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ORIGINAL RESEARCH

Mitochondrial DNA Content Is Linked to Cardiovascular Disease Patient Phenotypes

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BACKGROUND: We sought to determine whether mitochondrial DNA (mtDNA) content can be used as markers for 12 key phenotypes among cardiovascular disease patients, and whether these markers are valid across patients with diverse ancestries.

METHODS AND RESULTS: DNA was collected from the peripheral blood of 996 cardiovascular disease patients at the Cleveland Clinic. The mtDNA copy number and DNA-level variation were assessed from whole-genome sequence. Patients were also ascertained retrospectively for histories of 10 clinical events, as well as for maximum stenosis and extent of disease at baseline. Self-reported race and maternal ancestry inferred from mtDNA sequence were recorded. MtDNA copy number and overall mtDNA rare variant load were significantly lower in patients with histories of various adverse clinical events, and mtDNA copy number was inversely correlated with extent of disease. Strong associations were also found between absence of rare variants in the genes *MT-ATP6* and *MT-COII* and patient histories of hyperlipidemia and myocardial infarction, respectively. Importantly, associations were not ancestry dependent.

CONCLUSIONS: This study provides evidence that mtDNA copy number in circulation is associated with a variety of cardiovascular disease patient phenotypes. Results also suggest a protective role for some rare inherited mtDNA variants. Overall, the study supports the potential of mtDNA content and abundance as biomarkers in heart disease, in a manner that is valid across diverse ancestries.

Key Words: cardiovascular disease ■ mitochondrial DNA ■ blood-based biomarkers

It is well established that properly functioning mitochondria are crucial to energy requirements in the vascular epithelium[1] and the heart itself.[2] The 13 proteins encoded by mitochondrial DNA (mtDNA) genes are all part of complexes in the electron transport chain. These genes are tightly packed in each ≈16.5-kb copy of mtDNA, along with 2 rRNA genes, 22 tRNA genes, and noncoding regions that have roles in replication and transcription. Unlike nuclear chromosomes, the number of copies of the mitochondrial chromosome per human cell is quite fluid and differs from tissue to tissue and across developmental time.

Although many studies have queried the nuclear genome for variants that are associated with heart disease,[3,4] we hypothesized that mitochondrial DNA may also harbor variants that affect risk for cardiovascular disease (CVD)-related traits. In addition, recent work from Ashar et al.[5] has indicated that individuals with a lower mtDNA copy number (CN) in circulation have higher incident CVD. The same group also implicated lower mtDNA CN as an indicator of risk for sudden cardiac arrest.[6] We therefore sought to examine CN in circulation, using whole-genome sequence data, to query for associations with multiple CVD-related events. To this end, we collected deep sequencing mitochondrial genome data from cases at the Cleveland Clinic. Whole-genome sequencing has the advantage of allowing comprehensive examination of mtDNA variants, as well as mtDNA CN.

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CLINICAL PERSPECTIVE

What Is New?

- This large retrospective study examines relationships between clinical characteristics of patients with cardiovascular disease and mitochondrial DNA (mtDNA) content in circulation.
- Abundance of mtDNA in circulation was strongly inversely associated with histories of many types of adverse events and phenotypes.
- Analysis of inherited mtDNA variants uncovered evidence that links rare gene variants to an absence of past myocardial infarction events and hyperlipidemia.

What Are the Clinical Implications?

- The mtDNA content in blood may potentially serve as a biomarker for cardiovascular disease-related phenotypes.
- Further study is required to determine whether mtDNA content in circulation reflects its characteristics in cardiomyocytes; if so, there are implications for the pathogenesis of cardiovascular disease.

Nonstandard Abbreviations and Acronyms

CN	copy number
EOD	extent of disease
mtDNA	mitochondrial DNA

METHODS

The authors declare that all supporting data are available within the article and its online supplementary files.

Study Population, Sample Collection, Processing, and Sequencing

We collected high-coverage whole-genome sequencing data from the blood samples of 996 patients with CVD at the Cleveland Clinic. These patients were enrolled in the Cleveland Clinic GeneBank, a prospective study from 2001 to 2006. Each patient underwent an elective diagnostic cardiac catheterization procedure without acute coronary syndrome. All participants gave written informed consent approved by the Cleveland Clinic Institutional Review Board, and had well-documented clinical features at enrollment. Longitudinal outcomes were ascertained over 3 years. As a straightforward measure of the extent of disease, we adopted the coronary artery surgery study-50 (CASS-50) system, which is essentially a count of the number of coronary vessels affected (at stenosis >50%). Although simple, the CASS-50 scoring system has strong agreement with other scoring systems.[7] Details of the system can be found in Table S1. Peripheral blood samples were processed for DNA sequencing as previously described.[8] Patient characteristics are summarized in Table 1, and details for each patient are provided in Table S2. The definitions for clinical features are shown in Table S1.

Alignment and Extraction of chrM and chr22 Reads

Whole-genome sequencing was performed with Illumina HiSeq X10TM platform with 30× mean coverage in 150-bp pair-end form, and reads alignment was conducted using the ISAAC pipeline[9] to reference build hg38. Reads mapping to chromosome 22, positions 46 000 000 to 46 100 000, and to the mitochondrial chromosome were extracted from the BAM whole-genome sequencing files using SAMtools.[10] The mitochondrial reads were realigned to the revised Cambridge Reference Sequence using the Burrows-Wheeler Alignment tool.[11]

Copy Number Estimation

To estimate the mtDNA CN of each sample, chromosome 22 positions 46 000 000 to 46 100 000 (build hg38) was chosen as a region being representative of 2 copies per cell because it contains only very rare population CN variants.[12] Using read depth as a proxy for DNA CN, the mtDNA CN was estimated as $\frac{D_m}{D_n} \times 2$, where D_m denotes the average read depth across the mitochondrial chromosome, and D_n denotes the average read depth of the chromosome 22 two-copy region.

Variant Calling and Downstream Quality Control

We used the Genome Analysis Toolkit[13] to call single nucleotide variants. To minimize false positives, we omitted all variants in the regions from base positions 302 to 316, 513 to 526, 566 to 573, 8860, and 16181 to 16194, which are known to yield false variant calls.[14] Because heteroplasmic variants generally impact disease phenotypes only at levels around 80%,[15] all variants with heteroplasmy levels less than this were omitted from further consideration. We used SnpEff[16] to categorize the effects of each mtDNA variant. Population frequency for each variant was determined from GenBank.[17] Variants that appeared in fewer than 1% of GenBank sequences covering the variant's position were deemed rare for the purposes of this study. We used HaploGrep2.1.13[18] to obtain the haplogroup of each sample.

Table 1. Patient Characteristics

			Self-Reported Maternal Ancestry			
	Age, y, Median	Sex, % Women	White	Black	Asian	Other
Overall	56	30.4%	82.1%	14.5%	1.2%	2.2%
History of						
Coronary artery bypass graft (13.2%)	60	18.9%	82.6%	14.4%	0.8%	2.3%
Coronary artery disease (47.1%)	58	19.6%	80.4%	15.6%	1.3%	2.8%
Congestive heart failure (14.2%)	57	30.0%	76.6%	21.3%	0.0%	2.1%
Diabetes mellitus (31.9%)	57	29.2%	81.8%	15.1%	1.9%	1.3%
Hypertension (64.4%)	57	30.9%	78.8%	18.4%	1.1%	1.7%
Hyperlipidemia (74.1%)	57	27.0%	85.1%	12.1%	1.1%	1.8%
Myocardial infarction (18.3%)	59	19.8%	77.5%	19.8%	1.1%	1.6%
Percutaneous coronary intervention (16.8%)	59	22.2%	76.6%	18.6%	1.2%	3.6%
Stroke (5.0%)	57	42.0%	76.0%	20.0%	2.0%	2.0%
Ventricular arrhythmias (8.5%)	57	29.4%	87.1%	11.8%	0.0%	1.2%
Maximum stenosis >50% (48.3%)	59	18.7%	80.5%	15.8%	1.2%	2.5%
Extent of disease 0 (51.8%)	54	41.3%	83.7%	13.2%	1.2%	1.9%
Extent of disease 1 (13.7%)	58	20.6%	81.6%	13.2%	1.5%	3.7%
Extent of disease 2 (12.4%)	59	22.6%	73.4%	21.8%	2.4%	2.4%
Extent of disease 3 (22.1%)	59	15.5%	83.6%	14.1%	0.5%	1.8%

Age, sex, and ancestry characteristics are given for the entire cohort (Overall row) and within groups of patients with specific clinical characteristics (other rows). Percentage of patients with each clinical characteristic is provided after row name.

Statistical Procedures

All statistical computations were performed using R version 3.6.1. Associations among the 11 binary clinical features (history of clinical events and maximum stenosis at least 50%) were computed as odds ratios, with corresponding *P* values computed using the Fisher exact test. Associations between mtDNA CN and binary clinical features were tested using the following logistic regression model:

$$\mathrm{logit}\,(p) = \alpha + \beta_0 \times \log(\mathrm{CN}) + \beta_1 \times \mathrm{age} + \beta_2 \times \mathrm{sex} \tag{1}$$

where $p = $ probability binary clinical feature. *P* values were extracted from the model fit with the ANOVA (analysis of variance) function, using the χ^2 test argument. To compute the age- and sex-adjusted odds ratio for a binary clinical outcome associated with 1 standard deviation decrease in CN, CN was first converted to a *Z* score, which was used in place of the log(CN) term in Equation 1 above. The odds ratio was computed as $\exp(-\widehat{\beta}_0)$, where $\widehat{\beta}_0$ is the CN coefficient estimate in the model, and the 95% CI computed as exp(-β ± 1.96 × standard error). Odds ratio for first versus fourth quartiles was computed using only patients with CN in these quartiles, and the log(CN) term in Equation 1 above was instead coded as an indicator variable for the quartile 1 CN. Odds ratio and 95% CIs were computed as above. To test for association with the ordinal variable extent of disease (EOD), P_{trend} was computed with proportional odds logistic regression, using the polr() function in the MASS package. The 2-sided *P* value was computed using the normal-distribution quantile of the *t* value corresponding to the CN's coefficient. We also performed these regression analyses while adjusting for maternal race/ancestry, self-reported and inferred from mitochondrial haplogroup. Specifically, we added terms

$$I\ \mathrm{Whitemother} + I(\mathrm{Blackmother})$$

and

$$I\ \mathrm{haplogroup\ H} + I\ \mathrm{haplogroup\ L} + I\ \mathrm{haplogroup\ U}$$

to the models, where here $I(\cdot)$ denotes the indicator function:

$$I \bullet = \begin{cases} 1\text{if } \bullet \text{is true} \\ 0\text{if } \bullet \text{is false} \end{cases}$$

Rare variant association analyses were performed using a similar model,

$$\mathrm{logit}\ p = \alpha + \beta_0 \times \mathrm{rare\ variant} \tag{2}$$

Here, rare variant is either the numerical variable log (total number of rare mtDNA variants), or a binary variable indicating presence or absence of a rare variant in the mtDNA feature of interest (e.g., specific mRNA genes, any tRNA). *P* values were computed as above. To correct for multiple tests, we converted *P* values to *q* values[19] using the R package `qvalue`.

RESULTS

Patient Cohort

Cleveland Clinic patients were ascertained for history of prior events/disease (Table 1). Maximum stenosis was also assessed. Table S1 provides the working definitions for each of these events/histories. Unsurprisingly, there was substantial correlation among many of these clinical features (Figure 1). Patients also reported ancestries of both parents in broad terms (Asian, Black, White). Because mtDNA is the subject of our study, we focused solely on maternal ancestry. As a complementary, objective assessment of maternal ancestry, we determined haplogroups using each patient's mtDNA sequence. As expected, the reported maternal ancestry tracked closely with mtDNA continental haplogroups (Figure S1).

mtDNA CN Is Lower in Patients With Specific Clinical Histories

Prior studies have found that low mtDNA CN in blood is associated with risk of CVD and sudden cardiac death,[5,6] demonstrating the utility of mtDNA CN as a predictor of risk. We reasoned that mtDNA CN may also be associated with other specific patient histories. To this end, we tested the 10 clinical histories and maximum stenosis for association with mtDNA CN.

For all of these 11 clinical variables, those with the corresponding history/feature had lower median mtDNA CN than those without. Seven of the 11 attained nominal statistical significance (Figure 2). The relationships between mtDNA CN and history of coronary artery disease ($P=3.7\times10^{-4}$, after adjusting for age and sex), history of myocardial infarction ($P=9.7\times10^{-5}$), history of coronary artery bypass graft ($P=1.2\times10^{-5}$), and maximum stenosis >50% ($P=3.5\times10^{-5}$) were all significant after correction for multiple testing. One standard deviation decrease in CN was associated with odds ratios of 1.29 (95% CI, 1.21–1.39), 1.43 (95% CI, 1.13–1.57), 1.58 (95% CI, 1.42–1.76), and 1.35 (1.18–1.55), respectively, for these phenotypes after adjusting for

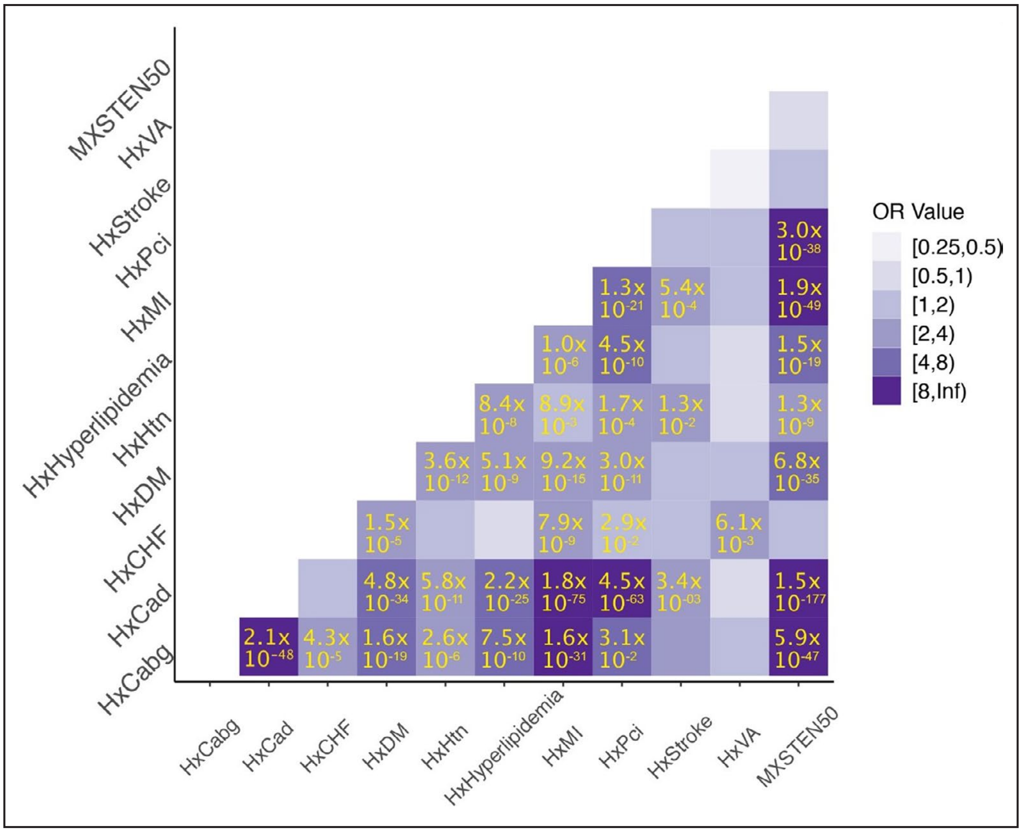

Figure 1. Correlations among clinical features of the cardiovascular disease cohort.
Each pixel is shaded according to the OR between the pairs of clinical features in the corresponding row and column, with darker shades indicating stronger correlation (see scale). Phenotype abbreviations are explained in Table S1. Fisher exact test *P* values are provided for each significant pair tested. OR indicates odds ratio.

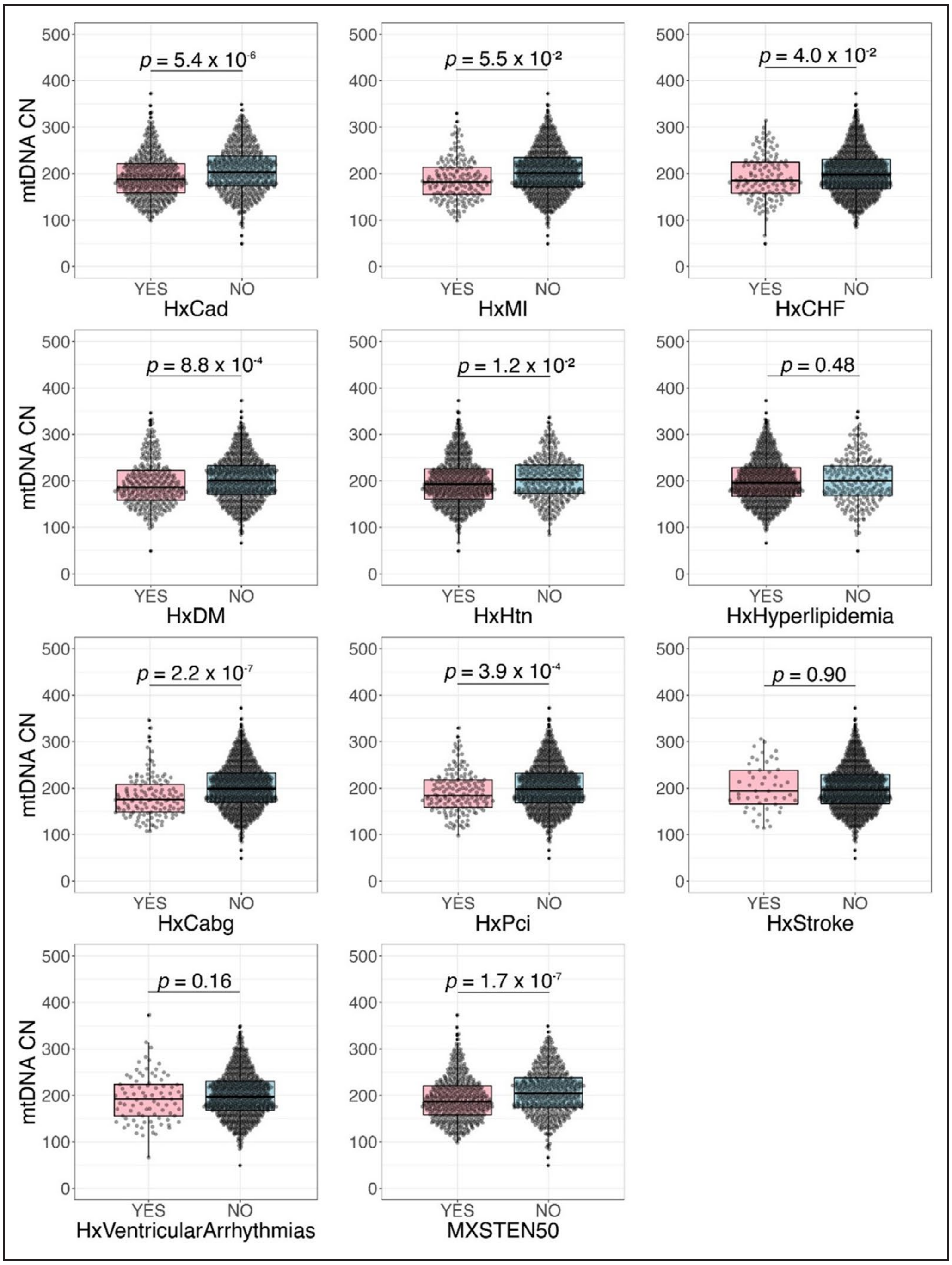

Figure 2. Clinical features associated with lower mitochondrial DNA (mtDNA) copy number (CN).
Each panel represents a different clinical feature, given at the bottom of the panel. The 2 groups in each panel represent individuals that do (YES) or do not (NO) have the clinical feature, with each point representing a patient and the vertical axis indicating that patient's mtDNA CN. The overlaid boxplots give the 25th, 50th, and 75th percentiles, and the whiskers extended either to the maximum/minimum values or 1.5×interquartile range (IQR) from the box (where IQR is the distance between the first and third quartiles), whichever is less extreme. *P* values were computed using a logistic regression model that adjusts for age and sex (see Methods section for details). Phenotype abbreviations are explained in Table S1.

age and sex (Table 2). Correspondingly, we observed significantly more prevalent history of these events among individuals with mtDNA CN in the first quartile (Table 2).

Race is a potential confounder in testing for association between event history and CN, as rates of specific clinical histories are not uniform across self-reported ancestries (Table S3). However, the association between event histories and mtDNA CN remain significant when we additionally control for maternal ancestry, both self-reported and inferred from mtDNA haplogroup (Table S4). The associations also remain largely significant when we restrict to subsets of patients within different maternal ancestral groups (self-reported, as well as the haplogroups [H, L, and U] that have at least 10% frequency in the cohort), and in all cases the associations are in the same direction (Table 2, Figures S2-S6). We conclude that the observed association between mtDNA CN and clinical features is independent of ancestry.

Extent of Disease Is Negatively Correlated With mtDNA CN

For each patient, severity of CVD (EOD) was scored as 0, 1, 2, or 3, on the basis of the number of diseased vessels (see Table S1 for details). There was a statistically significant trend toward lower mtDNA CN for more severe EOD ($P_{\text{trend}}=1.8\times10^{-8}$). Correspondingly, individuals in higher quartiles of the mtDNA CN were significantly more likely to have less severe EOD (Figure 3).

As with event histories, EOD's association with mtDNA CN was not confounded by ancestry, as the statistical relationship holds when we control for self-reported ancestry ($P_{\text{trend}}=8.2\times10^{-6}$) and mtDNA haplogroups ($P_{\text{trend}}=7.3\times10^{-6}$). The association also holds within the various self-reported ancestries and haplogroups (Figure S7).

Rare mtDNA Variant Burden Is Negatively Associated With Past Clinical Histories

Deep sequencing of 996 mitochondrial genomes allowed us to interrogate the impact of mtDNA variants on patient phenotypes. Overall, the cohort had 26 805 nonreference variants (2089 unique variants), among which 4959 (1746 unique) were deemed rare (population frequency <1%; Table S5). We chose to focus on rare variants for 2 reasons. First, they are more likely to exert a large effect than common variants. Second, common variants often track very closely with, or even define, ancestral mtDNA haplogroups, making it difficult to distinguish common variant associations with disease from associations with ancestry.

We tested for association of rare variants with each of the 11 aforementioned clinical features. By definition, each specific variant would be expected to appear in at most a handful of cases. As such, and because there are large numbers of rare variants, for any particular variant we are substantially underpowered to detect statistical enrichment that would withstand multiple-test correction. We therefore collapsed rare variants by mtDNA features (all tRNAs combined, all rRNAs combined, control region, and nonsynonymous variants in individual mRNA genes). We tested for association between presence/absence of rare variants in each of these 16 mitochondrial genome entities and each of the 11 clinical features. We also tested overall rare variant burden for association with each clinical feature. Overall, this resulted in 187 (11×17) statistical tests,

Table 2. Clinical Features' Associations With 1 Standard Deviation Decrease in Mitochondrial DNA Copy Number and for First Quartile Mitochondrial DNA Versus Fourth

		Overall, n=996	White Mother, n=818	Black Mother, n=144	Haplogroup H, n=365	Haplogroup L, n=137	Haplogroup U, n=112
HxCabg OR (95% CI)	1 SD CN decrease	1.58 (1.29–1.76)	1.53 (1.22–1.91)	1.73 (1.01–2.99)	1.81 (1.23–2.66)	2.04 (1.08–3.85)	2.13 (1.08–4.20)
	1st quartile vs. 4th	5.16 (2.66–10.01)	3.97 (2.01–7.85)	4.37 (0.80–23.90)	5.09 (1.62–15.97)	6.07 (0.64–57.61)	NA
HxCad OR (95% CI)	1 SD CN decrease	1.29 (1.13–1.48)	1.24 (1.07–1.45)	1.51 (1.06–2.15)	1.37 (1.08–1.74)	1.43 (1.00 – 2.04)	1.32 (0.87–2.00)
	1st quartile vs. 4th	1.97 (1.36–2.86)	1.74 (1.14–2.67)	2.77 (1.06–7.21)	2.56 (1.31–4.97)	2.14 (0.82–5.60)	2.34 (0.63–8.74)
HxMI OR (95% CI)	1 SD CN decrease	1.43 (1.20–1.71)	1.38 (1.14–1.69)	2.06 (1.30–3.25)	1.35 (1.00–1.83)	2.25 (1.38 – 3.68)	1.43 (0.78–2.63)
	1st quartile vs. 4th	2.51 (1.54–4.12)	2.14 (1.23–3.71)	6.31 (1.74–22.83)	2.01 (0.90–4.47)	6.40 (1.78–22.95)	2.22 (0.35–13.94)
MXSTEN50 OR (95% CI)	1 SD CN decrease	1.35 (1.18–1.55)	1.37 (1.17–1.60)	1.33 (1.08–1.62)	1.48 (1.16–1.88)	1.39 (0.97–1.98)	1.52 (0.98–2.34)
	1st quartile vs. 4th	2.25 (1.54–3.28)	2.28 (1.49–3.50)	2.83 (1.07–7.47)	3.14 (1.61–6.16)	2.43 (0.92–6.46)	3.51 (0.96–12.81)

ORs and CIs adjusted for age and sex are shown overall and stratified by patient ancestry (self-reported and assessed by haplogroup). CN indicates copy number; HxCabg, history of coronary artery bypass graft; HxCad, history of coronary artery disease; HxMI, history of myocardial infarction; MXSTEN50, maximum stenosis at least 50%; NA, insufficient numbers to calculate; and OR, odds ratio.

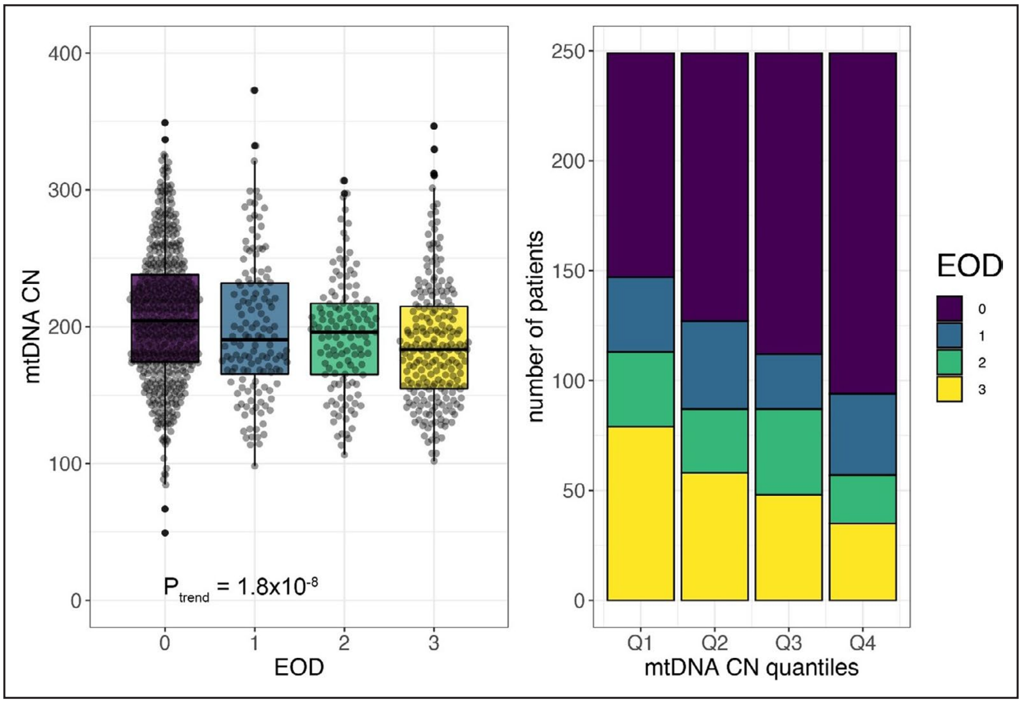

Figure 3. Extent of disease (EOD) is inversely associated with mitochondrial DNA (mtDNA) copy number (CN). The mtDNA CN for each patient is plotted, stratified by EOD (left panel).
Here, P_{trend} is computed using a proportional odds logistic regression model that adjusts for age and sex. In the right panel, the proportion of patients with each EOD score is shown for each mtDNA CN quartile. Higher mtDNA CN quartiles have fewer patients with more severe EOD.

necessitating adjustment for multiple testing. We corrected for multiple tests by computing *q* values for each *P* value to control for the false discovery rate.

As shown in Figure 4A, the *P* values largely follow the expected null distribution, with the 3 most significant (q<0.15) deviating from expectation. Intriguingly, all of these associations are consistent with rare mtDNA variants being protective against various clinical histories. Individuals with history of hyperlipidemia have a significantly higher overall rare variant burden than patients without the history (P=2.3×10^{-3}; q=0.14; Figure 4B). None of the 27 individuals with rare nonsynonymous variants in the *MT-COII* gene have history of myocardial infarction (P=7.6×10^{-4}; q=0.071; all variants shown in Figure 4C, colored by patient haplogroup). Presence of rare nonsynonymous variants in the *MT-ATP6* gene is significantly less common in individuals with history of hyperlipidemia (P=7.6×10^{-4}; q = 0.071). These analyses were not adjusted for age or sex because mtDNA variants are maternally inherited at conception and are therefore influenced by neither age nor sex. On the other hand, mtDNA variants are strongly associated with race/ancestry. However, as shown in Figure 4D, the associations are all in the same direction when stratified by maternal ancestry.

DISCUSSION

Here we have presented results from the first study, to our knowledge, to investigate the relationship between phenotypes of patients with CVD and mtDNA content. Although genome-wide association studies number in the thousands for the nuclear genome, there are few corresponding studies focusing on the mitochondrial genome.

We were able to expand upon the results of a prior study[5] that showed an inverse association between mtDNA CN and CVD. In our retrospective study, patients were ascertained for clinical histories/features at the time of the sample collection that was used for mtDNA analysis. Although the associations reported here are quite robust, it is impossible from our data to determine whether the lower mtDNA CN portends these events, or is instead the result of their occurrence. Making such a determination would require a prospective longitudinal study of patients with CVD. We also considered single nucleotide variants and their relationship with patient clinical characteristics. MtDNA variants are fairly stable over space and time, and as such, homoplasmic or near-homoplasmic variants detected in blood are likely to have been present in nearly all of the individual's tissue, including the heart, since birth. Our examination of the relationship

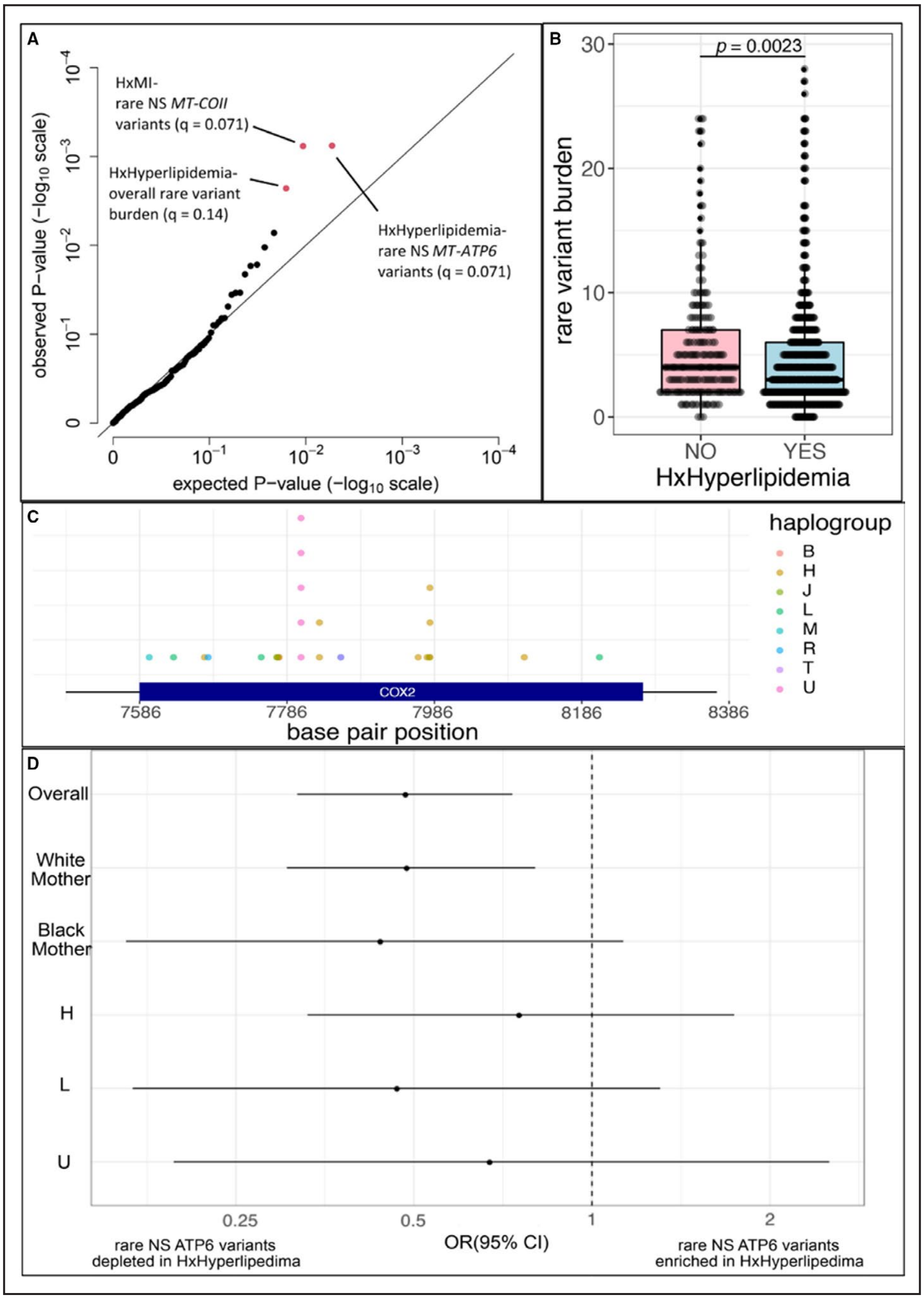

Figure 4. Significant associations between rare mitochondrial DNA (mtDNA) variants and clinical features.

A, A quantile-quantile (QQ) plot of 187 association tests shows 3 (in red) with *q* values below 0.15, including HxHyperlipidemia being associated with lower rare variant burden **(B**), HxMI associated with absence of rare NS *MT-COII* variants (all 27 rare *MT-COII* variants shown appear in individuals without HxMI) **(C)**, and HxHyperlipidemia being associated with absence of rare NS *MT-ATP6* variants **(D**). Here the *P* values are computed using a logistic regression model (see Methods section), and *q* values are computed using the qvalue package in R. Note that **(D)** shows that the association holds across maternal ancestries, with H, L, and U indicating haplogroup. Disease abbreviations are explained in Table S1. NS indicates nonsynonymous; and OR, odds ratio.

between mtDNA variants and patient characteristics implicated the mitochondria-encoded genes *MT-ATP6* and *MT-COII*. Rare variants in *MT-ATP6* were significantly less common in individuals with a history of hyperlipidemia, and none of the 182 individuals with a history of myocardial infarction harbor were among the 27 individuals with rare variants in *MT-COII*. We were initially surprised to find evidence that some rare germline variants may be protective against hyperlipidemia and myocardial infarction. However, from an evolutionary perspective, this is perhaps not so surprising. Because the examined traits generally have late age of onset, any selective advantage conferred by the variants needs not manifest in higher allele frequencies in the population. Furthermore, multiple studies have found protective associations between similar phenotypes and minor allele variants in both mtDNA[20,21] and nuclear DNA.[22] In the mitochondrial realm, a Japanese study found a specific mitochondrial haplotype to be protective against myocardial infarction.[23] Another study[24] reported 2 rare variants in *MT-ATP6* as being potentially protective against Leigh syndrome, a genetic disorder associated with hypertrophic cardiomyopathy. Interestingly, one of that study's reported variants, A8795G (H90R), affects the same amino acid as an *MT-ATP6* variant (C8794T [H90Y]) found in 2 patients in our study.

Here, we have focused on mtDNA CN and germline point substitutions, but a natural extension of our work would be to query whole-genome sequence for large deletions and low-heteroplasmy somatic mtDNA mutations. Studies have reported elevated levels of large mtDNA deletions in the heart tissue[25] and blood[26] of patients with coronary artery disease, and such deletions can be detected in whole-genome sequencing data.[27] Additionally, clonal hematopoiesis, the clonal expansion of hematopoietic stem cells harboring age-related somatic mutations, has been shown to be associated with CVD.[28] Whether somatic mtDNA mutations also play a role in CVD has not been investigated. Additional studies using deep sequencing of mtDNA in heart tissues and blood would yield further insight into the impact of germline and somatic mutations in mitochondrial function and its role in CVD.

Our study does have certain limitations. Interrogating mtDNA in peripheral blood is, at best, an indirect measure of the mtDNA content in cardiomyocytes, the primary tissue of interest. Although this may be an issue when analyzing CN, it should not be a problem when examining mtDNA sequence content, which should largely be the same in all tissues. Another limitation is a sample size (n=996), which left us underpowered to detect associations with individual rare variants. We also did not interrogate all classes of mtDNA variants.

Despite these limitations, our study design does have several strengths. Our patient cohort comprises a fairly large, well-annotated collection of disease cases. The use of whole-genome sequence yields extremely high depth coverage of the mitochondrial genome, which enables comprehensive and sensitive detection of all mtDNA substitutions. Imputation, which is known to be error prone, is unnecessary here. Because all patients were ascertained at the same center, and sequencing protocols were performed in a uniform manner, batch effects are not likely to be an issue, and meta-analysis is not needed. This overall uniformity is probably one of the reasons that we were able to uncover significant associations in a sample size below 1000.

In summary, we have presented an analysis of mtDNA content in the peripheral blood of patients with CVD. We detected robust associations between the patients' clinical characteristics and both mtDNA CN and rare mtDNA variants. All significant associations held true across different patient ancestries. Future studies are needed to validate these findings in other cohorts. Incorporating mtDNA analysis of cardiomyocytes would shed light on the implication of lower mtDNA content in the blood of more severely affected individuals.

ARTICLE INFORMATION

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Disclosures

Dr Tang has served as consultant to Sequana Medical AG, and has received honoraria from Springer Nature and American Board of Internal Medicine for authorship/editorship. Dr Hazen is named as co-inventor on pending and issued patents held by the Cleveland Clinic relating to cardiovascular diagnostics and therapeutics, is a paid consultant for Proctor & Gamble, has received research funds from Proctor & Gamble and Roche Diagnostics, and is eligible to receive royalty payments for inventions or discoveries related to cardiovascular diagnostics or therapeutics from Quest Diagnostics/Cleveland HeartLab or Proctor & Gamble. The remaining authors have no disclosures to report.

Supplementary Material

Tables S1–S5
Figures S1–S7

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SUPPLEMENTAL MATERIAL

Table S1. Patient clinical data used in the study.

Abbreviation	Label	Definition
Age	Age at time of procedure	Age at time of procedure
Sex	Sex	Male of Female
Asian mother	Mother Asian?	Subject reports mother is at least part or all Asian
Black.AA mother	Mother Black or African American?	Subject reports mother is at least part or all Black or African American
White mother	Mother White?	Subject reports mother is at least part or all white
EOD	Extent of disease. Number of diseased (>50% stenosis) vessels; coded 0, 1, 2, 3 (a value of 3 also includes LMT and RCA) (calculated)	0 = if RCA, LAD, LMT, LCX are all <50% 1 = if RCA, LAD or LCX are >= 50% 2 = If LMT >=50% or two out of three RCA, LAD and LCX are >= 50% 3 = If LMT and RCA are >= 50% OR RCA, LAD and LCX are all >= 50% Else NULL
HxCabg	History of Cabg?	Previous coronary artery bypass graft (CABG) surgery as documented in the medical record.
HxCad	History of CAD?	At least 1 vessel w/ >50% stenosis established by previous catheterization, history of myocardial infarction, PCI, or CABG.
HxCHF	History of CHF?	Documented history of Congestive Heart Failure.
HxDM	History of DM?	Hx of Type I Diabetes Mellitus or Type II DM (diet controlled DM), or taking oral hypoglycemic agent or insulin (not to include diagnosis or notation of borderline DM)
HxHtn	History of Htn?	Documented hx of HTN (hypertension) in chart or measurement of blood pressure: SBP>160 or DBP>90. Do not answer “yes” based on hypertension medications.
HxHyperlipidemia	History of Hyperlipidemia?	Chart documentation of any type of dyslipidemia; total cholesterol >ULN, LDL>ULN, HDL<LLN Triglycerides > ULN, as reported by laboratory; hx or current use of prescribed meds (statins, fibrates). (UNL= upper limit of lab normals range / LLN = lower limit of lab normals range)
HxMI	History of MI?	Documented history of an MI (myocardial infarction) per physician note, ie. Note in the H & P, Clinical Notes, Patient Letter, Physician correspondence or Discharge Summary in addition to one of the following criteria being met*: 1. As documented by cardiac enzymes (CK/MB $\underline{>}$ 2 X upper limit of normal.); 2. positive troponin**; 3.significant Q wave or 4.definite MI in CCF ECG text interpretation; 5. akinesis by echo or nuclear ventriculography or CT Scan***, or treated with thrombolytics (Streptokinase, Tissue Plasminogen Activator or t-PA, Alteplase, Retaplase, Urokinase or UK), Direct Intervention. ***Note: Thallium scars are not accurate, but PET, MRI scars are OK for diagnosis. *Note: In the absence of a physician note supporting h/o MI but with evidence of one of the above criteria being met, adjudicate MI with Dr. Ellis or Dr. Francis. ***Re: Elevated Troponins: If ↑ troponin with renal history but no MI history – not an MI patient. If CPKs are normal and troponin ↑ after CPR or multiple AICD firings, this may be troponin leak not an MI. If ↑ troponin, with renal history AND MI history with no other MI source documentation – adjudicate.*
HxPci	History of Pci?	Previous PTCA(Percutaneous Transluminal Coronary Angioplasty), PCI(Percutaneous Coronary Intervention), or Coronary Stenting as documented in the medical record. Unsuccessful or Failed PCI should be marked “Yes” to H/o Previous PCI.
HxStroke	History of Stroke?	Stroke- (*ACC-NCDR CE 34-1)* Patient has a history of stroke, i.e., loss of neurological function caused by an ischemic event with residual symptoms continuing at least 24 hours after onset. (Not to include TIA’s, or microvascular infarcts, or amarosis fugax)
HxVA	History of Ventricular Arrhythmias?	Documented history of Ventricular tachycardia (sustained VT / non sustained VT / runs of at least 3 beats), Ventricular fibrillation, not to include complete heart block (CHB) or bundle branch block (BBB)
MXSTEN50	At least one of the following must be true to be YES. If MaxStenosis <50% then NO, otherwise NULL: 1. MAXLAD ≥ 50% 2. MAXRCA ≥ 50% 3. MAXLCX ≥ 50% 4. MAXLMT ≥ 50% 5. MaxStenosis ≥ 50%	If MAXLAD, MAXRCA, MAXLCX, MAXLMT or MaxStenosis ≥ 50% then =1. If MaxStenosis <50%, then 0. Otherwise NULL.

Table S2. Characteristics of all patients in the cohort.

ID	Age	Sex	haplogroup	mtDNA CN	HxCad	MXSTEN50	HxMI	HxCHF	HxDM	HxHtn	HxHyperlipidemia	HxCabg	HxPci	HxStroke	HxVentricularArrhythmias	White mother	Black.AA mother	Asian mother	EOD
HLI-0001	59	M	N	159	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0002	56	M	H	155	1	1	0	0	0	1	1	0	0	0	NA	1	0	0	2
HLI-0003	52	F	V	207	1	1	1	0	1	1	1	1	1	0	1	1	0	0	3
HLI-0004	56	F	J	182	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0005	63	M	I	212	1	0	0	0	0	1	1	0	1	1	0	1	0	0	0
HLI-0006	64	F	H	176	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0008	59	M	H	239	1	1	1	0	0	1	1	0	1	1	NA	1	0	0	1
HLI-0009	54	M	H	191	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0010	64	M	W	143	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0011	49	M	X	141	1	1	1	0	0	1	1	1	1	0	0	1	0	0	3
HLI-0012	60	M	N	156	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0013	54	M	U	161	1	1	0	1	1	1	0	0	0	0	1	1	0	0	1
HLI-0014	57	M	H	147	1	1	0	0	1	1	1	0	0	0	1	1	0	0	1
HLI-0015	41	M	L	168	1	1	1	0	0	0	0	0	0	0	NA	0	1	0	1
HLI-0016	61	M	M	205	1	1	0	0	1	1	1	0	0	1	0	1	0	0	2
HLI-0017	37	M	H	203	1	1	0	0	1	0	1	0	0	0	NA	1	0	0	2
HLI-0018	64	M	H	149	1	1	0	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0019	58	M	U	141	1	1	NA	0	1	1	1	0	0	0	NA	1	0	0	3
HLI-0020	46	M	H	199	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0021	53	M	L	174	1	1	1	0	0	1	0	0	0	0	0	0	1	0	3
HLI-0023	55	M	U	226	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0024	61	M	J	157	1	1	0	0	1	1	1	1	0	0	NA	1	0	0	3
HLI-0025	54	M	H	167	1	1	0	0	1	0	1	0	1	0	NA	1	0	0	1
HLI-0026	51	F	L	217	1	1	0	0	1	1	1	1	0	0	0	0	1	0	2
HLI-0027	58	M	H	184	1	1	0	1	1	1	1	1	1	0	NA	1	0	0	3
HLI-0028	48	F	H	211	0	0	0	0	0	1	0	0	0	0	NA	1	0	0	0
HLI-0029	59	F	L	316	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0030	53	M	T	121	1	1	0	0	1	1	1	1	1	0	0	1	0	0	2
HLI-0031	43	M	H	203	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0032	59	M	H	177	1	1	0	0	0	0	1	0	0	0	NA	1	0	0	1
HLI-0033	59	F	H	182	0	0	0	0	1	1	0	0	0	0	NA	1	0	0	0
HLI-0034	37	M	J	228	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0035	58	F	T	235	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0036	46	M	T	221	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0037	65	M	K	133	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0038	53	M	T	187	1	1	0	0	0	1	1	1	0	0	NA	1	0	0	3
HLI-0039	40	F	H	192	0	0	0	0	1	1	1	0	0	0	NA	1	0	0	0
HLI-0040	39	F	J	192	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0041	61	F	H	183	1	1	1	0	0	1	1	1	1	0	0	1	0	0	3
HLI-0042	52	F	C	165	NA	1	NA	1	1	1	1	0	0	0	0	1	0	0	2
HLI-0043	64	M	H	175	1	1	1	0	1	1	1	0	0	0	NA	1	0	0	1
HLI-0044	57	M	H	198	1	1	0	0	1	1	1	0	0	0	NA	1	0	0	2
HLI-0045	44	M	H	207	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0
HLI-0046	62	M	J	130	1	1	0	0	0	1	1	0	0	0	1	1	0	0	3
HLI-0047	56	F	H	181	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0

HLI-0048	61	F	H	208	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0049	54	F	A	227	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0050	48	F	H	243	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0051	58	F	H	257	1	0	1	0	0	1	1	0	1	1	0	1	0	0	0
HLI-0052	65	M	H	271	1	1	0	0	0	1	1	0	1	0	NA	1	0	0	3
HLI-0053	62	M	H	180	1	1	1	0	1	0	1	0	1	0	0	1	0	0	2
HLI-0054	64	M	I	221	1	1	0	0	0	1	1	0	0	0	NA	1	0	0	3
HLI-0055	55	M	J	173	1	1	1	0	1	0	1	0	0	0	NA	1	0	0	1
HLI-0056	52	M	U	180	0	0	0	0	1	1	1	0	0	0	NA	1	0	0	0
HLI-0057	44	F	L	266	1	1	1	0	0	1	1	0	0	1	0	0	0	0	1
HLI-0058	30	M	H	277	1	1	0	1	1	1	1	0	0	0	0	1	0	0	3
HLI-0059	63	M	K	206	1	1	1	1	0	1	1	0	1	0	0	1	0	0	3
HLI-0060	54	M	K	174	1	0	NA	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0061	55	M	T	248	1	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0062	65	F	L	216	1	1	0	0	1	1	1	1	1	0	0	0	1	0	2
HLI-0063	35	F	H	292	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0064	64	M	H	218	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0065	57	M	I	174	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0066	50	M	H	158	1	1	0	0	1	1	1	0	1	0	0	1	0	0	2
HLI-0067	45	M	N	49	0	0	0	1	1	1	0	0	0	0	0	0	1	0	0
HLI-0068	62	M	U	184	1	1	0	0	1	0	0	0	0	0	NA	1	0	0	3
HLI-0069	50	M	J	268	0	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0070	52	M	J	206	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0071	62	M	W	251	1	1	1	0	1	0	1	1	1	0	0	1	0	0	3
HLI-0072	46	M	U	218	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0073	55	M	H	239	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0074	51	M	L	276	0	0	0	1	1	1	0	0	0	0	1	0	1	0	0
HLI-0075	60	M	H	215	1	1	0	0	0	0	1	0	1	0	0	1	0	0	1
HLI-0076	43	F	H	274	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0077	58	M	U	170	0	1	0	0	1	1	1	0	0	0	1	1	0	0	0
HLI-0078	57	M	H	269	1	0	1	0	1	0	1	0	0	0	0	1	0	0	0
HLI-0079	52	M	U	218	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0080	59	F	H	228	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0081	62	F	L	260	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0
HLI-0082	49	M	K	224	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0
HLI-0083	62	F	K	230	1	1	0	0	1	1	0	1	1	0	0	1	0	0	3
HLI-0084	57	M	U	230	0	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0085	48	F	T	259	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0086	52	M	H	187	1	1	0	0	1	1	1	0	0	0	0	1	0	0	1
HLI-0087	62	M	U	129	1	1	1	1	0	0	0	1	1	1	0	1	0	0	3
HLI-0088	47	M	L	218	0	0	0	1	1	1	0	0	0	0	0	0	1	0	0
HLI-0089	60	M	H	198	1	1	1	0	0	0	1	0	1	0	0	1	0	0	1
HLI-0090	55	M	H	161	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0091	56	F	U	182	1	0	1	0	1	1	1	0	1	0	1	1	0	0	0
HLI-0092	53	F	H	224	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0093	52	M	V	188	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0094	60	M	L	179	1	1	0	0	1	1	1	0	1	0	NA	0	1	0	1
HLI-0095	55	M	H	225	1	1	1	0	0	1	0	0	0	0	NA	1	0	0	2

HLI-0096	50	F	X	175	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0097	60	M	U	272	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0098	60	M	U	255	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0099	57	M	J	225	1	1	0	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0100	46	M	L	236	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0
HLI-0101	51	M	U	180	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0102	39	M	L	261	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0103	57	M	L	184	1	1	1	1	0	1	0	0	1	0	0	0	1	0	3
HLI-0104	54	M	H	230	1	1	1	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0105	56	M	J	235	1	0	1	1	0	1	1	0	0	1	0	1	0	0	0
HLI-0106	50	F	V	209	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0107	62	M	T	222	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0108	37	M	T	272	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0109	51	M	H	211	1	1	1	0	1	0	1	1	0	0	0	1	0	0	3
HLI-0110	63	M	T	207	1	1	0	0	1	1	1	0	0	0	NA	1	0	0	2
HLI-0111	54	F	H	187	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0112	53	F	H	206	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0113	61	M	T	229	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0114	51	F	H	271	1	1	0	1	1	1	1	0	0	0	0	1	0	0	1
HLI-0115	63	M	J	203	1	0	0	0	0	0	1	0	1	0	1	1	0	0	0
HLI-0116	62	M	T	176	1	1	1	1	1	0	NA	1	1	0	0	1	0	0	3
HLI-0117	49	F	J	248	1	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0118	55	M	H	179	1	1	1	0	0	1	1	1	1	1	1	1	0	0	3
HLI-0119	62	F	U	250	1	1	1	0	1	1	1	0	1	0	0	1	0	0	2
HLI-0120	51	F	T	216	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0
HLI-0121	58	M	T	213	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0122	53	M	H	223	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0123	53	F	H	244	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0
HLI-0124	44	M	H	155	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0125	64	M	L	181	1	1	0	0	0	1	1	0	1	0	0	0	1	0	2
HLI-0126	60	M	J	205	1	1	0	0	1	1	1	0	0	0	NA	1	0	0	2
HLI-0127	52	M	H	301	1	1	1	0	0	1	1	1	1	0	0	0	1	0	3
HLI-0128	47	M	H	255	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0129	52	F	H	193	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0130	63	F	K	248	1	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0131	49	F	K	191	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
HLI-0132	33	F	H	177	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0133	60	F	L	291	1	1	0	0	0	0	1	0	1	0	NA	0	1	0	1
HLI-0134	52	M	H	192	0	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0135	32	M	I	172	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0136	62	M	T	209	1	1	1	0	0	1	1	0	1	0	0	1	0	0	2
HLI-0137	64	M	H	162	1	0	0	1	0	1	1	0	1	0	0	1	0	0	0
HLI-0138	49	M	L	290	0	1	0	0	0	1	1	0	0	0	0	0	1	0	3
HLI-0139	65	F	K	200	1	1	1	1	1	1	1	1	0	0	0	1	0	0	2
HLI-0140	59	M	H	226	1	1	1	1	1	1	0	0	0	0	0	1	0	0	3
HLI-0141	65	M	U	219	1	0	0	0	0	0	1	0	1	0	0	1	0	0	0
HLI-0142	61	M	T	205	0	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0143	47	M	H	246	1	1	0	0	0	1	0	0	0	0	0	1	0	0	2

HLI-0144	50	F	H	159	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0145	38	M	B	217	1	0	0	0	0	1	1	0	0	0	0	0	0	1	0
HLI-0146	52	M	T	168	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0147	59	M	H	155	1	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0148	61	M	K	185	1	0	0	0	0	1	1	0	1	0	0	1	0	0	0
HLI-0149	59	M	V	216	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0150	58	M	L	245	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HLI-0151	62	M	L	241	1	1	0	1	0	1	0	1	1	0	0	0	1	0	1
HLI-0152	57	F	J	226	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0153	55	F	H	188	1	1	1	1	1	1	1	0	0	0	0	1	0	0	3
HLI-0154	55	M	I	201	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0155	51	F	L	202	1	1	0	0	1	1	1	0	1	0	0	0	1	0	1
HLI-0156	62	F	H	166	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0157	64	M	H	235	0	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0158	64	F	H	198	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0
HLI-0159	61	F	K	270	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0160	64	M	V	322	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0161	38	F	U	123	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0
HLI-0162	56	F	H	195	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0163	58	M	H	214	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0164	34	F	J	225	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0165	51	F	D	286	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0166	51	M	H	198	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0167	58	M	W	196	1	1	0	0	0	1	0	0	0	0	0	1	0	0	3
HLI-0168	62	M	J	189	1	1	1	0	0	1	1	1	0	0	0	1	0	0	3
HLI-0169	60	M	J	205	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0170	63	M	K	224	1	1	1	0	1	0	1	1	1	1	0	1	0	0	3
HLI-0171	58	M	H	141	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0172	55	M	K	234	1	1	0	0	0	0	1	0	0	0	1	1	0	0	1
HLI-0173	48	F	L	218	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0174	55	M	H	199	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1
HLI-0175	60	F	K	240	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0176	51	F	X	88	NA	0	NA	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0177	63	M	H	128	1	1	0	0	1	1	1	0	1	0	0	1	0	0	3
HLI-0178	63	F	H	92	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0179	51	F	H	135	1	1	1	0	1	1	NA	0	0	0	0	1	0	0	1
HLI-0180	56	M	R	261	1	1	NA	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0181	51	M	H	175	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0182	52	M	H	130	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0183	48	F	H	137	0	1	0	0	0	0	1	0	0	0	NA	1	0	0	1
HLI-0184	63	F	L	168	0	1	0	0	1	1	0	0	0	0	1	0	1	0	2
HLI-0185	50	M	U	148	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0186	58	M	U	118	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0187	46	F	H	116	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0188	34	M	H	227	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0189	40	M	R	194	1	1	1	0	1	0	1	1	0	0	0	1	0	0	3
HLI-0190	62	M	H	253	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0191	63	F	H	146	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0

HLI-0192	54	F	H	186	1	1	NA	0	1	1	1	1	1	1	NA	1	0	0	3
HLI-0193	48	M	U	194	1	1	NA	0	0	1	1	1	1	1	0	1	0	0	3
HLI-0194	55	F	H	223	1	0	1	0	1	1	1	0	0	1	0	1	0	0	0
HLI-0195	48	M	T	172	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0196	62	M	H	281	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0197	63	M	T	160	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0198	60	M	U	119	1	1	1	1	NA	1	1	1	1	0	0	1	0	0	3
HLI-0199	62	M	U	183	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0200	59	M	L	192	1	1	1	1	0	1	1	1	1	0	1	0	1	0	2
HLI-0201	57	M	X	187	1	1	1	0	0	1	1	0	0	1	0	1	0	0	3
HLI-0202	61	M	H	130	1	1	1	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0203	42	F	H	214	0	NA	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0204	49	M	U	192	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0205	56	M	T	143	1	1	0	1	0	1	1	0	0	0	0	1	0	0	2
HLI-0206	60	M	K	176	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0207	57	F	L	130	1	1	0	0	0	1	1	0	0	1	0	0	1	0	3
HLI-0208	40	M	H	166	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0209	64	M	U	139	0	0	0	0	0	1	NA	0	0	0	0	1	0	0	0
HLI-0210	55	M	T	160	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0
HLI-0211	57	M	X	165	1	1	0	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0212	53	M	T	280	1	1	0	0	1	1	1	0	0	1	0	1	0	0	1
HLI-0213	60	F	H	96	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0214	43	M	H	147	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0216	46	M	U	148	1	1	0	0	1	1	1	1	1	0	NA	1	0	0	3
HLI-0217	52	F	H	173	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0218	43	F	J	117	1	1	0	0	1	1	1	0	0	0	NA	1	0	0	3
HLI-0219	51	M	U	161	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0220	63	M	J	197	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0221	51	M	U	168	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0222	59	F	V	178	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0223	59	M	V	169	1	1	0	0	1	0	1	0	0	0	0	1	0	0	1
HLI-0224	63	M	L	309	0	0	0	0	1	1	0	0	0	0	0	0	1	0	0
HLI-0225	64	M	H	171	1	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0226	64	F	U	155	0	0	NA	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0227	62	M	T	210	1	1	0	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0228	56	F	H	175	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0229	60	M	L	161	1	1	NA	0	1	1	1	0	0	0	0	0	1	0	2
HLI-0230	54	M	N	215	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0231	52	M	H	175	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0232	48	M	R	166	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0233	63	M	L	139	1	1	1	0	1	1	0	0	0	0	0	0	1	0	2
HLI-0234	62	M	X	246	1	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0235	46	M	U	228	0	0	0	1	0	0	1	0	0	0	NA	1	0	0	0
HLI-0236	61	M	R	175	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0237	63	M	H	159	1	1	1	1	0	1	1	0	0	0	0	1	0	0	3
HLI-0238	47	M	H	228	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0239	64	F	J	225	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0240	56	M	H	123	0	1	0	0	0	0	1	0	0	0	0	1	0	0	1

HLI-0241	64	M	L	222	1	1	1	0	1	1	1	0	0	0	0	0	1	0	3
HLI-0242	48	F	L	213	1	1	1	0	1	1	0	0	1	0	0	0	1	0	2
HLI-0243	65	M	L	218	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0244	59	M	H	228	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0245	56	F	L	196	0	0	0	0	0	0	0	0	0	0	NA	0	1	0	0
HLI-0246	57	F	H	166	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0247	43	M	H	193	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0248	50	F	L	303	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0249	60	F	L	191	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0250	52	F	K	177	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0251	53	M	H	113	1	1	NA	0	0	1	1	0	1	0	0	0	1	0	2
HLI-0252	59	M	J	198	1	1	0	0	1	0	1	1	1	0	0	1	0	0	3
HLI-0253	57	M	L	268	0	0	0	1	1	1	0	0	0	0	1	0	1	0	0
HLI-0254	61	F	U	143	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0255	47	M	L	156	1	1	0	0	0	1	1	0	0	1	0	0	1	0	3
HLI-0256	55	M	H	173	1	0	NA	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0257	49	M	H	150	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0258	50	F	J	169	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0259	60	M	H	142	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0260	63	M	U	130	1	1	0	0	0	1	1	1	0	0	1	1	0	0	3
HLI-0261	31	F	H	246	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0262	55	F	L	302	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0263	54	F	L	200	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0264	55	M	T	200	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0265	53	M	H	158	1	1	1	0	1	1	1	1	0	1	NA	1	0	0	2
HLI-0266	38	M	V	210	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0267	63	F	I	277	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0
HLI-0268	47	F	J	212	0	0	0	0	0	0	NA	0	0	0	0	0	0	0	0
HLI-0269	64	M	R	119	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0270	42	M	H	284	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0
HLI-0271	47	F	H	219	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0272	48	M	L	224	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0273	57	M	H	250	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0274	57	M	H	151	1	1	1	0	1	0	0	0	0	0	0	1	0	0	3
HLI-0275	44	M	L	168	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1
HLI-0276	36	F	L	233	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0277	62	M	H	200	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0278	49	M	H	233	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0279	54	M	L	314	0	0	0	1	0	1	0	0	0	0	1	0	1	0	0
HLI-0280	47	M	L	267	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0281	59	M	H	134	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0282	58	F	H	298	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0283	34	M	D	242	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HLI-0284	37	M	H	220	0	0	0	1	0	1	1	0	0	0	1	1	0	0	0
HLI-0285	58	M	K	171	1	1	0	0	0	1	NA	0	0	0	0	1	0	0	3
HLI-0286	60	M	J	159	1	1	0	0	1	0	1	1	1	0	0	1	0	0	3
HLI-0287	64	M	H	145	1	1	1	1	0	0	1	0	0	0	0	1	0	0	3
HLI-0288	48	M	H	131	1	1	0	0	1	1	1	0	1	0	0	1	0	0	2

HLI-0289	63	F	T	171	1	1	0	NA	0	1	1	0	0	0	0	0	1	0	3
HLI-0290	65	M	T	206	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0291	52	M	L	204	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0292	48	F	L	224	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0293	49	M	I	185	1	1	0	0	1	0	1	0	0	0	0	1	0	0	2
HLI-0294	64	M	T	168	1	1	1	0	1	1	1	1	0	1	0	1	0	0	3
HLI-0295	64	M	J	179	0	1	0	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0296	51	M	L	181	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0297	54	M	H	202	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0298	61	M	L	178	1	1	0	0	1	1	1	1	0	0	0	0	1	0	3
HLI-0299	54	F	J	282	1	1	1	1	1	0	1	0	0	0	0	1	0	0	3
HLI-0300	48	M	L	194	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0301	59	M	H	187	1	1	1	1	1	1	1	1	0	0	1	1	0	0	3
HLI-0302	61	M	NA	214	1	1	1	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0303	60	M	V	191	1	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0304	61	M	L	266	0	0	0	1	0	1	0	0	0	0	0	0	1	0	0
HLI-0305	55	F	H	151	0	0	0	0	1	1	0	0	0	0	NA	1	0	0	0
HLI-0306	61	M	T	283	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0307	57	F	H	259	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0308	52	F	L	232	0	0	0	1	1	1	NA	0	0	0	0	0	1	0	0
HLI-0309	46	M	H	194	1	1	0	0	0	1	0	0	0	1	0	1	0	0	1
HLI-0310	64	M	H	224	0	0	0	0	0	1	0	0	0	0	1	1	0	0	0
HLI-0311	65	M	U	145	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0312	54	M	H	214	1	0	0	0	1	1	1	0	1	0	0	1	0	0	0
HLI-0313	64	M	T	223	1	1	0	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0314	43	M	U	151	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0315	61	M	H	185	1	1	0	0	1	1	0	0	0	0	0	1	0	0	2
HLI-0316	61	M	I	119	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0317	55	F	L	148	0	0	0	0	1	1	1	0	0	0	NA	0	1	0	0
HLI-0318	57	M	U	195	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0319	54	M	U	194	1	1	0	0	1	1	1	0	1	0	1	0	1	0	3
HLI-0320	63	M	H	202	0	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0321	38	F	J	165	1	1	0	0	1	0	1	0	0	0	0	0	0	0	2
HLI-0322	53	M	L	196	1	1	0	0	0	1	1	1	1	0	NA	0	1	0	3
HLI-0323	54	F	H	184	0	0	0	1	1	1	1	0	0	0	0	1	0	0	0
HLI-0324	46	M	B	265	1	1	0	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0325	59	M	H	215	1	1	0	0	0	1	NA	0	0	0	0	1	0	0	1
HLI-0326	64	M	H	297	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0327	51	M	H	185	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0328	64	M	J	206	1	1	0	0	1	0	0	0	1	0	0	1	0	0	2
HLI-0329	63	F	T	131	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0330	53	F	L	275	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0331	55	M	H	134	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0332	60	F	J	223	1	1	NA	0	1	0	1	0	1	0	NA	1	0	0	2
HLI-0333	36	M	H	67	0	0	0	1	0	1	1	0	0	0	1	1	0	0	0
HLI-0334	64	M	H	169	1	1	0	0	0	1	1	1	0	0	0	1	0	0	3
HLI-0335	58	F	U	187	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0336	41	M	I	137	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0

HLI-0337	49	M	T	127	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0338	55	M	X	200	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0339	62	M	H	180	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0340	62	F	X	150	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0341	48	M	L	204	0	0	0	0	0	0	1	0	0	0	NA	0	1	0	0
HLI-0342	63	M	H	131	1	1	1	0	0	1	1	1	0	0	0	1	0	0	3
HLI-0343	61	M	U	119	1	1	0	0	0	0	0	0	0	0	1	1	0	0	1
HLI-0344	64	F	C	117	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0
HLI-0345	48	M	H	92	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0346	46	M	U	157	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0347	60	F	NA	102	1	1	0	1	1	1	1	0	0	0	0	1	0	0	3
HLI-0348	45	M	H	104	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0349	61	M	U	116	1	1	NA	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0350	57	M	L	150	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0
HLI-0351	64	F	H	243	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0
HLI-0352	52	M	H	143	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0353	51	M	J	120	1	1	1	0	0	0	1	1	1	0	1	1	0	0	2
HLI-0354	60	M	W	245	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0355	60	M	U	129	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
HLI-0356	60	F	X	170	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0
HLI-0357	63	F	H	144	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0358	49	F	L	243	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0359	60	M	N	174	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0
HLI-0361	60	M	T	197	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0362	49	F	H	205	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0363	58	M	U	156	0	0	0	1	0	1	1	0	0	0	1	1	0	0	0
HLI-0364	62	F	H	117	1	1	1	1	0	1	0	1	0	1	0	0	1	0	3
HLI-0365	47	M	U	217	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0366	57	F	L	142	1	1	1	1	1	1	1	1	1	0	1	0	1	0	3
HLI-0367	59	M	I	127	0	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0368	41	F	H	193	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0369	41	M	H	199	1	1	1	0	1	0	1	0	0	0	1	1	0	0	1
HLI-0370	46	M	T	186	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0371	50	M	T	201	1	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0372	53	F	U	234	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0373	63	M	L	107	1	1	1	NA	1	NA	1	1	0	0	0	0	1	0	3
HLI-0374	40	F	H	156	0	0	0	0	0	0	NA	0	0	0	0	1	0	0	0
HLI-0375	56	M	K	219	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0376	61	F	X	246	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0377	54	M	H	199	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0378	56	M	H	234	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0379	59	F	L	174	1	1	NA	0	0	1	1	0	1	1	0	1	0	0	3
HLI-0380	59	F	L	203	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0381	62	F	H	136	1	1	1	1	1	1	1	1	0	0	1	1	0	0	3
HLI-0382	59	M	H	132	1	1	1	1	0	1	1	0	0	0	1	1	0	0	3
HLI-0383	49	F	L	213	0	0	0	0	0	1	1	0	0	0	NA	0	1	0	0
HLI-0384	58	F	T	181	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HLI-0385	56	M	T	175	1	1	0	0	1	1	1	1	1	0	0	1	0	0	2

HLI-0386	56	M	U	211	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0387	65	F	K	231	1	0	1	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0388	55	M	H	171	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0389	58	M	H	183	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0390	51	M	L	286	1	1	0	0	0	1	1	0	0	0	0	0	1	0	2
HLI-0391	47	M	H	183	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0392	56	M	H	151	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0393	55	M	T	198	1	1	1	1	1	1	1	1	0	0	0	1	0	0	2
HLI-0394	45	M	J	203	1	1	1	0	0	0	1	0	1	0	0	1	0	0	3
HLI-0395	49	M	L	237	1	1	NA	0	0	1	1	0	0	0	NA	0	1	0	2
HLI-0396	38	M	L	171	0	0	0	0	0	0	NA	0	0	0	1	0	1	0	0
HLI-0397	65	M	H	219	1	0	0	0	0	1	1	0	1	0	0	1	0	0	0
HLI-0398	62	M	H	219	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0399	52	F	L	176	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0400	57	F	H	244	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0401	64	M	L	143	1	1	1	1	1	1	1	1	0	0	0	0	1	0	3
HLI-0402	56	M	K	172	1	1	0	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0403	47	M	H	213	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0404	45	M	C	213	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0405	56	M	T	247	1	1	0	0	1	1	1	0	1	0	0	1	0	0	2
HLI-0406	59	M	T	167	1	1	1	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0407	63	M	T	142	1	1	0	1	0	1	1	0	0	0	0	1	0	0	2
HLI-0408	46	M	L	187	1	0	1	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0409	46	M	J	137	0	0	0	0	0	0	NA	0	0	0	0	1	0	0	0
HLI-0410	61	F	V	156	1	1	0	0	0	1	1	0	1	0	1	1	0	0	1
HLI-0411	55	M	K	196	1	1	1	0	0	1	1	0	1	0	0	0	1	0	2
HLI-0412	63	M	H	139	1	1	1	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0413	37	M	H	207	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0414	52	F	U	238	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0415	55	F	U	153	0	0	0	0	0	NA	1	0	0	0	NA	1	0	0	0
HLI-0416	52	M	H	136	1	1	0	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0417	57	F	J	175	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0418	62	M	K	179	0	1	NA	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0419	62	M	V	176	0	0	0	0	0	NA	0	0	0	0	0	1	0	0	0
HLI-0420	63	M	H	136	NA	1	0	1	1	0	0	0	0	0	NA	1	0	0	3
HLI-0421	48	M	W	156	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0422	50	F	X	179	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0
HLI-0423	53	M	K	204	1	1	1	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0424	54	F	H	175	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0425	60	M	U	126	1	1	NA	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0426	62	M	H	176	0	1	0	0	0	0	1	0	0	NA	0	1	0	0	1
HLI-0427	63	M	W	185	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0428	60	M	J	171	1	1	1	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0429	58	M	H	151	1	1	0	0	1	0	1	0	1	0	0	0	0	0	1
HLI-0430	35	M	L	129	0	0	0	1	1	1	1	0	0	NA	0	0	1	0	0
HLI-0431	37	M	H	161	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0432	50	F	H	119	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0433	64	M	J	107	1	1	0	0	0	0	1	1	0	0	0	1	0	0	3

HLI-0434	63	F	H	217	0	0	0	1	0	0	0	0	0	0	1	1	0	0	0
HLI-0435	50	M	U	174	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0436	57	F	K	139	1	1	1	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0437	51	M	H	187	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0438	63	M	H	188	1	0	1	1	1	1	1	0	1	0	0	1	0	0	0
HLI-0439	50	M	H	155	1	1	0	0	0	1	1	1	0	0	0	0	1	0	3
HLI-0440	64	F	H	129	1	0	0	0	1	1	1	0	0	0	0	0	1	0	0
HLI-0441	53	F	U	194	1	NA	NA	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0442	54	M	K	207	0	1	NA	1	1	0	0	0	0	0	0	1	0	0	3
HLI-0444	43	M	T	172	1	1	1	1	0	0	1	1	1	0	0	1	0	0	2
HLI-0445	61	M	H	139	0	1	0	0	0	NA	1	0	0	0	NA	1	0	0	1
HLI-0446	54	F	L	145	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
HLI-0447	61	M	U	236	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0448	63	M	K	203	0	1	0	0	0	0	1	0	0	0	NA	1	0	0	1
HLI-0449	59	F	V	230	1	1	1	0	1	0	1	1	1	0	0	1	0	0	2
HLI-0450	56	M	H	136	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0451	65	M	H	143	1	1	1	0	1	1	1	1	0	1	0	1	0	0	3
HLI-0452	61	M	L	154	1	1	1	0	0	1	1	1	0	0	0	0	1	0	3
HLI-0453	61	F	I	226	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0454	34	M	T	205	1	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0455	50	F	U	84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HLI-0456	62	M	K	145	0	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0457	64	M	K	136	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0458	55	M	H	137	1	1	1	1	1	0	1	1	1	0	1	1	0	0	2
HLI-0459	45	M	H	230	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0460	56	M	K	180	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0461	49	M	H	120	1	1	1	1	1	1	NA	1	0	0	NA	1	0	0	3
HLI-0462	62	F	L	155	1	0	1	0	0	1	NA	0	0	0	0	0	1	0	0
HLI-0463	51	M	L	223	0	0	0	0	1	1	NA	0	0	1	0	0	1	0	0
HLI-0464	65	M	B	178	1	1	0	0	1	1	1	0	1	0	0	0	0	1	1
HLI-0465	56	M	U	185	0	0	0	1	0	1	1	0	0	0	NA	1	0	0	0
HLI-0466	60	M	H	125	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0467	62	M	H	161	1	1	1	0	NA	1	1	1	1	0	0	1	0	0	3
HLI-0468	62	M	J	274	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0469	55	M	H	132	1	1	1	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0470	46	F	U	156	1	1	0	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0471	62	M	W	200	1	1	0	0	0	1	1	0	1	0	0	1	0	0	2
HLI-0472	37	F	H	151	0	0	0	0	0	0	1	0	0	NA	1	1	0	0	0
HLI-0473	43	M	L	230	1	1	1	0	0	1	1	0	1	0	0	0	1	0	1
HLI-0474	60	M	H	199	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0475	52	M	H	265	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0476	59	M	K	196	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0
HLI-0477	58	M	U	195	0	0	0	0	0	0	NA	0	0	0	NA	1	0	0	0
HLI-0478	44	M	J	221	0	0	0	0	0	1	NA	0	0	0	0	1	0	0	0
HLI-0479	60	F	H	147	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0480	59	M	J	214	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0481	62	F	H	143	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0482	50	M	U	144	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0

HLI-0483	60	M	T	116	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0484	39	F	H	232	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0485	50	M	H	182	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0486	55	F	H	136	1	1	NA	0	0	1	1	0	0	0	0	0	0	0	2
HLI-0488	62	M	J	157	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0
HLI-0489	56	F	T	223	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0490	49	M	H	250	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0491	65	F	T	257	0	0	0	1	0	NA	NA	0	0	0	NA	1	0	0	0
HLI-0492	63	F	H	136	1	1	1	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0493	41	M	H	192	1	1	0	0	1	1	1	0	0	0	0	1	0	0	1
HLI-0494	40	F	W	238	0	0	0	0	0	1	NA	0	0	0	0	1	0	0	0
HLI-0495	55	F	H	156	1	1	1	0	1	1	1	0	0	0	1	1	0	0	3
HLI-0496	61	M	H	146	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0497	64	F	L	135	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0498	38	M	M	152	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0499	49	M	K	219	0	0	0	1	1	1	1	0	0	0	0	1	0	0	0
HLI-0500	64	F	L	246	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0501	52	M	U	114	1	1	1	0	NA	1	1	0	0	0	1	1	0	0	1
HLI-0502	59	M	H	152	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0503	55	M	H	182	1	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0504	59	M	H	186	1	1	1	1	1	1	1	1	0	0	0	1	0	0	3
HLI-0505	61	M	J	279	1	1	1	0	0	1	1	1	0	0	0	1	0	0	2
HLI-0506	57	F	W	299	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0507	58	M	Y	167	1	0	1	0	0	0	1	0	1	0	0	0	0	1	0
HLI-0508	47	F	H	209	1	1	0	0	1	1	1	0	0	1	0	1	0	0	2
HLI-0509	50	F	H	247	0	0	0	0	0	1	0	0	0	0	NA	1	0	0	0
HLI-0510	59	F	K	213	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0511	63	M	T	325	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0
HLI-0512	64	M	L	303	0	0	0	0	1	1	1	0	0	0	0	0	1	0	0
HLI-0513	61	M	H	299	0	0	0	0	0	1	0	0	0	1	0	1	0	0	0
HLI-0514	47	M	U	285	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0515	56	M	L	188	1	1	0	0	0	1	1	0	0	0	0	0	1	0	2
HLI-0516	49	F	H	182	NA	0	NA	0	1	1	0	0	0	0	0	1	0	0	0
HLI-0517	57	M	H	186	1	1	0	0	0	0	0	0	0	0	0	1	0	0	1
HLI-0518	42	M	H	200	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0519	55	F	U	179	0	0	0	0	0	1	0	0	0	1	NA	1	0	0	0
HLI-0520	50	F	V	208	0	0	0	NA	0	0	1	0	0	0	0	1	0	0	0
HLI-0521	64	M	H	181	1	1	1	1	1	NA	1	1	0	0	0	1	0	0	3
HLI-0522	40	F	H	159	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0523	56	F	H	228	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0524	61	F	U	154	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0525	41	M	X	135	0	0	0	1	0	NA	0	0	0	0	0	1	0	0	0
HLI-0526	62	M	L	182	1	1	1	1	1	1	1	1	1	0	0	0	1	0	3
HLI-0527	56	F	K	179	0	0	0	1	0	0	0	0	0	1	0	1	0	0	0
HLI-0528	44	M	T	168	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0529	54	M	T	155	1	0	1	1	1	0	1	0	0	1	0	1	0	0	0
HLI-0530	64	M	U	143	0	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0531	35	F	H	158	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0

HLI-0532	61	F	H	159	1	1	NA	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0533	60	M	K	220	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0534	58	M	L	221	1	1	1	0	0	1	1	0	1	0	0	0	1	0	2
HLI-0535	19	M	H	171	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0536	37	M	J	179	1	1	1	0	1	1	1	0	0	0	0	1	0	0	1
HLI-0537	49	F	H	168	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0538	51	M	H	193	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0539	45	M	T	137	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0
HLI-0540	50	M	H	158	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0541	64	F	H	199	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0542	54	M	H	150	1	1	0	1	1	1	1	0	1	0	0	1	0	0	2
HLI-0543	57	F	J	199	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0544	50	M	H	185	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0545	61	M	H	141	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0546	58	M	H	194	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0547	64	F	H	159	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0548	61	M	L	199	1	1	1	1	1	1	1	0	1	0	0	0	1	0	2
HLI-0549	62	M	T	137	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0550	61	M	H	143	0	0	0	0	0	0	1	0	0	0	1	1	0	0	0
HLI-0551	64	F	K	167	1	1	1	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0552	53	M	H	181	1	1	0	0	1	1	1	1	0	1	NA	1	0	0	3
HLI-0553	58	M	L	173	1	1	1	0	0	1	0	0	0	0	0	0	1	0	2
HLI-0554	55	F	M	148	1	1	NA	0	0	1	NA	1	1	0	NA	0	0	0	3
HLI-0555	61	M	I	160	0	1	0	0	0	1	0	0	0	0	NA	1	0	0	1
HLI-0556	63	M	T	176	1	1	1	1	1	1	1	1	1	0	0	1	0	0	3
HLI-0557	54	M	K	195	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0558	65	F	J	155	0	0	0	0	1	1	1	0	0	0	NA	1	0	0	0
HLI-0559	64	F	J	213	0	0	0	1	1	0	1	0	0	0	0	1	0	0	0
HLI-0560	46	F	U	173	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0
HLI-0561	62	F	L	208	1	1	NA	0	0	1	1	0	0	0	NA	0	1	0	2
HLI-0562	48	M	H	138	0	1	0	0	0	1	0	0	0	0	NA	1	0	0	1
HLI-0563	42	F	H	232	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0564	51	M	K	249	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0565	52	F	J	106	1	1	1	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0566	42	M	H	201	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0567	52	F	U	142	0	1	0	1	1	1	0	0	0	0	0	1	0	0	1
HLI-0568	58	F	U	163	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0569	52	M	H	257	0	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0570	55	F	H	173	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0571	42	M	H	155	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0572	52	M	K	159	1	1	0	0	0	1	NA	0	0	0	0	1	0	0	2
HLI-0573	47	F	X	299	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0574	60	F	U	214	1	1	0	0	0	0	1	0	1	0	0	NA	NA	NA	2
HLI-0575	48	M	T	172	1	1	1	0	NA	0	1	0	1	0	0	1	0	0	2
HLI-0576	55	M	K	260	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0577	63	M	L	230	0	0	0	1	1	1	1	0	0	0	NA	0	1	0	0
HLI-0578	46	M	H	215	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0579	57	F	H	254	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0

HLI-0580	59	M	U	162	1	1	0	0	1	0	1	1	0	0	0	1	0	0	3
HLI-0581	50	M	L	128	1	1	1	1	1	1	1	1	0	0	0	1	0	0	3
HLI-0582	56	M	H	179	0	0	0	1	1	1	1	0	0	0	0	1	0	0	0
HLI-0583	58	F	L	228	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0584	58	M	L	284	1	1	1	0	1	1	1	0	1	0	0	0	1	0	3
HLI-0585	48	M	L	135	1	1	1	0	1	1	1	0	0	0	0	0	1	0	2
HLI-0586	64	M	W	187	0	1	0	0	0	1	1	0	0	0	NA	1	0	0	2
HLI-0587	53	M	L	165	1	1	0	1	1	1	0	0	1	0	0	0	1	0	3
HLI-0588	52	M	H	188	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0589	60	M	K	186	1	1	0	1	0	1	1	0	0	0	0	1	0	0	1
HLI-0590	43	M	T	145	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0
HLI-0591	64	M	W	174	0	0	0	1	0	1	0	0	0	0	0	1	0	0	0
HLI-0592	44	F	U	165	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0593	61	M	L	192	1	0	1	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0594	35	M	L	153	0	0	0	0	0	1	NA	0	0	0	0	1	0	0	0
HLI-0595	46	M	J	179	1	1	0	0	0	1	1	0	1	0	NA	1	0	0	1
HLI-0596	64	M	H	142	1	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0597	62	F	H	270	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0598	43	M	H	218	0	0	0	1	0	1	1	0	0	0	1	1	0	0	0
HLI-0599	55	F	J	204	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0600	36	M	H	301	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0601	63	M	L	179	1	1	1	1	0	1	1	0	1	0	0	0	1	0	2
HLI-0602	31	M	J	169	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0603	60	M	J	197	1	1	1	0	1	1	1	0	1	0	0	1	0	0	3
HLI-0604	64	M	K	133	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0606	59	F	U	288	0	0	0	1	0	NA	1	0	0	0	NA	NA	NA	NA	0
HLI-0607	54	M	H	272	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0608	56	M	I	175	1	1	0	0	1	0	1	0	0	0	0	1	0	0	1
HLI-0609	42	M	L	290	1	1	0	0	1	0	0	0	0	0	0	0	1	0	1
HLI-0610	58	M	H	233	1	1	NA	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0611	63	F	H	275	0	1	0	0	0	1	0	0	0	0	0	0	1	0	2
HLI-0612	61	M	T	121	1	1	1	1	1	1	1	1	0	0	0	1	0	0	3
HLI-0613	64	F	T	152	1	1	1	1	1	1	1	1	1	0	0	1	0	0	3
HLI-0614	48	F	T	226	1	1	0	0	0	1	1	1	0	0	0	1	0	0	3
HLI-0615	57	M	H	295	1	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0616	55	M	U	246	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0617	52	M	J	311	1	1	NA	0	1	1	1	1	1	0	NA	1	0	0	3
HLI-0618	55	F	T	179	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0619	62	M	T	152	1	1	1	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0620	62	M	L	165	1	1	1	1	1	1	0	0	0	0	0	0	1	0	3
HLI-0621	58	F	L	196	1	1	0	0	0	1	1	1	0	0	NA	0	1	0	3
HLI-0622	61	F	H	193	1	1	NA	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0623	50	M	R	199	1	1	0	0	1	1	1	0	0	0	0	0	0	1	3
HLI-0624	64	M	H	211	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0625	62	M	T	157	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0626	65	F	T	203	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0627	36	M	L	203	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0628	62	M	U	198	1	1	NA	0	0	1	1	0	1	0	0	1	0	0	1

HLI-0629	64	M	X	149	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0630	64	M	H	215	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0631	55	M	V	182	1	1	1	0	1	1	1	1	0	0	1	1	0	0	3
HLI-0632	55	F	H	175	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0633	61	F	V	203	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0634	54	F	H	191	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0635	57	F	R	178	1	1	0	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0636	41	F	T	181	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0637	40	M	U	166	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0638	53	M	H	264	0	0	0	0	1	1	1	0	0	0	NA	1	0	0	0
HLI-0639	61	M	H	257	0	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0640	61	M	N	144	1	1	1	0	1	1	1	1	0	0	0	1	0	0	2
HLI-0641	61	F	L	199	1	1	NA	0	1	1	1	1	1	0	0	0	1	0	2
HLI-0642	45	F	L	161	0	0	0	0	1	1	1	0	0	0	0	0	1	0	0
HLI-0643	53	F	T	281	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0644	63	M	H	260	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0645	62	M	H	257	1	1	0	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0646	52	M	T	182	1	1	1	1	1	1	1	1	0	0	0	1	0	0	3
HLI-0647	47	F	H	223	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0648	53	F	V	212	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0649	22	M	I	268	0	0	0	0	0	NA	0	0	0	1	0	1	0	0	0
HLI-0650	46	F	H	238	0	1	0	1	0	0	0	0	0	0	0	1	0	0	2
HLI-0651	65	M	H	199	1	1	1	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0652	62	F	T	215	1	1	0	0	0	1	1	1	0	0	0	1	0	0	3
HLI-0653	54	F	U	144	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0654	55	M	H	274	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0655	63	M	T	179	1	1	1	1	1	0	1	0	0	0	0	1	0	0	3
HLI-0656	57	M	H	220	1	1	0	0	0	1	1	0	0	0	NA	1	0	0	1
HLI-0657	55	M	H	208	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0658	43	F	K	200	1	1	1	0	0	0	1	0	1	0	0	1	0	0	1
HLI-0659	53	M	H	197	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0660	55	M	J	241	0	NA	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0661	54	F	U	150	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0662	41	F	H	258	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0663	33	M	T	303	0	0	0	0	1	1	1	0	0	0	1	1	0	0	0
HLI-0664	54	M	H	250	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0665	59	F	L	290	0	0	0	0	0	1	1	0	0	1	NA	0	1	0	0
HLI-0666	53	M	H	203	0	0	0	0	0	0	0	0	0	0	0	NA	NA	NA	0
HLI-0667	59	M	X	185	1	1	1	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0668	46	F	U	282	0	0	0	0	0	0	NA	0	0	0	0	1	0	0	0
HLI-0669	63	M	J	153	0	0	0	1	1	1	1	0	0	0	NA	1	0	0	0
HLI-0670	52	M	H	210	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0671	56	F	L	187	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0672	64	M	V	231	1	1	1	0	1	1	1	0	1	0	NA	1	0	0	1
HLI-0673	62	M	H	278	0	0	0	1	0	0	1	0	0	0	NA	1	0	0	0
HLI-0674	59	F	U	280	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0675	42	M	H	279	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0676	36	M	H	201	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0

HLI-0677	52	M	H	273	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0678	57	F	U	279	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0679	62	M	H	139	1	1	NA	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0680	59	M	L	235	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0
HLI-0681	61	M	U	245	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0682	62	M	J	269	0	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0683	62	M	H	206	1	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0684	49	F	J	213	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0685	45	M	L	297	1	1	0	0	0	1	1	0	0	0	0	0	1	0	2
HLI-0686	56	M	B	237	0	0	0	0	1	1	1	0	0	0	0	0	0	1	0
HLI-0687	59	M	K	275	0	0	0	0	0	1	0	0	0	0	NA	1	0	0	0
HLI-0688	65	M	L	252	0	0	0	0	0	0	0	0	0	0	NA	0	1	0	0
HLI-0689	63	M	R	221	0	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0690	65	F	M	213	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0691	64	M	J	227	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0692	60	M	U	226	1	1	1	1	1	1	1	1	1	0	0	1	0	0	3
HLI-0693	62	M	M	232	1	1	0	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0694	49	M	H	197	1	1	1	1	0	1	1	0	0	0	0	1	0	0	3
HLI-0695	51	M	L	291	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0696	57	M	T	142	1	1	1	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0697	63	M	U	148	1	1	0	0	0	1	1	0	0	0	NA	1	0	0	3
HLI-0698	49	M	L	249	1	1	NA	0	0	1	1	0	0	0	NA	NA	NA	NA	1
HLI-0699	55	M	L	246	1	1	0	0	0	1	1	0	1	0	0	0	1	0	2
HLI-0700	65	M	L	349	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0701	56	M	V	194	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0702	51	F	U	225	1	1	0	0	1	0	1	0	1	0	0	1	0	0	1
HLI-0703	60	M	H	211	1	1	1	1	0	1	1	1	0	0	0	1	0	0	3
HLI-0704	53	F	T	195	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0705	55	M	R	195	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0
HLI-0706	65	M	H	146	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0707	47	F	L	234	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HLI-0708	40	M	K	126	1	0	NA	0	0	0	NA	0	0	0	0	0	0	0	0
HLI-0709	61	F	I	264	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0710	48	M	L	288	1	1	1	1	0	1	1	1	1	0	0	0	1	0	3
HLI-0711	57	M	H	153	NA	1	NA	0	0	1	1	0	0	0	NA	1	0	0	1
HLI-0712	55	M	H	214	1	1	1	0	1	0	1	0	1	0	1	1	0	0	1
HLI-0713	21	M	H	219	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0714	51	F	U	174	1	1	0	0	0	0	0	0	0	0	0	NA	NA	NA	3
HLI-0715	53	M	H	179	1	1	0	0	1	0	1	0	0	0	0	1	0	0	2
HLI-0716	62	F	R	242	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0717	36	M	I	218	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0718	60	M	K	271	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0719	62	M	L	214	1	1	0	0	0	0	1	0	0	1	0	0	1	0	2
HLI-0720	60	M	H	219	1	1	1	0	0	0	NA	0	0	0	0	1	0	0	3
HLI-0721	59	F	T	268	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0
HLI-0722	62	M	H	143	1	1	1	0	0	1	1	1	0	0	1	1	0	0	3
HLI-0723	60	M	J	285	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0724	52	M	C	189	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3

HLI-0725	56	M	L	200	1	1	NA	0	0	1	1	0	0	0	0	0	1	0	2
HLI-0726	64	F	L	332	1	1	0	0	1	1	1	0	0	0	0	0	1	0	1
HLI-0727	43	M	U	220	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0728	62	M	I	257	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0729	49	M	K	320	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0730	50	M	K	255	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0731	61	M	H	198	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0732	54	F	K	153	1	1	0	0	1	1	1	1	1	0	0	1	0	0	1
HLI-0733	48	M	H	260	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0734	62	F	U	246	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0735	60	M	U	181	1	1	1	1	1	0	1	0	0	0	1	1	0	0	1
HLI-0736	62	M	I	183	1	1	1	0	1	1	1	1	0	0	1	1	0	0	3
HLI-0737	64	M	N	224	1	1	1	1	0	1	1	1	0	0	0	1	0	0	3
HLI-0738	46	M	W	210	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0739	65	F	L	219	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HLI-0740	46	F	H	223	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0741	61	M	L	231	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
HLI-0742	63	M	NA	240	0	0	0	0	0	1	1	0	0	1	1	1	0	0	0
HLI-0743	57	F	H	200	1	1	0	0	1	0	1	0	0	0	0	1	0	0	1
HLI-0744	59	M	K	230	1	1	NA	0	0	1	1	1	0	0	0	1	0	0	3
HLI-0745	41	F	H	326	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0746	62	M	J	257	1	1	1	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0747	61	M	L	260	0	0	0	1	0	1	1	0	0	0	0	0	1	0	0
HLI-0748	59	M	K	287	1	1	1	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0749	53	M	J	224	1	1	0	0	0	1	0	0	0	0	0	1	0	0	1
HLI-0750	28	M	H	282	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0751	59	M	H	217	1	1	0	0	0	0	1	0	0	0	0	1	0	0	2
HLI-0752	53	M	T	261	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0753	50	M	H	253	1	1	1	0	1	0	1	0	0	0	0	1	0	0	1
HLI-0754	41	F	L	232	1	1	1	0	0	1	0	0	0	0	0	0	1	0	1
HLI-0755	63	M	H	183	1	1	0	1	0	1	1	0	0	0	0	1	0	0	2
HLI-0756	55	M	K	186	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0
HLI-0757	51	M	K	213	1	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0758	42	M	U	197	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0759	64	M	H	180	0	0	0	0	0	0	1	0	0	0	NA	1	0	0	0
HLI-0760	64	F	L	172	0	0	0	1	1	1	1	0	0	0	0	0	1	0	0
HLI-0761	39	M	T	176	1	1	0	0	0	1	1	0	0	0	0	0	0	0	1
HLI-0762	64	M	K	242	1	1	1	0	NA	0	0	0	0	0	0	1	0	0	1
HLI-0763	65	F	T	261	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0
HLI-0764	50	F	H	232	1	1	0	0	1	0	1	0	0	0	0	1	0	0	1
HLI-0765	51	F	J	180	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0766	54	F	U	189	1	1	1	0	1	1	1	1	0	0	NA	1	0	0	1
HLI-0767	62	M	H	212	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0768	64	F	L	241	1	1	0	0	0	1	1	0	0	0	NA	0	1	0	3
HLI-0769	50	F	M	148	1	1	1	0	1	1	1	0	1	1	0	1	0	0	2
HLI-0770	50	M	M	158	1	1	1	0	1	0	0	0	1	0	0	1	0	0	3
HLI-0771	57	F	H	172	1	1	NA	0	1	1	1	0	1	0	NA	1	0	0	2
HLI-0772	60	F	T	306	0	0	0	0	0	0	1	0	0	1	0	1	0	0	0

HLI-0773	59	M	T	256	1	1	0	1	1	1	1	0	0	0	1	1	0	0	2
HLI-0774	61	M	T	217	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0775	61	M	H	160	1	1	0	0	0	1	0	0	0	0	0	1	0	0	1
HLI-0776	57	F	H	159	1	1	1	0	1	1	1	1	1	0	NA	1	0	0	3
HLI-0777	62	M	H	283	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0
HLI-0778	62	M	W	201	0	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0779	44	M	L	212	0	0	0	1	1	1	1	0	0	0	0	0	1	0	0
HLI-0780	62	M	T	216	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0781	49	F	L	172	1	0	0	0	1	1	1	0	1	0	0	1	0	0	0
HLI-0782	57	M	K	195	1	1	1	1	1	1	1	1	0	0	1	1	0	0	3
HLI-0783	45	F	L	295	1	1	1	0	1	1	1	0	1	0	0	0	1	0	1
HLI-0784	52	F	V	178	1	1	0	1	0	1	1	0	1	0	0	0	0	0	1
HLI-0785	53	M	H	158	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0
HLI-0786	60	F	L	165	0	1	0	0	0	1	1	0	0	1	NA	0	1	0	2
HLI-0787	56	F	L	234	1	1	0	0	0	1	1	0	1	1	0	0	1	0	3
HLI-0788	57	M	H	131	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0789	55	F	H	188	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0790	61	M	T	118	1	1	NA	0	0	1	1	0	1	0	NA	1	0	0	2
HLI-0791	61	F	H	189	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0792	50	M	J	168	1	1	0	1	1	1	1	0	1	0	0	1	0	0	1
HLI-0793	34	M	L	200	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0794	50	F	H	173	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0795	45	M	K	204	1	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0796	53	M	H	271	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0797	59	M	U	205	NA	1	0	0	0	1	0	0	0	0	0	1	0	0	1
HLI-0798	56	M	T	122	1	1	NA	0	0	1	1	0	1	0	0	1	0	0	2
HLI-0799	60	M	T	258	1	1	0	0	1	1	1	0	0	0	NA	1	0	0	1
HLI-0800	62	M	H	171	1	1	0	1	0	1	1	0	1	0	0	1	0	0	1
HLI-0801	61	M	H	193	0	1	0	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0802	55	M	L	164	0	1	0	0	0	0	1	0	0	0	0	0	1	0	3
HLI-0803	61	M	H	154	1	1	NA	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0804	60	F	L	216	0	0	0	1	0	1	1	0	0	0	1	0	1	0	0
HLI-0805	63	M	H	250	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0806	55	F	H	228	0	0	0	0	0	0	0	0	0	0	NA	1	0	0	0
HLI-0807	54	M	J	175	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0808	51	M	L	164	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0809	49	F	L	262	1	1	0	0	1	1	1	0	0	0	0	0	1	0	1
HLI-0810	63	M	T	236	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0811	61	M	J	214	1	1	0	0	1	1	0	0	0	0	0	1	0	0	2
HLI-0812	61	F	H	266	1	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0813	56	M	K	234	1	1	0	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0814	41	M	H	235	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0815	42	M	H	221	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
HLI-0816	53	M	H	259	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0817	60	M	H	186	1	1	0	1	0	0	1	0	1	0	0	1	0	0	3
HLI-0818	55	F	U	196	1	1	NA	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0819	59	M	H	254	1	1	NA	0	1	1	1	0	1	0	0	1	0	0	2
HLI-0820	62	M	T	170	NA	1	0	0	0	1	1	0	0	0	0	1	0	0	1

HLI-0821	53	M	J	311	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0822	55	M	W	347	1	1	0	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0823	62	M	H	373	1	1	0	0	0	1	1	0	0	0	1	1	0	0	1
HLI-0824	65	M	M	250	0	1	0	0	1	0	0	0	0	0	0	0	0	1	2
HLI-0825	64	M	H	299	1	1	0	0	0	0	0	0	0	0	0	1	0	0	1
HLI-0826	42	M	X	179	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0827	62	M	V	330	1	1	1	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0828	55	M	U	279	1	1	0	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0829	52	F	W	292	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0830	35	M	N	209	1	1	NA	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0831	58	F	H	161	1	1	NA	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0832	60	M	H	186	1	1	0	0	1	1	1	0	0	0	0	1	0	0	1
HLI-0833	65	M	C	240	1	1	0	0	0	0	1	0	1	0	0	1	0	0	1
HLI-0834	57	F	B	225	0	0	0	0	1	1	1	0	0	0	0	0	0	1	0
HLI-0835	61	M	B	246	1	1	0	0	0	1	0	0	0	0	0	1	0	0	3
HLI-0836	62	M	H	158	1	1	1	1	0	NA	1	1	1	0	0	1	0	0	2
HLI-0837	60	M	T	261	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0838	58	M	M	247	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0839	65	M	NA	316	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0840	45	F	T	307	1	1	0	0	1	0	1	0	0	0	NA	1	0	0	2
HLI-0841	58	M	U	243	1	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0842	54	F	A	280	0	0	0	0	1	1	1	0	0	0	0	0	1	0	0
HLI-0843	58	M	J	212	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0844	52	F	R	232	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0845	60	M	T	225	1	1	0	0	0	0	1	1	0	0	0	1	0	0	3
HLI-0846	47	M	J	263	0	0	0	1	0	1	1	0	0	1	0	1	0	0	0
HLI-0847	48	F	U	298	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0848	48	M	U	295	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0849	42	M	H	221	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0850	43	F	T	248	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0851	47	F	H	175	1	1	1	1	1	1	1	1	0	1	0	1	0	0	3
HLI-0852	53	M	U	238	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0853	50	M	T	174	1	1	1	0	0	0	1	1	0	0	0	1	0	0	3
HLI-0854	58	M	U	241	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0855	43	F	L	230	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0856	49	M	T	196	0	0	0	0	0	1	1	0	0	0	NA	1	0	0	0
HLI-0857	64	M	K	215	1	1	1	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0858	58	F	H	229	1	1	1	0	1	1	1	0	1	0	NA	1	0	0	2
HLI-0859	57	M	H	125	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0860	59	M	J	193	1	1	1	1	1	1	1	0	0	0	0	1	0	0	2
HLI-0861	57	F	L	299	1	1	0	1	1	1	1	0	0	0	0	0	1	0	1
HLI-0862	59	M	H	174	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0863	64	M	H	168	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0864	44	F	L	153	1	1	1	1	1	0	0	0	0	0	0	0	1	0	3
HLI-0865	51	M	J	203	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0866	58	M	U	230	1	1	0	0	0	1	1	0	0	NA	0	1	0	0	2
HLI-0867	58	M	K	252	0	0	0	0	0	1	1	0	0	1	0	1	0	0	0
HLI-0868	53	M	H	174	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0

HLI-0869	61	M	T	275	1	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0870	62	M	H	167	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0871	58	F	U	210	1	1	NA	0	1	1	1	0	0	0	0	1	0	0	2
HLI-0872	47	M	J	192	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0873	56	M	U	244	1	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0874	52	M	H	228	0	0	0	1	0	0	1	0	0	0	0	1	0	0	0
HLI-0875	61	M	V	230	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0876	52	M	R	231	1	0	0	0	1	0	1	0	0	0	1	1	0	0	0
HLI-0877	64	M	H	223	0	0	0	0	0	NA	1	0	0	0	1	1	0	0	0
HLI-0878	63	M	W	146	1	1	0	0	1	0	1	1	0	0	0	1	0	0	3
HLI-0879	57	M	H	227	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0880	44	M	J	145	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0881	63	M	K	176	1	1	1	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0882	48	M	U	261	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0883	56	M	T	219	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0884	60	M	J	193	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0885	47	F	K	219	1	0	0	0	0	1	1	0	1	0	0	1	0	0	0
HLI-0886	64	M	H	234	1	1	NA	0	0	0	1	1	0	0	0	1	0	0	3
HLI-0887	42	M	H	159	1	1	NA	0	0	1	1	0	1	0	0	0	1	0	3
HLI-0888	45	M	J	249	0	1	0	0	1	0	1	0	0	0	0	1	0	0	3
HLI-0889	56	M	U	213	1	1	1	0	0	1	1	1	1	0	0	0	0	0	3
HLI-0890	57	M	U	157	1	1	1	1	0	1	1	1	1	0	0	NA	NA	NA	3
HLI-0891	63	M	U	221	1	1	NA	0	1	1	1	0	1	0	0	1	0	0	2
HLI-0892	59	M	H	148	1	1	1	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0893	56	M	L	187	1	1	1	0	1	0	1	1	1	0	0	0	1	0	3
HLI-0894	55	F	L	219	0	0	NA	0	0	0	1	0	0	0	0	0	1	0	0
HLI-0895	52	F	H	179	0	0	0	0	1	1	1	0	0	0	NA	1	0	0	0
HLI-0896	51	M	U	166	1	1	1	0	1	1	1	0	1	0	0	1	0	0	2
HLI-0897	57	F	T	141	1	1	1	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0898	61	M	H	240	1	0	1	0	0	0	1	0	1	0	0	1	0	0	0
HLI-0899	60	M	H	181	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0900	59	M	H	168	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0901	64	F	U	232	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0902	60	F	T	244	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0903	62	M	J	238	0	1	0	0	0	0	1	0	0	0	0	1	0	0	2
HLI-0904	57	M	K	236	1	1	1	0	0	0	1	0	0	0	0	1	0	0	3
HLI-0906	51	M	H	203	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0907	57	M	U	139	1	1	0	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0908	61	M	H	98	1	1	1	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0909	48	M	H	178	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0910	54	F	U	197	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0911	46	M	W	146	1	1	1	0	1	1	1	1	0	0	0	1	0	0	3
HLI-0912	61	F	H	202	0	0	0	1	0	1	1	0	0	0	0	1	0	0	0
HLI-0913	55	M	H	312	1	1	1	NA	0	NA	1	0	0	0	0	1	0	0	3
HLI-0914	54	M	H	129	1	1	0	1	1	1	0	0	0	0	0	1	0	0	1
HLI-0915	50	M	K	181	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0916	63	M	J	255	1	1	0	0	1	1	1	0	0	0	0	1	0	0	1
HLI-0917	65	M	H	161	1	1	1	0	1	NA	1	0	0	0	0	1	0	0	3

HLI-0918	62	M	H	177	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0919	64	M	H	143	1	1	1	0	0	1	1	1	1	0	0	0	1	0	3
HLI-0920	59	F	K	131	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0921	51	F	L	221	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
HLI-0922	46	F	H	220	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0923	57	M	H	206	1	1	0	0	0	1	1	0	0	1	0	1	0	0	3
HLI-0924	54	M	H	182	1	1	1	0	0	0	0	0	0	0	0	0	0	1	1
HLI-0925	64	M	K	186	1	1	NA	0	0	1	1	0	1	0	0	1	0	0	3
HLI-0926	65	M	H	192	1	1	1	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0927	54	F	L	224	0	1	0	1	0	1	1	0	0	0	0	0	1	0	1
HLI-0928	48	M	U	168	1	1	1	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0929	62	F	H	180	1	1	0	NA	NA	1	1	0	0	0	0	1	0	0	2
HLI-0930	60	M	T	218	1	1	1	0	0	0	1	1	1	0	0	1	0	0	3
HLI-0931	64	M	U	181	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0932	55	F	L	226	0	0	0	0	0	1	NA	0	0	0	0	0	1	0	0
HLI-0933	51	F	W	180	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0934	58	M	K	121	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0935	62	M	R	221	1	1	0	0	0	1	1	0	1	0	0	1	0	0	1
HLI-0936	59	F	H	206	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0937	61	M	H	206	1	1	0	0	1	1	1	1	1	0	0	1	0	0	3
HLI-0938	65	M	H	157	0	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0939	54	M	H	196	1	1	1	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0940	56	M	B	287	1	1	0	0	1	1	1	0	0	0	0	0	1	0	1
HLI-0941	45	M	M	201	0	1	0	0	0	0	0	0	0	0	0	0	0	1	2
HLI-0942	57	M	H	168	0	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-0943	59	M	T	179	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0944	64	M	H	179	1	1	1	0	1	0	1	0	0	0	1	1	0	0	2
HLI-0945	50	M	K	152	1	1	NA	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0946	54	F	N	240	1	1	0	0	1	1	0	0	1	0	0	1	0	0	2
HLI-0947	57	F	H	314	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0948	59	F	J	273	1	1	0	0	1	1	1	0	1	0	0	1	0	0	1
HLI-0949	52	M	H	262	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0950	55	M	L	226	1	1	1	0	0	NA	NA	0	0	0	NA	0	1	0	3
HLI-0951	62	M	X	148	1	1	1	0	1	1	1	0	1	1	NA	1	0	0	2
HLI-0952	55	M	K	192	1	1	1	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0953	60	M	U	156	1	1	NA	0	0	0	1	1	1	0	0	1	0	0	3
HLI-0954	40	M	H	191	1	1	NA	1	1	1	1	1	1	0	1	1	0	0	3
HLI-0955	59	M	H	182	1	1	0	0	0	1	1	0	0	0	0	1	0	0	1
HLI-0956	60	M	K	157	1	1	1	1	0	1	1	1	1	0	0	1	0	0	3
HLI-0957	64	M	B	126	1	1	0	0	1	1	1	1	0	0	0	0	0	1	2
HLI-0958	55	M	X	141	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0959	62	M	J	129	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0960	57	M	K	139	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
HLI-0961	61	F	I	337	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0962	52	F	K	186	0	1	0	0	1	1	1	0	0	0	0	1	0	0	3
HLI-0963	44	M	K	210	1	1	1	0	1	1	1	1	1	0	NA	1	0	0	2
HLI-0964	62	F	H	198	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0965	50	M	H	293	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0

HLI-0966	55	M	N	192	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0967	54	F	H	183	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0968	61	F	T	248	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0969	64	M	H	220	1	1	0	0	0	1	1	1	0	0	0	1	0	0	2
HLI-0970	48	M	T	239	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0971	65	M	J	193	1	1	1	0	0	1	0	0	0	0	0	1	0	0	1
HLI-0972	56	M	H	138	1	1	0	0	1	1	0	1	1	0	0	1	0	0	3
HLI-0973	60	M	J	184	1	1	1	0	0	1	1	0	0	0	0	1	0	0	2
HLI-0974	46	M	K	179	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-0975	41	M	U	224	0	0	0	0	1	1	1	0	0	0	0	1	0	0	0
HLI-0976	56	M	H	174	1	1	0	0	1	1	1	1	0	1	0	1	0	0	3
HLI-0977	52	F	H	190	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0978	64	F	L	158	1	1	1	0	1	1	1	0	0	1	0	0	1	0	1
HLI-0979	56	M	J	223	1	1	1	0	0	1	0	0	0	0	0	0	1	0	2
HLI-0980	57	M	T	164	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0981	60	M	H	250	1	1	0	1	1	1	1	1	1	0	0	1	0	0	3
HLI-0982	60	F	H	180	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0
HLI-0983	60	F	H	219	0	1	0	1	1	1	1	0	0	0	0	1	0	0	1
HLI-0984	43	F	K	167	0	0	0	1	1	1	1	0	0	0	1	1	0	0	0
HLI-0985	57	M	H	175	1	1	0	0	1	1	1	0	1	0	0	1	0	0	3
HLI-0986	53	M	H	213	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0987	63	M	H	169	1	1	1	0	1	1	0	1	1	0	0	1	0	0	2
HLI-0988	61	M	J	146	1	1	1	1	0	0	1	0	1	0	1	1	0	0	3
HLI-0989	35	M	V	232	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0
HLI-0990	60	M	L	114	1	1	1	1	1	1	1	0	1	1	0	0	1	0	1
HLI-0991	62	M	W	194	0	0	0	0	0	1	1	0	0	0	0	1	0	0	0
HLI-0992	55	M	U	170	0	0	0	0	0	1	1	0	0	0	1	1	0	0	0
HLI-0993	48	F	H	114	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0994	58	M	U	257	1	1	1	0	0	0	1	0	1	0	1	1	0	0	1
HLI-0995	55	M	J	257	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0
HLI-0996	46	M	H	210	1	1	1	1	1	0	1	0	0	0	0	1	0	0	1
HLI-0997	55	M	U	141	1	1	1	0	0	1	1	0	0	0	0	1	0	0	3
HLI-0998	48	F	L	321	1	1	0	0	0	1	1	0	0	0	0	0	1	0	1
HLI-0999	59	M	H	235	1	1	1	0	1	1	1	0	0	0	0	1	0	0	2
HLI-1000	64	F	V	196	1	1	0	0	0	1	1	0	0	0	0	1	0	0	2
HLI-1001	62	M	U	166	1	1	NA	0	NA	0	1	1	1	0	0	1	0	0	3
HLI-1002	53	M	H	256	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
HLI-1003	56	M	H	225	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
HLI-1004	57	M	K	240	1	1	1	0	0	0	1	0	0	0	0	1	0	0	3

Table S3. Proportion of patients with specific clinical features, stratified by self-reported maternal ancestry.

	White Mother	Black Mother	Other
HxCabg	0.133	0.132	0.118
HxCad	0.465	0.507	0.559
HxCHF	0.133	0.211	0.088
HxDM	0.321	0.333	0.294
HxHtn	0.626	0.831	0.545
HxHyperlipidemia	0.783	0.645	0.677
HxMI	0.181	0.265	0.167
HxPci	0.156	0.215	0.235
HxStroke	0.047	0.070	0.059
HxVentricularArrhythmias	0.103	0.079	0.032
MXSTEN50	0.475	0.528	0.529

Table S4. Odds ratio with 95% confidence intervals (adjusted for age, sex, and maternal ancestry (self-reported and inferred by mtDNA haplogroup)) for clinical features' associations with one standard deviation decrease in mtDNA copy number, and for first quartile mtDNA vs. fourth quartile.

		Self reported maternal ancestry adjusted	Adjusted for mtDNA haplogroup
HxCabg OR (95% CI)	**one s.d. CN decrease**	1.57 (1.28-1.94)	1.62 (1.32-2.00)
	1st quartile vs. 4th	5.17 (2.65-10.09)	5.18 (2.65-10.12)
HxCad OR (95% CI)	**one s.d. CN decrease**	1.31 (1.14-1.51)	1.32 (1.15-1.52)
	1st quartile vs. 4th	2.04 (1.39-2.98)	2.06 (1.40-3.03)
HxMI OR (95% CI)	**one s.d. CN decrease**	1.47 (1.23-1.75)	1.50 (1.25-1.80)
	1st quartile vs. 4th	2.62 (1.58-4.32)	2.71 (1.63-4.50)
MXSTEN50 (95% CI)	**one s.d. CN decrease**	1.38 (1.20-1.58)	1.38 (1.20-1.58)
	1st quartile vs. 4th	2.36 (1.61-3.46)	2.35 (1.60-3.47)

Table S5. Non-reference mtDNA variants.

ID	position (rCRS)	reference allele	alternate allele	reference depth	alternate depth	SNPeff effect	SNPeff term	gene	Genbank frequency
HLI-0001	73	A	G	1	324	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0001	152	T	C	2	557	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0001	263	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0001	750	A	G	1	691	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0001	1438	A	G	1	680	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0001	1598	G	A	1	601	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0001	1719	G	A	3	498	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0001	2639	C	T	0	652	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0001	2706	A	G	0	729	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0001	3921	C	A	6	622	synonymous_variant	LOW	ND1	0.0026
HLI-0001	4769	A	G	1	578	synonymous_variant	LOW	ND2	0.9767
HLI-0001	4960	C	T	6	595	missense_variant	MODERATE	ND2	0.0028
HLI-0001	5471	G	A	4	669	synonymous_variant	LOW	ND2	0.0128
HLI-0001	7028	C	T	3	698	synonymous_variant	LOW	COX1	0.8089
HLI-0001	8251	G	A	5	541	synonymous_variant	LOW	COX2	0.058
HLI-0001	8472	C	T	1	432	missense_variant	MODERATE	ATP8	0.0027
HLI-0001	8836	A	G	0	665	missense_variant	MODERATE	ATP6	0.0029
HLI-0001	9335	C	T	0	685	synonymous_variant	LOW	COX3	0.0021
HLI-0001	10238	T	C	0	694	synonymous_variant	LOW	ND3	0.0623
HLI-0001	11362	A	G	0	642	synonymous_variant	LOW	ND4	0.0024
HLI-0001	11719	G	A	1	675	synonymous_variant	LOW	ND4	0.7756
HLI-0001	12501	G	A	5	493	synonymous_variant	LOW	ND5	0.0258
HLI-0001	12705	C	T	1	611	synonymous_variant	LOW	ND5	0.4212
HLI-0001	12822	A	G	12	612	synonymous_variant	LOW	ND5	0.0026
HLI-0001	14766	C	T	2	694	missense_variant	MODERATE	CYTB	0.7696
HLI-0001	15326	A	G	2	534	missense_variant	MODERATE	CYTB	0.9868
HLI-0001	16075	T	C	1	473	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0001	16145	G	A	1	550	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0001	16176	C	A	4	547	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0001	16223	C	T	0	553	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0001	16311	T	C	2	560	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0001	16390	G	A	0	514	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0001	16519	T	C	1	317	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0002	263	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0002	750	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0002	1438	A	G	1	635	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0002	4502	T	C	2	587	synonymous_variant	LOW	ND2	0.0013
HLI-0002	4769	A	G	2	540	synonymous_variant	LOW	ND2	0.9767
HLI-0002	9948	G	A	0	599	missense_variant	MODERATE	COX3	0.0015
HLI-0002	15326	A	G	0	459	missense_variant	MODERATE	CYTB	0.9868
HLI-0002	15784	T	C	0	431	synonymous_variant	LOW	CYTB	0.0363
HLI-0002	16519	T	C	0	292	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0003	72	T	C	0	377	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0003	204	T	C	1	467	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0003	207	G	A	1	459	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0003	263	A	G	1	256	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0003	750	A	G	2	723	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0003	1438	A	G	1	761	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0003	2706	A	G	0	744	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0003	4580	G	A	1	684	synonymous_variant	LOW	ND2	0.0169
HLI-0003	4769	A	G	1	664	synonymous_variant	LOW	ND2	0.9767
HLI-0003	7028	C	T	4	823	synonymous_variant	LOW	COX1	0.8089
HLI-0003	8179	A	G	0	761	synonymous_variant	LOW	COX2	9.00E-04
HLI-0003	11581	C	T	2	693	synonymous_variant	LOW	ND4	5.00E-04
HLI-0003	12645	C	T	4	737	synonymous_variant	LOW	ND5	0
HLI-0003	13759	G	A	0	515	missense_variant	MODERATE	ND5	0.0348
HLI-0003	15326	A	G	0	719	missense_variant	MODERATE	CYTB	0.9868
HLI-0003	15904	C	T	0	789	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0003	16219	A	G	2	805	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0003	16502	T	C	24	419	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0004	73	A	G	1	309	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0004	242	C	T	1	447	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0004	263	A	G	1	414	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0004	295	C	T	0	349	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0004	462	C	T	0	470	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0004	489	T	C	0	552	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0004	750	A	G	0	554	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0004	1438	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0004	2158	T	C	0	302	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0004	2706	A	G	0	592	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0004	3010	G	A	1	503	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0004	4216	T	C	2	444	missense_variant	MODERATE	ND1	0.0991
HLI-0004	4769	A	G	1	522	synonymous_variant	LOW	ND2	0.9767
HLI-0004	5460	G	A	5	541	missense_variant	MODERATE	ND2	0.0651
HLI-0004	5463	C	T	5	542	missense_variant	MODERATE	ND2	4.00E-04

HLI-0004	6911	T	C	6	735	synonymous_variant	LOW	COX1	6.00E-04
HLI-0004	7028	C	T	2	611	synonymous_variant	LOW	COX1	0.8089
HLI-0004	8269	G	A	5	549	stop_retained_variant	LOW	COX2	0.0127
HLI-0004	8557	G	A	0	471	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0004	10398	A	G	4	572	missense_variant	MODERATE	ND3	0.445
HLI-0004	11251	A	G	1	556	synonymous_variant	LOW	ND4	0.0932
HLI-0004	11719	G	A	0	595	synonymous_variant	LOW	ND4	0.7756
HLI-0004	12007	G	A	1	466	synonymous_variant	LOW	ND4	0.0639
HLI-0004	12612	A	G	5	522	synonymous_variant	LOW	ND5	0.0506
HLI-0004	13708	G	A	0	374	missense_variant	MODERATE	ND5	0.0717
HLI-0004	13879	T	C	1	499	missense_variant	MODERATE	ND5	0.0073
HLI-0004	14766	C	T	1	745	missense_variant	MODERATE	CYTB	0.7696
HLI-0004	15326	A	G	0	420	missense_variant	MODERATE	CYTB	0.9868
HLI-0004	15452	C	A	1	415	missense_variant	MODERATE	CYTB	0.0933
HLI-0004	16069	C	T	0	434	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0004	16126	T	C	1	458	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0004	16145	G	A	0	481	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0004	16172	T	C	1	474	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0004	16222	C	T	0	474	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0004	16261	C	T	4	504	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0005	73	A	G	0	41	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0005	199	T	C	1	60	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0005	250	T	C	0	31	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0005	263	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0005	750	A	G	0	63	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0005	1719	G	A	0	53	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0005	2706	A	G	0	64	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0005	4529	A	T	0	57	synonymous_variant	LOW	ND2	0.015
HLI-0005	4769	A	G	0	59	synonymous_variant	LOW	ND2	0.9767
HLI-0005	7028	C	T	0	71	synonymous_variant	LOW	COX1	0.8089
HLI-0005	8251	G	A	0	59	synonymous_variant	LOW	COX2	0.058
HLI-0005	8519	G	A	0	54	missense_variant	MODERATE	ATP8	0.0024
HLI-0005	10034	T	C	0	66	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0005	10238	T	C	0	49	synonymous_variant	LOW	ND3	0.0623
HLI-0005	10398	A	G	0	81	missense_variant	MODERATE	ND3	0.445
HLI-0005	10819	A	G	1	59	synonymous_variant	LOW	ND4	0.0228
HLI-0005	11719	G	A	0	64	synonymous_variant	LOW	ND4	0.7756
HLI-0005	12501	G	A	0	70	synonymous_variant	LOW	ND5	0.0258
HLI-0005	12705	C	T	0	73	synonymous_variant	LOW	ND5	0.4212

HLI-0005	13780	A	G	1	40	missense_variant	MODERATE	ND5	0.0179
HLI-0005	14766	C	T	0	61	missense_variant	MODERATE	CYTB	0.7696
HLI-0005	14861	G	A	0	65	missense_variant	MODERATE	CYTB	0.0029
HLI-0005	15043	G	A	0	81	synonymous_variant	LOW	CYTB	0.2362
HLI-0005	15326	A	G	0	57	missense_variant	MODERATE	CYTB	0.9868
HLI-0005	15773	G	A	0	95	missense_variant	MODERATE	CYTB	0.0011
HLI-0005	15924	A	G	0	66	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0005	16129	G	A	0	71	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0005	16223	C	T	0	56	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0005	16304	T	C	0	60	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0005	16391	G	A	0	60	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0005	16519	T	C	0	24	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0006	73	A	G	1	305	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0006	152	T	C	1	547	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0006	263	A	G	2	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0006	750	A	G	0	645	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0006	1438	A	G	0	694	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0006	3010	G	A	2	703	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0006	4769	A	G	1	654	synonymous_variant	LOW	ND2	0.9767
HLI-0006	6365	T	C	0	609	synonymous_variant	LOW	COX1	0.0026
HLI-0006	15326	A	G	1	649	missense_variant	MODERATE	CYTB	0.9868
HLI-0006	16162	A	G	1	631	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0006	16209	T	C	1	685	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0006	16519	T	C	0	288	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0008	152	T	C	0	552	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0008	263	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0008	750	A	G	0	699	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0008	1438	A	G	0	835	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0008	3010	G	A	0	734	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0008	4769	A	G	0	625	synonymous_variant	LOW	ND2	0.9767
HLI-0008	15326	A	G	0	647	missense_variant	MODERATE	CYTB	0.9868
HLI-0008	16519	T	C	0	343	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0009	73	A	G	1	370	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0009	263	A	G	0	320	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0009	750	A	G	0	741	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0009	1438	A	G	1	779	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0009	3010	G	A	1	768	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0009	3421	G	A	2	686	missense_variant	MODERATE	ND1	0.0015
HLI-0009	4769	A	G	1	719	synonymous_variant	LOW	ND2	0.9767

HLI-0009	8752	A	G	1	753	missense_variant	MODERATE	ATP6	2.00E-04
HLI-0009	9621	G	A	0	782	missense_variant	MODERATE	COX3	3.00E-04
HLI-0009	15326	A	G	0	680	missense_variant	MODERATE	CYTB	0.9868
HLI-0009	16051	A	G	0	690	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0009	16162	A	G	3	740	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0009	16519	T	C	2	395	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0010	73	A	G	0	326	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0010	119	T	C	10	481	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0010	189	A	G	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0010	195	T	C	0	408	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0010	204	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0010	207	G	A	0	407	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0010	263	A	G	0	284	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0010	709	G	A	2	697	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0010	750	A	G	0	743	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0010	1243	T	C	2	694	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0010	1438	A	G	0	721	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0010	2706	A	G	0	680	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0010	3505	A	G	6	692	missense_variant	MODERATE	ND1	0.0144
HLI-0010	4769	A	G	1	700	synonymous_variant	LOW	ND2	0.9767
HLI-0010	5046	G	A	4	662	missense_variant	MODERATE	ND2	0.018
HLI-0010	5460	G	A	7	726	missense_variant	MODERATE	ND2	0.0651
HLI-0010	7028	C	T	6	784	synonymous_variant	LOW	COX1	0.8089
HLI-0010	7853	G	A	4	755	missense_variant	MODERATE	COX2	0.0197
HLI-0010	7864	C	T	8	809	synonymous_variant	LOW	COX2	0.0041
HLI-0010	8251	G	A	4	646	synonymous_variant	LOW	COX2	0.058
HLI-0010	8994	G	A	0	683	synonymous_variant	LOW	ATP6	0.0167
HLI-0010	11204	T	C	1	657	missense_variant	MODERATE	ND4	0.003
HLI-0010	11674	C	T	1	678	synonymous_variant	LOW	ND4	0.0116
HLI-0010	11719	G	A	1	755	synonymous_variant	LOW	ND4	0.7756
HLI-0010	11947	A	G	2	625	synonymous_variant	LOW	ND4	0.011
HLI-0010	12414	T	C	3	631	synonymous_variant	LOW	ND5	0.0139
HLI-0010	12648	A	G	7	723	synonymous_variant	LOW	ND5	2.00E-04
HLI-0010	12705	C	T	0	792	synonymous_variant	LOW	ND5	0.4212
HLI-0010	14148	A	G	1	654	stop_retained_variant	LOW	ND5	0.0065
HLI-0010	14766	C	T	2	682	missense_variant	MODERATE	CYTB	0.7696
HLI-0010	15326	A	G	0	605	missense_variant	MODERATE	CYTB	0.9868
HLI-0010	15884	G	C	1	702	missense_variant	MODERATE	CYTB	0.011
HLI-0010	16223	C	T	3	714	upstream_gene_variant	MODIFIER	DLoop	0.4009

HLI-0010	16519	T	C	1	364	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0011	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0011	195	T	C	1	467	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0011	198	C	T	1	471	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0011	263	A	G	0	313	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0011	537	C	T	2	491	upstream_gene_variant	MODIFIER	DLoop	0.0022
HLI-0011	750	A	G	1	657	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0011	1438	A	G	2	666	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0011	1719	G	A	0	580	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0011	2706	A	G	1	670	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0011	4769	A	G	1	626	synonymous_variant	LOW	ND2	0.9767
HLI-0011	6221	T	C	0	631	synonymous_variant	LOW	COX1	0.0306
HLI-0011	6371	C	T	0	667	synonymous_variant	LOW	COX1	0.0097
HLI-0011	7028	C	T	2	690	synonymous_variant	LOW	COX1	0.8089
HLI-0011	11719	G	A	1	639	synonymous_variant	LOW	ND4	0.7756
HLI-0011	12705	C	T	2	561	synonymous_variant	LOW	ND5	0.4212
HLI-0011	13966	A	G	1	590	missense_variant	MODERATE	ND5	0.0126
HLI-0011	14470	T	C	1	584	synonymous_variant	LOW	ND6	0.0166
HLI-0011	14766	C	T	2	667	missense_variant	MODERATE	CYTB	0.7696
HLI-0011	15326	A	G	1	533	missense_variant	MODERATE	CYTB	0.9868
HLI-0011	16223	C	T	1	355	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0011	16278	C	T	1	517	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0011	16519	T	C	0	255	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0012	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0012	152	T	C	2	510	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0012	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0012	750	A	G	0	562	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0012	1438	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0012	1598	G	A	0	580	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0012	1703	C	T	3	486	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0012	1719	G	A	3	530	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0012	2639	C	T	1	569	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0012	2706	A	G	0	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0012	3921	C	A	0	550	synonymous_variant	LOW	ND1	0.0026
HLI-0012	4735	C	A	0	574	missense_variant	MODERATE	ND2	7.00E-04
HLI-0012	4769	A	G	1	592	synonymous_variant	LOW	ND2	0.9767
HLI-0012	4917	A	G	0	561	missense_variant	MODERATE	ND2	0.0477
HLI-0012	4960	C	T	0	591	missense_variant	MODERATE	ND2	0.0028
HLI-0012	5471	G	A	4	550	synonymous_variant	LOW	ND2	0.0128

HLI-0012	7028	C	T	1	588	synonymous_variant	LOW	COX1	0.8089
HLI-0012	8251	G	A	0	470	synonymous_variant	LOW	COX2	0.058
HLI-0012	8472	C	T	0	426	missense_variant	MODERATE	ATP8	0.0027
HLI-0012	8836	A	G	0	545	missense_variant	MODERATE	ATP6	0.0029
HLI-0012	10238	T	C	2	616	synonymous_variant	LOW	ND3	0.0623
HLI-0012	10846	C	T	67	434	synonymous_variant	LOW	ND4	1.00E-04
HLI-0012	11719	G	A	1	509	synonymous_variant	LOW	ND4	0.7756
HLI-0012	11928	A	G	0	523	missense_variant	MODERATE	ND4	0.0028
HLI-0012	12092	C	T	4	507	missense_variant	MODERATE	ND4	7.00E-04
HLI-0012	12501	G	A	10	531	synonymous_variant	LOW	ND5	0.0258
HLI-0012	12705	C	T	3	559	synonymous_variant	LOW	ND5	0.4212
HLI-0012	12822	A	G	14	543	synonymous_variant	LOW	ND5	0.0026
HLI-0012	13129	C	T	11	620	missense_variant	MODERATE	ND5	0.0046
HLI-0012	13710	A	G	0	488	synonymous_variant	LOW	ND5	0.0018
HLI-0012	14581	T	C	2	728	synonymous_variant	LOW	ND6	0.0023
HLI-0012	14766	C	T	4	720	missense_variant	MODERATE	CYTB	0.7696
HLI-0012	15326	A	G	0	387	missense_variant	MODERATE	CYTB	0.9868
HLI-0012	16145	G	A	1	479	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0012	16166	A	C	38	496	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0012	16176	C	A	3	532	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0012	16223	C	T	3	507	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0012	16390	G	A	2	442	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0012	16519	T	C	0	235	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0013	73	A	G	0	325	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0013	263	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0013	750	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0013	1438	A	G	0	711	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0013	1700	T	C	1	614	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0013	2706	A	G	0	660	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0013	3197	T	C	1	613	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0013	4769	A	G	1	596	synonymous_variant	LOW	ND2	0.9767
HLI-0013	7028	C	T	5	735	synonymous_variant	LOW	COX1	0.8089
HLI-0013	8269	G	A	4	649	stop_retained_variant	LOW	COX2	0.0127
HLI-0013	9012	T	C	2	691	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0013	9477	G	A	1	626	missense_variant	MODERATE	COX3	0.0387
HLI-0013	10326	T	A	0	606	missense_variant	MODERATE	ND3	1.00E-04
HLI-0013	11467	A	G	0	660	synonymous_variant	LOW	ND4	0.1231
HLI-0013	11719	G	A	1	673	synonymous_variant	LOW	ND4	0.7756
HLI-0013	12308	A	G	0	604	upstream_gene_variant	MODIFIER	TRNL2	0.1227

HLI-0013	12346	C	T	0	651	missense_variant	MODERATE	ND5	0.0056
HLI-0013	12372	G	A	1	620	synonymous_variant	LOW	ND5	0.1329
HLI-0013	13105	A	G	0	631	missense_variant	MODERATE	ND5	0.076
HLI-0013	13617	T	C	2	680	synonymous_variant	LOW	ND5	0.038
HLI-0013	14278	T	C	0	575	synonymous_variant	LOW	ND6	4.00E-04
HLI-0013	14766	C	T	2	668	missense_variant	MODERATE	CYTB	0.7696
HLI-0013	14793	A	G	0	739	missense_variant	MODERATE	CYTB	0.0199
HLI-0013	15218	A	G	2	675	missense_variant	MODERATE	CYTB	0.0169
HLI-0013	15326	A	G	0	625	missense_variant	MODERATE	CYTB	0.9868
HLI-0013	16256	C	T	1	575	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0013	16270	C	T	1	646	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0013	16399	A	G	0	567	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0014	263	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0014	750	A	G	1	563	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0014	980	T	C	2	717	upstream_gene_variant	MODIFIER	RNR1	0.0112
HLI-0014	1438	A	G	0	625	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0014	3010	G	A	1	583	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0014	4688	T	C	1	639	synonymous_variant	LOW	ND2	0.0078
HLI-0014	4769	A	G	1	642	synonymous_variant	LOW	ND2	0.9767
HLI-0014	15326	A	G	0	560	missense_variant	MODERATE	CYTB	0.9868
HLI-0014	16519	T	C	0	260	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0015	73	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0015	146	T	C	1	389	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0015	152	T	C	1	398	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0015	182	C	T	1	351	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0015	186	C	A	1	333	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0015	189	A	C	1	326	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0015	247	G	A	0	147	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0015	263	A	G	0	159	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0015	750	A	G	0	625	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0015	769	G	A	2	673	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0015	825	T	A	2	662	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0015	1018	G	A	0	622	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0015	1438	A	G	0	641	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0015	2387	T	C	1	683	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0015	2706	A	G	0	665	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0015	2758	G	A	0	691	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0015	2885	T	C	0	644	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0015	3105	A	G	0	625	upstream_gene_variant	MODIFIER	RNR2	0.0017

HLI-0015	3594	C	T	2	606	synonymous_variant	LOW	ND1	0.0789
HLI-0015	3666	G	A	4	643	synonymous_variant	LOW	ND1	0.0233
HLI-0015	4104	A	G	1	555	synonymous_variant	LOW	ND1	0.0785
HLI-0015	4769	A	G	1	635	synonymous_variant	LOW	ND2	0.9767
HLI-0015	5951	A	G	1	640	synonymous_variant	LOW	COX1	0.0128
HLI-0015	6071	T	C	2	635	synonymous_variant	LOW	COX1	0.0129
HLI-0015	6221	T	A	1	663	synonymous_variant	LOW	COX1	0.0027
HLI-0015	6260	G	A	1	751	synonymous_variant	LOW	COX1	0.009
HLI-0015	6531	C	T	3	650	synonymous_variant	LOW	COX1	0.001
HLI-0015	6917	G	A	0	639	synonymous_variant	LOW	COX1	0.0036
HLI-0015	7028	C	T	2	537	synonymous_variant	LOW	COX1	0.8089
HLI-0015	7146	A	G	0	277	missense_variant	MODERATE	COX1	0.0497
HLI-0015	7256	C	T	0	456	synonymous_variant	LOW	COX1	0.0784
HLI-0015	7389	T	C	0	462	missense_variant	MODERATE	COX1	0.0201
HLI-0015	7498	G	A	0	345	upstream_gene_variant	MODIFIER	TRNS1	0.0019
HLI-0015	7521	G	A	1	416	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0015	7789	G	A	3	635	synonymous_variant	LOW	COX2	0.0092
HLI-0015	7897	G	A	2	654	synonymous_variant	LOW	COX2	0.0024
HLI-0015	8027	G	A	3	633	missense_variant	MODERATE	COX2	0.0334
HLI-0015	8468	C	T	1	578	synonymous_variant	LOW	ATP8	0.0501
HLI-0015	8655	C	T	4	535	synonymous_variant	LOW	ATP6	0.0511
HLI-0015	8701	A	G	1	571	missense_variant	MODERATE	ATP6	0.3391
HLI-0015	9072	A	G	0	658	synonymous_variant	LOW	ATP6	0.0124
HLI-0015	9540	T	C	0	688	synonymous_variant	LOW	COX3	0.339
HLI-0015	9966	G	A	0	678	missense_variant	MODERATE	COX3	0.0069
HLI-0015	10398	A	G	0	641	missense_variant	MODERATE	ND3	0.445
HLI-0015	10586	G	A	2	612	synonymous_variant	LOW	ND4L	0.0177
HLI-0015	10688	G	A	2	616	synonymous_variant	LOW	ND4L	0.0515
HLI-0015	10810	T	C	1	605	synonymous_variant	LOW	ND4	0.0522
HLI-0015	10873	T	C	2	690	synonymous_variant	LOW	ND4	0.3389
HLI-0015	11302	C	T	1	599	synonymous_variant	LOW	ND4	0.0028
HLI-0015	11719	G	A	3	642	synonymous_variant	LOW	ND4	0.7756
HLI-0015	12019	C	T	2	652	synonymous_variant	LOW	ND4	0.0015
HLI-0015	12501	G	A	0	668	synonymous_variant	LOW	ND5	0.0258
HLI-0015	12616	T	C	0	676	synonymous_variant	LOW	ND5	0.0016
HLI-0015	12705	C	T	3	676	synonymous_variant	LOW	ND5	0.4212
HLI-0015	12810	A	G	2	693	synonymous_variant	LOW	ND5	0.0198
HLI-0015	13105	A	G	2	620	missense_variant	MODERATE	ND5	0.076
HLI-0015	13485	A	G	1	666	synonymous_variant	LOW	ND5	0.0122

HLI-0015	13506	C	T	1	729	synonymous_variant	LOW	ND5	0.0506
HLI-0015	13650	C	T	1	586	synonymous_variant	LOW	ND5	0.079
HLI-0015	13789	T	C	0	479	missense_variant	MODERATE	ND5	0.0185
HLI-0015	14000	T	A	0	606	missense_variant	MODERATE	ND5	0.0126
HLI-0015	14178	T	C	1	645	missense_variant	MODERATE	ND6	0.0225
HLI-0015	14560	G	A	1	679	synonymous_variant	LOW	ND6	0.0235
HLI-0015	14766	C	T	0	613	missense_variant	MODERATE	CYTB	0.7696
HLI-0015	14911	C	T	0	662	synonymous_variant	LOW	CYTB	0.0124
HLI-0015	15226	A	G	2	671	synonymous_variant	LOW	CYTB	0.0034
HLI-0015	15326	A	G	0	596	missense_variant	MODERATE	CYTB	0.9868
HLI-0015	15905	T	C	0	637	upstream_gene_variant	MODIFIER	TRNT	0.005
HLI-0015	15949	G	A	2	680	upstream_gene_variant	MODIFIER	TRNT	3.00E-04
HLI-0015	15978	C	T	1	707	upstream_gene_variant	MODIFIER	TRNP	0.0032
HLI-0015	16129	G	A	1	343	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0015	16215	A	G	1	206	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0015	16223	C	T	2	232	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0015	16278	C	T	2	376	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0015	16294	C	T	2	425	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0015	16311	T	C	2	478	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0015	16360	C	T	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0015	16519	T	C	0	205	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0016	73	A	G	0	351	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0016	263	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0016	482	T	C	1	447	upstream_gene_variant	MODIFIER	DLoop	0.0094
HLI-0016	489	T	C	1	473	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0016	750	A	G	0	706	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0016	1438	A	G	0	743	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0016	2706	A	G	0	734	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0016	4580	G	A	1	680	synonymous_variant	LOW	ND2	0.0169
HLI-0016	4769	A	G	0	687	synonymous_variant	LOW	ND2	0.9767
HLI-0016	5783	G	A	1	755	upstream_gene_variant	MODIFIER	TRNC	9.00E-04
HLI-0016	6635	T	C	0	829	synonymous_variant	LOW	COX1	0.0012
HLI-0016	7028	C	T	8	750	synonymous_variant	LOW	COX1	0.8089
HLI-0016	8701	A	G	1	677	missense_variant	MODERATE	ATP6	0.3391
HLI-0016	9540	T	C	0	702	synonymous_variant	LOW	COX3	0.339
HLI-0016	10398	A	G	0	752	missense_variant	MODERATE	ND3	0.445
HLI-0016	10400	C	T	0	758	synonymous_variant	LOW	ND3	0.2131
HLI-0016	10727	C	T	1	606	synonymous_variant	LOW	ND4L	6.00E-04
HLI-0016	10873	T	C	0	647	synonymous_variant	LOW	ND4	0.3389

HLI-0016	11377	G	A	1	646	synonymous_variant	LOW	ND4	0.0125
HLI-0016	11719	G	A	0	725	synonymous_variant	LOW	ND4	0.7756
HLI-0016	12393	C	T	5	678	synonymous_variant	LOW	ND5	1.00E-04
HLI-0016	12705	C	T	2	702	synonymous_variant	LOW	ND5	0.4212
HLI-0016	14766	C	T	5	701	missense_variant	MODERATE	CYTB	0.7696
HLI-0016	14783	T	C	2	800	synonymous_variant	LOW	CYTB	0.2126
HLI-0016	15043	G	A	0	747	synonymous_variant	LOW	CYTB	0.2362
HLI-0016	15301	G	A	0	661	synonymous_variant	LOW	CYTB	0.2912
HLI-0016	15326	A	G	0	716	missense_variant	MODERATE	CYTB	0.9868
HLI-0016	16126	T	C	0	719	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0016	16223	C	T	3	675	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0016	16278	C	T	1	665	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0016	16519	T	C	1	345	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0017	294	T	C	0	298	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0017	6632	T	C	1	878	synonymous_variant	LOW	COX1	6.00E-04
HLI-0017	8185	T	C	0	756	synonymous_variant	LOW	COX2	3.00E-04
HLI-0017	16051	A	G	1	557	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0018	73	A	G	0	334	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0018	151	C	T	1	567	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0018	263	A	G	0	374	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0018	750	A	G	1	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0018	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0018	3010	G	A	0	533	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0018	4769	A	G	1	531	synonymous_variant	LOW	ND2	0.9767
HLI-0018	11893	A	G	1	502	synonymous_variant	LOW	ND4	0.0017
HLI-0018	15326	A	G	0	466	missense_variant	MODERATE	CYTB	0.9868
HLI-0018	16162	A	G	1	234	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0018	16519	T	C	0	270	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0019	73	A	G	0	336	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0019	150	C	T	3	631	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0019	263	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0019	750	A	G	1	689	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0019	1438	A	G	0	753	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0019	1721	C	T	0	731	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0019	2706	A	G	1	719	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0019	3197	T	C	0	689	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0019	3212	C	T	0	770	upstream_gene_variant	MODIFIER	RNR2	0.0012
HLI-0019	3639	A	G	1	720	synonymous_variant	LOW	ND1	2.00E-04
HLI-0019	4732	A	G	1	756	missense_variant	MODERATE	ND2	0.0059

HLI-0019	4769	A	G	1	798	synonymous_variant	LOW	ND2	0.9767
HLI-0019	7028	C	T	6	733	synonymous_variant	LOW	COX1	0.8089
HLI-0019	7768	A	G	3	653	synonymous_variant	LOW	COX2	0.0186
HLI-0019	9477	G	A	1	708	missense_variant	MODERATE	COX3	0.0387
HLI-0019	9682	T	C	2	731	missense_variant	MODERATE	COX3	0.0012
HLI-0019	11467	A	G	3	702	synonymous_variant	LOW	ND4	0.1231
HLI-0019	11719	G	A	1	666	synonymous_variant	LOW	ND4	0.7756
HLI-0019	12136	T	C	0	758	synonymous_variant	LOW	ND4	0.0016
HLI-0019	12308	A	G	1	671	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0019	12372	G	A	0	724	synonymous_variant	LOW	ND5	0.1329
HLI-0019	13617	T	C	0	712	synonymous_variant	LOW	ND5	0.038
HLI-0019	13637	A	G	0	740	missense_variant	MODERATE	ND5	0.0074
HLI-0019	14182	T	C	0	678	synonymous_variant	LOW	ND6	0.0254
HLI-0019	14766	C	T	4	690	missense_variant	MODERATE	CYTB	0.7696
HLI-0019	15326	A	G	0	591	missense_variant	MODERATE	CYTB	0.9868
HLI-0019	16270	C	T	2	726	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0019	16398	G	A	1	591	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0020	263	A	G	0	267	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0020	7229	C	T	2	722	synonymous_variant	LOW	COX1	0.001
HLI-0020	11914	G	A	1	772	synonymous_variant	LOW	ND4	0.1112
HLI-0020	12954	T	C	5	638	synonymous_variant	LOW	ND5	0.0017
HLI-0020	14305	G	A	1	546	synonymous_variant	LOW	ND6	0.0069
HLI-0020	15326	A	G	0	610	missense_variant	MODERATE	CYTB	0.9868
HLI-0020	16235	A	G	3	631	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0020	16291	C	T	2	632	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0021	73	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0021	263	A	G	1	177	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0021	750	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0021	1438	A	G	0	528	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0021	2706	A	G	0	529	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0021	3450	C	T	0	476	synonymous_variant	LOW	ND1	0.0084
HLI-0021	3866	T	C	0	509	missense_variant	MODERATE	ND1	0.0029
HLI-0021	4769	A	G	0	517	synonymous_variant	LOW	ND2	0.9767
HLI-0021	5773	G	A	0	546	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0021	6221	T	C	1	471	synonymous_variant	LOW	COX1	0.0306
HLI-0021	7028	C	T	3	586	synonymous_variant	LOW	COX1	0.8089
HLI-0021	8701	A	G	1	510	missense_variant	MODERATE	ATP6	0.3391
HLI-0021	9055	G	A	1	521	missense_variant	MODERATE	ATP6	0.0425
HLI-0021	9449	C	T	2	614	synonymous_variant	LOW	COX3	0.0125

HLI-0021	9540	T	C	1	490	synonymous_variant	LOW	COX3	0.339
HLI-0021	10086	A	G	1	528	missense_variant	MODERATE	ND3	0.0088
HLI-0021	10373	G	A	3	583	synonymous_variant	LOW	ND3	0.0117
HLI-0021	10398	A	G	2	608	missense_variant	MODERATE	ND3	0.445
HLI-0021	10873	T	C	1	372	synonymous_variant	LOW	ND4	0.3389
HLI-0021	11002	A	G	1	365	synonymous_variant	LOW	ND4	0.0124
HLI-0021	11719	G	A	2	542	synonymous_variant	LOW	ND4	0.7756
HLI-0021	12705	C	T	1	586	synonymous_variant	LOW	ND5	0.4212
HLI-0021	13105	A	G	2	567	missense_variant	MODERATE	ND5	0.076
HLI-0021	13914	C	A	1	434	synonymous_variant	LOW	ND5	0.0091
HLI-0021	14512	T	C	2	512	synonymous_variant	LOW	ND6	3.00E-04
HLI-0021	14766	C	T	1	537	missense_variant	MODERATE	CYTB	0.7696
HLI-0021	14791	C	T	1	574	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0021	15301	G	A	1	481	synonymous_variant	LOW	CYTB	0.2912
HLI-0021	15311	A	G	1	495	missense_variant	MODERATE	CYTB	0.008
HLI-0021	15326	A	G	1	497	missense_variant	MODERATE	CYTB	0.9868
HLI-0021	15824	A	G	0	493	missense_variant	MODERATE	CYTB	0.0083
HLI-0021	15884	G	A	2	550	missense_variant	MODERATE	CYTB	0.0082
HLI-0021	16124	T	C	1	508	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0021	16223	C	T	0	471	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0021	16278	C	T	2	474	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0021	16362	T	C	0	429	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0021	16519	T	C	1	226	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0023	73	A	G	1	253	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0023	146	T	C	2	475	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0023	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0023	285	C	T	1	194	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0023	750	A	G	1	571	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0023	1438	A	G	1	558	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0023	2387	T	C	0	518	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0023	2706	A	G	0	522	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0023	3426	A	G	0	499	synonymous_variant	LOW	ND1	1.00E-04
HLI-0023	4769	A	G	1	534	synonymous_variant	LOW	ND2	0.9767
HLI-0023	5460	G	A	0	494	missense_variant	MODERATE	ND2	0.0651
HLI-0023	6365	T	C	0	515	synonymous_variant	LOW	COX1	0.0026
HLI-0023	7028	C	T	1	570	synonymous_variant	LOW	COX1	0.8089
HLI-0023	8395	C	T	0	489	synonymous_variant	LOW	ATP8	0.001
HLI-0023	8640	C	T	1	478	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0023	10885	T	C	1	521	synonymous_variant	LOW	ND4	0.001

HLI-0023	11467	A	G	1	551	synonymous_variant	LOW	ND4	0.1231
HLI-0023	11566	A	G	0	538	synonymous_variant	LOW	ND4	8.00E-04
HLI-0023	11719	G	A	0	526	synonymous_variant	LOW	ND4	0.7756
HLI-0023	11969	G	A	0	477	missense_variant	MODERATE	ND4	0.0135
HLI-0023	12308	A	G	0	520	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0023	12372	G	A	0	512	synonymous_variant	LOW	ND5	0.1329
HLI-0023	12879	T	C	2	577	synonymous_variant	LOW	ND5	0.0058
HLI-0023	13104	A	G	0	546	synonymous_variant	LOW	ND5	0.0057
HLI-0023	14766	C	T	4	558	missense_variant	MODERATE	CYTB	0.7696
HLI-0023	15110	G	A	0	577	missense_variant	MODERATE	CYTB	0.009
HLI-0023	15148	G	A	1	624	synonymous_variant	LOW	CYTB	0.0058
HLI-0023	15172	G	A	1	619	synonymous_variant	LOW	CYTB	0.0075
HLI-0023	15326	A	G	0	451	missense_variant	MODERATE	CYTB	0.9868
HLI-0023	15954	A	C	1	542	upstream_gene_variant	MODIFIER	Unannotated	0.0036
HLI-0023	16104	C	T	26	469	upstream_gene_variant	MODIFIER	DLoop	0.0023
HLI-0023	16111	C	T	1	491	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0023	16249	T	C	1	544	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0023	16327	C	T	1	524	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0023	16519	T	C	1	244	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0024	73	A	G	0	251	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0024	185	G	A	0	375	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0024	228	G	A	0	312	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0024	263	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0024	295	C	T	0	192	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0024	462	C	T	3	348	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0024	489	T	C	0	426	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0024	750	A	G	0	538	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0024	1438	A	G	1	593	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0024	2706	A	G	4	565	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0024	3010	G	A	1	587	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0024	4216	T	C	2	497	missense_variant	MODERATE	ND1	0.0991
HLI-0024	4769	A	G	0	524	synonymous_variant	LOW	ND2	0.9767
HLI-0024	6617	C	T	4	566	synonymous_variant	LOW	COX1	2.00E-04
HLI-0024	7028	C	T	2	616	synonymous_variant	LOW	COX1	0.8089
HLI-0024	10398	A	G	1	532	missense_variant	MODERATE	ND3	0.445
HLI-0024	11251	A	G	1	507	synonymous_variant	LOW	ND4	0.0932
HLI-0024	11719	G	A	0	534	synonymous_variant	LOW	ND4	0.7756
HLI-0024	12612	A	G	0	623	synonymous_variant	LOW	ND5	0.0506
HLI-0024	13708	G	A	0	484	missense_variant	MODERATE	ND5	0.0717

HLI-0024	13763	C	T	3	541	missense_variant	MODERATE	ND5	1.00E-04
HLI-0024	13934	C	T	0	484	missense_variant	MODERATE	ND5	0.0122
HLI-0024	14766	C	T	2	562	missense_variant	MODERATE	CYTB	0.7696
HLI-0024	14798	T	C	0	646	missense_variant	MODERATE	CYTB	0.0651
HLI-0024	15326	A	G	0	485	missense_variant	MODERATE	CYTB	0.9868
HLI-0024	15452	C	A	4	466	missense_variant	MODERATE	CYTB	0.0933
HLI-0024	16069	C	T	2	533	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0024	16126	T	C	0	519	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0024	16316	A	G	0	506	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0024	16390	G	A	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0024	16519	T	C	0	246	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0025	152	T	C	0	511	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0025	263	A	G	0	184	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0025	477	T	C	1	457	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0025	750	A	G	0	628	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0025	1438	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0025	3010	G	A	0	578	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0025	4769	A	G	0	581	synonymous_variant	LOW	ND2	0.9767
HLI-0025	15326	A	G	2	553	missense_variant	MODERATE	CYTB	0.9868
HLI-0025	16519	T	C	2	228	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0026	73	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0026	146	T	C	1	495	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0026	150	C	T	1	512	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0026	195	T	C	1	463	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0026	199	T	C	1	457	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0026	263	A	G	0	205	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0026	456	C	T	5	499	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0026	499	G	A	3	614	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0026	750	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0026	769	G	A	0	737	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0026	870	C	T	0	650	upstream_gene_variant	MODIFIER	RNR1	0.0013
HLI-0026	1018	G	A	1	647	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0026	1438	A	G	0	634	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0026	2159	T	C	0	590	upstream_gene_variant	MODIFIER	RNR2	7.00E-04
HLI-0026	2332	C	T	0	606	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0026	2416	T	C	0	647	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0026	2706	A	G	0	662	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0026	3254	C	A	4	642	upstream_gene_variant	MODIFIER	TRNL1	5.00E-04
HLI-0026	3434	A	G	1	614	missense_variant	MODERATE	ND1	0.0088

HLI-0026	3594	C	T	3	607	synonymous_variant	LOW	ND1	0.0789
HLI-0026	3693	G	A	0	656	synonymous_variant	LOW	ND1	0.0091
HLI-0026	4104	A	G	1	562	synonymous_variant	LOW	ND1	0.0785
HLI-0026	4769	A	G	2	573	synonymous_variant	LOW	ND2	0.9767
HLI-0026	6231	C	T	1	621	synonymous_variant	LOW	COX1	9.00E-04
HLI-0026	7028	C	T	2	687	synonymous_variant	LOW	COX1	0.8089
HLI-0026	7256	C	T	1	581	synonymous_variant	LOW	COX1	0.0784
HLI-0026	7521	G	A	2	547	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0026	8206	G	A	0	621	synonymous_variant	LOW	COX2	0.0287
HLI-0026	8701	A	G	0	621	missense_variant	MODERATE	ATP6	0.3391
HLI-0026	9221	A	G	1	628	synonymous_variant	LOW	COX3	0.0277
HLI-0026	9540	T	C	3	653	synonymous_variant	LOW	COX3	0.339
HLI-0026	9554	G	A	3	647	synonymous_variant	LOW	COX3	0.014
HLI-0026	9941	A	G	2	709	synonymous_variant	LOW	COX3	0.001
HLI-0026	10115	T	C	1	700	synonymous_variant	LOW	ND3	0.0278
HLI-0026	10398	A	G	1	648	missense_variant	MODERATE	ND3	0.445
HLI-0026	10873	T	C	0	485	synonymous_variant	LOW	ND4	0.3389
HLI-0026	10955	C	T	6	447	synonymous_variant	LOW	ND4	5.00E-04
HLI-0026	11353	T	C	1	620	synonymous_variant	LOW	ND4	0.0029
HLI-0026	11719	G	A	0	680	synonymous_variant	LOW	ND4	0.7756
HLI-0026	11944	T	C	1	585	synonymous_variant	LOW	ND4	0.0331
HLI-0026	12705	C	T	1	641	synonymous_variant	LOW	ND5	0.4212
HLI-0026	13590	G	A	1	635	synonymous_variant	LOW	ND5	0.0586
HLI-0026	13650	C	T	1	642	synonymous_variant	LOW	ND5	0.079
HLI-0026	14766	C	T	2	726	missense_variant	MODERATE	CYTB	0.7696
HLI-0026	14845	C	T	2	750	synonymous_variant	LOW	CYTB	7.00E-04
HLI-0026	15301	G	A	0	607	synonymous_variant	LOW	CYTB	0.2912
HLI-0026	15326	A	G	0	659	missense_variant	MODERATE	CYTB	0.9868
HLI-0026	15777	G	C	1	641	missense_variant	MODERATE	CYTB	5.00E-04
HLI-0026	16129	G	A	0	358	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0026	16278	C	T	0	400	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0026	16300	A	G	1	459	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0026	16354	C	T	1	393	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0026	16390	G	A	1	478	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0026	16399	A	G	0	459	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0026	16519	T	C	0	210	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0027	263	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0027	750	A	G	0	669	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0027	1438	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0027	2755	A	G	7	678	upstream_gene_variant	MODIFIER	RNR2	0.0047
HLI-0027	4769	A	G	0	574	synonymous_variant	LOW	ND2	0.9767
HLI-0027	15326	A	G	0	595	missense_variant	MODERATE	CYTB	0.9868
HLI-0027	16299	A	G	1	570	upstream_gene_variant	MODIFIER	DLoop	0.0032
HLI-0027	16519	T	C	1	371	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0028	207	G	A	2	455	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0028	263	A	G	0	170	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0028	456	C	T	4	455	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0028	750	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0028	1438	A	G	1	598	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0028	4769	A	G	1	490	synonymous_variant	LOW	ND2	0.9767
HLI-0028	10410	T	C	1	550	upstream_gene_variant	MODIFIER	TRNR	0.0049
HLI-0028	13725	C	T	1	489	synonymous_variant	LOW	ND5	4.00E-04
HLI-0028	15326	A	G	0	496	missense_variant	MODERATE	CYTB	0.9868
HLI-0028	16304	T	C	0	461	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0028	16311	T	C	0	481	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0029	73	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0029	150	C	T	1	477	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0029	195	T	C	0	452	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0029	198	C	T	0	447	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0029	263	A	G	0	157	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0029	499	G	A	3	388	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0029	750	A	G	2	582	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0029	1438	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0029	2352	T	C	0	612	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0029	2706	A	G	0	560	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0029	4769	A	G	1	501	synonymous_variant	LOW	ND2	0.9767
HLI-0029	4823	T	C	0	554	synonymous_variant	LOW	ND2	0.0049
HLI-0029	6413	T	C	0	559	synonymous_variant	LOW	COX1	0.0062
HLI-0029	7028	C	T	2	601	synonymous_variant	LOW	COX1	0.8089
HLI-0029	8701	A	G	2	592	missense_variant	MODERATE	ATP6	0.3391
HLI-0029	9540	T	C	0	562	synonymous_variant	LOW	COX3	0.339
HLI-0029	10398	A	G	0	556	missense_variant	MODERATE	ND3	0.445
HLI-0029	10819	A	G	0	573	synonymous_variant	LOW	ND4	0.0228
HLI-0029	10873	T	C	1	573	synonymous_variant	LOW	ND4	0.3389
HLI-0029	11719	G	A	0	540	synonymous_variant	LOW	ND4	0.7756
HLI-0029	12705	C	T	0	606	synonymous_variant	LOW	ND5	0.4212
HLI-0029	13105	A	G	0	520	missense_variant	MODERATE	ND5	0.076
HLI-0029	14212	T	C	1	548	synonymous_variant	LOW	ND6	0.0204

HLI-0029	14766	C	T	1	563	missense_variant	MODERATE	CYTB	0.7696
HLI-0029	14869	G	A	1	616	synonymous_variant	LOW	CYTB	0.0023
HLI-0029	14905	G	A	1	666	synonymous_variant	LOW	CYTB	0.0526
HLI-0029	15301	G	A	2	541	synonymous_variant	LOW	CYTB	0.2912
HLI-0029	15326	A	G	1	574	missense_variant	MODERATE	CYTB	0.9868
HLI-0029	15670	T	C	0	540	synonymous_variant	LOW	CYTB	0.0176
HLI-0029	16223	C	T	7	542	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0029	16320	C	T	2	499	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0029	16399	A	G	1	467	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0029	16519	T	C	0	229	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0030	73	A	G	0	257	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0030	709	G	A	1	554	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0030	750	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0030	930	G	A	2	566	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0030	1438	A	G	0	569	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0030	1888	G	A	2	524	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0030	2706	A	G	1	482	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0030	4216	T	C	2	501	missense_variant	MODERATE	ND1	0.0991
HLI-0030	4769	A	G	0	534	synonymous_variant	LOW	ND2	0.9767
HLI-0030	4917	A	G	1	581	missense_variant	MODERATE	ND2	0.0477
HLI-0030	5147	G	A	0	434	synonymous_variant	LOW	ND2	0.0437
HLI-0030	7028	C	T	6	586	synonymous_variant	LOW	COX1	0.8089
HLI-0030	8697	G	A	0	623	synonymous_variant	LOW	ATP6	0.0466
HLI-0030	10463	T	C	1	601	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0030	11251	A	G	2	557	synonymous_variant	LOW	ND4	0.0932
HLI-0030	11719	G	A	0	574	synonymous_variant	LOW	ND4	0.7756
HLI-0030	11812	A	G	0	540	synonymous_variant	LOW	ND4	0.0332
HLI-0030	13368	G	A	1	592	synonymous_variant	LOW	ND5	0.0495
HLI-0030	14233	A	G	3	568	synonymous_variant	LOW	ND6	0.0369
HLI-0030	14766	C	T	2	582	missense_variant	MODERATE	CYTB	0.7696
HLI-0030	14905	G	A	2	688	synonymous_variant	LOW	CYTB	0.0526
HLI-0030	15172	G	A	4	498	synonymous_variant	LOW	CYTB	0.0075
HLI-0030	15326	A	G	0	426	missense_variant	MODERATE	CYTB	0.9868
HLI-0030	15452	C	A	1	423	missense_variant	MODERATE	CYTB	0.0933
HLI-0030	15607	A	G	2	490	synonymous_variant	LOW	CYTB	0.0508
HLI-0030	15928	G	A	3	600	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0030	16126	T	C	0	547	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0030	16294	C	T	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0030	16296	C	T	1	481	upstream_gene_variant	MODIFIER	DLoop	0.0228

HLI-0030	16304	T	C	1	506	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0030	16519	T	C	1	219	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0031	263	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0031	750	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0031	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0031	4769	A	G	0	571	synonymous_variant	LOW	ND2	0.9767
HLI-0031	6647	A	G	0	710	synonymous_variant	LOW	COX1	0.0033
HLI-0031	13785	C	T	3	525	synonymous_variant	LOW	ND5	4.00E-04
HLI-0031	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0031	15927	G	A	0	502	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0031	16093	T	C	21	514	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0031	16311	T	C	0	501	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0031	16519	T	C	1	258	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0032	73	A	G	0	298	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0032	263	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0032	750	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0032	1438	A	G	0	676	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0032	1822	T	C	0	674	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0032	3010	G	A	1	672	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0032	4769	A	G	2	574	synonymous_variant	LOW	ND2	0.9767
HLI-0032	6365	T	C	2	663	synonymous_variant	LOW	COX1	0.0026
HLI-0032	15326	A	G	0	483	missense_variant	MODERATE	CYTB	0.9868
HLI-0032	16162	A	G	2	747	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0032	16209	T	C	0	651	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0032	16311	T	C	1	485	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0032	16519	T	C	0	294	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0033	263	A	G	0	305	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0033	750	A	G	0	710	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0033	1438	A	G	0	741	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0033	4769	A	G	2	632	synonymous_variant	LOW	ND2	0.9767
HLI-0033	8200	T	C	6	761	synonymous_variant	LOW	COX2	0.0025
HLI-0033	12133	C	T	13	685	synonymous_variant	LOW	ND4	8.00E-04
HLI-0033	14979	T	C	9	753	missense_variant	MODERATE	CYTB	0.0034
HLI-0033	15326	A	G	1	637	missense_variant	MODERATE	CYTB	0.9868
HLI-0033	16519	T	C	1	298	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0034	73	A	G	0	385	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0034	150	C	T	0	680	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0034	152	T	C	0	681	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0034	263	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0034	295	C	T	0	280	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0034	489	T	C	0	522	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0034	750	A	G	1	719	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0034	1438	A	G	0	781	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0034	2706	A	G	0	811	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0034	4216	T	C	3	742	missense_variant	MODERATE	ND1	0.0991
HLI-0034	4769	A	G	1	685	synonymous_variant	LOW	ND2	0.9767
HLI-0034	5633	C	T	4	750	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0034	7028	C	T	1	789	synonymous_variant	LOW	COX1	0.8089
HLI-0034	7476	C	T	0	813	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0034	8911	T	C	1	784	synonymous_variant	LOW	ATP6	0.0028
HLI-0034	10172	G	A	1	776	synonymous_variant	LOW	ND3	0.0084
HLI-0034	10398	A	G	1	739	missense_variant	MODERATE	ND3	0.445
HLI-0034	11251	A	G	1	704	synonymous_variant	LOW	ND4	0.0932
HLI-0034	11719	G	A	0	754	synonymous_variant	LOW	ND4	0.7756
HLI-0034	12612	A	G	3	775	synonymous_variant	LOW	ND5	0.0506
HLI-0034	13708	G	A	0	698	missense_variant	MODERATE	ND5	0.0717
HLI-0034	14766	C	T	2	731	missense_variant	MODERATE	CYTB	0.7696
HLI-0034	15257	G	A	1	733	missense_variant	MODERATE	CYTB	0.0155
HLI-0034	15326	A	G	0	758	missense_variant	MODERATE	CYTB	0.9868
HLI-0034	15452	C	A	6	722	missense_variant	MODERATE	CYTB	0.0933
HLI-0034	15812	G	A	0	786	missense_variant	MODERATE	CYTB	0.0096
HLI-0034	16069	C	T	2	733	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0034	16126	T	C	2	769	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0034	16217	T	C	0	786	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0035	73	A	G	0	336	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0035	207	G	A	13	405	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0035	263	A	G	1	282	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0035	321	T	C	1	207	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0035	709	G	A	1	717	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0035	750	A	G	1	740	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0035	930	G	A	3	754	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0035	1438	A	G	0	720	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0035	1888	G	A	0	717	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0035	2706	A	G	1	745	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0035	4216	T	C	1	738	missense_variant	MODERATE	ND1	0.0991
HLI-0035	4769	A	G	1	564	synonymous_variant	LOW	ND2	0.9767
HLI-0035	4917	A	G	0	622	missense_variant	MODERATE	ND2	0.0477
HLI-0035	5147	G	A	1	662	synonymous_variant	LOW	ND2	0.0437

HLI-0035	7028	C	T	1	743	synonymous_variant	LOW	COX1	0.8089
HLI-0035	8697	G	A	2	669	synonymous_variant	LOW	ATP6	0.0466
HLI-0035	10463	T	C	1	739	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0035	11251	A	G	0	699	synonymous_variant	LOW	ND4	0.0932
HLI-0035	11719	G	A	0	678	synonymous_variant	LOW	ND4	0.7756
HLI-0035	11812	A	G	0	706	synonymous_variant	LOW	ND4	0.0332
HLI-0035	13368	G	A	3	731	synonymous_variant	LOW	ND5	0.0495
HLI-0035	14233	A	G	0	713	synonymous_variant	LOW	ND6	0.0369
HLI-0035	14766	C	T	2	715	missense_variant	MODERATE	CYTB	0.7696
HLI-0035	14905	G	A	0	717	synonymous_variant	LOW	CYTB	0.0526
HLI-0035	15326	A	G	0	679	missense_variant	MODERATE	CYTB	0.9868
HLI-0035	15452	C	A	5	643	missense_variant	MODERATE	CYTB	0.0933
HLI-0035	15607	A	G	0	687	synonymous_variant	LOW	CYTB	0.0508
HLI-0035	15928	G	A	1	733	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0035	16126	T	C	1	664	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0035	16294	C	T	0	655	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0035	16296	C	T	0	657	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0035	16304	T	C	0	674	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0035	16519	T	C	0	408	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0036	73	A	G	0	355	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0036	195	T	C	1	485	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0036	263	A	G	0	300	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0036	709	G	A	1	779	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0036	750	A	G	1	796	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0036	1438	A	G	0	743	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0036	1888	G	A	2	817	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0036	2706	A	G	0	733	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0036	4216	T	C	1	785	missense_variant	MODERATE	ND1	0.0991
HLI-0036	4769	A	G	1	694	synonymous_variant	LOW	ND2	0.9767
HLI-0036	4917	A	G	0	650	missense_variant	MODERATE	ND2	0.0477
HLI-0036	5277	T	C	2	702	missense_variant	MODERATE	ND2	0.0022
HLI-0036	5426	T	C	1	733	synonymous_variant	LOW	ND2	0.0091
HLI-0036	6489	C	A	1	725	missense_variant	MODERATE	COX1	0.0016
HLI-0036	7028	C	T	2	755	synonymous_variant	LOW	COX1	0.8089
HLI-0036	8697	G	A	2	664	synonymous_variant	LOW	ATP6	0.0466
HLI-0036	10463	T	C	0	767	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0036	11251	A	G	0	635	synonymous_variant	LOW	ND4	0.0932
HLI-0036	11719	G	A	0	725	synonymous_variant	LOW	ND4	0.7756
HLI-0036	11812	A	G	3	704	synonymous_variant	LOW	ND4	0.0332

HLI-0036	13368	G	A	1	712	synonymous_variant	LOW	ND5	0.0495
HLI-0036	14233	A	G	1	698	synonymous_variant	LOW	ND6	0.0369
HLI-0036	14766	C	T	3	714	missense_variant	MODERATE	CYTB	0.7696
HLI-0036	14905	G	A	1	734	synonymous_variant	LOW	CYTB	0.0526
HLI-0036	15028	C	A	1	766	synonymous_variant	LOW	CYTB	0.0016
HLI-0036	15043	G	A	1	846	synonymous_variant	LOW	CYTB	0.2362
HLI-0036	15326	A	G	0	711	missense_variant	MODERATE	CYTB	0.9868
HLI-0036	15452	C	A	4	661	missense_variant	MODERATE	CYTB	0.0933
HLI-0036	15607	A	G	0	706	synonymous_variant	LOW	CYTB	0.0508
HLI-0036	15928	G	A	0	779	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0036	16126	T	C	0	359	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0036	16294	C	T	0	515	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0036	16298	T	C	0	524	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0036	16519	T	C	1	243	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0037	73	A	G	0	378	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0037	152	T	C	0	673	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0037	263	A	G	0	290	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0037	325	C	T	0	241	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0037	497	C	T	3	529	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0037	750	A	G	1	685	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0037	1189	T	C	1	700	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0037	1438	A	G	1	644	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0037	1811	A	G	1	668	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0037	2706	A	G	0	709	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0037	3480	A	G	0	589	synonymous_variant	LOW	ND1	0.0392
HLI-0037	4769	A	G	1	649	synonymous_variant	LOW	ND2	0.9767
HLI-0037	6260	G	A	0	714	synonymous_variant	LOW	COX1	0.009
HLI-0037	7028	C	T	3	722	synonymous_variant	LOW	COX1	0.8089
HLI-0037	9055	G	A	0	686	missense_variant	MODERATE	ATP6	0.0425
HLI-0037	9698	T	C	1	678	synonymous_variant	LOW	COX3	0.0405
HLI-0037	10029	A	G	0	653	upstream_gene_variant	MODIFIER	TRNG	2.00E-04
HLI-0037	10398	A	G	1	642	missense_variant	MODERATE	ND3	0.445
HLI-0037	10550	A	G	0	719	synonymous_variant	LOW	ND4L	0.0376
HLI-0037	11299	T	C	0	693	synonymous_variant	LOW	ND4	0.0417
HLI-0037	11467	A	G	1	718	synonymous_variant	LOW	ND4	0.1231
HLI-0037	11485	T	C	0	784	synonymous_variant	LOW	ND4	0.0081
HLI-0037	11719	G	A	0	672	synonymous_variant	LOW	ND4	0.7756
HLI-0037	11840	C	T	1	762	synonymous_variant	LOW	ND4	0.0041
HLI-0037	12308	A	G	0	600	upstream_gene_variant	MODIFIER	TRNL2	0.1227

HLI-0037	12372	G	A	0	650	synonymous_variant	LOW	ND5	0.1329
HLI-0037	13740	T	C	1	610	synonymous_variant	LOW	ND5	0.0041
HLI-0037	14167	C	T	1	640	synonymous_variant	LOW	ND6	0.0385
HLI-0037	14766	C	T	4	685	missense_variant	MODERATE	CYTB	0.7696
HLI-0037	14798	T	C	0	768	missense_variant	MODERATE	CYTB	0.0651
HLI-0037	15326	A	G	0	697	missense_variant	MODERATE	CYTB	0.9868
HLI-0037	16224	T	C	1	647	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0037	16311	T	C	2	608	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0037	16519	T	C	0	355	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0038	73	A	G	0	341	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0038	263	A	G	0	218	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0038	338	C	T	1	241	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0038	709	G	A	2	663	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0038	750	A	G	0	709	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0038	1438	A	G	2	643	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0038	1888	G	A	0	639	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0038	2706	A	G	1	684	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0038	4216	T	C	2	662	missense_variant	MODERATE	ND1	0.0991
HLI-0038	4769	A	G	1	582	synonymous_variant	LOW	ND2	0.9767
HLI-0038	4917	A	G	0	604	missense_variant	MODERATE	ND2	0.0477
HLI-0038	6260	G	A	1	692	synonymous_variant	LOW	COX1	0.009
HLI-0038	7028	C	T	4	719	synonymous_variant	LOW	COX1	0.8089
HLI-0038	8697	G	A	0	616	synonymous_variant	LOW	ATP6	0.0466
HLI-0038	10463	T	C	0	700	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0038	11251	A	G	0	657	synonymous_variant	LOW	ND4	0.0932
HLI-0038	11719	G	A	2	674	synonymous_variant	LOW	ND4	0.7756
HLI-0038	11812	A	G	4	687	synonymous_variant	LOW	ND4	0.0332
HLI-0038	12397	A	G	4	599	missense_variant	MODERATE	ND5	0.0069
HLI-0038	13368	G	A	0	667	synonymous_variant	LOW	ND5	0.0495
HLI-0038	14233	A	G	2	613	synonymous_variant	LOW	ND6	0.0369
HLI-0038	14766	C	T	2	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0038	14905	G	A	2	711	synonymous_variant	LOW	CYTB	0.0526
HLI-0038	15326	A	G	1	594	missense_variant	MODERATE	CYTB	0.9868
HLI-0038	15452	C	A	5	625	missense_variant	MODERATE	CYTB	0.0933
HLI-0038	15607	A	G	0	665	synonymous_variant	LOW	CYTB	0.0508
HLI-0038	15928	G	A	3	647	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0038	16126	T	C	0	569	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0038	16294	C	T	0	588	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0038	16296	C	T	0	591	upstream_gene_variant	MODIFIER	DLoop	0.0228

HLI-0038	16519	T	C	1	269	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0039	263	A	G	0	219	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0039	750	A	G	1	388	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0039	1438	A	G	0	523	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0039	4769	A	G	1	425	synonymous_variant	LOW	ND2	0.9767
HLI-0039	6776	T	C	2	360	synonymous_variant	LOW	COX1	0.0226
HLI-0039	7158	A	G	0	492	missense_variant	MODERATE	COX1	7.00E-04
HLI-0039	11086	A	G	2	439	synonymous_variant	LOW	ND4	1.00E-04
HLI-0039	15326	A	G	0	150	missense_variant	MODERATE	CYTB	0.9868
HLI-0039	16519	T	C	0	182	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0040	73	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0040	185	G	A	4	492	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0040	228	G	A	0	383	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0040	263	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0040	295	C	T	0	231	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0040	462	C	T	2	447	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0040	489	T	C	0	508	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0040	750	A	G	0	562	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0040	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0040	3010	G	A	1	577	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0040	4216	T	C	0	476	missense_variant	MODERATE	ND1	0.0991
HLI-0040	4769	A	G	0	548	synonymous_variant	LOW	ND2	0.9767
HLI-0040	7028	C	T	1	554	synonymous_variant	LOW	COX1	0.8089
HLI-0040	10398	A	G	1	641	missense_variant	MODERATE	ND3	0.445
HLI-0040	11251	A	G	2	520	synonymous_variant	LOW	ND4	0.0932
HLI-0040	11719	G	A	0	597	synonymous_variant	LOW	ND4	0.7756
HLI-0040	12612	A	G	9	706	synonymous_variant	LOW	ND5	0.0506
HLI-0040	13708	G	A	0	506	missense_variant	MODERATE	ND5	0.0717
HLI-0040	13934	C	T	0	486	missense_variant	MODERATE	ND5	0.0122
HLI-0040	14605	A	G	0	670	synonymous_variant	LOW	ND6	0.0022
HLI-0040	14766	C	T	0	636	missense_variant	MODERATE	CYTB	0.7696
HLI-0040	14798	T	C	0	733	missense_variant	MODERATE	CYTB	0.0651
HLI-0040	15326	A	G	1	405	missense_variant	MODERATE	CYTB	0.9868
HLI-0040	15452	C	A	3	376	missense_variant	MODERATE	CYTB	0.0933
HLI-0040	16069	C	T	1	666	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0040	16126	T	C	1	673	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0040	16222	C	T	0	562	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0041	263	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0041	456	C	T	4	520	upstream_gene_variant	MODIFIER	DLoop	0.025

HLI-0041	750	A	G	2	714	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0041	1438	A	G	0	778	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0041	2851	A	G	2	691	upstream_gene_variant	MODIFIER	RNR2	9.00E-04
HLI-0041	4095	C	T	1	657	synonymous_variant	LOW	ND1	2.00E-04
HLI-0041	4336	T	C	2	676	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0041	4769	A	G	3	719	synonymous_variant	LOW	ND2	0.9767
HLI-0041	9055	G	A	0	702	missense_variant	MODERATE	ATP6	0.0425
HLI-0041	13105	A	G	0	700	missense_variant	MODERATE	ND5	0.076
HLI-0041	13194	G	A	2	735	synonymous_variant	LOW	ND5	0.0046
HLI-0041	15326	A	G	0	647	missense_variant	MODERATE	CYTB	0.9868
HLI-0041	15833	C	T	1	749	synonymous_variant	LOW	CYTB	0.0051
HLI-0041	16304	T	C	1	630	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0042	73	A	G	0	359	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0042	489	T	C	0	444	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0042	493	A	G	0	456	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0042	750	A	G	2	706	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0042	1438	A	G	0	679	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0042	2706	A	G	0	698	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0042	3552	T	A	1	600	synonymous_variant	LOW	ND1	0.0337
HLI-0042	4242	C	T	1	702	synonymous_variant	LOW	ND1	7.00E-04
HLI-0042	4715	A	G	4	810	synonymous_variant	LOW	ND2	0.0416
HLI-0042	4769	A	G	1	816	synonymous_variant	LOW	ND2	0.9767
HLI-0042	7013	G	A	8	750	synonymous_variant	LOW	COX1	0.0013
HLI-0042	7028	C	T	6	818	synonymous_variant	LOW	COX1	0.8089
HLI-0042	7196	C	A	6	738	synonymous_variant	LOW	COX1	0.0389
HLI-0042	8584	G	A	0	735	missense_variant	MODERATE	ATP6	0.0521
HLI-0042	8701	A	G	0	719	missense_variant	MODERATE	ATP6	0.3391
HLI-0042	9540	T	C	2	793	synonymous_variant	LOW	COX3	0.339
HLI-0042	9545	A	G	2	790	synonymous_variant	LOW	COX3	0.0469
HLI-0042	9557	C	T	3	794	synonymous_variant	LOW	COX3	6.00E-04
HLI-0042	10398	A	G	0	769	missense_variant	MODERATE	ND3	0.445
HLI-0042	10400	C	T	0	777	synonymous_variant	LOW	ND3	0.2131
HLI-0042	10873	T	C	3	713	synonymous_variant	LOW	ND4	0.3389
HLI-0042	11719	G	A	0	693	synonymous_variant	LOW	ND4	0.7756
HLI-0042	11914	G	A	2	714	synonymous_variant	LOW	ND4	0.1112
HLI-0042	12454	G	A	0	790	missense_variant	MODERATE	ND5	6.00E-04
HLI-0042	12705	C	T	1	760	synonymous_variant	LOW	ND5	0.4212
HLI-0042	13263	A	G	2	759	synonymous_variant	LOW	ND5	0.0354
HLI-0042	14318	T	C	0	611	missense_variant	MODERATE	ND6	0.0339

HLI-0042	14766	C	T	3	732	missense_variant	MODERATE	CYTB	0.7696
HLI-0042	14783	T	C	0	824	synonymous_variant	LOW	CYTB	0.2126
HLI-0042	15043	G	A	1	758	synonymous_variant	LOW	CYTB	0.2362
HLI-0042	15301	G	A	0	628	synonymous_variant	LOW	CYTB	0.2912
HLI-0042	15326	A	G	0	685	missense_variant	MODERATE	CYTB	0.9868
HLI-0042	15487	A	T	0	623	synonymous_variant	LOW	CYTB	0.0391
HLI-0042	16223	C	T	3	691	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0042	16298	T	C	1	714	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0042	16325	T	C	14	657	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0042	16327	C	T	0	668	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0042	16519	T	C	1	364	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0043	263	A	G	1	269	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0043	750	A	G	0	705	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0043	1438	A	G	0	809	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0043	4769	A	G	1	763	synonymous_variant	LOW	ND2	0.9767
HLI-0043	11788	C	T	4	726	synonymous_variant	LOW	ND4	7.00E-04
HLI-0043	15326	A	G	1	693	missense_variant	MODERATE	CYTB	0.9868
HLI-0043	16519	T	C	0	380	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0044	152	T	C	21	564	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0044	153	A	G	2	587	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0044	204	T	C	1	525	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0044	263	A	G	1	177	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0044	750	A	G	1	720	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0044	1438	A	G	0	743	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0044	4769	A	G	0	639	synonymous_variant	LOW	ND2	0.9767
HLI-0044	6809	A	G	1	756	synonymous_variant	LOW	COX1	0
HLI-0044	10646	G	A	1	638	synonymous_variant	LOW	ND4L	0.0032
HLI-0044	12576	C	T	0	683	synonymous_variant	LOW	ND5	0
HLI-0044	15326	A	G	1	643	missense_variant	MODERATE	CYTB	0.9868
HLI-0044	16519	T	C	0	288	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0045	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0045	293	T	C	0	258	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0045	750	A	G	1	657	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0045	1438	A	G	0	669	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0045	4769	A	G	0	598	synonymous_variant	LOW	ND2	0.9767
HLI-0045	6776	T	C	2	741	synonymous_variant	LOW	COX1	0.0226
HLI-0045	8937	T	C	0	670	synonymous_variant	LOW	ATP6	0.0016
HLI-0045	12346	C	T	1	620	missense_variant	MODERATE	ND5	0.0056
HLI-0045	15326	A	G	0	582	missense_variant	MODERATE	CYTB	0.9868

HLI-0045	15530	T	C	1	606	synonymous_variant	LOW	CYTB	0.0036
HLI-0045	16209	T	C	0	626	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0045	16519	T	C	0	347	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0046	73	A	G	0	334	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0046	185	G	A	2	558	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0046	188	A	G	3	549	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0046	228	G	A	4	478	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0046	263	A	G	0	172	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0046	295	C	T	1	211	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0046	462	C	T	1	287	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0046	489	T	C	0	360	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0046	750	A	G	0	725	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0046	1438	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0046	2706	A	G	2	757	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0046	3010	G	A	1	742	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0046	4216	T	C	1	728	missense_variant	MODERATE	ND1	0.0991
HLI-0046	4769	A	G	0	685	synonymous_variant	LOW	ND2	0.9767
HLI-0046	7028	C	T	3	783	synonymous_variant	LOW	COX1	0.8089
HLI-0046	10398	A	G	0	735	missense_variant	MODERATE	ND3	0.445
HLI-0046	11002	A	G	1	561	synonymous_variant	LOW	ND4	0.0124
HLI-0046	11251	A	G	0	684	synonymous_variant	LOW	ND4	0.0932
HLI-0046	11719	G	A	1	709	synonymous_variant	LOW	ND4	0.7756
HLI-0046	12612	A	G	16	731	synonymous_variant	LOW	ND5	0.0506
HLI-0046	13032	A	G	17	677	synonymous_variant	LOW	ND5	6.00E-04
HLI-0046	13708	G	A	0	653	missense_variant	MODERATE	ND5	0.0717
HLI-0046	14325	T	C	0	628	missense_variant	MODERATE	ND6	0.001
HLI-0046	14766	C	T	4	752	missense_variant	MODERATE	CYTB	0.7696
HLI-0046	14798	T	C	1	835	missense_variant	MODERATE	CYTB	0.0651
HLI-0046	15326	A	G	0	656	missense_variant	MODERATE	CYTB	0.9868
HLI-0046	15452	C	A	3	666	missense_variant	MODERATE	CYTB	0.0933
HLI-0046	16069	C	T	2	762	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0046	16126	T	C	1	778	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0046	16519	T	C	0	339	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0047	263	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0047	750	A	G	0	748	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0047	1393	G	A	2	779	upstream_gene_variant	MODIFIER	RNR1	0.0017
HLI-0047	1438	A	G	1	837	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0047	4769	A	G	1	680	synonymous_variant	LOW	ND2	0.9767
HLI-0047	6293	T	C	0	767	synonymous_variant	LOW	COX1	0.0036

HLI-0047	6776	T	C	6	800	synonymous_variant	LOW	COX1	0.0226
HLI-0047	14180	T	C	1	702	missense_variant	MODERATE	ND6	0.0036
HLI-0047	15326	A	G	1	642	missense_variant	MODERATE	CYTB	0.9868
HLI-0047	16038	A	G	0	692	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0047	16214	C	T	1	711	upstream_gene_variant	MODIFIER	DLoop	0.008
HLI-0047	16311	T	C	1	718	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0047	16519	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0048	263	A	G	1	257	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0048	750	A	G	0	807	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0048	1438	A	G	0	729	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0048	4769	A	G	3	674	synonymous_variant	LOW	ND2	0.9767
HLI-0048	4793	A	G	4	751	synonymous_variant	LOW	ND2	0.0073
HLI-0048	5348	C	T	14	767	synonymous_variant	LOW	ND2	0.0016
HLI-0048	7521	G	A	8	696	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0048	12351	T	C	0	676	synonymous_variant	LOW	ND5	7.00E-04
HLI-0048	12768	A	G	7	763	synonymous_variant	LOW	ND5	0.0016
HLI-0048	15326	A	G	1	688	missense_variant	MODERATE	CYTB	0.9868
HLI-0048	16042	G	A	3	714	upstream_gene_variant	MODIFIER	DLoop	0.0016
HLI-0048	16519	T	C	1	362	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0049	73	A	G	0	354	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0049	146	T	C	2	645	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0049	153	A	G	2	652	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0049	235	A	G	0	371	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0049	263	A	G	0	320	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0049	663	A	G	1	747	upstream_gene_variant	MODIFIER	RNR1	0.0285
HLI-0049	750	A	G	0	780	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0049	1438	A	G	0	767	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0049	1736	A	G	2	806	upstream_gene_variant	MODIFIER	RNR2	0.0282
HLI-0049	2706	A	G	1	786	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0049	4248	T	C	1	747	synonymous_variant	LOW	ND1	0.0364
HLI-0049	4769	A	G	0	691	synonymous_variant	LOW	ND2	0.9767
HLI-0049	4824	A	G	4	773	missense_variant	MODERATE	ND2	0.0294
HLI-0049	7028	C	T	2	783	synonymous_variant	LOW	COX1	0.8089
HLI-0049	8027	G	A	3	782	missense_variant	MODERATE	COX2	0.0334
HLI-0049	8794	C	T	0	737	missense_variant	MODERATE	ATP6	0.0283
HLI-0049	11653	A	G	0	752	synonymous_variant	LOW	ND4	0.0049
HLI-0049	11719	G	A	2	806	synonymous_variant	LOW	ND4	0.7756
HLI-0049	12007	G	A	2	746	synonymous_variant	LOW	ND4	0.0639
HLI-0049	12705	C	T	3	926	synonymous_variant	LOW	ND5	0.4212

HLI-0049	13731	A	G	0	637	synonymous_variant	LOW	ND5	5.00E-04
HLI-0049	14766	C	T	3	724	missense_variant	MODERATE	CYTB	0.7696
HLI-0049	15326	A	G	0	701	missense_variant	MODERATE	CYTB	0.9868
HLI-0049	16111	C	T	1	747	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0049	16223	C	T	1	760	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0049	16290	C	T	2	680	upstream_gene_variant	MODIFIER	DLoop	0.0394
HLI-0049	16319	G	A	2	669	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0049	16362	T	C	0	656	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0050	263	A	G	1	277	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0050	750	A	G	0	745	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0050	1438	A	G	0	771	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0050	3010	G	A	0	791	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0050	4769	A	G	0	664	synonymous_variant	LOW	ND2	0.9767
HLI-0050	5162	T	C	1	747	synonymous_variant	LOW	ND2	5.00E-04
HLI-0050	7119	G	A	3	693	missense_variant	MODERATE	COX1	9.00E-04
HLI-0050	8311	T	C	0	659	upstream_gene_variant	MODIFIER	TRNK	0.0012
HLI-0050	9923	C	T	0	739	synonymous_variant	LOW	COX3	8.00E-04
HLI-0050	10667	T	C	2	723	synonymous_variant	LOW	ND4L	0.0047
HLI-0050	15082	C	T	1	760	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0050	15326	A	G	1	689	missense_variant	MODERATE	CYTB	0.9868
HLI-0050	16519	T	C	0	293	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0051	263	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0051	750	A	G	0	673	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0051	1438	A	G	0	748	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0051	3010	G	A	1	750	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0051	3796	A	G	0	648	missense_variant	MODERATE	ND1	0.0048
HLI-0051	4769	A	G	0	700	synonymous_variant	LOW	ND2	0.9767
HLI-0051	15326	A	G	1	657	missense_variant	MODERATE	CYTB	0.9868
HLI-0051	16356	T	C	0	606	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0051	16362	T	C	0	629	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0051	16519	T	C	0	238	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0052	152	T	C	72	464	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0052	263	A	G	1	255	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0052	593	T	C	1	514	upstream_gene_variant	MODIFIER	TRNF	0.0041
HLI-0052	750	A	G	1	706	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0052	1438	A	G	1	656	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0052	4769	A	G	1	602	synonymous_variant	LOW	ND2	0.9767
HLI-0052	5912	C	T	2	652	synonymous_variant	LOW	COX1	1.00E-04
HLI-0052	6776	T	C	4	766	synonymous_variant	LOW	COX1	0.0226

HLI-0052	8572	G	A	2	602	missense_variant	MODERATE	ATP6/8	0.0023
HLI-0052	15326	A	G	1	635	missense_variant	MODERATE	CYTB	0.9868
HLI-0052	16311	T	C	0	513	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0052	16519	T	C	1	316	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0053	263	A	G	1	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0053	477	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0053	750	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0053	1438	A	G	0	731	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0053	3010	G	A	1	666	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0053	4769	A	G	0	633	synonymous_variant	LOW	ND2	0.9767
HLI-0053	8994	G	A	0	671	synonymous_variant	LOW	ATP6	0.0167
HLI-0053	9150	A	G	0	675	synonymous_variant	LOW	ATP6	0.0072
HLI-0053	15326	A	G	1	597	missense_variant	MODERATE	CYTB	0.9868
HLI-0053	16263	T	C	1	588	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0053	16519	T	C	0	353	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0054	73	A	G	1	284	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0054	152	T	C	0	462	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0054	199	T	C	1	342	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0054	204	T	C	1	317	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0054	207	G	A	1	307	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0054	250	T	C	0	207	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0054	263	A	G	0	165	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0054	750	A	G	0	684	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0054	1438	A	G	0	700	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0054	1719	G	A	1	672	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0054	2706	A	G	0	725	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0054	4529	A	T	2	660	synonymous_variant	LOW	ND2	0.015
HLI-0054	4561	T	C	2	725	missense_variant	MODERATE	ND2	0.0065
HLI-0054	4769	A	G	0	634	synonymous_variant	LOW	ND2	0.9767
HLI-0054	7028	C	T	4	707	synonymous_variant	LOW	COX1	0.8089
HLI-0054	8251	G	A	2	648	synonymous_variant	LOW	COX2	0.058
HLI-0054	10034	T	C	0	703	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0054	10238	T	C	0	633	synonymous_variant	LOW	ND3	0.0623
HLI-0054	10398	A	G	0	759	missense_variant	MODERATE	ND3	0.445
HLI-0054	11353	T	C	0	639	synonymous_variant	LOW	ND4	0.0029
HLI-0054	11719	G	A	3	642	synonymous_variant	LOW	ND4	0.7756
HLI-0054	12501	G	A	1	769	synonymous_variant	LOW	ND5	0.0258
HLI-0054	12705	C	T	2	715	synonymous_variant	LOW	ND5	0.4212
HLI-0054	13780	A	G	1	494	missense_variant	MODERATE	ND5	0.0179

HLI-0054	14290	T	C	1	588	synonymous_variant	LOW	ND6	0.0012
HLI-0054	14766	C	T	2	653	missense_variant	MODERATE	CYTB	0.7696
HLI-0054	15043	G	A	0	688	synonymous_variant	LOW	CYTB	0.2362
HLI-0054	15326	A	G	0	615	missense_variant	MODERATE	CYTB	0.9868
HLI-0054	15758	A	G	1	715	missense_variant	MODERATE	CYTB	0.0076
HLI-0054	15924	A	G	0	706	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0054	16129	G	A	1	684	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0054	16223	C	T	0	639	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0054	16391	G	A	2	497	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0054	16519	T	C	0	295	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0055	73	A	G	1	368	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0055	185	G	A	1	569	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0055	188	A	G	1	570	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0055	228	G	A	2	427	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0055	263	A	G	0	307	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0055	295	C	T	0	249	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0055	462	C	T	3	480	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0055	489	T	C	2	587	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0055	750	A	G	0	730	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0055	1438	A	G	0	771	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0055	2706	A	G	1	718	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0055	3010	G	A	1	729	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0055	4216	T	C	1	805	missense_variant	MODERATE	ND1	0.0991
HLI-0055	4769	A	G	2	684	synonymous_variant	LOW	ND2	0.9767
HLI-0055	7028	C	T	3	799	synonymous_variant	LOW	COX1	0.8089
HLI-0055	9055	G	A	2	766	missense_variant	MODERATE	ATP6	0.0425
HLI-0055	10398	A	G	1	734	missense_variant	MODERATE	ND3	0.445
HLI-0055	11251	A	G	0	731	synonymous_variant	LOW	ND4	0.0932
HLI-0055	11719	G	A	2	736	synonymous_variant	LOW	ND4	0.7756
HLI-0055	12612	A	G	13	733	synonymous_variant	LOW	ND5	0.0506
HLI-0055	13708	G	A	1	656	missense_variant	MODERATE	ND5	0.0717
HLI-0055	14766	C	T	2	744	missense_variant	MODERATE	CYTB	0.7696
HLI-0055	14798	T	C	1	830	missense_variant	MODERATE	CYTB	0.0651
HLI-0055	14992	T	C	1	770	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0055	15326	A	G	0	705	missense_variant	MODERATE	CYTB	0.9868
HLI-0055	15452	C	A	2	718	missense_variant	MODERATE	CYTB	0.0933
HLI-0055	16069	C	T	1	754	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0055	16126	T	C	3	780	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0055	16519	T	C	0	397	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0056	73	A	G	0	422	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0056	152	T	C	0	684	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0056	195	T	C	0	632	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0056	263	A	G	0	241	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0056	499	G	A	0	523	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0056	750	A	G	0	742	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0056	1438	A	G	0	783	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0056	1811	A	G	1	819	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0056	2706	A	G	0	799	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0056	4646	T	C	1	855	synonymous_variant	LOW	ND2	0.0124
HLI-0056	4769	A	G	1	721	synonymous_variant	LOW	ND2	0.9767
HLI-0056	5999	T	C	2	799	synonymous_variant	LOW	COX1	0.0127
HLI-0056	6047	A	G	2	839	synonymous_variant	LOW	COX1	0.0114
HLI-0056	7028	C	T	3	788	synonymous_variant	LOW	COX1	0.8089
HLI-0056	8818	C	T	0	789	synonymous_variant	LOW	ATP6	0.0061
HLI-0056	9804	G	A	1	830	missense_variant	MODERATE	COX3	0.0028
HLI-0056	11332	C	T	1	749	synonymous_variant	LOW	ND4	0.0115
HLI-0056	11467	A	G	1	780	synonymous_variant	LOW	ND4	0.1231
HLI-0056	11719	G	A	0	777	synonymous_variant	LOW	ND4	0.7756
HLI-0056	12308	A	G	2	735	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0056	12372	G	A	2	849	synonymous_variant	LOW	ND5	0.1329
HLI-0056	12937	A	G	8	727	missense_variant	MODERATE	ND5	0.0026
HLI-0056	14620	C	T	5	794	synonymous_variant	LOW	ND6	0.0126
HLI-0056	14766	C	T	1	765	missense_variant	MODERATE	CYTB	0.7696
HLI-0056	15326	A	G	0	765	missense_variant	MODERATE	CYTB	0.9868
HLI-0056	15693	T	C	2	772	missense_variant	MODERATE	CYTB	0.0114
HLI-0056	16134	C	T	1	761	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0056	16240	A	G	2	744	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0056	16286	C	A	3	763	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0056	16356	T	C	1	674	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0056	16519	T	C	2	406	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0057	73	A	G	0	365	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0057	146	T	C	0	580	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0057	152	T	C	0	601	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0057	195	T	C	0	369	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0057	217	T	C	0	388	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0057	263	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0057	750	A	G	0	791	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0057	769	G	A	0	841	upstream_gene_variant	MODIFIER	RNR1	0.0819

HLI-0057	1018	G	A	1	778	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0057	1438	A	G	0	782	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0057	2416	T	C	1	779	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0057	2706	A	G	0	814	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0057	2789	C	T	0	868	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0057	3594	C	T	1	635	synonymous_variant	LOW	ND1	0.0789
HLI-0057	3918	G	A	0	714	synonymous_variant	LOW	ND1	0.009
HLI-0057	4104	A	G	1	624	synonymous_variant	LOW	ND1	0.0785
HLI-0057	4769	A	G	0	735	synonymous_variant	LOW	ND2	0.9767
HLI-0057	5285	A	G	1	793	synonymous_variant	LOW	ND2	0.0049
HLI-0057	7028	C	T	3	751	synonymous_variant	LOW	COX1	0.8089
HLI-0057	7175	T	C	0	766	synonymous_variant	LOW	COX1	0.0224
HLI-0057	7256	C	T	4	741	synonymous_variant	LOW	COX1	0.0784
HLI-0057	7274	C	T	3	746	synonymous_variant	LOW	COX1	0.0214
HLI-0057	7521	G	A	0	605	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0057	7771	A	G	1	755	synonymous_variant	LOW	COX2	0.0223
HLI-0057	8206	G	A	0	742	synonymous_variant	LOW	COX2	0.0287
HLI-0057	8701	A	G	1	721	missense_variant	MODERATE	ATP6	0.3391
HLI-0057	9221	A	G	1	735	synonymous_variant	LOW	COX3	0.0277
HLI-0057	9540	T	C	0	817	synonymous_variant	LOW	COX3	0.339
HLI-0057	10115	T	C	0	785	synonymous_variant	LOW	ND3	0.0278
HLI-0057	10398	A	G	2	749	missense_variant	MODERATE	ND3	0.445
HLI-0057	10873	T	C	1	742	synonymous_variant	LOW	ND4	0.3389
HLI-0057	11719	G	A	1	782	synonymous_variant	LOW	ND4	0.7756
HLI-0057	11914	G	A	0	828	synonymous_variant	LOW	ND4	0.1112
HLI-0057	11944	T	C	0	832	synonymous_variant	LOW	ND4	0.0331
HLI-0057	12693	A	G	4	836	synonymous_variant	LOW	ND5	0.0205
HLI-0057	12705	C	T	4	917	synonymous_variant	LOW	ND5	0.4212
HLI-0057	13590	G	A	0	717	synonymous_variant	LOW	ND5	0.0586
HLI-0057	13650	C	T	2	752	synonymous_variant	LOW	ND5	0.079
HLI-0057	13803	A	G	2	578	synonymous_variant	LOW	ND5	0.0216
HLI-0057	14566	A	G	1	791	synonymous_variant	LOW	ND6	0.0214
HLI-0057	14766	C	T	1	742	missense_variant	MODERATE	CYTB	0.7696
HLI-0057	15244	A	G	1	748	synonymous_variant	LOW	CYTB	0.0103
HLI-0057	15301	G	A	2	799	synonymous_variant	LOW	CYTB	0.2912
HLI-0057	15326	A	G	0	771	missense_variant	MODERATE	CYTB	0.9868
HLI-0057	15629	T	C	2	750	synonymous_variant	LOW	CYTB	0.0062
HLI-0057	15784	T	C	1	729	synonymous_variant	LOW	CYTB	0.0363
HLI-0057	16223	C	T	2	828	upstream_gene_variant	MODIFIER	DLoop	0.4009

HLI-0057	16278	C	T	0	778	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0057	16294	C	T	0	741	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0057	16309	A	G	1	724	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0057	16390	G	A	2	647	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0057	16519	T	C	2	425	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0058	263	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0058	15326	A	G	0	638	missense_variant	MODERATE	CYTB	0.9868
HLI-0058	16136	T	C	0	657	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0058	16235	A	G	0	681	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0058	16291	C	T	0	695	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0058	16293	A	G	0	694	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0059	73	A	G	0	335	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0059	150	C	T	1	567	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0059	189	A	G	2	555	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0059	263	A	G	1	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0059	497	C	T	5	509	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0059	750	A	G	0	719	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0059	1189	T	C	1	665	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0059	1438	A	G	0	719	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0059	1811	A	G	2	729	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0059	2706	A	G	0	664	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0059	3480	A	G	2	608	synonymous_variant	LOW	ND1	0.0392
HLI-0059	4769	A	G	1	667	synonymous_variant	LOW	ND2	0.9767
HLI-0059	7028	C	T	3	740	synonymous_variant	LOW	COX1	0.8089
HLI-0059	8053	A	G	0	655	synonymous_variant	LOW	COX2	0
HLI-0059	8723	G	A	1	663	missense_variant	MODERATE	ATP6	0.0016
HLI-0059	9055	G	A	1	695	missense_variant	MODERATE	ATP6	0.0425
HLI-0059	9698	T	C	0	668	synonymous_variant	LOW	COX3	0.0405
HLI-0059	10398	A	G	2	676	missense_variant	MODERATE	ND3	0.445
HLI-0059	10550	A	G	1	690	synonymous_variant	LOW	ND4L	0.0376
HLI-0059	11299	T	C	0	666	synonymous_variant	LOW	ND4	0.0417
HLI-0059	11467	A	G	1	724	synonymous_variant	LOW	ND4	0.1231
HLI-0059	11470	A	G	1	736	synonymous_variant	LOW	ND4	0.0029
HLI-0059	11719	G	A	0	687	synonymous_variant	LOW	ND4	0.7756
HLI-0059	11914	G	A	0	717	synonymous_variant	LOW	ND4	0.1112
HLI-0059	12308	A	G	5	658	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0059	12372	G	A	3	698	synonymous_variant	LOW	ND5	0.1329
HLI-0059	14167	C	T	3	699	synonymous_variant	LOW	ND6	0.0385
HLI-0059	14766	C	T	7	619	missense_variant	MODERATE	CYTB	0.7696

HLI-0059	14798	T	C	2	738	missense_variant	MODERATE	CYTB	0.0651
HLI-0059	15191	T	C	2	730	synonymous_variant	LOW	CYTB	0.0014
HLI-0059	15326	A	G	0	636	missense_variant	MODERATE	CYTB	0.9868
HLI-0059	15924	A	G	1	704	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0059	15930	G	A	1	725	upstream_gene_variant	MODIFIER	TRNT	0.0224
HLI-0059	16093	T	C	10	694	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0059	16224	T	C	0	627	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0059	16311	T	C	0	637	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0059	16519	T	C	1	284	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0060	73	A	G	0	349	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0060	146	T	C	0	627	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0060	152	T	C	0	637	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0060	263	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0060	750	A	G	1	695	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0060	1189	T	C	0	703	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0060	1438	A	G	1	705	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0060	1811	A	G	0	785	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0060	2706	A	G	0	686	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0060	3480	A	G	0	611	synonymous_variant	LOW	ND1	0.0392
HLI-0060	4769	A	G	3	687	synonymous_variant	LOW	ND2	0.9767
HLI-0060	7028	C	T	2	729	synonymous_variant	LOW	COX1	0.8089
HLI-0060	9055	G	A	1	719	missense_variant	MODERATE	ATP6	0.0425
HLI-0060	9093	A	G	1	798	synonymous_variant	LOW	ATP6	0.0031
HLI-0060	9698	T	C	0	745	synonymous_variant	LOW	COX3	0.0405
HLI-0060	10398	A	G	0	722	missense_variant	MODERATE	ND3	0.445
HLI-0060	10550	A	G	0	721	synonymous_variant	LOW	ND4L	0.0376
HLI-0060	10685	G	A	0	677	synonymous_variant	LOW	ND4L	0.0055
HLI-0060	11299	T	C	1	664	synonymous_variant	LOW	ND4	0.0417
HLI-0060	11377	G	A	0	729	synonymous_variant	LOW	ND4	0.0125
HLI-0060	11467	A	G	0	691	synonymous_variant	LOW	ND4	0.1231
HLI-0060	11719	G	A	0	687	synonymous_variant	LOW	ND4	0.7756
HLI-0060	12308	A	G	2	660	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0060	12372	G	A	0	700	synonymous_variant	LOW	ND5	0.1329
HLI-0060	14167	C	T	4	657	synonymous_variant	LOW	ND6	0.0385
HLI-0060	14766	C	T	3	735	missense_variant	MODERATE	CYTB	0.7696
HLI-0060	14798	T	C	2	826	missense_variant	MODERATE	CYTB	0.0651
HLI-0060	15326	A	G	0	641	missense_variant	MODERATE	CYTB	0.9868
HLI-0060	16224	T	C	0	672	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0060	16311	T	C	0	637	upstream_gene_variant	MODIFIER	DLoop	0.1969

HLI-0060	16519	T	C	1	383	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0061	73	A	G	0	373	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0061	195	T	C	0	532	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0061	263	A	G	1	244	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0061	709	G	A	0	717	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0061	750	A	G	1	778	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0061	1438	A	G	1	709	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0061	1888	G	A	1	736	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0061	2706	A	G	0	712	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0061	3705	G	A	1	677	synonymous_variant	LOW	ND1	0.0138
HLI-0061	4216	T	C	1	681	missense_variant	MODERATE	ND1	0.0991
HLI-0061	4769	A	G	1	701	synonymous_variant	LOW	ND2	0.9767
HLI-0061	4917	A	G	0	656	missense_variant	MODERATE	ND2	0.0477
HLI-0061	7028	C	T	0	758	synonymous_variant	LOW	COX1	0.8089
HLI-0061	8697	G	A	1	663	synonymous_variant	LOW	ATP6	0.0466
HLI-0061	9899	T	C	1	686	synonymous_variant	LOW	COX3	0.0108
HLI-0061	10463	T	C	1	794	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0061	10940	C	T	4	632	synonymous_variant	LOW	ND4	0
HLI-0061	11251	A	G	0	709	synonymous_variant	LOW	ND4	0.0932
HLI-0061	11719	G	A	1	740	synonymous_variant	LOW	ND4	0.7756
HLI-0061	11770	T	C	1	784	synonymous_variant	LOW	ND4	7.00E-04
HLI-0061	12633	C	A	9	755	synonymous_variant	LOW	ND5	0.0123
HLI-0061	13368	G	A	0	686	synonymous_variant	LOW	ND5	0.0495
HLI-0061	14766	C	T	5	710	missense_variant	MODERATE	CYTB	0.7696
HLI-0061	14905	G	A	1	768	synonymous_variant	LOW	CYTB	0.0526
HLI-0061	15217	G	A	1	688	synonymous_variant	LOW	CYTB	0.0104
HLI-0061	15326	A	G	0	671	missense_variant	MODERATE	CYTB	0.9868
HLI-0061	15452	C	A	3	635	missense_variant	MODERATE	CYTB	0.0933
HLI-0061	15607	A	G	0	704	synonymous_variant	LOW	CYTB	0.0508
HLI-0061	15928	G	A	1	745	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0061	16126	T	C	1	625	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0061	16163	A	G	1	687	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0061	16294	C	T	2	627	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0061	16519	T	C	0	347	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0062	73	A	G	0	405	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0062	152	T	C	3	682	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0062	263	A	G	1	216	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0062	750	A	G	0	736	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0062	921	T	C	1	752	upstream_gene_variant	MODIFIER	RNR1	0.0084

HLI-0062	1438	A	G	0	802	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0062	2706	A	G	0	748	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0062	4769	A	G	1	607	synonymous_variant	LOW	ND2	0.9767
HLI-0062	5147	G	A	1	645	synonymous_variant	LOW	ND2	0.0437
HLI-0062	6680	T	C	0	777	synonymous_variant	LOW	COX1	0.0226
HLI-0062	7028	C	T	0	768	synonymous_variant	LOW	COX1	0.8089
HLI-0062	7229	C	T	1	791	synonymous_variant	LOW	COX1	0.001
HLI-0062	7424	A	G	3	706	synonymous_variant	LOW	COX1	0.0115
HLI-0062	7765	A	G	0	685	synonymous_variant	LOW	COX2	0.0019
HLI-0062	8618	T	C	1	449	missense_variant	MODERATE	ATP6	0.0103
HLI-0062	8701	A	G	2	644	missense_variant	MODERATE	ATP6	0.3391
HLI-0062	9540	T	C	1	775	synonymous_variant	LOW	COX3	0.339
HLI-0062	10398	A	G	1	750	missense_variant	MODERATE	ND3	0.445
HLI-0062	10873	T	C	1	680	synonymous_variant	LOW	ND4	0.3389
HLI-0062	11719	G	A	0	685	synonymous_variant	LOW	ND4	0.7756
HLI-0062	12705	C	T	0	736	synonymous_variant	LOW	ND5	0.4212
HLI-0062	13105	A	G	1	728	missense_variant	MODERATE	ND5	0.076
HLI-0062	13886	T	C	0	563	missense_variant	MODERATE	ND5	0.0088
HLI-0062	14284	C	T	0	666	synonymous_variant	LOW	ND6	0.0087
HLI-0062	14766	C	T	2	704	missense_variant	MODERATE	CYTB	0.7696
HLI-0062	15301	G	A	0	734	synonymous_variant	LOW	CYTB	0.2912
HLI-0062	15326	A	G	0	795	missense_variant	MODERATE	CYTB	0.9868
HLI-0062	15672	T	C	0	735	missense_variant	MODERATE	CYTB	0.0014
HLI-0062	16124	T	C	2	680	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0062	16223	C	T	3	689	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0062	16256	C	T	5	729	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0062	16368	T	C	0	572	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0063	73	A	G	0	377	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0063	200	A	G	7	471	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0063	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0063	750	A	G	1	758	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0063	1438	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0063	3010	G	A	1	702	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0063	4769	A	G	2	696	synonymous_variant	LOW	ND2	0.9767
HLI-0063	5460	G	A	0	733	missense_variant	MODERATE	ND2	0.0651
HLI-0063	15326	A	G	0	692	missense_variant	MODERATE	CYTB	0.9868
HLI-0063	15817	A	G	0	760	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0063	16362	T	C	0	601	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0063	16519	T	C	0	316	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0064	152	T	C	1	597	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0064	263	A	G	1	272	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0064	750	A	G	1	734	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0064	1438	A	G	0	744	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0064	3010	G	A	1	708	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0064	4769	A	G	0	648	synonymous_variant	LOW	ND2	0.9767
HLI-0064	8065	G	A	2	725	synonymous_variant	LOW	COX2	6.00E-04
HLI-0064	15326	A	G	0	678	missense_variant	MODERATE	CYTB	0.9868
HLI-0064	16519	T	C	0	264	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0065	73	A	G	0	303	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0065	152	T	C	0	493	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0065	199	T	C	1	383	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0065	204	T	C	1	376	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0065	207	G	A	1	376	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0065	250	T	C	1	147	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0065	263	A	G	1	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0065	750	A	G	2	691	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0065	1438	A	G	0	733	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0065	1719	G	A	0	673	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0065	2706	A	G	0	663	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0065	4529	A	T	0	654	synonymous_variant	LOW	ND2	0.015
HLI-0065	4769	A	G	1	695	synonymous_variant	LOW	ND2	0.9767
HLI-0065	7028	C	T	3	754	synonymous_variant	LOW	COX1	0.8089
HLI-0065	8251	G	A	3	641	synonymous_variant	LOW	COX2	0.058
HLI-0065	10034	T	C	1	689	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0065	10238	T	C	1	633	synonymous_variant	LOW	ND3	0.0623
HLI-0065	10398	A	G	0	672	missense_variant	MODERATE	ND3	0.445
HLI-0065	11719	G	A	1	659	synonymous_variant	LOW	ND4	0.7756
HLI-0065	12501	G	A	7	726	synonymous_variant	LOW	ND5	0.0258
HLI-0065	12705	C	T	1	786	synonymous_variant	LOW	ND5	0.4212
HLI-0065	13780	A	G	2	413	missense_variant	MODERATE	ND5	0.0179
HLI-0065	14766	C	T	1	661	missense_variant	MODERATE	CYTB	0.7696
HLI-0065	15043	G	A	0	716	synonymous_variant	LOW	CYTB	0.2362
HLI-0065	15326	A	G	0	646	missense_variant	MODERATE	CYTB	0.9868
HLI-0065	15758	A	G	0	695	missense_variant	MODERATE	CYTB	0.0076
HLI-0065	15924	A	G	1	683	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0065	16129	G	A	1	714	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0065	16176	C	T	0	699	upstream_gene_variant	MODIFIER	DLoop	0.0061
HLI-0065	16223	C	T	1	676	upstream_gene_variant	MODIFIER	DLoop	0.4009

HLI-0065	16391	G	A	4	535	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0065	16519	T	C	1	311	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0066	72	T	C	0	334	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0066	204	T	C	0	358	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0066	263	A	G	0	219	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0066	750	A	G	2	728	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0066	1438	A	G	1	747	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0066	2706	A	G	1	674	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0066	4580	G	A	5	721	synonymous_variant	LOW	ND2	0.0169
HLI-0066	4769	A	G	2	639	synonymous_variant	LOW	ND2	0.9767
HLI-0066	7028	C	T	4	702	synonymous_variant	LOW	COX1	0.8089
HLI-0066	8311	T	C	1	606	upstream_gene_variant	MODIFIER	TRNK	0.0012
HLI-0066	15326	A	G	1	621	missense_variant	MODERATE	CYTB	0.9868
HLI-0066	15904	C	T	2	759	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0066	15930	G	A	3	797	upstream_gene_variant	MODIFIER	TRNT	0.0224
HLI-0066	16298	T	C	1	608	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0066	16519	T	C	0	358	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0067	73	A	G	1	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0067	150	C	T	2	517	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0067	189	A	G	3	509	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0067	195	T	C	3	498	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0067	263	A	G	0	216	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0067	750	A	G	0	654	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0067	1438	A	G	1	654	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0067	2352	T	C	2	582	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0067	2706	A	G	10	681	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0067	4769	A	G	2	546	synonymous_variant	LOW	ND2	0.9767
HLI-0067	4823	T	C	1	589	synonymous_variant	LOW	ND2	0.0049
HLI-0067	5396	C	T	2	621	synonymous_variant	LOW	ND2	0
HLI-0067	6044	T	C	3	706	synonymous_variant	LOW	COX1	2.00E-04
HLI-0067	7028	C	T	8	682	synonymous_variant	LOW	COX1	0.8089
HLI-0067	8701	A	G	3	590	missense_variant	MODERATE	ATP6	0.3391
HLI-0067	9540	T	C	4	623	synonymous_variant	LOW	COX3	0.339
HLI-0067	10398	A	G	2	549	missense_variant	MODERATE	ND3	0.445
HLI-0067	10819	A	G	4	630	synonymous_variant	LOW	ND4	0.0228
HLI-0067	10873	T	C	2	685	synonymous_variant	LOW	ND4	0.3389
HLI-0067	11719	G	A	0	600	synonymous_variant	LOW	ND4	0.7756
HLI-0067	12705	C	T	4	699	synonymous_variant	LOW	ND5	0.4212
HLI-0067	13105	A	G	4	705	missense_variant	MODERATE	ND5	0.076

HLI-0067	14212	T	C	5	622	synonymous_variant	LOW	ND6	0.0204
HLI-0067	14766	C	T	2	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0067	14869	G	A	11	693	synonymous_variant	LOW	CYTB	0.0023
HLI-0067	14905	G	A	12	762	synonymous_variant	LOW	CYTB	0.0526
HLI-0067	15301	G	A	5	599	synonymous_variant	LOW	CYTB	0.2912
HLI-0067	15326	A	G	0	656	missense_variant	MODERATE	CYTB	0.9868
HLI-0067	16223	C	T	2	608	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0067	16258	A	T	3	655	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0067	16320	C	T	3	600	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0067	16519	T	C	1	302	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0068	73	A	G	1	356	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0068	150	C	T	2	620	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0068	263	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0068	750	A	G	1	680	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0068	1438	A	G	1	723	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0068	1811	A	G	3	696	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0068	2652	G	A	2	687	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0068	2706	A	G	2	760	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0068	4188	A	G	0	713	synonymous_variant	LOW	ND1	0.003
HLI-0068	4640	C	A	2	707	missense_variant	MODERATE	ND2	0.0029
HLI-0068	4769	A	G	0	657	synonymous_variant	LOW	ND2	0.9767
HLI-0068	5333	T	C	1	624	synonymous_variant	LOW	ND2	3.00E-04
HLI-0068	7028	C	T	6	724	synonymous_variant	LOW	COX1	0.8089
HLI-0068	9656	T	C	3	710	synonymous_variant	LOW	COX3	0.0035
HLI-0068	11467	A	G	0	710	synonymous_variant	LOW	ND4	0.1231
HLI-0068	11719	G	A	1	697	synonymous_variant	LOW	ND4	0.7756
HLI-0068	12308	A	G	1	628	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0068	12372	G	A	1	689	synonymous_variant	LOW	ND5	0.1329
HLI-0068	13743	T	C	1	481	synonymous_variant	LOW	ND5	0.0037
HLI-0068	13980	G	C	0	626	synonymous_variant	LOW	ND5	1.00E-04
HLI-0068	14139	A	G	2	647	synonymous_variant	LOW	ND5	0.0056
HLI-0068	14766	C	T	1	643	missense_variant	MODERATE	CYTB	0.7696
HLI-0068	15326	A	G	0	671	missense_variant	MODERATE	CYTB	0.9868
HLI-0068	15454	T	C	0	660	synonymous_variant	LOW	CYTB	0.0072
HLI-0068	16343	A	G	3	598	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0069	73	A	G	1	360	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0069	152	T	C	0	580	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0069	185	G	A	7	583	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0069	228	G	A	0	238	upstream_gene_variant	MODIFIER	DLoop	0.0255

HLI-0069	263	A	G	2	281	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0069	295	C	T	0	251	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0069	462	C	T	3	509	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0069	489	T	C	2	627	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0069	750	A	G	0	729	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0069	1438	A	G	1	742	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0069	2706	A	G	0	752	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0069	3010	G	A	0	792	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0069	4216	T	C	1	724	missense_variant	MODERATE	ND1	0.0991
HLI-0069	4769	A	G	0	696	synonymous_variant	LOW	ND2	0.9767
HLI-0069	5198	A	G	0	749	synonymous_variant	LOW	ND2	0.0023
HLI-0069	7028	C	T	2	777	synonymous_variant	LOW	COX1	0.8089
HLI-0069	10398	A	G	0	784	missense_variant	MODERATE	ND3	0.445
HLI-0069	11251	A	G	2	700	synonymous_variant	LOW	ND4	0.0932
HLI-0069	11719	G	A	1	738	synonymous_variant	LOW	ND4	0.7756
HLI-0069	12612	A	G	5	733	synonymous_variant	LOW	ND5	0.0506
HLI-0069	13708	G	A	0	691	missense_variant	MODERATE	ND5	0.0717
HLI-0069	14766	C	T	2	829	missense_variant	MODERATE	CYTB	0.7696
HLI-0069	14798	T	C	1	824	missense_variant	MODERATE	CYTB	0.0651
HLI-0069	15326	A	G	0	689	missense_variant	MODERATE	CYTB	0.9868
HLI-0069	15452	C	A	2	715	missense_variant	MODERATE	CYTB	0.0933
HLI-0069	16069	C	T	0	710	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0069	16126	T	C	0	735	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0070	73	A	G	0	395	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0070	146	T	C	2	621	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0070	185	G	A	1	596	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0070	188	A	G	1	594	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0070	222	C	T	1	529	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0070	228	G	A	1	503	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0070	263	A	G	1	136	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0070	295	C	T	0	181	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0070	462	C	T	1	483	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0070	489	T	C	0	544	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0070	750	A	G	2	746	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0070	1438	A	G	1	789	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0070	2706	A	G	0	794	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0070	2707	A	G	0	801	upstream_gene_variant	MODIFIER	RNR2	8.00E-04
HLI-0070	3010	G	A	0	792	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0070	4216	T	C	1	776	missense_variant	MODERATE	ND1	0.0991

HLI-0070	4769	A	G	0	678	synonymous_variant	LOW	ND2	0.9767
HLI-0070	7028	C	T	3	808	synonymous_variant	LOW	COX1	0.8089
HLI-0070	10398	A	G	0	787	missense_variant	MODERATE	ND3	0.445
HLI-0070	10685	G	A	0	690	synonymous_variant	LOW	ND4L	0.0055
HLI-0070	11251	A	G	1	825	synonymous_variant	LOW	ND4	0.0932
HLI-0070	11719	G	A	0	699	synonymous_variant	LOW	ND4	0.7756
HLI-0070	12612	A	G	8	766	synonymous_variant	LOW	ND5	0.0506
HLI-0070	13281	T	C	1	824	synonymous_variant	LOW	ND5	0.0033
HLI-0070	13708	G	A	1	673	missense_variant	MODERATE	ND5	0.0717
HLI-0070	13933	A	G	1	683	missense_variant	MODERATE	ND5	0.0022
HLI-0070	14766	C	T	1	849	missense_variant	MODERATE	CYTB	0.7696
HLI-0070	14798	T	C	0	836	missense_variant	MODERATE	CYTB	0.0651
HLI-0070	15326	A	G	0	757	missense_variant	MODERATE	CYTB	0.9868
HLI-0070	15452	C	A	8	698	missense_variant	MODERATE	CYTB	0.0933
HLI-0070	16069	C	T	2	726	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0070	16126	T	C	1	752	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0070	16519	T	C	1	371	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0071	73	A	G	1	288	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0071	143	G	A	4	371	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0071	189	A	G	0	369	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0071	204	T	C	1	367	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0071	207	G	A	1	366	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0071	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0071	709	G	A	1	748	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0071	750	A	G	0	795	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0071	1243	T	C	2	731	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0071	1438	A	G	0	747	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0071	2706	A	G	2	765	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0071	3505	A	G	0	671	missense_variant	MODERATE	ND1	0.0144
HLI-0071	4769	A	G	0	722	synonymous_variant	LOW	ND2	0.9767
HLI-0071	5046	G	A	1	714	missense_variant	MODERATE	ND2	0.018
HLI-0071	5460	G	A	2	765	missense_variant	MODERATE	ND2	0.0651
HLI-0071	7028	C	T	2	752	synonymous_variant	LOW	COX1	0.8089
HLI-0071	8251	G	A	5	709	synonymous_variant	LOW	COX2	0.058
HLI-0071	8994	G	A	0	729	synonymous_variant	LOW	ATP6	0.0167
HLI-0071	11674	C	T	2	735	synonymous_variant	LOW	ND4	0.0116
HLI-0071	11719	G	A	0	757	synonymous_variant	LOW	ND4	0.7756
HLI-0071	11947	A	G	1	716	synonymous_variant	LOW	ND4	0.011
HLI-0071	12414	T	C	1	705	synonymous_variant	LOW	ND5	0.0139

HLI-0071	12705	C	T	1	757	synonymous_variant	LOW	ND5	0.4212
HLI-0071	14000	T	A	1	631	missense_variant	MODERATE	ND5	0.0126
HLI-0071	14766	C	T	2	734	missense_variant	MODERATE	CYTB	0.7696
HLI-0071	15326	A	G	0	671	missense_variant	MODERATE	CYTB	0.9868
HLI-0071	15884	G	C	1	794	missense_variant	MODERATE	CYTB	0.011
HLI-0071	16145	G	A	0	457	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0071	16223	C	T	1	422	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0071	16292	C	T	0	574	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0071	16320	C	T	0	630	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0071	16519	T	C	0	199	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0072	73	A	G	0	346	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0072	195	T	C	1	464	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0072	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0072	499	G	A	2	499	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0072	750	A	G	0	724	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0072	1438	A	G	0	744	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0072	1811	A	G	0	746	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0072	2706	A	G	2	718	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0072	3672	A	G	0	676	synonymous_variant	LOW	ND1	0.0013
HLI-0072	4646	T	C	2	747	synonymous_variant	LOW	ND2	0.0124
HLI-0072	4769	A	G	1	622	synonymous_variant	LOW	ND2	0.9767
HLI-0072	5999	T	C	1	756	synonymous_variant	LOW	COX1	0.0127
HLI-0072	6047	A	G	3	788	synonymous_variant	LOW	COX1	0.0114
HLI-0072	7028	C	T	5	755	synonymous_variant	LOW	COX1	0.8089
HLI-0072	7705	T	C	1	650	synonymous_variant	LOW	COX2	0.0034
HLI-0072	10876	A	G	1	698	synonymous_variant	LOW	ND4	0.0098
HLI-0072	11143	C	T	1	699	synonymous_variant	LOW	ND4	0.0076
HLI-0072	11176	G	A	2	763	synonymous_variant	LOW	ND4	0.0181
HLI-0072	11332	C	T	0	661	synonymous_variant	LOW	ND4	0.0115
HLI-0072	11339	T	C	0	690	synonymous_variant	LOW	ND4	0.0028
HLI-0072	11467	A	G	0	708	synonymous_variant	LOW	ND4	0.1231
HLI-0072	11719	G	A	2	690	synonymous_variant	LOW	ND4	0.7756
HLI-0072	12308	A	G	1	652	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0072	12372	G	A	1	722	synonymous_variant	LOW	ND5	0.1329
HLI-0072	12609	T	C	3	714	synonymous_variant	LOW	ND5	0.0024
HLI-0072	13708	G	A	2	600	missense_variant	MODERATE	ND5	0.0717
HLI-0072	14620	C	T	3	719	synonymous_variant	LOW	ND6	0.0126
HLI-0072	14766	C	T	5	692	missense_variant	MODERATE	CYTB	0.7696
HLI-0072	15067	T	C	1	754	synonymous_variant	LOW	CYTB	0.0035

HLI-0072	15326	A	G	0	636	missense_variant	MODERATE	CYTB	0.9868
HLI-0072	15693	T	C	1	667	missense_variant	MODERATE	CYTB	0.0114
HLI-0072	16356	T	C	0	533	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0072	16519	T	C	2	326	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0073	263	A	G	1	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0073	750	A	G	0	680	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0073	1438	A	G	0	694	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0073	3010	G	A	2	714	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0073	4131	A	G	1	638	synonymous_variant	LOW	ND1	0.0012
HLI-0073	4769	A	G	1	637	synonymous_variant	LOW	ND2	0.9767
HLI-0073	8116	A	G	2	666	synonymous_variant	LOW	COX2	8.00E-04
HLI-0073	11914	G	A	1	678	synonymous_variant	LOW	ND4	0.1112
HLI-0073	14041	C	T	4	600	missense_variant	MODERATE	ND5	4.00E-04
HLI-0073	15326	A	G	0	667	missense_variant	MODERATE	CYTB	0.9868
HLI-0073	16519	T	C	0	232	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0074	73	A	G	0	150	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0074	93	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0074	95	A	C	0	186	upstream_gene_variant	MODIFIER	DLoop	0.0076
HLI-0074	146	T	C	0	282	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0074	150	C	T	0	294	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0074	152	T	C	0	288	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0074	182	C	T	0	311	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0074	185	G	A	0	313	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0074	195	T	C	1	342	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0074	198	C	T	1	352	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0074	263	A	G	1	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0074	325	C	T	9	236	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0074	680	T	C	0	696	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0074	709	G	A	1	805	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0074	750	A	G	0	765	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0074	769	G	A	0	744	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0074	1018	G	A	0	756	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0074	1438	A	G	0	739	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0074	1442	G	A	0	766	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0074	2332	C	T	1	714	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0074	2416	T	C	1	776	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0074	2706	A	G	1	761	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0074	3200	T	A	0	635	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0074	3594	C	T	0	537	synonymous_variant	LOW	ND1	0.0789

HLI-0074	4104	A	G	0	610	synonymous_variant	LOW	ND1	0.0785
HLI-0074	4769	A	G	1	623	synonymous_variant	LOW	ND2	0.9767
HLI-0074	7028	C	T	1	736	synonymous_variant	LOW	COX1	0.8089
HLI-0074	7211	G	A	0	718	synonymous_variant	LOW	COX1	7.00E-04
HLI-0074	7256	C	T	1	725	synonymous_variant	LOW	COX1	0.0784
HLI-0074	7262	A	G	1	715	synonymous_variant	LOW	COX1	2.00E-04
HLI-0074	7521	G	A	1	584	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0074	7624	T	A	2	720	synonymous_variant	LOW	COX2	0.0047
HLI-0074	8206	G	A	1	680	synonymous_variant	LOW	COX2	0.0287
HLI-0074	8701	A	G	0	670	missense_variant	MODERATE	ATP6	0.3391
HLI-0074	9221	A	G	0	651	synonymous_variant	LOW	COX3	0.0277
HLI-0074	9540	T	C	0	717	synonymous_variant	LOW	COX3	0.339
HLI-0074	10115	T	C	2	773	synonymous_variant	LOW	ND3	0.0278
HLI-0074	10398	A	G	1	702	missense_variant	MODERATE	ND3	0.445
HLI-0074	10873	T	C	0	734	synonymous_variant	LOW	ND4	0.3389
HLI-0074	11719	G	A	1	689	synonymous_variant	LOW	ND4	0.7756
HLI-0074	11944	T	C	0	653	synonymous_variant	LOW	ND4	0.0331
HLI-0074	12236	G	A	1	676	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0074	12705	C	T	0	685	synonymous_variant	LOW	ND5	0.4212
HLI-0074	13590	G	A	0	677	synonymous_variant	LOW	ND5	0.0586
HLI-0074	13650	C	T	3	740	synonymous_variant	LOW	ND5	0.079
HLI-0074	13928	G	C	0	701	missense_variant	MODERATE	ND5	0.0484
HLI-0074	13958	G	C	0	770	missense_variant	MODERATE	ND5	0.0028
HLI-0074	14766	C	T	0	704	missense_variant	MODERATE	CYTB	0.7696
HLI-0074	15110	G	A	0	676	missense_variant	MODERATE	CYTB	0.009
HLI-0074	15217	G	A	1	665	synonymous_variant	LOW	CYTB	0.0104
HLI-0074	15301	G	A	0	717	synonymous_variant	LOW	CYTB	0.2912
HLI-0074	15326	A	G	0	716	missense_variant	MODERATE	CYTB	0.9868
HLI-0074	15849	C	T	1	706	missense_variant	MODERATE	CYTB	0.0027
HLI-0074	16223	C	T	4	694	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0074	16278	C	T	4	641	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0074	16390	G	A	0	433	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0074	16519	T	C	0	277	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0075	152	T	C	1	635	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0075	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0075	750	A	G	1	738	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0075	1438	A	G	0	727	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0075	4769	A	G	0	661	synonymous_variant	LOW	ND2	0.9767
HLI-0075	9071	C	T	2	733	missense_variant	MODERATE	ATP6	3.00E-04

HLI-0075	10394	C	T	0	687	synonymous_variant	LOW	ND3	0.002
HLI-0075	11461	A	T	0	725	synonymous_variant	LOW	ND4	0
HLI-0075	15326	A	G	0	658	missense_variant	MODERATE	CYTB	0.9868
HLI-0075	16519	T	C	0	365	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0076	263	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0076	327	C	T	0	244	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0076	750	A	G	0	716	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0076	1438	A	G	1	764	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0076	3010	G	A	1	776	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0076	4769	A	G	0	729	synonymous_variant	LOW	ND2	0.9767
HLI-0076	6620	T	C	8	729	synonymous_variant	LOW	COX1	0.0128
HLI-0076	11428	C	T	1	764	synonymous_variant	LOW	ND4	5.00E-04
HLI-0076	15326	A	G	2	726	missense_variant	MODERATE	CYTB	0.9868
HLI-0076	16324	T	C	0	511	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0076	16519	T	C	0	247	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0077	73	A	G	0	358	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0077	152	T	C	0	630	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0077	263	A	G	1	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0077	750	A	G	2	696	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0077	1438	A	G	1	755	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0077	1700	T	C	2	732	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0077	2706	A	G	1	789	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0077	3197	T	C	3	652	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0077	3745	G	A	1	667	missense_variant	MODERATE	ND1	0.0021
HLI-0077	3816	A	G	1	713	synonymous_variant	LOW	ND1	0.0042
HLI-0077	4769	A	G	0	720	synonymous_variant	LOW	ND2	0.9767
HLI-0077	5495	T	C	2	729	synonymous_variant	LOW	ND2	0.0051
HLI-0077	7028	C	T	2	789	synonymous_variant	LOW	COX1	0.8089
HLI-0077	9477	G	A	1	646	missense_variant	MODERATE	COX3	0.0387
HLI-0077	11467	A	G	4	668	synonymous_variant	LOW	ND4	0.1231
HLI-0077	11719	G	A	3	709	synonymous_variant	LOW	ND4	0.7756
HLI-0077	12308	A	G	1	713	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0077	12372	G	A	0	745	synonymous_variant	LOW	ND5	0.1329
HLI-0077	13617	T	C	0	647	synonymous_variant	LOW	ND5	0.038
HLI-0077	14766	C	T	2	700	missense_variant	MODERATE	CYTB	0.7696
HLI-0077	14793	A	G	2	767	missense_variant	MODERATE	CYTB	0.0199
HLI-0077	15218	A	G	1	709	missense_variant	MODERATE	CYTB	0.0169
HLI-0077	15326	A	G	0	686	missense_variant	MODERATE	CYTB	0.9868
HLI-0077	15924	A	G	0	737	upstream_gene_variant	MODIFIER	TRNT	0.0354

HLI-0077	16256	C	T	0	695	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0077	16270	C	T	0	748	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0077	16399	A	G	0	605	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0078	93	A	G	3	463	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0078	263	A	G	0	283	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0078	750	A	G	2	738	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0078	1438	A	G	0	734	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0078	4769	A	G	1	651	synonymous_variant	LOW	ND2	0.9767
HLI-0078	6776	T	C	4	824	synonymous_variant	LOW	COX1	0.0226
HLI-0078	8718	A	G	1	665	synonymous_variant	LOW	ATP6	0.0025
HLI-0078	15326	A	G	0	690	missense_variant	MODERATE	CYTB	0.9868
HLI-0078	15859	A	G	0	722	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0078	16129	G	A	2	648	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0078	16519	T	C	3	402	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0079	73	A	G	0	369	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0079	150	C	T	1	635	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0079	207	G	A	2	481	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0079	263	A	G	0	330	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0079	750	A	G	0	817	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0079	1438	A	G	0	803	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0079	2706	A	G	0	761	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0079	3197	T	C	2	718	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0079	4769	A	G	0	681	synonymous_variant	LOW	ND2	0.9767
HLI-0079	5656	A	G	3	709	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0079	7028	C	T	1	827	synonymous_variant	LOW	COX1	0.8089
HLI-0079	7385	A	G	0	719	synonymous_variant	LOW	COX1	0.0032
HLI-0079	7768	A	G	1	721	synonymous_variant	LOW	COX2	0.0186
HLI-0079	9477	G	A	1	671	missense_variant	MODERATE	COX3	0.0387
HLI-0079	10907	T	C	0	661	missense_variant	MODERATE	ND4	0.0022
HLI-0079	10927	T	C	1	667	synonymous_variant	LOW	ND4	0.0044
HLI-0079	11467	A	G	1	754	synonymous_variant	LOW	ND4	0.1231
HLI-0079	11719	G	A	0	718	synonymous_variant	LOW	ND4	0.7756
HLI-0079	12308	A	G	2	728	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0079	12372	G	A	0	783	synonymous_variant	LOW	ND5	0.1329
HLI-0079	12618	G	A	2	798	synonymous_variant	LOW	ND5	0.0137
HLI-0079	13617	T	C	0	723	synonymous_variant	LOW	ND5	0.038
HLI-0079	14182	T	C	3	674	synonymous_variant	LOW	ND6	0.0254
HLI-0079	14766	C	T	3	737	missense_variant	MODERATE	CYTB	0.7696
HLI-0079	15326	A	G	0	713	missense_variant	MODERATE	CYTB	0.9868

HLI-0079	16144	T	C	0	449	upstream_gene_variant	MODIFIER	DLoop	0.0047
HLI-0079	16270	C	T	5	603	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0080	263	A	G	0	267	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0080	750	A	G	1	689	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0080	1438	A	G	0	750	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0080	4769	A	G	1	610	synonymous_variant	LOW	ND2	0.9767
HLI-0080	4793	A	G	0	670	synonymous_variant	LOW	ND2	0.0073
HLI-0080	15326	A	G	0	695	missense_variant	MODERATE	CYTB	0.9868
HLI-0080	16519	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0081	73	A	G	0	333	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0081	263	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0081	750	A	G	1	690	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0081	1438	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0081	2706	A	G	1	665	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0081	3441	A	G	2	583	synonymous_variant	LOW	ND1	3.00E-04
HLI-0081	3450	C	T	2	608	synonymous_variant	LOW	ND1	0.0084
HLI-0081	4769	A	G	2	646	synonymous_variant	LOW	ND2	0.9767
HLI-0081	5773	G	A	1	732	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0081	6221	T	C	0	645	synonymous_variant	LOW	COX1	0.0306
HLI-0081	7028	C	T	1	711	synonymous_variant	LOW	COX1	0.8089
HLI-0081	8210	A	G	0	634	missense_variant	MODERATE	COX2	1.00E-04
HLI-0081	8701	A	G	1	645	missense_variant	MODERATE	ATP6	0.3391
HLI-0081	9449	C	T	2	647	synonymous_variant	LOW	COX3	0.0125
HLI-0081	9540	T	C	1	661	synonymous_variant	LOW	COX3	0.339
HLI-0081	10086	A	G	3	647	missense_variant	MODERATE	ND3	0.0088
HLI-0081	10373	G	A	0	647	synonymous_variant	LOW	ND3	0.0117
HLI-0081	10398	A	G	1	684	missense_variant	MODERATE	ND3	0.445
HLI-0081	10873	T	C	0	439	synonymous_variant	LOW	ND4	0.3389
HLI-0081	11002	A	G	0	482	synonymous_variant	LOW	ND4	0.0124
HLI-0081	11719	G	A	0	671	synonymous_variant	LOW	ND4	0.7756
HLI-0081	11800	A	G	3	696	synonymous_variant	LOW	ND4	0.0052
HLI-0081	11944	T	C	0	628	synonymous_variant	LOW	ND4	0.0331
HLI-0081	12705	C	T	0	779	synonymous_variant	LOW	ND5	0.4212
HLI-0081	13105	A	G	1	667	missense_variant	MODERATE	ND5	0.076
HLI-0081	13708	G	A	2	559	missense_variant	MODERATE	ND5	0.0717
HLI-0081	13914	C	A	3	546	synonymous_variant	LOW	ND5	0.0091
HLI-0081	14766	C	T	1	701	missense_variant	MODERATE	CYTB	0.7696
HLI-0081	15262	T	C	1	628	synonymous_variant	LOW	CYTB	0.0036
HLI-0081	15301	G	A	1	670	synonymous_variant	LOW	CYTB	0.2912

HLI-0081	15311	A	G	1	674	missense_variant	MODERATE	CYTB	0.008
HLI-0081	15326	A	G	1	665	missense_variant	MODERATE	CYTB	0.9868
HLI-0081	15824	A	G	1	702	missense_variant	MODERATE	CYTB	0.0083
HLI-0081	16093	T	C	15	610	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0081	16124	T	C	1	663	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0081	16223	C	T	0	628	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0081	16278	C	T	1	659	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0081	16519	T	C	0	264	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0082	73	A	G	0	352	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0082	146	T	C	1	588	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0082	152	T	C	1	596	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0082	263	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0082	750	A	G	1	689	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0082	1189	T	C	0	686	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0082	1438	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0082	1811	A	G	1	657	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0082	2706	A	G	1	679	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0082	3480	A	G	1	608	synonymous_variant	LOW	ND1	0.0392
HLI-0082	4769	A	G	0	654	synonymous_variant	LOW	ND2	0.9767
HLI-0082	7028	C	T	1	692	synonymous_variant	LOW	COX1	0.8089
HLI-0082	7521	G	A	0	638	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0082	9055	G	A	0	674	missense_variant	MODERATE	ATP6	0.0425
HLI-0082	9093	A	G	1	758	synonymous_variant	LOW	ATP6	0.0031
HLI-0082	9698	T	C	0	695	synonymous_variant	LOW	COX3	0.0405
HLI-0082	10398	A	G	0	653	missense_variant	MODERATE	ND3	0.445
HLI-0082	10550	A	G	1	647	synonymous_variant	LOW	ND4L	0.0376
HLI-0082	11299	T	C	1	687	synonymous_variant	LOW	ND4	0.0417
HLI-0082	11377	G	A	1	738	synonymous_variant	LOW	ND4	0.0125
HLI-0082	11467	A	G	1	659	synonymous_variant	LOW	ND4	0.1231
HLI-0082	11719	G	A	0	669	synonymous_variant	LOW	ND4	0.7756
HLI-0082	12130	T	C	0	641	synonymous_variant	LOW	ND4	0.0019
HLI-0082	12308	A	G	1	634	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0082	12372	G	A	3	714	synonymous_variant	LOW	ND5	0.1329
HLI-0082	14167	C	T	5	668	synonymous_variant	LOW	ND6	0.0385
HLI-0082	14766	C	T	6	656	missense_variant	MODERATE	CYTB	0.7696
HLI-0082	14798	T	C	1	732	missense_variant	MODERATE	CYTB	0.0651
HLI-0082	15326	A	G	0	622	missense_variant	MODERATE	CYTB	0.9868
HLI-0082	15853	C	T	1	687	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0082	16224	T	C	0	630	upstream_gene_variant	MODIFIER	DLoop	0.0423

HLI-0082	16311	T	C	1	592	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0082	16519	T	C	0	330	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0083	73	A	G	1	362	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0083	263	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0083	497	C	T	5	582	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0083	750	A	G	0	696	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0083	1189	T	C	0	718	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0083	1438	A	G	1	719	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0083	1811	A	G	0	769	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0083	2706	A	G	0	734	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0083	3480	A	G	0	601	synonymous_variant	LOW	ND1	0.0392
HLI-0083	3552	T	C	0	668	synonymous_variant	LOW	ND1	0.0028
HLI-0083	4769	A	G	1	696	synonymous_variant	LOW	ND2	0.9767
HLI-0083	7028	C	T	2	825	synonymous_variant	LOW	COX1	0.8089
HLI-0083	8764	G	A	0	705	missense_variant	MODERATE	ATP6	0.0016
HLI-0083	9055	G	A	0	758	missense_variant	MODERATE	ATP6	0.0425
HLI-0083	9698	T	C	1	770	synonymous_variant	LOW	COX3	0.0405
HLI-0083	10398	A	G	0	712	missense_variant	MODERATE	ND3	0.445
HLI-0083	10550	A	G	1	738	synonymous_variant	LOW	ND4L	0.0376
HLI-0083	11299	T	C	0	698	synonymous_variant	LOW	ND4	0.0417
HLI-0083	11467	A	G	0	733	synonymous_variant	LOW	ND4	0.1231
HLI-0083	11719	G	A	0	686	synonymous_variant	LOW	ND4	0.7756
HLI-0083	11914	G	A	0	676	synonymous_variant	LOW	ND4	0.1112
HLI-0083	12308	A	G	0	638	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0083	12372	G	A	0	681	synonymous_variant	LOW	ND5	0.1329
HLI-0083	14167	C	T	4	668	synonymous_variant	LOW	ND6	0.0385
HLI-0083	14766	C	T	5	764	missense_variant	MODERATE	CYTB	0.7696
HLI-0083	14798	T	C	0	799	missense_variant	MODERATE	CYTB	0.0651
HLI-0083	15326	A	G	0	675	missense_variant	MODERATE	CYTB	0.9868
HLI-0083	16224	T	C	0	653	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0083	16311	T	C	0	588	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0083	16519	T	C	0	370	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0084	73	A	G	0	369	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0084	263	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0084	750	A	G	0	759	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0084	1438	A	G	0	768	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0084	2706	A	G	0	771	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0084	3197	T	C	0	699	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0084	4769	A	G	0	680	synonymous_variant	LOW	ND2	0.9767

HLI-0084	7028	C	T	5	802	synonymous_variant	LOW	COX1	0.8089
HLI-0084	9477	G	A	1	688	missense_variant	MODERATE	COX3	0.0387
HLI-0084	9667	A	G	1	758	missense_variant	MODERATE	COX3	0.0055
HLI-0084	11467	A	G	1	765	synonymous_variant	LOW	ND4	0.1231
HLI-0084	11719	G	A	1	719	synonymous_variant	LOW	ND4	0.7756
HLI-0084	12308	A	G	2	725	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0084	12372	G	A	1	784	synonymous_variant	LOW	ND5	0.1329
HLI-0084	12582	A	G	2	742	synonymous_variant	LOW	ND5	2.00E-04
HLI-0084	13617	T	C	0	749	synonymous_variant	LOW	ND5	0.038
HLI-0084	14581	T	C	0	781	synonymous_variant	LOW	ND6	0.0023
HLI-0084	14766	C	T	1	725	missense_variant	MODERATE	CYTB	0.7696
HLI-0084	14793	A	G	0	815	missense_variant	MODERATE	CYTB	0.0199
HLI-0084	15218	A	G	0	729	missense_variant	MODERATE	CYTB	0.0169
HLI-0084	15326	A	G	0	671	missense_variant	MODERATE	CYTB	0.9868
HLI-0084	16092	T	C	11	705	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0084	16256	C	T	0	758	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0084	16270	C	T	0	728	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0084	16291	C	T	0	674	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0084	16294	C	T	0	680	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0084	16399	A	G	0	589	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0085	41	C	T	1	191	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0085	73	A	G	2	361	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0085	150	C	T	1	640	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0085	263	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0085	709	G	A	1	763	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0085	750	A	G	0	774	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0085	1438	A	G	0	787	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0085	1888	G	A	1	720	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0085	2308	A	G	1	709	upstream_gene_variant	MODIFIER	RNR2	0.0044
HLI-0085	2706	A	G	1	768	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0085	4216	T	C	0	753	missense_variant	MODERATE	ND1	0.0991
HLI-0085	4769	A	G	1	664	synonymous_variant	LOW	ND2	0.9767
HLI-0085	4917	A	G	0	650	missense_variant	MODERATE	ND2	0.0477
HLI-0085	7028	C	T	4	790	synonymous_variant	LOW	COX1	0.8089
HLI-0085	7828	A	G	0	741	synonymous_variant	LOW	COX2	0.0063
HLI-0085	8697	G	A	1	655	synonymous_variant	LOW	ATP6	0.0466
HLI-0085	8790	G	A	2	662	synonymous_variant	LOW	ATP6	0.0083
HLI-0085	10463	T	C	0	763	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0085	11251	A	G	0	710	synonymous_variant	LOW	ND4	0.0932

HLI-0085	11719	G	A	0	719	synonymous_variant	LOW	ND4	0.7756
HLI-0085	11812	A	G	1	694	synonymous_variant	LOW	ND4	0.0332
HLI-0085	13368	G	A	0	733	synonymous_variant	LOW	ND5	0.0495
HLI-0085	14233	A	G	1	709	synonymous_variant	LOW	ND6	0.0369
HLI-0085	14766	C	T	1	707	missense_variant	MODERATE	CYTB	0.7696
HLI-0085	14905	G	A	1	699	synonymous_variant	LOW	CYTB	0.0526
HLI-0085	15244	A	G	1	742	synonymous_variant	LOW	CYTB	0.0103
HLI-0085	15326	A	G	0	780	missense_variant	MODERATE	CYTB	0.9868
HLI-0085	15452	C	A	6	687	missense_variant	MODERATE	CYTB	0.0933
HLI-0085	15607	A	G	1	717	synonymous_variant	LOW	CYTB	0.0508
HLI-0085	15928	G	A	0	755	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0085	16093	T	C	25	681	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0085	16126	T	C	0	725	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0085	16153	G	A	0	709	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0085	16294	C	T	0	642	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0085	16301	C	T	0	672	upstream_gene_variant	MODIFIER	DLoop	0.0064
HLI-0085	16519	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0086	750	A	G	0	13	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0086	4769	A	G	0	10	synonymous_variant	LOW	ND2	0.9767
HLI-0086	6776	T	C	0	16	synonymous_variant	LOW	COX1	0.0226
HLI-0086	7976	G	A	0	10	missense_variant	MODERATE	COX2	1.00E-04
HLI-0086	15326	A	G	0	12	missense_variant	MODERATE	CYTB	0.9868
HLI-0087	73	A	G	1	359	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0087	263	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0087	750	A	G	0	665	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0087	1438	A	G	0	729	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0087	2706	A	G	2	754	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0087	3197	T	C	2	681	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0087	4615	A	G	4	669	missense_variant	MODERATE	ND2	9.00E-04
HLI-0087	4769	A	G	1	694	synonymous_variant	LOW	ND2	0.9767
HLI-0087	7028	C	T	6	746	synonymous_variant	LOW	COX1	0.8089
HLI-0087	9477	G	A	0	681	missense_variant	MODERATE	COX3	0.0387
HLI-0087	9667	A	G	1	669	missense_variant	MODERATE	COX3	0.0055
HLI-0087	11467	A	G	1	689	synonymous_variant	LOW	ND4	0.1231
HLI-0087	11719	G	A	1	665	synonymous_variant	LOW	ND4	0.7756
HLI-0087	12308	A	G	1	669	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0087	12372	G	A	1	714	synonymous_variant	LOW	ND5	0.1329
HLI-0087	13617	T	C	2	668	synonymous_variant	LOW	ND5	0.038
HLI-0087	14766	C	T	4	754	missense_variant	MODERATE	CYTB	0.7696

HLI-0087	14793	A	G	2	792	missense_variant	MODERATE	CYTB	0.0199
HLI-0087	15218	A	G	3	725	missense_variant	MODERATE	CYTB	0.0169
HLI-0087	15326	A	G	0	696	missense_variant	MODERATE	CYTB	0.9868
HLI-0087	16256	C	T	3	773	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0087	16270	C	T	1	768	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0087	16399	A	G	2	578	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0088	73	A	G	0	353	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0088	150	C	T	0	585	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0088	195	T	C	1	558	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0088	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0088	750	A	G	0	681	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0088	1438	A	G	3	698	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0088	2352	T	C	3	693	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0088	2483	T	C	2	670	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0088	2706	A	G	3	684	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0088	4769	A	G	0	644	synonymous_variant	LOW	ND2	0.9767
HLI-0088	5580	T	C	2	601	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0088	7028	C	T	2	702	synonymous_variant	LOW	COX1	0.8089
HLI-0088	8701	A	G	0	681	missense_variant	MODERATE	ATP6	0.3391
HLI-0088	9377	A	G	4	666	synonymous_variant	LOW	COX3	0.0084
HLI-0088	9540	T	C	0	664	synonymous_variant	LOW	COX3	0.339
HLI-0088	10398	A	G	1	679	missense_variant	MODERATE	ND3	0.445
HLI-0088	10819	A	G	2	657	synonymous_variant	LOW	ND4	0.0228
HLI-0088	10873	T	C	1	742	synonymous_variant	LOW	ND4	0.3389
HLI-0088	11337	A	G	2	652	missense_variant	MODERATE	ND4	6.00E-04
HLI-0088	11719	G	A	2	674	synonymous_variant	LOW	ND4	0.7756
HLI-0088	12705	C	T	2	676	synonymous_variant	LOW	ND5	0.4212
HLI-0088	14212	T	C	3	660	synonymous_variant	LOW	ND6	0.0204
HLI-0088	14766	C	T	1	702	missense_variant	MODERATE	CYTB	0.7696
HLI-0088	14905	G	A	2	705	synonymous_variant	LOW	CYTB	0.0526
HLI-0088	15301	G	A	0	720	synonymous_variant	LOW	CYTB	0.2912
HLI-0088	15326	A	G	0	722	missense_variant	MODERATE	CYTB	0.9868
HLI-0088	16172	T	C	0	331	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0088	16223	C	T	1	427	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0088	16320	C	T	0	618	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0088	16519	T	C	0	322	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0089	263	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0089	750	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0089	1438	A	G	1	631	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0089	3010	G	A	4	604	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0089	4769	A	G	0	576	synonymous_variant	LOW	ND2	0.9767
HLI-0089	15326	A	G	0	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0089	16519	T	C	0	274	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0090	263	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0090	750	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0090	1438	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0090	4025	C	T	4	568	missense_variant	MODERATE	ND1	0.0072
HLI-0090	4769	A	G	2	635	synonymous_variant	LOW	ND2	0.9767
HLI-0090	6710	A	G	10	709	synonymous_variant	LOW	COX1	9.00E-04
HLI-0090	6776	T	C	5	742	synonymous_variant	LOW	COX1	0.0226
HLI-0090	10364	G	A	4	578	synonymous_variant	LOW	ND3	8.00E-04
HLI-0090	12811	T	C	16	608	missense_variant	MODERATE	ND5	0.0125
HLI-0090	15326	A	G	0	579	missense_variant	MODERATE	CYTB	0.9868
HLI-0090	16311	T	C	1	541	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0090	16519	T	C	0	242	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0091	73	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0091	150	C	T	1	437	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0091	263	A	G	0	160	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0091	750	A	G	0	538	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0091	1438	A	G	1	550	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0091	1721	C	T	0	576	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0091	1811	A	G	1	640	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0091	2706	A	G	3	558	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0091	3197	T	C	1	501	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0091	4129	A	G	0	521	missense_variant	MODERATE	ND1	0.001
HLI-0091	4732	A	G	2	551	missense_variant	MODERATE	ND2	0.0059
HLI-0091	4769	A	G	3	602	synonymous_variant	LOW	ND2	0.9767
HLI-0091	7028	C	T	5	572	synonymous_variant	LOW	COX1	0.8089
HLI-0091	7768	A	G	0	507	synonymous_variant	LOW	COX2	0.0186
HLI-0091	9477	G	A	1	478	missense_variant	MODERATE	COX3	0.0387
HLI-0091	11467	A	G	1	542	synonymous_variant	LOW	ND4	0.1231
HLI-0091	11719	G	A	2	485	synonymous_variant	LOW	ND4	0.7756
HLI-0091	12308	A	G	3	487	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0091	12372	G	A	0	520	synonymous_variant	LOW	ND5	0.1329
HLI-0091	13359	G	A	0	525	synonymous_variant	LOW	ND5	0.0041
HLI-0091	13617	T	C	1	512	synonymous_variant	LOW	ND5	0.038
HLI-0091	13637	A	G	0	539	missense_variant	MODERATE	ND5	0.0074
HLI-0091	14182	T	C	0	480	synonymous_variant	LOW	ND6	0.0254

HLI-0091	14766	C	T	5	492	missense_variant	MODERATE	CYTB	0.7696
HLI-0091	15326	A	G	0	518	missense_variant	MODERATE	CYTB	0.9868
HLI-0091	16266	C	T	0	279	upstream_gene_variant	MODIFIER	DLoop	0.0135
HLI-0091	16270	C	T	0	289	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0092	263	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0092	750	A	G	0	628	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0092	1438	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0092	3943	A	G	0	557	missense_variant	MODERATE	ND1	2.00E-04
HLI-0092	4769	A	G	2	530	synonymous_variant	LOW	ND2	0.9767
HLI-0092	7337	G	A	1	584	synonymous_variant	LOW	COX1	0.0119
HLI-0092	15326	A	G	1	556	missense_variant	MODERATE	CYTB	0.9868
HLI-0092	16172	T	C	0	531	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0092	16519	T	C	0	280	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0093	72	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0093	93	A	G	0	398	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0093	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0093	750	A	G	3	602	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0093	1438	A	G	0	621	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0093	2706	A	G	1	618	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0093	4580	G	A	1	550	synonymous_variant	LOW	ND2	0.0169
HLI-0093	4769	A	G	0	590	synonymous_variant	LOW	ND2	0.9767
HLI-0093	7028	C	T	1	672	synonymous_variant	LOW	COX1	0.8089
HLI-0093	7444	G	A	1	669	stop_lost	HIGH	COX1	0.0035
HLI-0093	8910	C	T	0	609	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0093	14121	C	T	1	518	synonymous_variant	LOW	ND5	3.00E-04
HLI-0093	15326	A	G	1	557	missense_variant	MODERATE	CYTB	0.9868
HLI-0093	15904	C	T	1	719	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0093	16114	C	T	0	558	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0094	73	A	G	0	216	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0094	152	T	C	0	345	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0094	182	C	T	2	316	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0094	185	G	T	2	314	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0094	189	A	G	2	313	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0094	195	T	C	2	311	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0094	247	G	A	0	128	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0094	263	A	G	0	148	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0094	357	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0094	709	G	A	0	548	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0094	710	T	C	0	553	upstream_gene_variant	MODIFIER	RNR1	0.0071

HLI-0094	750	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0094	769	G	A	1	585	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0094	825	T	A	1	593	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0094	1018	G	A	0	588	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0094	1738	T	C	0	637	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0094	2352	T	C	1	551	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0094	2706	A	G	0	600	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0094	2758	G	A	1	632	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0094	2768	A	G	2	622	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0094	2885	T	C	2	600	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0094	3308	T	C	0	564	start_lost	HIGH	ND1	0.0073
HLI-0094	3594	C	T	2	426	synonymous_variant	LOW	ND1	0.0789
HLI-0094	3666	G	A	2	557	synonymous_variant	LOW	ND1	0.0233
HLI-0094	3693	G	A	3	562	synonymous_variant	LOW	ND1	0.0091
HLI-0094	4104	A	G	1	508	synonymous_variant	LOW	ND1	0.0785
HLI-0094	4769	A	G	0	573	synonymous_variant	LOW	ND2	0.9767
HLI-0094	5036	A	G	0	577	synonymous_variant	LOW	ND2	0.006
HLI-0094	5046	G	A	0	617	missense_variant	MODERATE	ND2	0.018
HLI-0094	5393	T	C	0	524	synonymous_variant	LOW	ND2	0.0059
HLI-0094	5655	T	C	1	601	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0094	6548	C	T	2	610	synonymous_variant	LOW	COX1	0.0061
HLI-0094	6719	T	C	1	661	synonymous_variant	LOW	COX1	0.041
HLI-0094	6827	T	C	1	566	synonymous_variant	LOW	COX1	0.0072
HLI-0094	6989	A	G	0	662	synonymous_variant	LOW	COX1	0.0061
HLI-0094	7028	C	T	1	637	synonymous_variant	LOW	COX1	0.8089
HLI-0094	7055	A	G	1	565	synonymous_variant	LOW	COX1	0.0188
HLI-0094	7146	A	G	2	302	missense_variant	MODERATE	COX1	0.0497
HLI-0094	7256	C	T	1	447	synonymous_variant	LOW	COX1	0.0784
HLI-0094	7389	T	C	0	430	missense_variant	MODERATE	COX1	0.0201
HLI-0094	7521	G	A	0	393	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0094	7867	C	T	1	598	synonymous_variant	LOW	COX2	0.0076
HLI-0094	7915	C	T	4	649	synonymous_variant	LOW	COX2	5.00E-04
HLI-0094	8248	A	G	1	530	synonymous_variant	LOW	COX2	0.0061
HLI-0094	8468	C	T	1	471	synonymous_variant	LOW	ATP8	0.0501
HLI-0094	8655	C	T	3	417	synonymous_variant	LOW	ATP6	0.0511
HLI-0094	8701	A	G	0	457	missense_variant	MODERATE	ATP6	0.3391
HLI-0094	9540	T	C	2	566	synonymous_variant	LOW	COX3	0.339
HLI-0094	10398	A	G	0	574	missense_variant	MODERATE	ND3	0.445
HLI-0094	10688	G	A	0	569	synonymous_variant	LOW	ND4L	0.0515

HLI-0094	10810	T	C	0	547	synonymous_variant	LOW	ND4	0.0522
HLI-0094	10873	T	C	0	572	synonymous_variant	LOW	ND4	0.3389
HLI-0094	11719	G	A	1	573	synonymous_variant	LOW	ND4	0.7756
HLI-0094	12519	T	C	0	581	synonymous_variant	LOW	ND5	0.007
HLI-0094	12705	C	T	0	639	synonymous_variant	LOW	ND5	0.4212
HLI-0094	13105	A	G	1	536	missense_variant	MODERATE	ND5	0.076
HLI-0094	13506	C	T	1	537	synonymous_variant	LOW	ND5	0.0506
HLI-0094	13650	C	T	2	520	synonymous_variant	LOW	ND5	0.079
HLI-0094	13789	T	C	0	356	missense_variant	MODERATE	ND5	0.0185
HLI-0094	13880	C	A	5	445	missense_variant	MODERATE	ND5	0.0055
HLI-0094	13980	G	A	2	503	synonymous_variant	LOW	ND5	0.0023
HLI-0094	14178	T	C	1	538	missense_variant	MODERATE	ND6	0.0225
HLI-0094	14182	T	C	1	554	synonymous_variant	LOW	ND6	0.0254
HLI-0094	14203	A	G	1	588	synonymous_variant	LOW	ND6	0.0061
HLI-0094	14560	G	A	1	585	synonymous_variant	LOW	ND6	0.0235
HLI-0094	14766	C	T	0	576	missense_variant	MODERATE	CYTB	0.7696
HLI-0094	14769	A	G	0	591	missense_variant	MODERATE	CYTB	0.0121
HLI-0094	15115	T	C	1	596	synonymous_variant	LOW	CYTB	0.0093
HLI-0094	15326	A	G	0	544	missense_variant	MODERATE	CYTB	0.9868
HLI-0094	16093	T	C	8	515	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0094	16126	T	C	0	534	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0094	16223	C	T	4	417	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0094	16264	C	T	0	391	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0094	16270	C	T	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0094	16278	C	T	1	370	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0094	16293	A	G	1	357	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0094	16311	T	C	1	351	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0094	16519	T	C	0	135	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0095	152	T	C	0	493	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0095	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0095	483	C	T	3	342	upstream_gene_variant	MODIFIER	DLoop	2.00E-04
HLI-0095	750	A	G	0	610	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0095	1438	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0095	1888	G	A	1	570	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0095	3010	G	A	0	596	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0095	3796	A	G	0	516	missense_variant	MODERATE	ND1	0.0048
HLI-0095	4769	A	G	2	539	synonymous_variant	LOW	ND2	0.9767
HLI-0095	15326	A	G	0	580	missense_variant	MODERATE	CYTB	0.9868
HLI-0095	16172	T	C	0	207	upstream_gene_variant	MODIFIER	DLoop	0.0748

HLI-0095	16356	T	C	3	441	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0095	16519	T	C	0	182	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0096	73	A	G	0	250	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0096	153	A	G	0	422	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0096	195	T	C	0	370	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0096	225	G	A	0	331	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0096	226	T	C	0	332	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0096	263	A	G	0	67	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0096	750	A	G	0	555	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0096	1438	A	G	0	580	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0096	1719	G	A	0	574	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0096	2706	A	G	0	589	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0096	3705	G	A	2	544	synonymous_variant	LOW	ND1	0.0138
HLI-0096	4769	A	G	4	525	synonymous_variant	LOW	ND2	0.9767
HLI-0096	5582	A	G	0	612	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0096	6221	T	C	0	518	synonymous_variant	LOW	COX1	0.0306
HLI-0096	6371	C	T	2	553	synonymous_variant	LOW	COX1	0.0097
HLI-0096	7028	C	T	0	578	synonymous_variant	LOW	COX1	0.8089
HLI-0096	8393	C	T	1	583	missense_variant	MODERATE	ATP8	0.0036
HLI-0096	11719	G	A	1	571	synonymous_variant	LOW	ND4	0.7756
HLI-0096	12705	C	T	0	568	synonymous_variant	LOW	ND5	0.4212
HLI-0096	13708	G	A	2	450	missense_variant	MODERATE	ND5	0.0717
HLI-0096	13966	A	G	3	502	missense_variant	MODERATE	ND5	0.0126
HLI-0096	14470	T	C	0	428	synonymous_variant	LOW	ND6	0.0166
HLI-0096	14766	C	T	2	504	missense_variant	MODERATE	CYTB	0.7696
HLI-0096	15326	A	G	0	500	missense_variant	MODERATE	CYTB	0.9868
HLI-0096	15927	G	A	0	574	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0096	16223	C	T	1	224	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0096	16278	C	T	0	346	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0096	16519	T	C	1	173	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0097	73	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0097	150	C	T	0	473	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0097	263	A	G	0	184	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0097	750	A	G	0	535	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0097	1438	A	G	0	596	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0097	1811	A	G	1	557	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0097	2706	A	G	0	576	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0097	3546	C	A	7	469	synonymous_variant	LOW	ND1	9.00E-04
HLI-0097	4188	A	G	2	533	synonymous_variant	LOW	ND1	0.003

HLI-0097	4640	C	A	0	552	missense_variant	MODERATE	ND2	0.0029
HLI-0097	4769	A	G	1	487	synonymous_variant	LOW	ND2	0.9767
HLI-0097	6359	A	G	0	627	synonymous_variant	LOW	COX1	0.0014
HLI-0097	7028	C	T	2	657	synonymous_variant	LOW	COX1	0.8089
HLI-0097	8867	T	C	0	538	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0097	9656	T	C	0	507	synonymous_variant	LOW	COX3	0.0035
HLI-0097	11467	A	G	0	543	synonymous_variant	LOW	ND4	0.1231
HLI-0097	11719	G	A	0	553	synonymous_variant	LOW	ND4	0.7756
HLI-0097	12308	A	G	2	584	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0097	12372	G	A	0	561	synonymous_variant	LOW	ND5	0.1329
HLI-0097	12720	A	G	0	570	synonymous_variant	LOW	ND5	0.0302
HLI-0097	13743	T	C	0	362	synonymous_variant	LOW	ND5	0.0037
HLI-0097	14139	A	G	0	481	synonymous_variant	LOW	ND5	0.0056
HLI-0097	14766	C	T	1	491	missense_variant	MODERATE	CYTB	0.7696
HLI-0097	15326	A	G	0	507	missense_variant	MODERATE	CYTB	0.9868
HLI-0097	15454	T	C	0	471	synonymous_variant	LOW	CYTB	0.0072
HLI-0097	16343	A	G	2	418	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0098	73	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0098	152	T	C	0	426	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0098	195	T	C	0	394	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0098	263	A	G	0	170	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0098	499	G	A	0	158	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0098	750	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0098	961	T	C	2	91	upstream_gene_variant	MODIFIER	RNR1	0.0087
HLI-0098	1438	A	G	0	596	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0098	1811	A	G	1	579	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0098	2706	A	G	0	603	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0098	4646	T	C	0	620	synonymous_variant	LOW	ND2	0.0124
HLI-0098	4769	A	G	0	529	synonymous_variant	LOW	ND2	0.9767
HLI-0098	5999	T	C	0	636	synonymous_variant	LOW	COX1	0.0127
HLI-0098	6047	A	G	2	682	synonymous_variant	LOW	COX1	0.0114
HLI-0098	7028	C	T	2	639	synonymous_variant	LOW	COX1	0.8089
HLI-0098	8818	C	T	0	538	synonymous_variant	LOW	ATP6	0.0061
HLI-0098	11332	C	T	1	531	synonymous_variant	LOW	ND4	0.0115
HLI-0098	11467	A	G	0	591	synonymous_variant	LOW	ND4	0.1231
HLI-0098	11719	G	A	0	545	synonymous_variant	LOW	ND4	0.7756
HLI-0098	12308	A	G	1	596	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0098	12372	G	A	1	543	synonymous_variant	LOW	ND5	0.1329
HLI-0098	12937	A	G	2	517	missense_variant	MODERATE	ND5	0.0026

HLI-0098	14620	C	T	5	512	synonymous_variant	LOW	ND6	0.0126
HLI-0098	14766	C	T	2	539	missense_variant	MODERATE	CYTB	0.7696
HLI-0098	15326	A	G	0	505	missense_variant	MODERATE	CYTB	0.9868
HLI-0098	15693	T	C	1	512	missense_variant	MODERATE	CYTB	0.0114
HLI-0098	16134	C	T	2	576	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0098	16356	T	C	2	393	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0098	16519	T	C	0	201	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0099	73	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0099	185	G	A	0	270	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0099	195	T	C	0	275	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0099	198	C	T	0	269	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0099	228	G	A	0	223	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0099	263	A	G	0	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0099	295	C	T	0	133	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0099	462	C	T	0	317	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0099	489	T	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0099	750	A	G	0	568	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0099	1438	A	G	0	529	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0099	2706	A	G	1	563	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0099	3010	G	A	0	533	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0099	4216	T	C	0	585	missense_variant	MODERATE	ND1	0.0991
HLI-0099	4769	A	G	1	520	synonymous_variant	LOW	ND2	0.9767
HLI-0099	6464	C	A	1	546	synonymous_variant	LOW	COX1	0.0011
HLI-0099	6554	C	T	0	501	synonymous_variant	LOW	COX1	0.0016
HLI-0099	7028	C	T	4	574	synonymous_variant	LOW	COX1	0.8089
HLI-0099	10398	A	G	1	557	missense_variant	MODERATE	ND3	0.445
HLI-0099	11251	A	G	1	524	synonymous_variant	LOW	ND4	0.0932
HLI-0099	11719	G	A	0	533	synonymous_variant	LOW	ND4	0.7756
HLI-0099	12127	G	A	2	516	synonymous_variant	LOW	ND4	0.0058
HLI-0099	12534	A	G	2	584	synonymous_variant	LOW	ND5	2.00E-04
HLI-0099	12612	A	G	0	623	synonymous_variant	LOW	ND5	0.0506
HLI-0099	13681	A	G	1	476	missense_variant	MODERATE	ND5	0.0035
HLI-0099	13708	G	A	0	505	missense_variant	MODERATE	ND5	0.0717
HLI-0099	14766	C	T	1	575	missense_variant	MODERATE	CYTB	0.7696
HLI-0099	14798	T	C	0	649	missense_variant	MODERATE	CYTB	0.0651
HLI-0099	15326	A	G	0	476	missense_variant	MODERATE	CYTB	0.9868
HLI-0099	15452	C	A	7	473	missense_variant	MODERATE	CYTB	0.0933
HLI-0099	16069	C	T	3	549	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0099	16092	T	C	7	536	upstream_gene_variant	MODIFIER	DLoop	0.0137

HLI-0099	16126	T	C	1	539	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0099	16261	C	T	1	473	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0100	73	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0100	152	T	C	1	504	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0100	263	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0100	750	A	G	1	572	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0100	921	T	C	0	571	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0100	1438	A	G	2	601	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0100	2706	A	G	1	624	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0100	4769	A	G	1	497	synonymous_variant	LOW	ND2	0.9767
HLI-0100	5147	G	A	1	499	synonymous_variant	LOW	ND2	0.0437
HLI-0100	6680	T	C	7	603	synonymous_variant	LOW	COX1	0.0226
HLI-0100	7028	C	T	0	620	synonymous_variant	LOW	COX1	0.8089
HLI-0100	7424	A	G	3	493	synonymous_variant	LOW	COX1	0.0115
HLI-0100	7765	A	G	3	577	synonymous_variant	LOW	COX2	0.0019
HLI-0100	8618	T	C	0	381	missense_variant	MODERATE	ATP6	0.0103
HLI-0100	8701	A	G	1	479	missense_variant	MODERATE	ATP6	0.3391
HLI-0100	8709	C	T	1	489	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0100	9151	A	G	0	617	missense_variant	MODERATE	ATP6	0.0013
HLI-0100	9540	T	C	0	558	synonymous_variant	LOW	COX3	0.339
HLI-0100	10398	A	G	3	566	missense_variant	MODERATE	ND3	0.445
HLI-0100	10873	T	C	1	522	synonymous_variant	LOW	ND4	0.3389
HLI-0100	11719	G	A	1	558	synonymous_variant	LOW	ND4	0.7756
HLI-0100	12705	C	T	1	629	synonymous_variant	LOW	ND5	0.4212
HLI-0100	13105	A	G	0	569	missense_variant	MODERATE	ND5	0.076
HLI-0100	13886	T	C	1	500	missense_variant	MODERATE	ND5	0.0088
HLI-0100	14128	A	G	2	510	missense_variant	MODERATE	ND5	0.0018
HLI-0100	14284	C	T	1	504	synonymous_variant	LOW	ND6	0.0087
HLI-0100	14766	C	T	0	556	missense_variant	MODERATE	CYTB	0.7696
HLI-0100	15301	G	A	0	560	synonymous_variant	LOW	CYTB	0.2912
HLI-0100	15326	A	G	0	596	missense_variant	MODERATE	CYTB	0.9868
HLI-0100	15924	A	G	1	575	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0100	16124	T	C	1	525	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0100	16223	C	T	1	541	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0100	16256	C	T	0	551	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0100	16368	T	C	1	438	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0101	73	A	G	0	276	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0101	263	A	G	1	195	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0101	750	A	G	1	545	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0101	1438	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0101	2352	T	C	1	590	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0101	2706	A	G	0	560	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0101	3197	T	C	2	602	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0101	4769	A	G	0	558	synonymous_variant	LOW	ND2	0.9767
HLI-0101	5471	G	A	0	599	synonymous_variant	LOW	ND2	0.0128
HLI-0101	7028	C	T	2	579	synonymous_variant	LOW	COX1	0.8089
HLI-0101	9477	G	A	3	509	missense_variant	MODERATE	COX3	0.0387
HLI-0101	9548	G	A	0	500	synonymous_variant	LOW	COX3	0.0149
HLI-0101	11467	A	G	1	570	synonymous_variant	LOW	ND4	0.1231
HLI-0101	11719	G	A	2	570	synonymous_variant	LOW	ND4	0.7756
HLI-0101	12308	A	G	1	529	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0101	12372	G	A	2	499	synonymous_variant	LOW	ND5	0.1329
HLI-0101	12441	T	C	1	503	synonymous_variant	LOW	ND5	0.0012
HLI-0101	13617	T	C	1	526	synonymous_variant	LOW	ND5	0.038
HLI-0101	14766	C	T	2	568	missense_variant	MODERATE	CYTB	0.7696
HLI-0101	14793	A	G	0	643	missense_variant	MODERATE	CYTB	0.0199
HLI-0101	15326	A	G	2	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0101	16256	C	T	1	536	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0101	16265	A	G	0	521	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0101	16270	C	T	1	513	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0101	16526	G	A	1	216	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0102	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0102	150	C	T	1	496	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0102	195	T	C	0	455	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0102	263	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0102	408	T	A	0	383	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0102	750	A	G	1	646	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0102	1438	A	G	0	677	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0102	2352	T	C	0	566	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0102	2483	T	C	0	652	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0102	2706	A	G	0	632	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0102	4769	A	G	0	568	synonymous_variant	LOW	ND2	0.9767
HLI-0102	5580	T	C	0	540	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0102	7028	C	T	2	638	synonymous_variant	LOW	COX1	0.8089
HLI-0102	8701	A	G	3	562	missense_variant	MODERATE	ATP6	0.3391
HLI-0102	9323	C	T	1	646	synonymous_variant	LOW	COX3	1.00E-04
HLI-0102	9377	A	G	0	713	synonymous_variant	LOW	COX3	0.0084
HLI-0102	9540	T	C	0	566	synonymous_variant	LOW	COX3	0.339

HLI-0102	10398	A	G	0	684	missense_variant	MODERATE	ND3	0.445
HLI-0102	10819	A	G	0	627	synonymous_variant	LOW	ND4	0.0228
HLI-0102	10873	T	C	0	628	synonymous_variant	LOW	ND4	0.3389
HLI-0102	11719	G	A	0	573	synonymous_variant	LOW	ND4	0.7756
HLI-0102	11722	T	C	0	582	synonymous_variant	LOW	ND4	5.00E-04
HLI-0102	12705	C	T	2	608	synonymous_variant	LOW	ND5	0.4212
HLI-0102	14097	C	T	0	493	synonymous_variant	LOW	ND5	8.00E-04
HLI-0102	14212	T	C	0	572	synonymous_variant	LOW	ND6	0.0204
HLI-0102	14580	A	G	0	573	synonymous_variant	LOW	ND6	1.00E-04
HLI-0102	14766	C	T	4	530	missense_variant	MODERATE	CYTB	0.7696
HLI-0102	14905	G	A	1	608	synonymous_variant	LOW	CYTB	0.0526
HLI-0102	15301	G	A	0	549	synonymous_variant	LOW	CYTB	0.2912
HLI-0102	15326	A	G	0	594	missense_variant	MODERATE	CYTB	0.9868
HLI-0102	15932	T	C	0	571	upstream_gene_variant	MODIFIER	TRNT	4.00E-04
HLI-0102	16172	T	C	0	189	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0102	16223	C	T	1	262	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0102	16320	C	T	1	401	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0102	16519	T	C	0	193	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0103	73	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0103	189	A	G	0	331	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0103	200	A	G	0	352	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0103	207	G	A	0	351	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0103	263	A	G	0	129	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0103	750	A	G	0	558	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0103	1438	A	G	0	553	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0103	1822	T	C	1	590	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0103	2706	A	G	0	625	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0103	3396	T	C	3	505	synonymous_variant	LOW	ND1	0.0082
HLI-0103	4218	T	C	0	542	synonymous_variant	LOW	ND1	0.0057
HLI-0103	4769	A	G	0	524	synonymous_variant	LOW	ND2	0.9767
HLI-0103	5601	C	T	7	624	upstream_gene_variant	MODIFIER	TRNA	0.0101
HLI-0103	7028	C	T	1	615	synonymous_variant	LOW	COX1	0.8089
HLI-0103	7819	C	A	5	586	synonymous_variant	LOW	COX2	0.0045
HLI-0103	8527	A	G	3	518	initiator_codon_variant	LOW	ATP6/8	0.0044
HLI-0103	8701	A	G	0	535	missense_variant	MODERATE	ATP6	0.3391
HLI-0103	8932	C	T	2	573	missense_variant	MODERATE	ATP6	0.0044
HLI-0103	9540	T	C	0	558	synonymous_variant	LOW	COX3	0.339
HLI-0103	9950	T	C	1	647	synonymous_variant	LOW	COX3	0.0362
HLI-0103	10398	A	G	1	574	missense_variant	MODERATE	ND3	0.445

HLI-0103	10873	T	C	0	489	synonymous_variant	LOW	ND4	0.3389
HLI-0103	11440	G	A	0	589	synonymous_variant	LOW	ND4	0.0081
HLI-0103	11719	G	A	0	566	synonymous_variant	LOW	ND4	0.7756
HLI-0103	12705	C	T	1	670	synonymous_variant	LOW	ND5	0.4212
HLI-0103	14766	C	T	0	531	missense_variant	MODERATE	CYTB	0.7696
HLI-0103	14769	A	G	0	547	missense_variant	MODERATE	CYTB	0.0121
HLI-0103	15301	G	A	0	554	synonymous_variant	LOW	CYTB	0.2912
HLI-0103	15326	A	G	0	596	missense_variant	MODERATE	CYTB	0.9868
HLI-0103	15514	T	C	1	514	synonymous_variant	LOW	CYTB	0.0071
HLI-0103	16209	T	C	0	500	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0103	16223	C	T	1	533	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0103	16292	C	T	0	482	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0103	16295	C	T	0	474	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0103	16311	T	C	0	462	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0103	16519	T	C	0	167	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0104	152	T	C	0	463	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0104	263	A	G	0	209	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0104	750	A	G	0	618	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0104	1438	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0104	1809	T	C	0	675	upstream_gene_variant	MODIFIER	RNR2	0.0012
HLI-0104	4769	A	G	0	549	synonymous_variant	LOW	ND2	0.9767
HLI-0104	15204	T	C	0	605	missense_variant	MODERATE	CYTB	0.0125
HLI-0104	15326	A	G	0	568	missense_variant	MODERATE	CYTB	0.9868
HLI-0104	16311	T	C	1	473	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0104	16519	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0105	73	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0105	150	C	T	1	458	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0105	195	T	C	0	429	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0105	263	A	G	1	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0105	295	C	T	1	189	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0105	489	T	C	1	385	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0105	750	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0105	1438	A	G	0	646	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0105	2706	A	G	1	681	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0105	4216	T	C	0	584	missense_variant	MODERATE	ND1	0.0991
HLI-0105	4769	A	G	3	552	synonymous_variant	LOW	ND2	0.9767
HLI-0105	6671	T	C	1	650	synonymous_variant	LOW	COX1	0.0071
HLI-0105	7028	C	T	0	700	synonymous_variant	LOW	COX1	0.8089
HLI-0105	7476	C	T	0	641	upstream_gene_variant	MODIFIER	TRNS1	0.0134

HLI-0105	10398	A	G	0	670	missense_variant	MODERATE	ND3	0.445
HLI-0105	10499	A	G	0	617	synonymous_variant	LOW	ND4L	0.0093
HLI-0105	11002	A	G	1	472	synonymous_variant	LOW	ND4	0.0124
HLI-0105	11251	A	G	1	647	synonymous_variant	LOW	ND4	0.0932
HLI-0105	11377	G	A	1	630	synonymous_variant	LOW	ND4	0.0125
HLI-0105	11719	G	A	0	575	synonymous_variant	LOW	ND4	0.7756
HLI-0105	12570	A	G	3	620	synonymous_variant	LOW	ND5	0.0016
HLI-0105	12612	A	G	3	702	synonymous_variant	LOW	ND5	0.0506
HLI-0105	13708	G	A	0	485	missense_variant	MODERATE	ND5	0.0717
HLI-0105	14766	C	T	0	588	missense_variant	MODERATE	CYTB	0.7696
HLI-0105	15257	G	A	1	661	missense_variant	MODERATE	CYTB	0.0155
HLI-0105	15326	A	G	0	668	missense_variant	MODERATE	CYTB	0.9868
HLI-0105	15452	C	A	5	579	missense_variant	MODERATE	CYTB	0.0933
HLI-0105	15679	A	G	0	578	synonymous_variant	LOW	CYTB	0.0018
HLI-0105	16069	C	T	2	589	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0105	16126	T	C	0	626	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0105	16231	T	C	1	457	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0106	72	T	C	0	284	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0106	195	T	C	0	390	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0106	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0106	750	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0106	1438	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0106	2706	A	G	0	697	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0106	4580	G	A	2	649	synonymous_variant	LOW	ND2	0.0169
HLI-0106	4769	A	G	0	576	synonymous_variant	LOW	ND2	0.9767
HLI-0106	7028	C	T	1	690	synonymous_variant	LOW	COX1	0.8089
HLI-0106	9844	C	T	2	693	missense_variant	MODERATE	COX3	0
HLI-0106	13105	A	G	1	661	missense_variant	MODERATE	ND5	0.076
HLI-0106	15326	A	G	0	564	missense_variant	MODERATE	CYTB	0.9868
HLI-0106	15904	C	T	2	659	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0106	16270	C	T	1	688	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0106	16298	T	C	1	637	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0107	73	A	G	1	309	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0107	152	T	C	1	544	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0107	195	T	C	1	510	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0107	263	A	G	0	221	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0107	709	G	A	0	715	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0107	750	A	G	0	791	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0107	1438	A	G	1	737	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0107	1888	G	A	0	715	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0107	2706	A	G	0	732	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0107	4216	T	C	1	759	missense_variant	MODERATE	ND1	0.0991
HLI-0107	4769	A	G	2	620	synonymous_variant	LOW	ND2	0.9767
HLI-0107	4917	A	G	5	624	missense_variant	MODERATE	ND2	0.0477
HLI-0107	7028	C	T	7	716	synonymous_variant	LOW	COX1	0.8089
HLI-0107	7269	G	A	3	676	missense_variant	MODERATE	COX1	0.0016
HLI-0107	8697	G	A	1	640	synonymous_variant	LOW	ATP6	0.0466
HLI-0107	9425	A	G	2	716	synonymous_variant	LOW	COX3	4.00E-04
HLI-0107	9899	T	C	1	669	synonymous_variant	LOW	COX3	0.0108
HLI-0107	10463	T	C	2	671	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0107	11251	A	G	1	665	synonymous_variant	LOW	ND4	0.0932
HLI-0107	11719	G	A	0	689	synonymous_variant	LOW	ND4	0.7756
HLI-0107	12633	C	A	9	721	synonymous_variant	LOW	ND5	0.0123
HLI-0107	13368	G	A	0	757	synonymous_variant	LOW	ND5	0.0495
HLI-0107	14766	C	T	3	672	missense_variant	MODERATE	CYTB	0.7696
HLI-0107	14905	G	A	0	678	synonymous_variant	LOW	CYTB	0.0526
HLI-0107	15326	A	G	0	610	missense_variant	MODERATE	CYTB	0.9868
HLI-0107	15452	C	A	5	650	missense_variant	MODERATE	CYTB	0.0933
HLI-0107	15607	A	G	0	727	synonymous_variant	LOW	CYTB	0.0508
HLI-0107	15928	G	A	0	690	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0107	16126	T	C	0	630	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0107	16163	A	G	2	626	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0107	16294	C	T	1	629	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0107	16362	T	C	0	589	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0107	16519	T	C	1	268	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0108	73	A	G	0	325	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0108	152	T	C	0	546	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0108	263	A	G	1	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0108	709	G	A	2	682	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0108	750	A	G	2	726	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0108	930	G	A	1	649	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0108	1438	A	G	1	732	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0108	1888	G	A	0	602	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0108	2706	A	G	0	672	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0108	4216	T	C	1	693	missense_variant	MODERATE	ND1	0.0991
HLI-0108	4769	A	G	1	574	synonymous_variant	LOW	ND2	0.9767
HLI-0108	4917	A	G	1	570	missense_variant	MODERATE	ND2	0.0477
HLI-0108	5147	G	A	1	588	synonymous_variant	LOW	ND2	0.0437

HLI-0108	6401	A	G	0	626	synonymous_variant	LOW	COX1	9.00E-04
HLI-0108	7028	C	T	2	676	synonymous_variant	LOW	COX1	0.8089
HLI-0108	8697	G	A	0	617	synonymous_variant	LOW	ATP6	0.0466
HLI-0108	9254	A	G	0	607	synonymous_variant	LOW	COX3	0.0083
HLI-0108	10463	T	C	0	621	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0108	11251	A	G	0	631	synonymous_variant	LOW	ND4	0.0932
HLI-0108	11719	G	A	0	705	synonymous_variant	LOW	ND4	0.7756
HLI-0108	11812	A	G	1	633	synonymous_variant	LOW	ND4	0.0332
HLI-0108	11872	C	T	2	691	synonymous_variant	LOW	ND4	3.00E-04
HLI-0108	13368	G	A	0	641	synonymous_variant	LOW	ND5	0.0495
HLI-0108	14233	A	G	1	589	synonymous_variant	LOW	ND6	0.0369
HLI-0108	14766	C	T	4	606	missense_variant	MODERATE	CYTB	0.7696
HLI-0108	14905	G	A	2	674	synonymous_variant	LOW	CYTB	0.0526
HLI-0108	15326	A	G	1	579	missense_variant	MODERATE	CYTB	0.9868
HLI-0108	15452	C	A	2	555	missense_variant	MODERATE	CYTB	0.0933
HLI-0108	15607	A	G	0	645	synonymous_variant	LOW	CYTB	0.0508
HLI-0108	15928	G	A	0	685	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0108	16126	T	C	0	625	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0108	16294	C	T	0	605	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0108	16304	T	C	0	642	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0108	16519	T	C	1	317	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0109	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0109	263	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0109	750	A	G	2	649	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0109	1438	A	G	1	697	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0109	3010	G	A	1	675	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0109	4769	A	G	1	565	synonymous_variant	LOW	ND2	0.9767
HLI-0109	6365	T	C	1	660	synonymous_variant	LOW	COX1	0.0026
HLI-0109	15326	A	G	1	608	missense_variant	MODERATE	CYTB	0.9868
HLI-0109	16162	A	G	1	326	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0109	16209	T	C	0	319	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0109	16519	T	C	0	223	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0110	73	A	G	1	310	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0110	195	T	C	0	453	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0110	263	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0110	709	G	A	0	686	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0110	750	A	G	1	721	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0110	1438	A	G	0	635	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0110	1888	G	A	0	632	upstream_gene_variant	MODIFIER	RNR2	0.0558

HLI-0110	2706	A	G	0	668	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0110	4216	T	C	3	672	missense_variant	MODERATE	ND1	0.0991
HLI-0110	4769	A	G	1	588	synonymous_variant	LOW	ND2	0.9767
HLI-0110	4917	A	G	0	574	missense_variant	MODERATE	ND2	0.0477
HLI-0110	5277	T	C	0	598	missense_variant	MODERATE	ND2	0.0022
HLI-0110	5426	T	C	0	640	synonymous_variant	LOW	ND2	0.0091
HLI-0110	6489	C	A	4	729	missense_variant	MODERATE	COX1	0.0016
HLI-0110	7028	C	T	3	706	synonymous_variant	LOW	COX1	0.8089
HLI-0110	8697	G	A	0	601	synonymous_variant	LOW	ATP6	0.0466
HLI-0110	10463	T	C	1	603	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0110	11251	A	G	0	646	synonymous_variant	LOW	ND4	0.0932
HLI-0110	11719	G	A	0	648	synonymous_variant	LOW	ND4	0.7756
HLI-0110	11812	A	G	1	668	synonymous_variant	LOW	ND4	0.0332
HLI-0110	13368	G	A	3	655	synonymous_variant	LOW	ND5	0.0495
HLI-0110	14233	A	G	2	673	synonymous_variant	LOW	ND6	0.0369
HLI-0110	14766	C	T	2	664	missense_variant	MODERATE	CYTB	0.7696
HLI-0110	14905	G	A	0	680	synonymous_variant	LOW	CYTB	0.0526
HLI-0110	15028	C	A	4	719	synonymous_variant	LOW	CYTB	0.0016
HLI-0110	15043	G	A	3	781	synonymous_variant	LOW	CYTB	0.2362
HLI-0110	15326	A	G	0	583	missense_variant	MODERATE	CYTB	0.9868
HLI-0110	15452	C	A	6	553	missense_variant	MODERATE	CYTB	0.0933
HLI-0110	15607	A	G	0	649	synonymous_variant	LOW	CYTB	0.0508
HLI-0110	15928	G	A	0	634	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0110	16126	T	C	1	309	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0110	16294	C	T	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0110	16296	C	T	0	384	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0110	16298	T	C	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0110	16519	T	C	0	182	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0111	263	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0111	456	C	T	4	455	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0111	750	A	G	1	679	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0111	1438	A	G	0	676	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0111	4336	T	C	1	677	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0111	4769	A	G	0	648	synonymous_variant	LOW	ND2	0.9767
HLI-0111	5839	C	T	1	668	upstream_gene_variant	MODIFIER	TRNY	0.0011
HLI-0111	15326	A	G	1	598	missense_variant	MODERATE	CYTB	0.9868
HLI-0111	16304	T	C	1	528	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0112	263	A	G	0	219	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0112	279	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.0046

HLI-0112	750	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0112	951	G	A	1	661	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0112	15326	A	G	2	570	missense_variant	MODERATE	CYTB	0.9868
HLI-0112	16354	C	T	2	477	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0113	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0113	263	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0113	709	G	A	2	581	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0113	750	A	G	1	620	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0113	930	G	A	4	612	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0113	1438	A	G	0	598	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0113	1888	G	A	3	575	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0113	2706	A	G	1	546	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0113	4216	T	C	2	589	missense_variant	MODERATE	ND1	0.0991
HLI-0113	4769	A	G	0	532	synonymous_variant	LOW	ND2	0.9767
HLI-0113	4917	A	G	3	488	missense_variant	MODERATE	ND2	0.0477
HLI-0113	5147	G	A	5	529	synonymous_variant	LOW	ND2	0.0437
HLI-0113	7028	C	T	1	664	synonymous_variant	LOW	COX1	0.8089
HLI-0113	7859	G	A	4	548	missense_variant	MODERATE	COX2	0.003
HLI-0113	8697	G	A	1	477	synonymous_variant	LOW	ATP6	0.0466
HLI-0113	10463	T	C	1	648	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0113	11251	A	G	0	549	synonymous_variant	LOW	ND4	0.0932
HLI-0113	11719	G	A	0	562	synonymous_variant	LOW	ND4	0.7756
HLI-0113	11812	A	G	0	508	synonymous_variant	LOW	ND4	0.0332
HLI-0113	13368	G	A	0	532	synonymous_variant	LOW	ND5	0.0495
HLI-0113	14233	A	G	1	520	synonymous_variant	LOW	ND6	0.0369
HLI-0113	14766	C	T	2	504	missense_variant	MODERATE	CYTB	0.7696
HLI-0113	14905	G	A	0	570	synonymous_variant	LOW	CYTB	0.0526
HLI-0113	15326	A	G	0	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0113	15452	C	A	5	506	missense_variant	MODERATE	CYTB	0.0933
HLI-0113	15607	A	G	2	557	synonymous_variant	LOW	CYTB	0.0508
HLI-0113	15928	G	A	2	591	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0113	16126	T	C	0	516	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0113	16294	C	T	0	538	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0113	16296	C	T	0	530	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0113	16304	T	C	0	516	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0113	16519	T	C	1	204	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0114	263	A	G	0	205	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0114	750	A	G	0	548	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0114	1438	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0114	4769	A	G	1	499	synonymous_variant	LOW	ND2	0.9767
HLI-0114	4793	A	G	0	561	synonymous_variant	LOW	ND2	0.0073
HLI-0114	15326	A	G	0	548	missense_variant	MODERATE	CYTB	0.9868
HLI-0114	16355	C	T	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0114	16519	T	C	4	236	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0115	73	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0115	146	T	C	0	391	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0115	185	G	A	0	376	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0115	188	A	G	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0115	228	G	A	0	136	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0115	263	A	G	0	162	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0115	295	C	T	0	143	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0115	462	C	T	2	303	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0115	489	T	C	0	353	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0115	750	A	G	0	541	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0115	1438	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0115	2706	A	G	0	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0115	3010	G	A	1	529	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0115	4216	T	C	0	534	missense_variant	MODERATE	ND1	0.0991
HLI-0115	4769	A	G	0	506	synonymous_variant	LOW	ND2	0.9767
HLI-0115	7028	C	T	1	571	synonymous_variant	LOW	COX1	0.8089
HLI-0115	8865	G	A	0	520	synonymous_variant	LOW	ATP6	0.003
HLI-0115	10398	A	G	0	571	missense_variant	MODERATE	ND3	0.445
HLI-0115	10685	G	A	0	530	synonymous_variant	LOW	ND4L	0.0055
HLI-0115	11251	A	G	2	510	synonymous_variant	LOW	ND4	0.0932
HLI-0115	11719	G	A	2	527	synonymous_variant	LOW	ND4	0.7756
HLI-0115	12612	A	G	2	575	synonymous_variant	LOW	ND5	0.0506
HLI-0115	13281	T	C	0	591	synonymous_variant	LOW	ND5	0.0033
HLI-0115	13708	G	A	0	411	missense_variant	MODERATE	ND5	0.0717
HLI-0115	13933	A	G	1	432	missense_variant	MODERATE	ND5	0.0022
HLI-0115	14766	C	T	0	484	missense_variant	MODERATE	CYTB	0.7696
HLI-0115	14798	T	C	1	546	missense_variant	MODERATE	CYTB	0.0651
HLI-0115	15326	A	G	0	507	missense_variant	MODERATE	CYTB	0.9868
HLI-0115	15452	C	A	8	464	missense_variant	MODERATE	CYTB	0.0933
HLI-0115	16069	C	T	1	555	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0115	16126	T	C	1	553	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0115	16519	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0116	73	A	G	1	261	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0116	152	T	C	0	468	upstream_gene_variant	MODIFIER	DLoop	0.2668

HLI-0116	263	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0116	709	G	A	1	566	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0116	750	A	G	2	618	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0116	1438	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0116	1888	G	A	0	587	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0116	2706	A	G	1	630	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0116	4216	T	C	0	571	missense_variant	MODERATE	ND1	0.0991
HLI-0116	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767
HLI-0116	4917	A	G	2	550	missense_variant	MODERATE	ND2	0.0477
HLI-0116	5378	A	G	0	525	synonymous_variant	LOW	ND2	0.0011
HLI-0116	5592	A	G	2	624	upstream_gene_variant	MODIFIER	TRNA	5.00E-04
HLI-0116	6040	A	G	2	586	missense_variant	MODERATE	COX1	0.0018
HLI-0116	6152	T	C	2	531	synonymous_variant	LOW	COX1	0.0077
HLI-0116	7028	C	T	4	622	synonymous_variant	LOW	COX1	0.8089
HLI-0116	8697	G	A	0	501	synonymous_variant	LOW	ATP6	0.0466
HLI-0116	10463	T	C	0	639	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0116	11251	A	G	2	516	synonymous_variant	LOW	ND4	0.0932
HLI-0116	11719	G	A	1	529	synonymous_variant	LOW	ND4	0.7756
HLI-0116	12406	G	A	4	531	missense_variant	MODERATE	ND5	0.0262
HLI-0116	12633	C	A	7	646	synonymous_variant	LOW	ND5	0.0123
HLI-0116	13368	G	A	1	534	synonymous_variant	LOW	ND5	0.0495
HLI-0116	14766	C	T	2	546	missense_variant	MODERATE	CYTB	0.7696
HLI-0116	14905	G	A	0	546	synonymous_variant	LOW	CYTB	0.0526
HLI-0116	14969	T	C	0	589	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0116	15326	A	G	1	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0116	15452	C	A	3	498	missense_variant	MODERATE	CYTB	0.0933
HLI-0116	15607	A	G	1	620	synonymous_variant	LOW	CYTB	0.0508
HLI-0116	15928	G	A	0	603	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0116	16126	T	C	0	490	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0116	16163	A	G	1	500	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0116	16294	C	T	0	453	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0116	16304	T	C	0	479	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0116	16519	T	C	0	220	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0117	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0117	185	G	A	2	379	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0117	228	G	A	2	369	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0117	263	A	G	1	177	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0117	295	C	T	1	198	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0117	462	C	T	4	433	upstream_gene_variant	MODIFIER	DLoop	0.0341

HLI-0117	489	T	C	1	333	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0117	750	A	G	0	555	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0117	1438	A	G	1	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0117	2706	A	G	0	565	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0117	3010	G	A	1	594	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0117	3221	A	G	1	540	upstream_gene_variant	MODIFIER	RNR2	0.0013
HLI-0117	4216	T	C	3	581	missense_variant	MODERATE	ND1	0.0991
HLI-0117	4769	A	G	0	528	synonymous_variant	LOW	ND2	0.9767
HLI-0117	7028	C	T	4	636	synonymous_variant	LOW	COX1	0.8089
HLI-0117	8805	A	G	0	541	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0117	10398	A	G	0	605	missense_variant	MODERATE	ND3	0.445
HLI-0117	11251	A	G	0	577	synonymous_variant	LOW	ND4	0.0932
HLI-0117	11719	G	A	0	531	synonymous_variant	LOW	ND4	0.7756
HLI-0117	12366	A	G	1	546	synonymous_variant	LOW	ND5	0.0014
HLI-0117	12612	A	G	7	595	synonymous_variant	LOW	ND5	0.0506
HLI-0117	13145	G	A	1	531	missense_variant	MODERATE	ND5	0.0094
HLI-0117	13708	G	A	0	413	missense_variant	MODERATE	ND5	0.0717
HLI-0117	13934	C	T	1	463	missense_variant	MODERATE	ND5	0.0122
HLI-0117	14296	A	G	0	497	synonymous_variant	LOW	ND6	3.00E-04
HLI-0117	14766	C	T	0	519	missense_variant	MODERATE	CYTB	0.7696
HLI-0117	14798	T	C	1	609	missense_variant	MODERATE	CYTB	0.0651
HLI-0117	15326	A	G	0	532	missense_variant	MODERATE	CYTB	0.9868
HLI-0117	15452	C	A	4	520	missense_variant	MODERATE	CYTB	0.0933
HLI-0117	16069	C	T	2	559	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0117	16126	T	C	0	592	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0117	16390	G	A	0	406	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0118	152	T	C	1	452	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0118	263	A	G	0	163	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0118	750	A	G	0	612	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0118	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0118	4769	A	G	0	544	synonymous_variant	LOW	ND2	0.9767
HLI-0118	6776	T	C	2	703	synonymous_variant	LOW	COX1	0.0226
HLI-0118	14198	G	A	1	494	missense_variant	MODERATE	ND6	0.001
HLI-0118	15326	A	G	0	552	missense_variant	MODERATE	CYTB	0.9868
HLI-0118	16519	T	C	0	239	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0119	73	A	G	0	260	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0119	185	G	A	4	348	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0119	263	A	G	0	208	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0119	750	A	G	0	547	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0119	1438	A	G	0	598	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0119	1700	T	C	0	619	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0119	2706	A	G	0	605	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0119	3197	T	C	1	552	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0119	4769	A	G	1	557	synonymous_variant	LOW	ND2	0.9767
HLI-0119	5319	A	G	0	524	missense_variant	MODERATE	ND2	0.0031
HLI-0119	6629	A	G	4	634	synonymous_variant	LOW	COX1	0.0019
HLI-0119	6719	T	C	2	720	synonymous_variant	LOW	COX1	0.041
HLI-0119	7028	C	T	0	660	synonymous_variant	LOW	COX1	0.8089
HLI-0119	9021	T	C	1	542	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0119	9477	G	A	2	603	missense_variant	MODERATE	COX3	0.0387
HLI-0119	11467	A	G	4	572	synonymous_variant	LOW	ND4	0.1231
HLI-0119	11719	G	A	0	571	synonymous_variant	LOW	ND4	0.7756
HLI-0119	12308	A	G	1	561	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0119	12346	C	T	0	625	missense_variant	MODERATE	ND5	0.0056
HLI-0119	12372	G	A	1	613	synonymous_variant	LOW	ND5	0.1329
HLI-0119	13617	T	C	0	536	synonymous_variant	LOW	ND5	0.038
HLI-0119	14766	C	T	6	572	missense_variant	MODERATE	CYTB	0.7696
HLI-0119	14793	A	G	3	646	missense_variant	MODERATE	CYTB	0.0199
HLI-0119	15218	A	G	1	607	missense_variant	MODERATE	CYTB	0.0169
HLI-0119	15326	A	G	1	537	missense_variant	MODERATE	CYTB	0.9868
HLI-0119	16256	C	T	0	610	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0119	16270	C	T	0	610	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0119	16399	A	G	1	433	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0120	73	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0120	263	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0120	709	G	A	2	582	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0120	750	A	G	3	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0120	1438	A	G	1	580	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0120	1888	G	A	0	587	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0120	2706	A	G	0	636	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0120	2850	T	C	0	584	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0120	4216	T	C	2	581	missense_variant	MODERATE	ND1	0.0991
HLI-0120	4769	A	G	2	569	synonymous_variant	LOW	ND2	0.9767
HLI-0120	4917	A	G	0	517	missense_variant	MODERATE	ND2	0.0477
HLI-0120	6425	T	C	0	533	synonymous_variant	LOW	COX1	7.00E-04
HLI-0120	7022	T	C	2	688	synonymous_variant	LOW	COX1	0.0024
HLI-0120	7028	C	T	2	690	synonymous_variant	LOW	COX1	0.8089
HLI-0120	8697	G	A	0	515	synonymous_variant	LOW	ATP6	0.0466

HLI-0120	10463	T	C	0	607	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0120	11251	A	G	0	560	synonymous_variant	LOW	ND4	0.0932
HLI-0120	11719	G	A	2	514	synonymous_variant	LOW	ND4	0.7756
HLI-0120	11812	A	G	1	527	synonymous_variant	LOW	ND4	0.0332
HLI-0120	13368	G	A	0	587	synonymous_variant	LOW	ND5	0.0495
HLI-0120	13965	T	C	0	432	synonymous_variant	LOW	ND5	0.005
HLI-0120	14233	A	G	0	455	synonymous_variant	LOW	ND6	0.0369
HLI-0120	14687	A	G	2	552	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0120	14766	C	T	1	589	missense_variant	MODERATE	CYTB	0.7696
HLI-0120	14905	G	A	0	555	synonymous_variant	LOW	CYTB	0.0526
HLI-0120	15326	A	G	0	464	missense_variant	MODERATE	CYTB	0.9868
HLI-0120	15452	C	A	4	512	missense_variant	MODERATE	CYTB	0.0933
HLI-0120	15607	A	G	2	546	synonymous_variant	LOW	CYTB	0.0508
HLI-0120	15928	G	A	0	594	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0120	16126	T	C	0	531	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0120	16256	C	T	1	540	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0120	16294	C	T	0	542	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0120	16296	C	T	0	530	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0120	16519	T	C	0	216	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0121	73	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0121	150	C	T	1	416	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0121	263	A	G	0	144	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0121	709	G	A	0	579	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0121	750	A	G	3	622	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0121	1438	A	G	0	541	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0121	1888	G	A	0	541	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0121	2706	A	G	1	547	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0121	4216	T	C	0	583	missense_variant	MODERATE	ND1	0.0991
HLI-0121	4769	A	G	0	515	synonymous_variant	LOW	ND2	0.9767
HLI-0121	4917	A	G	2	484	missense_variant	MODERATE	ND2	0.0477
HLI-0121	7028	C	T	3	601	synonymous_variant	LOW	COX1	0.8089
HLI-0121	8269	G	A	0	474	stop_retained_variant	LOW	COX2	0.0127
HLI-0121	8697	G	A	1	490	synonymous_variant	LOW	ATP6	0.0466
HLI-0121	10463	T	C	0	592	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0121	11251	A	G	3	539	synonymous_variant	LOW	ND4	0.0932
HLI-0121	11719	G	A	0	515	synonymous_variant	LOW	ND4	0.7756
HLI-0121	11812	A	G	0	558	synonymous_variant	LOW	ND4	0.0332
HLI-0121	13368	G	A	1	559	synonymous_variant	LOW	ND5	0.0495
HLI-0121	14233	A	G	0	447	synonymous_variant	LOW	ND6	0.0369

HLI-0121	14766	C	T	1	441	missense_variant	MODERATE	CYTB	0.7696
HLI-0121	14905	G	A	0	535	synonymous_variant	LOW	CYTB	0.0526
HLI-0121	15326	A	G	0	458	missense_variant	MODERATE	CYTB	0.9868
HLI-0121	15452	C	A	7	511	missense_variant	MODERATE	CYTB	0.0933
HLI-0121	15607	A	G	0	507	synonymous_variant	LOW	CYTB	0.0508
HLI-0121	15928	G	A	1	574	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0121	16126	T	C	0	445	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0121	16153	G	A	2	472	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0121	16294	C	T	3	468	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0121	16296	C	T	3	470	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0121	16519	T	C	1	171	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0122	64	C	T	0	227	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0122	72	T	C	0	253	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0122	195	T	C	0	352	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0122	263	A	G	0	198	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0122	750	A	G	0	581	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0122	1438	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0122	2706	A	G	1	640	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0122	4769	A	G	0	554	synonymous_variant	LOW	ND2	0.9767
HLI-0122	7028	C	T	2	660	synonymous_variant	LOW	COX1	0.8089
HLI-0122	7543	A	G	2	676	upstream_gene_variant	MODIFIER	TRND	8.00E-04
HLI-0122	10463	T	C	0	543	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0122	15110	G	A	1	637	missense_variant	MODERATE	CYTB	0.009
HLI-0122	15326	A	G	1	549	missense_variant	MODERATE	CYTB	0.9868
HLI-0122	16298	T	C	1	591	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0123	199	T	C	0	49	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0123	263	A	G	0	20	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0123	750	A	G	0	35	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0123	1438	A	G	0	35	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0123	4769	A	G	0	39	synonymous_variant	LOW	ND2	0.9767
HLI-0123	6776	T	C	0	45	synonymous_variant	LOW	COX1	0.0226
HLI-0123	8557	G	A	0	29	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0123	10915	T	C	0	22	synonymous_variant	LOW	ND4	0.0411
HLI-0123	15326	A	G	0	47	missense_variant	MODERATE	CYTB	0.9868
HLI-0123	16519	T	C	0	16	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0124	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0124	263	A	G	0	199	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0124	750	A	G	1	519	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0124	1438	A	G	3	582	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0124	3992	C	T	0	477	missense_variant	MODERATE	ND1	0.0062
HLI-0124	4024	A	G	0	498	missense_variant	MODERATE	ND1	0.0049
HLI-0124	4769	A	G	2	500	synonymous_variant	LOW	ND2	0.9767
HLI-0124	5004	T	C	8	529	synonymous_variant	LOW	ND2	0.0067
HLI-0124	8269	G	A	0	513	stop_retained_variant	LOW	COX2	0.0127
HLI-0124	9123	G	A	0	580	synonymous_variant	LOW	ATP6	0.0485
HLI-0124	10044	A	G	0	530	upstream_gene_variant	MODIFIER	TRNG	0.0027
HLI-0124	13545	C	T	1	498	synonymous_variant	LOW	ND5	2.00E-04
HLI-0124	14325	T	C	0	421	missense_variant	MODERATE	ND6	0.001
HLI-0124	14365	C	T	2	506	synonymous_variant	LOW	ND6	0.0046
HLI-0124	14582	A	G	2	488	missense_variant	MODERATE	ND6	0.005
HLI-0124	15326	A	G	0	540	missense_variant	MODERATE	CYTB	0.9868
HLI-0125	73	A	G	0	169	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0125	146	T	C	0	255	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0125	150	C	T	0	259	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0125	152	T	C	0	257	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0125	182	C	T	0	265	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0125	195	T	C	0	252	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0125	198	C	T	0	251	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0125	204	T	C	0	262	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0125	263	A	G	0	140	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0125	709	G	A	0	549	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0125	750	A	G	0	631	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0125	769	G	A	0	626	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0125	1018	G	A	0	589	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0125	1438	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0125	1442	G	A	0	590	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0125	1706	C	T	1	568	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0125	2332	C	T	1	595	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0125	2358	A	G	3	649	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0125	2416	T	C	1	625	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0125	2706	A	G	0	610	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0125	3594	C	T	1	472	synonymous_variant	LOW	ND1	0.0789
HLI-0125	4104	A	G	1	479	synonymous_variant	LOW	ND1	0.0785
HLI-0125	4158	A	G	1	506	synonymous_variant	LOW	ND1	0.0023
HLI-0125	4370	T	C	0	530	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0125	4767	A	G	0	557	missense_variant	MODERATE	ND2	0.0029
HLI-0125	4769	A	G	0	563	synonymous_variant	LOW	ND2	0.9767
HLI-0125	5027	C	T	1	577	synonymous_variant	LOW	ND2	0.003

HLI-0125	5331	C	A	3	592	missense_variant	MODERATE	ND2	0.0022
HLI-0125	5814	T	C	0	578	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0125	6614	T	C	0	622	synonymous_variant	LOW	COX1	0.001
HLI-0125	6713	C	T	1	627	synonymous_variant	LOW	COX1	0.0028
HLI-0125	6806	A	G	1	597	synonymous_variant	LOW	COX1	0.0012
HLI-0125	7028	C	T	1	635	synonymous_variant	LOW	COX1	0.8089
HLI-0125	7256	C	T	2	534	synonymous_variant	LOW	COX1	0.0784
HLI-0125	7521	G	A	1	424	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0125	7624	T	A	4	556	synonymous_variant	LOW	COX2	0.0047
HLI-0125	8080	C	T	3	547	synonymous_variant	LOW	COX2	0.0022
HLI-0125	8206	G	A	2	538	synonymous_variant	LOW	COX2	0.0287
HLI-0125	8387	G	A	1	521	missense_variant	MODERATE	ATP8	0.0028
HLI-0125	8503	T	C	0	416	synonymous_variant	LOW	ATP8	0.0019
HLI-0125	8701	A	G	0	467	missense_variant	MODERATE	ATP6	0.3391
HLI-0125	8790	G	A	1	419	synonymous_variant	LOW	ATP6	0.0083
HLI-0125	9221	A	G	0	557	synonymous_variant	LOW	COX3	0.0277
HLI-0125	9350	A	G	0	570	synonymous_variant	LOW	COX3	5.00E-04
HLI-0125	9540	T	C	0	509	synonymous_variant	LOW	COX3	0.339
HLI-0125	10115	T	C	0	667	synonymous_variant	LOW	ND3	0.0278
HLI-0125	10398	A	G	2	623	missense_variant	MODERATE	ND3	0.445
HLI-0125	10873	T	C	1	529	synonymous_variant	LOW	ND4	0.3389
HLI-0125	11719	G	A	0	548	synonymous_variant	LOW	ND4	0.7756
HLI-0125	11944	T	C	0	511	synonymous_variant	LOW	ND4	0.0331
HLI-0125	12236	G	A	3	522	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0125	12705	C	T	3	614	synonymous_variant	LOW	ND5	0.4212
HLI-0125	12948	A	G	4	533	synonymous_variant	LOW	ND5	0.0022
HLI-0125	13590	G	A	0	564	synonymous_variant	LOW	ND5	0.0586
HLI-0125	13650	C	T	2	549	synonymous_variant	LOW	ND5	0.079
HLI-0125	13966	A	G	0	534	missense_variant	MODERATE	ND5	0.0126
HLI-0125	14059	A	G	1	469	missense_variant	MODERATE	ND5	0.0022
HLI-0125	14407	C	T	1	458	synonymous_variant	LOW	ND6	7.00E-04
HLI-0125	14766	C	T	2	514	missense_variant	MODERATE	CYTB	0.7696
HLI-0125	15110	G	A	0	569	missense_variant	MODERATE	CYTB	0.009
HLI-0125	15217	G	A	0	528	synonymous_variant	LOW	CYTB	0.0104
HLI-0125	15301	G	A	0	550	synonymous_variant	LOW	CYTB	0.2912
HLI-0125	15326	A	G	0	567	missense_variant	MODERATE	CYTB	0.9868
HLI-0125	16114	C	A	1	485	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0125	16129	G	A	1	509	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0125	16175	A	G	1	493	upstream_gene_variant	MODIFIER	DLoop	6.00E-04

HLI-0125	16213	G	A	0	519	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0125	16223	C	T	0	521	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0125	16278	C	T	1	498	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0125	16354	C	T	1	385	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0125	16390	G	A	2	400	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0126	73	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0126	185	G	A	0	466	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0126	188	A	G	0	470	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0126	200	A	G	0	426	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0126	228	G	A	0	356	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0126	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0126	295	C	T	0	201	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0126	462	C	T	1	349	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0126	489	T	C	0	460	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0126	750	A	G	0	796	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0126	1438	A	G	1	711	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0126	2706	A	G	2	735	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0126	3010	G	A	0	730	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0126	4216	T	C	2	805	missense_variant	MODERATE	ND1	0.0991
HLI-0126	4769	A	G	1	632	synonymous_variant	LOW	ND2	0.9767
HLI-0126	7028	C	T	6	817	synonymous_variant	LOW	COX1	0.8089
HLI-0126	10398	A	G	1	736	missense_variant	MODERATE	ND3	0.445
HLI-0126	11251	A	G	4	703	synonymous_variant	LOW	ND4	0.0932
HLI-0126	11719	G	A	2	734	synonymous_variant	LOW	ND4	0.7756
HLI-0126	12612	A	G	6	741	synonymous_variant	LOW	ND5	0.0506
HLI-0126	13708	G	A	0	633	missense_variant	MODERATE	ND5	0.0717
HLI-0126	14766	C	T	5	717	missense_variant	MODERATE	CYTB	0.7696
HLI-0126	14798	T	C	1	799	missense_variant	MODERATE	CYTB	0.0651
HLI-0126	15172	G	A	1	680	synonymous_variant	LOW	CYTB	0.0075
HLI-0126	15326	A	G	0	718	missense_variant	MODERATE	CYTB	0.9868
HLI-0126	15452	C	A	2	678	missense_variant	MODERATE	CYTB	0.0933
HLI-0126	15773	G	A	1	771	missense_variant	MODERATE	CYTB	0.0011
HLI-0126	16069	C	T	3	721	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0126	16126	T	C	2	705	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0126	16366	C	T	4	535	upstream_gene_variant	MODIFIER	DLoop	0.0014
HLI-0126	16519	T	C	0	395	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0127	263	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0127	750	A	G	1	777	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0127	1438	A	G	0	751	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0127	3010	G	A	0	772	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0127	4769	A	G	0	665	synonymous_variant	LOW	ND2	0.9767
HLI-0127	5111	C	T	0	713	synonymous_variant	LOW	ND2	0.0012
HLI-0127	10257	C	T	1	686	synonymous_variant	LOW	ND3	5.00E-04
HLI-0127	12236	G	A	2	666	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0127	15326	A	G	0	750	missense_variant	MODERATE	CYTB	0.9868
HLI-0127	16145	G	A	0	684	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0127	16222	C	T	3	733	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0127	16259	C	A	8	717	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0127	16519	T	C	0	399	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0128	263	A	G	0	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0128	477	T	C	1	476	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0128	750	A	G	0	684	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0128	1438	A	G	0	804	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0128	3010	G	A	2	747	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0128	4769	A	G	0	676	synonymous_variant	LOW	ND2	0.9767
HLI-0128	8188	A	G	1	767	synonymous_variant	LOW	COX2	0.0069
HLI-0128	14467	A	G	1	692	synonymous_variant	LOW	ND6	2.00E-04
HLI-0128	15326	A	G	0	687	missense_variant	MODERATE	CYTB	0.9868
HLI-0128	16519	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0129	195	T	C	1	562	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0129	257	A	G	2	272	upstream_gene_variant	MODIFIER	DLoop	0.0025
HLI-0129	263	A	G	2	278	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0129	477	T	C	1	353	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0129	750	A	G	0	694	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0129	1438	A	G	0	729	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0129	3010	G	A	1	684	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0129	4769	A	G	1	652	synonymous_variant	LOW	ND2	0.9767
HLI-0129	5147	G	A	2	518	synonymous_variant	LOW	ND2	0.0437
HLI-0129	8473	T	C	0	513	synonymous_variant	LOW	ATP8	0.0105
HLI-0129	15326	A	G	0	521	missense_variant	MODERATE	CYTB	0.9868
HLI-0129	16519	T	C	1	315	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0130	73	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0130	263	A	G	0	209	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0130	497	C	T	4	416	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0130	750	A	G	2	580	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0130	1189	T	C	0	571	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0130	1438	A	G	0	577	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0130	1811	A	G	2	621	upstream_gene_variant	MODIFIER	RNR2	0.0763

HLI-0130	2706	A	G	0	562	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0130	3480	A	G	1	425	synonymous_variant	LOW	ND1	0.0392
HLI-0130	3796	A	G	1	502	missense_variant	MODERATE	ND1	0.0048
HLI-0130	4769	A	G	2	521	synonymous_variant	LOW	ND2	0.9767
HLI-0130	4823	T	C	0	586	synonymous_variant	LOW	ND2	0.0049
HLI-0130	6528	C	T	1	633	synonymous_variant	LOW	COX1	0.0013
HLI-0130	7028	C	T	5	624	synonymous_variant	LOW	COX1	0.8089
HLI-0130	8842	A	C	0	489	missense_variant	MODERATE	ATP6	1.00E-04
HLI-0130	9055	G	A	0	483	missense_variant	MODERATE	ATP6	0.0425
HLI-0130	9698	T	C	0	536	synonymous_variant	LOW	COX3	0.0405
HLI-0130	10398	A	G	1	605	missense_variant	MODERATE	ND3	0.445
HLI-0130	10550	A	G	1	537	synonymous_variant	LOW	ND4L	0.0376
HLI-0130	11299	T	C	0	571	synonymous_variant	LOW	ND4	0.0417
HLI-0130	11467	A	G	0	607	synonymous_variant	LOW	ND4	0.1231
HLI-0130	11470	A	G	0	616	synonymous_variant	LOW	ND4	0.0029
HLI-0130	11719	G	A	0	520	synonymous_variant	LOW	ND4	0.7756
HLI-0130	11914	G	A	0	519	synonymous_variant	LOW	ND4	0.1112
HLI-0130	12308	A	G	1	554	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0130	12372	G	A	2	566	synonymous_variant	LOW	ND5	0.1329
HLI-0130	14167	C	T	3	512	synonymous_variant	LOW	ND6	0.0385
HLI-0130	14766	C	T	2	573	missense_variant	MODERATE	CYTB	0.7696
HLI-0130	14798	T	C	1	607	missense_variant	MODERATE	CYTB	0.0651
HLI-0130	15326	A	G	1	524	missense_variant	MODERATE	CYTB	0.9868
HLI-0130	15924	A	G	0	602	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0130	16093	T	C	10	521	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0130	16224	T	C	0	521	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0130	16311	T	C	0	508	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0130	16519	T	C	0	275	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0131	73	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0131	263	A	G	0	207	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0131	264	C	T	0	207	upstream_gene_variant	MODIFIER	DLoop	0.0014
HLI-0131	497	C	T	4	317	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0131	750	A	G	0	509	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0131	1189	T	C	0	543	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0131	1438	A	G	0	538	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0131	1811	A	G	0	614	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0131	2706	A	G	1	589	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0131	3480	A	G	0	488	synonymous_variant	LOW	ND1	0.0392
HLI-0131	4769	A	G	2	481	synonymous_variant	LOW	ND2	0.9767

HLI-0131	7028	C	T	2	586	synonymous_variant	LOW	COX1	0.8089
HLI-0131	9055	G	A	0	461	missense_variant	MODERATE	ATP6	0.0425
HLI-0131	9698	T	C	0	561	synonymous_variant	LOW	COX3	0.0405
HLI-0131	10398	A	G	2	596	missense_variant	MODERATE	ND3	0.445
HLI-0131	10550	A	G	2	518	synonymous_variant	LOW	ND4L	0.0376
HLI-0131	10586	G	A	0	535	synonymous_variant	LOW	ND4L	0.0177
HLI-0131	11299	T	C	0	490	synonymous_variant	LOW	ND4	0.0417
HLI-0131	11467	A	G	0	557	synonymous_variant	LOW	ND4	0.1231
HLI-0131	11485	T	C	0	612	synonymous_variant	LOW	ND4	0.0081
HLI-0131	11719	G	A	1	559	synonymous_variant	LOW	ND4	0.7756
HLI-0131	12308	A	G	0	572	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0131	12372	G	A	0	543	synonymous_variant	LOW	ND5	0.1329
HLI-0131	14167	C	T	2	454	synonymous_variant	LOW	ND6	0.0385
HLI-0131	14280	A	G	1	415	missense_variant	MODERATE	ND6	0.0014
HLI-0131	14766	C	T	6	514	missense_variant	MODERATE	CYTB	0.7696
HLI-0131	14798	T	C	0	574	missense_variant	MODERATE	CYTB	0.0651
HLI-0131	15326	A	G	1	493	missense_variant	MODERATE	CYTB	0.9868
HLI-0131	15530	T	C	1	456	synonymous_variant	LOW	CYTB	0.0036
HLI-0131	16093	T	C	8	482	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0131	16224	T	C	0	482	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0131	16311	T	C	0	382	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0131	16519	T	C	0	162	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0132	263	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0132	477	T	C	0	301	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0132	750	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0132	1438	A	G	0	601	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0132	3010	G	A	1	600	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0132	4769	A	G	1	517	synonymous_variant	LOW	ND2	0.9767
HLI-0132	14350	C	T	3	484	synonymous_variant	LOW	ND6	3.00E-04
HLI-0132	15326	A	G	0	518	missense_variant	MODERATE	CYTB	0.9868
HLI-0132	16519	T	C	0	266	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0133	73	A	G	0	279	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0133	263	A	G	1	229	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0133	750	A	G	1	584	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0133	1438	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0133	2706	A	G	2	591	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0133	3450	C	T	0	525	synonymous_variant	LOW	ND1	0.0084
HLI-0133	3866	T	C	1	506	missense_variant	MODERATE	ND1	0.0029
HLI-0133	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767

HLI-0133	5773	G	A	2	643	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0133	6221	T	C	1	545	synonymous_variant	LOW	COX1	0.0306
HLI-0133	7028	C	T	2	674	synonymous_variant	LOW	COX1	0.8089
HLI-0133	7581	T	C	1	651	upstream_gene_variant	MODIFIER	TRND	0.0044
HLI-0133	8701	A	G	0	490	missense_variant	MODERATE	ATP6	0.3391
HLI-0133	9055	G	A	0	559	missense_variant	MODERATE	ATP6	0.0425
HLI-0133	9449	C	T	1	531	synonymous_variant	LOW	COX3	0.0125
HLI-0133	9540	T	C	0	508	synonymous_variant	LOW	COX3	0.339
HLI-0133	10086	A	G	0	645	missense_variant	MODERATE	ND3	0.0088
HLI-0133	10373	G	A	0	668	synonymous_variant	LOW	ND3	0.0117
HLI-0133	10398	A	G	0	689	missense_variant	MODERATE	ND3	0.445
HLI-0133	10873	T	C	0	372	synonymous_variant	LOW	ND4	0.3389
HLI-0133	11002	A	G	0	394	synonymous_variant	LOW	ND4	0.0124
HLI-0133	11719	G	A	1	570	synonymous_variant	LOW	ND4	0.7756
HLI-0133	12705	C	T	2	640	synonymous_variant	LOW	ND5	0.4212
HLI-0133	13105	A	G	0	560	missense_variant	MODERATE	ND5	0.076
HLI-0133	13914	C	A	3	480	synonymous_variant	LOW	ND5	0.0091
HLI-0133	14766	C	T	7	584	missense_variant	MODERATE	CYTB	0.7696
HLI-0133	14791	C	T	0	638	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0133	15301	G	A	0	590	synonymous_variant	LOW	CYTB	0.2912
HLI-0133	15311	A	G	0	623	missense_variant	MODERATE	CYTB	0.008
HLI-0133	15326	A	G	0	638	missense_variant	MODERATE	CYTB	0.9868
HLI-0133	15824	A	G	1	588	missense_variant	MODERATE	CYTB	0.0083
HLI-0133	16124	T	C	1	550	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0133	16223	C	T	3	533	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0133	16278	C	T	0	545	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0133	16362	T	C	1	424	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0133	16519	T	C	0	215	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0134	263	A	G	0	189	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0134	750	A	G	1	613	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0134	1438	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0134	3010	G	A	0	640	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0134	4769	A	G	1	546	synonymous_variant	LOW	ND2	0.9767
HLI-0134	9078	T	C	0	581	synonymous_variant	LOW	ATP6	9.00E-04
HLI-0134	15326	A	G	0	543	missense_variant	MODERATE	CYTB	0.9868
HLI-0134	15646	C	T	4	565	synonymous_variant	LOW	CYTB	7.00E-04
HLI-0134	16357	T	C	1	441	upstream_gene_variant	MODIFIER	DLoop	0.01
HLI-0134	16519	T	C	0	246	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0135	73	A	G	0	21	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0135	152	T	C	0	42	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0135	199	T	C	0	35	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0135	204	T	C	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0135	250	T	C	0	27	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0135	263	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0135	750	A	G	0	41	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0135	1438	A	G	0	54	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0135	1719	G	A	0	33	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0135	2220	A	G	0	35	upstream_gene_variant	MODIFIER	RNR2	0.0029
HLI-0135	2706	A	G	0	44	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0135	4529	A	T	0	36	synonymous_variant	LOW	ND2	0.015
HLI-0135	4769	A	G	0	42	synonymous_variant	LOW	ND2	0.9767
HLI-0135	6227	T	C	0	54	synonymous_variant	LOW	COX1	0.0019
HLI-0135	6734	G	A	0	58	synonymous_variant	LOW	COX1	0.0062
HLI-0135	7028	C	T	1	51	synonymous_variant	LOW	COX1	0.8089
HLI-0135	8251	G	A	0	12	synonymous_variant	LOW	COX2	0.058
HLI-0135	9966	G	A	0	58	missense_variant	MODERATE	COX3	0.0069
HLI-0135	10034	T	C	0	52	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0135	10238	T	C	0	47	synonymous_variant	LOW	ND3	0.0623
HLI-0135	10398	A	G	0	34	missense_variant	MODERATE	ND3	0.445
HLI-0135	10915	T	C	0	35	synonymous_variant	LOW	ND4	0.0411
HLI-0135	11719	G	A	0	36	synonymous_variant	LOW	ND4	0.7756
HLI-0135	12501	G	A	0	54	synonymous_variant	LOW	ND5	0.0258
HLI-0135	12705	C	T	1	45	synonymous_variant	LOW	ND5	0.4212
HLI-0135	13780	A	G	0	30	missense_variant	MODERATE	ND5	0.0179
HLI-0135	14766	C	T	0	39	missense_variant	MODERATE	CYTB	0.7696
HLI-0135	15043	G	A	0	48	synonymous_variant	LOW	CYTB	0.2362
HLI-0135	15326	A	G	0	51	missense_variant	MODERATE	CYTB	0.9868
HLI-0135	15924	A	G	0	59	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0135	16223	C	T	0	52	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0135	16311	T	C	0	46	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0135	16352	T	C	0	39	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0135	16391	G	A	0	38	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0136	73	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0136	152	T	C	1	491	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0136	263	A	G	0	201	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0136	709	G	A	0	591	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0136	750	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0136	930	G	A	1	560	upstream_gene_variant	MODIFIER	RNR1	0.0202

HLI-0136	1438	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0136	1888	G	A	1	564	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0136	2706	A	G	2	550	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0136	4216	T	C	0	549	missense_variant	MODERATE	ND1	0.0991
HLI-0136	4769	A	G	3	504	synonymous_variant	LOW	ND2	0.9767
HLI-0136	4917	A	G	0	517	missense_variant	MODERATE	ND2	0.0477
HLI-0136	5147	G	A	1	516	synonymous_variant	LOW	ND2	0.0437
HLI-0136	7028	C	T	6	639	synonymous_variant	LOW	COX1	0.8089
HLI-0136	8697	G	A	1	459	synonymous_variant	LOW	ATP6	0.0466
HLI-0136	10463	T	C	1	592	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0136	11242	C	G	1	548	synonymous_variant	LOW	ND4	4.00E-04
HLI-0136	11251	A	G	1	575	synonymous_variant	LOW	ND4	0.0932
HLI-0136	11719	G	A	1	653	synonymous_variant	LOW	ND4	0.7756
HLI-0136	11812	A	G	1	593	synonymous_variant	LOW	ND4	0.0332
HLI-0136	13368	G	A	1	546	synonymous_variant	LOW	ND5	0.0495
HLI-0136	14233	A	G	1	492	synonymous_variant	LOW	ND6	0.0369
HLI-0136	14766	C	T	2	471	missense_variant	MODERATE	CYTB	0.7696
HLI-0136	14905	G	A	1	548	synonymous_variant	LOW	CYTB	0.0526
HLI-0136	15326	A	G	0	516	missense_variant	MODERATE	CYTB	0.9868
HLI-0136	15452	C	A	7	541	missense_variant	MODERATE	CYTB	0.0933
HLI-0136	15607	A	G	1	563	synonymous_variant	LOW	CYTB	0.0508
HLI-0136	15928	G	A	0	577	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0136	16126	T	C	0	562	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0136	16294	C	T	3	509	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0136	16519	T	C	0	247	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0137	263	A	G	0	151	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0137	750	A	G	0	519	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0137	1438	A	G	1	570	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0137	2259	C	T	0	553	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0137	4745	A	G	1	540	synonymous_variant	LOW	ND2	0.0039
HLI-0137	4769	A	G	0	556	synonymous_variant	LOW	ND2	0.9767
HLI-0137	7337	G	A	2	572	synonymous_variant	LOW	COX1	0.0119
HLI-0137	13326	T	C	0	583	synonymous_variant	LOW	ND5	0.0032
HLI-0137	13680	C	T	0	431	synonymous_variant	LOW	ND5	0.005
HLI-0137	14727	T	C	0	577	upstream_gene_variant	MODIFIER	TRNE	0.0025
HLI-0137	14872	C	T	2	593	synonymous_variant	LOW	CYTB	0.0061
HLI-0137	15326	A	G	0	520	missense_variant	MODERATE	CYTB	0.9868
HLI-0138	73	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0138	152	T	C	0	455	upstream_gene_variant	MODIFIER	DLoop	0.2668

HLI-0138	195	T	C	0	432	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0138	263	A	G	0	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0138	750	A	G	2	562	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0138	921	T	C	0	619	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0138	1438	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0138	2706	A	G	1	619	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0138	4769	A	G	0	515	synonymous_variant	LOW	ND2	0.9767
HLI-0138	5046	G	A	1	544	missense_variant	MODERATE	ND2	0.018
HLI-0138	5147	G	A	2	513	synonymous_variant	LOW	ND2	0.0437
HLI-0138	6119	C	T	1	587	synonymous_variant	LOW	COX1	8.00E-04
HLI-0138	6680	T	C	2	644	synonymous_variant	LOW	COX1	0.0226
HLI-0138	7028	C	T	2	645	synonymous_variant	LOW	COX1	0.8089
HLI-0138	7424	A	G	0	606	synonymous_variant	LOW	COX1	0.0115
HLI-0138	8618	T	C	1	361	missense_variant	MODERATE	ATP6	0.0103
HLI-0138	8701	A	G	2	459	missense_variant	MODERATE	ATP6	0.3391
HLI-0138	9540	T	C	0	563	synonymous_variant	LOW	COX3	0.339
HLI-0138	10398	A	G	0	589	missense_variant	MODERATE	ND3	0.445
HLI-0138	10873	T	C	0	431	synonymous_variant	LOW	ND4	0.3389
HLI-0138	10933	C	T	0	383	synonymous_variant	LOW	ND4	0
HLI-0138	11719	G	A	0	583	synonymous_variant	LOW	ND4	0.7756
HLI-0138	12705	C	T	2	618	synonymous_variant	LOW	ND5	0.4212
HLI-0138	13105	A	G	2	636	missense_variant	MODERATE	ND5	0.076
HLI-0138	13886	T	C	0	518	missense_variant	MODERATE	ND5	0.0088
HLI-0138	13899	T	C	0	516	synonymous_variant	LOW	ND5	0.001
HLI-0138	14110	T	C	0	483	missense_variant	MODERATE	ND5	0.0096
HLI-0138	14284	C	T	1	475	synonymous_variant	LOW	ND6	0.0087
HLI-0138	14311	T	C	1	527	synonymous_variant	LOW	ND6	0.0017
HLI-0138	14766	C	T	2	481	missense_variant	MODERATE	CYTB	0.7696
HLI-0138	15301	G	A	2	563	synonymous_variant	LOW	CYTB	0.2912
HLI-0138	15326	A	G	1	616	missense_variant	MODERATE	CYTB	0.9868
HLI-0138	16124	T	C	1	521	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0138	16223	C	T	5	551	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0138	16519	T	C	0	252	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0139	73	A	G	1	229	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0139	146	T	C	1	400	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0139	152	T	C	1	412	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0139	263	A	G	0	166	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0139	709	G	A	0	601	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0139	750	A	G	2	618	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0139	1438	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0139	1811	A	G	1	657	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0139	2706	A	G	1	613	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0139	3480	A	G	0	566	synonymous_variant	LOW	ND1	0.0392
HLI-0139	4561	T	C	1	596	missense_variant	MODERATE	ND2	0.0065
HLI-0139	4769	A	G	1	543	synonymous_variant	LOW	ND2	0.9767
HLI-0139	7028	C	T	5	630	synonymous_variant	LOW	COX1	0.8089
HLI-0139	9055	G	A	3	585	missense_variant	MODERATE	ATP6	0.0425
HLI-0139	9698	T	C	1	612	synonymous_variant	LOW	COX3	0.0405
HLI-0139	9716	T	C	2	668	synonymous_variant	LOW	COX3	0.0108
HLI-0139	10550	A	G	1	581	synonymous_variant	LOW	ND4L	0.0376
HLI-0139	11299	T	C	0	618	synonymous_variant	LOW	ND4	0.0417
HLI-0139	11467	A	G	1	616	synonymous_variant	LOW	ND4	0.1231
HLI-0139	11719	G	A	0	611	synonymous_variant	LOW	ND4	0.7756
HLI-0139	12308	A	G	1	562	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0139	12372	G	A	1	547	synonymous_variant	LOW	ND5	0.1329
HLI-0139	14167	C	T	3	516	synonymous_variant	LOW	ND6	0.0385
HLI-0139	14766	C	T	8	584	missense_variant	MODERATE	CYTB	0.7696
HLI-0139	14798	T	C	1	628	missense_variant	MODERATE	CYTB	0.0651
HLI-0139	15326	A	G	0	518	missense_variant	MODERATE	CYTB	0.9868
HLI-0139	16224	T	C	0	513	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0139	16311	T	C	0	408	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0139	16519	T	C	0	244	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0140	248	A	G	1	267	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0140	263	A	G	1	269	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0140	750	A	G	0	613	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0140	1438	A	G	0	666	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0140	4769	A	G	0	558	synonymous_variant	LOW	ND2	0.9767
HLI-0140	6776	T	C	2	699	synonymous_variant	LOW	COX1	0.0226
HLI-0140	15326	A	G	1	559	missense_variant	MODERATE	CYTB	0.9868
HLI-0141	73	A	G	1	236	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0141	146	T	C	2	429	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0141	263	A	G	0	179	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0141	285	C	T	0	172	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0141	750	A	G	0	543	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0141	1438	A	G	0	542	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0141	2387	T	C	0	566	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0141	2706	A	G	3	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0141	3426	A	G	0	505	synonymous_variant	LOW	ND1	1.00E-04

HLI-0141	4769	A	G	2	517	synonymous_variant	LOW	ND2	0.9767
HLI-0141	5460	G	A	3	543	missense_variant	MODERATE	ND2	0.0651
HLI-0141	6365	T	C	1	544	synonymous_variant	LOW	COX1	0.0026
HLI-0141	7028	C	T	3	646	synonymous_variant	LOW	COX1	0.8089
HLI-0141	8395	C	T	0	452	synonymous_variant	LOW	ATP8	0.001
HLI-0141	10885	T	C	1	495	synonymous_variant	LOW	ND4	0.001
HLI-0141	11467	A	G	2	556	synonymous_variant	LOW	ND4	0.1231
HLI-0141	11566	A	G	1	522	synonymous_variant	LOW	ND4	8.00E-04
HLI-0141	11719	G	A	1	534	synonymous_variant	LOW	ND4	0.7756
HLI-0141	11969	G	A	0	512	missense_variant	MODERATE	ND4	0.0135
HLI-0141	12308	A	G	3	493	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0141	12372	G	A	2	520	synonymous_variant	LOW	ND5	0.1329
HLI-0141	12879	T	C	5	535	synonymous_variant	LOW	ND5	0.0058
HLI-0141	13104	A	G	1	512	synonymous_variant	LOW	ND5	0.0057
HLI-0141	14766	C	T	2	493	missense_variant	MODERATE	CYTB	0.7696
HLI-0141	15110	G	A	2	604	missense_variant	MODERATE	CYTB	0.009
HLI-0141	15148	G	A	3	610	synonymous_variant	LOW	CYTB	0.0058
HLI-0141	15172	G	A	2	590	synonymous_variant	LOW	CYTB	0.0075
HLI-0141	15326	A	G	0	481	missense_variant	MODERATE	CYTB	0.9868
HLI-0141	15954	A	C	0	569	upstream_gene_variant	MODIFIER	Unannotated	0.0036
HLI-0141	16104	C	T	20	530	upstream_gene_variant	MODIFIER	DLoop	0.0023
HLI-0141	16111	C	T	0	547	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0141	16249	T	C	0	495	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0141	16327	C	T	0	480	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0141	16519	T	C	0	190	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0142	73	A	G	1	285	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0142	195	T	C	1	361	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0142	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0142	709	G	A	1	606	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0142	750	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0142	1438	A	G	0	620	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0142	1888	G	A	0	515	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0142	2706	A	G	1	633	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0142	4216	T	C	0	569	missense_variant	MODERATE	ND1	0.0991
HLI-0142	4769	A	G	1	520	synonymous_variant	LOW	ND2	0.9767
HLI-0142	4917	A	G	1	545	missense_variant	MODERATE	ND2	0.0477
HLI-0142	7028	C	T	2	625	synonymous_variant	LOW	COX1	0.8089
HLI-0142	7984	G	A	1	595	synonymous_variant	LOW	COX2	5.00E-04
HLI-0142	8697	G	A	0	510	synonymous_variant	LOW	ATP6	0.0466

HLI-0142	10463	T	C	1	586	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0142	10873	T	C	0	619	synonymous_variant	LOW	ND4	0.3389
HLI-0142	11251	A	G	1	581	synonymous_variant	LOW	ND4	0.0932
HLI-0142	11719	G	A	2	587	synonymous_variant	LOW	ND4	0.7756
HLI-0142	11812	A	G	2	561	synonymous_variant	LOW	ND4	0.0332
HLI-0142	13368	G	A	0	624	synonymous_variant	LOW	ND5	0.0495
HLI-0142	14233	A	G	3	524	synonymous_variant	LOW	ND6	0.0369
HLI-0142	14569	G	A	0	553	synonymous_variant	LOW	ND6	0.0259
HLI-0142	14766	C	T	3	636	missense_variant	MODERATE	CYTB	0.7696
HLI-0142	14905	G	A	1	604	synonymous_variant	LOW	CYTB	0.0526
HLI-0142	15326	A	G	0	557	missense_variant	MODERATE	CYTB	0.9868
HLI-0142	15452	C	A	3	501	missense_variant	MODERATE	CYTB	0.0933
HLI-0142	15607	A	G	0	546	synonymous_variant	LOW	CYTB	0.0508
HLI-0142	15928	G	A	1	590	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0142	16126	T	C	1	294	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0142	16140	T	C	1	255	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0142	16294	C	T	0	350	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0142	16296	C	T	0	351	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0142	16311	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0142	16519	T	C	0	183	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0143	263	A	G	0	24	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0143	8931	A	G	0	42	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0143	15326	A	G	0	47	missense_variant	MODERATE	CYTB	0.9868
HLI-0143	16235	A	G	0	51	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0143	16291	C	T	0	57	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0144	239	T	C	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0144	263	A	G	0	36	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0144	750	A	G	0	49	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0144	1438	A	G	0	44	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0144	3915	G	A	0	39	synonymous_variant	LOW	ND1	0.0106
HLI-0144	4727	A	G	0	52	synonymous_variant	LOW	ND2	0.0063
HLI-0144	4769	A	G	0	45	synonymous_variant	LOW	ND2	0.9767
HLI-0144	9380	G	A	0	57	synonymous_variant	LOW	COX3	0.0094
HLI-0144	11253	T	C	0	40	missense_variant	MODERATE	ND4	0.0053
HLI-0144	14798	T	C	0	50	missense_variant	MODERATE	CYTB	0.0651
HLI-0144	15326	A	G	1	42	missense_variant	MODERATE	CYTB	0.9868
HLI-0144	16362	T	C	0	49	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0144	16482	A	G	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0145	73	A	C	1	239	upstream_gene_variant	MODIFIER	DLoop	1.00E-04

HLI-0145	75	G	A	1	249	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0145	89	T	C	1	290	upstream_gene_variant	MODIFIER	DLoop	0.0038
HLI-0145	263	A	G	0	170	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0145	709	G	A	1	586	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0145	750	A	G	1	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0145	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0145	2706	A	G	1	604	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0145	4769	A	G	0	573	synonymous_variant	LOW	ND2	0.9767
HLI-0145	5252	G	A	0	493	synonymous_variant	LOW	ND2	0.0027
HLI-0145	5465	T	C	1	609	synonymous_variant	LOW	ND2	0.0434
HLI-0145	7028	C	T	0	655	synonymous_variant	LOW	COX1	0.8089
HLI-0145	9123	G	A	10	640	synonymous_variant	LOW	ATP6	0.0485
HLI-0145	9254	A	G	5	517	synonymous_variant	LOW	COX3	0.0083
HLI-0145	10238	T	C	2	583	synonymous_variant	LOW	ND3	0.0623
HLI-0145	11719	G	A	1	602	synonymous_variant	LOW	ND4	0.7756
HLI-0145	14766	C	T	1	560	missense_variant	MODERATE	CYTB	0.7696
HLI-0145	15292	C	T	4	590	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0145	15326	A	G	1	662	missense_variant	MODERATE	CYTB	0.9868
HLI-0145	16217	T	C	0	160	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0145	16261	C	T	0	268	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0145	16519	T	C	1	208	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0146	73	A	G	0	285	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0146	152	T	C	3	519	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0146	263	A	G	0	196	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0146	709	G	A	0	564	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0146	750	A	G	3	623	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0146	827	A	G	1	605	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0146	1438	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0146	1888	G	A	1	603	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0146	2706	A	G	1	563	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0146	4216	T	C	5	494	missense_variant	MODERATE	ND1	0.0991
HLI-0146	4769	A	G	2	522	synonymous_variant	LOW	ND2	0.9767
HLI-0146	4917	A	G	0	545	missense_variant	MODERATE	ND2	0.0477
HLI-0146	4973	T	C	0	645	synonymous_variant	LOW	ND2	0.0018
HLI-0146	7028	C	T	0	656	synonymous_variant	LOW	COX1	0.8089
HLI-0146	8697	G	A	1	619	synonymous_variant	LOW	ATP6	0.0466
HLI-0146	9254	A	G	1	477	synonymous_variant	LOW	COX3	0.0083
HLI-0146	9932	G	A	1	621	synonymous_variant	LOW	COX3	0.0062
HLI-0146	10463	T	C	0	595	upstream_gene_variant	MODIFIER	TRNR	0.0474

HLI-0146	11251	A	G	2	635	synonymous_variant	LOW	ND4	0.0932
HLI-0146	11719	G	A	1	535	synonymous_variant	LOW	ND4	0.7756
HLI-0146	11839	T	G	0	558	synonymous_variant	LOW	ND4	0
HLI-0146	12633	C	A	14	585	synonymous_variant	LOW	ND5	0.0123
HLI-0146	13368	G	A	1	548	synonymous_variant	LOW	ND5	0.0495
HLI-0146	14766	C	T	2	531	missense_variant	MODERATE	CYTB	0.7696
HLI-0146	14905	G	A	1	593	synonymous_variant	LOW	CYTB	0.0526
HLI-0146	15326	A	G	0	525	missense_variant	MODERATE	CYTB	0.9868
HLI-0146	15452	C	A	8	472	missense_variant	MODERATE	CYTB	0.0933
HLI-0146	15607	A	G	0	519	synonymous_variant	LOW	CYTB	0.0508
HLI-0146	15928	G	A	0	560	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0146	16126	T	C	0	511	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0146	16163	A	G	0	513	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0146	16220	A	G	2	531	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0146	16294	C	T	1	514	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0146	16519	T	C	0	233	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0147	72	T	C	0	261	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0147	195	T	C	0	341	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0147	263	A	G	1	208	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0147	750	A	G	1	535	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0147	1275	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	1.00E-04
HLI-0147	1438	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0147	2706	A	G	0	511	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0147	4769	A	G	1	528	synonymous_variant	LOW	ND2	0.9767
HLI-0147	7028	C	T	1	580	synonymous_variant	LOW	COX1	0.8089
HLI-0147	8706	A	G	3	563	synonymous_variant	LOW	ATP6	7.00E-04
HLI-0147	15326	A	G	0	481	missense_variant	MODERATE	CYTB	0.9868
HLI-0147	16261	C	T	4	523	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0147	16298	T	C	2	508	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0148	73	A	G	1	283	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0148	263	A	G	0	208	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0148	497	C	T	1	411	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0148	750	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0148	1189	T	C	1	697	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0148	1438	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0148	1811	A	G	2	618	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0148	2706	A	G	0	614	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0148	3480	A	G	2	450	synonymous_variant	LOW	ND1	0.0392
HLI-0148	4491	G	A	1	609	missense_variant	MODERATE	ND2	0.0182

HLI-0148	4769	A	G	2	591	synonymous_variant	LOW	ND2	0.9767
HLI-0148	6155	C	A	1	590	synonymous_variant	LOW	COX1	0
HLI-0148	7028	C	T	4	710	synonymous_variant	LOW	COX1	0.8089
HLI-0148	7118	A	G	4	625	synonymous_variant	LOW	COX1	5.00E-04
HLI-0148	9055	G	A	2	581	missense_variant	MODERATE	ATP6	0.0425
HLI-0148	9477	G	A	4	611	missense_variant	MODERATE	COX3	0.0387
HLI-0148	9698	T	C	3	532	synonymous_variant	LOW	COX3	0.0405
HLI-0148	10398	A	G	1	636	missense_variant	MODERATE	ND3	0.445
HLI-0148	10550	A	G	2	603	synonymous_variant	LOW	ND4L	0.0376
HLI-0148	11299	T	C	1	597	synonymous_variant	LOW	ND4	0.0417
HLI-0148	11467	A	G	1	604	synonymous_variant	LOW	ND4	0.1231
HLI-0148	11485	T	C	2	654	synonymous_variant	LOW	ND4	0.0081
HLI-0148	11719	G	A	0	564	synonymous_variant	LOW	ND4	0.7756
HLI-0148	12017	A	G	1	571	missense_variant	MODERATE	ND4	1.00E-04
HLI-0148	12308	A	G	3	564	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0148	12372	G	A	1	585	synonymous_variant	LOW	ND5	0.1329
HLI-0148	14167	C	T	1	569	synonymous_variant	LOW	ND6	0.0385
HLI-0148	14182	T	C	1	605	synonymous_variant	LOW	ND6	0.0254
HLI-0148	14766	C	T	2	601	missense_variant	MODERATE	CYTB	0.7696
HLI-0148	14798	T	C	1	661	missense_variant	MODERATE	CYTB	0.0651
HLI-0148	15326	A	G	0	541	missense_variant	MODERATE	CYTB	0.9868
HLI-0148	16093	T	C	3	599	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0148	16224	T	C	0	584	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0148	16311	T	C	0	505	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0148	16519	T	C	0	254	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0149	72	T	C	0	285	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0149	89	T	C	0	352	upstream_gene_variant	MODIFIER	DLoop	0.0038
HLI-0149	93	A	G	0	363	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0149	195	T	C	1	423	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0149	263	A	G	0	176	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0149	750	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0149	930	G	A	1	674	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0149	1438	A	G	0	652	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0149	2706	A	G	0	611	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0149	4580	G	A	2	621	synonymous_variant	LOW	ND2	0.0169
HLI-0149	4769	A	G	1	568	synonymous_variant	LOW	ND2	0.9767
HLI-0149	7028	C	T	2	659	synonymous_variant	LOW	COX1	0.8089
HLI-0149	7444	G	A	1	671	stop_lost	HIGH	COX1	0.0035
HLI-0149	11899	T	C	0	615	synonymous_variant	LOW	ND4	0.0108

HLI-0149	12753	A	G	0	655	synonymous_variant	LOW	ND5	0.0011
HLI-0149	15326	A	G	2	585	missense_variant	MODERATE	CYTB	0.9868
HLI-0149	15904	C	T	0	731	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0149	16153	G	A	0	639	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0149	16298	T	C	3	500	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0150	73	A	G	1	206	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0150	150	C	T	1	326	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0150	152	T	C	1	332	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0150	182	C	T	1	307	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0150	195	T	C	1	295	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0150	198	C	T	1	298	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0150	204	T	C	0	304	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0150	263	A	G	0	138	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0150	418	C	T	0	328	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0150	750	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0150	769	G	A	1	634	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0150	1018	G	A	0	578	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0150	1438	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0150	1442	G	A	0	679	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0150	1706	C	T	0	573	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0150	2332	C	T	0	580	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0150	2358	A	G	2	623	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0150	2416	T	C	0	596	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0150	2706	A	G	0	640	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0150	3594	C	T	1	487	synonymous_variant	LOW	ND1	0.0789
HLI-0150	4104	A	G	1	519	synonymous_variant	LOW	ND1	0.0785
HLI-0150	4158	A	G	0	598	synonymous_variant	LOW	ND1	0.0023
HLI-0150	4370	T	C	0	504	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0150	4767	A	G	2	578	missense_variant	MODERATE	ND2	0.0029
HLI-0150	4769	A	G	2	581	synonymous_variant	LOW	ND2	0.9767
HLI-0150	5027	C	T	0	590	synonymous_variant	LOW	ND2	0.003
HLI-0150	5331	C	A	0	539	missense_variant	MODERATE	ND2	0.0022
HLI-0150	5814	T	C	0	613	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0150	6026	G	A	0	621	synonymous_variant	LOW	COX1	0.0163
HLI-0150	6713	C	T	5	734	synonymous_variant	LOW	COX1	0.0028
HLI-0150	7028	C	T	3	623	synonymous_variant	LOW	COX1	0.8089
HLI-0150	7256	C	T	3	483	synonymous_variant	LOW	COX1	0.0784
HLI-0150	7521	G	A	0	464	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0150	7624	T	A	1	592	synonymous_variant	LOW	COX2	0.0047

HLI-0150	8080	C	T	1	535	synonymous_variant	LOW	COX2	0.0022
HLI-0150	8206	G	A	0	527	synonymous_variant	LOW	COX2	0.0287
HLI-0150	8387	G	A	0	525	missense_variant	MODERATE	ATP8	0.0028
HLI-0150	8701	A	G	0	563	missense_variant	MODERATE	ATP6	0.3391
HLI-0150	8856	G	A	0	534	synonymous_variant	LOW	ATP6	0.004
HLI-0150	9221	A	G	2	582	synonymous_variant	LOW	COX3	0.0277
HLI-0150	9540	T	C	0	540	synonymous_variant	LOW	COX3	0.339
HLI-0150	10115	T	C	0	697	synonymous_variant	LOW	ND3	0.0278
HLI-0150	10398	A	G	1	597	missense_variant	MODERATE	ND3	0.445
HLI-0150	10828	T	C	2	585	synonymous_variant	LOW	ND4	0.0015
HLI-0150	10873	T	C	1	592	synonymous_variant	LOW	ND4	0.3389
HLI-0150	11719	G	A	0	540	synonymous_variant	LOW	ND4	0.7756
HLI-0150	11944	T	C	2	566	synonymous_variant	LOW	ND4	0.0331
HLI-0150	12236	G	A	2	564	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0150	12705	C	T	1	640	synonymous_variant	LOW	ND5	0.4212
HLI-0150	12948	A	G	5	556	synonymous_variant	LOW	ND5	0.0022
HLI-0150	13590	G	A	0	572	synonymous_variant	LOW	ND5	0.0586
HLI-0150	13650	C	T	0	617	synonymous_variant	LOW	ND5	0.079
HLI-0150	13924	C	T	1	577	missense_variant	MODERATE	ND5	0.0013
HLI-0150	14059	A	G	0	505	missense_variant	MODERATE	ND5	0.0022
HLI-0150	14766	C	T	4	576	missense_variant	MODERATE	CYTB	0.7696
HLI-0150	15110	G	A	1	615	missense_variant	MODERATE	CYTB	0.009
HLI-0150	15217	G	A	0	565	synonymous_variant	LOW	CYTB	0.0104
HLI-0150	15301	G	A	0	610	synonymous_variant	LOW	CYTB	0.2912
HLI-0150	15326	A	G	0	580	missense_variant	MODERATE	CYTB	0.9868
HLI-0150	16114	C	A	0	558	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0150	16129	G	A	1	587	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0150	16145	G	A	1	583	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0150	16213	G	A	0	597	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0150	16223	C	T	0	606	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0150	16278	C	T	3	548	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0150	16355	C	T	1	406	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0150	16362	T	C	2	432	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0150	16390	G	A	3	441	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0151	73	A	G	1	250	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0151	143	G	A	2	466	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0151	146	T	C	2	479	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0151	152	T	C	2	492	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0151	195	T	C	2	505	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0151	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0151	750	A	G	0	699	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0151	769	G	A	0	771	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0151	1018	G	A	1	668	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0151	1438	A	G	0	710	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0151	2416	T	C	0	685	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0151	2706	A	G	1	670	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0151	2789	C	T	1	761	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0151	3594	C	T	1	521	synonymous_variant	LOW	ND1	0.0789
HLI-0151	4104	A	G	1	566	synonymous_variant	LOW	ND1	0.0785
HLI-0151	4769	A	G	1	619	synonymous_variant	LOW	ND2	0.9767
HLI-0151	6164	C	T	1	636	synonymous_variant	LOW	COX1	0.0025
HLI-0151	7028	C	T	1	629	synonymous_variant	LOW	COX1	0.8089
HLI-0151	7175	T	C	0	665	synonymous_variant	LOW	COX1	0.0224
HLI-0151	7256	C	T	5	671	synonymous_variant	LOW	COX1	0.0784
HLI-0151	7274	C	T	6	646	synonymous_variant	LOW	COX1	0.0214
HLI-0151	7521	G	A	2	538	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0151	7751	T	C	1	612	missense_variant	MODERATE	COX2	0
HLI-0151	7771	A	G	0	679	synonymous_variant	LOW	COX2	0.0223
HLI-0151	8206	G	A	5	676	synonymous_variant	LOW	COX2	0.0287
HLI-0151	8701	A	G	2	616	missense_variant	MODERATE	ATP6	0.3391
HLI-0151	9221	A	G	0	667	synonymous_variant	LOW	COX3	0.0277
HLI-0151	9540	T	C	1	620	synonymous_variant	LOW	COX3	0.339
HLI-0151	10115	T	C	0	811	synonymous_variant	LOW	ND3	0.0278
HLI-0151	10398	A	G	0	646	missense_variant	MODERATE	ND3	0.445
HLI-0151	10873	T	C	1	617	synonymous_variant	LOW	ND4	0.3389
HLI-0151	10920	C	T	1	619	missense_variant	MODERATE	ND4	0.0037
HLI-0151	11719	G	A	0	671	synonymous_variant	LOW	ND4	0.7756
HLI-0151	11914	G	A	1	662	synonymous_variant	LOW	ND4	0.1112
HLI-0151	11944	T	C	1	691	synonymous_variant	LOW	ND4	0.0331
HLI-0151	12693	A	G	0	705	synonymous_variant	LOW	ND5	0.0205
HLI-0151	12705	C	T	0	776	synonymous_variant	LOW	ND5	0.4212
HLI-0151	13590	G	A	1	672	synonymous_variant	LOW	ND5	0.0586
HLI-0151	13650	C	T	1	705	synonymous_variant	LOW	ND5	0.079
HLI-0151	13803	A	G	0	443	synonymous_variant	LOW	ND5	0.0216
HLI-0151	14566	A	G	0	674	synonymous_variant	LOW	ND6	0.0214
HLI-0151	14766	C	T	0	674	missense_variant	MODERATE	CYTB	0.7696
HLI-0151	15229	T	C	0	627	synonymous_variant	LOW	CYTB	0.0014
HLI-0151	15301	G	A	1	653	synonymous_variant	LOW	CYTB	0.2912

HLI-0151	15326	A	G	0	643	missense_variant	MODERATE	CYTB	0.9868
HLI-0151	15784	T	C	0	683	synonymous_variant	LOW	CYTB	0.0363
HLI-0151	16278	C	T	1	514	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0151	16294	C	T	1	523	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0151	16362	T	C	1	508	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0151	16390	G	A	0	510	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0152	73	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0152	228	G	A	1	255	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0152	263	A	G	0	209	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0152	295	C	T	0	142	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0152	462	C	T	0	389	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0152	482	T	C	0	445	upstream_gene_variant	MODIFIER	DLoop	0.0094
HLI-0152	489	T	C	0	461	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0152	750	A	G	1	613	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0152	1438	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0152	2706	A	G	0	606	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0152	3010	G	A	2	631	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0152	3394	T	C	1	613	missense_variant	MODERATE	ND1	0.013
HLI-0152	4216	T	C	3	632	missense_variant	MODERATE	ND1	0.0991
HLI-0152	4769	A	G	1	555	synonymous_variant	LOW	ND2	0.9767
HLI-0152	7028	C	T	3	679	synonymous_variant	LOW	COX1	0.8089
HLI-0152	8897	C	T	1	641	missense_variant	MODERATE	ATP6	5.00E-04
HLI-0152	10398	A	G	0	621	missense_variant	MODERATE	ND3	0.445
HLI-0152	11251	A	G	1	618	synonymous_variant	LOW	ND4	0.0932
HLI-0152	11719	G	A	3	561	synonymous_variant	LOW	ND4	0.7756
HLI-0152	12612	A	G	5	635	synonymous_variant	LOW	ND5	0.0506
HLI-0152	13708	G	A	4	500	missense_variant	MODERATE	ND5	0.0717
HLI-0152	14766	C	T	7	623	missense_variant	MODERATE	CYTB	0.7696
HLI-0152	14798	T	C	3	651	missense_variant	MODERATE	CYTB	0.0651
HLI-0152	15326	A	G	0	595	missense_variant	MODERATE	CYTB	0.9868
HLI-0152	15452	C	A	5	574	missense_variant	MODERATE	CYTB	0.0933
HLI-0152	16069	C	T	4	586	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0152	16126	T	C	1	600	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0153	263	A	G	0	190	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0153	750	A	G	2	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0153	1438	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0153	4769	A	G	1	575	synonymous_variant	LOW	ND2	0.9767
HLI-0153	14470	T	A	0	565	synonymous_variant	LOW	ND6	0.0031
HLI-0153	15326	A	G	1	584	missense_variant	MODERATE	CYTB	0.9868

HLI-0153	16519	T	C	3	249	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0154	73	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0154	199	T	C	0	293	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0154	203	G	A	0	300	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0154	204	T	C	0	303	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0154	250	T	C	0	119	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0154	263	A	G	0	132	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0154	750	A	G	1	530	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0154	1438	A	G	1	612	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0154	1719	G	A	2	595	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0154	1836	A	G	1	637	upstream_gene_variant	MODIFIER	RNR2	4.00E-04
HLI-0154	2706	A	G	1	531	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0154	3447	A	G	1	512	synonymous_variant	LOW	ND1	0.0053
HLI-0154	3990	C	T	1	544	synonymous_variant	LOW	ND1	0.0031
HLI-0154	4023	T	C	0	582	synonymous_variant	LOW	ND1	9.00E-04
HLI-0154	4529	A	T	3	590	synonymous_variant	LOW	ND2	0.015
HLI-0154	4769	A	G	1	569	synonymous_variant	LOW	ND2	0.9767
HLI-0154	6734	G	A	9	659	synonymous_variant	LOW	COX1	0.0062
HLI-0154	7028	C	T	5	669	synonymous_variant	LOW	COX1	0.8089
HLI-0154	8251	G	A	1	502	synonymous_variant	LOW	COX2	0.058
HLI-0154	8616	G	T	0	494	missense_variant	MODERATE	ATP6	0.0032
HLI-0154	9947	G	A	0	626	synonymous_variant	LOW	COX3	0.0092
HLI-0154	10034	T	C	1	640	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0154	10238	T	C	2	524	synonymous_variant	LOW	ND3	0.0623
HLI-0154	10398	A	G	0	606	missense_variant	MODERATE	ND3	0.445
HLI-0154	10915	T	C	0	527	synonymous_variant	LOW	ND4	0.0411
HLI-0154	11719	G	A	0	547	synonymous_variant	LOW	ND4	0.7756
HLI-0154	12501	G	A	3	610	synonymous_variant	LOW	ND5	0.0258
HLI-0154	12705	C	T	2	585	synonymous_variant	LOW	ND5	0.4212
HLI-0154	13488	T	C	0	594	synonymous_variant	LOW	ND5	0.0014
HLI-0154	13780	A	G	0	401	missense_variant	MODERATE	ND5	0.0179
HLI-0154	14766	C	T	1	528	missense_variant	MODERATE	CYTB	0.7696
HLI-0154	15043	G	A	0	615	synonymous_variant	LOW	CYTB	0.2362
HLI-0154	15326	A	G	1	522	missense_variant	MODERATE	CYTB	0.9868
HLI-0154	15924	A	G	2	571	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0154	16129	G	A	0	380	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0154	16172	T	C	2	246	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0154	16223	C	T	0	262	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0154	16311	T	C	0	413	upstream_gene_variant	MODIFIER	DLoop	0.1969

HLI-0154	16391	G	A	0	384	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0154	16519	T	C	1	162	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0155	64	C	T	0	187	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0155	93	A	G	1	274	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0155	185	G	A	0	303	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0155	189	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0155	200	A	G	1	291	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0155	236	T	C	0	238	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0155	247	G	A	0	224	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0155	263	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0155	750	A	G	0	528	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0155	769	G	A	0	574	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0155	825	T	A	0	612	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0155	1018	G	A	1	558	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0155	1048	C	T	3	604	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0155	1117	A	G	2	611	upstream_gene_variant	MODIFIER	RNR1	6.00E-04
HLI-0155	1438	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0155	2245	A	C	0	533	upstream_gene_variant	MODIFIER	RNR2	8.00E-04
HLI-0155	2706	A	G	0	522	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0155	2758	G	A	0	569	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0155	2885	T	C	0	600	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0155	3516	C	A	1	428	synonymous_variant	LOW	ND1	0.0315
HLI-0155	3594	C	T	2	454	synonymous_variant	LOW	ND1	0.0789
HLI-0155	3866	T	C	1	520	missense_variant	MODERATE	ND1	0.0029
HLI-0155	4104	A	G	0	397	synonymous_variant	LOW	ND1	0.0785
HLI-0155	4312	C	T	2	442	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0155	4586	T	C	3	542	synonymous_variant	LOW	ND2	0.018
HLI-0155	4769	A	G	0	548	synonymous_variant	LOW	ND2	0.9767
HLI-0155	5096	T	C	0	550	synonymous_variant	LOW	ND2	0.0063
HLI-0155	5231	G	A	0	483	synonymous_variant	LOW	ND2	0.0232
HLI-0155	5442	T	C	0	534	missense_variant	MODERATE	ND2	0.0493
HLI-0155	5460	G	A	0	596	missense_variant	MODERATE	ND2	0.0651
HLI-0155	5603	C	T	2	594	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0155	6185	T	C	0	497	synonymous_variant	LOW	COX1	0.0325
HLI-0155	7028	C	T	2	531	synonymous_variant	LOW	COX1	0.8089
HLI-0155	7146	A	G	1	269	missense_variant	MODERATE	COX1	0.0497
HLI-0155	7256	C	T	3	426	synonymous_variant	LOW	COX1	0.0784
HLI-0155	7521	G	A	0	380	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0155	8428	C	T	3	461	synonymous_variant	LOW	ATP8	0.0144

HLI-0155	8468	C	T	4	462	synonymous_variant	LOW	ATP8	0.0501
HLI-0155	8566	A	G	1	411	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0155	8655	C	T	1	413	synonymous_variant	LOW	ATP6	0.0511
HLI-0155	8701	A	G	0	470	missense_variant	MODERATE	ATP6	0.3391
HLI-0155	9042	C	T	2	576	synonymous_variant	LOW	ATP6	0.0316
HLI-0155	9347	A	G	0	516	synonymous_variant	LOW	COX3	0.0314
HLI-0155	9540	T	C	1	478	synonymous_variant	LOW	COX3	0.339
HLI-0155	9755	G	A	0	613	synonymous_variant	LOW	COX3	0.0303
HLI-0155	9818	C	T	0	703	synonymous_variant	LOW	COX3	0.0179
HLI-0155	10398	A	G	2	547	missense_variant	MODERATE	ND3	0.445
HLI-0155	10589	G	A	1	504	synonymous_variant	LOW	ND4L	0.0355
HLI-0155	10664	C	T	0	578	synonymous_variant	LOW	ND4L	0.0315
HLI-0155	10688	G	A	0	567	synonymous_variant	LOW	ND4L	0.0515
HLI-0155	10810	T	C	0	503	synonymous_variant	LOW	ND4	0.0522
HLI-0155	10873	T	C	0	444	synonymous_variant	LOW	ND4	0.3389
HLI-0155	10915	T	C	0	492	synonymous_variant	LOW	ND4	0.0411
HLI-0155	11176	G	A	1	542	synonymous_variant	LOW	ND4	0.0181
HLI-0155	11641	A	G	0	551	synonymous_variant	LOW	ND4	0.0158
HLI-0155	11719	G	A	0	573	synonymous_variant	LOW	ND4	0.7756
HLI-0155	11914	G	A	1	609	synonymous_variant	LOW	ND4	0.1112
HLI-0155	12007	G	A	1	517	synonymous_variant	LOW	ND4	0.0639
HLI-0155	12175	T	C	0	543	upstream_gene_variant	MODIFIER	TRNH	6.00E-04
HLI-0155	12705	C	T	1	594	synonymous_variant	LOW	ND5	0.4212
HLI-0155	12720	A	G	0	641	synonymous_variant	LOW	ND5	0.0302
HLI-0155	13105	A	G	0	586	missense_variant	MODERATE	ND5	0.076
HLI-0155	13276	A	G	0	563	missense_variant	MODERATE	ND5	0.0312
HLI-0155	13506	C	T	1	519	synonymous_variant	LOW	ND5	0.0506
HLI-0155	13650	C	T	2	523	synonymous_variant	LOW	ND5	0.079
HLI-0155	14308	T	C	0	439	synonymous_variant	LOW	ND6	0.0209
HLI-0155	14766	C	T	0	515	missense_variant	MODERATE	CYTB	0.7696
HLI-0155	15136	C	T	2	573	synonymous_variant	LOW	CYTB	0.0153
HLI-0155	15326	A	G	0	449	missense_variant	MODERATE	CYTB	0.9868
HLI-0155	15431	G	A	1	466	missense_variant	MODERATE	CYTB	0.0182
HLI-0155	16129	G	A	1	500	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0155	16148	C	T	0	485	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0155	16168	C	T	0	440	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0155	16172	T	C	0	441	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0155	16223	C	T	0	433	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0155	16230	A	G	0	438	upstream_gene_variant	MODIFIER	DLoop	0.0309

HLI-0155	16311	T	C	1	440	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0155	16320	C	T	1	440	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0156	263	A	G	1	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0156	750	A	G	1	613	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0156	1438	A	G	0	601	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0156	3010	G	A	0	577	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0156	4769	A	G	1	546	synonymous_variant	LOW	ND2	0.9767
HLI-0156	15326	A	G	1	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0156	16148	C	T	0	181	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0156	16221	C	T	0	183	upstream_gene_variant	MODIFIER	DLoop	0.007
HLI-0156	16239	C	T	1	231	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0156	16356	T	C	2	431	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0156	16519	T	C	0	221	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0157	150	C	T	1	524	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0157	263	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0157	750	A	G	1	644	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0157	1438	A	G	0	628	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0157	3010	G	A	2	646	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0157	4688	T	C	6	633	synonymous_variant	LOW	ND2	0.0078
HLI-0157	4769	A	G	2	633	synonymous_variant	LOW	ND2	0.9767
HLI-0157	6216	T	C	0	600	synonymous_variant	LOW	COX1	0.0056
HLI-0157	15326	A	G	1	573	missense_variant	MODERATE	CYTB	0.9868
HLI-0157	15924	A	G	0	633	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0157	16297	T	C	0	567	upstream_gene_variant	MODIFIER	DLoop	0.0139
HLI-0157	16519	T	C	1	263	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0158	263	A	G	1	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0158	750	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0158	1438	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0158	3010	G	A	0	674	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0158	4769	A	G	0	584	synonymous_variant	LOW	ND2	0.9767
HLI-0158	15326	A	G	0	597	missense_variant	MODERATE	CYTB	0.9868
HLI-0158	16239	C	T	4	615	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0158	16519	T	C	0	317	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0159	73	A	G	1	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0159	146	T	C	2	550	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0159	152	T	C	2	553	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0159	263	A	G	1	221	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0159	750	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0159	1189	T	C	3	651	upstream_gene_variant	MODIFIER	RNR1	0.0318

HLI-0159	1438	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0159	1811	A	G	2	657	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0159	2706	A	G	0	607	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0159	3480	A	G	1	531	synonymous_variant	LOW	ND1	0.0392
HLI-0159	4769	A	G	2	596	synonymous_variant	LOW	ND2	0.9767
HLI-0159	7028	C	T	5	682	synonymous_variant	LOW	COX1	0.8089
HLI-0159	9006	A	G	0	607	synonymous_variant	LOW	ATP6	0.0014
HLI-0159	9055	G	A	0	661	missense_variant	MODERATE	ATP6	0.0425
HLI-0159	9090	T	C	0	688	synonymous_variant	LOW	ATP6	0.0038
HLI-0159	9452	G	A	0	648	synonymous_variant	LOW	COX3	0.0028
HLI-0159	9698	T	C	0	617	synonymous_variant	LOW	COX3	0.0405
HLI-0159	10398	A	G	4	639	missense_variant	MODERATE	ND3	0.445
HLI-0159	10550	A	G	1	633	synonymous_variant	LOW	ND4L	0.0376
HLI-0159	11299	T	C	0	598	synonymous_variant	LOW	ND4	0.0417
HLI-0159	11467	A	G	2	625	synonymous_variant	LOW	ND4	0.1231
HLI-0159	11719	G	A	1	599	synonymous_variant	LOW	ND4	0.7756
HLI-0159	12308	A	G	0	534	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0159	12372	G	A	0	574	synonymous_variant	LOW	ND5	0.1329
HLI-0159	14002	A	G	2	515	missense_variant	MODERATE	ND5	0.0025
HLI-0159	14040	G	A	0	563	synonymous_variant	LOW	ND5	0.0047
HLI-0159	14167	C	T	5	590	synonymous_variant	LOW	ND6	0.0385
HLI-0159	14207	G	A	1	650	missense_variant	MODERATE	ND6	7.00E-04
HLI-0159	14766	C	T	3	589	missense_variant	MODERATE	CYTB	0.7696
HLI-0159	14798	T	C	2	659	missense_variant	MODERATE	CYTB	0.0651
HLI-0159	15326	A	G	0	535	missense_variant	MODERATE	CYTB	0.9868
HLI-0159	16224	T	C	3	538	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0159	16311	T	C	0	514	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0159	16320	C	T	0	533	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0159	16519	T	C	1	260	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0160	72	T	C	1	293	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0160	263	A	G	2	180	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0160	750	A	G	1	603	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0160	1438	A	G	0	552	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0160	2706	A	G	2	615	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0160	4580	G	A	1	520	synonymous_variant	LOW	ND2	0.0169
HLI-0160	4639	T	C	0	592	missense_variant	MODERATE	ND2	0.0034
HLI-0160	4769	A	G	4	559	synonymous_variant	LOW	ND2	0.9767
HLI-0160	4991	G	A	1	565	synonymous_variant	LOW	ND2	0.0052
HLI-0160	5263	C	T	2	472	missense_variant	MODERATE	ND2	0.0058

HLI-0160	7028	C	T	4	633	synonymous_variant	LOW	COX1	0.8089
HLI-0160	7080	T	C	1	666	missense_variant	MODERATE	COX1	0.001
HLI-0160	8602	T	C	0	519	missense_variant	MODERATE	ATP6	0.0017
HLI-0160	8869	A	G	0	559	missense_variant	MODERATE	ATP6	0.0028
HLI-0160	14845	C	T	1	600	synonymous_variant	LOW	CYTB	7.00E-04
HLI-0160	15326	A	G	0	561	missense_variant	MODERATE	CYTB	0.9868
HLI-0160	15904	C	T	0	589	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0160	16298	T	C	1	491	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0160	16519	T	C	0	285	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0161	73	A	G	1	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0161	263	A	G	1	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0161	750	A	G	2	576	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0161	1187	T	C	2	605	upstream_gene_variant	MODIFIER	RNR1	8.00E-04
HLI-0161	1438	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0161	2706	A	G	1	635	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0161	3197	T	C	2	584	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0161	4769	A	G	0	592	synonymous_variant	LOW	ND2	0.9767
HLI-0161	7028	C	T	5	688	synonymous_variant	LOW	COX1	0.8089
HLI-0161	9055	G	A	0	564	missense_variant	MODERATE	ATP6	0.0425
HLI-0161	9477	G	A	2	586	missense_variant	MODERATE	COX3	0.0387
HLI-0161	9667	A	G	2	588	missense_variant	MODERATE	COX3	0.0055
HLI-0161	11467	A	G	1	640	synonymous_variant	LOW	ND4	0.1231
HLI-0161	11719	G	A	4	632	synonymous_variant	LOW	ND4	0.7756
HLI-0161	12308	A	G	1	572	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0161	12372	G	A	1	608	synonymous_variant	LOW	ND5	0.1329
HLI-0161	13617	T	C	1	566	synonymous_variant	LOW	ND5	0.038
HLI-0161	14433	C	T	9	566	missense_variant	MODERATE	ND6	8.00E-04
HLI-0161	14766	C	T	4	626	missense_variant	MODERATE	CYTB	0.7696
HLI-0161	14793	A	G	3	688	missense_variant	MODERATE	CYTB	0.0199
HLI-0161	15218	A	G	4	630	missense_variant	MODERATE	CYTB	0.0169
HLI-0161	15326	A	G	0	554	missense_variant	MODERATE	CYTB	0.9868
HLI-0161	16172	T	C	94	485	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0161	16256	C	T	0	593	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0161	16270	C	T	0	585	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0161	16291	C	T	1	540	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0161	16399	A	G	1	466	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0162	263	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0162	750	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0162	1438	A	G	0	562	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0162	3010	G	A	1	583	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0162	4769	A	G	0	581	synonymous_variant	LOW	ND2	0.9767
HLI-0162	15326	A	G	0	491	missense_variant	MODERATE	CYTB	0.9868
HLI-0162	15466	G	A	0	485	synonymous_variant	LOW	CYTB	0.0152
HLI-0162	16172	T	C	0	528	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0162	16256	C	T	1	535	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0162	16519	T	C	0	234	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0163	263	A	G	0	180	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0163	480	T	C	0	370	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0163	750	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0163	1438	A	G	1	608	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0163	2706	A	G	0	598	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0163	4655	G	A	0	717	synonymous_variant	LOW	ND2	0.0072
HLI-0163	4769	A	G	2	629	synonymous_variant	LOW	ND2	0.9767
HLI-0163	7028	C	T	4	674	synonymous_variant	LOW	COX1	0.8089
HLI-0163	11830	T	C	0	605	synonymous_variant	LOW	ND4	3.00E-04
HLI-0163	15115	T	C	0	626	synonymous_variant	LOW	CYTB	0.0093
HLI-0163	15326	A	G	0	547	missense_variant	MODERATE	CYTB	0.9868
HLI-0163	16168	C	T	0	601	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0163	16311	T	C	1	523	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0164	73	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0164	150	C	T	0	437	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0164	152	T	C	0	440	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0164	195	T	C	1	405	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0164	215	A	G	1	385	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0164	263	A	G	0	167	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0164	295	C	T	0	187	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0164	319	T	C	0	186	upstream_gene_variant	MODIFIER	DLoop	0.0041
HLI-0164	489	T	C	2	399	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0164	750	A	G	0	581	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0164	1438	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0164	1850	T	C	0	607	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0164	2706	A	G	1	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0164	3447	A	G	0	558	synonymous_variant	LOW	ND1	0.0053
HLI-0164	4216	T	C	0	562	missense_variant	MODERATE	ND1	0.0991
HLI-0164	4769	A	G	1	564	synonymous_variant	LOW	ND2	0.9767
HLI-0164	7028	C	T	1	639	synonymous_variant	LOW	COX1	0.8089
HLI-0164	7476	C	T	1	613	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0164	7789	G	A	1	569	synonymous_variant	LOW	COX2	0.0092

HLI-0164	10398	A	G	1	596	missense_variant	MODERATE	ND3	0.445
HLI-0164	10499	A	G	2	625	synonymous_variant	LOW	ND4L	0.0093
HLI-0164	11251	A	G	1	565	synonymous_variant	LOW	ND4	0.0932
HLI-0164	11377	G	A	1	533	synonymous_variant	LOW	ND4	0.0125
HLI-0164	11719	G	A	1	586	synonymous_variant	LOW	ND4	0.7756
HLI-0164	12612	A	G	8	608	synonymous_variant	LOW	ND5	0.0506
HLI-0164	13708	G	A	0	523	missense_variant	MODERATE	ND5	0.0717
HLI-0164	13722	A	G	0	566	synonymous_variant	LOW	ND5	0.0077
HLI-0164	14133	A	G	0	531	synonymous_variant	LOW	ND5	0.0094
HLI-0164	14766	C	T	1	583	missense_variant	MODERATE	CYTB	0.7696
HLI-0164	15257	G	A	1	519	missense_variant	MODERATE	CYTB	0.0155
HLI-0164	15326	A	G	2	581	missense_variant	MODERATE	CYTB	0.9868
HLI-0164	15452	C	A	1	474	missense_variant	MODERATE	CYTB	0.0933
HLI-0164	16069	C	T	2	602	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0164	16126	T	C	0	591	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0164	16145	G	A	0	572	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0164	16209	T	C	0	526	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0164	16231	T	C	0	526	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0164	16261	C	T	0	522	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0165	73	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0165	146	T	C	0	461	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0165	151	C	T	0	469	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0165	183	A	G	0	445	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0165	263	A	G	0	206	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0165	489	T	C	0	337	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0165	750	A	G	0	598	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0165	1438	A	G	1	524	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0165	2092	C	T	0	563	upstream_gene_variant	MODIFIER	RNR2	0.0087
HLI-0165	2706	A	G	0	596	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0165	3010	G	A	0	573	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0165	4769	A	G	0	585	synonymous_variant	LOW	ND2	0.9767
HLI-0165	4883	C	T	1	513	synonymous_variant	LOW	ND2	0.0483
HLI-0165	5178	C	A	0	502	missense_variant	MODERATE	ND2	0.0478
HLI-0165	7028	C	T	0	627	synonymous_variant	LOW	COX1	0.8089
HLI-0165	7747	C	T	0	546	synonymous_variant	LOW	COX2	5.00E-04
HLI-0165	8414	C	T	1	448	missense_variant	MODERATE	ATP8	0.0398
HLI-0165	8701	A	G	0	535	missense_variant	MODERATE	ATP6	0.3391
HLI-0165	9174	T	C	0	577	synonymous_variant	LOW	ATP6	4.00E-04
HLI-0165	9540	T	C	0	553	synonymous_variant	LOW	COX3	0.339

HLI-0165	10398	A	G	0	556	missense_variant	MODERATE	ND3	0.445
HLI-0165	10400	C	T	0	563	synonymous_variant	LOW	ND3	0.2131
HLI-0165	10873	T	C	3	500	synonymous_variant	LOW	ND4	0.3389
HLI-0165	11719	G	A	0	550	synonymous_variant	LOW	ND4	0.7756
HLI-0165	12705	C	T	0	592	synonymous_variant	LOW	ND5	0.4212
HLI-0165	14668	C	T	1	526	synonymous_variant	LOW	ND6	0.0417
HLI-0165	14766	C	T	1	497	missense_variant	MODERATE	CYTB	0.7696
HLI-0165	14783	T	C	1	563	synonymous_variant	LOW	CYTB	0.2126
HLI-0165	15043	G	A	2	563	synonymous_variant	LOW	CYTB	0.2362
HLI-0165	15301	G	A	0	498	synonymous_variant	LOW	CYTB	0.2912
HLI-0165	15326	A	G	0	537	missense_variant	MODERATE	CYTB	0.9868
HLI-0165	15760	C	T	2	561	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0165	16221	C	T	0	520	upstream_gene_variant	MODIFIER	DLoop	0.007
HLI-0165	16223	C	T	0	524	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0165	16325	T	C	0	458	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0165	16362	T	C	0	469	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0166	263	A	G	0	26	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0166	750	A	G	0	56	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0166	1438	A	G	0	48	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0166	3169	C	T	0	38	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0166	4769	A	G	0	53	synonymous_variant	LOW	ND2	0.9767
HLI-0166	9091	A	G	0	53	missense_variant	MODERATE	ATP6	3.00E-04
HLI-0166	12153	C	T	0	45	upstream_gene_variant	MODIFIER	TRNH	7.00E-04
HLI-0166	14470	T	A	0	55	synonymous_variant	LOW	ND6	0.0031
HLI-0166	15326	A	G	0	48	missense_variant	MODERATE	CYTB	0.9868
HLI-0166	16519	T	C	0	30	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0167	73	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0167	189	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0167	194	C	T	0	285	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0167	195	T	C	0	286	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0167	204	T	C	0	289	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0167	207	G	A	0	298	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0167	263	A	G	0	82	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0167	709	G	A	1	575	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0167	750	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0167	1243	T	C	1	608	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0167	1438	A	G	1	550	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0167	2706	A	G	1	537	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0167	3505	A	G	1	522	missense_variant	MODERATE	ND1	0.0144

HLI-0167	4363	T	C	0	479	upstream_gene_variant	MODIFIER	TRNQ	9.00E-04
HLI-0167	4769	A	G	1	525	synonymous_variant	LOW	ND2	0.9767
HLI-0167	5046	G	A	1	529	missense_variant	MODERATE	ND2	0.018
HLI-0167	5460	G	A	0	518	missense_variant	MODERATE	ND2	0.0651
HLI-0167	6528	C	T	1	561	synonymous_variant	LOW	COX1	0.0013
HLI-0167	7028	C	T	2	598	synonymous_variant	LOW	COX1	0.8089
HLI-0167	8251	G	A	1	534	synonymous_variant	LOW	COX2	0.058
HLI-0167	8994	G	A	1	503	synonymous_variant	LOW	ATP6	0.0167
HLI-0167	9275	A	G	0	535	synonymous_variant	LOW	COX3	3.00E-04
HLI-0167	10097	A	G	1	576	synonymous_variant	LOW	ND3	0.0011
HLI-0167	10410	T	C	1	568	upstream_gene_variant	MODIFIER	TRNR	0.0049
HLI-0167	11674	C	T	1	558	synonymous_variant	LOW	ND4	0.0116
HLI-0167	11719	G	A	3	603	synonymous_variant	LOW	ND4	0.7756
HLI-0167	11947	A	G	0	539	synonymous_variant	LOW	ND4	0.011
HLI-0167	12414	T	C	1	530	synonymous_variant	LOW	ND5	0.0139
HLI-0167	12705	C	T	0	558	synonymous_variant	LOW	ND5	0.4212
HLI-0167	14766	C	T	1	494	missense_variant	MODERATE	CYTB	0.7696
HLI-0167	15326	A	G	0	458	missense_variant	MODERATE	CYTB	0.9868
HLI-0167	15775	A	G	0	554	synonymous_variant	LOW	CYTB	0.0011
HLI-0167	15884	G	C	0	621	missense_variant	MODERATE	CYTB	0.011
HLI-0167	16223	C	T	4	483	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0167	16292	C	T	1	513	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0167	16362	T	C	0	442	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0167	16519	T	C	0	217	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0168	73	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0168	152	T	C	0	478	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0168	263	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0168	271	C	T	0	242	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0168	295	C	T	0	210	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0168	462	C	T	0	374	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0168	489	T	C	0	466	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0168	750	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0168	1438	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0168	2706	A	G	0	624	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0168	3010	G	A	1	611	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0168	4216	T	C	0	582	missense_variant	MODERATE	ND1	0.0991
HLI-0168	4769	A	G	0	588	synonymous_variant	LOW	ND2	0.9767
HLI-0168	5460	G	A	0	586	missense_variant	MODERATE	ND2	0.0651
HLI-0168	7028	C	T	1	612	synonymous_variant	LOW	COX1	0.8089

HLI-0168	8269	G	A	0	518	stop_retained_variant	LOW	COX2	0.0127
HLI-0168	9083	T	C	0	585	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0168	9192	G	A	0	659	synonymous_variant	LOW	ATP6	0.0012
HLI-0168	10398	A	G	1	669	missense_variant	MODERATE	ND3	0.445
HLI-0168	11719	G	A	0	552	synonymous_variant	LOW	ND4	0.7756
HLI-0168	12612	A	G	10	612	synonymous_variant	LOW	ND5	0.0506
HLI-0168	13269	A	G	2	693	synonymous_variant	LOW	ND5	0.0023
HLI-0168	13708	G	A	1	505	missense_variant	MODERATE	ND5	0.0717
HLI-0168	13879	T	C	1	456	missense_variant	MODERATE	ND5	0.0073
HLI-0168	14766	C	T	0	605	missense_variant	MODERATE	CYTB	0.7696
HLI-0168	15326	A	G	2	558	missense_variant	MODERATE	CYTB	0.9868
HLI-0168	15452	C	A	2	538	missense_variant	MODERATE	CYTB	0.0933
HLI-0168	16069	C	T	4	602	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0168	16126	T	C	0	571	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0168	16145	G	A	0	532	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0168	16222	C	T	1	518	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0168	16224	T	C	1	521	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0168	16235	A	G	1	515	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0168	16261	C	T	0	534	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0168	16519	T	C	0	211	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0169	73	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0169	185	G	A	7	403	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0169	263	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0169	295	C	T	0	186	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0169	462	C	T	3	433	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0169	489	T	C	0	523	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0169	750	A	G	1	638	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0169	1438	A	G	1	644	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0169	2706	A	G	2	577	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0169	3010	G	A	1	636	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0169	4216	T	C	0	610	missense_variant	MODERATE	ND1	0.0991
HLI-0169	4769	A	G	1	571	synonymous_variant	LOW	ND2	0.9767
HLI-0169	5237	G	A	0	558	synonymous_variant	LOW	ND2	0.0039
HLI-0169	6261	G	A	3	634	missense_variant	MODERATE	COX1	0.007
HLI-0169	7028	C	T	5	662	synonymous_variant	LOW	COX1	0.8089
HLI-0169	10398	A	G	1	672	missense_variant	MODERATE	ND3	0.445
HLI-0169	11251	A	G	0	607	synonymous_variant	LOW	ND4	0.0932
HLI-0169	11719	G	A	1	588	synonymous_variant	LOW	ND4	0.7756
HLI-0169	12612	A	G	4	637	synonymous_variant	LOW	ND5	0.0506

HLI-0169	13708	G	A	2	499	missense_variant	MODERATE	ND5	0.0717
HLI-0169	13934	C	T	1	501	missense_variant	MODERATE	ND5	0.0122
HLI-0169	14766	C	T	5	568	missense_variant	MODERATE	CYTB	0.7696
HLI-0169	14798	T	C	0	657	missense_variant	MODERATE	CYTB	0.0651
HLI-0169	15326	A	G	1	517	missense_variant	MODERATE	CYTB	0.9868
HLI-0169	15367	C	T	11	555	synonymous_variant	LOW	CYTB	6.00E-04
HLI-0169	15452	C	A	7	572	missense_variant	MODERATE	CYTB	0.0933
HLI-0169	16069	C	T	8	599	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0169	16126	T	C	3	579	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0169	16519	T	C	1	284	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0170	73	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0170	146	T	C	0	521	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0170	263	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0170	296	C	T	2	175	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0170	750	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0170	1438	A	G	0	680	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0170	1811	A	G	1	668	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0170	2706	A	G	0	709	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0170	3348	A	G	1	679	synonymous_variant	LOW	ND1	0.0065
HLI-0170	3480	A	G	0	589	synonymous_variant	LOW	ND1	0.0392
HLI-0170	4561	T	C	0	618	missense_variant	MODERATE	ND2	0.0065
HLI-0170	4769	A	G	1	600	synonymous_variant	LOW	ND2	0.9767
HLI-0170	5081	T	C	1	591	synonymous_variant	LOW	ND2	0.0012
HLI-0170	5130	T	C	0	680	synonymous_variant	LOW	ND2	7.00E-04
HLI-0170	7028	C	T	3	717	synonymous_variant	LOW	COX1	0.8089
HLI-0170	7076	A	G	4	717	synonymous_variant	LOW	COX1	0.0053
HLI-0170	9055	G	A	0	656	missense_variant	MODERATE	ATP6	0.0425
HLI-0170	9698	T	C	1	686	synonymous_variant	LOW	COX3	0.0405
HLI-0170	9716	T	C	1	750	synonymous_variant	LOW	COX3	0.0108
HLI-0170	10550	A	G	0	688	synonymous_variant	LOW	ND4L	0.0376
HLI-0170	11299	T	C	0	614	synonymous_variant	LOW	ND4	0.0417
HLI-0170	11467	A	G	2	644	synonymous_variant	LOW	ND4	0.1231
HLI-0170	11719	G	A	0	623	synonymous_variant	LOW	ND4	0.7756
HLI-0170	12308	A	G	1	672	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0170	12372	G	A	2	628	synonymous_variant	LOW	ND5	0.1329
HLI-0170	14167	C	T	1	588	synonymous_variant	LOW	ND6	0.0385
HLI-0170	14766	C	T	3	622	missense_variant	MODERATE	CYTB	0.7696
HLI-0170	14798	T	C	0	706	missense_variant	MODERATE	CYTB	0.0651
HLI-0170	15326	A	G	0	588	missense_variant	MODERATE	CYTB	0.9868

HLI-0170	16224	T	C	0	614	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0170	16311	T	C	2	535	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0170	16519	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0171	114	C	T	1	47	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0171	263	A	G	0	29	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0171	750	A	G	0	59	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0171	1438	A	G	0	52	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0171	4769	A	G	0	38	synonymous_variant	LOW	ND2	0.9767
HLI-0171	6776	T	C	0	69	synonymous_variant	LOW	COX1	0.0226
HLI-0171	9053	G	A	0	59	missense_variant	MODERATE	ATP6	0.0196
HLI-0171	13419	A	G	0	62	synonymous_variant	LOW	ND5	8.00E-04
HLI-0171	15326	A	G	0	55	missense_variant	MODERATE	CYTB	0.9868
HLI-0171	16519	T	C	0	35	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0172	73	A	G	0	282	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0172	195	T	C	3	365	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0172	263	A	G	1	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0172	497	C	T	5	455	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0172	750	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0172	1189	T	C	1	632	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0172	1438	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0172	1811	A	G	1	618	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0172	2706	A	G	0	621	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0172	3480	A	G	0	519	synonymous_variant	LOW	ND1	0.0392
HLI-0172	4769	A	G	0	566	synonymous_variant	LOW	ND2	0.9767
HLI-0172	7028	C	T	0	613	synonymous_variant	LOW	COX1	0.8089
HLI-0172	9055	G	A	1	592	missense_variant	MODERATE	ATP6	0.0425
HLI-0172	9698	T	C	0	586	synonymous_variant	LOW	COX3	0.0405
HLI-0172	10398	A	G	0	674	missense_variant	MODERATE	ND3	0.445
HLI-0172	10550	A	G	1	603	synonymous_variant	LOW	ND4L	0.0376
HLI-0172	11299	T	C	0	535	synonymous_variant	LOW	ND4	0.0417
HLI-0172	11467	A	G	0	664	synonymous_variant	LOW	ND4	0.1231
HLI-0172	11719	G	A	0	626	synonymous_variant	LOW	ND4	0.7756
HLI-0172	11914	G	A	1	572	synonymous_variant	LOW	ND4	0.1112
HLI-0172	12308	A	G	2	572	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0172	12372	G	A	0	566	synonymous_variant	LOW	ND5	0.1329
HLI-0172	14167	C	T	0	516	synonymous_variant	LOW	ND6	0.0385
HLI-0172	14766	C	T	3	616	missense_variant	MODERATE	CYTB	0.7696
HLI-0172	14798	T	C	1	636	missense_variant	MODERATE	CYTB	0.0651
HLI-0172	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868

HLI-0172	16093	T	C	9	570	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0172	16224	T	C	0	530	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0172	16311	T	C	0	510	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0172	16519	T	C	0	279	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0172	16524	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0173	73	A	G	0	175	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0173	151	C	T	1	272	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0173	152	T	C	1	274	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0173	182	C	T	1	260	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0173	185	G	T	1	257	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0173	189	A	G	1	255	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0173	195	T	C	1	263	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0173	247	G	A	0	136	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0173	263	A	G	0	149	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0173	357	A	G	0	219	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0173	709	G	A	1	601	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0173	710	T	C	2	603	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0173	750	A	G	0	576	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0173	769	G	A	0	572	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0173	825	T	A	0	592	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0173	1018	G	A	0	566	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0173	1738	T	C	2	613	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0173	2352	T	C	0	586	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0173	2706	A	G	1	617	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0173	2758	G	A	0	665	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0173	2768	A	G	0	651	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0173	2885	T	C	1	630	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0173	3308	T	C	3	598	start_lost	HIGH	ND1	0.0073
HLI-0173	3594	C	T	0	502	synonymous_variant	LOW	ND1	0.0789
HLI-0173	3666	G	A	4	610	synonymous_variant	LOW	ND1	0.0233
HLI-0173	3693	G	A	2	641	synonymous_variant	LOW	ND1	0.0091
HLI-0173	4104	A	G	1	535	synonymous_variant	LOW	ND1	0.0785
HLI-0173	4769	A	G	1	593	synonymous_variant	LOW	ND2	0.9767
HLI-0173	5036	A	G	1	601	synonymous_variant	LOW	ND2	0.006
HLI-0173	5046	G	A	1	640	missense_variant	MODERATE	ND2	0.018
HLI-0173	5393	T	C	0	528	synonymous_variant	LOW	ND2	0.0059
HLI-0173	5655	T	C	1	602	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0173	6548	C	T	3	658	synonymous_variant	LOW	COX1	0.0061
HLI-0173	6827	T	C	1	577	synonymous_variant	LOW	COX1	0.0072

HLI-0173	6989	A	G	3	629	synonymous_variant	LOW	COX1	0.0061
HLI-0173	7028	C	T	3	604	synonymous_variant	LOW	COX1	0.8089
HLI-0173	7055	A	G	1	528	synonymous_variant	LOW	COX1	0.0188
HLI-0173	7146	A	G	0	268	missense_variant	MODERATE	COX1	0.0497
HLI-0173	7256	C	T	2	412	synonymous_variant	LOW	COX1	0.0784
HLI-0173	7389	T	C	1	442	missense_variant	MODERATE	COX1	0.0201
HLI-0173	7521	G	A	0	414	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0173	7753	A	C	2	527	synonymous_variant	LOW	COX2	0
HLI-0173	7867	C	T	1	610	synonymous_variant	LOW	COX2	0.0076
HLI-0173	8248	A	G	0	560	synonymous_variant	LOW	COX2	0.0061
HLI-0173	8468	C	T	2	444	synonymous_variant	LOW	ATP8	0.0501
HLI-0173	8655	C	T	3	428	synonymous_variant	LOW	ATP6	0.0511
HLI-0173	8701	A	G	1	454	missense_variant	MODERATE	ATP6	0.3391
HLI-0173	9540	T	C	3	602	synonymous_variant	LOW	COX3	0.339
HLI-0173	10398	A	G	0	645	missense_variant	MODERATE	ND3	0.445
HLI-0173	10688	G	A	0	559	synonymous_variant	LOW	ND4L	0.0515
HLI-0173	10810	T	C	0	555	synonymous_variant	LOW	ND4	0.0522
HLI-0173	10873	T	C	1	573	synonymous_variant	LOW	ND4	0.3389
HLI-0173	11719	G	A	4	610	synonymous_variant	LOW	ND4	0.7756
HLI-0173	12519	T	C	0	581	synonymous_variant	LOW	ND5	0.007
HLI-0173	12705	C	T	2	592	synonymous_variant	LOW	ND5	0.4212
HLI-0173	13105	A	G	1	597	missense_variant	MODERATE	ND5	0.076
HLI-0173	13506	C	T	5	570	synonymous_variant	LOW	ND5	0.0506
HLI-0173	13650	C	T	2	519	synonymous_variant	LOW	ND5	0.079
HLI-0173	13789	T	C	1	398	missense_variant	MODERATE	ND5	0.0185
HLI-0173	13879	T	C	1	484	missense_variant	MODERATE	ND5	0.0073
HLI-0173	13880	C	A	1	484	missense_variant	MODERATE	ND5	0.0055
HLI-0173	14178	T	C	2	519	missense_variant	MODERATE	ND6	0.0225
HLI-0173	14203	A	G	2	584	synonymous_variant	LOW	ND6	0.0061
HLI-0173	14560	G	A	0	591	synonymous_variant	LOW	ND6	0.0235
HLI-0173	14766	C	T	0	575	missense_variant	MODERATE	CYTB	0.7696
HLI-0173	14769	A	G	0	584	missense_variant	MODERATE	CYTB	0.0121
HLI-0173	15115	T	C	1	639	synonymous_variant	LOW	CYTB	0.0093
HLI-0173	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0173	16126	T	C	3	591	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0173	16223	C	T	3	489	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0173	16264	C	T	1	460	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0173	16270	C	T	0	454	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0173	16278	C	T	0	451	upstream_gene_variant	MODIFIER	DLoop	0.1057

HLI-0173	16311	T	C	0	428	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0173	16519	T	C	0	146	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0174	146	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0174	152	T	C	0	407	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0174	263	A	G	1	150	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0174	750	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0174	1438	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0174	4769	A	G	2	594	synonymous_variant	LOW	ND2	0.9767
HLI-0174	6253	T	C	1	580	missense_variant	MODERATE	COX1	0.0106
HLI-0174	6750	C	T	3	751	synonymous_variant	LOW	COX1	0
HLI-0174	8757	T	C	1	554	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0174	11410	T	C	0	601	synonymous_variant	LOW	ND4	0.002
HLI-0174	11914	G	A	0	572	synonymous_variant	LOW	ND4	0.1112
HLI-0174	14953	C	T	4	599	synonymous_variant	LOW	CYTB	0.0019
HLI-0174	15326	A	G	0	544	missense_variant	MODERATE	CYTB	0.9868
HLI-0175	73	A	G	0	320	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0175	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0175	497	C	T	3	486	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0175	750	A	G	0	634	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0175	1189	T	C	0	621	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0175	1438	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0175	1811	A	G	0	631	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0175	2706	A	G	1	610	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0175	3480	A	G	0	519	synonymous_variant	LOW	ND1	0.0392
HLI-0175	4769	A	G	1	602	synonymous_variant	LOW	ND2	0.9767
HLI-0175	6260	G	A	2	619	synonymous_variant	LOW	COX1	0.009
HLI-0175	7028	C	T	1	736	synonymous_variant	LOW	COX1	0.8089
HLI-0175	9055	G	A	0	634	missense_variant	MODERATE	ATP6	0.0425
HLI-0175	9698	T	C	0	613	synonymous_variant	LOW	COX3	0.0405
HLI-0175	10398	A	G	0	658	missense_variant	MODERATE	ND3	0.445
HLI-0175	10550	A	G	2	589	synonymous_variant	LOW	ND4L	0.0376
HLI-0175	11299	T	C	1	598	synonymous_variant	LOW	ND4	0.0417
HLI-0175	11467	A	G	2	626	synonymous_variant	LOW	ND4	0.1231
HLI-0175	11485	T	C	1	679	synonymous_variant	LOW	ND4	0.0081
HLI-0175	11719	G	A	2	616	synonymous_variant	LOW	ND4	0.7756
HLI-0175	11840	C	T	1	683	synonymous_variant	LOW	ND4	0.0041
HLI-0175	12308	A	G	2	620	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0175	12372	G	A	1	642	synonymous_variant	LOW	ND5	0.1329
HLI-0175	13740	T	C	0	491	synonymous_variant	LOW	ND5	0.0041

HLI-0175	14167	C	T	6	524	synonymous_variant	LOW	ND6	0.0385
HLI-0175	14766	C	T	3	633	missense_variant	MODERATE	CYTB	0.7696
HLI-0175	14798	T	C	1	719	missense_variant	MODERATE	CYTB	0.0651
HLI-0175	15326	A	G	0	554	missense_variant	MODERATE	CYTB	0.9868
HLI-0175	16224	T	C	0	646	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0175	16311	T	C	1	564	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0175	16519	T	C	1	313	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0176	73	A	G	1	403	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0176	153	A	G	6	626	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0176	195	T	C	2	579	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0176	225	G	A	1	546	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0176	227	A	G	1	544	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0176	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0176	1438	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0176	1719	G	A	3	369	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0176	2706	A	G	0	602	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0176	4769	A	G	2	390	synonymous_variant	LOW	ND2	0.9767
HLI-0176	6221	T	C	0	823	synonymous_variant	LOW	COX1	0.0306
HLI-0176	6371	C	T	1	761	synonymous_variant	LOW	COX1	0.0097
HLI-0176	7028	C	T	5	444	synonymous_variant	LOW	COX1	0.8089
HLI-0176	8705	T	C	0	375	missense_variant	MODERATE	ATP6	0.0039
HLI-0176	11719	G	A	0	504	synonymous_variant	LOW	ND4	0.7756
HLI-0176	12705	C	T	2	395	synonymous_variant	LOW	ND5	0.4212
HLI-0176	13966	A	G	0	340	missense_variant	MODERATE	ND5	0.0126
HLI-0176	14470	T	C	2	626	synonymous_variant	LOW	ND6	0.0166
HLI-0176	14766	C	T	0	842	missense_variant	MODERATE	CYTB	0.7696
HLI-0176	15326	A	G	0	233	missense_variant	MODERATE	CYTB	0.9868
HLI-0176	16108	C	T	1	167	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0176	16223	C	T	2	172	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0176	16255	G	A	0	272	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0176	16278	C	T	1	341	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0176	16519	T	C	0	284	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0177	263	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0177	750	A	G	0	732	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0177	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0177	4654	C	T	0	631	missense_variant	MODERATE	ND2	2.00E-04
HLI-0177	4769	A	G	0	589	synonymous_variant	LOW	ND2	0.9767
HLI-0177	11788	C	T	3	528	synonymous_variant	LOW	ND4	7.00E-04
HLI-0177	13145	G	A	5	697	missense_variant	MODERATE	ND5	0.0094

HLI-0177	13389	C	T	0	574	synonymous_variant	LOW	ND5	1.00E-04
HLI-0177	15326	A	G	0	509	missense_variant	MODERATE	CYTB	0.9868
HLI-0177	16519	T	C	1	291	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0178	239	T	C	2	438	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0178	263	A	G	0	393	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0178	750	A	G	0	904	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0178	1438	A	G	1	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0178	3915	G	A	8	849	synonymous_variant	LOW	ND1	0.0106
HLI-0178	4727	A	G	5	489	synonymous_variant	LOW	ND2	0.0063
HLI-0178	4769	A	G	1	546	synonymous_variant	LOW	ND2	0.9767
HLI-0178	7280	C	T	5	488	synonymous_variant	LOW	COX1	2.00E-04
HLI-0178	9380	G	A	16	857	synonymous_variant	LOW	COX3	0.0094
HLI-0178	11253	T	C	0	455	missense_variant	MODERATE	ND4	0.0053
HLI-0178	15326	A	G	0	370	missense_variant	MODERATE	CYTB	0.9868
HLI-0178	16362	T	C	6	546	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0179	263	A	G	0	320	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0179	456	C	T	3	533	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0179	750	A	G	0	733	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0179	1438	A	G	0	522	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0179	3357	G	A	1	547	synonymous_variant	LOW	ND1	0.0012
HLI-0179	4336	T	C	1	526	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0179	4769	A	G	0	357	synonymous_variant	LOW	ND2	0.9767
HLI-0179	8440	A	G	1	315	synonymous_variant	LOW	ATP8	0.0046
HLI-0179	15326	A	G	0	341	missense_variant	MODERATE	CYTB	0.9868
HLI-0179	15833	C	T	1	143	synonymous_variant	LOW	CYTB	0.0051
HLI-0179	16304	T	C	0	426	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0180	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0180	146	T	C	27	440	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0180	152	T	C	0	481	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0180	263	A	G	0	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0180	709	G	A	27	661	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0180	750	A	G	0	749	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0180	1438	A	G	0	657	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0180	1674	A	G	25	612	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0180	1811	A	G	34	636	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0180	2706	A	G	0	689	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0180	3480	A	G	25	543	synonymous_variant	LOW	ND1	0.0392
HLI-0180	4561	T	C	25	552	missense_variant	MODERATE	ND2	0.0065
HLI-0180	4769	A	G	0	548	synonymous_variant	LOW	ND2	0.9767

HLI-0180	7028	C	T	1	653	synonymous_variant	LOW	COX1	0.8089
HLI-0180	9055	G	A	29	581	missense_variant	MODERATE	ATP6	0.0425
HLI-0180	9698	T	C	30	680	synonymous_variant	LOW	COX3	0.0405
HLI-0180	9716	T	C	32	745	synonymous_variant	LOW	COX3	0.0108
HLI-0180	10550	A	G	24	618	synonymous_variant	LOW	ND4L	0.0376
HLI-0180	11299	T	C	38	653	synonymous_variant	LOW	ND4	0.0417
HLI-0180	11467	A	G	30	623	synonymous_variant	LOW	ND4	0.1231
HLI-0180	11719	G	A	1	614	synonymous_variant	LOW	ND4	0.7756
HLI-0180	12308	A	G	25	593	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0180	12372	G	A	31	631	synonymous_variant	LOW	ND5	0.1329
HLI-0180	12950	A	G	28	579	missense_variant	MODERATE	ND5	0.0043
HLI-0180	14167	C	T	33	566	synonymous_variant	LOW	ND6	0.0385
HLI-0180	14766	C	T	4	599	missense_variant	MODERATE	CYTB	0.7696
HLI-0180	14798	T	C	38	640	missense_variant	MODERATE	CYTB	0.0651
HLI-0180	15326	A	G	1	669	missense_variant	MODERATE	CYTB	0.9868
HLI-0180	16224	T	C	10	559	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0180	16270	C	T	21	537	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0180	16311	T	C	21	502	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0180	16519	T	C	9	253	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0181	263	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0181	750	A	G	1	739	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0181	1438	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0181	4769	A	G	2	474	synonymous_variant	LOW	ND2	0.9767
HLI-0181	6776	T	C	9	741	synonymous_variant	LOW	COX1	0.0226
HLI-0181	12811	T	C	4	646	missense_variant	MODERATE	ND5	0.0125
HLI-0181	13967	C	T	0	428	missense_variant	MODERATE	ND5	0.003
HLI-0181	15326	A	G	0	457	missense_variant	MODERATE	CYTB	0.9868
HLI-0181	16311	T	C	1	467	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0181	16519	T	C	1	360	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0182	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0182	750	A	G	1	676	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0182	1438	A	G	2	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0182	4769	A	G	0	480	synonymous_variant	LOW	ND2	0.9767
HLI-0182	6776	T	C	2	783	synonymous_variant	LOW	COX1	0.0226
HLI-0182	8415	T	C	1	345	missense_variant	MODERATE	ATP8	0
HLI-0182	11746	A	G	3	639	synonymous_variant	LOW	ND4	1.00E-04
HLI-0182	15326	A	G	0	470	missense_variant	MODERATE	CYTB	0.9868
HLI-0182	16519	T	C	0	344	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0183	263	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0183	750	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0183	1438	A	G	0	602	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0183	4769	A	G	0	553	synonymous_variant	LOW	ND2	0.9767
HLI-0183	9545	A	G	1	650	synonymous_variant	LOW	COX3	0.0469
HLI-0183	11152	T	C	0	577	synonymous_variant	LOW	ND4	0.0024
HLI-0183	13500	T	C	0	544	synonymous_variant	LOW	ND5	0.0173
HLI-0183	15326	A	G	0	487	missense_variant	MODERATE	CYTB	0.9868
HLI-0183	16362	T	C	0	468	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0183	16519	T	C	0	371	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0184	73	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0184	152	T	C	1	422	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0184	182	C	T	0	391	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0184	185	G	T	0	386	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0184	189	A	G	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0184	195	T	C	0	375	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0184	199	T	C	0	384	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0184	247	G	A	0	209	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0184	263	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0184	357	A	G	0	370	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0184	709	G	A	1	533	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0184	710	T	C	1	533	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0184	750	A	G	0	571	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0184	769	G	A	0	589	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0184	825	T	A	1	661	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0184	1018	G	A	1	702	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0184	1738	T	C	1	157	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0184	2352	T	C	1	305	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0184	2706	A	G	2	545	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0184	2758	G	A	0	572	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0184	2768	A	G	0	578	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0184	2885	T	C	0	465	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0184	3308	T	C	2	526	start_lost	HIGH	ND1	0.0073
HLI-0184	3594	C	T	0	449	synonymous_variant	LOW	ND1	0.0789
HLI-0184	3666	G	A	1	514	synonymous_variant	LOW	ND1	0.0233
HLI-0184	3693	G	A	1	520	synonymous_variant	LOW	ND1	0.0091
HLI-0184	4104	A	G	0	442	synonymous_variant	LOW	ND1	0.0785
HLI-0184	4219	G	A	0	302	missense_variant	MODERATE	ND1	0.001
HLI-0184	4769	A	G	1	351	synonymous_variant	LOW	ND2	0.9767
HLI-0184	5036	A	G	0	379	synonymous_variant	LOW	ND2	0.006

HLI-0184	5046	G	A	0	403	missense_variant	MODERATE	ND2	0.018
HLI-0184	5393	T	C	1	364	synonymous_variant	LOW	ND2	0.0059
HLI-0184	5655	T	C	2	652	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0184	6548	C	T	1	566	synonymous_variant	LOW	COX1	0.0061
HLI-0184	6827	T	C	2	766	synonymous_variant	LOW	COX1	0.0072
HLI-0184	6989	A	G	0	589	synonymous_variant	LOW	COX1	0.0061
HLI-0184	7028	C	T	1	562	synonymous_variant	LOW	COX1	0.8089
HLI-0184	7055	A	G	1	504	synonymous_variant	LOW	COX1	0.0188
HLI-0184	7146	A	G	0	287	missense_variant	MODERATE	COX1	0.0497
HLI-0184	7256	C	T	2	243	synonymous_variant	LOW	COX1	0.0784
HLI-0184	7389	T	C	2	243	missense_variant	MODERATE	COX1	0.0201
HLI-0184	7521	G	A	0	207	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0184	7867	C	T	1	735	synonymous_variant	LOW	COX2	0.0076
HLI-0184	8248	A	G	1	440	synonymous_variant	LOW	COX2	0.0061
HLI-0184	8468	C	T	1	214	synonymous_variant	LOW	ATP8	0.0501
HLI-0184	8655	C	T	1	215	synonymous_variant	LOW	ATP6	0.0511
HLI-0184	8701	A	G	0	264	missense_variant	MODERATE	ATP6	0.3391
HLI-0184	9540	T	C	0	484	synonymous_variant	LOW	COX3	0.339
HLI-0184	10398	A	G	1	303	missense_variant	MODERATE	ND3	0.445
HLI-0184	10688	G	A	1	373	synonymous_variant	LOW	ND4L	0.0515
HLI-0184	10810	T	C	1	335	synonymous_variant	LOW	ND4	0.0522
HLI-0184	10873	T	C	1	407	synonymous_variant	LOW	ND4	0.3389
HLI-0184	11719	G	A	2	558	synonymous_variant	LOW	ND4	0.7756
HLI-0184	12519	T	C	0	218	synonymous_variant	LOW	ND5	0.007
HLI-0184	12705	C	T	2	326	synonymous_variant	LOW	ND5	0.4212
HLI-0184	13105	A	G	1	542	missense_variant	MODERATE	ND5	0.076
HLI-0184	13506	C	T	1	345	synonymous_variant	LOW	ND5	0.0506
HLI-0184	13650	C	T	0	374	synonymous_variant	LOW	ND5	0.079
HLI-0184	13789	T	C	0	279	missense_variant	MODERATE	ND5	0.0185
HLI-0184	13880	C	A	3	339	missense_variant	MODERATE	ND5	0.0055
HLI-0184	14178	T	C	0	298	missense_variant	MODERATE	ND6	0.0225
HLI-0184	14203	A	G	0	354	synonymous_variant	LOW	ND6	0.0061
HLI-0184	14560	G	A	0	712	synonymous_variant	LOW	ND6	0.0235
HLI-0184	14766	C	T	0	768	missense_variant	MODERATE	CYTB	0.7696
HLI-0184	14769	A	G	0	785	missense_variant	MODERATE	CYTB	0.0121
HLI-0184	15077	G	A	0	633	missense_variant	MODERATE	CYTB	0.0021
HLI-0184	15103	C	T	1	686	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0184	15115	T	C	1	677	synonymous_variant	LOW	CYTB	0.0093
HLI-0184	15326	A	G	0	280	missense_variant	MODERATE	CYTB	0.9868

HLI-0184	16126	T	C	1	219	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0184	16223	C	T	3	242	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0184	16264	C	T	1	231	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0184	16270	C	T	1	219	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0184	16278	C	T	1	226	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0184	16293	A	G	1	242	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0184	16311	T	C	1	249	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0184	16355	C	T	1	244	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0184	16519	T	C	0	124	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0185	73	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0185	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0185	750	A	G	1	688	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0185	1438	A	G	0	648	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0185	2706	A	G	1	663	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0185	3197	T	C	3	622	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0185	4769	A	G	2	527	synonymous_variant	LOW	ND2	0.9767
HLI-0185	7028	C	T	6	635	synonymous_variant	LOW	COX1	0.8089
HLI-0185	7843	A	G	3	686	synonymous_variant	LOW	COX2	0.0011
HLI-0185	9477	G	A	1	590	missense_variant	MODERATE	COX3	0.0387
HLI-0185	9758	T	C	1	701	synonymous_variant	LOW	COX3	0.0034
HLI-0185	11467	A	G	2	573	synonymous_variant	LOW	ND4	0.1231
HLI-0185	11719	G	A	2	507	synonymous_variant	LOW	ND4	0.7756
HLI-0185	12308	A	G	3	544	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0185	12372	G	A	1	583	synonymous_variant	LOW	ND5	0.1329
HLI-0185	12807	A	G	5	664	synonymous_variant	LOW	ND5	1.00E-04
HLI-0185	13617	T	C	0	547	synonymous_variant	LOW	ND5	0.038
HLI-0185	14766	C	T	2	623	missense_variant	MODERATE	CYTB	0.7696
HLI-0185	14793	A	G	2	721	missense_variant	MODERATE	CYTB	0.0199
HLI-0185	15326	A	G	0	571	missense_variant	MODERATE	CYTB	0.9868
HLI-0185	16256	C	T	1	490	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0185	16270	C	T	1	473	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0185	16287	C	T	1	432	upstream_gene_variant	MODIFIER	DLoop	0.0051
HLI-0185	16294	C	T	1	442	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0185	16295	C	T	1	443	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0185	16526	G	A	0	186	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0186	73	A	G	0	343	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0186	152	T	C	0	580	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0186	217	T	C	1	391	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0186	263	A	G	1	290	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0186	340	C	T	1	306	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0186	508	A	G	2	415	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0186	750	A	G	3	728	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0186	1438	A	G	0	625	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0186	1811	A	G	1	602	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0186	2706	A	G	3	622	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0186	3116	C	T	0	555	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0186	3720	A	G	1	678	synonymous_variant	LOW	ND1	0.0069
HLI-0186	4204	T	A	0	694	missense_variant	MODERATE	ND1	0
HLI-0186	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767
HLI-0186	5390	A	G	1	543	synonymous_variant	LOW	ND2	0.0069
HLI-0186	5426	T	C	1	623	synonymous_variant	LOW	ND2	0.0091
HLI-0186	6045	C	T	0	792	synonymous_variant	LOW	COX1	0.0065
HLI-0186	6152	T	C	1	753	synonymous_variant	LOW	COX1	0.0077
HLI-0186	7028	C	T	7	594	synonymous_variant	LOW	COX1	0.8089
HLI-0186	10876	A	G	2	394	synonymous_variant	LOW	ND4	0.0098
HLI-0186	11197	C	T	2	459	synonymous_variant	LOW	ND4	0.0021
HLI-0186	11467	A	G	0	583	synonymous_variant	LOW	ND4	0.1231
HLI-0186	11719	G	A	0	573	synonymous_variant	LOW	ND4	0.7756
HLI-0186	11732	T	C	0	628	synonymous_variant	LOW	ND4	0.002
HLI-0186	12308	A	G	0	505	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0186	12372	G	A	1	566	synonymous_variant	LOW	ND5	0.1329
HLI-0186	13020	T	C	0	706	synonymous_variant	LOW	ND5	0.0106
HLI-0186	13734	T	C	0	409	synonymous_variant	LOW	ND5	0.0067
HLI-0186	14226	G	A	2	503	missense_variant	MODERATE	ND6	6.00E-04
HLI-0186	14766	C	T	8	669	missense_variant	MODERATE	CYTB	0.7696
HLI-0186	15218	A	G	0	550	missense_variant	MODERATE	CYTB	0.0169
HLI-0186	15326	A	G	0	392	missense_variant	MODERATE	CYTB	0.9868
HLI-0186	15907	A	G	2	406	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0186	16051	A	G	1	410	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0186	16129	G	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0186	16362	T	C	1	466	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0186	16519	T	C	0	305	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0187	73	A	G	1	341	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0187	263	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0187	750	A	G	0	703	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0187	1438	A	G	0	616	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0187	3010	G	A	0	509	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0187	4639	T	C	1	641	missense_variant	MODERATE	ND2	0.0034

HLI-0187	4769	A	G	0	546	synonymous_variant	LOW	ND2	0.9767
HLI-0187	6365	T	C	0	639	synonymous_variant	LOW	COX1	0.0026
HLI-0187	10993	G	A	0	233	synonymous_variant	LOW	ND4	0.0014
HLI-0187	15326	A	G	0	392	missense_variant	MODERATE	CYTB	0.9868
HLI-0187	16162	A	G	1	450	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0187	16209	T	C	1	529	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0187	16519	T	C	0	371	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0188	263	A	G	1	179	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0188	750	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0188	1438	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0188	4769	A	G	2	566	synonymous_variant	LOW	ND2	0.9767
HLI-0188	11560	A	G	0	612	synonymous_variant	LOW	ND4	0.0015
HLI-0188	15326	A	G	0	465	missense_variant	MODERATE	CYTB	0.9868
HLI-0188	16519	T	C	1	223	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0189	73	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0189	119	T	C	6	329	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0189	189	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0189	195	T	C	0	255	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0189	204	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0189	207	G	A	0	248	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0189	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0189	709	G	A	6	530	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0189	750	A	G	0	568	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0189	1243	T	C	5	546	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0189	1438	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0189	2706	A	G	1	537	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0189	3505	A	G	7	460	missense_variant	MODERATE	ND1	0.0144
HLI-0189	4769	A	G	3	495	synonymous_variant	LOW	ND2	0.9767
HLI-0189	5046	G	A	6	558	missense_variant	MODERATE	ND2	0.018
HLI-0189	5460	G	A	7	540	missense_variant	MODERATE	ND2	0.0651
HLI-0189	5785	T	C	8	630	upstream_gene_variant	MODIFIER	TRNC	4.00E-04
HLI-0189	7028	C	T	1	615	synonymous_variant	LOW	COX1	0.8089
HLI-0189	7864	C	T	5	566	synonymous_variant	LOW	COX2	0.0041
HLI-0189	8251	G	A	7	470	synonymous_variant	LOW	COX2	0.058
HLI-0189	8994	G	A	4	518	synonymous_variant	LOW	ATP6	0.0167
HLI-0189	11674	C	T	6	511	synonymous_variant	LOW	ND4	0.0116
HLI-0189	11719	G	A	1	566	synonymous_variant	LOW	ND4	0.7756
HLI-0189	11947	A	G	7	492	synonymous_variant	LOW	ND4	0.011
HLI-0189	12414	T	C	9	490	synonymous_variant	LOW	ND5	0.0139

HLI-0189	12705	C	T	6	601	synonymous_variant	LOW	ND5	0.4212
HLI-0189	14766	C	T	3	479	missense_variant	MODERATE	CYTB	0.7696
HLI-0189	15326	A	G	0	502	missense_variant	MODERATE	CYTB	0.9868
HLI-0189	15884	G	C	6	602	missense_variant	MODERATE	CYTB	0.011
HLI-0189	16223	C	T	4	548	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0189	16292	C	T	1	489	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0189	16295	C	T	1	494	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0189	16519	T	C	1	207	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0190	73	A	G	24	242	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0190	195	T	C	28	442	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0190	263	A	G	0	190	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0190	709	G	A	26	595	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0190	750	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0190	1438	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0190	1888	G	A	35	543	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0190	2706	A	G	40	564	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0190	4216	T	C	35	565	missense_variant	MODERATE	ND1	0.0991
HLI-0190	4769	A	G	4	584	synonymous_variant	LOW	ND2	0.9767
HLI-0190	4917	A	G	25	542	missense_variant	MODERATE	ND2	0.0477
HLI-0190	5277	T	C	26	523	missense_variant	MODERATE	ND2	0.0022
HLI-0190	5426	T	C	37	537	synonymous_variant	LOW	ND2	0.0091
HLI-0190	6489	C	A	29	590	missense_variant	MODERATE	COX1	0.0016
HLI-0190	7028	C	T	45	633	synonymous_variant	LOW	COX1	0.8089
HLI-0190	8697	G	A	34	513	synonymous_variant	LOW	ATP6	0.0466
HLI-0190	10463	T	C	29	616	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0190	11251	A	G	28	608	synonymous_variant	LOW	ND4	0.0932
HLI-0190	11719	G	A	35	541	synonymous_variant	LOW	ND4	0.7756
HLI-0190	11812	A	G	25	519	synonymous_variant	LOW	ND4	0.0332
HLI-0190	13368	G	A	27	620	synonymous_variant	LOW	ND5	0.0495
HLI-0190	14233	A	G	29	542	synonymous_variant	LOW	ND6	0.0369
HLI-0190	14766	C	T	27	511	missense_variant	MODERATE	CYTB	0.7696
HLI-0190	14905	G	A	25	599	synonymous_variant	LOW	CYTB	0.0526
HLI-0190	15028	C	A	36	609	synonymous_variant	LOW	CYTB	0.0016
HLI-0190	15043	G	A	35	680	synonymous_variant	LOW	CYTB	0.2362
HLI-0190	15326	A	G	0	554	missense_variant	MODERATE	CYTB	0.9868
HLI-0190	15452	C	A	29	529	missense_variant	MODERATE	CYTB	0.0933
HLI-0190	15607	A	G	26	512	synonymous_variant	LOW	CYTB	0.0508
HLI-0190	15928	G	A	25	599	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0190	16126	T	C	33	308	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0190	16294	C	T	41	329	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0190	16296	C	T	41	331	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0190	16298	T	C	40	339	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0190	16519	T	C	11	173	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0191	73	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0191	185	G	A	1	370	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0191	195	T	C	1	374	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0191	228	G	A	0	277	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0191	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0191	295	C	T	0	136	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0191	462	C	T	7	350	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0191	489	T	C	9	418	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0191	750	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0191	1438	A	G	1	602	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0191	2706	A	G	2	647	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0191	3010	G	A	8	666	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0191	4216	T	C	8	622	missense_variant	MODERATE	ND1	0.0991
HLI-0191	4491	G	A	6	580	missense_variant	MODERATE	ND2	0.0182
HLI-0191	4769	A	G	0	548	synonymous_variant	LOW	ND2	0.9767
HLI-0191	7028	C	T	7	638	synonymous_variant	LOW	COX1	0.8089
HLI-0191	8940	C	T	7	561	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0191	9120	A	G	4	579	synonymous_variant	LOW	ATP6	8.00E-04
HLI-0191	10398	A	G	10	591	missense_variant	MODERATE	ND3	0.445
HLI-0191	11251	A	G	11	559	synonymous_variant	LOW	ND4	0.0932
HLI-0191	11719	G	A	1	580	synonymous_variant	LOW	ND4	0.7756
HLI-0191	12612	A	G	12	566	synonymous_variant	LOW	ND5	0.0506
HLI-0191	13708	G	A	8	430	missense_variant	MODERATE	ND5	0.0717
HLI-0191	14766	C	T	6	621	missense_variant	MODERATE	CYTB	0.7696
HLI-0191	14798	T	C	14	679	missense_variant	MODERATE	CYTB	0.0651
HLI-0191	15326	A	G	0	523	missense_variant	MODERATE	CYTB	0.9868
HLI-0191	15452	C	A	12	562	missense_variant	MODERATE	CYTB	0.0933
HLI-0191	16069	C	T	5	573	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0191	16093	T	C	6	598	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0191	16126	T	C	9	572	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0191	16261	C	T	4	572	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0191	16274	G	A	1	557	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0191	16355	C	T	7	436	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0192	263	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0192	750	A	G	0	631	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0192	951	G	A	2	577	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0192	4769	A	G	1	553	synonymous_variant	LOW	ND2	0.9767
HLI-0192	6260	G	A	1	667	synonymous_variant	LOW	COX1	0.009
HLI-0192	8679	A	G	2	507	synonymous_variant	LOW	ATP6	0.0011
HLI-0192	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0192	16354	C	T	1	449	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0193	73	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0193	150	C	T	0	528	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0193	263	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0193	326	A	G	5	209	upstream_gene_variant	MODIFIER	DLoop	0.001
HLI-0193	750	A	G	2	582	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0193	1438	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0193	1709	G	A	0	565	upstream_gene_variant	MODIFIER	RNR2	0.0035
HLI-0193	2706	A	G	2	598	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0193	3197	T	C	0	587	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0193	5656	A	G	1	607	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0193	6570	G	T	2	573	missense_variant	MODERATE	COX1	7.00E-04
HLI-0193	7028	C	T	3	759	synonymous_variant	LOW	COX1	0.8089
HLI-0193	7768	A	G	0	527	synonymous_variant	LOW	COX2	0.0186
HLI-0193	8084	A	G	1	575	missense_variant	MODERATE	COX2	3.00E-04
HLI-0193	9086	C	T	0	594	missense_variant	MODERATE	ATP6	0
HLI-0193	9477	G	A	2	609	missense_variant	MODERATE	COX3	0.0387
HLI-0193	11467	A	G	2	605	synonymous_variant	LOW	ND4	0.1231
HLI-0193	11719	G	A	2	603	synonymous_variant	LOW	ND4	0.7756
HLI-0193	12308	A	G	2	562	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0193	12372	G	A	2	604	synonymous_variant	LOW	ND5	0.1329
HLI-0193	13617	T	C	0	551	synonymous_variant	LOW	ND5	0.038
HLI-0193	14182	T	C	1	518	synonymous_variant	LOW	ND6	0.0254
HLI-0193	14766	C	T	4	539	missense_variant	MODERATE	CYTB	0.7696
HLI-0193	15326	A	G	0	554	missense_variant	MODERATE	CYTB	0.9868
HLI-0193	16270	C	T	1	339	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0193	16519	T	C	1	236	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0194	263	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0194	477	T	C	0	350	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0194	750	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0194	1438	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0194	3010	G	A	2	563	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0194	4769	A	G	2	548	synonymous_variant	LOW	ND2	0.9767
HLI-0194	14136	C	A	2	566	synonymous_variant	LOW	ND5	0

HLI-0194	15325	A	C	0	548	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0194	15326	A	G	0	552	missense_variant	MODERATE	CYTB	0.9868
HLI-0194	16292	C	T	0	516	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0194	16519	T	C	0	253	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0195	73	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0195	152	T	C	1	473	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0195	263	A	G	0	183	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0195	709	G	A	1	546	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0195	750	A	G	0	591	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0195	930	G	A	3	556	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0195	1438	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0195	1888	G	A	0	549	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0195	2706	A	G	3	574	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0195	4216	T	C	2	599	missense_variant	MODERATE	ND1	0.0991
HLI-0195	4769	A	G	0	492	synonymous_variant	LOW	ND2	0.9767
HLI-0195	4917	A	G	1	513	missense_variant	MODERATE	ND2	0.0477
HLI-0195	5147	G	A	2	487	synonymous_variant	LOW	ND2	0.0437
HLI-0195	7028	C	T	2	614	synonymous_variant	LOW	COX1	0.8089
HLI-0195	7521	G	A	0	545	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0195	8697	G	A	3	522	synonymous_variant	LOW	ATP6	0.0466
HLI-0195	8934	C	T	4	543	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0195	10463	T	C	3	650	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0195	11251	A	G	1	541	synonymous_variant	LOW	ND4	0.0932
HLI-0195	11719	G	A	1	563	synonymous_variant	LOW	ND4	0.7756
HLI-0195	11812	A	G	1	540	synonymous_variant	LOW	ND4	0.0332
HLI-0195	13368	G	A	2	575	synonymous_variant	LOW	ND5	0.0495
HLI-0195	14233	A	G	0	505	synonymous_variant	LOW	ND6	0.0369
HLI-0195	14766	C	T	3	528	missense_variant	MODERATE	CYTB	0.7696
HLI-0195	14905	G	A	2	574	synonymous_variant	LOW	CYTB	0.0526
HLI-0195	15326	A	G	0	475	missense_variant	MODERATE	CYTB	0.9868
HLI-0195	15452	C	A	3	487	missense_variant	MODERATE	CYTB	0.0933
HLI-0195	15607	A	G	0	482	synonymous_variant	LOW	CYTB	0.0508
HLI-0195	15928	G	A	2	611	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0195	16126	T	C	0	567	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0195	16129	G	A	0	565	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0195	16294	C	T	0	491	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0195	16296	C	T	0	491	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0195	16304	T	C	0	513	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0195	16519	T	C	0	235	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0196	263	A	G	0	216	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0196	750	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0196	1438	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0196	4769	A	G	0	573	synonymous_variant	LOW	ND2	0.9767
HLI-0196	8557	G	A	0	512	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0196	12603	C	T	2	610	synonymous_variant	LOW	ND5	7.00E-04
HLI-0196	14470	T	A	0	521	synonymous_variant	LOW	ND6	0.0031
HLI-0196	15326	A	G	0	570	missense_variant	MODERATE	CYTB	0.9868
HLI-0196	16093	T	C	21	668	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0196	16265	A	T	2	586	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0196	16295	C	T	2	612	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0196	16519	T	C	0	279	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0197	73	A	G	0	253	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0197	263	A	G	0	184	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0197	709	G	A	0	520	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0197	750	A	G	1	576	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0197	930	G	A	1	545	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0197	1438	A	G	1	561	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0197	1888	G	A	0	556	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0197	2706	A	G	3	509	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0197	4216	T	C	1	535	missense_variant	MODERATE	ND1	0.0991
HLI-0197	4769	A	G	3	513	synonymous_variant	LOW	ND2	0.9767
HLI-0197	4917	A	G	0	548	missense_variant	MODERATE	ND2	0.0477
HLI-0197	5147	G	A	2	394	synonymous_variant	LOW	ND2	0.0437
HLI-0197	7028	C	T	10	598	synonymous_variant	LOW	COX1	0.8089
HLI-0197	8697	G	A	0	504	synonymous_variant	LOW	ATP6	0.0466
HLI-0197	9254	A	G	0	514	synonymous_variant	LOW	COX3	0.0083
HLI-0197	10463	T	C	0	563	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0197	11251	A	G	0	559	synonymous_variant	LOW	ND4	0.0932
HLI-0197	11719	G	A	1	511	synonymous_variant	LOW	ND4	0.7756
HLI-0197	11812	A	G	2	509	synonymous_variant	LOW	ND4	0.0332
HLI-0197	13368	G	A	0	569	synonymous_variant	LOW	ND5	0.0495
HLI-0197	14233	A	G	1	463	synonymous_variant	LOW	ND6	0.0369
HLI-0197	14766	C	T	1	511	missense_variant	MODERATE	CYTB	0.7696
HLI-0197	14905	G	A	0	619	synonymous_variant	LOW	CYTB	0.0526
HLI-0197	15326	A	G	0	456	missense_variant	MODERATE	CYTB	0.9868
HLI-0197	15452	C	A	5	409	missense_variant	MODERATE	CYTB	0.0933
HLI-0197	15607	A	G	1	484	synonymous_variant	LOW	CYTB	0.0508
HLI-0197	15928	G	A	2	550	upstream_gene_variant	MODIFIER	TRNT	0.049

HLI-0197	16126	T	C	0	550	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0197	16294	C	T	0	497	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0197	16304	T	C	0	521	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0197	16519	T	C	0	227	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0198	73	A	G	0	253	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0198	152	T	C	0	434	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0198	217	T	C	0	239	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0198	263	A	G	0	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0198	508	A	G	2	322	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0198	750	A	G	0	518	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0198	1438	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0198	1811	A	G	1	614	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0198	2706	A	G	1	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0198	3720	A	G	0	540	synonymous_variant	LOW	ND1	0.0069
HLI-0198	3849	G	A	1	520	synonymous_variant	LOW	ND1	0.0035
HLI-0198	4553	T	C	4	469	synonymous_variant	LOW	ND2	0.0023
HLI-0198	4736	T	C	0	324	synonymous_variant	LOW	ND2	0.0012
HLI-0198	4769	A	G	8	370	synonymous_variant	LOW	ND2	0.9767
HLI-0198	5390	A	G	2	558	synonymous_variant	LOW	ND2	0.0069
HLI-0198	5426	T	C	1	611	synonymous_variant	LOW	ND2	0.0091
HLI-0198	6045	C	T	4	611	synonymous_variant	LOW	COX1	0.0065
HLI-0198	6152	T	C	0	551	synonymous_variant	LOW	COX1	0.0077
HLI-0198	7028	C	T	2	679	synonymous_variant	LOW	COX1	0.8089
HLI-0198	8473	T	C	0	392	synonymous_variant	LOW	ATP8	0.0105
HLI-0198	10876	A	G	0	540	synonymous_variant	LOW	ND4	0.0098
HLI-0198	11467	A	G	1	570	synonymous_variant	LOW	ND4	0.1231
HLI-0198	11719	G	A	0	574	synonymous_variant	LOW	ND4	0.7756
HLI-0198	12308	A	G	2	556	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0198	12372	G	A	0	554	synonymous_variant	LOW	ND5	0.1329
HLI-0198	12557	C	T	7	574	missense_variant	MODERATE	ND5	0.0028
HLI-0198	13020	T	C	3	527	synonymous_variant	LOW	ND5	0.0106
HLI-0198	13734	T	C	0	447	synonymous_variant	LOW	ND5	0.0067
HLI-0198	14766	C	T	2	547	missense_variant	MODERATE	CYTB	0.7696
HLI-0198	15326	A	G	0	488	missense_variant	MODERATE	CYTB	0.9868
HLI-0198	15907	A	G	0	581	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0198	16051	A	G	0	479	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0198	16092	T	C	4	404	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0198	16129	G	C	2	270	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0198	16362	T	C	0	422	upstream_gene_variant	MODIFIER	DLoop	0.1763

HLI-0198	16519	T	C	0	184	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0199	73	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0199	150	C	T	2	452	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0199	263	A	G	0	197	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0199	750	A	G	1	514	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0199	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0199	1721	C	T	3	548	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0199	2706	A	G	3	535	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0199	2757	A	G	0	573	upstream_gene_variant	MODIFIER	RNR2	0.002
HLI-0199	3197	T	C	0	609	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0199	3212	C	T	1	599	upstream_gene_variant	MODIFIER	RNR2	0.0012
HLI-0199	4732	A	G	0	512	missense_variant	MODERATE	ND2	0.0059
HLI-0199	4769	A	G	0	531	synonymous_variant	LOW	ND2	0.9767
HLI-0199	4843	C	T	0	538	missense_variant	MODERATE	ND2	5.00E-04
HLI-0199	7028	C	T	1	625	synonymous_variant	LOW	COX1	0.8089
HLI-0199	7768	A	G	1	484	synonymous_variant	LOW	COX2	0.0186
HLI-0199	9477	G	A	2	535	missense_variant	MODERATE	COX3	0.0387
HLI-0199	11467	A	G	0	553	synonymous_variant	LOW	ND4	0.1231
HLI-0199	11719	G	A	0	488	synonymous_variant	LOW	ND4	0.7756
HLI-0199	12308	A	G	2	447	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0199	12372	G	A	1	495	synonymous_variant	LOW	ND5	0.1329
HLI-0199	13617	T	C	2	517	synonymous_variant	LOW	ND5	0.038
HLI-0199	13637	A	G	2	548	missense_variant	MODERATE	ND5	0.0074
HLI-0199	14182	T	C	0	465	synonymous_variant	LOW	ND6	0.0254
HLI-0199	14766	C	T	3	466	missense_variant	MODERATE	CYTB	0.7696
HLI-0199	14956	T	C	1	541	synonymous_variant	LOW	CYTB	0.001
HLI-0199	15326	A	G	0	477	missense_variant	MODERATE	CYTB	0.9868
HLI-0199	16398	G	A	0	371	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0200	73	A	G	0	179	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0200	151	C	T	0	289	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0200	152	T	C	0	289	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0200	182	C	T	0	246	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0200	186	C	A	0	243	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0200	189	A	C	0	238	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0200	195	T	C	0	236	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0200	198	C	T	0	238	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0200	247	G	A	0	137	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0200	263	A	G	0	152	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0200	297	A	G	1	175	upstream_gene_variant	MODIFIER	DLoop	0.0107

HLI-0200	750	A	G	0	553	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0200	769	G	A	0	614	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0200	825	T	A	1	609	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0200	1018	G	A	0	616	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0200	1438	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0200	1598	G	A	0	582	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0200	2220	A	G	0	445	upstream_gene_variant	MODIFIER	RNR2	0.0029
HLI-0200	2706	A	G	1	583	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0200	2758	G	A	1	596	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0200	2885	T	C	0	631	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0200	3594	C	T	1	458	synonymous_variant	LOW	ND1	0.0789
HLI-0200	3666	G	A	0	570	synonymous_variant	LOW	ND1	0.0233
HLI-0200	4104	A	G	1	449	synonymous_variant	LOW	ND1	0.0785
HLI-0200	4769	A	G	0	477	synonymous_variant	LOW	ND2	0.9767
HLI-0200	5951	A	G	0	663	synonymous_variant	LOW	COX1	0.0128
HLI-0200	6071	T	C	0	667	synonymous_variant	LOW	COX1	0.0129
HLI-0200	6150	G	A	0	670	missense_variant	MODERATE	COX1	0.0049
HLI-0200	6253	T	C	0	601	missense_variant	MODERATE	COX1	0.0106
HLI-0200	6962	G	A	1	594	synonymous_variant	LOW	COX1	0.0235
HLI-0200	7028	C	T	1	551	synonymous_variant	LOW	COX1	0.8089
HLI-0200	7055	A	G	0	477	synonymous_variant	LOW	COX1	0.0188
HLI-0200	7076	A	G	0	422	synonymous_variant	LOW	COX1	0.0053
HLI-0200	7146	A	G	0	280	missense_variant	MODERATE	COX1	0.0497
HLI-0200	7256	C	T	3	408	synonymous_variant	LOW	COX1	0.0784
HLI-0200	7337	G	A	1	423	synonymous_variant	LOW	COX1	0.0119
HLI-0200	7389	T	C	0	396	missense_variant	MODERATE	COX1	0.0201
HLI-0200	7521	G	A	2	352	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0200	8027	G	A	3	561	missense_variant	MODERATE	COX2	0.0334
HLI-0200	8468	C	T	2	327	synonymous_variant	LOW	ATP8	0.0501
HLI-0200	8655	C	T	1	336	synonymous_variant	LOW	ATP6	0.0511
HLI-0200	8701	A	G	1	368	missense_variant	MODERATE	ATP6	0.3391
HLI-0200	8784	A	G	0	429	synonymous_variant	LOW	ATP6	0.006
HLI-0200	8877	T	C	0	463	synonymous_variant	LOW	ATP6	0.0053
HLI-0200	9072	A	G	1	549	synonymous_variant	LOW	ATP6	0.0124
HLI-0200	9540	T	C	0	471	synonymous_variant	LOW	COX3	0.339
HLI-0200	10031	T	C	0	573	upstream_gene_variant	MODIFIER	TRNG	0.0033
HLI-0200	10321	T	C	0	483	missense_variant	MODERATE	ND3	0.0106
HLI-0200	10398	A	G	0	523	missense_variant	MODERATE	ND3	0.445
HLI-0200	10586	G	A	3	519	synonymous_variant	LOW	ND4L	0.0177

HLI-0200	10688	G	A	1	517	synonymous_variant	LOW	ND4L	0.0515
HLI-0200	10792	A	G	0	548	synonymous_variant	LOW	ND4	0.0044
HLI-0200	10793	C	T	0	551	synonymous_variant	LOW	ND4	0.0043
HLI-0200	10810	T	C	0	583	synonymous_variant	LOW	ND4	0.0522
HLI-0200	10873	T	C	0	447	synonymous_variant	LOW	ND4	0.3389
HLI-0200	11164	A	G	0	552	synonymous_variant	LOW	ND4	0.0023
HLI-0200	11252	A	G	0	544	missense_variant	MODERATE	ND4	9.00E-04
HLI-0200	11654	A	G	1	539	missense_variant	MODERATE	ND4	0.0045
HLI-0200	11719	G	A	1	583	synonymous_variant	LOW	ND4	0.7756
HLI-0200	11959	A	G	0	507	synonymous_variant	LOW	ND4	0.0027
HLI-0200	12049	C	T	2	399	synonymous_variant	LOW	ND4	0.0052
HLI-0200	12477	T	C	2	438	synonymous_variant	LOW	ND5	0.0054
HLI-0200	12540	A	G	1	535	synonymous_variant	LOW	ND5	3.00E-04
HLI-0200	12705	C	T	1	527	synonymous_variant	LOW	ND5	0.4212
HLI-0200	12810	A	G	3	536	synonymous_variant	LOW	ND5	0.0198
HLI-0200	13105	A	G	0	563	missense_variant	MODERATE	ND5	0.076
HLI-0200	13149	A	G	4	620	synonymous_variant	LOW	ND5	0.0053
HLI-0200	13485	A	G	2	573	synonymous_variant	LOW	ND5	0.0122
HLI-0200	13506	C	T	1	577	synonymous_variant	LOW	ND5	0.0506
HLI-0200	13650	C	T	0	484	synonymous_variant	LOW	ND5	0.079
HLI-0200	13789	T	C	0	320	missense_variant	MODERATE	ND5	0.0185
HLI-0200	14000	T	A	0	439	missense_variant	MODERATE	ND5	0.0126
HLI-0200	14058	C	T	3	474	synonymous_variant	LOW	ND5	6.00E-04
HLI-0200	14178	T	C	0	473	missense_variant	MODERATE	ND6	0.0225
HLI-0200	14560	G	A	0	518	synonymous_variant	LOW	ND6	0.0235
HLI-0200	14766	C	T	3	510	missense_variant	MODERATE	CYTB	0.7696
HLI-0200	14911	C	T	5	631	synonymous_variant	LOW	CYTB	0.0124
HLI-0200	15326	A	G	0	450	missense_variant	MODERATE	CYTB	0.9868
HLI-0200	15929	A	G	1	381	upstream_gene_variant	MODIFIER	TRNT	6.00E-04
HLI-0200	16129	G	A	1	424	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0200	16223	C	T	5	315	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0200	16265	A	C	0	297	upstream_gene_variant	MODIFIER	DLoop	0.0087
HLI-0200	16286	C	G	0	279	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0200	16294	C	T	0	281	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0200	16311	T	C	0	286	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0200	16360	C	T	1	283	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0200	16519	T	C	0	159	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0200	16527	C	T	0	161	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0201	73	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0201	153	A	G	1	412	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0201	195	T	C	0	391	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0201	225	G	A	2	375	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0201	263	A	G	0	141	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0201	750	A	G	1	492	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0201	1438	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0201	1703	C	T	0	549	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0201	1719	G	A	0	607	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0201	2706	A	G	1	485	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0201	4769	A	G	0	495	synonymous_variant	LOW	ND2	0.9767
HLI-0201	5250	T	C	0	488	synonymous_variant	LOW	ND2	0.0013
HLI-0201	6221	T	C	1	508	synonymous_variant	LOW	COX1	0.0306
HLI-0201	6371	C	T	1	466	synonymous_variant	LOW	COX1	0.0097
HLI-0201	6680	T	C	4	588	synonymous_variant	LOW	COX1	0.0226
HLI-0201	7028	C	T	2	569	synonymous_variant	LOW	COX1	0.8089
HLI-0201	11719	G	A	1	490	synonymous_variant	LOW	ND4	0.7756
HLI-0201	12705	C	T	2	564	synonymous_variant	LOW	ND5	0.4212
HLI-0201	13966	A	G	0	428	missense_variant	MODERATE	ND5	0.0126
HLI-0201	14470	T	C	1	484	synonymous_variant	LOW	ND6	0.0166
HLI-0201	14766	C	T	4	497	missense_variant	MODERATE	CYTB	0.7696
HLI-0201	14818	A	G	0	528	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0201	15326	A	G	0	404	missense_variant	MODERATE	CYTB	0.9868
HLI-0201	16127	A	G	0	515	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0201	16223	C	T	1	430	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0201	16278	C	T	2	454	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0201	16519	T	C	0	193	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0202	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0202	750	A	G	1	545	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0202	1438	A	G	0	550	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0202	3010	G	A	2	573	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0202	4769	A	G	0	515	synonymous_variant	LOW	ND2	0.9767
HLI-0202	5460	G	A	1	561	missense_variant	MODERATE	ND2	0.0651
HLI-0202	8512	A	G	3	552	synonymous_variant	LOW	ATP8	0.0036
HLI-0202	14902	C	T	0	616	synonymous_variant	LOW	CYTB	0.0024
HLI-0202	15326	A	G	0	566	missense_variant	MODERATE	CYTB	0.9868
HLI-0202	16093	T	C	12	575	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0202	16519	T	C	0	244	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0203	73	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0203	263	A	G	1	210	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0203	750	A	G	0	546	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0203	1438	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0203	3010	G	A	0	590	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0203	4769	A	G	2	524	synonymous_variant	LOW	ND2	0.9767
HLI-0203	5460	G	A	1	543	missense_variant	MODERATE	ND2	0.0651
HLI-0203	15326	A	G	0	541	missense_variant	MODERATE	CYTB	0.9868
HLI-0203	15817	A	G	0	562	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0203	16519	T	C	0	256	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0204	73	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0204	150	C	T	1	503	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0204	263	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0204	750	A	G	0	594	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0204	1438	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0204	1811	A	G	0	626	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0204	2706	A	G	0	583	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0204	2833	A	G	2	579	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0204	3546	C	A	7	495	synonymous_variant	LOW	ND1	9.00E-04
HLI-0204	4188	A	G	0	545	synonymous_variant	LOW	ND1	0.003
HLI-0204	4640	C	A	0	642	missense_variant	MODERATE	ND2	0.0029
HLI-0204	4769	A	G	0	554	synonymous_variant	LOW	ND2	0.9767
HLI-0204	7028	C	T	0	659	synonymous_variant	LOW	COX1	0.8089
HLI-0204	8895	T	C	0	642	synonymous_variant	LOW	ATP6	4.00E-04
HLI-0204	9656	T	C	0	613	synonymous_variant	LOW	COX3	0.0035
HLI-0204	11467	A	G	1	603	synonymous_variant	LOW	ND4	0.1231
HLI-0204	11719	G	A	2	598	synonymous_variant	LOW	ND4	0.7756
HLI-0204	12308	A	G	2	588	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0204	12372	G	A	0	614	synonymous_variant	LOW	ND5	0.1329
HLI-0204	12738	T	C	8	660	synonymous_variant	LOW	ND5	0.002
HLI-0204	13743	T	C	1	408	synonymous_variant	LOW	ND5	0.0037
HLI-0204	14139	A	G	0	514	synonymous_variant	LOW	ND5	0.0056
HLI-0204	14766	C	T	3	561	missense_variant	MODERATE	CYTB	0.7696
HLI-0204	15326	A	G	0	532	missense_variant	MODERATE	CYTB	0.9868
HLI-0204	15454	T	C	0	511	synonymous_variant	LOW	CYTB	0.0072
HLI-0204	16343	A	G	2	453	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0205	73	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0205	263	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0205	709	G	A	2	391	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0205	750	A	G	0	491	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0205	930	G	A	3	510	upstream_gene_variant	MODIFIER	RNR1	0.0202

HLI-0205	1438	A	G	0	528	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0205	1888	G	A	0	464	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0205	2706	A	G	0	410	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0205	3826	T	C	0	519	synonymous_variant	LOW	ND1	0.0014
HLI-0205	4216	T	C	1	446	missense_variant	MODERATE	ND1	0.0991
HLI-0205	4769	A	G	0	469	synonymous_variant	LOW	ND2	0.9767
HLI-0205	4917	A	G	0	522	missense_variant	MODERATE	ND2	0.0477
HLI-0205	5147	G	A	0	408	synonymous_variant	LOW	ND2	0.0437
HLI-0205	5201	T	C	0	451	synonymous_variant	LOW	ND2	0.0015
HLI-0205	7028	C	T	5	508	synonymous_variant	LOW	COX1	0.8089
HLI-0205	8504	T	C	0	530	missense_variant	MODERATE	ATP8	3.00E-04
HLI-0205	8697	G	A	0	500	synonymous_variant	LOW	ATP6	0.0466
HLI-0205	10463	T	C	2	550	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0205	11251	A	G	1	531	synonymous_variant	LOW	ND4	0.0932
HLI-0205	11719	G	A	1	487	synonymous_variant	LOW	ND4	0.7756
HLI-0205	11812	A	G	1	514	synonymous_variant	LOW	ND4	0.0332
HLI-0205	13368	G	A	1	492	synonymous_variant	LOW	ND5	0.0495
HLI-0205	14233	A	G	1	452	synonymous_variant	LOW	ND6	0.0369
HLI-0205	14766	C	T	3	476	missense_variant	MODERATE	CYTB	0.7696
HLI-0205	14905	G	A	1	576	synonymous_variant	LOW	CYTB	0.0526
HLI-0205	15326	A	G	0	297	missense_variant	MODERATE	CYTB	0.9868
HLI-0205	15452	C	A	1	314	missense_variant	MODERATE	CYTB	0.0933
HLI-0205	15607	A	G	0	378	synonymous_variant	LOW	CYTB	0.0508
HLI-0205	15928	G	A	0	612	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0205	16126	T	C	1	551	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0205	16294	C	T	0	423	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0205	16304	T	C	0	440	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0205	16519	T	C	1	185	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0206	73	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0206	152	T	C	1	439	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0206	199	T	C	2	411	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0206	263	A	G	0	123	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0206	286	A	G	0	150	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0206	497	C	T	1	304	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0206	750	A	G	0	443	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0206	1189	T	C	0	567	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0206	1438	A	G	0	543	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0206	1811	A	G	1	610	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0206	2706	A	G	0	382	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0206	3480	A	G	0	355	synonymous_variant	LOW	ND1	0.0392
HLI-0206	4769	A	G	6	563	synonymous_variant	LOW	ND2	0.9767
HLI-0206	5074	T	C	0	384	missense_variant	MODERATE	ND2	0.0017
HLI-0206	7028	C	T	3	515	synonymous_variant	LOW	COX1	0.8089
HLI-0206	9055	G	A	0	392	missense_variant	MODERATE	ATP6	0.0425
HLI-0206	9698	T	C	0	410	synonymous_variant	LOW	COX3	0.0405
HLI-0206	10398	A	G	2	578	missense_variant	MODERATE	ND3	0.445
HLI-0206	10550	A	G	2	412	synonymous_variant	LOW	ND4L	0.0376
HLI-0206	11017	T	C	0	364	synonymous_variant	LOW	ND4	0.0028
HLI-0206	11299	T	C	1	486	synonymous_variant	LOW	ND4	0.0417
HLI-0206	11467	A	G	0	473	synonymous_variant	LOW	ND4	0.1231
HLI-0206	11719	G	A	0	503	synonymous_variant	LOW	ND4	0.7756
HLI-0206	12308	A	G	1	542	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0206	12372	G	A	1	559	synonymous_variant	LOW	ND5	0.1329
HLI-0206	14167	C	T	2	462	synonymous_variant	LOW	ND6	0.0385
HLI-0206	14766	C	T	0	568	missense_variant	MODERATE	CYTB	0.7696
HLI-0206	14767	T	C	0	572	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0206	14798	T	C	0	580	missense_variant	MODERATE	CYTB	0.0651
HLI-0206	15326	A	G	0	332	missense_variant	MODERATE	CYTB	0.9868
HLI-0206	16093	T	C	22	553	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0206	16172	T	C	0	514	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0206	16224	T	C	0	417	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0206	16231	T	C	0	413	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0206	16311	T	C	0	357	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0206	16519	T	C	0	201	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0207	73	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0207	152	T	C	0	280	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0207	182	C	T	0	258	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0207	185	G	T	0	258	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0207	195	T	C	0	237	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0207	198	C	T	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0207	247	G	A	0	87	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0207	263	A	G	0	95	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0207	357	A	G	0	205	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0207	709	G	A	3	487	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0207	710	T	C	3	493	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0207	750	A	G	1	518	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0207	769	G	A	3	512	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0207	825	T	A	0	527	upstream_gene_variant	MODIFIER	RNR1	0.0509

HLI-0207	1018	G	A	2	617	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0207	1738	T	C	1	578	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0207	2352	T	C	1	544	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0207	2706	A	G	0	569	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0207	2758	G	A	1	609	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0207	2768	A	G	1	586	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0207	2885	T	C	1	603	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0207	3308	T	C	1	544	start_lost	HIGH	ND1	0.0073
HLI-0207	3594	C	T	1	446	synonymous_variant	LOW	ND1	0.0789
HLI-0207	3666	G	A	1	518	synonymous_variant	LOW	ND1	0.0233
HLI-0207	3693	G	A	1	539	synonymous_variant	LOW	ND1	0.0091
HLI-0207	4104	A	G	4	469	synonymous_variant	LOW	ND1	0.0785
HLI-0207	4769	A	G	0	539	synonymous_variant	LOW	ND2	0.9767
HLI-0207	5036	A	G	0	559	synonymous_variant	LOW	ND2	0.006
HLI-0207	5046	G	A	0	598	missense_variant	MODERATE	ND2	0.018
HLI-0207	5393	T	C	0	517	synonymous_variant	LOW	ND2	0.0059
HLI-0207	5563	G	A	1	594	upstream_gene_variant	MODIFIER	TRNW	0.0018
HLI-0207	5655	T	C	1	566	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0207	6548	C	T	2	619	synonymous_variant	LOW	COX1	0.0061
HLI-0207	6827	T	C	2	587	synonymous_variant	LOW	COX1	0.0072
HLI-0207	6989	A	G	1	599	synonymous_variant	LOW	COX1	0.0061
HLI-0207	7028	C	T	0	596	synonymous_variant	LOW	COX1	0.8089
HLI-0207	7055	A	G	2	540	synonymous_variant	LOW	COX1	0.0188
HLI-0207	7146	A	G	3	275	missense_variant	MODERATE	COX1	0.0497
HLI-0207	7256	C	T	7	401	synonymous_variant	LOW	COX1	0.0784
HLI-0207	7389	T	C	4	451	missense_variant	MODERATE	COX1	0.0201
HLI-0207	7521	G	A	1	377	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0207	7867	C	T	2	593	synonymous_variant	LOW	COX2	0.0076
HLI-0207	8248	A	G	1	511	synonymous_variant	LOW	COX2	0.0061
HLI-0207	8468	C	T	2	425	synonymous_variant	LOW	ATP8	0.0501
HLI-0207	8655	C	T	6	478	synonymous_variant	LOW	ATP6	0.0511
HLI-0207	8701	A	G	0	529	missense_variant	MODERATE	ATP6	0.3391
HLI-0207	9540	T	C	1	505	synonymous_variant	LOW	COX3	0.339
HLI-0207	10398	A	G	3	599	missense_variant	MODERATE	ND3	0.445
HLI-0207	10688	G	A	1	522	synonymous_variant	LOW	ND4L	0.0515
HLI-0207	10810	T	C	0	508	synonymous_variant	LOW	ND4	0.0522
HLI-0207	10873	T	C	0	487	synonymous_variant	LOW	ND4	0.3389
HLI-0207	11605	A	G	0	535	synonymous_variant	LOW	ND4	0
HLI-0207	11719	G	A	2	565	synonymous_variant	LOW	ND4	0.7756

HLI-0207	12519	T	C	4	558	synonymous_variant	LOW	ND5	0.007
HLI-0207	12705	C	T	4	610	synonymous_variant	LOW	ND5	0.4212
HLI-0207	13105	A	G	1	484	missense_variant	MODERATE	ND5	0.076
HLI-0207	13506	C	T	2	553	synonymous_variant	LOW	ND5	0.0506
HLI-0207	13650	C	T	3	474	synonymous_variant	LOW	ND5	0.079
HLI-0207	13789	T	C	0	381	missense_variant	MODERATE	ND5	0.0185
HLI-0207	13880	C	A	3	433	missense_variant	MODERATE	ND5	0.0055
HLI-0207	14178	T	C	0	545	missense_variant	MODERATE	ND6	0.0225
HLI-0207	14203	A	G	0	577	synonymous_variant	LOW	ND6	0.0061
HLI-0207	14560	G	A	3	582	synonymous_variant	LOW	ND6	0.0235
HLI-0207	14766	C	T	1	534	missense_variant	MODERATE	CYTB	0.7696
HLI-0207	14769	A	G	1	543	missense_variant	MODERATE	CYTB	0.0121
HLI-0207	14894	T	C	1	585	missense_variant	MODERATE	CYTB	2.00E-04
HLI-0207	15115	T	C	2	581	synonymous_variant	LOW	CYTB	0.0093
HLI-0207	15326	A	G	0	503	missense_variant	MODERATE	CYTB	0.9868
HLI-0207	16126	T	C	1	552	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0207	16223	C	T	7	420	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0207	16264	C	T	0	344	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0207	16270	C	T	0	332	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0207	16278	C	T	0	325	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0207	16293	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0207	16311	T	C	0	296	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0207	16362	T	C	2	289	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0207	16400	C	T	3	376	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0207	16519	T	C	0	128	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0208	152	T	C	0	470	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0208	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0208	750	A	G	0	559	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0208	1438	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0208	2222	T	C	0	567	upstream_gene_variant	MODIFIER	RNR2	5.00E-04
HLI-0208	2706	A	G	1	569	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0208	4769	A	G	1	536	synonymous_variant	LOW	ND2	0.9767
HLI-0208	7028	C	T	3	632	synonymous_variant	LOW	COX1	0.8089
HLI-0208	8568	C	A	2	552	missense_variant	MODERATE	ATP6/8	0
HLI-0208	12131	T	C	0	579	missense_variant	MODERATE	ND4	1.00E-04
HLI-0208	14128	A	G	0	498	missense_variant	MODERATE	ND5	0.0018
HLI-0208	15326	A	G	0	519	missense_variant	MODERATE	CYTB	0.9868
HLI-0208	15773	G	A	2	571	missense_variant	MODERATE	CYTB	0.0011
HLI-0208	16311	T	C	0	507	upstream_gene_variant	MODIFIER	DLoop	0.1969

HLI-0209	73	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0209	150	C	T	0	418	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0209	152	T	C	27	393	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0209	195	T	C	1	401	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0209	263	A	G	1	175	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0209	499	G	A	1	276	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0209	750	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0209	1438	A	G	0	582	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0209	1811	A	G	1	674	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0209	2706	A	G	0	600	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0209	4646	T	C	1	602	synonymous_variant	LOW	ND2	0.0124
HLI-0209	4769	A	G	0	561	synonymous_variant	LOW	ND2	0.9767
HLI-0209	4811	A	G	3	621	synonymous_variant	LOW	ND2	0.0017
HLI-0209	5999	T	C	0	650	synonymous_variant	LOW	COX1	0.0127
HLI-0209	6047	A	G	0	688	synonymous_variant	LOW	COX1	0.0114
HLI-0209	6146	A	G	0	623	synonymous_variant	LOW	COX1	0.0013
HLI-0209	7028	C	T	3	662	synonymous_variant	LOW	COX1	0.8089
HLI-0209	9070	T	G	0	553	missense_variant	MODERATE	ATP6	0.0012
HLI-0209	10649	T	C	1	529	synonymous_variant	LOW	ND4L	3.00E-04
HLI-0209	10907	T	C	0	302	missense_variant	MODERATE	ND4	0.0022
HLI-0209	11009	T	C	0	392	synonymous_variant	LOW	ND4	0.002
HLI-0209	11332	C	T	1	601	synonymous_variant	LOW	ND4	0.0115
HLI-0209	11467	A	G	1	596	synonymous_variant	LOW	ND4	0.1231
HLI-0209	11719	G	A	2	590	synonymous_variant	LOW	ND4	0.7756
HLI-0209	12308	A	G	3	540	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0209	12372	G	A	0	543	synonymous_variant	LOW	ND5	0.1329
HLI-0209	14620	C	T	6	561	synonymous_variant	LOW	ND6	0.0126
HLI-0209	14766	C	T	1	528	missense_variant	MODERATE	CYTB	0.7696
HLI-0209	14866	C	T	2	578	synonymous_variant	LOW	CYTB	0.0012
HLI-0209	15326	A	G	0	578	missense_variant	MODERATE	CYTB	0.9868
HLI-0209	15693	T	C	1	585	missense_variant	MODERATE	CYTB	0.0114
HLI-0209	16179	C	T	3	588	upstream_gene_variant	MODIFIER	DLoop	0.0082
HLI-0209	16356	T	C	1	422	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0209	16519	T	C	0	216	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0210	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0210	152	T	C	0	483	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0210	263	A	G	0	179	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0210	709	G	A	1	553	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0210	750	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0210	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0210	1888	G	A	0	566	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0210	2706	A	G	1	543	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0210	4216	T	C	0	561	missense_variant	MODERATE	ND1	0.0991
HLI-0210	4769	A	G	0	524	synonymous_variant	LOW	ND2	0.9767
HLI-0210	4917	A	G	0	466	missense_variant	MODERATE	ND2	0.0477
HLI-0210	5747	A	G	4	644	upstream_gene_variant	MODIFIER	Unannotated	9.00E-04
HLI-0210	7028	C	T	4	615	synonymous_variant	LOW	COX1	0.8089
HLI-0210	7598	G	A	78	493	missense_variant	MODERATE	COX2	0.0125
HLI-0210	8697	G	A	0	527	synonymous_variant	LOW	ATP6	0.0466
HLI-0210	10398	A	G	0	594	missense_variant	MODERATE	ND3	0.445
HLI-0210	10463	T	C	2	630	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0210	11251	A	G	0	527	synonymous_variant	LOW	ND4	0.0932
HLI-0210	11719	G	A	0	544	synonymous_variant	LOW	ND4	0.7756
HLI-0210	11812	A	G	0	530	synonymous_variant	LOW	ND4	0.0332
HLI-0210	13260	T	C	0	574	synonymous_variant	LOW	ND5	0.0017
HLI-0210	13368	G	A	1	579	synonymous_variant	LOW	ND5	0.0495
HLI-0210	13708	G	A	0	458	missense_variant	MODERATE	ND5	0.0717
HLI-0210	13934	C	T	2	474	missense_variant	MODERATE	ND5	0.0122
HLI-0210	14233	A	G	1	485	synonymous_variant	LOW	ND6	0.0369
HLI-0210	14766	C	T	1	507	missense_variant	MODERATE	CYTB	0.7696
HLI-0210	14905	G	A	2	604	synonymous_variant	LOW	CYTB	0.0526
HLI-0210	15326	A	G	0	493	missense_variant	MODERATE	CYTB	0.9868
HLI-0210	15452	C	A	3	466	missense_variant	MODERATE	CYTB	0.0933
HLI-0210	15607	A	G	0	522	synonymous_variant	LOW	CYTB	0.0508
HLI-0210	15928	G	A	2	616	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0210	16086	T	C	2	550	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0210	16126	T	C	0	578	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0210	16294	C	T	0	494	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0210	16296	C	T	0	496	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0210	16368	T	C	1	464	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0210	16519	T	C	0	247	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0211	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0211	153	A	G	3	433	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0211	195	T	C	1	441	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0211	225	G	A	1	425	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0211	227	A	G	0	427	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0211	263	A	G	0	401	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0211	750	A	G	0	536	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0211	1438	A	G	0	540	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0211	1719	G	A	1	441	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0211	2706	A	G	0	488	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0211	4769	A	G	0	497	synonymous_variant	LOW	ND2	0.9767
HLI-0211	5021	T	C	1	425	synonymous_variant	LOW	ND2	9.00E-04
HLI-0211	6221	T	C	2	549	synonymous_variant	LOW	COX1	0.0306
HLI-0211	6371	C	T	4	477	synonymous_variant	LOW	COX1	0.0097
HLI-0211	7028	C	T	2	561	synonymous_variant	LOW	COX1	0.8089
HLI-0211	8705	T	C	0	523	missense_variant	MODERATE	ATP6	0.0039
HLI-0211	11719	G	A	0	525	synonymous_variant	LOW	ND4	0.7756
HLI-0211	12705	C	T	0	456	synonymous_variant	LOW	ND5	0.4212
HLI-0211	13966	A	G	0	390	missense_variant	MODERATE	ND5	0.0126
HLI-0211	14470	T	C	2	442	synonymous_variant	LOW	ND6	0.0166
HLI-0211	14766	C	T	1	501	missense_variant	MODERATE	CYTB	0.7696
HLI-0211	15313	T	C	0	385	synonymous_variant	LOW	CYTB	0.0022
HLI-0211	15326	A	G	1	422	missense_variant	MODERATE	CYTB	0.9868
HLI-0211	16223	C	T	0	246	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0211	16255	G	A	0	309	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0211	16278	C	T	0	362	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0211	16519	T	C	0	183	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0212	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0212	263	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0212	709	G	A	4	588	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0212	750	A	G	1	635	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0212	1438	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0212	1888	G	A	0	575	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0212	2141	T	C	0	493	upstream_gene_variant	MODIFIER	RNR2	0.0013
HLI-0212	2706	A	G	0	594	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0212	4216	T	C	1	517	missense_variant	MODERATE	ND1	0.0991
HLI-0212	4769	A	G	2	517	synonymous_variant	LOW	ND2	0.9767
HLI-0212	4917	A	G	0	467	missense_variant	MODERATE	ND2	0.0477
HLI-0212	5894	A	G	2	631	upstream_gene_variant	MODIFIER	Unannotated	0.0034
HLI-0212	7028	C	T	1	649	synonymous_variant	LOW	COX1	0.8089
HLI-0212	8697	G	A	0	488	synonymous_variant	LOW	ATP6	0.0466
HLI-0212	9117	T	C	0	529	synonymous_variant	LOW	ATP6	0.0018
HLI-0212	10463	T	C	0	597	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0212	11251	A	G	0	582	synonymous_variant	LOW	ND4	0.0932
HLI-0212	11719	G	A	0	514	synonymous_variant	LOW	ND4	0.7756
HLI-0212	11812	A	G	1	551	synonymous_variant	LOW	ND4	0.0332

HLI-0212	12741	C	T	5	613	synonymous_variant	LOW	ND5	9.00E-04
HLI-0212	13260	T	C	0	576	synonymous_variant	LOW	ND5	0.0017
HLI-0212	13368	G	A	0	546	synonymous_variant	LOW	ND5	0.0495
HLI-0212	13965	T	C	0	499	synonymous_variant	LOW	ND5	0.005
HLI-0212	13966	A	G	0	498	missense_variant	MODERATE	ND5	0.0126
HLI-0212	14233	A	G	1	513	synonymous_variant	LOW	ND6	0.0369
HLI-0212	14687	A	G	3	553	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0212	14766	C	T	4	572	missense_variant	MODERATE	CYTB	0.7696
HLI-0212	14905	G	A	0	566	synonymous_variant	LOW	CYTB	0.0526
HLI-0212	15326	A	G	0	542	missense_variant	MODERATE	CYTB	0.9868
HLI-0212	15452	C	A	4	499	missense_variant	MODERATE	CYTB	0.0933
HLI-0212	15607	A	G	0	558	synonymous_variant	LOW	CYTB	0.0508
HLI-0212	15928	G	A	1	568	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0212	16126	T	C	1	547	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0212	16174	C	T	2	531	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0212	16294	C	T	0	482	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0212	16296	C	T	0	485	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0212	16324	T	C	3	479	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0212	16519	T	C	0	202	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0213	263	A	G	0	222	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0213	477	T	C	5	305	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0213	750	A	G	0	552	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0213	1438	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0213	3010	G	A	0	593	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0213	4769	A	G	0	584	synonymous_variant	LOW	ND2	0.9767
HLI-0213	9150	A	G	8	566	synonymous_variant	LOW	ATP6	0.0072
HLI-0213	15326	A	G	0	515	missense_variant	MODERATE	CYTB	0.9868
HLI-0213	16263	T	C	6	469	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0213	16519	T	C	0	319	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0214	152	T	C	3	502	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0214	153	A	G	3	504	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0214	263	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0214	750	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0214	1438	A	G	0	571	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0214	4722	A	G	2	585	missense_variant	MODERATE	ND2	0.0019
HLI-0214	4769	A	G	1	654	synonymous_variant	LOW	ND2	0.9767
HLI-0214	5051	A	G	2	541	synonymous_variant	LOW	ND2	6.00E-04
HLI-0214	5390	A	G	0	568	synonymous_variant	LOW	ND2	0.0069
HLI-0214	15326	A	G	0	509	missense_variant	MODERATE	CYTB	0.9868

HLI-0216	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0216	150	C	T	3	546	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0216	263	A	G	1	209	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0216	723	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.002
HLI-0216	750	A	G	0	693	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0216	1290	C	T	4	616	upstream_gene_variant	MODIFIER	RNR1	5.00E-04
HLI-0216	1438	A	G	1	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0216	1721	C	T	1	669	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0216	2706	A	G	1	636	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0216	3197	T	C	0	579	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0216	3861	A	G	0	529	synonymous_variant	LOW	ND1	0.0011
HLI-0216	4769	A	G	0	574	synonymous_variant	LOW	ND2	0.9767
HLI-0216	5836	A	G	0	663	upstream_gene_variant	MODIFIER	TRNY	0.0018
HLI-0216	7028	C	T	2	638	synonymous_variant	LOW	COX1	0.8089
HLI-0216	7768	A	G	1	593	synonymous_variant	LOW	COX2	0.0186
HLI-0216	9477	G	A	2	589	missense_variant	MODERATE	COX3	0.0387
HLI-0216	10262	A	G	0	582	synonymous_variant	LOW	ND3	5.00E-04
HLI-0216	11467	A	G	1	599	synonymous_variant	LOW	ND4	0.1231
HLI-0216	11719	G	A	0	545	synonymous_variant	LOW	ND4	0.7756
HLI-0216	12308	A	G	1	621	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0216	12372	G	A	1	618	synonymous_variant	LOW	ND5	0.1329
HLI-0216	13017	A	G	2	585	synonymous_variant	LOW	ND5	7.00E-04
HLI-0216	13617	T	C	1	532	synonymous_variant	LOW	ND5	0.038
HLI-0216	13637	A	G	0	566	missense_variant	MODERATE	ND5	0.0074
HLI-0216	14182	T	C	2	543	synonymous_variant	LOW	ND6	0.0254
HLI-0216	14766	C	T	1	567	missense_variant	MODERATE	CYTB	0.7696
HLI-0216	15326	A	G	0	507	missense_variant	MODERATE	CYTB	0.9868
HLI-0216	16249	T	C	1	588	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0216	16270	C	T	0	552	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0217	195	T	C	0	399	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0217	263	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0217	750	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0217	961	T	G	2	653	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0217	1438	A	G	0	648	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0217	4769	A	G	0	549	synonymous_variant	LOW	ND2	0.9767
HLI-0217	8448	T	C	0	596	missense_variant	MODERATE	ATP8	0.0041
HLI-0217	13759	G	A	2	391	missense_variant	MODERATE	ND5	0.0348
HLI-0217	14869	G	A	0	613	synonymous_variant	LOW	CYTB	0.0023
HLI-0217	15326	A	G	1	606	missense_variant	MODERATE	CYTB	0.9868

HLI-0217	16293	A	G	1	564	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0217	16311	T	C	0	592	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0218	73	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0218	185	G	A	3	394	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0218	263	A	G	1	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0218	295	C	T	0	212	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0218	462	C	T	1	328	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0218	489	T	C	0	394	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0218	750	A	G	1	578	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0218	1438	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0218	2706	A	G	0	625	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0218	3010	G	A	0	644	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0218	4216	T	C	1	544	missense_variant	MODERATE	ND1	0.0991
HLI-0218	4769	A	G	2	547	synonymous_variant	LOW	ND2	0.9767
HLI-0218	5228	C	T	4	523	synonymous_variant	LOW	ND2	1.00E-04
HLI-0218	7028	C	T	3	646	synonymous_variant	LOW	COX1	0.8089
HLI-0218	9477	G	A	2	605	missense_variant	MODERATE	COX3	0.0387
HLI-0218	10398	A	G	1	569	missense_variant	MODERATE	ND3	0.445
HLI-0218	11251	A	G	0	568	synonymous_variant	LOW	ND4	0.0932
HLI-0218	11719	G	A	0	566	synonymous_variant	LOW	ND4	0.7756
HLI-0218	12358	A	G	2	552	missense_variant	MODERATE	ND5	0.0154
HLI-0218	12612	A	G	2	559	synonymous_variant	LOW	ND5	0.0506
HLI-0218	13708	G	A	0	488	missense_variant	MODERATE	ND5	0.0717
HLI-0218	13934	C	T	3	477	missense_variant	MODERATE	ND5	0.0122
HLI-0218	14766	C	T	2	537	missense_variant	MODERATE	CYTB	0.7696
HLI-0218	14798	T	C	1	635	missense_variant	MODERATE	CYTB	0.0651
HLI-0218	15326	A	G	0	520	missense_variant	MODERATE	CYTB	0.9868
HLI-0218	15452	C	A	2	543	missense_variant	MODERATE	CYTB	0.0933
HLI-0218	16069	C	T	0	540	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0218	16126	T	C	0	586	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0219	73	A	G	0	285	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0219	150	C	T	1	490	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0219	189	A	G	0	469	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0219	263	A	G	0	196	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0219	750	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0219	1438	A	G	0	694	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0219	2706	A	G	0	533	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0219	3348	A	G	0	545	synonymous_variant	LOW	ND1	0.0065
HLI-0219	4769	A	G	0	567	synonymous_variant	LOW	ND2	0.9767

HLI-0219	4955	C	T	0	581	synonymous_variant	LOW	ND2	2.00E-04
HLI-0219	5460	G	A	1	587	missense_variant	MODERATE	ND2	0.0651
HLI-0219	7028	C	T	3	627	synonymous_variant	LOW	COX1	0.8089
HLI-0219	7805	G	A	2	573	missense_variant	MODERATE	COX2	0.0077
HLI-0219	11467	A	G	1	576	synonymous_variant	LOW	ND4	0.1231
HLI-0219	11719	G	A	1	584	synonymous_variant	LOW	ND4	0.7756
HLI-0219	12246	C	T	1	525	upstream_gene_variant	MODIFIER	TRNS2	2.00E-04
HLI-0219	12308	A	G	3	584	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0219	12372	G	A	0	537	synonymous_variant	LOW	ND5	0.1329
HLI-0219	13674	T	C	0	458	synonymous_variant	LOW	ND5	0.001
HLI-0219	14179	A	G	0	493	synonymous_variant	LOW	ND6	0.0053
HLI-0219	14215	T	C	0	548	synonymous_variant	LOW	ND6	0.0011
HLI-0219	14766	C	T	0	530	missense_variant	MODERATE	CYTB	0.7696
HLI-0219	15326	A	G	2	518	missense_variant	MODERATE	CYTB	0.9868
HLI-0219	15862	T	C	1	507	synonymous_variant	LOW	CYTB	8.00E-04
HLI-0219	16134	C	T	1	516	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0219	16172	T	C	0	550	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0219	16219	A	G	1	537	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0219	16278	C	T	1	503	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0219	16519	T	C	0	226	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0220	73	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0220	185	G	A	3	391	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0220	228	G	A	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0220	263	A	G	1	235	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0220	295	C	T	0	198	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0220	462	C	T	5	387	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0220	489	T	C	0	466	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0220	750	A	G	0	619	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0220	1438	A	G	0	610	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0220	1811	A	G	4	650	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0220	2706	A	G	0	622	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0220	3010	G	A	1	647	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0220	3203	A	G	0	591	upstream_gene_variant	MODIFIER	RNR2	0.001
HLI-0220	4216	T	C	1	557	missense_variant	MODERATE	ND1	0.0991
HLI-0220	4769	A	G	1	580	synonymous_variant	LOW	ND2	0.9767
HLI-0220	7028	C	T	3	755	synonymous_variant	LOW	COX1	0.8089
HLI-0220	10398	A	G	0	579	missense_variant	MODERATE	ND3	0.445
HLI-0220	11251	A	G	1	615	synonymous_variant	LOW	ND4	0.0932
HLI-0220	11719	G	A	1	587	synonymous_variant	LOW	ND4	0.7756

HLI-0220	12612	A	G	5	607	synonymous_variant	LOW	ND5	0.0506
HLI-0220	13708	G	A	1	523	missense_variant	MODERATE	ND5	0.0717
HLI-0220	13934	C	T	1	514	missense_variant	MODERATE	ND5	0.0122
HLI-0220	14766	C	T	2	600	missense_variant	MODERATE	CYTB	0.7696
HLI-0220	14798	T	C	1	680	missense_variant	MODERATE	CYTB	0.0651
HLI-0220	15326	A	G	1	545	missense_variant	MODERATE	CYTB	0.9868
HLI-0220	15452	C	A	8	517	missense_variant	MODERATE	CYTB	0.0933
HLI-0220	16069	C	T	1	568	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0220	16126	T	C	0	624	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0221	73	A	G	0	31	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0221	195	T	C	1	49	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0221	263	A	G	0	29	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0221	285	C	T	0	24	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0221	385	A	G	0	31	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0221	750	A	G	0	49	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0221	1438	A	G	0	44	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0221	2218	C	T	0	35	upstream_gene_variant	MODIFIER	RNR2	0.0031
HLI-0221	2706	A	G	0	41	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0221	3591	G	A	0	30	synonymous_variant	LOW	ND1	0.0082
HLI-0221	4769	A	G	0	48	synonymous_variant	LOW	ND2	0.9767
HLI-0221	4991	G	A	0	36	synonymous_variant	LOW	ND2	0.0052
HLI-0221	6026	G	A	0	61	synonymous_variant	LOW	COX1	0.0163
HLI-0221	7028	C	T	0	82	synonymous_variant	LOW	COX1	0.8089
HLI-0221	7581	T	C	0	41	upstream_gene_variant	MODIFIER	TRND	0.0044
HLI-0221	9302	C	T	0	48	synonymous_variant	LOW	COX3	6.00E-04
HLI-0221	9386	T	C	1	48	synonymous_variant	LOW	COX3	7.00E-04
HLI-0221	10586	G	A	0	54	synonymous_variant	LOW	ND4L	0.0177
HLI-0221	11467	A	G	0	60	synonymous_variant	LOW	ND4	0.1231
HLI-0221	11719	G	A	0	59	synonymous_variant	LOW	ND4	0.7756
HLI-0221	12308	A	G	0	28	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0221	12372	G	A	0	29	synonymous_variant	LOW	ND5	0.1329
HLI-0221	12879	T	C	1	60	synonymous_variant	LOW	ND5	0.0058
HLI-0221	13104	A	G	0	54	synonymous_variant	LOW	ND5	0.0057
HLI-0221	13422	A	G	0	51	synonymous_variant	LOW	ND5	0.0021
HLI-0221	14070	A	G	0	47	synonymous_variant	LOW	ND5	0.0038
HLI-0221	14364	G	A	0	55	synonymous_variant	LOW	ND6	0.0076
HLI-0221	14766	C	T	0	47	missense_variant	MODERATE	CYTB	0.7696
HLI-0221	15047	G	A	0	62	missense_variant	MODERATE	CYTB	6.00E-04
HLI-0221	15148	G	A	0	60	synonymous_variant	LOW	CYTB	0.0058

HLI-0221	15954	A	C	0	35	upstream_gene_variant	MODIFIER	Unannotated	0.0036
HLI-0221	16129	G	A	0	23	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0221	16249	T	C	0	22	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0221	16288	T	C	0	37	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0222	72	T	C	0	238	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0222	263	A	G	1	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0222	750	A	G	1	491	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0222	1438	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0222	2706	A	G	0	557	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0222	4254	T	C	0	392	synonymous_variant	LOW	ND1	3.00E-04
HLI-0222	4580	G	A	1	504	synonymous_variant	LOW	ND2	0.0169
HLI-0222	4769	A	G	1	492	synonymous_variant	LOW	ND2	0.9767
HLI-0222	7028	C	T	3	595	synonymous_variant	LOW	COX1	0.8089
HLI-0222	8251	G	A	1	451	synonymous_variant	LOW	COX2	0.058
HLI-0222	11620	A	G	0	579	synonymous_variant	LOW	ND4	3.00E-04
HLI-0222	15326	A	G	0	399	missense_variant	MODERATE	CYTB	0.9868
HLI-0222	15904	C	T	3	451	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0222	16298	T	C	0	426	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0222	16519	T	C	0	211	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0223	72	T	C	4	254	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0223	89	T	C	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0038
HLI-0223	93	A	G	0	315	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0223	195	T	C	0	356	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0223	263	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0223	750	A	G	0	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0223	930	G	A	1	586	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0223	1438	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0223	2706	A	G	0	564	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0223	4580	G	A	3	491	synonymous_variant	LOW	ND2	0.0169
HLI-0223	4769	A	G	2	542	synonymous_variant	LOW	ND2	0.9767
HLI-0223	7028	C	T	0	597	synonymous_variant	LOW	COX1	0.8089
HLI-0223	7444	G	A	0	534	stop_lost	HIGH	COX1	0.0035
HLI-0223	11899	T	C	0	525	synonymous_variant	LOW	ND4	0.0108
HLI-0223	15326	A	G	0	494	missense_variant	MODERATE	CYTB	0.9868
HLI-0223	15904	C	T	2	604	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0223	16153	G	A	3	636	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0223	16298	T	C	0	450	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0224	73	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0224	146	T	C	0	446	upstream_gene_variant	MODIFIER	DLoop	0.1945

HLI-0224	152	T	C	0	449	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0224	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0224	750	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0224	769	G	A	0	628	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0224	1018	G	A	1	571	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0224	1438	A	G	0	563	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0224	2416	T	C	1	516	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0224	2706	A	G	0	560	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0224	2789	C	T	3	620	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0224	3594	C	T	2	474	synonymous_variant	LOW	ND1	0.0789
HLI-0224	4104	A	G	0	423	synonymous_variant	LOW	ND1	0.0785
HLI-0224	4769	A	G	0	520	synonymous_variant	LOW	ND2	0.9767
HLI-0224	7028	C	T	0	588	synonymous_variant	LOW	COX1	0.8089
HLI-0224	7175	T	C	0	617	synonymous_variant	LOW	COX1	0.0224
HLI-0224	7256	C	T	0	536	synonymous_variant	LOW	COX1	0.0784
HLI-0224	7274	C	T	0	517	synonymous_variant	LOW	COX1	0.0214
HLI-0224	7521	G	A	0	412	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0224	7771	A	G	0	528	synonymous_variant	LOW	COX2	0.0223
HLI-0224	8014	A	G	0	586	synonymous_variant	LOW	COX2	0.001
HLI-0224	8206	G	A	1	518	synonymous_variant	LOW	COX2	0.0287
HLI-0224	8701	A	G	0	437	missense_variant	MODERATE	ATP6	0.3391
HLI-0224	9221	A	G	0	542	synonymous_variant	LOW	COX3	0.0277
HLI-0224	9540	T	C	0	526	synonymous_variant	LOW	COX3	0.339
HLI-0224	10115	T	C	0	635	synonymous_variant	LOW	ND3	0.0278
HLI-0224	10398	A	G	0	646	missense_variant	MODERATE	ND3	0.445
HLI-0224	10873	T	C	0	507	synonymous_variant	LOW	ND4	0.3389
HLI-0224	11719	G	A	1	558	synonymous_variant	LOW	ND4	0.7756
HLI-0224	11914	G	A	0	589	synonymous_variant	LOW	ND4	0.1112
HLI-0224	11944	T	C	1	635	synonymous_variant	LOW	ND4	0.0331
HLI-0224	12693	A	G	0	596	synonymous_variant	LOW	ND5	0.0205
HLI-0224	12705	C	T	2	640	synonymous_variant	LOW	ND5	0.4212
HLI-0224	13590	G	A	0	501	synonymous_variant	LOW	ND5	0.0586
HLI-0224	13650	C	T	4	507	synonymous_variant	LOW	ND5	0.079
HLI-0224	13803	A	G	0	376	synonymous_variant	LOW	ND5	0.0216
HLI-0224	14281	C	T	2	469	synonymous_variant	LOW	ND6	0.0017
HLI-0224	14566	A	G	3	513	synonymous_variant	LOW	ND6	0.0214
HLI-0224	14766	C	T	5	487	missense_variant	MODERATE	CYTB	0.7696
HLI-0224	15301	G	A	0	520	synonymous_variant	LOW	CYTB	0.2912
HLI-0224	15326	A	G	0	562	missense_variant	MODERATE	CYTB	0.9868

HLI-0224	15784	T	C	0	521	synonymous_variant	LOW	CYTB	0.0363
HLI-0224	16131	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0224	16223	C	T	0	160	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0224	16225	C	T	0	165	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0224	16234	C	T	0	193	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0224	16278	C	T	0	279	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0224	16294	C	T	0	320	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0224	16309	A	G	15	353	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0224	16390	G	A	0	381	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0225	146	T	C	0	419	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0225	263	A	G	1	165	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0225	456	C	T	3	221	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0225	721	T	C	1	562	upstream_gene_variant	MODIFIER	RNR1	0.002
HLI-0225	750	A	G	1	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0225	956	C	T	3	543	upstream_gene_variant	MODIFIER	RNR1	2.00E-04
HLI-0225	1438	A	G	0	509	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0225	4336	T	C	0	456	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0225	4769	A	G	1	506	synonymous_variant	LOW	ND2	0.9767
HLI-0225	15326	A	G	0	482	missense_variant	MODERATE	CYTB	0.9868
HLI-0225	15706	A	G	0	508	synonymous_variant	LOW	CYTB	3.00E-04
HLI-0225	15833	C	T	0	503	synonymous_variant	LOW	CYTB	0.0051
HLI-0225	16304	T	C	2	477	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0226	73	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0226	150	C	T	0	395	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0226	152	T	C	0	393	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0226	195	T	C	0	363	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0226	263	A	G	0	130	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0226	750	A	G	3	562	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0226	1438	A	G	0	560	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0226	2234	C	T	5	544	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0226	2706	A	G	0	587	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0226	3197	T	C	1	580	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0226	4769	A	G	2	505	synonymous_variant	LOW	ND2	0.9767
HLI-0226	5656	A	G	3	597	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0226	7028	C	T	6	608	synonymous_variant	LOW	COX1	0.8089
HLI-0226	7768	A	G	0	498	synonymous_variant	LOW	COX2	0.0186
HLI-0226	9477	G	A	1	579	missense_variant	MODERATE	COX3	0.0387
HLI-0226	11467	A	G	1	562	synonymous_variant	LOW	ND4	0.1231
HLI-0226	11719	G	A	0	533	synonymous_variant	LOW	ND4	0.7756

HLI-0226	12308	A	G	1	529	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0226	12372	G	A	3	552	synonymous_variant	LOW	ND5	0.1329
HLI-0226	13617	T	C	0	458	synonymous_variant	LOW	ND5	0.038
HLI-0226	14182	T	C	0	466	synonymous_variant	LOW	ND6	0.0254
HLI-0226	14766	C	T	2	487	missense_variant	MODERATE	CYTB	0.7696
HLI-0226	15122	A	G	0	635	missense_variant	MODERATE	CYTB	2.00E-04
HLI-0226	15326	A	G	0	476	missense_variant	MODERATE	CYTB	0.9868
HLI-0226	16172	T	C	1	166	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0226	16270	C	T	0	325	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0226	16274	G	A	0	328	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0226	16311	T	C	1	333	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0226	16325	T	C	1	338	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0226	16357	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.01
HLI-0226	16465	C	T	2	273	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0226	16519	T	C	0	178	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0227	73	A	G	1	267	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0227	195	T	C	0	427	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0227	263	A	G	0	196	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0227	709	G	A	2	577	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0227	750	A	G	0	641	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0227	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0227	1888	G	A	0	587	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0227	2706	A	G	0	601	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0227	4216	T	C	2	616	missense_variant	MODERATE	ND1	0.0991
HLI-0227	4769	A	G	4	561	synonymous_variant	LOW	ND2	0.9767
HLI-0227	4917	A	G	0	498	missense_variant	MODERATE	ND2	0.0477
HLI-0227	5277	T	C	0	474	missense_variant	MODERATE	ND2	0.0022
HLI-0227	5426	T	C	1	524	synonymous_variant	LOW	ND2	0.0091
HLI-0227	6489	C	A	3	559	missense_variant	MODERATE	COX1	0.0016
HLI-0227	7028	C	T	4	680	synonymous_variant	LOW	COX1	0.8089
HLI-0227	8697	G	A	1	485	synonymous_variant	LOW	ATP6	0.0466
HLI-0227	10463	T	C	0	627	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0227	11251	A	G	3	555	synonymous_variant	LOW	ND4	0.0932
HLI-0227	11719	G	A	2	562	synonymous_variant	LOW	ND4	0.7756
HLI-0227	11812	A	G	2	562	synonymous_variant	LOW	ND4	0.0332
HLI-0227	13368	G	A	1	556	synonymous_variant	LOW	ND5	0.0495
HLI-0227	14233	A	G	0	498	synonymous_variant	LOW	ND6	0.0369
HLI-0227	14766	C	T	2	558	missense_variant	MODERATE	CYTB	0.7696
HLI-0227	14905	G	A	1	602	synonymous_variant	LOW	CYTB	0.0526

HLI-0227	15028	C	A	1	660	synonymous_variant	LOW	CYTB	0.0016
HLI-0227	15043	G	A	1	656	synonymous_variant	LOW	CYTB	0.2362
HLI-0227	15326	A	G	0	582	missense_variant	MODERATE	CYTB	0.9868
HLI-0227	15452	C	A	8	496	missense_variant	MODERATE	CYTB	0.0933
HLI-0227	15607	A	G	0	548	synonymous_variant	LOW	CYTB	0.0508
HLI-0227	15928	G	A	0	587	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0227	16126	T	C	0	326	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0227	16294	C	T	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0227	16296	C	T	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0227	16298	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0227	16519	T	C	0	165	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0228	146	T	C	0	393	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0228	152	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0228	195	T	C	1	357	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0228	210	A	G	1	337	upstream_gene_variant	MODIFIER	DLoop	0.0108
HLI-0228	263	A	G	0	95	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0228	709	G	A	1	565	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0228	750	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0228	1438	A	G	0	506	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0228	4769	A	G	0	499	synonymous_variant	LOW	ND2	0.9767
HLI-0228	9114	A	G	0	535	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0228	13101	A	C	0	559	synonymous_variant	LOW	ND5	0.0055
HLI-0228	13711	G	A	0	392	missense_variant	MODERATE	ND5	0.0011
HLI-0228	15326	A	G	0	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0228	16153	G	A	0	543	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0228	16288	T	C	2	459	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0228	16362	T	C	0	425	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0229	73	A	G	0	195	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0229	146	T	C	2	339	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0229	152	T	C	2	348	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0229	195	T	C	0	356	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0229	263	A	G	1	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0229	750	A	G	5	502	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0229	769	G	A	6	549	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0229	1018	G	A	8	536	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0229	1438	A	G	0	539	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0229	2416	T	C	15	543	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0229	2706	A	G	1	576	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0229	2789	C	T	19	576	upstream_gene_variant	MODIFIER	RNR2	0.0216

HLI-0229	3594	C	T	12	431	synonymous_variant	LOW	ND1	0.0789
HLI-0229	3918	G	A	9	473	synonymous_variant	LOW	ND1	0.009
HLI-0229	4104	A	G	14	438	synonymous_variant	LOW	ND1	0.0785
HLI-0229	4769	A	G	1	472	synonymous_variant	LOW	ND2	0.9767
HLI-0229	5285	A	G	14	472	synonymous_variant	LOW	ND2	0.0049
HLI-0229	7028	C	T	5	606	synonymous_variant	LOW	COX1	0.8089
HLI-0229	7175	T	C	11	544	synonymous_variant	LOW	COX1	0.0224
HLI-0229	7256	C	T	22	511	synonymous_variant	LOW	COX1	0.0784
HLI-0229	7274	C	T	23	544	synonymous_variant	LOW	COX1	0.0214
HLI-0229	7521	G	A	16	411	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0229	7771	A	G	12	471	synonymous_variant	LOW	COX2	0.0223
HLI-0229	8206	G	A	11	476	synonymous_variant	LOW	COX2	0.0287
HLI-0229	8701	A	G	1	435	missense_variant	MODERATE	ATP6	0.3391
HLI-0229	9221	A	G	11	508	synonymous_variant	LOW	COX3	0.0277
HLI-0229	9540	T	C	1	526	synonymous_variant	LOW	COX3	0.339
HLI-0229	10115	T	C	11	549	synonymous_variant	LOW	ND3	0.0278
HLI-0229	10398	A	G	0	555	missense_variant	MODERATE	ND3	0.445
HLI-0229	10454	T	C	16	587	upstream_gene_variant	MODIFIER	TRNR	0.0037
HLI-0229	10873	T	C	1	577	synonymous_variant	LOW	ND4	0.3389
HLI-0229	11719	G	A	2	509	synonymous_variant	LOW	ND4	0.7756
HLI-0229	11914	G	A	12	573	synonymous_variant	LOW	ND4	0.1112
HLI-0229	11944	T	C	12	564	synonymous_variant	LOW	ND4	0.0331
HLI-0229	12693	A	G	10	599	synonymous_variant	LOW	ND5	0.0205
HLI-0229	12705	C	T	3	670	synonymous_variant	LOW	ND5	0.4212
HLI-0229	13590	G	A	11	533	synonymous_variant	LOW	ND5	0.0586
HLI-0229	13650	C	T	9	572	synonymous_variant	LOW	ND5	0.079
HLI-0229	13803	A	G	3	369	synonymous_variant	LOW	ND5	0.0216
HLI-0229	14566	A	G	8	522	synonymous_variant	LOW	ND6	0.0214
HLI-0229	14766	C	T	2	537	missense_variant	MODERATE	CYTB	0.7696
HLI-0229	15211	C	T	10	507	synonymous_variant	LOW	CYTB	0.0015
HLI-0229	15244	A	G	10	530	synonymous_variant	LOW	CYTB	0.0103
HLI-0229	15301	G	A	0	487	synonymous_variant	LOW	CYTB	0.2912
HLI-0229	15326	A	G	0	510	missense_variant	MODERATE	CYTB	0.9868
HLI-0229	15421	A	G	7	492	synonymous_variant	LOW	CYTB	6.00E-04
HLI-0229	15629	T	C	9	499	synonymous_variant	LOW	CYTB	0.0062
HLI-0229	15784	T	C	14	484	synonymous_variant	LOW	CYTB	0.0363
HLI-0229	16093	T	C	35	469	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0229	16223	C	T	1	468	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0229	16278	C	T	10	425	upstream_gene_variant	MODIFIER	DLoop	0.1057

HLI-0229	16286	C	T	8	407	upstream_gene_variant	MODIFIER	DLoop	0.0052
HLI-0229	16294	C	T	8	411	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0229	16309	A	G	9	388	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0229	16390	G	A	6	365	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0229	16519	T	C	0	181	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0230	73	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0230	152	T	C	0	398	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0230	263	A	G	1	131	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0230	750	A	G	3	502	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0230	1438	A	G	1	514	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0230	1598	G	A	0	574	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0230	1703	C	T	0	538	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0230	1719	G	A	0	587	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0230	2639	C	T	0	502	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0230	2706	A	G	1	548	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0230	3921	C	A	3	452	synonymous_variant	LOW	ND1	0.0026
HLI-0230	4735	C	A	1	544	missense_variant	MODERATE	ND2	7.00E-04
HLI-0230	4769	A	G	3	538	synonymous_variant	LOW	ND2	0.9767
HLI-0230	4917	A	G	1	530	missense_variant	MODERATE	ND2	0.0477
HLI-0230	4960	C	T	2	592	missense_variant	MODERATE	ND2	0.0028
HLI-0230	5471	G	A	0	507	synonymous_variant	LOW	ND2	0.0128
HLI-0230	7028	C	T	3	547	synonymous_variant	LOW	COX1	0.8089
HLI-0230	8251	G	A	3	465	synonymous_variant	LOW	COX2	0.058
HLI-0230	8472	C	T	4	365	missense_variant	MODERATE	ATP8	0.0027
HLI-0230	8836	A	G	0	518	missense_variant	MODERATE	ATP6	0.0029
HLI-0230	10238	T	C	1	525	synonymous_variant	LOW	ND3	0.0623
HLI-0230	11719	G	A	0	466	synonymous_variant	LOW	ND4	0.7756
HLI-0230	11928	A	G	0	472	missense_variant	MODERATE	ND4	0.0028
HLI-0230	12092	C	T	4	482	missense_variant	MODERATE	ND4	7.00E-04
HLI-0230	12501	G	A	0	506	synonymous_variant	LOW	ND5	0.0258
HLI-0230	12705	C	T	0	512	synonymous_variant	LOW	ND5	0.4212
HLI-0230	12822	A	G	2	529	synonymous_variant	LOW	ND5	0.0026
HLI-0230	13129	C	T	3	480	missense_variant	MODERATE	ND5	0.0046
HLI-0230	13710	A	G	0	419	synonymous_variant	LOW	ND5	0.0018
HLI-0230	14581	T	C	0	498	synonymous_variant	LOW	ND6	0.0023
HLI-0230	14766	C	T	5	465	missense_variant	MODERATE	CYTB	0.7696
HLI-0230	15326	A	G	0	425	missense_variant	MODERATE	CYTB	0.9868
HLI-0230	16145	G	A	0	458	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0230	16176	C	A	5	502	upstream_gene_variant	MODIFIER	DLoop	6.00E-04

HLI-0230	16223	C	T	1	469	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0230	16390	G	A	1	396	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0230	16519	T	C	0	178	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0231	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0231	711	T	C	0	544	upstream_gene_variant	MODIFIER	RNR1	0.0031
HLI-0231	750	A	G	0	573	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0231	1438	A	G	0	529	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0231	3918	G	A	1	493	synonymous_variant	LOW	ND1	0.009
HLI-0231	4769	A	G	1	462	synonymous_variant	LOW	ND2	0.9767
HLI-0231	7775	G	A	0	486	missense_variant	MODERATE	COX2	0.0015
HLI-0231	12115	C	T	1	483	synonymous_variant	LOW	ND4	1.00E-04
HLI-0231	14119	C	T	6	440	missense_variant	MODERATE	ND5	2.00E-04
HLI-0231	14891	C	T	1	529	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0231	15326	A	G	0	448	missense_variant	MODERATE	CYTB	0.9868
HLI-0231	16519	T	C	1	241	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0232	64	C	T	0	192	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0232	263	A	G	0	154	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0232	750	A	G	0	494	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0232	1438	A	G	0	503	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0232	2442	T	C	3	535	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0232	2706	A	G	1	498	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0232	3847	T	C	5	448	synonymous_variant	LOW	ND1	0.0061
HLI-0232	4769	A	G	0	483	synonymous_variant	LOW	ND2	0.9767
HLI-0232	7028	C	T	2	581	synonymous_variant	LOW	COX1	0.8089
HLI-0232	10586	G	A	0	487	synonymous_variant	LOW	ND4L	0.0177
HLI-0232	10775	G	A	0	442	missense_variant	MODERATE	ND4	3.00E-04
HLI-0232	12474	C	T	2	504	synonymous_variant	LOW	ND5	2.00E-04
HLI-0232	13188	C	T	3	527	synonymous_variant	LOW	ND5	0.0053
HLI-0232	14766	C	T	2	476	missense_variant	MODERATE	CYTB	0.7696
HLI-0232	15326	A	G	0	433	missense_variant	MODERATE	CYTB	0.9868
HLI-0232	15466	G	A	1	436	synonymous_variant	LOW	CYTB	0.0152
HLI-0232	15674	T	C	2	470	missense_variant	MODERATE	CYTB	0.003
HLI-0232	16126	T	C	0	272	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0232	16172	T	C	20	128	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0232	16362	T	C	0	321	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0233	73	A	G	1	176	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0233	152	T	C	0	283	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0233	182	C	T	0	265	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0233	185	G	T	0	265	upstream_gene_variant	MODIFIER	DLoop	0.0056

HLI-0233	189	A	G	0	257	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0233	195	T	C	0	263	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0233	247	G	A	0	128	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0233	263	A	G	0	134	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0233	357	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0233	709	G	A	0	394	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0233	710	T	C	0	401	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0233	750	A	G	0	432	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0233	769	G	A	3	435	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0233	825	T	A	3	487	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0233	1018	G	A	2	559	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0233	1530	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	3.00E-04
HLI-0233	1738	T	C	1	522	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0233	2352	T	C	0	434	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0233	2706	A	G	0	470	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0233	2758	G	A	0	496	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0233	2768	A	G	0	494	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0233	2885	T	C	1	487	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0233	3308	T	C	0	484	start_lost	HIGH	ND1	0.0073
HLI-0233	3594	C	T	1	353	synonymous_variant	LOW	ND1	0.0789
HLI-0233	3666	G	A	1	409	synonymous_variant	LOW	ND1	0.0233
HLI-0233	3693	G	A	0	406	synonymous_variant	LOW	ND1	0.0091
HLI-0233	4104	A	G	0	344	synonymous_variant	LOW	ND1	0.0785
HLI-0233	4769	A	G	1	490	synonymous_variant	LOW	ND2	0.9767
HLI-0233	5036	A	G	1	427	synonymous_variant	LOW	ND2	0.006
HLI-0233	5046	G	A	2	459	missense_variant	MODERATE	ND2	0.018
HLI-0233	5393	T	C	2	489	synonymous_variant	LOW	ND2	0.0059
HLI-0233	5655	T	C	3	621	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0233	6548	C	T	3	444	synonymous_variant	LOW	COX1	0.0061
HLI-0233	6827	T	C	3	461	synonymous_variant	LOW	COX1	0.0072
HLI-0233	6989	A	G	2	510	synonymous_variant	LOW	COX1	0.0061
HLI-0233	7028	C	T	2	509	synonymous_variant	LOW	COX1	0.8089
HLI-0233	7055	A	G	1	446	synonymous_variant	LOW	COX1	0.0188
HLI-0233	7146	A	G	0	232	missense_variant	MODERATE	COX1	0.0497
HLI-0233	7256	C	T	5	396	synonymous_variant	LOW	COX1	0.0784
HLI-0233	7389	T	C	1	381	missense_variant	MODERATE	COX1	0.0201
HLI-0233	7521	G	A	1	301	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0233	7867	C	T	0	580	synonymous_variant	LOW	COX2	0.0076
HLI-0233	8248	A	G	2	463	synonymous_variant	LOW	COX2	0.0061

HLI-0233	8468	C	T	1	369	synonymous_variant	LOW	ATP8	0.0501
HLI-0233	8655	C	T	3	384	synonymous_variant	LOW	ATP6	0.0511
HLI-0233	8701	A	G	1	440	missense_variant	MODERATE	ATP6	0.3391
HLI-0233	9540	T	C	1	479	synonymous_variant	LOW	COX3	0.339
HLI-0233	10398	A	G	2	419	missense_variant	MODERATE	ND3	0.445
HLI-0233	10688	G	A	1	422	synonymous_variant	LOW	ND4L	0.0515
HLI-0233	10810	T	C	2	429	synonymous_variant	LOW	ND4	0.0522
HLI-0233	10873	T	C	2	443	synonymous_variant	LOW	ND4	0.3389
HLI-0233	11719	G	A	1	462	synonymous_variant	LOW	ND4	0.7756
HLI-0233	12519	T	C	5	487	synonymous_variant	LOW	ND5	0.007
HLI-0233	12705	C	T	0	485	synonymous_variant	LOW	ND5	0.4212
HLI-0233	13105	A	G	1	432	missense_variant	MODERATE	ND5	0.076
HLI-0233	13198	G	T	3	495	missense_variant	MODERATE	ND5	0
HLI-0233	13506	C	T	1	411	synonymous_variant	LOW	ND5	0.0506
HLI-0233	13650	C	T	0	355	synonymous_variant	LOW	ND5	0.079
HLI-0233	13789	T	C	1	270	missense_variant	MODERATE	ND5	0.0185
HLI-0233	13880	C	A	2	363	missense_variant	MODERATE	ND5	0.0055
HLI-0233	13980	G	A	0	362	synonymous_variant	LOW	ND5	0.0023
HLI-0233	14178	T	C	0	415	missense_variant	MODERATE	ND6	0.0225
HLI-0233	14180	T	C	0	416	missense_variant	MODERATE	ND6	0.0036
HLI-0233	14203	A	G	0	453	synonymous_variant	LOW	ND6	0.0061
HLI-0233	14560	G	A	2	527	synonymous_variant	LOW	ND6	0.0235
HLI-0233	14766	C	T	0	478	missense_variant	MODERATE	CYTB	0.7696
HLI-0233	14769	A	G	0	489	missense_variant	MODERATE	CYTB	0.0121
HLI-0233	15115	T	C	0	537	synonymous_variant	LOW	CYTB	0.0093
HLI-0233	15326	A	G	0	320	missense_variant	MODERATE	CYTB	0.9868
HLI-0233	16126	T	C	0	531	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0233	16223	C	T	3	385	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0233	16264	C	T	1	356	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0233	16270	C	T	1	342	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0233	16278	C	T	1	349	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0233	16293	A	G	1	337	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0233	16311	T	C	1	331	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0233	16519	T	C	0	117	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0234	73	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0234	153	A	G	7	394	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0234	195	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0234	225	G	A	0	270	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0234	226	T	C	0	269	upstream_gene_variant	MODIFIER	DLoop	0.0035

HLI-0234	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0234	750	A	G	0	529	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0234	1438	A	G	1	537	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0234	1719	G	A	0	522	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0234	2706	A	G	1	479	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0234	4769	A	G	0	485	synonymous_variant	LOW	ND2	0.9767
HLI-0234	6221	T	C	0	511	synonymous_variant	LOW	COX1	0.0306
HLI-0234	6371	C	T	1	543	synonymous_variant	LOW	COX1	0.0097
HLI-0234	7028	C	T	7	621	synonymous_variant	LOW	COX1	0.8089
HLI-0234	8393	C	T	1	414	missense_variant	MODERATE	ATP8	0.0036
HLI-0234	11719	G	A	2	504	synonymous_variant	LOW	ND4	0.7756
HLI-0234	11963	G	A	0	482	missense_variant	MODERATE	ND4	0.002
HLI-0234	12696	T	C	0	547	synonymous_variant	LOW	ND5	0.0027
HLI-0234	12705	C	T	0	552	synonymous_variant	LOW	ND5	0.4212
HLI-0234	13708	G	A	1	413	missense_variant	MODERATE	ND5	0.0717
HLI-0234	13966	A	G	0	418	missense_variant	MODERATE	ND5	0.0126
HLI-0234	14470	T	C	0	450	synonymous_variant	LOW	ND6	0.0166
HLI-0234	14766	C	T	5	463	missense_variant	MODERATE	CYTB	0.7696
HLI-0234	15326	A	G	0	399	missense_variant	MODERATE	CYTB	0.9868
HLI-0234	15927	G	A	0	497	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0234	16223	C	T	0	141	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0234	16278	C	T	0	234	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0234	16519	T	C	0	163	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0235	73	A	G	0	184	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0235	150	C	T	1	388	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0235	151	C	T	1	386	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0235	263	A	G	0	135	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0235	750	A	G	0	453	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0235	1438	A	G	0	509	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0235	1721	C	T	0	457	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0235	2706	A	G	0	462	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0235	3197	T	C	0	459	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0235	4732	A	G	0	494	missense_variant	MODERATE	ND2	0.0059
HLI-0235	4769	A	G	2	505	synonymous_variant	LOW	ND2	0.9767
HLI-0235	7028	C	T	3	579	synonymous_variant	LOW	COX1	0.8089
HLI-0235	7768	A	G	1	457	synonymous_variant	LOW	COX2	0.0186
HLI-0235	8706	A	G	2	440	synonymous_variant	LOW	ATP6	7.00E-04
HLI-0235	9055	G	A	0	456	missense_variant	MODERATE	ATP6	0.0425
HLI-0235	9477	G	A	1	473	missense_variant	MODERATE	COX3	0.0387

HLI-0235	10654	C	T	3	418	missense_variant	MODERATE	ND4L	7.00E-04
HLI-0235	11467	A	G	0	510	synonymous_variant	LOW	ND4	0.1231
HLI-0235	11719	G	A	0	492	synonymous_variant	LOW	ND4	0.7756
HLI-0235	11725	A	G	0	517	synonymous_variant	LOW	ND4	2.00E-04
HLI-0235	12308	A	G	0	465	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0235	12372	G	A	2	431	synonymous_variant	LOW	ND5	0.1329
HLI-0235	13617	T	C	1	446	synonymous_variant	LOW	ND5	0.038
HLI-0235	13637	A	G	1	492	missense_variant	MODERATE	ND5	0.0074
HLI-0235	14182	T	C	1	407	synonymous_variant	LOW	ND6	0.0254
HLI-0235	14766	C	T	4	402	missense_variant	MODERATE	CYTB	0.7696
HLI-0235	15326	A	G	0	383	missense_variant	MODERATE	CYTB	0.9868
HLI-0235	15940	T	C	1	494	upstream_gene_variant	MODIFIER	TRNT	0.0018
HLI-0235	16270	C	T	0	225	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0235	16311	T	C	1	284	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0236	58	T	C	0	189	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0236	64	C	T	0	211	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0236	146	T	C	0	470	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0236	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0236	336	A	G	2	177	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0236	750	A	G	0	518	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0236	827	A	G	3	576	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0236	1438	A	G	0	552	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0236	2442	T	C	2	528	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0236	2706	A	G	0	532	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0236	3847	T	C	1	474	synonymous_variant	LOW	ND1	0.0061
HLI-0236	4769	A	G	1	533	synonymous_variant	LOW	ND2	0.9767
HLI-0236	5387	C	T	0	501	synonymous_variant	LOW	ND2	6.00E-04
HLI-0236	7028	C	T	4	564	synonymous_variant	LOW	COX1	0.8089
HLI-0236	8292	G	A	3	452	upstream_gene_variant	MODIFIER	Unannotated	0.0024
HLI-0236	11761	C	T	1	506	synonymous_variant	LOW	ND4	0.0016
HLI-0236	13188	C	T	5	509	synonymous_variant	LOW	ND5	0.0053
HLI-0236	14766	C	T	3	458	missense_variant	MODERATE	CYTB	0.7696
HLI-0236	15236	A	G	0	487	missense_variant	MODERATE	CYTB	0.016
HLI-0236	15326	A	G	0	457	missense_variant	MODERATE	CYTB	0.9868
HLI-0236	16111	C	T	0	523	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0236	16126	T	C	0	551	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0236	16355	C	T	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0236	16362	T	C	0	399	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0237	143	G	A	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0191

HLI-0237	195	T	C	1	291	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0237	263	A	G	1	198	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0237	750	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0237	1211	G	A	0	612	upstream_gene_variant	MODIFIER	RNR1	0.0012
HLI-0237	1438	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0237	4769	A	G	0	539	synonymous_variant	LOW	ND2	0.9767
HLI-0237	6776	T	C	3	681	synonymous_variant	LOW	COX1	0.0226
HLI-0237	12957	T	C	3	536	synonymous_variant	LOW	ND5	0.0032
HLI-0237	14305	G	A	0	422	synonymous_variant	LOW	ND6	0.0069
HLI-0237	15326	A	G	0	521	missense_variant	MODERATE	CYTB	0.9868
HLI-0237	16153	G	A	1	539	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0237	16176	C	T	2	522	upstream_gene_variant	MODIFIER	DLoop	0.0061
HLI-0237	16298	T	C	1	454	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0238	152	T	C	1	476	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0238	263	A	G	0	209	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0238	750	A	G	2	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0238	1438	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0238	4769	A	G	1	547	synonymous_variant	LOW	ND2	0.9767
HLI-0238	4793	A	G	1	598	synonymous_variant	LOW	ND2	0.0073
HLI-0238	15326	A	G	0	528	missense_variant	MODERATE	CYTB	0.9868
HLI-0238	16519	T	C	0	268	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0239	73	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0239	263	A	G	0	204	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0239	295	C	T	0	176	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0239	462	C	T	5	371	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0239	489	T	C	2	451	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0239	750	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0239	1438	A	G	0	616	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0239	2706	A	G	0	562	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0239	3010	G	A	0	573	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0239	4216	T	C	1	591	missense_variant	MODERATE	ND1	0.0991
HLI-0239	4769	A	G	2	506	synonymous_variant	LOW	ND2	0.9767
HLI-0239	5393	T	C	0	503	synonymous_variant	LOW	ND2	0.0059
HLI-0239	7028	C	T	3	642	synonymous_variant	LOW	COX1	0.8089
HLI-0239	9055	G	A	1	580	missense_variant	MODERATE	ATP6	0.0425
HLI-0239	10398	A	G	2	651	missense_variant	MODERATE	ND3	0.445
HLI-0239	11251	A	G	0	533	synonymous_variant	LOW	ND4	0.0932
HLI-0239	11582	A	C	0	604	missense_variant	MODERATE	ND4	0
HLI-0239	11719	G	A	0	534	synonymous_variant	LOW	ND4	0.7756

HLI-0239	12612	A	G	3	598	synonymous_variant	LOW	ND5	0.0506
HLI-0239	13708	G	A	0	419	missense_variant	MODERATE	ND5	0.0717
HLI-0239	13934	C	T	0	503	missense_variant	MODERATE	ND5	0.0122
HLI-0239	14766	C	T	3	601	missense_variant	MODERATE	CYTB	0.7696
HLI-0239	14798	T	C	0	617	missense_variant	MODERATE	CYTB	0.0651
HLI-0239	15326	A	G	0	486	missense_variant	MODERATE	CYTB	0.9868
HLI-0239	15452	C	A	3	482	missense_variant	MODERATE	CYTB	0.0933
HLI-0239	16069	C	T	1	561	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0239	16126	T	C	0	574	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0239	16172	T	C	0	534	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0240	146	T	C	0	422	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0240	263	A	G	0	186	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0240	750	A	G	1	556	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0240	1438	A	G	0	581	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0240	4769	A	G	2	518	synonymous_variant	LOW	ND2	0.9767
HLI-0240	7444	G	A	2	626	stop_lost	HIGH	COX1	0.0035
HLI-0240	10562	A	G	0	531	synonymous_variant	LOW	ND4L	1.00E-04
HLI-0240	11152	T	C	1	564	synonymous_variant	LOW	ND4	0.0024
HLI-0240	15326	A	G	0	483	missense_variant	MODERATE	CYTB	0.9868
HLI-0240	16129	G	A	3	508	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0240	16519	T	C	1	202	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0241	73	A	G	0	127	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0241	151	C	T	1	216	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0241	152	T	C	1	217	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0241	182	C	T	0	196	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0241	186	C	A	0	196	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0241	189	A	C	0	193	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0241	195	T	C	0	197	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0241	247	G	A	0	95	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0241	263	A	G	0	100	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0241	297	A	G	0	111	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0241	750	A	G	0	470	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0241	769	G	A	0	527	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0241	825	T	A	0	515	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0241	1018	G	A	0	511	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0241	1438	A	G	0	530	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0241	1762	A	G	1	527	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0241	2706	A	G	1	424	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0241	2758	G	A	0	430	upstream_gene_variant	MODIFIER	RNR2	0.0503

HLI-0241	2885	T	C	0	467	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0241	3386	T	C	0	454	missense_variant	MODERATE	ND1	0
HLI-0241	3594	C	T	3	353	synonymous_variant	LOW	ND1	0.0789
HLI-0241	3666	G	A	0	401	synonymous_variant	LOW	ND1	0.0233
HLI-0241	3796	A	T	0	465	missense_variant	MODERATE	ND1	0.0045
HLI-0241	3843	A	G	1	542	synonymous_variant	LOW	ND1	0.0046
HLI-0241	3969	C	T	1	387	synonymous_variant	LOW	ND1	7.00E-04
HLI-0241	4104	A	G	0	385	synonymous_variant	LOW	ND1	0.0785
HLI-0241	4219	G	A	0	407	missense_variant	MODERATE	ND1	0.001
HLI-0241	4225	A	G	0	388	missense_variant	MODERATE	ND1	0.0026
HLI-0241	4454	T	A	1	398	upstream_gene_variant	MODIFIER	TRNM	0.0029
HLI-0241	4769	A	G	1	454	synonymous_variant	LOW	ND2	0.9767
HLI-0241	4937	T	C	2	493	synonymous_variant	LOW	ND2	0.0019
HLI-0241	5951	A	G	3	604	synonymous_variant	LOW	COX1	0.0128
HLI-0241	6071	T	C	3	585	synonymous_variant	LOW	COX1	0.0129
HLI-0241	6578	A	C	3	475	synonymous_variant	LOW	COX1	0
HLI-0241	7028	C	T	1	431	synonymous_variant	LOW	COX1	0.8089
HLI-0241	7055	A	G	3	412	synonymous_variant	LOW	COX1	0.0188
HLI-0241	7146	A	G	0	225	missense_variant	MODERATE	COX1	0.0497
HLI-0241	7256	C	T	3	375	synonymous_variant	LOW	COX1	0.0784
HLI-0241	7389	T	C	2	378	missense_variant	MODERATE	COX1	0.0201
HLI-0241	7521	G	A	1	343	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0241	8027	G	A	2	478	missense_variant	MODERATE	COX2	0.0334
HLI-0241	8087	T	C	1	489	synonymous_variant	LOW	COX2	0.0031
HLI-0241	8468	C	T	2	401	synonymous_variant	LOW	ATP8	0.0501
HLI-0241	8655	C	T	2	369	synonymous_variant	LOW	ATP6	0.0511
HLI-0241	8701	A	G	0	389	missense_variant	MODERATE	ATP6	0.3391
HLI-0241	8841	C	T	1	394	synonymous_variant	LOW	ATP6	2.00E-04
HLI-0241	9072	A	G	2	403	synonymous_variant	LOW	ATP6	0.0124
HLI-0241	9540	T	C	0	495	synonymous_variant	LOW	COX3	0.339
HLI-0241	9830	C	T	0	537	synonymous_variant	LOW	COX3	4.00E-04
HLI-0241	10321	T	C	1	436	missense_variant	MODERATE	ND3	0.0106
HLI-0241	10398	A	G	1	531	missense_variant	MODERATE	ND3	0.445
HLI-0241	10586	G	A	2	501	synonymous_variant	LOW	ND4L	0.0177
HLI-0241	10688	G	A	1	450	synonymous_variant	LOW	ND4L	0.0515
HLI-0241	10810	T	C	1	482	synonymous_variant	LOW	ND4	0.0522
HLI-0241	10873	T	C	1	355	synonymous_variant	LOW	ND4	0.3389
HLI-0241	10976	C	T	5	276	synonymous_variant	LOW	ND4	0.0027
HLI-0241	11044	C	T	4	335	synonymous_variant	LOW	ND4	3.00E-04

HLI-0241	11719	G	A	0	495	synonymous_variant	LOW	ND4	0.7756
HLI-0241	11899	T	C	0	442	synonymous_variant	LOW	ND4	0.0108
HLI-0241	12281	C	T	2	485	upstream_gene_variant	MODIFIER	TRNL2	0
HLI-0241	12705	C	T	0	501	synonymous_variant	LOW	ND5	0.4212
HLI-0241	12810	A	G	0	464	synonymous_variant	LOW	ND5	0.0198
HLI-0241	13105	A	G	0	410	missense_variant	MODERATE	ND5	0.076
HLI-0241	13260	T	C	1	482	synonymous_variant	LOW	ND5	0.0017
HLI-0241	13485	A	G	2	390	synonymous_variant	LOW	ND5	0.0122
HLI-0241	13506	C	T	1	407	synonymous_variant	LOW	ND5	0.0506
HLI-0241	13539	A	G	1	403	synonymous_variant	LOW	ND5	2.00E-04
HLI-0241	13650	C	T	3	389	synonymous_variant	LOW	ND5	0.079
HLI-0241	13789	T	C	0	301	missense_variant	MODERATE	ND5	0.0185
HLI-0241	14000	T	A	1	414	missense_variant	MODERATE	ND5	0.0126
HLI-0241	14088	T	C	0	427	synonymous_variant	LOW	ND5	0.0046
HLI-0241	14148	A	G	1	426	stop_retained_variant	LOW	ND5	0.0065
HLI-0241	14178	T	C	2	426	missense_variant	MODERATE	ND6	0.0225
HLI-0241	14422	T	C	4	392	synonymous_variant	LOW	ND6	2.00E-04
HLI-0241	14560	G	A	3	459	synonymous_variant	LOW	ND6	0.0235
HLI-0241	14766	C	T	4	487	missense_variant	MODERATE	CYTB	0.7696
HLI-0241	14911	C	T	4	504	synonymous_variant	LOW	CYTB	0.0124
HLI-0241	15326	A	G	0	359	missense_variant	MODERATE	CYTB	0.9868
HLI-0241	16093	T	C	13	433	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0241	16129	G	A	3	457	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0241	16223	C	T	4	232	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0241	16263	T	C	1	185	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0241	16278	C	T	1	199	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0241	16293	A	G	1	217	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0241	16294	C	T	1	218	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0241	16311	T	C	2	219	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0241	16360	C	T	2	218	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0241	16368	T	C	3	219	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0241	16519	T	C	1	95	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0242	73	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0242	150	C	T	0	408	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0242	189	A	G	0	394	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0242	200	A	G	0	379	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0242	263	A	G	0	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0242	750	A	G	1	455	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0242	1438	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0242	2352	T	C	0	501	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0242	2706	A	G	1	408	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0242	4769	A	G	1	443	synonymous_variant	LOW	ND2	0.9767
HLI-0242	5999	T	C	1	524	synonymous_variant	LOW	COX1	0.0127
HLI-0242	6221	T	C	1	452	synonymous_variant	LOW	COX1	0.0306
HLI-0242	6587	C	T	2	461	synonymous_variant	LOW	COX1	0.0084
HLI-0242	7028	C	T	2	502	synonymous_variant	LOW	COX1	0.8089
HLI-0242	8701	A	G	0	445	missense_variant	MODERATE	ATP6	0.3391
HLI-0242	9540	T	C	0	431	synonymous_variant	LOW	COX3	0.339
HLI-0242	10398	A	G	1	584	missense_variant	MODERATE	ND3	0.445
HLI-0242	10819	A	G	1	502	synonymous_variant	LOW	ND4	0.0228
HLI-0242	10873	T	C	1	505	synonymous_variant	LOW	ND4	0.3389
HLI-0242	11719	G	A	0	435	synonymous_variant	LOW	ND4	0.7756
HLI-0242	12705	C	T	0	546	synonymous_variant	LOW	ND5	0.4212
HLI-0242	14152	A	G	1	433	synonymous_variant	LOW	ND6	0.0086
HLI-0242	14212	T	C	1	495	synonymous_variant	LOW	ND6	0.0204
HLI-0242	14766	C	T	3	526	missense_variant	MODERATE	CYTB	0.7696
HLI-0242	15301	G	A	2	360	synonymous_variant	LOW	CYTB	0.2912
HLI-0242	15326	A	G	0	390	missense_variant	MODERATE	CYTB	0.9868
HLI-0242	15670	T	C	1	362	synonymous_variant	LOW	CYTB	0.0176
HLI-0242	15942	T	C	1	574	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0242	16223	C	T	0	460	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0242	16327	C	T	0	397	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0243	73	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0243	143	G	A	0	342	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0243	146	T	C	0	350	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0243	152	T	C	0	365	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0243	189	A	G	0	374	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0243	195	T	C	0	359	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0243	263	A	G	0	174	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0243	750	A	G	0	570	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0243	769	G	A	0	621	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0243	1018	G	A	0	680	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0243	1438	A	G	0	555	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0243	2416	T	C	0	589	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0243	2706	A	G	2	551	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0243	2789	C	T	1	584	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0243	3594	C	T	1	527	synonymous_variant	LOW	ND1	0.0789
HLI-0243	4104	A	G	0	506	synonymous_variant	LOW	ND1	0.0785

HLI-0243	4769	A	G	0	463	synonymous_variant	LOW	ND2	0.9767
HLI-0243	5147	G	A	0	482	synonymous_variant	LOW	ND2	0.0437
HLI-0243	6152	T	C	0	558	synonymous_variant	LOW	COX1	0.0077
HLI-0243	7028	C	T	0	625	synonymous_variant	LOW	COX1	0.8089
HLI-0243	7175	T	C	1	583	synonymous_variant	LOW	COX1	0.0224
HLI-0243	7256	C	T	0	570	synonymous_variant	LOW	COX1	0.0784
HLI-0243	7274	C	T	0	603	synonymous_variant	LOW	COX1	0.0214
HLI-0243	7521	G	A	0	464	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0243	7771	A	G	1	534	synonymous_variant	LOW	COX2	0.0223
HLI-0243	8206	G	A	1	520	synonymous_variant	LOW	COX2	0.0287
HLI-0243	8701	A	G	0	482	missense_variant	MODERATE	ATP6	0.3391
HLI-0243	9221	A	G	1	558	synonymous_variant	LOW	COX3	0.0277
HLI-0243	9540	T	C	0	476	synonymous_variant	LOW	COX3	0.339
HLI-0243	10115	T	C	0	655	synonymous_variant	LOW	ND3	0.0278
HLI-0243	10398	A	G	1	604	missense_variant	MODERATE	ND3	0.445
HLI-0243	10604	T	C	0	513	synonymous_variant	LOW	ND4L	9.00E-04
HLI-0243	10873	T	C	1	536	synonymous_variant	LOW	ND4	0.3389
HLI-0243	11719	G	A	1	558	synonymous_variant	LOW	ND4	0.7756
HLI-0243	11914	G	A	1	627	synonymous_variant	LOW	ND4	0.1112
HLI-0243	11944	T	C	0	628	synonymous_variant	LOW	ND4	0.0331
HLI-0243	12693	A	G	0	644	synonymous_variant	LOW	ND5	0.0205
HLI-0243	12705	C	T	0	661	synonymous_variant	LOW	ND5	0.4212
HLI-0243	13590	G	A	1	500	synonymous_variant	LOW	ND5	0.0586
HLI-0243	13650	C	T	3	502	synonymous_variant	LOW	ND5	0.079
HLI-0243	13803	A	G	0	396	synonymous_variant	LOW	ND5	0.0216
HLI-0243	14566	A	G	3	571	synonymous_variant	LOW	ND6	0.0214
HLI-0243	14766	C	T	0	558	missense_variant	MODERATE	CYTB	0.7696
HLI-0243	15301	G	A	2	532	synonymous_variant	LOW	CYTB	0.2912
HLI-0243	15326	A	G	1	559	missense_variant	MODERATE	CYTB	0.9868
HLI-0243	15784	T	C	0	563	synonymous_variant	LOW	CYTB	0.0363
HLI-0243	16129	G	A	0	432	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0243	16223	C	T	4	379	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0243	16278	C	T	2	405	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0243	16294	C	T	0	415	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0243	16309	A	G	0	428	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0243	16390	G	A	1	396	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0243	16400	C	T	2	422	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0244	263	A	G	1	204	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0244	750	A	G	0	522	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0244	3010	G	A	0	524	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0244	4769	A	G	3	490	synonymous_variant	LOW	ND2	0.9767
HLI-0244	5054	G	C	0	452	synonymous_variant	LOW	ND2	5.00E-04
HLI-0244	7471	C	T	2	536	upstream_gene_variant	MODIFIER	TRNS1	3.00E-04
HLI-0244	8429	C	T	2	479	missense_variant	MODERATE	ATP8	3.00E-04
HLI-0244	11087	T	C	0	604	missense_variant	MODERATE	ND4	0.0019
HLI-0244	15326	A	G	0	413	missense_variant	MODERATE	CYTB	0.9868
HLI-0244	16519	T	C	0	294	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0245	73	A	G	0	162	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0245	151	C	T	1	319	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0245	152	T	C	1	323	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0245	182	C	T	2	305	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0245	186	C	A	1	306	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0245	189	A	C	1	303	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0245	247	G	A	0	105	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0245	263	A	G	0	114	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0245	750	A	G	0	554	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0245	769	G	A	0	595	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0245	783	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	3.00E-04
HLI-0245	825	T	A	0	578	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0245	1018	G	A	0	612	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0245	1438	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0245	2706	A	G	1	540	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0245	2758	G	A	1	562	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0245	2885	T	C	0	592	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0245	3105	A	G	0	587	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0245	3594	C	T	0	459	synonymous_variant	LOW	ND1	0.0789
HLI-0245	3666	G	A	10	570	synonymous_variant	LOW	ND1	0.0233
HLI-0245	4104	A	G	0	510	synonymous_variant	LOW	ND1	0.0785
HLI-0245	4375	C	T	20	460	upstream_gene_variant	MODIFIER	TRNQ	1.00E-04
HLI-0245	4769	A	G	0	549	synonymous_variant	LOW	ND2	0.9767
HLI-0245	5951	A	G	2	631	synonymous_variant	LOW	COX1	0.0128
HLI-0245	6071	T	C	2	584	synonymous_variant	LOW	COX1	0.0129
HLI-0245	6221	T	A	1	545	synonymous_variant	LOW	COX1	0.0027
HLI-0245	6260	G	A	3	620	synonymous_variant	LOW	COX1	0.009
HLI-0245	6917	G	A	7	621	synonymous_variant	LOW	COX1	0.0036
HLI-0245	7028	C	T	1	564	synonymous_variant	LOW	COX1	0.8089
HLI-0245	7146	A	G	2	269	missense_variant	MODERATE	COX1	0.0497
HLI-0245	7256	C	T	5	397	synonymous_variant	LOW	COX1	0.0784

HLI-0245	7389	T	C	7	424	missense_variant	MODERATE	COX1	0.0201
HLI-0245	7498	G	A	2	316	upstream_gene_variant	MODIFIER	TRNS1	0.0019
HLI-0245	7521	G	A	1	362	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0245	7789	G	A	2	581	synonymous_variant	LOW	COX2	0.0092
HLI-0245	8027	G	A	5	541	missense_variant	MODERATE	COX2	0.0334
HLI-0245	8468	C	T	1	428	synonymous_variant	LOW	ATP8	0.0501
HLI-0245	8655	C	T	0	416	synonymous_variant	LOW	ATP6	0.0511
HLI-0245	8668	T	C	1	462	missense_variant	MODERATE	ATP6	7.00E-04
HLI-0245	8701	A	G	0	481	missense_variant	MODERATE	ATP6	0.3391
HLI-0245	9072	A	G	1	539	synonymous_variant	LOW	ATP6	0.0124
HLI-0245	9540	T	C	0	566	synonymous_variant	LOW	COX3	0.339
HLI-0245	9966	G	A	1	588	missense_variant	MODERATE	COX3	0.0069
HLI-0245	10398	A	G	0	609	missense_variant	MODERATE	ND3	0.445
HLI-0245	10586	G	A	3	562	synonymous_variant	LOW	ND4L	0.0177
HLI-0245	10688	G	A	1	499	synonymous_variant	LOW	ND4L	0.0515
HLI-0245	10810	T	C	1	526	synonymous_variant	LOW	ND4	0.0522
HLI-0245	10873	T	C	1	458	synonymous_variant	LOW	ND4	0.3389
HLI-0245	11302	C	T	5	567	synonymous_variant	LOW	ND4	0.0028
HLI-0245	11719	G	A	1	558	synonymous_variant	LOW	ND4	0.7756
HLI-0245	12019	C	T	4	542	synonymous_variant	LOW	ND4	0.0015
HLI-0245	12501	G	A	3	624	synonymous_variant	LOW	ND5	0.0258
HLI-0245	12705	C	T	0	583	synonymous_variant	LOW	ND5	0.4212
HLI-0245	12810	A	G	0	585	synonymous_variant	LOW	ND5	0.0198
HLI-0245	13105	A	G	0	512	missense_variant	MODERATE	ND5	0.076
HLI-0245	13485	A	G	1	597	synonymous_variant	LOW	ND5	0.0122
HLI-0245	13506	C	T	2	651	synonymous_variant	LOW	ND5	0.0506
HLI-0245	13650	C	T	0	513	synonymous_variant	LOW	ND5	0.079
HLI-0245	13789	T	C	2	385	missense_variant	MODERATE	ND5	0.0185
HLI-0245	14000	T	A	2	454	missense_variant	MODERATE	ND5	0.0126
HLI-0245	14178	T	C	1	519	missense_variant	MODERATE	ND6	0.0225
HLI-0245	14560	G	A	1	586	synonymous_variant	LOW	ND6	0.0235
HLI-0245	14766	C	T	3	502	missense_variant	MODERATE	CYTB	0.7696
HLI-0245	14911	C	T	4	589	synonymous_variant	LOW	CYTB	0.0124
HLI-0245	15226	A	G	2	558	synonymous_variant	LOW	CYTB	0.0034
HLI-0245	15326	A	G	0	502	missense_variant	MODERATE	CYTB	0.9868
HLI-0245	15905	T	C	0	632	upstream_gene_variant	MODIFIER	TRNT	0.005
HLI-0245	15978	C	T	4	629	upstream_gene_variant	MODIFIER	TRNP	0.0032
HLI-0245	16093	T	C	12	335	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0245	16129	G	A	0	255	upstream_gene_variant	MODIFIER	DLoop	0.1301

HLI-0245	16215	A	G	0	149	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0245	16223	C	T	1	160	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0245	16278	C	T	0	213	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0245	16294	C	T	0	234	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0245	16311	T	C	0	267	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0245	16327	C	T	0	288	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0245	16355	C	T	2	249	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0245	16360	C	T	3	263	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0245	16390	G	A	2	321	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0245	16519	T	C	0	115	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0246	263	A	G	0	256	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0246	750	A	G	1	536	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0246	1438	A	G	0	608	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0246	3010	G	A	0	620	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0246	4769	A	G	1	550	synonymous_variant	LOW	ND2	0.9767
HLI-0246	15326	A	G	0	479	missense_variant	MODERATE	CYTB	0.9868
HLI-0246	16239	C	T	6	529	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0246	16519	T	C	2	289	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0247	263	A	G	1	162	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0247	750	A	G	1	475	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0247	1438	A	G	1	526	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0247	4769	A	G	1	463	synonymous_variant	LOW	ND2	0.9767
HLI-0247	15326	A	G	0	461	missense_variant	MODERATE	CYTB	0.9868
HLI-0247	16304	T	C	0	398	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0248	73	A	G	0	276	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0248	146	T	C	0	474	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0248	152	T	C	0	491	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0248	195	T	C	2	468	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0248	263	A	G	2	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0248	750	A	G	0	658	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0248	769	G	A	0	680	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0248	1018	G	A	4	615	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0248	1438	A	G	0	621	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0248	1719	G	A	0	622	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0248	2416	T	C	4	596	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0248	2706	A	G	2	652	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0248	2789	C	T	3	686	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0248	3594	C	T	2	504	synonymous_variant	LOW	ND1	0.0789
HLI-0248	4104	A	G	2	576	synonymous_variant	LOW	ND1	0.0785

HLI-0248	4769	A	G	4	585	synonymous_variant	LOW	ND2	0.9767
HLI-0248	7028	C	T	3	651	synonymous_variant	LOW	COX1	0.8089
HLI-0248	7175	T	C	1	637	synonymous_variant	LOW	COX1	0.0224
HLI-0248	7256	C	T	4	595	synonymous_variant	LOW	COX1	0.0784
HLI-0248	7274	C	T	5	582	synonymous_variant	LOW	COX1	0.0214
HLI-0248	7521	G	A	1	477	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0248	7771	A	G	1	542	synonymous_variant	LOW	COX2	0.0223
HLI-0248	8206	G	A	5	533	synonymous_variant	LOW	COX2	0.0287
HLI-0248	8701	A	G	2	523	missense_variant	MODERATE	ATP6	0.3391
HLI-0248	9221	A	G	1	596	synonymous_variant	LOW	COX3	0.0277
HLI-0248	9540	T	C	2	573	synonymous_variant	LOW	COX3	0.339
HLI-0248	10115	T	C	1	734	synonymous_variant	LOW	ND3	0.0278
HLI-0248	10143	G	A	1	712	missense_variant	MODERATE	ND3	0.0075
HLI-0248	10398	A	G	5	602	missense_variant	MODERATE	ND3	0.445
HLI-0248	10873	T	C	0	596	synonymous_variant	LOW	ND4	0.3389
HLI-0248	11719	G	A	1	584	synonymous_variant	LOW	ND4	0.7756
HLI-0248	11914	G	A	2	696	synonymous_variant	LOW	ND4	0.1112
HLI-0248	11944	T	C	4	672	synonymous_variant	LOW	ND4	0.0331
HLI-0248	12693	A	G	1	665	synonymous_variant	LOW	ND5	0.0205
HLI-0248	12705	C	T	3	719	synonymous_variant	LOW	ND5	0.4212
HLI-0248	13590	G	A	4	547	synonymous_variant	LOW	ND5	0.0586
HLI-0248	13650	C	T	2	571	synonymous_variant	LOW	ND5	0.079
HLI-0248	13803	A	G	2	440	synonymous_variant	LOW	ND5	0.0216
HLI-0248	14566	A	G	1	551	synonymous_variant	LOW	ND6	0.0214
HLI-0248	14766	C	T	1	532	missense_variant	MODERATE	CYTB	0.7696
HLI-0248	15301	G	A	0	566	synonymous_variant	LOW	CYTB	0.2912
HLI-0248	15326	A	G	0	606	missense_variant	MODERATE	CYTB	0.9868
HLI-0248	15735	C	T	3	580	missense_variant	MODERATE	CYTB	0.0052
HLI-0248	15784	T	C	3	615	synonymous_variant	LOW	CYTB	0.0363
HLI-0248	16223	C	T	0	196	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0248	16278	C	T	3	330	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0248	16294	C	T	3	362	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0248	16309	A	G	2	403	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0248	16390	G	A	1	442	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0248	16519	T	C	1	157	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0249	73	A	G	0	144	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0249	93	A	G	0	162	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0249	146	T	C	0	258	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0249	150	C	T	0	270	upstream_gene_variant	MODIFIER	DLoop	0.1339

HLI-0249	152	T	C	0	269	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0249	182	C	T	1	293	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0249	195	T	C	1	274	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0249	198	C	T	1	277	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0249	263	A	G	1	165	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0249	325	C	T	2	185	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0249	680	T	C	1	595	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0249	709	G	A	1	661	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0249	750	A	G	1	647	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0249	769	G	A	0	632	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0249	1018	G	A	0	623	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0249	1438	A	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0249	1442	G	A	0	638	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0249	2332	C	T	0	599	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0249	2416	T	C	1	614	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0249	2706	A	G	0	598	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0249	3200	T	A	0	557	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0249	3594	C	T	0	520	synonymous_variant	LOW	ND1	0.0789
HLI-0249	3745	G	A	1	578	missense_variant	MODERATE	ND1	0.0021
HLI-0249	4104	A	G	0	562	synonymous_variant	LOW	ND1	0.0785
HLI-0249	4769	A	G	1	603	synonymous_variant	LOW	ND2	0.9767
HLI-0249	6272	A	G	0	605	synonymous_variant	LOW	COX1	0.0018
HLI-0249	7028	C	T	1	692	synonymous_variant	LOW	COX1	0.8089
HLI-0249	7256	C	T	3	579	synonymous_variant	LOW	COX1	0.0784
HLI-0249	7521	G	A	0	524	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0249	7624	T	A	0	628	synonymous_variant	LOW	COX2	0.0047
HLI-0249	8206	G	A	0	576	synonymous_variant	LOW	COX2	0.0287
HLI-0249	8701	A	G	0	542	missense_variant	MODERATE	ATP6	0.3391
HLI-0249	9221	A	G	1	580	synonymous_variant	LOW	COX3	0.0277
HLI-0249	9540	T	C	0	569	synonymous_variant	LOW	COX3	0.339
HLI-0249	10115	T	C	1	677	synonymous_variant	LOW	ND3	0.0278
HLI-0249	10398	A	G	0	695	missense_variant	MODERATE	ND3	0.445
HLI-0249	10873	T	C	0	612	synonymous_variant	LOW	ND4	0.3389
HLI-0249	11719	G	A	2	614	synonymous_variant	LOW	ND4	0.7756
HLI-0249	11944	T	C	1	554	synonymous_variant	LOW	ND4	0.0331
HLI-0249	12236	G	A	4	573	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0249	12705	C	T	2	597	synonymous_variant	LOW	ND5	0.4212
HLI-0249	13416	A	G	1	546	synonymous_variant	LOW	ND5	2.00E-04
HLI-0249	13590	G	A	0	540	synonymous_variant	LOW	ND5	0.0586

HLI-0249	13650	C	T	0	559	synonymous_variant	LOW	ND5	0.079
HLI-0249	13928	G	C	1	567	missense_variant	MODERATE	ND5	0.0484
HLI-0249	13958	G	C	0	621	missense_variant	MODERATE	ND5	0.0028
HLI-0249	14766	C	T	2	570	missense_variant	MODERATE	CYTB	0.7696
HLI-0249	15110	G	A	0	628	missense_variant	MODERATE	CYTB	0.009
HLI-0249	15217	G	A	0	585	synonymous_variant	LOW	CYTB	0.0104
HLI-0249	15301	G	A	0	612	synonymous_variant	LOW	CYTB	0.2912
HLI-0249	15326	A	G	0	606	missense_variant	MODERATE	CYTB	0.9868
HLI-0249	15849	C	T	3	626	missense_variant	MODERATE	CYTB	0.0027
HLI-0249	16223	C	T	0	570	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0249	16278	C	T	3	601	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0249	16318	A	G	0	525	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0249	16390	G	A	1	438	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0250	73	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0250	114	C	T	2	359	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0250	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0250	497	C	T	2	428	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0250	750	A	G	0	563	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0250	1189	T	C	1	609	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0250	1438	A	G	1	619	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0250	1811	A	G	1	536	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0250	2706	A	G	0	589	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0250	3480	A	G	1	556	synonymous_variant	LOW	ND1	0.0392
HLI-0250	4769	A	G	2	529	synonymous_variant	LOW	ND2	0.9767
HLI-0250	7028	C	T	0	588	synonymous_variant	LOW	COX1	0.8089
HLI-0250	9055	G	A	0	565	missense_variant	MODERATE	ATP6	0.0425
HLI-0250	9698	T	C	0	536	synonymous_variant	LOW	COX3	0.0405
HLI-0250	10398	A	G	2	653	missense_variant	MODERATE	ND3	0.445
HLI-0250	10550	A	G	0	593	synonymous_variant	LOW	ND4L	0.0376
HLI-0250	10978	A	G	0	384	synonymous_variant	LOW	ND4	0.0036
HLI-0250	11299	T	C	1	543	synonymous_variant	LOW	ND4	0.0417
HLI-0250	11467	A	G	0	565	synonymous_variant	LOW	ND4	0.1231
HLI-0250	11470	A	G	0	581	synonymous_variant	LOW	ND4	0.0029
HLI-0250	11719	G	A	1	545	synonymous_variant	LOW	ND4	0.7756
HLI-0250	11914	G	A	0	563	synonymous_variant	LOW	ND4	0.1112
HLI-0250	12308	A	G	1	519	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0250	12372	G	A	0	521	synonymous_variant	LOW	ND5	0.1329
HLI-0250	12954	T	C	2	554	synonymous_variant	LOW	ND5	0.0017
HLI-0250	14167	C	T	3	510	synonymous_variant	LOW	ND6	0.0385

HLI-0250	14766	C	T	5	522	missense_variant	MODERATE	CYTB	0.7696
HLI-0250	14798	T	C	0	597	missense_variant	MODERATE	CYTB	0.0651
HLI-0250	15326	A	G	1	504	missense_variant	MODERATE	CYTB	0.9868
HLI-0250	15924	A	G	0	606	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0250	16093	T	C	12	549	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0250	16223	C	T	0	542	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0250	16224	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0250	16234	C	T	1	536	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0250	16311	T	C	0	441	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0250	16519	T	C	0	198	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0251	73	A	G	45	186	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0251	146	T	C	87	381	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0251	152	T	C	0	464	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0251	263	A	G	0	241	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0251	750	A	G	0	454	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0251	1438	A	G	1	468	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0251	4769	A	G	2	571	synonymous_variant	LOW	ND2	0.9767
HLI-0251	7028	C	T	111	453	synonymous_variant	LOW	COX1	0.8089
HLI-0251	8014	A	G	101	435	synonymous_variant	LOW	COX2	0.001
HLI-0251	8701	A	G	95	417	missense_variant	MODERATE	ATP6	0.3391
HLI-0251	9540	T	C	81	346	synonymous_variant	LOW	COX3	0.339
HLI-0251	11914	G	A	89	422	synonymous_variant	LOW	ND4	0.1112
HLI-0251	11944	T	C	89	446	synonymous_variant	LOW	ND4	0.0331
HLI-0251	12693	A	G	119	481	synonymous_variant	LOW	ND5	0.0205
HLI-0251	12705	C	T	128	517	synonymous_variant	LOW	ND5	0.4212
HLI-0251	13803	A	G	61	264	synonymous_variant	LOW	ND5	0.0216
HLI-0251	15326	A	G	0	394	missense_variant	MODERATE	CYTB	0.9868
HLI-0251	15784	T	C	87	375	synonymous_variant	LOW	CYTB	0.0363
HLI-0252	73	A	G	0	284	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0252	146	T	C	2	500	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0252	242	C	T	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0252	263	A	G	0	200	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0252	295	C	T	0	174	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0252	462	C	T	2	267	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0252	489	T	C	0	308	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0252	750	A	G	1	604	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0252	1438	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0252	2158	T	C	0	591	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0252	2706	A	G	0	594	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0252	3010	G	A	1	560	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0252	4216	T	C	0	541	missense_variant	MODERATE	ND1	0.0991
HLI-0252	4769	A	G	5	556	synonymous_variant	LOW	ND2	0.9767
HLI-0252	5460	G	A	0	621	missense_variant	MODERATE	ND2	0.0651
HLI-0252	7028	C	T	1	663	synonymous_variant	LOW	COX1	0.8089
HLI-0252	8269	G	A	1	482	stop_retained_variant	LOW	COX2	0.0127
HLI-0252	8557	G	A	0	464	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0252	10398	A	G	1	623	missense_variant	MODERATE	ND3	0.445
HLI-0252	11251	A	G	2	608	synonymous_variant	LOW	ND4	0.0932
HLI-0252	11719	G	A	1	545	synonymous_variant	LOW	ND4	0.7756
HLI-0252	12007	G	A	0	551	synonymous_variant	LOW	ND4	0.0639
HLI-0252	12498	C	T	0	619	synonymous_variant	LOW	ND5	5.00E-04
HLI-0252	12612	A	G	1	559	synonymous_variant	LOW	ND5	0.0506
HLI-0252	13651	A	G	0	495	missense_variant	MODERATE	ND5	0.0053
HLI-0252	13708	G	A	0	280	missense_variant	MODERATE	ND5	0.0717
HLI-0252	13879	T	C	0	516	missense_variant	MODERATE	ND5	0.0073
HLI-0252	14766	C	T	0	518	missense_variant	MODERATE	CYTB	0.7696
HLI-0252	15326	A	G	0	531	missense_variant	MODERATE	CYTB	0.9868
HLI-0252	15452	C	A	2	538	missense_variant	MODERATE	CYTB	0.0933
HLI-0252	16069	C	T	2	569	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0252	16126	T	C	1	572	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0252	16145	G	A	0	552	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0252	16172	T	C	1	530	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0252	16222	C	T	2	540	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0252	16261	C	T	1	538	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0253	73	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0253	143	G	A	0	420	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0253	146	T	C	0	429	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0253	152	T	C	0	444	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0253	195	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0253	228	G	A	3	267	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0253	263	A	G	0	207	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0253	750	A	G	0	654	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0253	769	G	A	2	696	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0253	1018	G	A	1	652	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0253	1438	A	G	0	599	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0253	2416	T	C	1	605	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0253	2706	A	G	0	593	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0253	2789	C	T	3	677	upstream_gene_variant	MODIFIER	RNR2	0.0216

HLI-0253	3495	C	A	4	476	synonymous_variant	LOW	ND1	3.00E-04
HLI-0253	3594	C	T	2	527	synonymous_variant	LOW	ND1	0.0789
HLI-0253	4104	A	G	1	571	synonymous_variant	LOW	ND1	0.0785
HLI-0253	4769	A	G	3	589	synonymous_variant	LOW	ND2	0.9767
HLI-0253	7028	C	T	1	629	synonymous_variant	LOW	COX1	0.8089
HLI-0253	7175	T	C	1	627	synonymous_variant	LOW	COX1	0.0224
HLI-0253	7256	C	T	1	623	synonymous_variant	LOW	COX1	0.0784
HLI-0253	7274	C	T	0	592	synonymous_variant	LOW	COX1	0.0214
HLI-0253	7521	G	A	1	511	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0253	7771	A	G	0	544	synonymous_variant	LOW	COX2	0.0223
HLI-0253	8206	G	A	2	570	synonymous_variant	LOW	COX2	0.0287
HLI-0253	8701	A	G	0	543	missense_variant	MODERATE	ATP6	0.3391
HLI-0253	8790	G	A	1	524	synonymous_variant	LOW	ATP6	0.0083
HLI-0253	9221	A	G	0	599	synonymous_variant	LOW	COX3	0.0277
HLI-0253	9540	T	C	0	544	synonymous_variant	LOW	COX3	0.339
HLI-0253	9833	T	C	1	717	synonymous_variant	LOW	COX3	0.0013
HLI-0253	10115	T	C	0	685	synonymous_variant	LOW	ND3	0.0278
HLI-0253	10398	A	G	0	585	missense_variant	MODERATE	ND3	0.445
HLI-0253	10873	T	C	1	599	synonymous_variant	LOW	ND4	0.3389
HLI-0253	11719	G	A	0	622	synonymous_variant	LOW	ND4	0.7756
HLI-0253	11914	G	A	0	599	synonymous_variant	LOW	ND4	0.1112
HLI-0253	11944	T	C	1	645	synonymous_variant	LOW	ND4	0.0331
HLI-0253	12630	G	A	0	601	synonymous_variant	LOW	ND5	0.0053
HLI-0253	12693	A	G	0	691	synonymous_variant	LOW	ND5	0.0205
HLI-0253	12705	C	T	2	698	synonymous_variant	LOW	ND5	0.4212
HLI-0253	13590	G	A	1	638	synonymous_variant	LOW	ND5	0.0586
HLI-0253	13650	C	T	0	590	synonymous_variant	LOW	ND5	0.079
HLI-0253	13803	A	G	1	465	synonymous_variant	LOW	ND5	0.0216
HLI-0253	13818	T	C	1	511	synonymous_variant	LOW	ND5	6.00E-04
HLI-0253	14566	A	G	0	548	synonymous_variant	LOW	ND6	0.0214
HLI-0253	14766	C	T	3	525	missense_variant	MODERATE	CYTB	0.7696
HLI-0253	15190	C	T	3	603	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0253	15301	G	A	0	601	synonymous_variant	LOW	CYTB	0.2912
HLI-0253	15326	A	G	0	637	missense_variant	MODERATE	CYTB	0.9868
HLI-0253	15784	T	C	0	621	synonymous_variant	LOW	CYTB	0.0363
HLI-0253	15927	G	A	0	612	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0253	16223	C	T	3	610	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0253	16278	C	T	1	531	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0253	16294	C	T	0	509	upstream_gene_variant	MODIFIER	DLoop	0.0934

HLI-0253	16390	G	A	0	404	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0253	16519	T	C	0	233	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0254	73	A	G	0	276	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0254	263	A	G	2	243	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0254	282	T	C	0	203	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0254	750	A	G	1	515	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0254	1438	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0254	1811	A	G	1	545	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0254	2706	A	G	0	551	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0254	3738	C	T	3	550	synonymous_variant	LOW	ND1	0.0019
HLI-0254	4129	A	G	1	470	missense_variant	MODERATE	ND1	0.001
HLI-0254	4769	A	G	1	534	synonymous_variant	LOW	ND2	0.9767
HLI-0254	5240	A	G	1	481	synonymous_variant	LOW	ND2	0.0015
HLI-0254	6392	T	C	0	575	synonymous_variant	LOW	COX1	0.0359
HLI-0254	6455	C	T	1	600	synonymous_variant	LOW	COX1	0.0319
HLI-0254	7028	C	T	9	616	synonymous_variant	LOW	COX1	0.8089
HLI-0254	7055	A	G	5	678	synonymous_variant	LOW	COX1	0.0188
HLI-0254	9365	C	T	3	628	synonymous_variant	LOW	COX3	0.002
HLI-0254	9554	G	A	0	432	synonymous_variant	LOW	COX3	0.014
HLI-0254	9698	T	C	3	542	synonymous_variant	LOW	COX3	0.0405
HLI-0254	10733	C	T	0	516	synonymous_variant	LOW	ND4L	0.0016
HLI-0254	11467	A	G	2	601	synonymous_variant	LOW	ND4	0.1231
HLI-0254	11719	G	A	2	594	synonymous_variant	LOW	ND4	0.7756
HLI-0254	12135	C	A	3	383	missense_variant	MODERATE	ND4	0.0011
HLI-0254	12308	A	G	0	359	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0254	12372	G	A	1	366	synonymous_variant	LOW	ND5	0.1329
HLI-0254	13145	G	A	9	571	missense_variant	MODERATE	ND5	0.0094
HLI-0254	14766	C	T	2	495	missense_variant	MODERATE	CYTB	0.7696
HLI-0254	15326	A	G	0	468	missense_variant	MODERATE	CYTB	0.9868
HLI-0254	16209	T	C	0	544	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0254	16342	T	C	1	463	upstream_gene_variant	MODIFIER	DLoop	0.0042
HLI-0255	73	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0255	152	T	C	0	412	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0255	182	C	T	1	413	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0255	185	G	T	1	410	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0255	195	T	C	1	393	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0255	247	G	A	0	175	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0255	263	A	G	0	189	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0255	357	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.0057

HLI-0255	709	G	A	0	445	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0255	710	T	C	0	447	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0255	750	A	G	0	483	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0255	769	G	A	0	480	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0255	825	T	A	0	538	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0255	1018	G	A	1	624	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0255	1738	T	C	0	630	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0255	2352	T	C	0	462	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0255	2706	A	G	0	438	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0255	2758	G	A	0	491	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0255	2768	A	G	0	474	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0255	2885	T	C	0	518	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0255	3308	T	C	1	461	start_lost	HIGH	ND1	0.0073
HLI-0255	3594	C	T	2	384	synonymous_variant	LOW	ND1	0.0789
HLI-0255	3666	G	A	0	481	synonymous_variant	LOW	ND1	0.0233
HLI-0255	3693	G	A	0	485	synonymous_variant	LOW	ND1	0.0091
HLI-0255	4104	A	G	0	420	synonymous_variant	LOW	ND1	0.0785
HLI-0255	4769	A	G	1	556	synonymous_variant	LOW	ND2	0.9767
HLI-0255	5036	A	G	0	460	synonymous_variant	LOW	ND2	0.006
HLI-0255	5046	G	A	0	497	missense_variant	MODERATE	ND2	0.018
HLI-0255	5393	T	C	0	488	synonymous_variant	LOW	ND2	0.0059
HLI-0255	5655	T	C	0	610	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0255	6548	C	T	2	483	synonymous_variant	LOW	COX1	0.0061
HLI-0255	6827	T	C	0	537	synonymous_variant	LOW	COX1	0.0072
HLI-0255	6989	A	G	0	536	synonymous_variant	LOW	COX1	0.0061
HLI-0255	7028	C	T	3	545	synonymous_variant	LOW	COX1	0.8089
HLI-0255	7055	A	G	2	510	synonymous_variant	LOW	COX1	0.0188
HLI-0255	7146	A	G	1	256	missense_variant	MODERATE	COX1	0.0497
HLI-0255	7256	C	T	3	458	synonymous_variant	LOW	COX1	0.0784
HLI-0255	7389	T	C	1	443	missense_variant	MODERATE	COX1	0.0201
HLI-0255	7521	G	A	0	359	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0255	7867	C	T	1	554	synonymous_variant	LOW	COX2	0.0076
HLI-0255	8248	A	G	0	541	synonymous_variant	LOW	COX2	0.0061
HLI-0255	8468	C	T	3	429	synonymous_variant	LOW	ATP8	0.0501
HLI-0255	8655	C	T	2	423	synonymous_variant	LOW	ATP6	0.0511
HLI-0255	8701	A	G	0	485	missense_variant	MODERATE	ATP6	0.3391
HLI-0255	9540	T	C	1	463	synonymous_variant	LOW	COX3	0.339
HLI-0255	10398	A	G	0	538	missense_variant	MODERATE	ND3	0.445
HLI-0255	10688	G	A	0	491	synonymous_variant	LOW	ND4L	0.0515

HLI-0255	10810	T	C	0	536	synonymous_variant	LOW	ND4	0.0522
HLI-0255	10873	T	C	0	546	synonymous_variant	LOW	ND4	0.3389
HLI-0255	11719	G	A	1	521	synonymous_variant	LOW	ND4	0.7756
HLI-0255	12519	T	C	2	615	synonymous_variant	LOW	ND5	0.007
HLI-0255	12705	C	T	4	576	synonymous_variant	LOW	ND5	0.4212
HLI-0255	13105	A	G	0	494	missense_variant	MODERATE	ND5	0.076
HLI-0255	13506	C	T	0	446	synonymous_variant	LOW	ND5	0.0506
HLI-0255	13650	C	T	1	414	synonymous_variant	LOW	ND5	0.079
HLI-0255	13789	T	C	0	358	missense_variant	MODERATE	ND5	0.0185
HLI-0255	13880	C	A	2	413	missense_variant	MODERATE	ND5	0.0055
HLI-0255	14178	T	C	0	495	missense_variant	MODERATE	ND6	0.0225
HLI-0255	14203	A	G	0	538	synonymous_variant	LOW	ND6	0.0061
HLI-0255	14560	G	A	0	668	synonymous_variant	LOW	ND6	0.0235
HLI-0255	14766	C	T	1	571	missense_variant	MODERATE	CYTB	0.7696
HLI-0255	14769	A	G	1	589	missense_variant	MODERATE	CYTB	0.0121
HLI-0255	15115	T	C	1	585	synonymous_variant	LOW	CYTB	0.0093
HLI-0255	15326	A	G	0	369	missense_variant	MODERATE	CYTB	0.9868
HLI-0255	16126	T	C	1	603	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0255	16212	A	G	0	452	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0255	16223	C	T	1	424	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0255	16264	C	T	0	407	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0255	16270	C	T	0	402	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0255	16278	C	T	1	396	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0255	16311	T	C	1	379	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0255	16519	T	C	0	147	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0256	204	T	C	1	401	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0256	263	A	G	0	170	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0256	750	A	G	3	495	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0256	1438	A	G	1	515	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0256	3010	G	A	1	511	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0256	4769	A	G	2	530	synonymous_variant	LOW	ND2	0.9767
HLI-0256	5460	G	A	0	537	missense_variant	MODERATE	ND2	0.0651
HLI-0256	9377	A	G	0	590	synonymous_variant	LOW	COX3	0.0084
HLI-0256	9554	G	A	1	487	synonymous_variant	LOW	COX3	0.014
HLI-0256	15326	A	G	0	420	missense_variant	MODERATE	CYTB	0.9868
HLI-0256	15817	A	G	2	551	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0256	16519	T	C	1	199	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0257	263	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0257	750	A	G	0	576	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0257	1438	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0257	3010	G	A	1	579	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0257	3796	A	G	0	563	missense_variant	MODERATE	ND1	0.0048
HLI-0257	4769	A	G	0	512	synonymous_variant	LOW	ND2	0.9767
HLI-0257	6635	T	C	1	639	synonymous_variant	LOW	COX1	0.0012
HLI-0257	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0257	16172	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0257	16356	T	C	0	431	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0257	16362	T	C	0	455	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0257	16519	T	C	1	204	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0258	73	A	G	0	284	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0258	185	G	A	0	442	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0258	188	A	G	0	443	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0258	263	A	G	0	217	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0258	295	C	T	0	207	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0258	462	C	T	3	415	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0258	489	T	C	1	487	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0258	750	A	G	0	594	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0258	1438	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0258	2706	A	G	0	635	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0258	3010	G	A	2	611	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0258	4216	T	C	0	639	missense_variant	MODERATE	ND1	0.0991
HLI-0258	4769	A	G	0	605	synonymous_variant	LOW	ND2	0.9767
HLI-0258	7028	C	T	1	729	synonymous_variant	LOW	COX1	0.8089
HLI-0258	10398	A	G	1	612	missense_variant	MODERATE	ND3	0.445
HLI-0258	10876	A	G	0	575	synonymous_variant	LOW	ND4	0.0098
HLI-0258	11251	A	G	0	579	synonymous_variant	LOW	ND4	0.0932
HLI-0258	11719	G	A	0	612	synonymous_variant	LOW	ND4	0.7756
HLI-0258	12612	A	G	5	657	synonymous_variant	LOW	ND5	0.0506
HLI-0258	13708	G	A	0	515	missense_variant	MODERATE	ND5	0.0717
HLI-0258	13827	A	G	1	471	synonymous_variant	LOW	ND5	0.0047
HLI-0258	14766	C	T	2	552	missense_variant	MODERATE	CYTB	0.7696
HLI-0258	14798	T	C	1	613	missense_variant	MODERATE	CYTB	0.0651
HLI-0258	15326	A	G	1	550	missense_variant	MODERATE	CYTB	0.9868
HLI-0258	15452	C	A	4	544	missense_variant	MODERATE	CYTB	0.0933
HLI-0258	16069	C	T	1	633	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0258	16126	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0258	16519	T	C	1	286	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0259	263	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0259	750	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0259	1438	A	G	1	512	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0259	4769	A	G	1	516	synonymous_variant	LOW	ND2	0.9767
HLI-0259	11719	G	A	1	534	synonymous_variant	LOW	ND4	0.7756
HLI-0259	13827	A	G	0	422	synonymous_variant	LOW	ND5	0.0047
HLI-0259	15326	A	G	0	463	missense_variant	MODERATE	CYTB	0.9868
HLI-0259	16129	G	A	0	499	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0259	16291	C	T	0	493	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0259	16316	A	G	0	519	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0259	16519	T	C	0	196	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0260	73	A	G	0	279	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0260	195	T	C	0	423	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0260	215	A	G	2	431	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0260	263	A	G	1	139	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0260	499	G	A	1	267	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0260	629	T	C	1	545	upstream_gene_variant	MODIFIER	TRNF	0.0026
HLI-0260	750	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0260	1438	A	G	0	661	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0260	1811	A	G	0	553	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0260	2706	A	G	2	656	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0260	2772	C	T	2	627	upstream_gene_variant	MODIFIER	RNR2	0.0034
HLI-0260	4646	T	C	0	623	synonymous_variant	LOW	ND2	0.0124
HLI-0260	4769	A	G	0	583	synonymous_variant	LOW	ND2	0.9767
HLI-0260	5999	T	C	3	674	synonymous_variant	LOW	COX1	0.0127
HLI-0260	6047	A	G	3	698	synonymous_variant	LOW	COX1	0.0114
HLI-0260	7028	C	T	5	658	synonymous_variant	LOW	COX1	0.8089
HLI-0260	11332	C	T	0	598	synonymous_variant	LOW	ND4	0.0115
HLI-0260	11467	A	G	1	618	synonymous_variant	LOW	ND4	0.1231
HLI-0260	11719	G	A	1	612	synonymous_variant	LOW	ND4	0.7756
HLI-0260	12308	A	G	0	504	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0260	12372	G	A	1	549	synonymous_variant	LOW	ND5	0.1329
HLI-0260	13398	A	G	3	584	synonymous_variant	LOW	ND5	3.00E-04
HLI-0260	14620	C	T	3	577	synonymous_variant	LOW	ND6	0.0126
HLI-0260	14766	C	T	1	575	missense_variant	MODERATE	CYTB	0.7696
HLI-0260	15326	A	G	1	522	missense_variant	MODERATE	CYTB	0.9868
HLI-0260	15693	T	C	0	552	missense_variant	MODERATE	CYTB	0.0114
HLI-0260	16356	T	C	2	524	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0260	16519	T	C	0	255	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0261	263	A	G	0	183	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0261	480	T	C	1	397	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0261	750	A	G	0	577	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0261	1438	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0261	2706	A	G	2	611	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0261	4655	G	A	3	592	synonymous_variant	LOW	ND2	0.0072
HLI-0261	4769	A	G	0	575	synonymous_variant	LOW	ND2	0.9767
HLI-0261	7028	C	T	1	645	synonymous_variant	LOW	COX1	0.8089
HLI-0261	11830	T	C	0	579	synonymous_variant	LOW	ND4	3.00E-04
HLI-0261	15115	T	C	0	659	synonymous_variant	LOW	CYTB	0.0093
HLI-0261	15326	A	G	0	524	missense_variant	MODERATE	CYTB	0.9868
HLI-0261	16168	C	T	2	636	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0261	16169	C	T	2	637	upstream_gene_variant	MODIFIER	DLoop	0.0074
HLI-0261	16311	T	C	0	474	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0262	73	A	G	0	272	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0262	146	T	C	0	461	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0262	152	T	C	0	479	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0262	195	T	C	0	471	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0262	263	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0262	750	A	G	1	606	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0262	769	G	A	0	653	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0262	1018	G	A	1	621	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0262	1438	A	G	0	594	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0262	2416	T	C	1	668	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0262	2706	A	G	0	596	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0262	2789	C	T	2	644	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0262	3594	C	T	0	477	synonymous_variant	LOW	ND1	0.0789
HLI-0262	4104	A	G	0	490	synonymous_variant	LOW	ND1	0.0785
HLI-0262	4769	A	G	2	553	synonymous_variant	LOW	ND2	0.9767
HLI-0262	5581	A	G	0	599	upstream_gene_variant	MODIFIER	Unannotated	0.005
HLI-0262	7028	C	T	2	635	synonymous_variant	LOW	COX1	0.8089
HLI-0262	7175	T	C	0	563	synonymous_variant	LOW	COX1	0.0224
HLI-0262	7256	C	T	0	549	synonymous_variant	LOW	COX1	0.0784
HLI-0262	7274	C	T	2	546	synonymous_variant	LOW	COX1	0.0214
HLI-0262	7521	G	A	1	473	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0262	7771	A	G	0	518	synonymous_variant	LOW	COX2	0.0223
HLI-0262	8206	G	A	1	540	synonymous_variant	LOW	COX2	0.0287
HLI-0262	8668	T	C	0	519	missense_variant	MODERATE	ATP6	7.00E-04
HLI-0262	8701	A	G	0	545	missense_variant	MODERATE	ATP6	0.3391
HLI-0262	8764	G	A	0	552	missense_variant	MODERATE	ATP6	0.0016

HLI-0262	9221	A	G	0	557	synonymous_variant	LOW	COX3	0.0277
HLI-0262	9540	T	C	0	545	synonymous_variant	LOW	COX3	0.339
HLI-0262	10115	T	C	0	602	synonymous_variant	LOW	ND3	0.0278
HLI-0262	10398	A	G	0	585	missense_variant	MODERATE	ND3	0.445
HLI-0262	10873	T	C	0	494	synonymous_variant	LOW	ND4	0.3389
HLI-0262	11692	C	T	0	596	synonymous_variant	LOW	ND4	2.00E-04
HLI-0262	11719	G	A	1	636	synonymous_variant	LOW	ND4	0.7756
HLI-0262	11914	G	A	0	565	synonymous_variant	LOW	ND4	0.1112
HLI-0262	11944	T	C	1	603	synonymous_variant	LOW	ND4	0.0331
HLI-0262	12693	A	G	1	641	synonymous_variant	LOW	ND5	0.0205
HLI-0262	12705	C	T	1	694	synonymous_variant	LOW	ND5	0.4212
HLI-0262	13590	G	A	0	523	synonymous_variant	LOW	ND5	0.0586
HLI-0262	13650	C	T	2	542	synonymous_variant	LOW	ND5	0.079
HLI-0262	13803	A	G	0	442	synonymous_variant	LOW	ND5	0.0216
HLI-0262	14766	C	T	3	528	missense_variant	MODERATE	CYTB	0.7696
HLI-0262	15301	G	A	0	553	synonymous_variant	LOW	CYTB	0.2912
HLI-0262	15326	A	G	0	601	missense_variant	MODERATE	CYTB	0.9868
HLI-0262	15784	T	C	0	586	synonymous_variant	LOW	CYTB	0.0363
HLI-0262	16114	C	T	4	409	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0262	16173	C	T	6	251	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0262	16223	C	T	5	299	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0262	16278	C	T	0	379	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0262	16294	C	T	0	409	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0262	16309	A	G	0	432	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0262	16390	G	A	0	438	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0262	16519	T	C	0	220	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0263	64	C	T	0	229	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0263	93	A	G	0	326	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0263	152	T	C	0	391	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0263	189	A	G	0	391	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0263	204	T	C	0	385	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0263	207	G	A	0	381	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0263	236	T	C	1	398	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0263	247	G	A	1	388	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0263	263	A	G	1	377	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0263	750	A	G	0	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0263	769	G	A	0	643	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0263	825	T	A	0	667	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0263	1018	G	A	1	689	upstream_gene_variant	MODIFIER	RNR1	0.0817

HLI-0263	1048	C	T	2	751	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0263	1438	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0263	2245	A	G	0	438	upstream_gene_variant	MODIFIER	RNR2	0.0145
HLI-0263	2706	A	G	0	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0263	2758	G	A	0	621	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0263	2885	T	C	0	626	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0263	3516	C	A	12	523	synonymous_variant	LOW	ND1	0.0315
HLI-0263	3594	C	T	0	523	synonymous_variant	LOW	ND1	0.0789
HLI-0263	4104	A	G	1	452	synonymous_variant	LOW	ND1	0.0785
HLI-0263	4312	C	T	0	409	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0263	4586	T	C	0	603	synonymous_variant	LOW	ND2	0.018
HLI-0263	4769	A	G	1	531	synonymous_variant	LOW	ND2	0.9767
HLI-0263	4907	T	C	2	531	synonymous_variant	LOW	ND2	0.0047
HLI-0263	5147	G	A	0	461	synonymous_variant	LOW	ND2	0.0437
HLI-0263	5231	G	A	0	540	synonymous_variant	LOW	ND2	0.0232
HLI-0263	5442	T	C	1	571	missense_variant	MODERATE	ND2	0.0493
HLI-0263	5460	G	A	0	604	missense_variant	MODERATE	ND2	0.0651
HLI-0263	5603	C	T	1	643	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0263	5711	A	G	0	648	upstream_gene_variant	MODIFIER	TRNN	0.008
HLI-0263	6185	T	C	1	593	synonymous_variant	LOW	COX1	0.0325
HLI-0263	6257	G	A	0	647	synonymous_variant	LOW	COX1	0.0085
HLI-0263	7028	C	T	1	579	synonymous_variant	LOW	COX1	0.8089
HLI-0263	7146	A	G	0	333	missense_variant	MODERATE	COX1	0.0497
HLI-0263	7256	C	T	6	472	synonymous_variant	LOW	COX1	0.0784
HLI-0263	7521	G	A	2	371	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0263	8428	C	T	4	418	synonymous_variant	LOW	ATP8	0.0144
HLI-0263	8460	A	G	1	446	missense_variant	MODERATE	ATP8	0.0085
HLI-0263	8468	C	T	0	437	synonymous_variant	LOW	ATP8	0.0501
HLI-0263	8566	A	G	2	434	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0263	8655	C	T	2	453	synonymous_variant	LOW	ATP6	0.0511
HLI-0263	8701	A	G	3	535	missense_variant	MODERATE	ATP6	0.3391
HLI-0263	9042	C	T	2	588	synonymous_variant	LOW	ATP6	0.0316
HLI-0263	9347	A	G	0	589	synonymous_variant	LOW	COX3	0.0314
HLI-0263	9540	T	C	0	564	synonymous_variant	LOW	COX3	0.339
HLI-0263	9545	A	G	0	570	synonymous_variant	LOW	COX3	0.0469
HLI-0263	9554	G	A	0	557	synonymous_variant	LOW	COX3	0.014
HLI-0263	9755	G	A	1	636	synonymous_variant	LOW	COX3	0.0303
HLI-0263	9818	C	T	1	751	synonymous_variant	LOW	COX3	0.0179
HLI-0263	10398	A	G	0	538	missense_variant	MODERATE	ND3	0.445

HLI-0263	10589	G	A	1	536	synonymous_variant	LOW	ND4L	0.0355
HLI-0263	10664	C	T	1	615	synonymous_variant	LOW	ND4L	0.0315
HLI-0263	10688	G	A	0	601	synonymous_variant	LOW	ND4L	0.0515
HLI-0263	10810	T	C	1	487	synonymous_variant	LOW	ND4	0.0522
HLI-0263	10873	T	C	0	551	synonymous_variant	LOW	ND4	0.3389
HLI-0263	10915	T	C	1	526	synonymous_variant	LOW	ND4	0.0411
HLI-0263	11143	C	T	2	533	synonymous_variant	LOW	ND4	0.0076
HLI-0263	11172	A	G	0	625	missense_variant	MODERATE	ND4	0.0086
HLI-0263	11176	G	A	0	629	synonymous_variant	LOW	ND4	0.0181
HLI-0263	11641	A	G	2	605	synonymous_variant	LOW	ND4	0.0158
HLI-0263	11719	G	A	3	619	synonymous_variant	LOW	ND4	0.7756
HLI-0263	11914	G	A	2	558	synonymous_variant	LOW	ND4	0.1112
HLI-0263	12007	G	A	3	532	synonymous_variant	LOW	ND4	0.0639
HLI-0263	12705	C	T	0	554	synonymous_variant	LOW	ND5	0.4212
HLI-0263	12720	A	G	3	593	synonymous_variant	LOW	ND5	0.0302
HLI-0263	13105	A	G	1	537	missense_variant	MODERATE	ND5	0.076
HLI-0263	13116	C	T	1	589	synonymous_variant	LOW	ND5	0.0047
HLI-0263	13276	A	G	0	623	missense_variant	MODERATE	ND5	0.0312
HLI-0263	13506	C	T	1	503	synonymous_variant	LOW	ND5	0.0506
HLI-0263	13650	C	T	1	531	synonymous_variant	LOW	ND5	0.079
HLI-0263	14308	T	C	0	584	synonymous_variant	LOW	ND6	0.0209
HLI-0263	14755	A	G	0	612	synonymous_variant	LOW	CYTB	0.0074
HLI-0263	14766	C	T	2	656	missense_variant	MODERATE	CYTB	0.7696
HLI-0263	15136	C	T	1	656	synonymous_variant	LOW	CYTB	0.0153
HLI-0263	15326	A	G	0	470	missense_variant	MODERATE	CYTB	0.9868
HLI-0263	15431	G	A	1	448	missense_variant	MODERATE	CYTB	0.0182
HLI-0263	16148	C	T	0	507	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0263	16172	T	C	0	488	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0263	16223	C	T	0	448	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0263	16230	A	G	0	446	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0263	16311	T	C	0	432	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0263	16320	C	T	0	434	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0263	16519	T	C	0	187	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0264	73	A	G	0	277	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0264	204	T	C	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0264	263	A	G	0	256	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0264	709	G	A	2	642	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0264	750	A	G	1	682	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0264	1438	A	G	0	636	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0264	1888	G	A	2	582	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0264	2706	A	G	0	598	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0264	4216	T	C	0	548	missense_variant	MODERATE	ND1	0.0991
HLI-0264	4769	A	G	0	559	synonymous_variant	LOW	ND2	0.9767
HLI-0264	4917	A	G	4	550	missense_variant	MODERATE	ND2	0.0477
HLI-0264	6152	T	C	5	588	synonymous_variant	LOW	COX1	0.0077
HLI-0264	7028	C	T	0	647	synonymous_variant	LOW	COX1	0.8089
HLI-0264	8697	G	A	2	539	synonymous_variant	LOW	ATP6	0.0466
HLI-0264	8703	C	T	3	567	synonymous_variant	LOW	ATP6	0.0033
HLI-0264	10463	T	C	2	611	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0264	11251	A	G	0	585	synonymous_variant	LOW	ND4	0.0932
HLI-0264	11719	G	A	1	596	synonymous_variant	LOW	ND4	0.7756
HLI-0264	12633	C	A	2	582	synonymous_variant	LOW	ND5	0.0123
HLI-0264	13368	G	A	0	607	synonymous_variant	LOW	ND5	0.0495
HLI-0264	14766	C	T	4	550	missense_variant	MODERATE	CYTB	0.7696
HLI-0264	14905	G	A	1	620	synonymous_variant	LOW	CYTB	0.0526
HLI-0264	15326	A	G	1	505	missense_variant	MODERATE	CYTB	0.9868
HLI-0264	15452	C	A	7	520	missense_variant	MODERATE	CYTB	0.0933
HLI-0264	15607	A	G	2	589	synonymous_variant	LOW	CYTB	0.0508
HLI-0264	15928	G	A	0	603	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0264	16126	T	C	0	524	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0264	16163	A	G	0	564	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0264	16294	C	T	3	511	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0264	16390	G	A	0	470	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0264	16519	T	C	0	304	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0265	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0265	750	A	G	2	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0265	1438	A	G	1	631	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0265	3010	G	A	0	650	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0265	4769	A	G	3	569	synonymous_variant	LOW	ND2	0.9767
HLI-0265	5539	A	G	100	572	upstream_gene_variant	MODIFIER	TRNW	2.00E-04
HLI-0265	8602	T	C	0	554	missense_variant	MODERATE	ATP6	0.0017
HLI-0265	14212	T	C	1	578	synonymous_variant	LOW	ND6	0.0204
HLI-0265	15326	A	G	0	549	missense_variant	MODERATE	CYTB	0.9868
HLI-0265	16519	T	C	1	222	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0266	72	T	C	0	262	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0266	263	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0266	750	A	G	1	577	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0266	1438	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0266	2706	A	G	0	591	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0266	4580	G	A	1	512	synonymous_variant	LOW	ND2	0.0169
HLI-0266	4769	A	G	0	546	synonymous_variant	LOW	ND2	0.9767
HLI-0266	7028	C	T	5	642	synonymous_variant	LOW	COX1	0.8089
HLI-0266	13105	A	G	4	524	missense_variant	MODERATE	ND5	0.076
HLI-0266	13260	T	C	2	631	synonymous_variant	LOW	ND5	0.0017
HLI-0266	15326	A	G	0	533	missense_variant	MODERATE	CYTB	0.9868
HLI-0266	15904	C	T	0	571	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0266	16129	G	A	1	479	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0266	16298	T	C	0	441	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0267	73	A	G	0	34	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0267	199	T	C	0	42	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0267	250	T	C	0	23	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0267	263	A	G	0	23	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0267	750	A	G	0	32	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0267	1719	G	A	0	34	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0267	2706	A	G	0	44	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0267	4529	A	T	0	56	synonymous_variant	LOW	ND2	0.015
HLI-0267	4769	A	G	0	52	synonymous_variant	LOW	ND2	0.9767
HLI-0267	7028	C	T	0	48	synonymous_variant	LOW	COX1	0.8089
HLI-0267	8251	G	A	0	44	synonymous_variant	LOW	COX2	0.058
HLI-0267	8519	G	A	0	44	missense_variant	MODERATE	ATP8	0.0024
HLI-0267	10034	T	C	0	63	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0267	10238	T	C	0	58	synonymous_variant	LOW	ND3	0.0623
HLI-0267	10398	A	G	0	53	missense_variant	MODERATE	ND3	0.445
HLI-0267	10819	A	G	0	54	synonymous_variant	LOW	ND4	0.0228
HLI-0267	11719	G	A	0	58	synonymous_variant	LOW	ND4	0.7756
HLI-0267	12501	G	A	0	56	synonymous_variant	LOW	ND5	0.0258
HLI-0267	12705	C	T	0	37	synonymous_variant	LOW	ND5	0.4212
HLI-0267	13780	A	G	0	38	missense_variant	MODERATE	ND5	0.0179
HLI-0267	14766	C	T	0	47	missense_variant	MODERATE	CYTB	0.7696
HLI-0267	14861	G	A	0	46	missense_variant	MODERATE	CYTB	0.0029
HLI-0267	15043	G	A	0	43	synonymous_variant	LOW	CYTB	0.2362
HLI-0267	15326	A	G	0	46	missense_variant	MODERATE	CYTB	0.9868
HLI-0267	15773	G	A	0	49	missense_variant	MODERATE	CYTB	0.0011
HLI-0267	15924	A	G	0	42	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0267	16093	T	C	3	31	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0267	16129	G	A	0	34	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0267	16223	C	T	0	39	upstream_gene_variant	MODIFIER	DLoop	0.4009

HLI-0267	16304	T	C	0	36	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0267	16391	G	A	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0267	16519	T	C	0	19	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0268	73	A	G	1	273	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0268	185	G	A	1	413	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0268	188	A	G	1	414	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0268	228	G	A	2	302	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0268	263	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0268	295	C	T	0	166	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0268	462	C	T	1	434	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0268	489	T	C	0	497	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0268	750	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0268	1438	A	G	1	635	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0268	2706	A	G	0	566	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0268	3010	G	A	0	596	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0268	4216	T	C	0	588	missense_variant	MODERATE	ND1	0.0991
HLI-0268	4769	A	G	2	540	synonymous_variant	LOW	ND2	0.9767
HLI-0268	6293	T	C	0	610	synonymous_variant	LOW	COX1	0.0036
HLI-0268	7028	C	T	0	646	synonymous_variant	LOW	COX1	0.8089
HLI-0268	10398	A	G	0	572	missense_variant	MODERATE	ND3	0.445
HLI-0268	11251	A	G	0	658	synonymous_variant	LOW	ND4	0.0932
HLI-0268	11719	G	A	0	562	synonymous_variant	LOW	ND4	0.7756
HLI-0268	12612	A	G	3	580	synonymous_variant	LOW	ND5	0.0506
HLI-0268	13708	G	A	1	510	missense_variant	MODERATE	ND5	0.0717
HLI-0268	14766	C	T	3	611	missense_variant	MODERATE	CYTB	0.7696
HLI-0268	14798	T	C	0	637	missense_variant	MODERATE	CYTB	0.0651
HLI-0268	15326	A	G	0	492	missense_variant	MODERATE	CYTB	0.9868
HLI-0268	15452	C	A	5	554	missense_variant	MODERATE	CYTB	0.0933
HLI-0268	16069	C	T	3	613	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0268	16126	T	C	0	589	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0268	16138	A	C	0	585	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0268	16519	T	C	0	277	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0269	58	T	C	0	195	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0269	64	C	T	0	217	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0269	146	T	C	0	433	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0269	263	A	G	0	134	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0269	750	A	G	0	540	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0269	827	A	G	1	530	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0269	1438	A	G	0	521	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0269	2442	T	C	3	477	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0269	2706	A	G	0	541	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0269	3847	T	C	0	478	synonymous_variant	LOW	ND1	0.0061
HLI-0269	4659	G	A	1	542	missense_variant	MODERATE	ND2	0.0013
HLI-0269	4769	A	G	4	496	synonymous_variant	LOW	ND2	0.9767
HLI-0269	7028	C	T	1	616	synonymous_variant	LOW	COX1	0.8089
HLI-0269	8292	G	A	0	463	upstream_gene_variant	MODIFIER	Unannotated	0.0024
HLI-0269	11761	C	T	1	517	synonymous_variant	LOW	ND4	0.0016
HLI-0269	13188	C	T	9	522	synonymous_variant	LOW	ND5	0.0053
HLI-0269	14766	C	T	1	510	missense_variant	MODERATE	CYTB	0.7696
HLI-0269	15326	A	G	0	476	missense_variant	MODERATE	CYTB	0.9868
HLI-0269	16126	T	C	2	492	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0269	16355	C	T	0	398	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0269	16362	T	C	0	397	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0270	263	A	G	0	166	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0270	750	A	G	0	538	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0270	10810	T	C	0	585	synonymous_variant	LOW	ND4	0.0522
HLI-0270	15326	A	G	0	514	missense_variant	MODERATE	CYTB	0.9868
HLI-0270	15511	T	C	0	486	synonymous_variant	LOW	CYTB	0.0023
HLI-0270	16274	G	A	0	461	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0270	16519	T	C	0	257	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0271	263	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0271	750	A	G	0	544	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0271	1438	A	G	1	595	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0271	3010	G	A	0	581	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0271	4769	A	G	2	514	synonymous_variant	LOW	ND2	0.9767
HLI-0271	8251	G	A	3	503	synonymous_variant	LOW	COX2	0.058
HLI-0271	15326	A	G	0	522	missense_variant	MODERATE	CYTB	0.9868
HLI-0271	16080	A	G	0	427	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0271	16335	A	G	1	341	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0271	16356	T	C	1	386	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0272	73	A	G	0	155	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0272	152	T	C	0	278	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0272	182	C	T	0	283	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0272	185	G	T	0	280	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0272	195	T	C	0	281	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0272	247	G	A	0	134	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0272	263	A	G	0	140	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0272	357	A	G	1	180	upstream_gene_variant	MODIFIER	DLoop	0.0057

HLI-0272	709	G	A	0	363	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0272	710	T	C	0	363	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0272	750	A	G	1	384	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0272	769	G	A	1	384	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0272	825	T	A	0	443	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0272	1018	G	A	0	510	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0272	1738	T	C	0	479	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0272	2352	T	C	1	382	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0272	2706	A	G	0	397	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0272	2758	G	A	0	418	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0272	2768	A	G	0	418	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0272	2885	T	C	0	437	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0272	3308	T	C	0	408	start_lost	HIGH	ND1	0.0073
HLI-0272	3594	C	T	0	300	synonymous_variant	LOW	ND1	0.0789
HLI-0272	3666	G	A	2	398	synonymous_variant	LOW	ND1	0.0233
HLI-0272	3693	G	A	0	400	synonymous_variant	LOW	ND1	0.0091
HLI-0272	4104	A	G	0	327	synonymous_variant	LOW	ND1	0.0785
HLI-0272	4769	A	G	0	454	synonymous_variant	LOW	ND2	0.9767
HLI-0272	5036	A	G	1	410	synonymous_variant	LOW	ND2	0.006
HLI-0272	5046	G	A	1	437	missense_variant	MODERATE	ND2	0.018
HLI-0272	5393	T	C	0	419	synonymous_variant	LOW	ND2	0.0059
HLI-0272	5655	T	C	0	491	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0272	5806	T	C	0	495	upstream_gene_variant	MODIFIER	TRNC	4.00E-04
HLI-0272	6378	T	C	1	432	synonymous_variant	LOW	COX1	0.0011
HLI-0272	6548	C	T	1	423	synonymous_variant	LOW	COX1	0.0061
HLI-0272	6827	T	C	1	431	synonymous_variant	LOW	COX1	0.0072
HLI-0272	6989	A	G	3	487	synonymous_variant	LOW	COX1	0.0061
HLI-0272	7028	C	T	3	464	synonymous_variant	LOW	COX1	0.8089
HLI-0272	7055	A	G	3	397	synonymous_variant	LOW	COX1	0.0188
HLI-0272	7146	A	G	0	220	missense_variant	MODERATE	COX1	0.0497
HLI-0272	7256	C	T	3	346	synonymous_variant	LOW	COX1	0.0784
HLI-0272	7389	T	C	0	337	missense_variant	MODERATE	COX1	0.0201
HLI-0272	7521	G	A	0	252	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0272	7632	T	C	0	385	missense_variant	MODERATE	COX2	0
HLI-0272	7867	C	T	2	512	synonymous_variant	LOW	COX2	0.0076
HLI-0272	8248	A	G	1	412	synonymous_variant	LOW	COX2	0.0061
HLI-0272	8468	C	T	3	317	synonymous_variant	LOW	ATP8	0.0501
HLI-0272	8655	C	T	3	366	synonymous_variant	LOW	ATP6	0.0511
HLI-0272	8701	A	G	0	431	missense_variant	MODERATE	ATP6	0.3391

HLI-0272	9540	T	C	0	351	synonymous_variant	LOW	COX3	0.339
HLI-0272	10398	A	G	0	413	missense_variant	MODERATE	ND3	0.445
HLI-0272	10481	T	C	0	430	synonymous_variant	LOW	ND4L	1.00E-04
HLI-0272	10688	G	A	0	398	synonymous_variant	LOW	ND4L	0.0515
HLI-0272	10810	T	C	0	415	synonymous_variant	LOW	ND4	0.0522
HLI-0272	10873	T	C	0	448	synonymous_variant	LOW	ND4	0.3389
HLI-0272	11719	G	A	0	392	synonymous_variant	LOW	ND4	0.7756
HLI-0272	12519	T	C	0	505	synonymous_variant	LOW	ND5	0.007
HLI-0272	12705	C	T	4	473	synonymous_variant	LOW	ND5	0.4212
HLI-0272	13105	A	G	0	365	missense_variant	MODERATE	ND5	0.076
HLI-0272	13506	C	T	1	414	synonymous_variant	LOW	ND5	0.0506
HLI-0272	13650	C	T	2	348	synonymous_variant	LOW	ND5	0.079
HLI-0272	13789	T	C	1	248	missense_variant	MODERATE	ND5	0.0185
HLI-0272	13880	C	A	4	368	missense_variant	MODERATE	ND5	0.0055
HLI-0272	14178	T	C	0	475	missense_variant	MODERATE	ND6	0.0225
HLI-0272	14203	A	G	1	518	synonymous_variant	LOW	ND6	0.0061
HLI-0272	14560	G	A	0	425	synonymous_variant	LOW	ND6	0.0235
HLI-0272	14766	C	T	0	431	missense_variant	MODERATE	CYTB	0.7696
HLI-0272	14769	A	G	0	444	missense_variant	MODERATE	CYTB	0.0121
HLI-0272	15115	T	C	1	471	synonymous_variant	LOW	CYTB	0.0093
HLI-0272	15326	A	G	0	306	missense_variant	MODERATE	CYTB	0.9868
HLI-0272	16126	T	C	1	449	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0272	16223	C	T	1	297	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0272	16264	C	T	0	250	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0272	16270	C	T	0	241	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0272	16278	C	T	0	244	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0272	16311	T	C	1	237	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0272	16519	T	C	0	111	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0273	239	T	C	0	204	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0273	263	A	G	0	188	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0273	750	A	G	3	531	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0273	1438	A	G	2	557	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0273	3915	G	A	0	501	synonymous_variant	LOW	ND1	0.0106
HLI-0273	4727	A	G	4	476	synonymous_variant	LOW	ND2	0.0063
HLI-0273	4769	A	G	1	532	synonymous_variant	LOW	ND2	0.9767
HLI-0273	9380	G	A	1	543	synonymous_variant	LOW	COX3	0.0094
HLI-0273	10589	G	A	0	513	synonymous_variant	LOW	ND4L	0.0355
HLI-0273	14007	A	G	0	420	synonymous_variant	LOW	ND5	0.0052
HLI-0273	15326	A	G	1	484	missense_variant	MODERATE	CYTB	0.9868

HLI-0273	16362	T	C	0	402	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0274	263	A	G	0	148	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0274	750	A	G	1	490	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0274	1438	A	G	0	507	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0274	2259	C	T	0	507	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0274	4745	A	G	1	537	synonymous_variant	LOW	ND2	0.0039
HLI-0274	4769	A	G	0	580	synonymous_variant	LOW	ND2	0.9767
HLI-0274	7337	G	A	0	592	synonymous_variant	LOW	COX1	0.0119
HLI-0274	12397	A	G	1	410	missense_variant	MODERATE	ND5	0.0069
HLI-0274	13326	T	C	0	513	synonymous_variant	LOW	ND5	0.0032
HLI-0274	13680	C	T	3	416	synonymous_variant	LOW	ND5	0.005
HLI-0274	14872	C	T	3	538	synonymous_variant	LOW	CYTB	0.0061
HLI-0274	15326	A	G	0	485	missense_variant	MODERATE	CYTB	0.9868
HLI-0275	73	A	G	0	22	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0275	150	C	T	0	60	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0275	200	A	G	0	54	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0275	263	A	G	1	31	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0275	750	A	G	0	58	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0275	1438	A	G	0	36	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0275	2352	T	C	1	26	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0275	2416	T	C	0	32	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0275	2706	A	G	1	41	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0275	4769	A	G	0	59	synonymous_variant	LOW	ND2	0.9767
HLI-0275	6221	T	C	0	39	synonymous_variant	LOW	COX1	0.0306
HLI-0275	6587	C	T	0	51	synonymous_variant	LOW	COX1	0.0084
HLI-0275	7028	C	T	1	76	synonymous_variant	LOW	COX1	0.8089
HLI-0275	8701	A	G	0	48	missense_variant	MODERATE	ATP6	0.3391
HLI-0275	9540	T	C	0	40	synonymous_variant	LOW	COX3	0.339
HLI-0275	9932	G	A	0	43	synonymous_variant	LOW	COX3	0.0062
HLI-0275	10398	A	G	1	45	missense_variant	MODERATE	ND3	0.445
HLI-0275	10819	A	G	0	45	synonymous_variant	LOW	ND4	0.0228
HLI-0275	10873	T	C	0	48	synonymous_variant	LOW	ND4	0.3389
HLI-0275	11719	G	A	1	53	synonymous_variant	LOW	ND4	0.7756
HLI-0275	12705	C	T	0	53	synonymous_variant	LOW	ND5	0.4212
HLI-0275	14152	A	G	0	53	synonymous_variant	LOW	ND6	0.0086
HLI-0275	14212	T	C	0	51	synonymous_variant	LOW	ND6	0.0204
HLI-0275	14766	C	T	0	57	missense_variant	MODERATE	CYTB	0.7696
HLI-0275	15301	G	A	0	50	synonymous_variant	LOW	CYTB	0.2912
HLI-0275	15326	A	G	0	49	missense_variant	MODERATE	CYTB	0.9868

HLI-0275	15670	T	C	0	43	synonymous_variant	LOW	CYTB	0.0176
HLI-0275	15942	T	C	0	44	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0275	16223	C	T	0	25	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0275	16327	C	T	0	49	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0275	16343	A	T	0	50	upstream_gene_variant	MODIFIER	DLoop	3.00E-04
HLI-0276	73	A	G	0	8	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0276	93	A	G	0	12	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0276	146	T	C	0	24	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0276	150	C	T	0	27	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0276	152	T	C	0	26	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0276	182	C	T	0	30	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0276	195	T	C	0	29	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0276	198	C	T	0	29	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0276	263	A	G	0	19	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0276	325	C	T	0	18	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0276	680	T	C	0	51	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0276	709	G	A	0	55	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0276	750	A	G	0	42	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0276	769	G	A	0	43	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0276	1018	G	A	0	42	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0276	1438	A	G	0	44	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0276	1442	G	A	0	44	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0276	2332	C	T	0	30	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0276	2416	T	C	0	24	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0276	2706	A	G	0	37	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0276	2857	T	C	0	50	upstream_gene_variant	MODIFIER	RNR2	9.00E-04
HLI-0276	3200	T	A	0	47	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0276	3594	C	T	0	42	synonymous_variant	LOW	ND1	0.0789
HLI-0276	4104	A	G	0	25	synonymous_variant	LOW	ND1	0.0785
HLI-0276	4769	A	G	0	36	synonymous_variant	LOW	ND2	0.9767
HLI-0276	7028	C	T	0	65	synonymous_variant	LOW	COX1	0.8089
HLI-0276	7256	C	T	0	40	synonymous_variant	LOW	COX1	0.0784
HLI-0276	7521	G	A	0	24	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0276	7624	T	A	0	35	synonymous_variant	LOW	COX2	0.0047
HLI-0276	8206	G	A	0	37	synonymous_variant	LOW	COX2	0.0287
HLI-0276	8701	A	G	0	32	missense_variant	MODERATE	ATP6	0.3391
HLI-0276	9221	A	G	0	48	synonymous_variant	LOW	COX3	0.0277
HLI-0276	9540	T	C	0	40	synonymous_variant	LOW	COX3	0.339
HLI-0276	10115	T	C	0	50	synonymous_variant	LOW	ND3	0.0278

HLI-0276	10398	A	G	0	48	missense_variant	MODERATE	ND3	0.445
HLI-0276	10873	T	C	0	49	synonymous_variant	LOW	ND4	0.3389
HLI-0276	11719	G	A	0	46	synonymous_variant	LOW	ND4	0.7756
HLI-0276	11944	T	C	0	44	synonymous_variant	LOW	ND4	0.0331
HLI-0276	12236	G	A	0	39	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0276	12705	C	T	0	46	synonymous_variant	LOW	ND5	0.4212
HLI-0276	13590	G	A	0	45	synonymous_variant	LOW	ND5	0.0586
HLI-0276	13650	C	T	0	37	synonymous_variant	LOW	ND5	0.079
HLI-0276	13928	G	C	0	27	missense_variant	MODERATE	ND5	0.0484
HLI-0276	13958	G	C	0	36	missense_variant	MODERATE	ND5	0.0028
HLI-0276	14101	C	T	0	37	missense_variant	MODERATE	ND5	0
HLI-0276	14766	C	T	1	43	missense_variant	MODERATE	CYTB	0.7696
HLI-0276	15110	G	A	0	55	missense_variant	MODERATE	CYTB	0.009
HLI-0276	15217	G	A	0	35	synonymous_variant	LOW	CYTB	0.0104
HLI-0276	15301	G	A	0	35	synonymous_variant	LOW	CYTB	0.2912
HLI-0276	15326	A	G	0	33	missense_variant	MODERATE	CYTB	0.9868
HLI-0276	15849	C	T	0	26	missense_variant	MODERATE	CYTB	0.0027
HLI-0276	16092	T	C	0	46	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0276	16223	C	T	0	39	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0276	16278	C	T	0	41	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0276	16318	A	G	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0276	16390	G	A	0	41	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0277	263	A	G	0	142	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0277	456	C	T	1	273	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0277	750	A	G	0	518	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0277	961	T	C	0	88	upstream_gene_variant	MODIFIER	RNR1	0.0087
HLI-0277	1438	A	G	1	537	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0277	4336	T	C	2	495	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0277	4736	T	C	1	326	synonymous_variant	LOW	ND2	0.0012
HLI-0277	4769	A	G	2	360	synonymous_variant	LOW	ND2	0.9767
HLI-0277	15326	A	G	0	468	missense_variant	MODERATE	CYTB	0.9868
HLI-0277	15833	C	T	2	516	synonymous_variant	LOW	CYTB	0.0051
HLI-0277	16304	T	C	1	445	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0278	152	T	C	0	435	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0278	263	A	G	0	151	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0278	750	A	G	0	581	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0278	1438	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0278	4769	A	G	0	496	synonymous_variant	LOW	ND2	0.9767
HLI-0278	6776	T	C	0	627	synonymous_variant	LOW	COX1	0.0226

HLI-0278	11590	A	G	0	535	synonymous_variant	LOW	ND4	0.0021
HLI-0278	12217	A	G	2	526	upstream_gene_variant	MODIFIER	TRNS2	2.00E-04
HLI-0278	14687	A	G	3	604	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0278	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0278	16519	T	C	0	197	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0279	73	A	G	0	140	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0279	151	C	T	0	188	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0279	152	T	C	0	190	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0279	182	C	T	0	174	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0279	186	C	A	0	172	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0279	189	A	C	0	169	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0279	195	T	C	1	173	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0279	198	C	T	1	176	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0279	247	G	A	0	49	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0279	263	A	G	0	55	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0279	297	A	G	0	58	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0279	750	A	G	2	526	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0279	769	G	A	0	577	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0279	825	T	A	0	578	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0279	1018	G	A	0	608	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0279	1438	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0279	2706	A	G	3	594	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0279	2758	G	A	2	620	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0279	2885	T	C	4	559	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0279	3594	C	T	0	470	synonymous_variant	LOW	ND1	0.0789
HLI-0279	3666	G	A	1	566	synonymous_variant	LOW	ND1	0.0233
HLI-0279	3796	A	T	0	521	missense_variant	MODERATE	ND1	0.0045
HLI-0279	3843	A	G	1	576	synonymous_variant	LOW	ND1	0.0046
HLI-0279	4104	A	G	0	445	synonymous_variant	LOW	ND1	0.0785
HLI-0279	4167	C	T	3	550	synonymous_variant	LOW	ND1	3.00E-04
HLI-0279	4769	A	G	3	541	synonymous_variant	LOW	ND2	0.9767
HLI-0279	5108	T	C	1	576	synonymous_variant	LOW	ND2	0.012
HLI-0279	5460	G	A	1	571	missense_variant	MODERATE	ND2	0.0651
HLI-0279	5951	A	G	2	561	synonymous_variant	LOW	COX1	0.0128
HLI-0279	6071	T	C	0	564	synonymous_variant	LOW	COX1	0.0129
HLI-0279	7028	C	T	2	520	synonymous_variant	LOW	COX1	0.8089
HLI-0279	7055	A	G	3	510	synonymous_variant	LOW	COX1	0.0188
HLI-0279	7146	A	G	0	258	missense_variant	MODERATE	COX1	0.0497
HLI-0279	7256	C	T	0	396	synonymous_variant	LOW	COX1	0.0784

HLI-0279	7389	T	C	1	356	missense_variant	MODERATE	COX1	0.0201
HLI-0279	7521	G	A	0	315	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0279	7948	C	T	2	531	synonymous_variant	LOW	COX2	9.00E-04
HLI-0279	8027	G	A	0	553	missense_variant	MODERATE	COX2	0.0334
HLI-0279	8468	C	T	0	435	synonymous_variant	LOW	ATP8	0.0501
HLI-0279	8655	C	T	1	475	synonymous_variant	LOW	ATP6	0.0511
HLI-0279	8657	C	T	1	481	missense_variant	MODERATE	ATP6	1.00E-04
HLI-0279	8701	A	G	1	500	missense_variant	MODERATE	ATP6	0.3391
HLI-0279	9072	A	G	0	516	synonymous_variant	LOW	ATP6	0.0124
HLI-0279	9540	T	C	0	429	synonymous_variant	LOW	COX3	0.339
HLI-0279	10321	T	C	1	593	missense_variant	MODERATE	ND3	0.0106
HLI-0279	10398	A	G	0	595	missense_variant	MODERATE	ND3	0.445
HLI-0279	10586	G	A	0	503	synonymous_variant	LOW	ND4L	0.0177
HLI-0279	10688	G	A	0	541	synonymous_variant	LOW	ND4L	0.0515
HLI-0279	10810	T	C	2	551	synonymous_variant	LOW	ND4	0.0522
HLI-0279	10873	T	C	0	449	synonymous_variant	LOW	ND4	0.3389
HLI-0279	11719	G	A	0	555	synonymous_variant	LOW	ND4	0.7756
HLI-0279	11899	T	C	0	584	synonymous_variant	LOW	ND4	0.0108
HLI-0279	11914	G	A	0	589	synonymous_variant	LOW	ND4	0.1112
HLI-0279	12127	G	A	0	547	synonymous_variant	LOW	ND4	0.0058
HLI-0279	12705	C	T	1	589	synonymous_variant	LOW	ND5	0.4212
HLI-0279	12810	A	G	2	559	synonymous_variant	LOW	ND5	0.0198
HLI-0279	13105	A	G	2	537	missense_variant	MODERATE	ND5	0.076
HLI-0279	13485	A	G	0	631	synonymous_variant	LOW	ND5	0.0122
HLI-0279	13506	C	T	1	615	synonymous_variant	LOW	ND5	0.0506
HLI-0279	13650	C	T	0	490	synonymous_variant	LOW	ND5	0.079
HLI-0279	13789	T	C	0	370	missense_variant	MODERATE	ND5	0.0185
HLI-0279	14000	T	A	0	432	missense_variant	MODERATE	ND5	0.0126
HLI-0279	14148	A	G	0	506	stop_retained_variant	LOW	ND5	0.0065
HLI-0279	14178	T	C	0	592	missense_variant	MODERATE	ND6	0.0225
HLI-0279	14560	G	A	2	508	synonymous_variant	LOW	ND6	0.0235
HLI-0279	14766	C	T	0	522	missense_variant	MODERATE	CYTB	0.7696
HLI-0279	14911	C	T	3	499	synonymous_variant	LOW	CYTB	0.0124
HLI-0279	15280	C	T	2	458	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0279	15301	G	A	3	516	synonymous_variant	LOW	CYTB	0.2912
HLI-0279	15326	A	G	0	510	missense_variant	MODERATE	CYTB	0.9868
HLI-0279	15626	C	T	0	543	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0279	16038	A	G	0	530	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0279	16223	C	T	2	415	upstream_gene_variant	MODIFIER	DLoop	0.4009

HLI-0279	16274	G	A	0	289	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0279	16278	C	T	0	295	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0279	16293	A	G	0	315	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0279	16294	C	T	0	316	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0279	16311	T	C	0	324	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0279	16360	C	T	1	306	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0279	16519	T	C	0	153	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0280	73	A	G	0	58	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0280	93	A	G	0	67	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0280	95	A	C	0	67	upstream_gene_variant	MODIFIER	DLoop	0.0076
HLI-0280	146	T	C	0	116	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0280	150	C	T	0	121	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0280	152	T	C	0	118	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0280	153	A	G	0	120	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0280	182	C	T	0	147	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0280	195	T	C	0	159	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0280	198	C	T	0	159	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0280	263	A	G	0	91	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0280	325	C	T	0	127	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0280	680	T	C	0	392	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0280	709	G	A	0	457	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0280	750	A	G	1	473	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0280	769	G	A	1	479	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0280	1018	G	A	3	501	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0280	1438	A	G	1	524	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0280	1442	G	A	1	537	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0280	2332	C	T	2	521	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0280	2416	T	C	2	508	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0280	2706	A	G	1	492	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0280	3200	T	A	2	489	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0280	3594	C	T	0	405	synonymous_variant	LOW	ND1	0.0789
HLI-0280	4104	A	G	0	402	synonymous_variant	LOW	ND1	0.0785
HLI-0280	4769	A	G	0	491	synonymous_variant	LOW	ND2	0.9767
HLI-0280	5258	A	G	0	414	synonymous_variant	LOW	ND2	3.00E-04
HLI-0280	6791	A	G	0	515	synonymous_variant	LOW	COX1	0.0022
HLI-0280	7028	C	T	1	536	synonymous_variant	LOW	COX1	0.8089
HLI-0280	7256	C	T	1	427	synonymous_variant	LOW	COX1	0.0784
HLI-0280	7521	G	A	0	397	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0280	7624	T	A	1	504	synonymous_variant	LOW	COX2	0.0047

HLI-0280	8206	G	A	0	413	synonymous_variant	LOW	COX2	0.0287
HLI-0280	8701	A	G	0	509	missense_variant	MODERATE	ATP6	0.3391
HLI-0280	9221	A	G	0	445	synonymous_variant	LOW	COX3	0.0277
HLI-0280	9540	T	C	0	447	synonymous_variant	LOW	COX3	0.339
HLI-0280	10115	T	C	2	604	synonymous_variant	LOW	ND3	0.0278
HLI-0280	10398	A	G	1	501	missense_variant	MODERATE	ND3	0.445
HLI-0280	10873	T	C	1	454	synonymous_variant	LOW	ND4	0.3389
HLI-0280	11719	G	A	0	490	synonymous_variant	LOW	ND4	0.7756
HLI-0280	11944	T	C	0	430	synonymous_variant	LOW	ND4	0.0331
HLI-0280	12236	G	A	2	486	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0280	12705	C	T	2	510	synonymous_variant	LOW	ND5	0.4212
HLI-0280	13590	G	A	0	481	synonymous_variant	LOW	ND5	0.0586
HLI-0280	13650	C	T	3	467	synonymous_variant	LOW	ND5	0.079
HLI-0280	13928	G	C	0	460	missense_variant	MODERATE	ND5	0.0484
HLI-0280	13958	G	C	0	504	missense_variant	MODERATE	ND5	0.0028
HLI-0280	14766	C	T	4	431	missense_variant	MODERATE	CYTB	0.7696
HLI-0280	15110	G	A	0	502	missense_variant	MODERATE	CYTB	0.009
HLI-0280	15217	G	A	0	490	synonymous_variant	LOW	CYTB	0.0104
HLI-0280	15301	G	A	1	451	synonymous_variant	LOW	CYTB	0.2912
HLI-0280	15326	A	G	0	439	missense_variant	MODERATE	CYTB	0.9868
HLI-0280	15849	C	T	2	525	missense_variant	MODERATE	CYTB	0.0027
HLI-0280	16223	C	T	3	479	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0280	16278	C	T	2	447	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0280	16390	G	A	0	316	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0281	263	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0281	750	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0281	1438	A	G	1	620	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0281	4216	T	C	2	575	missense_variant	MODERATE	ND1	0.0991
HLI-0281	4769	A	G	0	596	synonymous_variant	LOW	ND2	0.9767
HLI-0281	11150	G	A	1	586	missense_variant	MODERATE	ND4	0.0024
HLI-0281	14410	G	A	0	502	synonymous_variant	LOW	ND6	9.00E-04
HLI-0281	15326	A	G	1	591	missense_variant	MODERATE	CYTB	0.9868
HLI-0281	16291	C	T	1	538	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0281	16519	T	C	0	249	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0282	263	A	G	0	123	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0282	750	A	G	0	544	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0282	1438	A	G	0	601	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0282	2706	A	G	0	587	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0282	4769	A	G	0	512	synonymous_variant	LOW	ND2	0.9767

HLI-0282	6040	A	G	1	585	missense_variant	MODERATE	COX1	0.0018
HLI-0282	7028	C	T	1	623	synonymous_variant	LOW	COX1	0.8089
HLI-0282	7964	T	C	0	505	missense_variant	MODERATE	COX2	3.00E-04
HLI-0282	9000	A	G	1	562	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0282	10283	A	G	1	518	synonymous_variant	LOW	ND3	0.002
HLI-0282	15326	A	G	0	566	missense_variant	MODERATE	CYTB	0.9868
HLI-0282	15775	A	G	1	577	synonymous_variant	LOW	CYTB	0.0011
HLI-0282	16311	T	C	1	471	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0283	73	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0283	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0283	489	T	C	0	271	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0283	750	A	G	0	587	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0283	1438	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0283	2706	A	G	0	606	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0283	3010	G	A	2	614	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0283	4769	A	G	1	577	synonymous_variant	LOW	ND2	0.9767
HLI-0283	4883	C	T	0	521	synonymous_variant	LOW	ND2	0.0483
HLI-0283	5178	C	A	1	519	missense_variant	MODERATE	ND2	0.0478
HLI-0283	6881	A	G	0	642	synonymous_variant	LOW	COX1	0.0012
HLI-0283	7028	C	T	2	643	synonymous_variant	LOW	COX1	0.8089
HLI-0283	8020	G	A	1	551	synonymous_variant	LOW	COX2	0.0093
HLI-0283	8414	C	T	1	506	missense_variant	MODERATE	ATP8	0.0398
HLI-0283	8701	A	G	1	508	missense_variant	MODERATE	ATP6	0.3391
HLI-0283	9540	T	C	0	489	synonymous_variant	LOW	COX3	0.339
HLI-0283	10181	C	T	1	602	synonymous_variant	LOW	ND3	0.0025
HLI-0283	10398	A	G	0	613	missense_variant	MODERATE	ND3	0.445
HLI-0283	10400	C	T	0	621	synonymous_variant	LOW	ND3	0.2131
HLI-0283	10873	T	C	0	498	synonymous_variant	LOW	ND4	0.3389
HLI-0283	11383	T	C	2	566	synonymous_variant	LOW	ND4	0.0013
HLI-0283	11719	G	A	3	588	synonymous_variant	LOW	ND4	0.7756
HLI-0283	12705	C	T	1	588	synonymous_variant	LOW	ND5	0.4212
HLI-0283	13720	C	T	2	425	synonymous_variant	LOW	ND5	8.00E-04
HLI-0283	14122	A	C	0	464	missense_variant	MODERATE	ND5	2.00E-04
HLI-0283	14668	C	T	1	623	synonymous_variant	LOW	ND6	0.0417
HLI-0283	14766	C	T	0	545	missense_variant	MODERATE	CYTB	0.7696
HLI-0283	14783	T	C	0	629	synonymous_variant	LOW	CYTB	0.2126
HLI-0283	14815	C	T	7	621	synonymous_variant	LOW	CYTB	8.00E-04
HLI-0283	14927	A	G	2	591	missense_variant	MODERATE	CYTB	0.003
HLI-0283	15043	G	A	4	584	synonymous_variant	LOW	CYTB	0.2362

HLI-0283	15301	G	A	0	523	synonymous_variant	LOW	CYTB	0.2912
HLI-0283	15326	A	G	0	543	missense_variant	MODERATE	CYTB	0.9868
HLI-0283	15370	C	T	0	515	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0283	15440	T	C	2	511	synonymous_variant	LOW	CYTB	0.0035
HLI-0283	15951	A	G	4	604	upstream_gene_variant	MODIFIER	TRNT	0.0074
HLI-0283	16173	C	T	1	545	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0283	16223	C	T	3	571	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0283	16319	G	A	2	494	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0283	16362	T	C	0	514	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0284	93	A	G	0	362	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0284	263	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0284	456	C	T	4	443	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0284	750	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0284	1438	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0284	4336	T	C	1	550	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0284	4769	A	G	2	549	synonymous_variant	LOW	ND2	0.9767
HLI-0284	5839	C	T	0	673	upstream_gene_variant	MODIFIER	TRNY	0.0011
HLI-0284	11101	A	G	1	678	synonymous_variant	LOW	ND4	0.0012
HLI-0284	15326	A	G	0	544	missense_variant	MODERATE	CYTB	0.9868
HLI-0284	16304	T	C	1	375	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0285	73	A	G	1	307	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0285	263	A	G	2	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0285	497	C	T	3	428	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0285	750	A	G	1	579	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0285	1189	T	C	0	662	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0285	1438	A	G	0	666	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0285	2706	A	G	0	576	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0285	3480	A	G	4	531	synonymous_variant	LOW	ND1	0.0392
HLI-0285	4769	A	G	1	581	synonymous_variant	LOW	ND2	0.9767
HLI-0285	5582	A	G	6	649	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0285	6260	G	A	2	540	synonymous_variant	LOW	COX1	0.009
HLI-0285	7028	C	T	3	662	synonymous_variant	LOW	COX1	0.8089
HLI-0285	8098	A	G	4	573	synonymous_variant	LOW	COX2	4.00E-04
HLI-0285	9055	G	A	1	623	missense_variant	MODERATE	ATP6	0.0425
HLI-0285	9438	G	A	2	625	missense_variant	MODERATE	COX3	0.0112
HLI-0285	9698	T	C	0	570	synonymous_variant	LOW	COX3	0.0405
HLI-0285	9804	G	A	0	679	missense_variant	MODERATE	COX3	0.0028
HLI-0285	10398	A	G	2	580	missense_variant	MODERATE	ND3	0.445
HLI-0285	10550	A	G	1	561	synonymous_variant	LOW	ND4L	0.0376

HLI-0285	11299	T	C	0	522	synonymous_variant	LOW	ND4	0.0417
HLI-0285	11467	A	G	0	610	synonymous_variant	LOW	ND4	0.1231
HLI-0285	11485	T	C	0	662	synonymous_variant	LOW	ND4	0.0081
HLI-0285	11719	G	A	0	570	synonymous_variant	LOW	ND4	0.7756
HLI-0285	11840	C	T	2	615	synonymous_variant	LOW	ND4	0.0041
HLI-0285	12308	A	G	2	557	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0285	12372	G	A	0	612	synonymous_variant	LOW	ND5	0.1329
HLI-0285	12528	G	A	1	603	synonymous_variant	LOW	ND5	6.00E-04
HLI-0285	13740	T	C	0	434	synonymous_variant	LOW	ND5	0.0041
HLI-0285	14167	C	T	3	558	synonymous_variant	LOW	ND6	0.0385
HLI-0285	14766	C	T	7	621	missense_variant	MODERATE	CYTB	0.7696
HLI-0285	14798	T	C	2	671	missense_variant	MODERATE	CYTB	0.0651
HLI-0285	15175	C	T	1	545	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0285	15326	A	G	0	521	missense_variant	MODERATE	CYTB	0.9868
HLI-0285	16224	T	C	1	585	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0285	16261	C	T	5	564	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0285	16311	T	C	0	494	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0285	16519	T	C	0	283	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0286	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0286	185	G	A	8	388	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0286	228	G	A	5	387	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0286	263	A	G	0	155	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0286	295	C	T	1	160	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0286	462	C	T	3	413	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0286	482	T	C	3	428	upstream_gene_variant	MODIFIER	DLoop	0.0094
HLI-0286	489	T	C	2	429	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0286	750	A	G	1	546	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0286	1438	A	G	0	601	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0286	2706	A	G	0	528	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0286	3010	G	A	8	569	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0286	3394	T	C	5	518	missense_variant	MODERATE	ND1	0.013
HLI-0286	4216	T	C	6	559	missense_variant	MODERATE	ND1	0.0991
HLI-0286	4248	T	C	6	591	synonymous_variant	LOW	ND1	0.0364
HLI-0286	4769	A	G	1	575	synonymous_variant	LOW	ND2	0.9767
HLI-0286	7028	C	T	3	605	synonymous_variant	LOW	COX1	0.8089
HLI-0286	10398	A	G	3	551	missense_variant	MODERATE	ND3	0.445
HLI-0286	11251	A	G	4	530	synonymous_variant	LOW	ND4	0.0932
HLI-0286	11719	G	A	1	538	synonymous_variant	LOW	ND4	0.7756
HLI-0286	12612	A	G	10	603	synonymous_variant	LOW	ND5	0.0506

HLI-0286	13708	G	A	1	501	missense_variant	MODERATE	ND5	0.0717
HLI-0286	14766	C	T	4	580	missense_variant	MODERATE	CYTB	0.7696
HLI-0286	14798	T	C	2	676	missense_variant	MODERATE	CYTB	0.0651
HLI-0286	15326	A	G	0	445	missense_variant	MODERATE	CYTB	0.9868
HLI-0286	15452	C	A	7	431	missense_variant	MODERATE	CYTB	0.0933
HLI-0286	16069	C	T	2	581	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0286	16126	T	C	2	626	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0287	263	A	G	1	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0287	477	T	C	2	340	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0287	750	A	G	1	546	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0287	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0287	3010	G	A	1	585	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0287	4769	A	G	3	549	synonymous_variant	LOW	ND2	0.9767
HLI-0287	8764	G	A	0	554	missense_variant	MODERATE	ATP6	0.0016
HLI-0287	11255	T	C	0	551	missense_variant	MODERATE	ND4	7.00E-04
HLI-0287	12858	C	T	9	581	synonymous_variant	LOW	ND5	7.00E-04
HLI-0287	15326	A	G	0	437	missense_variant	MODERATE	CYTB	0.9868
HLI-0287	16519	T	C	0	193	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0288	146	T	C	1	464	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0288	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0288	456	C	T	2	330	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0288	750	A	G	1	504	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0288	1438	A	G	0	554	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0288	4336	T	C	2	465	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0288	4769	A	G	0	506	synonymous_variant	LOW	ND2	0.9767
HLI-0288	7025	A	G	1	670	synonymous_variant	LOW	COX1	2.00E-04
HLI-0288	15326	A	G	0	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0288	16304	T	C	2	452	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0289	73	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0289	263	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0289	321	T	C	0	169	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0289	709	G	A	1	622	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0289	750	A	G	1	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0289	930	G	A	2	598	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0289	1438	A	G	0	739	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0289	1888	G	A	0	593	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0289	2706	A	G	1	615	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0289	3777	T	C	0	507	synonymous_variant	LOW	ND1	0.0015
HLI-0289	4216	T	C	2	588	missense_variant	MODERATE	ND1	0.0991

HLI-0289	4769	A	G	3	524	synonymous_variant	LOW	ND2	0.9767
HLI-0289	4917	A	G	0	541	missense_variant	MODERATE	ND2	0.0477
HLI-0289	5147	G	A	0	490	synonymous_variant	LOW	ND2	0.0437
HLI-0289	7028	C	T	3	628	synonymous_variant	LOW	COX1	0.8089
HLI-0289	8697	G	A	1	530	synonymous_variant	LOW	ATP6	0.0466
HLI-0289	10463	T	C	0	591	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0289	11251	A	G	1	545	synonymous_variant	LOW	ND4	0.0932
HLI-0289	11719	G	A	0	577	synonymous_variant	LOW	ND4	0.7756
HLI-0289	11812	A	G	1	610	synonymous_variant	LOW	ND4	0.0332
HLI-0289	13368	G	A	0	594	synonymous_variant	LOW	ND5	0.0495
HLI-0289	14233	A	G	2	511	synonymous_variant	LOW	ND6	0.0369
HLI-0289	14766	C	T	3	539	missense_variant	MODERATE	CYTB	0.7696
HLI-0289	14905	G	A	2	594	synonymous_variant	LOW	CYTB	0.0526
HLI-0289	15326	A	G	0	490	missense_variant	MODERATE	CYTB	0.9868
HLI-0289	15452	C	A	1	439	missense_variant	MODERATE	CYTB	0.0933
HLI-0289	15607	A	G	2	571	synonymous_variant	LOW	CYTB	0.0508
HLI-0289	15928	G	A	2	564	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0289	16126	T	C	0	576	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0289	16294	C	T	1	528	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0289	16296	C	T	1	532	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0289	16304	T	C	1	526	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0289	16519	T	C	1	319	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0290	73	A	G	0	307	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0290	152	T	C	3	547	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0290	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0290	533	A	G	1	52	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0290	709	G	A	3	543	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0290	750	A	G	1	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0290	1438	A	G	1	639	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0290	1842	A	G	1	655	upstream_gene_variant	MODIFIER	RNR2	0.0028
HLI-0290	1888	G	A	0	700	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0290	2695	G	A	3	661	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0290	2706	A	G	2	703	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0290	4216	T	C	0	594	missense_variant	MODERATE	ND1	0.0991
HLI-0290	4769	A	G	2	585	synonymous_variant	LOW	ND2	0.9767
HLI-0290	4917	A	G	3	572	missense_variant	MODERATE	ND2	0.0477
HLI-0290	6261	G	A	4	608	missense_variant	MODERATE	COX1	0.007
HLI-0290	7028	C	T	6	677	synonymous_variant	LOW	COX1	0.8089
HLI-0290	8455	C	T	4	501	synonymous_variant	LOW	ATP8	6.00E-04

HLI-0290	8697	G	A	0	555	synonymous_variant	LOW	ATP6	0.0466
HLI-0290	10463	T	C	0	658	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0290	10822	C	T	1	579	synonymous_variant	LOW	ND4	0.0036
HLI-0290	11251	A	G	0	626	synonymous_variant	LOW	ND4	0.0932
HLI-0290	11719	G	A	1	595	synonymous_variant	LOW	ND4	0.7756
HLI-0290	11812	A	G	0	559	synonymous_variant	LOW	ND4	0.0332
HLI-0290	13368	G	A	1	631	synonymous_variant	LOW	ND5	0.0495
HLI-0290	13770	C	T	6	406	synonymous_variant	LOW	ND5	1.00E-04
HLI-0290	13928	G	C	0	505	missense_variant	MODERATE	ND5	0.0484
HLI-0290	13973	A	T	0	544	missense_variant	MODERATE	ND5	5.00E-04
HLI-0290	14233	A	G	0	513	synonymous_variant	LOW	ND6	0.0369
HLI-0290	14766	C	T	2	578	missense_variant	MODERATE	CYTB	0.7696
HLI-0290	14905	G	A	0	622	synonymous_variant	LOW	CYTB	0.0526
HLI-0290	15326	A	G	0	553	missense_variant	MODERATE	CYTB	0.9868
HLI-0290	15452	C	A	3	538	missense_variant	MODERATE	CYTB	0.0933
HLI-0290	15607	A	G	1	595	synonymous_variant	LOW	CYTB	0.0508
HLI-0290	15928	G	A	0	682	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0290	16126	T	C	0	568	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0290	16172	T	C	0	607	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0290	16266	C	T	1	564	upstream_gene_variant	MODIFIER	DLoop	0.0135
HLI-0290	16292	C	T	0	585	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0290	16294	C	T	0	586	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0290	16519	T	C	1	266	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0291	73	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0291	185	G	A	0	372	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0291	189	A	G	0	381	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0291	200	A	G	0	381	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0291	263	A	G	0	151	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0291	750	A	G	1	546	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0291	980	T	C	4	610	upstream_gene_variant	MODIFIER	RNR1	0.0112
HLI-0291	1438	A	G	0	591	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0291	1822	T	C	0	608	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0291	2706	A	G	1	581	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0291	3396	T	C	0	506	synonymous_variant	LOW	ND1	0.0082
HLI-0291	4218	T	C	4	513	synonymous_variant	LOW	ND1	0.0057
HLI-0291	4769	A	G	1	500	synonymous_variant	LOW	ND2	0.9767
HLI-0291	5601	C	T	9	603	upstream_gene_variant	MODIFIER	TRNA	0.0101
HLI-0291	7028	C	T	0	561	synonymous_variant	LOW	COX1	0.8089
HLI-0291	7819	C	A	5	525	synonymous_variant	LOW	COX2	0.0045

HLI-0291	8527	A	G	2	472	initiator_codon_variant	LOW	ATP6/8	0.0044
HLI-0291	8701	A	G	1	512	missense_variant	MODERATE	ATP6	0.3391
HLI-0291	8932	C	T	3	523	missense_variant	MODERATE	ATP6	0.0044
HLI-0291	8998	G	A	3	551	missense_variant	MODERATE	ATP6	4.00E-04
HLI-0291	9540	T	C	0	543	synonymous_variant	LOW	COX3	0.339
HLI-0291	9950	T	C	5	580	synonymous_variant	LOW	COX3	0.0362
HLI-0291	10398	A	G	0	628	missense_variant	MODERATE	ND3	0.445
HLI-0291	10873	T	C	0	501	synonymous_variant	LOW	ND4	0.3389
HLI-0291	11440	G	A	0	556	synonymous_variant	LOW	ND4	0.0081
HLI-0291	11719	G	A	0	519	synonymous_variant	LOW	ND4	0.7756
HLI-0291	12705	C	T	0	583	synonymous_variant	LOW	ND5	0.4212
HLI-0291	14766	C	T	0	568	missense_variant	MODERATE	CYTB	0.7696
HLI-0291	14769	A	G	1	581	missense_variant	MODERATE	CYTB	0.0121
HLI-0291	15301	G	A	0	490	synonymous_variant	LOW	CYTB	0.2912
HLI-0291	15326	A	G	0	529	missense_variant	MODERATE	CYTB	0.9868
HLI-0291	15514	T	C	5	538	synonymous_variant	LOW	CYTB	0.0071
HLI-0291	15924	A	G	0	560	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0291	16209	T	C	0	542	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0291	16223	C	T	0	530	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0291	16292	C	T	0	415	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0291	16295	C	T	0	412	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0291	16311	T	C	0	394	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0291	16519	T	C	0	169	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0292	73	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0292	150	C	T	0	433	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0292	195	T	C	1	406	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0292	198	C	T	0	402	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0292	263	A	G	0	149	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0292	750	A	G	0	546	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0292	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0292	1888	G	A	2	541	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0292	2352	T	C	1	531	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0292	2706	A	G	1	566	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0292	4769	A	G	1	537	synonymous_variant	LOW	ND2	0.9767
HLI-0292	4823	T	C	0	600	synonymous_variant	LOW	ND2	0.0049
HLI-0292	6413	T	C	0	543	synonymous_variant	LOW	COX1	0.0062
HLI-0292	7028	C	T	2	636	synonymous_variant	LOW	COX1	0.8089
HLI-0292	8701	A	G	2	473	missense_variant	MODERATE	ATP6	0.3391
HLI-0292	9540	T	C	0	557	synonymous_variant	LOW	COX3	0.339

HLI-0292	10398	A	G	0	573	missense_variant	MODERATE	ND3	0.445
HLI-0292	10819	A	G	1	529	synonymous_variant	LOW	ND4	0.0228
HLI-0292	10873	T	C	0	546	synonymous_variant	LOW	ND4	0.3389
HLI-0292	11699	A	G	1	571	missense_variant	MODERATE	ND4	0
HLI-0292	11719	G	A	1	605	synonymous_variant	LOW	ND4	0.7756
HLI-0292	12705	C	T	3	649	synonymous_variant	LOW	ND5	0.4212
HLI-0292	13105	A	G	2	571	missense_variant	MODERATE	ND5	0.076
HLI-0292	14212	T	C	1	463	synonymous_variant	LOW	ND6	0.0204
HLI-0292	14750	A	G	1	499	missense_variant	MODERATE	CYTB	8.00E-04
HLI-0292	14766	C	T	3	552	missense_variant	MODERATE	CYTB	0.7696
HLI-0292	14869	G	A	2	621	synonymous_variant	LOW	CYTB	0.0023
HLI-0292	14905	G	A	2	624	synonymous_variant	LOW	CYTB	0.0526
HLI-0292	15301	G	A	0	527	synonymous_variant	LOW	CYTB	0.2912
HLI-0292	15326	A	G	0	556	missense_variant	MODERATE	CYTB	0.9868
HLI-0292	16086	T	C	0	620	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0292	16223	C	T	3	559	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0292	16320	C	T	0	482	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0292	16519	T	C	0	197	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0293	73	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0293	199	T	C	0	305	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0293	204	T	C	0	307	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0293	250	T	C	0	236	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0293	263	A	G	0	216	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0293	750	A	G	0	458	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0293	1438	A	G	0	499	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0293	1719	G	A	0	571	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0293	2706	A	G	0	480	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0293	4529	A	T	1	526	synonymous_variant	LOW	ND2	0.015
HLI-0293	4769	A	G	2	529	synonymous_variant	LOW	ND2	0.9767
HLI-0293	7028	C	T	1	577	synonymous_variant	LOW	COX1	0.8089
HLI-0293	8251	G	A	5	491	synonymous_variant	LOW	COX2	0.058
HLI-0293	8519	G	A	0	451	missense_variant	MODERATE	ATP8	0.0024
HLI-0293	10034	T	C	1	607	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0293	10238	T	C	0	545	synonymous_variant	LOW	ND3	0.0623
HLI-0293	10398	A	G	0	563	missense_variant	MODERATE	ND3	0.445
HLI-0293	10819	A	G	0	494	synonymous_variant	LOW	ND4	0.0228
HLI-0293	11719	G	A	1	514	synonymous_variant	LOW	ND4	0.7756
HLI-0293	12501	G	A	5	562	synonymous_variant	LOW	ND5	0.0258
HLI-0293	12705	C	T	0	595	synonymous_variant	LOW	ND5	0.4212

HLI-0293	13780	A	G	0	332	missense_variant	MODERATE	ND5	0.0179
HLI-0293	14766	C	T	1	447	missense_variant	MODERATE	CYTB	0.7696
HLI-0293	15043	G	A	1	561	synonymous_variant	LOW	CYTB	0.2362
HLI-0293	15326	A	G	0	390	missense_variant	MODERATE	CYTB	0.9868
HLI-0293	15924	A	G	1	543	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0293	16129	G	A	0	525	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0293	16223	C	T	4	446	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0293	16391	G	A	1	376	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0293	16519	T	C	0	235	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0294	73	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0294	152	T	C	2	396	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0294	263	A	G	0	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0294	709	G	A	1	454	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0294	750	A	G	1	501	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0294	930	G	A	3	512	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0294	1438	A	G	0	514	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0294	1888	G	A	0	466	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0294	2706	A	G	1	525	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0294	3338	T	C	0	489	missense_variant	MODERATE	ND1	0.002
HLI-0294	4216	T	C	1	475	missense_variant	MODERATE	ND1	0.0991
HLI-0294	4769	A	G	0	466	synonymous_variant	LOW	ND2	0.9767
HLI-0294	4917	A	G	2	485	missense_variant	MODERATE	ND2	0.0477
HLI-0294	5147	G	A	0	402	synonymous_variant	LOW	ND2	0.0437
HLI-0294	7028	C	T	1	582	synonymous_variant	LOW	COX1	0.8089
HLI-0294	8697	G	A	1	443	synonymous_variant	LOW	ATP6	0.0466
HLI-0294	10463	T	C	1	520	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0294	10750	A	G	1	494	missense_variant	MODERATE	ND4L	0.0045
HLI-0294	11251	A	G	0	509	synonymous_variant	LOW	ND4	0.0932
HLI-0294	11719	G	A	2	477	synonymous_variant	LOW	ND4	0.7756
HLI-0294	11812	A	G	1	516	synonymous_variant	LOW	ND4	0.0332
HLI-0294	13368	G	A	1	554	synonymous_variant	LOW	ND5	0.0495
HLI-0294	13722	A	G	1	411	synonymous_variant	LOW	ND5	0.0077
HLI-0294	14233	A	G	0	445	synonymous_variant	LOW	ND6	0.0369
HLI-0294	14766	C	T	4	458	missense_variant	MODERATE	CYTB	0.7696
HLI-0294	14905	G	A	3	540	synonymous_variant	LOW	CYTB	0.0526
HLI-0294	15326	A	G	0	437	missense_variant	MODERATE	CYTB	0.9868
HLI-0294	15452	C	A	5	420	missense_variant	MODERATE	CYTB	0.0933
HLI-0294	15607	A	G	1	440	synonymous_variant	LOW	CYTB	0.0508
HLI-0294	15928	G	A	2	513	upstream_gene_variant	MODIFIER	TRNT	0.049

HLI-0294	16126	T	C	0	471	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0294	16294	C	T	1	420	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0294	16296	C	T	1	422	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0294	16304	T	C	1	429	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0294	16519	T	C	0	161	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0295	73	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0295	150	C	T	0	436	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0295	152	T	C	0	435	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0295	263	A	G	0	183	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0295	295	C	T	0	145	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0295	489	T	C	0	275	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0295	750	A	G	1	513	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0295	1438	A	G	0	518	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0295	2706	A	G	0	450	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0295	4216	T	C	0	465	missense_variant	MODERATE	ND1	0.0991
HLI-0295	4769	A	G	0	527	synonymous_variant	LOW	ND2	0.9767
HLI-0295	5633	C	T	2	537	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0295	7028	C	T	3	541	synonymous_variant	LOW	COX1	0.8089
HLI-0295	7476	C	T	3	537	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0295	8911	T	C	0	520	synonymous_variant	LOW	ATP6	0.0028
HLI-0295	10172	G	A	0	536	synonymous_variant	LOW	ND3	0.0084
HLI-0295	10398	A	G	0	526	missense_variant	MODERATE	ND3	0.445
HLI-0295	11251	A	G	0	493	synonymous_variant	LOW	ND4	0.0932
HLI-0295	11719	G	A	0	472	synonymous_variant	LOW	ND4	0.7756
HLI-0295	12612	A	G	5	527	synonymous_variant	LOW	ND5	0.0506
HLI-0295	13708	G	A	1	405	missense_variant	MODERATE	ND5	0.0717
HLI-0295	14766	C	T	4	492	missense_variant	MODERATE	CYTB	0.7696
HLI-0295	15257	G	A	0	429	missense_variant	MODERATE	CYTB	0.0155
HLI-0295	15326	A	G	1	417	missense_variant	MODERATE	CYTB	0.9868
HLI-0295	15443	C	T	0	372	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0295	15452	C	A	0	387	missense_variant	MODERATE	CYTB	0.0933
HLI-0295	15812	G	A	2	476	missense_variant	MODERATE	CYTB	0.0096
HLI-0295	16069	C	T	5	521	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0295	16126	T	C	0	492	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0295	16265	A	T	0	447	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0296	73	A	G	0	173	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0296	152	T	C	1	272	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0296	182	C	T	1	261	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0296	185	G	T	1	256	upstream_gene_variant	MODIFIER	DLoop	0.0056

HLI-0296	189	A	G	1	251	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0296	195	T	C	1	266	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0296	247	G	A	1	124	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0296	263	A	G	1	135	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0296	357	A	G	0	219	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0296	709	G	A	1	461	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0296	710	T	C	1	462	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0296	750	A	G	0	517	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0296	769	G	A	1	531	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0296	825	T	A	3	568	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0296	1018	G	A	4	584	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0296	1738	T	C	5	542	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0296	2352	T	C	3	432	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0296	2706	A	G	0	473	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0296	2758	G	A	6	517	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0296	2768	A	G	6	520	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0296	2885	T	C	3	537	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0296	3308	T	C	3	494	start_lost	HIGH	ND1	0.0073
HLI-0296	3594	C	T	1	410	synonymous_variant	LOW	ND1	0.0789
HLI-0296	3666	G	A	5	436	synonymous_variant	LOW	ND1	0.0233
HLI-0296	3693	G	A	3	459	synonymous_variant	LOW	ND1	0.0091
HLI-0296	4104	A	G	0	399	synonymous_variant	LOW	ND1	0.0785
HLI-0296	4769	A	G	2	491	synonymous_variant	LOW	ND2	0.9767
HLI-0296	5036	A	G	1	464	synonymous_variant	LOW	ND2	0.006
HLI-0296	5046	G	A	1	496	missense_variant	MODERATE	ND2	0.018
HLI-0296	5393	T	C	3	490	synonymous_variant	LOW	ND2	0.0059
HLI-0296	5655	T	C	3	601	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0296	6548	C	T	5	514	synonymous_variant	LOW	COX1	0.0061
HLI-0296	6719	T	C	9	596	synonymous_variant	LOW	COX1	0.041
HLI-0296	6827	T	C	7	518	synonymous_variant	LOW	COX1	0.0072
HLI-0296	6989	A	G	4	543	synonymous_variant	LOW	COX1	0.0061
HLI-0296	7028	C	T	2	536	synonymous_variant	LOW	COX1	0.8089
HLI-0296	7055	A	G	4	487	synonymous_variant	LOW	COX1	0.0188
HLI-0296	7146	A	G	2	254	missense_variant	MODERATE	COX1	0.0497
HLI-0296	7256	C	T	4	446	synonymous_variant	LOW	COX1	0.0784
HLI-0296	7389	T	C	1	404	missense_variant	MODERATE	COX1	0.0201
HLI-0296	7521	G	A	0	326	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0296	7867	C	T	5	566	synonymous_variant	LOW	COX2	0.0076
HLI-0296	7915	C	T	4	664	synonymous_variant	LOW	COX2	5.00E-04

HLI-0296	8248	A	G	3	509	synonymous_variant	LOW	COX2	0.0061
HLI-0296	8468	C	T	5	407	synonymous_variant	LOW	ATP8	0.0501
HLI-0296	8655	C	T	6	392	synonymous_variant	LOW	ATP6	0.0511
HLI-0296	8701	A	G	1	426	missense_variant	MODERATE	ATP6	0.3391
HLI-0296	9540	T	C	3	452	synonymous_variant	LOW	COX3	0.339
HLI-0296	10398	A	G	0	508	missense_variant	MODERATE	ND3	0.445
HLI-0296	10688	G	A	5	475	synonymous_variant	LOW	ND4L	0.0515
HLI-0296	10810	T	C	4	472	synonymous_variant	LOW	ND4	0.0522
HLI-0296	10873	T	C	2	516	synonymous_variant	LOW	ND4	0.3389
HLI-0296	11719	G	A	0	510	synonymous_variant	LOW	ND4	0.7756
HLI-0296	12519	T	C	7	539	synonymous_variant	LOW	ND5	0.007
HLI-0296	12705	C	T	1	564	synonymous_variant	LOW	ND5	0.4212
HLI-0296	13105	A	G	3	536	missense_variant	MODERATE	ND5	0.076
HLI-0296	13506	C	T	3	479	synonymous_variant	LOW	ND5	0.0506
HLI-0296	13650	C	T	3	437	synonymous_variant	LOW	ND5	0.079
HLI-0296	13789	T	C	2	318	missense_variant	MODERATE	ND5	0.0185
HLI-0296	13880	C	A	12	414	missense_variant	MODERATE	ND5	0.0055
HLI-0296	13980	G	A	2	406	synonymous_variant	LOW	ND5	0.0023
HLI-0296	14178	T	C	3	473	missense_variant	MODERATE	ND6	0.0225
HLI-0296	14203	A	G	3	522	synonymous_variant	LOW	ND6	0.0061
HLI-0296	14560	G	A	5	512	synonymous_variant	LOW	ND6	0.0235
HLI-0296	14766	C	T	0	520	missense_variant	MODERATE	CYTB	0.7696
HLI-0296	14769	A	G	0	537	missense_variant	MODERATE	CYTB	0.0121
HLI-0296	15115	T	C	0	564	synonymous_variant	LOW	CYTB	0.0093
HLI-0296	15326	A	G	0	421	missense_variant	MODERATE	CYTB	0.9868
HLI-0296	16126	T	C	5	504	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0296	16223	C	T	1	410	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0296	16264	C	T	4	334	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0296	16270	C	T	4	320	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0296	16278	C	T	3	316	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0296	16293	A	G	3	297	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0296	16305	A	G	3	288	upstream_gene_variant	MODIFIER	DLoop	0.001
HLI-0296	16311	T	C	3	289	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0296	16519	T	C	0	120	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0297	195	T	C	0	370	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0297	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0297	750	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0297	951	G	A	2	659	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0297	6261	G	A	2	661	missense_variant	MODERATE	COX1	0.007

HLI-0297	12940	G	A	4	535	missense_variant	MODERATE	ND5	0.0054
HLI-0297	13395	A	G	0	585	synonymous_variant	LOW	ND5	0.0056
HLI-0297	14494	T	C	0	458	synonymous_variant	LOW	ND6	3.00E-04
HLI-0297	15326	A	G	0	566	missense_variant	MODERATE	CYTB	0.9868
HLI-0297	16519	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0298	73	A	G	0	18	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0298	152	T	C	0	38	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0298	185	G	T	0	36	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0298	189	A	G	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0298	195	T	C	0	35	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0298	210	A	G	0	37	upstream_gene_variant	MODIFIER	DLoop	0.0108
HLI-0298	247	G	A	0	23	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0298	263	A	G	0	17	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0298	357	A	G	0	24	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0298	709	G	A	0	36	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0298	710	T	C	0	36	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0298	750	A	G	0	44	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0298	769	G	A	0	49	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0298	825	T	A	0	60	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0298	1018	G	A	0	54	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0298	1738	T	C	0	37	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0298	2352	T	C	0	45	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0298	2706	A	G	0	37	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0298	2758	G	A	0	34	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0298	2768	A	G	0	36	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0298	2885	T	C	0	41	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0298	3308	T	C	0	56	start_lost	HIGH	ND1	0.0073
HLI-0298	3594	C	T	0	32	synonymous_variant	LOW	ND1	0.0789
HLI-0298	3666	G	A	0	28	synonymous_variant	LOW	ND1	0.0233
HLI-0298	3693	G	A	0	22	synonymous_variant	LOW	ND1	0.0091
HLI-0298	4104	A	G	0	41	synonymous_variant	LOW	ND1	0.0785
HLI-0298	4769	A	G	0	50	synonymous_variant	LOW	ND2	0.9767
HLI-0298	5036	A	G	0	44	synonymous_variant	LOW	ND2	0.006
HLI-0298	5046	G	A	0	47	missense_variant	MODERATE	ND2	0.018
HLI-0298	5393	T	C	0	43	synonymous_variant	LOW	ND2	0.0059
HLI-0298	5655	T	C	0	71	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0298	6548	C	T	0	38	synonymous_variant	LOW	COX1	0.0061
HLI-0298	6827	T	C	0	55	synonymous_variant	LOW	COX1	0.0072
HLI-0298	6989	A	G	0	82	synonymous_variant	LOW	COX1	0.0061

HLI-0298	7028	C	T	0	80	synonymous_variant	LOW	COX1	0.8089
HLI-0298	7055	A	G	0	68	synonymous_variant	LOW	COX1	0.0188
HLI-0298	7146	A	G	0	30	missense_variant	MODERATE	COX1	0.0497
HLI-0298	7256	C	T	0	54	synonymous_variant	LOW	COX1	0.0784
HLI-0298	7389	T	C	0	39	missense_variant	MODERATE	COX1	0.0201
HLI-0298	7521	G	A	0	39	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0298	7867	C	T	1	74	synonymous_variant	LOW	COX2	0.0076
HLI-0298	8248	A	G	0	48	synonymous_variant	LOW	COX2	0.0061
HLI-0298	8468	C	T	0	25	synonymous_variant	LOW	ATP8	0.0501
HLI-0298	8655	C	T	0	40	synonymous_variant	LOW	ATP6	0.0511
HLI-0298	8701	A	G	0	31	missense_variant	MODERATE	ATP6	0.3391
HLI-0298	9540	T	C	0	45	synonymous_variant	LOW	COX3	0.339
HLI-0298	10398	A	G	0	32	missense_variant	MODERATE	ND3	0.445
HLI-0298	10688	G	A	0	49	synonymous_variant	LOW	ND4L	0.0515
HLI-0298	10810	T	C	0	46	synonymous_variant	LOW	ND4	0.0522
HLI-0298	10873	T	C	0	46	synonymous_variant	LOW	ND4	0.3389
HLI-0298	11719	G	A	0	52	synonymous_variant	LOW	ND4	0.7756
HLI-0298	12519	T	C	0	67	synonymous_variant	LOW	ND5	0.007
HLI-0298	12609	T	C	0	64	synonymous_variant	LOW	ND5	0.0024
HLI-0298	12630	G	A	0	66	synonymous_variant	LOW	ND5	0.0053
HLI-0298	12696	T	C	0	60	synonymous_variant	LOW	ND5	0.0027
HLI-0298	12705	C	T	0	62	synonymous_variant	LOW	ND5	0.4212
HLI-0298	13105	A	G	0	62	missense_variant	MODERATE	ND5	0.076
HLI-0298	13506	C	T	0	42	synonymous_variant	LOW	ND5	0.0506
HLI-0298	13650	C	T	0	43	synonymous_variant	LOW	ND5	0.079
HLI-0298	13789	T	C	0	24	missense_variant	MODERATE	ND5	0.0185
HLI-0298	13880	C	A	0	33	missense_variant	MODERATE	ND5	0.0055
HLI-0298	14178	T	C	0	55	missense_variant	MODERATE	ND6	0.0225
HLI-0298	14203	A	G	0	58	synonymous_variant	LOW	ND6	0.0061
HLI-0298	14560	G	A	0	43	synonymous_variant	LOW	ND6	0.0235
HLI-0298	14766	C	T	1	65	missense_variant	MODERATE	CYTB	0.7696
HLI-0298	14769	A	G	1	65	missense_variant	MODERATE	CYTB	0.0121
HLI-0298	15115	T	C	0	65	synonymous_variant	LOW	CYTB	0.0093
HLI-0298	15326	A	G	0	45	missense_variant	MODERATE	CYTB	0.9868
HLI-0298	16126	T	C	0	58	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0298	16223	C	T	0	53	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0298	16264	C	T	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0298	16270	C	T	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0298	16278	C	T	0	42	upstream_gene_variant	MODIFIER	DLoop	0.1057

HLI-0298	16293	A	G	0	42	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0298	16311	T	C	0	41	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0298	16519	T	C	0	23	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0299	73	A	G	1	282	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0299	185	G	A	0	406	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0299	188	A	G	0	407	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0299	228	G	A	0	293	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0299	263	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0299	295	C	T	0	188	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0299	462	C	T	1	224	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0299	489	T	C	0	271	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0299	750	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0299	1438	A	G	1	659	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0299	2706	A	G	0	624	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0299	3010	G	A	2	635	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0299	4216	T	C	0	562	missense_variant	MODERATE	ND1	0.0991
HLI-0299	4769	A	G	0	556	synonymous_variant	LOW	ND2	0.9767
HLI-0299	7028	C	T	1	657	synonymous_variant	LOW	COX1	0.8089
HLI-0299	10398	A	G	0	624	missense_variant	MODERATE	ND3	0.445
HLI-0299	11002	A	G	2	454	synonymous_variant	LOW	ND4	0.0124
HLI-0299	11251	A	G	3	581	synonymous_variant	LOW	ND4	0.0932
HLI-0299	11719	G	A	0	567	synonymous_variant	LOW	ND4	0.7756
HLI-0299	12612	A	G	3	614	synonymous_variant	LOW	ND5	0.0506
HLI-0299	13032	A	G	3	620	synonymous_variant	LOW	ND5	6.00E-04
HLI-0299	13708	G	A	1	447	missense_variant	MODERATE	ND5	0.0717
HLI-0299	14325	T	C	1	468	missense_variant	MODERATE	ND6	0.001
HLI-0299	14766	C	T	1	562	missense_variant	MODERATE	CYTB	0.7696
HLI-0299	14798	T	C	0	645	missense_variant	MODERATE	CYTB	0.0651
HLI-0299	15326	A	G	1	514	missense_variant	MODERATE	CYTB	0.9868
HLI-0299	15452	C	A	1	524	missense_variant	MODERATE	CYTB	0.0933
HLI-0299	16069	C	T	1	570	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0299	16126	T	C	1	590	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0299	16519	T	C	2	279	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0300	73	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0300	150	C	T	1	370	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0300	152	T	C	1	379	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0300	182	C	T	1	343	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0300	195	T	C	1	329	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0300	198	C	T	1	327	upstream_gene_variant	MODIFIER	DLoop	0.0245

HLI-0300	263	A	G	0	161	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0300	418	C	T	2	309	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0300	750	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0300	769	G	A	1	620	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0300	1018	G	A	1	616	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0300	1438	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0300	1442	G	A	0	606	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0300	1706	C	T	0	598	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0300	2332	C	T	0	544	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0300	2358	A	G	0	597	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0300	2416	T	C	1	568	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0300	2706	A	G	2	587	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0300	3594	C	T	1	460	synonymous_variant	LOW	ND1	0.0789
HLI-0300	4104	A	G	0	542	synonymous_variant	LOW	ND1	0.0785
HLI-0300	4158	A	G	1	539	synonymous_variant	LOW	ND1	0.0023
HLI-0300	4370	T	C	0	584	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0300	4767	A	G	0	558	missense_variant	MODERATE	ND2	0.0029
HLI-0300	4769	A	G	0	564	synonymous_variant	LOW	ND2	0.9767
HLI-0300	5027	C	T	0	577	synonymous_variant	LOW	ND2	0.003
HLI-0300	5331	C	A	0	586	missense_variant	MODERATE	ND2	0.0022
HLI-0300	5342	C	T	0	586	synonymous_variant	LOW	ND2	1.00E-04
HLI-0300	5418	T	C	0	586	missense_variant	MODERATE	ND2	2.00E-04
HLI-0300	5471	G	A	0	602	synonymous_variant	LOW	ND2	0.0128
HLI-0300	5814	T	C	1	592	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0300	6026	G	A	1	592	synonymous_variant	LOW	COX1	0.0163
HLI-0300	6713	C	T	12	741	synonymous_variant	LOW	COX1	0.0028
HLI-0300	7028	C	T	6	687	synonymous_variant	LOW	COX1	0.8089
HLI-0300	7256	C	T	3	524	synonymous_variant	LOW	COX1	0.0784
HLI-0300	7521	G	A	2	425	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0300	7624	T	A	1	557	synonymous_variant	LOW	COX2	0.0047
HLI-0300	7702	G	A	0	641	synonymous_variant	LOW	COX2	0.001
HLI-0300	8065	G	A	0	573	synonymous_variant	LOW	COX2	6.00E-04
HLI-0300	8080	C	T	1	612	synonymous_variant	LOW	COX2	0.0022
HLI-0300	8206	G	A	1	511	synonymous_variant	LOW	COX2	0.0287
HLI-0300	8387	G	A	1	482	missense_variant	MODERATE	ATP8	0.0028
HLI-0300	8701	A	G	1	515	missense_variant	MODERATE	ATP6	0.3391
HLI-0300	9221	A	G	0	591	synonymous_variant	LOW	COX3	0.0277
HLI-0300	9540	T	C	0	546	synonymous_variant	LOW	COX3	0.339
HLI-0300	10115	T	C	0	645	synonymous_variant	LOW	ND3	0.0278

HLI-0300	10398	A	G	0	624	missense_variant	MODERATE	ND3	0.445
HLI-0300	10469	A	G	1	637	upstream_gene_variant	MODIFIER	TRNR	0
HLI-0300	10828	T	C	0	521	synonymous_variant	LOW	ND4	0.0015
HLI-0300	10873	T	C	0	544	synonymous_variant	LOW	ND4	0.3389
HLI-0300	11719	G	A	0	555	synonymous_variant	LOW	ND4	0.7756
HLI-0300	11944	T	C	3	560	synonymous_variant	LOW	ND4	0.0331
HLI-0300	12236	G	A	2	569	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0300	12705	C	T	1	697	synonymous_variant	LOW	ND5	0.4212
HLI-0300	12948	A	G	3	561	synonymous_variant	LOW	ND5	0.0022
HLI-0300	13590	G	A	2	576	synonymous_variant	LOW	ND5	0.0586
HLI-0300	13650	C	T	2	568	synonymous_variant	LOW	ND5	0.079
HLI-0300	13924	C	T	0	490	missense_variant	MODERATE	ND5	0.0013
HLI-0300	14059	A	G	3	460	missense_variant	MODERATE	ND5	0.0022
HLI-0300	14766	C	T	5	557	missense_variant	MODERATE	CYTB	0.7696
HLI-0300	15110	G	A	0	614	missense_variant	MODERATE	CYTB	0.009
HLI-0300	15217	G	A	2	557	synonymous_variant	LOW	CYTB	0.0104
HLI-0300	15301	G	A	0	543	synonymous_variant	LOW	CYTB	0.2912
HLI-0300	15326	A	G	0	541	missense_variant	MODERATE	CYTB	0.9868
HLI-0300	16114	C	A	1	550	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0300	16213	G	A	0	518	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0300	16223	C	T	1	506	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0300	16278	C	T	0	471	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0300	16355	C	T	0	396	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0300	16362	T	C	0	415	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0300	16390	G	A	0	421	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0301	263	A	G	0	181	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0301	750	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0301	1438	A	G	1	607	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0301	2706	A	G	0	610	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0301	3360	A	G	1	608	synonymous_variant	LOW	ND1	0.0013
HLI-0301	4769	A	G	1	600	synonymous_variant	LOW	ND2	0.9767
HLI-0301	6755	G	A	5	754	synonymous_variant	LOW	COX1	0.0065
HLI-0301	7028	C	T	3	714	synonymous_variant	LOW	COX1	0.8089
HLI-0301	15326	A	G	0	611	missense_variant	MODERATE	CYTB	0.9868
HLI-0301	16172	T	C	0	265	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0301	16311	T	C	1	457	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0303	72	T	C	0	278	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0303	263	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0303	508	A	G	0	344	upstream_gene_variant	MODIFIER	DLoop	0.0072

HLI-0303	750	A	G	1	586	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0303	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0303	2706	A	G	2	606	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0303	4580	G	A	1	579	synonymous_variant	LOW	ND2	0.0169
HLI-0303	4769	A	G	1	569	synonymous_variant	LOW	ND2	0.9767
HLI-0303	7028	C	T	3	644	synonymous_variant	LOW	COX1	0.8089
HLI-0303	7762	G	A	1	501	synonymous_variant	LOW	COX2	0.0025
HLI-0303	8589	A	G	0	542	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0303	14914	A	C	0	615	synonymous_variant	LOW	CYTB	3.00E-04
HLI-0303	15326	A	G	1	572	missense_variant	MODERATE	CYTB	0.9868
HLI-0303	15355	G	A	0	634	synonymous_variant	LOW	CYTB	0.0032
HLI-0303	15904	C	T	3	633	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0303	16298	T	C	0	496	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0304	73	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0304	150	C	T	1	448	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0304	195	T	C	1	428	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0304	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0304	750	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0304	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0304	2352	T	C	0	592	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0304	2706	A	G	0	658	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0304	3504	T	C	1	536	synonymous_variant	LOW	ND1	9.00E-04
HLI-0304	4769	A	G	1	582	synonymous_variant	LOW	ND2	0.9767
HLI-0304	4823	T	C	1	554	synonymous_variant	LOW	ND2	0.0049
HLI-0304	7028	C	T	2	617	synonymous_variant	LOW	COX1	0.8089
HLI-0304	8701	A	G	0	537	missense_variant	MODERATE	ATP6	0.3391
HLI-0304	8745	A	G	0	566	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0304	9540	T	C	2	546	synonymous_variant	LOW	COX3	0.339
HLI-0304	10361	T	C	1	598	synonymous_variant	LOW	ND3	4.00E-04
HLI-0304	10398	A	G	2	628	missense_variant	MODERATE	ND3	0.445
HLI-0304	10819	A	G	1	560	synonymous_variant	LOW	ND4	0.0228
HLI-0304	10873	T	C	3	607	synonymous_variant	LOW	ND4	0.3389
HLI-0304	11719	G	A	0	529	synonymous_variant	LOW	ND4	0.7756
HLI-0304	12092	C	T	1	511	missense_variant	MODERATE	ND4	7.00E-04
HLI-0304	12705	C	T	0	623	synonymous_variant	LOW	ND5	0.4212
HLI-0304	13105	A	G	0	629	missense_variant	MODERATE	ND5	0.076
HLI-0304	14182	T	C	0	525	synonymous_variant	LOW	ND6	0.0254
HLI-0304	14212	T	C	0	587	synonymous_variant	LOW	ND6	0.0204
HLI-0304	14766	C	T	1	528	missense_variant	MODERATE	CYTB	0.7696

HLI-0304	14869	G	A	0	605	synonymous_variant	LOW	CYTB	0.0023
HLI-0304	14905	G	A	0	644	synonymous_variant	LOW	CYTB	0.0526
HLI-0304	15301	G	A	0	566	synonymous_variant	LOW	CYTB	0.2912
HLI-0304	15326	A	G	0	610	missense_variant	MODERATE	CYTB	0.9868
HLI-0304	16223	C	T	5	511	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0304	16320	C	T	3	480	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0304	16519	T	C	1	233	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0305	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0305	477	T	C	0	361	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0305	750	A	G	0	577	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0305	1438	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0305	3010	G	A	3	699	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0305	4769	A	G	0	544	synonymous_variant	LOW	ND2	0.9767
HLI-0305	6284	A	G	4	623	synonymous_variant	LOW	COX1	0.0011
HLI-0305	12858	C	T	15	590	synonymous_variant	LOW	ND5	7.00E-04
HLI-0305	15326	A	G	0	540	missense_variant	MODERATE	CYTB	0.9868
HLI-0305	16519	T	C	2	330	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0306	41	C	T	0	157	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0306	73	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0306	150	C	T	1	534	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0306	263	A	G	0	205	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0306	709	G	A	1	614	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0306	750	A	G	0	666	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0306	1438	A	G	0	568	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0306	1888	G	A	0	602	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0306	2706	A	G	2	642	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0306	3798	C	T	7	521	synonymous_variant	LOW	ND1	2.00E-04
HLI-0306	4216	T	C	1	648	missense_variant	MODERATE	ND1	0.0991
HLI-0306	4769	A	G	1	568	synonymous_variant	LOW	ND2	0.9767
HLI-0306	4917	A	G	3	505	missense_variant	MODERATE	ND2	0.0477
HLI-0306	7028	C	T	2	592	synonymous_variant	LOW	COX1	0.8089
HLI-0306	8697	G	A	0	489	synonymous_variant	LOW	ATP6	0.0466
HLI-0306	8790	G	A	1	469	synonymous_variant	LOW	ATP6	0.0083
HLI-0306	10463	T	C	1	606	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0306	11251	A	G	2	530	synonymous_variant	LOW	ND4	0.0932
HLI-0306	11719	G	A	0	557	synonymous_variant	LOW	ND4	0.7756
HLI-0306	11812	A	G	0	542	synonymous_variant	LOW	ND4	0.0332
HLI-0306	13368	G	A	1	597	synonymous_variant	LOW	ND5	0.0495
HLI-0306	14233	A	G	0	581	synonymous_variant	LOW	ND6	0.0369

HLI-0306	14766	C	T	3	572	missense_variant	MODERATE	CYTB	0.7696
HLI-0306	14905	G	A	0	611	synonymous_variant	LOW	CYTB	0.0526
HLI-0306	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0306	15452	C	A	2	498	missense_variant	MODERATE	CYTB	0.0933
HLI-0306	15607	A	G	0	539	synonymous_variant	LOW	CYTB	0.0508
HLI-0306	15928	G	A	0	579	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0306	16126	T	C	1	530	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0306	16153	G	A	1	561	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0306	16256	C	T	1	567	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0306	16294	C	T	4	593	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0307	263	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0307	456	C	T	2	357	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0307	750	A	G	1	608	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0307	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0307	4336	T	C	2	584	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0307	4769	A	G	2	544	synonymous_variant	LOW	ND2	0.9767
HLI-0307	15326	A	G	1	559	missense_variant	MODERATE	CYTB	0.9868
HLI-0307	15833	C	T	0	616	synonymous_variant	LOW	CYTB	0.0051
HLI-0307	16304	T	C	0	477	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0308	73	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0308	150	C	T	3	414	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0308	152	T	C	3	422	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0308	195	T	C	2	409	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0308	263	A	G	0	165	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0308	750	A	G	0	535	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0308	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0308	2352	T	C	0	541	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0308	2706	A	G	1	507	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0308	4769	A	G	0	518	synonymous_variant	LOW	ND2	0.9767
HLI-0308	7028	C	T	2	602	synonymous_variant	LOW	COX1	0.8089
HLI-0308	7858	C	T	1	551	synonymous_variant	LOW	COX2	3.00E-04
HLI-0308	8701	A	G	0	497	missense_variant	MODERATE	ATP6	0.3391
HLI-0308	9540	T	C	0	563	synonymous_variant	LOW	COX3	0.339
HLI-0308	10398	A	G	5	625	missense_variant	MODERATE	ND3	0.445
HLI-0308	10819	A	G	0	555	synonymous_variant	LOW	ND4	0.0228
HLI-0308	10873	T	C	1	579	synonymous_variant	LOW	ND4	0.3389
HLI-0308	11719	G	A	0	505	synonymous_variant	LOW	ND4	0.7756
HLI-0308	12705	C	T	1	549	synonymous_variant	LOW	ND5	0.4212
HLI-0308	13422	A	G	0	508	synonymous_variant	LOW	ND5	0.0021

HLI-0308	14212	T	C	0	503	synonymous_variant	LOW	ND6	0.0204
HLI-0308	14766	C	T	0	472	missense_variant	MODERATE	CYTB	0.7696
HLI-0308	14905	G	A	0	589	synonymous_variant	LOW	CYTB	0.0526
HLI-0308	15301	G	A	0	500	synonymous_variant	LOW	CYTB	0.2912
HLI-0308	15326	A	G	0	564	missense_variant	MODERATE	CYTB	0.9868
HLI-0308	16172	T	C	0	213	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0308	16223	C	T	0	223	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0308	16261	C	T	1	281	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0308	16320	C	T	0	384	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0308	16519	T	C	0	162	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0309	263	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0309	750	A	G	1	603	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0309	1438	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0309	4769	A	G	1	537	synonymous_variant	LOW	ND2	0.9767
HLI-0309	11788	C	T	0	563	synonymous_variant	LOW	ND4	7.00E-04
HLI-0309	15326	A	G	0	589	missense_variant	MODERATE	CYTB	0.9868
HLI-0309	15355	G	A	0	612	synonymous_variant	LOW	CYTB	0.0032
HLI-0309	16519	T	C	1	309	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0310	72	T	C	1	249	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0310	263	A	G	0	161	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0310	750	A	G	1	540	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0310	1438	A	G	0	544	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0310	2706	A	G	0	506	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0310	4769	A	G	3	564	synonymous_variant	LOW	ND2	0.9767
HLI-0310	7028	C	T	3	664	synonymous_variant	LOW	COX1	0.8089
HLI-0310	8577	A	G	2	578	synonymous_variant	LOW	ATP6	0.0012
HLI-0310	12342	C	G	1	527	synonymous_variant	LOW	ND5	0
HLI-0310	15326	A	G	0	532	missense_variant	MODERATE	CYTB	0.9868
HLI-0310	15904	C	T	0	596	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0310	16298	T	C	1	495	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0311	73	A	G	3	248	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0311	150	C	T	2	470	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0311	263	A	G	0	186	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0311	750	A	G	0	491	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0311	1438	A	G	0	564	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0311	1721	C	T	1	499	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0311	2361	G	A	0	608	upstream_gene_variant	MODIFIER	RNR2	0.0027
HLI-0311	2706	A	G	2	523	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0311	3197	T	C	1	467	upstream_gene_variant	MODIFIER	RNR2	0.039

HLI-0311	3397	A	G	1	492	missense_variant	MODERATE	ND1	0.0029
HLI-0311	4732	A	G	1	535	missense_variant	MODERATE	ND2	0.0059
HLI-0311	4769	A	G	0	587	synonymous_variant	LOW	ND2	0.9767
HLI-0311	6293	T	C	2	578	synonymous_variant	LOW	COX1	0.0036
HLI-0311	7028	C	T	1	642	synonymous_variant	LOW	COX1	0.8089
HLI-0311	7768	A	G	2	514	synonymous_variant	LOW	COX2	0.0186
HLI-0311	9477	G	A	2	525	missense_variant	MODERATE	COX3	0.0387
HLI-0311	11173	C	T	0	499	synonymous_variant	LOW	ND4	0
HLI-0311	11467	A	G	1	566	synonymous_variant	LOW	ND4	0.1231
HLI-0311	11719	G	A	2	521	synonymous_variant	LOW	ND4	0.7756
HLI-0311	12308	A	G	1	505	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0311	12372	G	A	3	497	synonymous_variant	LOW	ND5	0.1329
HLI-0311	13368	G	A	2	541	synonymous_variant	LOW	ND5	0.0495
HLI-0311	13617	T	C	0	508	synonymous_variant	LOW	ND5	0.038
HLI-0311	13637	A	G	1	506	missense_variant	MODERATE	ND5	0.0074
HLI-0311	14182	T	C	2	517	synonymous_variant	LOW	ND6	0.0254
HLI-0311	14766	C	T	0	492	missense_variant	MODERATE	CYTB	0.7696
HLI-0311	14767	T	C	0	497	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0311	15326	A	G	1	451	missense_variant	MODERATE	CYTB	0.9868
HLI-0311	16270	C	T	2	361	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0312	152	T	C	1	436	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0312	263	A	G	0	156	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0312	477	T	C	0	327	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0312	750	A	G	0	598	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0312	1438	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0312	3010	G	A	2	578	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0312	4769	A	G	2	604	synonymous_variant	LOW	ND2	0.9767
HLI-0312	11020	A	G	1	412	synonymous_variant	LOW	ND4	0.0019
HLI-0312	14530	T	C	0	367	synonymous_variant	LOW	ND6	9.00E-04
HLI-0312	15326	A	G	0	518	missense_variant	MODERATE	CYTB	0.9868
HLI-0312	16519	T	C	1	258	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0313	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0313	195	T	C	1	330	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0313	263	A	G	0	207	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0313	709	G	A	1	538	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0313	750	A	G	0	577	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0313	1438	A	G	0	666	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0313	1888	G	A	0	412	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0313	2706	A	G	1	552	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0313	4216	T	C	0	460	missense_variant	MODERATE	ND1	0.0991
HLI-0313	4769	A	G	1	525	synonymous_variant	LOW	ND2	0.9767
HLI-0313	4917	A	G	3	531	missense_variant	MODERATE	ND2	0.0477
HLI-0313	6489	C	A	2	592	missense_variant	MODERATE	COX1	0.0016
HLI-0313	7028	C	T	2	648	synonymous_variant	LOW	COX1	0.8089
HLI-0313	8380	T	C	0	324	synonymous_variant	LOW	ATP8	3.00E-04
HLI-0313	8697	G	A	0	486	synonymous_variant	LOW	ATP6	0.0466
HLI-0313	10463	T	C	0	552	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0313	11251	A	G	0	555	synonymous_variant	LOW	ND4	0.0932
HLI-0313	11719	G	A	0	563	synonymous_variant	LOW	ND4	0.7756
HLI-0313	11812	A	G	0	536	synonymous_variant	LOW	ND4	0.0332
HLI-0313	13368	G	A	0	570	synonymous_variant	LOW	ND5	0.0495
HLI-0313	14233	A	G	1	482	synonymous_variant	LOW	ND6	0.0369
HLI-0313	14766	C	T	2	563	missense_variant	MODERATE	CYTB	0.7696
HLI-0313	14905	G	A	0	668	synonymous_variant	LOW	CYTB	0.0526
HLI-0313	15326	A	G	0	440	missense_variant	MODERATE	CYTB	0.9868
HLI-0313	15452	C	A	4	411	missense_variant	MODERATE	CYTB	0.0933
HLI-0313	15607	A	G	0	427	synonymous_variant	LOW	CYTB	0.0508
HLI-0313	15928	G	A	0	406	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0313	16126	T	C	1	268	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0313	16294	C	T	0	309	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0313	16296	C	T	0	309	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0313	16519	T	C	0	164	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0314	73	A	G	2	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0314	195	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0314	198	C	T	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0314	263	A	G	1	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0314	750	A	G	2	570	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0314	1438	A	G	2	631	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0314	2706	A	G	1	592	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0314	3197	T	C	1	592	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0314	4769	A	G	1	615	synonymous_variant	LOW	ND2	0.9767
HLI-0314	7028	C	T	2	695	synonymous_variant	LOW	COX1	0.8089
HLI-0314	9477	G	A	2	637	missense_variant	MODERATE	COX3	0.0387
HLI-0314	11467	A	G	1	626	synonymous_variant	LOW	ND4	0.1231
HLI-0314	11719	G	A	0	585	synonymous_variant	LOW	ND4	0.7756
HLI-0314	12308	A	G	1	533	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0314	12372	G	A	0	505	synonymous_variant	LOW	ND5	0.1329
HLI-0314	13617	T	C	0	607	synonymous_variant	LOW	ND5	0.038

HLI-0314	13802	C	T	1	436	missense_variant	MODERATE	ND5	6.00E-04
HLI-0314	14766	C	T	0	584	missense_variant	MODERATE	CYTB	0.7696
HLI-0314	14793	A	G	1	670	missense_variant	MODERATE	CYTB	0.0199
HLI-0314	15218	A	G	1	574	missense_variant	MODERATE	CYTB	0.0169
HLI-0314	15326	A	G	1	524	missense_variant	MODERATE	CYTB	0.9868
HLI-0314	16256	C	T	0	612	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0314	16270	C	T	0	600	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0314	16320	C	T	0	521	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0314	16399	A	G	0	468	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0315	73	A	G	1	254	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0315	143	G	A	2	483	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0315	263	A	G	1	251	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0315	709	G	A	0	565	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0315	750	A	G	2	621	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0315	1040	T	C	0	674	upstream_gene_variant	MODIFIER	RNR1	0.0024
HLI-0315	1438	A	G	0	596	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0315	2259	C	T	0	443	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0315	2873	A	G	0	565	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0315	4769	A	G	1	502	synonymous_variant	LOW	ND2	0.9767
HLI-0315	12406	G	A	1	347	missense_variant	MODERATE	ND5	0.0262
HLI-0315	12904	A	G	6	541	missense_variant	MODERATE	ND5	0.0011
HLI-0315	13762	T	G	1	406	missense_variant	MODERATE	ND5	7.00E-04
HLI-0315	14872	C	T	6	606	synonymous_variant	LOW	CYTB	0.0061
HLI-0315	15326	A	G	0	392	missense_variant	MODERATE	CYTB	0.9868
HLI-0315	16212	A	G	0	536	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0316	73	A	G	0	31	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0316	152	T	C	0	61	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0316	199	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0316	204	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0316	207	G	A	0	51	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0316	250	T	C	0	30	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0316	263	A	G	0	28	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0316	750	A	G	0	59	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0316	1438	A	G	0	38	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0316	1719	G	A	0	30	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0316	2706	A	G	0	50	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0316	4529	A	T	0	45	synonymous_variant	LOW	ND2	0.015
HLI-0316	4769	A	G	1	47	synonymous_variant	LOW	ND2	0.9767
HLI-0316	5492	T	C	0	47	synonymous_variant	LOW	ND2	0.0029

HLI-0316	5561	T	C	0	54	upstream_gene_variant	MODIFIER	TRNW	2.00E-04
HLI-0316	7028	C	T	0	84	synonymous_variant	LOW	COX1	0.8089
HLI-0316	8251	G	A	0	42	synonymous_variant	LOW	COX2	0.058
HLI-0316	10034	T	C	0	43	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0316	10238	T	C	0	46	synonymous_variant	LOW	ND3	0.0623
HLI-0316	10398	A	G	0	42	missense_variant	MODERATE	ND3	0.445
HLI-0316	11719	G	A	0	48	synonymous_variant	LOW	ND4	0.7756
HLI-0316	12501	G	A	0	33	synonymous_variant	LOW	ND5	0.0258
HLI-0316	12705	C	T	0	50	synonymous_variant	LOW	ND5	0.4212
HLI-0316	12715	A	G	0	46	missense_variant	MODERATE	ND5	0.001
HLI-0316	13780	A	G	0	29	missense_variant	MODERATE	ND5	0.0179
HLI-0316	14766	C	T	0	60	missense_variant	MODERATE	CYTB	0.7696
HLI-0316	15043	G	A	0	76	synonymous_variant	LOW	CYTB	0.2362
HLI-0316	15326	A	G	0	45	missense_variant	MODERATE	CYTB	0.9868
HLI-0316	15758	A	G	0	31	missense_variant	MODERATE	CYTB	0.0076
HLI-0316	15924	A	G	0	21	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0316	16129	G	A	0	51	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0316	16223	C	T	0	52	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0316	16391	G	A	0	53	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0316	16519	T	C	0	32	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0317	73	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0317	146	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0317	150	C	T	0	388	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0317	152	T	C	0	389	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0317	195	T	C	0	370	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0317	263	A	G	0	144	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0317	750	A	G	1	514	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0317	769	G	A	0	556	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0317	1018	G	A	3	627	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0317	1438	A	G	0	500	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0317	2416	T	C	0	322	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0317	2706	A	G	2	470	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0317	2789	C	T	1	532	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0317	3594	C	T	1	388	synonymous_variant	LOW	ND1	0.0789
HLI-0317	4104	A	G	1	362	synonymous_variant	LOW	ND1	0.0785
HLI-0317	4769	A	G	1	442	synonymous_variant	LOW	ND2	0.9767
HLI-0317	5581	A	G	0	563	upstream_gene_variant	MODIFIER	Unannotated	0.005
HLI-0317	6227	T	C	0	419	synonymous_variant	LOW	COX1	0.0019
HLI-0317	7028	C	T	3	574	synonymous_variant	LOW	COX1	0.8089

HLI-0317	7175	T	C	0	493	synonymous_variant	LOW	COX1	0.0224
HLI-0317	7256	C	T	2	507	synonymous_variant	LOW	COX1	0.0784
HLI-0317	7274	C	T	1	461	synonymous_variant	LOW	COX1	0.0214
HLI-0317	7521	G	A	0	296	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0317	7771	A	G	0	473	synonymous_variant	LOW	COX2	0.0223
HLI-0317	8206	G	A	1	389	synonymous_variant	LOW	COX2	0.0287
HLI-0317	8701	A	G	1	389	missense_variant	MODERATE	ATP6	0.3391
HLI-0317	9221	A	G	0	549	synonymous_variant	LOW	COX3	0.0277
HLI-0317	9540	T	C	0	347	synonymous_variant	LOW	COX3	0.339
HLI-0317	10115	T	C	0	536	synonymous_variant	LOW	ND3	0.0278
HLI-0317	10398	A	G	0	403	missense_variant	MODERATE	ND3	0.445
HLI-0317	10873	T	C	0	359	synonymous_variant	LOW	ND4	0.3389
HLI-0317	11719	G	A	0	511	synonymous_variant	LOW	ND4	0.7756
HLI-0317	11914	G	A	1	447	synonymous_variant	LOW	ND4	0.1112
HLI-0317	11944	T	C	1	451	synonymous_variant	LOW	ND4	0.0331
HLI-0317	12693	A	G	2	484	synonymous_variant	LOW	ND5	0.0205
HLI-0317	12705	C	T	2	498	synonymous_variant	LOW	ND5	0.4212
HLI-0317	13590	G	A	1	396	synonymous_variant	LOW	ND5	0.0586
HLI-0317	13650	C	T	1	421	synonymous_variant	LOW	ND5	0.079
HLI-0317	13803	A	G	0	277	synonymous_variant	LOW	ND5	0.0216
HLI-0317	14566	A	G	0	500	synonymous_variant	LOW	ND6	0.0214
HLI-0317	14766	C	T	5	555	missense_variant	MODERATE	CYTB	0.7696
HLI-0317	15301	G	A	0	352	synonymous_variant	LOW	CYTB	0.2912
HLI-0317	15326	A	G	0	364	missense_variant	MODERATE	CYTB	0.9868
HLI-0317	15784	T	C	0	334	synonymous_variant	LOW	CYTB	0.0363
HLI-0317	16223	C	T	2	407	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0317	16278	C	T	1	363	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0317	16294	C	T	0	351	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0317	16309	A	G	0	336	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0317	16390	G	A	0	318	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0317	16519	T	C	0	165	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0318	73	A	G	0	307	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0318	195	T	C	1	389	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0318	263	A	G	1	176	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0318	499	G	A	1	340	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0318	629	T	C	0	569	upstream_gene_variant	MODIFIER	TRNF	0.0026
HLI-0318	750	A	G	1	636	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0318	1438	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0318	1811	A	G	2	674	upstream_gene_variant	MODIFIER	RNR2	0.0763

HLI-0318	2706	A	G	1	665	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0318	2772	C	T	1	690	upstream_gene_variant	MODIFIER	RNR2	0.0034
HLI-0318	4646	T	C	4	698	synonymous_variant	LOW	ND2	0.0124
HLI-0318	4769	A	G	1	561	synonymous_variant	LOW	ND2	0.9767
HLI-0318	5984	A	G	2	639	synonymous_variant	LOW	COX1	0.002
HLI-0318	5999	T	C	2	689	synonymous_variant	LOW	COX1	0.0127
HLI-0318	6047	A	G	2	700	synonymous_variant	LOW	COX1	0.0114
HLI-0318	6938	C	T	6	670	synonymous_variant	LOW	COX1	0.0024
HLI-0318	7028	C	T	0	751	synonymous_variant	LOW	COX1	0.8089
HLI-0318	8260	T	C	2	527	synonymous_variant	LOW	COX2	0.001
HLI-0318	11332	C	T	1	615	synonymous_variant	LOW	ND4	0.0115
HLI-0318	11467	A	G	1	636	synonymous_variant	LOW	ND4	0.1231
HLI-0318	11719	G	A	0	645	synonymous_variant	LOW	ND4	0.7756
HLI-0318	12308	A	G	2	599	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0318	12372	G	A	1	601	synonymous_variant	LOW	ND5	0.1329
HLI-0318	14620	C	T	2	595	synonymous_variant	LOW	ND6	0.0126
HLI-0318	14766	C	T	4	579	missense_variant	MODERATE	CYTB	0.7696
HLI-0318	15326	A	G	1	596	missense_variant	MODERATE	CYTB	0.9868
HLI-0318	15693	T	C	1	678	missense_variant	MODERATE	CYTB	0.0114
HLI-0318	16356	T	C	1	550	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0318	16519	T	C	0	309	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0319	73	A	G	0	290	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0319	189	A	G	0	446	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0319	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0319	750	A	G	1	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0319	1438	A	G	1	613	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0319	2706	A	G	1	638	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0319	3348	A	G	2	658	synonymous_variant	LOW	ND1	0.0065
HLI-0319	3591	G	A	0	587	synonymous_variant	LOW	ND1	0.0082
HLI-0319	4769	A	G	2	606	synonymous_variant	LOW	ND2	0.9767
HLI-0319	5261	G	A	0	575	synonymous_variant	LOW	ND2	0.0021
HLI-0319	7028	C	T	2	698	synonymous_variant	LOW	COX1	0.8089
HLI-0319	7642	G	A	0	536	synonymous_variant	LOW	COX2	0.0018
HLI-0319	7805	G	A	0	636	missense_variant	MODERATE	COX2	0.0077
HLI-0319	10978	A	G	0	436	synonymous_variant	LOW	ND4	0.0036
HLI-0319	11467	A	G	0	672	synonymous_variant	LOW	ND4	0.1231
HLI-0319	11719	G	A	0	569	synonymous_variant	LOW	ND4	0.7756
HLI-0319	12308	A	G	0	482	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0319	12372	G	A	0	489	synonymous_variant	LOW	ND5	0.1329

HLI-0319	12406	G	A	0	472	missense_variant	MODERATE	ND5	0.0262
HLI-0319	13590	G	A	0	588	synonymous_variant	LOW	ND5	0.0586
HLI-0319	14179	A	G	0	552	synonymous_variant	LOW	ND6	0.0053
HLI-0319	14674	T	C	0	612	upstream_gene_variant	MODIFIER	TRNE	1.00E-04
HLI-0319	14766	C	T	1	585	missense_variant	MODERATE	CYTB	0.7696
HLI-0319	15326	A	G	0	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0319	15927	G	A	0	625	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0319	16172	T	C	1	544	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0319	16219	A	G	0	564	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0319	16278	C	T	2	536	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0319	16519	T	C	0	229	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0320	263	A	G	1	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0320	750	A	G	1	576	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0320	1438	A	G	0	602	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0320	4769	A	G	1	565	synonymous_variant	LOW	ND2	0.9767
HLI-0320	8155	G	A	0	649	synonymous_variant	LOW	COX2	0.0031
HLI-0320	11440	G	A	0	627	synonymous_variant	LOW	ND4	0.0081
HLI-0320	15326	A	G	0	564	missense_variant	MODERATE	CYTB	0.9868
HLI-0320	16519	T	C	0	270	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0321	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0321	150	C	T	1	475	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0321	152	T	C	1	471	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0321	263	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0321	295	C	T	0	142	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0321	489	T	C	0	307	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0321	709	G	A	2	585	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0321	750	A	G	0	613	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0321	1438	A	G	1	561	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0321	2706	A	G	0	617	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0321	4216	T	C	2	616	missense_variant	MODERATE	ND1	0.0991
HLI-0321	4769	A	G	2	543	synonymous_variant	LOW	ND2	0.9767
HLI-0321	5633	C	T	0	611	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0321	7028	C	T	4	617	synonymous_variant	LOW	COX1	0.8089
HLI-0321	7476	C	T	2	557	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0321	9909	T	C	1	622	missense_variant	MODERATE	COX3	2.00E-04
HLI-0321	10172	G	A	2	554	synonymous_variant	LOW	ND3	0.0084
HLI-0321	10398	A	G	1	568	missense_variant	MODERATE	ND3	0.445
HLI-0321	11251	A	G	4	538	synonymous_variant	LOW	ND4	0.0932
HLI-0321	11719	G	A	1	607	synonymous_variant	LOW	ND4	0.7756

HLI-0321	12612	A	G	0	597	synonymous_variant	LOW	ND5	0.0506
HLI-0321	13708	G	A	1	446	missense_variant	MODERATE	ND5	0.0717
HLI-0321	14766	C	T	5	531	missense_variant	MODERATE	CYTB	0.7696
HLI-0321	15257	G	A	2	534	missense_variant	MODERATE	CYTB	0.0155
HLI-0321	15326	A	G	0	557	missense_variant	MODERATE	CYTB	0.9868
HLI-0321	15452	C	A	6	484	missense_variant	MODERATE	CYTB	0.0933
HLI-0321	15812	G	A	2	572	missense_variant	MODERATE	CYTB	0.0096
HLI-0321	16069	C	T	4	511	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0321	16126	T	C	0	542	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0321	16278	C	T	4	475	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0321	16519	T	C	0	225	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0322	64	C	T	0	197	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0322	93	A	G	1	256	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0322	152	T	C	0	276	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0322	185	G	A	0	261	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0322	189	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0322	200	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0322	236	T	C	0	236	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0322	247	G	A	0	238	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0322	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0322	750	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0322	769	G	A	0	676	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0322	825	T	A	0	653	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0322	1018	G	A	1	666	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0322	1048	C	T	0	722	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0322	1438	A	G	1	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0322	2245	A	G	1	568	upstream_gene_variant	MODIFIER	RNR2	0.0145
HLI-0322	2706	A	G	0	618	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0322	2758	G	A	2	655	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0322	2885	T	C	0	621	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0322	3516	C	A	4	514	synonymous_variant	LOW	ND1	0.0315
HLI-0322	3594	C	T	3	522	synonymous_variant	LOW	ND1	0.0789
HLI-0322	3866	T	C	2	557	missense_variant	MODERATE	ND1	0.0029
HLI-0322	4104	A	G	0	449	synonymous_variant	LOW	ND1	0.0785
HLI-0322	4312	C	T	2	507	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0322	4586	T	C	0	551	synonymous_variant	LOW	ND2	0.018
HLI-0322	4769	A	G	0	616	synonymous_variant	LOW	ND2	0.9767
HLI-0322	5096	T	C	1	599	synonymous_variant	LOW	ND2	0.0063
HLI-0322	5231	G	A	2	530	synonymous_variant	LOW	ND2	0.0232

HLI-0322	5442	T	C	0	619	missense_variant	MODERATE	ND2	0.0493
HLI-0322	5460	G	A	0	655	missense_variant	MODERATE	ND2	0.0651
HLI-0322	5603	C	T	3	582	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0322	6185	T	C	0	580	synonymous_variant	LOW	COX1	0.0325
HLI-0322	7028	C	T	1	558	synonymous_variant	LOW	COX1	0.8089
HLI-0322	7146	A	G	1	278	missense_variant	MODERATE	COX1	0.0497
HLI-0322	7256	C	T	4	401	synonymous_variant	LOW	COX1	0.0784
HLI-0322	7521	G	A	2	406	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0322	8428	C	T	3	526	synonymous_variant	LOW	ATP8	0.0144
HLI-0322	8468	C	T	1	544	synonymous_variant	LOW	ATP8	0.0501
HLI-0322	8566	A	G	0	482	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0322	8655	C	T	7	447	synonymous_variant	LOW	ATP6	0.0511
HLI-0322	8701	A	G	3	500	missense_variant	MODERATE	ATP6	0.3391
HLI-0322	9042	C	T	4	604	synonymous_variant	LOW	ATP6	0.0316
HLI-0322	9347	A	G	1	598	synonymous_variant	LOW	COX3	0.0314
HLI-0322	9540	T	C	2	613	synonymous_variant	LOW	COX3	0.339
HLI-0322	9755	G	A	2	644	synonymous_variant	LOW	COX3	0.0303
HLI-0322	9818	C	T	0	744	synonymous_variant	LOW	COX3	0.0179
HLI-0322	10398	A	G	2	570	missense_variant	MODERATE	ND3	0.445
HLI-0322	10589	G	A	0	559	synonymous_variant	LOW	ND4L	0.0355
HLI-0322	10664	C	T	0	584	synonymous_variant	LOW	ND4L	0.0315
HLI-0322	10688	G	A	0	563	synonymous_variant	LOW	ND4L	0.0515
HLI-0322	10810	T	C	0	562	synonymous_variant	LOW	ND4	0.0522
HLI-0322	10873	T	C	0	428	synonymous_variant	LOW	ND4	0.3389
HLI-0322	10915	T	C	0	499	synonymous_variant	LOW	ND4	0.0411
HLI-0322	11176	G	A	2	572	synonymous_variant	LOW	ND4	0.0181
HLI-0322	11641	A	G	2	561	synonymous_variant	LOW	ND4	0.0158
HLI-0322	11719	G	A	2	666	synonymous_variant	LOW	ND4	0.7756
HLI-0322	11914	G	A	0	567	synonymous_variant	LOW	ND4	0.1112
HLI-0322	12007	G	A	2	575	synonymous_variant	LOW	ND4	0.0639
HLI-0322	12705	C	T	1	671	synonymous_variant	LOW	ND5	0.4212
HLI-0322	12720	A	G	5	742	synonymous_variant	LOW	ND5	0.0302
HLI-0322	13105	A	G	0	614	missense_variant	MODERATE	ND5	0.076
HLI-0322	13276	A	G	1	597	missense_variant	MODERATE	ND5	0.0312
HLI-0322	13506	C	T	1	570	synonymous_variant	LOW	ND5	0.0506
HLI-0322	13650	C	T	2	544	synonymous_variant	LOW	ND5	0.079
HLI-0322	14308	T	C	1	471	synonymous_variant	LOW	ND6	0.0209
HLI-0322	14766	C	T	4	533	missense_variant	MODERATE	CYTB	0.7696
HLI-0322	15136	C	T	1	666	synonymous_variant	LOW	CYTB	0.0153

HLI-0322	15326	A	G	0	565	missense_variant	MODERATE	CYTB	0.9868
HLI-0322	15431	G	A	3	540	missense_variant	MODERATE	CYTB	0.0182
HLI-0322	16069	C	T	2	581	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0322	16129	G	A	0	433	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0322	16148	C	T	0	491	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0322	16168	C	T	0	455	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0322	16172	T	C	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0322	16223	C	T	0	411	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0322	16230	A	G	0	402	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0322	16278	C	T	0	390	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0322	16309	A	G	0	371	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0322	16311	T	C	0	371	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0322	16320	C	T	0	370	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0323	263	A	G	0	127	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0323	750	A	G	0	550	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0323	1438	A	G	1	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0323	1508	C	T	4	592	upstream_gene_variant	MODIFIER	RNR1	5.00E-04
HLI-0323	3010	G	A	2	559	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0323	4769	A	G	0	541	synonymous_variant	LOW	ND2	0.9767
HLI-0323	7830	G	A	2	590	missense_variant	MODERATE	COX2	9.00E-04
HLI-0323	15326	A	G	0	582	missense_variant	MODERATE	CYTB	0.9868
HLI-0323	16519	T	C	0	144	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0324	73	A	G	0	253	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0324	159	T	C	3	436	upstream_gene_variant	MODIFIER	DLoop	0.001
HLI-0324	263	A	G	0	173	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0324	499	G	A	1	347	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0324	750	A	G	0	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0324	827	A	G	2	656	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0324	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0324	2706	A	G	0	621	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0324	2804	A	G	1	578	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0324	3547	A	G	1	574	missense_variant	MODERATE	ND1	0.0176
HLI-0324	4769	A	G	0	487	synonymous_variant	LOW	ND2	0.9767
HLI-0324	4820	G	A	0	506	synonymous_variant	LOW	ND2	0.0239
HLI-0324	4977	T	C	1	549	synonymous_variant	LOW	ND2	0.0177
HLI-0324	6473	C	T	4	595	synonymous_variant	LOW	COX1	0.0173
HLI-0324	6647	A	C	2	655	synonymous_variant	LOW	COX1	1.00E-04
HLI-0324	7028	C	T	3	645	synonymous_variant	LOW	COX1	0.8089
HLI-0324	9950	T	C	3	630	synonymous_variant	LOW	COX3	0.0362

HLI-0324	11177	C	T	0	557	missense_variant	MODERATE	ND4	0.019
HLI-0324	11719	G	A	1	552	synonymous_variant	LOW	ND4	0.7756
HLI-0324	13590	G	A	0	579	synonymous_variant	LOW	ND5	0.0586
HLI-0324	14106	T	C	0	474	synonymous_variant	LOW	ND5	8.00E-04
HLI-0324	14766	C	T	2	537	missense_variant	MODERATE	CYTB	0.7696
HLI-0324	15326	A	G	0	519	missense_variant	MODERATE	CYTB	0.9868
HLI-0324	15535	C	T	3	458	synonymous_variant	LOW	CYTB	0.023
HLI-0324	16092	T	C	4	354	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0324	16217	T	C	0	147	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0324	16519	T	C	0	170	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0325	55	T	C	0	235	upstream_gene_variant	MODIFIER	DLoop	0.0022
HLI-0325	57	T	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0325	263	A	G	0	183	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0325	750	A	G	1	639	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0325	1438	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0325	4769	A	G	1	621	synonymous_variant	LOW	ND2	0.9767
HLI-0325	6253	T	C	2	706	missense_variant	MODERATE	COX1	0.0106
HLI-0325	11050	T	C	0	532	synonymous_variant	LOW	ND4	0.001
HLI-0325	11410	T	C	1	631	synonymous_variant	LOW	ND4	0.002
HLI-0325	14953	C	T	2	648	synonymous_variant	LOW	CYTB	0.0019
HLI-0325	15326	A	G	0	617	missense_variant	MODERATE	CYTB	0.9868
HLI-0325	16129	G	A	2	603	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0326	72	T	G	1	326	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0326	146	T	C	2	513	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0326	195	T	C	1	497	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0326	263	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0326	750	A	G	0	674	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0326	1438	A	G	2	714	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0326	4769	A	G	1	637	synonymous_variant	LOW	ND2	0.9767
HLI-0326	7930	A	T	1	647	synonymous_variant	LOW	COX2	0.001
HLI-0326	10771	A	G	0	557	synonymous_variant	LOW	ND4	0.001
HLI-0326	15326	A	G	1	568	missense_variant	MODERATE	CYTB	0.9868
HLI-0326	16319	G	A	2	529	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0326	16519	T	C	1	248	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0327	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0327	750	A	G	0	665	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0327	980	T	C	1	742	upstream_gene_variant	MODIFIER	RNR1	0.0112
HLI-0327	1438	A	G	1	674	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0327	3010	G	A	2	664	upstream_gene_variant	MODIFIER	RNR2	0.1449

HLI-0327	4769	A	G	0	618	synonymous_variant	LOW	ND2	0.9767
HLI-0327	15326	A	G	0	586	missense_variant	MODERATE	CYTB	0.9868
HLI-0327	16209	T	C	2	712	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0327	16519	T	C	0	306	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0328	73	A	G	1	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0328	242	C	T	0	287	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0328	263	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0328	295	C	T	0	210	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0328	462	C	T	2	417	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0328	489	T	C	0	506	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0328	750	A	G	0	654	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0328	1438	A	G	0	668	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0328	2158	T	C	1	571	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0328	2706	A	G	1	678	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0328	3010	G	A	1	690	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0328	4216	T	C	0	627	missense_variant	MODERATE	ND1	0.0991
HLI-0328	4769	A	G	1	606	synonymous_variant	LOW	ND2	0.9767
HLI-0328	5460	G	A	0	653	missense_variant	MODERATE	ND2	0.0651
HLI-0328	7028	C	T	3	736	synonymous_variant	LOW	COX1	0.8089
HLI-0328	8269	G	A	0	570	stop_retained_variant	LOW	COX2	0.0127
HLI-0328	8557	G	A	1	543	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0328	10398	A	G	0	624	missense_variant	MODERATE	ND3	0.445
HLI-0328	11251	A	G	1	661	synonymous_variant	LOW	ND4	0.0932
HLI-0328	11719	G	A	2	638	synonymous_variant	LOW	ND4	0.7756
HLI-0328	12007	G	A	0	543	synonymous_variant	LOW	ND4	0.0639
HLI-0328	12612	A	G	2	614	synonymous_variant	LOW	ND5	0.0506
HLI-0328	13708	G	A	0	362	missense_variant	MODERATE	ND5	0.0717
HLI-0328	13879	T	C	0	468	missense_variant	MODERATE	ND5	0.0073
HLI-0328	14766	C	T	2	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0328	15326	A	G	0	607	missense_variant	MODERATE	CYTB	0.9868
HLI-0328	15452	C	A	5	564	missense_variant	MODERATE	CYTB	0.0933
HLI-0328	16069	C	T	0	596	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0328	16126	T	C	0	633	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0328	16145	G	A	0	605	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0328	16172	T	C	0	633	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0328	16261	C	T	1	634	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0329	73	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0329	152	T	C	0	520	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0329	195	T	C	2	486	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0329	263	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0329	709	G	A	0	581	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0329	750	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0329	1438	A	G	0	634	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0329	1888	G	A	0	383	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0329	2706	A	G	2	559	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0329	4216	T	C	0	495	missense_variant	MODERATE	ND1	0.0991
HLI-0329	4769	A	G	1	560	synonymous_variant	LOW	ND2	0.9767
HLI-0329	4917	A	G	7	555	missense_variant	MODERATE	ND2	0.0477
HLI-0329	7028	C	T	4	674	synonymous_variant	LOW	COX1	0.8089
HLI-0329	8697	G	A	0	524	synonymous_variant	LOW	ATP6	0.0466
HLI-0329	9899	T	C	0	644	synonymous_variant	LOW	COX3	0.0108
HLI-0329	10463	T	C	1	534	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0329	11170	C	T	1	533	synonymous_variant	LOW	ND4	2.00E-04
HLI-0329	11251	A	G	1	584	synonymous_variant	LOW	ND4	0.0932
HLI-0329	11719	G	A	0	571	synonymous_variant	LOW	ND4	0.7756
HLI-0329	12633	C	A	4	475	synonymous_variant	LOW	ND5	0.0123
HLI-0329	13368	G	A	0	620	synonymous_variant	LOW	ND5	0.0495
HLI-0329	14178	T	C	1	427	missense_variant	MODERATE	ND6	0.0225
HLI-0329	14766	C	T	2	593	missense_variant	MODERATE	CYTB	0.7696
HLI-0329	14905	G	A	0	752	synonymous_variant	LOW	CYTB	0.0526
HLI-0329	15326	A	G	0	462	missense_variant	MODERATE	CYTB	0.9868
HLI-0329	15452	C	A	1	396	missense_variant	MODERATE	CYTB	0.0933
HLI-0329	15607	A	G	0	417	synonymous_variant	LOW	CYTB	0.0508
HLI-0329	15928	G	A	2	424	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0329	16126	T	C	1	517	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0329	16163	A	G	0	550	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0329	16294	C	T	0	515	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0329	16519	T	C	1	324	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0330	64	C	T	0	216	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0330	93	A	G	0	317	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0330	152	T	C	1	344	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0330	185	G	A	1	369	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0330	189	A	G	1	359	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0330	200	A	G	2	347	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0330	236	T	C	0	137	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0330	247	G	A	0	146	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0330	263	A	G	1	163	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0330	709	G	A	0	631	upstream_gene_variant	MODIFIER	RNR1	0.1279

HLI-0330	750	A	G	0	695	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0330	769	G	A	0	673	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0330	825	T	A	0	660	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0330	1018	G	A	0	687	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0330	1048	C	T	0	758	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0330	1438	A	G	2	645	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0330	2245	A	G	0	622	upstream_gene_variant	MODIFIER	RNR2	0.0145
HLI-0330	2706	A	G	1	651	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0330	2758	G	A	1	672	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0330	2885	T	C	0	684	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0330	2951	A	G	2	714	upstream_gene_variant	MODIFIER	RNR2	2.00E-04
HLI-0330	3516	C	A	8	625	synonymous_variant	LOW	ND1	0.0315
HLI-0330	3594	C	T	0	624	synonymous_variant	LOW	ND1	0.0789
HLI-0330	3866	T	C	0	596	missense_variant	MODERATE	ND1	0.0029
HLI-0330	3924	A	G	0	667	synonymous_variant	LOW	ND1	0
HLI-0330	4104	A	G	0	482	synonymous_variant	LOW	ND1	0.0785
HLI-0330	4312	C	T	0	524	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0330	4586	T	C	0	545	synonymous_variant	LOW	ND2	0.018
HLI-0330	4769	A	G	2	563	synonymous_variant	LOW	ND2	0.9767
HLI-0330	5096	T	C	2	617	synonymous_variant	LOW	ND2	0.0063
HLI-0330	5231	G	A	1	577	synonymous_variant	LOW	ND2	0.0232
HLI-0330	5442	T	C	0	682	missense_variant	MODERATE	ND2	0.0493
HLI-0330	5460	G	A	0	732	missense_variant	MODERATE	ND2	0.0651
HLI-0330	5603	C	T	2	714	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0330	6185	T	C	2	646	synonymous_variant	LOW	COX1	0.0325
HLI-0330	7028	C	T	0	615	synonymous_variant	LOW	COX1	0.8089
HLI-0330	7146	A	G	0	343	missense_variant	MODERATE	COX1	0.0497
HLI-0330	7256	C	T	5	483	synonymous_variant	LOW	COX1	0.0784
HLI-0330	7258	T	C	5	489	missense_variant	MODERATE	COX1	0.001
HLI-0330	7521	G	A	0	377	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0330	8428	C	T	3	564	synonymous_variant	LOW	ATP8	0.0144
HLI-0330	8468	C	T	0	581	synonymous_variant	LOW	ATP8	0.0501
HLI-0330	8566	A	G	1	530	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0330	8655	C	T	2	535	synonymous_variant	LOW	ATP6	0.0511
HLI-0330	8701	A	G	1	581	missense_variant	MODERATE	ATP6	0.3391
HLI-0330	9042	C	T	0	676	synonymous_variant	LOW	ATP6	0.0316
HLI-0330	9181	A	G	1	693	missense_variant	MODERATE	ATP6	0.0018
HLI-0330	9347	A	G	0	683	synonymous_variant	LOW	COX3	0.0314
HLI-0330	9540	T	C	0	669	synonymous_variant	LOW	COX3	0.339

HLI-0330	9755	G	A	0	687	synonymous_variant	LOW	COX3	0.0303
HLI-0330	9818	C	T	2	738	synonymous_variant	LOW	COX3	0.0179
HLI-0330	10398	A	G	1	714	missense_variant	MODERATE	ND3	0.445
HLI-0330	10589	G	A	1	574	synonymous_variant	LOW	ND4L	0.0355
HLI-0330	10664	C	T	2	608	synonymous_variant	LOW	ND4L	0.0315
HLI-0330	10688	G	A	3	601	synonymous_variant	LOW	ND4L	0.0515
HLI-0330	10810	T	C	0	570	synonymous_variant	LOW	ND4	0.0522
HLI-0330	10873	T	C	0	471	synonymous_variant	LOW	ND4	0.3389
HLI-0330	10915	T	C	1	524	synonymous_variant	LOW	ND4	0.0411
HLI-0330	11176	G	A	2	602	synonymous_variant	LOW	ND4	0.0181
HLI-0330	11641	A	G	1	618	synonymous_variant	LOW	ND4	0.0158
HLI-0330	11719	G	A	0	702	synonymous_variant	LOW	ND4	0.7756
HLI-0330	11914	G	A	1	654	synonymous_variant	LOW	ND4	0.1112
HLI-0330	12007	G	A	0	566	synonymous_variant	LOW	ND4	0.0639
HLI-0330	12705	C	T	1	702	synonymous_variant	LOW	ND5	0.4212
HLI-0330	12720	A	G	1	763	synonymous_variant	LOW	ND5	0.0302
HLI-0330	13105	A	G	1	653	missense_variant	MODERATE	ND5	0.076
HLI-0330	13276	A	G	0	674	missense_variant	MODERATE	ND5	0.0312
HLI-0330	13506	C	T	0	616	synonymous_variant	LOW	ND5	0.0506
HLI-0330	13650	C	T	2	558	synonymous_variant	LOW	ND5	0.079
HLI-0330	14308	T	C	1	498	synonymous_variant	LOW	ND6	0.0209
HLI-0330	14766	C	T	3	624	missense_variant	MODERATE	CYTB	0.7696
HLI-0330	15136	C	T	0	644	synonymous_variant	LOW	CYTB	0.0153
HLI-0330	15326	A	G	0	575	missense_variant	MODERATE	CYTB	0.9868
HLI-0330	15431	G	A	3	560	missense_variant	MODERATE	CYTB	0.0182
HLI-0330	15721	T	C	0	616	synonymous_variant	LOW	CYTB	0.0033
HLI-0330	15839	C	T	0	596	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0330	16129	G	A	0	594	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0330	16148	C	T	0	539	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0330	16168	C	T	0	497	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0330	16172	T	C	0	496	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0330	16223	C	T	0	503	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0330	16230	A	G	0	506	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0330	16311	T	C	0	508	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0330	16320	C	T	0	511	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0330	16519	T	C	0	185	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0331	204	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0331	239	T	C	1	36	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0331	263	A	G	0	28	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0331	750	A	G	0	43	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0331	1438	A	G	0	34	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0331	3915	G	A	0	50	synonymous_variant	LOW	ND1	0.0106
HLI-0331	4727	A	G	0	42	synonymous_variant	LOW	ND2	0.0063
HLI-0331	4769	A	G	0	37	synonymous_variant	LOW	ND2	0.9767
HLI-0331	9380	G	A	0	64	synonymous_variant	LOW	COX3	0.0094
HLI-0331	10589	G	A	0	46	synonymous_variant	LOW	ND4L	0.0355
HLI-0331	15326	A	G	0	45	missense_variant	MODERATE	CYTB	0.9868
HLI-0331	16219	A	G	0	48	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0331	16362	T	C	0	54	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0331	16482	A	G	0	33	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0332	73	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0332	263	A	G	1	212	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0332	295	C	T	0	149	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0332	462	C	T	2	438	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0332	489	T	C	0	462	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0332	750	A	G	1	614	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0332	1438	A	G	0	612	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0332	2706	A	G	0	644	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0332	3010	G	A	0	580	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0332	4216	T	C	0	641	missense_variant	MODERATE	ND1	0.0991
HLI-0332	4769	A	G	2	524	synonymous_variant	LOW	ND2	0.9767
HLI-0332	7028	C	T	0	641	synonymous_variant	LOW	COX1	0.8089
HLI-0332	10398	A	G	1	623	missense_variant	MODERATE	ND3	0.445
HLI-0332	11251	A	G	1	556	synonymous_variant	LOW	ND4	0.0932
HLI-0332	11719	G	A	0	550	synonymous_variant	LOW	ND4	0.7756
HLI-0332	12612	A	G	4	532	synonymous_variant	LOW	ND5	0.0506
HLI-0332	13708	G	A	1	496	missense_variant	MODERATE	ND5	0.0717
HLI-0332	14766	C	T	6	587	missense_variant	MODERATE	CYTB	0.7696
HLI-0332	14798	T	C	1	649	missense_variant	MODERATE	CYTB	0.0651
HLI-0332	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868
HLI-0332	15452	C	A	7	515	missense_variant	MODERATE	CYTB	0.0933
HLI-0332	16069	C	T	4	539	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0332	16126	T	C	1	589	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0332	16261	C	T	1	534	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0333	263	A	G	0	186	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0333	750	A	G	2	610	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0333	1438	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0333	3010	G	A	2	794	upstream_gene_variant	MODIFIER	RNR2	0.1449

HLI-0333	3796	A	G	1	801	missense_variant	MODERATE	ND1	0.0048
HLI-0333	4769	A	G	1	610	synonymous_variant	LOW	ND2	0.9767
HLI-0333	8994	G	A	4	351	synonymous_variant	LOW	ATP6	0.0167
HLI-0333	15326	A	G	1	733	missense_variant	MODERATE	CYTB	0.9868
HLI-0333	16129	G	A	0	424	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0333	16355	C	T	2	434	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0333	16356	T	C	2	437	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0333	16362	T	C	2	460	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0333	16519	T	C	0	223	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0334	152	T	C	0	479	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0334	263	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0334	750	A	G	2	601	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0334	1438	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0334	2259	C	T	2	531	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0334	4745	A	G	0	606	synonymous_variant	LOW	ND2	0.0039
HLI-0334	4769	A	G	0	657	synonymous_variant	LOW	ND2	0.9767
HLI-0334	14872	C	T	2	616	synonymous_variant	LOW	CYTB	0.0061
HLI-0334	15326	A	G	1	542	missense_variant	MODERATE	CYTB	0.9868
HLI-0334	16234	C	T	3	592	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0334	16519	T	C	0	267	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0335	73	A	G	1	259	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0335	150	C	T	0	454	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0335	263	A	G	1	156	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0335	723	A	G	1	578	upstream_gene_variant	MODIFIER	RNR1	0.002
HLI-0335	750	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0335	1438	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0335	1721	C	T	0	577	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0335	2706	A	G	1	561	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0335	3197	T	C	0	524	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0335	4718	A	G	0	556	synonymous_variant	LOW	ND2	2.00E-04
HLI-0335	4769	A	G	2	598	synonymous_variant	LOW	ND2	0.9767
HLI-0335	7028	C	T	5	634	synonymous_variant	LOW	COX1	0.8089
HLI-0335	7768	A	G	2	508	synonymous_variant	LOW	COX2	0.0186
HLI-0335	9477	G	A	1	623	missense_variant	MODERATE	COX3	0.0387
HLI-0335	11467	A	G	1	543	synonymous_variant	LOW	ND4	0.1231
HLI-0335	11719	G	A	0	528	synonymous_variant	LOW	ND4	0.7756
HLI-0335	12308	A	G	0	533	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0335	12372	G	A	2	530	synonymous_variant	LOW	ND5	0.1329
HLI-0335	13017	A	G	6	545	synonymous_variant	LOW	ND5	7.00E-04

HLI-0335	13617	T	C	1	485	synonymous_variant	LOW	ND5	0.038
HLI-0335	13637	A	G	1	526	missense_variant	MODERATE	ND5	0.0074
HLI-0335	14182	T	C	0	510	synonymous_variant	LOW	ND6	0.0254
HLI-0335	14766	C	T	2	505	missense_variant	MODERATE	CYTB	0.7696
HLI-0335	15001	T	C	1	591	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0335	15326	A	G	1	461	missense_variant	MODERATE	CYTB	0.9868
HLI-0335	16270	C	T	0	551	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0336	73	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0336	152	T	C	0	52	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0336	204	T	C	0	40	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0336	207	G	A	0	40	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0336	250	T	C	0	24	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0336	263	A	G	0	19	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0336	750	A	G	0	40	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0336	1438	A	G	0	43	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0336	1719	G	A	0	25	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0336	2706	A	G	0	42	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0336	4529	A	T	0	44	synonymous_variant	LOW	ND2	0.015
HLI-0336	4769	A	G	0	42	synonymous_variant	LOW	ND2	0.9767
HLI-0336	6480	G	A	0	52	missense_variant	MODERATE	COX1	0.0031
HLI-0336	7028	C	T	0	70	synonymous_variant	LOW	COX1	0.8089
HLI-0336	8251	G	A	0	44	synonymous_variant	LOW	COX2	0.058
HLI-0336	10034	T	C	0	55	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0336	10238	T	C	0	39	synonymous_variant	LOW	ND3	0.0623
HLI-0336	10398	A	G	0	45	missense_variant	MODERATE	ND3	0.445
HLI-0336	11719	G	A	0	44	synonymous_variant	LOW	ND4	0.7756
HLI-0336	12501	G	A	1	40	synonymous_variant	LOW	ND5	0.0258
HLI-0336	12705	C	T	0	57	synonymous_variant	LOW	ND5	0.4212
HLI-0336	13780	A	G	0	38	missense_variant	MODERATE	ND5	0.0179
HLI-0336	14766	C	T	0	34	missense_variant	MODERATE	CYTB	0.7696
HLI-0336	15043	G	A	0	62	synonymous_variant	LOW	CYTB	0.2362
HLI-0336	15326	A	G	0	55	missense_variant	MODERATE	CYTB	0.9868
HLI-0336	15758	A	G	0	42	missense_variant	MODERATE	CYTB	0.0076
HLI-0336	15924	A	G	0	50	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0336	16129	G	A	0	46	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0336	16223	C	T	0	51	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0336	16311	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0336	16325	T	C	0	52	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0336	16391	G	A	0	39	upstream_gene_variant	MODIFIER	DLoop	0.0155

HLI-0336	16519	T	C	0	24	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0337	73	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0337	215	A	G	1	322	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0337	263	A	G	1	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0337	709	G	A	1	560	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0337	750	A	G	2	612	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0337	1438	A	G	0	616	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0337	1888	G	A	0	499	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0337	2706	A	G	0	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0337	4216	T	C	2	489	missense_variant	MODERATE	ND1	0.0991
HLI-0337	4769	A	G	0	518	synonymous_variant	LOW	ND2	0.9767
HLI-0337	4917	A	G	0	521	missense_variant	MODERATE	ND2	0.0477
HLI-0337	6662	A	G	7	667	synonymous_variant	LOW	COX1	1.00E-04
HLI-0337	7028	C	T	4	650	synonymous_variant	LOW	COX1	0.8089
HLI-0337	8697	G	A	0	512	synonymous_variant	LOW	ATP6	0.0466
HLI-0337	10463	T	C	0	484	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0337	11251	A	G	1	547	synonymous_variant	LOW	ND4	0.0932
HLI-0337	11719	G	A	0	582	synonymous_variant	LOW	ND4	0.7756
HLI-0337	11812	A	G	0	550	synonymous_variant	LOW	ND4	0.0332
HLI-0337	13135	G	A	11	619	missense_variant	MODERATE	ND5	0.0092
HLI-0337	13368	G	A	0	592	synonymous_variant	LOW	ND5	0.0495
HLI-0337	14233	A	G	0	465	synonymous_variant	LOW	ND6	0.0369
HLI-0337	14464	A	G	4	464	synonymous_variant	LOW	ND6	4.00E-04
HLI-0337	14569	G	A	1	535	synonymous_variant	LOW	ND6	0.0259
HLI-0337	14766	C	T	2	562	missense_variant	MODERATE	CYTB	0.7696
HLI-0337	14905	G	A	0	681	synonymous_variant	LOW	CYTB	0.0526
HLI-0337	15326	A	G	0	412	missense_variant	MODERATE	CYTB	0.9868
HLI-0337	15452	C	A	4	407	missense_variant	MODERATE	CYTB	0.0933
HLI-0337	15607	A	G	0	449	synonymous_variant	LOW	CYTB	0.0508
HLI-0337	15928	G	A	2	533	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0337	16126	T	C	0	544	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0337	16294	C	T	0	494	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0337	16519	T	C	0	270	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0338	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0338	153	A	G	6	425	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0338	195	T	C	1	234	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0338	225	G	A	1	238	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0338	227	A	G	1	230	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0338	263	A	G	0	157	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0338	750	A	G	1	560	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0338	1438	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0338	1719	G	A	1	558	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0338	2706	A	G	0	595	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0338	4769	A	G	1	572	synonymous_variant	LOW	ND2	0.9767
HLI-0338	6221	T	C	0	547	synonymous_variant	LOW	COX1	0.0306
HLI-0338	6284	A	G	0	587	synonymous_variant	LOW	COX1	0.0011
HLI-0338	6338	A	G	0	592	synonymous_variant	LOW	COX1	0.0037
HLI-0338	6371	C	T	0	557	synonymous_variant	LOW	COX1	0.0097
HLI-0338	7028	C	T	1	616	synonymous_variant	LOW	COX1	0.8089
HLI-0338	8705	T	C	0	531	missense_variant	MODERATE	ATP6	0.0039
HLI-0338	9007	A	G	1	571	missense_variant	MODERATE	ATP6	0.0022
HLI-0338	11719	G	A	0	537	synonymous_variant	LOW	ND4	0.7756
HLI-0338	12705	C	T	3	587	synonymous_variant	LOW	ND5	0.4212
HLI-0338	13966	A	G	0	436	missense_variant	MODERATE	ND5	0.0126
HLI-0338	14470	T	C	0	424	synonymous_variant	LOW	ND6	0.0166
HLI-0338	14766	C	T	0	481	missense_variant	MODERATE	CYTB	0.7696
HLI-0338	15326	A	G	0	517	missense_variant	MODERATE	CYTB	0.9868
HLI-0338	16223	C	T	0	217	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0338	16255	G	A	0	270	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0338	16278	C	T	0	306	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0338	16519	T	C	0	162	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0339	151	C	T	2	510	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0339	263	A	G	0	206	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0339	750	A	G	2	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0339	1438	A	G	0	619	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0339	4769	A	G	1	559	synonymous_variant	LOW	ND2	0.9767
HLI-0339	7109	C	A	11	636	synonymous_variant	LOW	COX1	0
HLI-0339	13819	T	C	3	448	missense_variant	MODERATE	ND5	0.0028
HLI-0339	15326	A	G	0	548	missense_variant	MODERATE	CYTB	0.9868
HLI-0339	16519	T	C	0	257	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0340	73	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0340	153	A	G	3	426	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0340	195	T	C	1	414	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0340	225	G	A	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0340	226	T	C	0	384	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0340	263	A	G	0	121	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0340	750	A	G	0	581	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0340	1438	A	G	1	601	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0340	1719	G	A	0	468	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0340	2706	A	G	1	587	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0340	4769	A	G	0	532	synonymous_variant	LOW	ND2	0.9767
HLI-0340	5892	T	C	0	594	upstream_gene_variant	MODIFIER	Unannotated	0.0018
HLI-0340	6221	T	C	0	571	synonymous_variant	LOW	COX1	0.0306
HLI-0340	6371	C	T	0	547	synonymous_variant	LOW	COX1	0.0097
HLI-0340	7028	C	T	2	650	synonymous_variant	LOW	COX1	0.8089
HLI-0340	8393	C	T	3	418	missense_variant	MODERATE	ATP8	0.0036
HLI-0340	11719	G	A	0	585	synonymous_variant	LOW	ND4	0.7756
HLI-0340	12705	C	T	0	587	synonymous_variant	LOW	ND5	0.4212
HLI-0340	13708	G	A	3	492	missense_variant	MODERATE	ND5	0.0717
HLI-0340	13966	A	G	3	481	missense_variant	MODERATE	ND5	0.0126
HLI-0340	14470	T	C	0	493	synonymous_variant	LOW	ND6	0.0166
HLI-0340	14766	C	T	3	547	missense_variant	MODERATE	CYTB	0.7696
HLI-0340	15326	A	G	0	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0340	15927	G	A	1	446	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0340	16278	C	T	1	366	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0340	16519	T	C	0	196	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0341	73	A	G	0	178	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0341	146	T	C	0	265	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0341	150	C	T	0	271	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0341	152	T	C	0	277	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0341	182	C	T	0	285	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0341	195	T	C	0	268	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0341	198	C	T	0	268	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0341	204	T	C	0	278	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0341	263	A	G	0	149	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0341	418	C	T	0	367	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0341	750	A	G	1	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0341	769	G	A	0	679	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0341	1018	G	A	2	660	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0341	1438	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0341	1442	G	A	0	622	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0341	1706	C	T	0	523	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0341	2332	C	T	0	542	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0341	2358	A	G	2	563	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0341	2416	T	C	3	532	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0341	2706	A	G	0	573	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0341	3594	C	T	0	529	synonymous_variant	LOW	ND1	0.0789

HLI-0341	4104	A	G	0	526	synonymous_variant	LOW	ND1	0.0785
HLI-0341	4158	A	G	0	552	synonymous_variant	LOW	ND1	0.0023
HLI-0341	4370	T	C	0	537	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0341	4767	A	G	0	560	missense_variant	MODERATE	ND2	0.0029
HLI-0341	4769	A	G	0	568	synonymous_variant	LOW	ND2	0.9767
HLI-0341	5027	C	T	0	537	synonymous_variant	LOW	ND2	0.003
HLI-0341	5249	T	C	1	556	synonymous_variant	LOW	ND2	0.0014
HLI-0341	5331	C	A	5	618	missense_variant	MODERATE	ND2	0.0022
HLI-0341	5814	T	C	1	627	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0341	6026	G	A	1	667	synonymous_variant	LOW	COX1	0.0163
HLI-0341	6267	G	A	0	616	missense_variant	MODERATE	COX1	0.0016
HLI-0341	6713	C	T	1	737	synonymous_variant	LOW	COX1	0.0028
HLI-0341	7028	C	T	0	649	synonymous_variant	LOW	COX1	0.8089
HLI-0341	7256	C	T	2	500	synonymous_variant	LOW	COX1	0.0784
HLI-0341	7521	G	A	0	402	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0341	7624	T	A	0	519	synonymous_variant	LOW	COX2	0.0047
HLI-0341	8080	C	T	3	582	synonymous_variant	LOW	COX2	0.0022
HLI-0341	8206	G	A	0	551	synonymous_variant	LOW	COX2	0.0287
HLI-0341	8387	G	A	1	429	missense_variant	MODERATE	ATP8	0.0028
HLI-0341	8701	A	G	0	472	missense_variant	MODERATE	ATP6	0.3391
HLI-0341	8856	G	A	0	509	synonymous_variant	LOW	ATP6	0.004
HLI-0341	9221	A	G	3	628	synonymous_variant	LOW	COX3	0.0277
HLI-0341	9377	A	G	0	642	synonymous_variant	LOW	COX3	0.0084
HLI-0341	9540	T	C	0	512	synonymous_variant	LOW	COX3	0.339
HLI-0341	10115	T	C	0	618	synonymous_variant	LOW	ND3	0.0278
HLI-0341	10398	A	G	0	560	missense_variant	MODERATE	ND3	0.445
HLI-0341	10828	T	C	0	591	synonymous_variant	LOW	ND4	0.0015
HLI-0341	10873	T	C	0	640	synonymous_variant	LOW	ND4	0.3389
HLI-0341	11719	G	A	0	611	synonymous_variant	LOW	ND4	0.7756
HLI-0341	11944	T	C	0	527	synonymous_variant	LOW	ND4	0.0331
HLI-0341	12236	G	A	0	505	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0341	12705	C	T	2	552	synonymous_variant	LOW	ND5	0.4212
HLI-0341	12948	A	G	0	567	synonymous_variant	LOW	ND5	0.0022
HLI-0341	13590	G	A	1	562	synonymous_variant	LOW	ND5	0.0586
HLI-0341	13650	C	T	2	587	synonymous_variant	LOW	ND5	0.079
HLI-0341	13924	C	T	0	519	missense_variant	MODERATE	ND5	0.0013
HLI-0341	14059	A	G	0	485	missense_variant	MODERATE	ND5	0.0022
HLI-0341	14766	C	T	0	548	missense_variant	MODERATE	CYTB	0.7696
HLI-0341	15110	G	A	2	622	missense_variant	MODERATE	CYTB	0.009

HLI-0341	15217	G	A	1	574	synonymous_variant	LOW	CYTB	0.0104
HLI-0341	15301	G	A	0	595	synonymous_variant	LOW	CYTB	0.2912
HLI-0341	15326	A	G	0	565	missense_variant	MODERATE	CYTB	0.9868
HLI-0341	16114	C	A	1	500	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0341	16129	G	A	1	540	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0341	16213	G	A	1	512	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0341	16223	C	T	1	511	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0341	16274	G	A	2	448	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0341	16278	C	T	2	445	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0341	16355	C	T	0	396	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0341	16362	T	C	0	421	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0341	16390	G	A	1	423	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0342	263	A	G	0	205	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0342	750	A	G	2	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0342	951	G	A	1	592	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0342	3834	G	A	1	539	synonymous_variant	LOW	ND1	0.0087
HLI-0342	15326	A	G	0	492	missense_variant	MODERATE	CYTB	0.9868
HLI-0342	16354	C	T	2	459	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0342	16519	T	C	0	308	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0343	73	A	G	0	338	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0343	263	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0343	750	A	G	0	686	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0343	1438	A	G	0	560	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0343	2706	A	G	0	563	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0343	3348	A	G	2	781	synonymous_variant	LOW	ND1	0.0065
HLI-0343	3969	C	T	3	716	synonymous_variant	LOW	ND1	7.00E-04
HLI-0343	4172	T	A	1	560	missense_variant	MODERATE	ND1	6.00E-04
HLI-0343	4769	A	G	0	498	synonymous_variant	LOW	ND2	0.9767
HLI-0343	7028	C	T	2	582	synonymous_variant	LOW	COX1	0.8089
HLI-0343	7805	G	A	0	454	missense_variant	MODERATE	COX2	0.0077
HLI-0343	11467	A	G	0	405	synonymous_variant	LOW	ND4	0.1231
HLI-0343	11569	T	C	0	413	synonymous_variant	LOW	ND4	0.0051
HLI-0343	11719	G	A	0	437	synonymous_variant	LOW	ND4	0.7756
HLI-0343	11938	C	T	1	452	synonymous_variant	LOW	ND4	9.00E-04
HLI-0343	12308	A	G	0	482	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0343	12372	G	A	0	527	synonymous_variant	LOW	ND5	0.1329
HLI-0343	13071	C	T	0	704	synonymous_variant	LOW	ND5	2.00E-04
HLI-0343	14179	A	G	0	539	synonymous_variant	LOW	ND6	0.0053
HLI-0343	14766	C	T	2	662	missense_variant	MODERATE	CYTB	0.7696

HLI-0343	14927	A	G	1	767	missense_variant	MODERATE	CYTB	0.003
HLI-0343	15326	A	G	0	576	missense_variant	MODERATE	CYTB	0.9868
HLI-0343	16172	T	C	0	178	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0343	16219	A	G	1	231	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0343	16239	C	T	3	287	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0343	16278	C	T	1	399	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0344	73	A	G	0	29	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0344	146	T	C	0	61	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0344	195	T	C	0	53	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0344	263	A	G	0	24	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0344	489	T	C	0	33	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0344	750	A	G	0	59	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0344	1438	A	G	0	32	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0344	1503	G	A	0	30	upstream_gene_variant	MODIFIER	RNR1	0.0053
HLI-0344	2706	A	G	0	49	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0344	3552	T	A	1	48	synonymous_variant	LOW	ND1	0.0337
HLI-0344	4047	T	C	0	42	synonymous_variant	LOW	ND1	0.0014
HLI-0344	4715	A	G	0	42	synonymous_variant	LOW	ND2	0.0416
HLI-0344	4769	A	G	0	41	synonymous_variant	LOW	ND2	0.9767
HLI-0344	5821	G	A	0	49	upstream_gene_variant	MODIFIER	TRNC	0.0069
HLI-0344	5987	C	T	0	66	synonymous_variant	LOW	COX1	5.00E-04
HLI-0344	6338	A	G	0	48	synonymous_variant	LOW	COX1	0.0037
HLI-0344	7028	C	T	0	58	synonymous_variant	LOW	COX1	0.8089
HLI-0344	7196	C	A	1	33	synonymous_variant	LOW	COX1	0.0389
HLI-0344	7853	G	A	1	38	missense_variant	MODERATE	COX2	0.0197
HLI-0344	8014	A	G	0	44	synonymous_variant	LOW	COX2	0.001
HLI-0344	8584	G	A	0	35	missense_variant	MODERATE	ATP6	0.0521
HLI-0344	8701	A	G	0	55	missense_variant	MODERATE	ATP6	0.3391
HLI-0344	9540	T	C	0	66	synonymous_variant	LOW	COX3	0.339
HLI-0344	9545	A	G	0	68	synonymous_variant	LOW	COX3	0.0469
HLI-0344	10398	A	G	0	26	missense_variant	MODERATE	ND3	0.445
HLI-0344	10400	C	T	0	25	synonymous_variant	LOW	ND3	0.2131
HLI-0344	10873	T	C	0	31	synonymous_variant	LOW	ND4	0.3389
HLI-0344	11719	G	A	0	39	synonymous_variant	LOW	ND4	0.7756
HLI-0344	11914	G	A	0	33	synonymous_variant	LOW	ND4	0.1112
HLI-0344	12705	C	T	0	60	synonymous_variant	LOW	ND5	0.4212
HLI-0344	12957	T	C	0	50	synonymous_variant	LOW	ND5	0.0032
HLI-0344	13263	A	G	0	51	synonymous_variant	LOW	ND5	0.0354
HLI-0344	14318	T	C	0	27	missense_variant	MODERATE	ND6	0.0339

HLI-0344	14766	C	T	0	60	missense_variant	MODERATE	CYTB	0.7696
HLI-0344	14783	T	C	0	63	synonymous_variant	LOW	CYTB	0.2126
HLI-0344	14978	A	G	0	48	missense_variant	MODERATE	CYTB	0.0033
HLI-0344	15043	G	A	0	61	synonymous_variant	LOW	CYTB	0.2362
HLI-0344	15301	G	A	0	41	synonymous_variant	LOW	CYTB	0.2912
HLI-0344	15326	A	G	0	44	missense_variant	MODERATE	CYTB	0.9868
HLI-0344	15487	A	T	0	43	synonymous_variant	LOW	CYTB	0.0391
HLI-0344	16223	C	T	0	48	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0344	16263	T	C	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0344	16298	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0344	16327	C	T	0	47	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0344	16519	T	C	0	29	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0345	195	T	C	1	582	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0345	263	A	G	0	283	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0345	750	A	G	0	845	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0345	961	T	G	2	830	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0345	1438	A	G	1	605	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0345	4769	A	G	0	467	synonymous_variant	LOW	ND2	0.9767
HLI-0345	8448	T	C	1	420	missense_variant	MODERATE	ATP8	0.0041
HLI-0345	9521	C	T	0	672	synonymous_variant	LOW	COX3	1.00E-04
HLI-0345	13759	G	A	1	350	missense_variant	MODERATE	ND5	0.0348
HLI-0345	14587	A	G	2	783	synonymous_variant	LOW	ND6	0.006
HLI-0345	15326	A	G	1	550	missense_variant	MODERATE	CYTB	0.9868
HLI-0345	16092	T	C	12	607	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0345	16140	T	C	0	652	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0345	16293	A	G	0	641	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0345	16311	T	C	0	674	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0346	73	A	G	0	338	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0346	263	A	G	0	277	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0346	750	A	G	1	674	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0346	1438	A	G	0	641	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0346	2706	A	G	0	604	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0346	3197	T	C	2	625	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0346	4769	A	G	2	496	synonymous_variant	LOW	ND2	0.9767
HLI-0346	7028	C	T	0	617	synonymous_variant	LOW	COX1	0.8089
HLI-0346	9477	G	A	2	679	missense_variant	MODERATE	COX3	0.0387
HLI-0346	9667	A	G	0	638	missense_variant	MODERATE	COX3	0.0055
HLI-0346	11467	A	G	0	495	synonymous_variant	LOW	ND4	0.1231
HLI-0346	11719	G	A	0	468	synonymous_variant	LOW	ND4	0.7756

HLI-0346	12308	A	G	2	527	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0346	12372	G	A	0	587	synonymous_variant	LOW	ND5	0.1329
HLI-0346	13617	T	C	0	529	synonymous_variant	LOW	ND5	0.038
HLI-0346	14766	C	T	5	702	missense_variant	MODERATE	CYTB	0.7696
HLI-0346	14793	A	G	1	822	missense_variant	MODERATE	CYTB	0.0199
HLI-0346	15218	A	G	2	564	missense_variant	MODERATE	CYTB	0.0169
HLI-0346	15326	A	G	0	575	missense_variant	MODERATE	CYTB	0.9868
HLI-0346	16270	C	T	2	676	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0346	16399	A	G	0	556	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0347	185	G	A	6	566	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0348	152	T	C	1	461	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0348	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0348	750	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0348	1438	A	G	0	663	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0348	3010	G	A	0	592	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0348	4769	A	G	0	536	synonymous_variant	LOW	ND2	0.9767
HLI-0348	11695	A	G	1	584	synonymous_variant	LOW	ND4	1.00E-04
HLI-0348	11864	T	C	1	553	synonymous_variant	LOW	ND4	0.0013
HLI-0348	15326	A	G	0	512	missense_variant	MODERATE	CYTB	0.9868
HLI-0348	16519	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0349	73	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0349	150	C	T	1	551	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0349	263	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0349	750	A	G	2	644	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0349	1438	A	G	1	598	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0349	2706	A	G	0	601	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0349	3197	T	C	0	538	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0349	4769	A	G	0	442	synonymous_variant	LOW	ND2	0.9767
HLI-0349	7028	C	T	2	610	synonymous_variant	LOW	COX1	0.8089
HLI-0349	9477	G	A	3	647	missense_variant	MODERATE	COX3	0.0387
HLI-0349	9548	G	A	2	565	synonymous_variant	LOW	COX3	0.0149
HLI-0349	11467	A	G	1	585	synonymous_variant	LOW	ND4	0.1231
HLI-0349	11719	G	A	1	534	synonymous_variant	LOW	ND4	0.7756
HLI-0349	12308	A	G	0	432	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0349	12372	G	A	1	455	synonymous_variant	LOW	ND5	0.1329
HLI-0349	13246	T	C	1	735	missense_variant	MODERATE	ND5	2.00E-04
HLI-0349	13351	C	T	3	607	synonymous_variant	LOW	ND5	3.00E-04
HLI-0349	13617	T	C	2	495	synonymous_variant	LOW	ND5	0.038
HLI-0349	14684	C	T	0	642	upstream_gene_variant	MODIFIER	TRNE	5.00E-04

HLI-0349	14766	C	T	4	671	missense_variant	MODERATE	CYTB	0.7696
HLI-0349	14793	A	G	3	710	missense_variant	MODERATE	CYTB	0.0199
HLI-0349	15326	A	G	1	499	missense_variant	MODERATE	CYTB	0.9868
HLI-0349	16168	C	T	2	567	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0349	16256	C	T	0	580	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0349	16270	C	T	1	605	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0349	16526	G	A	2	305	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0350	73	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0350	143	G	A	0	469	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0350	146	T	C	0	481	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0350	152	T	C	0	486	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0350	195	T	C	0	478	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0350	263	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0350	750	A	G	0	689	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0350	769	G	A	0	738	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0350	1018	G	A	0	639	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0350	1391	T	C	0	685	upstream_gene_variant	MODIFIER	RNR1	0.0027
HLI-0350	1438	A	G	0	728	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0350	2416	T	C	1	579	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0350	2706	A	G	0	644	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0350	2789	C	T	2	708	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0350	3594	C	T	2	558	synonymous_variant	LOW	ND1	0.0789
HLI-0350	4104	A	G	0	556	synonymous_variant	LOW	ND1	0.0785
HLI-0350	4769	A	G	4	525	synonymous_variant	LOW	ND2	0.9767
HLI-0350	5814	T	C	0	755	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0350	7028	C	T	6	707	synonymous_variant	LOW	COX1	0.8089
HLI-0350	7175	T	C	2	646	synonymous_variant	LOW	COX1	0.0224
HLI-0350	7256	C	T	2	538	synonymous_variant	LOW	COX1	0.0784
HLI-0350	7274	C	T	6	523	synonymous_variant	LOW	COX1	0.0214
HLI-0350	7521	G	A	0	492	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0350	7771	A	G	0	624	synonymous_variant	LOW	COX2	0.0223
HLI-0350	8206	G	A	1	608	synonymous_variant	LOW	COX2	0.0287
HLI-0350	8701	A	G	0	500	missense_variant	MODERATE	ATP6	0.3391
HLI-0350	9221	A	G	2	646	synonymous_variant	LOW	COX3	0.0277
HLI-0350	9540	T	C	0	654	synonymous_variant	LOW	COX3	0.339
HLI-0350	10115	T	C	0	588	synonymous_variant	LOW	ND3	0.0278
HLI-0350	10398	A	G	1	578	missense_variant	MODERATE	ND3	0.445
HLI-0350	10497	C	T	1	545	synonymous_variant	LOW	ND4L	0.0019
HLI-0350	10873	T	C	1	437	synonymous_variant	LOW	ND4	0.3389

HLI-0350	11719	G	A	1	534	synonymous_variant	LOW	ND4	0.7756
HLI-0350	11914	G	A	0	569	synonymous_variant	LOW	ND4	0.1112
HLI-0350	11944	T	C	0	557	synonymous_variant	LOW	ND4	0.0331
HLI-0350	12693	A	G	1	647	synonymous_variant	LOW	ND5	0.0205
HLI-0350	12705	C	T	1	705	synonymous_variant	LOW	ND5	0.4212
HLI-0350	13153	A	G	2	632	missense_variant	MODERATE	ND5	4.00E-04
HLI-0350	13590	G	A	2	521	synonymous_variant	LOW	ND5	0.0586
HLI-0350	13650	C	T	2	489	synonymous_variant	LOW	ND5	0.079
HLI-0350	13803	A	G	3	368	synonymous_variant	LOW	ND5	0.0216
HLI-0350	14566	A	G	1	609	synonymous_variant	LOW	ND6	0.0214
HLI-0350	14766	C	T	3	645	missense_variant	MODERATE	CYTB	0.7696
HLI-0350	15301	G	A	2	547	synonymous_variant	LOW	CYTB	0.2912
HLI-0350	15326	A	G	0	618	missense_variant	MODERATE	CYTB	0.9868
HLI-0350	15784	T	C	1	560	synonymous_variant	LOW	CYTB	0.0363
HLI-0350	16223	C	T	4	306	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0350	16278	C	T	0	367	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0350	16284	A	G	0	365	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0350	16294	C	T	0	382	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0350	16390	G	A	1	426	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0351	263	A	G	0	29	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0351	444	A	G	1	31	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0351	750	A	G	0	51	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0351	1438	A	G	0	51	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0351	3010	G	A	0	49	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0351	3337	G	A	0	45	missense_variant	MODERATE	ND1	0.0016
HLI-0351	4769	A	G	0	44	synonymous_variant	LOW	ND2	0.9767
HLI-0351	6125	A	G	0	67	synonymous_variant	LOW	COX1	0.0011
HLI-0351	8224	A	G	0	49	synonymous_variant	LOW	COX2	1.00E-04
HLI-0351	15326	A	G	0	45	missense_variant	MODERATE	CYTB	0.9868
HLI-0351	16519	T	C	0	41	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0352	263	A	G	1	320	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0352	750	A	G	0	811	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0352	1438	A	G	0	748	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0352	3010	G	A	0	708	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0352	4769	A	G	0	592	synonymous_variant	LOW	ND2	0.9767
HLI-0352	4772	T	C	0	607	synonymous_variant	LOW	ND2	0.0021
HLI-0352	15326	A	G	1	644	missense_variant	MODERATE	CYTB	0.9868
HLI-0352	16209	T	C	0	730	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0352	16519	T	C	0	460	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0353	73	A	G	0	415	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0353	152	T	C	0	754	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0353	263	A	G	0	347	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0353	295	C	T	0	294	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0353	462	C	T	3	629	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0353	489	T	C	1	686	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0353	750	A	G	0	825	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0353	1438	A	G	0	672	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0353	2706	A	G	2	654	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0353	3010	G	A	2	638	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0353	4136	A	G	0	673	missense_variant	MODERATE	ND1	0.0012
HLI-0353	4216	T	C	0	686	missense_variant	MODERATE	ND1	0.0991
HLI-0353	4769	A	G	0	518	synonymous_variant	LOW	ND2	0.9767
HLI-0353	7028	C	T	0	635	synonymous_variant	LOW	COX1	0.8089
HLI-0353	7789	G	A	2	591	synonymous_variant	LOW	COX2	0.0092
HLI-0353	7963	A	G	0	650	synonymous_variant	LOW	COX2	0.0019
HLI-0353	9041	A	G	0	692	missense_variant	MODERATE	ATP6	0.001
HLI-0353	9531	A	G	0	836	missense_variant	MODERATE	COX3	0.0015
HLI-0353	10398	A	G	1	503	missense_variant	MODERATE	ND3	0.445
HLI-0353	11251	A	G	1	550	synonymous_variant	LOW	ND4	0.0932
HLI-0353	11719	G	A	0	543	synonymous_variant	LOW	ND4	0.7756
HLI-0353	12612	A	G	0	549	synonymous_variant	LOW	ND5	0.0506
HLI-0353	13708	G	A	0	490	missense_variant	MODERATE	ND5	0.0717
HLI-0353	14766	C	T	1	742	missense_variant	MODERATE	CYTB	0.7696
HLI-0353	15326	A	G	0	553	missense_variant	MODERATE	CYTB	0.9868
HLI-0353	15452	C	A	2	462	missense_variant	MODERATE	CYTB	0.0933
HLI-0353	16069	C	T	1	581	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0353	16126	T	C	0	654	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0353	16519	T	C	0	478	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0354	73	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0354	189	A	G	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0354	194	C	T	0	307	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0354	195	T	C	0	306	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0354	204	T	C	0	302	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0354	207	G	A	0	298	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0354	263	A	G	0	197	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0354	709	G	A	0	646	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0354	750	A	G	0	701	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0354	1243	T	C	2	688	upstream_gene_variant	MODIFIER	RNR1	0.0161

HLI-0354	1406	T	C	0	691	upstream_gene_variant	MODIFIER	RNR1	0.0034
HLI-0354	1438	A	G	0	760	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0354	2706	A	G	0	660	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0354	3505	A	G	1	651	missense_variant	MODERATE	ND1	0.0144
HLI-0354	4769	A	G	0	561	synonymous_variant	LOW	ND2	0.9767
HLI-0354	5046	G	A	0	544	missense_variant	MODERATE	ND2	0.018
HLI-0354	5211	C	T	1	578	missense_variant	MODERATE	ND2	2.00E-04
HLI-0354	5460	G	A	1	665	missense_variant	MODERATE	ND2	0.0651
HLI-0354	6267	G	A	1	695	missense_variant	MODERATE	COX1	0.0016
HLI-0354	7028	C	T	2	704	synonymous_variant	LOW	COX1	0.8089
HLI-0354	7269	G	A	1	645	missense_variant	MODERATE	COX1	0.0016
HLI-0354	8251	G	A	2	562	synonymous_variant	LOW	COX2	0.058
HLI-0354	8994	G	A	0	645	synonymous_variant	LOW	ATP6	0.0167
HLI-0354	11674	C	T	2	632	synonymous_variant	LOW	ND4	0.0116
HLI-0354	11719	G	A	0	703	synonymous_variant	LOW	ND4	0.7756
HLI-0354	11947	A	G	0	544	synonymous_variant	LOW	ND4	0.011
HLI-0354	12414	T	C	3	545	synonymous_variant	LOW	ND5	0.0139
HLI-0354	12705	C	T	1	642	synonymous_variant	LOW	ND5	0.4212
HLI-0354	13263	A	G	0	696	synonymous_variant	LOW	ND5	0.0354
HLI-0354	14025	T	C	0	558	synonymous_variant	LOW	ND5	0.0033
HLI-0354	14766	C	T	0	617	missense_variant	MODERATE	CYTB	0.7696
HLI-0354	15326	A	G	0	592	missense_variant	MODERATE	CYTB	0.9868
HLI-0354	15784	T	C	0	594	synonymous_variant	LOW	CYTB	0.0363
HLI-0354	15884	G	C	0	633	missense_variant	MODERATE	CYTB	0.011
HLI-0354	16223	C	T	4	653	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0354	16292	C	T	1	622	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0354	16519	T	C	1	280	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0355	73	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0355	195	T	C	0	59	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0355	263	A	G	0	33	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0355	750	A	G	0	49	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0355	1438	A	G	0	45	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0355	2706	A	G	0	50	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0355	3027	T	C	0	31	upstream_gene_variant	MODIFIER	RNR2	0.0117
HLI-0355	3197	T	C	0	53	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0355	3552	T	C	0	55	synonymous_variant	LOW	ND1	0.0028
HLI-0355	4769	A	G	0	46	synonymous_variant	LOW	ND2	0.9767
HLI-0355	4823	T	C	0	50	synonymous_variant	LOW	ND2	0.0049
HLI-0355	5583	C	T	0	53	upstream_gene_variant	MODIFIER	Unannotated	5.00E-04

HLI-0355	6584	C	T	0	47	synonymous_variant	LOW	COX1	3.00E-04
HLI-0355	6836	C	T	1	57	synonymous_variant	LOW	COX1	4.00E-04
HLI-0355	7028	C	T	1	64	synonymous_variant	LOW	COX1	0.8089
HLI-0355	9325	T	C	1	56	missense_variant	MODERATE	COX3	5.00E-04
HLI-0355	9477	G	A	0	56	missense_variant	MODERATE	COX3	0.0387
HLI-0355	10837	C	T	0	49	synonymous_variant	LOW	ND4	1.00E-04
HLI-0355	11467	A	G	0	54	synonymous_variant	LOW	ND4	0.1231
HLI-0355	11719	G	A	0	53	synonymous_variant	LOW	ND4	0.7756
HLI-0355	12308	A	G	0	41	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0355	12372	G	A	0	48	synonymous_variant	LOW	ND5	0.1329
HLI-0355	13617	T	C	0	60	synonymous_variant	LOW	ND5	0.038
HLI-0355	14766	C	T	0	60	missense_variant	MODERATE	CYTB	0.7696
HLI-0355	14793	A	G	0	65	missense_variant	MODERATE	CYTB	0.0199
HLI-0355	15218	A	G	1	57	missense_variant	MODERATE	CYTB	0.0169
HLI-0355	15326	A	G	0	54	missense_variant	MODERATE	CYTB	0.9868
HLI-0355	16145	G	A	1	43	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0355	16256	C	T	0	42	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0355	16270	C	T	0	39	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0355	16399	A	G	0	54	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0356	73	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0356	153	A	G	0	57	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0356	195	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0356	225	G	A	0	41	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0356	226	T	C	0	40	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0356	263	A	G	0	22	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0356	750	A	G	0	62	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0356	1438	A	G	0	40	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0356	1719	G	A	0	42	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0356	2706	A	G	0	50	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0356	4769	A	G	0	57	synonymous_variant	LOW	ND2	0.9767
HLI-0356	5892	T	C	0	47	upstream_gene_variant	MODIFIER	Unannotated	0.0018
HLI-0356	6221	T	C	1	41	synonymous_variant	LOW	COX1	0.0306
HLI-0356	6371	C	T	0	47	synonymous_variant	LOW	COX1	0.0097
HLI-0356	7028	C	T	0	62	synonymous_variant	LOW	COX1	0.8089
HLI-0356	8393	C	T	0	43	missense_variant	MODERATE	ATP8	0.0036
HLI-0356	11719	G	A	0	46	synonymous_variant	LOW	ND4	0.7756
HLI-0356	12705	C	T	0	62	synonymous_variant	LOW	ND5	0.4212
HLI-0356	13708	G	A	0	50	missense_variant	MODERATE	ND5	0.0717
HLI-0356	13966	A	G	0	52	missense_variant	MODERATE	ND5	0.0126

HLI-0356	14470	T	C	0	51	synonymous_variant	LOW	ND6	0.0166
HLI-0356	14766	C	T	0	45	missense_variant	MODERATE	CYTB	0.7696
HLI-0356	15326	A	G	0	63	missense_variant	MODERATE	CYTB	0.9868
HLI-0356	15927	G	A	0	53	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0356	16223	C	T	0	27	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0356	16278	C	T	0	43	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0356	16519	T	C	0	31	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0357	152	T	C	0	64	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0357	263	A	G	0	41	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0357	750	A	G	0	57	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0357	1438	A	G	0	46	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0357	4769	A	G	0	52	synonymous_variant	LOW	ND2	0.9767
HLI-0357	7444	G	A	0	40	stop_lost	HIGH	COX1	0.0035
HLI-0357	15326	A	G	0	71	missense_variant	MODERATE	CYTB	0.9868
HLI-0357	16287	C	T	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0051
HLI-0357	16519	T	C	0	38	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0358	73	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0358	143	G	A	1	441	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0358	146	T	C	1	449	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0358	152	T	C	1	468	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0358	195	T	C	0	488	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0358	200	A	G	14	468	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0358	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0358	750	A	G	0	699	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0358	769	G	A	0	770	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0358	1018	G	A	1	679	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0358	1438	A	G	0	673	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0358	2416	T	C	0	620	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0358	2706	A	G	0	617	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0358	2789	C	T	2	713	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0358	3594	C	T	2	547	synonymous_variant	LOW	ND1	0.0789
HLI-0358	4104	A	G	2	536	synonymous_variant	LOW	ND1	0.0785
HLI-0358	4769	A	G	0	548	synonymous_variant	LOW	ND2	0.9767
HLI-0358	6164	C	T	2	662	synonymous_variant	LOW	COX1	0.0025
HLI-0358	7028	C	T	4	660	synonymous_variant	LOW	COX1	0.8089
HLI-0358	7175	T	C	1	604	synonymous_variant	LOW	COX1	0.0224
HLI-0358	7256	C	T	1	578	synonymous_variant	LOW	COX1	0.0784
HLI-0358	7274	C	T	1	561	synonymous_variant	LOW	COX1	0.0214
HLI-0358	7521	G	A	1	472	upstream_gene_variant	MODIFIER	TRND	0.082

HLI-0358	7771	A	G	1	571	synonymous_variant	LOW	COX2	0.0223
HLI-0358	8206	G	A	0	597	synonymous_variant	LOW	COX2	0.0287
HLI-0358	8701	A	G	1	577	missense_variant	MODERATE	ATP6	0.3391
HLI-0358	9221	A	G	1	665	synonymous_variant	LOW	COX3	0.0277
HLI-0358	9540	T	C	0	689	synonymous_variant	LOW	COX3	0.339
HLI-0358	10115	T	C	0	657	synonymous_variant	LOW	ND3	0.0278
HLI-0358	10398	A	G	1	623	missense_variant	MODERATE	ND3	0.445
HLI-0358	10873	T	C	0	474	synonymous_variant	LOW	ND4	0.3389
HLI-0358	10920	C	T	2	548	missense_variant	MODERATE	ND4	0.0037
HLI-0358	11719	G	A	0	640	synonymous_variant	LOW	ND4	0.7756
HLI-0358	11914	G	A	1	615	synonymous_variant	LOW	ND4	0.1112
HLI-0358	11944	T	C	1	657	synonymous_variant	LOW	ND4	0.0331
HLI-0358	12693	A	G	0	627	synonymous_variant	LOW	ND5	0.0205
HLI-0358	12705	C	T	0	688	synonymous_variant	LOW	ND5	0.4212
HLI-0358	13590	G	A	0	556	synonymous_variant	LOW	ND5	0.0586
HLI-0358	13650	C	T	1	600	synonymous_variant	LOW	ND5	0.079
HLI-0358	13803	A	G	0	445	synonymous_variant	LOW	ND5	0.0216
HLI-0358	14566	A	G	0	552	synonymous_variant	LOW	ND6	0.0214
HLI-0358	14766	C	T	0	599	missense_variant	MODERATE	CYTB	0.7696
HLI-0358	15229	T	C	0	641	synonymous_variant	LOW	CYTB	0.0014
HLI-0358	15301	G	A	0	655	synonymous_variant	LOW	CYTB	0.2912
HLI-0358	15326	A	G	0	648	missense_variant	MODERATE	CYTB	0.9868
HLI-0358	15784	T	C	0	528	synonymous_variant	LOW	CYTB	0.0363
HLI-0358	16223	C	T	4	309	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0358	16278	C	T	0	378	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0358	16294	C	T	1	396	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0358	16362	T	C	1	386	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0358	16390	G	A	2	449	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0359	73	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0359	152	T	C	0	544	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0359	200	A	G	7	494	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0359	263	A	G	0	200	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0359	750	A	G	2	654	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0359	1438	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0359	1598	G	A	2	616	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0359	1703	C	T	1	604	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0359	1719	G	A	2	648	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0359	2639	C	T	0	603	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0359	2706	A	G	0	682	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0359	3921	C	A	1	590	synonymous_variant	LOW	ND1	0.0026
HLI-0359	4769	A	G	0	571	synonymous_variant	LOW	ND2	0.9767
HLI-0359	4960	C	T	0	621	missense_variant	MODERATE	ND2	0.0028
HLI-0359	5471	G	A	2	623	synonymous_variant	LOW	ND2	0.0128
HLI-0359	7028	C	T	1	679	synonymous_variant	LOW	COX1	0.8089
HLI-0359	8251	G	A	1	547	synonymous_variant	LOW	COX2	0.058
HLI-0359	8472	C	T	0	456	missense_variant	MODERATE	ATP8	0.0027
HLI-0359	8836	A	G	0	606	missense_variant	MODERATE	ATP6	0.0029
HLI-0359	9266	G	A	1	638	synonymous_variant	LOW	COX3	0.0049
HLI-0359	9335	C	T	1	709	synonymous_variant	LOW	COX3	0.0021
HLI-0359	9957	T	C	0	689	missense_variant	MODERATE	COX3	8.00E-04
HLI-0359	10238	T	C	1	537	synonymous_variant	LOW	ND3	0.0623
HLI-0359	11362	A	G	0	662	synonymous_variant	LOW	ND4	0.0024
HLI-0359	11719	G	A	1	598	synonymous_variant	LOW	ND4	0.7756
HLI-0359	12501	G	A	5	547	synonymous_variant	LOW	ND5	0.0258
HLI-0359	12705	C	T	1	591	synonymous_variant	LOW	ND5	0.4212
HLI-0359	12822	A	G	3	678	synonymous_variant	LOW	ND5	0.0026
HLI-0359	13830	T	C	0	521	synonymous_variant	LOW	ND5	0.0021
HLI-0359	14766	C	T	2	625	missense_variant	MODERATE	CYTB	0.7696
HLI-0359	15326	A	G	0	564	missense_variant	MODERATE	CYTB	0.9868
HLI-0359	15514	T	C	0	505	synonymous_variant	LOW	CYTB	0.0071
HLI-0359	16145	G	A	1	673	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0359	16176	C	G	5	662	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0359	16223	C	T	2	659	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0359	16390	G	A	0	518	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0359	16519	T	C	0	289	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0361	73	A	G	0	26	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0361	263	A	G	0	22	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0361	709	G	A	0	48	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0361	750	A	G	0	46	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0361	1438	A	G	0	46	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0361	1888	G	A	0	32	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0361	2706	A	G	0	40	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0361	2850	T	C	0	42	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0361	4216	T	C	0	36	missense_variant	MODERATE	ND1	0.0991
HLI-0361	4769	A	G	0	36	synonymous_variant	LOW	ND2	0.9767
HLI-0361	4917	A	G	0	53	missense_variant	MODERATE	ND2	0.0477
HLI-0361	7022	T	C	0	56	synonymous_variant	LOW	COX1	0.0024
HLI-0361	7028	C	T	0	56	synonymous_variant	LOW	COX1	0.8089

HLI-0361	8697	G	A	0	41	synonymous_variant	LOW	ATP6	0.0466
HLI-0361	10463	T	C	0	46	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0361	11251	A	G	0	52	synonymous_variant	LOW	ND4	0.0932
HLI-0361	11719	G	A	0	34	synonymous_variant	LOW	ND4	0.7756
HLI-0361	11812	A	G	0	41	synonymous_variant	LOW	ND4	0.0332
HLI-0361	11824	A	G	0	43	synonymous_variant	LOW	ND4	1.00E-04
HLI-0361	13368	G	A	0	41	synonymous_variant	LOW	ND5	0.0495
HLI-0361	13965	T	C	0	40	synonymous_variant	LOW	ND5	0.005
HLI-0361	14233	A	G	0	38	synonymous_variant	LOW	ND6	0.0369
HLI-0361	14687	A	G	1	52	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0361	14766	C	T	0	47	missense_variant	MODERATE	CYTB	0.7696
HLI-0361	14905	G	A	0	55	synonymous_variant	LOW	CYTB	0.0526
HLI-0361	15326	A	G	0	45	missense_variant	MODERATE	CYTB	0.9868
HLI-0361	15452	C	A	0	48	missense_variant	MODERATE	CYTB	0.0933
HLI-0361	15607	A	G	0	49	synonymous_variant	LOW	CYTB	0.0508
HLI-0361	15928	G	A	0	55	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0361	16126	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0361	16294	C	T	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0361	16296	C	T	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0361	16519	T	C	0	25	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0362	73	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0362	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0362	750	A	G	2	676	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0362	1438	A	G	0	674	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0362	3010	G	A	1	682	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0362	3746	C	T	3	632	missense_variant	MODERATE	ND1	3.00E-04
HLI-0362	4769	A	G	1	582	synonymous_variant	LOW	ND2	0.9767
HLI-0362	11969	G	A	0	557	missense_variant	MODERATE	ND4	0.0135
HLI-0362	15326	A	G	1	584	missense_variant	MODERATE	CYTB	0.9868
HLI-0362	16051	A	G	1	630	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0362	16162	A	G	1	606	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0362	16278	C	T	0	562	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0362	16519	T	C	1	365	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0363	73	A	G	0	297	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0363	195	T	C	0	411	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0363	263	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0363	499	G	A	2	416	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0363	750	A	G	0	589	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0363	1438	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0363	1811	A	G	1	641	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0363	2706	A	G	1	637	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0363	4646	T	C	3	635	synonymous_variant	LOW	ND2	0.0124
HLI-0363	4769	A	G	0	581	synonymous_variant	LOW	ND2	0.9767
HLI-0363	5999	T	C	0	692	synonymous_variant	LOW	COX1	0.0127
HLI-0363	6047	A	G	0	724	synonymous_variant	LOW	COX1	0.0114
HLI-0363	7028	C	T	2	651	synonymous_variant	LOW	COX1	0.8089
HLI-0363	7762	G	A	1	589	synonymous_variant	LOW	COX2	0.0025
HLI-0363	8705	T	C	0	589	missense_variant	MODERATE	ATP6	0.0039
HLI-0363	10118	T	C	0	689	synonymous_variant	LOW	ND3	0.0017
HLI-0363	10676	C	T	0	537	synonymous_variant	LOW	ND4L	3.00E-04
HLI-0363	10907	T	C	0	542	missense_variant	MODERATE	ND4	0.0022
HLI-0363	11332	C	T	2	610	synonymous_variant	LOW	ND4	0.0115
HLI-0363	11467	A	G	0	729	synonymous_variant	LOW	ND4	0.1231
HLI-0363	11497	C	T	0	721	synonymous_variant	LOW	ND4	5.00E-04
HLI-0363	11719	G	A	1	615	synonymous_variant	LOW	ND4	0.7756
HLI-0363	12308	A	G	1	554	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0363	12372	G	A	2	577	synonymous_variant	LOW	ND5	0.1329
HLI-0363	14620	C	T	2	635	synonymous_variant	LOW	ND6	0.0126
HLI-0363	14766	C	T	3	585	missense_variant	MODERATE	CYTB	0.7696
HLI-0363	15326	A	G	0	526	missense_variant	MODERATE	CYTB	0.9868
HLI-0363	15516	C	T	1	559	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0363	15693	T	C	1	568	missense_variant	MODERATE	CYTB	0.0114
HLI-0363	16261	C	T	2	532	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0363	16356	T	C	0	488	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0364	263	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0364	750	A	G	0	669	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0364	1438	A	G	0	619	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0364	3010	G	A	1	655	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0364	4769	A	G	2	609	synonymous_variant	LOW	ND2	0.9767
HLI-0364	8602	T	C	2	600	missense_variant	MODERATE	ATP6	0.0017
HLI-0364	14212	T	C	1	560	synonymous_variant	LOW	ND6	0.0204
HLI-0364	15326	A	G	0	573	missense_variant	MODERATE	CYTB	0.9868
HLI-0364	16519	T	C	0	228	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0365	73	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0365	150	C	T	2	422	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0365	242	C	T	1	259	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0365	263	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0365	750	A	G	1	529	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0365	1438	A	G	0	567	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0365	1822	T	C	0	422	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0365	2706	A	G	1	527	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0365	3197	T	C	4	565	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0365	4769	A	G	0	500	synonymous_variant	LOW	ND2	0.9767
HLI-0365	5081	T	C	1	476	synonymous_variant	LOW	ND2	0.0012
HLI-0365	5656	A	G	4	567	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0365	5788	T	C	2	621	upstream_gene_variant	MODIFIER	TRNC	4.00E-04
HLI-0365	7028	C	T	1	610	synonymous_variant	LOW	COX1	0.8089
HLI-0365	7385	A	G	0	505	synonymous_variant	LOW	COX1	0.0032
HLI-0365	7768	A	G	0	513	synonymous_variant	LOW	COX2	0.0186
HLI-0365	9477	G	A	2	563	missense_variant	MODERATE	COX3	0.0387
HLI-0365	10301	A	G	0	455	synonymous_variant	LOW	ND3	1.00E-04
HLI-0365	10927	T	C	0	374	synonymous_variant	LOW	ND4	0.0044
HLI-0365	11467	A	G	1	636	synonymous_variant	LOW	ND4	0.1231
HLI-0365	11719	G	A	0	519	synonymous_variant	LOW	ND4	0.7756
HLI-0365	12308	A	G	1	383	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0365	12372	G	A	0	413	synonymous_variant	LOW	ND5	0.1329
HLI-0365	12618	G	A	6	491	synonymous_variant	LOW	ND5	0.0137
HLI-0365	13617	T	C	1	506	synonymous_variant	LOW	ND5	0.038
HLI-0365	14182	T	C	1	411	synonymous_variant	LOW	ND6	0.0254
HLI-0365	14470	T	C	0	448	synonymous_variant	LOW	ND6	0.0166
HLI-0365	14766	C	T	3	559	missense_variant	MODERATE	CYTB	0.7696
HLI-0365	15326	A	G	0	455	missense_variant	MODERATE	CYTB	0.9868
HLI-0365	15533	A	G	0	401	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0365	16074	A	G	0	376	upstream_gene_variant	MODIFIER	DLoop	2.00E-04
HLI-0365	16270	C	T	1	361	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0366	73	A	G	0	337	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0366	150	C	T	1	567	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0366	195	T	C	0	535	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0366	263	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0366	750	A	G	0	699	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0366	1438	A	G	0	664	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0366	2352	T	C	1	541	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0366	2483	T	C	0	630	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0366	2706	A	G	0	641	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0366	4769	A	G	2	599	synonymous_variant	LOW	ND2	0.9767
HLI-0366	5580	T	C	4	593	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0366	6261	G	A	6	708	missense_variant	MODERATE	COX1	0.007

HLI-0366	7028	C	T	4	729	synonymous_variant	LOW	COX1	0.8089
HLI-0366	8450	T	C	1	428	synonymous_variant	LOW	ATP8	3.00E-04
HLI-0366	8701	A	G	2	553	missense_variant	MODERATE	ATP6	0.3391
HLI-0366	9377	A	G	6	792	synonymous_variant	LOW	COX3	0.0084
HLI-0366	9540	T	C	0	751	synonymous_variant	LOW	COX3	0.339
HLI-0366	10398	A	G	0	557	missense_variant	MODERATE	ND3	0.445
HLI-0366	10819	A	G	1	587	synonymous_variant	LOW	ND4	0.0228
HLI-0366	10873	T	C	1	470	synonymous_variant	LOW	ND4	0.3389
HLI-0366	11654	A	G	11	730	missense_variant	MODERATE	ND4	0.0045
HLI-0366	11719	G	A	6	711	synonymous_variant	LOW	ND4	0.7756
HLI-0366	11722	T	C	7	714	synonymous_variant	LOW	ND4	5.00E-04
HLI-0366	12061	C	T	5	445	synonymous_variant	LOW	ND4	0.0014
HLI-0366	12285	T	C	5	442	upstream_gene_variant	MODIFIER	TRNL2	9.00E-04
HLI-0366	12705	C	T	2	590	synonymous_variant	LOW	ND5	0.4212
HLI-0366	14212	T	C	3	569	synonymous_variant	LOW	ND6	0.0204
HLI-0366	14766	C	T	3	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0366	14905	G	A	4	837	synonymous_variant	LOW	CYTB	0.0526
HLI-0366	15301	G	A	1	586	synonymous_variant	LOW	CYTB	0.2912
HLI-0366	15326	A	G	0	618	missense_variant	MODERATE	CYTB	0.9868
HLI-0366	16172	T	C	2	286	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0366	16223	C	T	4	312	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0366	16320	C	T	4	566	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0366	16519	T	C	0	288	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0367	73	A	G	0	26	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0367	199	T	C	0	52	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0367	204	T	C	0	51	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0367	250	T	C	0	30	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0367	263	A	G	0	26	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0367	750	A	G	0	48	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0367	1438	A	G	0	44	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0367	1719	G	A	0	41	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0367	2706	A	G	0	56	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0367	4529	A	T	1	54	synonymous_variant	LOW	ND2	0.015
HLI-0367	4769	A	G	0	58	synonymous_variant	LOW	ND2	0.9767
HLI-0367	6845	C	T	0	54	synonymous_variant	LOW	COX1	4.00E-04
HLI-0367	7028	C	T	0	64	synonymous_variant	LOW	COX1	0.8089
HLI-0367	8251	G	A	0	49	synonymous_variant	LOW	COX2	0.058
HLI-0367	8519	G	A	0	48	missense_variant	MODERATE	ATP8	0.0024
HLI-0367	10034	T	C	0	52	upstream_gene_variant	MODIFIER	TRNG	0.0157

HLI-0367	10238	T	C	0	56	synonymous_variant	LOW	ND3	0.0623
HLI-0367	10398	A	G	0	49	missense_variant	MODERATE	ND3	0.445
HLI-0367	10819	A	G	0	54	synonymous_variant	LOW	ND4	0.0228
HLI-0367	11465	T	C	0	58	synonymous_variant	LOW	ND4	0.0022
HLI-0367	11719	G	A	0	53	synonymous_variant	LOW	ND4	0.7756
HLI-0367	12501	G	A	0	19	synonymous_variant	LOW	ND5	0.0258
HLI-0367	12705	C	T	0	42	synonymous_variant	LOW	ND5	0.4212
HLI-0367	12892	T	C	1	65	synonymous_variant	LOW	ND5	4.00E-04
HLI-0367	13780	A	G	0	34	missense_variant	MODERATE	ND5	0.0179
HLI-0367	14766	C	T	0	53	missense_variant	MODERATE	CYTB	0.7696
HLI-0367	15043	G	A	0	63	synonymous_variant	LOW	CYTB	0.2362
HLI-0367	15326	A	G	0	49	missense_variant	MODERATE	CYTB	0.9868
HLI-0367	15924	A	G	0	35	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0367	16129	G	A	0	53	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0367	16223	C	T	0	53	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0367	16391	G	A	1	49	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0367	16519	T	C	0	26	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0368	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0368	750	A	G	0	637	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0368	1438	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0368	2581	A	G	5	611	upstream_gene_variant	MODIFIER	RNR2	0.0031
HLI-0368	4769	A	G	0	549	synonymous_variant	LOW	ND2	0.9767
HLI-0368	6776	T	C	7	731	synonymous_variant	LOW	COX1	0.0226
HLI-0368	15326	A	G	1	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0368	16129	G	A	0	554	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0368	16519	T	C	0	346	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0369	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0369	750	A	G	0	567	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0369	1438	A	G	1	568	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0369	2626	T	C	3	519	upstream_gene_variant	MODIFIER	RNR2	0.0045
HLI-0369	4769	A	G	1	628	synonymous_variant	LOW	ND2	0.9767
HLI-0369	4793	A	G	3	671	synonymous_variant	LOW	ND2	0.0073
HLI-0369	5348	C	T	3	573	synonymous_variant	LOW	ND2	0.0016
HLI-0369	15119	G	A	1	613	missense_variant	MODERATE	CYTB	0.0016
HLI-0369	15326	A	G	1	443	missense_variant	MODERATE	CYTB	0.9868
HLI-0369	16519	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0370	73	A	G	2	148	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0370	189	A	G	1	256	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0370	263	A	G	0	85	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0370	709	G	A	2	376	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0370	750	A	G	1	402	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0370	1438	A	G	1	430	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0370	1888	G	A	0	400	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0370	2706	A	G	0	371	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0370	4216	T	C	0	363	missense_variant	MODERATE	ND1	0.0991
HLI-0370	4769	A	G	0	430	synonymous_variant	LOW	ND2	0.9767
HLI-0370	4917	A	G	0	380	missense_variant	MODERATE	ND2	0.0477
HLI-0370	6392	T	C	0	391	synonymous_variant	LOW	COX1	0.0359
HLI-0370	7028	C	T	1	455	synonymous_variant	LOW	COX1	0.8089
HLI-0370	8697	G	A	0	426	synonymous_variant	LOW	ATP6	0.0466
HLI-0370	9003	C	T	3	378	synonymous_variant	LOW	ATP6	0
HLI-0370	10463	T	C	0	451	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0370	11251	A	G	0	386	synonymous_variant	LOW	ND4	0.0932
HLI-0370	11719	G	A	0	390	synonymous_variant	LOW	ND4	0.7756
HLI-0370	11812	A	G	0	408	synonymous_variant	LOW	ND4	0.0332
HLI-0370	13368	G	A	0	409	synonymous_variant	LOW	ND5	0.0495
HLI-0370	14233	A	G	0	340	synonymous_variant	LOW	ND6	0.0369
HLI-0370	14766	C	T	1	411	missense_variant	MODERATE	CYTB	0.7696
HLI-0370	14905	G	A	1	427	synonymous_variant	LOW	CYTB	0.0526
HLI-0370	15326	A	G	0	296	missense_variant	MODERATE	CYTB	0.9868
HLI-0370	15452	C	A	3	315	missense_variant	MODERATE	CYTB	0.0933
HLI-0370	15607	A	G	1	308	synonymous_variant	LOW	CYTB	0.0508
HLI-0370	15928	G	A	0	404	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0370	16126	T	C	2	174	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0370	16259	C	T	3	150	upstream_gene_variant	MODIFIER	DLoop	0.0053
HLI-0370	16294	C	T	1	208	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0370	16296	C	T	1	211	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0370	16519	T	C	1	102	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0371	73	A	G	0	178	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0371	204	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0371	207	G	A	0	293	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0371	263	A	G	0	116	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0371	709	G	A	1	410	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0371	750	A	G	1	450	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0371	930	G	A	1	446	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0371	1438	A	G	0	454	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0371	1888	G	A	0	413	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0371	2706	A	G	0	460	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0371	4216	T	C	0	456	missense_variant	MODERATE	ND1	0.0991
HLI-0371	4769	A	G	2	420	synonymous_variant	LOW	ND2	0.9767
HLI-0371	4917	A	G	2	422	missense_variant	MODERATE	ND2	0.0477
HLI-0371	5147	G	A	2	399	synonymous_variant	LOW	ND2	0.0437
HLI-0371	5783	G	A	1	586	upstream_gene_variant	MODIFIER	TRNC	9.00E-04
HLI-0371	7028	C	T	2	531	synonymous_variant	LOW	COX1	0.8089
HLI-0371	8697	G	A	0	382	synonymous_variant	LOW	ATP6	0.0466
HLI-0371	10463	T	C	1	540	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0371	11251	A	G	0	459	synonymous_variant	LOW	ND4	0.0932
HLI-0371	11719	G	A	1	427	synonymous_variant	LOW	ND4	0.7756
HLI-0371	11812	A	G	0	455	synonymous_variant	LOW	ND4	0.0332
HLI-0371	13359	G	A	0	435	synonymous_variant	LOW	ND5	0.0041
HLI-0371	13368	G	A	0	455	synonymous_variant	LOW	ND5	0.0495
HLI-0371	14233	A	G	0	427	synonymous_variant	LOW	ND6	0.0369
HLI-0371	14766	C	T	1	423	missense_variant	MODERATE	CYTB	0.7696
HLI-0371	14905	G	A	0	525	synonymous_variant	LOW	CYTB	0.0526
HLI-0371	15326	A	G	1	366	missense_variant	MODERATE	CYTB	0.9868
HLI-0371	15452	C	A	2	354	missense_variant	MODERATE	CYTB	0.0933
HLI-0371	15607	A	G	0	361	synonymous_variant	LOW	CYTB	0.0508
HLI-0371	15928	G	A	1	460	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0371	16126	T	C	0	414	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0371	16294	C	T	0	389	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0371	16296	C	T	0	393	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0371	16304	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0371	16519	T	C	0	196	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0372	73	A	G	0	15	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0372	263	A	G	0	19	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0372	750	A	G	1	32	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0372	1438	A	G	0	29	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0372	2706	A	G	0	34	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0372	3197	T	C	0	22	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0372	4769	A	G	0	20	synonymous_variant	LOW	ND2	0.9767
HLI-0372	7028	C	T	1	45	synonymous_variant	LOW	COX1	0.8089
HLI-0372	9477	G	A	0	30	missense_variant	MODERATE	COX3	0.0387
HLI-0372	11467	A	G	0	34	synonymous_variant	LOW	ND4	0.1231
HLI-0372	11719	G	A	0	28	synonymous_variant	LOW	ND4	0.7756
HLI-0372	12308	A	G	0	27	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0372	12372	G	A	0	14	synonymous_variant	LOW	ND5	0.1329
HLI-0372	13617	T	C	0	31	synonymous_variant	LOW	ND5	0.038

HLI-0372	13827	A	G	0	36	synonymous_variant	LOW	ND5	0.0047
HLI-0372	13928	G	C	0	31	missense_variant	MODERATE	ND5	0.0484
HLI-0372	14766	C	T	0	32	missense_variant	MODERATE	CYTB	0.7696
HLI-0372	14793	A	G	0	35	missense_variant	MODERATE	CYTB	0.0199
HLI-0372	15326	A	G	0	38	missense_variant	MODERATE	CYTB	0.9868
HLI-0372	15844	A	G	1	25	synonymous_variant	LOW	CYTB	3.00E-04
HLI-0372	16114	C	A	0	40	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0372	16256	C	T	0	26	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0372	16270	C	T	0	27	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0372	16294	C	T	0	31	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0372	16526	G	A	0	16	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0373	73	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0373	150	C	T	2	319	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0373	195	T	C	1	323	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0373	263	A	G	0	141	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0373	750	A	G	2	360	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0373	1438	A	G	1	387	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0373	2352	T	C	0	204	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0373	2483	T	C	0	297	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0373	2706	A	G	1	354	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0373	4769	A	G	0	394	synonymous_variant	LOW	ND2	0.9767
HLI-0373	5210	C	T	1	295	synonymous_variant	LOW	ND2	1.00E-04
HLI-0373	5580	T	C	2	374	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0373	6722	G	A	5	561	synonymous_variant	LOW	COX1	0.001
HLI-0373	7028	C	T	1	477	synonymous_variant	LOW	COX1	0.8089
HLI-0373	8701	A	G	2	348	missense_variant	MODERATE	ATP6	0.3391
HLI-0373	9377	A	G	1	413	synonymous_variant	LOW	COX3	0.0084
HLI-0373	9540	T	C	0	283	synonymous_variant	LOW	COX3	0.339
HLI-0373	9575	G	A	0	307	synonymous_variant	LOW	COX3	0.0071
HLI-0373	10398	A	G	2	399	missense_variant	MODERATE	ND3	0.445
HLI-0373	10819	A	G	1	370	synonymous_variant	LOW	ND4	0.0228
HLI-0373	10873	T	C	0	367	synonymous_variant	LOW	ND4	0.3389
HLI-0373	11719	G	A	0	397	synonymous_variant	LOW	ND4	0.7756
HLI-0373	11722	T	C	0	405	synonymous_variant	LOW	ND4	5.00E-04
HLI-0373	12705	C	T	0	349	synonymous_variant	LOW	ND5	0.4212
HLI-0373	14212	T	C	3	308	synonymous_variant	LOW	ND6	0.0204
HLI-0373	14766	C	T	0	439	missense_variant	MODERATE	CYTB	0.7696
HLI-0373	14905	G	A	4	509	synonymous_variant	LOW	CYTB	0.0526
HLI-0373	15301	G	A	1	318	synonymous_variant	LOW	CYTB	0.2912

HLI-0373	15326	A	G	0	306	missense_variant	MODERATE	CYTB	0.9868
HLI-0373	15519	T	C	0	236	missense_variant	MODERATE	CYTB	0.002
HLI-0373	16172	T	C	0	149	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0373	16223	C	T	0	148	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0373	16320	C	T	0	289	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0373	16519	T	C	1	129	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0374	150	C	T	1	479	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0374	263	A	G	0	146	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0374	750	A	G	0	511	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0374	1438	A	G	0	510	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0374	4769	A	G	0	508	synonymous_variant	LOW	ND2	0.9767
HLI-0374	4793	A	G	0	575	synonymous_variant	LOW	ND2	0.0073
HLI-0374	6296	C	A	5	586	synonymous_variant	LOW	COX1	0.001
HLI-0374	13959	C	T	3	398	synonymous_variant	LOW	ND5	2.00E-04
HLI-0374	15326	A	G	1	379	missense_variant	MODERATE	CYTB	0.9868
HLI-0374	16244	G	A	1	483	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0374	16519	T	C	0	189	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0375	73	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0375	146	T	C	0	55	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0375	195	T	C	0	52	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0375	263	A	G	0	24	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0375	750	A	G	0	45	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0375	1438	A	G	0	47	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0375	1811	A	G	0	49	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0375	2217	C	T	0	48	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0375	2706	A	G	0	47	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0375	3480	A	G	0	46	synonymous_variant	LOW	ND1	0.0392
HLI-0375	4769	A	G	0	55	synonymous_variant	LOW	ND2	0.9767
HLI-0375	5054	G	A	1	50	synonymous_variant	LOW	ND2	0.0033
HLI-0375	5231	G	A	1	50	synonymous_variant	LOW	ND2	0.0232
HLI-0375	6002	A	G	0	59	synonymous_variant	LOW	COX1	6.00E-04
HLI-0375	7028	C	T	0	55	synonymous_variant	LOW	COX1	0.8089
HLI-0375	9055	G	A	0	54	missense_variant	MODERATE	ATP6	0.0425
HLI-0375	9698	T	C	0	47	synonymous_variant	LOW	COX3	0.0405
HLI-0375	9716	T	C	0	45	synonymous_variant	LOW	COX3	0.0108
HLI-0375	10550	A	G	0	60	synonymous_variant	LOW	ND4L	0.0376
HLI-0375	11016	G	A	0	35	missense_variant	MODERATE	ND4	0.0062
HLI-0375	11299	T	C	0	57	synonymous_variant	LOW	ND4	0.0417
HLI-0375	11467	A	G	0	58	synonymous_variant	LOW	ND4	0.1231

HLI-0375	11719	G	A	0	54	synonymous_variant	LOW	ND4	0.7756
HLI-0375	11869	C	A	0	60	synonymous_variant	LOW	ND4	0.0015
HLI-0375	12308	A	G	0	39	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0375	12372	G	A	0	32	synonymous_variant	LOW	ND5	0.1329
HLI-0375	12501	G	A	0	59	synonymous_variant	LOW	ND5	0.0258
HLI-0375	14037	A	G	0	30	synonymous_variant	LOW	ND5	0.0017
HLI-0375	14167	C	T	0	38	synonymous_variant	LOW	ND6	0.0385
HLI-0375	14766	C	T	0	49	missense_variant	MODERATE	CYTB	0.7696
HLI-0375	14798	T	C	0	57	missense_variant	MODERATE	CYTB	0.0651
HLI-0375	15326	A	G	0	44	missense_variant	MODERATE	CYTB	0.9868
HLI-0375	16129	G	A	0	46	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0375	16224	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0375	16311	T	C	0	41	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0375	16519	T	C	0	23	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0376	73	A	G	1	199	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0376	153	A	G	2	333	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0376	195	T	C	0	310	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0376	263	A	G	0	129	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0376	750	A	G	5	447	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0376	1438	A	G	1	471	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0376	1719	G	A	1	455	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0376	2706	A	G	0	430	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0376	4769	A	G	1	410	synonymous_variant	LOW	ND2	0.9767
HLI-0376	6221	T	C	0	405	synonymous_variant	LOW	COX1	0.0306
HLI-0376	6371	C	T	0	386	synonymous_variant	LOW	COX1	0.0097
HLI-0376	7028	C	T	1	451	synonymous_variant	LOW	COX1	0.8089
HLI-0376	8393	C	T	0	325	missense_variant	MODERATE	ATP8	0.0036
HLI-0376	9083	T	C	1	422	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0376	11719	G	A	0	392	synonymous_variant	LOW	ND4	0.7756
HLI-0376	12705	C	T	1	452	synonymous_variant	LOW	ND5	0.4212
HLI-0376	13708	G	A	0	347	missense_variant	MODERATE	ND5	0.0717
HLI-0376	13966	A	G	1	359	missense_variant	MODERATE	ND5	0.0126
HLI-0376	14470	T	C	1	327	synonymous_variant	LOW	ND6	0.0166
HLI-0376	14766	C	T	1	387	missense_variant	MODERATE	CYTB	0.7696
HLI-0376	15326	A	G	0	376	missense_variant	MODERATE	CYTB	0.9868
HLI-0376	15927	G	A	0	472	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0376	16223	C	T	1	127	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0376	16278	C	T	0	237	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0376	16519	T	C	0	141	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0377	152	T	C	0	470	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0377	263	A	G	0	181	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0377	477	T	C	0	374	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0377	750	A	G	1	608	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0377	1438	A	G	0	633	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0377	3010	G	A	0	613	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0377	4769	A	G	0	553	synonymous_variant	LOW	ND2	0.9767
HLI-0377	8824	A	G	2	547	missense_variant	MODERATE	ATP6	0
HLI-0377	10523	A	G	0	638	synonymous_variant	LOW	ND4L	9.00E-04
HLI-0377	15326	A	G	0	503	missense_variant	MODERATE	CYTB	0.9868
HLI-0377	15565	T	C	0	602	synonymous_variant	LOW	CYTB	0.0021
HLI-0377	16519	T	C	0	244	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0378	146	T	C	0	495	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0378	153	A	G	0	507	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0378	263	A	G	0	201	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0378	750	A	G	0	645	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0378	1438	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0378	2581	A	G	1	615	upstream_gene_variant	MODIFIER	RNR2	0.0031
HLI-0378	4769	A	G	1	506	synonymous_variant	LOW	ND2	0.9767
HLI-0378	5147	G	A	0	504	synonymous_variant	LOW	ND2	0.0437
HLI-0378	6776	T	C	2	743	synonymous_variant	LOW	COX1	0.0226
HLI-0378	13813	G	A	1	452	missense_variant	MODERATE	ND5	5.00E-04
HLI-0378	15326	A	G	0	551	missense_variant	MODERATE	CYTB	0.9868
HLI-0378	16111	C	T	0	557	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0378	16129	G	A	0	594	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0378	16256	C	T	3	533	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0378	16519	T	C	0	263	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0379	73	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0379	189	A	G	0	336	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0379	200	A	G	0	341	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0379	263	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0379	750	A	G	0	514	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0379	1438	A	G	1	536	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0379	1692	A	G	1	508	upstream_gene_variant	MODIFIER	RNR2	0.003
HLI-0379	1822	T	C	1	548	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0379	2706	A	G	1	501	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0379	3396	T	C	0	478	synonymous_variant	LOW	ND1	0.0082
HLI-0379	4218	T	C	0	465	synonymous_variant	LOW	ND1	0.0057
HLI-0379	4769	A	G	1	549	synonymous_variant	LOW	ND2	0.9767

HLI-0379	5601	C	T	4	557	upstream_gene_variant	MODIFIER	TRNA	0.0101
HLI-0379	7028	C	T	2	592	synonymous_variant	LOW	COX1	0.8089
HLI-0379	7819	C	A	7	533	synonymous_variant	LOW	COX2	0.0045
HLI-0379	8527	A	G	0	472	initiator_codon_variant	LOW	ATP6/8	0.0044
HLI-0379	8701	A	G	1	528	missense_variant	MODERATE	ATP6	0.3391
HLI-0379	8932	C	T	0	577	missense_variant	MODERATE	ATP6	0.0044
HLI-0379	9540	T	C	0	496	synonymous_variant	LOW	COX3	0.339
HLI-0379	9950	T	C	0	587	synonymous_variant	LOW	COX3	0.0362
HLI-0379	10398	A	G	0	486	missense_variant	MODERATE	ND3	0.445
HLI-0379	10873	T	C	0	499	synonymous_variant	LOW	ND4	0.3389
HLI-0379	11440	G	A	0	573	synonymous_variant	LOW	ND4	0.0081
HLI-0379	11582	A	G	3	603	missense_variant	MODERATE	ND4	2.00E-04
HLI-0379	11719	G	A	1	549	synonymous_variant	LOW	ND4	0.7756
HLI-0379	12340	A	G	0	465	missense_variant	MODERATE	ND5	1.00E-04
HLI-0379	12705	C	T	0	627	synonymous_variant	LOW	ND5	0.4212
HLI-0379	13879	T	C	0	429	missense_variant	MODERATE	ND5	0.0073
HLI-0379	14766	C	T	1	574	missense_variant	MODERATE	CYTB	0.7696
HLI-0379	14769	A	G	1	575	missense_variant	MODERATE	CYTB	0.0121
HLI-0379	15301	G	A	0	399	synonymous_variant	LOW	CYTB	0.2912
HLI-0379	15326	A	G	1	432	missense_variant	MODERATE	CYTB	0.9868
HLI-0379	15514	T	C	0	400	synonymous_variant	LOW	CYTB	0.0071
HLI-0379	16209	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0379	16223	C	T	0	567	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0379	16292	C	T	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0379	16311	T	C	0	409	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0379	16519	T	C	0	211	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0380	64	C	T	1	192	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0380	93	A	G	1	277	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0380	185	G	A	1	282	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0380	189	A	G	1	282	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0380	195	T	C	1	270	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0380	200	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0380	236	T	C	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0380	247	G	A	0	230	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0380	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0380	750	A	G	0	558	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0380	769	G	A	0	603	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0380	825	T	A	0	663	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0380	1018	G	A	3	640	upstream_gene_variant	MODIFIER	RNR1	0.0817

HLI-0380	1048	C	T	1	704	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0380	1438	A	G	0	558	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0380	2245	A	C	0	387	upstream_gene_variant	MODIFIER	RNR2	8.00E-04
HLI-0380	2706	A	G	0	576	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0380	2758	G	A	1	583	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0380	2885	T	C	0	597	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0380	3516	C	A	2	538	synonymous_variant	LOW	ND1	0.0315
HLI-0380	3594	C	T	0	476	synonymous_variant	LOW	ND1	0.0789
HLI-0380	3866	T	C	0	549	missense_variant	MODERATE	ND1	0.0029
HLI-0380	4104	A	G	0	360	synonymous_variant	LOW	ND1	0.0785
HLI-0380	4312	C	T	2	388	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0380	4586	T	C	1	574	synonymous_variant	LOW	ND2	0.018
HLI-0380	4769	A	G	0	527	synonymous_variant	LOW	ND2	0.9767
HLI-0380	5096	T	C	0	483	synonymous_variant	LOW	ND2	0.0063
HLI-0380	5231	G	A	0	480	synonymous_variant	LOW	ND2	0.0232
HLI-0380	5442	T	C	0	515	missense_variant	MODERATE	ND2	0.0493
HLI-0380	5460	G	A	1	596	missense_variant	MODERATE	ND2	0.0651
HLI-0380	5603	C	T	3	605	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0380	6185	T	C	2	546	synonymous_variant	LOW	COX1	0.0325
HLI-0380	7028	C	T	1	560	synonymous_variant	LOW	COX1	0.8089
HLI-0380	7146	A	G	1	306	missense_variant	MODERATE	COX1	0.0497
HLI-0380	7256	C	T	2	441	synonymous_variant	LOW	COX1	0.0784
HLI-0380	7521	G	A	1	297	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0380	8428	C	T	4	436	synonymous_variant	LOW	ATP8	0.0144
HLI-0380	8468	C	T	3	449	synonymous_variant	LOW	ATP8	0.0501
HLI-0380	8566	A	G	0	431	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0380	8655	C	T	4	406	synonymous_variant	LOW	ATP6	0.0511
HLI-0380	8701	A	G	3	463	missense_variant	MODERATE	ATP6	0.3391
HLI-0380	9042	C	T	2	527	synonymous_variant	LOW	ATP6	0.0316
HLI-0380	9347	A	G	0	538	synonymous_variant	LOW	COX3	0.0314
HLI-0380	9540	T	C	0	530	synonymous_variant	LOW	COX3	0.339
HLI-0380	9755	G	A	0	591	synonymous_variant	LOW	COX3	0.0303
HLI-0380	9818	C	T	0	745	synonymous_variant	LOW	COX3	0.0179
HLI-0380	10398	A	G	0	532	missense_variant	MODERATE	ND3	0.445
HLI-0380	10589	G	A	1	554	synonymous_variant	LOW	ND4L	0.0355
HLI-0380	10664	C	T	1	602	synonymous_variant	LOW	ND4L	0.0315
HLI-0380	10688	G	A	1	580	synonymous_variant	LOW	ND4L	0.0515
HLI-0380	10810	T	C	0	537	synonymous_variant	LOW	ND4	0.0522
HLI-0380	10873	T	C	1	427	synonymous_variant	LOW	ND4	0.3389

HLI-0380	10915	T	C	2	480	synonymous_variant	LOW	ND4	0.0411
HLI-0380	11176	G	A	3	506	synonymous_variant	LOW	ND4	0.0181
HLI-0380	11641	A	G	2	593	synonymous_variant	LOW	ND4	0.0158
HLI-0380	11719	G	A	0	617	synonymous_variant	LOW	ND4	0.7756
HLI-0380	11914	G	A	0	515	synonymous_variant	LOW	ND4	0.1112
HLI-0380	12007	G	A	0	476	synonymous_variant	LOW	ND4	0.0639
HLI-0380	12477	T	C	2	445	synonymous_variant	LOW	ND5	0.0054
HLI-0380	12705	C	T	0	490	synonymous_variant	LOW	ND5	0.4212
HLI-0380	12720	A	G	2	525	synonymous_variant	LOW	ND5	0.0302
HLI-0380	13105	A	G	1	508	missense_variant	MODERATE	ND5	0.076
HLI-0380	13276	A	G	2	575	missense_variant	MODERATE	ND5	0.0312
HLI-0380	13506	C	T	1	499	synonymous_variant	LOW	ND5	0.0506
HLI-0380	13650	C	T	1	477	synonymous_variant	LOW	ND5	0.079
HLI-0380	14308	T	C	0	468	synonymous_variant	LOW	ND6	0.0209
HLI-0380	14488	T	C	0	479	synonymous_variant	LOW	ND6	6.00E-04
HLI-0380	14766	C	T	2	499	missense_variant	MODERATE	CYTB	0.7696
HLI-0380	15136	C	T	0	607	synonymous_variant	LOW	CYTB	0.0153
HLI-0380	15244	A	G	0	481	synonymous_variant	LOW	CYTB	0.0103
HLI-0380	15326	A	G	0	419	missense_variant	MODERATE	CYTB	0.9868
HLI-0380	15431	G	A	0	388	missense_variant	MODERATE	CYTB	0.0182
HLI-0380	15773	G	A	0	370	missense_variant	MODERATE	CYTB	0.0011
HLI-0380	15777	G	A	0	376	missense_variant	MODERATE	CYTB	0.0019
HLI-0380	16129	G	A	0	377	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0380	16148	C	T	0	394	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0380	16168	C	T	0	385	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0380	16172	T	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0380	16213	G	A	0	342	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0380	16223	C	T	0	352	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0380	16230	A	G	0	364	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0380	16311	T	C	0	370	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0380	16320	C	T	1	383	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0381	73	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0381	152	T	C	0	462	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0381	246	T	C	1	234	upstream_gene_variant	MODIFIER	DLoop	0.0022
HLI-0381	263	A	G	1	228	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0381	750	A	G	0	465	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0381	1438	A	G	0	538	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0381	2706	A	G	0	457	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0381	4769	A	G	1	514	synonymous_variant	LOW	ND2	0.9767

HLI-0381	5147	G	A	0	372	synonymous_variant	LOW	ND2	0.0437
HLI-0381	6491	C	T	2	468	synonymous_variant	LOW	COX1	0.002
HLI-0381	7028	C	T	1	506	synonymous_variant	LOW	COX1	0.8089
HLI-0381	7193	T	C	0	531	synonymous_variant	LOW	COX1	8.00E-04
HLI-0381	9336	A	G	3	472	missense_variant	MODERATE	COX3	0.0016
HLI-0381	11935	T	C	1	456	synonymous_variant	LOW	ND4	0.002
HLI-0381	12061	C	T	3	488	synonymous_variant	LOW	ND4	0.0014
HLI-0381	15326	A	G	0	364	missense_variant	MODERATE	CYTB	0.9868
HLI-0381	16214	C	T	1	548	upstream_gene_variant	MODIFIER	DLoop	0.008
HLI-0381	16217	T	C	1	548	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0381	16311	T	C	1	405	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0381	16335	A	G	1	403	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0381	16519	T	C	0	220	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0382	263	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0382	750	A	G	1	567	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0382	1438	A	G	0	577	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0382	4769	A	G	1	562	synonymous_variant	LOW	ND2	0.9767
HLI-0382	9129	C	T	1	613	synonymous_variant	LOW	ATP6	6.00E-04
HLI-0382	10394	C	T	1	566	synonymous_variant	LOW	ND3	0.002
HLI-0382	15326	A	G	0	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0382	16519	T	C	1	285	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0383	73	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0383	150	C	T	0	444	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0383	195	T	C	2	460	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0383	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0383	750	A	G	1	495	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0383	1438	A	G	1	517	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0383	2352	T	C	0	359	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0383	2483	T	C	0	451	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0383	2706	A	G	1	510	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0383	4769	A	G	1	518	synonymous_variant	LOW	ND2	0.9767
HLI-0383	5580	T	C	0	581	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0383	7028	C	T	2	591	synonymous_variant	LOW	COX1	0.8089
HLI-0383	8701	A	G	1	544	missense_variant	MODERATE	ATP6	0.3391
HLI-0383	9377	A	G	0	510	synonymous_variant	LOW	COX3	0.0084
HLI-0383	9540	T	C	0	404	synonymous_variant	LOW	COX3	0.339
HLI-0383	10398	A	G	0	536	missense_variant	MODERATE	ND3	0.445
HLI-0383	10819	A	G	1	471	synonymous_variant	LOW	ND4	0.0228
HLI-0383	10873	T	C	0	504	synonymous_variant	LOW	ND4	0.3389

HLI-0383	11337	A	G	1	505	missense_variant	MODERATE	ND4	6.00E-04
HLI-0383	11719	G	A	0	483	synonymous_variant	LOW	ND4	0.7756
HLI-0383	12705	C	T	2	515	synonymous_variant	LOW	ND5	0.4212
HLI-0383	14212	T	C	0	457	synonymous_variant	LOW	ND6	0.0204
HLI-0383	14766	C	T	4	552	missense_variant	MODERATE	CYTB	0.7696
HLI-0383	14905	G	A	0	636	synonymous_variant	LOW	CYTB	0.0526
HLI-0383	15301	G	A	0	418	synonymous_variant	LOW	CYTB	0.2912
HLI-0383	15326	A	G	0	422	missense_variant	MODERATE	CYTB	0.9868
HLI-0383	16172	T	C	0	284	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0383	16223	C	T	2	281	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0383	16320	C	T	0	413	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0383	16519	T	C	1	179	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0384	73	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0384	709	G	A	0	579	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0384	750	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0384	930	G	A	2	643	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0384	1438	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0384	1888	G	A	1	548	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0384	2706	A	G	0	570	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0384	4216	T	C	2	617	missense_variant	MODERATE	ND1	0.0991
HLI-0384	4769	A	G	1	493	synonymous_variant	LOW	ND2	0.9767
HLI-0384	4917	A	G	0	553	missense_variant	MODERATE	ND2	0.0477
HLI-0384	5147	G	A	0	472	synonymous_variant	LOW	ND2	0.0437
HLI-0384	7028	C	T	1	680	synonymous_variant	LOW	COX1	0.8089
HLI-0384	8697	G	A	0	528	synonymous_variant	LOW	ATP6	0.0466
HLI-0384	10463	T	C	2	658	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0384	11251	A	G	0	579	synonymous_variant	LOW	ND4	0.0932
HLI-0384	11719	G	A	1	612	synonymous_variant	LOW	ND4	0.7756
HLI-0384	11812	A	G	1	601	synonymous_variant	LOW	ND4	0.0332
HLI-0384	13368	G	A	0	575	synonymous_variant	LOW	ND5	0.0495
HLI-0384	14233	A	G	1	501	synonymous_variant	LOW	ND6	0.0369
HLI-0384	14766	C	T	1	536	missense_variant	MODERATE	CYTB	0.7696
HLI-0384	14905	G	A	1	605	synonymous_variant	LOW	CYTB	0.0526
HLI-0384	15172	G	A	1	529	synonymous_variant	LOW	CYTB	0.0075
HLI-0384	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868
HLI-0384	15452	C	A	3	461	missense_variant	MODERATE	CYTB	0.0933
HLI-0384	15607	A	G	0	532	synonymous_variant	LOW	CYTB	0.0508
HLI-0384	15928	G	A	1	675	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0384	16126	T	C	1	631	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0384	16294	C	T	1	541	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0384	16296	C	T	1	538	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0384	16304	T	C	1	533	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0384	16519	T	C	0	267	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0385	73	A	G	0	32	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0385	195	T	C	0	56	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0385	263	A	G	0	30	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0385	709	G	A	0	61	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0385	750	A	G	0	55	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0385	930	G	A	1	50	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0385	1438	A	G	0	47	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0385	1888	G	A	0	43	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0385	2706	A	G	0	53	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0385	4216	T	C	0	56	missense_variant	MODERATE	ND1	0.0991
HLI-0385	4769	A	G	1	35	synonymous_variant	LOW	ND2	0.9767
HLI-0385	4917	A	G	0	57	missense_variant	MODERATE	ND2	0.0477
HLI-0385	5147	G	A	0	31	synonymous_variant	LOW	ND2	0.0437
HLI-0385	7028	C	T	0	69	synonymous_variant	LOW	COX1	0.8089
HLI-0385	8697	G	A	1	38	synonymous_variant	LOW	ATP6	0.0466
HLI-0385	10463	T	C	0	50	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0385	11251	A	G	0	54	synonymous_variant	LOW	ND4	0.0932
HLI-0385	11719	G	A	0	48	synonymous_variant	LOW	ND4	0.7756
HLI-0385	11812	A	G	0	60	synonymous_variant	LOW	ND4	0.0332
HLI-0385	13368	G	A	0	65	synonymous_variant	LOW	ND5	0.0495
HLI-0385	14233	A	G	0	47	synonymous_variant	LOW	ND6	0.0369
HLI-0385	14766	C	T	0	56	missense_variant	MODERATE	CYTB	0.7696
HLI-0385	14905	G	A	0	65	synonymous_variant	LOW	CYTB	0.0526
HLI-0385	15001	T	C	1	69	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0385	15326	A	G	0	68	missense_variant	MODERATE	CYTB	0.9868
HLI-0385	15452	C	A	0	54	missense_variant	MODERATE	CYTB	0.0933
HLI-0385	15607	A	G	0	35	synonymous_variant	LOW	CYTB	0.0508
HLI-0385	15928	G	A	0	40	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0385	16126	T	C	0	47	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0385	16294	C	T	0	48	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0385	16296	C	T	0	48	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0385	16304	T	C	0	48	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0385	16519	T	C	0	20	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0386	73	A	G	0	250	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0386	152	T	C	0	455	upstream_gene_variant	MODIFIER	DLoop	0.2668

HLI-0386	195	T	C	2	428	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0386	263	A	G	0	150	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0386	285	C	T	0	165	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0386	385	A	G	0	314	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0386	750	A	G	0	552	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0386	1438	A	G	1	595	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0386	2218	C	T	2	459	upstream_gene_variant	MODIFIER	RNR2	0.0031
HLI-0386	2706	A	G	0	553	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0386	3591	G	A	1	469	synonymous_variant	LOW	ND1	0.0082
HLI-0386	4769	A	G	1	518	synonymous_variant	LOW	ND2	0.9767
HLI-0386	4991	G	A	2	473	synonymous_variant	LOW	ND2	0.0052
HLI-0386	6026	G	A	0	609	synonymous_variant	LOW	COX1	0.0163
HLI-0386	7028	C	T	0	617	synonymous_variant	LOW	COX1	0.8089
HLI-0386	7581	T	C	0	556	upstream_gene_variant	MODIFIER	TRND	0.0044
HLI-0386	9302	C	T	2	550	synonymous_variant	LOW	COX3	6.00E-04
HLI-0386	10586	G	A	0	538	synonymous_variant	LOW	ND4L	0.0177
HLI-0386	11467	A	G	2	603	synonymous_variant	LOW	ND4	0.1231
HLI-0386	11719	G	A	0	556	synonymous_variant	LOW	ND4	0.7756
HLI-0386	12308	A	G	0	472	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0386	12372	G	A	0	458	synonymous_variant	LOW	ND5	0.1329
HLI-0386	12879	T	C	1	574	synonymous_variant	LOW	ND5	0.0058
HLI-0386	13104	A	G	1	541	synonymous_variant	LOW	ND5	0.0057
HLI-0386	13422	A	G	2	529	synonymous_variant	LOW	ND5	0.0021
HLI-0386	14070	A	G	0	421	synonymous_variant	LOW	ND5	0.0038
HLI-0386	14364	G	A	0	447	synonymous_variant	LOW	ND6	0.0076
HLI-0386	14766	C	T	2	556	missense_variant	MODERATE	CYTB	0.7696
HLI-0386	15148	G	A	0	563	synonymous_variant	LOW	CYTB	0.0058
HLI-0386	15954	A	C	3	534	upstream_gene_variant	MODIFIER	Unannotated	0.0036
HLI-0386	16129	G	A	1	309	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0386	16249	T	C	1	270	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0386	16288	T	C	0	336	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0386	16362	T	C	1	394	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0387	73	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0387	195	T	C	0	333	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0387	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0387	497	C	T	3	328	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0387	750	A	G	0	456	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0387	1189	T	C	0	558	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0387	1438	A	G	0	469	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0387	1811	A	G	1	547	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0387	2706	A	G	0	447	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0387	3480	A	G	1	372	synonymous_variant	LOW	ND1	0.0392
HLI-0387	4769	A	G	0	487	synonymous_variant	LOW	ND2	0.9767
HLI-0387	7028	C	T	5	533	synonymous_variant	LOW	COX1	0.8089
HLI-0387	9055	G	A	1	476	missense_variant	MODERATE	ATP6	0.0425
HLI-0387	9698	T	C	0	480	synonymous_variant	LOW	COX3	0.0405
HLI-0387	10398	A	G	0	384	missense_variant	MODERATE	ND3	0.445
HLI-0387	10550	A	G	0	418	synonymous_variant	LOW	ND4L	0.0376
HLI-0387	11299	T	C	2	488	synonymous_variant	LOW	ND4	0.0417
HLI-0387	11467	A	G	2	509	synonymous_variant	LOW	ND4	0.1231
HLI-0387	11719	G	A	0	509	synonymous_variant	LOW	ND4	0.7756
HLI-0387	12063	C	T	0	505	missense_variant	MODERATE	ND4	6.00E-04
HLI-0387	12308	A	G	0	497	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0387	12372	G	A	0	474	synonymous_variant	LOW	ND5	0.1329
HLI-0387	14167	C	T	1	444	synonymous_variant	LOW	ND6	0.0385
HLI-0387	14766	C	T	5	552	missense_variant	MODERATE	CYTB	0.7696
HLI-0387	14798	T	C	0	619	missense_variant	MODERATE	CYTB	0.0651
HLI-0387	15326	A	G	0	348	missense_variant	MODERATE	CYTB	0.9868
HLI-0387	16224	T	C	1	507	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0387	16311	T	C	0	402	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0387	16519	T	C	0	179	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0388	195	T	C	2	398	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0388	263	A	G	0	222	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0388	750	A	G	1	566	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0388	961	T	G	5	655	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0388	1438	A	G	1	616	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0388	4769	A	G	0	601	synonymous_variant	LOW	ND2	0.9767
HLI-0388	7521	G	A	0	550	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0388	8448	T	C	0	469	missense_variant	MODERATE	ATP8	0.0041
HLI-0388	8898	C	T	0	650	synonymous_variant	LOW	ATP6	0.0011
HLI-0388	13759	G	A	0	412	missense_variant	MODERATE	ND5	0.0348
HLI-0388	15326	A	G	3	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0388	16278	C	T	3	554	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0388	16311	T	C	0	577	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0389	263	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0389	750	A	G	0	521	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0389	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0389	4769	A	G	0	541	synonymous_variant	LOW	ND2	0.9767

HLI-0389	10704	G	A	2	566	missense_variant	MODERATE	ND4L	2.00E-04
HLI-0389	11440	G	A	0	574	synonymous_variant	LOW	ND4	0.0081
HLI-0389	14239	C	T	3	509	synonymous_variant	LOW	ND6	0.0014
HLI-0389	15326	A	G	0	484	missense_variant	MODERATE	CYTB	0.9868
HLI-0389	16519	T	C	0	251	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0390	64	C	T	1	228	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0390	93	A	G	1	330	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0390	152	T	C	0	403	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0390	185	G	A	2	420	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0390	189	A	G	1	405	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0390	236	T	C	1	148	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0390	247	G	A	1	157	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0390	263	A	G	1	174	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0390	750	A	G	0	641	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0390	769	G	A	1	691	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0390	825	T	A	0	698	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0390	1018	G	A	0	703	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0390	1048	C	T	1	764	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0390	1438	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0390	1822	T	C	0	642	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0390	2245	A	G	1	640	upstream_gene_variant	MODIFIER	RNR2	0.0145
HLI-0390	2626	T	C	0	684	upstream_gene_variant	MODIFIER	RNR2	0.0045
HLI-0390	2706	A	G	1	658	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0390	2758	G	A	0	614	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0390	2759	T	C	0	614	upstream_gene_variant	MODIFIER	RNR2	3.00E-04
HLI-0390	2885	T	C	1	625	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0390	3516	C	A	2	520	synonymous_variant	LOW	ND1	0.0315
HLI-0390	3594	C	T	0	537	synonymous_variant	LOW	ND1	0.0789
HLI-0390	3866	T	C	0	642	missense_variant	MODERATE	ND1	0.0029
HLI-0390	4104	A	G	0	435	synonymous_variant	LOW	ND1	0.0785
HLI-0390	4312	C	T	0	508	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0390	4586	T	C	0	613	synonymous_variant	LOW	ND2	0.018
HLI-0390	4769	A	G	0	584	synonymous_variant	LOW	ND2	0.9767
HLI-0390	5096	T	C	0	583	synonymous_variant	LOW	ND2	0.0063
HLI-0390	5231	G	A	0	570	synonymous_variant	LOW	ND2	0.0232
HLI-0390	5442	T	C	0	633	missense_variant	MODERATE	ND2	0.0493
HLI-0390	5460	G	A	0	692	missense_variant	MODERATE	ND2	0.0651
HLI-0390	5603	C	T	1	695	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0390	6185	T	C	0	646	synonymous_variant	LOW	COX1	0.0325

HLI-0390	7028	C	T	2	589	synonymous_variant	LOW	COX1	0.8089
HLI-0390	7146	A	G	2	334	missense_variant	MODERATE	COX1	0.0497
HLI-0390	7256	C	T	2	457	synonymous_variant	LOW	COX1	0.0784
HLI-0390	7521	G	A	0	428	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0390	8428	C	T	2	532	synonymous_variant	LOW	ATP8	0.0144
HLI-0390	8468	C	T	2	527	synonymous_variant	LOW	ATP8	0.0501
HLI-0390	8566	A	G	0	512	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0390	8655	C	T	1	459	synonymous_variant	LOW	ATP6	0.0511
HLI-0390	8701	A	G	1	516	missense_variant	MODERATE	ATP6	0.3391
HLI-0390	8764	G	A	1	558	missense_variant	MODERATE	ATP6	0.0016
HLI-0390	9042	C	T	1	647	synonymous_variant	LOW	ATP6	0.0316
HLI-0390	9347	A	G	0	640	synonymous_variant	LOW	COX3	0.0314
HLI-0390	9540	T	C	0	617	synonymous_variant	LOW	COX3	0.339
HLI-0390	9755	G	A	1	670	synonymous_variant	LOW	COX3	0.0303
HLI-0390	9818	C	T	0	760	synonymous_variant	LOW	COX3	0.0179
HLI-0390	10398	A	G	3	658	missense_variant	MODERATE	ND3	0.445
HLI-0390	10589	G	A	0	626	synonymous_variant	LOW	ND4L	0.0355
HLI-0390	10664	C	T	0	665	synonymous_variant	LOW	ND4L	0.0315
HLI-0390	10688	G	A	0	643	synonymous_variant	LOW	ND4L	0.0515
HLI-0390	10810	T	C	0	559	synonymous_variant	LOW	ND4	0.0522
HLI-0390	10873	T	C	0	635	synonymous_variant	LOW	ND4	0.3389
HLI-0390	10915	T	C	2	595	synonymous_variant	LOW	ND4	0.0411
HLI-0390	11176	G	A	2	619	synonymous_variant	LOW	ND4	0.0181
HLI-0390	11641	A	G	0	602	synonymous_variant	LOW	ND4	0.0158
HLI-0390	11719	G	A	0	623	synonymous_variant	LOW	ND4	0.7756
HLI-0390	11914	G	A	0	626	synonymous_variant	LOW	ND4	0.1112
HLI-0390	12007	G	A	0	620	synonymous_variant	LOW	ND4	0.0639
HLI-0390	12705	C	T	1	637	synonymous_variant	LOW	ND5	0.4212
HLI-0390	12720	A	G	1	704	synonymous_variant	LOW	ND5	0.0302
HLI-0390	13105	A	G	0	602	missense_variant	MODERATE	ND5	0.076
HLI-0390	13276	A	G	3	635	missense_variant	MODERATE	ND5	0.0312
HLI-0390	13506	C	T	0	562	synonymous_variant	LOW	ND5	0.0506
HLI-0390	13650	C	T	2	532	synonymous_variant	LOW	ND5	0.079
HLI-0390	14308	T	C	0	493	synonymous_variant	LOW	ND6	0.0209
HLI-0390	14766	C	T	4	596	missense_variant	MODERATE	CYTB	0.7696
HLI-0390	15136	C	T	2	671	synonymous_variant	LOW	CYTB	0.0153
HLI-0390	15326	A	G	0	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0390	15431	G	A	2	565	missense_variant	MODERATE	CYTB	0.0182
HLI-0390	16093	T	C	28	543	upstream_gene_variant	MODIFIER	DLoop	0.0573

HLI-0390	16129	G	A	1	559	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0390	16148	C	T	1	561	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0390	16168	C	T	1	524	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0390	16172	T	C	1	519	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0390	16223	C	T	0	462	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0390	16230	A	G	0	452	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0390	16301	C	T	0	411	upstream_gene_variant	MODIFIER	DLoop	0.0064
HLI-0390	16311	T	C	0	439	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0390	16320	C	T	0	452	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0391	263	A	G	1	188	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0391	750	A	G	0	554	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0391	1438	A	G	0	628	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0391	4769	A	G	1	564	synonymous_variant	LOW	ND2	0.9767
HLI-0391	14470	T	A	1	450	synonymous_variant	LOW	ND6	0.0031
HLI-0391	15326	A	G	1	495	missense_variant	MODERATE	CYTB	0.9868
HLI-0391	16519	T	C	1	238	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0392	263	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0392	750	A	G	0	544	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0392	1438	A	G	0	562	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0392	3010	G	A	0	556	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0392	4769	A	G	1	534	synonymous_variant	LOW	ND2	0.9767
HLI-0392	8602	T	C	0	538	missense_variant	MODERATE	ATP6	0.0017
HLI-0392	9098	T	C	1	544	missense_variant	MODERATE	ATP6	0.0011
HLI-0392	14212	T	C	0	506	synonymous_variant	LOW	ND6	0.0204
HLI-0392	15326	A	G	0	433	missense_variant	MODERATE	CYTB	0.9868
HLI-0392	16209	T	C	0	185	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0392	16519	T	C	0	168	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0393	73	A	G	1	315	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0393	152	T	C	1	579	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0393	263	A	G	1	235	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0393	709	G	A	0	616	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0393	750	A	G	2	649	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0393	930	G	A	3	628	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0393	1438	A	G	1	648	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0393	1888	G	A	1	590	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0393	2706	A	G	1	578	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0393	4216	T	C	0	631	missense_variant	MODERATE	ND1	0.0991
HLI-0393	4769	A	G	1	615	synonymous_variant	LOW	ND2	0.9767
HLI-0393	4917	A	G	0	594	missense_variant	MODERATE	ND2	0.0477

HLI-0393	5147	G	A	2	540	synonymous_variant	LOW	ND2	0.0437
HLI-0393	7028	C	T	0	707	synonymous_variant	LOW	COX1	0.8089
HLI-0393	8697	G	A	0	575	synonymous_variant	LOW	ATP6	0.0466
HLI-0393	10463	T	C	1	689	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0393	11242	C	G	0	589	synonymous_variant	LOW	ND4	4.00E-04
HLI-0393	11251	A	G	0	620	synonymous_variant	LOW	ND4	0.0932
HLI-0393	11719	G	A	1	572	synonymous_variant	LOW	ND4	0.7756
HLI-0393	11812	A	G	3	582	synonymous_variant	LOW	ND4	0.0332
HLI-0393	13368	G	A	1	618	synonymous_variant	LOW	ND5	0.0495
HLI-0393	14233	A	G	1	525	synonymous_variant	LOW	ND6	0.0369
HLI-0393	14766	C	T	4	556	missense_variant	MODERATE	CYTB	0.7696
HLI-0393	14905	G	A	1	617	synonymous_variant	LOW	CYTB	0.0526
HLI-0393	15326	A	G	0	548	missense_variant	MODERATE	CYTB	0.9868
HLI-0393	15452	C	A	6	528	missense_variant	MODERATE	CYTB	0.0933
HLI-0393	15607	A	G	1	572	synonymous_variant	LOW	CYTB	0.0508
HLI-0393	15928	G	A	0	598	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0393	16126	T	C	0	567	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0393	16294	C	T	3	527	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0393	16311	T	C	0	556	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0393	16519	T	C	0	317	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0394	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0394	185	G	A	3	439	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0394	263	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0394	295	C	T	1	193	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0394	462	C	T	0	433	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0394	489	T	C	0	493	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0394	750	A	G	0	536	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0394	1438	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0394	2706	A	G	1	518	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0394	3010	G	A	0	593	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0394	4216	T	C	0	491	missense_variant	MODERATE	ND1	0.0991
HLI-0394	4769	A	G	1	532	synonymous_variant	LOW	ND2	0.9767
HLI-0394	5198	A	G	0	492	synonymous_variant	LOW	ND2	0.0023
HLI-0394	7028	C	T	4	594	synonymous_variant	LOW	COX1	0.8089
HLI-0394	10398	A	G	0	580	missense_variant	MODERATE	ND3	0.445
HLI-0394	11251	A	G	1	580	synonymous_variant	LOW	ND4	0.0932
HLI-0394	11719	G	A	1	541	synonymous_variant	LOW	ND4	0.7756
HLI-0394	12612	A	G	5	640	synonymous_variant	LOW	ND5	0.0506
HLI-0394	13708	G	A	0	513	missense_variant	MODERATE	ND5	0.0717

HLI-0394	14766	C	T	5	573	missense_variant	MODERATE	CYTB	0.7696
HLI-0394	14798	T	C	0	668	missense_variant	MODERATE	CYTB	0.0651
HLI-0394	15326	A	G	0	429	missense_variant	MODERATE	CYTB	0.9868
HLI-0394	15452	C	A	5	449	missense_variant	MODERATE	CYTB	0.0933
HLI-0394	16069	C	T	0	613	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0395	73	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0395	150	C	T	0	484	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0395	195	T	C	1	478	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0395	263	A	G	0	205	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0395	750	A	G	1	576	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0395	1438	A	G	0	605	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0395	2352	T	C	1	583	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0395	2483	T	C	2	555	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0395	2706	A	G	1	578	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0395	3277	G	A	0	599	upstream_gene_variant	MODIFIER	TRNL1	7.00E-04
HLI-0395	4769	A	G	1	546	synonymous_variant	LOW	ND2	0.9767
HLI-0395	7028	C	T	2	650	synonymous_variant	LOW	COX1	0.8089
HLI-0395	8701	A	G	1	553	missense_variant	MODERATE	ATP6	0.3391
HLI-0395	9377	A	G	0	600	synonymous_variant	LOW	COX3	0.0084
HLI-0395	9540	T	C	0	542	synonymous_variant	LOW	COX3	0.339
HLI-0395	10398	A	G	0	608	missense_variant	MODERATE	ND3	0.445
HLI-0395	10819	A	G	0	576	synonymous_variant	LOW	ND4	0.0228
HLI-0395	10873	T	C	1	576	synonymous_variant	LOW	ND4	0.3389
HLI-0395	11719	G	A	1	632	synonymous_variant	LOW	ND4	0.7756
HLI-0395	12406	G	A	0	539	missense_variant	MODERATE	ND5	0.0262
HLI-0395	12705	C	T	2	665	synonymous_variant	LOW	ND5	0.4212
HLI-0395	14212	T	C	0	536	synonymous_variant	LOW	ND6	0.0204
HLI-0395	14766	C	T	2	619	missense_variant	MODERATE	CYTB	0.7696
HLI-0395	14905	G	A	0	606	synonymous_variant	LOW	CYTB	0.0526
HLI-0395	15301	G	A	0	561	synonymous_variant	LOW	CYTB	0.2912
HLI-0395	15326	A	G	0	602	missense_variant	MODERATE	CYTB	0.9868
HLI-0395	15514	T	C	1	458	synonymous_variant	LOW	CYTB	0.0071
HLI-0395	16172	T	C	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0395	16223	C	T	2	310	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0395	16320	C	T	3	469	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0395	16519	T	C	0	255	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0396	73	A	G	1	159	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0396	151	C	T	0	264	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0396	152	T	C	0	263	upstream_gene_variant	MODIFIER	DLoop	0.2668

HLI-0396	182	C	T	0	237	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0396	186	C	A	0	236	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0396	189	A	C	0	232	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0396	195	T	C	0	234	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0396	198	C	T	0	234	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0396	204	T	C	0	249	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0396	247	G	A	0	121	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0396	263	A	G	0	138	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0396	297	A	G	0	173	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0396	750	A	G	0	466	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0396	769	G	A	0	509	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0396	825	T	A	0	536	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0396	1018	G	A	0	624	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0396	1438	A	G	0	526	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0396	2220	A	G	0	516	upstream_gene_variant	MODIFIER	RNR2	0.0029
HLI-0396	2706	A	G	0	483	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0396	2758	G	A	1	505	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0396	2885	T	C	1	465	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0396	3594	C	T	1	393	synonymous_variant	LOW	ND1	0.0789
HLI-0396	3666	G	A	2	436	synonymous_variant	LOW	ND1	0.0233
HLI-0396	4104	A	G	1	340	synonymous_variant	LOW	ND1	0.0785
HLI-0396	4769	A	G	1	524	synonymous_variant	LOW	ND2	0.9767
HLI-0396	5074	T	C	2	413	missense_variant	MODERATE	ND2	0.0017
HLI-0396	5087	T	C	2	462	synonymous_variant	LOW	ND2	0.0014
HLI-0396	5951	A	G	3	592	synonymous_variant	LOW	COX1	0.0128
HLI-0396	6071	T	C	1	525	synonymous_variant	LOW	COX1	0.0129
HLI-0396	6150	G	A	0	591	missense_variant	MODERATE	COX1	0.0049
HLI-0396	6253	T	C	0	515	missense_variant	MODERATE	COX1	0.0106
HLI-0396	6480	G	A	1	414	missense_variant	MODERATE	COX1	0.0031
HLI-0396	7028	C	T	0	425	synonymous_variant	LOW	COX1	0.8089
HLI-0396	7055	A	G	0	434	synonymous_variant	LOW	COX1	0.0188
HLI-0396	7076	A	G	0	394	synonymous_variant	LOW	COX1	0.0053
HLI-0396	7146	A	G	0	283	missense_variant	MODERATE	COX1	0.0497
HLI-0396	7256	C	T	2	439	synonymous_variant	LOW	COX1	0.0784
HLI-0396	7337	G	A	1	464	synonymous_variant	LOW	COX1	0.0119
HLI-0396	7389	T	C	3	416	missense_variant	MODERATE	COX1	0.0201
HLI-0396	7521	G	A	0	389	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0396	8027	G	A	5	585	missense_variant	MODERATE	COX2	0.0334
HLI-0396	8468	C	T	1	415	synonymous_variant	LOW	ATP8	0.0501

HLI-0396	8655	C	T	3	427	synonymous_variant	LOW	ATP6	0.0511
HLI-0396	8701	A	G	1	479	missense_variant	MODERATE	ATP6	0.3391
HLI-0396	8784	A	G	1	423	synonymous_variant	LOW	ATP6	0.006
HLI-0396	8877	T	C	0	424	synonymous_variant	LOW	ATP6	0.0053
HLI-0396	9072	A	G	0	448	synonymous_variant	LOW	ATP6	0.0124
HLI-0396	9108	A	G	1	508	synonymous_variant	LOW	ATP6	0.0014
HLI-0396	9540	T	C	0	411	synonymous_variant	LOW	COX3	0.339
HLI-0396	10031	T	C	0	575	upstream_gene_variant	MODIFIER	TRNG	0.0033
HLI-0396	10321	T	C	1	452	missense_variant	MODERATE	ND3	0.0106
HLI-0396	10398	A	G	1	457	missense_variant	MODERATE	ND3	0.445
HLI-0396	10586	G	A	1	474	synonymous_variant	LOW	ND4L	0.0177
HLI-0396	10688	G	A	0	442	synonymous_variant	LOW	ND4L	0.0515
HLI-0396	10792	A	G	0	473	synonymous_variant	LOW	ND4	0.0044
HLI-0396	10793	C	T	0	477	synonymous_variant	LOW	ND4	0.0043
HLI-0396	10810	T	C	0	499	synonymous_variant	LOW	ND4	0.0522
HLI-0396	10873	T	C	1	467	synonymous_variant	LOW	ND4	0.3389
HLI-0396	11164	A	G	0	439	synonymous_variant	LOW	ND4	0.0023
HLI-0396	11654	A	G	0	493	missense_variant	MODERATE	ND4	0.0045
HLI-0396	11719	G	A	1	507	synonymous_variant	LOW	ND4	0.7756
HLI-0396	11963	G	A	1	517	missense_variant	MODERATE	ND4	0.002
HLI-0396	12049	C	T	0	556	synonymous_variant	LOW	ND4	0.0052
HLI-0396	12669	C	T	2	607	synonymous_variant	LOW	ND5	0.0021
HLI-0396	12705	C	T	1	647	synonymous_variant	LOW	ND5	0.4212
HLI-0396	12810	A	G	1	468	synonymous_variant	LOW	ND5	0.0198
HLI-0396	13105	A	G	0	489	missense_variant	MODERATE	ND5	0.076
HLI-0396	13149	A	G	1	557	synonymous_variant	LOW	ND5	0.0053
HLI-0396	13485	A	G	0	446	synonymous_variant	LOW	ND5	0.0122
HLI-0396	13506	C	T	1	515	synonymous_variant	LOW	ND5	0.0506
HLI-0396	13650	C	T	1	406	synonymous_variant	LOW	ND5	0.079
HLI-0396	13789	T	C	0	288	missense_variant	MODERATE	ND5	0.0185
HLI-0396	14000	T	A	0	416	missense_variant	MODERATE	ND5	0.0126
HLI-0396	14178	T	C	0	481	missense_variant	MODERATE	ND6	0.0225
HLI-0396	14560	G	A	1	615	synonymous_variant	LOW	ND6	0.0235
HLI-0396	14587	A	G	3	648	synonymous_variant	LOW	ND6	0.006
HLI-0396	14766	C	T	1	532	missense_variant	MODERATE	CYTB	0.7696
HLI-0396	14911	C	T	1	644	synonymous_variant	LOW	CYTB	0.0124
HLI-0396	15326	A	G	0	319	missense_variant	MODERATE	CYTB	0.9868
HLI-0396	15924	A	G	1	535	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0396	16129	G	A	0	624	upstream_gene_variant	MODIFIER	DLoop	0.1301

HLI-0396	16214	C	T	0	480	upstream_gene_variant	MODIFIER	DLoop	0.008
HLI-0396	16223	C	T	3	453	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0396	16265	A	C	0	360	upstream_gene_variant	MODIFIER	DLoop	0.0087
HLI-0396	16278	C	T	0	330	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0396	16286	C	A	0	314	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0396	16291	C	T	0	317	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0396	16294	C	T	0	311	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0396	16311	T	C	0	308	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0396	16360	C	T	0	298	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0396	16519	T	C	0	105	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0396	16527	C	T	0	99	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0397	263	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0397	750	A	G	0	564	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0397	1438	A	G	1	578	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0397	3010	G	A	0	564	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0397	4769	A	G	1	526	synonymous_variant	LOW	ND2	0.9767
HLI-0397	8764	G	A	0	508	missense_variant	MODERATE	ATP6	0.0016
HLI-0397	10790	T	C	0	560	synonymous_variant	LOW	ND4	0.0027
HLI-0397	12507	A	G	2	556	synonymous_variant	LOW	ND5	0.0015
HLI-0397	12546	A	G	1	613	synonymous_variant	LOW	ND5	0
HLI-0397	15326	A	G	0	525	missense_variant	MODERATE	CYTB	0.9868
HLI-0397	16519	T	C	1	287	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0398	72	T	C	0	279	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0398	195	T	C	2	377	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0398	263	A	G	1	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0398	750	A	G	1	592	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0398	1438	A	G	1	664	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0398	2706	A	G	0	599	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0398	4769	A	G	2	495	synonymous_variant	LOW	ND2	0.9767
HLI-0398	7028	C	T	3	641	synonymous_variant	LOW	COX1	0.8089
HLI-0398	13461	T	C	0	607	synonymous_variant	LOW	ND5	3.00E-04
HLI-0398	15326	A	G	1	533	missense_variant	MODERATE	CYTB	0.9868
HLI-0398	15617	G	A	0	498	missense_variant	MODERATE	CYTB	0.0013
HLI-0398	16298	T	C	1	517	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0398	16311	T	C	1	548	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0399	73	A	G	0	195	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0399	152	T	C	0	359	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0399	182	C	T	0	337	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0399	185	G	T	0	325	upstream_gene_variant	MODIFIER	DLoop	0.0056

HLI-0399	195	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0399	198	C	T	0	311	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0399	228	G	A	0	363	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0399	247	G	A	0	369	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0399	263	A	G	0	146	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0399	357	A	G	0	334	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0399	709	G	A	1	414	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0399	710	T	C	1	418	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0399	750	A	G	0	472	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0399	769	G	A	0	491	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0399	825	T	A	0	544	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0399	1018	G	A	0	623	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0399	1738	T	C	1	553	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0399	2352	T	C	1	500	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0399	2706	A	G	0	446	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0399	2758	G	A	0	479	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0399	2768	A	G	0	480	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0399	2885	T	C	0	434	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0399	3308	T	C	0	449	start_lost	HIGH	ND1	0.0073
HLI-0399	3594	C	T	1	370	synonymous_variant	LOW	ND1	0.0789
HLI-0399	3666	G	A	3	417	synonymous_variant	LOW	ND1	0.0233
HLI-0399	3693	G	A	0	394	synonymous_variant	LOW	ND1	0.0091
HLI-0399	4104	A	G	0	309	synonymous_variant	LOW	ND1	0.0785
HLI-0399	4769	A	G	2	505	synonymous_variant	LOW	ND2	0.9767
HLI-0399	5036	A	G	1	410	synonymous_variant	LOW	ND2	0.006
HLI-0399	5046	G	A	1	439	missense_variant	MODERATE	ND2	0.018
HLI-0399	5393	T	C	1	474	synonymous_variant	LOW	ND2	0.0059
HLI-0399	5655	T	C	1	630	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0399	6378	T	C	0	368	synonymous_variant	LOW	COX1	0.0011
HLI-0399	6548	C	T	0	469	synonymous_variant	LOW	COX1	0.0061
HLI-0399	6827	T	C	3	474	synonymous_variant	LOW	COX1	0.0072
HLI-0399	6989	A	G	2	532	synonymous_variant	LOW	COX1	0.0061
HLI-0399	7028	C	T	2	498	synonymous_variant	LOW	COX1	0.8089
HLI-0399	7055	A	G	1	465	synonymous_variant	LOW	COX1	0.0188
HLI-0399	7146	A	G	0	297	missense_variant	MODERATE	COX1	0.0497
HLI-0399	7256	C	T	2	445	synonymous_variant	LOW	COX1	0.0784
HLI-0399	7389	T	C	0	479	missense_variant	MODERATE	COX1	0.0201
HLI-0399	7521	G	A	0	374	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0399	7867	C	T	1	579	synonymous_variant	LOW	COX2	0.0076

HLI-0399	8248	A	G	0	517	synonymous_variant	LOW	COX2	0.0061
HLI-0399	8468	C	T	4	484	synonymous_variant	LOW	ATP8	0.0501
HLI-0399	8655	C	T	2	423	synonymous_variant	LOW	ATP6	0.0511
HLI-0399	8701	A	G	1	446	missense_variant	MODERATE	ATP6	0.3391
HLI-0399	9540	T	C	0	394	synonymous_variant	LOW	COX3	0.339
HLI-0399	10398	A	G	0	532	missense_variant	MODERATE	ND3	0.445
HLI-0399	10688	G	A	1	496	synonymous_variant	LOW	ND4L	0.0515
HLI-0399	10810	T	C	0	505	synonymous_variant	LOW	ND4	0.0522
HLI-0399	10873	T	C	1	521	synonymous_variant	LOW	ND4	0.3389
HLI-0399	11719	G	A	0	489	synonymous_variant	LOW	ND4	0.7756
HLI-0399	12519	T	C	5	683	synonymous_variant	LOW	ND5	0.007
HLI-0399	12705	C	T	0	614	synonymous_variant	LOW	ND5	0.4212
HLI-0399	13105	A	G	1	421	missense_variant	MODERATE	ND5	0.076
HLI-0399	13506	C	T	0	409	synonymous_variant	LOW	ND5	0.0506
HLI-0399	13650	C	T	1	385	synonymous_variant	LOW	ND5	0.079
HLI-0399	13789	T	C	0	300	missense_variant	MODERATE	ND5	0.0185
HLI-0399	13880	C	A	4	376	missense_variant	MODERATE	ND5	0.0055
HLI-0399	14053	A	G	1	463	missense_variant	MODERATE	ND5	0.0046
HLI-0399	14178	T	C	0	541	missense_variant	MODERATE	ND6	0.0225
HLI-0399	14203	A	G	0	585	synonymous_variant	LOW	ND6	0.0061
HLI-0399	14560	G	A	0	650	synonymous_variant	LOW	ND6	0.0235
HLI-0399	14766	C	T	0	563	missense_variant	MODERATE	CYTB	0.7696
HLI-0399	14769	A	G	0	581	missense_variant	MODERATE	CYTB	0.0121
HLI-0399	15115	T	C	1	574	synonymous_variant	LOW	CYTB	0.0093
HLI-0399	15224	C	T	5	451	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0399	15326	A	G	0	279	missense_variant	MODERATE	CYTB	0.9868
HLI-0399	16126	T	C	2	623	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0399	16223	C	T	0	427	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0399	16264	C	T	0	357	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0399	16270	C	T	0	350	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0399	16278	C	T	0	348	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0399	16293	A	G	0	337	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0399	16311	T	C	0	320	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0399	16519	T	C	0	103	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0400	263	A	G	0	251	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0400	750	A	G	0	620	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0400	951	G	A	0	667	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0400	3834	G	A	0	556	synonymous_variant	LOW	ND1	0.0087
HLI-0400	12172	A	G	1	669	upstream_gene_variant	MODIFIER	TRNH	0.0064

HLI-0400	15326	A	G	0	433	missense_variant	MODERATE	CYTB	0.9868
HLI-0400	16224	T	C	1	526	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0400	16354	C	T	2	464	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0400	16519	T	C	0	237	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0401	73	A	G	0	31	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0401	150	C	T	0	70	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0401	185	G	A	0	63	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0401	189	A	G	0	63	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0401	200	A	G	0	65	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0401	263	A	G	0	37	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0401	750	A	G	0	66	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0401	1438	A	G	0	47	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0401	2352	T	C	0	27	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0401	2706	A	G	0	58	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0401	3438	G	A	0	51	synonymous_variant	LOW	ND1	0.0132
HLI-0401	4769	A	G	0	63	synonymous_variant	LOW	ND2	0.9767
HLI-0401	6221	T	C	0	63	synonymous_variant	LOW	COX1	0.0306
HLI-0401	6587	C	T	0	72	synonymous_variant	LOW	COX1	0.0084
HLI-0401	7028	C	T	0	81	synonymous_variant	LOW	COX1	0.8089
HLI-0401	8650	C	T	1	52	synonymous_variant	LOW	ATP6	0.0012
HLI-0401	8701	A	G	0	59	missense_variant	MODERATE	ATP6	0.3391
HLI-0401	9540	T	C	0	56	synonymous_variant	LOW	COX3	0.339
HLI-0401	10398	A	G	0	65	missense_variant	MODERATE	ND3	0.445
HLI-0401	10819	A	G	0	57	synonymous_variant	LOW	ND4	0.0228
HLI-0401	10873	T	C	0	63	synonymous_variant	LOW	ND4	0.3389
HLI-0401	11719	G	A	0	62	synonymous_variant	LOW	ND4	0.7756
HLI-0401	12705	C	T	0	41	synonymous_variant	LOW	ND5	0.4212
HLI-0401	14152	A	G	0	43	synonymous_variant	LOW	ND6	0.0086
HLI-0401	14212	T	C	0	35	synonymous_variant	LOW	ND6	0.0204
HLI-0401	14766	C	T	0	54	missense_variant	MODERATE	CYTB	0.7696
HLI-0401	15301	G	A	0	52	synonymous_variant	LOW	CYTB	0.2912
HLI-0401	15326	A	G	0	48	missense_variant	MODERATE	CYTB	0.9868
HLI-0401	15670	T	C	0	51	synonymous_variant	LOW	CYTB	0.0176
HLI-0401	15942	T	C	0	32	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0401	16169	C	T	0	53	upstream_gene_variant	MODIFIER	DLoop	0.0074
HLI-0401	16223	C	T	0	65	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0401	16311	T	C	0	58	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0401	16327	C	T	0	60	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0402	73	A	G	0	267	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0402	150	C	T	0	525	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0402	263	A	G	0	144	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0402	497	C	T	3	509	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0402	750	A	G	1	574	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0402	1189	T	C	0	666	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0402	1438	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0402	1811	A	G	0	578	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0402	2706	A	G	1	583	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0402	3480	A	G	3	542	synonymous_variant	LOW	ND1	0.0392
HLI-0402	4769	A	G	0	558	synonymous_variant	LOW	ND2	0.9767
HLI-0402	6392	T	C	1	551	synonymous_variant	LOW	COX1	0.0359
HLI-0402	7028	C	T	3	587	synonymous_variant	LOW	COX1	0.8089
HLI-0402	9055	G	A	1	521	missense_variant	MODERATE	ATP6	0.0425
HLI-0402	9698	T	C	1	527	synonymous_variant	LOW	COX3	0.0405
HLI-0402	10398	A	G	0	659	missense_variant	MODERATE	ND3	0.445
HLI-0402	10523	A	G	0	564	synonymous_variant	LOW	ND4L	9.00E-04
HLI-0402	10550	A	G	3	611	synonymous_variant	LOW	ND4L	0.0376
HLI-0402	11299	T	C	1	569	synonymous_variant	LOW	ND4	0.0417
HLI-0402	11467	A	G	1	637	synonymous_variant	LOW	ND4	0.1231
HLI-0402	11719	G	A	1	565	synonymous_variant	LOW	ND4	0.7756
HLI-0402	12308	A	G	1	476	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0402	12372	G	A	1	538	synonymous_variant	LOW	ND5	0.1329
HLI-0402	14167	C	T	0	479	synonymous_variant	LOW	ND6	0.0385
HLI-0402	14766	C	T	3	681	missense_variant	MODERATE	CYTB	0.7696
HLI-0402	14798	T	C	0	706	missense_variant	MODERATE	CYTB	0.0651
HLI-0402	15326	A	G	0	447	missense_variant	MODERATE	CYTB	0.9868
HLI-0402	15650	G	A	0	467	missense_variant	MODERATE	CYTB	4.00E-04
HLI-0402	16093	T	C	9	635	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0402	16224	T	C	0	525	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0402	16290	C	T	0	542	upstream_gene_variant	MODIFIER	DLoop	0.0394
HLI-0402	16311	T	C	0	519	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0402	16519	T	C	0	231	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0403	263	A	G	0	331	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0403	750	A	G	1	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0403	1438	A	G	0	681	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0403	3010	G	A	5	640	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0403	4769	A	G	0	608	synonymous_variant	LOW	ND2	0.9767
HLI-0403	11293	A	T	0	643	synonymous_variant	LOW	ND4	0
HLI-0403	14502	T	C	0	584	missense_variant	MODERATE	ND6	0.0037

HLI-0403	15326	A	G	0	542	missense_variant	MODERATE	CYTB	0.9868
HLI-0403	16519	T	C	0	296	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0404	73	A	G	0	298	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0404	143	G	A	0	516	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0404	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0404	489	T	C	2	424	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0404	493	A	G	2	418	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0404	750	A	G	0	710	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0404	1555	A	G	0	718	upstream_gene_variant	MODIFIER	RNR1	0.0015
HLI-0404	2706	A	G	0	690	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0404	3552	T	A	0	629	synonymous_variant	LOW	ND1	0.0337
HLI-0404	4167	C	T	4	659	synonymous_variant	LOW	ND1	3.00E-04
HLI-0404	4715	A	G	2	696	synonymous_variant	LOW	ND2	0.0416
HLI-0404	4769	A	G	2	730	synonymous_variant	LOW	ND2	0.9767
HLI-0404	7028	C	T	2	739	synonymous_variant	LOW	COX1	0.8089
HLI-0404	7196	C	A	7	724	synonymous_variant	LOW	COX1	0.0389
HLI-0404	8584	G	A	4	664	missense_variant	MODERATE	ATP6	0.0521
HLI-0404	8701	A	G	1	628	missense_variant	MODERATE	ATP6	0.3391
HLI-0404	9540	T	C	1	614	synonymous_variant	LOW	COX3	0.339
HLI-0404	9545	A	G	2	603	synonymous_variant	LOW	COX3	0.0469
HLI-0404	10398	A	G	0	753	missense_variant	MODERATE	ND3	0.445
HLI-0404	10400	C	T	0	764	synonymous_variant	LOW	ND3	0.2131
HLI-0404	10873	T	C	1	621	synonymous_variant	LOW	ND4	0.3389
HLI-0404	11719	G	A	1	663	synonymous_variant	LOW	ND4	0.7756
HLI-0404	11914	G	A	1	663	synonymous_variant	LOW	ND4	0.1112
HLI-0404	12705	C	T	0	770	synonymous_variant	LOW	ND5	0.4212
HLI-0404	13263	A	G	3	673	synonymous_variant	LOW	ND5	0.0354
HLI-0404	14318	T	C	0	533	missense_variant	MODERATE	ND6	0.0339
HLI-0404	14524	A	G	2	602	synonymous_variant	LOW	ND6	2.00E-04
HLI-0404	14766	C	T	1	712	missense_variant	MODERATE	CYTB	0.7696
HLI-0404	14783	T	C	1	777	synonymous_variant	LOW	CYTB	0.2126
HLI-0404	15043	G	A	1	727	synonymous_variant	LOW	CYTB	0.2362
HLI-0404	15301	G	A	0	612	synonymous_variant	LOW	CYTB	0.2912
HLI-0404	15326	A	G	0	694	missense_variant	MODERATE	CYTB	0.9868
HLI-0404	15487	A	T	1	602	synonymous_variant	LOW	CYTB	0.0391
HLI-0404	16086	T	C	3	569	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0404	16223	C	T	3	294	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0404	16278	C	T	3	436	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0404	16298	T	C	3	465	upstream_gene_variant	MODIFIER	DLoop	0.0655

HLI-0404	16325	T	C	1	469	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0404	16327	C	T	1	476	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0405	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0405	152	T	C	0	586	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0405	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0405	709	G	A	1	728	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0405	750	A	G	0	802	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0405	930	G	A	5	662	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0405	1438	A	G	1	711	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0405	1888	G	A	1	687	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0405	2706	A	G	0	675	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0405	3316	G	A	2	668	missense_variant	MODERATE	ND1	0.0101
HLI-0405	4216	T	C	2	644	missense_variant	MODERATE	ND1	0.0991
HLI-0405	4529	A	G	3	644	synonymous_variant	LOW	ND2	6.00E-04
HLI-0405	4769	A	G	2	581	synonymous_variant	LOW	ND2	0.9767
HLI-0405	4917	A	G	0	610	missense_variant	MODERATE	ND2	0.0477
HLI-0405	5147	G	A	1	577	synonymous_variant	LOW	ND2	0.0437
HLI-0405	7028	C	T	3	775	synonymous_variant	LOW	COX1	0.8089
HLI-0405	8697	G	A	0	637	synonymous_variant	LOW	ATP6	0.0466
HLI-0405	9254	A	G	2	629	synonymous_variant	LOW	COX3	0.0083
HLI-0405	10463	T	C	1	725	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0405	11251	A	G	1	692	synonymous_variant	LOW	ND4	0.0932
HLI-0405	11719	G	A	0	646	synonymous_variant	LOW	ND4	0.7756
HLI-0405	11812	A	G	2	689	synonymous_variant	LOW	ND4	0.0332
HLI-0405	13368	G	A	3	661	synonymous_variant	LOW	ND5	0.0495
HLI-0405	14233	A	G	0	648	synonymous_variant	LOW	ND6	0.0369
HLI-0405	14766	C	T	3	647	missense_variant	MODERATE	CYTB	0.7696
HLI-0405	14905	G	A	3	674	synonymous_variant	LOW	CYTB	0.0526
HLI-0405	15326	A	G	0	594	missense_variant	MODERATE	CYTB	0.9868
HLI-0405	15452	C	A	7	657	missense_variant	MODERATE	CYTB	0.0933
HLI-0405	15607	A	G	0	659	synonymous_variant	LOW	CYTB	0.0508
HLI-0405	15928	G	A	1	699	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0405	16126	T	C	0	611	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0405	16304	T	C	1	554	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0405	16519	T	C	0	321	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0406	73	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0406	152	T	C	0	439	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0406	195	T	C	0	465	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0406	263	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0406	709	G	A	0	563	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0406	750	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0406	1438	A	G	0	596	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0406	1888	G	A	0	398	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0406	2706	A	G	0	547	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0406	4216	T	C	1	484	missense_variant	MODERATE	ND1	0.0991
HLI-0406	4769	A	G	1	512	synonymous_variant	LOW	ND2	0.9767
HLI-0406	4917	A	G	0	560	missense_variant	MODERATE	ND2	0.0477
HLI-0406	5414	A	G	0	570	synonymous_variant	LOW	ND2	9.00E-04
HLI-0406	5558	A	G	0	667	upstream_gene_variant	MODIFIER	TRNW	0.0021
HLI-0406	7028	C	T	1	609	synonymous_variant	LOW	COX1	0.8089
HLI-0406	8697	G	A	0	534	synonymous_variant	LOW	ATP6	0.0466
HLI-0406	9899	T	C	1	638	synonymous_variant	LOW	COX3	0.0108
HLI-0406	10045	T	C	1	607	upstream_gene_variant	MODIFIER	TRNG	3.00E-04
HLI-0406	10463	T	C	0	589	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0406	11251	A	G	0	565	synonymous_variant	LOW	ND4	0.0932
HLI-0406	11719	G	A	1	596	synonymous_variant	LOW	ND4	0.7756
HLI-0406	12633	C	A	11	540	synonymous_variant	LOW	ND5	0.0123
HLI-0406	13368	G	A	1	584	synonymous_variant	LOW	ND5	0.0495
HLI-0406	14766	C	T	1	567	missense_variant	MODERATE	CYTB	0.7696
HLI-0406	14905	G	A	1	724	synonymous_variant	LOW	CYTB	0.0526
HLI-0406	15326	A	G	0	421	missense_variant	MODERATE	CYTB	0.9868
HLI-0406	15412	T	C	0	425	synonymous_variant	LOW	CYTB	0.0015
HLI-0406	15452	C	A	2	445	missense_variant	MODERATE	CYTB	0.0933
HLI-0406	15607	A	G	0	411	synonymous_variant	LOW	CYTB	0.0508
HLI-0406	15928	G	A	1	483	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0406	16126	T	C	0	551	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0406	16163	A	G	0	614	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0406	16294	C	T	0	461	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0406	16519	T	C	0	231	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0407	73	A	G	0	285	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0407	263	A	G	0	342	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0407	709	G	A	0	453	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0407	750	A	G	1	494	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0407	1438	A	G	0	541	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0407	1888	G	A	1	410	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0407	2141	T	C	1	407	upstream_gene_variant	MODIFIER	RNR2	0.0013
HLI-0407	2706	A	G	0	505	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0407	4216	T	C	1	428	missense_variant	MODERATE	ND1	0.0991

HLI-0407	4769	A	G	0	541	synonymous_variant	LOW	ND2	0.9767
HLI-0407	4917	A	G	1	545	missense_variant	MODERATE	ND2	0.0477
HLI-0407	7028	C	T	1	571	synonymous_variant	LOW	COX1	0.8089
HLI-0407	8697	G	A	0	535	synonymous_variant	LOW	ATP6	0.0466
HLI-0407	9117	T	C	1	516	synonymous_variant	LOW	ATP6	0.0018
HLI-0407	10463	T	C	0	464	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0407	11251	A	G	0	517	synonymous_variant	LOW	ND4	0.0932
HLI-0407	11719	G	A	0	559	synonymous_variant	LOW	ND4	0.7756
HLI-0407	11812	A	G	1	485	synonymous_variant	LOW	ND4	0.0332
HLI-0407	13368	G	A	0	530	synonymous_variant	LOW	ND5	0.0495
HLI-0407	13965	T	C	0	433	synonymous_variant	LOW	ND5	0.005
HLI-0407	13966	A	G	1	441	missense_variant	MODERATE	ND5	0.0126
HLI-0407	14233	A	G	1	487	synonymous_variant	LOW	ND6	0.0369
HLI-0407	14687	A	G	1	693	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0407	14766	C	T	0	727	missense_variant	MODERATE	CYTB	0.7696
HLI-0407	14905	G	A	0	718	synonymous_variant	LOW	CYTB	0.0526
HLI-0407	15110	G	A	2	608	missense_variant	MODERATE	CYTB	0.009
HLI-0407	15326	A	G	0	339	missense_variant	MODERATE	CYTB	0.9868
HLI-0407	15452	C	A	2	339	missense_variant	MODERATE	CYTB	0.0933
HLI-0407	15607	A	G	0	334	synonymous_variant	LOW	CYTB	0.0508
HLI-0407	15928	G	A	2	515	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0407	16126	T	C	2	729	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0407	16292	C	T	1	519	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0407	16294	C	T	1	521	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0407	16296	C	T	1	522	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0407	16324	T	C	1	504	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0407	16519	T	C	1	245	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0408	73	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0408	146	T	C	0	475	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0408	150	C	T	0	487	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0408	152	T	C	0	491	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0408	195	T	C	1	492	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0408	263	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0408	750	A	G	1	525	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0408	769	G	A	0	569	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0408	1018	G	A	1	731	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0408	1438	A	G	0	553	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0408	2416	T	C	0	366	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0408	2706	A	G	1	547	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0408	2789	C	T	0	593	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0408	3594	C	T	2	506	synonymous_variant	LOW	ND1	0.0789
HLI-0408	4104	A	G	1	448	synonymous_variant	LOW	ND1	0.0785
HLI-0408	4769	A	G	0	584	synonymous_variant	LOW	ND2	0.9767
HLI-0408	5581	A	G	1	648	upstream_gene_variant	MODIFIER	Unannotated	0.005
HLI-0408	6227	T	C	1	501	synonymous_variant	LOW	COX1	0.0019
HLI-0408	7028	C	T	1	622	synonymous_variant	LOW	COX1	0.8089
HLI-0408	7175	T	C	0	646	synonymous_variant	LOW	COX1	0.0224
HLI-0408	7256	C	T	0	683	synonymous_variant	LOW	COX1	0.0784
HLI-0408	7274	C	T	0	664	synonymous_variant	LOW	COX1	0.0214
HLI-0408	7521	G	A	1	430	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0408	7771	A	G	1	582	synonymous_variant	LOW	COX2	0.0223
HLI-0408	8206	G	A	1	524	synonymous_variant	LOW	COX2	0.0287
HLI-0408	8701	A	G	0	529	missense_variant	MODERATE	ATP6	0.3391
HLI-0408	9221	A	G	0	593	synonymous_variant	LOW	COX3	0.0277
HLI-0408	9540	T	C	1	406	synonymous_variant	LOW	COX3	0.339
HLI-0408	10115	T	C	2	746	synonymous_variant	LOW	ND3	0.0278
HLI-0408	10398	A	G	1	587	missense_variant	MODERATE	ND3	0.445
HLI-0408	10873	T	C	0	506	synonymous_variant	LOW	ND4	0.3389
HLI-0408	11719	G	A	0	570	synonymous_variant	LOW	ND4	0.7756
HLI-0408	11914	G	A	0	611	synonymous_variant	LOW	ND4	0.1112
HLI-0408	11944	T	C	1	622	synonymous_variant	LOW	ND4	0.0331
HLI-0408	12693	A	G	0	503	synonymous_variant	LOW	ND5	0.0205
HLI-0408	12705	C	T	1	553	synonymous_variant	LOW	ND5	0.4212
HLI-0408	13590	G	A	0	459	synonymous_variant	LOW	ND5	0.0586
HLI-0408	13650	C	T	0	496	synonymous_variant	LOW	ND5	0.079
HLI-0408	13803	A	G	2	324	synonymous_variant	LOW	ND5	0.0216
HLI-0408	14566	A	G	0	667	synonymous_variant	LOW	ND6	0.0214
HLI-0408	14766	C	T	2	670	missense_variant	MODERATE	CYTB	0.7696
HLI-0408	15301	G	A	0	392	synonymous_variant	LOW	CYTB	0.2912
HLI-0408	15326	A	G	0	407	missense_variant	MODERATE	CYTB	0.9868
HLI-0408	15784	T	C	1	334	synonymous_variant	LOW	CYTB	0.0363
HLI-0408	16223	C	T	4	531	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0408	16278	C	T	0	500	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0408	16294	C	T	0	472	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0408	16309	A	G	0	458	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0408	16390	G	A	0	384	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0408	16519	T	C	0	214	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0409	73	A	G	3	281	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0409	150	C	T	2	543	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0409	263	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0409	295	C	T	0	227	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0409	489	T	C	0	379	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0409	750	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0409	1438	A	G	0	594	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0409	2706	A	G	0	550	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0409	4216	T	C	0	420	missense_variant	MODERATE	ND1	0.0991
HLI-0409	4769	A	G	2	557	synonymous_variant	LOW	ND2	0.9767
HLI-0409	5474	A	G	0	537	synonymous_variant	LOW	ND2	3.00E-04
HLI-0409	5633	C	T	0	599	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0409	7028	C	T	2	636	synonymous_variant	LOW	COX1	0.8089
HLI-0409	7476	C	T	0	468	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0409	9016	A	G	1	534	missense_variant	MODERATE	ATP6	3.00E-04
HLI-0409	9494	A	G	1	544	synonymous_variant	LOW	COX3	0.0024
HLI-0409	10172	G	A	1	598	synonymous_variant	LOW	ND3	0.0084
HLI-0409	10398	A	G	0	545	missense_variant	MODERATE	ND3	0.445
HLI-0409	11251	A	G	1	596	synonymous_variant	LOW	ND4	0.0932
HLI-0409	11719	G	A	0	598	synonymous_variant	LOW	ND4	0.7756
HLI-0409	12612	A	G	10	489	synonymous_variant	LOW	ND5	0.0506
HLI-0409	13708	G	A	1	519	missense_variant	MODERATE	ND5	0.0717
HLI-0409	14766	C	T	2	569	missense_variant	MODERATE	CYTB	0.7696
HLI-0409	15257	G	A	0	445	missense_variant	MODERATE	CYTB	0.0155
HLI-0409	15326	A	G	0	446	missense_variant	MODERATE	CYTB	0.9868
HLI-0409	15452	C	A	5	396	missense_variant	MODERATE	CYTB	0.0933
HLI-0409	15662	A	G	0	401	missense_variant	MODERATE	CYTB	0.0038
HLI-0409	15812	G	A	0	405	missense_variant	MODERATE	CYTB	0.0096
HLI-0409	16069	C	T	2	451	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0409	16126	T	C	1	562	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0409	16278	C	T	0	540	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0409	16519	T	C	0	256	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0410	72	T	C	0	270	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0410	263	A	G	1	359	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0410	750	A	G	0	464	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0410	1438	A	G	0	493	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0410	2706	A	G	0	446	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0410	4221	C	T	0	339	synonymous_variant	LOW	ND1	4.00E-04
HLI-0410	4580	G	A	0	571	synonymous_variant	LOW	ND2	0.0169
HLI-0410	4769	A	G	0	490	synonymous_variant	LOW	ND2	0.9767

HLI-0410	4907	T	C	0	472	synonymous_variant	LOW	ND2	0.0047
HLI-0410	7028	C	T	2	556	synonymous_variant	LOW	COX1	0.8089
HLI-0410	10308	C	T	0	519	synonymous_variant	LOW	ND3	3.00E-04
HLI-0410	15326	A	G	0	293	missense_variant	MODERATE	CYTB	0.9868
HLI-0410	15904	C	T	1	450	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0410	16298	T	C	1	531	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0411	73	A	G	0	313	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0411	195	T	C	1	482	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0411	263	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0411	497	C	T	1	488	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0411	750	A	G	0	587	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0411	1189	T	C	2	685	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0411	1438	A	G	0	637	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0411	1811	A	G	1	605	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0411	2706	A	G	0	564	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0411	3480	A	G	1	492	synonymous_variant	LOW	ND1	0.0392
HLI-0411	4769	A	G	4	558	synonymous_variant	LOW	ND2	0.9767
HLI-0411	7028	C	T	5	641	synonymous_variant	LOW	COX1	0.8089
HLI-0411	9055	G	A	1	587	missense_variant	MODERATE	ATP6	0.0425
HLI-0411	9698	T	C	0	565	synonymous_variant	LOW	COX3	0.0405
HLI-0411	10370	T	C	0	633	synonymous_variant	LOW	ND3	0.0019
HLI-0411	10398	A	G	0	712	missense_variant	MODERATE	ND3	0.445
HLI-0411	10550	A	G	0	608	synonymous_variant	LOW	ND4L	0.0376
HLI-0411	11299	T	C	1	621	synonymous_variant	LOW	ND4	0.0417
HLI-0411	11467	A	G	0	671	synonymous_variant	LOW	ND4	0.1231
HLI-0411	11719	G	A	1	574	synonymous_variant	LOW	ND4	0.7756
HLI-0411	12308	A	G	3	601	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0411	12372	G	A	2	610	synonymous_variant	LOW	ND5	0.1329
HLI-0411	14167	C	T	1	561	synonymous_variant	LOW	ND6	0.0385
HLI-0411	14766	C	T	3	643	missense_variant	MODERATE	CYTB	0.7696
HLI-0411	14798	T	C	0	715	missense_variant	MODERATE	CYTB	0.0651
HLI-0411	15326	A	G	0	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0411	16048	G	A	1	603	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0411	16093	T	C	23	647	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0411	16224	T	C	1	521	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0411	16291	C	T	1	561	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0411	16311	T	C	0	557	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0411	16519	T	C	0	290	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0412	263	A	G	0	348	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0412	750	A	G	0	461	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0412	1438	A	G	0	469	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0412	3010	G	A	3	392	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0412	4769	A	G	0	450	synonymous_variant	LOW	ND2	0.9767
HLI-0412	13704	C	T	0	344	synonymous_variant	LOW	ND5	0
HLI-0412	15326	A	G	0	264	missense_variant	MODERATE	CYTB	0.9868
HLI-0412	16209	T	G	4	426	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0412	16519	T	C	0	183	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0413	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0413	456	C	T	6	546	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0413	750	A	G	2	679	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0413	1438	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0413	2581	A	G	1	640	upstream_gene_variant	MODIFIER	RNR2	0.0031
HLI-0413	4336	T	C	1	489	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0413	4769	A	G	2	604	synonymous_variant	LOW	ND2	0.9767
HLI-0413	5839	C	T	2	679	upstream_gene_variant	MODIFIER	TRNY	0.0011
HLI-0413	13833	A	G	1	488	synonymous_variant	LOW	ND5	1.00E-04
HLI-0413	15326	A	G	1	466	missense_variant	MODERATE	CYTB	0.9868
HLI-0413	16304	T	C	1	468	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0414	73	A	G	1	345	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0414	195	T	C	1	456	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0414	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0414	499	G	A	2	426	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0414	750	A	G	1	619	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0414	1438	A	G	1	672	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0414	1811	A	G	1	528	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0414	2706	A	G	2	637	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0414	4646	T	C	1	644	synonymous_variant	LOW	ND2	0.0124
HLI-0414	4769	A	G	1	591	synonymous_variant	LOW	ND2	0.9767
HLI-0414	5999	T	C	1	768	synonymous_variant	LOW	COX1	0.0127
HLI-0414	6047	A	G	3	823	synonymous_variant	LOW	COX1	0.0114
HLI-0414	7028	C	T	6	684	synonymous_variant	LOW	COX1	0.8089
HLI-0414	8818	C	T	1	597	synonymous_variant	LOW	ATP6	0.0061
HLI-0414	11332	C	T	1	643	synonymous_variant	LOW	ND4	0.0115
HLI-0414	11467	A	G	2	713	synonymous_variant	LOW	ND4	0.1231
HLI-0414	11719	G	A	2	689	synonymous_variant	LOW	ND4	0.7756
HLI-0414	12308	A	G	1	567	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0414	12372	G	A	1	571	synonymous_variant	LOW	ND5	0.1329
HLI-0414	13759	G	A	1	426	missense_variant	MODERATE	ND5	0.0348

HLI-0414	14620	C	T	2	707	synonymous_variant	LOW	ND6	0.0126
HLI-0414	14766	C	T	5	726	missense_variant	MODERATE	CYTB	0.7696
HLI-0414	15326	A	G	1	548	missense_variant	MODERATE	CYTB	0.9868
HLI-0414	15693	T	C	0	546	missense_variant	MODERATE	CYTB	0.0114
HLI-0414	16519	T	C	0	309	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0415	73	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0415	150	C	T	2	641	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0415	263	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0415	750	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0415	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0415	1721	C	T	2	454	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0415	2361	G	A	2	430	upstream_gene_variant	MODIFIER	RNR2	0.0027
HLI-0415	2706	A	G	0	589	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0415	3197	T	C	2	652	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0415	3397	A	G	1	629	missense_variant	MODERATE	ND1	0.0029
HLI-0415	4732	A	G	1	603	missense_variant	MODERATE	ND2	0.0059
HLI-0415	4769	A	G	1	645	synonymous_variant	LOW	ND2	0.9767
HLI-0415	6293	T	C	1	711	synonymous_variant	LOW	COX1	0.0036
HLI-0415	7028	C	T	0	674	synonymous_variant	LOW	COX1	0.8089
HLI-0415	7768	A	G	1	594	synonymous_variant	LOW	COX2	0.0186
HLI-0415	9477	G	A	0	640	missense_variant	MODERATE	COX3	0.0387
HLI-0415	11173	C	T	2	557	synonymous_variant	LOW	ND4	0
HLI-0415	11467	A	G	2	710	synonymous_variant	LOW	ND4	0.1231
HLI-0415	11719	G	A	2	577	synonymous_variant	LOW	ND4	0.7756
HLI-0415	12308	A	G	0	376	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0415	12372	G	A	0	327	synonymous_variant	LOW	ND5	0.1329
HLI-0415	13368	G	A	1	632	synonymous_variant	LOW	ND5	0.0495
HLI-0415	13617	T	C	0	574	synonymous_variant	LOW	ND5	0.038
HLI-0415	13637	A	G	0	615	missense_variant	MODERATE	ND5	0.0074
HLI-0415	14182	T	C	0	469	synonymous_variant	LOW	ND6	0.0254
HLI-0415	14766	C	T	0	709	missense_variant	MODERATE	CYTB	0.7696
HLI-0415	14767	T	C	0	716	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0415	15326	A	G	0	465	missense_variant	MODERATE	CYTB	0.9868
HLI-0415	16270	C	T	3	501	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0416	152	T	C	0	593	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0416	263	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0416	477	T	C	1	461	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0416	750	A	G	1	600	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0416	1438	A	G	0	633	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0416	3010	G	A	0	630	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0416	4769	A	G	0	593	synonymous_variant	LOW	ND2	0.9767
HLI-0416	11020	A	G	1	547	synonymous_variant	LOW	ND4	0.0019
HLI-0416	11986	C	T	2	628	synonymous_variant	LOW	ND4	1.00E-04
HLI-0416	15326	A	G	1	532	missense_variant	MODERATE	CYTB	0.9868
HLI-0416	16519	T	C	1	309	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0417	73	A	G	0	266	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0417	228	G	A	1	408	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0417	263	A	G	2	339	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0417	295	C	T	0	260	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0417	462	C	T	2	448	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0417	489	T	C	1	462	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0417	750	A	G	2	450	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0417	1438	A	G	0	506	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0417	2706	A	G	1	457	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0417	3010	G	A	0	485	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0417	3316	G	A	0	507	missense_variant	MODERATE	ND1	0.0101
HLI-0417	4216	T	C	6	378	missense_variant	MODERATE	ND1	0.0991
HLI-0417	4769	A	G	1	538	synonymous_variant	LOW	ND2	0.9767
HLI-0417	7028	C	T	3	571	synonymous_variant	LOW	COX1	0.8089
HLI-0417	9548	G	A	5	402	synonymous_variant	LOW	COX3	0.0149
HLI-0417	9836	T	C	1	799	synonymous_variant	LOW	COX3	3.00E-04
HLI-0417	10398	A	G	2	472	missense_variant	MODERATE	ND3	0.445
HLI-0417	11251	A	G	0	516	synonymous_variant	LOW	ND4	0.0932
HLI-0417	11719	G	A	1	529	synonymous_variant	LOW	ND4	0.7756
HLI-0417	12612	A	G	7	593	synonymous_variant	LOW	ND5	0.0506
HLI-0417	13515	C	T	2	504	synonymous_variant	LOW	ND5	1.00E-04
HLI-0417	13708	G	A	0	422	missense_variant	MODERATE	ND5	0.0717
HLI-0417	13934	C	T	2	378	missense_variant	MODERATE	ND5	0.0122
HLI-0417	14766	C	T	1	676	missense_variant	MODERATE	CYTB	0.7696
HLI-0417	14798	T	C	0	735	missense_variant	MODERATE	CYTB	0.0651
HLI-0417	15326	A	G	1	334	missense_variant	MODERATE	CYTB	0.9868
HLI-0417	15452	C	A	4	292	missense_variant	MODERATE	CYTB	0.0933
HLI-0417	16069	C	T	3	594	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0417	16126	T	C	2	678	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0418	73	A	G	0	308	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0418	146	T	C	1	602	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0418	263	A	G	0	315	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0418	750	A	G	0	645	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0418	1438	A	G	0	641	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0418	1811	A	G	1	479	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0418	2217	C	T	1	417	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0418	2706	A	G	0	658	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0418	3480	A	G	0	578	synonymous_variant	LOW	ND1	0.0392
HLI-0418	4769	A	G	1	595	synonymous_variant	LOW	ND2	0.9767
HLI-0418	5231	G	A	3	517	synonymous_variant	LOW	ND2	0.0232
HLI-0418	7028	C	T	3	695	synonymous_variant	LOW	COX1	0.8089
HLI-0418	9055	G	A	0	589	missense_variant	MODERATE	ATP6	0.0425
HLI-0418	9698	T	C	0	643	synonymous_variant	LOW	COX3	0.0405
HLI-0418	9716	T	C	0	730	synonymous_variant	LOW	COX3	0.0108
HLI-0418	10550	A	G	1	680	synonymous_variant	LOW	ND4L	0.0376
HLI-0418	11299	T	C	1	652	synonymous_variant	LOW	ND4	0.0417
HLI-0418	11467	A	G	2	675	synonymous_variant	LOW	ND4	0.1231
HLI-0418	11719	G	A	0	642	synonymous_variant	LOW	ND4	0.7756
HLI-0418	11869	C	A	3	571	synonymous_variant	LOW	ND4	0.0015
HLI-0418	12308	A	G	0	418	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0418	12372	G	A	0	384	synonymous_variant	LOW	ND5	0.1329
HLI-0418	13135	G	A	2	626	missense_variant	MODERATE	ND5	0.0092
HLI-0418	14037	A	G	1	459	synonymous_variant	LOW	ND5	0.0017
HLI-0418	14167	C	T	1	498	synonymous_variant	LOW	ND6	0.0385
HLI-0418	14766	C	T	2	646	missense_variant	MODERATE	CYTB	0.7696
HLI-0418	14798	T	C	0	764	missense_variant	MODERATE	CYTB	0.0651
HLI-0418	15326	A	G	0	476	missense_variant	MODERATE	CYTB	0.9868
HLI-0418	16222	C	T	51	483	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0418	16224	T	C	0	544	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0418	16270	C	T	2	583	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0418	16311	T	C	0	534	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0418	16519	T	C	0	300	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0419	72	T	C	1	257	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0419	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0419	750	A	G	2	493	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0419	1438	A	G	0	564	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0419	2706	A	G	1	493	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0419	4580	G	A	1	649	synonymous_variant	LOW	ND2	0.0169
HLI-0419	4639	T	C	0	600	missense_variant	MODERATE	ND2	0.0034
HLI-0419	4769	A	G	2	573	synonymous_variant	LOW	ND2	0.9767
HLI-0419	7028	C	T	4	581	synonymous_variant	LOW	COX1	0.8089
HLI-0419	8869	A	G	0	547	missense_variant	MODERATE	ATP6	0.0028

HLI-0419	11965	C	A	0	541	synonymous_variant	LOW	ND4	1.00E-04
HLI-0419	14016	G	A	0	420	synonymous_variant	LOW	ND5	0.003
HLI-0419	15326	A	G	0	414	missense_variant	MODERATE	CYTB	0.9868
HLI-0419	15904	C	T	0	513	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0419	16298	T	C	0	477	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0419	16519	T	C	1	200	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0420	263	A	G	1	277	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0420	456	C	T	4	530	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0420	750	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0420	1438	A	G	0	592	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0420	3819	C	T	0	619	synonymous_variant	LOW	ND1	0.0012
HLI-0420	4769	A	G	0	547	synonymous_variant	LOW	ND2	0.9767
HLI-0420	12127	G	A	1	350	synonymous_variant	LOW	ND4	0.0058
HLI-0420	15326	A	G	0	394	missense_variant	MODERATE	CYTB	0.9868
HLI-0420	16213	G	A	0	532	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0420	16216	A	G	0	540	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0420	16304	T	C	2	489	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0421	73	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0421	189	A	G	1	321	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0421	194	C	T	1	323	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0421	195	T	C	1	323	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0421	204	T	C	1	315	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0421	207	G	A	1	319	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0421	263	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0421	709	G	A	0	624	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0421	750	A	G	2	671	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0421	1243	T	C	0	684	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0421	1406	T	C	2	707	upstream_gene_variant	MODIFIER	RNR1	0.0034
HLI-0421	1438	A	G	0	775	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0421	2706	A	G	1	635	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0421	3505	A	G	1	603	missense_variant	MODERATE	ND1	0.0144
HLI-0421	4769	A	G	0	618	synonymous_variant	LOW	ND2	0.9767
HLI-0421	5046	G	A	0	562	missense_variant	MODERATE	ND2	0.018
HLI-0421	5460	G	A	1	623	missense_variant	MODERATE	ND2	0.0651
HLI-0421	7028	C	T	1	697	synonymous_variant	LOW	COX1	0.8089
HLI-0421	8251	G	A	1	578	synonymous_variant	LOW	COX2	0.058
HLI-0421	8994	G	A	2	592	synonymous_variant	LOW	ATP6	0.0167
HLI-0421	11674	C	T	9	644	synonymous_variant	LOW	ND4	0.0116
HLI-0421	11719	G	A	1	714	synonymous_variant	LOW	ND4	0.7756

HLI-0421	11947	A	G	2	570	synonymous_variant	LOW	ND4	0.011
HLI-0421	12414	T	C	4	442	synonymous_variant	LOW	ND5	0.0139
HLI-0421	12705	C	T	2	664	synonymous_variant	LOW	ND5	0.4212
HLI-0421	13263	A	G	1	712	synonymous_variant	LOW	ND5	0.0354
HLI-0421	14766	C	T	1	641	missense_variant	MODERATE	CYTB	0.7696
HLI-0421	15326	A	G	0	516	missense_variant	MODERATE	CYTB	0.9868
HLI-0421	15784	T	C	0	559	synonymous_variant	LOW	CYTB	0.0363
HLI-0421	15884	G	C	0	548	missense_variant	MODERATE	CYTB	0.011
HLI-0421	16223	C	T	0	516	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0421	16234	C	T	0	567	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0421	16245	C	T	1	577	upstream_gene_variant	MODIFIER	DLoop	0.0041
HLI-0421	16292	C	T	0	492	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0421	16519	T	C	1	270	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0422	73	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0422	195	T	C	0	403	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0422	263	A	G	0	320	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0422	750	A	G	2	502	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0422	1438	A	G	0	528	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0422	1719	G	A	0	414	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0422	2706	A	G	1	483	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0422	4769	A	G	1	510	synonymous_variant	LOW	ND2	0.9767
HLI-0422	6221	T	C	1	500	synonymous_variant	LOW	COX1	0.0306
HLI-0422	6371	C	T	0	471	synonymous_variant	LOW	COX1	0.0097
HLI-0422	6791	A	G	2	712	synonymous_variant	LOW	COX1	0.0022
HLI-0422	7028	C	T	1	571	synonymous_variant	LOW	COX1	0.8089
HLI-0422	8503	T	C	0	363	synonymous_variant	LOW	ATP8	0.0019
HLI-0422	11719	G	A	0	524	synonymous_variant	LOW	ND4	0.7756
HLI-0422	11878	T	C	1	490	synonymous_variant	LOW	ND4	7.00E-04
HLI-0422	12705	C	T	0	524	synonymous_variant	LOW	ND5	0.4212
HLI-0422	13708	G	A	1	474	missense_variant	MODERATE	ND5	0.0717
HLI-0422	13966	A	G	0	400	missense_variant	MODERATE	ND5	0.0126
HLI-0422	14470	T	C	2	506	synonymous_variant	LOW	ND6	0.0166
HLI-0422	14766	C	T	3	608	missense_variant	MODERATE	CYTB	0.7696
HLI-0422	15326	A	G	1	401	missense_variant	MODERATE	CYTB	0.9868
HLI-0422	16223	C	T	0	234	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0422	16278	C	T	1	343	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0422	16311	T	C	0	428	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0422	16505	T	C	0	230	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0422	16519	T	C	1	238	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0423	73	A	G	1	257	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0423	153	A	G	5	526	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0423	263	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0423	497	C	T	4	347	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0423	723	A	C	0	494	upstream_gene_variant	MODIFIER	RNR1	9.00E-04
HLI-0423	750	A	G	1	534	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0423	1189	T	C	0	619	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0423	1438	A	G	0	505	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0423	1811	A	G	1	448	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0423	2706	A	G	0	512	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0423	3480	A	G	1	364	synonymous_variant	LOW	ND1	0.0392
HLI-0423	4769	A	G	2	510	synonymous_variant	LOW	ND2	0.9767
HLI-0423	7028	C	T	0	584	synonymous_variant	LOW	COX1	0.8089
HLI-0423	9055	G	A	0	513	missense_variant	MODERATE	ATP6	0.0425
HLI-0423	9698	T	C	0	488	synonymous_variant	LOW	COX3	0.0405
HLI-0423	10398	A	G	1	483	missense_variant	MODERATE	ND3	0.445
HLI-0423	10550	A	G	0	503	synonymous_variant	LOW	ND4L	0.0376
HLI-0423	11071	C	T	5	498	synonymous_variant	LOW	ND4	7.00E-04
HLI-0423	11299	T	C	0	549	synonymous_variant	LOW	ND4	0.0417
HLI-0423	11467	A	G	1	566	synonymous_variant	LOW	ND4	0.1231
HLI-0423	11485	T	C	1	635	synonymous_variant	LOW	ND4	0.0081
HLI-0423	11719	G	A	1	526	synonymous_variant	LOW	ND4	0.7756
HLI-0423	12308	A	G	2	445	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0423	12372	G	A	1	373	synonymous_variant	LOW	ND5	0.1329
HLI-0423	14167	C	T	2	465	synonymous_variant	LOW	ND6	0.0385
HLI-0423	14766	C	T	1	602	missense_variant	MODERATE	CYTB	0.7696
HLI-0423	14798	T	C	0	698	missense_variant	MODERATE	CYTB	0.0651
HLI-0423	15326	A	G	0	379	missense_variant	MODERATE	CYTB	0.9868
HLI-0423	15355	G	A	0	402	synonymous_variant	LOW	CYTB	0.0032
HLI-0423	16224	T	C	1	503	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0423	16311	T	C	0	406	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0423	16519	T	C	0	190	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0424	72	T	C	0	28	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0424	263	A	G	0	36	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0424	750	A	G	0	53	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0424	1438	A	G	0	56	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0424	3010	G	A	0	50	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0424	4769	A	G	0	38	synonymous_variant	LOW	ND2	0.9767
HLI-0424	6261	G	A	0	67	missense_variant	MODERATE	COX1	0.007

HLI-0424	9914	A	G	0	46	synonymous_variant	LOW	COX3	0
HLI-0424	15326	A	G	0	66	missense_variant	MODERATE	CYTB	0.9868
HLI-0424	16291	C	T	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0424	16519	T	C	0	17	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0425	73	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0425	114	C	T	33	388	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0425	263	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0425	497	C	T	27	382	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0425	750	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0425	1189	T	C	52	560	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0425	1438	A	G	0	557	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0425	1811	A	G	34	546	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0425	2706	A	G	0	540	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0425	3480	A	G	37	409	synonymous_variant	LOW	ND1	0.0392
HLI-0425	3796	A	G	41	528	missense_variant	MODERATE	ND1	0.0048
HLI-0425	4769	A	G	1	616	synonymous_variant	LOW	ND2	0.9767
HLI-0425	4823	T	C	53	547	synonymous_variant	LOW	ND2	0.0049
HLI-0425	6528	C	T	44	494	synonymous_variant	LOW	COX1	0.0013
HLI-0425	7028	C	T	2	585	synonymous_variant	LOW	COX1	0.8089
HLI-0425	8842	A	C	48	532	missense_variant	MODERATE	ATP6	1.00E-04
HLI-0425	9055	G	A	1	533	missense_variant	MODERATE	ATP6	0.0425
HLI-0425	9698	T	C	43	469	synonymous_variant	LOW	COX3	0.0405
HLI-0425	10398	A	G	44	401	missense_variant	MODERATE	ND3	0.445
HLI-0425	10550	A	G	37	495	synonymous_variant	LOW	ND4L	0.0376
HLI-0425	11299	T	C	41	495	synonymous_variant	LOW	ND4	0.0417
HLI-0425	11467	A	G	2	606	synonymous_variant	LOW	ND4	0.1231
HLI-0425	11470	A	G	50	566	synonymous_variant	LOW	ND4	0.0029
HLI-0425	11719	G	A	0	553	synonymous_variant	LOW	ND4	0.7756
HLI-0425	11914	G	A	46	579	synonymous_variant	LOW	ND4	0.1112
HLI-0425	12308	A	G	1	491	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0425	12372	G	A	0	492	synonymous_variant	LOW	ND5	0.1329
HLI-0425	14167	C	T	36	482	synonymous_variant	LOW	ND6	0.0385
HLI-0425	14766	C	T	2	672	missense_variant	MODERATE	CYTB	0.7696
HLI-0425	14798	T	C	54	648	missense_variant	MODERATE	CYTB	0.0651
HLI-0425	15326	A	G	1	439	missense_variant	MODERATE	CYTB	0.9868
HLI-0425	15924	A	G	30	462	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0425	16093	T	C	51	522	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0425	16224	T	C	31	510	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0425	16311	T	C	0	477	upstream_gene_variant	MODIFIER	DLoop	0.1969

HLI-0425	16519	T	C	0	243	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0426	146	T	C	0	447	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0426	263	A	G	0	357	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0426	750	A	G	0	551	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0426	1438	A	G	0	548	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0426	2098	G	A	0	398	upstream_gene_variant	MODIFIER	RNR2	0.0013
HLI-0426	2847	C	A	1	526	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0426	3010	G	A	1	548	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0426	3394	T	C	2	533	missense_variant	MODERATE	ND1	0.013
HLI-0426	4769	A	G	0	549	synonymous_variant	LOW	ND2	0.9767
HLI-0426	11339	T	C	0	640	synonymous_variant	LOW	ND4	0.0028
HLI-0426	13722	A	G	1	512	synonymous_variant	LOW	ND5	0.0077
HLI-0426	15326	A	G	0	439	missense_variant	MODERATE	CYTB	0.9868
HLI-0426	15742	C	A	4	428	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0426	16270	C	T	1	508	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0426	16519	T	C	0	288	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0427	73	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0427	119	T	C	5	302	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0427	185	G	A	0	228	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0427	189	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0427	194	C	T	0	237	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0427	195	T	C	0	237	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0427	204	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0427	207	G	A	0	254	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0427	263	A	G	0	298	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0427	709	G	A	2	532	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0427	750	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0427	1243	T	C	0	638	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0427	1438	A	G	1	561	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0427	2706	A	G	0	546	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0427	3505	A	G	3	517	missense_variant	MODERATE	ND1	0.0144
HLI-0427	4769	A	G	2	550	synonymous_variant	LOW	ND2	0.9767
HLI-0427	5046	G	A	4	474	missense_variant	MODERATE	ND2	0.018
HLI-0427	5460	G	A	3	508	missense_variant	MODERATE	ND2	0.0651
HLI-0427	7028	C	T	2	650	synonymous_variant	LOW	COX1	0.8089
HLI-0427	7702	G	A	3	538	synonymous_variant	LOW	COX2	0.001
HLI-0427	8251	G	A	3	494	synonymous_variant	LOW	COX2	0.058
HLI-0427	8994	G	A	0	569	synonymous_variant	LOW	ATP6	0.0167
HLI-0427	11674	C	T	6	573	synonymous_variant	LOW	ND4	0.0116

HLI-0427	11719	G	A	2	642	synonymous_variant	LOW	ND4	0.7756
HLI-0427	11947	A	G	0	520	synonymous_variant	LOW	ND4	0.011
HLI-0427	12414	T	C	2	431	synonymous_variant	LOW	ND5	0.0139
HLI-0427	12705	C	T	0	514	synonymous_variant	LOW	ND5	0.4212
HLI-0427	14766	C	T	4	596	missense_variant	MODERATE	CYTB	0.7696
HLI-0427	15326	A	G	0	459	missense_variant	MODERATE	CYTB	0.9868
HLI-0427	15884	G	C	0	408	missense_variant	MODERATE	CYTB	0.011
HLI-0427	16213	G	A	0	555	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0427	16223	C	T	1	551	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0427	16292	C	T	0	481	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0427	16519	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0428	73	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0428	263	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0428	295	C	T	2	185	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0428	462	C	T	4	394	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0428	489	T	C	0	468	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0428	750	A	G	0	526	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0428	1438	A	G	1	592	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0428	2706	A	G	1	490	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0428	3010	G	A	1	511	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0428	4216	T	C	2	474	missense_variant	MODERATE	ND1	0.0991
HLI-0428	4769	A	G	1	495	synonymous_variant	LOW	ND2	0.9767
HLI-0428	7028	C	T	2	600	synonymous_variant	LOW	COX1	0.8089
HLI-0428	10398	A	G	3	608	missense_variant	MODERATE	ND3	0.445
HLI-0428	11251	A	G	2	572	synonymous_variant	LOW	ND4	0.0932
HLI-0428	11719	G	A	0	557	synonymous_variant	LOW	ND4	0.7756
HLI-0428	12612	A	G	5	477	synonymous_variant	LOW	ND5	0.0506
HLI-0428	13708	G	A	0	463	missense_variant	MODERATE	ND5	0.0717
HLI-0428	14766	C	T	0	581	missense_variant	MODERATE	CYTB	0.7696
HLI-0428	14798	T	C	0	676	missense_variant	MODERATE	CYTB	0.0651
HLI-0428	15326	A	G	0	418	missense_variant	MODERATE	CYTB	0.9868
HLI-0428	15452	C	A	4	375	missense_variant	MODERATE	CYTB	0.0933
HLI-0428	16069	C	T	2	520	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0428	16126	T	C	0	578	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0428	16261	C	T	1	435	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0429	263	A	G	0	256	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0429	408	T	A	1	311	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0429	750	A	G	1	525	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0429	1438	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0429	3345	T	C	0	504	synonymous_variant	LOW	ND1	4.00E-04
HLI-0429	4769	A	G	0	526	synonymous_variant	LOW	ND2	0.9767
HLI-0429	6776	T	C	0	695	synonymous_variant	LOW	COX1	0.0226
HLI-0429	8841	C	T	0	521	synonymous_variant	LOW	ATP6	2.00E-04
HLI-0429	9117	T	C	0	475	synonymous_variant	LOW	ATP6	0.0018
HLI-0429	10685	G	A	0	545	synonymous_variant	LOW	ND4L	0.0055
HLI-0429	15326	A	G	0	372	missense_variant	MODERATE	CYTB	0.9868
HLI-0429	16519	T	C	0	227	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0430	73	A	G	0	169	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0430	93	A	G	1	204	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0430	146	T	C	1	316	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0430	150	C	T	1	330	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0430	152	T	C	1	325	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0430	182	C	T	0	346	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0430	195	T	C	0	342	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0430	198	C	T	0	344	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0430	263	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0430	325	C	T	0	266	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0430	680	T	C	0	562	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0430	709	G	A	0	638	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0430	750	A	G	0	628	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0430	769	G	A	0	635	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0430	1018	G	A	0	729	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0430	1040	T	C	0	786	upstream_gene_variant	MODIFIER	RNR1	0.0024
HLI-0430	1438	A	G	0	675	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0430	1442	G	A	0	688	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0430	2332	C	T	0	570	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0430	2416	T	C	0	592	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0430	2706	A	G	1	605	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0430	3200	T	A	1	611	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0430	3594	C	T	2	539	synonymous_variant	LOW	ND1	0.0789
HLI-0430	4104	A	G	0	490	synonymous_variant	LOW	ND1	0.0785
HLI-0430	4769	A	G	0	634	synonymous_variant	LOW	ND2	0.9767
HLI-0430	7028	C	T	7	678	synonymous_variant	LOW	COX1	0.8089
HLI-0430	7256	C	T	7	551	synonymous_variant	LOW	COX1	0.0784
HLI-0430	7521	G	A	0	459	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0430	7624	T	A	0	558	synonymous_variant	LOW	COX2	0.0047
HLI-0430	8206	G	A	0	656	synonymous_variant	LOW	COX2	0.0287
HLI-0430	8701	A	G	0	526	missense_variant	MODERATE	ATP6	0.3391

HLI-0430	9221	A	G	0	653	synonymous_variant	LOW	COX3	0.0277
HLI-0430	9540	T	C	1	616	synonymous_variant	LOW	COX3	0.339
HLI-0430	10115	T	C	0	747	synonymous_variant	LOW	ND3	0.0278
HLI-0430	10398	A	G	1	614	missense_variant	MODERATE	ND3	0.445
HLI-0430	10873	T	C	0	576	synonymous_variant	LOW	ND4	0.3389
HLI-0430	11719	G	A	0	609	synonymous_variant	LOW	ND4	0.7756
HLI-0430	11944	T	C	0	564	synonymous_variant	LOW	ND4	0.0331
HLI-0430	12236	G	A	5	483	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0430	12705	C	T	0	578	synonymous_variant	LOW	ND5	0.4212
HLI-0430	13590	G	A	1	533	synonymous_variant	LOW	ND5	0.0586
HLI-0430	13650	C	T	0	554	synonymous_variant	LOW	ND5	0.079
HLI-0430	13928	G	C	0	531	missense_variant	MODERATE	ND5	0.0484
HLI-0430	13958	G	C	1	584	missense_variant	MODERATE	ND5	0.0028
HLI-0430	14766	C	T	3	592	missense_variant	MODERATE	CYTB	0.7696
HLI-0430	15110	G	A	0	652	missense_variant	MODERATE	CYTB	0.009
HLI-0430	15217	G	A	0	529	synonymous_variant	LOW	CYTB	0.0104
HLI-0430	15301	G	A	0	536	synonymous_variant	LOW	CYTB	0.2912
HLI-0430	15326	A	G	0	523	missense_variant	MODERATE	CYTB	0.9868
HLI-0430	15514	T	C	0	447	synonymous_variant	LOW	CYTB	0.0071
HLI-0430	15849	C	T	1	547	missense_variant	MODERATE	CYTB	0.0027
HLI-0430	16223	C	T	4	610	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0430	16278	C	T	6	577	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0430	16390	G	A	0	430	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0431	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0431	750	A	G	0	577	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0431	2352	T	C	0	536	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0431	10993	G	A	0	440	synonymous_variant	LOW	ND4	0.0014
HLI-0431	13708	G	A	0	467	missense_variant	MODERATE	ND5	0.0717
HLI-0431	15266	A	G	0	550	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0431	15326	A	G	0	553	missense_variant	MODERATE	CYTB	0.9868
HLI-0431	16362	T	C	1	428	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0431	16519	T	C	0	290	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0432	263	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0432	750	A	G	0	61	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0432	1438	A	G	0	39	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0432	4769	A	G	1	46	synonymous_variant	LOW	ND2	0.9767
HLI-0432	6776	T	C	0	68	synonymous_variant	LOW	COX1	0.0226
HLI-0432	15326	A	G	0	61	missense_variant	MODERATE	CYTB	0.9868
HLI-0432	16218	C	T	0	43	upstream_gene_variant	MODIFIER	DLoop	0.0062

HLI-0432	16298	T	C	0	51	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0432	16519	T	C	0	32	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0433	73	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0433	185	G	A	0	48	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0433	188	A	G	0	47	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0433	228	G	A	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0433	263	A	G	0	29	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0433	295	C	T	0	10	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0433	462	C	T	2	47	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0433	489	T	C	2	50	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0433	750	A	G	0	65	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0433	1438	A	G	0	54	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0433	2706	A	G	0	53	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0433	3010	G	A	0	55	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0433	4216	T	C	0	50	missense_variant	MODERATE	ND1	0.0991
HLI-0433	4454	T	C	0	50	upstream_gene_variant	MODIFIER	TRNM	0.0043
HLI-0433	4769	A	G	0	53	synonymous_variant	LOW	ND2	0.9767
HLI-0433	7028	C	T	0	63	synonymous_variant	LOW	COX1	0.8089
HLI-0433	10398	A	G	0	54	missense_variant	MODERATE	ND3	0.445
HLI-0433	11251	A	G	1	52	synonymous_variant	LOW	ND4	0.0932
HLI-0433	11719	G	A	0	43	synonymous_variant	LOW	ND4	0.7756
HLI-0433	12612	A	G	0	52	synonymous_variant	LOW	ND5	0.0506
HLI-0433	13708	G	A	0	40	missense_variant	MODERATE	ND5	0.0717
HLI-0433	14766	C	T	0	75	missense_variant	MODERATE	CYTB	0.7696
HLI-0433	14798	T	C	0	73	missense_variant	MODERATE	CYTB	0.0651
HLI-0433	15326	A	G	0	46	missense_variant	MODERATE	CYTB	0.9868
HLI-0433	15452	C	A	0	53	missense_variant	MODERATE	CYTB	0.0933
HLI-0433	16069	C	T	0	64	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0433	16126	T	C	0	71	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0433	16519	T	C	0	26	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0434	152	T	C	0	58	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0434	263	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0434	750	A	G	0	58	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0434	1438	A	G	0	58	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0434	2779	C	T	1	62	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0434	3591	G	A	0	32	synonymous_variant	LOW	ND1	0.0082
HLI-0434	4310	A	G	0	55	upstream_gene_variant	MODIFIER	TRNI	8.00E-04
HLI-0434	4769	A	G	0	70	synonymous_variant	LOW	ND2	0.9767
HLI-0434	8839	G	A	0	60	missense_variant	MODERATE	ATP6	0.0012

HLI-0434	13020	T	C	1	48	synonymous_variant	LOW	ND5	0.0106
HLI-0434	15326	A	G	0	55	missense_variant	MODERATE	CYTB	0.9868
HLI-0434	16168	C	T	0	52	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0434	16519	T	C	0	29	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0435	73	A	G	0	30	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0435	150	C	T	0	68	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0435	263	A	G	0	38	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0435	742	T	C	0	45	upstream_gene_variant	MODIFIER	RNR1	3.00E-04
HLI-0435	750	A	G	0	46	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0435	1438	A	G	0	53	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0435	2706	A	G	0	50	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0435	3197	T	C	0	51	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0435	4769	A	G	0	40	synonymous_variant	LOW	ND2	0.9767
HLI-0435	5437	C	T	0	54	missense_variant	MODERATE	ND2	5.00E-04
HLI-0435	5656	A	G	1	66	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0435	7028	C	T	0	78	synonymous_variant	LOW	COX1	0.8089
HLI-0435	7768	A	G	0	50	synonymous_variant	LOW	COX2	0.0186
HLI-0435	8814	C	T	0	57	synonymous_variant	LOW	ATP6	2.00E-04
HLI-0435	9477	G	A	0	57	missense_variant	MODERATE	COX3	0.0387
HLI-0435	11467	A	G	0	66	synonymous_variant	LOW	ND4	0.1231
HLI-0435	11719	G	A	1	67	synonymous_variant	LOW	ND4	0.7756
HLI-0435	12308	A	G	0	35	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0435	12372	G	A	0	39	synonymous_variant	LOW	ND5	0.1329
HLI-0435	13617	T	C	0	57	synonymous_variant	LOW	ND5	0.038
HLI-0435	14182	T	C	0	53	synonymous_variant	LOW	ND6	0.0254
HLI-0435	14766	C	T	0	76	missense_variant	MODERATE	CYTB	0.7696
HLI-0435	15326	A	G	0	53	missense_variant	MODERATE	CYTB	0.9868
HLI-0435	15355	G	A	0	56	synonymous_variant	LOW	CYTB	0.0032
HLI-0435	15721	T	C	0	46	synonymous_variant	LOW	CYTB	0.0033
HLI-0435	16270	C	T	0	59	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0436	73	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0436	195	T	C	1	456	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0436	263	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0436	497	C	T	6	450	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0436	750	A	G	2	562	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0436	1189	T	C	0	624	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0436	1438	A	G	0	569	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0436	1811	A	G	0	570	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0436	2706	A	G	0	575	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0436	3480	A	G	0	546	synonymous_variant	LOW	ND1	0.0392
HLI-0436	4769	A	G	1	591	synonymous_variant	LOW	ND2	0.9767
HLI-0436	4937	T	C	2	575	synonymous_variant	LOW	ND2	0.0019
HLI-0436	7028	C	T	5	603	synonymous_variant	LOW	COX1	0.8089
HLI-0436	9055	G	A	0	512	missense_variant	MODERATE	ATP6	0.0425
HLI-0436	9698	T	C	1	615	synonymous_variant	LOW	COX3	0.0405
HLI-0436	10398	A	G	2	621	missense_variant	MODERATE	ND3	0.445
HLI-0436	10550	A	G	2	556	synonymous_variant	LOW	ND4L	0.0376
HLI-0436	11299	T	C	3	571	synonymous_variant	LOW	ND4	0.0417
HLI-0436	11467	A	G	1	604	synonymous_variant	LOW	ND4	0.1231
HLI-0436	11719	G	A	0	629	synonymous_variant	LOW	ND4	0.7756
HLI-0436	12308	A	G	2	561	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0436	12372	G	A	0	558	synonymous_variant	LOW	ND5	0.1329
HLI-0436	14167	C	T	2	539	synonymous_variant	LOW	ND6	0.0385
HLI-0436	14766	C	T	5	640	missense_variant	MODERATE	CYTB	0.7696
HLI-0436	14798	T	C	2	708	missense_variant	MODERATE	CYTB	0.0651
HLI-0436	15326	A	G	0	534	missense_variant	MODERATE	CYTB	0.9868
HLI-0436	16048	G	A	1	707	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0436	16093	T	C	16	745	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0436	16224	T	C	0	703	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0436	16291	C	T	1	583	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0436	16311	T	C	1	566	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0436	16519	T	C	0	308	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0437	263	A	G	0	24	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0437	750	A	G	0	55	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0437	1438	A	G	0	34	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0437	2706	A	G	0	48	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0437	3421	G	A	2	39	missense_variant	MODERATE	ND1	0.0015
HLI-0437	4769	A	G	0	53	synonymous_variant	LOW	ND2	0.9767
HLI-0437	7028	C	T	0	77	synonymous_variant	LOW	COX1	0.8089
HLI-0437	8014	A	T	2	53	synonymous_variant	LOW	COX2	0.0024
HLI-0437	15218	A	G	1	47	missense_variant	MODERATE	CYTB	0.0169
HLI-0437	15326	A	G	0	59	missense_variant	MODERATE	CYTB	0.9868
HLI-0437	16067	C	T	1	50	upstream_gene_variant	MODIFIER	DLoop	0.0033
HLI-0437	16327	C	A	5	56	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0438	152	T	C	0	518	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0438	263	A	G	0	251	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0438	750	A	G	0	542	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0438	1438	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0438	3010	G	A	0	486	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0438	4674	A	G	1	589	missense_variant	MODERATE	ND2	5.00E-04
HLI-0438	4769	A	G	0	532	synonymous_variant	LOW	ND2	0.9767
HLI-0438	8566	A	G	0	478	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0438	12477	T	C	2	393	synonymous_variant	LOW	ND5	0.0054
HLI-0438	13287	C	T	0	570	synonymous_variant	LOW	ND5	8.00E-04
HLI-0438	15326	A	G	0	326	missense_variant	MODERATE	CYTB	0.9868
HLI-0438	16211	C	T	3	502	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0438	16519	T	C	0	265	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0439	73	A	G	40	175	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0439	195	T	C	74	304	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0439	198	C	T	71	305	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0439	263	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0439	325	C	T	16	218	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0439	680	T	C	86	471	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0439	709	G	A	95	519	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0439	750	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0439	769	G	A	76	530	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0439	1018	G	A	96	593	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0439	1040	T	C	104	646	upstream_gene_variant	MODIFIER	RNR1	0.0024
HLI-0439	1438	A	G	0	634	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0439	1442	G	A	79	572	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0439	2083	T	C	52	379	upstream_gene_variant	MODIFIER	RNR2	0.0011
HLI-0439	2332	C	T	58	368	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0439	2416	T	C	59	392	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0439	2706	A	G	0	549	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0439	3200	T	A	72	500	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0439	3594	C	T	48	430	synonymous_variant	LOW	ND1	0.0789
HLI-0439	4104	A	G	65	374	synonymous_variant	LOW	ND1	0.0785
HLI-0439	4769	A	G	1	562	synonymous_variant	LOW	ND2	0.9767
HLI-0439	7028	C	T	1	618	synonymous_variant	LOW	COX1	0.8089
HLI-0439	7256	C	T	78	483	synonymous_variant	LOW	COX1	0.0784
HLI-0439	7521	G	A	72	370	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0439	7624	T	A	73	394	synonymous_variant	LOW	COX2	0.0047
HLI-0439	8206	G	A	57	439	synonymous_variant	LOW	COX2	0.0287
HLI-0439	8701	A	G	76	475	missense_variant	MODERATE	ATP6	0.3391
HLI-0439	8870	T	C	83	593	missense_variant	MODERATE	ATP6	8.00E-04
HLI-0439	9221	A	G	69	508	synonymous_variant	LOW	COX3	0.0277
HLI-0439	9540	T	C	81	441	synonymous_variant	LOW	COX3	0.339

HLI-0439	10115	T	C	89	588	synonymous_variant	LOW	ND3	0.0278
HLI-0439	10398	A	G	91	506	missense_variant	MODERATE	ND3	0.445
HLI-0439	10873	T	C	73	512	synonymous_variant	LOW	ND4	0.3389
HLI-0439	11719	G	A	91	476	synonymous_variant	LOW	ND4	0.7756
HLI-0439	11944	T	C	64	425	synonymous_variant	LOW	ND4	0.0331
HLI-0439	12236	G	A	57	331	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0439	12705	C	T	77	398	synonymous_variant	LOW	ND5	0.4212
HLI-0439	13590	G	A	69	445	synonymous_variant	LOW	ND5	0.0586
HLI-0439	13650	C	T	81	458	synonymous_variant	LOW	ND5	0.079
HLI-0439	13928	G	C	78	412	missense_variant	MODERATE	ND5	0.0484
HLI-0439	13958	G	C	83	448	missense_variant	MODERATE	ND5	0.0028
HLI-0439	14766	C	T	84	534	missense_variant	MODERATE	CYTB	0.7696
HLI-0439	15043	G	A	83	608	synonymous_variant	LOW	CYTB	0.2362
HLI-0439	15110	G	A	93	656	missense_variant	MODERATE	CYTB	0.009
HLI-0439	15217	G	A	70	436	synonymous_variant	LOW	CYTB	0.0104
HLI-0439	15301	G	A	66	381	synonymous_variant	LOW	CYTB	0.2912
HLI-0439	15326	A	G	0	432	missense_variant	MODERATE	CYTB	0.9868
HLI-0439	15849	C	T	56	354	missense_variant	MODERATE	CYTB	0.0027
HLI-0439	16223	C	T	74	494	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0439	16264	C	T	87	489	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0439	16278	C	T	88	464	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0439	16390	G	A	68	406	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0440	150	C	T	1	470	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0440	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0440	750	A	G	2	528	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0440	1007	G	A	2	604	upstream_gene_variant	MODIFIER	RNR1	0.0015
HLI-0440	1438	A	G	2	574	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0440	3010	G	A	2	566	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0440	4769	A	G	1	562	synonymous_variant	LOW	ND2	0.9767
HLI-0440	7270	T	C	0	597	missense_variant	MODERATE	COX1	0.0016
HLI-0440	8167	T	C	3	575	synonymous_variant	LOW	COX2	0.0021
HLI-0440	12810	A	G	4	559	synonymous_variant	LOW	ND5	0.0198
HLI-0440	14053	A	G	2	453	missense_variant	MODERATE	ND5	0.0046
HLI-0440	15326	A	G	0	459	missense_variant	MODERATE	CYTB	0.9868
HLI-0440	16355	C	T	2	421	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0440	16519	T	C	0	236	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0441	73	A	G	0	40	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0441	152	T	C	0	61	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0441	217	T	C	0	42	upstream_gene_variant	MODIFIER	DLoop	0.0083

HLI-0441	263	A	G	0	37	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0441	394	C	T	0	37	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0441	508	A	G	0	23	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0441	575	C	T	0	27	upstream_gene_variant	MODIFIER	TRNF	9.00E-04
HLI-0441	750	A	G	0	48	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0441	1438	A	G	0	52	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0441	1811	A	G	0	35	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0441	2706	A	G	0	54	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0441	3170	C	A	0	55	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0441	3720	A	G	0	66	synonymous_variant	LOW	ND1	0.0069
HLI-0441	4769	A	G	0	46	synonymous_variant	LOW	ND2	0.9767
HLI-0441	5390	A	G	0	32	synonymous_variant	LOW	ND2	0.0069
HLI-0441	5426	T	C	0	35	synonymous_variant	LOW	ND2	0.0091
HLI-0441	6045	C	T	0	63	synonymous_variant	LOW	COX1	0.0065
HLI-0441	6152	T	C	0	75	synonymous_variant	LOW	COX1	0.0077
HLI-0441	7028	C	T	0	74	synonymous_variant	LOW	COX1	0.8089
HLI-0441	10876	A	G	0	41	synonymous_variant	LOW	ND4	0.0098
HLI-0441	11467	A	G	1	46	synonymous_variant	LOW	ND4	0.1231
HLI-0441	11719	G	A	0	45	synonymous_variant	LOW	ND4	0.7756
HLI-0441	12308	A	G	0	33	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0441	12372	G	A	0	32	synonymous_variant	LOW	ND5	0.1329
HLI-0441	13020	T	C	0	47	synonymous_variant	LOW	ND5	0.0106
HLI-0441	13734	T	C	0	44	synonymous_variant	LOW	ND5	0.0067
HLI-0441	14766	C	T	0	53	missense_variant	MODERATE	CYTB	0.7696
HLI-0441	15326	A	G	0	49	missense_variant	MODERATE	CYTB	0.9868
HLI-0441	15721	T	C	0	39	synonymous_variant	LOW	CYTB	0.0033
HLI-0441	15907	A	G	0	35	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0441	16051	A	G	0	30	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0441	16129	G	C	0	24	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0441	16260	C	T	0	31	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0441	16356	T	C	0	36	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0441	16362	T	C	0	40	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0441	16519	T	C	0	22	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0442	73	A	G	0	44	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0442	114	C	T	1	56	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0442	263	A	G	0	33	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0442	497	C	T	0	40	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0442	750	A	G	0	41	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0442	1189	T	C	0	62	upstream_gene_variant	MODIFIER	RNR1	0.0318

HLI-0442	1438	A	G	0	38	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0442	1811	A	G	0	38	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0442	2706	A	G	0	59	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0442	3480	A	G	0	40	synonymous_variant	LOW	ND1	0.0392
HLI-0442	4769	A	G	0	51	synonymous_variant	LOW	ND2	0.9767
HLI-0442	7028	C	T	0	64	synonymous_variant	LOW	COX1	0.8089
HLI-0442	9055	G	A	0	56	missense_variant	MODERATE	ATP6	0.0425
HLI-0442	9698	T	C	0	61	synonymous_variant	LOW	COX3	0.0405
HLI-0442	10398	A	G	2	48	missense_variant	MODERATE	ND3	0.445
HLI-0442	10550	A	G	0	59	synonymous_variant	LOW	ND4L	0.0376
HLI-0442	10978	A	G	0	26	synonymous_variant	LOW	ND4	0.0036
HLI-0442	11299	T	C	0	47	synonymous_variant	LOW	ND4	0.0417
HLI-0442	11467	A	G	0	67	synonymous_variant	LOW	ND4	0.1231
HLI-0442	11470	A	G	0	66	synonymous_variant	LOW	ND4	0.0029
HLI-0442	11719	G	A	0	57	synonymous_variant	LOW	ND4	0.7756
HLI-0442	11914	G	A	0	47	synonymous_variant	LOW	ND4	0.1112
HLI-0442	12308	A	G	0	38	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0442	12372	G	A	0	39	synonymous_variant	LOW	ND5	0.1329
HLI-0442	12954	T	C	0	53	synonymous_variant	LOW	ND5	0.0017
HLI-0442	14167	C	T	0	34	synonymous_variant	LOW	ND6	0.0385
HLI-0442	14766	C	T	1	56	missense_variant	MODERATE	CYTB	0.7696
HLI-0442	14798	T	C	0	68	missense_variant	MODERATE	CYTB	0.0651
HLI-0442	15326	A	G	1	49	missense_variant	MODERATE	CYTB	0.9868
HLI-0442	15924	A	G	0	24	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0442	16223	C	T	0	28	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0442	16224	T	C	0	28	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0442	16234	C	T	0	29	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0442	16311	T	C	0	39	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0442	16519	T	C	0	20	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0444	73	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0444	150	C	T	0	464	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0444	152	T	C	0	467	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0444	263	A	G	1	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0444	709	G	A	1	550	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0444	750	A	G	1	614	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0444	1438	A	G	0	592	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0444	1888	G	A	0	530	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0444	2706	A	G	1	633	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0444	3203	A	G	1	611	upstream_gene_variant	MODIFIER	RNR2	0.001

HLI-0444	4216	T	C	0	407	missense_variant	MODERATE	ND1	0.0991
HLI-0444	4769	A	G	0	579	synonymous_variant	LOW	ND2	0.9767
HLI-0444	4917	A	G	0	558	missense_variant	MODERATE	ND2	0.0477
HLI-0444	7028	C	T	0	668	synonymous_variant	LOW	COX1	0.8089
HLI-0444	8697	G	A	1	637	synonymous_variant	LOW	ATP6	0.0466
HLI-0444	10463	T	C	0	447	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0444	11251	A	G	0	532	synonymous_variant	LOW	ND4	0.0932
HLI-0444	11719	G	A	0	652	synonymous_variant	LOW	ND4	0.7756
HLI-0444	11812	A	G	0	569	synonymous_variant	LOW	ND4	0.0332
HLI-0444	13368	G	A	1	628	synonymous_variant	LOW	ND5	0.0495
HLI-0444	14233	A	G	0	544	synonymous_variant	LOW	ND6	0.0369
HLI-0444	14766	C	T	3	637	missense_variant	MODERATE	CYTB	0.7696
HLI-0444	14905	G	A	3	715	synonymous_variant	LOW	CYTB	0.0526
HLI-0444	15326	A	G	0	433	missense_variant	MODERATE	CYTB	0.9868
HLI-0444	15452	C	A	1	424	missense_variant	MODERATE	CYTB	0.0933
HLI-0444	15607	A	G	0	471	synonymous_variant	LOW	CYTB	0.0508
HLI-0444	15928	G	A	0	615	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0444	16092	T	C	8	691	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0444	16126	T	C	0	761	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0444	16153	G	A	0	726	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0444	16294	C	T	2	510	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0444	16519	T	C	0	246	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0445	73	A	G	0	282	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0445	263	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0445	750	A	G	0	525	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0445	951	G	A	4	662	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0445	9064	G	A	1	527	missense_variant	MODERATE	ATP6	0.0025
HLI-0445	15326	A	G	0	435	missense_variant	MODERATE	CYTB	0.9868
HLI-0445	15607	A	G	0	352	synonymous_variant	LOW	CYTB	0.0508
HLI-0445	16354	C	T	5	636	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0446	73	A	G	1	216	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0446	151	C	T	0	355	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0446	152	T	C	0	354	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0446	182	C	T	0	357	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0446	185	G	T	0	354	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0446	195	T	C	0	341	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0446	247	G	A	0	215	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0446	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0446	357	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.0057

HLI-0446	709	G	A	0	393	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0446	710	T	C	0	398	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0446	750	A	G	0	438	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0446	769	G	A	0	443	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0446	825	T	A	0	508	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0446	1018	G	A	1	553	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0446	1738	T	C	0	516	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0446	2352	T	C	1	531	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0446	2706	A	G	0	467	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0446	2758	G	A	1	515	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0446	2768	A	G	2	525	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0446	2885	T	C	2	533	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0446	3308	T	C	0	500	start_lost	HIGH	ND1	0.0073
HLI-0446	3594	C	T	0	332	synonymous_variant	LOW	ND1	0.0789
HLI-0446	3666	G	A	1	401	synonymous_variant	LOW	ND1	0.0233
HLI-0446	3693	G	A	2	389	synonymous_variant	LOW	ND1	0.0091
HLI-0446	4104	A	G	1	431	synonymous_variant	LOW	ND1	0.0785
HLI-0446	4769	A	G	0	581	synonymous_variant	LOW	ND2	0.9767
HLI-0446	5036	A	G	0	455	synonymous_variant	LOW	ND2	0.006
HLI-0446	5046	G	A	0	489	missense_variant	MODERATE	ND2	0.018
HLI-0446	5393	T	C	0	545	synonymous_variant	LOW	ND2	0.0059
HLI-0446	5655	T	C	0	643	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0446	6548	C	T	2	498	synonymous_variant	LOW	COX1	0.0061
HLI-0446	6827	T	C	5	594	synonymous_variant	LOW	COX1	0.0072
HLI-0446	6989	A	G	6	580	synonymous_variant	LOW	COX1	0.0061
HLI-0446	7028	C	T	4	508	synonymous_variant	LOW	COX1	0.8089
HLI-0446	7055	A	G	5	459	synonymous_variant	LOW	COX1	0.0188
HLI-0446	7146	A	G	0	330	missense_variant	MODERATE	COX1	0.0497
HLI-0446	7256	C	T	4	473	synonymous_variant	LOW	COX1	0.0784
HLI-0446	7389	T	C	5	456	missense_variant	MODERATE	COX1	0.0201
HLI-0446	7521	G	A	1	391	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0446	7867	C	T	0	577	synonymous_variant	LOW	COX2	0.0076
HLI-0446	8248	A	G	3	539	synonymous_variant	LOW	COX2	0.0061
HLI-0446	8468	C	T	2	435	synonymous_variant	LOW	ATP8	0.0501
HLI-0446	8655	C	T	5	434	synonymous_variant	LOW	ATP6	0.0511
HLI-0446	8701	A	G	2	485	missense_variant	MODERATE	ATP6	0.3391
HLI-0446	9540	T	C	0	408	synonymous_variant	LOW	COX3	0.339
HLI-0446	10398	A	G	1	540	missense_variant	MODERATE	ND3	0.445
HLI-0446	10688	G	A	0	477	synonymous_variant	LOW	ND4L	0.0515

HLI-0446	10810	T	C	3	543	synonymous_variant	LOW	ND4	0.0522
HLI-0446	10873	T	C	3	511	synonymous_variant	LOW	ND4	0.3389
HLI-0446	11719	G	A	0	530	synonymous_variant	LOW	ND4	0.7756
HLI-0446	12519	T	C	4	652	synonymous_variant	LOW	ND5	0.007
HLI-0446	12705	C	T	0	632	synonymous_variant	LOW	ND5	0.4212
HLI-0446	13105	A	G	0	503	missense_variant	MODERATE	ND5	0.076
HLI-0446	13506	C	T	0	459	synonymous_variant	LOW	ND5	0.0506
HLI-0446	13650	C	T	3	418	synonymous_variant	LOW	ND5	0.079
HLI-0446	13789	T	C	1	339	missense_variant	MODERATE	ND5	0.0185
HLI-0446	13880	C	A	3	410	missense_variant	MODERATE	ND5	0.0055
HLI-0446	14178	T	C	1	517	missense_variant	MODERATE	ND6	0.0225
HLI-0446	14203	A	G	2	560	synonymous_variant	LOW	ND6	0.0061
HLI-0446	14560	G	A	1	594	synonymous_variant	LOW	ND6	0.0235
HLI-0446	14766	C	T	0	594	missense_variant	MODERATE	CYTB	0.7696
HLI-0446	14769	A	G	0	604	missense_variant	MODERATE	CYTB	0.0121
HLI-0446	15115	T	C	0	603	synonymous_variant	LOW	CYTB	0.0093
HLI-0446	15326	A	G	2	390	missense_variant	MODERATE	CYTB	0.9868
HLI-0446	16126	T	C	2	680	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0446	16223	C	T	3	537	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0446	16264	C	T	2	485	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0446	16270	C	T	1	481	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0446	16278	C	T	0	475	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0446	16311	T	C	0	436	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0446	16519	T	C	0	157	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0447	73	A	G	1	336	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0447	152	T	C	1	559	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0447	189	A	G	0	353	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0447	217	T	C	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0447	263	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0447	340	C	T	0	250	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0447	508	A	G	1	365	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0447	750	A	G	0	700	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0447	1438	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0447	1811	A	G	0	530	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0447	2706	A	G	2	715	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0447	3116	C	T	1	616	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0447	3720	A	G	0	662	synonymous_variant	LOW	ND1	0.0069
HLI-0447	4769	A	G	2	529	synonymous_variant	LOW	ND2	0.9767
HLI-0447	4967	T	C	0	560	synonymous_variant	LOW	ND2	7.00E-04

HLI-0447	5390	A	G	1	613	synonymous_variant	LOW	ND2	0.0069
HLI-0447	5426	T	C	0	671	synonymous_variant	LOW	ND2	0.0091
HLI-0447	6045	C	T	1	724	synonymous_variant	LOW	COX1	0.0065
HLI-0447	6152	T	C	1	670	synonymous_variant	LOW	COX1	0.0077
HLI-0447	7028	C	T	0	700	synonymous_variant	LOW	COX1	0.8089
HLI-0447	10876	A	G	1	567	synonymous_variant	LOW	ND4	0.0098
HLI-0447	11197	C	T	2	621	synonymous_variant	LOW	ND4	0.0021
HLI-0447	11467	A	G	0	672	synonymous_variant	LOW	ND4	0.1231
HLI-0447	11719	G	A	0	685	synonymous_variant	LOW	ND4	0.7756
HLI-0447	11732	T	C	0	741	synonymous_variant	LOW	ND4	0.002
HLI-0447	12308	A	G	0	471	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0447	12372	G	A	2	487	synonymous_variant	LOW	ND5	0.1329
HLI-0447	13020	T	C	5	691	synonymous_variant	LOW	ND5	0.0106
HLI-0447	13734	T	C	0	500	synonymous_variant	LOW	ND5	0.0067
HLI-0447	14766	C	T	1	624	missense_variant	MODERATE	CYTB	0.7696
HLI-0447	15326	A	G	0	580	missense_variant	MODERATE	CYTB	0.9868
HLI-0447	15907	A	G	1	589	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0447	16051	A	G	0	463	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0447	16093	T	C	4	356	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0447	16129	G	C	0	234	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0447	16319	G	A	1	473	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0447	16362	T	C	0	547	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0447	16519	T	C	1	247	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0448	73	A	G	2	325	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0448	114	C	T	2	479	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0448	263	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0448	497	C	T	3	561	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0448	750	A	G	0	710	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0448	1189	T	C	0	671	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0448	1438	A	G	0	658	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0448	1811	A	G	0	673	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0448	2706	A	G	1	645	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0448	3480	A	G	3	535	synonymous_variant	LOW	ND1	0.0392
HLI-0448	4769	A	G	1	592	synonymous_variant	LOW	ND2	0.9767
HLI-0448	7028	C	T	5	726	synonymous_variant	LOW	COX1	0.8089
HLI-0448	9055	G	A	1	603	missense_variant	MODERATE	ATP6	0.0425
HLI-0448	9698	T	C	1	595	synonymous_variant	LOW	COX3	0.0405
HLI-0448	10398	A	G	0	604	missense_variant	MODERATE	ND3	0.445
HLI-0448	10550	A	G	0	595	synonymous_variant	LOW	ND4L	0.0376

HLI-0448	10978	A	G	2	443	synonymous_variant	LOW	ND4	0.0036
HLI-0448	11299	T	C	0	629	synonymous_variant	LOW	ND4	0.0417
HLI-0448	11467	A	G	0	668	synonymous_variant	LOW	ND4	0.1231
HLI-0448	11470	A	G	0	681	synonymous_variant	LOW	ND4	0.0029
HLI-0448	11719	G	A	0	605	synonymous_variant	LOW	ND4	0.7756
HLI-0448	11914	G	A	0	616	synonymous_variant	LOW	ND4	0.1112
HLI-0448	12308	A	G	0	531	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0448	12372	G	A	0	483	synonymous_variant	LOW	ND5	0.1329
HLI-0448	12954	T	C	1	642	synonymous_variant	LOW	ND5	0.0017
HLI-0448	14167	C	T	1	535	synonymous_variant	LOW	ND6	0.0385
HLI-0448	14766	C	T	1	606	missense_variant	MODERATE	CYTB	0.7696
HLI-0448	14798	T	C	0	709	missense_variant	MODERATE	CYTB	0.0651
HLI-0448	15326	A	G	0	626	missense_variant	MODERATE	CYTB	0.9868
HLI-0448	15924	A	G	0	617	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0448	16224	T	C	0	593	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0448	16234	C	T	0	632	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0448	16311	T	C	0	622	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0448	16519	T	C	0	356	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0449	72	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0449	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0449	750	A	G	1	671	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0449	1438	A	G	1	651	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0449	2706	A	G	0	634	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0449	4580	G	A	0	677	synonymous_variant	LOW	ND2	0.0169
HLI-0449	4769	A	G	1	599	synonymous_variant	LOW	ND2	0.9767
HLI-0449	7028	C	T	3	690	synonymous_variant	LOW	COX1	0.8089
HLI-0449	9368	A	G	0	724	synonymous_variant	LOW	COX3	8.00E-04
HLI-0449	15326	A	G	0	605	missense_variant	MODERATE	CYTB	0.9868
HLI-0449	15904	C	T	2	599	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0449	16261	C	T	4	637	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0449	16298	T	C	2	583	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0449	16311	T	C	2	562	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0449	16519	T	C	0	338	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0450	73	A	G	0	337	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0450	194	C	T	4	456	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0450	204	T	C	4	455	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0450	263	A	G	5	310	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0450	750	A	G	1	708	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0450	1438	A	G	0	668	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0450	1694	T	C	2	477	upstream_gene_variant	MODIFIER	RNR2	0.002
HLI-0450	3010	G	A	2	516	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0450	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767
HLI-0450	5051	A	G	2	474	synonymous_variant	LOW	ND2	6.00E-04
HLI-0450	9275	A	G	1	726	synonymous_variant	LOW	COX3	3.00E-04
HLI-0450	10376	A	G	2	602	synonymous_variant	LOW	ND3	6.00E-04
HLI-0450	15326	A	G	0	486	missense_variant	MODERATE	CYTB	0.9868
HLI-0450	16051	A	G	0	456	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0450	16162	A	G	3	553	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0450	16519	T	C	1	366	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0451	183	A	G	3	417	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0451	239	T	C	0	344	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0451	263	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0451	750	A	G	0	433	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0451	1438	A	G	0	486	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0451	3915	G	A	0	453	synonymous_variant	LOW	ND1	0.0106
HLI-0451	4727	A	G	5	507	synonymous_variant	LOW	ND2	0.0063
HLI-0451	4769	A	G	1	571	synonymous_variant	LOW	ND2	0.9767
HLI-0451	5785	T	C	1	685	upstream_gene_variant	MODIFIER	TRNC	4.00E-04
HLI-0451	9380	G	A	0	538	synonymous_variant	LOW	COX3	0.0094
HLI-0451	10045	T	G	2	578	upstream_gene_variant	MODIFIER	TRNG	0
HLI-0451	11253	T	C	1	481	missense_variant	MODERATE	ND4	0.0053
HLI-0451	14249	G	A	3	527	missense_variant	MODERATE	ND6	5.00E-04
HLI-0451	15326	A	G	0	352	missense_variant	MODERATE	CYTB	0.9868
HLI-0451	16362	T	C	0	424	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0451	16482	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0452	73	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0452	150	C	T	0	369	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0452	195	T	C	1	350	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0452	263	A	G	0	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0452	282	T	C	0	186	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0452	750	A	G	1	380	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0452	1438	A	G	3	404	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0452	2352	T	C	3	366	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0452	2483	T	C	2	391	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0452	2706	A	G	3	426	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0452	3277	G	A	3	459	upstream_gene_variant	MODIFIER	TRNL1	7.00E-04
HLI-0452	4769	A	G	2	482	synonymous_variant	LOW	ND2	0.9767
HLI-0452	7028	C	T	0	503	synonymous_variant	LOW	COX1	0.8089

HLI-0452	8701	A	G	4	466	missense_variant	MODERATE	ATP6	0.3391
HLI-0452	9377	A	G	2	512	synonymous_variant	LOW	COX3	0.0084
HLI-0452	9540	T	C	0	346	synonymous_variant	LOW	COX3	0.339
HLI-0452	10398	A	G	0	374	missense_variant	MODERATE	ND3	0.445
HLI-0452	10819	A	G	0	430	synonymous_variant	LOW	ND4	0.0228
HLI-0452	10873	T	C	0	476	synonymous_variant	LOW	ND4	0.3389
HLI-0452	11719	G	A	0	455	synonymous_variant	LOW	ND4	0.7756
HLI-0452	12406	G	A	6	422	missense_variant	MODERATE	ND5	0.0262
HLI-0452	12705	C	T	1	569	synonymous_variant	LOW	ND5	0.4212
HLI-0452	14212	T	C	1	488	synonymous_variant	LOW	ND6	0.0204
HLI-0452	14766	C	T	1	476	missense_variant	MODERATE	CYTB	0.7696
HLI-0452	14905	G	A	3	540	synonymous_variant	LOW	CYTB	0.0526
HLI-0452	15301	G	A	1	368	synonymous_variant	LOW	CYTB	0.2912
HLI-0452	15326	A	G	1	381	missense_variant	MODERATE	CYTB	0.9868
HLI-0452	16172	T	C	0	222	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0452	16223	C	T	0	244	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0452	16320	C	T	0	373	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0452	16519	T	C	0	131	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0453	73	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0453	199	T	C	0	318	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0453	203	G	A	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0453	204	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0453	250	T	C	0	126	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0453	263	A	G	0	134	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0453	750	A	G	1	571	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0453	1438	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0453	1719	G	A	0	466	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0453	1836	A	G	3	471	upstream_gene_variant	MODIFIER	RNR2	4.00E-04
HLI-0453	2706	A	G	0	509	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0453	3447	A	G	0	512	synonymous_variant	LOW	ND1	0.0053
HLI-0453	3990	C	T	1	458	synonymous_variant	LOW	ND1	0.0031
HLI-0453	4023	T	C	0	490	synonymous_variant	LOW	ND1	9.00E-04
HLI-0453	4529	A	T	1	552	synonymous_variant	LOW	ND2	0.015
HLI-0453	4769	A	G	3	502	synonymous_variant	LOW	ND2	0.9767
HLI-0453	6734	G	A	4	683	synonymous_variant	LOW	COX1	0.0062
HLI-0453	7028	C	T	4	597	synonymous_variant	LOW	COX1	0.8089
HLI-0453	8251	G	A	2	468	synonymous_variant	LOW	COX2	0.058
HLI-0453	8616	G	T	1	428	missense_variant	MODERATE	ATP6	0.0032
HLI-0453	9947	G	A	0	499	synonymous_variant	LOW	COX3	0.0092

HLI-0453	10034	T	C	0	555	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0453	10238	T	C	0	577	synonymous_variant	LOW	ND3	0.0623
HLI-0453	10398	A	G	0	577	missense_variant	MODERATE	ND3	0.445
HLI-0453	10915	T	C	0	459	synonymous_variant	LOW	ND4	0.0411
HLI-0453	11719	G	A	0	484	synonymous_variant	LOW	ND4	0.7756
HLI-0453	12501	G	A	6	451	synonymous_variant	LOW	ND5	0.0258
HLI-0453	12705	C	T	1	531	synonymous_variant	LOW	ND5	0.4212
HLI-0453	13488	T	C	0	468	synonymous_variant	LOW	ND5	0.0014
HLI-0453	13780	A	G	1	372	missense_variant	MODERATE	ND5	0.0179
HLI-0453	14766	C	T	2	485	missense_variant	MODERATE	CYTB	0.7696
HLI-0453	15043	G	A	0	618	synonymous_variant	LOW	CYTB	0.2362
HLI-0453	15326	A	G	0	432	missense_variant	MODERATE	CYTB	0.9868
HLI-0453	15924	A	G	1	446	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0453	16129	G	A	1	268	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0453	16172	T	C	0	155	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0453	16223	C	T	1	168	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0453	16311	T	C	0	380	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0453	16390	G	A	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0453	16391	G	A	0	392	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0453	16519	T	C	1	173	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0454	73	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0454	207	G	A	14	344	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0454	263	A	G	1	298	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0454	709	G	A	0	397	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0454	750	A	G	0	428	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0454	930	G	A	0	217	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0454	961	T	C	0	186	upstream_gene_variant	MODIFIER	RNR1	0.0087
HLI-0454	1438	A	G	0	397	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0454	1888	G	A	2	303	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0454	2706	A	G	0	418	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0454	3398	T	C	3	396	missense_variant	MODERATE	ND1	0.0039
HLI-0454	4216	T	C	1	315	missense_variant	MODERATE	ND1	0.0991
HLI-0454	4769	A	G	2	450	synonymous_variant	LOW	ND2	0.9767
HLI-0454	4917	A	G	2	430	missense_variant	MODERATE	ND2	0.0477
HLI-0454	5147	G	A	3	339	synonymous_variant	LOW	ND2	0.0437
HLI-0454	7028	C	T	1	501	synonymous_variant	LOW	COX1	0.8089
HLI-0454	8697	G	A	0	431	synonymous_variant	LOW	ATP6	0.0466
HLI-0454	10463	T	C	0	359	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0454	11251	A	G	0	440	synonymous_variant	LOW	ND4	0.0932

HLI-0454	11719	G	A	0	435	synonymous_variant	LOW	ND4	0.7756
HLI-0454	11812	A	G	0	374	synonymous_variant	LOW	ND4	0.0332
HLI-0454	13368	G	A	0	448	synonymous_variant	LOW	ND5	0.0495
HLI-0454	14233	A	G	0	428	synonymous_variant	LOW	ND6	0.0369
HLI-0454	14766	C	T	1	634	missense_variant	MODERATE	CYTB	0.7696
HLI-0454	14905	G	A	1	659	synonymous_variant	LOW	CYTB	0.0526
HLI-0454	15326	A	G	0	240	missense_variant	MODERATE	CYTB	0.9868
HLI-0454	15452	C	A	0	241	missense_variant	MODERATE	CYTB	0.0933
HLI-0454	15607	A	G	0	232	synonymous_variant	LOW	CYTB	0.0508
HLI-0454	15928	G	A	0	339	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0454	16126	T	C	0	581	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0454	16294	C	T	0	402	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0454	16296	C	T	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0454	16304	T	C	0	425	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0454	16519	T	C	0	161	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0455	73	A	G	0	174	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0455	150	C	T	0	373	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0455	263	A	G	0	167	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0455	750	A	G	0	388	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0455	1438	A	G	0	469	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0455	1721	C	T	0	418	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0455	2706	A	G	1	450	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0455	2757	A	G	4	498	upstream_gene_variant	MODIFIER	RNR2	0.002
HLI-0455	3197	T	C	0	557	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0455	3212	C	T	0	560	upstream_gene_variant	MODIFIER	RNR2	0.0012
HLI-0455	3381	A	G	2	431	synonymous_variant	LOW	ND1	1.00E-04
HLI-0455	4732	A	G	1	425	missense_variant	MODERATE	ND2	0.0059
HLI-0455	4769	A	G	1	488	synonymous_variant	LOW	ND2	0.9767
HLI-0455	4843	C	T	1	503	missense_variant	MODERATE	ND2	5.00E-04
HLI-0455	7028	C	T	4	489	synonymous_variant	LOW	COX1	0.8089
HLI-0455	7768	A	G	1	432	synonymous_variant	LOW	COX2	0.0186
HLI-0455	9007	A	G	1	454	missense_variant	MODERATE	ATP6	0.0022
HLI-0455	9477	G	A	2	465	missense_variant	MODERATE	COX3	0.0387
HLI-0455	11467	A	G	0	493	synonymous_variant	LOW	ND4	0.1231
HLI-0455	11719	G	A	0	476	synonymous_variant	LOW	ND4	0.7756
HLI-0455	12308	A	G	0	416	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0455	12372	G	A	2	416	synonymous_variant	LOW	ND5	0.1329
HLI-0455	13617	T	C	0	421	synonymous_variant	LOW	ND5	0.038
HLI-0455	13637	A	G	0	439	missense_variant	MODERATE	ND5	0.0074

HLI-0455	14182	T	C	1	431	synonymous_variant	LOW	ND6	0.0254
HLI-0455	14766	C	T	2	445	missense_variant	MODERATE	CYTB	0.7696
HLI-0455	14956	T	C	2	546	synonymous_variant	LOW	CYTB	0.001
HLI-0455	15326	A	G	0	424	missense_variant	MODERATE	CYTB	0.9868
HLI-0455	16270	C	T	2	321	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0455	16398	G	A	1	312	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0456	73	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0456	195	T	C	2	373	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0456	263	A	G	0	291	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0456	497	C	T	3	443	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0456	750	A	G	1	539	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0456	1189	T	C	4	602	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0456	1438	A	G	0	514	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0456	1811	A	G	2	419	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0456	2706	A	G	1	491	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0456	3480	A	G	0	477	synonymous_variant	LOW	ND1	0.0392
HLI-0456	4769	A	G	3	480	synonymous_variant	LOW	ND2	0.9767
HLI-0456	7028	C	T	2	581	synonymous_variant	LOW	COX1	0.8089
HLI-0456	9055	G	A	0	466	missense_variant	MODERATE	ATP6	0.0425
HLI-0456	9698	T	C	0	484	synonymous_variant	LOW	COX3	0.0405
HLI-0456	10398	A	G	1	489	missense_variant	MODERATE	ND3	0.445
HLI-0456	10550	A	G	1	587	synonymous_variant	LOW	ND4L	0.0376
HLI-0456	11299	T	C	0	537	synonymous_variant	LOW	ND4	0.0417
HLI-0456	11467	A	G	0	569	synonymous_variant	LOW	ND4	0.1231
HLI-0456	11719	G	A	1	513	synonymous_variant	LOW	ND4	0.7756
HLI-0456	12308	A	G	1	307	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0456	12372	G	A	1	275	synonymous_variant	LOW	ND5	0.1329
HLI-0456	14167	C	T	2	374	synonymous_variant	LOW	ND6	0.0385
HLI-0456	14766	C	T	3	665	missense_variant	MODERATE	CYTB	0.7696
HLI-0456	14798	T	C	0	691	missense_variant	MODERATE	CYTB	0.0651
HLI-0456	15326	A	G	0	349	missense_variant	MODERATE	CYTB	0.9868
HLI-0456	16048	G	A	0	359	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0456	16224	T	C	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0456	16291	C	T	0	443	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0456	16311	T	C	0	406	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0456	16519	T	C	0	208	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0457	73	A	G	0	272	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0457	151	C	T	0	506	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0457	152	T	C	0	511	upstream_gene_variant	MODIFIER	DLoop	0.2668

HLI-0457	263	A	G	0	207	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0457	497	C	T	3	427	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0457	750	A	G	1	581	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0457	1189	T	C	2	611	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0457	1438	A	G	0	546	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0457	1811	A	G	0	534	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0457	2706	A	G	0	530	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0457	3480	A	G	5	427	synonymous_variant	LOW	ND1	0.0392
HLI-0457	3644	T	C	6	488	missense_variant	MODERATE	ND1	0.0042
HLI-0457	4769	A	G	0	480	synonymous_variant	LOW	ND2	0.9767
HLI-0457	7028	C	T	5	574	synonymous_variant	LOW	COX1	0.8089
HLI-0457	9055	G	A	0	502	missense_variant	MODERATE	ATP6	0.0425
HLI-0457	9698	T	C	0	479	synonymous_variant	LOW	COX3	0.0405
HLI-0457	10398	A	G	0	515	missense_variant	MODERATE	ND3	0.445
HLI-0457	10550	A	G	1	493	synonymous_variant	LOW	ND4L	0.0376
HLI-0457	11299	T	C	2	513	synonymous_variant	LOW	ND4	0.0417
HLI-0457	11467	A	G	1	569	synonymous_variant	LOW	ND4	0.1231
HLI-0457	11719	G	A	1	555	synonymous_variant	LOW	ND4	0.7756
HLI-0457	12308	A	G	0	512	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0457	12372	G	A	3	482	synonymous_variant	LOW	ND5	0.1329
HLI-0457	13117	A	G	0	544	missense_variant	MODERATE	ND5	0.0014
HLI-0457	13708	G	A	2	449	missense_variant	MODERATE	ND5	0.0717
HLI-0457	14167	C	T	3	477	synonymous_variant	LOW	ND6	0.0385
HLI-0457	14766	C	T	2	522	missense_variant	MODERATE	CYTB	0.7696
HLI-0457	14798	T	C	1	624	missense_variant	MODERATE	CYTB	0.0651
HLI-0457	15326	A	G	0	486	missense_variant	MODERATE	CYTB	0.9868
HLI-0457	16224	T	C	1	514	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0457	16311	T	C	1	466	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0457	16519	T	C	0	261	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0458	60	T	C	1	178	upstream_gene_variant	MODIFIER	DLoop	8.00E-04
HLI-0458	152	T	C	0	401	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0458	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0458	750	A	G	0	439	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0458	1438	A	G	0	449	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0458	3992	C	T	2	449	missense_variant	MODERATE	ND1	0.0062
HLI-0458	4024	A	G	2	436	missense_variant	MODERATE	ND1	0.0049
HLI-0458	4769	A	G	2	466	synonymous_variant	LOW	ND2	0.9767
HLI-0458	5004	T	C	1	421	synonymous_variant	LOW	ND2	0.0067
HLI-0458	7741	T	C	0	474	synonymous_variant	LOW	COX2	9.00E-04

HLI-0458	8433	T	C	0	358	missense_variant	MODERATE	ATP8	8.00E-04
HLI-0458	9123	G	A	3	512	synonymous_variant	LOW	ATP6	0.0485
HLI-0458	14365	C	T	4	459	synonymous_variant	LOW	ND6	0.0046
HLI-0458	14582	A	G	2	552	missense_variant	MODERATE	ND6	0.005
HLI-0458	15326	A	G	0	322	missense_variant	MODERATE	CYTB	0.9868
HLI-0458	16300	A	G	0	396	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0459	73	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0459	263	A	G	0	198	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0459	750	A	G	1	421	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0459	1438	A	G	1	505	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0459	1842	A	G	2	460	upstream_gene_variant	MODIFIER	RNR2	0.0028
HLI-0459	4769	A	G	1	492	synonymous_variant	LOW	ND2	0.9767
HLI-0459	11641	A	G	2	485	synonymous_variant	LOW	ND4	0.0158
HLI-0459	15326	A	G	0	277	missense_variant	MODERATE	CYTB	0.9868
HLI-0459	16297	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	0.0139
HLI-0459	16519	T	C	1	165	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0460	73	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0460	195	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0460	263	A	G	0	161	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0460	497	C	T	2	386	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0460	750	A	G	1	480	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0460	1189	T	C	1	504	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0460	1438	A	G	0	497	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0460	1811	A	G	1	504	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0460	2706	A	G	2	443	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0460	3480	A	G	3	434	synonymous_variant	LOW	ND1	0.0392
HLI-0460	4769	A	G	2	468	synonymous_variant	LOW	ND2	0.9767
HLI-0460	7028	C	T	3	557	synonymous_variant	LOW	COX1	0.8089
HLI-0460	9055	G	A	1	495	missense_variant	MODERATE	ATP6	0.0425
HLI-0460	9698	T	C	0	448	synonymous_variant	LOW	COX3	0.0405
HLI-0460	10398	A	G	2	435	missense_variant	MODERATE	ND3	0.445
HLI-0460	10550	A	G	2	398	synonymous_variant	LOW	ND4L	0.0376
HLI-0460	11299	T	C	0	482	synonymous_variant	LOW	ND4	0.0417
HLI-0460	11467	A	G	0	482	synonymous_variant	LOW	ND4	0.1231
HLI-0460	11719	G	A	0	460	synonymous_variant	LOW	ND4	0.7756
HLI-0460	12308	A	G	0	436	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0460	12372	G	A	1	423	synonymous_variant	LOW	ND5	0.1329
HLI-0460	14167	C	T	1	419	synonymous_variant	LOW	ND6	0.0385
HLI-0460	14766	C	T	2	497	missense_variant	MODERATE	CYTB	0.7696

HLI-0460	14798	T	C	1	515	missense_variant	MODERATE	CYTB	0.0651
HLI-0460	15326	A	G	0	442	missense_variant	MODERATE	CYTB	0.9868
HLI-0460	16093	T	C	6	552	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0460	16224	T	C	1	468	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0460	16311	T	C	1	401	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0460	16519	T	C	1	232	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0460	16524	A	G	1	218	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0461	204	T	C	0	307	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0461	239	T	C	1	279	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0461	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0461	750	A	G	1	451	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0461	1438	A	G	2	481	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0461	3915	G	A	1	452	synonymous_variant	LOW	ND1	0.0106
HLI-0461	4727	A	G	5	463	synonymous_variant	LOW	ND2	0.0063
HLI-0461	4769	A	G	3	504	synonymous_variant	LOW	ND2	0.9767
HLI-0461	9380	G	A	1	506	synonymous_variant	LOW	COX3	0.0094
HLI-0461	10589	G	A	0	584	synonymous_variant	LOW	ND4L	0.0355
HLI-0461	12972	A	G	5	449	synonymous_variant	LOW	ND5	0.0012
HLI-0461	15326	A	G	0	328	missense_variant	MODERATE	CYTB	0.9868
HLI-0461	16219	A	G	0	467	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0461	16362	T	C	1	333	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0461	16482	A	G	4	251	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0462	73	A	G	0	180	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0462	152	T	C	2	313	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0462	182	C	T	1	304	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0462	185	G	T	1	291	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0462	189	A	G	1	278	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0462	195	T	C	1	287	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0462	199	T	C	1	296	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0462	247	G	A	0	154	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0462	263	A	G	0	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0462	357	A	G	1	315	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0462	709	G	A	0	428	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0462	710	T	C	0	428	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0462	750	A	G	0	466	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0462	769	G	A	0	480	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0462	825	T	A	0	559	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0462	1018	G	A	0	599	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0462	1738	T	C	2	325	upstream_gene_variant	MODIFIER	RNR2	0.0061

HLI-0462	2352	T	C	2	282	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0462	2706	A	G	2	474	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0462	2758	G	A	1	486	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0462	2768	A	G	1	485	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0462	2885	T	C	0	447	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0462	3308	T	C	0	431	start_lost	HIGH	ND1	0.0073
HLI-0462	3594	C	T	1	366	synonymous_variant	LOW	ND1	0.0789
HLI-0462	3666	G	A	1	420	synonymous_variant	LOW	ND1	0.0233
HLI-0462	3693	G	A	0	419	synonymous_variant	LOW	ND1	0.0091
HLI-0462	4104	A	G	0	326	synonymous_variant	LOW	ND1	0.0785
HLI-0462	4769	A	G	0	432	synonymous_variant	LOW	ND2	0.9767
HLI-0462	5036	A	G	0	345	synonymous_variant	LOW	ND2	0.006
HLI-0462	5046	G	A	0	378	missense_variant	MODERATE	ND2	0.018
HLI-0462	5393	T	C	0	339	synonymous_variant	LOW	ND2	0.0059
HLI-0462	5655	T	C	3	572	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0462	6548	C	T	2	510	synonymous_variant	LOW	COX1	0.0061
HLI-0462	6827	T	C	0	644	synonymous_variant	LOW	COX1	0.0072
HLI-0462	6989	A	G	0	525	synonymous_variant	LOW	COX1	0.0061
HLI-0462	7028	C	T	1	532	synonymous_variant	LOW	COX1	0.8089
HLI-0462	7055	A	G	0	492	synonymous_variant	LOW	COX1	0.0188
HLI-0462	7146	A	G	0	300	missense_variant	MODERATE	COX1	0.0497
HLI-0462	7256	C	T	1	369	synonymous_variant	LOW	COX1	0.0784
HLI-0462	7389	T	C	2	317	missense_variant	MODERATE	COX1	0.0201
HLI-0462	7521	G	A	1	234	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0462	7867	C	T	1	662	synonymous_variant	LOW	COX2	0.0076
HLI-0462	8248	A	G	0	353	synonymous_variant	LOW	COX2	0.0061
HLI-0462	8468	C	T	0	220	synonymous_variant	LOW	ATP8	0.0501
HLI-0462	8655	C	T	3	270	synonymous_variant	LOW	ATP6	0.0511
HLI-0462	8701	A	G	0	278	missense_variant	MODERATE	ATP6	0.3391
HLI-0462	9540	T	C	0	342	synonymous_variant	LOW	COX3	0.339
HLI-0462	10398	A	G	1	484	missense_variant	MODERATE	ND3	0.445
HLI-0462	10688	G	A	0	569	synonymous_variant	LOW	ND4L	0.0515
HLI-0462	10810	T	C	0	354	synonymous_variant	LOW	ND4	0.0522
HLI-0462	10873	T	C	0	393	synonymous_variant	LOW	ND4	0.3389
HLI-0462	11719	G	A	2	513	synonymous_variant	LOW	ND4	0.7756
HLI-0462	12519	T	C	0	345	synonymous_variant	LOW	ND5	0.007
HLI-0462	12705	C	T	0	382	synonymous_variant	LOW	ND5	0.4212
HLI-0462	13105	A	G	2	511	missense_variant	MODERATE	ND5	0.076
HLI-0462	13506	C	T	2	358	synonymous_variant	LOW	ND5	0.0506

HLI-0462	13650	C	T	0	317	synonymous_variant	LOW	ND5	0.079
HLI-0462	13789	T	C	1	242	missense_variant	MODERATE	ND5	0.0185
HLI-0462	13880	C	A	5	323	missense_variant	MODERATE	ND5	0.0055
HLI-0462	14178	T	C	1	362	missense_variant	MODERATE	ND6	0.0225
HLI-0462	14203	A	G	1	392	synonymous_variant	LOW	ND6	0.0061
HLI-0462	14560	G	A	0	525	synonymous_variant	LOW	ND6	0.0235
HLI-0462	14766	C	T	0	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0462	14769	A	G	0	640	missense_variant	MODERATE	CYTB	0.0121
HLI-0462	15077	G	A	2	654	missense_variant	MODERATE	CYTB	0.0021
HLI-0462	15103	C	T	1	693	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0462	15115	T	C	1	663	synonymous_variant	LOW	CYTB	0.0093
HLI-0462	15326	A	G	0	281	missense_variant	MODERATE	CYTB	0.9868
HLI-0462	16126	T	C	2	392	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0462	16223	C	T	1	326	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0462	16264	C	T	3	277	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0462	16270	C	T	3	262	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0462	16278	C	T	3	260	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0462	16293	A	G	3	254	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0462	16311	T	C	3	244	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0462	16355	C	T	2	242	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0462	16519	T	C	0	120	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0463	73	A	G	0	274	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0463	150	C	T	0	511	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0463	195	T	C	0	520	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0463	198	C	T	0	508	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0463	263	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0463	499	G	A	1	356	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0463	750	A	G	1	534	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0463	1438	A	G	1	549	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0463	1713	A	G	1	462	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0463	2352	T	C	0	382	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0463	2706	A	G	0	456	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0463	4769	A	G	0	534	synonymous_variant	LOW	ND2	0.9767
HLI-0463	4823	T	C	0	560	synonymous_variant	LOW	ND2	0.0049
HLI-0463	6413	T	C	0	514	synonymous_variant	LOW	COX1	0.0062
HLI-0463	7028	C	T	2	599	synonymous_variant	LOW	COX1	0.8089
HLI-0463	8701	A	G	0	435	missense_variant	MODERATE	ATP6	0.3391
HLI-0463	9540	T	C	0	535	synonymous_variant	LOW	COX3	0.339
HLI-0463	10398	A	G	2	530	missense_variant	MODERATE	ND3	0.445

HLI-0463	10819	A	G	1	502	synonymous_variant	LOW	ND4	0.0228
HLI-0463	10873	T	C	0	542	synonymous_variant	LOW	ND4	0.3389
HLI-0463	11204	T	C	0	510	missense_variant	MODERATE	ND4	0.003
HLI-0463	11719	G	A	0	530	synonymous_variant	LOW	ND4	0.7756
HLI-0463	12705	C	T	3	426	synonymous_variant	LOW	ND5	0.4212
HLI-0463	13105	A	G	1	513	missense_variant	MODERATE	ND5	0.076
HLI-0463	14212	T	C	0	435	synonymous_variant	LOW	ND6	0.0204
HLI-0463	14766	C	T	3	550	missense_variant	MODERATE	CYTB	0.7696
HLI-0463	14869	G	A	0	699	synonymous_variant	LOW	CYTB	0.0023
HLI-0463	14905	G	A	1	790	synonymous_variant	LOW	CYTB	0.0526
HLI-0463	15301	G	A	3	402	synonymous_variant	LOW	CYTB	0.2912
HLI-0463	15326	A	G	1	431	missense_variant	MODERATE	CYTB	0.9868
HLI-0463	16223	C	T	2	451	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0463	16320	C	T	2	429	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0463	16399	A	G	0	458	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0463	16519	T	C	0	300	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0464	73	A	G	0	29	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0464	103	G	A	0	46	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0464	152	T	C	0	64	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0464	204	T	C	0	59	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0464	263	A	G	0	36	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0464	709	G	A	0	66	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0464	750	A	G	1	58	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0464	1438	A	G	0	40	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0464	1598	G	A	0	53	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0464	2706	A	G	0	50	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0464	3480	A	G	0	46	synonymous_variant	LOW	ND1	0.0392
HLI-0464	3819	C	T	0	50	synonymous_variant	LOW	ND1	0.0012
HLI-0464	4769	A	G	0	50	synonymous_variant	LOW	ND2	0.9767
HLI-0464	5836	A	G	1	68	upstream_gene_variant	MODIFIER	TRNY	0.0018
HLI-0464	7028	C	T	1	78	synonymous_variant	LOW	COX1	0.8089
HLI-0464	7771	A	G	0	51	synonymous_variant	LOW	COX2	0.0223
HLI-0464	8467	C	T	0	42	synonymous_variant	LOW	ATP8	0.001
HLI-0464	8584	G	A	0	49	missense_variant	MODERATE	ATP6	0.0521
HLI-0464	8784	A	G	0	66	synonymous_variant	LOW	ATP6	0.006
HLI-0464	8829	C	T	0	66	synonymous_variant	LOW	ATP6	0.0031
HLI-0464	9950	T	C	0	60	synonymous_variant	LOW	COX3	0.0362
HLI-0464	10274	T	C	0	50	synonymous_variant	LOW	ND3	0.0024
HLI-0464	10398	A	G	0	43	missense_variant	MODERATE	ND3	0.445

HLI-0464	11719	G	A	0	63	synonymous_variant	LOW	ND4	0.7756
HLI-0464	12361	A	G	2	28	missense_variant	MODERATE	ND5	0.0054
HLI-0464	14766	C	T	1	59	missense_variant	MODERATE	CYTB	0.7696
HLI-0464	15223	C	T	1	51	synonymous_variant	LOW	CYTB	0.0034
HLI-0464	15326	A	G	0	60	missense_variant	MODERATE	CYTB	0.9868
HLI-0464	15508	C	T	0	55	synonymous_variant	LOW	CYTB	0.0033
HLI-0464	15662	A	G	0	47	missense_variant	MODERATE	CYTB	0.0038
HLI-0464	15851	A	G	0	55	missense_variant	MODERATE	CYTB	0.0034
HLI-0464	15927	G	A	0	50	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0464	16140	T	C	0	19	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0464	16243	T	C	0	26	upstream_gene_variant	MODIFIER	DLoop	0.021
HLI-0464	16519	T	C	0	37	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0465	73	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0465	185	G	A	6	480	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0465	263	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0465	478	A	G	0	402	upstream_gene_variant	MODIFIER	DLoop	2.00E-04
HLI-0465	709	G	A	1	636	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0465	750	A	G	1	677	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0465	1438	A	G	1	662	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0465	2706	A	G	2	648	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0465	3348	A	G	1	605	synonymous_variant	LOW	ND1	0.0065
HLI-0465	3847	T	C	1	567	synonymous_variant	LOW	ND1	0.0061
HLI-0465	4769	A	G	0	568	synonymous_variant	LOW	ND2	0.9767
HLI-0465	4820	G	A	1	593	synonymous_variant	LOW	ND2	0.0239
HLI-0465	7028	C	T	1	706	synonymous_variant	LOW	COX1	0.8089
HLI-0465	7805	G	A	1	622	missense_variant	MODERATE	COX2	0.0077
HLI-0465	11467	A	G	2	644	synonymous_variant	LOW	ND4	0.1231
HLI-0465	11719	G	A	1	620	synonymous_variant	LOW	ND4	0.7756
HLI-0465	12308	A	G	1	524	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0465	12372	G	A	1	546	synonymous_variant	LOW	ND5	0.1329
HLI-0465	14179	A	G	1	560	synonymous_variant	LOW	ND6	0.0053
HLI-0465	14766	C	T	1	539	missense_variant	MODERATE	CYTB	0.7696
HLI-0465	15326	A	G	0	586	missense_variant	MODERATE	CYTB	0.9868
HLI-0465	15790	C	T	0	607	synonymous_variant	LOW	CYTB	0.0013
HLI-0465	16093	T	C	7	443	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0465	16158	A	G	2	247	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0465	16172	T	C	1	213	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0465	16219	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0465	16278	C	T	1	395	upstream_gene_variant	MODIFIER	DLoop	0.1057

HLI-0466	146	T	C	0	510	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0466	152	T	C	0	523	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0466	195	T	C	1	504	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0466	263	A	G	1	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0466	709	G	A	2	649	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0466	750	A	G	1	711	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0466	1438	A	G	0	657	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0466	4769	A	G	0	572	synonymous_variant	LOW	ND2	0.9767
HLI-0466	8765	C	T	2	582	missense_variant	MODERATE	ATP6	3.00E-04
HLI-0466	13101	A	C	2	623	synonymous_variant	LOW	ND5	0.0055
HLI-0466	13711	G	A	1	492	missense_variant	MODERATE	ND5	0.0011
HLI-0466	15326	A	G	0	526	missense_variant	MODERATE	CYTB	0.9868
HLI-0466	16288	T	C	2	604	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0466	16362	T	C	2	593	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0467	263	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0467	474	T	C	0	36	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0467	750	A	G	0	64	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0467	1438	A	G	0	40	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0467	4386	T	C	0	47	upstream_gene_variant	MODIFIER	TRNQ	0.0033
HLI-0467	4769	A	G	0	51	synonymous_variant	LOW	ND2	0.9767
HLI-0467	7621	T	C	0	73	synonymous_variant	LOW	COX2	6.00E-04
HLI-0467	15326	A	G	0	58	missense_variant	MODERATE	CYTB	0.9868
HLI-0467	16519	T	C	0	24	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0468	73	A	G	0	340	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0468	185	G	A	6	546	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0468	228	G	A	0	411	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0468	263	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0468	295	C	T	0	218	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0468	462	C	T	3	490	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0468	489	T	C	0	579	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0468	750	A	G	0	679	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0468	1438	A	G	0	749	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0468	2706	A	G	0	718	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0468	3010	G	A	1	708	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0468	4216	T	C	1	717	missense_variant	MODERATE	ND1	0.0991
HLI-0468	4769	A	G	0	620	synonymous_variant	LOW	ND2	0.9767
HLI-0468	6464	C	A	3	719	synonymous_variant	LOW	COX1	0.0011
HLI-0468	6554	C	T	3	681	synonymous_variant	LOW	COX1	0.0016
HLI-0468	7028	C	T	0	765	synonymous_variant	LOW	COX1	0.8089

HLI-0468	10398	A	G	4	812	missense_variant	MODERATE	ND3	0.445
HLI-0468	11251	A	G	1	678	synonymous_variant	LOW	ND4	0.0932
HLI-0468	11719	G	A	0	685	synonymous_variant	LOW	ND4	0.7756
HLI-0468	12127	G	A	1	635	synonymous_variant	LOW	ND4	0.0058
HLI-0468	12612	A	G	1	796	synonymous_variant	LOW	ND5	0.0506
HLI-0468	13681	A	G	0	633	missense_variant	MODERATE	ND5	0.0035
HLI-0468	13708	G	A	1	672	missense_variant	MODERATE	ND5	0.0717
HLI-0468	14766	C	T	3	698	missense_variant	MODERATE	CYTB	0.7696
HLI-0468	14798	T	C	1	812	missense_variant	MODERATE	CYTB	0.0651
HLI-0468	15326	A	G	0	605	missense_variant	MODERATE	CYTB	0.9868
HLI-0468	15452	C	A	5	651	missense_variant	MODERATE	CYTB	0.0933
HLI-0468	15697	T	C	0	637	synonymous_variant	LOW	CYTB	0.0011
HLI-0468	16069	C	T	1	726	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0468	16092	T	C	19	758	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0468	16126	T	C	0	765	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0468	16261	C	T	1	658	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0469	151	C	T	0	568	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0469	152	T	C	0	576	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0469	263	A	G	1	277	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0469	750	A	G	0	596	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0469	1438	A	G	1	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0469	1664	G	A	3	530	upstream_gene_variant	MODIFIER	TRNV	0.003
HLI-0469	3010	G	A	0	591	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0469	4769	A	G	0	605	synonymous_variant	LOW	ND2	0.9767
HLI-0469	8488	C	T	0	366	synonymous_variant	LOW	ATP8	0
HLI-0469	15326	A	G	0	458	missense_variant	MODERATE	CYTB	0.9868
HLI-0469	16051	A	G	2	480	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0469	16093	T	C	27	566	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0469	16274	G	A	2	537	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0469	16311	T	C	1	555	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0469	16519	T	C	1	298	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0470	73	A	G	1	314	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0470	146	T	C	0	554	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0470	152	T	C	0	570	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0470	195	T	C	0	545	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0470	263	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0470	285	C	T	1	273	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0470	750	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0470	1393	G	A	3	673	upstream_gene_variant	MODIFIER	RNR1	0.0017

HLI-0470	1438	A	G	0	730	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0470	2387	T	C	0	457	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0470	2706	A	G	0	603	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0470	4769	A	G	0	631	synonymous_variant	LOW	ND2	0.9767
HLI-0470	7028	C	T	7	685	synonymous_variant	LOW	COX1	0.8089
HLI-0470	8395	C	T	1	430	synonymous_variant	LOW	ATP8	0.001
HLI-0470	10885	T	C	2	592	synonymous_variant	LOW	ND4	0.001
HLI-0470	11467	A	G	0	653	synonymous_variant	LOW	ND4	0.1231
HLI-0470	11566	A	G	1	609	synonymous_variant	LOW	ND4	8.00E-04
HLI-0470	11719	G	A	0	571	synonymous_variant	LOW	ND4	0.7756
HLI-0470	12308	A	G	1	457	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0470	12372	G	A	1	453	synonymous_variant	LOW	ND5	0.1329
HLI-0470	12879	T	C	5	584	synonymous_variant	LOW	ND5	0.0058
HLI-0470	13104	A	G	0	591	synonymous_variant	LOW	ND5	0.0057
HLI-0470	14070	A	G	0	474	synonymous_variant	LOW	ND5	0.0038
HLI-0470	14766	C	T	2	604	missense_variant	MODERATE	CYTB	0.7696
HLI-0470	15148	G	A	3	668	synonymous_variant	LOW	CYTB	0.0058
HLI-0470	15172	G	A	5	700	synonymous_variant	LOW	CYTB	0.0075
HLI-0470	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0470	15763	A	G	1	470	synonymous_variant	LOW	CYTB	3.00E-04
HLI-0470	15954	A	C	1	513	upstream_gene_variant	MODIFIER	Unannotated	0.0036
HLI-0470	16249	T	C	1	568	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0470	16311	T	C	0	560	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0470	16327	C	T	0	544	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0470	16519	T	C	0	293	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0471	73	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0471	189	A	G	1	366	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0471	194	C	T	1	367	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0471	195	T	C	1	367	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0471	204	T	C	1	358	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0471	207	G	A	1	358	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0471	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0471	709	G	A	1	654	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0471	750	A	G	0	668	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0471	1243	T	C	1	656	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0471	1438	A	G	1	681	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0471	2706	A	G	0	633	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0471	3505	A	G	0	629	missense_variant	MODERATE	ND1	0.0144
HLI-0471	4769	A	G	1	539	synonymous_variant	LOW	ND2	0.9767

HLI-0471	5046	G	A	1	541	missense_variant	MODERATE	ND2	0.018
HLI-0471	5460	G	A	0	674	missense_variant	MODERATE	ND2	0.0651
HLI-0471	6528	C	T	1	635	synonymous_variant	LOW	COX1	0.0013
HLI-0471	7028	C	T	0	668	synonymous_variant	LOW	COX1	0.8089
HLI-0471	8251	G	A	0	564	synonymous_variant	LOW	COX2	0.058
HLI-0471	8994	G	A	2	583	synonymous_variant	LOW	ATP6	0.0167
HLI-0471	10097	A	G	0	672	synonymous_variant	LOW	ND3	0.0011
HLI-0471	10398	A	G	0	624	missense_variant	MODERATE	ND3	0.445
HLI-0471	11674	C	T	4	592	synonymous_variant	LOW	ND4	0.0116
HLI-0471	11719	G	A	1	656	synonymous_variant	LOW	ND4	0.7756
HLI-0471	11947	A	G	0	583	synonymous_variant	LOW	ND4	0.011
HLI-0471	12414	T	C	4	508	synonymous_variant	LOW	ND5	0.0139
HLI-0471	12705	C	T	1	634	synonymous_variant	LOW	ND5	0.4212
HLI-0471	14766	C	T	1	597	missense_variant	MODERATE	CYTB	0.7696
HLI-0471	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868
HLI-0471	15775	A	G	1	570	synonymous_variant	LOW	CYTB	0.0011
HLI-0471	15884	G	C	0	611	missense_variant	MODERATE	CYTB	0.011
HLI-0471	16223	C	T	3	538	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0471	16292	C	T	1	544	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0471	16362	T	C	1	491	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0471	16519	T	C	0	314	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0472	263	A	G	1	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0472	750	A	G	0	695	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0472	1438	A	G	1	727	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0472	3010	G	A	1	736	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0472	4769	A	G	0	613	synonymous_variant	LOW	ND2	0.9767
HLI-0472	11084	A	G	0	698	missense_variant	MODERATE	ND4	0.004
HLI-0472	15326	A	G	0	661	missense_variant	MODERATE	CYTB	0.9868
HLI-0472	16519	T	C	0	391	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0473	73	A	G	1	241	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0473	151	C	T	0	353	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0473	152	T	C	0	354	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0473	182	C	T	1	317	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0473	186	C	A	1	309	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0473	189	A	C	1	304	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0473	195	T	C	1	297	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0473	204	T	C	1	305	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0473	247	G	A	0	338	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0473	263	A	G	1	162	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0473	297	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0473	750	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0473	769	G	A	0	687	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0473	825	T	A	0	702	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0473	1018	G	A	1	750	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0473	1438	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0473	2706	A	G	1	653	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0473	2758	G	A	1	693	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0473	2885	T	C	0	651	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0473	3594	C	T	0	518	synonymous_variant	LOW	ND1	0.0789
HLI-0473	3666	G	A	0	593	synonymous_variant	LOW	ND1	0.0233
HLI-0473	3796	A	T	0	628	missense_variant	MODERATE	ND1	0.0045
HLI-0473	3843	A	G	0	724	synonymous_variant	LOW	ND1	0.0046
HLI-0473	4104	A	G	0	461	synonymous_variant	LOW	ND1	0.0785
HLI-0473	4464	G	A	0	622	upstream_gene_variant	MODIFIER	TRNM	4.00E-04
HLI-0473	4769	A	G	0	568	synonymous_variant	LOW	ND2	0.9767
HLI-0473	5342	C	T	3	525	synonymous_variant	LOW	ND2	1.00E-04
HLI-0473	5460	G	A	2	588	missense_variant	MODERATE	ND2	0.0651
HLI-0473	5539	A	G	3	690	upstream_gene_variant	MODIFIER	TRNW	2.00E-04
HLI-0473	5951	A	G	0	656	synonymous_variant	LOW	COX1	0.0128
HLI-0473	6071	T	C	0	680	synonymous_variant	LOW	COX1	0.0129
HLI-0473	7028	C	T	1	624	synonymous_variant	LOW	COX1	0.8089
HLI-0473	7055	A	G	2	615	synonymous_variant	LOW	COX1	0.0188
HLI-0473	7146	A	G	1	356	missense_variant	MODERATE	COX1	0.0497
HLI-0473	7256	C	T	1	520	synonymous_variant	LOW	COX1	0.0784
HLI-0473	7257	A	G	1	524	missense_variant	MODERATE	COX1	0.0026
HLI-0473	7389	T	C	1	537	missense_variant	MODERATE	COX1	0.0201
HLI-0473	7521	G	A	0	390	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0473	8027	G	A	2	660	missense_variant	MODERATE	COX2	0.0334
HLI-0473	8400	T	C	0	436	missense_variant	MODERATE	ATP8	4.00E-04
HLI-0473	8468	C	T	0	433	synonymous_variant	LOW	ATP8	0.0501
HLI-0473	8655	C	T	2	438	synonymous_variant	LOW	ATP6	0.0511
HLI-0473	8701	A	G	4	492	missense_variant	MODERATE	ATP6	0.3391
HLI-0473	8832	A	G	1	558	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0473	9072	A	G	0	627	synonymous_variant	LOW	ATP6	0.0124
HLI-0473	9540	T	C	1	609	synonymous_variant	LOW	COX3	0.339
HLI-0473	9965	T	C	0	721	synonymous_variant	LOW	COX3	6.00E-04
HLI-0473	10083	A	G	0	716	missense_variant	MODERATE	ND3	0
HLI-0473	10321	T	C	0	681	missense_variant	MODERATE	ND3	0.0106

HLI-0473	10398	A	G	0	673	missense_variant	MODERATE	ND3	0.445
HLI-0473	10586	G	A	1	652	synonymous_variant	LOW	ND4L	0.0177
HLI-0473	10688	G	A	0	650	synonymous_variant	LOW	ND4L	0.0515
HLI-0473	10810	T	C	0	578	synonymous_variant	LOW	ND4	0.0522
HLI-0473	10873	T	C	0	614	synonymous_variant	LOW	ND4	0.3389
HLI-0473	11719	G	A	0	588	synonymous_variant	LOW	ND4	0.7756
HLI-0473	11899	T	C	2	594	synonymous_variant	LOW	ND4	0.0108
HLI-0473	11914	G	A	1	635	synonymous_variant	LOW	ND4	0.1112
HLI-0473	12705	C	T	0	508	synonymous_variant	LOW	ND5	0.4212
HLI-0473	12810	A	G	5	593	synonymous_variant	LOW	ND5	0.0198
HLI-0473	12936	A	G	0	583	synonymous_variant	LOW	ND5	0
HLI-0473	13105	A	G	1	605	missense_variant	MODERATE	ND5	0.076
HLI-0473	13485	A	G	0	534	synonymous_variant	LOW	ND5	0.0122
HLI-0473	13506	C	T	0	620	synonymous_variant	LOW	ND5	0.0506
HLI-0473	13650	C	T	2	540	synonymous_variant	LOW	ND5	0.079
HLI-0473	13789	T	C	0	379	missense_variant	MODERATE	ND5	0.0185
HLI-0473	14000	T	A	2	479	missense_variant	MODERATE	ND5	0.0126
HLI-0473	14079	A	G	2	454	synonymous_variant	LOW	ND5	0
HLI-0473	14148	A	G	1	495	stop_retained_variant	LOW	ND5	0.0065
HLI-0473	14178	T	C	0	531	missense_variant	MODERATE	ND6	0.0225
HLI-0473	14248	C	T	1	514	synonymous_variant	LOW	ND6	1.00E-04
HLI-0473	14560	G	A	0	711	synonymous_variant	LOW	ND6	0.0235
HLI-0473	14766	C	T	2	708	missense_variant	MODERATE	CYTB	0.7696
HLI-0473	14911	C	T	2	809	synonymous_variant	LOW	CYTB	0.0124
HLI-0473	15326	A	G	1	500	missense_variant	MODERATE	CYTB	0.9868
HLI-0473	15626	C	T	0	416	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0473	16038	A	G	0	474	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0473	16086	T	C	0	599	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0473	16223	C	T	3	532	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0473	16278	C	T	0	396	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0473	16292	C	T	0	421	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0473	16293	A	G	0	426	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0473	16294	C	T	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0473	16360	C	T	1	441	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0473	16519	T	C	0	199	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0474	263	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0474	750	A	G	1	559	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0474	1438	A	G	1	595	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0474	4216	T	C	1	528	missense_variant	MODERATE	ND1	0.0991

HLI-0474	4769	A	G	2	576	synonymous_variant	LOW	ND2	0.9767
HLI-0474	14470	T	A	1	474	synonymous_variant	LOW	ND6	0.0031
HLI-0474	15326	A	G	1	482	missense_variant	MODERATE	CYTB	0.9868
HLI-0474	16114	C	T	6	444	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0474	16519	T	C	1	266	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0475	239	T	C	0	294	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0475	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0475	750	A	G	1	592	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0475	1438	A	G	0	526	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0475	3915	G	A	0	479	synonymous_variant	LOW	ND1	0.0106
HLI-0475	4727	A	G	2	583	synonymous_variant	LOW	ND2	0.0063
HLI-0475	4769	A	G	0	628	synonymous_variant	LOW	ND2	0.9767
HLI-0475	9380	G	A	0	609	synonymous_variant	LOW	COX3	0.0094
HLI-0475	11253	T	C	0	538	missense_variant	MODERATE	ND4	0.0053
HLI-0475	15326	A	G	0	483	missense_variant	MODERATE	CYTB	0.9868
HLI-0475	16362	T	C	0	455	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0475	16482	A	G	0	316	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0476	73	A	G	0	294	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0476	150	C	T	0	532	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0476	195	T	C	0	523	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0476	263	A	G	0	241	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0476	497	C	T	1	490	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0476	750	A	G	1	554	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0476	1189	T	C	0	638	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0476	1438	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0476	1811	A	G	0	636	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0476	2706	A	G	1	571	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0476	3480	A	G	1	503	synonymous_variant	LOW	ND1	0.0392
HLI-0476	4769	A	G	1	585	synonymous_variant	LOW	ND2	0.9767
HLI-0476	5964	T	C	5	622	synonymous_variant	LOW	COX1	0.0033
HLI-0476	7028	C	T	1	645	synonymous_variant	LOW	COX1	0.8089
HLI-0476	9055	G	A	0	559	missense_variant	MODERATE	ATP6	0.0425
HLI-0476	9698	T	C	0	571	synonymous_variant	LOW	COX3	0.0405
HLI-0476	10398	A	G	0	568	missense_variant	MODERATE	ND3	0.445
HLI-0476	10550	A	G	2	565	synonymous_variant	LOW	ND4L	0.0376
HLI-0476	11299	T	C	0	582	synonymous_variant	LOW	ND4	0.0417
HLI-0476	11467	A	G	0	633	synonymous_variant	LOW	ND4	0.1231
HLI-0476	11719	G	A	2	601	synonymous_variant	LOW	ND4	0.7756
HLI-0476	12308	A	G	3	651	upstream_gene_variant	MODIFIER	TRNL2	0.1227

HLI-0476	12372	G	A	1	631	synonymous_variant	LOW	ND5	0.1329
HLI-0476	14167	C	T	2	516	synonymous_variant	LOW	ND6	0.0385
HLI-0476	14766	C	T	3	646	missense_variant	MODERATE	CYTB	0.7696
HLI-0476	14798	T	C	0	690	missense_variant	MODERATE	CYTB	0.0651
HLI-0476	15326	A	G	1	448	missense_variant	MODERATE	CYTB	0.9868
HLI-0476	15625	C	A	1	533	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0476	15791	A	G	1	560	missense_variant	MODERATE	CYTB	4.00E-04
HLI-0476	16145	G	A	0	575	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0476	16224	T	C	0	536	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0476	16311	T	C	0	482	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0476	16519	T	C	0	239	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0477	73	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0477	185	G	A	0	418	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0477	189	A	G	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0477	204	T	C	0	437	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0477	263	A	G	0	174	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0477	750	A	G	0	542	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0477	1438	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0477	1700	T	C	2	508	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0477	2706	A	G	1	581	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0477	3197	T	C	0	581	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0477	4769	A	G	1	557	synonymous_variant	LOW	ND2	0.9767
HLI-0477	5495	T	C	1	546	synonymous_variant	LOW	ND2	0.0051
HLI-0477	7028	C	T	4	649	synonymous_variant	LOW	COX1	0.8089
HLI-0477	9477	G	A	0	638	missense_variant	MODERATE	COX3	0.0387
HLI-0477	11467	A	G	1	582	synonymous_variant	LOW	ND4	0.1231
HLI-0477	11719	G	A	0	556	synonymous_variant	LOW	ND4	0.7756
HLI-0477	12308	A	G	1	371	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0477	12372	G	A	1	378	synonymous_variant	LOW	ND5	0.1329
HLI-0477	13617	T	C	1	517	synonymous_variant	LOW	ND5	0.038
HLI-0477	14766	C	T	5	595	missense_variant	MODERATE	CYTB	0.7696
HLI-0477	14793	A	G	0	659	missense_variant	MODERATE	CYTB	0.0199
HLI-0477	15218	A	G	0	505	missense_variant	MODERATE	CYTB	0.0169
HLI-0477	15326	A	G	0	453	missense_variant	MODERATE	CYTB	0.9868
HLI-0477	15924	A	G	0	394	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0477	16256	C	T	0	521	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0477	16270	C	T	0	541	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0477	16362	T	C	0	420	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0477	16399	A	G	0	449	upstream_gene_variant	MODIFIER	DLoop	0.0265

HLI-0478	73	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0478	185	G	A	2	447	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0478	263	A	G	1	180	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0478	295	C	T	0	201	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0478	462	C	T	1	446	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0478	489	T	C	0	500	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0478	750	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0478	1438	A	G	0	572	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0478	2706	A	G	1	570	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0478	3010	G	A	1	576	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0478	4216	T	C	0	515	missense_variant	MODERATE	ND1	0.0991
HLI-0478	4769	A	G	1	558	synonymous_variant	LOW	ND2	0.9767
HLI-0478	7028	C	T	3	614	synonymous_variant	LOW	COX1	0.8089
HLI-0478	10398	A	G	0	555	missense_variant	MODERATE	ND3	0.445
HLI-0478	10497	C	T	0	577	synonymous_variant	LOW	ND4L	0.0019
HLI-0478	11251	A	G	0	603	synonymous_variant	LOW	ND4	0.0932
HLI-0478	11719	G	A	0	579	synonymous_variant	LOW	ND4	0.7756
HLI-0478	12612	A	G	7	546	synonymous_variant	LOW	ND5	0.0506
HLI-0478	13708	G	A	0	462	missense_variant	MODERATE	ND5	0.0717
HLI-0478	13934	C	T	0	491	missense_variant	MODERATE	ND5	0.0122
HLI-0478	14766	C	T	0	597	missense_variant	MODERATE	CYTB	0.7696
HLI-0478	14798	T	C	0	667	missense_variant	MODERATE	CYTB	0.0651
HLI-0478	15326	A	G	0	486	missense_variant	MODERATE	CYTB	0.9868
HLI-0478	15452	C	A	5	521	missense_variant	MODERATE	CYTB	0.0933
HLI-0478	16069	C	T	1	497	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0478	16126	T	C	0	518	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0479	263	A	G	1	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0479	477	T	C	2	468	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0479	721	T	A	0	649	upstream_gene_variant	MODIFIER	RNR1	0
HLI-0479	750	A	G	0	677	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0479	1438	A	G	0	571	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0479	3010	G	A	0	564	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0479	4769	A	G	0	592	synonymous_variant	LOW	ND2	0.9767
HLI-0479	10679	A	G	0	581	synonymous_variant	LOW	ND4L	0.0017
HLI-0479	15326	A	G	0	596	missense_variant	MODERATE	CYTB	0.9868
HLI-0479	16519	T	C	2	253	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0480	73	A	G	0	316	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0480	150	C	T	1	583	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0480	263	A	G	0	251	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0480	295	C	T	0	187	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0480	489	T	C	0	428	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0480	750	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0480	1438	A	G	0	656	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0480	2706	A	G	0	616	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0480	4216	T	C	0	615	missense_variant	MODERATE	ND1	0.0991
HLI-0480	4769	A	G	1	559	synonymous_variant	LOW	ND2	0.9767
HLI-0480	5633	C	T	0	648	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0480	7028	C	T	1	695	synonymous_variant	LOW	COX1	0.8089
HLI-0480	7476	C	T	0	633	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0480	9016	A	G	1	656	missense_variant	MODERATE	ATP6	3.00E-04
HLI-0480	10172	G	A	0	651	synonymous_variant	LOW	ND3	0.0084
HLI-0480	10398	A	G	1	690	missense_variant	MODERATE	ND3	0.445
HLI-0480	11251	A	G	1	600	synonymous_variant	LOW	ND4	0.0932
HLI-0480	11719	G	A	1	605	synonymous_variant	LOW	ND4	0.7756
HLI-0480	12612	A	G	3	598	synonymous_variant	LOW	ND5	0.0506
HLI-0480	13708	G	A	1	593	missense_variant	MODERATE	ND5	0.0717
HLI-0480	14766	C	T	1	603	missense_variant	MODERATE	CYTB	0.7696
HLI-0480	15257	G	A	1	549	missense_variant	MODERATE	CYTB	0.0155
HLI-0480	15326	A	G	0	577	missense_variant	MODERATE	CYTB	0.9868
HLI-0480	15452	C	A	7	577	missense_variant	MODERATE	CYTB	0.0933
HLI-0480	15662	A	G	0	534	missense_variant	MODERATE	CYTB	0.0038
HLI-0480	15812	G	A	0	687	missense_variant	MODERATE	CYTB	0.0096
HLI-0480	16069	C	T	5	604	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0480	16126	T	C	0	659	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0480	16278	C	T	0	563	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0480	16519	T	C	0	295	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0481	151	C	T	2	465	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0481	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0481	750	A	G	0	523	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0481	990	T	C	2	615	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0481	1438	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0481	3010	G	A	0	537	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0481	4769	A	G	0	556	synonymous_variant	LOW	ND2	0.9767
HLI-0481	8251	G	A	0	528	synonymous_variant	LOW	COX2	0.058
HLI-0481	15326	A	G	0	417	missense_variant	MODERATE	CYTB	0.9868
HLI-0481	16080	A	G	2	534	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0481	16223	C	T	3	294	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0481	16356	T	C	0	416	upstream_gene_variant	MODIFIER	DLoop	0.024

HLI-0481	16519	T	C	1	190	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0482	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0482	150	C	T	0	509	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0482	263	A	G	0	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0482	750	A	G	0	475	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0482	1438	A	G	0	478	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0482	1721	C	T	0	456	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0482	2706	A	G	2	472	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0482	3197	T	C	2	531	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0482	3212	C	T	1	569	upstream_gene_variant	MODIFIER	RNR2	0.0012
HLI-0482	4732	A	G	6	544	missense_variant	MODERATE	ND2	0.0059
HLI-0482	4769	A	G	4	599	synonymous_variant	LOW	ND2	0.9767
HLI-0482	7028	C	T	3	614	synonymous_variant	LOW	COX1	0.8089
HLI-0482	7768	A	G	3	469	synonymous_variant	LOW	COX2	0.0186
HLI-0482	9477	G	A	0	499	missense_variant	MODERATE	COX3	0.0387
HLI-0482	9682	T	C	0	508	missense_variant	MODERATE	COX3	0.0012
HLI-0482	11467	A	G	0	572	synonymous_variant	LOW	ND4	0.1231
HLI-0482	11719	G	A	0	476	synonymous_variant	LOW	ND4	0.7756
HLI-0482	12136	T	C	1	518	synonymous_variant	LOW	ND4	0.0016
HLI-0482	12308	A	G	0	557	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0482	12372	G	A	0	563	synonymous_variant	LOW	ND5	0.1329
HLI-0482	13617	T	C	1	479	synonymous_variant	LOW	ND5	0.038
HLI-0482	13637	A	G	1	513	missense_variant	MODERATE	ND5	0.0074
HLI-0482	14182	T	C	2	494	synonymous_variant	LOW	ND6	0.0254
HLI-0482	14766	C	T	3	517	missense_variant	MODERATE	CYTB	0.7696
HLI-0482	15326	A	G	1	363	missense_variant	MODERATE	CYTB	0.9868
HLI-0482	16270	C	T	1	540	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0482	16398	G	A	0	482	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0483	73	A	G	2	256	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0483	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0483	709	G	A	0	459	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0483	750	A	G	3	503	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0483	1438	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0483	1888	G	A	2	352	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0483	2706	A	G	0	541	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0483	2850	T	C	1	504	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0483	4216	T	C	0	402	missense_variant	MODERATE	ND1	0.0991
HLI-0483	4769	A	G	1	546	synonymous_variant	LOW	ND2	0.9767
HLI-0483	4917	A	G	0	529	missense_variant	MODERATE	ND2	0.0477

HLI-0483	4931	C	T	0	581	synonymous_variant	LOW	ND2	1.00E-04
HLI-0483	7022	T	C	5	607	synonymous_variant	LOW	COX1	0.0024
HLI-0483	7028	C	T	5	630	synonymous_variant	LOW	COX1	0.8089
HLI-0483	8697	G	A	1	539	synonymous_variant	LOW	ATP6	0.0466
HLI-0483	10463	T	C	3	484	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0483	11251	A	G	1	525	synonymous_variant	LOW	ND4	0.0932
HLI-0483	11719	G	A	5	529	synonymous_variant	LOW	ND4	0.7756
HLI-0483	11812	A	G	2	468	synonymous_variant	LOW	ND4	0.0332
HLI-0483	13368	G	A	0	548	synonymous_variant	LOW	ND5	0.0495
HLI-0483	13965	T	C	1	366	synonymous_variant	LOW	ND5	0.005
HLI-0483	14233	A	G	2	495	synonymous_variant	LOW	ND6	0.0369
HLI-0483	14687	A	G	1	665	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0483	14766	C	T	1	702	missense_variant	MODERATE	CYTB	0.7696
HLI-0483	14905	G	A	1	738	synonymous_variant	LOW	CYTB	0.0526
HLI-0483	15326	A	G	0	330	missense_variant	MODERATE	CYTB	0.9868
HLI-0483	15452	C	A	3	297	missense_variant	MODERATE	CYTB	0.0933
HLI-0483	15607	A	G	3	307	synonymous_variant	LOW	CYTB	0.0508
HLI-0483	15928	G	A	3	464	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0483	16126	T	C	2	485	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0483	16294	C	T	1	462	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0483	16519	T	C	0	186	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0484	263	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0484	456	C	T	3	470	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0484	750	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0484	1438	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0484	3277	G	A	1	578	upstream_gene_variant	MODIFIER	TRNL1	7.00E-04
HLI-0484	4769	A	G	1	563	synonymous_variant	LOW	ND2	0.9767
HLI-0484	8975	T	C	1	627	missense_variant	MODERATE	ATP6	2.00E-04
HLI-0484	15326	A	G	0	503	missense_variant	MODERATE	CYTB	0.9868
HLI-0484	16114	C	T	4	571	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0484	16304	T	C	0	499	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0485	263	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0485	456	C	T	10	422	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0485	750	A	G	1	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0485	1438	A	G	0	637	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0485	3397	A	G	2	555	missense_variant	MODERATE	ND1	0.0029
HLI-0485	4336	T	C	2	471	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0485	4769	A	G	2	595	synonymous_variant	LOW	ND2	0.9767
HLI-0485	8727	C	A	4	424	synonymous_variant	LOW	ATP6	0

HLI-0485	15326	A	G	0	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0485	15833	C	T	1	439	synonymous_variant	LOW	CYTB	0.0051
HLI-0485	16209	T	C	1	598	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0485	16304	T	C	0	507	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0485	16519	T	C	0	281	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0486	73	A	G	1	302	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0486	263	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0486	750	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0486	1438	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0486	3010	G	A	1	662	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0486	4769	A	G	1	647	synonymous_variant	LOW	ND2	0.9767
HLI-0486	6365	T	C	0	669	synonymous_variant	LOW	COX1	0.0026
HLI-0486	14287	T	C	53	478	synonymous_variant	LOW	ND6	6.00E-04
HLI-0486	15326	A	G	0	497	missense_variant	MODERATE	CYTB	0.9868
HLI-0486	16162	A	G	0	716	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0486	16209	T	C	1	713	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0486	16519	T	C	0	290	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0488	73	A	G	0	316	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0488	185	G	A	9	554	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0488	228	G	A	4	477	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0488	263	A	G	0	402	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0488	295	C	T	1	316	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0488	462	C	T	3	530	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0488	489	T	C	1	554	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0488	750	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0488	1438	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0488	2706	A	G	0	617	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0488	3010	G	A	0	570	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0488	4216	T	C	0	457	missense_variant	MODERATE	ND1	0.0991
HLI-0488	4769	A	G	1	601	synonymous_variant	LOW	ND2	0.9767
HLI-0488	6261	G	A	9	622	missense_variant	MODERATE	COX1	0.007
HLI-0488	6480	G	A	6	599	missense_variant	MODERATE	COX1	0.0031
HLI-0488	7028	C	T	1	709	synonymous_variant	LOW	COX1	0.8089
HLI-0488	9181	A	G	0	687	missense_variant	MODERATE	ATP6	0.0018
HLI-0488	10398	A	G	0	673	missense_variant	MODERATE	ND3	0.445
HLI-0488	11251	A	G	0	604	synonymous_variant	LOW	ND4	0.0932
HLI-0488	11719	G	A	1	601	synonymous_variant	LOW	ND4	0.7756
HLI-0488	12612	A	G	7	541	synonymous_variant	LOW	ND5	0.0506
HLI-0488	12903	T	C	14	616	synonymous_variant	LOW	ND5	5.00E-04

HLI-0488	13708	G	A	0	509	missense_variant	MODERATE	ND5	0.0717
HLI-0488	13934	C	T	1	368	missense_variant	MODERATE	ND5	0.0122
HLI-0488	14766	C	T	2	722	missense_variant	MODERATE	CYTB	0.7696
HLI-0488	14798	T	C	0	813	missense_variant	MODERATE	CYTB	0.0651
HLI-0488	15326	A	G	0	423	missense_variant	MODERATE	CYTB	0.9868
HLI-0488	15452	C	A	4	369	missense_variant	MODERATE	CYTB	0.0933
HLI-0488	16069	C	T	3	414	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0488	16126	T	C	2	514	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0488	16278	C	T	3	488	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0488	16519	T	C	4	334	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0489	73	A	G	1	347	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0489	152	T	C	0	641	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0489	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0489	384	A	G	0	408	upstream_gene_variant	MODIFIER	DLoop	3.00E-04
HLI-0489	709	G	A	1	779	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0489	750	A	G	1	821	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0489	1438	A	G	0	748	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0489	1888	G	A	0	629	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0489	2706	A	G	0	745	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0489	4216	T	C	1	696	missense_variant	MODERATE	ND1	0.0991
HLI-0489	4769	A	G	1	695	synonymous_variant	LOW	ND2	0.9767
HLI-0489	4917	A	G	0	648	missense_variant	MODERATE	ND2	0.0477
HLI-0489	4959	G	A	0	702	missense_variant	MODERATE	ND2	0.0012
HLI-0489	5558	A	G	1	700	upstream_gene_variant	MODIFIER	TRNW	0.0021
HLI-0489	7028	C	T	7	800	synonymous_variant	LOW	COX1	0.8089
HLI-0489	7853	G	A	0	766	missense_variant	MODERATE	COX2	0.0197
HLI-0489	8697	G	A	1	604	synonymous_variant	LOW	ATP6	0.0466
HLI-0489	9300	G	A	2	661	missense_variant	MODERATE	COX3	0.0036
HLI-0489	10463	T	C	0	683	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0489	11251	A	G	0	667	synonymous_variant	LOW	ND4	0.0932
HLI-0489	11719	G	A	0	679	synonymous_variant	LOW	ND4	0.7756
HLI-0489	12633	C	A	1	730	synonymous_variant	LOW	ND5	0.0123
HLI-0489	13368	G	A	1	712	synonymous_variant	LOW	ND5	0.0495
HLI-0489	14544	G	A	1	618	synonymous_variant	LOW	ND6	0.0024
HLI-0489	14766	C	T	3	679	missense_variant	MODERATE	CYTB	0.7696
HLI-0489	14905	G	A	0	724	synonymous_variant	LOW	CYTB	0.0526
HLI-0489	15326	A	G	0	665	missense_variant	MODERATE	CYTB	0.9868
HLI-0489	15344	T	C	1	728	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0489	15452	C	A	3	626	missense_variant	MODERATE	CYTB	0.0933

HLI-0489	15607	A	G	1	688	synonymous_variant	LOW	CYTB	0.0508
HLI-0489	15928	G	A	1	687	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0489	16126	T	C	0	638	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0489	16163	A	G	0	655	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0489	16261	C	T	0	605	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0489	16270	C	T	0	592	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0489	16294	C	T	0	577	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0489	16519	T	C	1	328	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0490	73	A	G	0	357	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0490	263	A	G	0	279	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0490	750	A	G	0	719	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0490	1438	A	G	0	719	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0490	3992	C	T	2	644	missense_variant	MODERATE	ND1	0.0062
HLI-0490	4024	A	G	3	697	missense_variant	MODERATE	ND1	0.0049
HLI-0490	4769	A	G	0	646	synonymous_variant	LOW	ND2	0.9767
HLI-0490	5004	T	C	0	679	synonymous_variant	LOW	ND2	0.0067
HLI-0490	8269	G	A	2	657	stop_retained_variant	LOW	COX2	0.0127
HLI-0490	9123	G	A	0	718	synonymous_variant	LOW	ATP6	0.0485
HLI-0490	9286	T	C	1	680	missense_variant	MODERATE	COX3	3.00E-04
HLI-0490	10044	A	G	2	793	upstream_gene_variant	MODIFIER	TRNG	0.0027
HLI-0490	14365	C	T	0	591	synonymous_variant	LOW	ND6	0.0046
HLI-0490	14582	A	G	2	688	missense_variant	MODERATE	ND6	0.005
HLI-0490	15326	A	G	0	715	missense_variant	MODERATE	CYTB	0.9868
HLI-0491	73	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0491	263	A	G	0	266	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0491	709	G	A	1	678	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0491	750	A	G	0	712	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0491	930	G	A	1	707	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0491	1438	A	G	0	699	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0491	1888	G	A	0	558	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0491	2706	A	G	0	621	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0491	4216	T	C	2	590	missense_variant	MODERATE	ND1	0.0991
HLI-0491	4769	A	G	0	591	synonymous_variant	LOW	ND2	0.9767
HLI-0491	4917	A	G	5	660	missense_variant	MODERATE	ND2	0.0477
HLI-0491	5147	G	A	1	473	synonymous_variant	LOW	ND2	0.0437
HLI-0491	7028	C	T	0	694	synonymous_variant	LOW	COX1	0.8089
HLI-0491	8382	C	T	1	551	missense_variant	MODERATE	ATP8	1.00E-04
HLI-0491	8697	G	A	1	647	synonymous_variant	LOW	ATP6	0.0466
HLI-0491	9254	A	G	1	632	synonymous_variant	LOW	COX3	0.0083

HLI-0491	10463	T	C	1	696	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0491	11251	A	G	0	647	synonymous_variant	LOW	ND4	0.0932
HLI-0491	11719	G	A	0	592	synonymous_variant	LOW	ND4	0.7756
HLI-0491	11812	A	G	0	620	synonymous_variant	LOW	ND4	0.0332
HLI-0491	13368	G	A	0	676	synonymous_variant	LOW	ND5	0.0495
HLI-0491	13392	T	C	0	697	synonymous_variant	LOW	ND5	0.0014
HLI-0491	14233	A	G	0	588	synonymous_variant	LOW	ND6	0.0369
HLI-0491	14766	C	T	4	636	missense_variant	MODERATE	CYTB	0.7696
HLI-0491	14905	G	A	0	791	synonymous_variant	LOW	CYTB	0.0526
HLI-0491	15326	A	G	0	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0491	15452	C	A	2	491	missense_variant	MODERATE	CYTB	0.0933
HLI-0491	15607	A	G	0	497	synonymous_variant	LOW	CYTB	0.0508
HLI-0491	15928	G	A	0	626	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0491	16126	T	C	0	693	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0491	16172	T	C	0	730	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0491	16294	C	T	0	566	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0491	16304	T	C	0	596	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0491	16519	T	C	0	305	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0492	152	T	C	3	641	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0492	200	A	G	15	574	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0492	263	A	G	0	177	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0492	750	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0492	1438	A	G	0	732	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0492	4769	A	G	2	692	synonymous_variant	LOW	ND2	0.9767
HLI-0492	12952	G	A	2	653	missense_variant	MODERATE	ND5	5.00E-04
HLI-0492	15326	A	G	0	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0492	16519	T	C	2	345	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0493	152	T	C	0	562	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0493	199	T	C	3	573	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0493	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0493	750	A	G	0	634	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0493	1438	A	G	1	664	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0493	3010	G	A	0	722	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0493	4769	A	G	1	649	synonymous_variant	LOW	ND2	0.9767
HLI-0493	11864	T	C	2	689	synonymous_variant	LOW	ND4	0.0013
HLI-0493	15326	A	G	1	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0493	16129	G	A	1	558	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0493	16519	T	C	1	276	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0494	73	A	G	1	258	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0494	119	T	C	4	395	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0494	189	A	G	0	321	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0494	195	T	C	0	320	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0494	204	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0494	207	G	A	0	320	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0494	263	A	G	0	218	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0494	709	G	A	0	589	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0494	750	A	G	1	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0494	1243	T	C	0	646	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0494	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0494	2706	A	G	0	493	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0494	3505	A	G	1	564	missense_variant	MODERATE	ND1	0.0144
HLI-0494	4769	A	G	2	583	synonymous_variant	LOW	ND2	0.9767
HLI-0494	5046	G	A	0	491	missense_variant	MODERATE	ND2	0.018
HLI-0494	5460	G	A	2	629	missense_variant	MODERATE	ND2	0.0651
HLI-0494	7028	C	T	1	592	synonymous_variant	LOW	COX1	0.8089
HLI-0494	7864	C	T	0	685	synonymous_variant	LOW	COX2	0.0041
HLI-0494	8251	G	A	2	593	synonymous_variant	LOW	COX2	0.058
HLI-0494	8994	G	A	2	573	synonymous_variant	LOW	ATP6	0.0167
HLI-0494	11674	C	T	0	538	synonymous_variant	LOW	ND4	0.0116
HLI-0494	11719	G	A	0	634	synonymous_variant	LOW	ND4	0.7756
HLI-0494	11947	A	G	0	598	synonymous_variant	LOW	ND4	0.011
HLI-0494	12414	T	C	0	589	synonymous_variant	LOW	ND5	0.0139
HLI-0494	12705	C	T	0	600	synonymous_variant	LOW	ND5	0.4212
HLI-0494	14766	C	T	2	601	missense_variant	MODERATE	CYTB	0.7696
HLI-0494	15326	A	G	0	436	missense_variant	MODERATE	CYTB	0.9868
HLI-0494	15884	G	C	0	668	missense_variant	MODERATE	CYTB	0.011
HLI-0494	16223	C	T	1	590	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0494	16292	C	T	1	517	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0494	16519	T	C	1	250	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0495	73	A	G	2	299	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0495	263	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0495	750	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0495	1438	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0495	3010	G	A	1	629	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0495	4769	A	G	0	614	synonymous_variant	LOW	ND2	0.9767
HLI-0495	15326	A	G	1	473	missense_variant	MODERATE	CYTB	0.9868
HLI-0495	16162	A	G	1	646	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0495	16519	T	C	1	321	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0496	239	T	C	0	384	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0496	263	A	G	0	294	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0496	750	A	G	1	670	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0496	1438	A	G	0	727	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0496	3391	G	A	1	643	missense_variant	MODERATE	ND1	0.001
HLI-0496	3915	G	A	0	666	synonymous_variant	LOW	ND1	0.0106
HLI-0496	4727	A	G	1	720	synonymous_variant	LOW	ND2	0.0063
HLI-0496	4769	A	G	0	746	synonymous_variant	LOW	ND2	0.9767
HLI-0496	9380	G	A	1	757	synonymous_variant	LOW	COX3	0.0094
HLI-0496	11253	T	C	0	613	missense_variant	MODERATE	ND4	0.0053
HLI-0496	14527	A	G	0	677	synonymous_variant	LOW	ND6	0.0039
HLI-0496	15326	A	G	1	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0496	16362	T	C	0	537	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0496	16482	A	G	4	398	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0496	16526	G	A	2	362	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0497	64	C	T	2	249	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0497	93	A	G	0	359	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0497	185	G	A	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0497	189	A	G	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0497	200	A	G	0	416	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0497	236	T	C	0	367	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0497	247	G	A	0	345	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0497	263	A	G	0	291	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0497	750	A	G	0	643	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0497	769	G	A	0	701	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0497	825	T	A	0	708	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0497	1018	G	A	0	741	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0497	1048	C	T	1	804	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0497	1438	A	G	1	706	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0497	2245	A	C	1	561	upstream_gene_variant	MODIFIER	RNR2	8.00E-04
HLI-0497	2706	A	G	0	674	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0497	2758	G	A	2	724	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0497	2885	T	C	0	690	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0497	3516	C	A	4	554	synonymous_variant	LOW	ND1	0.0315
HLI-0497	3594	C	T	0	603	synonymous_variant	LOW	ND1	0.0789
HLI-0497	3866	T	C	3	638	missense_variant	MODERATE	ND1	0.0029
HLI-0497	4104	A	G	1	489	synonymous_variant	LOW	ND1	0.0785
HLI-0497	4312	C	T	2	537	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0497	4586	T	C	4	669	synonymous_variant	LOW	ND2	0.018

HLI-0497	4769	A	G	1	658	synonymous_variant	LOW	ND2	0.9767
HLI-0497	5096	T	C	1	533	synonymous_variant	LOW	ND2	0.0063
HLI-0497	5231	G	A	0	577	synonymous_variant	LOW	ND2	0.0232
HLI-0497	5442	T	C	0	655	missense_variant	MODERATE	ND2	0.0493
HLI-0497	5460	G	A	0	732	missense_variant	MODERATE	ND2	0.0651
HLI-0497	5603	C	T	2	723	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0497	6185	T	C	0	694	synonymous_variant	LOW	COX1	0.0325
HLI-0497	7028	C	T	5	654	synonymous_variant	LOW	COX1	0.8089
HLI-0497	7146	A	G	1	359	missense_variant	MODERATE	COX1	0.0497
HLI-0497	7256	C	T	2	534	synonymous_variant	LOW	COX1	0.0784
HLI-0497	7521	G	A	2	470	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0497	8428	C	T	2	495	synonymous_variant	LOW	ATP8	0.0144
HLI-0497	8468	C	T	5	520	synonymous_variant	LOW	ATP8	0.0501
HLI-0497	8566	A	G	1	512	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0497	8655	C	T	1	571	synonymous_variant	LOW	ATP6	0.0511
HLI-0497	8701	A	G	1	629	missense_variant	MODERATE	ATP6	0.3391
HLI-0497	9042	C	T	0	608	synonymous_variant	LOW	ATP6	0.0316
HLI-0497	9347	A	G	1	663	synonymous_variant	LOW	COX3	0.0314
HLI-0497	9540	T	C	1	593	synonymous_variant	LOW	COX3	0.339
HLI-0497	9755	G	A	0	688	synonymous_variant	LOW	COX3	0.0303
HLI-0497	9818	C	T	1	867	synonymous_variant	LOW	COX3	0.0179
HLI-0497	10398	A	G	1	662	missense_variant	MODERATE	ND3	0.445
HLI-0497	10589	G	A	0	676	synonymous_variant	LOW	ND4L	0.0355
HLI-0497	10664	C	T	1	744	synonymous_variant	LOW	ND4L	0.0315
HLI-0497	10688	G	A	0	711	synonymous_variant	LOW	ND4L	0.0515
HLI-0497	10810	T	C	0	576	synonymous_variant	LOW	ND4	0.0522
HLI-0497	10873	T	C	0	573	synonymous_variant	LOW	ND4	0.3389
HLI-0497	10915	T	C	0	549	synonymous_variant	LOW	ND4	0.0411
HLI-0497	11176	G	A	0	579	synonymous_variant	LOW	ND4	0.0181
HLI-0497	11641	A	G	4	682	synonymous_variant	LOW	ND4	0.0158
HLI-0497	11719	G	A	3	704	synonymous_variant	LOW	ND4	0.7756
HLI-0497	11914	G	A	0	667	synonymous_variant	LOW	ND4	0.1112
HLI-0497	12007	G	A	1	583	synonymous_variant	LOW	ND4	0.0639
HLI-0497	12705	C	T	2	575	synonymous_variant	LOW	ND5	0.4212
HLI-0497	12720	A	G	2	632	synonymous_variant	LOW	ND5	0.0302
HLI-0497	13105	A	G	0	625	missense_variant	MODERATE	ND5	0.076
HLI-0497	13276	A	G	0	726	missense_variant	MODERATE	ND5	0.0312
HLI-0497	13506	C	T	1	592	synonymous_variant	LOW	ND5	0.0506
HLI-0497	13650	C	T	2	565	synonymous_variant	LOW	ND5	0.079

HLI-0497	14308	T	C	2	578	synonymous_variant	LOW	ND6	0.0209
HLI-0497	14410	G	A	2	612	synonymous_variant	LOW	ND6	9.00E-04
HLI-0497	14766	C	T	4	653	missense_variant	MODERATE	CYTB	0.7696
HLI-0497	15136	C	T	1	677	synonymous_variant	LOW	CYTB	0.0153
HLI-0497	15326	A	G	0	537	missense_variant	MODERATE	CYTB	0.9868
HLI-0497	15431	G	A	1	519	missense_variant	MODERATE	CYTB	0.0182
HLI-0497	16129	G	A	0	574	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0497	16148	C	T	0	606	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0497	16168	C	T	0	567	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0497	16172	T	C	0	560	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0497	16223	C	T	0	554	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0497	16230	A	G	0	557	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0497	16311	T	C	0	537	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0497	16320	C	T	1	552	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0497	16519	T	C	2	221	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0498	73	A	G	0	291	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0498	263	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0498	489	T	C	0	367	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0498	750	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0498	789	T	C	0	632	upstream_gene_variant	MODIFIER	RNR1	0.0016
HLI-0498	1438	A	G	1	626	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0498	2706	A	G	1	586	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0498	4769	A	G	2	582	synonymous_variant	LOW	ND2	0.9767
HLI-0498	6755	G	A	4	707	synonymous_variant	LOW	COX1	0.0065
HLI-0498	7028	C	T	3	678	synonymous_variant	LOW	COX1	0.8089
HLI-0498	7599	C	T	0	544	missense_variant	MODERATE	COX2	0
HLI-0498	8701	A	G	0	490	missense_variant	MODERATE	ATP6	0.3391
HLI-0498	8925	A	G	1	647	synonymous_variant	LOW	ATP6	7.00E-04
HLI-0498	9540	T	C	0	548	synonymous_variant	LOW	COX3	0.339
HLI-0498	10398	A	G	1	591	missense_variant	MODERATE	ND3	0.445
HLI-0498	10400	C	T	1	596	synonymous_variant	LOW	ND3	0.2131
HLI-0498	10873	T	C	0	564	synonymous_variant	LOW	ND4	0.3389
HLI-0498	11719	G	A	0	589	synonymous_variant	LOW	ND4	0.7756
HLI-0498	12705	C	T	0	583	synonymous_variant	LOW	ND5	0.4212
HLI-0498	13542	A	G	2	534	synonymous_variant	LOW	ND5	0.002
HLI-0498	14766	C	T	0	606	missense_variant	MODERATE	CYTB	0.7696
HLI-0498	14783	T	C	0	712	synonymous_variant	LOW	CYTB	0.2126
HLI-0498	15043	G	A	1	673	synonymous_variant	LOW	CYTB	0.2362
HLI-0498	15229	T	C	2	548	synonymous_variant	LOW	CYTB	0.0014

HLI-0498	15301	G	A	0	533	synonymous_variant	LOW	CYTB	0.2912
HLI-0498	15326	A	G	0	531	missense_variant	MODERATE	CYTB	0.9868
HLI-0498	15721	T	C	0	487	synonymous_variant	LOW	CYTB	0.0033
HLI-0498	15954	A	G	2	506	upstream_gene_variant	MODIFIER	Unannotated	0.0018
HLI-0498	16179	C	T	3	516	upstream_gene_variant	MODIFIER	DLoop	0.0082
HLI-0498	16223	C	T	1	580	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0498	16294	C	T	0	548	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0498	16311	T	C	0	518	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0498	16325	T	C	0	522	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0498	16463	A	G	0	411	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0499	73	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0499	245	T	C	0	288	upstream_gene_variant	MODIFIER	DLoop	3.00E-04
HLI-0499	263	A	G	0	284	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0499	497	C	T	5	485	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0499	750	A	G	1	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0499	1189	T	C	0	653	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0499	1438	A	G	0	701	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0499	1811	A	G	0	581	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0499	2706	A	G	0	563	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0499	3480	A	G	0	521	synonymous_variant	LOW	ND1	0.0392
HLI-0499	4769	A	G	0	611	synonymous_variant	LOW	ND2	0.9767
HLI-0499	7028	C	T	3	640	synonymous_variant	LOW	COX1	0.8089
HLI-0499	7559	A	G	2	578	upstream_gene_variant	MODIFIER	TRND	8.00E-04
HLI-0499	8440	A	G	3	544	synonymous_variant	LOW	ATP8	0.0046
HLI-0499	9055	G	A	1	555	missense_variant	MODERATE	ATP6	0.0425
HLI-0499	9698	T	C	0	599	synonymous_variant	LOW	COX3	0.0405
HLI-0499	10398	A	G	0	610	missense_variant	MODERATE	ND3	0.445
HLI-0499	10550	A	G	0	610	synonymous_variant	LOW	ND4L	0.0376
HLI-0499	11299	T	C	1	596	synonymous_variant	LOW	ND4	0.0417
HLI-0499	11467	A	G	0	689	synonymous_variant	LOW	ND4	0.1231
HLI-0499	11719	G	A	0	599	synonymous_variant	LOW	ND4	0.7756
HLI-0499	12308	A	G	0	587	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0499	12372	G	A	0	597	synonymous_variant	LOW	ND5	0.1329
HLI-0499	13117	A	G	0	617	missense_variant	MODERATE	ND5	0.0014
HLI-0499	14167	C	T	1	523	synonymous_variant	LOW	ND6	0.0385
HLI-0499	14766	C	T	3	660	missense_variant	MODERATE	CYTB	0.7696
HLI-0499	14798	T	C	0	695	missense_variant	MODERATE	CYTB	0.0651
HLI-0499	15326	A	G	0	521	missense_variant	MODERATE	CYTB	0.9868
HLI-0499	16093	T	C	14	639	upstream_gene_variant	MODIFIER	DLoop	0.0573

HLI-0499	16224	T	C	0	611	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0499	16311	T	C	0	584	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0499	16519	T	C	0	306	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0500	73	A	G	1	317	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0500	152	T	C	0	553	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0500	263	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0500	750	A	G	0	657	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0500	921	T	C	0	742	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0500	1438	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0500	2706	A	G	0	664	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0500	4769	A	G	4	589	synonymous_variant	LOW	ND2	0.9767
HLI-0500	5147	G	A	1	579	synonymous_variant	LOW	ND2	0.0437
HLI-0500	6680	T	C	0	772	synonymous_variant	LOW	COX1	0.0226
HLI-0500	7028	C	T	0	726	synonymous_variant	LOW	COX1	0.8089
HLI-0500	7424	A	G	2	662	synonymous_variant	LOW	COX1	0.0115
HLI-0500	7765	A	G	3	652	synonymous_variant	LOW	COX2	0.0019
HLI-0500	8618	T	C	1	398	missense_variant	MODERATE	ATP6	0.0103
HLI-0500	8701	A	G	2	558	missense_variant	MODERATE	ATP6	0.3391
HLI-0500	8709	C	T	0	572	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0500	9151	A	G	0	737	missense_variant	MODERATE	ATP6	0.0013
HLI-0500	9540	T	C	0	664	synonymous_variant	LOW	COX3	0.339
HLI-0500	10398	A	G	0	680	missense_variant	MODERATE	ND3	0.445
HLI-0500	10873	T	C	2	585	synonymous_variant	LOW	ND4	0.3389
HLI-0500	11719	G	A	1	659	synonymous_variant	LOW	ND4	0.7756
HLI-0500	12705	C	T	1	645	synonymous_variant	LOW	ND5	0.4212
HLI-0500	13105	A	G	0	689	missense_variant	MODERATE	ND5	0.076
HLI-0500	13661	A	G	1	601	missense_variant	MODERATE	ND5	2.00E-04
HLI-0500	13886	T	C	0	558	missense_variant	MODERATE	ND5	0.0088
HLI-0500	14128	A	G	0	558	missense_variant	MODERATE	ND5	0.0018
HLI-0500	14284	C	T	3	567	synonymous_variant	LOW	ND6	0.0087
HLI-0500	14766	C	T	1	648	missense_variant	MODERATE	CYTB	0.7696
HLI-0500	15301	G	A	1	614	synonymous_variant	LOW	CYTB	0.2912
HLI-0500	15326	A	G	0	673	missense_variant	MODERATE	CYTB	0.9868
HLI-0500	16124	T	C	0	586	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0500	16256	C	T	1	613	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0500	16368	T	C	0	527	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0501	73	A	G	1	235	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0501	152	T	C	1	443	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0501	195	T	C	1	427	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0501	263	A	G	2	189	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0501	499	G	A	1	314	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0501	745	A	G	0	464	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0501	750	A	G	0	483	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0501	1438	A	G	0	518	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0501	1811	A	G	1	488	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0501	2706	A	G	2	506	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0501	3204	C	T	1	557	upstream_gene_variant	MODIFIER	RNR2	0.0034
HLI-0501	4646	T	C	0	532	synonymous_variant	LOW	ND2	0.0124
HLI-0501	4769	A	G	2	533	synonymous_variant	LOW	ND2	0.9767
HLI-0501	5471	G	A	2	512	synonymous_variant	LOW	ND2	0.0128
HLI-0501	5999	T	C	0	555	synonymous_variant	LOW	COX1	0.0127
HLI-0501	6047	A	G	0	609	synonymous_variant	LOW	COX1	0.0114
HLI-0501	7028	C	T	2	606	synonymous_variant	LOW	COX1	0.8089
HLI-0501	8818	C	T	3	533	synonymous_variant	LOW	ATP6	0.0061
HLI-0501	9098	T	C	0	520	missense_variant	MODERATE	ATP6	0.0011
HLI-0501	11332	C	T	0	560	synonymous_variant	LOW	ND4	0.0115
HLI-0501	11467	A	G	0	561	synonymous_variant	LOW	ND4	0.1231
HLI-0501	11719	G	A	0	460	synonymous_variant	LOW	ND4	0.7756
HLI-0501	12308	A	G	0	525	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0501	12372	G	A	0	510	synonymous_variant	LOW	ND5	0.1329
HLI-0501	12693	A	G	58	513	synonymous_variant	LOW	ND5	0.0205
HLI-0501	12937	A	G	0	537	missense_variant	MODERATE	ND5	0.0026
HLI-0501	14620	C	T	3	588	synonymous_variant	LOW	ND6	0.0126
HLI-0501	14766	C	T	2	529	missense_variant	MODERATE	CYTB	0.7696
HLI-0501	15326	A	G	1	401	missense_variant	MODERATE	CYTB	0.9868
HLI-0501	15693	T	C	0	418	missense_variant	MODERATE	CYTB	0.0114
HLI-0501	16134	C	T	1	641	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0501	16301	C	T	3	467	upstream_gene_variant	MODIFIER	DLoop	0.0064
HLI-0501	16356	T	C	1	477	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0501	16519	T	C	1	201	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0502	146	T	C	0	565	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0502	195	T	C	43	448	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0502	263	A	G	0	165	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0502	709	G	A	2	678	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0502	750	A	G	2	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0502	1438	A	G	0	701	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0502	3693	G	C	0	602	synonymous_variant	LOW	ND1	2.00E-04
HLI-0502	4769	A	G	2	638	synonymous_variant	LOW	ND2	0.9767

HLI-0502	5095	T	C	0	590	missense_variant	MODERATE	ND2	4.00E-04
HLI-0502	8107	A	G	0	602	synonymous_variant	LOW	COX2	2.00E-04
HLI-0502	8764	G	A	0	547	missense_variant	MODERATE	ATP6	0.0016
HLI-0502	13101	A	C	2	702	synonymous_variant	LOW	ND5	0.0055
HLI-0502	14121	C	T	3	573	synonymous_variant	LOW	ND5	3.00E-04
HLI-0502	15326	A	G	0	572	missense_variant	MODERATE	CYTB	0.9868
HLI-0502	16068	T	C	0	639	upstream_gene_variant	MODIFIER	DLoop	2.00E-04
HLI-0502	16288	T	C	0	573	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0502	16362	T	C	1	569	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0503	152	T	C	0	525	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0503	263	A	G	0	286	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0503	477	T	C	0	468	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0503	750	A	G	0	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0503	1438	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0503	3010	G	A	0	592	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0503	4769	A	G	0	628	synonymous_variant	LOW	ND2	0.9767
HLI-0503	8723	G	A	0	584	missense_variant	MODERATE	ATP6	0.0016
HLI-0503	13203	A	G	0	649	synonymous_variant	LOW	ND5	0.0012
HLI-0503	15326	A	G	1	474	missense_variant	MODERATE	CYTB	0.9868
HLI-0503	16519	T	C	1	294	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0504	195	T	C	0	427	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0504	263	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0504	750	A	G	1	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0504	1438	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0504	2706	A	G	1	571	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0504	4769	A	G	2	550	synonymous_variant	LOW	ND2	0.9767
HLI-0504	6962	G	A	0	658	synonymous_variant	LOW	COX1	0.0235
HLI-0504	7028	C	T	1	748	synonymous_variant	LOW	COX1	0.8089
HLI-0504	8706	A	G	2	566	synonymous_variant	LOW	ATP6	7.00E-04
HLI-0504	15326	A	G	0	540	missense_variant	MODERATE	CYTB	0.9868
HLI-0504	16298	T	C	2	580	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0505	73	A	G	1	243	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0505	185	G	A	3	418	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0505	228	G	A	1	304	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0505	263	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0505	295	C	T	1	239	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0505	462	C	T	3	468	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0505	489	T	C	1	463	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0505	750	A	G	0	504	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0505	1438	A	G	0	523	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0505	2706	A	G	1	513	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0505	3010	G	A	0	562	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0505	4216	T	C	0	446	missense_variant	MODERATE	ND1	0.0991
HLI-0505	4769	A	G	1	569	synonymous_variant	LOW	ND2	0.9767
HLI-0505	6464	C	A	2	473	synonymous_variant	LOW	COX1	0.0011
HLI-0505	6554	C	T	6	527	synonymous_variant	LOW	COX1	0.0016
HLI-0505	7028	C	T	4	581	synonymous_variant	LOW	COX1	0.8089
HLI-0505	7284	T	G	2	624	missense_variant	MODERATE	COX1	0
HLI-0505	8260	T	C	5	538	synonymous_variant	LOW	COX2	0.001
HLI-0505	10398	A	G	0	507	missense_variant	MODERATE	ND3	0.445
HLI-0505	10915	T	C	1	554	synonymous_variant	LOW	ND4	0.0411
HLI-0505	11251	A	G	0	544	synonymous_variant	LOW	ND4	0.0932
HLI-0505	11719	G	A	1	541	synonymous_variant	LOW	ND4	0.7756
HLI-0505	12127	G	A	1	650	synonymous_variant	LOW	ND4	0.0058
HLI-0505	12612	A	G	5	591	synonymous_variant	LOW	ND5	0.0506
HLI-0505	13681	A	G	0	487	missense_variant	MODERATE	ND5	0.0035
HLI-0505	13708	G	A	0	522	missense_variant	MODERATE	ND5	0.0717
HLI-0505	14766	C	T	2	578	missense_variant	MODERATE	CYTB	0.7696
HLI-0505	14798	T	C	0	646	missense_variant	MODERATE	CYTB	0.0651
HLI-0505	15326	A	G	1	450	missense_variant	MODERATE	CYTB	0.9868
HLI-0505	15452	C	A	2	382	missense_variant	MODERATE	CYTB	0.0933
HLI-0505	16069	C	T	2	652	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0505	16126	T	C	0	739	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0505	16261	C	T	1	500	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0506	73	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0506	189	A	G	0	413	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0506	195	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0506	204	T	C	0	409	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0506	207	G	A	0	423	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0506	263	A	G	0	160	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0506	709	G	A	2	448	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0506	750	A	G	4	506	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0506	1243	T	C	0	555	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0506	1438	A	G	0	502	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0506	2706	A	G	0	531	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0506	3505	A	G	1	503	missense_variant	MODERATE	ND1	0.0144
HLI-0506	4769	A	G	1	583	synonymous_variant	LOW	ND2	0.9767
HLI-0506	5046	G	A	1	496	missense_variant	MODERATE	ND2	0.018

HLI-0506	5460	G	A	1	584	missense_variant	MODERATE	ND2	0.0651
HLI-0506	6164	C	T	3	520	synonymous_variant	LOW	COX1	0.0025
HLI-0506	7028	C	T	5	647	synonymous_variant	LOW	COX1	0.8089
HLI-0506	7864	C	T	4	637	synonymous_variant	LOW	COX2	0.0041
HLI-0506	8251	G	A	3	591	synonymous_variant	LOW	COX2	0.058
HLI-0506	8994	G	A	1	513	synonymous_variant	LOW	ATP6	0.0167
HLI-0506	11674	C	T	2	599	synonymous_variant	LOW	ND4	0.0116
HLI-0506	11719	G	A	0	624	synonymous_variant	LOW	ND4	0.7756
HLI-0506	11947	A	G	2	559	synonymous_variant	LOW	ND4	0.011
HLI-0506	12414	T	C	2	524	synonymous_variant	LOW	ND5	0.0139
HLI-0506	12705	C	T	0	649	synonymous_variant	LOW	ND5	0.4212
HLI-0506	14148	A	G	0	462	stop_retained_variant	LOW	ND5	0.0065
HLI-0506	14766	C	T	2	582	missense_variant	MODERATE	CYTB	0.7696
HLI-0506	15326	A	G	0	386	missense_variant	MODERATE	CYTB	0.9868
HLI-0506	15812	G	A	0	479	missense_variant	MODERATE	CYTB	0.0096
HLI-0506	15884	G	C	0	597	missense_variant	MODERATE	CYTB	0.011
HLI-0506	16223	C	T	2	602	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0506	16292	C	T	2	514	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0506	16519	T	C	1	205	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0507	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0507	146	T	C	0	521	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0507	263	A	G	1	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0507	750	A	G	0	594	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0507	1438	A	G	0	619	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0507	2706	A	G	3	561	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0507	3834	G	A	2	546	synonymous_variant	LOW	ND1	0.0087
HLI-0507	4025	C	T	3	486	missense_variant	MODERATE	ND1	0.0072
HLI-0507	4769	A	G	1	548	synonymous_variant	LOW	ND2	0.9767
HLI-0507	5417	G	A	2	496	synonymous_variant	LOW	ND2	0.0109
HLI-0507	7028	C	T	3	653	synonymous_variant	LOW	COX1	0.8089
HLI-0507	8392	G	A	2	372	synonymous_variant	LOW	ATP8	0.0067
HLI-0507	10097	A	G	1	634	synonymous_variant	LOW	ND3	0.0011
HLI-0507	10238	T	C	2	689	synonymous_variant	LOW	ND3	0.0623
HLI-0507	10398	A	G	0	539	missense_variant	MODERATE	ND3	0.445
HLI-0507	11719	G	A	1	549	synonymous_variant	LOW	ND4	0.7756
HLI-0507	12705	C	T	3	469	synonymous_variant	LOW	ND5	0.4212
HLI-0507	14178	T	C	0	473	missense_variant	MODERATE	ND6	0.0225
HLI-0507	14693	A	G	1	654	upstream_gene_variant	MODIFIER	TRNE	0.0053
HLI-0507	14766	C	T	6	695	missense_variant	MODERATE	CYTB	0.7696

HLI-0507	15326	A	G	0	410	missense_variant	MODERATE	CYTB	0.9868
HLI-0507	15460	C	T	2	391	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0507	16231	T	C	2	586	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0507	16519	T	C	2	299	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0508	207	G	A	3	413	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0508	263	A	G	0	314	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0508	456	C	T	6	495	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0508	750	A	G	1	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0508	1438	A	G	0	716	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0508	4769	A	G	0	569	synonymous_variant	LOW	ND2	0.9767
HLI-0508	10410	T	C	2	573	upstream_gene_variant	MODIFIER	TRNR	0.0049
HLI-0508	13725	C	T	3	562	synonymous_variant	LOW	ND5	4.00E-04
HLI-0508	15326	A	G	1	496	missense_variant	MODERATE	CYTB	0.9868
HLI-0508	16304	T	C	1	481	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0508	16311	T	C	1	498	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0509	152	T	C	3	444	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0509	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0509	456	C	T	3	416	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0509	750	A	G	0	462	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0509	1438	A	G	0	445	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0509	4336	T	C	0	405	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0509	4769	A	G	0	503	synonymous_variant	LOW	ND2	0.9767
HLI-0509	5839	C	T	2	566	upstream_gene_variant	MODIFIER	TRNY	0.0011
HLI-0509	15326	A	G	0	352	missense_variant	MODERATE	CYTB	0.9868
HLI-0509	16213	G	A	0	607	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0509	16304	T	C	1	429	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0510	73	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0510	146	T	C	0	444	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0510	152	T	C	0	446	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0510	263	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0510	750	A	G	1	461	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0510	1189	T	C	1	586	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0510	1438	A	G	0	475	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0510	1811	A	G	2	400	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0510	2706	A	G	0	469	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0510	3480	A	G	1	430	synonymous_variant	LOW	ND1	0.0392
HLI-0510	4769	A	G	1	549	synonymous_variant	LOW	ND2	0.9767
HLI-0510	7028	C	T	4	582	synonymous_variant	LOW	COX1	0.8089
HLI-0510	9055	G	A	0	501	missense_variant	MODERATE	ATP6	0.0425

HLI-0510	9093	A	G	0	547	synonymous_variant	LOW	ATP6	0.0031
HLI-0510	9698	T	C	0	459	synonymous_variant	LOW	COX3	0.0405
HLI-0510	10398	A	G	2	459	missense_variant	MODERATE	ND3	0.445
HLI-0510	10550	A	G	1	433	synonymous_variant	LOW	ND4L	0.0376
HLI-0510	11299	T	C	1	540	synonymous_variant	LOW	ND4	0.0417
HLI-0510	11377	G	A	0	601	synonymous_variant	LOW	ND4	0.0125
HLI-0510	11467	A	G	0	523	synonymous_variant	LOW	ND4	0.1231
HLI-0510	11719	G	A	0	486	synonymous_variant	LOW	ND4	0.7756
HLI-0510	12308	A	G	1	526	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0510	12372	G	A	1	479	synonymous_variant	LOW	ND5	0.1329
HLI-0510	14167	C	T	4	458	synonymous_variant	LOW	ND6	0.0385
HLI-0510	14766	C	T	1	560	missense_variant	MODERATE	CYTB	0.7696
HLI-0510	14798	T	C	0	627	missense_variant	MODERATE	CYTB	0.0651
HLI-0510	15326	A	G	0	360	missense_variant	MODERATE	CYTB	0.9868
HLI-0510	16224	T	C	0	492	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0510	16311	T	C	0	427	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0510	16519	T	C	0	181	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0511	73	A	G	1	264	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0511	152	T	C	0	444	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0511	195	T	C	0	415	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0511	239	T	C	0	152	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0511	263	A	G	0	173	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0511	709	G	A	1	587	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0511	750	A	G	2	567	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0511	1438	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0511	1888	G	A	0	506	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0511	2706	A	G	0	531	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0511	4216	T	C	1	534	missense_variant	MODERATE	ND1	0.0991
HLI-0511	4769	A	G	1	497	synonymous_variant	LOW	ND2	0.9767
HLI-0511	4917	A	G	3	470	missense_variant	MODERATE	ND2	0.0477
HLI-0511	7028	C	T	3	609	synonymous_variant	LOW	COX1	0.8089
HLI-0511	8697	G	A	1	451	synonymous_variant	LOW	ATP6	0.0466
HLI-0511	9899	T	C	0	534	synonymous_variant	LOW	COX3	0.0108
HLI-0511	10463	T	C	0	574	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0511	11251	A	G	0	505	synonymous_variant	LOW	ND4	0.0932
HLI-0511	11719	G	A	0	529	synonymous_variant	LOW	ND4	0.7756
HLI-0511	12633	C	A	1	544	synonymous_variant	LOW	ND5	0.0123
HLI-0511	13368	G	A	1	515	synonymous_variant	LOW	ND5	0.0495
HLI-0511	14766	C	T	4	485	missense_variant	MODERATE	CYTB	0.7696

HLI-0511	14905	G	A	1	573	synonymous_variant	LOW	CYTB	0.0526
HLI-0511	15326	A	G	0	425	missense_variant	MODERATE	CYTB	0.9868
HLI-0511	15452	C	A	7	470	missense_variant	MODERATE	CYTB	0.0933
HLI-0511	15607	A	G	2	459	synonymous_variant	LOW	CYTB	0.0508
HLI-0511	15928	G	A	3	580	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0511	16126	T	C	0	546	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0511	16163	A	G	0	543	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0511	16294	C	T	2	426	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0511	16519	T	C	1	254	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0512	73	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0512	143	G	A	0	439	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0512	146	T	C	0	451	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0512	152	T	C	0	462	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0512	195	T	C	2	476	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0512	263	A	G	0	222	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0512	750	A	G	1	661	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0512	769	G	A	0	735	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0512	1018	G	A	0	642	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0512	1438	A	G	0	588	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0512	2416	T	C	0	538	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0512	2706	A	G	2	575	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0512	2789	C	T	2	570	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0512	3594	C	T	2	462	synonymous_variant	LOW	ND1	0.0789
HLI-0512	4104	A	G	0	505	synonymous_variant	LOW	ND1	0.0785
HLI-0512	4371	T	C	0	477	upstream_gene_variant	MODIFIER	TRNQ	3.00E-04
HLI-0512	4769	A	G	0	557	synonymous_variant	LOW	ND2	0.9767
HLI-0512	7028	C	T	4	612	synonymous_variant	LOW	COX1	0.8089
HLI-0512	7175	T	C	2	539	synonymous_variant	LOW	COX1	0.0224
HLI-0512	7256	C	T	1	542	synonymous_variant	LOW	COX1	0.0784
HLI-0512	7274	C	T	1	540	synonymous_variant	LOW	COX1	0.0214
HLI-0512	7521	G	A	0	491	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0512	7771	A	G	0	535	synonymous_variant	LOW	COX2	0.0223
HLI-0512	8206	G	A	2	518	synonymous_variant	LOW	COX2	0.0287
HLI-0512	8701	A	G	0	555	missense_variant	MODERATE	ATP6	0.3391
HLI-0512	9221	A	G	0	563	synonymous_variant	LOW	COX3	0.0277
HLI-0512	9535	C	T	0	542	missense_variant	MODERATE	COX3	0
HLI-0512	9540	T	C	0	529	synonymous_variant	LOW	COX3	0.339
HLI-0512	10115	T	C	2	570	synonymous_variant	LOW	ND3	0.0278
HLI-0512	10398	A	G	1	520	missense_variant	MODERATE	ND3	0.445

HLI-0512	10873	T	C	0	538	synonymous_variant	LOW	ND4	0.3389
HLI-0512	11719	G	A	0	506	synonymous_variant	LOW	ND4	0.7756
HLI-0512	11914	G	A	1	612	synonymous_variant	LOW	ND4	0.1112
HLI-0512	11944	T	C	1	574	synonymous_variant	LOW	ND4	0.0331
HLI-0512	12693	A	G	6	606	synonymous_variant	LOW	ND5	0.0205
HLI-0512	12705	C	T	3	622	synonymous_variant	LOW	ND5	0.4212
HLI-0512	13590	G	A	2	545	synonymous_variant	LOW	ND5	0.0586
HLI-0512	13650	C	T	1	554	synonymous_variant	LOW	ND5	0.079
HLI-0512	13752	T	C	0	329	synonymous_variant	LOW	ND5	7.00E-04
HLI-0512	13803	A	G	0	416	synonymous_variant	LOW	ND5	0.0216
HLI-0512	14566	A	G	1	586	synonymous_variant	LOW	ND6	0.0214
HLI-0512	14766	C	T	3	570	missense_variant	MODERATE	CYTB	0.7696
HLI-0512	15301	G	A	1	607	synonymous_variant	LOW	CYTB	0.2912
HLI-0512	15326	A	G	0	652	missense_variant	MODERATE	CYTB	0.9868
HLI-0512	15784	T	C	2	591	synonymous_variant	LOW	CYTB	0.0363
HLI-0512	16129	G	A	0	604	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0512	16223	C	T	3	463	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0512	16234	C	T	1	461	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0512	16278	C	T	2	392	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0512	16292	C	T	1	354	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0512	16294	C	T	1	356	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0512	16309	A	G	1	358	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0512	16390	G	A	1	423	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0513	263	A	G	1	222	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0513	750	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0513	1438	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0513	2259	C	T	0	609	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0513	4745	A	G	1	644	synonymous_variant	LOW	ND2	0.0039
HLI-0513	4769	A	G	1	620	synonymous_variant	LOW	ND2	0.9767
HLI-0513	13680	C	T	3	503	synonymous_variant	LOW	ND5	0.005
HLI-0513	14872	C	T	2	606	synonymous_variant	LOW	CYTB	0.0061
HLI-0513	15326	A	G	1	557	missense_variant	MODERATE	CYTB	0.9868
HLI-0514	73	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0514	150	C	T	1	576	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0514	263	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0514	499	G	A	3	406	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0514	750	A	G	0	599	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0514	1438	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0514	2706	A	G	1	574	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0514	3197	T	C	0	614	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0514	4769	A	G	1	557	synonymous_variant	LOW	ND2	0.9767
HLI-0514	5656	A	G	1	618	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0514	7028	C	T	0	640	synonymous_variant	LOW	COX1	0.8089
HLI-0514	7768	A	G	2	558	synonymous_variant	LOW	COX2	0.0186
HLI-0514	8435	A	G	3	504	missense_variant	MODERATE	ATP8	2.00E-04
HLI-0514	9477	G	A	5	681	missense_variant	MODERATE	COX3	0.0387
HLI-0514	10993	G	A	2	469	synonymous_variant	LOW	ND4	0.0014
HLI-0514	11467	A	G	0	622	synonymous_variant	LOW	ND4	0.1231
HLI-0514	11719	G	A	1	610	synonymous_variant	LOW	ND4	0.7756
HLI-0514	12308	A	G	2	567	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0514	12372	G	A	2	609	synonymous_variant	LOW	ND5	0.1329
HLI-0514	13617	T	C	2	540	synonymous_variant	LOW	ND5	0.038
HLI-0514	14182	T	C	0	572	synonymous_variant	LOW	ND6	0.0254
HLI-0514	14766	C	T	3	524	missense_variant	MODERATE	CYTB	0.7696
HLI-0514	15326	A	G	0	549	missense_variant	MODERATE	CYTB	0.9868
HLI-0514	16270	C	T	0	573	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0514	16311	T	C	0	537	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0515	73	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0515	151	C	T	1	370	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0515	152	T	C	1	370	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0515	182	C	T	1	329	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0515	185	G	T	1	319	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0515	189	A	G	1	306	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0515	195	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0515	200	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0515	247	G	A	0	147	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0515	263	A	G	1	154	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0515	357	A	G	1	320	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0515	709	G	A	0	490	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0515	710	T	C	0	494	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0515	750	A	G	0	536	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0515	769	G	A	0	539	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0515	825	T	A	0	605	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0515	1018	G	A	1	721	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0515	1738	T	C	0	421	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0515	2352	T	C	2	319	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0515	2706	A	G	2	503	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0515	2758	G	A	1	523	upstream_gene_variant	MODIFIER	RNR2	0.0503

HLI-0515	2768	A	G	1	521	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0515	2885	T	C	0	555	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0515	3308	T	C	0	520	start_lost	HIGH	ND1	0.0073
HLI-0515	3594	C	T	1	394	synonymous_variant	LOW	ND1	0.0789
HLI-0515	3666	G	A	0	495	synonymous_variant	LOW	ND1	0.0233
HLI-0515	3693	G	A	0	500	synonymous_variant	LOW	ND1	0.0091
HLI-0515	4104	A	G	0	347	synonymous_variant	LOW	ND1	0.0785
HLI-0515	4769	A	G	0	506	synonymous_variant	LOW	ND2	0.9767
HLI-0515	5036	A	G	0	422	synonymous_variant	LOW	ND2	0.006
HLI-0515	5046	G	A	0	459	missense_variant	MODERATE	ND2	0.018
HLI-0515	5393	T	C	1	412	synonymous_variant	LOW	ND2	0.0059
HLI-0515	5655	T	C	0	663	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0515	6548	C	T	2	544	synonymous_variant	LOW	COX1	0.0061
HLI-0515	6827	T	C	5	694	synonymous_variant	LOW	COX1	0.0072
HLI-0515	6989	A	G	5	629	synonymous_variant	LOW	COX1	0.0061
HLI-0515	7028	C	T	6	610	synonymous_variant	LOW	COX1	0.8089
HLI-0515	7055	A	G	6	578	synonymous_variant	LOW	COX1	0.0188
HLI-0515	7146	A	G	1	357	missense_variant	MODERATE	COX1	0.0497
HLI-0515	7256	C	T	1	439	synonymous_variant	LOW	COX1	0.0784
HLI-0515	7389	T	C	2	448	missense_variant	MODERATE	COX1	0.0201
HLI-0515	7521	G	A	0	331	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0515	7867	C	T	3	649	synonymous_variant	LOW	COX2	0.0076
HLI-0515	8248	A	G	1	428	synonymous_variant	LOW	COX2	0.0061
HLI-0515	8468	C	T	1	275	synonymous_variant	LOW	ATP8	0.0501
HLI-0515	8655	C	T	3	375	synonymous_variant	LOW	ATP6	0.0511
HLI-0515	8701	A	G	3	422	missense_variant	MODERATE	ATP6	0.3391
HLI-0515	9540	T	C	0	471	synonymous_variant	LOW	COX3	0.339
HLI-0515	10398	A	G	0	462	missense_variant	MODERATE	ND3	0.445
HLI-0515	10688	G	A	0	574	synonymous_variant	LOW	ND4L	0.0515
HLI-0515	10810	T	C	0	459	synonymous_variant	LOW	ND4	0.0522
HLI-0515	10873	T	C	0	448	synonymous_variant	LOW	ND4	0.3389
HLI-0515	11719	G	A	0	544	synonymous_variant	LOW	ND4	0.7756
HLI-0515	12519	T	C	0	396	synonymous_variant	LOW	ND5	0.007
HLI-0515	12705	C	T	1	399	synonymous_variant	LOW	ND5	0.4212
HLI-0515	13105	A	G	0	538	missense_variant	MODERATE	ND5	0.076
HLI-0515	13506	C	T	0	452	synonymous_variant	LOW	ND5	0.0506
HLI-0515	13650	C	T	2	427	synonymous_variant	LOW	ND5	0.079
HLI-0515	13789	T	C	0	285	missense_variant	MODERATE	ND5	0.0185
HLI-0515	13880	C	A	4	381	missense_variant	MODERATE	ND5	0.0055

HLI-0515	14178	T	C	1	443	missense_variant	MODERATE	ND6	0.0225
HLI-0515	14203	A	G	0	464	synonymous_variant	LOW	ND6	0.0061
HLI-0515	14560	G	A	3	633	synonymous_variant	LOW	ND6	0.0235
HLI-0515	14766	C	T	1	700	missense_variant	MODERATE	CYTB	0.7696
HLI-0515	14769	A	G	1	714	missense_variant	MODERATE	CYTB	0.0121
HLI-0515	15115	T	C	2	617	synonymous_variant	LOW	CYTB	0.0093
HLI-0515	15326	A	G	0	367	missense_variant	MODERATE	CYTB	0.9868
HLI-0515	16126	T	C	0	410	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0515	16223	C	T	2	375	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0515	16264	C	T	0	355	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0515	16270	C	T	0	342	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0515	16278	C	T	0	343	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0515	16311	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0515	16519	T	C	0	164	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0516	152	T	C	0	59	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0516	263	A	G	0	45	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0516	750	A	G	0	41	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0516	4769	A	G	0	43	synonymous_variant	LOW	ND2	0.9767
HLI-0516	5249	T	C	0	27	synonymous_variant	LOW	ND2	0.0014
HLI-0516	8598	T	C	0	58	synonymous_variant	LOW	ATP6	0.0015
HLI-0516	8925	A	G	0	41	synonymous_variant	LOW	ATP6	7.00E-04
HLI-0516	14259	G	A	1	39	missense_variant	MODERATE	ND6	8.00E-04
HLI-0516	15326	A	G	0	53	missense_variant	MODERATE	CYTB	0.9868
HLI-0516	16311	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0517	150	C	T	0	472	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0517	263	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0517	575	C	T	1	395	upstream_gene_variant	MODIFIER	TRNF	9.00E-04
HLI-0517	750	A	G	0	506	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0517	751	A	G	0	510	upstream_gene_variant	MODIFIER	RNR1	5.00E-04
HLI-0517	951	G	A	3	579	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0517	15326	A	G	0	374	missense_variant	MODERATE	CYTB	0.9868
HLI-0517	16124	T	C	0	531	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0517	16354	C	T	0	373	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0517	16519	T	C	0	255	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0518	239	T	C	0	264	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0518	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0518	750	A	G	0	568	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0518	1438	A	G	1	589	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0518	1503	G	A	2	668	upstream_gene_variant	MODIFIER	RNR1	0.0053

HLI-0518	3915	G	A	0	552	synonymous_variant	LOW	ND1	0.0106
HLI-0518	4011	C	T	1	468	synonymous_variant	LOW	ND1	8.00E-04
HLI-0518	4727	A	G	0	574	synonymous_variant	LOW	ND2	0.0063
HLI-0518	4769	A	G	1	614	synonymous_variant	LOW	ND2	0.9767
HLI-0518	8652	A	G	2	540	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0518	9142	G	A	1	582	missense_variant	MODERATE	ATP6	0.001
HLI-0518	9380	G	A	2	607	synonymous_variant	LOW	COX3	0.0094
HLI-0518	11253	T	C	1	546	missense_variant	MODERATE	ND4	0.0053
HLI-0518	15326	A	G	0	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0518	16362	T	C	1	442	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0518	16482	A	G	3	343	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0518	16519	T	C	1	314	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0519	73	A	G	0	311	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0519	263	A	G	2	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0519	750	A	G	2	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0519	1438	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0519	1700	T	C	0	573	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0519	2706	A	G	0	510	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0519	3197	T	C	0	489	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0519	4769	A	G	0	570	synonymous_variant	LOW	ND2	0.9767
HLI-0519	5495	T	C	3	619	synonymous_variant	LOW	ND2	0.0051
HLI-0519	7028	C	T	2	563	synonymous_variant	LOW	COX1	0.8089
HLI-0519	7158	A	G	0	586	missense_variant	MODERATE	COX1	7.00E-04
HLI-0519	9477	G	A	1	578	missense_variant	MODERATE	COX3	0.0387
HLI-0519	11467	A	G	2	616	synonymous_variant	LOW	ND4	0.1231
HLI-0519	11719	G	A	1	538	synonymous_variant	LOW	ND4	0.7756
HLI-0519	12308	A	G	1	556	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0519	12372	G	A	1	559	synonymous_variant	LOW	ND5	0.1329
HLI-0519	12441	T	C	4	576	synonymous_variant	LOW	ND5	0.0012
HLI-0519	13494	C	T	0	509	synonymous_variant	LOW	ND5	1.00E-04
HLI-0519	13617	T	C	1	523	synonymous_variant	LOW	ND5	0.038
HLI-0519	14766	C	T	9	556	missense_variant	MODERATE	CYTB	0.7696
HLI-0519	14793	A	G	2	672	missense_variant	MODERATE	CYTB	0.0199
HLI-0519	15218	A	G	0	548	missense_variant	MODERATE	CYTB	0.0169
HLI-0519	15326	A	G	0	547	missense_variant	MODERATE	CYTB	0.9868
HLI-0519	15924	A	G	1	604	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0519	16256	C	T	1	647	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0519	16270	C	T	1	585	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0519	16399	A	G	0	536	upstream_gene_variant	MODIFIER	DLoop	0.0265

HLI-0519	16519	T	C	0	333	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0520	72	T	C	1	273	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0520	263	A	G	0	204	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0520	750	A	G	1	555	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0520	1438	A	G	0	561	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0520	2706	A	G	1	502	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0520	4580	G	A	1	609	synonymous_variant	LOW	ND2	0.0169
HLI-0520	4769	A	G	0	547	synonymous_variant	LOW	ND2	0.9767
HLI-0520	7028	C	T	0	650	synonymous_variant	LOW	COX1	0.8089
HLI-0520	9210	A	G	3	560	missense_variant	MODERATE	COX3	0.0012
HLI-0520	13105	A	G	0	514	missense_variant	MODERATE	ND5	0.076
HLI-0520	14562	C	T	1	598	missense_variant	MODERATE	ND6	3.00E-04
HLI-0520	15326	A	G	0	398	missense_variant	MODERATE	CYTB	0.9868
HLI-0520	15904	C	T	0	464	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0520	16298	T	C	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0520	16311	T	C	1	513	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0521	263	A	G	0	348	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0521	750	A	G	0	475	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0521	1438	A	G	0	542	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0521	4769	A	G	1	598	synonymous_variant	LOW	ND2	0.9767
HLI-0521	10394	C	T	1	541	synonymous_variant	LOW	ND3	0.002
HLI-0521	15326	A	G	0	363	missense_variant	MODERATE	CYTB	0.9868
HLI-0521	16519	T	C	0	194	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0522	263	A	G	1	345	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0522	750	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0522	1438	A	G	0	642	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0522	3010	G	A	1	589	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0522	4769	A	G	1	569	synonymous_variant	LOW	ND2	0.9767
HLI-0522	10101	T	C	0	805	synonymous_variant	LOW	ND3	0.0026
HLI-0522	14470	T	C	1	676	synonymous_variant	LOW	ND6	0.0166
HLI-0522	15326	A	G	0	491	missense_variant	MODERATE	CYTB	0.9868
HLI-0522	16220	A	C	1	488	upstream_gene_variant	MODIFIER	DLoop	0.0054
HLI-0522	16519	T	C	0	339	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0523	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0523	263	A	G	1	260	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0523	480	T	C	1	396	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0523	750	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0523	1438	A	G	0	617	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0523	3010	G	A	2	613	upstream_gene_variant	MODIFIER	RNR2	0.1449

HLI-0523	4769	A	G	1	518	synonymous_variant	LOW	ND2	0.9767
HLI-0523	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0523	16051	A	G	2	543	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0523	16162	A	G	0	536	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0523	16304	T	C	1	541	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0523	16519	T	C	1	310	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0524	73	A	G	0	308	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0524	195	T	C	0	439	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0524	263	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0524	499	G	A	5	444	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0524	750	A	G	0	548	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0524	1438	A	G	2	601	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0524	1811	A	G	3	583	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0524	2706	A	G	0	540	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0524	4646	T	C	4	618	synonymous_variant	LOW	ND2	0.0124
HLI-0524	4769	A	G	1	589	synonymous_variant	LOW	ND2	0.9767
HLI-0524	4811	A	G	4	624	synonymous_variant	LOW	ND2	0.0017
HLI-0524	4841	G	A	3	620	synonymous_variant	LOW	ND2	7.00E-04
HLI-0524	5999	T	C	7	648	synonymous_variant	LOW	COX1	0.0127
HLI-0524	6047	A	G	6	700	synonymous_variant	LOW	COX1	0.0114
HLI-0524	6146	A	G	5	570	synonymous_variant	LOW	COX1	0.0013
HLI-0524	7028	C	T	4	622	synonymous_variant	LOW	COX1	0.8089
HLI-0524	9070	T	G	4	545	missense_variant	MODERATE	ATP6	0.0012
HLI-0524	10907	T	C	2	385	missense_variant	MODERATE	ND4	0.0022
HLI-0524	11009	T	C	2	469	synonymous_variant	LOW	ND4	0.002
HLI-0524	11332	C	T	4	566	synonymous_variant	LOW	ND4	0.0115
HLI-0524	11467	A	G	1	599	synonymous_variant	LOW	ND4	0.1231
HLI-0524	11719	G	A	1	589	synonymous_variant	LOW	ND4	0.7756
HLI-0524	12308	A	G	0	537	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0524	12372	G	A	3	524	synonymous_variant	LOW	ND5	0.1329
HLI-0524	14620	C	T	6	674	synonymous_variant	LOW	ND6	0.0126
HLI-0524	14766	C	T	2	604	missense_variant	MODERATE	CYTB	0.7696
HLI-0524	14866	C	T	4	708	synonymous_variant	LOW	CYTB	0.0012
HLI-0524	15326	A	G	0	425	missense_variant	MODERATE	CYTB	0.9868
HLI-0524	15693	T	C	2	487	missense_variant	MODERATE	CYTB	0.0114
HLI-0524	16179	C	T	3	654	upstream_gene_variant	MODIFIER	DLoop	0.0082
HLI-0524	16356	T	C	5	465	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0524	16519	T	C	0	290	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0525	73	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0525	153	A	G	0	466	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0525	195	T	C	0	334	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0525	225	G	A	1	408	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0525	227	A	G	1	410	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0525	263	A	G	0	390	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0525	750	A	G	1	576	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0525	1438	A	G	0	553	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0525	1719	G	A	2	545	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0525	2706	A	G	1	562	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0525	3386	T	C	0	523	missense_variant	MODERATE	ND1	0
HLI-0525	4769	A	G	1	531	synonymous_variant	LOW	ND2	0.9767
HLI-0525	6221	T	C	1	595	synonymous_variant	LOW	COX1	0.0306
HLI-0525	6371	C	T	1	563	synonymous_variant	LOW	COX1	0.0097
HLI-0525	7028	C	T	1	671	synonymous_variant	LOW	COX1	0.8089
HLI-0525	8705	T	C	0	526	missense_variant	MODERATE	ATP6	0.0039
HLI-0525	11719	G	A	1	546	synonymous_variant	LOW	ND4	0.7756
HLI-0525	12705	C	T	1	595	synonymous_variant	LOW	ND5	0.4212
HLI-0525	13966	A	G	0	513	missense_variant	MODERATE	ND5	0.0126
HLI-0525	14470	T	C	2	494	synonymous_variant	LOW	ND6	0.0166
HLI-0525	14766	C	T	0	574	missense_variant	MODERATE	CYTB	0.7696
HLI-0525	15326	A	G	0	491	missense_variant	MODERATE	CYTB	0.9868
HLI-0525	16108	C	T	0	353	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0525	16223	C	T	1	221	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0525	16255	G	A	0	283	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0525	16278	C	T	0	342	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0525	16519	T	C	0	195	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0526	73	A	G	0	303	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0526	150	C	T	0	572	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0526	152	T	C	0	574	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0526	189	A	G	1	553	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0526	263	A	G	0	277	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0526	750	A	G	1	646	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0526	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0526	2352	T	C	0	481	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0526	2706	A	G	0	647	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0526	4769	A	G	0	569	synonymous_variant	LOW	ND2	0.9767
HLI-0526	6221	T	C	0	649	synonymous_variant	LOW	COX1	0.0306
HLI-0526	6587	C	T	1	618	synonymous_variant	LOW	COX1	0.0084
HLI-0526	7028	C	T	1	709	synonymous_variant	LOW	COX1	0.8089

HLI-0526	8701	A	G	3	568	missense_variant	MODERATE	ATP6	0.3391
HLI-0526	9540	T	C	0	662	synonymous_variant	LOW	COX3	0.339
HLI-0526	10370	T	C	0	629	synonymous_variant	LOW	ND3	0.0019
HLI-0526	10398	A	G	0	680	missense_variant	MODERATE	ND3	0.445
HLI-0526	10819	A	G	2	596	synonymous_variant	LOW	ND4	0.0228
HLI-0526	10873	T	C	1	635	synonymous_variant	LOW	ND4	0.3389
HLI-0526	11719	G	A	1	618	synonymous_variant	LOW	ND4	0.7756
HLI-0526	12265	A	G	1	573	upstream_gene_variant	MODIFIER	TRNS2	0
HLI-0526	12705	C	T	0	543	synonymous_variant	LOW	ND5	0.4212
HLI-0526	14152	A	G	0	545	synonymous_variant	LOW	ND6	0.0086
HLI-0526	14212	T	C	0	630	synonymous_variant	LOW	ND6	0.0204
HLI-0526	14323	G	A	0	680	synonymous_variant	LOW	ND6	0.0058
HLI-0526	14766	C	T	2	628	missense_variant	MODERATE	CYTB	0.7696
HLI-0526	15301	G	A	3	485	synonymous_variant	LOW	CYTB	0.2912
HLI-0526	15326	A	G	0	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0526	15670	T	C	1	503	synonymous_variant	LOW	CYTB	0.0176
HLI-0526	15942	T	C	1	516	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0526	16327	C	T	0	525	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0526	16390	G	A	0	550	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0527	73	A	G	1	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0527	263	A	G	0	276	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0527	497	C	T	5	503	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0527	750	A	G	1	579	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0527	1189	T	C	0	643	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0527	1438	A	G	0	610	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0527	1811	A	G	1	499	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0527	2706	A	G	1	583	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0527	3480	A	G	0	536	synonymous_variant	LOW	ND1	0.0392
HLI-0527	4769	A	G	1	528	synonymous_variant	LOW	ND2	0.9767
HLI-0527	7028	C	T	0	629	synonymous_variant	LOW	COX1	0.8089
HLI-0527	9055	G	A	2	586	missense_variant	MODERATE	ATP6	0.0425
HLI-0527	9698	T	C	2	558	synonymous_variant	LOW	COX3	0.0405
HLI-0527	10398	A	G	1	545	missense_variant	MODERATE	ND3	0.445
HLI-0527	10550	A	G	1	621	synonymous_variant	LOW	ND4L	0.0376
HLI-0527	11299	T	C	1	534	synonymous_variant	LOW	ND4	0.0417
HLI-0527	11467	A	G	0	584	synonymous_variant	LOW	ND4	0.1231
HLI-0527	11719	G	A	0	540	synonymous_variant	LOW	ND4	0.7756
HLI-0527	12308	A	G	2	494	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0527	12372	G	A	1	412	synonymous_variant	LOW	ND5	0.1329

HLI-0527	13117	A	G	1	516	missense_variant	MODERATE	ND5	0.0014
HLI-0527	14167	C	T	2	483	synonymous_variant	LOW	ND6	0.0385
HLI-0527	14766	C	T	4	671	missense_variant	MODERATE	CYTB	0.7696
HLI-0527	14798	T	C	1	721	missense_variant	MODERATE	CYTB	0.0651
HLI-0527	15326	A	G	0	417	missense_variant	MODERATE	CYTB	0.9868
HLI-0527	16224	T	C	0	535	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0527	16311	T	C	0	474	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0527	16519	T	C	0	252	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0528	73	A	G	0	305	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0528	152	T	C	2	583	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0528	263	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0528	709	G	A	1	638	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0528	750	A	G	1	682	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0528	930	G	A	1	639	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0528	1438	A	G	0	582	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0528	1888	G	A	0	278	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0528	2706	A	G	2	569	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0528	4216	T	C	1	539	missense_variant	MODERATE	ND1	0.0991
HLI-0528	4769	A	G	1	538	synonymous_variant	LOW	ND2	0.9767
HLI-0528	4917	A	G	2	588	missense_variant	MODERATE	ND2	0.0477
HLI-0528	5147	G	A	0	442	synonymous_variant	LOW	ND2	0.0437
HLI-0528	7028	C	T	4	623	synonymous_variant	LOW	COX1	0.8089
HLI-0528	8697	G	A	0	445	synonymous_variant	LOW	ATP6	0.0466
HLI-0528	10463	T	C	0	588	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0528	10750	A	G	0	581	missense_variant	MODERATE	ND4L	0.0045
HLI-0528	11251	A	G	0	629	synonymous_variant	LOW	ND4	0.0932
HLI-0528	11719	G	A	2	674	synonymous_variant	LOW	ND4	0.7756
HLI-0528	11812	A	G	2	561	synonymous_variant	LOW	ND4	0.0332
HLI-0528	13368	G	A	0	594	synonymous_variant	LOW	ND5	0.0495
HLI-0528	13722	A	G	0	532	synonymous_variant	LOW	ND5	0.0077
HLI-0528	14233	A	G	1	452	synonymous_variant	LOW	ND6	0.0369
HLI-0528	14766	C	T	2	647	missense_variant	MODERATE	CYTB	0.7696
HLI-0528	14905	G	A	1	803	synonymous_variant	LOW	CYTB	0.0526
HLI-0528	15326	A	G	0	494	missense_variant	MODERATE	CYTB	0.9868
HLI-0528	15452	C	A	1	407	missense_variant	MODERATE	CYTB	0.0933
HLI-0528	15607	A	G	0	382	synonymous_variant	LOW	CYTB	0.0508
HLI-0528	15928	G	A	2	401	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0528	16126	T	C	1	514	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0528	16294	C	T	0	520	upstream_gene_variant	MODIFIER	DLoop	0.0934

HLI-0528	16296	C	T	0	520	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0528	16304	T	C	0	522	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0528	16519	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0529	73	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0529	263	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0529	709	G	A	0	55	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0529	750	A	G	0	57	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0529	930	G	A	0	44	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0529	1438	A	G	0	34	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0529	1888	G	A	0	33	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0529	2706	A	G	0	31	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0529	3826	T	C	0	48	synonymous_variant	LOW	ND1	0.0014
HLI-0529	4216	T	C	0	53	missense_variant	MODERATE	ND1	0.0991
HLI-0529	4769	A	G	0	52	synonymous_variant	LOW	ND2	0.9767
HLI-0529	4917	A	G	0	56	missense_variant	MODERATE	ND2	0.0477
HLI-0529	5147	G	A	0	37	synonymous_variant	LOW	ND2	0.0437
HLI-0529	5201	T	C	0	55	synonymous_variant	LOW	ND2	0.0015
HLI-0529	7028	C	T	0	78	synonymous_variant	LOW	COX1	0.8089
HLI-0529	8504	T	C	0	32	missense_variant	MODERATE	ATP8	3.00E-04
HLI-0529	8697	G	A	0	49	synonymous_variant	LOW	ATP6	0.0466
HLI-0529	10463	T	C	0	43	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0529	11251	A	G	0	56	synonymous_variant	LOW	ND4	0.0932
HLI-0529	11719	G	A	0	58	synonymous_variant	LOW	ND4	0.7756
HLI-0529	11812	A	G	1	62	synonymous_variant	LOW	ND4	0.0332
HLI-0529	13368	G	A	1	51	synonymous_variant	LOW	ND5	0.0495
HLI-0529	14233	A	G	1	53	synonymous_variant	LOW	ND6	0.0369
HLI-0529	14687	A	G	0	54	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0529	14766	C	T	2	51	missense_variant	MODERATE	CYTB	0.7696
HLI-0529	14905	G	A	0	62	synonymous_variant	LOW	CYTB	0.0526
HLI-0529	15326	A	G	0	41	missense_variant	MODERATE	CYTB	0.9868
HLI-0529	15452	C	A	0	53	missense_variant	MODERATE	CYTB	0.0933
HLI-0529	15607	A	G	0	45	synonymous_variant	LOW	CYTB	0.0508
HLI-0529	15928	G	A	0	39	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0529	16126	T	C	0	37	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0529	16249	T	C	0	58	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0529	16294	C	T	0	52	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0529	16296	C	T	0	51	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0529	16304	T	C	0	52	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0529	16519	T	C	0	20	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0530	73	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0530	150	C	T	0	527	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0530	263	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0530	750	A	G	0	529	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0530	1438	A	G	3	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0530	1721	C	T	2	520	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0530	2706	A	G	0	535	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0530	3197	T	C	0	526	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0530	3861	A	G	0	545	synonymous_variant	LOW	ND1	0.0011
HLI-0530	4749	T	C	0	608	missense_variant	MODERATE	ND2	1.00E-04
HLI-0530	4769	A	G	0	651	synonymous_variant	LOW	ND2	0.9767
HLI-0530	7028	C	T	4	615	synonymous_variant	LOW	COX1	0.8089
HLI-0530	7768	A	G	1	565	synonymous_variant	LOW	COX2	0.0186
HLI-0530	9197	A	G	1	596	missense_variant	MODERATE	ATP6	0
HLI-0530	9477	G	A	2	561	missense_variant	MODERATE	COX3	0.0387
HLI-0530	11467	A	G	0	575	synonymous_variant	LOW	ND4	0.1231
HLI-0530	11653	A	G	1	589	synonymous_variant	LOW	ND4	0.0049
HLI-0530	11719	G	A	1	604	synonymous_variant	LOW	ND4	0.7756
HLI-0530	12308	A	G	1	531	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0530	12372	G	A	2	451	synonymous_variant	LOW	ND5	0.1329
HLI-0530	12480	C	T	8	532	synonymous_variant	LOW	ND5	4.00E-04
HLI-0530	12634	A	G	8	534	missense_variant	MODERATE	ND5	0.0027
HLI-0530	13617	T	C	1	509	synonymous_variant	LOW	ND5	0.038
HLI-0530	13630	A	G	0	507	missense_variant	MODERATE	ND5	0.0018
HLI-0530	13637	A	G	0	512	missense_variant	MODERATE	ND5	0.0074
HLI-0530	14182	T	C	1	539	synonymous_variant	LOW	ND6	0.0254
HLI-0530	14766	C	T	4	551	missense_variant	MODERATE	CYTB	0.7696
HLI-0530	15326	A	G	0	488	missense_variant	MODERATE	CYTB	0.9868
HLI-0530	15497	G	A	1	414	missense_variant	MODERATE	CYTB	0.0043
HLI-0530	16270	C	T	0	521	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0530	16291	C	T	0	538	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0530	16292	C	T	0	537	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0530	16362	T	C	0	487	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0531	263	A	G	0	260	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0531	750	A	G	1	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0531	1438	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0531	2259	C	T	0	434	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0531	4745	A	G	0	600	synonymous_variant	LOW	ND2	0.0039
HLI-0531	4769	A	G	0	644	synonymous_variant	LOW	ND2	0.9767

HLI-0531	7337	G	A	0	599	synonymous_variant	LOW	COX1	0.0119
HLI-0531	11465	T	C	2	644	synonymous_variant	LOW	ND4	0.0022
HLI-0531	13326	T	C	3	613	synonymous_variant	LOW	ND5	0.0032
HLI-0531	13680	C	T	0	492	synonymous_variant	LOW	ND5	0.005
HLI-0531	14872	C	T	8	746	synonymous_variant	LOW	CYTB	0.0061
HLI-0531	15326	A	G	0	480	missense_variant	MODERATE	CYTB	0.9868
HLI-0531	16519	T	C	0	357	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0532	183	A	G	2	436	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0532	263	A	G	1	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0532	750	A	G	0	524	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0532	1438	A	G	0	604	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0532	3010	G	A	0	564	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0532	4769	A	G	1	575	synonymous_variant	LOW	ND2	0.9767
HLI-0532	8251	G	A	1	471	synonymous_variant	LOW	COX2	0.058
HLI-0532	8286	T	C	1	481	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0532	15326	A	G	0	457	missense_variant	MODERATE	CYTB	0.9868
HLI-0532	16080	A	G	2	458	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0532	16356	T	C	0	486	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0532	16360	C	T	0	505	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0533	73	A	G	0	330	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0533	152	T	C	0	609	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0533	263	A	G	3	276	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0533	325	C	T	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0533	497	C	T	2	512	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0533	750	A	G	1	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0533	1189	T	C	1	681	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0533	1438	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0533	1811	A	G	0	604	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0533	2706	A	G	1	635	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0533	3480	A	G	5	562	synonymous_variant	LOW	ND1	0.0392
HLI-0533	4769	A	G	3	560	synonymous_variant	LOW	ND2	0.9767
HLI-0533	6260	G	A	2	684	synonymous_variant	LOW	COX1	0.009
HLI-0533	7028	C	T	1	689	synonymous_variant	LOW	COX1	0.8089
HLI-0533	9055	G	A	0	615	missense_variant	MODERATE	ATP6	0.0425
HLI-0533	9698	T	C	1	624	synonymous_variant	LOW	COX3	0.0405
HLI-0533	10029	A	G	1	638	upstream_gene_variant	MODIFIER	TRNG	2.00E-04
HLI-0533	10398	A	G	1	623	missense_variant	MODERATE	ND3	0.445
HLI-0533	10550	A	G	2	596	synonymous_variant	LOW	ND4L	0.0376
HLI-0533	11299	T	C	1	646	synonymous_variant	LOW	ND4	0.0417

HLI-0533	11467	A	G	1	616	synonymous_variant	LOW	ND4	0.1231
HLI-0533	11485	T	C	1	663	synonymous_variant	LOW	ND4	0.0081
HLI-0533	11719	G	A	1	573	synonymous_variant	LOW	ND4	0.7756
HLI-0533	11840	C	T	0	575	synonymous_variant	LOW	ND4	0.0041
HLI-0533	12308	A	G	0	543	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0533	12372	G	A	5	553	synonymous_variant	LOW	ND5	0.1329
HLI-0533	13740	T	C	0	538	synonymous_variant	LOW	ND5	0.0041
HLI-0533	14167	C	T	2	574	synonymous_variant	LOW	ND6	0.0385
HLI-0533	14766	C	T	2	619	missense_variant	MODERATE	CYTB	0.7696
HLI-0533	14798	T	C	1	698	missense_variant	MODERATE	CYTB	0.0651
HLI-0533	15326	A	G	1	544	missense_variant	MODERATE	CYTB	0.9868
HLI-0533	16224	T	C	1	562	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0533	16311	T	C	0	524	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0533	16519	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0534	73	A	G	1	334	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0534	146	T	C	1	565	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0534	152	T	C	2	585	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0534	195	T	C	3	575	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0534	263	A	G	1	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0534	750	A	G	0	708	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0534	769	G	A	1	780	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0534	1018	G	A	0	745	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0534	1438	A	G	0	713	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0534	2416	T	C	0	670	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0534	2706	A	G	2	718	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0534	2789	C	T	0	810	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0534	3594	C	T	3	620	synonymous_variant	LOW	ND1	0.0789
HLI-0534	3918	G	A	0	655	synonymous_variant	LOW	ND1	0.009
HLI-0534	4104	A	G	1	630	synonymous_variant	LOW	ND1	0.0785
HLI-0534	4769	A	G	0	625	synonymous_variant	LOW	ND2	0.9767
HLI-0534	5285	A	G	0	672	synonymous_variant	LOW	ND2	0.0049
HLI-0534	7028	C	T	3	754	synonymous_variant	LOW	COX1	0.8089
HLI-0534	7175	T	C	1	699	synonymous_variant	LOW	COX1	0.0224
HLI-0534	7256	C	T	0	702	synonymous_variant	LOW	COX1	0.0784
HLI-0534	7274	C	T	0	684	synonymous_variant	LOW	COX1	0.0214
HLI-0534	7521	G	A	0	602	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0534	7771	A	G	1	681	synonymous_variant	LOW	COX2	0.0223
HLI-0534	8206	G	A	0	681	synonymous_variant	LOW	COX2	0.0287
HLI-0534	8701	A	G	2	702	missense_variant	MODERATE	ATP6	0.3391

HLI-0534	9067	A	G	0	708	missense_variant	MODERATE	ATP6	7.00E-04
HLI-0534	9221	A	G	2	691	synonymous_variant	LOW	COX3	0.0277
HLI-0534	9540	T	C	0	673	synonymous_variant	LOW	COX3	0.339
HLI-0534	10115	T	C	0	780	synonymous_variant	LOW	ND3	0.0278
HLI-0534	10398	A	G	2	730	missense_variant	MODERATE	ND3	0.445
HLI-0534	10873	T	C	0	626	synonymous_variant	LOW	ND4	0.3389
HLI-0534	11719	G	A	0	658	synonymous_variant	LOW	ND4	0.7756
HLI-0534	11914	G	A	1	672	synonymous_variant	LOW	ND4	0.1112
HLI-0534	11944	T	C	1	720	synonymous_variant	LOW	ND4	0.0331
HLI-0534	12693	A	G	0	737	synonymous_variant	LOW	ND5	0.0205
HLI-0534	12705	C	T	1	789	synonymous_variant	LOW	ND5	0.4212
HLI-0534	13590	G	A	0	687	synonymous_variant	LOW	ND5	0.0586
HLI-0534	13650	C	T	4	720	synonymous_variant	LOW	ND5	0.079
HLI-0534	13803	A	G	0	460	synonymous_variant	LOW	ND5	0.0216
HLI-0534	14566	A	G	0	650	synonymous_variant	LOW	ND6	0.0214
HLI-0534	14766	C	T	4	667	missense_variant	MODERATE	CYTB	0.7696
HLI-0534	15244	A	G	0	663	synonymous_variant	LOW	CYTB	0.0103
HLI-0534	15301	G	A	0	702	synonymous_variant	LOW	CYTB	0.2912
HLI-0534	15326	A	G	0	712	missense_variant	MODERATE	CYTB	0.9868
HLI-0534	15629	T	C	2	650	synonymous_variant	LOW	CYTB	0.0062
HLI-0534	15784	T	C	0	692	synonymous_variant	LOW	CYTB	0.0363
HLI-0534	16223	C	T	4	651	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0534	16278	C	T	0	663	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0534	16286	C	T	0	639	upstream_gene_variant	MODIFIER	DLoop	0.0052
HLI-0534	16294	C	T	0	635	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0534	16309	A	G	0	638	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0534	16390	G	A	0	583	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0534	16519	T	C	0	310	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0535	263	A	G	0	251	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0535	3388	C	A	0	578	missense_variant	MODERATE	ND1	3.00E-04
HLI-0535	4452	T	C	3	638	upstream_gene_variant	MODIFIER	TRNM	0.002
HLI-0535	15326	A	G	0	423	missense_variant	MODERATE	CYTB	0.9868
HLI-0535	16235	A	G	2	560	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0535	16291	C	T	0	566	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0535	16293	A	G	0	569	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0535	16400	C	T	2	442	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0536	73	A	G	0	301	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0536	185	G	A	3	429	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0536	228	G	A	1	350	upstream_gene_variant	MODIFIER	DLoop	0.0255

HLI-0536	263	A	G	0	266	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0536	295	C	T	0	173	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0536	462	C	T	2	471	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0536	489	T	C	0	552	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0536	750	A	G	0	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0536	1438	A	G	0	598	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0536	2706	A	G	0	553	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0536	3010	G	A	1	579	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0536	4216	T	C	3	546	missense_variant	MODERATE	ND1	0.0991
HLI-0536	4769	A	G	1	594	synonymous_variant	LOW	ND2	0.9767
HLI-0536	6464	C	A	3	590	synonymous_variant	LOW	COX1	0.0011
HLI-0536	6554	C	T	4	577	synonymous_variant	LOW	COX1	0.0016
HLI-0536	7028	C	T	2	649	synonymous_variant	LOW	COX1	0.8089
HLI-0536	10398	A	G	1	627	missense_variant	MODERATE	ND3	0.445
HLI-0536	11251	A	G	1	605	synonymous_variant	LOW	ND4	0.0932
HLI-0536	11719	G	A	0	565	synonymous_variant	LOW	ND4	0.7756
HLI-0536	12127	G	A	1	511	synonymous_variant	LOW	ND4	0.0058
HLI-0536	12612	A	G	7	580	synonymous_variant	LOW	ND5	0.0506
HLI-0536	13681	A	G	1	558	missense_variant	MODERATE	ND5	0.0035
HLI-0536	13708	G	A	2	606	missense_variant	MODERATE	ND5	0.0717
HLI-0536	14766	C	T	0	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0536	14798	T	C	1	714	missense_variant	MODERATE	CYTB	0.0651
HLI-0536	15326	A	G	0	478	missense_variant	MODERATE	CYTB	0.9868
HLI-0536	15452	C	A	2	473	missense_variant	MODERATE	CYTB	0.0933
HLI-0536	16069	C	T	0	573	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0536	16092	T	C	2	628	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0536	16126	T	C	0	629	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0536	16261	C	T	23	503	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0537	153	A	G	3	599	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0537	204	T	C	0	551	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0537	263	A	G	1	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0537	750	A	G	1	665	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0537	1438	A	G	0	659	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0537	4769	A	G	0	613	synonymous_variant	LOW	ND2	0.9767
HLI-0537	9948	G	A	0	708	missense_variant	MODERATE	COX3	0.0015
HLI-0537	10646	G	A	1	650	synonymous_variant	LOW	ND4L	0.0032
HLI-0537	13932	C	T	5	604	synonymous_variant	LOW	ND5	5.00E-04
HLI-0537	15326	A	G	0	571	missense_variant	MODERATE	CYTB	0.9868
HLI-0537	16519	T	C	0	274	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0538	263	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0538	750	A	G	1	731	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0538	1438	A	G	0	730	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0538	3010	G	A	0	723	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0538	3766	T	C	2	693	synonymous_variant	LOW	ND1	9.00E-04
HLI-0538	4769	A	G	2	721	synonymous_variant	LOW	ND2	0.9767
HLI-0538	6719	T	C	5	890	synonymous_variant	LOW	COX1	0.041
HLI-0538	8245	A	G	2	652	synonymous_variant	LOW	COX2	2.00E-04
HLI-0538	12618	G	A	3	737	synonymous_variant	LOW	ND5	0.0137
HLI-0538	13368	G	A	0	767	synonymous_variant	LOW	ND5	0.0495
HLI-0538	15326	A	G	0	698	missense_variant	MODERATE	CYTB	0.9868
HLI-0538	16519	T	C	0	401	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0539	73	A	G	0	328	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0539	263	A	G	1	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0539	458	C	T	3	522	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0539	709	G	A	1	651	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0539	750	A	G	0	688	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0539	930	G	A	2	673	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0539	1438	A	G	1	661	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0539	1709	G	A	1	629	upstream_gene_variant	MODIFIER	RNR2	0.0035
HLI-0539	1888	G	A	5	578	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0539	2706	A	G	1	585	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0539	4216	T	C	0	572	missense_variant	MODERATE	ND1	0.0991
HLI-0539	4769	A	G	0	568	synonymous_variant	LOW	ND2	0.9767
HLI-0539	4917	A	G	6	630	missense_variant	MODERATE	ND2	0.0477
HLI-0539	5147	G	A	4	473	synonymous_variant	LOW	ND2	0.0437
HLI-0539	6782	T	C	8	697	synonymous_variant	LOW	COX1	1.00E-04
HLI-0539	7028	C	T	2	705	synonymous_variant	LOW	COX1	0.8089
HLI-0539	8697	G	A	1	620	synonymous_variant	LOW	ATP6	0.0466
HLI-0539	9300	G	A	2	617	missense_variant	MODERATE	COX3	0.0036
HLI-0539	10463	T	C	0	681	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0539	11251	A	G	1	628	synonymous_variant	LOW	ND4	0.0932
HLI-0539	11533	C	T	3	620	synonymous_variant	LOW	ND4	4.00E-04
HLI-0539	11719	G	A	2	596	synonymous_variant	LOW	ND4	0.7756
HLI-0539	11812	A	G	1	612	synonymous_variant	LOW	ND4	0.0332
HLI-0539	13368	G	A	0	639	synonymous_variant	LOW	ND5	0.0495
HLI-0539	14233	A	G	0	609	synonymous_variant	LOW	ND6	0.0369
HLI-0539	14766	C	T	1	641	missense_variant	MODERATE	CYTB	0.7696
HLI-0539	14905	G	A	0	744	synonymous_variant	LOW	CYTB	0.0526

HLI-0539	15326	A	G	1	508	missense_variant	MODERATE	CYTB	0.9868
HLI-0539	15452	C	A	1	477	missense_variant	MODERATE	CYTB	0.0933
HLI-0539	15607	A	G	1	505	synonymous_variant	LOW	CYTB	0.0508
HLI-0539	15746	A	G	2	599	missense_variant	MODERATE	CYTB	0.0395
HLI-0539	15928	G	A	3	672	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0539	16126	T	C	2	807	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0539	16294	C	T	0	597	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0539	16296	C	T	0	599	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0539	16304	T	C	0	635	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0539	16519	T	C	0	320	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0540	263	A	G	1	301	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0540	750	A	G	1	684	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0540	1438	A	G	1	721	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0540	2248	T	C	3	620	upstream_gene_variant	MODIFIER	RNR2	2.00E-04
HLI-0540	3010	G	A	2	690	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0540	4769	A	G	0	640	synonymous_variant	LOW	ND2	0.9767
HLI-0540	8194	C	T	0	689	synonymous_variant	LOW	COX2	1.00E-04
HLI-0540	16311	T	C	1	591	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0540	16519	T	C	0	421	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0541	73	A	G	0	339	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0541	263	A	G	2	281	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0541	750	A	G	0	648	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0541	1438	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0541	2706	A	G	0	619	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0541	4769	A	G	1	608	synonymous_variant	LOW	ND2	0.9767
HLI-0541	6842	T	C	0	753	synonymous_variant	LOW	COX1	5.00E-04
HLI-0541	6890	A	G	1	795	synonymous_variant	LOW	COX1	5.00E-04
HLI-0541	7028	C	T	0	700	synonymous_variant	LOW	COX1	0.8089
HLI-0541	8014	A	T	0	692	synonymous_variant	LOW	COX2	0.0024
HLI-0541	8426	T	C	0	510	missense_variant	MODERATE	ATP8	3.00E-04
HLI-0541	9055	G	A	0	593	missense_variant	MODERATE	ATP6	0.0425
HLI-0541	10274	T	C	0	642	synonymous_variant	LOW	ND3	0.0024
HLI-0541	10897	C	T	0	623	synonymous_variant	LOW	ND4	5.00E-04
HLI-0541	15218	A	G	0	601	missense_variant	MODERATE	CYTB	0.0169
HLI-0541	15326	A	G	1	522	missense_variant	MODERATE	CYTB	0.9868
HLI-0541	16067	C	T	2	651	upstream_gene_variant	MODIFIER	DLoop	0.0033
HLI-0541	16240	A	G	1	653	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0541	16261	C	T	1	690	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0542	73	A	G	0	321	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0542	227	A	G	41	391	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0542	257	A	G	29	327	upstream_gene_variant	MODIFIER	DLoop	0.0025
HLI-0542	263	A	G	0	338	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0542	750	A	G	0	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0542	1438	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0542	2706	A	G	0	569	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0542	3027	T	C	2	630	upstream_gene_variant	MODIFIER	RNR2	0.0117
HLI-0542	3197	T	C	35	566	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0542	3552	T	C	39	496	synonymous_variant	LOW	ND1	0.0028
HLI-0542	4769	A	G	0	617	synonymous_variant	LOW	ND2	0.9767
HLI-0542	4924	G	C	40	560	missense_variant	MODERATE	ND2	4.00E-04
HLI-0542	6956	T	C	47	634	synonymous_variant	LOW	COX1	9.00E-04
HLI-0542	7028	C	T	0	721	synonymous_variant	LOW	COX1	0.8089
HLI-0542	7674	T	C	51	562	missense_variant	MODERATE	COX2	3.00E-04
HLI-0542	7711	T	C	52	617	synonymous_variant	LOW	COX2	0.002
HLI-0542	9477	G	A	42	599	missense_variant	MODERATE	COX3	0.0387
HLI-0542	10858	T	C	50	609	synonymous_variant	LOW	ND4	3.00E-04
HLI-0542	11467	A	G	57	601	synonymous_variant	LOW	ND4	0.1231
HLI-0542	11719	G	A	1	573	synonymous_variant	LOW	ND4	0.7756
HLI-0542	12308	A	G	39	466	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0542	12372	G	A	36	443	synonymous_variant	LOW	ND5	0.1329
HLI-0542	13617	T	C	34	509	synonymous_variant	LOW	ND5	0.038
HLI-0542	14110	T	C	29	502	missense_variant	MODERATE	ND5	0.0096
HLI-0542	14766	C	T	47	683	missense_variant	MODERATE	CYTB	0.7696
HLI-0542	14793	A	G	52	750	missense_variant	MODERATE	CYTB	0.0199
HLI-0542	15217	G	A	44	495	synonymous_variant	LOW	CYTB	0.0104
HLI-0542	15218	A	G	44	498	missense_variant	MODERATE	CYTB	0.0169
HLI-0542	15326	A	G	0	490	missense_variant	MODERATE	CYTB	0.9868
HLI-0542	16256	C	T	41	548	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0542	16270	C	T	40	512	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0542	16304	T	C	38	496	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0542	16399	A	G	35	494	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0543	73	A	G	0	260	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0543	185	G	A	1	485	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0543	188	A	G	1	488	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0543	228	G	A	2	439	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0543	263	A	G	0	358	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0543	295	C	T	0	312	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0543	462	C	T	2	433	upstream_gene_variant	MODIFIER	DLoop	0.0341

HLI-0543	489	T	C	0	474	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0543	750	A	G	0	396	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0543	1438	A	G	0	418	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0543	2706	A	G	2	409	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0543	3010	G	A	2	408	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0543	4216	T	C	1	371	missense_variant	MODERATE	ND1	0.0991
HLI-0543	4769	A	G	2	465	synonymous_variant	LOW	ND2	0.9767
HLI-0543	7028	C	T	6	495	synonymous_variant	LOW	COX1	0.8089
HLI-0543	10398	A	G	3	468	missense_variant	MODERATE	ND3	0.445
HLI-0543	11251	A	G	0	431	synonymous_variant	LOW	ND4	0.0932
HLI-0543	11719	G	A	0	535	synonymous_variant	LOW	ND4	0.7756
HLI-0543	12612	A	G	3	626	synonymous_variant	LOW	ND5	0.0506
HLI-0543	13708	G	A	3	429	missense_variant	MODERATE	ND5	0.0717
HLI-0543	14766	C	T	3	790	missense_variant	MODERATE	CYTB	0.7696
HLI-0543	14798	T	C	0	789	missense_variant	MODERATE	CYTB	0.0651
HLI-0543	15326	A	G	0	280	missense_variant	MODERATE	CYTB	0.9868
HLI-0543	15452	C	A	1	247	missense_variant	MODERATE	CYTB	0.0933
HLI-0543	15947	A	G	1	515	upstream_gene_variant	MODIFIER	TRNT	2.00E-04
HLI-0543	16069	C	T	3	625	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0543	16126	T	C	1	739	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0543	16519	T	C	1	211	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0544	263	A	G	1	313	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0544	750	A	G	1	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0544	1438	A	G	0	635	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0544	3010	G	A	0	633	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0544	4769	A	G	0	606	synonymous_variant	LOW	ND2	0.9767
HLI-0544	6719	T	C	11	764	synonymous_variant	LOW	COX1	0.041
HLI-0544	8245	A	G	0	540	synonymous_variant	LOW	COX2	2.00E-04
HLI-0544	12618	G	A	7	568	synonymous_variant	LOW	ND5	0.0137
HLI-0544	15326	A	G	0	472	missense_variant	MODERATE	CYTB	0.9868
HLI-0544	16519	T	C	2	292	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0545	263	A	G	2	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0545	629	T	C	18	580	upstream_gene_variant	MODIFIER	TRNF	0.0026
HLI-0545	750	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0545	1438	A	G	0	765	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0545	4769	A	G	4	621	synonymous_variant	LOW	ND2	0.9767
HLI-0545	4793	A	G	4	685	synonymous_variant	LOW	ND2	0.0073
HLI-0545	5348	C	T	9	611	synonymous_variant	LOW	ND2	0.0016
HLI-0545	15326	A	G	0	589	missense_variant	MODERATE	CYTB	0.9868

HLI-0545	16519	T	C	10	346	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0546	263	A	G	0	351	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0546	750	A	G	2	635	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0546	1438	A	G	0	576	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0546	4769	A	G	2	562	synonymous_variant	LOW	ND2	0.9767
HLI-0546	10211	C	T	0	829	synonymous_variant	LOW	ND3	0.0027
HLI-0546	15326	A	G	0	466	missense_variant	MODERATE	CYTB	0.9868
HLI-0546	16519	T	C	1	284	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0547	73	A	G	1	356	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0547	188	A	G	6	594	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0547	263	A	G	1	300	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0547	750	A	G	1	687	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0547	1438	A	G	1	750	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0547	3992	C	T	0	625	missense_variant	MODERATE	ND1	0.0062
HLI-0547	4024	A	G	1	667	missense_variant	MODERATE	ND1	0.0049
HLI-0547	4769	A	G	1	754	synonymous_variant	LOW	ND2	0.9767
HLI-0547	5004	T	C	0	681	synonymous_variant	LOW	ND2	0.0067
HLI-0547	8269	G	A	0	665	stop_retained_variant	LOW	COX2	0.0127
HLI-0547	9123	G	A	1	784	synonymous_variant	LOW	ATP6	0.0485
HLI-0547	10044	A	G	5	784	upstream_gene_variant	MODIFIER	TRNG	0.0027
HLI-0547	13545	C	T	1	633	synonymous_variant	LOW	ND5	2.00E-04
HLI-0547	14365	C	T	1	630	synonymous_variant	LOW	ND6	0.0046
HLI-0547	14582	A	G	2	704	missense_variant	MODERATE	ND6	0.005
HLI-0547	15326	A	G	0	632	missense_variant	MODERATE	CYTB	0.9868
HLI-0548	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0548	263	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0548	750	A	G	1	654	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0548	1438	A	G	0	660	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0548	2706	A	G	2	608	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0548	3420	C	T	1	618	synonymous_variant	LOW	ND1	4.00E-04
HLI-0548	3450	C	T	2	664	synonymous_variant	LOW	ND1	0.0084
HLI-0548	4769	A	G	1	666	synonymous_variant	LOW	ND2	0.9767
HLI-0548	5250	T	C	0	567	synonymous_variant	LOW	ND2	0.0013
HLI-0548	5773	G	A	1	758	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0548	6221	T	C	0	591	synonymous_variant	LOW	COX1	0.0306
HLI-0548	7028	C	T	3	704	synonymous_variant	LOW	COX1	0.8089
HLI-0548	7301	A	G	1	724	synonymous_variant	LOW	COX1	3.00E-04
HLI-0548	8131	C	T	1	620	synonymous_variant	LOW	COX2	1.00E-04
HLI-0548	8701	A	G	1	563	missense_variant	MODERATE	ATP6	0.3391

HLI-0548	9449	C	T	1	625	synonymous_variant	LOW	COX3	0.0125
HLI-0548	9540	T	C	0	670	synonymous_variant	LOW	COX3	0.339
HLI-0548	10086	A	G	0	781	missense_variant	MODERATE	ND3	0.0088
HLI-0548	10398	A	G	0	664	missense_variant	MODERATE	ND3	0.445
HLI-0548	10640	T	C	0	721	synonymous_variant	LOW	ND4L	0.0044
HLI-0548	10873	T	C	2	581	synonymous_variant	LOW	ND4	0.3389
HLI-0548	11150	G	A	2	580	missense_variant	MODERATE	ND4	0.0024
HLI-0548	11719	G	A	0	641	synonymous_variant	LOW	ND4	0.7756
HLI-0548	12705	C	T	0	572	synonymous_variant	LOW	ND5	0.4212
HLI-0548	13105	A	G	0	555	missense_variant	MODERATE	ND5	0.076
HLI-0548	13914	C	A	3	501	synonymous_variant	LOW	ND5	0.0091
HLI-0548	14766	C	T	1	614	missense_variant	MODERATE	CYTB	0.7696
HLI-0548	14914	A	T	0	742	synonymous_variant	LOW	CYTB	0
HLI-0548	15301	G	A	0	574	synonymous_variant	LOW	CYTB	0.2912
HLI-0548	15311	A	G	0	598	missense_variant	MODERATE	CYTB	0.008
HLI-0548	15326	A	G	0	582	missense_variant	MODERATE	CYTB	0.9868
HLI-0548	15824	A	G	0	585	missense_variant	MODERATE	CYTB	0.0083
HLI-0548	16124	T	C	1	418	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0548	16223	C	T	2	309	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0548	16278	C	T	2	482	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0548	16362	T	C	1	585	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0548	16527	C	T	2	292	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0549	65	T	C	0	304	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0549	73	A	G	13	332	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0549	152	T	C	1	677	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0549	263	A	G	0	307	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0549	709	G	A	1	692	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0549	750	A	G	0	757	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0549	930	G	A	5	755	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0549	1438	A	G	1	764	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0549	1888	G	A	0	674	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0549	2706	A	G	1	626	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0549	4216	T	C	0	663	missense_variant	MODERATE	ND1	0.0991
HLI-0549	4769	A	G	1	662	synonymous_variant	LOW	ND2	0.9767
HLI-0549	4917	A	G	0	674	missense_variant	MODERATE	ND2	0.0477
HLI-0549	5147	G	A	1	549	synonymous_variant	LOW	ND2	0.0437
HLI-0549	7028	C	T	2	787	synonymous_variant	LOW	COX1	0.8089
HLI-0549	8197	C	T	2	694	synonymous_variant	LOW	COX2	0
HLI-0549	8697	G	A	2	687	synonymous_variant	LOW	ATP6	0.0466

HLI-0549	9180	A	G	1	749	synonymous_variant	LOW	ATP6	0.0094
HLI-0549	9966	G	A	3	736	missense_variant	MODERATE	COX3	0.0069
HLI-0549	10463	T	C	0	704	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0549	11251	A	G	1	695	synonymous_variant	LOW	ND4	0.0932
HLI-0549	11719	G	A	0	635	synonymous_variant	LOW	ND4	0.7756
HLI-0549	11812	A	G	0	654	synonymous_variant	LOW	ND4	0.0332
HLI-0549	13368	G	A	0	720	synonymous_variant	LOW	ND5	0.0495
HLI-0549	13768	T	C	1	379	missense_variant	MODERATE	ND5	0.0019
HLI-0549	14233	A	G	0	613	synonymous_variant	LOW	ND6	0.0369
HLI-0549	14766	C	T	0	665	missense_variant	MODERATE	CYTB	0.7696
HLI-0549	14905	G	A	1	787	synonymous_variant	LOW	CYTB	0.0526
HLI-0549	15326	A	G	0	581	missense_variant	MODERATE	CYTB	0.9868
HLI-0549	15452	C	A	2	590	missense_variant	MODERATE	CYTB	0.0933
HLI-0549	15607	A	G	0	613	synonymous_variant	LOW	CYTB	0.0508
HLI-0549	15928	G	A	0	685	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0549	16126	T	C	0	663	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0549	16294	C	T	2	643	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0549	16296	C	T	2	630	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0549	16304	T	C	2	620	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0549	16519	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0550	263	A	G	0	298	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0550	750	A	G	0	715	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0550	1438	A	G	0	755	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0550	4769	A	G	0	677	synonymous_variant	LOW	ND2	0.9767
HLI-0550	6776	T	C	4	792	synonymous_variant	LOW	COX1	0.0226
HLI-0550	12811	T	C	16	672	missense_variant	MODERATE	ND5	0.0125
HLI-0550	15326	A	G	0	591	missense_variant	MODERATE	CYTB	0.9868
HLI-0550	16311	T	C	0	639	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0550	16519	T	C	1	412	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0551	73	A	G	0	32	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0551	263	A	G	0	39	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0551	497	C	T	1	41	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0551	750	A	G	0	57	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0551	1189	T	C	0	61	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0551	1438	A	G	0	57	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0551	1811	A	G	2	67	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0551	2706	A	G	0	57	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0551	3480	A	G	0	43	synonymous_variant	LOW	ND1	0.0392
HLI-0551	4697	C	T	0	68	synonymous_variant	LOW	ND2	9.00E-04

HLI-0551	4769	A	G	0	59	synonymous_variant	LOW	ND2	0.9767
HLI-0551	5585	G	A	0	74	upstream_gene_variant	MODIFIER	Unannotated	0.0097
HLI-0551	6134	C	T	1	53	synonymous_variant	LOW	COX1	2.00E-04
HLI-0551	6260	G	A	0	63	synonymous_variant	LOW	COX1	0.009
HLI-0551	6480	G	A	0	68	missense_variant	MODERATE	COX1	0.0031
HLI-0551	6605	A	G	0	92	synonymous_variant	LOW	COX1	5.00E-04
HLI-0551	7028	C	T	0	71	synonymous_variant	LOW	COX1	0.8089
HLI-0551	9055	G	A	0	51	missense_variant	MODERATE	ATP6	0.0425
HLI-0551	9698	T	C	0	66	synonymous_variant	LOW	COX3	0.0405
HLI-0551	10398	A	G	0	69	missense_variant	MODERATE	ND3	0.445
HLI-0551	10550	A	G	0	73	synonymous_variant	LOW	ND4L	0.0376
HLI-0551	11299	T	C	1	59	synonymous_variant	LOW	ND4	0.0417
HLI-0551	11467	A	G	0	73	synonymous_variant	LOW	ND4	0.1231
HLI-0551	11485	T	C	0	76	synonymous_variant	LOW	ND4	0.0081
HLI-0551	11719	G	A	0	57	synonymous_variant	LOW	ND4	0.7756
HLI-0551	11827	T	C	0	74	synonymous_variant	LOW	ND4	0.0015
HLI-0551	12308	A	G	0	64	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0551	12372	G	A	1	49	synonymous_variant	LOW	ND5	0.1329
HLI-0551	13830	T	C	0	47	synonymous_variant	LOW	ND5	0.0021
HLI-0551	14167	C	T	0	48	synonymous_variant	LOW	ND6	0.0385
HLI-0551	14766	C	T	2	65	missense_variant	MODERATE	CYTB	0.7696
HLI-0551	14798	T	C	0	65	missense_variant	MODERATE	CYTB	0.0651
HLI-0551	15326	A	G	0	67	missense_variant	MODERATE	CYTB	0.9868
HLI-0551	16168	C	T	0	79	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0551	16224	T	C	0	62	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0551	16311	T	C	0	47	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0551	16519	T	C	0	32	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0552	239	T	C	0	389	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0552	263	A	G	0	321	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0552	750	A	G	0	521	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0552	1438	A	G	0	576	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0552	3915	G	A	1	547	synonymous_variant	LOW	ND1	0.0106
HLI-0552	4727	A	G	1	656	synonymous_variant	LOW	ND2	0.0063
HLI-0552	4769	A	G	0	687	synonymous_variant	LOW	ND2	0.9767
HLI-0552	9380	G	A	1	626	synonymous_variant	LOW	COX3	0.0094
HLI-0552	11253	T	C	0	473	missense_variant	MODERATE	ND4	0.0053
HLI-0552	15326	A	G	0	360	missense_variant	MODERATE	CYTB	0.9868
HLI-0552	16298	T	C	0	559	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0552	16362	T	C	0	468	upstream_gene_variant	MODIFIER	DLoop	0.1763

HLI-0552	16482	A	G	0	291	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0553	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0553	150	C	T	0	564	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0553	152	T	C	0	565	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0553	195	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0553	263	A	G	0	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0553	750	A	G	0	589	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0553	1438	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0553	2352	T	C	0	597	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0553	2706	A	G	0	518	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0553	4769	A	G	0	615	synonymous_variant	LOW	ND2	0.9767
HLI-0553	7028	C	T	2	670	synonymous_variant	LOW	COX1	0.8089
HLI-0553	8701	A	G	3	616	missense_variant	MODERATE	ATP6	0.3391
HLI-0553	9540	T	C	1	544	synonymous_variant	LOW	COX3	0.339
HLI-0553	10088	C	T	1	729	synonymous_variant	LOW	ND3	3.00E-04
HLI-0553	10398	A	G	0	649	missense_variant	MODERATE	ND3	0.445
HLI-0553	10819	A	G	2	551	synonymous_variant	LOW	ND4	0.0228
HLI-0553	10861	T	C	2	589	synonymous_variant	LOW	ND4	8.00E-04
HLI-0553	10873	T	C	1	591	synonymous_variant	LOW	ND4	0.3389
HLI-0553	11719	G	A	2	605	synonymous_variant	LOW	ND4	0.7756
HLI-0553	12705	C	T	1	671	synonymous_variant	LOW	ND5	0.4212
HLI-0553	14212	T	C	1	611	synonymous_variant	LOW	ND6	0.0204
HLI-0553	14766	C	T	2	651	missense_variant	MODERATE	CYTB	0.7696
HLI-0553	14905	G	A	1	771	synonymous_variant	LOW	CYTB	0.0526
HLI-0553	15301	G	A	2	469	synonymous_variant	LOW	CYTB	0.2912
HLI-0553	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0553	16172	T	C	1	338	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0553	16223	C	T	0	329	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0553	16256	C	T	4	386	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0553	16320	C	T	1	471	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0553	16519	T	C	0	243	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0554	73	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0554	263	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0554	489	T	C	0	365	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0554	709	G	A	4	597	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0554	750	A	G	0	625	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0554	1303	G	A	1	751	upstream_gene_variant	MODIFIER	RNR1	9.00E-04
HLI-0554	1438	A	G	0	664	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0554	1888	G	A	0	564	upstream_gene_variant	MODIFIER	RNR2	0.0558

HLI-0554	2706	A	G	0	548	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0554	3921	C	T	1	566	synonymous_variant	LOW	ND1	0.003
HLI-0554	3954	C	T	1	593	synonymous_variant	LOW	ND1	5.00E-04
HLI-0554	4769	A	G	1	660	synonymous_variant	LOW	ND2	0.9767
HLI-0554	4916	A	G	1	620	synonymous_variant	LOW	ND2	0.0013
HLI-0554	6461	A	G	2	528	synonymous_variant	LOW	COX1	5.00E-04
HLI-0554	7028	C	T	3	609	synonymous_variant	LOW	COX1	0.8089
HLI-0554	8701	A	G	1	656	missense_variant	MODERATE	ATP6	0.3391
HLI-0554	9540	T	C	2	491	synonymous_variant	LOW	COX3	0.339
HLI-0554	9833	T	C	2	825	synonymous_variant	LOW	COX3	0.0013
HLI-0554	10398	A	G	0	686	missense_variant	MODERATE	ND3	0.445
HLI-0554	10400	C	T	0	691	synonymous_variant	LOW	ND3	0.2131
HLI-0554	10873	T	C	0	546	synonymous_variant	LOW	ND4	0.3389
HLI-0554	11719	G	A	2	585	synonymous_variant	LOW	ND4	0.7756
HLI-0554	12477	T	C	7	745	synonymous_variant	LOW	ND5	0.0054
HLI-0554	12705	C	T	0	803	synonymous_variant	LOW	ND5	0.4212
HLI-0554	14323	G	A	0	613	synonymous_variant	LOW	ND6	0.0058
HLI-0554	14766	C	T	2	634	missense_variant	MODERATE	CYTB	0.7696
HLI-0554	14783	T	C	1	738	synonymous_variant	LOW	CYTB	0.2126
HLI-0554	15043	G	A	2	693	synonymous_variant	LOW	CYTB	0.2362
HLI-0554	15287	T	C	1	451	missense_variant	MODERATE	CYTB	0.0015
HLI-0554	15301	G	A	1	475	synonymous_variant	LOW	CYTB	0.2912
HLI-0554	15326	A	G	1	462	missense_variant	MODERATE	CYTB	0.9868
HLI-0554	16129	G	A	0	773	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0554	16223	C	T	1	600	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0554	16291	C	T	1	543	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0554	16298	T	C	1	533	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0554	16519	T	C	0	264	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0555	73	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0555	189	A	G	0	358	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0555	199	T	C	0	366	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0555	203	G	A	0	357	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0555	204	T	C	0	355	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0555	250	T	C	1	308	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0555	263	A	G	0	267	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0555	750	A	G	0	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0555	1438	A	G	1	674	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0555	1719	G	A	1	695	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0555	2706	A	G	2	553	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0555	3398	T	C	1	598	missense_variant	MODERATE	ND1	0.0039
HLI-0555	3447	A	G	0	643	synonymous_variant	LOW	ND1	0.0053
HLI-0555	3990	C	T	1	540	synonymous_variant	LOW	ND1	0.0031
HLI-0555	4529	A	T	1	698	synonymous_variant	LOW	ND2	0.015
HLI-0555	4769	A	G	1	643	synonymous_variant	LOW	ND2	0.9767
HLI-0555	6734	G	A	3	779	synonymous_variant	LOW	COX1	0.0062
HLI-0555	7028	C	T	4	696	synonymous_variant	LOW	COX1	0.8089
HLI-0555	8107	A	G	3	607	synonymous_variant	LOW	COX2	2.00E-04
HLI-0555	8251	G	A	2	674	synonymous_variant	LOW	COX2	0.058
HLI-0555	8616	G	T	3	630	missense_variant	MODERATE	ATP6	0.0032
HLI-0555	9947	G	A	1	746	synonymous_variant	LOW	COX3	0.0092
HLI-0555	10034	T	C	3	725	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0555	10238	T	C	2	670	synonymous_variant	LOW	ND3	0.0623
HLI-0555	10398	A	G	0	679	missense_variant	MODERATE	ND3	0.445
HLI-0555	10915	T	C	4	517	synonymous_variant	LOW	ND4	0.0411
HLI-0555	11719	G	A	4	625	synonymous_variant	LOW	ND4	0.7756
HLI-0555	12501	G	A	5	735	synonymous_variant	LOW	ND5	0.0258
HLI-0555	12705	C	T	1	667	synonymous_variant	LOW	ND5	0.4212
HLI-0555	13780	A	G	1	410	missense_variant	MODERATE	ND5	0.0179
HLI-0555	14766	C	T	1	628	missense_variant	MODERATE	CYTB	0.7696
HLI-0555	15043	G	A	7	687	synonymous_variant	LOW	CYTB	0.2362
HLI-0555	15326	A	G	0	525	missense_variant	MODERATE	CYTB	0.9868
HLI-0555	15924	A	G	3	729	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0555	16129	G	A	1	822	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0555	16172	T	C	3	802	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0555	16223	C	T	3	713	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0555	16298	T	C	1	560	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0555	16311	T	C	1	602	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0555	16391	G	A	4	532	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0555	16519	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0556	73	A	G	1	293	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0556	152	T	C	0	531	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0556	195	T	C	0	502	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0556	239	T	C	0	215	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0556	263	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0556	709	G	A	0	563	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0556	750	A	G	1	611	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0556	1438	A	G	1	570	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0556	1888	G	A	0	446	upstream_gene_variant	MODIFIER	RNR2	0.0558

HLI-0556	2706	A	G	1	587	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0556	4216	T	C	0	448	missense_variant	MODERATE	ND1	0.0991
HLI-0556	4769	A	G	0	539	synonymous_variant	LOW	ND2	0.9767
HLI-0556	4917	A	G	1	536	missense_variant	MODERATE	ND2	0.0477
HLI-0556	7028	C	T	7	607	synonymous_variant	LOW	COX1	0.8089
HLI-0556	8697	G	A	0	532	synonymous_variant	LOW	ATP6	0.0466
HLI-0556	9899	T	C	0	649	synonymous_variant	LOW	COX3	0.0108
HLI-0556	10463	T	C	2	567	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0556	11251	A	G	0	581	synonymous_variant	LOW	ND4	0.0932
HLI-0556	11719	G	A	2	611	synonymous_variant	LOW	ND4	0.7756
HLI-0556	12633	C	A	4	574	synonymous_variant	LOW	ND5	0.0123
HLI-0556	13368	G	A	1	582	synonymous_variant	LOW	ND5	0.0495
HLI-0556	14766	C	T	3	593	missense_variant	MODERATE	CYTB	0.7696
HLI-0556	14905	G	A	1	717	synonymous_variant	LOW	CYTB	0.0526
HLI-0556	15326	A	G	0	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0556	15452	C	A	3	425	missense_variant	MODERATE	CYTB	0.0933
HLI-0556	15607	A	G	0	445	synonymous_variant	LOW	CYTB	0.0508
HLI-0556	15928	G	A	2	542	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0556	16126	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0556	16163	A	G	0	655	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0556	16294	C	T	2	509	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0556	16519	T	C	0	257	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0557	73	A	G	1	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0557	146	T	C	0	568	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0557	152	T	C	0	582	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0557	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0557	750	A	G	1	662	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0557	1189	T	C	3	700	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0557	1438	A	G	0	702	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0557	1811	A	G	2	642	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0557	2706	A	G	2	664	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0557	3480	A	G	2	589	synonymous_variant	LOW	ND1	0.0392
HLI-0557	4769	A	G	0	587	synonymous_variant	LOW	ND2	0.9767
HLI-0557	7028	C	T	4	726	synonymous_variant	LOW	COX1	0.8089
HLI-0557	9055	G	A	1	694	missense_variant	MODERATE	ATP6	0.0425
HLI-0557	9093	A	G	1	739	synonymous_variant	LOW	ATP6	0.0031
HLI-0557	9698	T	C	1	634	synonymous_variant	LOW	COX3	0.0405
HLI-0557	10398	A	G	0	638	missense_variant	MODERATE	ND3	0.445
HLI-0557	10550	A	G	1	650	synonymous_variant	LOW	ND4L	0.0376

HLI-0557	11299	T	C	2	605	synonymous_variant	LOW	ND4	0.0417
HLI-0557	11377	G	A	0	660	synonymous_variant	LOW	ND4	0.0125
HLI-0557	11467	A	G	0	676	synonymous_variant	LOW	ND4	0.1231
HLI-0557	11719	G	A	0	611	synonymous_variant	LOW	ND4	0.7756
HLI-0557	12308	A	G	0	562	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0557	12372	G	A	2	552	synonymous_variant	LOW	ND5	0.1329
HLI-0557	14167	C	T	2	534	synonymous_variant	LOW	ND6	0.0385
HLI-0557	14766	C	T	5	619	missense_variant	MODERATE	CYTB	0.7696
HLI-0557	14798	T	C	0	670	missense_variant	MODERATE	CYTB	0.0651
HLI-0557	15326	A	G	1	555	missense_variant	MODERATE	CYTB	0.9868
HLI-0557	16224	T	C	4	570	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0557	16311	T	C	2	562	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0557	16519	T	C	1	293	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0558	73	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0558	185	G	A	1	422	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0558	263	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0558	295	C	T	0	206	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0558	462	C	T	2	426	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0558	489	T	C	0	454	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0558	750	A	G	0	474	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0558	1438	A	G	0	474	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0558	2706	A	G	2	450	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0558	3010	G	A	1	499	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0558	4216	T	C	3	378	missense_variant	MODERATE	ND1	0.0991
HLI-0558	4769	A	G	0	489	synonymous_variant	LOW	ND2	0.9767
HLI-0558	7028	C	T	3	532	synonymous_variant	LOW	COX1	0.8089
HLI-0558	10398	A	G	1	426	missense_variant	MODERATE	ND3	0.445
HLI-0558	10497	C	T	0	456	synonymous_variant	LOW	ND4L	0.0019
HLI-0558	11251	A	G	0	488	synonymous_variant	LOW	ND4	0.0932
HLI-0558	11719	G	A	0	484	synonymous_variant	LOW	ND4	0.7756
HLI-0558	12612	A	G	0	560	synonymous_variant	LOW	ND5	0.0506
HLI-0558	13708	G	A	1	408	missense_variant	MODERATE	ND5	0.0717
HLI-0558	13934	C	T	1	390	missense_variant	MODERATE	ND5	0.0122
HLI-0558	14766	C	T	6	560	missense_variant	MODERATE	CYTB	0.7696
HLI-0558	14798	T	C	1	646	missense_variant	MODERATE	CYTB	0.0651
HLI-0558	15326	A	G	0	355	missense_variant	MODERATE	CYTB	0.9868
HLI-0558	15452	C	A	8	301	missense_variant	MODERATE	CYTB	0.0933
HLI-0558	16069	C	T	3	544	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0558	16126	T	C	0	639	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0559	73	A	G	1	304	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0559	185	G	A	3	465	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0559	228	G	A	2	353	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0559	263	A	G	1	278	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0559	295	C	T	2	226	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0559	462	C	T	3	493	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0559	489	T	C	1	558	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0559	750	A	G	1	711	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0559	1438	A	G	0	690	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0559	2706	A	G	1	631	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0559	3010	G	A	1	656	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0559	4025	C	T	0	525	missense_variant	MODERATE	ND1	0.0072
HLI-0559	4216	T	C	0	600	missense_variant	MODERATE	ND1	0.0991
HLI-0559	4769	A	G	2	602	synonymous_variant	LOW	ND2	0.9767
HLI-0559	7028	C	T	3	716	synonymous_variant	LOW	COX1	0.8089
HLI-0559	10398	A	G	0	667	missense_variant	MODERATE	ND3	0.445
HLI-0559	11251	A	G	2	599	synonymous_variant	LOW	ND4	0.0932
HLI-0559	11719	G	A	0	601	synonymous_variant	LOW	ND4	0.7756
HLI-0559	12612	A	G	7	664	synonymous_variant	LOW	ND5	0.0506
HLI-0559	13708	G	A	0	471	missense_variant	MODERATE	ND5	0.0717
HLI-0559	14766	C	T	3	591	missense_variant	MODERATE	CYTB	0.7696
HLI-0559	14798	T	C	1	662	missense_variant	MODERATE	CYTB	0.0651
HLI-0559	15326	A	G	0	529	missense_variant	MODERATE	CYTB	0.9868
HLI-0559	15452	C	A	5	548	missense_variant	MODERATE	CYTB	0.0933
HLI-0559	16069	C	T	1	598	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0559	16126	T	C	1	599	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0560	73	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0560	146	T	C	1	497	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0560	195	T	C	0	454	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0560	263	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0560	499	G	A	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0560	750	A	G	0	409	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0560	1438	A	G	0	488	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0560	1811	A	G	2	379	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0560	2706	A	G	0	404	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0560	3672	A	G	0	338	synonymous_variant	LOW	ND1	0.0013
HLI-0560	4646	T	C	2	553	synonymous_variant	LOW	ND2	0.0124
HLI-0560	4769	A	G	1	472	synonymous_variant	LOW	ND2	0.9767
HLI-0560	5999	T	C	2	503	synonymous_variant	LOW	COX1	0.0127

HLI-0560	6047	A	G	2	562	synonymous_variant	LOW	COX1	0.0114
HLI-0560	7028	C	T	1	527	synonymous_variant	LOW	COX1	0.8089
HLI-0560	7265	A	G	1	617	synonymous_variant	LOW	COX1	3.00E-04
HLI-0560	7705	T	C	0	463	synonymous_variant	LOW	COX2	0.0034
HLI-0560	9989	T	C	1	594	synonymous_variant	LOW	COX3	4.00E-04
HLI-0560	11332	C	T	0	466	synonymous_variant	LOW	ND4	0.0115
HLI-0560	11339	T	C	0	491	synonymous_variant	LOW	ND4	0.0028
HLI-0560	11467	A	G	0	517	synonymous_variant	LOW	ND4	0.1231
HLI-0560	11674	C	T	2	488	synonymous_variant	LOW	ND4	0.0116
HLI-0560	11719	G	A	1	520	synonymous_variant	LOW	ND4	0.7756
HLI-0560	12308	A	G	0	442	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0560	12372	G	A	1	417	synonymous_variant	LOW	ND5	0.1329
HLI-0560	14620	C	T	3	680	synonymous_variant	LOW	ND6	0.0126
HLI-0560	14766	C	T	1	610	missense_variant	MODERATE	CYTB	0.7696
HLI-0560	15326	A	G	0	284	missense_variant	MODERATE	CYTB	0.9868
HLI-0560	15693	T	C	2	316	missense_variant	MODERATE	CYTB	0.0114
HLI-0560	16356	T	C	2	408	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0560	16519	T	C	1	214	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0561	73	A	G	2	308	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0561	146	T	C	0	527	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0561	152	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0561	195	T	C	2	511	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0561	263	A	G	0	201	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0561	750	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0561	769	G	A	1	727	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0561	1018	G	A	0	707	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0561	1438	A	G	0	692	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0561	2416	T	C	0	591	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0561	2706	A	G	1	673	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0561	2789	C	T	2	716	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0561	3505	A	G	0	662	missense_variant	MODERATE	ND1	0.0144
HLI-0561	3594	C	T	1	612	synonymous_variant	LOW	ND1	0.0789
HLI-0561	4104	A	G	0	541	synonymous_variant	LOW	ND1	0.0785
HLI-0561	4703	T	C	1	622	synonymous_variant	LOW	ND2	0.0058
HLI-0561	4769	A	G	1	627	synonymous_variant	LOW	ND2	0.9767
HLI-0561	4772	T	C	0	628	synonymous_variant	LOW	ND2	0.0021
HLI-0561	7028	C	T	0	692	synonymous_variant	LOW	COX1	0.8089
HLI-0561	7175	T	C	2	633	synonymous_variant	LOW	COX1	0.0224
HLI-0561	7256	C	T	2	641	synonymous_variant	LOW	COX1	0.0784

HLI-0561	7274	C	T	2	627	synonymous_variant	LOW	COX1	0.0214
HLI-0561	7521	G	A	0	565	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0561	7771	A	G	1	629	synonymous_variant	LOW	COX2	0.0223
HLI-0561	8206	G	A	0	695	synonymous_variant	LOW	COX2	0.0287
HLI-0561	8701	A	G	0	585	missense_variant	MODERATE	ATP6	0.3391
HLI-0561	9221	A	G	0	693	synonymous_variant	LOW	COX3	0.0277
HLI-0561	9540	T	C	1	721	synonymous_variant	LOW	COX3	0.339
HLI-0561	10115	T	C	1	668	synonymous_variant	LOW	ND3	0.0278
HLI-0561	10398	A	G	1	662	missense_variant	MODERATE	ND3	0.445
HLI-0561	10873	T	C	0	552	synonymous_variant	LOW	ND4	0.3389
HLI-0561	11719	G	A	0	639	synonymous_variant	LOW	ND4	0.7756
HLI-0561	11914	G	A	1	656	synonymous_variant	LOW	ND4	0.1112
HLI-0561	11944	T	C	2	683	synonymous_variant	LOW	ND4	0.0331
HLI-0561	12693	A	G	1	696	synonymous_variant	LOW	ND5	0.0205
HLI-0561	12705	C	T	1	754	synonymous_variant	LOW	ND5	0.4212
HLI-0561	12976	C	T	0	689	synonymous_variant	LOW	ND5	6.00E-04
HLI-0561	13590	G	A	2	607	synonymous_variant	LOW	ND5	0.0586
HLI-0561	13650	C	T	2	670	synonymous_variant	LOW	ND5	0.079
HLI-0561	13764	C	T	1	613	synonymous_variant	LOW	ND5	3.00E-04
HLI-0561	13803	A	G	1	627	synonymous_variant	LOW	ND5	0.0216
HLI-0561	13824	A	G	1	606	synonymous_variant	LOW	ND5	4.00E-04
HLI-0561	14566	A	G	0	598	synonymous_variant	LOW	ND6	0.0214
HLI-0561	14766	C	T	3	616	missense_variant	MODERATE	CYTB	0.7696
HLI-0561	15301	G	A	0	609	synonymous_variant	LOW	CYTB	0.2912
HLI-0561	15326	A	G	0	647	missense_variant	MODERATE	CYTB	0.9868
HLI-0561	15784	T	C	0	602	synonymous_variant	LOW	CYTB	0.0363
HLI-0561	16223	C	T	0	505	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0561	16234	C	T	0	535	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0561	16249	T	C	0	538	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0561	16278	C	T	2	466	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0561	16294	C	T	0	455	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0561	16295	C	T	0	457	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0561	16390	G	A	1	489	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0562	195	T	C	2	468	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0562	263	A	G	1	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0562	750	A	G	0	672	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0562	961	T	G	0	729	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0562	1438	A	G	2	651	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0562	4769	A	G	1	625	synonymous_variant	LOW	ND2	0.9767

HLI-0562	5585	G	A	2	680	upstream_gene_variant	MODIFIER	Unannotated	0.0097
HLI-0562	8448	T	C	0	463	missense_variant	MODERATE	ATP8	0.0041
HLI-0562	11377	G	A	2	627	synonymous_variant	LOW	ND4	0.0125
HLI-0562	12235	T	C	3	526	upstream_gene_variant	MODIFIER	TRNS2	0.0044
HLI-0562	13759	G	A	1	417	missense_variant	MODERATE	ND5	0.0348
HLI-0562	14587	A	G	1	617	synonymous_variant	LOW	ND6	0.006
HLI-0562	15326	A	G	0	556	missense_variant	MODERATE	CYTB	0.9868
HLI-0562	15670	T	C	0	529	synonymous_variant	LOW	CYTB	0.0176
HLI-0562	16092	T	C	3	602	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0562	16140	T	C	0	669	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0562	16265	A	G	1	635	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0562	16293	A	G	1	650	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0562	16311	T	C	1	606	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0563	195	T	C	0	52	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0563	263	A	G	0	21	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0563	750	A	G	0	49	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0563	1438	A	G	0	37	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0563	4769	A	G	0	55	synonymous_variant	LOW	ND2	0.9767
HLI-0563	8404	T	C	0	33	synonymous_variant	LOW	ATP8	0.0015
HLI-0563	11560	A	G	2	45	synonymous_variant	LOW	ND4	0.0015
HLI-0563	15058	C	T	1	62	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0563	15326	A	G	0	44	missense_variant	MODERATE	CYTB	0.9868
HLI-0563	16519	T	C	0	30	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0564	73	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0564	152	T	C	1	524	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0564	199	T	C	1	483	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0564	263	A	G	1	184	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0564	750	A	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0564	1189	T	C	1	682	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0564	1438	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0564	1811	A	G	2	632	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0564	2706	A	G	1	627	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0564	3480	A	G	0	613	synonymous_variant	LOW	ND1	0.0392
HLI-0564	4646	T	C	1	663	synonymous_variant	LOW	ND2	0.0124
HLI-0564	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767
HLI-0564	5913	G	A	4	682	missense_variant	MODERATE	COX1	0.0097
HLI-0564	7028	C	T	1	693	synonymous_variant	LOW	COX1	0.8089
HLI-0564	9055	G	A	1	621	missense_variant	MODERATE	ATP6	0.0425
HLI-0564	9698	T	C	0	583	synonymous_variant	LOW	COX3	0.0405

HLI-0564	9962	G	A	1	645	synonymous_variant	LOW	COX3	0.0034
HLI-0564	10289	A	G	2	589	synonymous_variant	LOW	ND3	0.0032
HLI-0564	10398	A	G	1	703	missense_variant	MODERATE	ND3	0.445
HLI-0564	10550	A	G	1	681	synonymous_variant	LOW	ND4L	0.0376
HLI-0564	11204	T	C	0	564	missense_variant	MODERATE	ND4	0.003
HLI-0564	11299	T	C	1	589	synonymous_variant	LOW	ND4	0.0417
HLI-0564	11467	A	G	0	640	synonymous_variant	LOW	ND4	0.1231
HLI-0564	11719	G	A	1	647	synonymous_variant	LOW	ND4	0.7756
HLI-0564	11923	A	G	1	615	synonymous_variant	LOW	ND4	0.0023
HLI-0564	12308	A	G	0	593	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0564	12372	G	A	1	603	synonymous_variant	LOW	ND5	0.1329
HLI-0564	13967	C	T	0	563	missense_variant	MODERATE	ND5	0.003
HLI-0564	14167	C	T	2	536	synonymous_variant	LOW	ND6	0.0385
HLI-0564	14766	C	T	6	561	missense_variant	MODERATE	CYTB	0.7696
HLI-0564	14798	T	C	1	641	missense_variant	MODERATE	CYTB	0.0651
HLI-0564	15257	G	A	0	573	missense_variant	MODERATE	CYTB	0.0155
HLI-0564	15326	A	G	0	620	missense_variant	MODERATE	CYTB	0.9868
HLI-0564	15458	T	C	0	558	missense_variant	MODERATE	CYTB	0.0027
HLI-0564	15946	C	T	0	587	upstream_gene_variant	MODIFIER	TRNT	0.0018
HLI-0564	16093	T	C	11	521	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0564	16224	T	C	1	582	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0564	16311	T	C	0	542	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0564	16319	G	A	0	564	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0564	16463	A	G	1	439	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0564	16519	T	C	1	315	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0565	73	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0565	228	G	A	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0565	263	A	G	0	251	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0565	295	C	T	1	181	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0565	462	C	T	6	408	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0565	489	T	C	1	448	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0565	750	A	G	0	457	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0565	1438	A	G	3	513	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0565	2706	A	G	1	467	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0565	3010	G	A	1	558	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0565	4216	T	C	0	462	missense_variant	MODERATE	ND1	0.0991
HLI-0565	4767	A	G	0	532	missense_variant	MODERATE	ND2	0.0029
HLI-0565	4769	A	G	0	543	synonymous_variant	LOW	ND2	0.9767
HLI-0565	7028	C	T	4	521	synonymous_variant	LOW	COX1	0.8089

HLI-0565	9755	G	A	1	550	synonymous_variant	LOW	COX3	0.0303
HLI-0565	10398	A	G	1	520	missense_variant	MODERATE	ND3	0.445
HLI-0565	11251	A	G	0	487	synonymous_variant	LOW	ND4	0.0932
HLI-0565	11719	G	A	0	536	synonymous_variant	LOW	ND4	0.7756
HLI-0565	12612	A	G	16	614	synonymous_variant	LOW	ND5	0.0506
HLI-0565	13708	G	A	1	487	missense_variant	MODERATE	ND5	0.0717
HLI-0565	13934	C	T	3	441	missense_variant	MODERATE	ND5	0.0122
HLI-0565	14766	C	T	3	647	missense_variant	MODERATE	CYTB	0.7696
HLI-0565	14798	T	C	0	660	missense_variant	MODERATE	CYTB	0.0651
HLI-0565	15326	A	G	0	404	missense_variant	MODERATE	CYTB	0.9868
HLI-0565	15452	C	A	2	345	missense_variant	MODERATE	CYTB	0.0933
HLI-0565	16069	C	T	1	618	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0565	16126	T	C	0	670	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0565	16362	T	C	0	373	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0566	263	A	G	1	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0566	750	A	G	1	600	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0566	1438	A	G	0	662	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0566	4769	A	G	2	578	synonymous_variant	LOW	ND2	0.9767
HLI-0566	14470	T	A	1	525	synonymous_variant	LOW	ND6	0.0031
HLI-0566	15326	A	G	0	458	missense_variant	MODERATE	CYTB	0.9868
HLI-0566	16221	C	T	5	555	upstream_gene_variant	MODIFIER	DLoop	0.007
HLI-0566	16519	T	C	0	271	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0567	73	A	G	0	339	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0567	150	C	T	2	594	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0567	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0567	723	A	C	0	680	upstream_gene_variant	MODIFIER	RNR1	9.00E-04
HLI-0567	750	A	G	2	737	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0567	1438	A	G	0	682	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0567	1811	A	G	1	550	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0567	2294	A	G	0	556	upstream_gene_variant	MODIFIER	RNR2	0.0027
HLI-0567	2706	A	G	0	703	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0567	3010	G	A	3	599	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0567	4703	T	C	1	645	synonymous_variant	LOW	ND2	0.0058
HLI-0567	4769	A	G	1	682	synonymous_variant	LOW	ND2	0.9767
HLI-0567	6518	C	T	1	634	synonymous_variant	LOW	COX1	0.0025
HLI-0567	7028	C	T	2	712	synonymous_variant	LOW	COX1	0.8089
HLI-0567	9266	G	A	1	663	synonymous_variant	LOW	COX3	0.0049
HLI-0567	10506	A	G	0	652	missense_variant	MODERATE	ND4L	0.0025
HLI-0567	11467	A	G	0	648	synonymous_variant	LOW	ND4	0.1231

HLI-0567	11719	G	A	1	630	synonymous_variant	LOW	ND4	0.7756
HLI-0567	12308	A	G	0	494	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0567	12372	G	A	2	485	synonymous_variant	LOW	ND5	0.1329
HLI-0567	13934	C	T	0	486	missense_variant	MODERATE	ND5	0.0122
HLI-0567	14139	A	G	0	475	synonymous_variant	LOW	ND5	0.0056
HLI-0567	14766	C	T	2	630	missense_variant	MODERATE	CYTB	0.7696
HLI-0567	15326	A	G	0	569	missense_variant	MODERATE	CYTB	0.9868
HLI-0567	15454	T	C	0	518	synonymous_variant	LOW	CYTB	0.0072
HLI-0567	16343	A	G	2	551	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0567	16390	G	A	1	577	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0567	16519	T	C	0	329	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0568	73	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0568	152	T	C	0	469	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0568	217	T	C	0	357	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0568	263	A	G	0	315	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0568	340	C	T	0	296	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0568	508	A	G	6	395	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0568	750	A	G	1	498	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0568	988	G	A	0	652	upstream_gene_variant	MODIFIER	RNR1	8.00E-04
HLI-0568	1438	A	G	1	567	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0568	1811	A	G	0	431	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0568	2706	A	G	0	561	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0568	3720	A	G	1	492	synonymous_variant	LOW	ND1	0.0069
HLI-0568	4769	A	G	1	504	synonymous_variant	LOW	ND2	0.9767
HLI-0568	5390	A	G	0	422	synonymous_variant	LOW	ND2	0.0069
HLI-0568	5426	T	C	0	498	synonymous_variant	LOW	ND2	0.0091
HLI-0568	6045	C	T	0	621	synonymous_variant	LOW	COX1	0.0065
HLI-0568	6152	T	C	0	587	synonymous_variant	LOW	COX1	0.0077
HLI-0568	7028	C	T	0	637	synonymous_variant	LOW	COX1	0.8089
HLI-0568	7109	C	T	1	676	synonymous_variant	LOW	COX1	9.00E-04
HLI-0568	10876	A	G	1	488	synonymous_variant	LOW	ND4	0.0098
HLI-0568	11467	A	G	0	578	synonymous_variant	LOW	ND4	0.1231
HLI-0568	11719	G	A	1	549	synonymous_variant	LOW	ND4	0.7756
HLI-0568	11857	C	T	0	483	synonymous_variant	LOW	ND4	1.00E-04
HLI-0568	12308	A	G	1	357	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0568	12372	G	A	1	304	synonymous_variant	LOW	ND5	0.1329
HLI-0568	13020	T	C	11	528	synonymous_variant	LOW	ND5	0.0106
HLI-0568	13734	T	C	1	422	synonymous_variant	LOW	ND5	0.0067
HLI-0568	14766	C	T	1	602	missense_variant	MODERATE	CYTB	0.7696

HLI-0568	15326	A	G	1	383	missense_variant	MODERATE	CYTB	0.9868
HLI-0568	15784	T	C	0	369	synonymous_variant	LOW	CYTB	0.0363
HLI-0568	15907	A	G	0	423	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0568	16051	A	G	0	450	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0568	16129	G	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0568	16256	C	T	4	381	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0568	16519	T	C	0	195	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0569	263	A	G	1	105	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0569	750	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0569	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0569	2259	C	T	1	611	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0569	4745	A	G	1	611	synonymous_variant	LOW	ND2	0.0039
HLI-0569	4769	A	G	1	661	synonymous_variant	LOW	ND2	0.9767
HLI-0569	7337	G	A	0	605	synonymous_variant	LOW	COX1	0.0119
HLI-0569	13326	T	C	0	594	synonymous_variant	LOW	ND5	0.0032
HLI-0569	13680	C	T	1	496	synonymous_variant	LOW	ND5	0.005
HLI-0569	14727	T	C	2	545	upstream_gene_variant	MODIFIER	TRNE	0.0025
HLI-0569	14872	C	T	2	700	synonymous_variant	LOW	CYTB	0.0061
HLI-0569	15326	A	G	0	572	missense_variant	MODERATE	CYTB	0.9868
HLI-0569	16153	G	A	1	651	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0570	204	T	C	1	391	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0570	239	T	C	0	332	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0570	263	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0570	750	A	G	1	620	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0570	1438	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0570	3915	G	A	0	572	synonymous_variant	LOW	ND1	0.0106
HLI-0570	4727	A	G	4	594	synonymous_variant	LOW	ND2	0.0063
HLI-0570	4769	A	G	0	616	synonymous_variant	LOW	ND2	0.9767
HLI-0570	9380	G	A	0	686	synonymous_variant	LOW	COX3	0.0094
HLI-0570	10310	G	C	0	607	synonymous_variant	LOW	ND3	3.00E-04
HLI-0570	10589	G	A	2	595	synonymous_variant	LOW	ND4L	0.0355
HLI-0570	15326	A	G	0	518	missense_variant	MODERATE	CYTB	0.9868
HLI-0570	16219	A	G	0	628	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0570	16362	T	C	2	474	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0570	16482	A	G	3	362	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0571	263	A	G	0	42	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0571	750	A	G	0	54	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0571	1438	A	G	0	43	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0571	4769	A	G	0	56	synonymous_variant	LOW	ND2	0.9767

HLI-0571	11788	C	T	0	41	synonymous_variant	LOW	ND4	7.00E-04
HLI-0571	15326	A	G	0	61	missense_variant	MODERATE	CYTB	0.9868
HLI-0571	16519	T	C	0	29	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0572	73	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0572	195	T	C	0	448	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0572	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0572	497	C	T	3	449	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0572	750	A	G	0	551	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0572	1189	T	C	0	620	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0572	1438	A	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0572	1811	A	G	1	560	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0572	2706	A	G	1	561	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0572	2755	A	G	2	586	upstream_gene_variant	MODIFIER	RNR2	0.0047
HLI-0572	3010	G	A	0	582	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0572	3480	A	G	1	459	synonymous_variant	LOW	ND1	0.0392
HLI-0572	4029	C	A	2	421	missense_variant	MODERATE	ND1	4.00E-04
HLI-0572	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767
HLI-0572	7028	C	T	0	647	synonymous_variant	LOW	COX1	0.8089
HLI-0572	9055	G	A	1	539	missense_variant	MODERATE	ATP6	0.0425
HLI-0572	9698	T	C	0	523	synonymous_variant	LOW	COX3	0.0405
HLI-0572	10398	A	G	1	571	missense_variant	MODERATE	ND3	0.445
HLI-0572	10550	A	G	1	572	synonymous_variant	LOW	ND4L	0.0376
HLI-0572	11299	T	C	0	524	synonymous_variant	LOW	ND4	0.0417
HLI-0572	11467	A	G	1	611	synonymous_variant	LOW	ND4	0.1231
HLI-0572	11719	G	A	0	546	synonymous_variant	LOW	ND4	0.7756
HLI-0572	12308	A	G	1	515	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0572	12372	G	A	1	497	synonymous_variant	LOW	ND5	0.1329
HLI-0572	14167	C	T	1	508	synonymous_variant	LOW	ND6	0.0385
HLI-0572	14221	T	C	0	553	synonymous_variant	LOW	ND6	0.0027
HLI-0572	14766	C	T	0	571	missense_variant	MODERATE	CYTB	0.7696
HLI-0572	14798	T	C	1	660	missense_variant	MODERATE	CYTB	0.0651
HLI-0572	15326	A	G	0	461	missense_variant	MODERATE	CYTB	0.9868
HLI-0572	16093	T	C	17	483	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0572	16224	T	C	1	491	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0572	16311	T	C	1	458	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0572	16519	T	C	0	205	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0573	73	A	G	1	291	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0573	153	A	G	4	515	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0573	195	T	C	1	513	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0573	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0573	750	A	G	1	642	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0573	1438	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0573	1719	G	A	1	588	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0573	2706	A	G	1	619	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0573	4769	A	G	0	532	synonymous_variant	LOW	ND2	0.9767
HLI-0573	6221	T	C	3	563	synonymous_variant	LOW	COX1	0.0306
HLI-0573	6371	C	T	1	541	synonymous_variant	LOW	COX1	0.0097
HLI-0573	7028	C	T	1	609	synonymous_variant	LOW	COX1	0.8089
HLI-0573	8393	C	T	0	461	missense_variant	MODERATE	ATP8	0.0036
HLI-0573	9083	T	C	1	508	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0573	11719	G	A	2	558	synonymous_variant	LOW	ND4	0.7756
HLI-0573	12705	C	T	0	538	synonymous_variant	LOW	ND5	0.4212
HLI-0573	13708	G	A	1	474	missense_variant	MODERATE	ND5	0.0717
HLI-0573	13966	A	G	1	518	missense_variant	MODERATE	ND5	0.0126
HLI-0573	14470	T	C	0	445	synonymous_variant	LOW	ND6	0.0166
HLI-0573	14766	C	T	4	513	missense_variant	MODERATE	CYTB	0.7696
HLI-0573	15326	A	G	1	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0573	15927	G	A	0	575	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0573	16179	C	T	1	170	upstream_gene_variant	MODIFIER	DLoop	0.0082
HLI-0573	16223	C	T	1	242	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0573	16278	C	T	2	399	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0573	16519	T	C	2	205	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0574	73	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0574	150	C	T	1	559	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0574	263	A	G	1	197	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0574	750	A	G	1	601	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0574	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0574	1811	A	G	0	638	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0574	2706	A	G	0	568	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0574	3546	C	A	8	535	synonymous_variant	LOW	ND1	9.00E-04
HLI-0574	4188	A	G	0	565	synonymous_variant	LOW	ND1	0.003
HLI-0574	4640	C	A	2	642	missense_variant	MODERATE	ND2	0.0029
HLI-0574	4769	A	G	1	566	synonymous_variant	LOW	ND2	0.9767
HLI-0574	6359	A	G	0	580	synonymous_variant	LOW	COX1	0.0014
HLI-0574	7028	C	T	4	691	synonymous_variant	LOW	COX1	0.8089
HLI-0574	8867	T	C	0	571	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0574	9656	T	C	1	640	synonymous_variant	LOW	COX3	0.0035
HLI-0574	10469	A	G	1	609	upstream_gene_variant	MODIFIER	TRNR	0

HLI-0574	11467	A	G	0	605	synonymous_variant	LOW	ND4	0.1231
HLI-0574	11719	G	A	0	586	synonymous_variant	LOW	ND4	0.7756
HLI-0574	12308	A	G	0	506	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0574	12372	G	A	1	537	synonymous_variant	LOW	ND5	0.1329
HLI-0574	12720	A	G	1	676	synonymous_variant	LOW	ND5	0.0302
HLI-0574	13743	T	C	0	392	synonymous_variant	LOW	ND5	0.0037
HLI-0574	14139	A	G	0	479	synonymous_variant	LOW	ND5	0.0056
HLI-0574	14766	C	T	2	567	missense_variant	MODERATE	CYTB	0.7696
HLI-0574	15326	A	G	0	560	missense_variant	MODERATE	CYTB	0.9868
HLI-0574	15454	T	C	0	550	synonymous_variant	LOW	CYTB	0.0072
HLI-0574	16343	A	G	2	471	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0575	263	A	G	1	250	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0575	3350	T	C	1	507	missense_variant	MODERATE	ND1	4.00E-04
HLI-0575	15326	A	G	1	423	missense_variant	MODERATE	CYTB	0.9868
HLI-0575	16235	A	G	3	526	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0575	16291	C	T	4	481	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0576	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0576	114	C	T	1	427	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0576	263	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0576	497	C	T	3	519	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0576	750	A	G	0	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0576	1189	T	C	0	627	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0576	1438	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0576	1811	A	G	0	622	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0576	2706	A	G	1	622	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0576	3480	A	G	0	547	synonymous_variant	LOW	ND1	0.0392
HLI-0576	4769	A	G	0	530	synonymous_variant	LOW	ND2	0.9767
HLI-0576	7028	C	T	0	662	synonymous_variant	LOW	COX1	0.8089
HLI-0576	9055	G	A	0	634	missense_variant	MODERATE	ATP6	0.0425
HLI-0576	9698	T	C	0	603	synonymous_variant	LOW	COX3	0.0405
HLI-0576	10398	A	G	0	622	missense_variant	MODERATE	ND3	0.445
HLI-0576	10550	A	G	0	587	synonymous_variant	LOW	ND4L	0.0376
HLI-0576	10978	A	G	0	391	synonymous_variant	LOW	ND4	0.0036
HLI-0576	11084	A	G	1	587	missense_variant	MODERATE	ND4	0.004
HLI-0576	11299	T	C	0	606	synonymous_variant	LOW	ND4	0.0417
HLI-0576	11467	A	G	1	635	synonymous_variant	LOW	ND4	0.1231
HLI-0576	11470	A	G	1	654	synonymous_variant	LOW	ND4	0.0029
HLI-0576	11719	G	A	0	675	synonymous_variant	LOW	ND4	0.7756
HLI-0576	11914	G	A	1	554	synonymous_variant	LOW	ND4	0.1112

HLI-0576	12308	A	G	0	546	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0576	12372	G	A	1	606	synonymous_variant	LOW	ND5	0.1329
HLI-0576	12954	T	C	2	545	synonymous_variant	LOW	ND5	0.0017
HLI-0576	14167	C	T	1	498	synonymous_variant	LOW	ND6	0.0385
HLI-0576	14766	C	T	2	586	missense_variant	MODERATE	CYTB	0.7696
HLI-0576	14798	T	C	2	652	missense_variant	MODERATE	CYTB	0.0651
HLI-0576	15326	A	G	0	536	missense_variant	MODERATE	CYTB	0.9868
HLI-0576	15924	A	G	1	645	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0576	16223	C	T	0	531	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0576	16224	T	C	0	538	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0576	16234	C	T	1	549	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0576	16311	T	C	0	535	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0576	16519	T	C	1	234	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0577	73	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0577	152	T	C	1	515	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0577	263	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0577	750	A	G	2	636	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0577	921	T	C	0	619	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0577	1438	A	G	0	612	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0577	4769	A	G	1	565	synonymous_variant	LOW	ND2	0.9767
HLI-0577	5147	G	A	0	443	synonymous_variant	LOW	ND2	0.0437
HLI-0577	5580	T	C	0	511	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0577	6551	C	T	2	557	synonymous_variant	LOW	COX1	1.00E-04
HLI-0577	6680	T	C	1	662	synonymous_variant	LOW	COX1	0.0226
HLI-0577	7028	C	T	0	673	synonymous_variant	LOW	COX1	0.8089
HLI-0577	7424	A	G	2	610	synonymous_variant	LOW	COX1	0.0115
HLI-0577	8618	T	C	0	371	missense_variant	MODERATE	ATP6	0.0103
HLI-0577	8701	A	G	1	505	missense_variant	MODERATE	ATP6	0.3391
HLI-0577	8865	G	A	0	548	synonymous_variant	LOW	ATP6	0.003
HLI-0577	9540	T	C	0	581	synonymous_variant	LOW	COX3	0.339
HLI-0577	10398	A	G	0	588	missense_variant	MODERATE	ND3	0.445
HLI-0577	10873	T	C	1	498	synonymous_variant	LOW	ND4	0.3389
HLI-0577	11719	G	A	0	575	synonymous_variant	LOW	ND4	0.7756
HLI-0577	12705	C	T	0	572	synonymous_variant	LOW	ND5	0.4212
HLI-0577	13105	A	G	1	609	missense_variant	MODERATE	ND5	0.076
HLI-0577	13886	T	C	0	438	missense_variant	MODERATE	ND5	0.0088
HLI-0577	14284	C	T	2	490	synonymous_variant	LOW	ND6	0.0087
HLI-0577	14766	C	T	5	544	missense_variant	MODERATE	CYTB	0.7696
HLI-0577	15058	C	T	0	657	synonymous_variant	LOW	CYTB	5.00E-04

HLI-0577	15301	G	A	0	548	synonymous_variant	LOW	CYTB	0.2912
HLI-0577	15326	A	G	0	591	missense_variant	MODERATE	CYTB	0.9868
HLI-0577	16124	T	C	0	589	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0577	16223	C	T	1	551	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0577	16291	C	T	1	554	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0578	263	A	G	1	190	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0578	750	A	G	1	704	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0578	1438	A	G	0	682	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0578	2259	C	T	3	634	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0578	4745	A	G	0	650	synonymous_variant	LOW	ND2	0.0039
HLI-0578	4769	A	G	0	693	synonymous_variant	LOW	ND2	0.9767
HLI-0578	7337	G	A	0	675	synonymous_variant	LOW	COX1	0.0119
HLI-0578	7980	A	G	1	678	missense_variant	MODERATE	COX2	1.00E-04
HLI-0578	12906	C	A	10	635	missense_variant	MODERATE	ND5	6.00E-04
HLI-0578	13326	T	C	1	619	synonymous_variant	LOW	ND5	0.0032
HLI-0578	13680	C	T	0	546	synonymous_variant	LOW	ND5	0.005
HLI-0578	14872	C	T	3	682	synonymous_variant	LOW	CYTB	0.0061
HLI-0578	15326	A	G	0	602	missense_variant	MODERATE	CYTB	0.9868
HLI-0578	16519	T	C	0	213	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0579	195	T	C	0	416	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0579	239	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0579	263	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0579	750	A	G	1	638	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0579	1438	A	G	0	687	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0579	3915	G	A	1	582	synonymous_variant	LOW	ND1	0.0106
HLI-0579	4727	A	G	1	588	synonymous_variant	LOW	ND2	0.0063
HLI-0579	4769	A	G	5	656	synonymous_variant	LOW	ND2	0.9767
HLI-0579	9380	G	A	0	691	synonymous_variant	LOW	COX3	0.0094
HLI-0579	11253	T	C	0	589	missense_variant	MODERATE	ND4	0.0053
HLI-0579	14798	T	C	0	591	missense_variant	MODERATE	CYTB	0.0651
HLI-0579	15326	A	G	0	575	missense_variant	MODERATE	CYTB	0.9868
HLI-0579	16362	T	C	1	506	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0579	16482	A	G	2	433	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0579	16519	T	C	1	361	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0580	73	A	G	0	283	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0580	150	C	T	0	553	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0580	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0580	750	A	G	2	621	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0580	1438	A	G	0	551	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0580	1721	C	T	1	392	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0580	2706	A	G	0	579	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0580	3197	T	C	0	557	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0580	4769	A	G	0	462	synonymous_variant	LOW	ND2	0.9767
HLI-0580	7028	C	T	1	590	synonymous_variant	LOW	COX1	0.8089
HLI-0580	7768	A	G	1	567	synonymous_variant	LOW	COX2	0.0186
HLI-0580	9477	G	A	2	607	missense_variant	MODERATE	COX3	0.0387
HLI-0580	9670	A	G	0	517	missense_variant	MODERATE	COX3	7.00E-04
HLI-0580	11467	A	G	0	609	synonymous_variant	LOW	ND4	0.1231
HLI-0580	11653	A	G	0	622	synonymous_variant	LOW	ND4	0.0049
HLI-0580	11719	G	A	1	619	synonymous_variant	LOW	ND4	0.7756
HLI-0580	12308	A	G	1	345	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0580	12372	G	A	0	299	synonymous_variant	LOW	ND5	0.1329
HLI-0580	12634	A	G	8	415	missense_variant	MODERATE	ND5	0.0027
HLI-0580	13617	T	C	1	550	synonymous_variant	LOW	ND5	0.038
HLI-0580	13630	A	G	1	578	missense_variant	MODERATE	ND5	0.0018
HLI-0580	13637	A	G	1	578	missense_variant	MODERATE	ND5	0.0074
HLI-0580	14182	T	C	1	447	synonymous_variant	LOW	ND6	0.0254
HLI-0580	14766	C	T	3	621	missense_variant	MODERATE	CYTB	0.7696
HLI-0580	15326	A	G	0	495	missense_variant	MODERATE	CYTB	0.9868
HLI-0580	16270	C	T	0	363	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0580	16287	C	T	0	379	upstream_gene_variant	MODIFIER	DLoop	0.0051
HLI-0580	16519	T	C	0	238	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0581	73	A	G	1	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0581	146	T	C	1	546	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0581	152	T	C	1	552	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0581	263	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0581	750	A	G	0	474	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0581	921	T	C	2	576	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0581	1438	A	G	0	526	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0581	2706	A	G	2	518	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0581	2784	A	G	0	557	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0581	4769	A	G	1	502	synonymous_variant	LOW	ND2	0.9767
HLI-0581	5046	G	A	0	364	missense_variant	MODERATE	ND2	0.018
HLI-0581	5147	G	A	0	335	synonymous_variant	LOW	ND2	0.0437
HLI-0581	6680	T	C	2	659	synonymous_variant	LOW	COX1	0.0226
HLI-0581	7028	C	T	1	609	synonymous_variant	LOW	COX1	0.8089
HLI-0581	7079	C	T	4	635	synonymous_variant	LOW	COX1	1.00E-04
HLI-0581	7424	A	G	2	587	synonymous_variant	LOW	COX1	0.0115

HLI-0581	8618	T	C	0	389	missense_variant	MODERATE	ATP6	0.0103
HLI-0581	8701	A	G	2	501	missense_variant	MODERATE	ATP6	0.3391
HLI-0581	9464	T	C	1	590	synonymous_variant	LOW	COX3	0
HLI-0581	9540	T	C	1	441	synonymous_variant	LOW	COX3	0.339
HLI-0581	10398	A	G	0	623	missense_variant	MODERATE	ND3	0.445
HLI-0581	10873	T	C	0	517	synonymous_variant	LOW	ND4	0.3389
HLI-0581	10877	C	T	0	531	synonymous_variant	LOW	ND4	5.00E-04
HLI-0581	11719	G	A	1	526	synonymous_variant	LOW	ND4	0.7756
HLI-0581	12705	C	T	2	396	synonymous_variant	LOW	ND5	0.4212
HLI-0581	13105	A	G	0	505	missense_variant	MODERATE	ND5	0.076
HLI-0581	13886	T	C	1	372	missense_variant	MODERATE	ND5	0.0088
HLI-0581	14284	C	T	1	463	synonymous_variant	LOW	ND6	0.0087
HLI-0581	14634	T	C	0	657	missense_variant	MODERATE	ND6	0.001
HLI-0581	14766	C	T	0	623	missense_variant	MODERATE	CYTB	0.7696
HLI-0581	15110	G	A	1	574	missense_variant	MODERATE	CYTB	0.009
HLI-0581	15301	G	A	0	336	synonymous_variant	LOW	CYTB	0.2912
HLI-0581	15326	A	G	0	347	missense_variant	MODERATE	CYTB	0.9868
HLI-0581	16124	T	C	2	583	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0581	16223	C	T	4	536	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0582	195	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0582	263	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0582	750	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0582	961	T	G	2	690	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0582	1438	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0582	3948	A	G	0	518	synonymous_variant	LOW	ND1	7.00E-04
HLI-0582	4769	A	G	0	521	synonymous_variant	LOW	ND2	0.9767
HLI-0582	8448	T	C	0	323	missense_variant	MODERATE	ATP8	0.0041
HLI-0582	8757	T	C	0	481	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0582	8898	C	T	3	635	synonymous_variant	LOW	ATP6	0.0011
HLI-0582	13759	G	A	1	343	missense_variant	MODERATE	ND5	0.0348
HLI-0582	15326	A	G	0	437	missense_variant	MODERATE	CYTB	0.9868
HLI-0582	16278	C	T	0	471	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0582	16293	A	G	0	504	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0582	16311	T	C	0	479	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0583	73	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0583	151	C	T	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0583	152	T	C	0	369	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0583	186	C	A	0	329	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0583	189	A	C	0	329	upstream_gene_variant	MODIFIER	DLoop	0.0122

HLI-0583	195	T	C	0	325	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0583	204	T	C	0	331	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0583	247	G	A	0	143	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0583	263	A	G	0	155	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0583	297	A	G	1	186	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0583	467	C	T	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0016
HLI-0583	750	A	G	0	660	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0583	769	G	A	0	717	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0583	825	T	A	0	736	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0583	1018	G	A	1	738	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0583	1438	A	G	0	692	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0583	2308	A	G	0	514	upstream_gene_variant	MODIFIER	RNR2	0.0044
HLI-0583	2706	A	G	2	638	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0583	2758	G	A	1	705	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0583	2885	T	C	0	657	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0583	3594	C	T	1	597	synonymous_variant	LOW	ND1	0.0789
HLI-0583	3666	G	A	0	679	synonymous_variant	LOW	ND1	0.0233
HLI-0583	3796	A	T	1	625	missense_variant	MODERATE	ND1	0.0045
HLI-0583	3843	A	G	3	753	synonymous_variant	LOW	ND1	0.0046
HLI-0583	4104	A	G	1	591	synonymous_variant	LOW	ND1	0.0785
HLI-0583	4454	T	A	0	599	upstream_gene_variant	MODIFIER	TRNM	0.0029
HLI-0583	4769	A	G	1	579	synonymous_variant	LOW	ND2	0.9767
HLI-0583	5951	A	G	2	763	synonymous_variant	LOW	COX1	0.0128
HLI-0583	5984	A	G	3	820	synonymous_variant	LOW	COX1	0.002
HLI-0583	6071	T	C	2	693	synonymous_variant	LOW	COX1	0.0129
HLI-0583	6182	G	A	1	642	synonymous_variant	LOW	COX1	0.0033
HLI-0583	7028	C	T	0	604	synonymous_variant	LOW	COX1	0.8089
HLI-0583	7055	A	G	0	596	synonymous_variant	LOW	COX1	0.0188
HLI-0583	7146	A	G	1	315	missense_variant	MODERATE	COX1	0.0497
HLI-0583	7256	C	T	0	488	synonymous_variant	LOW	COX1	0.0784
HLI-0583	7389	T	C	0	484	missense_variant	MODERATE	COX1	0.0201
HLI-0583	7521	G	A	0	428	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0583	8027	G	A	1	633	missense_variant	MODERATE	COX2	0.0334
HLI-0583	8087	T	C	0	672	synonymous_variant	LOW	COX2	0.0031
HLI-0583	8468	C	T	2	426	synonymous_variant	LOW	ATP8	0.0501
HLI-0583	8655	C	T	0	454	synonymous_variant	LOW	ATP6	0.0511
HLI-0583	8701	A	G	3	518	missense_variant	MODERATE	ATP6	0.3391
HLI-0583	8928	T	C	0	648	synonymous_variant	LOW	ATP6	0.0013
HLI-0583	9072	A	G	0	600	synonymous_variant	LOW	ATP6	0.0124

HLI-0583	9311	T	C	0	627	synonymous_variant	LOW	COX3	0.001
HLI-0583	9540	T	C	0	665	synonymous_variant	LOW	COX3	0.339
HLI-0583	10321	T	C	0	626	missense_variant	MODERATE	ND3	0.0106
HLI-0583	10586	G	A	0	639	synonymous_variant	LOW	ND4L	0.0177
HLI-0583	10688	G	A	0	571	synonymous_variant	LOW	ND4L	0.0515
HLI-0583	10810	T	C	0	580	synonymous_variant	LOW	ND4	0.0522
HLI-0583	10873	T	C	0	612	synonymous_variant	LOW	ND4	0.3389
HLI-0583	11167	A	G	0	610	synonymous_variant	LOW	ND4	0.004
HLI-0583	11257	C	T	3	660	synonymous_variant	LOW	ND4	0.0027
HLI-0583	11719	G	A	0	621	synonymous_variant	LOW	ND4	0.7756
HLI-0583	11899	T	C	1	578	synonymous_variant	LOW	ND4	0.0108
HLI-0583	12236	G	A	84	398	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0583	12705	C	T	0	557	synonymous_variant	LOW	ND5	0.4212
HLI-0583	12810	A	G	2	626	synonymous_variant	LOW	ND5	0.0198
HLI-0583	12930	A	T	1	625	synonymous_variant	LOW	ND5	0.0016
HLI-0583	13105	A	G	2	624	missense_variant	MODERATE	ND5	0.076
HLI-0583	13485	A	G	0	619	synonymous_variant	LOW	ND5	0.0122
HLI-0583	13506	C	T	0	693	synonymous_variant	LOW	ND5	0.0506
HLI-0583	13650	C	T	1	535	synonymous_variant	LOW	ND5	0.079
HLI-0583	13789	T	C	0	437	missense_variant	MODERATE	ND5	0.0185
HLI-0583	14000	T	A	0	519	missense_variant	MODERATE	ND5	0.0126
HLI-0583	14034	T	C	0	529	synonymous_variant	LOW	ND5	0.0027
HLI-0583	14088	T	C	0	544	synonymous_variant	LOW	ND5	0.0046
HLI-0583	14148	A	G	1	579	stop_retained_variant	LOW	ND5	0.0065
HLI-0583	14178	T	C	1	597	missense_variant	MODERATE	ND6	0.0225
HLI-0583	14560	G	A	2	720	synonymous_variant	LOW	ND6	0.0235
HLI-0583	14766	C	T	4	612	missense_variant	MODERATE	CYTB	0.7696
HLI-0583	14911	C	T	2	762	synonymous_variant	LOW	CYTB	0.0124
HLI-0583	15326	A	G	0	558	missense_variant	MODERATE	CYTB	0.9868
HLI-0583	15663	T	C	1	506	missense_variant	MODERATE	CYTB	0.0016
HLI-0583	16129	G	A	2	510	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0583	16214	C	T	2	380	upstream_gene_variant	MODIFIER	DLoop	0.008
HLI-0583	16234	C	T	2	359	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0583	16249	T	C	2	338	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0583	16274	G	A	1	321	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0583	16278	C	T	1	326	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0583	16294	C	T	1	331	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0583	16311	T	C	1	335	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0583	16360	C	T	0	347	upstream_gene_variant	MODIFIER	DLoop	0.0153

HLI-0583	16519	T	C	0	154	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0584	73	A	G	0	321	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0584	150	C	T	1	548	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0584	189	A	G	1	525	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0584	200	A	G	11	511	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0584	263	A	G	1	173	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0584	750	A	G	1	675	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0584	1438	A	G	1	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0584	1822	T	C	1	663	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0584	2706	A	G	0	722	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0584	3396	T	C	1	639	synonymous_variant	LOW	ND1	0.0082
HLI-0584	3505	A	G	0	608	missense_variant	MODERATE	ND1	0.0144
HLI-0584	4218	T	C	0	628	synonymous_variant	LOW	ND1	0.0057
HLI-0584	4769	A	G	1	596	synonymous_variant	LOW	ND2	0.9767
HLI-0584	5601	C	T	3	690	upstream_gene_variant	MODIFIER	TRNA	0.0101
HLI-0584	7028	C	T	2	712	synonymous_variant	LOW	COX1	0.8089
HLI-0584	7819	C	A	4	714	synonymous_variant	LOW	COX2	0.0045
HLI-0584	8527	A	G	1	571	initiator_codon_variant	LOW	ATP6/8	0.0044
HLI-0584	8701	A	G	1	560	missense_variant	MODERATE	ATP6	0.3391
HLI-0584	8932	C	T	2	672	missense_variant	MODERATE	ATP6	0.0044
HLI-0584	9540	T	C	1	675	synonymous_variant	LOW	COX3	0.339
HLI-0584	9950	T	C	1	716	synonymous_variant	LOW	COX3	0.0362
HLI-0584	10398	A	G	0	704	missense_variant	MODERATE	ND3	0.445
HLI-0584	10873	T	C	1	623	synonymous_variant	LOW	ND4	0.3389
HLI-0584	11440	G	A	0	673	synonymous_variant	LOW	ND4	0.0081
HLI-0584	11719	G	A	1	649	synonymous_variant	LOW	ND4	0.7756
HLI-0584	12705	C	T	2	621	synonymous_variant	LOW	ND5	0.4212
HLI-0584	13167	A	G	0	664	synonymous_variant	LOW	ND5	0.0027
HLI-0584	14766	C	T	0	613	missense_variant	MODERATE	CYTB	0.7696
HLI-0584	14769	A	G	0	631	missense_variant	MODERATE	CYTB	0.0121
HLI-0584	15301	G	A	1	622	synonymous_variant	LOW	CYTB	0.2912
HLI-0584	15326	A	G	0	659	missense_variant	MODERATE	CYTB	0.9868
HLI-0584	15514	T	C	0	573	synonymous_variant	LOW	CYTB	0.0071
HLI-0584	16209	T	C	2	659	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0584	16223	C	T	3	706	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0584	16311	T	C	1	581	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0584	16519	T	C	0	340	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0585	73	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0585	143	G	A	0	510	upstream_gene_variant	MODIFIER	DLoop	0.0191

HLI-0585	146	T	C	0	526	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0585	152	T	C	1	539	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0585	195	T	C	1	558	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0585	198	C	T	1	550	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0585	263	A	G	0	272	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0585	750	A	G	0	660	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0585	769	G	A	0	702	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0585	1018	G	A	2	741	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0585	1438	A	G	0	631	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0585	2416	T	C	0	458	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0585	2706	A	G	0	630	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0585	2789	C	T	0	651	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0585	3010	G	A	3	571	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0585	3594	C	T	0	624	synonymous_variant	LOW	ND1	0.0789
HLI-0585	4104	A	G	0	547	synonymous_variant	LOW	ND1	0.0785
HLI-0585	4769	A	G	2	549	synonymous_variant	LOW	ND2	0.9767
HLI-0585	6663	A	G	3	817	missense_variant	MODERATE	COX1	0.0032
HLI-0585	7028	C	T	0	687	synonymous_variant	LOW	COX1	0.8089
HLI-0585	7175	T	C	2	632	synonymous_variant	LOW	COX1	0.0224
HLI-0585	7256	C	T	1	632	synonymous_variant	LOW	COX1	0.0784
HLI-0585	7274	C	T	1	597	synonymous_variant	LOW	COX1	0.0214
HLI-0585	7521	G	A	0	466	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0585	7771	A	G	1	620	synonymous_variant	LOW	COX2	0.0223
HLI-0585	8206	G	A	1	572	synonymous_variant	LOW	COX2	0.0287
HLI-0585	8701	A	G	1	511	missense_variant	MODERATE	ATP6	0.3391
HLI-0585	9221	A	G	0	659	synonymous_variant	LOW	COX3	0.0277
HLI-0585	9540	T	C	0	671	synonymous_variant	LOW	COX3	0.339
HLI-0585	10115	T	C	0	765	synonymous_variant	LOW	ND3	0.0278
HLI-0585	10398	A	G	1	631	missense_variant	MODERATE	ND3	0.445
HLI-0585	10873	T	C	1	582	synonymous_variant	LOW	ND4	0.3389
HLI-0585	11719	G	A	0	631	synonymous_variant	LOW	ND4	0.7756
HLI-0585	11914	G	A	2	482	synonymous_variant	LOW	ND4	0.1112
HLI-0585	11944	T	C	2	489	synonymous_variant	LOW	ND4	0.0331
HLI-0585	12693	A	G	0	554	synonymous_variant	LOW	ND5	0.0205
HLI-0585	12705	C	T	0	549	synonymous_variant	LOW	ND5	0.4212
HLI-0585	13260	T	C	1	680	synonymous_variant	LOW	ND5	0.0017
HLI-0585	13590	G	A	0	565	synonymous_variant	LOW	ND5	0.0586
HLI-0585	13650	C	T	1	593	synonymous_variant	LOW	ND5	0.079
HLI-0585	13803	A	G	1	415	synonymous_variant	LOW	ND5	0.0216

HLI-0585	14566	A	G	3	775	synonymous_variant	LOW	ND6	0.0214
HLI-0585	14766	C	T	1	667	missense_variant	MODERATE	CYTB	0.7696
HLI-0585	15301	G	A	0	506	synonymous_variant	LOW	CYTB	0.2912
HLI-0585	15326	A	G	0	527	missense_variant	MODERATE	CYTB	0.9868
HLI-0585	15784	T	C	1	363	synonymous_variant	LOW	CYTB	0.0363
HLI-0585	16129	G	A	1	429	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0585	16223	C	T	1	407	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0585	16278	C	T	0	458	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0585	16294	C	T	0	452	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0585	16309	A	G	1	441	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0585	16390	G	A	0	479	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0586	73	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0586	189	A	G	0	376	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0586	195	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0586	204	T	C	0	375	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0586	207	G	A	0	376	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0586	212	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0586	263	A	G	0	325	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0586	709	G	A	2	505	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0586	750	A	G	0	519	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0586	1243	T	C	0	620	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0586	1438	A	G	0	520	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0586	2706	A	G	0	514	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0586	3505	A	G	1	575	missense_variant	MODERATE	ND1	0.0144
HLI-0586	4769	A	G	0	532	synonymous_variant	LOW	ND2	0.9767
HLI-0586	5046	G	A	0	384	missense_variant	MODERATE	ND2	0.018
HLI-0586	5460	G	A	4	523	missense_variant	MODERATE	ND2	0.0651
HLI-0586	7028	C	T	3	635	synonymous_variant	LOW	COX1	0.8089
HLI-0586	7864	C	T	1	640	synonymous_variant	LOW	COX2	0.0041
HLI-0586	8251	G	A	5	453	synonymous_variant	LOW	COX2	0.058
HLI-0586	8531	A	G	0	493	missense_variant	MODERATE	ATP6/8	6.00E-04
HLI-0586	8994	G	A	1	487	synonymous_variant	LOW	ATP6	0.0167
HLI-0586	11674	C	T	3	588	synonymous_variant	LOW	ND4	0.0116
HLI-0586	11719	G	A	0	634	synonymous_variant	LOW	ND4	0.7756
HLI-0586	11947	A	G	0	526	synonymous_variant	LOW	ND4	0.011
HLI-0586	12414	T	C	5	407	synonymous_variant	LOW	ND5	0.0139
HLI-0586	12705	C	T	0	557	synonymous_variant	LOW	ND5	0.4212
HLI-0586	14766	C	T	2	708	missense_variant	MODERATE	CYTB	0.7696
HLI-0586	15326	A	G	0	347	missense_variant	MODERATE	CYTB	0.9868

HLI-0586	15884	G	C	0	380	missense_variant	MODERATE	CYTB	0.011
HLI-0586	16223	C	T	2	516	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0586	16320	C	T	0	443	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0586	16519	T	C	0	236	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0587	73	A	G	0	242	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0587	150	C	T	0	476	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0587	195	T	C	0	437	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0587	198	C	T	0	429	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0587	263	A	G	0	325	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0587	499	G	A	1	381	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0587	750	A	G	1	431	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0587	1438	A	G	0	434	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0587	2352	T	C	0	291	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0587	2706	A	G	0	443	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0587	4769	A	G	0	471	synonymous_variant	LOW	ND2	0.9767
HLI-0587	4823	T	C	2	501	synonymous_variant	LOW	ND2	0.0049
HLI-0587	4853	G	A	4	501	synonymous_variant	LOW	ND2	0.0026
HLI-0587	6413	T	C	0	430	synonymous_variant	LOW	COX1	0.0062
HLI-0587	7028	C	T	0	595	synonymous_variant	LOW	COX1	0.8089
HLI-0587	8701	A	G	1	483	missense_variant	MODERATE	ATP6	0.3391
HLI-0587	9540	T	C	0	293	synonymous_variant	LOW	COX3	0.339
HLI-0587	10398	A	G	1	492	missense_variant	MODERATE	ND3	0.445
HLI-0587	10819	A	G	0	462	synonymous_variant	LOW	ND4	0.0228
HLI-0587	10873	T	C	1	484	synonymous_variant	LOW	ND4	0.3389
HLI-0587	11719	G	A	0	525	synonymous_variant	LOW	ND4	0.7756
HLI-0587	12705	C	T	0	527	synonymous_variant	LOW	ND5	0.4212
HLI-0587	13105	A	G	0	498	missense_variant	MODERATE	ND5	0.076
HLI-0587	14180	T	C	0	404	missense_variant	MODERATE	ND6	0.0036
HLI-0587	14212	T	C	0	465	synonymous_variant	LOW	ND6	0.0204
HLI-0587	14750	A	G	2	688	missense_variant	MODERATE	CYTB	8.00E-04
HLI-0587	14766	C	T	1	733	missense_variant	MODERATE	CYTB	0.7696
HLI-0587	14869	G	A	1	711	synonymous_variant	LOW	CYTB	0.0023
HLI-0587	14905	G	A	1	786	synonymous_variant	LOW	CYTB	0.0526
HLI-0587	15244	A	G	0	417	synonymous_variant	LOW	CYTB	0.0103
HLI-0587	15301	G	A	0	351	synonymous_variant	LOW	CYTB	0.2912
HLI-0587	15326	A	G	0	302	missense_variant	MODERATE	CYTB	0.9868
HLI-0587	16223	C	T	2	403	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0587	16320	C	T	0	359	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0587	16399	A	G	0	373	upstream_gene_variant	MODIFIER	DLoop	0.0265

HLI-0587	16519	T	C	1	186	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0588	150	C	T	0	505	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0588	263	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0588	750	A	G	1	521	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0588	1438	A	G	1	582	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0588	3010	G	A	1	551	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0588	4769	A	G	1	556	synonymous_variant	LOW	ND2	0.9767
HLI-0588	14053	A	G	0	427	missense_variant	MODERATE	ND5	0.0046
HLI-0588	15326	A	G	0	411	missense_variant	MODERATE	CYTB	0.9868
HLI-0588	16144	T	C	2	584	upstream_gene_variant	MODIFIER	DLoop	0.0047
HLI-0588	16355	C	T	1	487	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0588	16519	T	C	2	277	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0589	73	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0589	263	A	G	1	353	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0589	497	C	T	1	453	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0589	750	A	G	0	465	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0589	1189	T	C	3	609	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0589	1438	A	G	0	456	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0589	1811	A	G	0	362	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0589	2706	A	G	1	455	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0589	3480	A	G	1	364	synonymous_variant	LOW	ND1	0.0392
HLI-0589	4769	A	G	0	526	synonymous_variant	LOW	ND2	0.9767
HLI-0589	5580	T	C	2	545	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0589	6179	G	A	4	481	synonymous_variant	LOW	COX1	0.0029
HLI-0589	6587	C	T	2	521	synonymous_variant	LOW	COX1	0.0084
HLI-0589	7028	C	T	2	596	synonymous_variant	LOW	COX1	0.8089
HLI-0589	7559	A	G	0	485	upstream_gene_variant	MODIFIER	TRND	8.00E-04
HLI-0589	8632	T	C	1	553	missense_variant	MODERATE	ATP6	3.00E-04
HLI-0589	9055	G	A	0	479	missense_variant	MODERATE	ATP6	0.0425
HLI-0589	9698	T	C	0	513	synonymous_variant	LOW	COX3	0.0405
HLI-0589	10398	A	G	1	481	missense_variant	MODERATE	ND3	0.445
HLI-0589	10550	A	G	1	511	synonymous_variant	LOW	ND4L	0.0376
HLI-0589	11299	T	C	0	524	synonymous_variant	LOW	ND4	0.0417
HLI-0589	11362	A	G	1	553	synonymous_variant	LOW	ND4	0.0024
HLI-0589	11467	A	G	0	565	synonymous_variant	LOW	ND4	0.1231
HLI-0589	11719	G	A	0	560	synonymous_variant	LOW	ND4	0.7756
HLI-0589	12308	A	G	0	362	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0589	12372	G	A	0	307	synonymous_variant	LOW	ND5	0.1329
HLI-0589	13117	A	G	0	482	missense_variant	MODERATE	ND5	0.0014

HLI-0589	14167	C	T	4	501	synonymous_variant	LOW	ND6	0.0385
HLI-0589	14766	C	T	2	680	missense_variant	MODERATE	CYTB	0.7696
HLI-0589	14798	T	C	1	754	missense_variant	MODERATE	CYTB	0.0651
HLI-0589	15326	A	G	0	297	missense_variant	MODERATE	CYTB	0.9868
HLI-0589	16093	T	C	9	469	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0589	16224	T	C	2	452	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0589	16311	T	C	0	375	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0589	16519	T	C	0	178	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0590	73	A	G	1	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0590	146	T	C	0	591	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0590	152	T	C	0	588	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0590	263	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0590	279	T	C	0	277	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0590	709	G	A	0	535	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0590	750	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0590	1438	A	G	1	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0590	1888	G	A	0	395	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0590	2706	A	G	1	566	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0590	4216	T	C	0	485	missense_variant	MODERATE	ND1	0.0991
HLI-0590	4769	A	G	1	544	synonymous_variant	LOW	ND2	0.9767
HLI-0590	4917	A	G	8	528	missense_variant	MODERATE	ND2	0.0477
HLI-0590	5187	C	T	3	495	synonymous_variant	LOW	ND2	0.0023
HLI-0590	6261	G	A	3	555	missense_variant	MODERATE	COX1	0.007
HLI-0590	7028	C	T	1	597	synonymous_variant	LOW	COX1	0.8089
HLI-0590	7873	C	T	6	679	synonymous_variant	LOW	COX2	0.0023
HLI-0590	8697	G	A	0	575	synonymous_variant	LOW	ATP6	0.0466
HLI-0590	10463	T	C	0	599	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0590	10822	C	T	0	579	synonymous_variant	LOW	ND4	0.0036
HLI-0590	11251	A	G	0	582	synonymous_variant	LOW	ND4	0.0932
HLI-0590	11719	G	A	0	609	synonymous_variant	LOW	ND4	0.7756
HLI-0590	11812	A	G	0	547	synonymous_variant	LOW	ND4	0.0332
HLI-0590	11914	G	A	0	530	synonymous_variant	LOW	ND4	0.1112
HLI-0590	13368	G	A	0	596	synonymous_variant	LOW	ND5	0.0495
HLI-0590	14233	A	G	0	506	synonymous_variant	LOW	ND6	0.0369
HLI-0590	14766	C	T	2	666	missense_variant	MODERATE	CYTB	0.7696
HLI-0590	14905	G	A	1	818	synonymous_variant	LOW	CYTB	0.0526
HLI-0590	15326	A	G	0	434	missense_variant	MODERATE	CYTB	0.9868
HLI-0590	15452	C	A	4	322	missense_variant	MODERATE	CYTB	0.0933
HLI-0590	15607	A	G	1	366	synonymous_variant	LOW	CYTB	0.0508

HLI-0590	15928	G	A	2	452	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0590	16126	T	C	0	644	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0590	16292	C	T	0	495	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0590	16294	C	T	0	505	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0590	16519	T	C	0	314	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0591	73	A	G	1	231	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0591	189	A	G	0	361	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0591	195	T	C	0	377	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0591	204	T	C	0	374	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0591	207	G	A	0	379	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0591	263	A	G	0	108	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0591	709	G	A	0	516	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0591	750	A	G	2	559	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0591	1243	T	C	1	590	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0591	1438	A	G	2	567	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0591	2706	A	G	0	504	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0591	3505	A	G	3	464	missense_variant	MODERATE	ND1	0.0144
HLI-0591	4769	A	G	4	496	synonymous_variant	LOW	ND2	0.9767
HLI-0591	5046	G	A	3	450	missense_variant	MODERATE	ND2	0.018
HLI-0591	5460	G	A	2	479	missense_variant	MODERATE	ND2	0.0651
HLI-0591	5964	T	C	1	613	synonymous_variant	LOW	COX1	0.0033
HLI-0591	7028	C	T	3	623	synonymous_variant	LOW	COX1	0.8089
HLI-0591	7864	C	T	3	550	synonymous_variant	LOW	COX2	0.0041
HLI-0591	8251	G	A	3	440	synonymous_variant	LOW	COX2	0.058
HLI-0591	8994	G	A	0	478	synonymous_variant	LOW	ATP6	0.0167
HLI-0591	11674	C	T	1	564	synonymous_variant	LOW	ND4	0.0116
HLI-0591	11719	G	A	0	624	synonymous_variant	LOW	ND4	0.7756
HLI-0591	11947	A	G	0	533	synonymous_variant	LOW	ND4	0.011
HLI-0591	12414	T	C	0	320	synonymous_variant	LOW	ND5	0.0139
HLI-0591	12630	G	A	2	438	synonymous_variant	LOW	ND5	0.0053
HLI-0591	12705	C	T	1	481	synonymous_variant	LOW	ND5	0.4212
HLI-0591	13395	A	G	1	547	synonymous_variant	LOW	ND5	0.0056
HLI-0591	14766	C	T	0	560	missense_variant	MODERATE	CYTB	0.7696
HLI-0591	14812	C	G	1	652	synonymous_variant	LOW	CYTB	0
HLI-0591	14851	A	G	1	685	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0591	15326	A	G	0	419	missense_variant	MODERATE	CYTB	0.9868
HLI-0591	15884	G	C	0	400	missense_variant	MODERATE	CYTB	0.011
HLI-0591	16223	C	T	0	475	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0591	16292	C	T	2	447	upstream_gene_variant	MODIFIER	DLoop	0.0243

HLI-0591	16320	C	T	0	412	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0591	16519	T	C	0	264	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0592	73	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0592	152	T	C	0	464	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0592	195	T	C	0	424	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0592	263	A	G	0	200	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0592	499	G	A	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0592	750	A	G	1	517	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0592	961	T	C	1	193	upstream_gene_variant	MODIFIER	RNR1	0.0087
HLI-0592	1438	A	G	0	579	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0592	1811	A	G	1	537	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0592	2706	A	G	0	513	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0592	4646	T	C	0	601	synonymous_variant	LOW	ND2	0.0124
HLI-0592	4769	A	G	3	573	synonymous_variant	LOW	ND2	0.9767
HLI-0592	5250	T	C	0	514	synonymous_variant	LOW	ND2	0.0013
HLI-0592	5999	T	C	0	607	synonymous_variant	LOW	COX1	0.0127
HLI-0592	6047	A	G	1	669	synonymous_variant	LOW	COX1	0.0114
HLI-0592	7028	C	T	3	660	synonymous_variant	LOW	COX1	0.8089
HLI-0592	8818	C	T	0	541	synonymous_variant	LOW	ATP6	0.0061
HLI-0592	11332	C	T	1	580	synonymous_variant	LOW	ND4	0.0115
HLI-0592	11467	A	G	1	593	synonymous_variant	LOW	ND4	0.1231
HLI-0592	11719	G	A	0	575	synonymous_variant	LOW	ND4	0.7756
HLI-0592	11986	C	T	0	533	synonymous_variant	LOW	ND4	1.00E-04
HLI-0592	12308	A	G	0	456	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0592	12372	G	A	1	430	synonymous_variant	LOW	ND5	0.1329
HLI-0592	12630	G	A	4	517	synonymous_variant	LOW	ND5	0.0053
HLI-0592	12937	A	G	3	515	missense_variant	MODERATE	ND5	0.0026
HLI-0592	14620	C	T	5	586	synonymous_variant	LOW	ND6	0.0126
HLI-0592	14766	C	T	1	618	missense_variant	MODERATE	CYTB	0.7696
HLI-0592	15326	A	G	0	429	missense_variant	MODERATE	CYTB	0.9868
HLI-0592	15693	T	C	0	360	missense_variant	MODERATE	CYTB	0.0114
HLI-0592	16134	C	T	0	484	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0592	16356	T	C	0	390	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0592	16519	T	C	1	228	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0593	73	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0593	185	G	A	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0593	189	A	G	0	438	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0593	263	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0593	750	A	G	0	530	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0593	1438	A	G	0	574	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0593	2706	A	G	0	491	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0593	3450	C	T	2	541	synonymous_variant	LOW	ND1	0.0084
HLI-0593	4769	A	G	0	598	synonymous_variant	LOW	ND2	0.9767
HLI-0593	5450	C	T	4	520	synonymous_variant	LOW	ND2	3.00E-04
HLI-0593	5773	G	A	5	620	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0593	6221	T	C	4	522	synonymous_variant	LOW	COX1	0.0306
HLI-0593	6527	A	G	3	553	synonymous_variant	LOW	COX1	8.00E-04
HLI-0593	7028	C	T	3	607	synonymous_variant	LOW	COX1	0.8089
HLI-0593	8555	T	C	0	545	missense_variant	MODERATE	ATP6/8	3.00E-04
HLI-0593	9007	A	G	0	510	missense_variant	MODERATE	ATP6	0.0022
HLI-0593	9449	C	T	0	589	synonymous_variant	LOW	COX3	0.0125
HLI-0593	9540	T	C	0	470	synonymous_variant	LOW	COX3	0.339
HLI-0593	10086	A	G	0	725	missense_variant	MODERATE	ND3	0.0088
HLI-0593	10398	A	G	0	641	missense_variant	MODERATE	ND3	0.445
HLI-0593	10873	T	C	0	541	synonymous_variant	LOW	ND4	0.3389
HLI-0593	11719	G	A	1	560	synonymous_variant	LOW	ND4	0.7756
HLI-0593	12705	C	T	0	511	synonymous_variant	LOW	ND5	0.4212
HLI-0593	13105	A	G	0	475	missense_variant	MODERATE	ND5	0.076
HLI-0593	13914	C	A	0	480	synonymous_variant	LOW	ND5	0.0091
HLI-0593	13934	C	T	0	518	missense_variant	MODERATE	ND5	0.0122
HLI-0593	14182	T	C	0	492	synonymous_variant	LOW	ND6	0.0254
HLI-0593	14766	C	T	5	534	missense_variant	MODERATE	CYTB	0.7696
HLI-0593	15301	G	A	0	470	synonymous_variant	LOW	CYTB	0.2912
HLI-0593	15311	A	G	0	508	missense_variant	MODERATE	CYTB	0.008
HLI-0593	15326	A	G	0	486	missense_variant	MODERATE	CYTB	0.9868
HLI-0593	15824	A	G	1	503	missense_variant	MODERATE	CYTB	0.0083
HLI-0593	16048	G	A	0	491	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0593	16124	T	C	0	614	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0593	16223	C	T	3	528	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0593	16278	C	T	1	524	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0593	16362	T	C	0	475	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0593	16519	T	C	0	234	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0594	73	A	G	2	248	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0594	150	C	T	2	452	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0594	195	T	C	0	442	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0594	263	A	G	0	183	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0594	750	A	G	0	512	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0594	1438	A	G	0	538	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0594	2352	T	C	0	317	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0594	2483	T	C	1	456	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0594	2706	A	G	0	518	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0594	3277	G	A	0	477	upstream_gene_variant	MODIFIER	TRNL1	7.00E-04
HLI-0594	4769	A	G	2	491	synonymous_variant	LOW	ND2	0.9767
HLI-0594	7028	C	T	3	614	synonymous_variant	LOW	COX1	0.8089
HLI-0594	8701	A	G	0	356	missense_variant	MODERATE	ATP6	0.3391
HLI-0594	9377	A	G	0	534	synonymous_variant	LOW	COX3	0.0084
HLI-0594	9540	T	C	1	421	synonymous_variant	LOW	COX3	0.339
HLI-0594	10398	A	G	0	547	missense_variant	MODERATE	ND3	0.445
HLI-0594	10819	A	G	0	554	synonymous_variant	LOW	ND4	0.0228
HLI-0594	10873	T	C	0	534	synonymous_variant	LOW	ND4	0.3389
HLI-0594	11719	G	A	0	552	synonymous_variant	LOW	ND4	0.7756
HLI-0594	12406	G	A	2	234	missense_variant	MODERATE	ND5	0.0262
HLI-0594	12705	C	T	0	325	synonymous_variant	LOW	ND5	0.4212
HLI-0594	13934	C	T	1	333	missense_variant	MODERATE	ND5	0.0122
HLI-0594	14212	T	C	0	343	synonymous_variant	LOW	ND6	0.0204
HLI-0594	14696	A	G	2	589	upstream_gene_variant	MODIFIER	TRNE	9.00E-04
HLI-0594	14766	C	T	1	624	missense_variant	MODERATE	CYTB	0.7696
HLI-0594	14905	G	A	0	683	synonymous_variant	LOW	CYTB	0.0526
HLI-0594	15301	G	A	3	417	synonymous_variant	LOW	CYTB	0.2912
HLI-0594	15326	A	G	0	417	missense_variant	MODERATE	CYTB	0.9868
HLI-0594	16172	T	C	1	191	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0594	16223	C	T	6	208	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0594	16320	C	T	1	376	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0594	16519	T	C	2	191	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0595	73	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0595	150	C	T	1	449	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0595	152	T	C	1	457	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0595	189	A	G	1	420	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0595	195	T	C	1	420	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0595	215	A	G	2	395	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0595	263	A	G	1	127	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0595	295	C	T	1	140	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0595	319	T	C	1	136	upstream_gene_variant	MODIFIER	DLoop	0.0041
HLI-0595	489	T	C	0	428	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0595	750	A	G	1	621	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0595	1438	A	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0595	2706	A	G	0	651	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0595	4216	T	C	1	591	missense_variant	MODERATE	ND1	0.0991
HLI-0595	4769	A	G	0	551	synonymous_variant	LOW	ND2	0.9767
HLI-0595	7028	C	T	5	645	synonymous_variant	LOW	COX1	0.8089
HLI-0595	7476	C	T	1	545	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0595	7789	G	A	0	597	synonymous_variant	LOW	COX2	0.0092
HLI-0595	10398	A	G	0	654	missense_variant	MODERATE	ND3	0.445
HLI-0595	10499	A	G	2	641	synonymous_variant	LOW	ND4L	0.0093
HLI-0595	11239	A	G	0	637	synonymous_variant	LOW	ND4	6.00E-04
HLI-0595	11251	A	G	0	661	synonymous_variant	LOW	ND4	0.0932
HLI-0595	11377	G	A	0	563	synonymous_variant	LOW	ND4	0.0125
HLI-0595	11719	G	A	1	599	synonymous_variant	LOW	ND4	0.7756
HLI-0595	12612	A	G	8	552	synonymous_variant	LOW	ND5	0.0506
HLI-0595	13708	G	A	0	534	missense_variant	MODERATE	ND5	0.0717
HLI-0595	13722	A	G	0	566	synonymous_variant	LOW	ND5	0.0077
HLI-0595	14133	A	G	0	531	synonymous_variant	LOW	ND5	0.0094
HLI-0595	14766	C	T	1	596	missense_variant	MODERATE	CYTB	0.7696
HLI-0595	15257	G	A	0	573	missense_variant	MODERATE	CYTB	0.0155
HLI-0595	15326	A	G	0	629	missense_variant	MODERATE	CYTB	0.9868
HLI-0595	15452	C	A	3	528	missense_variant	MODERATE	CYTB	0.0933
HLI-0595	16069	C	T	0	510	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0595	16145	G	A	0	559	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0595	16231	T	C	1	536	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0595	16261	C	T	1	569	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0596	263	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0596	750	A	G	0	567	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0596	1438	A	G	1	602	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0596	2259	C	T	1	416	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0596	4745	A	G	0	695	synonymous_variant	LOW	ND2	0.0039
HLI-0596	4769	A	G	0	688	synonymous_variant	LOW	ND2	0.9767
HLI-0596	7337	G	A	0	650	synonymous_variant	LOW	COX1	0.0119
HLI-0596	10694	A	G	0	673	synonymous_variant	LOW	ND4L	6.00E-04
HLI-0596	11025	T	C	3	493	missense_variant	MODERATE	ND4	0.0035
HLI-0596	13326	T	C	0	653	synonymous_variant	LOW	ND5	0.0032
HLI-0596	13680	C	T	0	517	synonymous_variant	LOW	ND5	0.005
HLI-0596	14872	C	T	4	787	synonymous_variant	LOW	CYTB	0.0061
HLI-0596	15326	A	G	0	423	missense_variant	MODERATE	CYTB	0.9868
HLI-0596	16213	G	A	0	440	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0597	183	A	G	1	545	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0597	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0597	750	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0597	1438	A	G	1	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0597	4769	A	G	0	638	synonymous_variant	LOW	ND2	0.9767
HLI-0597	15326	A	G	2	594	missense_variant	MODERATE	CYTB	0.9868
HLI-0597	16278	C	T	0	546	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0597	16519	T	C	2	303	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0598	263	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0598	750	A	G	1	685	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0598	1438	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0598	4769	A	G	2	589	synonymous_variant	LOW	ND2	0.9767
HLI-0598	9545	A	G	1	775	synonymous_variant	LOW	COX3	0.0469
HLI-0598	11152	T	C	2	667	synonymous_variant	LOW	ND4	0.0024
HLI-0598	13500	T	C	2	634	synonymous_variant	LOW	ND5	0.0173
HLI-0598	15326	A	G	1	582	missense_variant	MODERATE	CYTB	0.9868
HLI-0598	16519	T	C	0	371	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0599	73	A	G	2	302	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0599	185	G	A	6	533	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0599	188	A	G	6	526	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0599	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0599	295	C	T	2	289	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0599	462	C	T	7	506	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0599	489	T	C	5	535	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0599	750	A	G	1	636	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0599	1438	A	G	0	612	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0599	2706	A	G	0	604	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0599	3010	G	A	0	545	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0599	4216	T	C	2	470	missense_variant	MODERATE	ND1	0.0991
HLI-0599	4769	A	G	1	542	synonymous_variant	LOW	ND2	0.9767
HLI-0599	7028	C	T	1	692	synonymous_variant	LOW	COX1	0.8089
HLI-0599	10398	A	G	0	573	missense_variant	MODERATE	ND3	0.445
HLI-0599	10876	A	G	2	626	synonymous_variant	LOW	ND4	0.0098
HLI-0599	11251	A	G	1	633	synonymous_variant	LOW	ND4	0.0932
HLI-0599	11719	G	A	0	589	synonymous_variant	LOW	ND4	0.7756
HLI-0599	12612	A	G	2	538	synonymous_variant	LOW	ND5	0.0506
HLI-0599	13708	G	A	0	492	missense_variant	MODERATE	ND5	0.0717
HLI-0599	13827	A	G	0	454	synonymous_variant	LOW	ND5	0.0047
HLI-0599	14766	C	T	3	679	missense_variant	MODERATE	CYTB	0.7696
HLI-0599	14798	T	C	2	762	missense_variant	MODERATE	CYTB	0.0651
HLI-0599	15326	A	G	0	468	missense_variant	MODERATE	CYTB	0.9868

HLI-0599	15452	C	A	3	456	missense_variant	MODERATE	CYTB	0.0933
HLI-0599	16069	C	T	3	486	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0599	16126	T	C	1	553	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0599	16519	T	C	0	297	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0600	146	T	C	0	54	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0600	152	T	C	0	57	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0600	189	A	G	0	56	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0600	195	T	C	0	53	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0600	263	A	G	0	32	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0600	709	G	A	0	46	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0600	750	A	G	0	50	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0600	1438	A	G	0	55	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0600	4769	A	G	1	47	synonymous_variant	LOW	ND2	0.9767
HLI-0600	8412	T	C	0	49	missense_variant	MODERATE	ATP8	4.00E-04
HLI-0600	13101	A	C	0	50	synonymous_variant	LOW	ND5	0.0055
HLI-0600	13269	A	G	0	46	synonymous_variant	LOW	ND5	0.0023
HLI-0600	13899	T	C	0	51	synonymous_variant	LOW	ND5	0.001
HLI-0600	15326	A	G	0	54	missense_variant	MODERATE	CYTB	0.9868
HLI-0600	16362	T	C	0	42	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0600	16519	T	C	0	20	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0601	73	A	G	2	246	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0601	89	T	C	1	286	upstream_gene_variant	MODIFIER	DLoop	0.0038
HLI-0601	93	A	G	1	294	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0601	95	A	C	1	298	upstream_gene_variant	MODIFIER	DLoop	0.0076
HLI-0601	152	T	C	0	276	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0601	182	C	T	0	310	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0601	186	C	A	0	293	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0601	189	A	C	0	293	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0601	195	T	C	0	289	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0601	236	T	C	0	227	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0601	247	G	A	0	224	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0601	263	A	G	0	209	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0601	297	A	G	0	194	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0601	750	A	G	0	768	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0601	769	G	A	0	835	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0601	825	T	A	1	845	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0601	990	T	C	0	845	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0601	1018	G	A	0	916	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0601	1438	A	G	0	783	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0601	2706	A	G	1	773	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0601	2755	A	G	0	837	upstream_gene_variant	MODIFIER	RNR2	0.0047
HLI-0601	2758	G	A	0	841	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0601	2863	T	C	1	776	upstream_gene_variant	MODIFIER	RNR2	0.0017
HLI-0601	2885	T	C	0	878	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0601	3513	C	T	1	772	synonymous_variant	LOW	ND1	0.0015
HLI-0601	3594	C	T	0	777	synonymous_variant	LOW	ND1	0.0789
HLI-0601	3666	G	A	0	817	synonymous_variant	LOW	ND1	0.0233
HLI-0601	3796	A	T	0	754	missense_variant	MODERATE	ND1	0.0045
HLI-0601	3843	A	G	1	863	synonymous_variant	LOW	ND1	0.0046
HLI-0601	3927	A	G	1	821	synonymous_variant	LOW	ND1	0.0014
HLI-0601	4104	A	G	1	593	synonymous_variant	LOW	ND1	0.0785
HLI-0601	4363	T	C	0	645	upstream_gene_variant	MODIFIER	TRNQ	9.00E-04
HLI-0601	4454	T	A	0	698	upstream_gene_variant	MODIFIER	TRNM	0.0029
HLI-0601	4506	A	G	1	766	missense_variant	MODERATE	ND2	0.0012
HLI-0601	4769	A	G	2	633	synonymous_variant	LOW	ND2	0.9767
HLI-0601	5390	A	G	1	667	synonymous_variant	LOW	ND2	0.0069
HLI-0601	5951	A	G	2	840	synonymous_variant	LOW	COX1	0.0128
HLI-0601	6071	T	C	1	805	synonymous_variant	LOW	COX1	0.0129
HLI-0601	6752	A	G	3	730	synonymous_variant	LOW	COX1	0.0066
HLI-0601	7028	C	T	2	698	synonymous_variant	LOW	COX1	0.8089
HLI-0601	7055	A	G	3	702	synonymous_variant	LOW	COX1	0.0188
HLI-0601	7146	A	G	1	387	missense_variant	MODERATE	COX1	0.0497
HLI-0601	7202	A	G	3	513	synonymous_variant	LOW	COX1	0.0031
HLI-0601	7256	C	T	2	544	synonymous_variant	LOW	COX1	0.0784
HLI-0601	7389	T	C	0	491	missense_variant	MODERATE	COX1	0.0201
HLI-0601	7521	G	A	0	475	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0601	7660	T	C	1	733	synonymous_variant	LOW	COX2	0.0021
HLI-0601	7693	C	T	1	759	synonymous_variant	LOW	COX2	7.00E-04
HLI-0601	8027	G	A	1	742	missense_variant	MODERATE	COX2	0.0334
HLI-0601	8087	T	C	0	771	synonymous_variant	LOW	COX2	0.0031
HLI-0601	8468	C	T	1	458	synonymous_variant	LOW	ATP8	0.0501
HLI-0601	8655	C	T	4	475	synonymous_variant	LOW	ATP6	0.0511
HLI-0601	8701	A	G	0	540	missense_variant	MODERATE	ATP6	0.3391
HLI-0601	9072	A	G	1	792	synonymous_variant	LOW	ATP6	0.0124
HLI-0601	9272	C	T	2	753	synonymous_variant	LOW	COX3	7.00E-04
HLI-0601	9540	T	C	1	835	synonymous_variant	LOW	COX3	0.339
HLI-0601	9647	T	C	1	753	synonymous_variant	LOW	COX3	0.0022
HLI-0601	10321	T	C	0	393	missense_variant	MODERATE	ND3	0.0106

HLI-0601	10398	A	G	0	449	missense_variant	MODERATE	ND3	0.445
HLI-0601	10586	G	A	1	479	synonymous_variant	LOW	ND4L	0.0177
HLI-0601	10688	G	A	1	550	synonymous_variant	LOW	ND4L	0.0515
HLI-0601	10810	T	C	0	583	synonymous_variant	LOW	ND4	0.0522
HLI-0601	10873	T	C	1	644	synonymous_variant	LOW	ND4	0.3389
HLI-0601	11719	G	A	1	770	synonymous_variant	LOW	ND4	0.7756
HLI-0601	11899	T	C	0	668	synonymous_variant	LOW	ND4	0.0108
HLI-0601	12705	C	T	1	630	synonymous_variant	LOW	ND5	0.4212
HLI-0601	12768	A	G	1	680	synonymous_variant	LOW	ND5	0.0016
HLI-0601	12810	A	G	0	720	synonymous_variant	LOW	ND5	0.0198
HLI-0601	13105	A	G	0	740	missense_variant	MODERATE	ND5	0.076
HLI-0601	13485	A	G	2	702	synonymous_variant	LOW	ND5	0.0122
HLI-0601	13506	C	T	1	781	synonymous_variant	LOW	ND5	0.0506
HLI-0601	13650	C	T	0	708	synonymous_variant	LOW	ND5	0.079
HLI-0601	13789	T	C	0	606	missense_variant	MODERATE	ND5	0.0185
HLI-0601	14000	T	A	0	633	missense_variant	MODERATE	ND5	0.0126
HLI-0601	14088	T	C	0	590	synonymous_variant	LOW	ND5	0.0046
HLI-0601	14148	A	G	2	721	stop_retained_variant	LOW	ND5	0.0065
HLI-0601	14178	T	C	0	711	missense_variant	MODERATE	ND6	0.0225
HLI-0601	14560	G	A	2	720	synonymous_variant	LOW	ND6	0.0235
HLI-0601	14766	C	T	5	678	missense_variant	MODERATE	CYTB	0.7696
HLI-0601	14911	C	T	1	833	synonymous_variant	LOW	CYTB	0.0124
HLI-0601	15326	A	G	0	652	missense_variant	MODERATE	CYTB	0.9868
HLI-0601	16129	G	A	2	592	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0601	16223	C	T	1	495	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0601	16274	G	A	0	448	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0601	16278	C	T	0	444	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0601	16293	A	G	0	413	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0601	16294	C	T	0	416	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0601	16311	T	C	0	408	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0601	16360	C	T	0	359	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0601	16519	T	C	0	213	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0602	73	A	G	0	360	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0602	146	T	C	1	598	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0602	185	G	A	0	576	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0602	188	A	G	0	571	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0602	228	G	A	0	222	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0602	263	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0602	295	C	T	0	256	upstream_gene_variant	MODIFIER	DLoop	0.0469

HLI-0602	462	C	T	6	528	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0602	489	T	C	1	628	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0602	750	A	G	0	737	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0602	1438	A	G	0	743	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0602	2706	A	G	2	700	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0602	3010	G	A	2	682	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0602	4216	T	C	1	777	missense_variant	MODERATE	ND1	0.0991
HLI-0602	4769	A	G	0	681	synonymous_variant	LOW	ND2	0.9767
HLI-0602	7028	C	T	3	810	synonymous_variant	LOW	COX1	0.8089
HLI-0602	8865	G	A	0	692	synonymous_variant	LOW	ATP6	0.003
HLI-0602	10398	A	G	1	728	missense_variant	MODERATE	ND3	0.445
HLI-0602	10685	G	A	0	660	synonymous_variant	LOW	ND4L	0.0055
HLI-0602	11251	A	G	0	665	synonymous_variant	LOW	ND4	0.0932
HLI-0602	11719	G	A	2	639	synonymous_variant	LOW	ND4	0.7756
HLI-0602	12020	C	T	1	639	missense_variant	MODERATE	ND4	2.00E-04
HLI-0602	12612	A	G	1	730	synonymous_variant	LOW	ND5	0.0506
HLI-0602	13281	T	C	3	645	synonymous_variant	LOW	ND5	0.0033
HLI-0602	13708	G	A	1	563	missense_variant	MODERATE	ND5	0.0717
HLI-0602	13933	A	G	1	538	missense_variant	MODERATE	ND5	0.0022
HLI-0602	14766	C	T	0	719	missense_variant	MODERATE	CYTB	0.7696
HLI-0602	14798	T	C	1	806	missense_variant	MODERATE	CYTB	0.0651
HLI-0602	15326	A	G	1	648	missense_variant	MODERATE	CYTB	0.9868
HLI-0602	15452	C	A	5	617	missense_variant	MODERATE	CYTB	0.0933
HLI-0602	16069	C	T	3	660	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0602	16126	T	C	2	687	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0602	16519	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0603	73	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0603	185	G	A	0	477	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0603	188	A	G	0	480	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0603	228	G	A	0	396	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0603	263	A	G	0	327	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0603	295	C	T	0	268	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0603	462	C	T	4	498	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0603	489	T	C	1	521	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0603	750	A	G	0	591	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0603	1438	A	G	0	654	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0603	2706	A	G	0	638	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0603	3010	G	A	2	644	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0603	4216	T	C	1	522	missense_variant	MODERATE	ND1	0.0991

HLI-0603	4769	A	G	0	552	synonymous_variant	LOW	ND2	0.9767
HLI-0603	7028	C	T	2	700	synonymous_variant	LOW	COX1	0.8089
HLI-0603	10398	A	G	0	694	missense_variant	MODERATE	ND3	0.445
HLI-0603	11251	A	G	0	650	synonymous_variant	LOW	ND4	0.0932
HLI-0603	11719	G	A	2	615	synonymous_variant	LOW	ND4	0.7756
HLI-0603	12612	A	G	12	650	synonymous_variant	LOW	ND5	0.0506
HLI-0603	13708	G	A	2	540	missense_variant	MODERATE	ND5	0.0717
HLI-0603	14766	C	T	0	664	missense_variant	MODERATE	CYTB	0.7696
HLI-0603	14798	T	C	0	737	missense_variant	MODERATE	CYTB	0.0651
HLI-0603	15326	A	G	0	486	missense_variant	MODERATE	CYTB	0.9868
HLI-0603	15452	C	A	4	459	missense_variant	MODERATE	CYTB	0.0933
HLI-0603	16069	C	T	3	611	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0603	16126	T	C	0	644	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0603	16519	T	C	0	328	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0604	73	A	G	0	332	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0604	257	A	G	0	242	upstream_gene_variant	MODIFIER	DLoop	0.0025
HLI-0604	263	A	G	0	250	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0604	497	C	T	5	470	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0604	750	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0604	1189	T	C	1	773	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0604	1438	A	G	2	669	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0604	1811	A	G	4	648	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0604	2706	A	G	0	728	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0604	3480	A	G	1	522	synonymous_variant	LOW	ND1	0.0392
HLI-0604	4769	A	G	0	538	synonymous_variant	LOW	ND2	0.9767
HLI-0604	6260	G	A	1	681	synonymous_variant	LOW	COX1	0.009
HLI-0604	7028	C	T	4	771	synonymous_variant	LOW	COX1	0.8089
HLI-0604	9055	G	A	1	573	missense_variant	MODERATE	ATP6	0.0425
HLI-0604	9698	T	C	2	624	synonymous_variant	LOW	COX3	0.0405
HLI-0604	10398	A	G	0	642	missense_variant	MODERATE	ND3	0.445
HLI-0604	10550	A	G	1	587	synonymous_variant	LOW	ND4L	0.0376
HLI-0604	11152	T	C	0	582	synonymous_variant	LOW	ND4	0.0024
HLI-0604	11299	T	C	1	551	synonymous_variant	LOW	ND4	0.0417
HLI-0604	11467	A	G	0	629	synonymous_variant	LOW	ND4	0.1231
HLI-0604	11485	T	C	1	682	synonymous_variant	LOW	ND4	0.0081
HLI-0604	11719	G	A	1	585	synonymous_variant	LOW	ND4	0.7756
HLI-0604	11840	C	T	2	554	synonymous_variant	LOW	ND4	0.0041
HLI-0604	12308	A	G	1	522	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0604	12372	G	A	1	527	synonymous_variant	LOW	ND5	0.1329

HLI-0604	13740	T	C	0	447	synonymous_variant	LOW	ND5	0.0041
HLI-0604	14167	C	T	4	424	synonymous_variant	LOW	ND6	0.0385
HLI-0604	14766	C	T	2	595	missense_variant	MODERATE	CYTB	0.7696
HLI-0604	14798	T	C	0	657	missense_variant	MODERATE	CYTB	0.0651
HLI-0604	15326	A	G	0	641	missense_variant	MODERATE	CYTB	0.9868
HLI-0604	16224	T	C	3	557	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0604	16311	T	C	3	572	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0604	16519	T	C	1	260	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0606	73	A	G	1	377	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0606	152	T	C	0	609	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0606	217	T	C	0	336	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0606	263	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0606	508	A	G	4	508	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0606	750	A	G	1	758	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0606	1438	A	G	0	742	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0606	1811	A	G	1	642	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0606	1833	C	T	1	717	upstream_gene_variant	MODIFIER	RNR2	2.00E-04
HLI-0606	2706	A	G	0	731	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0606	3720	A	G	2	634	synonymous_variant	LOW	ND1	0.0069
HLI-0606	3849	G	A	1	693	synonymous_variant	LOW	ND1	0.0035
HLI-0606	4553	T	C	0	717	synonymous_variant	LOW	ND2	0.0023
HLI-0606	4769	A	G	0	624	synonymous_variant	LOW	ND2	0.9767
HLI-0606	5390	A	G	3	654	synonymous_variant	LOW	ND2	0.0069
HLI-0606	5426	T	C	1	735	synonymous_variant	LOW	ND2	0.0091
HLI-0606	5686	A	T	3	712	upstream_gene_variant	MODIFIER	TRNN	3.00E-04
HLI-0606	6045	C	T	3	787	synonymous_variant	LOW	COX1	0.0065
HLI-0606	6152	T	C	3	728	synonymous_variant	LOW	COX1	0.0077
HLI-0606	7028	C	T	4	826	synonymous_variant	LOW	COX1	0.8089
HLI-0606	8473	T	C	3	492	synonymous_variant	LOW	ATP8	0.0105
HLI-0606	10876	A	G	1	654	synonymous_variant	LOW	ND4	0.0098
HLI-0606	11467	A	G	0	752	synonymous_variant	LOW	ND4	0.1231
HLI-0606	11719	G	A	1	691	synonymous_variant	LOW	ND4	0.7756
HLI-0606	12308	A	G	1	601	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0606	12372	G	A	1	584	synonymous_variant	LOW	ND5	0.1329
HLI-0606	12557	C	T	1	626	missense_variant	MODERATE	ND5	0.0028
HLI-0606	13020	T	C	1	744	synonymous_variant	LOW	ND5	0.0106
HLI-0606	13734	T	C	0	580	synonymous_variant	LOW	ND5	0.0067
HLI-0606	14766	C	T	3	669	missense_variant	MODERATE	CYTB	0.7696
HLI-0606	15326	A	G	0	608	missense_variant	MODERATE	CYTB	0.9868

HLI-0606	15907	A	G	1	711	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0606	16051	A	G	1	550	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0606	16092	T	C	5	485	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0606	16129	G	C	1	359	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0606	16362	T	C	1	511	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0606	16519	T	C	0	254	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0607	263	A	G	1	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0607	750	A	G	0	674	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0607	1438	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0607	4769	A	G	0	557	synonymous_variant	LOW	ND2	0.9767
HLI-0607	7055	A	G	3	670	synonymous_variant	LOW	COX1	0.0188
HLI-0607	7386	C	T	1	593	synonymous_variant	LOW	COX1	0
HLI-0607	9545	A	G	0	682	synonymous_variant	LOW	COX3	0.0469
HLI-0607	11152	T	C	0	578	synonymous_variant	LOW	ND4	0.0024
HLI-0607	13500	T	C	0	576	synonymous_variant	LOW	ND5	0.0173
HLI-0607	15326	A	G	0	554	missense_variant	MODERATE	CYTB	0.9868
HLI-0607	15754	C	T	0	530	synonymous_variant	LOW	CYTB	3.00E-04
HLI-0607	16519	T	C	0	324	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0608	73	A	G	0	34	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0608	199	T	C	0	58	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0608	204	T	C	0	55	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0608	250	T	C	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0608	263	A	G	0	26	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0608	750	A	G	0	60	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0608	1438	A	G	0	39	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0608	1719	G	A	0	28	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0608	2706	A	G	0	53	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0608	4529	A	T	0	35	synonymous_variant	LOW	ND2	0.015
HLI-0608	4769	A	G	0	44	synonymous_variant	LOW	ND2	0.9767
HLI-0608	6267	G	A	0	54	missense_variant	MODERATE	COX1	0.0016
HLI-0608	6359	A	G	0	63	synonymous_variant	LOW	COX1	0.0014
HLI-0608	6734	G	A	1	59	synonymous_variant	LOW	COX1	0.0062
HLI-0608	7028	C	T	0	66	synonymous_variant	LOW	COX1	0.8089
HLI-0608	8251	G	A	0	50	synonymous_variant	LOW	COX2	0.058
HLI-0608	8573	G	A	0	41	missense_variant	MODERATE	ATP6	0.0011
HLI-0608	9386	T	C	0	69	synonymous_variant	LOW	COX3	7.00E-04
HLI-0608	9966	G	A	0	43	missense_variant	MODERATE	COX3	0.0069
HLI-0608	10034	T	C	0	48	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0608	10238	T	C	0	49	synonymous_variant	LOW	ND3	0.0623

HLI-0608	10398	A	G	0	47	missense_variant	MODERATE	ND3	0.445
HLI-0608	11719	G	A	0	49	synonymous_variant	LOW	ND4	0.7756
HLI-0608	12501	G	A	0	36	synonymous_variant	LOW	ND5	0.0258
HLI-0608	12705	C	T	0	43	synonymous_variant	LOW	ND5	0.4212
HLI-0608	13780	A	G	0	32	missense_variant	MODERATE	ND5	0.0179
HLI-0608	14766	C	T	3	65	missense_variant	MODERATE	CYTB	0.7696
HLI-0608	15043	G	A	0	71	synonymous_variant	LOW	CYTB	0.2362
HLI-0608	15326	A	G	0	53	missense_variant	MODERATE	CYTB	0.9868
HLI-0608	15924	A	G	0	43	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0608	16129	G	A	0	45	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0608	16223	C	T	0	28	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0608	16264	C	T	0	30	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0608	16270	C	T	0	31	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0608	16311	T	C	0	37	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0608	16319	G	A	0	36	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0608	16362	T	C	0	47	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0608	16391	G	A	0	47	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0608	16519	T	C	0	31	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0609	73	A	G	0	284	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0609	150	C	T	0	504	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0609	189	A	G	0	477	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0609	195	T	C	0	474	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0609	198	C	T	0	462	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0609	263	A	G	0	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0609	750	A	G	2	677	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0609	1438	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0609	2352	T	C	0	601	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0609	2706	A	G	0	618	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0609	2951	A	G	0	650	upstream_gene_variant	MODIFIER	RNR2	2.00E-04
HLI-0609	4769	A	G	2	636	synonymous_variant	LOW	ND2	0.9767
HLI-0609	4823	T	C	1	647	synonymous_variant	LOW	ND2	0.0049
HLI-0609	5082	T	C	2	578	synonymous_variant	LOW	ND2	0.0013
HLI-0609	6044	T	C	0	714	synonymous_variant	LOW	COX1	2.00E-04
HLI-0609	7028	C	T	1	745	synonymous_variant	LOW	COX1	0.8089
HLI-0609	8701	A	G	0	568	missense_variant	MODERATE	ATP6	0.3391
HLI-0609	9540	T	C	1	696	synonymous_variant	LOW	COX3	0.339
HLI-0609	10398	A	G	0	663	missense_variant	MODERATE	ND3	0.445
HLI-0609	10819	A	G	1	559	synonymous_variant	LOW	ND4	0.0228
HLI-0609	10873	T	C	2	596	synonymous_variant	LOW	ND4	0.3389

HLI-0609	11719	G	A	1	634	synonymous_variant	LOW	ND4	0.7756
HLI-0609	12705	C	T	1	620	synonymous_variant	LOW	ND5	0.4212
HLI-0609	13105	A	G	0	654	missense_variant	MODERATE	ND5	0.076
HLI-0609	14212	T	C	0	522	synonymous_variant	LOW	ND6	0.0204
HLI-0609	14766	C	T	0	608	missense_variant	MODERATE	CYTB	0.7696
HLI-0609	14869	G	A	1	737	synonymous_variant	LOW	CYTB	0.0023
HLI-0609	14905	G	A	2	844	synonymous_variant	LOW	CYTB	0.0526
HLI-0609	15301	G	A	0	576	synonymous_variant	LOW	CYTB	0.2912
HLI-0609	15326	A	G	0	614	missense_variant	MODERATE	CYTB	0.9868
HLI-0609	16223	C	T	0	557	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0609	16258	A	T	0	598	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0609	16299	A	G	2	546	upstream_gene_variant	MODIFIER	DLoop	0.0032
HLI-0609	16320	C	T	2	507	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0609	16519	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0610	263	A	G	0	221	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0610	327	C	T	1	189	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0610	456	C	T	5	541	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0610	750	A	G	1	738	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0610	1438	A	G	0	687	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0610	4769	A	G	1	541	synonymous_variant	LOW	ND2	0.9767
HLI-0610	5471	G	A	0	614	synonymous_variant	LOW	ND2	0.0128
HLI-0610	12864	T	C	9	701	synonymous_variant	LOW	ND5	8.00E-04
HLI-0610	15326	A	G	0	555	missense_variant	MODERATE	CYTB	0.9868
HLI-0610	16304	T	C	1	582	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0611	73	A	G	13	223	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0611	152	T	C	20	298	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0611	182	C	T	23	353	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0611	185	G	T	23	349	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0611	195	T	C	23	350	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0611	236	T	C	7	154	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0611	247	G	A	8	166	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0611	263	A	G	0	189	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0611	357	A	G	18	271	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0611	709	G	A	30	641	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0611	710	T	C	30	646	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0611	750	A	G	1	708	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0611	769	G	A	29	690	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0611	825	T	A	27	713	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0611	1018	G	A	27	660	upstream_gene_variant	MODIFIER	RNR1	0.0817

HLI-0611	1738	T	C	22	599	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0611	2352	T	C	22	535	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0611	2706	A	G	27	636	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0611	2758	G	A	31	668	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0611	2768	A	G	27	673	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0611	2885	T	C	25	643	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0611	3308	T	C	21	587	start_lost	HIGH	ND1	0.0073
HLI-0611	3594	C	T	25	539	synonymous_variant	LOW	ND1	0.0789
HLI-0611	3666	G	A	24	607	synonymous_variant	LOW	ND1	0.0233
HLI-0611	3693	G	A	30	616	synonymous_variant	LOW	ND1	0.0091
HLI-0611	4104	A	G	19	538	synonymous_variant	LOW	ND1	0.0785
HLI-0611	4769	A	G	0	602	synonymous_variant	LOW	ND2	0.9767
HLI-0611	5036	A	G	24	547	synonymous_variant	LOW	ND2	0.006
HLI-0611	5046	G	A	24	585	missense_variant	MODERATE	ND2	0.018
HLI-0611	5393	T	C	10	564	synonymous_variant	LOW	ND2	0.0059
HLI-0611	5655	T	C	22	645	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0611	6110	A	G	31	623	synonymous_variant	LOW	COX1	0
HLI-0611	6548	C	T	19	624	synonymous_variant	LOW	COX1	0.0061
HLI-0611	6827	T	C	20	587	synonymous_variant	LOW	COX1	0.0072
HLI-0611	6989	A	G	26	631	synonymous_variant	LOW	COX1	0.0061
HLI-0611	7028	C	T	28	608	synonymous_variant	LOW	COX1	0.8089
HLI-0611	7055	A	G	27	537	synonymous_variant	LOW	COX1	0.0188
HLI-0611	7146	A	G	25	281	missense_variant	MODERATE	COX1	0.0497
HLI-0611	7256	C	T	30	424	synonymous_variant	LOW	COX1	0.0784
HLI-0611	7389	T	C	32	466	missense_variant	MODERATE	COX1	0.0201
HLI-0611	7521	G	A	32	421	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0611	7867	C	T	37	622	synonymous_variant	LOW	COX2	0.0076
HLI-0611	8248	A	G	23	587	synonymous_variant	LOW	COX2	0.0061
HLI-0611	8468	C	T	16	462	synonymous_variant	LOW	ATP8	0.0501
HLI-0611	8655	C	T	29	466	synonymous_variant	LOW	ATP6	0.0511
HLI-0611	8701	A	G	28	508	missense_variant	MODERATE	ATP6	0.3391
HLI-0611	8790	G	A	22	447	synonymous_variant	LOW	ATP6	0.0083
HLI-0611	8988	A	G	27	585	synonymous_variant	LOW	ATP6	5.00E-04
HLI-0611	9540	T	C	30	598	synonymous_variant	LOW	COX3	0.339
HLI-0611	10398	A	G	27	613	missense_variant	MODERATE	ND3	0.445
HLI-0611	10688	G	A	21	551	synonymous_variant	LOW	ND4L	0.0515
HLI-0611	10810	T	C	22	565	synonymous_variant	LOW	ND4	0.0522
HLI-0611	10873	T	C	18	496	synonymous_variant	LOW	ND4	0.3389
HLI-0611	11719	G	A	23	629	synonymous_variant	LOW	ND4	0.7756

HLI-0611	12519	T	C	19	560	synonymous_variant	LOW	ND5	0.007
HLI-0611	12705	C	T	24	587	synonymous_variant	LOW	ND5	0.4212
HLI-0611	13105	A	G	20	579	missense_variant	MODERATE	ND5	0.076
HLI-0611	13506	C	T	27	573	synonymous_variant	LOW	ND5	0.0506
HLI-0611	13650	C	T	21	525	synonymous_variant	LOW	ND5	0.079
HLI-0611	13789	T	C	18	389	missense_variant	MODERATE	ND5	0.0185
HLI-0611	13880	C	A	19	462	missense_variant	MODERATE	ND5	0.0055
HLI-0611	14178	T	C	21	548	missense_variant	MODERATE	ND6	0.0225
HLI-0611	14203	A	G	21	591	synonymous_variant	LOW	ND6	0.0061
HLI-0611	14560	G	A	17	580	synonymous_variant	LOW	ND6	0.0235
HLI-0611	14766	C	T	31	628	missense_variant	MODERATE	CYTB	0.7696
HLI-0611	14769	A	G	32	637	missense_variant	MODERATE	CYTB	0.0121
HLI-0611	15115	T	C	27	655	synonymous_variant	LOW	CYTB	0.0093
HLI-0611	15326	A	G	0	585	missense_variant	MODERATE	CYTB	0.9868
HLI-0611	16114	C	A	22	540	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0611	16126	T	C	25	570	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0611	16223	C	T	27	444	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0611	16264	C	T	22	410	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0611	16270	C	T	22	406	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0611	16278	C	T	19	410	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0611	16293	A	G	20	403	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0611	16311	T	C	20	391	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0611	16519	T	C	0	160	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0612	73	A	G	0	349	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0612	152	T	C	1	618	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0612	263	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0612	709	G	A	0	664	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0612	750	A	G	2	703	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0612	930	G	A	4	643	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0612	1438	A	G	0	690	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0612	1888	G	A	0	664	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0612	2706	A	G	3	624	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0612	4216	T	C	2	641	missense_variant	MODERATE	ND1	0.0991
HLI-0612	4769	A	G	1	518	synonymous_variant	LOW	ND2	0.9767
HLI-0612	4917	A	G	1	613	missense_variant	MODERATE	ND2	0.0477
HLI-0612	5147	G	A	1	561	synonymous_variant	LOW	ND2	0.0437
HLI-0612	7028	C	T	4	747	synonymous_variant	LOW	COX1	0.8089
HLI-0612	8697	G	A	0	620	synonymous_variant	LOW	ATP6	0.0466
HLI-0612	10463	T	C	0	617	upstream_gene_variant	MODIFIER	TRNR	0.0474

HLI-0612	11242	C	G	0	631	synonymous_variant	LOW	ND4	4.00E-04
HLI-0612	11251	A	G	0	660	synonymous_variant	LOW	ND4	0.0932
HLI-0612	11719	G	A	0	657	synonymous_variant	LOW	ND4	0.7756
HLI-0612	11812	A	G	1	649	synonymous_variant	LOW	ND4	0.0332
HLI-0612	13368	G	A	2	625	synonymous_variant	LOW	ND5	0.0495
HLI-0612	14233	A	G	0	587	synonymous_variant	LOW	ND6	0.0369
HLI-0612	14766	C	T	3	585	missense_variant	MODERATE	CYTB	0.7696
HLI-0612	14905	G	A	1	683	synonymous_variant	LOW	CYTB	0.0526
HLI-0612	14927	A	G	0	719	missense_variant	MODERATE	CYTB	0.003
HLI-0612	15326	A	G	0	572	missense_variant	MODERATE	CYTB	0.9868
HLI-0612	15452	C	A	6	617	missense_variant	MODERATE	CYTB	0.0933
HLI-0612	15607	A	G	0	596	synonymous_variant	LOW	CYTB	0.0508
HLI-0612	15928	G	A	0	633	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0612	16126	T	C	1	647	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0612	16294	C	T	2	563	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0612	16519	T	C	0	336	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0613	73	A	G	0	351	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0613	152	T	C	1	631	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0613	195	T	C	5	560	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0613	263	A	G	1	179	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0613	504	T	C	1	278	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0613	709	G	A	6	606	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0613	750	A	G	2	726	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0613	1438	A	G	0	737	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0613	1888	G	A	2	617	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0613	2706	A	G	2	654	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0613	4216	T	C	4	621	missense_variant	MODERATE	ND1	0.0991
HLI-0613	4769	A	G	1	688	synonymous_variant	LOW	ND2	0.9767
HLI-0613	4917	A	G	2	650	missense_variant	MODERATE	ND2	0.0477
HLI-0613	7028	C	T	0	718	synonymous_variant	LOW	COX1	0.8089
HLI-0613	7337	G	A	1	727	synonymous_variant	LOW	COX1	0.0119
HLI-0613	8697	G	A	1	577	synonymous_variant	LOW	ATP6	0.0466
HLI-0613	9899	T	C	1	681	synonymous_variant	LOW	COX3	0.0108
HLI-0613	10463	T	C	1	696	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0613	11251	A	G	3	644	synonymous_variant	LOW	ND4	0.0932
HLI-0613	11719	G	A	0	653	synonymous_variant	LOW	ND4	0.7756
HLI-0613	12308	A	G	2	597	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0613	12633	C	A	2	658	synonymous_variant	LOW	ND5	0.0123
HLI-0613	13368	G	A	5	705	synonymous_variant	LOW	ND5	0.0495

HLI-0613	14766	C	T	0	609	missense_variant	MODERATE	CYTB	0.7696
HLI-0613	14905	G	A	4	739	synonymous_variant	LOW	CYTB	0.0526
HLI-0613	15326	A	G	1	588	missense_variant	MODERATE	CYTB	0.9868
HLI-0613	15452	C	A	1	546	missense_variant	MODERATE	CYTB	0.0933
HLI-0613	15607	A	G	3	569	synonymous_variant	LOW	CYTB	0.0508
HLI-0613	15928	G	A	1	625	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0613	16126	T	C	3	622	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0613	16163	A	G	2	657	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0613	16178	T	C	1	614	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0613	16256	C	T	1	653	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0613	16294	C	T	3	609	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0613	16519	T	C	1	310	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0614	73	A	G	0	401	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0614	152	T	C	6	738	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0614	263	A	G	1	295	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0614	709	G	A	2	790	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0614	750	A	G	0	848	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0614	930	G	A	2	827	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0614	1438	A	G	0	802	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0614	1888	G	A	1	717	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0614	2706	A	G	0	766	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0614	4216	T	C	3	696	missense_variant	MODERATE	ND1	0.0991
HLI-0614	4769	A	G	0	655	synonymous_variant	LOW	ND2	0.9767
HLI-0614	4917	A	G	1	628	missense_variant	MODERATE	ND2	0.0477
HLI-0614	5147	G	A	1	618	synonymous_variant	LOW	ND2	0.0437
HLI-0614	7028	C	T	0	835	synonymous_variant	LOW	COX1	0.8089
HLI-0614	8697	G	A	0	668	synonymous_variant	LOW	ATP6	0.0466
HLI-0614	10463	T	C	1	815	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0614	11242	C	G	0	708	synonymous_variant	LOW	ND4	4.00E-04
HLI-0614	11251	A	G	0	745	synonymous_variant	LOW	ND4	0.0932
HLI-0614	11719	G	A	0	734	synonymous_variant	LOW	ND4	0.7756
HLI-0614	11812	A	G	1	733	synonymous_variant	LOW	ND4	0.0332
HLI-0614	13368	G	A	1	736	synonymous_variant	LOW	ND5	0.0495
HLI-0614	14233	A	G	3	647	synonymous_variant	LOW	ND6	0.0369
HLI-0614	14766	C	T	2	670	missense_variant	MODERATE	CYTB	0.7696
HLI-0614	14905	G	A	1	820	synonymous_variant	LOW	CYTB	0.0526
HLI-0614	15326	A	G	0	691	missense_variant	MODERATE	CYTB	0.9868
HLI-0614	15452	C	A	7	710	missense_variant	MODERATE	CYTB	0.0933
HLI-0614	15607	A	G	0	742	synonymous_variant	LOW	CYTB	0.0508

HLI-0614	15928	G	A	0	705	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0614	16126	T	C	0	685	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0614	16294	C	T	2	633	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0614	16519	T	C	0	410	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0615	263	A	G	2	298	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0615	750	A	G	0	805	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0615	1438	A	G	0	786	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0615	3010	G	A	0	791	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0615	4769	A	G	1	722	synonymous_variant	LOW	ND2	0.9767
HLI-0615	6569	C	T	2	800	synonymous_variant	LOW	COX1	1.00E-04
HLI-0615	10101	T	C	0	820	synonymous_variant	LOW	ND3	0.0026
HLI-0615	15326	A	G	0	744	missense_variant	MODERATE	CYTB	0.9868
HLI-0615	16270	C	T	1	742	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0616	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0616	150	C	T	3	580	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0616	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0616	750	A	G	1	679	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0616	1438	A	G	0	699	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0616	1811	A	G	1	647	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0616	2706	A	G	1	698	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0616	4188	A	G	2	608	synonymous_variant	LOW	ND1	0.003
HLI-0616	4640	C	A	2	641	missense_variant	MODERATE	ND2	0.0029
HLI-0616	4769	A	G	0	622	synonymous_variant	LOW	ND2	0.9767
HLI-0616	6302	A	G	0	656	synonymous_variant	LOW	COX1	4.00E-04
HLI-0616	6603	C	T	0	684	synonymous_variant	LOW	COX1	2.00E-04
HLI-0616	7028	C	T	2	717	synonymous_variant	LOW	COX1	0.8089
HLI-0616	7853	G	A	0	652	missense_variant	MODERATE	COX2	0.0197
HLI-0616	9025	G	A	0	670	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0616	9656	T	C	0	684	synonymous_variant	LOW	COX3	0.0035
HLI-0616	10324	T	C	0	670	missense_variant	MODERATE	ND3	5.00E-04
HLI-0616	11467	A	G	0	628	synonymous_variant	LOW	ND4	0.1231
HLI-0616	11719	G	A	0	668	synonymous_variant	LOW	ND4	0.7756
HLI-0616	12308	A	G	0	613	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0616	12372	G	A	1	633	synonymous_variant	LOW	ND5	0.1329
HLI-0616	13743	T	C	0	447	synonymous_variant	LOW	ND5	0.0037
HLI-0616	14139	A	G	1	512	synonymous_variant	LOW	ND5	0.0056
HLI-0616	14389	C	T	2	474	synonymous_variant	LOW	ND6	1.00E-04
HLI-0616	14766	C	T	2	599	missense_variant	MODERATE	CYTB	0.7696
HLI-0616	15326	A	G	0	621	missense_variant	MODERATE	CYTB	0.9868

HLI-0616	15454	T	C	0	641	synonymous_variant	LOW	CYTB	0.0072
HLI-0616	15601	T	C	0	658	synonymous_variant	LOW	CYTB	0.0016
HLI-0616	16168	C	T	1	564	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0616	16288	T	C	0	610	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0616	16343	A	G	0	594	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0616	16355	C	T	0	581	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0617	73	A	G	0	391	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0617	150	C	T	0	657	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0617	195	T	C	0	658	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0617	263	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0617	295	C	T	0	282	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0617	456	C	T	4	606	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0617	489	T	C	0	654	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0617	750	A	G	1	808	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0617	1438	A	G	2	744	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0617	2706	A	G	3	888	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0617	4216	T	C	2	715	missense_variant	MODERATE	ND1	0.0991
HLI-0617	4769	A	G	2	688	synonymous_variant	LOW	ND2	0.9767
HLI-0617	6671	T	C	3	822	synonymous_variant	LOW	COX1	0.0071
HLI-0617	7028	C	T	1	760	synonymous_variant	LOW	COX1	0.8089
HLI-0617	7476	C	T	0	776	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0617	8065	G	A	1	740	synonymous_variant	LOW	COX2	6.00E-04
HLI-0617	9947	G	A	0	778	synonymous_variant	LOW	COX3	0.0092
HLI-0617	10398	A	G	1	750	missense_variant	MODERATE	ND3	0.445
HLI-0617	10499	A	G	0	653	synonymous_variant	LOW	ND4L	0.0093
HLI-0617	11002	A	G	0	584	synonymous_variant	LOW	ND4	0.0124
HLI-0617	11251	A	G	1	716	synonymous_variant	LOW	ND4	0.0932
HLI-0617	11377	G	A	0	723	synonymous_variant	LOW	ND4	0.0125
HLI-0617	11698	C	G	0	713	synonymous_variant	LOW	ND4	1.00E-04
HLI-0617	11719	G	A	0	769	synonymous_variant	LOW	ND4	0.7756
HLI-0617	12570	A	G	5	710	synonymous_variant	LOW	ND5	0.0016
HLI-0617	12612	A	G	3	713	synonymous_variant	LOW	ND5	0.0506
HLI-0617	13015	T	C	1	685	synonymous_variant	LOW	ND5	9.00E-04
HLI-0617	13708	G	A	4	582	missense_variant	MODERATE	ND5	0.0717
HLI-0617	13830	T	C	0	546	synonymous_variant	LOW	ND5	0.0021
HLI-0617	14766	C	T	3	687	missense_variant	MODERATE	CYTB	0.7696
HLI-0617	15257	G	A	0	714	missense_variant	MODERATE	CYTB	0.0155
HLI-0617	15326	A	G	1	778	missense_variant	MODERATE	CYTB	0.9868
HLI-0617	15452	C	A	3	710	missense_variant	MODERATE	CYTB	0.0933

HLI-0617	15679	A	G	0	708	synonymous_variant	LOW	CYTB	0.0018
HLI-0617	16069	C	T	3	745	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0617	16126	T	C	0	784	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0617	16241	A	G	1	722	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0618	73	A	G	2	391	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0618	263	A	G	0	308	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0618	709	G	A	2	767	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0618	750	A	G	0	811	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0618	930	G	A	0	793	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0618	1438	A	G	0	779	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0618	1888	G	A	0	778	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0618	2706	A	G	0	759	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0618	4216	T	C	0	731	missense_variant	MODERATE	ND1	0.0991
HLI-0618	4769	A	G	1	619	synonymous_variant	LOW	ND2	0.9767
HLI-0618	4917	A	G	2	684	missense_variant	MODERATE	ND2	0.0477
HLI-0618	5147	G	A	0	686	synonymous_variant	LOW	ND2	0.0437
HLI-0618	7028	C	T	0	788	synonymous_variant	LOW	COX1	0.8089
HLI-0618	8697	G	A	1	656	synonymous_variant	LOW	ATP6	0.0466
HLI-0618	10463	T	C	0	791	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0618	11251	A	G	0	734	synonymous_variant	LOW	ND4	0.0932
HLI-0618	11719	G	A	0	714	synonymous_variant	LOW	ND4	0.7756
HLI-0618	11812	A	G	0	678	synonymous_variant	LOW	ND4	0.0332
HLI-0618	13368	G	A	1	710	synonymous_variant	LOW	ND5	0.0495
HLI-0618	13692	C	T	6	642	synonymous_variant	LOW	ND5	6.00E-04
HLI-0618	14233	A	G	1	614	synonymous_variant	LOW	ND6	0.0369
HLI-0618	14766	C	T	2	728	missense_variant	MODERATE	CYTB	0.7696
HLI-0618	14905	G	A	0	757	synonymous_variant	LOW	CYTB	0.0526
HLI-0618	15326	A	G	0	717	missense_variant	MODERATE	CYTB	0.9868
HLI-0618	15452	C	A	6	709	missense_variant	MODERATE	CYTB	0.0933
HLI-0618	15607	A	G	1	729	synonymous_variant	LOW	CYTB	0.0508
HLI-0618	15928	G	A	1	731	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0618	16126	T	C	0	705	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0618	16294	C	T	2	717	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0618	16304	T	C	2	757	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0618	16519	T	C	1	401	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0619	41	C	T	0	227	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0619	73	A	G	0	406	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0619	150	C	T	0	754	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0619	263	A	G	0	364	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0619	709	G	A	1	706	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0619	750	A	G	0	799	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0619	1438	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0619	1888	G	A	0	310	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0619	2706	A	G	0	654	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0619	4216	T	C	1	533	missense_variant	MODERATE	ND1	0.0991
HLI-0619	4769	A	G	1	483	synonymous_variant	LOW	ND2	0.9767
HLI-0619	4917	A	G	0	530	missense_variant	MODERATE	ND2	0.0477
HLI-0619	7028	C	T	9	729	synonymous_variant	LOW	COX1	0.8089
HLI-0619	8460	A	G	1	371	missense_variant	MODERATE	ATP8	0.0085
HLI-0619	8697	G	A	0	525	synonymous_variant	LOW	ATP6	0.0466
HLI-0619	10463	T	C	0	598	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0619	11251	A	G	0	633	synonymous_variant	LOW	ND4	0.0932
HLI-0619	11719	G	A	0	634	synonymous_variant	LOW	ND4	0.7756
HLI-0619	11812	A	G	4	574	synonymous_variant	LOW	ND4	0.0332
HLI-0619	12681	T	C	0	592	synonymous_variant	LOW	ND5	0.0023
HLI-0619	13368	G	A	1	588	synonymous_variant	LOW	ND5	0.0495
HLI-0619	14233	A	G	1	485	synonymous_variant	LOW	ND6	0.0369
HLI-0619	14766	C	T	4	746	missense_variant	MODERATE	CYTB	0.7696
HLI-0619	14905	G	A	2	927	synonymous_variant	LOW	CYTB	0.0526
HLI-0619	15326	A	G	0	498	missense_variant	MODERATE	CYTB	0.9868
HLI-0619	15452	C	A	3	413	missense_variant	MODERATE	CYTB	0.0933
HLI-0619	15607	A	G	1	383	synonymous_variant	LOW	CYTB	0.0508
HLI-0619	15928	G	A	0	292	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0619	16126	T	C	0	436	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0619	16153	G	A	1	478	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0619	16294	C	T	0	488	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0619	16519	T	C	0	372	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0620	73	A	G	0	377	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0620	189	A	G	0	520	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0620	200	A	G	0	508	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0620	263	A	G	0	297	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0620	272	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0620	750	A	G	1	767	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0620	1438	A	G	0	753	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0620	1822	T	C	1	675	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0620	2706	A	G	0	745	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0620	3396	T	C	5	688	synonymous_variant	LOW	ND1	0.0082
HLI-0620	4218	T	C	1	675	synonymous_variant	LOW	ND1	0.0057

HLI-0620	4769	A	G	1	630	synonymous_variant	LOW	ND2	0.9767
HLI-0620	5601	C	T	6	793	upstream_gene_variant	MODIFIER	TRNA	0.0101
HLI-0620	7028	C	T	0	804	synonymous_variant	LOW	COX1	0.8089
HLI-0620	7819	C	A	7	783	synonymous_variant	LOW	COX2	0.0045
HLI-0620	8410	C	T	3	550	synonymous_variant	LOW	ATP8	0.0018
HLI-0620	8527	A	G	2	579	initiator_codon_variant	LOW	ATP6/8	0.0044
HLI-0620	8701	A	G	0	584	missense_variant	MODERATE	ATP6	0.3391
HLI-0620	8932	C	T	5	714	missense_variant	MODERATE	ATP6	0.0044
HLI-0620	9540	T	C	3	782	synonymous_variant	LOW	COX3	0.339
HLI-0620	9950	T	C	3	762	synonymous_variant	LOW	COX3	0.0362
HLI-0620	10070	C	T	0	770	synonymous_variant	LOW	ND3	8.00E-04
HLI-0620	10398	A	G	6	660	missense_variant	MODERATE	ND3	0.445
HLI-0620	10873	T	C	1	578	synonymous_variant	LOW	ND4	0.3389
HLI-0620	11440	G	A	0	714	synonymous_variant	LOW	ND4	0.0081
HLI-0620	11719	G	A	1	692	synonymous_variant	LOW	ND4	0.7756
HLI-0620	12705	C	T	5	656	synonymous_variant	LOW	ND5	0.4212
HLI-0620	14766	C	T	0	724	missense_variant	MODERATE	CYTB	0.7696
HLI-0620	14769	A	G	0	741	missense_variant	MODERATE	CYTB	0.0121
HLI-0620	15301	G	A	0	662	synonymous_variant	LOW	CYTB	0.2912
HLI-0620	15326	A	G	0	739	missense_variant	MODERATE	CYTB	0.9868
HLI-0620	15514	T	C	0	609	synonymous_variant	LOW	CYTB	0.0071
HLI-0620	16129	G	A	1	805	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0620	16209	T	C	0	793	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0620	16223	C	T	0	778	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0620	16292	C	T	2	657	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0620	16295	C	T	2	647	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0620	16311	T	C	2	623	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0620	16519	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0621	73	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0621	89	T	C	0	260	upstream_gene_variant	MODIFIER	DLoop	0.0038
HLI-0621	93	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0621	95	A	T	0	265	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0621	95	A	C	0	265	upstream_gene_variant	MODIFIER	DLoop	0.0076
HLI-0621	146	T	C	0	463	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0621	150	C	T	0	477	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0621	182	C	T	0	437	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0621	195	T	C	0	437	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0621	198	C	T	0	438	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0621	263	A	G	1	263	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0621	325	C	T	0	302	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0621	680	T	C	1	754	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0621	709	G	A	0	832	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0621	750	A	G	0	825	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0621	769	G	A	0	795	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0621	1018	G	A	0	787	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0621	1438	A	G	0	778	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0621	1442	G	A	0	799	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0621	2332	C	T	0	625	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0621	2416	T	C	0	653	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0621	2706	A	G	0	732	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0621	3200	T	A	0	732	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0621	3594	C	T	1	757	synonymous_variant	LOW	ND1	0.0789
HLI-0621	4104	A	G	3	593	synonymous_variant	LOW	ND1	0.0785
HLI-0621	4769	A	G	2	607	synonymous_variant	LOW	ND2	0.9767
HLI-0621	7028	C	T	3	770	synonymous_variant	LOW	COX1	0.8089
HLI-0621	7256	C	T	1	624	synonymous_variant	LOW	COX1	0.0784
HLI-0621	7521	G	A	1	564	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0621	7624	T	A	1	660	synonymous_variant	LOW	COX2	0.0047
HLI-0621	8206	G	A	1	702	synonymous_variant	LOW	COX2	0.0287
HLI-0621	8701	A	G	0	595	missense_variant	MODERATE	ATP6	0.3391
HLI-0621	9221	A	G	0	738	synonymous_variant	LOW	COX3	0.0277
HLI-0621	9540	T	C	1	785	synonymous_variant	LOW	COX3	0.339
HLI-0621	10115	T	C	1	719	synonymous_variant	LOW	ND3	0.0278
HLI-0621	10398	A	G	0	655	missense_variant	MODERATE	ND3	0.445
HLI-0621	10873	T	C	0	576	synonymous_variant	LOW	ND4	0.3389
HLI-0621	11362	A	G	0	668	synonymous_variant	LOW	ND4	0.0024
HLI-0621	11719	G	A	1	698	synonymous_variant	LOW	ND4	0.7756
HLI-0621	11944	T	C	0	592	synonymous_variant	LOW	ND4	0.0331
HLI-0621	12236	G	A	2	571	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0621	12630	G	A	2	645	synonymous_variant	LOW	ND5	0.0053
HLI-0621	12705	C	T	0	721	synonymous_variant	LOW	ND5	0.4212
HLI-0621	13590	G	A	0	650	synonymous_variant	LOW	ND5	0.0586
HLI-0621	13650	C	T	0	679	synonymous_variant	LOW	ND5	0.079
HLI-0621	13767	C	T	1	569	synonymous_variant	LOW	ND5	1.00E-04
HLI-0621	13928	G	C	0	576	missense_variant	MODERATE	ND5	0.0484
HLI-0621	13958	G	C	0	623	missense_variant	MODERATE	ND5	0.0028
HLI-0621	14766	C	T	2	687	missense_variant	MODERATE	CYTB	0.7696
HLI-0621	15110	G	A	0	737	missense_variant	MODERATE	CYTB	0.009

HLI-0621	15217	G	A	0	628	synonymous_variant	LOW	CYTB	0.0104
HLI-0621	15301	G	A	0	670	synonymous_variant	LOW	CYTB	0.2912
HLI-0621	15326	A	G	0	652	missense_variant	MODERATE	CYTB	0.9868
HLI-0621	15849	C	T	0	565	missense_variant	MODERATE	CYTB	0.0027
HLI-0621	16223	C	T	4	680	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0621	16390	G	A	1	499	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0622	204	T	C	1	437	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0622	239	T	C	0	416	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0622	263	A	G	0	356	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0622	750	A	G	0	757	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0622	1438	A	G	0	748	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0622	3915	G	A	1	734	synonymous_variant	LOW	ND1	0.0106
HLI-0622	4727	A	G	1	652	synonymous_variant	LOW	ND2	0.0063
HLI-0622	4769	A	G	1	676	synonymous_variant	LOW	ND2	0.9767
HLI-0622	9380	G	A	0	795	synonymous_variant	LOW	COX3	0.0094
HLI-0622	10589	G	A	2	717	synonymous_variant	LOW	ND4L	0.0355
HLI-0622	15326	A	G	1	646	missense_variant	MODERATE	CYTB	0.9868
HLI-0622	16219	A	G	1	631	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0622	16319	G	A	2	567	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0622	16362	T	C	0	615	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0622	16482	A	G	0	446	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0623	73	A	G	1	368	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0623	195	T	C	1	580	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0623	263	A	G	0	399	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0623	750	A	G	0	826	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0623	1438	A	G	0	703	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0623	1719	G	A	14	535	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0623	2706	A	G	0	738	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0623	4769	A	G	2	670	synonymous_variant	LOW	ND2	0.9767
HLI-0623	6221	T	C	23	722	synonymous_variant	LOW	COX1	0.0306
HLI-0623	6371	C	T	19	711	synonymous_variant	LOW	COX1	0.0097
HLI-0623	7028	C	T	1	791	synonymous_variant	LOW	COX1	0.8089
HLI-0623	7109	C	T	22	778	synonymous_variant	LOW	COX1	9.00E-04
HLI-0623	11719	G	A	0	667	synonymous_variant	LOW	ND4	0.7756
HLI-0623	12705	C	T	23	617	synonymous_variant	LOW	ND5	0.4212
HLI-0623	13134	A	G	13	712	synonymous_variant	LOW	ND5	2.00E-04
HLI-0623	13966	A	G	9	519	missense_variant	MODERATE	ND5	0.0126
HLI-0623	14470	T	C	11	547	synonymous_variant	LOW	ND6	0.0166
HLI-0623	14766	C	T	2	708	missense_variant	MODERATE	CYTB	0.7696

HLI-0623	15326	A	G	1	556	missense_variant	MODERATE	CYTB	0.9868
HLI-0623	16223	C	T	15	383	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0623	16278	C	T	11	529	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0623	16519	T	C	0	302	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0624	189	A	G	3	479	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0624	263	A	G	0	325	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0624	750	A	G	1	754	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0624	1438	A	G	0	716	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0624	4769	A	G	1	696	synonymous_variant	LOW	ND2	0.9767
HLI-0624	4793	A	G	1	758	synonymous_variant	LOW	ND2	0.0073
HLI-0624	5348	C	T	0	638	synonymous_variant	LOW	ND2	0.0016
HLI-0624	13323	C	T	0	668	synonymous_variant	LOW	ND5	3.00E-04
HLI-0624	15326	A	G	2	557	missense_variant	MODERATE	CYTB	0.9868
HLI-0624	15862	T	C	2	666	synonymous_variant	LOW	CYTB	8.00E-04
HLI-0624	16519	T	C	0	389	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0625	73	A	G	0	283	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0625	195	T	C	0	471	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0625	263	A	G	1	380	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0625	709	G	A	2	521	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0625	750	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0625	1438	A	G	1	502	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0625	1888	G	A	0	261	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0625	2706	A	G	0	538	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0625	4216	T	C	1	392	missense_variant	MODERATE	ND1	0.0991
HLI-0625	4769	A	G	0	512	synonymous_variant	LOW	ND2	0.9767
HLI-0625	4917	A	G	0	514	missense_variant	MODERATE	ND2	0.0477
HLI-0625	5277	T	C	0	457	missense_variant	MODERATE	ND2	0.0022
HLI-0625	5426	T	C	0	459	synonymous_variant	LOW	ND2	0.0091
HLI-0625	6489	C	A	0	589	missense_variant	MODERATE	COX1	0.0016
HLI-0625	7028	C	T	3	616	synonymous_variant	LOW	COX1	0.8089
HLI-0625	8697	G	A	0	497	synonymous_variant	LOW	ATP6	0.0466
HLI-0625	10463	T	C	2	723	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0625	11251	A	G	0	541	synonymous_variant	LOW	ND4	0.0932
HLI-0625	11719	G	A	0	572	synonymous_variant	LOW	ND4	0.7756
HLI-0625	11812	A	G	0	493	synonymous_variant	LOW	ND4	0.0332
HLI-0625	13368	G	A	1	483	synonymous_variant	LOW	ND5	0.0495
HLI-0625	14233	A	G	1	431	synonymous_variant	LOW	ND6	0.0369
HLI-0625	14766	C	T	3	728	missense_variant	MODERATE	CYTB	0.7696
HLI-0625	14905	G	A	0	855	synonymous_variant	LOW	CYTB	0.0526

HLI-0625	15028	C	A	4	774	synonymous_variant	LOW	CYTB	0.0016
HLI-0625	15043	G	A	1	832	synonymous_variant	LOW	CYTB	0.2362
HLI-0625	15326	A	G	0	360	missense_variant	MODERATE	CYTB	0.9868
HLI-0625	15452	C	A	2	269	missense_variant	MODERATE	CYTB	0.0933
HLI-0625	15607	A	G	0	253	synonymous_variant	LOW	CYTB	0.0508
HLI-0625	15928	G	A	0	294	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0625	16126	T	C	0	260	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0625	16294	C	T	0	352	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0625	16298	T	C	0	357	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0625	16519	T	C	2	174	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0626	73	A	G	1	285	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0626	263	A	G	0	328	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0626	709	G	A	1	575	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0626	750	A	G	5	625	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0626	1438	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0626	1888	G	A	0	416	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0626	2141	T	C	1	317	upstream_gene_variant	MODIFIER	RNR2	0.0013
HLI-0626	2706	A	G	0	583	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0626	4216	T	C	1	481	missense_variant	MODERATE	ND1	0.0991
HLI-0626	4769	A	G	1	596	synonymous_variant	LOW	ND2	0.9767
HLI-0626	4917	A	G	1	612	missense_variant	MODERATE	ND2	0.0477
HLI-0626	7028	C	T	4	670	synonymous_variant	LOW	COX1	0.8089
HLI-0626	8697	G	A	2	666	synonymous_variant	LOW	ATP6	0.0466
HLI-0626	10463	T	C	0	624	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0626	11251	A	G	0	573	synonymous_variant	LOW	ND4	0.0932
HLI-0626	11719	G	A	0	636	synonymous_variant	LOW	ND4	0.7756
HLI-0626	11812	A	G	1	560	synonymous_variant	LOW	ND4	0.0332
HLI-0626	13368	G	A	0	583	synonymous_variant	LOW	ND5	0.0495
HLI-0626	13965	T	C	0	500	synonymous_variant	LOW	ND5	0.005
HLI-0626	13966	A	G	0	510	missense_variant	MODERATE	ND5	0.0126
HLI-0626	14233	A	G	0	572	synonymous_variant	LOW	ND6	0.0369
HLI-0626	14687	A	G	0	746	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0626	14766	C	T	0	766	missense_variant	MODERATE	CYTB	0.7696
HLI-0626	14905	G	A	1	805	synonymous_variant	LOW	CYTB	0.0526
HLI-0626	15326	A	G	0	384	missense_variant	MODERATE	CYTB	0.9868
HLI-0626	15452	C	A	0	354	missense_variant	MODERATE	CYTB	0.0933
HLI-0626	15607	A	G	0	372	synonymous_variant	LOW	CYTB	0.0508
HLI-0626	15928	G	A	0	572	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0626	16126	T	C	0	673	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0626	16294	C	T	1	507	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0626	16324	T	C	0	518	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0626	16519	T	C	0	260	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0627	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0627	150	C	T	0	516	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0627	152	T	C	0	517	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0627	195	T	C	3	496	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0627	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0627	750	A	G	1	641	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0627	1438	A	G	0	618	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0627	2352	T	C	0	452	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0627	2706	A	G	0	602	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0627	4769	A	G	1	584	synonymous_variant	LOW	ND2	0.9767
HLI-0627	7028	C	T	0	677	synonymous_variant	LOW	COX1	0.8089
HLI-0627	8701	A	G	2	524	missense_variant	MODERATE	ATP6	0.3391
HLI-0627	9540	T	C	0	565	synonymous_variant	LOW	COX3	0.339
HLI-0627	10088	C	T	0	655	synonymous_variant	LOW	ND3	3.00E-04
HLI-0627	10398	A	G	0	609	missense_variant	MODERATE	ND3	0.445
HLI-0627	10819	A	G	1	582	synonymous_variant	LOW	ND4	0.0228
HLI-0627	10861	T	C	0	613	synonymous_variant	LOW	ND4	8.00E-04
HLI-0627	10873	T	C	0	616	synonymous_variant	LOW	ND4	0.3389
HLI-0627	11719	G	A	0	584	synonymous_variant	LOW	ND4	0.7756
HLI-0627	12705	C	T	0	484	synonymous_variant	LOW	ND5	0.4212
HLI-0627	14212	T	C	0	474	synonymous_variant	LOW	ND6	0.0204
HLI-0627	14766	C	T	6	643	missense_variant	MODERATE	CYTB	0.7696
HLI-0627	14905	G	A	0	770	synonymous_variant	LOW	CYTB	0.0526
HLI-0627	15301	G	A	1	495	synonymous_variant	LOW	CYTB	0.2912
HLI-0627	15326	A	G	0	544	missense_variant	MODERATE	CYTB	0.9868
HLI-0627	16172	T	C	1	207	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0627	16223	C	T	0	224	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0627	16256	C	T	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0627	16320	C	T	0	405	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0627	16519	T	C	0	225	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0628	73	A	G	0	327	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0628	150	C	T	4	624	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0628	263	A	G	0	326	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0628	750	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0628	1438	A	G	0	685	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0628	1811	A	G	4	554	upstream_gene_variant	MODIFIER	RNR2	0.0763

HLI-0628	2294	A	G	5	535	upstream_gene_variant	MODIFIER	RNR2	0.0027
HLI-0628	2706	A	G	2	655	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0628	3010	G	A	2	699	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0628	4703	T	C	4	677	synonymous_variant	LOW	ND2	0.0058
HLI-0628	4769	A	G	2	693	synonymous_variant	LOW	ND2	0.9767
HLI-0628	6518	C	T	0	686	synonymous_variant	LOW	COX1	0.0025
HLI-0628	7028	C	T	5	714	synonymous_variant	LOW	COX1	0.8089
HLI-0628	7289	A	G	1	657	synonymous_variant	LOW	COX1	2.00E-04
HLI-0628	9266	G	A	1	680	synonymous_variant	LOW	COX3	0.0049
HLI-0628	9887	T	C	0	846	synonymous_variant	LOW	COX3	0.0011
HLI-0628	10506	A	G	1	728	missense_variant	MODERATE	ND4L	0.0025
HLI-0628	11467	A	G	0	701	synonymous_variant	LOW	ND4	0.1231
HLI-0628	11719	G	A	1	648	synonymous_variant	LOW	ND4	0.7756
HLI-0628	12308	A	G	1	472	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0628	12372	G	A	1	447	synonymous_variant	LOW	ND5	0.1329
HLI-0628	13934	C	T	4	489	missense_variant	MODERATE	ND5	0.0122
HLI-0628	14139	A	G	3	587	synonymous_variant	LOW	ND5	0.0056
HLI-0628	14766	C	T	0	704	missense_variant	MODERATE	CYTB	0.7696
HLI-0628	14971	T	C	7	758	synonymous_variant	LOW	CYTB	0.003
HLI-0628	15326	A	G	0	542	missense_variant	MODERATE	CYTB	0.9868
HLI-0628	15454	T	C	5	487	synonymous_variant	LOW	CYTB	0.0072
HLI-0628	15643	C	T	1	485	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0628	16209	T	C	0	589	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0628	16343	A	G	1	564	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0628	16390	G	A	0	561	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0628	16519	T	C	2	291	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0629	73	A	G	0	344	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0629	195	T	C	0	490	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0629	263	A	G	0	341	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0629	750	A	G	1	670	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0629	1438	A	G	0	730	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0629	1719	G	A	1	608	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0629	2706	A	G	0	724	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0629	3866	T	C	1	656	missense_variant	MODERATE	ND1	0.0029
HLI-0629	4769	A	G	1	708	synonymous_variant	LOW	ND2	0.9767
HLI-0629	6221	T	C	0	675	synonymous_variant	LOW	COX1	0.0306
HLI-0629	6371	C	T	2	675	synonymous_variant	LOW	COX1	0.0097
HLI-0629	7028	C	T	1	773	synonymous_variant	LOW	COX1	0.8089
HLI-0629	11719	G	A	0	683	synonymous_variant	LOW	ND4	0.7756

HLI-0629	12705	C	T	1	578	synonymous_variant	LOW	ND5	0.4212
HLI-0629	13966	A	G	0	604	missense_variant	MODERATE	ND5	0.0126
HLI-0629	14470	T	C	1	606	synonymous_variant	LOW	ND6	0.0166
HLI-0629	14766	C	T	2	676	missense_variant	MODERATE	CYTB	0.7696
HLI-0629	15326	A	G	0	533	missense_variant	MODERATE	CYTB	0.9868
HLI-0629	16223	C	T	1	305	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0629	16248	C	T	1	385	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0629	16278	C	T	0	454	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0629	16519	T	C	0	272	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0630	263	A	G	0	316	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0630	750	A	G	0	760	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0630	1438	A	G	1	838	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0630	2706	A	G	2	889	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0630	4769	A	G	1	686	synonymous_variant	LOW	ND2	0.9767
HLI-0630	7028	C	T	8	827	synonymous_variant	LOW	COX1	0.8089
HLI-0630	12133	C	T	8	751	synonymous_variant	LOW	ND4	8.00E-04
HLI-0630	13105	A	G	6	828	missense_variant	MODERATE	ND5	0.076
HLI-0630	15326	A	G	0	711	missense_variant	MODERATE	CYTB	0.9868
HLI-0631	72	T	C	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0631	263	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0631	750	A	G	1	762	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0631	1438	A	G	0	785	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0631	2706	A	G	0	755	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0631	4580	G	A	1	755	synonymous_variant	LOW	ND2	0.0169
HLI-0631	4769	A	G	0	740	synonymous_variant	LOW	ND2	0.9767
HLI-0631	7028	C	T	4	819	synonymous_variant	LOW	COX1	0.8089
HLI-0631	9368	A	G	2	790	synonymous_variant	LOW	COX3	8.00E-04
HLI-0631	15326	A	G	0	684	missense_variant	MODERATE	CYTB	0.9868
HLI-0631	15904	C	T	2	714	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0631	16261	C	T	2	763	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0631	16298	T	C	0	713	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0631	16311	T	C	0	691	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0631	16519	T	C	0	422	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0632	263	A	G	0	363	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0632	750	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0632	1438	A	G	1	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0632	4769	A	G	0	637	synonymous_variant	LOW	ND2	0.9767
HLI-0632	4793	A	G	0	708	synonymous_variant	LOW	ND2	0.0073
HLI-0632	15326	A	G	0	421	missense_variant	MODERATE	CYTB	0.9868

HLI-0632	16519	T	C	0	291	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0633	72	T	C	1	337	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0633	263	A	G	1	334	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0633	750	A	G	0	676	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0633	1438	A	G	0	681	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0633	2706	A	G	1	667	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0633	4580	G	A	0	739	synonymous_variant	LOW	ND2	0.0169
HLI-0633	4769	A	G	0	645	synonymous_variant	LOW	ND2	0.9767
HLI-0633	7028	C	T	1	771	synonymous_variant	LOW	COX1	0.8089
HLI-0633	15326	A	G	0	510	missense_variant	MODERATE	CYTB	0.9868
HLI-0633	15904	C	T	0	570	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0633	16298	T	C	2	541	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0634	263	A	G	0	303	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0634	750	A	G	0	722	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0634	1438	A	G	0	750	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0634	2628	T	C	0	653	upstream_gene_variant	MODIFIER	RNR2	2.00E-04
HLI-0634	3010	G	A	1	681	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0634	4769	A	G	1	704	synonymous_variant	LOW	ND2	0.9767
HLI-0634	8622	C	T	5	606	synonymous_variant	LOW	ATP6	2.00E-04
HLI-0634	11084	A	G	0	743	missense_variant	MODERATE	ND4	0.004
HLI-0634	13827	A	G	2	535	synonymous_variant	LOW	ND5	0.0047
HLI-0634	15326	A	G	0	588	missense_variant	MODERATE	CYTB	0.9868
HLI-0634	16355	C	T	2	534	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0634	16519	T	C	1	373	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0635	73	A	G	1	362	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0635	152	T	C	65	589	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0635	195	T	C	3	607	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0635	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0635	709	G	A	70	633	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0635	750	A	G	1	758	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0635	1438	A	G	0	730	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0635	1888	G	A	42	506	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0635	2706	A	G	1	642	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0635	4216	T	C	39	554	missense_variant	MODERATE	ND1	0.0991
HLI-0635	4769	A	G	0	705	synonymous_variant	LOW	ND2	0.9767
HLI-0635	4917	A	G	56	663	missense_variant	MODERATE	ND2	0.0477
HLI-0635	7028	C	T	1	739	synonymous_variant	LOW	COX1	0.8089
HLI-0635	8697	G	A	49	602	synonymous_variant	LOW	ATP6	0.0466
HLI-0635	9120	A	G	72	651	synonymous_variant	LOW	ATP6	8.00E-04

HLI-0635	9899	T	C	70	679	synonymous_variant	LOW	COX3	0.0108
HLI-0635	10463	T	C	57	683	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0635	11251	A	G	49	657	synonymous_variant	LOW	ND4	0.0932
HLI-0635	11719	G	A	3	678	synonymous_variant	LOW	ND4	0.7756
HLI-0635	12633	C	A	51	592	synonymous_variant	LOW	ND5	0.0123
HLI-0635	13368	G	A	62	639	synonymous_variant	LOW	ND5	0.0495
HLI-0635	14766	C	T	2	714	missense_variant	MODERATE	CYTB	0.7696
HLI-0635	14905	G	A	81	800	synonymous_variant	LOW	CYTB	0.0526
HLI-0635	15236	A	G	50	521	missense_variant	MODERATE	CYTB	0.016
HLI-0635	15326	A	G	0	551	missense_variant	MODERATE	CYTB	0.9868
HLI-0635	15452	C	A	38	473	missense_variant	MODERATE	CYTB	0.0933
HLI-0635	15607	A	G	27	474	synonymous_variant	LOW	CYTB	0.0508
HLI-0635	15928	G	A	35	554	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0635	15965	A	G	40	607	upstream_gene_variant	MODIFIER	TRNP	2.00E-04
HLI-0635	16126	T	C	33	592	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0635	16163	A	G	33	645	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0635	16294	C	T	46	555	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0635	16519	T	C	1	402	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0636	73	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0636	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0636	709	G	A	2	509	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0636	750	A	G	1	559	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0636	1438	A	G	0	518	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0636	1888	G	A	1	413	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0636	2706	A	G	0	525	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0636	2850	T	C	0	542	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0636	4216	T	C	0	448	missense_variant	MODERATE	ND1	0.0991
HLI-0636	4688	T	C	1	640	synonymous_variant	LOW	ND2	0.0078
HLI-0636	4769	A	G	3	610	synonymous_variant	LOW	ND2	0.9767
HLI-0636	4917	A	G	0	571	missense_variant	MODERATE	ND2	0.0477
HLI-0636	7022	T	C	3	588	synonymous_variant	LOW	COX1	0.0024
HLI-0636	7028	C	T	3	608	synonymous_variant	LOW	COX1	0.8089
HLI-0636	8697	G	A	0	567	synonymous_variant	LOW	ATP6	0.0466
HLI-0636	10463	T	C	0	693	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0636	11251	A	G	2	580	synonymous_variant	LOW	ND4	0.0932
HLI-0636	11719	G	A	0	579	synonymous_variant	LOW	ND4	0.7756
HLI-0636	11812	A	G	1	527	synonymous_variant	LOW	ND4	0.0332
HLI-0636	13368	G	A	0	571	synonymous_variant	LOW	ND5	0.0495
HLI-0636	13965	T	C	2	430	synonymous_variant	LOW	ND5	0.005

HLI-0636	14233	A	G	1	492	synonymous_variant	LOW	ND6	0.0369
HLI-0636	14687	A	G	2	728	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0636	14766	C	T	3	753	missense_variant	MODERATE	CYTB	0.7696
HLI-0636	14905	G	A	1	797	synonymous_variant	LOW	CYTB	0.0526
HLI-0636	15326	A	G	1	340	missense_variant	MODERATE	CYTB	0.9868
HLI-0636	15452	C	A	2	340	missense_variant	MODERATE	CYTB	0.0933
HLI-0636	15607	A	G	0	315	synonymous_variant	LOW	CYTB	0.0508
HLI-0636	15928	G	A	0	456	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0636	16126	T	C	0	626	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0636	16294	C	T	0	485	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0636	16296	C	T	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0636	16519	T	C	0	233	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0637	73	A	G	0	326	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0637	150	C	T	2	622	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0637	263	A	G	0	290	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0637	750	A	G	1	657	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0637	1438	A	G	0	662	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0637	1721	C	T	1	570	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0637	2706	A	G	0	626	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0637	2757	A	G	0	690	upstream_gene_variant	MODIFIER	RNR2	0.002
HLI-0637	3197	T	C	1	639	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0637	3212	C	T	1	685	upstream_gene_variant	MODIFIER	RNR2	0.0012
HLI-0637	4732	A	G	2	638	missense_variant	MODERATE	ND2	0.0059
HLI-0637	4769	A	G	2	657	synonymous_variant	LOW	ND2	0.9767
HLI-0637	4843	C	T	1	615	missense_variant	MODERATE	ND2	5.00E-04
HLI-0637	7028	C	T	3	697	synonymous_variant	LOW	COX1	0.8089
HLI-0637	7768	A	G	0	675	synonymous_variant	LOW	COX2	0.0186
HLI-0637	9477	G	A	0	753	missense_variant	MODERATE	COX3	0.0387
HLI-0637	11467	A	G	2	684	synonymous_variant	LOW	ND4	0.1231
HLI-0637	11719	G	A	0	644	synonymous_variant	LOW	ND4	0.7756
HLI-0637	12308	A	G	4	452	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0637	12372	G	A	0	494	synonymous_variant	LOW	ND5	0.1329
HLI-0637	13617	T	C	1	598	synonymous_variant	LOW	ND5	0.038
HLI-0637	13637	A	G	1	625	missense_variant	MODERATE	ND5	0.0074
HLI-0637	14182	T	C	1	593	synonymous_variant	LOW	ND6	0.0254
HLI-0637	14766	C	T	1	650	missense_variant	MODERATE	CYTB	0.7696
HLI-0637	14956	T	C	2	761	synonymous_variant	LOW	CYTB	0.001
HLI-0637	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0637	16398	G	A	2	528	upstream_gene_variant	MODIFIER	DLoop	0.0013

HLI-0638	263	A	G	0	257	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0638	456	C	T	6	548	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0638	750	A	G	1	653	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0638	1438	A	G	1	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0638	4769	A	G	1	598	synonymous_variant	LOW	ND2	0.9767
HLI-0638	8473	T	C	1	498	synonymous_variant	LOW	ATP8	0.0105
HLI-0638	8593	A	G	1	634	missense_variant	MODERATE	ATP6	1.00E-04
HLI-0638	11404	A	G	0	633	synonymous_variant	LOW	ND4	0.0039
HLI-0638	15326	A	G	0	602	missense_variant	MODERATE	CYTB	0.9868
HLI-0638	16124	T	C	0	595	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0638	16304	T	C	0	502	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0638	16311	T	C	0	523	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0639	51	T	C	0	190	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0639	57	T	C	0	207	upstream_gene_variant	MODIFIER	DLoop	0.0028
HLI-0639	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0639	750	A	G	0	587	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0639	1438	A	G	1	562	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0639	4769	A	G	1	564	synonymous_variant	LOW	ND2	0.9767
HLI-0639	6253	T	C	5	656	missense_variant	MODERATE	COX1	0.0106
HLI-0639	11410	T	C	0	568	synonymous_variant	LOW	ND4	0.002
HLI-0639	13218	A	G	3	632	synonymous_variant	LOW	ND5	1.00E-04
HLI-0639	14953	C	T	2	642	synonymous_variant	LOW	CYTB	0.0019
HLI-0639	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0639	15927	G	A	0	512	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0640	73	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0640	152	T	C	1	509	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0640	195	T	C	0	522	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0640	198	C	T	0	517	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0640	263	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0640	750	A	G	1	525	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0640	1438	A	G	0	559	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0640	1598	G	A	2	552	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0640	1703	C	T	1	435	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0640	1719	G	A	1	481	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0640	2639	C	T	1	530	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0640	2706	A	G	1	582	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0640	3921	C	A	0	501	synonymous_variant	LOW	ND1	0.0026
HLI-0640	4769	A	G	2	558	synonymous_variant	LOW	ND2	0.9767
HLI-0640	4960	C	T	1	504	missense_variant	MODERATE	ND2	0.0028

HLI-0640	5471	G	A	1	496	synonymous_variant	LOW	ND2	0.0128
HLI-0640	5539	A	C	1	618	upstream_gene_variant	MODIFIER	TRNW	0
HLI-0640	5585	G	A	0	659	upstream_gene_variant	MODIFIER	Unannotated	0.0097
HLI-0640	7028	C	T	0	625	synonymous_variant	LOW	COX1	0.8089
HLI-0640	8251	G	A	3	458	synonymous_variant	LOW	COX2	0.058
HLI-0640	8472	C	T	2	351	missense_variant	MODERATE	ATP8	0.0027
HLI-0640	8836	A	G	1	572	missense_variant	MODERATE	ATP6	0.0029
HLI-0640	9335	C	T	1	534	synonymous_variant	LOW	COX3	0.0021
HLI-0640	10238	T	C	1	835	synonymous_variant	LOW	ND3	0.0623
HLI-0640	11362	A	G	1	533	synonymous_variant	LOW	ND4	0.0024
HLI-0640	11719	G	A	0	573	synonymous_variant	LOW	ND4	0.7756
HLI-0640	12297	T	C	0	408	upstream_gene_variant	MODIFIER	TRNL2	8.00E-04
HLI-0640	12501	G	A	9	481	synonymous_variant	LOW	ND5	0.0258
HLI-0640	12705	C	T	2	488	synonymous_variant	LOW	ND5	0.4212
HLI-0640	12822	A	G	7	536	synonymous_variant	LOW	ND5	0.0026
HLI-0640	14766	C	T	3	663	missense_variant	MODERATE	CYTB	0.7696
HLI-0640	15326	A	G	1	354	missense_variant	MODERATE	CYTB	0.9868
HLI-0640	16126	T	C	0	485	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0640	16145	G	A	0	539	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0640	16176	C	A	2	548	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0640	16390	G	A	0	382	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0640	16519	T	C	0	205	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0640	16527	C	T	0	210	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0641	73	A	G	0	241	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0641	150	C	T	0	411	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0641	152	T	C	0	413	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0641	182	C	T	0	392	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0641	195	T	C	0	383	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0641	198	C	T	0	375	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0641	204	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0641	263	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0641	292	T	A	0	241	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0641	418	C	T	1	483	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0641	750	A	G	1	618	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0641	769	G	A	0	659	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0641	1018	G	A	0	745	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0641	1438	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0641	1442	G	A	0	674	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0641	1706	C	T	2	525	upstream_gene_variant	MODIFIER	RNR2	0.0022

HLI-0641	2332	C	T	0	358	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0641	2358	A	G	0	371	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0641	2416	T	C	1	387	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0641	2706	A	G	1	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0641	3594	C	T	1	529	synonymous_variant	LOW	ND1	0.0789
HLI-0641	4104	A	G	3	482	synonymous_variant	LOW	ND1	0.0785
HLI-0641	4158	A	G	2	548	synonymous_variant	LOW	ND1	0.0023
HLI-0641	4370	T	C	1	581	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0641	4767	A	G	0	603	missense_variant	MODERATE	ND2	0.0029
HLI-0641	4769	A	G	0	613	synonymous_variant	LOW	ND2	0.9767
HLI-0641	5027	C	T	1	474	synonymous_variant	LOW	ND2	0.003
HLI-0641	5331	C	A	3	561	missense_variant	MODERATE	ND2	0.0022
HLI-0641	5814	T	C	0	778	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0641	6026	G	A	0	615	synonymous_variant	LOW	COX1	0.0163
HLI-0641	6713	C	T	2	796	synonymous_variant	LOW	COX1	0.0028
HLI-0641	7028	C	T	1	693	synonymous_variant	LOW	COX1	0.8089
HLI-0641	7256	C	T	7	668	synonymous_variant	LOW	COX1	0.0784
HLI-0641	7521	G	A	0	449	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0641	7569	A	G	2	548	upstream_gene_variant	MODIFIER	TRND	7.00E-04
HLI-0641	7624	T	A	1	584	synonymous_variant	LOW	COX2	0.0047
HLI-0641	8080	C	T	1	605	synonymous_variant	LOW	COX2	0.0022
HLI-0641	8093	T	C	0	669	synonymous_variant	LOW	COX2	0.0012
HLI-0641	8206	G	A	1	568	synonymous_variant	LOW	COX2	0.0287
HLI-0641	8387	G	A	0	466	missense_variant	MODERATE	ATP8	0.0028
HLI-0641	8701	A	G	0	585	missense_variant	MODERATE	ATP6	0.3391
HLI-0641	9221	A	G	0	649	synonymous_variant	LOW	COX3	0.0277
HLI-0641	9503	A	G	0	560	synonymous_variant	LOW	COX3	4.00E-04
HLI-0641	9540	T	C	0	560	synonymous_variant	LOW	COX3	0.339
HLI-0641	10115	T	C	0	810	synonymous_variant	LOW	ND3	0.0278
HLI-0641	10398	A	G	0	687	missense_variant	MODERATE	ND3	0.445
HLI-0641	10828	T	C	0	571	synonymous_variant	LOW	ND4	0.0015
HLI-0641	10873	T	C	0	616	synonymous_variant	LOW	ND4	0.3389
HLI-0641	11719	G	A	1	596	synonymous_variant	LOW	ND4	0.7756
HLI-0641	11944	T	C	0	609	synonymous_variant	LOW	ND4	0.0331
HLI-0641	12236	G	A	0	460	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0641	12705	C	T	0	517	synonymous_variant	LOW	ND5	0.4212
HLI-0641	12948	A	G	5	552	synonymous_variant	LOW	ND5	0.0022
HLI-0641	13590	G	A	2	570	synonymous_variant	LOW	ND5	0.0586
HLI-0641	13650	C	T	0	554	synonymous_variant	LOW	ND5	0.079

HLI-0641	13924	C	T	1	499	missense_variant	MODERATE	ND5	0.0013
HLI-0641	14040	G	A	1	502	synonymous_variant	LOW	ND5	0.0047
HLI-0641	14059	A	G	1	526	missense_variant	MODERATE	ND5	0.0022
HLI-0641	14152	A	G	2	469	synonymous_variant	LOW	ND6	0.0086
HLI-0641	14766	C	T	3	661	missense_variant	MODERATE	CYTB	0.7696
HLI-0641	15110	G	A	0	694	missense_variant	MODERATE	CYTB	0.009
HLI-0641	15217	G	A	0	527	synonymous_variant	LOW	CYTB	0.0104
HLI-0641	15301	G	A	3	461	synonymous_variant	LOW	CYTB	0.2912
HLI-0641	15326	A	G	0	458	missense_variant	MODERATE	CYTB	0.9868
HLI-0641	16114	C	A	3	491	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0641	16213	G	A	0	485	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0641	16223	C	T	1	485	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0641	16278	C	T	2	485	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0641	16355	C	T	1	431	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0641	16362	T	C	1	454	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0641	16390	G	A	2	457	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0642	73	A	G	0	279	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0642	150	C	T	1	548	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0642	182	C	T	0	540	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0642	185	G	T	0	543	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0642	195	T	C	0	532	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0642	247	G	A	0	282	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0642	263	A	G	0	298	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0642	357	A	G	1	387	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0642	709	G	A	3	618	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0642	710	T	C	3	620	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0642	750	A	G	0	670	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0642	769	G	A	0	676	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0642	825	T	A	0	756	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0642	1018	G	A	2	735	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0642	1738	T	C	0	655	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0642	2352	T	C	1	499	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0642	2706	A	G	1	625	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0642	2758	G	A	0	679	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0642	2768	A	G	0	679	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0642	2885	T	C	0	670	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0642	3308	T	C	1	620	start_lost	HIGH	ND1	0.0073
HLI-0642	3594	C	T	2	572	synonymous_variant	LOW	ND1	0.0789
HLI-0642	3666	G	A	2	572	synonymous_variant	LOW	ND1	0.0233

HLI-0642	3693	G	A	3	574	synonymous_variant	LOW	ND1	0.0091
HLI-0642	4104	A	G	3	569	synonymous_variant	LOW	ND1	0.0785
HLI-0642	4769	A	G	0	666	synonymous_variant	LOW	ND2	0.9767
HLI-0642	5036	A	G	1	595	synonymous_variant	LOW	ND2	0.006
HLI-0642	5046	G	A	1	640	missense_variant	MODERATE	ND2	0.018
HLI-0642	5393	T	C	2	584	synonymous_variant	LOW	ND2	0.0059
HLI-0642	5655	T	C	0	678	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0642	6548	C	T	1	651	synonymous_variant	LOW	COX1	0.0061
HLI-0642	6827	T	C	0	633	synonymous_variant	LOW	COX1	0.0072
HLI-0642	6989	A	G	1	697	synonymous_variant	LOW	COX1	0.0061
HLI-0642	7028	C	T	1	685	synonymous_variant	LOW	COX1	0.8089
HLI-0642	7055	A	G	0	619	synonymous_variant	LOW	COX1	0.0188
HLI-0642	7146	A	G	0	344	missense_variant	MODERATE	COX1	0.0497
HLI-0642	7256	C	T	6	552	synonymous_variant	LOW	COX1	0.0784
HLI-0642	7389	T	C	1	579	missense_variant	MODERATE	COX1	0.0201
HLI-0642	7521	G	A	1	431	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0642	7867	C	T	2	749	synonymous_variant	LOW	COX2	0.0076
HLI-0642	8248	A	G	0	596	synonymous_variant	LOW	COX2	0.0061
HLI-0642	8468	C	T	2	472	synonymous_variant	LOW	ATP8	0.0501
HLI-0642	8655	C	T	3	534	synonymous_variant	LOW	ATP6	0.0511
HLI-0642	8701	A	G	0	635	missense_variant	MODERATE	ATP6	0.3391
HLI-0642	9540	T	C	0	609	synonymous_variant	LOW	COX3	0.339
HLI-0642	10398	A	G	1	616	missense_variant	MODERATE	ND3	0.445
HLI-0642	10688	G	A	3	657	synonymous_variant	LOW	ND4L	0.0515
HLI-0642	10810	T	C	0	557	synonymous_variant	LOW	ND4	0.0522
HLI-0642	10873	T	C	0	551	synonymous_variant	LOW	ND4	0.3389
HLI-0642	11719	G	A	1	587	synonymous_variant	LOW	ND4	0.7756
HLI-0642	12519	T	C	1	639	synonymous_variant	LOW	ND5	0.007
HLI-0642	12705	C	T	0	702	synonymous_variant	LOW	ND5	0.4212
HLI-0642	13105	A	G	1	606	missense_variant	MODERATE	ND5	0.076
HLI-0642	13506	C	T	1	582	synonymous_variant	LOW	ND5	0.0506
HLI-0642	13650	C	T	1	570	synonymous_variant	LOW	ND5	0.079
HLI-0642	13789	T	C	0	417	missense_variant	MODERATE	ND5	0.0185
HLI-0642	13880	C	A	5	529	missense_variant	MODERATE	ND5	0.0055
HLI-0642	14178	T	C	0	607	missense_variant	MODERATE	ND6	0.0225
HLI-0642	14203	A	G	3	667	synonymous_variant	LOW	ND6	0.0061
HLI-0642	14560	G	A	0	720	synonymous_variant	LOW	ND6	0.0235
HLI-0642	14766	C	T	0	725	missense_variant	MODERATE	CYTB	0.7696
HLI-0642	14769	A	G	0	742	missense_variant	MODERATE	CYTB	0.0121

HLI-0642	15115	T	C	2	734	synonymous_variant	LOW	CYTB	0.0093
HLI-0642	15326	A	G	0	525	missense_variant	MODERATE	CYTB	0.9868
HLI-0642	16126	T	C	1	658	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0642	16223	C	T	2	599	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0642	16264	C	T	1	543	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0642	16270	C	T	1	517	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0642	16278	C	T	1	511	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0642	16311	T	C	1	499	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0642	16519	T	C	1	222	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0643	73	A	G	0	330	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0643	151	C	T	1	604	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0643	263	A	G	0	369	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0643	709	G	A	1	770	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0643	750	A	G	0	819	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0643	930	G	A	0	785	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0643	1438	A	G	0	712	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0643	1888	G	A	1	519	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0643	2706	A	G	0	713	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0643	4216	T	C	2	695	missense_variant	MODERATE	ND1	0.0991
HLI-0643	4561	T	C	2	718	missense_variant	MODERATE	ND2	0.0065
HLI-0643	4769	A	G	2	658	synonymous_variant	LOW	ND2	0.9767
HLI-0643	4917	A	G	0	663	missense_variant	MODERATE	ND2	0.0477
HLI-0643	5147	G	A	0	558	synonymous_variant	LOW	ND2	0.0437
HLI-0643	7028	C	T	3	721	synonymous_variant	LOW	COX1	0.8089
HLI-0643	8697	G	A	1	620	synonymous_variant	LOW	ATP6	0.0466
HLI-0643	10463	T	C	1	696	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0643	10750	A	G	0	663	missense_variant	MODERATE	ND4L	0.0045
HLI-0643	11233	T	C	0	665	synonymous_variant	LOW	ND4	6.00E-04
HLI-0643	11251	A	G	1	746	synonymous_variant	LOW	ND4	0.0932
HLI-0643	11719	G	A	0	716	synonymous_variant	LOW	ND4	0.7756
HLI-0643	11812	A	G	1	694	synonymous_variant	LOW	ND4	0.0332
HLI-0643	13368	G	A	1	766	synonymous_variant	LOW	ND5	0.0495
HLI-0643	14233	A	G	3	630	synonymous_variant	LOW	ND6	0.0369
HLI-0643	14766	C	T	1	768	missense_variant	MODERATE	CYTB	0.7696
HLI-0643	14905	G	A	0	866	synonymous_variant	LOW	CYTB	0.0526
HLI-0643	15326	A	G	0	565	missense_variant	MODERATE	CYTB	0.9868
HLI-0643	15452	C	A	4	532	missense_variant	MODERATE	CYTB	0.0933
HLI-0643	15607	A	G	1	545	synonymous_variant	LOW	CYTB	0.0508
HLI-0643	15928	G	A	1	548	upstream_gene_variant	MODIFIER	TRNT	0.049

HLI-0643	16126	T	C	0	635	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0643	16294	C	T	0	600	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0643	16296	C	T	0	602	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0643	16304	T	C	0	631	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0643	16519	T	C	0	367	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0644	93	A	G	1	458	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0644	263	A	G	2	221	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0644	750	A	G	0	763	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0644	1438	A	G	0	710	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0644	3010	G	A	0	691	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0644	4769	A	G	0	640	synonymous_variant	LOW	ND2	0.9767
HLI-0644	7013	G	A	0	803	synonymous_variant	LOW	COX1	0.0013
HLI-0644	11914	G	A	1	649	synonymous_variant	LOW	ND4	0.1112
HLI-0644	14798	T	C	0	648	missense_variant	MODERATE	CYTB	0.0651
HLI-0644	15326	A	G	0	672	missense_variant	MODERATE	CYTB	0.9868
HLI-0644	15737	G	A	0	680	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0644	16519	T	C	2	330	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0645	93	A	G	1	474	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0645	204	T	C	1	451	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0645	239	T	C	0	329	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0645	263	A	G	0	276	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0645	750	A	G	0	731	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0645	1438	A	G	0	731	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0645	3915	G	A	1	712	synonymous_variant	LOW	ND1	0.0106
HLI-0645	4727	A	G	6	656	synonymous_variant	LOW	ND2	0.0063
HLI-0645	4769	A	G	1	706	synonymous_variant	LOW	ND2	0.9767
HLI-0645	7773	C	T	0	718	missense_variant	MODERATE	COX2	1.00E-04
HLI-0645	9380	G	A	0	783	synonymous_variant	LOW	COX3	0.0094
HLI-0645	10589	G	A	2	691	synonymous_variant	LOW	ND4L	0.0355
HLI-0645	13748	A	G	0	550	missense_variant	MODERATE	ND5	0.0014
HLI-0645	15326	A	G	0	693	missense_variant	MODERATE	CYTB	0.9868
HLI-0645	16219	A	G	1	737	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0645	16362	T	C	2	555	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0645	16482	A	G	6	475	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0646	73	A	G	0	343	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0646	263	A	G	0	337	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0646	709	G	A	0	703	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0646	750	A	G	1	764	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0646	930	G	A	4	787	upstream_gene_variant	MODIFIER	RNR1	0.0202

HLI-0646	1438	A	G	0	706	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0646	1888	G	A	0	548	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0646	2706	A	G	1	704	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0646	4216	T	C	4	628	missense_variant	MODERATE	ND1	0.0991
HLI-0646	4769	A	G	1	604	synonymous_variant	LOW	ND2	0.9767
HLI-0646	4917	A	G	2	650	missense_variant	MODERATE	ND2	0.0477
HLI-0646	5147	G	A	0	557	synonymous_variant	LOW	ND2	0.0437
HLI-0646	7028	C	T	7	740	synonymous_variant	LOW	COX1	0.8089
HLI-0646	8697	G	A	0	563	synonymous_variant	LOW	ATP6	0.0466
HLI-0646	9254	A	G	2	744	synonymous_variant	LOW	COX3	0.0083
HLI-0646	10463	T	C	1	712	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0646	11251	A	G	0	682	synonymous_variant	LOW	ND4	0.0932
HLI-0646	11719	G	A	0	657	synonymous_variant	LOW	ND4	0.7756
HLI-0646	11812	A	G	1	632	synonymous_variant	LOW	ND4	0.0332
HLI-0646	13368	G	A	4	705	synonymous_variant	LOW	ND5	0.0495
HLI-0646	14233	A	G	2	543	synonymous_variant	LOW	ND6	0.0369
HLI-0646	14766	C	T	3	675	missense_variant	MODERATE	CYTB	0.7696
HLI-0646	14905	G	A	0	797	synonymous_variant	LOW	CYTB	0.0526
HLI-0646	15326	A	G	0	565	missense_variant	MODERATE	CYTB	0.9868
HLI-0646	15452	C	A	2	560	missense_variant	MODERATE	CYTB	0.0933
HLI-0646	15607	A	G	1	583	synonymous_variant	LOW	CYTB	0.0508
HLI-0646	15928	G	A	0	586	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0646	16126	T	C	3	656	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0646	16172	T	C	1	681	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0646	16294	C	T	0	642	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0646	16304	T	C	1	674	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0646	16519	T	C	0	340	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0647	73	A	G	0	302	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0647	263	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0647	750	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0647	1438	A	G	0	659	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0647	4769	A	G	0	618	synonymous_variant	LOW	ND2	0.9767
HLI-0647	6776	T	C	3	778	synonymous_variant	LOW	COX1	0.0226
HLI-0647	15326	A	G	0	472	missense_variant	MODERATE	CYTB	0.9868
HLI-0647	16298	T	C	1	586	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0647	16352	T	C	1	533	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0647	16519	T	C	0	300	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0648	72	T	C	0	330	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0648	195	T	C	1	499	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0648	263	A	G	0	313	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0648	750	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0648	1438	A	G	1	648	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0648	2706	A	G	0	615	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0648	4580	G	A	1	621	synonymous_variant	LOW	ND2	0.0169
HLI-0648	4769	A	G	1	637	synonymous_variant	LOW	ND2	0.9767
HLI-0648	7028	C	T	2	705	synonymous_variant	LOW	COX1	0.8089
HLI-0648	12810	A	G	7	669	synonymous_variant	LOW	ND5	0.0198
HLI-0648	15326	A	G	0	591	missense_variant	MODERATE	CYTB	0.9868
HLI-0648	15904	C	T	0	601	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0648	16240	A	G	0	557	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0648	16298	T	C	1	580	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0649	73	A	G	0	282	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0649	199	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0649	203	G	A	0	391	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0649	204	T	C	0	393	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0649	250	T	C	0	144	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0649	263	A	G	0	161	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0649	750	A	G	1	695	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0649	1438	A	G	0	682	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0649	1719	G	A	1	663	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0649	1836	A	G	1	669	upstream_gene_variant	MODIFIER	RNR2	4.00E-04
HLI-0649	2706	A	G	1	677	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0649	3447	A	G	0	602	synonymous_variant	LOW	ND1	0.0053
HLI-0649	3990	C	T	0	587	synonymous_variant	LOW	ND1	0.0031
HLI-0649	4023	T	C	0	623	synonymous_variant	LOW	ND1	9.00E-04
HLI-0649	4529	A	T	1	640	synonymous_variant	LOW	ND2	0.015
HLI-0649	4769	A	G	0	598	synonymous_variant	LOW	ND2	0.9767
HLI-0649	6734	G	A	2	720	synonymous_variant	LOW	COX1	0.0062
HLI-0649	7028	C	T	2	712	synonymous_variant	LOW	COX1	0.8089
HLI-0649	8251	G	A	3	628	synonymous_variant	LOW	COX2	0.058
HLI-0649	8616	G	T	0	602	missense_variant	MODERATE	ATP6	0.0032
HLI-0649	9947	G	A	1	671	synonymous_variant	LOW	COX3	0.0092
HLI-0649	10034	T	C	1	690	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0649	10238	T	C	2	642	synonymous_variant	LOW	ND3	0.0623
HLI-0649	10398	A	G	0	666	missense_variant	MODERATE	ND3	0.445
HLI-0649	10915	T	C	0	604	synonymous_variant	LOW	ND4	0.0411
HLI-0649	11719	G	A	0	688	synonymous_variant	LOW	ND4	0.7756
HLI-0649	12501	G	A	6	630	synonymous_variant	LOW	ND5	0.0258

HLI-0649	12705	C	T	0	663	synonymous_variant	LOW	ND5	0.4212
HLI-0649	13488	T	C	0	648	synonymous_variant	LOW	ND5	0.0014
HLI-0649	13780	A	G	1	443	missense_variant	MODERATE	ND5	0.0179
HLI-0649	14766	C	T	5	626	missense_variant	MODERATE	CYTB	0.7696
HLI-0649	15043	G	A	2	661	synonymous_variant	LOW	CYTB	0.2362
HLI-0649	15326	A	G	0	604	missense_variant	MODERATE	CYTB	0.9868
HLI-0649	15924	A	G	0	654	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0649	16129	G	A	1	461	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0649	16172	T	C	1	338	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0649	16223	C	T	4	387	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0649	16311	T	C	0	537	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0649	16391	G	A	1	519	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0649	16519	T	C	1	209	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0650	263	A	G	1	184	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0650	456	C	T	3	421	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0650	709	G	A	2	587	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0650	750	A	G	0	621	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0650	1438	A	G	0	637	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0650	4386	T	C	1	504	upstream_gene_variant	MODIFIER	TRNQ	0.0033
HLI-0650	4769	A	G	2	536	synonymous_variant	LOW	ND2	0.9767
HLI-0650	8251	G	A	0	537	synonymous_variant	LOW	COX2	0.058
HLI-0650	9530	T	C	2	516	synonymous_variant	LOW	COX3	0.0014
HLI-0650	15326	A	G	0	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0650	15774	T	C	2	572	missense_variant	MODERATE	CYTB	3.00E-04
HLI-0650	16304	T	C	1	562	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0651	72	T	C	0	314	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0651	263	A	G	0	301	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0651	750	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0651	1438	A	G	0	724	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0651	2706	A	G	0	612	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0651	4580	G	A	2	610	synonymous_variant	LOW	ND2	0.0169
HLI-0651	4769	A	G	0	566	synonymous_variant	LOW	ND2	0.9767
HLI-0651	6773	C	T	4	763	synonymous_variant	LOW	COX1	1.00E-04
HLI-0651	7028	C	T	4	699	synonymous_variant	LOW	COX1	0.8089
HLI-0651	8440	A	G	2	406	synonymous_variant	LOW	ATP8	0.0046
HLI-0651	15326	A	G	0	523	missense_variant	MODERATE	CYTB	0.9868
HLI-0651	15904	C	T	1	507	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0651	16298	T	C	3	457	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0652	73	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0652	152	T	C	1	544	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0652	195	T	C	4	525	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0652	263	A	G	1	233	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0652	709	G	A	1	547	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0652	750	A	G	1	586	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0652	1438	A	G	1	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0652	1888	G	A	1	450	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0652	2706	A	G	0	499	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0652	3337	G	A	1	569	missense_variant	MODERATE	ND1	0.0016
HLI-0652	4216	T	C	0	488	missense_variant	MODERATE	ND1	0.0991
HLI-0652	4769	A	G	0	576	synonymous_variant	LOW	ND2	0.9767
HLI-0652	4917	A	G	0	593	missense_variant	MODERATE	ND2	0.0477
HLI-0652	6002	A	G	0	593	synonymous_variant	LOW	COX1	6.00E-04
HLI-0652	7028	C	T	0	658	synonymous_variant	LOW	COX1	0.8089
HLI-0652	8697	G	A	1	550	synonymous_variant	LOW	ATP6	0.0466
HLI-0652	9899	T	C	1	683	synonymous_variant	LOW	COX3	0.0108
HLI-0652	10463	T	C	1	664	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0652	10873	T	C	0	556	synonymous_variant	LOW	ND4	0.3389
HLI-0652	11251	A	G	0	578	synonymous_variant	LOW	ND4	0.0932
HLI-0652	11719	G	A	1	573	synonymous_variant	LOW	ND4	0.7756
HLI-0652	12633	C	A	9	477	synonymous_variant	LOW	ND5	0.0123
HLI-0652	13368	G	A	0	606	synonymous_variant	LOW	ND5	0.0495
HLI-0652	14766	C	T	3	621	missense_variant	MODERATE	CYTB	0.7696
HLI-0652	14905	G	A	3	730	synonymous_variant	LOW	CYTB	0.0526
HLI-0652	15326	A	G	0	431	missense_variant	MODERATE	CYTB	0.9868
HLI-0652	15452	C	A	2	396	missense_variant	MODERATE	CYTB	0.0933
HLI-0652	15586	T	C	0	390	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0652	15607	A	G	0	424	synonymous_variant	LOW	CYTB	0.0508
HLI-0652	15928	G	A	1	390	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0652	16126	T	C	1	510	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0652	16163	A	G	2	557	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0652	16294	C	T	0	436	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0652	16519	T	C	1	250	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0653	73	A	G	0	356	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0653	152	T	C	0	619	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0653	195	T	C	1	611	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0653	263	A	G	0	301	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0653	296	C	T	0	287	upstream_gene_variant	MODIFIER	DLoop	4.00E-04
HLI-0653	499	G	A	0	464	upstream_gene_variant	MODIFIER	DLoop	0.0359

HLI-0653	745	A	G	0	685	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0653	750	A	G	0	710	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0653	1438	A	G	1	728	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0653	1811	A	G	0	746	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0653	2706	A	G	2	674	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0653	3204	C	T	1	676	upstream_gene_variant	MODIFIER	RNR2	0.0034
HLI-0653	4646	T	C	3	732	synonymous_variant	LOW	ND2	0.0124
HLI-0653	4769	A	G	1	733	synonymous_variant	LOW	ND2	0.9767
HLI-0653	5999	T	C	3	762	synonymous_variant	LOW	COX1	0.0127
HLI-0653	6047	A	G	4	806	synonymous_variant	LOW	COX1	0.0114
HLI-0653	7028	C	T	2	714	synonymous_variant	LOW	COX1	0.8089
HLI-0653	8818	C	T	1	632	synonymous_variant	LOW	ATP6	0.0061
HLI-0653	11332	C	T	1	733	synonymous_variant	LOW	ND4	0.0115
HLI-0653	11467	A	G	1	724	synonymous_variant	LOW	ND4	0.1231
HLI-0653	11719	G	A	1	683	synonymous_variant	LOW	ND4	0.7756
HLI-0653	12308	A	G	1	544	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0653	12372	G	A	2	550	synonymous_variant	LOW	ND5	0.1329
HLI-0653	12937	A	G	8	668	missense_variant	MODERATE	ND5	0.0026
HLI-0653	14620	C	T	9	755	synonymous_variant	LOW	ND6	0.0126
HLI-0653	14766	C	T	1	670	missense_variant	MODERATE	CYTB	0.7696
HLI-0653	15326	A	G	1	608	missense_variant	MODERATE	CYTB	0.9868
HLI-0653	15693	T	C	1	587	missense_variant	MODERATE	CYTB	0.0114
HLI-0653	16134	C	T	0	652	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0653	16356	T	C	0	509	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0653	16519	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0654	263	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0654	477	T	C	0	369	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0654	750	A	G	0	719	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0654	1438	A	G	0	741	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0654	3010	G	A	0	708	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0654	4769	A	G	1	642	synonymous_variant	LOW	ND2	0.9767
HLI-0654	9150	A	G	1	729	synonymous_variant	LOW	ATP6	0.0072
HLI-0654	15326	A	G	0	693	missense_variant	MODERATE	CYTB	0.9868
HLI-0654	16263	T	C	0	663	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0654	16311	T	C	0	689	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0654	16519	T	C	0	325	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0655	73	A	G	1	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0655	152	T	C	3	549	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0655	195	T	C	2	533	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0655	263	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0655	709	G	A	0	507	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0655	750	A	G	0	549	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0655	1438	A	G	0	509	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0655	1888	G	A	1	436	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0655	2706	A	G	0	484	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0655	4216	T	C	2	436	missense_variant	MODERATE	ND1	0.0991
HLI-0655	4769	A	G	0	577	synonymous_variant	LOW	ND2	0.9767
HLI-0655	4820	G	A	0	612	synonymous_variant	LOW	ND2	0.0239
HLI-0655	4917	A	G	2	576	missense_variant	MODERATE	ND2	0.0477
HLI-0655	7028	C	T	3	569	synonymous_variant	LOW	COX1	0.8089
HLI-0655	8697	G	A	0	625	synonymous_variant	LOW	ATP6	0.0466
HLI-0655	9554	G	A	0	407	synonymous_variant	LOW	COX3	0.014
HLI-0655	9899	T	C	1	699	synonymous_variant	LOW	COX3	0.0108
HLI-0655	10463	T	C	0	461	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0655	11251	A	G	0	546	synonymous_variant	LOW	ND4	0.0932
HLI-0655	11719	G	A	0	549	synonymous_variant	LOW	ND4	0.7756
HLI-0655	12633	C	A	5	640	synonymous_variant	LOW	ND5	0.0123
HLI-0655	13368	G	A	3	567	synonymous_variant	LOW	ND5	0.0495
HLI-0655	14766	C	T	1	655	missense_variant	MODERATE	CYTB	0.7696
HLI-0655	14905	G	A	0	699	synonymous_variant	LOW	CYTB	0.0526
HLI-0655	15326	A	G	0	383	missense_variant	MODERATE	CYTB	0.9868
HLI-0655	15452	C	A	4	351	missense_variant	MODERATE	CYTB	0.0933
HLI-0655	15607	A	G	0	377	synonymous_variant	LOW	CYTB	0.0508
HLI-0655	15928	G	A	1	586	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0655	16126	T	C	2	717	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0655	16163	A	G	3	765	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0655	16294	C	T	1	483	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0655	16519	T	C	0	291	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0656	263	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0656	750	A	G	0	659	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0656	1438	A	G	1	672	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0656	3010	G	A	2	608	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0656	4769	A	G	3	622	synonymous_variant	LOW	ND2	0.9767
HLI-0656	14650	C	T	3	715	synonymous_variant	LOW	ND6	1.00E-04
HLI-0656	15326	A	G	0	462	missense_variant	MODERATE	CYTB	0.9868
HLI-0656	16126	T	C	0	366	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0656	16519	T	C	0	244	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0657	195	T	C	4	487	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0657	263	A	G	0	366	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0657	750	A	G	0	505	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0657	961	T	G	3	656	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0657	1438	A	G	0	530	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0657	3145	A	G	5	587	upstream_gene_variant	MODIFIER	RNR2	4.00E-04
HLI-0657	4769	A	G	0	560	synonymous_variant	LOW	ND2	0.9767
HLI-0657	8448	T	C	2	494	missense_variant	MODERATE	ATP8	0.0041
HLI-0657	13759	G	A	2	306	missense_variant	MODERATE	ND5	0.0348
HLI-0657	14587	A	G	5	758	synonymous_variant	LOW	ND6	0.006
HLI-0657	15326	A	G	0	378	missense_variant	MODERATE	CYTB	0.9868
HLI-0657	16092	T	C	14	730	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0657	16140	T	C	1	794	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0657	16311	T	C	2	478	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0658	73	A	G	1	308	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0658	150	C	T	1	621	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0658	263	A	G	0	347	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0658	497	C	T	0	490	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0658	750	A	G	1	535	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0658	1189	T	C	0	665	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0658	1438	A	G	0	515	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0658	1811	A	G	0	417	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0658	2706	A	G	1	518	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0658	3480	A	G	0	490	synonymous_variant	LOW	ND1	0.0392
HLI-0658	4769	A	G	2	583	synonymous_variant	LOW	ND2	0.9767
HLI-0658	6155	C	A	3	573	synonymous_variant	LOW	COX1	0
HLI-0658	7028	C	T	5	655	synonymous_variant	LOW	COX1	0.8089
HLI-0658	7118	A	G	2	636	synonymous_variant	LOW	COX1	5.00E-04
HLI-0658	9055	G	A	0	524	missense_variant	MODERATE	ATP6	0.0425
HLI-0658	9477	G	A	1	539	missense_variant	MODERATE	COX3	0.0387
HLI-0658	9698	T	C	2	553	synonymous_variant	LOW	COX3	0.0405
HLI-0658	10398	A	G	1	396	missense_variant	MODERATE	ND3	0.445
HLI-0658	10550	A	G	0	457	synonymous_variant	LOW	ND4L	0.0376
HLI-0658	11299	T	C	2	555	synonymous_variant	LOW	ND4	0.0417
HLI-0658	11467	A	G	1	642	synonymous_variant	LOW	ND4	0.1231
HLI-0658	11485	T	C	0	713	synonymous_variant	LOW	ND4	0.0081
HLI-0658	11719	G	A	0	545	synonymous_variant	LOW	ND4	0.7756
HLI-0658	12017	A	G	1	548	missense_variant	MODERATE	ND4	1.00E-04
HLI-0658	12308	A	G	0	467	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0658	12372	G	A	1	478	synonymous_variant	LOW	ND5	0.1329

HLI-0658	14167	C	T	1	536	synonymous_variant	LOW	ND6	0.0385
HLI-0658	14182	T	C	0	556	synonymous_variant	LOW	ND6	0.0254
HLI-0658	14766	C	T	4	710	missense_variant	MODERATE	CYTB	0.7696
HLI-0658	14798	T	C	0	781	missense_variant	MODERATE	CYTB	0.0651
HLI-0658	15326	A	G	0	375	missense_variant	MODERATE	CYTB	0.9868
HLI-0658	16224	T	C	2	652	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0658	16311	T	C	0	510	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0658	16519	T	C	0	278	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0659	93	A	G	2	284	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0659	152	T	C	1	446	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0659	263	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0659	750	A	G	0	393	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0659	1438	A	G	1	481	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0659	3591	G	A	1	265	synonymous_variant	LOW	ND1	0.0082
HLI-0659	4310	A	G	1	421	upstream_gene_variant	MODIFIER	TRNI	8.00E-04
HLI-0659	4769	A	G	0	541	synonymous_variant	LOW	ND2	0.9767
HLI-0659	13020	T	C	1	415	synonymous_variant	LOW	ND5	0.0106
HLI-0659	15326	A	G	1	305	missense_variant	MODERATE	CYTB	0.9868
HLI-0659	16168	C	T	0	781	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0659	16519	T	C	0	226	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0660	73	A	G	0	305	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0660	185	G	A	9	540	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0660	228	G	A	1	430	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0660	263	A	G	0	323	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0660	295	C	T	0	224	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0660	462	C	T	2	451	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0660	489	T	C	1	538	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0660	750	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0660	1438	A	G	0	685	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0660	2706	A	G	1	577	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0660	3010	G	A	1	695	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0660	4216	T	C	0	579	missense_variant	MODERATE	ND1	0.0991
HLI-0660	4580	G	A	1	734	synonymous_variant	LOW	ND2	0.0169
HLI-0660	4769	A	G	0	708	synonymous_variant	LOW	ND2	0.9767
HLI-0660	7028	C	T	6	663	synonymous_variant	LOW	COX1	0.8089
HLI-0660	8865	G	A	0	622	synonymous_variant	LOW	ATP6	0.003
HLI-0660	9957	T	C	0	702	missense_variant	MODERATE	COX3	8.00E-04
HLI-0660	10398	A	G	1	669	missense_variant	MODERATE	ND3	0.445
HLI-0660	11251	A	G	0	629	synonymous_variant	LOW	ND4	0.0932

HLI-0660	11719	G	A	0	609	synonymous_variant	LOW	ND4	0.7756
HLI-0660	12612	A	G	5	670	synonymous_variant	LOW	ND5	0.0506
HLI-0660	13708	G	A	2	552	missense_variant	MODERATE	ND5	0.0717
HLI-0660	13934	C	T	2	594	missense_variant	MODERATE	ND5	0.0122
HLI-0660	14766	C	T	3	670	missense_variant	MODERATE	CYTB	0.7696
HLI-0660	14798	T	C	2	744	missense_variant	MODERATE	CYTB	0.0651
HLI-0660	15326	A	G	1	480	missense_variant	MODERATE	CYTB	0.9868
HLI-0660	15452	C	A	2	480	missense_variant	MODERATE	CYTB	0.0933
HLI-0660	16069	C	T	1	676	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0660	16126	T	C	0	742	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0660	16390	G	A	2	509	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0661	73	A	G	0	374	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0661	152	T	C	0	636	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0661	195	T	C	0	612	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0661	198	C	T	0	607	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0661	263	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0661	499	G	A	0	469	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0661	750	A	G	0	716	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0661	1438	A	G	0	728	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0661	1811	A	G	3	733	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0661	2706	A	G	0	718	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0661	4646	T	C	0	787	synonymous_variant	LOW	ND2	0.0124
HLI-0661	4769	A	G	0	692	synonymous_variant	LOW	ND2	0.9767
HLI-0661	5999	T	C	2	741	synonymous_variant	LOW	COX1	0.0127
HLI-0661	6047	A	G	2	803	synonymous_variant	LOW	COX1	0.0114
HLI-0661	7028	C	T	6	775	synonymous_variant	LOW	COX1	0.8089
HLI-0661	7705	T	C	1	692	synonymous_variant	LOW	COX2	0.0034
HLI-0661	11332	C	T	3	715	synonymous_variant	LOW	ND4	0.0115
HLI-0661	11339	T	C	4	756	synonymous_variant	LOW	ND4	0.0028
HLI-0661	11467	A	G	4	675	synonymous_variant	LOW	ND4	0.1231
HLI-0661	11719	G	A	2	716	synonymous_variant	LOW	ND4	0.7756
HLI-0661	11788	C	T	11	794	synonymous_variant	LOW	ND4	7.00E-04
HLI-0661	12308	A	G	2	669	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0661	12372	G	A	2	723	synonymous_variant	LOW	ND5	0.1329
HLI-0661	13528	A	G	7	709	missense_variant	MODERATE	ND5	9.00E-04
HLI-0661	14620	C	T	7	742	synonymous_variant	LOW	ND6	0.0126
HLI-0661	14766	C	T	1	704	missense_variant	MODERATE	CYTB	0.7696
HLI-0661	15514	T	C	6	688	synonymous_variant	LOW	CYTB	0.0071
HLI-0661	15693	T	C	2	712	missense_variant	MODERATE	CYTB	0.0114

HLI-0661	16140	T	C	6	754	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0661	16274	G	A	7	677	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0661	16356	T	C	3	623	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0661	16519	T	C	0	422	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0662	263	A	G	0	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0662	750	A	G	1	665	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0662	1438	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0662	4769	A	G	1	578	synonymous_variant	LOW	ND2	0.9767
HLI-0662	5054	G	C	0	589	synonymous_variant	LOW	ND2	5.00E-04
HLI-0662	6776	T	C	5	676	synonymous_variant	LOW	COX1	0.0226
HLI-0662	15326	A	G	0	538	missense_variant	MODERATE	CYTB	0.9868
HLI-0662	16519	T	C	1	345	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0663	73	A	G	1	386	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0663	263	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0663	709	G	A	0	786	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0663	750	A	G	0	841	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0663	1438	A	G	2	759	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0663	1709	G	A	1	708	upstream_gene_variant	MODIFIER	RNR2	0.0035
HLI-0663	1888	G	A	1	730	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0663	2706	A	G	1	697	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0663	4216	T	C	2	737	missense_variant	MODERATE	ND1	0.0991
HLI-0663	4769	A	G	0	738	synonymous_variant	LOW	ND2	0.9767
HLI-0663	4917	A	G	3	663	missense_variant	MODERATE	ND2	0.0477
HLI-0663	7028	C	T	4	794	synonymous_variant	LOW	COX1	0.8089
HLI-0663	7984	G	A	1	745	synonymous_variant	LOW	COX2	5.00E-04
HLI-0663	8697	G	A	1	671	synonymous_variant	LOW	ATP6	0.0466
HLI-0663	10463	T	C	0	741	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0663	11251	A	G	0	706	synonymous_variant	LOW	ND4	0.0932
HLI-0663	11719	G	A	0	695	synonymous_variant	LOW	ND4	0.7756
HLI-0663	11812	A	G	0	728	synonymous_variant	LOW	ND4	0.0332
HLI-0663	13368	G	A	0	725	synonymous_variant	LOW	ND5	0.0495
HLI-0663	14233	A	G	1	693	synonymous_variant	LOW	ND6	0.0369
HLI-0663	14766	C	T	0	700	missense_variant	MODERATE	CYTB	0.7696
HLI-0663	14905	G	A	1	769	synonymous_variant	LOW	CYTB	0.0526
HLI-0663	15326	A	G	2	669	missense_variant	MODERATE	CYTB	0.9868
HLI-0663	15452	C	A	1	726	missense_variant	MODERATE	CYTB	0.0933
HLI-0663	15607	A	G	1	690	synonymous_variant	LOW	CYTB	0.0508
HLI-0663	15928	G	A	0	735	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0663	16126	T	C	1	663	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0663	16140	T	C	1	733	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0663	16294	C	T	2	651	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0663	16296	C	T	2	658	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0663	16311	T	C	2	676	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0663	16519	T	C	1	380	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0664	263	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0664	750	A	G	1	740	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0664	951	G	A	1	783	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0664	15326	A	G	0	642	missense_variant	MODERATE	CYTB	0.9868
HLI-0664	16354	C	T	2	562	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0665	73	A	G	0	335	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0665	263	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0665	750	A	G	0	657	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0665	1211	G	A	0	673	upstream_gene_variant	MODIFIER	RNR1	0.0012
HLI-0665	1438	A	G	0	660	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0665	2706	A	G	0	653	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0665	3450	C	T	0	573	synonymous_variant	LOW	ND1	0.0084
HLI-0665	4769	A	G	0	600	synonymous_variant	LOW	ND2	0.9767
HLI-0665	5773	G	A	0	655	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0665	6221	T	C	0	633	synonymous_variant	LOW	COX1	0.0306
HLI-0665	7028	C	T	2	699	synonymous_variant	LOW	COX1	0.8089
HLI-0665	8701	A	G	0	579	missense_variant	MODERATE	ATP6	0.3391
HLI-0665	9449	C	T	2	626	synonymous_variant	LOW	COX3	0.0125
HLI-0665	9540	T	C	0	664	synonymous_variant	LOW	COX3	0.339
HLI-0665	10086	A	G	0	740	missense_variant	MODERATE	ND3	0.0088
HLI-0665	10365	G	A	0	670	missense_variant	MODERATE	ND3	0.0011
HLI-0665	10373	G	A	0	701	synonymous_variant	LOW	ND3	0.0117
HLI-0665	10398	A	G	0	710	missense_variant	MODERATE	ND3	0.445
HLI-0665	10873	T	C	1	450	synonymous_variant	LOW	ND4	0.3389
HLI-0665	11002	A	G	1	486	synonymous_variant	LOW	ND4	0.0124
HLI-0665	11719	G	A	0	630	synonymous_variant	LOW	ND4	0.7756
HLI-0665	12705	C	T	2	611	synonymous_variant	LOW	ND5	0.4212
HLI-0665	13105	A	G	1	581	missense_variant	MODERATE	ND5	0.076
HLI-0665	13326	T	C	1	628	synonymous_variant	LOW	ND5	0.0032
HLI-0665	13914	C	A	1	545	synonymous_variant	LOW	ND5	0.0091
HLI-0665	13967	C	T	2	610	missense_variant	MODERATE	ND5	0.003
HLI-0665	14696	A	G	1	657	upstream_gene_variant	MODIFIER	TRNE	9.00E-04
HLI-0665	14766	C	T	3	669	missense_variant	MODERATE	CYTB	0.7696
HLI-0665	15263	C	T	1	527	missense_variant	MODERATE	CYTB	5.00E-04

HLI-0665	15286	C	A	1	599	synonymous_variant	LOW	CYTB	0
HLI-0665	15301	G	A	1	574	synonymous_variant	LOW	CYTB	0.2912
HLI-0665	15311	A	G	0	578	missense_variant	MODERATE	CYTB	0.008
HLI-0665	15326	A	G	0	590	missense_variant	MODERATE	CYTB	0.9868
HLI-0665	15824	A	G	1	690	missense_variant	MODERATE	CYTB	0.0083
HLI-0665	16124	T	C	0	608	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0665	16223	C	T	1	637	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0665	16278	C	T	2	658	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0665	16362	T	C	0	574	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0665	16519	T	C	1	306	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0666	263	A	G	1	295	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0666	408	T	A	0	448	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0666	750	A	G	2	631	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0666	1438	A	G	0	733	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0666	4769	A	G	1	672	synonymous_variant	LOW	ND2	0.9767
HLI-0666	6776	T	C	3	715	synonymous_variant	LOW	COX1	0.0226
HLI-0666	15326	A	G	0	621	missense_variant	MODERATE	CYTB	0.9868
HLI-0666	16093	T	C	16	596	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0666	16519	T	C	0	310	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0667	73	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0667	153	A	G	3	495	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0667	195	T	C	2	507	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0667	225	G	A	0	492	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0667	226	T	C	0	497	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0667	263	A	G	0	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0667	750	A	G	0	501	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0667	1438	A	G	0	531	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0667	1719	G	A	0	412	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0667	2706	A	G	0	479	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0667	3705	G	A	0	395	synonymous_variant	LOW	ND1	0.0138
HLI-0667	4769	A	G	1	555	synonymous_variant	LOW	ND2	0.9767
HLI-0667	6221	T	C	0	488	synonymous_variant	LOW	COX1	0.0306
HLI-0667	6371	C	T	1	470	synonymous_variant	LOW	COX1	0.0097
HLI-0667	7028	C	T	4	628	synonymous_variant	LOW	COX1	0.8089
HLI-0667	7299	A	G	1	618	missense_variant	MODERATE	COX1	0.0014
HLI-0667	8393	C	T	1	487	missense_variant	MODERATE	ATP8	0.0036
HLI-0667	8994	G	A	0	463	synonymous_variant	LOW	ATP6	0.0167
HLI-0667	11016	G	A	0	388	missense_variant	MODERATE	ND4	0.0062
HLI-0667	11719	G	A	1	534	synonymous_variant	LOW	ND4	0.7756

HLI-0667	12705	C	T	1	485	synonymous_variant	LOW	ND5	0.4212
HLI-0667	13708	G	A	0	426	missense_variant	MODERATE	ND5	0.0717
HLI-0667	13966	A	G	0	397	missense_variant	MODERATE	ND5	0.0126
HLI-0667	14470	T	C	1	541	synonymous_variant	LOW	ND6	0.0166
HLI-0667	14766	C	T	0	650	missense_variant	MODERATE	CYTB	0.7696
HLI-0667	15326	A	G	0	344	missense_variant	MODERATE	CYTB	0.9868
HLI-0667	15784	T	C	0	416	synonymous_variant	LOW	CYTB	0.0363
HLI-0667	15927	G	A	0	442	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0667	16093	T	C	16	436	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0667	16223	C	T	2	383	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0667	16278	C	T	0	394	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0667	16519	T	C	0	198	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0668	73	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0668	152	T	C	0	554	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0668	217	T	C	1	356	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0668	263	A	G	1	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0668	340	C	T	0	171	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0668	508	A	G	0	342	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0668	750	A	G	0	550	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0668	1438	A	G	0	610	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0668	1811	A	G	0	607	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0668	2706	A	G	0	406	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0668	3116	C	T	1	492	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0668	3720	A	G	1	453	synonymous_variant	LOW	ND1	0.0069
HLI-0668	4769	A	G	2	548	synonymous_variant	LOW	ND2	0.9767
HLI-0668	5390	A	G	0	525	synonymous_variant	LOW	ND2	0.0069
HLI-0668	5426	T	C	0	644	synonymous_variant	LOW	ND2	0.0091
HLI-0668	6045	C	T	0	664	synonymous_variant	LOW	COX1	0.0065
HLI-0668	6152	T	C	0	525	synonymous_variant	LOW	COX1	0.0077
HLI-0668	7028	C	T	1	583	synonymous_variant	LOW	COX1	0.8089
HLI-0668	10127	A	G	1	631	synonymous_variant	LOW	ND3	2.00E-04
HLI-0668	10876	A	G	0	483	synonymous_variant	LOW	ND4	0.0098
HLI-0668	11197	C	T	0	437	synonymous_variant	LOW	ND4	0.0021
HLI-0668	11467	A	G	0	557	synonymous_variant	LOW	ND4	0.1231
HLI-0668	11719	G	A	0	601	synonymous_variant	LOW	ND4	0.7756
HLI-0668	11732	T	C	0	658	synonymous_variant	LOW	ND4	0.002
HLI-0668	11914	G	A	0	541	synonymous_variant	LOW	ND4	0.1112
HLI-0668	12308	A	G	2	576	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0668	12372	G	A	1	668	synonymous_variant	LOW	ND5	0.1329

HLI-0668	13020	T	C	1	477	synonymous_variant	LOW	ND5	0.0106
HLI-0668	13734	T	C	0	394	synonymous_variant	LOW	ND5	0.0067
HLI-0668	14766	C	T	3	565	missense_variant	MODERATE	CYTB	0.7696
HLI-0668	15326	A	G	0	331	missense_variant	MODERATE	CYTB	0.9868
HLI-0668	15907	A	G	0	646	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0668	16051	A	G	2	552	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0668	16129	G	C	2	378	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0668	16319	G	A	0	435	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0668	16362	T	C	1	444	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0668	16519	T	C	0	208	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0669	73	A	G	2	336	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0669	242	C	T	1	306	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0669	263	A	G	0	274	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0669	295	C	T	0	196	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0669	462	C	T	4	405	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0669	489	T	C	1	482	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0669	750	A	G	0	647	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0669	1438	A	G	1	633	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0669	2158	T	C	0	612	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0669	2706	A	G	0	668	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0669	3010	G	A	3	618	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0669	4216	T	C	3	656	missense_variant	MODERATE	ND1	0.0991
HLI-0669	4769	A	G	1	628	synonymous_variant	LOW	ND2	0.9767
HLI-0669	5460	G	A	3	695	missense_variant	MODERATE	ND2	0.0651
HLI-0669	7028	C	T	0	739	synonymous_variant	LOW	COX1	0.8089
HLI-0669	7979	G	A	1	652	missense_variant	MODERATE	COX2	3.00E-04
HLI-0669	8269	G	A	2	554	stop_retained_variant	LOW	COX2	0.0127
HLI-0669	8557	G	A	2	520	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0669	10398	A	G	5	602	missense_variant	MODERATE	ND3	0.445
HLI-0669	11251	A	G	0	676	synonymous_variant	LOW	ND4	0.0932
HLI-0669	11719	G	A	0	628	synonymous_variant	LOW	ND4	0.7756
HLI-0669	12007	G	A	1	578	synonymous_variant	LOW	ND4	0.0639
HLI-0669	12360	C	T	0	577	synonymous_variant	LOW	ND5	1.00E-04
HLI-0669	12612	A	G	5	654	synonymous_variant	LOW	ND5	0.0506
HLI-0669	13708	G	A	2	393	missense_variant	MODERATE	ND5	0.0717
HLI-0669	13879	T	C	2	596	missense_variant	MODERATE	ND5	0.0073
HLI-0669	14022	A	G	2	639	synonymous_variant	LOW	ND5	0.0366
HLI-0669	14766	C	T	2	613	missense_variant	MODERATE	CYTB	0.7696
HLI-0669	15326	A	G	0	602	missense_variant	MODERATE	CYTB	0.9868

HLI-0669	15452	C	A	3	560	missense_variant	MODERATE	CYTB	0.0933
HLI-0669	16069	C	T	0	626	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0669	16114	C	T	0	663	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0669	16126	T	C	0	639	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0669	16145	G	A	1	650	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0669	16172	T	C	1	646	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0669	16222	C	T	5	668	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0669	16261	C	T	4	646	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0670	263	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0670	750	A	G	1	683	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0670	1438	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0670	3010	G	A	1	739	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0670	4733	T	C	0	715	synonymous_variant	LOW	ND2	0.0029
HLI-0670	4769	A	G	2	762	synonymous_variant	LOW	ND2	0.9767
HLI-0670	15326	A	G	0	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0670	16519	T	C	0	353	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0671	73	A	G	0	308	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0671	150	C	T	0	583	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0671	152	T	C	0	590	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0671	195	T	C	1	564	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0671	263	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0671	750	A	G	1	612	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0671	1438	A	G	0	672	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0671	2352	T	C	0	612	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0671	2706	A	G	1	588	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0671	4769	A	G	2	653	synonymous_variant	LOW	ND2	0.9767
HLI-0671	7028	C	T	5	701	synonymous_variant	LOW	COX1	0.8089
HLI-0671	8701	A	G	0	671	missense_variant	MODERATE	ATP6	0.3391
HLI-0671	9540	T	C	0	630	synonymous_variant	LOW	COX3	0.339
HLI-0671	10088	C	T	5	666	synonymous_variant	LOW	ND3	3.00E-04
HLI-0671	10398	A	G	0	662	missense_variant	MODERATE	ND3	0.445
HLI-0671	10819	A	G	1	616	synonymous_variant	LOW	ND4	0.0228
HLI-0671	10861	T	C	0	668	synonymous_variant	LOW	ND4	8.00E-04
HLI-0671	10873	T	C	0	675	synonymous_variant	LOW	ND4	0.3389
HLI-0671	11719	G	A	1	614	synonymous_variant	LOW	ND4	0.7756
HLI-0671	12705	C	T	1	749	synonymous_variant	LOW	ND5	0.4212
HLI-0671	14212	T	C	1	615	synonymous_variant	LOW	ND6	0.0204
HLI-0671	14766	C	T	2	673	missense_variant	MODERATE	CYTB	0.7696
HLI-0671	14905	G	A	1	818	synonymous_variant	LOW	CYTB	0.0526

HLI-0671	15301	G	A	1	503	synonymous_variant	LOW	CYTB	0.2912
HLI-0671	15326	A	G	0	536	missense_variant	MODERATE	CYTB	0.9868
HLI-0671	16172	T	C	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0671	16223	C	T	1	373	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0671	16256	C	T	2	438	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0671	16320	C	T	0	539	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0671	16519	T	C	0	230	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0672	72	T	C	1	379	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0672	263	A	G	0	345	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0672	750	A	G	0	724	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0672	1438	A	G	0	760	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0672	2706	A	G	0	741	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0672	4580	G	A	2	663	synonymous_variant	LOW	ND2	0.0169
HLI-0672	4769	A	G	0	704	synonymous_variant	LOW	ND2	0.9767
HLI-0672	7028	C	T	2	779	synonymous_variant	LOW	COX1	0.8089
HLI-0672	9309	T	C	2	772	missense_variant	MODERATE	COX3	2.00E-04
HLI-0672	15326	A	G	0	648	missense_variant	MODERATE	CYTB	0.9868
HLI-0672	15904	C	T	2	750	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0672	16298	T	C	1	638	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0673	263	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0673	750	A	G	0	722	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0673	1438	A	G	0	718	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0673	3010	G	A	0	720	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0673	4769	A	G	0	676	synonymous_variant	LOW	ND2	0.9767
HLI-0673	4859	T	C	1	709	synonymous_variant	LOW	ND2	0.0017
HLI-0673	12136	T	C	1	699	synonymous_variant	LOW	ND4	0.0016
HLI-0673	15326	A	G	2	645	missense_variant	MODERATE	CYTB	0.9868
HLI-0673	16519	T	C	0	425	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0674	73	A	G	0	32	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0674	195	T	C	0	49	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0674	263	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0674	499	G	A	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0674	750	A	G	0	44	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0674	1438	A	G	0	50	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0674	1811	A	G	0	45	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0674	2083	T	C	0	42	upstream_gene_variant	MODIFIER	RNR2	0.0011
HLI-0674	2706	A	G	0	52	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0674	3672	A	G	0	50	synonymous_variant	LOW	ND1	0.0013
HLI-0674	4646	T	C	0	47	synonymous_variant	LOW	ND2	0.0124

HLI-0674	4769	A	G	0	50	synonymous_variant	LOW	ND2	0.9767
HLI-0674	5999	T	C	0	61	synonymous_variant	LOW	COX1	0.0127
HLI-0674	6047	A	G	0	53	synonymous_variant	LOW	COX1	0.0114
HLI-0674	7028	C	T	0	59	synonymous_variant	LOW	COX1	0.8089
HLI-0674	7705	T	C	0	42	synonymous_variant	LOW	COX2	0.0034
HLI-0674	8642	A	G	0	46	missense_variant	MODERATE	ATP6	4.00E-04
HLI-0674	11332	C	T	0	46	synonymous_variant	LOW	ND4	0.0115
HLI-0674	11339	T	C	0	41	synonymous_variant	LOW	ND4	0.0028
HLI-0674	11467	A	G	0	62	synonymous_variant	LOW	ND4	0.1231
HLI-0674	11719	G	A	0	56	synonymous_variant	LOW	ND4	0.7756
HLI-0674	12297	T	C	0	53	upstream_gene_variant	MODIFIER	TRNL2	8.00E-04
HLI-0674	12308	A	G	0	54	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0674	12372	G	A	0	48	synonymous_variant	LOW	ND5	0.1329
HLI-0674	14620	C	T	1	57	synonymous_variant	LOW	ND6	0.0126
HLI-0674	14766	C	T	0	42	missense_variant	MODERATE	CYTB	0.7696
HLI-0674	15326	A	G	0	47	missense_variant	MODERATE	CYTB	0.9868
HLI-0674	15693	T	C	0	45	missense_variant	MODERATE	CYTB	0.0114
HLI-0674	15789	C	T	0	46	missense_variant	MODERATE	CYTB	6.00E-04
HLI-0674	16295	C	T	1	57	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0674	16356	T	C	0	49	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0674	16362	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0674	16519	T	C	0	30	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0675	152	T	C	0	72	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0675	263	A	G	0	48	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0675	750	A	G	0	60	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0675	1438	A	G	0	55	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0675	2259	C	T	0	49	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0675	4745	A	G	0	61	synonymous_variant	LOW	ND2	0.0039
HLI-0675	4769	A	G	0	61	synonymous_variant	LOW	ND2	0.9767
HLI-0675	7337	G	A	0	67	synonymous_variant	LOW	COX1	0.0119
HLI-0675	13326	T	C	0	68	synonymous_variant	LOW	ND5	0.0032
HLI-0675	13680	C	T	0	57	synonymous_variant	LOW	ND5	0.005
HLI-0675	13851	C	T	0	46	synonymous_variant	LOW	ND5	2.00E-04
HLI-0675	14831	G	A	0	61	missense_variant	MODERATE	CYTB	0.0021
HLI-0675	14872	C	T	0	56	synonymous_variant	LOW	CYTB	0.0061
HLI-0675	15326	A	G	0	61	missense_variant	MODERATE	CYTB	0.9868
HLI-0676	263	A	G	0	30	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0676	750	A	G	0	60	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0676	1438	A	G	0	62	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0676	4769	A	G	0	61	synonymous_variant	LOW	ND2	0.9767
HLI-0676	14470	T	A	1	66	synonymous_variant	LOW	ND6	0.0031
HLI-0676	15326	A	G	0	72	missense_variant	MODERATE	CYTB	0.9868
HLI-0676	16093	T	C	1	51	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0676	16221	C	T	0	52	upstream_gene_variant	MODIFIER	DLoop	0.007
HLI-0676	16519	T	C	0	30	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0677	239	T	C	0	29	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0677	263	A	G	0	30	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0677	750	A	G	0	59	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0677	1438	A	G	0	64	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0677	4769	A	G	0	65	synonymous_variant	LOW	ND2	0.9767
HLI-0677	6869	C	T	0	68	synonymous_variant	LOW	COX1	7.00E-04
HLI-0677	9804	G	A	0	67	missense_variant	MODERATE	COX3	0.0028
HLI-0677	15326	A	G	0	51	missense_variant	MODERATE	CYTB	0.9868
HLI-0677	16362	T	C	0	50	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0677	16482	A	G	0	32	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0678	73	A	G	0	36	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0678	152	T	C	0	65	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0678	217	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0678	263	A	G	0	22	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0678	340	C	T	0	14	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0678	508	A	G	1	36	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0678	750	A	G	0	50	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0678	1438	A	G	0	57	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0678	1811	A	G	0	48	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0678	2706	A	G	0	55	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0678	3720	A	G	0	73	synonymous_variant	LOW	ND1	0.0069
HLI-0678	4132	G	A	0	54	missense_variant	MODERATE	ND1	1.00E-04
HLI-0678	4769	A	G	0	45	synonymous_variant	LOW	ND2	0.9767
HLI-0678	5390	A	G	0	60	synonymous_variant	LOW	ND2	0.0069
HLI-0678	5426	T	C	0	53	synonymous_variant	LOW	ND2	0.0091
HLI-0678	6045	C	T	0	73	synonymous_variant	LOW	COX1	0.0065
HLI-0678	6152	T	C	1	63	synonymous_variant	LOW	COX1	0.0077
HLI-0678	7028	C	T	1	62	synonymous_variant	LOW	COX1	0.8089
HLI-0678	8563	A	G	1	50	missense_variant	MODERATE	ATP6/8	0.0034
HLI-0678	10876	A	G	0	52	synonymous_variant	LOW	ND4	0.0098
HLI-0678	11467	A	G	0	72	synonymous_variant	LOW	ND4	0.1231
HLI-0678	11719	G	A	0	71	synonymous_variant	LOW	ND4	0.7756
HLI-0678	12308	A	G	0	60	upstream_gene_variant	MODIFIER	TRNL2	0.1227

HLI-0678	12372	G	A	0	59	synonymous_variant	LOW	ND5	0.1329
HLI-0678	13020	T	C	3	63	synonymous_variant	LOW	ND5	0.0106
HLI-0678	13734	T	C	0	60	synonymous_variant	LOW	ND5	0.0067
HLI-0678	14766	C	T	1	57	missense_variant	MODERATE	CYTB	0.7696
HLI-0678	15326	A	G	0	43	missense_variant	MODERATE	CYTB	0.9868
HLI-0678	15907	A	G	0	70	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0678	16051	A	G	0	52	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0678	16129	G	C	0	33	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0678	16362	T	C	0	67	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0679	263	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0679	750	A	G	1	601	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0679	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0679	2259	C	T	2	551	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0679	4745	A	G	0	679	synonymous_variant	LOW	ND2	0.0039
HLI-0679	4769	A	G	0	727	synonymous_variant	LOW	ND2	0.9767
HLI-0679	5060	C	T	0	520	synonymous_variant	LOW	ND2	3.00E-04
HLI-0679	13680	C	T	0	527	synonymous_variant	LOW	ND5	0.005
HLI-0679	14872	C	T	2	729	synonymous_variant	LOW	CYTB	0.0061
HLI-0679	15326	A	G	1	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0680	73	A	G	0	34	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0680	152	T	C	0	65	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0680	182	C	T	0	66	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0680	185	G	T	0	64	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0680	195	T	C	0	61	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0680	247	G	A	0	36	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0680	263	A	G	0	31	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0680	357	A	G	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0680	709	G	A	0	49	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0680	710	T	C	0	49	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0680	750	A	G	0	50	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0680	769	G	A	0	56	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0680	825	T	A	0	66	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0680	1018	G	A	0	66	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0680	1738	T	C	0	31	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0680	2352	T	C	0	34	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0680	2706	A	G	0	64	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0680	2758	G	A	0	66	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0680	2768	A	G	0	69	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0680	2885	T	C	0	59	upstream_gene_variant	MODIFIER	RNR2	0.05

HLI-0680	3308	T	C	0	60	start_lost	HIGH	ND1	0.0073
HLI-0680	3594	C	T	0	54	synonymous_variant	LOW	ND1	0.0789
HLI-0680	3666	G	A	1	75	synonymous_variant	LOW	ND1	0.0233
HLI-0680	3693	G	A	0	65	synonymous_variant	LOW	ND1	0.0091
HLI-0680	4104	A	G	0	58	synonymous_variant	LOW	ND1	0.0785
HLI-0680	4769	A	G	0	71	synonymous_variant	LOW	ND2	0.9767
HLI-0680	5036	A	G	0	52	synonymous_variant	LOW	ND2	0.006
HLI-0680	5046	G	A	0	54	missense_variant	MODERATE	ND2	0.018
HLI-0680	5393	T	C	0	57	synonymous_variant	LOW	ND2	0.0059
HLI-0680	5655	T	C	0	64	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0680	6378	T	C	0	57	synonymous_variant	LOW	COX1	0.0011
HLI-0680	6548	C	T	0	58	synonymous_variant	LOW	COX1	0.0061
HLI-0680	6827	T	C	0	67	synonymous_variant	LOW	COX1	0.0072
HLI-0680	6989	A	G	0	95	synonymous_variant	LOW	COX1	0.0061
HLI-0680	7028	C	T	0	88	synonymous_variant	LOW	COX1	0.8089
HLI-0680	7055	A	G	0	83	synonymous_variant	LOW	COX1	0.0188
HLI-0680	7146	A	G	0	32	missense_variant	MODERATE	COX1	0.0497
HLI-0680	7256	C	T	0	51	synonymous_variant	LOW	COX1	0.0784
HLI-0680	7389	T	C	0	55	missense_variant	MODERATE	COX1	0.0201
HLI-0680	7521	G	A	0	33	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0680	7867	C	T	0	80	synonymous_variant	LOW	COX2	0.0076
HLI-0680	8248	A	G	0	44	synonymous_variant	LOW	COX2	0.0061
HLI-0680	8468	C	T	0	29	synonymous_variant	LOW	ATP8	0.0501
HLI-0680	8655	C	T	1	40	synonymous_variant	LOW	ATP6	0.0511
HLI-0680	8701	A	G	0	40	missense_variant	MODERATE	ATP6	0.3391
HLI-0680	9540	T	C	0	70	synonymous_variant	LOW	COX3	0.339
HLI-0680	10398	A	G	0	50	missense_variant	MODERATE	ND3	0.445
HLI-0680	10688	G	A	0	63	synonymous_variant	LOW	ND4L	0.0515
HLI-0680	10810	T	C	0	38	synonymous_variant	LOW	ND4	0.0522
HLI-0680	10873	T	C	0	42	synonymous_variant	LOW	ND4	0.3389
HLI-0680	11719	G	A	0	65	synonymous_variant	LOW	ND4	0.7756
HLI-0680	12519	T	C	0	44	synonymous_variant	LOW	ND5	0.007
HLI-0680	12705	C	T	0	25	synonymous_variant	LOW	ND5	0.4212
HLI-0680	13105	A	G	0	66	missense_variant	MODERATE	ND5	0.076
HLI-0680	13506	C	T	0	60	synonymous_variant	LOW	ND5	0.0506
HLI-0680	13650	C	T	0	46	synonymous_variant	LOW	ND5	0.079
HLI-0680	13789	T	C	0	28	missense_variant	MODERATE	ND5	0.0185
HLI-0680	13880	C	A	1	34	missense_variant	MODERATE	ND5	0.0055
HLI-0680	14178	T	C	0	43	missense_variant	MODERATE	ND6	0.0225

HLI-0680	14203	A	G	0	50	synonymous_variant	LOW	ND6	0.0061
HLI-0680	14560	G	A	0	85	synonymous_variant	LOW	ND6	0.0235
HLI-0680	14766	C	T	0	66	missense_variant	MODERATE	CYTB	0.7696
HLI-0680	14769	A	G	0	67	missense_variant	MODERATE	CYTB	0.0121
HLI-0680	15115	T	C	0	64	synonymous_variant	LOW	CYTB	0.0093
HLI-0680	15326	A	G	0	47	missense_variant	MODERATE	CYTB	0.9868
HLI-0680	16126	T	C	0	26	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0680	16223	C	T	0	13	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0680	16264	C	T	0	18	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0680	16270	C	T	0	18	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0680	16278	C	T	0	21	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0680	16293	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0680	16311	T	C	0	31	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0680	16519	T	C	0	20	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0681	73	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0681	150	C	T	2	613	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0681	263	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0681	750	A	G	0	685	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0681	896	A	G	5	676	upstream_gene_variant	MODIFIER	RNR1	8.00E-04
HLI-0681	1438	A	G	0	695	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0681	1721	C	T	5	624	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0681	2706	A	G	0	633	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0681	3197	T	C	8	648	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0681	4732	A	G	4	688	missense_variant	MODERATE	ND2	0.0059
HLI-0681	4769	A	G	0	752	synonymous_variant	LOW	ND2	0.9767
HLI-0681	7028	C	T	1	738	synonymous_variant	LOW	COX1	0.8089
HLI-0681	7337	G	A	3	701	synonymous_variant	LOW	COX1	0.0119
HLI-0681	7768	A	G	7	633	synonymous_variant	LOW	COX2	0.0186
HLI-0681	9477	G	A	2	644	missense_variant	MODERATE	COX3	0.0387
HLI-0681	11329	A	G	3	672	synonymous_variant	LOW	ND4	6.00E-04
HLI-0681	11467	A	G	0	713	synonymous_variant	LOW	ND4	0.1231
HLI-0681	11719	G	A	0	632	synonymous_variant	LOW	ND4	0.7756
HLI-0681	12308	A	G	0	553	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0681	12372	G	A	1	584	synonymous_variant	LOW	ND5	0.1329
HLI-0681	13617	T	C	4	655	synonymous_variant	LOW	ND5	0.038
HLI-0681	13637	A	G	5	690	missense_variant	MODERATE	ND5	0.0074
HLI-0681	14182	T	C	2	615	synonymous_variant	LOW	ND6	0.0254
HLI-0681	14766	C	T	3	673	missense_variant	MODERATE	CYTB	0.7696
HLI-0681	15326	A	G	0	560	missense_variant	MODERATE	CYTB	0.9868

HLI-0681	15511	T	C	4	531	synonymous_variant	LOW	CYTB	0.0023
HLI-0681	16239	C	T	5	631	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0681	16311	T	C	5	568	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0682	11020	A	G	1	565	synonymous_variant	LOW	ND4	0.0019
HLI-0682	16231	T	C	0	703	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0682	16311	T	C	0	663	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0683	207	G	A	1	444	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0683	6216	T	C	0	675	synonymous_variant	LOW	COX1	0.0056
HLI-0683	6632	T	C	0	795	synonymous_variant	LOW	COX1	6.00E-04
HLI-0683	16051	A	G	0	472	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0684	73	A	G	0	330	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0684	242	C	T	0	314	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0684	263	A	G	0	286	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0684	295	C	T	0	204	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0684	462	C	T	3	550	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0684	489	T	C	1	630	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0684	750	A	G	0	681	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0684	1438	A	G	0	662	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0684	2158	T	C	1	484	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0684	2706	A	G	0	659	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0684	3010	G	A	3	646	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0684	4216	T	C	4	656	missense_variant	MODERATE	ND1	0.0991
HLI-0684	4769	A	G	1	552	synonymous_variant	LOW	ND2	0.9767
HLI-0684	5460	G	A	1	658	missense_variant	MODERATE	ND2	0.0651
HLI-0684	7028	C	T	1	696	synonymous_variant	LOW	COX1	0.8089
HLI-0684	8269	G	A	0	554	stop_retained_variant	LOW	COX2	0.0127
HLI-0684	8557	G	A	0	510	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0684	10398	A	G	1	606	missense_variant	MODERATE	ND3	0.445
HLI-0684	11251	A	G	0	627	synonymous_variant	LOW	ND4	0.0932
HLI-0684	11719	G	A	3	597	synonymous_variant	LOW	ND4	0.7756
HLI-0684	12007	G	A	2	503	synonymous_variant	LOW	ND4	0.0639
HLI-0684	12612	A	G	2	584	synonymous_variant	LOW	ND5	0.0506
HLI-0684	13708	G	A	1	551	missense_variant	MODERATE	ND5	0.0717
HLI-0684	13879	T	C	1	517	missense_variant	MODERATE	ND5	0.0073
HLI-0684	14022	A	G	1	551	synonymous_variant	LOW	ND5	0.0366
HLI-0684	14766	C	T	0	747	missense_variant	MODERATE	CYTB	0.7696
HLI-0684	15326	A	G	1	585	missense_variant	MODERATE	CYTB	0.9868
HLI-0684	15452	C	A	6	498	missense_variant	MODERATE	CYTB	0.0933
HLI-0684	16069	C	T	2	560	upstream_gene_variant	MODIFIER	DLoop	0.0496

HLI-0684	16126	T	C	0	584	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0684	16145	G	A	0	599	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0684	16172	T	C	0	594	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0684	16261	C	T	0	552	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0685	73	A	G	0	332	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0685	146	T	C	0	572	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0685	152	T	C	0	588	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0685	195	T	C	1	558	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0685	263	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0685	750	A	G	0	734	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0685	769	G	A	0	795	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0685	1018	G	A	0	743	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0685	1438	A	G	0	680	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0685	2416	T	C	1	635	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0685	2706	A	G	1	707	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0685	2789	C	T	3	777	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0685	3336	T	C	0	640	synonymous_variant	LOW	ND1	0.0039
HLI-0685	3594	C	T	2	593	synonymous_variant	LOW	ND1	0.0789
HLI-0685	3918	G	A	1	614	synonymous_variant	LOW	ND1	0.009
HLI-0685	4104	A	G	1	536	synonymous_variant	LOW	ND1	0.0785
HLI-0685	4769	A	G	1	634	synonymous_variant	LOW	ND2	0.9767
HLI-0685	5285	A	G	0	659	synonymous_variant	LOW	ND2	0.0049
HLI-0685	7028	C	T	2	742	synonymous_variant	LOW	COX1	0.8089
HLI-0685	7175	T	C	0	661	synonymous_variant	LOW	COX1	0.0224
HLI-0685	7256	C	T	0	685	synonymous_variant	LOW	COX1	0.0784
HLI-0685	7274	C	T	2	657	synonymous_variant	LOW	COX1	0.0214
HLI-0685	7521	G	A	0	545	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0685	7771	A	G	2	676	synonymous_variant	LOW	COX2	0.0223
HLI-0685	8206	G	A	0	666	synonymous_variant	LOW	COX2	0.0287
HLI-0685	8701	A	G	0	576	missense_variant	MODERATE	ATP6	0.3391
HLI-0685	9221	A	G	1	670	synonymous_variant	LOW	COX3	0.0277
HLI-0685	9428	T	C	1	698	synonymous_variant	LOW	COX3	5.00E-04
HLI-0685	9540	T	C	1	674	synonymous_variant	LOW	COX3	0.339
HLI-0685	10115	T	C	1	713	synonymous_variant	LOW	ND3	0.0278
HLI-0685	10398	A	G	0	627	missense_variant	MODERATE	ND3	0.445
HLI-0685	10873	T	C	0	652	synonymous_variant	LOW	ND4	0.3389
HLI-0685	11719	G	A	1	656	synonymous_variant	LOW	ND4	0.7756
HLI-0685	11896	C	T	1	664	synonymous_variant	LOW	ND4	0
HLI-0685	11914	G	A	1	717	synonymous_variant	LOW	ND4	0.1112

HLI-0685	11944	T	C	1	694	synonymous_variant	LOW	ND4	0.0331
HLI-0685	12693	A	G	3	648	synonymous_variant	LOW	ND5	0.0205
HLI-0685	12705	C	T	3	706	synonymous_variant	LOW	ND5	0.4212
HLI-0685	13590	G	A	1	634	synonymous_variant	LOW	ND5	0.0586
HLI-0685	13650	C	T	2	671	synonymous_variant	LOW	ND5	0.079
HLI-0685	13803	A	G	1	484	synonymous_variant	LOW	ND5	0.0216
HLI-0685	14566	A	G	1	665	synonymous_variant	LOW	ND6	0.0214
HLI-0685	14766	C	T	1	640	missense_variant	MODERATE	CYTB	0.7696
HLI-0685	15244	A	G	1	625	synonymous_variant	LOW	CYTB	0.0103
HLI-0685	15301	G	A	0	664	synonymous_variant	LOW	CYTB	0.2912
HLI-0685	15326	A	G	0	675	missense_variant	MODERATE	CYTB	0.9868
HLI-0685	15629	T	C	0	623	synonymous_variant	LOW	CYTB	0.0062
HLI-0685	15784	T	C	0	653	synonymous_variant	LOW	CYTB	0.0363
HLI-0685	16223	C	T	2	571	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0685	16278	C	T	0	574	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0685	16286	C	T	0	556	upstream_gene_variant	MODIFIER	DLoop	0.0052
HLI-0685	16294	C	T	0	553	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0685	16309	A	G	0	556	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0685	16390	G	A	0	548	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0686	73	A	G	1	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0686	207	G	A	1	326	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0686	263	A	G	0	198	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0686	499	G	A	1	368	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0686	750	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0686	827	A	G	1	643	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0686	1438	A	G	1	583	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0686	2706	A	G	0	601	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0686	2836	C	T	1	593	upstream_gene_variant	MODIFIER	RNR2	6.00E-04
HLI-0686	4769	A	G	0	515	synonymous_variant	LOW	ND2	0.9767
HLI-0686	4820	G	A	0	539	synonymous_variant	LOW	ND2	0.0239
HLI-0686	6023	G	A	1	444	synonymous_variant	LOW	COX1	0.008
HLI-0686	6216	T	C	0	542	synonymous_variant	LOW	COX1	0.0056
HLI-0686	6413	T	C	0	586	synonymous_variant	LOW	COX1	0.0062
HLI-0686	7028	C	T	3	627	synonymous_variant	LOW	COX1	0.8089
HLI-0686	11719	G	A	0	542	synonymous_variant	LOW	ND4	0.7756
HLI-0686	13590	G	A	3	495	synonymous_variant	LOW	ND5	0.0586
HLI-0686	14004	C	T	1	476	synonymous_variant	LOW	ND5	1.00E-04
HLI-0686	14053	A	G	0	488	missense_variant	MODERATE	ND5	0.0046
HLI-0686	14766	C	T	1	518	missense_variant	MODERATE	CYTB	0.7696

HLI-0686	15326	A	G	0	491	missense_variant	MODERATE	CYTB	0.9868
HLI-0686	15459	C	T	1	430	missense_variant	MODERATE	CYTB	3.00E-04
HLI-0686	15535	C	T	1	445	synonymous_variant	LOW	CYTB	0.023
HLI-0686	16131	T	C	0	235	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0686	16136	T	C	0	227	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0686	16217	T	C	0	139	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0686	16519	T	C	0	192	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0687	73	A	G	0	363	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0687	146	T	C	0	636	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0687	152	T	C	0	641	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0687	263	A	G	0	272	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0687	709	G	A	1	752	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0687	750	A	G	0	790	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0687	1438	A	G	0	732	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0687	1811	A	G	0	695	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0687	2706	A	G	0	724	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0687	3480	A	G	0	604	synonymous_variant	LOW	ND1	0.0392
HLI-0687	4561	T	C	1	625	missense_variant	MODERATE	ND2	0.0065
HLI-0687	4769	A	G	1	636	synonymous_variant	LOW	ND2	0.9767
HLI-0687	7028	C	T	3	768	synonymous_variant	LOW	COX1	0.8089
HLI-0687	9055	G	A	0	699	missense_variant	MODERATE	ATP6	0.0425
HLI-0687	9698	T	C	0	699	synonymous_variant	LOW	COX3	0.0405
HLI-0687	9716	T	C	1	773	synonymous_variant	LOW	COX3	0.0108
HLI-0687	10398	A	G	1	795	missense_variant	MODERATE	ND3	0.445
HLI-0687	10550	A	G	1	713	synonymous_variant	LOW	ND4L	0.0376
HLI-0687	11204	T	C	0	647	missense_variant	MODERATE	ND4	0.003
HLI-0687	11299	T	C	1	621	synonymous_variant	LOW	ND4	0.0417
HLI-0687	11467	A	G	0	659	synonymous_variant	LOW	ND4	0.1231
HLI-0687	11719	G	A	1	695	synonymous_variant	LOW	ND4	0.7756
HLI-0687	12308	A	G	2	674	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0687	12372	G	A	1	707	synonymous_variant	LOW	ND5	0.1329
HLI-0687	12870	C	T	4	696	synonymous_variant	LOW	ND5	5.00E-04
HLI-0687	14167	C	T	1	653	synonymous_variant	LOW	ND6	0.0385
HLI-0687	14750	A	G	0	689	missense_variant	MODERATE	CYTB	8.00E-04
HLI-0687	14766	C	T	1	755	missense_variant	MODERATE	CYTB	0.7696
HLI-0687	14798	T	C	1	721	missense_variant	MODERATE	CYTB	0.0651
HLI-0687	15326	A	G	1	651	missense_variant	MODERATE	CYTB	0.9868
HLI-0687	16124	T	C	0	638	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0687	16224	T	C	0	645	upstream_gene_variant	MODIFIER	DLoop	0.0423

HLI-0687	16293	A	G	0	687	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0687	16311	T	C	0	667	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0687	16519	T	C	0	303	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0688	73	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0688	93	A	G	2	251	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0688	146	T	C	0	342	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0688	150	C	T	0	350	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0688	152	T	C	0	356	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0688	182	C	T	0	397	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0688	195	T	C	0	402	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0688	198	C	T	0	409	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0688	263	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0688	325	C	T	0	266	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0688	680	T	C	0	671	upstream_gene_variant	MODIFIER	RNR1	0.0026
HLI-0688	709	G	A	0	731	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0688	750	A	G	1	707	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0688	769	G	A	0	681	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0688	1018	G	A	1	750	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0688	1040	T	C	1	844	upstream_gene_variant	MODIFIER	RNR1	0.0024
HLI-0688	1438	A	G	0	675	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0688	1442	G	A	1	699	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0688	2332	C	T	1	563	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0688	2416	T	C	0	594	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0688	2706	A	G	1	651	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0688	3200	T	A	0	681	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0688	3594	C	T	0	567	synonymous_variant	LOW	ND1	0.0789
HLI-0688	4104	A	G	2	478	synonymous_variant	LOW	ND1	0.0785
HLI-0688	4769	A	G	5	646	synonymous_variant	LOW	ND2	0.9767
HLI-0688	7028	C	T	0	683	synonymous_variant	LOW	COX1	0.8089
HLI-0688	7256	C	T	0	635	synonymous_variant	LOW	COX1	0.0784
HLI-0688	7521	G	A	0	570	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0688	7624	T	A	0	572	synonymous_variant	LOW	COX2	0.0047
HLI-0688	8206	G	A	0	692	synonymous_variant	LOW	COX2	0.0287
HLI-0688	8567	T	C	0	595	missense_variant	MODERATE	ATP6/8	0.0021
HLI-0688	8701	A	G	0	618	missense_variant	MODERATE	ATP6	0.3391
HLI-0688	8772	T	C	0	676	synonymous_variant	LOW	ATP6	0.0033
HLI-0688	9063	A	G	1	658	synonymous_variant	LOW	ATP6	6.00E-04
HLI-0688	9221	A	G	1	733	synonymous_variant	LOW	COX3	0.0277
HLI-0688	9540	T	C	0	638	synonymous_variant	LOW	COX3	0.339

HLI-0688	10115	T	C	0	722	synonymous_variant	LOW	ND3	0.0278
HLI-0688	10398	A	G	0	688	missense_variant	MODERATE	ND3	0.445
HLI-0688	10790	T	C	0	605	synonymous_variant	LOW	ND4	0.0027
HLI-0688	10873	T	C	0	611	synonymous_variant	LOW	ND4	0.3389
HLI-0688	11719	G	A	2	637	synonymous_variant	LOW	ND4	0.7756
HLI-0688	11944	T	C	1	645	synonymous_variant	LOW	ND4	0.0331
HLI-0688	12236	G	A	1	575	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0688	12705	C	T	0	622	synonymous_variant	LOW	ND5	0.4212
HLI-0688	13590	G	A	0	598	synonymous_variant	LOW	ND5	0.0586
HLI-0688	13650	C	T	0	641	synonymous_variant	LOW	ND5	0.079
HLI-0688	13928	G	C	0	645	missense_variant	MODERATE	ND5	0.0484
HLI-0688	13958	G	C	0	693	missense_variant	MODERATE	ND5	0.0028
HLI-0688	14766	C	T	2	660	missense_variant	MODERATE	CYTB	0.7696
HLI-0688	15110	G	A	0	757	missense_variant	MODERATE	CYTB	0.009
HLI-0688	15217	G	A	1	564	synonymous_variant	LOW	CYTB	0.0104
HLI-0688	15301	G	A	0	552	synonymous_variant	LOW	CYTB	0.2912
HLI-0688	15313	T	C	0	554	synonymous_variant	LOW	CYTB	0.0022
HLI-0688	15326	A	G	0	561	missense_variant	MODERATE	CYTB	0.9868
HLI-0688	15849	C	T	2	612	missense_variant	MODERATE	CYTB	0.0027
HLI-0688	16223	C	T	2	591	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0688	16264	C	T	1	616	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0688	16278	C	T	0	592	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0688	16311	T	C	0	521	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0688	16390	G	A	1	479	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0689	64	C	T	2	180	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0689	150	C	T	0	496	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0689	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0689	750	A	G	0	675	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0689	1438	A	G	1	666	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0689	2442	T	C	0	628	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0689	2706	A	G	2	658	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0689	3847	T	C	0	636	synonymous_variant	LOW	ND1	0.0061
HLI-0689	4769	A	G	2	615	synonymous_variant	LOW	ND2	0.9767
HLI-0689	7028	C	T	1	757	synonymous_variant	LOW	COX1	0.8089
HLI-0689	7679	T	C	3	677	missense_variant	MODERATE	COX2	0.0013
HLI-0689	13188	C	T	3	651	synonymous_variant	LOW	ND5	0.0053
HLI-0689	14766	C	T	1	632	missense_variant	MODERATE	CYTB	0.7696
HLI-0689	15326	A	G	0	599	missense_variant	MODERATE	CYTB	0.9868
HLI-0689	15628	A	G	1	698	synonymous_variant	LOW	CYTB	2.00E-04

HLI-0689	16126	T	C	1	605	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0689	16362	T	C	3	491	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0690	73	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0690	195	T	C	0	459	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0690	263	A	G	0	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0690	489	T	C	0	410	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0690	750	A	G	0	640	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0690	813	A	G	1	703	upstream_gene_variant	MODIFIER	RNR1	0.0044
HLI-0690	930	G	A	3	672	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0690	1438	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0690	2706	A	G	0	598	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0690	3705	G	A	0	600	synonymous_variant	LOW	ND1	0.0138
HLI-0690	4769	A	G	2	611	synonymous_variant	LOW	ND2	0.9767
HLI-0690	6446	G	A	10	660	synonymous_variant	LOW	COX1	0.0061
HLI-0690	6671	T	C	4	698	synonymous_variant	LOW	COX1	0.0071
HLI-0690	6680	T	C	4	712	synonymous_variant	LOW	COX1	0.0226
HLI-0690	7028	C	T	5	664	synonymous_variant	LOW	COX1	0.8089
HLI-0690	7853	G	A	3	620	missense_variant	MODERATE	COX2	0.0197
HLI-0690	8701	A	G	1	573	missense_variant	MODERATE	ATP6	0.3391
HLI-0690	8865	G	A	0	601	synonymous_variant	LOW	ATP6	0.003
HLI-0690	9540	T	C	1	581	synonymous_variant	LOW	COX3	0.339
HLI-0690	10398	A	G	0	612	missense_variant	MODERATE	ND3	0.445
HLI-0690	10400	C	T	0	621	synonymous_variant	LOW	ND3	0.2131
HLI-0690	10873	T	C	1	604	synonymous_variant	LOW	ND4	0.3389
HLI-0690	11353	T	C	1	596	synonymous_variant	LOW	ND4	0.0029
HLI-0690	11719	G	A	0	601	synonymous_variant	LOW	ND4	0.7756
HLI-0690	11914	G	A	0	642	synonymous_variant	LOW	ND4	0.1112
HLI-0690	12346	C	T	0	565	missense_variant	MODERATE	ND5	0.0056
HLI-0690	12403	C	T	3	565	missense_variant	MODERATE	ND5	0.0043
HLI-0690	12528	G	A	3	556	synonymous_variant	LOW	ND5	6.00E-04
HLI-0690	12705	C	T	4	584	synonymous_variant	LOW	ND5	0.4212
HLI-0690	12950	A	C	4	628	missense_variant	MODERATE	ND5	0.0043
HLI-0690	14110	T	C	0	531	missense_variant	MODERATE	ND5	0.0096
HLI-0690	14766	C	T	2	628	missense_variant	MODERATE	CYTB	0.7696
HLI-0690	14783	T	C	0	712	synonymous_variant	LOW	CYTB	0.2126
HLI-0690	15043	G	A	2	684	synonymous_variant	LOW	CYTB	0.2362
HLI-0690	15301	G	A	3	499	synonymous_variant	LOW	CYTB	0.2912
HLI-0690	15326	A	G	1	542	missense_variant	MODERATE	CYTB	0.9868
HLI-0690	16129	G	A	0	347	upstream_gene_variant	MODIFIER	DLoop	0.1301

HLI-0690	16249	T	C	2	289	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0690	16311	T	C	0	438	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0690	16359	T	C	0	398	upstream_gene_variant	MODIFIER	DLoop	0.0031
HLI-0690	16519	T	C	0	206	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0691	73	A	G	1	301	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0691	185	G	A	6	462	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0691	228	G	A	1	273	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0691	263	A	G	0	294	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0691	295	C	T	0	227	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0691	462	C	T	8	496	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0691	489	T	C	2	508	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0691	750	A	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0691	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0691	2706	A	G	0	610	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0691	3010	G	A	1	618	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0691	4216	T	C	0	620	missense_variant	MODERATE	ND1	0.0991
HLI-0691	4769	A	G	0	594	synonymous_variant	LOW	ND2	0.9767
HLI-0691	7028	C	T	3	673	synonymous_variant	LOW	COX1	0.8089
HLI-0691	9120	A	G	3	635	synonymous_variant	LOW	ATP6	8.00E-04
HLI-0691	9632	A	G	2	586	synonymous_variant	LOW	COX3	0.0015
HLI-0691	10398	A	G	0	593	missense_variant	MODERATE	ND3	0.445
HLI-0691	11251	A	G	0	609	synonymous_variant	LOW	ND4	0.0932
HLI-0691	11719	G	A	0	603	synonymous_variant	LOW	ND4	0.7756
HLI-0691	12083	T	G	3	558	missense_variant	MODERATE	ND4	0.001
HLI-0691	12612	A	G	3	615	synonymous_variant	LOW	ND5	0.0506
HLI-0691	13708	G	A	2	569	missense_variant	MODERATE	ND5	0.0717
HLI-0691	14766	C	T	4	597	missense_variant	MODERATE	CYTB	0.7696
HLI-0691	14798	T	C	1	698	missense_variant	MODERATE	CYTB	0.0651
HLI-0691	15326	A	G	0	536	missense_variant	MODERATE	CYTB	0.9868
HLI-0691	15452	C	A	4	517	missense_variant	MODERATE	CYTB	0.0933
HLI-0691	16069	C	T	4	629	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0691	16126	T	C	2	650	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0692	73	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0692	150	C	T	0	569	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0692	263	A	G	1	281	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0692	750	A	G	1	652	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0692	1303	G	A	0	741	upstream_gene_variant	MODIFIER	RNR1	9.00E-04
HLI-0692	1438	A	G	0	677	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0692	2706	A	G	1	597	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0692	3192	C	T	0	650	upstream_gene_variant	MODIFIER	RNR2	4.00E-04
HLI-0692	3197	T	C	0	654	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0692	3591	G	A	0	557	synonymous_variant	LOW	ND1	0.0082
HLI-0692	4592	T	C	0	611	synonymous_variant	LOW	ND2	0.0013
HLI-0692	4769	A	G	0	613	synonymous_variant	LOW	ND2	0.9767
HLI-0692	7028	C	T	5	640	synonymous_variant	LOW	COX1	0.8089
HLI-0692	9477	G	A	0	602	missense_variant	MODERATE	COX3	0.0387
HLI-0692	11296	C	T	2	641	synonymous_variant	LOW	ND4	0.0028
HLI-0692	11467	A	G	1	646	synonymous_variant	LOW	ND4	0.1231
HLI-0692	11719	G	A	1	602	synonymous_variant	LOW	ND4	0.7756
HLI-0692	11938	C	T	1	604	synonymous_variant	LOW	ND4	9.00E-04
HLI-0692	12308	A	G	0	591	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0692	12372	G	A	1	555	synonymous_variant	LOW	ND5	0.1329
HLI-0692	12618	G	A	2	636	synonymous_variant	LOW	ND5	0.0137
HLI-0692	13617	T	C	2	569	synonymous_variant	LOW	ND5	0.038
HLI-0692	14766	C	T	3	642	missense_variant	MODERATE	CYTB	0.7696
HLI-0692	14793	A	G	0	755	missense_variant	MODERATE	CYTB	0.0199
HLI-0692	15218	A	G	1	587	missense_variant	MODERATE	CYTB	0.0169
HLI-0692	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868
HLI-0692	16086	T	C	1	563	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0692	16239	C	T	2	596	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0692	16256	C	T	1	581	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0692	16270	C	T	0	537	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0692	16399	A	G	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0693	73	A	G	0	324	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0693	195	T	C	1	487	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0693	263	A	G	0	195	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0693	489	T	C	0	414	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0693	750	A	G	1	689	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0693	1438	A	G	1	685	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0693	2706	A	G	1	838	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0693	4769	A	G	2	636	synonymous_variant	LOW	ND2	0.9767
HLI-0693	6446	G	A	2	662	synonymous_variant	LOW	COX1	0.0061
HLI-0693	6680	T	C	5	737	synonymous_variant	LOW	COX1	0.0226
HLI-0693	7028	C	T	3	758	synonymous_variant	LOW	COX1	0.8089
HLI-0693	8701	A	G	0	660	missense_variant	MODERATE	ATP6	0.3391
HLI-0693	9380	G	A	1	746	synonymous_variant	LOW	COX3	0.0094
HLI-0693	9540	T	C	1	705	synonymous_variant	LOW	COX3	0.339
HLI-0693	10398	A	G	1	725	missense_variant	MODERATE	ND3	0.445

HLI-0693	10400	C	T	1	739	synonymous_variant	LOW	ND3	0.2131
HLI-0693	10873	T	C	1	677	synonymous_variant	LOW	ND4	0.3389
HLI-0693	10895	A	G	1	707	missense_variant	MODERATE	ND4	7.00E-04
HLI-0693	11719	G	A	0	658	synonymous_variant	LOW	ND4	0.7756
HLI-0693	12403	C	T	7	674	missense_variant	MODERATE	ND5	0.0043
HLI-0693	12705	C	T	4	701	synonymous_variant	LOW	ND5	0.4212
HLI-0693	12940	G	A	5	648	missense_variant	MODERATE	ND5	0.0054
HLI-0693	12950	A	C	5	698	missense_variant	MODERATE	ND5	0.0043
HLI-0693	13111	T	C	2	699	synonymous_variant	LOW	ND5	0.0021
HLI-0693	14110	T	C	0	581	missense_variant	MODERATE	ND5	0.0096
HLI-0693	14180	T	C	1	668	missense_variant	MODERATE	ND6	0.0036
HLI-0693	14766	C	T	1	643	missense_variant	MODERATE	CYTB	0.7696
HLI-0693	14783	T	C	1	706	synonymous_variant	LOW	CYTB	0.2126
HLI-0693	15043	G	A	3	723	synonymous_variant	LOW	CYTB	0.2362
HLI-0693	15262	T	C	3	654	synonymous_variant	LOW	CYTB	0.0036
HLI-0693	15301	G	A	1	709	synonymous_variant	LOW	CYTB	0.2912
HLI-0693	15326	A	G	1	712	missense_variant	MODERATE	CYTB	0.9868
HLI-0693	16093	T	C	9	465	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0693	16129	G	A	1	310	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0693	16223	C	T	2	213	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0693	16249	T	C	1	305	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0693	16311	T	C	2	454	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0693	16399	A	G	2	517	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0693	16519	T	C	3	211	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0694	263	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0694	750	A	G	0	524	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0694	951	G	A	1	603	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0694	11443	A	G	1	571	synonymous_variant	LOW	ND4	1.00E-04
HLI-0694	13395	A	G	0	509	synonymous_variant	LOW	ND5	0.0056
HLI-0694	15326	A	G	0	363	missense_variant	MODERATE	CYTB	0.9868
HLI-0694	16111	C	T	1	398	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0694	16354	C	T	0	389	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0695	73	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0695	146	T	C	0	338	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0695	152	T	C	0	343	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0695	182	C	T	0	316	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0695	185	G	T	0	313	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0695	189	A	G	0	310	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0695	247	G	A	0	112	upstream_gene_variant	MODIFIER	DLoop	0.0498

HLI-0695	263	A	G	0	127	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0695	357	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0695	709	G	A	0	571	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0695	710	T	C	0	577	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0695	750	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0695	769	G	A	0	629	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0695	825	T	A	0	637	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0695	1018	G	A	0	632	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0695	1738	T	C	0	581	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0695	2352	T	C	1	621	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0695	2706	A	G	0	610	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0695	2758	G	A	1	651	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0695	2768	A	G	0	651	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0695	2885	T	C	0	637	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0695	3308	T	C	0	603	start_lost	HIGH	ND1	0.0073
HLI-0695	3594	C	T	3	501	synonymous_variant	LOW	ND1	0.0789
HLI-0695	3666	G	A	0	590	synonymous_variant	LOW	ND1	0.0233
HLI-0695	3693	G	A	0	591	synonymous_variant	LOW	ND1	0.0091
HLI-0695	4104	A	G	1	513	synonymous_variant	LOW	ND1	0.0785
HLI-0695	4769	A	G	2	543	synonymous_variant	LOW	ND2	0.9767
HLI-0695	6548	C	T	3	661	synonymous_variant	LOW	COX1	0.0061
HLI-0695	6827	T	C	1	552	synonymous_variant	LOW	COX1	0.0072
HLI-0695	6989	A	G	2	624	synonymous_variant	LOW	COX1	0.0061
HLI-0695	7028	C	T	1	612	synonymous_variant	LOW	COX1	0.8089
HLI-0695	7055	A	G	1	553	synonymous_variant	LOW	COX1	0.0188
HLI-0695	7146	A	G	3	289	missense_variant	MODERATE	COX1	0.0497
HLI-0695	7256	C	T	0	457	synonymous_variant	LOW	COX1	0.0784
HLI-0695	7389	T	C	1	477	missense_variant	MODERATE	COX1	0.0201
HLI-0695	7521	G	A	1	381	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0695	7867	C	T	2	630	synonymous_variant	LOW	COX2	0.0076
HLI-0695	8248	A	G	1	609	synonymous_variant	LOW	COX2	0.0061
HLI-0695	8282	C	T	4	655	upstream_gene_variant	MODIFIER	Unannotated	7.00E-04
HLI-0695	8468	C	T	2	470	synonymous_variant	LOW	ATP8	0.0501
HLI-0695	8655	C	T	6	494	synonymous_variant	LOW	ATP6	0.0511
HLI-0695	8701	A	G	3	527	missense_variant	MODERATE	ATP6	0.3391
HLI-0695	9540	T	C	0	643	synonymous_variant	LOW	COX3	0.339
HLI-0695	10398	A	G	0	627	missense_variant	MODERATE	ND3	0.445
HLI-0695	10688	G	A	0	545	synonymous_variant	LOW	ND4L	0.0515
HLI-0695	10810	T	C	0	562	synonymous_variant	LOW	ND4	0.0522

HLI-0695	10873	T	C	0	553	synonymous_variant	LOW	ND4	0.3389
HLI-0695	11719	G	A	1	580	synonymous_variant	LOW	ND4	0.7756
HLI-0695	12171	A	G	2	530	upstream_gene_variant	MODIFIER	TRNH	0.0011
HLI-0695	12519	T	C	2	563	synonymous_variant	LOW	ND5	0.007
HLI-0695	12705	C	T	4	628	synonymous_variant	LOW	ND5	0.4212
HLI-0695	12891	C	T	3	625	synonymous_variant	LOW	ND5	7.00E-04
HLI-0695	13105	A	G	2	568	missense_variant	MODERATE	ND5	0.076
HLI-0695	13506	C	T	3	543	synonymous_variant	LOW	ND5	0.0506
HLI-0695	13650	C	T	3	569	synonymous_variant	LOW	ND5	0.079
HLI-0695	13789	T	C	0	418	missense_variant	MODERATE	ND5	0.0185
HLI-0695	13893	A	G	0	459	synonymous_variant	LOW	ND5	5.00E-04
HLI-0695	14178	T	C	0	542	missense_variant	MODERATE	ND6	0.0225
HLI-0695	14323	G	A	1	496	synonymous_variant	LOW	ND6	0.0058
HLI-0695	14560	G	A	3	586	synonymous_variant	LOW	ND6	0.0235
HLI-0695	14766	C	T	0	567	missense_variant	MODERATE	CYTB	0.7696
HLI-0695	14769	A	G	0	575	missense_variant	MODERATE	CYTB	0.0121
HLI-0695	15115	T	C	0	634	synonymous_variant	LOW	CYTB	0.0093
HLI-0695	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0695	15519	T	C	0	533	missense_variant	MODERATE	CYTB	0.002
HLI-0695	16093	T	C	23	474	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0695	16111	C	T	0	524	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0695	16126	T	C	0	511	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0695	16223	C	T	2	373	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0695	16239	C	T	2	373	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0695	16270	C	T	0	373	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0695	16278	C	T	0	387	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0695	16293	A	G	0	401	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0695	16311	T	C	0	398	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0695	16519	T	C	0	151	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0696	73	A	G	0	323	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0696	263	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0696	709	G	A	0	637	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0696	750	A	G	1	681	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0696	930	G	A	1	695	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0696	1438	A	G	0	694	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0696	1888	G	A	0	557	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0696	2706	A	G	1	653	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0696	4216	T	C	2	629	missense_variant	MODERATE	ND1	0.0991
HLI-0696	4769	A	G	0	581	synonymous_variant	LOW	ND2	0.9767

HLI-0696	4917	A	G	0	619	missense_variant	MODERATE	ND2	0.0477
HLI-0696	5147	G	A	2	513	synonymous_variant	LOW	ND2	0.0437
HLI-0696	7028	C	T	6	694	synonymous_variant	LOW	COX1	0.8089
HLI-0696	8697	G	A	2	601	synonymous_variant	LOW	ATP6	0.0466
HLI-0696	9254	A	G	2	645	synonymous_variant	LOW	COX3	0.0083
HLI-0696	10463	T	C	3	668	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0696	11251	A	G	0	672	synonymous_variant	LOW	ND4	0.0932
HLI-0696	11719	G	A	0	645	synonymous_variant	LOW	ND4	0.7756
HLI-0696	11812	A	G	0	587	synonymous_variant	LOW	ND4	0.0332
HLI-0696	13368	G	A	0	652	synonymous_variant	LOW	ND5	0.0495
HLI-0696	14233	A	G	1	571	synonymous_variant	LOW	ND6	0.0369
HLI-0696	14766	C	T	3	672	missense_variant	MODERATE	CYTB	0.7696
HLI-0696	14905	G	A	3	787	synonymous_variant	LOW	CYTB	0.0526
HLI-0696	15326	A	G	0	575	missense_variant	MODERATE	CYTB	0.9868
HLI-0696	15452	C	A	7	528	missense_variant	MODERATE	CYTB	0.0933
HLI-0696	15607	A	G	2	533	synonymous_variant	LOW	CYTB	0.0508
HLI-0696	15928	G	A	0	546	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0696	16126	T	C	0	633	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0696	16294	C	T	1	585	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0696	16304	T	C	1	612	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0696	16519	T	C	0	311	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0697	73	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0697	150	C	T	2	589	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0697	263	A	G	1	269	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0697	750	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0697	1438	A	G	1	650	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0697	2706	A	G	0	613	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0697	3197	T	C	0	603	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0697	4769	A	G	1	661	synonymous_variant	LOW	ND2	0.9767
HLI-0697	5656	A	G	5	724	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0697	6341	C	T	0	668	synonymous_variant	LOW	COX1	2.00E-04
HLI-0697	7028	C	T	1	688	synonymous_variant	LOW	COX1	0.8089
HLI-0697	7768	A	G	1	665	synonymous_variant	LOW	COX2	0.0186
HLI-0697	9477	G	A	1	649	missense_variant	MODERATE	COX3	0.0387
HLI-0697	11467	A	G	1	706	synonymous_variant	LOW	ND4	0.1231
HLI-0697	11719	G	A	1	634	synonymous_variant	LOW	ND4	0.7756
HLI-0697	12308	A	G	0	680	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0697	12372	G	A	2	692	synonymous_variant	LOW	ND5	0.1329
HLI-0697	13194	G	A	2	683	synonymous_variant	LOW	ND5	0.0046

HLI-0697	13617	T	C	0	548	synonymous_variant	LOW	ND5	0.038
HLI-0697	14182	T	C	1	606	synonymous_variant	LOW	ND6	0.0254
HLI-0697	14766	C	T	2	613	missense_variant	MODERATE	CYTB	0.7696
HLI-0697	15191	T	C	0	619	synonymous_variant	LOW	CYTB	0.0014
HLI-0697	15326	A	G	0	529	missense_variant	MODERATE	CYTB	0.9868
HLI-0697	16174	C	T	1	552	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0697	16270	C	T	0	517	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0697	16311	T	C	0	568	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0698	73	A	G	0	175	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0698	143	G	A	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0698	146	T	C	0	397	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0698	152	T	C	0	408	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0698	195	T	C	0	447	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0698	263	A	G	1	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0698	750	A	G	0	488	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0698	769	G	A	2	524	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0698	1018	G	A	0	697	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0698	1438	A	G	0	506	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0698	2416	T	C	0	399	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0698	2706	A	G	1	451	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0698	2789	C	T	0	485	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0698	3505	A	G	0	408	missense_variant	MODERATE	ND1	0.0144
HLI-0698	3594	C	T	0	349	synonymous_variant	LOW	ND1	0.0789
HLI-0698	4104	A	G	2	375	synonymous_variant	LOW	ND1	0.0785
HLI-0698	4703	T	C	2	572	synonymous_variant	LOW	ND2	0.0058
HLI-0698	4769	A	G	1	565	synonymous_variant	LOW	ND2	0.9767
HLI-0698	4772	T	C	1	560	synonymous_variant	LOW	ND2	0.0021
HLI-0698	7028	C	T	0	573	synonymous_variant	LOW	COX1	0.8089
HLI-0698	7175	T	C	0	523	synonymous_variant	LOW	COX1	0.0224
HLI-0698	7256	C	T	1	605	synonymous_variant	LOW	COX1	0.0784
HLI-0698	7274	C	T	0	584	synonymous_variant	LOW	COX1	0.0214
HLI-0698	7521	G	A	0	472	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0698	7771	A	G	0	530	synonymous_variant	LOW	COX2	0.0223
HLI-0698	8206	G	A	4	507	synonymous_variant	LOW	COX2	0.0287
HLI-0698	8701	A	G	1	554	missense_variant	MODERATE	ATP6	0.3391
HLI-0698	9221	A	G	1	473	synonymous_variant	LOW	COX3	0.0277
HLI-0698	9540	T	C	0	358	synonymous_variant	LOW	COX3	0.339
HLI-0698	10115	T	C	0	644	synonymous_variant	LOW	ND3	0.0278
HLI-0698	10398	A	G	0	644	missense_variant	MODERATE	ND3	0.445

HLI-0698	10873	T	C	0	457	synonymous_variant	LOW	ND4	0.3389
HLI-0698	11719	G	A	2	530	synonymous_variant	LOW	ND4	0.7756
HLI-0698	11914	G	A	1	530	synonymous_variant	LOW	ND4	0.1112
HLI-0698	11944	T	C	0	572	synonymous_variant	LOW	ND4	0.0331
HLI-0698	12693	A	G	2	520	synonymous_variant	LOW	ND5	0.0205
HLI-0698	12705	C	T	1	581	synonymous_variant	LOW	ND5	0.4212
HLI-0698	12976	C	T	0	404	synonymous_variant	LOW	ND5	6.00E-04
HLI-0698	13590	G	A	0	418	synonymous_variant	LOW	ND5	0.0586
HLI-0698	13650	C	T	1	423	synonymous_variant	LOW	ND5	0.079
HLI-0698	13764	C	T	5	387	synonymous_variant	LOW	ND5	3.00E-04
HLI-0698	13803	A	G	0	439	synonymous_variant	LOW	ND5	0.0216
HLI-0698	13824	A	G	0	442	synonymous_variant	LOW	ND5	4.00E-04
HLI-0698	14566	A	G	1	619	synonymous_variant	LOW	ND6	0.0214
HLI-0698	14766	C	T	5	613	missense_variant	MODERATE	CYTB	0.7696
HLI-0698	15301	G	A	0	341	synonymous_variant	LOW	CYTB	0.2912
HLI-0698	15326	A	G	0	339	missense_variant	MODERATE	CYTB	0.9868
HLI-0698	15784	T	C	2	415	synonymous_variant	LOW	CYTB	0.0363
HLI-0698	16223	C	T	0	502	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0698	16234	C	T	0	481	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0698	16249	T	C	0	491	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0698	16278	C	T	0	408	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0698	16294	C	T	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0698	16295	C	T	0	376	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0698	16390	G	A	0	343	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0699	73	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0699	146	T	C	0	322	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0699	152	T	C	0	328	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0699	182	C	T	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0699	185	G	C	0	298	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0699	195	T	C	0	275	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0699	198	C	T	0	275	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0699	204	T	C	0	289	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0699	207	G	A	0	295	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0699	263	A	G	0	135	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0699	750	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0699	769	G	A	3	703	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0699	1018	G	A	2	669	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0699	1438	A	G	0	672	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0699	1442	G	A	0	701	upstream_gene_variant	MODIFIER	RNR1	0.0061

HLI-0699	1706	C	T	0	622	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0699	2332	C	T	1	534	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0699	2358	A	G	0	584	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0699	2416	T	C	0	603	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0699	2706	A	G	0	551	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0699	3594	C	T	1	473	synonymous_variant	LOW	ND1	0.0789
HLI-0699	4104	A	G	0	547	synonymous_variant	LOW	ND1	0.0785
HLI-0699	4158	A	G	1	578	synonymous_variant	LOW	ND1	0.0023
HLI-0699	4370	T	C	0	503	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0699	4767	A	G	0	627	missense_variant	MODERATE	ND2	0.0029
HLI-0699	4769	A	G	0	640	synonymous_variant	LOW	ND2	0.9767
HLI-0699	5027	C	T	1	541	synonymous_variant	LOW	ND2	0.003
HLI-0699	5331	C	A	3	594	missense_variant	MODERATE	ND2	0.0022
HLI-0699	5814	T	C	0	699	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0699	6113	A	G	0	662	synonymous_variant	LOW	COX1	3.00E-04
HLI-0699	6713	C	T	2	703	synonymous_variant	LOW	COX1	0.0028
HLI-0699	7028	C	T	2	686	synonymous_variant	LOW	COX1	0.8089
HLI-0699	7256	C	T	1	605	synonymous_variant	LOW	COX1	0.0784
HLI-0699	7521	G	A	1	544	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0699	7624	T	A	2	578	synonymous_variant	LOW	COX2	0.0047
HLI-0699	8080	C	T	0	605	synonymous_variant	LOW	COX2	0.0022
HLI-0699	8206	G	A	0	614	synonymous_variant	LOW	COX2	0.0287
HLI-0699	8387	G	A	1	466	missense_variant	MODERATE	ATP8	0.0028
HLI-0699	8701	A	G	1	591	missense_variant	MODERATE	ATP6	0.3391
HLI-0699	9221	A	G	0	662	synonymous_variant	LOW	COX3	0.0277
HLI-0699	9540	T	C	0	626	synonymous_variant	LOW	COX3	0.339
HLI-0699	10101	T	C	0	707	synonymous_variant	LOW	ND3	0.0026
HLI-0699	10115	T	C	0	800	synonymous_variant	LOW	ND3	0.0278
HLI-0699	10172	G	A	2	829	synonymous_variant	LOW	ND3	0.0084
HLI-0699	10398	A	G	1	650	missense_variant	MODERATE	ND3	0.445
HLI-0699	10873	T	C	0	583	synonymous_variant	LOW	ND4	0.3389
HLI-0699	11719	G	A	0	549	synonymous_variant	LOW	ND4	0.7756
HLI-0699	11944	T	C	0	588	synonymous_variant	LOW	ND4	0.0331
HLI-0699	12011	T	C	1	586	missense_variant	MODERATE	ND4	2.00E-04
HLI-0699	12236	G	A	4	556	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0699	12705	C	T	2	575	synonymous_variant	LOW	ND5	0.4212
HLI-0699	12948	A	G	1	611	synonymous_variant	LOW	ND5	0.0022
HLI-0699	13590	G	A	1	554	synonymous_variant	LOW	ND5	0.0586
HLI-0699	13650	C	T	1	569	synonymous_variant	LOW	ND5	0.079

HLI-0699	14059	A	G	0	525	missense_variant	MODERATE	ND5	0.0022
HLI-0699	14766	C	T	3	593	missense_variant	MODERATE	CYTB	0.7696
HLI-0699	15110	G	A	0	619	missense_variant	MODERATE	CYTB	0.009
HLI-0699	15217	G	A	0	556	synonymous_variant	LOW	CYTB	0.0104
HLI-0699	15301	G	A	0	550	synonymous_variant	LOW	CYTB	0.2912
HLI-0699	15326	A	G	0	521	missense_variant	MODERATE	CYTB	0.9868
HLI-0699	16114	C	A	0	426	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0699	16129	G	A	0	363	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0699	16213	G	A	0	199	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0699	16223	C	T	0	217	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0699	16278	C	T	1	363	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0699	16390	G	A	0	413	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0700	73	A	G	0	350	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0700	263	A	G	0	341	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0700	750	A	G	1	713	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0700	1438	A	G	1	765	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0700	2706	A	G	1	685	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0700	3420	C	T	4	638	synonymous_variant	LOW	ND1	4.00E-04
HLI-0700	3450	C	T	3	692	synonymous_variant	LOW	ND1	0.0084
HLI-0700	4769	A	G	1	651	synonymous_variant	LOW	ND2	0.9767
HLI-0700	5773	G	A	3	798	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0700	6221	T	C	2	686	synonymous_variant	LOW	COX1	0.0306
HLI-0700	7028	C	T	0	766	synonymous_variant	LOW	COX1	0.8089
HLI-0700	8701	A	G	0	656	missense_variant	MODERATE	ATP6	0.3391
HLI-0700	9053	G	A	1	703	missense_variant	MODERATE	ATP6	0.0196
HLI-0700	9067	A	G	1	775	missense_variant	MODERATE	ATP6	7.00E-04
HLI-0700	9449	C	T	0	749	synonymous_variant	LOW	COX3	0.0125
HLI-0700	9540	T	C	0	729	synonymous_variant	LOW	COX3	0.339
HLI-0700	10086	A	G	0	757	missense_variant	MODERATE	ND3	0.0088
HLI-0700	10398	A	G	1	737	missense_variant	MODERATE	ND3	0.445
HLI-0700	10640	T	C	0	654	synonymous_variant	LOW	ND4L	0.0044
HLI-0700	10873	T	C	1	495	synonymous_variant	LOW	ND4	0.3389
HLI-0700	11069	A	G	2	653	missense_variant	MODERATE	ND4	1.00E-04
HLI-0700	11719	G	A	0	717	synonymous_variant	LOW	ND4	0.7756
HLI-0700	12705	C	T	0	715	synonymous_variant	LOW	ND5	0.4212
HLI-0700	13105	A	G	0	657	missense_variant	MODERATE	ND5	0.076
HLI-0700	13914	C	A	0	630	synonymous_variant	LOW	ND5	0.0091
HLI-0700	14766	C	T	4	642	missense_variant	MODERATE	CYTB	0.7696
HLI-0700	15301	G	A	0	654	synonymous_variant	LOW	CYTB	0.2912

HLI-0700	15311	A	G	0	686	missense_variant	MODERATE	CYTB	0.008
HLI-0700	15326	A	G	0	676	missense_variant	MODERATE	CYTB	0.9868
HLI-0700	15550	C	T	2	640	synonymous_variant	LOW	CYTB	0.0032
HLI-0700	15824	A	G	0	712	missense_variant	MODERATE	CYTB	0.0083
HLI-0700	16124	T	C	2	684	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0700	16223	C	T	1	692	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0700	16278	C	T	3	708	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0700	16362	T	C	0	570	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0700	16527	C	T	1	375	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0701	72	T	C	0	327	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0701	263	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0701	750	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0701	1438	A	G	0	741	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0701	2706	A	G	0	579	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0701	4580	G	A	5	678	synonymous_variant	LOW	ND2	0.0169
HLI-0701	4639	T	C	3	736	missense_variant	MODERATE	ND2	0.0034
HLI-0701	4769	A	G	2	628	synonymous_variant	LOW	ND2	0.9767
HLI-0701	5263	C	T	3	539	missense_variant	MODERATE	ND2	0.0058
HLI-0701	7028	C	T	3	683	synonymous_variant	LOW	COX1	0.8089
HLI-0701	8869	A	G	0	647	missense_variant	MODERATE	ATP6	0.0028
HLI-0701	14845	C	T	1	661	synonymous_variant	LOW	CYTB	7.00E-04
HLI-0701	15326	A	G	0	554	missense_variant	MODERATE	CYTB	0.9868
HLI-0701	15904	C	T	1	667	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0701	16298	T	C	0	571	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0702	73	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0702	263	A	G	0	313	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0702	750	A	G	0	481	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0702	1438	A	G	1	500	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0702	1700	T	C	1	523	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0702	2706	A	G	0	425	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0702	3197	T	C	1	566	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0702	4769	A	G	0	517	synonymous_variant	LOW	ND2	0.9767
HLI-0702	5495	T	C	0	647	synonymous_variant	LOW	ND2	0.0051
HLI-0702	7028	C	T	6	496	synonymous_variant	LOW	COX1	0.8089
HLI-0702	9477	G	A	1	534	missense_variant	MODERATE	COX3	0.0387
HLI-0702	11467	A	G	0	522	synonymous_variant	LOW	ND4	0.1231
HLI-0702	11719	G	A	1	522	synonymous_variant	LOW	ND4	0.7756
HLI-0702	12308	A	G	0	560	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0702	12372	G	A	0	586	synonymous_variant	LOW	ND5	0.1329

HLI-0702	13617	T	C	1	434	synonymous_variant	LOW	ND5	0.038
HLI-0702	14766	C	T	7	619	missense_variant	MODERATE	CYTB	0.7696
HLI-0702	14793	A	G	2	718	missense_variant	MODERATE	CYTB	0.0199
HLI-0702	15218	A	G	0	414	missense_variant	MODERATE	CYTB	0.0169
HLI-0702	15326	A	G	0	325	missense_variant	MODERATE	CYTB	0.9868
HLI-0702	15436	C	A	2	269	synonymous_variant	LOW	CYTB	0
HLI-0702	15924	A	G	2	684	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0702	16256	C	T	2	601	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0702	16270	C	T	3	633	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0702	16399	A	G	0	518	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0702	16519	T	C	0	319	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0703	152	T	C	4	534	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0703	263	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0703	408	T	A	3	368	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0703	750	A	G	0	523	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0703	4769	A	G	0	562	synonymous_variant	LOW	ND2	0.9767
HLI-0703	7444	G	A	4	598	stop_lost	HIGH	COX1	0.0035
HLI-0703	8598	T	C	8	572	synonymous_variant	LOW	ATP6	0.0015
HLI-0703	15326	A	G	0	370	missense_variant	MODERATE	CYTB	0.9868
HLI-0703	16311	T	C	4	502	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0703	16519	T	C	0	250	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0704	73	A	G	2	322	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0704	263	A	G	1	332	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0704	709	G	A	1	606	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0704	750	A	G	0	674	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0704	1438	A	G	4	619	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0704	1888	G	A	2	433	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0704	2706	A	G	0	684	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0704	2850	T	C	8	678	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0704	4216	T	C	3	518	missense_variant	MODERATE	ND1	0.0991
HLI-0704	4769	A	G	1	583	synonymous_variant	LOW	ND2	0.9767
HLI-0704	4917	A	G	7	626	missense_variant	MODERATE	ND2	0.0477
HLI-0704	7022	T	C	3	718	synonymous_variant	LOW	COX1	0.0024
HLI-0704	7028	C	T	3	746	synonymous_variant	LOW	COX1	0.8089
HLI-0704	8697	G	A	2	560	synonymous_variant	LOW	ATP6	0.0466
HLI-0704	10463	T	C	5	623	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0704	11251	A	G	5	644	synonymous_variant	LOW	ND4	0.0932
HLI-0704	11719	G	A	2	652	synonymous_variant	LOW	ND4	0.7756
HLI-0704	11812	A	G	2	598	synonymous_variant	LOW	ND4	0.0332

HLI-0704	13368	G	A	3	652	synonymous_variant	LOW	ND5	0.0495
HLI-0704	13965	T	C	3	529	synonymous_variant	LOW	ND5	0.005
HLI-0704	14233	A	G	5	527	synonymous_variant	LOW	ND6	0.0369
HLI-0704	14687	A	G	7	698	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0704	14766	C	T	5	696	missense_variant	MODERATE	CYTB	0.7696
HLI-0704	14905	G	A	5	820	synonymous_variant	LOW	CYTB	0.0526
HLI-0704	15326	A	G	0	509	missense_variant	MODERATE	CYTB	0.9868
HLI-0704	15452	C	A	3	428	missense_variant	MODERATE	CYTB	0.0933
HLI-0704	15607	A	G	2	459	synonymous_variant	LOW	CYTB	0.0508
HLI-0704	15928	G	A	5	460	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0704	15935	A	G	5	483	upstream_gene_variant	MODIFIER	TRNT	2.00E-04
HLI-0704	16126	T	C	2	547	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0704	16294	C	T	0	510	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0704	16296	C	T	0	513	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0704	16519	T	C	0	318	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0705	73	A	G	0	356	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0705	152	T	C	0	625	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0705	207	G	A	1	390	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0705	263	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0705	750	A	G	0	666	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0705	1438	A	G	1	727	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0705	2706	A	G	0	621	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0705	4496	C	T	0	638	synonymous_variant	LOW	ND2	5.00E-04
HLI-0705	4769	A	G	1	664	synonymous_variant	LOW	ND2	0.9767
HLI-0705	7028	C	T	3	690	synonymous_variant	LOW	COX1	0.8089
HLI-0705	8594	T	C	5	667	missense_variant	MODERATE	ATP6	0.0011
HLI-0705	10754	A	G	2	624	synonymous_variant	LOW	ND4L	0.0035
HLI-0705	11293	A	G	1	662	synonymous_variant	LOW	ND4	9.00E-04
HLI-0705	11719	G	A	0	633	synonymous_variant	LOW	ND4	0.7756
HLI-0705	13635	T	C	0	571	synonymous_variant	LOW	ND5	0.002
HLI-0705	14040	G	A	1	590	synonymous_variant	LOW	ND5	0.0047
HLI-0705	14544	G	A	0	651	synonymous_variant	LOW	ND6	0.0024
HLI-0705	14766	C	T	2	629	missense_variant	MODERATE	CYTB	0.7696
HLI-0705	15326	A	G	0	561	missense_variant	MODERATE	CYTB	0.9868
HLI-0705	15385	C	T	0	618	synonymous_variant	LOW	CYTB	8.00E-04
HLI-0705	16266	C	T	2	575	upstream_gene_variant	MODIFIER	DLoop	0.0135
HLI-0705	16304	T	C	0	590	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0705	16311	T	C	0	576	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0705	16356	T	C	0	529	upstream_gene_variant	MODIFIER	DLoop	0.024

HLI-0705	16524	A	G	2	367	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0706	73	A	G	2	303	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0706	150	C	T	3	566	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0706	214	A	G	4	433	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0706	263	A	G	0	409	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0706	709	G	A	7	580	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0706	750	A	G	1	621	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0706	1438	A	G	0	613	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0706	1888	G	A	4	335	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0706	2706	A	G	4	653	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0706	4216	T	C	2	471	missense_variant	MODERATE	ND1	0.0991
HLI-0706	4769	A	G	0	579	synonymous_variant	LOW	ND2	0.9767
HLI-0706	4917	A	G	0	540	missense_variant	MODERATE	ND2	0.0477
HLI-0706	7028	C	T	3	761	synonymous_variant	LOW	COX1	0.8089
HLI-0706	8697	G	A	5	561	synonymous_variant	LOW	ATP6	0.0466
HLI-0706	10463	T	C	7	602	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0706	11251	A	G	3	617	synonymous_variant	LOW	ND4	0.0932
HLI-0706	11719	G	A	8	545	synonymous_variant	LOW	ND4	0.7756
HLI-0706	12633	C	A	17	557	synonymous_variant	LOW	ND5	0.0123
HLI-0706	13368	G	A	3	635	synonymous_variant	LOW	ND5	0.0495
HLI-0706	13470	A	G	5	539	synonymous_variant	LOW	ND5	0.0033
HLI-0706	13708	G	A	5	461	missense_variant	MODERATE	ND5	0.0717
HLI-0706	14766	C	T	9	837	missense_variant	MODERATE	CYTB	0.7696
HLI-0706	14905	G	A	6	833	synonymous_variant	LOW	CYTB	0.0526
HLI-0706	15326	A	G	0	392	missense_variant	MODERATE	CYTB	0.9868
HLI-0706	15452	C	A	3	354	missense_variant	MODERATE	CYTB	0.0933
HLI-0706	15607	A	G	3	338	synonymous_variant	LOW	CYTB	0.0508
HLI-0706	15928	G	A	6	428	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0706	16126	T	C	3	573	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0706	16163	A	G	3	626	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0706	16294	C	T	2	452	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0706	16519	T	C	1	255	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0707	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0707	146	T	C	0	582	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0707	152	T	C	0	597	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0707	195	T	C	0	562	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0707	260	G	A	0	233	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0707	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0707	750	A	G	0	658	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0707	769	G	A	1	704	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0707	1018	G	A	0	740	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0707	1438	A	G	0	692	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0707	2416	T	C	2	667	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0707	2706	A	G	0	616	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0707	2789	C	T	1	669	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0707	3594	C	T	2	558	synonymous_variant	LOW	ND1	0.0789
HLI-0707	4104	A	G	0	546	synonymous_variant	LOW	ND1	0.0785
HLI-0707	4317	A	G	0	538	upstream_gene_variant	MODIFIER	TRNI	8.00E-04
HLI-0707	4769	A	G	1	688	synonymous_variant	LOW	ND2	0.9767
HLI-0707	6149	A	G	2	647	synonymous_variant	LOW	COX1	1.00E-04
HLI-0707	7028	C	T	2	698	synonymous_variant	LOW	COX1	0.8089
HLI-0707	7175	T	C	3	637	synonymous_variant	LOW	COX1	0.0224
HLI-0707	7256	C	T	3	701	synonymous_variant	LOW	COX1	0.0784
HLI-0707	7274	C	T	3	669	synonymous_variant	LOW	COX1	0.0214
HLI-0707	7521	G	A	0	637	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0707	7771	A	G	0	683	synonymous_variant	LOW	COX2	0.0223
HLI-0707	8206	G	A	2	746	synonymous_variant	LOW	COX2	0.0287
HLI-0707	8701	A	G	1	620	missense_variant	MODERATE	ATP6	0.3391
HLI-0707	9221	A	G	2	751	synonymous_variant	LOW	COX3	0.0277
HLI-0707	9540	T	C	0	644	synonymous_variant	LOW	COX3	0.339
HLI-0707	10115	T	C	2	789	synonymous_variant	LOW	ND3	0.0278
HLI-0707	10143	G	A	1	806	missense_variant	MODERATE	ND3	0.0075
HLI-0707	10398	A	G	0	744	missense_variant	MODERATE	ND3	0.445
HLI-0707	10873	T	C	0	628	synonymous_variant	LOW	ND4	0.3389
HLI-0707	11719	G	A	0	646	synonymous_variant	LOW	ND4	0.7756
HLI-0707	11914	G	A	0	668	synonymous_variant	LOW	ND4	0.1112
HLI-0707	11944	T	C	0	689	synonymous_variant	LOW	ND4	0.0331
HLI-0707	12693	A	G	1	689	synonymous_variant	LOW	ND5	0.0205
HLI-0707	12705	C	T	4	751	synonymous_variant	LOW	ND5	0.4212
HLI-0707	13590	G	A	1	608	synonymous_variant	LOW	ND5	0.0586
HLI-0707	13650	C	T	3	636	synonymous_variant	LOW	ND5	0.079
HLI-0707	13803	A	G	0	513	synonymous_variant	LOW	ND5	0.0216
HLI-0707	13965	T	C	1	611	synonymous_variant	LOW	ND5	0.005
HLI-0707	14566	A	G	0	772	synonymous_variant	LOW	ND6	0.0214
HLI-0707	14766	C	T	2	697	missense_variant	MODERATE	CYTB	0.7696
HLI-0707	15301	G	A	3	534	synonymous_variant	LOW	CYTB	0.2912
HLI-0707	15326	A	G	0	576	missense_variant	MODERATE	CYTB	0.9868
HLI-0707	15784	T	C	0	644	synonymous_variant	LOW	CYTB	0.0363

HLI-0707	16223	C	T	0	625	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0707	16278	C	T	2	571	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0707	16294	C	T	0	554	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0707	16309	A	G	1	540	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0707	16390	G	A	0	537	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0707	16519	T	C	0	268	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0708	73	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0708	263	A	G	1	333	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0708	497	C	T	4	457	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0708	750	A	G	0	525	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0708	1189	T	C	0	598	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0708	1438	A	G	0	506	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0708	1811	A	G	2	377	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0708	2706	A	G	0	574	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0708	3398	T	C	5	423	missense_variant	MODERATE	ND1	0.0039
HLI-0708	3480	A	G	2	434	synonymous_variant	LOW	ND1	0.0392
HLI-0708	4769	A	G	0	505	synonymous_variant	LOW	ND2	0.9767
HLI-0708	6260	G	A	4	530	synonymous_variant	LOW	COX1	0.009
HLI-0708	7028	C	T	1	617	synonymous_variant	LOW	COX1	0.8089
HLI-0708	8149	A	G	2	528	synonymous_variant	LOW	COX2	0.0074
HLI-0708	9055	G	A	2	491	missense_variant	MODERATE	ATP6	0.0425
HLI-0708	9698	T	C	1	486	synonymous_variant	LOW	COX3	0.0405
HLI-0708	10398	A	G	1	438	missense_variant	MODERATE	ND3	0.445
HLI-0708	10550	A	G	1	497	synonymous_variant	LOW	ND4L	0.0376
HLI-0708	11299	T	C	3	502	synonymous_variant	LOW	ND4	0.0417
HLI-0708	11467	A	G	0	586	synonymous_variant	LOW	ND4	0.1231
HLI-0708	11485	T	C	1	649	synonymous_variant	LOW	ND4	0.0081
HLI-0708	11719	G	A	1	499	synonymous_variant	LOW	ND4	0.7756
HLI-0708	11840	C	T	3	509	synonymous_variant	LOW	ND4	0.0041
HLI-0708	12308	A	G	1	381	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0708	12372	G	A	3	332	synonymous_variant	LOW	ND5	0.1329
HLI-0708	13740	T	C	1	371	synonymous_variant	LOW	ND5	0.0041
HLI-0708	14167	C	T	5	428	synonymous_variant	LOW	ND6	0.0385
HLI-0708	14766	C	T	4	694	missense_variant	MODERATE	CYTB	0.7696
HLI-0708	14798	T	C	5	783	missense_variant	MODERATE	CYTB	0.0651
HLI-0708	15326	A	G	1	321	missense_variant	MODERATE	CYTB	0.9868
HLI-0708	16224	T	C	0	596	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0708	16287	C	T	0	536	upstream_gene_variant	MODIFIER	DLoop	0.0051
HLI-0708	16311	T	C	0	517	upstream_gene_variant	MODIFIER	DLoop	0.1969

HLI-0708	16519	T	C	0	207	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0709	73	A	G	0	34	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0709	199	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0709	203	G	A	0	45	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0709	204	T	C	0	44	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0709	250	T	C	0	37	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0709	263	A	G	0	34	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0709	750	A	G	0	64	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0709	1438	A	G	0	73	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0709	1719	G	A	0	64	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0709	2706	A	G	0	81	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0709	3447	A	G	1	67	synonymous_variant	LOW	ND1	0.0053
HLI-0709	3990	C	T	0	63	synonymous_variant	LOW	ND1	0.0031
HLI-0709	4529	A	T	0	79	synonymous_variant	LOW	ND2	0.015
HLI-0709	4561	T	C	0	86	missense_variant	MODERATE	ND2	0.0065
HLI-0709	4769	A	G	1	55	synonymous_variant	LOW	ND2	0.9767
HLI-0709	6734	G	A	1	73	synonymous_variant	LOW	COX1	0.0062
HLI-0709	7028	C	T	0	109	synonymous_variant	LOW	COX1	0.8089
HLI-0709	8251	G	A	1	49	synonymous_variant	LOW	COX2	0.058
HLI-0709	8292	G	A	0	40	upstream_gene_variant	MODIFIER	Unannotated	0.0024
HLI-0709	8616	G	T	0	46	missense_variant	MODERATE	ATP6	0.0032
HLI-0709	9947	G	A	0	60	synonymous_variant	LOW	COX3	0.0092
HLI-0709	10034	T	C	0	58	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0709	10238	T	C	0	72	synonymous_variant	LOW	ND3	0.0623
HLI-0709	10398	A	G	0	61	missense_variant	MODERATE	ND3	0.445
HLI-0709	10915	T	C	0	57	synonymous_variant	LOW	ND4	0.0411
HLI-0709	11719	G	A	1	58	synonymous_variant	LOW	ND4	0.7756
HLI-0709	12501	G	A	0	36	synonymous_variant	LOW	ND5	0.0258
HLI-0709	12705	C	T	0	46	synonymous_variant	LOW	ND5	0.4212
HLI-0709	13780	A	G	0	32	missense_variant	MODERATE	ND5	0.0179
HLI-0709	14766	C	T	0	72	missense_variant	MODERATE	CYTB	0.7696
HLI-0709	15043	G	A	0	91	synonymous_variant	LOW	CYTB	0.2362
HLI-0709	15326	A	G	0	60	missense_variant	MODERATE	CYTB	0.9868
HLI-0709	15924	A	G	0	45	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0709	16129	G	A	0	60	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0709	16172	T	C	0	60	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0709	16223	C	T	1	58	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0709	16311	T	C	0	74	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0709	16391	G	A	0	71	upstream_gene_variant	MODIFIER	DLoop	0.0155

HLI-0709	16519	T	C	0	33	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0710	73	A	G	0	36	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0710	146	T	C	0	62	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0710	152	T	C	0	61	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0710	195	T	C	0	56	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0710	263	A	G	0	32	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0710	750	A	G	0	45	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0710	769	G	A	0	50	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0710	1018	G	A	0	60	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0710	1438	A	G	0	57	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0710	2416	T	C	1	44	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0710	2706	A	G	0	55	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0710	2789	C	T	0	49	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0710	3594	C	T	0	41	synonymous_variant	LOW	ND1	0.0789
HLI-0710	3918	G	A	0	51	synonymous_variant	LOW	ND1	0.009
HLI-0710	4104	A	G	0	42	synonymous_variant	LOW	ND1	0.0785
HLI-0710	4769	A	G	0	68	synonymous_variant	LOW	ND2	0.9767
HLI-0710	5285	A	G	0	63	synonymous_variant	LOW	ND2	0.0049
HLI-0710	6152	T	C	0	58	synonymous_variant	LOW	COX1	0.0077
HLI-0710	7028	C	T	0	76	synonymous_variant	LOW	COX1	0.8089
HLI-0710	7175	T	C	0	56	synonymous_variant	LOW	COX1	0.0224
HLI-0710	7256	C	T	0	68	synonymous_variant	LOW	COX1	0.0784
HLI-0710	7274	C	T	0	62	synonymous_variant	LOW	COX1	0.0214
HLI-0710	7521	G	A	0	54	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0710	7771	A	G	0	73	synonymous_variant	LOW	COX2	0.0223
HLI-0710	8206	G	A	0	73	synonymous_variant	LOW	COX2	0.0287
HLI-0710	8701	A	G	0	51	missense_variant	MODERATE	ATP6	0.3391
HLI-0710	9221	A	G	2	67	synonymous_variant	LOW	COX3	0.0277
HLI-0710	9540	T	C	0	45	synonymous_variant	LOW	COX3	0.339
HLI-0710	10115	T	C	0	74	synonymous_variant	LOW	ND3	0.0278
HLI-0710	10398	A	G	0	60	missense_variant	MODERATE	ND3	0.445
HLI-0710	10873	T	C	0	67	synonymous_variant	LOW	ND4	0.3389
HLI-0710	11719	G	A	0	58	synonymous_variant	LOW	ND4	0.7756
HLI-0710	11914	G	A	0	61	synonymous_variant	LOW	ND4	0.1112
HLI-0710	11944	T	C	0	59	synonymous_variant	LOW	ND4	0.0331
HLI-0710	12693	A	G	0	66	synonymous_variant	LOW	ND5	0.0205
HLI-0710	12705	C	T	0	69	synonymous_variant	LOW	ND5	0.4212
HLI-0710	13590	G	A	0	56	synonymous_variant	LOW	ND5	0.0586
HLI-0710	13650	C	T	0	43	synonymous_variant	LOW	ND5	0.079

HLI-0710	13803	A	G	0	40	synonymous_variant	LOW	ND5	0.0216
HLI-0710	14566	A	G	0	62	synonymous_variant	LOW	ND6	0.0214
HLI-0710	14766	C	T	0	59	missense_variant	MODERATE	CYTB	0.7696
HLI-0710	15244	A	G	0	70	synonymous_variant	LOW	CYTB	0.0103
HLI-0710	15301	G	A	0	65	synonymous_variant	LOW	CYTB	0.2912
HLI-0710	15326	A	G	0	65	missense_variant	MODERATE	CYTB	0.9868
HLI-0710	15391	C	T	0	44	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0710	15629	T	C	0	40	synonymous_variant	LOW	CYTB	0.0062
HLI-0710	15784	T	C	0	53	synonymous_variant	LOW	CYTB	0.0363
HLI-0710	16223	C	T	1	51	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0710	16278	C	T	0	56	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0710	16294	C	T	0	58	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0710	16309	A	G	0	61	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0710	16368	T	C	0	51	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0710	16390	G	A	0	47	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0710	16519	T	C	1	27	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0711	263	A	G	0	377	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0711	750	A	G	1	760	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0711	1438	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0711	1888	G	A	0	435	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0711	3010	G	A	4	518	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0711	4769	A	G	0	547	synonymous_variant	LOW	ND2	0.9767
HLI-0711	5460	G	A	1	675	missense_variant	MODERATE	ND2	0.0651
HLI-0711	15110	G	A	0	757	missense_variant	MODERATE	CYTB	0.009
HLI-0711	15326	A	G	0	450	missense_variant	MODERATE	CYTB	0.9868
HLI-0711	16519	T	C	1	325	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0712	263	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0712	750	A	G	1	669	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0712	1438	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0712	3010	G	A	0	690	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0712	4769	A	G	0	667	synonymous_variant	LOW	ND2	0.9767
HLI-0712	15326	A	G	0	600	missense_variant	MODERATE	CYTB	0.9868
HLI-0712	15883	G	A	3	695	synonymous_variant	LOW	CYTB	0.0078
HLI-0712	16239	C	T	0	603	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0712	16519	T	C	1	268	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0713	263	A	G	0	324	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0713	456	C	T	6	587	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0713	750	A	G	2	699	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0713	1438	A	G	0	743	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0713	4336	T	C	0	568	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0713	4769	A	G	0	710	synonymous_variant	LOW	ND2	0.9767
HLI-0713	5839	C	T	4	789	upstream_gene_variant	MODIFIER	TRNY	0.0011
HLI-0713	15326	A	G	0	522	missense_variant	MODERATE	CYTB	0.9868
HLI-0713	16304	T	C	0	555	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0714	73	A	G	0	323	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0714	263	A	G	0	374	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0714	750	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0714	1438	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0714	2706	A	G	0	595	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0714	3197	T	C	0	645	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0714	4769	A	G	3	609	synonymous_variant	LOW	ND2	0.9767
HLI-0714	7028	C	T	7	691	synonymous_variant	LOW	COX1	0.8089
HLI-0714	9477	G	A	3	656	missense_variant	MODERATE	COX3	0.0387
HLI-0714	9548	G	A	3	565	synonymous_variant	LOW	COX3	0.0149
HLI-0714	11467	A	G	0	647	synonymous_variant	LOW	ND4	0.1231
HLI-0714	11719	G	A	0	619	synonymous_variant	LOW	ND4	0.7756
HLI-0714	12308	A	G	1	446	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0714	12372	G	A	0	385	synonymous_variant	LOW	ND5	0.1329
HLI-0714	12441	T	C	4	425	synonymous_variant	LOW	ND5	0.0012
HLI-0714	13617	T	C	1	524	synonymous_variant	LOW	ND5	0.038
HLI-0714	14766	C	T	1	759	missense_variant	MODERATE	CYTB	0.7696
HLI-0714	14793	A	G	0	881	missense_variant	MODERATE	CYTB	0.0199
HLI-0714	15326	A	G	0	388	missense_variant	MODERATE	CYTB	0.9868
HLI-0714	16174	C	T	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0714	16256	C	T	0	531	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0714	16270	C	T	0	493	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0714	16526	G	A	0	222	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0715	263	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0715	750	A	G	1	733	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0715	1438	A	G	0	708	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0715	3010	G	A	2	695	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0715	4769	A	G	0	684	synonymous_variant	LOW	ND2	0.9767
HLI-0715	7980	A	G	3	790	missense_variant	MODERATE	COX2	1.00E-04
HLI-0715	8602	T	C	0	640	missense_variant	MODERATE	ATP6	0.0017
HLI-0715	14212	T	C	3	605	synonymous_variant	LOW	ND6	0.0204
HLI-0715	15326	A	G	0	528	missense_variant	MODERATE	CYTB	0.9868
HLI-0715	16519	T	C	0	256	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0716	73	A	G	0	314	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0716	263	A	G	2	406	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0716	497	C	T	43	532	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0716	723	A	C	47	581	upstream_gene_variant	MODIFIER	RNR1	9.00E-04
HLI-0716	750	A	G	1	675	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0716	1189	T	C	47	634	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0716	1438	A	G	0	625	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0716	1811	A	G	47	498	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0716	2706	A	G	0	641	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0716	3480	A	G	38	475	synonymous_variant	LOW	ND1	0.0392
HLI-0716	4769	A	G	0	636	synonymous_variant	LOW	ND2	0.9767
HLI-0716	7028	C	T	2	682	synonymous_variant	LOW	COX1	0.8089
HLI-0716	9055	G	A	58	521	missense_variant	MODERATE	ATP6	0.0425
HLI-0716	9698	T	C	50	616	synonymous_variant	LOW	COX3	0.0405
HLI-0716	10398	A	G	0	598	missense_variant	MODERATE	ND3	0.445
HLI-0716	10550	A	G	53	613	synonymous_variant	LOW	ND4L	0.0376
HLI-0716	11071	C	T	56	530	synonymous_variant	LOW	ND4	7.00E-04
HLI-0716	11299	T	C	71	649	synonymous_variant	LOW	ND4	0.0417
HLI-0716	11467	A	G	47	599	synonymous_variant	LOW	ND4	0.1231
HLI-0716	11485	T	C	54	660	synonymous_variant	LOW	ND4	0.0081
HLI-0716	11719	G	A	1	603	synonymous_variant	LOW	ND4	0.7756
HLI-0716	12308	A	G	34	447	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0716	12372	G	A	28	413	synonymous_variant	LOW	ND5	0.1329
HLI-0716	14167	C	T	47	557	synonymous_variant	LOW	ND6	0.0385
HLI-0716	14766	C	T	5	698	missense_variant	MODERATE	CYTB	0.7696
HLI-0716	14798	T	C	2	800	missense_variant	MODERATE	CYTB	0.0651
HLI-0716	15326	A	G	0	474	missense_variant	MODERATE	CYTB	0.9868
HLI-0716	15355	G	A	22	494	synonymous_variant	LOW	CYTB	0.0032
HLI-0716	16093	T	C	44	537	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0716	16224	T	C	28	587	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0716	16311	T	C	35	490	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0716	16519	T	C	0	274	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0717	73	A	G	0	333	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0717	152	T	C	1	538	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0717	199	T	C	0	428	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0717	204	T	C	0	412	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0717	207	G	A	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0717	250	T	C	0	169	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0717	263	A	G	0	186	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0717	750	A	G	0	755	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0717	1438	A	G	0	764	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0717	1719	G	A	1	705	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0717	2706	A	G	1	711	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0717	4529	A	T	2	739	synonymous_variant	LOW	ND2	0.015
HLI-0717	4769	A	G	0	676	synonymous_variant	LOW	ND2	0.9767
HLI-0717	7028	C	T	5	820	synonymous_variant	LOW	COX1	0.8089
HLI-0717	8251	G	A	3	653	synonymous_variant	LOW	COX2	0.058
HLI-0717	10034	T	C	1	737	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0717	10203	G	A	1	818	missense_variant	MODERATE	ND3	0.001
HLI-0717	10238	T	C	3	855	synonymous_variant	LOW	ND3	0.0623
HLI-0717	10398	A	G	3	696	missense_variant	MODERATE	ND3	0.445
HLI-0717	11719	G	A	1	685	synonymous_variant	LOW	ND4	0.7756
HLI-0717	12501	G	A	4	653	synonymous_variant	LOW	ND5	0.0258
HLI-0717	12705	C	T	0	648	synonymous_variant	LOW	ND5	0.4212
HLI-0717	13780	A	G	2	479	missense_variant	MODERATE	ND5	0.0179
HLI-0717	14374	T	C	2	727	synonymous_variant	LOW	ND6	0.0032
HLI-0717	14766	C	T	3	676	missense_variant	MODERATE	CYTB	0.7696
HLI-0717	15043	G	A	3	802	synonymous_variant	LOW	CYTB	0.2362
HLI-0717	15326	A	G	0	616	missense_variant	MODERATE	CYTB	0.9868
HLI-0717	15758	A	G	0	648	missense_variant	MODERATE	CYTB	0.0076
HLI-0717	15924	A	G	1	660	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0717	16129	G	A	1	674	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0717	16223	C	T	2	654	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0717	16519	T	C	0	329	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0718	73	A	G	0	346	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0718	146	T	C	0	571	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0718	152	T	C	0	590	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0718	263	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0718	750	A	G	0	741	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0718	1189	T	C	2	738	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0718	1438	A	G	0	753	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0718	1811	A	G	4	708	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0718	2706	A	G	1	748	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0718	3480	A	G	0	627	synonymous_variant	LOW	ND1	0.0392
HLI-0718	4767	A	G	0	666	missense_variant	MODERATE	ND2	0.0029
HLI-0718	4769	A	G	0	672	synonymous_variant	LOW	ND2	0.9767
HLI-0718	7028	C	T	0	724	synonymous_variant	LOW	COX1	0.8089
HLI-0718	7546	T	C	1	698	upstream_gene_variant	MODIFIER	TRND	1.00E-04
HLI-0718	9055	G	A	2	787	missense_variant	MODERATE	ATP6	0.0425

HLI-0718	9093	A	G	3	811	synonymous_variant	LOW	ATP6	0.0031
HLI-0718	9698	T	C	0	745	synonymous_variant	LOW	COX3	0.0405
HLI-0718	10398	A	G	0	696	missense_variant	MODERATE	ND3	0.445
HLI-0718	10550	A	G	1	707	synonymous_variant	LOW	ND4L	0.0376
HLI-0718	11299	T	C	0	671	synonymous_variant	LOW	ND4	0.0417
HLI-0718	11377	G	A	0	728	synonymous_variant	LOW	ND4	0.0125
HLI-0718	11467	A	G	1	731	synonymous_variant	LOW	ND4	0.1231
HLI-0718	11719	G	A	0	707	synonymous_variant	LOW	ND4	0.7756
HLI-0718	11914	G	A	1	686	synonymous_variant	LOW	ND4	0.1112
HLI-0718	12308	A	G	0	680	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0718	12372	G	A	0	710	synonymous_variant	LOW	ND5	0.1329
HLI-0718	14167	C	T	3	661	synonymous_variant	LOW	ND6	0.0385
HLI-0718	14766	C	T	2	723	missense_variant	MODERATE	CYTB	0.7696
HLI-0718	14798	T	C	0	813	missense_variant	MODERATE	CYTB	0.0651
HLI-0718	15326	A	G	3	649	missense_variant	MODERATE	CYTB	0.9868
HLI-0718	16224	T	C	1	627	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0718	16311	T	C	1	600	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0718	16368	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0718	16519	T	C	0	283	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0719	73	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0719	146	T	C	0	553	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0719	152	T	C	0	569	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0719	195	T	C	2	567	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0719	263	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0719	750	A	G	0	728	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0719	769	G	A	0	777	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0719	1018	G	A	0	755	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0719	1438	A	G	0	680	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0719	2416	T	C	0	511	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0719	2706	A	G	0	659	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0719	2789	C	T	3	725	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0719	3594	C	T	1	554	synonymous_variant	LOW	ND1	0.0789
HLI-0719	3918	G	A	3	570	synonymous_variant	LOW	ND1	0.009
HLI-0719	4104	A	G	2	494	synonymous_variant	LOW	ND1	0.0785
HLI-0719	4769	A	G	1	615	synonymous_variant	LOW	ND2	0.9767
HLI-0719	5285	A	G	2	647	synonymous_variant	LOW	ND2	0.0049
HLI-0719	7028	C	T	0	713	synonymous_variant	LOW	COX1	0.8089
HLI-0719	7175	T	C	1	621	synonymous_variant	LOW	COX1	0.0224
HLI-0719	7256	C	T	2	655	synonymous_variant	LOW	COX1	0.0784

HLI-0719	7274	C	T	1	615	synonymous_variant	LOW	COX1	0.0214
HLI-0719	7521	G	A	0	472	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0719	7771	A	G	0	635	synonymous_variant	LOW	COX2	0.0223
HLI-0719	8206	G	A	2	591	synonymous_variant	LOW	COX2	0.0287
HLI-0719	8701	A	G	0	570	missense_variant	MODERATE	ATP6	0.3391
HLI-0719	9221	A	G	0	693	synonymous_variant	LOW	COX3	0.0277
HLI-0719	9540	T	C	0	601	synonymous_variant	LOW	COX3	0.339
HLI-0719	10115	T	C	1	699	synonymous_variant	LOW	ND3	0.0278
HLI-0719	10398	A	G	0	585	missense_variant	MODERATE	ND3	0.445
HLI-0719	10873	T	C	0	568	synonymous_variant	LOW	ND4	0.3389
HLI-0719	11719	G	A	0	654	synonymous_variant	LOW	ND4	0.7756
HLI-0719	11914	G	A	2	618	synonymous_variant	LOW	ND4	0.1112
HLI-0719	11944	T	C	2	618	synonymous_variant	LOW	ND4	0.0331
HLI-0719	12693	A	G	9	583	synonymous_variant	LOW	ND5	0.0205
HLI-0719	12705	C	T	3	601	synonymous_variant	LOW	ND5	0.4212
HLI-0719	13590	G	A	1	613	synonymous_variant	LOW	ND5	0.0586
HLI-0719	13650	C	T	2	669	synonymous_variant	LOW	ND5	0.079
HLI-0719	13803	A	G	1	449	synonymous_variant	LOW	ND5	0.0216
HLI-0719	14566	A	G	2	675	synonymous_variant	LOW	ND6	0.0214
HLI-0719	14766	C	T	3	675	missense_variant	MODERATE	CYTB	0.7696
HLI-0719	15244	A	G	3	606	synonymous_variant	LOW	CYTB	0.0103
HLI-0719	15301	G	A	0	583	synonymous_variant	LOW	CYTB	0.2912
HLI-0719	15326	A	G	0	581	missense_variant	MODERATE	CYTB	0.9868
HLI-0719	15629	T	C	0	500	synonymous_variant	LOW	CYTB	0.0062
HLI-0719	15784	T	C	0	493	synonymous_variant	LOW	CYTB	0.0363
HLI-0719	16223	C	T	1	563	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0719	16278	C	T	1	593	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0719	16294	C	T	1	563	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0719	16309	A	G	1	553	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0719	16390	G	A	1	534	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0719	16519	T	C	1	283	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0720	263	A	G	1	303	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0720	750	A	G	0	670	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0720	1438	A	G	1	653	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0720	3010	G	A	1	589	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0720	4769	A	G	1	647	synonymous_variant	LOW	ND2	0.9767
HLI-0720	15326	A	G	0	488	missense_variant	MODERATE	CYTB	0.9868
HLI-0720	16051	A	G	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0720	16075	T	C	0	488	upstream_gene_variant	MODIFIER	DLoop	0.0027

HLI-0720	16311	T	C	1	496	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0720	16356	T	C	1	495	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0720	16519	T	C	0	237	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0721	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0721	263	A	G	1	259	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0721	596	T	C	0	596	upstream_gene_variant	MODIFIER	TRNF	3.00E-04
HLI-0721	709	G	A	1	604	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0721	750	A	G	0	680	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0721	1438	A	G	0	608	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0721	1888	G	A	0	394	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0721	2706	A	G	1	603	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0721	2850	T	C	0	630	upstream_gene_variant	MODIFIER	RNR2	0.0021
HLI-0721	4216	T	C	0	440	missense_variant	MODERATE	ND1	0.0991
HLI-0721	4688	T	C	1	639	synonymous_variant	LOW	ND2	0.0078
HLI-0721	4769	A	G	4	588	synonymous_variant	LOW	ND2	0.9767
HLI-0721	4917	A	G	1	569	missense_variant	MODERATE	ND2	0.0477
HLI-0721	7022	T	C	2	656	synonymous_variant	LOW	COX1	0.0024
HLI-0721	7028	C	T	2	686	synonymous_variant	LOW	COX1	0.8089
HLI-0721	8697	G	A	2	516	synonymous_variant	LOW	ATP6	0.0466
HLI-0721	10463	T	C	0	522	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0721	11251	A	G	0	615	synonymous_variant	LOW	ND4	0.0932
HLI-0721	11719	G	A	0	599	synonymous_variant	LOW	ND4	0.7756
HLI-0721	11812	A	G	2	619	synonymous_variant	LOW	ND4	0.0332
HLI-0721	13368	G	A	2	604	synonymous_variant	LOW	ND5	0.0495
HLI-0721	13965	T	C	0	500	synonymous_variant	LOW	ND5	0.005
HLI-0721	14233	A	G	0	516	synonymous_variant	LOW	ND6	0.0369
HLI-0721	14687	A	G	1	595	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0721	14766	C	T	3	672	missense_variant	MODERATE	CYTB	0.7696
HLI-0721	14905	G	A	0	703	synonymous_variant	LOW	CYTB	0.0526
HLI-0721	15326	A	G	0	436	missense_variant	MODERATE	CYTB	0.9868
HLI-0721	15452	C	A	0	469	missense_variant	MODERATE	CYTB	0.0933
HLI-0721	15607	A	G	0	441	synonymous_variant	LOW	CYTB	0.0508
HLI-0721	15928	G	A	1	418	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0721	16126	T	C	0	525	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0721	16294	C	T	0	494	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0721	16296	C	T	0	498	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0721	16519	T	C	1	250	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0722	263	A	G	1	298	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0722	750	A	G	0	591	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0722	1438	A	G	0	648	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0722	3010	G	A	1	586	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0722	4769	A	G	0	648	synonymous_variant	LOW	ND2	0.9767
HLI-0722	15326	A	G	0	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0722	16239	C	T	0	555	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0723	73	A	G	0	342	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0723	150	C	T	2	624	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0723	152	T	C	2	619	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0723	263	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0723	295	C	T	0	254	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0723	489	T	C	1	479	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0723	709	G	A	0	704	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0723	750	A	G	1	712	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0723	1438	A	G	0	693	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0723	2706	A	G	0	707	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0723	4216	T	C	0	661	missense_variant	MODERATE	ND1	0.0991
HLI-0723	4769	A	G	1	642	synonymous_variant	LOW	ND2	0.9767
HLI-0723	5633	C	T	1	660	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0723	7028	C	T	0	735	synonymous_variant	LOW	COX1	0.8089
HLI-0723	7476	C	T	0	683	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0723	10172	G	A	1	708	synonymous_variant	LOW	ND3	0.0084
HLI-0723	10398	A	G	0	723	missense_variant	MODERATE	ND3	0.445
HLI-0723	11251	A	G	2	630	synonymous_variant	LOW	ND4	0.0932
HLI-0723	11719	G	A	3	640	synonymous_variant	LOW	ND4	0.7756
HLI-0723	12612	A	G	4	679	synonymous_variant	LOW	ND5	0.0506
HLI-0723	13708	G	A	2	464	missense_variant	MODERATE	ND5	0.0717
HLI-0723	13830	T	C	1	506	synonymous_variant	LOW	ND5	0.0021
HLI-0723	14180	T	C	0	626	missense_variant	MODERATE	ND6	0.0036
HLI-0723	14766	C	T	0	665	missense_variant	MODERATE	CYTB	0.7696
HLI-0723	15257	G	A	1	599	missense_variant	MODERATE	CYTB	0.0155
HLI-0723	15326	A	G	0	643	missense_variant	MODERATE	CYTB	0.9868
HLI-0723	15452	C	A	4	651	missense_variant	MODERATE	CYTB	0.0933
HLI-0723	15812	G	A	4	654	missense_variant	MODERATE	CYTB	0.0096
HLI-0723	16066	A	G	1	668	upstream_gene_variant	MODIFIER	DLoop	0.0022
HLI-0723	16069	C	T	1	677	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0723	16126	T	C	1	658	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0723	16278	C	T	3	620	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0724	73	A	G	0	283	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0724	263	A	G	0	303	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0724	489	T	C	0	379	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0724	750	A	G	0	587	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0724	1438	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0724	1670	A	T	2	601	upstream_gene_variant	MODIFIER	TRNV	4.00E-04
HLI-0724	2706	A	G	2	528	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0724	3552	T	A	0	489	synonymous_variant	LOW	ND1	0.0337
HLI-0724	4715	A	G	3	660	synonymous_variant	LOW	ND2	0.0416
HLI-0724	4769	A	G	0	673	synonymous_variant	LOW	ND2	0.9767
HLI-0724	7028	C	T	2	601	synonymous_variant	LOW	COX1	0.8089
HLI-0724	7196	C	A	3	583	synonymous_variant	LOW	COX1	0.0389
HLI-0724	7694	C	T	2	581	synonymous_variant	LOW	COX2	5.00E-04
HLI-0724	8584	G	A	0	510	missense_variant	MODERATE	ATP6	0.0521
HLI-0724	8701	A	G	0	624	missense_variant	MODERATE	ATP6	0.3391
HLI-0724	9540	T	C	0	496	synonymous_variant	LOW	COX3	0.339
HLI-0724	9545	A	G	0	517	synonymous_variant	LOW	COX3	0.0469
HLI-0724	10398	A	G	1	595	missense_variant	MODERATE	ND3	0.445
HLI-0724	10400	C	T	1	603	synonymous_variant	LOW	ND3	0.2131
HLI-0724	10454	T	C	1	641	upstream_gene_variant	MODIFIER	TRNR	0.0037
HLI-0724	10873	T	C	0	544	synonymous_variant	LOW	ND4	0.3389
HLI-0724	11719	G	A	0	601	synonymous_variant	LOW	ND4	0.7756
HLI-0724	11914	G	A	1	651	synonymous_variant	LOW	ND4	0.1112
HLI-0724	12705	C	T	3	633	synonymous_variant	LOW	ND5	0.4212
HLI-0724	13263	A	G	0	668	synonymous_variant	LOW	ND5	0.0354
HLI-0724	14318	T	C	0	568	missense_variant	MODERATE	ND6	0.0339
HLI-0724	14766	C	T	2	626	missense_variant	MODERATE	CYTB	0.7696
HLI-0724	14783	T	C	1	725	synonymous_variant	LOW	CYTB	0.2126
HLI-0724	15043	G	A	1	697	synonymous_variant	LOW	CYTB	0.2362
HLI-0724	15301	G	A	0	458	synonymous_variant	LOW	CYTB	0.2912
HLI-0724	15326	A	G	0	484	missense_variant	MODERATE	CYTB	0.9868
HLI-0724	15487	A	T	0	387	synonymous_variant	LOW	CYTB	0.0391
HLI-0724	16093	T	C	19	507	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0724	16223	C	T	0	541	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0724	16234	C	T	0	582	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0724	16288	T	C	1	499	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0724	16298	T	C	1	483	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0724	16327	C	T	1	445	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0724	16497	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.0037
HLI-0724	16518	G	T	0	250	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0724	16519	T	C	0	249	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0724	16527	C	T	0	235	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0725	73	A	G	0	277	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0725	146	T	C	0	516	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0725	152	T	C	0	530	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0725	195	T	C	1	476	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0725	263	A	G	0	204	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0725	750	A	G	0	599	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0725	769	G	A	2	643	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0725	1018	G	A	0	675	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0725	1438	A	G	3	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0725	2416	T	C	0	484	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0725	2706	A	G	0	525	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0725	2789	C	T	2	597	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0725	3594	C	T	1	561	synonymous_variant	LOW	ND1	0.0789
HLI-0725	4104	A	G	1	446	synonymous_variant	LOW	ND1	0.0785
HLI-0725	4769	A	G	0	586	synonymous_variant	LOW	ND2	0.9767
HLI-0725	5581	A	G	0	661	upstream_gene_variant	MODIFIER	Unannotated	0.005
HLI-0725	7028	C	T	1	616	synonymous_variant	LOW	COX1	0.8089
HLI-0725	7175	T	C	0	580	synonymous_variant	LOW	COX1	0.0224
HLI-0725	7256	C	T	2	656	synonymous_variant	LOW	COX1	0.0784
HLI-0725	7274	C	T	1	644	synonymous_variant	LOW	COX1	0.0214
HLI-0725	7521	G	A	1	467	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0725	7771	A	G	1	558	synonymous_variant	LOW	COX2	0.0223
HLI-0725	8176	T	C	1	610	synonymous_variant	LOW	COX2	2.00E-04
HLI-0725	8206	G	A	1	623	synonymous_variant	LOW	COX2	0.0287
HLI-0725	8701	A	G	1	587	missense_variant	MODERATE	ATP6	0.3391
HLI-0725	9221	A	G	1	625	synonymous_variant	LOW	COX3	0.0277
HLI-0725	9540	T	C	1	539	synonymous_variant	LOW	COX3	0.339
HLI-0725	10115	T	C	1	713	synonymous_variant	LOW	ND3	0.0278
HLI-0725	10398	A	G	1	610	missense_variant	MODERATE	ND3	0.445
HLI-0725	10873	T	C	0	545	synonymous_variant	LOW	ND4	0.3389
HLI-0725	11719	G	A	1	609	synonymous_variant	LOW	ND4	0.7756
HLI-0725	11914	G	A	0	594	synonymous_variant	LOW	ND4	0.1112
HLI-0725	11944	T	C	0	637	synonymous_variant	LOW	ND4	0.0331
HLI-0725	12693	A	G	0	599	synonymous_variant	LOW	ND5	0.0205
HLI-0725	12705	C	T	0	652	synonymous_variant	LOW	ND5	0.4212
HLI-0725	13590	G	A	1	540	synonymous_variant	LOW	ND5	0.0586
HLI-0725	13650	C	T	3	542	synonymous_variant	LOW	ND5	0.079
HLI-0725	13803	A	G	0	390	synonymous_variant	LOW	ND5	0.0216

HLI-0725	14566	A	G	3	655	synonymous_variant	LOW	ND6	0.0214
HLI-0725	14766	C	T	0	579	missense_variant	MODERATE	CYTB	0.7696
HLI-0725	15301	G	A	2	454	synonymous_variant	LOW	CYTB	0.2912
HLI-0725	15326	A	G	1	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0725	15784	T	C	1	466	synonymous_variant	LOW	CYTB	0.0363
HLI-0725	16223	C	T	6	450	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0725	16278	C	T	1	483	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0725	16294	C	T	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0725	16309	A	G	1	474	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0725	16390	G	A	0	441	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0725	16519	T	C	0	199	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0726	73	A	G	0	299	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0726	152	T	C	0	548	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0726	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0726	750	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0726	1438	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0726	2706	A	G	0	578	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0726	3420	C	T	0	549	synonymous_variant	LOW	ND1	4.00E-04
HLI-0726	3450	C	T	0	595	synonymous_variant	LOW	ND1	0.0084
HLI-0726	4769	A	G	2	572	synonymous_variant	LOW	ND2	0.9767
HLI-0726	5250	T	C	0	558	synonymous_variant	LOW	ND2	0.0013
HLI-0726	5773	G	A	1	676	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0726	6221	T	C	0	505	synonymous_variant	LOW	COX1	0.0306
HLI-0726	7028	C	T	2	633	synonymous_variant	LOW	COX1	0.8089
HLI-0726	8701	A	G	1	539	missense_variant	MODERATE	ATP6	0.3391
HLI-0726	9449	C	T	0	643	synonymous_variant	LOW	COX3	0.0125
HLI-0726	9540	T	C	0	586	synonymous_variant	LOW	COX3	0.339
HLI-0726	10086	A	G	3	638	missense_variant	MODERATE	ND3	0.0088
HLI-0726	10398	A	G	0	572	missense_variant	MODERATE	ND3	0.445
HLI-0726	10640	T	C	0	648	synonymous_variant	LOW	ND4L	0.0044
HLI-0726	10873	T	C	0	553	synonymous_variant	LOW	ND4	0.3389
HLI-0726	11719	G	A	1	556	synonymous_variant	LOW	ND4	0.7756
HLI-0726	12705	C	T	0	585	synonymous_variant	LOW	ND5	0.4212
HLI-0726	13105	A	G	0	553	missense_variant	MODERATE	ND5	0.076
HLI-0726	13914	C	A	1	510	synonymous_variant	LOW	ND5	0.0091
HLI-0726	14766	C	T	3	555	missense_variant	MODERATE	CYTB	0.7696
HLI-0726	14905	G	A	0	688	synonymous_variant	LOW	CYTB	0.0526
HLI-0726	15301	G	A	0	525	synonymous_variant	LOW	CYTB	0.2912
HLI-0726	15311	A	G	0	554	missense_variant	MODERATE	CYTB	0.008

HLI-0726	15326	A	G	0	556	missense_variant	MODERATE	CYTB	0.9868
HLI-0726	15824	A	G	0	595	missense_variant	MODERATE	CYTB	0.0083
HLI-0726	16124	T	C	0	329	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0726	16223	C	T	0	195	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0726	16278	C	T	0	362	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0726	16362	T	C	0	479	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0726	16519	T	C	0	252	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0726	16527	C	T	0	229	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0727	73	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0727	151	C	T	1	562	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0727	152	T	C	1	565	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0727	263	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0727	750	A	G	0	643	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0727	1438	A	G	0	625	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0727	2706	A	G	2	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0727	3197	T	C	0	572	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0727	3768	A	G	5	603	synonymous_variant	LOW	ND1	0.002
HLI-0727	4769	A	G	1	571	synonymous_variant	LOW	ND2	0.9767
HLI-0727	7028	C	T	0	688	synonymous_variant	LOW	COX1	0.8089
HLI-0727	9477	G	A	0	607	missense_variant	MODERATE	COX3	0.0387
HLI-0727	11467	A	G	2	624	synonymous_variant	LOW	ND4	0.1231
HLI-0727	11719	G	A	1	573	synonymous_variant	LOW	ND4	0.7756
HLI-0727	12308	A	G	0	555	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0727	12372	G	A	1	536	synonymous_variant	LOW	ND5	0.1329
HLI-0727	13617	T	C	2	608	synonymous_variant	LOW	ND5	0.038
HLI-0727	14766	C	T	3	631	missense_variant	MODERATE	CYTB	0.7696
HLI-0727	14793	A	G	2	732	missense_variant	MODERATE	CYTB	0.0199
HLI-0727	15289	T	C	0	515	synonymous_variant	LOW	CYTB	0.0025
HLI-0727	15326	A	G	0	567	missense_variant	MODERATE	CYTB	0.9868
HLI-0727	16093	T	C	12	556	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0727	16256	C	T	0	604	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0727	16270	C	T	0	578	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0727	16311	T	C	0	533	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0727	16362	T	C	0	500	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0727	16526	G	A	1	260	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0728	73	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0728	199	T	C	1	395	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0728	204	T	C	1	397	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0728	250	T	C	0	244	upstream_gene_variant	MODIFIER	DLoop	0.0145

HLI-0728	263	A	G	0	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0728	574	A	C	1	199	upstream_gene_variant	MODIFIER	TRNF	0.0016
HLI-0728	750	A	G	2	690	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0728	1438	A	G	0	721	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0728	1719	G	A	0	725	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0728	2706	A	G	0	722	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0728	4529	A	T	3	661	synonymous_variant	LOW	ND2	0.015
HLI-0728	4769	A	G	3	621	synonymous_variant	LOW	ND2	0.9767
HLI-0728	5074	T	C	1	659	missense_variant	MODERATE	ND2	0.0017
HLI-0728	7028	C	T	3	748	synonymous_variant	LOW	COX1	0.8089
HLI-0728	8251	G	A	2	620	synonymous_variant	LOW	COX2	0.058
HLI-0728	10034	T	C	0	686	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0728	10238	T	C	0	653	synonymous_variant	LOW	ND3	0.0623
HLI-0728	10398	A	G	0	751	missense_variant	MODERATE	ND3	0.445
HLI-0728	11719	G	A	0	676	synonymous_variant	LOW	ND4	0.7756
HLI-0728	12408	T	A	2	620	synonymous_variant	LOW	ND5	1.00E-04
HLI-0728	12501	G	A	3	682	synonymous_variant	LOW	ND5	0.0258
HLI-0728	12705	C	T	3	736	synonymous_variant	LOW	ND5	0.4212
HLI-0728	14233	A	G	1	681	synonymous_variant	LOW	ND6	0.0369
HLI-0728	14766	C	T	3	659	missense_variant	MODERATE	CYTB	0.7696
HLI-0728	15043	G	A	2	721	synonymous_variant	LOW	CYTB	0.2362
HLI-0728	15244	A	G	2	665	synonymous_variant	LOW	CYTB	0.0103
HLI-0728	15326	A	G	0	746	missense_variant	MODERATE	CYTB	0.9868
HLI-0728	15924	A	G	3	728	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0728	16129	G	A	2	627	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0728	16148	C	T	3	675	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0728	16223	C	T	2	688	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0728	16294	C	T	2	635	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0728	16374	A	C	3	541	upstream_gene_variant	MODIFIER	DLoop	2.00E-04
HLI-0728	16391	G	A	5	581	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0728	16519	T	C	1	325	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0729	73	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0729	146	T	C	2	487	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0729	263	A	G	0	218	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0729	497	C	T	5	381	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0729	750	A	G	1	630	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0729	1189	T	C	0	636	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0729	1438	A	G	1	594	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0729	1811	A	G	0	614	upstream_gene_variant	MODIFIER	RNR2	0.0763

HLI-0729	2706	A	G	1	606	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0729	2887	T	C	1	614	upstream_gene_variant	MODIFIER	RNR2	0.0034
HLI-0729	3480	A	G	0	434	synonymous_variant	LOW	ND1	0.0392
HLI-0729	4769	A	G	1	561	synonymous_variant	LOW	ND2	0.9767
HLI-0729	7028	C	T	5	641	synonymous_variant	LOW	COX1	0.8089
HLI-0729	8311	T	C	0	571	upstream_gene_variant	MODIFIER	TRNK	0.0012
HLI-0729	9055	G	A	1	558	missense_variant	MODERATE	ATP6	0.0425
HLI-0729	9698	T	C	0	559	synonymous_variant	LOW	COX3	0.0405
HLI-0729	10398	A	G	1	685	missense_variant	MODERATE	ND3	0.445
HLI-0729	10550	A	G	2	626	synonymous_variant	LOW	ND4L	0.0376
HLI-0729	11299	T	C	2	549	synonymous_variant	LOW	ND4	0.0417
HLI-0729	11467	A	G	2	583	synonymous_variant	LOW	ND4	0.1231
HLI-0729	11719	G	A	1	565	synonymous_variant	LOW	ND4	0.7756
HLI-0729	12308	A	G	0	545	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0729	12372	G	A	0	552	synonymous_variant	LOW	ND5	0.1329
HLI-0729	14071	A	G	2	489	missense_variant	MODERATE	ND5	3.00E-04
HLI-0729	14167	C	T	0	520	synonymous_variant	LOW	ND6	0.0385
HLI-0729	14377	C	T	2	526	synonymous_variant	LOW	ND6	2.00E-04
HLI-0729	14766	C	T	7	508	missense_variant	MODERATE	CYTB	0.7696
HLI-0729	14798	T	C	2	595	missense_variant	MODERATE	CYTB	0.0651
HLI-0729	14857	T	C	1	585	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0729	15326	A	G	0	553	missense_variant	MODERATE	CYTB	0.9868
HLI-0729	16224	T	C	0	518	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0729	16311	T	C	1	488	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0729	16519	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0730	73	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0730	114	C	T	0	396	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0730	152	T	C	0	504	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0730	263	A	G	0	199	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0730	497	C	T	3	435	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0730	750	A	G	0	598	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0730	1189	T	C	0	596	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0730	1438	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0730	1811	A	G	0	575	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0730	2706	A	G	0	531	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0730	3480	A	G	0	393	synonymous_variant	LOW	ND1	0.0392
HLI-0730	3777	T	C	0	500	synonymous_variant	LOW	ND1	0.0015
HLI-0730	4769	A	G	0	558	synonymous_variant	LOW	ND2	0.9767
HLI-0730	7028	C	T	6	606	synonymous_variant	LOW	COX1	0.8089

HLI-0730	7729	A	G	1	578	synonymous_variant	LOW	COX2	2.00E-04
HLI-0730	9055	G	A	1	537	missense_variant	MODERATE	ATP6	0.0425
HLI-0730	9698	T	C	0	538	synonymous_variant	LOW	COX3	0.0405
HLI-0730	9800	T	C	0	689	synonymous_variant	LOW	COX3	2.00E-04
HLI-0730	10398	A	G	0	599	missense_variant	MODERATE	ND3	0.445
HLI-0730	10550	A	G	0	552	synonymous_variant	LOW	ND4L	0.0376
HLI-0730	11299	T	C	1	551	synonymous_variant	LOW	ND4	0.0417
HLI-0730	11467	A	G	0	585	synonymous_variant	LOW	ND4	0.1231
HLI-0730	11719	G	A	3	554	synonymous_variant	LOW	ND4	0.7756
HLI-0730	11914	G	A	0	525	synonymous_variant	LOW	ND4	0.1112
HLI-0730	12308	A	G	0	499	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0730	12372	G	A	2	474	synonymous_variant	LOW	ND5	0.1329
HLI-0730	13326	T	C	0	530	synonymous_variant	LOW	ND5	0.0032
HLI-0730	14167	C	T	1	525	synonymous_variant	LOW	ND6	0.0385
HLI-0730	14766	C	T	4	570	missense_variant	MODERATE	CYTB	0.7696
HLI-0730	14798	T	C	0	657	missense_variant	MODERATE	CYTB	0.0651
HLI-0730	15326	A	G	0	453	missense_variant	MODERATE	CYTB	0.9868
HLI-0730	15758	A	G	0	469	missense_variant	MODERATE	CYTB	0.0076
HLI-0730	15924	A	G	1	516	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0730	16093	T	C	20	474	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0730	16224	T	C	0	501	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0730	16234	C	T	0	535	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0730	16311	T	C	0	483	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0730	16519	T	C	1	228	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0731	196	T	C	5	420	upstream_gene_variant	MODIFIER	DLoop	0.0018
HLI-0731	263	A	G	0	163	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0731	750	A	G	0	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0731	1438	A	G	0	654	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0731	4769	A	G	1	675	synonymous_variant	LOW	ND2	0.9767
HLI-0731	9545	A	G	2	567	synonymous_variant	LOW	COX3	0.0469
HLI-0731	11152	T	C	0	605	synonymous_variant	LOW	ND4	0.0024
HLI-0731	12651	G	A	7	648	synonymous_variant	LOW	ND5	0.0027
HLI-0731	13500	T	C	0	572	synonymous_variant	LOW	ND5	0.0173
HLI-0731	14203	A	G	2	595	synonymous_variant	LOW	ND6	0.0061
HLI-0731	15326	A	G	0	560	missense_variant	MODERATE	CYTB	0.9868
HLI-0731	16519	T	C	0	279	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0732	73	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0732	152	T	C	1	433	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0732	263	A	G	2	162	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0732	497	C	T	5	358	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0732	750	A	G	1	454	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0732	1189	T	C	2	543	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0732	1438	A	G	0	514	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0732	1811	A	G	1	604	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0732	2706	A	G	0	563	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0732	3480	A	G	1	382	synonymous_variant	LOW	ND1	0.0392
HLI-0732	3736	G	A	0	432	missense_variant	MODERATE	ND1	0.0017
HLI-0732	4769	A	G	1	456	synonymous_variant	LOW	ND2	0.9767
HLI-0732	7028	C	T	4	609	synonymous_variant	LOW	COX1	0.8089
HLI-0732	9055	G	A	0	501	missense_variant	MODERATE	ATP6	0.0425
HLI-0732	9698	T	C	0	497	synonymous_variant	LOW	COX3	0.0405
HLI-0732	10398	A	G	0	500	missense_variant	MODERATE	ND3	0.445
HLI-0732	10550	A	G	0	544	synonymous_variant	LOW	ND4L	0.0376
HLI-0732	11299	T	C	2	439	synonymous_variant	LOW	ND4	0.0417
HLI-0732	11467	A	G	0	464	synonymous_variant	LOW	ND4	0.1231
HLI-0732	11470	A	G	0	473	synonymous_variant	LOW	ND4	0.0029
HLI-0732	11719	G	A	2	460	synonymous_variant	LOW	ND4	0.7756
HLI-0732	11914	G	A	1	542	synonymous_variant	LOW	ND4	0.1112
HLI-0732	12308	A	G	0	524	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0732	12372	G	A	1	524	synonymous_variant	LOW	ND5	0.1329
HLI-0732	14167	C	T	1	460	synonymous_variant	LOW	ND6	0.0385
HLI-0732	14766	C	T	3	502	missense_variant	MODERATE	CYTB	0.7696
HLI-0732	14798	T	C	0	565	missense_variant	MODERATE	CYTB	0.0651
HLI-0732	15326	A	G	0	507	missense_variant	MODERATE	CYTB	0.9868
HLI-0732	15924	A	G	2	548	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0732	16224	T	C	0	437	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0732	16311	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0732	16519	T	C	0	204	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0733	152	T	C	0	440	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0733	263	A	G	0	204	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0733	750	A	G	0	547	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0733	1438	A	G	0	527	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0733	4769	A	G	1	538	synonymous_variant	LOW	ND2	0.9767
HLI-0733	8628	C	T	0	455	synonymous_variant	LOW	ATP6	3.00E-04
HLI-0733	13581	T	C	0	536	synonymous_variant	LOW	ND5	6.00E-04
HLI-0733	15326	A	G	0	398	missense_variant	MODERATE	CYTB	0.9868
HLI-0733	16519	T	C	0	189	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0734	73	A	G	1	275	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0734	195	T	C	1	413	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0734	263	A	G	1	131	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0734	499	G	A	0	340	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0734	750	A	G	2	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0734	1438	A	G	0	620	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0734	1811	A	G	2	558	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0734	2706	A	G	2	574	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0734	4769	A	G	0	527	synonymous_variant	LOW	ND2	0.9767
HLI-0734	5999	T	C	0	604	synonymous_variant	LOW	COX1	0.0127
HLI-0734	6047	A	G	2	665	synonymous_variant	LOW	COX1	0.0114
HLI-0734	7028	C	T	2	641	synonymous_variant	LOW	COX1	0.8089
HLI-0734	8567	T	C	1	514	missense_variant	MODERATE	ATP6/8	0.0021
HLI-0734	8818	C	T	4	583	synonymous_variant	LOW	ATP6	0.0061
HLI-0734	9548	G	A	4	523	synonymous_variant	LOW	COX3	0.0149
HLI-0734	11332	C	T	3	565	synonymous_variant	LOW	ND4	0.0115
HLI-0734	11467	A	G	0	579	synonymous_variant	LOW	ND4	0.1231
HLI-0734	11719	G	A	0	561	synonymous_variant	LOW	ND4	0.7756
HLI-0734	12308	A	G	2	559	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0734	12372	G	A	1	535	synonymous_variant	LOW	ND5	0.1329
HLI-0734	14620	C	T	4	578	synonymous_variant	LOW	ND6	0.0126
HLI-0734	15326	A	G	0	475	missense_variant	MODERATE	CYTB	0.9868
HLI-0734	15693	T	C	0	497	missense_variant	MODERATE	CYTB	0.0114
HLI-0734	16356	T	C	0	452	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0734	16519	T	C	0	270	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0735	73	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0735	217	T	C	0	307	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0735	228	G	A	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0735	263	A	G	0	221	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0735	340	C	T	0	221	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0735	508	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0735	750	A	G	0	482	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0735	1438	A	G	1	497	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0735	1811	A	G	0	504	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0735	2706	A	G	0	464	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0735	3720	A	G	0	402	synonymous_variant	LOW	ND1	0.0069
HLI-0735	4769	A	G	0	538	synonymous_variant	LOW	ND2	0.9767
HLI-0735	5390	A	G	0	533	synonymous_variant	LOW	ND2	0.0069
HLI-0735	5426	T	C	0	586	synonymous_variant	LOW	ND2	0.0091
HLI-0735	6045	C	T	2	503	synonymous_variant	LOW	COX1	0.0065

HLI-0735	6152	T	C	2	489	synonymous_variant	LOW	COX1	0.0077
HLI-0735	7028	C	T	2	582	synonymous_variant	LOW	COX1	0.8089
HLI-0735	10876	A	G	0	508	synonymous_variant	LOW	ND4	0.0098
HLI-0735	11467	A	G	2	565	synonymous_variant	LOW	ND4	0.1231
HLI-0735	11719	G	A	0	480	synonymous_variant	LOW	ND4	0.7756
HLI-0735	12308	A	G	1	562	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0735	12372	G	A	1	528	synonymous_variant	LOW	ND5	0.1329
HLI-0735	13020	T	C	3	485	synonymous_variant	LOW	ND5	0.0106
HLI-0735	13734	T	C	2	374	synonymous_variant	LOW	ND5	0.0067
HLI-0735	14766	C	T	1	566	missense_variant	MODERATE	CYTB	0.7696
HLI-0735	15326	A	G	0	362	missense_variant	MODERATE	CYTB	0.9868
HLI-0735	15907	A	G	0	587	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0735	16051	A	G	2	520	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0735	16129	G	C	1	590	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0735	16362	T	C	1	373	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0735	16519	T	C	0	165	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0736	73	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0736	199	T	C	0	60	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0736	204	T	C	0	59	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0736	250	T	C	0	38	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0736	263	A	G	0	35	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0736	750	A	G	0	42	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0736	1438	A	G	0	43	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0736	1719	G	A	0	36	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0736	2706	A	G	0	43	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0736	4529	A	T	0	54	synonymous_variant	LOW	ND2	0.015
HLI-0736	4769	A	G	0	44	synonymous_variant	LOW	ND2	0.9767
HLI-0736	7028	C	T	1	75	synonymous_variant	LOW	COX1	0.8089
HLI-0736	8251	G	A	0	56	synonymous_variant	LOW	COX2	0.058
HLI-0736	8519	G	A	1	46	missense_variant	MODERATE	ATP8	0.0024
HLI-0736	10034	T	C	0	62	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0736	10238	T	C	0	80	synonymous_variant	LOW	ND3	0.0623
HLI-0736	10398	A	G	0	56	missense_variant	MODERATE	ND3	0.445
HLI-0736	10819	A	G	0	60	synonymous_variant	LOW	ND4	0.0228
HLI-0736	11719	G	A	0	54	synonymous_variant	LOW	ND4	0.7756
HLI-0736	12501	G	A	0	44	synonymous_variant	LOW	ND5	0.0258
HLI-0736	12705	C	T	1	69	synonymous_variant	LOW	ND5	0.4212
HLI-0736	13780	A	G	0	37	missense_variant	MODERATE	ND5	0.0179
HLI-0736	14766	C	T	0	71	missense_variant	MODERATE	CYTB	0.7696

HLI-0736	15043	G	A	0	76	synonymous_variant	LOW	CYTB	0.2362
HLI-0736	15326	A	G	0	36	missense_variant	MODERATE	CYTB	0.9868
HLI-0736	15924	A	G	0	47	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0736	16129	G	A	0	50	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0736	16223	C	T	0	47	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0736	16391	G	A	0	42	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0736	16519	T	C	1	25	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0737	73	A	G	0	313	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0737	152	T	C	2	574	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0737	263	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0737	750	A	G	2	633	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0737	1438	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0737	1598	G	A	0	614	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0737	1703	C	T	0	606	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0737	1719	G	A	0	660	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0737	2639	C	T	2	586	upstream_gene_variant	MODIFIER	RNR2	0.0026
HLI-0737	2706	A	G	1	672	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0737	3921	C	A	1	567	synonymous_variant	LOW	ND1	0.0026
HLI-0737	4769	A	G	1	547	synonymous_variant	LOW	ND2	0.9767
HLI-0737	4960	C	T	0	603	missense_variant	MODERATE	ND2	0.0028
HLI-0737	5471	G	A	1	591	synonymous_variant	LOW	ND2	0.0128
HLI-0737	7028	C	T	8	678	synonymous_variant	LOW	COX1	0.8089
HLI-0737	8251	G	A	4	547	synonymous_variant	LOW	COX2	0.058
HLI-0737	8472	C	T	1	493	missense_variant	MODERATE	ATP8	0.0027
HLI-0737	8836	A	G	0	597	missense_variant	MODERATE	ATP6	0.0029
HLI-0737	9335	C	T	1	589	synonymous_variant	LOW	COX3	0.0021
HLI-0737	10238	T	C	2	596	synonymous_variant	LOW	ND3	0.0623
HLI-0737	11362	A	G	0	593	synonymous_variant	LOW	ND4	0.0024
HLI-0737	11719	G	A	1	580	synonymous_variant	LOW	ND4	0.7756
HLI-0737	12501	G	A	2	613	synonymous_variant	LOW	ND5	0.0258
HLI-0737	12705	C	T	2	724	synonymous_variant	LOW	ND5	0.4212
HLI-0737	12822	A	G	1	634	synonymous_variant	LOW	ND5	0.0026
HLI-0737	14766	C	T	1	591	missense_variant	MODERATE	CYTB	0.7696
HLI-0737	15326	A	G	0	580	missense_variant	MODERATE	CYTB	0.9868
HLI-0737	16145	G	A	0	550	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0737	16176	C	G	2	589	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0737	16215	A	G	0	575	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0737	16223	C	T	1	577	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0737	16278	C	T	6	574	upstream_gene_variant	MODIFIER	DLoop	0.1057

HLI-0737	16390	G	A	0	506	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0737	16519	T	C	0	297	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0738	73	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0738	189	A	G	1	352	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0738	194	C	T	1	362	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0738	195	T	C	1	363	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0738	204	T	C	1	370	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0738	207	G	A	1	380	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0738	263	A	G	0	110	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0738	709	G	A	2	645	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0738	750	A	G	1	690	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0738	1243	T	C	1	624	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0738	1406	T	C	1	658	upstream_gene_variant	MODIFIER	RNR1	0.0034
HLI-0738	1438	A	G	0	720	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0738	2706	A	G	2	566	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0738	3505	A	G	2	512	missense_variant	MODERATE	ND1	0.0144
HLI-0738	3826	T	C	1	546	synonymous_variant	LOW	ND1	0.0014
HLI-0738	4769	A	G	3	569	synonymous_variant	LOW	ND2	0.9767
HLI-0738	5046	G	A	3	590	missense_variant	MODERATE	ND2	0.018
HLI-0738	5460	G	A	1	624	missense_variant	MODERATE	ND2	0.0651
HLI-0738	7028	C	T	6	671	synonymous_variant	LOW	COX1	0.8089
HLI-0738	8251	G	A	1	529	synonymous_variant	LOW	COX2	0.058
HLI-0738	8994	G	A	2	592	synonymous_variant	LOW	ATP6	0.0167
HLI-0738	11674	C	T	3	623	synonymous_variant	LOW	ND4	0.0116
HLI-0738	11719	G	A	1	677	synonymous_variant	LOW	ND4	0.7756
HLI-0738	11947	A	G	1	558	synonymous_variant	LOW	ND4	0.011
HLI-0738	12414	T	C	3	562	synonymous_variant	LOW	ND5	0.0139
HLI-0738	12705	C	T	1	606	synonymous_variant	LOW	ND5	0.4212
HLI-0738	13263	A	G	1	698	synonymous_variant	LOW	ND5	0.0354
HLI-0738	14766	C	T	3	570	missense_variant	MODERATE	CYTB	0.7696
HLI-0738	15326	A	G	0	562	missense_variant	MODERATE	CYTB	0.9868
HLI-0738	15784	T	C	0	628	synonymous_variant	LOW	CYTB	0.0363
HLI-0738	15884	G	C	3	581	missense_variant	MODERATE	CYTB	0.011
HLI-0738	16223	C	T	1	545	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0738	16292	C	T	0	525	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0738	16519	T	C	0	296	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0739	73	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0739	146	T	C	0	473	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0739	152	T	C	0	486	upstream_gene_variant	MODIFIER	DLoop	0.2668

HLI-0739	195	T	C	0	453	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0739	263	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0739	750	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0739	769	G	A	1	625	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0739	1018	G	A	1	690	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0739	1438	A	G	0	529	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0739	2416	T	C	1	381	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0739	2706	A	G	0	535	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0739	2789	C	T	1	582	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0739	3594	C	T	0	458	synonymous_variant	LOW	ND1	0.0789
HLI-0739	4104	A	G	2	367	synonymous_variant	LOW	ND1	0.0785
HLI-0739	4769	A	G	0	526	synonymous_variant	LOW	ND2	0.9767
HLI-0739	5090	T	C	0	454	synonymous_variant	LOW	ND2	0.0054
HLI-0739	5460	G	A	1	488	missense_variant	MODERATE	ND2	0.0651
HLI-0739	7028	C	T	1	619	synonymous_variant	LOW	COX1	0.8089
HLI-0739	7175	T	C	0	535	synonymous_variant	LOW	COX1	0.0224
HLI-0739	7256	C	T	0	498	synonymous_variant	LOW	COX1	0.0784
HLI-0739	7274	C	T	0	466	synonymous_variant	LOW	COX1	0.0214
HLI-0739	7521	G	A	2	352	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0739	7771	A	G	1	570	synonymous_variant	LOW	COX2	0.0223
HLI-0739	8206	G	A	0	505	synonymous_variant	LOW	COX2	0.0287
HLI-0739	8701	A	G	1	426	missense_variant	MODERATE	ATP6	0.3391
HLI-0739	9221	A	G	3	576	synonymous_variant	LOW	COX3	0.0277
HLI-0739	9540	T	C	0	477	synonymous_variant	LOW	COX3	0.339
HLI-0739	10115	T	C	1	671	synonymous_variant	LOW	ND3	0.0278
HLI-0739	10143	G	A	1	730	missense_variant	MODERATE	ND3	0.0075
HLI-0739	10398	A	G	1	534	missense_variant	MODERATE	ND3	0.445
HLI-0739	10873	T	C	0	484	synonymous_variant	LOW	ND4	0.3389
HLI-0739	11719	G	A	0	613	synonymous_variant	LOW	ND4	0.7756
HLI-0739	11914	G	A	2	465	synonymous_variant	LOW	ND4	0.1112
HLI-0739	11944	T	C	2	469	synonymous_variant	LOW	ND4	0.0331
HLI-0739	12693	A	G	0	451	synonymous_variant	LOW	ND5	0.0205
HLI-0739	12705	C	T	0	463	synonymous_variant	LOW	ND5	0.4212
HLI-0739	13590	G	A	2	513	synonymous_variant	LOW	ND5	0.0586
HLI-0739	13650	C	T	5	512	synonymous_variant	LOW	ND5	0.079
HLI-0739	13803	A	G	1	365	synonymous_variant	LOW	ND5	0.0216
HLI-0739	14566	A	G	3	609	synonymous_variant	LOW	ND6	0.0214
HLI-0739	14766	C	T	10	572	missense_variant	MODERATE	CYTB	0.7696
HLI-0739	15301	G	A	1	405	synonymous_variant	LOW	CYTB	0.2912

HLI-0739	15326	A	G	0	431	missense_variant	MODERATE	CYTB	0.9868
HLI-0739	15735	C	T	1	369	missense_variant	MODERATE	CYTB	0.0052
HLI-0739	15784	T	C	1	359	synonymous_variant	LOW	CYTB	0.0363
HLI-0739	16223	C	T	2	145	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0739	16278	C	T	2	250	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0739	16290	C	T	2	258	upstream_gene_variant	MODIFIER	DLoop	0.0394
HLI-0739	16294	C	T	2	263	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0739	16309	A	G	45	256	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0739	16390	G	A	1	348	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0740	73	A	G	0	283	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0740	263	A	G	2	421	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0740	750	A	G	0	499	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0740	1438	A	G	0	520	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0740	1555	A	G	1	537	upstream_gene_variant	MODIFIER	RNR1	0.0015
HLI-0740	3010	G	A	1	513	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0740	4639	T	C	0	542	missense_variant	MODERATE	ND2	0.0034
HLI-0740	4769	A	G	0	488	synonymous_variant	LOW	ND2	0.9767
HLI-0740	6365	T	C	1	505	synonymous_variant	LOW	COX1	0.0026
HLI-0740	15326	A	G	0	316	missense_variant	MODERATE	CYTB	0.9868
HLI-0740	16162	A	G	3	585	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0740	16209	T	C	1	587	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0740	16519	T	C	0	213	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0741	73	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0741	146	T	C	0	548	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0741	152	T	C	0	563	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0741	195	T	C	0	535	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0741	263	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0741	750	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0741	769	G	A	1	657	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0741	1018	G	A	2	677	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0741	1438	A	G	2	594	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0741	2416	T	C	1	513	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0741	2706	A	G	2	571	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0741	2789	C	T	2	606	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0741	3594	C	T	0	491	synonymous_variant	LOW	ND1	0.0789
HLI-0741	3918	G	A	2	556	synonymous_variant	LOW	ND1	0.009
HLI-0741	4104	A	G	0	451	synonymous_variant	LOW	ND1	0.0785
HLI-0741	4769	A	G	0	614	synonymous_variant	LOW	ND2	0.9767
HLI-0741	4772	T	C	0	629	synonymous_variant	LOW	ND2	0.0021

HLI-0741	5263	C	T	0	552	missense_variant	MODERATE	ND2	0.0058
HLI-0741	5285	A	G	0	589	synonymous_variant	LOW	ND2	0.0049
HLI-0741	6152	T	C	0	618	synonymous_variant	LOW	COX1	0.0077
HLI-0741	7028	C	T	2	666	synonymous_variant	LOW	COX1	0.8089
HLI-0741	7175	T	C	2	568	synonymous_variant	LOW	COX1	0.0224
HLI-0741	7256	C	T	7	578	synonymous_variant	LOW	COX1	0.0784
HLI-0741	7274	C	T	6	538	synonymous_variant	LOW	COX1	0.0214
HLI-0741	7521	G	A	0	456	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0741	7771	A	G	1	594	synonymous_variant	LOW	COX2	0.0223
HLI-0741	8206	G	A	1	550	synonymous_variant	LOW	COX2	0.0287
HLI-0741	8701	A	G	2	549	missense_variant	MODERATE	ATP6	0.3391
HLI-0741	9212	C	T	0	654	synonymous_variant	LOW	COX3	3.00E-04
HLI-0741	9221	A	G	0	687	synonymous_variant	LOW	COX3	0.0277
HLI-0741	9540	T	C	0	609	synonymous_variant	LOW	COX3	0.339
HLI-0741	10115	T	C	1	617	synonymous_variant	LOW	ND3	0.0278
HLI-0741	10398	A	G	0	618	missense_variant	MODERATE	ND3	0.445
HLI-0741	10873	T	C	1	549	synonymous_variant	LOW	ND4	0.3389
HLI-0741	11719	G	A	0	612	synonymous_variant	LOW	ND4	0.7756
HLI-0741	11914	G	A	0	578	synonymous_variant	LOW	ND4	0.1112
HLI-0741	11944	T	C	3	600	synonymous_variant	LOW	ND4	0.0331
HLI-0741	12693	A	G	0	556	synonymous_variant	LOW	ND5	0.0205
HLI-0741	12705	C	T	4	604	synonymous_variant	LOW	ND5	0.4212
HLI-0741	13590	G	A	0	583	synonymous_variant	LOW	ND5	0.0586
HLI-0741	13650	C	T	2	615	synonymous_variant	LOW	ND5	0.079
HLI-0741	13803	A	G	1	392	synonymous_variant	LOW	ND5	0.0216
HLI-0741	14566	A	G	1	639	synonymous_variant	LOW	ND6	0.0214
HLI-0741	14766	C	T	3	581	missense_variant	MODERATE	CYTB	0.7696
HLI-0741	15244	A	G	1	513	synonymous_variant	LOW	CYTB	0.0103
HLI-0741	15301	G	A	0	514	synonymous_variant	LOW	CYTB	0.2912
HLI-0741	15326	A	G	0	493	missense_variant	MODERATE	CYTB	0.9868
HLI-0741	15391	C	T	0	474	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0741	15629	T	C	0	435	synonymous_variant	LOW	CYTB	0.0062
HLI-0741	15784	T	C	0	474	synonymous_variant	LOW	CYTB	0.0363
HLI-0741	16223	C	T	6	522	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0741	16278	C	T	2	568	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0741	16294	C	T	2	538	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0741	16368	T	C	0	492	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0741	16390	G	A	1	492	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0741	16519	T	C	1	245	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0742	73	A	G	1	10	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0742	143	G	A	1	10	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0743	263	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0743	750	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0743	1438	A	G	0	561	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0743	4769	A	G	2	571	synonymous_variant	LOW	ND2	0.9767
HLI-0743	11788	C	T	2	560	synonymous_variant	LOW	ND4	7.00E-04
HLI-0743	15326	A	G	0	495	missense_variant	MODERATE	CYTB	0.9868
HLI-0743	16240	A	G	11	548	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0743	16519	T	C	1	249	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0744	73	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0744	152	T	C	0	536	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0744	199	T	C	2	540	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0744	263	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0744	750	A	G	0	592	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0744	1189	T	C	0	707	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0744	1438	A	G	2	579	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0744	1811	A	G	1	577	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0744	2706	A	G	0	584	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0744	3480	A	G	0	475	synonymous_variant	LOW	ND1	0.0392
HLI-0744	4646	T	C	1	673	synonymous_variant	LOW	ND2	0.0124
HLI-0744	4769	A	G	0	610	synonymous_variant	LOW	ND2	0.9767
HLI-0744	5913	G	A	2	714	missense_variant	MODERATE	COX1	0.0097
HLI-0744	7028	C	T	1	691	synonymous_variant	LOW	COX1	0.8089
HLI-0744	9055	G	A	1	631	missense_variant	MODERATE	ATP6	0.0425
HLI-0744	9698	T	C	2	542	synonymous_variant	LOW	COX3	0.0405
HLI-0744	9962	G	A	2	692	synonymous_variant	LOW	COX3	0.0034
HLI-0744	10289	A	G	1	611	synonymous_variant	LOW	ND3	0.0032
HLI-0744	10398	A	G	1	566	missense_variant	MODERATE	ND3	0.445
HLI-0744	10550	A	G	0	606	synonymous_variant	LOW	ND4L	0.0376
HLI-0744	11299	T	C	1	666	synonymous_variant	LOW	ND4	0.0417
HLI-0744	11467	A	G	0	690	synonymous_variant	LOW	ND4	0.1231
HLI-0744	11719	G	A	0	578	synonymous_variant	LOW	ND4	0.7756
HLI-0744	11923	A	G	0	635	synonymous_variant	LOW	ND4	0.0023
HLI-0744	12308	A	G	1	526	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0744	12372	G	A	2	489	synonymous_variant	LOW	ND5	0.1329
HLI-0744	13967	C	T	2	518	missense_variant	MODERATE	ND5	0.003
HLI-0744	14167	C	T	4	519	synonymous_variant	LOW	ND6	0.0385
HLI-0744	14766	C	T	3	652	missense_variant	MODERATE	CYTB	0.7696

HLI-0744	14798	T	C	0	740	missense_variant	MODERATE	CYTB	0.0651
HLI-0744	15257	G	A	0	507	missense_variant	MODERATE	CYTB	0.0155
HLI-0744	15326	A	G	0	516	missense_variant	MODERATE	CYTB	0.9868
HLI-0744	15946	C	T	1	487	upstream_gene_variant	MODIFIER	TRNT	0.0018
HLI-0744	16224	T	C	2	577	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0744	16311	T	C	1	484	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0744	16319	G	A	2	509	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0744	16463	A	G	2	365	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0744	16519	T	C	1	283	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0745	263	A	G	1	306	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0745	750	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0745	1438	A	G	0	692	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0745	3010	G	A	0	611	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0745	4769	A	G	1	622	synonymous_variant	LOW	ND2	0.9767
HLI-0745	7980	A	G	4	687	missense_variant	MODERATE	COX2	1.00E-04
HLI-0745	8602	T	C	0	641	missense_variant	MODERATE	ATP6	0.0017
HLI-0745	14212	T	C	1	617	synonymous_variant	LOW	ND6	0.0204
HLI-0745	15326	A	G	1	585	missense_variant	MODERATE	CYTB	0.9868
HLI-0745	16519	T	C	0	252	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0746	73	A	G	0	307	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0746	150	C	T	0	545	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0746	152	T	C	0	550	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0746	195	T	C	1	497	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0746	215	A	G	1	458	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0746	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0746	295	C	T	1	219	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0746	319	T	C	0	215	upstream_gene_variant	MODIFIER	DLoop	0.0041
HLI-0746	489	T	C	1	394	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0746	750	A	G	1	586	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0746	1438	A	G	0	637	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0746	1850	T	C	1	609	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0746	2706	A	G	1	555	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0746	4216	T	C	0	525	missense_variant	MODERATE	ND1	0.0991
HLI-0746	4769	A	G	1	600	synonymous_variant	LOW	ND2	0.9767
HLI-0746	7028	C	T	2	663	synonymous_variant	LOW	COX1	0.8089
HLI-0746	7476	C	T	1	649	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0746	7789	G	A	2	601	synonymous_variant	LOW	COX2	0.0092
HLI-0746	10398	A	G	1	648	missense_variant	MODERATE	ND3	0.445
HLI-0746	10499	A	G	1	650	synonymous_variant	LOW	ND4L	0.0093

HLI-0746	11251	A	G	2	606	synonymous_variant	LOW	ND4	0.0932
HLI-0746	11377	G	A	2	549	synonymous_variant	LOW	ND4	0.0125
HLI-0746	11719	G	A	0	620	synonymous_variant	LOW	ND4	0.7756
HLI-0746	12612	A	G	3	703	synonymous_variant	LOW	ND5	0.0506
HLI-0746	13708	G	A	1	657	missense_variant	MODERATE	ND5	0.0717
HLI-0746	13722	A	G	1	651	synonymous_variant	LOW	ND5	0.0077
HLI-0746	14133	A	G	2	579	synonymous_variant	LOW	ND5	0.0094
HLI-0746	14766	C	T	1	563	missense_variant	MODERATE	CYTB	0.7696
HLI-0746	15257	G	A	0	503	missense_variant	MODERATE	CYTB	0.0155
HLI-0746	15326	A	G	1	505	missense_variant	MODERATE	CYTB	0.9868
HLI-0746	15452	C	A	1	457	missense_variant	MODERATE	CYTB	0.0933
HLI-0746	16069	C	T	2	642	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0746	16126	T	C	0	672	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0746	16145	G	A	0	653	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0746	16261	C	T	0	545	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0746	16278	C	T	0	584	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0747	73	A	G	1	212	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0747	143	G	A	1	406	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0747	146	T	C	1	425	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0747	152	T	C	1	436	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0747	182	C	T	1	448	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0747	195	T	C	2	439	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0747	263	A	G	1	210	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0747	750	A	G	0	663	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0747	769	G	A	0	711	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0747	1018	G	A	2	641	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0747	1438	A	G	0	635	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0747	2416	T	C	1	475	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0747	2706	A	G	0	552	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0747	2789	C	T	3	570	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0747	3594	C	T	0	497	synonymous_variant	LOW	ND1	0.0789
HLI-0747	4104	A	G	1	432	synonymous_variant	LOW	ND1	0.0785
HLI-0747	4769	A	G	0	563	synonymous_variant	LOW	ND2	0.9767
HLI-0747	4812	G	C	0	604	missense_variant	MODERATE	ND2	1.00E-04
HLI-0747	5196	T	C	0	524	synonymous_variant	LOW	ND2	0.0021
HLI-0747	7028	C	T	2	635	synonymous_variant	LOW	COX1	0.8089
HLI-0747	7175	T	C	0	573	synonymous_variant	LOW	COX1	0.0224
HLI-0747	7256	C	T	0	589	synonymous_variant	LOW	COX1	0.0784
HLI-0747	7274	C	T	0	545	synonymous_variant	LOW	COX1	0.0214

HLI-0747	7521	G	A	0	425	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0747	7771	A	G	0	589	synonymous_variant	LOW	COX2	0.0223
HLI-0747	8206	G	A	1	571	synonymous_variant	LOW	COX2	0.0287
HLI-0747	8701	A	G	2	498	missense_variant	MODERATE	ATP6	0.3391
HLI-0747	9221	A	G	0	596	synonymous_variant	LOW	COX3	0.0277
HLI-0747	9356	C	T	1	626	synonymous_variant	LOW	COX3	8.00E-04
HLI-0747	9530	T	C	1	541	synonymous_variant	LOW	COX3	0.0014
HLI-0747	9540	T	C	1	561	synonymous_variant	LOW	COX3	0.339
HLI-0747	10115	T	C	2	642	synonymous_variant	LOW	ND3	0.0278
HLI-0747	10398	A	G	2	552	missense_variant	MODERATE	ND3	0.445
HLI-0747	10873	T	C	1	541	synonymous_variant	LOW	ND4	0.3389
HLI-0747	11386	T	C	0	583	synonymous_variant	LOW	ND4	0.0012
HLI-0747	11719	G	A	0	600	synonymous_variant	LOW	ND4	0.7756
HLI-0747	11914	G	A	0	574	synonymous_variant	LOW	ND4	0.1112
HLI-0747	11944	T	C	0	613	synonymous_variant	LOW	ND4	0.0331
HLI-0747	12612	A	G	2	471	synonymous_variant	LOW	ND5	0.0506
HLI-0747	12693	A	G	3	531	synonymous_variant	LOW	ND5	0.0205
HLI-0747	12705	C	T	1	542	synonymous_variant	LOW	ND5	0.4212
HLI-0747	13590	G	A	2	560	synonymous_variant	LOW	ND5	0.0586
HLI-0747	13650	C	T	2	597	synonymous_variant	LOW	ND5	0.079
HLI-0747	13803	A	G	0	366	synonymous_variant	LOW	ND5	0.0216
HLI-0747	13934	C	T	1	458	missense_variant	MODERATE	ND5	0.0122
HLI-0747	14566	A	G	1	592	synonymous_variant	LOW	ND6	0.0214
HLI-0747	14766	C	T	0	543	missense_variant	MODERATE	CYTB	0.7696
HLI-0747	15301	G	A	1	475	synonymous_variant	LOW	CYTB	0.2912
HLI-0747	15326	A	G	1	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0747	15596	G	A	0	466	missense_variant	MODERATE	CYTB	0.0018
HLI-0747	15784	T	C	0	469	synonymous_variant	LOW	CYTB	0.0363
HLI-0747	16223	C	T	0	492	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0747	16278	C	T	1	516	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0747	16294	C	T	17	478	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0747	16390	G	A	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0748	73	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0748	195	T	C	0	421	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0748	263	A	G	2	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0748	497	C	T	2	456	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0748	750	A	G	2	615	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0748	1187	T	C	0	643	upstream_gene_variant	MODIFIER	RNR1	8.00E-04
HLI-0748	1189	T	C	0	651	upstream_gene_variant	MODIFIER	RNR1	0.0318

HLI-0748	1438	A	G	0	628	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0748	1811	A	G	7	569	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0748	2706	A	G	0	520	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0748	3480	A	G	1	454	synonymous_variant	LOW	ND1	0.0392
HLI-0748	4113	G	A	1	485	synonymous_variant	LOW	ND1	0.0026
HLI-0748	4769	A	G	2	533	synonymous_variant	LOW	ND2	0.9767
HLI-0748	6357	C	T	0	588	synonymous_variant	LOW	COX1	3.00E-04
HLI-0748	7028	C	T	2	621	synonymous_variant	LOW	COX1	0.8089
HLI-0748	9055	G	A	0	585	missense_variant	MODERATE	ATP6	0.0425
HLI-0748	9698	T	C	0	567	synonymous_variant	LOW	COX3	0.0405
HLI-0748	10398	A	G	0	569	missense_variant	MODERATE	ND3	0.445
HLI-0748	10550	A	G	1	580	synonymous_variant	LOW	ND4L	0.0376
HLI-0748	11299	T	C	0	575	synonymous_variant	LOW	ND4	0.0417
HLI-0748	11467	A	G	1	601	synonymous_variant	LOW	ND4	0.1231
HLI-0748	11719	G	A	0	569	synonymous_variant	LOW	ND4	0.7756
HLI-0748	12308	A	G	1	475	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0748	12372	G	A	0	510	synonymous_variant	LOW	ND5	0.1329
HLI-0748	14167	C	T	1	509	synonymous_variant	LOW	ND6	0.0385
HLI-0748	14766	C	T	4	527	missense_variant	MODERATE	CYTB	0.7696
HLI-0748	14798	T	C	0	634	missense_variant	MODERATE	CYTB	0.0651
HLI-0748	15326	A	G	0	500	missense_variant	MODERATE	CYTB	0.9868
HLI-0748	16093	T	C	18	519	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0748	16224	T	C	0	503	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0748	16311	T	C	0	477	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0748	16519	T	C	0	272	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0749	73	A	G	1	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0749	150	C	T	0	522	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0749	185	G	A	6	520	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0749	228	G	A	0	486	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0749	263	A	G	0	188	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0749	295	C	T	2	242	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0749	462	C	T	3	389	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0749	489	T	C	0	379	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0749	750	A	G	0	601	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0749	1438	A	G	0	648	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0749	2706	A	G	0	592	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0749	3010	G	A	2	624	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0749	4216	T	C	3	535	missense_variant	MODERATE	ND1	0.0991
HLI-0749	4769	A	G	1	644	synonymous_variant	LOW	ND2	0.9767

HLI-0749	7028	C	T	1	674	synonymous_variant	LOW	COX1	0.8089
HLI-0749	7772	A	G	1	594	missense_variant	MODERATE	COX2	1.00E-04
HLI-0749	10398	A	G	3	632	missense_variant	MODERATE	ND3	0.445
HLI-0749	11204	T	C	1	600	missense_variant	MODERATE	ND4	0.003
HLI-0749	11251	A	G	2	694	synonymous_variant	LOW	ND4	0.0932
HLI-0749	11719	G	A	2	620	synonymous_variant	LOW	ND4	0.7756
HLI-0749	12612	A	G	14	549	synonymous_variant	LOW	ND5	0.0506
HLI-0749	13708	G	A	0	581	missense_variant	MODERATE	ND5	0.0717
HLI-0749	14766	C	T	4	626	missense_variant	MODERATE	CYTB	0.7696
HLI-0749	14798	T	C	2	713	missense_variant	MODERATE	CYTB	0.0651
HLI-0749	15326	A	G	1	477	missense_variant	MODERATE	CYTB	0.9868
HLI-0749	15452	C	A	6	517	missense_variant	MODERATE	CYTB	0.0933
HLI-0749	16069	C	T	1	564	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0749	16126	T	C	1	598	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0750	114	C	T	1	385	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0750	146	T	C	0	463	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0750	152	T	C	0	473	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0750	153	A	G	0	471	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0750	183	A	G	0	461	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0750	195	T	C	0	464	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0750	263	A	G	0	450	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0750	709	G	A	2	674	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0750	750	A	G	1	739	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0750	1438	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0750	4769	A	G	1	578	synonymous_variant	LOW	ND2	0.9767
HLI-0750	8864	T	C	0	587	missense_variant	MODERATE	ATP6	3.00E-04
HLI-0750	13101	A	C	4	654	synonymous_variant	LOW	ND5	0.0055
HLI-0750	13711	G	A	3	516	missense_variant	MODERATE	ND5	0.0011
HLI-0750	15326	A	G	1	589	missense_variant	MODERATE	CYTB	0.9868
HLI-0750	16288	T	C	1	475	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0750	16362	T	C	0	495	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0751	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0751	750	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0751	1438	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0751	4136	A	G	1	642	missense_variant	MODERATE	ND1	0.0012
HLI-0751	4769	A	G	1	628	synonymous_variant	LOW	ND2	0.9767
HLI-0751	11719	G	A	0	649	synonymous_variant	LOW	ND4	0.7756
HLI-0751	15326	A	G	0	644	missense_variant	MODERATE	CYTB	0.9868
HLI-0751	16129	G	A	1	660	upstream_gene_variant	MODIFIER	DLoop	0.1301

HLI-0751	16316	A	G	0	539	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0751	16519	T	C	1	359	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0752	73	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0752	240	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0752	263	A	G	0	275	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0752	709	G	A	1	665	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0752	750	A	G	1	727	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0752	930	G	A	4	619	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0752	1438	A	G	2	705	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0752	1888	G	A	0	708	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0752	2706	A	G	0	681	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0752	4216	T	C	0	701	missense_variant	MODERATE	ND1	0.0991
HLI-0752	4769	A	G	2	585	synonymous_variant	LOW	ND2	0.9767
HLI-0752	4917	A	G	3	595	missense_variant	MODERATE	ND2	0.0477
HLI-0752	5147	G	A	2	586	synonymous_variant	LOW	ND2	0.0437
HLI-0752	7028	C	T	2	701	synonymous_variant	LOW	COX1	0.8089
HLI-0752	8158	A	G	4	634	synonymous_variant	LOW	COX2	0.0021
HLI-0752	8697	G	A	0	635	synonymous_variant	LOW	ATP6	0.0466
HLI-0752	9947	G	A	0	731	synonymous_variant	LOW	COX3	0.0092
HLI-0752	10463	T	C	0	738	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0752	11251	A	G	1	657	synonymous_variant	LOW	ND4	0.0932
HLI-0752	11719	G	A	0	654	synonymous_variant	LOW	ND4	0.7756
HLI-0752	11812	A	G	2	644	synonymous_variant	LOW	ND4	0.0332
HLI-0752	12441	T	C	3	554	synonymous_variant	LOW	ND5	0.0012
HLI-0752	13368	G	A	0	696	synonymous_variant	LOW	ND5	0.0495
HLI-0752	13563	A	G	0	629	synonymous_variant	LOW	ND5	0.0072
HLI-0752	13743	T	C	1	521	synonymous_variant	LOW	ND5	0.0037
HLI-0752	14233	A	G	2	595	synonymous_variant	LOW	ND6	0.0369
HLI-0752	14766	C	T	0	598	missense_variant	MODERATE	CYTB	0.7696
HLI-0752	14905	G	A	0	697	synonymous_variant	LOW	CYTB	0.0526
HLI-0752	15326	A	G	0	587	missense_variant	MODERATE	CYTB	0.9868
HLI-0752	15452	C	A	3	588	missense_variant	MODERATE	CYTB	0.0933
HLI-0752	15607	A	G	0	631	synonymous_variant	LOW	CYTB	0.0508
HLI-0752	15928	G	A	1	671	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0752	16126	T	C	0	585	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0752	16147	C	T	0	646	upstream_gene_variant	MODIFIER	DLoop	0.0031
HLI-0752	16294	C	T	0	578	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0752	16296	C	T	0	568	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0752	16297	T	C	0	572	upstream_gene_variant	MODIFIER	DLoop	0.0139

HLI-0752	16304	T	C	0	550	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0752	16519	T	C	0	294	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0753	263	A	G	0	257	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0753	750	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0753	1438	A	G	0	732	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0753	3010	G	A	0	699	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0753	4769	A	G	0	614	synonymous_variant	LOW	ND2	0.9767
HLI-0753	12346	C	T	0	636	missense_variant	MODERATE	ND5	0.0056
HLI-0753	15326	A	G	1	646	missense_variant	MODERATE	CYTB	0.9868
HLI-0753	16093	T	C	40	612	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0753	16270	C	T	1	658	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0753	16519	T	C	0	361	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0754	73	A	G	0	291	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0754	146	T	C	0	534	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0754	152	T	C	0	541	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0754	195	T	C	1	510	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0754	263	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0754	750	A	G	0	533	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0754	769	G	A	0	579	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0754	1018	G	A	0	735	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0754	1438	A	G	0	559	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0754	2416	T	C	0	374	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0754	2706	A	G	1	535	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0754	2789	C	T	1	611	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0754	3594	C	T	2	483	synonymous_variant	LOW	ND1	0.0789
HLI-0754	3918	G	A	1	524	synonymous_variant	LOW	ND1	0.009
HLI-0754	4104	A	G	1	378	synonymous_variant	LOW	ND1	0.0785
HLI-0754	4769	A	G	0	532	synonymous_variant	LOW	ND2	0.9767
HLI-0754	5285	A	G	1	509	synonymous_variant	LOW	ND2	0.0049
HLI-0754	7028	C	T	0	594	synonymous_variant	LOW	COX1	0.8089
HLI-0754	7175	T	C	1	591	synonymous_variant	LOW	COX1	0.0224
HLI-0754	7256	C	T	1	615	synonymous_variant	LOW	COX1	0.0784
HLI-0754	7274	C	T	1	555	synonymous_variant	LOW	COX1	0.0214
HLI-0754	7521	G	A	0	384	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0754	7771	A	G	0	530	synonymous_variant	LOW	COX2	0.0223
HLI-0754	8206	G	A	2	513	synonymous_variant	LOW	COX2	0.0287
HLI-0754	8701	A	G	1	474	missense_variant	MODERATE	ATP6	0.3391
HLI-0754	9221	A	G	2	599	synonymous_variant	LOW	COX3	0.0277
HLI-0754	9540	T	C	0	426	synonymous_variant	LOW	COX3	0.339

HLI-0754	10115	T	C	0	682	synonymous_variant	LOW	ND3	0.0278
HLI-0754	10398	A	G	1	689	missense_variant	MODERATE	ND3	0.445
HLI-0754	10873	T	C	0	546	synonymous_variant	LOW	ND4	0.3389
HLI-0754	11719	G	A	0	570	synonymous_variant	LOW	ND4	0.7756
HLI-0754	11914	G	A	0	491	synonymous_variant	LOW	ND4	0.1112
HLI-0754	11944	T	C	0	476	synonymous_variant	LOW	ND4	0.0331
HLI-0754	12693	A	G	1	460	synonymous_variant	LOW	ND5	0.0205
HLI-0754	12705	C	T	1	508	synonymous_variant	LOW	ND5	0.4212
HLI-0754	13590	G	A	2	451	synonymous_variant	LOW	ND5	0.0586
HLI-0754	13650	C	T	0	496	synonymous_variant	LOW	ND5	0.079
HLI-0754	13803	A	G	0	315	synonymous_variant	LOW	ND5	0.0216
HLI-0754	14566	A	G	3	736	synonymous_variant	LOW	ND6	0.0214
HLI-0754	14766	C	T	5	643	missense_variant	MODERATE	CYTB	0.7696
HLI-0754	15244	A	G	3	521	synonymous_variant	LOW	CYTB	0.0103
HLI-0754	15301	G	A	1	460	synonymous_variant	LOW	CYTB	0.2912
HLI-0754	15326	A	G	1	433	missense_variant	MODERATE	CYTB	0.9868
HLI-0754	15629	T	C	0	346	synonymous_variant	LOW	CYTB	0.0062
HLI-0754	15784	T	C	1	317	synonymous_variant	LOW	CYTB	0.0363
HLI-0754	16223	C	T	3	374	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0754	16278	C	T	0	422	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0754	16294	C	T	0	416	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0754	16309	A	G	0	410	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0754	16390	G	A	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0754	16519	T	C	0	205	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0755	225	G	A	4	403	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0755	263	A	G	0	139	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0755	456	C	T	2	400	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0755	750	A	G	0	570	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0755	961	T	C	0	192	upstream_gene_variant	MODIFIER	RNR1	0.0087
HLI-0755	1438	A	G	1	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0755	4336	T	C	0	441	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0755	4769	A	G	1	559	synonymous_variant	LOW	ND2	0.9767
HLI-0755	15326	A	G	0	426	missense_variant	MODERATE	CYTB	0.9868
HLI-0755	15833	C	T	2	484	synonymous_variant	LOW	CYTB	0.0051
HLI-0755	16304	T	C	1	471	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0756	73	A	G	0	327	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0756	146	T	C	0	595	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0756	152	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0756	263	A	G	0	258	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0756	512	A	C	0	450	upstream_gene_variant	MODIFIER	DLoop	3.00E-04
HLI-0756	709	G	A	0	682	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0756	750	A	G	0	749	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0756	1438	A	G	0	682	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0756	1811	A	G	1	715	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0756	2706	A	G	1	648	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0756	3480	A	G	1	559	synonymous_variant	LOW	ND1	0.0392
HLI-0756	4561	T	C	4	760	missense_variant	MODERATE	ND2	0.0065
HLI-0756	4769	A	G	1	640	synonymous_variant	LOW	ND2	0.9767
HLI-0756	7028	C	T	6	694	synonymous_variant	LOW	COX1	0.8089
HLI-0756	8697	G	A	0	614	synonymous_variant	LOW	ATP6	0.0466
HLI-0756	9055	G	A	0	689	missense_variant	MODERATE	ATP6	0.0425
HLI-0756	9254	A	G	1	711	synonymous_variant	LOW	COX3	0.0083
HLI-0756	9698	T	C	1	691	synonymous_variant	LOW	COX3	0.0405
HLI-0756	9716	T	C	1	748	synonymous_variant	LOW	COX3	0.0108
HLI-0756	10550	A	G	1	684	synonymous_variant	LOW	ND4L	0.0376
HLI-0756	11299	T	C	2	678	synonymous_variant	LOW	ND4	0.0417
HLI-0756	11348	C	T	0	757	synonymous_variant	LOW	ND4	9.00E-04
HLI-0756	11467	A	G	1	706	synonymous_variant	LOW	ND4	0.1231
HLI-0756	11719	G	A	0	653	synonymous_variant	LOW	ND4	0.7756
HLI-0756	11914	G	A	0	672	synonymous_variant	LOW	ND4	0.1112
HLI-0756	12308	A	G	0	602	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0756	12372	G	A	3	657	synonymous_variant	LOW	ND5	0.1329
HLI-0756	14167	C	T	1	621	synonymous_variant	LOW	ND6	0.0385
HLI-0756	14766	C	T	2	628	missense_variant	MODERATE	CYTB	0.7696
HLI-0756	14798	T	C	0	705	missense_variant	MODERATE	CYTB	0.0651
HLI-0756	15116	A	G	1	688	missense_variant	MODERATE	CYTB	0
HLI-0756	15326	A	G	0	587	missense_variant	MODERATE	CYTB	0.9868
HLI-0756	16224	T	C	2	631	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0756	16311	T	C	0	573	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0756	16519	T	C	0	311	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0757	73	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0757	114	C	T	2	460	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0757	263	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0757	497	C	T	2	510	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0757	750	A	G	0	656	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0757	1189	T	C	0	672	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0757	1438	A	G	1	652	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0757	1462	G	A	0	722	upstream_gene_variant	MODIFIER	RNR1	0.0041

HLI-0757	1811	A	G	1	649	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0757	2706	A	G	0	686	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0757	3480	A	G	1	520	synonymous_variant	LOW	ND1	0.0392
HLI-0757	4769	A	G	0	599	synonymous_variant	LOW	ND2	0.9767
HLI-0757	7028	C	T	0	675	synonymous_variant	LOW	COX1	0.8089
HLI-0757	9055	G	A	0	623	missense_variant	MODERATE	ATP6	0.0425
HLI-0757	9698	T	C	0	587	synonymous_variant	LOW	COX3	0.0405
HLI-0757	10289	A	G	1	653	synonymous_variant	LOW	ND3	0.0032
HLI-0757	10398	A	G	1	589	missense_variant	MODERATE	ND3	0.445
HLI-0757	10550	A	G	0	647	synonymous_variant	LOW	ND4L	0.0376
HLI-0757	10978	A	G	0	450	synonymous_variant	LOW	ND4	0.0036
HLI-0757	11299	T	C	1	585	synonymous_variant	LOW	ND4	0.0417
HLI-0757	11467	A	G	0	626	synonymous_variant	LOW	ND4	0.1231
HLI-0757	11470	A	G	0	640	synonymous_variant	LOW	ND4	0.0029
HLI-0757	11719	G	A	1	596	synonymous_variant	LOW	ND4	0.7756
HLI-0757	11914	G	A	2	609	synonymous_variant	LOW	ND4	0.1112
HLI-0757	12308	A	G	1	551	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0757	12372	G	A	2	569	synonymous_variant	LOW	ND5	0.1329
HLI-0757	12954	T	C	7	597	synonymous_variant	LOW	ND5	0.0017
HLI-0757	14167	C	T	2	592	synonymous_variant	LOW	ND6	0.0385
HLI-0757	14766	C	T	3	663	missense_variant	MODERATE	CYTB	0.7696
HLI-0757	14798	T	C	0	746	missense_variant	MODERATE	CYTB	0.0651
HLI-0757	15326	A	G	0	515	missense_variant	MODERATE	CYTB	0.9868
HLI-0757	15924	A	G	1	595	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0757	16223	C	T	0	562	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0757	16224	T	C	0	567	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0757	16234	C	T	2	575	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0757	16311	T	C	0	544	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0757	16519	T	C	2	262	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0758	73	A	G	0	314	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0758	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0758	750	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0758	1438	A	G	0	662	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0758	2706	A	G	0	575	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0758	3348	A	G	1	584	synonymous_variant	LOW	ND1	0.0065
HLI-0758	3969	C	T	1	548	synonymous_variant	LOW	ND1	7.00E-04
HLI-0758	4172	T	A	1	584	missense_variant	MODERATE	ND1	6.00E-04
HLI-0758	4769	A	G	0	600	synonymous_variant	LOW	ND2	0.9767
HLI-0758	7028	C	T	0	677	synonymous_variant	LOW	COX1	0.8089

HLI-0758	7805	G	A	2	640	missense_variant	MODERATE	COX2	0.0077
HLI-0758	11467	A	G	0	643	synonymous_variant	LOW	ND4	0.1231
HLI-0758	11719	G	A	1	600	synonymous_variant	LOW	ND4	0.7756
HLI-0758	11938	C	T	1	592	synonymous_variant	LOW	ND4	9.00E-04
HLI-0758	12308	A	G	3	527	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0758	12372	G	A	1	482	synonymous_variant	LOW	ND5	0.1329
HLI-0758	12501	G	A	2	568	synonymous_variant	LOW	ND5	0.0258
HLI-0758	14179	A	G	0	609	synonymous_variant	LOW	ND6	0.0053
HLI-0758	14766	C	T	1	549	missense_variant	MODERATE	CYTB	0.7696
HLI-0758	14927	A	G	0	702	missense_variant	MODERATE	CYTB	0.003
HLI-0758	15326	A	G	0	550	missense_variant	MODERATE	CYTB	0.9868
HLI-0758	16172	T	C	1	211	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0758	16219	A	G	1	250	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0758	16239	C	T	1	297	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0758	16278	C	T	1	421	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0758	16362	T	C	1	487	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0759	263	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0759	750	A	G	0	658	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0759	1393	G	A	6	649	upstream_gene_variant	MODIFIER	RNR1	0.0017
HLI-0759	1438	A	G	2	704	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0759	1719	G	A	0	631	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0759	4769	A	G	1	616	synonymous_variant	LOW	ND2	0.9767
HLI-0759	4793	A	G	0	668	synonymous_variant	LOW	ND2	0.0073
HLI-0759	15326	A	G	0	482	missense_variant	MODERATE	CYTB	0.9868
HLI-0759	16176	C	T	3	601	upstream_gene_variant	MODIFIER	DLoop	0.0061
HLI-0759	16261	C	T	5	625	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0759	16519	T	C	1	303	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0760	73	A	G	0	168	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0760	89	T	C	0	189	upstream_gene_variant	MODIFIER	DLoop	0.0038
HLI-0760	93	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0760	151	C	T	0	274	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0760	152	T	C	0	273	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0760	182	C	T	0	280	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0760	186	C	A	0	280	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0760	189	A	C	0	286	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0760	195	T	C	0	292	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0760	247	G	A	0	138	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0760	248	A	G	0	139	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0760	263	A	G	1	151	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0760	710	T	C	0	477	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0760	750	A	G	0	499	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0760	769	G	A	0	506	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0760	825	T	A	0	589	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0760	1018	G	A	1	617	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0760	1438	A	G	1	602	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0760	2283	C	T	0	475	upstream_gene_variant	MODIFIER	RNR2	0.001
HLI-0760	2706	A	G	0	469	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0760	2758	G	A	0	492	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0760	2885	T	C	0	522	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0760	3525	C	T	2	451	synonymous_variant	LOW	ND1	6.00E-04
HLI-0760	3594	C	T	1	435	synonymous_variant	LOW	ND1	0.0789
HLI-0760	3666	G	A	0	494	synonymous_variant	LOW	ND1	0.0233
HLI-0760	4104	A	G	0	390	synonymous_variant	LOW	ND1	0.0785
HLI-0760	4769	A	G	1	539	synonymous_variant	LOW	ND2	0.9767
HLI-0760	4853	G	A	1	617	synonymous_variant	LOW	ND2	0.0026
HLI-0760	5951	A	G	9	622	synonymous_variant	LOW	COX1	0.0128
HLI-0760	6071	T	C	11	647	synonymous_variant	LOW	COX1	0.0129
HLI-0760	6221	T	A	9	504	synonymous_variant	LOW	COX1	0.0027
HLI-0760	6917	G	A	2	524	synonymous_variant	LOW	COX1	0.0036
HLI-0760	7028	C	T	0	482	synonymous_variant	LOW	COX1	0.8089
HLI-0760	7146	A	G	0	275	missense_variant	MODERATE	COX1	0.0497
HLI-0760	7256	C	T	2	421	synonymous_variant	LOW	COX1	0.0784
HLI-0760	7389	T	C	1	422	missense_variant	MODERATE	COX1	0.0201
HLI-0760	7521	G	A	1	334	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0760	8027	G	A	5	576	missense_variant	MODERATE	COX2	0.0334
HLI-0760	8468	C	T	2	382	synonymous_variant	LOW	ATP8	0.0501
HLI-0760	8655	C	T	1	415	synonymous_variant	LOW	ATP6	0.0511
HLI-0760	8701	A	G	2	494	missense_variant	MODERATE	ATP6	0.3391
HLI-0760	9072	A	G	3	474	synonymous_variant	LOW	ATP6	0.0124
HLI-0760	9540	T	C	0	441	synonymous_variant	LOW	COX3	0.339
HLI-0760	10398	A	G	0	591	missense_variant	MODERATE	ND3	0.445
HLI-0760	10586	G	A	2	555	synonymous_variant	LOW	ND4L	0.0177
HLI-0760	10688	G	A	0	480	synonymous_variant	LOW	ND4L	0.0515
HLI-0760	10810	T	C	0	530	synonymous_variant	LOW	ND4	0.0522
HLI-0760	10873	T	C	0	516	synonymous_variant	LOW	ND4	0.3389
HLI-0760	11302	C	T	3	537	synonymous_variant	LOW	ND4	0.0028
HLI-0760	11719	G	A	0	574	synonymous_variant	LOW	ND4	0.7756
HLI-0760	11984	T	C	1	493	missense_variant	MODERATE	ND4	0.0011

HLI-0760	12016	C	A	1	501	synonymous_variant	LOW	ND4	0
HLI-0760	12507	A	G	7	554	synonymous_variant	LOW	ND5	0.0015
HLI-0760	12705	C	T	0	585	synonymous_variant	LOW	ND5	0.4212
HLI-0760	12810	A	G	9	524	synonymous_variant	LOW	ND5	0.0198
HLI-0760	13105	A	G	1	448	missense_variant	MODERATE	ND5	0.076
HLI-0760	13485	A	G	3	442	synonymous_variant	LOW	ND5	0.0122
HLI-0760	13506	C	T	1	509	synonymous_variant	LOW	ND5	0.0506
HLI-0760	13650	C	T	2	455	synonymous_variant	LOW	ND5	0.079
HLI-0760	13789	T	C	4	327	missense_variant	MODERATE	ND5	0.0185
HLI-0760	14000	T	A	4	491	missense_variant	MODERATE	ND5	0.0126
HLI-0760	14178	T	C	1	558	missense_variant	MODERATE	ND6	0.0225
HLI-0760	14560	G	A	1	545	synonymous_variant	LOW	ND6	0.0235
HLI-0760	14669	A	G	3	638	missense_variant	MODERATE	ND6	6.00E-04
HLI-0760	14766	C	T	3	507	missense_variant	MODERATE	CYTB	0.7696
HLI-0760	14911	C	T	4	696	synonymous_variant	LOW	CYTB	0.0124
HLI-0760	15226	A	G	3	467	synonymous_variant	LOW	CYTB	0.0034
HLI-0760	15326	A	G	0	371	missense_variant	MODERATE	CYTB	0.9868
HLI-0760	15905	T	C	2	540	upstream_gene_variant	MODIFIER	TRNT	0.005
HLI-0760	15978	C	T	3	556	upstream_gene_variant	MODIFIER	TRNP	0.0032
HLI-0760	16129	G	A	2	550	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0760	16150	C	T	2	537	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0760	16223	C	T	0	354	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0760	16260	C	T	0	366	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0760	16278	C	T	0	334	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0760	16293	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0760	16294	C	T	0	320	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0760	16311	T	C	0	314	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0760	16360	C	T	0	288	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0760	16519	T	C	0	110	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0761	73	A	G	1	266	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0761	152	T	C	0	498	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0761	195	T	C	0	477	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0761	263	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0761	709	G	A	0	492	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0761	750	A	G	1	533	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0761	1438	A	G	0	508	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0761	1888	G	A	0	258	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0761	2706	A	G	0	510	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0761	3316	G	A	0	483	missense_variant	MODERATE	ND1	0.0101

HLI-0761	4216	T	C	0	362	missense_variant	MODERATE	ND1	0.0991
HLI-0761	4769	A	G	1	492	synonymous_variant	LOW	ND2	0.9767
HLI-0761	4917	A	G	0	516	missense_variant	MODERATE	ND2	0.0477
HLI-0761	5414	A	G	0	405	synonymous_variant	LOW	ND2	9.00E-04
HLI-0761	5558	A	G	2	590	upstream_gene_variant	MODIFIER	TRNW	0.0021
HLI-0761	7028	C	T	2	572	synonymous_variant	LOW	COX1	0.8089
HLI-0761	8697	G	A	1	518	synonymous_variant	LOW	ATP6	0.0466
HLI-0761	9899	T	C	3	693	synonymous_variant	LOW	COX3	0.0108
HLI-0761	10463	T	C	0	710	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0761	11251	A	G	0	521	synonymous_variant	LOW	ND4	0.0932
HLI-0761	11719	G	A	1	600	synonymous_variant	LOW	ND4	0.7756
HLI-0761	12064	C	T	1	244	synonymous_variant	LOW	ND4	0
HLI-0761	12633	C	A	3	433	synonymous_variant	LOW	ND5	0.0123
HLI-0761	13368	G	A	0	547	synonymous_variant	LOW	ND5	0.0495
HLI-0761	14766	C	T	3	666	missense_variant	MODERATE	CYTB	0.7696
HLI-0761	14905	G	A	2	744	synonymous_variant	LOW	CYTB	0.0526
HLI-0761	15326	A	G	0	321	missense_variant	MODERATE	CYTB	0.9868
HLI-0761	15412	T	C	0	293	synonymous_variant	LOW	CYTB	0.0015
HLI-0761	15452	C	A	2	275	missense_variant	MODERATE	CYTB	0.0933
HLI-0761	15607	A	G	0	290	synonymous_variant	LOW	CYTB	0.0508
HLI-0761	15928	G	A	0	285	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0761	16126	T	C	0	394	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0761	16163	A	G	0	477	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0761	16519	T	C	0	190	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0762	73	A	G	1	341	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0762	152	T	C	0	577	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0762	195	T	C	1	548	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0762	263	A	G	0	242	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0762	497	C	T	5	509	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0762	750	A	G	1	651	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0762	1189	T	C	1	654	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0762	1438	A	G	0	694	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0762	1811	A	G	1	651	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0762	2706	A	G	0	654	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0762	3480	A	G	0	521	synonymous_variant	LOW	ND1	0.0392
HLI-0762	3768	A	G	2	589	synonymous_variant	LOW	ND1	0.002
HLI-0762	4313	T	C	1	616	upstream_gene_variant	MODIFIER	TRNI	9.00E-04
HLI-0762	4769	A	G	1	584	synonymous_variant	LOW	ND2	0.9767
HLI-0762	7028	C	T	2	683	synonymous_variant	LOW	COX1	0.8089

HLI-0762	9055	G	A	0	638	missense_variant	MODERATE	ATP6	0.0425
HLI-0762	9064	G	A	0	669	missense_variant	MODERATE	ATP6	0.0025
HLI-0762	9698	T	C	0	624	synonymous_variant	LOW	COX3	0.0405
HLI-0762	10398	A	G	0	702	missense_variant	MODERATE	ND3	0.445
HLI-0762	10550	A	G	1	637	synonymous_variant	LOW	ND4L	0.0376
HLI-0762	11299	T	C	0	628	synonymous_variant	LOW	ND4	0.0417
HLI-0762	11467	A	G	0	733	synonymous_variant	LOW	ND4	0.1231
HLI-0762	11485	T	C	1	738	synonymous_variant	LOW	ND4	0.0081
HLI-0762	11719	G	A	2	629	synonymous_variant	LOW	ND4	0.7756
HLI-0762	12308	A	G	0	593	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0762	12372	G	A	2	607	synonymous_variant	LOW	ND5	0.1329
HLI-0762	14167	C	T	3	608	synonymous_variant	LOW	ND6	0.0385
HLI-0762	14766	C	T	4	649	missense_variant	MODERATE	CYTB	0.7696
HLI-0762	14798	T	C	0	699	missense_variant	MODERATE	CYTB	0.0651
HLI-0762	15326	A	G	1	576	missense_variant	MODERATE	CYTB	0.9868
HLI-0762	16224	T	C	1	596	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0762	16311	T	C	2	533	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0762	16519	T	C	2	275	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0763	73	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0763	263	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0763	709	G	A	0	641	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0763	750	A	G	1	725	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0763	930	G	A	1	667	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0763	1438	A	G	1	656	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0763	1888	G	A	0	588	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0763	2706	A	G	0	730	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0763	4216	T	C	0	670	missense_variant	MODERATE	ND1	0.0991
HLI-0763	4769	A	G	2	568	synonymous_variant	LOW	ND2	0.9767
HLI-0763	4917	A	G	0	630	missense_variant	MODERATE	ND2	0.0477
HLI-0763	5147	G	A	1	549	synonymous_variant	LOW	ND2	0.0437
HLI-0763	7028	C	T	3	719	synonymous_variant	LOW	COX1	0.8089
HLI-0763	8697	G	A	0	587	synonymous_variant	LOW	ATP6	0.0466
HLI-0763	9254	A	G	0	659	synonymous_variant	LOW	COX3	0.0083
HLI-0763	10463	T	C	0	676	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0763	11251	A	G	1	639	synonymous_variant	LOW	ND4	0.0932
HLI-0763	11719	G	A	0	661	synonymous_variant	LOW	ND4	0.7756
HLI-0763	11812	A	G	1	638	synonymous_variant	LOW	ND4	0.0332
HLI-0763	13368	G	A	0	672	synonymous_variant	LOW	ND5	0.0495
HLI-0763	14233	A	G	2	604	synonymous_variant	LOW	ND6	0.0369

HLI-0763	14766	C	T	2	612	missense_variant	MODERATE	CYTB	0.7696
HLI-0763	14905	G	A	0	730	synonymous_variant	LOW	CYTB	0.0526
HLI-0763	15326	A	G	0	556	missense_variant	MODERATE	CYTB	0.9868
HLI-0763	15452	C	A	6	618	missense_variant	MODERATE	CYTB	0.0933
HLI-0763	15607	A	G	2	590	synonymous_variant	LOW	CYTB	0.0508
HLI-0763	15928	G	A	0	600	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0763	16126	T	C	0	692	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0763	16294	C	T	1	568	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0763	16304	T	C	1	604	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0763	16519	T	C	2	298	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0764	263	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0764	750	A	G	1	647	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0764	1438	A	G	0	714	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0764	2706	A	G	1	673	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0764	4452	T	C	4	599	upstream_gene_variant	MODIFIER	TRNM	0.002
HLI-0764	4769	A	G	2	630	synonymous_variant	LOW	ND2	0.9767
HLI-0764	6230	C	T	5	622	synonymous_variant	LOW	COX1	2.00E-04
HLI-0764	7028	C	T	5	715	synonymous_variant	LOW	COX1	0.8089
HLI-0764	7094	T	C	9	763	synonymous_variant	LOW	COX1	0.0023
HLI-0764	9950	T	C	0	615	synonymous_variant	LOW	COX3	0.0362
HLI-0764	12043	C	A	2	598	synonymous_variant	LOW	ND4	1.00E-04
HLI-0764	13680	C	T	2	566	synonymous_variant	LOW	ND5	0.005
HLI-0764	15326	A	G	0	594	missense_variant	MODERATE	CYTB	0.9868
HLI-0764	16221	C	T	5	727	upstream_gene_variant	MODIFIER	DLoop	0.007
HLI-0764	16291	C	T	0	595	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0764	16355	C	T	1	522	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0765	73	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0765	185	G	A	1	444	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0765	195	T	C	1	439	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0765	228	G	A	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0765	263	A	G	1	327	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0765	295	C	T	0	275	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0765	462	C	T	0	460	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0765	482	T	C	0	482	upstream_gene_variant	MODIFIER	DLoop	0.0094
HLI-0765	489	T	C	0	480	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0765	750	A	G	1	510	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0765	1438	A	G	0	513	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0765	2706	A	G	2	479	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0765	3010	G	A	4	465	upstream_gene_variant	MODIFIER	RNR2	0.1449

HLI-0765	3394	T	C	1	501	missense_variant	MODERATE	ND1	0.013
HLI-0765	4216	T	C	4	371	missense_variant	MODERATE	ND1	0.0991
HLI-0765	4769	A	G	1	507	synonymous_variant	LOW	ND2	0.9767
HLI-0765	7028	C	T	2	576	synonymous_variant	LOW	COX1	0.8089
HLI-0765	7184	A	G	1	612	synonymous_variant	LOW	COX1	0.0017
HLI-0765	8952	T	C	1	539	synonymous_variant	LOW	ATP6	2.00E-04
HLI-0765	10398	A	G	1	773	missense_variant	MODERATE	ND3	0.445
HLI-0765	11251	A	G	1	536	synonymous_variant	LOW	ND4	0.0932
HLI-0765	11719	G	A	2	520	synonymous_variant	LOW	ND4	0.7756
HLI-0765	12612	A	G	4	529	synonymous_variant	LOW	ND5	0.0506
HLI-0765	13708	G	A	0	444	missense_variant	MODERATE	ND5	0.0717
HLI-0765	14766	C	T	1	661	missense_variant	MODERATE	CYTB	0.7696
HLI-0765	14798	T	C	1	764	missense_variant	MODERATE	CYTB	0.0651
HLI-0765	15326	A	G	1	353	missense_variant	MODERATE	CYTB	0.9868
HLI-0765	15452	C	A	3	266	missense_variant	MODERATE	CYTB	0.0933
HLI-0765	16069	C	T	2	405	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0765	16126	T	C	0	495	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0766	73	A	G	0	344	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0766	152	T	C	0	581	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0766	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0766	750	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0766	980	T	C	1	715	upstream_gene_variant	MODIFIER	RNR1	0.0112
HLI-0766	1438	A	G	0	703	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0766	1811	A	G	1	642	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0766	2706	A	G	0	619	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0766	3741	C	T	2	658	synonymous_variant	LOW	ND1	0.0092
HLI-0766	4769	A	G	2	608	synonymous_variant	LOW	ND2	0.9767
HLI-0766	5360	C	T	0	564	synonymous_variant	LOW	ND2	0.0093
HLI-0766	7028	C	T	2	666	synonymous_variant	LOW	COX1	0.8089
HLI-0766	8137	C	T	1	620	synonymous_variant	LOW	COX2	0.0092
HLI-0766	8684	C	T	2	581	missense_variant	MODERATE	ATP6	0.0106
HLI-0766	8962	A	T	2	618	missense_variant	MODERATE	ATP6	1.00E-04
HLI-0766	10084	T	C	0	662	missense_variant	MODERATE	ND3	0.0093
HLI-0766	10142	C	T	1	728	synonymous_variant	LOW	ND3	0.014
HLI-0766	11467	A	G	0	680	synonymous_variant	LOW	ND4	0.1231
HLI-0766	11719	G	A	2	596	synonymous_variant	LOW	ND4	0.7756
HLI-0766	12308	A	G	0	511	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0766	12372	G	A	0	521	synonymous_variant	LOW	ND5	0.1329
HLI-0766	13500	T	C	1	585	synonymous_variant	LOW	ND5	0.0173

HLI-0766	14569	G	A	0	694	synonymous_variant	LOW	ND6	0.0259
HLI-0766	14766	C	T	4	633	missense_variant	MODERATE	CYTB	0.7696
HLI-0766	14798	T	C	0	727	missense_variant	MODERATE	CYTB	0.0651
HLI-0766	15326	A	G	0	528	missense_variant	MODERATE	CYTB	0.9868
HLI-0766	16248	C	T	5	574	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0766	16318	A	T	1	573	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0766	16519	T	C	0	302	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0767	207	G	A	3	367	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0767	263	A	G	0	136	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0767	750	A	G	0	573	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0767	1438	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0767	4769	A	G	0	579	synonymous_variant	LOW	ND2	0.9767
HLI-0767	6323	A	G	0	584	synonymous_variant	LOW	COX1	4.00E-04
HLI-0767	10463	T	A	0	572	upstream_gene_variant	MODIFIER	TRNR	0
HLI-0767	15326	A	G	0	586	missense_variant	MODERATE	CYTB	0.9868
HLI-0767	16291	C	T	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0767	16343	A	G	0	436	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0767	16390	G	A	0	475	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0767	16519	T	C	1	251	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0768	73	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0768	151	C	T	0	380	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0768	152	T	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0768	186	C	A	0	346	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0768	189	A	C	0	338	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0768	195	T	C	0	343	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0768	198	C	T	0	352	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0768	247	G	A	0	137	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0768	263	A	G	0	160	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0768	297	A	G	0	194	upstream_gene_variant	MODIFIER	DLoop	0.0107
HLI-0768	750	A	G	0	593	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0768	769	G	A	0	650	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0768	794	T	C	0	671	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0768	825	T	A	0	698	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0768	1018	G	A	1	734	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0768	1438	A	G	0	675	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0768	2706	A	G	0	595	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0768	2758	G	A	0	625	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0768	2885	T	C	0	643	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0768	3594	C	T	0	492	synonymous_variant	LOW	ND1	0.0789

HLI-0768	3666	G	A	0	546	synonymous_variant	LOW	ND1	0.0233
HLI-0768	4094	C	T	2	511	missense_variant	MODERATE	ND1	2.00E-04
HLI-0768	4104	A	G	2	546	synonymous_variant	LOW	ND1	0.0785
HLI-0768	4722	A	G	2	645	missense_variant	MODERATE	ND2	0.0019
HLI-0768	4769	A	G	3	690	synonymous_variant	LOW	ND2	0.9767
HLI-0768	5951	A	G	0	686	synonymous_variant	LOW	COX1	0.0128
HLI-0768	6071	T	C	1	691	synonymous_variant	LOW	COX1	0.0129
HLI-0768	6150	G	A	1	726	missense_variant	MODERATE	COX1	0.0049
HLI-0768	6253	T	C	0	632	missense_variant	MODERATE	COX1	0.0106
HLI-0768	6500	C	T	3	606	synonymous_variant	LOW	COX1	1.00E-04
HLI-0768	7028	C	T	1	560	synonymous_variant	LOW	COX1	0.8089
HLI-0768	7055	A	G	3	562	synonymous_variant	LOW	COX1	0.0188
HLI-0768	7076	A	G	3	489	synonymous_variant	LOW	COX1	0.0053
HLI-0768	7146	A	G	0	305	missense_variant	MODERATE	COX1	0.0497
HLI-0768	7256	C	T	5	468	synonymous_variant	LOW	COX1	0.0784
HLI-0768	7337	G	A	5	577	synonymous_variant	LOW	COX1	0.0119
HLI-0768	7389	T	C	5	551	missense_variant	MODERATE	COX1	0.0201
HLI-0768	7521	G	A	2	384	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0768	8027	G	A	2	649	missense_variant	MODERATE	COX2	0.0334
HLI-0768	8468	C	T	4	454	synonymous_variant	LOW	ATP8	0.0501
HLI-0768	8567	T	C	0	503	missense_variant	MODERATE	ATP6/8	0.0021
HLI-0768	8655	C	T	3	498	synonymous_variant	LOW	ATP6	0.0511
HLI-0768	8701	A	G	1	575	missense_variant	MODERATE	ATP6	0.3391
HLI-0768	8784	A	G	0	532	synonymous_variant	LOW	ATP6	0.006
HLI-0768	8877	T	C	0	514	synonymous_variant	LOW	ATP6	0.0053
HLI-0768	9072	A	G	0	611	synonymous_variant	LOW	ATP6	0.0124
HLI-0768	9540	T	C	1	518	synonymous_variant	LOW	COX3	0.339
HLI-0768	10321	T	C	0	630	missense_variant	MODERATE	ND3	0.0106
HLI-0768	10398	A	G	0	621	missense_variant	MODERATE	ND3	0.445
HLI-0768	10586	G	A	0	542	synonymous_variant	LOW	ND4L	0.0177
HLI-0768	10688	G	A	2	652	synonymous_variant	LOW	ND4L	0.0515
HLI-0768	10792	A	G	0	567	synonymous_variant	LOW	ND4	0.0044
HLI-0768	10793	C	T	0	572	synonymous_variant	LOW	ND4	0.0043
HLI-0768	10810	T	C	0	591	synonymous_variant	LOW	ND4	0.0522
HLI-0768	10873	T	C	0	595	synonymous_variant	LOW	ND4	0.3389
HLI-0768	11164	A	G	2	583	synonymous_variant	LOW	ND4	0.0023
HLI-0768	11290	A	G	1	614	synonymous_variant	LOW	ND4	5.00E-04
HLI-0768	11654	A	G	0	644	missense_variant	MODERATE	ND4	0.0045
HLI-0768	11719	G	A	1	674	synonymous_variant	LOW	ND4	0.7756

HLI-0768	12049	C	T	1	552	synonymous_variant	LOW	ND4	0.0052
HLI-0768	12705	C	T	0	625	synonymous_variant	LOW	ND5	0.4212
HLI-0768	12810	A	G	1	588	synonymous_variant	LOW	ND5	0.0198
HLI-0768	13105	A	G	2	609	missense_variant	MODERATE	ND5	0.076
HLI-0768	13149	A	G	1	664	synonymous_variant	LOW	ND5	0.0053
HLI-0768	13269	A	G	0	675	synonymous_variant	LOW	ND5	0.0023
HLI-0768	13485	A	G	0	576	synonymous_variant	LOW	ND5	0.0122
HLI-0768	13506	C	T	1	653	synonymous_variant	LOW	ND5	0.0506
HLI-0768	13650	C	T	1	526	synonymous_variant	LOW	ND5	0.079
HLI-0768	13789	T	C	1	388	missense_variant	MODERATE	ND5	0.0185
HLI-0768	14000	T	A	0	509	missense_variant	MODERATE	ND5	0.0126
HLI-0768	14178	T	C	0	602	missense_variant	MODERATE	ND6	0.0225
HLI-0768	14560	G	A	2	650	synonymous_variant	LOW	ND6	0.0235
HLI-0768	14766	C	T	1	623	missense_variant	MODERATE	CYTB	0.7696
HLI-0768	14911	C	T	1	705	synonymous_variant	LOW	CYTB	0.0124
HLI-0768	15326	A	G	0	465	missense_variant	MODERATE	CYTB	0.9868
HLI-0768	15734	G	A	0	530	missense_variant	MODERATE	CYTB	0.0036
HLI-0768	15886	C	T	1	542	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0768	16078	A	G	0	513	upstream_gene_variant	MODIFIER	DLoop	3.00E-04
HLI-0768	16129	G	A	0	517	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0768	16223	C	T	2	475	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0768	16265	A	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.0087
HLI-0768	16286	C	A	0	361	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0768	16294	C	T	0	370	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0768	16311	T	C	0	364	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0768	16320	C	T	0	373	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0768	16360	C	T	0	392	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0768	16519	T	C	0	136	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0768	16527	C	T	0	133	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0769	73	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0769	194	C	T	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0769	195	T	C	0	390	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0769	263	A	G	0	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0769	489	T	C	0	397	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0769	750	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0769	813	A	G	0	702	upstream_gene_variant	MODIFIER	RNR1	0.0044
HLI-0769	1438	A	G	0	618	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0769	2706	A	G	0	544	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0769	4769	A	G	1	584	synonymous_variant	LOW	ND2	0.9767

HLI-0769	6446	G	A	5	548	synonymous_variant	LOW	COX1	0.0061
HLI-0769	6671	T	C	1	621	synonymous_variant	LOW	COX1	0.0071
HLI-0769	6680	T	C	3	665	synonymous_variant	LOW	COX1	0.0226
HLI-0769	7028	C	T	4	673	synonymous_variant	LOW	COX1	0.8089
HLI-0769	8701	A	G	2	580	missense_variant	MODERATE	ATP6	0.3391
HLI-0769	9540	T	C	0	614	synonymous_variant	LOW	COX3	0.339
HLI-0769	10398	A	G	1	678	missense_variant	MODERATE	ND3	0.445
HLI-0769	10400	C	T	1	686	synonymous_variant	LOW	ND3	0.2131
HLI-0769	10649	T	C	2	609	synonymous_variant	LOW	ND4L	3.00E-04
HLI-0769	10873	T	C	1	543	synonymous_variant	LOW	ND4	0.3389
HLI-0769	11719	G	A	2	581	synonymous_variant	LOW	ND4	0.7756
HLI-0769	12403	C	T	5	488	missense_variant	MODERATE	ND5	0.0043
HLI-0769	12414	T	C	6	544	synonymous_variant	LOW	ND5	0.0139
HLI-0769	12492	A	G	7	641	synonymous_variant	LOW	ND5	1.00E-04
HLI-0769	12705	C	T	2	682	synonymous_variant	LOW	ND5	0.4212
HLI-0769	12950	A	C	4	583	missense_variant	MODERATE	ND5	0.0043
HLI-0769	13637	A	G	1	553	missense_variant	MODERATE	ND5	0.0074
HLI-0769	14110	T	C	1	510	missense_variant	MODERATE	ND5	0.0096
HLI-0769	14766	C	T	1	614	missense_variant	MODERATE	CYTB	0.7696
HLI-0769	14783	T	C	1	702	synonymous_variant	LOW	CYTB	0.2126
HLI-0769	15043	G	A	1	647	synonymous_variant	LOW	CYTB	0.2362
HLI-0769	15301	G	A	0	511	synonymous_variant	LOW	CYTB	0.2912
HLI-0769	15326	A	G	0	566	missense_variant	MODERATE	CYTB	0.9868
HLI-0769	15519	T	C	0	489	missense_variant	MODERATE	CYTB	0.002
HLI-0769	16129	G	A	0	347	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0769	16249	T	C	1	300	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0769	16311	T	C	1	418	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0769	16519	T	C	2	203	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0770	73	A	G	0	310	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0770	195	T	C	0	399	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0770	263	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0770	489	T	C	0	430	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0770	750	A	G	0	618	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0770	813	A	G	1	706	upstream_gene_variant	MODIFIER	RNR1	0.0044
HLI-0770	1438	A	G	0	688	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0770	1503	G	A	0	766	upstream_gene_variant	MODIFIER	RNR1	0.0053
HLI-0770	2706	A	G	1	600	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0770	4048	G	A	0	436	missense_variant	MODERATE	ND1	0.0178
HLI-0770	4769	A	G	0	573	synonymous_variant	LOW	ND2	0.9767

HLI-0770	6253	T	C	0	624	missense_variant	MODERATE	COX1	0.0106
HLI-0770	6446	G	A	5	535	synonymous_variant	LOW	COX1	0.0061
HLI-0770	6671	T	C	2	733	synonymous_variant	LOW	COX1	0.0071
HLI-0770	6680	T	C	1	744	synonymous_variant	LOW	COX1	0.0226
HLI-0770	7028	C	T	2	644	synonymous_variant	LOW	COX1	0.8089
HLI-0770	8701	A	G	0	576	missense_variant	MODERATE	ATP6	0.3391
HLI-0770	9540	T	C	0	536	synonymous_variant	LOW	COX3	0.339
HLI-0770	10398	A	G	0	627	missense_variant	MODERATE	ND3	0.445
HLI-0770	10400	C	T	0	632	synonymous_variant	LOW	ND3	0.2131
HLI-0770	10873	T	C	1	545	synonymous_variant	LOW	ND4	0.3389
HLI-0770	11719	G	A	2	615	synonymous_variant	LOW	ND4	0.7756
HLI-0770	12403	C	T	4	416	missense_variant	MODERATE	ND5	0.0043
HLI-0770	12414	T	C	4	413	synonymous_variant	LOW	ND5	0.0139
HLI-0770	12705	C	T	1	599	synonymous_variant	LOW	ND5	0.4212
HLI-0770	12950	A	C	5	614	missense_variant	MODERATE	ND5	0.0043
HLI-0770	13637	A	G	1	585	missense_variant	MODERATE	ND5	0.0074
HLI-0770	14110	T	C	0	454	missense_variant	MODERATE	ND5	0.0096
HLI-0770	14766	C	T	0	660	missense_variant	MODERATE	CYTB	0.7696
HLI-0770	14783	T	C	0	750	synonymous_variant	LOW	CYTB	0.2126
HLI-0770	15043	G	A	0	739	synonymous_variant	LOW	CYTB	0.2362
HLI-0770	15301	G	A	0	523	synonymous_variant	LOW	CYTB	0.2912
HLI-0770	15326	A	G	0	558	missense_variant	MODERATE	CYTB	0.9868
HLI-0770	16249	T	C	0	330	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0770	16311	T	C	0	453	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0770	16519	T	C	0	187	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0771	73	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0771	263	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0771	456	C	T	2	450	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0771	750	A	G	0	561	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0771	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0771	4769	A	G	0	591	synonymous_variant	LOW	ND2	0.9767
HLI-0771	13827	A	G	4	424	synonymous_variant	LOW	ND5	0.0047
HLI-0771	15326	A	G	1	432	missense_variant	MODERATE	CYTB	0.9868
HLI-0771	15930	G	A	3	522	upstream_gene_variant	MODIFIER	TRNT	0.0224
HLI-0771	16304	T	C	2	460	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0771	16519	T	C	0	210	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0772	73	A	G	0	274	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0772	195	T	C	3	447	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0772	207	G	A	5	471	upstream_gene_variant	MODIFIER	DLoop	0.0472

HLI-0772	263	A	G	1	159	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0772	709	G	A	0	625	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0772	750	A	G	1	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0772	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0772	1888	G	A	0	646	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0772	2706	A	G	0	607	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0772	4216	T	C	0	533	missense_variant	MODERATE	ND1	0.0991
HLI-0772	4769	A	G	2	613	synonymous_variant	LOW	ND2	0.9767
HLI-0772	4917	A	G	0	573	missense_variant	MODERATE	ND2	0.0477
HLI-0772	5277	T	C	0	528	missense_variant	MODERATE	ND2	0.0022
HLI-0772	5426	T	C	1	579	synonymous_variant	LOW	ND2	0.0091
HLI-0772	6489	C	A	3	673	missense_variant	MODERATE	COX1	0.0016
HLI-0772	7028	C	T	2	633	synonymous_variant	LOW	COX1	0.8089
HLI-0772	8697	G	A	0	591	synonymous_variant	LOW	ATP6	0.0466
HLI-0772	10463	T	C	0	600	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0772	11251	A	G	0	608	synonymous_variant	LOW	ND4	0.0932
HLI-0772	11719	G	A	0	623	synonymous_variant	LOW	ND4	0.7756
HLI-0772	11812	A	G	1	635	synonymous_variant	LOW	ND4	0.0332
HLI-0772	13368	G	A	0	631	synonymous_variant	LOW	ND5	0.0495
HLI-0772	14233	A	G	0	582	synonymous_variant	LOW	ND6	0.0369
HLI-0772	14766	C	T	0	566	missense_variant	MODERATE	CYTB	0.7696
HLI-0772	14905	G	A	0	627	synonymous_variant	LOW	CYTB	0.0526
HLI-0772	15028	C	A	2	607	synonymous_variant	LOW	CYTB	0.0016
HLI-0772	15043	G	A	0	654	synonymous_variant	LOW	CYTB	0.2362
HLI-0772	15326	A	G	0	507	missense_variant	MODERATE	CYTB	0.9868
HLI-0772	15452	C	A	2	534	missense_variant	MODERATE	CYTB	0.0933
HLI-0772	15607	A	G	0	594	synonymous_variant	LOW	CYTB	0.0508
HLI-0772	15928	G	A	0	565	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0772	16126	T	C	0	309	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0772	16294	C	T	1	374	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0772	16296	C	T	0	374	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0772	16298	T	C	0	385	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0772	16519	T	C	1	178	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0773	73	A	G	0	315	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0773	263	A	G	1	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0773	709	G	A	0	664	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0773	750	A	G	1	718	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0773	930	G	A	2	686	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0773	1438	A	G	1	655	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0773	1888	G	A	0	611	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0773	2706	A	G	0	624	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0773	4216	T	C	1	578	missense_variant	MODERATE	ND1	0.0991
HLI-0773	4769	A	G	2	557	synonymous_variant	LOW	ND2	0.9767
HLI-0773	4917	A	G	0	692	missense_variant	MODERATE	ND2	0.0477
HLI-0773	5147	G	A	0	561	synonymous_variant	LOW	ND2	0.0437
HLI-0773	7028	C	T	3	678	synonymous_variant	LOW	COX1	0.8089
HLI-0773	8697	G	A	0	628	synonymous_variant	LOW	ATP6	0.0466
HLI-0773	10463	T	C	1	623	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0773	11251	A	G	0	671	synonymous_variant	LOW	ND4	0.0932
HLI-0773	11719	G	A	0	635	synonymous_variant	LOW	ND4	0.7756
HLI-0773	11812	A	G	0	633	synonymous_variant	LOW	ND4	0.0332
HLI-0773	13368	G	A	0	665	synonymous_variant	LOW	ND5	0.0495
HLI-0773	14233	A	G	1	632	synonymous_variant	LOW	ND6	0.0369
HLI-0773	14766	C	T	1	583	missense_variant	MODERATE	CYTB	0.7696
HLI-0773	14905	G	A	0	670	synonymous_variant	LOW	CYTB	0.0526
HLI-0773	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868
HLI-0773	15452	C	A	5	540	missense_variant	MODERATE	CYTB	0.0933
HLI-0773	15607	A	G	0	588	synonymous_variant	LOW	CYTB	0.0508
HLI-0773	15928	G	A	0	625	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0773	16126	T	C	0	632	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0773	16294	C	T	2	534	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0773	16296	C	T	2	536	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0773	16304	T	C	2	555	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0773	16519	T	C	0	268	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0774	73	A	G	0	300	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0774	263	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0774	709	G	A	0	645	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0774	750	A	G	0	680	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0774	930	G	A	2	664	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0774	1438	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0774	1888	G	A	0	555	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0774	2706	A	G	1	651	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0774	4216	T	C	0	565	missense_variant	MODERATE	ND1	0.0991
HLI-0774	4688	T	C	0	640	synonymous_variant	LOW	ND2	0.0078
HLI-0774	4769	A	G	0	606	synonymous_variant	LOW	ND2	0.9767
HLI-0774	4917	A	G	0	600	missense_variant	MODERATE	ND2	0.0477
HLI-0774	5147	G	A	0	484	synonymous_variant	LOW	ND2	0.0437
HLI-0774	7028	C	T	4	682	synonymous_variant	LOW	COX1	0.8089

HLI-0774	7100	A	G	2	683	synonymous_variant	LOW	COX1	2.00E-04
HLI-0774	7891	C	T	1	661	synonymous_variant	LOW	COX2	4.00E-04
HLI-0774	8697	G	A	0	580	synonymous_variant	LOW	ATP6	0.0466
HLI-0774	10463	T	C	1	635	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0774	11251	A	G	0	635	synonymous_variant	LOW	ND4	0.0932
HLI-0774	11719	G	A	1	629	synonymous_variant	LOW	ND4	0.7756
HLI-0774	11812	A	G	2	584	synonymous_variant	LOW	ND4	0.0332
HLI-0774	13368	G	A	1	661	synonymous_variant	LOW	ND5	0.0495
HLI-0774	13692	C	T	5	586	synonymous_variant	LOW	ND5	6.00E-04
HLI-0774	14233	A	G	3	585	synonymous_variant	LOW	ND6	0.0369
HLI-0774	14766	C	T	0	583	missense_variant	MODERATE	CYTB	0.7696
HLI-0774	14905	G	A	1	709	synonymous_variant	LOW	CYTB	0.0526
HLI-0774	15326	A	G	0	492	missense_variant	MODERATE	CYTB	0.9868
HLI-0774	15452	C	A	4	475	missense_variant	MODERATE	CYTB	0.0933
HLI-0774	15607	A	G	1	525	synonymous_variant	LOW	CYTB	0.0508
HLI-0774	15928	G	A	0	597	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0774	16126	T	C	1	620	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0774	16294	C	T	0	569	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0774	16296	C	T	0	560	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0774	16304	T	C	0	551	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0774	16519	T	C	1	278	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0775	263	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0775	750	A	G	0	683	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0775	1438	A	G	0	641	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0775	3992	C	T	1	600	missense_variant	MODERATE	ND1	0.0062
HLI-0775	4024	A	G	1	645	missense_variant	MODERATE	ND1	0.0049
HLI-0775	4769	A	G	1	653	synonymous_variant	LOW	ND2	0.9767
HLI-0775	5004	T	C	0	642	synonymous_variant	LOW	ND2	0.0067
HLI-0775	5634	A	G	0	666	upstream_gene_variant	MODIFIER	TRNA	5.00E-04
HLI-0775	6845	C	T	2	720	synonymous_variant	LOW	COX1	4.00E-04
HLI-0775	7581	T	C	0	704	upstream_gene_variant	MODIFIER	TRND	0.0044
HLI-0775	9106	A	G	0	651	missense_variant	MODERATE	ATP6	0
HLI-0775	9123	G	A	0	717	synonymous_variant	LOW	ATP6	0.0485
HLI-0775	14365	C	T	1	563	synonymous_variant	LOW	ND6	0.0046
HLI-0775	14582	A	G	0	675	missense_variant	MODERATE	ND6	0.005
HLI-0775	15326	A	G	1	627	missense_variant	MODERATE	CYTB	0.9868
HLI-0775	15497	G	A	1	619	missense_variant	MODERATE	CYTB	0.0043
HLI-0775	15930	G	A	0	713	upstream_gene_variant	MODIFIER	TRNT	0.0224
HLI-0776	263	A	G	0	196	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0776	477	T	C	0	482	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0776	750	A	G	2	633	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0776	1438	A	G	1	635	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0776	3010	G	A	0	602	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0776	4769	A	G	2	652	synonymous_variant	LOW	ND2	0.9767
HLI-0776	6267	G	A	1	686	missense_variant	MODERATE	COX1	0.0016
HLI-0776	11839	T	C	0	577	synonymous_variant	LOW	ND4	2.00E-04
HLI-0776	14050	T	A	3	517	missense_variant	MODERATE	ND5	0
HLI-0776	15326	A	G	0	552	missense_variant	MODERATE	CYTB	0.9868
HLI-0776	16519	T	C	2	354	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0777	73	A	G	0	334	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0777	152	T	C	0	599	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0777	263	A	G	0	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0777	750	A	G	1	695	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0777	1438	A	G	0	679	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0777	2010	T	C	0	649	upstream_gene_variant	MODIFIER	RNR2	8.00E-04
HLI-0777	3591	G	A	0	582	synonymous_variant	LOW	ND1	0.0082
HLI-0777	4310	A	G	0	690	upstream_gene_variant	MODIFIER	TRNI	8.00E-04
HLI-0777	4769	A	G	2	614	synonymous_variant	LOW	ND2	0.9767
HLI-0777	13020	T	C	4	622	synonymous_variant	LOW	ND5	0.0106
HLI-0777	13161	T	C	2	624	synonymous_variant	LOW	ND5	0.0015
HLI-0777	15326	A	G	0	622	missense_variant	MODERATE	CYTB	0.9868
HLI-0777	16111	C	T	1	655	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0777	16168	C	T	4	697	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0777	16254	A	G	0	688	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0777	16319	G	A	0	607	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0777	16519	T	C	1	295	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0778	73	A	G	1	293	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0778	189	A	G	2	383	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0778	195	T	C	2	382	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0778	204	T	C	2	355	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0778	207	G	A	2	353	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0778	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0778	709	G	A	0	657	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0778	750	A	G	0	725	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0778	1243	T	C	0	700	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0778	1438	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0778	2706	A	G	0	631	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0778	3505	A	G	0	698	missense_variant	MODERATE	ND1	0.0144

HLI-0778	4769	A	G	1	679	synonymous_variant	LOW	ND2	0.9767
HLI-0778	4917	A	G	1	648	missense_variant	MODERATE	ND2	0.0477
HLI-0778	5046	G	A	1	538	missense_variant	MODERATE	ND2	0.018
HLI-0778	5460	G	A	1	606	missense_variant	MODERATE	ND2	0.0651
HLI-0778	5582	A	G	1	720	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0778	7028	C	T	0	715	synonymous_variant	LOW	COX1	0.8089
HLI-0778	7864	C	T	2	708	synonymous_variant	LOW	COX2	0.0041
HLI-0778	8251	G	A	1	595	synonymous_variant	LOW	COX2	0.058
HLI-0778	8994	G	A	0	631	synonymous_variant	LOW	ATP6	0.0167
HLI-0778	11674	C	T	4	594	synonymous_variant	LOW	ND4	0.0116
HLI-0778	11719	G	A	0	660	synonymous_variant	LOW	ND4	0.7756
HLI-0778	11947	A	G	1	624	synonymous_variant	LOW	ND4	0.011
HLI-0778	12414	T	C	2	534	synonymous_variant	LOW	ND5	0.0139
HLI-0778	12705	C	T	0	605	synonymous_variant	LOW	ND5	0.4212
HLI-0778	13681	A	G	50	564	missense_variant	MODERATE	ND5	0.0035
HLI-0778	14766	C	T	4	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0778	15326	A	G	0	615	missense_variant	MODERATE	CYTB	0.9868
HLI-0778	15884	G	C	1	549	missense_variant	MODERATE	CYTB	0.011
HLI-0778	16145	G	A	1	647	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0778	16223	C	T	1	579	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0778	16265	A	G	1	581	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0778	16519	T	C	0	345	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0779	73	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0779	151	C	T	20	477	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0779	152	T	C	0	496	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0779	199	T	C	0	432	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0779	373	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0779	750	A	G	0	589	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0779	850	T	C	0	613	upstream_gene_variant	MODIFIER	RNR1	0.0025
HLI-0779	921	T	C	1	682	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0779	1438	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0779	2706	A	G	1	610	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0779	4769	A	G	1	507	synonymous_variant	LOW	ND2	0.9767
HLI-0779	5147	G	A	1	491	synonymous_variant	LOW	ND2	0.0437
HLI-0779	5252	G	A	1	509	synonymous_variant	LOW	ND2	0.0027
HLI-0779	7028	C	T	0	670	synonymous_variant	LOW	COX1	0.8089
HLI-0779	7424	A	G	0	567	synonymous_variant	LOW	COX1	0.0115
HLI-0779	8618	T	C	0	404	missense_variant	MODERATE	ATP6	0.0103
HLI-0779	8701	A	G	3	436	missense_variant	MODERATE	ATP6	0.3391

HLI-0779	9540	T	C	0	605	synonymous_variant	LOW	COX3	0.339
HLI-0779	10398	A	G	1	533	missense_variant	MODERATE	ND3	0.445
HLI-0779	10873	T	C	1	543	synonymous_variant	LOW	ND4	0.3389
HLI-0779	11719	G	A	1	594	synonymous_variant	LOW	ND4	0.7756
HLI-0779	12705	C	T	1	542	synonymous_variant	LOW	ND5	0.4212
HLI-0779	13105	A	G	0	612	missense_variant	MODERATE	ND5	0.076
HLI-0779	13886	T	C	0	497	missense_variant	MODERATE	ND5	0.0088
HLI-0779	14272	C	T	2	515	synonymous_variant	LOW	ND6	5.00E-04
HLI-0779	14284	C	T	2	559	synonymous_variant	LOW	ND6	0.0087
HLI-0779	14584	T	C	1	549	synonymous_variant	LOW	ND6	3.00E-04
HLI-0779	14766	C	T	3	514	missense_variant	MODERATE	CYTB	0.7696
HLI-0779	15301	G	A	0	523	synonymous_variant	LOW	CYTB	0.2912
HLI-0779	15326	A	G	0	563	missense_variant	MODERATE	CYTB	0.9868
HLI-0779	16111	C	T	0	602	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0779	16124	T	C	0	651	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0779	16223	C	T	0	560	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0779	16309	A	G	3	486	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0780	73	A	G	0	310	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0780	146	T	C	0	571	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0780	263	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0780	279	T	C	0	256	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0780	709	G	A	1	619	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0780	750	A	G	3	675	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0780	1438	A	G	0	600	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0780	1888	G	A	0	406	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0780	2706	A	G	0	600	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0780	4216	T	C	0	482	missense_variant	MODERATE	ND1	0.0991
HLI-0780	4769	A	G	2	560	synonymous_variant	LOW	ND2	0.9767
HLI-0780	4917	A	G	0	581	missense_variant	MODERATE	ND2	0.0477
HLI-0780	5187	C	T	0	550	synonymous_variant	LOW	ND2	0.0023
HLI-0780	6261	G	A	1	653	missense_variant	MODERATE	COX1	0.007
HLI-0780	7028	C	T	2	658	synonymous_variant	LOW	COX1	0.8089
HLI-0780	7873	C	T	0	724	synonymous_variant	LOW	COX2	0.0023
HLI-0780	8697	G	A	1	511	synonymous_variant	LOW	ATP6	0.0466
HLI-0780	10463	T	C	0	674	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0780	10822	C	T	0	570	synonymous_variant	LOW	ND4	0.0036
HLI-0780	11251	A	G	0	628	synonymous_variant	LOW	ND4	0.0932
HLI-0780	11719	G	A	0	602	synonymous_variant	LOW	ND4	0.7756
HLI-0780	11812	A	G	1	599	synonymous_variant	LOW	ND4	0.0332

HLI-0780	11914	G	A	0	572	synonymous_variant	LOW	ND4	0.1112
HLI-0780	12363	C	T	0	291	synonymous_variant	LOW	ND5	3.00E-04
HLI-0780	13368	G	A	0	622	synonymous_variant	LOW	ND5	0.0495
HLI-0780	14233	A	G	0	512	synonymous_variant	LOW	ND6	0.0369
HLI-0780	14766	C	T	3	602	missense_variant	MODERATE	CYTB	0.7696
HLI-0780	14905	G	A	1	756	synonymous_variant	LOW	CYTB	0.0526
HLI-0780	15326	A	G	0	457	missense_variant	MODERATE	CYTB	0.9868
HLI-0780	15452	C	A	2	413	missense_variant	MODERATE	CYTB	0.0933
HLI-0780	15607	A	G	0	429	synonymous_variant	LOW	CYTB	0.0508
HLI-0780	15928	G	A	0	420	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0780	16092	T	C	9	516	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0780	16126	T	C	0	610	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0780	16292	C	T	0	511	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0780	16294	C	T	0	523	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0780	16360	C	T	0	499	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0780	16519	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0781	90	G	A	0	172	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0781	97	G	A	0	186	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0781	150	C	T	0	331	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0781	189	A	G	0	395	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0781	195	T	C	0	402	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0781	200	A	G	0	406	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0781	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0781	750	A	G	0	624	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0781	1438	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0781	2352	T	C	1	539	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0781	2706	A	G	2	638	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0781	4562	A	G	0	670	synonymous_variant	LOW	ND2	0.0026
HLI-0781	4769	A	G	0	636	synonymous_variant	LOW	ND2	0.9767
HLI-0781	6221	T	C	0	637	synonymous_variant	LOW	COX1	0.0306
HLI-0781	6587	C	T	2	677	synonymous_variant	LOW	COX1	0.0084
HLI-0781	7028	C	T	3	663	synonymous_variant	LOW	COX1	0.8089
HLI-0781	8701	A	G	0	573	missense_variant	MODERATE	ATP6	0.3391
HLI-0781	9098	T	C	0	632	missense_variant	MODERATE	ATP6	0.0011
HLI-0781	9540	T	C	0	680	synonymous_variant	LOW	COX3	0.339
HLI-0781	10370	T	C	0	669	synonymous_variant	LOW	ND3	0.0019
HLI-0781	10398	A	G	0	656	missense_variant	MODERATE	ND3	0.445
HLI-0781	10819	A	G	2	569	synonymous_variant	LOW	ND4	0.0228
HLI-0781	10873	T	C	0	652	synonymous_variant	LOW	ND4	0.3389

HLI-0781	11719	G	A	1	657	synonymous_variant	LOW	ND4	0.7756
HLI-0781	12705	C	T	1	584	synonymous_variant	LOW	ND5	0.4212
HLI-0781	14152	A	G	0	572	synonymous_variant	LOW	ND6	0.0086
HLI-0781	14212	T	C	1	631	synonymous_variant	LOW	ND6	0.0204
HLI-0781	14766	C	T	5	604	missense_variant	MODERATE	CYTB	0.7696
HLI-0781	15301	G	A	0	571	synonymous_variant	LOW	CYTB	0.2912
HLI-0781	15326	A	G	0	615	missense_variant	MODERATE	CYTB	0.9868
HLI-0781	15670	T	C	0	507	synonymous_variant	LOW	CYTB	0.0176
HLI-0781	15942	T	C	0	526	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0781	16223	C	T	2	592	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0781	16327	C	T	0	465	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0782	73	A	G	0	371	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0782	146	T	C	1	633	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0782	152	T	C	2	638	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0782	263	A	G	0	286	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0782	750	A	G	1	728	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0782	1189	T	C	0	760	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0782	1438	A	G	0	746	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0782	1811	A	G	0	664	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0782	2706	A	G	0	686	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0782	3480	A	G	1	624	synonymous_variant	LOW	ND1	0.0392
HLI-0782	4769	A	G	1	625	synonymous_variant	LOW	ND2	0.9767
HLI-0782	7028	C	T	1	770	synonymous_variant	LOW	COX1	0.8089
HLI-0782	9055	G	A	4	694	missense_variant	MODERATE	ATP6	0.0425
HLI-0782	9093	A	G	3	759	synonymous_variant	LOW	ATP6	0.0031
HLI-0782	9698	T	C	0	690	synonymous_variant	LOW	COX3	0.0405
HLI-0782	10398	A	G	1	732	missense_variant	MODERATE	ND3	0.445
HLI-0782	10550	A	G	6	699	synonymous_variant	LOW	ND4L	0.0376
HLI-0782	11299	T	C	1	695	synonymous_variant	LOW	ND4	0.0417
HLI-0782	11377	G	A	2	711	synonymous_variant	LOW	ND4	0.0125
HLI-0782	11467	A	G	0	735	synonymous_variant	LOW	ND4	0.1231
HLI-0782	11719	G	A	1	682	synonymous_variant	LOW	ND4	0.7756
HLI-0782	12308	A	G	3	568	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0782	12372	G	A	2	578	synonymous_variant	LOW	ND5	0.1329
HLI-0782	14167	C	T	5	640	synonymous_variant	LOW	ND6	0.0385
HLI-0782	14766	C	T	4	715	missense_variant	MODERATE	CYTB	0.7696
HLI-0782	14798	T	C	0	815	missense_variant	MODERATE	CYTB	0.0651
HLI-0782	15326	A	G	1	591	missense_variant	MODERATE	CYTB	0.9868
HLI-0782	16224	T	C	1	680	upstream_gene_variant	MODIFIER	DLoop	0.0423

HLI-0782	16301	C	T	1	656	upstream_gene_variant	MODIFIER	DLoop	0.0064
HLI-0782	16311	T	C	1	636	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0782	16519	T	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0783	73	A	G	0	307	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0783	150	C	T	3	509	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0783	185	G	A	1	512	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0783	189	A	G	1	506	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0783	200	A	G	1	497	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0783	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0783	750	A	G	0	716	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0783	1438	A	G	0	657	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0783	2352	T	C	2	635	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0783	2706	A	G	5	672	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0783	3438	G	A	1	590	synonymous_variant	LOW	ND1	0.0132
HLI-0783	4769	A	G	2	676	synonymous_variant	LOW	ND2	0.9767
HLI-0783	6221	T	C	1	655	synonymous_variant	LOW	COX1	0.0306
HLI-0783	6587	C	T	4	690	synonymous_variant	LOW	COX1	0.0084
HLI-0783	7028	C	T	0	710	synonymous_variant	LOW	COX1	0.8089
HLI-0783	8650	C	T	0	620	synonymous_variant	LOW	ATP6	0.0012
HLI-0783	8701	A	G	1	631	missense_variant	MODERATE	ATP6	0.3391
HLI-0783	9540	T	C	0	713	synonymous_variant	LOW	COX3	0.339
HLI-0783	10398	A	G	0	673	missense_variant	MODERATE	ND3	0.445
HLI-0783	10819	A	G	2	602	synonymous_variant	LOW	ND4	0.0228
HLI-0783	10873	T	C	0	654	synonymous_variant	LOW	ND4	0.3389
HLI-0783	11719	G	A	0	661	synonymous_variant	LOW	ND4	0.7756
HLI-0783	12705	C	T	1	641	synonymous_variant	LOW	ND5	0.4212
HLI-0783	14152	A	G	0	641	synonymous_variant	LOW	ND6	0.0086
HLI-0783	14212	T	C	0	710	synonymous_variant	LOW	ND6	0.0204
HLI-0783	14766	C	T	2	606	missense_variant	MODERATE	CYTB	0.7696
HLI-0783	15301	G	A	1	566	synonymous_variant	LOW	CYTB	0.2912
HLI-0783	15326	A	G	1	626	missense_variant	MODERATE	CYTB	0.9868
HLI-0783	15670	T	C	4	595	synonymous_variant	LOW	CYTB	0.0176
HLI-0783	15942	T	C	0	620	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0783	16223	C	T	1	733	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0783	16311	T	C	0	581	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0783	16327	C	T	0	617	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0784	72	T	C	0	269	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0784	195	T	C	0	445	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0784	263	A	G	1	353	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0784	750	A	G	0	555	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0784	1438	A	G	1	579	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0784	2706	A	G	1	554	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0784	3277	G	A	0	577	upstream_gene_variant	MODIFIER	TRNL1	7.00E-04
HLI-0784	4580	G	A	1	641	synonymous_variant	LOW	ND2	0.0169
HLI-0784	4769	A	G	0	571	synonymous_variant	LOW	ND2	0.9767
HLI-0784	7028	C	T	2	619	synonymous_variant	LOW	COX1	0.8089
HLI-0784	9844	C	T	2	832	missense_variant	MODERATE	COX3	0
HLI-0784	13105	A	G	1	558	missense_variant	MODERATE	ND5	0.076
HLI-0784	15326	A	G	0	387	missense_variant	MODERATE	CYTB	0.9868
HLI-0784	15904	C	T	0	465	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0784	16270	C	T	0	501	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0784	16298	T	C	0	462	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0785	263	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0785	750	A	G	1	705	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0785	1438	A	G	0	726	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0785	3992	C	T	3	654	missense_variant	MODERATE	ND1	0.0062
HLI-0785	4024	A	G	1	697	missense_variant	MODERATE	ND1	0.0049
HLI-0785	4769	A	G	1	669	synonymous_variant	LOW	ND2	0.9767
HLI-0785	5004	T	C	0	602	synonymous_variant	LOW	ND2	0.0067
HLI-0785	8269	G	A	2	633	stop_retained_variant	LOW	COX2	0.0127
HLI-0785	9123	G	A	2	733	synonymous_variant	LOW	ATP6	0.0485
HLI-0785	12798	C	T	7	678	synonymous_variant	LOW	ND5	0.0015
HLI-0785	14365	C	T	3	683	synonymous_variant	LOW	ND6	0.0046
HLI-0785	14582	A	G	1	697	missense_variant	MODERATE	ND6	0.005
HLI-0785	15326	A	G	0	621	missense_variant	MODERATE	CYTB	0.9868
HLI-0786	73	A	G	1	308	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0786	146	T	C	1	511	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0786	152	T	C	1	528	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0786	195	T	C	2	505	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0786	263	A	G	0	237	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0786	750	A	G	1	606	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0786	769	G	A	1	657	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0786	1018	G	A	0	758	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0786	1438	A	G	0	652	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0786	2416	T	C	2	457	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0786	2706	A	G	1	606	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0786	2789	C	T	1	685	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0786	3594	C	T	1	588	synonymous_variant	LOW	ND1	0.0789

HLI-0786	3918	G	A	0	608	synonymous_variant	LOW	ND1	0.009
HLI-0786	4104	A	G	1	530	synonymous_variant	LOW	ND1	0.0785
HLI-0786	4769	A	G	3	583	synonymous_variant	LOW	ND2	0.9767
HLI-0786	5285	A	G	0	559	synonymous_variant	LOW	ND2	0.0049
HLI-0786	7028	C	T	0	643	synonymous_variant	LOW	COX1	0.8089
HLI-0786	7175	T	C	1	647	synonymous_variant	LOW	COX1	0.0224
HLI-0786	7256	C	T	3	724	synonymous_variant	LOW	COX1	0.0784
HLI-0786	7274	C	T	3	665	synonymous_variant	LOW	COX1	0.0214
HLI-0786	7521	G	A	4	483	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0786	7771	A	G	3	660	synonymous_variant	LOW	COX2	0.0223
HLI-0786	8206	G	A	0	556	synonymous_variant	LOW	COX2	0.0287
HLI-0786	8701	A	G	1	633	missense_variant	MODERATE	ATP6	0.3391
HLI-0786	9221	A	G	1	672	synonymous_variant	LOW	COX3	0.0277
HLI-0786	9540	T	C	0	548	synonymous_variant	LOW	COX3	0.339
HLI-0786	10115	T	C	0	696	synonymous_variant	LOW	ND3	0.0278
HLI-0786	10398	A	G	2	677	missense_variant	MODERATE	ND3	0.445
HLI-0786	10873	T	C	0	570	synonymous_variant	LOW	ND4	0.3389
HLI-0786	11719	G	A	1	600	synonymous_variant	LOW	ND4	0.7756
HLI-0786	11914	G	A	2	667	synonymous_variant	LOW	ND4	0.1112
HLI-0786	11944	T	C	3	715	synonymous_variant	LOW	ND4	0.0331
HLI-0786	12693	A	G	1	585	synonymous_variant	LOW	ND5	0.0205
HLI-0786	12705	C	T	1	643	synonymous_variant	LOW	ND5	0.4212
HLI-0786	13590	G	A	2	599	synonymous_variant	LOW	ND5	0.0586
HLI-0786	13650	C	T	2	580	synonymous_variant	LOW	ND5	0.079
HLI-0786	13803	A	G	1	425	synonymous_variant	LOW	ND5	0.0216
HLI-0786	14566	A	G	0	684	synonymous_variant	LOW	ND6	0.0214
HLI-0786	14766	C	T	4	613	missense_variant	MODERATE	CYTB	0.7696
HLI-0786	15244	A	G	0	541	synonymous_variant	LOW	CYTB	0.0103
HLI-0786	15301	G	A	0	498	synonymous_variant	LOW	CYTB	0.2912
HLI-0786	15326	A	G	0	461	missense_variant	MODERATE	CYTB	0.9868
HLI-0786	15629	T	C	3	481	synonymous_variant	LOW	CYTB	0.0062
HLI-0786	15784	T	C	0	441	synonymous_variant	LOW	CYTB	0.0363
HLI-0786	16223	C	T	1	572	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0786	16278	C	T	0	591	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0786	16294	C	T	0	578	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0786	16309	A	G	0	558	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0786	16390	G	A	0	485	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0786	16519	T	C	1	251	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0787	73	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0787	150	C	T	1	561	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0787	195	T	C	0	450	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0787	263	A	G	0	331	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0787	1438	A	G	0	684	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0787	2000	C	T	2	546	upstream_gene_variant	MODIFIER	RNR2	0.0045
HLI-0787	2352	T	C	0	567	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0787	2706	A	G	1	745	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0787	4655	G	A	1	692	synonymous_variant	LOW	ND2	0.0072
HLI-0787	4769	A	G	1	622	synonymous_variant	LOW	ND2	0.9767
HLI-0787	5262	G	A	1	631	missense_variant	MODERATE	ND2	0.0077
HLI-0787	6524	T	C	1	713	synonymous_variant	LOW	COX1	0.0053
HLI-0787	7028	C	T	3	698	synonymous_variant	LOW	COX1	0.8089
HLI-0787	8701	A	G	0	618	missense_variant	MODERATE	ATP6	0.3391
HLI-0787	9440	C	T	1	731	synonymous_variant	LOW	COX3	0
HLI-0787	9540	T	C	2	724	synonymous_variant	LOW	COX3	0.339
HLI-0787	9554	G	A	1	720	synonymous_variant	LOW	COX3	0.014
HLI-0787	10398	A	G	0	693	missense_variant	MODERATE	ND3	0.445
HLI-0787	10667	T	C	2	647	synonymous_variant	LOW	ND4L	0.0047
HLI-0787	10816	A	G	1	643	synonymous_variant	LOW	ND4	0.0044
HLI-0787	10819	A	G	1	658	synonymous_variant	LOW	ND4	0.0228
HLI-0787	10873	T	C	1	675	synonymous_variant	LOW	ND4	0.3389
HLI-0787	11719	G	A	1	656	synonymous_variant	LOW	ND4	0.7756
HLI-0787	12248	A	G	1	586	upstream_gene_variant	MODIFIER	TRNS2	0.0022
HLI-0787	12705	C	T	1	647	synonymous_variant	LOW	ND5	0.4212
HLI-0787	13101	A	C	1	708	synonymous_variant	LOW	ND5	0.0055
HLI-0787	13116	C	T	1	773	synonymous_variant	LOW	ND5	0.0047
HLI-0787	13197	C	T	5	772	synonymous_variant	LOW	ND5	0.0021
HLI-0787	13651	A	G	0	594	missense_variant	MODERATE	ND5	0.0053
HLI-0787	14212	T	C	0	610	synonymous_variant	LOW	ND6	0.0204
HLI-0787	14766	C	T	2	626	missense_variant	MODERATE	CYTB	0.7696
HLI-0787	15301	G	A	0	607	synonymous_variant	LOW	CYTB	0.2912
HLI-0787	15326	A	G	0	673	missense_variant	MODERATE	CYTB	0.9868
HLI-0787	15812	G	A	2	604	missense_variant	MODERATE	CYTB	0.0096
HLI-0787	16093	T	C	17	564	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0787	16148	C	T	2	657	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0787	16223	C	T	1	655	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0787	16265	A	T	2	622	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0787	16519	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0788	263	A	G	0	344	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0788	750	A	G	0	683	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0788	1438	A	G	0	637	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0788	4769	A	G	3	653	synonymous_variant	LOW	ND2	0.9767
HLI-0788	10211	C	T	2	724	synonymous_variant	LOW	ND3	0.0027
HLI-0788	15326	A	G	0	541	missense_variant	MODERATE	CYTB	0.9868
HLI-0788	16519	T	C	0	324	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0789	195	T	C	0	365	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0789	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0789	750	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0789	961	T	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0789	1438	A	G	0	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0789	4769	A	G	1	592	synonymous_variant	LOW	ND2	0.9767
HLI-0789	8448	T	C	0	278	missense_variant	MODERATE	ATP8	0.0041
HLI-0789	13759	G	A	0	355	missense_variant	MODERATE	ND5	0.0348
HLI-0789	15326	A	G	1	435	missense_variant	MODERATE	CYTB	0.9868
HLI-0789	16311	T	C	0	447	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0790	73	A	G	0	324	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0790	152	T	C	0	588	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0790	263	A	G	0	260	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0790	709	G	A	2	682	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0790	750	A	G	1	709	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0790	930	G	A	3	772	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0790	1438	A	G	0	669	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0790	1888	G	A	1	634	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0790	2706	A	G	1	716	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0790	4216	T	C	0	707	missense_variant	MODERATE	ND1	0.0991
HLI-0790	4769	A	G	2	599	synonymous_variant	LOW	ND2	0.9767
HLI-0790	4917	A	G	1	643	missense_variant	MODERATE	ND2	0.0477
HLI-0790	5147	G	A	2	619	synonymous_variant	LOW	ND2	0.0437
HLI-0790	7028	C	T	8	726	synonymous_variant	LOW	COX1	0.8089
HLI-0790	8697	G	A	1	616	synonymous_variant	LOW	ATP6	0.0466
HLI-0790	10463	T	C	0	615	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0790	11251	A	G	1	685	synonymous_variant	LOW	ND4	0.0932
HLI-0790	11719	G	A	1	698	synonymous_variant	LOW	ND4	0.7756
HLI-0790	11812	A	G	2	670	synonymous_variant	LOW	ND4	0.0332
HLI-0790	13368	G	A	1	736	synonymous_variant	LOW	ND5	0.0495
HLI-0790	14233	A	G	1	634	synonymous_variant	LOW	ND6	0.0369
HLI-0790	14766	C	T	2	642	missense_variant	MODERATE	CYTB	0.7696
HLI-0790	14905	G	A	3	741	synonymous_variant	LOW	CYTB	0.0526

HLI-0790	15326	A	G	0	614	missense_variant	MODERATE	CYTB	0.9868
HLI-0790	15452	C	A	4	607	missense_variant	MODERATE	CYTB	0.0933
HLI-0790	15607	A	G	2	638	synonymous_variant	LOW	CYTB	0.0508
HLI-0790	15928	G	A	0	663	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0790	16126	T	C	0	697	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0790	16294	C	T	0	569	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0790	16296	C	T	0	570	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0790	16304	T	C	0	589	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0790	16519	T	C	0	259	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0791	72	T	C	1	292	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0791	195	T	C	2	517	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0791	263	A	G	0	410	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0791	750	A	G	1	519	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0791	1438	A	G	0	524	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0791	2706	A	G	0	547	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0791	4769	A	G	0	517	synonymous_variant	LOW	ND2	0.9767
HLI-0791	7028	C	T	2	587	synonymous_variant	LOW	COX1	0.8089
HLI-0791	9110	T	C	0	551	missense_variant	MODERATE	ATP6	0.0013
HLI-0791	12172	A	G	1	447	upstream_gene_variant	MODIFIER	TRNH	0.0064
HLI-0791	14022	A	G	1	395	synonymous_variant	LOW	ND5	0.0366
HLI-0791	15326	A	G	0	366	missense_variant	MODERATE	CYTB	0.9868
HLI-0791	16129	G	A	2	495	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0791	16298	T	C	0	460	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0792	73	A	G	0	351	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0792	185	G	A	1	514	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0792	188	A	G	1	515	upstream_gene_variant	MODIFIER	DLoop	0.0106
HLI-0792	228	G	A	0	362	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0792	263	A	G	1	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0792	295	C	T	0	207	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0792	462	C	T	0	506	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0792	489	T	C	0	627	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0792	750	A	G	0	682	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0792	1438	A	G	0	695	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0792	2706	A	G	0	697	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0792	3010	G	A	1	708	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0792	4216	T	C	1	689	missense_variant	MODERATE	ND1	0.0991
HLI-0792	4769	A	G	0	697	synonymous_variant	LOW	ND2	0.9767
HLI-0792	4790	A	G	0	785	synonymous_variant	LOW	ND2	5.00E-04
HLI-0792	6293	T	C	1	759	synonymous_variant	LOW	COX1	0.0036

HLI-0792	7028	C	T	0	797	synonymous_variant	LOW	COX1	0.8089
HLI-0792	10398	A	G	2	795	missense_variant	MODERATE	ND3	0.445
HLI-0792	11251	A	G	1	684	synonymous_variant	LOW	ND4	0.0932
HLI-0792	11719	G	A	0	658	synonymous_variant	LOW	ND4	0.7756
HLI-0792	12612	A	G	13	729	synonymous_variant	LOW	ND5	0.0506
HLI-0792	13708	G	A	0	584	missense_variant	MODERATE	ND5	0.0717
HLI-0792	14766	C	T	3	784	missense_variant	MODERATE	CYTB	0.7696
HLI-0792	14798	T	C	1	795	missense_variant	MODERATE	CYTB	0.0651
HLI-0792	15043	G	A	2	701	synonymous_variant	LOW	CYTB	0.2362
HLI-0792	15326	A	G	0	653	missense_variant	MODERATE	CYTB	0.9868
HLI-0792	15452	C	A	2	666	missense_variant	MODERATE	CYTB	0.0933
HLI-0792	16069	C	T	7	720	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0792	16126	T	C	5	766	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0792	16519	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0793	73	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0793	152	T	C	1	540	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0793	189	A	G	2	545	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0793	200	A	G	2	526	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0793	263	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0793	750	A	G	1	657	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0793	1438	A	G	0	674	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0793	1822	T	C	0	689	upstream_gene_variant	MODIFIER	RNR2	0.0062
HLI-0793	2706	A	G	1	628	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0793	3396	T	C	0	658	synonymous_variant	LOW	ND1	0.0082
HLI-0793	4218	T	C	1	590	synonymous_variant	LOW	ND1	0.0057
HLI-0793	4769	A	G	0	615	synonymous_variant	LOW	ND2	0.9767
HLI-0793	5601	C	T	1	734	upstream_gene_variant	MODIFIER	TRNA	0.0101
HLI-0793	7028	C	T	1	701	synonymous_variant	LOW	COX1	0.8089
HLI-0793	7819	C	A	2	667	synonymous_variant	LOW	COX2	0.0045
HLI-0793	8410	C	T	1	488	synonymous_variant	LOW	ATP8	0.0018
HLI-0793	8527	A	G	1	551	initiator_codon_variant	LOW	ATP6/8	0.0044
HLI-0793	8701	A	G	1	610	missense_variant	MODERATE	ATP6	0.3391
HLI-0793	8932	C	T	5	664	missense_variant	MODERATE	ATP6	0.0044
HLI-0793	9540	T	C	1	624	synonymous_variant	LOW	COX3	0.339
HLI-0793	9950	T	C	1	701	synonymous_variant	LOW	COX3	0.0362
HLI-0793	10070	C	T	0	715	synonymous_variant	LOW	ND3	8.00E-04
HLI-0793	10398	A	G	0	595	missense_variant	MODERATE	ND3	0.445
HLI-0793	10873	T	C	1	623	synonymous_variant	LOW	ND4	0.3389
HLI-0793	11440	G	A	3	702	synonymous_variant	LOW	ND4	0.0081

HLI-0793	11719	G	A	0	618	synonymous_variant	LOW	ND4	0.7756
HLI-0793	12705	C	T	2	665	synonymous_variant	LOW	ND5	0.4212
HLI-0793	14766	C	T	0	641	missense_variant	MODERATE	CYTB	0.7696
HLI-0793	14769	A	G	0	651	missense_variant	MODERATE	CYTB	0.0121
HLI-0793	15301	G	A	0	604	synonymous_variant	LOW	CYTB	0.2912
HLI-0793	15326	A	G	0	633	missense_variant	MODERATE	CYTB	0.9868
HLI-0793	15514	T	C	1	544	synonymous_variant	LOW	CYTB	0.0071
HLI-0793	16129	G	A	0	588	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0793	16209	T	C	1	576	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0793	16223	C	T	2	586	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0793	16292	C	T	0	528	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0793	16295	C	T	0	526	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0793	16311	T	C	0	523	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0793	16519	T	C	0	277	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0794	263	A	G	0	285	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0794	456	C	T	2	466	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0794	750	A	G	0	646	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0794	1438	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0794	4336	T	C	1	537	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0794	4769	A	G	0	645	synonymous_variant	LOW	ND2	0.9767
HLI-0794	15326	A	G	1	516	missense_variant	MODERATE	CYTB	0.9868
HLI-0794	15833	C	T	1	557	synonymous_variant	LOW	CYTB	0.0051
HLI-0794	16304	T	C	2	555	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0795	73	A	G	1	341	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0795	146	T	C	1	606	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0795	263	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0795	750	A	G	0	718	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0795	1438	A	G	0	700	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0795	1811	A	G	3	712	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0795	2217	C	T	3	635	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0795	2706	A	G	0	709	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0795	3480	A	G	3	631	synonymous_variant	LOW	ND1	0.0392
HLI-0795	4769	A	G	0	608	synonymous_variant	LOW	ND2	0.9767
HLI-0795	5231	G	A	2	625	synonymous_variant	LOW	ND2	0.0232
HLI-0795	7028	C	T	1	708	synonymous_variant	LOW	COX1	0.8089
HLI-0795	9055	G	A	0	665	missense_variant	MODERATE	ATP6	0.0425
HLI-0795	9698	T	C	0	712	synonymous_variant	LOW	COX3	0.0405
HLI-0795	9716	T	C	0	777	synonymous_variant	LOW	COX3	0.0108
HLI-0795	10550	A	G	4	720	synonymous_variant	LOW	ND4L	0.0376

HLI-0795	11299	T	C	0	687	synonymous_variant	LOW	ND4	0.0417
HLI-0795	11467	A	G	1	712	synonymous_variant	LOW	ND4	0.1231
HLI-0795	11719	G	A	1	688	synonymous_variant	LOW	ND4	0.7756
HLI-0795	11869	C	A	5	655	synonymous_variant	LOW	ND4	0.0015
HLI-0795	12308	A	G	0	653	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0795	12372	G	A	0	682	synonymous_variant	LOW	ND5	0.1329
HLI-0795	13135	G	A	5	743	missense_variant	MODERATE	ND5	0.0092
HLI-0795	14037	A	G	4	578	synonymous_variant	LOW	ND5	0.0017
HLI-0795	14167	C	T	2	655	synonymous_variant	LOW	ND6	0.0385
HLI-0795	14766	C	T	2	659	missense_variant	MODERATE	CYTB	0.7696
HLI-0795	14798	T	C	0	746	missense_variant	MODERATE	CYTB	0.0651
HLI-0795	15326	A	G	1	628	missense_variant	MODERATE	CYTB	0.9868
HLI-0795	15586	T	C	3	685	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0795	16224	T	C	0	637	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0795	16311	T	C	0	549	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0795	16519	T	C	0	273	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0796	263	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0796	456	C	T	3	443	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0796	750	A	G	0	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0796	1438	A	G	0	701	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0796	3666	G	A	1	717	synonymous_variant	LOW	ND1	0.0233
HLI-0796	4769	A	G	0	627	synonymous_variant	LOW	ND2	0.9767
HLI-0796	5302	T	C	1	619	missense_variant	MODERATE	ND2	7.00E-04
HLI-0796	15326	A	G	0	634	missense_variant	MODERATE	CYTB	0.9868
HLI-0796	16304	T	C	0	562	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0796	16311	T	C	0	595	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0796	16391	G	A	2	549	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0797	73	A	G	0	35	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0797	195	T	C	0	62	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0797	263	A	G	0	25	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0797	750	A	G	0	58	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0797	1438	A	G	0	56	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0797	2706	A	G	0	61	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0797	3027	T	C	0	56	upstream_gene_variant	MODIFIER	RNR2	0.0117
HLI-0797	3197	T	C	0	48	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0797	3552	T	C	0	48	synonymous_variant	LOW	ND1	0.0028
HLI-0797	4769	A	G	1	50	synonymous_variant	LOW	ND2	0.9767
HLI-0797	4823	T	C	0	49	synonymous_variant	LOW	ND2	0.0049
HLI-0797	5583	C	T	0	59	upstream_gene_variant	MODIFIER	Unannotated	5.00E-04

HLI-0797	6584	C	T	0	67	synonymous_variant	LOW	COX1	3.00E-04
HLI-0797	6836	C	T	0	72	synonymous_variant	LOW	COX1	4.00E-04
HLI-0797	7028	C	T	0	79	synonymous_variant	LOW	COX1	0.8089
HLI-0797	9477	G	A	0	61	missense_variant	MODERATE	COX3	0.0387
HLI-0797	11467	A	G	0	58	synonymous_variant	LOW	ND4	0.1231
HLI-0797	11719	G	A	0	55	synonymous_variant	LOW	ND4	0.7756
HLI-0797	12308	A	G	0	60	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0797	12372	G	A	0	54	synonymous_variant	LOW	ND5	0.1329
HLI-0797	13617	T	C	0	54	synonymous_variant	LOW	ND5	0.038
HLI-0797	14766	C	T	0	76	missense_variant	MODERATE	CYTB	0.7696
HLI-0797	14793	A	G	0	82	missense_variant	MODERATE	CYTB	0.0199
HLI-0797	15218	A	G	1	58	missense_variant	MODERATE	CYTB	0.0169
HLI-0797	15326	A	G	0	70	missense_variant	MODERATE	CYTB	0.9868
HLI-0797	16145	G	A	0	50	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0797	16256	C	T	0	42	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0797	16270	C	T	0	39	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0797	16399	A	G	0	48	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0797	16519	T	C	0	27	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0798	73	A	G	0	310	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0798	152	T	C	0	561	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0798	195	T	C	1	556	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0798	263	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0798	709	G	A	1	613	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0798	750	A	G	2	655	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0798	930	G	A	2	665	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0798	1438	A	G	0	607	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0798	1888	G	A	0	430	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0798	2706	A	G	0	671	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0798	4216	T	C	2	459	missense_variant	MODERATE	ND1	0.0991
HLI-0798	4769	A	G	2	561	synonymous_variant	LOW	ND2	0.9767
HLI-0798	4917	A	G	0	576	missense_variant	MODERATE	ND2	0.0477
HLI-0798	5147	G	A	1	478	synonymous_variant	LOW	ND2	0.0437
HLI-0798	7028	C	T	3	691	synonymous_variant	LOW	COX1	0.8089
HLI-0798	8697	G	A	3	592	synonymous_variant	LOW	ATP6	0.0466
HLI-0798	10463	T	C	2	591	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0798	11251	A	G	1	635	synonymous_variant	LOW	ND4	0.0932
HLI-0798	11719	G	A	0	593	synonymous_variant	LOW	ND4	0.7756
HLI-0798	11812	A	G	2	590	synonymous_variant	LOW	ND4	0.0332
HLI-0798	13368	G	A	0	628	synonymous_variant	LOW	ND5	0.0495

HLI-0798	14233	A	G	1	577	synonymous_variant	LOW	ND6	0.0369
HLI-0798	14766	C	T	7	688	missense_variant	MODERATE	CYTB	0.7696
HLI-0798	14836	A	G	0	803	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0798	14905	G	A	0	847	synonymous_variant	LOW	CYTB	0.0526
HLI-0798	15326	A	G	0	455	missense_variant	MODERATE	CYTB	0.9868
HLI-0798	15452	C	A	2	445	missense_variant	MODERATE	CYTB	0.0933
HLI-0798	15607	A	G	1	393	synonymous_variant	LOW	CYTB	0.0508
HLI-0798	15928	G	A	0	449	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0798	16126	T	C	0	478	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0798	16294	C	T	1	516	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0798	16304	T	C	1	547	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0798	16519	T	C	0	272	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0799	73	A	G	0	353	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0799	195	T	C	0	498	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0799	263	A	G	1	278	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0799	709	G	A	1	741	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0799	750	A	G	0	791	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0799	1438	A	G	0	742	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0799	1888	G	A	1	677	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0799	2706	A	G	1	756	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0799	3705	G	A	1	690	synonymous_variant	LOW	ND1	0.0138
HLI-0799	4216	T	C	0	706	missense_variant	MODERATE	ND1	0.0991
HLI-0799	4769	A	G	2	722	synonymous_variant	LOW	ND2	0.9767
HLI-0799	4917	A	G	0	672	missense_variant	MODERATE	ND2	0.0477
HLI-0799	7028	C	T	4	803	synonymous_variant	LOW	COX1	0.8089
HLI-0799	8697	G	A	0	674	synonymous_variant	LOW	ATP6	0.0466
HLI-0799	9899	T	C	0	758	synonymous_variant	LOW	COX3	0.0108
HLI-0799	10463	T	C	0	693	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0799	11251	A	G	0	683	synonymous_variant	LOW	ND4	0.0932
HLI-0799	11719	G	A	1	667	synonymous_variant	LOW	ND4	0.7756
HLI-0799	12633	C	A	9	767	synonymous_variant	LOW	ND5	0.0123
HLI-0799	13368	G	A	0	725	synonymous_variant	LOW	ND5	0.0495
HLI-0799	14766	C	T	2	697	missense_variant	MODERATE	CYTB	0.7696
HLI-0799	14905	G	A	1	729	synonymous_variant	LOW	CYTB	0.0526
HLI-0799	15326	A	G	0	632	missense_variant	MODERATE	CYTB	0.9868
HLI-0799	15452	C	A	2	658	missense_variant	MODERATE	CYTB	0.0933
HLI-0799	15607	A	G	0	687	synonymous_variant	LOW	CYTB	0.0508
HLI-0799	15928	G	A	0	743	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0799	16126	T	C	1	690	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0799	16163	A	G	0	711	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0799	16292	C	T	0	647	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0799	16294	C	T	1	657	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0799	16519	T	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0800	152	T	C	0	534	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0800	263	A	G	2	360	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0800	456	C	T	4	521	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0800	750	A	G	1	655	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0800	1438	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0800	4336	T	C	1	429	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0800	4769	A	G	1	572	synonymous_variant	LOW	ND2	0.9767
HLI-0800	5319	A	G	0	526	missense_variant	MODERATE	ND2	0.0031
HLI-0800	8563	A	G	1	575	missense_variant	MODERATE	ATP6/8	0.0034
HLI-0800	15326	A	G	0	431	missense_variant	MODERATE	CYTB	0.9868
HLI-0800	16304	T	C	0	476	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0801	195	T	C	0	453	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0801	263	A	G	1	260	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0801	750	A	G	0	664	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0801	961	T	G	2	733	upstream_gene_variant	MODIFIER	RNR1	0.0035
HLI-0801	1438	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0801	4769	A	G	2	584	synonymous_variant	LOW	ND2	0.9767
HLI-0801	5585	G	A	0	635	upstream_gene_variant	MODIFIER	Unannotated	0.0097
HLI-0801	8448	T	C	1	369	missense_variant	MODERATE	ATP8	0.0041
HLI-0801	11698	C	T	0	678	synonymous_variant	LOW	ND4	1.00E-04
HLI-0801	13759	G	A	0	396	missense_variant	MODERATE	ND5	0.0348
HLI-0801	14587	A	G	3	658	synonymous_variant	LOW	ND6	0.006
HLI-0801	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0801	15670	T	C	0	463	synonymous_variant	LOW	CYTB	0.0176
HLI-0801	16092	T	C	8	523	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0801	16140	T	C	0	626	upstream_gene_variant	MODIFIER	DLoop	0.0177
HLI-0801	16265	A	G	0	523	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0801	16293	A	G	0	488	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0801	16311	T	C	0	473	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0802	73	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0802	146	T	C	0	460	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0802	152	T	C	0	471	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0802	182	C	T	0	409	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0802	186	C	A	0	398	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0802	189	A	C	0	391	upstream_gene_variant	MODIFIER	DLoop	0.0122

HLI-0802	194	C	T	1	397	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0802	247	G	A	0	220	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0802	263	A	G	0	243	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0802	750	A	G	2	699	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0802	769	G	A	0	762	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0802	825	T	A	0	810	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0802	1018	G	A	3	810	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0802	1438	A	G	0	651	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0802	2706	A	G	0	695	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0802	2758	G	A	0	732	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0802	2885	T	C	1	630	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0802	3594	C	T	0	579	synonymous_variant	LOW	ND1	0.0789
HLI-0802	3666	G	A	1	653	synonymous_variant	LOW	ND1	0.0233
HLI-0802	4104	A	G	0	523	synonymous_variant	LOW	ND1	0.0785
HLI-0802	4500	T	C	1	720	missense_variant	MODERATE	ND2	3.00E-04
HLI-0802	4703	T	C	2	619	synonymous_variant	LOW	ND2	0.0058
HLI-0802	4769	A	G	0	625	synonymous_variant	LOW	ND2	0.9767
HLI-0802	5951	A	G	2	746	synonymous_variant	LOW	COX1	0.0128
HLI-0802	6071	T	C	0	800	synonymous_variant	LOW	COX1	0.0129
HLI-0802	6221	T	A	2	699	synonymous_variant	LOW	COX1	0.0027
HLI-0802	6917	G	A	2	747	synonymous_variant	LOW	COX1	0.0036
HLI-0802	6965	T	C	0	779	synonymous_variant	LOW	COX1	1.00E-04
HLI-0802	7028	C	T	1	670	synonymous_variant	LOW	COX1	0.8089
HLI-0802	7146	A	G	0	335	missense_variant	MODERATE	COX1	0.0497
HLI-0802	7256	C	T	0	437	synonymous_variant	LOW	COX1	0.0784
HLI-0802	7389	T	C	0	428	missense_variant	MODERATE	COX1	0.0201
HLI-0802	7521	G	A	1	360	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0802	8027	G	A	2	793	missense_variant	MODERATE	COX2	0.0334
HLI-0802	8167	T	C	1	735	synonymous_variant	LOW	COX2	0.0021
HLI-0802	8251	G	A	1	624	synonymous_variant	LOW	COX2	0.058
HLI-0802	8468	C	T	5	353	synonymous_variant	LOW	ATP8	0.0501
HLI-0802	8655	C	T	2	403	synonymous_variant	LOW	ATP6	0.0511
HLI-0802	8659	A	G	2	423	missense_variant	MODERATE	ATP6	0.0022
HLI-0802	8701	A	G	3	483	missense_variant	MODERATE	ATP6	0.3391
HLI-0802	9072	A	G	1	644	synonymous_variant	LOW	ATP6	0.0124
HLI-0802	9377	A	G	0	731	synonymous_variant	LOW	COX3	0.0084
HLI-0802	9540	T	C	0	557	synonymous_variant	LOW	COX3	0.339
HLI-0802	10398	A	G	1	534	missense_variant	MODERATE	ND3	0.445
HLI-0802	10586	G	A	1	633	synonymous_variant	LOW	ND4L	0.0177

HLI-0802	10685	G	A	0	551	synonymous_variant	LOW	ND4L	0.0055
HLI-0802	10688	G	A	0	559	synonymous_variant	LOW	ND4L	0.0515
HLI-0802	10810	T	C	0	506	synonymous_variant	LOW	ND4	0.0522
HLI-0802	10873	T	C	0	506	synonymous_variant	LOW	ND4	0.3389
HLI-0802	11233	T	C	0	582	synonymous_variant	LOW	ND4	6.00E-04
HLI-0802	11302	C	T	0	625	synonymous_variant	LOW	ND4	0.0028
HLI-0802	11440	G	A	1	659	synonymous_variant	LOW	ND4	0.0081
HLI-0802	11719	G	A	1	645	synonymous_variant	LOW	ND4	0.7756
HLI-0802	12705	C	T	2	530	synonymous_variant	LOW	ND5	0.4212
HLI-0802	12810	A	G	2	570	synonymous_variant	LOW	ND5	0.0198
HLI-0802	12903	T	C	5	655	synonymous_variant	LOW	ND5	5.00E-04
HLI-0802	13105	A	G	1	652	missense_variant	MODERATE	ND5	0.076
HLI-0802	13485	A	G	0	535	synonymous_variant	LOW	ND5	0.0122
HLI-0802	13506	C	T	0	617	synonymous_variant	LOW	ND5	0.0506
HLI-0802	13650	C	T	2	579	synonymous_variant	LOW	ND5	0.079
HLI-0802	13789	T	C	0	395	missense_variant	MODERATE	ND5	0.0185
HLI-0802	13981	C	T	0	400	missense_variant	MODERATE	ND5	0.0011
HLI-0802	14000	T	A	0	436	missense_variant	MODERATE	ND5	0.0126
HLI-0802	14178	T	C	1	454	missense_variant	MODERATE	ND6	0.0225
HLI-0802	14560	G	A	0	902	synonymous_variant	LOW	ND6	0.0235
HLI-0802	14766	C	T	5	785	missense_variant	MODERATE	CYTB	0.7696
HLI-0802	14794	C	T	1	876	synonymous_variant	LOW	CYTB	0.001
HLI-0802	14798	T	C	1	879	missense_variant	MODERATE	CYTB	0.0651
HLI-0802	14911	C	T	2	897	synonymous_variant	LOW	CYTB	0.0124
HLI-0802	15226	A	G	4	622	synonymous_variant	LOW	CYTB	0.0034
HLI-0802	15326	A	G	1	494	missense_variant	MODERATE	CYTB	0.9868
HLI-0802	15905	T	C	0	252	upstream_gene_variant	MODIFIER	TRNT	0.005
HLI-0802	15924	A	G	0	283	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0802	15978	C	T	0	307	upstream_gene_variant	MODIFIER	TRNP	0.0032
HLI-0802	16086	T	C	2	376	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0802	16129	G	A	2	432	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0802	16223	C	T	1	381	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0802	16278	C	T	0	321	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0802	16294	C	T	0	354	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0802	16301	C	T	0	368	upstream_gene_variant	MODIFIER	DLoop	0.0064
HLI-0802	16311	T	C	0	369	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0802	16360	C	T	0	387	upstream_gene_variant	MODIFIER	DLoop	0.0153
HLI-0802	16519	T	C	0	230	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0803	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0803	750	A	G	1	619	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0803	1438	A	G	0	646	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0803	3915	G	A	2	699	synonymous_variant	LOW	ND1	0.0106
HLI-0803	4769	A	G	2	680	synonymous_variant	LOW	ND2	0.9767
HLI-0803	14798	T	C	0	757	missense_variant	MODERATE	CYTB	0.0651
HLI-0803	15326	A	G	0	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0803	16129	G	A	1	621	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0803	16519	T	C	3	360	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0804	73	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0804	143	G	A	0	592	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0804	146	T	C	0	609	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0804	195	T	C	1	608	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0804	263	A	G	0	303	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0804	480	T	C	2	529	upstream_gene_variant	MODIFIER	DLoop	0.0019
HLI-0804	750	A	G	1	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0804	769	G	A	3	740	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0804	1018	G	A	4	771	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0804	1438	A	G	0	780	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0804	2163	A	G	6	556	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0804	2416	T	C	4	541	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0804	2706	A	G	2	620	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0804	2789	C	T	0	713	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0804	3594	C	T	1	538	synonymous_variant	LOW	ND1	0.0789
HLI-0804	3918	G	A	1	593	synonymous_variant	LOW	ND1	0.009
HLI-0804	4104	A	G	0	484	synonymous_variant	LOW	ND1	0.0785
HLI-0804	4769	A	G	1	648	synonymous_variant	LOW	ND2	0.9767
HLI-0804	7028	C	T	0	714	synonymous_variant	LOW	COX1	0.8089
HLI-0804	7175	T	C	0	653	synonymous_variant	LOW	COX1	0.0224
HLI-0804	7256	C	T	2	692	synonymous_variant	LOW	COX1	0.0784
HLI-0804	7274	C	T	2	659	synonymous_variant	LOW	COX1	0.0214
HLI-0804	7521	G	A	0	511	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0804	7771	A	G	1	675	synonymous_variant	LOW	COX2	0.0223
HLI-0804	8206	G	A	0	663	synonymous_variant	LOW	COX2	0.0287
HLI-0804	8701	A	G	0	588	missense_variant	MODERATE	ATP6	0.3391
HLI-0804	9221	A	G	1	700	synonymous_variant	LOW	COX3	0.0277
HLI-0804	9540	T	C	0	599	synonymous_variant	LOW	COX3	0.339
HLI-0804	9716	T	C	2	649	synonymous_variant	LOW	COX3	0.0108
HLI-0804	10115	T	C	0	740	synonymous_variant	LOW	ND3	0.0278
HLI-0804	10398	A	G	0	639	missense_variant	MODERATE	ND3	0.445

HLI-0804	10873	T	C	0	625	synonymous_variant	LOW	ND4	0.3389
HLI-0804	11719	G	A	0	677	synonymous_variant	LOW	ND4	0.7756
HLI-0804	11914	G	A	3	701	synonymous_variant	LOW	ND4	0.1112
HLI-0804	11944	T	C	2	741	synonymous_variant	LOW	ND4	0.0331
HLI-0804	12693	A	G	0	601	synonymous_variant	LOW	ND5	0.0205
HLI-0804	12705	C	T	0	652	synonymous_variant	LOW	ND5	0.4212
HLI-0804	13590	G	A	5	671	synonymous_variant	LOW	ND5	0.0586
HLI-0804	13650	C	T	2	658	synonymous_variant	LOW	ND5	0.079
HLI-0804	13803	A	G	4	471	synonymous_variant	LOW	ND5	0.0216
HLI-0804	14566	A	G	3	712	synonymous_variant	LOW	ND6	0.0214
HLI-0804	14766	C	T	4	635	missense_variant	MODERATE	CYTB	0.7696
HLI-0804	15301	G	A	1	577	synonymous_variant	LOW	CYTB	0.2912
HLI-0804	15326	A	G	0	609	missense_variant	MODERATE	CYTB	0.9868
HLI-0804	15784	T	C	0	545	synonymous_variant	LOW	CYTB	0.0363
HLI-0804	16223	C	T	2	249	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0804	16278	C	T	1	415	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0804	16294	C	T	1	459	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0804	16309	A	G	1	504	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0804	16390	G	A	1	509	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0805	73	A	G	1	356	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0805	151	C	T	4	622	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0805	263	A	G	1	271	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0805	750	A	G	1	710	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0805	1438	A	G	1	728	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0805	3010	G	A	3	724	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0805	4769	A	G	4	664	synonymous_variant	LOW	ND2	0.9767
HLI-0805	7073	A	G	1	739	synonymous_variant	LOW	COX1	2.00E-04
HLI-0805	11893	A	G	0	629	synonymous_variant	LOW	ND4	0.0017
HLI-0805	15326	A	G	0	646	missense_variant	MODERATE	CYTB	0.9868
HLI-0805	16162	A	G	5	423	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0805	16519	T	C	1	332	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0806	263	A	G	0	311	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0806	477	T	C	0	493	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0806	750	A	G	1	708	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0806	1438	A	G	0	684	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0806	3010	G	A	1	658	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0806	3606	A	G	0	644	synonymous_variant	LOW	ND1	0.0124
HLI-0806	4769	A	G	0	605	synonymous_variant	LOW	ND2	0.9767
HLI-0806	15326	A	G	0	597	missense_variant	MODERATE	CYTB	0.9868

HLI-0806	15937	A	G	1	548	upstream_gene_variant	MODIFIER	TRNT	9.00E-04
HLI-0806	16519	T	C	0	375	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0807	73	A	G	1	334	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0807	150	C	T	0	562	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0807	152	T	C	0	567	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0807	195	T	C	0	467	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0807	215	A	G	1	400	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0807	263	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0807	295	C	T	0	239	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0807	319	T	C	0	253	upstream_gene_variant	MODIFIER	DLoop	0.0041
HLI-0807	489	T	C	1	490	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0807	750	A	G	0	672	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0807	1438	A	G	0	665	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0807	1850	T	C	0	535	upstream_gene_variant	MODIFIER	RNR2	0.0024
HLI-0807	2706	A	G	0	637	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0807	3434	A	G	1	619	missense_variant	MODERATE	ND1	0.0088
HLI-0807	4216	T	C	2	540	missense_variant	MODERATE	ND1	0.0991
HLI-0807	4769	A	G	1	619	synonymous_variant	LOW	ND2	0.9767
HLI-0807	7028	C	T	3	675	synonymous_variant	LOW	COX1	0.8089
HLI-0807	7476	C	T	1	541	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0807	7789	G	A	1	646	synonymous_variant	LOW	COX2	0.0092
HLI-0807	10398	A	G	0	602	missense_variant	MODERATE	ND3	0.445
HLI-0807	10499	A	G	0	625	synonymous_variant	LOW	ND4L	0.0093
HLI-0807	11251	A	G	1	714	synonymous_variant	LOW	ND4	0.0932
HLI-0807	11377	G	A	4	583	synonymous_variant	LOW	ND4	0.0125
HLI-0807	11719	G	A	0	644	synonymous_variant	LOW	ND4	0.7756
HLI-0807	12612	A	G	6	535	synonymous_variant	LOW	ND5	0.0506
HLI-0807	12876	C	T	10	614	synonymous_variant	LOW	ND5	6.00E-04
HLI-0807	13708	G	A	5	646	missense_variant	MODERATE	ND5	0.0717
HLI-0807	13722	A	G	5	699	synonymous_variant	LOW	ND5	0.0077
HLI-0807	14133	A	G	2	541	synonymous_variant	LOW	ND5	0.0094
HLI-0807	14766	C	T	2	637	missense_variant	MODERATE	CYTB	0.7696
HLI-0807	15257	G	A	0	587	missense_variant	MODERATE	CYTB	0.0155
HLI-0807	15326	A	G	0	607	missense_variant	MODERATE	CYTB	0.9868
HLI-0807	15452	C	A	4	470	missense_variant	MODERATE	CYTB	0.0933
HLI-0807	16069	C	T	3	539	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0807	16126	T	C	0	583	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0807	16145	G	A	0	594	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0807	16231	T	C	1	588	upstream_gene_variant	MODIFIER	DLoop	0.009

HLI-0807	16261	C	T	3	637	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0808	64	C	T	0	273	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0808	93	A	G	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0808	185	G	A	0	483	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0808	189	A	G	0	485	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0808	200	A	G	18	434	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0808	236	T	C	0	361	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0808	247	G	A	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0808	263	A	G	0	284	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0808	750	A	G	1	655	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0808	769	G	A	0	700	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0808	825	T	A	0	739	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0808	1018	G	A	0	732	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0808	1048	C	T	2	823	upstream_gene_variant	MODIFIER	RNR1	0.0355
HLI-0808	1438	A	G	0	704	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0808	2245	A	C	1	554	upstream_gene_variant	MODIFIER	RNR2	8.00E-04
HLI-0808	2706	A	G	1	672	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0808	2758	G	A	1	704	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0808	2885	T	C	0	712	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0808	3516	C	A	3	647	synonymous_variant	LOW	ND1	0.0315
HLI-0808	3594	C	T	1	643	synonymous_variant	LOW	ND1	0.0789
HLI-0808	3866	T	C	0	677	missense_variant	MODERATE	ND1	0.0029
HLI-0808	4104	A	G	1	449	synonymous_variant	LOW	ND1	0.0785
HLI-0808	4312	C	T	2	562	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0808	4586	T	C	4	661	synonymous_variant	LOW	ND2	0.018
HLI-0808	4769	A	G	1	624	synonymous_variant	LOW	ND2	0.9767
HLI-0808	5096	T	C	0	607	synonymous_variant	LOW	ND2	0.0063
HLI-0808	5231	G	A	1	636	synonymous_variant	LOW	ND2	0.0232
HLI-0808	5442	T	C	0	673	missense_variant	MODERATE	ND2	0.0493
HLI-0808	5460	G	A	1	731	missense_variant	MODERATE	ND2	0.0651
HLI-0808	5603	C	T	2	743	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0808	6185	T	C	0	629	synonymous_variant	LOW	COX1	0.0325
HLI-0808	7028	C	T	3	596	synonymous_variant	LOW	COX1	0.8089
HLI-0808	7146	A	G	1	330	missense_variant	MODERATE	COX1	0.0497
HLI-0808	7256	C	T	1	497	synonymous_variant	LOW	COX1	0.0784
HLI-0808	7521	G	A	2	455	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0808	8428	C	T	4	492	synonymous_variant	LOW	ATP8	0.0144
HLI-0808	8468	C	T	2	520	synonymous_variant	LOW	ATP8	0.0501
HLI-0808	8566	A	G	1	490	missense_variant	MODERATE	ATP6/8	0.0151

HLI-0808	8655	C	T	4	462	synonymous_variant	LOW	ATP6	0.0511
HLI-0808	8701	A	G	1	500	missense_variant	MODERATE	ATP6	0.3391
HLI-0808	9042	C	T	0	687	synonymous_variant	LOW	ATP6	0.0316
HLI-0808	9347	A	G	0	683	synonymous_variant	LOW	COX3	0.0314
HLI-0808	9540	T	C	0	604	synonymous_variant	LOW	COX3	0.339
HLI-0808	9755	G	A	1	720	synonymous_variant	LOW	COX3	0.0303
HLI-0808	9818	C	T	1	884	synonymous_variant	LOW	COX3	0.0179
HLI-0808	10398	A	G	3	663	missense_variant	MODERATE	ND3	0.445
HLI-0808	10589	G	A	3	678	synonymous_variant	LOW	ND4L	0.0355
HLI-0808	10664	C	T	5	692	synonymous_variant	LOW	ND4L	0.0315
HLI-0808	10688	G	A	1	637	synonymous_variant	LOW	ND4L	0.0515
HLI-0808	10810	T	C	1	597	synonymous_variant	LOW	ND4	0.0522
HLI-0808	10873	T	C	2	654	synonymous_variant	LOW	ND4	0.3389
HLI-0808	10915	T	C	3	646	synonymous_variant	LOW	ND4	0.0411
HLI-0808	11176	G	A	0	620	synonymous_variant	LOW	ND4	0.0181
HLI-0808	11641	A	G	0	677	synonymous_variant	LOW	ND4	0.0158
HLI-0808	11719	G	A	3	719	synonymous_variant	LOW	ND4	0.7756
HLI-0808	11914	G	A	0	636	synonymous_variant	LOW	ND4	0.1112
HLI-0808	12007	G	A	1	533	synonymous_variant	LOW	ND4	0.0639
HLI-0808	12705	C	T	3	615	synonymous_variant	LOW	ND5	0.4212
HLI-0808	12720	A	G	3	687	synonymous_variant	LOW	ND5	0.0302
HLI-0808	13105	A	G	0	678	missense_variant	MODERATE	ND5	0.076
HLI-0808	13276	A	G	2	713	missense_variant	MODERATE	ND5	0.0312
HLI-0808	13506	C	T	0	653	synonymous_variant	LOW	ND5	0.0506
HLI-0808	13650	C	T	2	603	synonymous_variant	LOW	ND5	0.079
HLI-0808	14308	T	C	1	586	synonymous_variant	LOW	ND6	0.0209
HLI-0808	14766	C	T	3	639	missense_variant	MODERATE	CYTB	0.7696
HLI-0808	15136	C	T	1	697	synonymous_variant	LOW	CYTB	0.0153
HLI-0808	15326	A	G	0	571	missense_variant	MODERATE	CYTB	0.9868
HLI-0808	15431	G	A	0	560	missense_variant	MODERATE	CYTB	0.0182
HLI-0808	15773	G	A	1	544	missense_variant	MODERATE	CYTB	0.0011
HLI-0808	16114	C	A	0	598	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0808	16129	G	A	0	633	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0808	16148	C	T	0	619	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0808	16168	C	T	0	597	upstream_gene_variant	MODIFIER	DLoop	0.011
HLI-0808	16172	T	C	0	604	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0808	16223	C	T	1	566	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0808	16230	A	G	1	570	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0808	16311	T	C	2	569	upstream_gene_variant	MODIFIER	DLoop	0.1969

HLI-0808	16320	C	T	2	563	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0809	73	A	G	1	249	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0809	146	T	C	1	555	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0809	152	T	C	1	564	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0809	263	A	G	0	375	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0809	750	A	G	0	488	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0809	769	G	A	1	533	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0809	1018	G	A	3	686	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0809	1438	A	G	1	484	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0809	2416	T	C	0	370	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0809	2706	A	G	0	494	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0809	2789	C	T	0	550	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0809	3594	C	T	2	428	synonymous_variant	LOW	ND1	0.0789
HLI-0809	4104	A	G	0	436	synonymous_variant	LOW	ND1	0.0785
HLI-0809	4769	A	G	2	510	synonymous_variant	LOW	ND2	0.9767
HLI-0809	5581	A	G	0	635	upstream_gene_variant	MODIFIER	Unannotated	0.005
HLI-0809	7028	C	T	1	602	synonymous_variant	LOW	COX1	0.8089
HLI-0809	7175	T	C	1	649	synonymous_variant	LOW	COX1	0.0224
HLI-0809	7256	C	T	0	729	synonymous_variant	LOW	COX1	0.0784
HLI-0809	7274	C	T	0	694	synonymous_variant	LOW	COX1	0.0214
HLI-0809	7521	G	A	1	440	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0809	7771	A	G	2	623	synonymous_variant	LOW	COX2	0.0223
HLI-0809	8206	G	A	0	506	synonymous_variant	LOW	COX2	0.0287
HLI-0809	8701	A	G	0	667	missense_variant	MODERATE	ATP6	0.3391
HLI-0809	9221	A	G	0	529	synonymous_variant	LOW	COX3	0.0277
HLI-0809	9540	T	C	0	384	synonymous_variant	LOW	COX3	0.339
HLI-0809	10115	T	C	2	690	synonymous_variant	LOW	ND3	0.0278
HLI-0809	10398	A	G	1	541	missense_variant	MODERATE	ND3	0.445
HLI-0809	10873	T	C	0	547	synonymous_variant	LOW	ND4	0.3389
HLI-0809	11719	G	A	1	586	synonymous_variant	LOW	ND4	0.7756
HLI-0809	11914	G	A	0	546	synonymous_variant	LOW	ND4	0.1112
HLI-0809	11944	T	C	1	593	synonymous_variant	LOW	ND4	0.0331
HLI-0809	12693	A	G	0	535	synonymous_variant	LOW	ND5	0.0205
HLI-0809	12705	C	T	0	578	synonymous_variant	LOW	ND5	0.4212
HLI-0809	13590	G	A	1	422	synonymous_variant	LOW	ND5	0.0586
HLI-0809	13650	C	T	1	477	synonymous_variant	LOW	ND5	0.079
HLI-0809	13803	A	G	1	323	synonymous_variant	LOW	ND5	0.0216
HLI-0809	14566	A	G	1	626	synonymous_variant	LOW	ND6	0.0214
HLI-0809	14766	C	T	4	660	missense_variant	MODERATE	CYTB	0.7696

HLI-0809	15221	G	A	1	456	missense_variant	MODERATE	CYTB	0.0014
HLI-0809	15301	G	A	0	394	synonymous_variant	LOW	CYTB	0.2912
HLI-0809	15326	A	G	0	384	missense_variant	MODERATE	CYTB	0.9868
HLI-0809	15784	T	C	0	353	synonymous_variant	LOW	CYTB	0.0363
HLI-0809	16223	C	T	2	448	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0809	16278	C	T	0	448	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0809	16294	C	T	0	439	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0809	16309	A	G	0	438	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0809	16390	G	A	0	362	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0809	16519	T	C	0	166	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0810	73	A	G	0	334	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0810	263	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0810	709	G	A	1	700	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0810	750	A	G	2	743	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0810	930	G	A	1	709	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0810	1438	A	G	0	688	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0810	1888	G	A	1	555	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0810	2706	A	G	0	655	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0810	4216	T	C	1	586	missense_variant	MODERATE	ND1	0.0991
HLI-0810	4769	A	G	2	565	synonymous_variant	LOW	ND2	0.9767
HLI-0810	4917	A	G	3	664	missense_variant	MODERATE	ND2	0.0477
HLI-0810	5147	G	A	1	557	synonymous_variant	LOW	ND2	0.0437
HLI-0810	7028	C	T	3	761	synonymous_variant	LOW	COX1	0.8089
HLI-0810	8697	G	A	0	613	synonymous_variant	LOW	ATP6	0.0466
HLI-0810	9254	A	G	3	649	synonymous_variant	LOW	COX3	0.0083
HLI-0810	10370	T	C	0	661	synonymous_variant	LOW	ND3	0.0019
HLI-0810	10463	T	C	0	698	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0810	11251	A	G	2	663	synonymous_variant	LOW	ND4	0.0932
HLI-0810	11719	G	A	0	714	synonymous_variant	LOW	ND4	0.7756
HLI-0810	11812	A	G	1	699	synonymous_variant	LOW	ND4	0.0332
HLI-0810	13368	G	A	0	701	synonymous_variant	LOW	ND5	0.0495
HLI-0810	13392	T	C	0	736	synonymous_variant	LOW	ND5	0.0014
HLI-0810	14233	A	G	1	626	synonymous_variant	LOW	ND6	0.0369
HLI-0810	14766	C	T	1	686	missense_variant	MODERATE	CYTB	0.7696
HLI-0810	14905	G	A	2	759	synonymous_variant	LOW	CYTB	0.0526
HLI-0810	15326	A	G	0	589	missense_variant	MODERATE	CYTB	0.9868
HLI-0810	15452	C	A	2	552	missense_variant	MODERATE	CYTB	0.0933
HLI-0810	15607	A	G	1	603	synonymous_variant	LOW	CYTB	0.0508
HLI-0810	15928	G	A	0	597	upstream_gene_variant	MODIFIER	TRNT	0.049

HLI-0810	16126	T	C	2	713	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0810	16172	T	C	0	789	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0810	16294	C	T	0	647	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0810	16304	T	C	0	687	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0810	16519	T	C	0	401	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0811	73	A	G	0	335	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0811	150	C	T	1	600	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0811	152	T	C	1	607	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0811	263	A	G	0	161	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0811	295	C	T	0	210	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0811	489	T	C	1	478	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0811	750	A	G	0	701	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0811	1438	A	G	0	706	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0811	2706	A	G	0	647	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0811	4216	T	C	1	624	missense_variant	MODERATE	ND1	0.0991
HLI-0811	4769	A	G	1	664	synonymous_variant	LOW	ND2	0.9767
HLI-0811	5633	C	T	2	649	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0811	7028	C	T	2	715	synonymous_variant	LOW	COX1	0.8089
HLI-0811	7476	C	T	0	699	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0811	10172	G	A	2	726	synonymous_variant	LOW	ND3	0.0084
HLI-0811	10398	A	G	1	659	missense_variant	MODERATE	ND3	0.445
HLI-0811	11061	C	T	1	657	missense_variant	MODERATE	ND4	0.0018
HLI-0811	11251	A	G	1	682	synonymous_variant	LOW	ND4	0.0932
HLI-0811	11719	G	A	0	617	synonymous_variant	LOW	ND4	0.7756
HLI-0811	12612	A	G	8	588	synonymous_variant	LOW	ND5	0.0506
HLI-0811	13708	G	A	1	608	missense_variant	MODERATE	ND5	0.0717
HLI-0811	14766	C	T	2	661	missense_variant	MODERATE	CYTB	0.7696
HLI-0811	15257	G	A	0	638	missense_variant	MODERATE	CYTB	0.0155
HLI-0811	15326	A	G	0	610	missense_variant	MODERATE	CYTB	0.9868
HLI-0811	15452	C	A	1	566	missense_variant	MODERATE	CYTB	0.0933
HLI-0811	15812	G	A	0	571	missense_variant	MODERATE	CYTB	0.0096
HLI-0811	16069	C	T	0	617	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0811	16126	T	C	0	631	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0811	16278	C	T	0	656	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0812	152	T	C	0	584	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0812	263	A	G	0	346	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0812	750	A	G	1	665	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0812	1438	A	G	0	662	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0812	1934	T	C	0	483	upstream_gene_variant	MODIFIER	RNR2	0

HLI-0812	4769	A	G	2	599	synonymous_variant	LOW	ND2	0.9767
HLI-0812	6776	T	C	0	816	synonymous_variant	LOW	COX1	0.0226
HLI-0812	10754	A	C	2	639	synonymous_variant	LOW	ND4L	0.0012
HLI-0812	15326	A	G	0	467	missense_variant	MODERATE	CYTB	0.9868
HLI-0812	16519	T	C	0	351	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0813	73	A	G	1	225	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0813	93	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0813	146	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0813	183	A	G	3	442	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0813	207	G	A	3	434	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0813	263	A	G	1	154	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0813	750	A	G	1	448	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0813	1438	A	G	0	547	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0813	1811	A	G	0	554	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0813	2217	C	T	0	543	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0813	2706	A	G	0	410	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0813	3480	A	G	2	355	synonymous_variant	LOW	ND1	0.0392
HLI-0813	4769	A	G	0	429	synonymous_variant	LOW	ND2	0.9767
HLI-0813	5231	G	A	0	371	synonymous_variant	LOW	ND2	0.0232
HLI-0813	7028	C	T	1	497	synonymous_variant	LOW	COX1	0.8089
HLI-0813	9055	G	A	1	425	missense_variant	MODERATE	ATP6	0.0425
HLI-0813	9698	T	C	1	447	synonymous_variant	LOW	COX3	0.0405
HLI-0813	9716	T	C	2	518	synonymous_variant	LOW	COX3	0.0108
HLI-0813	10550	A	G	0	403	synonymous_variant	LOW	ND4L	0.0376
HLI-0813	11299	T	C	1	488	synonymous_variant	LOW	ND4	0.0417
HLI-0813	11467	A	G	0	499	synonymous_variant	LOW	ND4	0.1231
HLI-0813	11719	G	A	0	490	synonymous_variant	LOW	ND4	0.7756
HLI-0813	11869	C	A	4	472	synonymous_variant	LOW	ND4	0.0015
HLI-0813	12308	A	G	2	532	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0813	12372	G	A	5	514	synonymous_variant	LOW	ND5	0.1329
HLI-0813	13135	G	A	1	413	missense_variant	MODERATE	ND5	0.0092
HLI-0813	14037	A	G	0	465	synonymous_variant	LOW	ND5	0.0017
HLI-0813	14167	C	T	2	478	synonymous_variant	LOW	ND6	0.0385
HLI-0813	14766	C	T	7	593	missense_variant	MODERATE	CYTB	0.7696
HLI-0813	14798	T	C	1	586	missense_variant	MODERATE	CYTB	0.0651
HLI-0813	15326	A	G	1	288	missense_variant	MODERATE	CYTB	0.9868
HLI-0813	16224	T	C	1	482	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0813	16311	T	C	0	380	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0813	16519	T	C	0	189	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0814	72	T	C	1	268	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0814	195	T	C	0	539	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0814	263	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0814	750	A	G	0	509	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0814	1438	A	G	0	477	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0814	2706	A	G	2	526	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0814	4769	A	G	2	496	synonymous_variant	LOW	ND2	0.9767
HLI-0814	4904	C	A	2	537	missense_variant	MODERATE	ND2	1.00E-04
HLI-0814	5046	G	A	0	397	missense_variant	MODERATE	ND2	0.018
HLI-0814	7028	C	T	4	572	synonymous_variant	LOW	COX1	0.8089
HLI-0814	15110	G	A	2	613	missense_variant	MODERATE	CYTB	0.009
HLI-0814	15326	A	G	0	324	missense_variant	MODERATE	CYTB	0.9868
HLI-0814	15968	T	C	0	307	upstream_gene_variant	MODIFIER	TRNP	0.004
HLI-0814	16298	T	C	0	437	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0815	152	T	C	0	587	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0815	207	G	A	3	563	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0815	263	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0815	750	A	G	0	700	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0815	1438	A	G	0	661	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0815	3010	G	A	3	669	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0815	4769	A	G	1	637	synonymous_variant	LOW	ND2	0.9767
HLI-0815	8618	T	C	1	437	missense_variant	MODERATE	ATP6	0.0103
HLI-0815	9621	G	A	1	688	missense_variant	MODERATE	COX3	3.00E-04
HLI-0815	14133	A	G	1	630	synonymous_variant	LOW	ND5	0.0094
HLI-0815	15326	A	G	0	602	missense_variant	MODERATE	CYTB	0.9868
HLI-0815	16172	T	C	0	641	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0815	16456	G	A	1	516	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0815	16519	T	C	1	400	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0816	143	G	A	0	510	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0816	152	T	C	0	532	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0816	263	A	G	1	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0816	750	A	G	0	640	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0816	1438	A	G	1	616	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0816	3197	T	C	0	619	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0816	4769	A	G	1	586	synonymous_variant	LOW	ND2	0.9767
HLI-0816	7645	T	C	0	590	synonymous_variant	LOW	COX2	0.0028
HLI-0816	7702	G	A	0	625	synonymous_variant	LOW	COX2	0.001
HLI-0816	10217	A	G	1	687	synonymous_variant	LOW	ND3	0.0016
HLI-0816	15326	A	G	1	589	missense_variant	MODERATE	CYTB	0.9868

HLI-0816	16270	C	T	1	558	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0817	152	T	C	0	580	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0817	263	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0817	750	A	G	3	732	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0817	1438	A	G	2	638	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0817	4688	T	C	0	425	synonymous_variant	LOW	ND2	0.0078
HLI-0817	4769	A	G	0	417	synonymous_variant	LOW	ND2	0.9767
HLI-0817	5496	A	G	0	579	missense_variant	MODERATE	ND2	1.00E-04
HLI-0817	6776	T	C	3	801	synonymous_variant	LOW	COX1	0.0226
HLI-0817	8251	G	A	2	526	synonymous_variant	LOW	COX2	0.058
HLI-0817	8763	T	C	2	518	synonymous_variant	LOW	ATP6	2.00E-04
HLI-0817	15326	A	G	0	482	missense_variant	MODERATE	CYTB	0.9868
HLI-0817	16519	T	C	0	340	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0818	73	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0818	263	A	G	0	218	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0818	750	A	G	0	677	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0818	1187	T	C	0	736	upstream_gene_variant	MODIFIER	RNR1	8.00E-04
HLI-0818	1438	A	G	0	563	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0818	2706	A	G	1	580	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0818	3197	T	C	1	539	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0818	3398	T	C	0	525	missense_variant	MODERATE	ND1	0.0039
HLI-0818	4769	A	G	3	428	synonymous_variant	LOW	ND2	0.9767
HLI-0818	7028	C	T	6	587	synonymous_variant	LOW	COX1	0.8089
HLI-0818	9055	G	A	0	602	missense_variant	MODERATE	ATP6	0.0425
HLI-0818	9477	G	A	0	654	missense_variant	MODERATE	COX3	0.0387
HLI-0818	9667	A	G	1	649	missense_variant	MODERATE	COX3	0.0055
HLI-0818	11467	A	G	1	631	synonymous_variant	LOW	ND4	0.1231
HLI-0818	11719	G	A	0	576	synonymous_variant	LOW	ND4	0.7756
HLI-0818	12308	A	G	2	297	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0818	12372	G	A	0	329	synonymous_variant	LOW	ND5	0.1329
HLI-0818	13617	T	C	1	530	synonymous_variant	LOW	ND5	0.038
HLI-0818	14766	C	T	6	760	missense_variant	MODERATE	CYTB	0.7696
HLI-0818	14793	A	G	2	868	missense_variant	MODERATE	CYTB	0.0199
HLI-0818	15218	A	G	0	537	missense_variant	MODERATE	CYTB	0.0169
HLI-0818	15326	A	G	0	439	missense_variant	MODERATE	CYTB	0.9868
HLI-0818	16256	C	T	1	433	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0818	16270	C	T	0	414	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0818	16291	C	T	0	401	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0818	16399	A	G	0	463	upstream_gene_variant	MODIFIER	DLoop	0.0265

HLI-0819	150	C	T	2	505	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0819	207	G	A	3	450	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0819	263	A	G	1	174	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0819	750	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0819	1438	A	G	2	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0819	4769	A	G	0	518	synonymous_variant	LOW	ND2	0.9767
HLI-0819	7987	A	G	0	637	synonymous_variant	LOW	COX2	0
HLI-0819	8865	G	A	0	533	synonymous_variant	LOW	ATP6	0.003
HLI-0819	10274	T	C	0	552	synonymous_variant	LOW	ND3	0.0024
HLI-0819	14211	C	T	0	536	missense_variant	MODERATE	ND6	5.00E-04
HLI-0819	14212	T	C	0	543	synonymous_variant	LOW	ND6	0.0204
HLI-0819	15326	A	G	0	457	missense_variant	MODERATE	CYTB	0.9868
HLI-0819	16093	T	C	11	391	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0820	73	A	G	1	314	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0820	114	C	T	0	444	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0820	263	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0820	709	G	A	2	564	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0820	750	A	G	1	642	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0820	930	G	A	1	616	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0820	1438	A	G	1	591	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0820	1888	G	A	0	565	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0820	2706	A	G	0	624	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0820	4216	T	C	2	571	missense_variant	MODERATE	ND1	0.0991
HLI-0820	4769	A	G	2	513	synonymous_variant	LOW	ND2	0.9767
HLI-0820	4917	A	G	2	577	missense_variant	MODERATE	ND2	0.0477
HLI-0820	5147	G	A	0	526	synonymous_variant	LOW	ND2	0.0437
HLI-0820	7028	C	T	5	646	synonymous_variant	LOW	COX1	0.8089
HLI-0820	8697	G	A	0	594	synonymous_variant	LOW	ATP6	0.0466
HLI-0820	9254	A	G	2	518	synonymous_variant	LOW	COX3	0.0083
HLI-0820	10463	T	C	0	616	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0820	11251	A	G	3	600	synonymous_variant	LOW	ND4	0.0932
HLI-0820	11719	G	A	0	562	synonymous_variant	LOW	ND4	0.7756
HLI-0820	11812	A	G	0	590	synonymous_variant	LOW	ND4	0.0332
HLI-0820	13368	G	A	2	677	synonymous_variant	LOW	ND5	0.0495
HLI-0820	14233	A	G	2	560	synonymous_variant	LOW	ND6	0.0369
HLI-0820	14766	C	T	0	589	missense_variant	MODERATE	CYTB	0.7696
HLI-0820	14905	G	A	1	677	synonymous_variant	LOW	CYTB	0.0526
HLI-0820	15326	A	G	1	548	missense_variant	MODERATE	CYTB	0.9868
HLI-0820	15452	C	A	3	520	missense_variant	MODERATE	CYTB	0.0933

HLI-0820	15607	A	G	0	537	synonymous_variant	LOW	CYTB	0.0508
HLI-0820	15928	G	A	0	644	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0820	16126	T	C	1	596	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0820	16172	T	C	0	639	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0820	16294	C	T	1	526	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0820	16304	T	C	1	557	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0820	16519	T	C	0	251	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0821	73	A	G	0	285	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0821	242	C	T	0	269	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0821	263	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0821	295	C	T	1	217	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0821	462	C	T	4	415	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0821	489	T	C	2	521	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0821	750	A	G	2	647	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0821	1438	A	G	0	654	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0821	2158	T	C	1	597	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0821	2706	A	G	0	612	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0821	3010	G	A	0	663	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0821	4216	T	C	1	604	missense_variant	MODERATE	ND1	0.0991
HLI-0821	4769	A	G	0	615	synonymous_variant	LOW	ND2	0.9767
HLI-0821	5460	G	A	3	608	missense_variant	MODERATE	ND2	0.0651
HLI-0821	5463	C	T	3	618	missense_variant	MODERATE	ND2	4.00E-04
HLI-0821	6911	T	C	8	642	synonymous_variant	LOW	COX1	6.00E-04
HLI-0821	7028	C	T	1	684	synonymous_variant	LOW	COX1	0.8089
HLI-0821	8269	G	A	2	498	stop_retained_variant	LOW	COX2	0.0127
HLI-0821	8557	G	A	6	581	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0821	10398	A	G	4	669	missense_variant	MODERATE	ND3	0.445
HLI-0821	11251	A	G	1	607	synonymous_variant	LOW	ND4	0.0932
HLI-0821	11719	G	A	3	574	synonymous_variant	LOW	ND4	0.7756
HLI-0821	12007	G	A	2	590	synonymous_variant	LOW	ND4	0.0639
HLI-0821	12612	A	G	4	621	synonymous_variant	LOW	ND5	0.0506
HLI-0821	13708	G	A	3	366	missense_variant	MODERATE	ND5	0.0717
HLI-0821	13879	T	C	2	493	missense_variant	MODERATE	ND5	0.0073
HLI-0821	14766	C	T	0	605	missense_variant	MODERATE	CYTB	0.7696
HLI-0821	15326	A	G	0	568	missense_variant	MODERATE	CYTB	0.9868
HLI-0821	15452	C	A	4	590	missense_variant	MODERATE	CYTB	0.0933
HLI-0821	16069	C	T	5	579	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0821	16126	T	C	0	583	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0821	16145	G	A	1	551	upstream_gene_variant	MODIFIER	DLoop	0.0286

HLI-0821	16172	T	C	4	545	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0821	16222	C	T	3	543	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0821	16261	C	T	2	532	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0822	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0822	189	A	G	0	376	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0822	194	C	T	0	376	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0822	195	T	C	0	376	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0822	204	T	C	0	371	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0822	207	G	A	0	364	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0822	263	A	G	1	250	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0822	709	G	A	1	736	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0822	750	A	G	1	793	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0822	1119	T	C	2	763	upstream_gene_variant	MODIFIER	RNR1	0.005
HLI-0822	1243	T	C	2	746	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0822	1438	A	G	0	737	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0822	2706	A	G	0	675	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0822	3394	T	C	0	650	missense_variant	MODERATE	ND1	0.013
HLI-0822	3505	A	G	1	608	missense_variant	MODERATE	ND1	0.0144
HLI-0822	4769	A	G	0	677	synonymous_variant	LOW	ND2	0.9767
HLI-0822	5046	G	A	2	622	missense_variant	MODERATE	ND2	0.018
HLI-0822	5460	G	A	2	730	missense_variant	MODERATE	ND2	0.0651
HLI-0822	6528	C	T	0	708	synonymous_variant	LOW	COX1	0.0013
HLI-0822	7028	C	T	2	746	synonymous_variant	LOW	COX1	0.8089
HLI-0822	8251	G	A	0	676	synonymous_variant	LOW	COX2	0.058
HLI-0822	8994	G	A	0	698	synonymous_variant	LOW	ATP6	0.0167
HLI-0822	9326	A	G	0	761	synonymous_variant	LOW	COX3	0
HLI-0822	11674	C	T	2	724	synonymous_variant	LOW	ND4	0.0116
HLI-0822	11719	G	A	1	791	synonymous_variant	LOW	ND4	0.7756
HLI-0822	11947	A	G	1	655	synonymous_variant	LOW	ND4	0.011
HLI-0822	12414	T	C	7	679	synonymous_variant	LOW	ND5	0.0139
HLI-0822	12705	C	T	0	803	synonymous_variant	LOW	ND5	0.4212
HLI-0822	14766	C	T	1	706	missense_variant	MODERATE	CYTB	0.7696
HLI-0822	15326	A	G	0	588	missense_variant	MODERATE	CYTB	0.9868
HLI-0822	15775	A	G	1	715	synonymous_variant	LOW	CYTB	0.0011
HLI-0822	15884	G	C	0	756	missense_variant	MODERATE	CYTB	0.011
HLI-0822	16173	C	T	1	720	upstream_gene_variant	MODIFIER	DLoop	0.0024
HLI-0822	16223	C	T	2	704	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0822	16292	C	T	1	624	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0822	16519	T	C	2	284	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0823	263	A	G	0	300	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0823	750	A	G	0	812	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0823	1438	A	G	0	751	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0823	3010	G	A	0	812	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0823	4769	A	G	0	735	synonymous_variant	LOW	ND2	0.9767
HLI-0823	4859	T	C	2	746	synonymous_variant	LOW	ND2	0.0017
HLI-0823	15326	A	G	0	715	missense_variant	MODERATE	CYTB	0.9868
HLI-0823	16519	T	C	2	377	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0824	73	A	G	0	311	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0824	263	A	G	0	343	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0824	461	C	T	0	621	upstream_gene_variant	MODIFIER	DLoop	7.00E-04
HLI-0824	489	T	C	0	642	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0824	750	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0824	2220	A	C	2	490	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0824	2706	A	G	1	689	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0824	3444	A	T	0	619	synonymous_variant	LOW	ND1	0
HLI-0824	4417	A	G	1	664	upstream_gene_variant	MODIFIER	TRNM	0
HLI-0824	4769	A	G	0	645	synonymous_variant	LOW	ND2	0.9767
HLI-0824	5225	A	G	1	672	synonymous_variant	LOW	ND2	0
HLI-0824	5301	A	G	0	692	missense_variant	MODERATE	ND2	0.0089
HLI-0824	5558	A	G	1	758	upstream_gene_variant	MODIFIER	TRNW	0.0021
HLI-0824	7028	C	T	1	675	synonymous_variant	LOW	COX1	0.8089
HLI-0824	8701	A	G	0	683	missense_variant	MODERATE	ATP6	0.3391
HLI-0824	9540	T	C	0	633	synonymous_variant	LOW	COX3	0.339
HLI-0824	10398	A	G	0	702	missense_variant	MODERATE	ND3	0.445
HLI-0824	10400	C	T	0	709	synonymous_variant	LOW	ND3	0.2131
HLI-0824	10640	T	C	0	747	synonymous_variant	LOW	ND4L	0.0044
HLI-0824	10873	T	C	0	652	synonymous_variant	LOW	ND4	0.3389
HLI-0824	11719	G	A	0	671	synonymous_variant	LOW	ND4	0.7756
HLI-0824	12705	C	T	1	613	synonymous_variant	LOW	ND5	0.4212
HLI-0824	12850	A	G	3	671	missense_variant	MODERATE	ND5	7.00E-04
HLI-0824	14128	A	G	0	618	missense_variant	MODERATE	ND5	0.0018
HLI-0824	14766	C	T	3	739	missense_variant	MODERATE	CYTB	0.7696
HLI-0824	14783	T	C	1	834	synonymous_variant	LOW	CYTB	0.2126
HLI-0824	14827	C	T	2	820	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0824	15043	G	A	0	774	synonymous_variant	LOW	CYTB	0.2362
HLI-0824	15299	T	C	0	563	synonymous_variant	LOW	CYTB	0.0014
HLI-0824	15301	G	A	0	568	synonymous_variant	LOW	CYTB	0.2912
HLI-0824	15326	A	G	0	570	missense_variant	MODERATE	CYTB	0.9868

HLI-0824	16086	T	C	1	641	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0824	16223	C	T	2	665	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0824	16311	T	C	0	536	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0824	16362	T	C	0	540	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0825	239	T	C	0	270	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0825	263	A	G	0	259	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0825	750	A	G	2	697	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0825	1438	A	G	0	685	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0825	3915	G	A	0	692	synonymous_variant	LOW	ND1	0.0106
HLI-0825	4727	A	G	1	656	synonymous_variant	LOW	ND2	0.0063
HLI-0825	4769	A	G	1	723	synonymous_variant	LOW	ND2	0.9767
HLI-0825	9380	G	A	2	714	synonymous_variant	LOW	COX3	0.0094
HLI-0825	10589	G	A	1	653	synonymous_variant	LOW	ND4L	0.0355
HLI-0825	15326	A	G	0	683	missense_variant	MODERATE	CYTB	0.9868
HLI-0825	16129	G	A	1	631	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0825	16249	T	C	0	593	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0825	16362	T	C	0	527	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0826	73	A	G	0	290	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0826	125	T	C	0	493	upstream_gene_variant	MODIFIER	DLoop	0.0033
HLI-0826	127	T	C	0	501	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0826	153	A	G	4	582	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0826	195	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0826	263	A	G	0	256	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0826	750	A	G	0	584	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0826	1438	A	G	0	656	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0826	1719	G	A	2	615	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0826	2706	A	G	0	558	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0826	3254	C	A	0	647	upstream_gene_variant	MODIFIER	TRNL1	5.00E-04
HLI-0826	4769	A	G	0	678	synonymous_variant	LOW	ND2	0.9767
HLI-0826	4884	A	G	1	699	missense_variant	MODERATE	ND2	2.00E-04
HLI-0826	5258	A	G	1	575	synonymous_variant	LOW	ND2	3.00E-04
HLI-0826	6221	T	C	0	582	synonymous_variant	LOW	COX1	0.0306
HLI-0826	6371	C	T	0	541	synonymous_variant	LOW	COX1	0.0097
HLI-0826	7028	C	T	6	662	synonymous_variant	LOW	COX1	0.8089
HLI-0826	9692	A	G	1	629	synonymous_variant	LOW	COX3	5.00E-04
HLI-0826	9986	G	A	1	723	synonymous_variant	LOW	COX3	0.0017
HLI-0826	10775	G	A	0	598	missense_variant	MODERATE	ND4	3.00E-04
HLI-0826	11719	G	A	0	596	synonymous_variant	LOW	ND4	0.7756
HLI-0826	12705	C	T	1	654	synonymous_variant	LOW	ND5	0.4212

HLI-0826	13966	A	G	0	527	missense_variant	MODERATE	ND5	0.0126
HLI-0826	14470	T	C	1	659	synonymous_variant	LOW	ND6	0.0166
HLI-0826	14766	C	T	1	675	missense_variant	MODERATE	CYTB	0.7696
HLI-0826	15326	A	G	1	444	missense_variant	MODERATE	CYTB	0.9868
HLI-0826	15734	G	A	0	498	missense_variant	MODERATE	CYTB	0.0036
HLI-0826	16223	C	T	1	385	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0826	16248	C	T	0	432	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0826	16278	C	T	0	469	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0826	16298	T	C	0	491	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0826	16519	T	C	2	224	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0827	72	T	C	0	378	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0827	263	A	G	1	285	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0827	750	A	G	0	763	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0827	1438	A	G	0	817	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0827	2706	A	G	0	800	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0827	4221	C	T	1	727	synonymous_variant	LOW	ND1	4.00E-04
HLI-0827	4580	G	A	1	706	synonymous_variant	LOW	ND2	0.0169
HLI-0827	4769	A	G	0	730	synonymous_variant	LOW	ND2	0.9767
HLI-0827	7028	C	T	3	798	synonymous_variant	LOW	COX1	0.8089
HLI-0827	10308	C	T	2	758	synonymous_variant	LOW	ND3	3.00E-04
HLI-0827	12531	C	T	1	745	synonymous_variant	LOW	ND5	0
HLI-0827	15326	A	G	2	735	missense_variant	MODERATE	CYTB	0.9868
HLI-0827	15904	C	T	1	773	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0827	16298	T	C	1	689	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0828	73	A	G	0	319	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0828	152	T	C	0	561	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0828	217	T	C	0	358	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0828	263	A	G	0	287	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0828	340	C	T	0	254	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0828	508	A	G	8	445	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0828	750	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0828	1438	A	G	0	707	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0828	1811	A	G	2	596	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0828	2706	A	G	3	664	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0828	3116	C	T	0	734	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0828	3720	A	G	6	620	synonymous_variant	LOW	ND1	0.0069
HLI-0828	4769	A	G	0	635	synonymous_variant	LOW	ND2	0.9767
HLI-0828	5390	A	G	3	658	synonymous_variant	LOW	ND2	0.0069
HLI-0828	5426	T	C	2	781	synonymous_variant	LOW	ND2	0.0091

HLI-0828	6045	C	T	5	768	synonymous_variant	LOW	COX1	0.0065
HLI-0828	6152	T	C	4	646	synonymous_variant	LOW	COX1	0.0077
HLI-0828	6290	C	T	5	713	synonymous_variant	LOW	COX1	3.00E-04
HLI-0828	7028	C	T	5	762	synonymous_variant	LOW	COX1	0.8089
HLI-0828	10586	G	A	3	663	synonymous_variant	LOW	ND4L	0.0177
HLI-0828	10876	A	G	2	664	synonymous_variant	LOW	ND4	0.0098
HLI-0828	11197	C	T	3	659	synonymous_variant	LOW	ND4	0.0021
HLI-0828	11467	A	G	3	729	synonymous_variant	LOW	ND4	0.1231
HLI-0828	11719	G	A	1	689	synonymous_variant	LOW	ND4	0.7756
HLI-0828	11732	T	C	1	761	synonymous_variant	LOW	ND4	0.002
HLI-0828	12308	A	G	0	552	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0828	12372	G	A	1	594	synonymous_variant	LOW	ND5	0.1329
HLI-0828	12544	A	G	3	636	missense_variant	MODERATE	ND5	0
HLI-0828	13020	T	C	3	632	synonymous_variant	LOW	ND5	0.0106
HLI-0828	13477	G	A	51	629	missense_variant	MODERATE	ND5	8.00E-04
HLI-0828	13734	T	C	0	558	synonymous_variant	LOW	ND5	0.0067
HLI-0828	14766	C	T	3	702	missense_variant	MODERATE	CYTB	0.7696
HLI-0828	15326	A	G	0	614	missense_variant	MODERATE	CYTB	0.9868
HLI-0828	15907	A	G	1	698	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0828	16051	A	G	1	654	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0828	16129	G	C	1	426	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0828	16222	C	T	1	300	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0828	16362	T	C	1	518	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0828	16519	T	C	1	259	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0829	73	A	G	0	297	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0829	194	C	T	1	431	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0829	195	T	C	1	430	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0829	204	T	C	1	407	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0829	207	G	A	1	406	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0829	263	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0829	709	G	A	3	717	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0829	750	A	G	1	800	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0829	1243	T	C	1	722	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0829	1406	T	C	1	784	upstream_gene_variant	MODIFIER	RNR1	0.0034
HLI-0829	1438	A	G	1	842	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0829	2706	A	G	1	658	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0829	3505	A	G	0	660	missense_variant	MODERATE	ND1	0.0144
HLI-0829	4769	A	G	1	660	synonymous_variant	LOW	ND2	0.9767
HLI-0829	5046	G	A	1	590	missense_variant	MODERATE	ND2	0.018

HLI-0829	5460	G	A	2	748	missense_variant	MODERATE	ND2	0.0651
HLI-0829	7028	C	T	2	758	synonymous_variant	LOW	COX1	0.8089
HLI-0829	7058	T	C	1	859	synonymous_variant	LOW	COX1	2.00E-04
HLI-0829	8251	G	A	6	696	synonymous_variant	LOW	COX2	0.058
HLI-0829	8994	G	A	0	648	synonymous_variant	LOW	ATP6	0.0167
HLI-0829	11674	C	T	1	706	synonymous_variant	LOW	ND4	0.0116
HLI-0829	11719	G	A	0	794	synonymous_variant	LOW	ND4	0.7756
HLI-0829	11947	A	G	0	719	synonymous_variant	LOW	ND4	0.011
HLI-0829	12414	T	C	5	683	synonymous_variant	LOW	ND5	0.0139
HLI-0829	12705	C	T	1	734	synonymous_variant	LOW	ND5	0.4212
HLI-0829	12923	G	T	6	682	missense_variant	MODERATE	ND5	8.00E-04
HLI-0829	14766	C	T	1	686	missense_variant	MODERATE	CYTB	0.7696
HLI-0829	15326	A	G	0	657	missense_variant	MODERATE	CYTB	0.9868
HLI-0829	15884	G	C	0	758	missense_variant	MODERATE	CYTB	0.011
HLI-0829	16223	C	T	2	756	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0829	16292	C	T	2	644	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0829	16519	T	C	0	310	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0830	73	A	G	2	297	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0830	153	A	G	6	544	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0830	195	T	C	2	467	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0830	225	G	A	1	407	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0830	226	T	C	1	404	upstream_gene_variant	MODIFIER	DLoop	0.0035
HLI-0830	263	A	G	1	314	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0830	750	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0830	1438	A	G	0	684	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0830	1719	G	A	2	666	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0830	2706	A	G	0	637	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0830	4769	A	G	1	666	synonymous_variant	LOW	ND2	0.9767
HLI-0830	6221	T	C	8	591	synonymous_variant	LOW	COX1	0.0306
HLI-0830	6371	C	T	5	594	synonymous_variant	LOW	COX1	0.0097
HLI-0830	6480	G	A	1	594	missense_variant	MODERATE	COX1	0.0031
HLI-0830	6896	T	C	3	748	synonymous_variant	LOW	COX1	7.00E-04
HLI-0830	7028	C	T	2	694	synonymous_variant	LOW	COX1	0.8089
HLI-0830	8393	C	T	4	549	missense_variant	MODERATE	ATP8	0.0036
HLI-0830	11719	G	A	2	676	synonymous_variant	LOW	ND4	0.7756
HLI-0830	12705	C	T	3	669	synonymous_variant	LOW	ND5	0.4212
HLI-0830	13708	G	A	1	645	missense_variant	MODERATE	ND5	0.0717
HLI-0830	13966	A	G	3	599	missense_variant	MODERATE	ND5	0.0126
HLI-0830	14384	G	A	0	716	missense_variant	MODERATE	ND6	0.0016

HLI-0830	14470	T	C	0	622	synonymous_variant	LOW	ND6	0.0166
HLI-0830	14766	C	T	0	656	missense_variant	MODERATE	CYTB	0.7696
HLI-0830	15326	A	G	0	509	missense_variant	MODERATE	CYTB	0.9868
HLI-0830	15927	G	A	0	589	upstream_gene_variant	MODIFIER	TRNT	0.0087
HLI-0830	16111	C	T	2	457	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0830	16223	C	T	0	317	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0830	16278	C	T	2	496	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0830	16519	T	C	0	230	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0831	263	A	G	0	311	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0831	750	A	G	1	586	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0831	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0831	4769	A	G	1	671	synonymous_variant	LOW	ND2	0.9767
HLI-0831	5585	G	A	1	742	upstream_gene_variant	MODIFIER	Unannotated	0.0097
HLI-0831	6152	T	C	2	650	synonymous_variant	LOW	COX1	0.0077
HLI-0831	13708	G	A	1	596	missense_variant	MODERATE	ND5	0.0717
HLI-0831	14364	G	A	2	688	synonymous_variant	LOW	ND6	0.0076
HLI-0831	15326	A	G	1	555	missense_variant	MODERATE	CYTB	0.9868
HLI-0831	16311	T	C	1	497	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0831	16519	T	C	0	279	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0832	263	A	G	1	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0832	750	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0832	1438	A	G	0	682	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0832	3010	G	A	4	596	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0832	4769	A	G	1	607	synonymous_variant	LOW	ND2	0.9767
HLI-0832	5460	G	A	2	696	missense_variant	MODERATE	ND2	0.0651
HLI-0832	8512	A	G	5	575	synonymous_variant	LOW	ATP8	0.0036
HLI-0832	14902	C	T	2	752	synonymous_variant	LOW	CYTB	0.0024
HLI-0832	15326	A	G	0	420	missense_variant	MODERATE	CYTB	0.9868
HLI-0832	16093	T	C	30	666	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0832	16519	T	C	1	283	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0833	73	A	G	0	294	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0833	263	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0833	489	T	C	0	375	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0833	750	A	G	1	663	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0833	1438	A	G	0	658	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0833	1670	A	T	1	651	upstream_gene_variant	MODIFIER	TRNV	4.00E-04
HLI-0833	2706	A	G	0	559	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0833	3552	T	A	0	543	synonymous_variant	LOW	ND1	0.0337
HLI-0833	4715	A	G	1	693	synonymous_variant	LOW	ND2	0.0416

HLI-0833	4769	A	G	2	683	synonymous_variant	LOW	ND2	0.9767
HLI-0833	7028	C	T	3	636	synonymous_variant	LOW	COX1	0.8089
HLI-0833	7196	C	A	6	643	synonymous_variant	LOW	COX1	0.0389
HLI-0833	7694	C	T	0	596	synonymous_variant	LOW	COX2	5.00E-04
HLI-0833	8020	G	A	1	657	synonymous_variant	LOW	COX2	0.0093
HLI-0833	8584	G	A	1	619	missense_variant	MODERATE	ATP6	0.0521
HLI-0833	8701	A	G	1	636	missense_variant	MODERATE	ATP6	0.3391
HLI-0833	9540	T	C	1	584	synonymous_variant	LOW	COX3	0.339
HLI-0833	9545	A	G	1	584	synonymous_variant	LOW	COX3	0.0469
HLI-0833	10398	A	G	0	658	missense_variant	MODERATE	ND3	0.445
HLI-0833	10400	C	T	0	664	synonymous_variant	LOW	ND3	0.2131
HLI-0833	10454	T	C	0	700	upstream_gene_variant	MODIFIER	TRNR	0.0037
HLI-0833	10873	T	C	0	588	synonymous_variant	LOW	ND4	0.3389
HLI-0833	11719	G	A	1	631	synonymous_variant	LOW	ND4	0.7756
HLI-0833	11914	G	A	1	630	synonymous_variant	LOW	ND4	0.1112
HLI-0833	12705	C	T	1	658	synonymous_variant	LOW	ND5	0.4212
HLI-0833	13263	A	G	3	662	synonymous_variant	LOW	ND5	0.0354
HLI-0833	14318	T	C	1	612	missense_variant	MODERATE	ND6	0.0339
HLI-0833	14766	C	T	0	649	missense_variant	MODERATE	CYTB	0.7696
HLI-0833	14783	T	C	0	750	synonymous_variant	LOW	CYTB	0.2126
HLI-0833	15043	G	A	1	644	synonymous_variant	LOW	CYTB	0.2362
HLI-0833	15301	G	A	0	534	synonymous_variant	LOW	CYTB	0.2912
HLI-0833	15326	A	G	0	547	missense_variant	MODERATE	CYTB	0.9868
HLI-0833	15487	A	T	0	493	synonymous_variant	LOW	CYTB	0.0391
HLI-0833	16093	T	C	13	667	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0833	16223	C	T	1	556	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0833	16234	C	T	1	585	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0833	16288	T	C	4	502	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0833	16298	T	C	4	494	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0833	16327	C	T	0	478	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0833	16355	C	T	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0833	16518	G	T	0	304	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0833	16519	T	C	0	304	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0833	16527	C	T	0	276	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0834	73	A	G	0	34	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0834	207	G	A	0	61	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0834	263	A	G	0	35	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0834	499	G	A	0	35	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0834	709	G	A	0	55	upstream_gene_variant	MODIFIER	RNR1	0.1279

HLI-0834	750	A	G	1	53	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0834	827	A	G	0	66	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0834	1438	A	G	0	49	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0834	2706	A	G	0	49	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0834	4769	A	G	0	38	synonymous_variant	LOW	ND2	0.9767
HLI-0834	4820	G	A	0	40	synonymous_variant	LOW	ND2	0.0239
HLI-0834	6023	G	A	1	50	synonymous_variant	LOW	COX1	0.008
HLI-0834	6216	T	C	0	48	synonymous_variant	LOW	COX1	0.0056
HLI-0834	6413	T	C	0	62	synonymous_variant	LOW	COX1	0.0062
HLI-0834	7028	C	T	0	75	synonymous_variant	LOW	COX1	0.8089
HLI-0834	7609	T	C	0	52	synonymous_variant	LOW	COX2	0.0011
HLI-0834	7775	G	A	0	56	missense_variant	MODERATE	COX2	0.0015
HLI-0834	9591	G	A	1	64	missense_variant	MODERATE	COX3	6.00E-04
HLI-0834	11719	G	A	0	68	synonymous_variant	LOW	ND4	0.7756
HLI-0834	13590	G	A	0	52	synonymous_variant	LOW	ND5	0.0586
HLI-0834	14766	C	T	0	70	missense_variant	MODERATE	CYTB	0.7696
HLI-0834	15326	A	G	0	57	missense_variant	MODERATE	CYTB	0.9868
HLI-0834	15535	C	T	0	49	synonymous_variant	LOW	CYTB	0.023
HLI-0834	16136	T	C	0	28	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0834	16217	T	C	1	26	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0834	16519	T	C	0	35	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0835	58	T	A	0	94	upstream_gene_variant	MODIFIER	DLoop	8.00E-04
HLI-0835	73	A	G	0	160	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0835	143	G	A	1	388	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0835	152	T	C	1	419	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0835	263	A	G	0	266	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0835	499	G	A	2	443	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0835	750	A	G	0	621	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0835	827	A	G	1	673	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0835	1438	A	G	0	627	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0835	2706	A	G	0	625	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0835	3547	A	G	0	583	missense_variant	MODERATE	ND1	0.0176
HLI-0835	4769	A	G	1	550	synonymous_variant	LOW	ND2	0.9767
HLI-0835	4820	G	A	0	609	synonymous_variant	LOW	ND2	0.0239
HLI-0835	4977	T	C	0	527	synonymous_variant	LOW	ND2	0.0177
HLI-0835	6473	C	T	0	598	synonymous_variant	LOW	COX1	0.0173
HLI-0835	7028	C	T	2	622	synonymous_variant	LOW	COX1	0.8089
HLI-0835	9221	A	T	1	585	synonymous_variant	LOW	COX3	0
HLI-0835	9950	T	C	2	604	synonymous_variant	LOW	COX3	0.0362

HLI-0835	11177	C	T	2	558	missense_variant	MODERATE	ND4	0.019
HLI-0835	11719	G	A	2	586	synonymous_variant	LOW	ND4	0.7756
HLI-0835	13590	G	A	0	545	synonymous_variant	LOW	ND5	0.0586
HLI-0835	14766	C	T	4	577	missense_variant	MODERATE	CYTB	0.7696
HLI-0835	15326	A	G	0	459	missense_variant	MODERATE	CYTB	0.9868
HLI-0835	15535	C	T	0	443	synonymous_variant	LOW	CYTB	0.023
HLI-0835	15884	G	A	3	495	missense_variant	MODERATE	CYTB	0.0082
HLI-0835	16217	T	C	0	136	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0835	16519	T	C	0	167	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0836	239	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0836	263	A	G	0	340	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0836	750	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0836	1438	A	G	0	667	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0836	4769	A	G	2	615	synonymous_variant	LOW	ND2	0.9767
HLI-0836	6869	C	T	8	712	synonymous_variant	LOW	COX1	7.00E-04
HLI-0836	9804	G	A	1	823	missense_variant	MODERATE	COX3	0.0028
HLI-0836	14185	A	T	4	561	synonymous_variant	LOW	ND6	4.00E-04
HLI-0836	15326	A	G	0	500	missense_variant	MODERATE	CYTB	0.9868
HLI-0836	16362	T	C	1	486	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0836	16400	C	T	2	545	upstream_gene_variant	MODIFIER	DLoop	0.003
HLI-0836	16482	A	G	4	382	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0837	73	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0837	263	A	G	1	265	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0837	709	G	A	5	633	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0837	750	A	G	3	656	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0837	930	G	A	2	668	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0837	1438	A	G	1	628	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0837	1888	G	A	0	530	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0837	2706	A	G	1	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0837	4216	T	C	1	546	missense_variant	MODERATE	ND1	0.0991
HLI-0837	4769	A	G	1	570	synonymous_variant	LOW	ND2	0.9767
HLI-0837	4917	A	G	0	615	missense_variant	MODERATE	ND2	0.0477
HLI-0837	5147	G	A	0	488	synonymous_variant	LOW	ND2	0.0437
HLI-0837	6719	T	C	1	763	synonymous_variant	LOW	COX1	0.041
HLI-0837	7028	C	T	2	640	synonymous_variant	LOW	COX1	0.8089
HLI-0837	8697	G	A	1	583	synonymous_variant	LOW	ATP6	0.0466
HLI-0837	10463	T	C	1	676	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0837	11251	A	G	0	613	synonymous_variant	LOW	ND4	0.0932
HLI-0837	11719	G	A	0	616	synonymous_variant	LOW	ND4	0.7756

HLI-0837	11812	A	G	2	595	synonymous_variant	LOW	ND4	0.0332
HLI-0837	13368	G	A	2	677	synonymous_variant	LOW	ND5	0.0495
HLI-0837	14233	A	G	0	564	synonymous_variant	LOW	ND6	0.0369
HLI-0837	14766	C	T	3	629	missense_variant	MODERATE	CYTB	0.7696
HLI-0837	14905	G	A	2	712	synonymous_variant	LOW	CYTB	0.0526
HLI-0837	15326	A	G	0	479	missense_variant	MODERATE	CYTB	0.9868
HLI-0837	15452	C	A	3	451	missense_variant	MODERATE	CYTB	0.0933
HLI-0837	15607	A	G	1	474	synonymous_variant	LOW	CYTB	0.0508
HLI-0837	15928	G	A	2	554	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0837	16126	T	C	5	613	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0837	16294	C	T	0	474	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0837	16296	C	T	0	476	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0837	16304	T	C	0	499	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0837	16519	T	C	1	257	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0838	73	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0838	195	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0838	215	A	G	0	297	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0838	263	A	G	2	195	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0838	489	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0838	750	A	G	1	573	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0838	813	A	G	0	659	upstream_gene_variant	MODIFIER	RNR1	0.0044
HLI-0838	930	G	A	1	563	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0838	1438	A	G	0	569	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0838	2706	A	G	1	545	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0838	3705	G	A	2	506	synonymous_variant	LOW	ND1	0.0138
HLI-0838	4769	A	G	0	501	synonymous_variant	LOW	ND2	0.9767
HLI-0838	6164	C	T	2	534	synonymous_variant	LOW	COX1	0.0025
HLI-0838	6446	G	A	2	529	synonymous_variant	LOW	COX1	0.0061
HLI-0838	6671	T	C	4	573	synonymous_variant	LOW	COX1	0.0071
HLI-0838	6680	T	C	5	580	synonymous_variant	LOW	COX1	0.0226
HLI-0838	7028	C	T	3	590	synonymous_variant	LOW	COX1	0.8089
HLI-0838	7853	G	A	1	587	missense_variant	MODERATE	COX2	0.0197
HLI-0838	8701	A	G	0	470	missense_variant	MODERATE	ATP6	0.3391
HLI-0838	9181	A	G	14	538	missense_variant	MODERATE	ATP6	0.0018
HLI-0838	9540	T	C	0	537	synonymous_variant	LOW	COX3	0.339
HLI-0838	10398	A	G	0	574	missense_variant	MODERATE	ND3	0.445
HLI-0838	10400	C	T	0	580	synonymous_variant	LOW	ND3	0.2131
HLI-0838	10873	T	C	1	501	synonymous_variant	LOW	ND4	0.3389
HLI-0838	11719	G	A	2	526	synonymous_variant	LOW	ND4	0.7756

HLI-0838	11809	T	C	1	574	synonymous_variant	LOW	ND4	0.0015
HLI-0838	12346	C	T	0	550	missense_variant	MODERATE	ND5	0.0056
HLI-0838	12403	C	T	3	549	missense_variant	MODERATE	ND5	0.0043
HLI-0838	12705	C	T	1	578	synonymous_variant	LOW	ND5	0.4212
HLI-0838	12950	A	C	2	546	missense_variant	MODERATE	ND5	0.0043
HLI-0838	14110	T	C	0	487	missense_variant	MODERATE	ND5	0.0096
HLI-0838	14766	C	T	1	566	missense_variant	MODERATE	CYTB	0.7696
HLI-0838	14769	A	G	1	577	missense_variant	MODERATE	CYTB	0.0121
HLI-0838	14783	T	C	1	616	synonymous_variant	LOW	CYTB	0.2126
HLI-0838	15043	G	A	1	556	synonymous_variant	LOW	CYTB	0.2362
HLI-0838	15301	G	A	0	489	synonymous_variant	LOW	CYTB	0.2912
HLI-0838	15326	A	G	0	535	missense_variant	MODERATE	CYTB	0.9868
HLI-0838	16129	G	A	1	301	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0838	16223	C	T	1	207	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0838	16249	T	C	0	282	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0838	16311	T	C	0	431	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0838	16359	T	C	0	350	upstream_gene_variant	MODIFIER	DLoop	0.0031
HLI-0838	16519	T	C	0	182	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0840	73	A	G	0	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0840	152	T	C	0	507	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0840	195	T	C	1	480	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0840	263	A	G	0	171	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0840	709	G	A	0	599	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0840	750	A	G	2	635	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0840	1438	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0840	1888	G	A	0	564	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0840	2706	A	G	0	573	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0840	4216	T	C	0	572	missense_variant	MODERATE	ND1	0.0991
HLI-0840	4769	A	G	3	575	synonymous_variant	LOW	ND2	0.9767
HLI-0840	4917	A	G	1	510	missense_variant	MODERATE	ND2	0.0477
HLI-0840	6002	A	G	0	661	synonymous_variant	LOW	COX1	6.00E-04
HLI-0840	7028	C	T	3	626	synonymous_variant	LOW	COX1	0.8089
HLI-0840	8697	G	A	1	518	synonymous_variant	LOW	ATP6	0.0466
HLI-0840	9052	A	G	0	595	missense_variant	MODERATE	ATP6	0.0015
HLI-0840	9899	T	C	1	580	synonymous_variant	LOW	COX3	0.0108
HLI-0840	10463	T	C	1	595	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0840	10873	T	C	0	545	synonymous_variant	LOW	ND4	0.3389
HLI-0840	11251	A	G	2	561	synonymous_variant	LOW	ND4	0.0932
HLI-0840	11719	G	A	0	613	synonymous_variant	LOW	ND4	0.7756

HLI-0840	12633	C	A	3	614	synonymous_variant	LOW	ND5	0.0123
HLI-0840	13368	G	A	0	643	synonymous_variant	LOW	ND5	0.0495
HLI-0840	14766	C	T	2	568	missense_variant	MODERATE	CYTB	0.7696
HLI-0840	14905	G	A	2	641	synonymous_variant	LOW	CYTB	0.0526
HLI-0840	15326	A	G	0	547	missense_variant	MODERATE	CYTB	0.9868
HLI-0840	15452	C	A	3	514	missense_variant	MODERATE	CYTB	0.0933
HLI-0840	15586	T	C	0	576	synonymous_variant	LOW	CYTB	5.00E-04
HLI-0840	15607	A	G	0	613	synonymous_variant	LOW	CYTB	0.0508
HLI-0840	15928	G	A	1	598	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0840	16126	T	C	0	549	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0840	16163	A	G	0	587	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0840	16294	C	T	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0840	16519	T	C	0	299	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0841	73	A	G	1	280	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0841	263	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0841	282	T	C	0	225	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0841	750	A	G	3	591	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0841	1438	A	G	0	608	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0841	1811	A	G	1	618	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0841	2706	A	G	1	579	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0841	3738	C	T	1	547	synonymous_variant	LOW	ND1	0.0019
HLI-0841	4129	A	G	2	524	missense_variant	MODERATE	ND1	0.001
HLI-0841	4769	A	G	0	631	synonymous_variant	LOW	ND2	0.9767
HLI-0841	5240	A	G	0	527	synonymous_variant	LOW	ND2	0.0015
HLI-0841	6392	T	C	1	585	synonymous_variant	LOW	COX1	0.0359
HLI-0841	6455	C	T	1	573	synonymous_variant	LOW	COX1	0.0319
HLI-0841	7028	C	T	3	629	synonymous_variant	LOW	COX1	0.8089
HLI-0841	7055	A	G	2	682	synonymous_variant	LOW	COX1	0.0188
HLI-0841	9365	C	T	1	579	synonymous_variant	LOW	COX3	0.002
HLI-0841	9698	T	C	0	565	synonymous_variant	LOW	COX3	0.0405
HLI-0841	10733	C	T	2	519	synonymous_variant	LOW	ND4L	0.0016
HLI-0841	11467	A	G	0	614	synonymous_variant	LOW	ND4	0.1231
HLI-0841	11719	G	A	0	580	synonymous_variant	LOW	ND4	0.7756
HLI-0841	11969	G	A	0	533	missense_variant	MODERATE	ND4	0.0135
HLI-0841	12135	C	A	2	587	missense_variant	MODERATE	ND4	0.0011
HLI-0841	12308	A	G	1	545	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0841	12372	G	A	1	572	synonymous_variant	LOW	ND5	0.1329
HLI-0841	13145	G	A	2	613	missense_variant	MODERATE	ND5	0.0094
HLI-0841	14766	C	T	0	568	missense_variant	MODERATE	CYTB	0.7696

HLI-0841	15326	A	G	0	472	missense_variant	MODERATE	CYTB	0.9868
HLI-0841	16209	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0841	16342	T	C	0	458	upstream_gene_variant	MODIFIER	DLoop	0.0042
HLI-0842	54	G	C	0	143	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0842	64	C	T	0	170	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0842	73	A	G	1	208	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0842	146	T	C	0	423	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0842	235	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0842	263	A	G	0	218	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0842	548	C	T	1	55	upstream_gene_variant	MODIFIER	DLoop	9.00E-04
HLI-0842	663	A	G	1	365	upstream_gene_variant	MODIFIER	RNR1	0.0285
HLI-0842	750	A	G	0	496	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0842	1438	A	G	1	502	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0842	1516	G	A	1	596	upstream_gene_variant	MODIFIER	RNR1	0
HLI-0842	1736	A	G	0	482	upstream_gene_variant	MODIFIER	RNR2	0.0282
HLI-0842	2706	A	G	0	509	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0842	4092	G	A	1	366	synonymous_variant	LOW	ND1	0.0026
HLI-0842	4248	T	C	1	386	synonymous_variant	LOW	ND1	0.0364
HLI-0842	4769	A	G	1	469	synonymous_variant	LOW	ND2	0.9767
HLI-0842	4824	A	G	0	487	missense_variant	MODERATE	ND2	0.0294
HLI-0842	7028	C	T	1	512	synonymous_variant	LOW	COX1	0.8089
HLI-0842	8027	G	A	1	519	missense_variant	MODERATE	COX2	0.0334
HLI-0842	8794	C	T	2	533	missense_variant	MODERATE	ATP6	0.0283
HLI-0842	11440	G	A	1	549	synonymous_variant	LOW	ND4	0.0081
HLI-0842	11719	G	A	0	483	synonymous_variant	LOW	ND4	0.7756
HLI-0842	12007	G	A	0	474	synonymous_variant	LOW	ND4	0.0639
HLI-0842	12705	C	T	1	548	synonymous_variant	LOW	ND5	0.4212
HLI-0842	14766	C	T	4	493	missense_variant	MODERATE	CYTB	0.7696
HLI-0842	15326	A	G	0	370	missense_variant	MODERATE	CYTB	0.9868
HLI-0842	16111	C	T	0	522	upstream_gene_variant	MODIFIER	DLoop	0.0263
HLI-0842	16124	T	C	0	572	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0842	16209	T	C	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0842	16223	C	T	0	493	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0842	16290	C	T	0	389	upstream_gene_variant	MODIFIER	DLoop	0.0394
HLI-0842	16311	T	C	0	395	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0842	16319	G	A	0	392	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0842	16362	T	C	0	354	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0843	73	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0843	185	G	A	3	452	upstream_gene_variant	MODIFIER	DLoop	0.0397

HLI-0843	228	G	A	0	359	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0843	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0843	295	C	T	0	215	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0843	462	C	T	2	471	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0843	489	T	C	0	512	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0843	750	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0843	1438	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0843	3010	G	A	0	563	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0843	4216	T	C	3	514	missense_variant	MODERATE	ND1	0.0991
HLI-0843	4769	A	G	2	609	synonymous_variant	LOW	ND2	0.9767
HLI-0843	6164	C	T	4	570	synonymous_variant	LOW	COX1	0.0025
HLI-0843	7028	C	T	7	608	synonymous_variant	LOW	COX1	0.8089
HLI-0843	8847	C	T	2	585	synonymous_variant	LOW	ATP6	0
HLI-0843	10398	A	G	0	540	missense_variant	MODERATE	ND3	0.445
HLI-0843	11251	A	G	2	577	synonymous_variant	LOW	ND4	0.0932
HLI-0843	11719	G	A	2	605	synonymous_variant	LOW	ND4	0.7756
HLI-0843	12612	A	G	0	582	synonymous_variant	LOW	ND5	0.0506
HLI-0843	13708	G	A	1	496	missense_variant	MODERATE	ND5	0.0717
HLI-0843	13934	C	T	1	538	missense_variant	MODERATE	ND5	0.0122
HLI-0843	14766	C	T	6	580	missense_variant	MODERATE	CYTB	0.7696
HLI-0843	14798	T	C	1	662	missense_variant	MODERATE	CYTB	0.0651
HLI-0843	15326	A	G	0	447	missense_variant	MODERATE	CYTB	0.9868
HLI-0843	15452	C	A	1	447	missense_variant	MODERATE	CYTB	0.0933
HLI-0843	16069	C	T	2	577	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0843	16126	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0843	16222	C	T	3	519	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0844	73	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0844	150	C	T	2	516	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0844	185	G	A	8	528	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0844	263	A	G	0	536	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0844	750	A	G	1	513	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0844	1438	A	G	0	579	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0844	1721	C	T	2	481	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0844	2706	A	G	0	519	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0844	2784	A	C	8	521	upstream_gene_variant	MODIFIER	RNR2	0
HLI-0844	3197	T	C	4	562	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0844	4769	A	G	1	535	synonymous_variant	LOW	ND2	0.9767
HLI-0844	7028	C	T	2	589	synonymous_variant	LOW	COX1	0.8089
HLI-0844	7768	A	G	13	595	synonymous_variant	LOW	COX2	0.0186

HLI-0844	9477	G	A	6	505	missense_variant	MODERATE	COX3	0.0387
HLI-0844	11016	G	A	9	404	missense_variant	MODERATE	ND4	0.0062
HLI-0844	11467	A	G	5	603	synonymous_variant	LOW	ND4	0.1231
HLI-0844	11653	A	G	11	626	synonymous_variant	LOW	ND4	0.0049
HLI-0844	11719	G	A	0	620	synonymous_variant	LOW	ND4	0.7756
HLI-0844	12308	A	G	11	487	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0844	12372	G	A	7	442	synonymous_variant	LOW	ND5	0.1329
HLI-0844	12634	A	G	8	698	missense_variant	MODERATE	ND5	0.0027
HLI-0844	13617	T	C	14	411	synonymous_variant	LOW	ND5	0.038
HLI-0844	13630	A	G	15	445	missense_variant	MODERATE	ND5	0.0018
HLI-0844	13637	A	G	14	457	missense_variant	MODERATE	ND5	0.0074
HLI-0844	14182	T	C	9	541	synonymous_variant	LOW	ND6	0.0254
HLI-0844	14766	C	T	2	648	missense_variant	MODERATE	CYTB	0.7696
HLI-0844	15326	A	G	0	333	missense_variant	MODERATE	CYTB	0.9868
HLI-0844	16176	C	T	12	595	upstream_gene_variant	MODIFIER	DLoop	0.0061
HLI-0844	16270	C	T	8	501	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0844	16316	A	G	7	433	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0844	16519	T	C	1	164	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0845	73	A	G	0	295	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0845	150	C	T	0	577	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0845	263	A	G	1	289	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0845	709	G	A	2	668	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0845	750	A	G	0	687	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0845	1438	A	G	0	659	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0845	1888	G	A	1	471	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0845	2706	A	G	3	627	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0845	4216	T	C	1	570	missense_variant	MODERATE	ND1	0.0991
HLI-0845	4769	A	G	0	600	synonymous_variant	LOW	ND2	0.9767
HLI-0845	4917	A	G	2	613	missense_variant	MODERATE	ND2	0.0477
HLI-0845	7028	C	T	2	659	synonymous_variant	LOW	COX1	0.8089
HLI-0845	7966	C	T	1	740	synonymous_variant	LOW	COX2	1.00E-04
HLI-0845	8697	G	A	1	647	synonymous_variant	LOW	ATP6	0.0466
HLI-0845	10463	T	C	0	612	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0845	11251	A	G	0	696	synonymous_variant	LOW	ND4	0.0932
HLI-0845	11719	G	A	1	635	synonymous_variant	LOW	ND4	0.7756
HLI-0845	11812	A	G	1	605	synonymous_variant	LOW	ND4	0.0332
HLI-0845	13368	G	A	0	672	synonymous_variant	LOW	ND5	0.0495
HLI-0845	14016	G	A	1	560	synonymous_variant	LOW	ND5	0.003
HLI-0845	14233	A	G	0	541	synonymous_variant	LOW	ND6	0.0369

HLI-0845	14766	C	T	1	629	missense_variant	MODERATE	CYTB	0.7696
HLI-0845	14905	G	A	0	763	synonymous_variant	LOW	CYTB	0.0526
HLI-0845	15326	A	G	0	534	missense_variant	MODERATE	CYTB	0.9868
HLI-0845	15452	C	A	2	517	missense_variant	MODERATE	CYTB	0.0933
HLI-0845	15607	A	G	1	531	synonymous_variant	LOW	CYTB	0.0508
HLI-0845	15928	G	A	3	469	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0845	16126	T	C	2	583	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0845	16153	G	A	2	636	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0845	16294	C	T	0	522	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0845	16296	C	T	0	524	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0845	16519	T	C	0	262	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0846	73	A	G	0	328	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0846	185	G	A	26	483	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0846	263	A	G	0	266	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0846	295	C	T	0	220	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0846	462	C	T	1	547	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0846	489	T	C	0	592	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0846	750	A	G	0	687	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0846	1438	A	G	1	735	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0846	2706	A	G	0	718	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0846	3010	G	A	0	700	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0846	4216	T	C	0	689	missense_variant	MODERATE	ND1	0.0991
HLI-0846	4769	A	G	0	689	synonymous_variant	LOW	ND2	0.9767
HLI-0846	7028	C	T	1	745	synonymous_variant	LOW	COX1	0.8089
HLI-0846	8347	A	T	2	672	upstream_gene_variant	MODIFIER	TRNK	0
HLI-0846	10398	A	G	0	671	missense_variant	MODERATE	ND3	0.445
HLI-0846	11251	A	G	0	693	synonymous_variant	LOW	ND4	0.0932
HLI-0846	11719	G	A	0	674	synonymous_variant	LOW	ND4	0.7756
HLI-0846	12612	A	G	13	666	synonymous_variant	LOW	ND5	0.0506
HLI-0846	13708	G	A	2	605	missense_variant	MODERATE	ND5	0.0717
HLI-0846	13934	C	T	0	678	missense_variant	MODERATE	ND5	0.0122
HLI-0846	14766	C	T	5	681	missense_variant	MODERATE	CYTB	0.7696
HLI-0846	14798	T	C	0	763	missense_variant	MODERATE	CYTB	0.0651
HLI-0846	15326	A	G	0	600	missense_variant	MODERATE	CYTB	0.9868
HLI-0846	15367	C	T	1	639	synonymous_variant	LOW	CYTB	6.00E-04
HLI-0846	15452	C	A	6	670	missense_variant	MODERATE	CYTB	0.0933
HLI-0846	16069	C	T	1	687	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0846	16126	T	C	0	751	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0847	73	A	G	0	214	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0847	150	C	T	0	407	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0847	195	T	C	0	400	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0847	263	A	G	1	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0847	499	G	A	2	353	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0847	750	A	G	0	484	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0847	1438	A	G	0	521	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0847	1811	A	G	0	495	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0847	4646	T	C	0	525	synonymous_variant	LOW	ND2	0.0124
HLI-0847	4769	A	G	0	483	synonymous_variant	LOW	ND2	0.9767
HLI-0847	5999	T	C	0	543	synonymous_variant	LOW	COX1	0.0127
HLI-0847	6047	A	G	0	623	synonymous_variant	LOW	COX1	0.0114
HLI-0847	7028	C	T	1	552	synonymous_variant	LOW	COX1	0.8089
HLI-0847	7705	T	C	0	461	synonymous_variant	LOW	COX2	0.0034
HLI-0847	11332	C	T	1	502	synonymous_variant	LOW	ND4	0.0115
HLI-0847	11467	A	G	0	547	synonymous_variant	LOW	ND4	0.1231
HLI-0847	11719	G	A	1	468	synonymous_variant	LOW	ND4	0.7756
HLI-0847	12308	A	G	0	490	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0847	12372	G	A	0	451	synonymous_variant	LOW	ND5	0.1329
HLI-0847	14053	A	G	0	433	missense_variant	MODERATE	ND5	0.0046
HLI-0847	14203	A	G	0	481	synonymous_variant	LOW	ND6	0.0061
HLI-0847	14620	C	T	3	502	synonymous_variant	LOW	ND6	0.0126
HLI-0847	14766	C	T	1	517	missense_variant	MODERATE	CYTB	0.7696
HLI-0847	15326	A	G	0	417	missense_variant	MODERATE	CYTB	0.9868
HLI-0847	15693	T	C	2	394	missense_variant	MODERATE	CYTB	0.0114
HLI-0847	16356	T	C	0	374	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0847	16519	T	C	0	208	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0848	73	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0848	263	A	G	1	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0848	750	A	G	0	571	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0848	1438	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0848	2706	A	G	0	574	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0848	3197	T	C	0	630	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0848	4769	A	G	2	553	synonymous_variant	LOW	ND2	0.9767
HLI-0848	5460	G	A	2	602	missense_variant	MODERATE	ND2	0.0651
HLI-0848	7028	C	T	0	643	synonymous_variant	LOW	COX1	0.8089
HLI-0848	9477	G	A	2	549	missense_variant	MODERATE	COX3	0.0387
HLI-0848	11467	A	G	0	585	synonymous_variant	LOW	ND4	0.1231
HLI-0848	11719	G	A	3	577	synonymous_variant	LOW	ND4	0.7756
HLI-0848	12308	A	G	2	516	upstream_gene_variant	MODIFIER	TRNL2	0.1227

HLI-0848	12372	G	A	0	560	synonymous_variant	LOW	ND5	0.1329
HLI-0848	13617	T	C	1	573	synonymous_variant	LOW	ND5	0.038
HLI-0848	13827	A	G	0	425	synonymous_variant	LOW	ND5	0.0047
HLI-0848	13928	G	C	0	518	missense_variant	MODERATE	ND5	0.0484
HLI-0848	14766	C	T	1	571	missense_variant	MODERATE	CYTB	0.7696
HLI-0848	14793	A	G	2	630	missense_variant	MODERATE	CYTB	0.0199
HLI-0848	15326	A	G	0	524	missense_variant	MODERATE	CYTB	0.9868
HLI-0848	16114	C	A	0	555	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0848	16256	C	T	1	533	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0848	16270	C	T	0	528	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0848	16294	C	T	1	506	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0848	16526	G	A	0	295	upstream_gene_variant	MODIFIER	DLoop	0.0137
HLI-0849	146	T	C	0	557	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0849	263	A	G	1	324	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0849	750	A	G	0	631	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0849	951	G	A	2	745	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0849	15326	A	G	0	526	missense_variant	MODERATE	CYTB	0.9868
HLI-0849	16354	C	T	1	511	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0850	73	A	G	0	331	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0850	263	A	G	0	300	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0850	709	G	A	1	697	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0850	750	A	G	0	715	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0850	930	G	A	1	715	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0850	1438	A	G	0	670	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0850	1888	G	A	1	548	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0850	2706	A	G	0	646	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0850	4216	T	C	0	571	missense_variant	MODERATE	ND1	0.0991
HLI-0850	4769	A	G	2	586	synonymous_variant	LOW	ND2	0.9767
HLI-0850	4917	A	G	0	624	missense_variant	MODERATE	ND2	0.0477
HLI-0850	5147	G	A	0	531	synonymous_variant	LOW	ND2	0.0437
HLI-0850	7028	C	T	2	684	synonymous_variant	LOW	COX1	0.8089
HLI-0850	8292	G	A	2	574	upstream_gene_variant	MODIFIER	Unannotated	0.0024
HLI-0850	8697	G	A	1	573	synonymous_variant	LOW	ATP6	0.0466
HLI-0850	9254	A	G	0	631	synonymous_variant	LOW	COX3	0.0083
HLI-0850	10463	T	C	1	656	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0850	11251	A	G	0	648	synonymous_variant	LOW	ND4	0.0932
HLI-0850	11719	G	A	0	632	synonymous_variant	LOW	ND4	0.7756
HLI-0850	11812	A	G	0	644	synonymous_variant	LOW	ND4	0.0332
HLI-0850	13368	G	A	0	634	synonymous_variant	LOW	ND5	0.0495

HLI-0850	14233	A	G	0	597	synonymous_variant	LOW	ND6	0.0369
HLI-0850	14766	C	T	0	595	missense_variant	MODERATE	CYTB	0.7696
HLI-0850	14905	G	A	2	745	synonymous_variant	LOW	CYTB	0.0526
HLI-0850	15326	A	G	0	583	missense_variant	MODERATE	CYTB	0.9868
HLI-0850	15452	C	A	1	531	missense_variant	MODERATE	CYTB	0.0933
HLI-0850	15607	A	G	0	540	synonymous_variant	LOW	CYTB	0.0508
HLI-0850	15928	G	A	0	532	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0850	16126	T	C	1	604	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0850	16294	C	T	0	565	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0850	16304	T	C	1	601	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0850	16519	T	C	0	331	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0851	263	A	G	0	376	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0851	750	A	G	0	413	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0851	1438	A	G	0	434	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0851	3010	G	A	1	417	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0851	4769	A	G	1	446	synonymous_variant	LOW	ND2	0.9767
HLI-0851	8224	A	G	1	390	synonymous_variant	LOW	COX2	1.00E-04
HLI-0851	8477	T	C	1	411	missense_variant	MODERATE	ATP8	6.00E-04
HLI-0851	15326	A	G	0	299	missense_variant	MODERATE	CYTB	0.9868
HLI-0851	16519	T	C	1	204	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0852	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0852	263	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0852	750	A	G	0	582	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0852	1438	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0852	1700	T	C	1	555	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0852	2706	A	G	1	528	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0852	3197	T	C	0	605	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0852	4769	A	G	1	577	synonymous_variant	LOW	ND2	0.9767
HLI-0852	5495	T	C	1	500	synonymous_variant	LOW	ND2	0.0051
HLI-0852	7028	C	T	4	616	synonymous_variant	LOW	COX1	0.8089
HLI-0852	9477	G	A	1	532	missense_variant	MODERATE	COX3	0.0387
HLI-0852	11467	A	G	0	597	synonymous_variant	LOW	ND4	0.1231
HLI-0852	11719	G	A	0	521	synonymous_variant	LOW	ND4	0.7756
HLI-0852	12308	A	G	0	529	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0852	12372	G	A	2	522	synonymous_variant	LOW	ND5	0.1329
HLI-0852	13617	T	C	1	524	synonymous_variant	LOW	ND5	0.038
HLI-0852	14766	C	T	2	524	missense_variant	MODERATE	CYTB	0.7696
HLI-0852	14793	A	G	1	595	missense_variant	MODERATE	CYTB	0.0199
HLI-0852	15218	A	G	0	525	missense_variant	MODERATE	CYTB	0.0169

HLI-0852	15326	A	G	1	465	missense_variant	MODERATE	CYTB	0.9868
HLI-0852	15924	A	G	0	500	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0852	16256	C	T	0	528	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0852	16270	C	T	0	560	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0852	16399	A	G	0	442	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0853	73	A	G	0	302	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0853	146	T	C	1	570	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0853	263	A	G	0	254	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0853	279	T	C	0	258	upstream_gene_variant	MODIFIER	DLoop	0.0046
HLI-0853	709	G	A	1	602	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0853	750	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0853	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0853	1888	G	A	0	601	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0853	2706	A	G	0	578	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0853	4216	T	C	1	567	missense_variant	MODERATE	ND1	0.0991
HLI-0853	4769	A	G	0	549	synonymous_variant	LOW	ND2	0.9767
HLI-0853	4917	A	G	2	580	missense_variant	MODERATE	ND2	0.0477
HLI-0853	5187	C	T	2	581	synonymous_variant	LOW	ND2	0.0023
HLI-0853	6261	G	A	1	614	missense_variant	MODERATE	COX1	0.007
HLI-0853	7028	C	T	4	627	synonymous_variant	LOW	COX1	0.8089
HLI-0853	7258	T	C	2	626	missense_variant	MODERATE	COX1	0.001
HLI-0853	7873	C	T	0	615	synonymous_variant	LOW	COX2	0.0023
HLI-0853	8697	G	A	1	602	synonymous_variant	LOW	ATP6	0.0466
HLI-0853	10463	T	C	2	616	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0853	10822	C	T	3	598	synonymous_variant	LOW	ND4	0.0036
HLI-0853	11251	A	G	0	664	synonymous_variant	LOW	ND4	0.0932
HLI-0853	11719	G	A	0	566	synonymous_variant	LOW	ND4	0.7756
HLI-0853	11812	A	G	0	564	synonymous_variant	LOW	ND4	0.0332
HLI-0853	11914	G	A	0	592	synonymous_variant	LOW	ND4	0.1112
HLI-0853	13368	G	A	1	624	synonymous_variant	LOW	ND5	0.0495
HLI-0853	14233	A	G	1	538	synonymous_variant	LOW	ND6	0.0369
HLI-0853	14544	G	A	0	574	synonymous_variant	LOW	ND6	0.0024
HLI-0853	14766	C	T	0	612	missense_variant	MODERATE	CYTB	0.7696
HLI-0853	14905	G	A	1	691	synonymous_variant	LOW	CYTB	0.0526
HLI-0853	15326	A	G	0	533	missense_variant	MODERATE	CYTB	0.9868
HLI-0853	15452	C	A	1	537	missense_variant	MODERATE	CYTB	0.0933
HLI-0853	15607	A	G	0	529	synonymous_variant	LOW	CYTB	0.0508
HLI-0853	15928	G	A	0	542	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0853	16126	T	C	0	557	upstream_gene_variant	MODIFIER	DLoop	0.1127

HLI-0853	16292	C	T	0	545	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0853	16294	C	T	0	549	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0853	16519	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0854	73	A	G	0	359	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0854	150	C	T	0	682	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0854	263	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0854	750	A	G	1	722	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0854	1438	A	G	1	737	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0854	1721	C	T	3	703	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0854	2706	A	G	0	659	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0854	3197	T	C	0	737	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0854	3927	A	G	2	639	synonymous_variant	LOW	ND1	0.0014
HLI-0854	4732	A	G	1	736	missense_variant	MODERATE	ND2	0.0059
HLI-0854	4769	A	G	1	771	synonymous_variant	LOW	ND2	0.9767
HLI-0854	7028	C	T	2	743	synonymous_variant	LOW	COX1	0.8089
HLI-0854	7768	A	G	0	694	synonymous_variant	LOW	COX2	0.0186
HLI-0854	8706	A	G	1	693	synonymous_variant	LOW	ATP6	7.00E-04
HLI-0854	9055	G	A	1	669	missense_variant	MODERATE	ATP6	0.0425
HLI-0854	9477	G	A	0	695	missense_variant	MODERATE	COX3	0.0387
HLI-0854	10654	C	T	1	777	missense_variant	MODERATE	ND4L	7.00E-04
HLI-0854	11467	A	G	1	719	synonymous_variant	LOW	ND4	0.1231
HLI-0854	11719	G	A	0	696	synonymous_variant	LOW	ND4	0.7756
HLI-0854	11725	A	G	0	728	synonymous_variant	LOW	ND4	2.00E-04
HLI-0854	12308	A	G	1	566	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0854	12372	G	A	3	580	synonymous_variant	LOW	ND5	0.1329
HLI-0854	13617	T	C	0	677	synonymous_variant	LOW	ND5	0.038
HLI-0854	13637	A	G	0	725	missense_variant	MODERATE	ND5	0.0074
HLI-0854	13830	T	C	0	499	synonymous_variant	LOW	ND5	0.0021
HLI-0854	14182	T	C	2	635	synonymous_variant	LOW	ND6	0.0254
HLI-0854	14766	C	T	1	755	missense_variant	MODERATE	CYTB	0.7696
HLI-0854	15326	A	G	0	560	missense_variant	MODERATE	CYTB	0.9868
HLI-0854	16270	C	T	0	473	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0854	16311	T	C	0	547	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0855	73	A	G	0	165	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0855	263	A	G	0	138	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0855	750	A	G	0	382	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0855	1438	A	G	1	399	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0855	2706	A	G	0	407	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0855	3450	C	T	1	360	synonymous_variant	LOW	ND1	0.0084

HLI-0855	4769	A	G	4	366	synonymous_variant	LOW	ND2	0.9767
HLI-0855	5773	G	A	0	411	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0855	6221	T	C	1	398	synonymous_variant	LOW	COX1	0.0306
HLI-0855	6237	C	T	2	433	synonymous_variant	LOW	COX1	0
HLI-0855	7028	C	T	1	434	synonymous_variant	LOW	COX1	0.8089
HLI-0855	8701	A	G	0	363	missense_variant	MODERATE	ATP6	0.3391
HLI-0855	9449	C	T	1	353	synonymous_variant	LOW	COX3	0.0125
HLI-0855	9540	T	C	0	287	synonymous_variant	LOW	COX3	0.339
HLI-0855	10086	A	G	0	443	missense_variant	MODERATE	ND3	0.0088
HLI-0855	10373	G	A	1	397	synonymous_variant	LOW	ND3	0.0117
HLI-0855	10398	A	G	1	397	missense_variant	MODERATE	ND3	0.445
HLI-0855	10873	T	C	0	262	synonymous_variant	LOW	ND4	0.3389
HLI-0855	11002	A	G	0	241	synonymous_variant	LOW	ND4	0.0124
HLI-0855	11719	G	A	1	416	synonymous_variant	LOW	ND4	0.7756
HLI-0855	11800	A	G	0	428	synonymous_variant	LOW	ND4	0.0052
HLI-0855	12705	C	T	1	359	synonymous_variant	LOW	ND5	0.4212
HLI-0855	13105	A	G	0	379	missense_variant	MODERATE	ND5	0.076
HLI-0855	13914	C	A	1	317	synonymous_variant	LOW	ND5	0.0091
HLI-0855	14766	C	T	1	346	missense_variant	MODERATE	CYTB	0.7696
HLI-0855	15301	G	A	0	341	synonymous_variant	LOW	CYTB	0.2912
HLI-0855	15311	A	G	0	336	missense_variant	MODERATE	CYTB	0.008
HLI-0855	15326	A	G	0	337	missense_variant	MODERATE	CYTB	0.9868
HLI-0855	15824	A	G	1	310	missense_variant	MODERATE	CYTB	0.0083
HLI-0855	15883	G	A	0	307	synonymous_variant	LOW	CYTB	0.0078
HLI-0855	15902	A	G	0	316	upstream_gene_variant	MODIFIER	TRNT	2.00E-04
HLI-0855	16124	T	C	1	336	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0855	16223	C	T	4	293	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0855	16278	C	T	0	308	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0855	16362	T	C	0	275	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0855	16519	T	C	0	144	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0856	73	A	G	1	196	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0856	152	T	C	1	354	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0856	195	T	C	1	325	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0856	263	A	G	0	105	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0856	469	C	T	4	246	upstream_gene_variant	MODIFIER	DLoop	3.00E-04
HLI-0856	709	G	A	1	441	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0856	750	A	G	3	457	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0856	1284	T	C	0	486	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0856	1438	A	G	0	461	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0856	1888	G	A	1	415	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0856	2706	A	G	0	412	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0856	4216	T	C	0	438	missense_variant	MODERATE	ND1	0.0991
HLI-0856	4769	A	G	3	454	synonymous_variant	LOW	ND2	0.9767
HLI-0856	4917	A	G	1	371	missense_variant	MODERATE	ND2	0.0477
HLI-0856	7028	C	T	4	498	synonymous_variant	LOW	COX1	0.8089
HLI-0856	8697	G	A	0	396	synonymous_variant	LOW	ATP6	0.0466
HLI-0856	9899	T	C	0	426	synonymous_variant	LOW	COX3	0.0108
HLI-0856	10463	T	C	1	425	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0856	11251	A	G	0	447	synonymous_variant	LOW	ND4	0.0932
HLI-0856	11719	G	A	1	429	synonymous_variant	LOW	ND4	0.7756
HLI-0856	12633	C	A	3	442	synonymous_variant	LOW	ND5	0.0123
HLI-0856	13368	G	A	0	508	synonymous_variant	LOW	ND5	0.0495
HLI-0856	14766	C	T	3	396	missense_variant	MODERATE	CYTB	0.7696
HLI-0856	14905	G	A	1	455	synonymous_variant	LOW	CYTB	0.0526
HLI-0856	15326	A	G	0	364	missense_variant	MODERATE	CYTB	0.9868
HLI-0856	15452	C	A	5	414	missense_variant	MODERATE	CYTB	0.0933
HLI-0856	15607	A	G	0	403	synonymous_variant	LOW	CYTB	0.0508
HLI-0856	15928	G	A	2	440	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0856	16126	T	C	0	386	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0856	16163	A	G	1	419	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0856	16294	C	T	3	360	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0856	16519	T	C	0	148	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0857	73	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0857	195	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0857	263	A	G	0	167	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0857	497	C	T	1	291	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0857	750	A	G	0	488	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0857	1189	T	C	0	566	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0857	1438	A	G	0	533	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0857	1811	A	G	0	522	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0857	2706	A	G	0	469	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0857	3480	A	G	0	443	synonymous_variant	LOW	ND1	0.0392
HLI-0857	4769	A	G	0	465	synonymous_variant	LOW	ND2	0.9767
HLI-0857	5291	T	C	0	446	synonymous_variant	LOW	ND2	0.001
HLI-0857	7028	C	T	0	522	synonymous_variant	LOW	COX1	0.8089
HLI-0857	9055	G	A	1	491	missense_variant	MODERATE	ATP6	0.0425
HLI-0857	9698	T	C	0	463	synonymous_variant	LOW	COX3	0.0405
HLI-0857	10398	A	G	1	462	missense_variant	MODERATE	ND3	0.445

HLI-0857	10550	A	G	2	514	synonymous_variant	LOW	ND4L	0.0376
HLI-0857	11299	T	C	0	531	synonymous_variant	LOW	ND4	0.0417
HLI-0857	11467	A	G	0	538	synonymous_variant	LOW	ND4	0.1231
HLI-0857	11719	G	A	1	456	synonymous_variant	LOW	ND4	0.7756
HLI-0857	12308	A	G	0	445	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0857	12372	G	A	0	424	synonymous_variant	LOW	ND5	0.1329
HLI-0857	12397	A	G	0	441	missense_variant	MODERATE	ND5	0.0069
HLI-0857	14167	C	T	1	435	synonymous_variant	LOW	ND6	0.0385
HLI-0857	14766	C	T	3	528	missense_variant	MODERATE	CYTB	0.7696
HLI-0857	14798	T	C	2	594	missense_variant	MODERATE	CYTB	0.0651
HLI-0857	15326	A	G	0	404	missense_variant	MODERATE	CYTB	0.9868
HLI-0857	15924	A	G	0	481	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0857	16093	T	C	16	409	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0857	16224	T	C	0	423	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0857	16311	T	C	0	406	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0857	16519	T	C	0	212	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0858	195	T	C	0	233	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0858	263	A	G	1	131	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0858	750	A	G	0	436	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0858	1438	A	G	0	458	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0858	3936	C	T	0	398	synonymous_variant	LOW	ND1	2.00E-04
HLI-0858	4769	A	G	4	469	synonymous_variant	LOW	ND2	0.9767
HLI-0858	12372	G	A	1	348	synonymous_variant	LOW	ND5	0.1329
HLI-0858	14552	A	G	3	422	missense_variant	MODERATE	ND6	6.00E-04
HLI-0858	15326	A	G	0	385	missense_variant	MODERATE	CYTB	0.9868
HLI-0858	16287	C	T	4	368	upstream_gene_variant	MODIFIER	DLoop	0.0051
HLI-0858	16519	T	C	0	171	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0859	239	T	C	0	147	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0859	263	A	G	0	123	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0859	750	A	G	1	450	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0859	1438	A	G	0	471	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0859	3915	G	A	1	428	synonymous_variant	LOW	ND1	0.0106
HLI-0859	4727	A	G	2	464	synonymous_variant	LOW	ND2	0.0063
HLI-0859	4769	A	G	3	517	synonymous_variant	LOW	ND2	0.9767
HLI-0859	9380	G	A	1	447	synonymous_variant	LOW	COX3	0.0094
HLI-0859	11253	T	C	1	416	missense_variant	MODERATE	ND4	0.0053
HLI-0859	15326	A	G	0	393	missense_variant	MODERATE	CYTB	0.9868
HLI-0859	15886	C	T	0	489	synonymous_variant	LOW	CYTB	4.00E-04
HLI-0859	16362	T	C	1	342	upstream_gene_variant	MODIFIER	DLoop	0.1763

HLI-0859	16482	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0860	152	T	C	0	366	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0860	10454	T	C	1	488	upstream_gene_variant	MODIFIER	TRNR	0.0037
HLI-0861	73	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0861	150	C	T	0	374	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0861	189	A	G	0	374	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0861	200	A	G	1	356	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0861	263	A	G	0	143	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0861	750	A	G	0	433	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0861	1438	A	G	0	462	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0861	2352	T	C	1	448	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0861	2706	A	G	0	483	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0861	4769	A	G	1	409	synonymous_variant	LOW	ND2	0.9767
HLI-0861	6221	T	C	1	448	synonymous_variant	LOW	COX1	0.0306
HLI-0861	6587	C	T	0	418	synonymous_variant	LOW	COX1	0.0084
HLI-0861	7028	C	T	1	493	synonymous_variant	LOW	COX1	0.8089
HLI-0861	8701	A	G	0	404	missense_variant	MODERATE	ATP6	0.3391
HLI-0861	9540	T	C	0	430	synonymous_variant	LOW	COX3	0.339
HLI-0861	10370	T	C	1	455	synonymous_variant	LOW	ND3	0.0019
HLI-0861	10398	A	G	0	498	missense_variant	MODERATE	ND3	0.445
HLI-0861	10819	A	G	1	428	synonymous_variant	LOW	ND4	0.0228
HLI-0861	10873	T	C	2	452	synonymous_variant	LOW	ND4	0.3389
HLI-0861	11719	G	A	0	394	synonymous_variant	LOW	ND4	0.7756
HLI-0861	12705	C	T	0	428	synonymous_variant	LOW	ND5	0.4212
HLI-0861	14152	A	G	0	363	synonymous_variant	LOW	ND6	0.0086
HLI-0861	14212	T	C	1	450	synonymous_variant	LOW	ND6	0.0204
HLI-0861	14766	C	T	2	383	missense_variant	MODERATE	CYTB	0.7696
HLI-0861	15301	G	A	0	376	synonymous_variant	LOW	CYTB	0.2912
HLI-0861	15326	A	G	0	409	missense_variant	MODERATE	CYTB	0.9868
HLI-0861	15670	T	C	0	378	synonymous_variant	LOW	CYTB	0.0176
HLI-0861	15942	T	C	0	434	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0861	16129	G	A	0	420	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0861	16223	C	T	1	376	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0861	16309	A	G	1	399	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0861	16327	C	T	0	406	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0862	150	C	T	1	431	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0862	263	A	G	0	181	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0862	750	A	G	1	490	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0862	1438	A	G	0	503	upstream_gene_variant	MODIFIER	RNR1	0.9501

HLI-0862	3010	G	A	0	516	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0862	4769	A	G	0	509	synonymous_variant	LOW	ND2	0.9767
HLI-0862	5460	G	A	1	506	missense_variant	MODERATE	ND2	0.0651
HLI-0862	15326	A	G	2	429	missense_variant	MODERATE	CYTB	0.9868
HLI-0862	15670	T	C	0	473	synonymous_variant	LOW	CYTB	0.0176
HLI-0862	15817	A	G	0	507	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0862	16519	T	C	2	259	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0863	263	A	G	0	160	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0863	477	T	C	0	327	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0863	750	A	G	1	490	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0863	1438	A	G	0	565	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0863	3010	G	A	1	513	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0863	4769	A	G	1	492	synonymous_variant	LOW	ND2	0.9767
HLI-0863	8108	A	G	2	486	missense_variant	MODERATE	COX2	0.0014
HLI-0863	8730	A	G	0	473	synonymous_variant	LOW	ATP6	0.002
HLI-0863	15326	A	G	1	416	missense_variant	MODERATE	CYTB	0.9868
HLI-0863	16519	T	C	0	174	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0864	73	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0864	152	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0864	182	C	T	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0864	185	G	T	0	296	upstream_gene_variant	MODIFIER	DLoop	0.0056
HLI-0864	189	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0864	195	T	C	0	298	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0864	247	G	A	0	142	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0864	263	A	G	0	161	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0864	357	A	G	0	230	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0864	709	G	A	1	520	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0864	710	T	C	1	521	upstream_gene_variant	MODIFIER	RNR1	0.0071
HLI-0864	750	A	G	1	531	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0864	769	G	A	0	540	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0864	825	T	A	0	579	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0864	1018	G	A	0	597	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0864	1738	T	C	1	574	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0864	2352	T	C	0	456	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0864	2706	A	G	0	550	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0864	2758	G	A	1	568	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0864	2768	A	G	1	551	upstream_gene_variant	MODIFIER	RNR2	0.0063
HLI-0864	2885	T	C	1	533	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0864	3308	T	C	0	470	start_lost	HIGH	ND1	0.0073

HLI-0864	3594	C	T	0	442	synonymous_variant	LOW	ND1	0.0789
HLI-0864	3666	G	A	1	520	synonymous_variant	LOW	ND1	0.0233
HLI-0864	3693	G	A	0	523	synonymous_variant	LOW	ND1	0.0091
HLI-0864	4104	A	G	1	434	synonymous_variant	LOW	ND1	0.0785
HLI-0864	4769	A	G	4	543	synonymous_variant	LOW	ND2	0.9767
HLI-0864	5036	A	G	0	546	synonymous_variant	LOW	ND2	0.006
HLI-0864	5046	G	A	0	588	missense_variant	MODERATE	ND2	0.018
HLI-0864	5393	T	C	0	496	synonymous_variant	LOW	ND2	0.0059
HLI-0864	5655	T	C	1	553	upstream_gene_variant	MODIFIER	TRNA	0.0066
HLI-0864	6548	C	T	1	498	synonymous_variant	LOW	COX1	0.0061
HLI-0864	6827	T	C	0	493	synonymous_variant	LOW	COX1	0.0072
HLI-0864	6989	A	G	2	590	synonymous_variant	LOW	COX1	0.0061
HLI-0864	7028	C	T	1	582	synonymous_variant	LOW	COX1	0.8089
HLI-0864	7055	A	G	4	507	synonymous_variant	LOW	COX1	0.0188
HLI-0864	7146	A	G	1	243	missense_variant	MODERATE	COX1	0.0497
HLI-0864	7256	C	T	2	391	synonymous_variant	LOW	COX1	0.0784
HLI-0864	7389	T	C	2	375	missense_variant	MODERATE	COX1	0.0201
HLI-0864	7521	G	A	0	309	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0864	7867	C	T	0	533	synonymous_variant	LOW	COX2	0.0076
HLI-0864	8248	A	G	1	493	synonymous_variant	LOW	COX2	0.0061
HLI-0864	8468	C	T	3	391	synonymous_variant	LOW	ATP8	0.0501
HLI-0864	8655	C	T	4	424	synonymous_variant	LOW	ATP6	0.0511
HLI-0864	8701	A	G	2	499	missense_variant	MODERATE	ATP6	0.3391
HLI-0864	9540	T	C	0	526	synonymous_variant	LOW	COX3	0.339
HLI-0864	10398	A	G	0	497	missense_variant	MODERATE	ND3	0.445
HLI-0864	10688	G	A	0	532	synonymous_variant	LOW	ND4L	0.0515
HLI-0864	10810	T	C	1	516	synonymous_variant	LOW	ND4	0.0522
HLI-0864	10873	T	C	1	515	synonymous_variant	LOW	ND4	0.3389
HLI-0864	11719	G	A	1	525	synonymous_variant	LOW	ND4	0.7756
HLI-0864	12082	A	G	1	525	synonymous_variant	LOW	ND4	4.00E-04
HLI-0864	12342	C	T	1	512	synonymous_variant	LOW	ND5	2.00E-04
HLI-0864	12519	T	C	1	538	synonymous_variant	LOW	ND5	0.007
HLI-0864	12705	C	T	2	536	synonymous_variant	LOW	ND5	0.4212
HLI-0864	13105	A	G	1	539	missense_variant	MODERATE	ND5	0.076
HLI-0864	13506	C	T	2	497	synonymous_variant	LOW	ND5	0.0506
HLI-0864	13650	C	T	0	446	synonymous_variant	LOW	ND5	0.079
HLI-0864	13789	T	C	1	346	missense_variant	MODERATE	ND5	0.0185
HLI-0864	13880	C	A	2	433	missense_variant	MODERATE	ND5	0.0055
HLI-0864	14178	T	C	0	512	missense_variant	MODERATE	ND6	0.0225

HLI-0864	14203	A	G	0	558	synonymous_variant	LOW	ND6	0.0061
HLI-0864	14560	G	A	2	531	synonymous_variant	LOW	ND6	0.0235
HLI-0864	14766	C	T	1	552	missense_variant	MODERATE	CYTB	0.7696
HLI-0864	14769	A	G	1	559	missense_variant	MODERATE	CYTB	0.0121
HLI-0864	15077	G	A	0	592	missense_variant	MODERATE	CYTB	0.0021
HLI-0864	15103	C	T	0	659	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0864	15115	T	C	0	656	synonymous_variant	LOW	CYTB	0.0093
HLI-0864	15326	A	G	1	468	missense_variant	MODERATE	CYTB	0.9868
HLI-0864	16126	T	C	0	492	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0864	16223	C	T	2	359	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0864	16264	C	T	0	338	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0864	16270	C	T	0	325	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0864	16278	C	T	0	321	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0864	16293	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0216
HLI-0864	16311	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0864	16519	T	C	0	137	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0865	73	A	G	0	206	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0865	146	T	C	0	372	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0865	185	G	A	9	359	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0865	228	G	A	0	162	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0865	263	A	G	0	189	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0865	295	C	T	0	167	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0865	462	C	T	1	342	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0865	489	T	C	0	394	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0865	750	A	G	0	424	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0865	1438	A	G	0	454	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0865	2706	A	G	0	394	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0865	3010	G	A	0	453	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0865	3702	A	G	0	393	synonymous_variant	LOW	ND1	3.00E-04
HLI-0865	4216	T	C	0	433	missense_variant	MODERATE	ND1	0.0991
HLI-0865	4769	A	G	2	509	synonymous_variant	LOW	ND2	0.9767
HLI-0865	6464	C	A	3	421	synonymous_variant	LOW	COX1	0.0011
HLI-0865	6554	C	T	1	489	synonymous_variant	LOW	COX1	0.0016
HLI-0865	7028	C	T	1	542	synonymous_variant	LOW	COX1	0.8089
HLI-0865	10398	A	G	0	385	missense_variant	MODERATE	ND3	0.445
HLI-0865	11251	A	G	0	417	synonymous_variant	LOW	ND4	0.0932
HLI-0865	11719	G	A	0	434	synonymous_variant	LOW	ND4	0.7756
HLI-0865	12127	G	A	0	444	synonymous_variant	LOW	ND4	0.0058
HLI-0865	12612	A	G	9	470	synonymous_variant	LOW	ND5	0.0506

HLI-0865	13681	A	G	1	386	missense_variant	MODERATE	ND5	0.0035
HLI-0865	13708	G	A	0	411	missense_variant	MODERATE	ND5	0.0717
HLI-0865	14766	C	T	3	448	missense_variant	MODERATE	CYTB	0.7696
HLI-0865	14798	T	C	1	511	missense_variant	MODERATE	CYTB	0.0651
HLI-0865	15326	A	G	0	334	missense_variant	MODERATE	CYTB	0.9868
HLI-0865	15452	C	A	5	355	missense_variant	MODERATE	CYTB	0.0933
HLI-0865	16069	C	T	1	458	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0865	16126	T	C	0	490	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0865	16261	C	T	0	383	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0866	73	A	G	0	236	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0866	263	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0866	750	A	G	1	497	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0866	1438	A	G	0	502	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0866	1700	T	C	0	439	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0866	2706	A	G	0	469	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0866	3197	T	C	0	508	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0866	4769	A	G	3	492	synonymous_variant	LOW	ND2	0.9767
HLI-0866	5495	T	C	0	504	synonymous_variant	LOW	ND2	0.0051
HLI-0866	7028	C	T	2	563	synonymous_variant	LOW	COX1	0.8089
HLI-0866	9477	G	A	0	540	missense_variant	MODERATE	COX3	0.0387
HLI-0866	11467	A	G	0	531	synonymous_variant	LOW	ND4	0.1231
HLI-0866	11719	G	A	0	480	synonymous_variant	LOW	ND4	0.7756
HLI-0866	12308	A	G	2	371	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0866	12372	G	A	1	357	synonymous_variant	LOW	ND5	0.1329
HLI-0866	13617	T	C	0	425	synonymous_variant	LOW	ND5	0.038
HLI-0866	14766	C	T	2	505	missense_variant	MODERATE	CYTB	0.7696
HLI-0866	14793	A	G	1	571	missense_variant	MODERATE	CYTB	0.0199
HLI-0866	15218	A	G	0	424	missense_variant	MODERATE	CYTB	0.0169
HLI-0866	15326	A	G	1	432	missense_variant	MODERATE	CYTB	0.9868
HLI-0866	15924	A	G	0	384	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0866	16256	C	T	0	437	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0866	16270	C	T	0	460	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0866	16399	A	G	0	369	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0867	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0867	150	C	T	1	484	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0867	152	T	C	1	484	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0867	263	A	G	0	206	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0867	497	C	T	5	420	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0867	750	A	G	0	545	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0867	1189	T	C	0	598	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0867	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0867	1811	A	G	1	591	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0867	2706	A	G	0	574	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0867	3480	A	G	0	550	synonymous_variant	LOW	ND1	0.0392
HLI-0867	4769	A	G	1	493	synonymous_variant	LOW	ND2	0.9767
HLI-0867	7028	C	T	4	592	synonymous_variant	LOW	COX1	0.8089
HLI-0867	9055	G	A	0	524	missense_variant	MODERATE	ATP6	0.0425
HLI-0867	9698	T	C	2	539	synonymous_variant	LOW	COX3	0.0405
HLI-0867	10398	A	G	1	535	missense_variant	MODERATE	ND3	0.445
HLI-0867	10550	A	G	0	540	synonymous_variant	LOW	ND4L	0.0376
HLI-0867	11299	T	C	0	516	synonymous_variant	LOW	ND4	0.0417
HLI-0867	11467	A	G	0	564	synonymous_variant	LOW	ND4	0.1231
HLI-0867	11719	G	A	1	535	synonymous_variant	LOW	ND4	0.7756
HLI-0867	12308	A	G	1	512	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0867	12372	G	A	2	579	synonymous_variant	LOW	ND5	0.1329
HLI-0867	14167	C	T	3	483	synonymous_variant	LOW	ND6	0.0385
HLI-0867	14766	C	T	8	491	missense_variant	MODERATE	CYTB	0.7696
HLI-0867	14798	T	C	0	576	missense_variant	MODERATE	CYTB	0.0651
HLI-0867	15326	A	G	0	507	missense_variant	MODERATE	CYTB	0.9868
HLI-0867	15653	A	T	1	502	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0867	16093	T	C	29	489	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0867	16224	T	C	1	505	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0867	16311	T	C	0	469	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0867	16519	T	C	1	237	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0868	152	T	C	0	469	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0868	263	A	G	0	194	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0868	750	A	G	0	558	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0868	1438	A	G	0	569	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0868	2772	C	T	1	505	upstream_gene_variant	MODIFIER	RNR2	0.0034
HLI-0868	4769	A	G	0	564	synonymous_variant	LOW	ND2	0.9767
HLI-0868	6743	T	C	7	626	synonymous_variant	LOW	COX1	3.00E-04
HLI-0868	10754	A	G	1	594	synonymous_variant	LOW	ND4L	0.0035
HLI-0868	15326	A	G	0	510	missense_variant	MODERATE	CYTB	0.9868
HLI-0868	16519	T	C	1	303	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0869	73	A	G	0	189	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0869	263	A	G	0	164	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0869	709	G	A	0	449	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0869	750	A	G	0	448	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0869	930	G	A	1	413	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0869	1438	A	G	0	414	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0869	1888	G	A	2	330	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0869	2706	A	G	0	419	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0869	4216	T	C	0	409	missense_variant	MODERATE	ND1	0.0991
HLI-0869	4769	A	G	0	307	synonymous_variant	LOW	ND2	0.9767
HLI-0869	4917	A	G	0	321	missense_variant	MODERATE	ND2	0.0477
HLI-0869	5147	G	A	0	344	synonymous_variant	LOW	ND2	0.0437
HLI-0869	5237	G	A	0	357	synonymous_variant	LOW	ND2	0.0039
HLI-0869	7028	C	T	2	471	synonymous_variant	LOW	COX1	0.8089
HLI-0869	8697	G	A	1	358	synonymous_variant	LOW	ATP6	0.0466
HLI-0869	10463	T	C	1	458	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0869	11251	A	G	1	407	synonymous_variant	LOW	ND4	0.0932
HLI-0869	11719	G	A	1	414	synonymous_variant	LOW	ND4	0.7756
HLI-0869	11812	A	G	0	423	synonymous_variant	LOW	ND4	0.0332
HLI-0869	13368	G	A	4	423	synonymous_variant	LOW	ND5	0.0495
HLI-0869	14233	A	G	0	413	synonymous_variant	LOW	ND6	0.0369
HLI-0869	14766	C	T	1	360	missense_variant	MODERATE	CYTB	0.7696
HLI-0869	14905	G	A	0	404	synonymous_variant	LOW	CYTB	0.0526
HLI-0869	15326	A	G	0	342	missense_variant	MODERATE	CYTB	0.9868
HLI-0869	15452	C	A	0	325	missense_variant	MODERATE	CYTB	0.0933
HLI-0869	15607	A	G	0	369	synonymous_variant	LOW	CYTB	0.0508
HLI-0869	15928	G	A	0	427	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0869	16126	T	C	0	409	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0869	16172	T	C	0	382	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0869	16294	C	T	0	316	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0869	16296	C	T	0	316	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0869	16304	T	C	0	323	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0869	16519	T	C	0	180	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0870	263	A	G	0	172	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0870	750	A	G	1	565	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0870	1438	A	G	0	554	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0870	4769	A	G	1	548	synonymous_variant	LOW	ND2	0.9767
HLI-0870	6776	T	C	1	638	synonymous_variant	LOW	COX1	0.0226
HLI-0870	14900	G	A	1	584	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0870	15326	A	G	0	510	missense_variant	MODERATE	CYTB	0.9868
HLI-0870	16519	T	C	0	257	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0871	73	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0871	150	C	T	1	484	upstream_gene_variant	MODIFIER	DLoop	0.1339

HLI-0871	263	A	G	0	184	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0871	723	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.002
HLI-0871	750	A	G	1	579	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0871	1438	A	G	0	569	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0871	1721	C	T	2	564	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0871	2706	A	G	0	581	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0871	3197	T	C	0	573	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0871	3861	A	G	0	550	synonymous_variant	LOW	ND1	0.0011
HLI-0871	4769	A	G	0	533	synonymous_variant	LOW	ND2	0.9767
HLI-0871	5836	A	G	0	634	upstream_gene_variant	MODIFIER	TRNY	0.0018
HLI-0871	7028	C	T	2	626	synonymous_variant	LOW	COX1	0.8089
HLI-0871	7768	A	G	0	511	synonymous_variant	LOW	COX2	0.0186
HLI-0871	9477	G	A	1	565	missense_variant	MODERATE	COX3	0.0387
HLI-0871	10262	A	G	1	610	synonymous_variant	LOW	ND3	5.00E-04
HLI-0871	11467	A	G	1	605	synonymous_variant	LOW	ND4	0.1231
HLI-0871	11719	G	A	0	562	synonymous_variant	LOW	ND4	0.7756
HLI-0871	12308	A	G	1	528	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0871	12372	G	A	0	505	synonymous_variant	LOW	ND5	0.1329
HLI-0871	13017	A	G	3	527	synonymous_variant	LOW	ND5	7.00E-04
HLI-0871	13617	T	C	0	494	synonymous_variant	LOW	ND5	0.038
HLI-0871	13637	A	G	0	541	missense_variant	MODERATE	ND5	0.0074
HLI-0871	14182	T	C	0	485	synonymous_variant	LOW	ND6	0.0254
HLI-0871	14766	C	T	2	527	missense_variant	MODERATE	CYTB	0.7696
HLI-0871	15326	A	G	0	462	missense_variant	MODERATE	CYTB	0.9868
HLI-0871	16249	T	C	0	514	upstream_gene_variant	MODIFIER	DLoop	0.0192
HLI-0871	16270	C	T	0	475	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0872	73	A	G	0	324	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0872	185	G	A	5	481	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0872	228	G	A	0	272	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0872	263	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0872	295	C	T	0	228	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0872	462	C	T	0	469	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0872	482	T	C	0	540	upstream_gene_variant	MODIFIER	DLoop	0.0094
HLI-0872	489	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0872	750	A	G	0	646	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0872	1438	A	G	1	661	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0872	2706	A	G	2	646	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0872	3010	G	A	1	632	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0872	3394	T	C	1	605	missense_variant	MODERATE	ND1	0.013

HLI-0872	4216	T	C	2	634	missense_variant	MODERATE	ND1	0.0991
HLI-0872	4769	A	G	2	614	synonymous_variant	LOW	ND2	0.9767
HLI-0872	5411	A	G	1	600	synonymous_variant	LOW	ND2	1.00E-04
HLI-0872	5773	G	A	0	682	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0872	7028	C	T	3	705	synonymous_variant	LOW	COX1	0.8089
HLI-0872	7184	A	G	3	650	synonymous_variant	LOW	COX1	0.0017
HLI-0872	10398	A	G	2	684	missense_variant	MODERATE	ND3	0.445
HLI-0872	11251	A	G	0	636	synonymous_variant	LOW	ND4	0.0932
HLI-0872	11719	G	A	2	599	synonymous_variant	LOW	ND4	0.7756
HLI-0872	12612	A	G	9	632	synonymous_variant	LOW	ND5	0.0506
HLI-0872	13368	G	A	1	677	synonymous_variant	LOW	ND5	0.0495
HLI-0872	13708	G	A	1	630	missense_variant	MODERATE	ND5	0.0717
HLI-0872	14200	T	C	0	563	synonymous_variant	LOW	ND6	0.0032
HLI-0872	14766	C	T	3	593	missense_variant	MODERATE	CYTB	0.7696
HLI-0872	14798	T	C	0	699	missense_variant	MODERATE	CYTB	0.0651
HLI-0872	15326	A	G	1	573	missense_variant	MODERATE	CYTB	0.9868
HLI-0872	15452	C	A	6	499	missense_variant	MODERATE	CYTB	0.0933
HLI-0872	16069	C	T	3	600	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0872	16126	T	C	1	611	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0872	16271	T	C	0	612	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0873	73	A	G	1	328	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0873	152	T	C	0	536	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0873	217	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0873	263	A	G	0	247	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0873	340	C	T	0	228	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0873	508	A	G	1	400	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0873	750	A	G	0	622	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0873	988	G	A	3	652	upstream_gene_variant	MODIFIER	RNR1	8.00E-04
HLI-0873	1438	A	G	0	660	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0873	1811	A	G	2	665	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0873	2706	A	G	0	645	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0873	3720	A	G	2	586	synonymous_variant	LOW	ND1	0.0069
HLI-0873	4769	A	G	2	601	synonymous_variant	LOW	ND2	0.9767
HLI-0873	5390	A	G	1	631	synonymous_variant	LOW	ND2	0.0069
HLI-0873	5426	T	C	1	668	synonymous_variant	LOW	ND2	0.0091
HLI-0873	6045	C	T	1	659	synonymous_variant	LOW	COX1	0.0065
HLI-0873	6152	T	C	0	570	synonymous_variant	LOW	COX1	0.0077
HLI-0873	6425	T	C	0	651	synonymous_variant	LOW	COX1	7.00E-04
HLI-0873	7028	C	T	3	697	synonymous_variant	LOW	COX1	0.8089

HLI-0873	7109	C	T	3	716	synonymous_variant	LOW	COX1	9.00E-04
HLI-0873	10876	A	G	0	611	synonymous_variant	LOW	ND4	0.0098
HLI-0873	11467	A	G	0	679	synonymous_variant	LOW	ND4	0.1231
HLI-0873	11719	G	A	1	620	synonymous_variant	LOW	ND4	0.7756
HLI-0873	12308	A	G	1	614	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0873	12372	G	A	1	619	synonymous_variant	LOW	ND5	0.1329
HLI-0873	13020	T	C	4	629	synonymous_variant	LOW	ND5	0.0106
HLI-0873	13734	T	C	0	537	synonymous_variant	LOW	ND5	0.0067
HLI-0873	14766	C	T	1	578	missense_variant	MODERATE	CYTB	0.7696
HLI-0873	15326	A	G	1	552	missense_variant	MODERATE	CYTB	0.9868
HLI-0873	15784	T	C	1	602	synonymous_variant	LOW	CYTB	0.0363
HLI-0873	15907	A	G	1	645	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0873	16051	A	G	2	625	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0873	16129	G	C	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0873	16256	C	T	4	461	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0873	16519	T	C	1	245	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0874	151	C	T	0	405	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0874	152	T	C	0	409	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0874	263	A	G	2	214	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0874	750	A	G	0	446	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0874	1438	A	G	0	447	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0874	4769	A	G	0	479	synonymous_variant	LOW	ND2	0.9767
HLI-0874	4793	A	G	0	532	synonymous_variant	LOW	ND2	0.0073
HLI-0874	8038	T	C	2	494	synonymous_variant	LOW	COX2	2.00E-04
HLI-0874	15326	A	G	1	354	missense_variant	MODERATE	CYTB	0.9868
HLI-0874	16519	T	C	0	194	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0875	72	T	C	0	237	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0875	263	A	G	0	192	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0875	750	A	G	0	517	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0875	1438	A	G	0	587	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0875	2706	A	G	0	464	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0875	4580	G	A	1	506	synonymous_variant	LOW	ND2	0.0169
HLI-0875	4769	A	G	0	493	synonymous_variant	LOW	ND2	0.9767
HLI-0875	7028	C	T	1	534	synonymous_variant	LOW	COX1	0.8089
HLI-0875	9368	A	G	1	565	synonymous_variant	LOW	COX3	8.00E-04
HLI-0875	15326	A	G	1	422	missense_variant	MODERATE	CYTB	0.9868
HLI-0875	15904	C	T	1	582	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0875	16261	C	T	3	508	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0875	16298	T	C	0	458	upstream_gene_variant	MODIFIER	DLoop	0.0655

HLI-0875	16311	T	C	0	454	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0875	16519	T	C	2	235	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0876	73	A	G	0	267	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0876	263	A	G	0	195	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0876	295	C	A	2	166	upstream_gene_variant	MODIFIER	DLoop	0.0012
HLI-0876	750	A	G	0	543	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0876	1391	T	C	0	596	upstream_gene_variant	MODIFIER	RNR1	0.0027
HLI-0876	1438	A	G	0	636	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0876	2706	A	G	0	513	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0876	3360	A	G	0	529	synonymous_variant	LOW	ND1	0.0013
HLI-0876	4769	A	G	0	503	synonymous_variant	LOW	ND2	0.9767
HLI-0876	4917	A	G	0	466	missense_variant	MODERATE	ND2	0.0477
HLI-0876	5586	C	T	0	559	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0876	5823	A	G	1	544	upstream_gene_variant	MODIFIER	TRNC	0.0014
HLI-0876	6557	C	T	1	488	synonymous_variant	LOW	COX1	0.0011
HLI-0876	6671	T	C	3	593	synonymous_variant	LOW	COX1	0.0071
HLI-0876	7028	C	T	1	567	synonymous_variant	LOW	COX1	0.8089
HLI-0876	7547	T	C	1	552	upstream_gene_variant	MODIFIER	TRND	0.0012
HLI-0876	7711	T	C	0	463	synonymous_variant	LOW	COX2	0.002
HLI-0876	7859	G	A	1	491	missense_variant	MODERATE	COX2	0.003
HLI-0876	8388	T	C	1	481	missense_variant	MODERATE	ATP8	0.0013
HLI-0876	8887	A	G	0	539	missense_variant	MODERATE	ATP6	0.0016
HLI-0876	10496	A	G	2	579	synonymous_variant	LOW	ND4L	5.00E-04
HLI-0876	10658	A	G	1	579	synonymous_variant	LOW	ND4L	0.0026
HLI-0876	10825	A	G	0	526	synonymous_variant	LOW	ND4	0.0011
HLI-0876	11719	G	A	0	526	synonymous_variant	LOW	ND4	0.7756
HLI-0876	13053	C	T	2	512	synonymous_variant	LOW	ND5	3.00E-04
HLI-0876	13948	C	T	4	459	missense_variant	MODERATE	ND5	0.0013
HLI-0876	14632	C	T	0	517	synonymous_variant	LOW	ND6	0.0012
HLI-0876	14766	C	T	1	502	missense_variant	MODERATE	CYTB	0.7696
HLI-0876	15326	A	G	0	438	missense_variant	MODERATE	CYTB	0.9868
HLI-0876	15721	T	C	1	500	synonymous_variant	LOW	CYTB	0.0033
HLI-0876	16311	T	C	0	479	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0876	16519	T	C	0	243	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0877	263	A	G	0	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0877	750	A	G	1	583	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0877	1438	A	G	0	585	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0877	2392	T	C	2	514	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0877	4769	A	G	1	521	synonymous_variant	LOW	ND2	0.9767

HLI-0877	7337	G	A	1	570	synonymous_variant	LOW	COX1	0.0119
HLI-0877	8167	T	C	0	540	synonymous_variant	LOW	COX2	0.0021
HLI-0877	9548	G	A	7	496	synonymous_variant	LOW	COX3	0.0149
HLI-0877	11465	T	C	0	589	synonymous_variant	LOW	ND4	0.0022
HLI-0877	15326	A	G	0	503	missense_variant	MODERATE	CYTB	0.9868
HLI-0877	16162	A	G	1	627	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0878	73	A	G	0	274	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0878	150	C	T	1	427	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0878	189	A	G	1	373	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0878	194	C	T	1	356	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0878	195	T	C	1	354	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0878	204	T	C	2	372	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0878	207	G	A	2	375	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0878	263	A	G	0	156	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0878	709	G	A	1	638	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0878	750	A	G	0	660	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0878	1243	T	C	1	684	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0878	1438	A	G	1	664	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0878	2706	A	G	1	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0878	3505	A	G	0	639	missense_variant	MODERATE	ND1	0.0144
HLI-0878	3644	T	C	2	608	missense_variant	MODERATE	ND1	0.0042
HLI-0878	4769	A	G	0	648	synonymous_variant	LOW	ND2	0.9767
HLI-0878	5046	G	A	2	550	missense_variant	MODERATE	ND2	0.018
HLI-0878	5460	G	A	1	601	missense_variant	MODERATE	ND2	0.0651
HLI-0878	6528	C	T	1	631	synonymous_variant	LOW	COX1	0.0013
HLI-0878	7028	C	T	3	803	synonymous_variant	LOW	COX1	0.8089
HLI-0878	7142	T	C	0	645	synonymous_variant	LOW	COX1	0.0028
HLI-0878	8251	G	A	3	573	synonymous_variant	LOW	COX2	0.058
HLI-0878	8994	G	A	1	643	synonymous_variant	LOW	ATP6	0.0167
HLI-0878	10097	A	G	2	715	synonymous_variant	LOW	ND3	0.0011
HLI-0878	11674	C	T	3	570	synonymous_variant	LOW	ND4	0.0116
HLI-0878	11719	G	A	0	658	synonymous_variant	LOW	ND4	0.7756
HLI-0878	11947	A	G	0	556	synonymous_variant	LOW	ND4	0.011
HLI-0878	12414	T	C	4	527	synonymous_variant	LOW	ND5	0.0139
HLI-0878	12705	C	T	4	644	synonymous_variant	LOW	ND5	0.4212
HLI-0878	14766	C	T	5	594	missense_variant	MODERATE	CYTB	0.7696
HLI-0878	15326	A	G	0	525	missense_variant	MODERATE	CYTB	0.9868
HLI-0878	15775	A	G	0	537	synonymous_variant	LOW	CYTB	0.0011
HLI-0878	15884	G	C	0	609	missense_variant	MODERATE	CYTB	0.011

HLI-0878	16223	C	T	3	620	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0878	16292	C	T	3	575	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0878	16362	T	C	1	522	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0878	16519	T	C	2	264	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0879	263	A	G	1	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0879	750	A	G	0	497	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0879	1438	A	G	0	484	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0879	2706	A	G	0	556	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0879	3507	C	T	0	436	synonymous_variant	LOW	ND1	3.00E-04
HLI-0879	4310	A	G	1	388	upstream_gene_variant	MODIFIER	TRNI	8.00E-04
HLI-0879	4769	A	G	0	483	synonymous_variant	LOW	ND2	0.9767
HLI-0879	6755	G	A	2	590	synonymous_variant	LOW	COX1	0.0065
HLI-0879	7028	C	T	1	572	synonymous_variant	LOW	COX1	0.8089
HLI-0879	15326	A	G	0	386	missense_variant	MODERATE	CYTB	0.9868
HLI-0879	16172	T	C	1	495	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0879	16311	T	C	0	404	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0880	73	A	G	1	296	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0880	150	C	T	2	565	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0880	152	T	C	2	562	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0880	263	A	G	0	241	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0880	295	C	T	0	220	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0880	489	T	C	0	400	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0880	750	A	G	0	605	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0880	1438	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0880	1719	G	A	1	624	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0880	2706	A	G	2	554	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0880	4216	T	C	1	589	missense_variant	MODERATE	ND1	0.0991
HLI-0880	4769	A	G	0	625	synonymous_variant	LOW	ND2	0.9767
HLI-0880	5633	C	T	2	666	upstream_gene_variant	MODIFIER	TRNA	0.0068
HLI-0880	7028	C	T	5	697	synonymous_variant	LOW	COX1	0.8089
HLI-0880	7476	C	T	3	654	upstream_gene_variant	MODIFIER	TRNS1	0.0134
HLI-0880	10172	G	A	2	669	synonymous_variant	LOW	ND3	0.0084
HLI-0880	10398	A	G	0	599	missense_variant	MODERATE	ND3	0.445
HLI-0880	11251	A	G	0	607	synonymous_variant	LOW	ND4	0.0932
HLI-0880	11719	G	A	1	592	synonymous_variant	LOW	ND4	0.7756
HLI-0880	12612	A	G	12	616	synonymous_variant	LOW	ND5	0.0506
HLI-0880	13708	G	A	0	601	missense_variant	MODERATE	ND5	0.0717
HLI-0880	14569	G	A	2	646	synonymous_variant	LOW	ND6	0.0259
HLI-0880	14766	C	T	3	632	missense_variant	MODERATE	CYTB	0.7696

HLI-0880	15257	G	A	7	507	missense_variant	MODERATE	CYTB	0.0155
HLI-0880	15326	A	G	0	523	missense_variant	MODERATE	CYTB	0.9868
HLI-0880	15452	C	A	7	417	missense_variant	MODERATE	CYTB	0.0933
HLI-0880	15812	G	A	2	507	missense_variant	MODERATE	CYTB	0.0096
HLI-0880	16069	C	T	1	565	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0880	16126	T	C	1	630	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0880	16278	C	T	0	576	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0881	73	A	G	0	270	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0881	146	T	C	1	510	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0881	153	A	G	1	523	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0881	263	A	G	2	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0881	750	A	G	1	568	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0881	1438	A	G	0	602	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0881	1811	A	G	1	613	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0881	2217	C	T	3	511	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0881	2706	A	G	0	566	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0881	3480	A	G	1	477	synonymous_variant	LOW	ND1	0.0392
HLI-0881	4769	A	G	0	574	synonymous_variant	LOW	ND2	0.9767
HLI-0881	5231	G	A	1	509	synonymous_variant	LOW	ND2	0.0232
HLI-0881	7028	C	T	2	659	synonymous_variant	LOW	COX1	0.8089
HLI-0881	9055	G	A	0	576	missense_variant	MODERATE	ATP6	0.0425
HLI-0881	9698	T	C	1	555	synonymous_variant	LOW	COX3	0.0405
HLI-0881	9716	T	C	2	620	synonymous_variant	LOW	COX3	0.0108
HLI-0881	10550	A	G	1	588	synonymous_variant	LOW	ND4L	0.0376
HLI-0881	11299	T	C	0	583	synonymous_variant	LOW	ND4	0.0417
HLI-0881	11467	A	G	1	618	synonymous_variant	LOW	ND4	0.1231
HLI-0881	11719	G	A	0	566	synonymous_variant	LOW	ND4	0.7756
HLI-0881	11869	C	A	4	610	synonymous_variant	LOW	ND4	0.0015
HLI-0881	12308	A	G	0	531	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0881	12372	G	A	0	499	synonymous_variant	LOW	ND5	0.1329
HLI-0881	13135	G	A	5	594	missense_variant	MODERATE	ND5	0.0092
HLI-0881	14037	A	G	3	469	synonymous_variant	LOW	ND5	0.0017
HLI-0881	14167	C	T	3	500	synonymous_variant	LOW	ND6	0.0385
HLI-0881	14766	C	T	4	573	missense_variant	MODERATE	CYTB	0.7696
HLI-0881	14798	T	C	2	664	missense_variant	MODERATE	CYTB	0.0651
HLI-0881	15326	A	G	0	464	missense_variant	MODERATE	CYTB	0.9868
HLI-0881	15484	A	G	0	434	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0881	16222	C	T	0	631	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0881	16224	T	C	0	629	upstream_gene_variant	MODIFIER	DLoop	0.0423

HLI-0881	16270	C	T	1	600	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0881	16311	T	C	1	539	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0881	16519	T	C	2	281	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0882	73	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0882	185	G	A	0	532	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0882	189	A	G	0	527	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0882	204	T	C	0	494	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0882	263	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0882	750	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0882	1438	A	G	1	685	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0882	1700	T	C	0	594	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0882	2706	A	G	2	681	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0882	3197	T	C	2	690	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0882	4769	A	G	0	565	synonymous_variant	LOW	ND2	0.9767
HLI-0882	5495	T	C	1	680	synonymous_variant	LOW	ND2	0.0051
HLI-0882	6425	T	C	1	650	synonymous_variant	LOW	COX1	7.00E-04
HLI-0882	7028	C	T	1	767	synonymous_variant	LOW	COX1	0.8089
HLI-0882	9477	G	A	0	659	missense_variant	MODERATE	COX3	0.0387
HLI-0882	11467	A	G	1	650	synonymous_variant	LOW	ND4	0.1231
HLI-0882	11719	G	A	0	620	synonymous_variant	LOW	ND4	0.7756
HLI-0882	12308	A	G	1	666	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0882	12372	G	A	0	694	synonymous_variant	LOW	ND5	0.1329
HLI-0882	12774	C	A	5	741	synonymous_variant	LOW	ND5	4.00E-04
HLI-0882	13617	T	C	0	615	synonymous_variant	LOW	ND5	0.038
HLI-0882	14766	C	T	3	620	missense_variant	MODERATE	CYTB	0.7696
HLI-0882	14793	A	G	0	665	missense_variant	MODERATE	CYTB	0.0199
HLI-0882	15218	A	G	1	656	missense_variant	MODERATE	CYTB	0.0169
HLI-0882	15326	A	G	1	635	missense_variant	MODERATE	CYTB	0.9868
HLI-0882	15924	A	G	2	663	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0882	16256	C	T	0	708	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0882	16270	C	T	0	692	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0882	16362	T	C	1	527	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0882	16399	A	G	2	576	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0883	73	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0883	263	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0883	709	G	A	0	591	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0883	750	A	G	2	649	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0883	1438	A	G	0	630	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0883	1888	G	A	0	608	upstream_gene_variant	MODIFIER	RNR2	0.0558

HLI-0883	2141	T	C	0	566	upstream_gene_variant	MODIFIER	RNR2	0.0013
HLI-0883	2706	A	G	0	615	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0883	3335	T	C	0	587	missense_variant	MODERATE	ND1	0.0011
HLI-0883	3350	T	C	0	639	missense_variant	MODERATE	ND1	4.00E-04
HLI-0883	4216	T	C	0	587	missense_variant	MODERATE	ND1	0.0991
HLI-0883	4769	A	G	1	546	synonymous_variant	LOW	ND2	0.9767
HLI-0883	4917	A	G	0	513	missense_variant	MODERATE	ND2	0.0477
HLI-0883	7028	C	T	1	606	synonymous_variant	LOW	COX1	0.8089
HLI-0883	8697	G	A	0	574	synonymous_variant	LOW	ATP6	0.0466
HLI-0883	9117	T	C	1	586	synonymous_variant	LOW	ATP6	0.0018
HLI-0883	10463	T	C	1	662	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0883	11251	A	G	2	582	synonymous_variant	LOW	ND4	0.0932
HLI-0883	11719	G	A	2	571	synonymous_variant	LOW	ND4	0.7756
HLI-0883	11812	A	G	0	584	synonymous_variant	LOW	ND4	0.0332
HLI-0883	12741	C	T	12	637	synonymous_variant	LOW	ND5	9.00E-04
HLI-0883	13368	G	A	4	585	synonymous_variant	LOW	ND5	0.0495
HLI-0883	13965	T	C	0	505	synonymous_variant	LOW	ND5	0.005
HLI-0883	13966	A	G	0	508	missense_variant	MODERATE	ND5	0.0126
HLI-0883	14233	A	G	0	521	synonymous_variant	LOW	ND6	0.0369
HLI-0883	14687	A	G	2	544	upstream_gene_variant	MODIFIER	TRNE	0.0059
HLI-0883	14766	C	T	1	569	missense_variant	MODERATE	CYTB	0.7696
HLI-0883	14905	G	A	1	573	synonymous_variant	LOW	CYTB	0.0526
HLI-0883	15326	A	G	1	515	missense_variant	MODERATE	CYTB	0.9868
HLI-0883	15452	C	A	3	552	missense_variant	MODERATE	CYTB	0.0933
HLI-0883	15607	A	G	0	568	synonymous_variant	LOW	CYTB	0.0508
HLI-0883	15772	A	G	6	571	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0883	15928	G	A	0	554	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0883	16126	T	C	3	559	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0883	16294	C	T	0	539	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0883	16296	C	T	0	541	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0883	16324	T	C	2	561	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0883	16519	T	C	0	265	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0884	6866	T	C	4	548	synonymous_variant	LOW	COX1	1.00E-04
HLI-0884	9506	C	T	1	482	synonymous_variant	LOW	COX3	0
HLI-0884	15383	T	C	2	424	missense_variant	MODERATE	CYTB	4.00E-04
HLI-0885	73	A	G	0	265	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0885	146	T	C	0	482	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0885	152	T	C	0	486	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0885	263	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.9513

HLI-0885	750	A	G	0	539	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0885	1189	T	C	0	586	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0885	1438	A	G	0	575	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0885	1811	A	G	1	528	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0885	2706	A	G	1	511	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0885	3480	A	G	3	561	synonymous_variant	LOW	ND1	0.0392
HLI-0885	4769	A	G	2	503	synonymous_variant	LOW	ND2	0.9767
HLI-0885	7028	C	T	3	613	synonymous_variant	LOW	COX1	0.8089
HLI-0885	9006	A	G	0	572	synonymous_variant	LOW	ATP6	0.0014
HLI-0885	9055	G	A	0	610	missense_variant	MODERATE	ATP6	0.0425
HLI-0885	9698	T	C	1	507	synonymous_variant	LOW	COX3	0.0405
HLI-0885	10398	A	G	0	515	missense_variant	MODERATE	ND3	0.445
HLI-0885	10550	A	G	2	574	synonymous_variant	LOW	ND4L	0.0376
HLI-0885	11299	T	C	2	512	synonymous_variant	LOW	ND4	0.0417
HLI-0885	11467	A	G	0	555	synonymous_variant	LOW	ND4	0.1231
HLI-0885	11719	G	A	0	533	synonymous_variant	LOW	ND4	0.7756
HLI-0885	12308	A	G	2	471	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0885	12372	G	A	0	456	synonymous_variant	LOW	ND5	0.1329
HLI-0885	14002	A	G	0	452	missense_variant	MODERATE	ND5	0.0025
HLI-0885	14040	G	A	0	486	synonymous_variant	LOW	ND5	0.0047
HLI-0885	14167	C	T	2	492	synonymous_variant	LOW	ND6	0.0385
HLI-0885	14766	C	T	5	518	missense_variant	MODERATE	CYTB	0.7696
HLI-0885	14798	T	C	1	570	missense_variant	MODERATE	CYTB	0.0651
HLI-0885	15326	A	G	0	464	missense_variant	MODERATE	CYTB	0.9868
HLI-0885	16224	T	C	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0885	16311	T	C	0	403	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0885	16320	C	T	0	398	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0885	16519	T	C	0	226	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0886	73	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0886	263	A	G	0	188	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0886	750	A	G	0	517	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0886	1116	A	G	1	553	upstream_gene_variant	MODIFIER	RNR1	2.00E-04
HLI-0886	1438	A	G	0	549	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0886	3010	G	A	1	521	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0886	4769	A	G	0	459	synonymous_variant	LOW	ND2	0.9767
HLI-0886	6365	T	C	3	564	synonymous_variant	LOW	COX1	0.0026
HLI-0886	7961	T	C	1	554	synonymous_variant	LOW	COX2	0.0044
HLI-0886	15326	A	G	0	425	missense_variant	MODERATE	CYTB	0.9868
HLI-0886	16162	A	G	1	529	upstream_gene_variant	MODIFIER	DLoop	0.0176

HLI-0886	16209	T	C	2	548	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0886	16519	T	C	0	278	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0887	73	A	G	4	275	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0887	263	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0887	750	A	G	1	585	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0887	1438	A	G	0	640	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0887	2706	A	G	9	585	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0887	3420	C	T	23	601	synonymous_variant	LOW	ND1	4.00E-04
HLI-0887	3450	C	T	20	628	synonymous_variant	LOW	ND1	0.0084
HLI-0887	4769	A	G	1	562	synonymous_variant	LOW	ND2	0.9767
HLI-0887	5773	G	A	15	654	upstream_gene_variant	MODIFIER	TRNC	0.0143
HLI-0887	6221	T	C	8	564	synonymous_variant	LOW	COX1	0.0306
HLI-0887	7028	C	T	11	669	synonymous_variant	LOW	COX1	0.8089
HLI-0887	8701	A	G	22	605	missense_variant	MODERATE	ATP6	0.3391
HLI-0887	9053	G	A	8	609	missense_variant	MODERATE	ATP6	0.0196
HLI-0887	9067	A	G	8	670	missense_variant	MODERATE	ATP6	7.00E-04
HLI-0887	9449	C	T	17	640	synonymous_variant	LOW	COX3	0.0125
HLI-0887	9540	T	C	14	506	synonymous_variant	LOW	COX3	0.339
HLI-0887	10086	A	G	14	583	missense_variant	MODERATE	ND3	0.0088
HLI-0887	10398	A	G	19	619	missense_variant	MODERATE	ND3	0.445
HLI-0887	10640	T	C	25	588	synonymous_variant	LOW	ND4L	0.0044
HLI-0887	10873	T	C	21	492	synonymous_variant	LOW	ND4	0.3389
HLI-0887	11719	G	A	11	541	synonymous_variant	LOW	ND4	0.7756
HLI-0887	12705	C	T	17	515	synonymous_variant	LOW	ND5	0.4212
HLI-0887	13105	A	G	10	563	missense_variant	MODERATE	ND5	0.076
HLI-0887	13914	C	A	17	476	synonymous_variant	LOW	ND5	0.0091
HLI-0887	14766	C	T	15	574	missense_variant	MODERATE	CYTB	0.7696
HLI-0887	15301	G	A	13	499	synonymous_variant	LOW	CYTB	0.2912
HLI-0887	15311	A	G	16	537	missense_variant	MODERATE	CYTB	0.008
HLI-0887	15326	A	G	0	533	missense_variant	MODERATE	CYTB	0.9868
HLI-0887	15550	C	T	14	448	synonymous_variant	LOW	CYTB	0.0032
HLI-0887	15824	A	G	15	520	missense_variant	MODERATE	CYTB	0.0083
HLI-0887	16124	T	C	17	561	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0887	16223	C	T	19	575	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0887	16278	C	T	16	559	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0887	16362	T	C	14	479	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0887	16527	C	T	1	260	upstream_gene_variant	MODIFIER	DLoop	0.0113
HLI-0888	73	A	G	0	252	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0888	185	G	A	8	449	upstream_gene_variant	MODIFIER	DLoop	0.0397

HLI-0888	228	G	A	0	237	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0888	263	A	G	2	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0888	295	C	T	0	220	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0888	462	C	T	1	373	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0888	489	T	C	0	429	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0888	750	A	G	0	504	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0888	1438	A	G	0	507	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0888	2706	A	G	0	513	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0888	3010	G	A	2	482	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0888	4216	T	C	1	444	missense_variant	MODERATE	ND1	0.0991
HLI-0888	4769	A	G	1	478	synonymous_variant	LOW	ND2	0.9767
HLI-0888	7028	C	T	0	564	synonymous_variant	LOW	COX1	0.8089
HLI-0888	10345	T	C	1	539	missense_variant	MODERATE	ND3	0.0016
HLI-0888	11251	A	G	0	505	synonymous_variant	LOW	ND4	0.0932
HLI-0888	11719	G	A	0	453	synonymous_variant	LOW	ND4	0.7756
HLI-0888	12612	A	G	1	510	synonymous_variant	LOW	ND5	0.0506
HLI-0888	13708	G	A	0	403	missense_variant	MODERATE	ND5	0.0717
HLI-0888	14180	T	C	1	492	missense_variant	MODERATE	ND6	0.0036
HLI-0888	14766	C	T	1	540	missense_variant	MODERATE	CYTB	0.7696
HLI-0888	14798	T	C	0	628	missense_variant	MODERATE	CYTB	0.0651
HLI-0888	15326	A	G	0	409	missense_variant	MODERATE	CYTB	0.9868
HLI-0888	15452	C	A	1	387	missense_variant	MODERATE	CYTB	0.0933
HLI-0888	16069	C	T	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0888	16126	T	C	0	498	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0888	16294	C	T	0	355	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0889	73	A	G	0	273	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0889	150	C	T	0	516	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0889	152	T	C	0	513	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0889	263	A	G	1	232	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0889	750	A	G	0	592	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0889	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0889	1721	C	T	2	548	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0889	2706	A	G	0	523	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0889	3197	T	C	0	595	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0889	3344	T	C	98	429	missense_variant	MODERATE	ND1	0
HLI-0889	4732	A	G	3	558	missense_variant	MODERATE	ND2	0.0059
HLI-0889	4769	A	G	3	611	synonymous_variant	LOW	ND2	0.9767
HLI-0889	5918	T	C	0	612	synonymous_variant	LOW	COX1	7.00E-04
HLI-0889	6158	A	G	0	545	synonymous_variant	LOW	COX1	1.00E-04

HLI-0889	7028	C	T	1	613	synonymous_variant	LOW	COX1	0.8089
HLI-0889	7768	A	G	2	487	synonymous_variant	LOW	COX2	0.0186
HLI-0889	9477	G	A	0	486	missense_variant	MODERATE	COX3	0.0387
HLI-0889	11467	A	G	0	612	synonymous_variant	LOW	ND4	0.1231
HLI-0889	11719	G	A	0	547	synonymous_variant	LOW	ND4	0.7756
HLI-0889	12308	A	G	2	531	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0889	12372	G	A	2	498	synonymous_variant	LOW	ND5	0.1329
HLI-0889	13617	T	C	0	514	synonymous_variant	LOW	ND5	0.038
HLI-0889	13637	A	G	0	541	missense_variant	MODERATE	ND5	0.0074
HLI-0889	14182	T	C	1	517	synonymous_variant	LOW	ND6	0.0254
HLI-0889	14323	G	A	1	499	synonymous_variant	LOW	ND6	0.0058
HLI-0889	14766	C	T	1	509	missense_variant	MODERATE	CYTB	0.7696
HLI-0889	15326	A	G	0	448	missense_variant	MODERATE	CYTB	0.9868
HLI-0889	16325	T	C	0	425	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0890	73	A	G	0	272	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0890	263	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0890	709	G	A	0	520	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0890	750	A	G	0	557	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0890	1438	A	G	0	567	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0890	2706	A	G	0	505	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0890	3197	T	C	0	558	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0890	4769	A	G	0	517	synonymous_variant	LOW	ND2	0.9767
HLI-0890	7028	C	T	6	598	synonymous_variant	LOW	COX1	0.8089
HLI-0890	9477	G	A	1	545	missense_variant	MODERATE	COX3	0.0387
HLI-0890	9667	A	G	0	442	missense_variant	MODERATE	COX3	0.0055
HLI-0890	11353	T	C	0	493	synonymous_variant	LOW	ND4	0.0029
HLI-0890	11467	A	G	0	531	synonymous_variant	LOW	ND4	0.1231
HLI-0890	11719	G	A	2	504	synonymous_variant	LOW	ND4	0.7756
HLI-0890	12308	A	G	0	516	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0890	12372	G	A	2	477	synonymous_variant	LOW	ND5	0.1329
HLI-0890	13617	T	C	1	499	synonymous_variant	LOW	ND5	0.038
HLI-0890	14766	C	T	2	557	missense_variant	MODERATE	CYTB	0.7696
HLI-0890	14793	A	G	0	654	missense_variant	MODERATE	CYTB	0.0199
HLI-0890	15218	A	G	1	472	missense_variant	MODERATE	CYTB	0.0169
HLI-0890	15326	A	G	0	408	missense_variant	MODERATE	CYTB	0.9868
HLI-0890	16256	C	T	0	552	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0890	16270	C	T	0	516	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0890	16291	C	T	0	489	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0890	16399	A	G	0	419	upstream_gene_variant	MODIFIER	DLoop	0.0265

HLI-0891	73	A	G	0	27	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0891	195	T	C	0	47	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0891	263	A	G	0	20	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0891	499	G	A	1	20	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0891	750	A	G	0	53	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0891	1438	A	G	0	46	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0891	1811	A	G	0	50	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0891	2706	A	G	0	29	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0891	4646	T	C	0	43	synonymous_variant	LOW	ND2	0.0124
HLI-0891	4769	A	G	0	44	synonymous_variant	LOW	ND2	0.9767
HLI-0891	5999	T	C	0	54	synonymous_variant	LOW	COX1	0.0127
HLI-0891	6047	A	G	0	58	synonymous_variant	LOW	COX1	0.0114
HLI-0891	7028	C	T	0	61	synonymous_variant	LOW	COX1	0.8089
HLI-0891	8818	C	T	0	44	synonymous_variant	LOW	ATP6	0.0061
HLI-0891	11332	C	T	0	43	synonymous_variant	LOW	ND4	0.0115
HLI-0891	11467	A	G	0	52	synonymous_variant	LOW	ND4	0.1231
HLI-0891	11719	G	A	0	37	synonymous_variant	LOW	ND4	0.7756
HLI-0891	12308	A	G	0	57	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0891	12372	G	A	0	50	synonymous_variant	LOW	ND5	0.1329
HLI-0891	13533	A	T	0	58	synonymous_variant	LOW	ND5	0
HLI-0891	14620	C	T	1	55	synonymous_variant	LOW	ND6	0.0126
HLI-0891	14766	C	T	0	41	missense_variant	MODERATE	CYTB	0.7696
HLI-0891	15326	A	G	0	59	missense_variant	MODERATE	CYTB	0.9868
HLI-0891	15693	T	C	0	54	missense_variant	MODERATE	CYTB	0.0114
HLI-0891	16311	T	C	0	54	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0891	16356	T	C	0	55	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0891	16519	T	C	0	29	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0892	263	A	G	0	207	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0892	750	A	G	0	568	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0892	1438	A	G	0	578	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0892	3010	G	A	1	579	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0892	4769	A	G	1	573	synonymous_variant	LOW	ND2	0.9767
HLI-0892	5460	G	A	2	598	missense_variant	MODERATE	ND2	0.0651
HLI-0892	6815	T	C	3	616	synonymous_variant	LOW	COX1	0.0157
HLI-0892	8895	T	C	1	592	synonymous_variant	LOW	ATP6	4.00E-04
HLI-0892	10463	T	C	1	533	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0892	15326	A	G	1	500	missense_variant	MODERATE	CYTB	0.9868
HLI-0892	15817	A	G	3	572	synonymous_variant	LOW	CYTB	9.00E-04
HLI-0892	16212	A	G	2	614	upstream_gene_variant	MODIFIER	DLoop	0.0034

HLI-0892	16261	C	T	2	611	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0892	16519	T	C	0	328	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0893	73	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0893	146	T	C	0	395	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0893	152	T	C	0	407	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0893	189	A	G	1	387	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0893	195	T	C	1	387	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0893	200	A	G	1	385	upstream_gene_variant	MODIFIER	DLoop	0.0308
HLI-0893	263	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0893	750	A	G	1	553	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0893	769	G	A	1	603	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0893	1018	G	A	1	626	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0893	1438	A	G	0	530	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0893	2416	T	C	1	402	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0893	2706	A	G	0	546	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0893	2789	C	T	2	511	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0893	3594	C	T	1	415	synonymous_variant	LOW	ND1	0.0789
HLI-0893	3918	G	A	1	525	synonymous_variant	LOW	ND1	0.009
HLI-0893	4104	A	G	1	419	synonymous_variant	LOW	ND1	0.0785
HLI-0893	4769	A	G	0	547	synonymous_variant	LOW	ND2	0.9767
HLI-0893	5285	A	G	0	479	synonymous_variant	LOW	ND2	0.0049
HLI-0893	7028	C	T	2	597	synonymous_variant	LOW	COX1	0.8089
HLI-0893	7175	T	C	0	531	synonymous_variant	LOW	COX1	0.0224
HLI-0893	7256	C	T	0	583	synonymous_variant	LOW	COX1	0.0784
HLI-0893	7274	C	T	0	557	synonymous_variant	LOW	COX1	0.0214
HLI-0893	7521	G	A	1	423	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0893	7771	A	G	1	544	synonymous_variant	LOW	COX2	0.0223
HLI-0893	8206	G	A	1	493	synonymous_variant	LOW	COX2	0.0287
HLI-0893	8701	A	G	1	543	missense_variant	MODERATE	ATP6	0.3391
HLI-0893	9221	A	G	0	557	synonymous_variant	LOW	COX3	0.0277
HLI-0893	9540	T	C	0	402	synonymous_variant	LOW	COX3	0.339
HLI-0893	10115	T	C	0	605	synonymous_variant	LOW	ND3	0.0278
HLI-0893	10398	A	G	0	536	missense_variant	MODERATE	ND3	0.445
HLI-0893	10873	T	C	0	475	synonymous_variant	LOW	ND4	0.3389
HLI-0893	11719	G	A	1	546	synonymous_variant	LOW	ND4	0.7756
HLI-0893	11914	G	A	0	613	synonymous_variant	LOW	ND4	0.1112
HLI-0893	11944	T	C	2	610	synonymous_variant	LOW	ND4	0.0331
HLI-0893	12693	A	G	1	559	synonymous_variant	LOW	ND5	0.0205
HLI-0893	12705	C	T	1	566	synonymous_variant	LOW	ND5	0.4212

HLI-0893	13590	G	A	0	473	synonymous_variant	LOW	ND5	0.0586
HLI-0893	13650	C	T	1	487	synonymous_variant	LOW	ND5	0.079
HLI-0893	13803	A	G	2	355	synonymous_variant	LOW	ND5	0.0216
HLI-0893	14566	A	G	1	591	synonymous_variant	LOW	ND6	0.0214
HLI-0893	14766	C	T	1	574	missense_variant	MODERATE	CYTB	0.7696
HLI-0893	15244	A	G	1	430	synonymous_variant	LOW	CYTB	0.0103
HLI-0893	15301	G	A	1	422	synonymous_variant	LOW	CYTB	0.2912
HLI-0893	15326	A	G	0	408	missense_variant	MODERATE	CYTB	0.9868
HLI-0893	15629	T	C	0	418	synonymous_variant	LOW	CYTB	0.0062
HLI-0893	15784	T	C	0	388	synonymous_variant	LOW	CYTB	0.0363
HLI-0893	16223	C	T	1	479	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0893	16278	C	T	1	487	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0893	16286	C	T	1	459	upstream_gene_variant	MODIFIER	DLoop	0.0052
HLI-0893	16294	C	T	1	451	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0893	16309	A	G	1	440	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0893	16390	G	A	0	415	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0893	16519	T	C	1	190	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0894	73	A	G	0	301	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0894	150	C	T	2	550	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0894	189	A	G	1	538	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0894	263	A	G	1	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0894	750	A	G	0	645	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0894	1438	A	G	1	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0894	2352	T	C	0	534	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0894	2706	A	G	1	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0894	4769	A	G	0	580	synonymous_variant	LOW	ND2	0.9767
HLI-0894	6221	T	C	0	593	synonymous_variant	LOW	COX1	0.0306
HLI-0894	6587	C	T	1	644	synonymous_variant	LOW	COX1	0.0084
HLI-0894	7028	C	T	2	660	synonymous_variant	LOW	COX1	0.8089
HLI-0894	8701	A	G	0	526	missense_variant	MODERATE	ATP6	0.3391
HLI-0894	9540	T	C	1	623	synonymous_variant	LOW	COX3	0.339
HLI-0894	10370	T	C	0	642	synonymous_variant	LOW	ND3	0.0019
HLI-0894	10398	A	G	1	681	missense_variant	MODERATE	ND3	0.445
HLI-0894	10819	A	G	2	604	synonymous_variant	LOW	ND4	0.0228
HLI-0894	10873	T	C	2	632	synonymous_variant	LOW	ND4	0.3389
HLI-0894	11719	G	A	0	632	synonymous_variant	LOW	ND4	0.7756
HLI-0894	12705	C	T	2	611	synonymous_variant	LOW	ND5	0.4212
HLI-0894	14152	A	G	1	518	synonymous_variant	LOW	ND6	0.0086
HLI-0894	14212	T	C	1	633	synonymous_variant	LOW	ND6	0.0204

HLI-0894	14766	C	T	1	627	missense_variant	MODERATE	CYTB	0.7696
HLI-0894	15301	G	A	0	516	synonymous_variant	LOW	CYTB	0.2912
HLI-0894	15326	A	G	0	553	missense_variant	MODERATE	CYTB	0.9868
HLI-0894	15670	T	C	0	538	synonymous_variant	LOW	CYTB	0.0176
HLI-0894	15942	T	C	0	589	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0894	16179	C	T	4	624	upstream_gene_variant	MODIFIER	DLoop	0.0082
HLI-0894	16223	C	T	1	605	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0894	16327	C	T	0	514	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0894	16519	T	C	2	309	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0895	263	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0895	750	A	G	1	559	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0895	1438	A	G	1	577	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0895	4769	A	G	0	547	synonymous_variant	LOW	ND2	0.9767
HLI-0895	4793	A	G	0	618	synonymous_variant	LOW	ND2	0.0073
HLI-0895	15326	A	G	0	371	missense_variant	MODERATE	CYTB	0.9868
HLI-0895	16519	T	C	0	240	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0896	73	A	G	0	303	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0896	152	T	C	1	534	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0896	217	T	C	1	293	upstream_gene_variant	MODIFIER	DLoop	0.0083
HLI-0896	263	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0896	508	A	G	0	450	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0896	750	A	G	1	627	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0896	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0896	1811	A	G	4	671	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0896	2706	A	G	0	599	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0896	3720	A	G	0	555	synonymous_variant	LOW	ND1	0.0069
HLI-0896	3849	G	A	0	572	synonymous_variant	LOW	ND1	0.0035
HLI-0896	4553	T	C	3	618	synonymous_variant	LOW	ND2	0.0023
HLI-0896	4769	A	G	0	624	synonymous_variant	LOW	ND2	0.9767
HLI-0896	5390	A	G	0	642	synonymous_variant	LOW	ND2	0.0069
HLI-0896	5426	T	C	0	684	synonymous_variant	LOW	ND2	0.0091
HLI-0896	5894	A	G	1	682	upstream_gene_variant	MODIFIER	Unannotated	0.0034
HLI-0896	6045	C	T	1	739	synonymous_variant	LOW	COX1	0.0065
HLI-0896	6152	T	C	3	618	synonymous_variant	LOW	COX1	0.0077
HLI-0896	7028	C	T	5	680	synonymous_variant	LOW	COX1	0.8089
HLI-0896	8473	T	C	0	427	synonymous_variant	LOW	ATP8	0.0105
HLI-0896	10876	A	G	0	602	synonymous_variant	LOW	ND4	0.0098
HLI-0896	11467	A	G	0	642	synonymous_variant	LOW	ND4	0.1231
HLI-0896	11719	G	A	1	604	synonymous_variant	LOW	ND4	0.7756

HLI-0896	12308	A	G	1	572	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0896	12372	G	A	3	631	synonymous_variant	LOW	ND5	0.1329
HLI-0896	12557	C	T	7	578	missense_variant	MODERATE	ND5	0.0028
HLI-0896	13020	T	C	8	680	synonymous_variant	LOW	ND5	0.0106
HLI-0896	13734	T	C	1	546	synonymous_variant	LOW	ND5	0.0067
HLI-0896	14766	C	T	1	582	missense_variant	MODERATE	CYTB	0.7696
HLI-0896	15326	A	G	0	521	missense_variant	MODERATE	CYTB	0.9868
HLI-0896	15907	A	G	0	646	upstream_gene_variant	MODIFIER	TRNT	0.0066
HLI-0896	16051	A	G	0	626	upstream_gene_variant	MODIFIER	DLoop	0.0252
HLI-0896	16129	G	C	1	393	upstream_gene_variant	MODIFIER	DLoop	0.0063
HLI-0896	16362	T	C	0	500	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0896	16519	T	C	1	262	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0897	73	A	G	0	309	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0897	146	T	C	0	578	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0897	263	A	G	0	248	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0897	458	C	T	3	600	upstream_gene_variant	MODIFIER	DLoop	6.00E-04
HLI-0897	709	G	A	0	655	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0897	750	A	G	0	700	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0897	930	G	A	2	666	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0897	1438	A	G	0	633	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0897	1709	G	A	2	619	upstream_gene_variant	MODIFIER	RNR2	0.0035
HLI-0897	1888	G	A	2	644	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0897	2706	A	G	0	644	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0897	4216	T	C	1	594	missense_variant	MODERATE	ND1	0.0991
HLI-0897	4769	A	G	2	591	synonymous_variant	LOW	ND2	0.9767
HLI-0897	4917	A	G	2	607	missense_variant	MODERATE	ND2	0.0477
HLI-0897	5147	G	A	4	593	synonymous_variant	LOW	ND2	0.0437
HLI-0897	7028	C	T	1	632	synonymous_variant	LOW	COX1	0.8089
HLI-0897	8697	G	A	0	558	synonymous_variant	LOW	ATP6	0.0466
HLI-0897	9300	G	A	1	639	missense_variant	MODERATE	COX3	0.0036
HLI-0897	10463	T	C	1	632	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0897	11251	A	G	0	638	synonymous_variant	LOW	ND4	0.0932
HLI-0897	11533	C	T	3	739	synonymous_variant	LOW	ND4	4.00E-04
HLI-0897	11719	G	A	1	633	synonymous_variant	LOW	ND4	0.7756
HLI-0897	11812	A	G	3	610	synonymous_variant	LOW	ND4	0.0332
HLI-0897	12007	G	A	2	566	synonymous_variant	LOW	ND4	0.0639
HLI-0897	13368	G	A	0	607	synonymous_variant	LOW	ND5	0.0495
HLI-0897	14233	A	G	1	584	synonymous_variant	LOW	ND6	0.0369
HLI-0897	14766	C	T	2	550	missense_variant	MODERATE	CYTB	0.7696

HLI-0897	14905	G	A	2	683	synonymous_variant	LOW	CYTB	0.0526
HLI-0897	15326	A	G	0	587	missense_variant	MODERATE	CYTB	0.9868
HLI-0897	15452	C	A	0	582	missense_variant	MODERATE	CYTB	0.0933
HLI-0897	15607	A	G	0	549	synonymous_variant	LOW	CYTB	0.0508
HLI-0897	15928	G	A	0	592	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0897	16126	T	C	0	607	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0897	16294	C	T	2	554	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0897	16296	C	T	2	560	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0897	16304	T	C	2	595	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0897	16519	T	C	0	308	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0898	263	A	G	0	267	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0898	750	A	G	0	668	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0898	1438	A	G	0	693	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0898	3010	G	A	1	686	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0898	3796	A	G	0	564	missense_variant	MODERATE	ND1	0.0048
HLI-0898	4769	A	G	2	619	synonymous_variant	LOW	ND2	0.9767
HLI-0898	14178	T	C	1	701	missense_variant	MODERATE	ND6	0.0225
HLI-0898	15326	A	G	0	620	missense_variant	MODERATE	CYTB	0.9868
HLI-0898	16356	T	C	0	529	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0898	16362	T	C	0	552	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0898	16519	T	C	0	291	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0899	263	A	G	1	300	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0899	750	A	G	0	557	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0899	1438	A	G	0	674	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0899	3010	G	A	29	550	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0899	4452	T	C	29	624	upstream_gene_variant	MODIFIER	TRNM	0.002
HLI-0899	4769	A	G	1	586	synonymous_variant	LOW	ND2	0.9767
HLI-0899	9066	A	G	31	507	synonymous_variant	LOW	ATP6	0.0012
HLI-0899	15326	A	G	0	526	missense_variant	MODERATE	CYTB	0.9868
HLI-0899	16519	T	C	1	237	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0900	263	A	G	0	244	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0900	750	A	G	2	666	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0900	1438	A	G	1	682	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0900	2259	C	T	0	601	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0900	4745	A	G	1	687	synonymous_variant	LOW	ND2	0.0039
HLI-0900	4769	A	G	2	681	synonymous_variant	LOW	ND2	0.9767
HLI-0900	7337	G	A	1	632	synonymous_variant	LOW	COX1	0.0119
HLI-0900	7830	G	A	4	695	missense_variant	MODERATE	COX2	9.00E-04
HLI-0900	13326	T	C	1	599	synonymous_variant	LOW	ND5	0.0032

HLI-0900	13680	C	T	2	549	synonymous_variant	LOW	ND5	0.005
HLI-0900	14872	C	T	5	659	synonymous_variant	LOW	CYTB	0.0061
HLI-0900	15326	A	G	0	617	missense_variant	MODERATE	CYTB	0.9868
HLI-0901	73	A	G	0	355	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0901	150	C	T	0	620	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0901	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0901	750	A	G	1	673	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0901	1438	A	G	0	692	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0901	1811	A	G	1	660	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0901	2294	A	G	0	609	upstream_gene_variant	MODIFIER	RNR2	0.0027
HLI-0901	2706	A	G	0	601	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0901	3010	G	A	0	622	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0901	4703	T	C	0	617	synonymous_variant	LOW	ND2	0.0058
HLI-0901	4769	A	G	2	625	synonymous_variant	LOW	ND2	0.9767
HLI-0901	6518	C	T	0	647	synonymous_variant	LOW	COX1	0.0025
HLI-0901	7028	C	T	4	653	synonymous_variant	LOW	COX1	0.8089
HLI-0901	7521	G	A	1	608	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0901	9266	G	A	0	577	synonymous_variant	LOW	COX3	0.0049
HLI-0901	10506	A	G	0	639	missense_variant	MODERATE	ND4L	0.0025
HLI-0901	11467	A	G	1	608	synonymous_variant	LOW	ND4	0.1231
HLI-0901	11719	G	A	0	597	synonymous_variant	LOW	ND4	0.7756
HLI-0901	12308	A	G	0	592	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0901	12372	G	A	0	628	synonymous_variant	LOW	ND5	0.1329
HLI-0901	13785	C	T	1	542	synonymous_variant	LOW	ND5	4.00E-04
HLI-0901	13934	C	T	1	499	missense_variant	MODERATE	ND5	0.0122
HLI-0901	14139	A	G	1	560	synonymous_variant	LOW	ND5	0.0056
HLI-0901	14258	G	A	1	495	missense_variant	MODERATE	ND6	5.00E-04
HLI-0901	14766	C	T	1	593	missense_variant	MODERATE	CYTB	0.7696
HLI-0901	15326	A	G	1	548	missense_variant	MODERATE	CYTB	0.9868
HLI-0901	15454	T	C	0	546	synonymous_variant	LOW	CYTB	0.0072
HLI-0901	16343	A	G	1	521	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0901	16390	G	A	0	557	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0901	16519	T	C	2	311	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0902	73	A	G	0	302	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0902	152	T	C	0	507	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0902	195	T	C	0	486	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0902	263	A	G	0	204	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0902	709	G	A	3	672	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0902	750	A	G	0	717	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0902	1438	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0902	1888	G	A	0	626	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0902	2706	A	G	0	597	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0902	4216	T	C	0	628	missense_variant	MODERATE	ND1	0.0991
HLI-0902	4769	A	G	1	651	synonymous_variant	LOW	ND2	0.9767
HLI-0902	4917	A	G	0	570	missense_variant	MODERATE	ND2	0.0477
HLI-0902	7028	C	T	2	669	synonymous_variant	LOW	COX1	0.8089
HLI-0902	8697	G	A	0	625	synonymous_variant	LOW	ATP6	0.0466
HLI-0902	9899	T	C	1	610	synonymous_variant	LOW	COX3	0.0108
HLI-0902	10463	T	C	1	680	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0902	11251	A	G	1	617	synonymous_variant	LOW	ND4	0.0932
HLI-0902	11719	G	A	0	609	synonymous_variant	LOW	ND4	0.7756
HLI-0902	12633	C	A	5	638	synonymous_variant	LOW	ND5	0.0123
HLI-0902	13368	G	A	1	665	synonymous_variant	LOW	ND5	0.0495
HLI-0902	14766	C	T	0	636	missense_variant	MODERATE	CYTB	0.7696
HLI-0902	14905	G	A	0	656	synonymous_variant	LOW	CYTB	0.0526
HLI-0902	15326	A	G	0	590	missense_variant	MODERATE	CYTB	0.9868
HLI-0902	15452	C	A	5	566	missense_variant	MODERATE	CYTB	0.0933
HLI-0902	15607	A	G	0	568	synonymous_variant	LOW	CYTB	0.0508
HLI-0902	15928	G	A	1	623	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0902	16126	T	C	1	588	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0902	16163	A	G	3	619	upstream_gene_variant	MODIFIER	DLoop	0.0136
HLI-0902	16294	C	T	1	542	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0902	16519	T	C	1	303	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0903	73	A	G	0	337	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0903	185	G	A	3	486	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0903	228	G	A	1	357	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0903	263	A	G	1	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0903	295	C	T	0	229	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0903	462	C	T	1	455	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0903	489	T	C	0	567	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0903	750	A	G	0	647	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0903	1438	A	G	0	634	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0903	2706	A	G	1	671	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0903	3010	G	A	0	604	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0903	4216	T	C	0	670	missense_variant	MODERATE	ND1	0.0991
HLI-0903	4769	A	G	0	607	synonymous_variant	LOW	ND2	0.9767
HLI-0903	7028	C	T	4	720	synonymous_variant	LOW	COX1	0.8089
HLI-0903	9755	G	A	2	668	synonymous_variant	LOW	COX3	0.0303

HLI-0903	10398	A	G	0	667	missense_variant	MODERATE	ND3	0.445
HLI-0903	11251	A	G	1	599	synonymous_variant	LOW	ND4	0.0932
HLI-0903	11719	G	A	0	594	synonymous_variant	LOW	ND4	0.7756
HLI-0903	12612	A	G	6	612	synonymous_variant	LOW	ND5	0.0506
HLI-0903	13708	G	A	1	541	missense_variant	MODERATE	ND5	0.0717
HLI-0903	13934	C	T	0	496	missense_variant	MODERATE	ND5	0.0122
HLI-0903	14766	C	T	1	595	missense_variant	MODERATE	CYTB	0.7696
HLI-0903	14798	T	C	0	684	missense_variant	MODERATE	CYTB	0.0651
HLI-0903	15326	A	G	1	590	missense_variant	MODERATE	CYTB	0.9868
HLI-0903	15452	C	A	0	607	missense_variant	MODERATE	CYTB	0.0933
HLI-0903	16069	C	T	3	626	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0903	16126	T	C	3	637	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0904	73	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0904	195	T	C	0	422	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0904	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0904	497	C	T	3	447	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0904	750	A	G	0	590	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0904	1189	T	C	1	561	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0904	1438	A	G	0	594	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0904	1811	A	G	0	591	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0904	2706	A	G	1	611	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0904	3480	A	G	0	513	synonymous_variant	LOW	ND1	0.0392
HLI-0904	4769	A	G	1	547	synonymous_variant	LOW	ND2	0.9767
HLI-0904	7028	C	T	1	649	synonymous_variant	LOW	COX1	0.8089
HLI-0904	9055	G	A	0	549	missense_variant	MODERATE	ATP6	0.0425
HLI-0904	9698	T	C	0	629	synonymous_variant	LOW	COX3	0.0405
HLI-0904	10398	A	G	0	553	missense_variant	MODERATE	ND3	0.445
HLI-0904	10550	A	G	0	617	synonymous_variant	LOW	ND4L	0.0376
HLI-0904	11299	T	C	1	591	synonymous_variant	LOW	ND4	0.0417
HLI-0904	11467	A	G	0	584	synonymous_variant	LOW	ND4	0.1231
HLI-0904	11719	G	A	1	537	synonymous_variant	LOW	ND4	0.7756
HLI-0904	12308	A	G	0	527	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0904	12372	G	A	1	541	synonymous_variant	LOW	ND5	0.1329
HLI-0904	14167	C	T	1	548	synonymous_variant	LOW	ND6	0.0385
HLI-0904	14766	C	T	5	587	missense_variant	MODERATE	CYTB	0.7696
HLI-0904	14798	T	C	1	647	missense_variant	MODERATE	CYTB	0.0651
HLI-0904	15326	A	G	0	501	missense_variant	MODERATE	CYTB	0.9868
HLI-0904	16093	T	C	4	537	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0904	16224	T	C	1	497	upstream_gene_variant	MODIFIER	DLoop	0.0423

HLI-0904	16311	T	C	2	460	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0904	16519	T	C	0	252	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0904	16524	A	G	0	257	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0906	263	A	G	0	262	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0906	456	C	T	6	563	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0906	750	A	G	0	664	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0906	1438	A	G	1	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0906	4336	T	C	0	592	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0906	4769	A	G	0	579	synonymous_variant	LOW	ND2	0.9767
HLI-0906	5839	C	T	1	706	upstream_gene_variant	MODIFIER	TRNY	0.0011
HLI-0906	15326	A	G	1	560	missense_variant	MODERATE	CYTB	0.9868
HLI-0906	16304	T	C	2	513	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0906	16343	A	G	4	555	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0907	73	A	G	1	322	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0907	183	A	G	1	414	upstream_gene_variant	MODIFIER	DLoop	0.0057
HLI-0907	195	T	C	1	398	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0907	263	A	G	0	163	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0907	499	G	A	2	437	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0907	750	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0907	1438	A	G	0	643	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0907	1811	A	G	0	675	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0907	2706	A	G	0	658	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0907	4646	T	C	5	607	synonymous_variant	LOW	ND2	0.0124
HLI-0907	4769	A	G	1	559	synonymous_variant	LOW	ND2	0.9767
HLI-0907	5437	C	T	3	622	missense_variant	MODERATE	ND2	5.00E-04
HLI-0907	5999	T	C	2	689	synonymous_variant	LOW	COX1	0.0127
HLI-0907	6047	A	G	0	734	synonymous_variant	LOW	COX1	0.0114
HLI-0907	6524	T	C	2	657	synonymous_variant	LOW	COX1	0.0053
HLI-0907	7028	C	T	9	664	synonymous_variant	LOW	COX1	0.8089
HLI-0907	7299	A	G	1	568	missense_variant	MODERATE	COX1	0.0014
HLI-0907	8658	C	T	1	605	synonymous_variant	LOW	ATP6	4.00E-04
HLI-0907	8818	C	T	0	603	synonymous_variant	LOW	ATP6	0.0061
HLI-0907	11332	C	T	1	550	synonymous_variant	LOW	ND4	0.0115
HLI-0907	11467	A	G	0	639	synonymous_variant	LOW	ND4	0.1231
HLI-0907	11719	G	A	1	619	synonymous_variant	LOW	ND4	0.7756
HLI-0907	12308	A	G	1	601	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0907	12372	G	A	0	625	synonymous_variant	LOW	ND5	0.1329
HLI-0907	14161	A	G	1	537	synonymous_variant	LOW	ND6	3.00E-04
HLI-0907	14620	C	T	4	562	synonymous_variant	LOW	ND6	0.0126

HLI-0907	14766	C	T	1	576	missense_variant	MODERATE	CYTB	0.7696
HLI-0907	15326	A	G	0	611	missense_variant	MODERATE	CYTB	0.9868
HLI-0907	15693	T	C	1	634	missense_variant	MODERATE	CYTB	0.0114
HLI-0907	16086	T	C	0	575	upstream_gene_variant	MODIFIER	DLoop	0.0233
HLI-0907	16356	T	C	2	462	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0907	16519	T	C	0	258	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0908	189	A	G	2	415	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0908	195	T	C	2	413	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0908	257	A	G	1	283	upstream_gene_variant	MODIFIER	DLoop	0.0025
HLI-0908	263	A	G	1	273	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0908	477	T	C	1	400	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0908	750	A	G	0	532	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0908	1438	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0908	3010	G	A	2	604	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0908	4769	A	G	1	555	synonymous_variant	LOW	ND2	0.9767
HLI-0908	8473	T	C	1	476	synonymous_variant	LOW	ATP8	0.0105
HLI-0908	15326	A	G	0	469	missense_variant	MODERATE	CYTB	0.9868
HLI-0908	16519	T	C	0	258	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0909	263	A	G	0	142	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0909	750	A	G	0	441	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0909	1438	A	G	0	419	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0909	4688	T	C	3	495	synonymous_variant	LOW	ND2	0.0078
HLI-0909	4769	A	G	1	434	synonymous_variant	LOW	ND2	0.9767
HLI-0909	4793	A	G	1	458	synonymous_variant	LOW	ND2	0.0073
HLI-0909	5348	C	T	0	415	synonymous_variant	LOW	ND2	0.0016
HLI-0909	5911	C	T	4	465	missense_variant	MODERATE	COX1	0.005
HLI-0909	13708	G	A	0	334	missense_variant	MODERATE	ND5	0.0717
HLI-0909	15326	A	G	0	412	missense_variant	MODERATE	CYTB	0.9868
HLI-0909	16266	C	T	2	391	upstream_gene_variant	MODIFIER	DLoop	0.0135
HLI-0909	16519	T	C	0	165	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0910	73	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0910	263	A	G	0	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0910	282	T	C	0	234	upstream_gene_variant	MODIFIER	DLoop	0.0021
HLI-0910	750	A	G	1	633	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0910	827	A	G	0	707	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0910	1438	A	G	0	606	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0910	1700	T	C	1	639	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0910	1811	A	G	1	674	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0910	2706	A	G	0	606	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0910	4769	A	G	1	586	synonymous_variant	LOW	ND2	0.9767
HLI-0910	6392	T	C	1	601	synonymous_variant	LOW	COX1	0.0359
HLI-0910	6455	C	T	2	700	synonymous_variant	LOW	COX1	0.0319
HLI-0910	7028	C	T	7	677	synonymous_variant	LOW	COX1	0.8089
HLI-0910	7055	A	G	7	760	synonymous_variant	LOW	COX1	0.0188
HLI-0910	9365	C	T	1	631	synonymous_variant	LOW	COX3	0.002
HLI-0910	9698	T	C	0	621	synonymous_variant	LOW	COX3	0.0405
HLI-0910	11467	A	G	2	617	synonymous_variant	LOW	ND4	0.1231
HLI-0910	11719	G	A	0	607	synonymous_variant	LOW	ND4	0.7756
HLI-0910	12308	A	G	1	585	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0910	12372	G	A	0	589	synonymous_variant	LOW	ND5	0.1329
HLI-0910	13145	G	A	7	665	missense_variant	MODERATE	ND5	0.0094
HLI-0910	14040	G	A	0	491	synonymous_variant	LOW	ND5	0.0047
HLI-0910	14766	C	T	2	598	missense_variant	MODERATE	CYTB	0.7696
HLI-0910	15326	A	G	1	623	missense_variant	MODERATE	CYTB	0.9868
HLI-0911	73	A	G	0	240	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0911	189	A	G	0	364	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0911	195	T	C	0	368	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0911	204	T	C	0	350	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0911	207	G	A	0	341	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0911	263	A	G	0	261	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0911	709	G	A	1	617	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0911	750	A	G	0	656	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0911	1243	T	C	0	552	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0911	1438	A	G	1	616	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0911	2706	A	G	1	544	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0911	3505	A	G	1	527	missense_variant	MODERATE	ND1	0.0144
HLI-0911	4769	A	G	0	565	synonymous_variant	LOW	ND2	0.9767
HLI-0911	4775	A	G	0	592	synonymous_variant	LOW	ND2	8.00E-04
HLI-0911	5046	G	A	1	569	missense_variant	MODERATE	ND2	0.018
HLI-0911	5460	G	A	0	662	missense_variant	MODERATE	ND2	0.0651
HLI-0911	7028	C	T	3	583	synonymous_variant	LOW	COX1	0.8089
HLI-0911	7864	C	T	1	658	synonymous_variant	LOW	COX2	0.0041
HLI-0911	8251	G	A	0	622	synonymous_variant	LOW	COX2	0.058
HLI-0911	8994	G	A	3	551	synonymous_variant	LOW	ATP6	0.0167
HLI-0911	11674	C	T	2	578	synonymous_variant	LOW	ND4	0.0116
HLI-0911	11719	G	A	0	662	synonymous_variant	LOW	ND4	0.7756
HLI-0911	11947	A	G	1	567	synonymous_variant	LOW	ND4	0.011
HLI-0911	12414	T	C	8	524	synonymous_variant	LOW	ND5	0.0139

HLI-0911	12705	C	T	1	618	synonymous_variant	LOW	ND5	0.4212
HLI-0911	13746	C	T	0	443	synonymous_variant	LOW	ND5	2.00E-04
HLI-0911	14766	C	T	2	564	missense_variant	MODERATE	CYTB	0.7696
HLI-0911	15326	A	G	0	561	missense_variant	MODERATE	CYTB	0.9868
HLI-0911	15884	G	C	1	598	missense_variant	MODERATE	CYTB	0.011
HLI-0911	16223	C	T	1	554	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0911	16292	C	T	0	548	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0911	16295	C	T	0	546	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0911	16519	T	C	0	253	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0912	93	A	G	1	358	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0912	263	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0912	750	A	G	1	610	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0912	1438	A	G	2	624	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0912	4769	A	G	0	558	synonymous_variant	LOW	ND2	0.9767
HLI-0912	6776	T	C	3	678	synonymous_variant	LOW	COX1	0.0226
HLI-0912	8718	A	G	0	555	synonymous_variant	LOW	ATP6	0.0025
HLI-0912	15326	A	G	0	588	missense_variant	MODERATE	CYTB	0.9868
HLI-0912	15859	A	G	3	611	synonymous_variant	LOW	CYTB	1.00E-04
HLI-0912	16129	G	A	0	538	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0912	16519	T	C	0	262	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0913	72	T	C	2	307	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0913	240	A	G	3	268	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0913	263	A	G	0	225	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0913	750	A	G	0	665	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0913	1438	A	G	0	663	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0913	2706	A	G	11	669	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0913	4580	G	A	3	579	synonymous_variant	LOW	ND2	0.0169
HLI-0913	4769	A	G	1	557	synonymous_variant	LOW	ND2	0.9767
HLI-0913	7028	C	T	11	652	synonymous_variant	LOW	COX1	0.8089
HLI-0913	9254	A	G	7	552	synonymous_variant	LOW	COX3	0.0083
HLI-0913	9368	A	G	16	655	synonymous_variant	LOW	COX3	8.00E-04
HLI-0913	14221	T	C	9	507	synonymous_variant	LOW	ND6	0.0027
HLI-0913	15326	A	G	1	597	missense_variant	MODERATE	CYTB	0.9868
HLI-0913	15904	C	T	7	685	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0913	16298	T	C	4	551	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0913	16519	T	C	0	303	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0914	73	A	G	7	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0914	185	G	A	25	461	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0914	188	A	G	26	451	upstream_gene_variant	MODIFIER	DLoop	0.0106

HLI-0914	228	G	A	20	384	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0914	263	A	G	0	125	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0914	295	C	T	7	169	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0914	462	C	T	18	403	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0914	489	T	C	18	470	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0914	750	A	G	1	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0914	1438	A	G	0	587	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0914	2706	A	G	11	572	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0914	3010	G	A	19	561	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0914	4216	T	C	19	501	missense_variant	MODERATE	ND1	0.0991
HLI-0914	4454	T	C	20	583	upstream_gene_variant	MODIFIER	TRNM	0.0043
HLI-0914	4769	A	G	3	529	synonymous_variant	LOW	ND2	0.9767
HLI-0914	7028	C	T	10	645	synonymous_variant	LOW	COX1	0.8089
HLI-0914	8853	A	G	27	580	synonymous_variant	LOW	ATP6	0.0026
HLI-0914	10398	A	G	30	508	missense_variant	MODERATE	ND3	0.445
HLI-0914	11251	A	G	19	545	synonymous_variant	LOW	ND4	0.0932
HLI-0914	11719	G	A	9	558	synonymous_variant	LOW	ND4	0.7756
HLI-0914	12612	A	G	27	515	synonymous_variant	LOW	ND5	0.0506
HLI-0914	13506	C	T	17	493	synonymous_variant	LOW	ND5	0.0506
HLI-0914	13708	G	A	13	526	missense_variant	MODERATE	ND5	0.0717
HLI-0914	14470	T	C	22	503	synonymous_variant	LOW	ND6	0.0166
HLI-0914	14766	C	T	17	573	missense_variant	MODERATE	CYTB	0.7696
HLI-0914	14798	T	C	22	577	missense_variant	MODERATE	CYTB	0.0651
HLI-0914	15326	A	G	0	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0914	15452	C	A	19	484	missense_variant	MODERATE	CYTB	0.0933
HLI-0914	16069	C	T	18	503	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0914	16126	T	C	13	542	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0914	16519	T	C	6	280	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0915	73	A	G	0	263	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0915	150	C	T	1	466	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0915	199	T	C	0	416	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0915	263	A	G	0	163	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0915	497	C	T	5	497	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0915	750	A	G	1	609	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0915	1189	T	C	1	581	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0915	1438	A	G	0	580	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0915	1811	A	G	0	608	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0915	2706	A	G	1	578	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0915	3480	A	G	0	403	synonymous_variant	LOW	ND1	0.0392

HLI-0915	4769	A	G	1	570	synonymous_variant	LOW	ND2	0.9767
HLI-0915	7028	C	T	1	657	synonymous_variant	LOW	COX1	0.8089
HLI-0915	9055	G	A	1	513	missense_variant	MODERATE	ATP6	0.0425
HLI-0915	9698	T	C	0	535	synonymous_variant	LOW	COX3	0.0405
HLI-0915	9938	T	C	0	674	synonymous_variant	LOW	COX3	0.0016
HLI-0915	10398	A	G	1	600	missense_variant	MODERATE	ND3	0.445
HLI-0915	10550	A	G	2	592	synonymous_variant	LOW	ND4L	0.0376
HLI-0915	11299	T	C	0	571	synonymous_variant	LOW	ND4	0.0417
HLI-0915	11467	A	G	1	605	synonymous_variant	LOW	ND4	0.1231
HLI-0915	11719	G	A	3	601	synonymous_variant	LOW	ND4	0.7756
HLI-0915	12308	A	G	0	589	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0915	12372	G	A	1	569	synonymous_variant	LOW	ND5	0.1329
HLI-0915	14167	C	T	1	541	synonymous_variant	LOW	ND6	0.0385
HLI-0915	14766	C	T	2	571	missense_variant	MODERATE	CYTB	0.7696
HLI-0915	14798	T	C	0	621	missense_variant	MODERATE	CYTB	0.0651
HLI-0915	15326	A	G	0	464	missense_variant	MODERATE	CYTB	0.9868
HLI-0915	16129	G	A	0	494	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0915	16224	T	C	0	543	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0915	16311	T	C	0	497	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0915	16519	T	C	0	224	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0916	73	A	G	0	318	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0916	185	G	A	3	502	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0916	228	G	A	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0916	263	A	G	1	201	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0916	295	C	T	0	249	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0916	462	C	T	2	406	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0916	489	T	C	0	440	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0916	750	A	G	0	629	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0916	1438	A	G	0	703	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0916	2706	A	G	0	644	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0916	3010	G	A	1	622	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0916	4216	T	C	0	664	missense_variant	MODERATE	ND1	0.0991
HLI-0916	4769	A	G	1	629	synonymous_variant	LOW	ND2	0.9767
HLI-0916	4838	T	C	0	596	synonymous_variant	LOW	ND2	2.00E-04
HLI-0916	5198	A	G	0	588	synonymous_variant	LOW	ND2	0.0023
HLI-0916	7028	C	T	0	673	synonymous_variant	LOW	COX1	0.8089
HLI-0916	9100	A	G	1	623	missense_variant	MODERATE	ATP6	7.00E-04
HLI-0916	10398	A	G	0	599	missense_variant	MODERATE	ND3	0.445
HLI-0916	11251	A	G	2	614	synonymous_variant	LOW	ND4	0.0932

HLI-0916	11719	G	A	0	595	synonymous_variant	LOW	ND4	0.7756
HLI-0916	12612	A	G	8	644	synonymous_variant	LOW	ND5	0.0506
HLI-0916	13708	G	A	0	514	missense_variant	MODERATE	ND5	0.0717
HLI-0916	14766	C	T	5	603	missense_variant	MODERATE	CYTB	0.7696
HLI-0916	14798	T	C	0	685	missense_variant	MODERATE	CYTB	0.0651
HLI-0916	15326	A	G	1	601	missense_variant	MODERATE	CYTB	0.9868
HLI-0916	15452	C	A	2	513	missense_variant	MODERATE	CYTB	0.0933
HLI-0916	16069	C	T	1	592	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0916	16126	T	C	0	606	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0917	263	A	G	0	206	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0917	750	A	G	0	549	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0917	1438	A	G	1	517	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0917	3010	G	A	4	537	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0917	4763	C	T	0	461	synonymous_variant	LOW	ND2	2.00E-04
HLI-0917	4769	A	G	0	480	synonymous_variant	LOW	ND2	0.9767
HLI-0917	15326	A	G	0	460	missense_variant	MODERATE	CYTB	0.9868
HLI-0917	16220	A	C	1	502	upstream_gene_variant	MODIFIER	DLoop	0.0054
HLI-0917	16324	T	C	3	432	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0917	16362	T	C	4	431	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0917	16519	T	C	4	239	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0918	263	A	G	0	217	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0918	750	A	G	0	656	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0918	1438	A	G	0	647	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0918	3010	G	A	0	650	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0918	4769	A	G	0	559	synonymous_variant	LOW	ND2	0.9767
HLI-0918	6386	C	T	4	606	synonymous_variant	LOW	COX1	5.00E-04
HLI-0918	15326	A	G	0	613	missense_variant	MODERATE	CYTB	0.9868
HLI-0918	16270	C	T	6	586	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0918	16519	T	C	1	324	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0919	73	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0919	152	T	C	2	529	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0919	263	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0919	750	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0919	921	T	C	5	664	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0919	1438	A	G	0	636	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0919	2706	A	G	3	666	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0919	3523	A	G	8	560	missense_variant	MODERATE	ND1	6.00E-04
HLI-0919	4769	A	G	0	593	synonymous_variant	LOW	ND2	0.9767
HLI-0919	5147	G	A	5	545	synonymous_variant	LOW	ND2	0.0437

HLI-0919	5492	T	C	6	599	synonymous_variant	LOW	ND2	0.0029
HLI-0919	7028	C	T	5	720	synonymous_variant	LOW	COX1	0.8089
HLI-0919	7424	A	G	3	595	synonymous_variant	LOW	COX1	0.0115
HLI-0919	8473	T	C	2	362	synonymous_variant	LOW	ATP8	0.0105
HLI-0919	8618	T	C	5	410	missense_variant	MODERATE	ATP6	0.0103
HLI-0919	8658	C	T	5	480	synonymous_variant	LOW	ATP6	4.00E-04
HLI-0919	8701	A	G	6	530	missense_variant	MODERATE	ATP6	0.3391
HLI-0919	9300	G	A	7	642	missense_variant	MODERATE	COX3	0.0036
HLI-0919	9540	T	C	5	655	synonymous_variant	LOW	COX3	0.339
HLI-0919	10398	A	G	7	591	missense_variant	MODERATE	ND3	0.445
HLI-0919	10873	T	C	7	399	synonymous_variant	LOW	ND4	0.3389
HLI-0919	11719	G	A	3	583	synonymous_variant	LOW	ND4	0.7756
HLI-0919	12705	C	T	5	687	synonymous_variant	LOW	ND5	0.4212
HLI-0919	13105	A	G	8	666	missense_variant	MODERATE	ND5	0.076
HLI-0919	13886	T	C	7	525	missense_variant	MODERATE	ND5	0.0088
HLI-0919	14284	C	T	1	495	synonymous_variant	LOW	ND6	0.0087
HLI-0919	14766	C	T	5	597	missense_variant	MODERATE	CYTB	0.7696
HLI-0919	15223	C	T	4	592	synonymous_variant	LOW	CYTB	0.0034
HLI-0919	15301	G	A	2	637	synonymous_variant	LOW	CYTB	0.2912
HLI-0919	15326	A	G	1	655	missense_variant	MODERATE	CYTB	0.9868
HLI-0919	16223	C	T	4	626	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0919	16260	C	T	5	666	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0920	73	A	G	1	287	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0920	195	T	C	0	472	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0920	263	A	G	1	245	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0920	497	C	T	2	484	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0920	750	A	G	1	532	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0920	1189	T	C	2	623	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0920	1438	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0920	1811	A	G	0	582	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0920	2706	A	G	3	609	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0920	3480	A	G	1	470	synonymous_variant	LOW	ND1	0.0392
HLI-0920	4769	A	G	0	595	synonymous_variant	LOW	ND2	0.9767
HLI-0920	4994	A	G	0	525	synonymous_variant	LOW	ND2	2.00E-04
HLI-0920	5460	G	A	1	538	missense_variant	MODERATE	ND2	0.0651
HLI-0920	7028	C	T	5	625	synonymous_variant	LOW	COX1	0.8089
HLI-0920	7521	G	A	1	529	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0920	9055	G	A	1	559	missense_variant	MODERATE	ATP6	0.0425
HLI-0920	9698	T	C	1	536	synonymous_variant	LOW	COX3	0.0405

HLI-0920	10398	A	G	3	475	missense_variant	MODERATE	ND3	0.445
HLI-0920	10550	A	G	2	530	synonymous_variant	LOW	ND4L	0.0376
HLI-0920	11299	T	C	3	596	synonymous_variant	LOW	ND4	0.0417
HLI-0920	11467	A	G	0	625	synonymous_variant	LOW	ND4	0.1231
HLI-0920	11719	G	A	1	584	synonymous_variant	LOW	ND4	0.7756
HLI-0920	12308	A	G	2	525	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0920	12372	G	A	2	493	synonymous_variant	LOW	ND5	0.1329
HLI-0920	14167	C	T	0	507	synonymous_variant	LOW	ND6	0.0385
HLI-0920	14766	C	T	2	580	missense_variant	MODERATE	CYTB	0.7696
HLI-0920	14798	T	C	3	659	missense_variant	MODERATE	CYTB	0.0651
HLI-0920	15326	A	G	0	484	missense_variant	MODERATE	CYTB	0.9868
HLI-0920	16224	T	C	2	502	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0920	16311	T	C	1	462	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0920	16519	T	C	0	259	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0921	73	A	G	0	256	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0921	150	C	T	1	428	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0921	152	T	C	1	429	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0921	182	C	T	0	392	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0921	195	T	C	0	385	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0921	198	C	T	0	385	upstream_gene_variant	MODIFIER	DLoop	0.0245
HLI-0921	204	T	C	0	398	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0921	263	A	G	0	170	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0921	418	C	T	0	386	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0921	750	A	G	0	571	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0921	769	G	A	1	623	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0921	1018	G	A	0	583	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0921	1438	A	G	1	643	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0921	1442	G	A	1	663	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0921	1706	C	T	1	578	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0921	2332	C	T	1	568	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0921	2358	A	G	3	591	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0921	2416	T	C	1	549	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0921	2706	A	G	1	595	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0921	3594	C	T	2	506	synonymous_variant	LOW	ND1	0.0789
HLI-0921	4104	A	G	1	571	synonymous_variant	LOW	ND1	0.0785
HLI-0921	4158	A	G	2	627	synonymous_variant	LOW	ND1	0.0023
HLI-0921	4370	T	C	0	560	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0921	4767	A	G	0	610	missense_variant	MODERATE	ND2	0.0029
HLI-0921	4769	A	G	0	619	synonymous_variant	LOW	ND2	0.9767

HLI-0921	5027	C	T	0	550	synonymous_variant	LOW	ND2	0.003
HLI-0921	5331	C	A	1	581	missense_variant	MODERATE	ND2	0.0022
HLI-0921	5814	T	C	0	648	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0921	6026	G	A	2	657	synonymous_variant	LOW	COX1	0.0163
HLI-0921	6713	C	T	8	675	synonymous_variant	LOW	COX1	0.0028
HLI-0921	7028	C	T	4	609	synonymous_variant	LOW	COX1	0.8089
HLI-0921	7256	C	T	2	588	synonymous_variant	LOW	COX1	0.0784
HLI-0921	7521	G	A	2	442	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0921	7624	T	A	0	558	synonymous_variant	LOW	COX2	0.0047
HLI-0921	8080	C	T	1	601	synonymous_variant	LOW	COX2	0.0022
HLI-0921	8206	G	A	0	637	synonymous_variant	LOW	COX2	0.0287
HLI-0921	8387	G	A	0	584	missense_variant	MODERATE	ATP8	0.0028
HLI-0921	8701	A	G	0	542	missense_variant	MODERATE	ATP6	0.3391
HLI-0921	8856	G	A	0	571	synonymous_variant	LOW	ATP6	0.004
HLI-0921	9221	A	G	1	636	synonymous_variant	LOW	COX3	0.0277
HLI-0921	9540	T	C	1	570	synonymous_variant	LOW	COX3	0.339
HLI-0921	10115	T	C	0	639	synonymous_variant	LOW	ND3	0.0278
HLI-0921	10398	A	G	1	551	missense_variant	MODERATE	ND3	0.445
HLI-0921	10828	T	C	1	590	synonymous_variant	LOW	ND4	0.0015
HLI-0921	10873	T	C	1	624	synonymous_variant	LOW	ND4	0.3389
HLI-0921	11719	G	A	1	594	synonymous_variant	LOW	ND4	0.7756
HLI-0921	11944	T	C	2	579	synonymous_variant	LOW	ND4	0.0331
HLI-0921	12236	G	A	0	563	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0921	12705	C	T	0	652	synonymous_variant	LOW	ND5	0.4212
HLI-0921	12948	A	G	1	619	synonymous_variant	LOW	ND5	0.0022
HLI-0921	13590	G	A	1	580	synonymous_variant	LOW	ND5	0.0586
HLI-0921	13650	C	T	1	595	synonymous_variant	LOW	ND5	0.079
HLI-0921	13924	C	T	0	549	missense_variant	MODERATE	ND5	0.0013
HLI-0921	14059	A	G	0	496	missense_variant	MODERATE	ND5	0.0022
HLI-0921	14766	C	T	2	614	missense_variant	MODERATE	CYTB	0.7696
HLI-0921	15110	G	A	0	647	missense_variant	MODERATE	CYTB	0.009
HLI-0921	15217	G	A	3	609	synonymous_variant	LOW	CYTB	0.0104
HLI-0921	15301	G	A	3	616	synonymous_variant	LOW	CYTB	0.2912
HLI-0921	15326	A	G	0	576	missense_variant	MODERATE	CYTB	0.9868
HLI-0921	16114	C	A	0	584	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0921	16129	G	A	0	627	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0921	16213	G	A	0	571	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0921	16223	C	T	0	596	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0921	16278	C	T	1	592	upstream_gene_variant	MODIFIER	DLoop	0.1057

HLI-0921	16355	C	T	1	486	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0921	16362	T	C	0	490	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0921	16390	G	A	1	480	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0922	152	T	C	0	457	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0922	263	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0922	750	A	G	0	564	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0922	1438	A	G	0	563	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0922	4769	A	G	0	491	synonymous_variant	LOW	ND2	0.9767
HLI-0922	6776	T	C	2	700	synonymous_variant	LOW	COX1	0.0226
HLI-0922	15326	A	G	0	392	missense_variant	MODERATE	CYTB	0.9868
HLI-0922	16519	T	C	0	223	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0923	263	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0923	456	C	T	2	365	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0923	721	T	C	1	636	upstream_gene_variant	MODIFIER	RNR1	0.002
HLI-0923	750	A	G	0	661	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0923	1438	A	G	1	615	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0923	4336	T	C	5	520	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0923	4769	A	G	0	519	synonymous_variant	LOW	ND2	0.9767
HLI-0923	13468	C	A	1	546	missense_variant	MODERATE	ND5	0
HLI-0923	15326	A	G	0	492	missense_variant	MODERATE	CYTB	0.9868
HLI-0923	15833	C	T	2	514	synonymous_variant	LOW	CYTB	0.0051
HLI-0923	16093	T	C	11	536	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0923	16304	T	C	1	481	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0924	73	A	G	9	229	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0924	263	A	G	0	368	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0924	447	C	G	7	291	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0924	489	T	C	4	295	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0924	750	A	G	3	508	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0924	930	G	A	16	547	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0924	1438	A	G	0	534	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0924	1598	G	A	18	529	upstream_gene_variant	MODIFIER	RNR1	0.0114
HLI-0924	1780	T	C	18	499	upstream_gene_variant	MODIFIER	RNR2	0.0053
HLI-0924	1888	G	A	13	381	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0924	2706	A	G	23	455	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0924	3438	G	A	14	465	synonymous_variant	LOW	ND1	0.0132
HLI-0924	3729	A	C	16	425	synonymous_variant	LOW	ND1	1.00E-04
HLI-0924	4216	T	C	11	428	missense_variant	MODERATE	ND1	0.0991
HLI-0924	4769	A	G	5	590	synonymous_variant	LOW	ND2	0.9767
HLI-0924	7028	C	T	20	543	synonymous_variant	LOW	COX1	0.8089

HLI-0924	8701	A	G	12	494	missense_variant	MODERATE	ATP6	0.3391
HLI-0924	9540	T	C	18	455	synonymous_variant	LOW	COX3	0.339
HLI-0924	10157	A	G	19	694	synonymous_variant	LOW	ND3	1.00E-04
HLI-0924	10398	A	G	19	488	missense_variant	MODERATE	ND3	0.445
HLI-0924	10400	C	T	19	493	synonymous_variant	LOW	ND3	0.2131
HLI-0924	10873	T	C	16	311	synonymous_variant	LOW	ND4	0.3389
HLI-0924	11083	A	G	15	482	synonymous_variant	LOW	ND4	0.0047
HLI-0924	11719	G	A	10	470	synonymous_variant	LOW	ND4	0.7756
HLI-0924	12705	C	T	11	439	synonymous_variant	LOW	ND5	0.4212
HLI-0924	13212	C	T	19	455	synonymous_variant	LOW	ND5	0.0016
HLI-0924	14766	C	T	15	501	missense_variant	MODERATE	CYTB	0.7696
HLI-0924	14783	T	C	14	598	synonymous_variant	LOW	CYTB	0.2126
HLI-0924	14800	C	T	15	594	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0924	15043	G	A	14	575	synonymous_variant	LOW	CYTB	0.2362
HLI-0924	15077	G	A	17	601	missense_variant	MODERATE	CYTB	0.0021
HLI-0924	15152	G	A	17	535	missense_variant	MODERATE	CYTB	1.00E-04
HLI-0924	15301	G	A	3	403	synonymous_variant	LOW	CYTB	0.2912
HLI-0924	15326	A	G	2	426	missense_variant	MODERATE	CYTB	0.9868
HLI-0924	15670	T	C	9	375	synonymous_variant	LOW	CYTB	0.0176
HLI-0924	15929	A	G	15	431	upstream_gene_variant	MODIFIER	TRNT	6.00E-04
HLI-0924	16223	C	T	7	98	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0924	16227	A	G	6	99	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0924	16258	A	C	12	144	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0924	16263	T	C	6	179	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0924	16274	G	A	6	198	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0925	73	A	G	1	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0925	146	T	C	1	492	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0925	152	T	C	1	493	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0925	263	A	G	0	201	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0925	709	G	A	0	530	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0925	750	A	G	2	560	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0925	1438	A	G	0	532	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0925	1811	A	G	2	541	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0925	2706	A	G	1	504	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0925	3480	A	G	0	446	synonymous_variant	LOW	ND1	0.0392
HLI-0925	4561	T	C	4	542	missense_variant	MODERATE	ND2	0.0065
HLI-0925	4769	A	G	1	561	synonymous_variant	LOW	ND2	0.9767
HLI-0925	7028	C	T	3	548	synonymous_variant	LOW	COX1	0.8089
HLI-0925	9055	G	A	0	518	missense_variant	MODERATE	ATP6	0.0425

HLI-0925	9698	T	C	0	525	synonymous_variant	LOW	COX3	0.0405
HLI-0925	9716	T	C	0	580	synonymous_variant	LOW	COX3	0.0108
HLI-0925	10550	A	G	0	606	synonymous_variant	LOW	ND4L	0.0376
HLI-0925	11299	T	C	1	519	synonymous_variant	LOW	ND4	0.0417
HLI-0925	11467	A	G	0	571	synonymous_variant	LOW	ND4	0.1231
HLI-0925	11719	G	A	0	523	synonymous_variant	LOW	ND4	0.7756
HLI-0925	12308	A	G	1	500	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0925	12372	G	A	0	486	synonymous_variant	LOW	ND5	0.1329
HLI-0925	14167	C	T	1	439	synonymous_variant	LOW	ND6	0.0385
HLI-0925	14766	C	T	2	507	missense_variant	MODERATE	CYTB	0.7696
HLI-0925	14798	T	C	2	562	missense_variant	MODERATE	CYTB	0.0651
HLI-0925	15326	A	G	0	439	missense_variant	MODERATE	CYTB	0.9868
HLI-0925	16224	T	C	0	525	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0925	16311	T	C	0	430	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0925	16519	T	C	0	223	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0926	150	C	T	0	417	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0926	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0926	750	A	G	1	498	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0926	1438	A	G	0	503	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0926	3010	G	A	1	527	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0926	4254	T	C	0	453	synonymous_variant	LOW	ND1	3.00E-04
HLI-0926	4769	A	G	2	417	synonymous_variant	LOW	ND2	0.9767
HLI-0926	5147	G	A	0	373	synonymous_variant	LOW	ND2	0.0437
HLI-0926	15326	A	G	0	397	missense_variant	MODERATE	CYTB	0.9868
HLI-0926	16519	T	C	2	210	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0927	64	C	T	0	184	upstream_gene_variant	MODIFIER	DLoop	0.0315
HLI-0927	93	A	G	1	278	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0927	152	T	C	0	338	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0927	189	A	G	0	329	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0927	204	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0927	207	G	A	1	314	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0927	236	T	C	0	305	upstream_gene_variant	MODIFIER	DLoop	0.0162
HLI-0927	247	G	A	0	287	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0927	263	A	G	0	264	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0927	750	A	G	0	506	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0927	769	G	A	0	535	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0927	825	T	A	1	564	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0927	1018	G	A	1	565	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0927	1048	C	T	1	638	upstream_gene_variant	MODIFIER	RNR1	0.0355

HLI-0927	1438	A	G	0	566	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0927	2245	A	G	1	414	upstream_gene_variant	MODIFIER	RNR2	0.0145
HLI-0927	2706	A	G	0	492	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0927	2758	G	A	1	503	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0927	2885	T	C	0	538	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0927	3516	C	A	4	490	synonymous_variant	LOW	ND1	0.0315
HLI-0927	3594	C	T	1	512	synonymous_variant	LOW	ND1	0.0789
HLI-0927	4104	A	G	0	403	synonymous_variant	LOW	ND1	0.0785
HLI-0927	4312	C	T	3	426	upstream_gene_variant	MODIFIER	TRNI	0.0316
HLI-0927	4586	T	C	2	503	synonymous_variant	LOW	ND2	0.018
HLI-0927	4769	A	G	1	469	synonymous_variant	LOW	ND2	0.9767
HLI-0927	5147	G	A	0	339	synonymous_variant	LOW	ND2	0.0437
HLI-0927	5231	G	A	2	452	synonymous_variant	LOW	ND2	0.0232
HLI-0927	5442	T	C	0	491	missense_variant	MODERATE	ND2	0.0493
HLI-0927	5460	G	A	1	547	missense_variant	MODERATE	ND2	0.0651
HLI-0927	5603	C	T	0	586	upstream_gene_variant	MODIFIER	TRNA	0.0158
HLI-0927	5711	A	G	4	517	upstream_gene_variant	MODIFIER	TRNN	0.008
HLI-0927	6185	T	C	1	554	synonymous_variant	LOW	COX1	0.0325
HLI-0927	6257	G	A	0	539	synonymous_variant	LOW	COX1	0.0085
HLI-0927	7028	C	T	0	494	synonymous_variant	LOW	COX1	0.8089
HLI-0927	7146	A	G	0	269	missense_variant	MODERATE	COX1	0.0497
HLI-0927	7256	C	T	3	436	synonymous_variant	LOW	COX1	0.0784
HLI-0927	7521	G	A	1	277	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0927	8428	C	T	5	427	synonymous_variant	LOW	ATP8	0.0144
HLI-0927	8460	A	G	0	449	missense_variant	MODERATE	ATP8	0.0085
HLI-0927	8468	C	T	0	423	synonymous_variant	LOW	ATP8	0.0501
HLI-0927	8566	A	G	1	384	missense_variant	MODERATE	ATP6/8	0.0151
HLI-0927	8655	C	T	2	424	synonymous_variant	LOW	ATP6	0.0511
HLI-0927	8701	A	G	2	461	missense_variant	MODERATE	ATP6	0.3391
HLI-0927	9042	C	T	0	474	synonymous_variant	LOW	ATP6	0.0316
HLI-0927	9347	A	G	1	473	synonymous_variant	LOW	COX3	0.0314
HLI-0927	9540	T	C	0	463	synonymous_variant	LOW	COX3	0.339
HLI-0927	9545	A	G	0	474	synonymous_variant	LOW	COX3	0.0469
HLI-0927	9554	G	A	0	482	synonymous_variant	LOW	COX3	0.014
HLI-0927	9755	G	A	2	574	synonymous_variant	LOW	COX3	0.0303
HLI-0927	9818	C	T	0	676	synonymous_variant	LOW	COX3	0.0179
HLI-0927	10398	A	G	0	513	missense_variant	MODERATE	ND3	0.445
HLI-0927	10589	G	A	0	563	synonymous_variant	LOW	ND4L	0.0355
HLI-0927	10664	C	T	2	549	synonymous_variant	LOW	ND4L	0.0315

HLI-0927	10688	G	A	0	531	synonymous_variant	LOW	ND4L	0.0515
HLI-0927	10810	T	C	0	492	synonymous_variant	LOW	ND4	0.0522
HLI-0927	10873	T	C	0	449	synonymous_variant	LOW	ND4	0.3389
HLI-0927	10915	T	C	0	494	synonymous_variant	LOW	ND4	0.0411
HLI-0927	11143	C	T	1	494	synonymous_variant	LOW	ND4	0.0076
HLI-0927	11172	A	G	1	541	missense_variant	MODERATE	ND4	0.0086
HLI-0927	11176	G	A	1	540	synonymous_variant	LOW	ND4	0.0181
HLI-0927	11641	A	G	1	510	synonymous_variant	LOW	ND4	0.0158
HLI-0927	11719	G	A	1	551	synonymous_variant	LOW	ND4	0.7756
HLI-0927	11914	G	A	1	524	synonymous_variant	LOW	ND4	0.1112
HLI-0927	12007	G	A	1	400	synonymous_variant	LOW	ND4	0.0639
HLI-0927	12705	C	T	0	486	synonymous_variant	LOW	ND5	0.4212
HLI-0927	12720	A	G	0	532	synonymous_variant	LOW	ND5	0.0302
HLI-0927	13105	A	G	0	568	missense_variant	MODERATE	ND5	0.076
HLI-0927	13116	C	T	0	556	synonymous_variant	LOW	ND5	0.0047
HLI-0927	13276	A	G	0	544	missense_variant	MODERATE	ND5	0.0312
HLI-0927	13506	C	T	0	461	synonymous_variant	LOW	ND5	0.0506
HLI-0927	13650	C	T	4	422	synonymous_variant	LOW	ND5	0.079
HLI-0927	14308	T	C	0	452	synonymous_variant	LOW	ND6	0.0209
HLI-0927	14755	A	G	1	537	synonymous_variant	LOW	CYTB	0.0074
HLI-0927	14766	C	T	3	579	missense_variant	MODERATE	CYTB	0.7696
HLI-0927	15136	C	T	1	488	synonymous_variant	LOW	CYTB	0.0153
HLI-0927	15326	A	G	0	407	missense_variant	MODERATE	CYTB	0.9868
HLI-0927	15431	G	A	1	377	missense_variant	MODERATE	CYTB	0.0182
HLI-0927	16148	C	T	0	459	upstream_gene_variant	MODIFIER	DLoop	0.03
HLI-0927	16172	T	C	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0927	16223	C	T	0	386	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0927	16230	A	G	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0309
HLI-0927	16311	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0927	16320	C	T	0	387	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0927	16519	T	C	0	167	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0928	73	A	G	0	255	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0928	150	C	T	0	503	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0928	263	A	G	0	213	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0928	750	A	G	0	501	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0928	1438	A	G	1	591	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0928	1811	A	G	1	506	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0928	2294	A	G	0	457	upstream_gene_variant	MODIFIER	RNR2	0.0027
HLI-0928	2706	A	G	0	576	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0928	4703	T	C	2	534	synonymous_variant	LOW	ND2	0.0058
HLI-0928	4769	A	G	0	552	synonymous_variant	LOW	ND2	0.9767
HLI-0928	6518	C	T	2	632	synonymous_variant	LOW	COX1	0.0025
HLI-0928	7028	C	T	2	621	synonymous_variant	LOW	COX1	0.8089
HLI-0928	7256	C	T	3	546	synonymous_variant	LOW	COX1	0.0784
HLI-0928	9101	T	C	2	561	missense_variant	MODERATE	ATP6	8.00E-04
HLI-0928	9266	G	A	1	521	synonymous_variant	LOW	COX3	0.0049
HLI-0928	10506	A	G	0	516	missense_variant	MODERATE	ND4L	0.0025
HLI-0928	11050	T	C	0	472	synonymous_variant	LOW	ND4	0.001
HLI-0928	11467	A	G	0	543	synonymous_variant	LOW	ND4	0.1231
HLI-0928	11719	G	A	0	500	synonymous_variant	LOW	ND4	0.7756
HLI-0928	12308	A	G	3	446	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0928	12372	G	A	3	441	synonymous_variant	LOW	ND5	0.1329
HLI-0928	13708	G	A	2	441	missense_variant	MODERATE	ND5	0.0717
HLI-0928	13934	C	T	4	454	missense_variant	MODERATE	ND5	0.0122
HLI-0928	14139	A	G	4	411	synonymous_variant	LOW	ND5	0.0056
HLI-0928	14766	C	T	0	484	missense_variant	MODERATE	CYTB	0.7696
HLI-0928	15326	A	G	0	476	missense_variant	MODERATE	CYTB	0.9868
HLI-0928	15454	T	C	0	443	synonymous_variant	LOW	CYTB	0.0072
HLI-0928	15466	G	A	0	489	synonymous_variant	LOW	CYTB	0.0152
HLI-0928	16274	G	A	0	431	upstream_gene_variant	MODIFIER	DLoop	0.0234
HLI-0928	16343	A	G	0	428	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0928	16362	T	C	0	425	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0928	16390	G	A	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0928	16519	T	C	1	261	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0929	151	C	T	0	437	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0929	152	T	C	0	442	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0929	263	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0929	750	A	G	0	488	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0929	1438	A	G	0	502	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0929	3010	G	A	0	494	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0929	4562	A	T	1	552	synonymous_variant	LOW	ND2	0
HLI-0929	4769	A	G	1	505	synonymous_variant	LOW	ND2	0.9767
HLI-0929	6956	T	G	2	487	synonymous_variant	LOW	COX1	2.00E-04
HLI-0929	15326	A	G	0	386	missense_variant	MODERATE	CYTB	0.9868
HLI-0929	16519	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0930	73	A	G	0	257	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0930	263	A	G	1	177	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0930	709	G	A	0	578	upstream_gene_variant	MODIFIER	RNR1	0.1279

HLI-0930	750	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0930	930	G	A	4	523	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0930	1438	A	G	1	576	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0930	1888	G	A	1	541	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0930	2706	A	G	0	551	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0930	4216	T	C	0	573	missense_variant	MODERATE	ND1	0.0991
HLI-0930	4769	A	G	0	445	synonymous_variant	LOW	ND2	0.9767
HLI-0930	4917	A	G	0	485	missense_variant	MODERATE	ND2	0.0477
HLI-0930	5147	G	A	0	420	synonymous_variant	LOW	ND2	0.0437
HLI-0930	7028	C	T	0	599	synonymous_variant	LOW	COX1	0.8089
HLI-0930	8233	A	G	0	474	synonymous_variant	LOW	COX2	0
HLI-0930	8697	G	A	0	470	synonymous_variant	LOW	ATP6	0.0466
HLI-0930	10463	T	C	0	612	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0930	10750	A	G	3	510	missense_variant	MODERATE	ND4L	0.0045
HLI-0930	11054	C	T	0	545	synonymous_variant	LOW	ND4	0
HLI-0930	11251	A	G	0	543	synonymous_variant	LOW	ND4	0.0932
HLI-0930	11719	G	A	2	559	synonymous_variant	LOW	ND4	0.7756
HLI-0930	11812	A	G	0	509	synonymous_variant	LOW	ND4	0.0332
HLI-0930	13368	G	A	1	525	synonymous_variant	LOW	ND5	0.0495
HLI-0930	13722	A	G	0	345	synonymous_variant	LOW	ND5	0.0077
HLI-0930	13812	T	C	0	395	synonymous_variant	LOW	ND5	0.0017
HLI-0930	14233	A	G	2	499	synonymous_variant	LOW	ND6	0.0369
HLI-0930	14766	C	T	0	492	missense_variant	MODERATE	CYTB	0.7696
HLI-0930	14905	G	A	2	524	synonymous_variant	LOW	CYTB	0.0526
HLI-0930	15326	A	G	1	500	missense_variant	MODERATE	CYTB	0.9868
HLI-0930	15452	C	A	4	495	missense_variant	MODERATE	CYTB	0.0933
HLI-0930	15607	A	G	0	509	synonymous_variant	LOW	CYTB	0.0508
HLI-0930	15928	G	A	1	567	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0930	16126	T	C	1	535	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0930	16136	T	C	2	574	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0930	16294	C	T	0	485	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0930	16296	C	T	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0930	16304	T	C	0	513	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0930	16519	T	C	0	280	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0931	73	A	G	0	26	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0931	150	C	T	0	55	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0931	194	C	T	0	55	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0931	263	A	G	0	35	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0931	750	A	G	0	53	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0931	1438	A	G	0	37	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0931	1721	C	T	0	44	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0931	2706	A	G	0	46	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0931	3197	T	C	0	40	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0931	4732	A	G	1	53	missense_variant	MODERATE	ND2	0.0059
HLI-0931	4769	A	G	0	53	synonymous_variant	LOW	ND2	0.9767
HLI-0931	7028	C	T	0	69	synonymous_variant	LOW	COX1	0.8089
HLI-0931	7768	A	G	0	38	synonymous_variant	LOW	COX2	0.0186
HLI-0931	9477	G	A	0	56	missense_variant	MODERATE	COX3	0.0387
HLI-0931	11467	A	G	0	54	synonymous_variant	LOW	ND4	0.1231
HLI-0931	11719	G	A	0	50	synonymous_variant	LOW	ND4	0.7756
HLI-0931	12308	A	G	0	41	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0931	12372	G	A	0	39	synonymous_variant	LOW	ND5	0.1329
HLI-0931	13617	T	C	0	49	synonymous_variant	LOW	ND5	0.038
HLI-0931	13637	A	G	0	43	missense_variant	MODERATE	ND5	0.0074
HLI-0931	14182	T	C	0	36	synonymous_variant	LOW	ND6	0.0254
HLI-0931	14766	C	T	1	52	missense_variant	MODERATE	CYTB	0.7696
HLI-0931	15326	A	G	0	57	missense_variant	MODERATE	CYTB	0.9868
HLI-0931	15511	T	C	0	45	synonymous_variant	LOW	CYTB	0.0023
HLI-0931	16290	C	T	0	47	upstream_gene_variant	MODIFIER	DLoop	0.0394
HLI-0931	16311	T	C	0	45	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0932	73	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0932	150	C	T	1	470	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0932	185	G	A	0	475	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0932	189	A	G	0	469	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0932	263	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0932	750	A	G	0	522	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0932	1438	A	G	2	532	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0932	2352	T	C	0	454	upstream_gene_variant	MODIFIER	RNR2	0.0265
HLI-0932	2706	A	G	0	470	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0932	3826	T	C	1	481	synonymous_variant	LOW	ND1	0.0014
HLI-0932	4769	A	G	0	539	synonymous_variant	LOW	ND2	0.9767
HLI-0932	6221	T	C	1	482	synonymous_variant	LOW	COX1	0.0306
HLI-0932	6587	C	T	0	486	synonymous_variant	LOW	COX1	0.0084
HLI-0932	7028	C	T	0	539	synonymous_variant	LOW	COX1	0.8089
HLI-0932	8577	A	G	1	494	synonymous_variant	LOW	ATP6	0.0012
HLI-0932	8701	A	G	1	512	missense_variant	MODERATE	ATP6	0.3391
HLI-0932	9540	T	C	1	509	synonymous_variant	LOW	COX3	0.339
HLI-0932	10398	A	G	0	580	missense_variant	MODERATE	ND3	0.445

HLI-0932	10819	A	G	0	435	synonymous_variant	LOW	ND4	0.0228
HLI-0932	10873	T	C	1	472	synonymous_variant	LOW	ND4	0.3389
HLI-0932	11719	G	A	0	523	synonymous_variant	LOW	ND4	0.7756
HLI-0932	12192	G	A	0	535	upstream_gene_variant	MODIFIER	TRNH	0.0022
HLI-0932	12705	C	T	0	510	synonymous_variant	LOW	ND5	0.4212
HLI-0932	14152	A	G	4	432	synonymous_variant	LOW	ND6	0.0086
HLI-0932	14212	T	C	0	554	synonymous_variant	LOW	ND6	0.0204
HLI-0932	14766	C	T	2	485	missense_variant	MODERATE	CYTB	0.7696
HLI-0932	14926	A	G	0	564	synonymous_variant	LOW	CYTB	0.0015
HLI-0932	15301	G	A	0	375	synonymous_variant	LOW	CYTB	0.2912
HLI-0932	15326	A	G	0	392	missense_variant	MODERATE	CYTB	0.9868
HLI-0932	15670	T	C	0	445	synonymous_variant	LOW	CYTB	0.0176
HLI-0932	15942	T	C	0	490	upstream_gene_variant	MODIFIER	TRNT	0.0086
HLI-0932	16223	C	T	2	448	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0932	16327	C	T	0	417	upstream_gene_variant	MODIFIER	DLoop	0.0434
HLI-0933	73	A	G	0	235	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0933	119	T	C	6	359	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0933	189	A	G	1	343	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0933	195	T	C	1	362	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0933	207	G	A	1	382	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0933	263	A	G	0	160	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0933	709	G	A	0	492	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0933	750	A	G	2	526	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0933	1243	T	C	0	531	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0933	1438	A	G	0	515	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0933	2706	A	G	1	423	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0933	3505	A	G	1	416	missense_variant	MODERATE	ND1	0.0144
HLI-0933	4769	A	G	0	496	synonymous_variant	LOW	ND2	0.9767
HLI-0933	5046	G	A	0	427	missense_variant	MODERATE	ND2	0.018
HLI-0933	5460	G	A	0	464	missense_variant	MODERATE	ND2	0.0651
HLI-0933	7028	C	T	3	553	synonymous_variant	LOW	COX1	0.8089
HLI-0933	7864	C	T	0	535	synonymous_variant	LOW	COX2	0.0041
HLI-0933	8251	G	A	1	454	synonymous_variant	LOW	COX2	0.058
HLI-0933	8994	G	A	1	444	synonymous_variant	LOW	ATP6	0.0167
HLI-0933	11422	C	T	0	478	synonymous_variant	LOW	ND4	7.00E-04
HLI-0933	11674	C	T	1	465	synonymous_variant	LOW	ND4	0.0116
HLI-0933	11719	G	A	0	522	synonymous_variant	LOW	ND4	0.7756
HLI-0933	11947	A	G	1	557	synonymous_variant	LOW	ND4	0.011
HLI-0933	12414	T	C	4	500	synonymous_variant	LOW	ND5	0.0139

HLI-0933	12705	C	T	2	472	synonymous_variant	LOW	ND5	0.4212
HLI-0933	14766	C	T	0	427	missense_variant	MODERATE	CYTB	0.7696
HLI-0933	15326	A	G	1	381	missense_variant	MODERATE	CYTB	0.9868
HLI-0933	15884	G	C	0	520	missense_variant	MODERATE	CYTB	0.011
HLI-0933	16223	C	T	0	446	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0933	16292	C	T	1	429	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0933	16519	T	C	1	228	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0934	73	A	G	0	292	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0934	195	T	C	0	450	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0934	263	A	G	1	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0934	497	C	T	1	415	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0934	750	A	G	1	530	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0934	1189	T	C	0	583	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0934	1438	A	G	0	570	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0934	1811	A	G	0	538	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0934	2706	A	G	1	541	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0934	3480	A	G	1	470	synonymous_variant	LOW	ND1	0.0392
HLI-0934	4769	A	G	1	515	synonymous_variant	LOW	ND2	0.9767
HLI-0934	7028	C	T	6	633	synonymous_variant	LOW	COX1	0.8089
HLI-0934	9055	G	A	0	543	missense_variant	MODERATE	ATP6	0.0425
HLI-0934	9698	T	C	0	546	synonymous_variant	LOW	COX3	0.0405
HLI-0934	10398	A	G	0	510	missense_variant	MODERATE	ND3	0.445
HLI-0934	10550	A	G	0	580	synonymous_variant	LOW	ND4L	0.0376
HLI-0934	11299	T	C	1	590	synonymous_variant	LOW	ND4	0.0417
HLI-0934	11337	A	G	2	634	missense_variant	MODERATE	ND4	6.00E-04
HLI-0934	11467	A	G	0	564	synonymous_variant	LOW	ND4	0.1231
HLI-0934	11719	G	A	1	544	synonymous_variant	LOW	ND4	0.7756
HLI-0934	12308	A	G	2	508	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0934	12372	G	A	1	574	synonymous_variant	LOW	ND5	0.1329
HLI-0934	14167	C	T	2	466	synonymous_variant	LOW	ND6	0.0385
HLI-0934	14766	C	T	2	524	missense_variant	MODERATE	CYTB	0.7696
HLI-0934	14798	T	C	1	607	missense_variant	MODERATE	CYTB	0.0651
HLI-0934	15326	A	G	0	464	missense_variant	MODERATE	CYTB	0.9868
HLI-0934	16093	T	C	6	517	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0934	16224	T	C	0	494	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0934	16311	T	C	0	480	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0934	16519	T	C	0	312	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0934	16524	A	G	0	297	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0935	73	A	G	0	207	upstream_gene_variant	MODIFIER	DLoop	0.7599

HLI-0935	263	A	G	0	172	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0935	295	C	A	0	137	upstream_gene_variant	MODIFIER	DLoop	0.0012
HLI-0935	750	A	G	0	449	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0935	1391	T	C	2	477	upstream_gene_variant	MODIFIER	RNR1	0.0027
HLI-0935	1438	A	G	0	501	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0935	2706	A	G	2	471	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0935	3360	A	G	0	429	synonymous_variant	LOW	ND1	0.0013
HLI-0935	4026	A	G	0	353	synonymous_variant	LOW	ND1	8.00E-04
HLI-0935	4216	T	C	1	422	missense_variant	MODERATE	ND1	0.0991
HLI-0935	4769	A	G	4	415	synonymous_variant	LOW	ND2	0.9767
HLI-0935	4917	A	G	0	417	missense_variant	MODERATE	ND2	0.0477
HLI-0935	5378	A	G	1	447	synonymous_variant	LOW	ND2	0.0011
HLI-0935	5586	C	T	1	483	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0935	5823	A	G	1	497	upstream_gene_variant	MODIFIER	TRNC	0.0014
HLI-0935	6557	C	T	0	464	synonymous_variant	LOW	COX1	0.0011
HLI-0935	6671	T	C	1	410	synonymous_variant	LOW	COX1	0.0071
HLI-0935	7028	C	T	2	490	synonymous_variant	LOW	COX1	0.8089
HLI-0935	7424	A	G	2	416	synonymous_variant	LOW	COX1	0.0115
HLI-0935	7547	T	C	0	440	upstream_gene_variant	MODIFIER	TRND	0.0012
HLI-0935	8388	T	C	0	351	missense_variant	MODERATE	ATP8	0.0013
HLI-0935	8887	A	G	0	452	missense_variant	MODERATE	ATP6	0.0016
HLI-0935	10658	A	G	0	477	synonymous_variant	LOW	ND4L	0.0026
HLI-0935	10825	A	G	0	410	synonymous_variant	LOW	ND4	0.0011
HLI-0935	11719	G	A	0	429	synonymous_variant	LOW	ND4	0.7756
HLI-0935	13105	A	G	1	486	missense_variant	MODERATE	ND5	0.076
HLI-0935	13368	G	A	1	471	synonymous_variant	LOW	ND5	0.0495
HLI-0935	13948	C	T	2	401	missense_variant	MODERATE	ND5	0.0013
HLI-0935	14632	C	T	0	434	synonymous_variant	LOW	ND6	0.0012
HLI-0935	14766	C	T	0	443	missense_variant	MODERATE	CYTB	0.7696
HLI-0935	15326	A	G	0	411	missense_variant	MODERATE	CYTB	0.9868
HLI-0935	15721	T	C	0	420	synonymous_variant	LOW	CYTB	0.0033
HLI-0935	16311	T	C	1	395	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0935	16519	T	C	1	222	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0936	263	A	G	0	188	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0936	456	C	T	4	303	upstream_gene_variant	MODIFIER	DLoop	0.025
HLI-0936	750	A	G	0	544	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0936	1438	A	G	0	549	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0936	4336	T	C	6	486	upstream_gene_variant	MODIFIER	TRNQ	0.0085
HLI-0936	4769	A	G	2	549	synonymous_variant	LOW	ND2	0.9767

HLI-0936	15326	A	G	0	481	missense_variant	MODERATE	CYTB	0.9868
HLI-0936	15833	C	T	1	575	synonymous_variant	LOW	CYTB	0.0051
HLI-0936	16304	T	C	1	457	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0937	73	A	G	9	238	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0937	263	A	G	0	142	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0937	295	C	A	5	136	upstream_gene_variant	MODIFIER	DLoop	0.0012
HLI-0937	750	A	G	0	556	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0937	1391	T	C	19	564	upstream_gene_variant	MODIFIER	RNR1	0.0027
HLI-0937	1438	A	G	0	608	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0937	2706	A	G	12	494	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0937	3360	A	G	13	484	synonymous_variant	LOW	ND1	0.0013
HLI-0937	4026	A	G	8	379	synonymous_variant	LOW	ND1	8.00E-04
HLI-0937	4769	A	G	1	520	synonymous_variant	LOW	ND2	0.9767
HLI-0937	4917	A	G	17	512	missense_variant	MODERATE	ND2	0.0477
HLI-0937	5378	A	G	17	419	synonymous_variant	LOW	ND2	0.0011
HLI-0937	5586	C	T	16	553	upstream_gene_variant	MODIFIER	Unannotated	0.0011
HLI-0937	5823	A	G	13	520	upstream_gene_variant	MODIFIER	TRNC	0.0014
HLI-0937	6557	C	T	12	490	synonymous_variant	LOW	COX1	0.0011
HLI-0937	6671	T	C	16	565	synonymous_variant	LOW	COX1	0.0071
HLI-0937	7028	C	T	16	628	synonymous_variant	LOW	COX1	0.8089
HLI-0937	7424	A	G	18	491	synonymous_variant	LOW	COX1	0.0115
HLI-0937	7547	T	C	23	538	upstream_gene_variant	MODIFIER	TRND	0.0012
HLI-0937	8388	T	C	12	312	missense_variant	MODERATE	ATP8	0.0013
HLI-0937	8887	A	G	29	529	missense_variant	MODERATE	ATP6	0.0016
HLI-0937	10658	A	G	31	595	synonymous_variant	LOW	ND4L	0.0026
HLI-0937	10825	A	G	21	472	synonymous_variant	LOW	ND4	0.0011
HLI-0937	11719	G	A	12	506	synonymous_variant	LOW	ND4	0.7756
HLI-0937	13948	C	T	14	352	missense_variant	MODERATE	ND5	0.0013
HLI-0937	14632	C	T	26	535	synonymous_variant	LOW	ND6	0.0012
HLI-0937	14766	C	T	10	487	missense_variant	MODERATE	CYTB	0.7696
HLI-0937	15326	A	G	1	422	missense_variant	MODERATE	CYTB	0.9868
HLI-0937	15721	T	C	10	372	synonymous_variant	LOW	CYTB	0.0033
HLI-0937	16311	T	C	14	352	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0937	16519	T	C	7	193	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0938	263	A	G	0	200	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0938	750	A	G	1	445	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0938	1438	A	G	0	447	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0938	2392	T	C	0	375	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0938	2706	A	G	0	445	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0938	4769	A	G	0	445	synonymous_variant	LOW	ND2	0.9767
HLI-0938	7028	C	T	1	515	synonymous_variant	LOW	COX1	0.8089
HLI-0938	7094	T	C	1	546	synonymous_variant	LOW	COX1	0.0023
HLI-0938	12941	C	T	9	437	missense_variant	MODERATE	ND5	1.00E-04
HLI-0938	15326	A	G	0	385	missense_variant	MODERATE	CYTB	0.9868
HLI-0938	15514	T	C	0	322	synonymous_variant	LOW	CYTB	0.0071
HLI-0939	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0939	750	A	G	1	494	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0939	1438	A	G	0	503	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0939	1719	G	A	0	543	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0939	3010	G	A	0	468	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0939	4769	A	G	5	459	synonymous_variant	LOW	ND2	0.9767
HLI-0939	5814	T	C	0	555	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0939	7337	G	A	0	521	synonymous_variant	LOW	COX1	0.0119
HLI-0939	15326	A	G	0	454	missense_variant	MODERATE	CYTB	0.9868
HLI-0939	15601	T	C	89	440	synonymous_variant	LOW	CYTB	0.0016
HLI-0939	15758	A	G	1	507	missense_variant	MODERATE	CYTB	0.0076
HLI-0939	16311	T	C	0	390	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0939	16519	T	C	0	221	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0940	73	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0940	146	T	C	1	414	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0940	263	A	G	0	159	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0940	750	A	G	1	497	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0940	1438	A	G	0	483	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0940	1473	C	T	0	505	upstream_gene_variant	MODIFIER	RNR1	0.0126
HLI-0940	2706	A	G	0	522	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0940	3423	T	A	1	420	synonymous_variant	LOW	ND1	0.0126
HLI-0940	4769	A	G	1	460	synonymous_variant	LOW	ND2	0.9767
HLI-0940	5465	T	C	0	526	synonymous_variant	LOW	ND2	0.0434
HLI-0940	6719	T	C	2	569	synonymous_variant	LOW	COX1	0.041
HLI-0940	7028	C	T	3	555	synonymous_variant	LOW	COX1	0.8089
HLI-0940	9123	G	A	0	558	synonymous_variant	LOW	ATP6	0.0485
HLI-0940	10238	T	C	0	441	synonymous_variant	LOW	ND3	0.0623
HLI-0940	11719	G	A	0	490	synonymous_variant	LOW	ND4	0.7756
HLI-0940	12239	C	T	0	461	upstream_gene_variant	MODIFIER	TRNS2	0.0389
HLI-0940	14022	A	G	0	386	synonymous_variant	LOW	ND5	0.0366
HLI-0940	14766	C	T	1	446	missense_variant	MODERATE	CYTB	0.7696
HLI-0940	15326	A	G	0	453	missense_variant	MODERATE	CYTB	0.9868
HLI-0940	15746	A	G	0	452	missense_variant	MODERATE	CYTB	0.0395

HLI-0940	16217	T	C	0	136	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0940	16247	A	G	0	190	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-0940	16261	C	T	1	227	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0940	16519	T	C	1	140	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0941	73	A	G	0	256	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0941	152	T	C	0	470	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0941	195	T	C	0	287	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0941	225	G	T	0	306	upstream_gene_variant	MODIFIER	DLoop	0
HLI-0941	263	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0941	489	T	C	0	397	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0941	709	G	A	1	564	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0941	750	A	G	2	595	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0941	1438	A	G	0	591	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0941	1888	G	A	0	529	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0941	2706	A	G	3	540	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0941	3921	C	T	0	516	synonymous_variant	LOW	ND1	0.003
HLI-0941	4541	G	A	1	617	synonymous_variant	LOW	ND2	0.0031
HLI-0941	4769	A	G	2	542	synonymous_variant	LOW	ND2	0.9767
HLI-0941	5592	A	G	2	610	upstream_gene_variant	MODIFIER	TRNA	5.00E-04
HLI-0941	7028	C	T	5	648	synonymous_variant	LOW	COX1	0.8089
HLI-0941	8206	G	A	0	513	synonymous_variant	LOW	COX2	0.0287
HLI-0941	8701	A	G	1	483	missense_variant	MODERATE	ATP6	0.3391
HLI-0941	9540	T	C	0	515	synonymous_variant	LOW	COX3	0.339
HLI-0941	10398	A	G	1	540	missense_variant	MODERATE	ND3	0.445
HLI-0941	10400	C	T	1	546	synonymous_variant	LOW	ND3	0.2131
HLI-0941	10873	T	C	1	499	synonymous_variant	LOW	ND4	0.3389
HLI-0941	11719	G	A	0	521	synonymous_variant	LOW	ND4	0.7756
HLI-0941	11914	G	A	0	581	synonymous_variant	LOW	ND4	0.1112
HLI-0941	12477	T	C	6	511	synonymous_variant	LOW	ND5	0.0054
HLI-0941	12705	C	T	4	649	synonymous_variant	LOW	ND5	0.4212
HLI-0941	14071	A	G	0	433	missense_variant	MODERATE	ND5	3.00E-04
HLI-0941	14323	G	A	0	451	synonymous_variant	LOW	ND6	0.0058
HLI-0941	14766	C	T	0	536	missense_variant	MODERATE	CYTB	0.7696
HLI-0941	14783	T	C	0	607	synonymous_variant	LOW	CYTB	0.2126
HLI-0941	15043	G	A	1	613	synonymous_variant	LOW	CYTB	0.2362
HLI-0941	15301	G	A	1	482	synonymous_variant	LOW	CYTB	0.2912
HLI-0941	15326	A	G	1	513	missense_variant	MODERATE	CYTB	0.9868
HLI-0941	15672	T	C	1	469	missense_variant	MODERATE	CYTB	0.0014
HLI-0941	16086	T	C	4	568	upstream_gene_variant	MODIFIER	DLoop	0.0233

HLI-0941	16129	G	A	0	590	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0941	16209	T	C	1	505	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0941	16223	C	T	1	517	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0941	16261	C	T	3	518	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0941	16319	G	A	0	451	upstream_gene_variant	MODIFIER	DLoop	0.0592
HLI-0941	16355	C	T	0	419	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0941	16519	T	C	2	213	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0942	72	T	C	1	193	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0942	195	T	C	1	314	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0942	263	A	G	0	134	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0942	750	A	G	0	433	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0942	1438	A	G	0	450	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0942	2706	A	G	1	398	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0942	4769	A	G	1	444	synonymous_variant	LOW	ND2	0.9767
HLI-0942	7028	C	T	1	517	synonymous_variant	LOW	COX1	0.8089
HLI-0942	10931	T	C	0	242	missense_variant	MODERATE	ND4	1.00E-04
HLI-0942	11950	A	G	4	463	synonymous_variant	LOW	ND4	0.0012
HLI-0942	15326	A	G	0	302	missense_variant	MODERATE	CYTB	0.9868
HLI-0942	15914	A	G	1	404	upstream_gene_variant	MODIFIER	TRNT	1.00E-04
HLI-0942	16291	C	T	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0942	16298	T	C	0	333	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0943	73	A	G	0	227	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0943	152	T	C	2	426	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0943	263	A	G	0	153	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0943	709	G	A	0	499	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0943	750	A	G	3	526	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0943	930	G	A	4	489	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0943	1438	A	G	0	487	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0943	1888	G	A	0	465	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0943	2706	A	G	4	450	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0943	4216	T	C	3	481	missense_variant	MODERATE	ND1	0.0991
HLI-0943	4769	A	G	2	392	synonymous_variant	LOW	ND2	0.9767
HLI-0943	4917	A	G	0	455	missense_variant	MODERATE	ND2	0.0477
HLI-0943	5147	G	A	1	444	synonymous_variant	LOW	ND2	0.0437
HLI-0943	7028	C	T	2	540	synonymous_variant	LOW	COX1	0.8089
HLI-0943	8697	G	A	1	484	synonymous_variant	LOW	ATP6	0.0466
HLI-0943	10463	T	C	1	504	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0943	11251	A	G	0	465	synonymous_variant	LOW	ND4	0.0932
HLI-0943	11719	G	A	1	482	synonymous_variant	LOW	ND4	0.7756

HLI-0943	11812	A	G	0	447	synonymous_variant	LOW	ND4	0.0332
HLI-0943	13368	G	A	1	535	synonymous_variant	LOW	ND5	0.0495
HLI-0943	14233	A	G	0	434	synonymous_variant	LOW	ND6	0.0369
HLI-0943	14766	C	T	3	417	missense_variant	MODERATE	CYTB	0.7696
HLI-0943	14905	G	A	1	514	synonymous_variant	LOW	CYTB	0.0526
HLI-0943	15326	A	G	0	456	missense_variant	MODERATE	CYTB	0.9868
HLI-0943	15452	C	A	5	443	missense_variant	MODERATE	CYTB	0.0933
HLI-0943	15607	A	G	0	480	synonymous_variant	LOW	CYTB	0.0508
HLI-0943	15928	G	A	0	474	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0943	16126	T	C	0	457	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0943	16294	C	T	0	387	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0943	16296	C	T	0	390	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0943	16304	T	C	0	412	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0943	16519	T	C	0	191	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0944	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0944	750	A	G	0	429	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0944	870	C	T	1	443	upstream_gene_variant	MODIFIER	RNR1	0.0013
HLI-0944	1438	A	G	0	502	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0944	3010	G	A	1	479	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0944	3796	A	G	0	397	missense_variant	MODERATE	ND1	0.0048
HLI-0944	4769	A	G	1	482	synonymous_variant	LOW	ND2	0.9767
HLI-0944	10873	T	C	0	388	synonymous_variant	LOW	ND4	0.3389
HLI-0944	15326	A	G	1	357	missense_variant	MODERATE	CYTB	0.9868
HLI-0944	16356	T	C	0	324	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0944	16362	T	C	0	349	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0944	16519	T	C	0	150	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0945	73	A	G	0	228	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0945	146	T	C	0	408	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0945	195	T	C	0	387	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0945	263	A	G	0	162	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0945	750	A	G	1	460	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0945	1438	A	G	0	469	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0945	1811	A	G	1	514	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0945	2217	C	T	2	438	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0945	2706	A	G	0	449	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0945	3480	A	G	0	334	synonymous_variant	LOW	ND1	0.0392
HLI-0945	4769	A	G	1	454	synonymous_variant	LOW	ND2	0.9767
HLI-0945	5054	G	A	0	398	synonymous_variant	LOW	ND2	0.0033
HLI-0945	5231	G	A	0	388	synonymous_variant	LOW	ND2	0.0232

HLI-0945	6002	A	G	0	475	synonymous_variant	LOW	COX1	6.00E-04
HLI-0945	7028	C	T	2	565	synonymous_variant	LOW	COX1	0.8089
HLI-0945	9055	G	A	1	428	missense_variant	MODERATE	ATP6	0.0425
HLI-0945	9698	T	C	0	464	synonymous_variant	LOW	COX3	0.0405
HLI-0945	9716	T	C	0	521	synonymous_variant	LOW	COX3	0.0108
HLI-0945	10550	A	G	0	476	synonymous_variant	LOW	ND4L	0.0376
HLI-0945	11016	G	A	0	375	missense_variant	MODERATE	ND4	0.0062
HLI-0945	11299	T	C	0	443	synonymous_variant	LOW	ND4	0.0417
HLI-0945	11467	A	G	1	497	synonymous_variant	LOW	ND4	0.1231
HLI-0945	11719	G	A	1	413	synonymous_variant	LOW	ND4	0.7756
HLI-0945	11869	C	A	1	513	synonymous_variant	LOW	ND4	0.0015
HLI-0945	12308	A	G	0	394	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0945	12372	G	A	0	326	synonymous_variant	LOW	ND5	0.1329
HLI-0945	12501	G	A	2	416	synonymous_variant	LOW	ND5	0.0258
HLI-0945	14037	A	G	0	402	synonymous_variant	LOW	ND5	0.0017
HLI-0945	14167	C	T	2	403	synonymous_variant	LOW	ND6	0.0385
HLI-0945	14766	C	T	4	486	missense_variant	MODERATE	CYTB	0.7696
HLI-0945	14798	T	C	0	553	missense_variant	MODERATE	CYTB	0.0651
HLI-0945	15326	A	G	0	343	missense_variant	MODERATE	CYTB	0.9868
HLI-0945	16129	G	A	1	451	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0945	16224	T	C	0	405	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0945	16311	T	C	0	381	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0945	16519	T	C	2	188	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0946	73	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0946	151	C	T	1	420	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0946	152	T	C	1	420	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0946	263	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0946	489	T	C	1	257	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0946	740	G	A	2	481	upstream_gene_variant	MODIFIER	RNR1	7.00E-04
HLI-0946	750	A	G	2	509	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0946	1438	A	G	0	520	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0946	2706	A	G	0	523	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0946	4715	A	G	11	647	synonymous_variant	LOW	ND2	0.0416
HLI-0946	4769	A	G	2	661	synonymous_variant	LOW	ND2	0.9767
HLI-0946	6752	A	G	3	689	synonymous_variant	LOW	COX1	0.0066
HLI-0946	7028	C	T	0	608	synonymous_variant	LOW	COX1	0.8089
HLI-0946	7196	C	A	6	562	synonymous_variant	LOW	COX1	0.0389
HLI-0946	8584	G	A	9	608	missense_variant	MODERATE	ATP6	0.0521
HLI-0946	8701	A	G	11	558	missense_variant	MODERATE	ATP6	0.3391

HLI-0946	9090	T	C	4	477	synonymous_variant	LOW	ATP6	0.0038
HLI-0946	9494	A	G	2	480	synonymous_variant	LOW	COX3	0.0024
HLI-0946	9540	T	C	5	488	synonymous_variant	LOW	COX3	0.339
HLI-0946	10325	G	A	5	533	synonymous_variant	LOW	ND3	0.0041
HLI-0946	10398	A	G	0	527	missense_variant	MODERATE	ND3	0.445
HLI-0946	10400	C	T	0	531	synonymous_variant	LOW	ND3	0.2131
HLI-0946	10873	T	C	8	461	synonymous_variant	LOW	ND4	0.3389
HLI-0946	11719	G	A	1	568	synonymous_variant	LOW	ND4	0.7756
HLI-0946	12705	C	T	1	648	synonymous_variant	LOW	ND5	0.4212
HLI-0946	12930	A	G	13	510	synonymous_variant	LOW	ND5	8.00E-04
HLI-0946	14766	C	T	1	564	missense_variant	MODERATE	CYTB	0.7696
HLI-0946	14783	T	C	12	606	synonymous_variant	LOW	CYTB	0.2126
HLI-0946	15043	G	A	1	608	synonymous_variant	LOW	CYTB	0.2362
HLI-0946	15261	G	A	6	433	missense_variant	MODERATE	CYTB	0.0019
HLI-0946	15301	G	A	2	486	synonymous_variant	LOW	CYTB	0.2912
HLI-0946	15326	A	G	1	483	missense_variant	MODERATE	CYTB	0.9868
HLI-0946	15487	A	T	5	465	synonymous_variant	LOW	CYTB	0.0391
HLI-0946	15784	T	C	5	639	synonymous_variant	LOW	CYTB	0.0363
HLI-0946	16129	G	A	4	606	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0946	16223	C	T	0	587	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0946	16224	T	C	13	563	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0946	16260	C	T	10	520	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0946	16298	T	C	4	463	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0946	16519	T	C	2	235	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0947	204	T	C	0	306	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0947	239	T	C	0	248	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0947	263	A	G	0	191	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0947	750	A	G	0	516	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0947	1438	A	G	0	573	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0947	3915	G	A	0	501	synonymous_variant	LOW	ND1	0.0106
HLI-0947	4727	A	G	1	647	synonymous_variant	LOW	ND2	0.0063
HLI-0947	4769	A	G	0	660	synonymous_variant	LOW	ND2	0.9767
HLI-0947	9380	G	A	1	502	synonymous_variant	LOW	COX3	0.0094
HLI-0947	10463	T	C	0	578	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0947	10589	G	A	0	683	synonymous_variant	LOW	ND4L	0.0355
HLI-0947	13768	T	C	0	320	missense_variant	MODERATE	ND5	0.0019
HLI-0947	15326	A	G	0	480	missense_variant	MODERATE	CYTB	0.9868
HLI-0947	16219	A	G	2	626	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0947	16362	T	C	0	412	upstream_gene_variant	MODIFIER	DLoop	0.1763

HLI-0947	16482	A	G	3	299	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0948	73	A	G	0	234	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0948	185	G	A	3	393	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0948	228	G	A	1	396	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0948	263	A	G	0	116	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0948	295	C	T	0	156	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0948	462	C	T	1	337	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0948	489	T	C	0	355	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0948	750	A	G	1	489	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0948	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0948	3010	G	A	0	610	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0948	4216	T	C	1	632	missense_variant	MODERATE	ND1	0.0991
HLI-0948	4769	A	G	0	608	synonymous_variant	LOW	ND2	0.9767
HLI-0948	7028	C	T	3	639	synonymous_variant	LOW	COX1	0.8089
HLI-0948	9527	C	T	2	561	synonymous_variant	LOW	COX3	6.00E-04
HLI-0948	10398	A	G	1	531	missense_variant	MODERATE	ND3	0.445
HLI-0948	11251	A	G	0	659	synonymous_variant	LOW	ND4	0.0932
HLI-0948	11719	G	A	1	595	synonymous_variant	LOW	ND4	0.7756
HLI-0948	12612	A	G	3	646	synonymous_variant	LOW	ND5	0.0506
HLI-0948	13708	G	A	0	551	missense_variant	MODERATE	ND5	0.0717
HLI-0948	13934	C	T	1	605	missense_variant	MODERATE	ND5	0.0122
HLI-0948	14766	C	T	1	533	missense_variant	MODERATE	CYTB	0.7696
HLI-0948	14798	T	C	1	581	missense_variant	MODERATE	CYTB	0.0651
HLI-0948	15326	A	G	0	550	missense_variant	MODERATE	CYTB	0.9868
HLI-0948	15452	C	A	4	577	missense_variant	MODERATE	CYTB	0.0933
HLI-0948	16069	C	T	1	631	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0948	16126	T	C	0	663	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0948	16160	A	G	10	628	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0948	16222	C	T	4	588	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0949	146	T	C	0	528	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0949	263	A	G	0	183	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0949	750	A	G	1	571	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0949	1438	A	G	0	670	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0949	4769	A	G	1	732	synonymous_variant	LOW	ND2	0.9767
HLI-0949	6776	T	C	3	785	synonymous_variant	LOW	COX1	0.0226
HLI-0949	8245	A	G	1	718	synonymous_variant	LOW	COX2	2.00E-04
HLI-0949	9007	A	G	1	600	missense_variant	MODERATE	ATP6	0.0022
HLI-0949	15326	A	G	0	617	missense_variant	MODERATE	CYTB	0.9868
HLI-0949	15885	C	T	2	770	missense_variant	MODERATE	CYTB	8.00E-04

HLI-0949	16222	C	T	2	688	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0949	16299	A	G	0	606	upstream_gene_variant	MODIFIER	DLoop	0.0032
HLI-0949	16519	T	C	1	352	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0950	73	A	G	0	172	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0950	151	C	T	0	293	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0950	152	T	C	0	294	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0950	182	C	T	0	284	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0950	186	C	A	0	283	upstream_gene_variant	MODIFIER	DLoop	0.013
HLI-0950	189	A	C	0	280	upstream_gene_variant	MODIFIER	DLoop	0.0122
HLI-0950	247	G	A	0	112	upstream_gene_variant	MODIFIER	DLoop	0.0498
HLI-0950	263	A	G	0	123	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0950	408	T	A	0	331	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0950	494	C	T	8	362	upstream_gene_variant	MODIFIER	DLoop	0.0012
HLI-0950	750	A	G	0	499	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0950	769	G	A	0	544	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0950	825	T	A	1	587	upstream_gene_variant	MODIFIER	RNR1	0.0509
HLI-0950	1018	G	A	1	652	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0950	1438	A	G	0	548	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0950	2706	A	G	0	490	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0950	2758	G	A	0	549	upstream_gene_variant	MODIFIER	RNR2	0.0503
HLI-0950	2885	T	C	0	553	upstream_gene_variant	MODIFIER	RNR2	0.05
HLI-0950	3594	C	T	1	426	synonymous_variant	LOW	ND1	0.0789
HLI-0950	3666	G	A	0	487	synonymous_variant	LOW	ND1	0.0233
HLI-0950	4104	A	G	0	428	synonymous_variant	LOW	ND1	0.0785
HLI-0950	4769	A	G	1	589	synonymous_variant	LOW	ND2	0.9767
HLI-0950	5951	A	G	2	546	synonymous_variant	LOW	COX1	0.0128
HLI-0950	6040	A	G	40	517	missense_variant	MODERATE	COX1	0.0018
HLI-0950	6071	T	C	3	611	synonymous_variant	LOW	COX1	0.0129
HLI-0950	6221	T	A	0	511	synonymous_variant	LOW	COX1	0.0027
HLI-0950	6260	G	A	0	597	synonymous_variant	LOW	COX1	0.009
HLI-0950	6917	G	A	1	590	synonymous_variant	LOW	COX1	0.0036
HLI-0950	7022	T	C	0	600	synonymous_variant	LOW	COX1	0.0024
HLI-0950	7028	C	T	0	615	synonymous_variant	LOW	COX1	0.8089
HLI-0950	7146	A	G	3	282	missense_variant	MODERATE	COX1	0.0497
HLI-0950	7256	C	T	3	483	synonymous_variant	LOW	COX1	0.0784
HLI-0950	7389	T	C	1	516	missense_variant	MODERATE	COX1	0.0201
HLI-0950	7498	G	A	1	387	upstream_gene_variant	MODIFIER	TRNS1	0.0019
HLI-0950	7521	G	A	1	427	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0950	7789	G	A	1	584	synonymous_variant	LOW	COX2	0.0092

HLI-0950	8027	G	A	8	632	missense_variant	MODERATE	COX2	0.0334
HLI-0950	8468	C	T	0	484	synonymous_variant	LOW	ATP8	0.0501
HLI-0950	8655	C	T	1	504	synonymous_variant	LOW	ATP6	0.0511
HLI-0950	8701	A	G	0	583	missense_variant	MODERATE	ATP6	0.3391
HLI-0950	9072	A	G	0	531	synonymous_variant	LOW	ATP6	0.0124
HLI-0950	9540	T	C	0	462	synonymous_variant	LOW	COX3	0.339
HLI-0950	9966	G	A	0	602	missense_variant	MODERATE	COX3	0.0069
HLI-0950	10398	A	G	1	630	missense_variant	MODERATE	ND3	0.445
HLI-0950	10586	G	A	2	605	synonymous_variant	LOW	ND4L	0.0177
HLI-0950	10688	G	A	0	599	synonymous_variant	LOW	ND4L	0.0515
HLI-0950	10810	T	C	0	531	synonymous_variant	LOW	ND4	0.0522
HLI-0950	10873	T	C	0	513	synonymous_variant	LOW	ND4	0.3389
HLI-0950	11302	C	T	1	549	synonymous_variant	LOW	ND4	0.0028
HLI-0950	11719	G	A	1	585	synonymous_variant	LOW	ND4	0.7756
HLI-0950	12019	C	T	0	573	synonymous_variant	LOW	ND4	0.0015
HLI-0950	12501	G	A	1	684	synonymous_variant	LOW	ND5	0.0258
HLI-0950	12705	C	T	1	616	synonymous_variant	LOW	ND5	0.4212
HLI-0950	12810	A	G	4	554	synonymous_variant	LOW	ND5	0.0198
HLI-0950	13105	A	G	1	491	missense_variant	MODERATE	ND5	0.076
HLI-0950	13485	A	G	3	561	synonymous_variant	LOW	ND5	0.0122
HLI-0950	13506	C	T	4	632	synonymous_variant	LOW	ND5	0.0506
HLI-0950	13650	C	T	1	528	synonymous_variant	LOW	ND5	0.079
HLI-0950	13789	T	C	1	443	missense_variant	MODERATE	ND5	0.0185
HLI-0950	14000	T	A	1	546	missense_variant	MODERATE	ND5	0.0126
HLI-0950	14178	T	C	0	569	missense_variant	MODERATE	ND6	0.0225
HLI-0950	14560	G	A	0	589	synonymous_variant	LOW	ND6	0.0235
HLI-0950	14766	C	T	0	530	missense_variant	MODERATE	CYTB	0.7696
HLI-0950	14911	C	T	2	656	synonymous_variant	LOW	CYTB	0.0124
HLI-0950	15119	G	A	2	657	missense_variant	MODERATE	CYTB	0.0016
HLI-0950	15226	A	G	0	508	synonymous_variant	LOW	CYTB	0.0034
HLI-0950	15326	A	G	0	511	missense_variant	MODERATE	CYTB	0.9868
HLI-0950	15905	T	C	2	689	upstream_gene_variant	MODIFIER	TRNT	0.005
HLI-0950	15978	C	T	1	707	upstream_gene_variant	MODIFIER	TRNP	0.0032
HLI-0950	16129	G	A	0	349	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0950	16223	C	T	0	194	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0950	16278	C	T	0	348	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0950	16294	C	T	0	387	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0950	16311	T	C	0	416	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0950	16519	T	C	0	169	upstream_gene_variant	MODIFIER	DLoop	0.6293

HLI-0951	73	A	G	0	196	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0951	195	T	C	3	262	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0951	263	A	G	0	143	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0951	750	A	G	1	464	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0951	1438	A	G	0	492	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0951	1719	G	A	4	492	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0951	2706	A	G	0	445	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0951	4769	A	G	0	440	synonymous_variant	LOW	ND2	0.9767
HLI-0951	6221	T	C	1	412	synonymous_variant	LOW	COX1	0.0306
HLI-0951	6371	C	T	1	448	synonymous_variant	LOW	COX1	0.0097
HLI-0951	7028	C	T	2	507	synonymous_variant	LOW	COX1	0.8089
HLI-0951	11719	G	A	1	450	synonymous_variant	LOW	ND4	0.7756
HLI-0951	12705	C	T	1	511	synonymous_variant	LOW	ND5	0.4212
HLI-0951	13966	A	G	1	401	missense_variant	MODERATE	ND5	0.0126
HLI-0951	14470	T	C	1	371	synonymous_variant	LOW	ND6	0.0166
HLI-0951	14569	G	A	1	401	synonymous_variant	LOW	ND6	0.0259
HLI-0951	14766	C	T	6	413	missense_variant	MODERATE	CYTB	0.7696
HLI-0951	15326	A	G	2	382	missense_variant	MODERATE	CYTB	0.9868
HLI-0951	15734	G	A	2	491	missense_variant	MODERATE	CYTB	0.0036
HLI-0951	16150	C	T	2	159	upstream_gene_variant	MODIFIER	DLoop	0.002
HLI-0951	16223	C	T	0	163	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0951	16245	C	T	0	205	upstream_gene_variant	MODIFIER	DLoop	0.0041
HLI-0951	16248	C	T	0	215	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0951	16278	C	T	0	269	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0951	16519	T	C	0	145	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0952	73	A	G	1	178	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0952	195	T	C	1	201	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0952	263	A	G	0	116	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0952	497	C	T	2	207	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0952	750	A	G	1	377	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0952	1189	T	C	0	349	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0952	1438	A	G	1	390	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0952	1811	A	G	0	441	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0952	2706	A	G	0	391	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0952	3480	A	G	2	301	synonymous_variant	LOW	ND1	0.0392
HLI-0952	4769	A	G	3	394	synonymous_variant	LOW	ND2	0.9767
HLI-0952	7028	C	T	0	420	synonymous_variant	LOW	COX1	0.8089
HLI-0952	9055	G	A	0	380	missense_variant	MODERATE	ATP6	0.0425
HLI-0952	9698	T	C	0	396	synonymous_variant	LOW	COX3	0.0405

HLI-0952	10370	T	C	1	450	synonymous_variant	LOW	ND3	0.0019
HLI-0952	10398	A	G	2	449	missense_variant	MODERATE	ND3	0.445
HLI-0952	10550	A	G	0	369	synonymous_variant	LOW	ND4L	0.0376
HLI-0952	11299	T	C	1	406	synonymous_variant	LOW	ND4	0.0417
HLI-0952	11467	A	G	0	383	synonymous_variant	LOW	ND4	0.1231
HLI-0952	11719	G	A	1	384	synonymous_variant	LOW	ND4	0.7756
HLI-0952	12308	A	G	2	362	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0952	12372	G	A	2	376	synonymous_variant	LOW	ND5	0.1329
HLI-0952	14167	C	T	1	331	synonymous_variant	LOW	ND6	0.0385
HLI-0952	14766	C	T	0	313	missense_variant	MODERATE	CYTB	0.7696
HLI-0952	14798	T	C	3	366	missense_variant	MODERATE	CYTB	0.0651
HLI-0952	15326	A	G	0	331	missense_variant	MODERATE	CYTB	0.9868
HLI-0952	16048	G	A	0	358	upstream_gene_variant	MODIFIER	DLoop	0.0027
HLI-0952	16093	T	C	18	347	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0952	16224	T	C	1	308	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0952	16291	C	T	0	317	upstream_gene_variant	MODIFIER	DLoop	0.0275
HLI-0952	16311	T	C	0	295	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0952	16519	T	C	0	128	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0953	73	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0953	152	T	C	1	461	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0953	195	T	C	2	404	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0953	263	A	G	0	118	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0953	499	G	A	0	293	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0953	750	A	G	1	531	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0953	1438	A	G	0	574	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0953	1811	A	G	1	588	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0953	2706	A	G	0	524	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0953	4646	T	C	2	589	synonymous_variant	LOW	ND2	0.0124
HLI-0953	4769	A	G	1	557	synonymous_variant	LOW	ND2	0.9767
HLI-0953	5999	T	C	3	594	synonymous_variant	LOW	COX1	0.0127
HLI-0953	6047	A	G	5	651	synonymous_variant	LOW	COX1	0.0114
HLI-0953	7028	C	T	6	615	synonymous_variant	LOW	COX1	0.8089
HLI-0953	8818	C	T	2	534	synonymous_variant	LOW	ATP6	0.0061
HLI-0953	11332	C	T	0	610	synonymous_variant	LOW	ND4	0.0115
HLI-0953	11467	A	G	1	522	synonymous_variant	LOW	ND4	0.1231
HLI-0953	11719	G	A	0	535	synonymous_variant	LOW	ND4	0.7756
HLI-0953	12308	A	G	0	519	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0953	12372	G	A	2	490	synonymous_variant	LOW	ND5	0.1329
HLI-0953	12937	A	G	4	567	missense_variant	MODERATE	ND5	0.0026

HLI-0953	14620	C	T	3	509	synonymous_variant	LOW	ND6	0.0126
HLI-0953	14766	C	T	2	473	missense_variant	MODERATE	CYTB	0.7696
HLI-0953	15326	A	G	0	505	missense_variant	MODERATE	CYTB	0.9868
HLI-0953	15693	T	C	2	478	missense_variant	MODERATE	CYTB	0.0114
HLI-0953	16134	C	T	3	486	upstream_gene_variant	MODIFIER	DLoop	0.0036
HLI-0953	16356	T	C	2	404	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-0953	16519	T	C	0	216	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0954	263	A	G	1	238	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0954	477	T	C	0	403	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0954	750	A	G	2	543	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0954	1438	A	G	0	568	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0954	3010	G	A	0	615	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0954	4769	A	G	3	591	synonymous_variant	LOW	ND2	0.9767
HLI-0954	9150	A	G	2	597	synonymous_variant	LOW	ATP6	0.0072
HLI-0954	15326	A	G	0	427	missense_variant	MODERATE	CYTB	0.9868
HLI-0954	16263	T	C	0	561	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0954	16316	A	G	1	451	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0954	16519	T	C	0	285	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0955	151	C	T	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0955	152	T	C	0	432	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0955	263	A	G	0	197	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0955	750	A	G	0	497	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0955	1438	A	G	0	546	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0955	4769	A	G	0	523	synonymous_variant	LOW	ND2	0.9767
HLI-0955	6776	T	C	4	639	synonymous_variant	LOW	COX1	0.0226
HLI-0955	13404	T	C	1	459	synonymous_variant	LOW	ND5	0.0015
HLI-0955	14125	C	T	2	421	synonymous_variant	LOW	ND5	3.00E-04
HLI-0955	15326	A	G	0	367	missense_variant	MODERATE	CYTB	0.9868
HLI-0955	16239	C	G	2	463	upstream_gene_variant	MODIFIER	DLoop	5.00E-04
HLI-0955	16519	T	C	0	204	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0956	73	A	G	0	212	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0956	152	T	C	0	392	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0956	263	A	G	0	158	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0956	497	C	T	0	320	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0956	750	A	G	0	438	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0956	1189	T	C	1	475	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0956	1438	A	G	1	480	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0956	1811	A	G	3	473	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0956	2706	A	G	0	396	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0956	3480	A	G	1	393	synonymous_variant	LOW	ND1	0.0392
HLI-0956	4769	A	G	3	431	synonymous_variant	LOW	ND2	0.9767
HLI-0956	7028	C	T	1	504	synonymous_variant	LOW	COX1	0.8089
HLI-0956	9055	G	A	1	425	missense_variant	MODERATE	ATP6	0.0425
HLI-0956	9698	T	C	1	417	synonymous_variant	LOW	COX3	0.0405
HLI-0956	10398	A	G	2	463	missense_variant	MODERATE	ND3	0.445
HLI-0956	10550	A	G	1	454	synonymous_variant	LOW	ND4L	0.0376
HLI-0956	11299	T	C	3	439	synonymous_variant	LOW	ND4	0.0417
HLI-0956	11467	A	G	1	480	synonymous_variant	LOW	ND4	0.1231
HLI-0956	11719	G	A	0	409	synonymous_variant	LOW	ND4	0.7756
HLI-0956	12308	A	G	2	412	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0956	12338	T	C	1	439	start_lost	HIGH	ND5	0.0034
HLI-0956	12372	G	A	1	381	synonymous_variant	LOW	ND5	0.1329
HLI-0956	14167	C	T	2	346	synonymous_variant	LOW	ND6	0.0385
HLI-0956	14766	C	T	3	398	missense_variant	MODERATE	CYTB	0.7696
HLI-0956	14798	T	C	1	464	missense_variant	MODERATE	CYTB	0.0651
HLI-0956	15326	A	G	0	366	missense_variant	MODERATE	CYTB	0.9868
HLI-0956	16224	T	C	1	406	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0956	16311	T	C	3	337	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0956	16519	T	C	0	218	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0957	73	A	G	0	260	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0957	263	A	G	0	186	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0957	499	G	A	0	296	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-0957	750	A	G	1	515	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0957	827	A	G	1	590	upstream_gene_variant	MODIFIER	RNR1	0.025
HLI-0957	1438	A	G	0	500	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0957	2706	A	G	0	504	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0957	3338	T	C	0	503	missense_variant	MODERATE	ND1	0.002
HLI-0957	4769	A	G	0	526	synonymous_variant	LOW	ND2	0.9767
HLI-0957	4820	G	A	2	560	synonymous_variant	LOW	ND2	0.0239
HLI-0957	7028	C	T	5	574	synonymous_variant	LOW	COX1	0.8089
HLI-0957	7521	G	A	0	448	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0957	9101	T	G	4	523	missense_variant	MODERATE	ATP6	2.00E-04
HLI-0957	11239	A	G	2	517	synonymous_variant	LOW	ND4	6.00E-04
HLI-0957	11719	G	A	1	494	synonymous_variant	LOW	ND4	0.7756
HLI-0957	13590	G	A	0	480	synonymous_variant	LOW	ND5	0.0586
HLI-0957	14587	A	G	0	512	synonymous_variant	LOW	ND6	0.006
HLI-0957	14766	C	T	3	458	missense_variant	MODERATE	CYTB	0.7696
HLI-0957	15172	G	A	0	486	synonymous_variant	LOW	CYTB	0.0075

HLI-0957	15326	A	G	0	390	missense_variant	MODERATE	CYTB	0.9868
HLI-0957	15535	C	T	1	376	synonymous_variant	LOW	CYTB	0.023
HLI-0957	16136	T	C	0	226	upstream_gene_variant	MODIFIER	DLoop	0.009
HLI-0957	16217	T	C	0	126	upstream_gene_variant	MODIFIER	DLoop	0.0734
HLI-0957	16218	C	T	0	128	upstream_gene_variant	MODIFIER	DLoop	0.0062
HLI-0957	16311	T	C	1	309	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0957	16324	T	C	1	321	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0957	16519	T	C	1	159	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0958	73	A	G	0	250	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0958	153	A	G	8	408	upstream_gene_variant	MODIFIER	DLoop	0.034
HLI-0958	195	T	C	5	414	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0958	225	G	A	4	363	upstream_gene_variant	MODIFIER	DLoop	0.0077
HLI-0958	227	A	G	4	356	upstream_gene_variant	MODIFIER	DLoop	0.0034
HLI-0958	263	A	G	1	102	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0958	750	A	G	0	528	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0958	1438	A	G	1	533	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0958	1719	G	A	3	507	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0958	2706	A	G	3	576	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0958	3386	T	C	0	514	missense_variant	MODERATE	ND1	0
HLI-0958	4769	A	G	1	525	synonymous_variant	LOW	ND2	0.9767
HLI-0958	6221	T	C	6	504	synonymous_variant	LOW	COX1	0.0306
HLI-0958	6371	C	T	2	513	synonymous_variant	LOW	COX1	0.0097
HLI-0958	7028	C	T	3	577	synonymous_variant	LOW	COX1	0.8089
HLI-0958	8705	T	C	1	491	missense_variant	MODERATE	ATP6	0.0039
HLI-0958	11719	G	A	1	535	synonymous_variant	LOW	ND4	0.7756
HLI-0958	12705	C	T	5	632	synonymous_variant	LOW	ND5	0.4212
HLI-0958	13966	A	G	0	509	missense_variant	MODERATE	ND5	0.0126
HLI-0958	14470	T	C	1	454	synonymous_variant	LOW	ND6	0.0166
HLI-0958	14766	C	T	8	484	missense_variant	MODERATE	CYTB	0.7696
HLI-0958	15326	A	G	0	520	missense_variant	MODERATE	CYTB	0.9868
HLI-0958	16108	C	T	2	256	upstream_gene_variant	MODIFIER	DLoop	0.0071
HLI-0958	16223	C	T	3	181	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0958	16255	G	A	0	253	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0958	16278	C	T	1	305	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0958	16519	T	C	0	191	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0959	73	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0959	242	C	T	0	347	upstream_gene_variant	MODIFIER	DLoop	0.0039
HLI-0959	263	A	G	0	312	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0959	295	C	T	0	227	upstream_gene_variant	MODIFIER	DLoop	0.0469

HLI-0959	462	C	T	4	438	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0959	489	T	C	1	521	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0959	750	A	G	0	653	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0959	1438	A	G	0	626	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0959	2158	T	C	1	476	upstream_gene_variant	MODIFIER	RNR2	0.0041
HLI-0959	2706	A	G	2	663	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0959	3010	G	A	0	642	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0959	4216	T	C	2	528	missense_variant	MODERATE	ND1	0.0991
HLI-0959	4769	A	G	1	623	synonymous_variant	LOW	ND2	0.9767
HLI-0959	5460	G	A	2	576	missense_variant	MODERATE	ND2	0.0651
HLI-0959	7028	C	T	6	686	synonymous_variant	LOW	COX1	0.8089
HLI-0959	8269	G	A	1	475	stop_retained_variant	LOW	COX2	0.0127
HLI-0959	8557	G	A	0	432	missense_variant	MODERATE	ATP6/8	0.0058
HLI-0959	10398	A	G	1	593	missense_variant	MODERATE	ND3	0.445
HLI-0959	11251	A	G	0	632	synonymous_variant	LOW	ND4	0.0932
HLI-0959	11719	G	A	0	608	synonymous_variant	LOW	ND4	0.7756
HLI-0959	12007	G	A	0	524	synonymous_variant	LOW	ND4	0.0639
HLI-0959	12612	A	G	9	558	synonymous_variant	LOW	ND5	0.0506
HLI-0959	13708	G	A	2	394	missense_variant	MODERATE	ND5	0.0717
HLI-0959	13879	T	C	0	565	missense_variant	MODERATE	ND5	0.0073
HLI-0959	14022	A	G	0	560	synonymous_variant	LOW	ND5	0.0366
HLI-0959	14766	C	T	3	597	missense_variant	MODERATE	CYTB	0.7696
HLI-0959	15326	A	G	0	502	missense_variant	MODERATE	CYTB	0.9868
HLI-0959	15452	C	A	1	484	missense_variant	MODERATE	CYTB	0.0933
HLI-0959	16069	C	T	2	559	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0959	16126	T	C	1	582	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0959	16145	G	A	1	602	upstream_gene_variant	MODIFIER	DLoop	0.0286
HLI-0959	16172	T	C	1	574	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0959	16222	C	T	2	549	upstream_gene_variant	MODIFIER	DLoop	0.0079
HLI-0959	16261	C	T	1	567	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0960	73	A	G	0	311	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0960	195	T	C	0	417	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0960	263	A	G	1	275	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0960	497	C	T	3	453	upstream_gene_variant	MODIFIER	DLoop	0.0213
HLI-0960	631	A	G	0	552	upstream_gene_variant	MODIFIER	TRNF	0
HLI-0960	739	C	T	0	567	upstream_gene_variant	MODIFIER	RNR1	0.0018
HLI-0960	748	G	A	0	600	upstream_gene_variant	MODIFIER	RNR1	1.00E-04
HLI-0960	750	A	G	0	611	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0960	1189	T	C	1	656	upstream_gene_variant	MODIFIER	RNR1	0.0318

HLI-0960	1438	A	G	0	623	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0960	1811	A	G	0	596	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0960	2706	A	G	0	645	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0960	3434	A	G	0	576	missense_variant	MODERATE	ND1	0.0088
HLI-0960	3480	A	G	1	574	synonymous_variant	LOW	ND1	0.0392
HLI-0960	4769	A	G	1	623	synonymous_variant	LOW	ND2	0.9767
HLI-0960	5252	G	A	0	540	synonymous_variant	LOW	ND2	0.0027
HLI-0960	7028	C	T	7	690	synonymous_variant	LOW	COX1	0.8089
HLI-0960	9055	G	A	1	544	missense_variant	MODERATE	ATP6	0.0425
HLI-0960	9698	T	C	0	546	synonymous_variant	LOW	COX3	0.0405
HLI-0960	10398	A	G	1	532	missense_variant	MODERATE	ND3	0.445
HLI-0960	10550	A	G	0	622	synonymous_variant	LOW	ND4L	0.0376
HLI-0960	11299	T	C	0	541	synonymous_variant	LOW	ND4	0.0417
HLI-0960	11467	A	G	0	618	synonymous_variant	LOW	ND4	0.1231
HLI-0960	11719	G	A	0	553	synonymous_variant	LOW	ND4	0.7756
HLI-0960	12007	G	A	0	550	synonymous_variant	LOW	ND4	0.0639
HLI-0960	12308	A	G	0	595	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0960	12372	G	A	1	576	synonymous_variant	LOW	ND5	0.1329
HLI-0960	14167	C	T	0	530	synonymous_variant	LOW	ND6	0.0385
HLI-0960	14766	C	T	2	586	missense_variant	MODERATE	CYTB	0.7696
HLI-0960	14798	T	C	0	678	missense_variant	MODERATE	CYTB	0.0651
HLI-0960	15326	A	G	1	546	missense_variant	MODERATE	CYTB	0.9868
HLI-0960	16093	T	C	9	571	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0960	16224	T	C	0	508	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0960	16311	T	C	1	460	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0960	16519	T	C	1	269	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0961	73	A	G	1	264	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0961	199	T	C	0	332	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0961	203	G	A	0	338	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0961	204	T	C	0	338	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0961	250	T	C	0	139	upstream_gene_variant	MODIFIER	DLoop	0.0145
HLI-0961	263	A	G	0	156	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0961	750	A	G	0	612	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0961	1438	A	G	0	652	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0961	1719	G	A	0	617	upstream_gene_variant	MODIFIER	RNR2	0.0474
HLI-0961	2706	A	G	0	652	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0961	3447	A	G	2	561	synonymous_variant	LOW	ND1	0.0053
HLI-0961	3990	C	T	2	552	synonymous_variant	LOW	ND1	0.0031
HLI-0961	4529	A	T	5	584	synonymous_variant	LOW	ND2	0.015

HLI-0961	4769	A	G	1	527	synonymous_variant	LOW	ND2	0.9767
HLI-0961	6734	G	A	3	750	synonymous_variant	LOW	COX1	0.0062
HLI-0961	7028	C	T	0	650	synonymous_variant	LOW	COX1	0.8089
HLI-0961	8251	G	A	3	518	synonymous_variant	LOW	COX2	0.058
HLI-0961	8616	G	T	1	563	missense_variant	MODERATE	ATP6	0.0032
HLI-0961	9947	G	A	1	648	synonymous_variant	LOW	COX3	0.0092
HLI-0961	10034	T	C	2	654	upstream_gene_variant	MODIFIER	TRNG	0.0157
HLI-0961	10238	T	C	0	517	synonymous_variant	LOW	ND3	0.0623
HLI-0961	10398	A	G	0	726	missense_variant	MODERATE	ND3	0.445
HLI-0961	10915	T	C	2	470	synonymous_variant	LOW	ND4	0.0411
HLI-0961	11719	G	A	0	586	synonymous_variant	LOW	ND4	0.7756
HLI-0961	12501	G	A	1	571	synonymous_variant	LOW	ND5	0.0258
HLI-0961	12705	C	T	3	682	synonymous_variant	LOW	ND5	0.4212
HLI-0961	13404	T	C	0	577	synonymous_variant	LOW	ND5	0.0015
HLI-0961	13780	A	G	2	421	missense_variant	MODERATE	ND5	0.0179
HLI-0961	14766	C	T	1	581	missense_variant	MODERATE	CYTB	0.7696
HLI-0961	15043	G	A	0	625	synonymous_variant	LOW	CYTB	0.2362
HLI-0961	15326	A	G	0	539	missense_variant	MODERATE	CYTB	0.9868
HLI-0961	15924	A	G	2	597	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0961	16129	G	A	0	622	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0961	16172	T	C	1	602	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0961	16223	C	T	3	604	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0961	16311	T	C	0	545	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0961	16391	G	A	2	491	upstream_gene_variant	MODIFIER	DLoop	0.0155
HLI-0961	16519	T	C	0	258	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0962	73	A	G	0	278	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0962	146	T	C	1	504	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0962	152	T	C	1	516	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0962	204	T	C	0	480	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0962	207	G	A	0	479	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0962	263	A	G	0	211	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0962	709	G	A	1	542	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0962	750	A	G	1	594	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0962	1438	A	G	1	588	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0962	1811	A	G	0	542	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0962	2706	A	G	1	517	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0962	3480	A	G	0	435	synonymous_variant	LOW	ND1	0.0392
HLI-0962	4561	T	C	0	637	missense_variant	MODERATE	ND2	0.0065
HLI-0962	4769	A	G	1	587	synonymous_variant	LOW	ND2	0.9767

HLI-0962	5495	T	C	0	641	synonymous_variant	LOW	ND2	0.0051
HLI-0962	7028	C	T	3	657	synonymous_variant	LOW	COX1	0.8089
HLI-0962	9055	G	A	0	567	missense_variant	MODERATE	ATP6	0.0425
HLI-0962	9698	T	C	0	625	synonymous_variant	LOW	COX3	0.0405
HLI-0962	9716	T	C	1	670	synonymous_variant	LOW	COX3	0.0108
HLI-0962	10550	A	G	1	619	synonymous_variant	LOW	ND4L	0.0376
HLI-0962	11299	T	C	1	587	synonymous_variant	LOW	ND4	0.0417
HLI-0962	11467	A	G	1	613	synonymous_variant	LOW	ND4	0.1231
HLI-0962	11719	G	A	0	570	synonymous_variant	LOW	ND4	0.7756
HLI-0962	12308	A	G	0	494	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0962	12372	G	A	0	472	synonymous_variant	LOW	ND5	0.1329
HLI-0962	14167	C	T	1	480	synonymous_variant	LOW	ND6	0.0385
HLI-0962	14766	C	T	3	693	missense_variant	MODERATE	CYTB	0.7696
HLI-0962	14798	T	C	0	800	missense_variant	MODERATE	CYTB	0.0651
HLI-0962	15326	A	G	0	444	missense_variant	MODERATE	CYTB	0.9868
HLI-0962	16224	T	C	0	308	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0962	16286	C	T	1	398	upstream_gene_variant	MODIFIER	DLoop	0.0052
HLI-0962	16311	T	C	1	440	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0962	16519	T	C	0	182	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0963	73	A	G	0	338	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0963	195	T	C	1	495	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0963	263	A	G	0	215	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0963	750	A	G	0	655	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0963	1189	T	C	0	666	upstream_gene_variant	MODIFIER	RNR1	0.0318
HLI-0963	1438	A	G	0	713	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0963	1811	A	G	0	796	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0963	2706	A	G	1	717	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0963	3480	A	G	1	619	synonymous_variant	LOW	ND1	0.0392
HLI-0963	4769	A	G	0	495	synonymous_variant	LOW	ND2	0.9767
HLI-0963	4856	T	C	0	518	synonymous_variant	LOW	ND2	0.0021
HLI-0963	5592	A	G	1	683	upstream_gene_variant	MODIFIER	TRNA	5.00E-04
HLI-0963	7028	C	T	4	752	synonymous_variant	LOW	COX1	0.8089
HLI-0963	8901	A	G	0	691	synonymous_variant	LOW	ATP6	0.0023
HLI-0963	9055	G	A	0	663	missense_variant	MODERATE	ATP6	0.0425
HLI-0963	9698	T	C	4	684	synonymous_variant	LOW	COX3	0.0405
HLI-0963	10398	A	G	1	631	missense_variant	MODERATE	ND3	0.445
HLI-0963	10550	A	G	1	693	synonymous_variant	LOW	ND4L	0.0376
HLI-0963	11299	T	C	0	621	synonymous_variant	LOW	ND4	0.0417
HLI-0963	11467	A	G	1	709	synonymous_variant	LOW	ND4	0.1231

HLI-0963	11719	G	A	1	645	synonymous_variant	LOW	ND4	0.7756
HLI-0963	12308	A	G	1	650	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0963	12372	G	A	1	687	synonymous_variant	LOW	ND5	0.1329
HLI-0963	14167	C	T	0	618	synonymous_variant	LOW	ND6	0.0385
HLI-0963	14766	C	T	4	662	missense_variant	MODERATE	CYTB	0.7696
HLI-0963	14798	T	C	2	731	missense_variant	MODERATE	CYTB	0.0651
HLI-0963	15326	A	G	0	643	missense_variant	MODERATE	CYTB	0.9868
HLI-0963	16224	T	C	1	579	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0963	16311	T	C	0	557	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0963	16362	T	C	0	602	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0963	16519	T	C	0	273	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0964	73	A	G	0	325	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0964	146	T	C	2	553	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0964	263	A	G	0	279	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0964	750	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0964	1438	A	G	0	663	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0964	3010	G	A	1	622	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0964	4769	A	G	2	629	synonymous_variant	LOW	ND2	0.9767
HLI-0964	15326	A	G	0	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0964	16162	A	G	0	595	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0964	16519	T	C	2	287	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0965	152	T	C	17	540	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0965	263	A	G	0	229	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0965	709	G	A	1	655	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0965	750	A	G	2	724	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0965	1438	A	G	0	649	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0965	2706	A	G	0	651	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0965	4769	A	G	1	574	synonymous_variant	LOW	ND2	0.9767
HLI-0965	7028	C	T	0	703	synonymous_variant	LOW	COX1	0.8089
HLI-0965	8014	A	T	0	634	synonymous_variant	LOW	COX2	0.0024
HLI-0965	8251	G	A	1	564	synonymous_variant	LOW	COX2	0.058
HLI-0965	15218	A	G	0	602	missense_variant	MODERATE	CYTB	0.0169
HLI-0965	15326	A	G	0	582	missense_variant	MODERATE	CYTB	0.9868
HLI-0965	16067	C	T	3	584	upstream_gene_variant	MODIFIER	DLoop	0.0033
HLI-0965	16129	G	A	1	658	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0965	16368	T	C	1	477	upstream_gene_variant	MODIFIER	DLoop	0.006
HLI-0966	73	A	G	1	257	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0966	189	A	G	6	462	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0966	195	T	C	7	451	upstream_gene_variant	MODIFIER	DLoop	0.196

HLI-0966	204	T	C	7	448	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0966	207	G	A	7	452	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0966	263	A	G	0	148	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0966	709	G	A	9	630	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0966	750	A	G	0	701	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0966	1243	T	C	9	717	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0966	1438	A	G	0	671	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0966	2706	A	G	0	652	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0966	3505	A	G	2	599	missense_variant	MODERATE	ND1	0.0144
HLI-0966	4769	A	G	2	596	synonymous_variant	LOW	ND2	0.9767
HLI-0966	5046	G	A	7	615	missense_variant	MODERATE	ND2	0.018
HLI-0966	5460	G	A	5	648	missense_variant	MODERATE	ND2	0.0651
HLI-0966	7028	C	T	1	720	synonymous_variant	LOW	COX1	0.8089
HLI-0966	7864	C	T	6	631	synonymous_variant	LOW	COX2	0.0041
HLI-0966	8251	G	A	10	595	synonymous_variant	LOW	COX2	0.058
HLI-0966	8659	A	G	5	599	missense_variant	MODERATE	ATP6	0.0022
HLI-0966	8887	A	G	4	674	missense_variant	MODERATE	ATP6	0.0016
HLI-0966	8994	G	A	1	601	synonymous_variant	LOW	ATP6	0.0167
HLI-0966	10398	A	G	1	648	missense_variant	MODERATE	ND3	0.445
HLI-0966	11674	C	T	11	631	synonymous_variant	LOW	ND4	0.0116
HLI-0966	11719	G	A	2	694	synonymous_variant	LOW	ND4	0.7756
HLI-0966	11947	A	G	8	588	synonymous_variant	LOW	ND4	0.011
HLI-0966	12414	T	C	1	606	synonymous_variant	LOW	ND5	0.0139
HLI-0966	12705	C	T	1	629	synonymous_variant	LOW	ND5	0.4212
HLI-0966	14766	C	T	5	625	missense_variant	MODERATE	CYTB	0.7696
HLI-0966	15326	A	G	0	588	missense_variant	MODERATE	CYTB	0.9868
HLI-0966	15884	G	C	3	657	missense_variant	MODERATE	CYTB	0.011
HLI-0966	16223	C	T	4	571	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0966	16292	C	T	1	559	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0966	16295	C	T	3	559	upstream_gene_variant	MODIFIER	DLoop	0.0196
HLI-0966	16324	T	C	1	509	upstream_gene_variant	MODIFIER	DLoop	0.0086
HLI-0966	16519	T	C	0	319	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0967	114	C	T	4	453	upstream_gene_variant	MODIFIER	DLoop	0.0044
HLI-0967	146	T	C	0	542	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0967	152	T	C	0	548	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0967	195	T	C	2	481	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0967	263	A	G	0	194	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0967	709	G	A	0	629	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0967	750	A	G	2	686	upstream_gene_variant	MODIFIER	RNR1	0.9821

HLI-0967	1438	A	G	0	650	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0967	4769	A	G	0	590	synonymous_variant	LOW	ND2	0.9767
HLI-0967	5093	T	C	3	614	synonymous_variant	LOW	ND2	0.0014
HLI-0967	11623	C	T	4	610	synonymous_variant	LOW	ND4	6.00E-04
HLI-0967	13101	A	C	1	622	synonymous_variant	LOW	ND5	0.0055
HLI-0967	13711	G	A	2	504	missense_variant	MODERATE	ND5	0.0011
HLI-0967	13752	T	C	1	533	synonymous_variant	LOW	ND5	7.00E-04
HLI-0967	15326	A	G	0	598	missense_variant	MODERATE	CYTB	0.9868
HLI-0967	16258	A	G	0	596	upstream_gene_variant	MODIFIER	DLoop	0.0012
HLI-0967	16263	T	C	0	579	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0967	16288	T	C	0	551	upstream_gene_variant	MODIFIER	DLoop	0.0072
HLI-0967	16362	T	C	0	441	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0968	73	A	G	0	132	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0968	263	A	G	1	249	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0968	709	G	A	3	247	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0968	750	A	G	1	278	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0968	930	G	A	1	375	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0968	1438	A	G	0	244	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0968	1888	G	A	3	269	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0968	2706	A	G	3	268	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0968	4216	T	C	0	301	missense_variant	MODERATE	ND1	0.0991
HLI-0968	4769	A	G	0	338	synonymous_variant	LOW	ND2	0.9767
HLI-0968	4917	A	G	0	453	missense_variant	MODERATE	ND2	0.0477
HLI-0968	5147	G	A	1	401	synonymous_variant	LOW	ND2	0.0437
HLI-0968	6593	A	G	5	385	synonymous_variant	LOW	COX1	2.00E-04
HLI-0968	7028	C	T	2	348	synonymous_variant	LOW	COX1	0.8089
HLI-0968	8697	G	A	2	623	synonymous_variant	LOW	ATP6	0.0466
HLI-0968	9254	A	G	0	297	synonymous_variant	LOW	COX3	0.0083
HLI-0968	10463	T	C	0	484	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0968	11251	A	G	1	298	synonymous_variant	LOW	ND4	0.0932
HLI-0968	11719	G	A	0	410	synonymous_variant	LOW	ND4	0.7756
HLI-0968	11812	A	G	0	283	synonymous_variant	LOW	ND4	0.0332
HLI-0968	13368	G	A	0	393	synonymous_variant	LOW	ND5	0.0495
HLI-0968	14233	A	G	2	631	synonymous_variant	LOW	ND6	0.0369
HLI-0968	14766	C	T	3	695	missense_variant	MODERATE	CYTB	0.7696
HLI-0968	14905	G	A	1	452	synonymous_variant	LOW	CYTB	0.0526
HLI-0968	15326	A	G	0	243	missense_variant	MODERATE	CYTB	0.9868
HLI-0968	15452	C	A	4	239	missense_variant	MODERATE	CYTB	0.0933
HLI-0968	15607	A	G	1	257	synonymous_variant	LOW	CYTB	0.0508

HLI-0968	15928	G	A	1	438	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0968	16126	T	C	0	610	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0968	16172	T	C	0	575	upstream_gene_variant	MODIFIER	DLoop	0.0748
HLI-0968	16266	C	T	87	378	upstream_gene_variant	MODIFIER	DLoop	0.0135
HLI-0968	16294	C	T	6	435	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0968	16304	T	C	6	426	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0968	16519	T	C	0	131	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0969	263	A	G	1	217	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0969	750	A	G	0	569	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0969	1438	A	G	0	614	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0969	4769	A	G	0	635	synonymous_variant	LOW	ND2	0.9767
HLI-0969	4793	A	G	0	608	synonymous_variant	LOW	ND2	0.0073
HLI-0969	15326	A	G	0	489	missense_variant	MODERATE	CYTB	0.9868
HLI-0969	16519	T	C	0	302	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0970	73	A	G	0	271	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0970	263	A	G	0	185	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0970	338	C	T	0	158	upstream_gene_variant	MODIFIER	DLoop	0.0011
HLI-0970	709	G	A	2	575	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0970	750	A	G	2	612	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0970	1438	A	G	0	639	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0970	1888	G	A	0	562	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0970	2706	A	G	1	565	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0970	4216	T	C	3	514	missense_variant	MODERATE	ND1	0.0991
HLI-0970	4769	A	G	0	544	synonymous_variant	LOW	ND2	0.9767
HLI-0970	4917	A	G	0	479	missense_variant	MODERATE	ND2	0.0477
HLI-0970	6260	G	A	2	562	synonymous_variant	LOW	COX1	0.009
HLI-0970	7028	C	T	4	611	synonymous_variant	LOW	COX1	0.8089
HLI-0970	8697	G	A	0	483	synonymous_variant	LOW	ATP6	0.0466
HLI-0970	10463	T	C	0	554	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0970	11251	A	G	0	516	synonymous_variant	LOW	ND4	0.0932
HLI-0970	11719	G	A	2	520	synonymous_variant	LOW	ND4	0.7756
HLI-0970	11812	A	G	0	535	synonymous_variant	LOW	ND4	0.0332
HLI-0970	12397	A	G	2	429	missense_variant	MODERATE	ND5	0.0069
HLI-0970	13368	G	A	1	580	synonymous_variant	LOW	ND5	0.0495
HLI-0970	14233	A	G	0	451	synonymous_variant	LOW	ND6	0.0369
HLI-0970	14766	C	T	0	471	missense_variant	MODERATE	CYTB	0.7696
HLI-0970	14905	G	A	0	590	synonymous_variant	LOW	CYTB	0.0526
HLI-0970	15326	A	G	0	477	missense_variant	MODERATE	CYTB	0.9868
HLI-0970	15452	C	A	4	470	missense_variant	MODERATE	CYTB	0.0933

HLI-0970	15607	A	G	1	475	synonymous_variant	LOW	CYTB	0.0508
HLI-0970	15928	G	A	0	538	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0970	16126	T	C	1	575	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0970	16294	C	T	0	533	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0970	16296	C	T	0	539	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0970	16519	T	C	0	230	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0971	73	A	G	0	289	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0971	182	C	T	1	458	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0971	185	G	A	14	452	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0971	228	G	A	0	160	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0971	263	A	G	0	187	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0971	295	C	T	0	165	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0971	462	C	T	2	445	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0971	489	T	C	0	353	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0971	750	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0971	1438	A	G	0	619	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0971	2706	A	G	2	593	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0971	3010	G	A	3	556	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0971	4216	T	C	3	531	missense_variant	MODERATE	ND1	0.0991
HLI-0971	4769	A	G	2	513	synonymous_variant	LOW	ND2	0.9767
HLI-0971	7028	C	T	4	694	synonymous_variant	LOW	COX1	0.8089
HLI-0971	10398	A	G	1	606	missense_variant	MODERATE	ND3	0.445
HLI-0971	11251	A	G	2	538	synonymous_variant	LOW	ND4	0.0932
HLI-0971	11719	G	A	1	599	synonymous_variant	LOW	ND4	0.7756
HLI-0971	12612	A	G	7	599	synonymous_variant	LOW	ND5	0.0506
HLI-0971	13708	G	A	0	461	missense_variant	MODERATE	ND5	0.0717
HLI-0971	13934	C	T	1	517	missense_variant	MODERATE	ND5	0.0122
HLI-0971	14766	C	T	4	553	missense_variant	MODERATE	CYTB	0.7696
HLI-0971	14798	T	C	0	612	missense_variant	MODERATE	CYTB	0.0651
HLI-0971	15326	A	G	0	522	missense_variant	MODERATE	CYTB	0.9868
HLI-0971	15452	C	A	2	554	missense_variant	MODERATE	CYTB	0.0933
HLI-0971	16069	C	T	3	583	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0971	16126	T	C	0	561	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0972	263	A	G	1	230	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0972	750	A	G	2	579	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0972	1438	A	G	1	570	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0972	3010	G	A	1	560	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0972	4769	A	G	0	567	synonymous_variant	LOW	ND2	0.9767
HLI-0972	11084	A	G	0	535	missense_variant	MODERATE	ND4	0.004

HLI-0972	15326	A	G	1	502	missense_variant	MODERATE	CYTB	0.9868
HLI-0972	16519	T	C	0	326	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0973	73	A	G	0	304	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0973	185	G	A	4	453	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0973	228	G	A	1	380	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0973	263	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0973	295	C	T	0	237	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0973	462	C	T	3	481	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0973	489	T	C	0	528	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0973	750	A	G	1	650	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0973	1438	A	G	0	646	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0973	2706	A	G	0	625	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0973	3010	G	A	0	658	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0973	4216	T	C	2	566	missense_variant	MODERATE	ND1	0.0991
HLI-0973	4769	A	G	1	591	synonymous_variant	LOW	ND2	0.9767
HLI-0973	6617	C	T	1	741	synonymous_variant	LOW	COX1	2.00E-04
HLI-0973	7028	C	T	4	709	synonymous_variant	LOW	COX1	0.8089
HLI-0973	10398	A	G	0	622	missense_variant	MODERATE	ND3	0.445
HLI-0973	11251	A	G	1	629	synonymous_variant	LOW	ND4	0.0932
HLI-0973	11719	G	A	0	570	synonymous_variant	LOW	ND4	0.7756
HLI-0973	12612	A	G	6	660	synonymous_variant	LOW	ND5	0.0506
HLI-0973	13708	G	A	0	574	missense_variant	MODERATE	ND5	0.0717
HLI-0973	13763	C	T	6	595	missense_variant	MODERATE	ND5	1.00E-04
HLI-0973	13934	C	T	1	500	missense_variant	MODERATE	ND5	0.0122
HLI-0973	14766	C	T	4	591	missense_variant	MODERATE	CYTB	0.7696
HLI-0973	14798	T	C	1	693	missense_variant	MODERATE	CYTB	0.0651
HLI-0973	15326	A	G	0	492	missense_variant	MODERATE	CYTB	0.9868
HLI-0973	15452	C	A	6	470	missense_variant	MODERATE	CYTB	0.0933
HLI-0973	16069	C	T	1	546	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0973	16126	T	C	1	617	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0973	16316	A	G	0	481	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0973	16390	G	A	0	518	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0973	16519	T	C	1	285	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0974	73	A	G	0	344	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0974	146	T	C	0	557	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0974	195	T	C	2	519	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0974	263	A	G	0	203	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0974	750	A	G	2	683	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0974	1189	T	C	1	716	upstream_gene_variant	MODIFIER	RNR1	0.0318

HLI-0974	1438	A	G	0	700	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0974	1811	A	G	1	747	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0974	2706	A	G	0	675	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0974	3480	A	G	0	653	synonymous_variant	LOW	ND1	0.0392
HLI-0974	4769	A	G	2	646	synonymous_variant	LOW	ND2	0.9767
HLI-0974	5237	G	A	0	636	synonymous_variant	LOW	ND2	0.0039
HLI-0974	5913	G	A	2	723	missense_variant	MODERATE	COX1	0.0097
HLI-0974	6845	C	T	3	782	synonymous_variant	LOW	COX1	4.00E-04
HLI-0974	7028	C	T	3	787	synonymous_variant	LOW	COX1	0.8089
HLI-0974	9055	G	A	1	659	missense_variant	MODERATE	ATP6	0.0425
HLI-0974	9698	T	C	1	700	synonymous_variant	LOW	COX3	0.0405
HLI-0974	10154	A	G	1	669	synonymous_variant	LOW	ND3	4.00E-04
HLI-0974	10398	A	G	1	706	missense_variant	MODERATE	ND3	0.445
HLI-0974	10550	A	G	2	659	synonymous_variant	LOW	ND4L	0.0376
HLI-0974	11299	T	C	3	648	synonymous_variant	LOW	ND4	0.0417
HLI-0974	11467	A	G	3	668	synonymous_variant	LOW	ND4	0.1231
HLI-0974	11719	G	A	2	620	synonymous_variant	LOW	ND4	0.7756
HLI-0974	12308	A	G	1	642	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0974	12372	G	A	2	678	synonymous_variant	LOW	ND5	0.1329
HLI-0974	12738	T	G	6	742	synonymous_variant	LOW	ND5	0.0019
HLI-0974	14167	C	T	2	565	synonymous_variant	LOW	ND6	0.0385
HLI-0974	14766	C	T	2	603	missense_variant	MODERATE	CYTB	0.7696
HLI-0974	14798	T	C	1	699	missense_variant	MODERATE	CYTB	0.0651
HLI-0974	15301	G	A	0	690	synonymous_variant	LOW	CYTB	0.2912
HLI-0974	15326	A	G	0	747	missense_variant	MODERATE	CYTB	0.9868
HLI-0974	16224	T	C	0	627	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0974	16311	T	C	0	599	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0974	16519	T	C	0	347	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0975	73	A	G	0	360	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0975	150	C	T	2	647	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0975	263	A	G	1	256	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0975	750	A	G	1	695	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0975	1438	A	G	0	698	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0975	2652	G	A	0	718	upstream_gene_variant	MODIFIER	RNR2	1.00E-04
HLI-0975	2706	A	G	0	708	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0975	3197	T	C	0	644	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0975	4769	A	G	2	623	synonymous_variant	LOW	ND2	0.9767
HLI-0975	5656	A	G	1	671	upstream_gene_variant	MODIFIER	Unannotated	0.0121
HLI-0975	7028	C	T	2	758	synonymous_variant	LOW	COX1	0.8089

HLI-0975	7768	A	G	2	633	synonymous_variant	LOW	COX2	0.0186
HLI-0975	9477	G	A	1	712	missense_variant	MODERATE	COX3	0.0387
HLI-0975	10370	T	C	0	714	synonymous_variant	LOW	ND3	0.0019
HLI-0975	11467	A	G	0	640	synonymous_variant	LOW	ND4	0.1231
HLI-0975	11719	G	A	1	632	synonymous_variant	LOW	ND4	0.7756
HLI-0975	12308	A	G	1	649	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0975	12372	G	A	1	674	synonymous_variant	LOW	ND5	0.1329
HLI-0975	13617	T	C	0	535	synonymous_variant	LOW	ND5	0.038
HLI-0975	14182	T	C	1	546	synonymous_variant	LOW	ND6	0.0254
HLI-0975	14766	C	T	0	554	missense_variant	MODERATE	CYTB	0.7696
HLI-0975	15326	A	G	0	653	missense_variant	MODERATE	CYTB	0.9868
HLI-0975	15388	T	C	1	659	synonymous_variant	LOW	CYTB	8.00E-04
HLI-0975	16270	C	T	1	411	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-0975	16519	T	C	0	259	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0976	263	A	G	1	246	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0976	750	A	G	1	616	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0976	1438	A	G	1	691	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0976	3010	G	A	0	643	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0976	4769	A	G	2	609	synonymous_variant	LOW	ND2	0.9767
HLI-0976	5460	G	A	3	603	missense_variant	MODERATE	ND2	0.0651
HLI-0976	6587	C	T	3	666	synonymous_variant	LOW	COX1	0.0084
HLI-0976	8512	A	G	3	573	synonymous_variant	LOW	ATP8	0.0036
HLI-0976	14902	C	T	5	759	synonymous_variant	LOW	CYTB	0.0024
HLI-0976	15326	A	G	0	504	missense_variant	MODERATE	CYTB	0.9868
HLI-0976	16093	T	C	21	591	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0976	16519	T	C	0	315	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0976	16523	A	G	0	321	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-0977	263	A	G	0	193	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0977	750	A	G	0	536	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0977	951	G	A	0	603	upstream_gene_variant	MODIFIER	RNR1	0.0077
HLI-0977	3834	G	A	3	553	synonymous_variant	LOW	ND1	0.0087
HLI-0977	12172	A	G	2	510	upstream_gene_variant	MODIFIER	TRNH	0.0064
HLI-0977	15326	A	G	0	412	missense_variant	MODERATE	CYTB	0.9868
HLI-0977	16224	T	C	0	531	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0977	16354	C	T	0	439	upstream_gene_variant	MODIFIER	DLoop	0.0092
HLI-0977	16519	T	C	0	292	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0978	73	A	G	0	249	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0978	143	G	A	0	457	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0978	146	T	C	0	474	upstream_gene_variant	MODIFIER	DLoop	0.1945

HLI-0978	152	T	C	0	483	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0978	195	T	C	1	469	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0978	263	A	G	0	233	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0978	534	C	T	1	457	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0978	750	A	G	0	579	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0978	769	G	A	0	625	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0978	1018	G	A	0	640	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0978	1438	A	G	0	603	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0978	2416	T	C	0	417	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0978	2706	A	G	0	573	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0978	2789	C	T	1	624	upstream_gene_variant	MODIFIER	RNR2	0.0216
HLI-0978	3594	C	T	1	542	synonymous_variant	LOW	ND1	0.0789
HLI-0978	4104	A	G	0	422	synonymous_variant	LOW	ND1	0.0785
HLI-0978	4769	A	G	1	573	synonymous_variant	LOW	ND2	0.9767
HLI-0978	7028	C	T	4	612	synonymous_variant	LOW	COX1	0.8089
HLI-0978	7175	T	C	1	543	synonymous_variant	LOW	COX1	0.0224
HLI-0978	7256	C	T	5	619	synonymous_variant	LOW	COX1	0.0784
HLI-0978	7274	C	T	5	580	synonymous_variant	LOW	COX1	0.0214
HLI-0978	7521	G	A	0	546	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0978	7771	A	G	1	653	synonymous_variant	LOW	COX2	0.0223
HLI-0978	8206	G	A	0	543	synonymous_variant	LOW	COX2	0.0287
HLI-0978	8701	A	G	0	581	missense_variant	MODERATE	ATP6	0.3391
HLI-0978	9221	A	G	1	597	synonymous_variant	LOW	COX3	0.0277
HLI-0978	9386	T	C	1	617	synonymous_variant	LOW	COX3	7.00E-04
HLI-0978	9540	T	C	1	561	synonymous_variant	LOW	COX3	0.339
HLI-0978	10115	T	C	1	657	synonymous_variant	LOW	ND3	0.0278
HLI-0978	10398	A	G	0	475	missense_variant	MODERATE	ND3	0.445
HLI-0978	10873	T	C	2	536	synonymous_variant	LOW	ND4	0.3389
HLI-0978	11719	G	A	0	569	synonymous_variant	LOW	ND4	0.7756
HLI-0978	11914	G	A	1	567	synonymous_variant	LOW	ND4	0.1112
HLI-0978	11944	T	C	2	603	synonymous_variant	LOW	ND4	0.0331
HLI-0978	12408	T	C	1	473	synonymous_variant	LOW	ND5	0.0016
HLI-0978	12693	A	G	1	556	synonymous_variant	LOW	ND5	0.0205
HLI-0978	12705	C	T	1	606	synonymous_variant	LOW	ND5	0.4212
HLI-0978	13590	G	A	0	497	synonymous_variant	LOW	ND5	0.0586
HLI-0978	13650	C	T	0	495	synonymous_variant	LOW	ND5	0.079
HLI-0978	13803	A	G	0	352	synonymous_variant	LOW	ND5	0.0216
HLI-0978	14566	A	G	1	536	synonymous_variant	LOW	ND6	0.0214
HLI-0978	14766	C	T	1	567	missense_variant	MODERATE	CYTB	0.7696

HLI-0978	15301	G	A	0	458	synonymous_variant	LOW	CYTB	0.2912
HLI-0978	15326	A	G	0	492	missense_variant	MODERATE	CYTB	0.9868
HLI-0978	15784	T	C	1	471	synonymous_variant	LOW	CYTB	0.0363
HLI-0978	15880	A	G	0	537	synonymous_variant	LOW	CYTB	2.00E-04
HLI-0978	16093	T	C	23	511	upstream_gene_variant	MODIFIER	DLoop	0.0573
HLI-0978	16124	T	C	1	577	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0978	16223	C	T	0	450	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0978	16278	C	T	0	446	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0978	16294	C	T	0	438	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0978	16309	A	G	0	426	upstream_gene_variant	MODIFIER	DLoop	0.029
HLI-0978	16390	G	A	0	444	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0978	16519	T	C	0	198	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0979	73	A	G	0	238	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0979	185	G	A	2	425	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0979	263	A	G	0	316	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0979	295	C	T	0	262	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0979	462	C	T	0	371	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0979	489	T	C	1	398	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0979	750	A	G	0	330	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0979	1438	A	G	0	365	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0979	1888	G	A	0	286	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0979	2706	A	G	1	370	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0979	3010	G	A	3	378	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0979	4216	T	C	0	319	missense_variant	MODERATE	ND1	0.0991
HLI-0979	4769	A	G	1	487	synonymous_variant	LOW	ND2	0.9767
HLI-0979	7028	C	T	0	479	synonymous_variant	LOW	COX1	0.8089
HLI-0979	9301	C	T	0	459	missense_variant	MODERATE	COX3	4.00E-04
HLI-0979	10398	A	G	1	544	missense_variant	MODERATE	ND3	0.445
HLI-0979	11251	A	G	1	398	synonymous_variant	LOW	ND4	0.0932
HLI-0979	11719	G	A	0	460	synonymous_variant	LOW	ND4	0.7756
HLI-0979	12612	A	G	2	507	synonymous_variant	LOW	ND5	0.0506
HLI-0979	13708	G	A	2	408	missense_variant	MODERATE	ND5	0.0717
HLI-0979	13934	C	T	1	336	missense_variant	MODERATE	ND5	0.0122
HLI-0979	14766	C	T	2	749	missense_variant	MODERATE	CYTB	0.7696
HLI-0979	14798	T	C	0	728	missense_variant	MODERATE	CYTB	0.0651
HLI-0979	15326	A	G	0	297	missense_variant	MODERATE	CYTB	0.9868
HLI-0979	15367	C	T	1	242	synonymous_variant	LOW	CYTB	6.00E-04
HLI-0979	15452	C	A	0	258	missense_variant	MODERATE	CYTB	0.0933
HLI-0979	16069	C	T	0	573	upstream_gene_variant	MODIFIER	DLoop	0.0496

HLI-0979	16126	T	C	0	676	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0979	16224	T	C	4	361	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0980	73	A	G	0	314	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0980	151	C	T	2	590	upstream_gene_variant	MODIFIER	DLoop	0.0343
HLI-0980	263	A	G	0	268	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0980	709	G	A	1	639	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0980	750	A	G	0	683	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0980	930	G	A	1	646	upstream_gene_variant	MODIFIER	RNR1	0.0202
HLI-0980	1438	A	G	1	674	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0980	1888	G	A	0	572	upstream_gene_variant	MODIFIER	RNR2	0.0558
HLI-0980	2706	A	G	1	674	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0980	4216	T	C	2	600	missense_variant	MODERATE	ND1	0.0991
HLI-0980	4769	A	G	2	577	synonymous_variant	LOW	ND2	0.9767
HLI-0980	4917	A	G	3	661	missense_variant	MODERATE	ND2	0.0477
HLI-0980	5147	G	A	4	456	synonymous_variant	LOW	ND2	0.0437
HLI-0980	7028	C	T	3	702	synonymous_variant	LOW	COX1	0.8089
HLI-0980	8697	G	A	1	628	synonymous_variant	LOW	ATP6	0.0466
HLI-0980	10463	T	C	0	638	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0980	11251	A	G	0	613	synonymous_variant	LOW	ND4	0.0932
HLI-0980	11719	G	A	2	611	synonymous_variant	LOW	ND4	0.7756
HLI-0980	11812	A	G	3	628	synonymous_variant	LOW	ND4	0.0332
HLI-0980	13368	G	A	0	672	synonymous_variant	LOW	ND5	0.0495
HLI-0980	14233	A	G	1	553	synonymous_variant	LOW	ND6	0.0369
HLI-0980	14766	C	T	2	632	missense_variant	MODERATE	CYTB	0.7696
HLI-0980	14905	G	A	0	807	synonymous_variant	LOW	CYTB	0.0526
HLI-0980	15326	A	G	0	453	missense_variant	MODERATE	CYTB	0.9868
HLI-0980	15452	C	A	2	478	missense_variant	MODERATE	CYTB	0.0933
HLI-0980	15607	A	G	0	499	synonymous_variant	LOW	CYTB	0.0508
HLI-0980	15928	G	A	0	667	upstream_gene_variant	MODIFIER	TRNT	0.049
HLI-0980	16126	T	C	1	675	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0980	16294	C	T	0	554	upstream_gene_variant	MODIFIER	DLoop	0.0934
HLI-0980	16296	C	T	0	556	upstream_gene_variant	MODIFIER	DLoop	0.0228
HLI-0980	16304	T	C	0	592	upstream_gene_variant	MODIFIER	DLoop	0.0746
HLI-0980	16519	T	C	0	294	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0981	263	A	G	0	288	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0981	750	A	G	0	724	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0981	1438	A	G	0	696	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0981	3010	G	A	1	725	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0981	3766	T	C	1	634	synonymous_variant	LOW	ND1	9.00E-04

HLI-0981	4769	A	G	0	629	synonymous_variant	LOW	ND2	0.9767
HLI-0981	6719	T	C	5	826	synonymous_variant	LOW	COX1	0.041
HLI-0981	8245	A	G	4	748	synonymous_variant	LOW	COX2	2.00E-04
HLI-0981	12618	G	A	4	714	synonymous_variant	LOW	ND5	0.0137
HLI-0981	13368	G	A	0	700	synonymous_variant	LOW	ND5	0.0495
HLI-0981	15326	A	G	0	589	missense_variant	MODERATE	CYTB	0.9868
HLI-0981	16519	T	C	0	338	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0982	146	T	C	0	556	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0982	195	T	C	1	516	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0982	263	A	G	1	231	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0982	750	A	G	0	615	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0982	1438	A	G	0	663	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0982	4769	A	G	1	636	synonymous_variant	LOW	ND2	0.9767
HLI-0982	7930	A	T	0	698	synonymous_variant	LOW	COX2	0.001
HLI-0982	10771	A	G	2	567	synonymous_variant	LOW	ND4	0.001
HLI-0982	15299	T	C	0	585	synonymous_variant	LOW	CYTB	0.0014
HLI-0982	15326	A	G	0	617	missense_variant	MODERATE	CYTB	0.9868
HLI-0982	16519	T	C	1	316	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0983	263	A	G	0	280	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0983	477	T	C	0	487	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0983	750	A	G	0	708	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0983	1438	A	G	0	750	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0983	3010	G	A	0	725	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0983	4769	A	G	1	601	synonymous_variant	LOW	ND2	0.9767
HLI-0983	9078	T	C	0	669	synonymous_variant	LOW	ATP6	9.00E-04
HLI-0983	9150	A	G	1	777	synonymous_variant	LOW	ATP6	0.0072
HLI-0983	9380	G	A	0	723	synonymous_variant	LOW	COX3	0.0094
HLI-0983	15326	A	G	1	619	missense_variant	MODERATE	CYTB	0.9868
HLI-0983	16263	T	C	0	609	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0983	16519	T	C	1	385	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0984	73	A	G	0	355	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0984	146	T	C	0	631	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-0984	195	T	C	1	619	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0984	263	A	G	0	306	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0984	750	A	G	1	686	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0984	1438	A	G	0	668	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0984	1811	A	G	0	575	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0984	2217	C	T	0	453	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-0984	2706	A	G	0	646	upstream_gene_variant	MODIFIER	RNR2	0.7914

HLI-0984	3480	A	G	0	504	synonymous_variant	LOW	ND1	0.0392
HLI-0984	4769	A	G	1	656	synonymous_variant	LOW	ND2	0.9767
HLI-0984	5054	G	A	1	503	synonymous_variant	LOW	ND2	0.0033
HLI-0984	5231	G	A	2	547	synonymous_variant	LOW	ND2	0.0232
HLI-0984	6002	A	G	1	697	synonymous_variant	LOW	COX1	6.00E-04
HLI-0984	7028	C	T	4	701	synonymous_variant	LOW	COX1	0.8089
HLI-0984	9055	G	A	0	618	missense_variant	MODERATE	ATP6	0.0425
HLI-0984	9698	T	C	0	577	synonymous_variant	LOW	COX3	0.0405
HLI-0984	9716	T	C	0	657	synonymous_variant	LOW	COX3	0.0108
HLI-0984	10550	A	G	1	744	synonymous_variant	LOW	ND4L	0.0376
HLI-0984	11016	G	A	3	547	missense_variant	MODERATE	ND4	0.0062
HLI-0984	11299	T	C	2	656	synonymous_variant	LOW	ND4	0.0417
HLI-0984	11467	A	G	1	660	synonymous_variant	LOW	ND4	0.1231
HLI-0984	11719	G	A	0	651	synonymous_variant	LOW	ND4	0.7756
HLI-0984	11869	C	A	3	637	synonymous_variant	LOW	ND4	0.0015
HLI-0984	12308	A	G	0	461	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0984	12372	G	A	1	423	synonymous_variant	LOW	ND5	0.1329
HLI-0984	12501	G	A	3	567	synonymous_variant	LOW	ND5	0.0258
HLI-0984	14037	A	G	0	458	synonymous_variant	LOW	ND5	0.0017
HLI-0984	14167	C	T	2	549	synonymous_variant	LOW	ND6	0.0385
HLI-0984	14766	C	T	3	694	missense_variant	MODERATE	CYTB	0.7696
HLI-0984	14798	T	C	1	803	missense_variant	MODERATE	CYTB	0.0651
HLI-0984	15326	A	G	0	461	missense_variant	MODERATE	CYTB	0.9868
HLI-0984	16129	G	A	0	579	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0984	16224	T	C	1	584	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-0984	16311	T	C	0	561	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0984	16519	T	C	0	271	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0985	263	A	G	0	286	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0985	709	G	A	2	743	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0985	750	A	G	2	789	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0985	2259	C	T	2	700	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-0985	4769	A	G	0	689	synonymous_variant	LOW	ND2	0.9767
HLI-0985	8266	A	G	4	685	synonymous_variant	LOW	COX2	3.00E-04
HLI-0985	9548	G	A	3	706	synonymous_variant	LOW	COX3	0.0149
HLI-0985	13762	T	G	0	507	missense_variant	MODERATE	ND5	7.00E-04
HLI-0985	14066	C	T	0	587	missense_variant	MODERATE	ND5	1.00E-04
HLI-0985	14872	C	T	2	710	synonymous_variant	LOW	CYTB	0.0061
HLI-0985	15217	G	A	0	722	synonymous_variant	LOW	CYTB	0.0104
HLI-0985	15326	A	G	0	678	missense_variant	MODERATE	CYTB	0.9868

HLI-0986	263	A	G	0	227	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0986	477	T	C	2	503	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0986	750	A	G	2	749	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0986	1438	A	G	0	781	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0986	3010	G	A	3	719	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0986	4769	A	G	2	693	synonymous_variant	LOW	ND2	0.9767
HLI-0986	6482	C	T	2	720	synonymous_variant	LOW	COX1	3.00E-04
HLI-0986	6959	C	T	4	815	synonymous_variant	LOW	COX1	4.00E-04
HLI-0986	14260	A	G	1	580	synonymous_variant	LOW	ND6	0.0034
HLI-0986	15326	A	G	0	661	missense_variant	MODERATE	CYTB	0.9868
HLI-0986	16362	T	C	0	605	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0986	16519	T	C	1	383	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0987	204	T	C	0	361	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0987	239	T	C	0	291	upstream_gene_variant	MODIFIER	DLoop	0.0114
HLI-0987	263	A	G	0	232	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0987	750	A	G	0	527	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0987	1438	A	G	0	647	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0987	3915	G	A	0	523	synonymous_variant	LOW	ND1	0.0106
HLI-0987	4727	A	G	1	575	synonymous_variant	LOW	ND2	0.0063
HLI-0987	4769	A	G	1	617	synonymous_variant	LOW	ND2	0.9767
HLI-0987	9380	G	A	0	560	synonymous_variant	LOW	COX3	0.0094
HLI-0987	10463	T	C	1	517	upstream_gene_variant	MODIFIER	TRNR	0.0474
HLI-0987	10589	G	A	1	592	synonymous_variant	LOW	ND4L	0.0355
HLI-0987	13768	T	C	0	273	missense_variant	MODERATE	ND5	0.0019
HLI-0987	15326	A	G	0	424	missense_variant	MODERATE	CYTB	0.9868
HLI-0987	16219	A	G	2	553	upstream_gene_variant	MODIFIER	DLoop	0.0073
HLI-0987	16362	T	C	0	410	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0987	16482	A	G	0	323	upstream_gene_variant	MODIFIER	DLoop	0.0067
HLI-0988	73	A	G	0	341	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0988	185	G	A	5	484	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0988	228	G	A	1	404	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0988	263	A	G	1	309	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0988	295	C	T	1	256	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0988	462	C	T	4	531	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0988	489	T	C	2	568	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0988	750	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0988	1438	A	G	0	717	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0988	2706	A	G	1	603	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0988	3010	G	A	2	648	upstream_gene_variant	MODIFIER	RNR2	0.1449

HLI-0988	4216	T	C	0	610	missense_variant	MODERATE	ND1	0.0991
HLI-0988	4769	A	G	0	679	synonymous_variant	LOW	ND2	0.9767
HLI-0988	7028	C	T	1	746	synonymous_variant	LOW	COX1	0.8089
HLI-0988	10398	A	G	2	641	missense_variant	MODERATE	ND3	0.445
HLI-0988	11251	A	G	2	641	synonymous_variant	LOW	ND4	0.0932
HLI-0988	11719	G	A	1	584	synonymous_variant	LOW	ND4	0.7756
HLI-0988	12612	A	G	7	685	synonymous_variant	LOW	ND5	0.0506
HLI-0988	13708	G	A	0	525	missense_variant	MODERATE	ND5	0.0717
HLI-0988	13934	C	T	1	581	missense_variant	MODERATE	ND5	0.0122
HLI-0988	14766	C	T	2	620	missense_variant	MODERATE	CYTB	0.7696
HLI-0988	14798	T	C	3	728	missense_variant	MODERATE	CYTB	0.0651
HLI-0988	15326	A	G	0	530	missense_variant	MODERATE	CYTB	0.9868
HLI-0988	15452	C	A	2	521	missense_variant	MODERATE	CYTB	0.0933
HLI-0988	15838	C	T	0	539	synonymous_variant	LOW	CYTB	0
HLI-0988	16069	C	T	2	534	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0988	16126	T	C	1	347	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0988	16290	C	T	1	426	upstream_gene_variant	MODIFIER	DLoop	0.0394
HLI-0988	16362	T	C	1	526	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0989	72	T	C	0	341	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-0989	263	A	G	0	239	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0989	750	A	G	1	667	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0989	1438	A	G	0	652	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0989	2706	A	G	0	631	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0989	4580	G	A	1	578	synonymous_variant	LOW	ND2	0.0169
HLI-0989	4769	A	G	0	517	synonymous_variant	LOW	ND2	0.9767
HLI-0989	7028	C	T	3	676	synonymous_variant	LOW	COX1	0.8089
HLI-0989	9368	A	G	0	671	synonymous_variant	LOW	COX3	8.00E-04
HLI-0989	15326	A	G	0	564	missense_variant	MODERATE	CYTB	0.9868
HLI-0989	15904	C	T	1	615	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-0989	16261	C	T	1	586	upstream_gene_variant	MODIFIER	DLoop	0.0754
HLI-0989	16298	T	C	0	599	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-0989	16311	T	C	0	586	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-0989	16519	T	C	0	291	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0990	73	A	G	1	242	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0990	150	C	T	0	416	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0990	152	T	C	0	419	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0990	182	C	T	1	423	upstream_gene_variant	MODIFIER	DLoop	0.0281
HLI-0990	195	T	C	1	410	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0990	198	C	T	1	398	upstream_gene_variant	MODIFIER	DLoop	0.0245

HLI-0990	204	T	C	1	413	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0990	263	A	G	0	223	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0990	418	C	T	0	491	upstream_gene_variant	MODIFIER	DLoop	0.0013
HLI-0990	750	A	G	1	558	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0990	769	G	A	0	602	upstream_gene_variant	MODIFIER	RNR1	0.0819
HLI-0990	1018	G	A	0	720	upstream_gene_variant	MODIFIER	RNR1	0.0817
HLI-0990	1438	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0990	1442	G	A	0	650	upstream_gene_variant	MODIFIER	RNR1	0.0061
HLI-0990	1706	C	T	0	555	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0990	2332	C	T	2	460	upstream_gene_variant	MODIFIER	RNR2	0.0056
HLI-0990	2358	A	G	2	496	upstream_gene_variant	MODIFIER	RNR2	0.0022
HLI-0990	2416	T	C	3	525	upstream_gene_variant	MODIFIER	RNR2	0.0337
HLI-0990	2706	A	G	1	619	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0990	3594	C	T	1	431	synonymous_variant	LOW	ND1	0.0789
HLI-0990	4104	A	G	1	405	synonymous_variant	LOW	ND1	0.0785
HLI-0990	4158	A	G	3	452	synonymous_variant	LOW	ND1	0.0023
HLI-0990	4370	T	C	0	580	upstream_gene_variant	MODIFIER	TRNQ	0.0023
HLI-0990	4767	A	G	0	648	missense_variant	MODERATE	ND2	0.0029
HLI-0990	4769	A	G	0	655	synonymous_variant	LOW	ND2	0.9767
HLI-0990	5027	C	T	2	474	synonymous_variant	LOW	ND2	0.003
HLI-0990	5331	C	A	1	605	missense_variant	MODERATE	ND2	0.0022
HLI-0990	5814	T	C	1	693	upstream_gene_variant	MODIFIER	TRNC	0.003
HLI-0990	6026	G	A	0	579	synonymous_variant	LOW	COX1	0.0163
HLI-0990	6713	C	T	5	883	synonymous_variant	LOW	COX1	0.0028
HLI-0990	7028	C	T	1	673	synonymous_variant	LOW	COX1	0.8089
HLI-0990	7256	C	T	4	674	synonymous_variant	LOW	COX1	0.0784
HLI-0990	7521	G	A	0	495	upstream_gene_variant	MODIFIER	TRND	0.082
HLI-0990	7624	T	A	1	521	synonymous_variant	LOW	COX2	0.0047
HLI-0990	8080	C	T	1	673	synonymous_variant	LOW	COX2	0.0022
HLI-0990	8206	G	A	1	559	synonymous_variant	LOW	COX2	0.0287
HLI-0990	8387	G	A	0	476	missense_variant	MODERATE	ATP8	0.0028
HLI-0990	8580	C	T	0	554	synonymous_variant	LOW	ATP6	1.00E-04
HLI-0990	8701	A	G	1	603	missense_variant	MODERATE	ATP6	0.3391
HLI-0990	8856	G	A	0	584	synonymous_variant	LOW	ATP6	0.004
HLI-0990	9221	A	G	1	607	synonymous_variant	LOW	COX3	0.0277
HLI-0990	9540	T	C	0	424	synonymous_variant	LOW	COX3	0.339
HLI-0990	10115	T	C	0	790	synonymous_variant	LOW	ND3	0.0278
HLI-0990	10398	A	G	0	691	missense_variant	MODERATE	ND3	0.445
HLI-0990	10828	T	C	0	518	synonymous_variant	LOW	ND4	0.0015

HLI-0990	10873	T	C	0	549	synonymous_variant	LOW	ND4	0.3389
HLI-0990	11719	G	A	3	577	synonymous_variant	LOW	ND4	0.7756
HLI-0990	11944	T	C	0	621	synonymous_variant	LOW	ND4	0.0331
HLI-0990	12236	G	A	4	618	upstream_gene_variant	MODIFIER	TRNS2	0.0075
HLI-0990	12705	C	T	1	629	synonymous_variant	LOW	ND5	0.4212
HLI-0990	12948	A	G	4	547	synonymous_variant	LOW	ND5	0.0022
HLI-0990	13590	G	A	0	488	synonymous_variant	LOW	ND5	0.0586
HLI-0990	13650	C	T	0	528	synonymous_variant	LOW	ND5	0.079
HLI-0990	13924	C	T	0	474	missense_variant	MODERATE	ND5	0.0013
HLI-0990	14059	A	G	1	483	missense_variant	MODERATE	ND5	0.0022
HLI-0990	14766	C	T	2	582	missense_variant	MODERATE	CYTB	0.7696
HLI-0990	15110	G	A	0	693	missense_variant	MODERATE	CYTB	0.009
HLI-0990	15217	G	A	1	523	synonymous_variant	LOW	CYTB	0.0104
HLI-0990	15301	G	A	0	445	synonymous_variant	LOW	CYTB	0.2912
HLI-0990	15326	A	G	0	434	missense_variant	MODERATE	CYTB	0.9868
HLI-0990	16114	C	A	2	590	upstream_gene_variant	MODIFIER	DLoop	0.005
HLI-0990	16129	G	A	1	662	upstream_gene_variant	MODIFIER	DLoop	0.1301
HLI-0990	16213	G	A	0	575	upstream_gene_variant	MODIFIER	DLoop	0.0118
HLI-0990	16223	C	T	0	618	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0990	16278	C	T	2	571	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-0990	16355	C	T	0	472	upstream_gene_variant	MODIFIER	DLoop	0.0147
HLI-0990	16362	T	C	0	472	upstream_gene_variant	MODIFIER	DLoop	0.1763
HLI-0990	16390	G	A	2	426	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0991	73	A	G	0	241	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0991	143	G	A	2	379	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-0991	189	A	G	2	351	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0991	195	T	C	1	342	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0991	204	T	C	0	325	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-0991	207	G	A	0	325	upstream_gene_variant	MODIFIER	DLoop	0.0472
HLI-0991	263	A	G	0	126	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0991	709	G	A	0	547	upstream_gene_variant	MODIFIER	RNR1	0.1279
HLI-0991	750	A	G	3	574	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0991	1243	T	C	2	571	upstream_gene_variant	MODIFIER	RNR1	0.0161
HLI-0991	1438	A	G	0	511	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0991	2706	A	G	1	522	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0991	3505	A	G	1	431	missense_variant	MODERATE	ND1	0.0144
HLI-0991	4769	A	G	0	520	synonymous_variant	LOW	ND2	0.9767
HLI-0991	5046	G	A	0	511	missense_variant	MODERATE	ND2	0.018
HLI-0991	5460	G	A	0	510	missense_variant	MODERATE	ND2	0.0651

HLI-0991	5580	T	C	1	462	upstream_gene_variant	MODIFIER	Unannotated	0.0038
HLI-0991	7028	C	T	6	588	synonymous_variant	LOW	COX1	0.8089
HLI-0991	7080	T	C	2	623	missense_variant	MODERATE	COX1	0.001
HLI-0991	7864	C	T	1	575	synonymous_variant	LOW	COX2	0.0041
HLI-0991	8251	G	A	2	475	synonymous_variant	LOW	COX2	0.058
HLI-0991	8994	G	A	1	550	synonymous_variant	LOW	ATP6	0.0167
HLI-0991	11674	C	T	4	520	synonymous_variant	LOW	ND4	0.0116
HLI-0991	11719	G	A	0	575	synonymous_variant	LOW	ND4	0.7756
HLI-0991	11947	A	G	0	509	synonymous_variant	LOW	ND4	0.011
HLI-0991	12414	T	C	2	440	synonymous_variant	LOW	ND5	0.0139
HLI-0991	12705	C	T	0	609	synonymous_variant	LOW	ND5	0.4212
HLI-0991	14766	C	T	1	505	missense_variant	MODERATE	CYTB	0.7696
HLI-0991	15326	A	G	0	455	missense_variant	MODERATE	CYTB	0.9868
HLI-0991	15884	G	C	0	588	missense_variant	MODERATE	CYTB	0.011
HLI-0991	16292	C	T	0	454	upstream_gene_variant	MODIFIER	DLoop	0.0243
HLI-0991	16519	T	C	0	257	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0992	73	A	G	0	281	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0992	150	C	T	0	523	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0992	263	A	G	0	175	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0992	750	A	G	1	567	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0992	1438	A	G	0	583	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0992	1811	A	G	2	655	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-0992	2706	A	G	0	593	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0992	3546	C	A	5	460	synonymous_variant	LOW	ND1	9.00E-04
HLI-0992	4188	A	G	1	492	synonymous_variant	LOW	ND1	0.003
HLI-0992	4640	C	A	1	574	missense_variant	MODERATE	ND2	0.0029
HLI-0992	4769	A	G	0	544	synonymous_variant	LOW	ND2	0.9767
HLI-0992	6359	A	G	2	544	synonymous_variant	LOW	COX1	0.0014
HLI-0992	7028	C	T	2	595	synonymous_variant	LOW	COX1	0.8089
HLI-0992	8867	T	C	0	510	missense_variant	MODERATE	ATP6	6.00E-04
HLI-0992	9656	T	C	0	601	synonymous_variant	LOW	COX3	0.0035
HLI-0992	11467	A	G	0	555	synonymous_variant	LOW	ND4	0.1231
HLI-0992	11719	G	A	1	527	synonymous_variant	LOW	ND4	0.7756
HLI-0992	12308	A	G	1	550	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0992	12372	G	A	0	512	synonymous_variant	LOW	ND5	0.1329
HLI-0992	12720	A	G	1	601	synonymous_variant	LOW	ND5	0.0302
HLI-0992	13743	T	C	0	382	synonymous_variant	LOW	ND5	0.0037
HLI-0992	14139	A	G	1	439	synonymous_variant	LOW	ND5	0.0056
HLI-0992	14766	C	T	4	478	missense_variant	MODERATE	CYTB	0.7696

HLI-0992	15326	A	G	1	551	missense_variant	MODERATE	CYTB	0.9868
HLI-0992	15454	T	C	0	518	synonymous_variant	LOW	CYTB	0.0072
HLI-0992	16343	A	G	1	428	upstream_gene_variant	MODIFIER	DLoop	0.0097
HLI-0993	150	C	T	0	399	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0993	263	A	G	0	222	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0993	750	A	G	0	457	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0993	1438	A	G	0	471	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0993	3010	G	A	1	482	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0993	4769	A	G	1	487	synonymous_variant	LOW	ND2	0.9767
HLI-0993	5460	G	A	1	531	missense_variant	MODERATE	ND2	0.0651
HLI-0993	12372	G	A	0	500	synonymous_variant	LOW	ND5	0.1329
HLI-0993	15326	A	G	0	331	missense_variant	MODERATE	CYTB	0.9868
HLI-0993	16519	T	C	0	180	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0994	73	A	G	0	226	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0994	199	T	C	0	327	upstream_gene_variant	MODIFIER	DLoop	0.061
HLI-0994	263	A	G	0	131	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0994	466	T	C	0	160	upstream_gene_variant	MODIFIER	DLoop	0.0015
HLI-0994	750	A	G	2	441	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0994	1007	G	A	0	444	upstream_gene_variant	MODIFIER	RNR1	0.0015
HLI-0994	1438	A	G	0	447	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0994	1700	T	C	0	448	upstream_gene_variant	MODIFIER	RNR2	0.0061
HLI-0994	2706	A	G	0	437	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0994	3197	T	C	0	456	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0994	4769	A	G	0	414	synonymous_variant	LOW	ND2	0.9767
HLI-0994	5495	T	C	0	448	synonymous_variant	LOW	ND2	0.0051
HLI-0994	7028	C	T	2	505	synonymous_variant	LOW	COX1	0.8089
HLI-0994	9477	G	A	1	404	missense_variant	MODERATE	COX3	0.0387
HLI-0994	11467	A	G	1	473	synonymous_variant	LOW	ND4	0.1231
HLI-0994	11719	G	A	0	411	synonymous_variant	LOW	ND4	0.7756
HLI-0994	12308	A	G	2	443	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0994	12372	G	A	0	413	synonymous_variant	LOW	ND5	0.1329
HLI-0994	13617	T	C	0	425	synonymous_variant	LOW	ND5	0.038
HLI-0994	14766	C	T	4	415	missense_variant	MODERATE	CYTB	0.7696
HLI-0994	14793	A	G	0	465	missense_variant	MODERATE	CYTB	0.0199
HLI-0994	15218	A	G	0	397	missense_variant	MODERATE	CYTB	0.0169
HLI-0994	15326	A	G	0	408	missense_variant	MODERATE	CYTB	0.9868
HLI-0994	15924	A	G	1	460	upstream_gene_variant	MODIFIER	TRNT	0.0354
HLI-0994	16256	C	T	0	434	upstream_gene_variant	MODIFIER	DLoop	0.0328
HLI-0994	16270	C	T	0	422	upstream_gene_variant	MODIFIER	DLoop	0.0465

HLI-0994	16399	A	G	1	321	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-0995	73	A	G	0	389	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0995	185	G	A	6	534	upstream_gene_variant	MODIFIER	DLoop	0.0397
HLI-0995	228	G	A	1	371	upstream_gene_variant	MODIFIER	DLoop	0.0255
HLI-0995	263	A	G	0	293	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0995	295	C	T	0	235	upstream_gene_variant	MODIFIER	DLoop	0.0469
HLI-0995	462	C	T	1	488	upstream_gene_variant	MODIFIER	DLoop	0.0341
HLI-0995	489	T	C	0	603	upstream_gene_variant	MODIFIER	DLoop	0.2578
HLI-0995	750	A	G	0	732	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0995	1438	A	G	0	740	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0995	2706	A	G	0	764	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0995	3010	G	A	1	745	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0995	4216	T	C	1	761	missense_variant	MODERATE	ND1	0.0991
HLI-0995	4769	A	G	2	676	synonymous_variant	LOW	ND2	0.9767
HLI-0995	6617	C	T	3	708	synonymous_variant	LOW	COX1	2.00E-04
HLI-0995	7028	C	T	0	815	synonymous_variant	LOW	COX1	0.8089
HLI-0995	10398	A	G	0	731	missense_variant	MODERATE	ND3	0.445
HLI-0995	11251	A	G	2	694	synonymous_variant	LOW	ND4	0.0932
HLI-0995	11719	G	A	1	708	synonymous_variant	LOW	ND4	0.7756
HLI-0995	12612	A	G	3	745	synonymous_variant	LOW	ND5	0.0506
HLI-0995	13708	G	A	2	623	missense_variant	MODERATE	ND5	0.0717
HLI-0995	13763	C	T	2	695	missense_variant	MODERATE	ND5	1.00E-04
HLI-0995	13934	C	T	3	660	missense_variant	MODERATE	ND5	0.0122
HLI-0995	14766	C	T	2	717	missense_variant	MODERATE	CYTB	0.7696
HLI-0995	14798	T	C	1	815	missense_variant	MODERATE	CYTB	0.0651
HLI-0995	15326	A	G	0	694	missense_variant	MODERATE	CYTB	0.9868
HLI-0995	15452	C	A	3	679	missense_variant	MODERATE	CYTB	0.0933
HLI-0995	16069	C	T	5	720	upstream_gene_variant	MODIFIER	DLoop	0.0496
HLI-0995	16126	T	C	5	773	upstream_gene_variant	MODIFIER	DLoop	0.1127
HLI-0995	16316	A	G	0	635	upstream_gene_variant	MODIFIER	DLoop	0.0084
HLI-0995	16390	G	A	2	654	upstream_gene_variant	MODIFIER	DLoop	0.0598
HLI-0995	16519	T	C	1	325	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0996	263	A	G	0	170	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0996	477	T	C	0	349	upstream_gene_variant	MODIFIER	DLoop	0.0093
HLI-0996	750	A	G	0	546	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0996	1438	A	G	0	644	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0996	3010	G	A	1	585	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0996	4769	A	G	0	520	synonymous_variant	LOW	ND2	0.9767
HLI-0996	14350	C	T	4	455	synonymous_variant	LOW	ND6	3.00E-04

HLI-0996	15326	A	G	1	497	missense_variant	MODERATE	CYTB	0.9868
HLI-0996	16519	T	C	0	240	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-0997	73	A	G	0	216	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0997	150	C	T	0	419	upstream_gene_variant	MODIFIER	DLoop	0.1339
HLI-0997	152	T	C	0	423	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0997	263	A	G	0	202	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0997	750	A	G	0	431	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0997	1438	A	G	1	518	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0997	1721	C	T	0	453	upstream_gene_variant	MODIFIER	RNR2	0.0058
HLI-0997	2706	A	G	0	450	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-0997	3197	T	C	0	523	upstream_gene_variant	MODIFIER	RNR2	0.039
HLI-0997	4732	A	G	0	526	missense_variant	MODERATE	ND2	0.0059
HLI-0997	4769	A	G	0	567	synonymous_variant	LOW	ND2	0.9767
HLI-0997	5918	T	C	0	530	synonymous_variant	LOW	COX1	7.00E-04
HLI-0997	7028	C	T	2	565	synonymous_variant	LOW	COX1	0.8089
HLI-0997	7768	A	G	0	502	synonymous_variant	LOW	COX2	0.0186
HLI-0997	9477	G	A	1	457	missense_variant	MODERATE	COX3	0.0387
HLI-0997	11467	A	G	0	489	synonymous_variant	LOW	ND4	0.1231
HLI-0997	11719	G	A	0	455	synonymous_variant	LOW	ND4	0.7756
HLI-0997	11963	G	A	1	477	missense_variant	MODERATE	ND4	0.002
HLI-0997	12308	A	G	2	526	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-0997	12372	G	A	0	520	synonymous_variant	LOW	ND5	0.1329
HLI-0997	13617	T	C	0	435	synonymous_variant	LOW	ND5	0.038
HLI-0997	13637	A	G	0	460	missense_variant	MODERATE	ND5	0.0074
HLI-0997	14182	T	C	1	462	synonymous_variant	LOW	ND6	0.0254
HLI-0997	14323	G	A	0	443	synonymous_variant	LOW	ND6	0.0058
HLI-0997	14766	C	T	2	495	missense_variant	MODERATE	CYTB	0.7696
HLI-0997	15326	A	G	0	306	missense_variant	MODERATE	CYTB	0.9868
HLI-0997	16300	A	G	0	322	upstream_gene_variant	MODIFIER	DLoop	0.0049
HLI-0997	16325	T	C	0	343	upstream_gene_variant	MODIFIER	DLoop	0.0332
HLI-0998	73	A	G	0	199	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0998	152	T	C	0	399	upstream_gene_variant	MODIFIER	DLoop	0.2668
HLI-0998	189	A	G	0	424	upstream_gene_variant	MODIFIER	DLoop	0.0565
HLI-0998	195	T	C	0	424	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-0998	263	A	G	0	201	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0998	750	A	G	0	454	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0998	921	T	C	0	537	upstream_gene_variant	MODIFIER	RNR1	0.0084
HLI-0998	1438	A	G	0	499	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0998	2706	A	G	0	493	upstream_gene_variant	MODIFIER	RNR2	0.7914

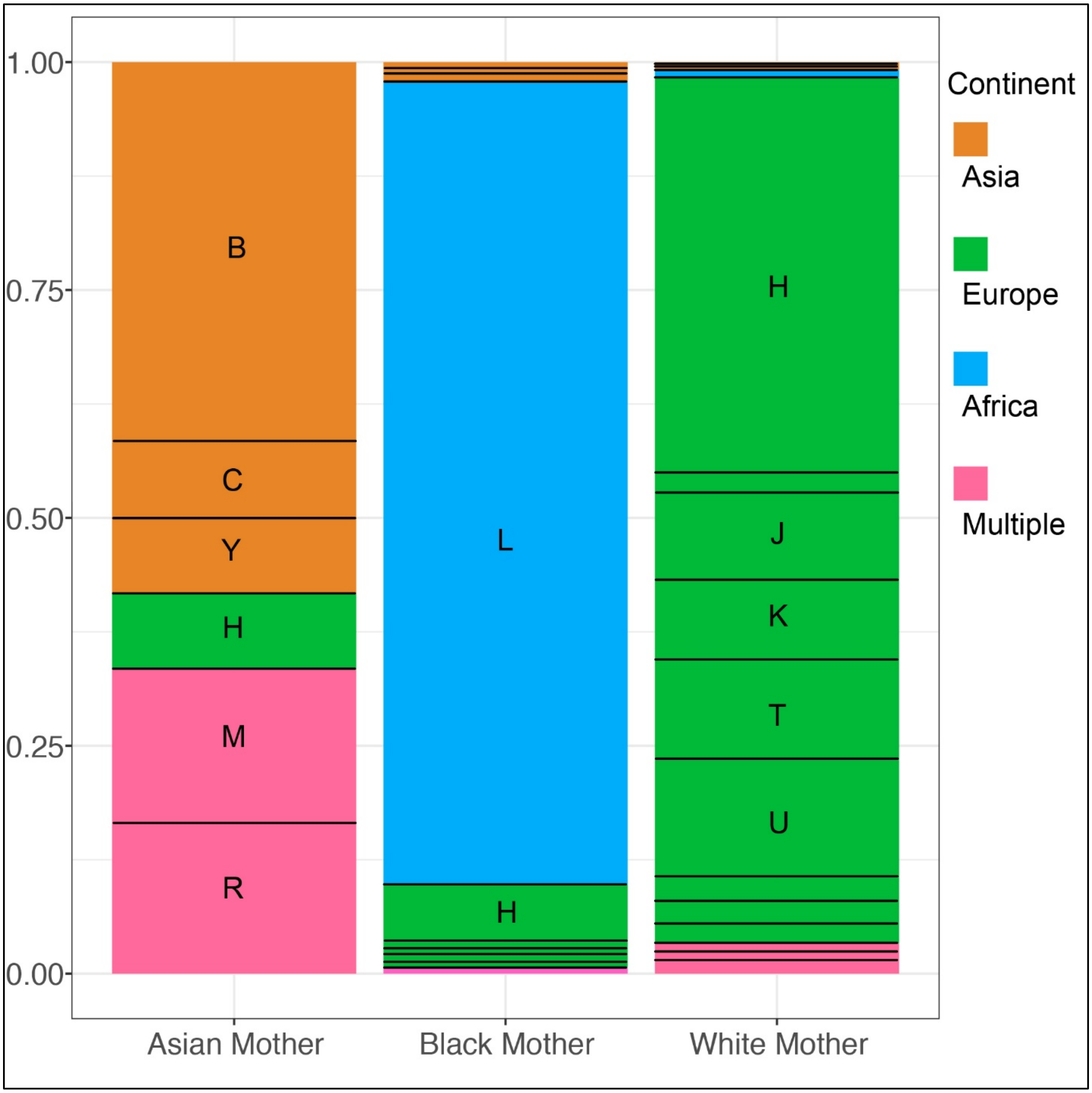
HLI-0998	4769	A	G	0	519	synonymous_variant	LOW	ND2	0.9767
HLI-0998	5147	G	A	0	369	synonymous_variant	LOW	ND2	0.0437
HLI-0998	7028	C	T	2	625	synonymous_variant	LOW	COX1	0.8089
HLI-0998	7424	A	G	0	531	synonymous_variant	LOW	COX1	0.0115
HLI-0998	8618	T	C	0	363	missense_variant	MODERATE	ATP6	0.0103
HLI-0998	8701	A	G	2	515	missense_variant	MODERATE	ATP6	0.3391
HLI-0998	9540	T	C	0	340	synonymous_variant	LOW	COX3	0.339
HLI-0998	10398	A	G	0	617	missense_variant	MODERATE	ND3	0.445
HLI-0998	10873	T	C	0	467	synonymous_variant	LOW	ND4	0.3389
HLI-0998	11719	G	A	0	561	synonymous_variant	LOW	ND4	0.7756
HLI-0998	12599	T	C	7	550	missense_variant	MODERATE	ND5	3.00E-04
HLI-0998	12705	C	T	1	517	synonymous_variant	LOW	ND5	0.4212
HLI-0998	13105	A	G	0	486	missense_variant	MODERATE	ND5	0.076
HLI-0998	13886	T	C	0	432	missense_variant	MODERATE	ND5	0.0088
HLI-0998	14284	C	T	2	471	synonymous_variant	LOW	ND6	0.0087
HLI-0998	14766	C	T	4	575	missense_variant	MODERATE	CYTB	0.7696
HLI-0998	15301	G	A	3	439	synonymous_variant	LOW	CYTB	0.2912
HLI-0998	15326	A	G	0	446	missense_variant	MODERATE	CYTB	0.9868
HLI-0998	16124	T	C	0	564	upstream_gene_variant	MODIFIER	DLoop	0.0156
HLI-0998	16223	C	T	2	489	upstream_gene_variant	MODIFIER	DLoop	0.4009
HLI-0998	16260	C	T	2	501	upstream_gene_variant	MODIFIER	DLoop	0.0112
HLI-0999	73	A	G	0	220	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-0999	263	A	G	0	182	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-0999	750	A	G	0	519	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-0999	1438	A	G	0	537	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-0999	3010	G	A	3	519	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-0999	4769	A	G	1	483	synonymous_variant	LOW	ND2	0.9767
HLI-0999	9341	A	T	2	512	synonymous_variant	LOW	COX3	1.00E-04
HLI-0999	15326	A	G	0	464	missense_variant	MODERATE	CYTB	0.9868
HLI-0999	16162	A	G	3	447	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-0999	16519	T	C	0	195	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-1000	72	T	C	0	277	upstream_gene_variant	MODIFIER	DLoop	0.0178
HLI-1000	204	T	C	2	445	upstream_gene_variant	MODIFIER	DLoop	0.0645
HLI-1000	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-1000	750	A	G	0	567	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-1000	1438	A	G	0	596	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-1000	2706	A	G	0	591	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-1000	4580	G	A	0	610	synonymous_variant	LOW	ND2	0.0169
HLI-1000	4769	A	G	1	574	synonymous_variant	LOW	ND2	0.9767

HLI-1000	7028	C	T	5	637	synonymous_variant	LOW	COX1	0.8089
HLI-1000	15326	A	G	0	519	missense_variant	MODERATE	CYTB	0.9868
HLI-1000	15904	C	T	1	617	upstream_gene_variant	MODIFIER	TRNT	0.0161
HLI-1000	15930	G	A	1	658	upstream_gene_variant	MODIFIER	TRNT	0.0224
HLI-1000	16298	T	C	2	449	upstream_gene_variant	MODIFIER	DLoop	0.0655
HLI-1001	73	A	G	0	298	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-1001	143	G	A	2	558	upstream_gene_variant	MODIFIER	DLoop	0.0191
HLI-1001	195	T	C	2	505	upstream_gene_variant	MODIFIER	DLoop	0.196
HLI-1001	263	A	G	0	165	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-1001	499	G	A	1	381	upstream_gene_variant	MODIFIER	DLoop	0.0359
HLI-1001	750	A	G	0	597	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-1001	1438	A	G	0	632	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-1001	1811	A	G	1	640	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-1001	2706	A	G	1	612	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-1001	4646	T	C	1	729	synonymous_variant	LOW	ND2	0.0124
HLI-1001	4769	A	G	0	596	synonymous_variant	LOW	ND2	0.9767
HLI-1001	5999	T	C	0	698	synonymous_variant	LOW	COX1	0.0127
HLI-1001	6047	A	G	0	752	synonymous_variant	LOW	COX1	0.0114
HLI-1001	6164	C	T	3	596	synonymous_variant	LOW	COX1	0.0025
HLI-1001	7028	C	T	0	673	synonymous_variant	LOW	COX1	0.8089
HLI-1001	8818	C	T	1	581	synonymous_variant	LOW	ATP6	0.0061
HLI-1001	11332	C	T	0	611	synonymous_variant	LOW	ND4	0.0115
HLI-1001	11467	A	G	1	652	synonymous_variant	LOW	ND4	0.1231
HLI-1001	11719	G	A	0	613	synonymous_variant	LOW	ND4	0.7756
HLI-1001	12308	A	G	1	610	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-1001	12372	G	A	0	594	synonymous_variant	LOW	ND5	0.1329
HLI-1001	14620	C	T	6	635	synonymous_variant	LOW	ND6	0.0126
HLI-1001	14766	C	T	5	556	missense_variant	MODERATE	CYTB	0.7696
HLI-1001	15326	A	G	1	525	missense_variant	MODERATE	CYTB	0.9868
HLI-1001	15693	T	C	1	539	missense_variant	MODERATE	CYTB	0.0114
HLI-1001	16356	T	C	0	504	upstream_gene_variant	MODIFIER	DLoop	0.024
HLI-1001	16519	T	C	2	246	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-1002	263	A	G	1	169	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-1002	750	A	G	1	608	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-1002	1438	A	G	0	610	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-1002	2259	C	T	1	585	upstream_gene_variant	MODIFIER	RNR2	0.0054
HLI-1002	4745	A	G	1	633	synonymous_variant	LOW	ND2	0.0039
HLI-1002	4769	A	G	1	614	synonymous_variant	LOW	ND2	0.9767
HLI-1002	12061	C	T	0	544	synonymous_variant	LOW	ND4	0.0014

HLI-1002	13680	C	T	2	532	synonymous_variant	LOW	ND5	0.005
HLI-1002	14560	G	A	0	527	synonymous_variant	LOW	ND6	0.0235
HLI-1002	14872	C	T	3	592	synonymous_variant	LOW	CYTB	0.0061
HLI-1002	15326	A	G	0	556	missense_variant	MODERATE	CYTB	0.9868
HLI-1002	16270	C	T	0	560	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-1002	16278	C	T	0	582	upstream_gene_variant	MODIFIER	DLoop	0.1057
HLI-1002	16311	T	C	0	545	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-1003	73	A	G	0	269	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-1003	263	A	G	0	224	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-1003	750	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-1003	1438	A	G	0	586	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-1003	3010	G	A	4	575	upstream_gene_variant	MODIFIER	RNR2	0.1449
HLI-1003	4769	A	G	0	558	synonymous_variant	LOW	ND2	0.9767
HLI-1003	6365	T	C	1	600	synonymous_variant	LOW	COX1	0.0026
HLI-1003	7961	T	C	1	556	synonymous_variant	LOW	COX2	0.0044
HLI-1003	15326	A	G	0	544	missense_variant	MODERATE	CYTB	0.9868
HLI-1003	16162	A	G	0	532	upstream_gene_variant	MODIFIER	DLoop	0.0176
HLI-1003	16209	T	C	0	573	upstream_gene_variant	MODIFIER	DLoop	0.0265
HLI-1003	16234	C	T	1	547	upstream_gene_variant	MODIFIER	DLoop	0.0314
HLI-1003	16519	T	C	0	275	upstream_gene_variant	MODIFIER	DLoop	0.6293
HLI-1004	73	A	G	0	315	upstream_gene_variant	MODIFIER	DLoop	0.7599
HLI-1004	146	T	C	2	557	upstream_gene_variant	MODIFIER	DLoop	0.1945
HLI-1004	263	A	G	1	234	upstream_gene_variant	MODIFIER	DLoop	0.9513
HLI-1004	488	A	G	1	439	upstream_gene_variant	MODIFIER	DLoop	1.00E-04
HLI-1004	750	A	G	1	643	upstream_gene_variant	MODIFIER	RNR1	0.9821
HLI-1004	1438	A	G	0	678	upstream_gene_variant	MODIFIER	RNR1	0.9501
HLI-1004	1811	A	G	1	626	upstream_gene_variant	MODIFIER	RNR2	0.0763
HLI-1004	2217	C	T	4	672	upstream_gene_variant	MODIFIER	RNR2	0.0016
HLI-1004	2706	A	G	2	668	upstream_gene_variant	MODIFIER	RNR2	0.7914
HLI-1004	3480	A	G	2	570	synonymous_variant	LOW	ND1	0.0392
HLI-1004	4769	A	G	2	586	synonymous_variant	LOW	ND2	0.9767
HLI-1004	5231	G	A	1	562	synonymous_variant	LOW	ND2	0.0232
HLI-1004	7028	C	T	0	665	synonymous_variant	LOW	COX1	0.8089
HLI-1004	8911	T	C	0	662	synonymous_variant	LOW	ATP6	0.0028
HLI-1004	9055	G	A	2	686	missense_variant	MODERATE	ATP6	0.0425
HLI-1004	9698	T	C	0	708	synonymous_variant	LOW	COX3	0.0405
HLI-1004	9716	T	C	0	726	synonymous_variant	LOW	COX3	0.0108
HLI-1004	10550	A	G	0	643	synonymous_variant	LOW	ND4L	0.0376
HLI-1004	11299	T	C	2	588	synonymous_variant	LOW	ND4	0.0417

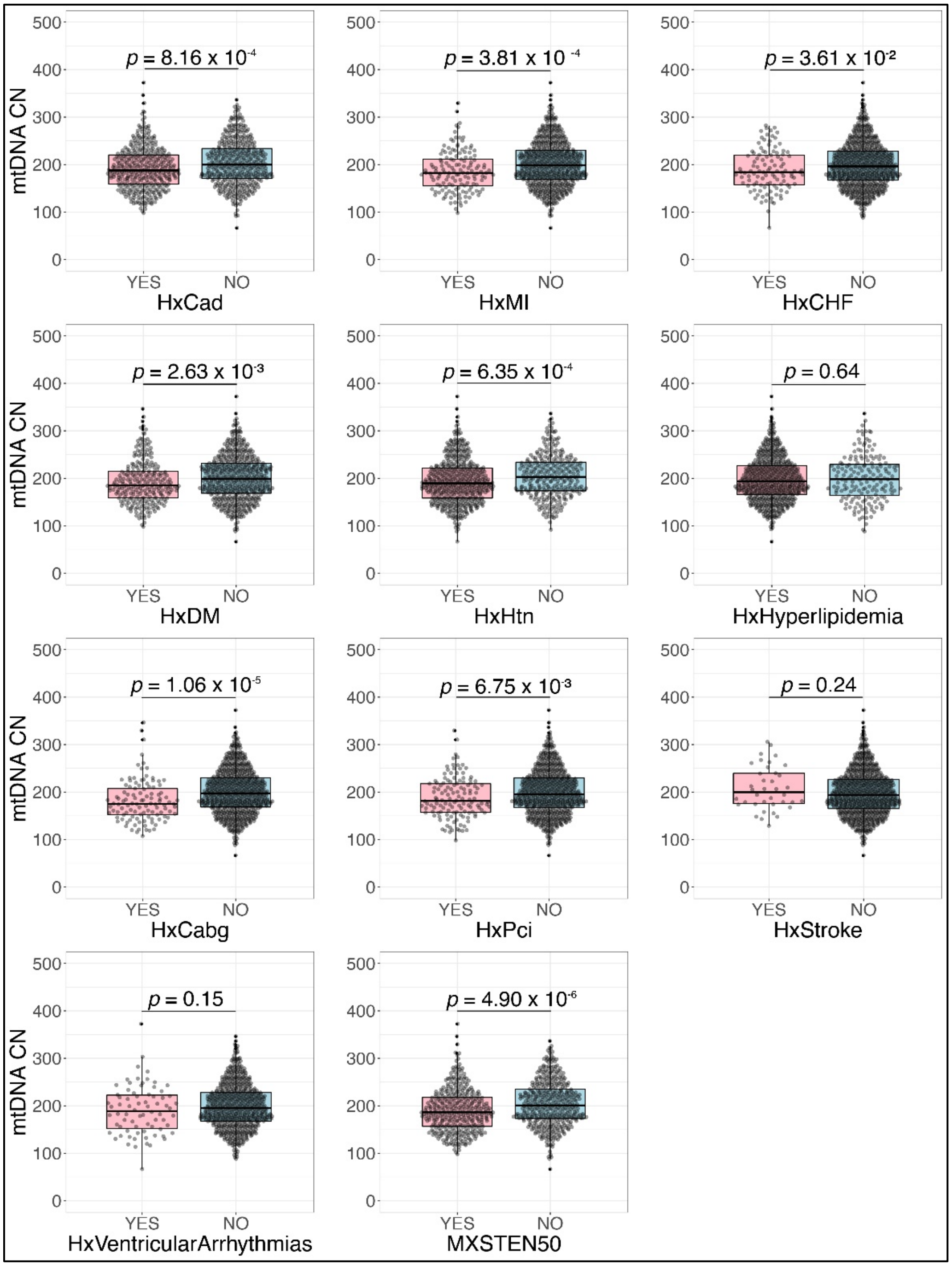
HLI-1004	11467	A	G	0	639	synonymous_variant	LOW	ND4	0.1231
HLI-1004	11719	G	A	1	643	synonymous_variant	LOW	ND4	0.7756
HLI-1004	11869	C	A	7	622	synonymous_variant	LOW	ND4	0.0015
HLI-1004	12308	A	G	0	597	upstream_gene_variant	MODIFIER	TRNL2	0.1227
HLI-1004	12372	G	A	1	615	synonymous_variant	LOW	ND5	0.1329
HLI-1004	13135	G	A	2	629	missense_variant	MODERATE	ND5	0.0092
HLI-1004	14037	A	G	0	480	synonymous_variant	LOW	ND5	0.0017
HLI-1004	14167	C	T	8	569	synonymous_variant	LOW	ND6	0.0385
HLI-1004	14766	C	T	2	626	missense_variant	MODERATE	CYTB	0.7696
HLI-1004	14798	T	C	0	690	missense_variant	MODERATE	CYTB	0.0651
HLI-1004	15326	A	G	0	588	missense_variant	MODERATE	CYTB	0.9868
HLI-1004	16224	T	C	0	657	upstream_gene_variant	MODIFIER	DLoop	0.0423
HLI-1004	16270	C	T	3	639	upstream_gene_variant	MODIFIER	DLoop	0.0465
HLI-1004	16311	T	C	0	595	upstream_gene_variant	MODIFIER	DLoop	0.1969
HLI-1004	16519	T	C	1	297	upstream_gene_variant	MODIFIER	DLoop	0.6293

Figure S1. Patients' self-reported maternal ancestry largely corresponds to mtDNA haplogroups.



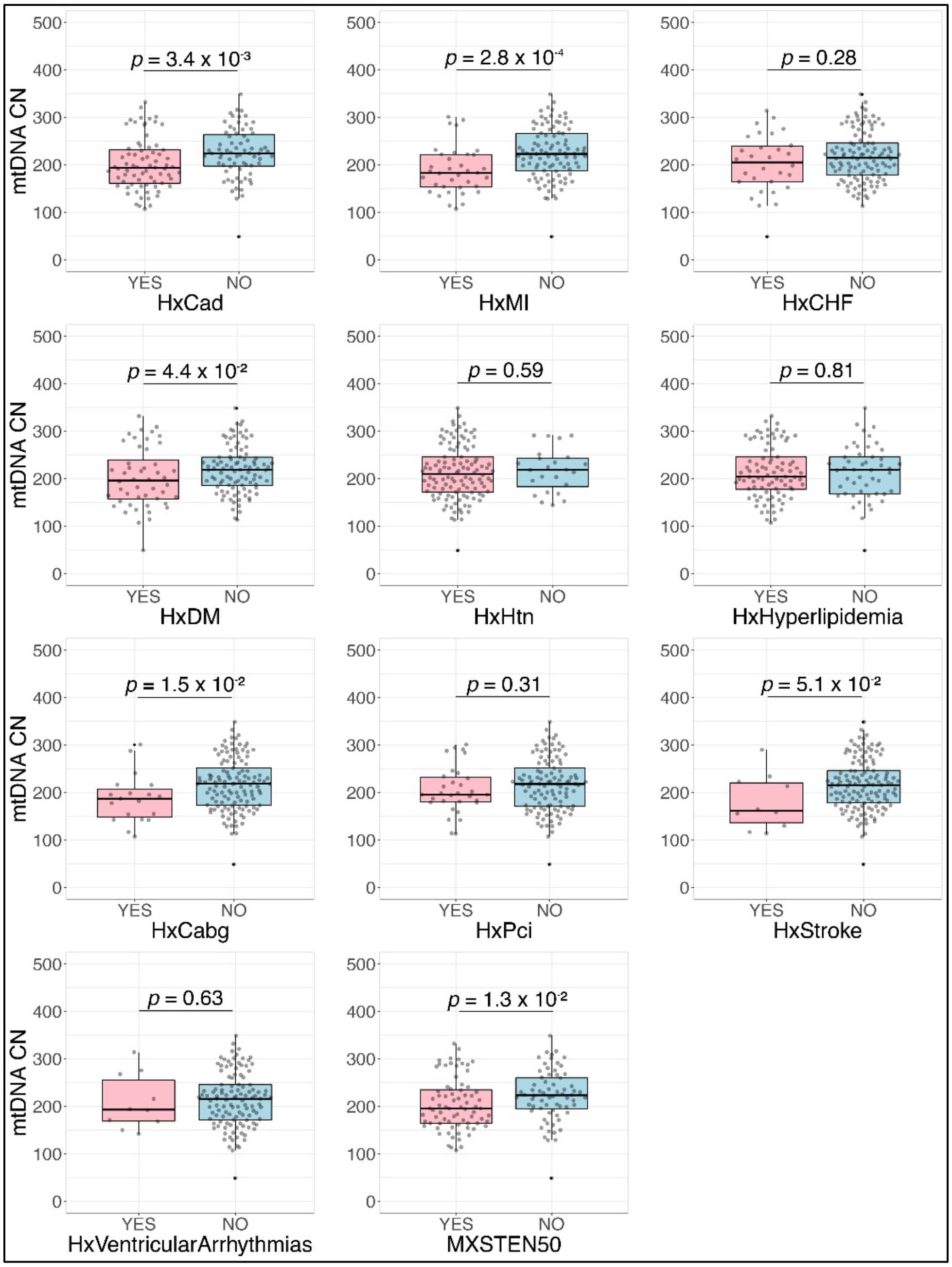
Each bar shows the composition of mtDNA haplogroups among individuals who report an Asian mother (left), black mother (middle), or white mother (right). Bars are sectioned by haplogroup and colored according to the haplogroup's continent (some haplogroups are associated with multiple continents, as labelled). Bar sections corresponding to haplogroups with only a very small number of patients in the corresponding bar are not labelled, but are still colored by continent.

Figure S2. Clinical features associated with lower mtDNA CN among individuals with self-reported white mothers.



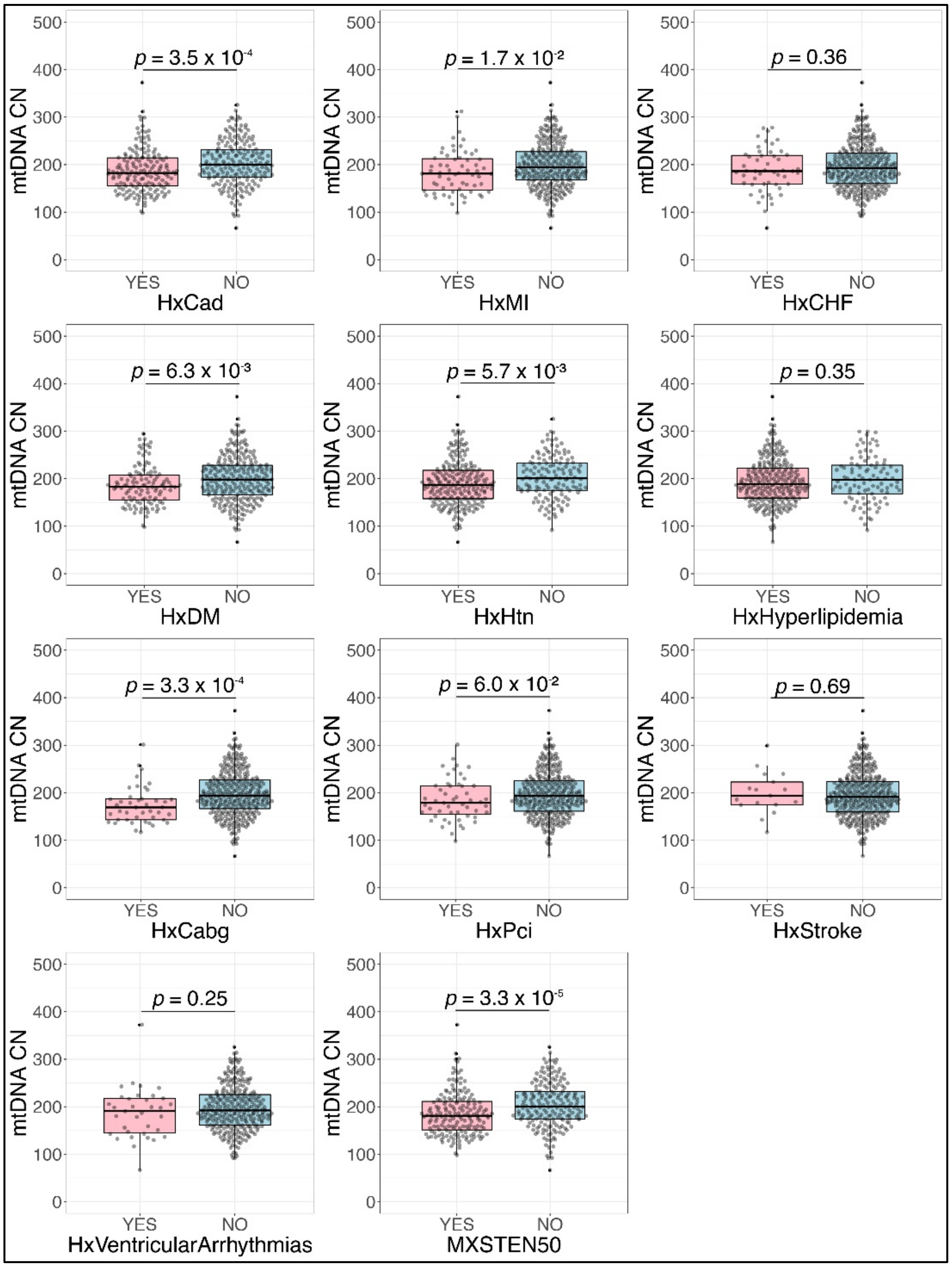
Each panel represents a different clinical feature, given at the bottom of the panel. The two groups in each panel represent individuals (those with white mothers) that do (YES) or do not (NO) have the clinical feature, with each point representing a patient and the vertical axis indicating that patient's mtDNA CN. The overlaid boxplots give the 25th, 50th, and 75th percentiles, and the whiskers extended either to the maximum/minimum values or 1.5 x IQR from the box (where IQR is the inter-quartile range, or distance between the first and third quartiles), whichever is less extreme. P-values were computed using a logistic regression model that adjusts for age and sex (see Methods for details).

Figure S3. Clinical features associated with lower mtDNA CN among individuals with self-reported black mothers.



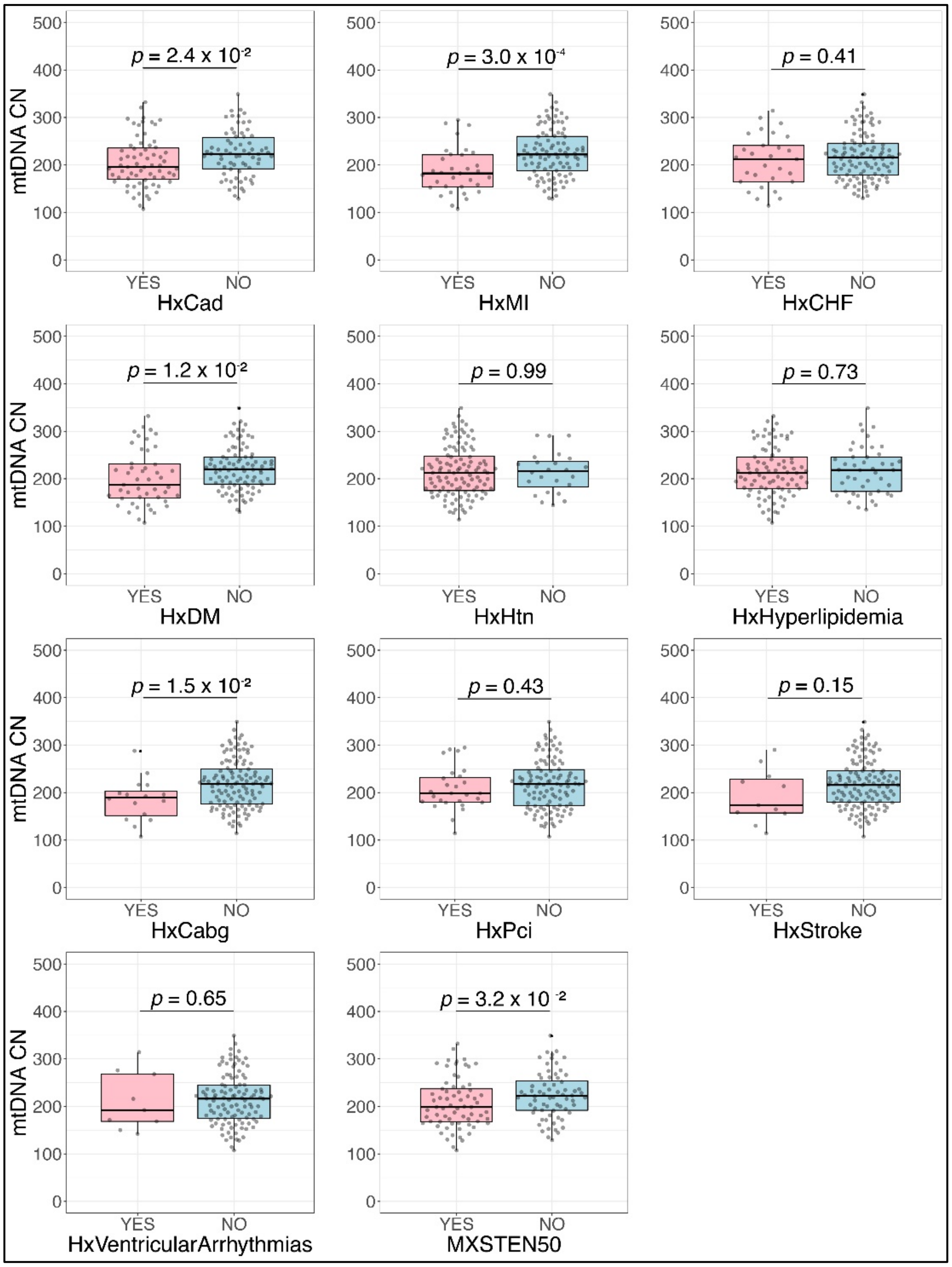
Each panel represents a different clinical feature, given at the bottom of the panel. The two groups in each panel represent individuals (with black mothers) that do (YES) or do not (NO) have the clinical feature, with each point representing a patient and the vertical axis indicating that patient's mtDNA CN. The overlaid boxplots give the 25th, 50th, and 75th percentiles, and the whiskers extended either to the maximum/minimum values or 1.5 x IQR from the box (where IQR is the inter-quartile range, or distance between the first and third quartiles), whichever is less extreme. P-values were computed using a logistic regression model that adjusts for age and sex (see Methods for details).

Figure S4. Clinical features associated with lower mtDNA CN among individuals with mtDNA haplogroup H.



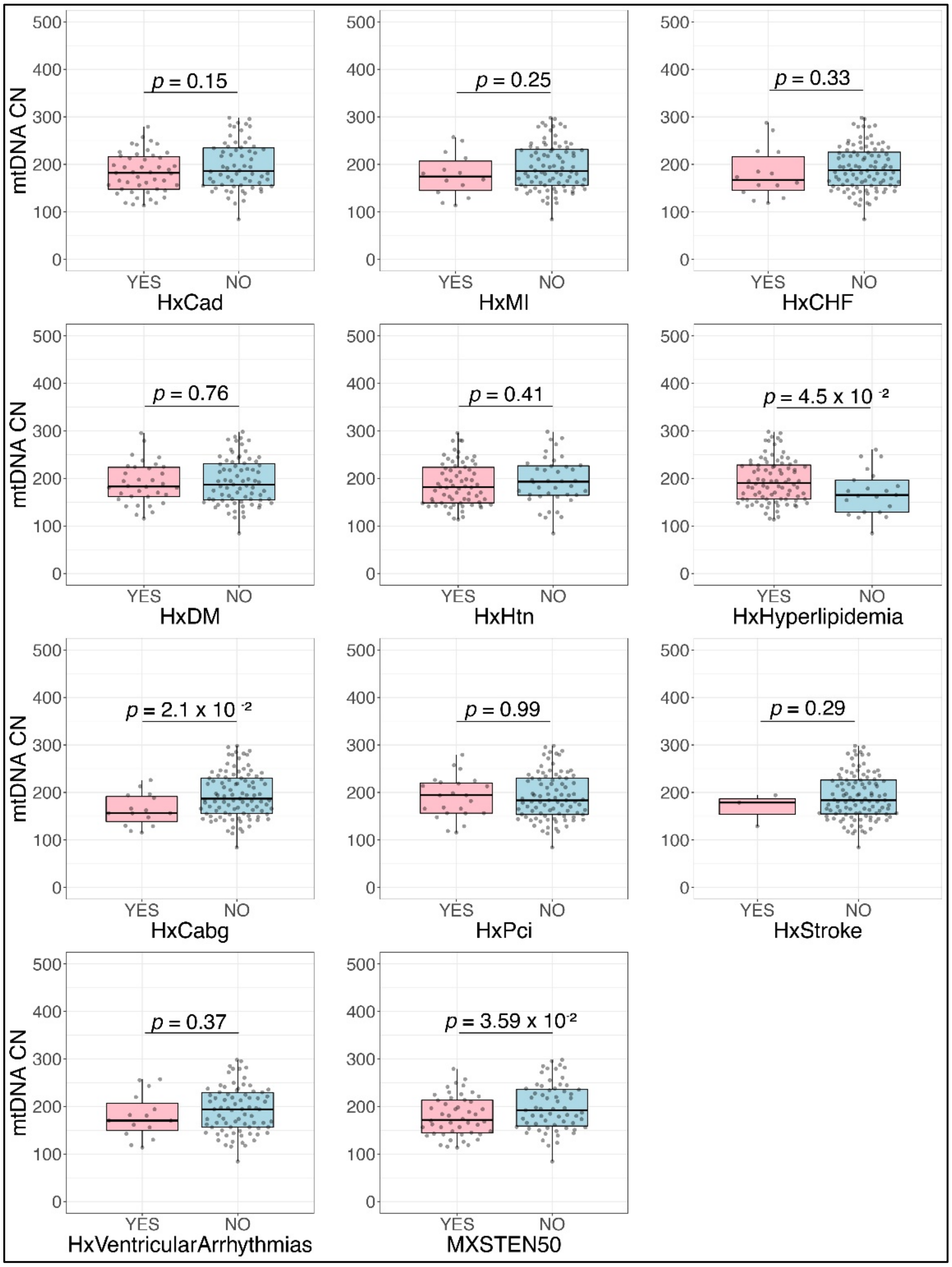
Each panel represents a different clinical feature, given at the bottom of the panel. The two groups in each panel represent individuals (those with haplogroup H) that do (YES) or do not (NO) have the clinical feature, with each point representing a patient and the vertical axis indicating that patient's mtDNA CN. The overlaid boxplots give the 25th, 50th, and 75th percentiles, and the whiskers extended either to the maximum/minimum values or 1.5 x IQR from the box (where IQR is the inter-quartile range, or distance between the first and third quartiles), whichever is less extreme. P-values were computed using a logistic regression model that adjusts for age and sex (see Methods for details).

Figure S5. Clinical features associated with lower mtDNA CN among individuals with mtDNA haplogroup L.



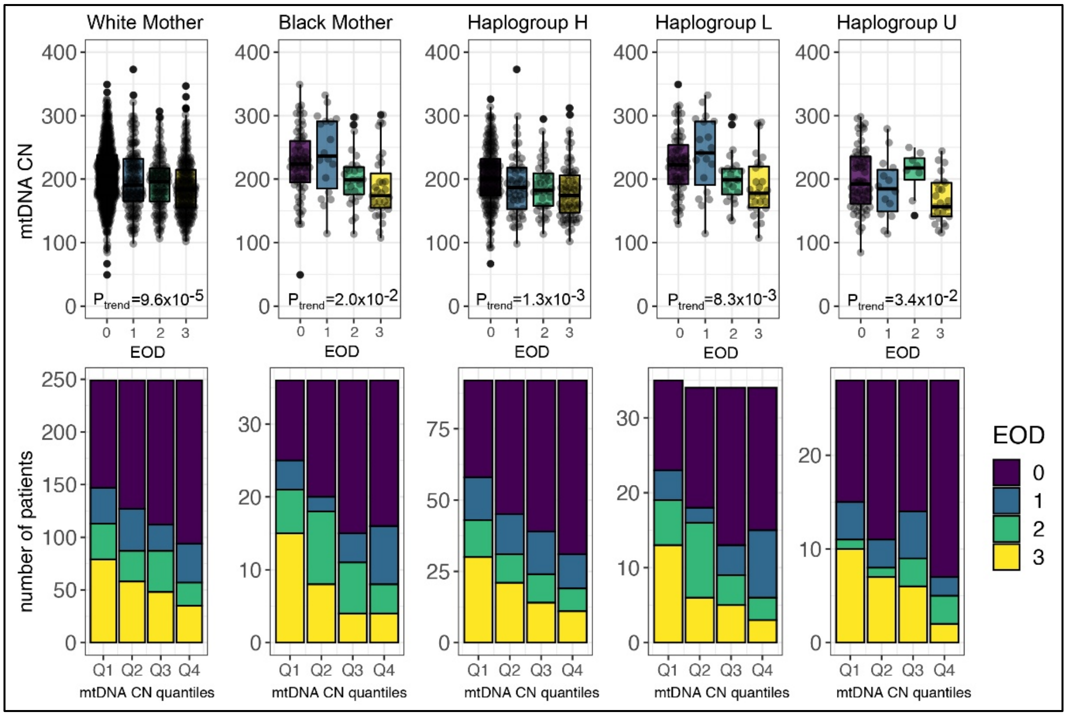
Each panel represents a different clinical feature, given at the bottom of the panel. The two groups in each panel represent individuals (those with haplogroup L) that do (YES) or do not (NO) have the clinical feature, with each point representing a patient and the vertical axis indicating that patient's mtDNA CN. The overlaid boxplots give the 25th, 50th, and 75th percentiles, and the whiskers extended either to the maximum/minimum values or 1.5 x IQR from the box (where IQR is the inter-quartile range, or distance between the first and third quartiles), whichever is less extreme. P-values were computed using a logistic regression model that adjusts for age and sex (see Methods for details).

Figure S6. Clinical features associated with lower mtDNA CN among individuals with mtDNA haplogroup U.



Each panel represents a different clinical feature, given at the bottom of the panel. The two groups in each panel represent individuals (those with haplogroup U) that do (YES) or do not (NO) have the clinical feature, with each point representing a patient and the vertical axis indicating that patient's mtDNA CN. The overlaid boxplots give the 25th, 50th, and 75th percentiles, and the whiskers extended either to the maximum/minimum values or 1.5 x IQR from the box (where IQR is the inter-quartile range, or distance between the first and third quartiles), whichever is less extreme. P-values were computed using a logistic regression model that adjusts for age and sex (see Methods for details).

Figure S7. Extent of disease (EOD) is inversely associated with mtDNA CN across maternal ancestries.



MtDNA for each patient is plotted for various maternal ancestral groups, stratified by EOD (top panels). In the bottom panels, proportion of patients with each EOD score is shown for each mtDNA quartile, within individual maternal ancestral groups. The trend of higher mtDNA quartiles having fewer patients with more severe EOD, observed for the cohort as a whole (Figure 3), holds across ancestral groups.