

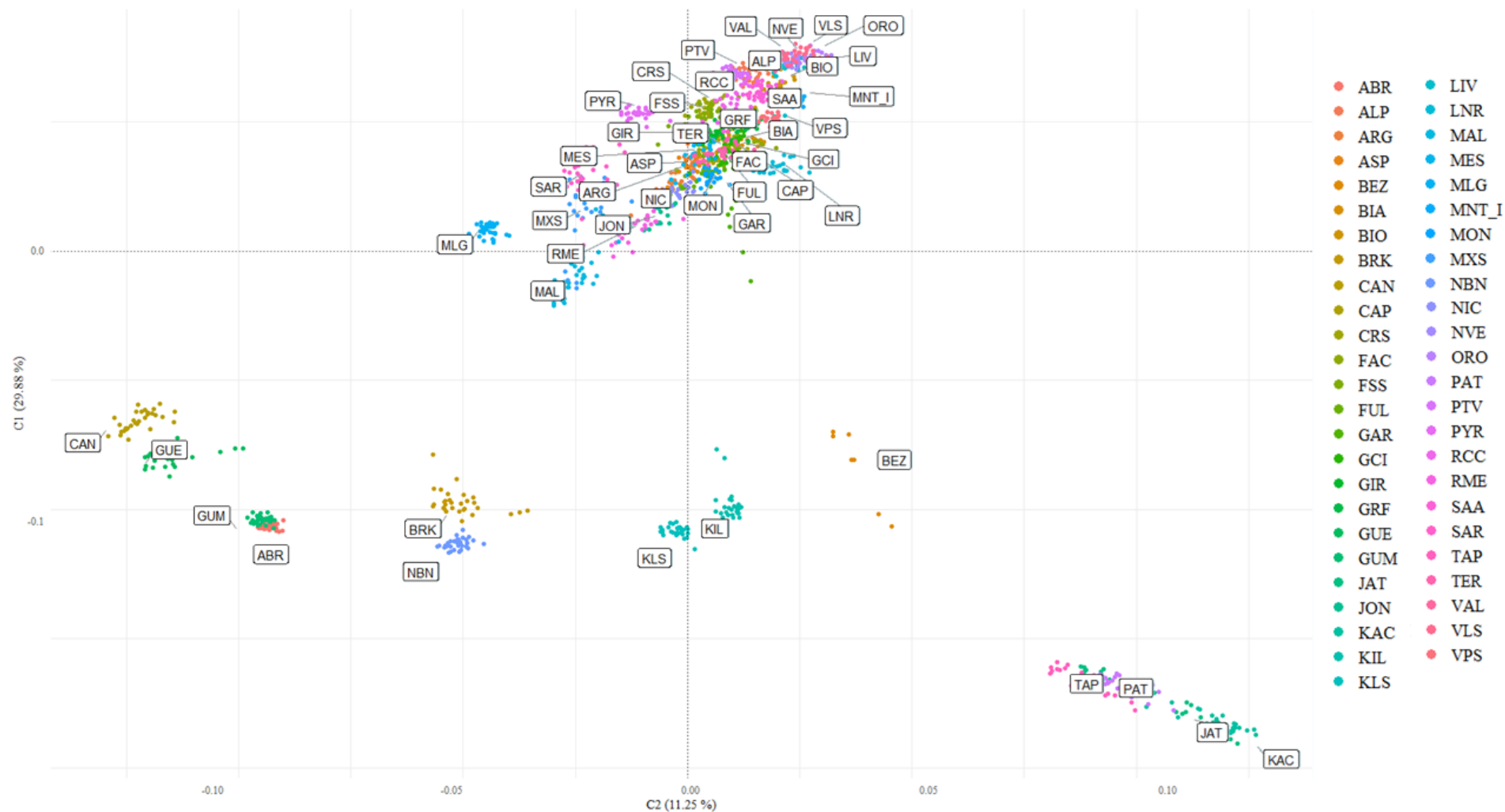
## **Characterization of heterozygosity-rich regions in Italian and worldwide goat breeds**

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**Supplementary Table S1** Summary statistics of genetic diversity. Geographic cluster (CODE), breed's acronym (Breed), observed heterozygosity ( $H_0$ ), expected heterozygosity ( $H_E$ ), fixation index ( $F_{IS}$ ) and minus allele frequency (MAF) per breed. The mean value of each index per geographical cluster is also reported. See Table 1 for a full definition of the dataset.

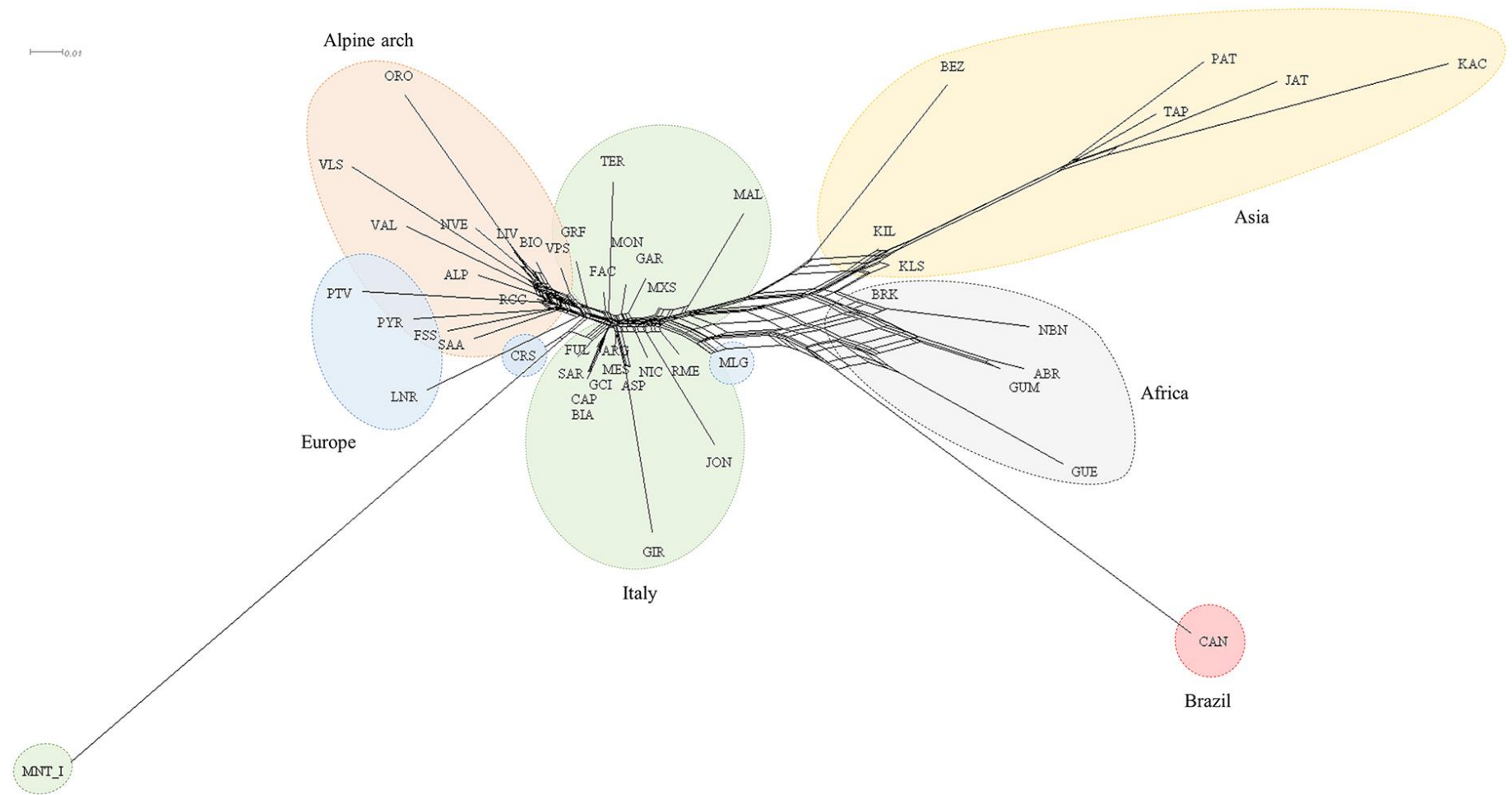
| CODE        | Breed       | $H_o$ |       | $H_E$ |       | $F_{IS}$ |       | $MAF$ |       | CODE        | Breed       | $H_o$ |       | $H_E$ |       | $F_{IS}$ |       | $MAF$ |       |       |
|-------------|-------------|-------|-------|-------|-------|----------|-------|-------|-------|-------------|-------------|-------|-------|-------|-------|----------|-------|-------|-------|-------|
|             |             | mean  | s.d.  | mean  | s.d.  | mean     | s.d.  | mean  | s.d.  |             |             | mean  | s.d.  | mean  | s.d.  | mean     | s.d.  | mean  | s.d.  |       |
| Italy       | ARG         | 0.416 | 0.128 | 0.412 | 0.100 | 0.051    | 0.018 | 0.326 | 0.118 | Alpine arch | ALP         | 0.409 | 0.133 | 0.405 | 0.107 | 0.066    | 0.018 | 0.319 | 0.122 |       |
|             | ASP         | 0.401 | 0.138 | 0.403 | 0.109 | 0.086    | 0.057 | 0.317 | 0.123 |             | BIO         | 0.403 | 0.141 | 0.401 | 0.111 | 0.081    | 0.039 | 0.316 | 0.124 |       |
|             | BIA         | 0.392 | 0.140 | 0.399 | 0.112 | 0.106    | 0.077 | 0.314 | 0.125 |             | LIV         | 0.404 | 0.146 | 0.396 | 0.115 | 0.078    | 0.019 | 0.311 | 0.127 |       |
|             | CAP         | 0.405 | 0.141 | 0.401 | 0.109 | 0.074    | 0.080 | 0.315 | 0.123 |             | NVE         | 0.391 | 0.159 | 0.385 | 0.126 | 0.108    | 0.044 | 0.300 | 0.133 |       |
|             | FAC         | 0.395 | 0.135 | 0.407 | 0.105 | 0.098    | 0.099 | 0.322 | 0.121 |             | ORO         | 0.358 | 0.169 | 0.352 | 0.146 | 0.183    | 0.046 | 0.268 | 0.143 |       |
|             | FUL         | 0.413 | 0.139 | 0.408 | 0.105 | 0.057    | 0.027 | 0.322 | 0.120 |             | RCC         | 0.399 | 0.126 | 0.414 | 0.098 | 0.089    | 0.080 | 0.328 | 0.116 |       |
|             | GAR         | 0.407 | 0.134 | 0.403 | 0.107 | 0.071    | 0.070 | 0.316 | 0.121 |             | SAA         | 0.413 | 0.134 | 0.405 | 0.106 | 0.057    | 0.024 | 0.319 | 0.121 |       |
|             | GCI         | 0.403 | 0.130 | 0.408 | 0.104 | 0.079    | 0.056 | 0.322 | 0.120 |             | VAL         | 0.369 | 0.152 | 0.376 | 0.132 | 0.158    | 0.095 | 0.291 | 0.136 |       |
|             | GIR         | 0.362 | 0.157 | 0.364 | 0.140 | 0.174    | 0.084 | 0.280 | 0.140 |             | VLS         | 0.351 | 0.167 | 0.358 | 0.144 | 0.199    | 0.094 | 0.275 | 0.142 |       |
|             | GRF         | 0.397 | 0.137 | 0.401 | 0.111 | 0.093    | 0.048 | 0.315 | 0.124 |             | VPS         | 0.400 | 0.138 | 0.404 | 0.109 | 0.087    | 0.047 | 0.319 | 0.123 |       |
|             | JON         | 0.415 | 0.181 | 0.373 | 0.133 | 0.055    | 0.029 | 0.288 | 0.136 |             | <i>mean</i> | 0.390 | 0.147 | 0.390 | 0.119 | 0.111    | 0.051 | 0.305 | 0.129 |       |
|             | MAL         | 0.369 | 0.142 | 0.384 | 0.124 | 0.134    | 0.102 | 0.298 | 0.132 |             | Africa      | ABR   | 0.364 | 0.162 | 0.361 | 0.144    | 0.169 | 0.038 | 0.279 | 0.143 |
|             | MES         | 0.413 | 0.138 | 0.406 | 0.106 | 0.058    | 0.024 | 0.320 | 0.121 | BRK         |             | 0.399 | 0.138 | 0.399 | 0.114 | 0.089    | 0.026 | 0.314 | 0.126 |       |
|             | MNT_I       | 0.271 | 0.208 | 0.263 | 0.191 | 0.381    | 0.016 | 0.198 | 0.165 | GUE         |             | 0.370 | 0.185 | 0.344 | 0.154 | 0.156    | 0.051 | 0.263 | 0.148 |       |
|             | MON         | 0.405 | 0.139 | 0.405 | 0.107 | 0.074    | 0.097 | 0.320 | 0.122 | GUM         |             | 0.369 | 0.158 | 0.367 | 0.140 | 0.157    | 0.032 | 0.284 | 0.140 |       |
|             | M×S         | 0.406 | 0.127 | 0.412 | 0.101 | 0.072    | 0.048 | 0.327 | 0.118 | NBN         |             | 0.355 | 0.159 | 0.361 | 0.143 | 0.190    | 0.032 | 0.277 | 0.142 |       |
|             | NIC         | 0.394 | 0.138 | 0.404 | 0.108 | 0.101    | 0.078 | 0.318 | 0.122 | <i>mean</i> |             | 0.371 | 0.160 | 0.366 | 0.139 | 0.152    | 0.036 | 0.283 | 0.140 |       |
|             | RME         | 0.396 | 0.132 | 0.402 | 0.109 | 0.137    | 0.105 | 0.316 | 0.123 | Asia        |             | BEZ   | 0.276 | 0.197 | 0.329 | 0.166    | 0.371 | 0.076 | 0.252 | 0.155 |
|             | SAR         | 0.404 | 0.129 | 0.408 | 0.104 | 0.079    | 0.043 | 0.321 | 0.120 |             |             | JAT   | 0.308 | 0.180 | 0.313 | 0.164    | 0.296 | 0.128 | 0.234 | 0.152 |
|             | TER         | 0.384 | 0.152 | 0.382 | 0.125 | 0.123    | 0.080 | 0.297 | 0.133 |             | KAC         | 0.281 | 0.204 | 0.278 | 0.186 | 0.359    | 0.064 | 0.209 | 0.163 |       |
| <i>mean</i> | 0.392       | 0.143 | 0.392 | 0.116 | 0.105 | 0.062    | 0.308 | 0.126 | KIL   |             | 0.401       | 0.147 | 0.394 | 0.117 | 0.085 | 0.028    | 0.309 | 0.128 |       |       |
| Europe      | CRS         | 0.400 | 0.134 | 0.401 | 0.109 | 0.087    | 0.030 | 0.315 | 0.123 |             | KLS         | 0.398 | 0.140 | 0.396 | 0.117 | 0.091    | 0.044 | 0.311 | 0.128 |       |
|             | FSS         | 0.393 | 0.145 | 0.391 | 0.118 | 0.104    | 0.080 | 0.304 | 0.128 |             | PAT         | 0.328 | 0.177 | 0.328 | 0.162 | 0.251    | 0.073 | 0.249 | 0.152 |       |
|             | LNR         | 0.358 | 0.144 | 0.379 | 0.130 | 0.184    | 0.107 | 0.295 | 0.135 |             | TAP         | 0.331 | 0.174 | 0.340 | 0.158 | 0.245    | 0.074 | 0.260 | 0.150 |       |
|             | MLG         | 0.415 | 0.131 | 0.409 | 0.104 | 0.054    | 0.032 | 0.324 | 0.120 |             | <i>mean</i> | 0.332 | 0.174 | 0.340 | 0.153 | 0.243    | 0.070 | 0.261 | 0.147 |       |
|             | PTV         | 0.374 | 0.153 | 0.372 | 0.133 | 0.146    | 0.047 | 0.287 | 0.137 | Brazil      | CAN         | 0.333 | 0.209 | 0.304 | 0.174 | 0.246    | 0.056 | 0.229 | 0.158 |       |
|             | PYR         | 0.373 | 0.148 | 0.382 | 0.127 | 0.149    | 0.088 | 0.297 | 0.133 |             |             |       |       |       |       |          |       |       |       |       |
|             | <i>mean</i> | 0.386 | 0.143 | 0.389 | 0.120 | 0.121    | 0.064 | 0.304 | 0.129 |             |             |       |       |       |       |          |       |       |       |       |

Supplementary Figure S1



Multidimensional scaling (MDS) plot of the goat dataset, according to the components C1 (29.88%) and C2 (11.25%). Each breed is represented by a different color. See Table 1 for a full definition of the dataset.

Supplementary Figure S2



Neighbor-Net based on pairwise Reynold's genetic distances among the 49 goat breeds. The breeds are highlighted according to their geographic group. See Table 1 for a full definition of the dataset.

**Supplementary Table S2** HRR and HRR islands per breed. Each breed reports the number of total HRR by Consecutive Runs (CR) and Sliding Window (SW) methods, the number of islands (HRR islands) and the number of harbored SNPs (SNPs in island). Each statistic is aggregated for geographic group (CODE). See Table 1 for a full definition of the dataset.

| CODE         | Breed        | HRR<br>CR | HRR<br>SW | HRR<br>islands | SNPs in<br>island | CODE           | Breed        | HRR<br>CR | HRR<br>SW | HRR<br>islands | SNPs in<br>island |
|--------------|--------------|-----------|-----------|----------------|-------------------|----------------|--------------|-----------|-----------|----------------|-------------------|
| Italy        | ARG          | 341       | 340       | 2              | 22                | Alpine<br>arch | ALP          | 520       | 518       | 5              | 50                |
|              | ASP          | 262       | 261       | 1              | 9                 |                | BIO          | 257       | 255       | 3              | 30                |
|              | BIA          | 261       | 260       | 5              | 51                |                | LIV          | 273       | 272       | 3              | 32                |
|              | CAP          | 294       | 293       | 5              | 53                |                | NVE          | 219       | 218       | 1              | 10                |
|              | FAC          | 301       | 300       | 4              | 37                |                | ORO          | 252       | 252       | 7              | 62                |
|              | FUL          | 278       | 278       | 4              | 32                |                | RCC          | 386       | 385       | 2              | 15                |
|              | GAR          | 389       | 389       | 2              | 22                |                | SAA          | 544       | 540       | 3              | 30                |
|              | GCI          | 332       | 332       | 3              | 24                |                | VAL          | 250       | 250       | 5              | 46                |
|              | GIR          | 262       | 261       | 2              | 24                |                | VLS          | 252       | 249       | 5              | 49                |
|              | GRF          | 326       | 325       | 3              | 26                |                | VPS          | 273       | 273       | 5              | 51                |
|              | JON          | 178       | 176       | 2              | 20                |                | <i>total</i> | 3226      | 3212      | 39             | 375               |
|              | MAL          | 383       | 378       | 3              | 31                |                |              |           |           |                |                   |
|              | MES          | 275       | 275       | 2              | 21                | Africa         | ABR          | 205       | 204       | 2              | 20                |
|              | MNT_I        | 205       | 205       | 16             | 171               |                | BRK          | 221       | 220       | 0              | 0                 |
|              | MON          | 326       | 326       | 4              | 34                |                | GUE          | 205       | 204       | 5              | 58                |
|              | M×S          | 407       | 403       | 4              | 40                |                | GUM          | 215       | 214       | 3              | 26                |
|              | NIC          | 250       | 250       | 2              | 26                |                | NBN          | 187       | 187       | 2              | 21                |
|              | RME          | 344       | 342       | 3              | 34                |                | <i>total</i> | 1033      | 1029      | 12             | 125               |
|              | SAR          | 363       | 361       | 4              | 42                |                |              |           |           |                |                   |
| TER          | 339          | 338       | 4         | 40             | Asia              | BEZ            | 13           | 13        | 1         | 10             |                   |
| <i>total</i> | 6116         | 6093      | 75        | 759            |                   | JAT            | 83           | 83        | 2         | 20             |                   |
|              |              |           |           |                |                   | KAC            | 53           | 53        | 1         | 10             |                   |
| Europe       | CRS          | 359       | 358       | 3              |                   | 22             | KIL          | 249       | 249       | 2              | 20                |
|              | FSS          | 361       | 359       | 2              |                   | 15             | KLS          | 255       | 253       | 2              | 21                |
|              | LNR          | 345       | 343       | 7              |                   | 69             | PAT          | 126       | 126       | 3              | 26                |
|              | MLG          | 387       | 385       | 4              | 50                | TAP            | 95           | 95        | 3         | 31             |                   |
|              | PTV          | 345       | 345       | 4              | 49                | <i>total</i>   | 874          | 872       | 14        | 138            |                   |
|              | PYR          | 308       | 304       | 1              | 11                |                |              |           |           |                |                   |
|              | <i>total</i> | 2105      | 2094      | 21             | 216               | Brazil         | CAN          | 258       | 258       | 5              | 52                |

**Supplementary Table S3** Gene enrichment analysis based on annotated genes within HRR islands. Per each HRR island, the table reports the type of process (type), the GO and KEGG analysis output (term), genes involved in given term (genes), the significance level ( $> 0.05$ ) of the gene-term enrichment (p-value), the measure of the enrichment's magnitude (Fold Enrichment) and the correction of significance levels for multiple observations (Bonferroni p-value). For the full definition of breeds, see Table 1. BP = Biological process; CC = Cellular component; MF = Molecular function; KP = KEGG pathway.

| HRR island | Type | Term                                                                               | Genes                      | p-value | Fold enrichment | Bonferroni p-value |
|------------|------|------------------------------------------------------------------------------------|----------------------------|---------|-----------------|--------------------|
| CHI3-D     | BP   | GO:0030183~B cell differentiation                                                  | <i>GON4L, YY1AP1</i>       | 0.049   | 35.78           | 1.000              |
| CHI7-A     | BP   | GO:0051960~regulation of nervous system development                                | <i>LRRTM2, CTNNA1</i>      | 0.043   | 23.38           | 0.982              |
| CHI7-C     | BP   | GO:0045935~positive regulation of nucleobase-containing compound metabolic process | <i>NSD1, UIMC1, FGFR4</i>  | 0.038   | 7.15            | 0.998              |
|            | BP   | GO:0051173~positive regulation of nitrogen compound metabolic process              | <i>NSD1, UIMC1, FGFR4</i>  | 0.045   | 6.53            | 0.999              |
| CHI8-C     | BP   | GO:0032649~regulation of interferon-gamma production                               | <i>CD274, JAK2</i>         | 0.012   | 107.34          | 0.966              |
|            | BP   | GO:1903555~regulation of tumor necrosis factor superfamily cytokine production     | <i>CD274, JAK2</i>         | 0.017   | 78.78           | 0.990              |
|            | BP   | GO:0046631~alpha-beta T cell activation                                            | <i>CD274, JAK2</i>         | 0.017   | 78.78           | 0.990              |
|            | BP   | GO:0042098~T cell proliferation                                                    | <i>CD274, JAK2</i>         | 0.021   | 64.57           | 0.996              |
|            | BP   | GO:0050870~positive regulation of T cell activation                                | <i>CD274, JAK2</i>         | 0.022   | 61.34           | 0.997              |
|            | BP   | GO:0050670~regulation of lymphocyte proliferation                                  | <i>CD274, JAK2</i>         | 0.023   | 58.82           | 0.998              |
|            | BP   | GO:0032944~regulation of mononuclear cell proliferation                            | <i>CD274, JAK2</i>         | 0.023   | 57.25           | 0.998              |
|            | BP   | GO:1903039~positive regulation of leukocyte cell-cell adhesion                     | <i>CD274, JAK2</i>         | 0.024   | 55.76           | 0.999              |
|            | BP   | GO:0070663~regulation of leukocyte proliferation                                   | <i>CD274, JAK2</i>         | 0.025   | 54.01           | 0.999              |
|            | BP   | GO:0022409~positive regulation of cell-cell adhesion                               | <i>CD274, JAK2</i>         | 0.028   | 47.44           | 1.000              |
|            | BP   | GO:0046651~lymphocyte proliferation                                                | <i>CD274, JAK2</i>         | 0.029   | 46.42           | 1.000              |
|            | BP   | GO:0051251~positive regulation of lymphocyte activation                            | <i>CD274, JAK2</i>         | 0.029   | 45.92           | 1.000              |
|            | BP   | GO:0045862~positive regulation of proteolysis                                      | <i>PLGRKT, JAK2</i>        | 0.031   | 42.09           | 1.000              |
|            | BP   | GO:0002696~positive regulation of leukocyte activation                             | <i>CD274, JAK2</i>         | 0.033   | 40.13           | 1.000              |
|            | BP   | GO:0050863~regulation of T cell activation                                         | <i>CD274, JAK2</i>         | 0.034   | 38.86           | 1.000              |
|            | BP   | GO:0050867~positive regulation of cell activation                                  | <i>CD274, JAK2</i>         | 0.035   | 38.00           | 1.000              |
|            | BP   | GO:1903037~regulation of leukocyte cell-cell adhesion                              | <i>CD274, JAK2</i>         | 0.038   | 34.91           | 1.000              |
|            | BP   | GO:0007159~leukocyte cell-cell adhesion                                            | <i>CD274, JAK2</i>         | 0.042   | 31.34           | 1.000              |
|            | BP   | GO:0051249~regulation of lymphocyte activation                                     | <i>CD274, JAK2</i>         | 0.046   | 28.91           | 1.000              |
|            | CC   | GO:0044459~plasma membrane part                                                    | <i>CD274, PLGRKT, JAK2</i> | 0.014   | 8.54            | 0.383              |
|            | KP   | chx05235:PD-L1 expression and PD-1 checkpoint pathway in cancer                    | <i>CD274, JAK2</i>         | 0.010   | 101.10          | 0.220              |

|         |    |                                                                                    |                                               |       |        |       |
|---------|----|------------------------------------------------------------------------------------|-----------------------------------------------|-------|--------|-------|
| CHI11-A | BP | GO:0019219~regulation of nucleobase-containing compound metabolic process          | <i>EFEMP1, PNPT1, PPP4R3B</i>                 | 0.035 | 5.35   | 0.988 |
| CHI11-C | BP | GO:0042472~inner ear morphogenesis                                                 | <i>WDPCP, OTX1</i>                            | 0.006 | 159.02 | 0.377 |
|         | BP | GO:0042471~ear morphogenesis                                                       | <i>WDPCP, OTX1</i>                            | 0.008 | 130.11 | 0.439 |
|         | BP | GO:0048839~inner ear development                                                   | <i>WDPCP, OTX1</i>                            | 0.011 | 88.83  | 0.572 |
|         | BP | GO:0043583~ear development                                                         | <i>WDPCP, OTX1</i>                            | 0.013 | 76.22  | 0.629 |
|         | BP | GO:0090596~sensory organ morphogenesis                                             | <i>WDPCP, OTX1</i>                            | 0.016 | 61.05  | 0.710 |
|         | BP | GO:0048562~embryonic organ morphogenesis                                           | <i>WDPCP, OTX1</i>                            | 0.018 | 55.05  | 0.747 |
|         | BP | GO:0048568~embryonic organ development                                             | <i>WDPCP, OTX1</i>                            | 0.027 | 37.66  | 0.867 |
|         | BP | GO:0007423~sensory organ development                                               | <i>WDPCP, OTX1</i>                            | 0.032 | 31.04  | 0.914 |
|         | BP | GO:0048598~embryonic morphogenesis                                                 | <i>WDPCP, OTX1</i>                            | 0.035 | 28.43  | 0.932 |
| CHI12-A | BP | GO:1990349~gap junction-mediated intercellular transport                           | <i>GJB2, GJA3, GJB6</i>                       | 0.000 | 552.04 | 0.002 |
|         | BP | GO:1902585~single-organism intercellular transport                                 | <i>GJB2, GJA3, GJB6</i>                       | 0.000 | 552.04 | 0.002 |
|         | BP | GO:0051253~negative regulation of RNA metabolic process                            | <i>PSPC1, ZMYM5, SAP18, MPHOSPH8</i>          | 0.030 | 5.28   | 0.999 |
|         | BP | GO:0045934~negative regulation of nucleobase-containing compound metabolic process | <i>PSPC1, ZMYM5, SAP18, MPHOSPH8</i>          | 0.043 | 4.57   | 1.000 |
|         | BP | GO:0031324~negative regulation of cellular metabolic process                       | <i>LATS2, PSPC1, ZMYM5, SAP18, MPHOSPH8</i>   | 0.047 | 3.22   | 1.000 |
|         | CC | GO:0005922~connexin complex                                                        | <i>GJB2, GJA3, GJB6</i>                       | 0.000 | 120.96 | 0.019 |
|         | CC | GO:0044430~cytoskeletal part                                                       | <i>IFT88, PARP4, LATS2, GJB6, CENPJ, SKA3</i> | 0.020 | 3.37   | 0.815 |
|         | CC | GO:0098797~plasma membrane protein complex                                         | <i>GJB2, GJA3, GJB6</i>                       | 0.023 | 11.77  | 0.856 |
|         | CC | GO:0044450~microtubule organizing center part                                      | <i>IFT88, LATS2, CENPJ</i>                    | 0.025 | 11.34  | 0.875 |
|         | CC | GO:0015630~microtubule cytoskeleton                                                | <i>IFT88, PARP4, LATS2, CENPJ, SKA3</i>       | 0.031 | 3.80   | 0.921 |
|         | CC | GO:0005819~spindle                                                                 | <i>PARP4, LATS2, SKA3</i>                     | 0.046 | 8.09   | 0.980 |
|         | MF | GO:0022829~wide pore channel activity                                              | <i>GJB2, GJA3, GJB6</i>                       | 0.000 | 136.85 | 0.006 |
| CHI13-B | BP | GO:0051347~positive regulation of transferase activity                             | <i>PRNP, PCNA, RASSF2, PRP</i>                | 0.003 | 25.93  | 0.396 |

|         |    |                                                                                                        |                                                                                           |       |        |       |
|---------|----|--------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------|-------|--------|-------|
| CHI16-D | BP | GO:0061756~leukocyte adhesion to vascular endothelial cell                                             | <i>SELP, SELL, SELE</i>                                                                   | 0.000 | 234.20 | 0.003 |
|         | BP | GO:0045123~cellular extravasation                                                                      | <i>SELP, SELL, SELE</i>                                                                   | 0.000 | 164.44 | 0.007 |
|         | BP | GO:0050900~leukocyte migration                                                                         | <i>SELP, SELL, SELE</i>                                                                   | 0.002 | 31.94  | 0.173 |
|         | BP | GO:0007159~leukocyte cell-cell adhesion                                                                | <i>SELP, SELL, SELE</i>                                                                   | 0.003 | 28.21  | 0.215 |
|         | BP | GO:0016339~calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules            | <i>SELP, SELL</i>                                                                         | 0.004 | 429.37 | 0.290 |
|         | BP | GO:0007157~heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules                 | <i>SELP, SELE</i>                                                                         | 0.007 | 234.20 | 0.467 |
|         | BP | GO:0016477~cell migration                                                                              | <i>SELP, SELL, SELE</i>                                                                   | 0.029 | 8.18   | 0.935 |
|         | BP | GO:0007596~blood coagulation                                                                           | <i>SELP, F5</i>                                                                           | 0.037 | 42.23  | 0.970 |
|         | CC | GO:0031091~platelet alpha granule                                                                      | <i>SELP, F5</i>                                                                           | 0.006 | 257.04 | 0.203 |
|         | CC | GO:0005887~integral component of plasma membrane                                                       | <i>SELP, SELL, SELE</i>                                                                   | 0.024 | 9.71   | 0.570 |
|         | CC | GO:0031226~intrinsic component of plasma membrane                                                      | <i>SELP, SELL, SELE</i>                                                                   | 0.027 | 9.02   | 0.622 |
|         | MF | GO:0033691~sialic acid binding                                                                         | <i>SELP, SELE</i>                                                                         | 0.003 | 609.94 | 0.036 |
|         | KP | chx04514:Cell adhesion molecules                                                                       | <i>SELP, SELL, SELE</i>                                                                   | 0.003 | 26.80  | 0.058 |
|         | KP | chx05144:Malaria                                                                                       | <i>SELP, SELE</i>                                                                         | 0.029 | 57.03  | 0.410 |
| CHI18-A | BP | GO:0033365~protein localization to organelle                                                           | <i>RIPOR1, ACD, PARD6A, NUTF2, CTCF</i>                                                   | 0.014 | 4.95   | 0.998 |
|         | BP | GO:0006349~regulation of gene expression by genetic imprinting                                         | <i>PRMT7, CTCF</i>                                                                        | 0.021 | 90.08  | 1.000 |
|         | BP | GO:0071514~genetic imprinting                                                                          | <i>PRMT7, CTCF</i>                                                                        | 0.027 | 68.88  | 1.000 |
|         | CC | GO:0005654~nucleoplasm                                                                                 | <i>EDC4, PLA2G15, DDX28, CENPT, ACD, PRMT7, ESRP2, NFATC3, NUTF2, CTCF, THAP11, PSKH1</i> | 0.025 | 1.90   | 0.863 |
| CHI24-A | BP | GO:0007188~adenylate cyclase-modulating G-protein coupled receptor signaling pathway                   | <i>MC2R, MC5R</i>                                                                         | 0.042 | 39.39  | 1.000 |
|         | BP | GO:0007187~G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger | <i>MC2R, MC5R</i>                                                                         | 0.043 | 38.34  | 1.000 |
|         | MF | GO:0004977~melanocortin receptor activity                                                              | <i>MC2R, MC5R</i>                                                                         | 0.002 | 889.50 | 0.015 |
|         | MF | GO:0008528~G-protein coupled peptide receptor activity                                                 | <i>MC2R, MC5R</i>                                                                         | 0.029 | 51.82  | 0.230 |
| CHI27-B | BP | GO:0018022~peptidyl-lysine methylation                                                                 | <i>NSD3, ASH2L</i>                                                                        | 0.041 | 40.89  | 0.999 |
|         | BP | GO:0016571~histone methylation                                                                         | <i>NSD3, ASH2L</i>                                                                        | 0.045 | 37.17  | 1.000 |
|         | MF | GO:0008170~N-methyltransferase activity                                                                | <i>NSD3, ASH2L</i>                                                                        | 0.045 | 37.65  | 0.599 |
|         | MF | GO:0008276~protein methyltransferase activity                                                          | <i>NSD3, ASH2L</i>                                                                        | 0.047 | 35.88  | 0.617 |