

**BRIEF COMMUNICATION**

Utility of Clinical Exome Sequencing in Dystonia: A Single-Center Study From India

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ABSTRACT

Objective With the use of next-generation sequencing in clinical practice, several genetic etiologies of dystonia have been identified. This study aimed to ascertain the utility of clinical exome sequencing (CES) in dystonia and factors suggestive of a genetic etiology.

Methods This study was a retrospective chart review of patients with dystonia who had undergone CES for the evaluation of dystonia.

Results Forty-eight patients (35 males, 46 families) with dystonia were studied, with a mean age at onset of 16.0 ± 14.1 (1–58) years. A pathogenic/likely pathogenic variant was found in 20 patients (41.7%) among which 14 patients (29.2%) carried a novel variant. CES was more likely to detect a genetic diagnosis in patients with an early age at onset, i.e., ≤ 20 years.

Conclusion CES is a useful tool in the diagnostic evaluation of dystonia, with a yield of close to 40%. Patients with an earlier age at onset have a higher likelihood of having dystonia due to a genetic cause than those with a later age at onset.

Keywords Clinical exome sequencing; Dystonia; Next-generation sequencing.

Dystonia is a common hyperkinetic movement disorder characterized by sustained or intermittent muscle contractions causing abnormal, often repetitive, movements or postures or both.¹ Clinical details such as family history, onset age, dystonia pattern, associated abnormal movements, and neurological and systemic involvement aid in formulating a diagnosis of dystonia.² Imaging and genetic assessments provide additional information that is often sufficient to confirm the diagnosis. However, owing to the numerous, complex and undescribed etiologies, a diagnosis may not be possible in every patient.

Genetic assessments are particularly helpful in the identification of monogenic forms, but individual gene testing is tedious and time-consuming due to the phenotypic heterogeneity of single-gene disorders and the phenotypic overlap of many different

genetic disorders. Next-generation sequencing (NGS) technology allows quick screening of thousands of genes and the simultaneous identification of known and novel variants. This technology has expedited the process of confirming genetic diagnoses and the discovery of novel pathogenic genes and variants.

In a clinical setting, NGS can be used to evaluate dystonia through various panels, such as targeted gene panels, clinical exome sequencing (CES), whole-exome sequencing (WES), or whole-genome sequencing (WGS), in the order of increasing coverage, diagnostic yield, interpretation complexity, and cost. As the name suggests, WGS and WES involve sequencing the whole genome and whole exome of over 21,000 genes identified so far, respectively. However, CES involves the sequencing of an exome subset of approximately 3,000–6,000 genes chosen

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based on association with the disease, and the subset may vary depending on the technology provider and with time based on the newly available literature. The diagnostic yield varies from 1% to 37.5% among different studies based on the subjects studied and the techniques used.³⁻¹⁰ In this study, we retrospectively reviewed the CES results of patients presenting with dystonia as the predominant symptom who had undergone CES as part of their diagnostic evaluation to assess the utility of CES and ascertain factors suggestive of a positive genetic diagnosis.

MATERIALS & METHODS

In this retrospective chart review, we reviewed our movement disorders database from 2016 to 2020 to identify those patients who had undergone CES as part of the evaluation of dystonia as their prominent phenotypic feature. Patient details were anonymized to maintain patient privacy. The clinical data, investigations and genetic reports of these patients were reviewed. All these patients were examined by movement disorder specialists (PKP, RY, NK, VVH). Dystonia in each patient was classified according to the recent consensus update on the classification and phenomenology of dystonia.¹ Additionally, based on the associated neurological features, dystonia was classified as isolated dystonia (IsoD), combined dystonia (CombD) or complex dystonia (CxD). Patients with IsoD had dystonia as the predominant feature, whereas patients with CombD had dystonia with other movement disorders, such as myoclonus, chorea, or parkinsonism. Patients with CxD had other neurological or systemic features.¹¹ CES (Supplementary Materials 1 and 2 in the online-only Data Supplement) was performed in all these patients, and the report was analyzed. The Institute Ethics Committee at the National Institute of Mental Health and Neurosciences granted an ethical clearance waiver owing to the retrospective nature of the study, with deidentified data being extracted from the files (No: NIMH/DO/DEAN [Basic Science]/2020-21). p value of < 0.05 considered statistically significant (Supplementary Material 1 in the online-only Data Supplement).

RESULTS

Forty-eight patients (35 males) belonging to 46 families were identified (Table 1). None of these patients had undergone single-gene or targeted-gene testing prior to CES. A positive family history was noted in 7 patients, including in 2 patients each from 2 families and in one patient each from 3 families (5 total families). Three patients from our center whose cases were previously published (patient 5,¹² patient 12,¹³ and patient 16¹⁴) were

included in this study. The demographic and clinical details and axis-1 classification details of this cohort are provided in Table 1.

Pathogenic/likely pathogenic (P/LP) variants were present in 20 patients (18 families) (Table 2). The genes in which the P/LP variants were observed were *PLA2G6* (4 patients from 3 families); *GLB1* (3 patients from 2 families); *TH*, *PRKN*, *TOR1A*, and *GCH1* in 2 patients each (a total of 8 patients from 8 families); and *THAP1*, *NDUFA12*, *NPC1*, *ATP7B*, and *FA2H* in one patient each (a total of 5 patients from 5 families) (Table 2). Among these, 14 patients (from 13 families) had novel variants that were classified as P/LP based on American College of Medical Genetics and Genomics (ACMG) causality criteria (Table 2). The age at onset (AAO), distribution of dystonia, associated features, and genetic abnormality in each patient are mentioned in Table 2. Among patients with a positive genetic diagnosis, *TOR1A* causing DYT1 was the most common genetic abnormality among those with IsoD, seen in 2 out of 6 patients, while *PLA2G6* causing *PLA2G6*-associated neurodegeneration (PLAN) was the most common genetic abnormality among those with CombD, observed in 4 out of 9 patients. In addition, 5 patients had P/LP variants in the heterozygous carrier state, and 8 patients had variants of unknown significance (VUSs) in genes relevant to dystonia (Supplementary Table 1 in the online-only Data Supplement).

When comparing patients with a positive genetic diagnosis to those with a negative genetic diagnosis, most of the patients with a positive genetic diagnosis had an early AAO of dystonia (≤ 20 yrs) (Table 1). Of an overall 36 patients with early-onset dystonia (≤ 20 years), 19 had P/LP mutations (52.8%). Among 12 patients with an adult onset of dystonia (> 20 years), only one had a P/LP mutation (8.3%) ($p = 0.007$). There was no significant difference in the diagnostic yield of genetic testing based on the distribution or the associated features.

DISCUSSION

In the present study, a cohort of 48 patients with heterogeneous dystonia who had undergone CES as part of their evaluation was analyzed. Our cohort had an early AAO of dystonia, with three-fourths of the patients having an AAO before 20 years. In comparison, earlier studies reported a relatively equal distribution of the AAO (Supplementary Table 2 in the online-only Data Supplement).^{5,6,8-10} Dystonia with an underlying genetic cause often has an early AAO and presentation. The yield of genetic testing in our cohort was higher (39.1%) than that in previous studies (11.7% to 37.5%) (Supplementary Table 2 in the online-only Data Supplement). This variability in diagnostic yield is most likely attributable to the inclusion criteria and possibly due to the differences in the population studied and the clinical

Table 1. Overall demographics and clinical manifestations of probands with dystonia

Features	Overall (n = 48)	Genetic diagnosis		p value
		Yes (n = 20)	No (n = 28)	
Sex (male/female)	35/13	15/5	20/8	0.78
Age at testing (years)	25.2 ± 14.0	22.5 ± 11.2	27.0 ± 16.1	0.28
Age at onset (years)	16.0 ± 14.1	11.9 ± 9.6	19.1 ± 16.3	0.08
Infantile onset	3 (6.2)	2 (10)	1 (3.5)	0.56
Childhood onset	25 (52)	11 (55)	14 (50)	0.77
Adolescence	8 (16.6)	6 (30)	2 (7.1)	0.05
Early adulthood	5 (10.4)	0	5 (17.8)	-
Late adulthood	7 (14.6)	1 (5)	6 (21.4)	0.21
Body distribution				-
Focal dystonia	7 (14.6)	1 (5)	6 (21.4)	0.21
Multifocal dystonia	4 (8.3)	4 (20)	0	-
Segmental dystonia	4 (8.3)	1 (5)	3 (10.7)	0.63
Generalized dystonia	33 (68.7)	14 (70)	19 (67.8)	> 0.99
Associated features				-
Isolated dystonia	18 (37.5)	6 (30)	12 (42.8)	0.54
Combined dystonia	18 (37.5)	9 (45)	9 (32.1)	0.4
Dystonia-parkinsonism	13 (72.2)	7 (77.8)	6 (66.7)	> 0.99
Dystonia-chorea	4 (22.2)	2 (22.2)	2 (22.2)	> 0.99
Dystonia-myoclonus	1 (5.6)	0 (0)	1 (11.1)	-
Complex dystonia	12 (25.0)	5 (25)	7 (25)	> 0.99
Dystonia-cerebellar ataxia	4 (33.3)	1 (20)	3 (42.8)	0.60
Dystonia-spasticity	5 (41.7)	1 (20)	4 (57.1)	0.30
Dystonia with cognitive decline	2 (16.7)	2 (40)	0	-
Dystonia with intellectual disability	1 (8.3)	1 (20)	0	-
Family history (families)	5/46 (10.9)	3 (16.6)	2 (7.1)	0.40

Data are presented as mean ± standard deviation or number (%).

characteristics of the enrolled patients. The higher yield seen in the present study may be due to the higher prevalence of young-onset dystonia and to selection bias. In previous studies, a higher yield of approximately 35% has been reported when the mean age of onset is in the 1st to 2nd decade.^{5,6,10} The lower positive rate in some of these studies could be due to the inclusion of patients with negative results in the initial targeted gene testing of a single gene or a set of genes.^{6,9}

Even though genetic testing plays a crucial role in the diagnosis of an underlying genetic abnormality, it may not always be accessible or financially feasible. An awareness of the predictors for positive genetic testing would help in the judicious use of NGS. The comparison of patients with and without a positive genetic test revealed the importance of an AAO of ≤ 20 years. None of the remaining clinical features had any impact on the outcome of genetic testing. Previous studies have shown that patients with an early AAO CombD or CxD have a higher likelihood of having a positive genetic diagnosis. However, patients with a later AAO isolated or focal dystonia have a lower likelihood of a positive genetic diagnosis.^{6,9,10} However, these findings

are inconsistent. The lack of such associations in the present study despite the presence of patients with IsoD, CombD, and CxD may be due to a lower sample size or different genetic population makeup than in previous studies.

The spectrum of affected genes seen in the present study was different from that in previous studies (Supplementary Table 2 in the online-only Data Supplement).^{3,5,6,8-10} In the present study, *PLA2G6* mutations were identified in 3 families (4 patients) with P/LP mutations (one novel mutation) and 2 families (2 patients) with VUSs. These patients presented with the typical dystonia-parkinsonism phenotypic subtype of PLAN. In another study from India,¹⁵ 3 patients had dystonia among 12 with genetically confirmed PLAN with a phenotype of neuronal axonal degeneration, suggesting that *PLA2G6* mutations may not be an uncommon genetic cause in the Indian population. However, this may be restricted to the population studied, and larger studies are required to ascertain the prevalence of *PLA2G6* mutations in patients with dystonia worldwide. *DYT-TOR1A* is considered to be the most common early-onset isolated genetic dystonia, which was the case in our study, and one-third of patients with

Table 2. Genetic causes identified in the present study

Case	AAO	Phenotype	Gene	Variant	Inheritance	ACMG classification
1	15	Focal, combined (DP)	<i>PLA2G6</i>	ENST00000332509;c.835delA;p.Ile279SerfsTer26 [†] ENST00000332509;c.991G>T;p.Asp331Tyr [†]	AR, CH	LP (PVS ₁ PM ₂) LP (PM ₂ PP ₂₋₅)
2	10	Generalised, combined (DP)	<i>PLA2G6</i>	ENST00000332509;c.2222G>A;p.arg742Gln	AR, Hm	P (PP ₅ PM _{2.5} PP ₂)
3*	18	Generalised, combined (DP)	<i>PLA2G6</i>	ENST00000332509;c.2222G>A;p.arg742Gln	AR, Hm	P (PP ₅ PM _{2.5} PP _{1.2})
4*	19	Generalised, combined (DP)	<i>PLA2G6</i>	ENST00000332509;c.2222G>A;p.arg742Gln	AR, Hm	P (PP ₅ PM _{2.5} PP _{1.2})
5	7	Generalised, isolated	<i>GLB1</i>	ENST00000307363;c.246-2A>G ENST00000307363;c.1325G>A;p.Arg442Gln	AR, CH	P (PVS ₁ PM ₂ PP ₃) P (PP ₅ PM _{2.3} PP _{2.3})
6*	4	Generalised, combined (DP)	<i>GLB1</i>	ENST00000307363;c.1325G>A;p.Arg442Gln ENST00000307363;c.1022G>T;p.Gly341Val [†]	AR, CH	P (PP ₅ PM ₂ PP ₁₋₃) LP (PM _{2.3} PP ₁₋₃)
7*	3	Generalised, combined (DP)	<i>GLB1</i>	ENST00000307363;c.1325G>A;p.Arg442Gln ENST00000307363;c.1022G>T;p.Gly341Val [†]	AR, CH	P (PP ₅ PM ₂ PP ₁₋₃) LP (PM _{2.3} PP ₁₋₃)
8	1	Multifocal, combined (DCh)	<i>GCH1</i>	ENST00000491895;c.542T>C;p.Val181Ala [†]	AR, Hm	LP (PM _{1.2} PP _{2.3})
9	1	Generalised, complex (DId)	<i>GCH1</i>	ENST00000491895;c.614T>C;p.Val205Ala [†] ENST00000491895;c.610G>A;p.Val204Ile	AR, CH	LP (PM _{1.2,5} PP _{2.3}) LP (PM _{1.2} PP _{2.3})
10	11	Generalised, isolated	<i>TOR1A</i>	ENST00000351698;c.907_909del;p.Glu303del	AD, Ht	P (PP ₅ PS ₃ PM _{1.2,4} PP ₃)
11	8	Multifocal, isolated	<i>TOR1A</i>	ENST00000351698;c.907_909del;p.Glu303del	AD, Ht	P (PP ₅ PS ₃ PM _{1.2,4} PP ₃)
12	20	Generalised, isolated	<i>TH</i>	ENST00000381178;c.525delG;p.Leu176SerfsTer61 [†] ENST00000381178;c.1481C>T;p.Thr494Met [†]	AR, CH	LP (PVS ₁ PM ₂) LP (PM ₂ PP _{2.3,5})
13	17	Multifocal, combined (DCh)	<i>TH</i>	ENST00000381178;c.1117C>T;p.Arg373Cys [†]	AR, Hm	LP (PM _{1.2} PP _{2.3})
14	20	Generalised, isolated	<i>PRKN</i>	ENST00000366898;c.124C>T;p.Arg42Cys [†] ENST00000366898;c.1076G>A;p.Gly359Asp [†]	AR, CH	LP (PM _{1.2,5} PP _{2.3}) LP (PM _{1.2} PP _{2.3})
15	17	Segmental, combined (DP)	<i>PRKN</i>	ENST00000366898;c.(171+1_172-1)_(412+1_413-1)del [†]	AR, Hm	
16	43	Multifocal, isolated	<i>THAP1</i>	ENST00000254250;c.71+1G>C [†]	AD, Ht	LPVS ₁ PM ₂ PP ₃)
17	6	Generalised, complex (DS)	<i>NDUFA12</i>	ENST00000327772;c.60_61delCCinsT; p.Arg21GlufsTer18 [†]	AR, Hm	LP (PVS ₁ PM ₂)
18	13	Generalised, complex (DCo)	<i>ATP7B</i>	ENST00000242839;c.3485C>T;p.Ser1162Phe [†]	AR, Hm	P (PS ₃ PM _{1.2} PP _{2.4})
19	10	Generalised, complex (DC)	<i>FA2H</i>	ENST00000219368;c.130C>A;p.Pro44Thr [†]	AR, Hm	LP (PM _{1.2,5})
20	2	Generalised, complex (DCo)	<i>NPC1</i>	ENST00000269228;c.2473T>C;p.Tyr825His [†]	AR, Hm	LP (PM _{2.5} PP _{2.3})

*belongs to same family and segregation analysis was performed by Sanger analysis; [†]novel mutations. AAO, age at onset; ACMG, American College of Medical Genetics and Genomics; AD, autosomal dominant; AR, autosomal recessive; CH, compound heterozygous; DC, dystonia cerebellar; DCh, dystonia chorea; DCo, dystonia with cognitive decline; DId, dystonia with intellectual disability; DP, dystonia parkinsonism; DS, dystonia spasticity; Hm, homozygous; Ht, heterozygous; LP, likely pathogenic; P, pathogenic; PVS, very strong evidence of pathogenicity; PS, strong evidence of pathogenicity; PM, moderate evidence of pathogenicity; PP, supportive evidence of pathogenicity.

IsoD had a previously reported pathogenic variant (p.Glu303del) in the *TOR1A* gene.⁹ Previous studies from India vary in this regard. None of the patients among a cohort of 178 IsoD patients harbored the p.Glu303del variant in *TOR1A*,¹⁶ while in a different study, only two patients belonging to a single family in a cohort of 321 patients with IsoD harbored this mutation.¹⁷ In the current study, a patient who presented with childhood-onset complex generalized dystonia was found to have an *NDUFA12* gene mutation leading to Leigh's syndrome. Although this is a known manifestation, it has not been described in previous studies of this nature. We did not observe any patients with *ANO3*, *GNAL*, or *KMT2B* mutations, which are among the recently described monogenic DYT_s. This is consistent with previous reports with only a single patient with dystonia each due to *GNAL*¹⁸ and *KMT2B*¹⁹ mutations described thus far from India and none

due to *ANO3* mutations. The frequency of a particular genetic mutation depends on population studies, which also has to be kept in mind when designing targeted gene panels to suit the population being tested.

With the introduction of NGS, the number of variants identified has increased. We found VUSs in nearly as many patients as those who had a P/LP mutation. With advancements in genomics, the status of these VUSs will be clarified, which may further improve detection rates. However, one needs to be aware of the benefits and limitations of the tests being ordered. Although NGS is time-saving and cost effective, many VUSs can be detected, which need to be interpreted with caution to determine pathogenicity. Additionally, with WES and WGS, VUSs unrelated to the disease being evaluated may be detected, further compounding the difficulty in interpretation and adding to the

psychological burden of patients owing to the presence of an additional unexpected abnormality. This possibility has to be discussed during pregenetic test counseling. Furthermore, a negative NGS result does not rule out a genetic disease, as NGS may miss copy number variants, large deletions and duplications, repeat disorders and diseases with imprinting phenomena. A genetic diagnosis has many clinical implications. Apart from identifying treatable disorders, an early genetic diagnosis will lead to proper prognostication, genetic counseling, family planning, and predicting the response to specific management options such as deep brain stimulation, which may have a differential response depending upon the genetic diagnosis.²⁰

Limitations

This study has several limitations owing to its retrospective nature. Not all patients with dystonia were offered or underwent genetic assessment. In addition, patients were not chosen consecutively or in any predefined manner, leading to a bias in ordering the genetic testing. The prevalence of patients with a younger AAO may be due to a clinical bias when ordering CES. It is likely that younger patients were advised CES more often in the hope of identifying a treatable cause. Biochemical estimations were not performed in patients with underlying enzyme defects, such as dopa-responsive dystonia, GM1 gangliosides, and Niemann-Pick disease type C. Segregation and functional studies could not be performed in several patients with VUSs to identify pathogenicity.

Conclusion

CES is a very useful tool in the evaluation of dystonia, with a yield of close to 40%. In particular, phenotypic and genotypic heterogeneity preclude single-gene tests, as they are time-consuming and not cost effective. An early AAO of dystonia could suggest a higher probability of a genetic cause and needs to be considered when ordering genetic testing.

Supplementary Materials

The online-only Data Supplement is available with this article at <https://doi.org/10.14802/jmd.21146>.

Conflicts of Interest

The authors have no financial conflicts of interest.

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Author Contributions

Conceptualization: Vikram Venkappayya Holla, Koti Neeraja, Albert Stezin, Pramod Kumar Pal. Data curation: Koti Neeraja, Vikram Venkappayya Holla, Albert Stezin, Shweta Prasad. Formal analysis: Vikram Venkappayya Holla, Koti Neeraja, Shweta Prasad. Investigation: Vikram Venkappayya Holla, Koti Neeraja, Bharat Kumar Suriseti. Methodology: Vikram Venkappayya Holla, Koti Neeraja, Pramod Kumar Pal. Project administration: Manjunath Netravathi, Nitish Kamble, Ravi Yadav, Pramod Kumar Pal. Resources: Vikram

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SUPPLEMENTARY MATERIAL 1

Clinical exome sequencing and statistical analysis

Clinical exome sequencing

Clinical exome sequencing (CES) was performed as part of evaluation in a commercial genetic lab using a standard pipeline for CES analysis. Customized exome sequencing of all clinically relevant genes was performed to identify relevant variations. A custom capture kit for targeted gene capture was used to assemble DNA library from the patients' genomic DNA. The libraries were sequenced to a mean >80–100× coverage on Illumina sequencing platform. The sequences obtained were aligned to human reference genome (GRCh37/hg19) and analyzed to identify variants. The best practices framework of Genome Analysis Tool Kit (Broad Institute, Cambridge, MA, USA) was followed for identification of variants in the sample. Gene annotation of the variants was performed against Ensembl human gene model (release 9–11) (EMBL-EBI, Cambridge, UK). Clinically relevant mutations were annotated using published variants in literature and a set of publicly available diseases databases (ClinVar, Online Mendelian Inheritance in Man, Genome Wide Association Study, Human Gene Mutation Database, and SwisVar). Common variants were filtered based on allele frequency in publicly available database of normal human variation (1000 Genome, Exome Aggregation Consortium, The Genome Aggregation Database, EVS, dbSNP, 1000 Japanese Genome) and internal Indian population database. Nonsynonymous variants effect was calculated using multiple algorithms such as PolyPhen-2, Scale-Invariant Feature Transform, MutationTaster2, and likelihood ratio test. Synonymous variants found in the CES panel consisting of customized gene panel were not used for clinical interpretation. The clinical effects of identified variants were classified based on the American College of Medical Genetics and Genomics (ACMG) standards and guidelines. A positive genetic diagnosis was considered if the variant was classified as likely pathogenic or pathogenic according to ACMG guidelines.^{S1} A variant was classified as novel if they are not published in literature and in publicly available disease database so far.

Statistical analysis

SPSS Statistics (Version 25, IBM Corp., Armonk, NY, USA) was used for statistical analysis. Descriptive statistical analysis (mean ± standard deviation for continuous variables and frequency and percentages for categorical variables) was performed for the demographic and clinical features. Appropriate statistical test (Fisher's exact for categorical variables, Student *t*-test for continuous variables of normal distribution and Mann-Whitney U test for continuous variables of non-normal distribution with Bonferroni correction) was applied for group comparison between individuals with positive genetic diagnosis and those with a negative genetic diagnosis. A threshold of *p*-values < 0.05 were considered as statistically significant.

REFERENCES

- S1. Richards S, Aziz N, Bale S, Bick D, Das S, Gastier-Foster J, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med* 2015;17:405-424.

SUPPLEMENTARY MATETIAL 2

List of genes analyzed in clinical exome sequencing

ABCE1	CFI	EVC	HNRNPD	N4BP2	PRDM5	SRD5A3	WDR19	BLNK
ABCG2	CHIC2	EVC2	HNRNPDL	NAA15	PRDM8	SRP72	WFS1	BMII
ADAMTS3	CHRNA9	FII	HPGD	NAF1	PRIMPOL	STAP1	WHSC1	BMPRIA
ADD1	CISD2	FII-AS1	HSD17B11	NAT8L	PRKG2	STIM2	WWC2	BMS1
ADGRA3	CLCN3	FABP2	HTN3	NDST3	PRMT9	SULT1B1	YTHDC1	BTAF1
ADH1A	CLNK	FAM175A	HTT	NDST4	PROM1	SULT1E1	ZGRF1	BTRC
ADH1B	CLOCK	FAT1	IBSP	NDUFC1	PRSS12	TACC3	ZNF141	BUB3
ADH1C	CNGA1	FAT4	IDUA	NEK1	PSAPL1	TACR3	ZNF518B	C10orf105
ADH4	COL25A1	FBXW7	IGFBP7	NELFA	PTPN13	TAPT1	ZNF721	C10orf11
ADH5	COQ2	FGA	IGFBP7-AS1	NFKB1	QDPR	TBC1D1	ABCC2	C10orf2
ADH6	CORIN	FGB	IL2	NFXL1	RAB28	TBC1D9	ABLIM1	C10orf53
ADH7	COX18	FGF2	IL21	NIPAL1	RAB33B	TBCK	ACADSB	C10orf55
ADRA2C	COX7B2	FGF5	INTU	NKX3-2	RAP1GDS1	TDO2	ACBD5	CACNB2
AFF1	CPE	FGFBP1	IRF2	NKX6-1	RASGEF1B	TEC	ACSL5	CALHM1
AFP	CPLX1	FGFR3	KCNIP4	NMU	RBPJ	TECRL	ACTA2	CAMK2G
AGA	CPZ	FGFRL1	KDR	NOA1	RCHY1	TENM3	ADAM12	CC2D2B
AIMP1	CTBP1	FGG	KIAA0232	NPFFR2	REST	TET2	ADD3	CCDC6
ALB	CXCL10	FIP1L1	KIAA1109	NPNT	RFC1	TLL1	ADK	CDH23
AMBN	CXCL11	FRAS1	KIT	NPY1R	RGS12	TLR1	ADRA2A	CDHR1
ANAPC10	CXCL5	FREM3	KLB	NPY2R	RHOH	TLR10	ADRB1	CFAP58
ANK2	CXCL8	FRG1	KLKB1	NR3C2	RNF212	TLR2	AGAP6	CH25H
ANKRD50	CYP2U1	GAB1	LARP7	NSUN7	RRH	TLR3	AIFM2	CHAT
ANTXR2	CYP4V2	GABRA2	LEF1	NUDT6	SCARB2	TLR6	AKRIC2	CHST3
ANXA5	DCHS2	GABRA4	LETM1	OTUD4	SCLT1	TMEM165	AKRIC3	CHUK
APBB2	DCK	GABRB1	LIAS	PABPC4L	SEC24B	TMPRSS11A	AKRIC4	CNNM2
ARHGAP24	DCLK2	GABRG1	LOC100507053	PALLD	SEC24D	TRAPPC11	AKRIE2	COL13A1
ATP10D	DCTD	GAK	LOC344967	PARM1	SEC31A	TRIM2	ALDH18A1	COL17A1 COMMD3- BMII
ATP5I	DKK2	GALNT7	LRAT	PCDH10	SEPSECS	TRMT10A	ALOX5	COX15
BANK1	DMP1	GALNTL6	LRBA	PCDH18	SCCB	TRMT44	ANK3	CPN1
BBS12	DOK7	GAR1	LRIT3	PCDH7	SH3BP2	TRPC3	ANKRD1	CSTF2T
BBS7	DRD5	GBA3	LRPAP1	PDE5A	SHROOM3	UCHL1	ANKRD22	CTBP2
BMP2K	DSPP	GC	MAB21L2	PDE6B	SLBP	UCP1	ANKRD26	CTNNA3
BMPRI1B	DTHD1	GK2	MAD2L1	PDGFC	SLC25A31	UFSP2	ANXA11	CUBN
BST1	DUX2 DUX4- chr4	GLRB	MAEA	PDGFRA	SLC25A4	UGDH	APBB1IP	CUL2
BTC	DUX4- chr4	GNRHR	MANBA	PDLIM3	SLC26A1	UGT2A1	ARHGAP21	CUL2
C4orf19	DUX4- chr4	GPRIN3	MAPK10	PDLIM5	SLC2A9	UGT2A3	ARL3	CUTC
C4orf26	DUX4L2 DUX4L3- chr4	GRID2	MED28	PHOX2B	SLC34A2	UGT2B10	ARMC4	CUZD1
C4orf29	DUX4L5	GRK4	MEPE	PIGG	SLC39A8	UGT2B15	ARMS2	CWF19L1
CAMK2D	DUX4L5	GRPEL1	METTL14	PIGY	SLC4A4	UGT2B17	AS3MT	CXCL12
CASP3	DUX4L5	GRXCR1	MFSDB	PITX2	SLC7A11	UGT2B28	ASAH2	CYP17A1
CBR4	DUX4L6	GUCY1A3	MGST2	PKD2	SLC9B1	UGT2B4	ASCC1	CYP26A1
CC2D2A	DUX4L6	GUF1	MMAA	PLK4	SLIT2	UGT2B7	ATE1	CYP26C1
CCDC109B	EDNRA	GYPA	MRPL1	POLR2B	SMAD1	UGT8	ATOH7	CYP2C18
CCKAR	EGF	GYPB	MRPS18C	PPA2	SMARCD1	UNC5C	ATP5C1	CYP2C19
CCNA2	EIF4E	GYPE	MSMO1	PPARGC1A	SNCA	USP38	ATRNL1	CYP2C8
CD38	ELMOD2	HADH	MSX1	PPAT	SOD3	USP46	BAG3	CYP2C9
CDKN2A1P	ENAM	HAND2	MTNR1A	PPEF2	SORBS2	UVSSA	BAMBI	CYP2E1
CDS1	EPHA5	HELQ	MTTP	PPM1K	SPATA5	VEGFC	BBIP1	DCLRE1A
CENPE	ETFDH	HHIP	MUC7	PPP2R2C	SPP1	WDFY3	BCCIP	DCLRE1C
CEP135	ETNPPL	HMX1	MYOZZ	PPP3CA	SPRY1	WDR1	BICC1	DHTKD1
DIP2C	HMX2	MPP7	PLCE1-AS1	ST8SIA6	ALPK3	CYP1A1	IPW	NEO1
DKK1	HNRNPH3	MRC1	PLEKHA1	STAMBPL1	AP3B2	CYP1A2	IQGAP1	NIPA1

DLG5	HOGA1	MRPL43	PNLIP	STOX1	AP3S2	DLL4	IREB2	NIPA2
DMBT1	HPS1	MRPS16	POLL	SUFU	AP4E1	DMXL2	ITGA11	NMB
DNA2	HPS6	MSMB	POLR3A	SVIL	APBA2	DNAJA4	IVD	NOP10
DNAJC12	HPSE2	MSRB2	PPP1R3C	SYCE1	APH1B	DNAJC17	JMJD7 JMJD7- PLA2G4B	NPAP1
DNAJC9	HTR7	MTPAP	PRF1	TACC2	ARIH1	DUOX1		NPTN
DPCD	HTRA1	MXI1	PRKCQ	TCF7L2	ARNT2	DUOX2	KBTBD13	NR2E3
DUX4- chr10	IDE	MYO3A	PRKG1	TCTN3	ATP10A	DUOXA1	KIF23	NR2F2
DUX4L3- chr10	IKZF5	MYOF	PRLHR	TECTB	B2M	DUOXA2	KIF7	NTRK3
EBF3	IL2RA	MYOZ1	PSAP	TET1	BBS4	DYX1C1 DYX1C1- CCPG1	KLHL25	OCA2
ECHS1	INA	MYPN	PTCHD3	TFAM	BCL2A1		LACTB	OR4M2
EDRF1	IPMK	NANOS1	PTEN	TIAL1	BLM	EDC3	LDHAL6B	PAK6
EGR2	ITGA8	NCOA4	PTF1A	TLX1	BLOC1S6	EIF2AK4	LINS1	PDIA3
EMX2	ITGB1	NDST2	PTPLA	TM9SF3	BUB1B	EMC4	LIPC	PEX11A
ENTPD1	ITPRIP	NDUFB8	RAB18	TRIM8	C15orf41	EPB42	LOXL1	PGBD4
ENTPD1- AS1	JMJD1C	NEBL	RASSF4	TUBAL3	C15orf62	ETFA	LRRRC28	PIAS1
EPC1	KAT6B	NET1	RBM20	TUBB8	C15orf65	FAH	LRRK1	PIF1
ERCC6	KCNK18	NEUROG3	RBP3	UPF2	CA12	FAM63B	LTK	PIGB
ERCC6- PGBD3	KCNMA1	NFKB2	RBP4	UROS	CAPN3	FAN1	LYSMD4	PKM
ERLIN1	KIAA1217	NKX2-3	RET	USMG5	CASC4	FANCI	MAGEL2	PLIN1
FAM160B1	KIAA1279	NMT2	RGR	USP54	CASC5	FBN1	MAP2K1	PML
FAM175B	KIAA1462	NODAL	RNLS	USP6NL	CATSPER2	FEM1B	MAPKBP1	POLG
FAS	KIF11	NRG3	RPP30	UTF1	CCNDBP1	FES	MCTP2	POLR2M
FBXO18	KIF20B	NRP1	RPS24	VAX1	CCPG1	FMN1	MEF2A	PPIB
FBXW4	KIF5B	NT5C2	RUFY2	VCL	CDAN1	FRMD5	MEGF11	PRTG
FFAR4	KIN	OAT	SEMA4G	VIM	CELF6	FURIN	MEIS2	PSMA4
FGF8	KLF6	OBFC1	SFTPA1	VIM-AS1	CEMIP	GABRA5	MESDC2	PSTPIP1
FGFR2	KLLN	OGDHL	SFTPA2	VTI1A	CEP152	GABRB3	MESP1	PWAR1
FRA10AC1	LDB1	OPN4	SFTPD	WAC	CERS3	GABRG3	MESP2	PWARSN
FRMD4A	LDB3	OPTN	SFXN4	WDFY4	CHD2	GALK2	MFGE8	PWRN1
GAD2	LGII	PAPSS2	SH3PX2A	WDR11	CHRFAM7A	GATM	MGA	PYGO1
GATA3	LIPA	PARD3	SHOC2	XPNPEP1	CHRNA3	GCOM1	MIR184	RAB27A
GBF1	LIPK	PAX2	SIRT1	YME1L1	CHRNA5	GJD2	MKRN3	RAD51
GDF2	LIPN	PBLD	SLC16A12	ZEB1	CHRNA7	GLCE	MNS1	RASGRP1
GFRA1	MAP3K8	PCBD1	SLC18A2	ZEB1-AS1	CHRN4	GLDN	MPI	RGMA
GJD4	MAPK8	PCDH15	SLC18A3	ZFYVE27	CHST14	GNB5	MRPL46	RLBP1
GLUD1	MASTL	PDCD11	SLC25A16	ZMYND11	CHSY1	GREM1	MRPS11	RORA
GOT1	MAT1A	PDE6C	SLC25A28	ZNF33A	CIB2	HCN4	MTFMT	RPS17
GPAM	MBL2	PDSS1	SLC29A3	ZNF365	CILP	HDC	MTHFS	RTF1
GPRIN2	MCM10	PDZD7	SLC39A12	AAGAB	CLN6	HERC1	MYEF2	RYR3
GRID1	MCU	PGAM1	SLIT1	ACAN	CLPX	HERC2	MYO1E	SCAPER
GRK5	MGEA5	PGBD3	SLK	ACTC1	COPS2	HEXA	MYO5A	SCG3
GSTO1	MGMT	PHYH	SMC3	ADAM10	COX5A	HIGD2B	MYO5C	SEMA6D
GSTO2	MICU1	PIK3AP1	SMNDC1	ADAMTS17	CSNK1G1	HOMER2	MYO9A	SEMA7A
HABP2	MINPP1	PIP4K2A	SNCG	ADAMTSL3	CTSH	HYKK	NDN	SIN3A
HELLS	MKI67	PITRM1	SORBS1	AGBL1	CTXN2	IDH2	NDNL2	SLC12A1
HHEX	MLLT10	PITX3	SORCS1	AKAP13	CYFIP1	IGF1R	NDUFAF1	SLC12A6
HIF1AN	MMP21	PLAU	SPAG6	ALDH1A2	CYP11A1	IL16	NEDD4	SLC24A1
HK1	MMRN2	PLCE1	SPRN	ALDH1A3	CYP19A1	INO80	NEIL1	SLC24A5
SLC28A1	VIMP	BMPER	CYP3A7- CYP3AP1	GCK	IRF5	NDUFA5	PRSS37	SNX10

SLC28A2	VPS13C	BPGM	CYP51A1	GHRHR	ISPD	NDUFB2	PRSS3P2	SP8
SLCO3A1	VPS33B	BRAF	DAGLB	GIMAP8	KCND2	NME8	PRSS58	SRI
SMAD3	VPS39	BRAT1	DBNL	GJC3	KCNH2	NOBOX	PSMC2	SRPK2
SMAD6	WDR72	C1GALT1	DDC	GLCCI1	KCTD7	NOD1	PSPH	ST7
SNAPC5	WDR73	C7orf43	DFNA5	GLI3	KDM7A	NOS3	PTCD1	ST7-AS1
SNORD115-1	WDR93	C7orf55	DGKB	GNAI1	KEL	NPC1L1	PTPN12	ST7-OT3
SNORD116-1	ZNF592	C7orf60	DGKI	GNB2	KIAA1549	NPSR1	PTPRN2	STAG3
SNORD116-10	ZNF774	CACNA2D1	DLD	GPNMB	KLHL7	NPTX2	PTPRZ1	STEAP4
SNRPN	ZSCAN29	CADPS2	DLX5	GPR37	KMT2C	NPY	RABGEF1	STX1A
SNUPN	AASS	CALCR	DLX6	GPR85	KMT2E	NRCAM	RAC1	STYXL1
SNURF	ABCA13	CALU	DMTF1	GRB10	KPNA7	NT5C3A	RAMP3	SUGCT
SNX1	ABCB1	CAMK2B	DNAAF5	GRM3	KRIT1	NUB1	RBM28	SUN1
SNX22	ABCB4	CARD11	DNAH11	GRM8	LAMB1	NUDT1	RBM48	TAF6
SPATA5L1	ABCB5	CASP2	DNAJB6	GSTK1	LAMB4	NUP205	RELN	TAS2R16
SPG11	ABCB8	CAVI	DNAJC30	GTF2I	LEP	OGDH	RFC2	TAS2R3
SPG21	ACHE	CBX3	DOCK4	GTF2IRD1	LFNG	OPN1SW	RHBDD2	TAS2R38
SPRED1	ACTB	CCDC136	DPP6	GTF2IRD2	LIMK1	OR2F1	RHEB	TBX20
SPTBN5	ACTL6B	CCL26	DUS4L	GUSB	LMBR1	OSBPL3	RINT1	TBXAS1
ST20-MTHFS	ACTR3C	CCM2	EEPDI	H2AFV	LOC100129427	PAX4	RNF216	TFR2
ST8SIA2	ADAM22	CD36	EGFR	HDAC9	LOC100506136	PAXIP1	RNF32	THSD7A
STARD9	ADCY1	CDCA7L	EGFR-AS1	HEPACAM2	LOC101926943	PCLO	RP9	TMEM139
STRA6	AEBP1	CDK13	EIF3B	HGF	LRGUK	PCOLCE	RUNDC3B	TNPO3
STRC	AGK	CDK5	EIF4H	HIBADH	LRRC4	PDGFA	SAMD9	TNRC18
SV2B	AGMO	CDK6	ELN	HIP1	LSMEM1	PDIA4	SAMD9L	TNS3
SYNM	AHR	CEP41	EN2	HNRNPA2B1	MACC1	PDK4	SBDS	TPK1
TBC1D2B	AIMP2	CFTR	EPHA1	HOXA1	MAD1L1	PEX1	SCRN1	TRA2A
TCF12	AKAP9	CHCHD2	EPHB4	HOXA10	MAGI2	PGAM2	SEMA3A	TRB
TGM5	AKR1B1	CHPF2	EPHB6	HOXA11	MCM7	PHKG1	SEMA3C	TRBV9
THBS1	AKRID1	CHRM2	EPO	HOXA13	MDH2	PIK3CG	SEMA3D	TRGC1
TLN2	AMZ1	CHST12	ETV1	HOXA2	MEST	PKD1L1	SEMA3E	TRGC2
TMC3	ANLN	CLCN1	EXOC4	HOXA3	MET	PLOD3	39326	TRGV1
TP53BP1	AOAH	CLIP2	EZH2	HOXA4	METTTL2B	PLXNA4	SERPINE1	TRIL
TPM1	AOC1	CNOT4	FAM126A	HOXA9	MIOS	PMS2	SFRP4	TRIM24
TRIP4	AP1S1	CNTNAP2	FAM188B	HSPB1	MIR96	PMS2P3	SGCE	TRPV5
TRPM1	AP4M1	COG5	FAM20C	HTR5A	MLXIPL	PNPLA8	SHFM1	TRRAP
TRPM7	AP5Z1	COL1A2	FBXL18	IFRD1	MMD2	PODXL	SHH	TSPAN12
TTBK2	AQP1	COX19	FEZF1	IGFBP1	MNX1	POM121C	SLC13A1	TWIST1
TUBGCP4	ASB10	CPA1	FKBP14	IGFBP3	MPLKIP	PON1	SLC25A13	TYW1
TUBGCP5	ASIC3	CPA4	FKBP6	IKZF1	MPP6	PON2	SLC25A40	UBE3C
TYRO3	ASL	CPVL	FLNC	IL6	MRPL32	PON3	SLC26A3	UBN2
UACA	ASNS	CREB5	FO XK1	IMMP2L	MRPS17	POR	SLC26A4	URGCP-
UBE3A	ATG9B	CTTNBP2	FOXP2	IMPDH1	MRPS24	POT1	SLC26A4-AS1	MRPS24
UBR1	ATP5J2-PTCD1	CUX1	FZD1	ING3	MRPS33	POU6F2	SLC26A5	VSTM2A
ULK4P1	ATP6V0A4	CYCS	FZD9	INHBA	MUC17	PPIA	SLC29A4	WBSCR16
ULK4P1	AUTS2	CYP2W1	GAL3ST4	INMT	MUC3A	PPP1R17	SLC37A3	WBSCR17
ULK4P2	AZGP1	CYP3A4	GALNT11	INMT-FAM188B	MYO1G	PPP1R3A	SMARCD3	WBSCR22
UNC13C	BAZ1B	CYP3A43	GALNTL5	INSIG1	NAMPT	PRKAG2	SMO	WDR60
USP3	BBS9	CYP3A5	GARS	INTS1	NCF1	PRKAR1B	SND1	WIP12
USP8	BLVRA	CYP3A7	GATAD1	IQCE	NDUFA4	PRSS1	SNORD56- chr7	XRCC2

YAEID1 ATP5G3 CHRNG DFNB59 FSHR IFIH1 LMAN2L MSH6 PER2

ZAN	ATP6VIB1	CHST10	DGKD	FZD5	IFT172	LOC100271832	MSTN	PEX13
ZC3HAV1	AUP1	CIAO1	DGUOK DGUOK- AS1	G6PC2	IGFBP5	LOC100507600	MXD1	PGAP1
ZKSCAN5	B3GALT1	CKAP2L		GAD1	IGKC	LOC101928371	MYCN	PIGF
ZNHIT1	B3GNT2	CLASPI	DHRS9	GAL3ST2	IGKV	LOC101929680	MYL1	PIKFYVE
ZBPB	B3GNT7	CLHC1	DIS3L2	GALNT13	IHH	LOC102724058	MYO3B	PKP4
ABCA12	BARD1	CMPK2	DLX2	GALNT14	IL18R1	LOC654841	MYO7B	PLA2R1
ABCB11	BBS5	CNGA3	DNAH6	GALNT3	IL18RAP	LOXL3	MYTIL	PLB1
ABCB6	BCL11A	CNNM3	DNAH7	GALNT5	IL1A	LPIN1	NAT8	PLCD4
ABCG5	BCL2L11	CNNM4	DNAJB2	GCKR	IL1B	LRPIB	NBAS	PLEKHH2
ABCG8	BCS1L	CNTNAP5	DNMT3A	GEN1	IL1R1	LRP2	NCAPH	PMS1
ACADL	BIN1	COA5	DOK1	GFPT1	IL1RL1	LRPPRC	NCK2	PNKD
ACMSD	BIRC6	COL3A1	DPP10	GGCX	IL1RN	LRRTM1	NCKAP1	PNPT1
ACPI	BMP10	COL4A3	DPP4	GIGYF2	IL36B	LRRTM4	NCOA1	POLR1A
ACTG2	BMPR2	COL4A4	DRC1	GLI2	IL36RN	LTBP1	NDUFA10	POMC
ACTR3	BOLA3	COL5A2	DTNB	GLS	IMMT	LY75	NDUFAF7	PPIG
ACVRI	BUB1	COL6A3	DYNC2LI1	GMPPA	INHA	MAL	NDUFB3	PPM1B
ACVRI1C	C2orf42	COLEC11	DYSF	GPBAR1	INHBB	MAP2	NDUFS1	PPM1G
ACVR2A	C2orf71	COMMD1	ECEL1	GPC1	INO80D	MAP4K3	NEB	PPP1CB
ADAM17	CACNB4	COX5B	EDAR	GPD2	INPP4A	MAP4K4	NEU2	PPP3R1
ADAM23	CAD	COX7A2L	EEF1B2	GPR1	INPP5D	MARS2	NEUROD1	PRADC1
ADCY3	CALCRL	CPO	EFEMP1	GPR35	INSIG2	MAT2A	NFE2L2	PREPL
ADD2	CALM2	CPS1	EHBP1	GPR55	IRS1	MATN3	NFU1	PRKAG3
ADRA2B	CAMKMT	CPSF3	EIF2AK3	GPR75	ITGA4	MBD5	NHEJ1	PRKD3
AFF3	CAPN10	CREB1	EIF2B4	GRB14	ITGA6	MCEE	NLRC4	PRKRA
AGAP1	CAPN13	CRIM1	ELMOD3	GRHL1	ITGB1BP1	MCFD2	NMS	PRLH
AGBL5	CASP10	CRIP1	EMILIN1	GTF2A1L	ITGB6	MCM6	NPAS2	PROC
AGPS	CASP8	CRYBA2	EMX1	GTF3C2	ITM2C	MDH1	NPHP1	PROKR1
AGXT	CCDC115	CRYGA	EN1	GYPC	ITSN2	MEIS1	NPPC	PRSS56
ALK	CCDC141	CRYGB	EPAS1	HADHA	KCNE4	MERTK	NR4A2	PTH2R
ALLC	CCDC88A	CRYGC	EPC2	HADHB	KCNH7	METTL8	NRP2	PTPN18
ALMS1	CCNT2	CRYGD	EPCAM	HDAC4	KCNJ13	MFF	NRXN1	PUS10
ALS2	CCT7	CRYGEP	EPHA4	HDLBP	KCNJ3	MGAT4A	NT5C1B NT5C1B- RDH14	PXDN
ANAPC1	CD207	CTLA4	EPT1	HECW2	KCNK3	MGAT5		RAB10
ANO7	CD8A	CTNNA2	ERBB4	HES6	KCNS3	MLPH	NTSR2	RAB11FIP5
ANTXR1	CDCA7	CUL3	ERCC3	HIBCH	KDM3A	MLTK	OBSL1	RAB3GAP1
AOX1	CEBPZ	CXCR1	EXOC6B	HK2	KHK	MMADHC	ODC1	RANBP2
AP1S3	CENPO	CXCR2	FABP1	HNMT	KIDINS220	MOB4	ORC4	RAPGEF4
APOB	CEP68	CXCR4	FAM136A	HOXD10	KIF1A	MOGS	OSR1	RBM43
ARHGEF4	CERKL	CYBRD1	FAM161A	HOXD11	KIF3C	MPHOSPH10	OTOF	REEP1
ARID5A	CERS6	CYP1B1	FAM228B	HOXD13	KIF5C	MPP4	PARD3B	REG1A
ARL6IP6	CFC1	CYP26B1	FANCL	HOXD4	KLF11	MPV17	PASK	REL
ASAP2	CFC1B	CYP27A1	FASTKD2	HS1BP3	KLF7	MREG	PAX3	RFX8
ASB1	CFLAR CFLAR- AS1	CYS1	FBXO11	HS6ST1	KLHL41	MRPL19	PAX8	RHOB
ASIC4		D2HGDH	FEV	HSPD1	KRTCAP3	MRPL35	PAX8-AS1	RIF1
ASPRV1	CGREF1	DARS	FHL2	HSPE1	KYNU	MRPL44	PDCD1	RMDN2
ASTL	CHN1	DBI	FIGLA	HTR2B	LCT	MRPL53	PDE11A	RNASEH1
ASXL2	CHPF	DCAF17	FN1	HTRA2	LHCGR	MRPS5	PDE6D	RNU4ATAC
ATG16L1	CHRNA1	DCTN1	FOXN2	ICOS	LIMS2	MRPS9	PDK1	ROCK2
ATIC	CHRND	DES	FRZB	IDH1	LIPT1	MSH2	PECR	RPIA

RPL31	SRSF7	UGGT1	ALDH3B2	CAPN1	CUL5	FLI1	IL18	MMP20
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RPS27A	ST3GAL5	UGT1A1	ALG8	CAPN5	CWF19L2	FLRT1	ILK	MMP3
RPS7	ST6GAL2	UGT1A10	ALG9	CAPRIN1	CYP2R1	FNBP4	INCENP	MMP7
SAG	STAMBP	UGT1A3	ALX4	CASP1	DCDC1	FOLH1	INPPL1	MMP8
SATB2	STAT1	UGT1A4	AMPD3	CASP12	DCDC5	FOLR1	INS	MOGAT2
SCG2	STAT4	UGT1A5	ANGPTL5	CASP5	DCHS1	FOXRED1	INTS5	MPEG1
SCN1A	STEAP3	UGT1A6	ANKK1	CAT	DCPS	FSHB	IRF7	MRE11A
SCN2A	STK11IP	UGT1A7	ANO3	CATSPER 1	DDB1	FTH1	JAM3	MRPL11
SCN3A	STK36	UGT1A8	ANO5	CBL	DDB2	FXYD2	KAT5	MRPL16
SCN7A	STK39	UGT1A9	AP001350. 1	CCDC86	DDX25	FXYD6	KBTBD4	MRPL17
SCN9A	SUCLG1	UNC50	APBB1	CCDC90B	DEAF1 DENND5 A	FXYD6-FXYD2	KCNA4	MRPL21
SEMA4C	SULT1C2	UNC80	APIP	CCKBR	A	FZD4	KCNC1	MRPL23
SF3B1	SULT1C3	USP34	APLN	CCND1	DGAT2	GAB2	KCNE3	MRPL48
SFTPB	SULT1C4	VIL1	APOA1	CCS	DGKZ	GAL	KCNJ1	MRPL49
SGPP2	SUMO1	VPS54	APOA4	CD151	DHCR7	GAL3ST3	KCNJ11	MS4A1
SH3BP4	TACR1	VRK2	APOA5	CD3D	DKK3	GALNT18	KCNJ5	MS4A10
SIX2	TANC1	VWA3B	APOC3	CD3E	DLAT	GANAB	KCNQ1 KCNQ10T 1	MS4A12
SIX3	TBR1	WDPCP	ARAP1	CD3G	DLG2	GDPD5	1	MS4A2
SLC11A1	TCF7L1	WDR35	ARCNI ARHGAP3 2	CD44	DNAJB13	GIF	KDEL2	MS4A3
SLC19A3	TFPI TGFBRAP 1	WIPF1	2	CD5	DPAGT1	GLYAT	KIAA1377	MS4A6A
SLC1A4	1	WNT10A	ARHGEF12	CD59	DPP3	GNG3	KIF18A	MS4A6E
SLC25A12	THADA	WNT6	ARL14EP	CD81	DRD2	GPR152	KIRREL3	MS4A7
SLC30A3	THSD7B	XDH	ASRGL1	CD82	DRD4	GRIK4	KLC2	MTA2
SLC30A6	TIA1	XIRP2	ATL3	CDKN1C	DSCAML1	GRM5	KMT2A	MTCH2
SLC35F5	TLK1	XRCC5	ATM	CDON	DYNC2H1	GSTP1	LDHA	MTMR2
SLC3A1	TLX2	ZAP70	B3GAT1	CEP164	EED	GTF2H1	LGALS12	MTNR1B
SLC40A1	TM4SF20	ZC3H6	B3GAT3	CEP57	EFEMP2	GYLTL1B	LGR4	MUC15
SLC4A10	TMEM127	ZDBF2	B3GNT6	CHEK1	ELP4	H19	LMO2	MUC2
SLC4A3	TMEM17	ZEB2	B4GALNT4	CHRM1	EPS8L2	HBB	LRFN4	MUC5B
SLC4A5	TMEM18	ZEB2-AS1	B4GAT1	CHST1	ESAM	HBD	LRP4	MUC6
SLC5A6	TMEM237	ZFP36L2	BACE1	CLCF1	ESRRA	HBE1	LRP4-AS1	MUS81
SLC5A7	TMEM87B	ZNF2	BANF1	CLMP	ETS1	HBG1	LRP5	MYBPC3
SLC8A1	TNP1	ZNF385B	BARX2	CLNS1A	EXPH5	HBC2	LRR10B	MYO7A
SMARCAL1 SNORD56- chr2	TNS1	ZNF513	BBS1	CLP1	EXT2	HEPACAM	LRR10B	MYO7A
SNRNP200	TP53I3	ZNF638	BCL9L	CLPB	F2	HEPN1	LRTOMT	NARS2
	TPO	ZNF804A	BDNF	CNGA4	FADD	HMBS HNRNPUL2- BSCL2	LTBP3	NAT10
SNTG2	TRAF3IP1	ABCC8	BDNF-AS	CNTF	FADS1	BSCL2	MADD	NAV2
SNX17	TRAK2	ACAD8	BEST1	CNTN5	FADS2	HPS5	MAML2	NCAM1
SOS1	TRIB2	ACAT1	BIRC3	COX8A	FAM111A	HRAS	MAP4K2	NCAPD3
SOX11	TRIM54	ACCS	BRSK2	CPT1A	FAM111B	HSPA8	MAP6	NDUFC2 NDUFC2- KCTD14
SP100	TRIP12	ACCSL	BSCL2	CRY2	FANCF	HTR3A	MAPK8IP1	KCTD14
SP110	TTC21B	ACER3	C11orf40	CRYAB	FAR1	HTR3B	MDK	NDUFS3
SPAG16	TTC7A	ACP2	C11orf73	CSNK2A3	FAT3	HYLS1	MED17	NDUFS8
SPAST	TTN	ACTN3 ADAMTS1 5	C11orf91	CSRP3	FDXACB1	IFITM3	MEN1	NDUFV1
SPEG	TTN-AS1	5	C1QTNF5	CST6	FEN1	IFITM5	MFRP	NELL1
SPP2	TUBA3E	ADM	C2CD3	CTNND1	FERMT3	IGF2	MICALCL	NLRP10
SPR	TUBA4A	AGBL2	CABP2	CTR9	FEZ1	IGF2-AS	MMP1	NLRP14
SPRED2	TWIST2	AHNAK	CABP4	CTSC	FGF3	IGHMBP2	MMP10	NLRX1
SPTBN1	UBR3	AIP	CADM1	CTSD	FIBIN	IGSF22	MMP12	NNMT
SRD5A2	UCN	ALDH3B1	CALCA	CTSF	FIBP	IL10RA	MMP13	NPAT
NRIH3	PTPRJ	SIAE	TH	ZFPL1	B3GNT5	CIDEC	EIF4G1	HTR3E

NRGN	PTS	SIGIRR	TIRAP	ZNF143	B4GALT4	CISH	EOGT	HYAL1
NRXN2	PUS3	SIK2	TMEM126 A	ZNF202	BAP1	CLCN2	EOMES	HYAL2
NUCB2	PVRL1	SIK3	TMEM126 B	ZNF408	BCHE	CLDN1	EPHA3	IFT122
NUMA1	PYGM	SIPA1	TMEM132 A	ZP1	BCL6	CLDN16	EPHB1	IFT80
NUP98	QSER1	SIRT3	TMEM135	A4GNT	BFSP2	CLEC3B	ETV5	IGF2BP2
OPCML	RAD9A	SLC1A2	TMEM138	AADAC	BOC	CLRN1	FANCD2 FANCD2O S	IGSF10
OR10V1	RAG1	SLC22A11	TMEM216	AADAACL2	BRPF1	CLSTN2		IL12A
OR51G1	RAG2	SLC22A12	TMPRSS4	ABCC5	BSN	CMC1	FBLN2	IL17RB
OR52H1	RAPSN	SLC22A18 SLC22A18A S	TMPRSS5	ABHD14A ABHD14A- ACY1	BTD	CMSS1	FBXO45	IL17RC
OR52N4	RASGRP2		TNNI2		BTLA	CNBP	FEZF2	IL17RD
OR8H1	RBM14 RBM14- RBM4	SLC22A25	TNNT3	ABHD5	C3orf17	CNTN3	FGF12	IL20RB
OR8K3	RBM4	SLC22A6	TOLLIP	ABI3BP	CACNA1D	CNTN4	FHIT	ILDRI
OSBPL5	RBM7	SLC22A8	TP53AIP1	ACAA1	CACNA2D2	CNTN6 COL6A4P 2	FLNB	IMPDH2
OTOG	RBMXL2	SLC22A9	TPCN2	ACAD11	CACNA2D3 CACNA2D3 -AS1	COL6A5	FOXL2	IMPG2
OVCH2	RDX	SLC25A22	TPH1	ACAD9		COL6A5	FOXP1	IQCB1
P2RY2	RELA	SLC25A45	TPP1	ACOX2	CADM2	COL6A6	FSTL1	IQCG
PACS1 PAFAH1B 2	RELT	SLC29A2	TRAF6	ACTL6A	CADPS	COL7A1	FYCO1	ITGA9
PAMR1	RHOG	SLC35C1	TREH	ACVR2B	CAMK1	COLQ	GAP43	ITIH1
PANX1	RIC3 RNASEH2 C	SLC37A4	TRIM21	ACY1	CAMP	COX17	GATA2	ITIH3
PAX6	ROBO3	SLC39A13	TRIM22	ADCY5	CASR	CP	GBE1	ITIH4
PC	ROM1	SLC6A5	TRIM44	ADIPQ ADIPQ- AS1	CAV3	CPOX	GFM1	ITPR1
PCSK7	RPL27A	SLCO2B1	TRIM5		CBLB	CRBN	GHRL	JAGN1
PDE3B	RPS3	SMPD1	TRMT112	AGTR1	CCDC14	CRELD1	GHRLOS	KALRN
PDHX	RPS6KB2	SMTNL1 SNORD56- chr11	TRPC6	AHSG	CCDC174	CRTAP	GHSR	KAT2B
PEX16	RRAS2	TSG101	TRM7B	ALAS1	CCDC39	CRYBG3	GLB1	KCNAB1
PGAP2	RRM1	SNX19	TSSC4	ALCAM	CCDC50	CRYGS	GLYCTK	KCNMB3
PGR	RRP8	SORL1	TUB	ALG3	CCDC66	CSTA	GMPPB	KCTD6
PHLDA2	RRP8	SOX6	TUT1	ALS2CL	CCK	CTNNB1	GMPS	KIAA2018
PHLDB1	SAA1	SPA17	TYR	AMT	CCR1	CX3CR1	GNAI2	KLHDC8B
PHOX2A	SAA2	SPDYC	U4atac- chr11	ANO10	CCR2	CYP8B1	GNAT1	KLHL24
PICALM	SAA4	SPI1	UBQLNL	APOD	CCR3	DAG1	GNB4	KLHL40
PIK3C2A	SART1	SPTBN2	UCP2	APPL1	CCR5	DALRD3	GORASP1	KLHL6
PITPNM1	SBF2	ST14	UCP3	ARF4	CCRL2	DAZL	GP5	KNG1
PIWIL4	SBF2-AS1	ST3GAL4	UNC93B1	ARHGAP31	CD200	DGKG	GP9	KPNA1
PKP3	SC5D	ST5	UPK2	ARL13B	CD80	DHX36	GPD1L	KY
PNPLA2	SCGB1A1	STIM1	UQCC3	ARL6	CD86	DIRC2	GPR149	LAMB2
POLD3	SCGB1D2	STK33	USH1C	ARL6IP5	CD96	DLEC1	GPX1	LARS2
PPP2R1B	SCN2B	STT3A	VEGFB	ASTE1	CDC25A	DLG1	GRM7	LIMD1
PPP2R5B	SCN3B	STX3	VPS11	ATG7	CDV3	DNAH1	GSK3B	LINC00852
PPP6R3	SCN4B	SUV420H1	WEE1	ATP11B	CELSR3	DNAJC13	GTF2E1	LIPH
PRCP	SCT	SYT9	WNT11	ATP13A4	CEP19	DNAJC19	GXYLT2	LMOD3 LOC10192888 2
PRDM10	SCUBE2	SYVN1	WT1	ATP13A5	CEP63	DNASE1L3	GYG1	LPP
PRDM11	SCYL1	TALDO1	WT1-AS	ATP2B2	CEP97	DOCK3	HACL1	LRIG1
PRMT3	SDHAF2	TBX10	WTAPP1	ATP2C1	CHDH	DRD3	HCLS1	LRRC2
PRSS23	SDHD	TCIRG1	YAP1	ATP6V1A	CHL1	DVL3	HESX1	LRRFIP2
PTGDR2	SERPING1	TCN1	ZBTB16	ATR	CHMP2B	ECE2	HGD	LSM3
PTH	SERPINH1	TEAD1	ZDHHC24	ATRIP	CHRD	EDEM1	HPS3	LTF
PTPRCAP	SF1	TECTA	ZDHHC5	ATXN7	CHST13	EHHADH	HRG	LXN
	SHANK2	TENM4	ZFP91	B3GALNT1	CHST2	EIF2B5	HTR3C	

LZTFL1	NPHP3-ACAD11	PTPN23	SLC25A38	TNFSF10	ACTN4	CALM3	CRX	FEM1A
MAATS1	NPRL2	PTPRG	SLC26A6	TNIK	ADAMTS10	CALR	CSNK1G2	FFAR1
MAGI1	NR1D2	PVRL3	SLC2A2	TNK2	ADAT3	CALR3	CYP2A13	FGF22
MANF	NR1I2	QARS	SLC33A1	TNNC1	ADCK4	CAPN12	CYP2A6	FKBP8
MAP3K13	NRROS	QRICH1	SLC35G2	TOPBP1	ADGRE2	CARD8	CYP2A7	FKRP
MAP4	NSUN3	QTRTD1	SLC4A7	TP63	ADGRL1	CARM1	CYP2B6	FOXA3
MAPKAPK3	NUP210	RAB7A	SLC6A1	TRAIP	AKT2	CASP14	CYP2F1	FPR1
MASP1	NXPE3	RAD18	SLC6A11	TRAK1	ALDH16A1	CBLC	CYP2G1P	FPR2
MBD4	OGG1	RAD54L2	SLC6A20	TREX1	ALKBH7	CC2D1A	CYP2S1	FTL
MBNL1	OPA1	RAF1	SLC6A6	TRH	AMH	CCDC114	CYP4F11	FUT1
MCCC1	OPA1-AS1	RARB	SLC7A14	TRMT10C	ANGPTL4	CCDC151	CYP4F12	FUT2
MCF2L2	OR5AC2	RASA2	SLC9A9	TRNT1	ANGPTL6	CCDC8	CYP4F2	FUT3
MCM2	OR5H6	RASSF1	SLCO2A1	TRPC1	AP2A1	CCER2	CYP4F22	FUT6
MECOM	OXSRI	RASSF1-AS1	SLMAP	TSEN2	AP2S1	CCNE1	CYP4F3	FUZ
MED12L	OXTR	RBP1	SMARCC1	TTC14	AP3D1	CD177	CYP4F8	GADD45B
MF12	P2RY12	RFC4	SNRK	U4atac-chr3	APC2	CD209	DAPK3	GALP
MGLL	P3H2	RFT1	SNRK-AS1	UBA3	APOC1	CD22	DHDH	GAMT
MIR191	PAQR9	RHO	SOX2	UBA5	APOC2	CD320	DHX34	GAPDHS
MITF	PARL	RHOA	SPATA16	UBA7	APOC4	CD33	DLL3	GCDH
MLF1	PBRM1	RNF168	SRGAP3	ULK4	APOC2	CD3EAP	DMPK	GDF1
MLH1	PCCB	ROBO1	SST	UMPS	APOE	CD79A	DNAAF3	GDF15
MME	PCOLCE2	ROBO2	SSUH2	UQCRC1	ARHGEF18	CDKN2D	DNASE2	GIPC1
MRPL3	PCYT1A	RPL15	ST3GAL6	UROC1	ATCAY	CEACAM16	DNM2	GIPC3
MRPL47	PDCD10	RPL24	ST6GAL1	VHL	ATF5	CEACAM5	DNMT1	GIPR
MRPS22	PDCD6IP	RPL35A	STAG1	VPS8	ATPIA3	CEBPA	DOCK6	GLTSCR1
MRPS25	PDHB	RPSA	STT3B	VWA5B2	ATP4A	CEBPG	DOTIL	GMIP
MST1	PHF7	RPUSD3	STXBP5L	WDR48	ATP5D	CEP89	DYRK1B	GNA11
MST1R	PIGZ	RSRC1	SUCLG2	WDR6	ATP5SL	CERS1	ECSIT	GNG7
MTMR14	PIK3CA	RUBCN	SUMF1	WNT5A	ATP8B3	CFD	EEF2	GP6
MUC13	PIK3CB	RUVBL1	SYN2	WNT7A	AURKC	CGB	EGLN2	GPI
MUC4	PIK3R4	RYK	SYNPR	WWTR1	AXL	CHAF1A	EHD2	GPX4
MYD88	PLCD1	SCAP	TBC1D23	XCR1	B3GNT3	CHMP2A	EIF3G	GRIK5
MYH15	PLOD2	SCN10A	TBL1XR1	XIRP1	B3GNT8	CHST8	ELANE	GRIN2D
MYL3	PLXNA1	SCN11A	TCTEX1D2	XPC	B9D2	CIC	ELL	GTPBP3
MYLK	PLXNB1	SCN5A	TDGF1	ZBTB11	BAX	CILP2	EMR1	GSY1
NAALADL2	PLXND1	SEC61A1	TERC	ZBTB11-AS1	BCAM	CKM	EPOR	HAMP
NAT6	POC1A	SEMA3F	TF	ZBTB20	BCAT2	CLECT1A	ERCC1	HAPLN4
NBEAL2	POGLUT1	SERPINI1	TFG	ZFYVE20	BCKDHA	CLEC4M	ERCC2	HAS1
NCKIPSD	POLQ	SERPINI2	TFRC	ZIC1	BCL3	CLPP	ERF	HAUS8
NDUFAF3	POMGNT2	SETD2	TGFBR2	ZIC4	BLOC1S3	CLPTM1	ETFB	HCN2
NDUFB4	POU1F1	SETD5	TGM4	ZMYND10	BRD4	CNOT3	ETHE1	HCST
NDUFB5	PPARG	SGOL1	THPO	ZNF148	BRSK1	COL5A3	EVI5L	HDGFRP2
NEK1	PRICKLE2	SHOX2	THRB	ZNF35	BSG	COMP	EXOSC5	HMHA1
NEK4	PRICKLE2-AS1	SI	TKT	ZNF445	C19orf12	COX6B1	FAAP24	HNRNPA1P10-chr19
NFKBIZ	PRICKLE2-AS3	SKIL	TLR9	ZNF589	C19orf18	COX7A1	FARSA	HNRNPUL1
NGLY1	PRKCD	SLC15A2	TM4SF19	ZNF620	C19orf70	CPAMD8	FBN3	HRC
NICN1	PROK2	SLC22A13	TM4SF19-TCTEX1D2	ZNF80	C19orf80	CPTIC	FCAR	HSD17B14
NISCH	PROS1	SLC22A14	TMEM39A	ABCA7	C3	CREB3L3	FCER2	HSPB6
NLG1	PSMD2	SLC25A20	TMEM43	ACP5	C5AR2	CRLF1	FCGRT	ICAM1
NPHP3	PTH1R	SLC25A26	TMIE	ACPT	CACNA1A	CRTC1	FDX1L	ICAM4
ICAM5	LIPE	NR2C2AP	PSG8	SLC44A2	ZFP14	CABIN1	GSTT2	PRODH

IER2	LMNB2	NRTN	PSPN	SLC5A5	ZFP30	CACNA1I	GSTT2B	RAC2
IFI30	LMTK3	NTF4	PTGIR	SLC7A10	ZFP36	CACNG2	HIRA	RANGAP1
IFNL3	LONP1	NUMBL	PTPRS	SLC7A9	ZNF175	CBY1	HMOX1	RBFOX2
IFNL4	LRP3	NUP62	PVR	SMARCA4	ZNF224	CCT8L2	HPS4	RIBC2
IL11	LTBP4	NWD1	PVRL2 RAB4B- EGLN2	SMG9	ZNF331	CDC45	IFT27	RTN4R
IL12RB1	LYL1	NXNL1		SPC24	ZNF350	CECR1	IGLL1	SBF1
IL27RA	MAG	OAZ1	RAX2	SPINT2	ZNF419	CECR2	IL17RA	SCARF2
IL4I1	MAN2B1	OCEL1	RDH8	STK11	ZNF420	CELSR1	IL17REL	SCO2
ILF3	MAP2K2	OLFM2	REEP6	STXBP2	ZNF426	CERK	KCTD17	38596
ILVBL	MAP2K7	OPA3	RETN	SULT2A1	ZNF433	CHCHD10	KREMEN1	SEPT5-GP1BB
INSL3	MARK4	OR7D4	RFX2	SULT2B1	ZNF45	CHEK2	LARGE	SERPIND1
INSR	MAST1	P2RY11	RFXANK	SUPT5H	ZNF480	CHKB CHKB- CPTIB	LGALS1	SEZ6L
IRF3	MBD3	PAFAH1B3	RGS9BP	SYCE2	ZNF490		LGALS2	SGSM3
ISYNA1	MBOAT7	PBX4	RHPN2	SYNE4	ZNF507	CLTCL1	LIF	SHANK3
ITPKC	MCOLN1	PDCD5	RINL	TBCB	ZNF526	COMT	LOC284889	SLC16A8
JAK3	MED25	PDE4C	RNASEH2A	TBXA2R	ZNF536	CPTIB	LZTR1	SLC25A1
JUNB	MED29	PEPD	RPL36	TCF3	ZNF543	CRELD2	MAPK1	SLC25A17
KANK2	MEF2B MEF2BNB- MEF2B	PET100	RPS11	TECR	ZNF551	CRKL	MCAT	SLC5A1
KCNC3	MEGF8	PEX11G	RPS15	TGFB1	ZNF559	CRYBA4	MCHR1	SMARCB1
KCNK6	MIA	PIK3R2	RPS19	TICAM1	ZNF582	CRYBB1	MCM5	SMC1B
KCNN4		PIN1	RPS28	TIMM44	ZNF607	CRYBB2	MGAT3	SNAP29 SNORD56- chr22
KEAP1	MLLT1	PIP5K1C	RPS5	TIMM50	ZNF610	CRYBB3	MIAT	
KIR2DL1	MR11	PLA2G4C	RRAS	TLE6	ZNF627	CSF2RB	MICAL3	SOX10
KIR2DL3	MRPL34	PLAUR	RTN2	TMEM91	ZNF77	CSNK1E CTA- 373H7.7 CTA- 373H7.7	MIF	SPECC1L SPECC1L- ADORA2A
KIR2DL4	MRPL4	PLD3	RUVBL2	TNFSF14	ZNF780B		MKL1	
KIR3DL1	MRPL54	PLEKHG2	RYR1	TNNI3	ZNF813		MLC1	SREBF2
KIR3DL2	MRPS12	PLIN4	S1PR2	TNNT1	ZNF829	CYB5R3	MN1	SULT4A1
KISS1R	MUM1	PLVAP	SAFB2	TNPO2	ZNF844	CYP2D6	MORC2	SUN2
KLC3	MYBPC2	PNKP	SARS2	TOMM40	A4GALT	CYP2D7P1	MPST	SYN3
KLF1	MYH14	PNPLA6	SBK3	TPM4	ACO2	DEPDC5	MRPL40	SYNGR1
KLK1	MYO1F	POLD1	SCN1B	TRMT1	ADORA2A	DGCR14	MYH9	TANGO2
KLK12	MYO9B	POLR2E	SDHAF1	TRPM4	ADRBK2	DGCR2	MYO18B	TBX1
KLK15	NACC1	POLRMT PPAN- P2RY11	SEMA6B	TSEN34	ADSL	DGCR5	NAGA	TCF20
KLK3	NANOS3		SERTAD1	TSHZ3	ALG12	DGCR6	NCAPH2	TCN2
KLK4	NCAN	PPP1R13L	SH3GL1	TSKS	APOBEC3B	DGCR8	NCF4	TIMP3
KLK7	NDUFA11	PPP2R1A	SHANK1	TUBB4A	APOBEC3G	DMC1	NDUFA6	TMPRSS6
KMT2B	NDUFA13	PRDX2	SHKBP1	TYK2	APOBEC3H	DNAJB7	NEFH	TNFRSF13C
KPTN	NDUFA3	PRKACA	SIGLEC12	TYROBP	APOL1	DNAL4	NF2	TNRC6B
KXD1	NDUFA7	PRKCG	SIGLEC14	UBA2	APOL2	DRG1	NIPSNAP1	TRIOBP
LDLR	NDUFB7	PRKCSH	SIGLEC16	UNC13A	APOL3	EIF4ENIF1	PDGFB	TRMU
LENG1	NDUFS7	PRKD2	SIPA1L3	UQCR11	APOL4	EP300	PEX26	TSPO
LGALS13	NFIX	PRODH2	SIRT6	UQCERS1	APOL5	EWSR1	PI4KA	TSSK2
LG14	NLRP12	PRPF31	SIX5	VAV1	ARSA	FBLN1	PICK1	TST
LHB	NLRP2	PRR19	SLC1A5	WDR62	ARVCF	FBXO7	PIWIL3	TTC28
LIG1	NLRP5	PRX	SLC25A23	WDR87	ATP6V1E1	GAL3ST1	PLA2G6	TLL1
LILRA3	NLRP7	PSENE1	SLC25A41	WDR88	ATXN10	GGT5	PNPLA3	TUBA8
LILRB2	NOTCH3	PSG1	SLC25A42	WIZ	BCR	GNBIL	POLR2F	TUBGCP6
LIM2	NPHS1	PSG2	SLC27A1	XRCC1	BRD1	GP1BB	POLR3H	TXN2
LIN7B	NR1H2	PSG7	SLC27A5	ZBTB45	C22orf39	GSTT1	PPARA	TXNRD2

TYMP	BTN1A1	CYP39A1	FLOT1	HIST1H4I	LAMA2	NEU1	PRPH2	SLC22A23
UFDIL	BTN2A1	DAAM2	FOXC1	HIVEP1	LAMA4	NFKBIL1	PRRC2A	SLC22A3
UPB1	BTNL2	DAXX	FOXF2	HIVEP2	LATS1	NHLRC1	PRSS16	SLC22A7
UPK3A	BVES	DCBLD1	FOXO3	HLA-A	LCA5	NKAIN2	PSMB8	SLC25A27
UQCR10	C2	DCDC2	FOXP4	HLA-B	LEMD2	NOTCH4	PSMB9	SLC26A8
USP18	C4A	DDAH2	FRK	HLA-C	LHFPL5	NOX3	PSORS1C1	SLC29A1
VPREB1	C4B	DDO	FUCA2	HLA-DMB	LIN28B	NQO2	PTK7	SLC35A1
XBP1	C6orf132	DDR1	GABBR1	HLA-DOA	LINC01016	NR2E1	PTPRK	SLC35B2
XPNPEP3	C6orf136	DDX39B	GABRR1	HLA-DOB	LMBRD1	NT5DC1	QKI	SLC35D3
XRCC6	C6orf15	DEF6	GABRR2	HLA-DPA1	LOC100129518	NT5E	QRSL1	SMOC2
ZDHC8	C6orf165	DEK	GCLC	HLA-DPB1	LPA	NUS1	RAB23	SNHG5
MT-TC	C6ORF165	DHX16	GCM2	HLA-DPB2	LRFN2	OARD1	RAETIL	SNX14
MT-TF	C6orf222	DLL1	GCNT2	HLA-DQA1	LTA	OPRM1	RARS2	SNX3
MT-TK	C6orf47	DNAH8	GFOD1	HLA-DQB1	LY6G6F	OR10C1	REV3L	SOBP
AARS2	CCDC170	DOPEY1	GJA1	HLA-DQB2	LYRM4	OR2J3	RFX6	SOD2
ABCC10	CCHCR1	DSE	GLO1	HLA-DRA	MAK	ORC3	RGL2	SOGA3
ACAT2	CCND3	DSP	GLP1R	HLA-DRB1	MAP3K7	OSTM1	RHAG	STK19
ADGRF1	CCR6	DST	GMDS	HLA-DRB5	MAPK13	PACRG	RIMS1	STX11
ADGRF4	CD109	DTNBP1	GMNN	HLA-E	MCM9	PAQR8	RIPPLY2	STX7
ADGRG6	CD164	DXO	GNMT	HLA-G	MDC1	PARK2	RMND1	STXBP5-AS1
ADTRP	CD2AP	E2F3	GOPC	HMGA1	MDN1	PCMT1	RNASSET2	STXBP5-AS1
AGER	CDC5L	ECT2L	GPANK1	HSF2	MED20	PDE10A	RNF8	SUMO4
AH1I	CDK19	EDN1	GPRC6A	HSPA1A	MED23	PDE7B	ROS1	SYNCRIP
AIF1	CDKAL1	EFHC1	GPSM3	HSPA1B	MICA	PDSS2	RPS10	SYNE1
AK9	CDKN1A	EHMT2	GPX5	HSPA1L	MICAL1	PEX3	RPS10-NUDT3	SYNGAP1
AKAP12	CDSN	ELOVL2	GPX6	HTR1B	MICB	PEX6	RPS12	SYTL3
ALDH5A1	CDYL	ELOVL4	GRIK2	HUS1B	MIR206	PEX7	RPS6KA2	T
ALDH8A1	CENPW	ELOVL5	GRM1	HYMAI	MOCS1	PGBD1	RREB1	TAAR1
AMD1	CEP85L	ENPP1	GSTA1	ICK	MOG	PGC	RSPH3	TAAR2
ANKRD6	CFB	EPB41L2	GSTA2	ID4	MPC1	PGM3	RSPH4A	TAAR6
ANKS1A	CGA	EPHA7	GSTA3	IFNGR1	MRAP2	PHACTR1	RSPH9	TAAR9
APOBEC2	CITED2	EPM2A	GSTA4	IGF2R	MRPL14	PHF10	RTN4IP1	TAB2
APOM	CLIC5	ERMARD	GSTA5	IL17A	MRPL18	PHF3	RUNX2	TAP1
ARG1	CLPS	ESR1	GTF2H4	IL17F	MRPL2	PHIP	SASH1	TAP2
ARHGAP18	CNPY3	EYA4	GTF2H5	IL20RA	MRPS10	PIM1	SCAF8	TAPBP
ARID1B	CNR1	EYS	GTPBP2	IMPG1	MRPS18A	PKHD1	SCGN	TAPSAR1
ASCC3	COL10A1	EZR	GUCA1A	IPCEF1	MRPS18B	PLA2G7	SEC63	TBC1D22B
ATG5	COL11A2	FI3A1	GUCA1B	IRF4	MSH5	PLAGL1	SERAC1	TBC1D32
ATP6V1G2-DDX39B	COL12A1	FABP7	HACE1	ITPR3	MSH5-SAPCD1	PLG	SERPINB6	TBC1D7
ATXN1	COL19A1	FAM120B	HBS1L	IYD	MTHFD1L	PLN	SGK1	TBP
B3GAT2	COL21A1	FAM65B	HCP5	JARID2	MTO1	PNPLA1	SHPRH	TBX18
BAG6	COL9A1	FAM8A1	HCRTR2	KCNK17	MUT	POLH	SIM1	TCF21
BAI3	COQ3	FANCE	HDAC2	KCNK5	MYB	POLR1C	SIRT5	TCPI
BCKDHB	COX7A2	FARS2	HEY2	KCNQ5	MYCT1	POU5F1	SKIV2L	TCTE1
BCLAF1	CRISP2	FBXL4	HFE	KHDC3L	MYLIP	PPARD	SLC17A1	TCTE3
BLOC1S5	CTGF	FBXO9	HIST1H1E	KIAA0319	MYO6	PPP2R5D	SLC17A3	TDP2
BMP5	CUL7	FIG4	HIST1H2AE	KIAA1244	NCR3	PPT2	SLC17A5	TDRD6
BMP6	CYBSR4	FILIP1	HIST1H2BE	KIAA1919	NDUFAF4	PRDM1	SLC22A1	TFAP2A-AS1
BRD2	CYP21A1P	FKBP5	HIST1H3B	KIF6	NEDD9	PRDM13	SLC22A16	TFAP2A-AS1
BTBD9	CYP21A2	FKBPL	HIST1H4B	KLC4	NELFE	PRL	SLC22A2	TFAP2B

TFAP2D	ADRA1A	DEFB1	GSR	MYC	PVT1	SULF1	CD24-chrY	AMHR2
TFB1M	ADRB3	DEFB4A	GTF2E2	MYOM2	PXDNL	TAF2	CDY1-chrY	ANAPC5
THBS2	AGO2	DGAT1	GULOP	NAPRT1	PYCR1	TATDN1	CDY2A-chrY	ANAPC7
TIAM2	ANGPT1	DLC1	HAS2	NAT1	RAB2A	TEX15	CRLF2-chrY	ANKLE2
TINAG	ANGPT2	DLGAP2	HEY1	NAT2	RAD21	TG	CSF2RA-chrY	ANKRD13A
TNF	ANK1	DOK2	HGSNAT	NBN	RAD54B	THAP1	DAZ1-chrY	ANKS1B
TNFAIP3	ARC	DPYS	HR	NCALD	RB1CC1	TMEM249	DAZ2-chrY	ANO6
TNFRSF21	ARFGF1	DPYSL2	HSF1	NCOA2	RDH10	TMEM67	DAZ3-chrY	APAF1
TNXB	ARHGFE10	E2F5	IDO1	NDRG1	RECQL4	TMEM70	DAZ4-chrY	APOBEC1
TPBG	ASAH1	EBAG9	IKBKB	NDUFAF6	RHOBTB2	TNFRSF10A	DDX3Y-chrY	APOF
TPMT	ASAP1	EEF1D	IL7	NDUFB9	RIMS2	TNFRSF10B	HSFY1-chrY	APPL2
TRAF3IP2	ASH2L	EFR3A	IMPA1	NEFL	RIPK2	TNFRSF11B	IL3RA-chrY	AQP2
TRDN	ASPH	EGR3	IMPAD1	NEFM	RNF139	TNKS	IL9R-chrY	AQP5
TREM2	ATP6V0D2	EIF3E	JPH1	NEIL2	RNF170	TONSL	KDM5D-chrY	ARHGAP9
TREML2	ATP6V1B2	EIF3H	JRK	NKAIN3	RNF19A	TOP1MT	NLGN4Y-chrY	ARID2
TREML4	ATP6VIH	ENPP2	KAT6A	NKX2-6	RP1	TRAPPC9	PRY-chrY	ARPC3
TRERF1	BAALC	EPHX2	KCNB2	NKX3-1	RP11-463D19.2	TRHR	PRY2-chrY	ART4
TSPYL1	BLK	EPPK1	KCNK9	NRG1	RP1L1	TRIB1	RBMV1A1-chrY	ASCL1
TTK	BMP1	ERLIN2	KCNQ3	NSMCE2	RPS20	TRIM55	RPS4Y1-chrY	ASUN
TUBB	C8orf37	ESCO2	KCNS2	OPLAH	RRM2B	TRPA1	RPS4Y2-chrY	ATF1
TUBB2A	CA1	EXOSC4	KCNU1	OPRK1	RUNX1T1	TRPS1	SHOX-chrY	ATN1
TUBB2B	CA2	EXT1	KCNV1	PARP10	SCRIB	TTI2	SPRY3-chrY	ATP2A2
TULP1	CA8	EXTL3	KIAA0196	PCM1	SFRP1	TTPA	SRY-chrY	ATP5B
TXLNB	CCAR2	EYA1	KIAA1429	PDGFRL	SFTPC	TUSC3	TBL1Y-chrY	ATP5G2
UBD	CHD7	FABP4	KIF13B	PDP1	SGCZ	UBE2W	TTY13-chrY	ATP6V0A2
UFL1	CHRNA2	FABP5	KLF10	PENK	SGK223	UBR5	USP9Y-chrY	ATXN2
UHRF1BP1	CLDN23	FAM160B2	LAPTM4B	PEX2	SHARPIN	UQCRB	VAMP7-chrY	AVIL
UNC5CL	CLN8	FAM83H	LINC00599	PII5	SLC18A1	VPS13B	VCY-chrY	AVPR1A
UNC93A	CLU	FAM86B2	LOC100132891	PINX1	SLC20A2	VPS37A	XKRY-chrY	B3GNT4
UQCC2	CNGB3	FAM91A1	LOXL2	PKHD1L1	SLC25A32	WHSCIL1	ZFY-chrY	B4GALNT1
UST	COL14A1	FBXL6	LPL	PLAG1	SLC25A37	WRN	A2M	B4GALNT3
UTRN	COX6C	FBXO32	LRRC6	PLAT	SLC30A8	WWP1	A2M-AS1	BBS10
VARS	CPA6	FDFT1	LRRC69	PLEC	SLC35G5	XKR4	A2ML1	BCAT1
VARS2	CRH	FGF17	LY6E	PMP2	SLC39A14	XKR6	AAAS	BCL7A
VEGFA	CSGALNACT1	FGF20	LY96	POLB	SLC39A4	XKR9	ABCC9	BHLHE41
VIP	CSMD1	FGFR1	LYN	POLR3D	SLC52A2	XPO7	ACACB	BICD1
VNN1	CSMD3	FGL1	LZTS1	POMK	SLC7A2	YWHAZ	ACAD10	BLOC1S1
WISP3	CSPP1	FOXH1	MAFA	POP1	SLCO5A1	ZBTB10	ACADS	BLOC1S1-RDH5
XPO5	CTHRC1	FSBP	MAK16	POU5F1B	SLURP1	ZC3H3	ACVR1B	BRAP
YIPF3	CTSB	FZD3	MCM4	PPP2CB	SNAI2	ZDHHC2	ACVRL1	C12orf10
ZBTB12	CYC1	FZD6	MCPH1	PPP2R2A	SNTB1	ZFAT	ADCY6	C12orf29
ZBTB24	CYP11B1	GATA4	MRPL13	PREX2	SNTG1	ZFAT-AS1	ADIPOR2	C12orf4
ZFP57	CYP11B2	GDAP1	MRPL15	PRKDC	SNX31	ZFHX4	AGAP2	C12orf43
ZNF292	CYP7A1	GDF6	MRPS28	PROSC	SOX17	ZFPM2	AICDA	C12orf57
ZNF311	CYP7B1	GFRA2	MSC	PSCA	SOX7	ZHX2	AKAP3	C12orf65
ZNF451	DCAF13	GGH	MSR1	PSD3	SPAG1	ZNF34	ALDH1L2	C1R
ADAM7	DCSTAMP	GNRH1	MSRA	PTDSS1	SQLE	AMELY-chrY	ALDH2	C1S
ADAM9	DDHD2	GPIHBP1	MTMR9	PTK2	ST3GAL1	ASMT-chrY	ALG10	C2CD5
ADCY8	DECR1	GPT	MTSS1	PTK2B	STAR	ASMTL-chrY	ALG10B	C3AR1
ADHFE1	DEFA4	GRHL2	MTUS1	PUF60	STK3	BPY2-chrY	ALX1	CACNA1C

CACNA1C-AS1	DNMIL	HOXC13-AS	KRT82	NR1H4	RAD52	SSPN	VEZT	C8G
CACNA2D4	DPY19L2	HPD	KRT83	NR4A1	RAN	ST8SIA1	VPS33A	C9orf114
CAMKK2	DTX1	HSP90B1	KRT85	NTF3	RASAL1	STAB2	VWF	C9orf117
CBX5	DUSP6	HSPB8	KRT86	NUAK1	RDH5	STAC3	WDR66	C9orf139
CCDC65	DYRK4	HVCN1	KSR2	NUP107	RECQL	STAT2	WIF1	C9orf172
CCND2	EEA1	IAPP	LDHB	NUP37	RHNO1	STAT6	WNK1	C9orf173
CCT2	EIF2B1	IFNG	LEMD3	OAS1	RNFT2	STK38L	WNT1	C9orf37
CD163	ELK3	IFT81	LGR5	OAS2	RPL6	SUOX	WNT10B	C9orf66
CD163L1	EMG1	IGF1	LOC101593348	OAS3	RPS26	SYCP3	WNT5B	C9orf72
CD27	EP400	IKBIP	LOC101927318	OLR1	RPSAP52	SYTI	XPOT	CACNA1B
CD4	EPS8	IQSEC3	LOC338817	ORAI1	RSRC2	TAC3	YARS2	CARD9
CD9	EPYC	IRAK3	LRP1	OTOGL	SART3	TAS2R19	ZC3H10	CCDC107
CDK2	ERBB3	IRAK4	LRP6	P2RX2	SBNO1	TAS2R43	ZCCHC8	CD72
CDK4	ESPL1	ISCU	LRRC10	P2RX4	SCARB1	TAS2R46	ZDHHC17	CDK20
CDKN1B	ETV6	ITGA5	LRRIQ1	P2RX7	SCN8A	TAS2R50	ABCA1	CDK5RAP2
CELA1	FAM186B	ITGA7	LRRK2	PAH	SCNNA1	TAS2R9	ABCA2	CDK9
CEP290	FAM222A	ITPR2	LTBR	PAWR	SDR9C7	TBC1D30	ABL1	CDKN2A
CEP83	FAM71C	KANSL2	LUM	PDE3A	SELPLG	TBK1	ABO	CDKN2B-AS1
CHD4	FGD4	KCNA1	LYZ	PDE6H	SENP1	TBX3	ACO1	CEL
CHFR	FGF23	KCNA5	MANSC1	PEX5	SETD1B	TBX5	ACTL7B	CEP78
CHPT1	FKBP4	KCNA6	MARS	PFKM	SETD8	TCP11L2	ADAMTS13	CER1
CHST11	FOXM1	KCNH3	MBD6	PGAM5	SH2B3	TCTN1	ADAMTSL2	CIZ1
CIT	FZD10	KCNJ8	MDM1	PHB2	SLC11A2	TCTN2	AGPAT2	CNTNAP3
CLEC2D	GABARAPL1	KCNMB4	MDM2	PHC1	SLC17A8	TDG	AGTPBP1	COL15A1
CLEC4C	GALNT6	KDM2B	MED13L	PIK3C2G	SLC25A3	TENC1	AK1	COL27A1
CLEC4D	GALNT8	KDM5A	MFAP5	PKP2	SLC26A10	TFCP2	AK8	COL5A1
CLEC7A	GALNT9	KERA	MGAT4C	PLCZ1	SLC2A3	TIMELESS	AKAP2	COQ4
CLIP1	GAPDH	KIAA1033	MGP	PLEKHG7	SLC39A5	TMEM132D	ALAD	CRAT
CNTN1	GDF11	KIF21A	MGST1	PMEL	SLC48A1	TMEM5	ALDH1A1	CRB2
COL2A1	GDF3	KIF5A	MIP	POC1B	SLC6A12	TMPO	ALDH1B1	CREB3
COQ5	GLI1	KITLG	MMAB	POLE	SLC6A13	TMPO-AS1	ALDOB	DAPK1
COX14	GLIPRIL2	KLRC1	MMP19	POLR3B	SLC8B1	TMTC3	ALG2	DBH
COX6A1	GNB3	KLRC4-KLRK1	MRPL42	PPP1R1A	SLCO1A2	TNFRSF1A	ANKRD18A	DBH-AS1
CRADD	GNPTAB	KLRK1	MRPL51	PRB1	SLCO1B1	TPCN1	ANKS6	DDX58
CRY1	GNS	KMT2D	MRPS35	PRB3	SLCO1B3	TPH2	ANXA1	DFNB31
CUX2	GOLGA3	KRAS	MSRB3	PRB4	SLCO1B7	TPI1	APTX	DMRT1
CYP27B1	GPD1	KRT1	MVK	PRICKLE1	SLCO1C1	TROAP	AQP3	DMRT2
DAO	GRIN2B	KRT18	MYBPC1	PRPH	SMARCC2	TRPV4	AQP7	DNAI1
DCN	GRIP1	KRT2	MYF5	PTHLH	SMARCD1	TSFM	ARID3C	DNAJB5
DCPIB	GUCY2C	KRT3	MYF6	PTPN11	SMUG1	TSPAN11	ASPN	DNM1
DCTN2	GYS2	KRT4	MYL2	PTPN6	SNORA34	TUBA1A	ASS1	DOCK8
DDIT3	HAL	KRT5	MYO1A	PTPRB	SNORD56- chr12	TULP3	ASTN2	DOLK
DDX11	HCAR1	KRT6A	NAV3	PTPRO	SOAT2	U4atac- chr12	AUH	DOLPP1
DDX47	HMGA2	KRT6B	NCAPD2	PTPRQ	SOCS2	UBE3B	B4GALT1	DPM2
DENR	HNFA	KRT6C	NCOR2	PTPRR	SOX5	UNG	BAAT	ECM2
DHH	HNRNPA1	KRT71	NDUFA12	PUS1	SP1	USP15	BARX1	EGFL7
DHX37	HNRNPA1P10- chr12	KRT74	NDUFA9	PXMP2	SP7	USP30	BICD2	EHMT1
DIABLO	HOXC11	KRT75	NECAP1	PXN	SPSB2	USP44	BNC2	ELAVL2
DIP2B	HOXC12	KRT8	NEDD1	PYROXD1	SRGAP1	VAMP1	BRD3	
DNAH10	HOXC13	KRT81	NOS1	PZP	SSH1	VDR	C5	

ENG	GSN	MUSK	RAD23B	TLN1	AURKA	FLRT3	NKX2-2	SLC13A3
ENHO	GSN-AS1	NAA35	RALGDS	TLR4	AVP	FOXA2	NOP56	SLC17A9
ERCC6L2	HAUS6	NANS	RANBP6	TMC1	B4GALT5	GATA5	NPEPL1	SLC2A10
EXD3	HNRNPK	NCS1	RAPGEF1	TMEM2	BCL2L1	GDF5	OPRL1	SLC4A11
EXOSC2	HSD17B3	NDOR1	REXO4	TMEM203	BFSP1	GHRH	OSBPL2	SLC52A3
EXOSC3	HSPA5	NDUFA8	RFX3	TMEM38B	BMP2	GNAS	OSER1	SLMO2
FAM120A	IARS	NDUFB6	RMI1	TMEM8C	BMP7	GNAS-AS1	OTOR	SLMO2-ATP5E
FAM120AOS	IFNA10	NFIB	RMRP	TNC	BPI	GSS	OVOL2	SNAP25
FAM166A	IFNA17	NINJ1	RNF20	TNFSF15	BPIFA1	HAO1	PAK7	SNORD56- chr20
FAM189A2	IFNA2	NIPSNAP3A	RNF38	TNFSF8	BPIFA3	HCK	PANK2	SNORD57
FAM205A	IFNB1	NOTCH1	ROR2	TOPORS TOPORS- AS1	C20orf197	HNF4A	PAX1	SNRPB
FANCC	IFT74	NPR2	RRAGA	TOR1A	CBFA2T2	HRH3	PCK1	SNTA1
FANCG	IKBKAP	NR4A3	RUSC2	TPM2	CD40	IDH3B	PCNA	SNX5
FBP1	IL11RA	NR5A1	RXRA	TPRN	CDH22	IFT52	PCSK2	SOX18
FBP2	INPP5E	NSMF	SIPR3	TRIM32	CDH4	ITCH	PDYN	SPTLC3
FBXO10	INSL6	NTNG2	SARDH	TRPM3	CEP250	ITPA	PHF20	SRC
FCN1	INVS	NTRK2	SDCCAG3	TRPM6	CHD6	JAG1	PI3	SS18L1
FCN2	JAK2	NUP214	SEC16A	TSC1	CHGB	JPH2	PIGT	STK35
FGD3	KANK1	ORIB1	SECISBP2	TTF1	CHMP4B	KCNB1	PLCB1	STK4
FKTN	KCNT1	OR1J1	SET	TLL1	CHRNA4	KCNQ2	PLCB4	STK4-AS1
FOCAD	KCNV2	PALM2	SETX	TYRP1	COL9A3	KCNS1	PLCG1	STX16
FOXD4	KDM4C	PALM2- AKAP2	SIGMARI	U4atac- chr9	COX4I2	KIAA1755	PLTP	STX16- NPEPL1
FOXE1	KIAA1432	PAPPA	SLC1A1	UBAP2	CPNE1	KIZ	POFUT1	SULF2
FPGS	KIF24	PAX5	SLC24A2	UBE2R2	CRLS1	L3MBTL1	PRND	SUN5
FREM1	KIF27	PCSK5	SLC27A4	UBQLN1	CSNK2A1	LAMA5	PRNP	SYCP2
FRMPD1	KLF4	PHF19	SLC28A3	UGCG	CSR2BP	LBP	PROCR	TBC1D20
FRRS1L	KLHL9	PHF2	SLC2A6	UNC13B	CST3	LPIN3	PROKR2	TGM2
FSD1L	LAMC3	PIGO	SLC31A1	VCP	CST9	MACROD2	PRPF6	TGM3
FUT7	LCN10	PIP5K1B	SLC34A3	VLDR	CTSA	MAFB	PSMA7	TGM6
FXN	LHX3	PKN3	SMARCA2	VPS13A	CTSZ	MATN4	PTGIS	THBD
GABBR2	LHX6	PLAA	SMC5	VPS13A- AS1	CYP24A1	MAVS	PTPN1	TLDC2
GALNT12	LMX1B	PMPCA	SNAPC4	WDR31	DDR1	MC3R	PTPRA	TMEM230
GALT	LOC100507346	POMT1	SOHLH1	WDR34	DEFB124	MCM8	PTPRT	TNFRSF6B
GAS1	LOC101448202	PPAPDC2	SPAG8	WDR5	DEFB126	MGME1	RAD21L1	TOP1
GBA2	LPAR1	PPP6C	SPATA31C1	XPA	DNAJC5	MKKS	RBCK1	TP53RK
GBGT1	LRR8A	PRDM12	SPATA6L	ZNF79	DNMT3B	MMP9	RBL1	TRIB3
GCNT1	LRSAM1	PRKACG	SPTAN1	AAR2	DOK5	MROH8	RBM12	TSHZ2
GDA	MAMDC4	PRPF4	SPTLC1	ABHD12	DPM1	MRPS26	RIN2	TTI1
GFI1B	MAN1B1	PRUNE2	ST6GALNAC4	ACSS2	DTD1	MTG2	RNF114	TUBB1
GLDC	MAPKAP1	PSAT1	ST6GALNAC6	ADA	DUSP15	MYBL2	RPN2	U4atac- chr20
GLE1	MIR204	PSMB7	STOM	ADAM33	E2F1	MYH7B	RSPO4	VAPB
GLIS3	MIR24-1	PTCH1	STXBP1	ADNP	EBF4	MYLK2	RTEL1	VPS16
GNA14	MLLT3	PTGDS	SURF1	ADRA1D	EDN3	MYT1	RTEL1- TNFRSF6B	VSX1
GNAQ	MPDZ	PTGES2	SYK	AHCY	EEF1A2	NANP	SALL4	XRN2
GNE	MRPL41	PTGS1	TAFIL	ARFGEF2	EIF2S2	NCOA3	SAMHD1	YWHAB
GNG10	MRPL50	PTPN3	TAL2	ASIP	ELMO2	NCOA6	SEC23B	ZHX3
GOLGA2	MRPS2	PTPRD	TDRD7	ASXL1	EPB41L1	NDUFAF5	SEMG1	ZNF133
GRHR	MRRF	PTRH1	TEK	ATP5E	FAM83C	NEURL2	SIGLEC1	ZNF217
GRIN1	MTAP	RAB14	TGFBR1	ATRN	FERMT1	NFATC2	SLA2	ZNF335
GRIN3A	MURC	RABL6	TJP2	FKBP1A	NFS1		SLC12A5	ZNF512B

ABCD4	DCAF11	HIF1A	NRL	SERPINA3	VSX2	HMSD	SERPINB4	ANKRD11
ACTN1	DCAF4	HIF1A-AS1	NRXN3	SERPINA5	WARS	IER3IP1	SERPINB5	ANKS3
ADSSL1	DCAF5	HOMEZ	NUBPL	SERPINA6	XRCC3	IMPA2	SERPINB7	APIG1
AHNAK2	DDHD1	HSP90AA1	NYNRIN	SIPAIL1	YY1	KATNAL2	SERPINB8	APRT
AK7	DDX24	IFT43	OTX2	SIX1	ZBTB1	KCTD1	SETBP1	ARL2BP
AKT1	DHRS1	IGHA1	OXA1L	SIX6	ZBTB42	LAMA1	SKA1	ARL6IP1
ALDH6A1	DHRS2	IGHG1	PABPN1	SLC10A1	ZC3H14	LAMA3	SLC14A1	ARMC5
AMN	DHRS4	IGHG2	PARP2	SLC22A17	ZFP36L1	LDLRAD4	SLC14A2	ATP2A1
ANG	DHRS4-AS1	IGHM	PAX9	SLC24A4	ZFYVE26	LINC00470	SMAD2	ATP6V0C
AP4S1	DHRS4L1	INF2	PCK2	SLC25A21	ADCYAP1	LIPG	SMAD4	AXIN1
APEX1	DHRS4L2	IRF9	PLEKHH1	SLC25A21-AS1	AFG3L2	LMAN1	SMAD7	BAIAP3
APOPT1	DHRS7	ISCA2	PNN	SLC25A29	APCDD1	LOC100505549	SMCHD1	BBS2
AREL1	DICER1	ITPK1	PNP	SLC7A7	AQP4	LOC100652770	ST8SIA3	BCAR1
ARID4A	DIO2	JAG2	POLE2	SLC7A8	ASXL3	LOC101927322	ST8SIA5	BCKDK
ATL1	DLST	KCNH5	POMT2	SMOC1	ATP5A1	LOXHD1	TAF4B	BCO1
ATP5S	DNAAF2	KIAA0586	PPP2R5C	SOCS4	ATP8B1	LPIN2	TCF4	BEAN1
ATXN3	DNAL1	KLC1	PRIMA1	SOS2	B4GALT6	MALT1	TGIF1	C16orf58
BAZIA	DYNCH1	KLHDC1	PRKCH	SPATA7	BCL2	MAPRE2	TMX3	C16orf93
BCL11B	EIF2B2	L2HGDH	PRKD1	SPTB	C18orf56	MBD1	TNFRSF11A	CA5A
BCL2L2	EML1	LGALS3	PROX2	SPTLC2	C18orf8	MBP	TSHZ1	CACNA1H
BCL2L2-PABPN1	ENTPD5	LINC00523	PRPF39	STRN3	CCBE1	MC2R	TTR	CACNG3
BDKRB2	ERH	LOC100506071	PSEN1	SUPT16H	CD226	MC4R	TWSG1	CAPN15
BMP4	ESR2	LOC100506321	PSMA3	SYNE2	CDH7	ME2	TXNL4A	CASC16
BRF1	ESRRB	LOC102724153	PSMA6	TCL1A	CELF4	MEP1B	TYMS	CBFA2T3
C14orf105	EXD2	LRFN5	PTCSC3	TDP1	CFAP53	MIB1	VPS4B	CBFB
C14orf142	FAM161B	LTBP2	PTGDR	TECPR2	CHST9	MOCOS	YES1	CCDC78
C14orf2	FAM177A1	MAP3K9	PTGER2	TEP1	CIDEA	MYO5B	ZNF236	CCL17
C14orf28	FANCM	MAP4K5	PTPN21	TGFB3	CLUL1	MYOM1	ZNF24	CCL22
CALM1	FBLN5	MAX	PYGL	TGM1	CNDP1	NARS	ZNF407	CCNF
CCDC176	FLVCR2	MDGA2	RABGGTA	TINF2	CNDP2	NDUFV2	ZNF519	CD19
CCDC85C	FOS	MGAT2	RAD51B	TNFAIP2	CTDP1	NEDD4L	ZNF532	CDH1
CCDC88C	FOXA1	MIPOL1	RALGAPA1	TRAC	CYB5A	NETO1	AARS	CDH11
CDC42BPB	FOXG1	MIS18BP1	RCOR1	TRAF3	DCC	NFATC1	ABAT	CDH13
CDKN3	FOXN3	MLH3	RDH11	TRAJ29	DLGAP1	NPC1	ABCA3	CDH15
CEBPE	FRMD6	MMP14	RDH12	TRAJ32	DSC2	OSBPL1A	ABCC1	CDH16
CEP170B	FSCB	MOK	RGS6	TRAJ54	DSC3	PIEZO2	ABCC11	CDH3
CFL2	FUT8	MRPL52	RIPK3	TRAV38-2DV8	DSG1	PIGN	ABCC12	CDH5
CHD8	GALC	MTA1	RNASE2	TRD	DSG2	PIK3C3	ABCC6	CDH8
CHGA	GCH1	MTHFD1	RNASE3	TRDV2	DSG3	PMAIP1	ACD	CDIP1
CINP	GEMIN2	MYH6	RNASE4	TRIP11	DSG4	PSTPIP2	ACSF3	CDK10
CMA1	GLRX5	MYH7	RNF31	TRMT5	DTNA	PTPN2	ACSM2B	CDT1
COCH	GOLGA5	NDUFB1	RPGRIP1	TSHR	DYM	RAB27B	ACSM3	CENPBD1
COQ6	GPHN	NEK9	RPS29	TSSK4	DYNAP	RAX	ADAMTS18	CES1
COX8C	GPR132	NFATC4	RPS6KL1	TTC5	ELP2	RBBP8	ADCY9	CES2
CPSF2	GPR33	NFKBIA	SALL2	TTC8	ENOSF1	RIT2	ADGRG1	CES4A
CTSG	GPR68	NID2	SDR39U1	TLL5	EPG5	RNF125	AGRP	CETP
CYP46A1	GPX2	NIN	SEC23A	UBR7	FECH	ROCK1	AHSP	CFDP1
DAAM1	GSC	NKX2-1	SELIL	UNC79	FHOD3	RTTN	AKTIP	CHMP1A
DACT1	GSTZ1	NPAS3	SERPINA1	VIPAS39	GATA6	SERPINB11	ALDOA	CHST5
DAD1	GZMB	NPC2	SERPINA10	VRK1	GNAL	SERPINB3	ALG1	CHST6

CIAPIN1	FANCA	KCTD19	ORC6	SEZ6L2	TRAP1	APOH	CCR7	EFTUD2
CIITA	FBXL19	KIAA0430	OSGIN1	SH2B1	TRIM72	ARHGDI1A	CD300LF	EIF4A3
CIRH1A	FBXO31	KIAA0513	OTOA	SLC12A3	TSC2	ARHGEF15	CD79B	ELAC2
CLCN7	FOXC2	KIAA0556	PALB2	SLC12A4	TUBB3	ARSG	CDC27	EME1
CLEC16A	FOXF1	KIF22	PAM16	SLC38A8	TUFM	ASGR1	CDC6	ENDOV
CLEC3A	FOXL1	LAT	PARD6A	SLC5A11	UBE2I	ASPA	CDK12	ENO3
CLN3	FTO	LCAT	PARN	SLC5A2	UBN1	ASPSCR1	CDK5R1	EPX
CLUAP1	FUS	LITAF	PDF	SLC6A2	UMOD	ATAD5	CDK5RAP3	ERBB2
CNGB1	GALNS	LMF1	PDP2	SLC7A5	UNKL	ATP2A3	CHD3	ETV4
CNOT1	GAN	LOC100289092	PDPK1	SLC7A6	UQCRC2	ATP5G1	CHRNBI	EZH1
CNTNAP4	GAS8	LOC606724	PDPR	SLC7A6OS	USB1	ATP6V0A1	CHRNE	FAM104A
COG4	GCSH	LRRC29	PHKB	SLX4	USP10	ATPAF2	CLEC10A	FAM134C
COG7	GFER	LUC7L	PHKG2	SMG1	USP7	AURKB	CLTC	FAM20A
COG8	GLG1	MAF	PHLPP2	SMPD3	VAC14	AXIN2	CNTNAP1	FASN
COQ7	GLIS2	MAPK3	PIEZO1	SNAI3	VKORC1	B4GALNT2	CNTROB	FBXO39
COQ9	GNAO1	MC1R	PIGQ	SNTB2	VPS35	B9D1	COA3	FKBP10
CORO1A	GNPTG	MEFV	PKD1	SOCS1	VPS4A	BAIAP2	COASY	FLCN
COX4I1	GP2	METTL22	PLA2G10	SOX8	WVVOX	BHLHA9	COG1	FN3K
COX6A2	GPR139	MGRN1	PLCG2	SPATA33	WWP2	BIRC5	COL1A1	FN3KRP
CPPED1	GPT2	MKL2	PLEKHG4	SPG7	XYLT1	BLMH	COX10	FOXJ1
CREBBP	GRIN2A	MLYCD	PLK1	SRCAP	ZFH3	BPTF	COX10-AS1	FOXN1
CRYM	GSE1	MMP2	PMFBP1	SRL	ZFP90	BRCA1	COX11	FSCN2
CSNK2A2	GSPT1	MPG	PMM2	SRRM2	ZNF213	BRIP1	CRHR1	FZD2
CTCF	GTF3C1	MRPL28	PPL	SSTR5	ZNF276	BZRAP1	CRK	G6PC
CTD-2258A20.5	HAGH	MRPS34	PRKCB	ST3GAL2	ZNF423	C17orf107	CRYBA1	G6PC3
CTF1	HBA1	MT1A	PRM1	STUB1	ZNF469	C17orf66	CSH1	GAA
CTU2	HBA2	MT1X	PRM2	STX1B	ZNF668	C1QTNF1	CSHL1	GALK1
CYBA	HBM	MT2A	PRM3	SULT1A1	ZNRF1	CA10	CSNK1D	GAS2L2
CYLD	HBQ1	MT3	PRMT7	SULT1A3	AANAT	CA4	CTC1	GAST
DCTN5	HBZ	MTSS1L	PRRT2	SYT17	AATF	CACNA1G	CTNS	GCGR
DHODH	HMOX2	MVD	PRSS22	TAF1C	ABCA10	CACNG1	CUEDC1	GEMIN4
DHX38	HP	MYH11	PRSS8	TAT	ABCA5	CACNG4	CXCL16	GFAP
DNAAF1	HSD11B2	MYLPF	PSMD7	TBC1D10B	ABCA8	CAMKK1	CYGB	GH1
DNASE1	HSD17B2	NAGPA	PYCARD	TBC1D24	ABCC3	CANT1	DBF4B	GH2
DNASE1L2	HSD3B7	NDE1	RABEP2	TBX6	ACACA	CARD14	DCAKD	GIP
DOC2A	HSF4	NDRG4	RBBP6	TEKT5	ACADVL	CBX2	DCXR	GIT1
DPEP1	HYDIN	NDUFAB1	RBFOX1	TELO2	ACE	CBX4	DDX5	GJC1
DPEP2	IFT140	NDUFB10	RBL2	TERF2IP	ACLY	CBX8	DGKE	GNA13
DUS2	IGFALS	NECAB2	RHBDF1	THOC6	ACOX1	CCDC103	DHRS7C	GOSR2
E2F4	IL21R	NFAT5	RLTPR	TIGD7	ACTG1	CCDC40	DLG4	GP1BA
EARS2	IL21R-AS1	NFATC3	ROGDI	TK2	ADPRM	CCDC47	DLX3	GPATCH8
EC11	IL4R	NIP7	RPGRIP1L	TMEM114	AIPL1	CCDC57	DLX4	GPR179
EEF2K	IQCK	NLRC5	RPS15A	TMEM219	AKAP10	CCL11	DNAH2	GPS1
EIF3C	IRF8	NOD2	RPS2	TMEM231	ALDH3A1	CCL13	DNAH9	GRB2
EME2	IRX5	NOL3	RSPRY1	TMEM8A	ALDH3A2	CCL2	DNAI2	GRB7
EMP2	ITGAM	NPRL3	SALL1	TNRC6A	ALOX12	CCL3	DPH1	GRN
ERCC4	JPH3	NQO1	SCNN1B	TOX3	ALOX12B	CCL3L1	DUSP3	GSDMA
ERI2	KARS	NTHL1	SCNN1G	TPSB2	ALOX15	CCL4L1	DVL2	GSDMB
FA2H	KATNB1	NUDT7	41153	TRADD	ALOXE3	CCL5	EFCAB13	GUCY2D
FAM86A	KCTD13	NUP93	SETD1A	TRAF7	AOC2	CCL7	EFCAB5	HAP1

HCRT	LGALS9B	NEK8	PPY	SHBG	STH	UTP6	DAOA-AS1	MIPEP
HELZ	LHX1	NF1	PRCD	SHMT1	STRADA	UTS2R	DCLK1	MIR17HG
HES7	LIG3	NFE2L1	PRKARIA	SHPK	STXBP4	VPS53	DGKH	MPHOSPH8
HEXDC	LLGL1	NGFR	PRKCA	SLC13A2	SUPT6H	VTN	DIAPH3	MRPS31
HID1	LLGL2	NLGN2	PRPF8	SLC13A5	SUZ12	WBP2	DIAPH3-AS1	MYCBP2
HNF1B	LOC100287042	NLK	PSMC3IP	SLC16A3	TACO1	WDR45B	DNAJC3	MYO16
HOXB1	LOC100288866	NLRP1	PTRF	SLC25A10	TAF15	WDR81	DOCK9	N4BP2L2
HOXB13	LOC100294362	NME1	PTRH2	SLC25A11	TANC2	WNK4	EDNRB	NALCN
HOXB6	LRRC46	NME1-NME2	PYCR1	SLC25A19	TBCD	WNT3	EFNB2	NALCN-AS1
HOXB8	MAP2K3	NOG	PYY	SLC25A35	TBX2	WNT9B	ENOX1	NBEA
HSD17B1	MAP2K4	NOL1	RAB34	SLC25A39	TBX21	WRAP53	ERCC5	NUDT15
IGFBP4	MAP3K14	NOS2	RAD51C	SLC26A11	TBX4	XAF1	EXOSC8	PARP4
IKZF3	MAPT	NPEPPS	RAD51D	SLC2A4	TCAP	XYLT2	F10	PCCA
INPP5K	MED13	NR1D1	RAD51L3-RFFL	SLC46A1	TEN1-CDK3	YBX2	F7	PCDH9
ITGA2B	MEOX1	NT5C	RAI1	SLC47A1	TEX14	YWHAE	FGF14	PCID2
ITGA3	METTL23	NXPH3	RANGRF	SLC47A2	THRA	ZACN	FGF9	PDX1
ITGAE	MFAP4	OMG	RARA	SLC4A1	TIMP2	ZMYND15	FLT1	PHF11
ITGB3	MFSD6L	ORMDL3	RARA-AS1	SLC52A1	TK1	ZNF750	FLT3	PIBF1
ITGB4	MGAT5B	P2RX1	RBFOX3	SLC6A4	TLK2	ZPBP2	FOXO1	POLR1D
JUP	MKS1	P2RX5	RCVRN	SLC9A3R1	TMC6	ZSWIM7	FREM2	POMP
KANSL1	MLX	P4HB	RECQL5	SLFN14	TMC8	ABCC4	FRY	POSTN
KAT2A	MPDU1	PAFAH1B1	RFNG	SLFN5	TMEM107	ALG11	GAS6	PROZ
KCNH6	MPO	PCGF2	RGS9	SMARCD2	TMEM132E	ALG5	GGACT	PSPC1
KCNJ12	MPP3	PDE6G	RHBDF2	SMARCE1	TMEM199	ALOX5AP	GJA3	RB1
KCNJ16	MRC2	PDK2	RILP	SMG6	TMEM92	ARHGEF7	GJB2	RCBTB1
KCNJ2	MRPL10	PECAM1	RNF135	SNORD118	TMEM98	ARL11	GJB6	RFXAP
KDM6B	MRPL12	PEMT	RNF213	SOCS3	TMEM99	ATP7B	GPC5	RNASEH2B
KIAA0100	MRPL27	PER1	RNF43	SOST	TNFAIP1	ATP8A2	GPC6	RNF219-AS1
KIAA0753	MRPL38	PEX12	RPA1	SOX15	TNFRSF13B	ATXN8OS	GPR12	RNF6
KIF19	MRPL45	PFAS	RPH3AL	SOX9	TNFSF12	B3GLCT	GPR180	RPL21
KIF1C	MRPS23	PFN1	RPL19	SPAG5	TNFSF12-TNFSF13	BIVM	GRK1	RPL21P28- chr13
KIF2B	MRPS7	PGAP3	RPL23	SPAG5-AS1	TNRC6C	BIVM-ERCC5	HSPH1	RXFP2
KLHL10	MSI2	PGS1	RPL26	SPAG9	TOP2A	BRCA2	HTR2A	SACS
KRT10	MYADML2	PHB	RPL27	SPATA22	TP53	CARS2	IFT88	SETDB2
KRT12	MYBBP1A	PIGL	RPL38	SPATA32	TP53I13	CDX2	ING1	SGCG
KRT13	MYH10	PIGS	RPS6KB1	SPECC1	TRIM37	CENPJ	INTS6	SLC10A2
KRT14	MYH13	PIGW	RPTOR	SPOP	TRPV1	CHAMP1	IRS2	SLC15A1
KRT15	MYH2	PIK3R5	RTN4RL1	SRCIN1	TRPV3	CLN5	ITM2B	SLC25A15
KRT16	MYH3	PITPNA	RUNDC1	SREBF1	TSEN54	CLYBL	KL	SLC25A30
KRT17	MYH4	PITPNM3	RUNDC3A	SRR	TSR1	COG3	KLF12	SLC7A1
KRT20	MYH8	PLD2	SARM1	SRSF2	TTC19	COG6	KLF5	SLITRK1
KRT24	MYL4	PLEKHM1	SCN4A	SSH2	TTC25	COL4A1	KLHL1	SLITRK5
KRT25	MYO15A	PLSCR3	SCO1	SSTR2	TUBG1	COL4A2	LACC1	SLITRK6
KRT31	MYO18A	PMP22	40057	ST6GALNAC1	UBB	CPB2	LAMP1	SMAD9
KRT37	MYO1C	PNMT	SERPINF1	ST6GALNAC2	ULK2	CRYL1	LHFP	SOHLH2
KRT38	MYO1D	PNPO	SERPINF2	STAC2	UNC119	CSNK1A1L	LIG4	SOX1
KRT9	MYOCD	POLG2	SEZ6	STARD3	UNC13D	CUL4A	LNX2	SPATA13
KRTAP1-1	NAGLU	POLR2A	SGCA	STAT3	UNC45B	CYSLTR2	LPAR6	SPERT
KRTAP4-8	NAGS	PPM1D	SGSH	STAT5A	USH1G	DACH1	LRCH1	SPG20
KRTAP9-3	NCOR1	PPM1E	SGSM2	STAT5B	USP6	DAOA	MCF2L	SPRY2

STARD13	ERG	TIAM1	ATRX	CT47A8	FTHL17	IL3RA	NLGN3	PRPS1
SUCLA2	ETS2	TMEM50B	ATXN3L	CT47A9	FTSJ1	IL9R	NLGN4X	PRPS2
TBCID4	FTCD	TMPRSS15	AVPR2	CUL4B	FUNDC2	INE1	NONO	PTCHD1
TGDS	GABPA	TMPRSS3	BCAP31	CXCR3	G6PD	IQSEC2	NOX1	RAB39B
THSD1	GRIK1	TPTE TRAPPC1 0	BCOR	CXorf36	GABRA3	IRAK1	NR0B1	RAB40AL
TMCO3	GRIK1-AS2		BCORL1	CYBB	GABRE	IRS4	NSDHL	RBBP7
TNFSF11 TNFSF13 B	HLCS IFNAR1	TRPM2	BEND2	CYSLTR1	GABRQ	ITIH6	NXF3	RBM10
TPP2	IFNAR2	TSPEAR TSPEAR- AS1	BEX4	DACH2	GATA1	KCNE1L	NXF5	RBMX
TPTE2P5	IFNGR2	TTC3	BGN	DCX	GDI1	KDM5C	NYX	RENBP
TRIM13	IL10RB	U2AF1	BMP15	DDX3X	GJB1	KDM6A	OCRL	REPS2
TRPC4	ITGB2	URB1	BRCC3	DDX53	GK	KIAA1210	OFD1	RHOXF2
UBAC2	ITSN1	WDR4	BRWD3	DGAT2L6	GLA	KIAA2022	OGT	RIPPLY1
UGGT2	KCNE1	WDR4	BTK C1GALTIC 1	DGKK	GLRA2	KIF4A	OPHN1	RLIM
UTP14C	KCNE2	YBEY		DIAPH2	GLRA4	KLF8	OPN1LW	RNF113A
WASF3	KCNJ15	ABCB7	CACNA1F	DKC1	GLUD2	KLHL13	OPN1MW OPN1MW 2	RNF128
ZIC2	KCNJ6	ABCD1	CASK	DLG3	GNL3L	KLHL15		RP2
ZMYM2	LIPI	ACSL4	CCDC160	DMD	GPC3	L1CAM	OR13H1	RPA4
ZMYM5	LSS	ADGRG2	CCDC22	DNASE1L1	GPC4	LAMP2	OTC	RPGR
ABCG1	LTN1	AFF2	CD40LG	DRP2	GPR101	LASIL	P2RY4	RPL10 RPL36A- HNRNPH2
ADAMTS1	MCM3AP	AGTR2	CD99L2	EBP	GPR112	LUZP4	PAK3	
ADARB1	MRAP	AIFM1	CDK16	EDA	GPR143	MAGEA4	PCDH11X	RPS4X
AIRE	MRPL39	ALAS2	CDKL5	EDA2R	GPR174	MAGEC3	PCDH19	RPS6KA3
APP	MRPS6	ALG13	CDR1	EFHC2	GRIA3	MAGED2	PDHA1	RRAGB
ATP5J	MX1	AMELX	CFP	EFNB1	GRIPAP1	MAGEE2	PDK3	RS1
ATP5O	NDUFV3	AMER1	CHM	EIF2S3	GRPR	MAGT1	PFKFB1	S100G
B3GALT5	NRIP1	AMMECR1	CHRD1	ELF4	GSPT2	MAMLD1	PGK1	SAGE1
BRWD1	OLIG2	AMOT	CHST7	ELK1	GUCY2F	MAOA	PGRMC1	SAT1
C21orf2	PCBP3	ANOS1	CLCN4	EMD	GYG2	MAOB	PHEX	SATL1
C21orf33	PCNT	AP1S2	CLCN5	F8	H2BFWT	MAP3K15	PHF6	38961
C21orf59	PCP4	APEX2	CLDN2	F9	HCCS	MAP7D3	PHF8	SERPINA7
C21orf91	PDXK	APLN	CLIC2	FAAH2	HCFC1	MBTPS2	PHKA1	SH2D1A
CBR1	PFKL	APOOL	CNGA2	FAM104B	HDAC6	MCF2	PHKA2 PHKA2- AS1	SHOX
CBR3	PKNOX1	AR	CNKS2	FAM120C	HDAC8	MCTS1		SHROOM4
CBS	POFUT2	ARAF	COL4A5	FAM199X	HDX	MECP2	PIGA	SLC10A3
CHAF1B	RCAN1	ARHGAP4	COL4A6	FAM47B	HEPH	MED12	PIH1D3	SLC16A2
CLDN14	RIPK4	ARHGAP6	COX7B	FAM58A	HMGB3	MID1	PIR	SLC25A14
CLIC6	RRP1B	ARHGEF6	CRLF2	FAM9C	HNRNPH2	MIDI1P1	PLP1	SLC25A43
COL18A1	RSPH1	ARHGEF9	CSAG1	FANCB	HPRT1	MID2	PLP2	SLC25A5 SLC25A5- AS1
COL6A1	RUNX1	ARSE	CSF2RA	FGD1	HSD17B10	MMGT1	PLS3	
COL6A2	S100B	ARSF	CSTF2	FGF13	HTATSF1	MSN	PLXNA3	SLC35A2
CRYAA	SIK1	ARSH	CT45A5	FGF16	HTR2C	MTM1	PLXNB3	SLC6A14
CRYZL1	SIM2	ARX	CT47A1	FHL1	HUWE1	MTMR1	PNPLA4	SLC6A8
CSTB	SLC19A1	ASMT	CT47A10	FIGF	IDH3G	MTMR8	POF1B	SLC7A3
CXADR	SLC37A1	ASMTL	CT47A11	FLNA	IDS	MXRA5	POLA1	SLC9A6
DIP2A	SLC5A3	ATP11C	CT47A12	FMR1	IGBP1	NAA10	PORCN	SLC9A7
DNMT3L	SOD1	ATP1B4	CT47A2	FMR1-AS1	IGSF1	NAP1L2	POU3F4	SMARCA1
DSCAM	SON	ATP2B3	CT47A3	FOXO4	IKBK3	NDP	PQBP1	SMC1A
DSCR8	SYNJ1	ATP6AP1	CT47A4	FOXP3	IL1RAPL1	NDUFA1	PRAF2	SMPX
DYRK1A	TFF1	ATP6AP2	CT47A5	FRMD7	IL1RAPL2	NDUFB11	PRDX4	SMS
		ATP7A	CT47A6	FRMPD4	IL2RG	NHS	PRICKLE3	SOX3

SPANXN5	USP27X	ALDH7A1	COX7C	FST	IL6ST	MTRR	PCDHB4	RASA1
SPRY3	USP9X	AMACR	CPLX2	FTMT	IL7R	MYO10	PCDHGA1	REEP2
SRPK3	VAMP7	ANKH	CSF1R	FYB	IL9	MYOT	PCDHGA10	RIOK2
SRPX	VCX2	ANKHD1	CSF2	G3BP1	IQGAP2	NADK2	PCDHGA11	ROPN1L
SRPX2	VCX3A	ANKRD31	CSNK1G3 CTD-	GABRA1	IRF1	NAIP	PCDHGA12	RPS14
SSR4	VGLL1	AP3B1	2201118.1	GABRA6	IRGM	NDST1	PCDHGA2	SAR1B
SSX1	VMA21	APBB3	CTNNA1	GABRB2	IRX4	NDUFA2	PCDHGA3	SCGB3A2
SSX2	VSIG4	APC	CTNND2	GABRG2	ISL1	NDUFAF2	PCDHGA4	SDHA
SSX7	WAS	ARHGAP26	DAB2	GABRP	ITGA1	NDUFS4	PCDHGA5	SEMA5A
STAG2	WDR13	ARHGEF28	DDX41	GDF9	ITGA2	NDUFS6	PCDHGA6	SEPP1
STS	WDR44	ARSB	DHFR	GDNF	ITK	NEUROG1	PCDHGA7	SETD9
SYN1	WDR45	ARSI	DIAPH1	GFM2	KCNMB1	NHP2	PCDHGA8	SGCD
SYP	WNK3	ATG12	DMGDH	GFPT2	KCNN2	NIM1K	PCDHGA9	SH3PXD2B
SYP-AS1	WWC3	B4GALT7	DMXL1	GHR	KDM3B	NIPAL4	PCDHGB1	SH3TC2
SYTL5	XG	BDP1	DNAH5	GLRA1	KIF2A	NIPBL	PCDHGB2	SHROOM1
TAF1	XIAP	BHMT	DNAJC21	GM2A	KLHL3	NKX2-5	PCDHGB3	SIL1
TAF7L	XIST	BHMT2	DND1	GPRIN1	LARS	NME5	PCDHGB4	SKP2
TAF9B	XK	BOD1 C1QTNF3-	DOCK2	GPX3	LECT2	NNT	PCDHGB5	SLC12A2
TAZ	XPNPEP2	AMACR	DRD1	GRIA1	LIFR	NPM1	PCDHGB6	SLC12A7
TBL1X	YY2	C5orf15	DROSHA	GRM6	LMNB1	NPR3	PCDHGB7	SLC1A3
TBX22	ZBTB33	C5orf42	EFNA5	GRPEL2	LOC100130744	NR2F1	PCDHGC3	SLC22A4
TENM1	ZC3H12B	C5orf66	EGR1	GRXCR2	LOC257396	NR3C1	PCDHGC4	SLC22A5
TEX11	ZC4H2	C6	EIF4E1B	HAND1	LOC553103	NSD1	PCDHGC5	SLC23A1
TEX13B	ZCCHC12	C7	EPB41L4A	HAPLN1	LOX	NSG2	PCSK1	SLC25A2
TFE3	ZCCHC13	C9	ERAP1	HARS	LTC4S	NSUN2	PDE4D	SLC25A46
THOC2	ZCCHC16	CAMK2A	ERAP2	HARS2	LYRM7	NUP155	PDE6A	SLC26A2
TIMM8A	ZDHHC15	CAMK4	ERBB2IP	HAVCRI	LYSMD3	OCN	PDE8B	SLC30A5
TIMP1	ZDHHC9	CARTPT	ERCC8	HBEGF	MAML1	OSMR	PDGFRB	SLC34A1
TLR7	ZFX	CAST	FI2	HCN1	MAN2A1	OTULIN	PDLIM4	SLC36A2
TLR8	ZIC3	CATSPER3	F2R	HDAC3	MAP3K1	OXCT1	PDLIM7	SLC45A2
TMEM185A	ZMYM3	CCDC127	F2RL1	HEXB	MAPK9	P4HA2	PDZD2	SLC6A18
TMEM187	ZNF157	CCDC152	FABP6	HIGD2A	MARVELD2	PAPD4	PHYKPL	SLC6A19
TMEM47	ZNF41	CCNO	FAF2	HINT1	MAST4	PAPD7	PIK3R1	SLC6A3
TMLHE	ZNF674	CCT5	FAM134B	HMGCR	MATR3	PCDH12	PITX1	SLC9A3
TRAPPC2	ZNF711	CD14	FAM81B	HMMR	MCC	PCDHA1	PLCXD3	SLCO4C1
TREX2	ZNF75D	CD74	FASTKD3	HNRNPA0	MCCC2	PCDHA10	POC5	SLCO6A1
TRPC5	ZNF81	CDH12	FAT2	HNRNPH1	MCIDAS	PCDHA11	POLK	SLIT3
TSIX	ZRSR2	CDH18	FAXDC2	HOMER1	MEF2C	PCDHA12	POU4F3	SMAD5
TSPAN7	ACSL6	CDH6	FBN2	HRH2	MEGF10	PCDHA13	PPARGC1B	SMIM3
TSPYL2	ADAM19	CDK7	FBXL17	HSD17B4	MGAT1	PCDHA2	PPP2R2B	SMN1
TSR2	ADAMTS16	CDKL3	FBXO38	HSPA9	MGAT4B	PCDHA3	PRDM6	SMN2
TXLNG	ADAMTS19	CDO1	FBXW11	HSPB3	MOCS2	PCDHA4	PRDM9	SNCAIP
UBA1	ADAMTS2	CDX1	FER	HTR1A	MRPL22	PCDHA5	PRLR	SNCB
UBE2A	ADAMTS6	CEP120	FGF1	IK	MRPL36	PCDHA6	PROP1	SNHG4
UBE2NL	ADGRV1	CHD1	FGF10	IL12B	MRPS27	PCDHA7	PTGER4	SPARC
UBL4A	ADRB2	CHSY3	FGF10-AS1	IL13	MRPS30	PCDHA8	PURA	SPEF2
UBQLN2	AFF4	CKS1B-chr5	FGFR4	IL3	MRPS36	PCDHA9	PWWP2A	SPINK1
UPF3B	AGGF1	CLPTM1L	FLT4	IL31RA	MSH3	PCDHAC1	RAD1	SPINK5
USP11	AGXT2	CMYA5	FNIP1	IL4	MSX2	PCDHAC2	RAD50	SPOCK1
USP26	AHRR	COL4A3BP	FOXI1	IL5	MTMR12	PCDHB16	RARS	SPRY4

SQSTM1	ACTN2	ATPIA2	CD244	COL8A2	DNAJC6	FAM72A	GJB4	HSD3B2
SRA1	ADAMTSL4	ATPIB1	CD247	COL9A2	DOCK7	FASLG	GJC2	HSPB7
SREK1	ADAR	ATP2B4	CD46	COPA	DPM3	FBLIM1	GLMN	HSPG2
SRP19	ADC	ATP5F1	CD55	COX20	DPYD	FBXO2	GLUL	HTR6
ST8SIA4	ADCK3	ATPAF1	CD58	CPT2	DRAM2	FCER1A	GNAI3	IARS2
STK10	ADCY10	ATPIF1	CDA	CR1	DSTYK	FCER1G	GNAT2	IBA57
STK32A	ADIPOR1	AVPR1B	CDC14A	CR1L	DUSP23	FCGR1A	GNB1	ID3
SYNPO	ADORA1	AXDND1	CDC42	CR2	DVL1	FCGR2A	GNPAT	IFI16
TAF9	ADORA3	B3GALNT2	CDC73	CRB1	ECE1	FCGR2B	GON4L	IFI44L
TCF7	AGBL4	B3GALT2	CDK11A	CRP	ECM1	FCGR2C	GORAB	IGSF3
TCOF1	AGL	B3GALT6	CDK11B	CSDE1	EDARADD	FCGR3A	GPR161	IGSF8
TENM2	AGO1	B4GALT2	CDK18	CSF1	EDN2	FCGR3B	GPR88	IL10
TERT	AGRN	B4GALT3	CDKN2C	CSF3R	EFCAB7	FCN3	GPSM2	IL12RB2
TGFBI	AGT	BCAN	CELSR2	CSMD2	EFNA3	FCRL3	GREM2	IL19
THBS4	AHCYL1	BCL10	CENPF	CTBS	EFNA4	FCRL4	GRHL3	IL23R
THG1L	AHDC1	BCL9	CEP104	CTH	EGLN1	FCRL6	GRIK3	IL6R
TIGD6	AIM2	BGLAP	CEP170	CTPS1	EIF2B3	FDPS	GSTM1	INPP5B
TLX3	AK2	BRINP2	CFH	CTRC	EIF2D	FH	GSTM2	INSRR
TMCO6	AKR7A2	BSND	CFHR1	CTSK	EIF4G3	FLAD1	GSTM3	IPP
TMEM173	AKR7A3	BTG2	CFHR2	CYP2J2	ELAVL4	FLG	GSTM4	IQGAP3
TNPO1	AKT3	C1orf100	CFHR3	CYP4A11	ELK4	FLG2	GSTM5	IRF2BP2
TRIO	ALDH4A1	C1orf106	CFHR4	CYP4A22	EMC1	FLVCR1	GUCA2B	IRF6
TRIP13	ALDH9A1	C1orf127	CFHR5	CYP4B1	ENO1	FMN2	H3F3A	ISG15
TRPC7	ALG14	C1orf145	CHD1L	CYP4Z1	ENSA	FMO1	H6PD	JAK1
TSLP	ALG6	C1orf168	CHD5	CYR61	EPB41	FMO2	HAX1	JUN
TSPAN17	ALPL	C1orf172	CHI3L1	DARS2	EPHA2	FMO3	HCN3	KANK4
TTC1	ALX3	C1QA	CHI3L2	DBT	EPHA8	FMO4	HCRTR1	KCNA2
TTC37 U4atac- chr5	AMPD1	C1QB	CHIA	DCAF6	EPHB2	FMO5	HDAC1	KCNA3
UBE2B	AMPD2	C1QC	CHIT1	DCAF8	EPHX1	FMO6P	HENMT1	KCNAB2
UIMC1	ANGPTL3	C4BPA	CHML	DCST1	EPS15	FMOD	HFE2	KCND3
UQCRCQ	AP4B1	C8A	CHRM3	DDAH1	EPS8L3	FOXD3	HFM1	KCNH1
VCAN	APH1A	C8B	CHRN2B CKS1B- chr1	DDI2	ERMAP	FOXE3 FPGT- TNNI3K	HHAT	KCNJ10
VDAC1	APOA1BP	CA6	DDOST	ERRFI1	ERRFI1	HIST2H2BF	HIST2H2BF	KCNJ9
WDR36	APOA2	CACHD1	CLCA1	DDR2	ESPN	FUBP1	HIST2H4A	KCNN3
WDR55	ARF1	CACNA1E	CLCA2	DDX20	ESRRG	FUCA1	HIST2H4B	KCNQ4
WNT8A	ARHGAP29	CACNA1S	CLCC1	DDX59	EVI5	GABRD	HIST3H3	KDF1
WWC1	ARHGEF10L	CAMSAP2	CLCN6	DENND2C	EXO1	GADD45A	HIVEP3	KDM1A
XRCC4	ARHGEF11	CAMTA1	CLCNKA	DHCR24	EXO5	GALE	HLX	KDM5B
ZFR	ARID1A	CAPN9	CLCNKB	DHDDS	EXOC8	GALNT2	HMCN1	KIAA1614
ZNF454	ARID4B	CASP9	CLDN19	DHRS3	EXTL1	GATAD2B	HMGCL	KIF14
ZSWIM6	ARNT	CASQ1	CLK2	DHX9	EXTL2	GBA	HMGCS2	KIF17
ABCA4	ARV1	CASQ2	CLSPN	DIO1	F13B	GBP2	HNRNPR	KIF1B
ABCD3	ASH1L	CASZ1	CLSTN1	DIRAS3	F3	GBP4	HNRNPU	KIF21B
ABL2	ASPM	CATSPER4	CMPK1	DISC1	F5	GCLM	HOOK1	KIF26B
ACADM	ASTN1	CCDC18	CNKSR1	DISC2	FAAH	GFI1	HORMAD1	KIFAP3
ACBD6	ATAD3A	CCDC19	CNR2	DISP1	FABP3	GJA4	HPCA	KISS1
ACKR1	ATF3	CCDC28B	CNTN2	DLGAP3	FAM212B	GJA5	HPCAL4	KLHL17
ACP6	ATF6	CCDC30	COA6	DMBX1	FAM213B	GJA8	HRNR	KLHL20
ACTA1	ATP13A2	CD1A	COG2	DMRTA2	FAM46C	GJA9	HSD11B1	KMO
	ATPIA1	CD1E	COL11A1	DNAH14	FAM71A	GJB3	HSD3B1	LAD1

LAMB3	MGST3	NMNATI	PGM1	PTAFR	RSP01	SLC9A1	TMCO1	USP48
LAMC1	MIA3	NOSIAP	PHC2	PTCH2	RUNX3	SMAP2	TMEM167B	UTS2
LAMC2	MIIP	NOTCH2	PHGDH	PTGS2	RXRG	SMIM1	TMEM201	VANGL1
LAMTOR2	MLLTI1	NPHP4	PIGC	PTPN14	RYR2	SMYD3	TMEM240	VANGL2
LAMTOR5	MMACHC	NPHS2	PIGM	PTPN22	SI00A14	SNIP1	TMEM69	VAV3
LAPTM5	MMEL1	NPL	PIGR	PTPRC	SI00A3	SNRPE	TMEM81	VCAM1
LBR	MOV10	NPPA NPPA- AS1	PIGV	PTPRF	SIPRI	SNX27	TMEM9	VPS13D
LCE3B	MPL	NPPB	PIK3C2B	PTPRU	SAMD11	SOAT1	TNFRSF14	VPS45
LCE3C	MPZ	NPPB	PIK3CD	PVRL4	SARS	SORT1	TNFRSF1B	WARS2
LCE5A	MR1	NPR1	PIK3R3	PYCR2	SASS6	SPAG17	TNFRSF25	WDR26
LCK	MRPL20	NR0B2	PINK1	PYGO2	SCNM1	SPATA21	TNFRSF4	WDR64
LDLRAD2	MRPL24	NR1I3	PINK1-AS	PYHIN1	SCNN1D	SPEN	TNFRSF9	WDR65
LDLRAP1	MRPL37	NR5A2	PKLR	RAB25	SCP2	SPRR3	TNFSF18	WNT3A
LEFTY2	MRPL55	NRAS	PKP1	RAB29	SDC3	SPRTN	TNFSF4	WNT4
LEPR	MRPL9	NT5C1A	PLA2G2A	RAB3GAP2	SDCCAG8	SPSB1	TNN	XPR1
LEPROT	MRPS14	NTNG1	PLA2G2D	RABGAP1L	SDHB	SPTA1	TNNI3K	YARS
LHX4	MRPS15	NTRK1	PLA2G4A	RAD54L	SDHC	SRGAP2	TNNT2	YTHDF2
LHX8	MRPS21	NUDC	PLA2G5	RASSF5	SEC16B	ST3GAL3	TNR	YY1AP1
LHX9	MRTO4	NVL	PLEKHA6	RBBP5	SELE	ST6GALNAC3	TOE1	ZBTB18
LIN28A	MSH4	OAZ3	PLEKHG5	RBM15	SELL	ST6GALNAC5	TOMM40L	ZBTB40
LMNA	MSTO2P	OBSCN	PLEKHM2	RBM8A	SELP	STIL	TORIAIP1	ZBTB41
LMO4	MTF1	OPRD1	PLOD1	RC3H1	SEMA4A	STMN1	TP53BP2	ZFP69
LOC100505666	MTHFR	OPTC	PMVK	RCOR3	42248	STXBP3	TP73	ZMPSTE24
LOC100506801	MTOR	OR10X1	POGZ	RD3	SEPN1	SUCO	TPM3	ZMYM6
LOC100527964	MTR	OR13G1	POMGNT1	REN	SERPINC1	SV2A	TPR	ZMYM6NB
LOC148413	MUC1	OR2M2	PPFIA4	RERE	SESN2	SYTI1	TRIM11	ZNF326
LOR	MUTYH	OR2W3	PPOX	RFWD2	SETDB1	SYTI4	TRIM17	ZNF644
LPAR3	MXRA8	ORC1	PPP1R12B	RFX5	SF3B4	SYT2	TRIM33	ZNF683
LPHN2	MYBPHL	OVGP1	PPP1R15B	RGL1	SFPQ	SZT2	TRIM63	ZNF687
LRIG2	MYCL	P3H1	PPT1	RGS2	SH2D2A	TACSTD2	TRIT1	ZNHIT6
LRP8	MYOC	PADI2	PQLC2	RGS5	SHC1	TAFI3	TROVE2	ZP4
LRRC41	MYSM1	PADI3	PRAMEF2	RGS7	SKI	TAGLN2	TSEN15	ZRANB2
LRRC7	NADK	PADI4	PRCC	RHCE	SLC16A1	TAL1	TSHB	
LUZP1	NAV1	PADI6	PRDM16	RHD	SLC19A2	TARDBP	TSNAX TSNAX- DISC1	
LYPLAL1	NBPF1	PAPPA2	PRDM2	RIMS3	SLC22A15	TARS2	TSSK3	
LYST	NCF2	PARK7	PRDX1	RITI	SLC25A33	TAS1R1	TTC4	
MACF1	NCSTN	PARP1	PRG4	RLF	SLC25A34	TAS1R2	TTF2	
MAD2L2	NDUFS2	PARS2	PRKAA2	RNASEL	SLC25A44	TAS1R3	TXNIP	
MAN1A2	NDUFS5	PAX7	PRKACB	RNF207	SLC26A9	TBCE	UBE2T	
MAP3K6	NEGR1	PBX1	PRKCZ	RNPC3	SLC2A1	TBX15	UBIAD1	
MAP7D1	NEK2	PCSK9	PROK1	RORC	SLC2A5	TBX19	UBQLN4	
MASP2	NEXN	PDE4B	PROX1	RPE65	SLC30A10	TCEB3	UBR4	
MAST2	NFASC	PDE4DIP	PRPF3	RPL11 RPL21P28- chr1	SLC30A2	TCHH	UHMK1	
MCL1	NFIA	PEAR1	PRRC2C	RPL5	SLC35A3	TCHHL1	UQCRH	
MDM4	NFYC	PER3	PRRX1	RPL5	SLC35D1	TEKT2	UROD	
MECR	NGF	PEX10	PRSS38	RPS27	SLC35F3	TESK2	USF1	
MED8	NID1	PEX11B	PRUNE	RPS6KA1	SLC41A1	TGFB2	USH2A	
MEF2D	NIPAL3	PEX14	PSEN2	RPS6KC1	SLC5A9	TGFBR3	USP1	
MFN2	NLRP3	PEX19	PSMB4	RRAGC	SLC6A17	THRAP3	USP24	
MFSD2A	NME7	PGD	PSMD4	RSC1A1	SLC6A9	TLR5		

Supplementary Table 1. Patients with P/LP variant in heterozygous carrier state, B/LB variant or VUS

Case	AAO	Phenotype	Gene	Variant	Inheritance	Type	ACMG classification
21	3	Generalised, isolated	<i>PRKRA</i>	ENST00000325748:c.380C>T; p.Pro127Leu	Ht, AR	Missense	LB (PP ₃ BP _{1,6})
			<i>PRKRA</i>	ENST00000325748:c.318-2A>T	Ht, AR	Splice site	P (PVS ₁ PM ₂ PP ₃)
			<i>TAF1</i>	ENST00000276072:c.1241G>T;p.Arg444Gly	Ht, XR	Missense	LB (PP ₂ BS ₁ BP ₄)
22	5	Generalised, combined (DP)	<i>CACNA1B</i>	ENST00000371372:c.3346G>A;p.Val1116Met	Ht, AD	Missense	LB (BS ₂ BP _{1,4})
23	42	Focal, combined (DP)	<i>GBA</i>	ENST00000327247:c.476G>A;p.Arg159Gln	Ht, AR	Missense	LP (PM _{1,2,5} PP _{2,3,5})
			<i>SPR</i>	ENST00000234454:c.628C>T;p.Arg210Trp	Ht, AD/AR	Missense	VUS (PM ₂ PP _{2,3})
24	12	Focal, paroxysmal	<i>ATM</i>	ENST00000278616;c.3449G>C;p.Arg1150Thr	Ht, AR	Missense	VUS (PM ₂ PP ₃)
			<i>ATM</i>	ENST00000278616:c.7435G>A;p.Glu2479Lys	Ht, AR	Missense	VUS (PM _{1,2})
25	6	Focal, isolated	<i>DCC</i>	ENST00000442544:c.3050T>C;p.Met1017Thr	Ht, AD	Missense	LB (PM ₂ BP _{1,4})
26	15	Generalised, complex (DC)	<i>SPG7</i>	ENST00000268704:c.1660G>A;p.Ala554Thr	Ht, AR	Missense	VUS (PM ₂ PP _{2,3})
27	26	Generalised, complex (DC)	<i>SLC20A2</i>	ENST00000342228:c.1423A>C;p.Lys475Gln	Ht, AD	Missense	B (PP ₂ BS _{1,2} BP ₄)
28	7	Generalised, isolated	<i>CACNA1B</i>	ENST00000371372:c.92G>T;p.Gly31Val	Ht, AD	Missense	VUS (PP ₃ BP ₁)
29	23	Generalised, complex (DC)	<i>SPTBN2</i>	ENST00000533211:c.5695C>T;p.Arg1899Cys	Ht, AD	Missense	VUS (PM ₂ PP ₃ BP ₁)
30	10	Generalised, complex (DS)	<i>LRRK2</i>	ENST00000298910:c.4883G>C;p.Arg1628Pro	Ht, AD	Missense	LB (PP _{2,3} BS ₁ BP ₆)
31	5	Generalised, combined (DCh)	<i>PRKRA</i>	ENST00000325748:c.380C>T;p.Pro127Leu	Ht, AR	Missense	LB (PP ₃ BP _{1,6})
			<i>ATP13A2</i>	ENST00000326735:c.767A>T;p.Tyr256Phe	Ht, AR	Missense	VUS (PM ₂ PP ₃ BP ₁)
			<i>ALS2</i>	ENST00000264276:c.2909G>T;p.Gly970Val	Ht, AR	Missense	VUS (PM ₂ PP ₂ BP ₄)
32	7	Generalised, complex (DS)	<i>PRKN</i>	ENST00000366898:c.838G>A;p.Asp280Asn	Ht, AR	Missense	LP (PM _{1,2} PP _{2,5} BP ₄)
33	3	Generalised, combined (DCh)	<i>PLA2G6</i>	ENST00000332509:c.898G>A;p.Ala300Thr	Ht, AR	Missense	VUS (PM ₂ PP _{2,5} BP ₄)
34	2	Generalised, complex (DS)	<i>PLA2G6</i>	ENST00000332509:c.2222G>A;p.Arg741Gln	Ht, AR	Missense	P (PP ₅ PM _{2,5} PP ₂)
			<i>NAGA</i>	ENST00000396398:c.838C>A;p.Leu280Lys	Ht, AR	Missense	VUS (PM ₂ PP _{2,3})
			<i>GCDH</i>	ENST00000222214:c.38G>A;p.Arg13His	Ht, AR	Missense	VUS (PM ₂ PP _{2,3})
35	43	Segmental, combined (DP)	<i>GCH1</i>	ENST00000491895:c.610G>A;p.Val204Ile	Ht, AR	Missense	LP (PM _{1,2} PP _{2,3})

AAO, age at onset; ACMG, American College of Medical Genetics and Genomics; AD, autosomal dominant; AR, autosomal recessive; B, benign; BP, supporting evidence of benign impact; BS, strong evidence of benign impact; DC, dystonia cerebellar; DCh, dystonia chorea; DP, dystonia parkinsonism; DS, dystonia spasticity; Ht, heterozygous; Hz, hemizygous; XR, X-linked recessive; LB, likely benign; LP, likely pathogenic; P, pathogenic; PM, moderate evidence of pathogenicity; PP, supportive evidence of pathogenicity; PVS, very strong evidence of pathogenicity; VUS, variant of unknown significance.

Supplementary Table 2. Previous studies of NGS in dystonia

Study	Country	Patients cohort	Age at onset	NGS	Yield	Genes (P/LP)
van Egmond et al. ³	Netherlands	61, main feature dystonia	< 21 in 72%	TGS	P/LP: 14.8%	<i>PRKRA, MECP2, GCDH, PRRT2, TH, NPC</i>
Zech et al. ⁵	Germany, Austria, Italy	16, EOGD	9.86 ± 6.9	WES	P/LP: 37.5%	<i>GCH1, THAP1, TOR1A, ANO3, ADCY5</i>
Ma et al. ⁸	China	65, main feature dystonia	22.7 ± 13.3	TGS	P/LP: 24.6% VUS: 6.2%	<i>TOR1A, PANK2, ATP1A3, PRRT2, GCH1, THAP</i>
Powis et al. ⁹	USA	189, main feature dystonia	13.7*	WES	Po/LPo: 21.7% U: 16.4%	<i>ADAR, ADCY5, ANO3, COL4A1, ECHS1, FA2H, GCH1, GLB1, GNAO1, KCNQ2, NACC1, NKX2-1, SLC16A2, PANK-2, WARS-2, KMT2B</i>
Kumar et al. ⁶	Australia, India	111, main feature dystonia	32.9 ± 21.4	WGS	P/LP: 11.7% VUS: 28.9%	<i>ADCY5, ATM, GNAL, GLB1, KMT2B, PRKN, PRRT2, SGCE, THAP1</i>
Wirth et al. ¹⁰	Netherlands	32, main feature dystonia	11.9	WES	P/LP: 34.4%	<i>CTNNB1, SUCLG1, NUS1, CNTNAP1, KCNB1, RELN, GNAO1, HIBCH, ADCK3</i>
Present study	India	48 (46 families), main feature dystonia	16.0 ± 14.1	CES	P/LP: 39.1% VUS: 16.7% P/LP carrier state: 10.4%	<i>PLA2G6, GLB1, TH, PRKN, TOR1A, ATP7B, FA2H, GCH1, GLB, THAP1, NDUFA12, NPC1</i>

*average age at testing. NGS, next-generation sequencing; EOGD, early onset generalised dystonia (< 30 yrs); TGS, targeted gene sequencing; WES, whole-exome sequencing; WGS, whole-genome sequencing; CES, clinical exome sequencing; P/LP, pathogenic/likely pathogenic; VUS, variant of uncertain significance; Po/Lpo, positive/likely positive; U, uncertain/uncharacterised (criteria for variant information not clearly stated).