



Supplementary Tables: Multi-ancestry genome-wide association study of major depression aids locus discovery, fine mapping, gene prioritization and causal inference

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Supplementary Table 1. Descriptive characteristics of the datasets included in this study.

| Study | Type of data | Ancestry | Location | N cases | N controls | Depression definition | Depression measure | Cut on for phenotype definition | Clinical Depression | Gender (% female) | Age (mean, SD) | ChrX available |
|--|--------------------|-------------------------|--|---------|------------|-----------------------|--|--|---------------------|-------------------|----------------|----------------|
| China Kadoorie Biobank | Summary statistics | East Asian | Gansu, Haikou, Harbin, Henan, Hunan, Liuzhou, Qingdao, Sichuan, Suzhou, Zhejiang | 5,376 | 69,998 | Symptom-based | CIDI-A trigger symptoms | Had experienced at least one of the four CIDI trigger symptoms | No | 44847 (59.5%) | 52.2 (10.7) | |
| CONVERGE | Summary statistics | East Asian | Hainan, Beijing, Chongqing | 5,303 | 5,337 | Structured interview | Psychiatric diagnosis (ICD10) | | Yes | 10640 (100%) | 46.1 (N/A) | Yes |
| 23andMe | Summary statistics | East Asian | USA | 2,729 | 90,310 | Self-report | Self-reported diagnosis | | No | 56708 (60.95%) | N/A | Yes |
| | | African | USA | 5,045 | 102,098 | | | | | 62049 (57.91%) | N/A | No |
| * Taiwan Major Depressive Disorder study - Platform 1 and Platform 2 | Summary statistics | East Asian | Taiwan | 988 | 6,075 | Multiple | DSM-IV/self-reported | | No | 5596 (57.5%) | 49.2 (11.3) | No |
| | | | | 360 | 2,317 | | | | | | | No |
| Women's Health Initiative | Raw genotype data | East Asian | USA | 454 | 2,553 | Symptom-based | 6-item CES-D | >=5 | No | 3007 (100%) | 62.7 (7.5) | Yes |
| | | African | | 1,790 | 7,622 | | | | | 9412 (100%) | 61.5 (7.1) | Yes |
| | | Hispanic/Latin American | | 1,218 | 3,254 | | | | | 4472 (100%) | 60.3 (6.7) | Yes |
| Intern Health Study | Raw genotype data | East Asian | USA | 294 | 544 | Symptom-based | PHQ-9 | >=10 | No | 459 (54.8%) | 27.4 (2.4) | No |
| | | African | | 98 | 188 | | | | | 181 (63.3%) | 27.8 (2.7) | No |
| | | South Asian | | 253 | 438 | | | | | 324 (46.9%) | 26.6 (2.1) | No |
| UK Biobank | Raw genotype data | East Asian | UK | 133 | 366 | Structured interview | Lifetime CIDI/ICD10 | | Yes | 360 (72.1%) | 52.1 (7.3) | No |
| | | African | | 505 | 904 | | | | | 859 (61%) | 50.7 (7.4) | No |
| | | South Asian | | 504 | 804 | | | | | 573 (43.8%) | 53.0 (8.3) | No |
| Army-STARRS | Raw genotype data | East Asian | USA | 74 | 442 | Structured interview | CIDI (DSM MDE) | | Yes | 66 (12.5%) | 24.5 (6.3) | No |
| | | African | | 172 | 1,856 | | | | | 434 (21.4%) | 23.5 (5.7) | No |
| | | Hispanic/Latin American | | 338 | 2,547 | | | | | 444 (15.4%) | 22.8 (5.1) | No |
| BioMe | Summary statistics | East Asian | USA | 60 | 835 | Medical records | ICD10 | | Yes | 58.7%** | 58.9** (N/A) | No |
| | | African | | 1,613 | 6,399 | | | | | | | |
| | | Hispanic/Latin American | | 95 | 8,553 | | | | | | | No |
| Genes & Health | Summary statistics | South Asian | UK | 3,748 | 25,934 | Medical records | ICD10 | | Yes | | | Yes |
| Biobank Japan | Summary statistics | East Asian | Japan | 3,893 | 174,747 | Multiple | medical history or prescribed medication | | No | N/A (46.3%)** | 63.0 (N/A)** | Yes |
| Million Veteran Program | Summary statistics | African | USA | 25,843 | 33,757 | Medical records | ICD9/10 codes | | Yes | N/A | N/A | No |
| | | East Asian | | 2,090 | 3,710 | | | | | N/A | N/A | No |
| † Australian Genetics of Depression Study (AGDS) | Summary statistics | European | Australia | 12,123 | 12,684 | Self-report | DSM-5 | | Yes | 9836 (75.1%) | 44.1 (15.1) | No |
| Genetic Epidemiology Research on Aging | Raw genotype data | East Asian | USA | 226 | 3,722 | Medical records | ICD9 | | Yes | 1627 41.2%) | N/A | Yes |
| | | African | | 206 | 1,598 | | | | | 662 (36.7%) | N/A | Yes |
| | | Hispanic/Latin American | | 415 | 2,808 | | | | | 1249 (38.8%) | N/A | Yes |
| Jackson Heart Study | Raw genotype data | African | USA | 299 | 990 | Symptom-based | 20-item CES-D | >=16 | No | 820 (63.6%) | 55.2 (12.2) | No |
| Drakenstein Child Health Study | Raw genotype data | African | South Africa | 139 | 346 | Symptom-based | BDI-II score | >=20 | No | 485 (100%) | 26.4 (5.6) | No |
| Vanderbilt University Biobank (BioVU) | Summary statistics | African | USA | 998 | 4,938 | Medical records | ICD9/10 codes | | Yes | N/A | N/A | No |

| | | | | | | | | | | | | |
|--|--------------------|-------------------------|----------|---------|---------|----------------------|--|--|--|---------------|-------------|-----|
| Hispanic Community Health Study/Study of Latinos | Summary statistics | Hispanic/Latin American | USA | 3,979 | 6,499 | Symptom-based | 10-item CES-D | cases >=10; controls <=6 | No | 7264 (59%)** | 46 (14)** | Yes |
| Detroit Neighborhood Health Study (DNHS) | Raw genotype data | African | USA | 58 | 436 | Symptom-based | PHQ-9 | no cut-off score - The study used PHQ-9 to identify a MDD case using DSM-IV criteria | No | 288 (58.3%) | 53.2 (16.6) | No |
| Prevention Intervention Research Center (PIRC) 1st Generation Trial | Summary statistics | African | USA | 52 | 547 | Structured interview | DIS-III-R | | Yes | 629 (58.5%)** | 29 (N/A) | No |
| Mexican Adolescent Mental Health Survey (MAMHS) | Summary statistics | Hispanic/Latin American | Mecico | 105 | 996 | Structured interview | Computer assisted version of adolescent CIDI (DSM IV criteria) | | Yes | 757 (68.8%) | 14.28 (N/A) | No |
| Pregnancy Outcomes, Maternal and Infant Study (PROMIS) | Summary statistics | Hispanic/Latin American | Peru | 1,076 | 2,328 | Symptom-based | PHQ-9 | no cut-off score - The study used depression severity scores. As a symptom measure, the scores ranged from 0 to 27 (mean PHQ-9 score was 8.2 (SD=5.3)) | No | 3404 (100%) | 28.2 (6.3) | No |
| ‡ Psychiatric Genomics Consortium Major Depressive Disorder 2 Study (PGC-MDD2) | Summary statistics | European | Multiple | 246,241 | 558,568 | Multiple | Multiple | | Yes (except for UKB and 23andMe Europeans) | N/A | N/A | No |

* The Taiwan Major Depressive Disorder study - Platform 1 and Platform 2 studies are considered and counted as one study.

† The AGDS includes samples of European ancestry only, and therefore it is not included in the set of 21 studies with ancestrally diverse participants, used for our primary analyses. Data from the ADGS were included in our multi-ancestry meta-analysis of MD.

‡ The PGC-MDD2 includes samples of European ancestry only, and therefore it is not included in the set of 21 studies with ancestrally diverse participants, used for our primary analyses. Data from the PGC-MDD2 were included in our multi-ancestry meta-analysis of MD.

N= number; SD= standard deviation; N/A= not available. **These numbers correspond to the overall dataset.

PGC MDD2: published data from Howard D.M., et al. (<https://www.nature.com/articles/s41593-018-0326-7>), please refer to the previous publication for detailed information.

Supplementary Table 2. Estimates of inflation for the different analyses

| Analysis | Outcome | lambda1 (LDSC) | Number of SNPs used to compute lambda1 | lambda2 (GenABEL) | Number of SNPs used to compute lambda2 | lambda1000 | LDSC intercept |
|---------------------------------------|---------------------------|----------------|--|-------------------|--|------------|----------------|
| Multi-ancestry meta-analysis | broad major depression | 1.687 | 1200864 | 1.573 | 9280125 | 1.001 | 1.019 |
| African ancestry meta-analysis | broad major depression | 1.0679 | 1079112 | 1.038 | 17147808 | 1.001 | 1.0357 |
| East Asian ancestry meta-analysis | broad major depression | 1.068 | 966673 | 1.045 | 8580346 | 1.002 | 1.0261 |
| South Asian ancestry meta-analysis | broad major depression | 1.017 | 971699 | 1.008 | 5723806 | 1.002 | 1.0139 |
| Hispanic/Latin American meta-analysis | broad major depression | 1.1491 | 1091289 | 1.092 | 13936624 | 1.002 | 1.05 |
| Multi-ancestry meta-analysis | clinical major depressior | 1.3169 | 243773 | 1.091 | 18477306 | 1.001 | 1.001 |
| African ancestry meta-analysis | clinical major depressior | 1.0405 | 693128 | 1.027 | 15113389 | 1.001 | 1.0283 |
| East Asian ancestry meta-analysis | clinical major depressior | 1.0649 | 424203 | 1.046 | 7675198 | 1.005 | 1.0228 |
| South Asian ancestry meta-analysis | clinical major depressior | 1.0165 | 912493 | 1.005 | 5344716 | 1.001 | 1.0142 |
| Hispanic/Latin American meta-analysis | clinical major depressior | 1.0016 | 1083897 | 1.002 | 10753379 | 1.001 | 1.0007 |

Lambda GC calculated by LDSC: first merge summary statistics with a 1.2m SNPs list of HapMap 3, and calculate lambda GC, LDSC intercept with the LDSC regression

Lambda GC calculated by the GenABEL R package: estlambda(df\$P,proportion=0.95)

Lambda 1000 were calculated with the reported lambda GC values.

Supplementary Table 3. Colocalisation of genes at 2q24.2 and 6q16.2 locus.

| Gene | Ensembl ID | nsnps | PP.H0.abf | PP.H1.abf | PP.H2.abf | PP.H3.abf | PP.H4.abf | QTLdataset | Ancestry | PMID |
|---------|---------------|-------|-----------|-----------|-----------|-----------|-----------|----------------|-------------------|----------|
| MCHR2 | ENSG000001520 | N/A | | | | | | | | |
| ASCC3 | ENSG000001122 | 4579 | 0.00% | 0.00% | 6.50% | 93.46% | 0.04% | mmQTL_brain | African | 3.5E+07 |
| GRIK2 | ENSG000001644 | 2312 | 3.75% | 0.13% | 92.33% | 3.22% | 0.58% | mmQTL_brain | African | 3.5E+07 |
| SIM1 | ENSG000001122 | N/A | | | | | | mmQTL_brain | African | 3.5E+07 |
| ASCC3 | ENSG000001122 | 5088 | 0.00% | 0.00% | 0.03% | 99.97% | 0.00% | mmQTL_brain | European | 3.5E+07 |
| GRIK2 | ENSG000001644 | 2645 | 0.00% | 3.65% | 0.03% | 91.04% | 5.28% | mmQTL_brain | European | 3.5E+07 |
| SLC4A11 | ENSG000001442 | N/A | | | | | | mmQTL_brain | European | 3.5E+07 |
| DPP4 | ENSG000001976 | 4158 | 0.00% | 0.00% | 4.45% | 95.54% | 0.01% | mmQTL_brain | European | 3.5E+07 |
| GCG | ENSG000001152 | N/A | | | | | | mmQTL_brain | European | 3.5E+07 |
| TBR1 | ENSG000001365 | N/A | | | | | | mmQTL_brain | European | 3.5E+07 |
| PSMD14 | ENSG000001152 | 4540 | 0.87% | 44.60% | 1.02% | 51.94% | 1.57% | mmQTL_brain | European | 3.5E+07 |
| RBMS1 | ENSG000001532 | 3604 | 0.02% | 1.24% | 1.82% | 96.11% | 0.81% | mmQTL_brain | European | 3.5E+07 |
| TANK | ENSG000001365 | 4698 | 0.00% | 0.15% | 1.89% | 97.85% | 0.10% | mmQTL_brain | European | 3.5E+07 |
| TBR1 | ENSG000001365 | N/A | | | | | | mmQTL_brain | European | 3.5E+07 |
| DPP4 | ENSG000001976 | 3900 | 0.00% | 0.00% | 0.30% | 99.70% | 0.00% | mmQTL_brain | Hispanic/Latin Am | 3.5E+07 |
| PSMD14 | ENSG000001152 | 4481 | 0.14% | 45.58% | 0.16% | 51.48% | 2.65% | mmQTL_brain | Hispanic/Latin Am | 3.5E+07 |
| RBMS1 | ENSG000001532 | 3785 | 0.01% | 1.27% | 0.58% | 97.98% | 0.16% | mmQTL_brain | Hispanic/Latin Am | 3.5E+07 |
| TANK | ENSG000001365 | 4649 | 0.00% | 0.08% | 0.30% | 99.61% | 0.01% | mmQTL_brain | Hispanic/Latin Am | 3.5E+07 |
| MCHR2 | ENSG000001520 | 857 | 5.73% | 82.61% | 0.40% | 5.74% | 5.52% | eqtl_blood_gen | African | 32220292 |
| ASCC3 | ENSG000001122 | 1961 | 0.00% | 0.00% | 96.68% | 2.69% | 0.62% | eqtl_blood_gen | African | 32220292 |
| GRIK2 | ENSG000001644 | 339 | 97.73% | 0.36% | 1.88% | 0.01% | 0.02% | eqtl_blood_gen | African | 32220292 |
| SIM1 | ENSG000001122 | 748 | 93.57% | 1.08% | 5.20% | 0.06% | 0.09% | eqtl_blood_gen | African | 32220292 |
| MCHR2 | ENSG000001520 | N/A | | | | | | eqtlgen_blood_ | European | 34475573 |
| ASCC3 | ENSG000001122 | 4880 | 0.00% | 0.00% | 0.03% | 99.97% | 0.00% | eqtlgen_blood_ | European | 34475573 |
| GRIK2 | ENSG000001644 | N/A | | | | | | eqtlgen_blood_ | European | 34475573 |
| SIM1 | ENSG000001122 | N/A | | | | | | eqtlgen_blood_ | European | 34475573 |

| | | | | | | | | | | |
|--------------|----------------------|-------------|--------------|--------------|--------------|---------------|--------------|-----------------|--------------------------|----------|
| SLC4A1 | ENSG000001442 | 4564 | 0.66% | 17.66% | 2.93% | 78.54% | 0.21% | eqlgen_blood_ | European | 34475573 |
| DPP4 | ENSG000001976 | N/A | | | | | | eqlgen_blood_ | European | 34475573 |
| GCG | ENSG000001152 | N/A | | | | | | eqlgen_blood_ | European | 34475573 |
| TBR1 | ENSG000001365 | N/A | | | | | | eqlgen_blood_ | European | 34475573 |
| PSMD1 | ENSG000001152 | 4675 | 0.02% | 1.09% | 1.26% | 69.37% | 28.26% | eqlgen_blood_ | European | 34475573 |
| RBMS1 | ENSG000001532 | N/a | | | | | | eqlgen_blood_ | European | 34475573 |
| TANK | ENSG000001365 | N/a | | | | | | eqlgen_blood_ | European | 34475573 |
| TBR1 | ENSG000001365 | N/a | | | | | | eqlgen_blood_ | European | 34475573 |
| PSMD1 | ENSG000001152 | 4388 | 0.23% | 69.25% | 0.08% | 24.71% | 5.74% | mesa_his | Hispanic/Latin Am | 35202437 |
| RBMS1 | ENSG000001532 | 3631 | 0.00% | 0.17% | 0.69% | 99.12% | 0.02% | mesa_his | Hispanic/Latin Am | 35202437 |
| TANK | ENSG000001365 | 4374 | 0.22% | 67.30% | 0.09% | 26.40% | 5.99% | mesa_his | Hispanic/Latin Am | 35202437 |
| TANK | ENSG000001365 | N/A | | | | | | afr_pqtl_blood | African | 35501419 |
| DPP4 | ENSG000001976 | N/A | | | | | | afr_pqtl_blood | African | 35501419 |
| GCG | ENSG000001152 | N/A | | | | | | afr_pqtl_blood | African | 35501419 |
| TANK | ENSG000001365 | N/A | | | | | | eur_pqtl_blood | European | 35501419 |
| DPP4 | ENSG000001976 | N/A | | | | | | eur_pqtl_blood | European | 35501419 |
| GCG | ENSG000001152 | N/A | | | | | | eur_pqtl_blood | European | 35501419 |
| GCG | ENSG000001152 | 17 (Not eno | 99.73% | 0.05% | 0.21% | 0.00% | 0.01% | his_pqtl_blood | Hispanic/Latin Am | 35202437 |

PP= posterior probability; QTLdataset= shortname of the study; nsnp= number of SNPs; Ensembl= Ensembl ID of the gene; Gene= Symbol of the Gene; PMID= PubMed reference number

H0: no association with either trait in the region

H1: association with trait 1 only

H2: association with trait 2 only

H3: both traits are associated, but have different single causal variants

H4: both traits are associated and share the same single causal variant

The colocalization analysis was performed to obtain shared causal loci posterior probability of H3/H4 hypothesis (i.e. both traits -depression and tissue specific QTLs are associated and share H3 - two linked variants, or H4 - a single causal variant). The table shows the probability (H0-

H4) for gene (e) or protein (p) expression from blood and brain tissues from different QTL studies (see PMID column). The genes that were not found in the tissue are denoted as N/A. The genes with H3/H4 probability >90% are highlighted in red.

Supplementary Table 4. 196* loci identified in European ancestry analysis and their results in our multi ancestry meta-analysis.

| SNP | CHR | BP | EA | NEA | Multi ancestry meta-analysis | | | | | | | | | | | | |
|-----------|-----|----------|----|-----|------------------------------|---------|--------|----------|--------------|----------|---------|--------|----------|-------------|---------|--------|----------|
| | | | | | European meta-analysis | | | | | Broad MD | | | | Clinical MD | | | |
| | | | | | EAF | BETA | SE | P value | Source study | EAF | BETA | SE | P value | EAF | BETA | SE | P value |
| rs301799 | 1 | 8489302 | T | C | 0.5694 | -0.0258 | 0.0035 | 3.67E-14 | AGDS | 0.5894 | -0.0252 | 0.0031 | 7.96E-16 | 0.6031 | -0.0256 | 0.0063 | 4.49E-05 |
| rs2089358 | 1 | 37194103 | T | C | 0.7002 | -0.026 | 0.0038 | 4.37E-12 | AGDS | 0.635 | -0.0249 | 0.0034 | 3.97E-13 | 0.5579 | -0.0207 | 0.007 | 0.003156 |
| rs1466887 | 1 | 37709328 | T | C | 0.5511 | -0.019 | 0.0035 | 4.17E-08 | AGDS | 0.5502 | -0.018 | 0.0031 | 8.74E-09 | 0.5171 | -0.0148 | 0.0064 | 0.02053 |
| rs7534271 | 1 | 47693981 | C | G | 0.4051 | 0.0169 | 0.0035 | 3.42E-08 | MVP | 0.4398 | 0.0153 | 0.0033 | 4.35E-06 | 0.5082 | 0.0099 | 0.0069 | 0.1517 |
| rs1710547 | 1 | 49528403 | A | C | 0.0978 | -0.0359 | 0.0058 | 4.27E-10 | MVP | 0.1264 | -0.0366 | 0.005 | 4.07E-13 | 0.137 | -0.0504 | 0.0112 | 6.86E-06 |
| rs1157924 | 1 | 50559162 | A | G | 0.907 | 0.0394 | 0.0059 | 3.29E-11 | AGDS | 0.8674 | 0.0411 | 0.005 | 3.79E-16 | 0.8592 | 0.0554 | 0.0115 | 1.34E-06 |
| rs1890946 | 1 | 52342427 | T | C | 0.4671 | -0.0232 | 0.0034 | 1.40E-11 | AGDS | 0.4698 | -0.022 | 0.0031 | 2.04E-12 | 0.5121 | -0.0177 | 0.0064 | 0.005311 |
| rs2568960 | 1 | 72812249 | A | G | 0.3843 | -0.0377 | 0.0035 | 1.30E-27 | AGDS | 0.3749 | -0.0337 | 0.0031 | 4.68E-27 | 0.3885 | -0.0322 | 0.0063 | 2.87E-07 |
| rs1213698 | 1 | 73725998 | T | G | 0.5042 | -0.0291 | 0.0035 | 7.16E-17 | AGDS | 0.5307 | -0.0272 | 0.003 | 2.61E-19 | 0.5744 | -0.0324 | 0.0064 | 4.39E-07 |
| rs1131885 | 1 | 80809636 | A | G | 0.2845 | 0.0221 | 0.0038 | 1.05E-08 | AGDS | 0.2749 | 0.0205 | 0.0034 | 2.31E-09 | 0.2654 | 0.0191 | 0.007 | 0.006153 |
| rs1091311 | 1 | 1.76E+08 | T | C | 0.3751 | -0.0253 | 0.0036 | 4.27E-13 | AGDS | 0.3664 | -0.0221 | 0.0034 | 1.19E-10 | 0.3403 | -0.0204 | 0.0076 | 0.006844 |
| rs7272489 | 1 | 1.77E+08 | C | G | 0.0873 | 0.0411 | 0.0061 | 2.30E-11 | AGDS | 0.0921 | 0.0337 | 0.0051 | 5.85E-11 | 0.0958 | 0.0224 | 0.0102 | 0.02857 |
| rs169235 | 1 | 1.82E+08 | A | G | 0.7525 | -0.022 | 0.004 | 2.15E-08 | AGDS | 0.7467 | -0.0219 | 0.0035 | 5.64E-10 | 0.7318 | -0.0268 | 0.0071 | 0.000165 |
| rs1684184 | 1 | 1.98E+08 | A | C | 0.2158 | -0.0297 | 0.0042 | 1.03E-13 | MVP | 0.2075 | -0.0239 | 0.0037 | 1.55E-10 | 0.1976 | -0.01 | 0.0081 | 0.2164 |
| rs2062479 | 1 | 1.98E+08 | C | G | 0.5283 | 0.0117 | 0.0036 | 3.00E-08 | MVP | 0.5181 | 0.0082 | 0.0031 | 0.008767 | 0.4702 | -0.0066 | 0.0071 | 0.3554 |
| rs4846898 | 1 | 2.3E+08 | A | G | 0.5983 | -0.0167 | 0.0035 | 2.95E-08 | MVP | 0.5892 | -0.0161 | 0.0032 | 6.19E-07 | 0.5717 | -0.0166 | 0.0061 | 0.006529 |
| rs1463980 | 2 | 22567003 | A | G | 0.4931 | -0.0224 | 0.0034 | 2.37E-11 | AGDS | 0.462 | -0.0205 | 0.0032 | 2.18E-10 | 0.4159 | -0.0194 | 0.0068 | 0.004234 |
| rs7589705 | 2 | 51095502 | T | G | 0.0525 | 0.037 | 0.0079 | 2.76E-08 | MVP | 0.0512 | 0.0345 | 0.0076 | 5.16E-06 | 0.0639 | 0.0103 | 0.0167 | 0.5378 |
| rs4971586 | 2 | 52315585 | A | T | 0.4933 | -0.0188 | 0.0035 | 3.38E-08 | AGDS | 0.506 | -0.0144 | 0.003 | 1.97E-06 | 0.5259 | -0.0192 | 0.0064 | 0.002519 |
| rs1568452 | 2 | 58012833 | T | C | 0.3857 | 0.0257 | 0.0035 | 2.10E-13 | AGDS | 0.3704 | 0.0238 | 0.0031 | 2.80E-14 | 0.3382 | 0.0221 | 0.0065 | 0.000718 |
| rs4852252 | 2 | 71539301 | T | C | 0.4317 | -0.0185 | 0.0035 | 2.85E-08 | AGDS | 0.4713 | -0.017 | 0.003 | 1.97E-08 | 0.5266 | -0.0156 | 0.0063 | 0.01378 |
| rs7586028 | 2 | 86819409 | T | C | 0.845 | -0.0276 | 0.0047 | 8.52E-09 | AGDS | 0.8135 | -0.0236 | 0.0041 | 1.17E-08 | 0.7524 | -0.0236 | 0.0079 | 0.002706 |
| rs2582954 | 2 | 1.04E+08 | T | C | 0.4018 | -0.0191 | 0.0035 | 1.84E-08 | AGDS | 0.424 | -0.0151 | 0.0031 | 1.39E-06 | 0.4212 | -0.0107 | 0.0066 | 0.1038 |
| rs1437336 | 2 | 1.42E+08 | T | G | 0.8991 | -0.0212 | 0.0057 | 2.25E-08 | MVP | 0.8377 | -0.0191 | 0.0045 | 2.60E-05 | 0.7522 | -0.0144 | 0.0081 | 0.07688 |
| rs1226412 | 2 | 1.57E+08 | T | C | 0.7919 | 0.0266 | 0.0042 | 4.56E-10 | AGDS | 0.7609 | 0.0215 | 0.0036 | 3.26E-09 | 0.7126 | 0.0202 | 0.0069 | 0.003549 |
| rs1267042 | 2 | 1.62E+08 | T | C | 0.694 | 0.0201 | 0.0038 | 7.31E-09 | MVP | 0.7005 | 0.0171 | 0.0033 | 2.83E-07 | 0.7149 | 0.0167 | 0.0071 | 0.01844 |
| rs1168689 | 2 | 1.75E+08 | A | T | 0.4391 | -0.0155 | 0.0035 | 4.92E-13 | MVP | 0.4457 | -0.0169 | 0.0031 | 6.60E-08 | 0.4987 | -0.0288 | 0.0068 | 2.51E-05 |
| rs1168137 | 2 | 1.86E+08 | A | G | 0.6058 | 0.0158 | 0.0035 | 1.65E-08 | MVP | 0.6105 | 0.0131 | 0.0031 | 2.82E-05 | 0.6304 | 0.0189 | 0.0068 | 0.005462 |
| rs788022 | 2 | 1.98E+08 | T | C | 0.3262 | 0.0203 | 0.0037 | 1.26E-08 | AGDS | 0.3308 | 0.0189 | 0.0033 | 1.39E-08 | 0.3311 | 0.0187 | 0.0075 | 0.013 |
| rs6218862 | 2 | 2.08E+08 | A | G | 0.3141 | 0.0244 | 0.0037 | 6.46E-11 | AGDS | 0.291 | 0.0222 | 0.0034 | 9.81E-11 | 0.267 | 0.0348 | 0.0073 | 1.95E-06 |
| rs7293160 | 2 | 2.13E+08 | T | C | 0.847 | -0.025 | 0.0048 | 4.56E-08 | AGDS | 0.8539 | -0.0226 | 0.0046 | 1.13E-06 | 0.8583 | -0.0159 | 0.0106 | 0.134 |
| rs2592105 | 2 | 2.34E+08 | C | G | 0.6476 | -0.0147 | 0.0036 | 4.51E-08 | MVP | 0.6607 | -0.0153 | 0.0032 | 2.16E-06 | 0.672 | -0.0137 | 0.007 | 0.05059 |
| rs1331980 | 3 | 44635461 | A | G | 0.3905 | -0.0184 | 0.0035 | 4.17E-13 | MVP | 0.4043 | -0.0182 | 0.0031 | 5.98E-09 | 0.3912 | -0.0134 | 0.0064 | 0.03626 |
| rs1305882 | 3 | 44731730 | A | G | 0.312 | 0.0228 | 0.0037 | 8.16E-10 | AGDS | 0.3107 | 0.0195 | 0.0033 | 4.77E-09 | 0.3241 | 0.0122 | 0.0068 | 0.0736 |
| rs9831648 | 3 | 49214303 | T | G | 0.7725 | -0.0246 | 0.0041 | 4.24E-09 | AGDS | 0.7623 | -0.025 | 0.0036 | 5.94E-12 | 0.7311 | -0.0351 | 0.0073 | 1.48E-06 |
| rs7624336 | 3 | 53244151 | T | G | 0.2089 | 0.0233 | 0.0042 | 2.40E-08 | AGDS | 0.1958 | 0.0207 | 0.0039 | 1.45E-07 | 0.1723 | 0.0074 | 0.0087 | 0.3956 |
| rs843812 | 3 | 61255413 | A | G | 0.41 | 0.0231 | 0.0035 | 3.56E-11 | AGDS | 0.4492 | 0.0208 | 0.0033 | 4.22E-10 | 0.521 | 0.021 | 0.0069 | 0.002202 |
| rs9825208 | 3 | 1.01E+08 | T | G | 0.4462 | -0.0195 | 0.0035 | 2.68E-08 | AGDS | 0.4499 | -0.0157 | 0.003 | 2.15E-07 | 0.4241 | -0.0145 | 0.0063 | 0.02074 |
| rs6783233 | 3 | 1.18E+08 | T | C | 0.2836 | 0.0217 | 0.0038 | 1.04E-08 | AGDS | 0.2701 | 0.0201 | 0.0035 | 1.27E-08 | 0.2587 | 0.021 | 0.0073 | 0.004008 |
| rs827095 | 3 | 1.58E+08 | A | T | 0.5791 | -0.0264 | 0.0035 | 1.32E-14 | AGDS | 0.5522 | -0.0209 | 0.003 | 5.09E-12 | 0.5243 | -0.0197 | 0.0063 | 0.001879 |
| rs827120 | 3 | 1.58E+08 | A | G | 0.5743 | 0.0249 | 0.0035 | 8.21E-13 | MVP | 0.5877 | 0.0195 | 0.003 | 1.19E-10 | 0.5948 | 0.0132 | 0.0061 | 0.0306 |

| | | | | | | | | | | | | | | | | |
|-----------|-------------|---|---|--------|---------|--------|----------|------|--------|---------|--------|----------|--------|---------|--------|----------|
| rs1296714 | 18 53099012 | C | G | 0.6977 | -0.0332 | 0.0038 | 1.28E-18 | AGDS | 0.6383 | -0.0248 | 0.0032 | 1.60E-14 | 0.5595 | -0.0232 | 0.0066 | 0.000475 |
| rs1452787 | 18 53207207 | A | G | 0.7214 | -0.024 | 0.0038 | 1.78E-12 | MVP | 0.7129 | -0.0216 | 0.0033 | 8.83E-11 | 0.728 | -0.0183 | 0.0071 | 0.01047 |
| rs7241572 | 18 77580712 | A | G | 0.201 | 0.0278 | 0.0043 | 1.35E-10 | AGDS | 0.1925 | 0.0268 | 0.0039 | 9.82E-12 | 0.1817 | 0.0306 | 0.0092 | 0.000903 |
| rs33430 | 19 30939443 | A | G | 0.3738 | -0.0204 | 0.0036 | 1.89E-08 | AGDS | 0.4187 | -0.0163 | 0.0031 | 1.89E-07 | 0.4566 | -0.0058 | 0.0063 | 0.3591 |
| rs7497423 | 20 39987612 | A | G | 0.1794 | 0.0269 | 0.0045 | 9.17E-10 | AGDS | 0.1702 | 0.0231 | 0.0041 | 2.37E-08 | 0.1564 | 0.0171 | 0.009 | 0.05585 |
| rs1262443 | 20 44680853 | A | G | 0.2587 | 0.0232 | 0.0039 | 2.49E-09 | AGDS | 0.2529 | 0.0191 | 0.0035 | 6.40E-08 | 0.2369 | 0.0176 | 0.0077 | 0.02146 |
| rs6066242 | 20 45843856 | A | G | 0.6271 | 0.0161 | 0.0036 | 1.36E-10 | MVP | 0.6514 | 0.0175 | 0.0033 | 1.48E-07 | 0.6794 | 0.0277 | 0.0075 | 0.000243 |
| rs6012575 | 20 47598497 | C | G | 0.5901 | 0.0164 | 0.0035 | 1.20E-08 | MVP | 0.6007 | 0.014 | 0.0031 | 7.64E-06 | 0.6155 | 0.0099 | 0.0067 | 0.1395 |
| rs372519 | 21 46574554 | A | G | 0.5318 | 0.0181 | 0.0035 | 2.64E-08 | MVP | 0.5202 | 0.0167 | 0.003 | 3.47E-08 | 0.5129 | 0.0218 | 0.0063 | 0.000545 |
| rs5758265 | 22 41617897 | A | G | 0.2849 | 0.0274 | 0.0038 | 3.55E-13 | AGDS | 0.3041 | 0.0235 | 0.0034 | 7.45E-12 | 0.332 | 0.0162 | 0.0065 | 0.01325 |
| rs7511013 | 22 46447132 | C | G | 0.6719 | 0.0214 | 0.0038 | 2.11E-08 | AGDS | 0.6764 | 0.0214 | 0.0035 | 1.37E-09 | 0.6766 | 0.0286 | 0.0077 | 0.000187 |

MD= Major depression; SNP= Single nucleotide polymorphism; CHR= Chromosome; BP= Base pair; EA= Effect allele; NEA= Non effect allele; EAF= Effect allele frequency; BETA= Regression coefficient; SE= Standard error of BETA
AGDS= Australian Genetics of Depression Study; MVP= Million Veteran Program

Two-sided association P values of z statistics from inverse-variance -weighted fixed-effect model meta-analysis are given.

*Only 196 out of the 206 loci had results in at least one of the ancestry/ethnic groups in our analysis.

Supplementary Table 5. Transferability of 260c Ica previously identified in individuals of European ancestry to individuals of non-European ancestry.

Table with columns for individual ID, sex, and ancestry categories: African ancestry samples, East Asian ancestry samples, Head M, His/LatAm ancestry samples, South Asian ancestry samples, African ancestry samples, CHG/MT, East Asian ancestry samples, and South Asian ancestry samples. Each cell contains a list of SNP IDs and their corresponding p-values.

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------------|----|--------|---|---|----|--------|-----------|--------|---------|--------------|--------------|---------|---------|--------|---------|--------------|--------------|--------|--------|---------|---------|---------|--------------|--------|--------|--------|---------|--------------|--------------|--------|--------|--------|---------|--------------|--------------|---------|---------|--------|---------|--------------|--------------|--------|--------|---------|---------|--------------|--------------|--------|--------|--------|--------|--------------|--------------|
| r1201363 | 10 | 11E+08 | A | G | 4 | 0.1286 | 0.0042 | 0.0152 | 0.7838 | 0.76018 | underpowered | 0.1899 | 0.0188 | 0.0162 | 0.2462 | 0.63395 | underpowered | 0.2838 | 0.0191 | 0.0114 | 0.09443 | 0.83304 | No | 0.4487 | 0.0464 | 0.0247 | 0.06667 | 0.72033 | underpowered | 0.1216 | 0.0107 | 0.0183 | 0.5599 | 0.52326 | underpowered | 0.1127 | 0.0041 | 0.039 | 0.916 | 0.17898 | underpowered | 0.4494 | 0.0421 | 0.0252 | 0.09521 | 0.25915 | underpowered | | | | | | |
| r075123126 | 10 | 11E+08 | T | G | 39 | 0.0313 | -0.08 | 0.1472 | 0.8888 | 0.99399 | No | 0.0208 | 0.056 | 0.049 | 0.1083 | 0.075499 | underpowered | 0.1005 | 0.0556 | 0.0405 | 0.1495 | 0.63861 | underpowered | 0.1014 | 0.027 | 0.0466 | 0.919 | 0.20784 | underpowered | 0.2164 | 0.007 | 0.0145 | 0.9812 | 0.1012 | underpowered | 0.0284 | 0.0811 | 0.0777 | 0.2995 | 0.11837 | underpowered | 0.2409 | 0.0498 | 0.0287 | 0.037 | 0.20496 | underpowered | | | | | | |
| r144113151 | 11 | 3E+024 | A | G | 7 | 0.0106 | -0.0907 | 0.0371 | 0.13245 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | r111413551 | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1844893 | 11 | 3E+024 | A | G | 3 | 0.2985 | -5.00E-04 | 0.001 | 0.986 | 0.70277 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1808043 | 11 | 3E+024 | T | G | 1 | 0.7236 | -0.122 | 0.028 | 0.244 | 0.80896 | No | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r14567834 | 11 | 3E+024 | T | G | 2 | 0.002 | -0.0907 | 0.036 | 0.92969 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered | |
| r1390211 | 11 | 3E+024 | T | G | 64 | 0.4713 | -7.00E-04 | 0.0097 | 0.9399 | 0.72425 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1509805 | 11 | 3E+024 | T | G | 64 | 0.4713 | -7.00E-04 | 0.0097 | 0.9399 | 0.72425 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1509805 | 11 | 3E+024 | T | G | 64 | 0.4713 | -7.00E-04 | 0.0097 | 0.9399 | 0.72425 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1509805 | 11 | 3E+024 | T | G | 64 | 0.4713 | -7.00E-04 | 0.0097 | 0.9399 | 0.72425 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1509805 | 11 | 3E+024 | T | G | 64 | 0.4713 | -7.00E-04 | 0.0097 | 0.9399 | 0.72425 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |
| r1509805 | 11 | 3E+024 | T | G | 64 | 0.4713 | -7.00E-04 | 0.0097 | 0.9399 | 0.72425 | underpowered | 0.4735 | -0.0011 | 0.011 | 0.3745 | 0.79884 | underpowered | 0.1027 | 0.0395 | 0.0162 | 0.82027 | 0.82879 | Yes | 0.4698 | 0.0048 | 0.0005 | 0.6421 | 0.61117 | underpowered | 0.2814 | -0.009 | 0.0131 | 0.4929 | 0.51137 | underpowered | 0.3001 | -0.0165 | 0.0281 | 0.5527 | 0.17807 | underpowered | 0.4971 | 0.0442 | 0.0254 | 0.02848 | 0.1935 | underpowered | 0.2686 | 0.0397 | 0.0269 | 0.2277 | 0.16 | underpowered |

MAJ: Major depression; SNP: Single nucleotide polymorphism; CHR: Chromosome; BP: base pair; EA: Effect allele; EAF: Effect allele frequency; NvarCrD: Number of variants in credible set; BEA: Regression coefficient; SE: Standard error of BEA
 *Only 20% out of the 200 loci had results in at least one of the credible sets in our analysis.
 Two-sided association P-values of statistics from inverse-variance weighted fixed-effect meta-analysis are given.
 Transferable: A locus was classified as transferable if at least one variant in the credible set was associated to the lead variant. The lead variant may not be significant for a transferable locus.
 SMR_pHit_p: Provides the result of the association in the credible set that had the smallest p-value in the non-European ancestry lookup GWAS.

SNP= Single nucleotide polymorphism; SNV= Single nucleotide variant; CHR= Chromosome; BP= Base pair; EA= Effect allele; NEA= Non effect allele; Freq= Effect allele frequency; BETA= Regression coefficient; SE= Standard error of BETA

Two-sided association P values of z statistics from an inverse-variance -weighted fixed-effect model meta-analysis are given.

Novel: novel from previously reported loci

HetPVal: P value for heterogeneity of effect across ancestry

N of SNVs in credible set: Number of SNVs in 99% credible set from multi ancestry finemapping

RSIDs of SNVs in credible set: RSIDs for SNVs in 99% credible sets from multi ancestry finemapping, only credible sets of <10 SNVs were shown.

Supplementary Table 8. Seven independent significant variants from the multi ancestry meta-analysis on clinical depression

| SNP | loci | Chr | bp | Effect allele | Non-effect al Freq | BETA | SE | P value | HetPVal | |
|-------------------|--------------------|----------|-----------------|---------------|--------------------|---------------|----------------|---------------|-----------------|---------------|
| rs12129573 | 1:72337239_ | 1 | 73768366 | a | c | 0.3174 | 0.0382 | 0.0067 | 1.45E-08 | 0.8653 |
| rs2085224 | 3:34958054_ | 3 | 35458054 | a | g | 0.5649 | -0.0478 | 0.0083 | 1.02E-08 | 0.4978 |
| rs4861162 | 4:41605865_ | 4 | 42105865 | a | c | 0.3579 | -0.0429 | 0.0078 | 3.15E-08 | 0.1996 |
| rs78676209 | 5:43712359_ | 5 | 44212359 | c | g | 0.9463 | -0.1043 | 0.0183 | 1.21E-08 | 0.6958 |
| 5:103903810 | 5:103403810 | 5 | 103903810 | d | i | 0.6308 | -0.0587 | 0.0088 | 2.47E-11 | 0.0005844 |
| rs10759878 | 9:119230709 | 9 | 119730709 | a | g | 0.7696 | 0.0441 | 0.0078 | 1.74E-08 | 0.6056 |
| rs1950829 | 14:41597937 | 14 | 42097937 | a | g | 0.5815 | 0.0483 | 0.0066 | 2.02E-13 | 0.7717 |

Two-sided association P values of z statistics from an inverse-variance -weighted fixed-effect model meta-analysis are given.

SNP= Single nucleotide polymorphism; CHR= Chromosome; BP= Base pair; Freq= Effect allele frequency; BETA= Regression coefficient; SE= Standard error of BETA

HetPVal= P value for heterogeneity of effect across ancestry

bold= Novel

P.value_association_lambdaGC: P values for GWAS association after lambda GC correction

chisq_ancestry_het, ndf_ancestry_het, P.value_ancestry_het: test statistics, degree of the test statistics, and P values for heterogeneity due to ancestry.

chisq_residual_het, ndf_residual_het, P.value_residual_het: test statistics, degree of freedom of the test statistics, and P values for residual heterogeneity.

Ncohort: N of cohorts in which the SNV were available.

| | | | | | | | | | | | | | |
|-------------|------------------|----|-----------|---|---|--------|---------|--------|----------|-----|-----------------------------|-----|------------------------|
| rs4906349 | 14:104091115:A:T | 14 | 104091115 | a | g | 0.6627 | 0.0271 | 0.0033 | 4.05E-16 | 11 | 8721;rs2403202;rs4444269;rs | 4 | rs10149470;rs10141157 |
| rs4489961 | 15:37904054:C:T | 15 | 37904054 | t | c | 0.4814 | -0.0194 | 0.003 | 1.48E-10 | 46 | 5216;rs11073258;rs28885697 | 82 | rs8037355;rs12102100;r |
| rs8043085 | 15:38828140:G:T | 15 | 38828140 | t | c | 0.2584 | 0.0192 | 0.0034 | 2.20E-08 | 30 | 73334;rs11073333;rs7272739 | 67 | rs8043085;rs56059718;r |
| rs34488670 | 15:47684936:C:T | 15 | 47684936 | t | c | 0.7856 | -0.0228 | 0.0037 | 1.02E-09 | 34 | 3799;rs12910487;rs12901436 | 40 | rs6493274;rs34488670;r |
| rs1047399 | 15:74044966:A:G | 15 | 74044966 | a | g | 0.3885 | -0.018 | 0.0031 | 8.74E-09 | 25 | 42096;rs4887161;rs4887164;r | 28 | rs28485305;rs1047399;r |
| rs7193263 | 16:6315880:A:G | 16 | 6315880 | a | g | 0.6349 | -0.023 | 0.0032 | 1.06E-12 | 3 | 03 | 7 | rs7193263;rs8063603;rs |
| rs7198928 | 16:7666402:C:T | 16 | 7666402 | t | c | 0.6012 | 0.0231 | 0.0031 | 1.54E-13 | 16 | 77203;rs11077206;rs3785238 | 16 | rs9925434;rs7198928;rs |
| rs9936260 | 16:12351254:A:G | 16 | 12351254 | a | g | 0.7287 | 0.0207 | 0.0035 | 4.62E-09 | 54 | 3;rs6498272;rs8058876;rs170 | 73 | rs9936260;rs6498272;rs |
| rs7200826 | 16:13066833:C:T | 16 | 13066833 | t | c | 0.2391 | 0.0249 | 0.0036 | 7.20E-12 | 6 | 383;rs2866126;rs34564081;1 | 78 | rs7200826;rs12926477;r |
| rs2157065 | 16:13748843:C:G | 16 | 13748843 | c | g | 0.2623 | 0.0244 | 0.0034 | 1.15E-12 | 21 | 962725;rs12922437;rs129215 | 82 | rs56887639;rs11865150 |
| rs170194 | 16:15558272:A:G | 16 | 15558272 | a | g | 0.3869 | 0.0173 | 0.0031 | 3.21E-08 | 23 | 2;rs12148985;rs219426;rs168 | 51 | rs34792;rs170194;rs478 |
| rs1353162 | 16:17907269:A:G | 16 | 17907269 | a | g | 0.597 | 0.0176 | 0.003 | 6.13E-09 | 73 | 645;rs1493870;rs4780669;rs1 | 113 | rs35977842;rs12926255 |
| rs3091404 | 16:21658266:C:T | 16 | 21658266 | t | c | 0.4142 | 0.0216 | 0.0032 | 2.26E-11 | 3 | 3444 | 14 | rs2369818;rs12923444;r |
| rs4784655 | 16:56364030:C:G | 16 | 56364030 | c | g | 0.3455 | 0.0187 | 0.0033 | 1.97E-08 | 6 | 615;rs2241952;rs4784654;rs8 | 18 | rs4784655;rs899236;rs8 |
| rs75581564 | 17:27363750:A:G | 17 | 27363750 | a | g | 0.1117 | 0.0293 | 0.0051 | 1.25E-08 | 27 | 319813;rs7220662;rs7281579 | 9 | rs75581564;rs11799966 |
| rs56084168 | 17:79084574:C:T | 17 | 79084574 | t | c | 0.1551 | -0.0241 | 0.0042 | 1.30E-08 | 11 | 54126;rs8071392;rs6565535;r | 12 | rs8071392;rs1801833;rs |
| rs11374439 | 18:31365589:D:I | 18 | 31365589 | d | i | 0.5339 | -0.0202 | 0.0036 | 2.70E-08 | 57 | 55006;rs770110525;rs158698 | NA | NA |
| rs12967855 | 18:35138245:A:G | 18 | 35138245 | a | g | 0.3741 | 0.026 | 0.0032 | 8.22E-16 | 8 | 82011;rs11665070;rs1557341 | 24 | rs12967855;rs4799949;r |
| rs112226573 | 18:39305644:D:I | 18 | 39305644 | d | i | 0.7903 | 0.0219 | 0.0039 | 2.63E-08 | 24 | 960323;rs11877563;rs426741 | 32 | rs4267411;rs2217731;rs |
| rs11663393 | 18:50614732:A:G | 18 | 50614732 | a | g | 0.4307 | 0.0222 | 0.0031 | 1.29E-12 | 84 | 100765;rs17486305;rs621007 | 107 | rs11663393;rs7227069;r |
| rs7241572 | 18:77580712:A:G | 18 | 77580712 | a | g | 0.1925 | 0.0268 | 0.0039 | 9.82E-12 | 7 | 71367544;rs7236339;rs11664 | 7 | rs7241572;rs11664298;r |
| rs10853981 | 19:4965064:A:G | 19 | 4965064 | a | g | 0.3415 | -0.0181 | 0.0032 | 2.09E-08 | 8 | 413045;rs7253212;rs1040739 | 42 | rs58324296;rs262548;rs |
| rs7248481 | 19:13083967:C:T | 19 | 13083967 | t | c | 0.4024 | -0.019 | 0.0032 | 4.02E-09 | 2 | rs7248481;rs7408675 | 10 | rs4334415;rs7248481;rs |
| rs2748668 | 20:37406869:C:T | 20 | 37406869 | t | c | 0.5832 | 0.0167 | 0.003 | 3.47E-08 | 61 | 109;rs2254234;rs2254245;rs2 | 72 | rs2748668;rs2077109;rs |
| rs6102456 | 20:40172707:C:T | 20 | 40172707 | t | c | 0.6762 | -0.0215 | 0.0035 | 1.15E-09 | 64 | 412;rs2294564;rs6072392;rs6 | 130 | rs6072412;rs6102456;rs |
| rs4578918 | 20:44721656:C:T | 20 | 44721656 | t | c | 0.2543 | 0.0208 | 0.0036 | 1.03E-08 | 50 | 27066;rs6065926;rs2297200;r | 7 | rs12624433;rs13037326 |
| rs910187 | 20:45841052:A:G | 20 | 45841052 | a | g | 0.345 | -0.0183 | 0.0033 | 3.91E-08 | 137 | 969;rs910187;rs4555399;rs60 | 30 | rs910187;rs6063085;rs7 |
| rs74963256 | 20:51588847:C:T | 20 | 51588847 | t | c | 0.8985 | 0.0295 | 0.0052 | 1.90E-08 | 17 | 97356;rs6013578;rs1884889;r | 21 | rs74963256;rs6022191;r |
| rs372519 | 21:46574554:A:G | 21 | 46574554 | a | g | 0.5202 | 0.0167 | 0.003 | 3.47E-08 | 90 | 19;rs2838815;rs2838821;rs11 | 83 | rs372519;rs403694;rs40 |
| rs20551 | 22:41548008:A:G | 22 | 41548008 | a | g | 0.7143 | -0.0268 | 0.0035 | 3.27E-14 | 16 | 9;rs11090039;rs2092563;rs13 | 63 | rs5758265;rs5995992;rs |
| rs9627391 | 22:46447097:C:T | 22 | 46447097 | t | c | 0.3465 | -0.0225 | 0.0034 | 5.48E-11 | 27 | 989;rs7292527;rs8135712;rs4 | 25 | rs7511013;rs9627391;rs |

SNP= Single nucleotide polymorphism; CHR= Chromosome; BP= Base pair; EA= Effect allele; NEA= Non effect allele; EAF= Effect allele frequency; BETA= Regression coefficient; SE= Standard error of BETA

Two-sided association P values of z statistics from an inverse-variance -weighted fixed-effect model meta-analysis are given.

SNP: rsID for the SNP of smallest P value in each region

N_causal_I2: N of SNVs in 99% credible set based on multiple ancestry fine mapping

N_causal_European: Number of SNVs in 99% credible set based on European ancestry fine mapping.

MarkerName_causal_I2: RSIDs for the variants in 99% credible set from multi ancestry fine mapping

MarkerName_causal_European: RSIDs for the variants in 99% credible set from European ancestry fine mapping

Supplementary Table 11. Comparison of the current TWAS with previous TWASs of MD

| GENE ID | PREVIOUS TWASs of MD | | | | | Current TWAS of MD | | |
|------------|----------------------|-------------|----------------|----------------|--------------|--------------------|--------------------|-------|
| | Gaspar_TWAS.Z | Wray_TWAS.Z | Gerring_TWAS.Z | AllAgio_TWAS.Z | Levey_TWAS.P | Meng_Navoly_TWAS.Z | Meng_Navoly_TWAS.P | NOVEL |
| ABHD16A | NA | NA | NA | NA | NA | 5.0184 | 5.21E-07 | Yes |
| ACADS | NA | NA | 4.93 | 4.40 | NA | 6.7252 | 1.75E-11 | No |
| ACTG1P22 | NA | NA | NA | NA | NA | -5.08024 | 3.77E-07 | Yes |
| ACVRL1 | NA | NA | NA | NA | 6.13E-07 | NA | NA | No |
| ACYP1 | NA | NA | NA | NA | NA | -5.89582 | 3.73E-09 | Yes |
| ADARB2 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| AKAP9 | NA | NA | NA | NA | NA | -4.84084 | 1.29E-06 | Yes |
| AL022393.7 | NA | NA | -4.97 | -4.31 | NA | NA | NA | No |
| AL049840.1 | NA | NA | 4.68 | 5.14 | NA | NA | NA | No |
| ALG1L12P | NA | NA | NA | NA | NA | -5.3793 | 7.48E-08 | Yes |
| AMT | NA | NA | -4.36 | -4.56 | 9.47E-11 | -5.8458 | 5.04E-09 | No |
| ANKHD1 | NA | NA | NA | NA | NA | 5.57662 | 2.45E-08 | Yes |
| ANKK1 | NA | NA | NA | NA | 5.41E-13 | -6.756548 | 1.41E-11 | No |
| ANKRD44 | NA | NA | NA | -5.69 | NA | -6.22781 | 4.73E-10 | No |
| AP000662.4 | NA | NA | NA | -4.98 | NA | NA | NA | No |
| APBB3 | NA | NA | NA | NA | NA | 5.0511 | 4.39E-07 | Yes |
| APEH | NA | NA | NA | NA | 4.19E-10 | NA | NA | No |
| AREL1 | NA | NA | NA | -5.02 | 1.46E-13 | -6.8529 | 7.24E-12 | No |
| ARHGAP9 | NA | NA | NA | NA | NA | 4.8704 | 1.11E-06 | Yes |
| ASCC3 | NA | NA | NA | NA | 2.77E-08 | NA | NA | No |
| ASTN1 | NA | NA | NA | NA | NA | -5.8 | 6.78E-09 | Yes |
| ATP6V1G2 | NA | NA | NA | NA | NA | 4.8372 | 1.32E-06 | Yes |
| ATXN1 | NA | NA | NA | NA | NA | -5.24013 | 1.60E-07 | Yes |
| B3GLCT | NA | NA | NA | NA | NA | -6.6471 | 2.99E-11 | Yes |
| B4GALNT4 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| BAG5 | 5.24 | NA | NA | 4.63 | 3.63E-11 | 7.95674 | 1.77E-15 | No |
| BAG6 | NA | NA | NA | -5.58 | NA | -5.0561 | 4.28E-07 | No |
| BATF | NA | NA | -4.88 | NA | NA | NA | NA | No |
| BEND4 | NA | -4.64 | NA | -4.65 | NA | -5.0889 | 3.60E-07 | No |
| BSN | NA | NA | NA | NA | 2.01E-10 | -6.67345 | 2.50E-11 | No |
| BSN-AS2 | NA | NA | NA | NA | 3.53E-10 | NA | NA | No |
| BTN1A1 | -5.91 | NA | NA | NA | NA | NA | NA | No |
| BTN2A1 | NA | NA | NA | NA | 3.94E-10 | -4.9667 | 6.81E-07 | No |
| BTN2A2 | NA | NA | NA | NA | 9.54E-06 | -6.6667 | 2.62E-11 | No |
| BTN2A3P | NA | NA | NA | NA | NA | -5.5853 | 2.33E-08 | Yes |
| BTN3A1 | NA | NA | NA | NA | 5.60E-09 | -5.68684 | 1.29E-08 | No |
| BTN3A2 | 5.38 | NA | 5.38 | 5.90 | 4.61E-12 | 6.84617 | 7.59E-12 | No |
| BTN3A3 | NA | NA | -4.41 | -4.46 | 7.47E-09 | -7.27847 | 3.38E-13 | No |
| BVES-AS1 | NA | NA | NA | -5.58 | NA | NA | NA | No |
| C11orf49 | NA | NA | NA | NA | NA | 4.8943 | 9.87E-07 | Yes |
| C15orf59 | NA | NA | NA | NA | NA | 5.652123 | 1.58E-08 | Yes |
| C1QTNF4 | NA | NA | NA | NA | NA | 4.92271 | 8.54E-07 | Yes |
| C3orf62 | NA | NA | NA | NA | NA | -5.42836 | 5.69E-08 | Yes |
| C4B | NA | NA | NA | NA | NA | -5.3135 | 1.08E-07 | Yes |
| CACNA1E | NA | NA | NA | -4.99 | NA | -6.09332 | 1.11E-09 | No |
| CCDC175 | NA | NA | NA | -5.48 | NA | NA | NA | No |
| CCDC71 | NA | NA | NA | NA | 2.87E-09 | 6.9722 | 3.12E-12 | No |

| | | | | | | | | |
|---------------|----|-------|-------|-------|----------|-----------|----------|-----|
| CCDC92 | NA | NA | NA | NA | NA | -4.84146 | 1.29E-06 | Yes |
| CCHCR1 | NA | NA | NA | NA | NA | 4.8596 | 1.18E-06 | Yes |
| CD14 | NA | NA | NA | NA | NA | -5.2186 | 1.80E-07 | Yes |
| CD276 | NA | NA | NA | NA | NA | -5.0534 | 4.34E-07 | Yes |
| CD40 | NA | NA | NA | NA | 5.08E-07 | -5.78917 | 7.07E-09 | No |
| CDCA4P1 | NA | NA | NA | NA | NA | 5.12289 | 3.01E-07 | Yes |
| CDH13 | NA | NA | NA | NA | NA | -5.839468 | 5.24E-09 | Yes |
| CDH9 | NA | NA | NA | NA | NA | 5.59796 | 2.17E-08 | Yes |
| CELF4 | NA | NA | NA | NA | 5.04E-14 | 5.7366 | 9.66E-09 | No |
| CENPL | NA | NA | NA | NA | 0.00 | NA | NA | No |
| CHADL | NA | NA | 4.47 | 1.33 | 1.45E-09 | NA | NA | No |
| CHD6 | NA | NA | NA | NA | NA | -6.38089 | 1.76E-10 | Yes |
| CHMP3 | NA | NA | 4.51 | 2.09 | NA | 5.4651 | 4.63E-08 | No |
| CHRNB1 | NA | NA | -4.39 | -3.50 | NA | NA | NA | No |
| CITF22-92A6.1 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| CKB | NA | NA | NA | 5.35 | 0.00 | 7.8802 | 3.27E-15 | No |
| CLOCK | NA | NA | NA | NA | 0.00 | 5.1001 | 3.40E-07 | No |
| CLP1 | NA | NA | 5.24 | 5.20 | 1.69E-09 | 5.732694 | 9.88E-09 | No |
| COQ3 | NA | NA | NA | 5.15 | NA | NA | NA | No |
| CRB1 | NA | NA | NA | NA | 1.66E-13 | -6.5 | 8.03E-11 | No |
| CRH | NA | NA | NA | NA | NA | -5.117671 | 3.09E-07 | Yes |
| CSE1L | NA | -4.71 | NA | -4.71 | 4.54E-07 | NA | NA | No |
| CTA-14H9.5 | NA | NA | NA | NA | 3.24E-12 | NA | NA | No |
| CTC-467M3.3 | NA | NA | -6.28 | -7.09 | 9.59E-11 | -8.13004 | 4.29E-16 | No |
| CTC-498M16.4 | NA | NA | 4.47 | 5.40 | 4.94E-10 | 7.34164 | 2.11E-13 | No |
| CTD-2298J14.2 | NA | NA | NA | -5.68 | 3.32E-15 | -7.7667 | 8.06E-15 | No |
| CTD-2653B5.1 | NA | NA | NA | 5.11 | NA | NA | NA | No |
| CTDP1 | NA | NA | NA | NA | NA | 5.28405 | 1.26E-07 | Yes |
| CTNND1 | NA | NA | NA | NA | NA | -5.21496 | 1.84E-07 | Yes |
| CTTNBP2 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| CYP7B1 | NA | NA | NA | NA | NA | -5.04642 | 4.50E-07 | Yes |
| DAG1 | NA | NA | NA | NA | 3.07E-10 | NA | NA | No |
| DALRD3 | NA | NA | NA | NA | NA | -4.88581 | 1.03E-06 | Yes |
| DCAF4L1 | NA | NA | NA | -5.13 | NA | -5.222222 | 1.77E-07 | No |
| DCC | NA | NA | NA | NA | NA | 5.1459 | 2.66E-07 | Yes |
| DCP2 | NA | NA | NA | NA | 5.06E-06 | NA | NA | No |
| DDAH2 | NA | 5.34 | NA | 5.41 | NA | 6.27865 | 3.42E-10 | No |
| DDR1 | NA | NA | NA | NA | NA | 5.0584 | 4.23E-07 | Yes |
| DDX27 | NA | 4.84 | NA | 4.84 | 6.76E-07 | 4.9031 | 9.43E-07 | No |
| DDX39B | NA | NA | NA | NA | NA | 6.4079 | 1.48E-10 | Yes |
| DDX6 | NA | NA | NA | NA | NA | 5.2118 | 1.87E-07 | Yes |
| DENND1B | NA | 4.85 | 4.75 | -5.42 | 3.67E-15 | -6.33118 | 2.43E-10 | No |
| DHX38 | NA | NA | -4.49 | 3.73 | NA | NA | NA | No |
| DLST | NA | 4.98 | NA | 5.09 | NA | 6.0433 | 1.51E-09 | No |
| DNAJC24 | NA | 4.46 | NA | 4.50 | NA | 5.1334 | 2.84E-07 | No |
| DRD2 | NA | NA | NA | -5.07 | 7.80E-19 | -5.4931 | 3.95E-08 | No |
| DYSF | NA | NA | NA | NA | NA | -5.5235 | 3.32E-08 | Yes |
| EBLN3P | NA | NA | NA | NA | 2.36E-10 | NA | NA | No |
| EIF4E3 | NA | NA | NA | NA | 4.48E-05 | NA | NA | No |
| EIF4H | NA | NA | NA | NA | NA | -5.683279 | 1.32E-08 | Yes |
| EMILIN3 | NA | NA | NA | NA | NA | -5.4 | 6.66E-08 | Yes |
| EP300 | NA | NA | NA | 5.49 | 1.25E-13 | 6.02305 | 1.71E-09 | No |

| | | | | | | | | |
|-----------|-------|-------|-------|-------|----------|-----------|----------|-----|
| ESR2 | -5.43 | NA | -5.40 | -5.98 | NA | -5.9692 | 2.38E-09 | No |
| ETFDH | NA | NA | NA | NA | NA | -5.17711 | 2.25E-07 | Yes |
| FADS1 | NA | NA | -4.64 | -4.60 | 1.47E-06 | -5.43077 | 5.61E-08 | No |
| FADS2 | NA | NA | NA | NA | 1.58E-07 | NA | NA | No |
| FADS3 | NA | NA | NA | NA | NA | -5.23825 | 1.62E-07 | Yes |
| FAHD2B | NA | NA | NA | NA | NA | -5.24731 | 1.54E-07 | Yes |
| FAM120A | NA | NA | NA | NA | 3.44E-11 | NA | NA | No |
| FAM120AOS | NA | NA | NA | NA | 2.62E-10 | NA | NA | No |
| FAM180B | NA | NA | NA | NA | NA | -5.097227 | 3.45E-07 | Yes |
| FAM220A | NA | NA | NA | NA | NA | -4.8692 | 1.12E-06 | Yes |
| FANCL | NA | -5.18 | NA | -5.18 | NA | -6.80622 | 1.00E-11 | No |
| FARP1 | NA | NA | NA | NA | NA | 4.838 | 1.31E-06 | Yes |
| FBXL17 | NA | NA | NA | NA | NA | 4.98383 | 6.23E-07 | Yes |
| FBXO10 | NA | NA | NA | NA | NA | -5.76456 | 8.19E-09 | Yes |
| FCF1 | NA | NA | NA | NA | 9.15E-14 | NA | NA | No |
| FEN1 | NA | NA | NA | NA | NA | 4.9623 | 6.97E-07 | Yes |
| FES | NA | NA | NA | NA | NA | 4.96774 | 6.77E-07 | Yes |
| FLOT1 | NA | NA | NA | -5.56 | NA | -5.3714 | 7.81E-08 | No |
| FRAT2 | NA | NA | NA | NA | NA | -4.90404 | 9.39E-07 | Yes |
| FURIN | NA | NA | NA | NA | 2.27E-07 | -5.4037 | 6.53E-08 | No |
| GALNT2 | NA | NA | NA | NA | NA | 5.13 | 2.88E-07 | Yes |
| GIGYF2 | NA | NA | NA | NA | NA | -5.06449 | 4.09E-07 | Yes |
| GLT8D1 | NA | NA | NA | NA | NA | -5.033333 | 4.82E-07 | Yes |
| GLYCK | NA | NA | NA | NA | NA | 4.864515 | 1.15E-06 | Yes |
| GMPPB | NA | NA | NA | NA | NA | 5.65116 | 1.59E-08 | Yes |
| GNL3 | NA | NA | NA | NA | NA | 5.5106 | 3.58E-08 | Yes |
| GOLGA1 | NA | NA | NA | NA | NA | -5.2453 | 1.56E-07 | Yes |
| GPR27 | NA | NA | NA | NA | 4.25E-06 | NA | NA | No |
| GPR89P | NA | NA | NA | NA | NA | 6.7434 | 1.55E-11 | Yes |
| GPX1 | NA | NA | 4.63 | 4.60 | 1.22E-10 | 6.1765 | 6.56E-10 | No |
| GRIA1 | NA | NA | NA | NA | NA | -5.05677 | 4.26E-07 | Yes |
| GRK4 | NA | NA | NA | NA | NA | -5.36733 | 7.99E-08 | Yes |
| GRM5 | NA | NA | NA | NA | NA | -5.02 | 5.22E-07 | Yes |
| GSDME | NA | NA | NA | NA | NA | 5.181818 | 2.20E-07 | Yes |
| GTF2H4 | NA | NA | NA | NA | NA | 6.7802 | 1.20E-11 | Yes |
| H1-12P | NA | NA | NA | NA | NA | -4.85195 | 1.22E-06 | Yes |
| H2AC6 | NA | NA | NA | NA | NA | 5.6425 | 1.68E-08 | Yes |
| HACE1 | NA | NA | NA | NA | NA | 4.981 | 6.33E-07 | Yes |
| HARS1 | NA | NA | NA | NA | NA | 5.4413 | 5.29E-08 | Yes |
| HARS2 | NA | NA | NA | NA | NA | -5.5863 | 2.32E-08 | Yes |
| HCG11 | NA | NA | NA | NA | 7.66E-11 | 7.0223 | 2.18E-12 | No |
| HCG22 | NA | NA | NA | NA | NA | 5.0372 | 4.72E-07 | Yes |
| HCP5 | NA | NA | NA | 6.40 | NA | NA | NA | No |
| HFE | NA | NA | NA | NA | NA | 5.67261 | 1.41E-08 | Yes |
| HIST1H1B | NA | NA | NA | NA | 0.00 | NA | NA | No |
| HIST1H2AK | 6.50 | NA | NA | -0.81 | NA | NA | NA | No |
| HIST1H2BF | NA | NA | NA | NA | NA | -5.1812 | 2.20E-07 | Yes |
| HIST1H2BN | NA | NA | NA | NA | 7.45E-16 | NA | NA | No |
| HIST1H2BO | NA | NA | NA | NA | 2.36E-14 | NA | NA | No |
| HIST1H3B | NA | NA | NA | NA | NA | -5.7552 | 8.65E-09 | Yes |
| HIST1H4D | NA | NA | NA | -4.99 | NA | -5.0784 | 3.81E-07 | No |
| HIST1H4L | NA | NA | NA | 4.87 | NA | 6.9078 | 4.92E-12 | No |

| | | | | | | | | |
|--------------------|------|-------|-------|-------|----------|-----------|----------|-----|
| HLA-B | NA | NA | NA | NA | NA | 5.3043 | 1.13E-07 | Yes |
| HLA-C | NA | NA | NA | NA | NA | -4.9746 | 6.54E-07 | Yes |
| HLA-DOA | NA | NA | 4.41 | 2.11 | NA | NA | NA | No |
| HLA-S | NA | NA | NA | NA | NA | 6.4798 | 9.18E-11 | Yes |
| HMGN4 | NA | NA | NA | 5.40 | NA | NA | NA | No |
| HSDL2 | NA | NA | NA | NA | NA | 4.91186 | 9.02E-07 | Yes |
| HSPA1A | NA | NA | NA | NA | 1.08E-07 | NA | NA | No |
| HSPA1L | NA | NA | NA | NA | 0.00 | NA | NA | No |
| HSPA2 | NA | NA | NA | NA | NA | -4.91528 | 8.87E-07 | Yes |
| IER3 | NA | NA | NA | NA | NA | -6.143 | 8.10E-10 | Yes |
| IGSF6 | NA | NA | NA | NA | NA | -5.57161 | 2.52E-08 | Yes |
| IHO1 (CCDC36) | NA | NA | NA | NA | 2.23E-11 | -5.4768 | 4.33E-08 | No |
| IK | NA | NA | NA | NA | NA | -5.40329 | 6.54E-08 | Yes |
| INAFM1 | NA | NA | NA | NA | NA | 4.94852 | 7.48E-07 | Yes |
| INPP5B | NA | NA | NA | NA | NA | -5.0294 | 4.92E-07 | Yes |
| AS1 (C15orf59-AS1) | NA | NA | NA | NA | 6.90E-09 | 5.4333 | 5.53E-08 | No |
| IST1 | NA | NA | -4.58 | -3.91 | NA | NA | NA | No |
| ITPR3 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| JKAMP | NA | NA | NA | -5.13 | NA | NA | NA | No |
| KCNG2 | NA | NA | NA | NA | 4.32E-08 | 5.770982 | 7.88E-09 | No |
| KCNJ13 | NA | NA | NA | NA | NA | 5.13 | 2.98E-07 | Yes |
| KIAA1143 | NA | NA | NA | NA | 4.83E-08 | NA | NA | No |
| KLC1 | 5.34 | NA | 5.34 | -4.71 | 4.06E-10 | 7.0982 | 1.26E-12 | No |
| KLF7 | NA | NA | NA | NA | 2.25E-10 | NA | NA | No |
| KLHDC8B | NA | NA | NA | NA | 2.57E-13 | NA | NA | No |
| L3MBTL2 | NA | NA | NA | NA | 7.00E-14 | 5.1116 | 3.19E-07 | No |
| LAMB2 | NA | NA | NA | NA | 8.39E-11 | 5.12903 | 2.91E-07 | No |
| LAMB2P1 | NA | NA | NA | NA | NA | -6.176471 | 6.56E-10 | Yes |
| LIN28B | NA | -5.23 | NA | -5.23 | 1.32E-10 | -6.95218 | 3.60E-12 | No |
| LIN28B-AS1 | NA | NA | NA | NA | 8.64E-11 | 6.6743 | 2.48E-11 | No |
| LINC00461 | NA | NA | NA | NA | 1.31E-10 | -5.84848 | 4.96E-09 | No |
| LINC00533 | NA | NA | NA | NA | NA | -6.78 | 1.20E-11 | Yes |
| LINC00577 | NA | NA | 5.00 | 4.40 | NA | NA | NA | No |
| LINC00997 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| LINC01068 | NA | NA | NA | NA | NA | -5.4644 | 4.64E-08 | Yes |
| LINC01415 | NA | NA | NA | NA | 6.38E-10 | NA | NA | No |
| LINC01965 | NA | NA | NA | NA | NA | 4.86 | 1.17E-06 | Yes |
| LINC02060 | NA | NA | NA | NA | 1.91E-09 | 6.9157 | 4.66E-12 | No |
| LPXN | NA | NA | -4.87 | 1.67 | NA | NA | NA | No |
| LRFN5 | 5.23 | NA | 5.23 | 5.60 | 2.64E-14 | 7.8084 | 5.98E-15 | No |
| LY6G5C | NA | NA | NA | NA | NA | 5.0826 | 3.72E-07 | Yes |
| LY6G6C | NA | NA | NA | NA | NA | -5.8016 | 6.57E-09 | Yes |
| MANEA-DT | NA | NA | NA | NA | NA | -4.87018 | 1.11E-06 | Yes |
| MARCKSL1P1 | NA | NA | NA | NA | NA | -5.584 | 2.35E-08 | Yes |
| MARK3 | NA | NA | NA | NA | NA | 5.9062 | 3.50E-09 | Yes |
| METTL12 | NA | NA | 4.58 | 0.32 | NA | NA | NA | No |
| METTL9 | NA | NA | NA | NA | NA | -5.4319 | 5.58E-08 | Yes |
| MFAP3L | NA | NA | NA | NA | NA | -6.25714 | 3.92E-10 | Yes |
| MFF | 4.98 | NA | NA | 4.60 | NA | NA | NA | No |
| MICA | NA | NA | NA | NA | NA | -4.8482 | 1.25E-06 | Yes |
| MICB | NA | NA | NA | -5.56 | NA | -5.249 | 1.53E-07 | No |
| MIER1 | NA | NA | NA | NA | NA | -5.2016 | 1.98E-07 | Yes |

| | | | | | | | | |
|------------|------|------|-------|-------|----------|----------|----------|-----|
| MIRLET7BHG | NA | NA | NA | NA | NA | 5.2646 | 1.40E-07 | Yes |
| MLEC | NA | NA | NA | NA | NA | 4.9146 | 8.90E-07 | Yes |
| MLF1 | NA | NA | NA | NA | 1.16E-09 | NA | NA | No |
| MMAB | NA | NA | NA | NA | NA | -5.2064 | 1.93E-07 | Yes |
| MPIG6B | NA | NA | NA | NA | NA | 4.89529 | 9.82E-07 | Yes |
| MPP6 | NA | NA | NA | NA | NA | -5.63636 | 1.74E-08 | Yes |
| MPRIIP1 | NA | NA | NA | NA | NA | -6.17709 | 6.53E-10 | Yes |
| MRPS33 | NA | NA | NA | NA | NA | 4.9569 | 7.16E-07 | Yes |
| MRTFA | NA | NA | NA | NA | NA | -5.3261 | 1.00E-07 | Yes |
| MSH5 | NA | NA | NA | NA | 5.52E-08 | 5.86483 | 4.50E-09 | No |
| MTCH2 | NA | NA | NA | NA | NA | -4.9484 | 7.48E-07 | Yes |
| MTHFD1 | NA | NA | NA | NA | NA | -6.22581 | 4.79E-10 | Yes |
| MYBPC3 | NA | NA | NA | NA | NA | 6.12225 | 9.23E-10 | Yes |
| MYO18A | NA | NA | NA | -5.13 | NA | NA | NA | No |
| NDUFA2 | NA | 5.19 | NA | 5.19 | NA | 6.08107 | 1.19E-09 | No |
| NDUFAF3 | NA | NA | NA | NA | NA | -5.0785 | 3.80E-07 | Yes |
| NEGR1 | 7.35 | NA | 8.49 | 8.76 | 1.77E-25 | 10.67742 | 1.30E-26 | No |
| NEK4 | NA | NA | NA | NA | NA | 5.49457 | 3.92E-08 | Yes |
| NEK6 | NA | NA | NA | NA | NA | -4.91876 | 8.71E-07 | Yes |
| NICN1 | NA | NA | NA | NA | 3.46E-11 | -5.431 | 5.60E-08 | No |
| NKAPL | NA | NA | NA | 5.00 | NA | NA | NA | No |
| NLGN1 | NA | NA | NA | NA | 1.21E-07 | NA | NA | No |
| NOL5BP | NA | NA | 5.13 | NA | NA | NA | NA | No |
| NPM1P46 | NA | NA | NA | NA | NA | 5.9122 | 3.38E-09 | Yes |
| NRD1 | NA | NA | NA | NA | NA | 6.30218 | 2.93E-10 | Yes |
| NT5C2 | NA | NA | NA | NA | 0.00 | -5.6791 | 1.35E-08 | No |
| NT5DC2 | NA | NA | NA | NA | NA | 5.3525 | 8.68E-08 | Yes |
| OLFM4 | NA | 5.09 | NA | 5.09 | NA | 6.391 | 1.65E-10 | No |
| OPN3 | NA | NA | 4.62 | 4.37 | NA | NA | NA | No |
| OR1F12 | NA | NA | NA | NA | NA | -6.50023 | 8.02E-11 | Yes |
| OR2B7P | NA | NA | NA | NA | NA | -6.42857 | 1.29E-10 | Yes |
| OR2B8P | NA | NA | -5.50 | -4.18 | NA | -6.5429 | 6.04E-11 | No |
| OR7E102P | NA | NA | NA | NA | NA | -4.9375 | 7.91E-07 | Yes |
| OSBPL3 | NA | NA | NA | -5.62 | NA | NA | NA | No |
| OTOA | NA | NA | NA | NA | 1.55E-08 | NA | NA | No |
| P4HTM | NA | NA | NA | NA | NA | -5.85513 | 4.77E-09 | Yes |
| PACRG | NA | NA | NA | NA | NA | -5.0324 | 4.84E-07 | Yes |
| PARK2 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| PAX6 | NA | NA | NA | NA | 9.36E-12 | NA | NA | No |
| PBRM1 | NA | NA | NA | NA | NA | 5.111236 | 3.20E-07 | Yes |
| PCDH8P1 | NA | NA | NA | NA | NA | -8.3679 | 5.86E-17 | Yes |
| PCDHA1 | NA | NA | NA | NA | 9.37E-08 | 5.70654 | 1.15E-08 | No |
| PCDHA10 | NA | NA | NA | NA | NA | -5.76667 | 8.09E-09 | Yes |
| PCDHA13 | NA | NA | NA | NA | NA | 5.56824 | 2.57E-08 | Yes |
| PCDHA2 | NA | NA | 4.57 | 4.75 | 1.14E-06 | 5.65614 | 1.55E-08 | No |
| PCDHA3 | NA | NA | NA | NA | 1.50E-06 | 5.72134 | 1.06E-08 | No |
| PCDHA4 | NA | NA | NA | NA | NA | -5.7 | 1.20E-08 | Yes |
| PCDHA5 | NA | NA | NA | -5.40 | 0.00 | -5.28054 | 1.29E-07 | No |
| PCDHA7 | NA | NA | NA | NA | 3.86E-08 | -5.7 | 1.20E-08 | No |
| PCDHA8 | NA | NA | NA | -4.98 | 4.48E-07 | -5.74167 | 9.37E-09 | No |
| PCDHAC1 | NA | NA | NA | NA | NA | -5.32519 | 1.01E-07 | Yes |
| PCDHB13 | NA | NA | NA | NA | NA | -5.1333 | 2.85E-07 | Yes |

| | | | | | | | | |
|---------------|-------|------|-------|-------|----------|-----------|----------|-----|
| PCDHB17P | NA | NA | NA | NA | NA | -5.02693 | 4.98E-07 | Yes |
| PCMTD1 | -5.38 | NA | NA | -4.61 | NA | -4.8324 | 1.35E-06 | No |
| PEBP1 | NA | NA | NA | NA | NA | -5.125 | 2.98E-07 | Yes |
| PFDN1 | NA | NA | NA | NA | NA | 5.4311 | 5.60E-08 | Yes |
| PGBD1 | -5.80 | NA | -5.80 | -6.31 | 1.55E-12 | -7.4676 | 8.17E-14 | No |
| PIGFP2 | NA | NA | NA | -5.31 | NA | NA | NA | No |
| PLCB3 | NA | NA | NA | NA | NA | 5.6482 | 1.62E-08 | Yes |
| PLEKHB1 | NA | NA | NA | NA | NA | 4.9062 | 9.28E-07 | Yes |
| PMFBP1 | NA | NA | NA | -5.16 | NA | NA | NA | No |
| POC1A | NA | NA | NA | NA | NA | 4.8367 | 1.32E-06 | Yes |
| POGZ | NA | NA | NA | NA | NA | -5.550775 | 2.84E-08 | Yes |
| POLI | NA | NA | -4.30 | -4.34 | NA | NA | NA | No |
| POLR1E | NA | NA | NA | NA | NA | -5.0776 | 3.82E-07 | Yes |
| POU5F2 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| PPP1R18 | NA | NA | NA | 4.91 | NA | NA | NA | No |
| PPP3CC | NA | NA | 4.75 | 4.10 | 0.00 | NA | NA | No |
| PPP6C | NA | NA | NA | NA | NA | 5.4851 | 4.13E-08 | Yes |
| PRKAR2A | NA | NA | NA | NA | NA | 4.8857 | 1.03E-06 | Yes |
| PROX2 | NA | NA | NA | -5.76 | 0.00 | -6.51102 | 7.46E-11 | No |
| PRPS1P2 | NA | NA | NA | NA | NA | -5.26209 | 1.42E-07 | Yes |
| PRR16 | NA | NA | NA | NA | NA | 4.89394 | 9.88E-07 | Yes |
| PRRC2A | 6.29 | NA | NA | 3.76 | NA | NA | NA | No |
| PRSS16 | NA | NA | -4.82 | -5.92 | 0.00 | -7.6471 | 2.06E-14 | No |
| PSMB4 | NA | NA | NA | NA | NA | -5.15789 | 2.50E-07 | Yes |
| PSMB7 | NA | NA | NA | NA | NA | -6.75808 | 1.40E-11 | Yes |
| PSMC3 | NA | NA | NA | NA | NA | -5.41935 | 5.98E-08 | Yes |
| PSORS1C2 | NA | NA | NA | NA | NA | 4.8628 | 1.16E-06 | Yes |
| PTBP2 | NA | NA | NA | NA | NA | -4.96 | 7.05E-07 | Yes |
| PTCH1 | NA | NA | NA | NA | 7.82E-07 | 5.1973 | 2.02E-07 | No |
| PTGIS | NA | NA | NA | NA | NA | -5.4681 | 4.55E-08 | Yes |
| PTPMT1 | NA | NA | NA | NA | NA | 4.9794 | 6.38E-07 | Yes |
| PXDNL | NA | 5.89 | NA | 5.89 | NA | NA | NA | No |
| QRICH1 | NA | NA | NA | NA | NA | 5.3513 | 8.73E-08 | Yes |
| RAB27B | NA | NA | NA | 5.01 | 2.46E-08 | 6.201 | 5.61E-10 | No |
| RABEPK | NA | NA | NA | NA | NA | 5.36302 | 8.18E-08 | Yes |
| RABGAP1 | NA | NA | NA | NA | NA | -5.62018 | 1.91E-08 | Yes |
| RALGPS1 | NA | NA | NA | NA | NA | -5.4214 | 5.91E-08 | Yes |
| RANGAP1 | NA | NA | NA | -5.58 | NA | -5.79754 | 6.73E-09 | No |
| RAPSN | NA | NA | NA | NA | NA | 4.9606 | 7.03E-07 | Yes |
| RASGRP1 | NA | NA | NA | NA | 1.86E-06 | NA | NA | No |
| RBM26 | NA | NA | NA | NA | NA | 4.851 | 1.23E-06 | Yes |
| RBX1 | NA | NA | NA | NA | 1.30E-08 | NA | NA | No |
| RCC1L | NA | NA | NA | NA | NA | 5.042803 | 4.59E-07 | Yes |
| RCN1 | NA | NA | NA | NA | 7.67E-09 | NA | NA | No |
| REFE | -5.46 | NA | -5.19 | -5.31 | 1.03E-11 | -8.06452 | 7.35E-16 | No |
| RERE-AS1 | NA | NA | NA | NA | NA | -8.26 | 1.48E-16 | Yes |
| RFTN2 | NA | NA | NA | NA | NA | 5.24979 | 1.52E-07 | Yes |
| RFWD2 | NA | NA | NA | 5.04 | NA | -6.50412 | 7.82E-11 | No |
| RHOA | NA | NA | NA | NA | 6.35E-11 | 5.2591 | 1.45E-07 | No |
| RILPL1 | NA | NA | NA | NA | NA | -4.833629 | 1.34E-06 | Yes |
| RN7SL693P | NA | NA | NA | NA | NA | -5.36381 | 8.15E-08 | Yes |
| RNF34 | NA | NA | NA | NA | NA | 6.07702 | 1.22E-09 | Yes |

| | | | | | | | | |
|---------------|-------|-------|-------|-------|----------|-----------|----------|-----|
| RP1-153G14.4 | NA | NA | NA | 5.35 | 0.00 | 6.9 | 5.20E-12 | No |
| RP1-265C24.5 | NA | NA | 5.01 | 5.53 | NA | NA | NA | No |
| RP1-265C24.8 | NA | NA | NA | NA | 9.11E-12 | -6.98553 | 2.84E-12 | No |
| RP1-86C11.7 | NA | NA | NA | NA | 6.46E-11 | NA | NA | No |
| RP11-163N6.2 | NA | NA | NA | -5.34 | NA | NA | NA | No |
| RP11-112.1 | NA | NA | NA | NA | 1.29E-06 | -5.4147 | 6.14E-08 | No |
| RP11-220I1.5 | NA | NA | NA | NA | 2.79E-08 | NA | NA | No |
| RP11-239L20.6 | NA | NA | 4.69 | 0.87 | NA | NA | NA | No |
| RP11-24H2.3 | NA | NA | NA | NA | 2.67E-11 | -7.7175 | 1.19E-14 | No |
| RP11-318C24.2 | NA | NA | -4.83 | -5.03 | 2.41E-11 | -6.55 | 5.93E-11 | No |
| RP11-3B7.1 | NA | NA | NA | NA | 6.77E-12 | -5.71875 | 1.07E-08 | No |
| RP11-571M6.17 | NA | NA | NA | NA | 2.79E-06 | NA | NA | No |
| RP11-597G23.1 | NA | NA | 4.56 | 4.11 | NA | NA | NA | No |
| RP11-600F24.2 | NA | NA | NA | 5.19 | NA | NA | NA | No |
| RP11-73M18.6 | NA | NA | NA | 5.03 | NA | NA | NA | No |
| RP11-73M18.7 | NA | NA | NA | 4.86 | NA | NA | NA | No |
| RP11-73M18.8 | NA | NA | NA | 5.14 | NA | NA | NA | No |
| RP11-73M18.9 | NA | NA | 4.94 | 4.98 | NA | NA | NA | No |
| RP11-814H16.2 | NA | NA | NA | 5.01 | NA | NA | NA | No |
| RP11-894P9.2 | NA | NA | NA | -5.46 | NA | NA | NA | No |
| RP5-1115A15.1 | NA | NA | NA | -5.18 | NA | NA | NA | No |
| RP5-874C20.3 | NA | NA | 5.85 | 5.74 | NA | NA | NA | No |
| RPL10AP1 | NA | NA | NA | NA | NA | -5.3888 | 7.09E-08 | Yes |
| RPL31P12 | NA | NA | -7.85 | -7.79 | NA | -10.67952 | 1.27E-26 | No |
| RPRD1B | NA | NA | NA | NA | NA | -5.4265 | 5.75E-08 | Yes |
| RPS29P5 | NA | NA | NA | NA | NA | -6.25678 | 3.93E-10 | Yes |
| RPS6K11 | NA | NA | NA | -5.02 | NA | NA | NA | No |
| RTN1 | NA | NA | NA | -5.35 | NA | -5.73258 | 9.89E-09 | No |
| RYBP | NA | NA | NA | NA | NA | -4.91812 | 8.74E-07 | Yes |
| SCAI | NA | NA | NA | NA | NA | 4.8904 | 1.01E-06 | Yes |
| SCRN3 | NA | NA | NA | NA | 3.41E-07 | NA | NA | No |
| SDK1 | NA | NA | NA | NA | NA | -4.872625 | 1.10E-06 | Yes |
| SELENBP1 | NA | NA | NA | NA | NA | -5.57 | 2.57E-08 | Yes |
| SELENOH | NA | NA | NA | NA | 4.89E-11 | -6.115701 | 9.61E-10 | No |
| SEMA3G | NA | NA | NA | NA | NA | 5.03569 | 4.76E-07 | Yes |
| SERPING1 | NA | NA | NA | NA | NA | -6.077748 | 1.22E-09 | Yes |
| SF3B1 | NA | 4.45 | NA | 5.21 | 1.65E-07 | 5.96 | 2.46E-09 | No |
| SGIP1 | NA | NA | NA | NA | NA | 5.6711 | 1.42E-08 | Yes |
| SHISA9 | NA | NA | NA | NA | NA | 5.747212 | 9.07E-09 | Yes |
| SLC12A5 | NA | NA | NA | NA | 4.55E-13 | 5.54286 | 2.98E-08 | No |
| SLC25A17 | NA | -4.73 | NA | 5.08 | 3.34E-12 | 6.30088 | 2.96E-10 | No |
| SLC29A3 | NA | NA | NA | NA | NA | -5.1546 | 2.54E-07 | Yes |
| SLC30A9 | -5.46 | NA | -5.46 | -5.77 | NA | 6.486593 | 8.78E-11 | No |
| SLC39A13 | NA | NA | NA | NA | NA | -4.9093 | 9.14E-07 | Yes |
| SLC4A9 | NA | NA | NA | NA | NA | -7.01784 | 2.25E-12 | Yes |
| SLIT1 | NA | NA | NA | NA | NA | 4.9074 | 9.23E-07 | Yes |
| SMIM15P2 | NA | NA | NA | NA | NA | 8.2281 | 1.90E-16 | Yes |
| SMIM4 | NA | NA | NA | NA | 1.86E-06 | NA | NA | No |
| SNORA63 | NA | NA | NA | 4.85 | NA | NA | NA | No |
| SNRPGP2 | NA | NA | NA | NA | NA | -5.47944 | 4.27E-08 | Yes |
| SORBS3 | NA | NA | NA | NA | 7.15E-07 | NA | NA | No |
| SORCS3 | NA | NA | NA | NA | 1.02E-10 | -6.36302 | 1.98E-10 | No |

| | | | | | | | | |
|--------------|------|------|-------|-------|----------|-----------|----------|-----|
| SPCS1 | NA | NA | NA | NA | NA | -4.93333 | 8.08E-07 | Yes |
| SPP13 | NA | NA | -4.66 | -4.64 | 1.10E-10 | -7.0424 | 1.89E-12 | No |
| SRA1 | NA | NA | NA | NA | NA | 5.7891 | 7.08E-09 | Yes |
| ST13 | NA | NA | NA | NA | 0.00 | NA | NA | No |
| STAU1 | NA | NA | NA | NA | 8.25E-08 | -4.8688 | 1.12E-06 | No |
| STK24 | NA | NA | NA | NA | 2.51E-07 | NA | NA | No |
| SUDS3 | NA | NA | NA | NA | NA | 5.3492 | 8.84E-08 | Yes |
| SYNE2 | NA | NA | NA | 5.61 | NA | 5.8267 | 5.65E-09 | No |
| TAL1 | NA | NA | NA | NA | 5.30E-07 | NA | NA | No |
| TBCA | NA | NA | NA | NA | NA | -4.84107 | 1.29E-06 | Yes |
| TCAIM | NA | NA | NA | NA | 1.69E-09 | NA | NA | No |
| TCTA | NA | NA | NA | NA | 2.56E-11 | NA | NA | No |
| TCTEX1D1 | NA | NA | NA | NA | NA | -5.29438 | 1.19E-07 | Yes |
| TEC | NA | NA | NA | NA | NA | 6.34503 | 2.22E-10 | Yes |
| THAP5 | NA | NA | -4.69 | -4.19 | NA | NA | NA | No |
| TIAF1 | NA | NA | -4.73 | -5.36 | 3.07E-05 | NA | NA | No |
| TKT | NA | NA | NA | NA | NA | 5.0953 | 3.48E-07 | Yes |
| TLR4 | NA | NA | NA | NA | NA | -5.45146 | 5.00E-08 | Yes |
| TMCO6 | NA | NA | NA | NA | NA | -6.11993 | 9.36E-10 | Yes |
| TMEM106B | NA | NA | 5.70 | -5.79 | 0.00 | 7.8302 | 4.87E-15 | No |
| TMEM161B | NA | NA | -4.49 | 3.66 | 2.42E-15 | -5.8387 | 5.26E-09 | No |
| TMEM161B-AS1 | NA | NA | NA | 6.72 | NA | 6.91264 | 4.76E-12 | No |
| TMEM165 | NA | NA | NA | NA | NA | -5.31347 | 1.08E-07 | Yes |
| TMEM258 | NA | NA | NA | 5.02 | 1.06E-06 | 5.2727 | 1.34E-07 | No |
| TMEM33 | 5.16 | NA | 5.16 | 4.84 | NA | NA | NA | No |
| TMEM42 | NA | NA | NA | NA | 3.74E-10 | NA | NA | No |
| TMX2 | 5.52 | NA | NA | -0.13 | NA | NA | NA | No |
| TNKS1BP1 | NA | NA | NA | 4.92 | NA | 6.02571 | 1.68E-09 | No |
| TOB2P1 | NA | NA | NA | NA | NA | -5.3385 | 9.37E-08 | Yes |
| TP53111 | NA | NA | NA | NA | 1.35E-05 | NA | NA | No |
| TRAF3 | NA | NA | NA | NA | 2.48E-07 | 5.2 | 1.99E-07 | No |
| TRHDE-AS1 | NA | NA | NA | NA | NA | 4.96357 | 6.92E-07 | Yes |
| TRIAP1 | NA | NA | NA | NA | NA | -5.0329 | 4.83E-07 | Yes |
| TRIM8 | NA | NA | NA | NA | 2.71E-05 | NA | NA | No |
| TRMT61A | NA | 5.05 | NA | 5.05 | 5.90E-10 | 8.6347 | 5.89E-18 | No |
| TSKU | NA | NA | NA | NA | NA | 4.88776 | 1.02E-06 | Yes |
| TXNDC12 | NA | NA | NA | NA | NA | -6.49563 | 8.27E-11 | Yes |
| UBA7 | NA | NA | NA | NA | 5.49E-10 | NA | NA | No |
| UNC119B | NA | NA | NA | NA | NA | 5.1723 | 2.31E-07 | Yes |
| USMG5 | NA | NA | NA | NA | NA | 4.90664 | 9.26E-07 | Yes |
| USP15 | NA | NA | NA | NA | 8.14E-06 | NA | NA | No |
| USP3-AS1 | NA | NA | NA | NA | NA | -4.90395 | 9.39E-07 | Yes |
| USP4 | NA | NA | NA | NA | 2.84E-10 | 6.03315 | 1.61E-09 | No |
| VAMP2 | NA | NA | NA | NA | NA | 5.0309 | 4.88E-07 | Yes |
| VARS2 | NA | NA | NA | 6.32 | NA | 5.7459 | 9.14E-09 | No |
| VDAC2 | NA | NA | NA | NA | NA | -4.850507 | 1.23E-06 | Yes |
| VWA7 | NA | NA | NA | NA | NA | 5.2581 | 1.46E-07 | Yes |
| WASF5P | NA | NA | NA | -5.16 | NA | -5.6286 | 1.82E-08 | No |
| WDR55 | NA | NA | NA | NA | 7.08E-06 | -5.9676 | 2.41E-09 | No |
| WDR82 | NA | NA | NA | NA | NA | -4.96056 | 7.03E-07 | Yes |
| XPNPEP3 | NA | 5.11 | 4.54 | 5.11 | NA | 6.3325 | 2.41E-10 | No |
| XRCC3 | NA | NA | NA | NA | NA | 6.2751 | 3.49E-10 | Yes |

| | | | | | | | | |
|----------------|-------|-------|-------|-------|----------|----------|----------|-----|
| YLPM1 | NA | NA | NA | NA | 1.33E-12 | 6.4133 | 1.42E-10 | No |
| ZBTB12 | NA | NA | 5.23 | 3.76 | NA | 5.6052 | 2.08E-08 | No |
| ZC3H7B | NA | NA | 4.37 | 5.73 | 1.50E-09 | 6.05882 | 1.37E-09 | No |
| ZDHHC21 | NA | NA | NA | NA | NA | 5.02149 | 5.13E-07 | Yes |
| ZDHHCS | NA | NA | NA | NA | 1.65E-10 | 6.0954 | 1.09E-09 | No |
| ZFYVE21 | NA | NA | NA | NA | NA | 7.3023 | 2.83E-13 | Yes |
| ZKSCAN3 | 5.05 | NA | 5.05 | 6.09 | NA | 7.0152 | 2.30E-12 | No |
| ZKSCAN4 | -6.08 | NA | NA | -3.89 | 8.66E-25 | -8.5972 | 8.17E-18 | No |
| ZKSCAN7 | NA | NA | NA | NA | 1.44E-11 | NA | NA | No |
| ZKSCAN8 | NA | NA | NA | NA | 1.30E-08 | 8.13254 | 4.20E-16 | No |
| ZMAT2 | NA | NA | NA | NA | NA | -6.09238 | 1.11E-09 | Yes |
| ZMYND8 | 4.95 | NA | NA | -0.2 | NA | NA | NA | No |
| ZNF165 | -4.96 | NA | NA | 4.19 | 3.10E-13 | 4.92146 | 8.59E-07 | No |
| ZNF184 | -5.19 | NA | -5.19 | -6.33 | 1.02E-15 | -7.3843 | 1.53E-13 | No |
| ZNF192P1 | NA | NA | NA | NA | NA | -6.8879 | 5.66E-12 | Yes |
| ZNF197 | NA | NA | NA | NA | 3.11E-12 | -6.23175 | 4.61E-10 | No |
| ZNF204P | NA | NA | NA | -5.03 | NA | -7.9333 | 2.13E-15 | No |
| ZNF391 | NA | NA | NA | NA | NA | 5.15767 | 2.50E-07 | Yes |
| ZNF445 | NA | -5.11 | NA | -5.1 | 1.17E-10 | -6.40297 | 1.52E-10 | No |
| ZNF501 | NA | NA | NA | NA | 2.21E-08 | -4.84451 | 1.27E-06 | No |
| ZNF502 | NA | NA | NA | NA | 8.67E-09 | -5.0969 | 3.45E-07 | No |
| ZNF602P | NA | NA | NA | NA | NA | 7.5471 | 4.45E-14 | Yes |
| ZNF638 | NA | NA | NA | NA | NA | -5 | 5.64E-07 | Yes |
| ZNF660 | NA | NA | NA | NA | 1.26E-08 | NA | NA | No |
| ZNF684 | NA | NA | NA | NA | NA | 5.00313 | 5.64E-07 | Yes |
| ZNF852 | NA | NA | NA | NA | 9.97E-11 | NA | NA | No |
| ZNFX1 | NA | NA | NA | NA | 1.30E-05 | NA | NA | No |
| ZSCAN12 | NA | NA | NA | NA | 3.19E-20 | NA | NA | No |
| ZSCAN12P1 | NA | NA | NA | 6.27 | NA | 7.1867 | 6.64E-13 | No |
| ZSCAN16 | -5.47 | NA | NA | -6.11 | 1.64E-10 | -7.4977 | 6.49E-14 | No |
| ZSCAN16-AS1 | NA | NA | NA | NA | NA | 6.4549 | 1.08E-10 | Yes |
| ZSCAN23 | -5.66 | NA | -5.66 | -5.78 | NA | NA | NA | No |
| ZSCAN26 | NA | NA | NA | NA | NA | 6.85488 | 7.14E-12 | Yes |
| ZSCAN31 | -5.59 | NA | -5.59 | -5.08 | NA | -5.9996 | 1.98E-09 | No |
| ZSCAN9 | -5.14 | NA | -5.14 | -6.16 | 1.40E-20 | -8.42105 | 3.73E-17 | No |

TWAS= Transcriptome wide association study; MD= major depression; Novel= compared to the previous TWASes of MD on the left of the table.

The table in green (results from the current TWAS of MD) shows 330 significant gene associations out of the 354 gene associations of the current study in total. 24 processed pseudogenes, transcribed processed pseudogenes, unprocessed pseudogenes and lncRNAs are not shown.

In the current TWAS of MD (in green) 205 gene associations were novel and have not been previously reported across the five largest TWASs of MD (left).

80 gene associations are shared between the current TWAS (in green) and the Dall'Aglio et al. (2021) study (on the left)

89 gene associations are shared between the current TWAS (in green) and the Levey et al. (2021) study (on the left)

Genes in bold font (44) are shared associations across the three largest MD TWASs (Meng et al. 2023 (the current TWAS, in green), Levey et al. 2021 and Dall'Aglio et al. 2021)

The Z-scores of the current TWAS (in green) presented in column Meng_Navoly_TWAS.Z are the z-scores computed for each gene using each gene's best tissue MODELCV.PV p-value)

The Levey et al. (2021) study used S-MultiXcan to compute TWAS results. For this study, TWAS p-values are shown instead of TWAS z-scores.

The table on the left is an extension of the gene table from Dall'Aglio et al. (2021) supplementary material.

Supplementary Table 12. Genes prioritisation combining FUMA, MAGMA, Hi-C MAGMA and TWAS.

| ENSG ID | Gene symbol | FUMASig | MAGMASig | HiCMAGM | TWASSig | CHR | Start | End | FUMA.posl | FUMA.eqtl | FUMA.IndS | MAGMA.N | MAGMA.P | HiCMAGM | HiCMAGM | TWAS.Z | TWAS.P | TWAS.Nov | Magma.Novel |
|-----------------|------------------|---------|----------|---------|---------|-----|----------|----------|-----------|-----------|------------|---------|----------|---------|----------|-----------|----------|----------|-------------|
| ENSG00000116288 | <i>PARK7</i> | FALSE | FALSE | TRUE | FALSE | 1 | 8021723 | 8045565 | NA | NA | NA | NA | NA | 293 | 5.90E-06 | NA | NA | NA | TRUE |
| ENSG00000162426 | <i>SLC45A1</i> | TRUE | FALSE | FALSE | FALSE | 1 | 8377886 | 8404227 | 0 | 3 | rs301805 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000142599 | <i>RERE</i> | TRUE | TRUE | TRUE | TRUE | 1 | 8412457 | 8877702 | 142 | 13 | rs301805 | 847 | 3.48E-08 | 380 | 1.29E-09 | -8.06452 | 7.35E-16 | FALSE | FALSE |
| ENSG00000232912 | <i>RERE-AS1</i> | FALSE | TRUE | TRUE | TRUE | 1 | 8449705 | 8504898 | NA | NA | NA | 84 | 4.08E-08 | 20 | 7.30E-07 | -8.26 | 1.48E-16 | TRUE | TRUE |
| ENSG00000270282 | | FALSE | TRUE | TRUE | FALSE | 1 | 8537712 | 8583080 | NA | NA | NA | 83 | 2.08E-06 | 5 | 6.87E-05 | NA | NA | NA | TRUE |
| ENSG00000221083 | | FALSE | TRUE | TRUE | FALSE | 1 | 8561854 | 8606978 | NA | NA | NA | 65 | 3.53E-06 | 7 | 2.80E-06 | NA | NA | NA | TRUE |
| ENSG00000234619 | <i>RPL7P11</i> | FALSE | TRUE | FALSE | FALSE | 1 | 8775489 | 8821146 | NA | NA | NA | 68 | 0.000454 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000226545 | | FALSE | TRUE | FALSE | FALSE | 1 | 8823534 | 8869565 | NA | NA | NA | 77 | 0.005192 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000224315 | <i>RPL7P7</i> | FALSE | TRUE | FALSE | FALSE | 1 | 8836270 | 8881972 | NA | NA | NA | 76 | 0.037528 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000228423 | | FALSE | TRUE | FALSE | FALSE | 1 | 8855919 | 8902110 | NA | NA | NA | 91 | 0.048203 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000229716 | <i>RPL23AP19</i> | FALSE | TRUE | TRUE | FALSE | 1 | 8856066 | 8901434 | NA | NA | NA | 89 | 0.047858 | 5 | 0.024417 | NA | NA | NA | TRUE |
| ENSG00000234481 | | FALSE | TRUE | TRUE | FALSE | 1 | 37203741 | 37251369 | NA | NA | NA | 86 | 0.000271 | 3 | 0.024408 | NA | NA | NA | TRUE |
| ENSG00000207328 | <i>RNU6-636P</i> | FALSE | FALSE | TRUE | FALSE | 1 | 37669211 | 37669317 | NA | NA | NA | NA | NA | 187 | 3.75E-05 | NA | NA | NA | TRUE |
| ENSG00000223944 | | FALSE | TRUE | FALSE | FALSE | 1 | 37718340 | 37825701 | NA | NA | NA | 427 | 0.024596 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000252368 | <i>RNA5SP43</i> | FALSE | TRUE | FALSE | FALSE | 1 | 37720278 | 37765387 | NA | NA | NA | 153 | 0.006028 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000227416 | | FALSE | FALSE | TRUE | FALSE | 1 | 38248129 | 38248557 | NA | NA | NA | NA | NA | 6 | 0.033504 | NA | NA | NA | TRUE |
| ENSG00000204084 | <i>INPP5B</i> | FALSE | FALSE | FALSE | TRUE | 1 | 38326369 | 38412729 | NA | NA | NA | NA | NA | NA | NA | -5.0294 | 4.92E-07 | TRUE | NA |
| ENSG00000117010 | <i>ZNF684</i> | FALSE | FALSE | FALSE | TRUE | 1 | 40997245 | 41013839 | NA | NA | NA | NA | NA | NA | NA | 5.00313 | 5.64E-07 | TRUE | NA |
| ENSG00000186094 | <i>AGBL4</i> | TRUE | FALSE | FALSE | FALSE | 1 | 48998527 | 50489585 | 41 | 0 | rs1157924f | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000230114 | <i>AGBL4-AS1</i> | FALSE | FALSE | TRUE | FALSE | 1 | 49723083 | 49734957 | NA | NA | NA | NA | NA | 151 | 0.001951 | NA | NA | NA | TRUE |
| ENSG00000227839 | <i>NA</i> | TRUE | FALSE | TRUE | FALSE | 1 | 50459990 | 50461874 | 2 | 0 | rs1157924f | NA | NA | 27 | 0.001064 | NA | NA | NA | TRUE |
| ENSG00000233595 | <i>MTND2P29</i> | FALSE | FALSE | TRUE | FALSE | 1 | 50482764 | 50483175 | NA | NA | NA | NA | NA | 2 | 0.000751 | NA | NA | NA | TRUE |
| ENSG00000162374 | <i>ELAVL4</i> | TRUE | FALSE | FALSE | FALSE | 1 | 50513686 | 50669458 | 3 | 0 | rs1157924f | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000230828 | | FALSE | TRUE | FALSE | FALSE | 1 | 50545609 | 50590954 | NA | NA | NA | 68 | 0.00676 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000085832 | <i>EPS15</i> | FALSE | FALSE | TRUE | FALSE | 1 | 51819935 | 51985000 | NA | NA | NA | NA | NA | 223 | 0.000188 | NA | NA | NA | TRUE |
| ENSG00000078618 | <i>NRDC</i> | TRUE | TRUE | FALSE | TRUE | 1 | 52254863 | 52344477 | 31 | 9 | rs7551758 | 402 | 0.000959 | NA | NA | 5.94 | 2.81E-09 | TRUE | TRUE |
| ENSG00000266993 | | FALSE | FALSE | FALSE | TRUE | 1 | 52259606 | 52264826 | NA | NA | NA | NA | NA | NA | NA | 7 | 2.56E-12 | NA | NA |
| ENSG00000230604 | <i>TSEN15P2</i> | FALSE | TRUE | FALSE | FALSE | 1 | 52290450 | 52335807 | NA | NA | NA | 127 | 0.000163 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000212076 | <i>NA</i> | FALSE | TRUE | FALSE | FALSE | 1 | 52292013 | 52337082 | NA | NA | NA | 129 | 0.000157 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000212174 | <i>NA</i> | FALSE | TRUE | FALSE | FALSE | 1 | 52296305 | 52341381 | NA | NA | NA | 130 | 0.000669 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000169213 | <i>RAB3B</i> | TRUE | FALSE | FALSE | FALSE | 1 | 52373628 | 52456436 | 0 | 9 | rs7551758 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000117862 | <i>TXNDC12</i> | TRUE | FALSE | FALSE | TRUE | 1 | 52485803 | 52521843 | 0 | 2 | rs7551758 | NA | NA | NA | NA | -6.49563 | 8.27E-11 | TRUE | NA |
| ENSG00000154222 | <i>CC2D1B</i> | TRUE | FALSE | FALSE | FALSE | 1 | 52811395 | 52831865 | 0 | 1 | rs7551758 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000162378 | <i>ZYG11B</i> | TRUE | FALSE | FALSE | FALSE | 1 | 53192126 | 53293014 | 0 | 2 | rs7551758 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000118473 | <i>SGIP1</i> | FALSE | TRUE | FALSE | TRUE | 1 | 66964066 | 67223982 | NA | NA | NA | 973 | 0.001089 | NA | NA | 5.6711 | 1.42E-08 | TRUE | FALSE |
| ENSG00000248458 | | FALSE | TRUE | FALSE | FALSE | 1 | 67121547 | 67177710 | NA | NA | NA | 191 | 0.017572 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000152760 | <i>DYNLT5</i> | FALSE | TRUE | FALSE | TRUE | 1 | 67183143 | 67254470 | NA | NA | NA | 189 | 0.008732 | NA | NA | -5.29438 | 1.19E-07 | NA | TRUE |
| ENSG00000198160 | <i>MIER1</i> | FALSE | FALSE | FALSE | TRUE | 1 | 67390578 | 67454302 | NA | NA | NA | NA | NA | NA | NA | -5.2016 | 1.98E-07 | TRUE | NA |
| ENSG00000172260 | <i>NEGR1</i> | TRUE | TRUE | TRUE | TRUE | 1 | 71861623 | 72748417 | 10 | 29 | rs1432639 | 2079 | 2.31E-06 | 91 | 1.53E-07 | 10.67742 | 1.30E-26 | FALSE | FALSE |
| ENSG00000233994 | <i>GDI2P2</i> | FALSE | TRUE | TRUE | FALSE | 1 | 72705235 | 72750842 | NA | NA | NA | 77 | 2.79E-05 | 7 | 2.68E-05 | NA | NA | NA | TRUE |
| ENSG00000227207 | <i>RPL31P12</i> | FALSE | TRUE | TRUE | TRUE | 1 | 72732155 | 72777512 | NA | NA | NA | 78 | 3.25E-09 | 31 | 2.68E-05 | -10.67952 | 1.27E-26 | FALSE | TRUE |
| ENSG00000227016 | <i>LINC02796</i> | FALSE | TRUE | TRUE | FALSE | 1 | 73195714 | 73266965 | NA | NA | NA | 215 | 0.007989 | 17 | 4.62E-08 | NA | NA | NA | TRUE |
| ENSG00000225087 | | FALSE | TRUE | TRUE | FALSE | 1 | 73204604 | 73399823 | NA | NA | NA | 460 | 2.66E-08 | 37 | 5.94E-10 | NA | NA | NA | TRUE |
| ENSG00000280317 | | FALSE | TRUE | TRUE | FALSE | 1 | 73434697 | 73479997 | NA | NA | NA | 126 | 6.56E-07 | 10 | 3.40E-09 | NA | NA | NA | TRUE |
| ENSG00000229636 | <i>KRT8P21</i> | FALSE | TRUE | TRUE | FALSE | 1 | 73535475 | 73581965 | NA | NA | NA | 235 | 2.96E-09 | 73 | 1.84E-07 | NA | NA | NA | TRUE |
| ENSG00000251825 | <i>RN7SKP19</i> | FALSE | TRUE | TRUE | FALSE | 1 | 73647287 | 73692538 | NA | NA | NA | 83 | 1.08E-10 | 7 | 7.48E-06 | NA | NA | NA | TRUE |
| ENSG00000233973 | <i>LINC01360</i> | FALSE | TRUE | TRUE | FALSE | 1 | 73736853 | 73830936 | NA | NA | NA | 208 | 8.74E-10 | 49 | 2.11E-10 | NA | NA | NA | TRUE |

| | | | | | | | | | | | | | | | | | | | |
|-----------------|-----------|-------|-------|-------|-------|---|----------|----------|----|-----|------------|------|----------|-----|----------|-----------|----------|-------|-------|
| ENSG00000116783 | TNNI3K | FALSE | FALSE | TRUE | FALSE | 1 | 74701085 | 75010108 | NA | NA | NA | NA | NA | 65 | 3.85E-08 | NA | NA | NA | TRUE |
| ENSG00000162621 | LRRCS3 | FALSE | FALSE | TRUE | FALSE | 1 | 74935562 | 74978298 | NA | NA | NA | NA | NA | 40 | 2.44E-05 | NA | NA | NA | TRUE |
| ENSG00000266033 | NA | FALSE | TRUE | FALSE | FALSE | 1 | 80785064 | 80830173 | NA | NA | NA | 205 | 0.004108 | NA | NA | NA | NA | TRUE | |
| ENSG00000225598 | | FALSE | TRUE | FALSE | FALSE | 1 | 80829049 | 80875306 | NA | NA | NA | 202 | 0.011102 | NA | NA | NA | NA | TRUE | |
| ENSG00000117569 | PTBP2 | FALSE | FALSE | FALSE | TRUE | 1 | 97187221 | 97289294 | NA | NA | NA | NA | NA | NA | | -4.96 | 7.05E-07 | TRUE | NA |
| ENSG00000143393 | PI4KB | FALSE | FALSE | TRUE | FALSE | 1 | 1.51E+08 | 1.51E+08 | NA | NA | NA | NA | NA | 34 | 0.007532 | NA | NA | NA | TRUE |
| ENSG00000143416 | SELENBP1 | FALSE | FALSE | FALSE | TRUE | 1 | 1.51E+08 | 1.51E+08 | NA | NA | NA | NA | NA | NA | | -5.57 | 2.57E-08 | TRUE | NA |
| ENSG00000159377 | PSMB4 | FALSE | TRUE | FALSE | TRUE | 1 | 1.51E+08 | 1.51E+08 | NA | NA | NA | 89 | 0.014105 | NA | NA | -5.15789 | 2.50E-07 | TRUE | FALSE |
| ENSG00000143442 | POGZ | FALSE | TRUE | FALSE | TRUE | 1 | 1.51E+08 | 1.51E+08 | NA | NA | NA | 185 | 0.031779 | NA | NA | -5.550775 | 2.84E-08 | TRUE | FALSE |
| ENSG00000238711 | RNY4P25 | FALSE | TRUE | FALSE | FALSE | 1 | 1.51E+08 | 1.51E+08 | NA | NA | NA | 75 | 0.011256 | NA | NA | NA | NA | TRUE | |
| ENSG00000116147 | TNR | FALSE | FALSE | TRUE | FALSE | 1 | 1.75E+08 | 1.76E+08 | NA | NA | NA | NA | NA | 178 | 0.006663 | NA | NA | NA | TRUE |
| ENSG00000227740 | LINC02803 | FALSE | FALSE | FALSE | TRUE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | NA | NA | NA | | -6.55 | 5.93E-11 | NA | NA |
| ENSG00000230777 | RPS29P5 | FALSE | FALSE | FALSE | TRUE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | NA | NA | NA | | -6.25678 | 3.93E-10 | TRUE | NA |
| ENSG00000143207 | COP1 | TRUE | TRUE | FALSE | TRUE | 1 | 1.76E+08 | 1.76E+08 | 91 | 114 | rs35846375 | 761 | 0.000601 | NA | NA | -6.50412 | 7.82E-11 | NA | TRUE |
| ENSG00000252906 | SCARNA3 | FALSE | TRUE | FALSE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 113 | 0.015601 | NA | NA | NA | NA | TRUE | |
| ENSG00000228686 | | FALSE | TRUE | FALSE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 119 | 0.001575 | NA | NA | NA | NA | TRUE | |
| ENSG00000236021 | COP1-DT | FALSE | TRUE | FALSE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 176 | 5.36E-05 | NA | NA | NA | NA | TRUE | |
| ENSG00000232463 | | FALSE | TRUE | TRUE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 107 | 0.000956 | 17 | 0.004146 | NA | NA | NA | TRUE |
| ENSG00000253025 | RNU2-12P | FALSE | TRUE | FALSE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 97 | 0.000822 | NA | NA | NA | NA | TRUE | |
| ENSG00000227815 | | FALSE | TRUE | FALSE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 105 | 0.00181 | NA | NA | NA | NA | TRUE | |
| ENSG00000231020 | | FALSE | TRUE | TRUE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 151 | 0.003206 | 13 | 0.000999 | NA | NA | NA | TRUE |
| ENSG00000225904 | MORF4L1P7 | FALSE | TRUE | FALSE | FALSE | 1 | 1.76E+08 | 1.76E+08 | NA | NA | NA | 98 | 0.001582 | NA | NA | NA | NA | TRUE | |
| ENSG00000152092 | ASTN1 | FALSE | FALSE | FALSE | TRUE | 1 | 1.77E+08 | 1.77E+08 | NA | NA | NA | NA | NA | NA | | -5.8 | 6.78E-09 | TRUE | NA |
| ENSG00000198797 | BRINP2 | TRUE | FALSE | FALSE | FALSE | 1 | 1.77E+08 | 1.77E+08 | 0 | 124 | rs35846375 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000224968 | LINC01645 | FALSE | FALSE | TRUE | FALSE | 1 | 1.77E+08 | 1.81E+08 | NA | NA | NA | NA | NA | 54 | 0.002837 | NA | NA | NA | TRUE |
| ENSG00000153029 | MR1 | FALSE | FALSE | TRUE | FALSE | 1 | 1.81E+08 | 1.81E+08 | NA | NA | NA | NA | NA | 75 | 0.033248 | NA | NA | NA | FALSE |
| ENSG00000198216 | CACNA1E | TRUE | TRUE | FALSE | TRUE | 1 | 1.81E+08 | 1.82E+08 | 24 | 12 | rs199929 | 1050 | 2.54E-05 | NA | NA | -6.09332 | 1.11E-09 | FALSE | FALSE |
| ENSG00000252977 | RNA5SP70 | FALSE | TRUE | TRUE | FALSE | 1 | 1.82E+08 | 1.82E+08 | NA | NA | NA | 110 | 0.000193 | 12 | 3.69E-05 | NA | NA | NA | TRUE |
| ENSG00000272880 | | FALSE | FALSE | FALSE | TRUE | 1 | 1.82E+08 | 1.82E+08 | NA | NA | NA | NA | NA | NA | | 5.42 | 5.87E-08 | NA | NA |
| ENSG00000134376 | CRB1 | FALSE | FALSE | FALSE | TRUE | 1 | 1.97E+08 | 1.97E+08 | NA | NA | NA | NA | NA | NA | | -6.5 | 8.03E-11 | TRUE | NA |
| ENSG00000230260 | | FALSE | TRUE | FALSE | FALSE | 1 | 1.97E+08 | 1.97E+08 | NA | NA | NA | 51 | 2.62E-05 | NA | NA | NA | NA | TRUE | |
| ENSG00000213047 | DENND1B | FALSE | FALSE | FALSE | TRUE | 1 | 1.97E+08 | 1.98E+08 | NA | NA | NA | NA | NA | NA | | -6.33118 | 2.43E-10 | FALSE | NA |
| ENSG00000235582 | | FALSE | TRUE | TRUE | FALSE | 1 | 1.98E+08 | 1.98E+08 | NA | NA | NA | 52 | 0.025807 | 3 | 0.001828 | NA | NA | NA | TRUE |
| ENSG00000163050 | COQ8A | FALSE | TRUE | FALSE | FALSE | 1 | 2.27E+08 | 2.27E+08 | NA | NA | NA | 370 | 0.018828 | NA | NA | NA | NA | TRUE | |
| ENSG00000143641 | GALNT2 | FALSE | FALSE | FALSE | TRUE | 1 | 2.3E+08 | 2.3E+08 | NA | NA | NA | NA | NA | NA | | 5.13 | 2.88E-07 | TRUE | NA |
| ENSG00000186487 | MYT1L | FALSE | FALSE | TRUE | FALSE | 2 | 1792885 | 2334966 | NA | NA | NA | NA | NA | 803 | 0.038918 | NA | NA | NA | TRUE |
| ENSG00000271629 | | FALSE | FALSE | TRUE | FALSE | 2 | 21421390 | 21421768 | NA | NA | NA | NA | NA | 21 | 0.024013 | NA | NA | NA | TRUE |
| ENSG00000264192 | RN7SL117P | FALSE | TRUE | TRUE | FALSE | 2 | 22110865 | 22156160 | NA | NA | NA | 46 | 0.000213 | 2 | 0.003411 | NA | NA | NA | TRUE |
| ENSG00000231200 | NA | FALSE | TRUE | FALSE | FALSE | 2 | 22146208 | 22788977 | NA | NA | NA | 1532 | 5.88E-08 | NA | NA | NA | NA | TRUE | |
| ENSG00000228999 | | FALSE | FALSE | TRUE | FALSE | 2 | 22165050 | 22188552 | NA | NA | NA | NA | NA | 13 | 0.012737 | NA | NA | NA | TRUE |
| ENSG00000234189 | | FALSE | TRUE | FALSE | FALSE | 2 | 22504925 | 22550116 | NA | NA | NA | 95 | 9.93E-07 | NA | NA | NA | NA | TRUE | |
| ENSG00000206882 | RNA5SP87 | FALSE | TRUE | TRUE | FALSE | 2 | 22551758 | 22596875 | NA | NA | NA | 156 | 1.84E-07 | 13 | 5.21E-07 | NA | NA | NA | TRUE |
| ENSG00000234207 | LINC01830 | FALSE | TRUE | TRUE | FALSE | 2 | 22565466 | 22714876 | NA | NA | NA | 435 | 0.024677 | 15 | 0.000242 | NA | NA | NA | TRUE |
| ENSG00000179915 | NRXN1 | FALSE | FALSE | TRUE | FALSE | 2 | 50145643 | 51259699 | NA | NA | NA | NA | NA | 583 | 0.006262 | NA | NA | NA | TRUE |
| ENSG00000231918 | | FALSE | TRUE | FALSE | FALSE | 2 | 51224739 | 52645055 | NA | NA | NA | 5371 | 1.29E-07 | NA | NA | NA | NA | TRUE | |
| ENSG00000271615 | ACTG1P22 | FALSE | TRUE | FALSE | TRUE | 2 | 57947563 | 58003187 | NA | NA | NA | 99 | 2.14E-05 | NA | NA | -5.08024 | 3.77E-07 | TRUE | TRUE |
| ENSG00000028116 | VRK2 | TRUE | TRUE | TRUE | FALSE | 2 | 58134786 | 58387055 | 34 | 0 | rs1568452 | 645 | 7.69E-07 | 183 | 0.020225 | NA | NA | NA | FALSE |
| ENSG00000251738 | NA | FALSE | FALSE | TRUE | FALSE | 2 | 58289716 | 58289800 | NA | NA | NA | NA | NA | 20 | 9.53E-06 | NA | NA | NA | TRUE |
| ENSG00000115392 | FANCL | TRUE | TRUE | FALSE | TRUE | 2 | 58386378 | 58468507 | 0 | 1 | rs1568452 | 307 | 0.000704 | NA | NA | -6.80622 | 1.00E-11 | FALSE | FALSE |
| ENSG00000233723 | LINC01122 | FALSE | TRUE | TRUE | FALSE | 2 | 58619934 | 59300901 | NA | NA | NA | 1611 | 1.68E-06 | 182 | 0.041085 | NA | NA | NA | TRUE |
| ENSG00000163235 | TGFA | FALSE | FALSE | TRUE | FALSE | 2 | 70674412 | 70781147 | NA | NA | NA | NA | NA | 47 | 0.003846 | NA | NA | NA | TRUE |

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|-----------------|------------|-------|-------|-------|-------|---|----------|----------|----|-----|------------|------|----------|----------|----------|----------|----------|-------|-------|
| ENSG00000124370 | MCEE | FALSE | FALSE | TRUE | FALSE | 2 | 71336814 | 71357367 | NA | NA | NA | NA | 58 | 0.005926 | NA | NA | NA | TRUE | |
| ENSG00000075292 | ZNF638 | TRUE | TRUE | TRUE | TRUE | 2 | 71503691 | 71662199 | 82 | 0 | rs12474077 | 649 | 0.003176 | 260 | 0.004403 | -5 | 5.64E-07 | TRUE | FALSE |
| ENSG00000281195 | | FALSE | TRUE | TRUE | FALSE | 2 | 71566068 | 71613450 | NA | NA | NA | 169 | 0.015282 | 13 | 0.005308 | NA | NA | NA | TRUE |
| ENSG00000200779 | RNU6-105P | FALSE | TRUE | FALSE | FALSE | 2 | 71596885 | 71641988 | NA | NA | NA | 155 | 0.003165 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000135636 | DYSF | TRUE | FALSE | FALSE | TRUE | 2 | 71680852 | 71913898 | 3 | 0 | rs12474077 | NA | NA | NA | NA | -5.5235 | 3.32E-08 | TRUE | NA |
| ENSG00000132305 | IMMT | TRUE | FALSE | FALSE | FALSE | 2 | 86371055 | 86422893 | 0 | 96 | rs11365296 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000068615 | REEP1 | TRUE | FALSE | FALSE | FALSE | 2 | 86441116 | 86565206 | 5 | 0 | rs11365296 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000115548 | KDM3A | TRUE | TRUE | FALSE | FALSE | 2 | 86667770 | 86719839 | 62 | 2 | rs11365296 | 256 | 0.005589 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000115561 | CHMP3 | TRUE | TRUE | FALSE | TRUE | 2 | 86730554 | 86948245 | 81 | 141 | rs11365296 | 291 | 0.028755 | NA | NA | 5.4651 | 4.63E-08 | FALSE | FALSE |
| ENSG00000249884 | RNF103-CHM | TRUE | FALSE | FALSE | FALSE | 2 | 86732791 | 86948245 | 78 | 0 | rs11365296 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000239305 | RNF103 | TRUE | FALSE | FALSE | FALSE | 2 | 86830516 | 86850989 | 13 | 0 | rs11365296 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000153563 | CD8A | TRUE | FALSE | FALSE | FALSE | 2 | 87011729 | 87035519 | 0 | 13 | rs11365296 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000226114 | NDUFB4P5 | FALSE | FALSE | TRUE | FALSE | 2 | 87161585 | 87161945 | NA | NA | NA | NA | NA | 37 | 0.010253 | NA | NA | NA | TRUE |
| ENSG00000183281 | PLGLB1 | TRUE | FALSE | FALSE | FALSE | 2 | 87229682 | 87248975 | 0 | 133 | rs11365296 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000237308 | | FALSE | TRUE | TRUE | FALSE | 2 | 96151770 | 96197279 | NA | NA | NA | 41 | 0.048763 | 1 | 0.038834 | NA | NA | NA | TRUE |
| ENSG00000229689 | | FALSE | TRUE | TRUE | FALSE | 2 | 96156093 | 96208153 | NA | NA | NA | 49 | 0.043796 | 17 | 0.046021 | NA | NA | NA | TRUE |
| ENSG00000273305 | | FALSE | TRUE | FALSE | FALSE | 2 | 96168717 | 96214217 | NA | NA | NA | 40 | 0.029739 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000168992 | OR7E102P | FALSE | FALSE | FALSE | TRUE | 2 | 96212279 | 96213293 | NA | NA | NA | NA | NA | NA | NA | -4.9375 | 7.91E-07 | TRUE | NA |
| ENSG00000235584 | | FALSE | FALSE | FALSE | TRUE | 2 | 96326336 | 96334475 | NA | NA | NA | NA | NA | NA | NA | 4.92 | 8.79E-07 | NA | NA |
| ENSG00000144199 | FAHD2B | FALSE | FALSE | FALSE | TRUE | 2 | 97749320 | 97760619 | NA | NA | NA | NA | NA | NA | NA | -5.24731 | 1.54E-07 | TRUE | NA |
| ENSG00000256637 | LINC01965 | FALSE | TRUE | FALSE | TRUE | 2 | 1.04E+08 | 1.05E+08 | NA | NA | NA | 602 | 0.018637 | NA | NA | 4.86 | 1.17E-06 | TRUE | TRUE |
| ENSG00000232597 | | FALSE | TRUE | FALSE | FALSE | 2 | 1.04E+08 | 1.05E+08 | NA | NA | NA | 161 | 6.35E-05 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000236141 | | FALSE | TRUE | FALSE | FALSE | 2 | 1.04E+08 | 1.05E+08 | NA | NA | NA | 100 | 0.003671 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000235597 | LINC01102 | FALSE | TRUE | TRUE | FALSE | 2 | 1.05E+08 | 1.05E+08 | NA | NA | NA | 287 | 0.008819 | 66 | 0.000515 | NA | NA | NA | TRUE |
| ENSG00000155052 | CNTNAP5 | FALSE | TRUE | FALSE | FALSE | 2 | 1.25E+08 | 1.26E+08 | NA | NA | NA | 3059 | 0.002265 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000168702 | LRP1B | FALSE | TRUE | FALSE | FALSE | 2 | 1.41E+08 | 1.43E+08 | NA | NA | NA | 8288 | 0.002119 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000228655 | | FALSE | TRUE | FALSE | FALSE | 2 | 1.44E+08 | 1.44E+08 | NA | NA | NA | 617 | 0.018632 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000144354 | CDCA7 | FALSE | FALSE | TRUE | FALSE | 2 | 1.74E+08 | 1.74E+08 | NA | NA | NA | NA | NA | 98 | 0.046289 | NA | NA | NA | TRUE |
| ENSG00000138430 | OLA1 | TRUE | FALSE | FALSE | FALSE | 2 | 1.75E+08 | 1.75E+08 | 0 | 16 | rs17255455 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000280414 | | FALSE | TRUE | FALSE | FALSE | 2 | 1.75E+08 | 1.75E+08 | NA | NA | NA | 111 | 0.012876 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000268241 | NA | FALSE | TRUE | FALSE | FALSE | 2 | 1.75E+08 | 1.75E+08 | NA | NA | NA | 107 | 0.012485 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000138433 | CIR1 | TRUE | FALSE | FALSE | FALSE | 2 | 1.75E+08 | 1.75E+08 | 28 | 0 | rs17255455 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000144306 | SCRN3 | TRUE | FALSE | FALSE | FALSE | 2 | 1.75E+08 | 1.75E+08 | 0 | 2 | rs17255455 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000163328 | GPR155 | TRUE | FALSE | FALSE | FALSE | 2 | 1.75E+08 | 1.75E+08 | 0 | 8 | rs17255455 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000144320 | LNPK | TRUE | FALSE | FALSE | FALSE | 2 | 1.77E+08 | 1.77E+08 | 0 | 9 | rs13743697 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000128713 | HOXD11 | FALSE | TRUE | FALSE | FALSE | 2 | 1.77E+08 | 1.77E+08 | NA | NA | NA | 110 | 0.010967 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000216193 | NA | FALSE | TRUE | FALSE | FALSE | 2 | 1.77E+08 | 1.77E+08 | NA | NA | NA | 105 | 0.012024 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000174279 | EVX2 | TRUE | TRUE | FALSE | FALSE | 2 | 1.77E+08 | 1.77E+08 | 16 | 0 | rs6752623 | 119 | 0.006755 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000128714 | HOXD13 | TRUE | TRUE | FALSE | FALSE | 2 | 1.77E+08 | 1.77E+08 | 17 | 0 | rs6752623 | 127 | 0.003097 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000170178 | HOXD12 | TRUE | TRUE | FALSE | FALSE | 2 | 1.77E+08 | 1.77E+08 | 8 | 0 | rs6752623 | 115 | 0.003936 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000187944 | C2orf66 | FALSE | FALSE | TRUE | FALSE | 2 | 1.98E+08 | 1.98E+08 | NA | NA | NA | NA | NA | 27 | 0.013542 | NA | NA | NA | TRUE |
| ENSG00000197121 | PGAP1 | FALSE | FALSE | TRUE | FALSE | 2 | 1.98E+08 | 1.98E+08 | NA | NA | NA | NA | NA | 230 | 0.006315 | NA | NA | NA | TRUE |
| ENSG00000065413 | ANKRD44 | TRUE | FALSE | FALSE | TRUE | 2 | 1.98E+08 | 1.98E+08 | 47 | 21 | rs1563340 | NA | NA | NA | NA | -6.22781 | 4.73E-10 | FALSE | NA |
| ENSG00000213104 | NPM1P46 | FALSE | TRUE | FALSE | TRUE | 2 | 1.98E+08 | 1.98E+08 | NA | NA | NA | 78 | 0.000461 | NA | NA | 5.9122 | 3.38E-09 | TRUE | TRUE |
| ENSG00000202434 | | FALSE | TRUE | FALSE | FALSE | 2 | 1.98E+08 | 1.98E+08 | NA | NA | NA | 76 | 0.000574 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000115524 | SF3B1 | TRUE | TRUE | FALSE | TRUE | 2 | 1.98E+08 | 1.98E+08 | 26 | 365 | rs1563340 | 117 | 0.000993 | NA | NA | 5.96 | 2.46E-09 | FALSE | FALSE |
| ENSG00000206836 | RNU6-1029P | FALSE | TRUE | TRUE | FALSE | 2 | 1.98E+08 | 1.98E+08 | NA | NA | NA | 58 | 0.000349 | 5 | 0.009222 | NA | NA | NA | TRUE |
| ENSG00000115520 | COQ10B | TRUE | TRUE | FALSE | FALSE | 2 | 1.98E+08 | 1.98E+08 | 10 | 0 | rs1563340 | 80 | 0.023387 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000144381 | HSPD1 | TRUE | TRUE | TRUE | FALSE | 2 | 1.98E+08 | 1.98E+08 | 22 | 0 | rs1563340 | 69 | 0.00217 | 57 | 0.014383 | NA | NA | NA | FALSE |
| ENSG00000231699 | | FALSE | TRUE | FALSE | FALSE | 2 | 1.98E+08 | 1.98E+08 | NA | NA | NA | 55 | 0.003509 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000115541 | HSPE1 | TRUE | TRUE | TRUE | FALSE | 2 | 1.98E+08 | 1.98E+08 | 15 | 0 | rs1563340 | 61 | 0.002425 | 13 | 0.000431 | NA | NA | NA | FALSE |

| | | | | | | | | | | | | | | | | | | | |
|-----------------|--------------------|-------|-------|-------|-------|---|----------|----------|-----|-----|------------|------|----------|-----|----------|----------|----------|-------|-------|
| ENSG00000270757 | <i>HSPE1-MOB4</i> | TRUE | TRUE | FALSE | FALSE | 2 | 1.98E+08 | 1.98E+08 | 32 | 0 | rs1563340 | 130 | 0.003054 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000115540 | <i>MOB4</i> | TRUE | TRUE | FALSE | FALSE | 2 | 1.98E+08 | 1.98E+08 | 27 | 0 | rs1563340 | 116 | 0.001272 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000162944 | <i>RFTN2</i> | TRUE | TRUE | TRUE | TRUE | 2 | 1.98E+08 | 1.99E+08 | 72 | 230 | rs1563340 | 230 | 0.003205 | 297 | 0.000428 | 5.24979 | 1.52E-07 | TRUE | FALSE |
| ENSG00000222017 | | TRUE | FALSE | TRUE | FALSE | 2 | 1.99E+08 | 1.99E+08 | 36 | 0 | rs1563340 | NA | NA | 87 | 0.036198 | NA | NA | NA | TRUE |
| ENSG00000247626 | <i>MARS2</i> | TRUE | FALSE | FALSE | FALSE | 2 | 1.99E+08 | 1.99E+08 | 13 | 0 | rs1563340 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000152430 | <i>BOLL</i> | TRUE | FALSE | FALSE | FALSE | 2 | 1.99E+08 | 1.99E+08 | 22 | 0 | rs1563340 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000115896 | <i>PLCL1</i> | TRUE | TRUE | FALSE | FALSE | 2 | 1.99E+08 | 1.99E+08 | 156 | 219 | rs1563340 | 776 | 0.007652 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000236653 | <i>LINC01923</i> | FALSE | FALSE | TRUE | FALSE | 2 | 1.99E+08 | 1.99E+08 | NA | NA | NA | NA | NA | 137 | 0.000653 | NA | NA | NA | TRUE |
| ENSG00000118263 | <i>KLF7</i> | TRUE | TRUE | TRUE | FALSE | 2 | 2.08E+08 | 2.08E+08 | 25 | 0 | rs2111592 | 421 | 0.00118 | 421 | 0.007637 | NA | NA | NA | FALSE |
| ENSG00000224342 | | FALSE | TRUE | TRUE | FALSE | 2 | 2.08E+08 | 2.08E+08 | NA | NA | NA | 228 | 0.000203 | 6 | 0.031408 | NA | NA | NA | TRUE |
| ENSG00000234902 | | FALSE | TRUE | FALSE | FALSE | 2 | 2.08E+08 | 2.08E+08 | NA | NA | NA | 266 | 0.000112 | NA | NA | NA | NA | TRUE | |
| ENSG00000225916 | | FALSE | TRUE | FALSE | FALSE | 2 | 2.08E+08 | 2.08E+08 | NA | NA | NA | 117 | 0.002303 | NA | NA | NA | NA | TRUE | |
| ENSG00000178568 | <i>ERBB4</i> | TRUE | TRUE | FALSE | FALSE | 2 | 2.12E+08 | 2.13E+08 | 39 | 0 | rs7583068 | 4820 | 0.000832 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000197585 | | FALSE | TRUE | FALSE | FALSE | 2 | 2.15E+08 | 2.16E+08 | NA | NA | NA | 1483 | 0.001098 | NA | NA | NA | NA | TRUE | |
| ENSG00000174453 | <i>VWC2L</i> | TRUE | FALSE | FALSE | FALSE | 2 | 2.15E+08 | 2.15E+08 | 34 | 0 | rs13795929 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000144452 | <i>ABCA12</i> | FALSE | FALSE | TRUE | FALSE | 2 | 2.16E+08 | 2.16E+08 | NA | NA | NA | NA | NA | 150 | 0.015192 | NA | NA | NA | TRUE |
| ENSG00000115468 | <i>EFHD1</i> | TRUE | FALSE | FALSE | FALSE | 2 | 2.33E+08 | 2.34E+08 | 4 | 0 | rs283468 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000204120 | <i>GIGYF2</i> | TRUE | TRUE | FALSE | TRUE | 2 | 2.34E+08 | 2.34E+08 | 159 | 134 | rs283468 | 587 | 0.004304 | NA | NA | -5.06449 | 4.09E-07 | TRUE | TRUE |
| ENSG00000213055 | <i>EEF1B2P7</i> | FALSE | TRUE | TRUE | FALSE | 2 | 2.34E+08 | 2.34E+08 | NA | NA | NA | 119 | 0.017771 | 3 | 0.015531 | NA | NA | NA | TRUE |
| ENSG00000252452 | <i>RNU6-107P</i> | FALSE | TRUE | TRUE | FALSE | 2 | 2.34E+08 | 2.34E+08 | NA | NA | NA | 111 | 0.005005 | 9 | 0.003543 | NA | NA | NA | TRUE |
| ENSG00000241409 | | FALSE | TRUE | TRUE | FALSE | 2 | 2.34E+08 | 2.34E+08 | NA | NA | NA | 122 | 0.003494 | 7 | 0.032502 | NA | NA | NA | TRUE |
| ENSG00000115474 | <i>KCNJ13</i> | TRUE | TRUE | FALSE | TRUE | 2 | 2.34E+08 | 2.34E+08 | 27 | 0 | rs283468 | 115 | 0.004054 | NA | NA | 5.13 | 2.98E-07 | TRUE | TRUE |
| ENSG00000199781 | | FALSE | TRUE | FALSE | FALSE | 2 | 2.34E+08 | 2.34E+08 | NA | NA | NA | 106 | 0.02996 | NA | NA | NA | NA | TRUE | |
| ENSG00000182600 | <i>SNORC</i> | TRUE | TRUE | FALSE | FALSE | 2 | 2.34E+08 | 2.34E+08 | 35 | 172 | rs283468 | 161 | 0.008349 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000066248 | <i>NGEF</i> | TRUE | FALSE | FALSE | FALSE | 2 | 2.34E+08 | 2.34E+08 | 18 | 0 | rs283468 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000085978 | <i>ATG16L1</i> | FALSE | FALSE | TRUE | FALSE | 2 | 2.34E+08 | 2.34E+08 | NA | NA | NA | NA | NA | 157 | 0.012001 | NA | NA | NA | TRUE |
| ENSG00000231304 | <i>SGO1-AS1</i> | FALSE | TRUE | FALSE | FALSE | 3 | 20180736 | 21197459 | NA | NA | NA | 4167 | 0.012274 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000283563 | | FALSE | TRUE | FALSE | FALSE | 3 | 28355669 | 29819028 | NA | NA | NA | 5177 | 0.025559 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000144642 | <i>RBMS3</i> | TRUE | TRUE | FALSE | FALSE | 3 | 29322473 | 30051886 | 72 | 0 | rs6783423 | 3154 | 0.000143 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000173769 | <i>TOPAZ1</i> | FALSE | FALSE | TRUE | FALSE | 3 | 44283378 | 44373590 | NA | NA | NA | NA | NA | 87 | 6.90E-05 | NA | NA | NA | FALSE |
| ENSG00000179152 | <i>TCAIM</i> | TRUE | TRUE | TRUE | FALSE | 3 | 44379611 | 44450943 | 0 | 4 | rs1423456 | 248 | 0.045007 | 32 | 0.000797 | NA | NA | NA | FALSE |
| ENSG00000283036 | <i>LINC01988</i> | FALSE | TRUE | TRUE | FALSE | 3 | 44430626 | 44481021 | NA | NA | NA | 99 | 0.001643 | 12 | 0.008298 | NA | NA | NA | TRUE |
| ENSG00000225873 | <i>C3orf86</i> | FALSE | TRUE | TRUE | FALSE | 3 | 44452619 | 44516438 | NA | NA | NA | 114 | 0.000853 | 20 | 0.034354 | NA | NA | NA | TRUE |
| ENSG00000185219 | <i>ZNF445</i> | TRUE | TRUE | TRUE | TRUE | 3 | 44481262 | 44519162 | 0 | 41 | rs1423456 | 138 | 0.000335 | 113 | 0.000797 | -6.40297 | 1.52E-10 | FALSE | FALSE |
| ENSG00000178917 | <i>ZNF852</i> | TRUE | TRUE | FALSE | FALSE | 3 | 44540462 | 44552128 | 0 | 59 | rs1423456 | 114 | 0.000364 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000264774 | <i>NA</i> | FALSE | TRUE | FALSE | FALSE | 3 | 44546708 | 44591793 | NA | NA | NA | 103 | 0.000442 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000214825 | <i>EI24P3</i> | FALSE | TRUE | TRUE | FALSE | 3 | 44556236 | 44602297 | NA | NA | NA | 119 | 0.000364 | 66 | 0.023295 | NA | NA | NA | TRUE |
| ENSG00000277509 | | FALSE | TRUE | FALSE | FALSE | 3 | 44560447 | 44605883 | NA | NA | NA | 126 | 0.000525 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000236869 | <i>ZKSCAN7-AS1</i> | FALSE | TRUE | FALSE | FALSE | 3 | 44588849 | 44762145 | NA | NA | NA | 332 | 0.000181 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000144792 | <i>ZNF660</i> | FALSE | TRUE | FALSE | FALSE | 3 | 44591456 | 44651186 | NA | NA | NA | 138 | 0.000409 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000196345 | <i>ZKSCAN7</i> | TRUE | TRUE | TRUE | FALSE | 3 | 44596685 | 44624975 | 0 | 44 | rs1423456 | 196 | 0.000529 | 90 | 7.33E-05 | NA | NA | NA | FALSE |
| ENSG00000214820 | <i>MPRIPP1</i> | FALSE | TRUE | TRUE | TRUE | 3 | 44611430 | 44657518 | NA | NA | NA | 90 | 0.00043 | 12 | 0.000251 | -6.17709 | 6.53E-10 | TRUE | TRUE |
| ENSG00000186448 | <i>ZNF197</i> | TRUE | TRUE | TRUE | TRUE | 3 | 44626380 | 44689963 | 0 | 86 | rs1423456 | 104 | 0.000235 | 38 | 8.04E-05 | -6.23175 | 4.61E-10 | TRUE | FALSE |
| ENSG00000233509 | <i>ZNF197-AS1</i> | FALSE | TRUE | FALSE | FALSE | 3 | 44648620 | 44701289 | NA | NA | NA | 83 | 0.000196 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000272077 | | FALSE | TRUE | FALSE | FALSE | 3 | 44673904 | 44720856 | NA | NA | NA | 56 | 0.000171 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000169981 | <i>ZNF35</i> | TRUE | TRUE | TRUE | FALSE | 3 | 44690219 | 44702283 | 1 | 0 | rs1423456 | 81 | 0.000111 | 5 | 0.021997 | NA | NA | NA | FALSE |
| ENSG00000196653 | <i>ZNF502</i> | TRUE | TRUE | FALSE | TRUE | 3 | 44754135 | 44765323 | 19 | 101 | rs1423456 | 136 | 0.025526 | NA | NA | -5.0969 | 3.45E-07 | TRUE | TRUE |
| ENSG00000186446 | <i>ZNF501</i> | TRUE | FALSE | FALSE | TRUE | 3 | 44771088 | 44778575 | 26 | 93 | rs1423456 | NA | NA | NA | NA | -4.84451 | 1.27E-06 | TRUE | NA |
| ENSG00000163807 | <i>KIAA1143</i> | TRUE | TRUE | FALSE | FALSE | 3 | 44779153 | 44803154 | 35 | 93 | rs1423456 | 88 | 0.010924 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000163808 | <i>KIF15</i> | TRUE | TRUE | TRUE | FALSE | 3 | 44803209 | 44914868 | 71 | 0 | rs1423456 | 210 | 0.00337 | 250 | 0.000369 | NA | NA | NA | FALSE |
| ENSG00000238958 | <i>NA</i> | FALSE | TRUE | FALSE | FALSE | 3 | 44824507 | 44869597 | NA | NA | NA | 62 | 0.002174 | NA | NA | NA | NA | NA | TRUE |

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|-----------------|----------|-------|-------|-------|-------|---|----------|----------|----|-----|------------|-----|----------|-----|-----------|----------|----------|-------|
| ENSG00000207783 | NA | FALSE | TRUE | FALSE | FALSE | 3 | 44868380 | 44913473 | NA | NA | NA | 83 | 0.000181 | NA | NA | NA | NA | TRUE |
| ENSG00000169964 | TMEM42 | TRUE | TRUE | TRUE | FALSE | 3 | 44903361 | 44907162 | 11 | 0 | rs14234569 | 105 | 0.002167 | 53 | 0.000549 | NA | NA | FALSE |
| ENSG00000163810 | TGM4 | TRUE | FALSE | TRUE | FALSE | 3 | 44916100 | 44956482 | 5 | 0 | rs14234569 | NA | NA | 141 | 0.001028 | NA | NA | TRUE |
| ENSG00000164048 | ZNF589 | TRUE | FALSE | TRUE | FALSE | 3 | 48282590 | 48340743 | 0 | 1 | rs7617480 | NA | NA | 80 | 0.000824 | NA | NA | TRUE |
| ENSG00000232112 | TMA7 | TRUE | FALSE | FALSE | FALSE | 3 | 48481667 | 48485616 | 0 | 85 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000213689 | TREX1 | TRUE | FALSE | FALSE | FALSE | 3 | 48506445 | 48509044 | 0 | 84 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000164054 | SHISA5 | TRUE | FALSE | FALSE | FALSE | 3 | 48509197 | 48542259 | 0 | 2 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000114268 | PFKFB4 | FALSE | FALSE | TRUE | FALSE | 3 | 48555117 | 48594323 | NA | NA | NA | NA | NA | 108 | 0.024359 | NA | NA | TRUE |
| ENSG00000145040 | UCN2 | TRUE | FALSE | FALSE | FALSE | 3 | 48599160 | 48601206 | 0 | 1 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000114270 | COL7A1 | FALSE | FALSE | TRUE | FALSE | 3 | 48601506 | 48632700 | NA | NA | NA | NA | NA | 57 | 0.001739 | NA | NA | TRUE |
| ENSG0000010256 | UQCRC1 | FALSE | FALSE | TRUE | FALSE | 3 | 48636436 | 48647470 | NA | NA | NA | NA | NA | 41 | 0.004254 | NA | NA | TRUE |
| ENSG00000183396 | TMEM89 | FALSE | FALSE | TRUE | FALSE | 3 | 48658192 | 48659288 | NA | NA | NA | NA | NA | 54 | 0.033434 | NA | NA | TRUE |
| ENSG00000008300 | CELSR3 | FALSE | FALSE | TRUE | FALSE | 3 | 48673902 | 48700348 | NA | NA | NA | NA | NA | 71 | 0.006309 | NA | NA | TRUE |
| ENSG00000213672 | NCKIPSD | TRUE | FALSE | FALSE | FALSE | 3 | 48701364 | 48723797 | 0 | 160 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000114302 | PRKAR2A | TRUE | FALSE | TRUE | TRUE | 3 | 48782030 | 48885279 | 0 | 120 | rs7617480 | NA | NA | 124 | 0.002522 | 4.8857 | 1.03E-06 | TRUE |
| ENSG00000178537 | SLC25A20 | FALSE | FALSE | TRUE | FALSE | 3 | 48894364 | 48936426 | NA | NA | NA | NA | NA | 61 | 0.001496 | NA | NA | TRUE |
| ENSG00000221883 | ARIH2OS | FALSE | FALSE | TRUE | FALSE | 3 | 48955221 | 48956818 | NA | NA | NA | NA | NA | 5 | 0.005766 | NA | NA | TRUE |
| ENSG00000177479 | ARIH2 | TRUE | FALSE | FALSE | FALSE | 3 | 48956254 | 49023815 | 0 | 87 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000178467 | P4HTM | TRUE | FALSE | FALSE | TRUE | 3 | 49027319 | 49044587 | 0 | 154 | rs7617480 | NA | NA | NA | -5.85513 | 4.77E-09 | TRUE | NA |
| ENSG00000178252 | WDR6 | TRUE | FALSE | FALSE | FALSE | 3 | 49044495 | 49053386 | 0 | 151 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000178149 | DALRD3 | TRUE | FALSE | FALSE | TRUE | 3 | 49052921 | 49059726 | 0 | 147 | rs7617480 | NA | NA | NA | -4.88581 | 1.03E-06 | TRUE | NA |
| ENSG00000178057 | NDUFAF3 | FALSE | FALSE | TRUE | TRUE | 3 | 49057892 | 49060928 | NA | NA | NA | NA | NA | 41 | 0.004362 | -5.0785 | 3.80E-07 | TRUE |
| ENSG00000198218 | QRICH1 | TRUE | FALSE | FALSE | TRUE | 3 | 49067140 | 49131796 | 1 | 147 | rs7617480 | NA | NA | NA | 5.3513 | 8.73E-08 | TRUE | NA |
| ENSG00000172053 | QARS1 | TRUE | FALSE | FALSE | FALSE | 3 | 49133365 | 49142553 | 3 | 0 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000172046 | USP19 | TRUE | FALSE | FALSE | FALSE | 3 | 49145479 | 49158371 | 4 | 0 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000172037 | LAMB2 | TRUE | FALSE | FALSE | TRUE | 3 | 49158547 | 49170551 | 2 | 0 | rs7617480 | NA | NA | NA | 5.12903 | 2.91E-07 | TRUE | NA |
| ENSG00000270441 | LAMB2P1 | FALSE | TRUE | FALSE | TRUE | 3 | 49167519 | 49233284 | NA | NA | NA | 95 | 0.001039 | NA | -6.176471 | 6.56E-10 | TRUE | TRUE |
| ENSG00000177352 | CCDC71 | TRUE | TRUE | TRUE | TRUE | 3 | 49199968 | 49203754 | 2 | 145 | rs7617480 | 73 | 5.56E-05 | 33 | 0.039281 | 6.9722 | 3.12E-12 | TRUE |
| ENSG00000185909 | KLHDC8B | TRUE | TRUE | FALSE | FALSE | 3 | 49209044 | 49213917 | 10 | 2 | rs7617480 | 74 | 0.001454 | NA | NA | NA | NA | TRUE |
| ENSG00000236980 | C3orf84 | TRUE | TRUE | FALSE | FALSE | 3 | 49215065 | 49229291 | 16 | 0 | rs7617480 | 85 | 9.99E-05 | NA | NA | NA | NA | FALSE |
| ENSG00000173421 | IHO1 | TRUE | TRUE | FALSE | TRUE | 3 | 49235861 | 49295537 | 26 | 0 | rs7617480 | 147 | 0.000532 | NA | -5.4768 | 4.33E-08 | TRUE | TRUE |
| ENSG00000199546 | | FALSE | TRUE | TRUE | FALSE | 3 | 49272565 | 49317672 | NA | NA | NA | 62 | 0.014256 | 2 | 0.00087 | NA | NA | TRUE |
| ENSG00000225399 | | TRUE | TRUE | TRUE | TRUE | 3 | 49297518 | 49298744 | 6 | 3 | rs7617480 | 63 | 0.009713 | 6 | 0.003497 | -5.71875 | 1.07E-08 | TRUE |
| ENSG00000188315 | C3orf62 | TRUE | FALSE | FALSE | TRUE | 3 | 49306035 | 49315342 | 7 | 0 | rs7617480 | NA | NA | NA | -5.42836 | 5.69E-08 | TRUE | NA |
| ENSG00000264633 | MIR4271 | FALSE | FALSE | TRUE | FALSE | 3 | 49311553 | 49311619 | NA | NA | NA | NA | NA | 5 | 0.034816 | NA | NA | TRUE |
| ENSG00000114316 | USP4 | TRUE | FALSE | FALSE | TRUE | 3 | 49315264 | 49378145 | 20 | 63 | rs7617480 | NA | NA | NA | 6.03315 | 1.61E-09 | TRUE | NA |
| ENSG00000235908 | RHOA-IT1 | FALSE | TRUE | FALSE | FALSE | 3 | 49392578 | 49439439 | NA | NA | NA | 87 | 0.044035 | NA | NA | NA | NA | TRUE |
| ENSG00000233276 | GPX1 | TRUE | FALSE | FALSE | TRUE | 3 | 49394609 | 49396033 | 12 | 147 | rs7617480 | NA | NA | NA | 6.1765 | 6.56E-10 | FALSE | NA |
| ENSG00000067560 | RHOA | TRUE | TRUE | TRUE | TRUE | 3 | 49396578 | 49450431 | 47 | 0 | rs7617480 | 181 | 0.03117 | 59 | 0.019133 | 5.2591 | 1.45E-07 | TRUE |
| ENSG00000283189 | | FALSE | TRUE | FALSE | FALSE | 3 | 49444227 | 49501743 | NA | NA | NA | 92 | 0.049671 | NA | NA | NA | NA | TRUE |
| ENSG00000145022 | TCTA | TRUE | FALSE | TRUE | FALSE | 3 | 49449639 | 49453908 | 14 | 79 | rs7617480 | NA | NA | 8 | 0.012256 | NA | NA | TRUE |
| ENSG00000145020 | AMT | TRUE | FALSE | FALSE | TRUE | 3 | 49454211 | 49460186 | 13 | 147 | rs7617480 | NA | NA | NA | -5.8458 | 5.04E-09 | FALSE | NA |
| ENSG00000145029 | NICN1 | TRUE | FALSE | TRUE | TRUE | 3 | 49460379 | 49466759 | 11 | 146 | rs7617480 | NA | NA | 8 | 0.014112 | -5.431 | 5.60E-08 | TRUE |
| ENSG00000173402 | DAG1 | TRUE | FALSE | FALSE | FALSE | 3 | 49506146 | 49573048 | 39 | 0 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000226913 | BSN-DT | FALSE | TRUE | FALSE | FALSE | 3 | 49576739 | 49626799 | NA | NA | NA | 67 | 0.001044 | NA | NA | NA | NA | TRUE |
| ENSG00000164061 | BSN | TRUE | FALSE | FALSE | TRUE | 3 | 49591922 | 49708978 | 13 | 67 | rs7617480 | NA | NA | NA | -6.67345 | 2.50E-11 | TRUE | NA |
| ENSG00000173531 | MST1 | TRUE | FALSE | FALSE | FALSE | 3 | 49721380 | 49726934 | 0 | 11 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000164068 | RNF123 | TRUE | FALSE | FALSE | FALSE | 3 | 49726932 | 49758962 | 0 | 142 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000173540 | GMPPB | TRUE | FALSE | FALSE | TRUE | 3 | 49754277 | 49761384 | 0 | 168 | rs7617480 | NA | NA | NA | 5.65116 | 1.59E-08 | TRUE | NA |
| ENSG00000004534 | RBM6 | TRUE | FALSE | FALSE | FALSE | 3 | 49977440 | 50137478 | 0 | 1 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000186792 | HYAL3 | TRUE | FALSE | FALSE | FALSE | 3 | 50330262 | 50336899 | 0 | 100 | rs7617480 | NA | NA | NA | NA | NA | NA | NA |

| | | | | | | | | | | | | | | | | | | | |
|-----------------|------------|-------|-------|-------|-------|---|----------|----------|-----|-----|------------|------|----------|----------|-----------|----------|----------|-------|------|
| ENSG00000164087 | POC1A | FALSE | FALSE | FALSE | TRUE | 3 | 52109242 | 52188706 | NA | NA | NA | NA | NA | NA | 4.8367 | 1.32E-06 | TRUE | NA | |
| ENSG00000164091 | WDR82 | FALSE | FALSE | FALSE | TRUE | 3 | 52288450 | 52322036 | NA | NA | NA | NA | NA | NA | -4.96056 | 7.03E-07 | TRUE | NA | |
| ENSG00000168237 | GLYCK | FALSE | FALSE | FALSE | TRUE | 3 | 52321105 | 52329273 | NA | NA | NA | NA | NA | NA | 4.864515 | 1.15E-06 | TRUE | NA | |
| ENSG00000242797 | GLYCK-AS1 | FALSE | FALSE | TRUE | FALSE | 3 | 52322596 | 52333083 | NA | NA | NA | NA | 88 | 0.023348 | NA | NA | NA | TRUE | |
| ENSG00000114841 | DNAH1 | FALSE | FALSE | TRUE | FALSE | 3 | 52350335 | 52434507 | NA | NA | NA | NA | 105 | 0.024585 | NA | NA | NA | TRUE | |
| ENSG00000010319 | SEMA3G | FALSE | FALSE | FALSE | TRUE | 3 | 52467051 | 52479119 | NA | NA | NA | NA | NA | NA | 5.03569 | 4.76E-07 | TRUE | NA | |
| ENSG00000010322 | NISCH | FALSE | FALSE | TRUE | FALSE | 3 | 52489134 | 52527087 | NA | NA | NA | NA | 83 | 0.048227 | NA | NA | NA | TRUE | |
| ENSG00000168273 | SMIM4 | FALSE | TRUE | FALSE | FALSE | 3 | 52535618 | 52623253 | NA | NA | NA | 200 | 0.027143 | NA | NA | NA | NA | TRUE | |
| ENSG00000168268 | NT5DC2 | FALSE | TRUE | FALSE | TRUE | 3 | 52548403 | 52604070 | NA | NA | NA | 119 | 0.02274 | NA | NA | 5.3525 | 8.68E-08 | TRUE | TRUE |
| ENSG00000221518 | RNU6ATAC16 | FALSE | TRUE | FALSE | FALSE | 3 | 52559586 | 52604723 | NA | NA | NA | 96 | 0.035538 | NA | NA | NA | NA | TRUE | |
| ENSG00000163939 | PBRM1 | FALSE | FALSE | TRUE | TRUE | 3 | 52579368 | 52719852 | NA | NA | NA | NA | 120 | 0.016656 | 5.111236 | 3.20E-07 | TRUE | TRUE | |
| ENSG00000163938 | GNL3 | FALSE | FALSE | FALSE | TRUE | 3 | 52715172 | 52728513 | NA | NA | NA | NA | NA | NA | 5.5106 | 3.58E-08 | TRUE | NA | |
| ENSG00000016864 | GLT8D1 | FALSE | FALSE | FALSE | TRUE | 3 | 52728502 | 52740048 | NA | NA | NA | NA | NA | NA | -5.033333 | 4.82E-07 | TRUE | NA | |
| ENSG00000114902 | SPCS1 | FALSE | FALSE | FALSE | TRUE | 3 | 52738971 | 52745164 | NA | NA | NA | NA | NA | NA | -4.93333 | 8.08E-07 | TRUE | NA | |
| ENSG00000114904 | NEK4 | FALSE | FALSE | FALSE | TRUE | 3 | 52742460 | 52804962 | NA | NA | NA | NA | NA | NA | 5.49457 | 3.92E-08 | TRUE | NA | |
| ENSG00000275956 | | FALSE | FALSE | FALSE | TRUE | 3 | 52766563 | 52767883 | NA | NA | NA | NA | NA | NA | 5.36351 | 8.16E-08 | NA | NA | |
| ENSG00000270941 | | FALSE | FALSE | FALSE | TRUE | 3 | 52768751 | 52769029 | NA | NA | NA | NA | NA | NA | 5.11266 | 3.18E-07 | NA | NA | |
| ENSG00000163935 | SFMBT1 | FALSE | FALSE | TRUE | FALSE | 3 | 52937588 | 53080084 | NA | NA | NA | NA | 220 | 0.00879 | NA | NA | NA | TRUE | |
| ENSG00000163931 | TKT | FALSE | FALSE | FALSE | TRUE | 3 | 53258728 | 53290068 | NA | NA | NA | NA | NA | NA | 5.0953 | 3.48E-07 | TRUE | NA | |
| ENSG00000189283 | FHIT | TRUE | FALSE | FALSE | FALSE | 3 | 59735036 | 61237133 | 62 | 0 | rs9816087 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000237456 | ID2B | FALSE | FALSE | TRUE | FALSE | 3 | 62109878 | 62110282 | NA | NA | NA | NA | 122 | 0.000173 | NA | NA | NA | TRUE | |
| ENSG00000163602 | RYBP | FALSE | FALSE | FALSE | TRUE | 3 | 72420976 | 72495774 | NA | NA | NA | NA | NA | NA | -4.91812 | 8.74E-07 | TRUE | NA | |
| ENSG00000243396 | RPL32P7 | FALSE | TRUE | FALSE | FALSE | 3 | 1.01E+08 | 1.01E+08 | NA | NA | NA | 107 | 0.048121 | NA | NA | NA | NA | TRUE | |
| ENSG00000144821 | MYH15 | TRUE | TRUE | FALSE | FALSE | 3 | 1.08E+08 | 1.08E+08 | 38 | 12 | rs11368958 | 469 | 0.007178 | NA | NA | NA | NA | TRUE | |
| ENSG00000198919 | DZIP3 | TRUE | FALSE | FALSE | FALSE | 3 | 1.08E+08 | 1.08E+08 | 0 | 9 | rs11368958 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000138472 | GUCA1C | TRUE | FALSE | FALSE | FALSE | 3 | 1.09E+08 | 1.09E+08 | 0 | 15 | rs11368958 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000181722 | ZBTB20 | TRUE | FALSE | FALSE | FALSE | 3 | 1.14E+08 | 1.15E+08 | 24 | 0 | rs1357492 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000185565 | LSAMP | TRUE | FALSE | FALSE | FALSE | 3 | 1.16E+08 | 1.18E+08 | 136 | 0 | rs76954017 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000239268 | | FALSE | TRUE | FALSE | FALSE | 3 | 1.17E+08 | 1.18E+08 | NA | NA | NA | 1121 | 2.80E-05 | NA | NA | NA | NA | TRUE | |
| ENSG00000242816 | | FALSE | FALSE | TRUE | FALSE | 3 | 1.18E+08 | 1.18E+08 | NA | NA | NA | NA | NA | 4 | 3.94E-05 | NA | NA | TRUE | |
| ENSG00000248724 | NPHP3-AS1 | FALSE | FALSE | TRUE | FALSE | 3 | 1.32E+08 | 1.33E+08 | NA | NA | NA | NA | 259 | 0.032147 | NA | NA | NA | TRUE | |
| ENSG00000214237 | MINDY4B | FALSE | TRUE | FALSE | FALSE | 3 | 1.51E+08 | 1.51E+08 | NA | NA | NA | 248 | 0.030848 | NA | NA | NA | NA | TRUE | |
| ENSG00000260234 | | FALSE | FALSE | TRUE | FALSE | 3 | 1.51E+08 | 1.51E+08 | NA | NA | NA | NA | 6 | 0.042665 | NA | NA | NA | TRUE | |
| ENSG00000197415 | VEPH1 | FALSE | FALSE | TRUE | FALSE | 3 | 1.57E+08 | 1.57E+08 | NA | NA | NA | NA | 205 | 0.02403 | NA | NA | NA | TRUE | |
| ENSG00000174899 | SLC66A1L | TRUE | TRUE | TRUE | FALSE | 3 | 1.57E+08 | 1.57E+08 | 65 | 5 | rs9837424 | 604 | 6.70E-06 | 299 | 0.000639 | NA | NA | TRUE | |
| ENSG00000168779 | SHOX2 | TRUE | TRUE | TRUE | FALSE | 3 | 1.58E+08 | 1.58E+08 | 1 | 0 | rs1526193 | 158 | 0.002337 | 67 | 0.012874 | NA | NA | FALSE | |
| ENSG00000174891 | RSRC1 | TRUE | TRUE | TRUE | FALSE | 3 | 1.58E+08 | 1.58E+08 | 289 | 250 | rs1526193; | 1490 | 1.77E-06 | 244 | 3.50E-05 | NA | NA | FALSE | |
| ENSG00000241723 | | FALSE | TRUE | TRUE | FALSE | 3 | 1.58E+08 | 1.58E+08 | NA | NA | NA | 150 | 1.78E-07 | 10 | 5.33E-08 | NA | NA | TRUE | |
| ENSG00000277143 | | FALSE | TRUE | FALSE | FALSE | 3 | 1.58E+08 | 1.58E+08 | NA | NA | NA | 131 | 0.00349 | NA | NA | NA | NA | TRUE | |
| ENSG00000243314 | | FALSE | FALSE | TRUE | FALSE | 3 | 1.58E+08 | 1.58E+08 | NA | NA | NA | NA | 71 | 0.038333 | NA | NA | NA | TRUE | |
| ENSG00000178053 | MLF1 | TRUE | FALSE | FALSE | FALSE | 3 | 1.58E+08 | 1.58E+08 | 2 | 0 | rs1526193 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000168827 | GFM1 | TRUE | FALSE | FALSE | FALSE | 3 | 1.58E+08 | 1.58E+08 | 0 | 14 | rs1526193 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000079257 | LXN | TRUE | FALSE | FALSE | FALSE | 3 | 1.58E+08 | 1.58E+08 | 0 | 188 | rs1526193 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000118849 | RARRS1 | TRUE | FALSE | FALSE | FALSE | 3 | 1.58E+08 | 1.58E+08 | 0 | 272 | rs1526193 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000127249 | ATP13A4 | TRUE | FALSE | FALSE | FALSE | 3 | 1.93E+08 | 1.93E+08 | 12 | 5 | rs7649917 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000236297 | EEF1A1P23 | FALSE | FALSE | FALSE | TRUE | 3 | 1.93E+08 | 1.93E+08 | NA | NA | NA | NA | NA | NA | 5.1935 | 2.06E-07 | NA | NA | |
| ENSG00000198836 | OPA1 | TRUE | FALSE | FALSE | FALSE | 3 | 1.93E+08 | 1.93E+08 | 10 | 0 | rs7649917 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000125388 | GRK4 | TRUE | FALSE | FALSE | TRUE | 4 | 2965335 | 3042474 | 0 | 9 | rs3905238 | NA | NA | NA | -5.36733 | 7.99E-08 | TRUE | NA | |
| ENSG00000197386 | HTT | TRUE | FALSE | FALSE | FALSE | 4 | 3076408 | 3245676 | 64 | 0 | rs3905238 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000188981 | MSANTD1 | TRUE | TRUE | FALSE | FALSE | 4 | 3246096 | 3273465 | 5 | 11 | rs3905238 | 211 | 0.012032 | NA | NA | NA | NA | TRUE | |
| ENSG00000163956 | LRPAP1 | TRUE | FALSE | FALSE | FALSE | 4 | 3508103 | 3534286 | 0 | 2 | rs3905238 | NA | NA | NA | NA | NA | NA | NA | |

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|-----------------|------------|-------|-------|-------|-------|---|----------|----------|-----|-----|------------|------|----------|-----|----------|-----------|----------|-------|-------|
| ENSG00000048342 | CC2D2A | FALSE | TRUE | FALSE | FALSE | 4 | 15436489 | 15613180 | NA | NA | NA | 441 | 0.027165 | NA | NA | NA | NA | TRUE | |
| ENSG00000109133 | TMEM33 | TRUE | FALSE | FALSE | FALSE | 4 | 41937137 | 41962589 | 4 | 92 | rs34215984 | NA | NA | NA | NA | NA | FALSE | NA | |
| ENSG00000272862 | | FALSE | TRUE | FALSE | FALSE | 4 | 41980758 | 42026254 | NA | NA | NA | 189 | 0.0026 | NA | NA | NA | NA | TRUE | |
| ENSG00000182308 | DCAF4L1 | TRUE | FALSE | TRUE | TRUE | 4 | 41983713 | 41988476 | 37 | 106 | rs34215984 | NA | NA | 22 | 0.003566 | -5.222222 | 1.77E-07 | FALSE | FALSE |
| ENSG00000014824 | SLC30A9 | TRUE | TRUE | FALSE | TRUE | 4 | 41992489 | 42092474 | 297 | 315 | rs34215984 | 515 | 0.000566 | NA | 6.486593 | 8.78E-11 | FALSE | FALSE | |
| ENSG00000249212 | ATP1B1P1 | FALSE | TRUE | TRUE | FALSE | 4 | 41996226 | 42042140 | NA | NA | NA | 194 | 0.000646 | 17 | 0.000461 | NA | NA | NA | TRUE |
| ENSG00000188848 | BEND4 | TRUE | TRUE | FALSE | TRUE | 4 | 42112955 | 42154895 | 26 | 93 | rs34215984 | 323 | 0.001195 | NA | -5.0889 | 3.60E-07 | FALSE | FALSE | |
| ENSG00000128039 | SRD5A3 | FALSE | FALSE | TRUE | FALSE | 4 | 56212276 | 56239263 | NA | NA | NA | NA | NA | 223 | 0.045853 | NA | NA | NA | TRUE |
| ENSG00000249700 | SRD5A3-AS1 | FALSE | FALSE | TRUE | FALSE | 4 | 56230138 | 56262014 | NA | NA | NA | NA | NA | 351 | 0.018877 | NA | NA | NA | TRUE |
| ENSG00000134851 | TMEM165 | FALSE | FALSE | FALSE | TRUE | 4 | 56262124 | 56319564 | NA | NA | NA | NA | NA | NA | -5.31347 | 1.08E-07 | TRUE | NA | |
| ENSG00000134852 | CLOCK | FALSE | TRUE | FALSE | TRUE | 4 | 56284070 | 56448305 | NA | NA | NA | 605 | 0.018648 | NA | 5.1001 | 3.40E-07 | TRUE | TRUE | |
| ENSG00000238585 | | FALSE | TRUE | FALSE | FALSE | 4 | 56357762 | 56402875 | NA | NA | NA | 191 | 0.044235 | NA | NA | NA | NA | TRUE | |
| ENSG00000272969 | | FALSE | TRUE | TRUE | FALSE | 4 | 56378279 | 56424056 | NA | NA | NA | 184 | 0.037179 | 15 | 0.008156 | NA | NA | NA | TRUE |
| ENSG00000223305 | RN7SKP30 | FALSE | TRUE | TRUE | FALSE | 4 | 56396669 | 56442002 | NA | NA | NA | 173 | 0.01302 | 16 | 0.049075 | NA | NA | NA | TRUE |
| ENSG00000163440 | PDCL2 | FALSE | TRUE | FALSE | FALSE | 4 | 56412692 | 56493379 | NA | NA | NA | 281 | 0.034563 | NA | NA | NA | NA | TRUE | |
| ENSG00000251339 | | FALSE | TRUE | FALSE | FALSE | 4 | 59636791 | 59884870 | NA | NA | NA | 933 | 0.033928 | NA | NA | NA | NA | TRUE | |
| ENSG00000251266 | LINC02429 | FALSE | TRUE | TRUE | FALSE | 4 | 59815000 | 59922677 | NA | NA | NA | 491 | 0.001132 | 32 | 9.92E-05 | NA | NA | NA | TRUE |
| ENSG00000249382 | LINC02619 | FALSE | TRUE | FALSE | FALSE | 4 | 59842900 | 59888878 | NA | NA | NA | 169 | 0.000558 | NA | NA | NA | NA | TRUE | |
| ENSG00000250375 | | FALSE | FALSE | TRUE | FALSE | 4 | 59912738 | 59940974 | NA | NA | NA | NA | NA | 100 | 0.040806 | NA | NA | NA | TRUE |
| ENSG00000156269 | NAA11 | TRUE | FALSE | TRUE | FALSE | 4 | 80146848 | 80247204 | 47 | 0 | rs1038425 | NA | NA | 68 | 0.00179 | NA | NA | NA | TRUE |
| ENSG00000196782 | MAML3 | FALSE | TRUE | FALSE | FALSE | 4 | 1.41E+08 | 1.41E+08 | NA | NA | NA | 1285 | 0.001446 | NA | NA | NA | NA | FALSE | |
| ENSG00000151962 | RBM46 | FALSE | FALSE | TRUE | FALSE | 4 | 1.56E+08 | 1.56E+08 | NA | NA | NA | NA | NA | 33 | 0.015079 | NA | NA | NA | TRUE |
| ENSG00000250910 | | FALSE | FALSE | TRUE | FALSE | 4 | 1.56E+08 | 1.56E+08 | NA | NA | NA | NA | NA | 139 | 0.006889 | NA | NA | NA | TRUE |
| ENSG00000249924 | | FALSE | TRUE | FALSE | FALSE | 4 | 1.56E+08 | 1.56E+08 | NA | NA | NA | 154 | 0.023448 | NA | NA | NA | NA | TRUE | |
| ENSG00000171503 | ETFDH | FALSE | FALSE | FALSE | TRUE | 4 | 1.6E+08 | 1.6E+08 | NA | NA | NA | NA | NA | NA | -5.17711 | 2.25E-07 | TRUE | NA | |
| ENSG00000248319 | LINC02275 | FALSE | FALSE | TRUE | FALSE | 4 | 1.71E+08 | 1.71E+08 | NA | NA | NA | NA | NA | 180 | 0.012756 | NA | NA | NA | TRUE |
| ENSG00000198948 | MFAP3L | TRUE | TRUE | FALSE | TRUE | 4 | 1.71E+08 | 1.71E+08 | 20 | 29 | rs1904823 | 256 | 0.021927 | NA | -6.25714 | 3.92E-10 | TRUE | TRUE | |
| ENSG00000109576 | AADAT | TRUE | FALSE | FALSE | FALSE | 4 | 1.71E+08 | 1.71E+08 | 5 | 2 | rs1904823 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000113100 | CDH9 | TRUE | TRUE | TRUE | TRUE | 5 | 26880709 | 27121257 | 158 | 101 | rs3811921 | 581 | 0.003319 | 11 | 0.002186 | 5.59796 | 2.17E-08 | TRUE | FALSE |
| ENSG00000171530 | TBCA | FALSE | FALSE | TRUE | TRUE | 5 | 76986991 | 77164604 | NA | NA | NA | NA | NA | 217 | 0.042472 | -4.84107 | 1.29E-06 | TRUE | TRUE |
| ENSG00000248708 | LINC02144 | FALSE | FALSE | TRUE | FALSE | 5 | 87008952 | 87029086 | NA | NA | NA | NA | NA | 12 | 0.033765 | NA | NA | NA | TRUE |
| ENSG00000164180 | TMEM161B | TRUE | TRUE | TRUE | TRUE | 5 | 87485450 | 87565293 | 4 | 0 | rs3099439 | 212 | 2.79E-05 | 126 | 6.20E-08 | -5.8387 | 5.26E-09 | FALSE | FALSE |
| ENSG00000247828 | TMEM161B-D | FALSE | TRUE | TRUE | TRUE | 5 | 87529712 | 87742502 | NA | NA | NA | 385 | 9.19E-09 | 95 | 2.68E-05 | 6.91264 | 4.76E-12 | NA | TRUE |
| ENSG00000207129 | RNA55P187 | FALSE | TRUE | TRUE | FALSE | 5 | 87560075 | 87605193 | NA | NA | NA | 79 | 2.72E-08 | 6 | 0.000851 | NA | NA | NA | TRUE |
| ENSG00000240083 | RPS3AP22 | FALSE | TRUE | TRUE | FALSE | 5 | 87642774 | 87688542 | NA | NA | NA | 79 | 2.79E-05 | 7 | 3.89E-06 | NA | NA | NA | TRUE |
| ENSG00000206958 | | FALSE | TRUE | TRUE | FALSE | 5 | 87643589 | 87688724 | NA | NA | NA | 80 | 4.06E-10 | 27 | 6.30E-10 | NA | NA | NA | TRUE |
| ENSG00000250306 | | FALSE | TRUE | TRUE | FALSE | 5 | 87643765 | 87689077 | NA | NA | NA | 80 | 4.06E-10 | 9 | 2.12E-09 | NA | NA | NA | TRUE |
| ENSG00000250156 | LINC02060 | FALSE | TRUE | TRUE | TRUE | 5 | 87694799 | 87769907 | NA | NA | NA | 180 | 2.11E-08 | 17 | 8.45E-06 | 6.9157 | 4.66E-12 | TRUE | TRUE |
| ENSG00000271904 | | FALSE | TRUE | TRUE | TRUE | 5 | 87719709 | 87829514 | NA | NA | NA | 325 | 1.01E-05 | 8 | 0.002256 | 7.34164 | 2.11E-13 | NA | TRUE |
| ENSG00000245526 | LINC00461 | FALSE | TRUE | TRUE | TRUE | 5 | 87793363 | 88021858 | NA | NA | NA | 500 | 2.79E-05 | 430 | 2.68E-05 | -5.84848 | 4.96E-09 | TRUE | TRUE |
| ENSG00000250705 | H3P23 | FALSE | TRUE | TRUE | FALSE | 5 | 87863598 | 87908935 | NA | NA | NA | 70 | 7.72E-06 | 5 | 1.69E-06 | NA | NA | NA | TRUE |
| ENSG00000245864 | MEF2C-AS2 | FALSE | TRUE | TRUE | FALSE | 5 | 87937036 | 88028648 | NA | NA | NA | 162 | 2.79E-05 | 3 | 0.004135 | NA | NA | NA | TRUE |
| ENSG00000250555 | | FALSE | TRUE | TRUE | FALSE | 5 | 87953468 | 87998676 | NA | NA | NA | 75 | 2.03E-09 | 5 | 0.000147 | NA | NA | NA | TRUE |
| ENSG00000250377 | | FALSE | TRUE | TRUE | TRUE | 5 | 87978462 | 88024789 | NA | NA | NA | 83 | 2.09E-07 | 3 | 0.000778 | -8.13004 | 4.29E-16 | NA | TRUE |
| ENSG00000081189 | MEF2C | FALSE | TRUE | TRUE | FALSE | 5 | 88002934 | 88235074 | NA | NA | NA | 430 | 2.79E-05 | 460 | 0.011942 | NA | NA | NA | FALSE |
| ENSG00000248588 | | FALSE | FALSE | TRUE | FALSE | 5 | 92161962 | 92179711 | NA | NA | NA | NA | NA | 48 | 2.91E-07 | NA | NA | NA | TRUE |
| ENSG00000249958 | CCT7P2 | FALSE | FALSE | TRUE | FALSE | 5 | 92225094 | 92226547 | NA | NA | NA | NA | NA | 20 | 0.00073 | NA | NA | NA | TRUE |
| ENSG00000175745 | NR2F1 | FALSE | FALSE | TRUE | FALSE | 5 | 92919043 | 92930321 | NA | NA | NA | NA | NA | 86 | 0.002971 | NA | NA | NA | TRUE |
| ENSG00000113391 | FAM172A | TRUE | TRUE | FALSE | FALSE | 5 | 92953775 | 93447404 | 272 | 0 | rs7278664 | 828 | 2.79E-05 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000249353 | NPM1P27 | FALSE | TRUE | FALSE | FALSE | 5 | 93008544 | 93054373 | NA | NA | NA | 62 | 8.07E-07 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000272406 | | FALSE | TRUE | TRUE | FALSE | 5 | 93042346 | 93089206 | NA | NA | NA | 71 | 5.55E-07 | 1 | 2.67E-06 | NA | NA | NA | TRUE |

| | | | | | | | | | | | | | | | | | | | |
|-----------------|--------------------|-------|-------|-------|-------|---|----------|----------|-----|-----|---------------|------|----------|-----|----------|----------|----------|-------|-------|
| ENSG00000248483 | <i>POU5F2</i> | TRUE | TRUE | TRUE | FALSE | 5 | 93070508 | 93077343 | 18 | 0 | rs7278664 | 83 | 8.63E-08 | 13 | 0.005345 | NA | NA | NA | FALSE |
| ENSG00000251023 | | FALSE | TRUE | TRUE | FALSE | 5 | 93186375 | 93234531 | NA | NA | NA | 74 | 4.79E-07 | 8 | 9.00E-07 | NA | NA | NA | TRUE |
| ENSG00000185261 | <i>KIAA0825</i> | TRUE | FALSE | FALSE | FALSE | 5 | 93488671 | 93954309 | 1 | 0 | rs7278664 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000175471 | <i>MCTP1</i> | FALSE | FALSE | TRUE | FALSE | 5 | 94040805 | 94620279 | NA | NA | NA | NA | NA | 95 | 0.003119 | NA | NA | NA | TRUE |
| ENSG00000251574 | | FALSE | TRUE | TRUE | FALSE | 5 | 1.04E+08 | 1.05E+08 | NA | NA | NA | 3225 | 3.87E-07 | 91 | 0.038146 | NA | NA | NA | TRUE |
| ENSG00000278958 | | FALSE | TRUE | TRUE | FALSE | 5 | 1.04E+08 | 1.04E+08 | NA | NA | NA | 95 | 5.39E-10 | 8 | 2.81E-09 | NA | NA | NA | TRUE |
| ENSG00000145743 | <i>FBXL17</i> | TRUE | TRUE | FALSE | TRUE | 5 | 1.07E+08 | 1.08E+08 | 18 | 0 | rs288181 | 1503 | 0.001018 | NA | NA | 4.98383 | 6.23E-07 | TRUE | TRUE |
| ENSG00000184838 | <i>PRR16</i> | TRUE | TRUE | FALSE | TRUE | 5 | 1.2E+08 | 1.2E+08 | 21 | 12 | rs9285891 | 1080 | 0.001318 | NA | NA | 4.89394 | 9.88E-07 | TRUE | FALSE |
| ENSG00000222609 | <i>RNU4-69P</i> | FALSE | FALSE | TRUE | FALSE | 5 | 1.2E+08 | 1.2E+08 | NA | NA | NA | NA | NA | 13 | 0.016677 | NA | NA | NA | TRUE |
| ENSG00000170476 | <i>MZB1</i> | FALSE | FALSE | TRUE | FALSE | 5 | 1.39E+08 | 1.39E+08 | NA | NA | NA | NA | NA | 30 | 0.017084 | NA | NA | NA | TRUE |
| ENSG00000131508 | <i>UBE2D2</i> | FALSE | FALSE | TRUE | FALSE | 5 | 1.39E+08 | 1.39E+08 | NA | NA | NA | NA | NA | 146 | 0.000137 | NA | NA | NA | TRUE |
| ENSG00000207020 | | FALSE | FALSE | TRUE | FALSE | 5 | 1.39E+08 | 1.39E+08 | NA | NA | NA | NA | NA | 30 | 0.03886 | NA | NA | NA | TRUE |
| ENSG00000171604 | <i>CXXC5</i> | FALSE | FALSE | TRUE | FALSE | 5 | 1.39E+08 | 1.39E+08 | NA | NA | NA | NA | NA | 95 | 0.009648 | NA | NA | NA | TRUE |
| ENSG00000158458 | <i>NRG2</i> | FALSE | FALSE | TRUE | FALSE | 5 | 1.39E+08 | 1.39E+08 | NA | NA | NA | NA | NA | 156 | 0.012755 | NA | NA | NA | TRUE |
| ENSG00000245146 | <i>MALINC1</i> | FALSE | FALSE | TRUE | FALSE | 5 | 1.39E+08 | 1.39E+08 | NA | NA | NA | NA | NA | 55 | 0.000465 | NA | NA | NA | TRUE |
| ENSG00000185129 | <i>PURA</i> | TRUE | FALSE | FALSE | FALSE | 5 | 1.39E+08 | 1.39E+08 | 0 | 52 | rs3756335 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000254363 | | FALSE | TRUE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 107 | 0.003883 | 78 | 0.017569 | NA | NA | NA | TRUE |
| ENSG00000182700 | <i>IGIP</i> | TRUE | FALSE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 1 | 0 | rs175086 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000120306 | <i>CYSTM1</i> | TRUE | FALSE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 66 | 65 | rs175086 | NA | NA | 47 | 0.00233 | NA | NA | NA | TRUE |
| ENSG00000113068 | <i>PFDN1</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 54 | 0 | rs175086 | 194 | 0.025388 | 155 | 0.000294 | 5.4311 | 5.60E-08 | TRUE | TRUE |
| ENSG00000113070 | <i>HBEGF</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 97 | 0.032205 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000113073 | <i>SLC4A9</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 0 | 46 | rs175086 | 97 | 0.029351 | 48 | 0.001969 | -7.01784 | 2.25E-12 | TRUE | FALSE |
| ENSG00000249637 | <i>ANKHD1-DT</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 88 | 0.006575 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000131503 | <i>ANKHD1</i> | FALSE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 178 | 0.014921 | 173 | 0.00083 | 5.57662 | 2.45E-08 | TRUE | FALSE |
| ENSG00000254996 | <i>ANKHD1-EIF4</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 191 | 0.016637 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000222790 | <i>RNU4-14P</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 51 | 0.008632 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000243056 | <i>EIF4EBP3</i> | FALSE | TRUE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 49 | 0.038902 | 7 | 0.035709 | NA | NA | NA | TRUE |
| ENSG00000213523 | <i>SRA1</i> | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 0 | 241 | rs3756335 | NA | NA | NA | NA | 5.7891 | 7.08E-09 | TRUE | NA |
| ENSG00000113108 | <i>APBB3</i> | FALSE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | NA | NA | NA | NA | 5.0511 | 4.39E-07 | TRUE | NA |
| ENSG00000200235 | | FALSE | FALSE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | NA | NA | 6 | 0.023824 | NA | NA | NA | TRUE |
| ENSG00000170458 | <i>CD14</i> | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 0 | 121 | rs3756335 | NA | NA | NA | NA | -5.2186 | 1.80E-07 | TRUE | NA |
| ENSG00000131495 | <i>NDUFA2</i> | TRUE | TRUE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 20 | 131 | rs3756335 | 101 | 0.031831 | NA | NA | 6.08107 | 1.19E-09 | FALSE | TRUE |
| ENSG00000113119 | <i>TMCO6</i> | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 17 | 271 | rs3756335; NA | NA | NA | NA | NA | -6.11993 | 9.36E-10 | TRUE | NA |
| ENSG00000113141 | <i>IK</i> | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 26 | 186 | rs3756335 | NA | NA | NA | NA | -5.40329 | 6.54E-08 | TRUE | NA |
| ENSG00000120314 | <i>WDR55</i> | TRUE | TRUE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 18 | 238 | rs3756335; | 114 | 0.027793 | NA | NA | -5.9676 | 2.41E-09 | TRUE | FALSE |
| ENSG00000256453 | <i>DND1</i> | TRUE | TRUE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 13 | 0 | rs3756335 | 89 | 0.020205 | 6 | 0.013629 | NA | NA | NA | TRUE |
| ENSG00000170445 | <i>HARS1</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 30 | 229 | rs3756335 | 131 | 0.024393 | 86 | 0.016984 | 5.4413 | 5.29E-08 | TRUE | TRUE |
| ENSG00000199990 | <i>VTRNA1-1</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 93 | 0.018976 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000202111 | <i>VTRNA1-2</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 101 | 0.033328 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000202515 | <i>VTRNA1-3</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 109 | 0.028025 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000112855 | <i>HARS2</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 30 | 121 | rs3756335 | 99 | 0.018676 | 35 | 0.044418 | -5.5863 | 2.32E-08 | TRUE | FALSE |
| ENSG00000146007 | <i>ZMAT2</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 32 | 242 | rs3756335 | 98 | 0.013555 | 29 | 0.005484 | -6.09238 | 1.11E-09 | TRUE | FALSE |
| ENSG00000250515 | | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 165 | 0.002831 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000248106 | | FALSE | TRUE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 157 | 0.002349 | 29 | 0.006927 | NA | NA | NA | TRUE |
| ENSG00000279726 | | FALSE | TRUE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 170 | 0.001482 | 24 | 0.002651 | NA | NA | NA | TRUE |
| ENSG00000204970 | <i>PCDHA1</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 112 | 246 | rs3756335 | 712 | 0.015444 | 24 | 0.005455 | 5.70654 | 1.15E-08 | TRUE | FALSE |
| ENSG00000204969 | <i>PCDHA2</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 96 | 241 | rs3756335 | 662 | 0.031233 | 31 | 0.0102 | 5.65614 | 1.55E-08 | FALSE | FALSE |
| ENSG00000255408 | <i>PCDHA3</i> | TRUE | TRUE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 81 | 242 | rs3756335; | 646 | 0.043128 | 25 | 0.003694 | 5.72134 | 1.06E-08 | TRUE | FALSE |
| ENSG00000204967 | <i>PCDHA4</i> | TRUE | FALSE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 72 | 240 | rs3756335 | NA | NA | 84 | 0.00171 | -5.7 | 1.20E-08 | TRUE | FALSE |
| ENSG00000204965 | <i>PCDHA5</i> | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 43 | 20 | rs3756335 | NA | NA | NA | NA | -5.28054 | 1.29E-07 | FALSE | NA |
| ENSG00000249504 | <i>PCDHA14</i> | FALSE | TRUE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | NA | NA | NA | 110 | 0.023674 | NA | NA | NA | NA | NA | TRUE |

| | | | | | | | | | | | | | | | | | | | |
|------------------|-----------|-------|-------|-------|-------|---|----------|-------------|----|-----|---------------|------|----------|-----|----------|----------|----------|-------|-------|
| ENSG000000081842 | PCDHA6 | TRUE | FALSE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 32 | 136 | rs3756335; NA | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000204963 | PCDHA7 | TRUE | FALSE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 26 | 270 | rs3756335 NA | NA | NA | 20 | 0.003704 | -5.7 | 1.20E-08 | TRUE | FALSE |
| ENSG00000204962 | PCDHA8 | TRUE | FALSE | TRUE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 21 | 280 | rs3756335; NA | NA | NA | 12 | 0.015638 | -5.74167 | 9.37E-09 | FALSE | TRUE |
| ENSG00000204961 | PCDHA9 | TRUE | FALSE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 11 | 270 | rs3756335 NA | NA | NA | 55 | 0.013763 | NA | NA | NA | FALSE |
| ENSG00000250120 | PCDHA10 | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 0 | 244 | rs3756335 NA | NA | NA | NA | -5.76667 | 8.09E-09 | TRUE | NA | |
| ENSG00000249034 | NA | TRUE | FALSE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 0 | 2 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000249158 | PCDHA11 | TRUE | FALSE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 0 | 130 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000251664 | PCDHA12 | TRUE | FALSE | FALSE | FALSE | 5 | 1.4E+08 | 1.4E+08 | 0 | 107 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000239389 | PCDHA13 | TRUE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 | 0 | 270 | rs3756335 NA | NA | NA | NA | 5.56824 | 2.57E-08 | TRUE | NA | NA |
| ENSG00000248383 | PCDHAC1 | FALSE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.4E+08 NA | NA | NA | NA | NA | NA | NA | -5.32519 | 1.01E-07 | TRUE | NA | NA |
| ENSG00000279047 | | FALSE | FALSE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 NA | NA | NA | NA | NA | NA | 132 | 0.001836 | NA | NA | NA | TRUE |
| ENSG00000113205 | PCDHB3 | FALSE | FALSE | TRUE | FALSE | 5 | 1.4E+08 | 1.4E+08 NA | NA | NA | NA | NA | NA | 34 | 0.000856 | NA | NA | NA | TRUE |
| ENSG00000272108 | | FALSE | FALSE | FALSE | TRUE | 5 | 1.4E+08 | 1.41E+08 NA | NA | NA | NA | NA | NA | NA | 5.46667 | 4.59E-08 | NA | NA | NA |
| ENSG00000113209 | PCDHB5 | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 58 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000255622 | PCDHB17P | TRUE | FALSE | FALSE | TRUE | 5 | 1.41E+08 | 1.41E+08 | 0 | 1 | rs3756335 NA | NA | NA | NA | -5.02693 | 4.98E-07 | TRUE | NA | NA |
| ENSG00000113212 | PCDHB7 | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 1 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000196963 | NA | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 1 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000120324 | PCDHB10 | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 131 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000120328 | PCDHB12 | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 2 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000187372 | PCDHB13 | TRUE | FALSE | FALSE | TRUE | 5 | 1.41E+08 | 1.41E+08 | 0 | 1 | rs3756335 NA | NA | NA | NA | -5.1333 | 2.85E-07 | TRUE | NA | NA |
| ENSG00000113248 | PCDHB15 | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 33 | rs175086 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000253910 | PCDHGB2 | TRUE | FALSE | FALSE | FALSE | 5 | 1.41E+08 | 1.41E+08 | 0 | 47 | rs3756335 NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000113580 | NR3C1 | FALSE | TRUE | FALSE | FALSE | 5 | 1.43E+08 | 1.43E+08 NA | NA | NA | NA | 380 | 0.033215 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000155511 | GRIA1 | TRUE | FALSE | FALSE | TRUE | 5 | 1.53E+08 | 1.53E+08 | 17 | 0 | rs1466386 NA | NA | NA | NA | -5.05677 | 4.26E-07 | TRUE | NA | NA |
| ENSG00000242976 | RN7SL177P | FALSE | TRUE | TRUE | FALSE | 5 | 1.53E+08 | 1.53E+08 NA | NA | NA | NA | 191 | 0.014968 | 11 | 0.000561 | NA | NA | NA | TRUE |
| ENSG00000253538 | | FALSE | FALSE | TRUE | FALSE | 5 | 1.64E+08 | 1.64E+08 NA | NA | NA | NA | NA | NA | 79 | 6.11E-09 | NA | NA | NA | TRUE |
| ENSG00000241956 | | FALSE | TRUE | FALSE | FALSE | 5 | 1.64E+08 | 1.65E+08 NA | NA | NA | NA | 2549 | 2.58E-07 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000254066 | LINC01938 | FALSE | TRUE | TRUE | FALSE | 5 | 1.65E+08 | 1.65E+08 NA | NA | NA | NA | 183 | 1.80E-05 | 47 | 2.71E-05 | NA | NA | NA | TRUE |
| ENSG00000145934 | TENM2 | TRUE | TRUE | FALSE | FALSE | 5 | 1.67E+08 | 1.68E+08 | 92 | 29 | rs1218801(| 2646 | 2.10E-09 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000253357 | | FALSE | TRUE | FALSE | FALSE | 5 | 1.67E+08 | 1.67E+08 NA | NA | NA | NA | 127 | 0.003386 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000253065 | | FALSE | FALSE | TRUE | FALSE | 5 | 1.67E+08 | 1.67E+08 NA | NA | NA | NA | NA | NA | 49 | 0.030899 | NA | NA | NA | TRUE |
| ENSG00000124788 | ATXN1 | FALSE | FALSE | FALSE | TRUE | 6 | 16299343 | 16761722 NA | NA | NA | NA | NA | NA | NA | -5.24013 | 1.60E-07 | TRUE | NA | NA |
| ENSG00000146038 | DCDC2 | TRUE | FALSE | FALSE | FALSE | 6 | 24171984 | 24358280 | 25 | 11 | rs1219797: NA | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000124564 | SLC17A3 | FALSE | FALSE | TRUE | FALSE | 6 | 25845084 | 25882514 NA | NA | NA | NA | NA | NA | 82 | 0.011581 | NA | NA | NA | FALSE |
| ENSG00000272462 | | FALSE | FALSE | TRUE | FALSE | 6 | 25992890 | 26002003 NA | NA | NA | NA | NA | NA | 41 | 0.008199 | NA | NA | NA | TRUE |
| ENSG00000224447 | H3P26 | FALSE | FALSE | TRUE | FALSE | 6 | 26016607 | 26016829 NA | NA | NA | NA | NA | NA | 12 | 0.034442 | NA | NA | NA | TRUE |
| ENSG00000286522 | H3C2 | FALSE | FALSE | FALSE | TRUE | 6 | 26031817 | 26032327 NA | NA | NA | NA | NA | NA | NA | -5.7552 | 8.65E-09 | NA | NA | NA |
| ENSG00000274267 | NA | FALSE | FALSE | TRUE | FALSE | 6 | 26031878 | 26032288 NA | NA | NA | NA | NA | NA | 97 | 0.000105 | NA | NA | NA | TRUE |
| ENSG00000234816 | H2AC5P | FALSE | FALSE | TRUE | FALSE | 6 | 26044217 | 26044585 NA | NA | NA | NA | NA | NA | 102 | 0.00899 | NA | NA | NA | TRUE |
| ENSG00000010704 | HFE | FALSE | FALSE | FALSE | TRUE | 6 | 26087509 | 26098571 NA | NA | NA | NA | NA | NA | NA | 5.67261 | 1.41E-08 | TRUE | NA | NA |
| ENSG00000180573 | H2AC6 | FALSE | FALSE | FALSE | TRUE | 6 | 26124373 | 26139344 NA | NA | NA | NA | NA | NA | NA | 5.6425 | 1.68E-08 | TRUE | NA | NA |
| ENSG00000274290 | H2BC6 | FALSE | FALSE | TRUE | FALSE | 6 | 26172287 | 26184883 NA | NA | NA | NA | NA | NA | 104 | 0.011644 | NA | NA | NA | TRUE |
| ENSG00000277157 | H4C4 | FALSE | FALSE | FALSE | TRUE | 6 | 26188938 | 26189340 NA | NA | NA | NA | NA | NA | NA | -5.0784 | 3.81E-07 | NA | NA | NA |
| ENSG00000216331 | H1-12P | FALSE | FALSE | FALSE | TRUE | 6 | 26195782 | 26196861 NA | NA | NA | NA | NA | NA | NA | -4.85195 | 1.22E-06 | TRUE | NA | NA |
| ENSG00000277224 | H2BC7 | FALSE | FALSE | FALSE | TRUE | 6 | 26199744 | 26200216 NA | NA | NA | NA | NA | NA | NA | -5.1812 | 2.20E-07 | NA | NA | NA |
| ENSG00000187990 | NA | FALSE | FALSE | TRUE | FALSE | 6 | 26216428 | 26216872 NA | NA | NA | NA | NA | NA | 62 | 0.04912 | NA | NA | NA | TRUE |
| ENSG00000220875 | H3C9P | FALSE | TRUE | TRUE | FALSE | 6 | 26312104 | 26357520 NA | NA | NA | NA | 216 | 7.63E-05 | 165 | 0.022759 | NA | NA | NA | TRUE |
| ENSG00000186470 | BTN3A2 | FALSE | TRUE | TRUE | TRUE | 6 | 26330387 | 26388548 NA | NA | NA | NA | 325 | 1.30E-08 | 131 | 1.05E-08 | 6.84617 | 7.59E-12 | FALSE | FALSE |
| ENSG00000252399 | NA | FALSE | TRUE | TRUE | FALSE | 6 | 26343199 | 26388264 NA | NA | NA | NA | 271 | 1.65E-08 | 72 | 2.98E-05 | NA | NA | NA | TRUE |
| ENSG00000124508 | BTN2A2 | FALSE | TRUE | TRUE | TRUE | 6 | 26348324 | 26405102 NA | NA | NA | NA | 337 | 3.93E-08 | 160 | 7.75E-06 | -6.6667 | 2.62E-11 | TRUE | FALSE |
| ENSG00000215979 | NA | FALSE | TRUE | TRUE | FALSE | 6 | 26355704 | 26400780 NA | NA | NA | NA | 286 | 2.02E-08 | 2 | 0.022872 | NA | NA | NA | TRUE |

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|-----------------|------------------|-------|-------|-------|-------|---|----------|----------|----|----|----|-----|----------|-----|----------|----------|----------|-------|-------|
| ENSG00000026950 | <i>BTN3A1</i> | FALSE | TRUE | TRUE | TRUE | 6 | 26367465 | 26425444 | NA | NA | NA | 328 | 0.000271 | 89 | 0.013753 | -5.68684 | 1.29E-08 | TRUE | FALSE |
| ENSG00000124549 | <i>BTN2A3P</i> | FALSE | FALSE | TRUE | TRUE | 6 | 26421619 | 26432611 | NA | NA | NA | NA | NA | 161 | 6.07E-08 | -5.5853 | 2.33E-08 | TRUE | TRUE |
| ENSG00000112763 | <i>BTN2A1</i> | FALSE | TRUE | TRUE | TRUE | 6 | 26423132 | 26486849 | NA | NA | NA | 226 | 0.001372 | 100 | 9.19E-08 | -4.9667 | 6.81E-07 | TRUE | FALSE |
| ENSG00000111801 | <i>BTN3A3</i> | FALSE | FALSE | FALSE | TRUE | 6 | 26440700 | 26453643 | NA | NA | NA | NA | NA | NA | NA | -7.27847 | 3.38E-13 | FALSE | NA |
| ENSG00000124557 | <i>BTN1A1</i> | FALSE | TRUE | TRUE | FALSE | 6 | 26466449 | 26520650 | NA | NA | NA | 162 | 4.18E-07 | 97 | 0.000378 | NA | NA | FALSE | FALSE |
| ENSG00000228223 | <i>HCG11</i> | FALSE | TRUE | TRUE | TRUE | 6 | 26488678 | 26536807 | NA | NA | NA | 137 | 0.000804 | 63 | 4.09E-05 | 7.0223 | 2.18E-12 | TRUE | TRUE |
| ENSG00000261353 | <i>NA</i> | FALSE | TRUE | FALSE | FALSE | 6 | 26492291 | 26537632 | NA | NA | NA | 124 | 0.002069 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000182952 | <i>HMGNA4</i> | FALSE | TRUE | FALSE | FALSE | 6 | 26503633 | 26556482 | NA | NA | NA | 133 | 0.02942 | NA | NA | NA | NA | FALSE | FALSE |
| ENSG00000199289 | <i>RNU6-502P</i> | FALSE | TRUE | FALSE | FALSE | 6 | 26509579 | 26554686 | NA | NA | NA | 113 | 0.033506 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000146109 | <i>ABT1</i> | FALSE | TRUE | TRUE | FALSE | 6 | 26562180 | 26610972 | NA | NA | NA | 175 | 0.000292 | 55 | 3.99E-05 | NA | NA | NA | FALSE |
| ENSG00000275846 | | FALSE | TRUE | TRUE | FALSE | 6 | 26567961 | 26616889 | NA | NA | NA | 171 | 0.000431 | 20 | 5.18E-05 | NA | NA | NA | TRUE |
| ENSG00000271071 | | FALSE | TRUE | FALSE | FALSE | 6 | 26602131 | 26648337 | NA | NA | NA | 136 | 0.036791 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000181315 | <i>ZNF322</i> | FALSE | FALSE | TRUE | FALSE | 6 | 26634611 | 26659980 | NA | NA | NA | NA | NA | 64 | 6.25E-05 | NA | NA | NA | FALSE |
| ENSG00000261584 | | FALSE | FALSE | TRUE | FALSE | 6 | 26686469 | 26688192 | NA | NA | NA | NA | NA | 117 | 4.96E-10 | NA | NA | NA | TRUE |
| ENSG00000241549 | <i>GUSBP2</i> | FALSE | FALSE | TRUE | FALSE | 6 | 26839263 | 26924333 | NA | NA | NA | NA | NA | 694 | 6.24E-11 | NA | NA | NA | TRUE |
| ENSG00000243307 | <i>POM121L6P</i> | FALSE | FALSE | TRUE | FALSE | 6 | 26864731 | 26866556 | NA | NA | NA | NA | NA | 54 | 1.25E-05 | NA | NA | NA | TRUE |
| ENSG00000224843 | <i>LINC00240</i> | FALSE | FALSE | TRUE | FALSE | 6 | 26924771 | 26991703 | NA | NA | NA | NA | NA | 307 | 3.45E-10 | NA | NA | NA | TRUE |
| ENSG00000272312 | | FALSE | FALSE | TRUE | FALSE | 6 | 26968987 | 26969427 | NA | NA | NA | NA | NA | 143 | 1.09E-09 | NA | NA | NA | TRUE |
| ENSG00000219770 | <i>VN1R11P</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27016059 | 27061926 | NA | NA | NA | 102 | 0.013057 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000216762 | <i>VN1R13P</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27018144 | 27064028 | NA | NA | NA | 99 | 0.006799 | 22 | 9.90E-08 | NA | NA | NA | TRUE |
| ENSG00000196787 | <i>H2AC11</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27065821 | 27113070 | NA | NA | NA | 85 | 0.001922 | 7 | 0.044266 | NA | NA | NA | TRUE |
| ENSG00000222800 | <i>RNU2-62P</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27067569 | 27112759 | NA | NA | NA | 76 | 0.001202 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000276180 | <i>H4C9</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27071367 | 27117660 | NA | NA | NA | 82 | 0.008931 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000274997 | <i>H2AC12</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27079908 | 27125294 | NA | NA | NA | 83 | 0.047247 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000265565 | <i>MIR3143</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27080405 | 27125467 | NA | NA | NA | 81 | 0.042033 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000272468 | | FALSE | FALSE | TRUE | FALSE | 6 | 27090436 | 27091000 | NA | NA | NA | NA | NA | 8 | 3.82E-08 | NA | NA | NA | TRUE |
| ENSG00000124635 | <i>H2BC11</i> | FALSE | FALSE | TRUE | FALSE | 6 | 27093676 | 27100529 | NA | NA | NA | NA | NA | 75 | 6.46E-09 | NA | NA | NA | TRUE |
| ENSG00000197903 | <i>H2BC12</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27104197 | 27149577 | NA | NA | NA | 84 | 0.004675 | 89 | 2.30E-07 | NA | NA | NA | TRUE |
| ENSG00000174572 | <i>RPL10P2</i> | FALSE | FALSE | TRUE | FALSE | 6 | 27179023 | 27179692 | NA | NA | NA | NA | NA | 51 | 3.03E-10 | NA | NA | NA | TRUE |
| ENSG00000112812 | <i>PRSS16</i> | FALSE | FALSE | FALSE | TRUE | 6 | 27215480 | 27224403 | NA | NA | NA | NA | NA | NA | NA | -7.6471 | 2.06E-14 | FALSE | NA |
| ENSG00000204789 | <i>ZNF204P</i> | FALSE | FALSE | TRUE | TRUE | 6 | 27325604 | 27328000 | NA | NA | NA | NA | NA | 11 | 0.014402 | -7.9333 | 2.13E-15 | FALSE | TRUE |
| ENSG00000124613 | <i>ZNF391</i> | FALSE | FALSE | FALSE | TRUE | 6 | 27342394 | 27371687 | NA | NA | NA | NA | NA | NA | NA | 5.15767 | 2.50E-07 | TRUE | NA |
| ENSG00000271755 | | FALSE | TRUE | FALSE | TRUE | 6 | 27361789 | 27409743 | NA | NA | NA | 181 | 4.63E-06 | NA | NA | 6.9 | 5.20E-12 | NA | TRUE |
| ENSG00000237154 | <i>MCFD2P1</i> | FALSE | FALSE | TRUE | FALSE | 6 | 27375476 | 27375775 | NA | NA | NA | NA | NA | 6 | 9.02E-06 | NA | NA | NA | TRUE |
| ENSG00000096654 | <i>ZNF184</i> | FALSE | TRUE | FALSE | TRUE | 6 | 27408522 | 27475897 | NA | NA | NA | 217 | 0.000108 | NA | NA | -7.3843 | 1.53E-13 | FALSE | FALSE |
| ENSG00000270666 | | FALSE | TRUE | FALSE | FALSE | 6 | 27472818 | 27518053 | NA | NA | NA | 114 | 0.001699 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000219738 | <i>CD83P1</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27518601 | 27564523 | NA | NA | NA | 107 | 0.000464 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000206671 | <i>RNU6-471P</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27529191 | 27574296 | NA | NA | NA | 89 | 0.021818 | 6 | 4.14E-06 | NA | NA | NA | TRUE |
| ENSG00000238648 | <i>NA</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27564188 | 27609311 | NA | NA | NA | 70 | 0.000132 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000281706 | | FALSE | TRUE | FALSE | FALSE | 6 | 27626814 | 27688001 | NA | NA | NA | 191 | 0.028281 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000216915 | <i>GPR89P</i> | FALSE | TRUE | FALSE | TRUE | 6 | 27694779 | 27741273 | NA | NA | NA | 131 | 5.88E-09 | NA | NA | 6.7434 | 1.55E-11 | TRUE | TRUE |
| ENSG00000218069 | <i>RSL24D1P1</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27738398 | 27783890 | NA | NA | NA | 122 | 2.79E-05 | 28 | 2.13E-06 | NA | NA | NA | TRUE |
| ENSG00000217862 | <i>H4C10P</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27739853 | 27785117 | NA | NA | NA | 116 | 2.79E-05 | 10 | 1.54E-10 | NA | NA | NA | TRUE |
| ENSG00000196747 | <i>H2AC13</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27740977 | 27786479 | NA | NA | NA | 111 | 5.92E-09 | 4 | 7.55E-08 | NA | NA | NA | TRUE |
| ENSG00000278828 | <i>H3C10</i> | FALSE | TRUE | FALSE | FALSE | 6 | 27742842 | 27789078 | NA | NA | NA | 108 | 1.99E-08 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000273703 | <i>H2BC14</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27747822 | 27793202 | NA | NA | NA | 101 | 2.79E-05 | 10 | 1.54E-10 | NA | NA | NA | TRUE |
| ENSG00000197238 | <i>H4C11</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27756886 | 27802258 | NA | NA | NA | 100 | 2.79E-05 | 8 | 6.46E-08 | NA | NA | NA | TRUE |
| ENSG00000185130 | <i>H2BC13</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27765222 | 27810709 | NA | NA | NA | 100 | 1.37E-09 | 40 | 3.81E-05 | NA | NA | NA | TRUE |
| ENSG00000233822 | <i>H2BC15</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27770538 | 27843576 | NA | NA | NA | 169 | 2.79E-05 | 12 | 2.97E-12 | NA | NA | NA | TRUE |
| ENSG00000276368 | <i>H2AC14</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27772132 | 27817518 | NA | NA | NA | 99 | 1.43E-09 | 12 | 2.91E-10 | NA | NA | NA | TRUE |
| ENSG00000273542 | <i>H4C12</i> | FALSE | TRUE | TRUE | FALSE | 6 | 27788994 | 27834305 | NA | NA | NA | 97 | 2.79E-05 | 7 | 1.35E-05 | NA | NA | NA | TRUE |

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|-----------------|-------------|-------|-------|-------|-------|---|----------|----------|----|----|----|-----|----------|-----|----------|----------|----------|-------|-------|
| ENSG00000275221 | H2AC15 | FALSE | TRUE | TRUE | FALSE | 6 | 27795725 | 27841117 | NA | NA | NA | 110 | 3.32E-10 | 6 | 5.94E-11 | NA | NA | NA | TRUE |
| ENSG00000276903 | H2AC16 | FALSE | TRUE | TRUE | FALSE | 6 | 27798133 | 27843525 | NA | NA | NA | 108 | 2.79E-05 | 9 | 8.52E-08 | NA | NA | NA | TRUE |
| ENSG00000217646 | H2BC16P | FALSE | TRUE | TRUE | FALSE | 6 | 27821840 | 27867179 | NA | NA | NA | 114 | 2.79E-05 | 10 | 7.13E-11 | NA | NA | NA | TRUE |
| ENSG00000184357 | H1-5 | FALSE | TRUE | TRUE | FALSE | 6 | 27824627 | 27870307 | NA | NA | NA | 116 | 2.79E-05 | 16 | 2.11E-10 | NA | NA | NA | TRUE |
| ENSG00000274641 | H2BC17 | FALSE | TRUE | TRUE | FALSE | 6 | 27826241 | 27871621 | NA | NA | NA | 116 | 2.79E-05 | 6 | 1.06E-05 | NA | NA | NA | TRUE |
| ENSG00000275379 | H3C11 | FALSE | TRUE | TRUE | FALSE | 6 | 27829683 | 27875093 | NA | NA | NA | 122 | 2.79E-05 | 6 | 3.02E-05 | NA | NA | NA | TRUE |
| ENSG00000275126 | H4C13 | FALSE | TRUE | TRUE | TRUE | 6 | 27830977 | 27876288 | NA | NA | NA | 122 | 2.79E-05 | 6 | 0.001917 | 6.9078 | 4.92E-12 | NA | TRUE |
| ENSG00000197153 | H3C12 | FALSE | TRUE | TRUE | FALSE | 6 | 27848160 | 27893570 | NA | NA | NA | 124 | 2.14E-10 | 9 | 3.95E-10 | NA | NA | NA | TRUE |
| ENSG00000278677 | H2AC17 | FALSE | TRUE | TRUE | FALSE | 6 | 27850535 | 27895927 | NA | NA | NA | 131 | 7.99E-10 | 6 | 4.16E-11 | NA | NA | NA | TRUE |
| ENSG00000238610 | RNU7-26P | FALSE | TRUE | TRUE | FALSE | 6 | 27855282 | 27900344 | NA | NA | NA | 123 | 7.28E-09 | 10 | 1.16E-10 | NA | NA | NA | TRUE |
| ENSG00000168131 | OR2B2 | FALSE | FALSE | TRUE | FALSE | 6 | 27878963 | 27880174 | NA | NA | NA | NA | NA | 10 | 1.91E-07 | NA | NA | NA | FALSE |
| ENSG00000168126 | OR2W6P | FALSE | FALSE | TRUE | FALSE | 6 | 27905243 | 27906181 | NA | NA | NA | NA | NA | 11 | 7.34E-05 | NA | NA | NA | TRUE |
| ENSG00000214374 | RPLP2P1 | FALSE | FALSE | TRUE | FALSE | 6 | 27932953 | 27933292 | NA | NA | NA | NA | NA | 8 | 4.87E-08 | NA | NA | NA | TRUE |
| ENSG00000217539 | IQCB2P | FALSE | TRUE | TRUE | FALSE | 6 | 27943501 | 27990133 | NA | NA | NA | 149 | 0.01035 | 13 | 1.82E-05 | NA | NA | NA | TRUE |
| ENSG00000216629 | OR2W4P | FALSE | FALSE | TRUE | FALSE | 6 | 27944928 | 27945853 | NA | NA | NA | NA | NA | 8 | 1.43E-06 | NA | NA | NA | TRUE |
| ENSG00000199851 | | FALSE | TRUE | TRUE | FALSE | 6 | 27948346 | 27993553 | NA | NA | NA | 144 | 0.001216 | 38 | 8.33E-05 | NA | NA | NA | TRUE |
| ENSG00000217315 | OR2W2P | FALSE | TRUE | TRUE | FALSE | 6 | 27966725 | 28012633 | NA | NA | NA | 146 | 6.68E-06 | 8 | 0.000171 | NA | NA | NA | TRUE |
| ENSG00000187763 | OR2B7P | FALSE | TRUE | TRUE | TRUE | 6 | 27979212 | 28025145 | NA | NA | NA | 163 | 5.89E-05 | 13 | 0.000406 | -6.42857 | 1.29E-10 | TRUE | TRUE |
| ENSG00000220721 | OR1F12 | FALSE | TRUE | FALSE | TRUE | 6 | 28006094 | 28052011 | NA | NA | NA | 162 | 1.59E-06 | NA | NA | -6.50023 | 8.02E-11 | TRUE | TRUE |
| ENSG00000182477 | OR2B8P | FALSE | TRUE | TRUE | TRUE | 6 | 28011006 | 28056943 | NA | NA | NA | 158 | 9.10E-07 | 11 | 0.003978 | -6.5429 | 6.04E-11 | FALSE | TRUE |
| ENSG00000197279 | ZNF165 | FALSE | TRUE | TRUE | TRUE | 6 | 28013753 | 28067341 | NA | NA | NA | 187 | 2.85E-07 | 65 | 1.49E-08 | 4.92146 | 8.59E-07 | FALSE | FALSE |
| ENSG00000219891 | ZSCAN12P1 | FALSE | TRUE | TRUE | TRUE | 6 | 28023932 | 28071442 | NA | NA | NA | 163 | 7.17E-08 | 47 | 2.74E-09 | 7.1867 | 6.64E-13 | FALSE | TRUE |
| ENSG00000272009 | | FALSE | TRUE | TRUE | TRUE | 6 | 28036570 | 28083908 | NA | NA | NA | 163 | 1.27E-08 | 13 | 8.92E-06 | 6.49021 | 8.57E-11 | NA | TRUE |
| ENSG00000219392 | ZNF602P | FALSE | TRUE | TRUE | TRUE | 6 | 28048406 | 28094329 | NA | NA | NA | 161 | 3.15E-09 | 27 | 1.24E-07 | 7.5471 | 4.45E-14 | TRUE | TRUE |
| ENSG00000196812 | ZSCAN16 | FALSE | TRUE | TRUE | TRUE | 6 | 28057338 | 28107860 | NA | NA | NA | 172 | 1.11E-08 | 44 | 2.68E-05 | -7.4977 | 6.49E-14 | FALSE | FALSE |
| ENSG00000261839 | | FALSE | TRUE | TRUE | TRUE | 6 | 28069627 | 28117456 | NA | NA | NA | 160 | 4.53E-08 | 16 | 1.97E-05 | -6.98553 | 2.84E-12 | NA | TRUE |
| ENSG00000198315 | ZKSCAN8 | FALSE | TRUE | TRUE | TRUE | 6 | 28074716 | 28137250 | NA | NA | NA | 219 | 3.60E-08 | 147 | 1.26E-07 | 8.13254 | 4.20E-16 | TRUE | FALSE |
| ENSG00000269293 | ZSCAN16-AS1 | FALSE | TRUE | TRUE | TRUE | 6 | 28079573 | 28140071 | NA | NA | NA | 212 | 3.12E-08 | 17 | 6.94E-06 | 6.4549 | 1.08E-10 | TRUE | TRUE |
| ENSG00000226314 | ZKSCAN8P1 | FALSE | TRUE | TRUE | TRUE | 6 | 28094559 | 28147372 | NA | NA | NA | 173 | 1.03E-07 | 32 | 2.09E-09 | -6.8879 | 5.66E-12 | NA | TRUE |
| ENSG00000280107 | | FALSE | TRUE | TRUE | TRUE | 6 | 28103623 | 28150299 | NA | NA | NA | 163 | 1.29E-07 | 15 | 4.10E-09 | 6.34503 | 2.22E-10 | NA | TRUE |
| ENSG00000216901 | ZNF603P | FALSE | TRUE | TRUE | FALSE | 6 | 28108966 | 28154452 | NA | NA | NA | 153 | 4.70E-08 | 10 | 7.43E-07 | NA | NA | NA | TRUE |
| ENSG00000218016 | ZKSCAN8P2 | FALSE | TRUE | FALSE | FALSE | 6 | 28120828 | 28167210 | NA | NA | NA | 147 | 8.16E-08 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000137185 | ZSCAN9 | FALSE | TRUE | TRUE | TRUE | 6 | 28158042 | 28211260 | NA | NA | NA | 157 | 3.34E-09 | 27 | 1.93E-10 | -8.42105 | 3.73E-17 | FALSE | FALSE |
| ENSG00000176933 | TOB2P1 | FALSE | TRUE | TRUE | TRUE | 6 | 28175421 | 28221412 | NA | NA | NA | 135 | 6.07E-10 | 10 | 0.007378 | -5.3385 | 9.37E-08 | TRUE | TRUE |
| ENSG00000189134 | NKAPL | FALSE | TRUE | TRUE | FALSE | 6 | 28192098 | 28238736 | NA | NA | NA | 133 | 5.70E-09 | 11 | 3.54E-06 | NA | NA | FALSE | FALSE |
| ENSG00000197062 | ZSCAN26 | FALSE | TRUE | TRUE | TRUE | 6 | 28199788 | 28256001 | NA | NA | NA | 145 | 2.79E-05 | 29 | 1.01E-08 | 6.85488 | 7.14E-12 | TRUE | FALSE |
| ENSG00000276302 | | FALSE | TRUE | TRUE | FALSE | 6 | 28199899 | 28259357 | NA | NA | NA | 151 | 1.55E-08 | 9 | 2.00E-07 | NA | NA | NA | TRUE |
| ENSG00000187626 | ZKSCAN4 | FALSE | TRUE | TRUE | TRUE | 6 | 28202401 | 28255002 | NA | NA | NA | 133 | 6.48E-10 | 14 | 1.51E-06 | -8.5972 | 8.17E-18 | FALSE | FALSE |
| ENSG00000137338 | PGBD1 | FALSE | TRUE | TRUE | TRUE | 6 | 28214349 | 28280326 | NA | NA | NA | 199 | 1.31E-06 | 67 | 7.09E-08 | -7.4676 | 8.17E-14 | FALSE | FALSE |
| ENSG00000273712 | | FALSE | TRUE | FALSE | FALSE | 6 | 28273390 | 28318660 | NA | NA | NA | 168 | 1.21E-06 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000270326 | SMIM15P2 | FALSE | TRUE | TRUE | TRUE | 6 | 28277437 | 28322629 | NA | NA | NA | 174 | 1.10E-05 | 12 | 0.01742 | 8.2281 | 1.90E-16 | TRUE | TRUE |
| ENSG00000235109 | ZSCAN31 | FALSE | TRUE | TRUE | TRUE | 6 | 28282514 | 28359048 | NA | NA | NA | 297 | 0.007928 | 101 | 1.46E-06 | -5.9996 | 1.98E-09 | FALSE | FALSE |
| ENSG00000189298 | ZKSCAN3 | FALSE | TRUE | TRUE | TRUE | 6 | 28282691 | 28346954 | NA | NA | NA | 257 | 0.008276 | 85 | 4.53E-08 | 7.0152 | 2.30E-12 | FALSE | FALSE |
| ENSG00000235570 | LINC00533 | FALSE | FALSE | FALSE | TRUE | 6 | 28616063 | 28616843 | NA | NA | NA | NA | NA | NA | NA | -6.78 | 1.20E-11 | TRUE | NA |
| ENSG00000237425 | RPSAP2 | FALSE | TRUE | FALSE | FALSE | 6 | 28664794 | 28710681 | NA | NA | NA | 84 | 0.021207 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000235559 | NOP56P1 | FALSE | TRUE | FALSE | FALSE | 6 | 28741410 | 28786781 | NA | NA | NA | 74 | 0.002713 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000265764 | NA | FALSE | TRUE | TRUE | FALSE | 6 | 28753749 | 28798812 | NA | NA | NA | 77 | 0.001241 | 8 | 9.12E-07 | NA | NA | NA | TRUE |
| ENSG00000224157 | HCG14 | FALSE | FALSE | TRUE | FALSE | 6 | 28864307 | 28865099 | NA | NA | NA | NA | NA | 28 | 9.26E-05 | NA | NA | NA | TRUE |
| ENSG00000212240 | RNU6-930P | FALSE | FALSE | TRUE | FALSE | 6 | 28883422 | 28883521 | NA | NA | NA | NA | NA | 2 | 0.001684 | NA | NA | NA | TRUE |
| ENSG00000277661 | | FALSE | FALSE | TRUE | FALSE | 6 | 29003798 | 29044301 | NA | NA | NA | NA | NA | 10 | 0.046024 | NA | NA | NA | TRUE |
| ENSG00000112462 | OR12D3 | FALSE | FALSE | TRUE | FALSE | 6 | 29341200 | 29343068 | NA | NA | NA | NA | NA | 3 | 1.78E-05 | NA | NA | NA | FALSE |

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|-----------------|------------------|-------|-------|-------|-------|---|----------|----------|----|----|----|-----|----------|-----|----------|---------|----------|-------|-------|
| ENSG00000236405 | <i>UBQLN1P1</i> | FALSE | FALSE | TRUE | FALSE | 6 | 30330889 | 30332057 | NA | NA | NA | NA | NA | 99 | 0.024497 | NA | NA | NA | TRUE |
| ENSG00000137343 | <i>ATA1</i> | FALSE | FALSE | TRUE | FALSE | 6 | 30594619 | 30614600 | NA | NA | NA | NA | NA | 150 | 0.004345 | NA | NA | NA | TRUE |
| ENSG00000137312 | <i>FLOT1</i> | FALSE | FALSE | FALSE | TRUE | 6 | 30695486 | 30710509 | NA | NA | NA | NA | NA | NA | NA | -5.3714 | 7.81E-08 | FALSE | NA |
| ENSG00000137331 | <i>IER3</i> | FALSE | FALSE | FALSE | TRUE | 6 | 30710976 | 30712325 | NA | NA | NA | NA | NA | NA | NA | -6.143 | 8.10E-10 | TRUE | NA |
| ENSG00000204580 | <i>DDR1</i> | FALSE | FALSE | FALSE | TRUE | 6 | 30844198 | 30867933 | NA | NA | NA | NA | NA | NA | NA | 5.0584 | 4.23E-07 | TRUE | NA |
| ENSG00000213780 | <i>GTF2H4</i> | FALSE | FALSE | FALSE | TRUE | 6 | 30875984 | 30881883 | NA | NA | NA | NA | NA | NA | NA | 6.7802 | 1.20E-11 | TRUE | NA |
| ENSG00000137411 | <i>VARS2</i> | FALSE | FALSE | FALSE | TRUE | 6 | 30881982 | 30894236 | NA | NA | NA | NA | NA | NA | NA | 5.7459 | 9.14E-09 | FALSE | NA |
| ENSG00000228789 | <i>HCG22</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31021227 | 31027667 | NA | NA | NA | NA | NA | NA | NA | 5.0372 | 4.72E-07 | TRUE | NA |
| ENSG00000204540 | <i>PSORS1C1</i> | FALSE | TRUE | TRUE | FALSE | 6 | 31047608 | 31117869 | NA | NA | NA | 389 | 0.011189 | 91 | 0.008806 | NA | NA | NA | FALSE |
| ENSG00000204542 | <i>C6orf15</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31069000 | 31115336 | NA | NA | NA | 370 | 0.011295 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000204539 | <i>CDSN</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31072867 | 31123223 | NA | NA | NA | 379 | 0.01137 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000238211 | <i>POLR2LP1</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31073504 | 31118690 | NA | NA | NA | 370 | 0.011324 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000137310 | <i>TCF19</i> | FALSE | TRUE | TRUE | FALSE | 6 | 31091319 | 31141992 | NA | NA | NA | 213 | 0.001173 | 164 | 1.23E-06 | NA | NA | NA | TRUE |
| ENSG00000204538 | <i>PSORS1C2</i> | FALSE | TRUE | FALSE | TRUE | 6 | 31095313 | 31142127 | NA | NA | NA | 159 | 0.000756 | NA | NA | 4.8628 | 1.16E-06 | TRUE | FALSE |
| ENSG00000204536 | <i>CCHCR1</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31110216 | 31126015 | NA | NA | NA | NA | NA | NA | NA | 4.8596 | 1.18E-06 | TRUE | NA |
| ENSG00000272501 | | FALSE | FALSE | FALSE | TRUE | 6 | 31162977 | 31165814 | NA | NA | NA | NA | NA | NA | NA | -5.1531 | 2.56E-07 | NA | NA |
| ENSG00000206344 | <i>HCG27</i> | FALSE | FALSE | TRUE | FALSE | 6 | 31165537 | 31171745 | NA | NA | NA | NA | NA | 59 | 4.90E-05 | NA | NA | NA | TRUE |
| ENSG00000204525 | <i>HLA-C</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31236526 | 31239907 | NA | NA | NA | NA | NA | NA | NA | -4.9746 | 6.54E-07 | TRUE | NA |
| ENSG00000234745 | <i>HLA-B</i> | FALSE | FALSE | TRUE | TRUE | 6 | 31237268 | 31324964 | NA | NA | NA | NA | NA | 201 | 0.00037 | 5.3043 | 1.13E-07 | TRUE | FALSE |
| ENSG00000231402 | <i>WASF5P</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31255287 | 31256741 | NA | NA | NA | NA | NA | NA | NA | -5.6286 | 1.82E-08 | FALSE | NA |
| ENSG00000271581 | | FALSE | TRUE | TRUE | TRUE | 6 | 31289424 | 31335414 | NA | NA | NA | 446 | 2.26E-05 | 101 | 0.002541 | -4.9269 | 8.35E-07 | NA | TRUE |
| ENSG00000201658 | <i>RNU6-283P</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31302911 | 31348017 | NA | NA | NA | 451 | 7.72E-05 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000230994 | <i>FGFR3P1</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31310196 | 31355796 | NA | NA | NA | 455 | 6.81E-05 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000223702 | <i>ZDHHC20P2</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31313188 | 31358616 | NA | NA | NA | 443 | 6.89E-05 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000228432 | <i>DHFRP2</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31324129 | 31369675 | NA | NA | NA | 284 | 0.000183 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000225851 | <i>HLA-S</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31349851 | 31350065 | NA | NA | NA | NA | NA | NA | NA | 6.4798 | 9.18E-11 | TRUE | NA |
| ENSG00000204520 | <i>MICA</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31367561 | 31383092 | NA | NA | NA | NA | NA | NA | NA | -4.8482 | 1.25E-06 | TRUE | NA |
| ENSG00000233902 | | FALSE | TRUE | FALSE | FALSE | 6 | 31420505 | 31466113 | NA | NA | NA | 151 | 0.004972 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000204516 | <i>MICB</i> | FALSE | TRUE | TRUE | TRUE | 6 | 31427658 | 31488901 | NA | NA | NA | 264 | 0.035715 | 146 | 0.013283 | -5.249 | 1.53E-07 | FALSE | FALSE |
| ENSG00000256851 | | FALSE | TRUE | FALSE | FALSE | 6 | 31448756 | 31493988 | NA | NA | NA | 244 | 0.044734 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000201680 | | FALSE | TRUE | FALSE | FALSE | 6 | 31454466 | 31499567 | NA | NA | NA | 244 | 0.04245 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000225499 | <i>RPL15P4</i> | FALSE | TRUE | FALSE | FALSE | 6 | 31460891 | 31506470 | NA | NA | NA | 243 | 0.041976 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000198563 | <i>DDX39B</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31497996 | 31510225 | NA | NA | NA | NA | NA | NA | NA | 6.4079 | 1.48E-10 | TRUE | NA |
| ENSG00000213760 | <i>ATP6V1G2</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31512221 | 31516204 | NA | NA | NA | NA | NA | NA | NA | 4.8372 | 1.32E-06 | TRUE | NA |
| ENSG00000204498 | <i>NFKBIL1</i> | FALSE | FALSE | TRUE | FALSE | 6 | 31515358 | 31526606 | NA | NA | NA | NA | NA | 40 | 0.000246 | NA | NA | NA | TRUE |
| ENSG00000204482 | <i>LST1</i> | FALSE | FALSE | TRUE | FALSE | 6 | 31553901 | 31556686 | NA | NA | NA | NA | NA | 7 | 0.024387 | NA | NA | NA | FALSE |
| ENSG00000204463 | <i>BAG6</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31606805 | 31620482 | NA | NA | NA | NA | NA | NA | NA | -5.0561 | 4.28E-07 | FALSE | NA |
| ENSG00000204428 | <i>LY6G5C</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31644461 | 31651817 | NA | NA | NA | NA | NA | NA | NA | 5.0826 | 3.72E-07 | TRUE | NA |
| ENSG00000204427 | <i>ABHD16A</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31654732 | 31671133 | NA | NA | NA | NA | NA | NA | NA | 5.0184 | 5.21E-07 | TRUE | NA |
| ENSG00000204420 | <i>MPIG6B</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31686371 | 31694491 | NA | NA | NA | NA | NA | NA | NA | 4.89529 | 9.82E-07 | TRUE | NA |
| ENSG00000204421 | <i>LY6G6C</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31686425 | 31689523 | NA | NA | NA | NA | NA | NA | NA | -5.8016 | 6.57E-09 | TRUE | NA |
| ENSG00000213722 | <i>DDAH2</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31694815 | 31698394 | NA | NA | NA | NA | NA | NA | NA | 6.27865 | 3.42E-10 | FALSE | NA |
| ENSG00000204410 | <i>MSH5</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31707454 | 31730453 | NA | NA | NA | NA | NA | NA | NA | 5.86483 | 4.50E-09 | TRUE | NA |
| ENSG00000204396 | <i>VWA7</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31733367 | 31745105 | NA | NA | NA | NA | NA | NA | NA | 5.2581 | 1.46E-07 | TRUE | NA |
| ENSG00000204366 | <i>ZBTB12</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31867390 | 31869863 | NA | NA | NA | NA | NA | NA | NA | 5.6052 | 2.08E-08 | FALSE | NA |
| ENSG00000224389 | <i>C4B</i> | FALSE | FALSE | FALSE | TRUE | 6 | 31982572 | 32003195 | NA | NA | NA | NA | NA | NA | NA | -5.3135 | 1.08E-07 | TRUE | NA |
| ENSG00000030110 | <i>BAK1</i> | FALSE | TRUE | FALSE | FALSE | 6 | 33530324 | 33583070 | NA | NA | NA | 267 | 0.048075 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000197251 | <i>LINC00336</i> | FALSE | TRUE | FALSE | FALSE | 6 | 33543883 | 33596115 | NA | NA | NA | 277 | 0.042116 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000233859 | <i>ADH5P4</i> | FALSE | TRUE | FALSE | FALSE | 6 | 66536823 | 66582932 | NA | NA | NA | 337 | 0.000511 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000270521 | | FALSE | FALSE | TRUE | FALSE | 6 | 67420135 | 67420720 | NA | NA | NA | NA | NA | 260 | 0.00013 | NA | NA | NA | TRUE |
| ENSG00000172469 | <i>MANEA</i> | FALSE | TRUE | FALSE | FALSE | 6 | 95990419 | 96067333 | NA | NA | NA | 265 | 0.045021 | NA | NA | NA | NA | NA | FALSE |

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|-----------------|------------|-------|-------|-------|-------|---|----------|----------|-----|-----|-----------|------|----------|-----|----------|-----------|----------|-------|-------|
| ENSG00000261366 | MANEA-DT | FALSE | TRUE | FALSE | TRUE | 6 | 96013059 | 96060326 | NA | NA | NA | 173 | 0.048015 | NA | NA | -4.87018 | 1.11E-06 | TRUE | TRUE |
| ENSG00000152034 | MCHR2 | FALSE | FALSE | TRUE | FALSE | 6 | 1E+08 | 1E+08 | NA | NA | NA | NA | NA | 125 | 0.002 | NA | NA | NA | TRUE |
| ENSG00000112246 | SIM1 | TRUE | TRUE | FALSE | FALSE | 6 | 1.01E+08 | 1.01E+08 | 9 | 0 | rs1237461 | 327 | 0.009845 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000220695 | | FALSE | TRUE | TRUE | FALSE | 6 | 1.01E+08 | 1.01E+08 | NA | NA | NA | 75 | 0.000148 | 6 | 6.97E-05 | NA | NA | NA | TRUE |
| ENSG00000112249 | ASCC3 | TRUE | TRUE | FALSE | FALSE | 6 | 1.01E+08 | 1.01E+08 | 371 | 309 | rs1237461 | 1211 | 0.000705 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000260000 | | FALSE | TRUE | FALSE | TRUE | 6 | 1.01E+08 | 1.01E+08 | NA | NA | NA | 147 | 0.008605 | NA | NA | 5.8099 | 6.25E-09 | NA | TRUE |
| ENSG00000270987 | | FALSE | TRUE | TRUE | FALSE | 6 | 1.01E+08 | 1.01E+08 | NA | NA | NA | 148 | 0.002966 | 15 | 0.009392 | NA | NA | NA | TRUE |
| ENSG00000164418 | GRIK2 | TRUE | FALSE | FALSE | FALSE | 6 | 1.02E+08 | 1.03E+08 | 0 | 2 | rs1237461 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000085382 | HACE1 | TRUE | FALSE | FALSE | TRUE | 6 | 1.05E+08 | 1.05E+08 | 0 | 44 | rs1115642 | NA | NA | NA | NA | 4.981 | 6.33E-07 | TRUE | NA |
| ENSG00000203809 | LIN28B-AS1 | FALSE | TRUE | TRUE | TRUE | 6 | 1.05E+08 | 1.05E+08 | NA | NA | NA | 229 | 9.73E-06 | 11 | 8.37E-06 | 6.6743 | 2.48E-11 | TRUE | TRUE |
| ENSG00000187772 | LIN28B | TRUE | TRUE | FALSE | TRUE | 6 | 1.05E+08 | 1.06E+08 | 33 | 32 | rs1115642 | 297 | 2.46E-05 | NA | NA | -6.95218 | 3.60E-12 | FALSE | FALSE |
| ENSG00000164483 | SAMD3 | TRUE | TRUE | FALSE | FALSE | 6 | 1.3E+08 | 1.31E+08 | 344 | 233 | rs1044741 | 1244 | 0.024654 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000164484 | TMEM200A | TRUE | FALSE | FALSE | FALSE | 6 | 1.31E+08 | 1.31E+08 | 28 | 111 | rs1044741 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000236366 | | FALSE | TRUE | FALSE | FALSE | 6 | 1.43E+08 | 1.43E+08 | NA | NA | NA | 475 | 0.00262 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000229017 | LINC01277 | FALSE | FALSE | TRUE | FALSE | 6 | 1.43E+08 | 1.43E+08 | NA | NA | NA | NA | NA | 151 | 0.002244 | NA | NA | NA | TRUE |
| ENSG00000146416 | AIG1 | FALSE | FALSE | TRUE | FALSE | 6 | 1.43E+08 | 1.44E+08 | NA | NA | NA | NA | NA | 125 | 0.008489 | NA | NA | NA | TRUE |
| ENSG00000189007 | ADAT2 | FALSE | FALSE | TRUE | FALSE | 6 | 1.44E+08 | 1.44E+08 | NA | NA | NA | NA | NA | 93 | 0.02704 | NA | NA | NA | TRUE |
| ENSG00000203727 | SAMD5 | TRUE | FALSE | FALSE | FALSE | 6 | 1.48E+08 | 1.48E+08 | 21 | 11 | rs9497822 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000091831 | ESR1 | TRUE | FALSE | FALSE | FALSE | 6 | 1.52E+08 | 1.52E+08 | 47 | 6 | rs3757323 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000112530 | PACRG | FALSE | FALSE | FALSE | TRUE | 6 | 1.63E+08 | 1.64E+08 | NA | NA | NA | NA | NA | NA | NA | -5.0324 | 4.84E-07 | TRUE | NA |
| ENSG00000198517 | MAFK | TRUE | FALSE | FALSE | FALSE | 7 | 1570350 | 1582679 | 0 | 3 | rs3996329 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000230444 | TFAMP1 | FALSE | FALSE | TRUE | FALSE | 7 | 1654226 | 1654961 | NA | NA | NA | NA | NA | 202 | 0.012738 | NA | NA | NA | TRUE |
| ENSG00000002822 | MAD1L1 | TRUE | FALSE | FALSE | FALSE | 7 | 1855429 | 2272878 | 28 | 0 | rs3996329 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000176349 | | TRUE | TRUE | FALSE | FALSE | 7 | 1878222 | 1889567 | 0 | 24 | rs3996329 | 323 | 0.02146 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000122687 | MRM2 | TRUE | FALSE | FALSE | FALSE | 7 | 2273866 | 2281840 | 0 | 26 | rs3996329 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000146555 | SDK1 | FALSE | TRUE | FALSE | TRUE | 7 | 3306080 | 4318632 | NA | NA | NA | 4375 | 0.005388 | NA | NA | -4.872625 | 1.10E-06 | TRUE | FALSE |
| ENSG00000178397 | FAM220A | FALSE | FALSE | FALSE | TRUE | 7 | 6369042 | 6388612 | NA | NA | NA | NA | NA | NA | NA | -4.8692 | 1.12E-06 | TRUE | NA |
| ENSG00000005108 | THSD7A | TRUE | FALSE | TRUE | FALSE | 7 | 11409984 | 11871824 | 0 | 1 | rs1269932 | NA | NA | 564 | 8.44E-10 | NA | NA | NA | TRUE |
| ENSG00000106460 | TMEM106B | TRUE | TRUE | TRUE | TRUE | 7 | 12250867 | 12282993 | 123 | 116 | rs1269932 | 431 | 2.79E-05 | 98 | 1.57E-08 | 7.8302 | 4.87E-15 | FALSE | FALSE |
| ENSG00000146530 | VWDE | TRUE | FALSE | FALSE | FALSE | 7 | 12370511 | 12443567 | 0 | 66 | rs1269932 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000105926 | PALS2 | TRUE | FALSE | TRUE | TRUE | 7 | 24612887 | 24733812 | 60 | 64 | rs2529050 | NA | NA | 308 | 0.025526 | -5.63636 | 1.74E-08 | NA | TRUE |
| ENSG00000105928 | GSDME | TRUE | FALSE | FALSE | TRUE | 7 | 24737972 | 24809244 | 15 | 75 | rs2529050 | NA | NA | NA | NA | 5.181818 | 2.20E-07 | TRUE | NA |
| ENSG00000205756 | | FALSE | TRUE | FALSE | FALSE | 7 | 32792946 | 32838054 | NA | NA | NA | 234 | 0.003308 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000251999 | | FALSE | TRUE | TRUE | FALSE | 7 | 32796426 | 32841558 | NA | NA | NA | 240 | 0.004222 | 20 | 0.015463 | NA | NA | NA | TRUE |
| ENSG00000231952 | DPY19L1P2 | FALSE | TRUE | FALSE | FALSE | 7 | 32817369 | 32888182 | NA | NA | NA | 307 | 0.01722 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000226829 | | FALSE | FALSE | TRUE | FALSE | 7 | 67615270 | 67753220 | NA | NA | NA | NA | NA | 306 | 2.68E-05 | NA | NA | NA | TRUE |
| ENSG00000106089 | STX1A | TRUE | FALSE | FALSE | FALSE | 7 | 73113536 | 73134002 | 0 | 11 | rs2107745 | NA | NA | NA | NA | NA | NA | NA | NA |
| ENSG00000106077 | ABHD11 | FALSE | FALSE | TRUE | FALSE | 7 | 73150424 | 73153197 | NA | NA | NA | NA | NA | 39 | 0.029716 | NA | NA | NA | TRUE |
| ENSG00000175877 | TMEM270 | FALSE | FALSE | TRUE | FALSE | 7 | 73275489 | 73280223 | NA | NA | NA | NA | NA | 134 | 0.006602 | NA | NA | NA | TRUE |
| ENSG00000106682 | EIF4H | FALSE | FALSE | FALSE | TRUE | 7 | 73588561 | 73611452 | NA | NA | NA | NA | NA | NA | NA | -5.683279 | 1.32E-08 | TRUE | NA |
| ENSG00000006704 | GTF2IRD1 | TRUE | TRUE | TRUE | FALSE | 7 | 73868120 | 74016931 | 75 | 0 | rs2107745 | 472 | 0.000674 | 152 | 0.001646 | NA | NA | NA | FALSE |
| ENSG00000238391 | RNA5SP233 | FALSE | TRUE | TRUE | FALSE | 7 | 73891758 | 73936870 | NA | NA | NA | 139 | 0.019993 | 44 | 0.006079 | NA | NA | NA | TRUE |
| ENSG00000252378 | NA | FALSE | TRUE | FALSE | FALSE | 7 | 73950677 | 73995754 | NA | NA | NA | 98 | 0.008009 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000274523 | RCC1L | FALSE | FALSE | FALSE | TRUE | 7 | 74441226 | 74490064 | NA | NA | NA | NA | NA | NA | NA | 5.042803 | 4.59E-07 | TRUE | NA |
| ENSG00000153956 | CACNA2D1 | FALSE | TRUE | FALSE | FALSE | 7 | 81565760 | 82108114 | NA | NA | NA | 1785 | 0.020088 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000186472 | PCLO | TRUE | TRUE | TRUE | FALSE | 7 | 82383329 | 82792246 | 121 | 0 | rs2522836 | 1347 | 1.41E-06 | 143 | 6.40E-05 | NA | NA | NA | FALSE |
| ENSG00000127914 | AKAP9 | FALSE | FALSE | FALSE | TRUE | 7 | 91570154 | 91739987 | NA | NA | NA | NA | NA | NA | NA | -4.84084 | 1.29E-06 | TRUE | NA |
| ENSG00000234273 | | FALSE | TRUE | FALSE | FALSE | 7 | 1.09E+08 | 1.09E+08 | NA | NA | NA | 404 | 2.11E-05 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000077063 | CTTNBP2 | FALSE | TRUE | FALSE | FALSE | 7 | 1.17E+08 | 1.18E+08 | NA | NA | NA | 472 | 0.011372 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000224136 | | FALSE | TRUE | FALSE | FALSE | 7 | 1.17E+08 | 1.18E+08 | NA | NA | NA | 99 | 0.001531 | NA | NA | NA | NA | NA | TRUE |
| ENSG00000179603 | GRM8 | FALSE | TRUE | FALSE | FALSE | 7 | 1.26E+08 | 1.27E+08 | NA | NA | NA | 2428 | 7.81E-06 | NA | NA | NA | NA | NA | FALSE |

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|-----------------|------------|-------|-------|-------|-------|----|----------|----------|----|----|----|-----|----------------|------|----------|----------|----------|----------|----------|------|
| ENSG00000201080 | NA | FALSE | TRUE | TRUE | FALSE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | 137 | 0.043785 | 1 | 0.020386 | NA | NA | NA | TRUE | |
| ENSG00000213061 | PFN1P11 | FALSE | FALSE | TRUE | FALSE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | NA | NA | 71 | 0.01016 | NA | NA | NA | TRUE | |
| ENSG00000236937 | PTGES3P4 | FALSE | FALSE | TRUE | FALSE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | NA | NA | 12 | 0.012218 | NA | NA | NA | TRUE | |
| ENSG00000166275 | BORCS7 | TRUE | FALSE | TRUE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 11 | 4 rs7597093f | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000270316 | BORCS7-ASM | TRUE | TRUE | TRUE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 34 | 0 rs7597093f | 288 | 0.045148 | 18 | 0.005613 | NA | TRUE | |
| ENSG00000214435 | AS3MT | TRUE | TRUE | TRUE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 28 | 36 rs7597093f | 249 | 0.031297 | 141 | 0.002154 | NA | TRUE | |
| ENSG00000148842 | CNNM2 | TRUE | FALSE | FALSE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 74 | 128 rs7597093f | NA | NA | NA | NA | NA | NA | |
| ENSG00000076685 | NT5C2 | TRUE | FALSE | FALSE | TRUE | 10 | 1.05E+08 | 1.05E+08 | | | | 50 | 104 rs7597093f | NA | NA | NA | -5.6791 | 1.35E-08 | TRUE | |
| ENSG00000213277 | MARCKSL1P1 | FALSE | FALSE | FALSE | TRUE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | NA | NA | NA | -5.584 | 2.35E-08 | TRUE | NA | NA | |
| ENSG00000148798 | INA | TRUE | FALSE | FALSE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 1 | 90 rs7597093f | NA | NA | NA | NA | NA | NA | |
| ENSG00000156374 | PCGF6 | TRUE | FALSE | FALSE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 1 | 0 rs7597093f | NA | NA | NA | NA | NA | NA | |
| ENSG00000148843 | PDCD11 | FALSE | TRUE | FALSE | FALSE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | 149 | 0.00869 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000173915 | ATP5MK | FALSE | TRUE | TRUE | TRUE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | 84 | 0.011103 | 8 | 0.04877 | 4.90664 | 9.26E-07 | NA | TRUE | |
| ENSG00000221767 | NA | FALSE | TRUE | FALSE | FALSE | 10 | 1.05E+08 | 1.05E+08 | NA | NA | NA | 71 | 0.016963 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000138172 | CALHM2 | TRUE | FALSE | FALSE | FALSE | 10 | 1.05E+08 | 1.05E+08 | | | | 0 | 1 rs7597093f | NA | NA | NA | NA | NA | NA | |
| ENSG00000237761 | NA | FALSE | TRUE | FALSE | FALSE | 10 | 1.06E+08 | 1.06E+08 | NA | NA | NA | 102 | 0.035957 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000156395 | SORCS3 | TRUE | TRUE | TRUE | TRUE | 10 | 1.06E+08 | 1.07E+08 | | | | 40 | 0 rs1021363 | 2047 | 2.23E-13 | 101 | 1.28E-08 | -6.36302 | 1.98E-10 | TRUE |
| ENSG00000226387 | SORCS3-AS1 | FALSE | TRUE | FALSE | FALSE | 10 | 1.06E+08 | 1.06E+08 | NA | NA | NA | 92 | 2.86E-05 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000148704 | VAX1 | FALSE | TRUE | FALSE | FALSE | 10 | 1.19E+08 | 1.19E+08 | NA | NA | NA | 112 | 0.019366 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000154478 | GPR26 | FALSE | FALSE | TRUE | FALSE | 10 | 1.25E+08 | 1.25E+08 | NA | NA | NA | NA | NA | 41 | 0.005571 | NA | NA | NA | TRUE | |
| ENSG00000110693 | SOX6 | TRUE | TRUE | FALSE | FALSE | 11 | 15987995 | 16761138 | | | | 141 | 0 rs1083258f | 1162 | 0.010994 | NA | NA | NA | FALSE | |
| ENSG00000187398 | LUZP2 | TRUE | FALSE | FALSE | FALSE | 11 | 24518516 | 25104150 | | | | 164 | 2 rs1691279f | NA | NA | NA | NA | NA | NA | |
| ENSG00000152219 | ARL14EP | FALSE | FALSE | TRUE | FALSE | 11 | 30344598 | 30359774 | NA | NA | NA | NA | NA | 143 | 0.000103 | NA | NA | NA | TRUE | |
| ENSG00000242353 | RPL12P30 | FALSE | FALSE | TRUE | FALSE | 11 | 30389695 | 30390193 | NA | NA | NA | NA | NA | 61 | 0.001636 | NA | NA | NA | TRUE | |
| ENSG00000066382 | MPPED2 | FALSE | FALSE | TRUE | FALSE | 11 | 30406040 | 30607828 | NA | NA | NA | NA | NA | 50 | 3.43E-06 | NA | NA | NA | TRUE | |
| ENSG00000170959 | DCDC1 | TRUE | TRUE | FALSE | FALSE | 11 | 30851916 | 31391357 | | | | 125 | 0 rs2616792 | 855 | 9.46E-05 | NA | NA | NA | FALSE | |
| ENSG00000221629 | NA | FALSE | TRUE | FALSE | FALSE | 11 | 31192306 | 31237441 | NA | NA | NA | 92 | 0.020288 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000255370 | CYCSP25 | FALSE | TRUE | FALSE | FALSE | 11 | 31292219 | 31337534 | NA | NA | NA | 68 | 0.000477 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000255525 | NA | FALSE | TRUE | TRUE | FALSE | 11 | 31292232 | 31346095 | NA | NA | NA | 73 | 0.000307 | 9 | 0.00026 | NA | NA | NA | TRUE | |
| ENSG00000170946 | DNAJC24 | TRUE | TRUE | FALSE | TRUE | 11 | 31391387 | 31453396 | | | | 9 | 16 rs2616792 | 170 | 0.043066 | NA | 5.1334 | 2.84E-07 | FALSE | |
| ENSG00000109911 | ELP4 | TRUE | FALSE | FALSE | FALSE | 11 | 31531297 | 31805546 | | | | 2 | 0 rs1806152 | NA | NA | NA | NA | NA | NA | |
| ENSG00000007372 | PAX6 | TRUE | TRUE | TRUE | FALSE | 11 | 31806340 | 31839509 | | | | 32 | 0 rs1806152 | 118 | 0.000233 | 63 | 3.62E-06 | NA | FALSE | |
| ENSG00000281880 | PAUPAR | FALSE | TRUE | FALSE | FALSE | 11 | 31812894 | 31860858 | NA | NA | NA | 65 | 0.001047 | NA | NA | NA | NA | NA | TRUE | |
| ENSG00000049449 | RCN1 | TRUE | FALSE | TRUE | FALSE | 11 | 31833939 | 32127301 | | | | 30 | 0 rs1806152 | NA | NA | 60 | 2.53E-06 | NA | FALSE | |
| ENSG00000149100 | EIF3M | TRUE | FALSE | FALSE | FALSE | 11 | 32605344 | 32627808 | | | | 24 | 0 rs1438647f | NA | NA | NA | NA | NA | NA | |
| ENSG00000186714 | CCDC73 | TRUE | FALSE | FALSE | FALSE | 11 | 32623792 | 32816204 | | | | 56 | 0 rs1438647f | NA | NA | NA | NA | NA | NA | |
| ENSG00000135378 | PRRG4 | TRUE | FALSE | FALSE | FALSE | 11 | 32851489 | 32879669 | | | | 0 | 30 rs1438647f | NA | NA | NA | NA | NA | NA | |
| ENSG00000121690 | DEPDC7 | TRUE | FALSE | FALSE | FALSE | 11 | 33037410 | 33055128 | | | | 0 | 30 rs1438647f | NA | NA | NA | NA | NA | NA | |
| ENSG00000149091 | DGKZ | FALSE | FALSE | TRUE | FALSE | 11 | 46354455 | 46402104 | NA | NA | NA | NA | NA | 202 | 0.016335 | NA | NA | NA | TRUE | |
| ENSG00000110497 | AMBRA1 | TRUE | FALSE | FALSE | FALSE | 11 | 46417964 | 46615675 | | | | 3 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000175213 | ZNF408 | TRUE | FALSE | FALSE | FALSE | 11 | 46722368 | 46727462 | | | | 1 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000180210 | F2 | TRUE | FALSE | FALSE | FALSE | 11 | 46740730 | 46761056 | | | | 2 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000175216 | CKAP5 | TRUE | FALSE | FALSE | FALSE | 11 | 46764598 | 46867847 | | | | 1 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000134569 | LRP4 | FALSE | FALSE | TRUE | FALSE | 11 | 46878419 | 46940173 | NA | NA | NA | NA | NA | 210 | 0.002151 | NA | NA | NA | TRUE | |
| ENSG00000149179 | C11orf49 | TRUE | FALSE | FALSE | TRUE | 11 | 46958240 | 47185936 | | | | 14 | 0 rs7130107 | NA | NA | NA | 4.8943 | 9.87E-07 | TRUE | |
| ENSG00000149182 | ARFGAP2 | TRUE | FALSE | FALSE | FALSE | 11 | 47185848 | 47198676 | | | | 1 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000165912 | PAC3IN3 | TRUE | FALSE | FALSE | FALSE | 11 | 47199076 | 47207994 | | | | 1 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000134574 | DDB2 | TRUE | FALSE | FALSE | FALSE | 11 | 47236493 | 47260767 | | | | 3 | 1 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000134575 | ACP2 | TRUE | FALSE | FALSE | FALSE | 11 | 47260853 | 47270457 | | | | 4 | 2 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000025434 | NR1H3 | TRUE | FALSE | FALSE | FALSE | 11 | 47269851 | 47290396 | | | | 1 | 0 rs7130107 | NA | NA | NA | NA | NA | NA | |
| ENSG00000110514 | MADD | TRUE | FALSE | FALSE | FALSE | 11 | 47290712 | 47351582 | | | | 2 | 8 rs7130107 | NA | NA | NA | NA | NA | NA | |

| | | | | | | | | | | | | | | | | | | | |
|-----------------|-----------|-------|-------|-------|-------|----|----------|----------|-----|-----|------------|-----|----------|----------|----------|----------|----------|-------|-------|
| ENSG00000123329 | ARHGAP9 | FALSE | FALSE | FALSE | TRUE | 12 | 57866047 | 57882597 | NA | NA | NA | NA | NA | NA | 4.8704 | 1.11E-06 | TRUE | NA | |
| ENSG00000236333 | TRHDE-AS1 | FALSE | FALSE | TRUE | TRUE | 12 | 72647288 | 72668687 | NA | NA | NA | NA | 42 | 0.047941 | 4.96357 | 6.92E-07 | TRUE | TRUE | |
| ENSG00000258332 | LINC02394 | FALSE | TRUE | FALSE | FALSE | 12 | 74397866 | 74449608 | NA | NA | NA | 142 | 0.038601 | NA | NA | NA | NA | TRUE | |
| ENSG00000213270 | RPL6P25 | FALSE | FALSE | TRUE | FALSE | 12 | 83545110 | 83545969 | NA | NA | NA | NA | 58 | 0.038932 | NA | NA | NA | TRUE | |
| ENSG00000257124 | | FALSE | TRUE | FALSE | FALSE | 12 | 84044788 | 84090498 | NA | NA | NA | 202 | 0.001002 | NA | NA | NA | NA | TRUE | |
| ENSG00000221148 | | FALSE | TRUE | FALSE | FALSE | 12 | 84567103 | 84612227 | NA | NA | NA | 134 | 0.000378 | NA | NA | NA | NA | TRUE | |
| ENSG00000257729 | | FALSE | TRUE | TRUE | FALSE | 12 | 84630119 | 84698341 | NA | NA | NA | 308 | 0.001685 | 72 | 6.02E-07 | NA | NA | TRUE | |
| ENSG00000258358 | | FALSE | TRUE | FALSE | FALSE | 12 | 84832404 | 84878657 | NA | NA | NA | 136 | 0.012412 | NA | NA | NA | NA | TRUE | |
| ENSG00000139428 | MMAB | TRUE | FALSE | FALSE | TRUE | 12 | 1.1E+08 | 1.1E+08 | 0 | 8 | rs11065505 | NA | NA | NA | -5.2064 | 1.93E-07 | TRUE | NA | |
| ENSG00000139433 | GLTP | TRUE | FALSE | FALSE | FALSE | 12 | 1.1E+08 | 1.1E+08 | 0 | 14 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000139437 | TCHP | TRUE | FALSE | FALSE | FALSE | 12 | 1.1E+08 | 1.1E+08 | 2 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000139436 | GIT2 | TRUE | FALSE | FALSE | FALSE | 12 | 1.1E+08 | 1.1E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000076513 | ANKRD13A | TRUE | FALSE | FALSE | FALSE | 12 | 1.1E+08 | 1.1E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000122970 | IFT81 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 2 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000174437 | ATP2A2 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000111229 | ARPC3 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000111231 | GPN3 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000111237 | VPS29 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 0 | 9 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000151164 | RAD9B | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000196850 | PPTC7 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 3 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000204852 | TCTN1 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 1 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000122986 | HVCN1 | TRUE | FALSE | FALSE | FALSE | 12 | 1.11E+08 | 1.11E+08 | 3 | 0 | rs11065505 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000111445 | RFC5 | FALSE | FALSE | TRUE | FALSE | 12 | 1.18E+08 | 1.18E+08 | NA | NA | NA | NA | 95 | 0.009934 | NA | NA | NA | TRUE | |
| ENSG00000176834 | VSIG10 | TRUE | FALSE | TRUE | FALSE | 12 | 1.19E+08 | 1.19E+08 | 5 | 0 | rs795475 | NA | NA | 254 | 0.001082 | NA | NA | TRUE | |
| ENSG00000212800 | NA | FALSE | TRUE | FALSE | FALSE | 12 | 1.19E+08 | 1.19E+08 | NA | NA | NA | 113 | 0.005432 | NA | NA | NA | NA | TRUE | |
| ENSG00000089220 | PEBP1 | TRUE | FALSE | FALSE | TRUE | 12 | 1.19E+08 | 1.19E+08 | 8 | 50 | rs795475 | NA | NA | NA | -5.125 | 2.98E-07 | TRUE | NA | |
| ENSG00000135090 | TAOK3 | TRUE | TRUE | TRUE | FALSE | 12 | 1.19E+08 | 1.19E+08 | 55 | 0 | rs795475 | 604 | 0.001659 | 222 | 0.008166 | NA | NA | FALSE | |
| ENSG00000240342 | RPS2P5 | FALSE | TRUE | FALSE | FALSE | 12 | 1.19E+08 | 1.19E+08 | NA | NA | NA | 108 | 0.00124 | NA | NA | NA | NA | TRUE | |
| ENSG00000111707 | SUDS3 | TRUE | FALSE | FALSE | TRUE | 12 | 1.19E+08 | 1.19E+08 | 1 | 0 | rs795475 | NA | NA | NA | 5.3492 | 8.84E-08 | TRUE | NA | |
| ENSG00000275409 | | FALSE | FALSE | FALSE | TRUE | 12 | 1.19E+08 | 1.19E+08 | NA | NA | NA | NA | NA | NA | -5.3334 | 9.64E-08 | NA | NA | |
| ENSG00000135097 | MSI1 | FALSE | FALSE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | NA | 368 | 5.68E-07 | NA | NA | NA | TRUE | |
| ENSG00000170855 | TRIAP1 | FALSE | FALSE | FALSE | TRUE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | NA | NA | NA | -5.0329 | 4.83E-07 | TRUE | NA | |
| ENSG00000257218 | GATC | TRUE | FALSE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | 0 | 55 | rs7323035 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000088986 | DYNLL1 | FALSE | FALSE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | NA | 226 | 0.022371 | NA | NA | NA | TRUE | |
| ENSG00000110871 | COQ5 | TRUE | FALSE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | 0 | 3 | rs534415 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG0000022840 | RNF10 | FALSE | FALSE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | NA | 230 | 0.005522 | NA | NA | NA | TRUE | |
| ENSG00000167272 | POP5 | TRUE | FALSE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | 0 | 8 | rs534415 | NA | NA | NA | NA | NA | NA | NA | |
| ENSG00000256008 | CABP1-DT | FALSE | TRUE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 227 | 0.001336 | 149 | 0.002152 | NA | NA | TRUE | |
| ENSG00000157782 | CABP1 | TRUE | TRUE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | 23 | 0 | rs7323035 | 280 | 0.001309 | 313 | 1.61E-06 | NA | NA | FALSE | |
| ENSG00000277423 | | FALSE | TRUE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 157 | 0.030511 | NA | NA | NA | NA | TRUE | |
| ENSG00000276188 | | FALSE | TRUE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 163 | 0.022013 | NA | NA | NA | NA | TRUE | |
| ENSG00000110917 | MLEC | TRUE | TRUE | TRUE | TRUE | 12 | 1.21E+08 | 1.21E+08 | 7 | 65 | rs7323035 | 221 | 0.013032 | 105 | 1.32E-06 | 4.9146 | 8.90E-07 | TRUE | TRUE |
| ENSG00000175970 | UNC119B | TRUE | FALSE | TRUE | TRUE | 12 | 1.21E+08 | 1.21E+08 | 6 | 53 | rs7323035 | NA | NA | 42 | 0.006198 | 5.1723 | 2.31E-07 | TRUE | TRUE |
| ENSG00000122971 | ACADS | TRUE | FALSE | FALSE | TRUE | 12 | 1.21E+08 | 1.21E+08 | 5 | 80 | rs7323035 | NA | NA | NA | 6.7252 | 1.75E-11 | FALSE | NA | |
| ENSG00000255946 | | FALSE | TRUE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 232 | 1.97E-05 | 130 | 3.38E-07 | NA | NA | TRUE | |
| ENSG00000157837 | SPPL3 | TRUE | TRUE | TRUE | TRUE | 12 | 1.21E+08 | 1.21E+08 | 198 | 132 | rs7323035 | 611 | 3.60E-07 | 296 | 1.47E-07 | -7.0424 | 1.89E-12 | FALSE | FALSE |
| ENSG00000213137 | ARF1P2 | FALSE | TRUE | TRUE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 128 | 8.82E-07 | 32 | 0.000118 | NA | NA | TRUE | |
| ENSG00000231313 | CLIC1P1 | FALSE | TRUE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 173 | 2.04E-06 | NA | NA | NA | NA | TRUE | |
| ENSG00000244585 | RPL12P33 | FALSE | TRUE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 185 | 1.05E-06 | NA | NA | NA | NA | TRUE | |
| ENSG00000241388 | HNF1A-AS1 | FALSE | TRUE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | NA | NA | NA | 318 | 0.036582 | NA | NA | NA | NA | TRUE | |
| ENSG00000157895 | C12orf43 | TRUE | FALSE | FALSE | FALSE | 12 | 1.21E+08 | 1.21E+08 | 0 | 5 | rs534415 | NA | NA | NA | NA | NA | NA | NA | |

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|-----------------|-------------------|-------|-------|-------|-------|----|----------|----------|----|----|-----------|-----|----------|----|----------|--------|----------|------|-------|
| ENSG00000182257 | <i>PRR34</i> | TRUE | TRUE | FALSE | FALSE | 22 | 46445358 | 46450024 | 12 | 0 | rs9627391 | 118 | 4.00E-05 | NA | NA | NA | NA | NA | FALSE |
| ENSG00000197182 | <i>MIRLET7BHG</i> | TRUE | TRUE | FALSE | TRUE | 22 | 46449749 | 46509808 | 12 | 0 | rs9627391 | 305 | 0.001557 | NA | NA | 5.2646 | 1.40E-07 | TRUE | TRUE |
| ENSG00000235159 | | FALSE | FALSE | TRUE | FALSE | 22 | 46463236 | 46465771 | NA | NA | NA | NA | NA | 17 | 0.001705 | NA | NA | NA | TRUE |

FUMASig: whether gene has been mapped by FUMA positional mapping or FUMA eQTL mapping

MAGMASig: whether gene is significant in conventional MAGMA

HiCMAGMASig: whether gene is significant in Hi-C MAGMA

TWASSig: whether gene is significant in TWAS

FUMA.posMapSNPs: N of SNPs mapped to each gene by FUMA positional mapping

FUMA.eqtIMapSNPs: N of SNPs mapped to each gene by FUMA eQTL mapping

FUMA.IndSigSNPs: RSID for the independent lead SNP in each locus

MAGMA.NSNPs: N of SNPs mapped to each gene by MAGMA

MAGMA.P.Bonferroni: Bonferroni adjusted P value for MAGMA analysis

HiCMAGMA.NSNPs: N of SNPs mapped to each gene by Hi-C MAGMA

HiCMAGMA.P.Bonferroni: Bonferroni adjusted P value for Hi-C MAGMA analysis

TWAS.Novel: Whether TWAS significant genes are novel to previously identified genes by TWAS

Magma.Novel: Whether MAGMA or Hi-C MAGMA significant genes are novel to previously identified genes by MAGMA.

| | | | | | | | | | | | | | | | | | | | |
|-----------------|----------|----|----------|----------|----|------------|--------|----------|------------|----------|----|-------|----|-------------|----------|----------------|----|----------|-----------|
| ENSG00000198951 | NAGA | 22 | 42454358 | 42466846 | -1 | protein_ct | 4668 | NAGA | 2.02E-06 | 0.183467 | 0 | 0 | 5 | 0.000101399 | 7.04E-29 | GTEEx/v8/Brain | NA | NA | rs5758265 |
| ENSG00000100197 | CYP2D6 | 22 | 42522501 | 42526908 | -1 | protein_ct | 1565 | CYP2D6 | 9.23E-10 | 0.153954 | 0 | 0 | 11 | 2.97E-05 | 3.61E-26 | GTEEx/v8/Brain | - | 3.55E-13 | rs5758265 |
| ENSG00000182257 | C22orf26 | 22 | 46445358 | 46450024 | -1 | protein_ct | 55267 | C22orf26 | 0.03584602 | -0.05356 | 17 | 14.95 | 0 | NA | NA | NA | NA | 2.11E-08 | rs7511013 |
| ENSG00000197182 | FLJ27365 | 22 | 46449749 | 46509808 | 1 | protein_ct | 400931 | MIRLET7B | NA | NA | 17 | 14.95 | 0 | NA | NA | NA | NA | 2.11E-08 | rs7511013 |

Gene : ENSG ID

synonym : gene

^ . . .

entrezID : entrez ID

GenomicLocus : Index of genomic loci where mapped SNPs are from. This could contain more than one interval in the case that eQTLs are mapped to genes from distinct genomic risk loci.

chr : chromosome

start : Starting position of the gene

end : Ending position of the gene

strand : Strand of the gene

status : Status of the gene from Ensembl (not available for > v85)

type : Gene biotype from Ensembl

HUGO : HUGO (HGNC) gene symbol

pLI : pLI score from ExAC database. The probability of being loss-of-function intolerant. The higher the score is, the more intolerant to loss-of-function mutations the gene is.

ncRVIS : Non-coding residual variation intolerance score. The higher the score is, the more intolerant to non-coding variation the gene is.

posMapSNPs (posMap): The number of SNPs mapped to gene based on positional mapping (after functional filtering if parameters are given).

posMapMaxCADD (posMap): The maximum CADD score of mapped SNPs by positional mapping.

eqtlMapSNPs (eqtlMap): The number of SNPs mapped to the gene based on eQTL mapping.

eqtlMapminP (eqtlMap): The minimum eQTL P-value of mapped SNPs.

eqtlMapminI (eqtlMap): The minimum eQTL FDR of mapped SNPs.

eqtlMapts (eqtlMap): Tissue types of mapped eQTL SNPs.

eqtlDirection (eqtlMap): Consecutive direction of mapped eQTL SNPs after aligning risk increasing alleles in GWAS and tested alleles in eQTL data source.

minGwasP : The minimum P-value of mapped SNPs.

IndSigSNPs : rsID of the all independent significant SNPs of mapped SNPs.

Column header definitions: K. Watanabe, E. Taskesen, A. van Bochoven and D. Posthuma. Functional mapping and annotation of genetic associations with FUMA. Nat. Commun. 8:1826. (2017).

Supplementary Table 14. Genes significant from MAGMA annotation after Bonferroni correction.

| ENSG ID | Gene symbol | CHR | START | STOP | NSNPS | NPARAM | N | Z.STAT | P value | P.Bonferroni | FDR |
|-----------------|-------------------|-----|-----------|-----------|-------|--------|---------|--------|----------|--------------|----------|
| ENSG00000156395 | <i>SORCS3</i> | 10 | 106365859 | 107034993 | 2047 | 108 | 1010761 | 8.5995 | 4.00E-18 | 2.23E-13 | 2.23E-13 |
| ENSG00000078328 | <i>RBFOX1</i> | 16 | 6034132 | 7773340 | 11317 | 763 | 1010761 | 8.1422 | 1.94E-16 | 1.08E-11 | 5.42E-12 |
| ENSG00000251825 | <i>RN7SKP19</i> | 1 | 73647287 | 73692538 | 83 | 9 | 1010761 | 7.8586 | 1.94E-15 | 1.08E-10 | 2.48E-11 |
| ENSG00000125385 | <i>AL161781.1</i> | 9 | 37011832 | 37057234 | 98 | 27 | 1010761 | 7.8516 | 2.05E-15 | 1.15E-10 | 2.48E-11 |
| ENSG00000168959 | <i>GRM5</i> | 11 | 88227744 | 88834113 | 1925 | 99 | 1010761 | 7.8294 | 2.45E-15 | 1.37E-10 | 2.48E-11 |
| ENSG00000279325 | <i>AL136359.1</i> | 13 | 53732802 | 53782675 | 156 | 17 | 1010761 | 7.8189 | 2.66E-15 | 1.49E-10 | 2.48E-11 |
| ENSG00000197153 | <i>HIST1H3J</i> | 6 | 27848160 | 27893570 | 124 | 25 | 1010761 | 7.7731 | 3.83E-15 | 2.14E-10 | 3.05E-11 |
| ENSG00000241613 | <i>RN7SL618P</i> | 13 | 53797212 | 53842505 | 133 | 26 | 1010761 | 7.7496 | 4.61E-15 | 2.57E-10 | 3.14E-11 |
| ENSG00000275221 | <i>HIST1H2AK</i> | 6 | 27795725 | 27841117 | 110 | 20 | 1010761 | 7.7173 | 5.94E-15 | 3.32E-10 | 3.14E-11 |
| ENSG00000267028 | <i>TCF4-AS1</i> | 18 | 53084764 | 53160171 | 164 | 30 | 1010761 | 7.7104 | 6.27E-15 | 3.50E-10 | 3.14E-11 |
| ENSG00000206958 | <i>RF00156</i> | 5 | 87643589 | 87688724 | 80 | 15 | 1010761 | 7.6915 | 7.27E-15 | 4.06E-10 | 3.14E-11 |
| ENSG00000250306 | <i>AC091826.1</i> | 5 | 87643765 | 87689077 | 80 | 15 | 1010761 | 7.6915 | 7.27E-15 | 4.06E-10 | 3.14E-11 |
| ENSG00000225510 | <i>PCDH8P1</i> | 13 | 53739116 | 53786888 | 149 | 17 | 1010761 | 7.6839 | 7.72E-15 | 4.31E-10 | 3.14E-11 |
| ENSG00000256500 | <i>AL139300.1</i> | 14 | 103994299 | 104162261 | 432 | 35 | 1010761 | 7.6812 | 7.88E-15 | 4.40E-10 | 3.14E-11 |
| ENSG00000278958 | <i>AC091931.1</i> | 5 | 103735473 | 103781200 | 95 | 22 | 1010761 | 7.6551 | 9.66E-15 | 5.39E-10 | 3.59E-11 |
| ENSG00000176933 | <i>TOB2P1</i> | 6 | 28175421 | 28221412 | 135 | 23 | 1010761 | 7.6398 | 1.09E-14 | 6.07E-10 | 3.80E-11 |
| ENSG00000187626 | <i>ZKSCAN4</i> | 6 | 28202401 | 28255002 | 133 | 24 | 1010761 | 7.6315 | 1.16E-14 | 6.48E-10 | 3.81E-11 |
| ENSG00000278677 | <i>HIST1H2AM</i> | 6 | 27850535 | 27895927 | 131 | 27 | 1010761 | 7.6043 | 1.43E-14 | 7.99E-10 | 4.44E-11 |
| ENSG00000233973 | <i>LINC01360</i> | 1 | 73736853 | 73830936 | 208 | 15 | 1010761 | 7.5928 | 1.57E-14 | 8.74E-10 | 4.55E-11 |
| ENSG00000149295 | <i>DRD2</i> | 11 | 113270337 | 113381111 | 308 | 39 | 1010761 | 7.5874 | 1.63E-14 | 9.11E-10 | 4.55E-11 |
| ENSG00000185130 | <i>HIST1H2BL</i> | 6 | 27765222 | 27810709 | 100 | 19 | 1010761 | 7.5344 | 2.45E-14 | 1.37E-09 | 6.52E-11 |
| ENSG00000276368 | <i>HIST1H2AJ</i> | 6 | 27772132 | 27817518 | 99 | 16 | 1010761 | 7.5283 | 2.57E-14 | 1.43E-09 | 6.52E-11 |
| ENSG00000196628 | <i>TCF4</i> | 18 | 52879562 | 53338258 | 842 | 101 | 1010761 | 7.5065 | 3.04E-14 | 1.69E-09 | 7.37E-11 |
| ENSG00000250555 | <i>AC008525.2</i> | 5 | 87953468 | 87998676 | 75 | 21 | 1010761 | 7.4831 | 3.63E-14 | 2.03E-09 | 8.39E-11 |
| ENSG00000145934 | <i>TENM2</i> | 5 | 166676804 | 167701162 | 2646 | 321 | 1010761 | 7.4786 | 3.76E-14 | 2.10E-09 | 8.39E-11 |
| ENSG00000237515 | <i>SHISA9</i> | 16 | 12960477 | 13344270 | 1778 | 197 | 1010761 | 7.4439 | 4.89E-14 | 2.73E-09 | 1.05E-10 |
| ENSG00000229636 | <i>KRT8P21</i> | 1 | 73535475 | 73581965 | 235 | 11 | 1010761 | 7.4332 | 5.30E-14 | 2.96E-09 | 1.10E-10 |
| ENSG00000219392 | <i>ZNF602P</i> | 6 | 28048406 | 28094329 | 161 | 16 | 1010761 | 7.4247 | 5.65E-14 | 3.15E-09 | 1.11E-10 |
| ENSG00000227207 | <i>RPL31P12</i> | 1 | 72732155 | 72777512 | 78 | 11 | 1010761 | 7.4207 | 5.82E-14 | 3.25E-09 | 1.11E-10 |
| ENSG00000137185 | <i>ZSCAN9</i> | 6 | 28158042 | 28211260 | 157 | 22 | 1010761 | 7.4171 | 5.98E-14 | 3.34E-09 | 1.11E-10 |
| ENSG00000165379 | <i>LRFN5</i> | 14 | 42041773 | 42383752 | 968 | 81 | 1010761 | 7.3843 | 7.66E-14 | 4.28E-09 | 1.38E-10 |
| ENSG00000126214 | <i>KLC1</i> | 14 | 104060514 | 104190586 | 340 | 31 | 1010761 | 7.3659 | 8.80E-14 | 4.91E-09 | 1.53E-10 |
| ENSG00000264904 | | 14 | 104032305 | 104077396 | 127 | 15 | 1010761 | 7.3536 | 9.65E-14 | 5.39E-09 | 1.60E-10 |
| ENSG00000252469 | <i>RNU7-160P</i> | 14 | 103981682 | 104026743 | 115 | 17 | 1010761 | 7.351 | 9.84E-14 | 5.49E-09 | 1.60E-10 |
| ENSG00000189134 | <i>NKAPL</i> | 6 | 28192098 | 28238736 | 133 | 24 | 1010761 | 7.3461 | 1.02E-13 | 5.70E-09 | 1.60E-10 |
| ENSG00000216915 | <i>GPR89P</i> | 6 | 27694779 | 27741273 | 131 | 18 | 1010761 | 7.3418 | 1.05E-13 | 5.88E-09 | 1.60E-10 |
| ENSG00000196747 | <i>HIST1H2AI</i> | 6 | 27740977 | 27786479 | 111 | 20 | 1010761 | 7.3408 | 1.06E-13 | 5.92E-09 | 1.60E-10 |
| ENSG00000260285 | <i>AL133367.1</i> | 14 | 103981347 | 104030409 | 128 | 18 | 1010761 | 7.3221 | 1.22E-13 | 6.81E-09 | 1.79E-10 |

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|-----------------|---------------------|----|-----------|-----------|------|-----|---------|--------|----------|----------|----------|
| ENSG00000251858 | <i>RF00322</i> | 14 | 42028666 | 42073794 | 67 | 17 | 1010761 | 7.316 | 1.28E-13 | 7.13E-09 | 1.82E-10 |
| ENSG00000238610 | <i>RNU7-26P</i> | 6 | 27855282 | 27900344 | 123 | 28 | 1010761 | 7.3133 | 1.30E-13 | 7.28E-09 | 1.82E-10 |
| ENSG00000247828 | <i>TMEM161B-AS1</i> | 5 | 87529712 | 87742502 | 385 | 30 | 1010761 | 7.2819 | 1.65E-13 | 9.19E-09 | 2.24E-10 |
| ENSG00000258851 | <i>AL139300.2</i> | 14 | 103984758 | 104038214 | 126 | 16 | 1010761 | 7.263 | 1.89E-13 | 1.06E-08 | 2.52E-10 |
| ENSG00000196812 | <i>ZSCAN16</i> | 6 | 28057338 | 28107860 | 172 | 15 | 1010761 | 7.2568 | 1.98E-13 | 1.11E-08 | 2.57E-10 |
| ENSG00000272009 | <i>AL121944.1</i> | 6 | 28036570 | 28083908 | 163 | 15 | 1010761 | 7.2379 | 2.28E-13 | 1.27E-08 | 2.89E-10 |
| ENSG00000186470 | <i>BTN3A2</i> | 6 | 26330387 | 26388548 | 325 | 34 | 1010761 | 7.2349 | 2.33E-13 | 1.30E-08 | 2.89E-10 |
| ENSG00000101489 | <i>CELF4</i> | 18 | 34813010 | 35181000 | 1020 | 147 | 1010761 | 7.2135 | 2.73E-13 | 1.52E-08 | 3.29E-10 |
| ENSG00000276302 | <i>AL021997.3</i> | 6 | 28199899 | 28259357 | 151 | 25 | 1010761 | 7.2113 | 2.77E-13 | 1.55E-08 | 3.29E-10 |
| ENSG00000252399 | | 6 | 26343199 | 26388264 | 271 | 26 | 1010761 | 7.2027 | 2.95E-13 | 1.65E-08 | 3.43E-10 |
| ENSG00000278828 | <i>HIST1H3H</i> | 6 | 27742842 | 27789078 | 108 | 21 | 1010761 | 7.1767 | 3.57E-13 | 1.99E-08 | 4.04E-10 |
| ENSG00000215979 | | 6 | 26355704 | 26400780 | 286 | 28 | 1010761 | 7.1749 | 3.62E-13 | 2.02E-08 | 4.04E-10 |
| ENSG00000250156 | <i>LINC02060</i> | 5 | 87694799 | 87769907 | 180 | 16 | 1010761 | 7.1687 | 3.79E-13 | 2.11E-08 | 4.14E-10 |
| ENSG00000225087 | <i>AL583808.1</i> | 1 | 73204604 | 73399823 | 460 | 34 | 1010761 | 7.1369 | 4.77E-13 | 2.66E-08 | 5.12E-10 |
| ENSG00000207129 | <i>RNA5SP187</i> | 5 | 87560075 | 87605193 | 79 | 13 | 1010761 | 7.134 | 4.87E-13 | 2.72E-08 | 5.13E-10 |
| ENSG00000237092 | <i>LINC01065</i> | 13 | 53710674 | 53760943 | 125 | 17 | 1010761 | 7.1274 | 5.11E-13 | 2.85E-08 | 5.29E-10 |
| ENSG00000206784 | <i>RF00019</i> | 9 | 37287256 | 37332368 | 53 | 13 | 1010761 | 7.1184 | 5.46E-13 | 3.05E-08 | 5.48E-10 |
| ENSG00000220990 | | 13 | 53931980 | 53977091 | 137 | 20 | 1010761 | 7.1158 | 5.56E-13 | 3.11E-08 | 5.48E-10 |
| ENSG00000269293 | <i>ZSCAN16-AS1</i> | 6 | 28079573 | 28140071 | 212 | 17 | 1010761 | 7.1149 | 5.60E-13 | 3.12E-08 | 5.48E-10 |
| ENSG00000166165 | <i>CKB</i> | 14 | 103975996 | 104024448 | 128 | 18 | 1010761 | 7.1083 | 5.88E-13 | 3.28E-08 | 5.65E-10 |
| ENSG00000142599 | <i>RERE</i> | 1 | 8402457 | 8912702 | 847 | 62 | 1010761 | 7.1001 | 6.23E-13 | 3.48E-08 | 5.90E-10 |
| ENSG00000198315 | <i>ZKSCAN8</i> | 6 | 28074716 | 28137250 | 219 | 16 | 1010761 | 7.0953 | 6.45E-13 | 3.60E-08 | 6.00E-10 |
| ENSG00000201184 | <i>RNU4-68P</i> | 14 | 103998742 | 104043882 | 109 | 15 | 1010761 | 7.0885 | 6.78E-13 | 3.78E-08 | 6.17E-10 |
| ENSG00000273919 | <i>AL450423.1</i> | 13 | 53884346 | 53995015 | 383 | 37 | 1010761 | 7.087 | 6.85E-13 | 3.82E-08 | 6.17E-10 |
| ENSG00000124508 | <i>BTN2A2</i> | 6 | 26348324 | 26405102 | 337 | 32 | 1010761 | 7.0834 | 7.03E-13 | 3.93E-08 | 6.23E-10 |
| ENSG00000232912 | <i>AL096855.1</i> | 1 | 8449705 | 8504898 | 84 | 13 | 1010761 | 7.0779 | 7.32E-13 | 4.08E-08 | 6.38E-10 |
| ENSG00000261839 | <i>AL358933.1</i> | 6 | 28069627 | 28117456 | 160 | 14 | 1010761 | 7.0636 | 8.11E-13 | 4.53E-08 | 6.96E-10 |
| ENSG00000216901 | <i>ZNF603P</i> | 6 | 28108966 | 28154452 | 153 | 15 | 1010761 | 7.0586 | 8.41E-13 | 4.70E-08 | 7.11E-10 |
| ENSG00000231200 | <i>LINC01830</i> | 2 | 22146208 | 22788977 | 1532 | 122 | 1010761 | 7.0273 | 1.05E-12 | 5.88E-08 | 8.77E-10 |
| ENSG00000187323 | <i>DCC</i> | 18 | 49831542 | 51072273 | 5014 | 233 | 1010761 | 7.0097 | 1.19E-12 | 6.67E-08 | 9.80E-10 |
| ENSG00000219891 | <i>ZSCAN12P1</i> | 6 | 28023932 | 28071442 | 163 | 16 | 1010761 | 6.9994 | 1.29E-12 | 7.17E-08 | 1.04E-09 |
| ENSG00000218016 | <i>ZNF192P2</i> | 6 | 28120828 | 28167210 | 147 | 16 | 1010761 | 6.9813 | 1.46E-12 | 8.16E-08 | 1.17E-09 |
| ENSG00000252437 | <i>RNA5SP459</i> | 18 | 52803777 | 52848876 | 154 | 32 | 1010761 | 6.9782 | 1.49E-12 | 8.34E-08 | 1.17E-09 |
| ENSG00000248483 | <i>POU5F2</i> | 5 | 93058926 | 93112343 | 83 | 14 | 1010761 | 6.9734 | 1.55E-12 | 8.63E-08 | 1.20E-09 |
| ENSG00000243516 | <i>RPL12P40</i> | 18 | 35217652 | 35263139 | 113 | 15 | 1010761 | 6.9603 | 1.70E-12 | 9.48E-08 | 1.30E-09 |
| ENSG00000246451 | <i>AL049840.1</i> | 14 | 104138699 | 104185352 | 107 | 17 | 1010761 | 6.9528 | 1.79E-12 | 9.99E-08 | 1.35E-09 |
| ENSG00000226314 | <i>ZNF192P1</i> | 6 | 28094559 | 28147372 | 173 | 14 | 1010761 | 6.9489 | 1.84E-12 | 1.03E-07 | 1.37E-09 |
| ENSG00000269958 | <i>AL049840.4</i> | 14 | 104127690 | 104173500 | 105 | 17 | 1010761 | 6.9339 | 2.05E-12 | 1.14E-07 | 1.50E-09 |
| ENSG00000266530 | <i>MIR4318</i> | 18 | 35202098 | 35247178 | 106 | 16 | 1010761 | 6.919 | 2.27E-12 | 1.27E-07 | 1.63E-09 |
| ENSG00000231918 | <i>AC007402.1</i> | 2 | 51224739 | 52645055 | 5371 | 325 | 1010761 | 6.917 | 2.31E-12 | 1.29E-07 | 1.63E-09 |
| ENSG00000280107 | <i>AL022393.1</i> | 6 | 28103623 | 28150299 | 163 | 14 | 1010761 | 6.9169 | 2.31E-12 | 1.29E-07 | 1.63E-09 |
| ENSG00000216070 | | 9 | 37286020 | 37331101 | 52 | 13 | 1010761 | 6.9137 | 2.36E-12 | 1.32E-07 | 1.65E-09 |

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|-----------------|-------------------|----|-----------|-----------|------|-----|---------|--------|----------|----------|----------|
| ENSG00000140945 | <i>CDH13</i> | 16 | 82625408 | 83844245 | 7317 | 589 | 1010761 | 6.9048 | 2.51E-12 | 1.40E-07 | 1.73E-09 |
| ENSG00000256053 | <i>APOPT1</i> | 14 | 103994299 | 104068524 | 184 | 21 | 1010761 | 6.9004 | 2.59E-12 | 1.45E-07 | 1.76E-09 |
| ENSG00000224997 | | 14 | 104142607 | 104189149 | 110 | 19 | 1010761 | 6.8987 | 2.62E-12 | 1.46E-07 | 1.76E-09 |
| ENSG00000269940 | <i>AL049840.3</i> | 14 | 104125897 | 104171507 | 108 | 17 | 1010761 | 6.8797 | 3.00E-12 | 1.67E-07 | 1.99E-09 |
| ENSG00000241723 | <i>AC074276.1</i> | 3 | 157983598 | 158029210 | 150 | 12 | 1010761 | 6.8712 | 3.18E-12 | 1.78E-07 | 2.09E-09 |
| ENSG00000206882 | <i>RNA5SP87</i> | 2 | 22551758 | 22596875 | 156 | 15 | 1010761 | 6.8665 | 3.29E-12 | 1.84E-07 | 2.14E-09 |
| ENSG00000250377 | <i>AC008525.1</i> | 5 | 87978462 | 88024789 | 83 | 14 | 1010761 | 6.848 | 3.74E-12 | 2.09E-07 | 2.40E-09 |
| ENSG00000279877 | | 16 | 5254803 | 6836015 | 9051 | 687 | 1010761 | 6.8359 | 4.08E-12 | 2.27E-07 | 2.59E-09 |
| ENSG00000221130 | | 11 | 88810878 | 88855992 | 107 | 12 | 1010761 | 6.8307 | 4.22E-12 | 2.36E-07 | 2.65E-09 |
| ENSG00000241956 | <i>AC109466.1</i> | 5 | 163688702 | 164608649 | 2549 | 181 | 1010761 | 6.8179 | 4.62E-12 | 2.58E-07 | 2.86E-09 |
| ENSG00000197279 | <i>ZNF165</i> | 6 | 28013753 | 28067341 | 187 | 17 | 1010761 | 6.8035 | 5.11E-12 | 2.85E-07 | 3.13E-09 |
| ENSG00000270108 | <i>AL049840.5</i> | 14 | 104118913 | 104164464 | 103 | 17 | 1010761 | 6.7978 | 5.31E-12 | 2.96E-07 | 3.22E-09 |
| ENSG00000157837 | <i>SPPL3</i> | 12 | 121190313 | 121377174 | 611 | 42 | 1010761 | 6.7696 | 6.45E-12 | 3.60E-07 | 3.87E-09 |
| ENSG00000251574 | <i>AC099520.1</i> | 5 | 103708999 | 104763671 | 3225 | 157 | 1010761 | 6.7591 | 6.94E-12 | 3.87E-07 | 4.12E-09 |
| ENSG00000124557 | <i>BTN1A1</i> | 6 | 26466449 | 26520650 | 162 | 21 | 1010761 | 6.7483 | 7.48E-12 | 4.18E-07 | 4.40E-09 |
| ENSG00000251023 | <i>AC114980.1</i> | 5 | 93186375 | 93234531 | 74 | 12 | 1010761 | 6.7284 | 8.57E-12 | 4.79E-07 | 4.99E-09 |
| ENSG00000272406 | <i>AC108102.1</i> | 5 | 93042346 | 93089206 | 71 | 17 | 1010761 | 6.7069 | 9.94E-12 | 5.55E-07 | 5.72E-09 |
| ENSG00000166166 | <i>TRMT61A</i> | 14 | 103960521 | 104013410 | 139 | 17 | 1010761 | 6.6878 | 1.13E-11 | 6.32E-07 | 6.45E-09 |
| ENSG00000280317 | <i>AL732618.1</i> | 1 | 73434697 | 73479997 | 126 | 15 | 1010761 | 6.6825 | 1.17E-11 | 6.56E-07 | 6.62E-09 |
| ENSG00000028116 | <i>VRK2</i> | 2 | 58099786 | 58397055 | 645 | 57 | 1010761 | 6.6592 | 1.38E-11 | 7.69E-07 | 7.69E-09 |
| ENSG00000196092 | <i>PAX5</i> | 9 | 36823272 | 37069182 | 902 | 128 | 1010761 | 6.6568 | 1.40E-11 | 7.81E-07 | 7.73E-09 |
| ENSG00000249353 | <i>NPM1P27</i> | 5 | 93008544 | 93054373 | 62 | 18 | 1010761 | 6.652 | 1.45E-11 | 8.07E-07 | 7.91E-09 |
| ENSG00000263872 | <i>MIR4528</i> | 18 | 50728471 | 50773560 | 128 | 17 | 1010761 | 6.6473 | 1.49E-11 | 8.33E-07 | 8.09E-09 |
| ENSG00000213137 | <i>ARF1P2</i> | 12 | 121272913 | 121318450 | 128 | 16 | 1010761 | 6.6389 | 1.58E-11 | 8.82E-07 | 8.48E-09 |
| ENSG00000200502 | <i>RF00019</i> | 9 | 37125134 | 37170234 | 77 | 12 | 1010761 | 6.6356 | 1.62E-11 | 9.02E-07 | 8.59E-09 |
| ENSG00000182477 | <i>OR2B8P</i> | 6 | 28011006 | 28056943 | 158 | 15 | 1010761 | 6.6343 | 1.63E-11 | 9.10E-07 | 8.59E-09 |
| ENSG00000228292 | <i>AL512604.1</i> | 9 | 37195109 | 37240365 | 59 | 15 | 1010761 | 6.6233 | 1.76E-11 | 9.80E-07 | 9.16E-09 |
| ENSG00000234189 | <i>AC099799.1</i> | 2 | 22504925 | 22550116 | 95 | 16 | 1010761 | 6.6215 | 1.78E-11 | 9.93E-07 | 9.19E-09 |
| ENSG00000244585 | <i>RPL12P33</i> | 12 | 121319548 | 121365039 | 185 | 21 | 1010761 | 6.6126 | 1.89E-11 | 1.05E-06 | 9.67E-09 |
| ENSG00000273712 | <i>AL021997.2</i> | 6 | 28273390 | 28318660 | 168 | 27 | 1010761 | 6.592 | 2.17E-11 | 1.21E-06 | 1.10E-08 |
| ENSG00000041353 | <i>RAB27B</i> | 18 | 52460430 | 52572747 | 300 | 36 | 1010761 | 6.5903 | 2.20E-11 | 1.23E-06 | 1.10E-08 |
| ENSG00000137338 | <i>PGBD1</i> | 6 | 28214349 | 28280326 | 199 | 31 | 1010761 | 6.5801 | 2.35E-11 | 1.31E-06 | 1.17E-08 |
| ENSG00000147905 | <i>ZCCHC7</i> | 9 | 37085536 | 37368146 | 421 | 33 | 1010761 | 6.5774 | 2.39E-11 | 1.34E-06 | 1.18E-08 |
| ENSG00000186472 | <i>PCLO</i> | 7 | 82373329 | 82827246 | 1347 | 95 | 1010761 | 6.5689 | 2.53E-11 | 1.41E-06 | 1.24E-08 |
| ENSG00000261198 | <i>AC005774.1</i> | 16 | 7654232 | 7699994 | 227 | 36 | 1010761 | 6.5658 | 2.59E-11 | 1.44E-06 | 1.26E-08 |
| ENSG00000166170 | <i>BAG5</i> | 14 | 104012881 | 104064151 | 114 | 14 | 1010761 | 6.5643 | 2.61E-11 | 1.46E-06 | 1.26E-08 |
| ENSG00000220721 | <i>OR1F12</i> | 6 | 28006094 | 28052011 | 162 | 15 | 1010761 | 6.5518 | 2.84E-11 | 1.59E-06 | 1.36E-08 |
| ENSG00000233723 | <i>LINC01122</i> | 2 | 58619934 | 59300901 | 1611 | 176 | 1010761 | 6.5434 | 3.01E-11 | 1.68E-06 | 1.42E-08 |
| ENSG00000266175 | | 22 | 41446636 | 41491705 | 94 | 14 | 1010761 | 6.5394 | 3.09E-11 | 1.72E-06 | 1.45E-08 |
| ENSG00000174891 | <i>RSRC1</i> | 3 | 157788644 | 158273519 | 1490 | 45 | 1010761 | 6.5353 | 3.17E-11 | 1.77E-06 | 1.48E-08 |
| ENSG00000148219 | <i>ASTN2</i> | 9 | 119177504 | 120212348 | 3334 | 299 | 1010761 | 6.5256 | 3.39E-11 | 1.89E-06 | 1.56E-08 |
| ENSG00000231313 | <i>CLIC1P1</i> | 12 | 121317203 | 121362926 | 173 | 21 | 1010761 | 6.5141 | 3.66E-11 | 2.04E-06 | 1.67E-08 |

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|-----------------|------------|----|-----------|-----------|------|-----|---------|--------|----------|----------|----------|
| ENSG00000270282 | AL096855.2 | 1 | 8537712 | 8583080 | 83 | 13 | 1010761 | 6.5115 | 3.72E-11 | 2.08E-06 | 1.69E-08 |
| ENSG00000279972 | AL356596.1 | 14 | 41974175 | 42019553 | 103 | 17 | 1010761 | 6.5021 | 3.96E-11 | 2.21E-06 | 1.78E-08 |
| ENSG00000172260 | NEGR1 | 1 | 71851623 | 72783417 | 2079 | 155 | 1010761 | 6.4958 | 4.13E-11 | 2.31E-06 | 1.84E-08 |
| ENSG00000137872 | SEMA6D | 15 | 47441298 | 48076420 | 2081 | 124 | 1010761 | 6.4943 | 4.17E-11 | 2.33E-06 | 1.85E-08 |
| ENSG00000077498 | TYR | 11 | 88875620 | 89038927 | 461 | 33 | 1010761 | 6.4473 | 5.69E-11 | 3.18E-06 | 2.50E-08 |
| ENSG00000199515 | RF00019 | 22 | 41451558 | 41496650 | 91 | 15 | 1010761 | 6.443 | 5.86E-11 | 3.27E-06 | 2.54E-08 |
| ENSG00000119522 | DENND1A | 9 | 126131933 | 126727431 | 1598 | 110 | 1010761 | 6.4425 | 5.88E-11 | 3.28E-06 | 2.54E-08 |
| ENSG00000221083 | RF00599 | 1 | 8561854 | 8606978 | 65 | 11 | 1010761 | 6.4315 | 6.32E-11 | 3.53E-06 | 2.71E-08 |
| ENSG00000185053 | SGCZ | 8 | 13937373 | 15130848 | 7024 | 336 | 1010761 | 6.4113 | 7.21E-11 | 4.03E-06 | 3.07E-08 |
| ENSG00000271755 | AL031118.1 | 6 | 27361789 | 27409743 | 181 | 13 | 1010761 | 6.3899 | 8.30E-11 | 4.63E-06 | 3.51E-08 |
| ENSG00000221160 | | 22 | 41453517 | 41498570 | 90 | 14 | 1010761 | 6.3773 | 9.01E-11 | 5.03E-06 | 3.77E-08 |
| ENSG00000183098 | GPC6 | 13 | 93844095 | 95069655 | 3756 | 322 | 1010761 | 6.3768 | 9.04E-11 | 5.05E-06 | 3.77E-08 |
| ENSG00000259360 | AC009558.1 | 15 | 47679698 | 47726751 | 151 | 20 | 1010761 | 6.3628 | 9.90E-11 | 5.53E-06 | 4.09E-08 |
| ENSG00000269910 | AL049840.2 | 14 | 104150853 | 104196387 | 107 | 22 | 1010761 | 6.3344 | 1.19E-10 | 6.65E-06 | 4.85E-08 |
| ENSG00000217315 | OR2W2P | 6 | 27966725 | 28012633 | 146 | 19 | 1010761 | 6.3338 | 1.20E-10 | 6.68E-06 | 4.85E-08 |
| ENSG00000174899 | PQLC2L | 3 | 157226035 | 157405538 | 604 | 68 | 1010761 | 6.3333 | 1.20E-10 | 6.70E-06 | 4.85E-08 |
| ENSG00000259221 | AC023905.1 | 15 | 47641627 | 47723929 | 307 | 29 | 1010761 | 6.3278 | 1.24E-10 | 6.94E-06 | 4.99E-08 |
| ENSG00000250705 | AC008526.1 | 5 | 87863598 | 87908935 | 70 | 17 | 1010761 | 6.3114 | 1.38E-10 | 7.72E-06 | 5.51E-08 |
| ENSG00000179603 | GRM8 | 7 | 126068652 | 126928348 | 2428 | 138 | 1010761 | 6.3096 | 1.40E-10 | 7.81E-06 | 5.54E-08 |
| ENSG00000203809 | LIN28B-AS1 | 6 | 105302339 | 105424322 | 229 | 31 | 1010761 | 6.2754 | 1.74E-10 | 9.73E-06 | 6.86E-08 |
| ENSG00000271904 | AC091826.2 | 5 | 87719709 | 87829514 | 325 | 29 | 1010761 | 6.2702 | 1.80E-10 | 1.01E-05 | 7.04E-08 |
| ENSG00000237214 | AL080243.2 | 22 | 41425056 | 41470637 | 139 | 17 | 1010761 | 6.2669 | 1.84E-10 | 1.03E-05 | 7.14E-08 |
| ENSG00000102837 | OLFM4 | 13 | 53567894 | 53636192 | 215 | 51 | 1010761 | 6.2647 | 1.87E-10 | 1.04E-05 | 7.19E-08 |
| ENSG00000241990 | PRR34-AS1 | 22 | 46414585 | 46463090 | 120 | 18 | 1010761 | 6.2577 | 1.95E-10 | 1.09E-05 | 7.47E-08 |
| ENSG00000270326 | AL021997.1 | 6 | 28277437 | 28322629 | 174 | 27 | 1010761 | 6.2562 | 1.97E-10 | 1.10E-05 | 7.49E-08 |
| ENSG00000273289 | AL121672.3 | 22 | 46413973 | 46459440 | 115 | 16 | 1010761 | 6.2409 | 2.18E-10 | 1.21E-05 | 8.20E-08 |
| ENSG00000254066 | LINC01938 | 5 | 164637583 | 164703758 | 183 | 21 | 1010761 | 6.1794 | 3.22E-10 | 1.80E-05 | 1.21E-07 |
| ENSG00000251847 | | 9 | 120483653 | 120528749 | 208 | 21 | 1010761 | 6.1753 | 3.30E-10 | 1.84E-05 | 1.23E-07 |
| ENSG00000255946 | AC069234.1 | 12 | 121168273 | 121234395 | 232 | 32 | 1010761 | 6.1644 | 3.54E-10 | 1.97E-05 | 1.31E-07 |
| ENSG00000234273 | AC073071.1 | 7 | 109152038 | 109272223 | 404 | 50 | 1010761 | 6.1538 | 3.78E-10 | 2.11E-05 | 1.39E-07 |
| ENSG00000271615 | ACTG1P22 | 2 | 57947563 | 58003187 | 99 | 19 | 1010761 | 6.1517 | 3.83E-10 | 2.14E-05 | 1.40E-07 |
| ENSG00000258901 | AL121821.2 | 14 | 42014865 | 42060258 | 85 | 20 | 1010761 | 6.15 | 3.87E-10 | 2.16E-05 | 1.40E-07 |
| ENSG00000228512 | | 9 | 120510726 | 120640349 | 607 | 54 | 1010761 | 6.1471 | 3.94E-10 | 2.20E-05 | 1.42E-07 |
| ENSG00000271581 | AL671883.2 | 6 | 31289424 | 31335414 | 446 | 65 | 1010761 | 6.1433 | 4.04E-10 | 2.26E-05 | 1.45E-07 |
| ENSG00000187772 | LIN28B | 6 | 105353741 | 105541207 | 297 | 40 | 1010761 | 6.1298 | 4.40E-10 | 2.46E-05 | 1.51E-07 |
| ENSG00000281649 | EBLN3P | 9 | 37044854 | 37100504 | 134 | 20 | 1010761 | 6.1296 | 4.41E-10 | 2.46E-05 | 1.51E-07 |
| ENSG00000198216 | CACNA1E | 1 | 181417716 | 181787219 | 1050 | 123 | 1010761 | 6.1243 | 4.55E-10 | 2.54E-05 | 1.51E-07 |
| ENSG00000230260 | AL136322.1 | 1 | 197397106 | 197451599 | 51 | 17 | 1010761 | 6.1195 | 4.69E-10 | 2.62E-05 | 1.51E-07 |
| ENSG00000233994 | GDI2P2 | 1 | 72705235 | 72750842 | 77 | 12 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000164180 | TMEM161B | 5 | 87475450 | 87599674 | 212 | 28 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000240083 | RPS3AP22 | 5 | 87642774 | 87688542 | 79 | 15 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000245526 | LINC00461 | 5 | 87793363 | 88021858 | 500 | 59 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |

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|-----------------|-------------|----|-----------|-----------|------|----|---------|--------|----------|----------|----------|
| ENSG00000245864 | MEF2C-AS2 | 5 | 87937036 | 88028648 | 162 | 27 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000081189 | MEF2C | 5 | 88002934 | 88235074 | 430 | 47 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000113391 | FAM172A | 5 | 92943775 | 93482381 | 828 | 57 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000218069 | RSL24D1P1 | 6 | 27738398 | 27783890 | 122 | 21 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000217862 | HIST1H4PS1 | 6 | 27739853 | 27785117 | 116 | 21 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000273703 | HIST1H2BM | 6 | 27747822 | 27793202 | 101 | 20 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000197238 | HIST1H4J | 6 | 27756886 | 27802258 | 100 | 21 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000233822 | HIST1H2BN | 6 | 27770538 | 27843576 | 169 | 25 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000273542 | HIST1H4K | 6 | 27788994 | 27834305 | 97 | 21 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000276903 | HIST1H2AL | 6 | 27798133 | 27843525 | 108 | 20 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000217646 | HIST1H2BPS2 | 6 | 27821840 | 27867179 | 114 | 21 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000184357 | HIST1H1B | 6 | 27824627 | 27870307 | 116 | 20 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000274641 | HIST1H2BO | 6 | 27826241 | 27871621 | 116 | 21 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000275379 | HIST1H3I | 6 | 27829683 | 27875093 | 122 | 23 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000275126 | HIST1H4L | 6 | 27830977 | 27876288 | 122 | 23 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000197062 | ZSCAN26 | 6 | 28199788 | 28256001 | 145 | 25 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
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| ENSG00000250850 | AL161781.2 | 9 | 36967694 | 37018037 | 206 | 29 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
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| ENSG00000258636 | AL121821.1 | 14 | 42047064 | 42109059 | 96 | 18 | 1010761 | 6.1094 | 5.00E-10 | 2.79E-05 | 1.51E-07 |
| ENSG00000239268 | AC092691.1 | 3 | 117381001 | 117751439 | 1121 | 69 | 1010761 | 6.1088 | 5.02E-10 | 2.80E-05 | 1.51E-07 |
| ENSG00000226387 | SORCS3-AS1 | 10 | 106414366 | 106460958 | 92 | 19 | 1010761 | 6.1055 | 5.12E-10 | 2.86E-05 | 1.54E-07 |
| ENSG00000100711 | ZFYVE21 | 14 | 104147067 | 104210005 | 148 | 27 | 1010761 | 6.0976 | 5.38E-10 | 3.00E-05 | 1.61E-07 |
| ENSG00000231711 | LINC00899 | 22 | 46425787 | 46475733 | 109 | 20 | 1010761 | 6.0931 | 5.54E-10 | 3.09E-05 | 1.64E-07 |
| ENSG00000264571 | MIR4529 | 18 | 53111452 | 53156529 | 85 | 21 | 1010761 | 6.0868 | 5.76E-10 | 3.21E-05 | 1.70E-07 |
| ENSG00000119596 | YLPM1 | 14 | 75195069 | 75312984 | 196 | 17 | 1010761 | 6.0726 | 6.29E-10 | 3.51E-05 | 1.85E-07 |
| ENSG00000213857 | AL080243.1 | 22 | 41460184 | 41506243 | 86 | 14 | 1010761 | 6.0528 | 7.12E-10 | 3.97E-05 | 2.08E-07 |
| ENSG00000182257 | PRR34 | 22 | 46435358 | 46485024 | 118 | 24 | 1010761 | 6.0516 | 7.17E-10 | 4.00E-05 | 2.08E-07 |
| ENSG00000227835 | CARM1P1 | 9 | 2897073 | 3088408 | 662 | 88 | 1010761 | 6.0483 | 7.32E-10 | 4.09E-05 | 2.12E-07 |
| ENSG00000267013 | LINC01929 | 18 | 52763135 | 52826537 | 196 | 23 | 1010761 | 6.047 | 7.38E-10 | 4.12E-05 | 2.12E-07 |
| ENSG00000231010 | AL121672.1 | 22 | 46441620 | 46489040 | 112 | 27 | 1010761 | 6.0386 | 7.77E-10 | 4.34E-05 | 2.22E-07 |
| ENSG00000233242 | AL512604.2 | 9 | 37102545 | 37150487 | 91 | 12 | 1010761 | 6.0373 | 7.84E-10 | 4.37E-05 | 2.23E-07 |
| ENSG00000255266 | AP003484.1 | 11 | 57627794 | 57673043 | 69 | 12 | 1010761 | 6.0091 | 9.33E-10 | 5.21E-05 | 2.64E-07 |
| ENSG00000236021 | AL359265.3 | 1 | 176141784 | 176208466 | 176 | 28 | 1010761 | 6.0044 | 9.60E-10 | 5.36E-05 | 2.71E-07 |
| ENSG00000177352 | CCDC71 | 3 | 49189968 | 49238754 | 73 | 11 | 1010761 | 5.9984 | 9.96E-10 | 5.56E-05 | 2.80E-07 |
| ENSG00000187763 | OR2B7P | 6 | 27979212 | 28025145 | 163 | 17 | 1010761 | 5.9892 | 1.05E-09 | 5.89E-05 | 2.94E-07 |
| ENSG00000232203 | SLC25A6P2 | 9 | 31218899 | 31264775 | 233 | 18 | 1010761 | 5.9876 | 1.06E-09 | 5.94E-05 | 2.96E-07 |
| ENSG00000232597 | AC013727.1 | 2 | 104463117 | 104531667 | 161 | 39 | 1010761 | 5.9769 | 1.14E-09 | 6.35E-05 | 3.14E-07 |
| ENSG00000230994 | FGFR3P1 | 6 | 31310196 | 31355796 | 455 | 66 | 1010761 | 5.9655 | 1.22E-09 | 6.81E-05 | 3.35E-07 |
| ENSG00000223702 | ZDHHC20P2 | 6 | 31313188 | 31358616 | 443 | 64 | 1010761 | 5.9636 | 1.23E-09 | 6.89E-05 | 3.38E-07 |
| ENSG00000259434 | AC068875.1 | 15 | 37647228 | 37818009 | 524 | 45 | 1010761 | 5.9491 | 1.35E-09 | 7.52E-05 | 3.67E-07 |
| ENSG00000220875 | HIST1H3PS1 | 6 | 26312104 | 26357520 | 216 | 31 | 1010761 | 5.9468 | 1.37E-09 | 7.63E-05 | 3.71E-07 |

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|-----------------|-------------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000201658 | <i>RNU6-283P</i> | 6 | 31302911 | 31348017 | 451 | 65 | 1010761 | 5.945 | 1.38E-09 | 7.72E-05 | 3.73E-07 |
| ENSG00000255303 | <i>OR5BA1P</i> | 11 | 57623770 | 57669751 | 75 | 13 | 1010761 | 5.932 | 1.50E-09 | 8.35E-05 | 4.02E-07 |
| ENSG00000100399 | <i>CHADL</i> | 22 | 41615517 | 41671938 | 121 | 17 | 1010761 | 5.9276 | 1.54E-09 | 8.58E-05 | 4.10E-07 |
| ENSG00000187676 | <i>B3GLCT</i> | 13 | 31739073 | 31916413 | 508 | 51 | 1010761 | 5.9242 | 1.57E-09 | 8.76E-05 | 4.17E-07 |
| ENSG00000170959 | <i>DCDC1</i> | 11 | 30875151 | 31426321 | 855 | 58 | 1010761 | 5.9116 | 1.69E-09 | 9.46E-05 | 4.48E-07 |
| ENSG00000236980 | <i>C3orf84</i> | 3 | 49205065 | 49264291 | 85 | 12 | 1010761 | 5.9026 | 1.79E-09 | 9.99E-05 | 4.71E-07 |
| ENSG00000259428 | <i>HMGB3P26</i> | 14 | 103820576 | 103866157 | 115 | 17 | 1010761 | 5.8946 | 1.88E-09 | 0.0001048 | 4.92E-07 |
| ENSG00000096654 | <i>ZNF184</i> | 6 | 27408522 | 27475897 | 217 | 18 | 1010761 | 5.8902 | 1.93E-09 | 0.0001077 | 5.03E-07 |
| ENSG00000169981 | <i>ZNF35</i> | 3 | 44655219 | 44712283 | 81 | 16 | 1010761 | 5.8858 | 1.98E-09 | 0.0001106 | 5.14E-07 |
| ENSG00000234902 | <i>AC007879.3</i> | 2 | 208041441 | 208135790 | 266 | 43 | 1010761 | 5.8842 | 2.00E-09 | 0.0001116 | 5.17E-07 |
| ENSG00000222698 | <i>RF00019</i> | 22 | 41406501 | 41451595 | 156 | 18 | 1010761 | 5.8691 | 2.19E-09 | 0.0001223 | 5.63E-07 |
| ENSG00000238648 | | 6 | 27564188 | 27609311 | 70 | 19 | 1010761 | 5.856 | 2.37E-09 | 0.0001324 | 6.07E-07 |
| ENSG00000252859 | <i>RNU6-375P</i> | 22 | 41529221 | 41574320 | 89 | 19 | 1010761 | 5.8542 | 2.40E-09 | 0.0001338 | 6.11E-07 |
| ENSG00000243904 | <i>RPSAP5</i> | 14 | 103830370 | 103876253 | 109 | 14 | 1010761 | 5.8442 | 2.55E-09 | 0.0001421 | 6.46E-07 |
| ENSG00000075413 | <i>MARK3</i> | 14 | 103816729 | 103980168 | 432 | 27 | 1010761 | 5.8431 | 2.56E-09 | 0.000143 | 6.46E-07 |
| ENSG00000144642 | <i>RBMS3</i> | 3 | 29287473 | 30061882 | 3154 | 286 | 1010761 | 5.8427 | 2.57E-09 | 0.0001433 | 6.46E-07 |
| ENSG00000220695 | <i>Z86062.1</i> | 6 | 100943152 | 100988928 | 75 | 17 | 1010761 | 5.8377 | 2.65E-09 | 0.0001477 | 6.62E-07 |
| ENSG00000212076 | | 1 | 52292013 | 52337082 | 129 | 21 | 1010761 | 5.8274 | 2.81E-09 | 0.0001571 | 7.01E-07 |
| ENSG00000230604 | <i>TSEN15P2</i> | 1 | 52290450 | 52335807 | 127 | 20 | 1010761 | 5.8214 | 2.92E-09 | 0.0001628 | 7.24E-07 |
| ENSG00000267284 | <i>AC022031.2</i> | 18 | 53353294 | 53465992 | 220 | 29 | 1010761 | 5.8167 | 3.00E-09 | 0.0001675 | 7.41E-07 |
| ENSG00000272077 | <i>AC124045.1</i> | 3 | 44673904 | 44720856 | 56 | 14 | 1010761 | 5.8137 | 3.05E-09 | 0.0001705 | 7.51E-07 |
| ENSG00000236869 | <i>AC099669.1</i> | 3 | 44588849 | 44762145 | 332 | 31 | 1010761 | 5.8038 | 3.24E-09 | 0.0001809 | 7.90E-07 |
| ENSG00000207783 | | 3 | 44868380 | 44913473 | 83 | 17 | 1010761 | 5.8037 | 3.24E-09 | 0.000181 | 7.90E-07 |
| ENSG00000100401 | <i>RANGAP1</i> | 22 | 41631615 | 41717255 | 154 | 16 | 1010761 | 5.8025 | 3.27E-09 | 0.0001823 | 7.91E-07 |
| ENSG00000228432 | <i>DHFRP2</i> | 6 | 31324129 | 31369675 | 284 | 44 | 1010761 | 5.8022 | 3.27E-09 | 0.0001827 | 7.91E-07 |
| ENSG00000258587 | <i>AC006530.1</i> | 14 | 75305387 | 75350957 | 104 | 16 | 1010761 | 5.799 | 3.34E-09 | 0.0001862 | 8.02E-07 |
| ENSG00000252977 | <i>RNA5SP70</i> | 1 | 181705702 | 181750780 | 110 | 20 | 1010761 | 5.7933 | 3.45E-09 | 0.0001926 | 8.27E-07 |
| ENSG00000233509 | <i>ZNF197-AS1</i> | 3 | 44648620 | 44701289 | 83 | 15 | 1010761 | 5.7908 | 3.50E-09 | 0.0001956 | 8.36E-07 |
| ENSG00000224342 | <i>AC007879.1</i> | 2 | 208003358 | 208097514 | 228 | 29 | 1010761 | 5.7847 | 3.63E-09 | 0.0002027 | 8.63E-07 |
| ENSG00000119608 | <i>PROX2</i> | 14 | 75309574 | 75365537 | 137 | 18 | 1010761 | 5.7768 | 3.81E-09 | 0.0002125 | 8.99E-07 |
| ENSG00000264192 | <i>RN7SL117P</i> | 2 | 22110865 | 22156160 | 46 | 12 | 1010761 | 5.7764 | 3.82E-09 | 0.000213 | 8.99E-07 |
| ENSG00000119689 | <i>DLST</i> | 14 | 75313596 | 75380448 | 177 | 20 | 1010761 | 5.7709 | 3.94E-09 | 0.0002201 | 9.25E-07 |
| ENSG00000007372 | <i>PAX6</i> | 11 | 31796327 | 31874610 | 118 | 21 | 1010761 | 5.761 | 4.18E-09 | 0.0002334 | 9.77E-07 |
| ENSG00000186448 | <i>ZNF197</i> | 3 | 44631511 | 44699963 | 104 | 17 | 1010761 | 5.7602 | 4.20E-09 | 0.0002345 | 9.77E-07 |
| ENSG00000234481 | <i>AC117945.1</i> | 1 | 37203741 | 37251369 | 86 | 13 | 1010761 | 5.7358 | 4.85E-09 | 0.0002709 | 1.12E-06 |
| ENSG0000026950 | <i>BTN3A1</i> | 6 | 26367465 | 26425444 | 328 | 29 | 1010761 | 5.7355 | 4.86E-09 | 0.0002713 | 1.12E-06 |
| ENSG00000146109 | <i>ABT1</i> | 6 | 26562180 | 26610972 | 175 | 20 | 1010761 | 5.723 | 5.23E-09 | 0.000292 | 1.20E-06 |
| ENSG00000213592 | <i>PPIAP42</i> | 11 | 57475516 | 57521002 | 60 | 9 | 1010761 | 5.7143 | 5.51E-09 | 0.0003073 | 1.26E-06 |
| ENSG00000255525 | <i>AL137804.1</i> | 11 | 31292232 | 31346095 | 73 | 10 | 1010761 | 5.7143 | 5.51E-09 | 0.0003075 | 1.26E-06 |
| ENSG00000269104 | | 22 | 41675388 | 41720686 | 72 | 11 | 1010761 | 5.712 | 5.58E-09 | 0.0003116 | 1.27E-06 |
| ENSG00000211450 | <i>SELENOH</i> | 11 | 57473722 | 57520883 | 61 | 9 | 1010761 | 5.7012 | 5.95E-09 | 0.000332 | 1.34E-06 |
| ENSG00000185219 | <i>ZNF445</i> | 3 | 44463212 | 44554162 | 138 | 21 | 1010761 | 5.6994 | 6.01E-09 | 0.0003355 | 1.35E-06 |

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|-----------------|--------------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000206836 | <i>RNU6-1029P</i> | 2 | 198277469 | 198322575 | 58 | 12 | 1010761 | 5.6929 | 6.25E-09 | 0.0003487 | 1.40E-06 |
| ENSG00000178917 | <i>ZNF852</i> | 3 | 44530462 | 44587128 | 114 | 17 | 1010761 | 5.6855 | 6.52E-09 | 0.0003639 | 1.45E-06 |
| ENSG00000214825 | <i>E124P3</i> | 3 | 44556236 | 44602297 | 119 | 14 | 1010761 | 5.6853 | 6.53E-09 | 0.0003645 | 1.45E-06 |
| ENSG00000221148 | <i>RF00334</i> | 12 | 84567103 | 84612227 | 134 | 21 | 1010761 | 5.6791 | 6.77E-09 | 0.0003779 | 1.50E-06 |
| ENSG00000156603 | <i>MED19</i> | 11 | 57461186 | 57514795 | 80 | 11 | 1010761 | 5.6721 | 7.05E-09 | 0.0003937 | 1.56E-06 |
| ENSG00000267325 | <i>LINC01415</i> | 18 | 53433958 | 53483952 | 134 | 19 | 1010761 | 5.6659 | 7.31E-09 | 0.0004082 | 1.60E-06 |
| ENSG00000144792 | <i>ZNF660</i> | 3 | 44591456 | 44651186 | 138 | 15 | 1010761 | 5.6656 | 7.33E-09 | 0.0004089 | 1.60E-06 |
| ENSG00000213593 | <i>TMX2</i> | 11 | 57445075 | 57518445 | 109 | 14 | 1010761 | 5.6615 | 7.50E-09 | 0.0004188 | 1.64E-06 |
| ENSG00000254732 | <i>AP001931.1</i> | 11 | 57474635 | 57570715 | 135 | 16 | 1010761 | 5.658 | 7.66E-09 | 0.0004275 | 1.66E-06 |
| ENSG00000214820 | <i>MPRIPP1</i> | 3 | 44611430 | 44657518 | 90 | 13 | 1010761 | 5.6571 | 7.70E-09 | 0.0004297 | 1.67E-06 |
| ENSG00000275846 | <i>AL513548.3</i> | 6 | 26567961 | 26616889 | 171 | 21 | 1010761 | 5.6564 | 7.73E-09 | 0.0004314 | 1.67E-06 |
| ENSG00000264774 | | 3 | 44546708 | 44591793 | 103 | 13 | 1010761 | 5.6521 | 7.92E-09 | 0.0004423 | 1.70E-06 |
| ENSG00000234619 | <i>RPL7P11</i> | 1 | 8775489 | 8821146 | 68 | 16 | 1010761 | 5.6475 | 8.14E-09 | 0.0004545 | 1.74E-06 |
| ENSG00000213104 | <i>NPM1P46</i> | 2 | 198234425 | 198280616 | 78 | 14 | 1010761 | 5.6451 | 8.25E-09 | 0.0004606 | 1.76E-06 |
| ENSG00000219738 | <i>CD83P1</i> | 6 | 27518601 | 27564523 | 107 | 27 | 1010761 | 5.6437 | 8.32E-09 | 0.0004644 | 1.77E-06 |
| ENSG00000255370 | <i>CYCSP25</i> | 11 | 31292219 | 31337534 | 68 | 9 | 1010761 | 5.6391 | 8.55E-09 | 0.000477 | 1.81E-06 |
| ENSG00000185352 | <i>HS6ST3</i> | 13 | 96708093 | 97501816 | 1940 | 135 | 1010761 | 5.6354 | 8.73E-09 | 0.0004873 | 1.84E-06 |
| ENSG00000271314 | <i>AL161729.2</i> | 9 | 98222206 | 98267661 | 116 | 16 | 1010761 | 5.6334 | 8.83E-09 | 0.0004931 | 1.85E-06 |
| ENSG00000100393 | <i>EP300</i> | 22 | 41452790 | 41586083 | 248 | 28 | 1010761 | 5.6327 | 8.87E-09 | 0.000495 | 1.85E-06 |
| ENSG00000233859 | <i>ADH5P4</i> | 6 | 66536823 | 66582932 | 337 | 26 | 1010761 | 5.6272 | 9.16E-09 | 0.0005111 | 1.91E-06 |
| ENSG00000277509 | <i>AC099669.2</i> | 3 | 44560447 | 44605883 | 126 | 14 | 1010761 | 5.6225 | 9.41E-09 | 0.0005252 | 1.95E-06 |
| ENSG00000196345 | <i>ZKSCAN7</i> | 3 | 44561685 | 44634975 | 196 | 17 | 1010761 | 5.6213 | 9.48E-09 | 0.0005291 | 1.96E-06 |
| ENSG00000173421 | <i>CCDC36</i> | 3 | 49200861 | 49305537 | 147 | 17 | 1010761 | 5.6205 | 9.52E-09 | 0.0005315 | 1.96E-06 |
| ENSG00000100403 | <i>ZC3H7B</i> | 22 | 41662526 | 41766151 | 168 | 21 | 1010761 | 5.6177 | 9.68E-09 | 0.0005401 | 1.99E-06 |
| ENSG00000249382 | <i>AC097501.1</i> | 4 | 59842900 | 59888878 | 169 | 21 | 1010761 | 5.6119 | 1.00E-08 | 0.0005584 | 2.05E-06 |
| ENSG0000014824 | <i>SLC30A9</i> | 4 | 41957489 | 42102474 | 515 | 22 | 1010761 | 5.6097 | 1.01E-08 | 0.0005657 | 2.06E-06 |
| ENSG00000202434 | <i>RF00394</i> | 2 | 198234442 | 198279578 | 76 | 14 | 1010761 | 5.6072 | 1.03E-08 | 0.000574 | 2.08E-06 |
| ENSG00000256757 | <i>AP002840.1</i> | 11 | 113241043 | 113292839 | 149 | 17 | 1010761 | 5.6069 | 1.03E-08 | 0.000575 | 2.08E-06 |
| ENSG00000185920 | <i>PTCH1</i> | 9 | 98195262 | 98314339 | 299 | 32 | 1010761 | 5.6023 | 1.06E-08 | 0.0005905 | 2.13E-06 |
| ENSG00000143207 | <i>COP1</i> | 1 | 175903967 | 176211629 | 761 | 56 | 1010761 | 5.5991 | 1.08E-08 | 0.0006012 | 2.16E-06 |
| ENSG00000124177 | <i>CHD6</i> | 20 | 40020741 | 40282133 | 672 | 53 | 1010761 | 5.5897 | 1.14E-08 | 0.0006347 | 2.27E-06 |
| ENSG00000249212 | <i>ATP1B1P1</i> | 4 | 41996226 | 42042140 | 194 | 10 | 1010761 | 5.5867 | 1.16E-08 | 0.000646 | 2.31E-06 |
| ENSG00000254462 | <i>TMX2-CTNND1</i> | 11 | 57445077 | 57569058 | 182 | 19 | 1010761 | 5.582 | 1.19E-08 | 0.0006637 | 2.36E-06 |
| ENSG00000212174 | | 1 | 52296305 | 52341381 | 130 | 21 | 1010761 | 5.5806 | 1.20E-08 | 0.0006691 | 2.37E-06 |
| ENSG00000006704 | <i>GTF2IRD1</i> | 7 | 73833120 | 74026930 | 472 | 72 | 1010761 | 5.5792 | 1.21E-08 | 0.0006744 | 2.38E-06 |
| ENSG00000283458 | <i>AC011139.1</i> | 18 | 36859204 | 36917972 | 205 | 32 | 1010761 | 5.5717 | 1.26E-08 | 0.0007039 | 2.47E-06 |
| ENSG00000115392 | <i>FANCL</i> | 2 | 58376378 | 58503485 | 307 | 42 | 1010761 | 5.5717 | 1.26E-08 | 0.0007041 | 2.47E-06 |
| ENSG00000112249 | <i>ASCC3</i> | 6 | 100946070 | 101364240 | 1211 | 46 | 1010761 | 5.5713 | 1.26E-08 | 0.0007055 | 2.47E-06 |
| ENSG00000204538 | <i>PSORS1C2</i> | 6 | 31095313 | 31142127 | 159 | 35 | 1010761 | 5.5592 | 1.35E-08 | 0.0007562 | 2.63E-06 |
| ENSG00000228223 | <i>HCG11</i> | 6 | 26488678 | 26536807 | 137 | 16 | 1010761 | 5.5485 | 1.44E-08 | 0.0008042 | 2.79E-06 |
| ENSG00000253025 | <i>RNU2-12P</i> | 1 | 176202998 | 176248165 | 97 | 16 | 1010761 | 5.5446 | 1.47E-08 | 0.0008223 | 2.85E-06 |
| ENSG00000178568 | <i>ERBB4</i> | 2 | 212230442 | 213438565 | 4820 | 337 | 1010761 | 5.5426 | 1.49E-08 | 0.000832 | 2.87E-06 |

| | | | | | | | | | | | |
|-----------------|------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000243122 | AC016304.1 | 15 | 37747892 | 37793304 | 169 | 23 | 1010761 | 5.5393 | 1.52E-08 | 0.0008475 | 2.91E-06 |
| ENSG00000225873 | LINC00694 | 3 | 44452619 | 44516438 | 114 | 19 | 1010761 | 5.5381 | 1.53E-08 | 0.0008533 | 2.92E-06 |
| ENSG00000184226 | PCDH9 | 13 | 66866966 | 67839577 | 2455 | 229 | 1010761 | 5.5277 | 1.62E-08 | 0.0009054 | 3.09E-06 |
| ENSG00000108684 | ASIC2 | 17 | 31330105 | 32519313 | 4235 | 470 | 1010761 | 5.5211 | 1.68E-08 | 0.0009403 | 3.20E-06 |
| ENSG00000232463 | AL359265.2 | 1 | 176190336 | 176235966 | 107 | 16 | 1010761 | 5.5181 | 1.71E-08 | 0.0009562 | 3.24E-06 |
| ENSG00000078618 | NRDC | 1 | 52244863 | 52379609 | 402 | 44 | 1010761 | 5.5177 | 1.72E-08 | 0.0009588 | 3.24E-06 |
| ENSG00000244691 | RPL10AP1 | 14 | 103868456 | 103914098 | 129 | 12 | 1010761 | 5.512 | 1.77E-08 | 0.0009902 | 3.33E-06 |
| ENSG00000115524 | SF3B1 | 2 | 198244508 | 198334815 | 117 | 19 | 1010761 | 5.5115 | 1.78E-08 | 0.0009931 | 3.33E-06 |
| ENSG00000257124 | AC093025.1 | 12 | 84044788 | 84090498 | 202 | 18 | 1010761 | 5.5099 | 1.80E-08 | 0.001002 | 3.35E-06 |
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| ENSG00000270441 | AC135506.1 | 3 | 49167519 | 49233284 | 95 | 14 | 1010761 | 5.5036 | 1.86E-08 | 0.0010387 | 3.45E-06 |
| ENSG00000226913 | BSN-AS2 | 3 | 49576739 | 49626799 | 67 | 11 | 1010761 | 5.5027 | 1.87E-08 | 0.001044 | 3.45E-06 |
| ENSG00000281880 | PAUPAR | 11 | 31812894 | 31860858 | 65 | 11 | 1010761 | 5.5022 | 1.88E-08 | 0.0010468 | 3.45E-06 |
| ENSG00000118473 | SGIP1 | 1 | 66964066 | 67223982 | 973 | 62 | 1010761 | 5.4953 | 1.95E-08 | 0.0010888 | 3.58E-06 |
| ENSG00000197585 | AC068051.1 | 2 | 215104764 | 215583970 | 1483 | 104 | 1010761 | 5.4937 | 1.97E-08 | 0.0010984 | 3.60E-06 |
| ENSG00000271659 | AL161729.4 | 9 | 98241327 | 98286802 | 123 | 18 | 1010761 | 5.4894 | 2.02E-08 | 0.0011254 | 3.68E-06 |
| ENSG00000251266 | LINC02429 | 4 | 59815000 | 59922677 | 491 | 42 | 1010761 | 5.4885 | 2.03E-08 | 0.0011316 | 3.69E-06 |
| ENSG00000137310 | TCF19 | 6 | 31091319 | 31141992 | 213 | 36 | 1010761 | 5.4821 | 2.10E-08 | 0.0011733 | 3.81E-06 |
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| ENSG00000188848 | BEND4 | 4 | 42102955 | 42189895 | 323 | 32 | 1010761 | 5.4789 | 2.14E-08 | 0.0011948 | 3.85E-06 |
| ENSG00000222800 | RNU2-62P | 6 | 27067569 | 27112759 | 76 | 23 | 1010761 | 5.4777 | 2.15E-08 | 0.0012023 | 3.87E-06 |
| ENSG00000199851 | RF00012 | 6 | 27948346 | 27993553 | 144 | 23 | 1010761 | 5.4758 | 2.18E-08 | 0.0012158 | 3.90E-06 |
| ENSG00000240342 | RPS2P5 | 12 | 118648889 | 118694767 | 108 | 15 | 1010761 | 5.4723 | 2.22E-08 | 0.0012399 | 3.95E-06 |
| ENSG00000265764 | | 6 | 28753749 | 28798812 | 77 | 11 | 1010761 | 5.4721 | 2.22E-08 | 0.0012412 | 3.95E-06 |
| ENSG00000115540 | MOB4 | 2 | 198345295 | 198428423 | 116 | 17 | 1010761 | 5.4678 | 2.28E-08 | 0.0012719 | 4.04E-06 |
| ENSG00000157782 | CABP1 | 12 | 121043355 | 121115127 | 280 | 45 | 1010761 | 5.4626 | 2.35E-08 | 0.0013095 | 4.14E-06 |
| ENSG00000184838 | PRR16 | 5 | 119764973 | 120033027 | 1080 | 97 | 1010761 | 5.4615 | 2.36E-08 | 0.001318 | 4.16E-06 |
| ENSG00000272981 | | 11 | 126954221 | 127019630 | 252 | 29 | 1010761 | 5.4597 | 2.38E-08 | 0.0013308 | 4.18E-06 |
| ENSG00000256008 | AC125616.1 | 12 | 121057414 | 121114394 | 227 | 37 | 1010761 | 5.459 | 2.39E-08 | 0.0013362 | 4.19E-06 |
| ENSG00000206950 | RF00019 | 8 | 14155064 | 14200172 | 218 | 31 | 1010761 | 5.4544 | 2.46E-08 | 0.0013715 | 4.27E-06 |
| ENSG00000112763 | BTN2A1 | 6 | 26423132 | 26486849 | 226 | 25 | 1010761 | 5.4543 | 2.46E-08 | 0.001372 | 4.27E-06 |
| ENSG00000271155 | AL161729.1 | 9 | 98233517 | 98279918 | 118 | 18 | 1010761 | 5.4533 | 2.47E-08 | 0.0013798 | 4.29E-06 |
| ENSG00000260100 | AL512604.3 | 9 | 37068810 | 37114773 | 103 | 13 | 1010761 | 5.447 | 2.56E-08 | 0.0014294 | 4.43E-06 |
| ENSG00000196782 | MAML3 | 4 | 140627907 | 141110338 | 1285 | 174 | 1010761 | 5.4449 | 2.59E-08 | 0.0014464 | 4.46E-06 |
| ENSG00000185909 | KLHDC8B | 3 | 49174044 | 49223919 | 74 | 12 | 1010761 | 5.444 | 2.61E-08 | 0.0014542 | 4.47E-06 |
| ENSG00000183230 | CTNNA3 | 10 | 67662276 | 69490927 | 7333 | 338 | 1010761 | 5.442 | 2.63E-08 | 0.0014706 | 4.51E-06 |
| ENSG00000279726 | AC005609.5 | 5 | 140158042 | 140236778 | 170 | 13 | 1010761 | 5.4406 | 2.65E-08 | 0.0014819 | 4.53E-06 |
| ENSG00000135124 | P2RX4 | 12 | 121612660 | 121681909 | 284 | 34 | 1010761 | 5.4402 | 2.66E-08 | 0.0014854 | 4.53E-06 |
| ENSG00000105737 | GRIK5 | 19 | 42492473 | 42608650 | 98 | 24 | 1010761 | 5.4376 | 2.70E-08 | 0.0015071 | 4.58E-06 |
| ENSG00000224136 | AC007568.1 | 7 | 117487913 | 117533729 | 99 | 19 | 1010761 | 5.4348 | 2.74E-08 | 0.0015306 | 4.64E-06 |
| ENSG00000229115 | AL390774.1 | 9 | 126486499 | 126532054 | 112 | 20 | 1010761 | 5.4339 | 2.76E-08 | 0.0015389 | 4.65E-06 |
| ENSG00000197182 | MIRLET7BHG | 22 | 46414749 | 46519808 | 305 | 51 | 1010761 | 5.4319 | 2.79E-08 | 0.0015565 | 4.69E-06 |

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|-----------------|-------------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000132793 | <i>LPIN3</i> | 20 | 39934560 | 39999222 | 166 | 29 | 1010761 | 5.4305 | 2.81E-08 | 0.001568 | 4.71E-06 |
| ENSG00000228686 | <i>AL590723.1</i> | 1 | 175951413 | 175997896 | 119 | 21 | 1010761 | 5.4298 | 2.82E-08 | 0.0015747 | 4.71E-06 |
| ENSG00000225904 | <i>MORF4L1P7</i> | 1 | 176326835 | 176372537 | 98 | 17 | 1010761 | 5.4289 | 2.83E-08 | 0.0015822 | 4.72E-06 |
| ENSG00000283036 | <i>LINCO1988</i> | 3 | 44430626 | 44481021 | 99 | 18 | 1010761 | 5.4222 | 2.94E-08 | 0.0016428 | 4.89E-06 |
| ENSG00000135090 | <i>TAOK3</i> | 12 | 118577606 | 118845750 | 604 | 44 | 1010761 | 5.4205 | 2.97E-08 | 0.0016587 | 4.92E-06 |
| ENSG00000257729 | <i>AC090679.1</i> | 12 | 84630119 | 84698341 | 308 | 15 | 1010761 | 5.4177 | 3.02E-08 | 0.0016853 | 4.99E-06 |
| ENSG00000270666 | <i>AL021918.1</i> | 6 | 27472818 | 27518053 | 114 | 22 | 1010761 | 5.4162 | 3.04E-08 | 0.0016994 | 5.00E-06 |
| ENSG00000233436 | <i>BTBD18</i> | 11 | 57500986 | 57554253 | 71 | 14 | 1010761 | 5.4157 | 3.05E-08 | 0.0017038 | 5.00E-06 |
| ENSG00000221450 | | 9 | 2914323 | 2959410 | 183 | 32 | 1010761 | 5.4155 | 3.06E-08 | 0.0017062 | 5.00E-06 |
| ENSG00000198561 | <i>CTNND1</i> | 11 | 57485715 | 57597018 | 143 | 17 | 1010761 | 5.4096 | 3.16E-08 | 0.0017633 | 5.16E-06 |
| ENSG00000273951 | <i>AL031667.3</i> | 20 | 40104211 | 40149865 | 111 | 18 | 1010761 | 5.4087 | 3.17E-08 | 0.0017717 | 5.17E-06 |
| ENSG00000175893 | <i>ZDHC21</i> | 9 | 14601069 | 14728469 | 556 | 77 | 1010761 | 5.4067 | 3.21E-08 | 0.0017921 | 5.21E-06 |
| ENSG00000227815 | <i>AL359265.1</i> | 1 | 176206619 | 176252538 | 105 | 16 | 1010761 | 5.4049 | 3.24E-08 | 0.0018098 | 5.25E-06 |
| ENSG00000156599 | <i>ZDHC5</i> | 11 | 57400219 | 57478659 | 124 | 18 | 1010761 | 5.3992 | 3.35E-08 | 0.0018687 | 5.40E-06 |
| ENSG00000196787 | <i>HIST1H2AG</i> | 6 | 27065821 | 27113070 | 85 | 23 | 1010761 | 5.3941 | 3.44E-08 | 0.0019221 | 5.54E-06 |
| ENSG00000261353 | | 6 | 26492291 | 26537632 | 124 | 14 | 1010761 | 5.3808 | 3.71E-08 | 0.0020693 | 5.95E-06 |
| ENSG00000168702 | <i>LRP1B</i> | 2 | 140978992 | 142924270 | 8288 | 491 | 1010761 | 5.3765 | 3.80E-08 | 0.0021192 | 6.07E-06 |
| ENSG00000169964 | <i>TMEM42</i> | 3 | 44868361 | 44917162 | 105 | 20 | 1010761 | 5.3725 | 3.88E-08 | 0.0021672 | 6.17E-06 |
| ENSG00000144381 | <i>HSPD1</i> | 2 | 198341305 | 198399998 | 69 | 12 | 1010761 | 5.3723 | 3.89E-08 | 0.00217 | 6.17E-06 |
| ENSG00000238958 | | 3 | 44824507 | 44869597 | 62 | 14 | 1010761 | 5.372 | 3.89E-08 | 0.0021736 | 6.17E-06 |
| ENSG00000258439 | <i>AC007956.1</i> | 14 | 75089752 | 75135293 | 104 | 15 | 1010761 | 5.3646 | 4.06E-08 | 0.002264 | 6.40E-06 |
| ENSG00000155052 | <i>CNTNAP5</i> | 2 | 124747864 | 125682864 | 3059 | 209 | 1010761 | 5.3646 | 4.06E-08 | 0.0022646 | 6.40E-06 |
| ENSG00000225916 | <i>AC007879.2</i> | 2 | 208056673 | 208103032 | 117 | 20 | 1010761 | 5.3616 | 4.13E-08 | 0.0023026 | 6.49E-06 |
| ENSG00000168779 | <i>SHOX2</i> | 3 | 157803800 | 157859292 | 158 | 16 | 1010761 | 5.3589 | 4.19E-08 | 0.0023375 | 6.57E-06 |
| ENSG00000248106 | <i>AC116353.2</i> | 5 | 140108695 | 140154406 | 157 | 11 | 1010761 | 5.3579 | 4.21E-08 | 0.0023495 | 6.58E-06 |
| ENSG00000115541 | <i>HSPE1</i> | 2 | 198329718 | 198378181 | 61 | 10 | 1010761 | 5.3522 | 4.35E-08 | 0.0024255 | 6.78E-06 |
| ENSG00000272862 | <i>AC106052.1</i> | 4 | 41980758 | 42026254 | 189 | 13 | 1010761 | 5.3396 | 4.66E-08 | 0.0026002 | 7.24E-06 |
| ENSG00000236366 | <i>AL359313.1</i> | 6 | 142837592 | 142994026 | 475 | 43 | 1010761 | 5.3382 | 4.69E-08 | 0.0026204 | 7.28E-06 |
| ENSG00000235559 | <i>NOP56P1</i> | 6 | 28741410 | 28786781 | 74 | 10 | 1010761 | 5.3319 | 4.86E-08 | 0.0027126 | 7.51E-06 |
| ENSG00000250515 | <i>AC116353.3</i> | 5 | 140101875 | 140147448 | 165 | 11 | 1010761 | 5.3241 | 5.07E-08 | 0.0028314 | 7.82E-06 |
| ENSG00000232920 | <i>LINCO1400</i> | 9 | 37063528 | 37110789 | 110 | 14 | 1010761 | 5.3237 | 5.08E-08 | 0.002838 | 7.82E-06 |
| ENSG00000267402 | <i>TCF4-AS2</i> | 18 | 53124406 | 53173623 | 97 | 22 | 1010761 | 5.3183 | 5.24E-08 | 0.0029225 | 8.03E-06 |
| ENSG00000168496 | <i>FEN1</i> | 11 | 61525109 | 61574716 | 81 | 16 | 1010761 | 5.3162 | 5.30E-08 | 0.0029568 | 8.10E-06 |
| ENSG00000270987 | <i>AL133338.2</i> | 6 | 101302479 | 101348214 | 148 | 22 | 1010761 | 5.3157 | 5.31E-08 | 0.0029659 | 8.10E-06 |
| ENSG00000149972 | <i>CNTN5</i> | 11 | 98856871 | 100239616 | 6093 | 394 | 1010761 | 5.3135 | 5.38E-08 | 0.0030011 | 8.18E-06 |
| ENSG00000270757 | <i>HSPE1-MOB4</i> | 2 | 198330137 | 198425450 | 130 | 18 | 1010761 | 5.3103 | 5.47E-08 | 0.003054 | 8.30E-06 |
| ENSG00000128714 | <i>HOXD13</i> | 2 | 176922619 | 176970666 | 127 | 26 | 1010761 | 5.3078 | 5.55E-08 | 0.003097 | 8.39E-06 |
| ENSG00000200779 | <i>RNU6-105P</i> | 2 | 71596885 | 71641988 | 155 | 22 | 1010761 | 5.3038 | 5.67E-08 | 0.0031652 | 8.55E-06 |
| ENSG00000075292 | <i>ZNF638</i> | 2 | 71468723 | 71672191 | 649 | 50 | 1010761 | 5.3032 | 5.69E-08 | 0.0031762 | 8.56E-06 |
| ENSG00000162944 | <i>RFTN2</i> | 2 | 198422948 | 198575719 | 230 | 19 | 1010761 | 5.3015 | 5.74E-08 | 0.0032049 | 8.59E-06 |
| ENSG00000231020 | <i>AL591043.1</i> | 1 | 176264808 | 176310231 | 151 | 13 | 1010761 | 5.3015 | 5.74E-08 | 0.0032056 | 8.59E-06 |
| ENSG00000250756 | <i>AC018645.1</i> | 7 | 32792946 | 32838054 | 234 | 24 | 1010761 | 5.2957 | 5.93E-08 | 0.0033083 | 8.85E-06 |

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|-----------------|-------------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000113100 | <i>CDH9</i> | 5 | 26870709 | 27073693 | 581 | 54 | 1010761 | 5.2951 | 5.95E-08 | 0.003319 | 8.85E-06 |
| ENSG00000163808 | <i>KIF15</i> | 3 | 44768209 | 44904753 | 210 | 28 | 1010761 | 5.2924 | 6.04E-08 | 0.0033701 | 8.96E-06 |
| ENSG00000253357 | <i>AC008708.1</i> | 5 | 167113368 | 167166129 | 127 | 24 | 1010761 | 5.2915 | 6.07E-08 | 0.0033861 | 8.98E-06 |
| ENSG00000277143 | <i>AC074276.2</i> | 3 | 158044219 | 158089566 | 131 | 15 | 1010761 | 5.286 | 6.25E-08 | 0.0034901 | 9.22E-06 |
| ENSG00000241409 | <i>AC064852.1</i> | 2 | 233614856 | 233667659 | 122 | 16 | 1010761 | 5.2857 | 6.26E-08 | 0.0034945 | 9.22E-06 |
| ENSG00000231699 | <i>AC020550.1</i> | 2 | 198363527 | 198408689 | 55 | 9 | 1010761 | 5.2849 | 6.29E-08 | 0.0035093 | 9.23E-06 |
| ENSG00000236141 | <i>AC013727.2</i> | 2 | 104472204 | 104521146 | 100 | 31 | 1010761 | 5.2767 | 6.58E-08 | 0.0036713 | 9.64E-06 |
| ENSG00000254602 | <i>AP000662.1</i> | 11 | 57370497 | 57430263 | 103 | 13 | 1010761 | 5.2744 | 6.66E-08 | 0.0037165 | 9.73E-06 |
| ENSG00000126215 | <i>XRCC3</i> | 14 | 104153946 | 104216841 | 144 | 26 | 1010761 | 5.2675 | 6.91E-08 | 0.0038593 | 1.01E-05 |
| ENSG00000254363 | <i>AC011379.2</i> | 5 | 139501904 | 139562636 | 107 | 16 | 1010761 | 5.2664 | 6.96E-08 | 0.0038835 | 1.01E-05 |
| ENSG00000170178 | <i>HOXD12</i> | 2 | 176929458 | 176975921 | 115 | 23 | 1010761 | 5.2639 | 7.05E-08 | 0.0039358 | 1.02E-05 |
| ENSG00000115474 | <i>KCNJ13</i> | 2 | 233621174 | 233676278 | 115 | 14 | 1010761 | 5.2585 | 7.26E-08 | 0.0040538 | 1.05E-05 |
| ENSG00000266033 | | 1 | 80785064 | 80830173 | 205 | 12 | 1010761 | 5.256 | 7.36E-08 | 0.0041083 | 1.06E-05 |
| ENSG00000124915 | <i>AP002380.1</i> | 11 | 61503965 | 61560127 | 119 | 23 | 1010761 | 5.2541 | 7.44E-08 | 0.0041522 | 1.07E-05 |
| ENSG00000134571 | <i>MYBPC3</i> | 11 | 47342948 | 47409253 | 176 | 26 | 1010761 | 5.2513 | 7.55E-08 | 0.0042161 | 1.08E-05 |
| ENSG00000251999 | <i>RF00322</i> | 7 | 32796426 | 32841558 | 240 | 23 | 1010761 | 5.251 | 7.56E-08 | 0.0042215 | 1.08E-05 |
| ENSG00000267311 | <i>AC007673.1</i> | 18 | 52511688 | 52558040 | 92 | 19 | 1010761 | 5.2506 | 7.58E-08 | 0.0042304 | 1.08E-05 |
| ENSG00000204120 | <i>GIGYF2</i> | 2 | 233527015 | 233735285 | 587 | 46 | 1010761 | 5.2475 | 7.71E-08 | 0.0043038 | 1.10E-05 |
| ENSG00000253554 | <i>AC022639.1</i> | 8 | 64589737 | 65316115 | 1590 | 119 | 1010761 | 5.2429 | 7.90E-08 | 0.0044105 | 1.12E-05 |
| ENSG00000172409 | <i>CLP1</i> | 11 | 57389488 | 57439340 | 81 | 13 | 1010761 | 5.2375 | 8.14E-08 | 0.0045435 | 1.15E-05 |
| ENSG00000197903 | <i>HIST1H2BK</i> | 6 | 27104197 | 27149577 | 84 | 21 | 1010761 | 5.2322 | 8.38E-08 | 0.004675 | 1.18E-05 |
| ENSG00000261432 | <i>LINC01613</i> | 9 | 122662331 | 122710110 | 103 | 17 | 1010761 | 5.226 | 8.66E-08 | 0.0048343 | 1.22E-05 |
| ENSG00000233902 | <i>AL645933.1</i> | 6 | 31420505 | 31466113 | 151 | 32 | 1010761 | 5.2208 | 8.91E-08 | 0.0049718 | 1.25E-05 |
| ENSG00000252452 | <i>RNU6-107P</i> | 2 | 233612375 | 233657476 | 111 | 13 | 1010761 | 5.2196 | 8.97E-08 | 0.0050055 | 1.26E-05 |
| ENSG00000234881 | <i>PIGFP2</i> | 9 | 126570315 | 126615965 | 106 | 20 | 1010761 | 5.2185 | 9.02E-08 | 0.0050334 | 1.26E-05 |
| ENSG00000226545 | <i>AL357552.1</i> | 1 | 8823534 | 8869565 | 77 | 18 | 1010761 | 5.2128 | 9.30E-08 | 0.0051922 | 1.30E-05 |
| ENSG00000146555 | <i>SDK1</i> | 7 | 3306080 | 4318632 | 4375 | 215 | 1010761 | 5.2059 | 9.65E-08 | 0.0053883 | 1.34E-05 |
| ENSG00000258536 | <i>FKBP1BP1</i> | 14 | 42176842 | 42222166 | 179 | 15 | 1010761 | 5.2059 | 9.65E-08 | 0.0053887 | 1.34E-05 |
| ENSG00000221280 | | 12 | 118569604 | 118614676 | 113 | 23 | 1010761 | 5.2044 | 9.73E-08 | 0.0054317 | 1.35E-05 |
| ENSG00000115548 | <i>KDM3A</i> | 2 | 86632924 | 86729839 | 256 | 29 | 1010761 | 5.1991 | 1.00E-07 | 0.0055885 | 1.38E-05 |
| ENSG00000252368 | <i>RNA5SP43</i> | 1 | 37720278 | 37765387 | 153 | 20 | 1010761 | 5.185 | 1.08E-07 | 0.0060283 | 1.49E-05 |
| ENSG00000198846 | <i>TOX</i> | 8 | 59707977 | 60066767 | 985 | 130 | 1010761 | 5.1831 | 1.09E-07 | 0.0060892 | 1.50E-05 |
| ENSG00000235784 | <i>HNRNPA1P29</i> | 13 | 94037230 | 94083108 | 158 | 19 | 1010761 | 5.1808 | 1.10E-07 | 0.0061645 | 1.51E-05 |
| ENSG00000149485 | <i>FADS1</i> | 11 | 61557097 | 61619634 | 120 | 15 | 1010761 | 5.1784 | 1.12E-07 | 0.006246 | 1.53E-05 |
| ENSG00000267172 | <i>AC022031.1</i> | 18 | 53449398 | 53496990 | 117 | 19 | 1010761 | 5.1725 | 1.16E-07 | 0.006447 | 1.58E-05 |
| ENSG00000149292 | <i>TTC12</i> | 11 | 113150251 | 113264266 | 273 | 38 | 1010761 | 5.1707 | 1.17E-07 | 0.0065101 | 1.59E-05 |
| ENSG00000206969 | <i>RNU6-1316P</i> | 14 | 103297193 | 103342300 | 126 | 16 | 1010761 | 5.1701 | 1.17E-07 | 0.0065301 | 1.59E-05 |
| ENSG00000249637 | <i>AC008438.1</i> | 5 | 139740476 | 139815952 | 88 | 19 | 1010761 | 5.1688 | 1.18E-07 | 0.0065754 | 1.60E-05 |
| ENSG00000241204 | <i>AC022730.2</i> | 8 | 71326360 | 71371811 | 127 | 27 | 1010761 | 5.1676 | 1.19E-07 | 0.0066172 | 1.60E-05 |
| ENSG00000119682 | <i>AREL1</i> | 14 | 75117955 | 75214818 | 121 | 14 | 1010761 | 5.1655 | 1.20E-07 | 0.006692 | 1.62E-05 |
| ENSG00000174279 | <i>EVX2</i> | 2 | 176932200 | 176983641 | 119 | 25 | 1010761 | 5.1638 | 1.21E-07 | 0.0067545 | 1.62E-05 |
| ENSG00000230828 | <i>AL583843.1</i> | 1 | 50545609 | 50590954 | 68 | 16 | 1010761 | 5.1636 | 1.21E-07 | 0.0067596 | 1.62E-05 |

| | | | | | | | | | | | |
|-----------------|-------------------|----|-----------|-----------|------|----|---------|--------|----------|-----------|----------|
| ENSG00000216762 | <i>VN1R13P</i> | 6 | 27018144 | 27064028 | 99 | 19 | 1010761 | 5.1625 | 1.22E-07 | 0.0067992 | 1.63E-05 |
| ENSG00000124920 | <i>MYRF</i> | 11 | 61485121 | 61565990 | 157 | 27 | 1010761 | 5.1608 | 1.23E-07 | 0.0068611 | 1.64E-05 |
| ENSG00000166793 | <i>YPEL4</i> | 11 | 57402561 | 57452417 | 78 | 13 | 1010761 | 5.1573 | 1.25E-07 | 0.006994 | 1.67E-05 |
| ENSG00000211990 | | 14 | 103310958 | 103356075 | 140 | 18 | 1010761 | 5.1559 | 1.26E-07 | 0.0070442 | 1.68E-05 |
| ENSG00000165915 | <i>SLC39A13</i> | 11 | 47393683 | 47448052 | 140 | 16 | 1010761 | 5.1552 | 1.27E-07 | 0.0070727 | 1.68E-05 |
| ENSG00000144821 | <i>MYH15</i> | 3 | 108089216 | 108283169 | 469 | 60 | 1010761 | 5.1524 | 1.29E-07 | 0.0071776 | 1.70E-05 |
| ENSG00000066336 | <i>SPI1</i> | 11 | 47366411 | 47435127 | 187 | 20 | 1010761 | 5.152 | 1.29E-07 | 0.0071933 | 1.70E-05 |
| ENSG00000222722 | | 9 | 126337663 | 126382736 | 108 | 17 | 1010761 | 5.1497 | 1.30E-07 | 0.0072815 | 1.72E-05 |
| ENSG00000134824 | <i>FADS2</i> | 11 | 61525452 | 61644826 | 267 | 34 | 1010761 | 5.1462 | 1.33E-07 | 0.0074165 | 1.75E-05 |
| ENSG00000265910 | | 11 | 47397633 | 47442733 | 118 | 15 | 1010761 | 5.145 | 1.34E-07 | 0.0074679 | 1.75E-05 |
| ENSG00000207601 | | 11 | 61549967 | 61595033 | 55 | 7 | 1010761 | 5.1423 | 1.36E-07 | 0.0075739 | 1.77E-05 |
| ENSG00000115896 | <i>PLCL1</i> | 2 | 198634426 | 199024608 | 776 | 50 | 1010761 | 5.1404 | 1.37E-07 | 0.0076515 | 1.79E-05 |
| ENSG00000232132 | <i>NDFIP2-AS1</i> | 13 | 80041499 | 80090366 | 77 | 16 | 1010761 | 5.1386 | 1.38E-07 | 0.0077235 | 1.80E-05 |
| ENSG00000235109 | <i>ZSCAN31</i> | 6 | 28282514 | 28359048 | 297 | 34 | 1010761 | 5.1337 | 1.42E-07 | 0.0079284 | 1.84E-05 |
| ENSG00000227016 | <i>AL583808.2</i> | 1 | 73195714 | 73266965 | 215 | 17 | 1010761 | 5.1323 | 1.43E-07 | 0.0079892 | 1.85E-05 |
| ENSG00000252378 | | 7 | 73950677 | 73995754 | 98 | 23 | 1010761 | 5.1318 | 1.43E-07 | 0.0080088 | 1.85E-05 |
| ENSG00000189298 | <i>ZKSCAN3</i> | 6 | 28282691 | 28346954 | 257 | 33 | 1010761 | 5.1256 | 1.48E-07 | 0.0082756 | 1.91E-05 |
| ENSG00000182600 | <i>SNORC</i> | 2 | 233698724 | 233751116 | 161 | 21 | 1010761 | 5.124 | 1.50E-07 | 0.0083487 | 1.92E-05 |
| ENSG00000134825 | <i>TMEM258</i> | 11 | 61546435 | 61595274 | 66 | 8 | 1010761 | 5.1235 | 1.50E-07 | 0.0083705 | 1.92E-05 |
| ENSG00000260000 | <i>AL133338.1</i> | 6 | 101294347 | 101340863 | 147 | 21 | 1010761 | 5.1183 | 1.54E-07 | 0.0086049 | 1.97E-05 |
| ENSG00000222790 | <i>RNU4-14P</i> | 5 | 139766908 | 139812029 | 51 | 13 | 1010761 | 5.1177 | 1.55E-07 | 0.0086323 | 1.98E-05 |
| ENSG00000148843 | <i>PDCD11</i> | 10 | 105121405 | 105216049 | 149 | 28 | 1010761 | 5.1164 | 1.56E-07 | 0.0086903 | 1.98E-05 |
| ENSG00000152760 | <i>TCTEX1D1</i> | 1 | 67183143 | 67254470 | 189 | 24 | 1010761 | 5.1155 | 1.56E-07 | 0.0087322 | 1.99E-05 |
| ENSG00000235597 | <i>LINC01102</i> | 2 | 105014725 | 105147290 | 287 | 48 | 1010761 | 5.1136 | 1.58E-07 | 0.0088192 | 2.00E-05 |
| ENSG00000230826 | <i>AL390774.2</i> | 9 | 126463716 | 126524220 | 170 | 22 | 1010761 | 5.1132 | 1.58E-07 | 0.0088388 | 2.00E-05 |
| ENSG00000200818 | <i>RNU6-1204P</i> | 14 | 57256704 | 57301810 | 83 | 25 | 1010761 | 5.112 | 1.59E-07 | 0.0088985 | 2.01E-05 |
| ENSG00000276180 | <i>HIST1H4I</i> | 6 | 27071367 | 27117660 | 82 | 23 | 1010761 | 5.1113 | 1.60E-07 | 0.0089309 | 2.02E-05 |
| ENSG00000136158 | <i>SPRY2</i> | 13 | 80900111 | 80950086 | 133 | 29 | 1010761 | 5.1017 | 1.68E-07 | 0.0093925 | 2.12E-05 |
| ENSG00000225399 | <i>AC121247.1</i> | 3 | 49262518 | 49308749 | 63 | 13 | 1010761 | 5.0954 | 1.74E-07 | 0.0097129 | 2.18E-05 |
| ENSG00000112246 | <i>SIM1</i> | 6 | 100822891 | 100947805 | 327 | 46 | 1010761 | 5.0928 | 1.76E-07 | 0.0098446 | 2.21E-05 |
| ENSG00000208009 | <i>MIR130A</i> | 11 | 57373671 | 57418759 | 78 | 10 | 1010761 | 5.0881 | 1.81E-07 | 0.0100941 | 2.25E-05 |
| ENSG00000107105 | <i>ELAVL2</i> | 9 | 23680102 | 23861335 | 577 | 86 | 1010761 | 5.088 | 1.81E-07 | 0.0100975 | 2.25E-05 |
| ENSG00000217539 | <i>IQCB2P</i> | 6 | 27943501 | 27990133 | 149 | 23 | 1010761 | 5.0834 | 1.85E-07 | 0.0103498 | 2.31E-05 |
| ENSG00000163807 | <i>KIAA1143</i> | 3 | 44780236 | 44838154 | 88 | 17 | 1010761 | 5.0731 | 1.96E-07 | 0.0109236 | 2.42E-05 |
| ENSG00000170209 | <i>ANKK1</i> | 11 | 113223513 | 113281140 | 149 | 17 | 1010761 | 5.0728 | 1.96E-07 | 0.0109392 | 2.42E-05 |
| ENSG00000128713 | <i>HOXD11</i> | 2 | 176937014 | 176984316 | 110 | 24 | 1010761 | 5.0723 | 1.96E-07 | 0.0109666 | 2.42E-05 |
| ENSG00000222326 | | 11 | 61572633 | 61617712 | 90 | 13 | 1010761 | 5.0721 | 1.97E-07 | 0.0109827 | 2.42E-05 |
| ENSG00000110693 | <i>SOX6</i> | 11 | 15977995 | 16532935 | 1162 | 90 | 1010761 | 5.0719 | 1.97E-07 | 0.0109945 | 2.42E-05 |
| ENSG00000225598 | <i>AL606519.1</i> | 1 | 80829049 | 80875306 | 202 | 21 | 1010761 | 5.07 | 1.99E-07 | 0.0111016 | 2.43E-05 |
| ENSG00000173915 | <i>ATP5MD</i> | 10 | 105138798 | 105191223 | 84 | 20 | 1010761 | 5.07 | 1.99E-07 | 0.0111033 | 2.43E-05 |
| ENSG00000204540 | <i>PSORS1C1</i> | 6 | 31047608 | 31117869 | 389 | 43 | 1010761 | 5.0685 | 2.00E-07 | 0.0111893 | 2.45E-05 |
| ENSG00000238711 | <i>RNY4P25</i> | 1 | 151376476 | 151421571 | 75 | 9 | 1010761 | 5.0674 | 2.02E-07 | 0.0112563 | 2.46E-05 |

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|-----------------|------------------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000204542 | <i>C6orf15</i> | 6 | 31069000 | 31115336 | 370 | 39 | 1010761 | 5.0667 | 2.02E-07 | 0.0112948 | 2.46E-05 |
| ENSG00000238211 | <i>POLR2LP1</i> | 6 | 31073504 | 31118690 | 370 | 39 | 1010761 | 5.0662 | 2.03E-07 | 0.0113244 | 2.46E-05 |
| ENSG00000204539 | <i>CDSN</i> | 6 | 31072867 | 31123223 | 379 | 41 | 1010761 | 5.0655 | 2.04E-07 | 0.0113701 | 2.46E-05 |
| ENSG00000077063 | <i>CTTNBP2</i> | 7 | 117340705 | 117548561 | 472 | 76 | 1010761 | 5.0654 | 2.04E-07 | 0.0113724 | 2.46E-05 |
| ENSG00000201444 | <i>RNU6-1082P</i> | 9 | 120460274 | 120505380 | 133 | 30 | 1010761 | 5.064 | 2.05E-07 | 0.0114561 | 2.47E-05 |
| ENSG00000216193 | | 2 | 176938371 | 176983458 | 105 | 22 | 1010761 | 5.0548 | 2.15E-07 | 0.0120243 | 2.59E-05 |
| ENSG00000188981 | <i>MSANTD1</i> | 4 | 3211096 | 3274268 | 211 | 25 | 1010761 | 5.0547 | 2.16E-07 | 0.0120316 | 2.59E-05 |
| ENSG00000231304 | <i>SGO1-AS1</i> | 3 | 20180736 | 21197459 | 4167 | 285 | 1010761 | 5.0509 | 2.20E-07 | 0.0122738 | 2.63E-05 |
| ENSG00000258358 | <i>AC087888.1</i> | 12 | 84832404 | 84878657 | 136 | 19 | 1010761 | 5.0487 | 2.22E-07 | 0.0124117 | 2.66E-05 |
| ENSG00000268241 | | 2 | 175190601 | 175237151 | 107 | 20 | 1010761 | 5.0476 | 2.24E-07 | 0.0124848 | 2.67E-05 |
| ENSG00000101445 | <i>PPP1R16B</i> | 20 | 37399348 | 37561667 | 489 | 59 | 1010761 | 5.0419 | 2.30E-07 | 0.012861 | 2.74E-05 |
| ENSG00000280414 | <i>AC018470.1</i> | 2 | 175189166 | 175237294 | 111 | 20 | 1010761 | 5.0417 | 2.31E-07 | 0.0128755 | 2.74E-05 |
| ENSG00000268525 | | 19 | 42572740 | 42619259 | 38 | 16 | 1010761 | 5.0397 | 2.33E-07 | 0.0130106 | 2.75E-05 |
| ENSG00000223305 | <i>RN7SKP30</i> | 4 | 56396669 | 56442002 | 173 | 13 | 1010761 | 5.0396 | 2.33E-07 | 0.0130195 | 2.75E-05 |
| ENSG00000110917 | <i>MLEC</i> | 12 | 121089672 | 121149667 | 221 | 38 | 1010761 | 5.0394 | 2.33E-07 | 0.0130324 | 2.75E-05 |
| ENSG00000219770 | <i>VN1R11P</i> | 6 | 27016059 | 27061926 | 102 | 18 | 1010761 | 5.0391 | 2.34E-07 | 0.0130569 | 2.75E-05 |
| ENSG00000146007 | <i>ZMAT2</i> | 5 | 140044919 | 140096261 | 98 | 10 | 1010761 | 5.0319 | 2.43E-07 | 0.0135548 | 2.85E-05 |
| ENSG00000259275 | <i>AC087477.2</i> | 15 | 96862466 | 96957033 | 243 | 45 | 1010761 | 5.0259 | 2.51E-07 | 0.0139835 | 2.93E-05 |
| ENSG00000264583 | <i>MIR4487</i> | 11 | 47387521 | 47432593 | 126 | 15 | 1010761 | 5.0257 | 2.51E-07 | 0.0139986 | 2.93E-05 |
| ENSG00000159377 | <i>PSMB4</i> | 1 | 151337010 | 151384420 | 89 | 24 | 1010761 | 5.0243 | 2.53E-07 | 0.0141052 | 2.95E-05 |
| ENSG00000199546 | <i>RF00019</i> | 3 | 49272565 | 49317672 | 62 | 12 | 1010761 | 5.0222 | 2.55E-07 | 0.0142559 | 2.98E-05 |
| ENSG00000048740 | <i>CELF2</i> | 10 | 10805360 | 11388674 | 2003 | 205 | 1010761 | 5.0169 | 2.63E-07 | 0.0146595 | 3.05E-05 |
| ENSG00000131503 | <i>ANKHD1</i> | 5 | 139746399 | 139929441 | 178 | 31 | 1010761 | 5.0134 | 2.67E-07 | 0.0149213 | 3.10E-05 |
| ENSG00000242976 | <i>RN7SL177P</i> | 5 | 153099942 | 153145238 | 191 | 17 | 1010761 | 5.0128 | 2.68E-07 | 0.0149682 | 3.11E-05 |
| ENSG00000197692 | <i>CBX3P7</i> | 11 | 89016913 | 89062414 | 94 | 14 | 1010761 | 5.0106 | 2.71E-07 | 0.0151457 | 3.13E-05 |
| ENSG00000255197 | <i>AC090559.1</i> | 11 | 47394699 | 47465741 | 202 | 19 | 1010761 | 5.0104 | 2.72E-07 | 0.0151596 | 3.13E-05 |
| ENSG00000281195 | <i>AC007878.1</i> | 2 | 71566068 | 71613450 | 169 | 22 | 1010761 | 5.0088 | 2.74E-07 | 0.0152824 | 3.15E-05 |
| ENSG00000204970 | <i>PCDHA1</i> | 5 | 140130721 | 140401932 | 712 | 50 | 1010761 | 5.0068 | 2.77E-07 | 0.0154443 | 3.18E-05 |
| ENSG00000252906 | <i>SCARNA3</i> | 1 | 175927534 | 175972676 | 113 | 20 | 1010761 | 5.0049 | 2.80E-07 | 0.0156011 | 3.20E-05 |
| ENSG00000140009 | <i>ESR2</i> | 14 | 64540950 | 64839830 | 819 | 87 | 1010761 | 5.0018 | 2.84E-07 | 0.0158512 | 3.25E-05 |
| ENSG00000279297 | <i>AP000720.1</i> | 11 | 88995885 | 89041367 | 96 | 18 | 1010761 | 5.0001 | 2.87E-07 | 0.0159958 | 3.27E-05 |
| ENSG00000200376 | <i>RNU5E-10P</i> | 11 | 47588023 | 47633140 | 62 | 18 | 1010761 | 4.998 | 2.90E-07 | 0.0161632 | 3.30E-05 |
| ENSG00000254996 | <i>ANKHD1-EIF4EBP3</i> | 5 | 139746493 | 139939154 | 191 | 32 | 1010761 | 4.9925 | 2.98E-07 | 0.0166366 | 3.38E-05 |
| ENSG00000118058 | <i>KMT2A</i> | 11 | 118272205 | 118407547 | 184 | 27 | 1010761 | 4.9924 | 2.98E-07 | 0.0166472 | 3.38E-05 |
| ENSG00000221767 | | 10 | 105144010 | 105189158 | 71 | 18 | 1010761 | 4.9887 | 3.04E-07 | 0.0169625 | 3.44E-05 |
| ENSG00000231952 | <i>DPY19L1P2</i> | 7 | 32817369 | 32888182 | 307 | 24 | 1010761 | 4.9858 | 3.09E-07 | 0.0172204 | 3.49E-05 |
| ENSG00000255082 | <i>GRM5-AS1</i> | 11 | 88202744 | 88267222 | 207 | 24 | 1010761 | 4.9846 | 3.10E-07 | 0.0173293 | 3.50E-05 |
| ENSG00000266594 | <i>MIR4766</i> | 22 | 41199887 | 41244962 | 75 | 18 | 1010761 | 4.9834 | 3.12E-07 | 0.0174348 | 3.52E-05 |
| ENSG00000177125 | <i>ZBTB34</i> | 9 | 129587944 | 129658157 | 143 | 38 | 1010761 | 4.9828 | 3.13E-07 | 0.0174878 | 3.52E-05 |
| ENSG00000248458 | <i>AL139147.1</i> | 1 | 67121547 | 67177710 | 191 | 21 | 1010761 | 4.9819 | 3.15E-07 | 0.0175715 | 3.53E-05 |
| ENSG00000213055 | <i>EEF1B2P7</i> | 2 | 233584233 | 233629908 | 119 | 14 | 1010761 | 4.9797 | 3.18E-07 | 0.0177708 | 3.56E-05 |
| ENSG00000232493 | <i>RPL12P11</i> | 20 | 40141061 | 40186561 | 117 | 14 | 1010761 | 4.9777 | 3.22E-07 | 0.0179578 | 3.59E-05 |

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|-----------------|------------|----|-----------|-----------|------|-----|---------|--------|----------|-----------|----------|
| ENSG00000173611 | SCAI | 9 | 127694887 | 127940775 | 479 | 38 | 1010761 | 4.9732 | 3.29E-07 | 0.0183758 | 3.67E-05 |
| ENSG00000196666 | FAM180B | 11 | 47573245 | 47620746 | 63 | 20 | 1010761 | 4.9715 | 3.32E-07 | 0.018545 | 3.68E-05 |
| ENSG00000228655 | AC096558.1 | 2 | 144042990 | 144273358 | 617 | 70 | 1010761 | 4.9706 | 3.34E-07 | 0.018632 | 3.68E-05 |
| ENSG00000256637 | LINC01965 | 2 | 104455768 | 104704236 | 602 | 87 | 1010761 | 4.9705 | 3.34E-07 | 0.0186365 | 3.68E-05 |
| ENSG00000246662 | LINC00535 | 8 | 94215531 | 94747661 | 1153 | 112 | 1010761 | 4.9705 | 3.34E-07 | 0.0186387 | 3.68E-05 |
| ENSG00000134852 | CLOCK | 4 | 56284070 | 56448305 | 605 | 26 | 1010761 | 4.9704 | 3.34E-07 | 0.0186482 | 3.68E-05 |
| ENSG00000112855 | HARS2 | 5 | 140036011 | 140088876 | 99 | 10 | 1010761 | 4.9701 | 3.35E-07 | 0.0186756 | 3.68E-05 |
| ENSG00000163050 | COQ8A | 1 | 227050237 | 227185246 | 370 | 57 | 1010761 | 4.9685 | 3.37E-07 | 0.018828 | 3.71E-05 |
| ENSG00000199990 | VTRNA1-1 | 5 | 140055860 | 140100958 | 93 | 10 | 1010761 | 4.967 | 3.40E-07 | 0.0189764 | 3.73E-05 |
| ENSG00000148704 | VAX1 | 10 | 118878032 | 118932812 | 112 | 19 | 1010761 | 4.9631 | 3.47E-07 | 0.0193655 | 3.80E-05 |
| ENSG00000238391 | RNA5SP233 | 7 | 73891758 | 73936870 | 139 | 18 | 1010761 | 4.9569 | 3.58E-07 | 0.0199929 | 3.91E-05 |
| ENSG00000153956 | CACNA2D1 | 7 | 81565760 | 82108114 | 1785 | 196 | 1010761 | 4.9559 | 3.60E-07 | 0.0200883 | 3.92E-05 |
| ENSG00000256453 | DND1 | 5 | 140040379 | 140088171 | 89 | 9 | 1010761 | 4.9548 | 3.62E-07 | 0.020205 | 3.94E-05 |
| ENSG00000221629 | | 11 | 31192306 | 31237441 | 92 | 12 | 1010761 | 4.954 | 3.63E-07 | 0.0202882 | 3.95E-05 |
| ENSG00000110931 | CAMKK2 | 12 | 121665494 | 121771111 | 317 | 56 | 1010761 | 4.9533 | 3.65E-07 | 0.0203607 | 3.95E-05 |
| ENSG00000119616 | FCF1 | 14 | 75144847 | 75215323 | 93 | 12 | 1010761 | 4.9511 | 3.69E-07 | 0.0205918 | 3.99E-05 |
| ENSG00000237425 | RPSAP2 | 6 | 28664794 | 28710681 | 84 | 18 | 1010761 | 4.9454 | 3.80E-07 | 0.0212069 | 4.10E-05 |
| ENSG00000135503 | ACVR1B | 12 | 52310451 | 52400862 | 223 | 41 | 1010761 | 4.9434 | 3.84E-07 | 0.021428 | 4.13E-05 |
| ENSG00000176349 | AC104129.1 | 7 | 1843222 | 1899567 | 323 | 26 | 1010761 | 4.9431 | 3.84E-07 | 0.0214598 | 4.13E-05 |
| ENSG00000206671 | RNU6-471P | 6 | 27529191 | 27574296 | 89 | 25 | 1010761 | 4.9399 | 3.91E-07 | 0.0218181 | 4.20E-05 |
| ENSG00000198948 | MFAP3L | 4 | 170897748 | 170988363 | 256 | 35 | 1010761 | 4.9389 | 3.93E-07 | 0.021927 | 4.21E-05 |
| ENSG00000276188 | AC069234.4 | 12 | 121111915 | 121157326 | 163 | 29 | 1010761 | 4.9381 | 3.94E-07 | 0.0220129 | 4.22E-05 |
| ENSG00000107249 | GLIS3 | 9 | 3814127 | 4334916 | 2400 | 271 | 1010761 | 4.9357 | 3.99E-07 | 0.0222848 | 4.26E-05 |
| ENSG00000168268 | NT5DC2 | 3 | 52548403 | 52604070 | 119 | 17 | 1010761 | 4.9318 | 4.07E-07 | 0.0227403 | 4.34E-05 |
| ENSG0000048828 | FAM120A | 9 | 96179004 | 96338389 | 496 | 44 | 1010761 | 4.9295 | 4.12E-07 | 0.0230037 | 4.38E-05 |
| ENSG00000115520 | COQ10B | 2 | 198283147 | 198350032 | 80 | 14 | 1010761 | 4.9263 | 4.19E-07 | 0.0233872 | 4.45E-05 |
| ENSG00000249924 | AC097467.1 | 4 | 156197314 | 156243288 | 154 | 21 | 1010761 | 4.9258 | 4.20E-07 | 0.023448 | 4.45E-05 |
| ENSG00000249504 | PCDHA14 | 5 | 140205809 | 140253106 | 110 | 20 | 1010761 | 4.9239 | 4.24E-07 | 0.0236735 | 4.48E-05 |
| ENSG00000170445 | HARS | 5 | 140042758 | 140106609 | 131 | 12 | 1010761 | 4.9181 | 4.37E-07 | 0.024393 | 4.61E-05 |
| ENSG00000048471 | SNX29 | 16 | 12035595 | 12678146 | 3179 | 228 | 1010761 | 4.9176 | 4.38E-07 | 0.0244561 | 4.61E-05 |
| ENSG00000223944 | AL353604.1 | 1 | 37718340 | 37825701 | 427 | 55 | 1010761 | 4.9164 | 4.41E-07 | 0.0245962 | 4.63E-05 |
| ENSG00000164483 | SAMD3 | 6 | 130455460 | 130721570 | 1244 | 67 | 1010761 | 4.916 | 4.42E-07 | 0.0246537 | 4.63E-05 |
| ENSG00000234207 | AC096570.1 | 2 | 22565466 | 22714876 | 435 | 47 | 1010761 | 4.9158 | 4.42E-07 | 0.0246771 | 4.63E-05 |
| ENSG00000165588 | OTX2 | 14 | 57256623 | 57312197 | 119 | 28 | 1010761 | 4.9126 | 4.49E-07 | 0.0250813 | 4.70E-05 |
| ENSG00000113068 | PFDN1 | 5 | 139614624 | 139717706 | 194 | 17 | 1010761 | 4.9102 | 4.55E-07 | 0.0253877 | 4.75E-05 |
| ENSG00000196653 | ZNF502 | 3 | 44719135 | 44775323 | 136 | 20 | 1010761 | 4.9092 | 4.57E-07 | 0.0255261 | 4.76E-05 |
| ENSG00000283563 | AC098650.1 | 3 | 28355669 | 29819028 | 5177 | 449 | 1010761 | 4.9089 | 4.58E-07 | 0.0255591 | 4.76E-05 |
| ENSG00000235582 | AL365258.2 | 1 | 197669766 | 197715237 | 52 | 11 | 1010761 | 4.907 | 4.62E-07 | 0.0258069 | 4.80E-05 |
| ENSG00000131323 | TRAF3 | 14 | 103208813 | 103387837 | 564 | 51 | 1010761 | 4.9004 | 4.78E-07 | 0.0266866 | 4.95E-05 |
| ENSG00000168273 | SMIM4 | 3 | 52535618 | 52623253 | 200 | 20 | 1010761 | 4.8971 | 4.86E-07 | 0.0271432 | 5.02E-05 |
| ENSG00000048342 | CC2D2A | 4 | 15436489 | 15613180 | 441 | 59 | 1010761 | 4.897 | 4.87E-07 | 0.0271649 | 5.02E-05 |
| ENSG00000120314 | WDR55 | 5 | 140009261 | 140061930 | 114 | 16 | 1010761 | 4.8925 | 4.98E-07 | 0.0277935 | 5.13E-05 |

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|-----------------|-------------|----|-----------|-----------|-----|----|---------|--------|----------|-----------|----------|
| ENSG00000202515 | VTRNA1-3 | 5 | 140070743 | 140115831 | 109 | 10 | 1010761 | 4.8908 | 5.02E-07 | 0.0280251 | 5.16E-05 |
| ENSG00000175886 | RPL7AP66 | 18 | 36904836 | 36950636 | 155 | 23 | 1010761 | 4.8901 | 5.04E-07 | 0.028125 | 5.16E-05 |
| ENSG00000166126 | AMN | 14 | 103353993 | 103407529 | 151 | 33 | 1010761 | 4.8901 | 5.04E-07 | 0.0281323 | 5.16E-05 |
| ENSG00000281706 | LINC01012 | 6 | 27626814 | 27688001 | 191 | 26 | 1010761 | 4.889 | 5.07E-07 | 0.0282807 | 5.18E-05 |
| ENSG00000105732 | ZNF574 | 19 | 42537629 | 42595701 | 49 | 14 | 1010761 | 4.8879 | 5.09E-07 | 0.028437 | 5.20E-05 |
| ENSG00000115561 | CHMP3 | 2 | 86720554 | 86825602 | 291 | 28 | 1010761 | 4.8858 | 5.15E-07 | 0.0287552 | 5.25E-05 |
| ENSG00000113073 | SLC4A9 | 5 | 139704787 | 139764728 | 97 | 24 | 1010761 | 4.8817 | 5.26E-07 | 0.0293513 | 5.35E-05 |
| ENSG00000182952 | HMGNA4 | 6 | 26503633 | 26556482 | 133 | 11 | 1010761 | 4.8813 | 5.27E-07 | 0.02942 | 5.35E-05 |
| ENSG00000123444 | KBTBD4 | 11 | 47583749 | 47635567 | 73 | 19 | 1010761 | 4.8795 | 5.32E-07 | 0.0296846 | 5.39E-05 |
| ENSG00000273305 | AC009237.15 | 2 | 96168717 | 96214217 | 40 | 11 | 1010761 | 4.8791 | 5.33E-07 | 0.0297387 | 5.39E-05 |
| ENSG00000199781 | RF00019 | 2 | 233658363 | 233703461 | 106 | 18 | 1010761 | 4.8777 | 5.37E-07 | 0.0299598 | 5.42E-05 |
| ENSG00000255384 | AP001267.2 | 11 | 118293836 | 118340921 | 58 | 15 | 1010761 | 4.8746 | 5.45E-07 | 0.0304309 | 5.49E-05 |
| ENSG00000277423 | AC069234.5 | 12 | 121106670 | 121152085 | 157 | 30 | 1010761 | 4.8741 | 5.47E-07 | 0.0305112 | 5.50E-05 |
| ENSG00000214237 | MINDY4B | 3 | 150578832 | 150658226 | 248 | 59 | 1010761 | 4.8719 | 5.53E-07 | 0.0308478 | 5.55E-05 |
| ENSG00000067560 | RHOA | 3 | 49386578 | 49484635 | 181 | 18 | 1010761 | 4.8698 | 5.58E-07 | 0.0311699 | 5.60E-05 |
| ENSG00000204969 | PCDHA2 | 5 | 140139437 | 140401929 | 662 | 49 | 1010761 | 4.8694 | 5.60E-07 | 0.031233 | 5.60E-05 |
| ENSG00000214435 | AS3MT | 10 | 104594273 | 104671656 | 249 | 24 | 1010761 | 4.869 | 5.61E-07 | 0.0312966 | 5.60E-05 |
| ENSG00000197381 | ADARB1 | 21 | 46459515 | 46656475 | 605 | 66 | 1010761 | 4.8669 | 5.67E-07 | 0.0316365 | 5.65E-05 |
| ENSG00000143442 | POGZ | 1 | 151365200 | 151466941 | 185 | 17 | 1010761 | 4.866 | 5.69E-07 | 0.0317794 | 5.66E-05 |
| ENSG00000131495 | NDUFA2 | 5 | 140014870 | 140062370 | 101 | 14 | 1010761 | 4.8657 | 5.70E-07 | 0.0318313 | 5.66E-05 |
| ENSG00000259503 | AC048383.1 | 15 | 70578915 | 70629081 | 175 | 18 | 1010761 | 4.8643 | 5.74E-07 | 0.032058 | 5.69E-05 |
| ENSG00000113070 | HBEGF | 5 | 139702428 | 139761216 | 97 | 23 | 1010761 | 4.8634 | 5.77E-07 | 0.0322048 | 5.71E-05 |
| ENSG00000113580 | NR3C1 | 5 | 142647496 | 142850077 | 380 | 49 | 1010761 | 4.8573 | 5.95E-07 | 0.0332145 | 5.88E-05 |
| ENSG00000235102 | ADI1P1 | 20 | 39924763 | 39970300 | 113 | 20 | 1010761 | 4.8567 | 5.97E-07 | 0.0333077 | 5.88E-05 |
| ENSG00000202111 | VTRNA1-2 | 5 | 140063510 | 140108598 | 101 | 9 | 1010761 | 4.8566 | 5.97E-07 | 0.0333278 | 5.88E-05 |
| ENSG00000199289 | RNU6-502P | 6 | 26509579 | 26554686 | 113 | 11 | 1010761 | 4.8555 | 6.00E-07 | 0.0335064 | 5.90E-05 |
| ENSG00000275130 | AL592227.1 | 9 | 11608496 | 11653621 | 284 | 32 | 1010761 | 4.8534 | 6.07E-07 | 0.033867 | 5.95E-05 |
| ENSG00000251339 | AC017091.1 | 4 | 59636791 | 59884870 | 933 | 71 | 1010761 | 4.8531 | 6.08E-07 | 0.0339279 | 5.95E-05 |
| ENSG00000214670 | | 14 | 75148879 | 75214800 | 88 | 12 | 1010761 | 4.8519 | 6.11E-07 | 0.0341321 | 5.98E-05 |
| ENSG00000163440 | PDCL2 | 4 | 56412692 | 56493379 | 281 | 24 | 1010761 | 4.8494 | 6.19E-07 | 0.0345631 | 6.04E-05 |
| ENSG00000223212 | RNU4-74P | 7 | 140717049 | 140762209 | 89 | 13 | 1010761 | 4.8474 | 6.25E-07 | 0.0349114 | 6.09E-05 |
| ENSG00000232630 | PRPS1P2 | 9 | 127877932 | 127923868 | 113 | 10 | 1010761 | 4.8467 | 6.28E-07 | 0.0350437 | 6.11E-05 |
| ENSG00000267414 | AC120049.1 | 18 | 42246892 | 42294682 | 59 | 19 | 1010761 | 4.8443 | 6.35E-07 | 0.0354656 | 6.17E-05 |
| ENSG00000221518 | RNU6ATAC16P | 3 | 52559586 | 52604723 | 96 | 14 | 1010761 | 4.8439 | 6.37E-07 | 0.0355376 | 6.17E-05 |
| ENSG00000149131 | SERPING1 | 11 | 57329991 | 57392326 | 141 | 21 | 1010761 | 4.8436 | 6.38E-07 | 0.0355879 | 6.17E-05 |
| ENSG00000204516 | MICB | 6 | 31427658 | 31488901 | 264 | 35 | 1010761 | 4.8429 | 6.40E-07 | 0.0357146 | 6.18E-05 |
| ENSG00000237761 | AL161646.2 | 10 | 106340860 | 106386731 | 102 | 16 | 1010761 | 4.8415 | 6.44E-07 | 0.0359568 | 6.21E-05 |
| ENSG00000091656 | ZFHX4 | 8 | 77558454 | 77789521 | 513 | 63 | 1010761 | 4.8384 | 6.55E-07 | 0.0365385 | 6.29E-05 |
| ENSG00000241388 | HNF1A-AS1 | 12 | 121369531 | 121453768 | 318 | 38 | 1010761 | 4.8381 | 6.55E-07 | 0.036582 | 6.29E-05 |
| ENSG00000028277 | POU2F2 | 19 | 42580262 | 42671630 | 95 | 12 | 1010761 | 4.838 | 6.56E-07 | 0.036606 | 6.29E-05 |
| ENSG00000271071 | AL513548.2 | 6 | 26602131 | 26648337 | 136 | 15 | 1010761 | 4.837 | 6.59E-07 | 0.0367908 | 6.31E-05 |
| ENSG00000237153 | AL162725.2 | 9 | 16983706 | 17122813 | 523 | 40 | 1010761 | 4.8353 | 6.65E-07 | 0.0371 | 6.35E-05 |

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|-----------------|--------------------|----|-----------|-----------|-----|----|---------|--------|----------|-----------|----------|
| ENSG00000272969 | <i>AC024243.1</i> | 4 | 56378279 | 56424056 | 184 | 13 | 1010761 | 4.8349 | 6.66E-07 | 0.0371793 | 6.36E-05 |
| ENSG00000237169 | <i>RPL12P27</i> | 10 | 99058895 | 99104715 | 159 | 16 | 1010761 | 4.8341 | 6.69E-07 | 0.0373216 | 6.37E-05 |
| ENSG00000224315 | <i>RPL7P7</i> | 1 | 8836270 | 8881972 | 76 | 16 | 1010761 | 4.833 | 6.72E-07 | 0.0375281 | 6.39E-05 |
| ENSG00000258332 | <i>LINC02394</i> | 12 | 74397866 | 74449608 | 142 | 28 | 1010761 | 4.8274 | 6.92E-07 | 0.0386009 | 6.56E-05 |
| ENSG00000139970 | <i>RTN1</i> | 14 | 60052695 | 60372684 | 686 | 58 | 1010761 | 4.8267 | 6.94E-07 | 0.0387483 | 6.58E-05 |
| ENSG00000243056 | <i>EIF4EBP3</i> | 5 | 139892251 | 139939163 | 49 | 14 | 1010761 | 4.8259 | 6.97E-07 | 0.0389018 | 6.59E-05 |
| ENSG00000183798 | <i>EMILIN3</i> | 20 | 39978606 | 40030467 | 134 | 26 | 1010761 | 4.8245 | 7.02E-07 | 0.0391647 | 6.63E-05 |
| ENSG00000235332 | <i>RPSAP76</i> | 9 | 127946928 | 127993100 | 122 | 16 | 1010761 | 4.8195 | 7.19E-07 | 0.0401566 | 6.78E-05 |
| ENSG00000259542 | <i>AC087477.5</i> | 15 | 96926375 | 96983419 | 152 | 26 | 1010761 | 4.8191 | 7.21E-07 | 0.0402532 | 6.79E-05 |
| ENSG00000124160 | <i>NCOA5</i> | 20 | 44679624 | 44753591 | 209 | 32 | 1010761 | 4.8161 | 7.32E-07 | 0.0408593 | 6.88E-05 |
| ENSG00000119414 | <i>PPP6C</i> | 9 | 127898852 | 127987218 | 232 | 21 | 1010761 | 4.8157 | 7.33E-07 | 0.0409358 | 6.88E-05 |
| ENSG00000207196 | <i>RF00019</i> | 11 | 70541272 | 70586374 | 102 | 17 | 1010761 | 4.8112 | 7.50E-07 | 0.0418724 | 7.03E-05 |
| ENSG00000225499 | <i>RPL15P4</i> | 6 | 31460891 | 31506470 | 243 | 30 | 1010761 | 4.8107 | 7.52E-07 | 0.0419757 | 7.03E-05 |
| ENSG00000265565 | <i>MIR3143</i> | 6 | 27080405 | 27125467 | 81 | 23 | 1010761 | 4.8104 | 7.53E-07 | 0.0420332 | 7.03E-05 |
| ENSG00000197251 | <i>LINC00336</i> | 6 | 33543883 | 33596115 | 277 | 39 | 1010761 | 4.81 | 7.55E-07 | 0.0421158 | 7.03E-05 |
| ENSG00000201680 | <i>RF00019</i> | 6 | 31454466 | 31499567 | 244 | 30 | 1010761 | 4.8085 | 7.61E-07 | 0.0424501 | 7.08E-05 |
| ENSG00000170946 | <i>DNAJC24</i> | 11 | 31356387 | 31463396 | 170 | 20 | 1010761 | 4.8056 | 7.72E-07 | 0.0430658 | 7.16E-05 |
| ENSG00000255408 | <i>PCDHA3</i> | 5 | 140145613 | 140401929 | 646 | 48 | 1010761 | 4.8053 | 7.73E-07 | 0.0431283 | 7.16E-05 |
| ENSG00000201080 | | 10 | 104593178 | 104638276 | 137 | 17 | 1010761 | 4.8023 | 7.84E-07 | 0.0437848 | 7.25E-05 |
| ENSG00000229689 | <i>AC009237.3</i> | 2 | 96156093 | 96208153 | 49 | 12 | 1010761 | 4.8022 | 7.85E-07 | 0.0437959 | 7.25E-05 |
| ENSG00000235908 | <i>RHOA-IT1</i> | 3 | 49392578 | 49439439 | 87 | 12 | 1010761 | 4.8011 | 7.89E-07 | 0.0440354 | 7.28E-05 |
| ENSG00000238585 | <i>RF00019</i> | 4 | 56357762 | 56402875 | 191 | 13 | 1010761 | 4.8002 | 7.92E-07 | 0.0442346 | 7.30E-05 |
| ENSG00000149654 | <i>CDH22</i> | 20 | 44792372 | 44972137 | 503 | 95 | 1010761 | 4.7989 | 7.98E-07 | 0.0445149 | 7.33E-05 |
| ENSG00000256851 | <i>AL663061.1</i> | 6 | 31448756 | 31493988 | 244 | 30 | 1010761 | 4.798 | 8.01E-07 | 0.0447342 | 7.36E-05 |
| ENSG00000179152 | <i>TCAIM</i> | 3 | 44344611 | 44460943 | 248 | 24 | 1010761 | 4.7967 | 8.06E-07 | 0.0450072 | 7.37E-05 |
| ENSG00000259614 | <i>AC087477.6</i> | 15 | 96921443 | 96967285 | 134 | 19 | 1010761 | 4.7967 | 8.06E-07 | 0.0450077 | 7.37E-05 |
| ENSG00000172469 | <i>MANEA</i> | 6 | 95990419 | 96067333 | 265 | 21 | 1010761 | 4.7967 | 8.07E-07 | 0.0450211 | 7.37E-05 |
| ENSG00000270316 | <i>BORCS7-ASMT</i> | 10 | 104579029 | 104671656 | 288 | 28 | 1010761 | 4.7961 | 8.09E-07 | 0.0451478 | 7.38E-05 |
| ENSG00000274997 | <i>HIST1H2AH</i> | 6 | 27079908 | 27125294 | 83 | 23 | 1010761 | 4.787 | 8.46E-07 | 0.0472466 | 7.71E-05 |
| ENSG00000229716 | <i>RPL23AP19</i> | 1 | 8856066 | 8901434 | 89 | 14 | 1010761 | 4.7844 | 8.57E-07 | 0.0478584 | 7.79E-05 |
| ENSG00000261366 | <i>MANEA-AS1</i> | 6 | 96013059 | 96060326 | 173 | 14 | 1010761 | 4.7838 | 8.60E-07 | 0.0480152 | 7.80E-05 |
| ENSG00000030110 | <i>BAK1</i> | 6 | 33530324 | 33583070 | 267 | 40 | 1010761 | 4.7835 | 8.61E-07 | 0.0480749 | 7.80E-05 |
| ENSG00000243396 | <i>AC084198.1</i> | 3 | 101308087 | 101353488 | 107 | 15 | 1010761 | 4.7833 | 8.62E-07 | 0.0481207 | 7.80E-05 |
| ENSG00000228423 | <i>AL357552.2</i> | 1 | 8855919 | 8902110 | 91 | 15 | 1010761 | 4.783 | 8.64E-07 | 0.0482028 | 7.80E-05 |
| ENSG00000237308 | <i>AC009237.10</i> | 2 | 96151770 | 96197279 | 41 | 11 | 1010761 | 4.7807 | 8.74E-07 | 0.0487632 | 7.88E-05 |
| ENSG00000283189 | <i>AC104452.1</i> | 3 | 49444227 | 49501743 | 92 | 14 | 1010761 | 4.7769 | 8.90E-07 | 0.0496713 | 8.01E-05 |

Gene symbol: the gene ID as specified in the annotation file

CHR: the chromosome the gene is on

START/STOP: the annotation boundaries of the gene on that chromosome (this includes any window around the gene applied during annotation)

NSNPS: the number of SNPs annotated to that gene that were found in the data and were not excluded based on internal SNP QC

NRARE: the number of those SNPs classified as rare (when using the --burden option)

NPARAM: the number of relevant parameters used in the model. For the SNP-wise models this is an approximate value; for the principal components regression (raw data default) this is set to the number of principal components retained after pruning; for the multi- models this is the mean NPARAM value of the component base models

N: the sample size used when analysing that gene; can differ for allosomal chromosomes or when analysing SNP p-value input with variable sample size by SNP (due to missingness or differences in coverage in meta-analysis)

ZSTAT: the Z-value for the gene, based on its (permutation) p-value; this is what is used as the measure of gene association in the gene-level analyses

Pvalue: the two-sided gene p-value of z statistics, using asymptotic sampling distribution

For the complete MAGMA manual, please refer to: de Leeuw C, Mooij J, Heskes T, Posthuma D (2015): MAGMA: Generalized gene-set analysis of GWAS data. *PLoS Comput Biol* 11(4): e1004219.

FDR: false discovery rate

Supplementary Table 15. Genes significant from Hi-C MAGMA annotation after Bonferroni correction.

| ENSG ID | Gene symbol | CHR | START | STOP | NSNPS | NPARAM | N | ZSTAT | P | P.Bonferroni FDR | |
|-----------------|-------------|-----|-----------|-----------|-------|--------|---------|--------|----------|------------------|----------|
| ENSG00000233822 | HIST1H2BN | 6 | 27805538 | 27833576 | 12 | 7 | 1010761 | 8.2924 | 5.55E-17 | 2.97E-12 | 2.97E-12 |
| ENSG00000278677 | HIST1H2AM | 6 | 27860535 | 27860927 | 6 | 4 | 1010761 | 7.9726 | 7.77E-16 | 4.16E-11 | 1.43E-11 |
| ENSG00000275221 | HIST1H2AK | 6 | 27805725 | 27806117 | 6 | 3 | 1010761 | 7.9284 | 1.11E-15 | 5.94E-11 | 1.43E-11 |
| ENSG00000241549 | GUSBP2 | 6 | 26839263 | 26924333 | 694 | 97 | 1010761 | 7.9223 | 1.17E-15 | 6.24E-11 | 1.43E-11 |
| ENSG00000217646 | HIST1H2BPS2 | 6 | 27831840 | 27832179 | 10 | 4 | 1010761 | 7.9057 | 1.33E-15 | 7.13E-11 | 1.43E-11 |
| ENSG00000238610 | RNU7-26P | 6 | 27865282 | 27865344 | 10 | 5 | 1010761 | 7.845 | 2.16E-15 | 1.16E-10 | 1.72E-11 |
| ENSG00000217862 | HIST1H4PS1 | 6 | 27774853 | 27775117 | 10 | 3 | 1010761 | 7.8088 | 2.89E-15 | 1.54E-10 | 1.72E-11 |
| ENSG00000273703 | HIST1H2BM | 6 | 27782822 | 27783202 | 10 | 3 | 1010761 | 7.8088 | 2.89E-15 | 1.54E-10 | 1.72E-11 |
| ENSG00000225510 | PCDH8P1 | 13 | 53774116 | 53776888 | 17 | 4 | 1010761 | 7.8088 | 2.89E-15 | 1.54E-10 | 1.72E-11 |
| ENSG00000137185 | ZSCAN9 | 6 | 28193042 | 28201260 | 27 | 11 | 1010761 | 7.7806 | 3.61E-15 | 1.93E-10 | 1.76E-11 |
| ENSG00000233973 | LINC01360 | 1 | 73771853 | 73820936 | 49 | 9 | 1010761 | 7.7695 | 3.94E-15 | 2.11E-10 | 1.76E-11 |
| ENSG00000184357 | HIST1H1B | 6 | 27834627 | 27835307 | 16 | 5 | 1010761 | 7.7695 | 3.94E-15 | 2.11E-10 | 1.76E-11 |
| ENSG00000258851 | AL139300.2 | 14 | 104019758 | 104028214 | 6 | 2 | 1010761 | 7.7543 | 4.44E-15 | 2.38E-10 | 1.83E-11 |
| ENSG00000276368 | HIST1H2AJ | 6 | 27782132 | 27782518 | 12 | 3 | 1010761 | 7.7285 | 5.44E-15 | 2.91E-10 | 1.89E-11 |
| ENSG00000279056 | AP003400.3 | 11 | 89290028 | 89290373 | 35 | 13 | 1010761 | 7.7272 | 5.50E-15 | 2.94E-10 | 1.89E-11 |
| ENSG00000174572 | RPL10P2 | 6 | 27179023 | 27179692 | 51 | 16 | 1010761 | 7.7234 | 5.66E-15 | 3.03E-10 | 1.89E-11 |
| ENSG00000224843 | LINC00240 | 6 | 26924771 | 26991703 | 307 | 52 | 1010761 | 7.707 | 6.44E-15 | 3.45E-10 | 2.03E-11 |
| ENSG00000197153 | HIST1H3J | 6 | 27858160 | 27858570 | 9 | 4 | 1010761 | 7.6895 | 7.38E-15 | 3.95E-10 | 2.20E-11 |
| ENSG00000261584 | AL513548.1 | 6 | 26686469 | 26688192 | 117 | 35 | 1010761 | 7.6604 | 9.27E-15 | 4.96E-10 | 2.50E-11 |
| ENSG00000086991 | NOX4 | 11 | 89057524 | 89231355 | 444 | 80 | 1010761 | 7.6596 | 9.33E-15 | 4.99E-10 | 2.50E-11 |
| ENSG00000225087 | AL583808.1 | 1 | 73214604 | 73364823 | 37 | 10 | 1010761 | 7.6372 | 1.11E-14 | 5.94E-10 | 2.83E-11 |
| ENSG00000206958 | RF00156 | 5 | 87678589 | 87678724 | 27 | 6 | 1010761 | 7.6297 | 1.18E-14 | 6.30E-10 | 2.86E-11 |
| ENSG00000166682 | TMPRSS5 | 11 | 113558272 | 113577095 | 103 | 32 | 1010761 | 7.6028 | 1.45E-14 | 7.75E-10 | 3.26E-11 |
| ENSG00000149295 | DRD2 | 11 | 113280337 | 113346111 | 162 | 35 | 1010761 | 7.6018 | 1.46E-14 | 7.81E-10 | 3.26E-11 |
| ENSG00000005108 | THSD7A | 7 | 11409984 | 11871824 | 564 | 66 | 1010761 | 7.5919 | 1.58E-14 | 8.44E-10 | 3.37E-11 |
| ENSG00000272312 | AL133255.1 | 6 | 26968987 | 26969427 | 143 | 47 | 1010761 | 7.5582 | 2.04E-14 | 1.09E-09 | 4.21E-11 |
| ENSG00000142599 | RERE | 1 | 8412457 | 8877702 | 380 | 60 | 1010761 | 7.537 | 2.40E-14 | 1.29E-09 | 4.76E-11 |
| ENSG00000256053 | APOPT1 | 14 | 104029299 | 104058524 | 80 | 12 | 1010761 | 7.5111 | 2.93E-14 | 1.57E-09 | 5.60E-11 |
| ENSG00000226314 | ZNF192P1 | 6 | 28129559 | 28137372 | 32 | 6 | 1010761 | 7.4734 | 3.91E-14 | 2.09E-09 | 7.05E-11 |
| ENSG00000250306 | AC091826.1 | 5 | 87678765 | 87679077 | 9 | 3 | 1010761 | 7.4719 | 3.95E-14 | 2.12E-09 | 7.05E-11 |
| ENSG00000219891 | ZSCAN12P1 | 6 | 28058932 | 28061442 | 47 | 16 | 1010761 | 7.4377 | 5.12E-14 | 2.74E-09 | 8.78E-11 |
| ENSG00000278958 | AC091931.1 | 5 | 103770473 | 103771200 | 8 | 4 | 1010761 | 7.4344 | 5.25E-14 | 2.81E-09 | 8.78E-11 |
| ENSG00000280317 | AL732618.1 | 1 | 73444697 | 73444997 | 10 | 2 | 1010761 | 7.4093 | 6.35E-14 | 3.40E-09 | 1.03E-10 |
| ENSG00000206690 | RF00019 | 11 | 87833163 | 87833273 | 25 | 8 | 1010761 | 7.3931 | 7.17E-14 | 3.84E-09 | 1.13E-10 |
| ENSG00000280107 | AL022393.1 | 6 | 28138623 | 28140299 | 15 | 5 | 1010761 | 7.3844 | 7.66E-14 | 4.10E-09 | 1.17E-10 |
| ENSG00000279325 | AL136359.1 | 13 | 53767802 | 53772675 | 19 | 7 | 1010761 | 7.3695 | 8.57E-14 | 4.58E-09 | 1.27E-10 |
| ENSG00000253538 | AC008662.2 | 5 | 163636637 | 163638898 | 79 | 8 | 1010761 | 7.331 | 1.14E-13 | 6.11E-09 | 1.65E-10 |
| ENSG00000232920 | LINC01400 | 9 | 37073528 | 37075789 | 24 | 7 | 1010761 | 7.3278 | 1.17E-13 | 6.26E-09 | 1.65E-10 |
| ENSG00000124635 | HIST1H2BJ | 6 | 27093676 | 27100529 | 75 | 21 | 1010761 | 7.3237 | 1.21E-13 | 6.46E-09 | 1.66E-10 |

Supplementary Table 16. Bi-directional relationship between MD and cardiometabolic outcomes

A. Mendelian Randomisation (MR) results from multiple methods. Instruments selected using the 5x10-8 threshold are highlighted in blue.

| | | MR results | | | | | Pleiotropy | | | | | |
|---|-------------------|------------|------------|----------|--------------|-------------|------------|-----------------|-----------------|----------------------|-------------|------------------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| MD on BMI (African ancestry) | 1 MR Egger | 39 | 0.19706101 | 0.084899 | 0.02589473 | 0.03065995 | 0.363462 | 1.217818 | -0.01459535 | 0.008736636 | 0.1032 | |
| | 2 Weighted median | 39 | 0.06148706 | 0.070748 | 0.38479063 | -0.07717844 | 0.200153 | 1.063417 | | Heterogeneity | | |
| | 3 IVW | 39 | 0.07981394 | 0.048884 | 0.10252856 | -0.01599895 | 0.175627 | 1.083086 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 39 | -0.0530433 | 0.153296 | 0.7312376 | -0.35350374 | 0.247417 | 0.948339 | MR Egger | 38.86904 | 37 | 0.3855 |
| | 5 Weighted mode | 39 | 0.24850275 | 0.13176 | 0.06695295 | -0.00974775 | 0.506753 | 1.282104 | IVW | 41.80089 | 38 | 0.3092 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| MD on BMI (East Asian ancestry) | 1 MR Egger | 23 | -0.115509 | 0.197546 | 0.5649659 | -0.502699 | 0.271681 | 0.8909125 | 0.01159159 | 0.01743668 | 0.5134 | |
| | 2 Weighted median | 23 | -0.0539818 | 0.112604 | 0.6316578 | -0.274686 | 0.166722 | 0.9474493 | | Heterogeneity | | |
| | 3 IVW | 23 | 0.00535952 | 0.077246 | 0.9446854 | -0.1460432 | 0.156762 | 1.0053739 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 23 | 0.26537728 | 0.230735 | 0.2624356 | -0.1868631 | 0.717618 | 1.3039228 | MR Egger | 16.69318 | 21 | 0.7295 |
| | 5 Weighted mode | 23 | -0.1301923 | 0.207555 | 0.5369416 | -0.5370006 | 0.276616 | 0.8779266 | IVW | 17.13511 | 22 | 0.7559 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| MD on BMI (European ancestry) | 1 MR Egger | 113 | 0.03258395 | 0.17786 | 0.8549754 | -0.31602179 | 0.38119 | 1.033121 | 0.001561049 | 0.004554242 | 0.7324 | |
| | 2 Weighted median | 113 | 0.0095802 | 0.02485 | 4.851650e-05 | 0.05225159 | 0.149665 | 1.10623 | | Heterogeneity | | |
| | 3 IVW | 113 | 0.092351 | 0.034943 | 8.220631e-03 | 0.02386187 | 0.16084 | 1.09675 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 113 | 0.26772644 | 0.066204 | 9.683843e-05 | 0.13796693 | 0.397486 | 1.30699 | MR Egger | 1233.803 | 111 | 9E-189 |
| | 5 Weighted mode | 113 | 0.20603526 | 0.074403 | 6.578917e-03 | 0.06020636 | 0.351864 | 1.228797 | IVW | 1235.109 | 112 | 2E-188 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| MD on BMI (Hispanic/Latin American samples) | 1 MR Egger | 35 | 0.26793304 | 0.139283 | 0.06305909 | -0.00506149 | 0.540928 | 1.30726 | -0.02409003 | 0.01731338 | 0.1734 | |
| | 2 Weighted median | 35 | 0.21043604 | 0.149856 | 0.16024171 | -0.08328087 | 0.504153 | 1.234216 | | Heterogeneity | | |
| | 3 IVW | 35 | 0.12763136 | 0.096084 | 0.18407066 | -0.06069409 | 0.315957 | 1.136134 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 35 | 0.04608757 | 0.282977 | 0.87158724 | -0.50854638 | 0.600722 | 1.047166 | MR Egger | 21.40243 | 33 | 0.9401 |
| | 5 Weighted mode | 35 | 0.22679585 | 0.136378 | 0.10550704 | -0.04050555 | 0.494097 | 1.254574 | IVW | 23.33846 | 34 | 0.9157 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| MD on BMI (South Asian ancestry) | 1 MR Egger | 11 | 0.12222485 | 0.282515 | 0.6754648 | -0.43150539 | 0.675955 | 1.1300082 | -0.0151131 | 0.04253335 | 0.7305 | |
| | 2 Weighted median | 11 | 0.02003047 | 0.053506 | 0.7081367 | -0.08484119 | 0.124902 | 1.0202324 | | Heterogeneity | | |
| | 3 IVW | 11 | 0.02338169 | 0.047112 | 0.6196828 | -0.06895786 | 0.115721 | 1.0236572 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 11 | -0.0034138 | 0.097327 | 0.9727094 | -0.1941743 | 0.187347 | 0.996592 | MR Egger | 17.62269 | 9 | 0.0398 |
| | 5 Weighted mode | 11 | -0.011476 | 0.0955 | 0.9067308 | -0.19865696 | 0.175705 | 0.9885896 | IVW | 17.86991 | 10 | 0.0572 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| BMI on MD (African ancestry) | 1 MR Egger | 31 | 0.02288984 | 0.04511 | 0.6156968 | -0.06552604 | 0.111306 | 1.0231538 | -0.001777147 | 0.007102188 | 0.8042 | |
| | 2 Weighted median | 31 | -0.0062746 | 0.036559 | 0.8637279 | -0.07792978 | 0.065381 | 0.993745 | | Heterogeneity | | |
| | 3 IVW | 31 | 0.01343697 | 0.024265 | 0.5797465 | -0.0341228 | 0.060997 | 1.0135277 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 31 | -0.0708856 | 0.07182 | 0.3315431 | -0.21165323 | 0.069882 | 0.9315685 | MR Egger | 33.18401 | 29 | 0.2704 |
| | 5 Weighted mode | 31 | -0.0374145 | 0.058783 | 0.5292886 | -0.15262971 | 0.077801 | 0.9632767 | IVW | 33.25565 | 30 | 0.3116 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| BMI on MD (East Asian ancestry) | 1 MR Egger | 12 | 0.05165011 | 0.084436 | 0.5543839 | -0.11384482 | 0.217145 | 1.053007 | -0.0076976 | 0.01532312 | 0.6263 | |
| | 2 Weighted median | 12 | 0.04507423 | 0.039114 | 0.2491674 | -0.03158968 | 0.121738 | 1.046106 | | Heterogeneity | | |
| | 3 IVW | 12 | 0.01196062 | 0.029893 | 0.6885812 | -0.04660999 | 0.070571 | 1.012053 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 12 | 0.05239065 | 0.060948 | 0.4083577 | -0.06706813 | 0.171849 | 1.053787 | MR Egger | 6.520611 | 10 | 0.7698 |
| | 5 Weighted mode | 12 | 0.04934452 | 0.056355 | 0.399966 | -0.06111205 | 0.159801 | 1.050582 | IVW | 6.772968 | 11 | 0.8172 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| BMI on MD (European ancestry) | 1 MR Egger | 339 | 0.1151204 | 0.053438 | 3.19E-02 | 0.01038249 | 0.219858 | 1.122008 | 0.000616833 | 0.001305646 | 0.6369 | |
| | 2 Weighted median | 339 | 0.1268111 | 0.027994 | 1.38E-05 | 0.06681215 | 0.17655 | 1.129394 | | Heterogeneity | | |
| | 3 IVW | 339 | 0.1382895 | 0.0212 | 6.88E-11 | 0.09673794 | 0.179841 | 1.148308 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 339 | 0.182433 | 0.07364 | 1.37E-02 | 0.03809845 | 0.326768 | 1.200134 | MR Egger | 843.1192 | 337 | ##### |
| | 5 Weighted mode | 339 | 0.1313464 | 0.037454 | 5.15E-04 | 0.05793739 | 0.204756 | 1.140363 | IVW | 843.6776 | 338 | ##### |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| BMI on MD (Hispanic/Latin American samples) | 1 MR Egger | 18 | -0.0142569 | 0.028163 | 0.619603 | -0.06945672 | 0.040943 | 0.9858443 | -0.001011464 | 0.009805163 | 0.9191 | |
| | 2 Weighted median | 18 | -0.022179 | 0.01962 | 0.258292 | -0.06063378 | 0.016276 | 0.9780652 | | Heterogeneity | | |
| | 3 IVW | 18 | -0.0167172 | 0.01411 | 0.2346068 | -0.04442734 | 0.010885 | 0.9833687 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 18 | -0.0276599 | 0.033273 | 0.4173325 | -0.09287586 | 0.037556 | 0.9727191 | MR Egger | 15.95951 | 16 | 0.4558 |
| | 5 Weighted mode | 18 | -0.0305651 | 0.031085 | 0.3392572 | -0.09149128 | 0.030361 | 0.9698973 | IVW | 15.97015 | 17 | 0.526 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| BMI on MD (South Asian ancestry) | 1 MR Egger | 10 | -0.6471249 | 0.663394 | 0.3741249 | -1.9473774 | 0.653128 | 0.5235488 | 0.03559036 | 0.04484561 | 0.4634 | |
| | 2 Weighted median | 10 | -0.18138 | 0.216231 | 0.4015675 | -0.6051928 | 0.242433 | 0.8341183 | | Heterogeneity | | |
| | 3 IVW | 10 | -0.1365626 | 0.161906 | 0.3989652 | -0.4538974 | 0.180772 | 0.8723517 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 10 | 0.07758997 | 0.335647 | 0.8248676 | -0.802783 | 0.735458 | 1.0806795 | MR Egger | 4.410438 | 5 | 0.492 |
| | 5 Weighted mode | 10 | -0.2268987 | 0.312903 | 0.4956616 | -0.8401883 | 0.386391 | 0.7970015 | IVW | 5.04027 | 6 | 0.5387 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| MD on FG (African ancestry) | 1 MR Egger | 42 | -0.047873 | 0.038378 | 0.2195047 | -0.1230941 | 0.027348 | 0.9532549 | 0.00409836 | 0.00406448 | 0.3194 | |
| | 2 Weighted median | 42 | -0.0448345 | 0.029799 | 0.1324394 | -0.1032411 | 0.013572 | 0.9561557 | | Heterogeneity | | |
| | 3 IVW | 42 | -0.0154347 | 0.020932 | 0.4608947 | -0.0564612 | 0.025592 | 0.9846838 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 42 | -0.0443329 | 0.054672 | 0.4221079 | -0.1514892 | 0.062823 | 0.9566354 | MR Egger | 46.94145 | 40 | 0.2093 |
| | 5 Weighted mode | 42 | -0.0370446 | 0.045499 | 0.420244 | -0.1262229 | 0.052134 | 0.9636332 | IVW | 48.13464 | 41 | 0.2064 |
| | | MR results | | | | | Pleiotropy | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |

| | MD on FG (East Asian ancestry) | | | | | | | | | | | |
|--------------------------------|--------------------------------|-------------|------------|------------|-------------|-------------|-----------|-----------------|---------------|-------------|-----------|-----------|
| | 1 | 2 | 3 | 4 | 5 | | | | | | | |
| MD on FG (East Asian ancestry) | 1 MR Egger | 27 | 0.03239451 | 0.035089 | 0.3647278 | -0.03638063 | 0.10117 | 1.032925 | -0.00111941 | 0.003014762 | 0.7135 | |
| | 2 Weighted median | 27 | 0.02870473 | 0.021862 | 0.1891913 | -0.01414549 | 0.071555 | 1.029121 | Heterogeneity | | | |
| | 3 IVW | 27 | 0.02098196 | 0.016645 | 0.2074748 | -0.01164268 | 0.053607 | 1.021204 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 27 | 0.04873522 | 0.034783 | 0.1729976 | -0.01943884 | 0.116909 | 1.049942 | MR Egger | 32.26968 | 25 | 0.1504 |
| | 5 Weighted mode | 27 | 0.03686469 | 0.02926 | 0.2188926 | -0.02048433 | 0.094214 | 1.037553 | IVW | 32.44765 | 26 | 0.1787 |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 113 | 0.02612076 | 0.075008 | 0.7283202 | -0.12089517 | 0.173137 | 1.0264649 | -0.00797744 | 0.001920614 | 0.6787 | | |
| 2 Weighted median | 113 | 0.00119384 | 0.016135 | 0.941019 | -0.03043135 | 0.032819 | 1.0011946 | Heterogeneity | | | | |
| 3 IVW | 113 | -0.0044226 | 0.014739 | 0.7641348 | -0.033112 | 0.024466 | 0.9955872 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 113 | 0.01648686 | 0.04853 | 0.7346983 | -0.07863136 | 0.111605 | 1.0166235 | MR Egger | 233.9745 | 111 | ##### | |
| 5 Weighted mode | 113 | 0.01183181 | 0.049375 | 0.8110523 | -0.08494233 | 0.108606 | 1.0119021 | IVW | 234.3381 | 112 | ##### | |
| Pleiotropy | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 39 | -0.0190499 | 0.020167 | 0.3509949 | -0.05857776 | 0.020478 | 0.9811304 | 0.004574052 | 0.002624849 | 0.0897 | | |
| 2 Weighted median | 39 | -0.0006625 | 0.017441 | 0.9696973 | -0.03484658 | 0.033522 | 0.9993377 | Heterogeneity | | | | |
| 3 IVW | 39 | 0.00653714 | 0.01419 | 0.6450304 | -0.02127584 | 0.03435 | 1.0065586 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 39 | -0.0267805 | 0.030793 | 0.3899255 | -0.08713442 | 0.033573 | 0.9735749 | MR Egger | 51.65967 | 37 | 0.0553 | |
| 5 Weighted mode | 39 | -0.0030661 | 0.017565 | 0.8623579 | -0.03749424 | 0.031362 | 0.9969386 | IVW | 55.89945 | 38 | 0.0306 | |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 11 | 0.06173785 | 0.14098 | 0.6717657 | -0.21458215 | 0.338058 | 1.063683 | -0.009456204 | 0.0213017 | 0.6676 | | |
| 2 Weighted median | 11 | 0.02539053 | 0.033421 | 0.4474218 | -0.04011442 | 0.090895 | 1.025716 | Heterogeneity | | | | |
| 3 IVW | 11 | 0.0001808 | 0.025427 | 0.9943265 | -0.04965578 | 0.050017 | 1.000181 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 11 | 0.03388677 | 0.058433 | 0.574796 | -0.08064135 | 0.148415 | 1.034467 | MR Egger | 6.293823 | 9 | 0.7102 | |
| 5 Weighted mode | 11 | 0.03083684 | 0.049921 | 0.5505683 | -0.06700744 | 0.128681 | 1.031317 | IVW | 6.490886 | 10 | 0.7725 | |
| Pleiotropy | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 13 | 0.1477471 | 0.528291 | 0.826392 | -0.877028 | 1.183197 | 1.15922 | -0.002236418 | 0.03845369 | 0.963 | | |
| 2 Weighted median | 13 | 0.1180032 | 0.134765 | 0.3812343 | -0.1461354 | 0.382142 | 1.125248 | Heterogeneity | | | | |
| 3 IVW | 13 | 0.1177846 | 0.116945 | 0.313847 | -0.114269 | 0.346996 | 1.125002 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 13 | 0.1049621 | 0.155447 | 0.5691352 | -0.1997147 | 0.409639 | 1.110668 | MR Egger | 0.06121556 | 1 | 0.8046 | |
| 5 Weighted mode | 13 | 0.1186857 | 0.156368 | 0.5271 | -0.1877952 | 0.425167 | 1.126016 | IVW | 0.064598 | 2 | 0.9682 | |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 12 | -0.0521706 | 0.293107 | 0.8637712 | -0.626609 | 0.52232 | 0.949167 | -0.00623782 | 0.01210215 | 0.6221 | | |
| 2 Weighted median | 12 | -0.1816364 | 0.151966 | 0.2319916 | -0.4794897 | 0.116217 | 0.8339045 | Heterogeneity | | | | |
| 3 IVW | 12 | -0.1895292 | 0.116303 | 0.1031828 | -0.4174831 | 0.038425 | 0.8273486 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 12 | -0.0484928 | 0.233107 | 0.8404053 | -0.5053824 | 0.408397 | 0.9526642 | MR Egger | 9.071916 | 7 | 0.2475 | |
| 5 Weighted mode | 12 | -0.2240895 | 0.210822 | 0.3188423 | -0.6373005 | 0.189121 | 0.7992436 | IVW | 9.41622 | 8 | 0.3084 | |
| Pleiotropy | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 91 | -0.0379463 | 0.059598 | 0.5259486 | -0.15475756 | 0.078865 | 0.9627646 | 0.001287395 | 0.001748947 | 0.4636 | | |
| 2 Weighted median | 91 | -0.0104834 | 0.036108 | 0.7715611 | -0.08125518 | 0.060288 | 0.9895714 | Heterogeneity | | | | |
| 3 IVW | 91 | 0.17081E-05 | 0.029805 | 0.9997114 | -0.05840703 | 0.058429 | 1.0000108 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 91 | 0.00449994 | 0.069084 | 0.948209 | -0.13090418 | 0.139904 | 1.0045101 | MR Egger | 168.069 | 89 | ##### | |
| 5 Weighted mode | 91 | -0.0372891 | 0.03675 | 0.3129863 | -0.10931938 | 0.034741 | 0.9633976 | IVW | 169.0922 | 90 | ##### | |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 16 | 0.9197977 | 0.483927 | 0.13013469 | -0.02869995 | 1.868295 | 2.508783 | 0.02219213 | 0.06284301 | 0.7361 | | |
| 2 Weighted median | 16 | 0.3563328 | 0.154875 | 0.02140415 | -0.06277805 | 0.659888 | 1.428083 | Heterogeneity | | | | |
| 3 IVW | 16 | 0.2414407 | 0.139691 | 0.08391841 | -0.03235392 | 0.515235 | 1.273082 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 16 | 0.3724622 | 0.187975 | 0.10438509 | 0.00403114 | 0.740893 | 1.451304 | MR Egger | 4.115061 | 4 | 0.3907 | |
| 5 Weighted mode | 16 | 0.358964 | 0.161521 | 0.07689622 | 0.04238261 | 0.675546 | 1.431845 | IVW | 6.284514 | 5 | 0.2795 | |
| Pleiotropy | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 11 | -0.1222678 | 0.868891 | 0.7316156 | -2.0152944 | 1.390759 | 0.7317856 | 0.02219213 | 0.06284301 | 0.7361 | | |
| 2 Weighted median | 11 | -0.1213608 | 0.20388 | 0.5516712 | -0.5209646 | 0.278243 | 0.8857143 | Heterogeneity | | | | |
| 3 IVW | 11 | -0.0113029 | 0.158242 | 0.9430571 | -0.3214575 | 0.298852 | 0.9887607 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 11 | -0.147169 | 0.318055 | 0.6576079 | -0.7705563 | 0.476218 | 0.8631481 | MR Egger | 7.675764 | 6 | 0.2628 | |
| 5 Weighted mode | 11 | -0.1854494 | 0.288688 | 0.5410819 | -0.7512779 | 0.380379 | 0.8307309 | IVW | 7.835298 | 7 | 0.3473 | |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 44 | 0.01510314 | 0.021838 | 0.4930016 | -0.02770002 | 0.057906 | 1.015218 | -0.02185E-05 | 0.002445672 | 0.9707 | | |
| 2 Weighted median | 44 | 0.01960871 | 0.019335 | 0.3105046 | -0.01828761 | 0.057505 | 1.019802 | Heterogeneity | | | | |
| 3 IVW | 44 | 0.01445321 | 0.012753 | 0.2570759 | -0.01054242 | 0.039449 | 1.014558 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 44 | 0.02888896 | 0.031571 | 0.3652709 | -0.03299034 | 0.090768 | 1.02931 | MR Egger | 47.36304 | 42 | 0.263 | |
| 5 Weighted mode | 44 | 0.01883726 | 0.023989 | 0.4366179 | -0.02818149 | 0.065856 | 1.019016 | IVW | 47.36458 | 43 | 0.2991 | |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 29 | 0.05228802 | 0.030918 | 0.1023107 | -0.0083105 | 0.112887 | 1.053679 | -0.004989336 | 0.002916799 | 0.0986 | | |
| 2 Weighted median | 29 | 0.02061322 | 0.022084 | 0.3506197 | -0.02267202 | 0.063898 | 1.020827 | Heterogeneity | | | | |
| 3 IVW | 29 | 0.00615985 | 0.015634 | 0.6935768 | -0.02448261 | 0.036802 | 1.006179 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 29 | 0.00244864 | 0.043649 | 0.9556619 | -0.08310376 | 0.088001 | 1.002452 | MR Egger | 27.58295 | 27 | 0.4327 | |
| 5 Weighted mode | 29 | 0.02047808 | 0.036096 | 0.575013 | -0.05026958 | 0.091226 | 1.020689 | IVW | 30.57212 | 28 | 0.3364 | |
| Pleiotropy | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |
| 1 MR Egger | 113 | 0.2582416 | 0.11914 | 3.23E-02 | 0.02472629 | 0.491757 | 1.294652 | -0.003708472 | 0.003050661 | 0.2267 | | |
| 2 Weighted median | 113 | 0.1118202 | 0.020245 | 3.33E-08 | 0.07214013 | 0.1515 | 1.118312 | Heterogeneity | | | | |
| 3 IVW | 113 | 0.1162558 | 0.023548 | 7.93E-07 | 0.07010186 | 0.16241 | 1.123283 | Method | Q | Q_df | Q_p-value | |
| 4 Simple mode | 113 | 0.1644939 | 0.070663 | 2.17E-02 | 0.02599459 | 0.302993 | 1.178796 | MR Egger | 567.4199 | 111 | 2E-62 | |
| 5 Weighted mode | 113 | 0.1644939 | 0.071552 | 2.34E-02 | 0.02425287 | 0.304735 | 1.178796 | IVW | 574.974 | 112 | 2E-63 | |
| MR results | | | | | | | | | | | | |
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | | |

| | | | | | | | | | | | | |
|--|-------------------|----|------------|----------|-----------|-------------|----------|-----------|-------------|---------------|--------|-----------|
| MD on TG (Hispanic/Latin American samples) | 1 MR Egger | 40 | -0.0185295 | 0.023493 | 0.4351709 | -0.06457625 | 0.027517 | 0.9816411 | 0.002877725 | 0.002821604 | 0.3142 | |
| | 2 Weighted mediar | 40 | -0.0178907 | 0.023819 | 0.4525792 | -0.06457515 | 0.028794 | 0.9822684 | | Heterogeneity | | |
| | 3 IVW | 40 | -0.014386 | 0.015948 | 0.3670162 | -0.04564338 | 0.016871 | 0.985717 | Method | Q | Q_df | Q_p-value |
| | 4 Simple mode | 40 | -0.0113593 | 0.039298 | 0.7740706 | -0.08838343 | 0.065665 | 0.988705 | MR Egger | 27.14777 | 38 | 0.9048 |
| | 5 Weighted mode | 40 | -0.0201027 | 0.024493 | 0.4167741 | -0.06810868 | 0.027903 | 0.980098 | IVW | 28.18795 | 39 | 0.9002 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|----------|-----------------|------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 12 | 0.04780345 | 0.092415 | 0.6162142 | -0.13332915 | 0.228936 | 1.048964 | -0.004922415 | 0.01399761 | 0.7324 | |
| 2 Weighted mediar | 12 | 0.01000242 | 0.020989 | 0.6336849 | -0.03113675 | 0.051142 | 1.010053 | | | Heterogeneity | |
| 3 IVW | 12 | 0.01577644 | 0.015348 | 0.3039991 | -0.01430622 | 0.045859 | 1.015902 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 12 | 0.01535057 | 0.030301 | 0.6224344 | -0.04403949 | 0.074741 | 1.015469 | MR Egger | 10.44578 | 10 | 0.4023 |
| 5 Weighted mode | 12 | 0.01353333 | 0.031296 | 0.6737854 | -0.04780702 | 0.074874 | 1.013625 | IVW | 10.57496 | 11 | 0.4795 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|-----------|-----------------|-------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 28 | -0.000733 | 0.1068 | 0.9945767 | -0.2100613 | 0.208595 | 0.9992673 | 0.004856613 | 0.008214919 | 0.5595 | |
| 2 Weighted mediar | 28 | 0.01441763 | 0.085993 | 0.8668498 | -0.15412797 | 0.182963 | 1.0145221 | | | Heterogeneity | |
| 3 IVW | 28 | 0.04937217 | 0.064987 | 0.4474198 | -0.07800236 | 0.176747 | 1.0506113 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 28 | 0.02210073 | 0.136927 | 0.8729758 | -0.24627582 | 0.290477 | 1.0223468 | MR Egger | 13.52614 | 26 | 0.9787 |
| 5 Weighted mode | 28 | 0.01531686 | 0.088509 | 0.8638989 | -0.15815984 | 0.188794 | 1.0154348 | IVW | 13.87565 | 27 | 0.9824 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|--------------------|------------|----------|-----------|-----------------|-------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 31 | -0.2503079 | 0.101077 | 0.019349536 | -0.4484185 | -0.0522 | 0.778561 | 0.00853119 | 0.006141536 | 0.1754 | |
| 2 Weighted mediar | 31 | -0.1667542 | 0.069789 | 0.016875642 | -0.3035407 | -0.02997 | 0.8464076 | | | Heterogeneity | |
| 3 IVW | 31 | -0.1274703 | 0.048956 | 9.22E-03 | -0.2234241 | -0.03152 | 0.8803196 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 31 | -0.1629022 | 0.105898 | 0.13445798 | -0.3704618 | 0.044657 | 0.8496743 | MR Egger | 22.43171 | 29 | 0.8019 |
| 5 Weighted mode | 31 | -0.1578572 | 0.073467 | 0.039851618 | -0.3018521 | -0.01386 | 0.8539717 | IVW | 24.3613 | 30 | 0.7554 |

| MR results | | | | | | | | | | | |
|-------------------|-------|---------|----------|------------|-------------|----------|-----------|-----------------|-------------|---------------|--------------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 241 | 0.0023 | 0.027552 | 0.93238466 | -0.05166115 | 0.056341 | 1.0023428 | 0.001261971 | 0.000957798 | 0.1889 | |
| 2 Weighted mediar | 241 | -0.0142 | 0.020786 | 0.49467302 | -0.05493432 | 0.026545 | 0.9859058 | | | Heterogeneity | |
| 3 IVW | 241 | 0.0317 | 0.016273 | 0.05172288 | -0.0023704 | 0.063552 | 1.0321638 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 241 | -0.0257 | 0.043226 | 0.55295041 | -0.11040602 | 0.059038 | 0.9746432 | MR Egger | 423.527 | 239 | 2E-12 |
| 5 Weighted mode | 241 | -0.0090 | 0.0238 | 0.7057078 | -0.05564734 | 0.037651 | 0.991042 | IVW | 426.6033 | 240 | 1E-12 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|----------|-----------------|-------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 14 | 0.00487351 | 0.0565 | 0.9326844 | -0.10586597 | 0.115613 | 1.004885 | -1.66378E-05 | 0.007040405 | 0.9982 | |
| 2 Weighted mediar | 14 | 0.00940049 | 0.041746 | 0.8218388 | -0.07242261 | 0.091224 | 1.009445 | | | Heterogeneity | |
| 3 IVW | 14 | 0.00476225 | 0.03123 | 0.8787994 | -0.05644777 | 0.065972 | 1.004774 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 14 | 0.05497715 | 0.068161 | 0.4344162 | -0.07861786 | 0.188572 | 1.056516 | MR Egger | 10.91122 | 12 | 0.5365 |
| 5 Weighted mode | 14 | 0.01435162 | 0.040091 | 0.7261063 | -0.06422664 | 0.09293 | 1.014455 | IVW | 10.91123 | 13 | 0.6183 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|----------|-----------------|-------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 16 | 0.1007202 | 0.116364 | 0.3888015 | -0.32879318 | 0.127353 | 0.904186 | 0.01135386 | 0.006955711 | 0.1058 | |
| 2 Weighted mediar | 16 | 0.08319468 | 0.088306 | 0.3461321 | -0.08988506 | 0.256274 | 1.086753 | | | Heterogeneity | |
| 3 IVW | 16 | 0.0671848 | 0.054849 | 0.2206084 | -0.04031861 | 0.174688 | 1.069493 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 16 | 0.2464496 | 0.179682 | 0.173231 | -0.10572695 | 0.598626 | 1.279475 | MR Egger | 104.5455 | 100 | 0.3581 |
| 5 Weighted mode | 16 | 0.11836801 | 0.110631 | 0.2871978 | -0.09846833 | 0.335204 | 1.125658 | IVW | 107.331 | 101 | 0.3145 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|-----------|-----------------|-------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 39 | 0.00590712 | 0.083007 | 0.9436503 | -0.15678634 | 0.168601 | 1.0059246 | -0.001632005 | 0.008529178 | 0.8493 | |
| 2 Weighted mediar | 39 | -0.0273995 | 0.067135 | 0.6831838 | -0.1589849 | 0.104186 | 0.9729725 | | | Heterogeneity | |
| 3 IVW | 39 | -0.0072349 | 0.046019 | 0.8750739 | -0.09743151 | 0.092962 | 0.9927912 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 39 | 0.01965416 | 0.12787 | 0.8786566 | -0.23097161 | 0.27028 | 1.0198486 | MR Egger | 40.5156 | 37 | 0.318 |
| 5 Weighted mode | 39 | 0.01965416 | 0.098278 | 0.8425591 | -0.17297147 | 0.21228 | 1.0198486 | IVW | 40.55569 | 38 | 0.3583 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|--------------------|-------------|----------|----------|-----------------|-------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 28 | 0.07173585 | 0.022121 | 0.003339112 | 0.02838 | 0.115094 | 1.074372 | -0.004802966 | 0.002305867 | 0.0472 | |
| 2 Weighted mediar | 28 | 0.04351584 | 0.01809 | 0.016171634 | 0.00805 | 0.07898 | 1.044477 | | | Heterogeneity | |
| 3 IVW | 28 | 0.03418555 | 0.01282 | 0.007663783 | 0.00906 | 0.059313 | 1.034777 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 28 | 0.01880384 | 0.024633 | 0.451862054 | -0.02947621 | 0.067084 | 1.018982 | MR Egger | 19.22709 | 26 | 0.8267 |
| 5 Weighted mode | 28 | 0.03019618 | 0.019437 | 0.131944396 | -0.00790095 | 0.068293 | 1.030657 | IVW | 23.5657 | 27 | 0.6543 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|-----------|-----------------|-------------|---------------|--------------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 113 | 0.0539333 | 0.107628 | 0.6172875 | -0.15701781 | 0.264884 | 1.0554142 | -0.001983846 | 0.002755838 | 0.4731 | |
| 2 Weighted mediar | 113 | 0.01583364 | 0.01808 | 0.3811515 | -0.01960226 | 0.05127 | 1.0159597 | | | Heterogeneity | |
| 3 IVW | 113 | -0.0220231 | 0.021182 | 0.2984737 | -0.06353961 | 0.019493 | 0.9782177 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 113 | 0.06596041 | 0.052039 | 0.2075956 | -0.03603531 | 0.167956 | 1.0681844 | MR Egger | 532.0482 | 111 | 3E-56 |
| 5 Weighted mode | 113 | 0.04553581 | 0.045956 | 0.3238874 | -0.04453721 | 0.135609 | 1.0465885 | IVW | 534.5321 | 112 | 3E-56 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|------------|----------|-----------|-----------------|------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 35 | 0.0127466 | 0.126949 | 0.9206288 | -0.2360741 | 0.261567 | 1.0128282 | -0.01708207 | 0.01574935 | 0.286 | |
| 2 Weighted mediar | 35 | -0.0459637 | 0.138466 | 0.7399278 | -0.3173572 | 0.22543 | 0.9550767 | | | Heterogeneity | |
| 3 IVW | 35 | -0.0871227 | 0.087395 | 0.3188199 | -0.2584165 | 0.084171 | 0.9165647 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 35 | -0.159044 | 0.28178 | 0.5761695 | -0.7113334 | 0.393245 | 0.8529588 | MR Egger | 21.52096 | 33 | 0.9378 |
| 5 Weighted mode | 35 | -0.0998035 | 0.123455 | 0.42447 | -0.3417756 | 0.142169 | 0.9050152 | IVW | 22.69737 | 34 | 0.9303 |

| MR results | | | | | | | | | | | |
|-------------------|-------|------------|----------|-----------|-------------|----------|-----------|-----------------|------------|---------------|-----------|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
| 1 MR Egger | 11 | -0.0313274 | 0.310642 | 0.9218825 | -0.64018482 | 0.57753 | 0.9691582 | 0.01374562 | 0.04676208 | 0.7755 | |
| 2 Weighted mediar | 11 | 0.02792745 | 0.054796 | 0.6102852 | -0.07947182 | 0.135327 | 1.0283211 | | | Heterogeneity | |
| 3 IVW | 11 | 0.05858332 | 0.051686 | 0.2570248 | -0.04272082 | 0.159887 | 1.0603333 | Method | Q | Q_df | Q_p-value |
| 4 Simple mode | 11 | 0.02157588 | 0.093772 | 0.8226616 | -0.16221764 | 0.205369 | 1.0218103 | MR Egger | 21.28694 | 9 | 0.0114 |
| 5 Weighted mode | 11 | 0.01524665 | 0.093883 | 0.8742257 | -0.16876486 | 0.199258 | 1.0153635 | IVW | 21.4913 | 10 | 0.0179 |

| MR results | | | | | | | | | | | |
|------------|-------|------|----|---------|---------|---------|----|-----------------|----|---------|--|
| method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |

| | | method | n SNP | beta | se | p-value | 95%CI_L | 95%CI_U | OR | Egger intercept | se | p-value | |
|--|---|-----------------|-------|------------|----------|-----------|-------------|----------|-----------|-----------------|-------------|---------|-----------|
| HDL on MD (European ancestry) | 1 | MR Egger | 308 | 0.01676812 | 0.014429 | 0.2460957 | -0.01151274 | 0.045049 | 1.016909 | -0.000330034 | 0.000655615 | 0.615 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 308 | 0.01186975 | 0.010641 | 0.2646553 | -0.00898695 | 0.032726 | 1.01194 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 308 | 0.03183677 | 0.032273 | 0.324668 | -0.03141767 | 0.095091 | 1.032349 | MR Egger | 470.4639 | 306 | ##### |
| | 5 | Weighted mode | 308 | 0.01700096 | 0.012137 | 0.1622932 | -0.00678732 | 0.040789 | 1.017146 | IVW | 470.8535 | 307 | ##### |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| HDL on MD (Hispanic/Latin American samples) | 1 | MR Egger | 14 | 0.07861907 | 0.103906 | 0.4638626 | -0.12503579 | 0.282274 | 1.081792 | -0.002033945 | 0.008991807 | 0.8249 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 14 | 0.08447938 | 0.066662 | 0.2050566 | -0.0461785 | 0.215137 | 1.08815 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 14 | 0.05791445 | 0.049175 | 0.2389072 | -0.03846845 | 0.154297 | 1.059624 | MR Egger | 9.459227 | 12 | 0.6633 |
| | 5 | Weighted mode | 14 | 0.17017777 | 0.097675 | 0.1050497 | -0.02126544 | 0.361621 | 1.185516 | IVW | 9.510394 | 13 | 0.7334 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| HDL on MD (South Asian ancestry) | 1 | MR Egger | 18 | 1.00164589 | 2.104217 | 0.6809908 | -3.122619 | 5.125911 | 2.7227595 | -0.05397746 | 0.118751 | 0.694 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 18 | 0.05790688 | 0.293318 | 0.8434987 | -0.5169963 | 0.63281 | 1.0596163 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 18 | -0.3588987 | 0.54704 | 0.5586052 | -1.4310962 | 0.713299 | 0.6984451 | MR Egger | 3.195225 | 2 | 0.2024 |
| | 5 | Weighted mode | 18 | -0.3530906 | 0.597961 | 0.5963927 | -1.5250948 | 0.818914 | 0.7025135 | IVW | 3.525307 | 3 | 0.3175 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| MD on LDL (African ancestry) | 1 | MR Egger | 44 | -0.0068556 | 0.021175 | 0.7477256 | -0.04835866 | 0.034647 | 0.9931678 | -0.001619268 | 0.002378839 | 0.4998 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 44 | -0.0184753 | 0.012451 | 0.1378531 | -0.04287937 | 0.005929 | 0.9816943 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 44 | -0.0048693 | 0.033521 | 0.885184 | -0.07057089 | 0.060832 | 0.9951425 | MR Egger | 43.26685 | 42 | 0.417 |
| | 5 | Weighted mode | 44 | -0.0211317 | 0.02507 | 0.4039392 | -0.07026832 | 0.028005 | 0.97909 | IVW | 43.74417 | 43 | 0.4397 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| MD on LDL (East Asian ancestry) | 1 | MR Egger | 29 | 0.00814529 | 0.030823 | 0.7935869 | -0.052268 | 0.068559 | 1.0081786 | -0.001823905 | 0.002906783 | 0.5356 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 29 | -0.0197634 | 0.021541 | 0.3589033 | -0.06198471 | 0.022458 | 0.9804306 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 29 | -0.0087332 | 0.015049 | 0.5617121 | -0.03822997 | 0.020764 | 0.9913049 | MR Egger | 24.19602 | 27 | 0.6194 |
| | 5 | Weighted mode | 29 | -0.0245499 | 0.036319 | 0.5046107 | -0.09573421 | 0.046634 | 0.975749 | IVW | 24.58973 | 28 | 0.6501 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| MD on LDL (European ancestry) | 1 | MR Egger | 113 | 0.20220335 | 0.10767 | 0.0630 | -0.0088306 | 0.413237 | 1.224097 | -0.003866417 | 0.002756944 | 0.1636 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 113 | 0.01470564 | 0.017636 | 0.4044 | -0.01986011 | 0.049271 | 1.014814 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 113 | 0.05416919 | 0.021326 | 0.0111 | 0.01236934 | 0.095969 | 1.055663 | MR Egger | 446.2019 | 111 | 1E-41 |
| | 5 | Weighted mode | 113 | 0.00381041 | 0.041647 | 0.9273 | -0.07781681 | 0.085438 | 1.003818 | IVW | 454.1081 | 112 | 1E-42 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| MD on LDL (Hispanic/Latin American samples) | 1 | MR Egger | 40 | -0.0037539 | 0.024861 | 0.8807787 | -0.05248231 | 0.044974 | 0.9962531 | 0.001236258 | 0.003008836 | 0.6835 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 40 | -0.0120484 | 0.025333 | 0.6343524 | -0.06170011 | 0.037603 | 0.9880239 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 40 | 0.00375095 | 0.016685 | 0.8221296 | -0.02895205 | 0.036454 | 1.003758 | MR Egger | 41.20735 | 38 | 0.3321 |
| | 5 | Weighted mode | 40 | 0.01520643 | 0.045044 | 0.7374807 | -0.0730793 | 0.103492 | 1.0153226 | IVW | 41.39042 | 39 | 0.3667 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| MD on LDL (South Asian ancestry) | 1 | MR Egger | 12 | -0.0150615 | 0.10229 | 0.8858663 | -0.21554927 | 0.185426 | 0.9850514 | 0.001154969 | 0.01549099 | 0.942 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 12 | -0.0075455 | 0.016543 | 0.646314 | -0.04119664 | 0.040444 | 0.9996216 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 12 | 0.01885978 | 0.038576 | 0.6345163 | -0.05674955 | 0.094469 | 1.0190387 | MR Egger | 12.40374 | 10 | 0.2589 |
| | 5 | Weighted mode | 12 | 0.01666474 | 0.04128 | 0.6941687 | -0.06424365 | 0.097573 | 1.0168044 | IVW | 12.41063 | 11 | 0.3336 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| LDL on MD (African ancestry) | 1 | MR Egger | 38 | 0.02682697 | 0.096401 | 0.7823864 | -0.16211965 | 0.215774 | 1.02719 | 0.004591006 | 0.008182164 | 0.5782 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 38 | 0.06877426 | 0.060297 | 0.2540376 | -0.04940729 | 0.186956 | 1.071194 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 38 | 0.03861892 | 0.119981 | 0.7493589 | -0.19654407 | 0.273782 | 1.039374 | MR Egger | 45.12643 | 36 | 0.1416 |
| | 5 | Weighted mode | 38 | 0.08223271 | 0.070585 | 0.2514702 | -0.05611441 | 0.22058 | 1.085708 | IVW | 45.52108 | 37 | 0.1588 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| LDL on MD (East Asian ancestry) | 1 | MR Egger | 37 | -0.0924639 | 0.110045 | 0.4064788 | -0.3081521 | 0.123224 | 0.9116821 | 0.005947253 | 0.006311723 | 0.3525 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 37 | -0.0494943 | 0.071198 | 0.4869553 | -0.1890432 | 0.090055 | 0.9517106 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 37 | 0.00029946 | 0.049172 | 0.9951408 | -0.0960768 | 0.096676 | 1.0002995 | MR Egger | 32.59898 | 35 | 0.5846 |
| | 5 | Weighted mode | 37 | 0.02646381 | 0.144847 | 0.8560565 | -0.2574354 | 0.310363 | 1.0268171 | IVW | 33.48682 | 36 | 0.5887 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| LDL on MD (European ancestry) | 1 | MR Egger | 249 | 0.00855837 | 0.027495 | 0.7558619 | -0.04533273 | 0.062449 | 1.0085951 | -0.000196927 | 0.000981972 | 0.8412 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 249 | 0.00402678 | 0.015635 | 0.6736839 | -0.05088133 | 0.032885 | 0.991042 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 249 | -0.0231838 | 0.044904 | 0.6061104 | -0.11119634 | 0.064829 | 0.9770829 | MR Egger | 409.2674 | 247 | ##### |
| | 5 | Weighted mode | 249 | -0.0001543 | 0.02468 | 0.9950163 | -0.04852753 | 0.048219 | 0.9998457 | IVW | 409.3341 | 248 | ##### |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| LDL on MD (Hispanic/Latin American samples) | 1 | MR Egger | 13 | 0.0183935 | 0.056586 | 0.7512402 | -0.09251573 | 0.129303 | 1.0185637 | -0.001172338 | 0.006917493 | 0.8685 | |
| | 2 | Weighted median | | | | | | | | | | | |
| | 3 | IVW | 13 | -0.0327388 | 0.045488 | 0.4716989 | -0.12189617 | 0.056419 | 0.9677913 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 13 | -0.0307622 | 0.07502 | 0.6889938 | -0.17780195 | 0.116278 | 0.9697061 | MR Egger | 12.45076 | 11 | 0.3307 |
| | 5 | Weighted mode | 13 | -0.0115998 | 0.049248 | 0.8177604 | -0.1081251 | 0.084925 | 0.9884672 | IVW | 12.48327 | 12 | 0.4077 |
| MR results | | | | | | | | | | | | | |
| Pleiotropy | | | | | | | | | | | | | |
| method n SNP beta se p-value 95%CI_L 95%CI_U OR Egger intercept se p-value | | | | | | | | | | | | | |

| | 1 | MR Egger | 13 | 0.05937656 | 0.164376 | 0.7189618 | -0.26280108 | 0.381554 | 1.061175 | 0.000843086 | 0.008439762 | 0.9207 | |
|----------------------------------|---|-----------------|----|------------|----------|-----------|-------------|----------|----------|-------------|---------------|----------|-----------|
| LDL on MD (South Asian ancestry) | 2 | Weighted median | 13 | 0.01794743 | 0.126405 | 0.8870933 | -0.22980712 | 0.265702 | 1.018109 | | Heterogeneity | | |
| | 3 | IVW | 13 | 0.07413862 | 0.071984 | 0.3030427 | -0.06695023 | 0.215228 | 1.076956 | Method | Q | Q_df | Q_p-value |
| | 4 | Simple mode | 13 | 0.11566139 | 0.257636 | 0.6547748 | -0.38930599 | 0.620629 | 1.122616 | MR Egger | | 64.97889 | 74 0.7638 |
| | 5 | Weighted mode | 13 | 0.01660506 | 0.143034 | 0.90789 | -0.2637409 | 0.296951 | 1.016744 | IVW | | 64.98887 | 75 0.7887 |

B. Results of the MR-PRESSO analyses for significant heterogeneity observed.

| Ancestry | Expc Outcome | Caus Sd | IVW | | MR-PRESSO | | | | | | | |
|----------|--------------|---------|---------|--------------|-----------|---------|------------|-------------|----------------|--------|---------|-------|
| | | | P-value | Causal Estim | Sd | P-value | Nb outlier | global test | global test P- | on | on P- | |
| European | MDD BMI | ### | 0.0346 | 0.0128 | 0.1184 | 0.0231 | 2.05E-06 | 20 | 1281.457 | <0.001 | -26.048 | 0.388 |
| European | MDD FG | ### | 0.0145 | 0.7731 | -0.0099 | 0.0139 | 0.4778 | 2 | 239.7108 | <0.001 | 57.791 | 0.811 |
| European | MDD TG | ### | 0.0233 | 2.33E-06 | 0.1171 | 0.0189 | 1.19E-08 | 10 | 594.4885 | <0.001 | -1.156 | 0.937 |
| European | MDD SBP | ### | 0.0208 | 0.3095 | -0.0169 | 0.0163 | 0.3015 | 10 | 546.1281 | <0.001 | -25.940 | 0.691 |
| European | MDD HDL | ### | 0.0263 | 0.0371 | -0.0689 | 0.0194 | 6.05E-04 | 18 | 725.2331 | <0.001 | 19.353 | 0.516 |
| European | MDD LDL | ### | 0.0210 | 0.0136 | 0.0329 | 0.0153 | 0.0341 | 9 | 464.3117 | <0.001 | 59.841 | 0.085 |
| European | BMI MDD | ### | 0.0211 | 9.65E-10 | 0.1357 | 0.0191 | 8.04E-12 | 14 | 896.3895 | <0.001 | -2.247 | 0.867 |
| European | FG MDD | ### | 0.0296 | 0.9895 | 0.0031 | 0.0262 | 0.9070 | 2 | 172.138 | <0.001 | -87.245 | 0.956 |
| European | TG MDD | ### | 0.0159 | 0.0344 | 0.0192 | 0.0146 | 0.1887 | 5 | 435.9962 | <0.001 | 76.099 | 0.115 |
| European | SBP MDD | ### | 0.0246 | 0.6513 | -0.0300 | 0.0228 | 0.1896 | 6 | 420.2089 | <0.001 | 63.000 | 0.606 |
| European | HDL MDD | ### | 0.0106 | 0.2925 | 0.0189 | 0.0097 | 0.0525 | 6 | 483.5809 | <0.001 | -40.631 | 0.506 |
| European | LDL MDD | ### | 0.0155 | 0.7261 | 0.0097 | 0.0145 | 0.5053 | 3 | 414.162 | <0.001 | -43.932 | 0.807 |

Unadjusted two-sided association P values of z statistics are given.

MD= Major depression; MR= Mendelian Randomisation; BMI= Body mass index; FG= Fasting glucose; TG= Triglycerides; SBP= Systolic Blood Pressure; HDL= High density lipoprotein; LDL= Low density lipoprotein; nsnp= number of SNPs in model, OR= odds ratio, CI_L= Confidence interval lower bound; CI_U= Confidence interval upper bound; IVW= inverse variance weighted; df= degrees of freedom

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| Jared O'Connell | 23andMe Inc., Sunnyvale, CA, USA |
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| Catherine H. Weldon | 23andMe Inc., Sunnyvale, CA, USA |
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Supplementary Table 19. Members of the Genes and Health Research Team

| Published Name | Affiliation |
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| Shaheen Akhtar | Genes & Health Research Team |
| Mohammad Anwar | Genes & Health Research Team |
| Elena Arciero | Genes & Health Research Team |
| Samina Ashraf | Genes & Health Research Team |
| Gerome Breen | Genes & Health Research Team |
| Raymond Chung | Genes & Health Research Team |
| Charles J Curtis | Genes & Health Research Team |
| Maharun Chowdhury | Genes & Health Research Team |
| Grainne Colligan | Genes & Health Research Team |
| Panos Deloukas | Genes & Health Research Team |
| Ceri Durham | Genes & Health Research Team |
| Sarah Finer | Genes & Health Research Team |
| Chris Griffiths | Genes & Health Research Team |
| Qin Qin Huang | Genes & Health Research Team |
| Matt Hurles | Genes & Health Research Team |
| Karen A Hunt | Genes & Health Research Team |
| Shapna Hussain | Genes & Health Research Team |
| Kamrul Islam | Genes & Health Research Team |
| Ahsan Khan | Genes & Health Research Team |
| Amara Khan | Genes & Health Research Team |
| Cath Lavery | Genes & Health Research Team |
| Sang Hyuck Lee | Genes & Health Research Team |
| Robin Lerner | Genes & Health Research Team |
| Daniel MacArthur | Genes & Health Research Team |
| Bev MacLaughlin | Genes & Health Research Team |
| Hilary Martin | Genes & Health Research Team |
| Dan Mason | Genes & Health Research Team |

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| Shefa Miah | Genes & Health Research Team |
| Bill Newman | Genes & Health Research Team |
| Nishat Safa | Genes & Health Research Team |
| Farah Tahmasebi | Genes & Health Research Team |
| Richard C Trembath | Genes & Health Research Team |
| Bhavi Trivedi | Genes & Health Research Team |
| David A van Heel | Genes & Health Research Team |
| John Wright | Genes & Health Research Team |

Supplementary Table 20. Members of the China Kadoorie Biobank Collaborative Group

| Published Name | Affiliation |
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| International Steering Committee | |
| Junshi Chen, MD | CKB Collaborative Group |
| Zhengming Chen, DPhil (prin | CKB Collaborative Group |
| Robert Clarke, FRCP | CKB Collaborative Group |
| Rory Collins, FRS | CKB Collaborative Group |
| Yu Guo | CKB Collaborative Group |
| Liming Li, PhD (principal inve | CKB Collaborative Group |
| Jun Lv, MD | CKB Collaborative Group |
| Richard Peto, FRS | CKB Collaborative Group |
| Robin Walters PhD | CKB Collaborative Group |
| International Coordinating Centre, Oxford, England | |
| Daniel Avery, MSc | CKB Collaborative Group |
| Derrick Bennett, PhD | CKB Collaborative Group |
| Ruth Boxall, MD | CKB Collaborative Group |
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| Yiping Chen, DPhil, | CKB Collaborative Group |
| Zhengming Chen, DPhil | CKB Collaborative Group |
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| Huaidong Du, PhD | CKB Collaborative Group |
| Simon Gilbert, MSc | CKB Collaborative Group |
| Alex Hacker, BA, | CKB Collaborative Group |
| Michael Holmes, PhD | CKB Collaborative Group |
| Christiana Kartsonaki, DPhil | CKB Collaborative Group |
| Rene Kerosi, MSc | CKB Collaborative Group |
| Ling Kong, BSc | CKB Collaborative Group |
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| John McDonnell, GD(Comp S | CKB Collaborative Group |

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| Iona Millwood, DPhil | CKB Collaborative Group |
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| Jayakrishnan Radhakrishnan, | CKB Collaborative Group |
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| Iain Turnbull, MBBS, | CKB Collaborative Group |
| Robin Walters, PhD, | CKB Collaborative Group |
| Jenny Wang, MSc | CKB Collaborative Group |
| Lin Wang, MSc | CKB Collaborative Group |
| Neil Wright, MSc | CKB Collaborative Group |
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National Coordinating Centre, Beijing, China

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| Canqing Yu, PhD | CKB Collaborative Group |

10 Regional Coordinating Centres

Qingdao: Qingdao Centre for Disease Control and Prevention (CDC)

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| Shanpeng Li | CKB Collaborative Group |
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| Xiaocao Tian | CKB Collaborative Group |
| Hua Zhang | CKB Collaborative Group |
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| Feng Ning | CKB Collaborative Group |
| Xiaohui Sun, | CKB Collaborative Group |
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Licang CDC

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| Junzheng Wang | CKB Collaborative Group |
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Heilongjiang, Provincial CDC

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Nangang CDC

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| Bo Yu | CKB Collaborative Group |
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Hainan, Provincial CDC

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| Yan Fu | CKB Collaborative Group |
| Zhenwang Fu | CKB Collaborative Group |
| Xiaohuan Wang | CKB Collaborative Group |

Meilan CDC

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Suzhou CDC

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Sichuan, Provincial CDC

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Maiji CDC

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| Tao Wang | CKB Collaborative Group |
| Xi Zhang | CKB Collaborative Group |
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Huixian CDC

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| Pan He | CKB Collaborative Group |
| Chen Hu | CKB Collaborative Group |
| Xukui Zhang | CKB Collaborative Group |
| Huifang Wu | CKB Collaborative Group |
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Zhejiang, Provincial CDC

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Tongxiang CDC

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Supplementary Table 21. Members of the BioBank Japan Project

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