Translational studies support a role for serotonin 2B receptors in aggression-related cannabis response

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Supplementary Notes

Materials and Methods

Genotyping and Quality Control

Grady Trauma Project (GTP) sample:

SNPweights software17 was used to assign ancestry, focusing on African-American ancestry only. PLINK [1] was used to perform quality control analyses (e.g., to remove SNPs with a call rate < 95%); individuals with missingness > 2% or heterozygosity > |0.2|, those failing sex checks, and duplicates and relatives were also removed. We then removed SNPs with a call rate < 0.98, with differential missingness between cases and controls < 0.02 or significant deviation from Hardy-Weinberg proportions ($p<1\times10^{-6}$ in controls and $p<1\times10^{-10}$ in PTSD cases). Imputation to the 1000 Genomes phase 1 reference was performed within the PGC pipeline[16] using SHAPEIT for phasing[21] and IMPUTE2 for imputation.[22] Principal-component analysis (PCA) was conducted on high-quality SNPs with low LD passing filters and then used to remove outlier subjects.

Analysis of possible variant function

eQTL analysis using the Braineac Database

To investigate the effect of the GWS SNPs (*HTR2B* rs17440378 and *PSMD1* rs35750632) on gene expression level, we conducted an expression quantitative trait locus (eQTL) analysis using the Braineac database from the UK Brain Expression Consortium (UKBEC) (www.braineac.org). This database contains information collected from 10 brain regions of 134 neuropathologically normal individuals: cerebellar cortex, frontal cortex, hippocampus, medulla, occipital cortex, putamen, substantia nigra, temporal cortex, thalamus, and intralocular white matter.

eQTL analysis using the GTEx Database

We also conducted an eQTL analysis for both *HTR2B* rs17440378 and *PSMD1* rs35750632 using the Genotype-Tissue Expression (GTEx) Project database. We performed a single-tissue eQTL analysis and a multi-tissue comparison between the variant of interest and the target gene. The data used for the analyses described here were obtained from the GTEx portal (www.gtexportal.org)

Chromatin regulation analysis using HaploReg v4.1

We used HaploReg v4.1 (http://archive.broadinstitute.org/mammals/haploreg/haploreg.php) to explore chromatin states, protein binding, and regulatory motif alterations within the GWS SNPs (*HTR2B**rs17440378 and *PSMD1**rs35750632). This database contains 127 reference epigenomes from ENCODE 2012 and Roadmap Epigenomics. We used the following datasets: ChromHMM states corresponding to enhancer or promoter elements, from the 15-state core model and 25-state model incorporating imputed data; histone modification ChIP-seq peaks using the gappedPeak algorithm for H3K27ac, H3K9ac, H3K9me1, and K3K9me3; and DNase hypersensitivity data peaks using the narrowPeak algorithm. To examine the effect of GWS variants on regulatory motifs, we used the position weight matrix (PWM)-scanning process. For the analysis, we selected an LD threshold (r^2) of 0.8 and used the AFR 1000G Phase 1 population for LD calculation.

Polygenic risk score analysis

PRS analysis was conducted as previously reported [2]. Data were clumped by linkage disequilibrium with $r^2 < 0.2$ in a 200 kb window. The PRS was calculated based on a set of top SNPs (*P*-values 0.00001, 0.0001, 0.001, 0.005, 0.01, 0.05, 0.1, and 0.5) and multiplying the dosage of the risk alleles weighted by the effect sizes. The association between CRA and the PRS of each individual was analyzed in a logistic regression model embedded in GEE to correct for correlations among related individuals: CRA ~ PRS + age + sex + 3 PCs. The Yale-Penn 1 and Yale-Penn 2 datasets were analyzed separately and then combined by meta-analysis using METAL software. *P*-values smaller than 0.01 (0.05/5) were considered significant after multiple correction.

Htr2b knockout mice, THC administration and behavioral phenotyping

Aggressive behavior was investigated using the resident-intruder test adapted from Koolhaas and colleagues [3] and performed 1 hour after i.p. injection. Briefly, experimental mice were put in isolation for 10 days to induce aggression. An unfamiliar mouse of the same sex and strain, used as an intruder, was introduced in the cage for 30 minutes. Intruders were balanced based on the total number of encounters, so that each experimental resident mouse was not exposed to the same intruder. The behavioral parameters scored for both frequency and duration included: 1) social investigation behavior (anogenital sniff, nose sniff, body sniff, allogrooming), 2) aggressive behavior (aggressive grooming, offensive posture, attack, tail rattling, and digging), 3) locomotor activity (number of crossings).

Results

Manhattan plots are shown in Supplementary Figure 1. To determine whether both GWS SNPs reflect the same association signal, we conducted a conditional analysis by adjusting each for the other GWS variant. Adjusting for one variant in the conditional analysis eliminated the association for the other ($P_{\text{conditional}} = 0.34$ for rs17440378; $P_{\text{conditional}} = 0.23$ for rs35750632).

*Post-hoc analysis of association between HTR2B*rs17440378 and aggression or substance-dependence traits*

To investigate the specificity of the SNP association with CRA, we examined the association of *HTR2B**rs17440378 with other aggression-related and substance dependence traits (lower panel, Supplementary Figure 4). No association was observed for an aggression-related disorder or substance dependence. We also tested the association of *HTR2B**rs17440378 with aggression under the influence of other drugs, such as alcohol, cocaine, and opioids; there was no significant association found.

eQTLs analysis using the Braineac Database

Using the Braineac Database, we identified several rs17440378 eQTLs for *HTR2B* across all 10 of the brain regions analyzed (exprID = 2603401, aveALL $p = 7.3 \times 10^{-4}$) (Supplementary Table 4). The highest expression of *HTR2B* (exprID = 2603401) is in the medulla ($n = 119$) and substantia nigra ($n = 101$) (Supplementary Figure 5). eQTLs for *HTR2B**rs17440378 were also identified at genes across multiple brain regions: *PSMD1*, *DIS3L2*, *SP140*, *B3GNT7* (SupplementaryTable 4). No eQTLs were identified for rs35750632 in any of the brain regions examined.

eQTLs analysis using the GTEx Database

We used the GTEx database to identify additional eQTLs for *HTR2B**rs17440378 from 8,232 human samples in multiple tissues. We found 19 eQTLs for *HTR2B**rs17440378 in *HTR2B*, *C2orf72*, *ARMC9*, *RP11-223I10.1*, *AC017104.6*, and *B3GNT7* (Supplementary Table 5). The most significant result was the eQTL in *C2orf72* ($p = 3.8 \times 10^{-18}$, Effect size = 1.0). A multi-tissue eQTL comparison analysis between *C2orf72* and *HTR2B**rs17440378 eQTL showed a suggestive association in the putamen ($n = 82$, $\beta = 0.28$, $p = 1.0 \times 10^{-2}$) and in peripheral tissues (Supplementary Figure 6). A multi-tissue eQTL comparison between *HTR2B* and *HTR2B**rs17440378 revealed associations in the cerebellum ($n = 103$, $\beta = -0.37$, $p = 5.0 \times 10^{-2}$) and in peripheral tissue (Supplementary Figure 7). No eQTLs for rs35750632 were identified in any tissue.

Chromatin regulation analysis using HaploReg v4.1

We used HaploReg v4.1 to examine the regulatory role of GWS SNPs and variants with $r^2 > 0.8$. For *HTR2B**rs17440378, we identified multiple enhancer histone marks in embryonic stem cells (ESC), induced pluripotent stem cells (iPSC) and the anterior caudate and cingulate gyrus, among other tissues (Supplementary Table 6). Several regulatory motifs are altered by rs17440378, including Gfi-1, Nkx2-6, and Nkx3-4 (Supplementary Table 7A). Another variant in high LD with rs17440378 ($r^2 = 0.85$, D’ = 0.96), rs55637820, showed several enhancer histone marks in gastrointestinal tissue, pancreatic tissue, brain tissue (anterior caudate); it also alters 11 regulatory motifs (Supplementary Table 7B).

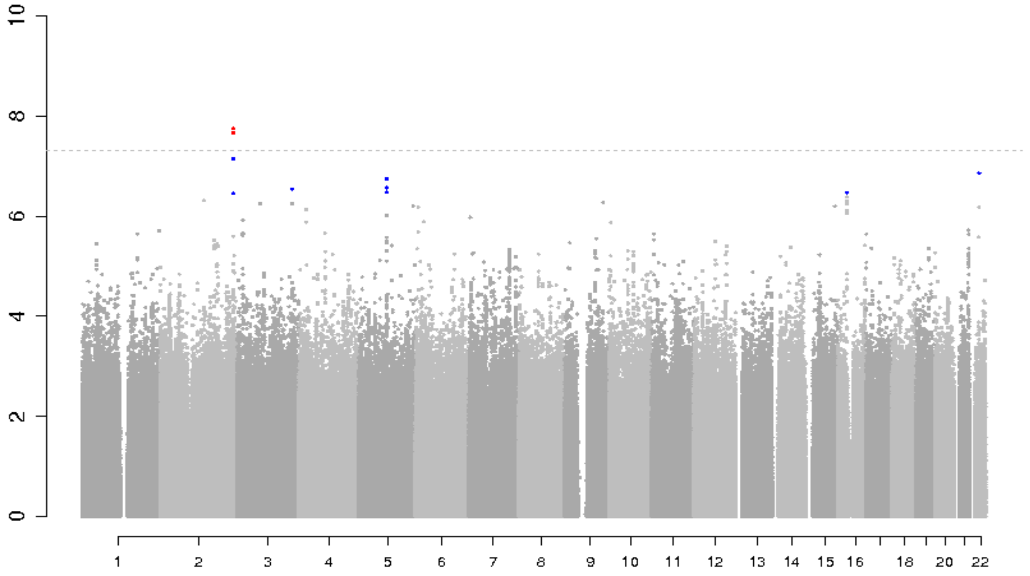
For rs35750632, we identified two promoter histone marks in gastrointestinal tissue and enhancer histone marks in epithelial tissue, adipose tissue, gastrointestinal tissue, and blood cells. Twelve regulatory motifs were altered by this genetic variant (Supplementary Table 7C).

References

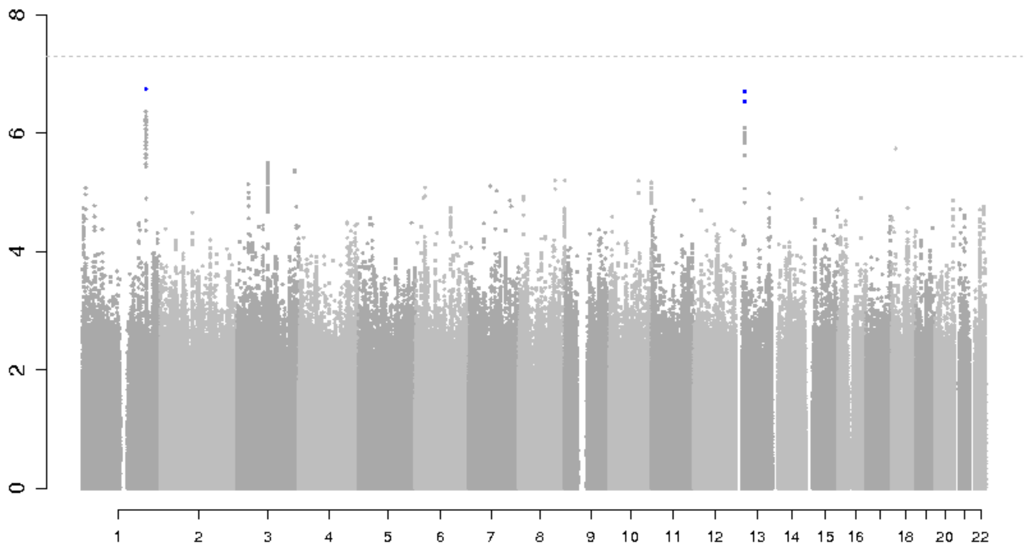
1. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, et al. PLINK: a tool set for whole-genome association and population-based linkage analyses. *American journal of human genetics.* 2007;81(3):559-575.
2. International Schizophrenia C, Purcell SM, Wray NR, Stone JL, Visscher PM, O'Donovan MC, et al. Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature.* 2009;460(7256):748-752.
3. Koolhaas JM, Coppens CM, de Boer SF, Buwalda B, Meerlo P, Timmermans PJ. The resident-intruder paradigm: a standardized test for aggression, violence and social stress. *Journal of visualized experiments : JoVE.* 2013(77):e4367.

Figure S1. Manhattan plots from cannabis-related aggression genome-wide association study.

AA



EA



African Americans (AAs) and European Americans (EAs). Y-axis shows $-\log_{10}$(P-value) and x-axis the 22 chromosomes. Each dot represents a SNP. Dotted line depicts *P* value cutoff of 5.0×10^{-8}.

Figure S2. QQ plot from genome-wide association study (GWAS) in African Americans (AAs).

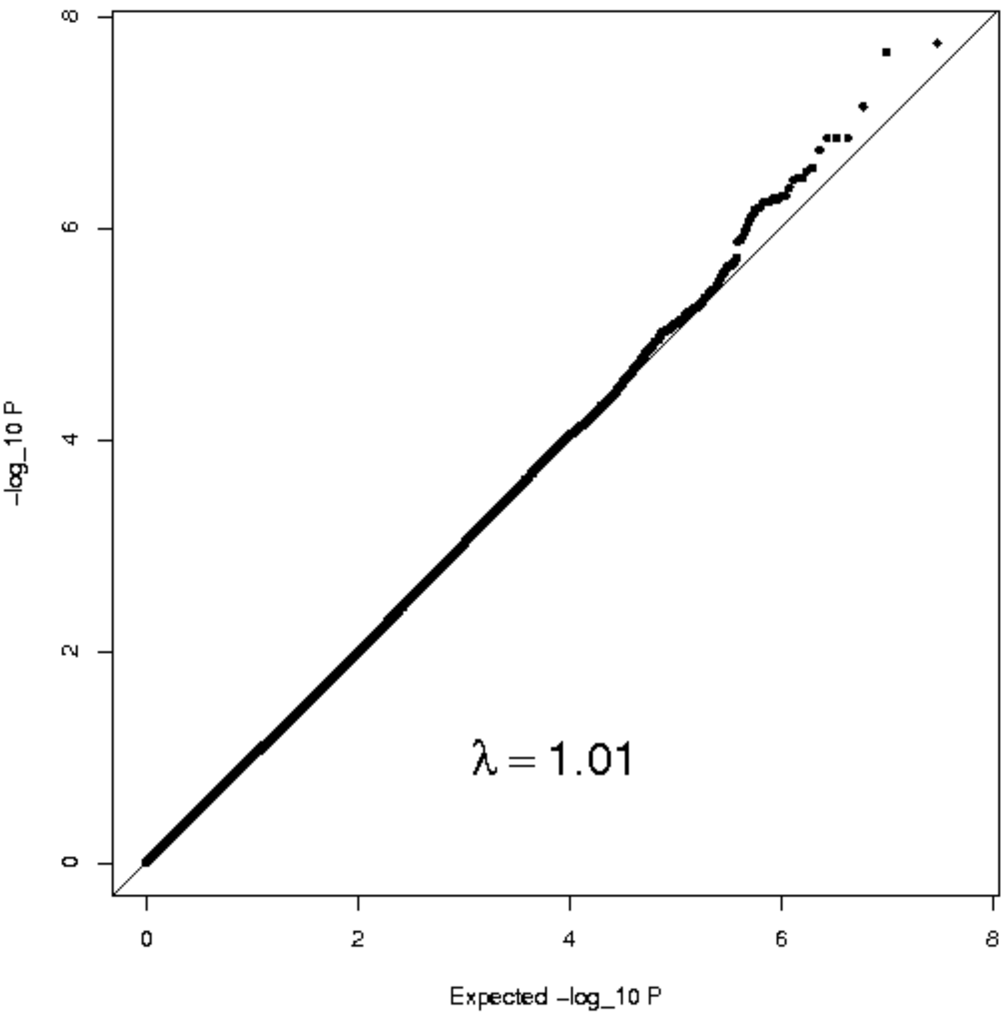


Figure S3. QQ plot from genome-wide association study (GWAS) in European Americans (EAs).

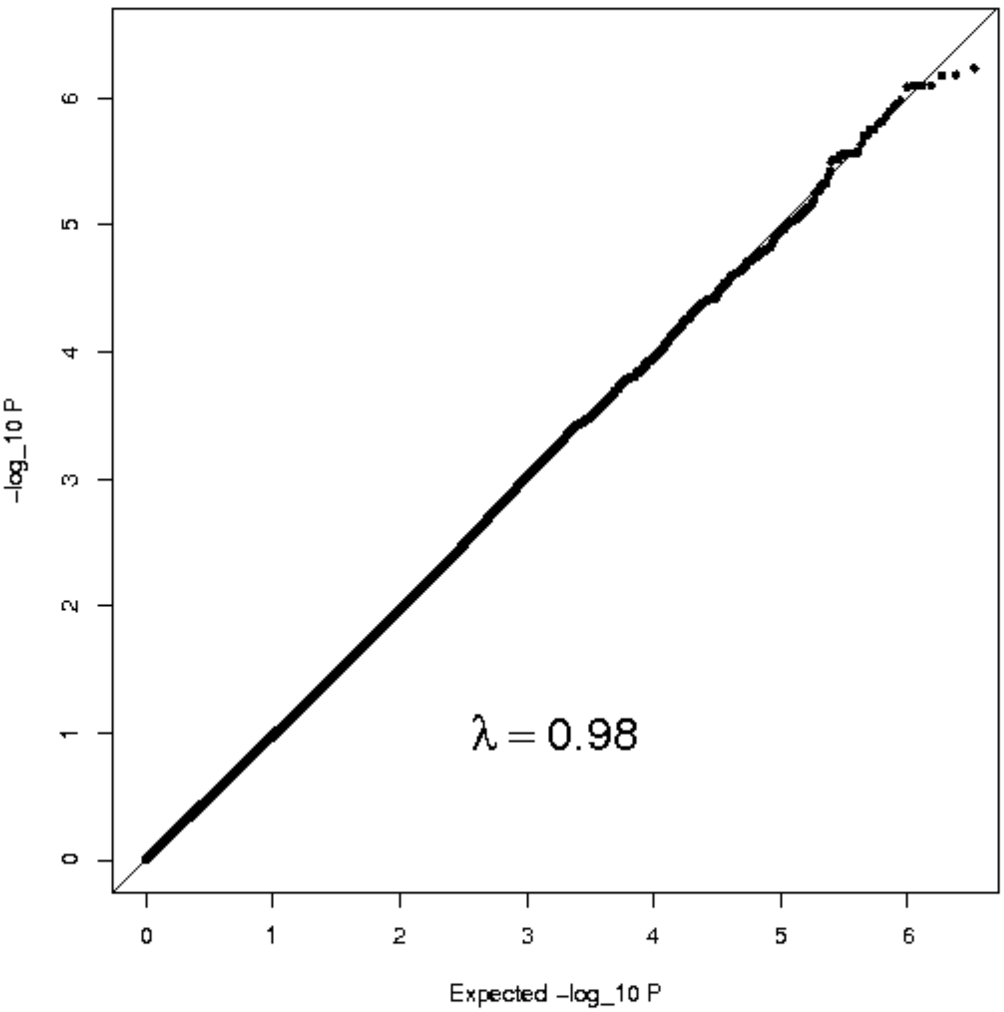


Figure S4. Cannabis-related aggression (CRA) stratified by rs17440378 genotype in African Americans (left) and European Americans (right).

Prevalence of CRA stratified by genotype for the GWS risk variants in African Americans (AAs) and European Americans (EAs). Cannabis-related aggression (CRA) is shown in percentage (%) stratified by genotype of the top SNP, rs17440378, in AAs and EAs.

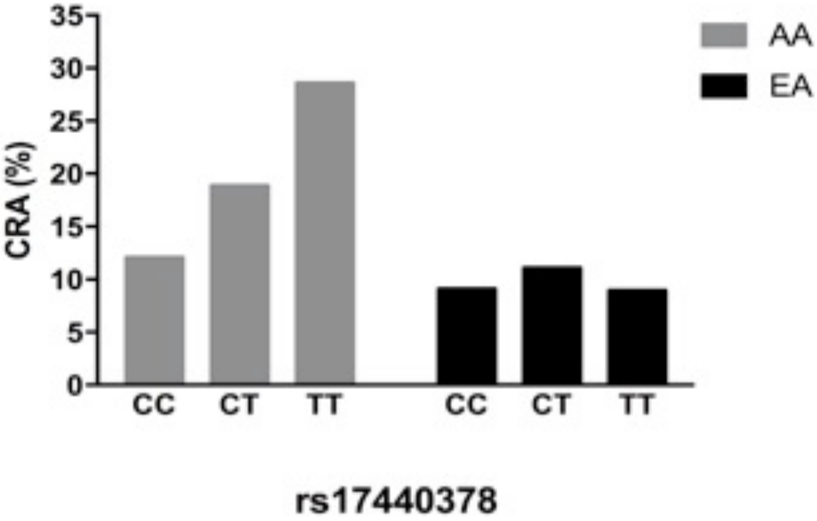
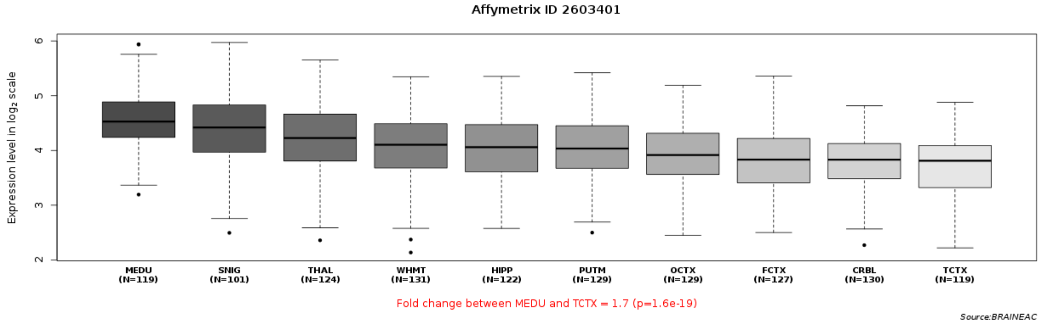
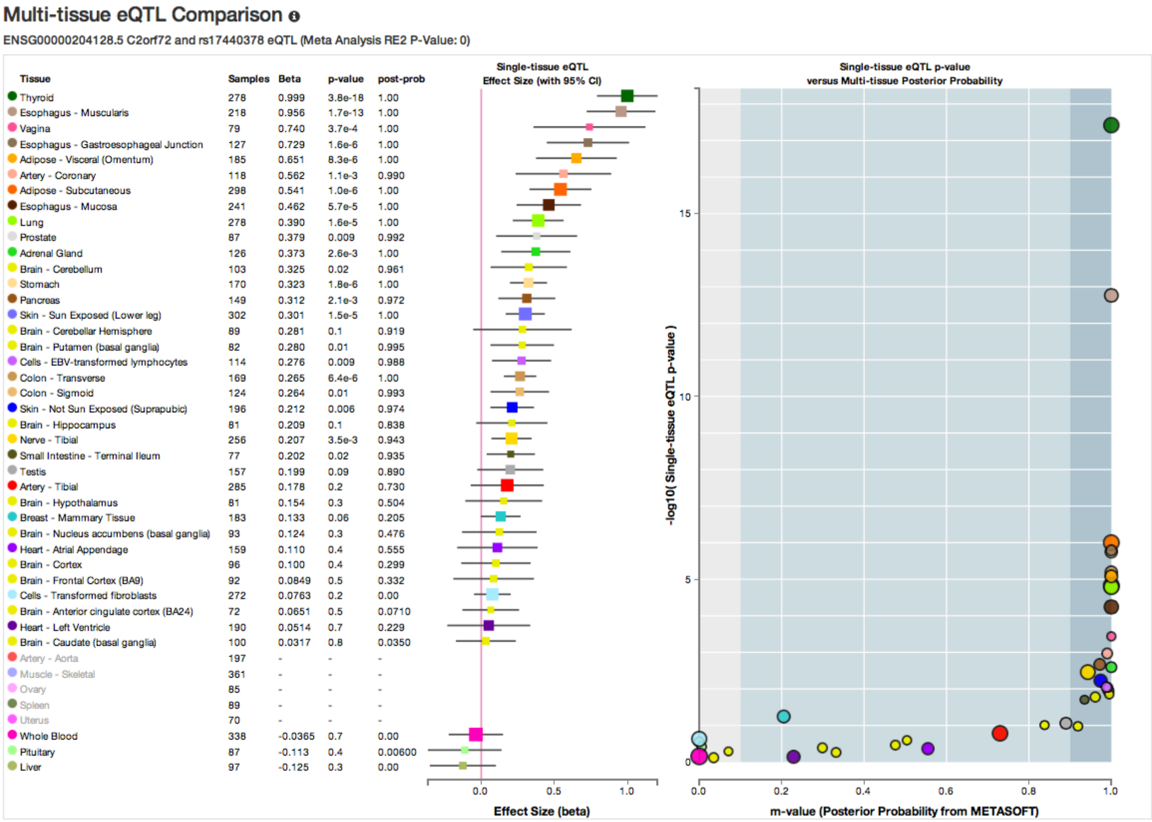


Figure S5. Gene expression patterns of *HTR2B* in human brain samples stratified by rs17440378 genotype using Braineac UK database.



Source:BRAINEAC

Figure S6. Multi-tissue eQTL comparison between *C2orf72* and rs17440378 eQTL using GTEx database.

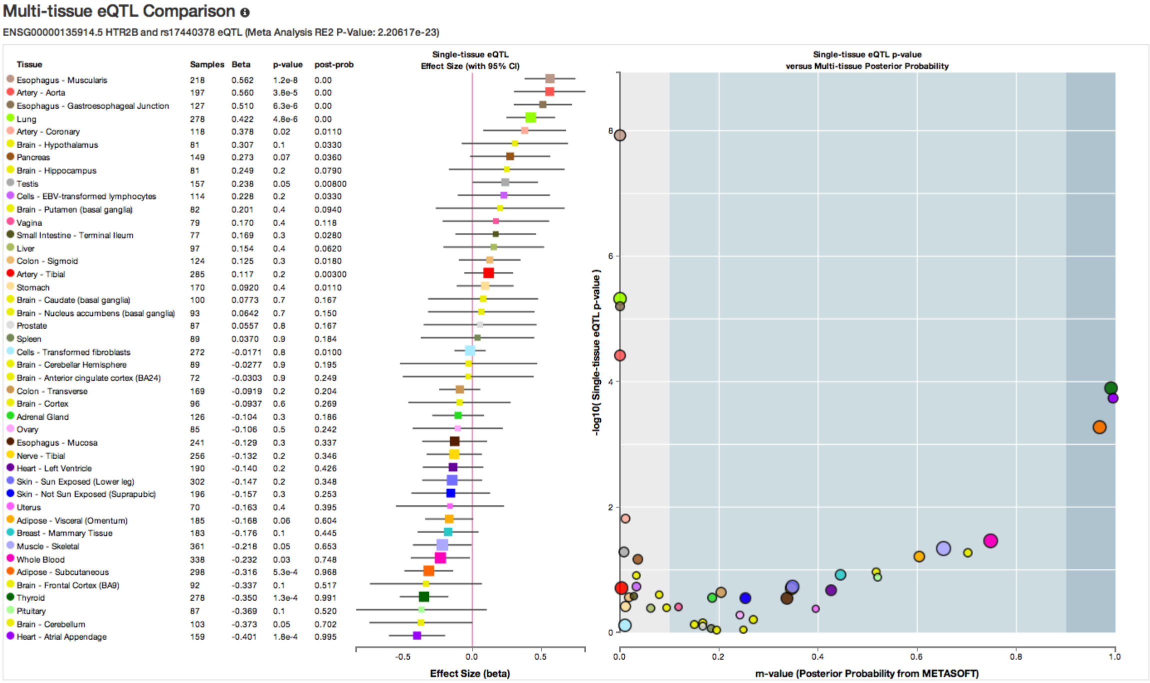


Multi-tissue eQTL Comparison

ENSG00000204128.5 C2orf72 and rs17440378 eQTL (Meta Analysis RE2 P-Value: 0)

Tissue	Samples	Beta	p-value	post-prob
Thyroid	278	0.999	3.8e-18	1.00
Esophagus - Muscularis	218	0.956	1.7e-13	1.00
Vagina	79	0.740	3.7e-4	1.00
Esophagus - Gastroesophageal Junction	127	0.729	1.6e-6	1.00
Adipose - Visceral (Omentum)	185	0.651	8.3e-6	1.00
Artery - Coronary	118	0.562	1.1e-3	0.990
Adipose - Subcutaneous	298	0.541	1.0e-6	1.00
Esophagus - Mucosa	241	0.462	5.7e-5	1.00
Lung	278	0.390	1.6e-5	1.00
Prostate	87	0.379	0.009	0.992
Adrenal Gland	126	0.373	2.6e-3	1.00
Brain - Cerebellum	103	0.325	0.02	0.961
Stomach	170	0.323	1.8e-6	1.00
Pancreas	149	0.312	2.1e-3	0.972
Skin - Sun Exposed (Lower leg)	302	0.301	1.5e-5	1.00
Brain - Cerebellar Hemisphere	89	0.281	0.1	0.919
Brain - Putamen (basal ganglia)	82	0.280	0.01	0.995
Cells - EBV-transformed lymphocytes	114	0.276	0.009	0.988
Colon - Transverse	169	0.265	6.4e-6	1.00
Colon - Sigmoid	124	0.264	0.01	0.993
Skin - Not Sun Exposed (Suprapubic)	196	0.212	0.006	0.974
Brain - Hippocampus	81	0.209	0.1	0.838
Nerve - Tibial	256	0.207	3.5e-3	0.943
Small Intestine - Terminal Ileum	77	0.202	0.02	0.935
Testis	157	0.199	0.09	0.890
Artery - Tibial	285	0.178	0.2	0.730
Brain - Hypothalamus	81	0.154	0.3	0.504
Breast - Mammary Tissue	183	0.133	0.06	0.205
Brain - Nucleus accumbens (basal ganglia)	93	0.124	0.3	0.476
Heart - Atrial Appendage	159	0.110	0.4	0.555
Brain - Cortex	96	0.100	0.4	0.299
Brain - Frontal Cortex (BA9)	92	0.0849	0.5	0.332
Cells - Transformed fibroblasts	272	0.0763	0.2	0.00
Brain - Anterior cingulate cortex (BA24)	72	0.0651	0.5	0.0710
Heart - Left Ventricle	190	0.0514	0.7	0.229
Brain - Caudate (basal ganglia)	100	0.0317	0.8	0.0350
Artery - Aorta	197	-	-	-
Muscle - Skeletal	361	-	-	-
Ovary	85	-	-	-
Spleen	89	-	-	-
Uterus	70	-	-	-
Whole Blood	338	-0.0365	0.7	0.00
Pituitary	87	-0.113	0.4	0.00600
Liver	97	-0.125	0.3	0.00

Figure S7. Multi-tissue eQTL comparison between *HTR2B* and rs17440378 eQTL using GTEx database.



Multi-tissue eQTL Comparison

ENSG00000135914.5 HTR2B and rs17440378 eQTL (Meta Analysis RE2 P-Value: 2.20617e-23)

Tissue	Samples	Beta	p-value	post-prob
● Esophagus - Muscularis	218	0.562	1.2e-8	0.00
● Artery - Aorta	197	0.560	3.8e-5	0.00
● Esophagus - Gastroesophageal Junction	127	0.510	6.3e-6	0.00
● Lung	278	0.422	4.8e-6	0.00
● Artery - Coronary	118	0.378	0.02	0.0110
● Brain - Hypothalamus	81	0.307	0.1	0.0330
● Pancreas	149	0.273	0.07	0.0360
● Brain - Hippocampus	81	0.249	0.2	0.0790
● Testis	157	0.238	0.05	0.00800
● Cells - EBV-transformed lymphocytes	114	0.228	0.2	0.0330
● Brain - Putamen (basal ganglia)	82	0.201	0.4	0.0940
● Vagina	79	0.170	0.4	0.118
● Small Intestine - Terminal Ileum	77	0.169	0.3	0.0280
● Liver	97	0.154	0.4	0.0620
● Colon - Sigmoid	124	0.125	0.3	0.0180
● Artery - Tibial	285	0.117	0.2	0.00300
● Stomach	170	0.0920	0.4	0.0110
● Brain - Caudate (basal ganglia)	100	0.0773	0.7	0.167
● Brain - Nucleus accumbens (basal ganglia)	93	0.0642	0.7	0.150
● Prostate	87	0.0557	0.8	0.167
● Spleen	89	0.0370	0.9	0.184
● Cells - Transformed fibroblasts	272	-0.0171	0.8	0.0100
● Brain - Cerebellar Hemisphere	89	-0.0277	0.9	0.195
● Brain - Anterior cingulate cortex (BA24)	72	-0.0303	0.9	0.249
● Colon - Transverse	169	-0.0919	0.2	0.204
● Brain - Cortex	96	-0.0937	0.6	0.269
● Adrenal Gland	126	-0.104	0.3	0.186
● Ovary	85	-0.106	0.5	0.242
● Esophagus - Mucosa	241	-0.129	0.3	0.337
● Nerve - Tibial	256	-0.132	0.2	0.346
● Heart - Left Ventricle	190	-0.140	0.2	0.426
● Skin - Sun Exposed (Lower leg)	302	-0.147	0.2	0.348
● Skin - Not Sun Exposed (Suprapubic)	196	-0.157	0.3	0.253
● Uterus	70	-0.163	0.4	0.395
● Adipose - Visceral (Omentum)	185	-0.168	0.06	0.604
● Breast - Mammary Tissue	183	-0.176	0.1	0.445
● Muscle - Skeletal	361	-0.218	0.05	0.653
● Whole Blood	338	-0.232	0.03	0.748
● Adipose - Subcutaneous	298	-0.316	5.3e-4	0.968
● Brain - Frontal Cortex (BA9)	92	-0.337	0.1	0.517
● Thyroid	278	-0.350	1.3e-4	0.991
● Pituitary	87	-0.369	0.1	0.520
● Brain - Cerebellum	103	-0.373	0.05	0.702
● Heart - Atrial Appendage	159	-0.401	1.8e-4	0.995

Figure S8. Effects of THC (10 mg/kg) on locomotor activity in *Htr2b*$^{-/-}$ *and WT mice.*

In agreement with our previous data, *Htr2b*$^{-/-}$ *mice* showed hyperactivity in basal condition (SAL group). THC (10 mg/kg, i.p.) treatment significantly decreased locomotion in both *Htr2b*$^{-/-}$ and WT (*Htr2b*$^{+/+}$) mice. Genotype effect: *** = $P < 0.001$. Treatment effect: *** and ** = $P < 0.001$ and 0.01, respectively.

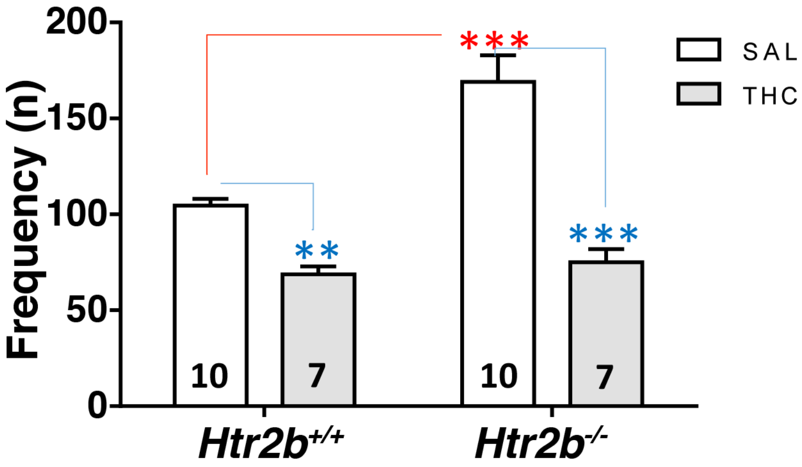


Table S1. Top Findings in African-Americans ($p < 5.0 \times 10^{-5}$).

Marker	Chr	Pos (hg19)	Gene Name	Eff Allele	Alt Allele	Alle Freq YP1	Beta YP1	SE YP1	*P* YP1	Alle Freq YP2	Beta YP2	SE YP2	*P* YP2	Alle Freq Meta	Beta Meta	SE Meta	*P* Meta	Direction
rs35750632	2	232022300	PSMD1	T	TG	0.877	-0.494	0.118	2.69E-05	0.869	-0.634	0.166	1.35E-04	0.875	-0.541	0.096	1.79E-08	--
rs17440378	2	231979355	HTR2B/PSMD1	T	C	0.109	0.56	0.125	6.93E-06	0.115	0.599	0.179	8.36E-04	0.111	0.573	0.102	2.16E-08	++
rs12468767	2	232036843	PSMD1	T	G	0.877	-0.496	0.12	3.75E-05	0.867	-0.6	0.171	4.55E-04	0.874	-0.53	0.098	7.10E-08	--
rs4823088	22	30696099	TBC1D10A	T	C					0.014	1.92	0.365	1.40E-07	0.014	1.92	0.365	1.40E-07	?+
rs757867	22	30715202	TBC1D10A	T	C					0.986	-1.92	0.365	1.40E-07	0.986	-1.92	0.365	1.40E-07	?-
rs2015035	22	30771554	CCDC157	T	G					0.014	1.92	0.365	1.40E-07	0.014	1.92	0.365	1.40E-07	?+
rs10057162	5	89525090		T	G	0.112	0.609	0.123	8.31E-07	0.11	0.378	0.19	4.63E-02	0.112	0.54	0.103	1.82E-07	++
rs34540120	5	89523174		T	TAC	0.887	-0.596	0.123	1.38E-06	0.89	-0.381	0.19	4.43E-02	0.888	-0.532	0.103	2.70E-07	--
rs149740722	3	177317870		C	G	0.026	0.729	0.244	2.83E-03	0.035	1.169	0.269	1.40E-05	0.03	0.928	0.181	2.89E-07	++
rs11949050	5	89523266		T	G	0.114	0.593	0.123	1.57E-06	0.111	0.375	0.19	4.78E-02	0.113	0.528	0.103	3.32E-07	++
rs16939648	16	27984243	GSG1L	A	G	0.227	0.476	0.105	5.33E-06	0.228	0.339	0.139	1.49E-02	0.227	0.426	0.084	3.38E-07	++
rs55637820	2	231935918	PSMD1	T	C	0.107	0.548	0.126	1.46E-05	0.109	0.489	0.182	7.25E-03	0.108	0.529	0.104	3.53E-07	++
rs34947651	16	27981236	GSG1L	T	C	0.229	0.471	0.104	5.76E-06	0.229	0.332	0.139	1.70E-02	0.229	0.421	0.083	4.13E-07	++
rs149345708	2	138308058	THSD7B	A	G	0.963	-0.961	0.191	4.89E-07					0.963	-0.961	0.191	4.89E-07	-?
rs4788020	16	27987389	GSG1L	A	C	0.236	0.469	0.104	6.18E-06	0.23	0.328	0.14	1.91E-02	0.234	0.419	0.083	4.97E-07	++
rs72759756	9	121909049		A	G	0.965	-0.95	0.189	5.30E-07					0.965	-0.95	0.19	5.30E-07	-?
rs17292799	9	121911162		A	G	0.965	-0.95	0.189	5.30E-07					0.965	-0.95	0.19	5.30E-07	-?
rs72759758	9	121911231		A	T	0.965	-0.95	0.189	5.30E-07					0.965	-0.95	0.19	5.30E-07	-?
rs72759765	9	121926039	BRINP1	A	G	0.035	0.95	0.189	5.30E-07					0.035	0.95	0.19	5.30E-07	+?
rs114270663	3	177320605		A	G	0.026	0.746	0.245	2.27E-03	0.034	1.114	0.272	4.28E-05	0.03	0.911	0.182	5.60E-07	++
rs111834647	3	74330779	CNTN3	A	G	0.015	1.342	0.268	5.60E-07					0.015	1.342	0.268	5.60E-07	+?
rs74015182	16	27982326	GSG1L	A	C	0.759	-0.46	0.102	6.48E-06	0.766	-0.32	0.138	2.08E-02	0.762	-0.411	0.082	5.66E-07	--
rs12932580	16	27981544	GSG1L	A	G	0.24	0.457	0.102	7.08E-06	0.234	0.323	0.138	1.97E-02	0.238	0.41	0.082	5.73E-07	++
rs73332709	5	173640890	NSG2	A	G	0.717	-0.479	0.096	6.30E-07					0.717	-0.479	0.096	6.30E-07	-?

rs72764138	15	92856395		T	G	0.116	0.5	0.125	6.25E-05	0.111	0.522	0.176	3.06E-03	0.115	0.507	0.102	6.40E-07	++
rs5997619	22	30752367	SF3A1	T	C					0.014	1.855	0.373	6.52E-07	0.014	1.855	0.373	6.52E-07	?+
rs112300838	6	9078153		C	G	0.959	-0.946	0.19	6.72E-07					0.959	-0.946	0.19	6.72E-07	-?
rs17882740	4	24796771	SOD3	A	G	0.011	1.516	0.306	7.47E-07					0.011	1.516	0.306	7.47E-07	+?
rs12927375	16	27987780	GSG1L	C	G	0.764	-0.469	0.104	6.18E-06	0.771	-0.309	0.141	2.81E-02	0.766	-0.413	0.084	7.72E-07	--
rs12444993	16	27980502	GSG1L	A	C	0.24	0.442	0.102	1.34E-05	0.232	0.331	0.138	1.65E-02	0.237	0.403	0.082	8.27E-07	++
rs12444955	16	27980343	GSG1L	T	C	0.229	0.455	0.103	1.10E-05	0.229	0.324	0.139	1.97E-02	0.229	0.408	0.083	8.68E-07	++
rs114717251	5	90216193	GPR98	T	C	0.023	0.94	0.237	7.15E-05	0.029	0.962	0.336	4.20E-03	0.025	0.947	0.194	9.83E-07	++
rs71535109	7	4436384		CT	C	0.475	-0.445	0.091	1.05E-06					0.475	-0.445	0.091	1.05E-06	-?
rs79001706	5	137050455	KLHL3	T	C	0.029	0.83	0.203	4.44E-05	0.024	0.895	0.336	7.71E-03	0.028	0.848	0.174	1.10E-06	++
rs384417	3	19871378		C	G	0.13	0.573	0.118	1.20E-06					0.13	0.573	0.118	1.20E-06	+?
rs187380	5	133411871		T	C	0.027	0.932	0.216	1.55E-05	0.033	0.68	0.294	2.08E-02	0.029	0.844	0.174	1.22E-06	++
rs576244464	6	27120517		A	AAAC	0.973	-0.95	0.23	3.70E-05	0.97	-0.774	0.301	1.01E-02	0.972	-0.885	0.183	1.29E-06	--
rs7689521	4	24797398	SOD3	C	G	0.989	-1.475	0.305	1.32E-06					0.989	-1.475	0.305	1.32E-06	-?
rs3736461	10	5855403	GDI2	C	G	0.043	0.752	0.184	4.34E-05	0.049	0.679	0.263	9.72E-03	0.045	0.728	0.151	1.35E-06	++
rs75339536	21	46011679	TSPEAR	A	G	0.102	0.617	0.13	1.91E-06					0.102	0.617	0.13	1.91E-06	+?
rs79041926	1	244316024		A	G	0.027	1.006	0.211	1.96E-06					0.026	1.006	0.211	1.96E-06	+?
rs9505639	6	9117717		A	G	0.029	1.013	0.213	2.07E-06					0.029	1.013	0.213	2.07E-06	+?
rs441117	3	19881723		A	G	0.13	0.576	0.118	1.16E-06	0.131	0.221	0.188	2.39E-01	0.131	0.475	0.1	2.14E-06	++
rs143747975	4	83752984	SEC31A	A	G	0.957	-0.822	0.174	2.22E-06					0.957	-0.822	0.174	2.22E-06	-?
rs570696747	1	175235513		A	C	0.011	1.456	0.308	2.26E-06					0.011	1.456	0.308	2.26E-06	+?
rs269377	3	19878733		T	C	0.132	0.56	0.118	2.27E-06					0.132	0.56	0.118	2.27E-06	+?
rs148697933	17	1027253	ABR	A	G	0.033	0.952	0.201	2.27E-06					0.033	0.952	0.201	2.27E-06	+?
rs11825707	11	8310456		T	C	0.95	-0.7	0.175	6.20E-05	0.94	-0.617	0.244	1.15E-02	0.947	-0.672	0.142	2.27E-06	--
rs77878914	21	46010039	TSPEAR	C	G	0.903	-0.623	0.132	2.34E-06					0.903	-0.623	0.132	2.34E-06	-?
rs269373	3	19857703		T	C	0.134	0.552	0.117	2.41E-06					0.134	0.552	0.117	2.41E-06	+?
rs7577721	2	231899645		T	C	0.118	0.507	0.126	5.56E-05	0.113	0.458	0.188	1.48E-02	0.117	0.492	0.104	2.54E-06	++
rs112431724	22	27971973		T	C	0.037	0.921	0.196	2.63E-06					0.037	0.921	0.196	2.63E-06	+?

rs10042483	5	89524771		A	G	0.907	-0.542	0.135	5.87E-05	0.912	-0.499	0.205	1.48E-02	0.908	-0.529	0.113	2.66E-06	--
rs116418533	5	90177946	GPR98	T	C	0.032	0.866	0.209	3.52E-05	0.034	0.678	0.298	2.27E-02	0.033	0.804	0.171	2.66E-06	++
rs7873111	9	99918645		T	C	0.62	-0.41	0.088	2.82E-06					0.62	-0.41	0.088	2.82E-06	-?
rs142759919	11	8322061		G	GT	0.049	0.715	0.177	5.22E-05	0.059	0.597	0.252	1.78E-02	0.052	0.676	0.145	2.97E-06	++
rs72882066	2	171027730		A	C	0.03	0.849	0.212	6.15E-05	0.038	0.677	0.276	1.43E-02	0.033	0.785	0.168	3.00E-06	++
rs76692579	5	90179044	GPR98	A	G	0.968	-0.866	0.209	3.52E-05	0.965	-0.66	0.297	2.64E-02	0.967	-0.798	0.171	3.15E-06	--
rs114831425	12	67638803		A	C	0.011	1.432	0.307	3.20E-06					0.011	1.432	0.307	3.20E-06	+?
rs114428454	5	90054631	GPR98	A	C	0.969	-0.799	0.213	1.74E-04	0.966	-0.802	0.293	6.17E-03	0.968	-0.8	0.172	3.36E-06	--
rs146987630	9	16120918		T	C	0.012	1.274	0.274	3.44E-06					0.012	1.274	0.274	3.44E-06	+?
rs13031656	2	181368613		C	G	0.151	0.392	0.118	8.77E-04	0.149	0.559	0.168	8.63E-04	0.15	0.447	0.097	3.52E-06	++
rs540376396	1	45138442	TMEM53	T	TAA	0.551	0.296	0.089	9.33E-04	0.542	0.438	0.13	7.69E-04	0.548	0.341	0.074	3.62E-06	++
rs11676228	2	181355237		A	T	0.148	0.391	0.118	9.67E-04	0.149	0.563	0.168	8.19E-04	0.148	0.448	0.097	3.75E-06	++
rs7422521	2	171029252		T	C	0.971	-0.825	0.214	1.19E-04	0.963	-0.714	0.277	1.00E-02	0.968	-0.783	0.17	3.84E-06	--
rs7424191	2	171029253		A	T	0.971	-0.825	0.214	1.19E-04	0.963	-0.714	0.277	1.00E-02	0.968	-0.783	0.17	3.84E-06	--
rs72812371	16	87034453		T	C	0.963	-0.89	0.193	3.84E-06					0.963	-0.89	0.193	3.84E-06	-?
rs73198371	5	105914822		T	G	0.041	0.83	0.18	3.88E-06					0.041	0.83	0.18	3.88E-06	+?
rs147184218	2	179829275	CCDC141	G	GC	0.031	0.948	0.199	1.87E-06	0.028	0.328	0.369	3.74E-01	0.031	0.808	0.175	3.88E-06	++
rs831430	12	104002077	STAB2	T	C	0.191	0.349	0.103	7.30E-04	0.165	0.536	0.163	1.01E-03	0.184	0.402	0.087	3.96E-06	++
rs13010875	2	181365923		A	G	0.852	-0.39	0.118	1.01E-03	0.851	-0.559	0.168	8.63E-04	0.852	-0.446	0.097	4.06E-06	--
rs7561337	2	181352806		T	G	0.849	-0.397	0.118	7.53E-04	0.851	-0.541	0.168	1.29E-03	0.85	-0.444	0.097	4.11E-06	--
rs12891188	14	60168943	RTN1	T	C	0.113	0.493	0.128	1.24E-04	0.108	0.472	0.186	1.13E-02	0.112	0.486	0.106	4.26E-06	++
rs79238552	17	17282172		T	C	0.969	-0.958	0.209	4.35E-06					0.969	-0.959	0.209	4.35E-06	-?
rs867437025	17	17282246		G	GTCA	0.032	0.921	0.2	4.38E-06					0.032	0.921	0.201	4.38E-06	+?
rs1424654	2	171029437		A	T	0.029	0.825	0.214	1.19E-04	0.038	0.698	0.276	1.15E-02	0.033	0.777	0.169	4.44E-06	++
rs1424652	2	171029691		T	C	0.029	0.825	0.214	1.19E-04	0.038	0.698	0.276	1.15E-02	0.033	0.777	0.169	4.44E-06	++
rs371934588	21	46010210	TSPEAR	A	G	0.099	0.602	0.131	4.48E-06					0.099	0.602	0.131	4.48E-06	+?
rs56011924	19	40923776		T	C	0.059	0.553	0.163	6.77E-04	0.06	0.709	0.226	1.74E-03	0.059	0.606	0.132	4.49E-06	++
rs17138931	6	4894001	CDYL	T	C	0.968	-0.951	0.207	4.53E-06					0.968	-0.951	0.207	4.53E-06	-?

rs369235400	7	129508264	UBE2H	CA	C	0.291	-0.448	0.108	3.22E-05	0.287	-0.322	0.159	4.29E-02	0.29	-0.408	0.089	4.70E-06	--
rs2019924	10	59771907		T	C	0.603	0.346	0.101	6.15E-04	0.598	0.431	0.141	2.21E-03	0.601	0.375	0.082	4.94E-06	++
rs34165368	9	97439214		A	G	0.028	0.698	0.228	2.17E-03	0.037	0.929	0.269	5.64E-04	0.032	0.794	0.174	4.94E-06	++
rs145862183	5	90013848	GPR98	A	G	0.016	0.863	0.279	1.97E-03	0.022	1.23	0.356	5.55E-04	0.018	1.002	0.22	4.99E-06	++
rs141163966	10	78075387	C10orf11	CT	C	0.065	0.683	0.157	1.41E-05	0.057	0.424	0.26	1.02E-01	0.063	0.613	0.135	5.09E-06	++
rs831683	12	103999401	STAB2	T	C	0.808	-0.347	0.103	7.76E-04	0.833	-0.525	0.163	1.29E-03	0.816	-0.398	0.087	5.10E-06	--
rs114648534	4	83745868	SEC31A	A	G	0.957	-0.797	0.175	5.11E-06					0.957	-0.797	0.175	5.11E-06	-?
rs186689544	7	13746927		T	C	0.985	-1.218	0.268	5.39E-06					0.985	-1.218	0.268	5.39E-06	-?
rs6084337	20	384898		A	G	0.711	0.473	0.104	5.41E-06					0.711	0.473	0.104	5.41E-06	+?
rs116776594	21	46010392	TSPEAR	C	G	0.9	-0.597	0.131	5.44E-06					0.9	-0.597	0.131	5.44E-06	-?
rs41281164	9	97419334		T	C	0.97	-0.498	0.225	2.67E-02	0.958	-1.089	0.251	1.43E-05	0.965	-0.761	0.167	5.51E-06	--
rs10261367	7	129509742	UBE2H	C	G	0.729	0.437	0.109	5.78E-05	0.731	0.353	0.164	3.09E-02	0.73	0.411	0.09	5.52E-06	++
rs199831803	7	129532098	UBE2H	CT	C	0.708	0.435	0.107	4.95E-05	0.714	0.337	0.16	3.53E-02	0.71	0.405	0.089	5.54E-06	++
rs374116165	21	46011406	TSPEAR	T	G	0.097	0.608	0.134	5.60E-06					0.097	0.608	0.134	5.60E-06	+?
rs144363824	21	46011409	TSPEAR	A	G	0.097	0.608	0.134	5.60E-06					0.097	0.608	0.134	5.60E-06	+?
rs1486831	7	129512093	UBE2H	C	G	0.293	-0.446	0.108	3.66E-05	0.287	-0.319	0.159	4.50E-02	0.291	-0.406	0.089	5.61E-06	--
rs79157838	7	10182601		T	C	0.987	-1.292	0.285	5.66E-06					0.987	-1.292	0.285	5.66E-06	-?
rs139899589	7	10183196		T	G	0.987	-1.292	0.285	5.66E-06					0.987	-1.292	0.285	5.66E-06	-?
rs525252	6	125429351		A	G	0.351	0.352	0.092	1.34E-04	0.357	0.325	0.132	1.40E-02	0.353	0.343	0.076	5.67E-06	++
rs4480118	8	61879363		A	C	0.627	0.354	0.091	1.03E-04	0.565	0.302	0.127	1.77E-02	0.606	0.336	0.074	5.70E-06	++
rs34487135	11	8325316		CAG	C	0.93	-0.614	0.151	5.07E-05	0.932	-0.495	0.238	3.76E-02	0.931	-0.58	0.128	5.76E-06	--
rs181998721	21	46010712	TSPEAR	T	C	0.9	-0.595	0.131	5.79E-06					0.9	-0.595	0.131	5.79E-06	-?
rs192724113	4	107447441		A	G	0.029	0.943	0.208	5.86E-06					0.029	0.943	0.208	5.86E-06	+?
rs79708490	12	101379068	ANO4	T	C	0.037	0.626	0.192	1.14E-03	0.04	0.914	0.28	1.10E-03	0.038	0.718	0.159	5.92E-06	++
rs148799648	15	43923717	STRC	A	G	0.056	0.751	0.159	2.35E-06	0.048	0.237	0.285	4.05E-01	0.054	0.629	0.139	5.97E-06	++
rs75209008	21	46009463	TSPEAR	A	G	0.902	-0.593	0.131	6.05E-06					0.902	-0.593	0.131	6.05E-06	-?
rs55682483	7	129508489	UBE2H	T	C	0.707	0.444	0.107	3.35E-05	0.711	0.305	0.157	5.14E-02	0.709	0.4	0.088	6.08E-06	++
rs6467267	7	129511036	UBE2H	T	C	0.271	-0.434	0.109	6.49E-05	0.269	-0.353	0.164	3.09E-02	0.27	-0.409	0.09	6.15E-06	--

rs6731739	2	235413286		A	G	0.278	0.412	0.093	9.31E-06	0.287	0.211	0.143	1.41E-01	0.281	0.352	0.078	6.17E-06	++
rs148402127	10	78120967	C10orf11	T	C	0.067	0.71	0.156	5.16E-06	0.059	0.309	0.265	2.45E-01	0.065	0.607	0.134	6.19E-06	++
rs112561380	7	129520535	UBE2H	T	TG	0.729	0.426	0.109	8.57E-05	0.732	0.372	0.165	2.44E-02	0.73	0.41	0.091	6.22E-06	++
rs10500121	7	129520583	UBE2H	T	C	0.729	0.426	0.109	8.57E-05	0.732	0.372	0.165	2.44E-02	0.73	0.41	0.091	6.22E-06	++
rs139636006	7	129572652	UBE2H	G	GTCTA	0.291	-0.438	0.108	4.85E-05	0.285	-0.33	0.16	3.99E-02	0.289	-0.404	0.089	6.24E-06	--
rs2275774	10	5799613	FAM208B	A	G	0.962	-0.765	0.191	6.13E-05	0.958	-0.605	0.283	3.27E-02	0.961	-0.715	0.158	6.27E-06	--
rs113913410	14	25909855		A	C	0.023	0.889	0.242	2.36E-04	0.017	1.025	0.388	8.35E-03	0.021	0.926	0.205	6.32E-06	++
rs74524297	21	46010025	TSPEAR	C	G	0.909	-0.61	0.135	6.33E-06					0.909	-0.61	0.135	6.33E-06	-?
rs114480957	21	46010464	TSPEAR	C	G	0.112	0.562	0.125	6.38E-06					0.112	0.562	0.125	6.38E-06	+?
rs35392308	7	149008043		A	G	0.936	-0.625	0.156	6.32E-05	0.95	-0.541	0.257	3.55E-02	0.94	-0.602	0.134	6.46E-06	--
rs12685159	9	97419146		A	C	0.031	0.485	0.224	3.05E-02	0.042	1.089	0.251	1.43E-05	0.035	0.753	0.167	6.65E-06	++
rs3807121	7	129505832	UBE2H	A	G	0.668	0.39	0.1	8.89E-05	0.674	0.336	0.15	2.52E-02	0.67	0.374	0.083	6.69E-06	++
rs4150990	19	40930577	SERTAD1	T	C	0.941	-0.531	0.161	9.76E-04	0.94	-0.709	0.226	1.74E-03	0.941	-0.591	0.131	6.72E-06	--
rs188073085	1	175225803		A	T	0.011	1.406	0.313	6.82E-06					0.011	1.406	0.312	6.82E-06	+?
rs76089179	18	7372568		T	C	0.021	1.097	0.244	6.95E-06					0.021	1.097	0.244	6.95E-06	+?
rs75823176	18	7372714		T	G	0.979	-1.097	0.244	6.95E-06					0.979	-1.097	0.244	6.95E-06	-?
rs116323131	18	7372732		A	G	0.979	-1.097	0.244	6.95E-06					0.979	-1.097	0.244	6.95E-06	-?
rs10817938	9	100462409		T	C	0.988	-1.248	0.278	6.98E-06					0.988	-1.248	0.278	6.98E-06	-?
rs1526323	7	129510308	UBE2H	A	T	0.273	-0.433	0.108	6.06E-05	0.27	-0.335	0.161	3.73E-02	0.272	-0.402	0.09	7.12E-06	--
rs587693578	21	46011718	TSPEAR	T	C	0.895	-0.578	0.129	7.15E-06					0.895	-0.578	0.129	7.15E-06	-?
rs7911724	10	59768336		T	G	0.6	0.347	0.101	6.12E-04	0.598	0.413	0.141	3.46E-03	0.599	0.37	0.082	7.19E-06	++
rs1930476	10	59768994		T	C	0.4	-0.347	0.101	6.12E-04	0.402	-0.413	0.141	3.46E-03	0.401	-0.37	0.082	7.19E-06	--
rs4405262	10	59769179		T	C	0.6	0.347	0.101	6.12E-04	0.598	0.413	0.141	3.46E-03	0.599	0.37	0.082	7.19E-06	++
rs142536865	10	59769818		A	AAAG	0.6	0.347	0.101	6.12E-04	0.598	0.413	0.141	3.46E-03	0.599	0.37	0.082	7.19E-06	++
rs145381340	1	175243401		A	G	0.988	-1.354	0.302	7.44E-06					0.988	-1.354	0.302	7.44E-06	-?
rs146159724	1	175248857		T	G	0.012	1.354	0.302	7.44E-06					0.012	1.354	0.302	7.44E-06	+?
rs147003316	1	175250175		A	G	0.988	-1.354	0.302	7.44E-06					0.988	-1.354	0.302	7.44E-06	-?
rs73046390	19	40933942		A	G	0.941	-0.538	0.161	8.42E-04	0.94	-0.687	0.226	2.42E-03	0.94	-0.588	0.131	7.49E-06	--

rs11570907	12	68623905		T	TG	0.948	-0.719	0.161	7.52E-06					0.948	-0.719	0.161	7.52E-06	-?
rs6668870	1	45141645	C1orf228	C	G	0.433	0.302	0.09	7.78E-04	0.446	0.378	0.126	2.70E-03	0.437	0.328	0.073	7.53E-06	++
rs11582807	1	45142157	C1orf228	A	G	0.567	-0.302	0.09	7.78E-04	0.554	-0.378	0.126	2.70E-03	0.563	-0.328	0.073	7.53E-06	--
rs11581074	1	45142209	C1orf228	A	G	0.433	0.302	0.09	7.78E-04	0.446	0.378	0.126	2.70E-03	0.437	0.328	0.073	7.53E-06	++
rs1344367	5	67845698		A	C	0.387	0.399	0.089	7.62E-06					0.387	0.399	0.089	7.62E-06	+?
rs28604351	7	129526340	UBE2H	T	G	0.746	0.444	0.109	4.86E-05	0.741	0.321	0.162	4.80E-02	0.744	0.406	0.091	7.68E-06	++
rs144609516	18	27668193		A	G	0.987	-1.226	0.289	2.26E-05	0.986	-0.758	0.453	9.46E-02	0.986	-1.091	0.244	7.77E-06	--
rs559573174	4	83757347	SEC31A	A	G	0.022	1.006	0.225	7.85E-06					0.022	1.006	0.225	7.85E-06	+?
rs77322363	5	90018628	GPR98	A	C	0.967	-0.74	0.207	3.39E-04	0.96	-0.762	0.285	7.57E-03	0.964	-0.748	0.167	7.86E-06	--
rs11448310	7	129521461	UBE2H	CT	C	0.273	-0.422	0.108	8.99E-05	0.269	-0.353	0.162	2.95E-02	0.272	-0.401	0.09	7.93E-06	--
rs62491499	7	129508277	UBE2H	A	G	0.724	0.419	0.107	9.71E-05	0.73	0.36	0.163	2.77E-02	0.726	0.401	0.09	7.95E-06	++
rs142223349	6	15920153		T	TG	0.02	1.101	0.256	1.68E-05	0.021	0.611	0.382	1.10E-01	0.02	0.95	0.213	7.96E-06	++
rs74317380	11	101841571	KIAA1377	T	C	0.017	1.164	0.261	7.99E-06					0.017	1.164	0.261	7.99E-06	+?
rs182008011	11	101793916	KIAA1377	T	C	0.017	1.161	0.26	8.09E-06					0.017	1.161	0.26	8.09E-06	+?
rs201360771	11	101793918	KIAA1377	A	AG	0.983	-1.161	0.26	8.09E-06					0.983	-1.161	0.26	8.09E-06	-?
rs146312926	21	46009947	TSPEAR	G	GTGA	0.903	-0.592	0.133	8.19E-06					0.903	-0.592	0.133	8.19E-06	-?
rs2037720	7	129506548	UBE2H	T	C	0.274	-0.42	0.108	9.60E-05	0.27	-0.357	0.163	2.89E-02	0.273	-0.401	0.09	8.22E-06	--
rs11334941	7	129510562	UBE2H	T	TA	0.289	-0.436	0.108	4.99E-05	0.285	-0.312	0.159	4.98E-02	0.288	-0.397	0.089	8.23E-06	--
rs34598210	7	48646412	ABCA13	T	C	0.011	1.225	0.309	7.50E-05	0.016	0.927	0.437	3.37E-02	0.013	1.126	0.253	8.26E-06	++
rs115276657	17	1025166	ABR	T	C	0.035	0.882	0.198	8.37E-06					0.035	0.882	0.198	8.37E-06	+?
rs146658424	11	22391195	SLC17A6	A	G	0.019	1.121	0.252	8.44E-06					0.019	1.121	0.252	8.44E-06	+?
rs184447374	14	44533372		T	C	0.021	1.06	0.238	8.45E-06					0.021	1.06	0.238	8.45E-06	+?
rs7789191	7	129583060	UBE2H	C	G	0.708	0.442	0.107	3.81E-05	0.714	0.292	0.156	6.17E-02	0.71	0.394	0.088	8.48E-06	++
rs57314877	7	129553263	UBE2H	T	C	0.708	0.431	0.107	5.78E-05	0.714	0.316	0.158	4.56E-02	0.71	0.395	0.089	8.58E-06	++
rs28473687	7	129555368	UBE2H	T	C	0.708	0.431	0.107	5.78E-05	0.714	0.316	0.158	4.56E-02	0.71	0.395	0.089	8.58E-06	++
rs7783328	7	129564637	UBE2H	C	G	0.707	0.427	0.107	6.25E-05	0.713	0.32	0.158	4.31E-02	0.709	0.394	0.088	8.59E-06	++
rs148426090	21	46009955	TSPEAR	C	G	0.097	0.59	0.133	8.59E-06					0.097	0.591	0.133	8.59E-06	+?
rs703607	12	104007349	STAB2	A	C	0.188	0.329	0.104	1.50E-03	0.161	0.552	0.167	9.30E-04	0.181	0.391	0.088	8.77E-06	++

rs62491518	7	129527572	UBE2H	T	C	0.292	-0.431	0.107	5.78E-05	0.286	-0.314	0.158	4.65E-02	0.29	-0.394	0.089	8.78E-06	--
rs10216153	7	129528249	UBE2H	T	C	0.292	-0.431	0.107	5.78E-05	0.286	-0.314	0.158	4.65E-02	0.29	-0.394	0.089	8.78E-06	--
rs146481131	7	129539083	UBE2H	T	TG	0.273	-0.415	0.108	1.26E-04	0.268	-0.373	0.165	2.39E-02	0.272	-0.402	0.09	8.78E-06	--
rs587610033	21	46010648	TSPEAR	A	G	0.099	0.587	0.132	8.98E-06					0.099	0.587	0.132	8.98E-06	+?
rs16933397	10	78106137	C10orf11	T	C	0.07	0.664	0.152	1.30E-05	0.06	0.348	0.26	1.80E-01	0.067	0.583	0.131	9.03E-06	++
rs12463656	2	232036396	PSMD1	A	G	0.157	0.383	0.11	5.05E-04	0.158	0.459	0.165	5.40E-03	0.157	0.407	0.092	9.10E-06	++
rs7566683	2	181349217		T	G	0.841	-0.344	0.116	3.01E-03	0.842	-0.584	0.167	4.58E-04	0.841	-0.422	0.095	9.11E-06	--
rs139921370	12	72402228	TPH2	T	G	0.013	1.108	0.314	4.15E-04	0.018	1.036	0.385	7.15E-03	0.015	1.079	0.243	9.17E-06	++
rs7803795	7	129561516	UBE2H	T	C	0.272	-0.421	0.108	9.90E-05	0.268	-0.351	0.163	3.11E-02	0.271	-0.4	0.09	9.17E-06	--
rs73161641	7	129530503	UBE2H	T	C	0.272	-0.419	0.108	1.05E-04	0.269	-0.353	0.162	2.95E-02	0.271	-0.399	0.09	9.23E-06	--
rs12993861	2	181375740		C	G	0.811	-0.332	0.11	2.47E-03	0.814	-0.533	0.156	6.55E-04	0.812	-0.398	0.09	9.25E-06	--
rs11570908	12	68623721		T	G	0.053	0.704	0.159	9.27E-06					0.053	0.704	0.159	9.27E-06	+?
rs17162295	7	129516157	UBE2H	A	C	0.271	-0.421	0.108	1.01E-04	0.269	-0.353	0.164	3.09E-02	0.27	-0.4	0.09	9.27E-06	--
rs10837583	11	41164213	LRRC4C	T	C	0.874	0.713	0.161	9.27E-06					0.874	0.713	0.161	9.27E-06	+?
rs114975594	21	46009991	TSPEAR	A	G	0.097	0.588	0.133	9.32E-06					0.097	0.588	0.133	9.32E-06	+?
rs74569492	18	7371726		A	C	0.021	1.078	0.243	9.34E-06					0.021	1.078	0.243	9.34E-06	+?
rs77236103	18	7371868		A	G	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs79085700	18	7371966		A	G	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs79167849	18	7372024		A	C	0.021	1.078	0.243	9.34E-06					0.021	1.078	0.243	9.34E-06	+?
rs143604981	18	7372071		T	C	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs145745578	18	7372077		T	C	0.021	1.078	0.243	9.34E-06					0.021	1.078	0.243	9.34E-06	+?
rs148540659	18	7372114		T	C	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs141096077	18	7372258		T	C	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs141927305	18	7372319		A	G	0.021	1.078	0.243	9.34E-06					0.021	1.078	0.243	9.34E-06	+?
rs74809813	18	7372418		T	C	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs79490721	18	7372426		A	C	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?
rs75261297	18	7372478		T	G	0.021	1.078	0.243	9.34E-06					0.021	1.078	0.243	9.34E-06	+?
rs78278535	18	7372541		T	G	0.979	-1.078	0.243	9.34E-06					0.979	-1.078	0.243	9.34E-06	-?

rs58731223	11	86433926		CA	C	0.337	0.418	0.094	9.35E-06					0.337	0.418	0.094	9.35E-06	+?
rs73804436	4	24819266	CCDC149	A	C	0.014	1.242	0.28	9.38E-06					0.013	1.242	0.28	9.38E-06	+?
rs11742479	5	178935867		A	G	0.666	-0.413	0.093	9.47E-06					0.666	-0.413	0.093	9.47E-06	-?
rs57369579	6	42176743	MRPS10	T	TG	0.765	-0.448	0.101	9.48E-06					0.765	-0.448	0.101	9.48E-06	-?
rs149105997	18	27642914		A	G	0.014	1.203	0.288	2.87E-05	0.014	0.758	0.453	9.46E-02	0.014	1.075	0.243	9.51E-06	++
rs13020623	2	181375915		T	C	0.814	-0.331	0.11	2.54E-03	0.814	-0.533	0.156	6.55E-04	0.814	-0.397	0.09	9.54E-06	--
rs144346907	11	41164369	LRRC4C	A	AT	0.126	-0.712	0.161	9.55E-06					0.126	-0.712	0.161	9.55E-06	-?
rs199780898	11	41164371	LRRC4C	A	G	0.126	-0.712	0.161	9.55E-06					0.126	-0.712	0.161	9.55E-06	-?
rs4660821	1	45144850	C1orf228	T	C	0.416	0.282	0.091	1.92E-03	0.437	0.405	0.124	1.12E-03	0.424	0.325	0.073	9.58E-06	++
rs189111952	14	44541075		A	T	0.98	-1.081	0.244	9.63E-06					0.98	-1.081	0.244	9.63E-06	-?
rs111854232	21	46011162	TSPEAR	T	C	0.094	0.592	0.134	9.68E-06					0.094	0.592	0.134	9.68E-06	+?
rs10240142	7	129560225	UBE2H	T	C	0.728	0.419	0.108	1.05E-04	0.732	0.351	0.163	3.11E-02	0.729	0.398	0.09	9.72E-06	++
rs147325163	2	179833623	CCDC141	A	G	0.031	0.916	0.201	5.11E-06	0.028	0.315	0.369	3.93E-01	0.031	0.779	0.176	1.02E-05	++
rs150717437	21	46011250	TSPEAR	A	G	0.098	0.587	0.133	1.03E-05					0.098	0.587	0.133	1.03E-05	+?
rs79382781	10	78113739	C10orf11	A	T	0.932	-0.661	0.153	1.53E-05	0.94	-0.348	0.26	1.80E-01	0.934	-0.581	0.132	1.05E-05	--
rs34760947	7	148980222	ZNF783	T	C	0.202	0.408	0.105	1.02E-04	0.19	0.336	0.159	3.46E-02	0.199	0.386	0.088	1.05E-05	++
rs13403531	2	725541		A	G	0.019	0.643	0.278	2.08E-02	0.013	1.868	0.417	7.58E-06	0.017	1.019	0.231	1.05E-05	++
rs200347539	4	83732683		G	GCTT	0.043	0.778	0.177	1.06E-05					0.043	0.778	0.177	1.06E-05	+?
rs78738570	20	1837957		A	G	0.017	1.15	0.261	1.06E-05					0.017	1.15	0.261	1.06E-05	+?
rs1407351	9	10166359	PTPRD	T	C	0.663	-0.304	0.093	1.11E-03	0.647	-0.401	0.133	2.57E-03	0.658	-0.336	0.076	1.08E-05	--
rs527968368	17	1025083	ABR	A	C	0.963	-0.858	0.195	1.09E-05					0.963	-0.858	0.195	1.09E-05	-?
rs193033936	9	15413833		C	G	0.978	-0.966	0.22	1.11E-05					0.978	-0.966	0.22	1.11E-05	-?
rs7801603	7	129573322	UBE2H	A	G	0.73	0.412	0.108	1.41E-04	0.734	0.365	0.166	2.75E-02	0.731	0.398	0.091	1.12E-05	++
rs111355324	1	238648609		A	G	0.038	0.831	0.189	1.12E-05					0.038	0.831	0.189	1.12E-05	+?
rs269370	3	19858681		T	C	0.191	0.472	0.108	1.13E-05					0.191	0.472	0.108	1.13E-05	+?
rs116327582	7	142416842		A	G	0.988	-1.251	0.285	1.13E-05					0.988	-1.251	0.285	1.13E-05	-?
rs12210021	6	47305805		A	G	0.166	0.347	0.117	3.02E-03	0.164	0.556	0.164	6.81E-04	0.166	0.418	0.095	1.14E-05	++
rs11768305	7	156244159		A	G	0.175	0.345	0.107	1.22E-03	0.179	0.481	0.158	2.29E-03	0.177	0.388	0.088	1.15E-05	++

rs7237755	18	22604326		T	C	0.491	-0.388	0.093	2.97E-05	0.501	-0.227	0.137	9.72E-02	0.494	-0.338	0.077	1.15E-05	--
rs4800613	18	22607723		A	G	0.509	0.388	0.093	2.97E-05	0.499	0.227	0.137	9.72E-02	0.506	0.338	0.077	1.15E-05	++
rs79125076	19	13657260	CACNA1A	A	C	0.928	-0.653	0.149	1.15E-05					0.928	-0.653	0.149	1.15E-05	-?
rs116899926	7	120903368	CPED1	C	G	0.99	-1.408	0.321	1.15E-05					0.99	-1.408	0.321	1.15E-05	-?
rs143859751	10	58534221		A	G	0.984	-0.873	0.287	2.36E-03	0.982	-1.314	0.4	1.02E-03	0.984	-1.023	0.233	1.15E-05	--
rs512296	6	125430128		T	C	0.681	-0.353	0.094	1.84E-04	0.665	-0.316	0.137	2.14E-02	0.676	-0.341	0.078	1.16E-05	--
rs4660822	1	45144856	C1orf228	A	G	0.583	-0.277	0.091	2.28E-03	0.563	-0.405	0.124	1.12E-03	0.576	-0.322	0.073	1.16E-05	--
rs75183205	7	77962515	MAGI2	A	G	0.012	0.885	0.325	6.45E-03	0.016	1.365	0.383	3.63E-04	0.013	1.086	0.248	1.17E-05	++
rs17150545	7	77963011	MAGI2	T	C	0.988	-0.885	0.325	6.45E-03	0.984	-1.365	0.383	3.63E-04	0.987	-1.086	0.248	1.17E-05	--
rs75623315	7	77964777	MAGI2	C	G	0.988	-0.885	0.325	6.45E-03	0.984	-1.365	0.383	3.63E-04	0.987	-1.086	0.248	1.17E-05	--
rs10025514	4	114786768		T	C	0.968	-0.837	0.202	3.38E-05	0.963	-0.506	0.3	9.16E-02	0.967	-0.734	0.168	1.18E-05	--
rs868256	4	4852156		A	G	0.924	-0.417	0.149	5.19E-03	0.901	-0.679	0.192	3.96E-04	0.915	-0.516	0.118	1.18E-05	--
rs115032837	8	3610483	CSMD1	A	T	0.05	0.758	0.173	1.19E-05					0.05	0.758	0.173	1.19E-05	+?
rs201273544	9	106828888		A	AAGAGACTG	0.104	0.475	0.125	1.52E-04	0.085	0.485	0.221	2.81E-02	0.1	0.477	0.109	1.20E-05	++
rs35621087	10	1181739		CT	C	0.272	0.406	0.096	2.51E-05	0.302	0.221	0.136	1.04E-01	0.282	0.344	0.079	1.20E-05	++
rs10980872	9	99913443		T	C	0.324	0.407	0.093	1.21E-05					0.324	0.407	0.093	1.21E-05	+?
rs16933471	10	78142829	C10orf11	T	C	0.059	0.683	0.164	3.03E-05	0.049	0.431	0.281	1.25E-01	0.056	0.619	0.141	1.21E-05	++
rs116100498	7	51809381		T	G	0.934	-0.669	0.153	1.22E-05					0.934	-0.669	0.153	1.22E-05	-?
rs4963941	12	26099201		T	C	0.03	0.394	0.248	1.12E-01	0.036	1.257	0.267	2.45E-06	0.033	0.794	0.182	1.23E-05	++
rs72772400	10	5865257	GDI2	T	C	0.95	-0.638	0.171	1.95E-04	0.942	-0.54	0.234	2.10E-02	0.947	-0.604	0.138	1.24E-05	--
rs13402242	2	232029568	PSMD1	A	G	0.844	-0.375	0.11	6.87E-04	0.842	-0.459	0.165	5.40E-03	0.843	-0.401	0.092	1.25E-05	--
rs16933248	10	78072512	C10orf11	T	C	0.071	0.618	0.151	4.47E-05	0.06	0.428	0.254	9.26E-02	0.068	0.568	0.13	1.25E-05	++
rs35296561	8	61883600		CT	C	0.368	-0.351	0.092	1.41E-04	0.429	-0.277	0.127	2.88E-02	0.389	-0.326	0.075	1.28E-05	--
rs565389564	18	46129438	CTIF	G	GTGGA	0.019	1.108	0.254	1.28E-05					0.019	1.108	0.254	1.28E-05	+?
rs13010533	2	181386683		T	G	0.827	-0.354	0.111	1.49E-03	0.825	-0.498	0.162	2.07E-03	0.827	-0.4	0.092	1.29E-05	--
rs9664798	10	78111873	C10orf11	A	G	0.931	-0.653	0.153	1.94E-05	0.94	-0.348	0.26	1.80E-01	0.933	-0.575	0.132	1.29E-05	--
rs10216157	7	129528319	UBE2H	C	G	0.73	0.412	0.109	1.53E-04	0.734	0.357	0.163	2.90E-02	0.732	0.395	0.09	1.29E-05	++

rs554295044	13	53759775		A	AC	0.985	-0.889	0.305	3.52E-03	0.988	-1.354	0.402	7.54E-04	0.986	-1.059	0.243	1.30E-05	--
rs61045241	7	97640967		T	C	0.714	0.375	0.099	1.49E-04	0.739	0.364	0.17	3.16E-02	0.721	0.373	0.086	1.31E-05	++
rs11817495	10	133251360		A	G	0.011	1.047	0.325	1.26E-03	0.011	1.399	0.467	2.74E-03	0.011	1.162	0.267	1.31E-05	++
rs76586525	19	46720605		T	C	0.989	-1.378	0.316	1.33E-05					0.989	-1.378	0.317	1.33E-05	-?
rs140791899	19	46725285		CA	C	0.989	-1.378	0.316	1.33E-05					0.989	-1.378	0.317	1.33E-05	-?
rs191791711	1	175217491		T	C	0.989	-1.344	0.309	1.34E-05					0.989	-1.344	0.309	1.34E-05	-?
rs189646905	1	175218407		T	G	0.011	1.344	0.309	1.34E-05					0.011	1.344	0.309	1.34E-05	+?
rs2600749	2	237609991		A	C	0.557	-0.393	0.09	1.36E-05					0.557	-0.393	0.09	1.36E-05	-?
rs7525994	1	160676947	CD48	T	C	0.036	0.852	0.196	1.37E-05					0.036	0.852	0.196	1.37E-05	+?
rs7548088	1	160677259	CD48	A	G	0.036	0.852	0.196	1.37E-05					0.036	0.852	0.196	1.37E-05	+?
rs571731771	3	87894018		A	G	0.016	0.803	0.275	3.53E-03	0.019	1.245	0.37	7.70E-04	0.017	0.961	0.221	1.37E-05	++
rs200313400	15	44001693	STRC	CA	C	0.049	0.813	0.173	2.63E-06	0.042	0.155	0.31	6.16E-01	0.047	0.656	0.151	1.39E-05	++
rs34838451	11	87862535	RAB38	A	G	0.037	0.896	0.197	5.52E-06	0.026	0.247	0.389	5.25E-01	0.035	0.764	0.176	1.42E-05	++
rs9953030	18	22609639		A	G	0.475	0.382	0.091	2.54E-05	0.473	0.209	0.142	1.42E-01	0.474	0.332	0.076	1.42E-05	++
rs12933234	16	27981362	GSG1L	A	T	0.273	0.415	0.101	3.98E-05	0.268	0.24	0.139	8.35E-02	0.271	0.354	0.082	1.42E-05	++
rs12933235	16	27981363	GSG1L	T	G	0.727	-0.415	0.101	3.98E-05	0.732	-0.24	0.139	8.35E-02	0.729	-0.354	0.082	1.42E-05	--
rs55845359	16	27981644	GSG1L	A	G	0.727	-0.415	0.101	3.98E-05	0.732	-0.24	0.139	8.35E-02	0.729	-0.354	0.082	1.42E-05	--
rs4572960	5	51572584		T	C	0.402	0.224	0.095	1.84E-02	0.417	0.511	0.125	4.66E-05	0.408	0.329	0.076	1.43E-05	++
rs190533586	1	156160458		T	C					0.012	1.887	0.435	1.43E-05	0.012	1.886	0.435	1.43E-05	?+
rs75272883	2	59610249		T	C	0.986	-1.154	0.281	3.88E-05	0.986	-0.723	0.454	1.11E-01	0.986	-1.035	0.239	1.44E-05	--
rs11265621	1	154442960	SHE	A	G	0.373	-0.308	0.093	9.29E-04	0.39	-0.402	0.141	4.28E-03	0.378	-0.337	0.078	1.44E-05	--
rs2929380	3	19941458	EFHB	A	G	0.192	0.458	0.104	1.01E-05	0.197	0.186	0.162	2.53E-01	0.194	0.379	0.087	1.44E-05	++
rs188075933	4	158095783		T	G	0.983	-1.118	0.249	7.15E-06	0.986	-0.313	0.577	5.88E-01	0.983	-0.992	0.229	1.45E-05	--
rs74079527	1	63473031		T	C	0.078	0.61	0.141	1.45E-05					0.078	0.61	0.141	1.45E-05	+?
rs192300427	10	122019656		A	T	0.984	-1.039	0.27	1.22E-04	0.988	-1.017	0.507	4.46E-02	0.985	-1.034	0.239	1.45E-05	--
rs6844034	4	59833690		T	G	0.311	0.358	0.095	1.80E-04	0.307	0.306	0.139	2.75E-02	0.309	0.341	0.079	1.45E-05	++
rs114521859	21	46010602	TSPEAR	T	G	0.907	-0.582	0.134	1.45E-05					0.907	-0.582	0.134	1.45E-05	-?
rs78872057	18	68457556		A	T	0.022	0.98	0.226	1.46E-05					0.022	0.98	0.226	1.46E-05	+?

rs1198415	14	82910064		A	G	0.273	0.306	0.096	1.48E-03	0.272	0.428	0.141	2.43E-03	0.272	0.345	0.08	1.46E-05	++
rs549695780	1	225285904	DNAH14	G	GA	0.222	-0.49	0.118	3.11E-05	0.242	-0.266	0.163	1.03E-01	0.229	-0.413	0.095	1.49E-05	--
rs74365341	6	17297964		A	C	0.013	1.27	0.293	1.49E-05					0.013	1.27	0.293	1.49E-05	+?
rs74733341	6	17299306		T	C	0.013	1.27	0.293	1.49E-05					0.013	1.27	0.293	1.49E-05	+?
rs111227041	6	17302215		C	G	0.987	-1.27	0.293	1.49E-05					0.987	-1.27	0.293	1.49E-05	-?
rs77701626	6	17304052		T	C	0.987	-1.27	0.293	1.49E-05					0.987	-1.27	0.293	1.49E-05	-?
rs70999394	6	17304528		T	TCA	0.987	-1.27	0.293	1.49E-05					0.987	-1.27	0.293	1.49E-05	-?
rs116339771	12	101377122	ANO4	A	G	0.038	0.603	0.19	1.48E-03	0.039	0.866	0.285	2.38E-03	0.038	0.684	0.158	1.49E-05	++
rs74875220	11	8302036		T	C	0.964	-0.869	0.201	1.50E-05					0.964	-0.869	0.201	1.50E-05	-?
rs703605	12	103995659	STAB2	A	G	0.198	0.335	0.102	1.01E-03	0.181	0.464	0.16	3.77E-03	0.193	0.372	0.086	1.50E-05	++
rs363374	10	118993483		A	G	0.293	0.427	0.099	1.51E-05					0.293	0.427	0.099	1.51E-05	+?
rs690874	7	49870026	VWC2	A	G	0.136	-0.693	0.16	1.52E-05					0.136	-0.693	0.16	1.52E-05	-?
rs9423376	10	4834556	AKR1E2	T	C	0.255	0.35	0.103	6.67E-04	0.261	0.365	0.137	7.70E-03	0.257	0.356	0.082	1.55E-05	++
rs75729329	18	68492090		T	G	0.02	1.031	0.239	1.60E-05					0.02	1.031	0.239	1.60E-05	+?
rs76115917	18	68492666		A	G	0.98	-1.031	0.239	1.60E-05					0.98	-1.031	0.239	1.60E-05	-?
rs74686437	18	68493130		T	C	0.98	-1.031	0.239	1.60E-05					0.98	-1.031	0.239	1.60E-05	-?
rs76494002	18	68493957		A	G	0.98	-1.031	0.239	1.60E-05					0.98	-1.031	0.239	1.60E-05	-?
rs142360392	18	46121359	CTIF	T	C	0.019	1.095	0.254	1.61E-05					0.019	1.095	0.254	1.61E-05	+?
rs199655286	3	87879869		G	GA	0.016	0.788	0.274	4.05E-03	0.019	1.245	0.37	7.70E-04	0.017	0.95	0.22	1.62E-05	++
rs13071420	3	168981877	MECOM	T	C	0.79	-0.454	0.105	1.63E-05					0.79	-0.454	0.105	1.63E-05	-?
rs189254565	4	83790534	SEC31A	T	C	0.04	0.8	0.182	1.04E-05	0.033	0.307	0.325	3.44E-01	0.038	0.683	0.158	1.64E-05	++
rs73188567	8	8376863		A	T	0.049	0.517	0.176	3.33E-03	0.049	0.778	0.237	1.05E-03	0.049	0.61	0.141	1.64E-05	++
rs112372099	7	129572114	UBE2H	A	C	0.249	-0.434	0.11	8.58E-05	0.252	-0.31	0.165	6.10E-02	0.25	-0.396	0.092	1.66E-05	--
rs145950432	2	184641814		T	C	0.018	0.729	0.275	8.04E-03	0.011	1.661	0.431	1.18E-04	0.016	0.999	0.232	1.67E-05	++
rs115521622	5	10365654		T	C	0.057	0.709	0.165	1.67E-05					0.057	0.709	0.165	1.67E-05	+?
rs10103425	8	61880958		T	C	0.554	0.374	0.087	1.68E-05					0.554	0.374	0.087	1.68E-05	+?
rs10110804	8	61882557		T	C	0.554	0.374	0.087	1.68E-05					0.554	0.374	0.087	1.68E-05	+?
rs12428701	13	108086788	FAM155A	T	G	0.789	-0.402	0.106	1.46E-04	0.793	-0.317	0.153	3.80E-02	0.79	-0.374	0.087	1.69E-05	--

rs1815102	7	97642988		A	G	0.274	-0.378	0.099	1.39E-04	0.247	-0.346	0.173	4.52E-02	0.267	-0.37	0.086	1.70E-05	--
rs115433897	7	68092763		T	C	0.028	0.822	0.213	1.16E-04	0.031	0.649	0.332	5.06E-02	0.029	0.772	0.179	1.70E-05	++
rs77348404	1	160678066	CD48	C	G	0.037	0.843	0.196	1.71E-05					0.037	0.843	0.196	1.71E-05	+?
rs10059711	5	51551758		T	C	0.41	0.236	0.094	1.22E-02	0.42	0.521	0.133	9.38E-05	0.413	0.33	0.077	1.72E-05	++
rs192081737	4	47748379	CORIN	T	C	0.989	-0.952	0.312	2.29E-03	0.985	-1.147	0.376	2.26E-03	0.987	-1.032	0.24	1.73E-05	--
rs7147005	14	98473288		A	G	0.334	0.315	0.098	1.25E-03	0.348	0.413	0.143	3.81E-03	0.339	0.346	0.081	1.73E-05	++
rs62489374	7	129581482	UBE2H	T	C	0.728	0.408	0.107	1.44E-04	0.732	0.329	0.161	4.10E-02	0.729	0.384	0.089	1.73E-05	++
rs187874943	12	4844565	RP11-234B24.6	T	C	0.968	-0.405	0.226	7.38E-02	0.975	-1.587	0.322	8.32E-07	0.97	-0.796	0.185	1.74E-05	--
rs28580019	18	22610199		T	C	0.524	-0.378	0.091	3.13E-05	0.526	-0.208	0.143	1.45E-01	0.525	-0.329	0.077	1.74E-05	--
rs4860464	4	59832534		A	T	0.313	0.355	0.095	1.98E-04	0.308	0.302	0.14	3.07E-02	0.311	0.338	0.079	1.77E-05	++
rs7186668	16	86522899		C	G	0.651	-0.294	0.092	1.34E-03	0.616	-0.395	0.135	3.53E-03	0.64	-0.326	0.076	1.77E-05	--
rs116219705	7	13100672		T	C	0.978	-1.027	0.239	1.78E-05					0.978	-1.027	0.239	1.78E-05	-?
rs12813085	12	68617828	IL26	T	C	0.055	0.677	0.158	1.78E-05					0.055	0.677	0.158	1.78E-05	+?
rs184756085	4	83786479	SEC31A	A	G	0.984	-1.145	0.267	1.79E-05					0.984	-1.145	0.267	1.79E-05	-?
rs143840340	2	10583762	ODC1	A	G	0.013	1.232	0.287	1.81E-05					0.013	1.232	0.287	1.81E-05	+?
rs144229860	2	10587373	ODC1	G	GTCAA	0.013	1.232	0.287	1.81E-05					0.013	1.232	0.287	1.81E-05	+?
rs113131728	1	219680667		T	G	0.054	-0.919	0.272	7.11E-04	0.052	-1.426	0.515	5.59E-03	0.054	-1.03	0.24	1.81E-05	--
rs2136601	10	1180935		A	G	0.742	-0.366	0.097	1.69E-04	0.713	-0.288	0.137	3.52E-02	0.732	-0.34	0.079	1.82E-05	--
rs55859212	14	92988685	RIN3	T	C	0.478	0.38	0.099	1.20E-04	0.514	0.28	0.141	4.78E-02	0.49	0.347	0.081	1.82E-05	++
rs11735450	4	59835392		T	C	0.313	0.356	0.095	1.84E-04	0.31	0.294	0.138	3.38E-02	0.312	0.336	0.078	1.83E-05	++
rs377744015	10	107041782		CTTCT	C	0.606	0.398	0.093	1.85E-05					0.606	0.398	0.093	1.85E-05	+?
rs77881904	3	142619764		T	C	0.909	-0.544	0.133	4.36E-05	0.915	-0.331	0.217	1.27E-01	0.911	-0.486	0.114	1.85E-05	--
rs4788016	16	27976503	GSG1L	T	C	0.185	0.43	0.109	8.26E-05	0.192	0.278	0.148	6.11E-02	0.188	0.377	0.088	1.86E-05	++
rs35588287	16	27977832	GSG1L	CAA	C	0.79	-0.375	0.106	3.96E-04	0.785	-0.339	0.14	1.58E-02	0.788	-0.362	0.085	1.86E-05	--
rs1358727	6	150504354	PPP1R14C	A	G	0.711	0.378	0.106	3.46E-04	0.705	0.351	0.149	1.85E-02	0.709	0.369	0.086	1.86E-05	++
rs869104053	6	120603039		CA	C	0.423	0.391	0.091	1.86E-05					0.423	0.391	0.091	1.86E-05	+?
rs2349238	8	61883127		C	G	0.368	-0.338	0.091	2.23E-04	0.429	-0.279	0.127	2.78E-02	0.389	-0.318	0.074	1.87E-05	--

rs143523331	4	158084289	GLRB	T	C	0.018	1.066	0.249	1.88E-05					0.018	1.066	0.249	1.88E-05	+?
rs9743857	14	98470051		T	G	0.333	0.309	0.098	1.51E-03	0.347	0.419	0.143	3.29E-03	0.338	0.344	0.081	1.88E-05	++
rs9743860	14	98470078		A	G	0.333	0.309	0.098	1.51E-03	0.347	0.419	0.143	3.29E-03	0.338	0.344	0.081	1.88E-05	++
rs13231525	7	149011410		T	C	0.076	0.583	0.147	7.20E-05	0.056	0.434	0.261	9.59E-02	0.071	0.547	0.128	1.90E-05	++
rs28515968	14	86001049	FLRT2	T	G	0.076	-0.729	0.216	7.50E-04	0.062	-1.134	0.409	5.58E-03	0.073	-0.817	0.191	1.91E-05	--
rs74721198	3	4775378	ITPR1	A	G	0.976	-0.983	0.23	1.92E-05					0.976	-0.983	0.23	1.92E-05	-?
rs74324161	11	12567697		A	G	0.202	0.439	0.103	1.92E-05					0.202	0.439	0.103	1.92E-05	+?
rs75295605	5	105934787		A	G	0.91	-0.574	0.134	1.93E-05					0.91	-0.574	0.134	1.93E-05	-?
rs75723213	10	48543372		A	T	0.011	1.262	0.295	1.93E-05					0.011	1.262	0.295	1.93E-05	+?
rs10101707	8	61883621		T	C	0.368	-0.338	0.091	2.23E-04	0.429	-0.277	0.127	2.90E-02	0.389	-0.317	0.074	1.94E-05	--
rs77161426	18	31385009		T	C					0.989	-1.801	0.422	1.94E-05	0.989	-1.801	0.422	1.94E-05	?-
rs116983213	18	31385088		T	G					0.989	-1.801	0.422	1.94E-05	0.989	-1.801	0.422	1.94E-05	?-
rs142463700	18	31387330		T	C					0.989	-1.801	0.422	1.94E-05	0.989	-1.801	0.422	1.94E-05	?-
rs28637115	22	50342638		A	G	0.281	0.429	0.1	1.95E-05					0.281	0.429	0.1	1.95E-05	+?
rs79584851	13	102142652	ITGBL1	A	G	0.054	0.522	0.169	1.95E-03	0.048	0.739	0.244	2.46E-03	0.052	0.592	0.139	1.96E-05	++
rs10253233	7	129542761	UBE2H	A	C	0.249	-0.428	0.11	1.00E-04	0.256	-0.303	0.162	6.10E-02	0.251	-0.389	0.091	1.96E-05	--
rs12747682	1	19354505		A	G	0.919	-0.591	0.151	9.36E-05	0.904	-0.404	0.218	6.36E-02	0.914	-0.53	0.124	1.98E-05	--
rs60907340	10	122669855		CAG	C	0.633	-0.278	0.091	2.39E-03	0.659	-0.411	0.132	1.88E-03	0.642	-0.321	0.075	1.99E-05	--
rs6924223	6	47309130		A	T	0.152	0.347	0.121	4.18E-03	0.144	0.564	0.17	8.81E-04	0.149	0.421	0.099	2.00E-05	++
rs185820158	7	68116729		A	T	0.029	0.803	0.213	1.58E-04	0.028	0.692	0.347	4.62E-02	0.029	0.773	0.181	2.01E-05	++
rs140439453	20	9919198		A	G	0.012	1.276	0.3	2.04E-05					0.012	1.276	0.3	2.04E-05	+?
rs75126122	10	16580055		T	C	0.986	-1.201	0.282	2.06E-05					0.986	-1.201	0.282	2.06E-05	-?
rs1490862	16	86524159		T	C	0.343	0.276	0.092	2.67E-03	0.38	0.434	0.137	1.55E-03	0.355	0.325	0.076	2.07E-05	++
rs142177056	6	154541085	OPRM1	A	C	0.027	0.988	0.22	7.11E-06	0.013	0.128	0.55	8.16E-01	0.025	0.869	0.204	2.08E-05	++
rs72962525	18	68773265		A	G	0.053	0.74	0.17	1.29E-05	0.059	0.287	0.263	2.77E-01	0.055	0.607	0.143	2.08E-05	++
rs10903375	10	1180536		A	G	0.743	-0.367	0.098	1.88E-04	0.712	-0.288	0.138	3.63E-02	0.733	-0.34	0.08	2.08E-05	--
rs56338410	9	97436423		T	C	0.973	-0.636	0.237	7.19E-03	0.964	-0.938	0.276	6.68E-04	0.97	-0.765	0.18	2.09E-05	--
rs67845333	9	97438758		A	G	0.027	0.636	0.237	7.19E-03	0.036	0.938	0.276	6.68E-04	0.03	0.765	0.18	2.09E-05	++

rs36025648	9	97439197		T	C	0.973	-0.636	0.237	7.19E-03	0.964	-0.938	0.276	6.68E-04	0.97	-0.765	0.18	2.09E-05	--
rs374907030	15	42672831	CAPN3	G	GTA	0.172	0.465	0.109	2.09E-05					0.172	0.466	0.109	2.09E-05	+?
rs10632320	8	95791447	DPY19L4	T	TA	0.599	-0.3	0.093	1.21E-03	0.571	-0.379	0.135	5.04E-03	0.59	-0.326	0.076	2.09E-05	--
rs74543577	10	78148277	C10orf11	T	C	0.062	0.644	0.159	4.81E-05	0.049	0.408	0.28	1.46E-01	0.059	0.587	0.138	2.10E-05	++
rs181387460	17	43829993	CRHR1	T	C	0.987	-1.313	0.309	2.11E-05					0.987	-1.313	0.309	2.11E-05	-?
rs11910228	21	42606393	BACE2	A	G	0.749	-0.418	0.098	2.12E-05					0.749	-0.418	0.098	2.12E-05	-?
rs56132227	7	7192901		A	G	0.884	-0.3	0.135	2.61E-02	0.899	-0.79	0.188	2.72E-05	0.889	-0.466	0.11	2.12E-05	--
rs112035191	7	78094898	MAGI2	T	C	0.984	-1.148	0.27	2.14E-05					0.984	-1.148	0.27	2.14E-05	-?
rs115954126	3	177432532		A	T	0.035	0.481	0.215	2.53E-02	0.04	1.031	0.26	7.34E-05	0.037	0.704	0.166	2.14E-05	++
rs115268512	1	183269022	NMNAT2	A	G	0.02	1.043	0.246	2.15E-05					0.02	1.043	0.245	2.15E-05	+?
rs35898647	7	129586883	UBE2H	G	GA	0.679	0.409	0.102	6.38E-05	0.678	0.251	0.15	9.33E-02	0.679	0.359	0.084	2.15E-05	++
rs2702703	11	19401373	NAV2	T	G	0.415	0.408	0.096	2.15E-05					0.415	0.408	0.096	2.15E-05	+?
rs6992440	8	61885271		T	C	0.368	-0.336	0.091	2.34E-04	0.428	-0.275	0.127	3.08E-02	0.388	-0.315	0.074	2.16E-05	--
rs7014286	8	61885496		A	G	0.368	-0.336	0.091	2.34E-04	0.428	-0.275	0.127	3.08E-02	0.388	-0.315	0.074	2.16E-05	--
rs16885929	7	77955555	MAGI2	T	C	0.988	-0.856	0.322	7.90E-03	0.984	-1.302	0.379	5.99E-04	0.986	-1.042	0.245	2.18E-05	--
rs141633909	14	54189343		T	C	0.984	-1.138	0.268	2.18E-05					0.984	-1.138	0.268	2.18E-05	-?
rs1370513	2	119195750		A	G	0.29	0.352	0.094	1.73E-04	0.284	0.289	0.143	4.41E-02	0.288	0.333	0.079	2.19E-05	++
rs187341728	11	99575800	CNTN5	A	G	0.048	0.679	0.168	5.18E-05	0.047	0.433	0.296	1.44E-01	0.047	0.619	0.146	2.21E-05	++
rs112725690	11	66578669	C11orf80	T	C					0.016	1.65	0.389	2.22E-05	0.016	1.65	0.389	2.22E-05	?+
rs6905409	6	150506330	PPP1R14C	A	G	0.527	0.29	0.091	1.41E-03	0.526	0.36	0.127	4.70E-03	0.527	0.314	0.074	2.22E-05	++
rs13228286	7	129574785	UBE2H	A	G	0.725	0.391	0.106	2.45E-04	0.732	0.347	0.162	3.23E-02	0.727	0.378	0.089	2.22E-05	++
rs142931410	2	31565423	XDH	A	C	0.013	1.232	0.291	2.24E-05					0.013	1.232	0.291	2.24E-05	+?
rs139480007	7	7181458		A	G	0.066	0.311	0.161	5.29E-02	0.068	0.994	0.219	5.83E-06	0.067	0.549	0.13	2.24E-05	++
rs182035407	7	70666640	WBSCR17	T	C	0.978	-0.926	0.239	1.09E-04	0.981	-0.722	0.405	7.45E-02	0.978	-0.873	0.206	2.24E-05	--
rs9923388	16	86522010		A	G	0.487	-0.272	0.088	1.94E-03	0.488	-0.423	0.139	2.42E-03	0.487	-0.315	0.074	2.25E-05	--
rs1875067	8	75087343		T	C	0.657	0.356	0.096	2.15E-04	0.623	0.309	0.149	3.74E-02	0.647	0.342	0.081	2.25E-05	++
rs147890976	18	27664580		T	C	0.013	1.226	0.289	2.26E-05					0.013	1.226	0.289	2.26E-05	+?
rs10215972	7	129586354	UBE2H	T	C	0.321	-0.409	0.102	6.38E-05	0.322	-0.248	0.15	9.72E-02	0.321	-0.358	0.084	2.27E-05	--

rs61358838	2	184647305		G	GCCG	0.982	-0.705	0.274	1.01E-02	0.989	-1.661	0.431	1.18E-04	0.984	-0.981	0.232	2.28E-05	--
rs76171415	14	78688399		A	G					0.989	-1.71	0.404	2.28E-05	0.989	-1.71	0.404	2.28E-05	?-
rs35060589	9	97447390		T	C	0.973	-0.643	0.237	6.65E-03	0.964	-0.917	0.275	8.48E-04	0.969	-0.759	0.179	2.30E-05	--
rs12461351	19	46696941		C	G	0.984	-1.126	0.266	2.31E-05					0.984	-1.126	0.266	2.31E-05	-?
rs78387553	1	167397729		C	G	0.979	-1.034	0.244	2.31E-05					0.979	-1.034	0.244	2.31E-05	-?
rs111465347	7	129574783	UBE2H	A	G	0.776	0.502	0.118	2.16E-05	0.768	0.221	0.165	1.80E-01	0.773	0.407	0.096	2.31E-05	++
rs58394833	14	92988648	RIN3	T	C	0.516	-0.358	0.098	2.45E-04	0.479	-0.296	0.138	3.26E-02	0.503	-0.337	0.08	2.34E-05	--
rs6970562	7	68107997		T	C	0.028	0.815	0.213	1.31E-04	0.03	0.641	0.346	6.37E-02	0.029	0.767	0.181	2.35E-05	++
rs116188248	2	62180673	COMMD1	C	G	0.974	-0.702	0.237	3.09E-03	0.975	-1.008	0.323	1.83E-03	0.975	-0.809	0.191	2.35E-05	--
rs13403522	2	725523		A	G	0.019	0.587	0.284	3.84E-02	0.013	1.868	0.417	7.58E-06	0.017	0.992	0.234	2.35E-05	++
rs145650262	2	729945		A	C	0.981	-0.587	0.284	3.84E-02	0.987	-1.868	0.417	7.58E-06	0.983	-0.992	0.234	2.35E-05	--
rs148812682	2	730184		A	C	0.019	0.587	0.284	3.84E-02	0.013	1.868	0.417	7.58E-06	0.017	0.992	0.234	2.35E-05	++
rs116498271	2	730651		C	G	0.981	-0.587	0.284	3.84E-02	0.987	-1.868	0.417	7.58E-06	0.983	-0.992	0.234	2.35E-05	--
rs76184806	12	26105260		T	C	0.029	0.343	0.253	1.75E-01	0.036	1.257	0.267	2.45E-06	0.033	0.777	0.184	2.36E-05	++
rs6979056	7	129580795	UBE2H	T	C	0.251	-0.417	0.11	1.47E-04	0.253	-0.316	0.163	5.33E-02	0.252	-0.386	0.091	2.36E-05	--
rs574110246	8	118652008		T	TA	0.989	-1.319	0.312	2.37E-05					0.99	-1.319	0.312	2.37E-05	-?
rs10689256	10	118996351		CTG	C	0.556	0.361	0.092	9.34E-05	0.547	0.253	0.147	8.40E-02	0.553	0.331	0.078	2.38E-05	++
rs12531403	7	7185752		T	C	0.066	0.31	0.164	5.93E-02	0.068	0.994	0.219	5.83E-06	0.067	0.555	0.131	2.38E-05	++
rs2956035	8	75086235		A	G	0.342	-0.359	0.097	2.02E-04	0.376	-0.301	0.148	4.19E-02	0.352	-0.342	0.081	2.39E-05	--
rs1930474	10	59768760		A	G	0.386	-0.326	0.099	1.02E-03	0.395	-0.378	0.142	7.56E-03	0.389	-0.343	0.081	2.41E-05	--
rs697197	12	104008584	STAB2	A	T	0.803	-0.307	0.102	2.64E-03	0.829	-0.519	0.164	1.56E-03	0.81	-0.366	0.087	2.41E-05	--
rs12126234	1	48575218		A	C	0.976	-0.818	0.224	2.68E-04	0.962	-0.625	0.285	2.85E-02	0.97	-0.744	0.176	2.46E-05	--
rs73282482	8	101815514		A	G	0.029	0.96	0.228	2.46E-05					0.029	0.96	0.228	2.46E-05	+?
rs144895577	2	184345928		A	G	0.989	-1.303	0.309	2.46E-05					0.99	-1.303	0.309	2.46E-05	-?
rs2931380	3	19936589	EFHB	A	C	0.191	0.451	0.104	1.41E-05	0.196	0.168	0.163	3.02E-01	0.193	0.369	0.087	2.48E-05	++
rs62325016	4	162317333	FSTL5	T	C	0.09	0.52	0.141	2.20E-04	0.094	0.428	0.207	3.91E-02	0.091	0.491	0.117	2.49E-05	++
rs12436459	14	98481337		A	G	0.656	-0.31	0.097	1.35E-03	0.643	-0.397	0.143	5.37E-03	0.652	-0.337	0.08	2.49E-05	--
rs114770586	1	113796385		A	G	0.974	-0.896	0.213	2.50E-05					0.974	-0.896	0.213	2.50E-05	-?

rs2468075	15	45060641		C	G	0.655	-0.388	0.092	2.51E-05					0.655	-0.388	0.092	2.51E-05	-?
rs200851232	2	213099290	ERBB4	T	TC	0.032	0.732	0.199	2.25E-04	0.032	0.703	0.345	4.16E-02	0.032	0.725	0.172	2.51E-05	++
rs139959483	2	213101005	ERBB4	A	G	0.032	0.732	0.199	2.25E-04	0.032	0.703	0.345	4.16E-02	0.032	0.725	0.172	2.51E-05	++
rs4366431	10	78153552	C10orf11	C	G	0.062	0.641	0.156	3.79E-05	0.049	0.356	0.287	2.15E-01	0.059	0.577	0.137	2.51E-05	++
rs10103373	8	61880764		T	G	0.567	0.369	0.088	2.52E-05					0.567	0.369	0.088	2.52E-05	+?
rs10090053	8	97067686		A	G	0.489	-0.279	0.091	2.17E-03	0.529	-0.407	0.136	2.74E-03	0.501	-0.319	0.076	2.52E-05	--
rs2956038	8	75114396		T	C	0.045	0.721	0.183	8.16E-05	0.041	0.471	0.283	9.58E-02	0.044	0.647	0.154	2.52E-05	++
rs78591730	13	102138784	ITGBL1	A	T	0.944	-0.504	0.164	2.12E-03	0.949	-0.676	0.23	3.24E-03	0.946	-0.562	0.134	2.53E-05	--
rs9582496	13	102140921	ITGBL1	T	C	0.056	0.504	0.164	2.12E-03	0.051	0.676	0.23	3.24E-03	0.054	0.562	0.134	2.53E-05	++
rs12973186	19	5102014	KDM4B	A	G	0.018	0.954	0.226	2.53E-05					0.018	0.954	0.227	2.53E-05	+?
rs10741741	11	18342081	HPS5	T	C	0.592	-0.322	0.092	4.39E-04	0.601	-0.287	0.123	1.98E-02	0.596	-0.31	0.073	2.54E-05	--
rs112168619	10	5872086	GDI2	T	C	0.04	0.799	0.19	2.54E-05					0.04	0.799	0.19	2.54E-05	+?
rs143440748	8	8387347		A	AGT	0.892	-0.323	0.133	1.54E-02	0.888	-0.7	0.183	1.30E-04	0.891	-0.454	0.108	2.55E-05	--
rs143776937	6	153663509	AL590867.1	CAACAA	C	0.369	0.343	0.094	2.69E-04	0.368	0.274	0.127	3.11E-02	0.368	0.319	0.076	2.55E-05	++
rs527855420	12	75165820		C	G	0.786	0.489	0.126	1.00E-04	0.796	0.317	0.176	7.22E-02	0.79	0.431	0.102	2.55E-05	++
rs76101583	2	62197756	COMMD1	A	G	0.974	-0.696	0.237	3.33E-03	0.975	-1.008	0.323	1.83E-03	0.974	-0.805	0.191	2.56E-05	--
rs148912611	2	62200036	COMMD1	C	G	0.974	-0.696	0.237	3.33E-03	0.975	-1.008	0.323	1.83E-03	0.974	-0.805	0.191	2.56E-05	--
rs534355048	2	62218047	COMMD1	A	C	0.974	-0.696	0.237	3.33E-03	0.975	-1.008	0.323	1.83E-03	0.974	-0.805	0.191	2.56E-05	--
rs147361733	2	62230138	COMMD1	T	C	0.026	0.696	0.237	3.33E-03	0.025	1.008	0.323	1.83E-03	0.026	0.805	0.191	2.56E-05	++
rs12444844	16	27990399	GSG1L	T	G	0.174	0.339	0.117	3.69E-03	0.162	0.514	0.162	1.52E-03	0.17	0.399	0.095	2.56E-05	++
rs17555093	7	149015327		C	G	0.949	-0.641	0.173	2.16E-04	0.957	-0.545	0.269	4.28E-02	0.951	-0.613	0.146	2.59E-05	--
rs7726317	5	117921244		A	G	0.05	0.308	0.191	1.06E-01	0.066	0.902	0.204	9.53E-06	0.058	0.586	0.139	2.60E-05	++
rs34089610	9	97443765		A	C	0.025	0.634	0.243	9.12E-03	0.036	0.938	0.276	6.68E-04	0.029	0.767	0.182	2.61E-05	++
rs7243003	18	56707448		T	C	0.401	0.381	0.091	2.61E-05					0.401	0.381	0.091	2.61E-05	+?
rs12195341	6	51749131	PKHD1	C	G	0.014	1.216	0.289	2.61E-05					0.013	1.216	0.289	2.61E-05	+?
rs12206293	6	51751389	PKHD1	T	C	0.986	-1.216	0.289	2.61E-05					0.987	-1.216	0.289	2.61E-05	-?
rs537927647	7	51789720		A	T	0.966	-0.847	0.202	2.62E-05					0.966	-0.847	0.202	2.62E-05	-?
rs571358545	7	120880850	CPED1	C	G	0.01	1.306	0.311	2.63E-05					0.01	1.306	0.311	2.63E-05	+?

rs185438958	7	55538647	VOPP1	T	C	0.971	-0.531	0.249	3.32E-02	0.97	-1.13	0.286	7.84E-05	0.971	-0.789	0.188	2.66E-05	--
rs73188570	8	8380281		T	C	0.951	-0.51	0.176	3.75E-03	0.949	-0.744	0.237	1.68E-03	0.95	-0.593	0.141	2.67E-05	--
rs41306045	6	117083172	FAM162B	T	C	0.011	0.977	0.33	3.10E-03	0.02	1.082	0.362	2.82E-03	0.015	1.025	0.244	2.70E-05	++
rs62424435	6	117084242	FAM162B	T	C	0.011	0.977	0.33	3.10E-03	0.02	1.082	0.362	2.82E-03	0.015	1.025	0.244	2.70E-05	++
rs116194294	1	201920542		T	C	0.981	-1.01	0.241	2.72E-05					0.981	-1.01	0.241	2.72E-05	-?
rs10878013	12	63636405		T	C	0.808	-0.356	0.105	6.95E-04	0.799	-0.38	0.154	1.34E-02	0.805	-0.363	0.087	2.73E-05	--
rs1699041	21	46011397	TSPEAR	A	G	0.904	-0.566	0.135	2.73E-05					0.904	-0.566	0.135	2.73E-05	-?
rs112225300	1	90262687	RP11-302M6.4	A	T	0.926	1.048	0.25	2.73E-05					0.926	1.048	0.25	2.73E-05	+?
rs1930470	10	59767845		A	G	0.387	-0.319	0.099	1.28E-03	0.396	-0.383	0.141	6.75E-03	0.39	-0.34	0.081	2.76E-05	--
rs1930472	10	59768050		A	G	0.613	0.319	0.099	1.28E-03	0.604	0.383	0.141	6.75E-03	0.61	0.34	0.081	2.76E-05	++
rs34646923	3	9550925	LHFPL4	A	AC	0.259	0.393	0.094	2.77E-05					0.259	0.393	0.094	2.77E-05	+?
rs35347475	19	8182938	FBN3	T	TAC	0.126	0.452	0.122	2.04E-04	0.14	0.346	0.173	4.50E-02	0.131	0.417	0.099	2.77E-05	++
rs4724952	7	7189717		A	C	0.932	-0.3	0.163	6.50E-02	0.929	-0.968	0.215	6.66E-06	0.931	-0.544	0.13	2.78E-05	--
rs142534252	3	142612482		A	G	0.091	0.546	0.133	3.81E-05	0.088	0.281	0.217	1.94E-01	0.09	0.474	0.113	2.79E-05	++
rs62424438	6	117092777		A	G	0.011	1.001	0.332	2.55E-03	0.018	1.099	0.377	3.58E-03	0.014	1.044	0.249	2.80E-05	++
rs2929384	3	19932499	EFHB	A	G	0.808	-0.449	0.104	1.49E-05	0.803	-0.163	0.162	3.15E-01	0.807	-0.366	0.087	2.81E-05	--
rs115540417	6	21453879		T	C	0.097	0.551	0.132	2.81E-05					0.098	0.551	0.132	2.81E-05	+?
rs75191634	11	120528226	GRIK4	A	G	0.963	-0.829	0.198	2.82E-05					0.963	-0.829	0.198	2.82E-05	-?
rs4081624	10	118996115		A	C	0.505	-0.362	0.09	6.09E-05	0.537	-0.216	0.146	1.40E-01	0.513	-0.321	0.077	2.83E-05	--
rs16831521	3	180076400		T	C	0.923	-0.595	0.143	3.28E-05	0.931	-0.289	0.233	2.16E-01	0.925	-0.511	0.122	2.83E-05	--
rs61247576	9	97429925		A	C	0.974	-0.615	0.241	1.05E-02	0.965	-0.952	0.277	5.87E-04	0.97	-0.76	0.182	2.84E-05	--
rs62325025	4	162332566	FSTL5	T	C	0.907	-0.53	0.138	1.26E-04	0.9	-0.369	0.205	7.16E-02	0.905	-0.48	0.115	2.84E-05	--
rs76912990	21	43240688	PRDM15	T	C	0.014	1.166	0.279	2.85E-05					0.014	1.166	0.279	2.85E-05	+?
rs369736478	7	125405126		A	C	0.945	-0.701	0.167	2.87E-05					0.945	-0.701	0.168	2.87E-05	-?
rs77442209	5	10451034	ROPN1L	T	C	0.058	0.688	0.164	2.89E-05					0.058	0.688	0.165	2.89E-05	+?
rs4788017	16	27976829	GSG1L	A	G	0.812	-0.397	0.109	2.56E-04	0.805	-0.306	0.147	3.68E-02	0.81	-0.365	0.087	2.90E-05	--
rs73037608	3	176686874		A	G	0.247	0.363	0.099	2.58E-04	0.229	0.303	0.147	3.95E-02	0.241	0.344	0.082	2.90E-05	++

rs115431271	18	55402395	ATP8B1	A	G	0.014	1.226	0.293	2.91E-05					0.013	1.226	0.293	2.91E-05	+?
rs9476981	6	15916893		T	C	0.962	-0.798	0.196	4.53E-05	0.964	-0.422	0.305	1.67E-01	0.962	-0.689	0.165	2.92E-05	--
rs34297290	7	129585784	UBE2H	T	C	0.678	0.405	0.102	6.59E-05	0.677	0.232	0.147	1.15E-01	0.677	0.35	0.084	2.93E-05	++
rs9792563	9	1322280		T	G	0.619	0.404	0.097	2.92E-05	0.613	0.183	0.143	2.00E-01	0.617	0.335	0.08	2.95E-05	++
rs9794407	10	1349262	ADARB2	A	C	0.848	-0.496	0.119	2.96E-05					0.848	-0.496	0.119	2.96E-05	-?
rs9505640	6	9120953		A	T	0.972	-0.916	0.219	2.96E-05					0.972	-0.916	0.219	2.96E-05	-?
rs149078994	4	158245818	GRIA2	A	G	0.982	-1.04	0.243	1.80E-05	0.983	-0.358	0.518	4.90E-01	0.983	-0.917	0.22	2.97E-05	--
rs7556919	2	119194761		T	C	0.29	0.343	0.094	2.41E-04	0.284	0.289	0.143	4.41E-02	0.288	0.327	0.078	2.98E-05	++
rs1370512	2	119194992		T	C	0.29	0.343	0.094	2.41E-04	0.284	0.289	0.143	4.41E-02	0.288	0.327	0.078	2.98E-05	++
rs566523351	1	90261018	RP11-302M6.4	T	TTTA	0.927	1.043	0.25	2.99E-05					0.926	1.043	0.25	2.99E-05	+?
rs111272652	17	1023802	ABR	T	C	0.04	0.794	0.19	2.99E-05					0.04	0.794	0.19	2.99E-05	+?
rs139760259	3	87986940		C	G	0.016	0.779	0.274	4.52E-03	0.019	1.175	0.37	1.48E-03	0.018	0.919	0.22	2.99E-05	++
rs12622630	2	232152297	ARMC9	A	G	0.803	-0.352	0.109	1.29E-03	0.805	-0.408	0.153	7.53E-03	0.804	-0.371	0.089	3.01E-05	--
rs575248632	4	83815426	SEC31A	CTTTGTGT	C	0.988	-1.244	0.298	3.02E-05					0.988	-1.244	0.298	3.02E-05	-?
rs56289902	7	7191986		T	C	0.069	0.297	0.164	7.00E-02	0.071	0.968	0.215	6.66E-06	0.07	0.543	0.13	3.04E-05	++
rs112308087	5	133401821		A	G	0.026	0.837	0.221	1.48E-04	0.037	0.552	0.291	5.77E-02	0.03	0.733	0.176	3.05E-05	++
rs35633351	2	174709261		T	C	0.069	0.64	0.153	3.05E-05					0.069	0.64	0.153	3.05E-05	+?
rs10464619	7	77969785	MAGI2	T	C	0.012	0.885	0.325	6.45E-03	0.015	1.277	0.393	1.16E-03	0.013	1.044	0.25	3.05E-05	++
rs117499799	7	77970782	MAGI2	T	C	0.012	0.885	0.325	6.45E-03	0.015	1.277	0.393	1.16E-03	0.013	1.044	0.25	3.05E-05	++
rs117870566	7	77970907	MAGI2	T	C	0.012	0.885	0.325	6.45E-03	0.015	1.277	0.393	1.16E-03	0.013	1.044	0.25	3.05E-05	++
rs200319268	7	77970943	MAGI2	A	AC	0.012	0.885	0.325	6.45E-03	0.015	1.277	0.393	1.16E-03	0.013	1.044	0.25	3.05E-05	++
rs190353615	2	722192		A	G	0.019	0.566	0.283	4.57E-02	0.013	1.868	0.417	7.58E-06	0.017	0.976	0.234	3.09E-05	++
rs77334734	21	42824293	MX1	C	G	0.985	-1.082	0.269	5.91E-05	0.984	-0.631	0.449	1.61E-01	0.985	-0.963	0.231	3.10E-05	--
rs73037611	3	176687914		T	C	0.247	0.362	0.099	2.77E-04	0.229	0.303	0.147	3.95E-02	0.242	0.343	0.082	3.10E-05	++
rs147688762	15	41790896	ITPKA	A	G					0.011	1.855	0.445	3.12E-05	0.011	1.855	0.445	3.12E-05	?+
rs72308925	15	41794465	ITPKA	G	GCTCCCGCCCCGCCTGCCCC		0.011	1.855	0.445	3.12E-05	0.011	1.855	0.445	3.12E-05	?+			

rs35089028	11	77164561	PAK1	T	TCCGCCCTTA	0.189	-0.423	0.126	7.82E-04	0.207	-0.423	0.172	1.38E-02	0.195	-0.423	0.102	3.12E-05	--
rs1930475	10	59768808		A	G	0.531	0.339	0.097	5.01E-04	0.53	0.316	0.138	2.21E-02	0.53	0.331	0.08	3.13E-05	++
rs111777972	9	97446540		A	G	0.025	0.634	0.243	9.12E-03	0.036	0.917	0.275	8.48E-04	0.03	0.758	0.182	3.13E-05	++
rs576418706	4	76369184		T	C	0.077	0.607	0.146	3.14E-05					0.077	0.607	0.146	3.14E-05	+?
rs76923085	17	18897732	SLC5A10	A	G	0.065	0.652	0.157	3.14E-05					0.065	0.652	0.157	3.14E-05	+?
rs6575264	14	92985113	RIN3	A	G	0.467	0.381	0.099	1.25E-04	0.496	0.252	0.142	7.54E-02	0.476	0.339	0.081	3.14E-05	++
rs13075932	3	88327613		T	C	0.978	-1.021	0.245	3.17E-05					0.979	-1.021	0.245	3.17E-05	-?
rs142128766	10	128224870	C10orf90	A	C	0.978	-0.689	0.263	8.76E-03	0.982	-1.375	0.388	3.92E-04	0.979	-0.905	0.218	3.19E-05	--
rs12983105	19	46696423		A	T	0.016	1.102	0.265	3.20E-05					0.017	1.102	0.265	3.20E-05	+?
rs79508892	1	113792932		C	G	0.027	0.883	0.212	3.20E-05					0.026	0.883	0.212	3.20E-05	+?
rs368417617	14	52061024	FRMD6	T	TTTTA	0.222	0.363	0.105	5.33E-04	0.256	0.326	0.141	2.08E-02	0.234	0.35	0.084	3.20E-05	++
rs114937444	4	174448570	HAND2	A	T	0.013	1.242	0.299	3.21E-05					0.013	1.242	0.299	3.21E-05	+?
rs201644806	14	98480386		T	TCTCCCTCCCTCCTTGC	0.33	0.299	0.098	2.21E-03	0.349	0.41	0.142	3.88E-03	0.337	0.334	0.08	3.21E-05	++
rs141247511	7	70670196	WBSCR17	A	G	0.022	0.92	0.246	1.81E-04	0.019	0.748	0.406	6.57E-02	0.021	0.874	0.21	3.23E-05	++
rs73989465	2	215244523	SPAG16	A	C	0.843	-0.455	0.11	3.27E-05					0.843	-0.455	0.11	3.27E-05	-?
rs80011419	6	117093451		A	C	0.011	0.981	0.33	2.97E-03	0.018	1.099	0.377	3.58E-03	0.014	1.032	0.248	3.27E-05	++
rs62424440	6	117095609		T	C	0.989	-0.981	0.33	2.97E-03	0.982	-1.099	0.377	3.58E-03	0.986	-1.032	0.248	3.27E-05	--
rs62424441	6	117095819		A	G	0.011	0.981	0.33	2.97E-03	0.018	1.099	0.377	3.58E-03	0.014	1.032	0.248	3.27E-05	++
rs543962900	7	70632681	WBSCR17	A	T	0.988	-1.287	0.31	3.27E-05					0.988	-1.287	0.31	3.27E-05	-?
rs140428124	21	21991033		A	G	0.974	-0.932	0.224	3.27E-05					0.974	-0.932	0.224	3.27E-05	-?
rs10843228	12	28797052		A	C	0.217	0.226	0.104	3.02E-02	0.248	0.589	0.144	4.32E-05	0.228	0.351	0.084	3.28E-05	++
rs17147824	7	77966192	MAGI2	A	G	0.988	-0.885	0.325	6.45E-03	0.985	-1.245	0.387	1.31E-03	0.987	-1.033	0.249	3.30E-05	--
rs199886226	7	77968691	MAGI2	G	GA	0.012	0.885	0.325	6.45E-03	0.015	1.245	0.387	1.31E-03	0.013	1.033	0.249	3.30E-05	++
rs528630024	7	77968693	MAGI2	A	G	0.988	-0.885	0.325	6.45E-03	0.985	-1.245	0.387	1.31E-03	0.987	-1.033	0.249	3.30E-05	--
rs17150550	7	77969112	MAGI2	T	G	0.988	-0.885	0.325	6.45E-03	0.985	-1.245	0.387	1.31E-03	0.987	-1.033	0.249	3.30E-05	--

rs184099020	16	19078547		A	T	0.014	1.235	0.298	3.30E-05					0.013	1.235	0.297	3.30E-05	+?
rs4408825	3	65581480	MAGI1	T	C	0.815	-0.368	0.105	4.46E-04	0.829	-0.372	0.168	2.69E-02	0.819	-0.369	0.089	3.32E-05	--
rs796644157	7	149014280		A	AT	0.078	0.55	0.146	1.61E-04	0.059	0.451	0.257	7.88E-02	0.073	0.526	0.127	3.33E-05	++
rs557930994	3	87982438		T	C	0.987	-0.951	0.298	1.40E-03	0.988	-1.233	0.457	6.99E-03	0.988	-1.035	0.249	3.34E-05	--
rs576495351	3	87982468		A	G	0.987	-0.951	0.298	1.40E-03	0.988	-1.233	0.457	6.99E-03	0.988	-1.035	0.249	3.34E-05	--
rs555317536	3	87982510		T	C	0.987	-0.951	0.298	1.40E-03	0.988	-1.233	0.457	6.99E-03	0.988	-1.035	0.249	3.34E-05	--
rs78972026	3	71955823		C	G	0.972	-0.844	0.221	1.35E-04	0.978	-0.62	0.363	8.77E-02	0.974	-0.784	0.189	3.35E-05	--
rs116497000	8	3611709	CSMD1	C	G	0.98	-1.046	0.252	3.36E-05					0.98	-1.046	0.252	3.36E-05	-?
rs149936787	1	27703088		A	T	0.987	-1.206	0.291	3.37E-05					0.987	-1.206	0.291	3.37E-05	-?
rs67658320	2	209703230	PTH2R	T	C	0.139	0.491	0.119	3.41E-05					0.139	0.491	0.119	3.41E-05	+?
rs7789336	7	129583129	UBE2H	T	C	0.251	-0.416	0.11	1.52E-04	0.253	-0.291	0.162	7.22E-02	0.251	-0.377	0.091	3.43E-05	--
rs3110675	15	45065642		A	T	0.344	0.379	0.092	3.43E-05					0.344	0.379	0.091	3.43E-05	+?
rs1563059	2	181414808		T	G	0.171	0.346	0.112	2.03E-03	0.173	0.462	0.163	4.72E-03	0.172	0.383	0.092	3.43E-05	++
rs143345370	15	43896940	CKMT1B	C	G	0.942	-0.687	0.157	1.22E-05	0.952	-0.175	0.297	5.55E-01	0.944	-0.575	0.139	3.44E-05	--
rs146980261	3	87942366		A	G	0.017	0.766	0.274	5.11E-03	0.019	1.175	0.37	1.48E-03	0.018	0.911	0.22	3.45E-05	++
rs143685564	3	87943504		A	T	0.017	0.766	0.274	5.11E-03	0.019	1.175	0.37	1.48E-03	0.018	0.911	0.22	3.45E-05	++
rs7175002	15	26447659		A	G	0.875	-0.497	0.12	3.46E-05					0.875	-0.497	0.12	3.46E-05	-?
rs13223718	7	149017184		A	T	0.068	0.597	0.152	8.14E-05	0.058	0.386	0.267	1.48E-01	0.065	0.546	0.132	3.47E-05	++
rs79216413	19	46681687		T	G	0.016	1.098	0.265	3.47E-05					0.017	1.098	0.265	3.47E-05	+?
rs534051742	2	62207710	COMMD1	T	C	0.026	0.681	0.237	4.05E-03	0.025	0.993	0.322	2.07E-03	0.026	0.79	0.191	3.48E-05	++
rs4903510	14	77355410		A	G	0.051	0.696	0.168	3.48E-05					0.051	0.696	0.168	3.48E-05	+?
rs62193731	2	232006786	PSMD1	A	G	0.145	0.36	0.112	1.35E-03	0.144	0.449	0.169	7.90E-03	0.145	0.387	0.094	3.49E-05	++
rs9549403	13	114054609		T	C	0.596	-0.358	0.087	3.50E-05					0.596	-0.358	0.087	3.50E-05	-?
rs7277567	21	27995962		A	T	0.959	-0.737	0.178	3.51E-05					0.959	-0.737	0.178	3.51E-05	-?
rs139495342	4	83738699		T	C	0.984	-1.118	0.27	3.51E-05					0.984	-1.118	0.27	3.51E-05	-?
rs6752436	2	181413253		A	G	0.171	0.346	0.112	2.03E-03	0.173	0.46	0.163	4.87E-03	0.172	0.383	0.092	3.52E-05	++
rs140304980	7	29758915		A	C	0.976	-0.888	0.224	7.25E-05	0.982	-0.55	0.397	1.66E-01	0.977	-0.806	0.195	3.52E-05	--
rs115557754	4	158130317	GRIA2	C	G	0.984	-1.08	0.253	1.94E-05	0.986	-0.323	0.576	5.75E-01	0.985	-0.958	0.232	3.53E-05	--

rs9582495	13	102136512	ITGBL1	C	G	0.944	-0.489	0.164	2.88E-03	0.949	-0.676	0.23	3.24E-03	0.945	-0.552	0.134	3.53E-05	--
rs11804107	1	113472147	SLC16A1	A	C	0.051	0.502	0.178	4.74E-03	0.053	0.789	0.25	1.56E-03	0.051	0.599	0.145	3.56E-05	++
rs58920012	1	113487149	SLC16A1	T	C	0.949	-0.502	0.178	4.74E-03	0.947	-0.789	0.25	1.56E-03	0.949	-0.599	0.145	3.56E-05	--
rs11801876	1	113489045	SLC16A1	A	T	0.949	-0.502	0.178	4.74E-03	0.947	-0.789	0.25	1.56E-03	0.949	-0.599	0.145	3.56E-05	--
rs191541620	1	110494121		T	C	0.981	-1.045	0.253	3.58E-05	0.986	14.744	426.113	9.72E-01	0.981	-1.045	0.253	3.58E-05	-+
rs5773988	1	48565411		A	AT	0.026	0.771	0.214	3.22E-04	0.039	0.595	0.284	3.61E-02	0.031	0.707	0.171	3.58E-05	++
rs17009775	2	30787943	LCLAT1	A	T	0.011	1.047	0.345	2.39E-03	0.012	1.257	0.445	4.70E-03	0.011	1.126	0.273	3.59E-05	++
rs183071534	2	30797090	LCLAT1	A	T	0.989	-1.047	0.345	2.39E-03	0.988	-1.257	0.445	4.70E-03	0.989	-1.126	0.273	3.59E-05	--
rs17164001	7	7192868		C	G	0.931	-0.289	0.164	7.80E-02	0.929	-0.968	0.215	6.66E-06	0.93	-0.538	0.13	3.60E-05	--
rs66506667	5	173631697	NSG2	CG	C	0.398	0.333	0.09	2.28E-04	0.408	0.259	0.135	5.48E-02	0.401	0.31	0.075	3.61E-05	++
rs6575640	14	98476907		T	C	0.336	0.293	0.097	2.62E-03	0.348	0.417	0.143	3.53E-03	0.34	0.332	0.081	3.63E-05	++
rs7735143	5	92726723		C	G	0.014	1.228	0.297	3.63E-05					0.013	1.228	0.297	3.63E-05	+?
rs139194449	5	92734101		A	G	0.014	1.228	0.297	3.63E-05					0.013	1.228	0.297	3.63E-05	+?
rs141029616	5	92735158		A	T	0.014	1.228	0.297	3.63E-05					0.013	1.228	0.297	3.63E-05	+?
rs143652265	5	92735752		A	T	0.986	-1.228	0.297	3.63E-05					0.987	-1.228	0.297	3.63E-05	-?
rs138449968	5	92736496		A	C	0.986	-1.228	0.297	3.63E-05					0.987	-1.228	0.297	3.63E-05	-?
rs4498940	10	59802063		C	G	0.375	-0.298	0.098	2.41E-03	0.385	-0.406	0.142	4.12E-03	0.378	-0.334	0.081	3.65E-05	--
rs1930495	10	59802660		A	G	0.625	0.298	0.098	2.41E-03	0.615	0.406	0.142	4.12E-03	0.622	0.334	0.081	3.65E-05	++
rs78570362	4	113051577		T	C	0.93	-0.369	0.156	1.76E-02	0.943	-0.872	0.227	1.24E-04	0.934	-0.53	0.128	3.66E-05	--
rs147913187	4	113052990		T	C	0.07	0.369	0.156	1.76E-02	0.057	0.872	0.227	1.24E-04	0.066	0.53	0.128	3.66E-05	++
rs149045446	3	177400901		T	TTCTC	0.035	0.419	0.22	5.71E-02	0.041	1.058	0.257	3.76E-05	0.037	0.69	0.167	3.66E-05	++
rs405177	19	30400632		T	C	0.012	1.217	0.295	3.67E-05					0.012	1.217	0.295	3.67E-05	+?
rs420160	19	30402013		T	C	0.012	1.217	0.295	3.67E-05					0.012	1.217	0.295	3.67E-05	+?
3:19932864	3	19932864	EFHB	GA	GAA	0.81	-0.45	0.105	1.78E-05	0.805	-0.156	0.162	3.37E-01	0.809	-0.363	0.088	3.69E-05	--
rs600859	9	79325558	PRUNE2	C	G	0.35	0.287	0.091	1.58E-03	0.347	0.359	0.133	7.15E-03	0.349	0.31	0.075	3.69E-05	++
rs116374491	2	62165741	COMMD1	T	C	0.026	0.679	0.234	3.65E-03	0.025	0.975	0.323	2.53E-03	0.026	0.781	0.189	3.70E-05	++
rs77498844	10	78098561	C10orf11	T	C	0.064	0.637	0.16	7.05E-05	0.056	0.37	0.264	1.61E-01	0.062	0.566	0.137	3.71E-05	++
rs74350986	10	78100631	C10orf1	A	C	0.064	0.637	0.16	7.05E-05	0.056	0.37	0.264	1.61E-01	0.062	0.566	0.137	3.71E-05	++

			1													
rs4723859	7	39366946	POU6F2	A	G	0.187	0.372	0.107	4.99E-04	0.175	0.366	0.166	2.72E-02	0.184	0.37	0.09	3.73E-05	++
rs76240807	3	89291465	EPHA3	A	T	0.049	0.691	0.175	7.97E-05	0.047	0.411	0.28	1.43E-01	0.048	0.613	0.149	3.74E-05	++
rs11767943	7	155735074		A	G	0.26	0.362	0.096	1.72E-04	0.328	0.254	0.14	7.01E-02	0.282	0.327	0.079	3.74E-05	++
rs146564943	13	53666675		T	G	0.987	-1.024	0.317	1.24E-03	0.988	-1.124	0.437	1.02E-02	0.987	-1.058	0.257	3.75E-05	--
rs4408686	2	28940526		T	C	0.651	-0.3	0.091	9.79E-04	0.648	-0.339	0.137	1.29E-02	0.65	-0.312	0.076	3.76E-05	--
rs78176579	14	26219269		A	C	0.053	0.663	0.161	3.78E-05					0.053	0.663	0.161	3.78E-05	+?
rs144623926	1	160676216	CD48	A	T	0.031	0.863	0.209	3.81E-05					0.031	0.863	0.209	3.81E-05	+?
rs115579283	1	160676291	CD48	T	C	0.969	-0.863	0.209	3.81E-05					0.969	-0.863	0.209	3.81E-05	-?
rs12698352	7	155734985		T	C	0.261	0.36	0.096	1.76E-04	0.328	0.254	0.14	7.01E-02	0.282	0.327	0.079	3.81E-05	++
rs13325223	3	66905590		A	G	0.91	-0.394	0.142	5.41E-03	0.908	-0.644	0.201	1.37E-03	0.909	-0.477	0.116	3.82E-05	--
rs140854658	3	184996397	EHHADH	T	G	0.011	1.042	0.308	7.04E-04	0.014	0.982	0.419	1.91E-02	0.012	1.021	0.248	3.82E-05	++
rs260249	6	42397088	TRERF1	A	G	0.761	-0.434	0.105	3.83E-05					0.761	-0.434	0.105	3.83E-05	-?
rs10165605	2	75828653		A	G	0.692	-0.33	0.094	4.23E-04	0.692	-0.303	0.142	3.30E-02	0.692	-0.322	0.078	3.84E-05	--
rs17044311	4	113049268		A	C	0.928	-0.378	0.152	1.28E-02	0.941	-0.829	0.226	2.38E-04	0.932	-0.518	0.126	3.84E-05	--
rs6964280	7	7185729		A	G	0.071	0.268	0.161	9.56E-02	0.071	1.01	0.217	3.13E-06	0.071	0.531	0.129	3.84E-05	++
rs111513694	7	78104164	MAGI2	A	G	0.016	1.072	0.274	8.94E-05	0.012	0.708	0.5	1.57E-01	0.015	0.988	0.24	3.86E-05	++
rs113872230	7	78104595	MAGI2	T	C	0.016	1.072	0.274	8.94E-05	0.012	0.708	0.5	1.57E-01	0.015	0.988	0.24	3.86E-05	++
rs76758768	1	164416436		A	T	0.957	-0.755	0.183	3.86E-05					0.957	-0.755	0.183	3.86E-05	-?
rs117291995	18	31328564	ASXL3	A	G					0.989	-1.709	0.415	3.87E-05	0.989	-1.709	0.415	3.87E-05	?-
rs140240199	18	31344103		T	C					0.989	-1.709	0.415	3.87E-05	0.989	-1.709	0.415	3.87E-05	?-
rs28372621	4	114721328		T	C	0.028	0.801	0.212	1.57E-04	0.033	0.54	0.305	7.69E-02	0.029	0.716	0.174	3.88E-05	++
rs75984171	5	128806174	ADAMTS19	T	C	0.019	1.004	0.244	3.89E-05					0.019	1.004	0.244	3.89E-05	+?
rs9977916	21	36423454	RUNX1	T	C	0.965	-0.801	0.195	3.89E-05					0.965	-0.801	0.195	3.89E-05	-?
rs577993	9	79321871	PRUNE2	T	C	0.454	0.283	0.09	1.61E-03	0.444	0.342	0.128	7.67E-03	0.45	0.303	0.074	3.90E-05	++
rs76501672	5	89970231	GPR98	T	C	0.943	-0.578	0.168	5.63E-04	0.939	-0.55	0.245	2.49E-02	0.942	-0.569	0.138	3.90E-05	--
rs67135813	2	171028736		T	C	0.962	-0.672	0.198	6.68E-04	0.957	-0.596	0.257	2.03E-02	0.96	-0.644	0.157	3.92E-05	--
rs57656489	17	19412550	SLC47A1	A	G	0.152	0.473	0.115	3.92E-05					0.152	0.473	0.115	3.92E-05	+?

rs73684022	7	27689695	HIBADH	T	C	0.988	-1.247	0.303	3.94E-05					0.988	-1.247	0.303	3.94E-05	-?
rs115390199	10	109951895		A	C	0.989	-1.254	0.305	3.94E-05					0.989	-1.254	0.305	3.94E-05	-?
rs2943811	11	61280720		A	G	0.386	-0.37	0.09	3.96E-05					0.386	-0.37	0.09	3.96E-05	-?
rs12488234	3	112191202	BTLA	T	G	0.873	-0.482	0.117	3.96E-05					0.873	-0.482	0.117	3.96E-05	-?
rs115363570	16	19610886	C16orf62	C	G	0.986	-1.028	0.295	4.95E-04	0.99	-1.071	0.491	2.91E-02	0.987	-1.039	0.253	3.96E-05	--
rs11677127	2	28945646		T	C	0.612	-0.29	0.09	1.34E-03	0.612	-0.351	0.135	9.42E-03	0.612	-0.309	0.075	3.98E-05	--
rs558693940	7	51751265		A	G	0.04	0.777	0.189	3.98E-05					0.04	0.777	0.189	3.98E-05	+?
rs80157892	7	78102623	MAGI2	T	C	0.984	-1.055	0.273	1.11E-04	0.988	-0.751	0.505	1.37E-01	0.985	-0.986	0.24	3.99E-05	--
rs557429455	3	87936836		T	G	0.017	0.753	0.273	5.79E-03	0.019	1.175	0.37	1.48E-03	0.018	0.902	0.22	4.00E-05	++
rs17049585	2	58828404		A	G	0.131	0.351	0.124	4.59E-03	0.121	0.581	0.185	1.65E-03	0.128	0.422	0.103	4.00E-05	++
rs17049586	2	58828603		A	G	0.131	0.351	0.124	4.59E-03	0.121	0.581	0.185	1.65E-03	0.128	0.422	0.103	4.00E-05	++
rs34193840	7	149009492		A	G	0.931	-0.583	0.152	1.28E-04	0.946	-0.418	0.265	1.15E-01	0.935	-0.542	0.132	4.01E-05	--
rs7558175	2	221176925		T	C	0.314	0.332	0.092	2.97E-04	0.292	0.279	0.142	4.90E-02	0.307	0.316	0.077	4.01E-05	++
rs60384186	10	1182830		T	C	0.662	-0.34	0.091	1.75E-04	0.643	-0.239	0.134	7.52E-02	0.656	-0.309	0.075	4.01E-05	--
rs142753018	7	70666937	WBSCR17	C	G	0.978	-0.913	0.245	1.99E-04	0.981	-0.722	0.405	7.45E-02	0.979	-0.862	0.21	4.03E-05	--
rs148723799	1	56504658		C	G	0.013	1.196	0.291	4.03E-05					0.013	1.196	0.291	4.03E-05	+?
rs575374	6	125427426		A	G	0.489	-0.276	0.093	3.06E-03	0.496	-0.374	0.129	3.63E-03	0.491	-0.31	0.075	4.05E-05	--
rs554882892	7	148964886	ZNF783	T	TA	0.885	-0.482	0.124	1.07E-04	0.892	-0.305	0.197	1.22E-01	0.887	-0.431	0.105	4.10E-05	--
rs10137906	14	98490569		A	G	0.354	0.341	0.094	3.07E-04	0.371	0.265	0.132	4.53E-02	0.36	0.315	0.077	4.11E-05	++
rs147239590	17	68033643		A	G	0.016	0.996	0.243	4.12E-05					0.016	0.996	0.243	4.12E-05	+?
rs10197001	2	231961582	PSMD1	T	G	0.146	0.351	0.112	1.81E-03	0.143	0.463	0.17	6.58E-03	0.145	0.385	0.094	4.12E-05	++
rs16844619	2	211422333	CPS1	A	C	0.697	-0.378	0.091	3.32E-05	0.698	-0.159	0.135	2.39E-01	0.697	-0.31	0.075	4.12E-05	--
rs188577120	20	1833298		A	C	0.011	1.258	0.307	4.13E-05					0.011	1.258	0.307	4.13E-05	+?
rs1471482	13	95804906	ABCC4	T	G	0.984	-1.093	0.267	4.13E-05					0.984	-1.093	0.267	4.13E-05	-?
rs17104164	1	48581550		A	C	0.975	-0.781	0.224	4.78E-04	0.962	-0.625	0.285	2.85E-02	0.97	-0.722	0.176	4.13E-05	--
rs10482934	21	24514388		T	C	0.027	0.624	0.215	3.66E-03	0.031	0.877	0.295	2.94E-03	0.028	0.712	0.174	4.13E-05	++
rs6577044	13	114072735		A	G	0.535	0.383	0.093	4.14E-05					0.535	0.383	0.093	4.14E-05	+?
rs77595058	2	159376166	PKP4	A	G	0.97	-0.706	0.219	1.27E-03	0.971	-0.789	0.31	1.10E-02	0.97	-0.734	0.179	4.14E-05	--

rs56357646	6	21454061		A	T	0.903	-0.544	0.133	4.15E-05					0.903	-0.544	0.133	4.15E-05	-?
rs72882068	2	171028588		A	G	0.962	-0.669	0.197	7.11E-04	0.957	-0.596	0.257	2.03E-02	0.96	-0.641	0.157	4.16E-05	--
rs183654244	19	51308240		A	G	0.028	0.891	0.217	4.16E-05					0.028	0.891	0.217	4.16E-05	+?
rs1454566	2	221175540		A	T	0.314	0.331	0.092	3.09E-04	0.292	0.279	0.142	4.90E-02	0.308	0.316	0.077	4.16E-05	++
rs80014032	12	7841342		A	G	0.943	-0.643	0.157	4.16E-05					0.943	-0.643	0.157	4.16E-05	-?
rs2392654	2	221178879		A	G	0.314	0.332	0.092	2.90E-04	0.293	0.276	0.142	5.20E-02	0.307	0.316	0.077	4.17E-05	++
rs2392656	2	221179018		A	G	0.314	0.332	0.092	2.90E-04	0.293	0.276	0.142	5.20E-02	0.307	0.316	0.077	4.17E-05	++
rs76775172	14	25881071		A	G	0.027	0.72	0.221	1.11E-03	0.021	0.905	0.359	1.17E-02	0.026	0.771	0.188	4.17E-05	++
rs77528954	2	29786204	ALK	C	G	0.024	0.941	0.232	4.84E-05	0.026	0.455	0.372	2.21E-01	0.025	0.805	0.197	4.19E-05	++
rs114510183	3	25715367		T	C	0.014	1.203	0.294	4.20E-05					0.013	1.203	0.294	4.20E-05	+?
rs75022956	8	101673826	SNX31	A	G	0.013	1.23	0.3	4.21E-05					0.013	1.23	0.3	4.21E-05	+?
rs2600777	2	237600633		A	G	0.545	-0.367	0.089	4.21E-05					0.545	-0.366	0.089	4.21E-05	-?
rs691211	7	49875085	VWC2	A	G	0.166	-0.565	0.138	4.22E-05					0.166	-0.565	0.138	4.22E-05	-?
rs494446	7	49875687	VWC2	T	C	0.166	-0.565	0.138	4.22E-05					0.166	-0.565	0.138	4.22E-05	-?
rs564198758	3	164914205	SLITRK3	C	G	0.035	0.642	0.209	2.11E-03	0.032	0.787	0.288	6.24E-03	0.034	0.692	0.169	4.22E-05	++
rs12120330	1	48682729		T	C	0.026	0.752	0.222	7.14E-04	0.037	0.662	0.285	2.04E-02	0.03	0.718	0.175	4.23E-05	++
rs11267622	9	79324135	PRUNE2	A	ATGACTGTTGCAG	0.568	-0.278	0.088	1.64E-03	0.58	-0.342	0.129	8.03E-03	0.572	-0.298	0.073	4.23E-05	--
rs9504286	6	4894705	CDYL	A	G	0.035	0.824	0.201	4.24E-05					0.035	0.824	0.201	4.24E-05	+?
rs13394402	2	231968920	PSMD1	T	G	0.146	0.35	0.112	1.86E-03	0.143	0.463	0.17	6.58E-03	0.145	0.384	0.094	4.24E-05	++
rs60484735	2	28959995		T	TG	0.616	-0.29	0.09	1.25E-03	0.617	-0.342	0.134	1.11E-02	0.616	-0.306	0.075	4.24E-05	--
rs7160380	14	77357190		A	G	0.949	-0.688	0.168	4.25E-05					0.949	-0.688	0.168	4.25E-05	-?
rs115322324	4	158155410	GRIA2	T	C	0.982	-1.01	0.243	3.14E-05	0.983	-0.395	0.518	4.46E-01	0.982	-0.899	0.22	4.25E-05	--
rs149805559	19	22403270		T	TG	0.419	-0.358	0.088	4.25E-05					0.419	-0.358	0.088	4.25E-05	-?
rs185197163	18	31092239		A	G	0.016	0.85	0.284	2.82E-03	0.013	1.331	0.453	3.30E-03	0.015	0.986	0.241	4.27E-05	++
rs79461887	5	105928001		T	G	0.953	-0.724	0.177	4.28E-05					0.953	-0.724	0.177	4.28E-05	-?
rs421842	10	132189360		A	G	0.679	0.366	0.098	2.00E-04	0.679	0.271	0.152	7.42E-02	0.679	0.338	0.083	4.29E-05	++
rs143377417	19	44302154	LYPD5	C	G	0.988	-1.441	0.309	3.14E-06	0.988	0.378	0.731	6.05E-01	0.988	-1.165	0.285	4.29E-05	-+

	7	118144654		.Cn0.	T									0.034	0.707	0.173	4.29E-05	++
rs1046691	7	129473739	UBE2H	T	C	0.253	-0.391	0.111	4.18E-04	0.25	-0.352	0.17	3.76E-02	0.252	-0.379	0.093	4.30E-05	--
rs72681775	4	162338341	FSTL5	A	C	0.093	0.53	0.138	1.26E-04	0.1	0.336	0.207	1.04E-01	0.095	0.47	0.115	4.31E-05	++
rs7541119	1	113448204		C	G	0.892	-0.383	0.126	2.27E-03	0.892	-0.517	0.186	5.32E-03	0.892	-0.425	0.104	4.33E-05	--
rs190379195	5	89223135		A	T	0.059	0.659	0.161	4.34E-05					0.059	0.659	0.161	4.34E-05	+?
rs147393275	20	40794675	PTPRT	T	C	0.014	1.284	0.314	4.35E-05					0.014	1.284	0.314	4.35E-05	+?
rs144562261	20	40823799	PTPRT	A	T	0.986	-1.284	0.314	4.35E-05					0.986	-1.284	0.314	4.35E-05	-?
rs146643653	4	83756238	SEC31A	A	G	0.027	0.878	0.215	4.35E-05					0.026	0.878	0.215	4.35E-05	+?
rs148801384	3	177357025		T	TTTA	0.044	0.518	0.195	7.88E-03	0.046	0.832	0.255	1.13E-03	0.045	0.634	0.155	4.36E-05	++
rs7175483	15	45068394		C	G	0.286	0.382	0.093	4.36E-05					0.286	0.382	0.093	4.36E-05	+?
rs145535352	7	125418024		T	C	0.055	0.688	0.168	4.37E-05					0.055	0.688	0.168	4.37E-05	+?
rs269367	3	19860421		A	C	0.829	-0.442	0.108	4.37E-05					0.829	-0.442	0.108	4.37E-05	-?
rs269366	3	19861406		T	C	0.171	0.442	0.108	4.37E-05					0.171	0.442	0.108	4.37E-05	+?
rs149460283	15	44082151	RP11-296A16.1	T	C	0.045	0.699	0.177	7.82E-05	0.038	0.405	0.3	1.78E-01	0.043	0.623	0.152	4.37E-05	++
rs374825463	15	44097811	MFAP1	A	ATTCT	0.045	0.699	0.177	7.82E-05	0.038	0.405	0.3	1.78E-01	0.043	0.623	0.152	4.37E-05	++
rs115362284	15	44101320	MFAP1	T	C	0.955	-0.699	0.177	7.82E-05	0.962	-0.405	0.3	1.78E-01	0.957	-0.623	0.152	4.37E-05	--
rs796638992	10	92095335		A	AAT	0.057	0.688	0.168	4.38E-05					0.057	0.688	0.168	4.38E-05	+?
rs550867697	19	40890200	HIPK4	T	TTTTG	0.976	-0.901	0.232	1.04E-04	0.984	-0.632	0.457	1.67E-01	0.977	-0.846	0.207	4.38E-05	--
rs55835850	2	28949296		T	C	0.62	-0.296	0.09	9.95E-04	0.618	-0.326	0.134	1.52E-02	0.619	-0.305	0.075	4.39E-05	--
rs683866	9	79322068	PRUNE2	T	G	0.431	0.277	0.088	1.74E-03	0.42	0.344	0.129	7.87E-03	0.427	0.298	0.073	4.40E-05	++
rs2760207	10	9103606		C	G	0.011	1.297	0.317	4.40E-05					0.011	1.297	0.317	4.40E-05	+?
rs1456999	14	98466345		A	G	0.328	0.271	0.097	5.16E-03	0.342	0.451	0.143	1.61E-03	0.332	0.328	0.08	4.42E-05	++
rs11263642	11	69147825	MYEOV	A	G	0.988	-1.275	0.312	4.44E-05					0.988	-1.275	0.312	4.44E-05	-?
rs11263459	11	69156605	MYEOV	A	G	0.012	1.275	0.312	4.44E-05					0.012	1.275	0.312	4.44E-05	+?
rs8031239	15	33071184	FMN1	A	C	0.948	-0.552	0.179	2.06E-03	0.949	-0.677	0.25	6.74E-03	0.949	-0.594	0.146	4.45E-05	--
rs191902897	15	44145965	WDR76	A	G	0.035	0.808	0.189	1.85E-05	0.024	0.19	0.407	6.40E-01	0.034	0.699	0.171	4.46E-05	++
rs76696690	5	67551343	PIK3R1	A	C	0.988	-1.083	0.33	1.04E-03	0.988	-1.131	0.465	1.50E-02	0.988	-1.099	0.269	4.47E-05	--

rs9978607	21	36435884	RUNX1	A	G	0.947	-0.733	0.163	6.78E-06	0.944	-0.087	0.295	7.68E-01	0.946	-0.582	0.142	4.47E-05	--
rs13050576	21	36444219	RUNX1	C	G	0.948	-0.73	0.163	7.54E-06	0.945	-0.097	0.297	7.44E-01	0.947	-0.583	0.143	4.47E-05	--
rs12447761	16	62760182		A	G	0.1	0.42	0.134	1.68E-03	0.116	0.471	0.18	8.91E-03	0.106	0.439	0.107	4.48E-05	++
rs1026684	14	98461877		A	T	0.674	-0.271	0.097	5.24E-03	0.658	-0.451	0.143	1.61E-03	0.669	-0.328	0.08	4.48E-05	--
rs114467552	4	83913889	LIN54	A	G	0.03	0.843	0.207	4.49E-05					0.03	0.843	0.207	4.49E-05	+?
rs187348106	4	83914623	LIN54	A	G	0.03	0.843	0.207	4.49E-05					0.03	0.843	0.207	4.49E-05	+?
rs58828596	4	83915164	LIN54	CA	C	0.97	-0.843	0.207	4.49E-05					0.97	-0.843	0.207	4.49E-05	-?
rs115657017	4	83923853	LIN54	T	G	0.03	0.843	0.207	4.49E-05					0.03	0.843	0.207	4.49E-05	+?
rs116252662	4	83928348	LIN54	T	C	0.97	-0.843	0.207	4.49E-05					0.97	-0.843	0.207	4.49E-05	-?
rs56689651	4	83928825	LIN54	A	G	0.03	0.843	0.207	4.49E-05					0.03	0.843	0.207	4.49E-05	+?
rs10590980	15	80516154		CA	C	0.577	0.32	0.093	5.84E-04	0.568	0.295	0.134	2.77E-02	0.574	0.312	0.076	4.50E-05	++
rs112565517	3	120740331	STXBP5L	A	G	0.043	0.767	0.188	4.51E-05					0.043	0.767	0.188	4.51E-05	+?
rs2523811	6	29849333		T	C	0.2	0.354	0.108	9.90E-04	0.19	0.362	0.151	1.61E-02	0.197	0.357	0.087	4.52E-05	++
rs201500531	15	44651787	CASC4	A	AAAAC	0.075	0.614	0.15	4.52E-05					0.075	0.614	0.15	4.52E-05	+?
rs534247	1	90239523	RP11-302M6.4	A	G	0.067	-1.107	0.271	4.53E-05					0.067	-1.107	0.272	4.53E-05	-?
rs77197270	3	136914848		A	G	0.018	0.987	0.26	1.48E-04	0.018	0.662	0.403	1.01E-01	0.018	0.892	0.219	4.54E-05	++
rs41361451	6	148402361		T	C	0.088	-0.658	0.195	7.46E-04	0.08	-0.701	0.305	2.16E-02	0.086	-0.67	0.164	4.54E-05	--
rs10444219	11	11771122		T	C	0.966	-0.815	0.2	4.54E-05					0.966	-0.815	0.2	4.54E-05	-?
rs73696166	8	97022789		A	T	0.018	1.059	0.26	4.55E-05					0.018	1.059	0.26	4.55E-05	+?
rs2206430	20	41320638	PTPRT	A	G	0.907	-0.439	0.135	1.09E-03	0.9	-0.441	0.181	1.47E-02	0.904	-0.44	0.108	4.55E-05	--
rs116809469	10	128206436	C10orf90	A	G	0.022	0.717	0.258	5.48E-03	0.017	1.288	0.4	1.30E-03	0.021	0.884	0.217	4.55E-05	++
rs12133441	1	41889513		A	C	0.368	-0.397	0.097	4.56E-05					0.368	-0.397	0.097	4.56E-05	-?
rs72572451	7	7192963		T	G	0.07	0.277	0.164	9.02E-02	0.071	0.968	0.215	6.66E-06	0.07	0.531	0.13	4.56E-05	++
rs12745431	1	104741819		A	G	0.035	0.503	0.204	1.37E-02	0.04	0.915	0.263	5.12E-04	0.036	0.657	0.161	4.58E-05	++
rs12128656	1	48625257		A	C	0.022	0.798	0.233	6.11E-04	0.035	0.656	0.293	2.51E-02	0.027	0.743	0.182	4.58E-05	++
rs6102997	20	41330578	PTPRT	A	C	0.907	-0.449	0.135	8.89E-04	0.899	-0.424	0.18	1.82E-02	0.904	-0.44	0.108	4.59E-05	--
rs11459392	11	77143347	PAK1	T	TA	0.254	0.309	0.103	2.61E-03	0.28	0.391	0.14	5.33E-03	0.263	0.338	0.083	4.60E-05	++

rs72983619	2	232004469	PSMD1	A	G	0.146	0.352	0.112	1.76E-03	0.144	0.449	0.169	7.90E-03	0.145	0.382	0.094	4.60E-05	++
rs34669904	19	5166659	PTPRS	C	G	0.016	0.978	0.24	4.61E-05					0.016	0.978	0.24	4.61E-05	+?
rs148816524	3	32508181	CMTM7	A	G	0.032	0.782	0.211	2.04E-04	0.029	0.568	0.322	7.76E-02	0.031	0.718	0.176	4.62E-05	++
rs142571666	3	32508182	CMTM7	T	C	0.032	0.782	0.211	2.04E-04	0.029	0.568	0.322	7.76E-02	0.031	0.718	0.176	4.62E-05	++
rs4383075	14	98485019		A	G	0.665	-0.309	0.098	1.60E-03	0.645	-0.366	0.141	9.40E-03	0.658	-0.328	0.08	4.62E-05	--
rs139094978	11	101771431	ANGPTL5	T	TG	0.019	1.022	0.251	4.62E-05					0.019	1.022	0.251	4.62E-05	+?
rs10809034	9	10171341	PTPRD	T	C	0.64	-0.254	0.092	5.91E-03	0.621	-0.435	0.136	1.38E-03	0.634	-0.311	0.076	4.63E-05	--
rs113000305	3	120792232	STXBP5L	T	C	0.957	-0.766	0.188	4.63E-05					0.957	-0.766	0.188	4.63E-05	-?
rs145057131	2	184700120		T	C	0.982	-0.675	0.273	1.34E-02	0.988	-1.537	0.419	2.45E-04	0.984	-0.932	0.229	4.63E-05	--
rs115455755	5	5395028		T	C	0.015	1.115	0.274	4.65E-05					0.015	1.115	0.274	4.65E-05	+?
rs78667814	12	12612913	LOH12CR1	T	C	0.017	0.711	0.261	6.37E-03	0.02	1.009	0.325	1.89E-03	0.018	0.828	0.203	4.65E-05	++
rs77282240	12	12612914	LOH12CR1	A	G	0.983	-0.711	0.261	6.37E-03	0.98	-1.009	0.325	1.89E-03	0.982	-0.828	0.203	4.65E-05	--
rs77977190	12	12613418	LOH12CR1	A	C	0.017	0.711	0.261	6.37E-03	0.02	1.009	0.325	1.89E-03	0.018	0.828	0.203	4.65E-05	++
rs9988866	11	18392983		A	T	0.457	0.285	0.089	1.38E-03	0.451	0.306	0.121	1.17E-02	0.455	0.293	0.072	4.67E-05	++
rs115364762	4	175342106		A	T	0.989	-1.08	0.317	6.57E-04	0.982	-0.918	0.408	2.44E-02	0.986	-1.019	0.25	4.67E-05	--
rs6963862	7	55360709		T	C	0.026	0.425	0.257	9.79E-02	0.028	1.242	0.291	1.91E-05	0.027	0.783	0.192	4.67E-05	++
rs11232877	11	81516733		A	C	0.232	0.348	0.102	6.25E-04	0.224	0.325	0.147	2.70E-02	0.229	0.341	0.084	4.68E-05	++
rs149616570	7	7179232		T	TTTTG	0.071	0.272	0.156	8.12E-02	0.071	0.986	0.217	5.45E-06	0.071	0.515	0.127	4.69E-05	++
rs17049573	2	58824027		A	G	0.934	-0.501	0.16	1.70E-03	0.94	-0.615	0.234	8.71E-03	0.935	-0.537	0.132	4.70E-05	--
rs546227723	5	179115420	CANX	A	G	0.986	-1.165	0.286	4.70E-05					0.986	-1.165	0.286	4.70E-05	-?
rs6876641	5	133394222		A	G	0.039	0.648	0.184	4.22E-04	0.049	0.541	0.263	3.94E-02	0.042	0.613	0.151	4.71E-05	++
rs12253810	10	15116387		T	C	0.13	0.399	0.124	1.31E-03	0.126	0.462	0.184	1.20E-02	0.129	0.419	0.103	4.71E-05	++
rs6102993	20	41325748	PTPRT	T	C	0.093	0.438	0.135	1.13E-03	0.1	0.441	0.181	1.47E-02	0.096	0.439	0.108	4.71E-05	++
rs79276019	11	87915452		A	C	0.032	0.933	0.211	9.62E-06	0.021	0.084	0.437	8.48E-01	0.03	0.773	0.19	4.71E-05	++
rs113311734	9	97432670		A	C	0.024	0.588	0.246	1.69E-02	0.035	0.952	0.277	5.87E-04	0.029	0.749	0.184	4.71E-05	++
rs7800072	7	84628989	SEMA3D	T	G	0.613	0.369	0.098	1.67E-04	0.642	0.243	0.142	8.74E-02	0.622	0.329	0.081	4.72E-05	++
rs113337491	17	19410528	SLC47A1	A	G	0.828	-0.455	0.112	4.72E-05					0.828	-0.455	0.112	4.72E-05	-?
rs75306303	6	120859306		A	G	0.044	0.613	0.181	6.88E-04	0.04	0.631	0.281	2.49E-02	0.043	0.618	0.152	4.73E-05	++

rs6872882	5	165523674		T	C	0.517	0.353	0.087	4.73E-05					0.517	0.353	0.087	4.73E-05	+?
rs111601119	16	87084565		T	G	0.015	1.146	0.282	4.73E-05					0.015	1.146	0.282	4.73E-05	+?
rs111279925	16	1233151	CACNA1H	A	C	0.847	-0.455	0.112	4.75E-05					0.847	-0.456	0.112	4.75E-05	-?
rs150876893	15	95548969		CAT	C	0.983	-1.099	0.27	4.77E-05					0.983	-1.099	0.27	4.77E-05	-?
rs288925	1	69832182		A	G	0.092	0.487	0.138	4.21E-04	0.095	0.421	0.206	4.12E-02	0.093	0.467	0.115	4.78E-05	++
rs190835	1	69833286		C	G	0.908	-0.487	0.138	4.21E-04	0.905	-0.421	0.206	4.12E-02	0.907	-0.467	0.115	4.78E-05	--
rs112761653	19	13656974	CACNA1A	C	G	0.943	-0.689	0.169	4.78E-05					0.944	-0.689	0.17	4.78E-05	-?
rs143318748	7	108570255		T	TTTG	0.022	0.622	0.266	1.92E-02	0.018	1.358	0.367	2.17E-04	0.021	0.875	0.215	4.80E-05	++
rs114897748	2	213097090	ERBB4	T	C	0.968	-0.732	0.199	2.25E-04	0.969	-0.609	0.351	8.28E-02	0.968	-0.702	0.173	4.80E-05	--
rs73445186	15	84915085		T	G	0.137	0.306	0.125	1.42E-02	0.13	0.588	0.168	4.48E-04	0.134	0.407	0.1	4.81E-05	++
rs73445187	15	84915095		A	G	0.863	-0.306	0.125	1.42E-02	0.87	-0.588	0.168	4.48E-04	0.866	-0.407	0.1	4.81E-05	--
rs150134041	10	78084476	C10orf11	A	AT	0.065	0.634	0.158	6.33E-05	0.058	0.326	0.265	2.19E-01	0.063	0.553	0.136	4.82E-05	++
rs188093489	3	185009943	MAP3K13	A	C	0.988	-1.015	0.306	9.00E-04	0.986	-0.982	0.419	1.91E-02	0.988	-1.004	0.247	4.84E-05	--
rs146629096	6	21454312		A	G	0.898	-0.535	0.132	4.85E-05					0.898	-0.535	0.132	4.85E-05	-?
rs55721532	2	28938968		A	G	0.645	-0.286	0.092	1.78E-03	0.645	-0.36	0.137	8.41E-03	0.645	-0.309	0.076	4.86E-05	--
rs78983383	5	89518212		C	G	0.895	-0.455	0.132	5.78E-04	0.902	-0.422	0.195	3.06E-02	0.897	-0.445	0.11	4.86E-05	--
rs112620303	19	13658598	CACNA1A	A	C	0.057	0.685	0.169	4.87E-05					0.057	0.685	0.169	4.87E-05	+?
rs57767815	11	81513081		A	C	0.251	0.371	0.102	2.87E-04	0.24	0.278	0.146	5.72E-02	0.247	0.34	0.084	4.87E-05	++
rs370517012	11	1905146	LSP1	G	GT	0.033	0.843	0.208	4.90E-05					0.033	0.843	0.208	4.90E-05	+?
rs6710959	2	28958603		T	C	0.615	-0.287	0.09	1.45E-03	0.617	-0.342	0.134	1.11E-02	0.615	-0.304	0.075	4.91E-05	--
rs57501094	2	28959965		CAGCTCACTGCAGCTTCAACCTCCCTGG	C	0.385	0.287	0.09	1.45E-03	0.383	0.342	0.134	1.11E-02	0.385	0.304	0.075	4.91E-05	++
rs140326363	2	62142426	COMMD1	A	C	0.026	0.671	0.236	4.50E-03	0.026	0.963	0.322	2.79E-03	0.026	0.773	0.19	4.92E-05	++
rs75613455	12	12209702	BCL2L14	A	G	0.088	-0.673	0.195	5.69E-04	0.08	-0.641	0.298	3.17E-02	0.086	-0.664	0.164	4.92E-05	--
rs12432932	14	92976023		T	C	0.03	0.885	0.218	4.93E-05					0.029	0.885	0.218	4.93E-05	+?
rs7132453	12	63636174		T	C	0.192	0.354	0.106	8.00E-04	0.209	0.35	0.153	2.22E-02	0.198	0.352	0.087	4.95E-05	++

rs115140013	3	197279694	BDH1	A	G	0.984	-1.17	0.288	4.96E-05					0.984	-1.17	0.288	4.96E-05	-?
rs182396116	3	197282754	BDH1	T	G	0.016	1.17	0.288	4.96E-05					0.016	1.17	0.288	4.96E-05	+?
rs112861115	22	45196607	PRR5-ARHGAP8	A	G	0.508	-0.347	0.085	4.97E-05					0.508	-0.347	0.086	4.97E-05	-?
rs7235954	18	22596041		C	G	0.492	0.389	0.092	2.19E-05	0.488	0.128	0.141	3.63E-01	0.491	0.312	0.077	4.97E-05	++
rs9711993	2	239684289		A	G	0.721	-0.391	0.096	4.98E-05					0.721	-0.391	0.096	4.98E-05	-?

Table S2. Top Findings in European-Americans ($p < 5.0 \times 10^{-5}$).

Marker	Chr	Pos (hg19)	Gene name	Eff Allele	Alt Allele	Alle Freq YP1	Beta YP1	SE YP1	*P* YP1	Alle Freq YP2	Beta YP1	SE YP2	*P* YP2	Alle Freq Meta	Beta Meta	SE Meta	*P* Meta	Direction
rs12684088	9	103880173	LPPR1	A	T	0.033	1.226	0.241	3.53E-07					0.033	1.226	0.241	3.53E-07	+?
rs56073857	8	2703779		A	C	0.011	1.989	0.397	5.61E-07					0.011	1.989	0.397	5.61E-07	+?
rs11030846	11	29872433		A	G	0.099	0.61	0.184	9.14E-04	0.096	0.803	0.211	1.45E-04	0.098	0.693	0.139	5.85E-07	++
rs7853968	9	103890732	LPPR1	C	G	0.966	-1.196	0.24	6.57E-07					0.966	-1.196	0.24	6.57E-07	-?
rs1501588	8	16640722		A	G	0.069	0.683	0.202	7.42E-04	0.08	0.818	0.223	2.35E-04	0.074	0.744	0.15	6.69E-07	++
rs118078748	11	29855828		T	C	0.09	0.617	0.191	1.21E-03	0.088	0.813	0.215	1.50E-04	0.089	0.703	0.142	7.92E-07	++
rs1483035	4	156510036		A	G	0.403	0.428	0.121	4.29E-04	0.4	0.537	0.153	4.58E-04	0.402	0.47	0.095	7.95E-07	++
rs11724400	4	156510748		T	C	0.597	-0.428	0.121	4.29E-04	0.6	-0.537	0.153	4.58E-04	0.598	-0.47	0.095	7.95E-07	--
rs2705447	4	156510320		T	C	0.596	-0.427	0.122	4.43E-04	0.6	-0.537	0.153	4.58E-04	0.598	-0.469	0.095	8.21E-07	--
rs2705464	4	156513652		A	G	0.594	-0.421	0.122	5.44E-04	0.6	-0.536	0.153	4.69E-04	0.596	-0.466	0.095	1.04E-06	--
rs1318278	8	16637512		A	G	0.07	0.67	0.207	1.19E-03	0.08	0.811	0.221	2.49E-04	0.075	0.735	0.151	1.13E-06	++
rs6816498	4	156506677		T	C	0.405	0.43	0.122	4.43E-04	0.4	0.517	0.153	7.57E-04	0.403	0.464	0.096	1.26E-06	++
rs4922233	8	16639069		T	C	0.076	0.61	0.199	2.17E-03	0.088	0.809	0.214	1.53E-04	0.082	0.703	0.146	1.40E-06	++
rs4681921	3	56904958	ARHGEF3	T	C	0.583	-0.361	0.12	2.57E-03	0.598	-0.593	0.151	8.34E-05	0.589	-0.451	0.094	1.52E-06	--
rs35886876	3	56907017	ARHGEF3	A	T	0.419	0.362	0.12	2.56E-03	0.402	0.589	0.15	9.08E-05	0.412	0.45	0.094	1.60E-06	++
rs73057290	3	35260436		T	C	0.014	1.716	0.351	1.04E-06	0.014	0.68	0.521	1.92E-01	0.014	1.392	0.291	1.76E-06	++
rs11030843	11	29868083		T	G	0.09	0.584	0.194	2.60E-03	0.088	0.813	0.215	1.50E-04	0.089	0.687	0.144	1.78E-06	++
rs11030844	11	29868278		T	C	0.091	0.612	0.19	1.30E-03	0.089	0.765	0.216	3.94E-04	0.09	0.679	0.143	1.97E-06	++
rs10567492	4	156485045		A	ATTCT	0.406	0.44	0.122	3.10E-04	0.406	0.477	0.154	1.90E-03	0.406	0.454	0.096	1.98E-06	++
rs73057274	3	35251812		T	C	0.986	-1.722	0.356	1.36E-06	0.986	-0.68	0.521	1.92E-01	0.986	-1.389	0.294	2.31E-06	--
rs2625274	4	156488140		A	T	0.569	-0.437	0.123	3.84E-04	0.575	-0.475	0.154	2.05E-03	0.571	-0.452	0.096	2.62E-06	--
rs567173013	4	156488055		G	GGTATTGGGT	0.569	-0.437	0.123	3.84E-04	0.574	-0.473	0.154	2.13E-03	0.571	-0.451	0.096	2.71E-06	--
rs73149268	3	25282624	RARB	T	C	0.01	1.71	0.365	2.75E-06					0.01	1.71	0.365	2.75E-06	+?

rs111940197	3	25283567	RARB	T	C	0.99	-1.71	0.365	2.75E-06					0.99	-1.71	0.365	2.75E-06	-?
rs140275615	3	25284679	RARB	T	C	0.99	-1.71	0.365	2.75E-06					0.99	-1.71	0.365	2.75E-06	-?
rs1843029	3	25288462	RARB	T	C	0.99	-1.71	0.365	2.75E-06					0.99	-1.71	0.365	2.75E-06	-?
rs113931895	3	25289172	RARB	T	C	0.01	1.71	0.365	2.75E-06					0.01	1.71	0.365	2.75E-06	+?
rs11030856	11	29886545		A	G	0.09	0.561	0.196	4.32E-03	0.087	0.818	0.214	1.36E-04	0.089	0.678	0.145	2.85E-06	++
rs11030857	11	29886723		A	G	0.09	0.561	0.196	4.32E-03	0.087	0.818	0.214	1.36E-04	0.089	0.678	0.145	2.85E-06	++
rs78923500	3	25289791	RARB	A	G	0.011	1.687	0.361	3.05E-06					0.011	1.687	0.361	3.05E-06	+?
rs145836613	3	25291057	RARB	A	AT	0.989	-1.687	0.361	3.05E-06					0.989	-1.687	0.361	3.05E-06	-?
rs73151265	3	25294450	RARB	A	G	0.011	1.687	0.361	3.05E-06					0.011	1.687	0.361	3.05E-06	+?
rs2254177	17	48358419	TMEM92	A	G	0.311	0.623	0.134	3.08E-06					0.311	0.623	0.134	3.08E-06	+?
rs72878918	11	29869921		A	G	0.898	-0.577	0.184	1.73E-03	0.902	-0.742	0.212	4.76E-04	0.899	-0.648	0.139	3.21E-06	--
rs4922234	8	16639271		C	G	0.924	-0.605	0.199	2.36E-03	0.915	-0.776	0.22	4.16E-04	0.92	-0.682	0.147	3.78E-06	--
rs2254318	17	48359928		C	G	0.314	0.617	0.134	4.16E-06					0.314	0.617	0.134	4.16E-06	+?
rs2586437	17	48360903		T	C	0.317	0.607	0.133	4.72E-06					0.317	0.607	0.133	4.72E-06	+?
rs80067087	14	95508157		T	C	0.972	-1.209	0.264	4.75E-06					0.972	-1.209	0.264	4.75E-06	-?
rs1466516	4	156517289		T	C	0.608	-0.422	0.126	8.00E-04	0.604	-0.476	0.152	1.78E-03	0.607	-0.444	0.097	4.76E-06	--
rs2705469	4	156515772		T	C	0.608	-0.421	0.126	8.17E-04	0.605	-0.477	0.152	1.74E-03	0.607	-0.444	0.097	4.77E-06	--
rs72878951	11	29899326		A	G	0.901	-0.563	0.189	2.93E-03	0.903	-0.752	0.213	4.12E-04	0.902	-0.646	0.141	4.87E-06	--
rs728230	17	48359421		A	G	0.311	0.609	0.134	5.35E-06					0.311	0.609	0.134	5.35E-06	+?
rs149927205	2	213240755	ERBB4	T	TGCCCTAATTGATGAA	0.05	0.488	0.247	4.78E-02	0.048	1.115	0.249	7.84E-06	0.049	0.798	0.175	5.37E-06	++
rs10501116	11	29880030		A	T	0.894	-0.573	0.179	1.34E-03	0.903	-0.697	0.214	1.14E-03	0.898	-0.624	0.137	5.43E-06	--
rs11529247	11	29852312		A	G	0.088	0.541	0.192	4.73E-03	0.089	0.786	0.215	2.53E-04	0.088	0.65	0.143	5.54E-06	++
rs72878978	11	29917439		A	C	0.106	0.537	0.18	2.87E-03	0.098	0.735	0.212	5.37E-04	0.103	0.62	0.137	6.40E-06	++
rs12420770	11	29890495		A	C	0.107	0.541	0.18	2.65E-03	0.098	0.729	0.212	5.99E-04	0.103	0.62	0.137	6.42E-06	++
rs3122707	9	15588214	CCDC171	C	G	0.905	-0.804	0.179	6.88E-06					0.905	-0.804	0.179	6.88E-06	-?

rs201800106	2	748110		T	C	0.614	0.599	0.134	7.11E-06					0.614	0.6	0.134	7.11E-06	+?
rs11161210	15	25969509	ATP10A	A	T	0.023	1.228	0.273	7.12E-06					0.023	1.228	0.273	7.12E-06	+?
rs187562906	6	71985782		T	C	0.011	1.742	0.388	7.14E-06					0.011	1.742	0.388	7.14E-06	+?
rs3122706	9	15588885	CCDC171	T	G	0.905	-0.796	0.177	7.18E-06					0.905	-0.796	0.177	7.18E-06	-?
rs72878920	11	29870591		A	G	0.883	-0.544	0.172	1.60E-03	0.894	-0.68	0.211	1.27E-03	0.887	-0.599	0.134	7.38E-06	--
rs4355814	8	16642227		C	G	0.913	-0.581	0.184	1.60E-03	0.909	-0.689	0.216	1.42E-03	0.911	-0.626	0.14	7.75E-06	--
rs2251405	1	114697134		A	G	0.763	0.721	0.171	2.39E-05	0.764	0.38	0.192	4.80E-02	0.764	0.571	0.128	7.77E-06	++
rs11525343	11	29854157		T	C	0.089	0.521	0.192	6.59E-03	0.089	0.786	0.215	2.53E-04	0.089	0.639	0.143	8.06E-06	++
rs62426129	6	149269199	UST	T	C	0.196	-0.62	0.188	9.76E-04	0.168	-0.788	0.258	2.30E-03	0.186	-0.678	0.152	8.19E-06	--
rs62426130	6	149269662	UST	T	G	0.804	0.62	0.188	9.76E-04	0.832	0.788	0.258	2.30E-03	0.814	0.678	0.152	8.19E-06	++
rs12918906	16	19889658	GPRC5B	T	C	0.059	0.92	0.206	8.22E-06					0.059	0.92	0.206	8.22E-06	+?
rs7611431	3	56910091	ARHGEF3	A	G	0.559	-0.32	0.122	8.55E-03	0.573	-0.582	0.152	1.24E-04	0.564	-0.423	0.095	8.46E-06	--
rs11030848	11	29877687		T	C	0.108	0.552	0.179	2.03E-03	0.097	0.695	0.214	1.16E-03	0.103	0.611	0.137	8.59E-06	++
rs247396	16	83814397	CDH13	C	G	0.239	0.351	0.148	1.75E-02	0.246	0.604	0.153	7.93E-05	0.242	0.473	0.106	8.62E-06	++
rs1364115	16	83815052	CDH13	C	G	0.233	0.347	0.149	1.99E-02	0.238	0.619	0.155	6.76E-05	0.236	0.477	0.107	9.04E-06	++
rs10835592	11	29848290		A	T	0.911	-0.485	0.195	1.29E-02	0.913	-0.836	0.216	1.10E-04	0.912	-0.643	0.145	9.09E-06	--
rs72876999	11	29848888		T	C	0.089	0.485	0.195	1.29E-02	0.087	0.836	0.216	1.10E-04	0.088	0.643	0.145	9.09E-06	++
rs59970673	15	45378884		A	G	0.01	1.862	0.42	9.21E-06					0.01	1.862	0.42	9.21E-06	+?
rs1981860	16	83813294	CDH13	T	C	0.767	-0.347	0.149	1.99E-02	0.761	-0.618	0.155	6.94E-05	0.764	-0.477	0.108	9.24E-06	--
rs57930285	16	83813511	CDH13	A	G	0.233	0.347	0.149	1.99E-02	0.239	0.618	0.155	6.94E-05	0.236	0.477	0.108	9.24E-06	++
rs143088710	2	52866377		T	C	0.02	1.022	0.33	1.96E-03	0.016	1.321	0.411	1.30E-03	0.018	1.139	0.257	9.50E-06	++
rs5790769	11	29884200		T	TA	0.909	-0.551	0.196	5.03E-03	0.911	-0.764	0.218	4.63E-04	0.91	-0.646	0.146	9.56E-06	--
11:29896975	11	29896975		CTT	TTT	0.892	-0.529	0.178	3.04E-03	0.901	-0.713	0.212	7.96E-04	0.896	-0.605	0.137	9.59E-06	--
rs10501120	11	29897097		A	G	0.108	0.529	0.178	3.04E-03	0.099	0.713	0.212	7.96E-04	0.104	0.605	0.137	9.59E-06	++
rs11134266	5	7945144		T	C	0.955	-0.423	0.286	1.39E-01	0.954	-1.239	0.266	3.13E-06	0.955	-0.86	0.195	9.83E-06	--
rs151051496	5	7948743		G	GAT	0.045	0.423	0.286	1.39E-01	0.046	1.239	0.266	3.13E-06	0.045	0.86	0.195	9.83E-06	++
rs11744470	5	7952808		A	G	0.955	-0.423	0.286	1.39E-01	0.954	-1.239	0.266	3.13E-06	0.955	-0.86	0.195	9.83E-06	--
rs4140764	12	13952222	GRIN2B	C	G	0.733	-0.404	0.136	2.89E-03	0.737	-0.559	0.167	8.33E-04	0.734	-0.465	0.105	9.91E-06	--

rs13081102	3	56910738	ARHGEF3	T	C	0.561	-0.318	0.121	8.61E-03	0.579	-0.576	0.152	1.55E-04	0.568	-0.418	0.095	1.03E-05	--
rs138053245	9	120221686		G	GA	0.972	-0.974	0.296	1.01E-03	0.974	-0.953	0.325	3.40E-03	0.973	-0.964	0.219	1.07E-05	--
rs114807580	12	20150910		T	C	0.985	-1.52	0.345	1.07E-05					0.985	-1.52	0.345	1.07E-05	-?
rs9495493	6	139802437		T	C	0.058	0.933	0.212	1.07E-05					0.058	0.933	0.212	1.07E-05	+?
rs12211515	6	149271813	UST	T	C	0.803	0.631	0.188	8.12E-04	0.832	0.722	0.252	4.19E-03	0.813	0.664	0.151	1.10E-05	++
rs6775150	3	56906056	ARHGEF3	C	G	0.435	0.3	0.12	1.26E-02	0.424	0.599	0.152	8.35E-05	0.431	0.415	0.094	1.10E-05	++
rs4681924	3	56906396	ARHGEF3	T	C	0.564	-0.308	0.121	1.10E-02	0.576	-0.587	0.152	1.12E-04	0.569	-0.416	0.095	1.11E-05	--
rs12222131	11	29931436		A	G	0.107	0.598	0.182	1.02E-03	0.097	0.631	0.216	3.52E-03	0.103	0.612	0.139	1.12E-05	++
rs116912917	20	43660394	STK4	A	G	0.917	-0.83	0.189	1.13E-05					0.917	-0.83	0.189	1.13E-05	-?
rs1403418	3	189804656	LEPREL1	A	G					0.99	-2.121	0.483	1.14E-05	0.99	-2.121	0.483	1.14E-05	?-
rs926757	22	45497187		A	G	0.112	0.415	0.172	1.55E-02	0.119	0.738	0.191	1.10E-04	0.115	0.56	0.128	1.15E-05	++
rs5820809	17	48360270		T	TAAAC	0.348	0.576	0.131	1.16E-05					0.348	0.576	0.131	1.16E-05	+?
rs11030840	11	29862369		C	G	0.883	-0.541	0.174	1.90E-03	0.894	-0.66	0.211	1.77E-03	0.887	-0.589	0.134	1.16E-05	--
rs10501119	11	29896698		T	C	0.884	-0.542	0.173	1.75E-03	0.892	-0.654	0.211	1.97E-03	0.888	-0.587	0.134	1.17E-05	--
rs16920003	11	29937234		C	G	0.115	0.606	0.177	6.04E-04	0.105	0.584	0.215	6.46E-03	0.111	0.598	0.136	1.19E-05	++
rs11130551	3	56906636	ARHGEF3	T	C	0.563	-0.305	0.121	1.19E-02	0.573	-0.588	0.152	1.11E-04	0.567	-0.415	0.095	1.21E-05	--
rs45501291	7	87029710		A	G	0.942	-0.672	0.226	2.99E-03	0.947	-0.857	0.264	1.17E-03	0.944	-0.75	0.172	1.26E-05	--
rs453991	9	15600548	CCDC171	A	G	0.086	0.804	0.184	1.27E-05					0.086	0.804	0.184	1.27E-05	+?
rs11030863	11	29910585		T	C	0.88	-0.564	0.17	8.93E-04	0.887	-0.591	0.209	4.69E-03	0.883	-0.575	0.132	1.29E-05	--
rs56090907	16	68401338	SMPD3	CGTGCGCTGCT	C	0.35	0.578	0.133	1.47E-05	0.346	0.256	0.155	9.86E-02	0.348	0.441	0.101	1.29E-05	++
rs11030862	11	29897704		C	G	0.115	0.552	0.173	1.46E-03	0.106	0.635	0.213	2.84E-03	0.112	0.585	0.134	1.34E-05	++
rs12469774	2	213259502	ERBB4	T	C	0.952	-0.576	0.241	1.70E-02	0.955	-1.007	0.263	1.27E-04	0.953	-0.773	0.178	1.36E-05	--
rs149574734	8	2851416	CSMD1	T	C	0.019	1.46	0.336	1.42E-05					0.019	1.46	0.336	1.42E-05	+?
rs55669429	3	63995599		A	G	0.912	-0.638	0.186	5.89E-04	0.907	-0.577	0.218	8.00E-03	0.91	-0.612	0.141	1.45E-05	--
rs7008098	8	141287438	TRAPPC9	A	T	0.336	0.382	0.125	2.16E-03	0.323	0.481	0.155	1.95E-03	0.331	0.421	0.097	1.48E-05	++
rs115263587	5	99707048		T	C	0.986	-1.565	0.361	1.49E-05					0.986	-1.565	0.361	1.49E-05	-?
rs139706388	10	125228664		T	TA	0.09	0.525	0.189	5.48E-03	0.085	0.763	0.223	6.25E-04	0.088	0.624	0.144	1.49E-05	++

rs34768432	14	30785974		T	C	0.933	-0.925	0.214	1.53E-05					0.933	-0.925	0.214	1.53E-05	-?
rs62426127	6	149259898	UST	A	G	0.819	0.61	0.191	1.39E-03	0.836	0.766	0.259	3.16E-03	0.825	0.665	0.154	1.53E-05	++
rs62426128	6	149260017	UST	T	C	0.819	0.61	0.191	1.39E-03	0.836	0.766	0.259	3.16E-03	0.825	0.665	0.154	1.53E-05	++
rs181885805	10	125228663		A	C	0.092	0.504	0.189	7.77E-03	0.084	0.81	0.228	3.69E-04	0.089	0.629	0.145	1.53E-05	++
rs16919890	11	29865389		C	G	0.894	-0.565	0.179	1.57E-03	0.901	-0.637	0.215	3.09E-03	0.897	-0.594	0.138	1.55E-05	--
rs397874352	3	177420306		A	AT	0.177	0.656	0.147	8.24E-06	0.178	0.247	0.188	1.89E-01	0.177	0.501	0.116	1.55E-05	++
rs9390640	6	149254024	UST	A	C	0.366	-0.565	0.139	4.89E-05	0.367	-0.313	0.166	6.01E-02	0.367	-0.461	0.107	1.55E-05	--
rs17080218	6	149258535	UST	T	C	0.18	-0.598	0.19	1.66E-03	0.163	-0.798	0.264	2.48E-03	0.174	-0.667	0.154	1.56E-05	--
rs144056943	7	86335993	GRM3	A	G	0.032	0.904	0.286	1.59E-03	0.03	0.996	0.337	3.15E-03	0.031	0.942	0.218	1.58E-05	++
rs79367729	12	49353087		T	TC	0.384	0.401	0.126	1.47E-03	0.39	0.439	0.15	3.46E-03	0.387	0.417	0.097	1.59E-05	++
rs9645813	12	49353138		C	G	0.384	0.401	0.126	1.47E-03	0.39	0.439	0.15	3.46E-03	0.387	0.417	0.097	1.59E-05	++
rs61942207	12	49353601		T	C	0.616	-0.401	0.126	1.47E-03	0.61	-0.439	0.15	3.46E-03	0.613	-0.417	0.097	1.59E-05	--
rs4760664	12	49354484		A	G	0.616	-0.401	0.126	1.47E-03	0.61	-0.439	0.15	3.46E-03	0.613	-0.417	0.097	1.59E-05	--
rs139355322	5	99770257		A	T	0.012	1.641	0.38	1.61E-05					0.012	1.641	0.38	1.61E-05	+?
rs141420537	19	33323510	SLC7A9	A	AG	0.231	0.217	0.143	1.31E-01	0.239	0.831	0.17	9.88E-07	0.235	0.472	0.11	1.62E-05	++
rs141924696	7	7602244		T	C	0.989	-1.623	0.376	1.62E-05					0.989	-1.623	0.376	1.62E-05	-?
rs10875902	12	49355292		A	G	0.384	0.401	0.126	1.47E-03	0.39	0.438	0.15	3.54E-03	0.387	0.416	0.097	1.63E-05	++
rs72878968	11	29910502		A	G	0.882	-0.515	0.174	3.00E-03	0.893	-0.671	0.211	1.48E-03	0.886	-0.578	0.134	1.63E-05	--
rs11919260	3	1086918		A	G	0.473	0.556	0.129	1.65E-05					0.473	0.556	0.129	1.65E-05	+?
rs190534068	2	213223091	ERBB4	A	T	0.95	-0.469	0.247	5.79E-02	0.952	-1.063	0.252	2.47E-05	0.951	-0.76	0.176	1.65E-05	--
rs75711731	11	29926303		T	C	0.884	-0.544	0.176	2.00E-03	0.894	-0.641	0.213	2.57E-03	0.888	-0.584	0.136	1.68E-05	--
rs2561074	5	65640352		A	G	0.606	-0.547	0.127	1.71E-05					0.607	-0.547	0.127	1.71E-05	-?
rs2801646	5	65640456		A	G	0.606	-0.547	0.127	1.71E-05					0.607	-0.547	0.127	1.71E-05	-?
rs10512246	9	98426095		C	G					0.01	1.969	0.458	1.73E-05	0.01	1.969	0.458	1.73E-05	?+
rs9521369	13	110082687		A	G	0.148	0.626	0.161	1.04E-04	0.15	0.385	0.185	3.67E-02	0.149	0.522	0.121	1.73E-05	++
rs12513726	5	177414179		T	C	0.264	0.366	0.14	9.06E-03	0.269	0.546	0.155	4.38E-04	0.267	0.446	0.104	1.76E-05	++
rs2307022	16	68381978	PRMT7	A	G	0.345	0.549	0.134	3.97E-05	0.343	0.279	0.154	7.02E-02	0.344	0.433	0.101	1.78E-05	++
rs73196422	7	87007744	CROT	T	C	0.942	-0.682	0.225	2.40E-03	0.946	-0.823	0.269	2.23E-03	0.944	-0.74	0.172	1.79E-05	--

rs73196425	7	87008223	CROT	T	C	0.058	0.682	0.225	2.40E-03	0.054	0.823	0.269	2.23E-03	0.056	0.74	0.172	1.79E-05	++
rs117503563	8	26815709		A	G	0.024	0.93	0.307	2.43E-03	0.016	1.245	0.402	1.96E-03	0.021	1.046	0.244	1.80E-05	++
rs79413760	9	79156095		T	C	0.011	1.578	0.368	1.81E-05					0.011	1.578	0.368	1.81E-05	+?
rs4696883	4	8644223		A	G	0.271	0.578	0.135	1.82E-05					0.271	0.578	0.135	1.82E-05	+?
rs3782353	12	49358880		A	G	0.384	0.402	0.126	1.41E-03	0.391	0.428	0.15	4.19E-03	0.387	0.413	0.096	1.82E-05	++
rs549799093	11	29921526		T	TA	0.134	0.542	0.164	9.75E-04	0.122	0.558	0.204	6.23E-03	0.129	0.548	0.128	1.83E-05	++
rs78527272	13	110022728		A	G	0.105	0.582	0.182	1.37E-03	0.103	0.593	0.208	4.41E-03	0.104	0.587	0.137	1.84E-05	++
rs4760662	12	49370857		A	G	0.387	0.393	0.125	1.66E-03	0.395	0.438	0.15	3.55E-03	0.39	0.411	0.096	1.85E-05	++
rs12069698	1	97352212		C	G	0.95	-0.972	0.233	3.02E-05	0.951	-0.484	0.302	1.09E-01	0.951	-0.79	0.184	1.86E-05	--
rs3741627	12	49359587	WNT10B	T	G	0.616	-0.402	0.126	1.41E-03	0.608	-0.427	0.15	4.33E-03	0.613	-0.412	0.096	1.87E-05	--
rs1051886	12	49359989	WNT10B	A	G	0.384	0.402	0.126	1.41E-03	0.392	0.427	0.15	4.33E-03	0.387	0.412	0.096	1.87E-05	++
rs73060918	3	35400750		A	C	0.983	-1.383	0.351	8.07E-05	0.986	-0.892	0.485	6.57E-02	0.984	-1.214	0.284	1.93E-05	--
rs73196416	7	87006287	CROT	A	G	0.942	-0.682	0.225	2.40E-03	0.946	-0.816	0.269	2.44E-03	0.943	-0.737	0.172	1.93E-05	--
rs2031277	13	31200712	USPL1	T	G	0.984	-1.494	0.35	1.94E-05					0.984	-1.494	0.35	1.94E-05	-?
rs60267144	13	31202445	USPL1	A	G	0.984	-1.494	0.35	1.94E-05					0.984	-1.494	0.35	1.94E-05	-?
rs11839042	13	31207246	USPL1	T	G	0.016	1.494	0.35	1.94E-05					0.016	1.494	0.35	1.94E-05	+?
rs11841258	13	31221745	USPL1	A	G	0.984	-1.494	0.35	1.94E-05					0.984	-1.494	0.35	1.94E-05	-?
rs11838483	13	31221768	USPL1	C	G	0.984	-1.494	0.35	1.94E-05					0.984	-1.494	0.35	1.94E-05	-?
rs140813066	13	31229326	USPL1	A	G	0.016	1.494	0.35	1.94E-05					0.016	1.494	0.35	1.94E-05	+?
rs78450603	9	137521989		A	G	0.987	-1.572	0.368	1.94E-05					0.987	-1.572	0.368	1.94E-05	-?
rs114344631	1	97373175		A	G	0.047	1.013	0.237	1.96E-05					0.047	1.012	0.237	1.96E-05	+?
rs7740363	6	149253509	UST	A	T	0.366	-0.566	0.139	4.52E-05	0.369	-0.295	0.166	7.54E-02	0.367	-0.454	0.106	1.97E-05	--
rs182034520	4	106309665	PPA2	T	C	0.018	1.511	0.354	2.00E-05	0.014	-15.048	683.825	9.82E-01	0.018	1.511	0.354	2.00E-05	+-
rs9377179	6	149252699	UST	A	T	0.366	-0.566	0.139	4.52E-05	0.369	-0.293	0.165	7.60E-02	0.367	-0.453	0.106	2.01E-05	--
rs9390639	6	149252978	UST	C	G	0.634	0.566	0.139	4.52E-05	0.631	0.293	0.166	7.65E-02	0.633	0.454	0.106	2.01E-05	++
rs6792738	3	1080996		A	G	0.55	-0.552	0.129	2.01E-05					0.55	-0.552	0.13	2.01E-05	-?
rs4760663	12	49368633		A	G	0.387	0.389	0.125	1.86E-03	0.395	0.438	0.15	3.55E-03	0.39	0.409	0.096	2.08E-05	++
rs9377178	6	149252604	UST	T	C	0.366	-0.566	0.139	4.52E-05	0.368	-0.291	0.165	7.88E-02	0.367	-0.453	0.106	2.10E-05	--

rs184158151	5	4779708		T	G	0.02	1.374	0.323	2.10E-05					0.02	1.374	0.323	2.10E-05	+?
rs145281604	6	70945711	COL9A1	A	G	0.029	1.175	0.276	2.11E-05					0.029	1.175	0.276	2.11E-05	+?
rs1026900	6	149246525	UST	T	C	0.368	-0.569	0.138	3.79E-05	0.367	-0.28	0.164	8.87E-02	0.367	-0.449	0.106	2.14E-05	--
rs72876992	11	29845123		T	C	0.103	0.489	0.179	6.32E-03	0.095	0.714	0.213	7.94E-04	0.1	0.582	0.137	2.15E-05	++
rs79104029	2	80901525		T	G	0.972	-1.169	0.275	2.15E-05					0.973	-1.169	0.275	2.15E-05	-?
rs143943848	5	99811021		T	C	0.99	-1.752	0.413	2.16E-05					0.99	-1.752	0.413	2.16E-05	-?
rs149593616	5	99833127		A	T	0.01	1.752	0.413	2.16E-05					0.01	1.752	0.413	2.16E-05	+?
rs146453521	6	70807017	COL19A1	T	G	0.975	-1.235	0.291	2.19E-05					0.975	-1.235	0.291	2.19E-05	-?
rs4376480	8	141282972	TRAPPC9	A	C	0.289	0.367	0.133	5.70E-03	0.291	0.518	0.157	9.62E-04	0.29	0.43	0.101	2.20E-05	++
rs114111786	4	106394997	PPA2	T	C	0.018	1.497	0.353	2.21E-05					0.018	1.497	0.353	2.21E-05	+?
rs144183314	4	106407068		C	G	0.018	1.497	0.353	2.21E-05					0.018	1.497	0.353	2.21E-05	+?
rs802025	7	86986632	CROT	T	C	0.058	0.683	0.225	2.36E-03	0.055	0.799	0.269	2.93E-03	0.057	0.731	0.172	2.22E-05	++
rs13228213	7	24558290		C	G	0.97	-0.947	0.302	1.72E-03	0.979	-1.094	0.381	4.08E-03	0.974	-1.004	0.237	2.23E-05	--
rs66964668	14	30796768		T	G	0.068	0.898	0.212	2.25E-05					0.068	0.898	0.212	2.25E-05	+?
rs6909559	6	149251418	UST	A	T	0.634	0.566	0.139	4.52E-05	0.632	0.286	0.164	8.22E-02	0.633	0.45	0.106	2.26E-05	++
rs577238531	13	37058031		G	GT	0.988	-1.653	0.39	2.26E-05					0.988	-1.653	0.39	2.26E-05	-?
rs55786056	13	110018992		T	C	0.11	0.543	0.18	2.52E-03	0.103	0.599	0.202	2.95E-03	0.107	0.568	0.134	2.30E-05	++
rs62385557	6	14028851		T	C	0.058	0.77	0.24	1.34E-03	0.062	0.765	0.277	5.76E-03	0.06	0.768	0.181	2.31E-05	++
rs150391166	10	120073184	FAM204A	T	C	0.011	1.659	0.392	2.31E-05					0.011	1.659	0.392	2.31E-05	+?
rs11168812	12	49361363	WNT10B	A	T	0.616	-0.402	0.126	1.41E-03	0.608	-0.415	0.149	5.48E-03	0.613	-0.407	0.096	2.33E-05	--
rs7728691	5	86767630		A	G	0.183	0.395	0.141	5.14E-03	0.168	0.574	0.175	1.07E-03	0.177	0.465	0.11	2.33E-05	++
rs60017145	3	13568756		T	C	0.468	0.637	0.133	1.79E-06	0.46	0.15	0.149	3.14E-01	0.464	0.42	0.099	2.34E-05	++
rs60420459	8	16637175		CAA	C	0.986	-1.488	0.398	1.87E-04	0.987	-1.014	0.477	3.37E-02	0.987	-1.293	0.306	2.34E-05	--
rs117751879	7	86276785	GRM3	A	G	0.968	-0.808	0.285	4.53E-03	0.968	-1.04	0.327	1.48E-03	0.968	-0.908	0.215	2.35E-05	--
rs9644815	9	15547189		T	G	0.086	0.766	0.181	2.36E-05					0.086	0.766	0.181	2.36E-05	+?
rs78675214	12	49350686	RP11-302B13.5	A	AG	0.384	0.401	0.126	1.47E-03	0.389	0.418	0.15	5.32E-03	0.386	0.408	0.097	2.36E-05	++
rs7672	16	68294800	PLA2G15	C	G	0.273	0.476	0.142	8.24E-04	0.264	0.414	0.159	9.30E-03	0.269	0.448	0.106	2.37E-05	++
rs560165688	1	217381532		CAAAAAAAA	C	0.659	-0.568	0.134	2.38E-05					0.659	-0.568	0.134	2.38E-05	-?

				AAAAA														
rs116327131	2	205805004	PARD3B	A	G	0.98	-1.268	0.3	2.38E-05					0.98	-1.268	0.3	2.38E-05	-?
rs12222280	11	29938269		T	C	0.883	-0.577	0.176	1.02E-03	0.894	-0.57	0.215	7.90E-03	0.887	-0.574	0.136	2.39E-05	--
rs57183663	9	126489993	DENND1A	G	GA	0.048	1.027	0.232	9.91E-06	0.049	0.356	0.31	2.51E-01	0.048	0.786	0.186	2.39E-05	++
rs802024	7	86985719	CROT	T	C	0.059	0.669	0.225	2.90E-03	0.055	0.814	0.269	2.51E-03	0.057	0.729	0.172	2.41E-05	++
rs11030859	11	29893775		A	G	0.106	0.547	0.18	2.30E-03	0.1	0.633	0.215	3.30E-03	0.104	0.582	0.138	2.41E-05	++
rs11168798	12	49345137	RP11-302B13.5	A	G	0.384	0.402	0.126	1.41E-03	0.389	0.415	0.15	5.71E-03	0.386	0.407	0.097	2.42E-05	++
rs11168800	12	49345657	RP11-302B13.5	T	C	0.384	0.402	0.126	1.41E-03	0.389	0.415	0.15	5.71E-03	0.386	0.407	0.097	2.42E-05	++
rs11168803	12	49346058	RP11-302B13.5	A	T	0.616	-0.402	0.126	1.41E-03	0.611	-0.415	0.15	5.71E-03	0.614	-0.407	0.097	2.42E-05	--
rs4747389	10	20218657	PLXDC2	C	G	0.136	0.556	0.165	7.52E-04	0.134	0.491	0.192	1.07E-02	0.135	0.528	0.125	2.45E-05	++
rs10875900	12	49344680	RP11-302B13.5	T	C	0.616	-0.402	0.126	1.43E-03	0.611	-0.415	0.15	5.71E-03	0.614	-0.407	0.097	2.46E-05	--
rs10501118	11	29895210		A	G	0.891	-0.516	0.18	4.06E-03	0.899	-0.67	0.214	1.72E-03	0.894	-0.58	0.138	2.48E-05	--
rs76077935	4	86536380	ARHGAP24	T	C	0.972	-1.112	0.264	2.49E-05					0.972	-1.112	0.264	2.49E-05	-?
rs75203428	18	33937953	FHOD3	CT	C	0.898	-0.537	0.178	2.55E-03	0.902	-0.654	0.22	2.95E-03	0.9	-0.583	0.138	2.49E-05	--
rs116905150	6	70884798	COL19A1	A	G	0.03	1.162	0.276	2.51E-05					0.03	1.162	0.276	2.51E-05	+?
rs62421864	6	111342098	RPF2	A	G	0.206	0.464	0.146	1.52E-03	0.189	0.475	0.171	5.51E-03	0.199	0.469	0.111	2.51E-05	++
rs12153853	6	10599496	GCNT2	T	C	0.476	-0.331	0.126	8.39E-03	0.512	-0.542	0.157	5.63E-04	0.49	-0.414	0.098	2.52E-05	--
rs4526804	12	49347581	RP11-302B13.5	T	C	0.384	0.401	0.126	1.47E-03	0.389	0.415	0.15	5.71E-03	0.386	0.407	0.097	2.53E-05	++
rs9783477	12	49347931	RP11-302B13.5	T	C	0.616	-0.401	0.126	1.47E-03	0.611	-0.415	0.15	5.71E-03	0.614	-0.407	0.097	2.53E-05	--
rs9783452	12	49349377	RP11-302B13.5	T	C	0.384	0.401	0.126	1.47E-03	0.389	0.415	0.15	5.71E-03	0.386	0.407	0.097	2.53E-05	++
rs6680664	1	97352971		T	G	0.05	0.96	0.233	3.72E-05	0.049	0.468	0.302	1.21E-01	0.05	0.777	0.184	2.53E-05	++
rs6669942	1	97353389		A	G	0.95	-0.96	0.233	3.72E-05	0.951	-0.468	0.302	1.21E-01	0.95	-0.777	0.184	2.53E-05	--
rs73133329	1	224728658	CNIH3	A	G	0.03	1.18	0.28	2.54E-05					0.03	1.18	0.28	2.54E-05	+?
rs56003829	2	1392929	TPO	A	G	0.351	0.53	0.126	2.55E-05					0.351	0.53	0.126	2.55E-05	+?
rs11030854	11	29882601		T	C	0.883	-0.551	0.172	1.37E-03	0.892	-0.584	0.214	6.27E-03	0.886	-0.564	0.134	2.57E-05	--
rs10140487	14	95500317		A	G	0.027	1.144	0.272	2.59E-05					0.027	1.144	0.272	2.59E-05	+?
rs112714763	7	86969315		A	T	0.059	0.669	0.225	2.90E-03	0.055	0.804	0.269	2.79E-03	0.057	0.725	0.172	2.64E-05	++
rs2339734	8	93781703		T	C	0.948	-0.74	0.23	1.32E-03	0.962	-0.819	0.301	6.58E-03	0.953	-0.769	0.183	2.65E-05	--

rs78763838	5	7926765		T	C	0.045	0.507	0.277	6.77E-02	0.044	1.106	0.271	4.45E-05	0.045	0.813	0.194	2.70E-05	++
rs117249777	6	94390462		T	C	0.952	-0.985	0.235	2.73E-05					0.952	-0.985	0.235	2.73E-05	-?
rs112796991	7	86983328	CROT	T	C	0.059	0.669	0.225	2.90E-03	0.055	0.802	0.269	2.90E-03	0.057	0.723	0.172	2.73E-05	++
rs6940841	6	149249546	UST	T	C	0.366	-0.566	0.139	4.52E-05	0.366	-0.274	0.165	9.60E-02	0.366	-0.445	0.106	2.78E-05	--
rs9404007	6	149252323	UST	T	C	0.366	-0.566	0.139	4.52E-05	0.366	-0.274	0.165	9.60E-02	0.366	-0.445	0.106	2.78E-05	--
rs371078415	2	213204401	ERBB4	A	AT	0.048	0.549	0.244	2.43E-02	0.046	0.959	0.258	2.05E-04	0.048	0.742	0.177	2.85E-05	++
rs10060927	5	177833721	COL23A1	A	G	0.012	1.607	0.384	2.85E-05					0.012	1.607	0.384	2.85E-05	+?
rs138002092	17	12391719		A	G	0.012	1.725	0.412	2.86E-05					0.012	1.725	0.412	2.86E-05	+?
rs7319068	13	23681661		T	G	0.74	0.668	0.173	1.10E-04	0.718	0.359	0.178	4.29E-02	0.729	0.518	0.124	2.87E-05	++
rs73201584	12	87825222		T	C	0.029	1.2	0.265	6.01E-06	0.029	0.305	0.39	4.35E-01	0.029	0.917	0.219	2.88E-05	++
rs73201588	12	87827514		A	T	0.971	-1.2	0.265	6.01E-06	0.971	-0.305	0.39	4.35E-01	0.971	-0.917	0.219	2.88E-05	--
rs73203510	12	87841055		T	C	0.971	-1.2	0.265	6.01E-06	0.971	-0.305	0.39	4.35E-01	0.971	-0.917	0.219	2.88E-05	--
rs73203516	12	87842263		T	C	0.029	1.2	0.265	6.01E-06	0.029	0.305	0.39	4.35E-01	0.029	0.917	0.219	2.88E-05	++
rs68045477	12	87842300		A	T	0.029	1.2	0.265	6.01E-06	0.029	0.305	0.39	4.35E-01	0.029	0.917	0.219	2.88E-05	++
rs67896401	12	87843550		T	C	0.029	1.2	0.265	6.01E-06	0.029	0.305	0.39	4.35E-01	0.029	0.917	0.219	2.88E-05	++
rs73203525	12	87846448		T	C	0.029	1.2	0.265	6.01E-06	0.029	0.305	0.39	4.35E-01	0.029	0.917	0.219	2.88E-05	++
rs55943699	12	87846643		A	C	0.971	-1.2	0.265	6.01E-06	0.971	-0.305	0.39	4.35E-01	0.971	-0.917	0.219	2.88E-05	--
rs73189250	12	87847141		A	C	0.029	1.2	0.265	6.01E-06	0.029	0.305	0.39	4.35E-01	0.029	0.917	0.219	2.88E-05	++
rs4624015	13	110087890		T	G	0.15	0.609	0.161	1.62E-04	0.152	0.372	0.181	4.03E-02	0.151	0.504	0.12	2.89E-05	++
rs62228689	21	45284209		A	G	0.028	1.247	0.274	5.45E-06	0.031	0.303	0.399	4.47E-01	0.029	0.944	0.226	2.95E-05	++
rs62228690	21	45284210		A	C	0.028	1.247	0.274	5.45E-06	0.031	0.303	0.399	4.47E-01	0.029	0.944	0.226	2.95E-05	++
rs711249	2	36731860	CRIM1	A	G	0.243	0.452	0.139	1.15E-03	0.244	0.44	0.168	8.74E-03	0.243	0.447	0.107	2.97E-05	++
rs1123423	5	7932244		A	G	0.045	0.497	0.277	7.26E-02	0.044	1.106	0.271	4.45E-05	0.045	0.808	0.194	2.99E-05	++
rs141428478	7	86968232		A	AT	0.059	0.669	0.225	2.90E-03	0.055	0.79	0.268	3.26E-03	0.057	0.719	0.172	3.01E-05	++
rs56409711	16	13267012	SHISA9	A	G	0.676	-0.532	0.128	3.05E-05					0.676	-0.532	0.128	3.05E-05	-?
rs573889921	16	29703745	QPRT	CA	C	0.031	1.067	0.256	3.06E-05					0.031	1.067	0.256	3.06E-05	+?
rs59390327	12	129323252		G	GA	0.307	0.473	0.127	2.06E-04	0.299	0.331	0.164	4.36E-02	0.304	0.419	0.101	3.06E-05	++
rs147106863	17	55620889	MSI2	G	GC	0.979	-1.301	0.312	3.12E-05					0.979	-1.301	0.312	3.12E-05	-?

rs9521368	13	110077751		T	G	0.85	-0.606	0.161	1.73E-04	0.848	-0.37	0.181	4.12E-02	0.849	-0.502	0.121	3.14E-05	--
rs12348143	9	79153853		C	G	0.015	1.411	0.339	3.16E-05					0.015	1.411	0.339	3.16E-05	+?
rs12344097	9	79153868		A	G	0.985	-1.411	0.339	3.16E-05					0.985	-1.411	0.339	3.16E-05	-?
rs7211577	17	14114280		A	G	0.515	0.542	0.13	3.17E-05					0.515	0.542	0.13	3.17E-05	+?
rs848530	2	36730786	CRIM1	C	G	0.758	-0.457	0.139	1.01E-03	0.758	-0.429	0.168	1.07E-02	0.758	-0.446	0.107	3.18E-05	--
rs12484168	22	48600443		T	C	0.878	-0.624	0.172	2.81E-04	0.875	-0.434	0.202	3.16E-02	0.877	-0.544	0.131	3.19E-05	--
rs9615279	22	48600677		T	C	0.122	0.624	0.172	2.81E-04	0.125	0.434	0.202	3.16E-02	0.123	0.544	0.131	3.19E-05	++
rs113433376	11	29922377		T	TTGATTCATCCTTGCC	0.118	0.515	0.174	3.00E-03	0.109	0.623	0.212	3.28E-03	0.114	0.558	0.134	3.20E-05	++
rs10847703	12	129340533	GLT1D1	A	G	0.276	0.419	0.129	1.19E-03	0.269	0.44	0.169	9.25E-03	0.274	0.426	0.103	3.23E-05	++
rs143366645	4	25027224	LGI2	T	TTGA	0.014	1.509	0.363	3.23E-05					0.014	1.509	0.363	3.23E-05	+?
rs10012345	4	25027371	LGI2	T	C	0.014	1.509	0.363	3.23E-05					0.014	1.509	0.363	3.23E-05	+?
rs78093441	8	43372298		T	C	0.05	0.927	0.223	3.29E-05					0.05	0.927	0.223	3.29E-05	+?
rs73654595	9	98431423		C	G					0.011	1.874	0.451	3.29E-05	0.011	1.874	0.451	3.29E-05	?+
rs117768394	6	70805125	COL19A1	C	G	0.974	-1.204	0.29	3.31E-05					0.974	-1.204	0.29	3.31E-05	-?
rs1044388	6	111346808	RPF2	A	G	0.207	0.45	0.146	2.01E-03	0.189	0.475	0.171	5.51E-03	0.199	0.46	0.111	3.32E-05	++
rs1044389	6	111346843	RPF2	A	G	0.207	0.45	0.146	2.01E-03	0.189	0.475	0.171	5.51E-03	0.199	0.46	0.111	3.32E-05	++
rs375417629	4	115328123		CAA	C	0.818	-0.644	0.155	3.34E-05					0.818	-0.644	0.155	3.34E-05	-?
rs144971853	12	87838452		CAA	C	0.972	-1.143	0.261	1.20E-05	0.976	-0.343	0.417	4.10E-01	0.973	-0.917	0.221	3.37E-05	--
rs1415120	11	29884095		T	C	0.109	0.517	0.179	3.78E-03	0.098	0.655	0.218	2.67E-03	0.104	0.573	0.138	3.42E-05	++
rs6914065	6	149251599	UST	A	C	0.634	0.566	0.139	4.52E-05	0.631	0.261	0.164	1.11E-01	0.633	0.439	0.106	3.44E-05	++
rs72878965	11	29910344		T	C	0.882	-0.515	0.174	3.00E-03	0.891	-0.618	0.212	3.57E-03	0.886	-0.556	0.134	3.45E-05	--
rs72848177	17	65578416	PITPNC1	T	G	0.97	-1.155	0.279	3.45E-05					0.97	-1.155	0.279	3.45E-05	-?
rs78463012	11	29884695		A	ATTC	0.106	0.551	0.18	2.22E-03	0.099	0.612	0.219	5.24E-03	0.103	0.575	0.139	3.53E-05	++
rs1026901	6	149246207	UST	C	G	0.633	0.579	0.14	3.55E-05	0.63	0.249	0.163	1.26E-01	0.632	0.439	0.106	3.58E-05	++
rs6570910	6	149245531	UST	A	G	0.365	-0.56	0.14	6.30E-05	0.366	-0.275	0.164	9.44E-02	0.365	-0.44	0.106	3.62E-05	--

rs6570911	6	149245564	UST	A	G	0.365	-0.56	0.14	6.30E-05	0.366	-0.275	0.164	9.44E-02	0.365	-0.44	0.106	3.62E-05	--
rs10431096	11	99820446	CNTN5	A	G	0.065	0.717	0.22	1.14E-03	0.064	0.636	0.249	1.07E-02	0.064	0.681	0.165	3.65E-05	++
rs11222007	11	99820883	CNTN5	C	G	0.935	-0.717	0.22	1.14E-03	0.936	-0.636	0.249	1.07E-02	0.936	-0.681	0.165	3.65E-05	--
rs117267411	8	2745380		T	C	0.99	-1.689	0.409	3.67E-05					0.99	-1.689	0.409	3.67E-05	-?
rs112152350	1	97314440		T	G	0.95	-0.878	0.235	1.89E-04	0.948	-0.563	0.289	5.13E-02	0.949	-0.753	0.182	3.68E-05	--
rs55780014	8	93705347		A	T	0.945	-0.729	0.225	1.18E-03	0.96	-0.767	0.301	1.07E-02	0.951	-0.742	0.18	3.70E-05	--
rs77652639	2	3275680	TSSC1	T	C	0.97	-1.154	0.28	3.77E-05					0.97	-1.154	0.28	3.77E-05	-?
rs17080176	6	149256469	UST	A	G	0.18	-0.558	0.185	2.54E-03	0.159	-0.754	0.263	4.09E-03	0.173	-0.623	0.151	3.77E-05	--
rs11831047	12	87840567		T	C	0.971	-1.2	0.265	6.01E-06	0.97	-0.262	0.39	5.01E-01	0.97	-0.903	0.219	3.78E-05	--
rs11832191	12	87841866		T	C	0.971	-1.2	0.265	6.01E-06	0.97	-0.262	0.39	5.01E-01	0.97	-0.903	0.219	3.78E-05	--
rs17040395	4	110318688		T	G	0.012	1.519	0.369	3.80E-05					0.012	1.519	0.369	3.80E-05	+?
rs17040401	4	110326576		T	G	0.988	-1.519	0.369	3.80E-05					0.988	-1.519	0.369	3.80E-05	-?
rs6845967	4	110332917		A	G	0.988	-1.519	0.369	3.80E-05					0.988	-1.519	0.369	3.80E-05	-?
rs143504774	1	184105545		T	G	0.052	0.667	0.225	3.00E-03	0.043	0.873	0.3	3.64E-03	0.049	0.741	0.18	3.81E-05	++
rs58373535	6	3132790	BPHL	T	C	0.986	-1.522	0.37	3.82E-05					0.986	-1.522	0.369	3.82E-05	-?
rs11587659	1	242673874	PLD5	A	G	0.167	0.559	0.156	3.30E-04	0.18	0.39	0.183	3.27E-02	0.173	0.488	0.118	3.82E-05	++
rs1222268	4	59329616		A	G	0.45	-0.56	0.136	3.83E-05					0.45	-0.56	0.136	3.83E-05	-?
rs10953423	7	77681979	MAGI2	T	C	0.3	-0.473	0.157	2.52E-03	0.294	-0.517	0.184	5.05E-03	0.298	-0.491	0.119	3.84E-05	--
rs2705452	4	156503942		A	C	0.479	-0.362	0.126	3.93E-03	0.47	-0.483	0.161	2.71E-03	0.476	-0.408	0.099	3.84E-05	--
rs4237854	12	49324179	RP11-302B13.5	C	G	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs11168794	12	49325142	RP11-302B13.5	A	G	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs12229275	12	49325840	RP11-302B13.5	A	T	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs61942166	12	49326147	RP11-302B13.5	A	C	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs61942167	12	49326440	RP11-302B13.5	T	C	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs1830192	12	49326687	RP11-302B13.5	T	C	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs1818996	12	49326774	RP11-302B13.5	A	G	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs11168795	12	49327458	RP11-302B13.5	T	C	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs10875897	12	49327694	RP11-302B13.5	T	C	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--

rs2073480	12	49332012	RP11-302B13.5	A	G	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs1054376	12	49332092	RP11-302B13.5	A	G	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs4760666	12	49332366	RP11-302B13.5	T	C	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs538033634	12	49333896	RP11-302B13.5	G	GA	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs10747557	12	49334982	RP11-302B13.5	C	G	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs2131713	12	49335511	RP11-302B13.5	T	C	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs2030900	12	49336402	RP11-302B13.5	T	G	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs4018510	12	49336789	RP11-302B13.5	T	C	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs4760667	12	49337287	RP11-302B13.5	T	C	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs10875898	12	49337537	RP11-302B13.5	C	G	0.615	-0.389	0.127	2.26E-03	0.611	-0.415	0.15	5.71E-03	0.613	-0.4	0.097	3.84E-05	--
rs78843695	12	49338778	RP11-302B13.5	T	TA	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs11168797	12	49338841	RP11-302B13.5	T	G	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs4760668	12	49341010	RP11-302B13.5	T	G	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs61942169	12	49341893	RP11-302B13.5	A	C	0.385	0.389	0.127	2.26E-03	0.389	0.415	0.15	5.71E-03	0.387	0.4	0.097	3.84E-05	++
rs111429154	9	15710546	CCDC171	A	G	0.079	0.793	0.193	3.84E-05					0.079	0.793	0.193	3.84E-05	+?
rs369804666	12	49338923	RP11-302B13.5	T	TAAA	0.396	0.389	0.126	2.00E-03	0.396	0.409	0.15	6.48E-03	0.396	0.397	0.097	3.84E-05	++
rs16971238	15	41255257		T	C	0.014	1.475	0.358	3.85E-05					0.014	1.474	0.358	3.85E-05	+?
rs73402541	15	41255492		T	C	0.014	1.475	0.358	3.85E-05					0.014	1.474	0.358	3.85E-05	+?
rs117188437	16	84199815	DNAAF1	A	T	0.083	0.328	0.225	1.44E-01	0.092	0.914	0.213	1.80E-05	0.088	0.636	0.155	3.86E-05	++
rs2696291	17	48353084	TMEM92	T	C	0.748	-0.572	0.139	3.93E-05					0.748	-0.572	0.139	3.93E-05	-?
rs6905041	6	110936144	CDK19	T	C	0.198	0.409	0.155	8.52E-03	0.189	0.547	0.17	1.30E-03	0.194	0.472	0.115	3.94E-05	++
rs2272311	12	49329695	RP11-302B13.5	A	G	0.615	-0.389	0.127	2.26E-03	0.61	-0.414	0.15	5.89E-03	0.613	-0.4	0.097	3.95E-05	--
rs141826252	2	213186294	ERBB4	T	C	0.041	0.521	0.262	4.68E-02	0.042	1.049	0.272	1.14E-04	0.042	0.776	0.189	3.96E-05	++
rs76509375	6	111353398		C	G	0.207	0.446	0.146	2.21E-03	0.189	0.47	0.171	6.07E-03	0.2	0.456	0.111	3.97E-05	++
rs62421895	6	111353642		A	G	0.793	-0.446	0.146	2.21E-03	0.811	-0.47	0.171	6.07E-03	0.8	-0.456	0.111	3.97E-05	--
rs62421896	6	111353658		A	G	0.207	0.446	0.146	2.21E-03	0.189	0.47	0.171	6.07E-03	0.2	0.456	0.111	3.97E-05	++
rs12527783	6	111355785		T	G	0.793	-0.446	0.146	2.21E-03	0.811	-0.47	0.171	6.07E-03	0.8	-0.456	0.111	3.97E-05	--

rs1550756	3	124065433	KALRN	C	G	0.354	0.45	0.132	6.50E-04	0.356	0.351	0.15	1.91E-02	0.355	0.407	0.099	4.00E-05	++
rs11584120	1	97316509		A	G	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs147911368	1	97319841		T	C	0.949	-0.871	0.235	2.09E-04	0.948	-0.563	0.289	5.13E-02	0.949	-0.749	0.182	4.01E-05	--
rs371592264	1	97320131		T	C	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs11497391	1	97321516		T	G	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs11497394	1	97321725		A	T	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs139762434	1	97323460		A	G	0.949	-0.871	0.235	2.09E-04	0.948	-0.563	0.289	5.13E-02	0.949	-0.749	0.182	4.01E-05	--
rs11485406	1	97323498		A	G	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs12077790	1	97324265		A	G	0.949	-0.871	0.235	2.09E-04	0.948	-0.563	0.289	5.13E-02	0.949	-0.749	0.182	4.01E-05	--
rs12093130	1	97324527		T	C	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs7533256	1	97325148		T	C	0.949	-0.871	0.235	2.09E-04	0.948	-0.563	0.289	5.13E-02	0.949	-0.749	0.182	4.01E-05	--
rs11485408	1	97325442		A	C	0.051	0.871	0.235	2.09E-04	0.052	0.563	0.289	5.13E-02	0.051	0.749	0.182	4.01E-05	++
rs11584817	1	97325914		T	G	0.949	-0.871	0.235	2.09E-04	0.948	-0.563	0.289	5.13E-02	0.949	-0.749	0.182	4.01E-05	--
rs10747558	12	49344401	RP11-302B13.5	C	G	0.616	-0.385	0.127	2.36E-03	0.611	-0.415	0.15	5.71E-03	0.614	-0.398	0.097	4.01E-05	--
rs11222004	11	99819795	CNTN5	A	T	0.935	-0.717	0.22	1.14E-03	0.936	-0.626	0.249	1.19E-02	0.936	-0.677	0.165	4.06E-05	--
rs9325143	12	49353027		A	G	0.375	0.359	0.125	3.97E-03	0.384	0.444	0.15	3.12E-03	0.379	0.394	0.096	4.06E-05	++
rs34851054	3	110109417		CCA	C	0.106	0.688	0.168	4.10E-05					0.106	0.688	0.168	4.10E-05	+?
rs117666456	12	87811639		A	G	0.037	1.031	0.251	3.89E-05	0.036	0.452	0.336	1.79E-01	0.036	0.824	0.201	4.11E-05	++
rs55996691	12	87815977		A	G	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs73201574	12	87817005		T	G	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs577511305	12	87817621		A	G	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs148496689	12	87818827		A	AGCTTCTCTTT	0.037	1.031	0.251	3.89E-05	0.036	0.452	0.336	1.79E-01	0.036	0.824	0.201	4.11E-05	++
rs145618836	12	87826643		A	AT	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs55668611	12	87835563		A	G	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs60791984	12	87835626		A	G	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs140048966	12	87836867		A	ACTC	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--

					ATATAT													
rs67469634	12	87837397		T	G	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs17014865	12	87838096		T	C	0.963	-1.031	0.251	3.89E-05	0.964	-0.452	0.336	1.79E-01	0.964	-0.824	0.201	4.11E-05	--
rs73782464	5	109743092	TMEM232	T	C	0.97	-0.945	0.289	1.09E-03	0.964	-0.788	0.314	1.22E-02	0.967	-0.873	0.213	4.11E-05	--
rs141983779	4	127500956		G	GTTTTTCTTTTTTTTTTTTTTTT	0.843	-0.646	0.158	4.13E-05					0.843	-0.646	0.158	4.13E-05	-?
rs2586435	17	48362186		A	C	0.319	0.544	0.133	4.19E-05					0.319	0.544	0.133	4.19E-05	+?
rs1689292	7	53004725		T	C	0.98	-0.836	0.327	1.07E-02	0.97	-1.031	0.319	1.23E-03	0.975	-0.936	0.228	4.20E-05	--
rs1731304	7	53005243		A	G	0.02	0.836	0.327	1.07E-02	0.03	1.031	0.319	1.23E-03	0.025	0.936	0.228	4.20E-05	++
rs1731305	7	53005343		T	C	0.02	0.836	0.327	1.07E-02	0.03	1.031	0.319	1.23E-03	0.025	0.936	0.228	4.20E-05	++
rs2888054	2	213195197	ERBB4	T	C	0.162	0.295	0.158	6.24E-02	0.155	0.735	0.18	4.43E-05	0.159	0.487	0.119	4.22E-05	++
rs35132287	3	110104657		T	G	0.107	0.686	0.168	4.26E-05					0.107	0.686	0.168	4.26E-05	+?
rs79625194	5	18133580		G	GT	0.622	0.496	0.132	1.76E-04	0.607	0.303	0.161	5.97E-02	0.616	0.418	0.102	4.26E-05	++
rs722102	1	97349337		A	G	0.049	0.927	0.235	8.16E-05	0.049	0.484	0.302	1.09E-01	0.049	0.759	0.186	4.27E-05	++
rs3122596	1	105685128		C	G	0.011	0.931	0.486	5.55E-02	0.016	1.438	0.388	2.10E-04	0.014	1.241	0.303	4.27E-05	++
rs12998	1	204161947	KISS1	T	C	0.04	1.017	0.249	4.29E-05					0.04	1.017	0.249	4.29E-05	+?
rs1044387	6	111346806	RPF2	T	C	0.207	0.446	0.146	2.21E-03	0.19	0.465	0.171	6.68E-03	0.2	0.454	0.111	4.34E-05	++
rs7773288	6	111348554	RPF2	T	C	0.207	0.446	0.146	2.21E-03	0.19	0.465	0.171	6.68E-03	0.2	0.454	0.111	4.34E-05	++
rs11180322	12	75383057		T	C	0.985	-0.87	0.445	5.05E-02	0.985	-1.44	0.387	2.01E-04	0.985	-1.194	0.292	4.34E-05	--
rs16915185	8	93677234		T	C	0.944	-0.72	0.225	1.38E-03	0.96	-0.763	0.3	1.09E-02	0.95	-0.736	0.18	4.36E-05	--
rs2339658	8	93680269		A	G	0.056	0.72	0.225	1.38E-03	0.04	0.763	0.3	1.09E-02	0.05	0.736	0.18	4.36E-05	++
rs141635543	1	97320482		A	C	0.948	-0.866	0.232	1.90E-04	0.947	-0.543	0.289	6.03E-02	0.947	-0.74	0.181	4.37E-05	--
rs77199232	11	99847805	CNTN5	A	G	0.938	-0.769	0.221	5.08E-04	0.935	-0.568	0.255	2.59E-02	0.936	-0.682	0.167	4.39E-05	--

rs186109742	5	99774096		A	T	0.989	-1.669	0.409	4.46E-05					0.989	-1.669	0.409	4.46E-05	-?
rs191813690	5	99774098		A	T	0.989	-1.669	0.409	4.46E-05					0.989	-1.669	0.409	4.46E-05	-?
rs147440771	6	3133466	BPHL	A	ACTCTT	0.015	1.475	0.361	4.47E-05					0.015	1.475	0.361	4.47E-05	+?
rs77638044	6	3133481	BPHL	T	C	0.985	-1.475	0.361	4.47E-05					0.985	-1.475	0.361	4.47E-05	-?
rs7315539	12	1661143	WNT5B	A	G	0.399	0.53	0.13	4.48E-05					0.399	0.53	0.13	4.48E-05	+?
rs34100237	5	30875576		C	G	0.959	-0.247	0.299	4.07E-01	0.954	-1.238	0.263	2.51E-06	0.956	-0.805	0.197	4.48E-05	--
rs12171615	7	52998078		A	G	0.02	0.836	0.327	1.07E-02	0.03	1.023	0.319	1.33E-03	0.025	0.932	0.228	4.49E-05	++
rs73351178	7	52999310		T	C	0.02	0.836	0.327	1.07E-02	0.03	1.023	0.319	1.33E-03	0.025	0.932	0.228	4.49E-05	++
rs4624980	7	53001604		T	C	0.02	0.836	0.327	1.07E-02	0.03	1.023	0.319	1.33E-03	0.025	0.932	0.228	4.49E-05	++
rs13219996	6	111357686		T	G	0.228	0.39	0.141	5.62E-03	0.204	0.506	0.166	2.37E-03	0.218	0.438	0.107	4.56E-05	++
rs142622080	3	110103953		T	TA	0.107	0.684	0.168	4.56E-05					0.107	0.684	0.168	4.56E-05	+?
rs35180502	3	110104952		G	GA	0.107	0.684	0.168	4.56E-05					0.107	0.684	0.168	4.56E-05	+?
rs12086129	1	97335336		A	T	0.951	-0.927	0.235	8.16E-05	0.951	-0.476	0.302	1.15E-01	0.951	-0.756	0.186	4.58E-05	--
rs138005861	1	97337931		G	GCAAAA	0.049	0.927	0.235	8.16E-05	0.049	0.476	0.302	1.15E-01	0.049	0.756	0.186	4.58E-05	++
rs12096480	1	97339253		A	G	0.049	0.927	0.235	8.16E-05	0.049	0.476	0.302	1.15E-01	0.049	0.756	0.186	4.58E-05	++
rs11165731	1	97340388		A	G	0.951	-0.927	0.235	8.16E-05	0.951	-0.476	0.302	1.15E-01	0.951	-0.756	0.186	4.58E-05	--
rs74107605	1	97341129		T	G	0.951	-0.927	0.235	8.16E-05	0.951	-0.476	0.302	1.15E-01	0.951	-0.756	0.186	4.58E-05	--
rs12094917	1	97341724		A	C	0.951	-0.927	0.235	8.16E-05	0.951	-0.476	0.302	1.15E-01	0.951	-0.756	0.186	4.58E-05	--
rs6660077	1	97344882		A	G	0.951	-0.927	0.235	8.16E-05	0.951	-0.476	0.302	1.15E-01	0.951	-0.756	0.186	4.58E-05	--
rs79741362	1	97347462		A	G	0.951	-0.927	0.235	8.16E-05	0.951	-0.476	0.302	1.15E-01	0.951	-0.756	0.186	4.58E-05	--
rs4665554	2	23350490		T	C	0.452	-0.538	0.132	4.59E-05					0.452	-0.538	0.132	4.59E-05	-?
rs9820608	3	124075754	KALRN	T	C	0.357	0.468	0.135	5.24E-04	0.357	0.336	0.15	2.52E-02	0.357	0.409	0.1	4.59E-05	++
rs16962894	16	84202227	DNAAF1	T	C	0.087	0.33	0.222	1.36E-01	0.093	0.892	0.212	2.52E-05	0.09	0.625	0.153	4.59E-05	++
rs11248530	10	125204321		T	C	0.07	0.36	0.225	1.09E-01	0.075	0.978	0.233	2.61E-05	0.072	0.658	0.162	4.65E-05	++
rs10270309	7	25298283		A	G	0.056	0.584	0.242	1.58E-02	0.068	0.82	0.245	8.05E-04	0.062	0.701	0.172	4.66E-05	++
rs75163401	4	60667036		T	TA	0.023	1.272	0.312	4.69E-05					0.023	1.272	0.312	4.69E-05	+?
rs192196005	5	28515522		A	G	0.99	-1.724	0.424	4.75E-05					0.99	-1.724	0.424	4.75E-05	-?

4:156505597	4	156505597		AT	ATTTGTT	0.477	-0.354	0.124	4.48E-03	0.469	-0.481	0.162	2.92E-03	0.474	-0.401	0.099	4.75E-05	--
rs8140738	22	48611036		A	G	0.121	0.61	0.173	4.22E-04	0.125	0.433	0.203	3.29E-02	0.123	0.535	0.132	4.75E-05	++
rs8140762	22	48611088		A	G	0.121	0.61	0.173	4.22E-04	0.125	0.433	0.203	3.29E-02	0.123	0.535	0.132	4.75E-05	++
rs8140892	22	48611116		T	C	0.879	-0.61	0.173	4.22E-04	0.875	-0.433	0.203	3.29E-02	0.877	-0.535	0.132	4.75E-05	--
rs8141097	22	48611310		T	C	0.879	-0.61	0.173	4.22E-04	0.875	-0.433	0.203	3.29E-02	0.877	-0.535	0.132	4.75E-05	--
rs9615804	22	48612068		C	G	0.879	-0.61	0.173	4.22E-04	0.875	-0.433	0.203	3.29E-02	0.877	-0.535	0.132	4.75E-05	--
rs371456582	13	79888008	RBM26	CA	C	0.486	-0.38	0.124	2.17E-03	0.48	-0.418	0.156	7.42E-03	0.483	-0.395	0.097	4.79E-05	--
rs12082277	1	97327501		A	G	0.951	-0.927	0.235	8.16E-05	0.95	-0.469	0.302	1.21E-01	0.951	-0.754	0.186	4.87E-05	--
rs12062222	1	97331544		T	C	0.049	0.927	0.235	8.16E-05	0.05	0.469	0.302	1.21E-01	0.049	0.754	0.186	4.87E-05	++
rs9615798	22	48609442		T	C	0.121	0.613	0.174	4.31E-04	0.125	0.433	0.203	3.29E-02	0.123	0.537	0.132	4.89E-05	++
rs9615799	22	48609485		T	C	0.879	-0.613	0.174	4.31E-04	0.875	-0.433	0.203	3.29E-02	0.877	-0.537	0.132	4.89E-05	--
rs2338675	22	48610856		T	G	0.121	0.613	0.174	4.31E-04	0.125	0.433	0.203	3.29E-02	0.123	0.537	0.132	4.89E-05	++
rs577209042	6	120301820		T	TATATACAC	0.746	-0.293	0.143	4.02E-02	0.738	-0.64	0.167	1.22E-04	0.743	-0.44	0.108	4.91E-05	--
rs71486660	10	125202585		A	G	0.066	0.308	0.231	1.82E-01	0.069	1.046	0.236	9.10E-06	0.068	0.669	0.165	4.91E-05	++
rs5751574	22	23416005	RTDR1	A	G	0.246	-0.53	0.166	1.38E-03	0.217	-0.525	0.21	1.25E-02	0.235	-0.528	0.13	4.92E-05	--
rs11222071	11	99834399	CNTN5	T	C	0.937	-0.764	0.221	5.54E-04	0.935	-0.564	0.255	2.68E-02	0.936	-0.678	0.167	4.93E-05	--
rs11222108	11	99843468	CNTN5	C	G	0.937	-0.764	0.221	5.54E-04	0.935	-0.564	0.255	2.68E-02	0.936	-0.678	0.167	4.93E-05	--
rs7704035	5	86750847		T	C	0.185	0.381	0.143	7.85E-03	0.168	0.56	0.177	1.55E-03	0.178	0.452	0.111	4.95E-05	++
rs34569968	6	3110639	RIPK1	T	C	0.011	1.679	0.414	4.96E-05					0.011	1.679	0.414	4.96E-05	+?
rs79373551	6	3111814	RIPK1	A	G	0.011	1.679	0.414	4.96E-05					0.011	1.679	0.414	4.96E-05	+?

Table S3. Top 10 eQTLs of rs17440378 in human brain samples (aveALL) using Braineac UK database.

Gene Symbol	Marker	rsID	exprID	Chr	Start	Stop	aveALL	CRBL	FCTX	HIPP	MEDU	OCTX	PUTM	SNIG	TCTX	THAL	WHMT
HTR2B	chr2:231979355	rs17440378	2603401	2	231972876	231989824	7.30E-04	4.20E-01	5.40E-01	2.90E-01	7.40E-01	3.40E-01	3.70E-02	5.00E-04	1.20E-01	6.70E-02	2.80E-02
HTR2B	chr2:231979355	rs17440378	2603400	2	231972876	231989824	1.10E-03	6.10E-01	4.60E-01	1.10E-01	3.60E-01	2.40E-01	6.30E-02	9.50E-03	7.30E-02	6.60E-01	7.40E-04
PSMD1	chr2:231979355	rs17440378	2531767	2	231921607	232037527	4.50E-03	5.70E-02	6.30E-02	2.80E-01	9.50E-01	2.00E-01	6.00E-02	2.70E-02	1.50E-02	7.60E-02	4.00E-01
DIS3L2	chr2:231979355	rs17440378	2532218	2	232825975	233209416	7.60E-03	5.50E-01	8.60E-01	1.90E-01	1.20E-01	2.50E-01	7.90E-01	2.20E-01	1.10E-01	5.60E-03	5.10E-01
HTR2B	chr2:231979355	rs17440378	t2603395	2	231972876	231989824	1.70E-02	2.70E-01	4.10E-01	3.60E-01	1.60E-01	1.20E-01	2.10E-02	5.20E-02	2.90E-01	3.50E-01	1.60E-02
SP140, SP140L	chr2:231979355	rs17440378	2531249	2	231090446	231177928	2.00E-02	2.80E-01	5.10E-02	1.10E-02	7.60E-01	4.70E-01	8.00E-01	1.20E-02	8.60E-01	5.20E-02	9.70E-02
B3GNT7	chr2:231979355	rs17440378	2531915	2	232259841	232273503	2.70E-02	4.30E-02	8.90E-01	4.00E-01	3.70E-01	2.80E-01	5.30E-01	2.80E-01	8.70E-01	4.60E-01	8.70E-01
HTR2B	chr2:231979355	rs17440378	2603398	2	231972876	231989824	3.80E-02	9.70E-01	9.90E-01	1.60E-01	8.20E-01	2.70E-01	2.90E-02	9.80E-02	3.00E-01	6.50E-01	2.50E-03
HTR2B	chr2:231979355	rs17440378	2603403	2	231972876	231989824	3.80E-02	4.40E-01	6.50E-02	4.80E-01	1.70E-01	1.90E-01	5.20E-01	2.80E-01	9.30E-01	3.60E-01	2.00E-02

Table S4. eQTLs of rs17440378 in human brain samples using GTEx database.

Gencode Id	Gene Symbol	SNP Id	P-Value	Effect Size	Tissue
ENSG00000204128.5	C2orf72	rs17440378	3.80E-18	1	Thyroid
ENSG00000204128.5	C2orf72	rs17440378	1.70E-13	0.96	Esophagus - Muscularis
ENSG00000135931.13	ARMC9	rs17440378	2.30E-11	0.61	Artery - Aorta
ENSG00000261829.1	RP11-223I10.1	rs17440378	7.40E-11	0.73	Thyroid
ENSG00000135931.13	ARMC9	rs17440378	6.40E-09	0.34	Artery - Tibial
ENSG00000135914.5	HTR2B	rs17440378	1.20E-08	0.56	Esophagus - Muscularis
ENSG00000135931.13	ARMC9	rs17440378	7.20E-07	0.5	Pancreas
ENSG00000204128.5	C2orf72	rs17440378	0.000001	0.54	Adipose - Subcutaneous
ENSG00000204128.5	C2orf72	rs17440378	0.0000016	0.73	Esophagus - Gastroesophageal Junction
ENSG00000204128.5	C2orf72	rs17440378	0.0000018	0.32	Stomach
ENSG00000135914.5	HTR2B	rs17440378	0.0000048	0.42	Lung
ENSG00000135914.5	HTR2B	rs17440378	0.0000063	0.51	Esophagus - Gastroesophageal Junction
ENSG00000204128.5	C2orf72	rs17440378	0.0000064	0.27	Colon - Transverse
ENSG00000204128.5	C2orf72	rs17440378	0.0000083	0.65	Adipose - Visceral (Omentum)
ENSG00000224376.1	AC017104.6	rs17440378	0.0000094	0.49	Artery - Aorta
ENSG00000204128.5	C2orf72	rs17440378	0.000015	0.3	Skin - Sun Exposed (Lower leg)
ENSG00000204128.5	C2orf72	rs17440378	0.000016	0.39	Lung
ENSG00000156966.6	B3GNT7	rs17440378	0.000027	-0.28	Colon - Transverse
ENSG00000135914.5	HTR2B	rs17440378	0.000038	0.56	Artery - Aorta

Table S5. Histone marks for 17440378 using HaploReg v4.1 database.

Epigenome ID (EID)	Group	Description	Chromatin states (15-S)	Chromatin states (25-S)	H3K4me1	H3K4me3	H3K27ac	H3K9ac
E017	IMR90	IMR90 fetal lung fibroblasts Cell Line			H3K4me1_Enh			
E002	ESC	ES-WA7 Cells		17_EnhW2	H3K4me1_Enh			
E001	ESC	ES-I3 Cells			H3K4me1_Enh			
E015	ESC	HUES6 Cells		17_EnhW2	H3K4me1_Enh		H3K27ac_Enh	
E014	ESC	HUES48 Cells	7_Enh	17_EnhW2	H3K4me1_Enh		H3K27ac_Enh	
E016	ESC	HUES64 Cells	7_Enh	17_EnhW2	H3K4me1_Enh		H3K27ac_Enh	
E003	ESC	H1 Cells			H3K4me1_Enh		H3K27ac_Enh	
E024	ESC	ES-UCSF4 Cells			H3K4me1_Enh			
E020	iPSC	iPS-20b Cells	7_Enh		H3K4me1_Enh			H3K9ac_Pro
E019	iPSC	iPS-18 Cells			H3K4me1_Enh			
E018	iPSC	iPS-15b Cells		17_EnhW2	H3K4me1_Enh			
E013	ES-deriv	hESC Derived CD56+ Mesoderm Cultured Cells					H3K27ac_Enh	
E025	Mesench	Adipose Derived Mesenchymal Stem Cell Cultured Cells			H3K4me1_Enh			H3K9ac_Pro
E023	Mesench	Mesenchymal Stem Cell Derived Adipocyte Cultured Cells			H3K4me1_Enh			
E055	Epithelial	Foreskin Fibroblast Primary Cells skin01			H3K4me1_Enh			
E061	Epithelial	Foreskin Melanocyte Primary Cells skin03			H3K4me1_Enh			
E068	Brain	Brain Anterior Caudate						H3K9ac_Pro
E069	Brain	Brain Cingulate Gyrus			H3K4me1_Enh			
E063	Adipose	Adipose Nuclei						H3K9ac_Pro
E078	Sm. Muscle	Duodenum Smooth Muscle					H3K27ac_Enh	
E076	Sm.	Colon Smooth			H3K4me1		H3K27	

	Muscle	Muscle			_Enh		ac_Enh	
E103	Sm. Muscle	Rectal Smooth Muscle			H3K4me1_Enh		H3K27ac_Enh	
E086	Other	Fetal Kidney			H3K4me1_Enh	H3K4me3_Pro		H3K9ac_Pro
E088	Other	Fetal Lung						H3K9ac_Pro
E087	Other	Pancreatic Islets			H3K4me1_Enh			
E114	ENCODE 2012	A549 EtOH 0.02pct Lung Carcinoma Cell Line			H3K4me1_Enh			
E119	ENCODE 2012	HMEC Mammary Epithelial Primary Cells						H3K9ac_Pro
E128	ENCODE 2012	NHLF Lung Fibroblast Primary Cells			H3K4me1_Enh			

Table S6. Regulatory motifs of rs17440378 using HaploReg v4.1 database.

A. rs17440378

Position Weight Matrix ID (Library from Kheradpour and Kellis, 2013)	Strand	Ref	Alt
Gfi1_1	+	12.1	11.6
Nkx2_6	+	9.8	11.6
Nkx3_4	+	12.2	11.8

B. rs55637820

Position Weight Matrix ID (Library from Kheradpour and Kellis, 2013)	Strand	Ref	Alt
Egr-1_disc2	+	12.9	0.9
Ets_known3	-	13	1
GATA_disc3	+	13.2	5.3
GATA_known8	-	1.4	13.3
Irf_disc5	-	13	1
Nrf-2_1	-	14.2	2.2
PU.1_disc3	-	12.8	0.8
Pax-5_disc4	+	13.8	10
Rad21_disc5	-	11.5	0.5
Rad21_disc6	-	11	0.3
SP1_disc3	-	15.5	11.9

C. rs35750632

Position Weight Matrix ID (Library from Kheradpour and Kellis, 2013)	Strand	Ref	Alt
AP-1_disc10	+	0	11.5
Glis2	-	11.7	12.6
MAZR	+	7.8	18.9
NF-I_1	+	4.1	12.3
RREB-1_2	-	-1.7	1.8
SP1_known1	+	9.3	11.4
UF1H3BETA	+	-13.8	-1.9
WT1	-	7.3	11.2
ZBTB7A_known2	-	14.1	13.3
ZNF219	-	9.8	11.6

Zfp281	-	9.3	12.9
Zfp740	-	13.4	13.1

Table S7. Polygenic risk score (PRS) results for extraversion and cannabis-related aggression

	Yale Penn 1				**Yale Penn 2**				**Meta**			
PT	**#SNPs**	**Beta**	**SE**	**P-value**	**#SNPs**	**Beta**	**SE**	**P-value**	**Direction**	**Beta**	**SE**	**P-value**
0.00001	5	0.210	0.29	4.74E-01	4	0.044	0.36	9.03E-01	++	0.144	0.23	5.28E-01
0.0001	19	0.224	0.29	4.40E-01	14	0.480	0.41	2.37E-01	++	0.312	0.24	1.88E-01
0.001	**1366**	**0.713**	**0.32**	**2.51E-02**	**863**	**0.603**	**0.37**	**1.02E-01**	**++**	**0.666**	**0.24**	**5.63E-03**
0.005	**5313**	**0.708**	**0.32**	**2.59E-02**	**3111**	**0.424**	**0.36**	**2.33E-01**	**++**	**0.582**	**0.24**	**1.40E-02**
0.01	9470	0.382	0.33	2.42E-01	5406	0.392	0.35	2.60E-01	++	0.387	0.24	1.04E-01
0.05	35173	0.399	0.27	1.38E-01	19139	0.077	0.36	8.30E-01	++	0.284	0.22	1.88E-01
0.1	60510	0.267	0.28	3.39E-01	32152	-0.095	0.35	7.86E-01	+-	0.127	0.22	5.63E-01
0.5	182633	0.249	0.29	3.83E-01	89487	-0.308	0.36	3.87E-01	+-	0.032	0.22	8.87E-01