SUPPLEMENTARY DATA

## Genotyping

Genotyping of the Malmö Men and Malmö Training Intervention studies was done simultaneously at Lund University on HumanOmniExpress 12v1 C chips (Illumina, California, USA) and genotype calling was done with the Illumina Genome studio software. A total of 103403 and 81424 SNPs from the Malmö Men and Malmö Training Intervention studies failed to pass the QC. Details on exclusion criteria and a more detailed decomposition of reasons for failure are available in the supplement. Genotyping of the MuTHER samples was completed as part of the larger TwinsUK dataset (N~6000) and was done with a combination of Illumina arrays (HumanHap300, HumanHap610Q, 1M-Duo and 1.2MDuo 1M). Intensity data for each of the three arrays were pooled separately (with 1M-Duo and 1.2MDuo 1M pooled together), and genotypes were called with the Illuminus26 calling algorithm.

## Genotyping quality control

The following exclusion criteria were applied to samples from all three cohorts:
(i) sample call rate <98%; (ii) evidence of non-European ancestry as assessed by principal component analysis or multidimensionality scaling comparisons with HapMap populations; (iii) genome-wide heterozygosity outliers detected on a plot of missingness vs. heterozygosity at genome-wide level. In the Malmö cohorts, we also checked for (iv) gender mismatches using standard settings in PLINK; (v) relatedness between individuals using the IBD-test as implemented in PLINK, excluding individuals from pairs with pi_hat ≥0.2 or outliers based upon average pi_hat. In the MuTHER dataset, the (v) IBD-test was used to identify samples suggestive of sample identity errors. Exclusion criteria for SNPs were: (i) SNP call rate < 98% (Malmö) or SNP call rate < 97% (SNPs with MAF ≥ 5%) or SNP call rate <99% (SNPs with 1% ≤ MAF < 5%) (MuTHER); (ii) Hardy-Weinberg equilibrium test performed in a set of unrelated samples, p-values < $5.7*10^{-7}$ (SNPs with MAF ≥ 5%) or p-values < 0.0001 (SNPs with 1% ≤ MAF < 5%) (Malmö) or Hardy-Weinberg equilibrium test p-values < $5.7*10^{-7}$ (MuTHER); (iii) MAF < 1% assessed in a set of unrelated samples.

## Imputation

In each study, we imputed individual genotypes to 1000 Genomes data, to provide a common set of SNPs for analysis. Imputation was carried out using IMPUTE2 (https://mathgen.stats.ox.ac.uk/impute/impute_v2) and the June 2011 release of the 1000 Genomes Phase I panel was used as a reference panel (http://mathgen.stats.ox.ac.uk/impute/data_download_1000G_phase1_interim). The MuTHER samples were imputed as part of the TwinsUK dataset (N~6000) and pre-phasing of this data was carried out using IMPUTE2. The two Malmö cohorts were pre-phased using SHAPEIT (http://www.shapeit.fr). For all analyses, probabilistic genotypes were used for the subsequent analyses. After imputation, SNPs were filtered using a minor allele frequency (MAF) > 5% and an IMPUTE2 info value of >0.8.

## Gene expression

Due to differences in gene expression arrays used across studies, we adopted a gene-centric approach to our analyses, selecting probes in each study that mapped to the 7006 genes common to all three. All probes were mapped to NCBI build 37 of the Genome Browser and only uniquely mapping probes, with no mismatches and either an Ensembl or RefSeq ID, were kept for analysis. Probes encompassing a common SNP (MAF>5%) were excluded from all studies. Expression profiling of the MuTHER samples was performed using the Illumina Human HT-12 V3 BeadChips (Illumina Inc.), including more than 48000 probes. 200ng of total RNA was processed according to the protocol supplied by Illumina. All samples were randomized before array hybridization, and technical replicates were always hybridized on different BeadChips. Log2-transformed expression signals were normalized with quantile normalization of the replicates of each individual, followed by quantile normalization across all individuals. Post–quality-control expression profiles were obtained for 42 individuals. The Illumina probe annotations were mapped to build 37 using the R package (illuminaHumanv3.db). After applying the probe inclusion criteria above, 9633 probes were left in the analysis. Gene expression analysis in the Malmo Men cohort was assayed using the Affymetrix HG-U133a platform, while the Affymetrix custom array NUGOhs1a520180 was used for the Malmo Intervention cohort (Affymetrix Inc.). All probes were mapped to NCBI build 37 and annotated with R packages hgu133a.db and nugohs1a520180.db. Log2-transformed expression signals of both Malmo cohorts were normalized using RMA (Robust Multichip Average) expression measure (16).

### Annotation and enrichment analysis

The program SnpEff (1) was used to annotate and predict the effects of both our eQTL SNPs and all *cis* SNPs tested in our study. We assed the enrichment of low p-values closer to TSSs using the Exact Binomial Test implemented in the R statistical environment. Specifically, we performed an exact test of a null hypothesis about the probability of success in a Bernoulli experiment, in which the number of successes corresponds to the number of eQTL SNPs where the associated gene is the closest. We only tested eQTL SNPs where the eQTL gene and the nearest gene were probed by our meta-analysis (within 250kb of TSS). The Test of Equal or Given Proportions, implemented in R, was used to test the null hypothesis that the proportions (probabilities of success) are the same, or that they are equal certain given values. Specifically, this test was performed to test eQTL SNP enrichment for each gene functional unit and for functional RegulomeDB categories in comparison with the background of all cis SNPs tested.

### Gene expression analysis of publicly available data sets

Raw expression data for ten public microarray studies were retrieved from ArrayExpress (http://www.ebi.ac.uk/arrayexpress/), all based on the Affymetrix HG-U133+2 array platform (Table S5). Data normalization was carried out with Robust Probabilistic Averaging (RPA) (2) with probesets mapped to Ensembl gene identifiers using the R/Bioconductor package customCDF v.1.2.1 (3), and quality controlled using the arrayQualityMetrics v3.14.0 (4). None of the selected samples failed quality control. Differential expression between subjects with type 2 diabetes (T2D) and normoglycemic (NGT) individuals was estimated by meta-analysis of three datasets with full annotation for these groups: E-GEOD-18732, E-GEOD-19420, and E-GEOD-25462, including 102 T2D and 87 NGT samples. The datasets were individually normalized with RPA and meta-analysed using the geneMeta R/Bioconductor package [http://www.bioconductor.org/packages/release/bioc/html/GeneMeta.html]. Association to BMI was calculated by retrieving all samples within the seven selected datasets, with annotation for BMI (Table S3), from the HG-U133+2 arrays and normalized as a single dataset using RPA, followed by a linear regression for BMI adjusted for sex.

### Integration of genome-wide association data from MAGIC and DIAGRAM

To investigate whether our significant eQTL are enriched for associations to T2D and glycaemic traits, we did a lookup of our significant eQTLs SNPs in GWAS data from the DIAGRAM consortium for T2D (5), and from the MAGIC consortium for HOMA-IR (6), 2 hour glucose, 2 hour glucose adjusted for BMI, fasting insulin, fasting insulin adjusted for BMI, fasting glucose and fasting glucose adjusted for BMI (7). We did a binomial sign test to quantify the extent of the enrichment in each of the GWAS studies, using only independent eQTL SNPs, by calculating the probability of observing the number of GWAS SNPs we found with a p-value < 0.05 amongst our eQTL SNPs. We also noted any eQTL SNP that was associated with any of the DIAGRAM and MAGIC phenotypes with genome-wide significance.

**Supplementary Table 1.** Top SNP per gene for all significant (FDR<5%, p-value=1.96E-05) eQTLs identified in the meta-analysis. Information on bimodality of gene expression, distance of eQTL SNPs to transcription start sites (TSS), functional annotation of eQTL SNPs and previously reported eQTLs are also detailed.

| SNP (dbSNP137) | Gene | Allele1 | Allele2 | Weight | Zscore | Pvalue | Direction | Het_$I^2$ | Het_ChiSq | Het_Df | Het_Pval | FDR | Bimodal gene expression | SNP within which gene | gene in our gene list | SNP_pos - TSS | SNP relative transcript location | RegulomeDB score | eQTL seen before |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2238479 | CRYM | a | g | 95,5 | -11,309 | 1,18E-29 | --- | 52 | 8,337 | 2 | 0,01548 | 2,46E-22 |  | CRYM | yes | 13 134 | intron | 6 |  |
| rs2296805 | PEX6 | t | g | 95,5 | 9,065 | 1,24E-19 | +++ | 86,3 | 29,248 | 2 | 4,46E-07 | 2,90E-13 |  | GNMT | - | -2 852 | intron | 1f | yes |
| rs7810193 | SEC61G | t | c | 95,5 | -8,896 | 5,78E-19 | --- | 74,3 | 15,569 | 2 | 0,0004162 | 4,15E-13 |  | - | - | -68 068 | intergenic | 6 |  |
| rs251851 | ERAP2 | a | t | 95,5 | 8,434 | 3,35E-17 | +++ | 74,8 | 15,875 | 2 | 0,0003571 | 6,65E-12 |  | LNPEP | yes | 113 375 | intron | 6 | yes |
| rs138616686 | NQO2 | a | g | 95,5 | -8,233 | 1,83E-16 | --- | -67,6 | 2,387 | 2 | 0,3032 | 2,90E-11 |  | NQO2 | yes | 3 904 | intron |  | yes |
| rs12483950 | DDT | c | g | 95,5 | 8,09 | 5,96E-16 | +++ | 77,5 | 17,814 | 2 | 0,0001354 | 9,39E-11 |  | - | - | -17 378 | downstream | 5 | yes |
| rs10073049 | PFDN1 | a | c | 95,5 | -8,089 | 6,03E-16 | --- | 34,4 | 6,099 | 2 | 0,04739 | 9,44E-11 |  | CYSTM1 | - | -18 515 | intron | 6 |  |
| rs80317390 | NUDT2 | a | g | 95,5 | 7,988 | 1,37E-15 | +++ | 0 | 1,049 | 2 | 0,5918 | 1,25E-10 |  | - | - | 49 182 | downstream, upstream | 5 | yes |
| rs58655904 | LDHC | t | c | 95,5 | 7,792 | 6,60E-15 | +++ | 68,5 | 12,691 | 2 | 0,001755 | 3,97E-10 | yes | - | - | -1 662 | downstream, upstream | 4 |  |
| rs1955657 | SERPINA5 | a | g | 95,5 | 7,718 | 1,19E-14 | +++ | 0 | 0,642 | 2 | 0,7252 | 6,69E-10 |  | SERPINA3 | - | 24 918 | intron | 6 |  |
| rs7503161 | EIF5A | a | c | 95,5 | -7,418 | 1,19E-13 | --- | 70 | 13,347 | 2 | 0,001264 | 5,62E-09 |  | - | - | -2 353 | upstream |  | yes |
| rs2278022 | ATMIN | t | c | 95,5 | 7,357 | 1,89E-13 | +++ | 55 | 8,895 | 2 | 0,01171 | 8,74E-09 |  | ATMIN | yes | 6 035 | missense |  |  |
| rs2409494 | TMEM50B | t | c | 95,5 | -6,828 | 8,61E-12 | --- | 71,9 | 14,23 | 2 | 0,000813 | 2,57E-07 |  | IFNGR2, TMEM50B | yes | 3 616 | intron |  | yes |
| rs3863496 | TIMM22 | t | c | 95,5 | 6,756 | 1,42E-11 | +++ | 70,4 | 13,527 | 2 | 0,001155 | 4,02E-07 | yes | TIMM22 | yes | 2 807 | intron |  | yes |
| rs2268177 | CDC42 | a | t | 95,5 | 6,624 | 3,49E-11 | +-+ | 93,4 | 60,627 | 2 | 6,84E-14 | 9,17E-07 |  | CDC42 | yes | 36 291 | intron | 5 | yes |
| rs9859086 | LRRFIP2 | a | c | 95,5 | 6,593 | 4,30E-11 | +++ | 0 | 0,548 | 2 | 0,7605 | 1,11E-06 |  | LRRFIP2 | yes | 52 075 | intron |  | yes |
| rs4374997 | PIWIL2 | a | c | 95,5 | 6,544 | 6,00E-11 | +++ | 0 | 0,469 | 2 | 0,7909 | 1,44E-06 | yes | PIWIL2 | yes | 36 517 | intron | 5 | yes |
| rs1055138 | FAM149A | c | g | 95,5 | 6,488 | 8,69E-11 | +++ | 28,8 | 5,62 | 2 | 0,06021 | 2,05E-06 |  | CYP4V2 | - | 47 405 | missense | 4 |  |
| rs8076632 | SPATA20 | c | g | 95,5 | -6,475 | 9,46E-11 | --- | 18,1 | 4,885 | 2 | 0,08696 | 2,22E-06 |  | SPATA20 | yes | 1 500 | missense | 1f | yes |
| rs7008207 | EPHX2 | a | c | 95,5 | 6,356 | 2,07E-10 | +++ | -52,9 | 2,616 | 2 | 0,2704 | 4,50E-06 |  | EPHX2 | yes | 42 547 | intron | 6 |  |
| rs11089856 | H1F0 | a | c | 95,5 | -6,26 | 3,85E-10 | --- | 42,4 | 6,939 | 2 | 0,03114 | 8,11E-06 |  | GCAT | - | 4 671 | intron | 5 |  |
| rs178092 | SNAP29 | a | c | 95,5 | 6,25 | 4,11E-10 | +++ | 37,7 | 6,419 | 2 | 0,04038 | 8,51E-06 |  | - | - | 45 001 | intergenic |  | yes |
| rs403908 | CARKD | a | g | 95,5 | -6,101 | 1,05E-09 | --- | 12 | 4,547 | 2 | 0,103 | 1,88E-05 |  | CARKD | yes | 17 752 | intron | 5 | yes |
| rs10872251 | FABP7 | a | g | 95,5 | 6,097 | 1,08E-09 | +-+ | 87,3 | 31,5 | 2 | 1,45E-07 | 1,91E-05 | yes | FABP7 | yes | 3 449 | intron | 6 |  |
| rs10861347 | KIAA1033 | t | c | 95,5 | 6,091 | 1,12E-09 | +++ | 78 | 18,148 | 2 | 0,0001146 | 1,98E-05 |  | ALDH1L2 | - | -24 081 | intron | 3a |  |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2491020 | KIAA1279 | a | g | 95,5 | -6,085 | 1,17E-09 | --- | 37,2 | 6,368 | 2 | 0,04143 | 2,05E-05 | | - | - | 30 090 | downstream | 4 | yes |
| rs1131017 | RPS26 | c | g | 95,5 | -5,999 | 1,98E-09 | --- | 80,2 | 20,194 | 2 | 4,12E-05 | 3,28E-05 | | RPS26 | yes | 244 | 5´UTR | 4 | yes |
| rs4443587 | KLHDC10 | t | g | 95,5 | 5,95 | 2,67E-09 | +++ | 78,2 | 18,332 | 2 | 0,0001045 | 4,34E-05 | | - | - | 68 170 | downstream | 6 | |
| rs1271970 | RPP40 | a | g | 95,5 | -5,886 | 3,95E-09 | --- | 42,9 | 7,004 | 2 | 0,03014 | 6,22E-05 | | RPP40 | yes | -207 | downstream | 6 | yes |
| rs34270592 | AMFR | a | c | 95,5 | 5,884 | 3,99E-09 | +++ | 42,9 | 7,009 | 2 | 0,03006 | 6,27E-05 | | AMFR | yes | 36 315 | intron | 6 | |
| rs17137288 | TYW1 | a | g | 95,5 | -5,849 | 4,94E-09 | --- | 46,2 | 7,437 | 2 | 0,02427 | 7,65E-05 | | TYW1 | yes | 120 179 | intron | 6 | yes |
| rs11779069 | LY96 | t | c | 95,5 | -5,804 | 6,49E-09 | --- | 44 | 7,14 | 2 | 0,02815 | 9,88E-05 | | UBE2W | yes | -134 803 | intron | 6 | |
| rs8070763 | STAT3 | t | c | 95,5 | -5,784 | 7,29E-09 | --- | 67,9 | 12,467 | 2 | 0,001963 | 0,00010992 | | STAT3 | yes | 71 054 | intron | | |
| rs12433361 | ARG2 | a | t | 95,5 | 5,761 | 8,38E-09 | +++ | 32,4 | 5,92 | 2 | 0,05182 | 0,00012319 | | ARG2 | yes | 8 488 | intron | | yes |
| rs141761164 | PSMG1 | t | c | 95,5 | -5,732 | 9,90E-09 | --- | 0 | 1,483 | 2 | 0,4764 | 0,00014325 | | - | - | -18 253 | intergenic | | |
| rs7646106 | ARL8B | t | c | 95,5 | 5,694 | 1,24E-08 | +++ | 0 | 0,088 | 2 | 0,9572 | 0,00016938 | | EDEM1 | yes | 94 042 | 3´UTR | | |
| rs3762815 | PDCD6IP | a | g | 95,5 | 5,646 | 1,64E-08 | +++ | 70 | 13,34 | 2 | 0,001269 | 0,00021789 | | PDCD6IP | yes | 23 658 | intron | 5 | |
| rs17354693 | HYDIN | a | g | 95,5 | 5,595 | 2,21E-08 | +++ | 28,8 | 5,621 | 2 | 0,06019 | 0,0002602 | | MARVELD3 | - | 822 416 | intron | 5 | yes |
| rs7487568 | CHD4 | t | c | 95,5 | 5,593 | 2,24E-08 | +++ | 0 | 1,781 | 2 | 0,4105 | 0,00026276 | | ANO2 | - | -686 186 | intron | | |
| rs3816864 | LPPR2 | t | g | 95,5 | -5,582 | 2,37E-08 | --- | -12,9 | 3,542 | 2 | 0,1702 | 0,00027352 | | RAB3D | - | -19 541 | intron | 5 | yes |
| rs6537035 | ZNF330 | a | g | 95,5 | 5,581 | 2,39E-08 | +++ | 51,6 | 8,262 | 2 | 0,01607 | 0,00027491 | | RNF150 | - | -20 349 | intergenic | | |
| rs11131799 | AGA | a | g | 95,5 | -5,56 | 2,69E-08 | --- | -8,7 | 3,678 | 2 | 0,1589 | 0,00028666 | yes | AGA | yes | 11 450 | intron | 4 | yes |
| rs113671109 | MKRN2 | t | c | 95,5 | 5,553 | 2,81E-08 | +++ | 0 | 1,01 | 2 | 0,6034 | 0,00029275 | yes | MKRN2 | yes | 22 292 | intron | 6 | yes |
| rs10902201 | TMEM80 | a | g | 95,5 | -5,527 | 3,25E-08 | --- | 0 | 0,803 | 2 | 0,6693 | 0,0003311 | | DEAF1,<br>EPS8L2,<br>TMEM80 | yes | 8 968 | downstream,<br>upstream | 5 | |
| rs118129429 | PCDH8 | a | g | 95,5 | -5,526 | 3,29E-08 | --- | 0 | 1,128 | 2 | 0,5688 | 0,0003311 | | LECT1 | yes | -136 623 | intron | 6 | |
| rs11237443 | GAB2 | a | c | 95,5 | -5,519 | 3,41E-08 | --- | 0 | 1,832 | 2 | 0,4 | 0,00034023 | | GAB2 | yes | 78 754 | intron | | yes |
| rs4737751 | ARMC1 | a | g | 95,5 | 5,515 | 3,49E-08 | +++ | 57 | 9,298 | 2 | 0,009572 | 0,00034776 | | MTFR1 | yes | 85 543 | intron | | |
| rs10816774 | CTNNAL1 | a | g | 95,5 | -5,475 | 4,36E-08 | --- | 40,2 | 6,688 | 2 | 0,0353 | 0,00042674 | | EPB41L4B | yes | 232 151 | intron | 5 | |
| rs4747339 | CACNB2 | t | c | 95,5 | -5,453 | 4,95E-08 | --- | -15,2 | 3,473 | 2 | 0,1761 | 0,00045885 | | CACNB2 | yes | 161 818 | intron | | |
| rs35962983 | NR1D2 | t | c | 95,5 | -5,399 | 6,70E-08 | --- | 0 | 1,292 | 2 | 0,524 | 0,00059798 | | NR1D2 | yes | 24 432 | intron | | |
| rs6781329 | HRG | a | g | 95,5 | -5,386 | 7,20E-08 | --- | 0 | 1,443 | 2 | 0,486 | 0,0006349 | | - | - | -203 576 | intergenic | 6 | |
| rs9428015 | CCBL2 | a | g | 95,5 | -5,353 | 8,65E-08 | --- | 0 | 1,046 | 2 | 0,5928 | 0,00074335 | | PKN2 | - | -132 115 | intron | 5 | yes |
| rs114624166 | PRR16 | t | g | 95,5 | -5,316 | 1,06E-07 | --- | 41,2 | 6,799 | 2 | 0,03339 | 0,00086608 | | - | - | -35 365 | intergenic | 6 | yes |

# SUPPLEMENTARY DATA

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2433611 | GATM | a | c | 95,5 | -5,274 | 1,34E-07 | --- | 0 | 0,583 | 2 | 0,747 | 0,00102064 | | GATM | yes | 12 332 | intron | | |
| rs62092421 | TCF4 | t | g | 95,5 | 5,243 | 1,58E-07 | +++ | 54,6 | 8,809 | 2 | 0,01222 | 0,00113307 | | - | - | -23 468 | intergenic | 5 | |
| rs11668620 | TMEM161A | c | g | 95,5 | -5,242 | 1,59E-07 | --- | -98,2 | 2,018 | 2 | 0,3646 | 0,00114013 | | SLC25A42 | yes | -11 939 | intron | 5 | yes |
| rs12048758 | CNIH4 | a | g | 95,5 | 5,235 | 1,65E-07 | +++ | 0 | 0,137 | 2 | 0,934 | 0,00117581 | | WDR26 | yes | 34 454 | intron | | |
| rs111584059 | DOPEY2 | a | g | 95,5 | 5,229 | 1,70E-07 | +++ | -59,3 | 2,51 | 2 | 0,285 | 0,00120534 | | DOPEY2 | yes | 25 465 | intron | 6 | yes |
| rs150478765 | WDR41 | a | g | 95,5 | 5,217 | 1,82E-07 | +++ | 29,3 | 5,659 | 2 | 0,05906 | 0,00126536 | | WDR41 | yes | 70 691 | intron | | |
| rs62580498 | CDK5RAP2 | a | g | 95,5 | 5,192 | 2,08E-07 | +++ | 56,7 | 9,237 | 2 | 0,00987 | 0,00141436 | | CDK5RAP2 | yes | 8 349 | intron | 5 | yes |
| rs6689008 | NUCKS1 | t | c | 95,5 | -5,188 | 2,13E-07 | --- | 0 | 1,969 | 2 | 0,3735 | 0,00144529 | yes | SLC45A3 | - | -32 773 | intron | 4 | |
| rs9819419 | FYCO1 | a | g | 95,5 | -5,182 | 2,20E-07 | --- | 41,3 | 6,811 | 2 | 0,03319 | 0,00147624 | | - | - | 177 969 | intergenic | 5 | |
| rs7289655 | GSTT1 | a | c | 95,5 | -5,168 | 2,37E-07 | --- | 82,2 | 22,445 | 2 | 1,34E-05 | 0,00158174 | | - | - | -40 910 | intergenic | 5 | yes |
| rs9296398 | PRPH2 | t | c | 95,5 | 5,144 | 2,69E-07 | +++ | -29,2 | 3,095 | 2 | 0,2128 | 0,00177154 | | PRPH2 | yes | 9 346 | intron | | yes |
| rs6572656 | ATP5S | a | c | 95,5 | 5,116 | 3,13E-07 | +++ | 19,8 | 4,987 | 2 | 0,08263 | 0,00201754 | | L2HGDH | - | -3 727 | intron | 1b | yes |
| rs246771 | KCNIP1 | c | g | 95,5 | -5,113 | 3,18E-07 | --- | 16,4 | 4,783 | 2 | 0,09148 | 0,00204533 | | DOCK2 | yes | -658 847 | intron | 6 | |
| rs2490273 | ZNF593 | t | g | 95,5 | 5,112 | 3,19E-07 | +-+ | 78,3 | 18,405 | 2 | 0,0001008 | 0,00204985 | | - | - | -6 629 | downstream | 5 | |
| rs3120065 | OSGEP | t | c | 95,5 | -5,09 | 3,58E-07 | --- | 19,5 | 4,971 | 2 | 0,08329 | 0,00225477 | | OSGEP | yes | 4 506 | intron | | yes |
| rs2359614 | EIF2B2 | a | t | 95,5 | -5,059 | 4,22E-07 | -+- | 66,1 | 11,786 | 2 | 0,002758 | 0,00253322 | | TMED10 | - | 160 173 | intron | 5 | yes |
| rs7657455 | MFAP3L | c | g | 95,5 | 5,048 | 4,46E-07 | +++ | 80,6 | 20,608 | 2 | 3,35E-05 | 0,00266691 | | - | - | 51 096 | intergenic | 5 | yes |
| rs17818245 | COX4I1 | a | g | 95,5 | 5,042 | 4,60E-07 | +++ | -0,1 | 3,995 | 2 | 0,1357 | 0,00272888 | yes | - | - | 241 929 | intergenic | | |
| rs59633892 | CDKAL1 | t | c | 95,5 | -5,016 | 5,28E-07 | --- | 60,3 | 10,068 | 2 | 0,006514 | 0,00309946 | | - | - | 698 658 | downstream | | yes |
| rs10823398 | TSPAN15 | a | c | 95,5 | -5,003 | 5,64E-07 | --- | 0 | 0,028 | 2 | 0,9862 | 0,00329182 | | - | - | 59 138 | downstream | | |
| rs72940355 | FECH | a | g | 95,5 | -4,984 | 6,22E-07 | --- | 30,9 | 5,793 | 2 | 0,05523 | 0,00358652 | | FECH | yes | 20 685 | intron | 6 | |
| 17-44619118 | NSF | a | g | 95,5 | 4,98 | 6,35E-07 | +++ | 0 | 0,575 | 2 | 0,7502 | 0,00364945 | | LRRC37A2,<br>ARL17A | - | -48 916 | intron | | |
| rs35030877 | COG7 | a | g | 95,5 | -4,977 | 6,46E-07 | --- | -7,5 | 3,722 | 2 | 0,1555 | 0,00370233 | | - | - | -4 785 | downstream | 6 | |
| rs75000818 | SGCB | a | g | 95,5 | 4,973 | 6,59E-07 | +++ | 0 | 1,685 | 2 | 0,4306 | 0,00377028 | | - | - | 196 337 | intergenic | | |
| rs1899288 | CPNE3 | t | c | 95,5 | 4,967 | 6,82E-07 | +++ | 71,9 | 14,226 | 2 | 0,0008143 | 0,00388201 | | CPNE3 | yes | 38 671 | intron | | |
| rs148654891 | FIBP | a | g | 95,5 | -4,952 | 7,34E-07 | --- | -19,1 | 3,359 | 2 | 0,1865 | 0,00410278 | | - | - | -75 947 | intergenic | | |
| rs10200594 | WIPF1 | a | g | 95,5 | -4,95 | 7,43E-07 | --- | -72,9 | 2,313 | 2 | 0,3146 | 0,00410278 | | - | - | -12 812 | upstream | 4 | |
| rs8007801 | EML1 | c | g | 95,5 | 4,942 | 7,72E-07 | +++ | -10 | 3,638 | 2 | 0,1622 | 0,00422405 | | - | - | 393 986 | intergenic | 5 | |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs78701930 | HMBOX1 | t | c | 95,5 | 4,935 | 8,00E-07 | +++ | 57,3 | 9,358 | 2 | 0,009289 | 0,00436969 | | KIF13B | yes | 215 862 | intron | | |
| rs2520180 | C17orf48 | t | c | 95,5 | 4,931 | 8,17E-07 | +++ | -12,3 | 3,561 | 2 | 0,1685 | 0,00443719 | | SCO1 | - | -6 597 | intron | | yes |
| rs12086750 | PPIE | c | g | 95,5 | 4,924 | 8,48E-07 | +++ | 70,5 | 13,546 | 2 | 0,001144 | 0,0045865 | | PPIE | yes | 5 952 | intron | 5 | yes |
| rs11204702 | ARNT | a | c | 95,5 | 4,924 | 8,49E-07 | +++ | 80,3 | 20,316 | 2 | 3,88E-05 | 0,00459016 | | GOLPH3L | yes | -118 673 | intron | | |
| rs61752479 | AMPD1 | a | g | 95,5 | -4,922 | 8,57E-07 | --- | 64,8 | 11,369 | 2 | 0,003398 | 0,00460719 | | AMPD1 | yes | 15 535 | missense | | |
| rs35044129 | PDLIM5 | a | t | 95,5 | 4,917 | 8,79E-07 | +++ | 27,8 | 5,538 | 2 | 0,06273 | 0,00469205 | | PDLIM5 | yes | 139 807 | intron | 6 | |
| rs73181350 | PCK1 | c | g | 95,5 | 4,913 | 8,97E-07 | ++- | 90,8 | 43,446 | 2 | 3,68E-10 | 0,00476031 | | - | - | 512 190 | intergenic | | |
| 11-36166998 | TRAF6 | a | g | 95,5 | -4,905 | 9,34E-07 | --- | 60 | 10,009 | 2 | 0,006708 | 0,00493152 | | LDLRAD3 | - | -338 318 | intron | | |
| rs13267051 | CCDC25 | a | g | 95,5 | 4,896 | 9,76E-07 | +++ | 0 | 1,28 | 2 | 0,5273 | 0,00511079 | | CCDC25 | yes | 22 484 | intron | 5 | |
| rs935074 | SPSB1 | a | g | 95,5 | 4,876 | 1,08E-06 | +++ | 0 | 0,071 | 2 | 0,9652 | 0,00558444 | | CTNNBIP1 | yes | 577 027 | intron | 5 | |
| rs2297811 | CYP4B1 | t | c | 95,5 | 4,876 | 1,08E-06 | +++ | 53,5 | 8,603 | 2 | 0,01355 | 0,00559199 | | CYP4B1 | yes | 15 120 | intron | 6 | yes |
| rs56007403 | LGMN | t | c | 95,5 | -4,872 | 1,11E-06 | --- | 0 | 0,469 | 2 | 0,791 | 0,00568303 | yes | SLC24A4 | - | -247 484 | intron | 5 | |
| rs1218556 | LENEP | t | g | 95,5 | -4,861 | 1,17E-06 | --- | -1 | 3,96 | 2 | 0,1381 | 0,00594316 | | KCNN3 | yes | -144 949 | intron | 5 | |
| rs72670883 | ZCCHC11 | t | c | 95,5 | -4,85 | 1,23E-06 | --- | 0 | 0,529 | 2 | 0,7675 | 0,006232 | | SLC1A7 | - | 709 213 | intron | | |
| rs76611793 | CPVL | t | c | 95,5 | -4,836 | 1,32E-06 | --- | -5,2 | 3,802 | 2 | 0,1494 | 0,00661326 | | CPVL, CHN2 | yes | 146 872 | intron | 5 | |
| rs2543519 | MPST | a | g | 95,5 | -4,833 | 1,35E-06 | --- | 0 | 1,268 | 2 | 0,5305 | 0,00671862 | | TMPRSS6 | yes | 64 568 | intron | 5 | |
| rs147990233 | RPS16 | a | t | 95,5 | 4,823 | 1,41E-06 | +++ | 54,2 | 8,728 | 2 | 0,01273 | 0,00698077 | | SUPT5H | yes | 28 629 | intron | | yes |
| rs11119673 | KCNH1 | a | t | 95,5 | -4,812 | 1,49E-06 | --- | -65,7 | 2,414 | 2 | 0,2992 | 0,00729092 | | KCNH1 | yes | 381 442 | intron | 5 | |
| rs686618 | PAMR1 | t | c | 95,5 | -4,811 | 1,50E-06 | --- | 0 | 1,812 | 2 | 0,4042 | 0,00730873 | | - | - | 113 019 | intergenic | | |
| rs56019197 | TMEM110 | t | c | 95,5 | -4,81 | 1,51E-06 | --- | 0 | 0,264 | 2 | 0,8764 | 0,0073618 | | TMEM110 | yes | 3 982 | intron | | |
| rs2032890 | ERAP1 | a | c | 95,5 | 4,797 | 1,61E-06 | +++ | 65,3 | 11,523 | 2 | 0,003146 | 0,00778284 | | ERAP1 | yes | 10 965 | intron | | yes |
| rs1033181 | MYCT1 | a | g | 95,5 | -4,791 | 1,66E-06 | --- | 0 | 1,768 | 2 | 0,4131 | 0,00795101 | | ESR1 | yes | -824 208 | intron | | |
| rs2517145 | PDGFRL | a | c | 95,5 | -4,769 | 1,85E-06 | --- | 0 | 0,94 | 2 | 0,6251 | 0,00875921 | | PDGFRL | yes | 11 892 | intron | 6 | |
| rs11057389 | ABCB9 | t | c | 95,5 | -4,769 | 1,85E-06 | --- | 14,9 | 4,7 | 2 | 0,09537 | 0,00877216 | | DNAH10 | - | 968 605 | intron | | |
| rs6739468 | CRIPT | t | g | 95,5 | 4,761 | 1,93E-06 | +++ | 0 | 1,336 | 2 | 0,5127 | 0,00907339 | | CRIPT | yes | 5 056 | intron | | yes |
| rs113265714 | ALAS1 | a | g | 95,5 | 4,752 | 2,02E-06 | +++ | 0 | 1,976 | 2 | 0,3724 | 0,00941876 | | WDR82 | - | 77 071 | intron | | |
| rs7503584 | PNPO | a | g | 95,5 | -4,751 | 2,03E-06 | --- | 0 | 1,26 | 2 | 0,5327 | 0,00945275 | | CDK5RAP3 | - | 36 148 | intron | 1f | |
| rs2194762 | ABI2 | t | c | 95,5 | -4,743 | 2,11E-06 | --- | 44,3 | 7,181 | 2 | 0,02758 | 0,00980376 | | - | - | 841 720 | intergenic | | yes |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs11169368 | CSRNP2 | t | c | 95,5 | 4,74 | 2,14E-06 | +++ | -1,8 | 3,928 | 2 | 0,1403 | 0,00993279 | | - | - | -755 947 | intergenic | | |
| rs2114308 | MMP20 | a | g | 95,5 | 4,731 | 2,23E-06 | +++ | 0 | 1,267 | 2 | 0,5307 | 0,01029151 | | YAP1 | yes | -399 232 | intron | 6 | |
| rs8010851 | WARS | t | c | 95,5 | 4,73 | 2,25E-06 | +++ | 18,9 | 4,931 | 2 | 0,08495 | 0,0103516 | | WARS | yes | 24 516 | intron | 6 | |
| rs6443851 | MCCC1 | a | g | 95,5 | 4,726 | 2,29E-06 | +++ | 17,1 | 4,823 | 2 | 0,08968 | 0,01051029 | | MCCC1 | yes | 86 044 | upstream | 6 | |
| rs4268913 | TMBIM1 | a | g | 95,5 | -4,719 | 2,37E-06 | --- | 0 | 1,809 | 2 | 0,4047 | 0,01082444 | | PNKD | - | 39 959 | intron | 6 | |
| rs35273276 | ZBTB16 | t | g | 95,5 | 4,718 | 2,39E-06 | +++ | 0 | 0,419 | 2 | 0,8109 | 0,01086709 | yes | - | - | 936 909 | intergenic | | |
| rs10829610 | MGMT | a | g | 95,5 | 4,716 | 2,40E-06 | +++ | -55,2 | 2,577 | 2 | 0,2756 | 0,01093736 | | MGMT | yes | 165 615 | intron | 6 | yes |
| rs200680626 | B3GALNT1 | a | g | 95,5 | -4,713 | 2,44E-06 | --- | -63,5 | 2,447 | 2 | 0,2942 | 0,01109586 | yes | - | - | 848 718 | intergenic | | |
| rs12510251 | ING2 | a | g | 95,5 | -4,693 | 2,70E-06 | --- | -48,6 | 2,691 | 2 | 0,2604 | 0,01191568 | | ODZ3 | yes | -811 635 | intron | 6 | |
| rs11265398 | S100A9 | a | g | 95,5 | -4,69 | 2,73E-06 | --- | 89,1 | 36,632 | 2 | 1,11E-08 | 0,01203476 | | UBAP2L | yes | 905 328 | intron | 5 | |
| rs7534861 | MOSC1 | a | g | 95,5 | -4,689 | 2,75E-06 | --- | 0 | 1,138 | 2 | 0,566 | 0,01211015 | | MARC1 | - | 25 862 | intron | 3a | |
| rs75701904 | KLHL2 | t | c | 95,5 | -4,687 | 2,77E-06 | --- | -19,5 | 3,346 | 2 | 0,1877 | 0,01218174 | | - | - | 318 830 | intergenic | | |
| rs13275128 | MSRA | c | g | 95,5 | -4,685 | 2,80E-06 | --- | 0 | 1,129 | 2 | 0,5687 | 0,01233604 | | MSRA | yes | 170 804 | intron | 6 | yes |
| rs7725534 | MRPL22 | t | c | 95,5 | -4,68 | 2,87E-06 | --- | 0 | 0,802 | 2 | 0,6698 | 0,01259078 | | - | - | 403 490 | intergenic | | |
| rs10509573 | IFIT2 | t | c | 95,5 | -4,674 | 2,96E-06 | --- | 0 | 1,034 | 2 | 0,5963 | 0,01284854 | | - | - | 127 516 | downstream | 6 | |
| rs4383259 | ZNF415 | a | g | 95,5 | -4,667 | 3,06E-06 | --- | -22,1 | 3,275 | 2 | 0,1945 | 0,01323687 | | ZNF347 | - | 50 206 | intron | 5 | |
| rs140929099 | COL4A2 | t | c | 95,5 | 4,66 | 3,17E-06 | +++ | -33 | 3,007 | 2 | 0,2224 | 0,01364047 | | COL4A1 | - | -54 157 | intron | | |
| rs3903399 | RBBP5 | t | c | 95,5 | 4,657 | 3,20E-06 | +++ | 64 | 11,101 | 2 | 0,003886 | 0,01376838 | | CNTN2 | yes | -13 727 | intron | 5 | |
| rs79079466 | UNC5B | t | c | 95,5 | -4,656 | 3,23E-06 | --- | 0 | 1,909 | 2 | 0,385 | 0,01384725 | | CDH23 | - | 423 042 | intron | 4 | |
| rs79028889 | CNGA1 | a | g | 95,5 | 4,65 | 3,32E-06 | +++ | 0 | 0,282 | 2 | 0,8684 | 0,01408365 | | CORIN | yes | -319 732 | intron | 6 | |
| rs12978924 | C19orf57 | t | c | 95,5 | 4,645 | 3,41E-06 | +++ | 0 | 1,794 | 2 | 0,4077 | 0,01436931 | | CACNA1A | yes | -454 970 | intron | | |
| rs12206195 | SMPDL3A | a | c | 95,5 | -4,641 | 3,47E-06 | --- | 0 | 1,75 | 2 | 0,4169 | 0,01452832 | | - | - | 73 794 | intergenic | 6 | |
| rs10194503 | DHX57 | c | g | 95,5 | -4,632 | 3,63E-06 | --- | 0 | 0,203 | 2 | 0,9034 | 0,01495591 | | GALM | - | -104 393 | intron | 6 | |
| rs79294885 | NOP10 | a | c | 95,5 | -4,628 | 3,69E-06 | --- | -33,8 | 2,989 | 2 | 0,2244 | 0,01518109 | | SLC12A6 | yes | -4 046 | intron | 4 | |
| rs36094466 | FOXI1 | a | g | 95,5 | 4,628 | 3,70E-06 | +++ | 0 | 0,67 | 2 | 0,7154 | 0,01521513 | | - | - | 37 769 | intergenic | | |
| rs2216704 | PPWD1 | a | g | 95,5 | 4,623 | 3,79E-06 | +++ | 0 | 0,139 | 2 | 0,9329 | 0,01543906 | | - | - | -921 047 | intergenic | 6 | yes |
| rs78291594 | PRPSAP2 | a | g | 95,5 | 4,62 | 3,85E-06 | +++ | 0 | 0,428 | 2 | 0,8075 | 0,01562557 | | FAM18B1 | - | -69 161 | intron | 5 | |
| rs10751259 | UVRAG | t | c | 95,5 | 4,619 | 3,86E-06 | +++ | 0,2 | 4,006 | 2 | 0,1349 | 0,01568339 | | LRRC32 | yes | 730 661 | intron | 5 | |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs114026170 | PPP2R2D | c | g | 95,5 | 4,616 | 3,92E-06 | +++ | 66,6 | 11,968 | 2 | 0,002519 | 0,01585021 | | PPP2R2D | yes | 18 892 | intron | 5 | |
| rs62179167 | AGPS | t | c | 95,5 | -4,616 | 3,92E-06 | --- | -80,8 | 2,213 | 2 | 0,3307 | 0,01585117 | | OSBPL6 | - | 902 043 | intron | 6 | |
| rs7534670 | USP1 | a | g | 95,5 | -4,613 | 3,97E-06 | --- | 0 | 0,969 | 2 | 0,616 | 0,01602956 | | ALG6 | yes | 963 636 | intron | 6 | |
| rs12653735 | COMMD10 | a | c | 95,5 | -4,605 | 4,13E-06 | --- | 0 | 0,648 | 2 | 0,7234 | 0,01646018 | | COMMD10 | yes | 301 808 | intron | 5 | |
| rs8062453 | DEXI | t | g | 95,5 | -4,603 | 4,16E-06 | --- | 0 | 0,247 | 2 | 0,8839 | 0,01650584 | yes | LITAF | yes | 651 635 | intron | | |
| rs4740353 | C9orf78 | t | c | 95,5 | -4,602 | 4,18E-06 | --- | -7,6 | 3,718 | 2 | 0,1558 | 0,01650584 | | HMCN2 | - | 658 805 | intron | 5 | |
| rs62223782 | DYRK1A | t | c | 95,5 | 4,6 | 4,24E-06 | +++ | -94,1 | 2,061 | 2 | 0,3569 | 0,01655952 | | HLCS | yes | -573 641 | intron | | |
| rs8063558 | ABAT | t | c | 95,5 | -4,596 | 4,30E-06 | --- | -15,5 | 3,463 | 2 | 0,177 | 0,01676633 | | - | - | -1 012 732 | intergenic | 6 | |
| rs1887353 | TPP2 | a | g | 95,5 | -4,594 | 4,34E-06 | --- | -25,4 | 3,19 | 2 | 0,2029 | 0,01687961 | | - | - | -12 082 | intergenic | 5 | |
| rs56039808 | NFKBIB | t | c | 95,5 | 4,592 | 4,39E-06 | +++ | 0 | 1,832 | 2 | 0,4001 | 0,01704252 | yes | SIPA1L3 | yes | -827 407 | intron | 5 | |
| rs184005941 | THAP7 | a | c | 95,5 | -4,592 | 4,39E-06 | --- | 0 | 0,439 | 2 | 0,8031 | 0,0170478 | | MAPK1 | yes | 774 756 | intron | | |
| rs1036951 | SLC22A3 | c | g | 95,5 | 4,591 | 4,41E-06 | +++ | 0 | 0,456 | 2 | 0,7963 | 0,01712683 | | IGF2R | yes | -309 342 | intron | | yes |
| rs7334264 | MPHOSPH8 | c | g | 95,5 | 4,591 | 4,42E-06 | +++ | 0 | 1,483 | 2 | 0,4765 | 0,01715148 | | - | - | 641 645 | intergenic | | |
| rs2332313 | COX11 | t | g | 95,5 | -4,588 | 4,48E-06 | --- | 0 | 1,67 | 2 | 0,4339 | 0,01735707 | | TOM1L1 | - | -10 433 | intron | 5 | |
| rs2811555 | GLUL | a | g | 95,5 | -4,587 | 4,49E-06 | --- | -83,6 | 2,178 | 2 | 0,3365 | 0,01738867 | | NMNAT2 | yes | 958 681 | intron | 6 | |
| rs9955053 | WDR7 | a | t | 95,5 | -4,587 | 4,51E-06 | --- | -21,9 | 3,281 | 2 | 0,1939 | 0,0174325 | | - | - | 382 825 | downstream | 6 | |
| rs74646715 | MRS2 | a | g | 95,5 | 4,585 | 4,54E-06 | +++ | -59,5 | 2,507 | 2 | 0,2855 | 0,01755546 | | MRS2 | yes | 18 587 | intron | 6 | |
| rs2232669 | POLR1D | t | c | 95,5 | -4,579 | 4,66E-06 | --- | -62 | 2,469 | 2 | 0,291 | 0,01796695 | | POLR1D | yes | -420 | intron | 4 | |
| rs12171327 | EXOSC9 | a | g | 95,5 | 4,577 | 4,71E-06 | +++ | 0 | 1,981 | 2 | 0,3715 | 0,01811298 | | - | - | -70 791 | intergenic | 6 | |
| rs7851652 | LHX3 | t | c | 95,5 | -4,575 | 4,76E-06 | --- | -85,4 | 2,157 | 2 | 0,34 | 0,01826053 | | - | - | -574 982 | downstream | 6 | |
| rs61946623 | FAM48A | a | g | 95,5 | -4,574 | 4,78E-06 | --- | 9 | 4,397 | 2 | 0,111 | 0,01832717 | | - | - | 530 953 | intergenic | 5 | |
| rs9535526 | RNASEH2B | t | c | 95,5 | -4,573 | 4,82E-06 | --- | 0 | 0,784 | 2 | 0,6756 | 0,01843265 | | RNASEH2B | yes | 632 | intron | 1b | yes |
| rs4938447 | PHLDB1 | a | c | 95,5 | 4,569 | 4,90E-06 | +++ | 0 | 1,372 | 2 | 0,5037 | 0,01869764 | | - | - | -720 862 | intergenic | | |
| rs78358857 | DLGAP1 | t | c | 95,5 | -4,568 | 4,92E-06 | --- | 0 | 1,612 | 2 | 0,4467 | 0,0187572 | | DLGAP1 | yes | 571 525 | intron | 6 | |
| rs7782374 | CHN2 | t | c | 95,5 | -4,565 | 5,00E-06 | --- | -6,7 | 3,75 | 2 | 0,1534 | 0,01902723 | | CHN2 | yes | -26 428 | intron | 5 | |
| rs6069006 | BCAS1 | a | g | 95,5 | 4,564 | 5,03E-06 | +++ | 0 | 0,313 | 2 | 0,8551 | 0,01912073 | | - | - | 900 116 | intergenic | 5 | |
| rs4254466 | PPP1CB | a | g | 95,5 | -4,558 | 5,16E-06 | --- | 50,2 | 8,027 | 2 | 0,01807 | 0,01952426 | | PPP1CB, SPDYA | yes | 34 436 | intron | | |
| rs2922932 | DLX5 | a | g | 95,5 | -4,555 | 5,23E-06 | --- | -14,7 | 3,488 | 2 | 0,1748 | 0,01973571 | | - | - | -254 891 | intergenic | 5 | |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs11168700 | C12orf41 | a | c | 95,5 | -4,552 | 5,31E-06 | --- | -21,8 | 3,284 | 2 | 0,1936 | 0,01991291 | | CCNT1 | yes | 34 204 | intron | 2b | |
| rs72844739 | CD151 | c | g | 95,5 | -4,548 | 5,41E-06 | --- | 44,8 | 7,24 | 2 | 0,02678 | 0,02026703 | | DEAF1 | yes | -175 399 | intron | 5 | |
| 4-7837218 | KIAA0232 | a | g | 95,5 | 4,543 | 5,54E-06 | +++ | 0 | 1,699 | 2 | 0,4275 | 0,02070535 | | AFAP1 | - | 1 052 760 | intron | | |
| rs2890662 | KLHL5 | a | g | 95,5 | -4,543 | 5,55E-06 | --- | 0 | 1,44 | 2 | 0,4867 | 0,02075025 | | KLHL5 | yes | 53 929 | intron | 6 | |
| rs7920643 | LARP4B | a | t | 95,5 | -4,538 | 5,69E-06 | --- | 0 | 0,749 | 2 | 0,6875 | 0,02114456 | | - | - | 999 011 | intergenic | 5 | |
| rs36073297 | OPA3 | t | c | 95,5 | 4,538 | 5,69E-06 | +++ | 0 | 1,122 | 2 | 0,5706 | 0,02114822 | | MARK4 | yes | -292 775 | intron | 5 | |
| rs143844677 | CDC14B | t | c | 95,5 | -4,535 | 5,76E-06 | --- | 0 | 1,275 | 2 | 0,5285 | 0,02131638 | | - | - | -401 822 | intergenic | | |
| rs71455663 | FLJ13224 | a | t | 95,5 | 4,533 | 5,82E-06 | +++ | -73,5 | 2,306 | 2 | 0,3157 | 0,02148959 | | DENND5B | - | 82 812 | intron | 6 | |
| rs8003968 | ESRRB | a | c | 95,5 | -4,532 | 5,85E-06 | --- | 0 | 1,265 | 2 | 0,5313 | 0,02158124 | | ESRRB | yes | -45 606 | intron | 6 | |
| rs6065703 | JPH2 | t | c | 95,5 | -4,527 | 5,99E-06 | --- | -24 | 3,225 | 2 | 0,1994 | 0,02202319 | | - | - | -3 388 | downstream | 4 | |
| rs9525501 | C13orf15 | c | g | 95,5 | 4,525 | 6,05E-06 | +++ | 0 | 1,059 | 2 | 0,5889 | 0,02221089 | | - | - | 25 148 | intergenic | | |
| rs115929263 | KIF1A | c | g | 95,5 | -4,524 | 6,06E-06 | --- | 0 | 0,2 | 2 | 0,9047 | 0,02221089 | | NDUFA10 | yes | -797 962 | intron | 6 | |
| rs74676427 | MRPL42 | a | g | 95,5 | 4,522 | 6,13E-06 | +++ | 0 | 0,968 | 2 | 0,6164 | 0,02243002 | | - | - | 625 267 | intergenic | 5 | |
| rs58809197 | ELAC2 | a | g | 95,5 | -4,52 | 6,18E-06 | --- | 0 | 1,739 | 2 | 0,4192 | 0,02254977 | | ELAC2 | yes | 25 332 | intron | 6 | yes |
| rs10271869 | GIMAP4 | t | c | 95,5 | 4,517 | 6,26E-06 | +++ | 0 | 1,779 | 2 | 0,4109 | 0,02278997 | | - | - | -211 469 | intergenic | 4 | |
| rs116939934 | ZNF550 | a | g | 95,5 | -4,514 | 6,37E-06 | --- | -40,3 | 2,851 | 2 | 0,2404 | 0,02313126 | | - | - | -263 286 | upstream | 5 | |
| rs581508, rs60228684 | OPN3 | c | g | 95,5 | 4,513 | 6,39E-06 | +++ | -26,8 | 3,154 | 2 | 0,2066 | 0,02320349 | | OPN3 | yes | 44 950 | intron | 4 | |
| rs12711940 | RALB | a | t | 95,5 | 4,509 | 6,51E-06 | +++ | 39,1 | 6,563 | 2 | 0,03757 | 0,02357759 | | RALB | yes | 25 973 | intron | 6 | yes |
| rs4351362 | FLNC | c | g | 95,5 | 4,505 | 6,64E-06 | +++ | 30,2 | 5,732 | 2 | 0,05691 | 0,02388425 | | - | - | 937 884 | downstream | 6 | |
| rs2810715 | MIPEP | c | g | 95,5 | -4,504 | 6,67E-06 | --- | 62,8 | 10,743 | 2 | 0,004647 | 0,0239468 | | - | - | 201 789 | intron | | |
| rs73164728 | MTMR3 | a | g | 95,5 | -4,504 | 6,68E-06 | --- | 27,1 | 5,489 | 2 | 0,06428 | 0,02398218 | | MTMR3, HORMAD2 | yes | 256 412 | intron | 6 | |
| rs1358085 | TMOD3 | a | g | 95,5 | -4,503 | 6,70E-06 | --- | 0 | 0,9 | 2 | 0,6377 | 0,02402141 | | - | - | 702 239 | upstream | | |
| rs10503718 | BIN3 | t | c | 95,5 | -4,503 | 6,71E-06 | --- | 0 | 0,058 | 2 | 0,9712 | 0,0240506 | | PEBP4 | - | 134 650 | intron | 4 | |
| rs246228 | ABCC1 | a | c | 95,5 | -4,502 | 6,72E-06 | --+ | 71,7 | 14,155 | 2 | 0,0008441 | 0,0240572 | | ABCC1 | yes | 92 209 | intron | 2b | |
| rs12456603 | OSBPL1A | c | g | 95,5 | -4,495 | 6,96E-06 | --- | 77,3 | 17,654 | 2 | 0,0001467 | 0,02463214 | | OSBPL1A | yes | 23 409 | intron | 5 | yes |
| rs9997795 | ANK2 | a | g | 95,5 | 4,49 | 7,14E-06 | +++ | 0 | 0,044 | 2 | 0,978 | 0,02463511 | | - | - | -351 220 | intergenic | | |
| rs60208411 | PIK3CD | t | c | 95,5 | 4,479 | 7,50E-06 | +++ | 0 | 1,605 | 2 | 0,4482 | 0,02507555 | | UBE4B | yes | 434 591 | intron | | |
| rs5050 | COG2 | t | g | 95,5 | 4,477 | 7,59E-06 | +++ | -62,9 | 2,455 | 2 | 0,293 | 0,02531486 | | AGT | yes | 71 685 | 5´UTR | 1a | |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs76826033 | FHOD3 | a | g | 95,5 | -4,475 | 7,64E-06 | --- | -24 | 3,226 | 2 | 0,1993 | 0,02544942 | yes | FHOD3 | yes | 114 632 | intron | | |
| rs4547172 | PFKM | a | g | 95,5 | -4,474 | 7,69E-06 | --- | 0 | 1,272 | 2 | 0,5294 | 0,02554614 | | - | - | -161 233 | intergenic | 5 | |
| rs2854181 | FTSJ3 | t | c | 95,5 | 4,474 | 7,69E-06 | +++ | 63,5 | 10,974 | 2 | 0,00414 | 0,02554871 | | - | - | 72 495 | downstream | | |
| rs10920310 | TIMM17A | c | g | 95,5 | 4,473 | 7,71E-06 | +++ | 0 | 0,553 | 2 | 0,7585 | 0,02561107 | | - | - | 73 323 | intergenic | 5 | yes |
| rs2273630 | KHNYN | t | c | 95,5 | 4,47 | 7,81E-06 | +++ | -31,1 | 3,05 | 2 | 0,2176 | 0,02574839 | | CBLN3, KHNYN | yes | 205 | 5´UTR, upstream | 2b | |
| rs2239325 | ABCC6 | a | c | 95,5 | -4,469 | 7,85E-06 | --- | -11,4 | 3,589 | 2 | 0,1662 | 0,02579527 | | ABCC6 | yes | 26 710 | intron | 6 | |
| rs4839353 | CSDE1 | t | g | 95,5 | 4,464 | 8,03E-06 | +++ | -0,2 | 3,991 | 2 | 0,136 | 0,02627248 | yes | - | - | -658 256 | intergenic | | |
| rs72669230 | MEAF6 | a | g | 95,5 | 4,461 | 8,16E-06 | +++ | 0 | 1,297 | 2 | 0,5227 | 0,02667234 | | - | - | 975 076 | intergenic | | |
| rs66708929 | RPL39L | a | c | 95,5 | 4,46 | 8,20E-06 | +++ | -72,3 | 2,322 | 2 | 0,3132 | 0,02675358 | | DGKG | - | -977 076 | downstream | 5 | |
| rs6982560 | ANXA13 | c | g | 95,5 | -4,458 | 8,27E-06 | --- | -33,1 | 3,004 | 2 | 0,2227 | 0,02687986 | | - | - | 734 981 | intergenic | | |
| rs62310596 | CLOCK | a | g | 95,5 | 4,456 | 8,35E-06 | +++ | 0 | 1,104 | 2 | 0,5759 | 0,02704948 | | KIAA1211 | - | 816 257 | intron | | |
| rs4736320 | LY6D | a | t | 95,5 | 4,455 | 8,38E-06 | +++ | -6,2 | 3,765 | 2 | 0,1522 | 0,02713658 | | GML, CYP11B2 | yes | 128 064 | intron | 5 | |
| rs10948137 | RANBP9 | t | c | 95,5 | 4,452 | 8,51E-06 | +++ | 0 | 0,263 | 2 | 0,8769 | 0,02737097 | | - | - | -961 440 | intergenic | 6 | |
| rs12363722 | UNC93B1 | a | c | 95,5 | 4,444 | 8,84E-06 | +++ | 0 | 0,37 | 2 | 0,8312 | 0,02804576 | | PPP6R3 | - | 477 717 | intron | 5 | |
| rs5805912, rs62941261 | CLDN10 | a | t | 95,5 | -4,441 | 8,96E-06 | --- | 0 | 0,234 | 2 | 0,8895 | 0,0283433 | | ABCC4 | yes | -194 420 | intron | 6 | |
| rs2690923 | CUX1 | a | g | 95,5 | 4,436 | 9,17E-06 | +++ | 0 | 0,13 | 2 | 0,9371 | 0,02878093 | yes | - | - | -24 313 | intergenic | | |
| rs28422906 | SLC25A22 | t | c | 95,5 | -4,436 | 9,17E-06 | --- | 0 | 1,344 | 2 | 0,5106 | 0,02878093 | | AP2A2 | yes | 205 161 | intron | 5 | |
| rs654533 | CD3E | t | c | 95,5 | -4,434 | 9,25E-06 | --- | 0 | 0,375 | 2 | 0,8292 | 0,02898132 | | - | - | 412 514 | intergenic | 5 | |
| rs12702047 | GPER | a | g | 95,5 | 4,432 | 9,35E-06 | +++ | 0 | 0,682 | 2 | 0,7109 | 0,02926389 | yes | C7orf50, GPER | yes | 6 278 | 3´UTR, intron | 4 | |
| rs10752954 | IVNS1ABP | a | g | 95,5 | -4,425 | 9,64E-06 | --- | 43 | 7,02 | 2 | 0,0299 | 0,02982545 | | - | - | 146 861 | intergenic | 5 | |
| rs4781128 | LITAF | a | g | 95,5 | 4,425 | 9,65E-06 | +++ | -64,5 | 2,431 | 2 | 0,2965 | 0,0298506 | | LITAF | yes | 65 994 | intron | 2b | |
| rs7616890 | ABHD5 | a | g | 95,5 | -4,421 | 9,82E-06 | --- | 0 | 1,149 | 2 | 0,5629 | 0,02992474 | | ANO10 | yes | -124 878 | intron | | |
| rs13195767 | CDYL | t | c | 95,5 | 4,421 | 9,85E-06 | +++ | -6,5 | 3,757 | 2 | 0,1528 | 0,02994204 | | - | - | -374 735 | intergenic | 5 | yes |
| rs4351859 | OAS1 | a | c | 95,5 | 4,419 | 9,94E-06 | +++ | -55,5 | 2,572 | 2 | 0,2764 | 0,03019668 | | - | - | 707 146 | intergenic | 6 | |
| rs112042189 | OXCT1 | t | c | 95,5 | 4,413 | 1,02E-05 | +++ | 0 | 0,136 | 2 | 0,934 | 0,03075482 | | - | - | 171 231 | upstream | | |
| rs2249888 | FN3KRP | a | g | 95,5 | 4,412 | 1,03E-05 | +++ | 58,9 | 9,741 | 2 | 0,007668 | 0,03089098 | | FN3KRP | yes | 1 157 | intron | 1f | yes |
| rs677991 | TULP3 | t | c | 95,5 | -4,404 | 1,06E-05 | --- | 38,3 | 6,488 | 2 | 0,03901 | 0,03178429 | | TSPAN9 | - | 358 751 | intron | 5 | |
| rs145785014 | FUS | t | c | 95,5 | 4,404 | 1,06E-05 | +++ | -6,4 | 3,761 | 2 | 0,1525 | 0,03180505 | | - | - | 398 896 | intergenic | | |

# SUPPLEMENTARY DATA

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs10249186 | INSIG1 | a | t | 95,5 | 4,401 | 1,08E-05 | +++ | 0 | 0,825 | 2 | 0,6618 | 0,03215427 | DPP6 | yes | -916 802 | intron | 6 |
| rs9301945 | ABCC4 | t | c | 95,5 | 4,4 | 1,08E-05 | +++ | 0 | 0,415 | 2 | 0,8126 | 0,03230546 | GPC6 | - | -796 774 | intron | 6 |
| rs28372678 | BAIAP3 | a | g | 95,5 | -4,394 | 1,11E-05 | --- | -53,2 | 2,611 | 2 | 0,2711 | 0,03274606 | SPSB3 | yes | 449 010 | upstream | 2a |
| rs139621578 | KIAA0922 | a | g | 95,5 | 4,391 | 1,13E-05 | +++ | 27,3 | 5,499 | 2 | 0,06395 | 0,03305217 | - | - | -478 849 | intergenic | |
| rs1391102 | ATP2C2 | c | g | 95,5 | -4,389 | 1,14E-05 | --- | -85,9 | 2,151 | 2 | 0,3411 | 0,03328447 | CRISPLD2 | yes | 541 168 | downstream | |
| rs658065 | FAM8A1 | a | t | 95,5 | -4,384 | 1,17E-05 | --- | -78,6 | 2,239 | 2 | 0,3264 | 0,03391939 | - | - | -808 814 | intergenic | 6 |
| rs9907526 | ITGB4 | c | g | 95,5 | 4,381 | 1,18E-05 | +++ | 0 | 0,779 | 2 | 0,6774 | 0,03420253 | PRPSAP1 | yes | 597 662 | intron | |
| rs10792434 | MEN1 | a | g | 95,5 | 4,38 | 1,19E-05 | +++ | -27,8 | 3,13 | 2 | 0,2091 | 0,03432872 | AP003774.4 | - | -352 575 | 3´UTR | |
| rs118122922 | POLDIP3 | t | g | 95,5 | -4,378 | 1,20E-05 | --- | -6,9 | 3,741 | 2 | 0,1541 | 0,03445416 | MPPED1 | - | 921 316 | intron | 5 |
| rs4461 | TOM1 | a | g | 95,5 | 4,378 | 1,20E-05 | +++ | 0 | 0,289 | 2 | 0,8656 | 0,03453109 | TOM1 | yes | 6 | intron | 4 |
| rs7474813 | ADO | t | c | 95,5 | -4,374 | 1,22E-05 | --- | 0 | 0,437 | 2 | 0,8038 | 0,03496645 | ZNF365 | yes | -175 568 | intron | |
| rs2300371 | IL10RB | t | c | 95,5 | -4,373 | 1,23E-05 | -+- | 70 | 13,32 | 2 | 0,001281 | 0,03513308 | IFNAR2 | - | 11 228 | intron | 6 |
| rs7521247 | CD244 | a | g | 95,5 | 4,371 | 1,24E-05 | +++ | 0 | 0,425 | 2 | 0,8087 | 0,03530857 | CD84 | yes | -259 389 | intron | 6 |
| rs882354 | CAMK2A | a | g | 95,5 | -4,37 | 1,24E-05 | --- | -59,7 | 2,505 | 2 | 0,2858 | 0,03541133 | SLC6A7 | yes | -1 893 | downstream | 5 |
| rs247902 | TAF1C | t | c | 95,5 | 4,369 | 1,25E-05 | +++ | 47 | 7,543 | 2 | 0,02301 | 0,03550585 | ATP2C2 | yes | 262 145 | intron | 6 |
| rs12216486 | IGF2R | a | g | 95,5 | -4,369 | 1,25E-05 | --- | -10,4 | 3,624 | 2 | 0,1633 | 0,0355864 | - | - | -60 514 | downstream | 6 |
| rs4695739 | SCRG1 | a | c | 95,5 | 4,368 | 1,25E-05 | +++ | 0 | 1,428 | 2 | 0,4896 | 0,03566205 | - | - | 274 873 | intergenic | 6 |
| rs7210280 | EVI2A | c | g | 95,5 | 4,368 | 1,25E-05 | +++ | 56,1 | 9,105 | 2 | 0,01054 | 0,03568076 | SUZ12P | - | -564 657 | intron | |
| rs13053864 | CRYBB1 | t | c | 95,5 | -4,36 | 1,30E-05 | --- | -59,4 | 2,51 | 2 | 0,2851 | 0,03669693 | - | - | 877 102 | intergenic | 5 |
| rs9481169 | LAMA4 | t | g | 95,5 | -4,36 | 1,30E-05 | --- | -82,2 | 2,195 | 2 | 0,3337 | 0,03676676 | - | - | -499 271 | upstream | 5 |
| rs4458132 | PDE4C | a | t | 95,5 | 4,358 | 1,31E-05 | +++ | 0 | 0,495 | 2 | 0,7806 | 0,03700917 | PDE4C | yes | 17 590 | intron | 5 |
| rs431691 | BLM | a | g | 95,5 | 4,354 | 1,34E-05 | +++ | 0 | 0,829 | 2 | 0,6607 | 0,03759998 | - | - | 99 177 | downstream | 5 |
| rs1858790 | KCNQ1DN | a | t | 95,5 | 4,351 | 1,36E-05 | +++ | 0 | 0,778 | 2 | 0,6776 | 0,03808836 | ZNF195 | yes | 474 308 | intron | 6 |
| rs2345055 | EIF2AK1 | a | c | 95,5 | -4,348 | 1,37E-05 | --- | 0 | 1,018 | 2 | 0,6011 | 0,03841638 | AIMP2 | yes | -1 259 | intron | 4 |
| rs35755011 | HOXB2 | t | c | 95,5 | 4,348 | 1,37E-05 | +++ | 0 | 0,104 | 2 | 0,9492 | 0,03843405 | - | - | -57 563 | intergenic | 4 |
| rs146608062 | SLC30A1 | a | g | 95,5 | -4,348 | 1,38E-05 | --- | 0 | 1,637 | 2 | 0,4412 | 0,03850772 | - | - | -340 285 | intergenic | |
| rs9318072 | C13orf34 | t | c | 95,5 | 4,34 | 1,43E-05 | +++ | 0 | 1,827 | 2 | 0,401 | 0,03959639 | - | - | -309 604 | intergenic | |
| rs2276419 | HYOU1 | t | c | 95,5 | -4,338 | 1,44E-05 | --- | 0 | 0,763 | 2 | 0,6827 | 0,03973891 | UBE4A | yes | -684 536 | 5´UTR | 4 |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs4919639 | PSD | c | g | 95,5 | 4,336 | 1,45E-05 | +++ | 41,6 | 6,853 | 2 | 0,03251 | 0,04011794 | | - | - | 54 484 | upstream | 5 | |
| rs4863686 | TBC1D9 | c | g | 95,5 | 4,336 | 1,45E-05 | +++ | -4,4 | 3,833 | 2 | 0,1471 | 0,04017954 | | MAML3 | yes | -863 769 | intron | 5 | |
| rs62449081 | GGCT | t | c | 95,5 | -4,32 | 1,56E-05 | --- | 0 | 0,806 | 2 | 0,6684 | 0,04224068 | yes | FAM188B | - | 350 034 | intron | 5 | |
| rs4982255 | PSMA6 | a | g | 95,5 | -4,317 | 1,58E-05 | --- | 0 | 1,591 | 2 | 0,4514 | 0,04270324 | | - | - | 45 196 | intergenic | | |
| rs56982547 | SNPH | a | g | 95,5 | -4,317 | 1,58E-05 | --- | 0 | 0,552 | 2 | 0,7589 | 0,04275174 | | RAD21L1, SNPH | yes | 16 742 | intron | 5 | |
| rs1790469 | GRIK4 | a | g | 95,5 | 4,317 | 1,59E-05 | +++ | 31,4 | 5,832 | 2 | 0,05414 | 0,04282169 | | - | - | -504 575 | intergenic | 5 | |
| rs75845312 | ANKZF1 | t | c | 95,5 | 4,316 | 1,59E-05 | +++ | 0 | 0,012 | 2 | 0,9939 | 0,04287016 | | - | - | 815 546 | intergenic | | |
| rs35787376 | RPL23A | c | g | 95,5 | -4,313 | 1,61E-05 | --- | 5,2 | 4,219 | 2 | 0,1213 | 0,04325673 | | - | - | -721 322 | intergenic | | |
| rs4326952 | ELF1 | t | c | 95,5 | -4,311 | 1,62E-05 | --- | -31,5 | 3,043 | 2 | 0,2184 | 0,0434435 | | - | - | 481 791 | intergenic | | |
| rs34302476 | HBQ1 | a | g | 95,5 | 4,31 | 1,63E-05 | +++ | 0 | 1,82 | 2 | 0,4025 | 0,04364955 | | - | - | 640 329 | intergenic | | |
| rs8078610 | EVI2B | t | c | 95,5 | -4,309 | 1,64E-05 | --- | 0 | 0,226 | 2 | 0,8932 | 0,04385082 | | - | - | 285 593 | intergenic | 6 | |
| rs3818508 | CELSR2 | t | c | 95,5 | 4,308 | 1,65E-05 | +++ | -78,1 | 2,246 | 2 | 0,3254 | 0,04399117 | | KIAA1324 | - | -52 167 | intron | 5 | |
| rs3796242 | TSC22D2 | a | t | 95,5 | 4,308 | 1,65E-05 | +++ | 0 | 1,805 | 2 | 0,4055 | 0,04401221 | yes | CLRN1 | - | 563 652 | synonymous | 5 | |
| rs3784330 | CIB2 | t | c | 95,5 | 4,308 | 1,65E-05 | +++ | 23 | 5,195 | 2 | 0,07445 | 0,04401632 | | CIB2 | yes | 23 321 | intron | 4 | yes |
| rs3008011 | RPS6KA2 | t | c | 95,5 | -4,307 | 1,65E-05 | --- | -9,5 | 3,652 | 2 | 0,161 | 0,04406808 | | PDE10A | yes | -809 093 | intron | 5 | |
| rs1044522 | TMEM134 | a | g | 95,5 | -4,302 | 1,69E-05 | --- | 0 | 0,819 | 2 | 0,6641 | 0,04478612 | | CTSF | yes | -895 986 | synonymous | 4 | |
| rs11582371 | SH3GLB1 | t | c | 95,5 | 4,302 | 1,69E-05 | +++ | 16,1 | 4,769 | 2 | 0,09213 | 0,04480688 | | - | - | -180 447 | intergenic | | |
| rs339985 | RORA | a | t | 95,5 | 4,298 | 1,72E-05 | +++ | 0 | 0,478 | 2 | 0,7872 | 0,04545507 | | RORA | yes | 137 621 | intron | 6 | |
| rs217401 | OGDH | a | c | 95,5 | -4,298 | 1,73E-05 | --- | 3,4 | 4,139 | 2 | 0,1263 | 0,04554332 | | - | - | -54 843 | intergenic | 6 | |
| rs35334347 | NIN | a | g | 95,5 | -4,296 | 1,74E-05 | --- | -90 | 2,105 | 2 | 0,3491 | 0,04576713 | yes | NIN | yes | 31 502 | intron | | |
| rs11895231 | DGKD | t | c | 95,5 | -4,295 | 1,74E-05 | --- | 13,2 | 4,609 | 2 | 0,09979 | 0,0458613 | | DGKD | yes | -2 250 | intron | | |
| rs12731262 | NECAP2 | t | c | 95,5 | 4,294 | 1,76E-05 | +++ | 0 | 1,198 | 2 | 0,5493 | 0,04612456 | | - | - | -686 224 | upstream | 6 | |
| rs77604319 | RPS6KC1 | a | c | 95,5 | -4,292 | 1,77E-05 | --- | 0 | 1,049 | 2 | 0,592 | 0,04648575 | | - | - | -536 591 | intergenic | 5 | |
| rs114111458 | TRAF5 | a | g | 95,5 | 4,288 | 1,80E-05 | +++ | -50,6 | 2,655 | 2 | 0,2651 | 0,04710087 | | HHAT | - | -901 611 | intron | 5 | |
| rs2600560 | DYNC1I1 | a | g | 95,5 | -4,286 | 1,82E-05 | --- | -11,8 | 3,579 | 2 | 0,167 | 0,04754005 | | DYNC1I1 | yes | 89 946 | intron | | |
| rs12438010 | PDE8A | t | g | 95,5 | 4,285 | 1,82E-05 | +++ | 0 | 0,528 | 2 | 0,7678 | 0,0475803 | | - | - | 329 662 | intergenic | 5 | |
| rs72665339 | EPHB2 | a | g | 95,5 | -4,285 | 1,83E-05 | --- | 0 | 0,297 | 2 | 0,862 | 0,04759446 | | - | - | -606 410 | intergenic | 3a | |
| rs4512352 | MATN2 | a | g | 95,5 | -4,285 | 1,83E-05 | --- | 0 | 1,937 | 2 | 0,3797 | 0,04760861 | | MATN2 | yes | 58 928 | intron | 6 | |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs533494 | IL19 | t | c | 95,5 | -4,284 | 1,83E-05 | --- | 0 | 1,524 | 2 | 0,4667 | 0,04776932 | | PIGR | yes | 107 570 | intron | |
| rs74444868 | ARFGAP3 | t | c | 95,5 | -4,283 | 1,85E-05 | --- | 0 | 0,527 | 2 | 0,7682 | 0,04798377 | | - | - | -7 277 | intergenic | |
| rs61921903 | USP15 | t | c | 95,5 | -4,281 | 1,86E-05 | --- | 32,8 | 5,949 | 2 | 0,05108 | 0,04826345 | | - | - | 194 750 | intergenic | |
| rs13003555 | SP110 | a | g | 95,5 | -4,28 | 1,87E-05 | --- | -67,2 | 2,392 | 2 | 0,3024 | 0,04849208 | | SP110 | yes | -55 795 | intron | 5 |
| rs12584413 | SACS | t | g | 95,5 | 4,277 | 1,90E-05 | +++ | 53,2 | 8,555 | 2 | 0,01387 | 0,04893561 | | SACS | yes | 15 074 | intron | |
| rs11622788 | ADAM20 | t | c | 95,5 | 4,275 | 1,91E-05 | +-+ | 53,7 | 8,648 | 2 | 0,01325 | 0,04926932 | | - | - | 298 423 | intergenic | 6 |
| rs62011588 | NR2F2 | a | c | 95,5 | 4,274 | 1,92E-05 | +++ | 0 | 0,121 | 2 | 0,9411 | 0,04928237 | | NR2F2-AS1 | - | -191 252 | intron | |
| rs13278111 | TNFRSF10D | t | c | 95,5 | 4,273 | 1,93E-05 | +++ | 0 | 1,322 | 2 | 0,5164 | 0,04928237 | | - | - | -432 912 | intergenic | 5 |
| rs12144062 | PHGDH | t | c | 95,5 | 4,271 | 1,95E-05 | +++ | 0 | 1,341 | 2 | 0,5113 | 0,04954813 | | - | - | -130 428 | intergenic | |
| rs2949950 | HELZ | t | c | 95,5 | -4,27 | 1,96E-05 | --- | 0 | 0,463 | 2 | 0,7934 | 0,04969809 | yes | PITPNC1 | yes | 386 347 | intron | 6 |

SUPPLEMENTARY DATA

**Supplementary Table 2.** Significant (FDR < 5%, p-value = 1.34E-04) associations identified between gene expression (standardized units) and fasting plasma insulin, HOMA-IR and BMI through meta-analysis.

| Gene | Phenotype | P-value | Direction | Het P-value |
|---|---|---|---|---|
| RCAN2 | BMI | 2,21E-08 | -+- | 0,015 |
| SH3GLB2 | BMI | 3,56E-08 | +++ | 0,508 |
| RBBP6 | BMI | 8,50E-08 | --- | 0,600 |
| ALDH1A2 | HOMA-IR | 9,22E-08 | +-+ | 0,009 |
| DBNDD1 | HOMA-IR | 2,11E-07 | +-+ | 0,015 |
| DBNDD1 | insulin | 3,34E-07 | +-+ | 0,006 |
| ARHGEF10L | insulin | 2,41E-06 | +++ | 0,221 |
| PITPNM1 | BMI | 3,44E-06 | --- | 0,018 |
| WSB2 | BMI | 9,29E-06 | -+- | 0,002 |
| GZMH | insulin | 9,89E-06 | +++ | 0,951 |
| BCL7A | HOMA-IR | 1,03E-05 | --- | 0,176 |
| BCL7A | insulin | 1,15E-05 | --- | 0,186 |
| ENPEP | BMI | 1,22E-05 | +++ | 0,440 |
| C17orf101 | insulin | 1,23E-05 | +++ | 0,229 |
| UGT8 | insulin | 1,45E-05 | --- | 0,112 |
| FHL2 | BMI | 1,53E-05 | -++ | 0,010 |
| CA2 | BMI | 1,55E-05 | +++ | 0,595 |
| MSTN | BMI | 1,82E-05 | +++ | 0,088 |
| DHRS7 | insulin | 1,84E-05 | +++ | 0,762 |
| IMPA2 | insulin | 2,39E-05 | +++ | 0,063 |
| ARID1A | BMI | 2,52E-05 | +++ | 0,560 |
| TRIO | BMI | 2,91E-05 | --- | 0,774 |
| RAF1 | BMI | 3,11E-05 | +++ | 0,490 |
| SPR | BMI | 3,36E-05 | --- | 0,011 |
| SPOCK1 | HOMA-IR | 3,52E-05 | --- | 0,175 |
| TMOD1 | BMI | 3,92E-05 | +++ | 0,036 |
| SLC30A10 | insulin | 4,00E-05 | --- | 0,817 |
| ARHGEF10L | HOMA-IR | 4,02E-05 | +++ | 0,211 |
| UGT8 | HOMA-IR | 4,36E-05 | --- | 0,041 |
| ALDH1A2 | insulin | 4,85E-05 | +-+ | 0,017 |
| C17orf101 | HOMA-IR | 5,15E-05 | +++ | 0,300 |
| DAK | insulin | 5,83E-05 | -++ | 0,000 |
| BCKDHB | BMI | 6,16E-05 | --- | 0,881 |
| EIF4E2 | insulin | 6,41E-05 | +++ | 0,173 |
| ARHGAP17 | BMI | 6,51E-05 | +++ | 0,083 |
| ATP6V0C | HOMA-IR | 6,66E-05 | -++ | 0,073 |
| GZMH | HOMA-IR | 6,82E-05 | +++ | 0,988 |

| | | | | |
|---|---|---|---|---|
| PDIA4 | BMI | 7,14E-05 | +++ | 0,797 |
| G3BP2 | insulin | 7,87E-05 | +++ | 0,371 |
| AGXT2L1 | BMI | 8,42E-05 | --- | 0,372 |
| CASQ1 | insulin | 8,54E-05 | +++ | 0,191 |
| SLC30A10 | HOMA-IR | 9,04E-05 | --- | 0,764 |
| TMED2 | insulin | 9,08E-05 | +++ | 0,077 |
| CD46 | BMI | 9,93E-05 | +++ | 0,781 |
| RNF111 | HOMA-IR | 1,07E-04 | +-+ | 0,024 |
| GAS6 | insulin | 1,20E-04 | --- | 0,367 |
| CTSF | BMI | 1,28E-04 | -+- | 0,001 |
| CALML4 | insulin | 1,33E-04 | +++ | 0,403 |
| PFKM | insulin | 1,34E-04 | +++ | 0,044 |

**Supplementary Table 3.** Significant (FDR < 5%, p-value = 7.14E-05) associations identified between gene expression (standardized units) and fasting plasma insulin adjusted for BMI, HOMA-IR adjusted for BMI and BMI through meta-analysis.

| Gene | Phenotype | P-value | Direction | Het P-value |
|---|---|---|---|---|
| RCAN2 | BMI | 2,21E-08 | -+- | 0,015 |
| SH3GLB2 | BMI | 3,56E-08 | +++ | 0,508 |
| RBBP6 | BMI | 8,50E-08 | --- | 0,600 |
| UNG | insulin(BMI) | 1,08E-06 | +++ | 0,329 |
| CKAP5 | insulin(BMI) | 1,11E-06 | --- | 0,433 |
| PITPNM1 | BMI | 3,44E-06 | --- | 0,018 |
| TBC1D1 | insulin(BMI) | 4,20E-06 | +++ | 0,196 |
| CALML4 | insulin(BMI) | 9,05E-06 | +++ | 0,192 |
| WSB2 | BMI | 9,29E-06 | -+- | 0,002 |
| ENPEP | BMI | 1,22E-05 | +++ | 0,440 |
| FHL2 | BMI | 1,53E-05 | -++ | 0,010 |
| CA2 | BMI | 1,55E-05 | +++ | 0,595 |
| MSTN | BMI | 1,82E-05 | +++ | 0,088 |
| ALDH1A2 | HOMA-IR(BMI) | 1,95E-05 | +-+ | 0,048 |
| PRRX1 | insulin(BMI) | 2,32E-05 | -+- | 0,003 |
| ARID1A | BMI | 2,52E-05 | +++ | 0,560 |
| TRIO | BMI | 2,91E-05 | --- | 0,774 |
| RAF1 | BMI | 3,11E-05 | +++ | 0,490 |
| NRXN3 | insulin(BMI) | 3,25E-05 | -+- | 0,008 |
| SPR | BMI | 3,36E-05 | --- | 0,011 |
| GAS6 | insulin(BMI) | 3,63E-05 | --- | 0,724 |
| TMOD1 | BMI | 3,92E-05 | +++ | 0,036 |
| BCKDHB | BMI | 6,16E-05 | --- | 0,881 |
| ING2 | HOMA- | 6,28E-05 | -++ | 0,014 |

SUPPLEMENTARY DATA

| | | | | |
|---|---|---|---|---|
| | IR(BMI) | | | |
| ARHGAP17 | BMI | 6,51E-05 | +++ | 0,083 |
| ATP1B1 | HOMA-IR(BMI) | 6,85E-05 | +++ | 0,534 |
| PDIA4 | BMI | 7,14E-05 | +++ | 0,797 |

**Supplementary Table 4.** Extended analysis in the MM-study of the influence of the PFKM eQTL SNP (rs4547172) on skeletal muscle metabolic phenotypes.

| | Non-T2D | | | | T2D | | | | All | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | beta | IQR | p-value | n | beta | IQR | p-value | n | beta | IQR | p-value | n |
| M-value | | | 0,27 | | 0,22 | 0.044-0.39 | 0,015 | 71 | 0,15 | 0.029-0.27 | 0,016 | 178 |
| Delta RQ | 0,017 | 0.003-0.031 | 0,016 | 102 | | | 0,4 | | 0,011 | 0.00012-0.022 | 0,048 | 173 |
| Glycogen | | | 0,56 | | 50,1 | 4.6-95.6 | 0,032 | 63 | | | 0,21 | |
| IMTG | 15,7 | 5.20-26.2 | 0,004 | 103 | | | 0,88 | | 8,69 | 0.26-17.12 | 0,043 | 167 |
| CGOXBW | | | 0,22 | | 0,25 | 0.022-0.48 | 0,032 | 71 | 0,19 | 0.025-0.36 | 0,025 | 178 |

Respiratory quotient (RQ), intra muscular triglycerides (IMTG), whole body glucose oxidation rate in the insulin stimulated state during clamp divided by body weight (CGOXBW). Delta RQ = RQclamp – RQbasal. All analysis was adjusted for age and BMI (except for M-value and CGOXBW), Delta RQ was in addition adjusted for RQbasal. M-value was square root transformed.

**Supplementary Table 5.** Public microarray gene expression data used.

| | All | | | T2D | | | Non-T2D | | | T2D vs. Non-T2D |
|---|---|---|---|---|---|---|---|---|---|---|
| | Mean | SD | n | Mean | SD | n | Mean | SD | n | p-value* |
| M-value (mg / kg / min) | 4.41 | 2.27 | 178 | 3.35 | 1.88 | 71 | 5.12 | 2.24 | 107 | $1.42 \times 10^{-7}$ |
| Delta RQ (AU) | 0.071 | 0.049 | 173 | 0.054 | 0.047 | 71 | 0.082 | 0.047 | 102 | $1.73 \times 10^{-4}$ |
| Glycogen (mmol / kg) | 373 | 101 | 166 | 371 | 117 | 63 | 374 | 90 | 103 | 0.88 |
| IMTG (mmol / kg) | 59.3 | 37.8 | 167 | 60.4 | 39.1 | 64 | 58.6 | 37.2 | 103 | 0.76 |
| CGOXBW (mg / kg / min) | 1.96 | 0.74 | 178 | 1.75 | 0.65 | 71 | 2.10 | 0.77 | 107 | $1.99 \times 10^{-3}$ |

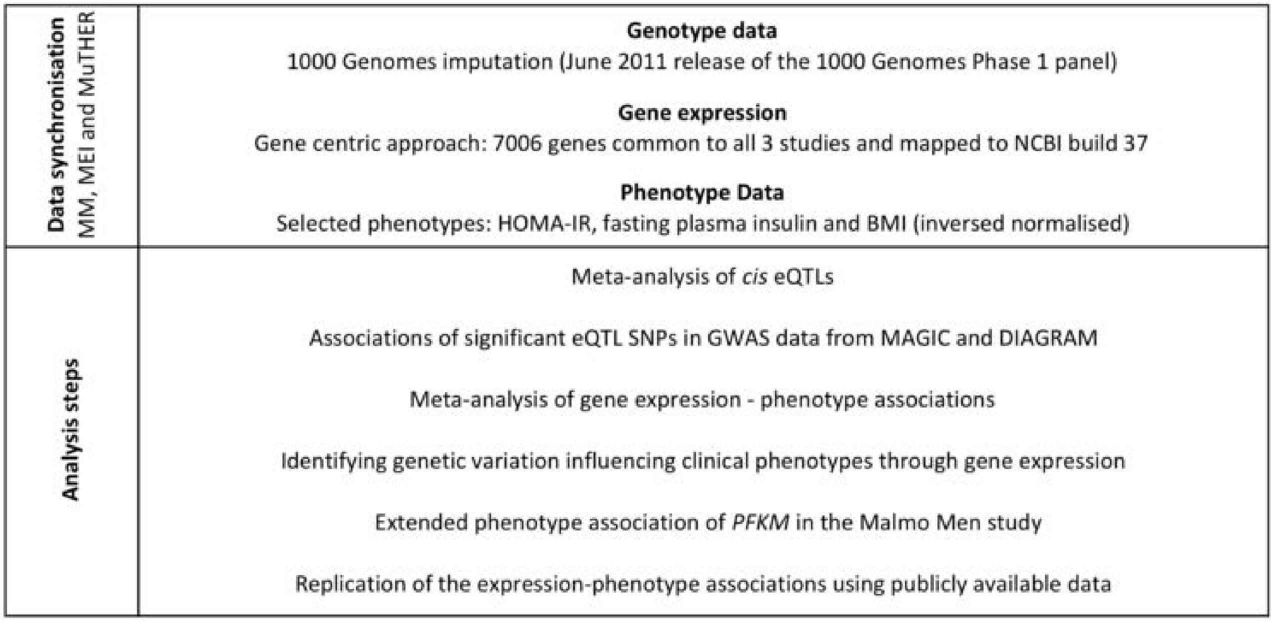
*analysed using student-t test, unadjusted. SD = standard deviation

**Supplementary Table 6.** Publicly available expression data sets used

| Study | N (T2D) | N (NGT) | N (BMI) |
|---|---|---|---|
| E-GEOD-18832 | - | - | 21 |
| E-GEOD-22435 | - | - | 17 |
| E-GEOD-28998 | - | - | 14 |
| E-GEOD-5109 | - | - | 6 |
| E-GEOD-6798 | - | - | 29 |
| E-GEOD-8157 | - | - | 13 |
| E-MEXP-2559 | - | - | 35 |
| E-GEOD-18732 | 66 | 40 | - |
| E-GEOD-19420 | 27 | 10 | - |
| E-GEOD-25462 | 9 | 37 | 50 |
| TOTAL | 102 | 87 | 185 |

SUPPLEMENTARY DATA

**Supplementary Figure 1.** Overview of methods



| | |
|---|---|
| **Data synchronisation**<br>MM, MEI and MuTHER | **Genotype data**<br>1000 Genomes imputation (June 2011 release of the 1000 Genomes Phase 1 panel)<br>**Gene expression**<br>Gene centric approach: 7006 genes common to all 3 studies and mapped to NCBI build 37<br>**Phenotype Data**<br>Selected phenotypes: HOMA-IR, fasting plasma insulin and BMI (inversed normalised) |
| **Analysis steps** | Meta-analysis of *cis* eQTLs<br>Associations of significant eQTL SNPs in GWAS data from MAGIC and DIAGRAM<br>Meta-analysis of gene expression - phenotype associations<br>Identifying genetic variation influencing clinical phenotypes through gene expression<br>Extended phenotype association of *PFKM* in the Malmo Men study<br>Replication of the expression-phenotype associations using publicly available data |

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