Supplementary Online Content

Smeland OB, Frei O, Kauppi K, et al; NeuroCHARGE (Cohorts for Heart and Aging Research in Genomic Epidemiology) Cognitive Working Group. Identification of genetic loci jointly influencing schizophrenia risk and the cognitive traits of verbal-numerical reasoning, reaction time, and general cognitive function. *JAMA Psychiatry.* Published online July 26, 2017. doi:10.1001/jamapsychiatry.2017.1986

eAppendix. Methods

Conditional True Discovery Rate

The 'enrichment' seen in the conditional Q-Q plots can be directly interpreted in terms of true discovery rate (TDR = 1 – false discovery rate (FDR))[1]. More specifically, for a given p-value cut-off, the FDR is defined as

$$\mathrm{FDR}(p) = \pi_0 F_0(p) / F(p), \qquad [1]$$

where π_0 is the proportion of null SNPs, F_0 is the null cumulative distribution function (cdf), and F is the cdf of all SNPs, both null and non-null[2]. Under the null hypothesis, F_0 is the cdf of the uniform distribution on the unit interval [0,1], so that Eq. [1] reduces to

$$\mathrm{FDR}(p) = \pi_0\, p / F(p), \qquad [2]$$

The cdf F can be estimated by the empirical cdf $q = N_p / N$, where N_p is the number of SNPs with p-values less than or equal to p, and N is the total number of SNPs. Replacing F by q in Eq. [2], we get

$$\text{Estimated FDR}(p) = \pi_0\, p / q, \qquad [3]$$

which is biased upwards as an estimate of the FDR[3]. Replacing π_0 in Equation [3] with unity gives an estimated FDR that is further biased upward;

$$q^* = p/q \qquad [4]$$

If π_0 is close to one, as is likely true for most GWASs, the increase in bias from Eq. [3] is minimal. The quantity $1 – p/q$, is therefore biased downward, and hence a conservative estimate of the TDR. Referring to the Q-Q plots, we see that q* is equivalent to the nominal p-value divided by the empirical quantile, as defined earlier. We can thus read the FDR estimate directly off the Q-Q plot as

$$-\log_{10}(q^*) = \log_{10}(q) – \log_{10}(p), \qquad [5]$$

i.e. the horizontal shift of the curves in the Q-Q plots from the expected line x = y, with a larger shift corresponding to a smaller FDR. This is illustrated in Figure 1 and Supplementary Figure 1.

Conditional Q-Q plots

In conditional Q-Q plots, earlier and steeper departures from the null line (leftward shift) with higher levels of association with a secondary trait indicate a greater proportion of true associations for a given nominal p-value. Q-Q plots compare a nominal probability distribution against an empirical distribution. In the presence of all null relationships, nominal p-values form a straight line on a Q-Q plot when plotted against the empirical distribution. For schizophrenia (SCZ) and all cognitive traits SNPs and for each categorical subset (strata), $-\log_{10}$ nominal p-values were plotted against $-\log_{10}$ empirical p-values (conditional Q-Q plots). Leftward deflections of the observed distribution from the projected null line reflect increased tail probabilities in the distribution of test statistics (z-scores) and consequently an over-abundance of low p-values compared to that expected by chance, also named 'enrichment'.

Under large-scale testing paradigms, such as GWAS, quantitative estimates of likely true associations can be estimated from the distributions of summary statistics[2,4]. One common method for visualizing the enrichment of statistical association relative to that expected under the global null hypothesis is through Q-Q plots of nominal p-values obtained from GWAS summary statistics. The usual Q-Q curve has as the y-ordinate the nominal p-value, denoted by "p", and as the x-ordinate the corresponding value of the empirical cdf, denoted by "q". Under the global null hypothesis the theoretical distribution is uniform on the interval [0,1]. As is common in GWAS, we instead plot $-\log_{10}$ p against $-\log_{10}$ q to emphasize tail probabilities of the theoretical and empirical distributions. Therefore, genetic enrichment results in a leftward shift in the Q-Q curve, corresponding to a larger fraction of SNPs with nominal $-\log_{10}$ p-value greater than or equal to a given threshold. Conditional Q-Q plots are constructed by creating subsets of SNPs based on levels of an auxiliary measure for each SNP, and computing Q-Q plots separately for each level. If SNP enrichment is captured by variation in the auxiliary measure, this is expressed as successive leftward deflections in a conditional Q-Q plot as levels of the auxiliary measure increase. We constructed conditional Q-Q plots of empirical quantiles of nominal $-\log_{10}$ values for SNP association with SCZ for all SNPs, and for subsets (strata) of SNPs determined by the nominal p-values of their association with cognitive traits, and vice versa. Specifically, we computed the empirical cumulative distribution of nominal p-values (cdf(p)) for a given phenotype for all SNPs and for SNPs with significance levels below the indicated cut-offs for the other phenotypes ($-\log_{10}(p) \geq 1$, $-\log_{10}(p) \geq 2$, $-\log_{10}(p) \geq 3$ corresponding to $p < 0.1$, $p < 0.01$, $p < 0.001$ respectively). The nominal p-values ($–\log_{10}(p)$) are plotted on the y-axis, and the empirical quantiles ($–\log_{10}(q)$, where $q=1-\mathrm{cdf}(p)$) are plotted on the x-axis. To assess for polygenic effects below the standard GWAS significance threshold, we focused the conditional Q-Q plots on SNPs with nominal $–\log_{10}(p) < 7.3$ (corresponding to $p > 5\times10^{-8}$). To control for spurious enrichment, all plots were constructed after random pruning averaged over 200 iterations. At each iteration, one SNP in every linkage disequilibrium (LD) block (defined by an $r^2>0.1$) was randomly selected and the empirical cumulative distribution functions were computed using the corresponding p-values. We also excluded SNPs within the extended major histocompatibility complex (MHC) (human genome build 19 location 25652429–33368333) and SNPs in LD ($r^2>0.1$) with such SNPs given the long range LD in this region and strong association with SCZ[5].

Detection of loci using conditional FDR

The standard FDR framework derives from a model assuming that the distribution of test statistics in a GWAS can be formulated as a mixture of null and non-null effects, with true associations (non-null effects) having more extreme test statistics than false associations (null effects). The FDR can be interpreted as the probability that a SNP is null given that its p-value is as small as or smaller than its observed p-value. Conjunctional FDR (conjFDR), denoted by $FDR_{trait1|trait2}$, is defined as the posterior probability that a given SNP is null for the first trait given that the p-values for both traits are as small as or smaller than the observed p-values[6-9]. Conjunctional cFDR, denoted by $FDR_{trait1\&trait2}$ is defined as the posterior probability that a SNP is null for either phenotype or both simultaneously, given that its p-values for both traits are as small as or smaller than the observed p-values[6-8]. We obtained an estimate of conjFDR via the cFDR. A conservative estimate of $FDR_{trait1\&trait2}$ is given by the maximum between $FDR_{trait1|trait2}$ and $FDR_{trait2|trait1}$[10]. It is important to note that ranking SNPs by standard FDRs or by p-values gives the same ordering of SNPs. In contrast, cFDR reorders SNPs which results in a different ranking than that based on p-values alone.

To visualize the location of the shared genetic variants associated with SCZ and cognitive traits, we constructed 'conjFDR Manhattan plots', showing all SNPs with a significant conjunctional cFDR within an LD block in relation to their chromosomal location. The strongest signal was identified after ranking all SNPs based on the conjunctional cFDR and removing SNPs in LD $r^2 > 0.1$ with any higher ranked SNP. The risk loci were annotated to the closest gene. We investigated the direction of allelic effects in the conjunctional loci by comparing their SCZ z-scores against their cognitive trait z-scores. For conjunctional loci showing ambiguous directionality of allelic effects, we identified SNPs in LD with these loci and compared their z-scores in SCZ and cognitive traits. We also constructed 'cFDR Manhattan plots' for COG, VNR and RT, showing all SNPs with a significant cFDR within an LD block in relation to their chromosomal location.

Brain gene expression

We determined the overall messenger RNA (mRNA) expression in the human brain of genes jointly implicated in SCZ and cognitive traits. Using the publically available dataset from the Human Brain Transcriptome project at http://hbatlas.org, we assessed mRNA expression trajectories in six regions of the developing and adult human brain. Spanning periods from embryonic development to late adulthood, this dataset provides genome-wide, exon-level transcriptome data generated using the Affymetrix GeneChip Human Exon 1.0 ST Arrays from over 1,340 tissue samples from both hemispheres of postmortem human brains (n=57)[11]. Additionally, we determined the regional distribution of mRNA expression of the implicated genes in the adult human brain using the publically available dataset from The UK Human Brain Expression Consortium (https://ukbec.wordpress.com/). This dataset is based on exon array profiling using the Affymetrix GeneChip Human Exon 1.0 ST Arrays of 1,231 samples from 10 brain areas originating from 134 individuals. A full description of the study is provided in Trabzuni et al (2011)[12]. The data was downloaded from http://www.braineac.org/.

Gene set enrichment analysis

To assess for enrichment of gene sets in the conjunctional loci shared between SCZ and COG, we applied a gene set enrichment method, DEPICT (Data-driven Expression Prioritized Integration for Complex Traits; www.broadinstitute.org/depict)[13]. DEPICT assesses whether any of 14,461 reconstituted gene sets are significantly enriched for genes in the associated loci, and prioritizes genes that share predicted functions with genes from the other associated loci more often than expected by chance. The reconstituted gene sets are defined by membership probability for each gene based on their functional characterization in a probabilistic framework rather than using a binary indication[13]. We applied DEPICT analysis on loci with conjFDR<.20 shared between SCZ and COG.

eFigure 1. Conditional Q-Q Plots of Cognitive Traits Given Association With Schizophrenia
Conditional Q-Q plots of nominal versus empirical $-\log_{10}$ p-values (corrected for inflation) in general cognitive function (COG) in the CHARGE cohort (COG CHARGE), COG in the COGENT cohort (COG COGENT), reaction time (RT) and verbal-numerical reasoning (VNR) as a function of significance of association with SCZ below the standard GWAS threshold of $p<5\times10^{-8}$ at the level of $-\log_{10}(p)\geq1$, $-\log_{10}(p)\geq2$, $-\log_{10}(p)\geq3$ corresponding to $p\leq0.1$, $p\leq0.01$, $p\leq0.001$, respectively. The blue lines indicate all SNPs. The dashed lines indicate the null hypothesis.

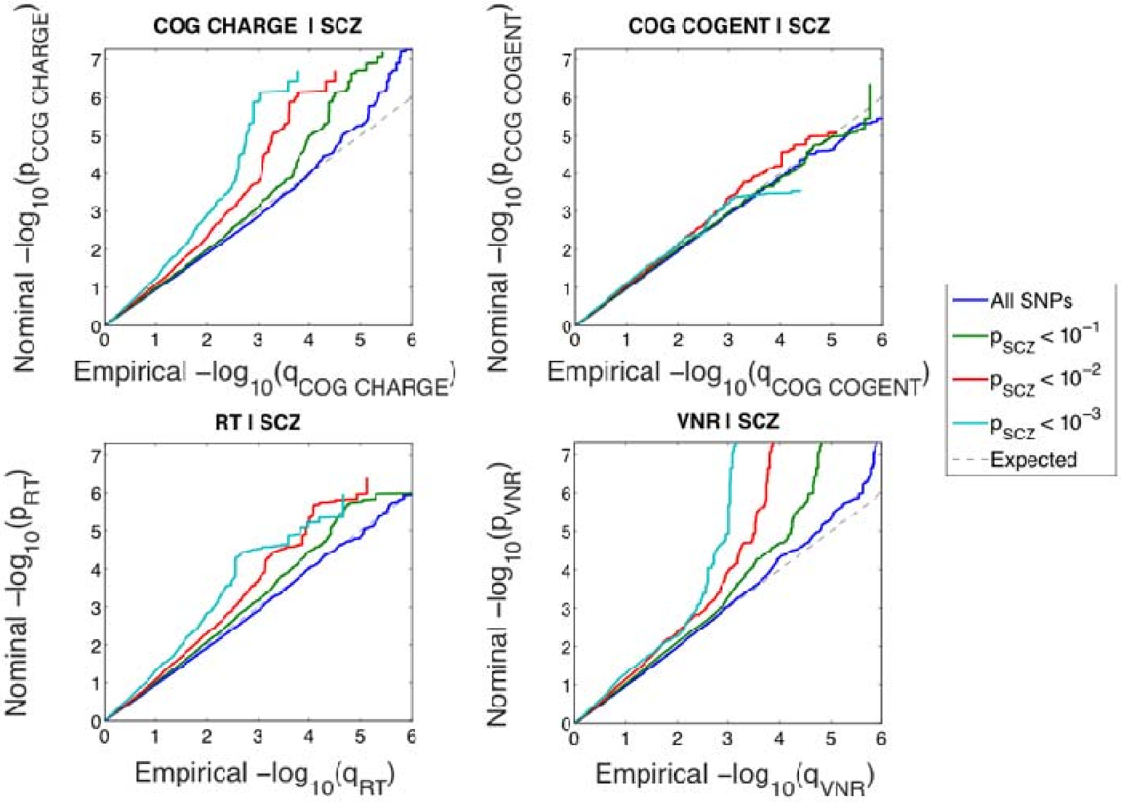
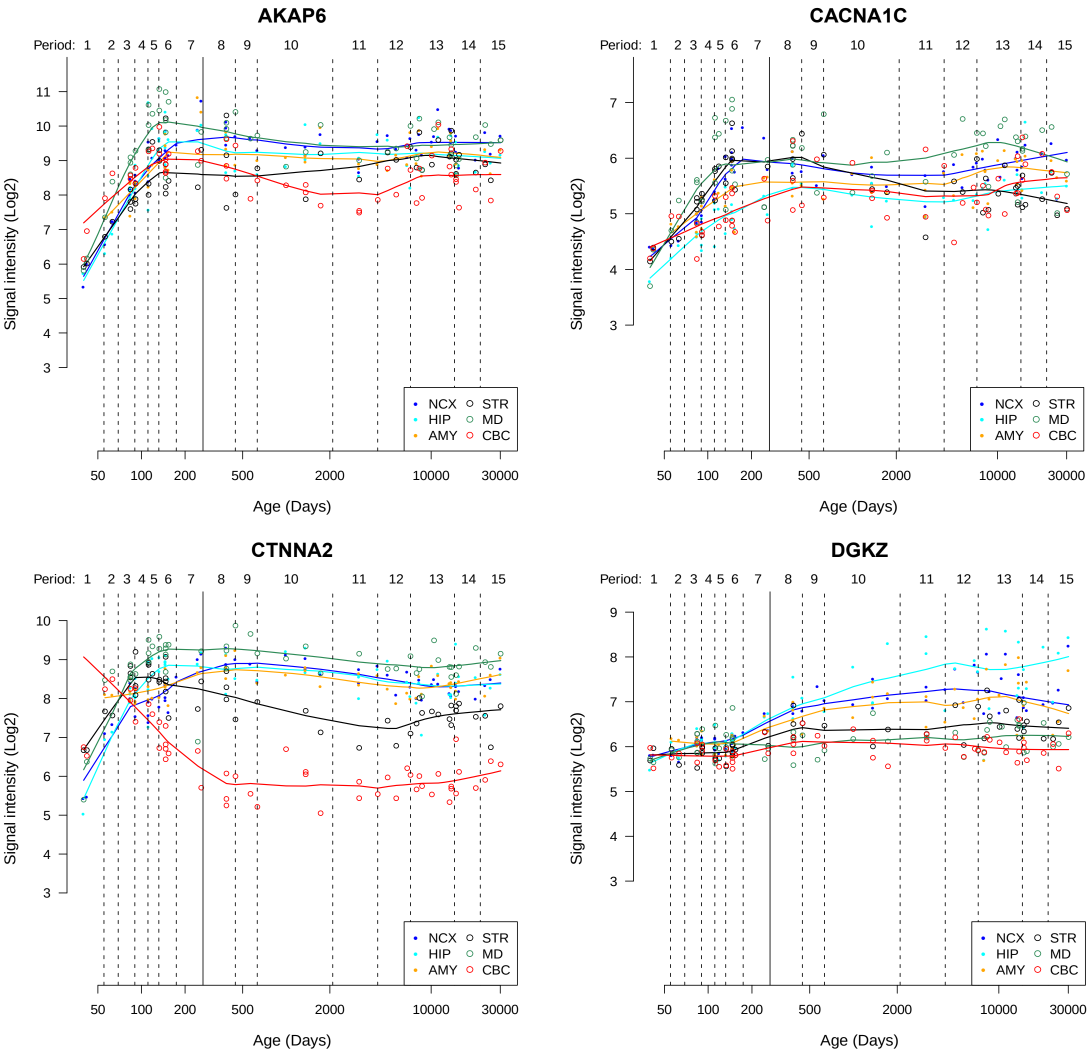


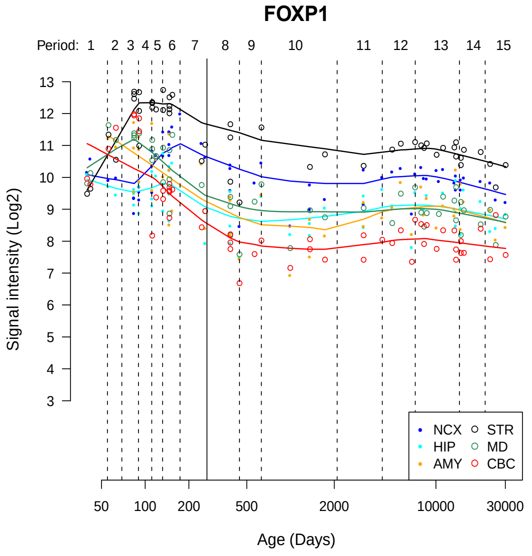
Figure 2. Averaged Regional mRNA Expression Distribution in the Adult Human Brain of Genes Implicated in Schizophrenia and General Cognitive Function, Verbal-Numerical Reasoning, and Reaction Time

Expression levels are indicated by color intensity in the $\log_2$ scale. Data is provided by The UK Human Brain Expression Consortium and downloaded from http://www.braineac.org/. Gene symbols are shown at the x axis. Brain structures shown at the y axis include temporal cortex (TCTX), occipital cortex (OCTX), frontal cortex (FCTX), intralobular white matter (WHMT), substantia nigra (SNIG), medulla (MEDU), cerebellar cortex (CRBL), thalamus (THAL), putamen (PUTM), hippocampus (HIPP) and the average of all structures (aveALL).

eFigure 3. Expression Trajectories of Genes Annotated to Loci Shared Between Schizophrenia and General Cognitive Function, Verbal-Numerical Reasoning, and Reaction Time in the Developmental and Adult Human Brain

Line plots show the $\log_2$-transformed gene exon array signal intensity from the early fetal period to late adulthood in six brain regions. The solid line between periods 7 and 8 (approximately post-conception day 280) separates prenatal from postnatal periods. Data were generated using Affymetrix GeneChip Human Exon 1.0 ST Arrays by the Human Brain Transcriptome project, and accessed via their publicly available database at http://hbatlas.org[11]. Abbreviations: NCX = neocortex; HIP = hippocampus; AMY = amygdala; STR = striatum; MD = mediodorsal nucleus of the thalamus; CBC = cerebellar cortex.

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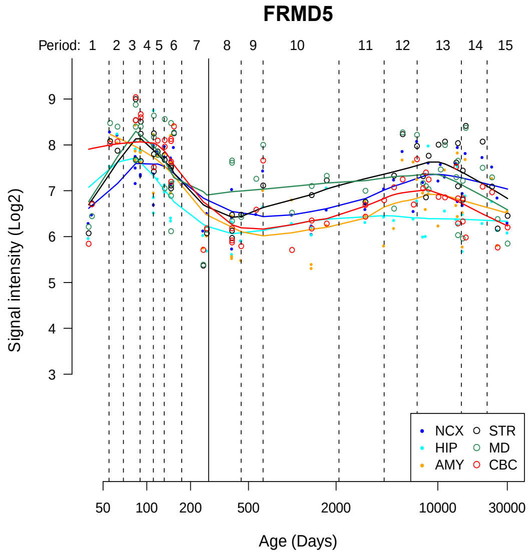
Age (Days)
NCX
STR
HIP
MD
AMY
CBC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STR
HIP
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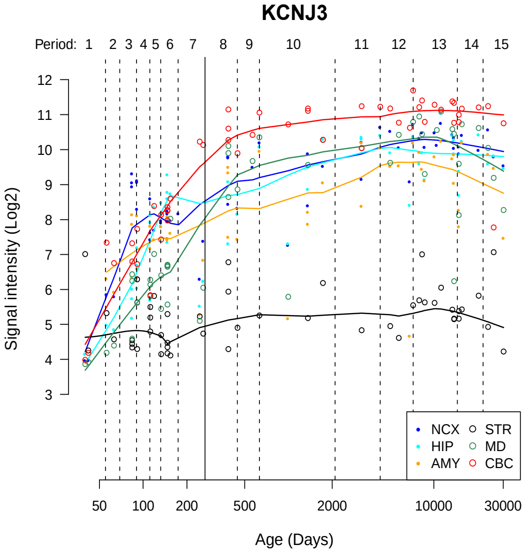
AMY
CBC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Age (Days)
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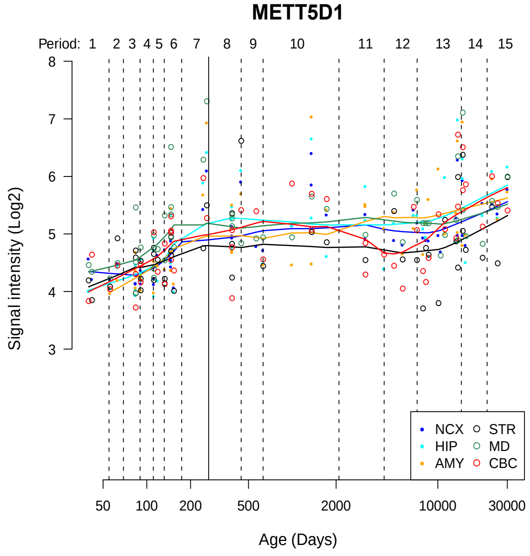
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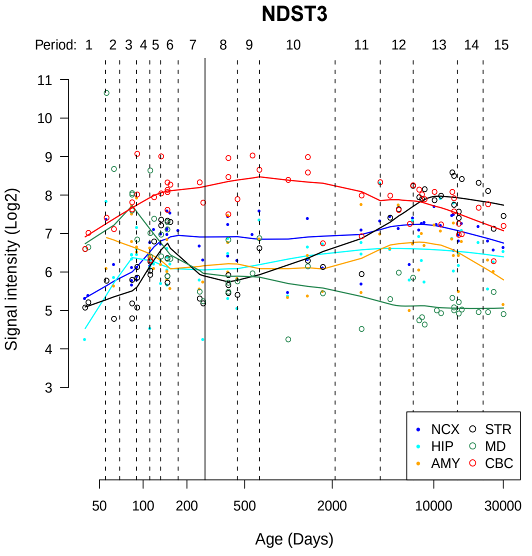
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Age (Days)
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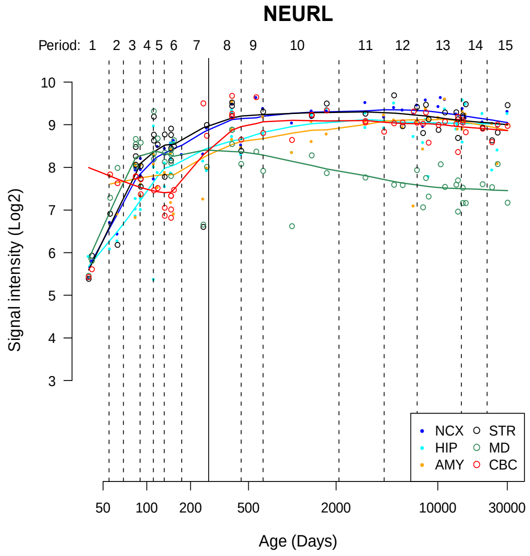
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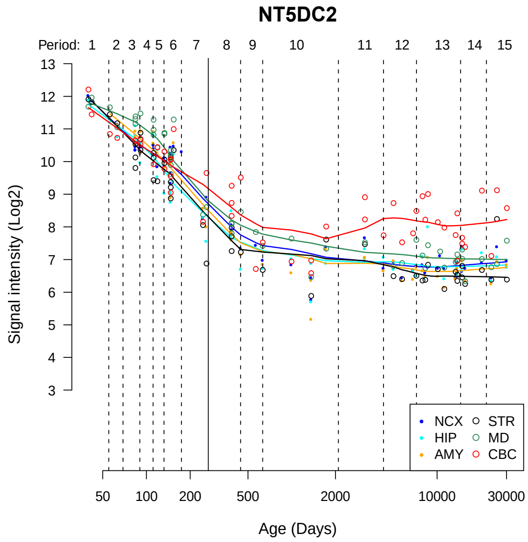
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Signal intensity (Log2)
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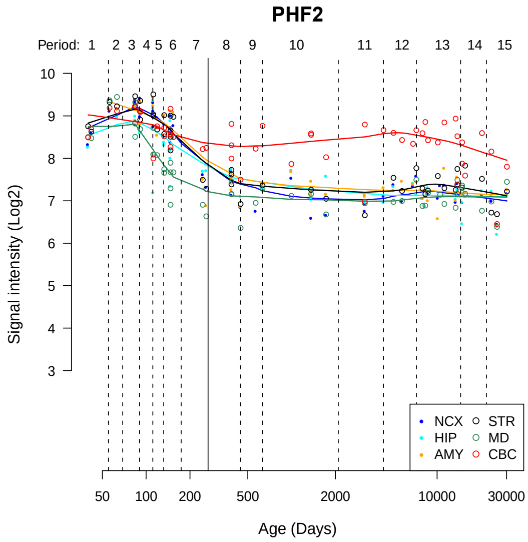
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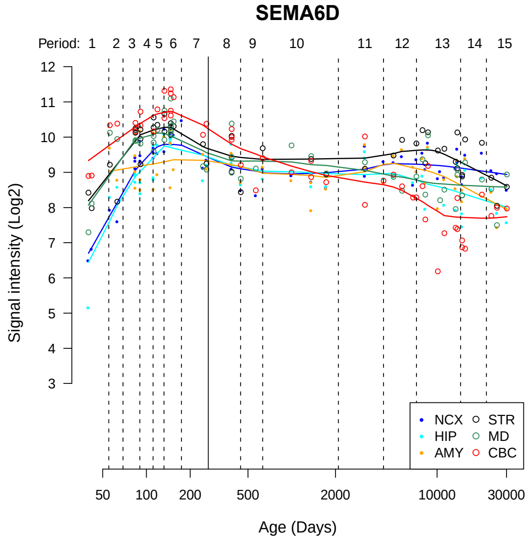
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Signal intensity (Log2)
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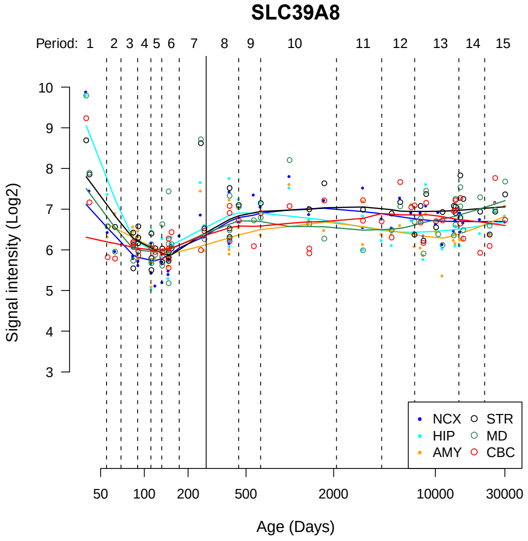
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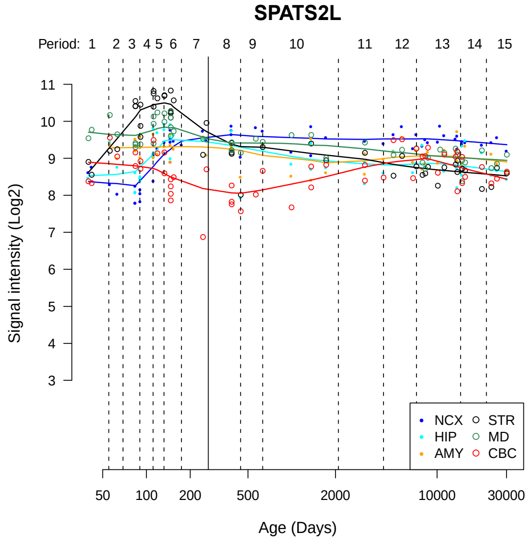
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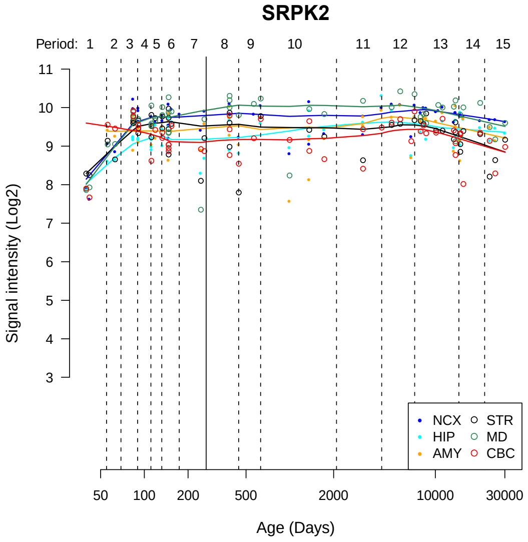
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Age (Days)
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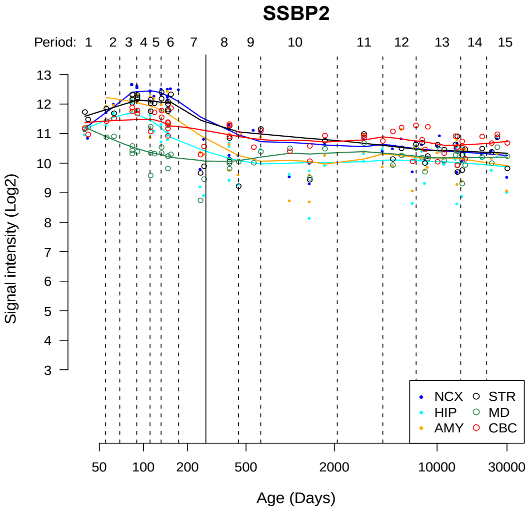
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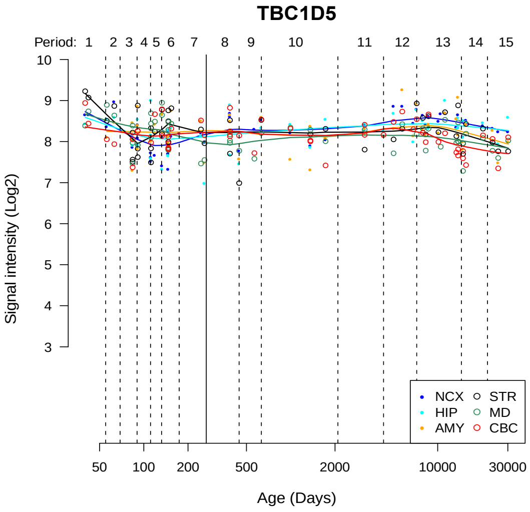
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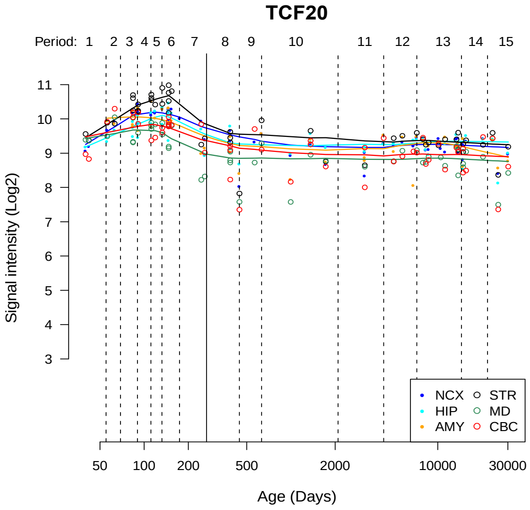
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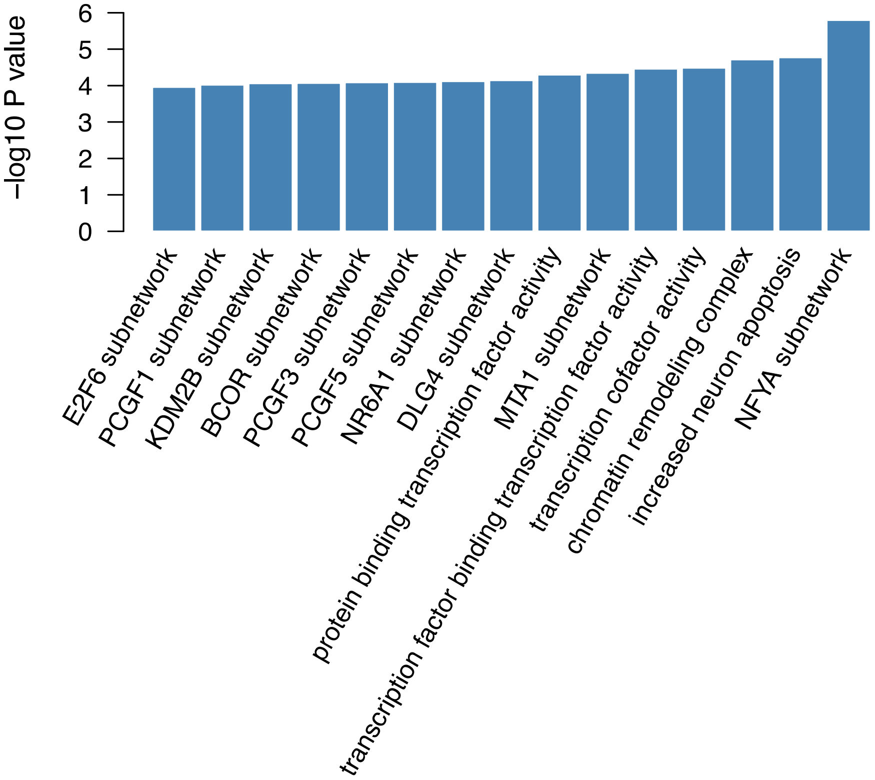

eFigure 4. Top-ranked gene sets enriched for genes in loci associated with schizophrenia and general cognitive function (conjunctional FDR<.20) identified using DEPICT analysis[13].

eTable 1. Loci With cFDR<.01 Associated With Cognitive Traits Given Association With Schizophrenia. cFDR Manhattan plots are presented in Figure 2.

Loci associated with general cognitive function (COG) in the CHARGE cohort at cFDR<.01

Locus	SNP	Gene Id	Chr	Position	P COG CHARGE	FDR COG CHARGE	cFDR COG CHARGE | SCZ
1	rs12986588	*CTNNA2*	2	80116325	2,74E-05	2,33E-01	4,58E-03
2	rs13303	*STAB1*	3	52558008	2,01E-05	2,11E-01	3,13E-03
3	rs6838310	*NDST3*	4	118878133	4,43E-06	1,79E-01	6,72E-04
4	rs6452790	*TMEM161B*	5	87756708	5,24E-06	1,79E-01	7,61E-03
5	rs1487441	*AK091365*	6	98553894	8,64E-08	2,96E-02	3,02E-04
6	rs17522122	*AKAP6*	14	33302882	1,87E-07	4,44E-02	3,67E-05
7	rs10119	*TOMM40*	19	45406673	4,98E-08	2,46E-02	5,62E-03
8	rs5758659	*TCF20*	22	42622003	4,74E-06	1,79E-01	8,39E-04

Loci associated with COG in the COGENT cohort at cFDR<.01

Locus	SNP	Gene Id	Chr	Position	P COG COGENT	FDR COG COGENT	cFDR COG COGENT | SCZ
1	rs7581162	*BCL11A*	2	60704484	2,64E-05	9,27E-01	8,16E-03
2	rs34349601	*AK096499*	2	199553892	5,15E-06	9,30E-01	8,85E-03
3	rs13098807	*ARPP-21*	3	35613088	4,13E-07	8,48E-01	7,64E-03

Loci associated with verbal-numerical reasoning (VNR) at cFDR<.01

Locus	SNP	Gene Id	Chr	Position	P VNR	FDR VNR	cFDR VNR | SCZ
1	rs1349265	*THRB*	3	24159387	2,33E-06	8,51E-02	2,22E-03
2	rs13105682	*BANK1*	4	102702364	8,77E-06	1,63E-01	1,56E-03
3	rs3897757	*APBA1*	9	72075130	2,38E-06	8,51E-02	6,83E-03
4	rs4295766	*FLJ00199*	9	131838821	2,73E-05	2,55E-01	5,91E-03
5	rs5758605	*CYP2D6*	22	42541349	8,28E-11	2,02E-04	2,13E-08

Loci associated with reaction time (RT) at cFDR<.01

Locus	**SNP**	**Gene Id**	**Chr**	**Position**	**P RT**	**FDR RT**	**cFDR RT | SCZ**
1	rs13020196	*SPATS2L*	2	201071942	5,19E-07	1,00E-01	1,10E-04
2	rs7785252	*SUN1*	7	902394	1,02E-06	1,10E-01	9,04E-03
3	rs55934002	*PHF2*	9	96369424	2,77E-05	2,39E-01	5,43E-03
4	rs12577142	*DGKZ*	11	46377770	8,86E-06	2,18E-01	1,78E-03

eTable 2. Effect Sizes of SNPs in LD With Conjunctional Loci With Ambiguous Effect Directionality

A. Effect sizes of SNPs in LD with rs13024343, rs1545424 and rs12253987 shared between schizophrenia (SCZ) and general cognitive function (COG) (conjFDR<.05) with ambiguous direction of allelic effects (Table 1)

					COG GWAS				Schizophrenia GWAS			
					Davies et al. (2015)				Schizophrenia Working Group et al. (2014)			
SNP	**Proxy**	**Distance**	**R^2**	**DPrime**	**SNP Id**	**A1/A2**	**Beta**	**P**	**SNP Id**	**A1/A2**	**or**	**p**
rs13024343	rs13034462	10816	0.908	1	rs13034462	t/g	-0.0603	7,13E-06	rs13034462	t/g	0,9035	1,20E-04
rs13024343	rs12986588	13985	0.822	0.907	rs12986588	t/c	0.0605	7,40E-06	rs12986588	t/c	1,1072	1,15E-04
rs13024343	rs12987105	7230	0.73	1	rs12987105	t/c	-0.0605	8,87E-06	rs12987105	t/c	0,8990	6,06E-05
rs13024343	rs4591366	52244	0.457	0.795	rs4591366	t/c	0.0173	4,45E-02	rs4591366	t/c	1,0163	3,03E-01
rs13024343	rs12713994	33751	0.423	0.793	rs12713994	a/g	0.0227	1,25E-02	rs12713994	a/g	1,0312	7,40E-02
rs1545424	rs1375817	16	1	1	rs1375817	t/c	-0.0243	2,02E-04	rs1375817	t/c	1,0527	2,31E-06
rs1545424	rs2596672	1016	1	1	rs2596672	a/g	0.0141	1,04E-02	rs2596672	a/g	0,9501	2,61E-06
rs1545424	rs2122368	4552	1	1	rs2122368	a/g	0.0141	1,07E-02	rs2122368	a/g	0,9499	2,38E-06
rs1545424	rs1375818	4893	1	1	rs1375818	t/c	-0.0141	1,04E-02	rs1375818	t/c	1,0523	2,77E-06
rs1545424	rs1597393	6250	1	1	rs1597393	t/c	-0.014	1,08E-02	rs1597393	t/c	1,0532	2,20E-06
rs12253987	rs11191727	8574	0.468	0.708	rs11191727	t/c	0.0179	3,17E-02	rs11191727	t/c	0,9562	3,49E-03
rs12253987	rs12413931	114641	0.433	1	rs12413931	t/c	0.0126	1,70E-01	rs12413931	t/c	0,9618	3,48E-02
rs12253987	rs11191724	12347	0.411	0.83	rs11191724	a/g	0.0181	1,50E-02	rs11191724	a/g	0,9389	4,33E-06
rs12253987	rs7904046	31041	0.407	0.638	rs7904046	a/c	0.0165	3,01E-02	rs7904046	a/c	0,9525	7,10E-04
rs12253987	rs7893473	21345	0.338	0.621	rs7893473	c/g	0.0167	2,84E-02	rs7893473	c/g	0,9480	2,21E-04

B. Effect sizes of SNPs in LD with rs7857165 shared between SCZ and reaction time (RT) (conjFDR<.05) with ambiguous direction of allelic effects (Table 1)

					RT GWAS. Davies et al. (2016)				Schizophrenia GWAS Schizophrenia Working Group et al. (2014)			
SNP	**Proxy**	**Distance**	**R^2**	**DPrime**	**SNP Id**	**A1/A2**	**RT Beta**	**RT P-value**	**SNP Id**	**A1/A2**	**or**	**p**
rs7857165	rs4146138	541	1	1	rs4146138	t/c	0,0590	7,72E-06	rs4146138	t/c	1,1294	5,09E-05
rs7857165	rs117162228	6075	0,661	1	rs117162228	a/g	0,0017	9,15E-01	rs117162228	a/g	1,0985	1,97E-02
rs7857165	rs7044283	830	0,496	1	rs7044283	t/g	0,0590	7,72E-06	rs7044283	t/g	1,1306	4,42E-05
rs7857165	rs117432403	10886	0,496	1	rs117432403	a/g	0,0184	3,65E-01	rs117432403	a/g	1,1088	1,01E-02
rs7857165	rs117640468	15047	0,496	1	rs117640468	t/c	0,0191	3,26E-01	rs117640468	t/c	1,1174	1,64E-02

eTable 3. List of Gene Loci (Unpruned) With Conjunctional False Discovery Rate (conjFDR<.10) Associated With Schizophrenia (SCZ) and General Cognitive Function in the CHARGE Cohort (COG CHARGE), COG in the COGENT Cohort (COG COGENT), Verbal-Numerical Reasoning (VNR) or Reaction Time (RT). Loci in MHC marked with *.

eTable 3A. Loci with conjFDR<.10 associated with SCZ and COG CHARGE

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
1	rs2782657	HYI	1	C	G	NaN	NaN	5,26E-02	1	1,58E-03	2,58E-04
1	rs3791034	KDM4A	1	G	A	-2,92E+00	3,47E+00	8,65E-02	0	3,45E-03	5,26E-04
1	rs4660257	KDM4A	1	C	T	-3,07E+00	3,38E+00	9,02E-02	0	2,15E-03	7,29E-04
1	rs11805774	KDM4A	1	A	G	-3,00E+00	3,44E+00	8,81E-02	0	2,74E-03	5,80E-04
1	rs17401357	KDM4A	1	C	G	NaN	NaN	9,93E-02	0	3,31E-03	5,94E-04
1	rs3791035	KDM4A	1	C	G	NaN	NaN	8,65E-02	0	3,10E-03	5,62E-04
1	rs2270972	KDM4A	1	G	C	NaN	NaN	9,93E-02	0	3,49E-03	6,17E-04
2	rs12561796	ANKRD45	1	T	C	-3,60E+00	3,20E+00	8,64E-02	1	3,21E-04	1,40E-03
3	rs6709302	BCL11A	2	A	G	3,63E+00	3,26E+00	8,64E-02	1	2,87E-04	1,12E-03
4	rs12986588	CTNNA2	2	T	C	3,21E+00	4,19E+00	4,44E-02	0	1,32E-03	2,74E-05
4	rs13034462	CTNNA2	2	G	T	3,21E+00	4,20E+00	4,44E-02	0	1,34E-03	2,65E-05
4	rs13024343	CTNNA2	2	A	T	NaN	NaN	2,64E-02	1	6,57E-04	2,92E-05
4	rs12987105	CTNNA2	2	C	T	3,34E+00	4,16E+00	3,15E-02	0	8,50E-04	3,21E-05
5	rs1545424	TBC1D5	3	A	T	NaN	NaN	3,35E-02	1	1,04E-04	3,02E-04
5	rs1375817	TBC1D5	3	C	T	-3,86E+00	3,48E+00	4,69E-02	0	1,15E-04	5,06E-04
6	rs352158	ALAS1	3	C	T	3,01E+00	-3,42E+00	8,81E-02	0	2,62E-03	6,36E-04
6	rs614288	ALAS1	3	T	C	3,14E+00	-3,52E+00	5,26E-02	0	1,71E-03	4,26E-04
6	rs181274	ALAS1	3	T	A	NaN	NaN	8,64E-02	0	9,42E-04	1,16E-03
6	rs352167	ALAS1	3	T	C	3,41E+00	-3,28E+00	7,47E-02	0	6,57E-04	1,02E-03
6	rs352166	ALAS1	3	C	T	3,39E+00	-3,29E+00	7,47E-02	0	7,09E-04	9,88E-04
6	rs352165	ALAS1	3	A	G	3,31E+00	-3,25E+00	8,64E-02	0	9,28E-04	1,13E-03

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
6	rs352163	ALAS1	3	G	A	3,29E+00	-3,57E+00	3,97E-02	0	1,01E-03	3,60E-04
6	rs164640	ALAS1	3	C	T	3,32E+00	-3,57E+00	3,97E-02	0	8,86E-04	3,58E-04
6	rs352162	TLR9	3	T	C	3,42E+00	-3,65E+00	2,81E-02	0	6,16E-04	2,63E-04
6	rs352140	TLR9	3	C	T	3,44E+00	-3,67E+00	2,81E-02	0	5,87E-04	2,40E-04
6	rs352139	TLR9	3	T	C	3,54E+00	-3,74E+00	2,35E-02	0	4,07E-04	1,85E-04
6	rs187084	TLR9	3	G	A	-4,33E+00	3,39E+00	5,50E-02	0	1,47E-05	7,07E-04
6	rs1060330	WDR82	3	T	C	4,57E+00	-3,65E+00	2,81E-02	0	4,80E-06	2,66E-04
6	rs7614727	WDR82	3	C	T	4,55E+00	-3,66E+00	2,81E-02	0	5,40E-06	2,48E-04
6	rs6445358	WDR82	3	C	G	NaN	NaN	2,81E-02	0	4,10E-06	2,78E-04
6	rs7622851	GLYCTK1	3	C	G	NaN	NaN	3,35E-02	0	3,75E-06	3,51E-04
6	rs13094687	PHF7	3	G	A	-3,91E+00	3,24E+00	8,64E-02	0	9,10E-05	1,21E-03
6	rs2272088	PHF7	3	G	A	-3,86E+00	3,27E+00	7,47E-02	0	1,15E-04	1,09E-03
6	rs648514	SEMA3G	3	A	G	3,42E+00	-3,45E+00	4,69E-02	0	6,30E-04	5,55E-04
6	rs731831	STAB1	3	A	G	-4,15E+00	3,56E+00	3,97E-02	0	3,30E-05	3,69E-04
6	rs1010553	STAB1	3	C	T	4,13E+00	-3,91E+00	1,33E-02	0	3,63E-05	9,11E-05
6	rs1010554	STAB1	3	C	T	3,93E+00	-4,04E+00	7,29E-03	0	8,39E-05	5,38E-05
6	rs2015971	STAB1	3	T	C	-3,25E+00	3,71E+00	4,44E-02	0	1,16E-03	2,05E-04
6	rs13081028	STAB1	3	G	A	3,65E+00	-4,22E+00	1,27E-02	0	2,66E-04	2,39E-05
6	rs9853056	STAB1	3	T	C	3,78E+00	-3,87E+00	1,33E-02	0	1,56E-04	1,09E-04
6	rs13303	STAB1	3	T	C	3,86E+00	-4,26E+00	7,15E-03	0	1,12E-04	2,01E-05
6	rs11711421	NT5DC2	3	T	C	-3,35E+00	3,71E+00	3,15E-02	0	8,07E-04	2,06E-04
6	rs4687625	NT5DC2	3	T	C	-3,19E+00	3,67E+00	4,44E-02	0	1,41E-03	2,43E-04
6	rs4282054	NT5DC2	3	T	C	3,88E+00	-4,29E+00	5,88E-03	1	1,04E-04	1,82E-05
6	rs7614981	NT5DC2	3	C	A	4,10E+00	-4,12E+00	5,92E-03	0	4,11E-05	3,78E-05
6	rs12489828	NT5DC2	3	G	T	4,07E+00	-4,07E+00	7,29E-03	0	4,62E-05	4,65E-05
6	rs6445528	LOC440957	3	G	A	-3,01E+00	3,73E+00	7,34E-02	0	2,61E-03	1,91E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
6	rs1133415	LOC440957	3	A	G	-2,99E+00	3,73E+00	8,65E-02	0	2,82E-03	1,90E-04
6	rs2878628	PB1	3	G	A	-3,75E+00	3,55E+00	3,97E-02	0	1,75E-04	3,81E-04
6	rs2251219	PB1	3	C	T	-4,17E+00	3,47E+00	4,69E-02	0	3,06E-05	5,12E-04
6	rs1961959	PB1	3	C	G	NaN	NaN	4,69E-02	0	4,94E-05	5,12E-04
6	rs1961958	PB1	3	G	A	-4,08E+00	3,48E+00	4,69E-02	0	4,51E-05	5,07E-04
6	rs17052259	PB1	3	G	A	-3,76E+00	3,56E+00	3,97E-02	0	1,68E-04	3,73E-04
6	rs3796353	PB1	3	T	C	-3,76E+00	3,56E+00	3,97E-02	0	1,70E-04	3,73E-04
6	rs6778844	PB1	3	C	T	-4,04E+00	3,48E+00	4,69E-02	0	5,35E-05	5,04E-04
6	rs2289249	PB1	3	A	G	-4,06E+00	3,48E+00	4,69E-02	0	4,81E-05	4,98E-04
6	rs6798246	PB1	3	A	G	-4,09E+00	3,48E+00	4,69E-02	0	4,25E-05	5,01E-04
6	rs11714565	PB1	3	T	C	-3,69E+00	3,56E+00	3,97E-02	0	2,26E-04	3,70E-04
6	rs6805156	PB1	3	C	T	-3,71E+00	3,56E+00	3,97E-02	0	2,08E-04	3,70E-04
6	rs7652191	PB1	3	C	T	-3,73E+00	3,56E+00	3,97E-02	0	1,94E-04	3,71E-04
6	rs17264436	PB1	3	A	T	NaN	NaN	4,69E-02	0	6,82E-05	5,06E-04
6	rs4687629	PB1	3	C	G	NaN	NaN	3,97E-02	0	1,93E-04	3,73E-04
6	rs11720159	PB1	3	G	T	-3,70E+00	3,56E+00	3,97E-02	0	2,17E-04	3,73E-04
6	rs11720243	PB1	3	C	T	-3,69E+00	3,56E+00	3,97E-02	0	2,28E-04	3,72E-04
6	rs12487445	PB1	3	C	A	-3,96E+00	3,48E+00	4,69E-02	0	7,38E-05	5,03E-04
6	rs2590838	PB1	3	G	A	4,66E+00	-3,97E+00	1,09E-02	0	3,13E-06	7,22E-05
6	rs2336146	PB1	3	G	A	-3,65E+00	3,60E+00	3,35E-02	0	2,59E-04	3,18E-04
6	rs11714419	PB1	3	G	A	-4,00E+00	3,49E+00	4,69E-02	0	6,33E-05	4,82E-04
6	rs2118540	PB1	3	C	T	-4,02E+00	3,51E+00	3,97E-02	0	5,77E-05	4,43E-04
6	rs2276824	PB1	3	C	G	NaN	NaN	6,42E-02	0	4,48E-06	8,87E-04
6	rs3774366	PB1	3	C	T	-3,71E+00	3,59E+00	3,35E-02	0	2,05E-04	3,32E-04
6	rs3774365	PB1	3	C	T	-4,14E+00	3,52E+00	3,97E-02	0	3,54E-05	4,31E-04
6	rs12487591	PB1	3	T	A	NaN	NaN	3,97E-02	0	3,53E-05	4,40E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
6	rs3733045	PB1	3	G	A	-3,74E+00	3,58E+00	3,35E-02	0	1,81E-04	3,42E-04
6	rs3755806	PB1	3	C	T	-4,14E+00	3,51E+00	4,69E-02	0	3,41E-05	4,52E-04
6	rs13083798	PB1	3	A	G	4,66E+00	-4,00E+00	8,94E-03	0	3,12E-06	6,23E-05
6	rs10510760	PB1	3	A	G	-4,22E+00	3,60E+00	3,35E-02	0	2,45E-05	3,16E-04
6	rs13064064	PB1	3	C	T	-4,14E+00	3,51E+00	3,97E-02	0	3,46E-05	4,43E-04
6	rs1561337	PB1	3	A	G	-4,15E+00	3,51E+00	3,97E-02	0	3,26E-05	4,44E-04
6	rs4687548	PB1	3	T	A	NaN	NaN	3,97E-02	0	3,27E-05	4,46E-04
6	rs2083180	PB1	3	T	G	-3,80E+00	3,64E+00	2,81E-02	0	1,45E-04	2,74E-04
6	rs13068293	PB1	3	A	C	-4,15E+00	3,51E+00	3,97E-02	0	3,27E-05	4,42E-04
6	rs11130312	PB1	3	C	A	-4,14E+00	3,51E+00	3,97E-02	0	3,45E-05	4,44E-04
6	rs13085895	PB1	3	C	G	NaN	NaN	3,97E-02	0	4,09E-05	4,39E-04
6	rs13085775	PB1	3	T	C	-3,72E+00	3,58E+00	3,35E-02	0	1,99E-04	3,50E-04
6	rs2028216	PB1	3	T	C	-4,01E+00	3,66E+00	2,81E-02	0	6,05E-05	2,51E-04
6	rs2289250	PB1	3	A	C	-4,15E+00	3,51E+00	3,97E-02	0	3,36E-05	4,41E-04
6	rs2336149	PB1	3	A	G	-3,73E+00	3,57E+00	3,35E-02	0	1,93E-04	3,54E-04
6	rs7611731	PB1	3	C	T	-3,73E+00	3,59E+00	3,35E-02	0	1,92E-04	3,25E-04
6	rs6804145	PB1	3	T	C	-3,73E+00	3,57E+00	3,35E-02	0	1,95E-04	3,55E-04
6	rs11130315	PB1	3	G	A	-4,14E+00	3,52E+00	3,97E-02	0	3,43E-05	4,39E-04
6	rs6803012	PB1	3	A	G	-4,14E+00	3,49E+00	4,69E-02	0	3,46E-05	4,81E-04
6	rs2336542	PB1	3	G	A	-4,15E+00	3,50E+00	4,69E-02	0	3,35E-05	4,65E-04
6	rs10865973	PBRM1	3	T	A	NaN	NaN	4,69E-02	0	5,54E-05	4,66E-04
6	rs10865974	PBRM1	3	T	G	-3,74E+00	3,55E+00	3,97E-02	0	1,87E-04	3,89E-04
6	rs1866268	PBRM1	3	A	C	-3,73E+00	3,55E+00	3,97E-02	0	1,93E-04	3,89E-04
6	rs1108842	GNL3	3	A	C	4,66E+00	-3,93E+00	1,09E-02	0	3,09E-06	8,58E-05
6	rs11177	GNL3	3	A	G	-4,00E+00	3,48E+00	4,69E-02	0	6,22E-05	5,00E-04
6	rs6762813	GNL3	3	T	C	-4,00E+00	3,50E+00	4,69E-02	0	6,38E-05	4,65E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
6	rs2289247	GNL3	3	A	G	-3,74E+00	3,55E+00	3,97E-02	0	1,85E-04	3,79E-04
6	rs6976	GLT8D1	3	T	C	-4,00E+00	3,50E+00	4,69E-02	0	6,37E-05	4,60E-04
6	rs2164885	GLT8D1	3	C	T	-3,66E+00	3,56E+00	3,97E-02	0	2,56E-04	3,67E-04
6	rs3733041	GLT8D1	3	C	T	-3,70E+00	3,55E+00	3,97E-02	0	2,20E-04	3,92E-04
6	rs12635140	GLT8D1	3	C	T	-3,69E+00	3,56E+00	3,97E-02	0	2,24E-04	3,74E-04
6	rs6617	SPCS1	3	G	C	NaN	NaN	1,95E-02	0	2,33E-04	1,76E-04
6	rs3755798	SPCS1	3	A	G	-3,69E+00	3,53E+00	3,97E-02	0	2,21E-04	4,13E-04
6	rs6445534	SPCS1	3	A	G	-3,69E+00	3,53E+00	3,97E-02	0	2,20E-04	4,13E-04
6	rs13079063	NEK4	3	G	A	-3,71E+00	3,54E+00	3,97E-02	0	2,05E-04	4,07E-04
6	rs11235	NEK4	3	C	T	4,57E+00	-3,27E+00	7,47E-02	0	4,80E-06	1,07E-03
6	rs2268027	NEK4	3	A	G	-3,99E+00	3,48E+00	4,69E-02	0	6,48E-05	4,97E-04
6	rs11130323	NEK4	3	C	T	-4,14E+00	3,47E+00	4,69E-02	0	3,45E-05	5,13E-04
6	rs2268026	NEK4	3	C	T	-4,13E+00	3,47E+00	4,69E-02	0	3,68E-05	5,25E-04
6	rs2072390	NEK4	3	T	A	NaN	NaN	3,97E-02	0	1,97E-04	4,30E-04
6	rs13082208	NEK4	3	G	T	-3,98E+00	3,39E+00	5,50E-02	0	6,92E-05	7,00E-04
6	rs13082960	NEK4	3	C	A	-4,16E+00	3,45E+00	5,50E-02	0	3,22E-05	5,70E-04
6	rs2336545	NEK4	3	C	T	-4,16E+00	3,40E+00	5,50E-02	0	3,19E-05	6,64E-04
6	rs12497998	NEK4	3	T	C	-3,80E+00	3,47E+00	4,69E-02	0	1,47E-04	5,14E-04
6	rs2268025	NEK4	3	T	A	NaN	NaN	5,50E-02	0	4,79E-05	6,88E-04
6	rs1029871	NEK4	3	C	G	NaN	NaN	5,50E-02	0	4,54E-05	6,54E-04
6	rs998909	NEK4	3	G	A	-3,89E+00	3,29E+00	7,47E-02	0	1,01E-04	9,93E-04
6	rs11717836	NEK4	3	G	A	-4,13E+00	3,47E+00	4,69E-02	0	3,70E-05	5,12E-04
6	rs2019065	ITIH1	3	C	T	-4,00E+00	3,52E+00	3,97E-02	0	6,29E-05	4,25E-04
6	rs2710323	ITIH1	3	T	C	5,12E+00	-3,93E+00	1,09E-02	0	3,14E-07	8,47E-05
6	rs3774354	ITIH1	3	A	G	-4,10E+00	3,49E+00	4,69E-02	0	4,18E-05	4,76E-04
6	rs3774355	ITIH1	3	A	G	-4,07E+00	3,48E+00	4,69E-02	0	4,74E-05	4,94E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
6	rs2239551	ITIH1	3	A	G	-4,00E+00	3,49E+00	4,69E-02	0	6,32E-05	4,78E-04
6	rs2268023	ITIH1	3	A	T	NaN	NaN	8,64E-02	0	2,03E-04	1,30E-03
6	rs678	ITIH1	3	T	A	NaN	NaN	6,42E-02	0	3,92E-05	7,34E-04
6	rs1042779	ITIH1	3	G	A	-4,19E+00	3,34E+00	6,42E-02	0	2,79E-05	8,45E-04
6	rs2286798	ITIH1	3	C	A	-4,10E+00	3,36E+00	6,42E-02	0	4,11E-05	7,78E-04
6	rs2300149	ITIH1	3	T	C	-3,99E+00	3,50E+00	4,69E-02	0	6,49E-05	4,70E-04
6	rs2239549	ITIH1	3	A	G	-4,06E+00	3,37E+00	6,42E-02	0	4,83E-05	7,45E-04
6	rs2240919	ITIH3	3	G	C	NaN	NaN	2,35E-02	0	3,51E-05	2,16E-04
6	rs2535629	ITIH3	3	A	G	-4,59E+00	3,35E+00	6,42E-02	0	4,46E-06	8,13E-04
6	rs3617	ITIH3	3	A	C	-5,27E+00	3,92E+00	1,09E-02	0	1,38E-07	8,84E-05
6	rs736408	ITIH3	3	T	C	-4,37E+00	3,26E+00	7,47E-02	0	1,21E-05	1,10E-03
6	rs4481150	ITIH3	3	T	C	5,26E+00	-3,92E+00	1,33E-02	0	1,42E-07	8,94E-05
6	rs2535627	AX746575	3	T	C	5,31E+00	-3,95E+00	1,09E-02	0	1,09E-07	7,93E-05
6	rs2071044	ITIH4	3	C	T	5,18E+00	-3,93E+00	1,09E-02	0	2,23E-07	8,33E-05
6	rs6445541	TMEM110	3	T	G	-4,78E+00	3,30E+00	7,47E-02	0	1,79E-06	9,66E-04
6	rs4687672	TMEM110	3	A	G	-4,48E+00	3,22E+00	8,64E-02	0	7,48E-06	1,29E-03
6	rs2276825	TMEM110	3	C	T	-4,35E+00	3,44E+00	5,50E-02	0	1,38E-05	5,79E-04
6	rs9682464	TMEM110	3	T	C	-4,36E+00	3,43E+00	5,50E-02	0	1,30E-05	5,94E-04
6	rs4302374	TMEM110	3	C	T	-4,23E+00	3,40E+00	5,50E-02	0	2,33E-05	6,80E-04
6	rs6445547	TMEM110	3	C	T	-4,19E+00	3,41E+00	5,50E-02	0	2,73E-05	6,59E-04
6	rs12492391	TMEM110	3	A	C	-4,70E+00	3,25E+00	8,64E-02	0	2,66E-06	1,16E-03
6	rs9876403	TMEM110	3	T	C	-3,99E+00	3,34E+00	6,42E-02	0	6,71E-05	8,40E-04
6	rs9880978	TMEM110	3	G	C	NaN	NaN	8,64E-02	0	3,93E-06	1,23E-03
6	rs9844736	TMEM110	3	T	G	-4,03E+00	3,20E+00	8,64E-02	0	5,64E-05	1,35E-03
6	rs1134546	SFMBT1	3	G	A	-3,72E+00	3,19E+00	9,95E-02	0	2,00E-04	1,42E-03
6	rs2581810	SFMBT1	3	C	T	-3,93E+00	3,28E+00	7,47E-02	0	8,33E-05	1,03E-03

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
6	rs2257216	SFMBT1	3	T	C	-5,15E+00	3,78E+00	1,95E-02	0	2,62E-07	1,60E-04
6	rs2710314	SFMBT1	3	T	C	-5,17E+00	3,78E+00	1,95E-02	0	2,38E-07	1,55E-04
6	rs2581801	SFMBT1	3	G	T	-3,96E+00	3,40E+00	5,50E-02	0	7,37E-05	6,81E-04
6	rs2581815	SFMBT1	3	G	C	NaN	NaN	5,50E-02	0	1,01E-04	6,95E-04
6	rs7648514	SFMBT1	3	G	C	NaN	NaN	5,50E-02	0	7,31E-05	6,90E-04
6	rs6445550	SFMBT1	3	A	G	-3,98E+00	3,39E+00	5,50E-02	0	6,99E-05	6,92E-04
6	rs9865094	SFMBT1	3	G	C	NaN	NaN	6,42E-02	0	1,07E-04	8,29E-04
6	rs9311485	SFMBT1	3	T	G	-3,91E+00	3,35E+00	6,42E-02	0	9,20E-05	8,13E-04
6	rs2336669	SFMBT1	3	G	A	-4,14E+00	3,38E+00	6,42E-02	0	3,52E-05	7,22E-04
6	rs4519686	SFMBT1	3	T	C	-3,92E+00	3,39E+00	5,50E-02	0	9,02E-05	6,91E-04
6	rs2336670	SFMBT1	3	T	G	-5,08E+00	3,72E+00	2,35E-02	0	3,79E-07	2,01E-04
6	rs9823697	SFMBT1	3	G	A	-5,07E+00	3,60E+00	3,35E-02	0	3,91E-07	3,13E-04
6	rs2245424	SFMBT1	3	G	C	NaN	NaN	2,35E-02	0	3,72E-07	1,91E-04
6	rs6792578	SFMBT1	3	A	G	-3,93E+00	3,40E+00	5,50E-02	0	8,61E-05	6,67E-04
6	rs6768844	SFMBT1	3	T	C	-3,91E+00	3,40E+00	5,50E-02	0	9,28E-05	6,80E-04
6	rs6771610	SFMBT1	3	C	T	-3,89E+00	3,23E+00	8,64E-02	0	9,99E-05	1,24E-03
6	rs2246556	SFMBT1	3	T	C	-4,56E+00	3,13E+00	9,95E-02	0	5,02E-06	1,77E-03
6	rs2564947	SFMBT1	3	C	T	-3,79E+00	3,25E+00	8,64E-02	0	1,48E-04	1,17E-03
6	rs2581780	SFMBT1	3	C	T	-3,80E+00	3,28E+00	7,47E-02	0	1,44E-04	1,05E-03
6	rs17304995	SFMBT1	3	G	A	-4,09E+00	3,14E+00	9,95E-02	0	4,25E-05	1,70E-03
6	rs11915851	SFMBT1	3	A	G	-4,99E+00	3,58E+00	3,35E-02	0	5,97E-07	3,38E-04
6	rs6794389	SFMBT1	3	G	A	-3,95E+00	3,28E+00	7,47E-02	0	7,92E-05	1,06E-03
6	rs6789219	SFMBT1	3	G	C	NaN	NaN	7,47E-02	0	7,22E-05	9,03E-04
7	rs11707890	HFKHLB	3	G	T	-3,84E+00	3,43E+00	5,50E-02	0	1,21E-04	5,94E-04
7	rs7632921	FOXP1	3	T	G	-4,06E+00	3,51E+00	3,97E-02	0	4,89E-05	4,45E-04
7	rs11720523	FOXP1	3	A	C	-4,01E+00	3,51E+00	4,69E-02	0	6,17E-05	4,48E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
7	rs6779258	FOXP1	3	C	T	-4,03E+00	3,46E+00	4,69E-02	0	5,50E-05	5,49E-04
7	rs1392226	FOXP1	3	A	G	-3,98E+00	3,53E+00	3,97E-02	0	7,01E-05	4,23E-04
7	rs9837383	FOXP1	3	C	T	-3,99E+00	3,57E+00	3,97E-02	0	6,63E-05	3,59E-04
7	rs9842406	FOXP1	3	G	T	-4,08E+00	3,58E+00	3,35E-02	1	4,58E-05	3,49E-04
7	rs6780776	FOXP1	3	T	C	-4,03E+00	3,50E+00	4,69E-02	0	5,62E-05	4,59E-04
7	rs17662328	FOXP1	3	A	G	-4,09E+00	3,51E+00	4,69E-02	0	4,25E-05	4,47E-04
7	rs1432611	FOXP1	3	T	G	-4,09E+00	3,49E+00	4,69E-02	0	4,27E-05	4,91E-04
7	rs6803008	FOXP1	3	T	C	-4,12E+00	3,46E+00	4,69E-02	0	3,75E-05	5,36E-04
7	rs6778026	FOXP1	3	A	G	-4,07E+00	3,47E+00	4,69E-02	0	4,60E-05	5,20E-04
7	rs1499895	FOXP1	3	C	T	-3,98E+00	3,46E+00	4,69E-02	0	7,03E-05	5,33E-04
7	rs1499894	FOXP1	3	T	C	-4,11E+00	3,44E+00	5,50E-02	0	3,91E-05	5,72E-04
7	rs7649993	FOXP1	3	G	C	NaN	NaN	5,50E-02	0	5,62E-05	6,51E-04
7	rs6764416	FOXP1	3	T	C	-4,02E+00	3,43E+00	5,50E-02	0	5,78E-05	6,01E-04
7	rs7624274	FOXP1	3	A	T	NaN	NaN	5,50E-02	0	6,43E-05	6,90E-04
7	rs7610856	FOXP1	3	A	C	-4,01E+00	3,48E+00	4,69E-02	0	6,09E-05	5,06E-04
8	rs4543205	NDST3	4	C	A	3,20E+00	-4,46E+00	4,44E-02	0	1,38E-03	8,30E-06
8	rs6848399	NDST3	4	T	C	3,08E+00	-4,47E+00	6,22E-02	0	2,10E-03	7,90E-06
8	rs4487434	NDST3	4	G	A	3,10E+00	-4,48E+00	6,22E-02	0	1,94E-03	7,41E-06
8	rs4560487	NDST3	4	G	A	3,14E+00	-4,51E+00	5,26E-02	0	1,69E-03	6,63E-06
8	rs7680858	NDST3	4	G	A	3,29E+00	-4,49E+00	3,74E-02	0	1,00E-03	7,01E-06
8	rs10461154	NDST3	4	T	C	3,17E+00	-4,50E+00	5,26E-02	0	1,52E-03	6,93E-06
8	rs7673016	NDST3	4	G	A	3,22E+00	-4,41E+00	4,44E-02	0	1,28E-03	1,05E-05
8	rs6834344	NDST3	4	A	G	3,16E+00	-4,51E+00	5,26E-02	0	1,57E-03	6,63E-06
8	rs936891	NDST3	4	A	G	3,22E+00	-4,49E+00	4,44E-02	0	1,27E-03	7,29E-06
8	rs1319937	NDST3	4	G	C	NaN	NaN	6,22E-02	0	2,00E-03	6,04E-06
8	rs11098412	NDST3	4	C	A	3,10E+00	-4,52E+00	6,22E-02	0	1,94E-03	6,31E-06

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
8	rs6534066	NDST3	4	G	A	3,10E+00	-4,07E+00	6,22E-02	0	1,94E-03	4,68E-05
8	rs6534067	NDST3	4	G	C	NaN	NaN	3,15E-02	0	7,51E-04	4,96E-06
8	rs11940384	NDST3	4	A	T	NaN	NaN	5,26E-02	0	1,71E-03	5,46E-06
8	rs6856081	NDST3	4	G	A	3,39E+00	-4,59E+00	2,64E-02	0	6,93E-04	4,48E-06
8	rs6838122	NDST3	4	T	C	3,37E+00	-4,58E+00	3,15E-02	0	7,61E-04	4,69E-06
8	rs6838310	NDST3	4	T	C	3,42E+00	-4,59E+00	2,64E-02	0	6,23E-04	4,43E-06
8	rs2389474	NDST3	4	A	G	3,22E+00	-4,56E+00	4,44E-02	0	1,26E-03	5,03E-06
8	rs4834648	NDST3	4	T	C	3,19E+00	-4,45E+00	4,44E-02	0	1,41E-03	8,51E-06
8	rs6816919	NDST3	4	T	C	3,19E+00	-4,54E+00	5,26E-02	0	1,43E-03	5,50E-06
8	rs11098414	NDST3	4	T	G	3,41E+00	-4,58E+00	2,64E-02	0	6,46E-04	4,62E-06
8	rs10031942	NDST3	4	T	C	3,21E+00	-4,55E+00	4,44E-02	0	1,34E-03	5,36E-06
8	rs6534071	NDST3	4	C	A	3,21E+00	-4,55E+00	4,44E-02	0	1,33E-03	5,41E-06
8	rs11098416	NDST3	4	G	A	3,44E+00	-4,58E+00	2,64E-02	0	5,84E-04	4,75E-06
8	rs2892782	NDST3	4	C	T	3,20E+00	-4,52E+00	4,44E-02	0	1,38E-03	6,31E-06
8	rs7684262	NDST3	4	T	G	3,20E+00	-4,31E+00	4,44E-02	0	1,38E-03	1,62E-05
8	rs6847160	NDST3	4	T	A	NaN	NaN	4,44E-02	0	1,26E-03	7,84E-06
8	rs2389471	NDST3	4	T	C	3,19E+00	-4,46E+00	5,26E-02	0	1,42E-03	8,23E-06
8	rs2389470	NDST3	4	T	A	NaN	NaN	4,44E-02	0	1,25E-03	8,94E-06
8	rs13113939	NDST3	4	G	A	3,42E+00	-4,47E+00	2,64E-02	0	6,26E-04	7,92E-06
8	rs2389467	NDST3	4	G	T	3,35E+00	-4,46E+00	3,15E-02	0	8,06E-04	8,04E-06
8	rs11936756	NDST3	4	G	A	3,11E+00	-4,45E+00	6,22E-02	0	1,85E-03	8,70E-06
8	rs12108300	NDST3	4	T	C	3,27E+00	-4,46E+00	3,74E-02	0	1,06E-03	8,35E-06
8	rs6841411	NDST3	4	T	C	3,13E+00	-4,42E+00	5,26E-02	0	1,77E-03	1,00E-05
8	rs4498201	NDST3	4	T	C	3,33E+00	-4,44E+00	3,15E-02	0	8,56E-04	8,95E-06
8	rs2389464	NDST3	4	A	G	3,38E+00	-4,45E+00	3,15E-02	0	7,26E-04	8,52E-06
8	rs2389463	NDST3	4	A	C	3,42E+00	-4,49E+00	2,64E-02	0	6,37E-04	7,14E-06

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
8	rs4833557	NDST3	4	A	G	3,42E+00	-4,36E+00	2,64E-02	0	6,21E-04	1,30E-05
8	rs4833558	NDST3	4	C	T	3,48E+00	-4,45E+00	2,21E-02	1	4,98E-04	8,42E-06
8	rs4590118	NDST3	4	T	G	3,40E+00	-3,93E+00	2,64E-02	0	6,74E-04	8,37E-05
8	rs12507486	NDST3	4	T	C	3,42E+00	-4,47E+00	2,64E-02	0	6,22E-04	7,82E-06
8	rs6534073	NDST3	4	T	A	NaN	NaN	2,64E-02	0	6,77E-04	6,78E-06
8	rs2892779	NDST3	4	A	C	3,19E+00	-4,49E+00	4,44E-02	0	1,41E-03	7,07E-06
9	rs159369	SMIM15	5	A	G	3,57E+00	-3,28E+00	7,47E-02	0	3,57E-04	1,04E-03
9	rs159366	SMIM15	5	T	C	3,44E+00	-3,21E+00	8,64E-02	0	5,74E-04	1,34E-03
9	rs34618	SMIM15	5	A	C	3,48E+00	-3,20E+00	8,64E-02	0	4,97E-04	1,40E-03
9	rs159363	SMIM15	5	A	G	3,71E+00	-3,17E+00	9,95E-02	0	2,08E-04	1,54E-03
9	rs159361	SMIM15	5	T	C	3,49E+00	-3,19E+00	8,64E-02	0	4,80E-04	1,41E-03
9	rs40506	SMIM15	5	T	C	5,21E+00	-3,28E+00	7,47E-02	0	1,90E-07	1,06E-03
9	rs34628	SMIM15	5	C	A	3,47E+00	-3,21E+00	8,64E-02	0	5,22E-04	1,33E-03
9	rs34627	SMIM15	5	G	A	5,22E+00	-3,27E+00	7,47E-02	0	1,76E-07	1,08E-03
9	rs159360	SMIM15	5	C	A	5,25E+00	-3,27E+00	7,47E-02	0	1,53E-07	1,08E-03
9	rs2055375	SMIM15	5	T	G	5,26E+00	-3,27E+00	7,47E-02	0	1,47E-07	1,09E-03
9	rs7443733	SMIM15	5	T	C	5,21E+00	-3,28E+00	7,47E-02	0	1,92E-07	1,05E-03
9	rs7444594	SMIM15	5	T	G	5,27E+00	-3,29E+00	7,47E-02	0	1,35E-07	1,01E-03
9	rs12516321	ZSWIM6	5	G	A	3,58E+00	-3,17E+00	9,95E-02	0	3,38E-04	1,51E-03
9	rs6868457	ZSWIM6	5	T	C	5,36E+00	-3,34E+00	6,42E-02	0	8,17E-08	8,37E-04
9	rs12523278	ZSWIM6	5	A	G	5,32E+00	-3,28E+00	7,47E-02	0	1,04E-07	1,06E-03
9	rs4352559	ZSWIM6	5	C	T	5,46E+00	-3,50E+00	4,69E-02	0	4,65E-08	4,69E-04
9	rs4546329	ZSWIM6	5	T	C	5,76E+00	-3,70E+00	2,35E-02	0	8,32E-09	2,16E-04
9	rs4391122	ZSWIM6	5	G	A	5,89E+00	-3,86E+00	1,62E-02	1	3,92E-09	1,13E-04
9	rs7701440	ZSWIM6	5	C	T	5,73E+00	-3,65E+00	2,81E-02	0	1,02E-08	2,66E-04
9	rs4700418	ZSWIM6	5	G	C	NaN	NaN	2,81E-02	0	7,14E-08	2,36E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
9	rs6449528	ZSWIM6	5	A	G	5,64E+00	-3,67E+00	2,81E-02	0	1,67E-08	2,40E-04
9	rs4604142	ZSWIM6	5	T	C	5,63E+00	-3,78E+00	1,95E-02	0	1,79E-08	1,57E-04
9	rs7724551	ZSWIM6	5	A	G	5,56E+00	-3,71E+00	2,35E-02	0	2,72E-08	2,07E-04
9	rs13169711	ZSWIM6	5	A	G	5,46E+00	-3,65E+00	2,81E-02	0	4,69E-08	2,60E-04
9	rs7734879	ZSWIM6	5	A	C	4,17E+00	-3,26E+00	8,64E-02	0	2,99E-05	1,13E-03
9	rs6449531	ZSWIM6	5	A	G	4,19E+00	-3,26E+00	8,64E-02	0	2,75E-05	1,12E-03
9	rs6449532	ZSWIM6	5	T	C	4,12E+00	-3,26E+00	7,47E-02	0	3,75E-05	1,11E-03
9	rs6894675	ZSWIM6	5	C	G	NaN	NaN	8,64E-02	0	3,77E-05	1,14E-03
9	rs6449533	ZSWIM6	5	C	T	4,24E+00	-3,20E+00	8,64E-02	0	2,26E-05	1,37E-03
9	rs10939902	ZSWIM6	5	C	T	5,56E+00	-3,37E+00	6,42E-02	0	2,65E-08	7,43E-04
9	rs6885005	ZSWIM6	5	A	T	NaN	NaN	8,64E-02	0	3,58E-05	1,19E-03
9	rs7709645	ZSWIM6	5	C	G	NaN	NaN	4,69E-02	0	2,50E-08	4,80E-04
9	rs7714712	ZSWIM6	5	A	C	4,08E+00	-3,27E+00	7,47E-02	0	4,46E-05	1,09E-03
9	rs7720894	ZSWIM6	5	C	G	NaN	NaN	6,42E-02	0	4,32E-07	7,77E-04
10	rs12521503	SSBP2	5	T	C	3,52E+00	3,61E+00	3,35E-02	1	4,32E-04	3,09E-04
10	rs458430	SSBP2	5	C	T	3,12E+00	3,66E+00	6,22E-02	0	1,82E-03	2,54E-04
10	rs378482	SSBP2	5	C	T	3,47E+00	3,62E+00	3,35E-02	0	5,24E-04	2,92E-04
10	rs401996	SSBP2	5	T	C	3,39E+00	3,27E+00	7,47E-02	0	6,92E-04	1,06E-03
10	rs384075	SSBP2	5	G	T	3,39E+00	3,26E+00	8,64E-02	0	7,11E-04	1,13E-03
10	rs391229	SSBP2	5	G	A	3,36E+00	3,37E+00	6,42E-02	0	7,79E-04	7,55E-04
10	rs456778	SSBP2	5	A	C	3,20E+00	3,41E+00	6,18E-02	0	1,39E-03	6,39E-04
10	rs463247	SSBP2	5	A	C	3,19E+00	3,41E+00	6,95E-02	0	1,41E-03	6,49E-04
10	rs457700	SSBP2	5	A	T	NaN	NaN	6,18E-02	0	1,36E-03	6,88E-04
10	rs386424	SSBP2	5	G	T	3,18E+00	3,41E+00	6,95E-02	0	1,49E-03	6,41E-04
10	rs462122	SSBP2	5	A	G	3,18E+00	3,49E+00	5,97E-02	0	1,47E-03	4,87E-04
11	rs6914964	SRF	6	G	A	-3,06E+00	3,39E+00	7,82E-02	0	2,19E-03	6,97E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
11	rs17209365	CUL9	6	G	A	-3,14E+00	3,29E+00	9,27E-02	0	1,68E-03	9,99E-04
11	rs16896344	CUL9	6	A	G	-3,32E+00	3,33E+00	6,42E-02	1	9,07E-04	8,75E-04
12	rs4727614	BC061919	7	A	C	4,69E+00	-3,24E+00	8,64E-02	0	2,72E-06	1,19E-03
12	rs6965384	LHFPL3	7	G	A	4,67E+00	-3,22E+00	8,64E-02	0	3,00E-06	1,29E-03
12	rs7776707	LHFPL3	7	A	C	4,72E+00	-3,20E+00	8,64E-02	0	2,41E-06	1,39E-03
12	rs3823752	CR591034	7	T	C	4,70E+00	-3,30E+00	7,47E-02	0	2,60E-06	9,56E-04
12	rs6948885	KMT2E	7	T	C	4,66E+00	-3,19E+00	9,95E-02	0	3,20E-06	1,42E-03
12	rs10953468	KMT2E	7	T	A	NaN	NaN	8,64E-02	0	3,61E-06	1,40E-03
12	rs6967587	KMT2E	7	T	C	4,64E+00	-3,19E+00	8,64E-02	0	3,56E-06	1,41E-03
12	rs1142	SRPK2	7	T	C	4,12E+00	-3,21E+00	8,64E-02	0	3,76E-05	1,35E-03
12	rs1144	SRPK2	7	C	T	3,96E+00	-3,22E+00	8,64E-02	0	7,54E-05	1,28E-03
12	rs7797912	SRPK2	7	C	T	4,61E+00	-3,19E+00	9,95E-02	0	4,04E-06	1,43E-03
12	rs2299304	SRPK2	7	C	T	4,55E+00	-3,27E+00	7,47E-02	0	5,44E-06	1,07E-03
12	rs10487150	SRPK2	7	C	A	4,78E+00	-3,40E+00	5,50E-02	0	1,74E-06	6,84E-04
12	rs10238507	SRPK2	7	C	A	4,82E+00	-3,31E+00	7,47E-02	0	1,45E-06	9,38E-04
12	rs10266871	SRPK2	7	A	G	4,74E+00	-3,26E+00	7,47E-02	0	2,12E-06	1,10E-03
12	rs3779210	SRPK2	7	T	C	4,63E+00	-3,28E+00	7,47E-02	0	3,71E-06	1,03E-03
12	rs4730072	SRPK2	7	T	A	NaN	NaN	7,47E-02	0	2,91E-06	9,59E-04
12	rs10277120	SRPK2	7	A	T	NaN	NaN	5,50E-02	0	3,37E-06	6,68E-04
12	rs2240463	SRPK2	7	T	C	4,70E+00	-3,33E+00	6,42E-02	0	2,65E-06	8,76E-04
12	rs10281422	SRPK2	7	A	G	4,69E+00	-3,33E+00	6,42E-02	0	2,68E-06	8,67E-04
12	rs41562	SRPK2	7	C	T	4,71E+00	-3,32E+00	6,42E-02	0	2,47E-06	8,88E-04
12	rs2237613	SRPK2	7	C	G	NaN	NaN	7,47E-02	0	2,56E-06	9,20E-04
12	rs41563	SRPK2	7	A	G	4,89E+00	-3,33E+00	6,42E-02	0	9,84E-07	8,66E-04
12	rs4730073	SRPK2	7	C	A	4,75E+00	-3,24E+00	8,64E-02	0	2,03E-06	1,18E-03
12	rs10953470	SRPK2	7	G	T	4,86E+00	-3,18E+00	9,95E-02	0	1,20E-06	1,48E-03

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
12	rs2299319	SRPK2	7	T	C	4,86E+00	-3,18E+00	9,95E-02	0	1,17E-06	1,48E-03
12	rs3801282	SRPK2	7	A	G	4,83E+00	-3,15E+00	9,95E-02	0	1,35E-06	1,61E-03
12	rs3801281	SRPK2	7	T	C	4,86E+00	-3,13E+00	9,95E-02	0	1,19E-06	1,77E-03
12	rs6466056	SRPK2	7	T	C	4,95E+00	-3,18E+00	9,95E-02	0	7,49E-07	1,49E-03
12	rs2057883	SRPK2	7	C	G	NaN	NaN	9,95E-02	0	8,80E-07	1,49E-03
12	rs2057884	SRPK2	7	T	C	4,87E+00	-3,17E+00	9,95E-02	0	1,14E-06	1,51E-03
12	rs10241415	SRPK2	7	A	G	4,86E+00	-3,24E+00	8,64E-02	0	1,19E-06	1,20E-03
12	rs6466057	SRPK2	7	T	C	4,68E+00	-3,20E+00	8,64E-02	0	2,87E-06	1,39E-03
12	rs1204056	SRPK2	7	G	A	4,67E+00	-3,18E+00	9,95E-02	0	3,06E-06	1,45E-03
12	rs1204058	SRPK2	7	T	G	4,69E+00	-3,20E+00	8,64E-02	0	2,80E-06	1,39E-03
12	rs12334245	SRPK2	7	C	T	4,52E+00	-3,29E+00	7,47E-02	0	6,16E-06	1,00E-03
12	rs2030776	SRPK2	7	G	C	NaN	NaN	7,47E-02	0	2,75E-06	9,33E-04
12	rs7357199	SRPK2	7	C	G	NaN	NaN	7,47E-02	0	2,71E-06	9,82E-04
12	rs6466064	SRPK2	7	C	T	4,75E+00	-3,35E+00	6,42E-02	0	2,05E-06	8,14E-04
12	rs3801999	SRPK2	7	G	A	4,64E+00	-3,37E+00	6,42E-02	0	3,55E-06	7,40E-04
12	rs3847071	SRPK2	7	A	T	NaN	NaN	3,97E-02	0	1,42E-05	3,91E-04
12	rs4266584	SRPK2	7	A	C	4,07E+00	-3,62E+00	3,35E-02	1	4,66E-05	2,96E-04
12	rs4282505	SRPK2	7	A	G	4,26E+00	-3,55E+00	3,97E-02	0	2,08E-05	3,90E-04
13	rs717349	MED30	8	C	T	-3,33E+00	3,13E+00	9,95E-02	1	8,65E-04	1,77E-03
13	rs17740505	MED30	8	C	A	-3,32E+00	3,14E+00	9,95E-02	0	9,14E-04	1,70E-03
14	rs4976976	TSNARE1	8	A	G	-5,33E+00	3,26E+00	7,47E-02	1	9,58E-08	1,12E-03
15	rs12253987	NEURL	10	A	T	NaN	NaN	4,69E-02	1	9,31E-04	4,51E-04
16	rs11030380	METTL15	11	A	T	NaN	NaN	5,26E-02	0	1,41E-03	5,84E-05
16	rs2582895	METTL15	11	A	C	-3,27E+00	3,45E+00	4,69E-02	0	1,07E-03	5,61E-04
16	rs2585817	METTL15	11	G	A	-3,27E+00	3,44E+00	5,50E-02	0	1,07E-03	5,82E-04
16	rs11030382	METTL15	11	T	C	-3,34E+00	3,44E+00	5,50E-02	0	8,52E-04	5,91E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
16	rs7952220	METTL15	11	C	T	-3,30E+00	3,39E+00	5,50E-02	0	9,57E-04	6,95E-04
16	rs4378371	METTL15	11	G	C	NaN	NaN	6,18E-02	0	1,19E-03	6,87E-04
16	rs4520584	METTL15	11	A	G	-3,26E+00	3,39E+00	5,50E-02	0	1,10E-03	7,05E-04
16	rs2585813	METTL15	11	T	A	NaN	NaN	7,19E-02	0	1,15E-03	7,62E-04
16	rs2582897	METTL15	11	C	T	-3,27E+00	3,23E+00	8,64E-02	0	1,09E-03	1,24E-03
16	rs2585811	METTL15	11	A	G	-3,26E+00	3,38E+00	6,42E-02	0	1,10E-03	7,33E-04
16	rs11030384	METTL15	11	T	A	NaN	NaN	9,27E-02	0	1,58E-03	9,44E-04
16	rs4442537	METTL15	11	T	C	-3,23E+00	3,31E+00	8,32E-02	0	1,25E-03	9,26E-04
16	rs10835362	METTL15	11	A	G	-3,22E+00	3,37E+00	7,19E-02	0	1,27E-03	7,56E-04
16	rs10835363	METTL15	11	C	T	-3,21E+00	3,31E+00	8,32E-02	0	1,31E-03	9,46E-04
16	rs11030385	METTL15	11	A	G	-3,25E+00	3,31E+00	8,32E-02	0	1,14E-03	9,24E-04
16	rs10835365	METTL15	11	G	A	-3,20E+00	3,32E+00	8,32E-02	0	1,37E-03	9,15E-04
16	rs11821132	METTL15	11	G	T	-3,15E+00	3,32E+00	9,27E-02	0	1,62E-03	9,08E-04
16	rs12226610	METTL15	11	C	G	NaN	NaN	8,32E-02	0	1,21E-03	9,33E-04
16	rs11030386	METTL15	11	A	C	-3,24E+00	3,31E+00	8,32E-02	0	1,18E-03	9,29E-04
16	rs11030387	METTL15	11	T	C	-3,22E+00	3,31E+00	8,32E-02	0	1,29E-03	9,32E-04
16	rs10767729	METTL15	11	T	C	-3,21E+00	3,31E+00	8,32E-02	0	1,35E-03	9,27E-04
16	rs4923549	METTL15	11	G	A	-3,24E+00	3,33E+00	7,19E-02	0	1,17E-03	8,84E-04
16	rs10767733	METTL15	11	A	G	-3,33E+00	3,33E+00	6,42E-02	0	8,74E-04	8,81E-04
16	rs10767734	METTL15	11	T	C	-3,47E+00	3,58E+00	3,35E-02	1	5,21E-04	3,49E-04
17	rs11062161	CACNA1C	12	C	T	6,09E+00	-3,15E+00	9,95E-02	0	1,12E-09	1,63E-03
17	rs2239030	CACNA1C	12	A	G	5,84E+00	-3,15E+00	9,95E-02	0	5,25E-09	1,65E-03
17	rs2283291	CACNA1C	12	A	G	5,86E+00	-3,15E+00	9,95E-02	0	4,74E-09	1,61E-03
17	rs3794297	CACNA1C	12	T	C	5,96E+00	-3,16E+00	9,95E-02	0	2,52E-09	1,56E-03
17	rs882195	CACNA1C	12	C	G	NaN	NaN	4,69E-02	0	1,11E-09	4,71E-04
17	rs882194	CACNA1C	12	G	A	5,95E+00	-3,22E+00	8,64E-02	0	2,64E-09	1,30E-03

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
17	rs2239038	CACNA1C	12	A	G	6,43E+00	-3,29E+00	7,47E-02	0	1,29E-10	9,88E-04
17	rs2238057	CACNA1C	12	G	T	6,46E+00	-3,66E+00	2,81E-02	1	1,02E-10	2,50E-04
17	rs1860002	CACNA1C	12	C	T	6,76E+00	-3,46E+00	4,69E-02	0	1,35E-11	5,38E-04
18	rs3783300	PRKD1	14	A	C	3,54E+00	-3,18E+00	9,95E-02	0	4,02E-04	1,46E-03
18	rs3783301	PRKD1	14	T	G	3,50E+00	-3,17E+00	9,95E-02	0	4,59E-04	1,51E-03
18	rs1108732	PRKD1	14	T	C	3,55E+00	-3,13E+00	9,95E-02	0	3,87E-04	1,72E-03
18	rs7158279	PRKD1	14	G	A	3,45E+00	-3,26E+00	7,47E-02	1	5,67E-04	1,10E-03
18	rs2333613	PRKD1	14	C	T	3,56E+00	-3,18E+00	9,95E-02	0	3,74E-04	1,48E-03
18	rs1959440	PRKD1	14	T	G	4,03E+00	-3,27E+00	7,47E-02	0	5,47E-05	1,06E-03
19	rs2239647	AKAP6	14	A	C	3,49E+00	-4,43E+00	2,21E-02	0	4,89E-04	9,40E-06
19	rs1051695	AKAP6	14	A	G	3,09E+00	-4,06E+00	6,22E-02	0	2,02E-03	4,81E-05
19	rs2300861	AKAP6	14	C	T	3,22E+00	-4,14E+00	4,44E-02	0	1,26E-03	3,54E-05
19	rs2143975	AKAP6	14	C	G	NaN	NaN	8,65E-02	0	3,18E-03	2,44E-06
19	rs10145461	AKAP6	14	T	G	-2,92E+00	4,31E+00	8,65E-02	0	3,52E-03	1,63E-05
19	rs17522122	AKAP6	14	T	G	3,41E+00	-5,21E+00	2,64E-02	0	6,57E-04	1,87E-07
19	rs12879159	AKAP6	14	A	G	3,52E+00	-4,96E+00	1,84E-02	1	4,27E-04	6,98E-07
19	rs12882859	AKAP6	14	T	A	NaN	NaN	1,84E-02	0	4,17E-04	7,68E-07
19	rs7146265	AKAP6	14	A	G	3,50E+00	-4,96E+00	2,21E-02	0	4,69E-04	7,08E-07
19	rs7145828	AKAP6	14	G	A	3,51E+00	-4,96E+00	2,21E-02	0	4,52E-04	7,02E-07
19	rs12885467	AKAP6	14	C	T	3,57E+00	-5,09E+00	1,84E-02	0	3,59E-04	3,58E-07
19	rs11623122	AKAP6	14	A	G	3,49E+00	-4,97E+00	2,21E-02	0	4,79E-04	6,72E-07
19	rs11623135	AKAP6	14	T	C	3,49E+00	-4,84E+00	2,21E-02	0	4,84E-04	1,29E-06
19	rs12894779	AKAP6	14	A	G	3,54E+00	-4,97E+00	1,84E-02	0	3,97E-04	6,83E-07
19	rs12894833	AKAP6	14	G	C	NaN	NaN	2,21E-02	0	4,77E-04	6,63E-07
19	rs12895330	AKAP6	14	C	G	NaN	NaN	6,22E-02	0	2,15E-03	9,68E-07
19	rs12896446	AKAP6	14	G	T	3,47E+00	-4,87E+00	2,21E-02	0	5,14E-04	1,14E-06

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
20	rs689767	TP53BP1	15	C	G	NaN	NaN	9,58E-02	0	1,37E-03	1,35E-03
20	rs2602141	TP53BP1	15	G	T	-3,20E+00	3,20E+00	9,58E-02	0	1,37E-03	1,37E-03
20	rs536313	TP53BP1	15	T	C	-3,22E+00	3,19E+00	9,58E-02	0	1,29E-03	1,41E-03
20	rs2244981	TP53BP1	15	C	T	-3,21E+00	3,21E+00	9,58E-02	0	1,32E-03	1,34E-03
20	rs493377	TP53BP1	15	T	C	-3,23E+00	3,22E+00	9,58E-02	0	1,22E-03	1,26E-03
20	rs1079309	TP53BP1	15	A	C	-3,36E+00	3,23E+00	8,64E-02	0	7,79E-04	1,25E-03
20	rs2927071	CATSPER2	15	C	T	-3,25E+00	3,27E+00	8,32E-02	0	1,14E-03	1,07E-03
20	rs11070410	PDIA3	15	A	G	-3,27E+00	3,23E+00	8,64E-02	0	1,08E-03	1,22E-03
20	rs686666	WDR76	15	A	G	-3,20E+00	3,26E+00	8,32E-02	0	1,35E-03	1,11E-03
20	rs667476	FRMD5	15	C	A	-3,21E+00	3,40E+00	6,18E-02	0	1,33E-03	6,75E-04
20	rs524908	FRMD5	15	C	A	-3,24E+00	3,56E+00	4,50E-02	1	1,20E-03	3,70E-04
21	rs7167194	CHD2	15	C	A	2,98E+00	-3,41E+00	9,93E-02	1	2,86E-03	6,57E-04
22	rs199504	WNT3	17	C	T	-2,96E+00	-3,61E+00	8,65E-02	1	3,10E-03	3,06E-04
22	rs199500	WNT3	17	T	C	-3,21E+00	-3,21E+00	9,58E-02	0	1,31E-03	1,33E-03
23	rs7259683	SCAF1	19	C	T	-3,77E+00	3,13E+00	9,95E-02	1	1,66E-04	1,75E-03
24	rs5996092	WBP2NL	22	G	A	-3,25E+00	3,53E+00	4,50E-02	0	1,16E-03	4,17E-04
24	rs5996094	WBP2NL	22	C	T	-3,28E+00	3,66E+00	3,74E-02	0	1,02E-03	2,53E-04
24	rs6002561	WBP2NL	22	G	A	-3,28E+00	3,68E+00	3,74E-02	0	1,05E-03	2,30E-04
24	rs5751191	WBP2NL	22	T	C	-4,69E+00	3,51E+00	3,97E-02	0	2,70E-06	4,45E-04
24	rs5758527	WBP2NL	22	G	T	4,27E+00	-3,73E+00	2,35E-02	0	1,98E-05	1,89E-04
24	rs6519301	WBP2NL	22	G	A	4,32E+00	-3,77E+00	1,95E-02	0	1,53E-05	1,65E-04
24	rs133300	WBP2NL	22	G	A	4,28E+00	-3,76E+00	1,95E-02	0	1,84E-05	1,70E-04
24	rs133301	WBP2NL	22	T	C	4,29E+00	-3,77E+00	1,95E-02	0	1,79E-05	1,64E-04
24	rs133303	WBP2NL	22	G	C	NaN	NaN	1,95E-02	0	2,51E-05	1,76E-04
24	rs133305	WBP2NL	22	T	C	4,31E+00	-3,75E+00	1,95E-02	0	1,65E-05	1,74E-04
24	rs133306	WBP2NL	22	A	G	4,31E+00	-3,75E+00	1,95E-02	0	1,66E-05	1,76E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
24	rs5758537	WBP2NL	22	T	G	4,31E+00	-3,76E+00	1,95E-02	0	1,67E-05	1,72E-04
24	rs129856	WBP2NL	22	G	C	NaN	NaN	1,95E-02	0	1,80E-05	1,74E-04
24	rs129857	WBP2NL	22	C	T	4,29E+00	-3,76E+00	1,95E-02	0	1,81E-05	1,71E-04
24	rs133330	WBP2NL	22	A	G	4,31E+00	-3,74E+00	2,35E-02	0	1,65E-05	1,84E-04
24	rs133335	WBP2NL	22	G	A	4,38E+00	-3,67E+00	2,81E-02	0	1,16E-05	2,44E-04
24	rs133340	WBP2NL	22	A	T	NaN	NaN	2,35E-02	0	1,77E-05	1,82E-04
24	rs133349	WBP2NL	22	T	A	NaN	NaN	2,35E-02	0	1,42E-05	2,03E-04
24	rs1063392	NAGA	22	G	A	4,26E+00	-3,82E+00	1,62E-02	0	2,02E-05	1,32E-04
24	rs133373	NAGA	22	A	G	3,89E+00	-3,94E+00	1,09E-02	0	1,00E-04	8,17E-05
24	rs7245	NDUFA6	22	G	A	4,07E+00	-3,87E+00	1,33E-02	0	4,66E-05	1,10E-04
24	rs2284087	NDUFA6	22	T	C	3,98E+00	-3,85E+00	1,62E-02	0	6,84E-05	1,17E-04
24	rs5751216	NDUFA6	22	G	T	3,93E+00	-3,85E+00	1,62E-02	0	8,46E-05	1,20E-04
24	rs6002626	NDUFA6	22	C	G	NaN	NaN	1,62E-02	0	4,80E-05	1,27E-04
24	rs5758589	NDUFA6	22	A	G	3,97E+00	-3,86E+00	1,62E-02	0	7,22E-05	1,13E-04
24	rs2142694	CYP2D6	22	A	G	4,40E+00	-3,89E+00	1,33E-02	0	1,09E-05	1,02E-04
24	rs742089	TCF20	22	A	G	4,12E+00	-3,48E+00	4,69E-02	0	3,82E-05	4,92E-04
24	rs5758645	TCF20	22	G	T	4,28E+00	-4,24E+00	3,13E-03	0	1,88E-05	2,21E-05
24	rs5758653	TCF20	22	T	G	4,70E+00	-4,45E+00	1,31E-03	0	2,54E-06	8,46E-06
24	rs5758659	TCF20	22	T	C	4,80E+00	-4,58E+00	8,39E-04	1	1,55E-06	4,74E-06
24	rs5758660	TCF20	22	A	C	4,76E+00	-4,47E+00	1,31E-03	0	1,98E-06	7,66E-06
24	rs5758670	TCF20	22	C	T	4,57E+00	-4,32E+00	2,52E-03	0	4,93E-06	1,57E-05
24	rs5751250	LOC388906	22	G	T	4,55E+00	-4,33E+00	2,52E-03	0	5,39E-06	1,47E-05
24	rs5751255	LOC388906	22	T	C	4,75E+00	-4,47E+00	1,31E-03	0	2,05E-06	7,78E-06
24	rs134873	LOC388906	22	G	T	5,01E+00	-4,43E+00	1,63E-03	0	5,53E-07	9,42E-06
24	rs134877	LOC388906	22	T	C	4,84E+00	-4,43E+00	1,63E-03	0	1,28E-06	9,57E-06
24	rs134900	LOC388906	22	C	G	NaN	NaN	1,31E-03	0	1,08E-06	7,20E-06

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG CHARGE	conjFDR	prune	p SCZ	p COG CHARGE
24	rs134902	LOC388906	22	A	G	4,86E+00	-4,52E+00	1,05E-03	0	1,17E-06	6,19E-06
24	rs80506	LOC388906	22	A	T	NaN	NaN	3,13E-03	0	1,62E-06	1,92E-05

eTable 3B. Loci with conjFDR<.10 associated with SCZ and COG COGENT

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score COG COGENT	conjFDR	prune	p SCZ	p COG COGENT
1	rs10189857	BCL11A	2	G	A	-3,91E+00	-3,60E+00	7,17E-02	1	9,41E-05	3,21E-04
***2**	rs3021303	HLA-DRB5	6	T	G	-4,20E+00	3,52E+00	8,65E-02	1	2,64E-05	4,27E-04
3	rs10106136	KCNV1	8	T	A	NaN	NaN	8,65E-02	0	2,83E-05	4,07E-04
3	rs10103911	KCNV1	8	C	T	4,21E+00	-3,52E+00	8,65E-02	0	2,51E-05	4,38E-04
3	rs62526783	KCNV1	8	A	G	5,15E+00	-3,61E+00	7,17E-02	1	2,56E-07	3,06E-04
4	rs7096655	BC032914	10	T	C	3,70E+00	3,54E+00	8,65E-02	1	2,14E-04	3,95E-04
4	rs7920501	BC032914	10	A	T	NaN	NaN	8,69E-02	0	2,78E-04	3,17E-04
4	rs1317707	BC032914	10	G	A	3,67E+00	3,51E+00	8,69E-02	0	2,47E-04	4,45E-04
4	rs7900126	BC032914	10	G	A	3,66E+00	3,60E+00	8,69E-02	0	2,56E-04	3,18E-04
4	rs10905650	BC032914	10	A	G	3,66E+00	3,60E+00	8,69E-02	0	2,54E-04	3,22E-04
4	rs7912446	BC032914	10	G	A	3,65E+00	3,57E+00	8,69E-02	0	2,61E-04	3,53E-04
4	rs11256437	BC032914	10	T	C	3,68E+00	3,52E+00	8,69E-02	0	2,36E-04	4,37E-04

eTable 3C. Loci with conjFDR<.10 associated with SCZ and VNR

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
1	rs4660731	TIE1	1	G	A	3,59E+00	-3,40E+00	8,26E-02	0	3,36E-04	6,79E-04
1	rs2782651	HYI	1	C	G	NaN	NaN	8,88E-02	0	3,90E-04	4,14E-04
1	rs1964952	HYI	1	A	G	3,59E+00	-3,52E+00	7,41E-02	1	3,35E-04	4,36E-04
1	rs11210887	PTPRF	1	G	A	4,74E+00	-3,36E+00	9,69E-02	0	2,10E-06	7,71E-04
1	rs549845	PTPRF	1	G	A	4,77E+00	-3,35E+00	9,69E-02	0	1,82E-06	8,13E-04
2	rs13126505	BANK1	4	A	G	4,52E+00	-3,89E+00	1,82E-02	0	6,27E-06	1,01E-04
2	rs13109404	BANK1	4	G	T	4,53E+00	-3,92E+00	1,47E-02	0	5,81E-06	8,87E-05
2	rs13127398	BANK1	4	A	T	NaN	NaN	1,19E-02	0	4,13E-06	6,98E-05
2	rs34592089	BANK1	4	A	G	4,72E+00	-3,61E+00	4,90E-02	0	2,35E-06	3,09E-04
2	rs1813006	BANK1	4	T	G	4,72E+00	-3,92E+00	1,47E-02	0	2,38E-06	8,79E-05
2	rs13101632	BANK1	4	A	G	3,96E+00	-3,54E+00	5,87E-02	0	7,63E-05	3,96E-04
2	rs35225200	SLC39A8	4	C	A	5,60E+00	-3,88E+00	1,82E-02	0	2,13E-08	1,03E-04
2	rs35518360	SLC39A8	4	T	A	NaN	NaN	1,82E-02	0	2,13E-08	1,02E-04
2	rs13107325	SLC39A8	4	T	C	5,51E+00	-4,38E+00	2,47E-03	1	3,52E-08	1,17E-05
2	rs13135092	SLC39A8	4	G	A	5,42E+00	-3,63E+00	4,90E-02	0	6,04E-08	2,86E-04
3	rs4946935	FOXO3	6	A	G	4,31E+00	-3,36E+00	9,69E-02	1	1,67E-05	7,86E-04
4	rs9611554	KIAA1031	22	G	C	NaN	NaN	5,87E-02	1	1,91E-04	3,98E-04
5	rs5758487	WBP2NL	22	T	C	-3,87E+00	4,75E+00	2,81E-02	0	1,08E-04	2,01E-06
5	rs9607850	WBP2NL	22	T	C	3,83E+00	-5,02E+00	3,43E-02	0	1,26E-04	5,24E-07
5	rs7288838	WBP2NL	22	C	T	3,64E+00	-5,01E+00	6,15E-02	0	2,76E-04	5,42E-07
5	rs4822076	WBP2NL	22	C	T	-4,07E+00	3,53E+00	5,87E-02	0	4,63E-05	4,12E-04
5	rs6519298	WBP2NL	22	T	C	4,21E+00	-5,92E+00	8,00E-03	0	2,54E-05	3,17E-09
5	rs739292	WBP2NL	22	A	G	4,07E+00	-5,98E+00	1,51E-02	0	4,69E-05	2,28E-09
5	rs5751191	WBP2NL	22	T	C	-4,69E+00	5,52E+00	9,13E-04	0	2,70E-06	3,30E-08
5	rs5758527	WBP2NL	22	G	T	4,27E+00	-5,93E+00	6,46E-03	0	1,98E-05	3,11E-09

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs5751195	WBP2NL	22	C	A	4,30E+00	-5,95E+00	5,21E-03	0	1,72E-05	2,76E-09
5	rs739294	WBP2NL	22	C	T	3,72E+00	-5,42E+00	5,08E-02	0	1,95E-04	6,02E-08
5	rs133292	WBP2NL	22	A	G	4,72E+00	-5,98E+00	9,13E-04	0	2,41E-06	2,20E-09
5	rs133293	WBP2NL	22	A	G	4,43E+00	-5,93E+00	3,38E-03	0	9,22E-06	3,07E-09
5	rs133294	WBP2NL	22	T	C	4,32E+00	-5,95E+00	5,21E-03	0	1,59E-05	2,61E-09
5	rs6519301	WBP2NL	22	G	A	4,32E+00	-5,99E+00	5,21E-03	0	1,53E-05	2,10E-09
5	rs133300	WBP2NL	22	G	A	4,28E+00	-6,02E+00	6,46E-03	0	1,84E-05	1,70E-09
5	rs133301	WBP2NL	22	T	C	4,29E+00	-5,96E+00	6,46E-03	0	1,79E-05	2,47E-09
5	rs133303	WBP2NL	22	G	C	NaN	NaN	8,00E-03	0	2,51E-05	1,85E-09
5	rs133305	WBP2NL	22	T	C	4,31E+00	-6,02E+00	5,21E-03	0	1,65E-05	1,79E-09
5	rs133306	WBP2NL	22	A	G	4,31E+00	-6,01E+00	5,21E-03	0	1,66E-05	1,85E-09
5	rs133307	WBP2NL	22	A	C	4,30E+00	-6,04E+00	5,21E-03	0	1,67E-05	1,59E-09
5	rs5758537	WBP2NL	22	T	G	4,31E+00	-6,04E+00	5,21E-03	0	1,67E-05	1,59E-09
5	rs129855	WBP2NL	22	A	G	4,30E+00	-6,04E+00	5,21E-03	0	1,75E-05	1,58E-09
5	rs129856	WBP2NL	22	G	C	NaN	NaN	6,46E-03	0	1,80E-05	1,64E-09
5	rs129857	WBP2NL	22	C	T	4,29E+00	-6,04E+00	6,46E-03	0	1,81E-05	1,58E-09
5	rs6002571	WBP2NL	22	A	G	4,29E+00	-6,04E+00	6,46E-03	0	1,82E-05	1,58E-09
5	rs133313	WBP2NL	22	T	G	4,28E+00	-6,06E+00	6,46E-03	0	1,87E-05	1,40E-09
5	rs133314	WBP2NL	22	A	G	4,28E+00	-6,03E+00	6,46E-03	0	1,87E-05	1,61E-09
5	rs133317	WBP2NL	22	A	G	3,58E+00	-5,48E+00	7,41E-02	0	3,40E-04	4,29E-08
5	rs133318	WBP2NL	22	A	G	4,37E+00	-6,05E+00	4,20E-03	0	1,25E-05	1,46E-09
5	rs133321	WBP2NL	22	G	A	4,30E+00	-6,03E+00	5,21E-03	0	1,72E-05	1,63E-09
5	rs133322	WBP2NL	22	G	A	4,30E+00	-6,16E+00	5,21E-03	0	1,72E-05	7,28E-10
5	rs133323	WBP2NL	22	C	T	4,31E+00	-6,05E+00	5,21E-03	0	1,65E-05	1,49E-09
5	rs133324	WBP2NL	22	A	C	4,30E+00	-6,02E+00	5,21E-03	0	1,71E-05	1,76E-09
5	rs133325	WBP2NL	22	A	G	4,30E+00	-6,00E+00	5,21E-03	0	1,74E-05	1,96E-09

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs133326	WBP2NL	22	A	G	4,31E+00	-6,02E+00	5,21E-03	0	1,65E-05	1,72E-09
5	rs133327	WBP2NL	22	C	T	4,31E+00	-6,03E+00	5,21E-03	0	1,61E-05	1,64E-09
5	rs133328	WBP2NL	22	C	T	4,30E+00	-6,03E+00	5,21E-03	0	1,68E-05	1,62E-09
5	rs133330	WBP2NL	22	A	G	4,31E+00	-6,01E+00	5,21E-03	0	1,65E-05	1,83E-09
5	rs133335	WBP2NL	22	G	A	4,38E+00	-6,09E+00	4,20E-03	0	1,16E-05	1,10E-09
5	rs133336	WBP2NL	22	T	C	4,29E+00	-6,04E+00	6,46E-03	0	1,81E-05	1,58E-09
5	rs133339	WBP2NL	22	G	A	4,42E+00	-6,15E+00	3,38E-03	0	9,96E-06	7,77E-10
5	rs133340	WBP2NL	22	A	T	NaN	NaN	5,21E-03	0	1,77E-05	1,50E-09
5	rs133346	WBP2NL	22	T	G	4,36E+00	-6,04E+00	4,20E-03	0	1,28E-05	1,58E-09
5	rs2301521	WBP2NL	22	G	C	NaN	NaN	2,47E-03	0	6,08E-06	1,30E-05
5	rs133347	WBP2NL	22	T	A	NaN	NaN	4,20E-03	0	1,36E-05	1,41E-09
5	rs133348	WBP2NL	22	T	C	4,05E+00	-6,08E+00	1,51E-02	0	5,10E-05	1,22E-09
5	rs133349	WBP2NL	22	T	A	NaN	NaN	5,21E-03	0	1,42E-05	1,43E-09
5	rs133350	WBP2NL	22	A	G	-4,50E+00	4,32E+00	3,11E-03	0	6,82E-06	1,55E-05
5	rs133351	WBP2NL	22	T	G	3,63E+00	-5,50E+00	7,41E-02	0	2,83E-04	3,76E-08
5	rs5758553	WBP2NL	22	A	G	4,35E+00	-6,03E+00	4,20E-03	0	1,39E-05	1,63E-09
5	rs5751204	WBP2NL	22	C	T	-4,53E+00	4,20E+00	4,90E-03	0	5,82E-06	2,70E-05
5	rs133352	WBP2NL	22	C	A	-4,41E+00	4,09E+00	7,67E-03	0	1,04E-05	4,27E-05
5	rs4822084	WBP2NL	22	T	C	4,38E+00	-6,06E+00	4,20E-03	0	1,20E-05	1,36E-09
5	rs133353	WBP2NL	22	G	A	-4,33E+00	4,10E+00	7,67E-03	0	1,48E-05	4,15E-05
5	rs133355	WBP2NL	22	G	A	-4,43E+00	4,22E+00	4,90E-03	0	9,21E-06	2,47E-05
5	rs133356	WBP2NL	22	G	A	-4,51E+00	4,21E+00	4,90E-03	0	6,39E-06	2,58E-05
5	rs6002586	WBP2NL	22	T	C	-4,54E+00	4,32E+00	3,11E-03	0	5,72E-06	1,53E-05
5	rs133357	WBP2NL	22	T	C	4,25E+00	-6,05E+00	6,46E-03	0	2,16E-05	1,46E-09
5	rs133358	WBP2NL	22	T	A	NaN	NaN	6,46E-03	0	1,85E-05	1,34E-09
5	rs34277770	WBP2NL	22	G	A	3,66E+00	-5,51E+00	6,15E-02	0	2,50E-04	3,64E-08

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs5758559	WBP2NL	22	G	A	-4,70E+00	4,11E+00	7,67E-03	0	2,55E-06	4,04E-05
5	rs10854749	WBP2NL	22	T	G	3,71E+00	-5,54E+00	5,08E-02	0	2,08E-04	3,06E-08
5	rs5758562	WBP2NL	22	C	G	NaN	NaN	4,90E-03	0	6,43E-06	2,74E-05
5	rs5751209	WBP2NL	22	A	G	-4,51E+00	4,14E+00	6,14E-03	0	6,60E-06	3,44E-05
5	rs5758566	WBP2NL	22	G	A	-4,36E+00	4,18E+00	6,14E-03	0	1,32E-05	2,94E-05
5	rs1063392	NAGA	22	G	A	4,26E+00	-6,06E+00	6,46E-03	0	2,02E-05	1,37E-09
5	rs2013960	NAGA	22	A	T	NaN	NaN	6,46E-03	0	1,98E-05	1,16E-09
5	rs2854837	NAGA	22	G	A	-4,56E+00	4,30E+00	3,11E-03	0	5,06E-06	1,73E-05
5	rs2413666	NAGA	22	C	T	-4,22E+00	4,17E+00	8,00E-03	0	2,49E-05	3,04E-05
5	rs133367	NAGA	22	C	T	-3,97E+00	4,27E+00	2,29E-02	0	7,30E-05	1,99E-05
5	rs133368	NAGA	22	T	C	-4,37E+00	4,25E+00	4,20E-03	0	1,22E-05	2,14E-05
5	rs133369	NAGA	22	C	T	-4,36E+00	4,19E+00	4,90E-03	0	1,30E-05	2,81E-05
5	rs133370	NAGA	22	T	C	-4,21E+00	4,14E+00	8,00E-03	0	2,52E-05	3,49E-05
5	rs133371	NAGA	22	G	A	-4,26E+00	4,14E+00	6,46E-03	0	2,07E-05	3,48E-05
5	rs133373	NAGA	22	A	G	3,89E+00	-6,24E+00	2,81E-02	0	1,00E-04	4,41E-10
5	rs133374	NAGA	22	G	A	-4,21E+00	4,14E+00	8,00E-03	0	2,58E-05	3,47E-05
5	rs133375	NAGA	22	C	G	NaN	NaN	7,67E-03	0	2,17E-05	3,77E-05
5	rs133376	NAGA	22	T	C	3,98E+00	-6,25E+00	1,86E-02	0	6,97E-05	4,18E-10
5	rs133377	NAGA	22	C	T	-4,19E+00	4,18E+00	8,00E-03	0	2,80E-05	2,98E-05
5	rs2859438	NAGA	22	A	T	NaN	NaN	8,00E-03	0	2,71E-05	3,48E-05
5	rs133378	NAGA	22	G	C	NaN	NaN	8,00E-03	0	2,69E-05	3,49E-05
5	rs28605764	NAGA	22	C	T	-3,67E+00	4,33E+00	6,15E-02	0	2,44E-04	1,46E-05
5	rs133379	NAGA	22	A	G	-4,35E+00	4,23E+00	4,90E-03	0	1,34E-05	2,38E-05
5	rs133380	FAM109B	22	C	T	-4,07E+00	4,35E+00	1,51E-02	0	4,74E-05	1,34E-05
5	rs13057094	FAM109B	22	T	C	-4,34E+00	4,20E+00	5,21E-03	0	1,42E-05	2,69E-05
5	rs4822088	FAM109B	22	G	C	NaN	NaN	3,43E-02	0	1,15E-04	3,66E-05

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs133381	FAM109B	22	C	G	NaN	NaN	1,86E-02	0	5,85E-05	3,80E-05
5	rs133382	FAM109B	22	C	T	-4,23E+00	4,12E+00	8,00E-03	0	2,39E-05	3,85E-05
5	rs133383	FAM109B	22	T	C	3,98E+00	-6,20E+00	1,86E-02	0	7,00E-05	5,77E-10
5	rs1807494	FAM109B	22	G	C	NaN	NaN	8,00E-03	0	2,43E-05	3,30E-05
5	rs8135801	FAM109B	22	G	A	-4,25E+00	4,16E+00	6,46E-03	0	2,16E-05	3,16E-05
5	rs2269524	SMDT1	22	G	T	-4,24E+00	4,17E+00	6,46E-03	0	2,23E-05	3,11E-05
5	rs6002592	C22ORF32	22	C	A	-4,20E+00	4,19E+00	8,00E-03	0	2,72E-05	2,84E-05
5	rs6002593	C22ORF32	22	T	A	NaN	NaN	9,90E-03	0	3,30E-05	3,55E-05
5	rs2071711	C22ORF32	22	C	G	NaN	NaN	9,90E-03	0	2,99E-05	1,73E-05
5	rs5758574	NDUFA6	22	G	C	NaN	NaN	1,86E-02	0	6,51E-05	3,63E-10
5	rs7245	NDUFA6	22	G	A	4,07E+00	-6,29E+00	1,51E-02	0	4,66E-05	3,26E-10
5	rs4147641	NDUFA6	22	G	C	NaN	NaN	6,46E-03	0	2,02E-05	2,02E-05
5	rs6002596	NDUFA6	22	A	G	-4,41E+00	4,20E+00	4,90E-03	0	1,05E-05	2,65E-05
5	rs4147640	NDUFA6	22	C	T	-4,31E+00	4,26E+00	5,21E-03	0	1,61E-05	2,03E-05
5	rs2284087	NDUFA6	22	T	C	3,98E+00	-6,29E+00	1,86E-02	0	6,84E-05	3,26E-10
5	rs1801311	NDUFA6	22	A	G	-4,35E+00	4,24E+00	4,20E-03	0	1,38E-05	2,21E-05
5	rs4147638	NDUFA6	22	A	G	-4,30E+00	4,27E+00	5,21E-03	0	1,73E-05	1,96E-05
5	rs6002597	CR597807	22	A	C	-4,19E+00	4,27E+00	8,00E-03	0	2,79E-05	2,00E-05
5	rs6002598	CR597807	22	G	A	-3,60E+00	4,23E+00	7,41E-02	0	3,16E-04	2,33E-05
5	rs6002600	CR597807	22	A	G	-4,35E+00	4,25E+00	4,20E-03	0	1,37E-05	2,15E-05
5	rs6002601	CR597807	22	T	A	NaN	NaN	4,20E-03	0	1,40E-05	2,09E-05
5	rs5758577	CR597807	22	G	C	NaN	NaN	1,22E-02	0	3,83E-05	2,55E-10
5	rs5758578	CR597807	22	A	C	4,02E+00	-6,32E+00	1,86E-02	0	5,83E-05	2,65E-10
5	rs61527837	CR597807	22	T	C	-4,33E+00	4,26E+00	5,21E-03	0	1,48E-05	2,00E-05
5	rs5996108	CR597807	22	T	C	-4,53E+00	4,36E+00	2,47E-03	0	5,82E-06	1,31E-05
5	rs8138500	CR597807	22	T	G	-4,34E+00	4,28E+00	4,20E-03	0	1,40E-05	1,84E-05

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs7292241	CR597807	22	A	G	-4,47E+00	4,24E+00	4,90E-03	0	7,90E-06	2,27E-05
5	rs7291996	CR597807	22	T	C	-4,32E+00	4,26E+00	5,21E-03	0	1,55E-05	2,01E-05
5	rs6002602	CR597807	22	A	G	-4,34E+00	4,26E+00	4,20E-03	0	1,41E-05	2,00E-05
5	rs6002603	CR597807	22	G	C	NaN	NaN	4,20E-03	0	1,29E-05	2,06E-05
5	rs73421049	CR597807	22	A	G	-4,26E+00	4,26E+00	6,46E-03	0	2,01E-05	2,06E-05
5	rs6002604	CR597807	22	T	A	NaN	NaN	5,21E-03	0	1,43E-05	1,57E-05
5	rs5996109	NDUFA6	22	G	A	-4,34E+00	4,32E+00	5,21E-03	0	1,44E-05	1,55E-05
5	rs5996110	CR597807	22	G	A	-4,16E+00	4,26E+00	9,90E-03	0	3,23E-05	2,06E-05
5	rs5996111	CR597807	22	T	C	-4,46E+00	4,24E+00	4,90E-03	0	8,17E-06	2,25E-05
5	rs6002605	CR597807	22	G	A	-4,31E+00	4,26E+00	5,21E-03	0	1,61E-05	2,00E-05
5	rs6002606	CR597807	22	C	T	-4,17E+00	4,26E+00	9,90E-03	0	3,11E-05	2,07E-05
5	rs6002607	CR597807	22	C	T	4,10E+00	-6,30E+00	1,22E-02	0	4,17E-05	3,05E-10
5	rs6002608	CR597807	22	T	C	4,10E+00	-6,31E+00	1,22E-02	0	4,18E-05	2,87E-10
5	rs6002609	CR597807	22	A	C	-4,50E+00	4,35E+00	2,47E-03	0	6,67E-06	1,34E-05
5	rs6002610	CR597807	22	T	C	-4,33E+00	4,25E+00	5,21E-03	0	1,51E-05	2,12E-05
5	rs12157818	CR597807	22	T	C	-4,30E+00	4,25E+00	5,21E-03	0	1,67E-05	2,13E-05
5	rs9620026	CR597807	22	T	C	-4,33E+00	4,25E+00	5,21E-03	0	1,50E-05	2,10E-05
5	rs28817600	CR597807	22	G	A	-4,25E+00	4,25E+00	6,46E-03	0	2,16E-05	2,10E-05
5	rs28791586	CR597807	22	G	A	-4,34E+00	4,25E+00	5,21E-03	0	1,45E-05	2,11E-05
5	rs2839708	NDUFA6	22	G	A	-4,33E+00	4,27E+00	5,21E-03	0	1,53E-05	1,95E-05
5	rs6519306	CR597807	22	C	T	-4,34E+00	4,29E+00	5,21E-03	0	1,45E-05	1,80E-05
5	rs6002614	CR597807	22	A	G	-4,34E+00	4,24E+00	5,21E-03	0	1,45E-05	2,26E-05
5	rs6002615	NDUFA6	22	G	A	-4,33E+00	4,21E+00	5,21E-03	0	1,51E-05	2,53E-05
5	rs6002616	NDUFA6	22	G	A	-4,27E+00	4,23E+00	6,46E-03	0	1,95E-05	2,35E-05
5	rs8141702	CR597807	22	A	G	-4,44E+00	4,19E+00	4,90E-03	0	8,88E-06	2,82E-05
5	rs2413668	CR597807	22	G	A	4,01E+00	-6,32E+00	1,86E-02	0	6,14E-05	2,66E-10

Locus	**SNP**	**Gene**	**Chr**	**A1**	**A2**	**z-score SCZ**	**z-score VNR**	**conjFDR**	**prune**	**p SCZ**	**p VNR**
5	rs5996113	CR597807	22	G	C	NaN	NaN	6,14E-03	0	1,01E-05	2,95E-05
5	rs7364289	CR597807	22	C	A	-4,34E+00	4,22E+00	5,21E-03	0	1,45E-05	2,44E-05
5	rs7364293	CR597807	22	T	C	-4,29E+00	4,25E+00	5,21E-03	0	1,75E-05	2,13E-05
5	rs2413669	NDUFA6	22	C	A	-4,33E+00	4,22E+00	5,21E-03	0	1,52E-05	2,45E-05
5	rs6002618	CR597807	22	C	G	NaN	NaN	5,21E-03	0	1,57E-05	2,46E-05
5	rs5751216	NDUFA6	22	G	T	3,93E+00	-6,27E+00	2,29E-02	0	8,46E-05	3,72E-10
5	rs5996115	CR597807	22	G	C	NaN	NaN	5,21E-03	0	1,51E-05	2,49E-05
5	rs6002621	NDUFA6	22	C	A	-4,34E+00	4,21E+00	4,90E-03	0	1,41E-05	2,52E-05
5	rs2839710	CR597807	22	C	T	-4,30E+00	4,21E+00	5,21E-03	0	1,72E-05	2,50E-05
5	rs2413670	CR597807	22	G	C	NaN	NaN	1,86E-02	0	6,04E-05	3,52E-10
5	rs2413671	CR597807	22	G	A	4,02E+00	-6,27E+00	1,86E-02	0	5,92E-05	3,71E-10
5	rs7286375	CR597807	22	C	G	NaN	NaN	1,22E-02	0	4,31E-05	2,43E-05
5	rs61665536	CR597807	22	G	A	-4,32E+00	4,22E+00	5,21E-03	0	1,53E-05	2,44E-05
5	rs2413672	NDUFA6	22	T	C	-4,32E+00	4,24E+00	5,21E-03	0	1,54E-05	2,28E-05
5	rs6002623	NDUFA6	22	A	G	-4,33E+00	4,22E+00	5,21E-03	0	1,49E-05	2,43E-05
5	rs6002624	CR597807	22	C	G	NaN	NaN	5,21E-03	0	1,74E-05	2,31E-05
5	rs11090076	NDUFA6	22	C	T	-4,41E+00	4,11E+00	7,67E-03	0	1,05E-05	3,99E-05
5	rs8143153	CR597807	22	C	G	NaN	NaN	6,46E-03	0	1,95E-05	2,74E-05
5	rs12161070	CR597807	22	A	C	-4,23E+00	4,04E+00	9,57E-03	0	2,32E-05	5,38E-05
5	rs12161096	CR597807	22	T	C	-4,20E+00	4,17E+00	8,00E-03	0	2,70E-05	3,01E-05
5	rs12157344	CR597807	22	A	G	-4,13E+00	4,05E+00	1,22E-02	0	3,58E-05	5,18E-05
5	rs5751220	CR597807	22	A	C	4,04E+00	-6,32E+00	1,51E-02	0	5,45E-05	2,54E-10
5	rs8138678	NDUFA6	22	G	A	-4,28E+00	4,18E+00	6,46E-03	0	1,85E-05	2,96E-05
5	rs12158568	CR597807	22	C	T	-4,26E+00	4,18E+00	6,46E-03	0	2,05E-05	2,87E-05
5	rs5996116	CR597807	22	A	G	-4,29E+00	4,10E+00	7,67E-03	0	1,76E-05	4,17E-05
5	rs5758587	CR597807	22	C	G	NaN	NaN	1,86E-02	0	6,35E-05	3,29E-10

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs6002625	CR597807	22	G	A	-4,35E+00	4,30E+00	4,20E-03	0	1,35E-05	1,73E-05
5	rs6002626	NDUFA6	22	C	G	NaN	NaN	1,51E-02	0	4,80E-05	2,92E-10
5	rs5758589	NDUFA6	22	A	G	3,97E+00	-6,26E+00	2,29E-02	0	7,22E-05	3,95E-10
5	rs764481	NDUFA6	22	A	G	-4,29E+00	4,18E+00	6,46E-03	0	1,79E-05	2,97E-05
5	rs34385013	AK123630	22	A	G	3,86E+00	-6,16E+00	3,43E-02	0	1,14E-04	7,21E-10
5	rs35028622	AK123630	22	A	C	3,82E+00	-6,10E+00	3,43E-02	0	1,33E-04	1,08E-09
5	rs116390392	AK123630	22	T	C	-4,55E+00	4,09E+00	7,67E-03	0	5,32E-06	4,31E-05
5	rs1135840	AK123630	22	C	G	NaN	NaN	3,43E-02	0	1,39E-04	1,06E-09
5	rs28371730	AK123630	22	T	C	-4,18E+00	4,05E+00	9,90E-03	0	2,94E-05	5,21E-05
5	rs16947	AK123630	22	A	G	-4,23E+00	4,07E+00	9,57E-03	0	2,30E-05	4,68E-05
5	rs1058164	AK123630	22	C	G	NaN	NaN	5,08E-02	0	2,17E-04	6,40E-10
5	rs28371699	AK123630	22	C	A	3,89E+00	-6,29E+00	2,81E-02	0	1,02E-04	3,22E-10
5	rs28633410	AK123630	22	T	C	-4,37E+00	4,15E+00	6,14E-03	0	1,23E-05	3,28E-05
5	rs28735595	AK123630	22	T	C	3,70E+00	-6,11E+00	5,08E-02	0	2,14E-04	9,78E-10
5	rs1080983	AK123630	22	T	C	-4,42E+00	4,07E+00	9,57E-03	0	9,96E-06	4,66E-05
5	rs28680494	AK123630	22	C	A	3,98E+00	-6,11E+00	1,86E-02	0	6,94E-05	9,71E-10
5	rs28439297	AK123630	22	T	C	3,98E+00	-6,11E+00	1,86E-02	0	6,95E-05	9,72E-10
5	rs28542726	AK123630	22	T	G	4,02E+00	-6,22E+00	1,86E-02	0	5,76E-05	5,12E-10
5	rs28369142	AK123630	22	C	A	-4,27E+00	4,31E+00	6,46E-03	0	1,94E-05	1,65E-05
5	rs28579115	AK123630	22	T	G	4,20E+00	-6,29E+00	8,00E-03	0	2,71E-05	3,17E-10
5	rs28670611	AK123630	22	T	C	4,17E+00	-6,12E+00	9,90E-03	0	3,01E-05	9,25E-10
5	rs9623531	AK123630	22	C	T	-4,58E+00	4,00E+00	1,19E-02	0	4,55E-06	6,22E-05
5	rs28712237	AK123630	22	A	G	-4,51E+00	3,99E+00	1,19E-02	0	6,61E-06	6,67E-05
5	rs4993393	AK123630	22	G	A	-4,48E+00	3,76E+00	2,75E-02	0	7,33E-06	1,71E-04
5	rs28515621	AK123630	22	G	T	-4,63E+00	4,06E+00	9,57E-03	0	3,74E-06	4,89E-05
5	rs2743449	AK123630	22	T	C	4,43E+00	-6,06E+00	3,38E-03	0	9,52E-06	1,37E-09

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs28570317	AK123630	22	C	G	NaN	NaN	7,67E-03	0	5,24E-06	4,13E-05
5	rs6002633	CYP2D7P1	22	T	C	-4,63E+00	3,91E+00	1,82E-02	0	3,66E-06	9,09E-05
5	rs2743451	CYP2D7P1	22	C	T	4,38E+00	-5,88E+00	4,20E-03	0	1,18E-05	4,15E-09
5	rs2860372	CYP2D7P1	22	C	T	-4,83E+00	5,24E+00	4,70E-04	0	1,39E-06	1,61E-07
5	rs28733092	CYP2D7P1	22	C	T	-5,00E+00	4,11E+00	7,67E-03	0	5,77E-07	4,00E-05
5	rs3020736	CYP2D7P1	22	A	G	-4,88E+00	4,14E+00	6,14E-03	0	1,04E-06	3,53E-05
5	rs56404506	CYP2D7P1	22	T	C	-4,12E+00	3,66E+00	4,06E-02	0	3,74E-05	2,56E-04
5	rs1800754	CYP2D7P1	22	G	A	4,42E+00	-6,29E+00	3,38E-03	0	1,00E-05	3,07E-10
5	rs1058167	CYP2D7P1	22	A	G	-4,73E+00	4,30E+00	3,11E-03	0	2,27E-06	1,67E-05
5	rs3021083	CYP2D7P1	22	C	T	4,42E+00	-6,18E+00	3,38E-03	0	9,77E-06	6,29E-10
5	rs28514673	CYP2D7P1	22	G	A	-4,56E+00	4,12E+00	7,67E-03	0	5,03E-06	3,87E-05
5	rs36093924	CYP2D7P1	22	T	C	4,11E+00	-6,39E+00	1,22E-02	0	3,92E-05	1,63E-10
5	rs2743459	CYP2D7P1	22	T	G	4,55E+00	-6,21E+00	1,76E-03	0	5,45E-06	5,39E-10
5	rs2854740	CYP2D7P1	22	G	A	4,49E+00	-6,13E+00	2,73E-03	0	7,09E-06	9,02E-10
5	rs2743461	CYP2D6	22	G	A	4,42E+00	-6,34E+00	3,38E-03	0	9,77E-06	2,30E-10
5	rs5758605	CYP2D6	22	A	G	4,41E+00	-6,50E+00	3,38E-03	0	1,02E-05	8,28E-11
5	rs2142694	CYP2D6	22	A	G	4,40E+00	-6,52E+00	3,38E-03	0	1,09E-05	7,18E-11
5	rs2854743	CYP2D6	22	A	C	-4,51E+00	4,63E+00	2,19E-03	0	6,41E-06	3,74E-06
5	rs2743462	CYP2D6	22	G	A	4,38E+00	-6,51E+00	4,20E-03	0	1,21E-05	7,37E-11
5	rs2743465	CYP2D6	22	A	G	4,38E+00	-5,99E+00	4,20E-03	0	1,20E-05	2,09E-09
5	rs2743467	TCF20	22	G	A	-4,35E+00	4,24E+00	4,20E-03	0	1,38E-05	2,21E-05
5	rs2743468	TCF20	22	A	G	-4,24E+00	4,23E+00	6,46E-03	0	2,22E-05	2,30E-05
5	rs5758619	TCF20	22	C	T	4,08E+00	-5,95E+00	1,51E-02	0	4,51E-05	2,65E-09
5	rs5758623	TCF20	22	C	G	NaN	NaN	5,21E-03	0	1,72E-05	4,48E-09
5	rs742089	TCF20	22	A	G	4,12E+00	-5,95E+00	1,22E-02	0	3,82E-05	2,73E-09
5	rs760648	TCF20	22	A	G	4,83E+00	-4,95E+00	4,70E-04	0	1,40E-06	7,54E-07

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs2413684	TCF20	22	T	C	4,46E+00	-5,94E+00	2,73E-03	0	8,08E-06	2,81E-09
5	rs2899355	TCF20	22	C	T	4,34E+00	-6,13E+00	5,21E-03	0	1,42E-05	8,99E-10
5	rs5758645	TCF20	22	G	T	4,28E+00	-5,79E+00	6,46E-03	0	1,88E-05	6,90E-09
5	rs17002876	TCF20	22	G	C	NaN	NaN	1,47E-02	0	2,33E-05	7,56E-05
5	rs5751241	TCF20	22	A	G	4,28E+00	-5,73E+00	6,46E-03	0	1,83E-05	1,03E-08
5	rs6002655	TCF20	22	T	C	5,01E+00	-5,17E+00	1,92E-04	1	5,48E-07	2,29E-07
5	rs5758653	TCF20	22	T	G	4,70E+00	-5,50E+00	9,13E-04	0	2,54E-06	3,90E-08
5	rs2143139	TCF20	22	G	C	NaN	NaN	1,47E-02	0	2,36E-05	8,14E-05
5	rs5758659	TCF20	22	T	C	4,80E+00	-5,49E+00	5,87E-04	0	1,55E-06	4,13E-08
5	rs5758660	TCF20	22	A	C	4,76E+00	-5,42E+00	7,32E-04	0	1,98E-06	5,93E-08
5	rs5758670	TCF20	22	C	T	4,57E+00	-5,35E+00	1,76E-03	0	4,93E-06	8,92E-08
5	rs5751250	LOC388906	22	G	T	4,55E+00	-5,36E+00	1,76E-03	0	5,39E-06	8,20E-08
5	rs5758677	LOC388906	22	C	A	4,74E+00	-5,53E+00	7,32E-04	0	2,09E-06	3,23E-08
5	rs5751255	LOC388906	22	T	C	4,75E+00	-5,52E+00	7,32E-04	0	2,05E-06	3,31E-08
5	rs134867	LOC388906	22	T	C	-4,14E+00	3,63E+00	4,90E-02	0	3,45E-05	2,84E-04
5	rs134869	LOC388906	22	A	G	4,67E+00	-5,49E+00	1,14E-03	0	2,99E-06	4,12E-08
5	rs134873	LOC388906	22	G	T	5,01E+00	-5,43E+00	1,92E-04	0	5,53E-07	5,64E-08
5	rs134874	LOC388906	22	A	G	-4,54E+00	3,75E+00	3,35E-02	0	5,69E-06	1,79E-04
5	rs134877	LOC388906	22	T	C	4,84E+00	-5,32E+00	4,70E-04	0	1,28E-06	1,01E-07
5	rs134878	LOC388906	22	A	G	-4,38E+00	3,85E+00	2,24E-02	0	1,20E-05	1,20E-04
5	rs134879	LOC388906	22	C	A	4,84E+00	-5,36E+00	4,70E-04	0	1,28E-06	8,23E-08
5	rs134882	LOC388906	22	C	T	4,85E+00	-5,44E+00	4,70E-04	0	1,24E-06	5,45E-08
5	rs134885	LOC388906	22	C	G	NaN	NaN	4,06E-02	0	1,20E-05	2,54E-04
5	rs134886	LOC388906	22	A	G	-4,36E+00	3,67E+00	4,06E-02	0	1,32E-05	2,47E-04
5	rs134887	LOC388906	22	A	G	-4,39E+00	3,68E+00	4,06E-02	0	1,15E-05	2,30E-04
5	rs134888	LOC388906	22	C	T	-4,45E+00	3,67E+00	4,06E-02	0	8,55E-06	2,41E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score VNR	conjFDR	prune	p SCZ	p VNR
5	rs134889	LOC388906	22	A	T	NaN	NaN	4,06E-02	0	1,39E-05	2,42E-04
5	rs134891	LOC388906	22	T	C	-4,33E+00	3,69E+00	3,35E-02	0	1,50E-05	2,22E-04
5	rs134899	LOC388906	22	T	G	-4,38E+00	3,73E+00	3,35E-02	0	1,21E-05	1,91E-04
5	rs134900	LOC388906	22	C	G	NaN	NaN	3,76E-04	0	1,08E-06	4,25E-08
5	rs134901	LOC388906	22	C	T	-4,40E+00	3,71E+00	3,35E-02	0	1,10E-05	2,09E-04
5	rs134902	LOC388906	22	A	G	4,86E+00	-5,49E+00	4,70E-04	0	1,17E-06	4,09E-08
5	rs134903	LOC388906	22	C	A	-4,43E+00	3,66E+00	4,06E-02	0	9,64E-06	2,51E-04
5	rs80506	LOC388906	22	A	T	NaN	NaN	5,87E-04	0	1,62E-06	6,09E-08
5	rs134906	LOC388906	22	T	C	4,68E+00	-5,23E+00	1,14E-03	0	2,84E-06	1,66E-07

eTable 3D. Loci with conjFDR<.10 associated with SCZ and RT

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
1	rs11264211	AGO4	1	G	A	-3,40E+00	-3,43E+00	8,57E-02	0	6,81E-04	6,02E-04
1	rs12083902	AGO4	1	A	G	-3,45E+00	-3,41E+00	8,57E-02	0	5,64E-04	6,60E-04
1	rs727005	AGO4	1	G	A	-3,42E+00	-3,40E+00	8,57E-02	0	6,29E-04	6,82E-04
1	rs11264213	EIF2C4	1	G	A	-3,51E+00	-3,45E+00	6,84E-02	1	4,44E-04	5,62E-04
1	rs11263828	EIF2C4	1	C	G	NaN	NaN	8,57E-02	0	6,19E-04	5,60E-04
2	rs34464261	KCNJ3	2	G	T	3,40E+00	-3,49E+00	8,57E-02	0	6,73E-04	4,76E-04
2	rs62176457	KCNJ3	2	T	G	3,43E+00	-3,55E+00	8,57E-02	0	6,09E-04	3,81E-04
2	rs34829140	KCNJ3	2	A	C	3,39E+00	-3,51E+00	8,57E-02	0	6,93E-04	4,56E-04
2	rs13004840	KCNJ3	2	T	C	3,48E+00	-3,37E+00	9,33E-02	0	5,00E-04	7,41E-04
2	rs13000491	KCNJ3	2	C	T	3,48E+00	-3,37E+00	9,33E-02	0	4,96E-04	7,57E-04
2	rs34643576	KCNJ3	2	G	C	NaN	NaN	8,57E-02	0	5,78E-04	5,28E-04
2	rs34578247	KCNJ3	2	C	T	3,41E+00	-3,48E+00	8,57E-02	0	6,42E-04	5,02E-04
2	rs34003363	KCNJ3	2	A	G	3,43E+00	-3,47E+00	8,57E-02	0	6,00E-04	5,26E-04
2	rs67338739	KCNJ3	2	C	T	3,44E+00	-3,61E+00	8,57E-02	0	5,84E-04	3,12E-04
2	rs12993822	KCNJ3	2	G	C	NaN	NaN	8,57E-02	0	5,84E-04	4,01E-04
2	rs35204416	KCNJ3	2	G	C	NaN	NaN	8,57E-02	0	5,86E-04	3,21E-04
2	rs62174923	KCNJ3	2	C	T	3,45E+00	-3,62E+00	7,21E-02	1	5,58E-04	2,94E-04
2	rs7593161	KCNJ3	2	G	C	NaN	NaN	8,57E-02	0	5,85E-04	3,22E-04
2	rs62174925	KCNJ3	2	T	A	NaN	NaN	8,57E-02	0	5,85E-04	3,28E-04
2	rs62174926	KCNJ3	2	A	G	3,48E+00	-3,60E+00	7,21E-02	0	5,03E-04	3,22E-04
2	rs13013475	KCNJ3	2	A	C	3,42E+00	-3,56E+00	8,57E-02	0	6,19E-04	3,70E-04
2	rs35072026	KCNJ3	2	C	T	3,39E+00	-3,60E+00	8,57E-02	0	7,07E-04	3,13E-04
3	rs13020196	SPATS2L	2	T	G	3,51E+00	5,02E+00	7,21E-02	0	4,56E-04	5,19E-07
3	rs1653301	SPATS2L	2	A	G	3,46E+00	4,88E+00	7,21E-02	0	5,47E-04	1,05E-06
3	rs10445790	SPATS2L	2	C	T	3,43E+00	4,85E+00	8,57E-02	0	5,99E-04	1,21E-06
3	rs13035874	SPATS2L	2	A	G	4,24E+00	4,97E+00	4,76E-03	0	2,19E-05	6,56E-07
3	rs1367858	SPATS2L	2	T	C	5,01E+00	4,59E+00	8,97E-04	0	5,49E-07	4,36E-06
3	rs4673905	SPATS2L	2	G	A	4,48E+00	4,53E+00	2,02E-03	0	7,42E-06	5,83E-06
3	rs6435048	SPATS2L	2	T	C	4,84E+00	4,71E+00	5,65E-04	1	1,31E-06	2,48E-06
3	rs3769484	SPATS2L	2	T	C	4,85E+00	4,68E+00	7,12E-04	0	1,26E-06	2,82E-06

Locus	**SNP**	**Gene**	**Chr**	**A1**	**A2**	**z-score SCZ**	**z-score RT**	**conjFDR**	**prune**	**p SCZ**	**p RT**
3	rs3769483	SPATS2L	2	G	A	4,85E+00	4,70E+00	5,65E-04	0	1,26E-06	2,60E-06
3	rs3769482	SPATS2L	2	G	C	NaN	NaN	7,12E-04	0	1,25E-06	2,84E-06
3	rs1347551	SPATS2L	2	T	C	4,78E+00	4,60E+00	8,97E-04	0	1,76E-06	4,27E-06
3	rs3769472	SPATS2L	2	A	G	4,82E+00	4,59E+00	8,97E-04	0	1,46E-06	4,38E-06
3	rs2033804	SPATS2L	2	T	A	NaN	NaN	6,74E-03	0	1,09E-05	2,93E-05
3	rs1975583	SPATS2L	2	C	A	4,52E+00	4,23E+00	5,43E-03	0	6,29E-06	2,38E-05
3	rs1369841	SPATS2L	2	G	A	4,67E+00	4,14E+00	6,74E-03	0	3,07E-06	3,44E-05
3	rs6743157	SPATS2L	2	T	C	4,67E+00	4,19E+00	5,43E-03	0	3,01E-06	2,79E-05
3	rs35417285	SPATS2L	2	C	T	4,58E+00	4,19E+00	6,74E-03	0	4,70E-06	2,84E-05
3	rs3856513	SPATS2L	2	A	G	4,64E+00	4,17E+00	6,74E-03	0	3,40E-06	3,00E-05
3	rs3769456	SPATS2L	2	T	C	4,67E+00	4,13E+00	8,36E-03	0	3,02E-06	3,59E-05
3	rs994280	SPATS2L	2	G	A	4,34E+00	4,23E+00	5,43E-03	0	1,44E-05	2,35E-05
3	rs12990174	SPATS2L	2	A	G	4,61E+00	4,18E+00	6,74E-03	0	4,08E-06	2,94E-05
3	rs3754797	SPATS2L	2	A	G	4,66E+00	4,24E+00	4,36E-03	0	3,10E-06	2,23E-05
3	rs6708345	SPATS2L	2	C	A	4,70E+00	3,50E+00	6,84E-02	0	2,57E-06	4,58E-04
4	rs832192	SCA7	3	T	C	3,42E+00	3,35E+00	9,33E-02	1	6,28E-04	8,16E-04
5	rs2764264	FOXO3	6	C	T	4,36E+00	3,35E+00	9,33E-02	0	1,32E-05	8,23E-04
5	rs13217795	FOXO3	6	C	T	4,36E+00	3,42E+00	8,01E-02	1	1,32E-05	6,34E-04
5	rs4946932	FOXO3	6	A	C	4,33E+00	3,35E+00	9,33E-02	0	1,48E-05	8,11E-04
5	rs9398171	FOXO3	6	C	T	4,57E+00	3,38E+00	9,33E-02	0	4,83E-06	7,37E-04
5	rs111727905	FOXO3	6	G	A	4,44E+00	3,39E+00	8,01E-02	0	8,95E-06	6,87E-04
6	rs7857165	PHF2	9	A	T	NaN	NaN	3,52E-02	1	2,16E-04	3,00E-05
6	rs10119832	PHF2	9	A	G	3,41E+00	4,14E+00	8,57E-02	0	6,56E-04	3,54E-05
6	rs55934002	PHF2	9	T	C	3,43E+00	4,19E+00	8,57E-02	0	6,02E-04	2,77E-05
7	rs1044796	CREB3L1	11	T	C	4,40E+00	4,14E+00	6,74E-03	0	1,07E-05	3,42E-05
7	rs12285419	CREB3L1	11	A	C	4,68E+00	4,15E+00	6,74E-03	0	2,85E-06	3,26E-05
7	rs11038864	DGKZ	11	A	G	4,38E+00	3,51E+00	6,84E-02	0	1,16E-05	4,53E-04
7	rs61882674	DGKZ	11	G	C	NaN	NaN	2,80E-03	0	1,69E-06	1,23E-05
7	rs61882678	DGKZ	11	T	A	NaN	NaN	2,80E-03	0	1,22E-06	1,28E-05
7	rs61882679	DGKZ	11	T	G	3,45E+00	4,03E+00	7,21E-02	0	5,60E-04	5,68E-05
7	rs876701	DGKZ	11	G	A	4,99E+00	4,38E+00	2,80E-03	0	6,12E-07	1,21E-05
7	rs7951870	DGKZ	11	C	T	5,25E+00	4,37E+00	2,80E-03	0	1,56E-07	1,22E-05

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
7	rs61882682	DGKZ	11	C	A	4,92E+00	4,35E+00	2,80E-03	0	8,58E-07	1,34E-05
7	rs61882683	DGKZ	11	A	G	4,89E+00	4,30E+00	3,50E-03	0	1,03E-06	1,71E-05
7	rs59319338	DGKZ	11	T	C	4,76E+00	4,30E+00	3,50E-03	0	1,92E-06	1,67E-05
7	rs12577142	DGKZ	11	C	T	5,13E+00	4,44E+00	1,78E-03	1	2,82E-07	8,86E-06
7	rs12576115	DGKZ	11	A	G	4,94E+00	4,39E+00	2,23E-03	0	7,77E-07	1,11E-05
7	rs61882686	DGKZ	11	A	C	3,47E+00	3,95E+00	7,21E-02	0	5,21E-04	7,77E-05
7	rs12575519	DGKZ	11	G	T	5,08E+00	4,36E+00	2,80E-03	0	3,71E-07	1,27E-05
7	rs3740977	DGKZ	11	C	T	4,85E+00	4,34E+00	3,50E-03	0	1,21E-06	1,41E-05
7	rs7936413	DGKZ	11	C	T	5,09E+00	4,36E+00	2,80E-03	0	3,65E-07	1,29E-05
7	rs2046768	DGKZ	11	C	T	5,08E+00	4,46E+00	1,78E-03	0	3,74E-07	8,08E-06
7	rs3740974	DGKZ	11	C	A	5,03E+00	4,35E+00	2,80E-03	0	4,92E-07	1,36E-05
7	rs34406563	DGKZ	11	C	T	4,67E+00	3,63E+00	4,10E-02	0	2,96E-06	2,79E-04
7	rs2279465	DGKZ	11	C	T	5,03E+00	4,36E+00	2,80E-03	0	5,00E-07	1,28E-05
7	rs35324223	MDK	11	G	A	5,10E+00	4,35E+00	2,80E-03	0	3,31E-07	1,38E-05
7	rs2067482	CHRM4	11	A	G	4,77E+00	4,14E+00	6,74E-03	0	1,82E-06	3,43E-05
7	rs7946705	AMBRA1	11	A	G	4,74E+00	4,18E+00	6,74E-03	0	2,10E-06	2,89E-05
7	rs12574668	AMBRA1	11	A	C	5,00E+00	4,21E+00	5,43E-03	0	5,67E-07	2,52E-05
7	rs111449880	AMBRA1	11	A	G	4,82E+00	4,18E+00	6,74E-03	0	1,40E-06	2,87E-05
7	rs61882691	AMBRA1	11	A	C	4,73E+00	4,15E+00	6,74E-03	0	2,19E-06	3,31E-05
7	rs12283172	AMBRA1	11	T	C	4,64E+00	4,15E+00	6,74E-03	0	3,53E-06	3,26E-05
7	rs61882701	AMBRA1	11	A	G	4,72E+00	4,15E+00	6,74E-03	0	2,40E-06	3,30E-05
7	rs6485682	AMBRA1	11	C	A	4,99E+00	4,17E+00	6,74E-03	0	6,06E-07	3,09E-05
7	rs61882702	AMBRA1	11	A	G	4,80E+00	4,14E+00	6,74E-03	0	1,62E-06	3,52E-05
7	rs16938506	AMBRA1	11	C	A	4,97E+00	4,18E+00	6,74E-03	0	6,60E-07	2,98E-05
7	rs2291487	AMBRA1	11	T	C	4,74E+00	4,15E+00	6,74E-03	0	2,11E-06	3,36E-05
7	rs75748389	AMBRA1	11	G	C	NaN	NaN	6,74E-03	0	2,18E-06	2,85E-05
7	rs2864076	AMBRA1	11	T	C	5,00E+00	4,19E+00	5,43E-03	0	5,80E-07	2,80E-05
7	rs61882706	AMBRA1	11	A	G	4,75E+00	4,16E+00	6,74E-03	0	2,02E-06	3,16E-05
7	rs2171668	AMBRA1	11	C	A	5,02E+00	4,18E+00	6,74E-03	0	5,06E-07	2,89E-05
7	rs2864072	AMBRA1	11	C	A	4,79E+00	4,14E+00	6,74E-03	0	1,70E-06	3,53E-05
7	rs7951579	AMBRA1	11	A	G	5,13E+00	4,16E+00	6,74E-03	0	2,97E-07	3,24E-05
7	rs11038897	AMBRA1	11	T	C	5,02E+00	4,16E+00	6,74E-03	0	5,06E-07	3,14E-05

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
7	rs61882709	AMBRA1	11	A	G	5,02E+00	4,16E+00	6,74E-03	0	5,05E-07	3,17E-05
7	rs61882710	AMBRA1	11	A	G	4,74E+00	4,15E+00	6,74E-03	0	2,10E-06	3,33E-05
7	rs61882711	AMBRA1	11	T	C	4,75E+00	4,11E+00	8,36E-03	0	2,03E-06	3,91E-05
7	rs80031726	AMBRA1	11	C	T	4,80E+00	4,15E+00	6,74E-03	0	1,61E-06	3,30E-05
7	rs61882712	AMBRA1	11	C	T	4,75E+00	4,13E+00	8,36E-03	0	2,08E-06	3,60E-05
7	rs7930103	AMBRA1	11	T	C	4,74E+00	4,13E+00	8,36E-03	0	2,11E-06	3,59E-05
7	rs1472001	AMBRA1	11	A	G	4,74E+00	4,13E+00	8,36E-03	0	2,14E-06	3,59E-05
7	rs79078082	AMBRA1	11	G	A	3,39E+00	3,73E+00	8,57E-02	0	6,94E-04	1,95E-04
7	rs12574250	AMBRA1	11	A	G	4,62E+00	4,10E+00	8,36E-03	0	3,76E-06	4,09E-05
7	rs11038900	AMBRA1	11	G	A	5,06E+00	4,17E+00	6,74E-03	0	4,22E-07	3,07E-05
7	rs7130141	AMBRA1	11	T	C	4,99E+00	4,14E+00	6,74E-03	0	5,96E-07	3,43E-05
7	rs58147945	AMBRA1	11	G	C	NaN	NaN	6,74E-03	0	5,34E-07	3,40E-05
7	rs1489192	AMBRA1	11	C	T	5,02E+00	4,15E+00	6,74E-03	0	5,04E-07	3,27E-05
7	rs7112229	AMBRA1	11	T	C	4,75E+00	4,13E+00	8,36E-03	0	2,06E-06	3,57E-05
7	rs12578042	AMBRA1	11	G	C	NaN	NaN	6,74E-03	0	5,00E-07	3,47E-05
7	rs3802888	AMBRA1	11	G	A	5,04E+00	4,16E+00	6,74E-03	0	4,70E-07	3,24E-05
7	rs2902858	AMBRA1	11	C	T	4,99E+00	4,18E+00	6,74E-03	0	6,15E-07	2,93E-05
7	rs12576359	AMBRA1	11	G	T	4,72E+00	4,14E+00	6,74E-03	0	2,39E-06	3,47E-05
7	rs10838602	AMBRA1	11	A	G	4,72E+00	4,15E+00	6,74E-03	0	2,39E-06	3,33E-05
7	rs11038906	AMBRA1	11	A	G	5,02E+00	4,15E+00	6,74E-03	0	5,15E-07	3,38E-05
7	rs61882720	AMBRA1	11	A	C	4,72E+00	4,07E+00	1,03E-02	0	2,37E-06	4,79E-05
7	rs12272795	AMBRA1	11	G	A	4,92E+00	4,09E+00	8,36E-03	0	8,71E-07	4,35E-05
7	rs7932866	AMBRA1	11	G	A	4,64E+00	4,11E+00	8,36E-03	0	3,44E-06	3,88E-05
7	rs61882743	AMBRA1	11	G	C	NaN	NaN	1,03E-02	0	2,15E-07	4,92E-05
7	rs10160701	AMBRA1	11	T	C	5,07E+00	4,10E+00	8,36E-03	0	3,93E-07	4,21E-05
7	rs112419908	AMBRA1	11	A	G	4,72E+00	4,08E+00	1,03E-02	0	2,39E-06	4,53E-05
7	rs11819869	AMBRA1	11	T	C	5,04E+00	4,09E+00	8,36E-03	0	4,71E-07	4,32E-05
7	rs11038914	AMBRA1	11	T	C	5,09E+00	4,08E+00	8,36E-03	0	3,66E-07	4,45E-05
7	rs61882746	AMBRA1	11	T	C	5,04E+00	4,11E+00	8,36E-03	0	4,56E-07	3,98E-05
7	rs57535407	AMBRA1	11	C	T	4,81E+00	4,09E+00	8,36E-03	0	1,53E-06	4,34E-05
7	rs12576317	AMBRA1	11	A	G	4,82E+00	4,15E+00	6,74E-03	0	1,46E-06	3,36E-05
7	rs12573978	AMBRA1	11	G	A	4,78E+00	4,07E+00	1,03E-02	0	1,71E-06	4,74E-05

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
7	rs61882748	AMBRA1	11	G	C	NaN	NaN	8,36E-03	0	1,42E-06	4,25E-05
7	rs7127529	AMBRA1	11	C	A	5,03E+00	4,12E+00	8,36E-03	0	4,98E-07	3,84E-05
7	rs61882750	AMBRA1	11	G	T	5,02E+00	4,11E+00	8,36E-03	0	5,07E-07	3,99E-05
7	rs11038919	AMBRA1	11	G	A	4,69E+00	4,02E+00	1,27E-02	0	2,68E-06	5,74E-05
7	rs112705011	AMBRA1	11	T	C	4,63E+00	4,09E+00	8,36E-03	0	3,62E-06	4,39E-05
7	rs79445785	AMBRA1	11	T	C	4,62E+00	4,08E+00	1,03E-02	0	3,82E-06	4,50E-05
7	rs7481312	AMBRA1	11	T	C	4,68E+00	4,08E+00	8,36E-03	0	2,81E-06	4,45E-05
7	rs11038927	AMBRA1	11	C	G	NaN	NaN	8,36E-03	0	6,30E-07	3,96E-05
7	rs139362284	AMBRA1	11	T	C	4,68E+00	4,14E+00	6,74E-03	0	2,85E-06	3,49E-05
7	rs12295266	AMBRA1	11	T	A	NaN	NaN	1,03E-02	0	2,98E-06	4,67E-05
7	rs61882756	AMBRA1	11	T	C	4,33E+00	4,06E+00	1,03E-02	0	1,49E-05	4,93E-05
7	rs61882757	AMBRA1	11	A	G	4,63E+00	4,11E+00	8,36E-03	0	3,72E-06	3,93E-05
7	rs61882758	AMBRA1	11	G	A	4,85E+00	4,16E+00	6,74E-03	0	1,25E-06	3,15E-05
7	rs73449983	AMBRA1	11	G	A	4,66E+00	4,11E+00	8,36E-03	0	3,14E-06	3,98E-05
7	rs7125907	HARBI1	11	T	C	4,62E+00	4,06E+00	1,03E-02	0	3,91E-06	5,00E-05
7	rs75966121	HARBI1	11	G	T	4,65E+00	4,18E+00	6,74E-03	0	3,37E-06	2,93E-05
7	rs55661562	HARBI1	11	C	A	4,68E+00	4,06E+00	1,03E-02	0	2,81E-06	4,98E-05
7	rs35623865	HARBI1	11	T	C	4,96E+00	4,15E+00	6,74E-03	0	7,21E-07	3,36E-05
7	rs61884262	HARBI1	11	A	G	4,75E+00	4,03E+00	1,27E-02	0	2,03E-06	5,62E-05
7	rs6485685	HARBI1	11	A	G	4,62E+00	4,06E+00	1,03E-02	0	3,75E-06	4,95E-05
7	rs55657382	HARBI1	11	A	T	NaN	NaN	1,03E-02	0	3,41E-06	4,95E-05
7	rs7924401	HARBI1	11	T	A	NaN	NaN	8,36E-03	0	8,74E-07	3,88E-05
7	rs61884264	KIAA0652	11	A	G	4,97E+00	4,09E+00	8,36E-03	0	6,53E-07	4,35E-05
7	rs7484002	ATG13	11	G	A	4,67E+00	4,07E+00	1,03E-02	0	3,03E-06	4,77E-05
7	rs79317378	KIAA0652	11	C	T	4,64E+00	4,05E+00	1,03E-02	0	3,49E-06	5,16E-05
7	rs12292425	ATG13	11	G	T	4,66E+00	4,07E+00	1,03E-02	0	3,11E-06	4,62E-05
7	rs7122039	ATG13	11	C	A	4,97E+00	4,05E+00	1,03E-02	0	6,60E-07	5,03E-05
7	rs7108770	KIAA0652	11	A	G	5,10E+00	4,12E+00	8,36E-03	0	3,36E-07	3,76E-05
7	rs60722866	KIAA0652	11	C	T	5,01E+00	4,10E+00	8,36E-03	0	5,55E-07	4,05E-05
7	rs60932698	KIAA0652	11	G	A	4,66E+00	4,06E+00	1,03E-02	0	3,12E-06	4,86E-05
7	rs61884270	KIAA0652	11	T	G	3,43E+00	3,64E+00	8,57E-02	0	6,09E-04	2,68E-04
7	rs61884271	KIAA0652	11	C	T	4,67E+00	4,05E+00	1,03E-02	0	3,04E-06	5,14E-05

Locus	**SNP**	**Gene**	**Chr**	**A1**	**A2**	**z-score SCZ**	**z-score RT**	**conjFDR**	**prune**	**p SCZ**	**p RT**
7	rs7128092	KIAA0652	11	A	T	NaN	NaN	1,03E-02	0	5,45E-06	4,69E-05
7	rs7126316	KIAA0652	11	A	T	NaN	NaN	1,03E-02	0	3,38E-06	4,74E-05
7	rs7126343	KIAA0652	11	C	T	4,54E+00	4,07E+00	1,03E-02	0	5,58E-06	4,76E-05
7	rs61884273	KIAA0652	11	G	T	4,63E+00	4,09E+00	8,36E-03	0	3,73E-06	4,40E-05
7	rs61884274	KIAA0652	11	G	A	4,63E+00	4,07E+00	1,03E-02	0	3,64E-06	4,70E-05
7	rs4307676	KIAA0652	11	A	G	4,63E+00	4,07E+00	1,03E-02	0	3,65E-06	4,67E-05
7	rs7109698	ATG13	11	T	C	4,84E+00	4,08E+00	8,36E-03	0	1,30E-06	4,43E-05
7	rs55896955	KIAA0652	11	G	C	NaN	NaN	1,03E-02	0	3,51E-06	4,98E-05
7	rs61884292	KIAA0652	11	T	A	NaN	NaN	1,03E-02	0	3,37E-06	5,06E-05
7	rs4423142	KIAA0652	11	G	T	4,65E+00	4,04E+00	1,03E-02	0	3,36E-06	5,25E-05
7	rs4606447	ATG13	11	A	G	3,49E+00	3,43E+00	8,01E-02	0	4,92E-04	5,95E-04
7	rs61884295	KIAA0652	11	A	G	4,36E+00	4,03E+00	1,03E-02	0	1,30E-05	5,59E-05
7	rs56349329	KIAA0652	11	A	G	4,38E+00	4,10E+00	8,36E-03	0	1,19E-05	4,21E-05
7	rs57744667	KIAA0652	11	T	C	4,41E+00	4,05E+00	1,03E-02	0	1,02E-05	5,08E-05
7	rs4319473	ARHGAP1	11	A	G	4,31E+00	4,07E+00	1,03E-02	0	1,60E-05	4,62E-05
7	rs12574259	ARHGAP1	11	G	A	4,50E+00	4,03E+00	1,03E-02	0	6,69E-06	5,61E-05
7	rs79443985	ARHGAP1	11	C	T	4,50E+00	3,99E+00	1,27E-02	0	6,64E-06	6,52E-05
7	rs10838613	ARHGAP1	11	A	C	4,34E+00	4,21E+00	5,43E-03	0	1,45E-05	2,54E-05
7	rs7926389	ARHGAP1	11	G	A	4,65E+00	4,00E+00	1,27E-02	0	3,40E-06	6,43E-05
7	rs57739486	ZNF408	11	T	C	4,49E+00	4,03E+00	1,03E-02	0	6,96E-06	5,59E-05
7	rs12574918	ZNF408	11	C	G	NaN	NaN	1,27E-02	0	6,88E-06	6,19E-05
7	rs11038973	ZNF408	11	C	G	NaN	NaN	1,03E-02	0	8,32E-06	5,60E-05
7	rs11038974	ZNF408	11	T	G	4,45E+00	4,03E+00	1,03E-02	0	8,47E-06	5,60E-05
7	rs61884301	ZNF408	11	T	G	4,48E+00	4,00E+00	1,27E-02	0	7,39E-06	6,23E-05
7	rs79175663	ZNF408	11	T	C	4,49E+00	3,96E+00	1,56E-02	0	6,97E-06	7,57E-05
7	rs61884307	F2	11	C	G	NaN	NaN	7,21E-02	0	4,98E-04	2,85E-04
7	rs3136487	F2	11	G	A	3,41E+00	3,81E+00	8,57E-02	0	6,43E-04	1,37E-04
7	rs11038985	CKAP5	11	G	T	3,60E+00	3,76E+00	5,07E-02	0	3,24E-04	1,67E-04
7	rs4500447	CKAP5	11	G	A	3,57E+00	3,76E+00	5,07E-02	0	3,54E-04	1,69E-04
7	rs10466476	CKAP5	11	T	A	NaN	NaN	6,05E-02	0	3,96E-04	1,76E-04
7	rs10466477	CKAP5	11	A	C	3,57E+00	3,76E+00	5,07E-02	0	3,54E-04	1,71E-04
7	rs7928445	CKAP5	11	C	A	3,58E+00	3,76E+00	5,07E-02	0	3,41E-04	1,71E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
7	rs11038987	CKAP5	11	T	A	NaN	NaN	5,07E-02	0	3,49E-04	1,75E-04
7	rs7947517	CKAP5	11	G	A	3,56E+00	3,76E+00	6,05E-02	0	3,67E-04	1,70E-04
7	rs7111811	CKAP5	11	C	A	3,68E+00	3,76E+00	4,23E-02	0	2,32E-04	1,70E-04
7	rs61897303	CKAP5	11	G	A	3,56E+00	3,76E+00	6,05E-02	0	3,73E-04	1,67E-04
7	rs57485117	CKAP5	11	G	C	NaN	NaN	6,05E-02	0	3,73E-04	1,45E-04
7	rs11822959	CKAP5	11	T	C	3,65E+00	3,74E+00	4,23E-02	0	2,61E-04	1,83E-04
7	rs7105052	CKAP5	11	C	T	3,49E+00	3,74E+00	7,21E-02	0	4,84E-04	1,83E-04
7	rs61897304	CKAP5	11	G	A	3,56E+00	3,78E+00	6,05E-02	0	3,67E-04	1,59E-04
7	rs9735937	CKAP5	11	A	G	3,61E+00	3,77E+00	5,07E-02	0	3,01E-04	1,63E-04
7	rs73456126	CKAP5	11	G	A	3,58E+00	3,77E+00	5,07E-02	0	3,39E-04	1,63E-04
7	rs56311746	CKAP5	11	T	A	NaN	NaN	5,07E-02	0	3,53E-04	1,59E-04
7	rs7118097	CKAP5	11	G	A	3,60E+00	3,77E+00	5,07E-02	0	3,18E-04	1,66E-04
7	rs7111760	LRP4	11	C	T	3,58E+00	3,76E+00	5,07E-02	0	3,38E-04	1,69E-04
7	rs7129622	LRP4	11	G	A	3,60E+00	3,76E+00	5,07E-02	0	3,16E-04	1,73E-04
7	rs7115986	LRP4	11	A	T	NaN	NaN	5,07E-02	0	3,23E-04	1,67E-04
7	rs7123729	CKAP5	11	C	T	3,58E+00	3,77E+00	5,07E-02	0	3,38E-04	1,66E-04
7	rs7108147	LRP4	11	A	G	3,58E+00	3,75E+00	5,07E-02	0	3,45E-04	1,74E-04
7	rs7102474	CKAP5	11	C	T	3,58E+00	3,76E+00	5,07E-02	0	3,43E-04	1,69E-04
7	rs4128315	LRP4	11	C	T	3,59E+00	3,77E+00	5,07E-02	0	3,35E-04	1,66E-04
7	rs7105217	CKAP5	11	A	T	NaN	NaN	5,07E-02	0	3,46E-04	1,66E-04
7	rs7106323	LRP4	11	A	C	3,58E+00	3,77E+00	5,07E-02	0	3,49E-04	1,62E-04
7	rs59197251	CKAP5	11	T	C	3,57E+00	3,77E+00	5,07E-02	0	3,52E-04	1,66E-04
7	rs12287376	CKAP5	11	T	C	3,57E+00	3,75E+00	6,05E-02	0	3,64E-04	1,80E-04
7	rs11824327	LRP4	11	C	T	3,52E+00	3,75E+00	6,05E-02	0	4,35E-04	1,78E-04
7	rs12277006	LRP4	11	A	G	3,47E+00	3,74E+00	7,21E-02	0	5,25E-04	1,87E-04
7	rs60940896	CR612190	11	C	T	3,56E+00	3,75E+00	6,05E-02	0	3,69E-04	1,77E-04
7	rs61898463	CR612190	11	G	A	3,50E+00	3,75E+00	7,21E-02	0	4,65E-04	1,78E-04
7	rs6485700	LRP4	11	G	A	3,47E+00	3,74E+00	7,21E-02	0	5,11E-04	1,81E-04
7	rs7938960	CR612190	11	C	T	3,49E+00	3,76E+00	7,21E-02	0	4,78E-04	1,69E-04
7	rs11039012	CR612190	11	A	C	3,51E+00	3,74E+00	7,21E-02	0	4,48E-04	1,82E-04
7	rs56331152	CR612190	11	T	C	3,54E+00	3,75E+00	6,05E-02	0	3,99E-04	1,78E-04
7	rs16938534	LRP4/LRP4	11	C	T	3,51E+00	3,75E+00	7,21E-02	0	4,48E-04	1,77E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
7	rs12273360	CR612190	11	C	T	3,51E+00	3,71E+00	7,21E-02	0	4,48E-04	2,10E-04
7	rs7112060	LRP4/LRP4	11	T	C	3,51E+00	3,75E+00	7,21E-02	0	4,55E-04	1,79E-04
7	rs7115038	LRP4	11	C	G	NaN	NaN	6,05E-02	0	4,38E-04	1,97E-04
7	rs11039015	LRP4	11	C	T	3,52E+00	3,72E+00	6,05E-02	0	4,38E-04	1,97E-04
7	rs7945548	LRP4	11	G	A	3,53E+00	3,73E+00	6,05E-02	0	4,20E-04	1,93E-04
7	rs11825434	LRP4	11	C	T	3,53E+00	3,76E+00	6,05E-02	0	4,10E-04	1,68E-04
7	rs61898529	LRP4	11	A	G	3,62E+00	3,78E+00	5,07E-02	0	2,95E-04	1,54E-04
7	rs7105172	LRP4	11	C	T	3,59E+00	3,73E+00	5,07E-02	0	3,35E-04	1,94E-04
7	rs12281784	LRP4	11	T	C	3,67E+00	3,78E+00	4,23E-02	0	2,45E-04	1,54E-04
7	rs11819969	LRP4	11	C	A	3,67E+00	3,78E+00	4,23E-02	0	2,46E-04	1,55E-04
7	rs12294921	LRP4	11	A	G	3,63E+00	3,79E+00	5,07E-02	0	2,88E-04	1,50E-04
7	rs7112518	LRP4	11	A	C	3,68E+00	3,82E+00	4,23E-02	0	2,35E-04	1,36E-04
7	rs57368576	LRP4	11	G	C	NaN	NaN	5,07E-02	0	2,89E-04	1,31E-04
7	rs61898531	LRP4	11	T	C	3,40E+00	3,84E+00	8,57E-02	0	6,73E-04	1,23E-04
7	rs61382645	LRP4	11	T	C	3,61E+00	3,80E+00	5,07E-02	0	3,10E-04	1,47E-04
7	rs6485706	LRP4	11	T	C	3,68E+00	3,81E+00	4,23E-02	0	2,29E-04	1,41E-04
7	rs7128102	LRP4	11	A	G	3,67E+00	3,76E+00	4,23E-02	0	2,45E-04	1,68E-04
7	rs7102325	LRP4	11	A	G	3,70E+00	3,75E+00	3,52E-02	0	2,14E-04	1,75E-04
7	rs7120113	LRP4	11	T	C	3,67E+00	3,76E+00	4,23E-02	0	2,39E-04	1,67E-04
7	rs9667108	LRP4	11	C	G	NaN	NaN	4,23E-02	0	2,39E-04	1,73E-04
7	rs61899283	C11ORF49	11	G	A	3,41E+00	3,72E+00	8,57E-02	0	6,57E-04	2,02E-04
7	rs7107703	C11ORF49	11	A	G	3,43E+00	3,71E+00	8,57E-02	0	6,05E-04	2,09E-04
7	rs61899292	C11ORF49	11	A	G	3,40E+00	3,70E+00	8,57E-02	0	6,72E-04	2,16E-04
7	rs61896127	C11ORF49	11	T	C	3,41E+00	3,77E+00	8,57E-02	0	6,60E-04	1,66E-04
7	rs118012321	C11ORF49	11	C	T	3,44E+00	3,76E+00	8,57E-02	0	5,86E-04	1,71E-04
7	rs1352307	C11ORF49	11	G	A	3,48E+00	3,76E+00	7,21E-02	0	4,99E-04	1,67E-04
7	rs61897848	ARFGAP2	11	T	C	3,59E+00	3,72E+00	5,07E-02	0	3,36E-04	1,99E-04
8	rs10773011	SBNO1	12	A	G	4,16E+00	3,40E+00	8,01E-02	1	3,23E-05	6,66E-04
8	rs10773012	SBNO1	12	A	C	3,82E+00	3,41E+00	8,01E-02	0	1,34E-04	6,58E-04
9	rs12879159	AKAP6	14	A	G	3,52E+00	3,39E+00	8,01E-02	1	4,27E-04	6,92E-04
9	rs12885124	AKAP6	14	G	T	3,51E+00	3,38E+00	9,33E-02	0	4,44E-04	7,20E-04
9	rs11623122	AKAP6	14	A	G	3,49E+00	3,35E+00	9,33E-02	0	4,79E-04	8,11E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
9	rs11156769	AKAP6	14	G	A	3,49E+00	3,33E+00	9,33E-02	0	4,86E-04	8,56E-04
9	rs12433255	AKAP6	14	A	G	3,43E+00	3,33E+00	9,33E-02	0	6,06E-04	8,64E-04
9	rs12894779	AKAP6	14	A	G	3,54E+00	3,34E+00	9,33E-02	0	3,97E-04	8,49E-04
10	rs1559677	SEMA6D	15	G	A	3,64E+00	3,54E+00	5,80E-02	0	2,69E-04	3,96E-04
10	rs1559678	SEMA6D	15	C	T	3,61E+00	3,49E+00	6,84E-02	0	3,03E-04	4,76E-04
10	rs1353580	SEMA6D	15	A	T	NaN	NaN	6,84E-02	0	2,97E-04	4,66E-04
10	rs1948572	SEMA6D	15	T	C	3,58E+00	3,47E+00	6,84E-02	0	3,41E-04	5,20E-04
10	rs6493279	SEMA6D	15	C	T	3,65E+00	3,47E+00	6,84E-02	0	2,67E-04	5,25E-04
10	rs6493280	SEMA6D	15	C	T	3,60E+00	3,49E+00	6,84E-02	0	3,13E-04	4,77E-04
10	rs1991206	SEMA6D	15	C	T	3,61E+00	3,52E+00	5,80E-02	0	3,10E-04	4,39E-04
10	rs1991207	SEMA6D	15	A	T	NaN	NaN	5,80E-02	0	3,16E-04	4,33E-04
10	rs1991208	SEMA6D	15	G	T	3,60E+00	3,51E+00	5,80E-02	0	3,16E-04	4,43E-04
10	rs1390869	SEMA6D	15	C	T	3,56E+00	3,49E+00	6,84E-02	0	3,67E-04	4,90E-04
10	rs1496897	SEMA6D	15	C	T	3,60E+00	3,59E+00	5,07E-02	1	3,22E-04	3,35E-04
10	rs13313462	SEMA6D	15	G	A	3,58E+00	3,54E+00	5,80E-02	0	3,43E-04	4,04E-04
10	rs12593841	SEMA6D	15	A	G	3,57E+00	3,53E+00	5,80E-02	0	3,55E-04	4,17E-04
10	rs11857221	SEMA6D	15	A	C	3,59E+00	3,52E+00	5,80E-02	0	3,26E-04	4,33E-04
10	rs7175662	SEMA6D	15	G	A	3,57E+00	3,54E+00	6,05E-02	0	3,55E-04	4,04E-04
10	rs7169840	SEMA6D	15	A	C	3,45E+00	3,56E+00	7,21E-02	0	5,59E-04	3,76E-04
10	rs28597109	SEMA6D	15	C	A	3,57E+00	3,52E+00	6,05E-02	0	3,58E-04	4,36E-04
10	rs2173093	SEMA6D	15	A	G	3,58E+00	3,53E+00	5,80E-02	0	3,40E-04	4,23E-04
10	rs11070586	SEMA6D	15	T	A	NaN	NaN	6,05E-02	0	3,63E-04	4,26E-04
11	rs216452	DQ584120	17	T	C	3,66E+00	3,65E+00	4,23E-02	1	2,50E-04	2,59E-04
12	rs17527878	AK127787	18	T	C	4,85E+00	3,42E+00	8,01E-02	1	1,21E-06	6,23E-04
12	rs12458596	AK127787	18	G	A	4,89E+00	3,44E+00	8,01E-02	0	1,03E-06	5,74E-04
12	rs57820851	AK127787	18	T	G	4,65E+00	3,41E+00	8,01E-02	0	3,30E-06	6,59E-04
13	rs6095357	ARFGEF2	20	A	C	-3,85E+00	-3,33E+00	9,33E-02	0	1,18E-04	8,60E-04
13	rs1997851	ARFGEF2	20	T	G	-3,63E+00	-3,35E+00	9,33E-02	0	2,87E-04	8,14E-04
13	rs6012555	ARFGEF2	20	A	C	-3,62E+00	-3,32E+00	9,33E-02	0	2,92E-04	8,89E-04
13	rs6066909	ARFGEF2	20	C	T	-3,63E+00	-3,34E+00	9,33E-02	0	2,82E-04	8,44E-04
13	rs6095359	ARFGEF2	20	T	C	-3,62E+00	-3,35E+00	9,33E-02	0	3,00E-04	8,19E-04
13	rs6019516	ARFGEF2	20	C	T	-3,61E+00	-3,35E+00	9,33E-02	0	3,04E-04	8,13E-04

Locus	SNP	Gene	Chr	A1	A2	z-score SCZ	z-score RT	conjFDR	prune	p SCZ	p RT
13	rs6019519	ARFGEF2	20	T	C	-3,67E+00	-3,41E+00	8,01E-02	1	2,47E-04	6,46E-04
13	rs4810894	ARFGEF2	20	A	G	-3,60E+00	-3,38E+00	9,33E-02	0	3,20E-04	7,22E-04
13	rs1467417	ARFGEF2	20	T	C	-3,60E+00	-3,37E+00	9,33E-02	0	3,23E-04	7,52E-04
13	rs4810896	ARFGEF2	20	A	C	-3,62E+00	-3,38E+00	9,33E-02	0	3,00E-04	7,19E-04

eTable 4. Significant eQTL Functionality of SNPs With Conjunction FDR<.05 Identified Using GTEx (www.gtexportal.org). The effect size is computed as the effect of the alternative allele relative to the reference allele.

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000162989.3	KCNJ3	rs67338739	C/T	0.000026	0.32	**Brain - Cerebellum**
ENSG00000196141.8	SPATS2L	rs6435048	C/T	0.0000020	0.29	Skin - Sun Exposed (Lower leg)
ENSG00000201499.1	RNU6-312P	rs6435048	C/T	0.0000026	0.52	Heart - Atrial Appendage
ENSG00000226124.2	FTCDNL1	rs6435048	C/T	0.000024	-0.29	Thyroid
ENSG00000226124.2	FTCDNL1	rs6435048	C/T	0.000027	-0.23	Muscle - Skeletal
ENSG00000232732.5	AC073043.1	rs6435048	C/T	0.00013	0.41	Testis
ENSG00000163939.14	PBRM1	rs4282054	C/T	1.4e-14	0.37	Thyroid
ENSG00000168268.6	NT5DC2	rs4282054	C/T	4.5e-14	-0.19	Cells - Transformed fibroblasts
ENSG00000168268.6	NT5DC2	rs4282054	C/T	1.1e-13	-0.31	Skin - Sun Exposed (Lower leg)
ENSG00000168237.13	GLYCTK	rs4282054	C/T	3.6e-12	-0.31	Thyroid
ENSG00000114904.8	NEK4	rs4282054	C/T	2.3e-11	-0.32	Cells - Transformed fibroblasts
ENSG00000168268.6	NT5DC2	rs4282054	C/T	3.1e-10	-0.51	Cells - EBV-transformed lymphocytes
ENSG00000168268.6	NT5DC2	rs4282054	C/T	8.8e-10	-0.28	Thyroid
ENSG00000163939.14	PBRM1	rs4282054	C/T	1.3e-9	0.17	Artery - Tibial
ENSG00000163938.12	GNL3	rs4282054	C/T	1.7e-9	-0.18	Cells - Transformed fibroblasts
ENSG00000055955.11	ITIH4	rs4282054	C/T	1.7e-9	0.47	Artery - Aorta
ENSG00000055955.11	ITIH4	rs4282054	C/T	1.1e-8	0.42	Artery - Tibial
ENSG00000163938.12	GNL3	rs4282054	C/T	1.5e-8	-0.22	Artery - Aorta
ENSG00000055955.11	ITIH4	rs4282054	C/T	1.7e-8	0.19	Muscle - Skeletal
ENSG00000168237.13	GLYCTK	rs4282054	C/T	2.1e-8	-0.21	Whole Blood
ENSG00000163938.12	GNL3	rs4282054	C/T	4.7e-8	-0.24	Esophagus - Muscularis
ENSG00000168268.6	NT5DC2	rs4282054	C/T	5.4e-8	-0.47	Colon - Sigmoid
ENSG00000163938.12	GNL3	rs4282054	C/T	1.1e-7	-0.22	Artery - Tibial
ENSG00000213533.7	TMEM110	rs4282054	C/T	3.0e-7	0.30	Artery - Aorta

Gencode Id	**Gene Symbol**	**SNP Id**	**A1/A2**	**P-value**	**Effect Size**	**Tissue**
ENSG00000168268.6	NT5DC2	rs4282054	C/T	3.6e-7	-0.26	Testis
ENSG00000114904.8	NEK4	rs4282054	C/T	4.1e-7	-0.25	Thyroid
ENSG00000168268.6	NT5DC2	rs4282054	C/T	4.8e-7	-0.28	Artery - Aorta
ENSG00000213533.7	TMEM110	rs4282054	C/T	5.2e-7	0.26	Adipose - Subcutaneous
ENSG00000213533.7	TMEM110	rs4282054	C/T	9.7e-7	0.21	Muscle - Skeletal
ENSG00000163939.14	PBRM1	rs4282054	C/T	0.0000010	-0.14	Cells - Transformed fibroblasts
ENSG00000272573.1	MUSTN1	rs4282054	C/T	0.0000011	0.38	Artery - Aorta
ENSG00000168268.6	NT5DC2	rs4282054	C/T	0.0000014	-0.30	Colon - Transverse
ENSG00000055955.11	ITIH4	rs4282054	C/T	0.0000022	0.31	Cells - Transformed fibroblasts
ENSG00000168268.6	NT5DC2	rs4282054	C/T	0.0000028	0.38	Heart - Atrial Appendage
ENSG00000163938.12	GNL3	rs4282054	C/T	0.0000036	-0.24	Heart - Left Ventricle
ENSG00000168237.13	GLYCTK	rs4282054	C/T	0.0000043	-0.21	Lung
ENSG00000114904.8	NEK4	rs4282054	C/T	0.0000043	-0.21	Artery - Tibial
ENSG00000168237.13	GLYCTK	rs4282054	C/T	0.0000044	-0.24	Esophagus - Mucosa
ENSG00000163938.12	GNL3	rs4282054	C/T	0.0000047	-0.17	Colon - Transverse
ENSG00000163938.12	GNL3	rs4282054	C/T	0.0000062	-0.53	**Brain - Cerebellum**
ENSG00000163938.12	GNL3	rs4282054	C/T	0.0000067	-0.29	Testis
ENSG00000163938.12	GNL3	rs4282054	C/T	0.0000079	-0.48	**Brain - Cerebellar Hemisphere**
ENSG00000055955.11	ITIH4	rs4282054	C/T	0.0000085	0.24	Whole Blood
ENSG00000114904.8	NEK4	rs4282054	C/T	0.0000090	-0.26	Breast - Mammary Tissue
ENSG00000163938.12	GNL3	rs4282054	C/T	0.000014	-0.33	**Brain - Frontal Cortex (BA9)**
ENSG00000055955.11	ITIH4	rs4282054	C/T	0.000016	0.18	Adipose - Subcutaneous
ENSG00000114904.8	NEK4	rs4282054	C/T	0.000017	-0.25	Nerve - Tibial
ENSG00000114904.8	NEK4	rs4282054	C/T	0.000021	-0.28	Esophagus - Mucosa
ENSG00000114904.8	NEK4	rs4282054	C/T	0.000021	-0.25	Adipose - Visceral (Omentum)
ENSG00000168268.6	NT5DC2	rs4282054	C/T	0.000022	-0.22	Skin - Not Sun Exposed (Suprapubic)

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000168237.13	GLYCTK	rs4282054	C/T	0.000026	-0.36	Spleen
ENSG00000114904.8	NEK4	rs4282054	C/T	0.000029	-0.19	Skin - Sun Exposed (Lower leg)
ENSG00000213533.7	TMEM110	rs4282054	C/T	0.000033	0.16	Whole Blood
ENSG00000114904.8	NEK4	rs4282054	C/T	0.000042	-0.19	Esophagus - Muscularis
ENSG00000168237.13	GLYCTK	rs4282054	C/T	0.000043	-0.16	Colon - Transverse
ENSG00000168268.6	NT5DC2	rs4282054	C/T	0.000043	-0.33	Spleen
ENSG00000163938.12	GNL3	rs4282054	C/T	0.000051	-0.15	Nerve - Tibial
ENSG00000168237.13	GLYCTK	rs4282054	C/T	0.000060	-0.20	Esophagus - Muscularis
ENSG00000168268.6	NT5DC2	rs4282054	C/T	0.000062	-0.22	Breast - Mammary Tissue
ENSG00000055955.11	ITIH4	rs4282054	C/T	0.000064	0.19	Skin - Sun Exposed (Lower leg)
ENSG00000114904.8	NEK4	rs4282054	C/T	0.000081	-0.17	Lung
ENSG00000272573.1	MUSTN1	rs4282054	C/T	0.000086	0.19	Whole Blood
ENSG00000168268.6	NT5DC2	rs4282054	C/T	0.00010	-0.22	Nerve - Tibial
ENSG00000168237.13	GLYCTK	rs4282054	C/T	0.00011	-0.33	**Brain - Cerebellum**
ENSG00000242094.1	FOXP1-IT1	rs9837383	T/C	0.000023	-0.29	Testis
ENSG00000049167.9	ERCC8	rs4391122	A/G	0.00014	0.18	Cells - Transformed fibroblasts
ENSG00000205464.7	ATP6AP1L	rs12521503	C/T	0.000037	-0.28	Skin - Sun Exposed (Lower leg)
ENSG00000237513.1	RP11-325F22.2	rs4266584	A/C	0.0000043	-0.16	Whole Blood
ENSG00000227603.1	RP11-165J3.6	rs7857165	T/A	0.000015	1.2	**Brain - Cerebellar Hemisphere**
ENSG00000227603.1	RP11-165J3.6	rs7857165	T/A	0.000029	0.72	Thyroid
ENSG00000107954.6	NEURL	rs12253987	T/A	0.0000064	-0.35	Cells - Transformed fibroblasts
ENSG00000175224.12	ATG13	rs2046768	T/C	1.5e-9	-0.32	Esophagus - Muscularis
ENSG00000175224.12	ATG13	rs2046768	T/C	2.1e-8	-0.24	Skin - Sun Exposed (Lower leg)
ENSG00000175224.12	ATG13	rs2046768	T/C	0.0000014	-0.21	Skin - Not Sun Exposed (Suprapubic)
ENSG00000165905.12	GYLTL1B	rs2046768	T/C	0.0000054	0.46	Muscle - Skeletal
ENSG00000180720.6	CHRM4	rs2046768	T/C	0.0000059	-0.42	Nerve - Tibial

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000110492.11	MDK	rs2046768	T/C	0.000011	-0.24	Artery - Tibial
ENSG00000175224.12	ATG13	rs2046768	T/C	0.000015	-0.15	Cells - Transformed fibroblasts
ENSG00000175224.12	ATG13	rs2046768	T/C	0.000037	-0.33	Adipose - Visceral (Omentum)
ENSG00000165912.11	PACSIN3	rs2046768	T/C	0.000048	0.31	Esophagus - Mucosa
ENSG00000110492.11	MDK	rs2046768	T/C	0.000088	-0.27	Heart - Left Ventricle
ENSG00000175224.12	ATG13	rs2046768	T/C	0.00010	-0.18	Nerve - Tibial
ENSG00000175224.12	ATG13	rs2046768	T/C	0.00011	-0.30	Thyroid
ENSG00000249839.1	AC011330.5	rs524908	A/C	2.9e-16	0.66	Thyroid
ENSG00000166763.7	STRCP1	rs524908	A/C	2.7e-14	-0.51	Thyroid
ENSG00000249839.1	AC011330.5	rs524908	A/C	5.1e-13	0.75	Testis
ENSG00000249839.1	AC011330.5	rs524908	A/C	7.3e-13	0.62	Lung
ENSG00000166763.7	STRCP1	rs524908	A/C	1.3e-12	-0.52	Nerve - Tibial
ENSG00000242866.5	STRC	rs524908	A/C	2.9e-11	-0.64	**Brain - Caudate (basal ganglia)**
ENSG00000166763.7	STRCP1	rs524908	A/C	6.0e-11	-0.55	Skin - Not Sun Exposed (Suprapubic)
ENSG00000249839.1	AC011330.5	rs524908	A/C	7.0e-11	0.90	**Brain - Cerebellar Hemisphere**
ENSG00000166763.7	STRCP1	rs524908	A/C	7.2e-11	-0.36	Skin - Sun Exposed (Lower leg)
ENSG00000205771.2	CATSPER2P1	rs524908	A/C	2.5e-10	-0.41	Cells - Transformed fibroblasts
ENSG00000166763.7	STRCP1	rs524908	A/C	2.7e-10	-0.63	Cells - EBV-transformed lymphocytes
ENSG00000242866.5	STRC	rs524908	A/C	5.0e-10	-0.39	Muscle - Skeletal
ENSG00000140265.8	ZSCAN29	rs524908	A/C	5.8e-10	0.31	Thyroid
ENSG00000166763.7	STRCP1	rs524908	A/C	9.3e-10	-0.41	Whole Blood
ENSG00000249839.1	AC011330.5	rs524908	A/C	1.1e-9	0.49	Artery - Tibial
ENSG00000249839.1	AC011330.5	rs524908	A/C	2.0e-9	0.57	Nerve - Tibial
ENSG00000168803.10	ADAL	rs524908	A/C	3.8e-9	0.93	**Brain - Anterior cingulate cortex (BA24)**
ENSG00000166763.7	STRCP1	rs524908	A/C	1.2e-8	-0.43	Esophagus - Muscularis
ENSG00000242866.5	STRC	rs524908	A/C	1.4e-8	-0.64	**Brain - Nucleus accumbens (basal ganglia)**

Gencode Id	**Gene Symbol**	**SNP Id**	**A1/A2**	**P-value**	**Effect Size**	**Tissue**
ENSG00000140265.8	ZSCAN29	rs524908	A/C	1.5e-8	0.31	Skin - Sun Exposed (Lower leg)
ENSG00000242866.5	STRC	rs524908	A/C	2.3e-8	-0.40	Thyroid
ENSG00000168803.10	ADAL	rs524908	A/C	3.6e-8	0.37	Nerve - Tibial
ENSG00000104055.10	TGM5	rs524908	A/C	7.5e-8	-0.61	Cells - EBV-transformed lymphocytes
ENSG00000140265.8	ZSCAN29	rs524908	A/C	8.5e-8	0.30	Breast - Mammary Tissue
ENSG00000249839.1	AC011330.5	rs524908	A/C	9.1e-8	0.50	Esophagus - Muscularis
ENSG00000166763.7	STRCP1	rs524908	A/C	1.1e-7	-0.30	Adipose - Subcutaneous
ENSG00000166763.7	STRCP1	rs524908	A/C	2.1e-7	-0.59	Liver
ENSG00000166763.7	STRCP1	rs524908	A/C	2.7e-7	-0.67	Ovary
ENSG00000223572.5	CKMT1A	rs524908	A/C	2.9e-7	0.33	Esophagus - Mucosa
ENSG00000159495.7	TGM7	rs524908	A/C	3.0e-7	-0.42	Esophagus - Mucosa
ENSG00000166763.7	STRCP1	rs524908	A/C	3.9e-7	-0.39	Artery - Tibial
ENSG00000242866.5	STRC	rs524908	A/C	4.0e-7	-0.44	Skin - Not Sun Exposed (Suprapubic)
ENSG00000249839.1	AC011330.5	rs524908	A/C	4.7e-7	0.76	**Brain - Cerebellum**
ENSG00000249839.1	AC011330.5	rs524908	A/C	4.8e-7	0.62	Heart - Atrial Appendage
ENSG00000242866.5	STRC	rs524908	A/C	5.5e-7	-0.34	Adipose - Subcutaneous
ENSG00000242866.5	STRC	rs524908	A/C	6.3e-7	-0.30	Skin - Sun Exposed (Lower leg)
ENSG00000242866.5	STRC	rs524908	A/C	6.4e-7	-0.61	**Brain - Cortex**
ENSG00000242866.5	STRC	rs524908	A/C	7.0e-7	-0.39	Testis
ENSG00000168803.10	ADAL	rs524908	A/C	0.0000011	0.23	Cells - Transformed fibroblasts
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000013	-0.56	Esophagus - Gastroesophageal Junction
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000013	0.67	Artery - Coronary
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000013	0.77	Uterus
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000016	-0.44	Testis
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000017	0.51	Breast - Mammary Tissue
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000018	-0.79	Uterus

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000019	-0.32	Lung
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000023	-0.70	Small Intestine - Terminal Ileum
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000024	0.39	Adipose - Subcutaneous
ENSG00000242866.5	STRC	rs524908	A/C	0.0000026	-0.36	Nerve - Tibial
ENSG00000168803.10	ADAL	rs524908	A/C	0.0000033	0.16	Muscle - Skeletal
ENSG00000140264.15	SERF2	rs524908	A/C	0.0000034	0.17	Whole Blood
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000035	0.38	Esophagus - Mucosa
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000038	0.63	Cells - EBV-transformed lymphocytes
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000041	0.50	Skin - Not Sun Exposed (Suprapubic)
ENSG00000242866.5	STRC	rs524908	A/C	0.0000045	-0.45	Colon - Transverse
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000046	-0.40	Artery - Aorta
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000050	0.38	Skin - Sun Exposed (Lower leg)
ENSG00000168803.10	ADAL	rs524908	A/C	0.0000051	0.29	Thyroid
ENSG00000242866.5	STRC	rs524908	A/C	0.0000056	-0.29	Breast - Mammary Tissue
ENSG00000168803.10	ADAL	rs524908	A/C	0.0000057	0.28	Lung
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.0000058	0.67	Prostate
ENSG00000242866.5	STRC	rs524908	A/C	0.0000062	-0.49	**Brain - Frontal Cortex (BA9)**
ENSG00000167004.8	PDIA3	rs524908	A/C	0.0000062	0.12	Whole Blood
ENSG00000166763.7	STRCP1	rs524908	A/C	0.0000065	-0.54	Prostate
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.0000066	0.27	Esophagus - Muscularis
ENSG00000242866.5	STRC	rs524908	A/C	0.0000072	-0.37	Esophagus - Muscularis
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.0000077	0.29	Adipose - Visceral (Omentum)
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.0000086	0.14	Cells - Transformed fibroblasts
ENSG00000242866.5	STRC	rs524908	A/C	0.000010	-0.49	**Brain - Putamen (basal ganglia)**
ENSG00000168803.10	ADAL	rs524908	A/C	0.000010	0.24	Breast - Mammary Tissue
ENSG00000168803.10	ADAL	rs524908	A/C	0.000013	0.28	Skin - Sun Exposed (Lower leg)

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000166763.7	STRCP1	rs524908	A/C	0.000016	-0.26	Breast - Mammary Tissue
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.000018	0.15	Muscle - Skeletal
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.000021	0.44	Artery - Aorta
ENSG00000205771.2	CATSPER2P1	rs524908	A/C	0.000028	-0.26	Muscle - Skeletal
ENSG00000168806.6	LCMT2	rs524908	A/C	0.000029	-0.22	Esophagus - Mucosa
ENSG00000205771.2	CATSPER2P1	rs524908	A/C	0.000029	-0.34	Skin - Sun Exposed (Lower leg)
ENSG00000166763.7	STRCP1	rs524908	A/C	0.000034	-0.63	Spleen
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.000039	0.22	Adipose - Subcutaneous
ENSG00000168803.10	ADAL	rs524908	A/C	0.000048	0.25	Adipose - Subcutaneous
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.000059	0.57	Colon - Sigmoid
ENSG00000205771.2	CATSPER2P1	rs524908	A/C	0.000066	-0.39	Skin - Not Sun Exposed (Suprapubic)
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.000066	0.58	Pituitary
ENSG00000067369.9	TP53BP1	rs524908	A/C	0.000072	0.15	Esophagus - Muscularis
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.000079	0.28	Colon - Transverse
ENSG00000168803.10	ADAL	rs524908	A/C	0.00011	0.32	Skin - Not Sun Exposed (Suprapubic)
ENSG00000166763.7	STRCP1	rs524908	A/C	0.00012	-0.49	Adrenal Gland
ENSG00000067369.9	TP53BP1	rs524908	A/C	0.00012	0.14	Cells - Transformed fibroblasts
ENSG00000205771.2	CATSPER2P1	rs524908	A/C	0.00013	-0.31	Lung
ENSG00000140265.8	ZSCAN29	rs524908	A/C	0.00015	0.22	Testis
ENSG00000249839.1	AC011330.5	rs524908	A/C	0.00015	0.47	Colon - Transverse
ENSG00000259928.1	RP11-218M11.1	rs216452	C/T	8.6e-7	-0.23	Testis
ENSG00000230113.1	AC091177.1	rs216452	C/T	0.000093	0.31	Artery - Aorta
ENSG00000167549.14	CORO6	rs216452	C/T	0.00015	0.29	Thyroid
ENSG00000100197.16	CYP2D6	rs134873	T/G	4.1e-33	-0.69	Whole Blood
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.9e-29	-0.76	Skin - Sun Exposed (Lower leg)
ENSG00000183066.10	WBP2NL	rs134873	T/G	8.2e-21	-0.48	Testis

Gencode Id	**Gene Symbol**	**SNP Id**	**A1/A2**	**P-value**	**Effect Size**	**Tissue**
ENSG00000100197.16	CYP2D6	rs134873	T/G	9.1e-21	-0.79	Esophagus - Mucosa
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.8e-20	-0.66	Thyroid
ENSG00000100197.16	CYP2D6	rs134873	T/G	2.0e-17	-0.66	Lung
ENSG00000198951.7	NAGA	rs134873	T/G	4.5e-17	0.47	Nerve - Tibial
ENSG00000198951.7	NAGA	rs134873	T/G	7.1e-17	0.45	Thyroid
ENSG00000100197.16	CYP2D6	rs134873	T/G	4.3e-16	-0.84	**Brain - Nucleus accumbens (basal ganglia)**
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.1e-15	-0.66	Artery - Tibial
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.1e-14	-0.63	Skin - Not Sun Exposed (Suprapubic)
ENSG00000100197.16	CYP2D6	rs134873	T/G	4.3e-14	-0.63	Esophagus - Muscularis
ENSG00000198951.7	NAGA	rs134873	T/G	7.6e-14	0.29	Cells - Transformed fibroblasts
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.4e-13	-0.56	Adipose - Subcutaneous
ENSG00000100197.16	CYP2D6	rs134873	T/G	3.6e-13	-0.94	**Brain - Cerebellar Hemisphere**
ENSG00000198951.7	NAGA	rs134873	T/G	5.2e-13	0.41	Muscle - Skeletal
ENSG00000100197.16	CYP2D6	rs134873	T/G	6.8e-12	-0.95	Spleen
ENSG00000198951.7	NAGA	rs134873	T/G	7.5e-12	0.30	Skin - Sun Exposed (Lower leg)
ENSG00000198951.7	NAGA	rs134873	T/G	1.2e-11	0.44	Esophagus - Muscularis
ENSG00000100197.16	CYP2D6	rs134873	T/G	3.2e-11	-0.70	**Brain - Caudate (basal ganglia)**
ENSG00000183172.8	SMDT1	rs134873	T/G	4.2e-11	0.32	Whole Blood
ENSG00000198951.7	NAGA	rs134873	T/G	4.3e-11	0.24	Adipose - Subcutaneous
ENSG00000100197.16	CYP2D6	rs134873	T/G	4.4e-11	-0.74	**Brain - Putamen (basal ganglia)**
ENSG00000100197.16	CYP2D6	rs134873	T/G	4.5e-11	-0.81	**Brain - Cerebellum**
ENSG00000198951.7	NAGA	rs134873	T/G	9.4e-11	0.55	Pancreas
ENSG00000198951.7	NAGA	rs134873	T/G	1.0e-10	0.41	Artery - Aorta
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.3e-10	-0.39	Colon - Transverse
ENSG00000198951.7	NAGA	rs134873	T/G	1.4e-10	0.33	Skin - Not Sun Exposed (Suprapubic)
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.6e-10	-0.72	**Brain - Hypothalamus**

Gencode Id	**Gene Symbol**	**SNP Id**	**A1/A2**	**P-value**	**Effect Size**	**Tissue**
ENSG00000198951.7	NAGA	rs134873	T/G	2.3e-10	0.32	Artery - Tibial
ENSG00000100197.16	CYP2D6	rs134873	T/G	2.7e-10	-0.46	Cells - Transformed fibroblasts
ENSG00000198951.7	NAGA	rs134873	T/G	2.9e-10	0.60	**Brain - Cerebellum**
ENSG00000100197.16	CYP2D6	rs134873	T/G	3.0e-10	-0.73	**Brain - Hippocampus**
ENSG00000183172.8	SMDT1	rs134873	T/G	3.3e-10	0.39	Adipose - Subcutaneous
ENSG00000183172.8	SMDT1	rs134873	T/G	4.3e-10	0.42	Skin - Sun Exposed (Lower leg)
ENSG00000227370.1	RP4-669P10.19	rs134873	T/G	1.5e-9	-0.46	Skin - Sun Exposed (Lower leg)
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.8e-9	-0.71	**Brain - Frontal Cortex (BA9)**
ENSG00000100197.16	CYP2D6	rs134873	T/G	3.6e-9	-0.63	Adipose - Visceral (Omentum)
ENSG00000198951.7	NAGA	rs134873	T/G	8.6e-9	0.40	Heart - Left Ventricle
ENSG00000183172.8	SMDT1	rs134873	T/G	1.2e-8	0.39	Artery - Aorta
ENSG00000100197.16	CYP2D6	rs134873	T/G	1.5e-8	-0.44	Nerve - Tibial
ENSG00000100197.16	CYP2D6	rs134873	T/G	2.6e-8	-0.80	Pituitary
ENSG00000232710.1	RP4-669P10.16	rs134873	T/G	3.2e-8	0.61	Testis
ENSG00000198951.7	NAGA	rs134873	T/G	5.1e-8	0.70	Pituitary
ENSG00000198951.7	NAGA	rs134873	T/G	5.4e-8	0.42	Heart - Atrial Appendage
ENSG00000100197.16	CYP2D6	rs134873	T/G	5.4e-8	-0.75	**Brain - Cortex**
ENSG00000198951.7	NAGA	rs134873	T/G	5.6e-8	0.28	Adipose - Visceral (Omentum)
ENSG00000198951.7	NAGA	rs134873	T/G	6.0e-8	0.60	**Brain - Cerebellar Hemisphere**
ENSG00000100197.16	CYP2D6	rs134873	T/G	6.8e-8	-0.50	Artery - Aorta
ENSG00000237037.5	NDUFA6-AS1	rs134873	T/G	8.9e-8	-0.34	Skin - Sun Exposed (Lower leg)
ENSG00000198951.7	NAGA	rs134873	T/G	1.2e-7	0.35	Stomach
ENSG00000100197.16	CYP2D6	rs134873	T/G	2.6e-7	-0.61	Cells - EBV-transformed lymphocytes
ENSG00000183172.8	SMDT1	rs134873	T/G	2.6e-7	0.38	Esophagus - Muscularis
ENSG00000198951.7	NAGA	rs134873	T/G	4.1e-7	0.22	Lung
ENSG00000213790.2	OLA1P1	rs134873	T/G	5.0e-7	0.75	Liver

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000183172.8	SMDT1	rs134873	T/G	5.3e-7	0.23	Muscle - Skeletal
ENSG00000183172.8	SMDT1	rs134873	T/G	7.2e-7	0.40	Adipose - Visceral (Omentum)
ENSG00000100197.16	CYP2D6	rs134873	T/G	7.5e-7	-0.59	Pancreas
ENSG00000100197.16	CYP2D6	rs134873	T/G	9.8e-7	-0.43	Stomach
ENSG00000100197.16	CYP2D6	rs134873	T/G	0.0000011	-0.62	Artery - Coronary
ENSG00000100197.16	CYP2D6	rs134873	T/G	0.0000011	-0.54	Adrenal Gland
ENSG00000198951.7	NAGA	rs134873	T/G	0.0000012	0.38	**Brain - Nucleus accumbens (basal ganglia)**
ENSG00000183172.8	SMDT1	rs134873	T/G	0.0000017	0.51	Esophagus - Gastroesophageal Junction
ENSG00000273366.1	CTA-989H11.1	rs134873	T/G	0.0000017	-0.35	Esophagus - Mucosa
ENSG00000183172.8	SMDT1	rs134873	T/G	0.0000021	0.52	Colon - Sigmoid
ENSG00000183172.8	SMDT1	rs134873	T/G	0.0000024	0.59	Cells - EBV-transformed lymphocytes
ENSG00000198951.7	NAGA	rs134873	T/G	0.0000027	0.30	Breast - Mammary Tissue
ENSG00000183172.8	SMDT1	rs134873	T/G	0.0000044	0.28	Thyroid
ENSG00000183172.8	SMDT1	rs134873	T/G	0.0000046	0.51	Pituitary
ENSG00000227370.1	RP4-669P10.19	rs134873	T/G	0.0000062	0.44	Testis
ENSG00000100197.16	CYP2D6	rs134873	T/G	0.0000065	-0.76	**Brain - Anterior cingulate cortex (BA24)**
ENSG00000270083.1	RP1-257I20.14	rs134873	T/G	0.0000071	0.60	**Brain - Cerebellum**
ENSG00000183172.8	SMDT1	rs134873	T/G	0.0000097	0.42	Skin - Not Sun Exposed (Suprapubic)
ENSG00000100197.16	CYP2D6	rs134873	T/G	0.000010	-0.63	Prostate
ENSG00000198951.7	NAGA	rs134873	T/G	0.000010	0.36	**Brain - Frontal Cortex (BA9)**
ENSG00000232710.1	RP4-669P10.16	rs134873	T/G	0.000010	0.67	Ovary
ENSG00000100197.16	CYP2D6	rs134873	T/G	0.000013	-0.40	Breast - Mammary Tissue
ENSG00000227370.1	RP4-669P10.19	rs134873	T/G	0.000013	-0.64	**Brain - Hypothalamus**
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000019	0.71	Ovary
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000020	0.48	Pancreas
ENSG00000182057.4	Z83851.3	rs134873	T/G	0.000021	0.42	Artery - Aorta

Gencode Id	Gene Symbol	SNP Id	A1/A2	P-value	Effect Size	Tissue
ENSG00000273366.1	CTA-989H11.1	rs134873	T/G	0.000027	-0.42	Testis
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000027	0.27	Esophagus - Mucosa
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000034	0.27	Nerve - Tibial
ENSG00000182057.4	Z83851.3	rs134873	T/G	0.000035	0.35	Thyroid
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000041	0.41	Colon - Transverse
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000042	0.33	Stomach
ENSG00000183172.8	SMDT1	rs134873	T/G	0.000055	0.22	Artery - Tibial
ENSG00000237037.5	NDUFA6-AS1	rs134873	T/G	0.000057	-0.32	Skin - Not Sun Exposed (Suprapubic)
ENSG00000270083.1	RP1-257I20.14	rs134873	T/G	0.000067	0.29	Thyroid
ENSG00000227370.1	RP4-669P10.19	rs134873	T/G	0.00011	-0.36	Esophagus - Muscularis

eTable 5. Cis-eQTL Data in Human Brain Using UK Brain Expression Consortium Data (www.braineac.org). Expression Affected by SNP Shown by the Exon-Specific Probeset or Transcript-Level ("t"+exprID; Winsorised mean over probesets). SNPs With Significant Brain eQTL Functionality Using GTEx Data Were Assessed (Table S4). Data for rs7857165 Were Not Available.

Gene	SNP	ExprID	Chr	Start	Stop	Average of brain tissues	Cere-bellum	Frontal cortex	Hippo-campus	Medulla	Occip. cortex	Puta-men	Subst. Nigra	Temp. Cortex	Thal-amus	White Matter
KCNJ3	rs67338739	2511170	chr2	155482391	155714866	2.5e-02	9.2e-02	9.0e-01	3.3e-03	1.4e-01	2.5e-01	1.9e-01	7.2e-01	7.6e-01	2.6e-01	1.2e-01
KCNJ3	rs67338739	2511169	chr2	155482391	155714866	2.3e-02	3.8e-02	8.4e-01	3.3e-03	1.5e-01	1.8e-01	2.5e-01	9.3e-01	6.8e-01	2.4e-01	1.0e-01
KCNJ3	rs67338739	t2511153	chr2	155482391	155714866	1.8e-02	1.3e-02	9.5e-01	4.3e-03	2.8e-01	2.1e-01	1.8e-01	4.5e-01	6.8e-01	2.5e-01	1.8e-01
KCNJ3	rs67338739	2511185	chr2	155482391	155714866	5.7e-03	9.7e-03	5.8e-01	4.9e-03	4.9e-01	2.0e-01	5.0e-01	1.2e-01	5.2e-01	4.9e-01	3.7e-02
KCNJ3	rs67338739	2511166	chr2	155482391	155714866	9.7e-03	8.8e-02	5.0e-01	5.5e-03	1.7e-01	1.8e-01	1.3e-01	3.4e-01	6.2e-01	2.5e-01	1.2e-01
KCNJ3	rs67338739	2511171	chr2	155482391	155714866	5.0e-02	1.4e-01	8.8e-01	1.1e-02	3.0e-02	6.0e-01	1.3e-01	3.5e-01	8.2e-01	3.0e-01	7.7e-01
KCNJ3	rs67338739	2511184	chr2	155482391	155714866	2.1e-02	9.0e-02	4.1e-01	1.9e-02	7.1e-01	3.2e-01	1.6e-01	6.5e-01	5.3e-01	2.0e-01	1.1e-01
KCNJ3	rs67338739	2511165	chr2	155482391	155714866	3.6e-02	4.3e-02	7.4e-01	3.6e-02	4.3e-01	8.6e-02	9.7e-01	7.8e-01	7.5e-01	2.5e-01	7.0e-01
KCNJ3	rs67338739	2511164	chr2	155482391	155714866	5.9e-01	3.3e-01	8.0e-01	9.2e-01	4.5e-02	5.2e-01	2.4e-01	3.6e-01	4.8e-01	5.6e-01	7.6e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624078	chr3	52719936	52730172	1.4e-04	9.0e-02	2.2e-02	1.9e-01	4.8e-04	1.4e-01	1.8e-01	5.6e-02	5.8e-01	4.2e-02	5.4e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624081	chr3	52719936	52730172	8.2e-04	3.8e-03	2.2e-01	1.3e-01	3.2e-01	2.0e-02	4.9e-01	5.3e-01	2.0e-01	1.8e-01	7.7e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624108	chr3	52719936	52730172	4.1e-01	8.1e-01	5.6e-01	6.8e-01	2.2e-01	4.9e-01	7.7e-01	4.8e-01	6.7e-01	1.1e-02	4.7e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624082	chr3	52719936	52730172	2.5e-02	1.1e-01	1.4e-01	3.9e-01	1.1e-01	2.5e-02	5.8e-01	4.0e-01	6.0e-01	8.3e-01	5.2e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624106	chr3	52719936	52730172	8.3e-01	4.7e-01	7.6e-01	8.0e-01	9.3e-01	5.8e-01	4.8e-02	2.7e-01	8.8e-01	9.9e-01	4.8e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624075	chr3	52719936	52730172	1.6e-01	5.8e-01	9.3e-02	8.9e-01	4.9e-01	5.6e-02	6.9e-01	1.8e-01	3.0e-01	1.4e-01	7.4e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624109	chr3	52719936	52730172	5.3e-01	2.5e-01	2.9e-01	6.3e-01	3.4e-01	8.1e-01	6.4e-02	3.5e-01	3.4e-01	5.6e-01	9.6e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624100	chr3	52719936	52730172	8.9e-02	7.3e-02	3.0e-01	1.6e-01	4.1e-01	1.3e-01	9.5e-01	3.2e-01	1.8e-01	8.1e-01	5.1e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624087	chr3	52719936	52730172	7.5e-02	1.8e-01	3.9e-01	8.0e-02	8.1e-01	1.9e-01	8.6e-01	2.1e-01	1.0e-01	7.7e-01	8.6e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624096	chr3	52719936	52730172	3.5e-01	2.3e-01	7.7e-01	8.0e-01	6.4e-01	3.4e-01	7.3e-01	9.4e-02	2.8e-01	4.1e-01	8.5e-01

Gene	SNP	ExprID	Chr	Start	Stop	Average of brain tissues	Cere-bellum	Frontal cortex	Hippo-campus	Medulla	Occip. cortex	Puta-men	Subst. Nigra	Temp. Cortex	Thal-amus	White Matter
GNL3,GLT8D1, SNORD19B	rs4282054	2624107	chr3	52719936	52730172	9.9e-01	1.7e-01	5.2e-01	5.6e-01	6.9e-01	5.4e-01	1.1e-01	7.3e-01	6.0e-01	5.1e-01	5.3e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624093	chr3	52719936	52730172	9.4e-01	9.3e-01	3.0e-01	4.8e-01	4.0e-01	7.2e-01	1.1e-01	5.8e-01	5.7e-01	9.6e-01	9.2e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624102	chr3	52719936	52730172	8.8e-01	7.5e-01	2.6e-01	8.8e-01	5.8e-01	6.6e-01	1.1e-01	2.7e-01	6.0e-01	3.8e-01	1.0e+00
GNL3,GLT8D1, SNORD19B	rs4282054	2624095	chr3	52719936	52730172	6.5e-01	7.7e-01	6.0e-01	5.0e-01	6.4e-01	5.6e-01	1.2e-01	2.9e-01	5.8e-01	5.2e-01	5.7e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624083	chr3	52719936	52730172	2.7e-01	2.3e-01	5.6e-01	5.6e-01	4.9e-01	1.4e-01	3.1e-01	1.8e-01	2.0e-01	2.9e-01	9.1e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624092	chr3	52719936	52730172	4.7e-01	8.7e-01	6.6e-01	5.5e-01	9.6e-01	9.4e-01	5.3e-01	7.8e-01	2.5e-01	1.5e-01	4.4e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624084	chr3	52719936	52730172	7.6e-01	1.6e-01	1.6e-01	2.7e-01	7.9e-01	4.9e-01	5.5e-01	1.0e+00	8.6e-01	6.4e-01	7.1e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624091	chr3	52719936	52730172	5.5e-01	9.7e-01	9.1e-01	9.3e-01	6.7e-01	9.8e-01	1.7e-01	7.9e-01	2.5e-01	3.8e-01	1.8e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624076	chr3	52719936	52730172	8.8e-01	5.3e-01	3.7e-01	9.6e-01	2.7e-01	2.0e-01	5.6e-01	2.0e-01	8.6e-01	3.4e-01	2.3e-01
GNL3,GLT8D1, SNORD19B	rs4282054	t2624074	chr3	52719936	52730172	3.2e-01	2.3e-01	4.4e-01	4.1e-01	9.0e-01	2.0e-01	3.2e-01	2.5e-01	6.1e-01	8.8e-01	9.6e-01
GNL3,GLT8D1, SNORD19B	rs4282054	2624098	chr3	52719936	52730172	5.2e-01	5.6e-01	9.4e-01	6.7e-01	8.6e-01	3.3e-01	7.8e-01	7.1e-01	7.8e-01	3.3e-01	7.6e-01
GLYCTK	rs4282054	2623622	chr3	52321125	52329252	1.6e-02	2.3e-01	1.4e-01	7.8e-01	6.4e-01	1.8e-01	9.8e-01	1.0e-02	5.7e-01	7.4e-01	5.5e-02
GLYCTK	rs4282054	2623625	chr3	52321125	52329252	9.2e-02	1.3e-01	7.3e-02	1.5e-01	1.3e-01	2.1e-02	2.5e-01	1.5e-01	5.2e-01	7.5e-01	4.3e-01
GLYCTK	rs4282054	2623618	chr3	52321125	52329252	7.9e-01	9.8e-01	2.8e-01	4.9e-01	7.5e-01	6.8e-01	5.5e-01	1.0e+00	4.7e-01	7.1e-01	4.8e-02
GLYCTK	rs4282054	2623623	chr3	52321125	52329252	6.7e-02	3.4e-01	6.9e-02	1.2e-01	3.2e-01	3.6e-01	3.0e-01	9.0e-02	8.5e-01	3.8e-01	4.9e-01
GLYCTK	rs4282054	2623629	chr3	52321125	52329252	3.3e-01	7.5e-01	2.2e-01	8.3e-01	8.3e-01	6.4e-01	6.7e-01	7.5e-02	8.1e-01	2.9e-01	7.9e-01
GLYCTK	rs4282054	2623632	chr3	52321125	52329252	2.9e-01	6.4e-01	9.3e-01	4.8e-01	6.6e-01	3.8e-01	5.8e-01	4.5e-01	3.6e-01	4.2e-01	7.7e-02
GLYCTK	rs4282054	2623630	chr3	52321125	52329252	7.5e-01	6.2e-01	8.2e-01	3.5e-01	1.6e-01	8.5e-01	5.3e-01	6.9e-01	7.9e-02	8.5e-01	5.5e-01
GLYCTK	rs4282054	2623631	chr3	52321125	52329252	3.7e-01	1.9e-01	8.3e-01	1.2e-01	2.1e-01	1.1e-01	5.2e-01	3.4e-01	6.6e-01	4.8e-01	4.1e-01
GLYCTK	rs4282054	2623621	chr3	52321125	52329252	2.6e-01	5.9e-01	8.3e-01	2.3e-01	6.0e-01	5.8e-01	7.9e-01	1.0e+00	1.4e-01	1.4e-01	1.4e-01
GLYCTK	rs4282054	2623616	chr3	52321125	52329252	7.9e-01	1.5e-01	5.7e-01	3.3e-01	1.7e-01	5.6e-01	2.9e-01	4.1e-01	2.9e-01	8.0e-01	4.7e-01

Gene	SNP	ExprID	Chr	Start	Stop	Average of brain tissues	Cerebellum	Frontal cortex	Hippocampus	Medulla	Occip. cortex	Putamen	Subst. Nigra	Temp. Cortex	Thalamus	White Matter
GLYCTK	rs4282054	t2623611	chr3	52321125	52329252	1.9e-01	2.1e-01	1.9e-01	3.0e-01	2.0e-01	9.4e-01	9.7e-01	3.4e-01	3.6e-01	9.6e-01	5.8e-01
GLYCTK	rs4282054	2623624	chr3	52321125	52329252	3.9e-01	4.8e-01	7.4e-01	3.7e-01	5.8e-01	5.4e-01	7.7e-01	5.2e-01	8.5e-01	5.0e-01	2.0e-01
GLYCTK	rs4282054	2623633	chr3	52321125	52329252	8.0e-01	7.8e-01	7.0e-01	5.3e-01	6.9e-01	4.7e-01	8.0e-01	4.8e-01	7.5e-01	4.3e-01	6.9e-01
GLYCTK	rs4282054	2623627	chr3	52321125	52329252	6.7e-01	8.6e-01	8.5e-01	7.6e-01	3.3e-01	3.3e-01	2.1e-01	6.6e-01	4.9e-01	4.9e-01	4.9e-01
ADAL	rs524908	3591367	chr15	43622052	43646685	2.1e-04	2.4e-03	2.1e-02	1.9e-02	6.7e-02	4.1e-02	8.1e-02	9.4e-02	1.7e-03	1.8e-02	1.8e-03
ADAL	rs524908	3591387	chr15	43622052	43646685	4.8e-02	6.4e-04	9.6e-01	7.0e-01	7.9e-01	5.2e-04	9.3e-01	3.2e-01	1.3e-01	3.8e-01	8.5e-01
ADAL	rs524908	3591384	chr15	43622052	43646685	2.3e-02	5.0e-01	3.9e-01	2.7e-01	1.3e-01	4.4e-02	3.3e-01	1.2e-03	9.8e-01	6.0e-01	7.9e-02
ADAL	rs524908	3591389	chr15	43622052	43646685	2.7e-02	8.2e-03	1.8e-01	4.9e-01	8.5e-02	1.5e-03	6.6e-01	2.3e-01	1.3e-01	1.0e-01	5.2e-01
ADAL	rs524908	3591383	chr15	43622052	43646685	5.2e-02	1.8e-01	7.7e-01	5.9e-01	2.5e-02	1.3e-01	7.5e-01	3.7e-03	7.1e-01	8.6e-01	9.4e-01
ADAL	rs524908	3591390	chr15	43622052	43646685	3.0e-02	8.5e-03	8.3e-01	4.6e-01	2.1e-01	4.9e-03	7.4e-01	4.5e-02	1.2e-02	5.4e-01	4.4e-01
ADAL	rs524908	3591370	chr15	43622052	43646685	2.4e-02	4.0e-01	2.8e-01	4.0e-01	6.9e-03	7.1e-02	1.7e-02	4.7e-02	5.8e-01	3.6e-01	9.6e-01
ADAL	rs524908	t3591365	chr15	43622052	43646685	1.0e-01	1.4e-02	9.5e-01	5.3e-01	8.2e-02	3.7e-02	4.8e-01	6.9e-02	2.9e-01	1.7e-01	9.6e-01
ADAL	rs524908	3591382	chr15	43622052	43646685	4.8e-01	8.2e-01	4.5e-01	5.9e-01	5.5e-01	2.9e-01	8.7e-01	5.3e-01	5.0e-01	2.2e-02	2.2e-01
ADAL	rs524908	3591372	chr15	43622052	43646685	8.0e-01	3.8e-01	8.2e-01	3.1e-01	5.1e-01	9.2e-01	4.7e-01	2.5e-02	6.4e-01	1.8e-01	9.7e-01
ADAL	rs524908	3591391	chr15	43622052	43646685	2.3e-01	3.1e-02	5.2e-01	8.0e-01	1.1e-01	5.2e-02	8.6e-01	4.6e-01	9.7e-02	2.3e-01	1.8e-01
ADAL	rs524908	3591385	chr15	43622052	43646685	2.2e-01	9.6e-01	1.0e-01	7.9e-01	3.3e-01	7.5e-01	2.7e-01	2.0e-01	3.1e-02	4.0e-01	3.7e-01
ADAL	rs524908	3591392	chr15	43622052	43646685	1.8e-01	3.5e-02	9.0e-01	5.6e-01	6.0e-02	4.7e-02	7.1e-01	1.6e-01	9.6e-01	3.5e-01	9.9e-01
ADAL	rs524908	3591379	chr15	43622052	43646685	2.0e-01	1.7e-01	7.0e-01	5.0e-01	7.9e-01	2.8e-01	5.4e-02	2.0e-01	9.1e-01	5.2e-01	7.6e-01
ADAL	rs524908	3591373	chr15	43622052	43646685	9.1e-01	6.7e-01	1.5e-01	6.2e-01	4.9e-01	9.8e-01	7.6e-01	3.9e-01	3.7e-01	6.0e-02	9.2e-01
ADAL	rs524908	3591381	chr15	43622052	43646685	1.9e-01	6.3e-01	3.9e-01	2.2e-01	9.4e-02	4.5e-01	1.8e-01	7.1e-02	9.4e-01	9.5e-01	9.5e-01
ADAL	rs524908	3591376	chr15	43622052	43646685	7.1e-01	7.4e-01	1.0e-01	9.7e-01	1.8e-01	5.2e-01	4.6e-01	7.9e-02	5.9e-01	3.3e-01	8.4e-01
ADAL	rs524908	3591388	chr15	43622052	43646685	7.5e-01	1.9e-01	1.8e-01	8.2e-02	4.6e-01	4.8e-01	2.5e-01	3.5e-01	1.0e-01	8.3e-01	1.9e-01
ADAL	rs524908	3591366	chr15	43622052	43646685	2.0e-01	6.2e-01	2.5e-01	7.8e-01	7.7e-01	1.5e-01	5.8e-01	1.4e-01	9.9e-02	6.9e-01	4.2e-01
STRC	rs524908	3621378	chr15	43891605	43910968	1.9e-06	3.6e-01	3.1e-03	1.6e-03	4.3e-02	2.1e-02	6.9e-02	5.6e-05	1.3e-05	3.4e-03	2.9e-03
STRC	rs524908	3621380	chr15	43891605	43910968	5.5e-05	1.1e-01	7.7e-04	2.0e-01	2.0e-02	3.2e-03	4.2e-01	7.3e-02	1.9e-05	1.7e-02	6.2e-02

Gene	SNP	ExprID	Chr	Start	Stop	Average of brain tissues	Cere-bellum	Frontal cortex	Hippo-campus	Medulla	Occip. cortex	Puta-men	Subst. Nigra	Temp. Cortex	Thal-amus	White Matter
STRC	rs524908	t3621351	chr15	43891605	43910968	3.1e-05	6.5e-02	8.9e-03	1.5e-01	3.4e-02	3.4e-03	2.0e-01	8.2e-03	5.8e-04	4.1e-03	4.0e-03
STRC	rs524908	3621376	chr15	43891605	43910968	2.1e-04	7.2e-02	1.9e-01	3.8e-03	1.3e-01	1.3e-01	5.3e-01	6.7e-02	4.0e-02	2.4e-02	2.7e-03
STRC	rs524908	3621366	chr15	43891605	43910968	2.3e-03	4.7e-01	4.0e-01	6.0e-01	1.4e-02	7.8e-01	6.0e-02	1.2e-02	1.7e-01	5.3e-01	8.0e-02
STRC	rs524908	3621373	chr15	43891605	43910968	6.2e-01	8.5e-01	6.3e-01	8.2e-01	6.7e-01	1.5e-02	7.4e-01	5.2e-01	9.1e-01	8.0e-01	6.7e-01
STRC	rs524908	3621367	chr15	43891605	43910968	2.2e-02	1.1e-01	3.4e-01	6.8e-01	8.0e-02	4.9e-02	4.7e-01	3.9e-02	2.1e-02	4.0e-02	4.0e-01
STRC	rs524908	3621352	chr15	43891605	43910968	4.5e-01	9.3e-01	3.0e-01	9.2e-01	6.7e-01	7.7e-01	1.7e-01	8.8e-01	3.5e-01	8.5e-01	6.4e-01
CYP2D7P1,CYP2D6	rs134873	t3962293	chr22	42535612	42551082	1.6e-05	2.8e-02	2.2e-01	9.1e-04	2.2e-01	1.7e-01	1.3e-01	1.9e-01	3.0e-01	2.0e-02	3.3e-02
CYP2D7P1,CYP2D6	rs134873	3962299	chr22	42535612	42551082	4.0e-05	9.1e-03	3.7e-02	2.4e-02	8.3e-01	4.4e-01	5.9e-02	1.8e-02	4.9e-01	1.2e-03	3.0e-02
CYP2D7P1,CYP2D6	rs134873	3962306	chr22	42535612	42551082	4.3e-04	1.0e-01	8.9e-01	6.0e-03	3.4e-01	5.6e-01	7.7e-01	8.6e-01	7.1e-02	6.6e-02	5.5e-03
CYP2D7P1,CYP2D6	rs134873	3962308	chr22	42535612	42551082	5.0e-03	4.4e-02	4.4e-01	4.5e-04	4.6e-01	8.6e-02	3.5e-01	5.3e-02	3.5e-01	2.6e-01	1.3e-02
CYP2D7P1,CYP2D6	rs134873	3962294	chr22	42535612	42551082	6.6e-03	4.2e-01	9.0e-02	9.3e-02	1.8e-01	8.6e-01	3.4e-01	6.6e-01	6.1e-01	3.1e-01	5.4e-01
CYP2D7P1,CYP2D6	rs134873	3962312	chr22	42535612	42551082	2.7e-02	6.3e-01	9.9e-02	7.9e-02	1.5e-01	3.8e-01	3.6e-01	6.1e-01	5.1e-01	7.8e-01	2.5e-01
CYP2D7P1,CYP2D6	rs134873	3962314	chr22	42535612	42551082	5.4e-02	7.9e-01	8.4e-02	6.1e-01	9.1e-01	2.8e-02	7.8e-01	1.4e-01	2.5e-01	1.2e-01	6.8e-01
CYP2D7P1,CYP2D6	rs134873	3962295	chr22	42535612	42551082	9.2e-01	1.8e-01	8.9e-01	4.1e-01	3.7e-02	3.8e-01	5.9e-01	6.0e-01	9.7e-01	8.7e-01	2.6e-01
NAGA	rs134873	3962245	chr22	42422833	42466846	2.5e-04	4.9e-02	3.0e-03	4.2e-01	7.4e-01	7.9e-02	3.7e-02	3.3e-03	9.4e-01	3.7e-02	5.0e-02
NAGA	rs134873	3962232	chr22	42422833	42466846	1.2e-02	9.1e-02	2.8e-03	8.4e-01	3.0e-02	3.4e-01	5.6e-01	1.7e-01	2.8e-04	9.4e-01	5.3e-01
NAGA	rs134873	t3962219	chr22	42422833	42466846	6.4e-02	3.8e-01	3.3e-04	9.1e-01	3.8e-01	7.9e-03	2.2e-02	3.6e-01	2.3e-03	9.3e-01	4.1e-01
NAGA	rs134873	3962231	chr22	42422833	42466846	1.6e-01	8.3e-01	5.5e-02	4.5e-01	1.3e-03	3.0e-01	2.5e-02	8.4e-01	4.4e-03	5.3e-01	8.3e-01
NAGA	rs134873	3962244	chr22	42422833	42466846	9.8e-02	7.2e-01	1.6e-03	9.5e-01	9.7e-01	2.7e-01	3.8e-01	3.3e-01	6.9e-02	6.0e-01	3.1e-01
NAGA	rs134873	3962239	chr22	42422833	42466846	7.7e-02	1.8e-01	1.1e-02	3.9e-01	9.0e-01	1.8e-03	1.2e-01	8.9e-01	1.1e-01	5.0e-01	3.3e-01
NAGA	rs134873	3962240	chr22	42422833	42466846	8.9e-01	7.1e-01	2.9e-01	3.3e-01	8.8e-01	9.9e-03	8.8e-01	6.5e-01	5.6e-02	4.3e-02	9.2e-02
NAGA	rs134873	3962237	chr22	42422833	42466846	1.6e-02	8.0e-01	7.6e-02	4.4e-01	1.3e-01	1.0e-02	5.6e-02	9.7e-01	9.6e-02	3.4e-01	7.5e-01

Gene	SNP	ExprID	Chr	Start	Stop	Average of brain tissues	Cere-bellum	Frontal cortex	Hippo-campus	Medulla	Occip. cortex	Puta-men	Subst. Nigra	Temp. Cortex	Thal-amus	White Matter
NAGA	rs134873	3962236	chr22	42422833	42466846	1.4e-01	9.4e-01	1.2e-01	7.7e-01	3.7e-01	5.7e-01	1.9e-01	4.0e-01	2.4e-01	1.7e-02	9.5e-01
NAGA	rs134873	3962238	chr22	42422833	42466846	2.1e-02	7.9e-01	2.3e-01	2.7e-01	6.5e-01	4.1e-02	7.3e-01	2.0e-01	5.8e-01	6.6e-01	1.8e-01
NAGA	rs134873	3962234	chr22	42422833	42466846	2.2e-02	3.7e-01	6.2e-01	4.7e-01	9.0e-01	8.1e-02	1.5e-01	1.3e-01	8.1e-01	4.8e-01	6.1e-02
NAGA	rs134873	3962247	chr22	42422833	42466846	4.0e-01	2.5e-02	9.3e-01	4.1e-01	2.0e-01	9.6e-02	4.3e-01	1.7e-01	5.8e-02	3.4e-01	1.8e-01
NAGA	rs134873	3962233	chr22	42422833	42466846	2.1e-01	3.7e-01	1.0e-01	2.8e-01	4.1e-02	4.8e-01	7.5e-01	4.1e-01	2.9e-02	9.3e-01	8.3e-01
NAGA	rs134873	3962249	chr22	42422833	42466846	1.3e-01	8.5e-01	2.1e-01	5.0e-01	9.4e-01	6.1e-01	4.3e-02	4.9e-01	3.2e-01	1.7e-01	1.4e-01
NAGA	rs134873	3962248	chr22	42422833	42466846	3.6e-01	1.8e-01	9.4e-01	2.4e-01	9.3e-01	9.5e-01	1.8e-01	5.3e-01	6.4e-01	3.1e-01	5.8e-02
NAGA	rs134873	3962243	chr22	42422833	42466846	6.3e-01	9.3e-01	1.1e-01	4.9e-01	4.8e-01	2.9e-01	4.7e-01	8.3e-01	2.4e-01	2.2e-01	2.1e-01
NAGA	rs134873	3962241	chr22	42422833	42466846	6.6e-01	1.8e-01	3.4e-01	7.6e-01	6.8e-01	2.9e-01	5.5e-01	3.4e-01	7.1e-01	3.6e-01	9.6e-01
NAGA	rs134873	3962221	chr22	42422833	42466846	4.1e-01	8.0e-01	1.9e-01	8.8e-01	8.0e-01	2.2e-01	6.3e-01	2.5e-01	2.3e-01	9.7e-01	8.7e-01

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