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Supplemental Information

Genetic Differences in the Immediate Transcriptome Response to Stress Predict Risk-Related Brain Function and Psychiatric Disorders

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SUPPLEMENTAL DATA

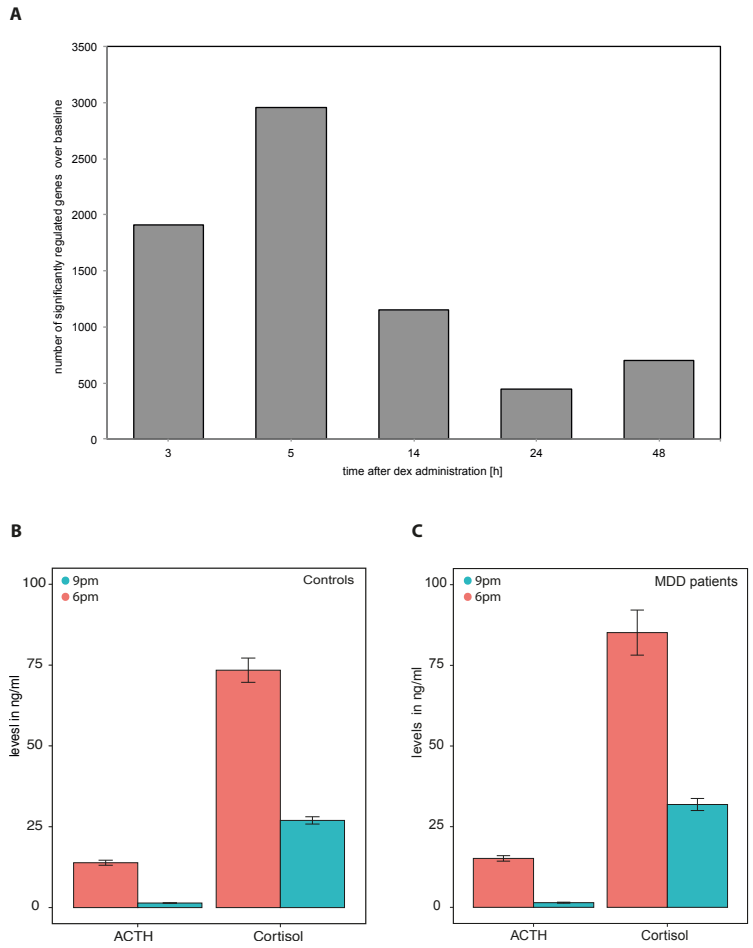

Figure S1. Related to Figure 2.

(A) Time course of gene expression changes after oral dexamethasone administration. The number of genes that are differently expressed at several time points after administration of 1.5 mg dexamethasone relative to baseline in 4 healthy male individuals are shown. The height of the bars indicates the total number of transcripts with nominally significant changes from baseline gene expression. Baseline blood samples were obtained at 6pm. This evening time point was chosen so that the stimulation experiments took place during the quiescent period of the stress hormone system. Baseline blood draws were immediately followed by oral administration of dexamethasone. Additional blood samples were drawn at 9pm and 11pm on the same day, at 8am and 6pm the next day and at 6pm on day 3. A comparison of baseline gene expression vs. gene expression after 3, 5, 14, 24 and 48 h shows an initial high number of gene expression changes, followed by a normalization within 24-48 hours. The highest number of differently expressed genes (highest bar in chart) was observed at 3 and 5 hours post dexamethasone ingestion. For practical reasons as well as to avoid secondary GR target effects, in the subsequent experiment we collected blood 3 hours after dexamethasone intake. (B), (C) Dexamethasone effect on cortisol and ACTH levels. Administration of dexamethasone resulted in a robust suppression of cortisol in all individuals. Cortisol levels were significantly suppressed in healthy controls (B; $F_{1,90} = 89.74$, $P = 3.57 \times 10^{-15}$) as well as in depressed patients (C; $F_{1,67} = 7.09$, $P = 0.0097$) 3h after dexamethasone challenge. Similar results were observed for ACTH, with a significant reduction in ACTH levels in healthy controls B; $F_{1,91} = 43.96$, $P = 2.33 \times 10^{-9}$) and in depressed patients (C; $F_{1,65} = 9.75$, $P = 0.0027$) after 3h.

P values in (A,B) derived from a linear model; error bars: ± sem

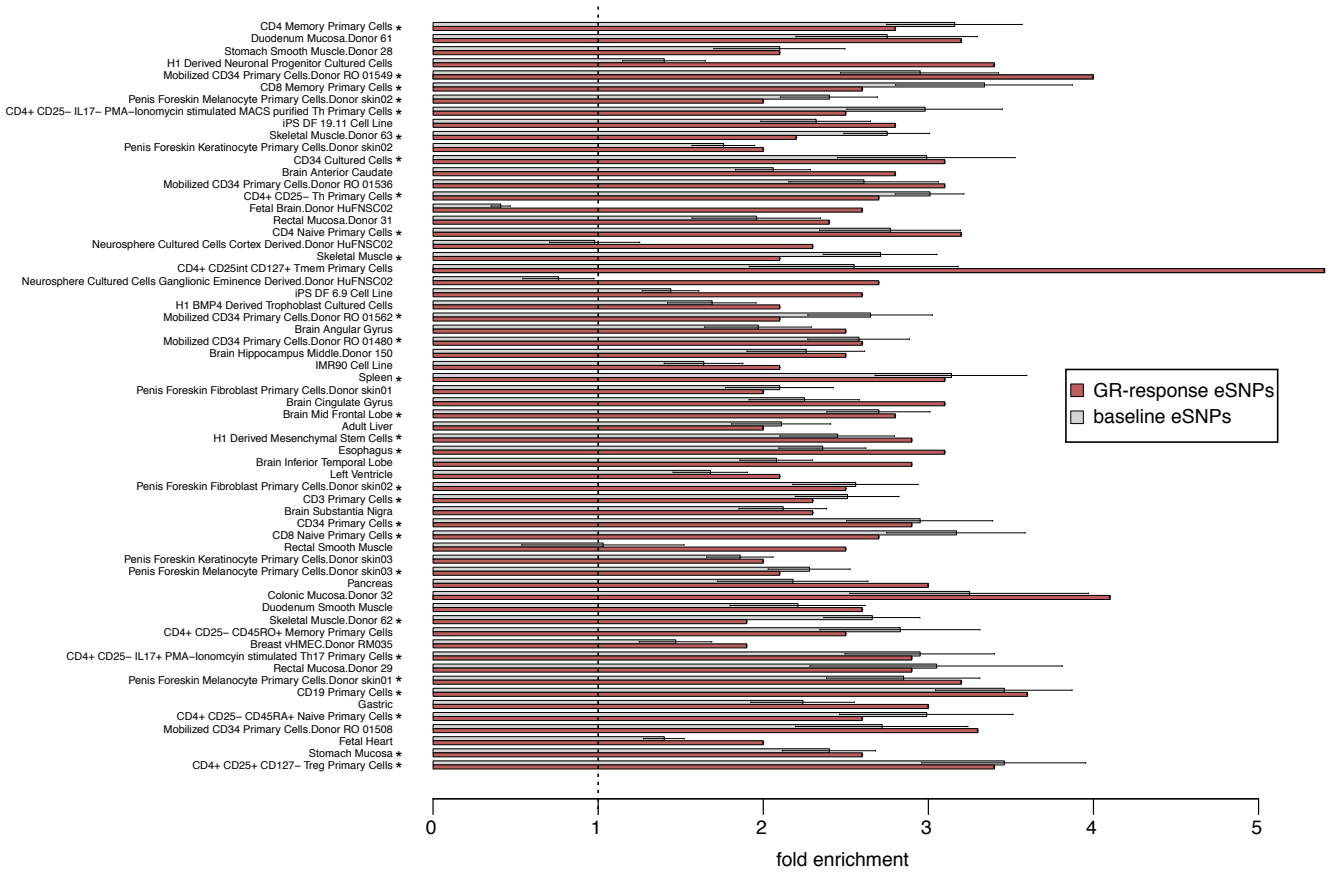

Figure S2. Related to Figure 3.

GR- eSNPs are enriched for enhancers in multiple tissues and cell lines from the Roadmap Epigenome Project. The x-axis shows the fold enrichment and the y-axis shows all enhancers that survived the Bonferroni multiple testing correction for the number of tested tissues or cells. GR-response eSNPs are illustrated in red and baseline eSNPs in gray. Out of the 62 presented enhancers, 28 additionally showed a significant enrichment within baseline eSNPs (marked with *).
P values derived from a binomial enrichment test; error bars: ± sd

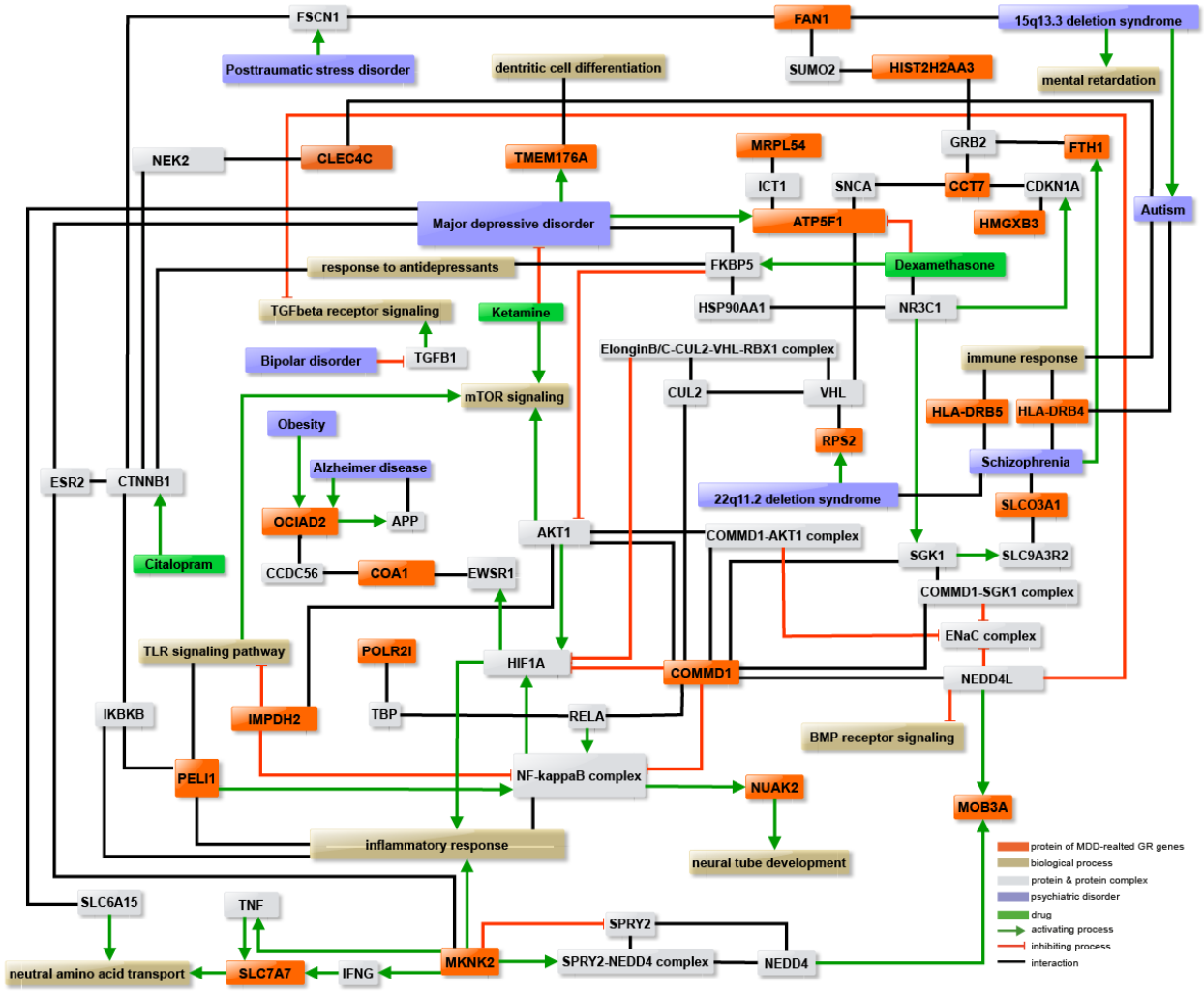

Figure S3. Related to Figure 6.
Disease-related network. For 22 of the 24 MDD-related GR genes a tightly interconnected disease-related network was generated from manually curated experimental data derived from the literature. Elements of the figure: Proteins from MDD-related GR genes (orange boxes), additional proteins and protein complexes (white boxes), biological processes (beige boxes), psychiatric disorders (blue boxes), drugs (green boxes), activating processes (green arrow-headed lines), inhibitory processes (red bar-headed lines) and interactions such as physical interactions, associations with diseases and differential regulation of signaling pathways (black line).

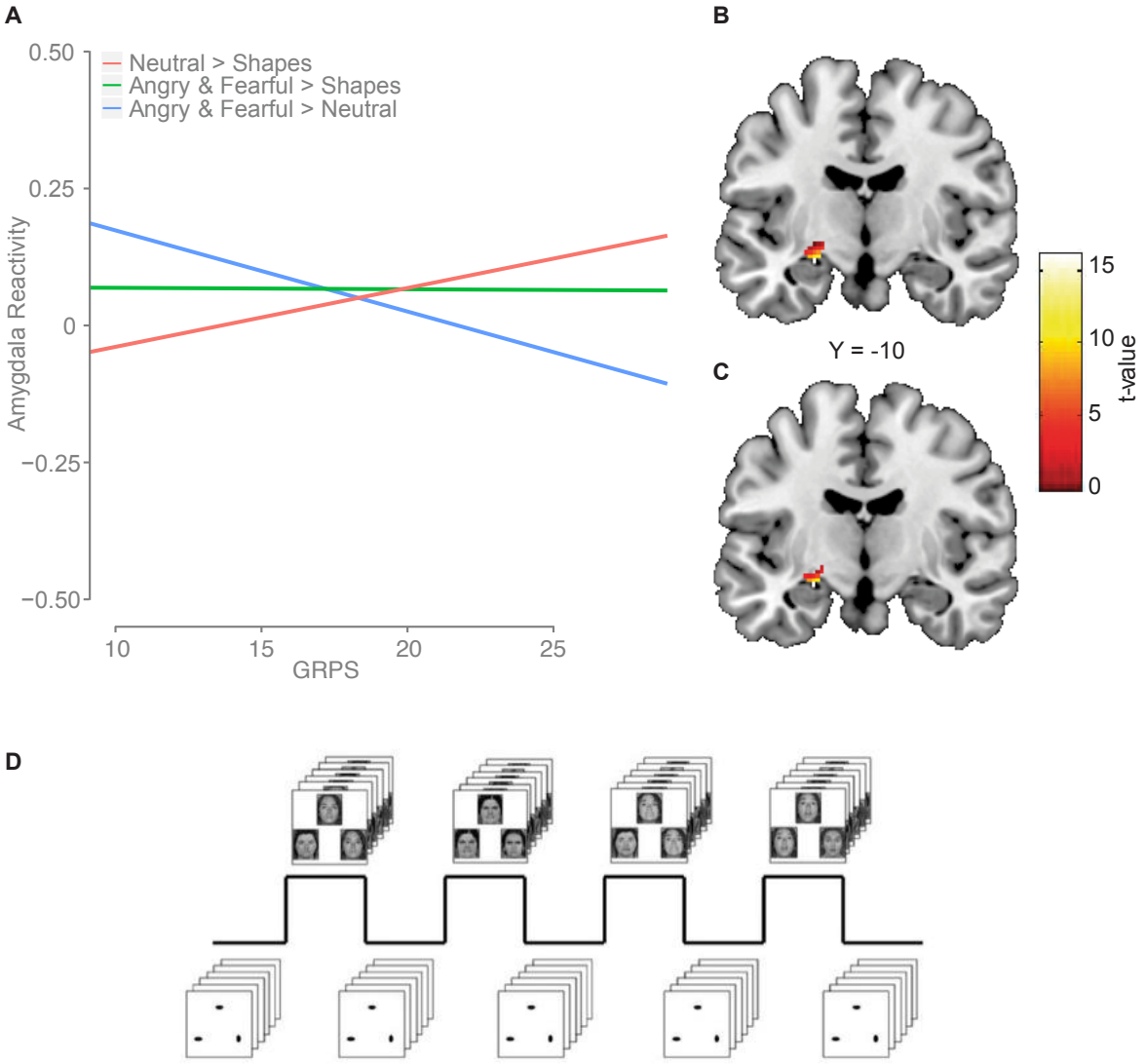

Figure S4. Related to Figure 7.
(A) Elevated genetic risk profile scores (GRPSs) correlate with dysfunctional amygdala reactivity in the entire DNS sample (*n* = 647). As previously found in the European-American subsample, elevated GRPSs predicted blunted amygdala reactivity to threat-related expressions in comparison to neutral expressions in the entire sample when controlling for patterns of population stratification. Post-hoc analyses revealed that GRPS was not predictive of reactivity to threat-related expressions, but that higher GRPSs predicted elevated amygdala reactivity to neutral expressions, in comparison to non-face control stimuli. (B), (C) Show the main effects of the post hoc contrasts for left centromedial amygdala reactivity used in imaging genetics analyses of GRPS in the entire sample. (B) "Angry & Fearful > Shapes" (49 contiguous voxels; max voxel MNI coordinate, x = -24, y = -10, z = -14, t = 22.59, $P < 4.41 \times 10^{-16}$), and (C) "Neutral > Shapes" (35 contiguous voxels; max voxel MNI coordinate, x = -24, y = -10, z = -14, t = 10.73, $P < 4.41 \times 10^{-16}$). (D) DNS fMRI Task: Participants completed four expression-specific (Neutral, Angry, Fear, Surprise) face-matching task blocks interleaved with five sensorimotor shape-matching control blocks. Order for task blocks was counterbalanced across participants.

Table S1. Related to Figure 2.
List of the 320 *cis*-eSNP-probe combinations (*cis*-eQTL bins).

(In separate Excel file.)

Table S2. Related to Figure 5. Overlap of GR-response *cis*-eSNP bin-probe combinations with SNPs nominally associated with MDD in the meta-analysis for MDD (meta-analysis $P \leq 0.05$; $n = 17,846$ samples).
List of 26 eSNP bins (23 tagging SNPs), representing the overlap of the 282 GR-response *cis*-eSNPs and SNPs from the meta-analysis for MDD.

	tag SNP eQTL b	Genes nearby tag SNP	SNP Locati	SNP Chr[a]	PGC A1[b]	PGC A2[c]	PGC OR[d]	PGC RiskA	PGC p-value[f]	P ID[g]	P Gene[h]	Q value[i]	Cross Disorder Association[j]	GR binding site
1	1-148440425	*PLEKHO1, ANP32E*	intergenic	1	T	G	1.09	T	0.013	ILMN_1695435	*HIST2H2AA3/4*	0.006	CDA, BPD, SCZ, ADHD	yes
2	19-40883657	*UPK1A, ZBTB32*	intergenic	19	C	G	0.91	G	0.001	ILMN_1720542	*POLR2I*	0.044	BPD	yes
3	rs10002500	*CNGA1*	intronic	4	T	C	1.07	T	0.043	ILMN_1700306	*OCIAD2*	0.024		no
4	rs10505733	*CLEC4C*	intronic	12	A	C	0.94	C	0.021	ILMN_1665457	*CLEC4C*	0.00021	SCZ	no
	rs10505733	*CLEC4C*	intronic	12	A	C	0.94	C	0.021	ILMN_1682259	*CLEC4C*	0.00021	SCZ	no
5	rs12432242	*SLC7A7*	intronic	14	T	C	0.94	C	0.008	ILMN_1810275	*SLC7A7*	0.041	CDA, BPD	no
6	rs12611262	*SEMA6B, TNFAIP8L1*	intergenic	19	T	C	1.06	T	0.022	ILMN_1658486	*MRPL54*	0.046		no
7	rs12620091	*ALMS1P*	ncRNA_intr	2	T	C	0.95	C	0.022	ILMN_1662954	*CCT7*	0.047		no
8	rs17239727	*BLVRA*	intronic	7	A	G	0.94	G	0.022	ILMN_2081335	*COA1*	0.024	CDA	yes
9	rs1873625	*BSN*	intronic	3	A	C	0.94	C	0.018	ILMN_1705737	*IMPDH2*	0.048		no
10	rs1981294	*LRIF1, DRAM2*	intergenic	1	T	C	1.07	T	0.021	ILMN_1721989	*ATP5F1*	0.037	CDA	no
11	rs2072443	*TMEM176B*	exonic	7	T	C	1.05	T	0.034	ILMN_1791511	*TMEM176A*	0.036		no
12	rs2269799	*SV2B*	intronic	15	T	C	0.95	C	0.04	ILMN_1663699	*SLCO3A1*	0.047		no
13	rs2395891	*BTBD2, MKNK2*	intergenic	19	T	G	1.07	T	0.031	ILMN_1721344	*MOB3A*	0.024	CDA, BPD	yes
	rs2395891	*BTBD2, MKNK2*	intergenic	19	T	G	1.07	T	0.031	ILMN_2347068	*MKNK2*	0.028	CDA, BPD	yes
14	rs2422008	*WDPCP*	intronic	2	A	C	1.05	A	0.036	ILMN_1679268	*PELI1*	0.042	CDA, ASD	yes
15	rs2956993	*GANAB*	intronic	11	T	G	0.95	G	0.032	ILMN_1746525	*FTH1*	0.044		no
16	rs35288741	*NFASC*	intronic	1	A	G	1.05	A	0.042	ILMN_2094952	*NUAK2*	0.044		no
17	rs6493387	*TRPM1*	intronic	15	T	C	0.93	C	0.001	ILMN_1778734	*FAN1*	0.045	CDA	no
18	rs6545924	*COMMD1, B3GNT2*	intergenic	2	T	G	1.06	T	0.018	ILMN_1761242	*COMMD1*	0.045		no
19	rs7194275	*C16orf91, CCDC154*	intergenic	16	T	C	0.92	C	0.021	ILMN_1688749	*RPS2*	0.049	CDA, BPD, SCZ	no
20	rs7252014	*KCNN1*	intronic	19	A	G	1.06	A	0.016	ILMN_1766487	*LRRC25*	0.038		no
21	rs917585	*SLC6A7*	intronic	5	C	G	1.05	C	0.029	ILMN_1694686	*HMGXB3*	0.045	CDA, SCZ	no
22	rs9268671	*HLA-DRA, HLA-DRB5*	intergenic	6	A	G	0.95	G	0.031	ILMN_1697499	*HLA-DRB5*	0.00021	CDA, SCZ, ASD	no
23	rs9268926	*HLA-DRA, HLA-DRB5*	intergenic	6	A	G	0.92	G	0.041	ILMN_1697499	*HLA-DRB5*	0.012	CDA, SCZ, ASD	no
	rs9268926	*HLA-DRA, HLA-DRB5*	intergenic	6	A	G	0.92	G	0.041	ILMN_2159694	*HLA-DRB4*	0.00073	CDA, SCZ, ASD, ADHD	no

[a] *SNP Chromosome*
[b] *code for allele 1 (reference allele, not necessary minor allele)*
[c] *code for allele 2*
[d] *odds ratio*
[f] *risk allele*
[f] *meta analysis p-value*
[g] *Illumina probe identifier (Human HT-12 v3)*
[h] *probe gene*
[i] *lowest Q value for eSNP bin*
[j] *probes that also had an eSNP associated with bipolar disorder (BPD), schizophrenia (SCZ), attention deficit-hyperactivity disorder (ADHD), autism spectrum disorder (ASD) or the cross disorder analysis (CDA)*
[k] *eSNP bins including a GR binding site based on ChIP-seq data*

Table S3. Related to Figure 5. MDD-related GR tagging eSNPs and their proxy SNPs used to generate the cumulative risk allele profile in the MARS cohort. Three SNPs deviated from HWE (rs12620091, rs9268671 and rs9268926) and were excluded from the analysis. As result the remaining 20 SNPs were used to generate a profile.

	tag SNP eQTL bin	Proxy for SNP[a]	Genes nearby tag SNP	SNP Chr	MARS A1[b]	MARS A2[c]	MARS MAF[c]	MARS HWE P value[e]	Used for analysis
1	1-148440425	rs72694971 (renamed)	*PLEKHO1, ANP32E*	1	G	T	0.12	0.56	yes
2	19-40883657	rs73048504 (renamed)	*UPK1A, ZBTB32*	19	C	G	0.18	0.22	yes
3	rs10002500		*CNGA1*	4	T	C	0.13	0.58	yes
4	rs10505733		*CLEC4C*	12	C	A	0.29	0.42	yes
5	rs12432242		*SLC7A7*	14	C	T	0.39	0.87	yes
6	rs12611262		*SEMA6B, TNFAIP8L1*	19	T	C	0.39	0.59	yes
7	rs12620091	rs34874205 (r^2=0.92)	*ALMS1P*	2	C	T	0.37	< 0.00001	no
8	rs17239727		*BLVRA*	7	T	C	0.21	0.48	yes
9	rs1873625		*BSN*	3	A	C	0.29	0.85	yes
10	rs1981294		*LRIF1, DRAM2*	1	C	T	0.17	0.47	yes
11	rs2072443		*TMEM176B*	7	T	C	0.41	0.75	yes
12	rs2269799		*SV2B*	15	C	T	0.32	0.23	yes
13	rs2395891		*BTBD2, MKNK2*	19	T	G	0.35	0.21	yes
14	rs2422008		*WDPCP*	2	A	C	0.43	1	yes
15	rs2956993		*GANAB*	11	G	T	0.38	0.30	yes
16	rs35288741		*NFASC*	1	G	A	0.35	0.25	yes
17	rs6493387		*TRPM1*	15	T	C	0.47	0.11	yes
18	rs6545924		*COMMD1, B3GNT2*	2	G	T	0.50	0.30	yes
19	rs7194275		*C16orf91, CCDC154*	16	C	T	0.12	0.0007	yes
20	rs7252014		*KCNN1*	19	A	G	0.48	0.054	yes
21	rs917585		*SLC6A7*	5	G	C	0.50	0.57	yes
22	rs9268671	rs116072659 (renamed)	*HLA-DRA, HLA-DRB5*	6	A	G	0.34	< 0.00001	no
23	rs9268926	rs114766558 (r^2=0.81)	*HLA-DRA, HLA-DRB5*	6	G	A	0.31	< 0.00001	no

[a] *r^2=LD from MPIP cohort*

[b] *code for allele 1 (reference allele, not necessary minor allele)*

[c] *code for allele 2*

[d] *minor allele frequency*

[e] *Hardy-Weinberg test statistics*

Table S4. Related to Figure 7 and S3. MDD-related GR tagging eSNPs and their proxy SNPs used to generate the cumulative risk allele profile in the DNS cohort. Four SNPs did not have a proxy available (rs12620091, rs917585, rs9268671 and rs9268926). No SNPs deviated from HWE.

							DNS MAF[d]		DNS HWE P values[e]					
	tag SNP eQTL bin	Proxy for SNP[a]	Genes nearby tag SNP	SNP Chr	DNS A1[b]	DNS A2[c]	EUR-AM	ALL	EUR-AM	AFR-AM	Latino/a	Asian1	Asian 2	Used in the analysis
1	1-148440425	rs11588837 (r^2=0.96)	*PLEKHO1, ANP32E*	1	A	G	0.15	0.34	0.48	0.95	0.34	0.99	0.72	yes
2	19-40883657	rs8106959 (r^2=0.95)	KMT2B	19	A	G	0.22	0.18	0.53	0.89	0.87	0.28	0.5	yes
3	rs10002500		*CNGA1*	4	T	C	0.1	0.19	0.28	0.74	0.65	0.48	0.5	yes
4	rs10505733	rs1894823 (r^2=1)	*CLEC4C*	12	T	C	0.31	0.28	0.34	0.4	0.16	0.14	0.35	yes
5	rs12432242	rs2281677 (r^2=0.93)	*SLC7A7*	14	A	G	0.38	0.39	0.96	0.29	0.04	0.16	0.31	yes
6	rs12611262		*SEMA6B, TNFAIP8L1*	19	T	C	0.37	0.44	0.49	0.84	0.57	0.26	0.55	yes
7	rs12620091	no Proxy												no
8	rs17239727	rs10229363 (r^2=1)	*BLVRA*	7	A	G	0.2	0.13	0.23	0.62	0.47	0.86	0.35	yes
9	rs1873625	rs9858280 (r^2=1)	*BSN*	3	T	C	0.37	0.28	0.39	0.6	0.71	0.52	0.24	yes
10	rs1981294	rs4838884 (r^2=1)	*LRIF1, DRAM2*	1	A	G	0.2	0.19	0.63	0.66	0.48	0.932	0.67	yes
11	rs2072443		*TMEM176B*	7	T	C	0.42	0.44	0.38	0.41	0.59	0.39	0.74	yes
12	rs2269799		*SV2B*	15	C	T	0.33	0.35	0.1	0.6	0.32	0.5	0.35	yes
13	rs2395891		*BTBD2, MKNK2*	19	T	G	0.34	0.38	0.49	0.18	0.26	0.3	0.03	yes
14	rs2422008		*WDPCP*	2	A	C	0.47	0.41	0.85	0.25	0.9	0.13	0.82	yes
15	rs2956993		*GANAB*	11	G	T	0.35	0.29	0.42	0.47	0.43	0.61	0.99	yes
16	rs35288741	rs7534993 (r^2=1)	*NFASC*	1	G	A	0.34	0.27	0.24	0.21	0.56	0.53	0.35	yes
17	rs6493387	rs12901022 (r^2=1)	*TRPM1*	15	C	T	0.48	0.46	0.79	0.44	0.41	0.94	0.82	yes
18	rs6545924	rs921320 (r^2=1)	*COMMD1, B3GNT2*	2	C	A	0.5	0.5	0.17	0.53	0.4	0.65	0.94	yes
19	rs7194275		*C16orf91, CCDC154*	16	C	T	0.19	0.19	0.5	0.92	0.73	0.051	1	yes
20	rs7252014		*KCNN1*	19	A	G	0.48	0.47	0.55	0.37	0.31	0.07	0.45	yes
21	rs917585	no Proxy												no
22	rs9268671	no Proxy												no
23	rs9268926	no Proxy												no

[a] *r^2=LD for CEU population from 1KGP (>0.90 for all subpopulations)*

[b] *code for allele 1 (i.e., reference risk allele, not necessary minor allele)*

[c] *code for allele 2*

[d] *minor allele frequencies*

[e] *Hardy-Weinberg test statistics for European Americans (EUR-AM), African Americans (AFR-AM), Latino/as, Asian Cluster 1 (Asian1) and Asian Cluster 2 (Asian2)*

Table S5. Related to Figure 7 and S3. Psychiatric Diagnoses in the Duke Neurogenetics Study (DNS). Of note, this table represents the number of diagnoses across DNS participants. Some individuals presented with a comorbid status.

	European American (*n*=306)	Full Sample (*n*=647)
Alcohol Abuse	22	41
Alcohol Dependence	19	31
Major Depressive Disorder	8	17
Marijuana Abuse	7	15
Gernalized Anxiety Disorder	7	11
Social Anxiety Disorder	3	8
Agoraphobia w/o Panic Disorder	6	8
Bipolar Disorder NOS	6	8
Marijuana Dependence	5	7
Bipolar II	3	6
OCD	4	6
Bulimia Nervosa	2	5
Panic Disorder	1	4
Dysthymia	0	1
PTSD	0	1
Anorexia Nervosa	0	1
Bipolar I	1	1
TOTAL	94	171

Table S6. Related to Figure 2. Sequence of primers used in this study.

List of primers and universal probe library number used for the qPCR for *ADORA3*, *HIST2H2AA3/4* and *TBP* in human whole blood.

Target Gene	Primer Set (5'-3')	UPL probe number
ADORA3	Forward: tcatttgcagccaggtagc	82
	Reverse: tgcttgggtgtggtctatca	
HIST2H2AA3, HIST2H2AA4 (short isoform)	Forward: cgacgaggaactgaacaagc	61
	Reverse: gcctggatgttaggcaagac	
HIST2H2AA3, HIST2H2AA4 (long isoform)	Forward: aaggggcacctgtgaactc	21
	Reverse: gactgagagtggccagcatt	
TBP	Forward: ctttgcagtgacccagcat	67
	Reverse: cgctggaactcgtctcacta	

List of primers used for the qPCR for *LONP1* and *GAPDH* in LCLs.

Target Gene	Primer Set (5'-3')
LONP1	Forward: TTGGTGGCATCAAGGAGAAG
	Reverse: CGGTAGTGTTCCACGAAGTG
GAPDH	Forward: CCAAGGTCATCCATGACAAC
	Reverse: GAGGCAGGGATGATGTTCTG

Oligonucleotides for Chromatin Conformation Capture (3C).

Primer	Sequence
C1	GCCTTACCCAGCACATTTTG
P1	CTGGAAGAGCTTGACCAAGTG
P2	CTCACTCCCCTTGCAATCTC
P3	ACTCGCTTTTTGCAGTAGGG
P4	TACCGCAGCCTACTGCATC
P5	CTTCCACACTGAATCTCACCTG
P6	ATCAATGACCCTCACTCCTCTC
P6	ATCAATGACCCTCACTCCTCTC

Primer set for DNA quantification of 3C samples.

Primer Set (5'-3')
Forward: TGGTGAAACCCCGTCTCTAC
Reverse: AATCTCAGCTCACTGCAACC

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Samples and study design.

MPIP cohort.

The subject pool for the eQTL analysis consisted of 164 male Caucasian individuals (90% of German origin) recruited for the MARS project (Ising et al., 2009): 93 healthy probands (age = 40.2 ± 12.4 years; body mass index (BMI) = 24.9 ± 3.1 kg/m^2) and 71 in-patients with MDD (age = 48.5 ± 13.5 years; HAM-D = 25.3 ± 8.0; BMI = 26.1 ± 3.6 kg/m^2). All were treated at the hospital of the Max Planck Institute of Psychiatry in Munich, Germany (MPIP; MPIP cohort). Only individuals not reporting a history of current psychiatric, major neurological nor general medical disorders were included in the control sample. Recruitment strategies and further characterization of the MPIP cohort have been described previously (Hennings et al., 2009; Menke et al., 2012). Of these participants, 4 were excluded due genotyping problems.

MARS cohort. This sample included 1,005 MDD patients (561 female, 444 males; age = 48.15 ± 14.13 years; HAM-D = 25.68 ± 6.5), as well as 478 controls (298 females, 180 males; age = 47.83 ± 13.7 years), recruited for the MARS project at the MPIP in Munich, Germany. All included patients were of European descent. Recruitment strategies and further characterization including population stratification of the MARS cohort have been described previously (Hennings et al., 2009; Menke et al., 2012). All individuals used within the eQTL study (MPIP cohort) were not part of this sample.

DNS cohort.

All participants from the Duke Neurogenetics Study (DNS) provided informed written consent, prior to participation, in accord with the guidelines of the Duke University Medical Center Institutional Review Board. All participants were in good general health and free of the following DNS exclusion criteria: (1) medical diagnosis of cancer, stroke, diabetes requiring insulin treatment, chronic kidney or liver disease or lifetime psychotic symptoms; (2) use of psychotropic, glucocorticoid or hypolipidemic medication, and (3) conditions affecting cerebral blood flow and metabolism (e.g., hypertension). Current DSM-IV Axis I and select Axis II disorders (Antisocial Personality Disorder

and Borderline Personality Disorder) were assessed with the electronic Mini International Neuropsychiatric Interview (Sheehan et al., 1998) and Structured Clinical Interview for the DSM-IV Axis II (SCID-II) (First et al., 1997) respectively. These disorders are not exclusionary as the DNS seeks to establish broad variability in multiple behavioral phenotypes related to psychopathology.

On January 6th, 2014, 726 participants had overlapping fMRI and genetic data that was fully processed and used for these analyses. Of these participants, 79 were excluded due to scanner-related artifacts in fMRI data (*n* = 6), incidental structural brain abnormalities (*n* = 2), a large number of movement outliers in fMRI data (*n* = 21; see ART description below), inadequate signal in our amygdala regions of interest (*n* = 14; see coverage description below), poor behavioral performance (*n* = 20; accuracy lower than 75%), outlier status according to ancestrally-informative principal components (*n* = 5), scanner malfunctions (*n* = 2), incomplete fMRI data collection (*n* = 1), and failed genotyping at one GRPS polymorphisms (without a proxy of $r^2 > 0.9$; *n* = 8). Thus, all imaging genetics analyses were conducted in a final European-American subsample of 306 participants (age = 19.72 ± 1.23 years; 148 males; 63 with DSM-IV Axis I disorder) and a full sample of 647 participants (age = 19.65 ± 1.24 years; 285 males; 117 with DSM-IV Axis I disorder; 306 European Americans, 72 African Americans, 170 Asians, 37 Latino/as, and 62 of Other/Multiple racial origins according to self-reported ethnicity; for a full description of diagnoses present in the sample see Table S5).

Mouse models.

The animal experiments were carried out in the animal facilities of the MPIP in Munich, Germany. Male C57BL/6N mice at an age of 12 weeks (mean bodyweight 26.8 ± 0.1 g) were used for the dexamethasone-stimulation test (DEX-mouse). The experiment was performed twice with two separate batches of mice (*n* = 22 per batch). Male 3-4 month old C57BL/6N mice (mean bodyweight 25.5 ± 2.12 g) were used for the acute social defeat mouse model (Stress-mouse). Two weeks before the experiment onset, mice were singly housed and

acclimated to the experimental room. All mice (DEX and Stress-mice) were kept under a 12 h light/dark cycle and standard conditions. Food and tap water were available *ad libitum*. All efforts were made to minimize animal suffering during the experiment. The committee for the Care and Use of Laboratory animals of the Government of Upper Bavaria, Germany approved the protocols.

(i) DEX-mouse: Animals were injected i.p. with either vehicle (VEH, *n* = 11) or 10 mg/kg dexamethasone (DEX, *n* = 11) between 9am and 11am. Animals were sacrificed 4 hours post injection, blood was collected and the brains were carefully removed. The prefrontal cortex (PFC; batch 1), hippocampus (HC; batch 1) and amygdala (AM; batch 2) were dissected immediately according to standard protocols (Spijker, 2011). Amygdala preparation was as follows: brains were cut into ca. 1 mm thick slices using a custom-mounting device. The amygdala (all subnuclei) (Paxinos and Franklin, 2003) was manually dissected with a scalpel under visual control using a binocular microscope. HC and PFC preparation: brain regions were manually dissected from the whole brain by trained personnel. Dissected tissues were directly transferred into RNA lysis solution (Applied Biosystems, USA) and frozen at -80°C. In addition, 300 µl of trunk blood (batch 1) was collected into microcentrifuge tubes containing PaxGene RNA stabilizer solution and frozen at -20°C.

(ii) Stress-mouse: The acute social defeat stress paradigm lasted 5 min and was conducted as previously described (Wagner et al., 2013). Briefly, experimental mice were placed in the home cage of a dominant aggressive CD1 resident mouse. Interaction between the mice was permitted for 5 min without any interference unless an animal was severely injured. When this was the case, the experimental animal was returned to his home cage and excluded from analysis. Prior to the experimental day, all CD1 resident mice received aggression tests to ensure dominance and were trained for aggressive behavior. The control mice were allowed to explore an empty cage (control condition) for 5 min. Exactly 4 h after

the onset of the stress paradigm, the mice were sacrificed and the tissue harvested for subsequent analyses. Briefly, mice were anesthetized with Isofluorane and then immediately killed by decapitation. In the same manner as for the DEX-mouse, 250µl of trunk blood was collected and the brains were carefully removed. The same brain regions i.e. the HC, AM and PFC were dissected out, snap-frozen, and stored in RNA lysis solution at -80°C until needed.

Gene expression data.

Human whole blood of the MPIP cohort was collected using PAXgene Blood RNA Tubes (PreAnalytiX), processed as described previously (Menke et al., 2012) and hybridized to Illumina HumanHT-12 v3.0 Expression Bead Chips. Samples had a mean RNA integrity number (RIN) of 7.97 ± 0.42 *SD*. The Illumina Bead Array Reader was used to scan the microarrays and summarized raw probe intensities were exported using Illumina's GenomeStudio v2011.1 Gene Expression module. Further processing was carried out using R version 2.14.0 (http://www.r-project.org/). All 48,750 probes present on the microarray were first filtered by an Illumina detection *P* value of 0.01 in at least 10% of the samples, leaving 14,168 expressed probes for further analysis. Each transcript was then transformed and normalized through variance stabilization and normalization (VSN) (Lin et al., 2008). Technical batches were adjusted using ComBat with fixed effects of amplification round (Johnson and Cheng, 2007). To test for hidden confounding effects within the ComBat corrected data, we applied a surrogate variable analysis (Leek and Storey, 2007). No significant surrogate variable could be identified suggesting that most of the confounding effects were captured by correcting for known batch effects. To further reduce batch effects baseline and dexamethasone stimulated RNA samples for each individual were processed within a single run. Finally for each probe, we constructed a linear model of the log fold change in gene expression between 6pm (baseline) and 9pm (GR-stimulation) standardized

to 6pm (baseline) controlling for age, disease status and BMI. Models were implemented in "R" using the "lm" function. The residuals (GR-response residuals) from this regression were used as phenotype values in the following analyses. The results did not change when the RIN factor, the dexamethasone serum levels (3 hours following administration) and the differential blood cell count (levels of monocytes, granulocytes and lymphocytes) were included as additional independent covariates.

To control if significant eQTLs might be biased due to SNPs within the probes, the Illumina re-annotation pipeline (ReMOAT version August 2009) (Barbosa-Morais et al., 2010) was used to annotate SNPs (relying on UCSC dbSNP 126 table) that were located within the gene expression probe sequence. No bias of eQTL misclassifications due to such sequence polymorphisms in the probe region could be identified. The probe gene names were updated using the NCBI build 36 (hg18) Reference Sequence (RefSeq) (Pruitt et al., 2012) gene annotation table obtained from the UCSC Table Browser (http://hgdownload.soe.ucsc.edu/goldenPath/hg18/database/refGene.txt.gz). The positions of the probes were annotated using ReMOAT and only autosomal probes were used for the GR-response eQTL analysis (n = 4,447 autosomal probes).

DEX-mouse und Stress-mouse RNA was extracted from whole blood using the PAXgene blood miRNA kit (PreAnalytiX) according to (Krawiec et al., 2009). RNA was extracted from the mouse brain regions using RNeasy Plus Universal Mini Kit (Qiagen) in the DEX-mouse experiment and using TRIzol (Life Technologies) in the Stress-mouse experiment, both according to manufacturer's protocol. RNA was quality checked using the Agilent 2100 Bioanalyser, amplified using the Illumina Total Prep 96-Amplification kit (Life Technology) and then hybridized on Illumina MouseRef-8 v2.0 (for DEX-mouse) and Illumina MouseWG-6 v2.0 BeadChips (for Stress-mouse). For each tissue and experiment the samples were processed together (RNA amplification, hybridization and scanning). All samples had a mean RIN of 7.5 ± 0.2 *SD* for DEX-mouse and 6.6 ± 0.5 *SD* for Stress-mouse

blood cells and a mean RIN of 9.2 ± 0.4 *SD* for DEX-mouse and 9.2 ± 0.3 *SD* Stress-mouse brain tissues. All probes present on the microarrays (MouseRef-8 = 25,700; MouseWG-6 = 45,200 probes) were first filtered using an Illumina detection *P* value of 0.05 in at least 15% of the samples. Secondly, each transcript was transformed, normalized and batch corrected, in the same fashion as for the human gene expression data. For differential gene expression analysis between the VEH and DEX animals, as well as between control and stress animals linear regression models implemented in R were used on the normalized, transformed and batch corrected expression values for each tissue. Multiple testing corrections were performed by controlling the false discovery rate (*FDR*) according to Benjamini and Hochberg. A *FDR* ≤ 10% was considered as significant. Results were illustrated as a heatmap in Figure 6B. If multiple array probes per gene existed, only the most significant one is shown in Figure 6B.

Genotype data.

Human DNA of the MPIP cohort samples was isolated from EDTA blood samples using the Gentra Puregene Blood Kit (Qiagen) with standardized protocols. Genome-wide SNP genotyping was performed using Illumina Human610-Quad and Illumina Human660W-Quad Genotyping BeadChips according to the manufacturer's standard protocols. In total, 582,539 genetic markers in 163 individuals of the MPIP cohort could be successfully genotyped. Individuals with low genotyping rate (<98%) and SNPs showing significant deviation from the Hardy-Weinberg equilibrium (HWE, *P* value < 1×10^{-5}) were excluded. Similarly, a low minor allele frequency (MAF;<10%) and SNPs with high rates of missing data (>2%) were excluded. This resulted in 436,643 SNPs and 160 individuals for further analysis. In the 160 samples that passed the quality control, imputation of additional variants was performed using IMPUTE v2 (Howie et al., 2009) on the basis of HapMap CEU Phase 3 (International HapMap Consortium, 2003) and 1,000 Genomes Project version June 2010 (hg18) CEU

data for ~8 million SNPs (Durbin et al., 2010). Imputed SNPs were excluded if their posterior probability averages were less than 90% for the most likely imputed genotype (INFO ≥ 0.9). SNPs were also excluded if their call rate was less than 98%, HWE *P* value was less than 1×10^{-5} and MAF < 10%. This yielded a total of 2,011,895 SNPs. To annotate SNPs for the closest gene, we used Annovar version November 2011 (Wang et al., 2010) with the RefSeq gene annotation SNP coordinates are given according to hg18.

Human DNA of the MARS cohort samples was extracted from EDTA blood samples using the Gentra Puregene Blood Kit (Qiagen) with standardized protocols. Whole-genome SNP genotyping was performed on Illumina Sentix Human-1, HumanHap300, Human610-Quad and HumanOmniExpress Genotyping BeadChips according to the manufacturer's standard protocols. Individuals as well as the genotype data have been subjected to the same quality control steps as the MPIP cohort (genotyping rate < 98%, MAF < 10%, HWE *P* value < 1×10^{-5}, SNP missingness < 98%). Missing genotype data were imputed via IMPUTE v2 based on the 1,000 Genomes Project version Nov. 2010 ALL reference panel. The MDD-related GR eSNP profile was derived from loci associated with both dexamethasone-induced differences in gene expression and MDD. It included alleles from 20 of the 23 tag eSNPs (3 SNPs diverged from HWE in the MARS sample, Table S3. Non-risk and risk alleles (according to association with depression in the PGC dataset) were coded 0 and 1, respectively, and summed in an additive fashion to create cumulative genetic risk profile scores (GRPS; 0 ,1 ,2). The MARS GRPSs ranged from 12-30.

Human DNA from participants of the DNS cohort was isolated from saliva derived from Oragene DNA self-collection kits (DNA Genotek) customized for 23andMe. DNA extraction and genotyping were performed by the National Genetics Institute (NGI), a CLIA-certified clinical laboratory and subsidiary of Laboratory Corporation of America. The Illumina HumanOmniExpress BeadChips and a custom array containing an additional ~300,000 SNPs were used to provide genome-wide data. Due to differences in genotyping array

content the DNS GRPSs included alleles from 19 of the 23 eSNPs (Table S4) and were coded in the same way as the MARS GRPSs. All SNPs used for the GRPSs had genotyping rates < 97%, MAF < 10%, HWE *P* value < 1×10^{-5} (Table S4). DNS GRPSs ranged from 10-28 and were normally distributed (Figure 7). To account for differences in ancestral background in the full sample, we used EIGENSTRAT (v, 5.0.1) (Price et al., 2006) to generate principal components and included the first 5 components as covariates in the analysis. Five participants were outliers for these components (± 6 *SD* from the mean on one of the top ten components) and hence were excluded from analyses.

DNS neuroimaging protocol.

*BOLD fMRI paradigm***.**

A widely used and reliable challenge paradigm was employed to elicit amygdala reactivity. The paradigm consists of 4 task blocks requiring face-matching interleaved with 5 control blocks requiring shape-matching (see Figure S4D). In each face-matching trial within a block, participants view a trio of faces derived from a standard set of facial affect pictures (expressing angry, fearful, surprised, or neutral emotions), and select which of the 2 faces presented on the bottom row of the display matches the target stimulus presented on the top row. Each emotion-specific block (e.g., fearful facial expressions only) consists of 6 individual trials, balanced for gender of the face. Block order is pseudo-randomized across participants. Each of the 6 face trios is presented for 4 seconds with a variable inter-stimulus interval of 2-6 seconds; total block length is 48 seconds. In the shape-matching control blocks, participants view a trio of geometric shapes (i.e., circles, horizontal and vertical ellipses) and select which of 2 shapes displayed on the bottom matches the target shape presented on top. Each control block consists of 6 different shape trios presented for 4 seconds with a fixed inter-stimulus interval of 2 seconds, comprising a total block length of 36 seconds. The total paradigm was 390 seconds in duration. Reaction times and accuracy are recorded through an MR-compatible button box.

BOLD fMRI acquisition.

Participants were scanned using a research-dedicated GE MR750 3T scanner equipped with high-power high-duty-cycle 50-mT/m gradients at 200 T/m/s slew rate, and an eight-channel head coil for parallel imaging at high bandwidth up to 1MHz at the Duke-UNC Brain Imaging and Analysis Center. A semi-automated high-order shimming program was used to ensure global field homogeneity. A series of 34 interleaved axial functional slices aligned with the anterior commissure-posterior commissure (AC-PC) plane were acquired for full-brain coverage using an inverse-spiral pulse sequence to reduce susceptibility artifact (TR/TE/flip angle = 2000 ms / 30 ms / 60; FOV = 240 mm; 3.75 × 3.75 × 4 mm voxels (selected to provide whole brain coverage while maintaining adequate signal-to-noise and optimizing acquisition times); interslice skip = 0). Four initial RF excitations were performed (and discarded) to achieve steady-state equilibrium. To allow for spatial registration of each participant's data to a standard coordinate system, high-resolution three-dimensional structural images were acquired in 34 axial slices co-planar with the functional scans (TR/TE/flip angle = 7.7s / 3.0 ms / 12; voxel size = 0.9 × 0.9 × 4 mm; FOV = 240 mm; interslice skip = 0).

BOLD fMRI data analysis.

The general linear model of Statistical Parametric Mapping 8 (SPM8) (http://www.fil.ion.ucl.ac.uk/spm) was used for whole-brain image analysis. Individual subject data were first realigned to the first volume in the time series to correct for head motion before being spatially normalized into the standard stereotactic space of the Montreal Neurological Institute (MNI) template using a 12-parameter affine model. Next, data were smoothed to minimize noise and residual differences in individual anatomy with a 6mm FWHM Gaussian filter. Voxel-wise signal intensities were ratio normalized to the whole-brain global mean. Then the ARTifact Detection Tool (ART; https://www.nitrc.org/docman/view.php/104/390/Artifact%20Detection%20Toolbox%20Manu

al) was used to generate regressors accounting for images due to large motion (i.e., > 0.6 mm relative to the previous time frame) or spikes (i.e., global mean intensity 2.5 standard deviations from the entire time series). Participants for whom more than 5% of acquisition volumes were flagged by ART (*n* = 21) were removed from analyses. An region of interest (ROI) mask (Automated Anatomical Labeling (AAL) atlas) from WFU pickatlas (Maldjian et al., 2003) was used to ensure adequate amygdala coverage for the face-matching and number-guessing tasks, respectively. Participants who had less than 90% coverage of the amygdala (*n* = 14) were excluded from analyses.

Following preprocessing steps outlined above, linear contrasts employing canonical hemodynamic response functions were used to estimate task-specific (i.e., "Angry & Fearful Faces > Neutral Faces", "Angry & Fearful > Shapes", "Neutral > Shapes") BOLD responses for each individual. The primary contrast of "Angry & Fearful > Neutral" was used to assay centromedial reactivity to cues that are conditioned social signals to threat in the environment (i.e., angry and fearful expressions) relative to signals that do not convey threat information about the environment (i.e., neutral expressions). Post-hoc analyses using the "Angry & Fearful > Shapes" and "Neutral > Shapes" contrasts were used to discern if the association with GRPS reflected relatively decreased reactivity to angry and fearful expressions or increased reactivity to neutral expressions. Individual contrast images (i.e., weighted sum of the beta images) were used in second-level random effects models accounting for scan-to-scan and participant-to-participant variability to determine mean contrast-specific responses using one-sample t-tests. A voxel-level statistical threshold of *P* value < 0.05, family wise error corrected for multiple comparisons across the bilateral centromedial amygdala ROIs, and a cluster-level extent threshold of 10 contiguous voxels was applied to these analyses. The bilateral centromedial amygdala ROIs were defined using anatomical probability maps (Amunts et al., 2005). The centromedial ROI was chosen because it includes the central nucleus of the amygdala (CeA). This specifically functions to drive physiologic, attentive, and

neuromodulatory responses to threat, as opposed to the basolateral complex of the amygdala (BLA), which primarily functions to relay information to the CeA. Thus, the expression of stress responsive behavior is more closely linked with the activity of the CeA and not the BLA (Davis and Whalen, 2001; LeDoux, 2007). Human research using such distinctions has shown that ROIs encompassing the CeA or BLA differentially respond to stimuli and share different patterns of functional as well as structural connectivity (Brown et al., 2014; Etkin et al., 2004; Lerner et al., 2012).

BOLD parameter estimates from a cluster within the left centromedial amygdala ROI exhibiting a main effect for the "Angry & Fearful > Neutral" contrast were extracted using the VOI tool in SPM8 and exported for regression analyses in SPSS (v.18). No significant cluster emerged in the right centromedial amygdala. Extracting parameter estimates from clusters activated by our fMRI paradigm, rather than those specifically correlated with our independent variables of interest, precludes the possibility of any correlation coefficient inflation that may result when an explanatory covariate is used to select a region of interest. We have successfully used this strategy in prior studies (Bogdan et al., 2012).

Statistical Analysis.

Cis-associations of baseline gene expression.

Using baseline gene expression of the 4,447 differently regulated autosomal array probes (absolute fold change ≥ 1.3 in at least 20% of all samples), 26,205 unique *cis*-SNPs and 764 gene expression probes corresponding to 31,541 *cis*-eQTLs were found to be significant after multiple testing correction with the same strategy as described for the GR-stimulated gene expression changes. The 26,205 unique eSNPs represented 1,010 uncorrelated eSNP bins (1,148 eSNP bin-probe combinations). The 775 eQTL bins (68%) were located within 100 kb upstream or downstream from the array probe ends, 911 eQTL bins (79%) within 200 kb and only 237 eQTLs bins > 200 kb (21%).

Validation GR-response cis-eQTL results

Validation of GR-response *cis*-eQTL results was carried out with a sample size-weighted Z-score meta-analysis (Evangelou and Ioannidis, 2013) in an additional independent data set using peripheral blood samples (baseline and after GR-stimulation with 1.5 mg dexamethasone) of 58 individuals (21 male controls, 14 male cases and 23 female cases). We applied the same strategy as used in the discovery sample (MPIP cohort) to filter, normalize and batch correct the gene expression data. We adjusted the analysis for the same covariates plus gender; applied the same SNP quality control checks and performed the *cis*-eQTL mapping in PLINK.

Enrichment of GR binding regions

To identify whether GR-response eSNPs were enriched for GR binding sites, we used the *E*NCODE (ENCODE Project Consortium, 2011) *NR3C1* ChIP-seq data from GM12878 LCLs (accession: ENCSR904YPP) from which no aligned tracks are currently available. Raw data were download at https://www.encodeproject.org/experiments and initial filtering was performed using FASTX Toolkit (v. 0.0.14, http://hannonlab.cshl.edu/fastx_toolkit/index.html) and Prinseq (v. 0.20.3) (Schmieder and Edwards, 2011) to eliminate artifacts and low quality reads. Alignment on hg19 was performed using BWA (v. 0.7.10) (Li and Durbin, 2009) allowing only uniquely mappable alignments with alignment quality of above 20. Reads from both ChIP and both control libraries were pooled leading to 46,453,650 and 68,227,580 used reads, respectively. Peak-calling was carried out by MACS14 (v. 1.4.2) (Zhang et al., 2008) using default settings, resulting in around 23,000 annotated signals. The average length of a ChIP signal as defined by the peak calling was 746.3 bps ± 370.6 bsp.

We mapped the GR-response eSNPs to these GR ChIP-seq peaks and compared the overlap observed with 1,000 equal sized sets of randomly drawn SNPs (n=3,662 SNPs) from of all analyzed SNPs (without replacement) matched in MAF (=null distribution). To match the MAF distributions of the random SNP sets with our GR-response eQTL data we

divided the SNPs into non-overlapping MAF bins, each of the width 0.05 as described previously (Nicolae et al., 2010). For every set we counted the percentage of SNPs within a GR ChIP-seq peak. Enrichment calculations with a permutation-based *FDR* < 10% were considered as statistically significant within the entire manuscript.

Enhancer enrichment analysis

We investigated whether GR-response eSNP binds are enriched for functional enhancer annotations using the online tool HaploReg version 2 (Ward and Kellis, 2012) based on the Roadmap Epigenome data (Roadmap Epigenomics Consortium et al., 2015) and using the 1,000 Genomes Project CEU data as a background data set. Additionally we performed the enrichment analysis on ten permuted baseline eSNP bin sets (size matched) to generate a realistic null distribution. The average enhancer enrichment over the ten permutations is present in Figure 3 and S2.

Chromatin interaction analysis with paired-end tag (ChIA-PET) mapping.

The combined set of the first two replicates of the RNA Polymerase II ChIA-PET data (Li et al., 2010; 2012) generated from K562 chronic myeloid leukemia cell lines (*n* > 400,000 interaction regions) was obtained from the UCSC Genome Browser (http://hgdownload.cse.ucsc.edu/goldenPath/hg19/encodeDCC/wgEncodeGisChiaPet/). Genomic coordinates of our GR-response eSNP bins were converted from hg18 to GRCh build 37 (hg19) using the UCSC Genome Browser liftOver tool (http://genome.ucsc.edu/cgi-bin/hgLiftOver) and the probe gene coordinates were updated with the hg19 RefSeq (Pruitt et al., 2012) gene table obtained from the UCSC Table Browser (http://hgdownload.soe.ucsc.edu/goldenPath/hg19/database/refGene.txt.gz; excluding 15 probe genes on hg19). To estimate the overlap of the direct chromatin interactions and GR-response eQTL bins (eSNP bin-probe gene combination) we tested if one ChIA-PET tag overlapped with the region of the eSNP bin ± 10kb as well as the relevant array probe gene

(10kb ± transcription start or end). To establish the null distribution, we permuted the distances between the GR-response eSNP bins and the transcription sites of the corresponding probe gene (*n* = 270 updated to hg19) and estimated the overlap with ChIA-PET interaction signals. We repeated the analysis 1,000 times and for each set we counted the number of genes with overlapping ChIA-PET data.

Enrichment of GWAS susceptibility markers.

To identify whether GR-response eSNPs were specifically enriched for association with psychiatric disorders and not with other diseases or traits, we generated 1,000 sets of permuted baseline eSNPs (conditional on MAF and number of GR-response eSNPs overlapping with the respective GWAS). For every set we counted the percentage of unique SNPs with a GWAS results at *P* value ≤ 0.05. On this basis we constructed the null distribution. A second null distribution was created based on all imputed SNPs of high quality.

1.) PGC MDD data: The MDD GWAS data was generated by conducting a meta-analysis based on the Psychiatric Genomics Consortium (PGC) GWAS mega-analysis for MDD (Major Depressive Disorder Working Group of the Psychiatric GWAS Consortium, 2012) data . We used the “meta-analysis” function in PLINK assuming a fixed effect model in 17,846 individuals of European ancestry (8,864 cases with MDD and 8,982 controls) from 8 of the 9 studies included in the PGC MDD data. All samples from the initial PGC MDD data (*n* = 18,759) that overlapped with our MARS cohort (*n* = 376 cases and 537 controls) were excluded, which was then used as validation sample. The PGC MDD analysis used SNP data imputed to the 1,000 Genomes Project (hg19).

2.) PGC cross-disorder data: The results of the PGC cross-disorder (CD) analysis (33,332 patients and 27,888 controls of European ancestry distributed among five disorders: SCZ, BPD, ADHD, ASD and MDD) (Cross-Disorder Group of the Psychiatric Genomics

Consortium, 2013; Cross-Disorder Group of the Psychiatric Genomics Consortium et al., 2013) were obtained from the PGC website (http://pgc.unc.edu). The PGC CD analysis applied a multinomial regression procedure and used SNP data imputed to the HapMap Phase 3 data (hg18).

3.) PGC SCZ2 data: The results of the multistage GWAS for SCZ (Schizophrenia Working Group of the Psychiatric Genomics, 2014) obtained from the PGC website (http://pgc.unc.edu). The PGC SCZ2 analysis used SNP data imputed to the 1,000 Genomes Project (hg19).

4.) Non psychiatric trait data: The GWAS data for height (Heid et al., 2010) and rheumatoid arthritis (RA) (Stahl et al., 2010) were obtained from the PGC website (http://pgc.unc.edu). Results of the Crohn's disease (CD) analysis were obtained from International Inflammatory Bowel Disease Genetics Consortium website (http://www.ibdgenetics.org). The RA analysis used SNP data imputed to the HapMap Phase 2 data (hg17) and the CD as well as height data was imputed based on HapMap Phase 3. For comparability we converted all our SNP coordinates to the relevant genome assembly of analyzed GWAS data using the UCSC Genome Browser liftOver tool.

Co-expression analysis

For the co-expression analysis we used the GR-response residuals from all array probes (*n* = 4,447) to determine if the 25 MDD-related GR array probes are more co-regulated than 1,000 sets of randomly chosen GR-stimulated transcripts. To realize this, we carried out a co-expression analysis in R using the function "dist" specifying the Euclidian distance as distance measure and calculated the mean distance of all pair-wise distances. We established the significance of co-expression network of the 25 MDD-related GR array probes by testing the observed mean distance versus the null distributions created by

calculating the mean distance of all pair-wise distances for 1,000 sets of 25 randomly chosen GR-stimulated transcripts. Next, we determined the number of sets, having lower mean distances than the actual MDD-related GR transcripts to measure the enrichment statistic.

*DNS neuroimaging analysis***.**

Statistical analyses of the imaging data were completed using linear regression in SPSS to test the association of the MDD-related GR tag eSNP GRPSs to amygdala reactivity in the independent DNS cohort. To maintain variability but constrain the influence of extreme outliers, prior to any analyses, all imaging variables were winsorized (i.e., following data quality control procedures, outliers more than ± 3 SD were set at ± 3 SD from the mean; for the "Angry and Fearful > Neutral faces" contrast, 13 outliers (2.01%) of the entire sample were moved to ± 3 SD from the mean). Gender, psychiatric diagnosis (0,1) and age were entered as covariates for both EUR-AM and entire sample analyses. Five ancestrally-informative principal components that distinguish the sample were added as additional covariates in the analyses of the entire sample. We computed permutations (n = 1,000) in which we constructed randomly generated SNP profiles that were matched for MAF, amount of SNPs (n = 19) and constrained by the max LD observed within the sample.

Graphs were generated with Haploview (Barrett et al., 2005), ggplot2 ((Wickham, 2009) and Circos (Krzywinski et al., 2009).

Chromatin conformation capture

Five human lymphoblastoid cell lines were cultured in RMPI media with stable l-glutamine (Biochrom) supplemented with 10% fetal bovine serum and 1% antibiotic-antimycotic (Life Technologies). Crosslinking and cell lysis were performed as described (Hagège et al., 2007). Nuclei were digested using 1,000 U of *Nco*I. Subsequent re-ligation, de-crosslinking and purification were conducted according to the manufacturer's protocol. Following assessment of digestion efficiency and sample purity, DNA concentration of the 3C samples

were determined by SybrGreen quantitative PCR using an “internal” primer set (see Table S6; primers that do not amplify across sites recognized by the restriction enzyme used) as described in (Hagège et al., 2007). Primers were designed with an anchor primer in the fragment containing the TSS of *LONP1* and in potential interacting fragments in and around eSNP bin of *NRTN* using Primer3Plus (http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi). Quantitative PCR was carried out using ABsolute Blue qPCR SYBR Green Master Mix (Thermo Fisher Scientific) and the Mini Opticon Real-Time PCR System (Bio-Rad) according to the manufacturer’s instructions. A 179-kb BAC clone (CTD-2522A4) containing the entire *LONP1-NRTN* genomic sequence was purchased from Life Technologies and served as PCR control template. The BAC clone was cut with *Nco*I and re-ligated by T4 DNA ligase. All primer pairs were tested on a standard curve of the BAC control library and yielded PCR efficiencies > 1.7. The presence of a single PCR product was confirmed by agarose gel electrophoresis and melting curve analysis. Cycling conditions were: 95 °C for 15min, 45 cycles of 95°C for 15s, 60°C for 15s, 72°C for 15s. Quantitative PCR data were normalized to *GAPDH* as a loading control. *GAPDH* cycling conditions were 95 °C for 15min, 45 cycles of 95°C for 15s, 60°C for 15s, 72°C for 15s. Data analysis was carried out according to (Hagège et al., 2007) and is presented as relative crosslinking frequency. Primers used for the chromatin conformation capture interaction studies are listed in Table S6. Linear mixed models were used for statistical analysis.

Quantitative real-time PCR (qPCR) validation.

Total RNA was reverse-transcribed to cDNA using random primers and the Superscript II reverse transcriptase (Invitrogen) for qPCR to validate microarray results. qPCR was carried out according to manufactures instructions using Roche-LightCycler 480 System (Roche Applied Science) and assays were designed using the Roche Universal Probe Library (http://qpcr.probefinder.com) for *ADORA3* (the probe with a significant GR-response eQTLs), *HIST2H2AA3/4* (the probe with the most eSNPs overlapping with the meta-analysis results

for MDD) and *TBP* as the endogenous control gene. Assays for *LONP1* and *GADPH* were designed using Primer3Plus (http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi). The association between eSNPs and GR-stimulated gene expression of the target genes could be validated using qPCR (see Figure 2C,D and 4A,B). Sequences of primers used are summarized in Table S6. All samples were run in duplicates and duplicates discordant in *CT* values by more than 0.2 cycles, were excluded from the analysis. Relative gene transcript levels were determined by Pfaffl's equation (Pfaffl, 2001) with: $\text{ratio} = \frac{(\text{E}_{\text{gene}})^{\Delta\text{CT}_{\text{gene}}(\text{baseline sample} - GR-\text{stimulated sample})}}{(\text{E}_{\text{housekeeper}})^{\Delta\text{CT}_{\text{housekeeper}}(\text{baseline sample} - GR-\text{stimulated sample})}}$. qPCR ratios shown in Figure 2D and were calculated using the following equations:

$$pre = \frac{(E_{housekeeper})^{CT_{housekeeper}(baseline\ sample)}}{(E_{gene})^{CT_{gene}(baseline\ sample)}}$$

and *post* = $\frac{(E_{housekeeper})^{CT_{housekeeper}(GR-stimulated\ sample)}}{(E_{gene})^{CT_{gene}(GR-stimulated\ sample)}}$.

qPCR validation results.

Two transcript variants encoding isoforms with a different 3'UTR length have been identified for *HIST2H2AA3/4*. The shorter gene product (isoform 1) is annotated by RefSeq while the alternatively spliced longer gene product (isoform 2) is annotated by Ensembl release 54 (HIST2H2AA3-001; ENST00000369161) and further predicted by AceView (HIST2H2AA3.aApr07-unspliced, HIST2H2AA4.aApr07-unspliced). This longer isoform is tagged by the significant Illumina probe (ILMN_1695435). Hence we designed two different assays- one covering the common part of both isoforms (assay 1) and the other tagging isoform 2 (assay 2). The expression levels measured with both assays were highly correlated (Spearman's test *P* value < 1.5×10^{-20}, *R* = 74%). We could replicate a significant SNP effect in 137 samples with a *P* value of 0.012 using assay 1 with a genotypic model and *P* = 0.017 using a carrier model, with the same direction of change as in the expression array.

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Table S1. List of the 320 *cis*-eSNP-probe combinations (*cis*-eQTL bins).

	tag SNP eQTL bin	Genes nearby tag SNP	SNP Position	SNP Location	SNP Chr[a]	Bin Position[b]	P ID[c]	P Gene[d]	P Start[e]	P End[f]	Q value[g]	FC[h]
1	rs9994839	*SPARCL1*	88612804	downstream	4	88612804:88612804	ILMN_1651354	*SPP1*	89122810	89122859	0.04493	1.14
2	rs9931197	*SCNN1G,SCNN1B*	23139419	intergenic	16	23134897:23144982	ILMN_1806908	*PRKCB*	24134561	24134610	0.04398	1.14
3	rs9873175	*RPL29,DUSP7*	52034676	intergenic	3	52034676:52034676	ILMN_1811063	*RPL29*	52002705	52002753	0.04811	-1.27
4	rs9526443	*MED4*	47560511	intronic	13	47365868:47599728	ILMN_1751708	*ITM2B*	47730310	47730359	0.04442	1.27
5	rs9525211	*RASA3*	113821535	intronic	13	113765493:113849035	ILMN_1727389	*CDC16*	114056045	114056176	0.04061	-1.14
6	rs9525211	*RASA3*	113821535	intronic	13	113765493:113849035	ILMN_1782292	*LAMP1*	113025482	113025532	0.01755	1.12
7	rs9503750	*PXDC1,FAM50B*	3769775	intergenic	6	3769775:3769775	ILMN_2186806	*HLA-B*	2771459	2771494	0.02504	1.16
8	rs9503168	*LOC100508120*	2327394	ncRNA_intronic	6	2327394:2327394	ILMN_2376205	*LTB*	2795982	2796031	0.04811	-1.36
9	rs9418982	*LOC619207,CYP2E1*	135170612	intergenic	10	135170612:135173515	ILMN_1708348	*ADAM8*	134926187	134926236	0.04686	1.24
10	rs9329125	*LOC728554,PROP1*	177334115	intergenic	5	177334115:177334115	ILMN_1910550	*DR980253*	177490041	177490085	0.04729	-1.14
11	rs9320357	*GSTM2P1,SLC16A10*	111506483	intergenic	6	111506483:111506483	ILMN_1676891	*CDC2L6*	111037966	111038015	0.04686	1.25
12	rs9268926	*HLA-DRA,HLA-DRB5*	32541045	intergenic	6	32453869:32790115	ILMN_1697499	*HLA-DRB5*	32593375	32593424	0.01205	-1.07
13	rs9268926	*HLA-DRA,HLA-DRB5*	32541045	intergenic	6	32453869:32790115	ILMN_2159694	*HLA-DRB4*	32593471	32593510	0.00073	-1.08
14	rs9268671	*HLA-DRA,HLA-DRB5*	32522268	intergenic	6	32227876:32886634	ILMN_1697499	*HLA-DRB5*	32593375	32593424	0.00021	-1.07
15	rs917585	*SLC6A7*	149553142	intronic	5	149548828:149553142	ILMN_1694686	*HMGXB3*	149412726	149412775	0.04488	-1.14
16	rs91710	*ARRDC2,IL12RB1*	18002123	intergenic	19	18002123:18002123	ILMN_1782977	*UBA52*	18546768	18546901	0.04671	1.08
17	rs914314	*SYNDIG1,CST7*	24845355	intergenic	20	24845355:24928143	ILMN_1679826	*CST7*	24888342	24888391	0.03386	1.14
18	rs885950	*POU5F1,PSORS1C3*	31248131	intergenic	6	31248131:31248131	ILMN_1673753	*ABCF1*	30647270	30647316	0.04488	-1.12
19	rs877836	*UQCRFS1,LOC284395*	34454402	intergenic	19	34454402:34454402	ILMN_1664920	*C19orf12*	34883977	34884026	0.0498	-1.12
20	rs843631	*ACYP2,C2orf73*	54400729	intergenic	2	54400729:54400729	ILMN_1755883	*RPS27A*	55313346	55313494	0.04861	-1.36
21	rs809972	*MIR34A,H6PD*	9156950	intergenic	1	9156950:9161140	ILMN_1716465	*RBP7*	9998450	9998499	0.02504	1.33
22	rs8082593	*UTP18,CA10*	46864801	intergenic	17	46864801:46868005	ILMN_1657884	*NME1*	46598740	46598789	0.04395	-1.1
23	rs8047140	*KCTD13*	29830489	intronic	16	29830489:29830489	ILMN_1759008	*ZNF689*	30522268	30522317	0.04196	-1.24
24	rs8041381	*RORA*	58650254	intronic	15	58650254:58650254	ILMN_1711899	*ANXA2*	58476751	58476800	0.04811	-1.14
25	rs8033385	*ITGA11,CORO2B*	66607543	intergenic	15	66605623:66615540	ILMN_2386530	*RPLP1*	67532389	67534587	0.04061	-1.3
26	rs8015121	*RBM23*	22445091	intronic	14	22445091:22492026	ILMN_2403889	*PRMT5*	22459840	22459889	0.01205	1.1
27	rs8007588	*STXBP6*	24356851	intronic	14	24353845:24416476	ILMN_2148944	*ADCY4*	23857548	23857597	0.02723	1.26
28	rs7955208	*PTPN11,RPH3A*	111687506	intergenic	12	111654550:111687640	ILMN_1674063	*OAS2*	111933815	111933864	0.01742	-1.25
29	rs7915524	*FAM171A1*	15333909	intronic	10	15333909:15333909	ILMN_1656378	*NMT2*	15190139	15190187	0.03563	-1.24
30	rs7870685	*LOC401497,ACO1*	31563188	intergenic	9	31532987:31563188	ILMN_1767980	*LOC401497*	30564835	30564884	0.02179	1.05
31	rs7826635	*CHMP7,R3HCC1*	23196358	intergenic	8	23196358:23207181	ILMN_1715969	*SLC25A37*	23485399	23485448	0.02774	1.24
32	rs7796045	*CCT6P3,ZNF92*	64405044	intergenic	7	64099514:64564258	ILMN_2118663	*ERV3*	64089139	64089188	0.02446	1.21
33	rs7755418	*FAM50B,PRPF4B*	3963885	intergenic	6	3960299:3963885	ILMN_1695311	*HLA-DMA*	4297264	4297313	0.04856	-1.37
34	rs7678870	*LOC340017,FAM198B*	158971780	intergenic	4	158971518:158982000	ILMN_2190851	*PPID*	159849823	159849872	0.04686	1.1
35	rs7673908	*CLOCK*	56089576	intronic	4	56023701:56131438	ILMN_1773760	*PAICS*	57021950	57021999	0.04493	-1.19
36	rs7622109	*TCAIM*	44377067	intronic	3	44235999:44408914	ILMN_1655702	*ABHD5*	43735013	43735062	0.02774	1.51
37	rs760657	*BPIFC,FBXO7*	31187285	intergenic	22	31187285:31187285	ILMN_1793934	*PISD*	30344925	30344974	0.03872	1.35
38	rs7556661	*ARNT,SETDB1*	149158633	intergenic	1	148990371:149222752	ILMN_1741200	*RFX5*	149580031	149580080	0.03563	-1.3
39	rs7544118	*ADORA3*	111833728	intronic	1	111833649:111833728	ILMN_1733259	*ADORA3*	111827625	111827674	0.00164	2.08
40	rs7535902	*LIN28A*	26614327	intronic	1	26614327:26614327	ILMN_1668270	*ZDHHC18*	27054486	27054535	0.04729	1.34
41	rs749326	*SH3BP1*	36380965	intronic	22	36380965:36380965	ILMN_2162367	*DMC1*	37245125	37245174	0.04727	1.07
42	rs745749	*MAPK9*	179648409	intronic	5	179648409:179648409	ILMN_2390227	*TBC1D9B*	179221819	179221868	0.04442	-1.12
43	rs736020	*DHRS9,LRP2*	169672578	intergenic	2	169668668:169672578	ILMN_2384181	*DHRS9*	169660307	169660356	0.04061	1.47
44	rs7349097	*PTPRF*	43806722	intronic	1	43806722:43806722	ILMN_1714445	*SLC6A9*	44234825	44234874	0.04488	1.09
45	rs734570	*SNRNP70*	54298261	intronic	19	54298261:54298261	ILMN_1759436	*NOSIP*	54751494	54751618	0.03121	-1.24
46	rs7256770	*ACP5*	11550911	upstream	19	11549460:11552040	ILMN_1656822	*DNM2*	10803221	10803270	0.04579	1.18
47	rs7256770	*ACP5*	11550911	upstream	19	11549460:11552040	ILMN_2339377	*DNM2*	10803299	10803348	0.02774	1.11
48	rs7252014	*KCNN1*	17941991	intronic	19	17941991:17941991	ILMN_1766487	*LRRC25*	18363434	18363483	0.0384	1.1

49	rs724208	*OLIG1,C21orf54*	33413854	intergenic	21	33411218:33417711	ILMN_1679476	*GART*	33798336	33798385	0.04493	-1.19
50	rs7198922	*SHISA9,ERCC4*	13800306	intergenic	16	13798866:13800306	ILMN_1814808	*BFAR*	14669840	14669889	0.04686	-1.15
51	rs7194275	*C16orf91,CCDC154*	1421021	intergenic	16	1421021:1421021	ILMN_1688749	*RPS2*	1952272	1952499	0.04856	-1.22
52	rs717450	*XCL1*	166818816	downstream	1	166818816:166818816	ILMN_1709233	*F5*	167754302	167754351	0.04442	1.31
53	rs7173954	*INO80*	39062306	intronic	15	39062306:39062306	ILMN_2234758	*SRP14*	38118441	38118586	0.04061	-1.11
54	rs7099954	*ITIH2*	7795738	intronic	10	7783672:7795738	ILMN_1685774	*ATP5C1*	7884320	7884369	0.04061	-1.26
55	rs7089504	*PRKCQ*	6556333	intronic	10	6556333:6556333	ILMN_1754178	*GDI2*	5847402	5847451	0.04686	-1.08
56	rs7071536	*ANKRD16*	5943524	downstream	10	5943091:5943524	ILMN_1795467	*LOC399715*	6417618	6417667	0.01755	1.19
57	rs7027886	*KCNV2,KIAA0020*	2788358	intergenic	9	2773113:2788358	ILMN_1818149		2785269	2785318	0.03728	-1.16
58	rs698915	*RPRD2*	148654942	intronic	1	148517158:148708051	ILMN_1664706	*HIST2H3D*	148051811	148051860	0.03386	1.13
59	rs698915	*RPRD2*	148654942	intronic	1	148517158:148708051	ILMN_1769027	*CDC42SE1*	149290632	149290681	0.04395	1.22
60	rs6904470	*TAAR5,TAAR3*	132969038	intergenic	6	132969038:132969038	ILMN_1782621	*RPS12*	133177861	133177910	0.04442	-1.09
61	rs6749185	*CYBRD1*	172088854	intronic	2	172087932:172138153	ILMN_1712305	*CYBRD1*	172122282	172122331	0.03872	1.13
62	rs6749185	*CYBRD1*	172088854	intronic	2	172087932:172138153	ILMN_1773847	*DYNC1I2*	172310679	172312576	0.04686	-1.16
63	rs6709463	*FAM117B*	203253443	intronic	2	203230594:203258986	ILMN_1739942	*FAM117B*	203342628	203342677	0.03728	-1.07
64	rs6651024	*C6orf10*	32446164	intronic	6	32446164:32497490	ILMN_1697499	*HLA-DRB5*	32593375	32593424	0.04061	-1.07
65	rs661552	*Sep-09*	72791228	intronic	17	72790904:72791228	ILMN_2391912	*SEC14L1*	72721073	72721122	0.04488	1.33
66	rs6607302	*HNF1B,LOC284100*	33268343	intergenic	17	33268343:33268343	ILMN_1748651	*PSMB3*	34172228	34172277	0.03563	1.12
67	rs6581076	*OR10P1,METTL7B*	54353493	intergenic	12	54353493:54355498	ILMN_1750636	*RPS26*	54722548	54722597	0.03563	-1.21
68	rs6545924	*COMMD1,B3GNT2*	62224740	intergenic	2	62224740:62224740	ILMN_1761242	*COMMD1*	62216595	62216644	0.04488	-1.22
69	rs6543137	*IL18RAP*	102432340	intronic	2	102432340:102460645	ILMN_1781700	*IL18R1*	102381204	102381253	0.01742	1.99
70	rs6531673	*TLR6*	38524312	intronic	4	38524100:38532779	ILMN_1670931	*PDS5A*	39501313	39501362	0.03758	-1.1
71	rs6493387	*TRPM1*	29099315	intronic	15	29095045:29100035	ILMN_1778734	*MTMR15*	29022465	29022514	0.04488	-1.16
72	rs6482235	*PIP4K2A,ARMC3*	23062972	intergenic	10	23055735:23072792	ILMN_1657977	*MSRB2*	23449816	23449865	0.03563	1.31
73	rs6439982	*SPSB4,ACPL2*	142422118	intergenic	3	142418014:142464580	ILMN_1706598	*ACPL2*	142495356	142495402	0.01664	1.25
74	rs6439982	*SPSB4,ACPL2*	142422118	intergenic	3	142418014:142464580	ILMN_2306955	*ACPL2*	142495345	142495394	0.04488	1.26
75	rs6433294	*DCAF17,CYBRD1*	172077315	intergenic	2	172004040:172082512	ILMN_1712305	*CYBRD1*	172122282	172122331	0.01664	1.13
76	rs6433294	*DCAF17,CYBRD1*	172077315	intergenic	2	172004040:172082512	ILMN_2087692	*CYBRD1*	172122506	172122555	0.02388	1.14
77	rs639459	*C7orf25*	42918461	upstream	7	42908379:42918461	ILMN_1751051	*C7orf25*	42915790	42915839	0.04686	1.16
78	rs633683	*PHLDB1*	118009952	intronic	11	118009952:118009952	ILMN_2181241	*RPL23AP64*	118378966	118379015	0.04442	-1.22
79	rs624420	*CPT1A,MRPL21*	68376799	intergenic	11	68376799:68376799	ILMN_1711994	*TCIRG1*	67574603	67574652	0.04861	1.3
80	rs62262832	*C3orf17,BOC*	114324550	intergenic	3	114324550:114325444	ILMN_2286514	*GTPBP8*	114194610	114194659	0.04488	-1.18
81	rs6070412	*PPP4R1L*	56298680	ncRNA_intronic	20	56252573:56300219	ILMN_1704079	*RBM38*	55417232	55417281	0.03563	1.11
82	rs6070412	*PPP4R1L*	56298680	ncRNA_intronic	20	56252573:56300219	ILMN_2404049	*RBM38*	55417464	55417513	0.03758	1.1
83	rs60492890	*C19orf24*	1226368	upstream	19	1226368:1226987	ILMN_1674926	*C19orf35*	2225969	2226018	0.02774	1.37
84	rs60157471	*IL36B*	113508723	intronic	2	113508723:113508723	ILMN_1775501	*IL1B*	113304124	113304173	0.04727	-1.47
85	rs6001675	*ENTHD1*	38495105	intronic	22	38487197:38499872	ILMN_1883491	*AI970822*	37570629	37570678	0.04686	1.08
86	rs5994328	*SLC35E4,DUSP18*	29376587	intergenic	22	29376587:29376587	ILMN_1832879	*CD237904*	30363535	30363584	0.04727	1.36
87	rs59562633	*LOC100128714*	23744670	ncRNA_intronic	15	23738959:23744670	ILMN_1764549	*UBE3A*	23133561	23133610	0.04395	-1.12
88	rs59464952	*NLRP1,LOC339166*	5526243	intergenic	17	5526243:5531668	ILMN_1682761	*C17orf87*	5054545	5054594	0.04488	-1.18
89	rs57988909	*OR5H15,OR5H6*	99447182	intergenic	3	99447182:99447744	ILMN_1710326	*CLDND1*	99717305	99717354	0.04442	-1.23
90	rs5763241	*RFPL1*	28169168	downstream	22	28169168:28169168	ILMN_2393169	*THOC5*	28234509	28237095	0.04515	1.15
91	rs5756520	*TMPRSS6,IL2RB*	35838453	intergenic	22	35836626:35838453	ILMN_1687306	*LGALS2*	36296553	36296602	0.04729	-1.18
92	rs5752890	*EMID1*	27972365	intronic	22	27972365:27980905	ILMN_1809433	*XBP1*	27520967	27521016	0.03563	-1.17
93	rs57057834	*SLC19A1,LOC100129027*	45879226	intergenic	21	45879226:46007444	ILMN_1785179	*UBE2G2*	45013511	45013560	0.04729	-1.25
94	rs55776343	*SLC41A3*	127232672	intronic	3	127232672:127232672	ILMN_1702055	*ROPN1B*	127170784	127170833	0.04488	1.13
95	rs55678304	*RAB3A,PDE4C*	18177629	intergenic	19	18176196:18178341	ILMN_1807277	*IFI30*	18149528	18149661	0.04493	-1.18
96	rs538645	*DDX6,CXCR5*	118216279	intergenic	11	118216279:118216279	ILMN_1726306	*HMBS*	118469305	118469354	0.04395	1.03
97	rs531815	*MAK*	10898737	intronic	6	10870983:10927080	ILMN_2209115	*MAK*	10871283	10871332	0.01664	1.13
98	rs524908	*FRMD5*	41975283	intronic	15	41717025:42014562	ILMN_1658743	*CCNDBP1*	41265312	41265361	0.04136	1.13
99	rs4990638	*TMEM132E,CCT6B*	29996842	intergenic	17	29996842:29996842	ILMN_1752520	*SLFN11*	30701915	30701964	0.03364	-1.2

100	rs4985671	*LOC339166,WSCD1*	5896735	intergenic	17	5896735:5896735	ILMN_1810045	*NLRP1*	5361803	5361852	0.03563	1.16
101	rs4976450	*SPOCK1*	136856221	intronic	5	136843093:136861052	ILMN_1706539	*KDM3B*	137800223	137800272	0.04488	1.13
102	rs4968392	*VMP1*	55153986	intronic	17	55153986:55197547	ILMN_1695157	*CA4*	55591585	55591634	0.04488	1.7
103	rs492799	*NAALADL1,CDCA5*	64591882	intergenic	11	64591882:64591882	ILMN_1756204	*RPS6KA4*	63896005	63896054	0.02774	-1.17
104	rs4924543	*ZNF770,ANP32AP1*	33193816	intergenic	15	33193816:33193871	ILMN_2103547	*GOLGA8A*	32605217	32605266	0.03328	-1.26
105	rs4924398	*GPR176*	37963256	intronic	15	37947099:37963256	ILMN_1686116	*THBS1*	37676117	37676166	0.04061	1.24
106	rs4902681	*ACTN1*	68496370	intronic	14	68496370:68496370	ILMN_1675448	*ZFP36L1*	68324290	68324339	0.04729	-1.06
107	rs4889991	*CARD14*	75772658	intronic	17	75772658:75772658	ILMN_1749722	*RNF213*	75984368	75984417	0.03728	1.13
108	rs4887017	*ACSBG1*	76291717	intronic	15	76291717:76291717	ILMN_1665887	*WDR61*	76365455	76365504	0.04395	-1.21
109	rs4845391	*KCNN3*	153005728	intronic	1	153005728:153005728	ILMN_1782057	*ATP8B2*	152590047	152590096	0.04686	-1.21
110	rs4845143	*IL19*	205069942	intronic	1	205061027:205081399	ILMN_1742601	*CR1*	205859986	205861942	0.04847	1.3
111	rs4845143	*IL19*	205069942	intronic	1	205061027:205081399	ILMN_1767193	*CR1*	205859954	205860003	0.04061	1.22
112	rs4845143	*IL19*	205069942	intronic	1	205061027:205081399	ILMN_2388112	*CR1*	205879575	205879624	0.04488	1.24
113	rs4795402	*ORMDL3,LRRC3C*	35338911	intergenic	17	35338911:35338911	ILMN_1805636	*PERLD1*	35081038	35081087	0.04488	-1.14
114	rs4777959	*SLCO3A1,ST8SIA2*	90663220	intergenic	15	90663040:90663544	ILMN_1654735	*SLCO3A1*	90507108	90507157	0.02471	1.23
115	rs4767092	*LHX5,RBM19*	112459392	intergenic	12	112459392:112459392	ILMN_1675640	*OAS1*	111839789	111839838	0.04856	-1.16
116	rs4688030	*MAATS1*	120923380	intronic	3	120923380:120929131	ILMN_2187718	*COX17*	120878851	120878900	0.04442	-1.16
117	rs4653108	*SMIM12,DLGAP3*	35100619	intergenic	1	35100619:35100619	ILMN_2260500	*KIAA0319L*	35677436	35677485	0.04625	1.34
118	rs4452682	*SLC22A23*	3360301	intronic	6	3360301:3360301	ILMN_1783158	*LY6G6F*	3124285	3124482	0.04856	1.12
119	rs444297	*LIMK1,EIF4H*	73191971	intergenic	7	73191971:73191971	ILMN_1761387		72286547	72286586	0.04395	1.31
120	rs4442562	*FOXR1*	118351023	intronic	11	118328358:118351023	ILMN_1746516	*RPS25*	118393973	118394202	0.04686	-1.25
121	rs4433629	*LOC338758,LINC00615*	88865586	intergenic	12	88850063:88865586	ILMN_1795835	*LOC338758*	88628314	88628363	0.04488	-1.16
122	rs4309551	*RRM2,C2orf48*	10190124	intergenic	2	10182160:10190124	ILMN_1775011	*NOL10*	10628711	10628760	0.01664	1.1
123	rs42931	*GAL3ST1*	29290412	intronic	22	29290412:29291048	ILMN_1803925	*MTMR3*	28756106	28756155	0.04061	1.26
124	rs4253082	*ERCC6*	50387592	intronic	10	50325185:50387592	ILMN_1679555	*TIMM23*	51262200	51262249	0.04579	-1.21
125	rs425181	*C1orf87,NFIA*	61008272	intergenic	1	61008272:61008272	ILMN_2143148	*TM2D1*	61919409	61919458	0.04811	-1.06
126	rs4242902	*DPPA3,CLEC4C*	7762703	intergenic	12	7762115:7764216	ILMN_1665457	*CLEC4C*	7790224	7790273	0.0299	1.19
127	rs417557	*CLDN14,SIM2*	36934876	intergenic	21	36934876:36934876	ILMN_1661194	*CLDN14*	36760535	36760584	0.04686	1.14
128	rs4147779	*NDUFS8*	67561383	downstream	11	67561383:67561383	ILMN_1692026	*SUV420H1*	67689973	67690022	0.04911	1.15
129	rs4075678	*GALNT18*	11275540	intronic	11	11275540:11275751	ILMN_2380946	*EIF4G2*	10775399	10775448	0.04061	-1.01
130	rs4075428	*CIZ1*	129979942	intronic	9	129971407:129982793	ILMN_1687857	*ST6GALNAC4*	129710161	129710210	0.04686	1.07
131	rs4075428	*CIZ1*	129979942	intronic	9	129971407:129982793	ILMN_1732049	*DPM2*	129737499	129737548	0.02607	1.12
132	rs4075428	*CIZ1*	129979942	intronic	9	129971407:129982793	ILMN_2413064	*ST6GALNAC4*	129710210	129710259	0.01888	1.08
133	rs3865451	*ADCK4*	45897379	intronic	19	45897379:45897379	ILMN_1654875	*CLC*	44916828	44916877	0.04911	-1.36
134	rs3853657	*MIR4456,CEP72*	620246	intergenic	5	620246:620246	ILMN_1655195	*SMA4*	922813	1276923	0.03563	-1.17
135	rs3826440	*POLR2A*	7352179	intronic	17	7336893:7352179	ILMN_1731546	*RPL26*	8226358	8227200	0.04395	-1.25
136	rs3825073	*SYVN1*	64656846	intronic	11	64656846:64656846	ILMN_1794364	*CTSW*	65407708	65407757	0.04395	-1.05
137	rs3802984	*ODF3*	187337	exonic	11	187337:187337	ILMN_1657932	*MUC6*	1006343	1006392	0.04861	1.11
138	rs3793243	*STX1A*	72759283	intronic	7	72759283:72759283	ILMN_1761387		72286547	72286586	0.04061	1.31
139	rs3771863	*TACR1*	75273222	intronic	2	75273222:75273222	ILMN_1696375	*TTC31*	74574864	74574913	0.04493	-1.16
140	rs3766746	*PLOD1*	11954453	intronic	1	11947940:11955707	ILMN_1651385	*MFN2*	11995702	11995751	0.04061	1.28
141	rs3761821	*OBP2B,ABO*	135075604	intergenic	9	135070093:135092020	ILMN_1683498	*RPL7A*	135207747	135207986	0.03872	-1.16
142	rs3760352	*ASGR2,ASGR1*	6960602	intergenic	17	6960602:6960602	ILMN_1703433	*PLSCR3*	7233856	7233905	0.02607	-1.26
143	rs3760352	*ASGR2,ASGR1*	6960602	intergenic	17	6960602:6960602	ILMN_1722900	*EIF4A1*	7422386	7422435	0.04061	-1.2
144	rs3758587	*ARHGAP19-SLIT1*	98936234	ncRNA_intronic	10	98936234:98936234	ILMN_1794914	*UBTD1*	99320582	99320631	0.02929	1.15
145	rs36074193	*TOB1-AS1,SPAG9*	46338098	intergenic	17	46320079:46338774	ILMN_1672004	*TOB1*	46295472	46295521	0.00198	1.46
146	rs35406858	*RPP25,SCAMP5*	73066722	intergenic	15	73066722:73143655	ILMN_1704477	*COX5A*	72999836	73003042	0.0384	-1.27
147	rs35406858	*RPP25,SCAMP5*	73066722	intergenic	15	73066722:73143655	ILMN_1733696	*IMP3*	73718652	73718701	0.04186	-1.27
148	rs35288741	*NFASC*	203194778	intronic	1	203191308:203194778	ILMN_2094952	*NUAK2*	203538143	203538192	0.04387	1.15
149	rs34771359	*CHN2,PRR15*	29532520	intergenic	7	29530510:29532686	ILMN_1821876	*AK024143*	30391669	30391718	0.04686	1.07
150	rs34764163	*DISP1*	221101110	intronic	1	221101110:221101110	ILMN_1901666	*AI445566*	221775124	221775173	0.04488	1.07

151	rs325828	*MROH2B*	41067989	intronic	5	41031410:41227685	ILMN_2357577	*PRKAA1*	40795743	40795792	0.02774	-1
152	rs3015983	*PAK1*	76842552	intronic	11	76842552:76842552	ILMN_1767365	*PAK1*	76710953	76711002	0.04686	1.22
153	rs300035	*FOXL1,C16orf95*	85245335	intergenic	16	85245335:85245335	ILMN_1666594	*IRF8*	84513378	84513427	0.04493	-1.06
154	rs2956993	*GANAB*	62162738	intronic	11	62162738:62162738	ILMN_1746525	*FTH1*	61488797	61488845	0.04395	1.11
155	rs2938387	*PPARG*	12414387	intronic	3	12404468:12425354	ILMN_1793724	*C3orf31*	11807055	11825991	0.03563	-1.18
156	rs2856728	*ELN*	73108718	intronic	7	73108718:73108718	ILMN_1791375	*STAG3L2*	73937376	73937425	0.04686	-1.25
157	rs2848122	*ANKRD36BP2,MIR4436A*	88888304	intergenic	2	88888304:88888304	ILMN_1652199	*IGKC*	89108078	89108248	0.04686	-1.16
158	rs2828337	*D21S2088E,LOC339622*	23917069	intergenic	21	23917069:23917131	ILMN_1653667	*TBX1*	24503066	24503115	0.04686	1.17
159	rs2812500	*C10orf35,COL13A1*	71090178	intergenic	10	71090178:71090178	ILMN_1740633	*PRF1*	72027390	72027439	0.04442	1.09
160	rs2749883	*NID2*	51585466	intronic	14	51574983:51585466	ILMN_1807925	*GNG2*	51505271	51505320	0.048	1.04
161	rs2730355	*GALNT15*	16203962	intronic	3	16203962:16216785	ILMN_1723414	*HACL1*	15577408	15579869	0.0299	-1.17
162	rs2712353	*ATP6V1A*	114978338	intronic	3	114978338:114978338	ILMN_2286514	*GTPBP8*	114194610	114194659	0.04686	-1.18
163	rs2672027	*MIR4456,CEP72*	619782	intergenic	5	619782:628683	ILMN_1744210	*SDHA*	289627	289676	0.04387	-1.16
164	rs2568032	*ST5*	8817653	intronic	11	8817620:8817653	ILMN_1752988	*C11orf17*	8898065	8898114	0.04488	-1.18
165	rs2567342	*BDH1*	198766894	intronic	3	198765490:198784408	ILMN_1756360	*RPL35A*	199161471	199162234	0.04442	-1.22
166	rs2524379	*EMR2*	14715034	intronic	19	14715034:14719882	ILMN_1688152	*IL27RA*	14024744	14024793	0.04686	-1.2
167	rs250145	*MAF,MIR548H4*	78214847	intergenic	16	78214847:78214847	ILMN_1719543	*MAF*	78190183	78190216	0.04493	-1.18
168	rs2473263	*WNT4,ZBTB40*	22415951	intergenic	1	22415032:22424400	ILMN_1701603	*ALPL*	21777338	21777387	0.04398	1.42
169	rs2460432	*ASL*	65191820	intronic	7	65166353:65877443	ILMN_1651950	*TPST1*	65462499	65462548	0.03325	2.3
170	rs2422008	*WDPCP*	63634109	intronic	2	63617436:63672852	ILMN_1679268	*PELI1*	64174168	64174217	0.04204	1.68
171	rs2420147	*LYRM7,CDC42SE2*	130589156	intergenic	5	130589156:130589156	ILMN_1737343	*FNIP1*	131005910	131005959	0.04847	1.25
172	rs2395891	*BTBD2,MKNK2*	1983148	intergenic	19	1982709:2000314	ILMN_1721344	*MOB3A*	2022058	2022107	0.02446	1.15
173	rs2395891	*BTBD2,MKNK2*	1983148	intergenic	19	1982709:2000314	ILMN_2347068	*MKNK2*	1988716	1988765	0.02774	1.18
174	rs2388881	*MCTP2,LOC440311*	93084371	intergenic	15	93084371:93084371	ILMN_1792682	*MCTP2*	92814577	92814626	0.04442	1.29
175	rs2387976	*NANP*	25547560	intronic	20	25155074:25547776	ILMN_1674394	*C20orf3*	24891888	24891937	0.01664	1.37
176	rs2387976	*NANP*	25547560	intronic	20	25155074:25547776	ILMN_2091792	*ENTPD6*	25154924	25154973	0.03872	-1.18
177	rs2385067	*TMEM104*	70321665	intronic	17	70321665:70321665	ILMN_1748797	*GRB2*	70833601	70833650	0.04061	1.21
178	rs2371129	*EIF1B-AS1*	40223397	ncRNA_intronic	3	40218470:40469694	ILMN_2404850	*RPL14*	40478782	40478831	0.00997	-1.14
179	rs2363536	*CD53*	111227572	intronic	1	111223235:111228031	ILMN_1721989	*ATP5F1*	111805082	111805131	0.04196	-1.13
180	rs2359795	*JDP2*	74982232	intronic	14	74979367:74982232	ILMN_1694233	*ACYP1*	74589991	74590040	0.04061	-1.14
181	rs2329844	*TSPEAR*	44911329	intronic	21	44897801:44915392	ILMN_1785179	*UBE2G2*	45013511	45013560	0.03325	-1.25
182	rs231478	*MPP2*	39339153	intronic	17	39335292:39346859	ILMN_1653711	*FZD2*	39992224	39992273	0.01755	-1.22
183	rs2305160	*NPAS2*	100957736	exonic	2	100957736:100961907	ILMN_1702806	*PDCL3*	100559358	100559407	0.04488	-1.15
184	rs2296887	*GBF1*	103995400	UTR5	10	103995400:104154200	ILMN_1682165	*NT5C2*	104837928	104837977	0.04061	1.23
185	rs2295281	*MFN2*	11981999	intronic	1	11905131:12018455	ILMN_1651385	*MFN2*	11995702	11995751	0.00026	1.28
186	rs2282444	*TOMM6,USP49*	41870786	intergenic	6	41862554:41904795	ILMN_1663489	*UBR2*	42765341	42766751	0.04729	1.15
187	rs2280516	*DRC1*	26531314	intronic	2	26531314:26531314	ILMN_1691090	*MPV17*	27386135	27386184	0.02446	-1.18
188	rs2277628	*MYCBPAP*	45956380	intronic	17	45955762:45956380	ILMN_2263718	*SPAG9*	46398289	46398338	0.02504	1.19
189	rs2269799	*SV2B*	89597587	intronic	15	89597587:89597587	ILMN_1663699	*SLCO3A1*	90198184	90198233	0.04686	1.11
190	rs2253693	*SIRPB1*	1493468	UTR3	20	1493468:1493468	ILMN_1841622	*AI655567*	1364588	1364637	0.04395	1.35
191	rs2240516	*COA1*	43653821	intronic	7	43653821:43653821	ILMN_2081335	*C7orf44*	43645572	43645621	0.03325	1.18
192	rs2237250	*FYN*	112091774	intronic	6	112085437:112111819	ILMN_2249920	*FYN*	112128094	112128143	0.04398	-1.19
193	rs2234768	*ACTA2*	90739923	intronic	10	90732604:90746143	ILMN_1799848	*ANKRD22*	90572755	90573017	0.04579	1.43
194	rs2209313	*SIRPB1*	1547142	intronic	20	1444909:1550206	ILMN_1742442	*SIRPB1*	1527582	1532456	0.00043	1.15
195	rs2178779	*OR4E2,DAD1*	21479411	intergenic	14	21479411:21479411	ILMN_1670272	*LRP10*	22416937	22416986	0.02929	1.31
196	rs2161343	*FLJ38109*	153760297	ncRNA_intronic	5	153760297:153760297	ILMN_1728742	*C5orf4*	154178618	154178667	0.04398	1.13
197	rs213637	*PAQR7*	26061212	UTR3	1	26061212:26061212	ILMN_1760556	*BC041843*	25443060	25443109	0.048	1.12
198	rs2072443	*TMEM176B*	150121309	exonic	7	150121309:150121309	ILMN_1791511	*TMEM176A*	150133038	150133087	0.03563	-1.15
199	rs2049490	*POC5,SV2C*	75264893	intergenic	5	75264893:75264893	ILMN_2221507	*F2R*	76066988	76067037	0.04686	1.09
200	rs2027237	*LOC728228*	4125104	downstream	20	4125104:4125104	ILMN_1717809	*RNF24*	3862010	3862059	0.04061	1.2
201	rs200891	*LOC100289473,SIRPA*	1739920	intergenic	20	1739920:1739920	ILMN_1758146	*SIRPA*	1868371	1868420	0.04442	1.4

202	rs1981294	*LRIF1,DRAM2*	111328262	intergenic	1	111328262:111333136	ILMN_1721989	*ATP5F1*	111805082	111805131	0.03653	-1.13
203	rs1893233	*PIEZO2,GNAL*	11401062	intergenic	18	11401062:11401062	ILMN_1667744	*MPPE1*	11874882	11874931	0.04196	1.19
204	rs1873625	*BSN*	49641968	intronic	3	49624993:49641968	ILMN_1705737	*IMPDH2*	49037239	49037333	0.048	-1.24
205	rs1859441	*COL2A1,SENP1*	46709500	intergenic	12	46671211:47058180	ILMN_1731666	*ZNF641*	47022351	47022400	0.03325	1.05
206	rs17849707	*CEP68*	65152343	exonic	2	65146074:65162727	ILMN_2388605	*ACTR2*	65351207	65351256	0.04811	1.06
207	rs17834472	*SLC38A6,TMEM30B*	60684493	intergenic	14	60684493:60712798	ILMN_2410516	*PPM1A*	59819329	59819378	0.02471	1.14
208	rs17654580	*ARRDC2,IL12RB1*	17989388	intergenic	19	17989388:17989388	ILMN_1782977	*UBA52*	18546768	18546901	0.04398	1.08
209	rs17586305	*D21S2088E,LOC339622*	23746337	intergenic	21	23733607:23747666	ILMN_1653667	*TBX1*	24503066	24503115	0.03325	1.17
210	rs17340646	*TPI1P2,LOC407835*	128509750	intergenic	7	128508960:128516364	ILMN_1683811	*TNPO3*	128382582	128382631	0.03386	1.18
211	rs17304079	*RBM6*	50060157	intronic	3	49962479:50111467	ILMN_1749662	*GPX1*	49369862	49369911	0.04442	1.09
212	rs17280306	*ZNF621,CTNNB1*	41143088	intergenic	3	41093454:41155349	ILMN_1786242	*RPL14*	40477928	40477977	0.04442	-1.32
213	rs17239727	*BLVRA*	43810846	intronic	7	43533029:43810846	ILMN_2081335	*C7orf44*	43645572	43645621	0.02446	1.18
214	rs171803	*SLCO6A1,PAM*	102164398	intergenic	5	102069646:102617353	ILMN_2313901	*PAM*	102393033	102393082	0.00026	1.13
215	rs17178720	*UGGT1*	128656269	exonic	2	128549279:128666687	ILMN_1765122	*MAP3K2*	127780309	127780358	0.04442	1.17
216	rs17173596	*GIMAP1-GIMAP5,TMEM176B*	150108317	intergenic	7	150087531:150122017	ILMN_1791511	*TMEM176A*	150133038	150133087	0.01749	-1.15
217	rs17108932	*PTEN,RNLS*	89856653	intergenic	10	89851613:89856653	ILMN_1701134	*PTEN*	89715816	89715865	0.03563	1.56
218	rs17108932	*PTEN,RNLS*	89856653	intergenic	10	89851613:89856653	ILMN_1880406	*PTEN*	89718328	89718377	0.03563	1.62
219	rs17034661	*VGLL4*	11577131	intronic	3	11577131:11577131	ILMN_1768480	*VGLL4*	11572660	11572709	0.04811	-1.16
220	rs17031905	*INPP4A*	98437334	intronic	2	98390151:98516378	ILMN_1719756	*ZAP70*	97722452	97722501	0.04294	-1.2
221	rs16858988	*GAD1*	171411206	intronic	2	171404718:171411206	ILMN_1712305	*CYBRD1*	172122282	172122331	0.03386	1.13
222	rs166211	*LOC283867,CDH5*	64480435	intergenic	16	64475158:64495025	ILMN_1712389	*CKLF*	65144146	65144195	0.04294	1.3
223	rs166211	*LOC283867,CDH5*	64480435	intergenic	16	64475158:64495025	ILMN_2414027	*CKLF*	65144132	65144181	0.04392	1.27
224	rs1647990	*RORA*	58703914	intronic	15	58695599:58703914	ILMN_1711899	*ANXA2*	58476751	58476800	0.03872	-1.14
225	rs1610037	*ADCYAP1*	900635	UTR3	18	900635:900635	ILMN_1803676	*ENOSF1*	664167	664216	0.01807	-1.14
226	rs158391	*ZNF33B,BMS1*	42463084	intergenic	10	42462526:42471703	ILMN_1799208	*CSGALNACT2*	42979374	42979423	0.03758	1.23
227	rs1562782	*ADM,AMPD3*	10299287	intergenic	11	9822432:10299287	ILMN_1678004	*TMEM41B*	9258922	9258971	0.04442	-1.06
228	rs1562782	*ADM,AMPD3*	10299287	intergenic	11	9822432:10299287	ILMN_2093500	*ZBED5*	10831172	10831221	0.03563	-1.12
229	rs1559155	*PPFIA3*	54324584	intronic	19	54324584:54324584	ILMN_1732053	*SNRNP70*	54303590	54303639	0.04856	-1.12
230	rs1532445	*LZTS1,LZTS1-AS1*	20176079	intergenic	8	20176079:20176079	ILMN_1679483	*INTS10*	19753619	19753668	0.04442	-1.11
231	rs1529505	*F2RL1*	76150719	UTR5	5	76142198:76164090	ILMN_2041190	*F2RL1*	76166727	76166776	0.03758	1.19
232	rs1423738	*HS3ST4,C16orf82*	26707229	intergenic	16	26707224:26707229	ILMN_1798204	*IL21R*	27369234	27369283	0.04488	-1.16
233	rs1408069	*KLF4,ACTL7B*	110258821	intergenic	9	110226442:110258821	ILMN_2137789	*KLF4*	109287322	109287371	0.03782	-1.11
234	rs1379868	*NRTN*	5778097	intronic	19	5778097:5783209	ILMN_1766125	*LONP1*	5643098	5643147	0.02446	-1.19
235	rs1352312	*MAP3K14*	40732544	intronic	17	40732230:40732544	ILMN_1762678	*NMT1*	40541739	40541788	0.048	-1.13
236	rs13332660	*SEZ6L2*	29813383	intronic	16	29813383:29813383	ILMN_2125747	*CORO1A*	30107703	30107752	0.04061	1.12
237	rs13285411	*DNM1*	130037689	intronic	9	130037689:130037689	ILMN_1692223	*LCN2*	129954359	129955223	0.04686	1.16
238	rs1317577	*N4BP2,RHOH*	39872944	intergenic	4	39871932:39872944	ILMN_1750507	*RPL9*	39136324	39136409	0.02774	-1.41
239	rs131430	*IGLL1,C22orf43*	22257134	intergenic	22	22257134:22257134	ILMN_2393765	*IGLL1*	22245479	22245528	0.04488	-1.13
240	rs13090	*MED16*	819115	exonic	19	819115:819115	ILMN_1777190	*CFD*	814271	814320	0.04395	1.11
241	rs13022989	*LOC440905*	130508683	ncRNA_intronic	2	130508683:130508683	ILMN_2156982	*IMP4*	130820595	130820644	0.04729	-1.19
242	rs12981801	*ZNF554*	2788468	downstream	19	2788468:2792360	ILMN_1674926	*C19orf35*	2225969	2226018	0.04686	1.37
243	rs12891572	*HNRNPC*	20808102	upstream	14	20750264:20808102	ILMN_1780533	*RNASE6*	20320082	20320131	0.04204	1.4
244	rs12886153	*KTN1,RPL13AP3*	55290826	intergenic	14	55290826:55290826	ILMN_1780132	*PELI2*	55837274	55837323	0.03653	1.17
245	rs1280984	*CASZ1,C1orf127*	10907149	intergenic	1	10900411:10907149	ILMN_1794165	*PGD*	10402399	10402448	0.01755	1.29
246	rs12766521	*SH2D4B,NRG3*	82523728	intergenic	10	82523405:82550940	ILMN_2380494	*ANXA11*	81904867	81904916	0.04442	1.22
247	rs12705071	*ZNF3,COPS6*	99519962	intergenic	7	99519962:99519962	ILMN_1804530	*ARPC1B*	98826745	98826794	0.04856	1.08
248	rs1265758	*C6orf10*	32431507	intronic	6	32429093:32441173	ILMN_1697499	*HLA-DRB5*	32593375	32593424	0.04387	-1.07
249	rs12620091	*ALMS1P*	73760327	ncRNA_intronic	2	73760327:73760327	ILMN_1662954	*CCT7*	73324681	73325224	0.04686	-1.17
250	rs12611262	*SEMA6B,TNFAIP8L1*	4566843	intergenic	19	4566843:4566843	ILMN_1658486	*MRPL54*	3716282	3718260	0.04579	-1.24
251	rs12548608	*KIF13B*	29058919	intronic	8	29042276:29062627	ILMN_1778226	*EXTL3*	28666791	28666840	0.03563	1.44
252	rs12497322	*XIRP1,CX3CR1*	39224757	intergenic	3	39224757:39228567	ILMN_1665148	*RPSA*	39427271	39427306	0.04442	-1.36

253	rs12497322	*XIRP1,CX3CR1*	39224757	intergenic	3	39224757:39228567	ILMN_1710885	*RPSA*	39425216	39427294	0.03872	-1.34
254	rs12443981	*SEPHS2,ITGAL*	30367556	intergenic	16	30367556:30367556	ILMN_1671854	*ZNF48*	30298858	30298907	0.03758	-1.18
255	rs12441390	*RASGRP1,C15orf53*	36737852	intergenic	15	36737314:36741243	ILMN_1768958	*RASGRP1*	36567825	36567874	0.04493	-1.17
256	rs12438495	*IGF1R*	97294581	intronic	15	97294581:97294581	ILMN_1744023	*IGF1R*	97324631	97324680	0.04686	1.17
257	rs12433896	*RNASE4,EDDM3A*	20252225	intergenic	14	20250408:20254322	ILMN_1780533	*RNASE6*	20320082	20320131	0.01755	1.4
258	rs12432242	*SLC7A7*	22353745	intronic	14	22352289:22354412	ILMN_1810275	*SLC7A7*	22312595	22312644	0.04061	-1.01
259	rs12423255	*PITPNM2*	122161017	upstream	12	122161017:122161017	ILMN_1725187	*PITPNM2*	122035951	122036000	0.04061	1.17
260	rs12417156	*CHRDL2*	74107635	intronic	11	74106228:74107635	ILMN_1652753	*PAAF1*	73316029	73316078	0.01664	-1.17
261	rs12372446	*KRT71,KRT74*	51240161	intergenic	12	51240161:51240161	ILMN_1695812	*KRT72*	51265803	51265852	0.04493	-1.02
262	rs12335026	*FABP12,IMPA1*	82616916	intergenic	8	82603595:82618996	ILMN_1690586	*DQ579214*	83366491	83366540	0.03073	-1.28
263	rs1228529	*PHACTR1*	13269124	intronic	6	13267877:13316842	ILMN_1736982	*PHACTR1*	13391737	13394369	0.03872	1.19
264	rs12216600	*PDE1C*	31932494	intronic	7	31932494:31932494	ILMN_1737947	*LSM5*	32493430	32493822	0.04686	-1.2
265	rs12206258	*GMDS*	1654702	intronic	6	1654702:1659676	ILMN_1738401	*FOXC1*	1557280	1557329	0.02366	1.42
266	rs12128782	*TBX19,MIR557*	166576671	intergenic	1	166574781:166578203	ILMN_1739103	*MPZL1*	166011934	166011983	0.04061	1.24
267	rs11859842	*SLC7A5P1,SPN*	29568718	intergenic	16	29567727:29568718	ILMN_2344373	*MVP*	29765045	29765094	0.03728	1.1
268	rs11760934	*POLR2J2,FAM185A*	102121342	intergenic	7	102121342:102121342	ILMN_1682368	*LRWD1*	101900431	101900480	0.04729	1.26
269	rs11760186	*PHACTR1*	13303990	intronic	6	13272634:13313608	ILMN_1736982	*PHACTR1*	13391737	13394369	0.005	1.19
270	rs11707455	*BBX*	109002467	intronic	3	108965483:109014759	ILMN_1771333	*CD47*	109245077	109245126	0.02504	-1.17
271	rs11686934	*MXD1,ASPRV1*	70025620	intergenic	2	70025620:70026831	ILMN_2388466	*TIA1*	70292835	70292837	0.04488	-1.1
272	rs11672145	*ZNF799*	12361149	downstream	19	12361149:12361149	ILMN_1694325	*NFIX*	13070426	13070475	0.02607	1.06
273	rs11672145	*ZNF799*	12361149	downstream	19	12361149:12361149	ILMN_1751571	*RAD23A*	12925269	12925318	0.03981	-1.05
274	rs11645488	*FLJ26245*	34918516	intergenic	16	34673963:35126825	ILMN_1689327	*CR617556*	34894369	34894418	0.03563	-1.05
275	rs11644259	*BRD7*	48928964	intronic	16	48927389:48958820	ILMN_1721349	*MAGT1*	48582679	48582721	0.04061	1.11
276	rs11638679	*C15orf54,THBS1*	37427440	intergenic	15	37427440:37427440	ILMN_1686116	*THBS1*	37676117	37676166	0.04715	1.24
277	rs11264449	*SEMA4A*	154401865	intronic	1	154393992:154401865	ILMN_1755123	*GBA*	153471726	153472096	0.04488	1.19
278	rs11249756	*BTNL3,BTNL9*	180387978	intergenic	5	180246943:180391419	ILMN_1783795	*BTNL3*	180365765	180365814	0.00581	1.16
279	rs11246074	*IFITM3,B4GALNT4*	326332	intergenic	11	326332:326332	ILMN_1698519	*AL137655*	154284	154333	0.04625	1.25
280	rs11238359	*EGFR,LANCL2*	55351381	intergenic	7	55338638:55382381	ILMN_1760338	*SUMO2*	55767228	55767277	0.04061	-1.1
281	rs11227523	*ZDHHC24*	66062514	downstream	11	66060430:66067587	ILMN_1657701	*RBM4*	66153904	66153953	0.04735	-1.15
282	rs11176799	*CAND1,DYRK2*	66280237	intergenic	12	66280237:66280237	ILMN_1794588	*DYRK2*	66339763	66339812	0.03758	-1.32
283	rs11123840	*PDCL3,NPAS2*	100670590	intergenic	2	100657569:100673431	ILMN_1665877	*RNF149*	101259473	101259522	0.01182	1.42
284	rs11083620	*C19orf69*	46640523	upstream	19	46640523:46640523	ILMN_1734878	*CD79A*	47077190	47077239	0.04061	-1.3
285	rs11078835	*GAS7*	10018374	intronic	17	10018374:10018374	ILMN_1745994	*GAS7*	9755048	9755097	0.04488	1.14
286	rs11055463	*DPPA3,CLEC4C*	7770921	intergenic	12	7770253:7813713	ILMN_1665457	*CLEC4C*	7790224	7790273	0.00164	1.19
287	rs11055463	*DPPA3,CLEC4C*	7770921	intergenic	12	7770253:7813713	ILMN_1682259	*CLEC4C*	7773603	7774660	0.04395	1.12
288	rs10939637	*SLC2A9*	9586675	intronic	4	9580847:9590987	ILMN_1675844	*WDR1*	9708466	9708515	0.04727	1.18
289	rs10931765	*PGAP1,ANKRD44*	197505469	intergenic	2	197505306:197506307	ILMN_1798543	*STK17B*	196710644	196710693	0.04121	1.42
290	rs10906402	*LOC399715,PRKCQ*	6470773	intergenic	10	6470773:6470773	ILMN_1733421	*PRKCQ*	6509403	6509452	0.04488	-1.2
291	rs10885031	*RBM20*	112488320	intronic	10	112487536:112488320	ILMN_1787378	*ADD3*	111882076	111882125	0.04488	-1.05
292	rs10881678	*KIF20B,LINC00865*	91560885	intergenic	10	91560353:91560885	ILMN_1682799	*STAMBPL1*	90672973	90673022	0.04925	-1.21
293	rs10835861	*RCN1,WT1*	32176427	intergenic	11	32160744:32176427	ILMN_1737806	*BX648962*	31864998	31865047	0.04686	1.05
294	rs10790231	*TMPRSS4*	117472686	intronic	11	117434172:117474332	ILMN_1746516	*RPS25*	118393973	118394202	0.01596	-1.25
295	rs10784359	*SLC2A13*	38732017	intronic	12	38684237:39072999	ILMN_1859584	*AK026751*	38822138	38822187	0.0181	1.22
296	rs10781518	*SDCCAG3*	138420368	intronic	9	138390427:138420368	ILMN_1764239	*PMPCA*	138437919	138437968	0.04488	-1.12
297	rs10746914	*ANXA1,RORB*	74994069	intergenic	9	74992209:75000116	ILMN_1795228	*ZFAND5*	74159606	74159655	0.04387	1.07
298	rs10505733	*CLEC4C*	7779822	intronic	12	7779822:7821438	ILMN_1665457	*CLEC4C*	7790224	7790273	0.00021	1.19
299	rs10505733	*CLEC4C*	7779822	intronic	12	7779822:7821438	ILMN_1682259	*CLEC4C*	7773603	7774660	0.00021	1.12
300	rs10489832	*OR10R2,OR6Y1*	156720980	intergenic	1	156720980:156720980	ILMN_1710937	*IFI16*	157288363	157288412	0.04686	1.29
301	rs10487531	*LOC730441,MTRNR2L6*	141837701	intergenic	7	141837701:141837701	ILMN_1701875	*ZYX*	142798238	142798287	0.04488	1.23
302	rs1041898	*SULF2,LINC00494*	45995024	intergenic	20	45978568:45995024	ILMN_2345142	*SULF2*	45719770	45719819	0.03386	1.17
303	rs10234768	*C7orf72*	50152625	intronic	7	50152625:50163789	ILMN_1669617	*GRB10*	50625510	50625559	0.04442	1.14

304	rs10180924	*ATOH8,LOC284950*	85875430	intergenic	2	85869833:85875430	ILMN_1790692	*GNLY*	85778306	85779241	0.01664	1.02
305	rs1007122	*COMMD7,DNMT3B*	30809662	intergenic	20	30808003:30814325	ILMN_1774250	*PLUNC*	31291793	31291842	0.04686	1.06
306	rs10039049	*ANXA6*	150498092	intronic	5	150498092:150522859	ILMN_1736567	*CD74*	149761687	149761736	0.04686	-1.25
307	rs10039049	*ANXA6*	150498092	intronic	5	150498092:150522859	ILMN_2379644	*CD74*	149761619	149761668	0.04488	-1.28
308	rs1001073	*MASP1*	188427399	intronic	3	188427399:188427399	ILMN_1685722	*EIF4A2*	187990260	187990309	0.04442	-1.26
309	rs10002500	*CNGA1*	47653436	intronic	4	47653436:47695545	ILMN_1700306	*OCIAD2*	48589546	48589595	0.02446	-1.32
310	5-50827997	*ISL1,PELO*	50827997	intergenic	5	50618846:50828051	ILMN_1806651	*PARP8*	49998725	49998774	0.04686	1.25
311	3-43101876	*GTDC2*	43101876	intronic	3	43094794:43124579	ILMN_1674522	*HIGD1A*	42801413	42801462	0.04395	-1.07
312	3-113567114	*CD200,BTLA*	113567114	intergenic	3	113566762:113576083	ILMN_2415786	*CD96*	112853372	112853421	0.04488	-1.29
313	19-40883657	*UPK1A,ZBTB32*	40883657	intergenic	19	40877452:40911365	ILMN_1720542	*POLR2I*	41296993	41297081	0.04442	-1.18
314	19-18810229	*UPF1*	18810229	intronic	19	18808384:18851396	ILMN_1805693	*GMIP*	19601535	19601584	0.04442	1.21
315	17-8005504	*VAMP2*	8005504	intronic	17	8005504:8005504	ILMN_1746883	*SSAT2*	7470481	7470530	0.04395	-1.17
316	15-20476475	*CYFIP1*	20476475	intronic	15	20476475:20477065	ILMN_1657478	*MAGEL2*	21440140	21440189	0.04686	1.09
317	10-44400544	*CXCL12,TMEM72-AS1*	44400544	intergenic	10	44400544:44400544	ILMN_1798533	*ZNF22*	44820311	44820360	0.04488	-1.16
318	1-20817476	*CDA*	20817476	intronic	1	20816817:20818566	ILMN_1734231	*DDOST*	20851298	20851347	0.04856	-1.19
319	1-155229343	*ARHGEF11*	155229343	intronic	1	155158234:155283683	ILMN_1695576	*MRPL24*	154973950	154974062	0.04061	-1.25
320	1-148440425	*PLEKHO1,ANP32E*	148440425	intergenic	1	148267857:148770679	ILMN_1695435	*HIST2H2AA3/4*	148080335	148080384	0.00581	1.22

[a] *SNP Chromosome*

[b] *Position of the eQTL bin (=set of SNPs in LD) denotes the region surrounding the tag SNP containing 1 or more SNPs in LD with the tag SNP (listed in bp hg 18)*

[c] *Illumina probe identifier (Human HT-12 v3)*

[d] *probe gene*

[e-f] *transcript position (listed in bp hg 18)*

[g] *lowest Q value for eQTL bin*

[h] *fold change of GR-stimulated/baseline gene expression*