**Online Supplemental Materials**

**Supplemental Methods**

***Participants***

The GENiAL cohort includes 273 men and 718 women. All lived in the Stockholm county, Sweden. 194 participants had type 2 diabetes, hypertension, or dyslipidemia alone or in different combinations. None were treated with insulin, glitazones or glucagon-like-peptide analogues. Fifty-seven percent were obese (defined as BMI >30kg/m2). The participants attended the Karolinska University Hospital’s clinical research center in the morning after an overnight fast for clinical examination and venous blood sampling for routine clinical chemistry.

***MR analyses***

The key approach of an MR analysis is to treat genotypes as naturally occurring randomizations to infer causal relationship between two phenotypes and can be viewed as analogous to a randomized clinical trial, albeit with some differences. To estimate the causal effect (γ) of a mediator (M), also known as exposure on the phenotype of interest (Y), also known as the outcome, and a variant Gj affects M and does not affect Y through pathways that are not mediated by M , then Gj can be viewed as an unconfounded proxy for M, also known as instrumental variables (IVs). Under these assumptions,

βY,j=γβM,j

where βY,j is the association of Gj with Y, and βM,j is the association of Gj with M.

For each analysis, the SNPs meeting the GWAS p-value threshold of 5x10-8 for the respective exposures were used IVs and the instruments were harmonised to the effect size increasing allele. The SNPs were pruned for linkage disequilibrium at a r2 threshold of 0.02 using the 1000 Genomes European superpopulation as a reference to retain only independent instruments.

Sensitivity analyses included MR Egger (1) that allows for some degree of uncorrelated horizontal pleiotropy but no correlated horizontal pleiotropy, leave-one out analyses to assess instrument outliers, and the weighted median (2) and mode (3) MR methods were used to infer a causal estimate that allows for a certain degree of both correlated and uncorrelated horizontal pleiotropy. MR Steiger (4) test was perform to assess the directionality of the exposure-outcome relationship to account for any potential reverse causation. MR Steiger calculates the causal direction of a relationship and the confidence of that direction using the correlation of SNP-exposure and SNP-outcome, under the assumption that there is no confounding or horizontal pleiotropy (5).

**Results**

***MR analyses***

A total of 9 instrumental variables (Supplementary Table 5) were used for fat cell number. For BMI as the outcome, 8 SNPs were available from the GWAS dataset. Fat cell number showed no significant causal association with BMI using the IVW method (OR 0.98, CI 95% 0.93-1.03, P=0.54). Similar estimates were obtained while accounting for uncorrelated horizontal pleiotropy with MR Egger (OR 0.92, CI 95% 0.73-1.151, P=0.52) and accounting for correlated horizontal pleiotropy using MR weighted median (OR 0.97, CI 95% 0.92-1.03, P=0.47) or weighted mode (OR 0.97, CI 95% 0.89-1.05, P=0.49). To check if BMI instead leads to a difference in fat cell number, MR was conducted using BMI as the exposure and fat cell number as the outcome. A total of 421 SNPs were used as instrumental variables. There was no significant association of the effect of BMI on fat cell number (Supplementary Table 6). MR Steiger estimated the direction of causality to be fat cell number leading to a difference in BMI (Steiger P=7.23x10-74). There was only 1 instrumental variable for an MR analysis of fat cell number as exposure and WHRadjBMI as outcome and the association estimate using Wald’s ratio was not significant (OR 1.04, CI 95% 0.81-1.34, P=0.72). MR analyses using WHRadjBMI as exposure and fat cell number as outcome, there were 28 SNPs available to be used as IVs. However, the causal association was not significant (Supplementary Table 5). MR Steiger estimated the causal direction to be from fat cell number to WHRadjBMI (Steiger P=1.21x10-8).

For MR analyses using fat cell number as exposure and type 2 diabetes as outcome, there was only 1 instrument available and showed no significant association (Wald’s ratio OR 0.93, CI 95% 0.58-1.48, P=0.77). There were 112 instruments for the MR analyses using type 2 diabetes as exposure and fat cell number as outcome, but the associations were not significant (Supplementary Table 5). MR Steiger estimated the direction of causality to be from fat cell number to type 2 diabetes (Steiger P=1.4x10-8).

**References**

1. Bowden J, Davey Smith G, Burgess S. Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. International journal of epidemiology. 2015;44(2):512-25.

2. Bowden J, Davey Smith G, Haycock PC, Burgess S. Consistent estimation in Mendelian randomization with some invalid instruments using a weighted median estimator. Genetic epidemiology. 2016;40(4):304-14.

3. Hartwig FP, Davey Smith G, Bowden J. Robust inference in summary data Mendelian randomization via the zero modal pleiotropy assumption. International journal of epidemiology. 2017;46(6):1985-98.

4. Hemani G, Tilling K, Davey Smith G. Orienting the causal relationship between imprecisely measured traits using GWAS summary data. PLoS genetics. 2017;13(11):e1007081.

5. Lutz SM, Wu AC, Hokanson JE, Vansteelandt S, Lange C. Caution against examining the role of reverse causality in Mendelian Randomization. Genetic epidemiology. 2021;45(5):445-54.

**Supplemental Figure Legends**

**Supplemental Figure 1** Regional plots for loci with at least one GWAS significant (p<5x10-8) SNP. Lead SNPs are presented for loci on A) chromosome 1, B) chromosome 2, C) chromosome 5, D) chromosome 6. The lead SNP (E) for the first chromosome 7 locus does not have LD information in the FUMA/Locuszoom reference data, so a proxy (F) is identified as the lead for this locus. Similarly, the lead SNP for the second chromosome 7 locus, 7:57587402\_T\_C, so FUMA presents G) rs112427936 as a proxy. Lead SNPs are presented for the H) chromosome 18 locus, I) and the chromosome 19 locus. The lead SNP (J) for the chromosome 20 locus lacks LD information in FUMA/locuszoom, so the lead SNP reported by FUMA (K) is also presented. Lead SNPs are presented as purple diamonds with other SNPs coloured by their LD with the lead SNP. Grey colouring indicates unknown LD. Solid lines indicate the threshold for GWAS significance, whilst the dashed line represents the threshold for suggestive significance.

**Supplemental Figure 2**: GWAS of fat cell number with additional adjustment for BMI. A) Manhattan plot of results. B) QQ plot of results. C) Comparison of effect of SNPs with suggestive associations (p<1x10-5) in the original analysis, with and without adjustment for BMI. D) Distribution of BMI in the GENiAL study.

**Supplemental Figure 3:** Effects of siRNA-mediated knock-down of candidate genes for fat cell number on human adipose-derived stem cell proliferation. hASCs were transfected with control siRNA oligonucleotide (siNegC) or siRNAs targeting SPATS2L, KCTD18, HSD17B12 and PEPD in proliferating cells 4 days prior induction of differentiation and followed until differentiation day 7, upon which accumulation of neutral lipids was evaluated by lipid staining.

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| **Supplementary Table 1. GWAS used to extract the summary statistics for BMI, T2D, and WHRadjBMI.** | | | | | | |
| **Outcome** | **Study ID** | **Total SNVs** | **Sample size** | **Consortium** | **Unit** | **Reference** |
| **BMI** | ukb-b-2303 | 9851867 | 454884 | UKBB /MRC-IEU | SD | Elsworth B, Lyon M, Alexander T, Liu Y, Matthews P, Hallett J, et al. The MRC IEU OpenGWAS data infrastructure. BioRxiv. 2020. |
| **T2D** | ebi-a-GCST006867 | 5030727 | 655666 | DIAGRAM + GERA + UKBB | logOR | Xue A, Wu Y, Zhu Z, Zhang F, Kemper KE, Zheng Z, et al. Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature communications. 2018;9(1):1-14. |
| **WHRadjBMI** | ieu-a-79 | 2542432 | 210082 | GIANT | SD | Shungin D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, Mägi R, et al. New genetic loci link adipose and insulin biology to body fat distribution. Nature. 2015;518(7538):187-96. |
| The study ID corresponds to the IEU GWAS database ID. UKBB: UK BioBank, GIANT: The Genetic Investigation of ANthropometric Traits, DIAGRAM: The DIAbetes Genetics Replication And Meta-analysis, GERA: Genetic Epidemiology Research on Aging. | | | | | | |

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| **Supplementary table 2. SNPs associated with abdominal subcutaneous fat cell number** | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|  |  |  |  |  |  |  |  | |  | |  |  | | |  | |  | |  | | **conditional lead** | | | | **conditional proxy** | | |
| **CHR** | **POS** | **ID** | **REF** | **ALT** | **A1** | **A1\_FREQ** | **BETA** | **SE** | | **P** | | | **lead/**  **proxy** | **r2 with lead** | | **r2 with proxy** | | **BETA** | | **SE** | | **P** | **BETA** | **SE** | | **P** |
| 1 | 18 981 408 | rs140068450 | A | G | A | 0.01 | 0.197 | 0.034 | | 6.09E-09 | | |  |  | |  | |  | |  | |  |  |  | |  |
| 2 | 54 781 601 | rs149660479 | G | T | G | 0.01 | 0.183 | 0.029 | | 8.71E-10 | | |  | lead | |  | |  | |  | |  |  |  | |  |
| 2 | 54 895 319 | rs139247782 | T | C | T | 0.01 | 0.177 | 0.029 | | 1.79E-09 | | |  |  | | 0.92 | |  | |  | |  |  |  | |  |
| 5 | 145 423 858 | rs186498547 | T | C | T | 0.01 | 0.166 | 0.028 | | 5.36E-09 | | |  |  | |  | |  | |  | |  |  |  | |  |
| 6 | 89 295 743 | rs150250345 | A | G | A | 0.01 | 0.151 | 0.026 | | 9.16E-09 | | |  |  | |  | |  | |  | |  |  |  | |  |
| 7 | 7 195 558 | rs12672133 | C | T | C | 0.04 | 0.092 | 0.016 | | 9.76E-09 | | |  | 0.61 | | 0.62 | | 0.042 | | 0.025 | | 0.0927 | 0.044 | 0.025 | | 0.0833 |
| 7 | 7 213 245 | rs73043785 | T | C | T | 0.04 | 0.088 | 0.016 | | 2.27E-08 | | |  | 0.60 | | 0.62 | | 0.036 | | 0.025 | | 0.1445 | 0.037 | 0.025 | | 0.1299 |
| 7 | 7 214 799 | rs73043789 | A | G | A | 0.04 | 0.088 | 0.016 | | 2.25E-08 | | |  | 0.60 | | 0.62 | | 0.036 | | 0.025 | | 0.1440 | 0.037 | 0.025 | | 0.1294 |
| 7 | 7 216 175 | rs12667853 | A | G | A | 0.04 | 0.089 | 0.016 | | 1.50E-08 | | |  | 0.62 | | 0.63 | | 0.038 | | 0.025 | | 0.1240 | 0.039 | 0.025 | | 0.1116 |
| 7 | 7 217 867 | rs55637396 | A | G | A | 0.04 | 0.092 | 0.016 | | 6.67E-09 | | |  | 0.64 | | 0.66 | | 0.044 | | 0.026 | | 0.0892 | 0.045 | 0.026 | | 0.0815 |
| 7 | 7 272 485 | rs73045769 | T | C | T | 0.04 | 0.093 | 0.016 | | 7.82E-09 | | |  | 0.67 | | 0.68 | | 0.042 | | 0.027 | | 0.1188 | 0.043 | 0.027 | | 0.1055 |
| 7 | 7 273 424 | rs73045773 | G | A | G | 0.04 | 0.091 | 0.016 | | 1.02E-08 | | |  | 0.64 | | 0.65 | | 0.040 | | 0.025 | | 0.1114 | 0.042 | 0.025 | | 0.1008 |
| 7 | 7 282 894 | rs73049974 | A | G | A | 0.04 | 0.091 | 0.016 | | 1.13E-08 | | |  | 0.66 | | 0.67 | | 0.039 | | 0.026 | | 0.1408 | 0.040 | 0.026 | | 0.1281 |
| 7 | 7 285 578 | rs114287739 | T | A | T | 0.04 | 0.092 | 0.016 | | 7.60E-09 | | |  | 0.69 | | 0.70 | | 0.041 | | 0.027 | | 0.1365 | 0.042 | 0.027 | | 0.1209 |
| 7 | 7 285 607 | rs73049983 | A | G | A | 0.04 | 0.092 | 0.016 | | 9.64E-09 | | |  | 0.69 | | 0.70 | | 0.039 | | 0.027 | | 0.1557 | 0.040 | 0.027 | | 0.1402 |
| 7 | 7 286 193 | rs5010182 | G | A | G | 0.04 | 0.092 | 0.016 | | 7.60E-09 | | |  | 0.69 | | 0.70 | | 0.041 | | 0.027 | | 0.1365 | 0.042 | 0.027 | | 0.1209 |
| 7 | 7 292 688 | rs73049994 | T | C | T | 0.04 | 0.092 | 0.016 | | 1.00E-08 | | |  | 0.69 | | 0.70 | | 0.039 | | 0.027 | | 0.1580 | 0.040 | 0.027 | | 0.1405 |
| 7 | 7 296 136 | rs73049999 | C | T | C | 0.04 | 0.093 | 0.016 | | 8.81E-09 | | |  | 0.69 | | 0.70 | | 0.040 | | 0.027 | | 0.1465 | 0.041 | 0.027 | | 0.1309 |
| 7 | 7 300 508 | rs112344846 | C | G | C | 0.03 | 0.093 | 0.016 | | 2.37E-08 | | |  | 0.76 | | 0.76 | | 0.027 | | 0.031 | | 0.3946 | 0.027 | 0.032 | | 0.4044 |
| 7 | 7 301 098 | rs73051710 | C | T | C | 0.03 | 0.092 | 0.016 | | 2.73E-08 | | |  | 0.76 | | 0.76 | | 0.025 | | 0.031 | | 0.4282 | 0.025 | 0.032 | | 0.4393 |
| 7 | 7 312 747 | rs58968692 | C | T | C | 0.04 | 0.090 | 0.016 | | 2.98E-08 | | |  | 0.76 | | 0.78 | | 0.025 | | 0.030 | | 0.4201 | 0.016 | 0.035 | | 0.6415 |
| 7 | 7 313 294 | rs6973768 | G | T | G | 0.04 | 0.093 | 0.017 | | 2.42E-08 | | |  | 0.81 | | 0.85 | | 0.023 | | 0.033 | | 0.4949 | 0.011 | 0.040 | | 0.7758 |
| 7 | 7 316 262 | rs6974699 | C | G | C | 0.03 | 0.104 | 0.018 | | 1.26E-08 | | |  | 0.93 | | 1.00 | | 0.007 | | 0.051 | | 0.8927 | -0.206 | 0.122 | | 0.0904 |
| 7 | 7 317 524 | rs2270081 | A | G | A | 0.03 | 0.104 | 0.018 | | 1.10E-08 | | |  | 0.92 | | 1.00 | | 0.009 | | 0.051 | | 0.8563 | NA | NA | | NA |
| 7 | 7 319 013 | rs147389390 | D | I | D | 0.03 | 0.113 | 0.018 | | 1.49E-09 | | | lead |  | | 0.95 | | NA | | NA | | NA | 0.063 | 0.052 | | 0.2270 |
| 7 | 7 321 075 | rs60008535 | G | A | G | 0.03 | 0.100 | 0.018 | | 2.50E-08 | | |  | 0.90 | | 0.97 | | -0.003 | | 0.047 | | 0.9543 | -0.160 | 0.094 | | 0.0872 |
| 7 | 7 321 130 | rs73051783 | C | G | C | 0.03 | 0.106 | 0.018 | | 7.93E-09 | | |  | 0.92 | | 1.00 | | 0.017 | | 0.052 | | 0.7502 | NA | NA | | NA |
| 7 | 7 328 241 | rs56405297 | G | A | G | 0.03 | 0.111 | 0.018 | | 2.29E-09 | | |  | 0.95 | | 1.00 | | 0.048 | | 0.052 | | 0.3628 | NA | NA | | NA |
| 7 | 7 328 318 | rs138278387 | D | I | D | 0.03 | 0.112 | 0.019 | | 3.89E-09 | | |  | 1.00 | | 0.94 | | NA | | NA | | NA | 0.041 | 0.052 | | 0.4309 |
| 7 | 7 329 539 | rs7779267 | T | C | T | 0.03 | 0.112 | 0.018 | | 1.84E-09 | | | proxy | 0.95 | |  | | 0.053 | | 0.052 | | 0.3050 | NA | NA | | NA |
| 7 | 7 332 244 | rs73053804 | C | G | C | 0.03 | 0.111 | 0.019 | | 3.07E-09 | | |  | 0.92 | | 1.00 | | 0.043 | | 0.050 | | 0.3836 | NA | NA | | NA |
| 7 | 7 332 460 | rs73053807 | A | C | A | 0.03 | 0.115 | 0.020 | | 9.80E-09 | | |  | 0.75 | | 0.81 | | 0.042 | | 0.039 | | 0.2727 | 0.027 | 0.051 | | 0.6022 |
| 7 | 57 521 560 | rs117553144 | C | T | C | 0.02 | 0.148 | 0.025 | | 2.82E-09 | | |  | 0.92 | | 1.00 | | -0.026 | | 0.092 | | 0.7753 | 0.036 | 0.086 | | 0.6771 |
| 7 | 57 573 899 | 7:57573899\_C\_G | G | C | G | 0.02 | 0.150 | 0.024 | | 1.15E-09 | | |  | 1.00 | |  | | -0.015 | | 0.119 | | 0.9024 | 0.079 | 0.095 | | 0.4059 |
| 7 | 57 587 402 | 7:57587402\_T\_C | C | T | C | 0.02 | 0.148 | 0.023 | | 4.11E-10 | | | lead |  | | 1.00 | | NA | | NA | | NA | 0.135 | 0.093 | | 0.1456 |
| 7 | 57 618 204 | rs112427936 | A | G | A | 0.02 | 0.159 | 0.026 | | 1.21E-09 | | | proxy | 1.00 | | 0.94 | | 0.015 | | 0.102 | | 0.8833 | NA | NA | | NA |
| 7 | 57 659 662 | rs528332416 | T | C | T | 0.01 | 0.162 | 0.028 | | 5.93E-09 | | |  | 1.00 | | 0.94 | | 0.006 | | 0.074 | | 0.9406 | -0.088 | 0.136 | | 0.5170 |
| 18 | 36 828 775 | rs141736521 | A | G | A | 0.01 | 0.179 | 0.032 | | 2.95E-08 | | |  |  | |  | |  | |  | |  |  |  | |  |
| 19 | 47 119 930 | 19:47119930\_C\_G | G | C | G | 0.01 | 0.181 | 0.032 | | 1.80E-08 | | |  | 0.92 | |  | |  | |  | |  |  |  | |  |
| 19 | 47 139 877 | rs115034159 | T | C | T | 0.01 | 0.185 | 0.030 | | 1.68E-09 | | | lead |  | |  | | BETA | | SE | | P | BETA | SE | | P |
| 20 | 32 162 067 | rs149392217 | C | G | C | 0.02 | 0.152 | 0.025 | | 2.02E-09 | | |  | 1.00 | | 0.89 | | 0.055 | | 0.039 | | 0.1583 | 0.051 | 0.046 | | 0.2677 |
| 20 | 32 178 376 | rs139163690 | T | C | T | 0.02 | 0.151 | 0.025 | | 2.56E-09 | | |  | 0.66 | | 0.89 | | 0.051 | | 0.039 | | 0.1906 | 0.046 | 0.047 | | 0.3261 |
| 20 | 32 275 289 | rs3213133 | D | I | D | 0.01 | 0.224 | 0.033 | | 2.54E-11 | | | lead |  | | 0.46 | | NA | | NA | | NA | 0.142 | 0.048 | | 0.0033 |
| 20 | 32 458 051 | rs150618140 | A | C | A | 0.02 | 0.163 | 0.025 | | 1.26E-10 | | | proxy | 0.46 | |  | | 0.085 | | 0.036 | | 0.0192 | NA | NA | | NA |

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| Supplementary table 3. SNPs associated abdominal subcutaneous fat cell numbera | | | | | | | | | | | | |  | |  |  |
| CHROM | POS | ID | REF | ALT | A1 | A1\_FREQ | MACH\_R2 | BETA\_A1 | SE | L95 | U95 | P | Consequence | Conseq-uence | | IMPACT |
| 1 | 5271487 | rs148400317 | D | I | D | 0.013 | 0.952 | 0.127 | 0.028 | 0.071 | 0.182 | 8.22E-06 | intergenic variant | 36 | | MODIFIER |
| 1 | 18981408 | rs140068450 | A | G | A | 0.012 | 0.718 | 0.197 | 0.034 | 0.131 | 0.263 | 6.09E-09 | intron variant | 23 | | MODIFIER |
| 1 | 47080679 | rs6671527 | A | G | G | 0.491 | 0.997 | -0.028 | 0.006 | -0.040 | -0.016 | 7.66E-06 | 5 prime UTR variant | 20 | | MODIFIER |
| 1 | 47080983 | rs35494693 | A | G | A | 0.490 | 0.980 | -0.028 | 0.006 | -0.040 | -0.016 | 9.02E-06 | intron variant | 23 | | MODIFIER |
| 1 | 47263237 | rs45544733 | C | G | C | 0.020 | 0.858 | 0.113 | 0.024 | 0.066 | 0.159 | 2.86E-06 | upstream gene variant | 26 | | MODIFIER |
| 1 | 47265429 | rs55693314 | T | C | T | 0.019 | 0.861 | 0.113 | 0.024 | 0.066 | 0.160 | 2.54E-06 | intron variant | 23 | | MODIFIER |
| 1 | 118376849 | rs548437178 | G | A | G | 0.013 | 0.812 | 0.137 | 0.030 | 0.078 | 0.196 | 6.94E-06 | intergenic variant | 36 | | MODIFIER |
| 1 | 118821005 | rs181890845 | C | T | C | 0.013 | 0.968 | 0.129 | 0.027 | 0.075 | 0.183 | 2.89E-06 | regulatory region variant | 34 | | MODIFIER |
| 1 | 118833583 | rs147848872 | C | A | C | 0.014 | 0.959 | 0.129 | 0.027 | 0.075 | 0.183 | 2.75E-06 | regulatory region variant | 34 | | MODIFIER |
| 1 | 159824835 | rs111439060 | C | G | C | 0.015 | 0.782 | 0.140 | 0.029 | 0.084 | 0.196 | 1.04E-06 | intron variant | 23 | | MODIFIER |
| 1 | 169625593 | rs116833969 | G | C | G | 0.024 | 0.902 | 0.094 | 0.021 | 0.053 | 0.135 | 8.26E-06 | regulatory region variant | 34 | | MODIFIER |
| 1 | 170154993 | rs111749519 | G | A | G | 0.013 | 0.894 | 0.139 | 0.028 | 0.084 | 0.195 | 1.15E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 1 | 172888353 | rs143922166 | C | T | C | 0.020 | 0.785 | 0.114 | 0.025 | 0.065 | 0.162 | 4.42E-06 | regulatory region variant | 34 | | MODIFIER |
| 1 | 173521743 | rs142810310 | D | I | D | 0.020 | 0.951 | 0.101 | 0.023 | 0.056 | 0.145 | 9.65E-06 | intron variant | 23 | | MODIFIER |
| 1 | 174095248 | rs139387250 | T | C | T | 0.014 | 0.891 | 0.129 | 0.028 | 0.074 | 0.184 | 4.38E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 1 | 175005858 | rs138727370 | T | C | T | 0.011 | 0.803 | 0.157 | 0.033 | 0.092 | 0.222 | 2.53E-06 | regulatory region variant | 34 | | MODIFIER |
| 1 | 247252153 | rs7512933 | T | C | T | 0.066 | 0.492 | 0.079 | 0.018 | 0.044 | 0.113 | 8.35E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 19735548 | rs62126633 | A | C | A | 0.428 | 1.009 | 0.028 | 0.006 | 0.015 | 0.040 | 9.49E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 19761314 | rs7561420 | C | T | T | 0.428 | 1.009 | 0.028 | 0.006 | 0.016 | 0.040 | 9.25E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 19765158 | rs4666492 | G | C | G | 0.424 | 0.988 | 0.028 | 0.006 | 0.016 | 0.040 | 8.72E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 23552507 | rs115409144 | A | G | A | 0.011 | 1.090 | 0.137 | 0.028 | 0.082 | 0.192 | 1.10E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 46133628 | rs111508080 | A | G | A | 0.029 | 0.961 | 0.085 | 0.019 | 0.048 | 0.122 | 6.87E-06 | intron variant | 23 | | MODIFIER |
| 2 | 46140574 | rs115299511 | T | C | T | 0.028 | 0.968 | 0.088 | 0.019 | 0.051 | 0.126 | 4.24E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54330976 | rs149611868 | C | T | C | 0.012 | 0.880 | 0.139 | 0.030 | 0.081 | 0.198 | 3.74E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54370169 | rs146575195 | T | G | T | 0.012 | 0.904 | 0.138 | 0.029 | 0.080 | 0.196 | 3.09E-06 | 3 prime UTR variant | 21 | | MODIFIER |
| 2 | 54712295 | rs116332364 | T | C | T | 0.046 | 1.009 | 0.066 | 0.015 | 0.037 | 0.095 | 7.09E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54781601 | rs149660479 | G | T | G | 0.012 | 0.906 | 0.183 | 0.029 | 0.125 | 0.241 | 8.71E-10 | intron variant | 23 | | MODIFIER |
| 2 | 54867769 | rs139099501 | I | D | I | 0.053 | 1.014 | 0.061 | 0.014 | 0.034 | 0.087 | 8.54E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54884074 | rs3769331 | C | T | C | 0.053 | 1.007 | 0.062 | 0.014 | 0.035 | 0.089 | 7.30E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54892506 | rs7583633 | G | C | G | 0.051 | 0.974 | 0.064 | 0.014 | 0.036 | 0.091 | 6.64E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54895319 | rs139247782 | T | C | T | 0.012 | 0.924 | 0.177 | 0.029 | 0.120 | 0.233 | 1.79E-09 | intron variant | 23 | | MODIFIER |
| 2 | 54898115 | rs3820856 | T | C | T | 0.058 | 1.001 | 0.068 | 0.013 | 0.042 | 0.094 | 3.11E-07 | 3 prime UTR variant | 21 | | MODIFIER |
| 2 | 54901455 | rs201313305 | D | I | D | 0.056 | 1.000 | 0.069 | 0.013 | 0.043 | 0.095 | 2.56E-07 | downstream gene variant | 27 | | MODIFIER |
| 2 | 54904820 | rs6740018 | G | C | G | 0.059 | 0.982 | 0.070 | 0.013 | 0.044 | 0.096 | 1.44E-07 | regulatory region variant | 34 | | MODIFIER |
| 2 | 54909741 | rs143157223 | A | G | A | 0.059 | 0.979 | 0.070 | 0.013 | 0.044 | 0.096 | 1.20E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54911968 | rs75654812 | C | T | C | 0.059 | 0.973 | 0.071 | 0.013 | 0.046 | 0.097 | 8.06E-08 | intergenic variant | 36 | | MODIFIER |
| 2 | 54913089 | rs151009419 | T | C | T | 0.059 | 0.974 | 0.071 | 0.013 | 0.046 | 0.097 | 8.16E-08 | intergenic variant | 36 | | MODIFIER |
| 2 | 54915221 | rs6705193 | A | G | A | 0.062 | 1.007 | 0.065 | 0.013 | 0.040 | 0.090 | 3.71E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54915327 | rs77334206 | G | A | G | 0.059 | 0.978 | 0.070 | 0.013 | 0.044 | 0.095 | 1.40E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54916241 | rs74518232 | C | G | C | 0.060 | 0.979 | 0.068 | 0.013 | 0.042 | 0.094 | 2.51E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54916618 | rs7561112 | T | C | T | 0.062 | 1.006 | 0.065 | 0.013 | 0.040 | 0.090 | 3.04E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54916629 | rs7587575 | T | A | T | 0.062 | 1.006 | 0.065 | 0.013 | 0.040 | 0.090 | 3.16E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54920691 | rs76988803 | G | C | G | 0.058 | 0.986 | 0.070 | 0.013 | 0.044 | 0.096 | 1.36E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54921349 | rs72911575 | C | G | C | 0.058 | 0.982 | 0.070 | 0.013 | 0.044 | 0.096 | 1.62E-07 | regulatory region variant | 34 | | MODIFIER |
| 2 | 54922692 | rs72911576 | G | A | G | 0.058 | 0.976 | 0.071 | 0.013 | 0.045 | 0.097 | 1.04E-07 | regulatory region variant | 34 | | MODIFIER |
| 2 | 54925159 | rs140858894 | D | I | D | 0.057 | 0.961 | 0.071 | 0.013 | 0.045 | 0.098 | 1.41E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54927885 | rs111404605 | G | A | G | 0.059 | 0.982 | 0.070 | 0.013 | 0.045 | 0.096 | 9.79E-08 | intergenic variant | 36 | | MODIFIER |
| 2 | 54934844 | rs79747576 | A | C | A | 0.058 | 0.978 | 0.073 | 0.013 | 0.047 | 0.099 | 5.32E-08 | intergenic variant | 36 | | MODIFIER |
| 2 | 54938035 | rs72389124 | D | I | D | 0.061 | 0.945 | 0.069 | 0.013 | 0.043 | 0.095 | 2.20E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54938475 | rs10169328 | A | G | A | 0.058 | 0.966 | 0.071 | 0.013 | 0.045 | 0.097 | 1.36E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54938926 | rs60307496 | G | T | G | 0.058 | 0.965 | 0.070 | 0.013 | 0.044 | 0.096 | 1.64E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54939411 | rs13404168 | C | T | C | 0.059 | 0.961 | 0.070 | 0.013 | 0.044 | 0.096 | 1.59E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54939481 | rs13404269 | C | T | C | 0.059 | 0.960 | 0.070 | 0.013 | 0.044 | 0.096 | 1.72E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54940174 | 2:54940174\_T\_C | C | T | C | 0.059 | 0.962 | 0.070 | 0.013 | 0.044 | 0.096 | 1.55E-07 |  |  | |  |
| 2 | 54941710 | rs13398208 | G | C | G | 0.058 | 0.963 | 0.073 | 0.013 | 0.047 | 0.099 | 6.71E-08 | intergenic variant | 36 | | MODIFIER |
| 2 | 54947126 | rs72913513 | G | A | G | 0.077 | 0.914 | 0.063 | 0.012 | 0.039 | 0.086 | 2.50E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 54948606 | rs72913519 | C | G | C | 0.070 | 0.945 | 0.062 | 0.012 | 0.038 | 0.086 | 6.29E-07 | upstream gene variant | 26 | | MODIFIER |
| 2 | 54949937 | rs59370148 | C | T | C | 0.058 | 0.950 | 0.071 | 0.013 | 0.045 | 0.098 | 1.59E-07 | upstream gene variant | 26 | | MODIFIER |
| 2 | 54951482 | rs72913521 | T | C | T | 0.057 | 0.952 | 0.071 | 0.013 | 0.045 | 0.098 | 1.63E-07 | upstream gene variant | 26 | | MODIFIER |
| 2 | 54955792 | rs116681291 | G | A | G | 0.038 | 0.909 | 0.077 | 0.017 | 0.044 | 0.111 | 5.62E-06 | intron variant | 23 | | MODIFIER |
| 2 | 54956566 | rs10170283 | C | A | C | 0.057 | 0.951 | 0.072 | 0.014 | 0.045 | 0.098 | 1.43E-07 | intron variant | 23 | | MODIFIER |
| 2 | 54959408 | rs13399055 | T | A | T | 0.057 | 0.952 | 0.070 | 0.014 | 0.044 | 0.097 | 2.78E-07 | intron variant | 23 | | MODIFIER |
| 2 | 56872143 | rs111609475 | A | G | A | 0.035 | 0.901 | 0.080 | 0.018 | 0.045 | 0.114 | 6.77E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 57361468 | rs555944479 | A | T | A | 0.046 | 0.842 | 0.071 | 0.016 | 0.040 | 0.103 | 8.04E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 80882232 | rs116120048 | G | C | G | 0.012 | 0.813 | 0.141 | 0.032 | 0.080 | 0.203 | 8.58E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 82111548 | rs138681844 | T | C | T | 0.015 | 0.784 | 0.139 | 0.028 | 0.083 | 0.195 | 1.21E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 84086257 | rs189227070 | G | A | G | 0.012 | 0.831 | 0.143 | 0.031 | 0.083 | 0.203 | 3.43E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 85236657 | rs71411813 | C | A | C | 0.014 | 0.871 | 0.154 | 0.028 | 0.099 | 0.210 | 5.70E-08 | intron variant | 23 | | MODIFIER |
| 2 | 167744332 | rs150083396 | G | A | G | 0.013 | 0.835 | 0.134 | 0.029 | 0.076 | 0.192 | 6.24E-06 | upstream gene variant | 26 | | MODIFIER |
| 2 | 167879413 | rs542353682 | T | C | T | 0.020 | 0.919 | 0.102 | 0.023 | 0.058 | 0.146 | 7.13E-06 | intron variant | 23 | | MODIFIER |
| 2 | 168430169 | rs79378767 | A | G | A | 0.023 | 0.838 | 0.121 | 0.022 | 0.077 | 0.165 | 9.16E-08 | intron variant | 23 | | MODIFIER |
| 2 | 200753271 | rs148890552 | A | G | A | 0.014 | 1.014 | 0.121 | 0.026 | 0.071 | 0.171 | 3.00E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200767076 | rs114847522 | A | G | A | 0.015 | 0.997 | 0.118 | 0.025 | 0.068 | 0.168 | 4.04E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200769914 | rs116615797 | A | G | A | 0.015 | 1.003 | 0.118 | 0.025 | 0.068 | 0.168 | 3.92E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200772896 | rs183372316 | T | C | T | 0.015 | 1.003 | 0.118 | 0.025 | 0.068 | 0.168 | 3.92E-06 | upstream gene variant | 26 | | MODIFIER |
| 2 | 200801380 | rs139474032 | G | A | G | 0.015 | 1.001 | 0.117 | 0.025 | 0.067 | 0.167 | 4.56E-06 | intron variant | 23 | | MODIFIER |
| 2 | 200871874 | rs78003233 | T | C | T | 0.015 | 1.000 | 0.117 | 0.025 | 0.068 | 0.167 | 3.91E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200891378 | rs115648719 | C | T | C | 0.015 | 1.004 | 0.115 | 0.025 | 0.066 | 0.165 | 6.13E-06 | regulatory region variant | 34 | | MODIFIER |
| 2 | 200901576 | rs114419000 | T | C | T | 0.015 | 1.012 | 0.114 | 0.025 | 0.065 | 0.163 | 7.05E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200962992 | rs149699386 | A | G | A | 0.011 | 1.051 | 0.153 | 0.029 | 0.096 | 0.209 | 1.51E-07 | intergenic variant | 36 | | MODIFIER |
| 2 | 200968208 | rs188401823 | C | T | C | 0.015 | 1.019 | 0.118 | 0.025 | 0.070 | 0.167 | 1.76E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200973255 | rs116835322 | A | G | A | 0.015 | 1.019 | 0.118 | 0.025 | 0.070 | 0.167 | 1.76E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200983853 | rs142988313 | C | A | C | 0.015 | 1.019 | 0.118 | 0.025 | 0.070 | 0.167 | 1.76E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 200995050 | rs140986905 | C | T | C | 0.011 | 1.047 | 0.152 | 0.029 | 0.096 | 0.208 | 1.33E-07 | regulatory region variant | 34 | | MODIFIER |
| 2 | 201002023 | rs114489156 | T | C | T | 0.016 | 1.027 | 0.119 | 0.024 | 0.071 | 0.167 | 1.33E-06 | regulatory region variant | 34 | | MODIFIER |
| 2 | 201006938 | rs74822948 | A | G | A | 0.016 | 1.034 | 0.119 | 0.024 | 0.071 | 0.166 | 1.29E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 201017463 | rs77852935 | A | G | A | 0.016 | 1.035 | 0.119 | 0.024 | 0.071 | 0.167 | 1.15E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 201020141 | rs141481897 | C | T | C | 0.016 | 1.035 | 0.119 | 0.024 | 0.071 | 0.167 | 1.15E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 201075633 | rs115519448 | A | G | A | 0.010 | 1.065 | 0.161 | 0.030 | 0.103 | 0.219 | 8.20E-08 | intergenic variant | 36 | | MODIFIER |
| 2 | 201076992 | rs78170266 | A | G | A | 0.010 | 1.068 | 0.160 | 0.030 | 0.102 | 0.218 | 9.58E-08 | regulatory region variant | 34 | | MODIFIER |
| 2 | 201119367 | rs115947566 | A | G | A | 0.031 | 1.065 | 0.077 | 0.017 | 0.044 | 0.111 | 6.97E-06 | intergenic variant | 36 | | MODIFIER |
| 2 | 201354937 | rs565245989 | D | I | D | 0.009 | 0.942 | 0.154 | 0.033 | 0.088 | 0.219 | 4.61E-06 | frameshift variant | 5 | | HIGH |
| 2 | 221944806 | rs151197313 | A | G | A | 0.011 | 0.544 | 0.185 | 0.039 | 0.107 | 0.262 | 3.32E-06 | intergenic variant | 36 | | MODIFIER |
| 3 | 25073712 | rs138514634 | A | G | A | 0.011 | 0.857 | 0.143 | 0.032 | 0.081 | 0.206 | 6.99E-06 | intron variant | 23 | | MODIFIER |
| 3 | 119372487 | rs188407911 | T | G | T | 0.012 | 0.930 | 0.128 | 0.029 | 0.072 | 0.184 | 9.84E-06 | intron variant | 23 | | MODIFIER |
| 3 | 131358627 | rs146215444 | G | A | G | 0.013 | 0.883 | 0.133 | 0.029 | 0.076 | 0.190 | 4.63E-06 | intron variant | 23 | | MODIFIER |
| 3 | 131900991 | rs114164672 | T | C | T | 0.014 | 0.965 | 0.121 | 0.026 | 0.069 | 0.172 | 4.83E-06 | intergenic variant | 36 | | MODIFIER |
| 3 | 131923754 | rs116639767 | C | G | C | 0.015 | 0.952 | 0.123 | 0.026 | 0.071 | 0.174 | 3.29E-06 | intergenic variant | 36 | | MODIFIER |
| 3 | 131987439 | rs186588368 | G | A | G | 0.013 | 0.954 | 0.136 | 0.028 | 0.081 | 0.191 | 1.38E-06 | intergenic variant | 36 | | MODIFIER |
| 3 | 132218621 | rs61748103 | A | G | A | 0.011 | 0.792 | 0.164 | 0.033 | 0.099 | 0.228 | 7.77E-07 | missense variant | 11 | | MODERATE |
| 3 | 190408786 | rs73184209 | A | T | A | 0.011 | 0.739 | 0.169 | 0.034 | 0.102 | 0.235 | 7.07E-07 | intergenic variant | 36 | | MODIFIER |
| 4 | 21719655 | rs191089506 | G | A | G | 0.012 | 0.611 | 0.189 | 0.035 | 0.120 | 0.258 | 1.16E-07 | intron variant | 23 | | MODIFIER |
| 4 | 21897281 | rs76563062 | T | C | T | 0.014 | 0.687 | 0.147 | 0.032 | 0.085 | 0.209 | 4.12E-06 | intron variant | 23 | | MODIFIER |
| 4 | 22093741 | rs138173324 | A | G | A | 0.014 | 0.711 | 0.144 | 0.030 | 0.084 | 0.203 | 2.78E-06 | regulatory region variant | 34 | | MODIFIER |
| 4 | 32122541 | rs10557314 | D | I | I | 0.148 | 0.941 | 0.043 | 0.009 | 0.026 | 0.061 | 1.30E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 4 | 48307565 | rs116076550 | G | A | G | 0.012 | 0.799 | 0.152 | 0.031 | 0.091 | 0.214 | 1.24E-06 | intergenic variant | 36 | | MODIFIER |
| 4 | 100398912 | rs116483546 | G | A | G | 0.044 | 0.987 | 0.068 | 0.015 | 0.039 | 0.098 | 6.17E-06 | intergenic variant | 36 | | MODIFIER |
| 4 | 100522458 | rs550156613 | A | T | A | 0.044 | 0.918 | 0.070 | 0.016 | 0.039 | 0.100 | 9.61E-06 | intron variant | 23 | | MODIFIER |
| 4 | 142128863 | rs186636723 | G | T | G | 0.012 | 1.034 | 0.127 | 0.027 | 0.073 | 0.180 | 3.52E-06 | intergenic variant | 36 | | MODIFIER |
| 4 | 142309016 | rs183930059 | G | T | G | 0.010 | 1.067 | 0.146 | 0.029 | 0.089 | 0.204 | 6.14E-07 | intergenic variant | 36 | | MODIFIER |
| 4 | 142963810 | rs183291101 | T | G | T | 0.011 | 0.900 | 0.163 | 0.031 | 0.102 | 0.224 | 2.14E-07 | intron variant | 23 | | MODIFIER |
| 4 | 148235861 | rs79684310 | C | T | C | 0.020 | 1.038 | 0.101 | 0.022 | 0.058 | 0.143 | 4.38E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 26903163 | rs138455466 | C | T | C | 0.010 | 0.901 | 0.145 | 0.033 | 0.082 | 0.209 | 8.82E-06 | intron variant | 23 | | MODIFIER |
| 5 | 66303886 | rs34698 | G | C | C | 0.124 | 1.005 | 0.042 | 0.009 | 0.024 | 0.060 | 7.19E-06 | intron variant | 23 | | MODIFIER |
| 5 | 66306930 | rs537382 | A | G | G | 0.124 | 1.000 | 0.042 | 0.009 | 0.024 | 0.060 | 6.70E-06 | intron variant | 23 | | MODIFIER |
| 5 | 66313583 | rs166091 | C | T | C | 0.123 | 1.010 | 0.042 | 0.009 | 0.023 | 0.060 | 9.05E-06 | intron variant | 23 | | MODIFIER |
| 5 | 66313721 | rs706703 | A | G | A | 0.122 | 1.011 | 0.042 | 0.009 | 0.024 | 0.060 | 8.26E-06 | intron variant | 23 | | MODIFIER |
| 5 | 66317317 | rs250278 | C | T | C | 0.124 | 1.016 | 0.041 | 0.009 | 0.023 | 0.059 | 9.36E-06 | intron variant | 23 | | MODIFIER |
| 5 | 66322736 | rs2548584 | A | G | A | 0.123 | 1.017 | 0.042 | 0.009 | 0.023 | 0.060 | 8.79E-06 | intron variant | 23 | | MODIFIER |
| 5 | 106293649 | rs78582752 | T | A | T | 0.011 | 0.867 | 0.147 | 0.031 | 0.086 | 0.208 | 2.94E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 5 | 112445413 | rs139994237 | C | T | C | 0.019 | 0.752 | 0.125 | 0.026 | 0.075 | 0.175 | 1.36E-06 | intron variant | 23 | | MODIFIER |
| 5 | 121506284 | rs114718578 | A | C | A | 0.041 | 0.836 | 0.077 | 0.017 | 0.043 | 0.110 | 7.31E-06 | intron variant | 23 | | MODIFIER |
| 5 | 121507211 | rs116596137 | C | G | C | 0.041 | 0.834 | 0.076 | 0.017 | 0.043 | 0.109 | 7.89E-06 | intron variant | 23 | | MODIFIER |
| 5 | 145323203 | rs186123088 | T | C | T | 0.012 | 0.923 | 0.148 | 0.029 | 0.091 | 0.204 | 3.64E-07 | intron variant | 23 | | MODIFIER |
| 5 | 145423858 | rs186498547 | T | C | T | 0.012 | 0.996 | 0.166 | 0.028 | 0.111 | 0.221 | 5.36E-09 | intron variant | 23 | | MODIFIER |
| 5 | 145491112 | rs151111196 | C | T | C | 0.018 | 0.750 | 0.119 | 0.026 | 0.067 | 0.171 | 7.09E-06 | downstream gene variant | 27 | | MODIFIER |
| 5 | 145761929 | rs33999729 | A | G | A | 0.029 | 0.959 | 0.094 | 0.019 | 0.057 | 0.131 | 7.13E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145781373 | rs34303875 | T | C | T | 0.031 | 0.931 | 0.092 | 0.018 | 0.056 | 0.128 | 6.47E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145782940 | rs13160043 | T | C | T | 0.031 | 0.926 | 0.092 | 0.018 | 0.056 | 0.128 | 6.75E-07 | regulatory region variant | 34 | | MODIFIER |
| 5 | 145783258 | rs13183864 | G | A | G | 0.031 | 0.929 | 0.092 | 0.018 | 0.056 | 0.128 | 7.23E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145783524 | rs149976158 | C | T | C | 0.031 | 0.926 | 0.092 | 0.018 | 0.056 | 0.128 | 6.75E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145784871 | rs34242710 | A | C | A | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.51E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145785181 | rs34926825 | T | G | T | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.60E-07 | regulatory region variant | 34 | | MODIFIER |
| 5 | 145785785 | rs56763657 | A | G | A | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.60E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145786058 | rs34567385 | C | G | C | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.60E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145786205 | rs34214546 | A | G | A | 0.027 | 0.913 | 0.091 | 0.020 | 0.051 | 0.130 | 6.53E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 145787743 | rs34694143 | T | C | T | 0.031 | 0.920 | 0.091 | 0.018 | 0.055 | 0.128 | 8.45E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145788362 | rs13182461 | G | A | G | 0.031 | 0.921 | 0.090 | 0.018 | 0.054 | 0.126 | 1.02E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 145788526 | rs60165325 | G | A | G | 0.031 | 0.921 | 0.090 | 0.018 | 0.054 | 0.126 | 1.02E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 145789406 | rs13167316 | T | G | T | 0.031 | 0.912 | 0.091 | 0.018 | 0.055 | 0.128 | 8.05E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145789613 | rs35713813 | G | A | G | 0.031 | 0.912 | 0.091 | 0.018 | 0.055 | 0.128 | 8.05E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145792710 | rs13166656 | T | A | T | 0.031 | 0.912 | 0.091 | 0.018 | 0.055 | 0.128 | 8.05E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145794521 | rs13157438 | T | C | T | 0.031 | 0.906 | 0.092 | 0.018 | 0.055 | 0.128 | 8.53E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145794905 | rs566018027 | D | I | D | 0.098 | 0.876 | 0.050 | 0.011 | 0.028 | 0.071 | 7.78E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 145794923 | rs35979619 | C | A | C | 0.031 | 0.906 | 0.092 | 0.018 | 0.055 | 0.128 | 8.53E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145798557 | rs13174030 | C | T | C | 0.029 | 0.911 | 0.102 | 0.019 | 0.065 | 0.139 | 1.04E-07 | intergenic variant | 36 | | MODIFIER |
| 5 | 145799833 | rs141025130 | A | T | A | 0.032 | 0.911 | 0.087 | 0.018 | 0.051 | 0.123 | 1.98E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 145800527 | rs71594532 | T | C | T | 0.029 | 0.908 | 0.102 | 0.019 | 0.065 | 0.139 | 9.73E-08 | intergenic variant | 36 | | MODIFIER |
| 5 | 145802546 | rs75584856 | C | A | C | 0.032 | 0.911 | 0.087 | 0.018 | 0.051 | 0.123 | 1.98E-06 | intergenic variant | 36 | | MODIFIER |
| 5 | 148667489 | rs149048112 | G | A | G | 0.012 | 0.816 | 0.143 | 0.032 | 0.080 | 0.206 | 8.57E-06 | intron variant | 23 | | MODIFIER |
| 5 | 149455731 | rs199692631 | D | I | D | 0.012 | 0.774 | 0.162 | 0.032 | 0.099 | 0.224 | 4.67E-07 | intron variant | 23 | | MODIFIER |
| 5 | 149461227 | rs149360747 | A | C | A | 0.012 | 0.898 | 0.134 | 0.030 | 0.076 | 0.192 | 7.15E-06 | intron variant | 23 | | MODIFIER |
| 5 | 154400477 | rs17570417 | T | G | T | 0.011 | 0.893 | 0.137 | 0.031 | 0.077 | 0.198 | 8.79E-06 | downstream gene variant | 27 | | MODIFIER |
| 5 | 180344389 | rs113893737 | C | T | C | 0.289 | 0.835 | -0.034 | 0.007 | -0.048 | -0.019 | 6.99E-06 | intron variant | 23 | | MODIFIER |
| 6 | 5391537 | rs72815688 | T | C | T | 0.015 | 0.985 | 0.113 | 0.025 | 0.064 | 0.163 | 8.84E-06 | intron variant | 23 | | MODIFIER |
| 6 | 5393015 | rs568431658 | D | I | D | 0.015 | 0.985 | 0.113 | 0.025 | 0.064 | 0.163 | 8.84E-06 | intron variant | 23 | | MODIFIER |
| 6 | 5394517 | rs56207004 | G | A | G | 0.015 | 0.982 | 0.116 | 0.026 | 0.065 | 0.167 | 8.25E-06 | intron variant | 23 | | MODIFIER |
| 6 | 5396091 | rs56142140 | A | G | A | 0.015 | 0.972 | 0.115 | 0.026 | 0.065 | 0.166 | 9.17E-06 | intron variant | 23 | | MODIFIER |
| 6 | 89295743 | rs150250345 | A | G | A | 0.015 | 0.951 | 0.151 | 0.026 | 0.100 | 0.202 | 9.16E-09 | intergenic variant | 36 | | MODIFIER |
| 6 | 89318627 | rs76794656 | A | G | A | 0.026 | 0.968 | 0.097 | 0.020 | 0.059 | 0.136 | 8.07E-07 | downstream gene variant | 27 | | MODIFIER |
| 6 | 89438628 | rs62429110 | T | C | T | 0.028 | 1.011 | 0.094 | 0.018 | 0.058 | 0.130 | 3.33E-07 | intron variant | 23 | | MODIFIER |
| 6 | 89566156 | rs150527950 | D | I | D | 0.024 | 0.897 | 0.109 | 0.021 | 0.068 | 0.151 | 3.16E-07 | intron variant | 23 | | MODIFIER |
| 6 | 96323283 | rs143740547 | A | C | A | 0.011 | 0.995 | 0.136 | 0.030 | 0.077 | 0.195 | 6.75E-06 | intergenic variant | 36 | | MODIFIER |
| 6 | 96330719 | rs117020483 | T | C | T | 0.010 | 0.954 | 0.156 | 0.032 | 0.093 | 0.219 | 1.43E-06 | intergenic variant | 36 | | MODIFIER |
| 6 | 96340424 | rs117471132 | G | A | G | 0.010 | 0.957 | 0.156 | 0.032 | 0.093 | 0.220 | 1.37E-06 | intergenic variant | 36 | | MODIFIER |
| 6 | 96356615 | rs116997611 | G | T | G | 0.009 | 0.990 | 0.165 | 0.032 | 0.103 | 0.227 | 2.38E-07 | intergenic variant | 36 | | MODIFIER |
| 6 | 96357883 | rs117134018 | A | T | A | 0.009 | 0.980 | 0.165 | 0.032 | 0.103 | 0.228 | 2.85E-07 | intergenic variant | 36 | | MODIFIER |
| 6 | 96359967 | 6:96359967\_A\_G | G | A | G | 0.010 | 0.968 | 0.162 | 0.031 | 0.100 | 0.223 | 3.13E-07 |  |  | |  |
| 6 | 109587963 | rs28590584 | G | A | G | 0.028 | 1.065 | 0.081 | 0.018 | 0.045 | 0.116 | 8.64E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109600710 | rs57715392 | T | C | T | 0.028 | 1.058 | 0.080 | 0.018 | 0.045 | 0.116 | 8.90E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109603881 | rs9487031 | T | C | T | 0.028 | 1.071 | 0.082 | 0.018 | 0.046 | 0.117 | 6.54E-06 | non coding transcript exon variant | 22 | | MODIFIER |
| 6 | 109622008 | rs78277738 | T | C | T | 0.025 | 1.058 | 0.085 | 0.019 | 0.048 | 0.123 | 9.64E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109623946 | rs74514583 | T | C | T | 0.025 | 1.059 | 0.085 | 0.019 | 0.047 | 0.122 | 1.00E-05 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109625017 | rs116455351 | A | G | A | 0.025 | 1.059 | 0.085 | 0.019 | 0.047 | 0.122 | 1.00E-05 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109625643 | rs143896733 | I | D | I | 0.025 | 1.059 | 0.085 | 0.019 | 0.047 | 0.122 | 1.00E-05 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109625847 | rs76863671 | C | T | C | 0.025 | 1.058 | 0.085 | 0.019 | 0.048 | 0.123 | 9.64E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109625994 | rs77096693 | C | T | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109626028 | rs373667111 | C | G | C | 0.025 | 1.064 | 0.085 | 0.019 | 0.048 | 0.123 | 8.70E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109626833 | rs77290030 | C | T | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109627632 | rs78191399 | T | C | T | 0.025 | 1.063 | 0.085 | 0.019 | 0.048 | 0.122 | 8.76E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109628720 | rs75394325 | T | C | T | 0.025 | 1.064 | 0.085 | 0.019 | 0.048 | 0.122 | 9.07E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109629019 | 6:109629019\_G\_C | C | G | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 |  |  | |  |
| 6 | 109630536 | rs78986376 | C | T | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109631935 | rs77156705 | G | A | G | 0.025 | 1.064 | 0.085 | 0.019 | 0.048 | 0.122 | 9.07E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109636490 | rs76906380 | A | G | A | 0.027 | 1.058 | 0.083 | 0.019 | 0.047 | 0.120 | 7.28E-06 | non coding transcript exon variant | 22 | | MODIFIER |
| 6 | 109636543 | rs150922062 | D | I | D | 0.027 | 1.026 | 0.083 | 0.019 | 0.047 | 0.120 | 9.16E-06 | non coding transcript exon variant | 22 | | MODIFIER |
| 6 | 109636621 | rs76809124 | G | A | G | 0.027 | 1.039 | 0.085 | 0.019 | 0.048 | 0.121 | 6.13E-06 | splice region variant, non coding transcript exon variant | 13 | | LOW |
| 6 | 109636754 | rs79921185 | A | T | A | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109636839 | rs79212539 | G | A | G | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109636882 | rs146728087 | D | I | D | 0.026 | 1.058 | 0.085 | 0.019 | 0.048 | 0.121 | 6.99E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109636916 | rs78553346 | A | C | A | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | regulatory region variant | 34 | | MODIFIER |
| 6 | 109636952 | rs79791278 | C | T | C | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637158 | rs79960228 | G | C | G | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637287 | rs77655476 | G | A | G | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637444 | rs139254193 | T | C | T | 0.027 | 1.052 | 0.084 | 0.019 | 0.048 | 0.120 | 7.23E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637475 | rs149578739 | G | A | G | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637657 | rs143778307 | A | G | A | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637747 | rs75219290 | A | G | A | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637838 | rs79642415 | A | G | A | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109637864 | rs74693235 | G | A | G | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109638417 | rs77946366 | T | C | T | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109638665 | rs57544850 | G | A | G | 0.027 | 1.051 | 0.084 | 0.019 | 0.048 | 0.121 | 7.22E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109638684 | 6:109638684\_G\_A | A | G | A | 0.027 | 1.051 | 0.084 | 0.019 | 0.048 | 0.121 | 7.22E-06 |  |  | |  |
| 6 | 109638885 | rs76422683 | T | C | T | 0.027 | 1.039 | 0.084 | 0.019 | 0.048 | 0.121 | 7.02E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109639641 | rs75638499 | A | G | A | 0.026 | 1.057 | 0.084 | 0.019 | 0.048 | 0.121 | 7.10E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 109640900 | rs75278348 | A | G | A | 0.027 | 0.990 | 0.087 | 0.019 | 0.050 | 0.125 | 5.48E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 6 | 115823340 | 6:115823340\_C\_T | T | C | T | 0.029 | 0.855 | 0.089 | 0.020 | 0.050 | 0.127 | 7.96E-06 |  |  | |  |
| 7 | 7195558 | rs12672133 | C | T | C | 0.038 | 0.996 | 0.092 | 0.016 | 0.061 | 0.124 | 9.76E-09 | intergenic variant | 36 | | MODIFIER |
| 7 | 7213245 | rs73043785 | T | C | T | 0.039 | 1.034 | 0.088 | 0.016 | 0.058 | 0.119 | 2.27E-08 | intergenic variant | 36 | | MODIFIER |
| 7 | 7214799 | rs73043789 | A | G | A | 0.039 | 1.036 | 0.088 | 0.016 | 0.058 | 0.119 | 2.25E-08 | regulatory region variant | 34 | | MODIFIER |
| 7 | 7216175 | rs12667853 | A | G | A | 0.039 | 1.029 | 0.089 | 0.016 | 0.058 | 0.120 | 1.50E-08 | regulatory region variant | 34 | | MODIFIER |
| 7 | 7217867 | rs55637396 | A | G | A | 0.038 | 1.024 | 0.092 | 0.016 | 0.062 | 0.123 | 6.67E-09 | upstream gene variant | 26 | | MODIFIER |
| 7 | 7272485 | rs73045769 | T | C | T | 0.036 | 1.079 | 0.093 | 0.016 | 0.062 | 0.124 | 7.82E-09 | intron variant | 23 | | MODIFIER |
| 7 | 7273424 | rs73045773 | G | A | G | 0.037 | 1.068 | 0.091 | 0.016 | 0.060 | 0.121 | 1.02E-08 | intron variant | 23 | | MODIFIER |
| 7 | 7282894 | rs73049974 | A | G | A | 0.037 | 1.058 | 0.091 | 0.016 | 0.060 | 0.121 | 1.13E-08 | intron variant | 23 | | MODIFIER |
| 7 | 7285578 | rs114287739 | T | A | T | 0.036 | 1.076 | 0.092 | 0.016 | 0.061 | 0.123 | 7.60E-09 | 3 prime UTR variant | 21 | | MODIFIER |
| 7 | 7285607 | rs73049983 | A | G | A | 0.036 | 1.069 | 0.092 | 0.016 | 0.061 | 0.124 | 9.64E-09 | 3 prime UTR variant | 21 | | MODIFIER |
| 7 | 7286193 | rs5010182 | G | A | G | 0.036 | 1.076 | 0.092 | 0.016 | 0.061 | 0.123 | 7.60E-09 | 3 prime UTR variant | 21 | | MODIFIER |
| 7 | 7292688 | rs73049994 | T | C | T | 0.036 | 1.060 | 0.092 | 0.016 | 0.061 | 0.123 | 1.00E-08 | upstream gene variant | 26 | | MODIFIER |
| 7 | 7296136 | rs73049999 | C | T | C | 0.036 | 1.059 | 0.093 | 0.016 | 0.061 | 0.124 | 8.81E-09 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7298191 | rs75122088 | T | C | T | 0.036 | 1.083 | 0.081 | 0.016 | 0.051 | 0.112 | 3.07E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7299469 | rs28617577 | T | C | T | 0.042 | 1.028 | 0.075 | 0.015 | 0.045 | 0.105 | 9.34E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7299480 | rs7803236 | A | G | A | 0.042 | 1.026 | 0.075 | 0.015 | 0.045 | 0.105 | 8.83E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7299654 | rs200521981 | I | D | I | 0.037 | 1.022 | 0.088 | 0.016 | 0.056 | 0.120 | 7.03E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7300508 | rs112344846 | C | G | C | 0.035 | 1.042 | 0.093 | 0.016 | 0.060 | 0.125 | 2.37E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7300574 | rs117303191 | A | G | A | 0.035 | 1.077 | 0.087 | 0.016 | 0.056 | 0.118 | 7.60E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7301098 | rs73051710 | C | T | C | 0.034 | 1.050 | 0.092 | 0.016 | 0.060 | 0.124 | 2.73E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7304999 | rs58465226 | D | I | D | 0.038 | 0.977 | 0.089 | 0.016 | 0.057 | 0.121 | 5.35E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7305003 | rs57240533 | A | T | A | 0.038 | 0.977 | 0.089 | 0.016 | 0.057 | 0.121 | 5.35E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7305712 | rs58285948 | C | T | C | 0.037 | 1.011 | 0.083 | 0.016 | 0.051 | 0.115 | 4.42E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7305787 | rs57402603 | C | T | C | 0.037 | 1.007 | 0.083 | 0.016 | 0.051 | 0.115 | 4.05E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7309344 | rs12673653 | G | A | G | 0.037 | 1.026 | 0.085 | 0.016 | 0.054 | 0.117 | 1.51E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7312747 | rs58968692 | C | T | C | 0.037 | 1.026 | 0.090 | 0.016 | 0.059 | 0.122 | 2.98E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7313294 | rs6973768 | G | T | G | 0.036 | 1.000 | 0.093 | 0.017 | 0.061 | 0.126 | 2.42E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7313485 | rs6953213 | A | G | A | 0.038 | 0.959 | 0.083 | 0.016 | 0.051 | 0.116 | 5.34E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7316262 | rs6974699 | C | G | C | 0.030 | 0.980 | 0.104 | 0.018 | 0.068 | 0.139 | 1.26E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 7317524 | rs2270081 | A | G | A | 0.030 | 0.981 | 0.104 | 0.018 | 0.069 | 0.139 | 1.10E-08 | non coding transcript exon variant | 22 | | MODIFIER |
| 7 | 7319013 | rs147389390 | D | I | D | 0.031 | 0.917 | 0.113 | 0.018 | 0.077 | 0.149 | 1.49E-09 | downstream gene variant | 27 | | MODIFIER |
| 7 | 7321075 | rs60008535 | G | A | G | 0.032 | 0.967 | 0.100 | 0.018 | 0.065 | 0.135 | 2.50E-08 | downstream gene variant | 27 | | MODIFIER |
| 7 | 7321130 | rs73051783 | C | G | C | 0.030 | 0.960 | 0.106 | 0.018 | 0.070 | 0.142 | 7.93E-09 | downstream gene variant | 27 | | MODIFIER |
| 7 | 7328241 | rs56405297 | G | A | G | 0.030 | 0.950 | 0.111 | 0.018 | 0.075 | 0.147 | 2.29E-09 | intergenic variant | 36 | | MODIFIER |
| 7 | 7328318 | rs138278387 | D | I | D | 0.029 | 0.932 | 0.112 | 0.019 | 0.075 | 0.149 | 3.89E-09 | intergenic variant | 36 | | MODIFIER |
| 7 | 7329539 | rs7779267 | T | C | T | 0.030 | 0.943 | 0.112 | 0.018 | 0.076 | 0.149 | 1.84E-09 | intergenic variant | 36 | | MODIFIER |
| 7 | 7332244 | rs73053804 | C | G | C | 0.030 | 0.935 | 0.111 | 0.019 | 0.075 | 0.147 | 3.07E-09 | regulatory region variant | 34 | | MODIFIER |
| 7 | 7332460 | rs73053807 | A | C | A | 0.026 | 0.932 | 0.115 | 0.020 | 0.076 | 0.154 | 9.80E-09 | regulatory region variant | 34 | | MODIFIER |
| 7 | 20898650 | rs113848802 | T | G | T | 0.020 | 0.834 | 0.108 | 0.024 | 0.061 | 0.155 | 7.10E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 7 | 22111219 | rs57914885 | C | T | C | 0.013 | 0.554 | 0.176 | 0.037 | 0.104 | 0.247 | 1.92E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 31611054 | rs147861251 | T | C | T | 0.014 | 0.914 | 0.130 | 0.027 | 0.076 | 0.183 | 2.49E-06 | intron variant | 23 | | MODIFIER |
| 7 | 32020525 | rs554724744 | T | C | T | 0.010 | 0.979 | 0.161 | 0.031 | 0.100 | 0.222 | 2.89E-07 | intron variant | 23 | | MODIFIER |
| 7 | 52003971 | rs56059073 | D | I | I | 0.013 | 0.682 | 0.150 | 0.033 | 0.085 | 0.215 | 7.46E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 52004711 | rs56182929 | D | I | I | 0.013 | 0.770 | 0.146 | 0.031 | 0.085 | 0.208 | 3.57E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 57405340 | 7:57405340\_T\_A | A | T | A | 0.019 | 0.931 | 0.103 | 0.023 | 0.058 | 0.149 | 9.48E-06 |  |  | |  |
| 7 | 57405804 | 7:57405804\_G\_A | A | G | A | 0.020 | 0.925 | 0.103 | 0.023 | 0.058 | 0.148 | 9.31E-06 |  |  | |  |
| 7 | 57406329 | 7:57406329\_A\_G | G | A | G | 0.020 | 0.931 | 0.102 | 0.023 | 0.057 | 0.146 | 8.60E-06 |  |  | |  |
| 7 | 57406704 | 7:57406704\_T\_C | C | T | C | 0.020 | 0.931 | 0.102 | 0.023 | 0.057 | 0.146 | 8.60E-06 |  |  | |  |
| 7 | 57406886 | 7:57406886\_C\_T | T | C | T | 0.020 | 0.931 | 0.102 | 0.023 | 0.057 | 0.146 | 8.60E-06 |  |  | |  |
| 7 | 57412385 | 7:57412385\_G\_C | C | G | C | 0.023 | 1.007 | 0.093 | 0.020 | 0.053 | 0.133 | 5.07E-06 |  |  | |  |
| 7 | 57413299 | 7:57413299\_T\_C | C | T | C | 0.024 | 1.023 | 0.099 | 0.020 | 0.061 | 0.138 | 5.76E-07 |  |  | |  |
| 7 | 57413991 | 7:57413991\_T\_C | C | T | C | 0.024 | 1.023 | 0.099 | 0.020 | 0.061 | 0.138 | 5.76E-07 |  |  | |  |
| 7 | 57416109 | 7:57416109\_T\_C | C | T | C | 0.024 | 1.022 | 0.100 | 0.020 | 0.061 | 0.138 | 5.56E-07 |  |  | |  |
| 7 | 57416833 | 7:57416833\_G\_A | A | G | A | 0.024 | 1.012 | 0.102 | 0.020 | 0.062 | 0.141 | 4.77E-07 |  |  | |  |
| 7 | 57417498 | 7:57417498\_C\_T | T | C | T | 0.024 | 1.012 | 0.102 | 0.020 | 0.062 | 0.141 | 4.77E-07 |  |  | |  |
| 7 | 57418093 | 7:57418093\_G\_A | A | G | A | 0.024 | 1.011 | 0.102 | 0.020 | 0.062 | 0.141 | 4.84E-07 |  |  | |  |
| 7 | 57419651 | 7:57419651\_C\_T | T | C | T | 0.025 | 0.987 | 0.091 | 0.020 | 0.053 | 0.130 | 4.08E-06 |  |  | |  |
| 7 | 57420031 | 7:57420031\_G\_A | A | G | A | 0.024 | 1.011 | 0.102 | 0.020 | 0.062 | 0.141 | 4.84E-07 |  |  | |  |
| 7 | 57422898 | 7:57422898\_A\_T | T | A | T | 0.023 | 1.007 | 0.103 | 0.020 | 0.063 | 0.142 | 3.90E-07 |  |  | |  |
| 7 | 57427008 | 7:57427008\_C\_G | G | C | G | 0.023 | 0.991 | 0.104 | 0.020 | 0.064 | 0.143 | 3.97E-07 |  |  | |  |
| 7 | 57427491 | 7:57427491\_G\_T | T | G | T | 0.023 | 0.991 | 0.104 | 0.020 | 0.064 | 0.143 | 3.97E-07 |  |  | |  |
| 7 | 57429011 | 7:57429011\_G\_A | A | G | A | 0.023 | 0.990 | 0.104 | 0.020 | 0.064 | 0.143 | 3.99E-07 |  |  | |  |
| 7 | 57429860 | 7:57429860\_A\_C | C | A | C | 0.024 | 0.966 | 0.105 | 0.021 | 0.065 | 0.145 | 3.87E-07 |  |  | |  |
| 7 | 57521560 | rs117553144 | C | T | C | 0.016 | 0.962 | 0.148 | 0.025 | 0.099 | 0.196 | 2.82E-09 | intron variant | 23 | | MODIFIER |
| 7 | 57573899 | 7:57573899\_C\_G | G | C | G | 0.016 | 0.959 | 0.150 | 0.024 | 0.103 | 0.198 | 1.15E-09 |  |  | |  |
| 7 | 57587402 | 7:57587402\_T\_C | C | T | C | 0.017 | 0.982 | 0.148 | 0.023 | 0.102 | 0.194 | 4.11E-10 |  |  | |  |
| 7 | 57618204 | rs112427936 | A | G | A | 0.015 | 0.914 | 0.159 | 0.026 | 0.109 | 0.210 | 1.21E-09 | intergenic variant | 36 | | MODIFIER |
| 7 | 57659662 | rs528332416 | T | C | T | 0.014 | 0.894 | 0.162 | 0.028 | 0.108 | 0.217 | 5.93E-09 | intergenic variant | 36 | | MODIFIER |
| 7 | 57744969 | rs116966023 | T | C | T | 0.013 | 0.904 | 0.148 | 0.028 | 0.093 | 0.203 | 1.88E-07 | intergenic variant | 36 | | MODIFIER |
| 7 | 57883125 | rs78388266 | G | A | G | 0.012 | 0.962 | 0.137 | 0.029 | 0.080 | 0.193 | 2.45E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 57884852 | 7:57884852\_A\_G | G | A | G | 0.013 | 0.986 | 0.129 | 0.027 | 0.076 | 0.181 | 1.75E-06 |  |  | |  |
| 7 | 57886097 | rs547171602 | T | A | T | 0.013 | 0.986 | 0.129 | 0.027 | 0.076 | 0.181 | 1.75E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 62033679 | rs117851918 | A | G | A | 0.011 | 0.773 | 0.148 | 0.033 | 0.083 | 0.212 | 8.49E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 62440909 | rs185713072 | A | G | A | 0.010 | 0.908 | 0.159 | 0.032 | 0.095 | 0.222 | 1.03E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 62459110 | rs182548138 | A | G | A | 0.011 | 0.904 | 0.154 | 0.031 | 0.093 | 0.216 | 1.11E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 62493807 | rs148446805 | G | A | G | 0.015 | 0.808 | 0.148 | 0.028 | 0.094 | 0.202 | 9.55E-08 | intergenic variant | 36 | | MODIFIER |
| 7 | 62600865 | rs146191764 | G | A | G | 0.010 | 0.904 | 0.146 | 0.032 | 0.083 | 0.209 | 5.80E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 85164769 | rs66841046 | A | C | A | 0.437 | 0.630 | 0.038 | 0.008 | 0.023 | 0.053 | 1.20E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 128482834 | rs71581921 | T | C | T | 0.014 | 0.792 | 0.158 | 0.029 | 0.102 | 0.215 | 5.60E-08 | intron variant | 23 | | MODIFIER |
| 7 | 136253593 | rs187398437 | A | T | A | 0.012 | 0.770 | 0.166 | 0.033 | 0.102 | 0.230 | 4.17E-07 | intergenic variant | 36 | | MODIFIER |
| 7 | 136866494 | rs147782262 | A | G | A | 0.042 | 0.940 | 0.070 | 0.016 | 0.039 | 0.101 | 9.94E-06 | regulatory region variant | 34 | | MODIFIER |
| 7 | 136892170 | rs12154638 | T | C | T | 0.044 | 1.008 | 0.067 | 0.015 | 0.037 | 0.096 | 9.12E-06 | intergenic variant | 36 | | MODIFIER |
| 7 | 142506482 | rs2018260 | G | T | G | 0.016 | 0.984 | 0.115 | 0.025 | 0.066 | 0.163 | 4.18E-06 | TF binding site variant | 30 | | MODIFIER |
| 8 | 41189261 | rs138170590 | A | G | A | 0.010 | 0.865 | 0.169 | 0.033 | 0.105 | 0.233 | 2.84E-07 | regulatory region variant | 34 | | MODIFIER |
| 8 | 51110797 | rs117254896 | G | A | G | 0.014 | 0.986 | 0.123 | 0.026 | 0.072 | 0.175 | 3.31E-06 | intron variant | 23 | | MODIFIER |
| 8 | 64343023 | rs545960082 | G | A | G | 0.240 | 0.659 | 0.048 | 0.009 | 0.030 | 0.065 | 8.37E-08 |  |  | |  |
| 8 | 74905075 | rs1481858 | A | G | A | 0.011 | 0.622 | 0.172 | 0.038 | 0.098 | 0.247 | 6.77E-06 | intron variant | 23 | | MODIFIER |
| 9 | 6706240 | rs75740146 | G | T | G | 0.016 | 0.901 | 0.116 | 0.026 | 0.065 | 0.167 | 8.51E-06 | intergenic variant | 36 | | MODIFIER |
| 9 | 24121894 | rs113838706 | C | A | C | 0.020 | 0.830 | 0.110 | 0.024 | 0.063 | 0.157 | 4.72E-06 | intergenic variant | 36 | | MODIFIER |
| 9 | 37645096 | rs200046053 | I | D | I | 0.103 | 0.940 | 0.048 | 0.010 | 0.028 | 0.068 | 4.41E-06 | intron variant | 23 | | MODIFIER |
| 9 | 115527016 | rs78025083 | C | T | C | 0.018 | 1.043 | 0.100 | 0.022 | 0.056 | 0.144 | 8.89E-06 | intron variant | 23 | | MODIFIER |
| 9 | 115568509 | rs118065136 | A | G | A | 0.018 | 1.009 | 0.103 | 0.023 | 0.058 | 0.148 | 9.21E-06 | intron variant | 23 | | MODIFIER |
| 9 | 115598800 | rs117078509 | A | G | A | 0.018 | 0.977 | 0.106 | 0.024 | 0.060 | 0.153 | 7.05E-06 | intron variant | 23 | | MODIFIER |
| 9 | 133499884 | rs183889908 | G | A | G | 0.010 | 0.990 | 0.147 | 0.031 | 0.086 | 0.207 | 2.35E-06 | intron variant | 23 | | MODIFIER |
| 10 | 1800041 | rs117791867 | G | C | G | 0.011 | 0.922 | 0.152 | 0.031 | 0.091 | 0.213 | 1.13E-06 | intergenic variant | 36 | | MODIFIER |
| 10 | 1805374 | rs116237299 | C | T | C | 0.011 | 0.894 | 0.146 | 0.030 | 0.086 | 0.206 | 2.05E-06 | intergenic variant | 36 | | MODIFIER |
| 10 | 24070171 | rs143713405 | T | G | T | 0.012 | 0.772 | 0.178 | 0.033 | 0.114 | 0.242 | 7.51E-08 | intron variant | 23 | | MODIFIER |
| 10 | 134968323 | rs111302573 | T | C | T | 0.021 | 0.978 | 0.096 | 0.022 | 0.054 | 0.139 | 9.28E-06 | intergenic variant | 36 | | MODIFIER |
| 11 | 18195609 | rs146132319 | T | C | T | 0.014 | 1.067 | 0.125 | 0.025 | 0.075 | 0.174 | 9.47E-07 | missense variant | 11 | | MODERATE |
| 11 | 18202180 | rs191961659 | T | G | T | 0.014 | 1.062 | 0.131 | 0.026 | 0.080 | 0.181 | 4.28E-07 | intergenic variant | 36 | | MODIFIER |
| 11 | 36840594 | rs188041487 | C | A | C | 0.011 | 1.020 | 0.130 | 0.029 | 0.074 | 0.186 | 6.60E-06 | intergenic variant | 36 | | MODIFIER |
| 11 | 38096613 | rs149272992 | A | C | A | 0.012 | 0.784 | 0.169 | 0.032 | 0.107 | 0.232 | 1.63E-07 | intergenic variant | 36 | | MODIFIER |
| 11 | 70682557 | 11:70682557\_T\_C | C | T | T | 0.376 | 0.949 | 0.030 | 0.007 | 0.017 | 0.043 | 5.95E-06 |  |  | |  |
| 11 | 95349908 | rs77008050 | A | G | A | 0.027 | 0.910 | 0.091 | 0.020 | 0.052 | 0.130 | 5.96E-06 | intergenic variant | 36 | | MODIFIER |
| 11 | 102488443 | rs17099108 | G | A | G | 0.011 | 0.932 | 0.153 | 0.030 | 0.094 | 0.213 | 5.55E-07 | intron variant | 23 | | MODIFIER |
| 12 | 47924811 | rs75633495 | T | C | T | 0.013 | 0.777 | 0.143 | 0.030 | 0.083 | 0.202 | 2.84E-06 | intergenic variant | 36 | | MODIFIER |
| 12 | 47946809 | rs149188661 | T | C | T | 0.012 | 0.829 | 0.162 | 0.031 | 0.101 | 0.222 | 2.17E-07 | intergenic variant | 36 | | MODIFIER |
| 12 | 73162092 | rs74333287 | T | C | T | 0.011 | 0.903 | 0.139 | 0.031 | 0.078 | 0.199 | 8.74E-06 | intergenic variant | 36 | | MODIFIER |
| 13 | 60431525 | rs78750293 | A | G | A | 0.014 | 1.067 | 0.116 | 0.025 | 0.066 | 0.166 | 5.17E-06 | intron variant | 23 | | MODIFIER |
| 13 | 60458404 | rs142445000 | T | G | T | 0.014 | 1.015 | 0.128 | 0.026 | 0.076 | 0.179 | 1.45E-06 | intron variant | 23 | | MODIFIER |
| 13 | 60479348 | rs192272125 | A | G | A | 0.013 | 0.970 | 0.141 | 0.027 | 0.088 | 0.195 | 3.30E-07 | intron variant | 23 | | MODIFIER |
| 13 | 60683393 | rs116916397 | C | G | C | 0.013 | 0.859 | 0.141 | 0.029 | 0.084 | 0.198 | 1.49E-06 | intron variant | 23 | | MODIFIER |
| 13 | 60707842 | rs75265795 | C | T | C | 0.013 | 0.897 | 0.135 | 0.028 | 0.080 | 0.190 | 1.62E-06 | intron variant | 23 | | MODIFIER |
| 13 | 60722442 | rs74456884 | T | C | T | 0.014 | 0.892 | 0.135 | 0.028 | 0.081 | 0.190 | 1.60E-06 | intron variant | 23 | | MODIFIER |
| 13 | 74866589 | rs376739799 | I | D | I | 0.055 | 0.857 | 0.067 | 0.014 | 0.038 | 0.095 | 4.92E-06 | intergenic variant | 36 | | MODIFIER |
| 13 | 106533249 | rs75846503 | T | C | T | 0.019 | 1.041 | 0.099 | 0.022 | 0.056 | 0.143 | 8.29E-06 | intergenic variant | 36 | | MODIFIER |
| 13 | 110772717 | rs78760186 | G | A | G | 0.022 | 0.978 | 0.110 | 0.021 | 0.068 | 0.151 | 2.68E-07 | upstream gene variant | 26 | | MODIFIER |
| 14 | 24998718 | rs142065939 | A | G | A | 0.016 | 0.715 | 0.152 | 0.029 | 0.096 | 0.208 | 1.59E-07 | intergenic variant | 36 | | MODIFIER |
| 14 | 24998759 | rs180908849 | A | G | A | 0.015 | 0.713 | 0.161 | 0.030 | 0.103 | 0.219 | 6.69E-08 | intergenic variant | 36 | | MODIFIER |
| 14 | 25032368 | rs148483440 | C | T | C | 0.015 | 0.854 | 0.145 | 0.027 | 0.091 | 0.198 | 1.81E-07 | intergenic variant | 36 | | MODIFIER |
| 14 | 25068098 | rs150795143 | A | G | A | 0.015 | 0.901 | 0.133 | 0.026 | 0.082 | 0.185 | 4.95E-07 | intergenic variant | 36 | | MODIFIER |
| 14 | 25078451 | rs144558932 | T | C | T | 0.015 | 0.915 | 0.132 | 0.026 | 0.080 | 0.183 | 6.14E-07 | intron variant | 23 | | MODIFIER |
| 14 | 83386038 | rs17117694 | T | C | T | 0.013 | 0.896 | 0.134 | 0.029 | 0.077 | 0.191 | 5.00E-06 | intergenic variant | 36 | | MODIFIER |
| 15 | 20559108 | rs201116352 | D | I | D | 0.013 | 0.561 | 0.164 | 0.037 | 0.093 | 0.236 | 7.87E-06 | regulatory region variant | 34 | | MODIFIER |
| 15 | 41533136 | rs144284546 | T | C | T | 0.011 | 0.717 | 0.179 | 0.034 | 0.111 | 0.246 | 2.62E-07 | intron variant | 23 | | MODIFIER |
| 15 | 58986249 | rs76308871 | G | A | G | 0.012 | 0.899 | 0.144 | 0.029 | 0.087 | 0.201 | 8.52E-07 | intron variant | 23 | | MODIFIER |
| 15 | 59000404 | rs138707472 | C | T | C | 0.013 | 0.893 | 0.142 | 0.029 | 0.085 | 0.199 | 1.16E-06 | intron variant | 23 | | MODIFIER |
| 15 | 59016170 | rs147294843 | A | C | A | 0.013 | 0.933 | 0.139 | 0.028 | 0.084 | 0.195 | 1.11E-06 | intron variant | 23 | | MODIFIER |
| 15 | 59043298 | rs141640215 | T | C | T | 0.013 | 0.931 | 0.137 | 0.028 | 0.082 | 0.193 | 1.37E-06 | upstream gene variant | 26 | | MODIFIER |
| 15 | 59088044 | rs79512009 | G | C | G | 0.013 | 0.915 | 0.133 | 0.028 | 0.078 | 0.189 | 3.08E-06 | intron variant | 23 | | MODIFIER |
| 15 | 59415891 | 15:59415891\_I\_D | D | I | D | 0.040 | 0.867 | 0.078 | 0.017 | 0.045 | 0.111 | 4.01E-06 |  |  | |  |
| 15 | 59454937 | rs73420830 | C | T | C | 0.044 | 0.982 | 0.073 | 0.015 | 0.044 | 0.103 | 1.51E-06 | intron variant | 23 | | MODIFIER |
| 15 | 61376919 | rs112928311 | A | C | A | 0.014 | 0.872 | 0.129 | 0.028 | 0.073 | 0.184 | 6.61E-06 | intron variant | 23 | | MODIFIER |
| 15 | 75940814 | rs117242252 | C | T | C | 0.011 | 0.796 | 0.151 | 0.033 | 0.087 | 0.215 | 4.18E-06 | 5 prime UTR variant | 20 | | MODIFIER |
| 15 | 80519402 | rs764503 | G | A | G | 0.302 | 0.960 | 0.031 | 0.007 | 0.017 | 0.044 | 7.17E-06 | intron variant | 23 | | MODIFIER |
| 16 | 8974775 | rs59454999 | D | I | I | 0.020 | 0.446 | 0.147 | 0.033 | 0.083 | 0.211 | 8.00E-06 | regulatory region variant | 34 | | MODIFIER |
| 16 | 50171697 | rs74651422 | C | G | C | 0.021 | 1.077 | 0.099 | 0.021 | 0.058 | 0.139 | 1.95E-06 | intergenic variant | 36 | | MODIFIER |
| 16 | 50174059 | rs75653698 | G | C | G | 0.021 | 1.073 | 0.098 | 0.021 | 0.058 | 0.139 | 2.04E-06 | intergenic variant | 36 | | MODIFIER |
| 16 | 50176176 | rs113710352 | T | C | T | 0.022 | 1.078 | 0.095 | 0.020 | 0.055 | 0.135 | 3.59E-06 | intergenic variant | 36 | | MODIFIER |
| 16 | 50181270 | rs9746569 | T | A | A | 0.022 | 1.076 | 0.094 | 0.020 | 0.054 | 0.134 | 4.49E-06 | regulatory region variant | 34 | | MODIFIER |
| 16 | 50181389 | rs112283677 | A | G | A | 0.022 | 1.078 | 0.095 | 0.020 | 0.055 | 0.135 | 3.59E-06 | regulatory region variant | 34 | | MODIFIER |
| 16 | 50190380 | rs111805222 | T | C | T | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.136 | 1.73E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50200087 | rs7192461 | G | A | A | 0.022 | 1.101 | 0.096 | 0.020 | 0.057 | 0.135 | 1.87E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50203171 | rs9302747 | A | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50203469 | rs9302748 | C | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50203510 | 16:50203510\_G\_C | C | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 |  |  | |  |
| 16 | 50206206 | rs11076520 | T | C | C | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50206891 | rs112755907 | A | G | A | 0.022 | 1.097 | 0.096 | 0.020 | 0.057 | 0.135 | 1.84E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50207731 | rs8043876 | A | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50217169 | rs111529120 | A | G | A | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.136 | 1.73E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50220836 | rs77594408 | G | T | G | 0.022 | 1.099 | 0.095 | 0.020 | 0.056 | 0.134 | 2.10E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50222326 | rs9925568 | C | T | T | 0.022 | 1.092 | 0.094 | 0.020 | 0.055 | 0.134 | 2.48E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50228844 | rs113177857 | C | T | C | 0.022 | 1.095 | 0.095 | 0.020 | 0.056 | 0.134 | 2.33E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50231036 | rs372992015 | I | D | I | 0.032 | 0.977 | 0.080 | 0.018 | 0.045 | 0.115 | 7.54E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50237262 | rs4581696 | A | G | G | 0.023 | 1.090 | 0.092 | 0.020 | 0.054 | 0.131 | 3.05E-06 | intron variant | 23 | | MODIFIER |
| 16 | 50243856 | rs6500301 | C | G | G | 0.023 | 1.070 | 0.090 | 0.020 | 0.051 | 0.129 | 5.65E-06 | intron variant | 23 | | MODIFIER |
| 18 | 9654474 | rs558769262 | G | T | G | 0.016 | 0.503 | 0.190 | 0.035 | 0.121 | 0.258 | 6.57E-08 | regulatory region variant | 34 | | MODIFIER |
| 18 | 33922847 | rs113423362 | G | A | G | 0.011 | 0.989 | 0.139 | 0.029 | 0.081 | 0.197 | 2.67E-06 | intron variant | 23 | | MODIFIER |
| 18 | 36783593 | rs75160699 | T | G | T | 0.011 | 0.808 | 0.171 | 0.033 | 0.106 | 0.236 | 3.44E-07 | downstream gene variant | 27 | | MODIFIER |
| 18 | 36807001 | rs150906740 | T | G | T | 0.011 | 0.829 | 0.170 | 0.033 | 0.106 | 0.234 | 2.32E-07 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 18 | 36828775 | rs141736521 | A | G | A | 0.011 | 0.836 | 0.179 | 0.032 | 0.116 | 0.241 | 2.95E-08 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 19 | 17543681 | rs12985272 | A | G | A | 0.040 | 0.963 | 0.073 | 0.016 | 0.041 | 0.104 | 6.62E-06 | downstream gene variant | 27 | | MODIFIER |
| 19 | 47119930 | 19:47119930\_C\_G | G | C | G | 0.010 | 0.912 | 0.181 | 0.032 | 0.119 | 0.244 | 1.80E-08 |  |  | |  |
| 19 | 47139877 | rs115034159 | T | C | T | 0.012 | 0.818 | 0.185 | 0.030 | 0.126 | 0.245 | 1.68E-09 | upstream gene variant | 26 | | MODIFIER |
| 19 | 55576645 | 19:55576645\_G\_A | A | G | A | 0.011 | 0.833 | 0.171 | 0.033 | 0.107 | 0.235 | 2.12E-07 |  |  | |  |
| 20 | 32162067 | rs149392217 | C | G | C | 0.018 | 0.819 | 0.152 | 0.025 | 0.103 | 0.201 | 2.02E-09 | missense variant, splice region variant | 11 | | MODERATE |
| 20 | 32178376 | rs139163690 | T | C | T | 0.018 | 0.825 | 0.151 | 0.025 | 0.102 | 0.200 | 2.56E-09 | intron variant | 23 | | MODIFIER |
| 20 | 32275289 | rs3213133 | D | I | D | 0.012 | 0.729 | 0.224 | 0.033 | 0.159 | 0.289 | 2.54E-11 | upstream gene variant | 26 | | MODIFIER |
| 20 | 32458051 | rs150618140 | A | C | A | 0.018 | 0.834 | 0.163 | 0.025 | 0.114 | 0.212 | 1.26E-10 | intergenic variant | 36 | | MODIFIER |
| 21 | 20723562 | rs2000587 | T | A | T | 0.402 | 0.803 | -0.033 | 0.007 | -0.047 | -0.019 | 2.98E-06 | intergenic variant | 36 | | MODIFIER |
| 21 | 24745658 | rs2828092 | T | C | T | 0.068 | 1.016 | 0.055 | 0.012 | 0.032 | 0.079 | 5.87E-06 | intron variant, non coding transcript variant | 23 | | MODIFIER |
| 21 | 24801169 | rs190939201 | G | A | G | 0.081 | 0.914 | 0.058 | 0.012 | 0.035 | 0.081 | 8.68E-07 | intergenic variant | 36 | | MODIFIER |
| 21 | 25074937 | rs2828440 | C | T | C | 0.033 | 1.038 | 0.081 | 0.017 | 0.048 | 0.114 | 1.70E-06 | intergenic variant | 36 | | MODIFIER |
| 21 | 46426355 | rs140901493 | I | D | I | 0.033 | 0.898 | 0.084 | 0.018 | 0.048 | 0.120 | 4.11E-06 | upstream gene variant | 26 | | MODIFIER |
| Shown are results for SNPs displaying suggestive association (p<10-5) with fat cell number. Beta is calculated for allelele A1. Information about functional consequence is from VEP. | | | | | | | | | | | | | | | | |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary table 4. Genetic loci associated with abdominal subcutaneous fat cell numbera** | | | | | | | | | | |  |  |  |
| **CHROM** | **POS** | **ID** | **REF** | **ALT** | **A1** | **A1\_FREQ** | **MACH\_R2** | **BETA** | **SE** | **L95** | **U95** | **P** | **eQTL** |
| 1 | 5271487 | rs148400317 | D | I | D | 0.013 | 0.952 | 0.127 | 0.028 | 0.071 | 0.182 | 8.22E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 1 | 47080679 | rs6671527 | A | G | G | 0.491 | 0.997 | -0.028 | 0.006 | -0.040 | -0.016 | 7.66E-06 | *LURAP* in SAT |
| 1 | 47080983 | rs35494693 | A | G | A | 0.490 | 0.980 | -0.028 | 0.006 | -0.040 | -0.016 | 9.02E-06 | *LURAP* in SAT |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | 19735548 | rs62126633 | A | C | A | 0.428 | 1.009 | 0.028 | 0.006 | 0.015 | 0.040 | 9.49E-06 | no |
| 2 | 19761314 | rs7561420 | C | T | T | 0.428 | 1.009 | 0.028 | 0.006 | 0.016 | 0.040 | 9.25E-06 | no |
| 2 | 19765158 | rs4666492 | G | C | G | 0.424 | 0.988 | 0.028 | 0.006 | 0.016 | 0.040 | 8.72E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | 54712295 | rs116332364 | T | C | T | 0.046 | 1.009 | 0.066 | 0.015 | 0.037 | 0.095 | 7.09E-06 | no |
| 2 | 54781601 | rs149660479 | G | T | G | 0.012 | 0.906 | 0.183 | 0.029 | 0.125 | 0.241 | 8.71E-10 | no |
| 2 | 54867769 | rs139099501 | I | D | I | 0.053 | 1.014 | 0.061 | 0.014 | 0.034 | 0.087 | 8.54E-06 | no |
| 2 | 54884074 | rs3769331 | C | T | C | 0.053 | 1.007 | 0.062 | 0.014 | 0.035 | 0.089 | 7.30E-06 | no |
| 2 | 54892506 | rs7583633 | G | C | G | 0.051 | 0.974 | 0.064 | 0.014 | 0.036 | 0.091 | 6.64E-06 | no |
| 2 | 54895319 | rs139247782 | T | C | T | 0.012 | 0.924 | 0.177 | 0.029 | 0.120 | 0.233 | 1.79E-09 | no |
| 2 | 54898115 | rs3820856 | T | C | T | 0.058 | 1.001 | 0.068 | 0.013 | 0.042 | 0.094 | 3.11E-07 | no |
| 2 | 54901455 | rs201313305 | D | I | D | 0.056 | 1.000 | 0.069 | 0.013 | 0.043 | 0.095 | 2.56E-07 | no |
| 2 | 54904820 | rs6740018 | G | C | G | 0.059 | 0.982 | 0.070 | 0.013 | 0.044 | 0.096 | 1.44E-07 | no |
| 2 | 54909741 | rs143157223 | A | G | A | 0.059 | 0.979 | 0.070 | 0.013 | 0.044 | 0.096 | 1.20E-07 | no |
| 2 | 54911968 | rs75654812 | C | T | C | 0.059 | 0.973 | 0.071 | 0.013 | 0.046 | 0.097 | 8.06E-08 | *PRORSD1P* (not SAT) |
| 2 | 54913089 | rs151009419 | T | C | T | 0.059 | 0.974 | 0.071 | 0.013 | 0.046 | 0.097 | 8.16E-08 | no |
| 2 | 54915221 | rs6705193 | A | G | A | 0.062 | 1.007 | 0.065 | 0.013 | 0.040 | 0.090 | 3.71E-07 | no |
| 2 | 54915327 | rs77334206 | G | A | G | 0.059 | 0.978 | 0.070 | 0.013 | 0.044 | 0.095 | 1.40E-07 | no |
| 2 | 54916241 | rs74518232 | C | G | C | 0.060 | 0.979 | 0.068 | 0.013 | 0.042 | 0.094 | 2.51E-07 | no |
| 2 | 54916618 | rs7561112 | T | C | T | 0.062 | 1.006 | 0.065 | 0.013 | 0.040 | 0.090 | 3.04E-07 | no |
| 2 | 54916629 | rs7587575 | T | A | T | 0.062 | 1.006 | 0.065 | 0.013 | 0.040 | 0.090 | 3.16E-07 | no |
| 2 | 54920691 | rs76988803 | G | C | G | 0.058 | 0.986 | 0.070 | 0.013 | 0.044 | 0.096 | 1.36E-07 | no |
| 2 | 54921349 | rs72911575 | C | G | C | 0.058 | 0.982 | 0.070 | 0.013 | 0.044 | 0.096 | 1.62E-07 | no |
| 2 | 54922692 | rs72911576 | G | A | G | 0.058 | 0.976 | 0.071 | 0.013 | 0.045 | 0.097 | 1.04E-07 | no |
| 2 | 54925159 | rs140858894 | D | I | D | 0.057 | 0.961 | 0.071 | 0.013 | 0.045 | 0.098 | 1.41E-07 | no |
| 2 | 54927885 | rs111404605 | G | A | G | 0.059 | 0.982 | 0.070 | 0.013 | 0.045 | 0.096 | 9.79E-08 | no |
| 2 | 54934844 | rs79747576 | A | C | A | 0.058 | 0.978 | 0.073 | 0.013 | 0.047 | 0.099 | 5.32E-08 | no |
| 2 | 54938035 | rs72389124 | D | I | D | 0.061 | 0.945 | 0.069 | 0.013 | 0.043 | 0.095 | 2.20E-07 | no |
| 2 | 54938475 | rs10169328 | A | G | A | 0.058 | 0.966 | 0.071 | 0.013 | 0.045 | 0.097 | 1.36E-07 | no |
| 2 | 54938926 | rs60307496 | G | T | G | 0.058 | 0.965 | 0.070 | 0.013 | 0.044 | 0.096 | 1.64E-07 | no |
| 2 | 54939411 | rs13404168 | C | T | C | 0.059 | 0.961 | 0.070 | 0.013 | 0.044 | 0.096 | 1.59E-07 | no |
| 2 | 54939481 | rs13404269 | C | T | C | 0.059 | 0.960 | 0.070 | 0.013 | 0.044 | 0.096 | 1.72E-07 | no |
| 2 | 54940174 | 2:54940174\_T\_C | C | T | C | 0.059 | 0.962 | 0.070 | 0.013 | 0.044 | 0.096 | 1.55E-07 | no |
| 2 | 54941710 | rs13398208 | G | C | G | 0.058 | 0.963 | 0.073 | 0.013 | 0.047 | 0.099 | 6.71E-08 | no |
| 2 | 54947126 | rs72913513 | G | A | G | 0.077 | 0.914 | 0.063 | 0.012 | 0.039 | 0.086 | 2.50E-07 | no |
| 2 | 54948606 | rs72913519 | C | G | C | 0.070 | 0.945 | 0.062 | 0.012 | 0.038 | 0.086 | 6.29E-07 | no |
| 2 | 54949937 | rs59370148 | C | T | C | 0.058 | 0.950 | 0.071 | 0.013 | 0.045 | 0.098 | 1.59E-07 | no |
| 2 | 54951482 | rs72913521 | T | C | T | 0.057 | 0.952 | 0.071 | 0.013 | 0.045 | 0.098 | 1.63E-07 | no |
| 2 | 54955792 | rs116681291 | G | A | G | 0.038 | 0.909 | 0.077 | 0.017 | 0.044 | 0.111 | 5.62E-06 | no |
| 2 | 54956566 | rs10170283 | C | A | C | 0.057 | 0.951 | 0.072 | 0.014 | 0.045 | 0.098 | 1.43E-07 | no |
| 2 | 54959408 | rs13399055 | T | A | T | 0.057 | 0.952 | 0.070 | 0.014 | 0.044 | 0.097 | 2.78E-07 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | 56872143 | rs111609475 | A | G | A | 0.035 | 0.901 | 0.080 | 0.018 | 0.045 | 0.114 | 6.77E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | 200753271 | rs148890552 | A | G | A | 0.014 | 1.014 | 0.121 | 0.026 | 0.071 | 0.171 | 3.00E-06 | no |
| 2 | 200767076 | rs114847522 | A | G | A | 0.015 | 0.997 | 0.118 | 0.025 | 0.068 | 0.168 | 4.04E-06 | no |
| 2 | 200769914 | rs116615797 | A | G | A | 0.015 | 1.003 | 0.118 | 0.025 | 0.068 | 0.168 | 3.92E-06 | *SATB2-AS1* in ileum |
| 2 | 200772896 | rs183372316 | T | C | T | 0.015 | 1.003 | 0.118 | 0.025 | 0.068 | 0.168 | 3.92E-06 | *SATB2-AS1* in ileum |
| 2 | 200801380 | rs139474032 | G | A | G | 0.015 | 1.001 | 0.117 | 0.025 | 0.067 | 0.167 | 4.56E-06 | *SATB2-AS1* in ileum |
| 2 | 200871874 | rs78003233 | T | C | T | 0.015 | 1.000 | 0.117 | 0.025 | 0.068 | 0.167 | 3.91E-06 | *SATB2-AS1* in ileum |
| 2 | 200891378 | rs115648719 | C | T | C | 0.015 | 1.004 | 0.115 | 0.025 | 0.066 | 0.165 | 6.13E-06 | *SATB2-AS1* in ileum |
| 2 | 200901576 | rs114419000 | T | C | T | 0.015 | 1.012 | 0.114 | 0.025 | 0.065 | 0.163 | 7.05E-06 | *SATB2-AS1* in ileum |
| 2 | 200962992 | rs149699386 | A | G | A | 0.011 | 1.051 | 0.153 | 0.029 | 0.096 | 0.209 | 1.51E-07 | *SATB2-AS1* in ileum |
| 2 | 200968208 | rs188401823 | C | T | C | 0.015 | 1.019 | 0.118 | 0.025 | 0.070 | 0.167 | 1.76E-06 | *SATB2-AS1* in ileum |
| 2 | 200973255 | rs116835322 | A | G | A | 0.015 | 1.019 | 0.118 | 0.025 | 0.070 | 0.167 | 1.76E-06 | *SATB2-AS1* in ileum |
| 2 | 200983853 | rs142988313 | C | A | C | 0.015 | 1.019 | 0.118 | 0.025 | 0.070 | 0.167 | 1.76E-06 | *SATB2-AS1* in ileum |
| 2 | 200995050 | rs140986905 | C | T | C | 0.011 | 1.047 | 0.152 | 0.029 | 0.096 | 0.208 | 1.33E-07 | *SATB2-AS1* in ileum |
| 2 | 201002023 | rs114489156 | T | C | T | 0.016 | 1.027 | 0.119 | 0.024 | 0.071 | 0.167 | 1.33E-06 | *SATB2-AS1* in ileum |
| 2 | 201006938 | rs74822948 | A | G | A | 0.016 | 1.034 | 0.119 | 0.024 | 0.071 | 0.166 | 1.29E-06 | *SATB2-AS1* in ileum |
| 2 | 201017463 | rs77852935 | A | G | A | 0.016 | 1.035 | 0.119 | 0.024 | 0.071 | 0.167 | 1.15E-06 | *SATB2-AS1* in ileum |
| 2 | 201020141 | rs141481897 | C | T | C | 0.016 | 1.035 | 0.119 | 0.024 | 0.071 | 0.167 | 1.15E-06 | *SATB2-AS1* in ileum |
| 2 | 201075633 | rs115519448 | A | G | A | 0.010 | 1.065 | 0.161 | 0.030 | 0.103 | 0.219 | 8.20E-08 | *SATB2-AS1* in ileum |
| 2 | 201076992 | rs78170266 | A | G | A | 0.010 | 1.068 | 0.160 | 0.030 | 0.102 | 0.218 | 9.58E-08 | *SATB2-AS1* in ileum |
| 2 | 201119367 | rs115947566 | A | G | A | 0.031 | 1.065 | 0.077 | 0.017 | 0.044 | 0.111 | 6.97E-06 | *SPATS2L* in skin |
| 2 | 201354937 | rs565245989 | D | I | D | 0.009 | 0.942 | 0.154 | 0.033 | 0.088 | 0.219 | 4.61E-06 | *KCTD18* in SAT |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | 100398912 | rs116483546 | G | A | G | 0.044 | 0.987 | 0.068 | 0.015 | 0.039 | 0.098 | 6.17E-06 | no |
| 4 | 100522458 | rs550156613 | A | T | A | 0.044 | 0.918 | 0.070 | 0.016 | 0.039 | 0.100 | 9.61E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | 66303886 | rs34698 | G | C | C | 0.124 | 1.005 | 0.042 | 0.009 | 0.024 | 0.060 | 7.19E-06 | *MAST-AS1* SAT, *MAST4* muscle |
| 5 | 66306930 | rs537382 | A | G | G | 0.124 | 1.000 | 0.042 | 0.009 | 0.024 | 0.060 | 6.70E-06 | *MAST-AS1* SAT, *MAST4* muscle |
| 5 | 66313583 | rs166091 | C | T | C | 0.123 | 1.010 | 0.042 | 0.009 | 0.023 | 0.060 | 9.05E-06 | *MAST-AS1* SAT, *MAST4* muscle |
| 5 | 66313721 | rs706703 | A | G | A | 0.122 | 1.011 | 0.042 | 0.009 | 0.024 | 0.060 | 8.26E-06 | *MAST-AS1* SAT, *MAST4* muscle |
| 5 | 66317317 | rs250278 | C | T | C | 0.124 | 1.016 | 0.041 | 0.009 | 0.023 | 0.059 | 9.36E-06 | *MAST-AS1* SAT, *MAST4* muscle |
| 5 | 66322736 | rs2548584 | A | G | A | 0.123 | 1.017 | 0.042 | 0.009 | 0.023 | 0.060 | 8.79E-06 | *MAST-AS1* SAT, *MAST4* muscle |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | 145491112 | rs151111196 | C | T | C | 0.018 | 0.750 | 0.119 | 0.026 | 0.067 | 0.171 | 7.09E-06 | *LARS* SAT |
| 5 | 145761929 | rs33999729 | A | G | A | 0.029 | 0.959 | 0.094 | 0.019 | 0.057 | 0.131 | 7.13E-07 | no |
| 5 | 145781373 | rs34303875 | T | C | T | 0.031 | 0.931 | 0.092 | 0.018 | 0.056 | 0.128 | 6.47E-07 | no |
| 5 | 145782940 | rs13160043 | T | C | T | 0.031 | 0.926 | 0.092 | 0.018 | 0.056 | 0.128 | 6.75E-07 | no |
| 5 | 145783258 | rs13183864 | G | A | G | 0.031 | 0.929 | 0.092 | 0.018 | 0.056 | 0.128 | 7.23E-07 | no |
| 5 | 145783524 | rs149976158 | C | T | C | 0.031 | 0.926 | 0.092 | 0.018 | 0.056 | 0.128 | 6.75E-07 | no |
| 5 | 145784871 | rs34242710 | A | C | A | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.51E-07 | no |
| 5 | 145785181 | rs34926825 | T | G | T | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.60E-07 | no |
| 5 | 145785785 | rs56763657 | A | G | A | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.60E-07 | no |
| 5 | 145786058 | rs34567385 | C | G | C | 0.031 | 0.928 | 0.092 | 0.018 | 0.056 | 0.128 | 6.60E-07 | no |
| 5 | 145786205 | rs34214546 | A | G | A | 0.027 | 0.913 | 0.091 | 0.020 | 0.051 | 0.130 | 6.53E-06 | no |
| 5 | 145787743 | rs34694143 | T | C | T | 0.031 | 0.920 | 0.091 | 0.018 | 0.055 | 0.128 | 8.45E-07 | no |
| 5 | 145788362 | rs13182461 | G | A | G | 0.031 | 0.921 | 0.090 | 0.018 | 0.054 | 0.126 | 1.02E-06 | no |
| 5 | 145788526 | rs60165325 | G | A | G | 0.031 | 0.921 | 0.090 | 0.018 | 0.054 | 0.126 | 1.02E-06 | no |
| 5 | 145789406 | rs13167316 | T | G | T | 0.031 | 0.912 | 0.091 | 0.018 | 0.055 | 0.128 | 8.05E-07 | no |
| 5 | 145789613 | rs35713813 | G | A | G | 0.031 | 0.912 | 0.091 | 0.018 | 0.055 | 0.128 | 8.05E-07 | no |
| 5 | 145792710 | rs13166656 | T | A | T | 0.031 | 0.912 | 0.091 | 0.018 | 0.055 | 0.128 | 8.05E-07 | no |
| 5 | 145794521 | rs13157438 | T | C | T | 0.031 | 0.906 | 0.092 | 0.018 | 0.055 | 0.128 | 8.53E-07 | no |
| 5 | 145794905 | rs566018027 | D | I | D | 0.098 | 0.876 | 0.050 | 0.011 | 0.028 | 0.071 | 7.78E-06 | no |
| 5 | 145794923 | rs35979619 | C | A | C | 0.031 | 0.906 | 0.092 | 0.018 | 0.055 | 0.128 | 8.53E-07 | no |
| 5 | 145798557 | rs13174030 | C | T | C | 0.029 | 0.911 | 0.102 | 0.019 | 0.065 | 0.139 | 1.04E-07 | no |
| 5 | 145799833 | rs141025130 | A | T | A | 0.032 | 0.911 | 0.087 | 0.018 | 0.051 | 0.123 | 1.98E-06 | no |
| 5 | 145800527 | rs71594532 | T | C | T | 0.029 | 0.908 | 0.102 | 0.019 | 0.065 | 0.139 | 9.73E-08 | no |
| 5 | 145802546 | rs75584856 | C | A | C | 0.032 | 0.911 | 0.087 | 0.018 | 0.051 | 0.123 | 1.98E-06 | no |
| 5 | 148667489 | rs149048112 | G | A | G | 0.012 | 0.816 | 0.143 | 0.032 | 0.080 | 0.206 | 8.57E-06 | no |
| 5 | 149455731 | rs199692631 | D | I | D | 0.012 | 0.774 | 0.162 | 0.032 | 0.099 | 0.224 | 4.67E-07 | no |
| 5 | 149461227 | rs149360747 | A | C | A | 0.012 | 0.898 | 0.134 | 0.030 | 0.076 | 0.192 | 7.15E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | 109587963 | rs28590584 | G | A | G | 0.028 | 1.065 | 0.081 | 0.018 | 0.045 | 0.116 | 8.64E-06 | *CCDC162P* in other tissue |
| 6 | 109600710 | rs57715392 | T | C | T | 0.028 | 1.058 | 0.080 | 0.018 | 0.045 | 0.116 | 8.90E-06 | *CCDC162P* in other tissue |
| 6 | 109603881 | rs9487031 | T | C | T | 0.028 | 1.071 | 0.082 | 0.018 | 0.046 | 0.117 | 6.54E-06 | *CCDC162P* in other tissue |
| 6 | 109622008 | rs78277738 | T | C | T | 0.025 | 1.058 | 0.085 | 0.019 | 0.048 | 0.123 | 9.64E-06 | *CCDC162P* in other tissue |
| 6 | 109623946 | rs74514583 | T | C | T | 0.025 | 1.059 | 0.085 | 0.019 | 0.047 | 0.122 | 1.00E-05 | *CCDC162P* SAT |
| 6 | 109625017 | rs116455351 | A | G | A | 0.025 | 1.059 | 0.085 | 0.019 | 0.047 | 0.122 | 1.00E-05 | *CCDC162P* SAT |
| 6 | 109625643 | rs143896733 | I | D | I | 0.025 | 1.059 | 0.085 | 0.019 | 0.047 | 0.122 | 1.00E-05 | *CCDC162P* SAT |
| 6 | 109625847 | rs76863671 | C | T | C | 0.025 | 1.058 | 0.085 | 0.019 | 0.048 | 0.123 | 9.64E-06 | *CCDC162P* SAT |
| 6 | 109625994 | rs77096693 | C | T | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 | *CCDC162P* SAT |
| 6 | 109626028 | rs373667111 | C | G | C | 0.025 | 1.064 | 0.085 | 0.019 | 0.048 | 0.123 | 8.70E-06 | *CCDC162P* in other tissue |
| 6 | 109626833 | rs77290030 | C | T | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 | *CCDC162P* SAT |
| 6 | 109627632 | rs78191399 | T | C | T | 0.025 | 1.063 | 0.085 | 0.019 | 0.048 | 0.122 | 8.76E-06 | *CCDC162P* SAT |
| 6 | 109628720 | rs75394325 | T | C | T | 0.025 | 1.064 | 0.085 | 0.019 | 0.048 | 0.122 | 9.07E-06 | *CCDC162P* SAT |
| 6 | 109629019 | 6:109629019\_G\_C | C | G | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 |  |
| 6 | 109630536 | rs78986376 | C | T | C | 0.025 | 1.065 | 0.085 | 0.019 | 0.048 | 0.122 | 9.41E-06 | *CCDC162P* SAT |
| 6 | 109631935 | rs77156705 | G | A | G | 0.025 | 1.064 | 0.085 | 0.019 | 0.048 | 0.122 | 9.07E-06 | *CCDC162P* in other tissue |
| 6 | 109636490 | rs76906380 | A | G | A | 0.027 | 1.058 | 0.083 | 0.019 | 0.047 | 0.120 | 7.28E-06 | *CCDC162P* in other tissue |
| 6 | 109636543 | rs150922062 | D | I | D | 0.027 | 1.026 | 0.083 | 0.019 | 0.047 | 0.120 | 9.16E-06 | *CCDC162P* SAT |
| 6 | 109636621 | rs76809124 | G | A | G | 0.027 | 1.039 | 0.085 | 0.019 | 0.048 | 0.121 | 6.13E-06 | *CCDC162P* SAT |
| 6 | 109636754 | rs79921185 | A | T | A | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | *CCDC162P* SAT |
| 6 | 109636839 | rs79212539 | G | A | G | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | *CCDC162P* SAT |
| 6 | 109636882 | rs146728087 | D | I | D | 0.026 | 1.058 | 0.085 | 0.019 | 0.048 | 0.121 | 6.99E-06 | *CCDC162P* SAT |
| 6 | 109636916 | rs78553346 | A | C | A | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | *CCDC162P* SAT |
| 6 | 109636952 | rs79791278 | C | T | C | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | *CCDC162P* SAT |
| 6 | 109637158 | rs79960228 | G | C | G | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | *CCDC162P* SAT |
| 6 | 109637287 | rs77655476 | G | A | G | 0.027 | 1.043 | 0.085 | 0.019 | 0.048 | 0.121 | 6.16E-06 | *CCDC162P* SAT |
| 6 | 109637444 | rs139254193 | T | C | T | 0.027 | 1.052 | 0.084 | 0.019 | 0.048 | 0.120 | 7.23E-06 | *CCDC162P* SAT |
| 6 | 109637475 | rs149578739 | G | A | G | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | *CCDC162P* SAT |
| 6 | 109637657 | rs143778307 | A | G | A | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | *CCDC162P* SAT |
| 6 | 109637747 | rs75219290 | A | G | A | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | *CCDC162P* SAT |
| 6 | 109637838 | rs79642415 | A | G | A | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | *CCDC162P* SAT |
| 6 | 109637864 | rs74693235 | G | A | G | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | *CCDC162P* SAT |
| 6 | 109638417 | rs77946366 | T | C | T | 0.027 | 1.053 | 0.084 | 0.019 | 0.048 | 0.121 | 7.03E-06 | *CCDC162P* SAT |
| 6 | 109638665 | rs57544850 | G | A | G | 0.027 | 1.051 | 0.084 | 0.019 | 0.048 | 0.121 | 7.22E-06 | *CCDC162P* in other tissue |
| 6 | 109638684 | 6:109638684\_G\_A | A | G | A | 0.027 | 1.051 | 0.084 | 0.019 | 0.048 | 0.121 | 7.22E-06 |  |
| 6 | 109638885 | rs76422683 | T | C | T | 0.027 | 1.039 | 0.084 | 0.019 | 0.048 | 0.121 | 7.02E-06 | *CCDC162P* in other tissue |
| 6 | 109639641 | rs75638499 | A | G | A | 0.026 | 1.057 | 0.084 | 0.019 | 0.048 | 0.121 | 7.10E-06 | *CCDC162P* in other tissue |
| 6 | 109640900 | rs75278348 | A | G | A | 0.027 | 0.990 | 0.087 | 0.019 | 0.050 | 0.125 | 5.48E-06 | *CCDC162P* in other tissue |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | 7195558 | rs12672133 | C | T | C | 0.038 | 0.996 | 0.092 | 0.016 | 0.061 | 0.124 | 9.76E-09 | no |
| 7 | 7213245 | rs73043785 | T | C | T | 0.039 | 1.034 | 0.088 | 0.016 | 0.058 | 0.119 | 2.27E-08 | no |
| 7 | 7214799 | rs73043789 | A | G | A | 0.039 | 1.036 | 0.088 | 0.016 | 0.058 | 0.119 | 2.25E-08 | no |
| 7 | 7216175 | rs12667853 | A | G | A | 0.039 | 1.029 | 0.089 | 0.016 | 0.058 | 0.120 | 1.50E-08 | no |
| 7 | 7217867 | rs55637396 | A | G | A | 0.038 | 1.024 | 0.092 | 0.016 | 0.062 | 0.123 | 6.67E-09 | no |
| 7 | 7272485 | rs73045769 | T | C | T | 0.036 | 1.079 | 0.093 | 0.016 | 0.062 | 0.124 | 7.82E-09 | no |
| 7 | 7273424 | rs73045773 | G | A | G | 0.037 | 1.068 | 0.091 | 0.016 | 0.060 | 0.121 | 1.02E-08 | no |
| 7 | 7282894 | rs73049974 | A | G | A | 0.037 | 1.058 | 0.091 | 0.016 | 0.060 | 0.121 | 1.13E-08 | no |
| 7 | 7285578 | rs114287739 | T | A | T | 0.036 | 1.076 | 0.092 | 0.016 | 0.061 | 0.123 | 7.60E-09 | no |
| 7 | 7285607 | rs73049983 | A | G | A | 0.036 | 1.069 | 0.092 | 0.016 | 0.061 | 0.124 | 9.64E-09 | no |
| 7 | 7286193 | rs5010182 | G | A | G | 0.036 | 1.076 | 0.092 | 0.016 | 0.061 | 0.123 | 7.60E-09 | no |
| 7 | 7292688 | rs73049994 | T | C | T | 0.036 | 1.060 | 0.092 | 0.016 | 0.061 | 0.123 | 1.00E-08 | no |
| 7 | 7296136 | rs73049999 | C | T | C | 0.036 | 1.059 | 0.093 | 0.016 | 0.061 | 0.124 | 8.81E-09 | no |
| 7 | 7298191 | rs75122088 | T | C | T | 0.036 | 1.083 | 0.081 | 0.016 | 0.051 | 0.112 | 3.07E-07 | no |
| 7 | 7299469 | rs28617577 | T | C | T | 0.042 | 1.028 | 0.075 | 0.015 | 0.045 | 0.105 | 9.34E-07 | no |
| 7 | 7299480 | rs7803236 | A | G | A | 0.042 | 1.026 | 0.075 | 0.015 | 0.045 | 0.105 | 8.83E-07 | no |
| 7 | 7299654 | rs200521981 | I | D | I | 0.037 | 1.022 | 0.088 | 0.016 | 0.056 | 0.120 | 7.03E-08 | no |
| 7 | 7300508 | rs112344846 | C | G | C | 0.035 | 1.042 | 0.093 | 0.016 | 0.060 | 0.125 | 2.37E-08 | no |
| 7 | 7300574 | rs117303191 | A | G | A | 0.035 | 1.077 | 0.087 | 0.016 | 0.056 | 0.118 | 7.60E-08 | no |
| 7 | 7301098 | rs73051710 | C | T | C | 0.034 | 1.050 | 0.092 | 0.016 | 0.060 | 0.124 | 2.73E-08 | no |
| 7 | 7304999 | rs58465226 | D | I | D | 0.038 | 0.977 | 0.089 | 0.016 | 0.057 | 0.121 | 5.35E-08 | no |
| 7 | 7305003 | rs57240533 | A | T | A | 0.038 | 0.977 | 0.089 | 0.016 | 0.057 | 0.121 | 5.35E-08 | no |
| 7 | 7305712 | rs58285948 | C | T | C | 0.037 | 1.011 | 0.083 | 0.016 | 0.051 | 0.115 | 4.42E-07 | no |
| 7 | 7305787 | rs57402603 | C | T | C | 0.037 | 1.007 | 0.083 | 0.016 | 0.051 | 0.115 | 4.05E-07 | no |
| 7 | 7309344 | rs12673653 | G | A | G | 0.037 | 1.026 | 0.085 | 0.016 | 0.054 | 0.117 | 1.51E-07 | no |
| 7 | 7312747 | rs58968692 | C | T | C | 0.037 | 1.026 | 0.090 | 0.016 | 0.059 | 0.122 | 2.98E-08 | no |
| 7 | 7313294 | rs6973768 | G | T | G | 0.036 | 1.000 | 0.093 | 0.017 | 0.061 | 0.126 | 2.42E-08 | no |
| 7 | 7313485 | rs6953213 | A | G | A | 0.038 | 0.959 | 0.083 | 0.016 | 0.051 | 0.116 | 5.34E-07 | no |
| 7 | 7316262 | rs6974699 | C | G | C | 0.030 | 0.980 | 0.104 | 0.018 | 0.068 | 0.139 | 1.26E-08 | no |
| 7 | 7317524 | rs2270081 | A | G | A | 0.030 | 0.981 | 0.104 | 0.018 | 0.069 | 0.139 | 1.10E-08 | no |
| 7 | 7319013 | rs147389390 | D | I | D | 0.031 | 0.917 | 0.113 | 0.018 | 0.077 | 0.149 | 1.49E-09 | no |
| 7 | 7321075 | rs60008535 | G | A | G | 0.032 | 0.967 | 0.100 | 0.018 | 0.065 | 0.135 | 2.50E-08 | no |
| 7 | 7321130 | rs73051783 | C | G | C | 0.030 | 0.960 | 0.106 | 0.018 | 0.070 | 0.142 | 7.93E-09 | no |
| 7 | 7328241 | rs56405297 | G | A | G | 0.030 | 0.950 | 0.111 | 0.018 | 0.075 | 0.147 | 2.29E-09 | no |
| 7 | 7328318 | rs138278387 | D | I | D | 0.029 | 0.932 | 0.112 | 0.019 | 0.075 | 0.149 | 3.89E-09 | no |
| 7 | 7329539 | rs7779267 | T | C | T | 0.030 | 0.943 | 0.112 | 0.018 | 0.076 | 0.149 | 1.84E-09 | no |
| 7 | 7332244 | rs73053804 | C | G | C | 0.030 | 0.935 | 0.111 | 0.019 | 0.075 | 0.147 | 3.07E-09 | no |
| 7 | 7332460 | rs73053807 | A | C | A | 0.026 | 0.932 | 0.115 | 0.020 | 0.076 | 0.154 | 9.80E-09 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | 136253593 | rs187398437 | A | T | A | 0.012 | 0.770 | 0.166 | 0.033 | 0.102 | 0.230 | 4.17E-07 | no |
| 7 | 136866494 | rs147782262 | A | G | A | 0.042 | 0.940 | 0.070 | 0.016 | 0.039 | 0.101 | 9.94E-06 | *PTN* esofagus |
| 7 | 136892170 | rs12154638 | T | C | T | 0.044 | 1.008 | 0.067 | 0.015 | 0.037 | 0.096 | 9.12E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 9 | 37645096 | rs200046053 | I | D | I | 0.103 | 0.940 | 0.048 | 0.010 | 0.028 | 0.068 | 4.41E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 15 | 80519402 | rs764503 | G | A | G | 0.302 | 0.960 | 0.031 | 0.007 | 0.017 | 0.044 | 7.17E-06 | *FAH* SAT *LINC01314* other organs |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 16 | 50171697 | rs74651422 | C | G | C | 0.021 | 1.077 | 0.099 | 0.021 | 0.058 | 0.139 | 1.95E-06 | no |
| 16 | 50174059 | rs75653698 | G | C | G | 0.021 | 1.073 | 0.098 | 0.021 | 0.058 | 0.139 | 2.04E-06 | no |
| 16 | 50176176 | rs113710352 | T | C | T | 0.022 | 1.078 | 0.095 | 0.020 | 0.055 | 0.135 | 3.59E-06 | no |
| 16 | 50181270 | rs9746569 | T | A | A | 0.022 | 1.076 | 0.094 | 0.020 | 0.054 | 0.134 | 4.49E-06 | *HEATR3* lung |
| 16 | 50181389 | rs112283677 | A | G | A | 0.022 | 1.078 | 0.095 | 0.020 | 0.055 | 0.135 | 3.59E-06 | no |
| 16 | 50190380 | rs111805222 | T | C | T | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.136 | 1.73E-06 | no |
| 16 | 50200087 | rs7192461 | G | A | A | 0.022 | 1.101 | 0.096 | 0.020 | 0.057 | 0.135 | 1.87E-06 | no |
| 16 | 50203171 | rs9302747 | A | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | *HEATR3* lung |
| 16 | 50203469 | rs9302748 | C | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | *HEATR3* lung |
| 16 | 50203510 | 16:50203510\_G\_C | C | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | no |
| 16 | 50206206 | rs11076520 | T | C | C | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | no |
| 16 | 50206891 | rs112755907 | A | G | A | 0.022 | 1.097 | 0.096 | 0.020 | 0.057 | 0.135 | 1.84E-06 | no |
| 16 | 50207731 | rs8043876 | A | G | G | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.135 | 1.99E-06 | *HEATR3* lung |
| 16 | 50217169 | rs111529120 | A | G | A | 0.022 | 1.099 | 0.096 | 0.020 | 0.057 | 0.136 | 1.73E-06 | no |
| 16 | 50220836 | rs77594408 | G | T | G | 0.022 | 1.099 | 0.095 | 0.020 | 0.056 | 0.134 | 2.10E-06 | no |
| 16 | 50222326 | rs9925568 | C | T | T | 0.022 | 1.092 | 0.094 | 0.020 | 0.055 | 0.134 | 2.48E-06 | no |
| 16 | 50228844 | rs113177857 | C | T | C | 0.022 | 1.095 | 0.095 | 0.020 | 0.056 | 0.134 | 2.33E-06 | no |
| 16 | 50231036 | rs372992015 | I | D | I | 0.032 | 0.977 | 0.080 | 0.018 | 0.045 | 0.115 | 7.54E-06 | no |
| 16 | 50237262 | rs4581696 | A | G | G | 0.023 | 1.090 | 0.092 | 0.020 | 0.054 | 0.131 | 3.05E-06 | *HEATR3* lung |
| 16 | 50243856 | rs6500301 | C | G | G | 0.023 | 1.070 | 0.090 | 0.020 | 0.051 | 0.129 | 5.65E-06 | *HEATR3* lung |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 21 | 24745658 | rs2828092 | T | C | T | 0.068 | 1.016 | 0.055 | 0.012 | 0.032 | 0.079 | 5.87E-06 | no |
| 21 | 24801169 | rs190939201 | G | A | G | 0.081 | 0.914 | 0.058 | 0.012 | 0.035 | 0.081 | 8.68E-07 | no |
| 21 | 25074937 | rs2828440 | C | T | C | 0.033 | 1.038 | 0.081 | 0.017 | 0.048 | 0.114 | 1.70E-06 | no |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 21 | 46426355 | rs140901493 | I | D | I | 0.033 | 0.898 | 0.084 | 0.018 | 0.048 | 0.120 | 4.11E-06 | no |
| a. SNPs associated with fat cell number with p<10-5 after filtering for genetic loci with >3 SNPs associated with fat cell number according to visual inspection in Locus Zoom and, for SNPs displaying suggestive but not GWAS-significant association with fat cell number, MAF >2%. Beta is calculated for allelele A1. | | | | | | | | | | | | | |

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Supplementary table 5. Bi-directional MR analysis was conducted to assess possible causal relationships between fat cell number and BMI, WHRadjBMI, or T2D** | | | | | | | |
| Exposure | Outcome | Instruments | Effect allele | Other allele | Wald's ratio | | |
| Beta | SE | P |
| Fat cell number | BMI | rs115034159 | T | C | -0.24 | 0.1 | 0.02 |
| rs117553144 | C | T | -0.08 | 0.05 | 0.13 |
| rs12672133 | C | T | 0.03 | 0.06 | 0.61 |
| rs140068450 | A | G | -0.01 | 0.06 | 0.83 |
| rs141736521 | A | G | -0.06 | 0.05 | 0.28 |
| rs149392217 | C | G | -0.03 | 0.05 | 0.56 |
| rs149660479 | G | T | 0.07 | 0.06 | 0.24 |
| rs150250345 | A | G | 0.08 | 0.06 | 0.22 |
| BMI | Fat cell number | rs10063055 | T | C | -0.08 | 0.57 | 0.89 |
| rs10160769 | G | C | -0.03 | 0.49 | 0.95 |
| rs1017529 | A | C | -0.06 | 0.57 | 0.92 |
| rs10182416 | G | A | 0.36 | 0.47 | 0.44 |
| rs10184537 | C | T | -0.1 | 0.4 | 0.8 |
| rs10217047 | A | C | 0.33 | 0.56 | 0.56 |
| rs10402950 | C | T | -0.15 | 0.53 | 0.77 |
| rs10417386 | C | T | -0.94 | 0.55 | 0.09 |
| rs10423928 | T | A | 0.2 | 0.22 | 0.36 |
| rs1048932 | C | A | -0.37 | 0.42 | 0.38 |
| rs10505836 | C | A | 0.87 | 0.52 | 0.1 |
| rs10510025 | T | C | 0.38 | 0.39 | 0.33 |
| rs1064213 | A | G | 0.01 | 0.42 | 0.99 |
| rs10756792 | C | T | -0.4 | 0.39 | 0.31 |
| rs10760277 | T | C | -0.08 | 0.45 | 0.87 |
| rs10771041 | T | C | -0.26 | 0.43 | 0.55 |
| rs10799778 | T | G | 0.51 | 0.47 | 0.28 |
| rs10903791 | A | G | -0.32 | 0.57 | 0.57 |
| rs10927006 | T | C | 0.85 | 0.54 | 0.11 |
| rs10938398 | A | G | 0.12 | 0.22 | 0.57 |
| rs10960294 | G | T | 0 | 0.49 | 1 |
| rs11000993 | C | T | 0.08 | 0.52 | 0.88 |
| rs11012732 | G | A | 0.41 | 0.3 | 0.17 |
| rs11017771 | G | C | -1.22 | 0.66 | 0.07 |
| rs11024271 | C | T | -0.7 | 0.55 | 0.2 |
| rs11057072 | G | A | 0.76 | 0.6 | 0.2 |
| rs1106761 | A | G | -0.03 | 0.46 | 0.95 |
| rs11071646 | G | A | 0.51 | 0.39 | 0.2 |
| rs11079849 | C | T | 0 | 0.32 | 0.99 |
| rs11099020 | C | T | -0.32 | 0.46 | 0.48 |
| rs11105846 | G | T | 0.51 | 0.56 | 0.37 |
| rs11115160 | G | A | 0.42 | 0.57 | 0.45 |
| rs11122450 | T | G | 0.41 | 0.56 | 0.46 |
| rs11134679 | G | A | -0.22 | 0.36 | 0.54 |
| rs1114166 | C | T | 0.62 | 0.56 | 0.27 |
| rs11150745 | A | G | -0.72 | 0.33 | 0.03 |
| rs11161044 | C | G | 0.01 | 0.45 | 0.99 |
| rs11165643 | T | C | 0.13 | 0.31 | 0.68 |
| rs111689389 | G | C | 0.65 | 0.5 | 0.2 |
| rs1126930 | C | G | 0.09 | 0.57 | 0.88 |
| rs113079574 | C | T | -0.05 | 0.49 | 0.92 |
| rs113603865 | T | C | -0.69 | 0.4 | 0.08 |
| rs113624107 | A | G | -0.14 | 0.5 | 0.78 |
| rs11525873 | T | C | -0.48 | 0.44 | 0.28 |
| rs11608710 | G | T | 0.11 | 0.47 | 0.82 |
| rs11610621 | A | T | 0.43 | 0.54 | 0.42 |
| rs116374395 | A | G | 0.96 | 0.49 | 0.05 |
| rs116377258 | G | A | 0.21 | 0.2 | 0.3 |
| rs1167311 | G | A | -0.11 | 0.34 | 0.75 |
| rs11691869 | C | A | 0.09 | 0.33 | 0.78 |
| rs11699828 | G | A | -0.02 | 0.65 | 0.97 |
| rs11709402 | G | A | 0.31 | 0.32 | 0.34 |
| rs117118217 | C | G | 0.3 | 0.44 | 0.49 |
| rs117342986 | T | C | -0.22 | 0.83 | 0.79 |
| rs11751591 | G | A | -0.33 | 0.47 | 0.48 |
| rs11757278 | T | C | 0.94 | 0.45 | 0.04 |
| rs118136827 | G | T | -0.01 | 0.53 | 0.98 |
| rs1183668 | C | G | 0.33 | 0.42 | 0.43 |
| rs11914525 | A | G | -0.28 | 0.35 | 0.42 |
| rs1191600 | C | A | 0.46 | 0.51 | 0.37 |
| rs12001437 | C | T | 0.16 | 0.52 | 0.76 |
| rs12033257 | A | G | 0.1 | 0.43 | 0.82 |
| rs1205593 | T | C | -0.62 | 0.59 | 0.3 |
| rs12072739 | G | A | -0.28 | 0.46 | 0.54 |
| rs12089815 | G | A | -0.41 | 0.5 | 0.42 |
| rs12140153 | G | T | 0.12 | 0.35 | 0.73 |
| rs12149660 | G | A | 0.43 | 0.41 | 0.3 |
| rs12259464 | A | G | 0.35 | 0.48 | 0.47 |
| rs12340969 | C | T | 0.26 | 0.29 | 0.38 |
| rs12364470 | G | T | -0.04 | 0.42 | 0.93 |
| rs12427047 | C | T | -0.2 | 0.41 | 0.61 |
| rs12462975 | A | G | -0.51 | 0.35 | 0.15 |
| rs1263629 | G | A | 0.49 | 0.57 | 0.39 |
| rs1266874 | G | A | 0.51 | 0.46 | 0.26 |
| rs12681792 | A | C | -0.18 | 0.52 | 0.74 |
| rs12692596 | T | C | 0.17 | 0.46 | 0.71 |
| rs12762034 | C | T | -0.23 | 0.41 | 0.58 |
| rs1286058 | A | T | 0.1 | 0.47 | 0.82 |
| rs12881629 | G | A | 0.33 | 0.5 | 0.51 |
| rs12885458 | T | G | 0.95 | 0.38 | 0.01 |
| rs12956148 | A | C | 0.5 | 0.48 | 0.3 |
| rs1296328 | A | C | 0.29 | 0.35 | 0.41 |
| rs12977787 | A | G | 0.82 | 0.46 | 0.07 |
| rs13012070 | G | A | 0.31 | 0.53 | 0.56 |
| rs13076052 | G | C | 0.62 | 0.48 | 0.2 |
| rs13107325 | T | C | -0.12 | 0.32 | 0.7 |
| rs13176429 | C | T | 0.13 | 0.44 | 0.77 |
| rs13218383 | C | G | 1.34 | 0.42 | 0 |
| rs1322842 | A | G | -0.59 | 0.49 | 0.23 |
| rs13248187 | C | T | 0.71 | 0.44 | 0.11 |
| rs1327259 | A | G | -0.29 | 0.42 | 0.49 |
| rs1330199 | G | T | 0.63 | 0.53 | 0.24 |
| rs13317303 | C | A | 0.44 | 0.56 | 0.43 |
| rs13427822 | A | G | -0.09 | 0.38 | 0.81 |
| rs1346841 | G | A | 0.11 | 0.52 | 0.82 |
| rs1360201 | T | C | -1.02 | 0.48 | 0.03 |
| rs140159717 | C | T | -0.26 | 0.49 | 0.59 |
| rs1412239 | G | C | 0.17 | 0.27 | 0.53 |
| rs1436348 | G | A | 0.07 | 0.41 | 0.87 |
| rs1438945 | T | A | 1.52 | 0.54 | 0 |
| rs1441264 | A | G | -0.15 | 0.36 | 0.67 |
| rs1446585 | A | G | 0.16 | 0.5 | 0.75 |
| rs1451963 | T | G | 0.14 | 0.65 | 0.83 |
| rs1458156 | T | C | -0.5 | 0.45 | 0.27 |
| rs1459190 | G | A | 0.18 | 0.43 | 0.68 |
| rs1471093 | A | G | 0.14 | 0.47 | 0.77 |
| rs1471740 | C | T | 0.05 | 0.39 | 0.9 |
| rs147568678 | T | C | 0.13 | 0.52 | 0.81 |
| rs1477290 | C | T | -0.17 | 0.27 | 0.53 |
| rs147730268 | G | T | -0.03 | 0.33 | 0.94 |
| rs149050217 | G | A | 0.23 | 0.48 | 0.63 |
| rs1503526 | C | T | 0.29 | 0.41 | 0.48 |
| rs1554654 | C | T | 0.25 | 0.5 | 0.61 |
| rs156201 | C | G | 0.8 | 0.54 | 0.14 |
| rs1582931 | G | A | -0.64 | 0.48 | 0.18 |
| rs1607659 | G | A | -0.93 | 0.55 | 0.09 |
| rs1609010 | G | A | -0.3 | 0.3 | 0.32 |
| rs16846140 | G | A | 0.25 | 0.51 | 0.62 |
| rs16868443 | C | G | -0.49 | 0.55 | 0.38 |
| rs16916303 | A | G | -0.04 | 0.49 | 0.93 |
| rs17056301 | C | T | -0.24 | 0.54 | 0.66 |
| rs17132130 | G | C | -0.08 | 0.4 | 0.83 |
| rs17149254 | T | C | -0.08 | 0.37 | 0.83 |
| rs17193211 | C | T | -0.2 | 0.5 | 0.69 |
| rs17289010 | A | G | -0.11 | 0.51 | 0.83 |
| rs17399739 | G | A | 0.57 | 0.45 | 0.21 |
| rs17446299 | G | C | 0.04 | 0.54 | 0.94 |
| rs17639546 | G | A | 0.73 | 0.42 | 0.08 |
| rs1778830 | A | G | -0.58 | 0.46 | 0.21 |
| rs1788808 | A | G | 0.03 | 0.29 | 0.93 |
| rs1793636 | G | C | -0.22 | 0.5 | 0.67 |
| rs1805123 | T | G | -0.63 | 0.48 | 0.2 |
| rs1834144 | C | A | -0.43 | 0.47 | 0.36 |
| rs1884897 | G | A | -0.28 | 0.34 | 0.41 |
| rs1919243 | C | T | -0.18 | 0.54 | 0.74 |
| rs1967772 | G | A | -0.48 | 0.44 | 0.28 |
| rs1999433 | C | T | -0.17 | 0.53 | 0.75 |
| rs2035936 | T | G | 0.59 | 0.41 | 0.15 |
| rs2051559 | C | T | -0.16 | 0.45 | 0.73 |
| rs2076603 | G | A | -0.44 | 0.52 | 0.4 |
| rs2102278 | G | A | -0.28 | 0.58 | 0.63 |
| rs2114210 | A | G | -0.34 | 0.5 | 0.49 |
| rs2133561 | A | T | -0.99 | 0.44 | 0.02 |
| rs213518 | C | T | -0.06 | 0.57 | 0.91 |
| rs2153740 | A | G | 0.56 | 0.54 | 0.3 |
| rs215634 | A | G | -0.05 | 0.44 | 0.92 |
| rs2164300 | C | T | -0.56 | 0.52 | 0.28 |
| rs2172131 | T | C | 0.33 | 0.4 | 0.41 |
| rs217672 | C | A | -0.32 | 0.41 | 0.44 |
| rs2178899 | A | T | 0.42 | 0.4 | 0.29 |
| rs2190887 | C | T | 1.14 | 0.58 | 0.05 |
| rs2192158 | A | G | 0.02 | 0.41 | 0.96 |
| rs2216931 | A | C | 0.42 | 0.41 | 0.3 |
| rs2234458 | C | T | -0.02 | 0.3 | 0.94 |
| rs2249825 | G | C | -0.37 | 0.47 | 0.43 |
| rs2253310 | G | C | -0.32 | 0.37 | 0.38 |
| rs2271189 | G | A | 0.01 | 0.39 | 0.98 |
| rs2275444 | G | A | -0.16 | 0.55 | 0.78 |
| rs2289379 | C | T | -0.24 | 0.42 | 0.56 |
| rs2306593 | C | T | 0 | 0.38 | 0.99 |
| rs2307111 | T | C | 0.3 | 0.22 | 0.18 |
| rs2342892 | T | G | -0.37 | 0.49 | 0.45 |
| rs2381404 | C | T | -0.93 | 0.53 | 0.08 |
| rs2398861 | G | A | 0.03 | 0.39 | 0.95 |
| rs2425816 | A | G | -0.17 | 0.52 | 0.74 |
| rs2433733 | G | A | -0.13 | 0.38 | 0.74 |
| rs2482356 | T | C | -0.31 | 0.58 | 0.59 |
| rs249293 | C | G | 1.1 | 0.54 | 0.04 |
| rs2512892 | C | T | 0.66 | 0.47 | 0.16 |
| rs252761 | G | T | -1.05 | 0.57 | 0.07 |
| rs2568958 | A | G | 0.12 | 0.28 | 0.68 |
| rs2569993 | C | T | 0.14 | 0.5 | 0.78 |
| rs2606228 | A | C | 0.22 | 0.48 | 0.64 |
| rs2616143 | G | A | 0.67 | 0.47 | 0.16 |
| rs2678204 | G | T | 0.43 | 0.28 | 0.13 |
| rs2725371 | A | G | -0.25 | 0.44 | 0.57 |
| rs2781668 | T | C | -0.73 | 0.55 | 0.19 |
| rs2836961 | C | A | -0.58 | 0.52 | 0.26 |
| rs28404639 | C | T | -0.45 | 0.56 | 0.42 |
| rs28457680 | A | T | 0.65 | 0.48 | 0.17 |
| rs28489620 | G | A | -0.68 | 0.46 | 0.14 |
| rs2861685 | T | C | -0.94 | 0.38 | 0.01 |
| rs28670671 | T | C | 0.23 | 0.54 | 0.67 |
| rs2875762 | C | G | -0.45 | 0.51 | 0.38 |
| rs2920503 | C | T | -0.89 | 0.49 | 0.07 |
| rs2962334 | T | G | -0.41 | 0.41 | 0.32 |
| rs317656 | T | A | 0.68 | 0.49 | 0.16 |
| rs329118 | C | T | 0.26 | 0.38 | 0.49 |
| rs329651 | T | G | 1.24 | 0.57 | 0.03 |
| rs34025316 | T | C | -0.91 | 0.57 | 0.11 |
| rs34045288 | T | C | 0.15 | 0.28 | 0.59 |
| rs34153025 | T | C | 0.42 | 0.58 | 0.47 |
| rs34234296 | G | A | -0.2 | 0.47 | 0.66 |
| rs34481751 | C | A | -0.36 | 0.44 | 0.42 |
| rs34517439 | A | C | 0.05 | 0.27 | 0.84 |
| rs34811474 | G | A | 0.4 | 0.27 | 0.13 |
| rs349071 | G | A | -0.98 | 0.49 | 0.04 |
| rs35154326 | A | G | 0.53 | 0.52 | 0.3 |
| rs35364449 | T | C | -0.54 | 0.44 | 0.21 |
| rs355393 | A | G | -0.34 | 0.54 | 0.53 |
| rs35809007 | G | A | 0.4 | 0.37 | 0.28 |
| rs35867081 | A | G | 0.04 | 0.44 | 0.93 |
| rs35957544 | G | T | -0.63 | 0.32 | 0.05 |
| rs35972789 | C | A | 0.05 | 0.68 | 0.95 |
| rs36007635 | G | A | -0.05 | 0.45 | 0.91 |
| rs36061954 | T | C | -0.57 | 0.5 | 0.25 |
| rs3751837 | T | C | 0.63 | 0.53 | 0.24 |
| rs3764625 | T | G | 0.12 | 0.55 | 0.83 |
| rs3766823 | A | G | -0.54 | 0.46 | 0.24 |
| rs3784710 | T | C | 0.22 | 0.25 | 0.38 |
| rs3803286 | A | G | -0.09 | 0.37 | 0.8 |
| rs3807566 | G | T | 0.96 | 0.51 | 0.06 |
| rs3814883 | T | C | -0.38 | 0.26 | 0.14 |
| rs3851998 | C | G | -0.01 | 0.52 | 0.98 |
| rs3866805 | A | C | 0.59 | 0.56 | 0.29 |
| rs3897102 | T | C | -1.13 | 0.51 | 0.03 |
| rs3901286 | C | A | 0.48 | 0.36 | 0.19 |
| rs3902951 | G | T | -0.03 | 0.49 | 0.95 |
| rs394608 | C | T | -0.04 | 0.33 | 0.89 |
| rs40071 | T | C | 0.13 | 0.31 | 0.66 |
| rs4055791 | C | T | 0.32 | 0.35 | 0.37 |
| rs406388 | G | C | 0.3 | 0.52 | 0.56 |
| rs4148155 | A | G | 0 | 0.48 | 1 |
| rs4261944 | G | T | 0.16 | 0.46 | 0.72 |
| rs4284600 | C | T | 0.78 | 0.52 | 0.13 |
| rs429343 | A | G | -0.18 | 0.36 | 0.62 |
| rs429358 | T | C | 0.07 | 0.32 | 0.83 |
| rs4307239 | G | A | 0.38 | 0.5 | 0.45 |
| rs4456769 | T | C | -0.7 | 0.46 | 0.13 |
| rs4477562 | T | C | 0.19 | 0.3 | 0.52 |
| rs4482463 | C | A | 0.01 | 0.38 | 0.98 |
| rs4562625 | C | G | -0.27 | 0.45 | 0.55 |
| rs4613074 | T | C | 0.05 | 0.35 | 0.89 |
| rs4625852 | G | A | 1.07 | 0.57 | 0.06 |
| rs4625888 | T | C | 0.2 | 0.53 | 0.71 |
| rs4648450 | C | A | 0.71 | 0.45 | 0.11 |
| rs4658403 | C | T | -0.3 | 0.48 | 0.53 |
| rs4671328 | T | G | 0.03 | 0.31 | 0.91 |
| rs4672338 | T | C | -0.13 | 0.5 | 0.8 |
| rs4718964 | T | G | 0.64 | 0.57 | 0.26 |
| rs4722398 | T | C | -0.27 | 0.53 | 0.61 |
| rs4757144 | A | G | 0.3 | 0.38 | 0.43 |
| rs4764949 | A | G | -0.51 | 0.37 | 0.17 |
| rs4790292 | C | A | 0.27 | 0.32 | 0.4 |
| rs4792716 | G | A | -0.17 | 0.45 | 0.71 |
| rs4832298 | C | T | -0.81 | 0.43 | 0.06 |
| rs4876611 | G | A | 0.44 | 0.37 | 0.24 |
| rs4895799 | T | C | -0.18 | 0.55 | 0.74 |
| rs4900590 | T | C | -0.38 | 0.43 | 0.38 |
| rs4919197 | T | C | 0.06 | 0.57 | 0.92 |
| rs4929923 | C | T | -0.53 | 0.34 | 0.12 |
| rs4958702 | T | C | -0.44 | 0.42 | 0.3 |
| rs4976553 | A | G | -0.29 | 0.54 | 0.59 |
| rs512121 | T | C | 0.68 | 0.51 | 0.18 |
| rs529200 | G | A | -0.35 | 0.37 | 0.35 |
| rs539515 | C | A | 0 | 0.16 | 0.98 |
| rs55658481 | A | G | 0.88 | 0.52 | 0.09 |
| rs55714539 | C | A | 0.55 | 0.36 | 0.12 |
| rs55726687 | A | G | 0.03 | 0.3 | 0.93 |
| rs558887 | A | G | 0.66 | 0.51 | 0.2 |
| rs55920177 | A | T | 0.67 | 0.57 | 0.24 |
| rs559231 | T | G | 0.19 | 0.5 | 0.71 |
| rs56038322 | A | G | 0.34 | 0.48 | 0.48 |
| rs56133507 | G | T | -0.37 | 0.56 | 0.51 |
| rs56161855 | T | A | -0.57 | 0.38 | 0.14 |
| rs56203622 | C | T | 0.81 | 0.49 | 0.1 |
| rs56352336 | T | C | -0.11 | 0.58 | 0.85 |
| rs56356382 | T | C | -0.02 | 0.37 | 0.96 |
| rs56399737 | C | T | 0.37 | 0.4 | 0.35 |
| rs56803094 | A | G | 0.24 | 0.51 | 0.64 |
| rs56858768 | A | G | 0.4 | 0.42 | 0.34 |
| rs56893062 | G | T | -0.01 | 0.51 | 0.99 |
| rs57488047 | T | C | 0.25 | 0.43 | 0.55 |
| rs57636386 | T | C | -0.14 | 0.29 | 0.62 |
| rs577525 | C | T | -0.14 | 0.33 | 0.67 |
| rs57989773 | C | T | 0.12 | 0.58 | 0.83 |
| rs58862095 | C | T | -0.25 | 0.28 | 0.37 |
| rs59227842 | G | A | -0.43 | 0.3 | 0.16 |
| rs59237168 | T | C | 0.52 | 0.48 | 0.28 |
| rs594024 | T | C | -0.11 | 0.42 | 0.79 |
| rs5995843 | A | G | -0.42 | 0.36 | 0.25 |
| rs6023655 | A | G | 0.14 | 0.52 | 0.78 |
| rs60764613 | T | G | -0.26 | 0.44 | 0.56 |
| rs6134916 | C | T | -0.41 | 0.57 | 0.48 |
| rs61813324 | T | C | -0.08 | 0.3 | 0.78 |
| rs61828088 | A | G | 0.51 | 0.48 | 0.29 |
| rs61903695 | G | A | 0.16 | 0.44 | 0.72 |
| rs61992671 | A | G | 0.31 | 0.42 | 0.46 |
| rs62007782 | G | A | 0.17 | 0.42 | 0.68 |
| rs62072006 | C | A | -1.09 | 0.64 | 0.09 |
| rs62107261 | T | C | 0.16 | 0.22 | 0.45 |
| rs62176243 | A | T | 0.49 | 0.46 | 0.29 |
| rs62190049 | G | C | 0.13 | 0.56 | 0.82 |
| rs62246311 | A | G | 0.19 | 0.52 | 0.71 |
| rs62379271 | G | T | -0.19 | 0.55 | 0.73 |
| rs6265 | C | T | -0.2 | 0.21 | 0.33 |
| rs6430068 | A | G | 0.53 | 0.5 | 0.29 |
| rs6444950 | A | G | -0.22 | 0.46 | 0.64 |
| rs6474856 | C | T | -0.18 | 0.57 | 0.75 |
| rs6504543 | C | T | 0.56 | 0.42 | 0.18 |
| rs6531639 | G | A | -0.46 | 0.57 | 0.42 |
| rs6545714 | G | A | -0.18 | 0.33 | 0.58 |
| rs6551304 | G | A | 0.19 | 0.47 | 0.7 |
| rs6560906 | T | C | 0.38 | 0.55 | 0.49 |
| rs6561937 | T | A | 0.31 | 0.45 | 0.48 |
| rs6567160 | C | T | -0.17 | 0.14 | 0.23 |
| rs6575340 | A | G | 0.34 | 0.3 | 0.26 |
| rs66679256 | T | C | -0.18 | 0.42 | 0.67 |
| rs6669189 | T | C | -0.86 | 0.36 | 0.02 |
| rs6669341 | A | G | 0.89 | 0.37 | 0.01 |
| rs6682438 | C | T | 0.43 | 0.53 | 0.42 |
| rs6688826 | C | T | -0.24 | 0.53 | 0.65 |
| rs66978877 | T | C | 0.35 | 0.43 | 0.41 |
| rs6705567 | T | C | -0.54 | 0.44 | 0.23 |
| rs6707827 | G | A | 0.26 | 0.6 | 0.66 |
| rs6710091 | C | G | -0.77 | 0.55 | 0.16 |
| rs6713781 | G | C | 0.14 | 0.51 | 0.78 |
| rs672313 | G | A | 0.16 | 0.45 | 0.71 |
| rs6744646 | G | A | -0.13 | 0.16 | 0.39 |
| rs6752979 | A | G | -0.09 | 0.55 | 0.87 |
| rs67609008 | C | T | -0.37 | 0.42 | 0.38 |
| rs6774894 | A | T | -0.41 | 0.53 | 0.44 |
| rs6777784 | T | G | 0.62 | 0.52 | 0.24 |
| rs6843852 | T | C | -0.51 | 0.47 | 0.28 |
| rs6909685 | C | T | -0.16 | 0.45 | 0.73 |
| rs6922607 | G | A | 0.34 | 0.57 | 0.55 |
| rs6938973 | C | T | 0.01 | 0.36 | 0.98 |
| rs6950388 | A | G | -0.32 | 0.44 | 0.47 |
| rs6962980 | A | C | 0.5 | 0.39 | 0.21 |
| rs698147 | A | G | -0.61 | 0.47 | 0.19 |
| rs6998660 | G | A | -0.04 | 0.52 | 0.94 |
| rs7024334 | T | G | 0.36 | 0.56 | 0.52 |
| rs7027304 | T | C | 0.37 | 0.44 | 0.4 |
| rs7034554 | A | G | -0.46 | 0.49 | 0.34 |
| rs7038943 | T | C | 0.23 | 0.46 | 0.62 |
| rs705145 | A | C | -0.48 | 0.47 | 0.31 |
| rs7070670 | C | T | 0.52 | 0.57 | 0.36 |
| rs7124681 | A | C | -0.2 | 0.24 | 0.41 |
| rs7132908 | A | G | -0.42 | 0.21 | 0.04 |
| rs7169847 | G | T | 0.32 | 0.46 | 0.48 |
| rs7201895 | G | A | -0.76 | 0.46 | 0.1 |
| rs7206608 | G | C | 0.13 | 0.5 | 0.8 |
| rs7232171 | T | G | 0.47 | 0.5 | 0.34 |
| rs723672 | T | C | -0.97 | 0.58 | 0.09 |
| rs7259070 | C | T | -0.04 | 0.3 | 0.9 |
| rs72617140 | C | A | 0.11 | 0.39 | 0.78 |
| rs72634826 | G | A | 0.61 | 0.34 | 0.08 |
| rs72673947 | G | A | -0.73 | 0.44 | 0.1 |
| rs72866851 | T | A | -0.01 | 0.6 | 0.99 |
| rs72892910 | T | G | 0.14 | 0.2 | 0.5 |
| rs72910629 | G | A | 0.51 | 0.57 | 0.37 |
| rs72948836 | A | G | -0.9 | 0.55 | 0.1 |
| rs73026725 | C | A | 0.23 | 0.42 | 0.59 |
| rs73052033 | T | C | -0.27 | 0.28 | 0.35 |
| rs73142879 | C | T | 0.2 | 0.31 | 0.51 |
| rs73193736 | A | G | 0.22 | 0.41 | 0.59 |
| rs73213484 | A | T | -0.66 | 0.4 | 0.1 |
| rs7331420 | G | A | 0.16 | 0.5 | 0.76 |
| rs7357754 | G | A | 0.13 | 0.45 | 0.77 |
| rs73601548 | T | C | 0.35 | 0.63 | 0.58 |
| rs7442137 | C | T | 0.98 | 0.52 | 0.06 |
| rs7442885 | C | G | -0.19 | 0.35 | 0.59 |
| rs745249 | T | C | 0.48 | 0.37 | 0.2 |
| rs7498044 | G | A | 0.05 | 0.44 | 0.9 |
| rs7498665 | G | A | 0.22 | 0.23 | 0.34 |
| rs75035127 | A | G | 0.43 | 0.52 | 0.4 |
| rs7516554 | T | C | -1.02 | 0.53 | 0.05 |
| rs7519259 | A | G | -0.9 | 0.45 | 0.05 |
| rs754635 | G | C | 0.14 | 0.38 | 0.71 |
| rs7549358 | G | C | 0.54 | 0.59 | 0.35 |
| rs75499503 | C | T | 0.08 | 0.41 | 0.85 |
| rs75557510 | A | G | -0.48 | 0.51 | 0.35 |
| rs7571496 | A | G | -0.55 | 0.45 | 0.23 |
| rs76183894 | T | C | -0.09 | 0.56 | 0.88 |
| rs7619139 | A | T | -0.05 | 0.49 | 0.91 |
| rs76387394 | G | A | 0.46 | 0.5 | 0.36 |
| rs7762794 | G | A | 0.53 | 0.46 | 0.24 |
| rs7774 | A | C | 0 | 0.44 | 1 |
| rs7805441 | T | C | 0.62 | 0.48 | 0.19 |
| rs7828631 | T | C | 0.01 | 0.59 | 0.99 |
| rs784257 | C | T | 0.5 | 0.48 | 0.29 |
| rs7852189 | G | A | -0.25 | 0.39 | 0.52 |
| rs7893571 | T | G | -0.81 | 0.47 | 0.09 |
| rs7916385 | C | T | -0.56 | 0.43 | 0.19 |
| rs79212998 | T | G | -0.46 | 0.54 | 0.39 |
| rs7924036 | G | T | 0.4 | 0.44 | 0.36 |
| rs7925100 | A | G | 0.79 | 0.44 | 0.08 |
| rs7942037 | G | C | 0.2 | 0.4 | 0.62 |
| rs7944782 | G | T | -0.13 | 0.4 | 0.75 |
| rs7947143 | G | A | 0.42 | 0.52 | 0.42 |
| rs7952102 | T | C | 0.3 | 0.46 | 0.51 |
| rs7975187 | G | A | -0.75 | 0.54 | 0.16 |
| rs79780963 | T | C | -0.44 | 0.43 | 0.3 |
| rs7996639 | A | G | 0.8 | 0.46 | 0.08 |
| rs8015400 | A | C | -0.02 | 0.3 | 0.94 |
| rs8020365 | A | T | -0.55 | 0.33 | 0.1 |
| rs8024137 | T | A | -0.97 | 0.64 | 0.13 |
| rs8047587 | T | G | 0 | 0.09 | 0.99 |
| rs8112818 | A | G | 0.04 | 0.32 | 0.89 |
| rs8132491 | G | A | 0.11 | 0.46 | 0.81 |
| rs815163 | T | C | 0.29 | 0.38 | 0.46 |
| rs862320 | C | T | -0.14 | 0.27 | 0.62 |
| rs879620 | T | C | 0.1 | 0.27 | 0.72 |
| rs909892 | G | A | 0.1 | 0.56 | 0.86 |
| rs9294260 | A | G | -0.63 | 0.43 | 0.14 |
| rs935166 | G | A | -0.03 | 0.39 | 0.95 |
| rs9366863 | T | C | -0.23 | 0.24 | 0.34 |
| rs9369370 | G | A | 0.65 | 0.55 | 0.24 |
| rs947088 | T | G | -0.08 | 0.55 | 0.89 |
| rs9478496 | C | T | -0.07 | 0.45 | 0.87 |
| rs9522173 | A | T | 0.21 | 0.52 | 0.68 |
| rs9571687 | C | A | 0.12 | 0.51 | 0.82 |
| rs9638713 | A | G | 1.86 | 0.59 | 0 |
| rs9673839 | G | A | -0.57 | 0.49 | 0.24 |
| rs9843653 | C | T | 0.02 | 0.22 | 0.92 |
| rs9860326 | G | C | 0.33 | 0.45 | 0.47 |
| rs9888533 | T | C | -0.11 | 0.52 | 0.83 |
| rs9906072 | T | C | 0.37 | 0.36 | 0.31 |
| rs9944241 | T | C | 0.2 | 0.45 | 0.66 |
| rs9951619 | G | T | -0.02 | 0.51 | 0.96 |
| rs9991259 | A | G | 0.03 | 0.58 | 0.96 |
| Fat cell number | WHRadjBMI | rs12672133 | C | T | 0.05 | 0.13 | 0.73 |
| WHRadjBMI | Fat cell number | rs1011731 | G | A | 0.21 | 0.33 | 0.52 |
| rs10245353 | A | C | -0.69 | 0.3 | 0.02 |
| rs10783615 | G | A | -0.19 | 0.25 | 0.45 |
| rs11048470 | T | G | 0.14 | 0.28 | 0.62 |
| rs1121980 | A | G | 0.03 | 0.15 | 0.86 |
| rs1128249 | G | T | 0.13 | 0.3 | 0.65 |
| rs11663816 | C | T | -0.24 | 0.28 | 0.39 |
| rs12549058 | G | T | 0.12 | 0.29 | 0.68 |
| rs1294421 | G | T | -0.05 | 0.26 | 0.86 |
| rs1316952 | T | C | 0.73 | 0.37 | 0.05 |
| rs1440372 | C | T | -0.09 | 0.33 | 0.78 |
| rs1563355 | C | T | 0.15 | 0.21 | 0.48 |
| rs1569135 | A | G | -0.15 | 0.27 | 0.58 |
| rs16996700 | T | C | 0.41 | 0.35 | 0.24 |
| rs17109256 | A | G | -0.61 | 0.36 | 0.09 |
| rs17451107 | T | C | 0.19 | 0.29 | 0.52 |
| rs2179129 | A | G | 0.23 | 0.31 | 0.45 |
| rs2207139 | G | A | 0.13 | 0.32 | 0.69 |
| rs2287019 | C | T | 0.25 | 0.3 | 0.42 |
| rs2765539 | T | C | 0.1 | 0.27 | 0.72 |
| rs2972164 | C | T | 0.41 | 0.33 | 0.22 |
| rs3786897 | G | A | -0.49 | 0.29 | 0.09 |
| rs459193 | A | G | -0.28 | 0.28 | 0.31 |
| rs4640244 | G | A | -0.02 | 0.3 | 0.96 |
| rs4929927 | G | A | -0.62 | 0.34 | 0.07 |
| rs929641 | A | G | 0.39 | 0.32 | 0.22 |
| rs9860730 | A | G | -0.02 | 0.3 | 0.96 |
| rs998584 | A | C | 0.37 | 0.22 | 0.09 |
| Fat cell number | T2D | rs12672133 | C | T | -0.07 | 0.24 | 0.78 |
| T2D | Fat cell number | rs10077431 | C | A | 0.05 | 0.16 | 0.75 |
| rs10087241 | G | A | -0.03 | 0.13 | 0.83 |
| rs10100265 | A | C | 0.01 | 0.13 | 0.92 |
| rs10114341 | T | C | 0.21 | 0.15 | 0.18 |
| rs10401969 | C | T | -0.11 | 0.12 | 0.37 |
| rs1050226 | A | G | -0.15 | 0.13 | 0.26 |
| rs1061813 | G | A | 0.07 | 0.15 | 0.62 |
| rs10740322 | A | G | 0.2 | 0.14 | 0.15 |
| rs10811661 | T | C | 0.05 | 0.05 | 0.36 |
| rs10830963 | G | C | -0.16 | 0.08 | 0.04 |
| rs10842994 | C | T | 0.12 | 0.1 | 0.25 |
| rs10974438 | C | A | -0.01 | 0.11 | 0.95 |
| rs11098676 | C | T | -0.18 | 0.14 | 0.2 |
| rs11107116 | T | G | 0.24 | 0.16 | 0.14 |
| rs11257655 | T | C | 0.04 | 0.1 | 0.7 |
| rs1127655 | C | T | -0.18 | 0.14 | 0.18 |
| rs11677557 | A | G | -0.15 | 0.13 | 0.25 |
| rs11925227 | G | A | 0.06 | 0.15 | 0.68 |
| rs11926707 | C | T | -0.32 | 0.14 | 0.02 |
| rs12088739 | A | G | 0.06 | 0.13 | 0.65 |
| rs12299509 | G | A | -0.04 | 0.14 | 0.76 |
| rs12910825 | G | A | 0.23 | 0.13 | 0.07 |
| rs12945601 | T | C | -0.04 | 0.14 | 0.77 |
| rs12970134 | A | G | -0.13 | 0.13 | 0.31 |
| rs13094957 | T | C | 0.13 | 0.1 | 0.18 |
| rs13239186 | T | C | 0.03 | 0.12 | 0.79 |
| rs13330951 | A | G | -0.13 | 0.14 | 0.36 |
| rs13389219 | C | T | 0.04 | 0.09 | 0.64 |
| rs1359790 | G | A | 0.08 | 0.09 | 0.37 |
| rs1552224 | A | C | 0.11 | 0.08 | 0.17 |
| rs16988333 | A | G | 0.08 | 0.16 | 0.63 |
| rs17086692 | G | T | 0.18 | 0.14 | 0.2 |
| rs17168486 | T | C | 0.16 | 0.11 | 0.15 |
| rs17334919 | C | T | -0.02 | 0.1 | 0.81 |
| rs17405722 | A | G | 0.04 | 0.12 | 0.76 |
| rs17411031 | C | G | 0.17 | 0.16 | 0.29 |
| rs1758632 | G | C | 0.05 | 0.13 | 0.7 |
| rs17631783 | C | T | 0.16 | 0.14 | 0.26 |
| rs17791483 | A | G | 0.24 | 0.11 | 0.03 |
| rs1801214 | T | C | -0.01 | 0.07 | 0.94 |
| rs1899951 | C | T | -0.05 | 0.07 | 0.51 |
| rs2191348 | T | G | 0.05 | 0.1 | 0.62 |
| rs2237892 | C | T | -0.44 | 0.13 | 0 |
| rs2261181 | T | C | -0.01 | 0.13 | 0.93 |
| rs2292662 | C | T | 0.02 | 0.13 | 0.9 |
| rs2294120 | A | G | -0.28 | 0.14 | 0.04 |
| rs2296173 | G | A | -0.1 | 0.12 | 0.41 |
| rs2299383 | T | C | 0.34 | 0.15 | 0.03 |
| rs243019 | C | T | -0.02 | 0.11 | 0.88 |
| rs2796441 | G | A | 0.03 | 0.09 | 0.77 |
| rs2820426 | G | A | 0.04 | 0.12 | 0.72 |
| rs2867125 | C | T | -0.12 | 0.14 | 0.39 |
| rs2908282 | A | G | 0.06 | 0.15 | 0.7 |
| rs2925979 | T | C | -0.06 | 0.12 | 0.62 |
| rs2972144 | G | A | 0.03 | 0.07 | 0.7 |
| rs340874 | C | T | -0.07 | 0.1 | 0.51 |
| rs348330 | G | A | -0.09 | 0.14 | 0.52 |
| rs35011184 | A | G | 0.01 | 0.03 | 0.77 |
| rs3756784 | G | T | -0.12 | 0.16 | 0.44 |
| rs3802177 | G | A | 0 | 0.05 | 0.99 |
| rs459193 | G | A | 0.1 | 0.1 | 0.31 |
| rs4686471 | C | T | -0.05 | 0.12 | 0.69 |
| rs4810426 | T | C | -0.07 | 0.13 | 0.57 |
| rs4823182 | G | A | -0.06 | 0.13 | 0.67 |
| rs4865796 | A | G | -0.22 | 0.12 | 0.08 |
| rs516946 | C | T | 0.11 | 0.09 | 0.26 |
| rs5215 | C | T | 0.16 | 0.09 | 0.09 |
| rs576674 | G | A | -0.04 | 0.13 | 0.78 |
| rs6059662 | G | A | -0.37 | 0.15 | 0.02 |
| rs6066138 | G | A | -0.12 | 0.15 | 0.4 |
| rs61953351 | G | T | 0.01 | 0.1 | 0.89 |
| rs622217 | T | C | -0.1 | 0.13 | 0.46 |
| rs6515236 | A | C | 0.31 | 0.14 | 0.03 |
| rs67232546 | T | C | -0.03 | 0.14 | 0.84 |
| rs6795735 | C | T | -0.07 | 0.11 | 0.51 |
| rs6798189 | G | A | -0.06 | 0.08 | 0.49 |
| rs6817471 | C | G | -0.01 | 0.13 | 0.93 |
| rs6878122 | G | A | 0 | 0.12 | 0.98 |
| rs7138300 | C | T | -0.04 | 0.14 | 0.76 |
| rs7144011 | T | G | -0.29 | 0.17 | 0.09 |
| rs7177055 | A | G | -0.02 | 0.11 | 0.88 |
| rs7185735 | G | A | 0.01 | 0.06 | 0.83 |
| rs7240767 | C | T | 0.06 | 0.14 | 0.68 |
| rs72892910 | T | G | 0.08 | 0.12 | 0.5 |
| rs735949 | T | C | 0 | 0.13 | 0.99 |
| rs753270 | C | T | 0.13 | 0.13 | 0.31 |
| rs7561798 | G | A | 0.08 | 0.16 | 0.62 |
| rs7572970 | G | A | 0.15 | 0.12 | 0.21 |
| rs7651090 | G | A | -0.02 | 0.06 | 0.78 |
| rs7674212 | G | T | 0.01 | 0.14 | 0.92 |
| rs7685296 | C | T | 0.1 | 0.14 | 0.48 |
| rs77258096 | C | A | -0.04 | 0.1 | 0.69 |
| rs7729395 | T | C | -0.11 | 0.1 | 0.28 |
| rs7756992 | G | A | -0.02 | 0.05 | 0.65 |
| rs7786095 | A | G | 0 | 0.15 | 0.98 |
| rs780094 | C | T | 0.07 | 0.1 | 0.47 |
| rs7845219 | T | C | 0.19 | 0.15 | 0.22 |
| rs7923866 | C | T | -0.01 | 0.07 | 0.93 |
| rs7929543 | C | A | 0.04 | 0.13 | 0.78 |
| rs8068804 | A | G | -0.25 | 0.12 | 0.03 |
| rs8108269 | G | T | 0.08 | 0.11 | 0.47 |
| rs825476 | T | C | 0.01 | 0.13 | 0.93 |
| rs835576 | C | T | -0.03 | 0.14 | 0.82 |
| rs840967 | C | A | -0.08 | 0.13 | 0.51 |
| rs849135 | G | A | 0.08 | 0.06 | 0.19 |
| rs853974 | T | C | -0.09 | 0.12 | 0.45 |
| rs9369425 | G | A | 0.21 | 0.12 | 0.09 |
| rs963740 | A | T | -0.05 | 0.15 | 0.75 |
| rs982077 | A | G | -0.06 | 0.14 | 0.69 |
| rs9844972 | C | G | 0.08 | 0.14 | 0.58 |
| rs9894220 | A | G | -0.06 | 0.11 | 0.59 |
| rs9940149 | G | A | -0.05 | 0.15 | 0.75 |
| **SNPs used as instrumental variables for various exposure-outcome pair and their respective Wald’s ratio estimate for the single-SNP MR analysis** | | | | | | | |

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| **Supplementary table 6. MR with BMI as the exposure and fat cell number as the outcome.** | | | | | | | | | |
| **Exposure** | **Outcome** | **MR method** | **OR** | **OR CI 95%** | | **SE** | **P** | **MR Steiger** | |
| **Lower** | **Upper** | **Causal direction** | **P** |
| Fat cell number | BMI | IVW | 0.98 | 0.93 | 1.04 | 0.03 | 0.54 | SANT | 7.34E-74 |
| MR Egger | 0.52 | 0.92 | 0.74 | 0.12 | 1.16 |
| Weighted median | 0.47 | 0.98 | 0.92 | 0.03 | 1.04 |
| Weighted mode | 0.5 | 0.97 | 0.89 | 0.04 | 1.05 |
| BMI | Fat cell number | IVW | 1.01 | 0.97 | 1.05 | 0.02 | 0.55 | FALSKT | 2.20E-78 |
| MR Egger | 1.01 | 0.91 | 1.12 | 0.05 | 0.85 |
| Weighted median | 1 | 0.94 | 1.07 | 0.03 | 0.91 |
| Weighted mode | 1.01 | 0.9 | 1.14 | 0.06 | 0.88 |
| Fat cell number | WHRadjBMI | Wald's ratio | 1.05 | 0.81 | 1.35 | 0.13 | 0.73 | SANT | 1.21E-08 |
| WHRadjBMI | Fat cell number | IVW | 1.02 | 0.91 | 1.14 | 0.06 | 0.72 | FALSKT | 1.16E-03 |
| MR Egger | 1.03 | 0.62 | 1.71 | 0.26 | 0.91 |
| Weighted median | 1.07 | 0.91 | 1.26 | 0.08 | 0.39 |
| Weighted mode | 1.09 | 0.86 | 1.38 | 0.12 | 0.48 |
| Fat cell number | T2D | Wald's ratio | 0.94 | 0.59 | 1.48 | 0.24 | 0.78 | SANT | 1.41E-08 |
| T2D | Fat cell number | IVW | 1 | 0.99 | 1.02 | 0.01 | 0.64 | SANT | 9.27E-01 |
| MR Egger | 1.01 | 0.96 | 1.06 | 0.02 | 0.64 |
| Weighted median | 1.01 | 0.97 | 1.04 | 0.02 | 0.72 |
| Weighted mode | 1 | 0.97 | 1.04 | 0.02 | 0.87 |
| Results for the bi-directional MR. | | |  |  |  |  |  |  |  |

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| **Supplementary table 7. BMI SNPs from GWAS associated with abdominal subcutaneous fat cell numbera** | | | | | | | | | | | | |  |  |  |
|  |  |  | **GWAS of fat cell number** | | | | | | | **Published GWAS of BMI** | | | | | |
| **consistent association** | **CHROM** | **ID** | **REF** | **ALT** | **A1** | **A1 FREQ** | **BETA** | **SE** | **P** | **PUBMEDID** | **RISK ALLELEb.** | **RISK ALLELE FREQUENCY** | **P-VALUE** | **OR or BETA** | **95% CI** |
| g. | 1 | rs72634819 | T | C | T | 0.26 | -0.01 | 0.01 | 0.045 | 30595370 |  |  | 1.00E-19 |  |  |
| g. | 1 | rs12144626 | C | T | T | 0.40 | 0.02 | 0.01 | 0.013 | 30595370 |  |  | 3.00E-17 |  |  |
| Yes | 1 | rs977747 | G | T | T | 0.39 | 0.02 | 0.01 | 0.010 | 25673413 | T | 0.403 | 2.00E-08 | 0.017 | increase |
| g. | 1 | rs7519259 | A | G | G | 0.45 | 0.01 | 0.01 | 0.049 | 30595370 |  |  | 3.00E-14 |  |  |
| No | 1 | rs1514177 | G | C | C | 0.45 | -0.02 | 0.01 | 0.007 | 30239722 | C | 0.426 | 8.00E-30 | 0.018 | increase |
| No | 1 | rs1514175 | G | A | A | 0.45 | -0.02 | 0.01 | 0.009 | 20935630 | A | 0.430 | 8.00E-14 | 0.070 | increase |
| No | 1 | rs1514174 | T | C | C | 0.47 | -0.01 | 0.01 | 0.023 | 26426971 | C | 0.430 | 3.00E-15 | 0.039 | increase |
| No | 1 | rs7526762 | G | A | A | 0.47 | -0.01 | 0.01 | 0.023 | 28448500 | A | 0.460 | 6.00E-08 | 0.022 | increase |
| No | 1 | rs7551507 | T | C | C | 0.47 | -0.01 | 0.01 | 0.028 | 28448500 | C | 0.443 | 4.00E-08 | 0.023 | increase |
| g. | 1 | rs12042908 | G | A | A | 0.47 | -0.01 | 0.01 | 0.030 | 30108127 | A |  | 1.00E-17 | 0.022 |  |
| No | 1 | rs12566985 | A | G | G | 0.47 | -0.01 | 0.01 | 0.024 | 25673413 | G | 0.446 | 3.00E-15 | 0.024 | increase |
| No | 1 | rs12041852 | A | G | G | 0.47 | -0.01 | 0.01 | 0.027 | 26604143 | G | 0.460 | 2.00E-10 | 0.046 | increase |
| No | 1 | rs7553348 | A | G | G | 0.47 | -0.01 | 0.01 | 0.021 | 26426971 | A | 0.558 | 4.00E-17 | 0.023 | decrease |
| g. | 1 | rs7553158 | A | G | G | 0.47 | -0.01 | 0.01 | 0.021 | 30595370 |  |  | 2.00E-19 |  |  |
| No | 1 | rs3843262 | A | T | A | 0.42 | -0.02 | 0.01 | 0.015 | 28448500 | A | 0.434 | 2.00E-08 | 0.029 | increase |
| g. | 1 | rs2798334 | C | T | T | 0.26 | 0.02 | 0.01 | 0.015 | 22589738 | C | 0.730 | 1.00E-06 |  |  |
| g. | 1 | rs6587552 | G | A | A | 0.26 | -0.02 | 0.01 | 0.016 | 30595370 |  |  | 3.00E-14 |  |  |
| No | 1 | rs6587553 | G | A | A | 0.20 | -0.02 | 0.01 | 0.046 | 30239722 | A | 0.197 | 5.00E-11 | 0.014 | increase |
| Yes | 1 | rs141845046 | T | C | T | 0.02 | 0.04 | 0.02 | 0.049 | 29273807 | T | 2.440 | 8.00E-18 | 0.048 | increase |
| No | 1 | rs2274319 | C | T | T | 0.35 | 0.01 | 0.01 | 0.048 | 30239722 | T | 0.346 | 2.00E-12 | 0.013 | decrease |
| Yes | 1 | rs199950 | T | C | C | 0.18 | 0.02 | 0.01 | 0.040 | 25378290 | G | 0.310 | 3.00E-06 | 1.000 | increase |
| No | 2 | rs2861685 | C | T | C | 0.39 | 0.02 | 0.01 | 0.014 | 30239722 | T | 0.586 | 8.00E-18 | 0.017 | increase |
| No | 2 | rs10196304 | C | A | C | 0.38 | 0.02 | 0.01 | 0.016 | 30239722 | A | 0.596 | 4.00E-16 | 0.014 | increase |
| Yes | 2 | rs4851057 | T | C | T | 0.10 | 0.03 | 0.01 | 0.008 | 30239722 | T | 0.127 | 3.00E-10 | 0.016 | increase |
| g. | 2 | rs3087523 | A | G | A | 0.10 | 0.03 | 0.01 | 0.006 | 30595370 |  |  | 1.00E-08 |  |  |
| g. | 2 | rs72851476 | C | A | C | 0.22 | -0.02 | 0.01 | 0.018 | 30595370 |  |  | 2.00E-09 |  |  |
| Yes | 2 | rs7560871 | A | G | A | 0.09 | 0.02 | 0.01 | 0.049 | 30239722 | A | 0.071 | 6.00E-11 | 0.022 | increase |
| g. | 2 | rs10208807 | T | C | T | 0.49 | 0.01 | 0.01 | 0.048 | 30595370 |  |  | 2.00E-09 |  |  |
| Yes | 3 | rs1452075 | T | C | C | 0.28 | -0.01 | 0.01 | 0.044 | 30239722 | T | 0.731 | 3.00E-12 | 0.013 | increase |
| g. | 3 | rs7630382 | T | C | C | 0.48 | 0.01 | 0.01 | 0.037 | 30595370 |  |  | 2.00E-17 |  |  |
| No | 3 | rs4273371 | C | T | T | 0.47 | 0.02 | 0.01 | 0.009 | 30239722 | T | 0.507 | 4.00E-12 | 0.011 | decrease |
| g. | 3 | rs1502172 | G | A | A | 0.36 | 0.02 | 0.01 | 0.008 | 22589738 | A | 0.340 | 3.00E-06 |  |  |
| g. | 3 | rs12634936 | C | T | C | 0.05 | 0.04 | 0.02 | 0.008 | 30595370 |  |  | 2.00E-10 |  |  |
| g. | 3 | rs6765877 | A | G | G | 0.43 | -0.01 | 0.01 | 0.045 | 30595370 |  |  | 2.00E-08 |  |  |
| Yes | 3 | rs11546878 | T | C | T | 0.18 | -0.02 | 0.01 | 0.017 | 29273807 | C | 0.835 | 2.00E-12 | 0.017 | increase |
| Yes | 4 | rs35851183 | G | A | G | 0.34 | 0.01 | 0.01 | 0.041 | 30239722 | A | 0.642 | 1.00E-09 | 0.012 | decrease |
| No | 4 | rs148636479 | T | A | T | 0.02 | 0.05 | 0.03 | 0.040 | 30239722 | A | 0.972 | 5.00E-10 | 0.039 | increase |
| Yes | 4 | rs1437842 | A | G | A | 0.44 | -0.02 | 0.01 | 0.001 | 30239722 | A | 0.491 | 8.00E-10 | 0.011 | decrease |
| g. | 5 | rs79125854 | C | A | C | 0.04 | 0.03 | 0.02 | 0.034 | 30595370 |  |  | 3.00E-11 |  |  |
| g. | 5 | rs2579040 | A | T | T | 0.26 | 0.02 | 0.01 | 0.004 | 30595370 |  |  | 7.00E-12 |  |  |
| Yes | 6 | rs11757278 | C | T | C | 0.34 | -0.01 | 0.01 | 0.038 | 30239722 | T | 0.696 | 7.00E-13 | 0.013 | increase |
| g. | 6 | rs9395520 | T | C | T | 0.35 | -0.01 | 0.01 | 0.044 | 30595370 |  |  | 2.00E-12 |  |  |
| g. | 6 | rs12203240 | C | T | C | 0.06 | 0.03 | 0.01 | 0.019 | 30595370 |  |  | 3.00E-09 |  |  |
| g. | 6 | rs2254336 | T | A | T | 0.49 | 0.02 | 0.01 | 0.019 | 30239722 | A | 0.476 | 3.00E-06 | 0.008 | decrease |
| Yes | 6 | rs9346455 | G | T | G | 0.10 | 0.02 | 0.01 | 0.027 | 26323598 | G | 0.087 | 6.00E-06 | 0.013 | increase |
| g. | 6 | rs13203153 | A | G | A | 0.20 | 0.02 | 0.01 | 0.036 | 30595370 |  |  | 8.00E-09 |  |  |
| g. | 6 | rs180963 | C | T | T | 0.50 | -0.02 | 0.01 | 0.007 | 30595370 |  |  | 2.00E-11 |  |  |
| No | 6 | rs12209887 | A | G | A | 0.49 | -0.02 | 0.01 | 0.007 | 30239722 | A | 0.463 | 2.00E-11 | 0.011 | increase |
| Yes | 6 | rs7752256 | A | G | A | 0.41 | -0.01 | 0.01 | 0.020 | 28552196 | A | 0.386 | 5.00E-07 | 0.035 | decrease |
| g. | 6 | rs13218383 | G | C | G | 0.33 | -0.02 | 0.01 | 0.002 | 30595370 |  |  | 1.00E-10 |  |  |
| Yes | 6 | rs9374842 | T | C | C | 0.24 | -0.02 | 0.01 | 0.007 | 26426971 | T | 0.745 | 8.00E-08 | 0.016 | increase |
| Yes | 6 | rs2357760 | A | G | G | 0.32 | -0.02 | 0.01 | 0.005 | 30239722 | A | 0.674 | 2.00E-16 | 0.014 | increase |
| Yes | 6 | rs2275215 | C | T | C | 0.28 | 0.01 | 0.01 | 0.040 | 20397748 | T | 0.730 | 4.00E-07 | 0.090 | decrease |
| g. | 6 | rs141198485 | D | I | D | 0.01 | 0.06 | 0.03 | 0.035 | 28552196 | A | 0.010 | 4.00E-06 | 0.185 | increase |
| Yes | 7 | rs9638713 | G | A | A | 0.02 | 0.07 | 0.02 | 0.002 | 30239722 | A | 0.027 | 9.00E-09 | 0.030 | increase |
| g. | 7 | rs2711111 | G | A | A | 0.42 | 0.01 | 0.01 | 0.046 | 30595370 |  |  | 2.00E-08 |  |  |
| Yes | 7 | rs1035010 | T | C | T | 0.25 | 0.02 | 0.01 | 0.021 | 30239722 | T | 0.252 | 2.00E-12 | 0.014 | increase |
| g. | 7 | rs6953344 | G | A | G | 0.24 | 0.02 | 0.01 | 0.015 | 30595370 |  |  | 1.00E-10 |  |  |
| No | 7 | rs6465468 | T | G | T | 0.29 | -0.01 | 0.01 | 0.038 | 26426971 | T | 0.308 | 3.00E-08 | 0.017 | increase |
| g. | 7 | rs12375196 | A | C | A | 0.46 | 0.01 | 0.01 | 0.044 | 30595370 |  |  | 2.00E-20 |  |  |
| Yes | 7 | rs11496125 | T | C | T | 0.46 | 0.01 | 0.01 | 0.041 | 30239722 | T | 0.405 | 9.00E-23 | 0.017 | increase |
| Yes | 7 | rs2299383 | T | C | T | 0.46 | 0.01 | 0.01 | 0.028 | 30239722 | T | 0.398 | 7.00E-23 | 0.016 | increase |
| Yes | 7 | rs2396625 | A | T | A | 0.41 | -0.02 | 0.01 | 0.004 | 30239722 | A | 0.418 | 3.00E-24 | 0.018 | decrease |
| Yes | 7 | rs1524445 | T | C | T | 0.41 | -0.02 | 0.01 | 0.004 | 30239722 | T | 0.416 | 3.00E-22 | 0.019 | decrease |
| g. | 8 | rs78686130 | T | C | T | 0.31 | 0.01 | 0.01 | 0.041 | 30595370 |  |  | 7.00E-09 |  |  |
| No | 8 | rs1982441 | T | G | T | 0.17 | -0.02 | 0.01 | 0.009 | 30239722 | T | 0.132 | 2.00E-11 | 0.017 | increase |
| No | 8 | rs890235 | G | A | G | 0.45 | 0.01 | 0.01 | 0.033 | 30239722 | A | 0.546 | 2.00E-09 | 0.010 | increase |
| g. | 8 | rs1808629 | A | G | G | 0.32 | -0.01 | 0.01 | 0.037 | 30595370 |  |  | 3.00E-24 |  |  |
| No | 8 | rs1459180 | G | T | T | 0.42 | 0.01 | 0.01 | 0.047 | 26426971 | G | 0.580 | 3.00E-09 | 0.027 | increase |
| g. | 8 | rs7838490 | A | G | A | 0.17 | -0.02 | 0.01 | 0.037 | 22417934 |  |  | 6.00E-08 |  |  |
| No | 8 | rs1383592 | A | G | A | 0.23 | -0.02 | 0.01 | 0.032 | 30239722 | A | 0.212 | 5.00E-09 | 0.012 | increase |
| No | 9 | rs1927702 | C | T | C | 0.41 | 0.01 | 0.01 | 0.048 | 19851299 | G | 0.420 | 6.00E-06 | 0.080 | increase |
| Yes | 9 | rs7864204 | G | A | A | 0.33 | -0.02 | 0.01 | 0.003 | 23192594 | A | 0.440 | 9.00E-07 | 0.040 | decrease |
| No | 9 | rs2134858 | T | C | C | 0.50 | -0.01 | 0.01 | 0.029 | 30239722 | T | 0.512 | 6.00E-12 | 0.012 | decrease |
| Yes | 9 | rs2777768 | G | A | G | 0.25 | -0.02 | 0.01 | 0.009 | 30239722 | A | 0.723 | 6.00E-10 | 0.012 | increase |
| g. | 9 | rs12376870 | A | G | A | 0.24 | 0.02 | 0.01 | 0.021 | 30595370 |  |  | 4.00E-09 |  |  |
| g. | 9 | rs6478538 | G | A | A | 0.34 | -0.01 | 0.01 | 0.028 | 30595370 |  |  | 1.00E-08 |  |  |
| Yes | 9 | rs4734 | G | T | G | 0.15 | 0.02 | 0.01 | 0.032 | 30239722 | T | 0.840 | 2.00E-13 | 0.018 | decrease |
| g. | 9 | rs113132247 | A | G | A | 0.15 | 0.02 | 0.01 | 0.028 | 30595370 |  |  | 3.00E-12 |  |  |
| Yes | 9 | rs7871866 | C | G | C | 0.15 | 0.02 | 0.01 | 0.027 | 30239722 | C | 0.160 | 8.00E-14 | 0.018 | increase |
| Yes | 10 | rs284860 | C | T | T | 0.44 | 0.01 | 0.01 | 0.038 | 29273807 | T | 0.411 | 9.00E-09 | 0.010 | increase |
| g. | 10 | rs7081254 | C | T | C | 0.14 | 0.02 | 0.01 | 0.039 | 30595370 |  |  | 3.00E-08 |  |  |
| Yes | 11 | rs2237892 | T | C | T | 0.07 | 0.04 | 0.01 | 0.001 | 24861553 | T | 0.360 | 9.00E-13 | 0.030 | increase |
| Yes | 11 | rs60808706 | A | G | A | 0.07 | 0.03 | 0.01 | 0.011 | 28892062 | A | 0.392 | 1.00E-38 | 0.046 | increase |
| No | 11 | rs17309930 | A | C | A | 0.23 | -0.02 | 0.01 | 0.025 | 26604143 | A | 0.210 | 1.00E-07 | 0.045 | increase |
| No | 11 | rs11555762 | T | C | T | 0.30 | -0.02 | 0.01 | 0.027 | 29273807 | T | 0.310 | 5.00E-14 | 0.014 | increase |
| g. | 11 | rs7115013 | T | C | T | 0.40 | 0.01 | 0.01 | 0.036 | 30595370 |  |  | 5.00E-11 |  |  |
| Yes | 11 | rs1458095 | T | C | T | 0.11 | -0.03 | 0.01 | 0.002 | 19851299 | G | 0.900 | 7.00E-06 | 0.190 | increase |
| No | 11 | rs349071 | A | G | G | 0.49 | -0.01 | 0.01 | 0.044 | 30239722 | A | 0.499 | 4.00E-13 | 0.014 | decrease |
| No | 11 | rs349088 | A | C | C | 0.49 | -0.02 | 0.01 | 0.012 | 30239722 | A | 0.478 | 4.00E-14 | 0.013 | decrease |
| g. | 11 | rs329651 | T | G | G | 0.14 | -0.02 | 0.01 | 0.030 | 30595370 |  |  | 1.00E-11 |  |  |
| Yes | 12 | rs7138803 | A | G | A | 0.42 | -0.01 | 0.01 | 0.031 | 26426971 | A | 0.387 | 2.00E-31 | 0.033 | increase |
| No | 12 | rs3205718 | T | C | T | 0.41 | -0.01 | 0.01 | 0.039 | 28892062 | T | 0.287 | 5.00E-10 | 0.023 | increase |
| No | 12 | rs7132908 | A | G | A | 0.42 | -0.01 | 0.01 | 0.043 | 30239722 | A | 0.390 | 5.00E-64 | 0.031 | increase |
| g. | 12 | rs1154752 | T | C | C | 0.38 | 0.01 | 0.01 | 0.029 | 30595370 |  |  | 9.00E-08 |  |  |
| Yes | 12 | rs7397059 | T | C | C | 0.40 | -0.01 | 0.01 | 0.040 | 30239722 | T | 0.560 | 6.00E-10 | 0.010 | increase |
| g. | 12 | rs6490030 | A | C | A | 0.39 | 0.01 | 0.01 | 0.021 | 30595370 |  |  | 2.00E-08 |  |  |
| g. | 12 | rs4304868 | A | C | A | 0.17 | 0.02 | 0.01 | 0.032 | 22589738 | A | 0.160 | 8.00E-06 |  |  |
| g. | 12 | rs3897102 | T | C | T | 0.39 | -0.01 | 0.01 | 0.028 | 30595370 |  |  | 2.00E-09 |  |  |
| g. | 13 | rs9544930 | A | G | A | 0.15 | 0.02 | 0.01 | 0.042 | 30595370 |  |  | 5.00E-08 |  |  |
| g. | 13 | rs11620399 | T | G | T | 0.07 | -0.03 | 0.01 | 0.024 | 22589738 | T | 0.040 | 5.00E-06 |  |  |
| No | 13 | rs8181823 | C | A | A | 0.23 | 0.02 | 0.01 | 0.023 | 30239722 | A | 0.234 | 4.00E-10 | 0.013 | decrease |
| g. | 13 | rs4435118 | A | G | G | 0.23 | 0.02 | 0.01 | 0.019 | 30595370 |  |  | 3.00E-10 |  |  |
| Yes | 14 | rs1491905 | C | T | T | 0.48 | 0.01 | 0.01 | 0.023 | 30239722 | T | 0.473 | 4.00E-18 | 0.015 | increase |
| g. | 14 | rs12885458 | G | T | T | 0.48 | 0.02 | 0.01 | 0.012 | 30595370 |  |  | 9.00E-19 |  |  |
| Yes | 14 | rs4900715 | A | G | G | 0.48 | 0.02 | 0.01 | 0.014 | 30239722 | A | 0.528 | 5.00E-18 | 0.015 | decrease |
| Yes | 14 | rs17105272 | T | C | T | 0.33 | 0.02 | 0.01 | 0.020 | 30239722 | T | 0.319 | 2.00E-10 | 0.012 | increase |
| g. | 15 | rs7175642 | G | T | T | 0.37 | 0.01 | 0.01 | 0.039 | 30595370 |  |  | 5.00E-10 |  |  |
| Yes | 15 | rs12914623 | C | G | C | 0.25 | -0.02 | 0.01 | 0.022 | 30239722 | C | 0.272 | 2.00E-16 | 0.016 | decrease |
| No | 16 | rs9302817 | G | T | G | 0.18 | 0.02 | 0.01 | 0.009 | 28892062 | G | 0.180 | 5.00E-08 | 0.016 | decrease |
| Yes | 16 | rs249293 | C | G | G | 0.28 | -0.01 | 0.01 | 0.040 | 30239722 | C | 0.699 | 3.00E-11 | 0.012 | increase |
| g. | 16 | rs4889606 | G | A | G | 0.40 | 0.02 | 0.01 | 0.015 | 30595370 |  |  | 4.00E-26 |  |  |
| g. | 16 | rs12716979 | G | T | G | 0.40 | 0.02 | 0.01 | 0.013 | 31453325 |  |  | 7.00E-24 |  |  |
| No | 16 | rs749670 | G | A | G | 0.40 | 0.01 | 0.01 | 0.023 | 29273807 | A | 0.624 | 7.00E-14 | 0.015 | increase |
| No | 16 | rs1564981 | A | G | A | 0.45 | 0.01 | 0.01 | 0.034 | 28892062 | G | 0.480 | 1.00E-08 | 0.018 | increase |
| g. | 16 | rs12920255 | T | C | T | 0.01 | 0.11 | 0.03 | 0.000 | 30595370 |  |  | 2.00E-08 |  |  |
| g. | 16 | rs2962466 | C | G | G | 0.37 | -0.02 | 0.01 | 0.014 | 30595370 |  |  | 1.00E-09 |  |  |
| g. | 16 | rs2317497 | T | A | T | 0.24 | -0.02 | 0.01 | 0.034 | 30595370 |  |  | 6.00E-10 |  |  |
| g. | 17 | rs2020942 | T | C | T | 0.42 | 0.02 | 0.01 | 0.016 | 30595370 |  |  | 4.00E-11 |  |  |
| Yes | 17 | rs17826219 | A | G | A | 0.12 | 0.02 | 0.01 | 0.019 | 28892062 | A | 0.090 | 3.00E-08 | 0.021 | increase |
| g. | 17 | rs62058023 | C | T | C | 0.10 | 0.02 | 0.01 | 0.048 | 30595370 |  |  | 2.00E-08 |  |  |
| g. | 17 | rs2586222 | G | A | A | 0.16 | -0.02 | 0.01 | 0.021 | 30595370 |  |  | 2.00E-08 |  |  |
| No | 17 | rs9910745 | T | C | T | 0.41 | 0.01 | 0.01 | 0.047 | 30239722 | T | 0.445 | 3.00E-26 | 0.018 | decrease |
| No | 17 | rs12939549 | G | A | G | 0.41 | 0.01 | 0.01 | 0.048 | 30239722 | A | 0.557 | 4.00E-28 | 0.018 | increase |
| No | 17 | rs12940622 | A | G | A | 0.41 | 0.01 | 0.01 | 0.041 | 25673413 | G | 0.575 | 2.00E-09 | 0.018 | increase |
| g. | 17 | rs11150745 | G | A | G | 0.31 | 0.02 | 0.01 | 0.029 | 30595370 |  |  | 3.00E-24 |  |  |
| g. | 18 | rs1791780 | A | G | A | 0.46 | 0.01 | 0.01 | 0.039 | 22589738 | G | 0.540 | 4.00E-07 |  |  |
| g. | 18 | rs7233512 | A | G | A | 0.34 | 0.02 | 0.01 | 0.008 | 30595370 |  |  | 4.00E-11 |  |  |
| No | 18 | rs11874040 | G | A | G | 0.34 | 0.02 | 0.01 | 0.012 | 30239722 | A | 0.714 | 2.00E-11 | 0.013 | increase |
| g. | 18 | rs12963831 | T | C | T | 0.05 | 0.04 | 0.01 | 0.020 | 30595370 |  |  | 6.00E-09 |  |  |
| No | 19 | rs7259325 | G | A | A | 0.48 | 0.01 | 0.01 | 0.042 | 30239722 | A | 0.483 | 4.00E-10 | 0.011 | decrease |
| g. | 20 | rs2327129 | A | G | G | 0.18 | 0.02 | 0.01 | 0.030 | 30595370 |  |  | 3.00E-09 |  |  |
| g. | 20 | rs4911382 | T | C | C | 0.37 | 0.01 | 0.01 | 0.026 | 30595370 |  |  | 8.00E-13 |  |  |
| No | 20 | rs6142067 | T | C | C | 0.37 | 0.01 | 0.01 | 0.032 | 30239722 | T | 0.602 | 4.00E-13 | 0.013 | increase |
| Yes | 21 | rs11702843 | A | G | A | 0.29 | 0.02 | 0.01 | 0.024 | 30239722 | A | 0.253 | 2.00E-09 | 0.012 | increase |
| g. | 22 | rs5771118 | C | T | T | 0.25 | 0.02 | 0.01 | 0.021 | 30595370 |  |  | 6.00E-09 |  |  |
| a. SNPs associated with BMI in GWAS catalogue were overlapped with SNPs nominally associated with abdominal fat cell number. Consistent association Yes = allele associated with increased risk of type 2 diabetes is associated with lower number of abdominal fat cells. | | | | | | | | | | | | | | | |
| b. The cell is left empty if no risk allele is reported in GWAS catalogue. | | | | | | | | | | | | | | | |
| d. Common allele | | | | | | | | | | | | | | | |
| e. If more tha one study has reported a specific SNP we have filtered for publications with alleles reported and for studies with large sample size. | | | | | | | | | | | | | | | |
| f. Only SNPs with consistent results for fat cell number and T2D risk have been chosen for eQTL analysis. | | | | | | | | | | | | | | | |
| g. Excluded due to unclear T2D-risk allele. | | | | | | | | | | | | | | | |