Supplementary material for **Genetic Determinants of Plasma Low-Density Lipoprotein Cholesterol Levels: Monogenicity, Polygenicity, and "Missing" Heritability.**

**Supplementary methods**

**Search for GWASs related to plasma LDL-c levels:** The GWAS Catalog (www.ebi.ac.uk/gwas) was accessed on August 18, 2021. After a search for the trait "low-density lipoprotein cholesterol measurement" (EFO_0004611), two .csv files were downloaded: a file with the published studies included in the database (study file) and a file with the SNVs associated with the trait in these studies (association file). The first step was to filter the "reported trait" field of the study file using "Low-density lipoprotein cholesterol levels", "LDL cholesterol", "LDL cholesterol levels", "Total cholesterol levels in LDL", "Lipid traits", "Cardiovascular disease risk factors", "Metabolite levels", "Cholesterol", "Lipid or lipoprotein levels", "Quantitative traits", "Biochemical measures", or "Cardiovascular risk factors." The next step was to choose discovery samples from the following groups: Europeans or European ancestry, East Asians, Afro-Americans or African ancestry, Native Americans or Hispanics, Middle-East populations, and Oceanians. Studies of multiethnic discovery samples were discarded. Studies with consigned background traits (usually a disease) were also discarded. The selected studies were used to extract SNVs associated with LDL-c in the association file. All the SNV were checked through the dbSNP (www.ncbi.nlm.nih.gov/snp) and the ClinVar (www.ncbi.nlm.nih.gov/clinvar) databases to determine the type of mutation. Polyphen (genetics.bwh.harvard.edu/pph2/) and Sift (sift.bii.a-star.edu.sg/) programs were used for the prediction of the functional effects of SNVs affecting exons.

**Table S1a:** SNVs associated with low-density lipoprotein cholesterol in European ancestry populations.

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *SKI* | | rs560221037 | 1 | 2,235,046 | | intronic | | | | | | 6E−12 | [22] |
| *TTC34 - ACTRT2* | | rs79316815 | 1 | 2,902,742 | | intergenic | | | | | | 3E−7 | [17] |
| *CASZ1* | | rs880315 | 1 | 10,736,809 | | intronic | | | | | | 7E−12 | [21] |
| *CASZ1* | | rs682178 | 1 | 10,738,495 | | intronic | | | | | | 5E−10 | [22] |
| *CLCN6* | | rs112521149 | 1 | 11,829,758 | | intronic | | | | | | 4E−8 | [22] |
| *EPHA2 - ARHGEF19-AS1* | | rs12078100 | 1 | 16,186,091 | | intergenic | | | | | | 7E−13; 9E−10; 2E−24 | [20][21][22] |
| *ASAP3* | | rs61778883 | 1 | 23,468,684 | | intronic | | | | | | 2E−9 | [21] |
| *ASAP3* | | rs375390883 | 1 | 23,468,691 | | intronic | | | | | | 3E−17 | [22] |
| *ELOA* | | chr1:23747996 | 1 | 23,747,996 | | intergenic | | | | | | 4E−9 | [20] |
| | | | 1 | 25,420,739 | | missense | c.48G>C | p.Trp16Cys | no interp. | benign | tolerated | 4E−9 | [13] |
| | | | 1 | 25,442,719 | | intronic | | | | | | 4E−36 | [20] |
| | | | 1 | 25,449,242 | | intronic | | | | | | 1E−10; 2E−14 | [8][12] |
| | | | 1 | 25,467,172 | | intronic | | | | | | 2E−35 | [21] |
| *ARID1A* | | rs114165349 | 1 | 26,695,422 | | intronic | | | | | | 4E−27; 8E−16 | [20][21] |
| *PIGV - RN7SL165P* | | rs12748152 | 1 | 26,811,902 | | intergenic | | | | | | 3E−12 | [12] |
| *KDF1* | | rs79598313 | 1 | 26,958,422 | | intronic | | | | | | 7E−10 | [13] |
| *MECR* | | rs2291609 | 1 | 29,224,479 | | intronic | | | | | | 2E−8 | [20] |
| | | | 1 | 54,646,717 | | intergenic | | | | | | 1E−7 | [15] |
| | | | 1 | 54,876,728 | | intronic | | | | | | 2E−9 | [15] |
| | | | 1 | 54,983,266 | | intronic | | | | | | 3E−9 | [15] |
| | | | 1 | 55,030,366 | | intergenic | | | | | | 4E−11; 4E−8; 1E−10 | [1][4][9] |
| | | | 1 | 55,038,977 | | 5'-UTR | c.-861G>A | | benign | | | 2E−28; 3E−50 | [8][12] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PCSK9* | *PCSK9* | rs11591147 | 1 | 55,039,974 | | missense | c.137G>T | p.Arg46Leu | benign/likely benign | benign | tolerated | 2E−44; 2E−92; 3E−563; 2E−421 | [2][13][20] [21] |
| *PCSK9* | | rs693668 | 1 | 55,055,436 | | intronic | | | | | | 9E−8 | [19] |
| *PCSK9* | | rs472495 | 1 | 55,055,640 | | intronic | | | | | | 6E−85 | [21] |
| *PCSK9* | | rs11206517 | 1 | 55,060,755 | | intronic | | | | | | 6E−32 | [21] |
| *USP24 - Y_RNA* | | chr1:55246601 | 1 | 55,246,601 | | intergenic | | | | | | 4E−16 | [15] |
| *USP24 - Y_RNA* | | chr1:55505647 | 1 | 55,505,647 | | intergenic | | | | | | 1E−29 | [15] |
| *USP24 - Y_RNA* | | chr1:55636240 | 1 | 55,636,240 | | intergenic | | | | | | 6E−25 | [15] |
| *USP24 - Y_RNA* | | chr1:55759138 | 1 | 55,759,138 | | intergenic | | | | | | 8E−21 | [15] |
| *USP24 - Y_RNA* | | chr1:55939497 | 1 | 55,939,497 | | intergenic | | | | | | 2E−18 | [15] |
| *USP24 - Y_RNA* | | chr1:56062375 | 1 | 56,062,375 | | intergenic | | | | | | 3E−17 | [15] |
| *ENSG00000284686* | | rs17457613 | 1 | 56,250,181 | | intronic | | | | | | 2E−9 | [20] |
| *ENSG00000284686* | | chr1:56304721 | 1 | 56,304,721 | | intronic | | | | | | 2E−15 | [15] |
| *ENSG00000284686* | | rs11206788 | 1 | 56,332,309 | | intronic | | | | | | 2E−10 | [21] |
| *ENSG00000284686* | | chr1:56480207 | 1 | 56,480,207 | | intronic | | | | | | 2E−15 | [15] |
| *FYB2 - C8A* | | chr1:56840574 | 1 | 56,840,574 | | intergenic | | | | | | 3E−14 | [15] |
| *DAB1* | | chr1:56995693 | 1 | 56,995,693 | | 3'-UTR | c.*2451C>? | | | | | 5E−9 | [15] |
| *DOCK7* | *DOCK7 - ANGPTL3* | rs2131925 | 1 | 62,560,271 | | intronic | | | | | | 3E−18; 3E−32 | [8][12] |
| *DOCK7* | | rs10889348 | 1 | 62,612,551 | | intronic | | | | | | 2E−11 | [13] |
| *DOCK7* | | rs10889353 | 1 | 62,652,525 | | intronic | | | | | | 8E−6 | [5] |
| *DOCK7* | | rs1168127 | 1 | 62,670,407 | | intronic | | | | | | 2E−70 | [21] |
| *ATG4C - FOXD3* | | chr1:62900811 | 1 | 62,900,811 | | intergenic | | | | | | 2E−6 | [15] |
| *ATG4C - FOXD3* | | chr1:62944947 | 1 | 62,944,947 | | intergenic | | | | | | 5E−101 | [20] |
| *ATG4C - FOXD3* | | chr1:63086001 | 1 | 63,086,001 | | intergenic | | | | | | 4E−6 | [15] |
| *GFI1 - EVI5* | | rs11164654 | 1 | 92,502,755 | | intergenic | | | | | | 2E−8 | [13] |
| *EVI5* | | rs1556562 | 1 | 92,568,466 | | intronic | | | | | | 2E−12; 2E−14 | [20][21] |
| *Y_RNA - PRMT6* | | rs3108680 | 1 | 107,030,375 | | intergenic | | | | | | 2E−9 | [20] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 1 | 108,925,836 | | intronic | | | | | | 6E−10 | [21] |
| | | | 1 | 109,233,663 | | intronic | | | | | | 8E−304 | [22] |
| | | | 1 | 109,255,141 | | intronic | | | | | | 3E−40 | [21] |
| | | | 1 | 109,264,661 | | intronic | | | | | | 1E−277 | [20] |
| | | | 1 | 109,272,258 | | intronic | | | | | | 2E−336 | [21] |
| | | | 1 | 109,274,968 | | 3'-UTR | c.*919G>T | | association | | | 2E−42 | [4] |
| | | | 1 | 109,275,216 | | 3'-UTR | c.*1167T>C | | np | | | 1E−26 | [9] |
| | | | 1 | 109,275,684 | | 3'-UTR | c.*1635G>C | | np | | | 1E−170; 5E−241; 2E−72 | [8][12][19] |
| | | | 1 | 109,275,908 | | intergenic | | | | | | 3E−29; 8E−23; 2E−12; 2E−91 | [2][5][6][13] |
| | | | 1 | 109,279,544 | | intergenic | | | | | | 6E−33; 1E−33 | [1][3] |
| | | | 1 | 109,519,352 | | intergenic | | | | | | 7E−11 | [21] |
| | | | 1 | 109,690,361 | | missense | c.451A>G | p.Asn151Asp | np | benign | tolerated | 6E−10 | [21] |
| | | | 1 | 109,817,590 | | intergenic | | | | | | 4E−15 | [15] |
| *CIART* | | rs2147324 | 1 | 150,283,177 | | intronic | | | | | | 3E−8 | [20] |
| *TARS2* | | rs77257036 | 1 | 150,503,710 | | intronic | | | | | | 4E−8 | [21] |
| *ANXA9* | | rs267733 | 1 | 150,986,360 | | missense | c.497A>G | p.Asp166Gly | np | probably damaging | tolerated | 5E−9 | [12] |
| *Y_RNA - EFNA1* | | rs11807418 | 1 | 155,122,129 | | intergenic | | | | | | 4E−8 | [20] |
| *EFNA1* | | rs4745 | 1 | 155,133,751 | | missense | c.476A>T | p.Asp159Val | np | benign | tolerated | 3E−10 | [16] |
| *LAMC21 - LAMC2* | | rs35221132 | 1 | 183,145,730 | | intergenic | | | | | | 8E−9 | [20] |
| *PTPRC - LINC01221* | | chr1:198994696 | 1 | 198,994,696 | | intergenic | | | | | | 2E−9 | [20] |
| *LINC01221* | | rs6667939 | 1 | 199,025,490 | | intergenic | | | | | | 7E−11 | [21] |
| *CR1L* | | rs4844614 | 1 | 207,701,830 | | intronic | | | | | | 2E−7 | [6] |
| | | | 1 | 220,796,686 | | missense | c.493A>G | p.Thr165Ala | np | benign | tolerated | 3E−33; 8E−29 | [20][21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *MTARC1* | *MTARC1* | rs2642442 | 1 | 220,800,221 | | intronic | | | | | | 6E−11; 5E−11 | [8][12] |
| *CNIH4, NVL* | | rs12751807 | 1 | 224,349,953 | | intergenic | | | | | | 1E−9 | [20] |
| *IRF2BP2 - TOMM20* | *IRF2BP2* | rs10910476 | 1 | 234,599,210 | | intergenic | | | | | | 4E−9 | [21] |
| *IRF2BP2 - TOMM20* | | rs556107 | 1 | 234,717,312 | | intergenic | | | | | | 1E−70; 8E−64 | [20][21] |
| *IRF2BP2 - TOMM20* | | rs514230 | 1 | 234,722,850 | | intergenic | | | | | | 9E−12; 9E−12; 1E−11 | [8][12][13] |
| *IRF2BP2 - TOMM20* | | rs28631087 | 1 | 234,973,467 | | intergenic | | | | | | 2E−10 | [21] |
| *RPS7, COLEC11* | | rs56236159 | 2 | 3,588,888 | | intergenic | | | | | | 7E−9 | [21] |
| *COLEC11, RPS7* | | rs6542680 | 2 | 3,592,552 | | intergenic | | | | | | 1E−9 | [20] |
| *COLEC11, RPS7* | | rs3820897 | 2 | 3,594,771 | | intergenic | | | | | | 2E−14 | [22] |
| *LINC01814* | | rs72784625 | 2 | 8,580,520 | | intergenic | | | | | | 6E−9 | [22] |
| *LINC00570* | | rs72774870 | 2 | 11,372,699 | | intergenic | | | | | | 4E−8 | [21] |
| *RN7SL140P, RPS16P2* | *APOB* | rs907866 | 2 | 20,171,619 | | intergenic | | | | | | 4E−17 | [21] |
| *LDAH* | | rs4971516 | 2 | 20,703,255 | | intronic | | | | | | 2E−52 | [10] |
| *APOB* | | rs13392272 | 2 | 20,994,618 | | intergenic | | | | | | 1E−306 | [20] |
| *APOB* | | rs693 | 2 | 21,009,323 | | synonymous | c.7545C>T | p.Thr2515= | benign | | | 1E−21; 4E−17; 3E−11 | [2][5][6] |
| *APOB* | | rs1367117 | 2 | 21,041,028 | | missense | c.293C>T | p.Thr98Ile | benign/likely benign | benign | deleterious | 4E−114; 1E−182 | [8][12] |
| *TDRD15, APOB* | | rs934197 | 2 | 21,044,589 | | intergenic | | | | | | 9E−312 | [21] |
| *TDRD15, APOB* | | rs7575840 | 2 | 21,050,618 | | intergenic | | | | | | 4E−28 | [19] |
| *APOB, TDRD15* | | rs515135 | 2 | 21,063,185 | | intergenic | | | | | | 5E−29; 2E−20; 2E−63 | [4][9][13] |
| *APOB, TDRD15* | | rs562338 | 2 | 21,065,449 | | intergenic | | | | | | 6E−22; 1E−9 | [1][3] |
| *TDRD15 - NUTF2P8* | | rs312976 | 2 | 21,152,474 | | intergenic | | | | | | 5E−324 | [22] |
| *TDRD15 - NUTF2P8* | | rs430096 | 2 | 21,211,708 | | intergenic | | | | | | 2E−103 | [21] |
| *TDRD15 - NUTF2P8* | | chr2:21281097 | 2 | 21,281,097 | | intergenic | | | | | | 8E−13 | [15] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *TDRD15 - NUTF2P8* | *APOB* | chr2:21383353 | 2 | 21,383,353 | | intergenic | | | | | | 4E−10 | [15] |
| *TDRD15 - NUTF2P8* | | rs11693526 | 2 | 22,124,628 | | intergenic | | | | | | 2E−8; 7E−6 | [20][21] |
| *ITSN2* | | rs77907512 | 2 | 24,267,100 | | intronic | | | | | | 5E−11 | [20] |
| *KCNK3* | | rs1731243 | 2 | 26,707,543 | | intronic | | | | | | 7E−10 | [21] |
| *GCKR* | *GCKR* | rs1260326 | 2 | 27,508,073 | | missense | c.1337T>C | p.Leu446Pro | benign, association | possibly damaging | tolerated | 4E−99; 6E−60 | [20][21] |
| *THADA* | *ABCG5/8* | rs12990177 | 2 | 43,455,520 | | intronic | | | | | | 1E−12 | [21] |
| *ABCG5* | | rs6756629 | 2 | 43,837,951 | | missense | c.148C>T | p.Arg50Cys | benign/likely benign | probably damaging | deleterious | 3E−10 | [5] |
| *ABCG8* | | rs4299376 | 2 | 43,845,437 | | intronic | | | | | | 2E−47; 4E−72; 5E−187; 4E−131 | [8][12][20] [21] |
| *ABCG8* | | rs41360247 | 2 | 43,846,517 | | intronic | | | | | | 1E−10 | [19] |
| *ABCG8* | | rs6544713 | 2 | 43,846,742 | | intronic | | | | | | 2E−20 | [4] |
| *ABCG8* | | rs72875462 | 2 | 43,852,171 | | intronic | | | | | | 2E−35 | [13] |
| *ABCG8* | | rs6709904 | 2 | 43,853,185 | | intronic | | | | | | 9E−40 | [21] |
| *EHBP1* | | rs4671050 | 2 | 62,761,034 | | intronic | | | | | | 1E−21 | [20] |
| *EHBP1* | | rs7562734 | 2 | 62,820,838 | | intronic | | | | | | 2E−19 | [21] |
| *EHBP1* | | rs2710642 | 2 | 62,922,422 | | intronic | | | | | | 6E−9 | [12] |
| *SERTAD2* | | rs1861398 | 2 | 64,679,666 | | intronic | | | | | | 8E−9 | [20] |
| *SERTAD2* | | rs12471768 | 2 | 64,701,469 | | intronic | | | | | | 3E−9 | [21] |
| *GCC2* | | rs763102966 | 2 | 108,449,778 | | intronic | | | | | | 1E−12 | [20] |
| *LIMS1* | | rs2718717 | 2 | 108,589,683 | | intronic | | | | | | 3E−10 | [21] |
| *IL1F10* | | rs3811055 | 2 | 113,073,605 | | intronic | | | | | | 2E−8 | [20] |
| *INSIG2, RN7SL111P* | *INSIG2* | rs10490626 | 2 | 118,078,265 | | intergenic | | | | | | 2E−12 | [12] |
| *RN7SL111P, INSIG2* | | rs150474434 | 2 | 118,087,545 | | intergenic | | | | | | 7E−22; 1E−23 | [20][21] |
| *LINC01101* | | rs17050272 | 2 | 120,548,864 | | intergenic | | | | | | 2E−24; 3E−22 | [20][21] |
| *Y_RNA, LINC01101* | | rs2030746 | 2 | 120,551,912 | | intergenic | | | | | | 9E−9 | [12] |
| *TMEM163* | | rs10928512 | 2 | 134,693,732 | | intronic | | | | | | 4E−8 | [19] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *ACMSD, CCNT2-AS1* | | rs4954192 | 2 | 134,875,411 | | intronic | | | | | | 6E−12 | [21] |
| *ZRANB3* | | rs151022760 | 2 | 135,340,991 | | intronic | | | | | | 4E−12 | [20] |
| *DARS1-AS1, CXCR4* | | rs6714750 | 2 | 136,025,599 | | intergenic | | | | | | 3E−8 | [21] |
| *ACVR1C* | | rs12614487 | 2 | 157,578,057 | | intronic | | | | | | 5E−10 | [20] |
| *ACVR1C* | | rs7601153 | 2 | 157,591,059 | | intronic | | | | | | 2E−7 | [21] |
| *GRB14, COBLL1* | | rs10184004 | 2 | 164,651,879 | | intergenic | | | | | | 1E−11 | [20] |
| *ABCB11* | | rs2287622 | 2 | 168,973,818 | | missense | c.1331T>C | p.Val444Ala | benign | benign | tolerated | 3E−23 | [21] |
| *UBR3* | | chr2:169829810 | 2 | 169,829,810 | | intronic | | | | | | 8E−24 | [20] |
| *FAM117B* | | rs7569317 | 2 | 202,663,256 | | intronic | | | | | | 9E−18 | [21] |
| *CARF* | | rs140244541 | 2 | 202,943,809 | | intronic | | | | | | 6E−9 | [13] |
| *RAPH1* | | rs7603427 | 2 | 203,452,830 | | intronic | | | | | | 9E−8 | [21] |
| *RAPH1 - CD28* | | chr2:203556224 | 2 | 203,556,224 | | intergenic | | | | | | 1E−24 | [20] |
| *FN1* | | rs1250258 | 2 | 215,435,462 | | intronic | | | | | | 7E−9 | [21] |
| *FN1* | | rs1250229 | 2 | 215,439,661 | | intergenic | | | | | | 3E−8 | [12] |
| *UGT1A3, UGT1A5, UGT1A9, UGT1A10, UGT1A4, UGT1A6, UGT1A8, UGT1A7* | | rs11568318 | 2 | 233,756,852 | | intronic | | | | | | 7E−10; 7E−19 | [21][22] |
| *UGT1A8, UGT1A9, UGT1A4, UGT1A7, UGT1A10, UGT1A6, UGT1A5, UGT1A1, UGT1A3* | | rs11563251 | 2 | 233,770,738 | | intronic | | | | | | 5E−8; 8E−13 | [12][20] |
| *FARP2* | | rs59916403 | 2 | 241,431,336 | | intronic | | | | | | 4E−9 | [22] |
| *GSTM5P1, PPARG* | *PPARG* | rs2920503 | 3 | 12,282,731 | | intergenic | | | | | | 3E−10 | [13] |
| *GSTM5P1, PPARG* | | rs13076933 | 3 | 12,285,932 | | intergenic | | | | | | 6E−26; 3E−18; 8E−49 | [20][21][22] |
| *CMTM6* | | rs7640978 | 3 | 32,491,518 | | intronic | | | | | | 1E−8 | [12] |
| *CMTM6* | | rs9834932 | 3 | 32,493,890 | | intronic | | | | | | 1E−18 | [21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *CMTM6* | | rs150605723 | 3 | 32,499,834 | | intronic | | | | | | 2E−19 | [20] |
| *PXK* | | rs9825431 | 3 | 58,420,967 | | intronic | | | | | | 4E−18 | [20] |
| *KCTD6, PDHB* | | rs71311871 | 3 | 58,434,886 | | intergenic | | | | | | 7E−14 | [21] |
| *MITF* | | rs55921103 | 3 | 69,761,143 | | intronic | | | | | | 3E−12; 5E−10 | [20][21] |
| *MITF* | | rs7623486 | 3 | 69,859,943 | | intronic | | | | | | 9E−7 | [17] |
| *NR1I2* | | rs3732359 | 3 | 119,817,582 | | 3'-UTR | c.*370G>A | | np | | | 5E−12 | [21] |
| *GSK3B* | | rs570238285 | 3 | 120,069,666 | | intronic | | | | | | 1E−8 | [20] |
| *CASR* | | chr3:122285218 | 3 | 122,285,218 | | 3'-UTR | c.*27A>? | | | | | 1E−19 | [20] |
| *PARP9* | | rs9841897 | 3 | 122,563,722 | | intronic | | | | | | 1E−10 | [21] |
| *PLXND1* | | rs56299595 | 3 | 129,559,339 | | intronic | | | | | | 2E−8 | [20] |
| *DNAJC13* | | rs17404153 | 3 | 132,444,356 | | intronic | | | | | | 2E−9 | [12] |
| *DNAJC13* | | rs113177823 | 3 | 132,498,859 | | intronic | | | | | | 8E−20; 1E−18 | [20][21] |
| *STAG1* | | rs28478252 | 3 | 136,402,758 | | intronic | | | | | | 4E−11 | [20] |
| *STAG1* | | rs3932048 | 3 | 136,540,082 | | intronic | | | | | | 6E−10 | [21] |
| *PAQR9, PCOLCE2* | | rs11709868 | 3 | 142,930,002 | | intergenic | | | | | | 4E−14 | [20] |
| *PCOLCE2, PAQR9* | | rs9832727 | 3 | 142,930,268 | | intergenic | | | | | | 2E−11; 3E−20 | [21][22] |
| *ZIC4, RPL21P71* | | rs113270900 | 3 | 147,316,110 | | intergenic | | | | | | 1E−8 | [22] |
| *RPL32P8, TM4SF1-AS1* | | rs7645585 | 3 | 149,406,996 | | intergenic | | | | | | 1E−8 | [22] |
| *SLC33A1* | | rs76440173 (rs138283229) | 3 | 155,828,335 | | missense | c.1525G>A | p.Gly509Ser | conflicting | probably damaging | deleterious | 5E−9 | [22] |
| *IFT80* | | rs4616688 | 3 | 160,324,671 | | intronic | | | | | | 5E−13 | [22] |
| *TNIK, SLC2A2* | | rs6785233 | 3 | 171,039,196 | | intergenic | | | | | | 3E−8; 4E−15 | [20][22] |
| *HGFAC* | *LRPAP1* | rs13108218 | 4 | 3,442,204 | | intronic | | | | | | 2E−26; 2E−16; 1E−43 | [20][21][22] |
| *DOK7* | | rs6831256 | 4 | 3,471,412 | | intronic | | | | | | 2E−8 | [12] |
| *SORCS2* | | rs4689653 | 4 | 7,221,592 | | intronic | | | | | | 6E−14 | [22] |
| *SORCS2* | | rs576573069 | 4 | 7,223,886 | | intronic | | | | | | 3E−9 | [21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *SH3TC1* | | rs2002574 | 4 | 8,222,549 | | intronic | | | | | | 2E−9 | [22] |
| *RBM47, RNU7-74P* | | rs203273 | 4 | 40,416,653 | | intergenic | | | | | | 5E−12 | [22] |
| *TMPRSS11E, UGT2B29P* | | rs9884390 | 4 | 68,507,689 | | intergenic | | | | | | 7E−24 | [21] |
| *UGT2B17, UGT2B15* | | rs4860987 | 4 | 68,625,566 | | intergenic | | | | | | 6E−49 | [22] |
| *UGT2B28 - UGT2B4* | | chr4:69455038 | 4 | 69,455,038 | | intergenic | | | | | | 4E−27 | [20] |
| *ADAMTS3* | | rs151193598 | 4 | 72,437,677 | | intronic | | | | | | 3E−10 | [15] |
| *ADAMTS3 - COX18* | | rs190671241 | 4 | 72,708,425 | | intergenic | | | | | | 2E−11 | [15] |
| *ADAMTS3 - COX18* | | chr4:72754788 | 4 | 72,754,788 | | intergenic | | | | | | 2E−6 | [15] |
| *ADAMTS3 - COX18* | | rs181948526 | 4 | 72,902,905 | | intergenic | | | | | | 9E−13 | [15] |
| *ADAMTS3 - COX18* | | chr4:72954415 | 4 | 72,954,415 | | intergenic | | | | | | 2E−6 | [15] |
| *ANKRD17* | | chr4:73134560 | 4 | 73,134,560 | | intronic | | | | | | 1E−7 | [15] |
| *ANKRD17* | | rs187918276 | 4 | 73,167,847 | | intronic | | | | | | 3E−13 | [15] |
| *ALB, ANKRD17* | | rs72663045 | 4 | 73,311,680 | | intergenic | | | | | | 6E−7 | [21] |
| *LINC02499* | | rs113759232 | 4 | 73,522,447 | | intergenic | | | | | | 2E−11 | [15] |
| *UMLILO, RASSF6* | | rs573930512 | 4 | 73,646,563 | | intergenic | | | | | | 8E−12 | [15] |
| *MTHFD2L* | | chr4:74133592 | 4 | 74,133,592 | | intronic | | | | | | 3E−6 | [15] |
| *MTHFD2L* | | rs182616603 | 4 | 74,219,015 | | intronic | | | | | | 2E−12 | [13] |
| *MTHFD2L* | | chr4:74265673 | 4 | 74,265,673 | | intronic | | | | | | 5E−12 | [15] |
| *AREG - BTC* | | chr4:74653273 | 4 | 74,653,273 | | intergenic | | | | | | 3E−8 | [15] |
| *BTC* | | chr4:74793806 | 4 | 74,793,806 | | intronic | | | | | | 2E−8 | [15] |
| *PARM1* | | chr4:74990001 | 4 | 74,990,001 | | intronic | | | | | | 8E−9 | [15] |
| *PARM1 - RCHY1* | | chr4:75242737 | 4 | 75,242,737 | | intergenic | | | | | | 6E−9 | [15] |
| *PARM1 - RCHY1* | | chr4:75422391 | 4 | 75,422,391 | | intergenic | | | | | | 1E−7 | [15] |
| *CDKL2* | | chr4:75583178 | 4 | 75,583,178 | | intronic | | | | | | 3E−6 | [15] |
| *G3BP2* | | chr4:75684215 | 4 | 75,684,215 | | intronic | | | | | | 4E−6 | [15] |
| *FGF5, PRDM8* | | rs1458038 | 4 | 80,243,569 | | intergenic | | | | | | 7E−16 | [21] |
| *AFF1* | | rs3775228 | 4 | 87,064,014 | | intronic | | | | | | 2E−12 | [20] |
| *ADH1B* | | rs1229984 | 4 | 99,318,162 | | missense | c.143A>G | p.His48Arg | protective | benign | tolerated | 1E−20; 7E−17 | [20][21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *SLC39A8* | | rs13107325 | 4 | 102,267,552 | | missense | c.970G>A | p.Ala391Thr | np | benign | tolerated | 1E−10; 6E−10 | [20][21] |
| *TRIM2* | | rs41280463 | 4 | 153,270,074 | | intronic | | | | | | 6E−10 | [20] |
| *FGB, PLRG1* | | rs114756490 | 4 | 154,555,475 | | intergenic | | | | | | 1E−11 | [20] |
| *FGB* | | rs6054 | 4 | 154,568,456 | | missense | c.794C>T | p.Pro265Leu | conflicting | probably damaging | tolerated | 6E−26 | [22] |
| *GUCY1A1* | | rs990619 | 4 | 155,586,526 | | intergenic | | | | | | 2E−8 | [21] |
| - | | rs2716769 | 4 | 179,549,287 | | intergenic | | | | | | 2E−7 | [17] |
| *CYP4V2* | | rs13146272 | 4 | 186,199,057 | | missense | c.775C>A | p.Gln259Lys | benign | benign | tolerated | 1E−7 | [16] |
| *RAI14* | | rs146433259 | 5 | 34,713,687 | | intronic | | | | | | 5E−8; 1E−9 | [21][22] |
| *IL7R, CAPSL* | | rs6871748 | 5 | 35,885,880 | | intergenic | | | | | | 5E−8 | [22] |
| *ITGA1* | | rs115421711 | 5 | 52,787,392 | | intergenic | | | | | | 2E−29 | [22] |
| *ITGA1, PELO* | | rs116734477 | 5 | 52,799,190 | | intronic | | | | | | 1E−20; 3E−19 | [20][21] |
| *ARL15* | | rs7735249 | 5 | 54,014,309 | | intronic | | | | | | 2E−8 | [22] |
| *C5orf67* | | rs547065676 | 5 | 56,561,722 | | intergenic | | | | | | 2E−31 | [22] |
| *C5orf67* | | rs3936511 | 5 | 56,564,954 | | intergenic | | | | | | 7E−18 | [20] |
| *C5orf67* | | rs9686661 | 5 | 56,565,959 | | intergenic | | | | | | 1E−8 | [21] |
| *LINC02056* | | rs2925677 | 5 | 72,657,802 | | intergenic | | | | | | 4E−14; 1E−13 | [20][21] |
| *LINC02056, RPL7P22* | | rs3010239 | 5 | 72,714,474 | | intergenic | | | | | | 2E−21 | [22] |
| *HMGCR, ANKRD31* | *HMGCR* | rs2335418 | 5 | 75,307,654 | | intergenic | | | | | | 5E−321 | [22] |
| *HMGCR* | | rs3843482 | 5 | 75,343,434 | | intronic | | | | | | 2E−45 | [13] |
| *HMGCR* | | rs12654264 | 5 | 75,352,778 | | intronic | c.1368+1176A>T | | association | | | 1E−20 | [2] |
| *HMGCR* | | rs3846662 | 5 | 75,355,259 | | intronic | | | | | | 2E−11 | [5] |
| *HMGCR, CERT1* | | rs3846663 | 5 | 75,359,901 | | intronic | | | | | | 8E−12; 2E−15; 5E−45; 1E−11; 8E−78; 1E−-222; 2E−187 | [4][19] [8][9][12] [20][21] |
| *HMGCR* | | rs12916 | 5 | 75,360,714 | | 3'-UTR | c.*372T>C | | np | | | | |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *CSNK1G3* | | rs7734476 | 5 | 123,513,182 | | intronic | | | | | | 2E−19; 4E−19 | [20][21] |
| *CSNK1G3* | | rs4530754 | 5 | 123,519,722 | | intronic | | | | | | 4E−12 | [12] |
| *SLC22A5* | | rs546280079 | 5 | 132,374,220 | | intronic | | | | | | 7E−9 | [20] |
| *SLC22A5, IRF1-AS1* | | rs1016988 | 5 | 132,408,882 | | intergenic | | | | | | 1E−12; 5E−11 | [16][21] |
| *CYSTM1* | | rs17118739 | 5 | 140,218,325 | | intronic | | | | | | 3E−9 | [20] |
| *HAVCR1, TIMD4* | *TIMD4* | rs6882076 | 5 | 156,963,286 | | intergenic | | | | | | 2E−22; 3E−31; 2E−69 | [8][12][20] |
| *HAVCR1, TIMD4* | | rs6874202 | 5 | 156,964,617 | | intergenic | | | | | | 1E−50 | [21] |
| *HAVCR1, TIMD4* | | rs1501908 | 5 | 156,971,158 | | intergenic | | | | | | 1E−11 | [4] |
| *HAVCR1* | | rs1553318 | 5 | 157,052,312 | | intronic | | | | | | 2E−15 | [13] |
| *FGFR4* | | rs351855 | 5 | 177,093,242 | | missense | c.1162G>A | p.Gly388Arg | uncertain | possibly damaging | tolerated | 1E−9 | [16] |
| *RN7SL554P* | | rs942922 | 6 | 6,972,360 | | intergenic | | | | | | 2E−8 | [22] |
| *ADTRP, AMD1P4* | | rs147539187 | 6 | 11,838,809 | | intergenic | | | | | | 1E−7 | [21] |
| *ADTRP, AMD1P4* | | rs771191353 | 6 | 11,856,024 | | intergenic | | | | | | 2E−8 | [20] |
| *AMD1P4* | | rs9470298 | 6 | 11,868,281 | | intergenic | | | | | | 5E−18 | [22] |
| *MYLIP, MDH1P2* | *MYLIP* | rs7746081 | 6 | 16,126,703 | | intergenic | | | | | | 1E−39; 5E−25 | [20][21] |
| *MYLIP, MDH1P2* | | rs3757354 | 6 | 16,127,176 | | intergenic | | | | | | 1E−11; 2E−17; 2E−9 | [8][12][13] |
| *MRPL42P2, RNU6-1114P* | | rs2142672 | 6 | 16,196,963 | | intergenic | | | | | | 2E−8 | [9] |
| *HFE* | *HFE* | rs1800562 | 6 | 26,092,913 | | missense | c.845G>A | p.Cys282Tyr | conflicting | possibly damaging | deleterious | 6E−10; 8E−14; 5E−44 | [8][12][20] |
| *HFE* | | rs79220007 | 6 | 26,098,246 | | 3'-UTR | c.*4020T>C | | np | | | 2E−48 | [21] |
| *MIR3143, RPL10P2* | | rs71559014 | 6 | 27,154,665 | | intergenic | | | | | | 1E−18 | [20] |
| *HIST1H1B* | | rs201148465 | 6 | 27,867,515 | | synonymous | c.15T>G | p.Ala5= | np | | tolerated | 3E−8 | [16] |
| *ZSCAN16-AS1* | | rs76079263 | 6 | 28,051,887 | | intergenic | | | | | | 4E−21 | [21] |
| *ZSCAN31* | | rs35814746 | 6 | 28,331,311 | | intronic | | | | | | 4E−16 | [20] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *HLA-H, HCP5B* | *HLA* | rs28849176 | 6 | 29,880,280 | | intergenic | | | | | | 1E−17 | [21] |
| *TRIM31-AS1, TRIM31* | | rs9378220 | 6 | 30,109,358 | | intronic | | | | | | 4E−18 | [20] |
| *HCG17* | | rs9391803 | 6 | 30,247,600 | | intronic | | | | | | 2E−19 | [21] |
| *HLA-B* | | rs3179865 | 6 | 31,356,417 | | synonymous | c.369C>T | p.Tyr123= | np | | tolerated | 2E−19 | [21] |
| *MICA, HLA-S* | | rs7741091 | 6 | 31,384,854 | | intergenic | | | | | | 3E−26 | [20] |
| *ATP6V1G2* | | rs34568880 | 6 | 31,546,671 | | 5'-UTR | c.-81G>A | | np | | | 6E−10 | [21] |
| *FKBPL - PRRT1* | | chr6:32153409 | 6 | 32,153,409 | | intergenic | | | | | | 3E−6 | [15] |
| *HLA-DRA* | | rs3177928 | 6 | 32,444,658 | | 3'-UTR | c.*18G>A | | np | | | 2E−15; 3E−17 | [8][12] |
| *HLA-DRB9, HLA-DRB5* | | rs114067101 | 6 | 32,490,183 | | intergenic | | | | | | 8E−13 | [13] |
| *HLA-DQA1* | | rs17205170 | 6 | 32,634,706 | | intronic | | | | | | 1E−44 | [20] |
| *MTCO3P1, HLA-DQB1* | | rs34392107 | 6 | 32,696,177 | | intergenic | | | | | | 6E−45 | [21] |
| *COL11A2* | *RXRB* | rs2254287 | 6 | 33,176,171 | | intronic | | | benign | | | 5E−8 | [1] |
| *ILRUN* | | rs76967117 | 6 | 34,635,914 | | intronic | | | | | | 2E−17 | [21] |
| *SNRPC* | | rs114863007 | 6 | 34,761,381 | | intronic | | | | | | 6E−15 | [20] |
| *COX6A1P2, RPL12P2* | | rs913499 | 6 | 37,070,656 | | intergenic | | | | | | 5E−11; 1E−8 | [20][21] |
| *KCNK17, KCNK5* | | rs4711589 | 6 | 39,262,795 | | intergenic | | | | | | 8E−9 | [20] |
| *KCNK17, KCNK5* | | rs55804343 | 6 | 39,267,131 | | intergenic | | | | | | 7E−8 | [21] |
| *CNPY3, RPL24P4* | | rs9471975 | 6 | 42,951,484 | | intergenic | | | | | | 1E−9 | [21] |
| *LINC02537, VEGFA* | | rs998584 | 6 | 43,790,159 | | intergenic | | | | | | 2E−10 | [20] |
| *TRAM2-AS1* | | rs2239619 | 6 | 52,588,422 | | intergenic | | | | | | 4E−15 | [16] |
| *LINC01564, KLHL31* | | rs12665537 | 6 | 53,644,654 | | intergenic | | | | | | 3E−11 | [20] |
| *PRDX2P4* | | rs9496567 | 6 | 100,154,877 | | intergenic | | | | | | 6E−13 | [21] |
| *PRDX2P4* | | rs17185536 | 6 | 100,173,055 | | intergenic | | | | | | 4E−15 | [20] |
| *PRDM1, RN7SKP211* | | rs4946713 | 6 | 105,926,140 | | intergenic | | | | | | 2E−8 | [20] |
| *FRK* | | rs9488822 | 6 | 115,991,730 | | intronic | | | | | | 3E−9; 2E−7 | [8][12] |
| *FRK* | | rs3822855 | 6 | 115,995,719 | | intronic | | | | | | 4E−17 | [21] |
| *FRK* | | rs35936182 | 6 | 116,023,963 | | intronic | | | | | | 1E−18 | [20] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *RSPO3* | | rs141783576 | 6 | 127,118,752 | | 5'-UTR | c.-441G>C | | np | | | 2E−11 | [20] |
| *RSPO3* | | rs9491699 | 6 | 127,150,388 | | intronic | | | | | | 2E−11 | [21] |
| *L3MBTL3* | | rs12197047 | 6 | 130,068,066 | | intronic | | | | | | 2E−9; 1E−9 | [20][21] |
| *HBS1L* | | rs7776054 | 6 | 135,097,778 | | intronic | | | | | | 7E−12 | [21] |
| *HBS1L* | | rs9389268 | 6 | 135,098,493 | | intronic | | | | | | 3E−15 | [20] |
| *REPS1, ABRACL* | | rs66883945 | 6 | 138,996,691 | | intergenic | | | | | | 3E−10 | [20] |
| *FNDC1 - SOD2* | *SLC22A1 - LPA* | rs12191504 | 6 | 159,537,803 | | intergenic | | | | | | 3E−8 | [20] |
| *IGF2R* | | rs73025516 | 6 | 160,099,774 | | intronic | | | | | | 9E−10 | [21] |
| *SLC22A1* | | rs12208357 | 6 | 160,122,116 | | missense | c.181C>T | p.Arg61Cys | np | probably damaging | deleterious | 3E−44 | [21] |
| *SLC22A1* | | rs2297374 | 6 | 160,154,953 | | intronic | | | | | | 5E−6 | [13] |
| *SLC22A1* | | rs146534110 | 6 | 160,157,037 | | intronic | | | | | | 9E−14 | [21] |
| *SLC22A1* | | rs1564348 | 6 | 160,157,828 | | intronic | | | | | | 2E−17; 3E−21; 2E−9 | [8][12][19] |
| *LPAL2* | | rs117733303 | 6 | 160,501,838 | | intronic | | | | | | 3E−27 | [21] |
| *LPA* | | rs118039278 | 6 | 160,564,494 | | intronic | | | | | | 6E−170; 2E−102 | [20][21] |
| *LPA* | | rs10455872 | 6 | 160,589,086 | | intronic | c.3947+467T>C | | drug response | | | 3E−321 | [22] |
| *LPA, PLG* | | rs186696265 | 6 | 160,690,668 | | intergenic | | | | | | 4E−14 | [13] |
| *C7orf50* | | rs10272002 | 7 | 1,007,979 | | intronic | | | | | | 3E−19 | [22] |
| *C7orf50* | | rs869412 | 7 | 1,034,498 | | intronic | | | | | | 1E−8 | [21] |
| *C7orf50* | | rs10275712 | 7 | 1,043,282 | | intronic | | | | | | 6E−12 | [20] |
| *RAC1* | | rs836550 | 7 | 6,400,806 | | intronic | | | | | | 5E−8 | [21] |
| *AHR* | | rs6968865 | 7 | 17,247,645 | | 5'-UTR | | | np | | | 4E−10 | [22] |
| *SP4, RNU1-15P* | *DNAH11* | rs28406917 | 7 | 21,409,833 | | intergenic | | | | | | 2E−8 | [21] |
| *DNAH11* | | rs56130071 | 7 | 21,559,135 | | intronic | | | | | | 2E−14; 5E−39 | [13][21] |
| *DNAH11* | | rs150169808 | 7 | 21,562,042 | | intronic | | | | | | 7E−50; 2E−87 | [20][22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *DNAH11* | *DNAH11* | rs12670798 | 7 | 21,567,734 | | intronic | | | | | | 6E−9; 7E−10; 5E−14 | [5][8][12] |
| *MIR148A* | | rs4722551 | 7 | 25,952,206 | | intergenic | | | | | | 4E−14; 2E−19; 1E−17; 6E−37 | [12][20][21] [22] |
| *JAZF1* | | rs12055996 | 7 | 28,152,174 | | intronic | | | | | | 4E−9 | [22] |
| *MARK2P13, EEPD1* | | rs67050321 | 7 | 36,129,593 | | intergenic | | | | | | 6E−13; 2E−11; 5E−20 | [20][21][22] |
| *INHBA-AS1* | | rs142220572 | 7 | 41,710,893 | | intergenic | | | | | | 2E−8 | [22] |
| *NPC1L1* | *NPC1L1* | rs2072183 | 7 | 44,539,581 | | synonymous | c.816C>G | p.Leu272= | benign | | tolerated | 4E−11; 7E−16 | [8][12] |
| *NPC1L1* | | rs41279633 | 7 | 44,541,277 | | 5'-UTR | c.-18C>A | | np | | | 1E−10 | [13] |
| *NPC1L1, DDX56* | | rs2073547 | 7 | 44,542,732 | | intergenic | | | | | | 5E−50; 2E−40; 4E−88 | [20][21][22] |
| *MLXIPL* | | rs799157 | 7 | 73,605,971 | | synonymous | c.759A>G | p.Ser253= | np | | tolerated | 9E−13 | [20] |
| *POR* | | rs2302429 | 7 | 75,985,459 | | intronic | | | | | | 1E−11 | [20] |
| *ABCB4* | | rs31674 | 7 | 87,439,148 | | intronic | | | | | | 6E−9 | [20] |
| *ABCB4* | | rs4148826 | 7 | 87,445,103 | | intronic | | | | | | 7E−9 | [21] |
| *BAIAP2L1* | | rs112758337 | 7 | 98,347,956 | | intronic | | | | | | 2E−9 | [21] |
| *PPIAP82, BAIAP2L1* | | rs377584195 | 7 | 98,405,352 | | intergenic | | | | | | 1E−12 | [20] |
| *MOSPD3, TFR2* | | rs10953298 | 7 | 100,619,150 | | intergenic | | | | | | 2E−17 | [20] |
| *EPO, ZAN* | | rs111338114 | 7 | 100,732,869 | | intergenic | | | | | | 5E−9 | [21] |
| *RPS29P15, MUC3A* | | rs10231941 | 7 | 100,934,914 | | intergenic | | | | | | 3E−13 | [21] |
| *PRKAR2B* | | rs257377 | 7 | 107,160,643 | | 3'-UTR | c.*1061G>T | | np | | | 2E−9 | [22] |
| *PPP1R3A* | | rs12705932 | 7 | 113,987,029 | | intronic | | | | | | 1E−6 | [17] |
| *CAPZA2* | | rs41785 | 7 | 116,845,966 | | intronic | | | | | | 9E−9 | [22] |
| *ZNF800* | | rs62621812 | 7 | 127,375,029 | | missense | c.307C>T | p.Pro103Ser | np | benign | tolerated | 3E−8 | [22] |
| *CEP41* | | chr7:130438531 | 7 | 130,438,531 | | intronic | | | | | | 4E−11 | [20] |
| *KLF14, H4P1* | | rs35363532 | 7 | 130,760,670 | | intergenic | | | | | | 3E−22 | [22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *BPGM, TUBB3P2* | | rs2347699 | 7 | 134,706,212 | | intergenic | | | | | | 3E−8 | [22] |
| *RN7SKP280, INSIG1-DT* | | rs4374942 | 7 | 155,235,097 | | intergenic | | | | | | 1E−12 | [22] |
| *MCPH1-AS1* | | rs2911987 | 8 | 6,707,055 | | intergenic | | | | | | 3E−11 | [22] |
| *RNU6-526P, RNU6-1151P* | *PPP1R3B* | rs7012637 | 8 | 9,315,699 | | intergenic | | | | | | 9E−45 | [20] |
| *RNU6-1151P, RNU6-526P* | | rs2169387 | 8 | 9,323,885 | | intergenic | | | | | | 3E−16 | [13] |
| *RNU6-526P, RNU6-1151P* | | rs9987289 | 8 | 9,325,848 | | intergenic | | | | | | 7E−15; 9E−24; 5E−36 | [8][12][21] |
| *RNU6-526P, RNU6-1151P* | | rs2126259 | 8 | 9,327,636 | | intergenic | | | | | | 7E−12 | [9] |
| *RNU6-1151P, RNU6-526P* | | rs1461729 | 8 | 9,329,732 | | intergenic | | | | | | 3E−6 | [19] |
| *TNKS* | | rs1350559 | 8 | 9,510,233 | | intergenic | | | | | | 2E−10 | [21] |
| *NAT2* | | rs1495741 | 8 | 18,415,371 | | intergenic | | | | | | 3E−28; 5E−12 | [20][21] |
| | | | 8 | 19,966,981 | | 3'-UTR | c.*1671T>C | | benign | | | 1E−21 | [20] |
| *DMTN* | | rs7386762 | 8 | 22,069,949 | | intronic | | | | | | 8E−13 | [20] |
| *DMTN* | | rs59328596 | 8 | 22,070,716 | | intronic | | | | | | 9E−10 | [21] |
| *KIF13B* | | rs117139027 | 8 | 29,167,426 | | missense | c.1105C>T | p.Arg369Trp | np | probably damaging | deleterious | 4E−15; 7E−13 | [20][21] |
| *ANK1* | | rs72638977 | 8 | 41,683,104 | | intronic | | | | | | 1E−8 | [21] |
| *TRMT112P7, RP1* | | rs10102164 | 8 | 54,509,054 | | intergenic | | | | | | 4E−11 | [12] |
| *RP1* | | rs9298506 | 8 | 54,524,964 | | intronic | | | | | | 3E−23; 3E−13 | [20][21] |
| | | | 8 | 58,476,006 | | intergenic | | | | | | 4E−9; 1E−7 | [8][12] |
| | | | 8 | 58,479,765 | | intergenic | | | | | | 2E−11 | [13] |
| | | | 8 | 58,480,714 | | intergenic | | | | | | 2E−56; 3E−46 | [20][21] |
| *RAB2A* | | rs5891768 | 8 | 60,563,015 | | intronic | | | | | | 2E−11 | [20] |
| *TMEM70* | | rs2306486 | 8 | 73,976,259 | | 5'-UTR | c.-23C>T | | benign | | | 4E−11 | [20] |
| *TMEM74 - TRHR* | | rs4620259 | 8 | 108,979,439 | | intergenic | | | | | | 5E−8 | [21] |
| *TRPS1* | | rs2737245 | 8 | 115,646,356 | | intronic | | | | | | 5E−30 | [20] |
| *TRPS1* | | rs2737265 | 8 | 115,655,407 | | intronic | | | | | | 2E−18 | [21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *TRIB1 - LRATD2* | *TRIB1* | rs2954021 | 8 | 125,469,835 | | intergenic | | | | | | 1E−7 | [9] |
| *TRIB1 - LRATD2* | | rs17321515 | 8 | 125,474,167 | | intergenic | | | | | | 5E−12 | [19] |
| *TRIB1 - LRATD2* | | rs2954029 | 8 | 125,478,730 | | intergenic | | | | | | 3E−29; 2E−50 | [8][12] |
| *TRIB1 - LRATD2* | | rs28601761 | 8 | 125,487,789 | | intergenic | | | | | | 6E−264; 1E−184 | [20][21] |
| *TRIB1 - LRATD2* | | rs6987702 | 8 | 125,492,484 | | intergenic | | | | | | 3E−6 | [5] |
| *TRIB1 - LRATD2* | | rs112875651 | 8 | 125,494,452 | | intergenic | | | | | | 4E−26 | [13] |
| *TRIB1 - LRATD2* | | chr8:126504383 | 8 | 126,504,383 | | intergenic | | | | | | 5E−324 | [22] |
| *PTK2* | | rs11997161 | 8 | 140,728,488 | | intronic | | | | | | 3E−8 | [22] |
| *PTK2* | | rs28768427 | 8 | 140,978,586 | | intronic | | | | | | 1E−8 | [21] |
| *PLEC* | | rs11781667 | 8 | 143,966,688 | | intergenic | | | | | | 4E−18 | [20] |
| *PLEC* | | rs11136341 | 8 | 143,969,375 | | intronic | | | | | | 4E−13; 7E−12 | [8][12] |
| *PLEC* | | rs11786083 | 8 | 143,976,190 | | intronic | | | | | | 7E−13 | [21] |
| *PARP10* | | rs1134027 | 8 | 143,977,246 | | 3'-UTR | c.*238C>T | | np | | | 2E−34 | [22] |
| *PARP10* | | rs11784833 | 8 | 143,989,244 | | intronic | | | | | | 2E−10 | [13] |
| *VLDLR* | *VLDLR* | rs3780181 | 9 | 2,640,759 | | intronic | | | | | | 2E−9; 2E−14; 3E−11; 1E−23 | [12][20][21] [22] |
| *BNC2* | | rs10810657 | 9 | 16,884,588 | | intergenic | | | | | | 1E−11; 5E−20 | [20][22] |
| *DENND4C* | | rs34150222 | 9 | 19,313,915 | | intronic | | | | | | 2E−12 | [20] |
| *RPS6* | | rs67710536 | 9 | 19,376,257 | | 3'-UTR | c.*36T>G | | np | | | 1E−10 | [16] |
| *CDKN2B-AS1* | | rs6475606 | 9 | 22,081,851 | | intergenic | | | | | | 2E−22 | [21] |
| *PCSK5* | | rs1571790 | 9 | 76,114,260 | | intronic | | | | | | 2E−11 | [20] |
| *PCSK5* | | rs6560499 | 9 | 76,115,850 | | intronic | | | | | | 8E−9 | [21] |
| *ABCA1* | *ABCA1* | rs2066714 | 9 | 104,824,472 | | missense | c.2649A>G | p.Ile883Met | benign | benign | tolerated | 2E−11 | [21] |
| *ABCA1* | | rs11789603 | 9 | 104,884,738 | | intronic | | | | | | 1E−13 | [21] |
| *ABCA1* | | rs2740488 | 9 | 104,899,461 | | intronic | | | | | | 5E−37; 8E−27 | [20][21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PKN3* | | rs13283282 | 9 | 128,703,202 | | intronic | | | | | | 3E−14; 3E−12 | [20][21] |
| | | | 9 | 133,266,456 | | intronic | | | association | | | 2E−228 | [22] |
| | | | 9 | 133,271,182 | | intronic | | | | | | 6E−20 | [13] |
| | | | 9 | 133,274,295 | | intronic | | | | | | 9E−96 | [21] |
| | | | 9 | 133,279,427 | | intergenic | | | | | | 8E−22 | [8] |
| | | | 9 | 133,279,427 | | intergenic | | | | | | 2E−41 | [12] |
| *TMEM250 - LHX3* | | chr9:136138765 | 9 | 136,138,765 | | intergenic | | | | | | 7E−136 | [20] |
| *INPP5E, PMPCA* | | rs10448340 | 9 | 136,425,617 | | intergenic | | | | | | 1E−11; 6E−16 | [21][22] |
| *PMPCA, INPP5E* | | rs34297856 | 9 | 136,427,993 | | intergenic | | | | | | 2E−9 | [20] |
| *SEC16A* | | rs3812594 | 9 | 136,474,501 | | missense | c.3115C>T | p.Arg1039Cys | np | benign | tolerated | 1E−12 | [16] |
| *RBM17, RPL32P23* | | rs75641219 | 10 | 6,087,347 | | intergenic | | | | | | 3E−8 | [22] |
| *GATA3* | | rs3824667 | 10 | 8,058,162 | | intronic | | | | | | 3E−8 | [22] |
| *TRDMT1, VIM-AS1* | | rs10795464 | 10 | 17,213,096 | | intergenic | | | | | | 3E−13 | [22] |
| *CACNB2* | | rs1757216 | 10 | 18,217,497 | | intronic | | | | | | 1E−8 | [22] |
| *CACNB2* | | rs11014204 | 10 | 18,431,916 | | intronic | | | | | | 3E−9 | [21] |
| *ARHGAP12, RPL34P19* | | rs201700897 (rs796526078) | 10 | 31,957,010 | | intronic | | | | | | 1E−10 | [22] |
| *MARCHF8* | | rs7908745 | 10 | 45,458,319 | | missense | c.1642T>C | p.Tyr548His | np | benign | tolerated | 6E−11 | [22] |
| *SGMS1* | | rs79828839 | 10 | 50,592,671 | | intronic | | | | | | 2E−8 | [21] |
| *A1CF* | | rs41274050 | 10 | 50,814,012 | | missense | c.1168G>A | p.Gly390Ser | likely benign | probably damaging | tolerated | 4E−13 | [20] |
| *JMJD1C* | | rs10761756 | 10 | 63,412,568 | | intronic | | | | | | 1E−9 | [20] |
| *REEP3* | | rs7090758 | 10 | 63,575,555 | | intronic | | | | | | 2E−8 | [21] |
| *HK1* | | rs16926246 | 10 | 69,333,636 | | intronic | | | | | | 2E−18 | [20] |
| *HK1* | | rs17476364 | 10 | 69,334,748 | | intronic | | | | | | 9E−11 | [21] |
| *CYP26A1, NIP7P1* | | rs2068888 | 10 | 93,079,885 | | intergenic | | | | | | 6E−32; 5E−20; 2E−46 | [20][21][22] |
| *PKD2L1* | | rs603424 | 10 | 100,315,722 | | intronic | | | | | | 3E−11 | [20] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *GPAM* | | rs1129555 | 10 | 112,150,963 | | 3'-UTR | c.*2587T>C | | np | | | 5E−7 | [13] |
| *GPAM* | | rs2250802 | 10 | 112,161,596 | | intronic | | | | | | 6E−15 | [21] |
| *GPAM* | | rs2792735 | 10 | 112,162,067 | | intronic | | | | | | 6E−19 | [20] |
| *GPAM* | | rs2255141 | 10 | 112,174,128 | | intronic | | | | | | 2E−9; 1E−13 | [8][12] |
| *ADRB1* | | rs72823013 | 10 | 114,026,474 | | intergenic | | | | | | 2E−10 | [22] |
| *ADRB1* | | rs72823020 | 10 | 114,038,188 | | intergenic | | | | | | 6E−12 | [21] |
| *PNLIPRP2* | | rs4751996 | 10 | 116,638,383 | | missense | c.1084G>A | p.Val361Ile | np | benign | tolerated | 4E−10;1E−17 | [20][22] |
| *PNLIPRP2* | | rs10885997 | 10 | 116,638,460 | | synonymous | c.1161A>G | p.Ser387= | np | | tolerated | 7E−9 | [16] |
| *FAM24B* | | rs1891110 | 10 | 122,850,511 | | missense | c.5C>T | p.Pro2Leu | np | benign | tolerated | 2E−31 | [16] |
| *C10orf88, FAM24A* | | rs10794579 | 10 | 122,927,140 | | intergenic | | | | | | 7E−20; 2E−25 | [20][22] |
| *C10orf88* | | rs12246352 | 10 | 122,945,791 | | intronic | | | | | | 7E−14 | [21] |
| *CEND1, GATD1* | | rs61876729 | 11 | 778,857 | | intergenic | | | | | | 6E−10 | [22] |
| *NAP1L4* | | rs61871243 | 11 | 2,977,392 | | intronic | | | | | | 7E−11 | [22] |
| *TRIM6-TRIM34, TRIM5* | | rs7108486 | 11 | 5,655,928 | | intronic | | | | | | 2E−8 | [21] |
| *TRIM5* | | rs11601507 | 11 | 5,679,844 | | missense | c.334G>A | p.Val112Phe | np | benign | deleterious | 3E−24; 2E−15; 3E−40 | [20][21][22] |
| *COPB1* | | rs769117329 | 11 | 14,477,390 | | intronic | | | | | | 2E−8 | [22] |
| *SPTY2D1* | | rs10128711 | 11 | 18,611,437 | | intronic | | | | | | 5E−13 | [20] |
| *SPTY2D1* | | rs10500834 | 11 | 18,617,165 | | intronic | | | | | | 1E−28 | [22] |
| *SPTY2D1, SRSF3P1* | | rs10832963 | 11 | 18,642,694 | | intergenic | | | | | | 4E−13 | [21] |
| *CSRP3-AS1, NAV2* | | rs4756996 | 11 | 19,333,933 | | intergenic | | | | | | 5E−7 | [17] |
| *LUZP2 - ANO3* | | rs1489502 | 11 | 26,061,460 | | intergenic | | | | | | 3E−9 | [22] |
| *THEM7P* | | rs79953563 | 11 | 32,131,922 | | intronic | | | | | | 9E−13 | [22] |
| *FADS1* | *FADS1* | rs174546 | 11 | 61,802,358 | | 3'-UTR | c.*53G>A | | np | | | 1E−7; 1E−21; 2E−39 | [6][8][12] |
| *FADS1* | | rs174547 | 11 | 61,803,311 | | intronic | | | | | | 6E−9 | [19] |
| *FADS1* | | rs174551 | 11 | 61,806,212 | | intronic | | | | | | 2E−27 | [13] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *FADS2* | *FADS1* | rs174564 | 11 | 61,820,833 | | intronic | | | | | | 6E−63; 3E−48 | [20][21] |
| *FADS2* | | rs174570 | 11 | 61,829,740 | | intronic | | | | | | 4E−13 | [5] |
| *NAA40* | | rs11373615 | 11 | 63,941,561 | | intronic | | | | | | 4E−8 | [20] |
| *RELA* | | rs11227247 | 11 | 65,655,382 | | intronic | | | | | | 6E−9 | [21] |
| *MRPL11* | | rs550317996 | 11 | 66,461,002 | | intronic | | | | | | 2E−10 | [20] |
| *ZDHHC24, BBS1* | | rs74869459 | 11 | 66,529,098 | | intronic | | | | | | 3E−12 | [21] |
| *PDGFD* | | rs115739682 | 11 | 103,999,912 | | intronic | | | | | | 1E−9 | [21] |
| *PDGFD* | | rs10791660 | 11 | 104,000,311 | | intronic | | | | | | 4E−11 | [20] |
| *TMPRSS5, MTRF1LP1* | | rs45543538 | 11 | 113,707,269 | | intergenic | | | | | | 2E−8 | [20] |
| *LINC02702, BUD13* | *APOA1-C3-A4-A5* | rs12272004 | 11 | 116,733,008 | | intergenic | | | | | | 5E−13 | [5] |
| *LINC02702, BUD13* | | rs1558861 | 11 | 116,736,721 | | intergenic | | | | | | 2E−6 | [9] |
| *ZPR1 (ZNF259)* | | rs964184 | 11 | 116,778,201 | | 3'-UTR | c.*724C>G | | np | | | 1E−26; 2E−26; 4E−18; 2E−163; 2E−78; 2E−316 | [8][12][13] [20][21][22] |
| *IFT46* | | rs7110984 | 11 | 118,571,519 | | intronic | | | | | | 9E−9 | [20] |
| *UBASH3B, GLULP3* | | rs6589939 | 11 | 122,647,817 | | intergenic | | | | | | 7E−10 | [21] |
| *UBASH3B, GLULP3* | | rs7941030 | 11 | 122,651,667 | | intergenic | | | | | | 3E−13 | [20] |
| *ST3GAL4* | *ST3GAL4* | rs112771035 | 11 | 126,355,981 | | intronic | | | | | | 8E−55 | [20] |
| *ST3GAL4* | | rs1893351 | 11 | 126,357,131 | | intronic | | | | | | 4E−10 | [22] |
| *ST3GAL4* | | rs59379014 | 11 | 126,358,105 | | intronic | | | | | | 3E−43 | [21] |
| *ST3GAL4* | | rs11220462 | 11 | 126,374,057 | | intronic | | | | | | 1E−15; 7E−21 | [8][12] |
| *ST3GAL4* | | rs4307732 | 11 | 126,375,060 | | intronic | | | | | | 3E−12 | [13] |
| *B4GALNT3* | | rs35882350 | 12 | 513,963 | | intronic | | | | | | 2E−14; 5E−9; 2E−18 | [20][21][22] |
| *CCND2* | | rs76895963 | 12 | 4,275,678 | | intronic | | | | | | 9E−11; 1E−21 | [20][22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *CD163L1, CD163* | | rs117692263 | 12 | 7,472,418 | | intronic | | | | | | 2E−8 | [22] |
| *LINC00612, VDAC2P2* | | rs881376 | 12 | 9,050,157 | | intergenic | | | | | | 5E−12 | [20] |
| *LINC00612, VDAC2P2* | | rs201319146 | 12 | 9,053,207 | | intergenic | | | | | | 2E−20 | [22] |
| *ETV6* | | rs117864888 | 12 | 11,744,963 | | intronic | | | | | | 3E−8 | [22] |
| *KRAS* | | rs12318598 | 12 | 25,254,792 | | intergenic | | | | | | 3E−11 | [22] |
| *ITPR2* | | rs1007938 | 12 | 26,649,616 | | intronic | | | | | | 1E−8 | [21] |
| *ITPR2* | | rs111626763 | 12 | 26,681,872 | | splice region | | | np | | | 2E−8 | [22] |
| *ERGIC2* | | rs10843391 | 12 | 29,355,709 | | intronic | | | | | | 3E−8 | [22] |
| *RESF1* | | rs4931005 | 12 | 31,992,066 | | intronic | | | | | | 2E−8 | [22] |
| *SLC2A13* | | rs10877955 | 12 | 40,027,315 | | intronic | | | | | | 5E−13 | [22] |
| *SLC2A13, LINC02555* | | rs2253736 | 12 | 40,139,535 | | intergenic | | | | | | 2E−9 | [20] |
| *LIMA1* | | rs2160994 | 12 | 50,256,274 | | intronic | | | | | | 7E−15; 4E−17 | [20][21] |
| *SCN8A* | | chr12:51779544 | 12 | 51,779,544 | | intronic | | | | | | 2E−11 | [20] |
| *R3HDM2* | | rs10649122 | 12 | 57,256,817 | | intronic | | | | | | 2E−12 | [20] |
| *RAB21* | | rs61754230 | 12 | 71,785,666 | | missense | c.671C>T | p.Ser224Phe | np | probably damaging | deleterious | 4E−12; 4E−15; 1E−8 | [16][20][21] |
| *SLC17A8* | | rs749921369 | 12 | 100,395,327 | | intergenic | | | | | | 7E−11 | [20] |
| *WASHC4 (KIAA1033)* | | rs1663564 | 12 | 105,152,394 | | missense | c.2701G>A | p.Val902Ile | np | benign | tolerated | 1E−8 | [20] |
| *MVK* | | rs71079573 | 12 | 109,583,090 | | intronic | | | | | | 3E−8 | [20] |
| *ATXN2* | | rs597808 | 12 | 111,535,554 | | intronic | | | | | | 4E−23; 2E−38 | [20][21] |
| *BRAP, ATXN2-AS* | | rs11065987 | 12 | 111,634,620 | | intergenic | | | | | | 2E−9; 1E−11 | [8][12] |
| *RPH3A* | | rs233721 | 12 | 112,593,739 | | intronic | | | | | | 2E−18 | [21] |
| *RPH3A* | | rs233716 | 12 | 112,602,139 | | intronic | | | | | | 5E−13 | [20] |
| *KSR2* | | rs4767631 | 12 | 117,873,938 | | intronic | | | | | | 6E−7 | [7] |
| | | | 12 | 120,951,159 | | intergenic | | | | | | 2E−8 | [4] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *HNF1A* | *HNF1A* | rs1169288 | 12 | 120,978,847 | | missense | c.79A>C | p.Ile27Leu | benign | benign | tolerated | 1E−15; 6E−21; 4E−45; 3E−76 | [8][12][20] [22] |
| *HNF1A* | | rs1169294 | 12 | 120,988,791 | | intronic | | | | | | 2E−27 | [21] |
| *C12orf43* | | rs1169314 | 12 | 121,005,313 | | intronic | | | | | | 2E−8 | [13] |
| *DNAH10* | | rs11057353 | 12 | 123,781,140 | | missense | c.499T>C | p.Ser167Pro | benign | benign | tolerated | 4E−12 | [20] |
| *SCARB1* | | rs112403212 | 12 | 124,818,708 | | intronic | | | | | | 1E−8 | [21] |
| *SCARB1* | | rs11057830 | 12 | 124,822,507 | | intronic | | | | | | 2E−15 | [20] |
| *FBRSL1* | | rs12826964 | 12 | 132,564,267 | | intronic | | | | | | 5E−9 | [20] |
| *HMGB1, UBE2L5* | | rs1331698 | 13 | 30,442,842 | | intergenic | | | | | | 8E−11 | [22] |
| *BRCA2* | | rs4942486 | 13 | 32,379,251 | | intronic | c.8755-66T>C | | benign | | | 2E−11 | [12] |
| *BRCA2, IFIT1P1* | | rs2238162 | 13 | 32,385,062 | | intronic | | | | | | 4E−15 | [21] |
| *PDS5B - KL* | | chr13:32976656 | 13 | 32,976,656 | | intergenic | | | | | | 8E−27; 4E−47 | [20][22] |
| *SETDB2* | | rs11386165 | 13 | 49,474,266 | | intronic | | | | | | 5E−8 | [22] |
| *DLEU1* | | rs201796 | 13 | 50,381,960 | | intergenic | | | | | | 2E−8 | [20] |
| *DLEU1* | | rs67854369 | 13 | 50,471,162 | | intergenic | | | | | | 4E−9 | [22] |
| *KLF12* | | rs112679104 | 13 | 74,132,814 | | intronic | | | | | | 6E−10 | [22] |
| *COL4A2* | | rs551473284 | 13 | 110,385,978 | | intronic | | | | | | 2E−9; 1E−9 | [20][21] |
| *COL4A2* | | rs75816352 | 13 | 110,385,979 | | intronic | | | | | | 7E−14 | [22] |
| *GAS6-AS1, GAS6* | | rs7140110 | 13 | 113,841,051 | | intronic | | | | | | 2E−28 | [20] |
| *GAS6-AS1, GAS6* | | rs6602912 | 13 | 113,843,576 | | intronic | | | | | | 6E−22 | [21] |
| *GAS6* | | rs6602909 | 13 | 113,849,020 | | intronic | | | | | | 3E−47 | [22] |
| | | | 14 | 24,402,720 | | intronic | | | | | | 2E−8; 9E−23; 1E−19; 5E−43 | [13][20][21] [22] |
| | | | 14 | 24,414,681 | | missense | c.2932G>A | p.Ala978Thr | np | benign | tolerated | 4E−11; 3E−15 | [8][12] |
| *HECTD1 - HEATR5A* | | rs139262716 | 14 | 31,255,905 | | intergenic | | | | | | 1E−8 | [22] |
| *CFL2, RPL12P6* | | rs11846704 | 14 | 34,717,488 | | intergenic | | | | | | 3E−9 | [22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *RPL12P6, CFL2* | | rs10151517 | 14 | 34,718,046 | | intergenic | | | | | | 5E−8 | [20] |
| *SYNE2* | | rs8008068 | 14 | 63,766,999 | | intronic | | | | | | 4E−8 | [21] |
| *ESR2* | | chr14:64236436 | 14 | 64,236,436 | | intronic | | | | | | 7E−12; 4E−17 | [20][22] |
| *ADAM21P1, COX16* | | rs8005362 | 14 | 70,304,150 | | intergenic | | | | | | 2E−25 | [22] |
| *ADAM20, MED6* | | rs6573971 | 14 | 70,544,752 | | intergenic | | | | | | 3E−10 | [21] |
| *RN7SL77P, TTC9* | | rs9646133 | 14 | 70,629,627 | | intergenic | | | | | | 5E−22 | [16] |
| *MAP3K9 - PCNX1* | | chr14:70874146 | 14 | 70,874,146 | | intergenic | | | | | | 4E−14 | [20] |
| *ZFYVE1* | | rs61988556 | 14 | 72,972,550 | | intronic | | | | | | 2E−9 | [21] |
| *MIDEAS* | | rs13379043 | 14 | 73,783,423 | | intronic | | | | | | 2E−6; 4E−13; 8E−24 | [16][20][22] |
| | | | 14 | 94,301,859 | | intergenic | | | | | | 4E−12 | [21] |
| | | | 14 | 94,378,610 | | missense | c.1096G>A | p.Glu366Lys | pathogenic | probably damaging | deleterious | 1E−21 | [16] |
| | | | 14 | 94,380,925 | | missense | c.863A>T | p.Glu288Val | conflicting | probably damaging | deleterious | 2E−15; 4E−30 | [20][22] |
| *LINC00637, ATP5MJ* | | rs12891477 | 14 | 103,866,422 | | intergenic | | | | | | 3E−12 | [22] |
| *SECISBP2L* | | rs7164309 | 15 | 49,025,561 | | intronic | | | | | | 3E−9 | [20] |
| *FAM227B* | | rs10851478 | 15 | 49,536,822 | | intronic | | | | | | 6E−9 | [21] |
| *FAM227B* | | rs566865466 | 15 | 49,550,054 | | intronic | | | | | | 6E−12 | [22] |
| *WDR72* | | rs79391862 | 15 | 53,447,229 | | intergenic | | | | | | 9E−11 | [22] |
| | | | 15 | 57,220,086 | | intronic | | | | | | 2E−9 | [21] |
| | | | 15 | 57,240,500 | | intronic | | | | | | 4E−17 | [20] |
| | | | 15 | 58,391,167 | | intronic | | | | | | 9E−16 | [21] |
| | | | 15 | 58,430,392 | | intronic | | | | | | 1E−43 | [22] |
| | | | 15 | 58,434,545 | | intronic | | | | | | 9E−18 | [21] |
| *ADAM10* | | chr15:58679807 | 15 | 58,679,807 | | intronic | | | | | | 2E−30 | [20] |
| *C2CD4A, NPM1P47* | | rs72749770 | 15 | 62,073,266 | | intergenic | | | | | | 9E−10 | [22] |
| *TPM1* | | rs76162994 | 15 | 63,036,763 | | intergenic | | | | | | 4E−8 | [22] |
| *USP3, LINC02568* | | rs11636087 | 15 | 63,496,068 | | intergenic | | | | | | 2E−17 | [22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *USP3, LINC02568* | | rs62011285 | 15 | 63,498,864 | | intergenic | | | | | | 2E−8 | [21] |
| *USP3, LINC02568* | | rs56369308 | 15 | 63,500,058 | | intergenic | | | | | | 1E−12 | [20] |
| *LMAN1L* | | rs112987086 | 15 | 74,814,378 | | intronic | | | | | | 1E−11 | [21] |
| *LMAN1L* | | rs12917376 | 15 | 74,823,826 | | intronic | | | | | | 4E−8 | [20] |
| *SCAMP2, MPI* | | rs9673065 | 15 | 74,888,551 | | intergenic | | | | | | 2E−11 | [22] |
| *CRTC3, IQGAP1* | | rs56402930 | 15 | 90,529,730 | | intergenic | | | | | | 8E−6 | [21] |
| *CRTC3* | | rs6496691 | 15 | 90,566,379 | | intronic | | | | | | 2E−9 | [22] |
| *PCSK6* | | rs34631529 | 15 | 101,305,277 | | missense | c.2891C>T | p.Thr964Met | likely benign | probably damaging | deleterious | 6E−9 | [22] |
| *LITAF* | | rs12445804 | 16 | 11,612,244 | | intronic | | | | | | 7E−14; 8E−9; 5E−23 | [20][21][22] |
| *Y_RNA, MIR193BHG* | | rs246179 | 16 | 14,287,318 | | intergenic | | | | | | 8E−9 | [22] |
| *STX1B* | | rs12920772 | 16 | 31,001,460 | | intronic | | | | | | 8E−11 | [20] |
| *FTO* | | rs62033400 | 16 | 53,777,876 | | intronic | | | | | | 1E−11 | [21] |
| *CETP, HERPUD1* | *CETP* | rs247617 | 16 | 56,956,804 | | intergenic | | | | | | 2E−24 | [13] |
| *HERPUD1, CETP* | | rs183130 | 16 | 56,957,451 | | intergenic | | | association | | | 8E−59 | [20] |
| *HERPUD1, CETP* | | rs3764261 | 16 | 56,959,412 | | intergenic | | | no interp. | | | 9E−13; 2E−34; 1E−49 | [8][12][21] |
| *WWP2* | | rs78432537 | 16 | 69,839,928 | | intronic | | | | | | 5E−9 | [20] |
| *HYDIN* | | rs56212732 | 16 | 70,896,467 | | intronic | | | | | | 2E−9 | [21] |
| *HYDIN* | | rs145090930 | 16 | 70,922,412 | | intronic | | | | | | 1E−11 | [20] |
| *MARVELD3, TAT-AS1* | *TNXL4B* | rs9929977 | 16 | 71,605,150 | | intergenic | | | | | | 1E−14 | [21] |
| *DHODH* | | rs11648003 | 16 | 72,018,449 | | intronic | | | | | | 2E−20 | [13] |
| *TXNL4B, HPR* | | rs34042070 | 16 | 72,067,626 | | intronic | | | | | | 5E−105; 2E−73; 1E−177 | [20][21][22] |
| *HPR, TXNL4B* | | rs2000999 | 16 | 72,074,194 | | intronic | | | | | | 2E−22; 4E−41 | [8][12] |
| *PMFBP1, LINC01572* | | rs7202323 | 16 | 72,183,214 | | intergenic | | | | | | 8E−25 | [21] |
| *MAF* | | rs1862719 | 16 | 79,470,160 | | intronic | | | | | | 8E−11 | [22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *OSGIN1, MLYCD* | | rs4782568 | 16 | 83,946,924 | | intronic | | | | | | 8E−15; 6E−15; 1E−24 | [20][21][22] |
| *ZFPM1* | | rs139829677 | 16 | 88,502,880 | | intronic | | | | | | 1E−13 | [22] |
| *ZFPM1* | | rs147032017 | 16 | 88,514,388 | | synonymous | c.270C>T | p.Asp90= | np | | tolerated | 5E−9 | [16] |
| *ZFPM1-AS1, ZFPM1* | | rs77013160 | 16 | 88,516,463 | | intronic | | | | | | 6E−9; 2E−8 | [20][21] |
| *WDR81* | | rs11431553 | 17 | 1,719,561 | | intronic | | | | | | 3E−10 | [22] |
| *DPH1* | | rs7207466 | 17 | 2,039,567 | | intronic | | | | | | 6E−10 | [22] |
| *ASGR1* | | rs55714927 | 17 | 7,176,997 | | synonymous | c.267G>A | p.Lys89= | np | | tolerated | 9E−12; 7E−37; 4E−23 | [13][20][21] |
| *DLG4* | | rs314253 | 17 | 7,188,331 | | 3'-UTR | c.*2377A>G | | np | | | 3E−10 | [12] |
| *TP53* | | rs9894946 | 17 | 7,667,762 | | intronic | | | | | | 2E−9 | [21] |
| *RAI1* | | rs71367412 | 17 | 17,717,693 | | intronic | | | | | | 6E−9 | [20] |
| *VTN* | | rs704 | 17 | 28,367,840 | | missense | c.1199C>T | p.Thr400Met | np | benign | tolerated | 5E−29; 3E−15; 9E−13 | [16][20][21] |
| *TAOK1, ABHD15* | | rs56208742 | 17 | 29,557,649 | | intergenic | | | | | | 1E−11; 2E−8 | [20][21] |
| *NF1* | | rs12603885 | 17 | 31,139,704 | | intronic | | | | | | 3E−14; 1E−14 | [20][21] |
| *NF1* | | rs11080150 | 17 | 31,302,308 | | intronic | | | | | | 1E−7 | [16] |
| *STAT5A* | | rs28727898 | 17 | 42,297,600 | | intronic | | | | | | 2E−9 | [20] |
| *EFCAB13* | *OSBPL7* | rs7206971 | 17 | 47,347,749 | | intronic | | | | | | 4E−9; 3E−7; 4E−10 | [8][12][13] |
| *NPEPPS* | | rs36043200 | 17 | 47,552,040 | | intronic | | | | | | 1E−36 | [21] |
| *NPEPPS* | | rs10445374 | 17 | 47,585,017 | | intronic | | | | | | 2E−46 | [20] |
| *LINC02086* | | rs3110609 | 17 | 48,676,181 | | intergenic | | | | | | 3E−12 | [21] |
| *LINC02086* | | rs3096644 | 17 | 48,680,213 | | intergenic | | | | | | 3E−13 | [20] |
| *APOH* | *APOH* | rs1801689 | 17 | 66,214,462 | | missense | c.973T>G | p.Cys325Gly | np | probably damaging | deleterious | 1E−11; 1E−30; 2E−24 | [12][20][21] |
| *ARSG* | *ABCA6* | rs12936113 | 17 | 68,404,922 | | intronic | | | | | | 2E−8 | [21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *ABCA6* | *ABCA6* | rs77542162 | 17 | 69,085,137 | | missense | c.4075T>C | p.Cys1359Arg | np | probably damaging | deleterious | 2E−18; 2E−98; 6E−74; 3E−169 | [13][20][21] [22] |
| *ABCA10* | | rs72631343 | 17 | 69,195,129 | | intronic | | | | | | 5E−21 | [21] |
| *H3-3B* | | rs73352129 | 17 | 75,782,528 | | intronic | | | | | | 1E−13 | [20] |
| *UNK* | | rs2125345 | 17 | 75,786,110 | | intronic | | | | | | 3E−22 | [16] |
| *TRIM65* | | rs56000661 | 17 | 75,882,573 | | intronic | | | | | | 1E−23 | [22] |
| *PGS1* | | rs12948394 | 17 | 78,386,710 | | intronic | | | | | | 5E−15; 5E−18; 2E−25 | [20][21][22] |
| *FOXK2* | | rs3736206 | 17 | 82,572,553 | | intronic | | | | | | 2E−9 | [22] |
| *B3GNTL1* | | rs111571253 | 17 | 83,051,228 | | intronic | | | | | | 1E−8 | [22] |
| *CTAGE1* | | rs79588679 | 18 | 22,327,807 | | intergenic | | | | | | 4E−8 | [13] |
| *NPC1* | *NPC1* | rs2510344 | 18 | 23,533,321 | | intronic | c.3754+34A>G | | benign | | | 2E−9 | [22] |
| *TAF4B* | | rs12960731 | 18 | 26,338,309 | | intronic | | | | | | 8E−7 | [17] |
| *LIPG* | *LIPG* | rs77960347 | 18 | 49,583,585 | | missense | c.1187A>G | p.Asn396Ser | np | probably damaging | tolerated | 6E−14; 8E−15; 3E−24 | [20][21][22] |
| *LIPG, SMUG1P1* | | rs7241918 | 18 | 49,634,583 | | intergenic | | | | | | 1E−8 | [21] |
| *ATP8B1* | | rs369298568 | 18 | 57,651,800 | | intronic | | | | | | 5E−12 | [22] |
| *THOP1* | | rs2741991 | 19 | 2,802,094 | | intronic | | | | | | 3E−9 | [20] |
| *THOP1* | | rs1640273 | 19 | 2,803,229 | | intronic | | | | | | 4E−11 | [22] |
| *HDGFL2* | | rs111174163 | 19 | 4,492,942 | | intronic | | | | | | 9E−10 | [22] |
| *S1PR5, ATG4D* | *LDLR* | rs549956721 | 19 | 10,526,288 | | intergenic | | | | | | 2E−10 | [21] |
| *DNM2* | | chr19:10734951 | 19 | 10,734,951 | | intronic | | | | | | 7E−10 | [15] |
| *YIPF2 - SMARCA4* | | chr19:10948031 | 19 | 10,948,031 | | intergenic | | | | | | 1E−11 | [15] |
| *SMARCA4* | | rs1122608 | 19 | 11,052,925 | | intronic | | | | | | 1E−14 | [19] |
| *SMARCA4* | | rs10423733 | 19 | 11,075,243 | | intronic | | | | | | 3E−428 | [20] |
| *SMARCA4* | | rs143020224 | 19 | 11,076,648 | | intronic | | | | | | 9E−605 | [21] |
| *SMARCA4* | | rs112374545 | 19 | 11,078,223 | | intronic | | | | | | 7E−142 | [13] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 19 | 11,084,354 | | intronic | | | | | | 2E−7 | [6] |
| | | | 19 | 11,091,630 | | intronic | c.67+2015G>T | | benign | | | 2E−26; 2E−51; 4E−26; 4E−117; 4E−262 | [1][2][4][8] [12] |
| | | | 19 | 11,100,236 | | synonymous | c.81C>T | p.Cys27= | benign | | tolerated | 4E−14 | [5] |
| | | | 19 | 11,116,804 | | intronic | c.1706-55A>C | | benign | | | 4E−89 | [21] |
| | | | 19 | 11,127,797 | | intronic | | | | | | 7E−6 | [9] |
| | | | 19 | 11,198,502 | | intergenic | | | | | | 2E−23 | [15] |
| | | | 19 | 11,224,801 | | intronic | | | | | | 6E−16 | [21] |
| *RGL3* | | chr19:11398422 | 19 | 11,398,422 | | intronic | | | | | | 5E−15 | [15] |
| *ECSIT* | | chr19:11507217 | 19 | 11,507,217 | | intronic | | | | | | 3E−8 | [15] |
| *ZNF441 - ZNF491* | | chr19:11789826 | 19 | 11,789,826 | | intergenic | | | | | | 2E−7 | [15] |
| *ZNF788P, ZNF20* | | rs117590032 | 19 | 12,095,815 | | intronic | | | | | | 5E−8 | [20] |
| *CYP4F12* | | rs4808360 | 19 | 15,687,205 | | intronic | | | | | | 8E−10 | [21] |
| *PDE4C* | | rs62120394 | 19 | 18,227,899 | | intronic | | | | | | 6E−12 | [21] |
| *PDE4C* | | rs8112975 | 19 | 18,230,100 | | intronic | | | | | | 6E−12 | [20] |
| | | | 19 | 19,259,532 | | intronic | | | | | | 3E−11 | [14] |
| | | | 19 | 19,268,740 | | missense | c.499G>A | p.Glu167Lys | np | possibly damaging | tolerated | 3E−186 | [20] |
| | | | 19 | 19,277,691 | | intronic | | | | | | 2E−158 | [21] |
| | | | 19 | 19,285,807 | | intronic | | | | | | 9E−37 | [21] |
| | | | 19 | 19,296,909 | | intronic | | | | | | 2E−8; 7E−22; 1E−11; 3E−54; 3E−8 | [4][8][9][12] [19] |
| | | | 19 | 19,349,732 | | intronic | | | | | | 3E−23 | [13] |
| | | | 19 | 19,394,368 | | intronic | | | | | | 4E−8 | [15] |
| | | | 19 | 19,494,483 | | intronic | | | | | | 2E−7 | [15] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 19 | 19,547,663 | | intergenic | | | | | | 3E−9; 3E−8 | [1][2] |
| | | | 19 | 19,678,719 | | intronic | | | | | | 3E−6 | [5] |
| | | | 19 | 19,727,152 | | intronic | | | | | | 3E−8 | [15] |
| *ZNF826P* | | rs144984216 | 19 | 20,369,092 | | intronic | | | | | | 3E−8 | [21] |
| *ZNF486 - ZNF737* | | chr19:20439917 | 19 | 20,439,917 | | intergenic | | | | | | 7E−14 | [20] |
| *CYP2A6* | | rs56113850 | 19 | 40,847,202 | | intronic | | | | | | 2E−10 | [21] |
| *CYP2A6* | | rs56267346 | 19 | 40,847,433 | | intronic | | | | | | 3E−14 | [20] |
| *ZNF574* | | rs201596848 | 19 | 42,080,806 | | missense | c.2200C>T | p.Arg734Cys | np | possibly damaging | tolerated | 1E−11 | [16] |
| *POU2F2* | | chr19:42103100 | 19 | 42,103,100 | | intronic | | | | | | 2E−8 | [15] |
| *XRCC1* | | chr19:43545210 | 19 | 43,545,210 | | intronic | | | | | | 1E−7 | [15] |
| *XRCC1* | | rs2021092 | 19 | 43,564,554 | | intronic | | | | | | 9E−10 | [21] |
| *XRCC1* | | rs3213282 | 19 | 43,568,728 | | intronic | | | | | | 3E−11 | [20] |
| *CEACAM20* | | rs62116889 | 19 | 44,518,526 | | intronic | | | | | | 2E−33 | [21] |
| *CEACAM20 - IGSF23* | | chr19:44603140 | 19 | 44,603,140 | | intergenic | | | | | | 3E−7 | [15] |
| *IGSF23* | | rs62119267 | 19 | 44,631,381 | | intronic | | | | | | 9E−295 | [20] |
| *CEACAM16-AS1, BCL3* | | rs1551891 | 19 | 44,728,555 | | intergenic | | | | | | 4E−490 | [21] |
| | | | 19 | 44,844,654 | | intergenic | | | | | | 7E−343 | [21] |
| | | | 19 | 44,888,997 | | 3'-UTR | c.*618C>T | | np | | | 1E−711 | [21] |
| | | | 19 | 44,892,009 | | intronic | | | | | | 2E−19; 5E−8 | [5][6] |
| | | | 19 | 44,908,822 | | missense | c.526C>T | p.Arg176Cys | drug response | probably damaging | deleterious | 3E−19; 1E−17 | [14][18] |
| | | | 19 | 44,909,976 | | intergenic | | | | | | 5E−324; 5E−50 | [13][15] |
| | | | 19 | 44,918,393 | | intronic | | | | | | 4E−323 | [22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 19 | 44,919,689 | | downstream | c.*459A>G | | no interp. | | | 3E−43; 1E−60; 1E−20; 4E−27; 9E−147; 2E−40; 1E−14; 2E−178; 5E−35 | [1][2][3][4] [8][9][11] [12][19] |
| | | | 19 | 44,987,027 | | intronic | | | | | | 9E−9 | [21] |
| | | | 19 | 45,114,005 | | intronic | | | | | | 5E−17 | [21] |
| | | | 19 | 45,531,618 | | intronic | | | | | | 2E−9 | [15] |
| | | | 19 | 45,791,965 | | intronic | | | | | | 2E−45 | [20] |
| | | | 19 | 45,933,306 | | intergenic | | | | | | 2E−31 | [21] |
| *IGFL1, IGFL1P2* | | rs145725232 | 19 | 46,249,284 | | intergenic | | | | | | 8E−7 | [21] |
| *HNRNPMP2, SLC1A5* | | rs16980741 | 19 | 46,792,101 | | intergenic | | | | | | 3E−8 | [20] |
| *FUT2* | | rs516316 | 19 | 48,702,888 | | intronic | | | | | | 1E−61; 1E−46 | [20][21] |
| *ZNF667-AS1* | | rs61469827 | 19 | 56,500,104 | | intergenic | | | | | | 3E−8 | [20] |
| *ZNF329* | | rs35081008 | 19 | 58,150,868 | | intergenic | | | | | | 3E−23; 1E−27; 9E−35 | [20][21][22] |
| *ZNF329, ZNF274* | | rs117492019 | 19 | 58,170,494 | | intergenic | | | | | | 1E−8 | [13] |
| *RBCK1* | | rs6139104 | 20 | 409,666 | | intronic | | | | | | 2E−11 | [22] |
| *GPCPD1* | | rs73075609 | 20 | 5,600,143 | | intronic | | | | | | 1E−11; 2E−8; 2E−16 | [20][21][22] |
| *LINC01723* | | rs438568 | 20 | 12,978,039 | | intergenic | | | | | | 1E−9; 4E−9; 7E−16 | [20][21][22] |
| *LINC01723* | | rs364585 | 20 | 12,982,070 | | intergenic | | | | | | 4E−10 | [12] |
| *BANF2, RNU6-192P* | | rs61433703 | 20 | 17,823,423 | | intergenic | | | | | | 3E−8 | [21] |
| *RNU6-192P* | | rs2618568 | 20 | 17,863,324 | | intergenic | | | | | | 7E−15 | [13] |
| *RNU6-192P* | | rs2618567 | 20 | 17,863,848 | | intergenic | | | | | | 8E−41; 3E−73 | [20][22] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *RNU6-192P* | | rs2618566 | 20 | 17,864,040 | | intergenic | | | | | | 1E−29 | [21] |
| *RNU6-192P* | | rs2328223 | 20 | 17,865,277 | | intergenic | | | | | | 6E−9 | [12] |
| *ENTPD6* | | rs1044573 | 20 | 25,226,018 | | 3'-UTR | c.*421A>G | | np | | | 4E−13 | [22] |
| *PYGB, ENTPD6* | | rs6050463 | 20 | 25,228,354 | | intergenic | | | | | | 6E−9; 2E−9 | [20][21] |
| *EIFE2S2 - ASIP* | | chr20:34120437 | 20 | 34,120,437 | | intergenic | | | | | | 4E−21 | [20] |
| *FER1L4* | | rs224424 | 20 | 35,560,231 | | intergenic | | | | | | 3E−16 | [21] |
| *DHX35 - MAFB* | | chr20:38966760 | 20 | 38,966,760 | | intronic | | | | | | 5E−8 | [15] |
| *DHX35 - MAFB* | | chr20:39116691 | 20 | 39,116,691 | | intergenic | | | | | | 4E−8 | [15] |
| *LOC105372618* | | rs2902940 | 20 | 40,462,847 | | intronic | | | | | | 1E−8; 2E−11 | [8][12] |
| *DHX35 - MAFB* | | rs1883711 | 20 | 40,551,182 | | intergenic | | | | | | 4E−16; 4E−96; 1E−63; 4E−171 | [13][20][21] [22] |
| *DHX35 - MAFB* | | rs191064657 | 20 | 40,563,663 | | intergenic | | | | | | 9E−10 | [21] |
| *DHX35 - MAFB* | | rs6102059 | 20 | 40,600,144 | | intergenic | | | | | | 4E−9 | [4] |
| *TOP1* | | rs6029526 | 20 | 41,043,978 | | intronic | | | | | | 3E−19; 5E−18 | [8][12] |
| *PLCG1* | | rs6093446 | 20 | 41,152,292 | | intronic | | | | | | 7E−22 | [21] |
| *PLCG1* | | rs753381 | 20 | 41,168,825 | | missense | c.2438T>C | p.Ile813Thr | np | benign | tolerated | 7E−8 | [19] |
| *CHD6* | | rs2866745 | 20 | 41,606,278 | | intronic | | | | | | 1E−21 | [20] |
| *HNF4A* | *HNF4A* | rs1800961 | 20 | 44,413,724 | | missense | c.416C>T | p.Thr139Ile | benign/likely benign | benign | tolerated | 5E−28; 4E−23 | [20][21] |
| *PLTP* | *PLTP* | rs6065904 | 20 | 45,906,012 | | intronic | | | | | | 5E−13 | [20] |
| *PCIF1, PLTP* | | rs6073958 | 20 | 45,923,216 | | intergenic | | | | | | 3E−11 | [21] |
| *SUMO1P1, BCAS1* | | rs6022850 | 20 | 53,918,861 | | intergenic | | | | | | 9E−11 | [22] |
| *NTSR1* | | rs3746778 | 20 | 62,710,120 | | intronic | | | | | | 1E−15 | [22] |
| *SLC2A4RG* | | rs2256814 | 20 | 63,742,630 | | intronic | | | | | | 7E−9 | [21] |
| *TCEA2* | | rs6090040 | 20 | 64,060,707 | | intronic | | | | | | 1E−8; 8E−19 | [20][22] |
| *TCEA2* | | rs6062343 | 20 | 64,064,578 | | intronic | | | | | | 1E−6 | [16] |
| *PCMTD2* | | rs6090101 | 20 | 64,278,167 | | intronic | | | | | | 3E−11 | [21] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *NRIP1 - USP25* | | rs62219001 | 21 | 15,210,560 | | intergenic | | | | | | 1E−12 | [22] |
| *NRIP1 - USP25* | | rs12106385 | 21 | 15,214,362 | | intergenic | | | | | | 5E−8 | [20] |
| *SCAF4* | | rs67038483 | 21 | 31,723,790 | | intronic | | | | | | 7E−6 | [21] |
| *SCAF4* | | rs73201545 | 21 | 31,733,452 | | intergenic | | | | | | 8E−13 | [22] |
| *DOP1B* | | rs11911615 | 21 | 36,180,834 | | intronic | | | | | | 5E−10 | [22] |
| *HMGN1, BRWD1-AS1* | | rs4818025 | 21 | 39,337,245 | | intergenic | | | | | | 9E−11 | [21] |
| *BRWD1-AS1, HMGN1* | | rs1963676 | 21 | 39,338,034 | | intergenic | | | | | | 1E−13; 2E−22 | [20][22] |
| *PKNOX1* | | rs2839619 | 21 | 43,016,067 | | intronic | | | | | | 8E−6 | [7] |
| *COMT* | | rs165722 | 22 | 19,961,490 | | intronic | | | | | | 3E−9 | [22] |
| *UBE2L3* | | rs5754102 | 22 | 21,561,983 | | intronic | | | | | | 2E−8 | [22] |
| *MTMR3* | | rs5763662 | 22 | 29,982,714 | | intronic | | | | | | 1E−8 | [12] |
| *LIF-AS1, HORMAD2* | | rs16988410 | 22 | 30,221,596 | | intergenic | | | | | | 7E−9 | [22] |
| *HMGXB4* | | rs35288294 | 22 | 35,280,146 | | intronic | | | | | | 7E−10 | [22] |
| *TOM1* | | rs138730 | 22 | 35,300,938 | | intronic | | | | | | 6E−9 | [20] |
| *SLC25A17* | | rs2076674 | 22 | 40,774,059 | | intronic | | | | | | 3E−12 | [16] |
| *XPNPEP3* | | rs138352 | 22 | 40,872,921 | | intronic | | | | | | 8E−16 | [22] |
| *XPNPEP3* | | rs5758128 | 22 | 40,918,008 | | intronic | | | | | | 6E−13 | [20] |
| *Y_RNA, RBX1* | | rs960596 | 22 | 40,997,516 | | intergenic | | | | | | 1E−9 | [21] |
| *PNPLA3* | | rs2294915 | 22 | 43,945,024 | | intronic | | | | | | 6E−10 | [22] |
| *FBLN1* | | rs13268 | 22 | 45,600,418 | | missense | c.2084A>G | His695Arg | benign | possibly damaging | tolerated | 4E−10; 9E−14 | [20][22] |
| | | | 22 | 46,231,706 | | intronic | | | | | | 3E−8 | [12] |
| *C22orf34, RN7SKP252* | | rs1807675 | 22 | 49,674,346 | | intergenic | | | | | | 7E−10 | [22] |
| *PPP6R2* | | rs9616822 | 22 | 50,402,144 | | intronic | | | | | | 4E−15 | [22] |
| *PPP6R2* | | rs12162782 | 22 | 50,415,197 | | intronic | | | | | | 9E−10; 4E−9 | [20][21] |
| *ARSL (ARSE)* | | rs35143646 | X | 2,938,114 | | missense | c.1270G>A | p.Gly424Ser | benign | possibly damaging | tolerated | 2E−25 | [22] |
| *EIF1AX* | | rs73447108 | X | 20,136,228 | | intronic | | | | | | 8E−18 | [22] |
| *AR* | | rs5031002 | X | 67,722,783 | | intronic | | | | | | 2E−7 | [6] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | LD[d] | Type[e] | cDNA | Protein | ClinVar[f] | Polyphen[g] | Sift[h] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *TDGF1P3* | | rs5942956 | X | 110,520,525 | | 5'-UTR | | | | | | 2E−102 | [22] |
| *M6PRP1, CHRDL1* | | rs144832584 | X | 110,662,875 | | intergenic | | | | | | 2E−8 | [22] |
| *GDI1, FAM50A* | | rs188437955 | X | 154,443,984 | | intergenic | | | | | | 1E−8 | [22] |

[a.]Gene affected by the variant, or the closest genes in case of intergenic variants. [b.]Identification in the dbSNPs database (www.ncbi.nlm.nih.gov/snp). [c.]Positions are relative to genome assembly GRCh38. [d.]Linkage disequilibrium (LD) tracks were taken from Berisa and Prickrel (2016) [23]. [e.]Type of mutation. [f.]Classification in the ClinVar database (www.ncbi.nlm.nih.gov/clinvar) of variants affecting coding regions: no interp., no interpretation; np, not present. [g.]Prediction of the functional effect using PolyPhen (genetics.bwh.harvard.edu/pph2/). [h.]Prediction of the functional effect using Sift (sift.bii.a-star.edu.sg/).

**Supplementary references for European populations**


1. Willer, C.J.; Sanna, S.; Jackson, A.U.; Scuteri, A.; Bonnycastle, L.L.; Clarke, R.; Heath, S.C.; Timpson, N.J.; Najjar, S.S.; Stringham, H.M., et al. Newly identified loci that influence lipid concentrations and risk of coronary artery disease. *Nat Genet* **2008**, *40*, 161-169, doi:10.1038/ng.76.
2. Kathiresan, S.; Melander, O.; Guiducci, C.; Surti, A.; Burtt, N.P.; Rieder, M.J.; Cooper, G.M.; Roos, C.; Voight, B.F.; Havulinna, A.S., et al. Six new loci associated with blood low-density lipoprotein cholesterol, high-density lipoprotein cholesterol or triglycerides in humans. *Nat Genet* **2008**, *40*, 189-197, doi:10.1038/ng.75.
3. Sandhu, M.S.; Waterworth, D.M.; Debenham, S.L.; Wheeler, E.; Papadakis, K.; Zhao, J.H.; Song, K.; Yuan, X.; Johnson, T.; Ashford, S., et al. LDL-cholesterol concentrations: a genome-wide association study. *Lancet* **2008**, *371*, 483-491, doi:10.1016/S0140-6736(08)60208-1.
4. Kathiresan, S.; Willer, C.J.; Peloso, G.M.; Demissie, S.; Musunuru, K.; Schadt, E.E.; Kaplan, L.; Bennett, D.; Li, Y.; Tanaka, T., et al. Common variants at 30 loci contribute to polygenic dyslipidemia. *Nat Genet* **2009**, *41*, 56-65, doi:10.1038/ng.291.
5. Aulchenko, Y.S.; Ripatti, S.; Lindqvist, I.; Boomsma, D.; Heid, I.M.; Pramstaller, P.P.; Penninx, B.W.J.H.; Janssens, A.C.J.W.; Wilson, J.F.; Spector, T., et al. Loci influencing lipid levels and coronary heart disease risk in 16 European population cohorts. *Nature Genetics* **2008**, *41*, 47, doi:10.1038/ng.269.
6. Sabatti, C.; Service, S.K.; Hartikainen, A.L.; Pouta, A.; Ripatti, S.; Brodsky, J.; Jones, C.G.; Zaitlen, N.A.; Varilo, T.; Kaakinen, M., et al. Genome-wide association analysis of metabolic traits in a birth cohort from a founder population. *Nat Genet* **2009**, *41*, 35-46, doi:10.1038/ng.271.
7. Zemunik, T.; Boban, M.; Lauc, G.; Janković, S.; Rotim, K.; Vatavuk, Z.; Bencić, G.; Dogas, Z.; Boraska, V.; Torlak, V., et al. Genome-wide association study of biochemical traits in Korcula Island, Croatia. *Croat Med J* **2009**, *50*, 23-33, doi:10.3325/cmj.2009.50.23.
8. Teslovich, T.M.; Musunuru, K.; Smith, A.V.; Edmondson, A.C.; Stylianou, I.M.; Koseki, M.; Pirruccello, J.P.; Ripatti, S.; Chasman, D.I.; Willer, C.J., et al. Biological, clinical and population relevance of 95 loci for blood lipids. *Nature* **2010**, *466*, 707-713, doi:10.1038/nature09270.
9. Waterworth, D.M.; Ricketts, S.L.; Song, K.; Chen, L.; Zhao, J.H.; Ripatti, S.; Aulchenko, Y.S.; Zhang, W.; Yuan, X.; Lim, N., et al. Genetic variants influencing circulating lipid levels and risk of coronary artery disease. *Arterioscler Thromb Vasc Biol* **2010**, *30*, 2264-2276, doi:10.1161/ATVBAHA.109.201020.
10. Shen, H.; Damcott, C.M.; Rampersaud, E.; Pollin, T.I.; Horenstein, R.B.; McArdle, P.F.; Peyser, P.A.; Bielak, L.F.; Post, W.S.; Chang, Y.P., et al. Familial defective apolipoprotein B-100 and increased low-density lipoprotein cholesterol and coronary artery calcification in the old order amish. *Arch Intern Med* **2010**, *170*, 1850-1855, doi:10.1001/archinternmed.2010.384.
11. Keller, M.; Schleinitz, D.; Förster, J.; Tönjes, A.; Böttcher, Y.; Fischer-Rosinsky, A.; Breitfeld, J.; Weidle, K.; Rayner, N.W.; Burkhardt, R., et al. THOC5: a novel gene involved in HDL-cholesterol metabolism. *J Lipid Res* **2013**, *54*, 3170-3176, doi:10.1194/jlr.M039420.
12. Willer, C.J.; Schmidt, E.M.; Sengupta, S.; Peloso, G.M.; Gustafsson, S.; Kanoni, S.; Ganna, A.; Chen, J.; Buchkovich, M.L.; Mora, S., et al. Discovery and refinement of loci associated with lipid levels. *Nat Genet* **2013**, *45*, 1274-1283, doi:10.1038/ng.2797.
13. Surakka, I.; Horikoshi, M.; Mägi, R.; Sarin, A.P.; Mahajan, A.; Lagou, V.; Marullo, L.; Ferreira, T.; Miraglio, B.; Timonen, S., et al. The impact of low-frequency and rare variants on lipid levels. *Nat Genet* **2015**, *47*, 589-597, doi:10.1038/ng.3300.
14. Southam, L.; Gilly, A.; Süveges, D.; Farmaki, A.E.; Schwartzentruber, J.; Tachmazidou, I.; Matchan, A.; Rayner, N.W.; Tsafantakis, E.; Karaleftheri, M., et al. Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. *Nat Commun* **2017**, *8*, 15606, doi:10.1038/ncomms15606.
15. Davis, J.P.; Huyghe, J.R.; Locke, A.E.; Jackson, A.U.; Sim, X.; Stringham, H.M.; Teslovich, T.M.; Welch, R.P.; Fuchsberger, C.; Narisu, N., et al. Common, low-frequency, and rare genetic

variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. *PLoS Genet* **2017**, *13*, e1007079, doi:10.1371/journal.pgen.1007079.
16. Liu, D.J.; Peloso, G.M.; Yu, H.; Butterworth, A.S.; Wang, X.; Mahajan, A.; Saleheen, D.; Emdin, C.; Alam, D.; Alves, A.C., et al. Exome-wide association study of plasma lipids in >300,000 individuals. *Nat Genet* **2017**, *49*, 1758-1766, doi:10.1038/ng.3977.
17. Lutz, M.W.; Casanova, R.; Saldana, S.; Kuchibhatla, M.; Plassman, B.L.; Hayden, K.M. Analysis of pleiotropic genetic effects on cognitive impairment, systemic inflammation, and plasma lipids in the Health and Retirement Study. *Neurobiol Aging* **2019**, *80*, 173-186, doi:10.1016/j.neurobiolaging.2018.10.028.
18. Tabassum, R.; Rämö, J.T.; Ripatti, P.; Koskela, J.T.; Kurki, M.; Karjalainen, J.; Palta, P.; Hassan, S.; Nunez-Fontarnau, J.; Kiiskinen, T.T.J., et al. Genetic architecture of human plasma lipidome and its link to cardiovascular disease. *Nat Commun* **2019**, *10*, 4329, doi:10.1038/s41467-019-11954-8.
19. Kulminski, A.M.; Loika, Y.; Nazarian, A.; Culminskaya, I. Quantitative and Qualitative Role of Antagonistic Heterogeneity in Genetics of Blood Lipids. *J Gerontol A Biol Sci Med Sci* **2020**, *75*, 1811-1819, doi:10.1093/gerona/glz225.
20. Ripatti, P.; Rämö, J.T.; Mars, N.J.; Fu, Y.; Lin, J.; Söderlund, S.; Benner, C.; Surakka, I.; Kiiskinen, T.; Havulinna, A.S., et al. Polygenic Hyperlipidemias and Coronary Artery Disease Risk. *Circ Genom Precis Med* **2020**, *13*, e002725, doi:10.1161/CIRCGEN.119.002725.
21. Richardson, T.G.; Sanderson, E.; Palmer, T.M.; Ala-Korpela, M.; Ference, B.A.; Davey Smith, G.; Holmes, M.V. Evaluating the relationship between circulating lipoprotein lipids and apolipoproteins with risk of coronary heart disease: A multivariable Mendelian randomisation analysis. *PLoS Med* **2020**, *17*, e1003062, doi:10.1371/journal.pmed.1003062.
22. Klimentidis, Y.C.; Arora, A.; Newell, M.; Zhou, J.; Ordovas, J.M.; Renquist, B.J.; Wood, A.C. Phenotypic and Genetic Characterization of Lower LDL Cholesterol and Increased Type 2 Diabetes Risk in the UK Biobank. *Diabetes* **2020**, *69*, 2194-2205, doi:10.2337/db19-1134.
23. Berisa, T.; Pickrell, J.K. Approximately independent linkage disequilibrium blocks in human populations. **2016**, doi:10.1093/bioinformatics/btv546.

**Table S1b:** SNVs associated with low-density lipoprotein cholesterol in East-Asian populations.

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 1 | 25,422,778 | intronic | | | | | | 1E−8 | [9] |
| | | | 1 | 25,434,429 | intronic | | | | | | 2E−18 | [5] |
| *PIGV, RN7SL165P* | | rs12748152 | 1 | 26,811,902 | intergenic | | | | | | 3E−12 | [5] |
| *BSND - PCSK9* | *PCSK9* | rs7523141 | 1 | 55,033,125 | intergenic | | | | | | 3E−25 | [7] |
| *BSND - PCSK9* | | rs7525649 | 1 | 55,033,483 | intergenic | | | | | | 3E−11 | [2] |
| *PCSK9, BSND* | | rs2479409 | 1 | 55,038,977 | 5'-UTR | c.-861G>A | | benign | | | 3E−42 | [5] |
| *PCSK9* | | rs151193009 | 1 | 55,043,912 | missense | c.277C>T | p.Arg93Cys | conflicting | probably damaging | deleterious | 6E−17; 8E−32 | [3][9] |
| *PCSK9* | | rs12136600 | 1 | 55,055,522 | intronic | | | | | | 4E−20 | [7] |
| *PCSK9* | | rs505151 | 1 | 55,063,514 | missense | c.2009G>A | p.Gly670Glu | | benign | tolerated | 8E−7; 9E−9 | [5] |
| *USP24 - Y_RNA* | | chr1:55509585 | 1 | 55,509,585 | intergenic | | | | | | 4E−36 | [10] |
| *LINC01755* | | rs147943615 | 1 | 55,902,364 | intergenic | | | | | | 1E−27 | [7] |
| *USP1* | *DOCK7 - ANGPTL3* | rs10158897 | 1 | 62,447,248 | intronic | | | | | | 9E−6 | [1] |
| *DOCK7 - ANGPTL3* | | rs636523 | 1 | 62,454,337 | intergenic | | | | | | 5E−7 | [1] |
| *DOCK7* | | rs11485618 | 1 | 62,628,536 | intronic | | | | | | 1E−31 | [5] |
| *ADGRL2* | | rs367881 | 1 | 81,883,032 | intronic | | | | | | 2E−6 | [8] |
| | | | 1 | 109,274,968 | 3'-UTR | c.*919G>T | | association | | | 3E−11 | [9] |
| | | | 1 | 109,275,216 | 3'-UTR | c.*1167T>C | | np | | | 2E−28 | [7] |
| | | | 1 | 109,275,684 | 3'-UTR | c.*1635G>T | | np | | | 2E−17 | [3] |
| | | | 1 | 109,279,544 | intergenic | | | | | | 2E−11; 2E−19; 2E−31; 4E−289; 7E−9 | [5][9] |
| | | | 1 | 109,817,590 | intergenic | | | | | | 2E−21 | [10] |
| *PRPF3* | | rs56047090 | 1 | 150,343,248 | intronic | | | | | | 5E−7 | [8] |
| *ANXA9* | | rs267733 | 1 | 150,986,360 | missense | c.497A>G | p.Asp166Gly | np | probably damaging | tolerated | 4E−8 | [5] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *MTARC1* | *MTAC1* | rs2642438 | 1 | 220,796,686 | missense | c.493A>G | p.Thr165Ala | np | benign | tolerated | 1E−19 | [5] |
| *LINC01132, LINC00184* | *IRF2BP2* | rs2587534 | 1 | 234,713,592 | intergenic | | | | | | 2E−23 | [5] |
| *LINC00184 - LINC01132* | | rs553427 | 1 | 234,717,013 | intergenic | | | | | | 1E−9 | [7] |
| *HS1BP3* | *APOB* | rs75352129 | 2 | 20,648,432 | intronic | | | | | | 6E−59 | [7] |
| *LDAH - APOB* | | rs10172650 | 2 | 20,982,585 | intergenic | | | | | | 1E−12; 4E−14 | [5] |
| *APOB* | | rs57825321 | 2 | 21,024,193 | intronic | | | | | | 4E−30 | [7] |
| *APOB* | | rs13306194 | 2 | 21,029,662 | missense | c.1594C>T | p.Arg532Trp | np | probably damaging | deleterious | 1E−12 | [3] |
| *APOB* | | rs1367117 | 2 | 21,041,028 | missense | c.293C>T | p.Thr98Ile | benign/likely benign | benign | deleterious | 2E−10; 2E−179 | [5][7] |
| *APOB - TDRD15* | | rs312949 | 2 | 21,111,411 | intergenic | | | | | | 3E−6 | [2] |
| *TDRD15* | | chr2:21242731 | 2 | 21,242,731 | intergenic | | | | | | 1E−18 | [10] |
| *TRD15 - NUTF2P8* | | rs12469758 | 2 | 21,310,235 | intergenic | | | | | | 5E−53 | [7] |
| *VN1R18P* | | rs77348447 | 2 | 48,003,689 | intronic | | | | | | 5E−6 | [8] |
| *FSHR, CTBP2P5* | | rs10490120 | 2 | 48,916,690 | intergenic | | | | | | 1E−6 | [8] |
| *EHBP1* | | rs2710642 | 2 | 62,922,422 | intronic | | | | | | 2E−10 | [5] |
| *Y_RNA, LINC01101* | | rs2030746 | 2 | 120,551,912 | intergenic | | | | | | 8E−9 | [5] |
| *FN1* | | rs1250229 | 2 | 215,439,661 | intergenic | | | | | | 2E−9 | [5] |
| *UGT1A8, UGT1A9, UGT1A4, UGT1A7, UGT1A10, UGT1A6, UGT1A5, UGT1A1, UGT1A3* | | rs11563251 | 2 | 233,770,738 | intronic | | | | | | 4E−8 | [5] |
| *CMTM6* | | rs3773777 | 3 | 32,496,755 | intronic | | | | | | 7E−8 | [5] |
| *WDR5B-DT, KPNA1* | | rs3762637 | 3 | 122,426,477 | intronic | | | | | | 3E−8 | [5] |
| *DNAJC13* | | rs17345563 | 3 | 132,490,359 | intronic | | | | | | 1E−9 | [5] |
| *TNK2* | | rs75454932 (rs141507877) | 3 | 195,894,179 | intronic | | | | | | 3E−6 | [8] |
| *RGS12* | *LRPAP1* | rs6818397 | 4 | 3,433,158 | intronic | | | | | | 3E−9 | [5] |
| *HEXB* | *HMGCR* | rs186072633 | 5 | 74,648,603 | intronic | | | | | | 6E−15 | [10] |
| *HMGCR, ANKRD31* | | rs6871667 | 5 | 75,308,917 | intergenic | | | | | | 7E−13 | [2] |
| *HMGCR* | | rs10045497 | 5 | 75,340,659 | intronic | | | | | | 1E−12 | [1] |
| *HMGCR* | | rs3846661 | 5 | 75,343,353 | intronic | | | | | | 5E−31 | [7] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 5 | 75,352,778 | intronic | c.1368+1176A>T | | association | | | 1E−6; 1E−9 | [9] |
| | | | 5 | 75,360,714 | 3'-UTR | c.*372T>C | | np | | | 1E−21; 3E−95 | [5] |
| | | | 5 | 75,513,055 | intronic | | | | | | 1E−16 | [5] |
| *CSNK1G3* | | rs4530754 | 5 | 123,519,722 | intronic | | | | | | 3E−12 | [5] |
| *HAVCR1, TIMD4* | | rs6882076 | 5 | 156,963,286 | intergenic | | | | | | 1E−33; 1E−8 | [5][7] |
| | | | 6 | 16,108,932 | intergenic | | | | | | 8E−17 | [5] |
| *HLA-C, USP8P1* | | rs9357121 | 6 | 31,272,702 | intergenic | | | | | | 3E−10 | [2] |
| *HLA-DRA* | | rs3177928 | 6 | 32,444,658 | 3'-UTR | c.*18G>A | | np | | | 5E−17 | [5] |
| *TRAM2-AS1* | | rs2239620 | 6 | 52,587,787 | intergenic | | | | | | 2E−8 | [5] |
| *FRK* | | rs6909746 | 6 | 116,031,587 | intronic | | | | | | 2E−9 | [5] |
| *HBS1L* | | rs7775698 | 6 | 135,097,497 | intronic | | | | | | 2E−8 | [5] |
| *HBS1L* | | rs7776054 | 6 | 135,097,778 | intronic | | | | | | 4E−8 | [5] |
| *H3P28* | | rs4870470 | 6 | 156,593,851 | intergenic | | | | | | 2E−6 | [8] |
| *DNAH11* | | rs12670798 | 7 | 21,567,734 | intronic | | | | | | 2E−12 | [5] |
| *MIR148A* | | rs28537499 | 7 | 25,975,772 | intergenic | | | | | | 2E−10 | [7] |
| | | | 7 | 44,539,581 | synonymous | c.816C>G | p.Leu272= | benign | | tolerated | 2E−14 | [5] |
| *TBL2* | | rs17145738 | 7 | 73,568,544 | 3'-UTR | c.*1963G>A | | | | | 5E−9 | [7] |
| *RN7SL265P, ABHD11-AS1* | | rs112959129 | 7 | 73,733,662 | intergenic | | | | | | 1E−6 | [8] |
| | | | 8 | 9,325,848 | intergenic | | | | | | 1E−22 | [5] |
| *TRMT112P7, RP1* | | rs10102164 | 8 | 54,509,054 | intergenic | | | | | | 8E−11 | [5] |
| *UBXN2B* | *CYP7A1* | rs13277801 | 8 | 58,440,975 | intronic | | | | | | 4E−19 | [5] |
| *CYP7A1, UBXN2B* | | rs75214121 | 8 | 58,485,717 | intergenic | | | | | | 9E−9 | [7] |
| *TRIB1* | *TRIB1* | rs2001846 | 8 | 125,466,208 | intergenic | | | | | | 6E−9 | [7] |
| *TRIB1* | | rs17321515 | 8 | 125,474,167 | intergenic | | | | | | 8E−7 | [1] |
| *TRIB1* | | rs2980869 | 8 | 125,476,008 | intergenic | | | | | | 3E−6; 4E−9 | [5] |
| *TRIB1* | | rs2954029 | 8 | 125,478,730 | intergenic | | | | | | 2E−56 | [5] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *COL22A1 - KCNK9* | | rs4588831 | 8 | 139,337,989 | intergenic | | | | | | 5E−6 | [8] |
| *PLEC* | | rs7832643 | 8 | 143,948,489 | intronic | | | | | | 2E−17 | [5] |
| | | | 9 | 2,640,759 | intronic | | | | | | 5E−10 | [5] |
| *ZNF618* | | rs59508358 (rs377752731) | 9 | 113,833,966 | intergenic | | | | | | 9E−6 | [8] |
| *ABO* | | rs9411378 | 9 | 133,270,015 | intronic | | | | | | 1E−19 | [7] |
| *ABO* | | rs507666 | 9 | 133,273,983 | intronic | c.28+1179T>C | | association | | | 2E−11 | [1] |
| *ABO, Y_RNA* | | rs579459 | 9 | 133,278,724 | intergenic | | | | | | 2E−51; 2E−9; 6E−13; 7E−13 | [2][5] |
| *TMEM250 - LHX3* | | chr9:136131651 | 9 | 136,131,651 | intergenic | | | | | | 5E−11 | [10] |
| *OIT3* | | rs41280378 | 10 | 72,932,888 | 3'-UTR | c.*364T>G | | np | | | 9E−15 | [7] |
| *GPAM* | | rs1129555 | 10 | 112,150,963 | 3'-UTR | c.*2587T>C | | np | | | 1E−15 | [5] |
| *MYRF, TMEM258* | *FADS1* | rs174533 | 11 | 61,781,553 | intronic | | | | | | 1E−9; 5E−7 | [5] |
| *FADS2* | | rs1535 | 11 | 61,830,500 | intronic | | | | | | 5E−45 | [5] |
| *ZPR1* | *APOA1-C3-A4-A5* | rs964184 | 11 | 116,778,201 | 3'-UTR | c.*724C>G | | np | | | 3E−18 | [5] |
| *ZPR1* | | rs113932726 | 11 | 116,779,922 | intronic | | | | | | 2E−8 | [7] |
| *GSEC, DCPS* | *ST3GAL4* | rs2401 | 11 | 126,341,832 | intronic | | | | | | 5E−8 | [5] |
| *GSEC, DCPS* | | rs17135399 | 11 | 126,348,646 | intronic | | | | | | 2E−22 | [5] |
| *NR1H4* | | rs75061399 | 12 | 100,548,299 | intronic | | | | | | 5E−8 | [7] |
| *CUX2* | | rs79105258 | 12 | 111,280,427 | intronic | | | | | | 3E−20 | [7] |
| *RPH3A* | | rs7315593 | 12 | 112,840,165 | intronic | | | | | | 8E−9 | [7] |
| | | | 12 | 120,978,847 | missense | c.79A>C | p.Ile27Leu | benign | benign | tolerated | 2E−22 | [5] |
| *BRCA2* | | rs1799955 | 13 | 32,355,095 | synonymous | c.7242A>G | p.Ser2414= | benign | | tolerated | 3E−8; 3E−9 | [5] |
| *BRCA2* | | rs4942486 | 13 | 32,379,251 | intronic | c.8755-66T>C | | benign | | | 5E−14 | [5] |
| | | | 14 | 24,414,681 | missense | c.2932G>A | p.Ala978Thr | np | benign | tolerated | 2E−14 | [5] |
| *OTX2-AS1* | | rs57618243 | 14 | 56,984,146 | intergenic | | | | | | 7E−6 | [8] |
| | | | 15 | 58,400,482 | intronic | | | | | | 2E−8 | [7] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *CASC22, LINC02180* | | rs12925859 | 16 | 52,194,027 | intergenic | | | | | | 4E−6 | [8] |
| *HERPUD1, CETP* | *CETP* | rs247616 | 16 | 56,955,678 | intergenic | | | | | | 1E−33 | [5] |
| *PKD1L3* | | rs7185272 | 16 | 71,979,898 | missense | c.1286C>G | p.Thr429Ser | np | benign | tolerated | 5E−8 | [3] |
| *PKD1L3* | | rs7192750 | 16 | 71,980,883 | intronic | | | | | | 1E−14 | [5] |
| *PKD1L3* | | rs8051431 | 16 | 71,981,352 | intronic | | | | | | 4E−15 | [5] |
| *PKD1L3* | | rs12927205 | 16 | 71,991,178 | intronic | | | | | | 8E−7 | [2] |
| *TXNL4B* | | rs77303550 | 16 | 72,045,758 | intronic | | | | | | 1E−8; 7E−16 | [7][9] |
| *HPR, TXNL4B* | | rs2000999 | 16 | 72,074,194 | intronic | | | | | | 2E−6; 5E−45 | [5] |
| *DLG4* | | rs314253 | 17 | 7,188,331 | 3'-UTR | c.*2377A>G | | np | | | 4E−10 | [5] |
| *PFAS* | | rs4791641 | 17 | 8,257,831 | missense | c.1100C>T | p.Pro367Leu | np | benign | tolerated | 1E−7 | [5] |
| *TNFAIP1* | | rs3093679 | 17 | 28,337,189 | intronic | | | | | | 2E−9 | [7] |
| | | | 19 | 11,106,639 | missense | c.769C>T | p.Arg257Trp | np | probably damaging | deleterious | 3E−8 | [3] |
| | | | 19 | 11,118,542 | intronic | | | | | | 5E−9 | [5] |
| | | | 19 | 11,131,631 | 3'-UTR | c.*315G>C | | benign/likely benign | | | 3E−15; 4E−40 | [5][7] |
| | | | 19 | 11,139,463 | intronic | | | | | | 1E−24 | [2] |
| | | | 19 | 11,143,211 | intronic | | | | | | 3E−9 | [9] |
| | | | 19 | 11,145,500 | 3'-UTR | c.*1683G>A | | np | | | 7E−6 | [1] |
| *ANGPTL8* | | rs2278426 | 19 | 11,239,812 | missense | c.175C>T | p.Arg59Trp | np | possibly damaging | deleterious | 2E−9 | [7] |
| *SUGP1* | *NCAN - TM6SF2* | rs10401969 | 19 | 19,296,909 | intronic | | | | | | 6E−51 | [5] |
| *NECTIN2* | *APOE-C1-C2-C4* | rs406456 | 19 | 44,879,460 | intronic | | | | | | 5E−6 | [8] |
| *TOMM40* | | rs1160985 | 19 | 44,900,155 | intronic | | | | | | 3E−6; 4E−13 | [1][4] |
| *TOMM40 - APOE* | | rs769446 | 19 | 44,905,371 | intergenic | | | | | | 3E−322 | [7] |
| *APOE* | | rs429358 | 19 | 44,908,684 | missense | c.388T>C | p.Cys130Arg | conflicting | benign | tolerated | 4E−71 | [7] |
| *APOE* | | rs7412 | 19 | 44,908,822 | missense | c.526C>T | p.Arg176Cys | drug response | probably damaging | deleterious | 2E−286; 7E−15 | [5][6] |
| *APOE - APOC1* | | rs1065853 | 19 | 44,909,976 | intergenic | | | | | | 3E−54 | [9] |

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 19 | 44,912,383 | intergenic | | | | | | 1E−129; 1E−13; 4E−59 | [5][6] |
| | | | 19 | 45,412,079 | intronic | | | | | | 9E−113 | [10] |
| *LINC01723* | | rs364585 | 20 | 12,982,070 | intergenic | | | | | | 4E−11 | [5] |
| *RNU6-192P* | | rs2328223 | 20 | 17,865,277 | intergenic | | | | | | 2E−10 | [5] |
| *TOP1* | | rs6065311 | 20 | 41,095,698 | intronic | | | | | | 2E−34; 3E−6 | [5] |
| *ZHX3* | | rs56668103 | 20 | 41,197,439 | intronic | | | | | | 7E−9 | [7] |
| *MTMR3* | | rs5763662 | 22 | 29,982,714 | intronic | | | | | | 3E−9 | [5] |

[a.]Gene affected by the variant, or the closest genes in case of intergenic variants. [b.]Identification in the dbSNPs database (www.ncbi.nlm.nih.gov/snp). [c.]Positions are relative to genome assembly GRCh38. [d.]Type of mutation. [e.]Classification in the ClinVar database (www.ncbi.nlm.nih.gov/clinvar) of variants affecting coding regions: no interp., no interpretation; np, not present. [f.]Prediction of the functional effect using PolyPhen (genetics.bwh.harvard.edu/pph2/). [g.]Prediction of the functional effect using Sift (sift.bii.a-star.edu.sg/).

**Supplementary references for East-Asian populations**


1. Zhou, L.; He, M.; Mo, Z.; Wu, C.; Yang, H.; Yu, D.; Yang, X.; Zhang, X.; Wang, Y.; Sun, J., et al. A genome wide association study identifies common variants associated with lipid levels in the Chinese population. *PLoS One* **2013**, *8*, e82420, doi:10.1371/journal.pone.0082420.
2. Lu, X.; Huang, J.; Mo, Z.; He, J.; Wang, L.; Yang, X.; Tan, A.; Chen, S.; Chen, J.; Gu, C.C., et al. Genetic Susceptibility to Lipid Levels and Lipid Change Over Time and Risk of Incident Hyperlipidemia in Chinese Populations. *Circ Cardiovasc Genet* **2016**, *9*, 37-44, doi:10.1161/CIRCGENETICS.115.001096.
3. Tang, C.S.; Zhang, H.; Cheung, C.Y.; Xu, M.; Ho, J.C.; Zhou, W.; Cherny, S.S.; Zhang, Y.; Holmen, O.; Au, K.W., et al. Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. *Nat Commun* **2015**, *6*, 10206, doi:10.1038/ncomms10206.
4. Kurano, M.; Tsukamoto, K.; Kamitsuji, S.; Kamatani, N.; Hara, M.; Ishikawa, T.; Kim, B.J.; Moon, S.; Jin Kim, Y.; Teramoto, T. Genome-wide association study of serum lipids confirms previously reported associations as well as new associations of common SNPs within PCSK7 gene with triglyceride. *J Hum Genet* **2016**, *61*, 427-433, doi:10.1038/jhg.2015.170.
5. Spracklen, C.N.; Chen, P.; Kim, Y.J.; Wang, X.; Cai, H.; Li, S.; Long, J.; Wu, Y.; Wang, Y.X.; Takeuchi, F., et al. Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. *Hum Mol Genet* **2017**, *26*, 1770-1784, doi:10.1093/hmg/ddx062.
6. Zhu, Y.; Zhang, D.; Zhou, D.; Li, Z.; Li, Z.; Fang, L.; Yang, M.; Shan, Z.; Li, H.; Chen, J., et al. Susceptibility loci for metabolic syndrome and metabolic components identified in Han Chinese: a multi-stage genome-wide association study. *J Cell Mol Med* **2017**, *21*, 1106-1116, doi:10.1111/jcmm.13042.
7. Kanai, M.; Akiyama, M.; Takahashi, A.; Matoba, N.; Momozawa, Y.; Ikeda, M.; Iwata, N.; Ikegawa, S.; Hirata, M.; Matsuda, K., et al. Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. *Nat Genet* **2018**, *50*, 390-400, doi:10.1038/s41588-018-0047-6.
8. Liu, H.; Wang, W.; Zhang, C.; Xu, C.; Duan, H.; Tian, X.; Zhang, D. Heritability and Genome-Wide Association Study of Plasma Cholesterol in Chinese Adult Twins. *Front Endocrinol (Lausanne)* **2018**, *9*, 677, doi:10.3389/fendo.2018.00677.
9. Moon, S.; Kim, Y.J.; Han, S.; Hwang, M.Y.; Shin, D.M.; Park, M.Y.; Lu, Y.; Yoon, K.; Jang, H.M.; Kim, Y.K., et al. The Korea Biobank Array: Design and Identification of Coding Variants Associated with Blood Biochemical Traits. *Sci Rep* **2019**, *9*, 1382, doi:10.1038/s41598-018-37832-9.
10. Han, S.; Hwang, M.Y.; Yoon, K.; Kim, Y.K.; Kim, Y.J.; Kim, B.J.; Moon, S. Exome chip-driven association study of lipidemia in >14,000 Koreans and evaluation of genetic effect on identified variants between different ethnic groups. *Genet Epidemiol* **2019**, *43*, 617-628, doi:10.1002/gepi.22208.

**Table S1c:** SNVs associated with low-density lipoprotein cholesterol in Afro-Americans or African ancestry populations.

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *PCSK9* | *PCSK9* | rs28362286 | 1 | 55,063,542 | nonsense | c.2037C>A | p.Cys679Ter | conflicting | | | 2E−42 | [3] |
| *CELSR2* | *CELSR2 - SORT1* | rs12740374 | 1 | 109,274,968 | 3'-UTR | c.*919G>T | | association | | | 2E−26; 9E−29 | [1][3] |
| *TARBP1 - IRF2BP2* | *IRF2BP2* | rs744487 | 1 | 234,590,266 | intergenic | | | | | | 5E−6 | [1] |
| | | | 2 | 20,901,018 | intergenic | | | | | | 1E−7 | [1] |
| | | | 2 | 21,191,270 | intergenic | | | | | | 3E−9 | [1] |
| | | | 2 | 22,599,287 | intergenic | | | | | | 4E−7 | [1] |
| *DTNB* | | rs11684202 | 2 | 25,664,689 | intronic | | | | | | 6E−6 | [1] |
| *MYO3B - SP5* | | rs2080401 | 2 | 170,684,313 | intergenic | | | | | | 7E−6 | [1] |
| *TNIK* | | rs11920719 | 3 | 171,116,770 | intronic | | | | | | 4E−6 | [1] |
| *SGCD* | | chr5:156378584 | 5 | 156,378,584 | intronic | | | | | | 5E−9 | [3] |
| *RNF130* | | rs13161895 | 5 | 180,044,201 | intronic | | | | | | 4E−7 | [1] |
| *PDGFD* | | rs10895547 | 11 | 103,937,424 | intronic | | | | | | 3E−6 | [1] |
| *PLEKHO2* | | rs12595292 | 15 | 64,861,491 | synonymous | c.399G>A | p.Lys133= | np | | | 9E−6 | [1] |
| *LITAF* | | rs7203193 | 16 | 11,547,324 | intergenic | | | | | | 3E−6 | [1] |
| *ZFHX3* | | rs16971384 | 16 | 72,897,186 | intronic | | | | | | 5E−6 | [1] |
| *DNM2* | *LDLR* | rs11671653 | 19 | 10,727,810 | intronic | | | | | | 9E−7 | [1] |
| *SMARCA4* | | rs11669133 | 19 | 10,981,463 | intronic | | | | | | 1E−8 | [1] |
| *SMARCA4 - LDLR* | | rs12151108 | 19 | 11,086,585 | intergenic | | | | | | 2E−32 | [3] |
| *LDLR* | | rs6511720 | 19 | 11,091,630 | intronic | | | benign | | | 7E−8 | [1] |
| *APOE* | *APOE-C1-C2-C4* | rs7412 | 19 | 44,908,822 | missense | c.526C>T | p.Arg176Cys | drug response | probably damaging | deleterious | 1E−189; 2E−9 | [2][3] |
| *LOC105373347* | | rs5904726 | X | 147,241,105 | intronic | | | | | | 9E−6 | [1] |

[a.]Gene affected by the variant, or the closest genes in case of intergenic variants. [b.]Identification in the dbSNPs database (www.ncbi.nlm.nih.gov/snp). [c.]Positions are relative to genome assembly GRCh38. [d.]Type of mutation. [e.]Classification in the ClinVar database (www.ncbi.nlm.nih.gov/clinvar) of variants affecting coding regions: no interp., no interpretation; np, not present. [f.]Prediction of the functional effect using PolyPhen (genetics.bwh.harvard.edu/pph2/). [g.]Prediction of the functional effect using Sift (sift.bii.a-star.edu.sg/).

**Table S1d:** SNVs associated with low-density lipoprotein cholesterol in Hispanic or Native-American ancestry populations.

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *CELSR2* | *CELSR2 - SORT1* | rs12740374 | 1 | 109,274,968 | 3'-UTR | c.*919G>T | | association | | | 1E−36 | [2] |
| *CELSR2* | | rs660240 | 1 | 109,275,216 | 3'-UTR | c.*1167T>C | | np | | | 1E−28 | [1] |
| *APOB* | *APOB* | rs13392272 | 2 | 20,994,618 | intergenic | | | | | | 2E−12 | [1] |
| *TDRD15, APOB* | | rs7575840 | 2 | 21,050,618 | intergenic | | | | | | 4E−18 | [2] |
| *APOB, TDRD15* | | rs562338 | 2 | 21,065,449 | intergenic | | | | | | 3E−19 | [2] |
| *ABCG8* | *ABCG5/G8* | rs4245791 | 2 | 43,847,292 | intronic | | | | | | 5E−8 | [2] |
| *HMGCR* | *HMGCR* | rs6882842 | 5 | 75,356,084 | intronic | | | | | | 4E−6 | [2] |
| *ZNF619P1* | | rs6944635 | 7 | 46,132,286 | intergenic | | | | | | 3E−6 | [2] |
| | | | 11 | 61,781,553 | intronic | | | | | | 6E−7 | [2] |
| *DHODH* | | rs8062895 | 16 | 72,014,733 | intronic | | | | | | 3E−6 | [2] |
| *PFAS* | | rs4791641 | 17 | 8,257,831 | missense | c.1100C>T | p.Pro367Leu | np | benign | tolerated | 1E−8 | [1] |
| *LDLR* | *LDLR* | rs6511720 | 19 | 11,091,630 | intronic | c.67+2015G>T | | benign | | | 2E−18 | [2] |
| *NCAN* | *NCAN - TM6SF2* | rs2238675 | 19 | 19,225,799 | intronic | | | | | | 2E−8 | [1] |
| *NECTIN2* | *APOE-C1-C2-C4* | rs7254892 | 19 | 44,886,339 | intronic | | | | | | 2E−38 | [2] |

[a.]Gene affected by the variant, or the closest genes in case of intergenic variants. [b.]Identification in the dbSNPs database (www.ncbi.nlm.nih.gov/snp). [c.]Positions are relative to genome assembly GRCh38. [d.]Type of mutation. [e.]Classification in the ClinVar database (www.ncbi.nlm.nih.gov/clinvar) of variants affecting coding regions: no interp., no interpretation; np, not present. [f.]Prediction of the functional effect using PolyPhen (genetics.bwh.harvard.edu/pph2/). [g.]Prediction of the functional effect using Sift (sift.bii.a-star.edu.sg/)

**Table S1e:** SNVs associated with low-density lipoprotein cholesterol in Middle-East populations.

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *CELSR2* | *CELSR2 - SORT1* | rs7528419 | 1 | 109,274,570 | 3'-UTR variant | c.*521A>G | | np | | | 5E−6 | [1] |
| *TDRD15* | *APOB* | rs70939068 (rs142138117) | 2 | 21,124,818 | intronic variant | | | | | | 7E−8 | [1] |
| *LOC105374317* | | rs10183198 | 2 | 21,248,115 | intronic variant | | | | | | 5E−7 | [1] |
| *INTS10, LPL* | *LPL* | rs10635970 | 8 | 19,887,529 | A repetition | | | | | | 2E−8 | [1] |
| *RPL30P9, LPL* | | rs7016880 | 8 | 20,019,235 | intergenic | | | | | | 5E−6 | [1] |
| *C8orf37-AS1, LINC01298* | | rs62522646 | 8 | 95,211,565 | intronic variant | | | | | | 1E−7 | [1] |
| | | | 19 | 11,165,580 | 3'-UTR variant | c.*978A>G | | np | | | 9E−8 | [1] |

[a.]Gene affected by the variant, or the closest genes in case of intergenic variants. [b.]Identification in the dbSNPs database (www.ncbi.nlm.nih.gov/snp). [c.]Positions are relative to genome assembly GRCh38. [d.]Type of mutation. [e.]Classification in the ClinVar database (www.ncbi.nlm.nih.gov/clinvar) of variants affecting coding regions: no interp., no interpretation; np, not present. [f.]Prediction of the functional effect using PolyPhen (genetics.bwh.harvard.edu/pph2/). [g.]Prediction of the functional effect using Sift (sift.bii.a-star.edu.sg

**Table S1f**: SNVs associated with low-density lipoprotein cholesterol in Oceanian populations.

| Mapped gene[a] | Region | SNPid[b] | Chr | Position[c] | Type[d] | cDNA | Protein | ClinVar[e] | Polyphen[f] | Sift[g] | p-value | References |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| *APOB - TDRD15* | *APOB* | rs754523 | 2 | 21,088,819 | intergenic | | | | | | 6E−6 | [2] |
| *ANKRD31, HMGCR* | *HMGCR* | rs7703051 | 5 | 75,329,662 | intergenic | | | | | | 1E−8 | [1] |
| *TOMM40* | *APOE-C1-C2-C4* | rs1160985 | 19 | 44,900,155 | intronic | | | | | | 2E−27 | [2] |
| *APOC1* | | rs4420638 | 19 | 44,919,689 | downstream | c.*459A>G | | no interp. | | | 2E−7 | [1] |

[a.]Gene affected by the variant, or the closest genes in case of intergenic variants. [b.]Identification in the dbSNPs database (www.ncbi.nlm.nih.gov/snp). [c.]Positions are relative to genome assembly GRCh38. [d.]Type of mutation. [e.]Classification in the ClinVar database (www.ncbi.nlm.nih.gov/clinvar) of variants affecting coding regions: no interp., no interpretation; np, not present. [f.]Prediction of the functional effect using PolyPhen (genetics.bwh.harvard.edu/pph2/). [g.]Prediction of the functional effect using Sift (sift.bii.a-star.edu.sg/).

**Supplementary references for Afro-American or African ancestry populations**


1. Lettre, G.; Palmer, C.D.; Young, T.; Ejebe, K.G.; Allayee, H.; Benjamin, E.J.; Bennett, F.; Bowden, D.W.; Chakravarti, A.; Dreisbach, A., et al. Genome-wide association study of coronary heart disease and its risk factors in 8,090 African Americans: the NHLBI CARe Project. *PLoS Genet* **2011**, *7*, e1001300, doi:10.1371/journal.pgen.1001300.
2. Rasmussen-Torvik, L.J.; Pacheco, J.A.; Wilke, R.A.; Thompson, W.K.; Ritchie, M.D.; Kho, A.N.; Muthalagu, A.; Hayes, M.G.; Armstrong, L.L.; Scheftner, D.A., et al. High density GWAS for LDL cholesterol in African Americans using electronic medical records reveals a strong protective variant in APOE. *Clin Transl Sci* **2012**, *5*, 394-399, doi:10.1111/j.1752-8062.2012.00446.x.
3. Gurdasani, D.; Carstensen, T.; Fatumo, S.; Chen, G.; Franklin, C.S.; Prado-Martinez, J.; Bouman, H.; Abascal, F.; Haber, M.; Tachmazidou, I., et al. Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell* **2019**, *179*, 984-1002 e1036, doi:10.1016/j.cell.2019.10.004.


**Supplementary references for Native American or Hispanic populations**


1. Below, J.E.; Parra, E.J.; Gamazon, E.R.; Torres, J.; Krithika, S.; Candille, S.; Lu, Y.; Manichakul, A.; Peralta-Romero, J.; Duan, Q., et al. Meta-analysis of lipid-traits in Hispanics identifies novel loci, population-specific effects, and tissue-specific enrichment of eQTLs. *Sci Rep* **2016**, *6*, 19429, doi:10.1038/srep19429.
2. Andaleon, A.; Mogil, L.S.; Wheeler, H.E. Genetically regulated gene expression underlies lipid traits in Hispanic cohorts. *PLoS One* **2019**, *14*, e0220827, doi:10.1371/journal.pone.0220827.


**Supplementary references for Middle-East populations.**


1. Hebbar, P.; Abubaker, J.A.; Abu-Farha, M.; Alsmadi, O.; Elkum, N.; Alkayal, F.; John, S.E.; Channanath, A.; Iqbal, R.; Pitkaniemi, J., et al. Genome-wide landscape establishes novel association signals for metabolic traits in the Arab population. *Hum Genet* **2021**, *140*, 505-528, doi:10.1007/s00439-020-02222-7.


**Supplementary references for Oceanian populations.**


1. Burkhardt, R.; Kenny, E.E.; Lowe, J.K.; Birkeland, A.; Josowitz, R.; Noel, M.; Salit, J.; Maller, J.B.; Pe'er, I.; Daly, M.J., et al. Common SNPs in HMGCR in micronesians and whites associated with LDL-cholesterol levels affect alternative splicing of exon13. *Arterioscler Thromb Vasc Biol* **2008**, *28*, 2078-2084, doi:10.1161/ATVBAHA.108.172288.
2. Carlson, J.C.; Weeks, D.E.; Hawley, N.L.; Sun, G.; Cheng, H.; Naseri, T.; Reupena, M.S.; Tuitele, J.; Deka, R.; McGarvey, S.T., et al. Genome-wide association studies in Samoans give insight into the genetic architecture of fasting serum lipid levels. *J Hum Genet* **2020**, *66*, 111-121, doi:10.1038/s10038-020-0816-9.