

A Genome-Wide Association Study of Depressive Symptoms

Supplemental Information

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Table S1. Genotyping and quality control information.

Cohort	Platform	Calling algorithm	Sample QC			Imputation QC			Imputation		Analysis	
			Call rate	Other exclusions	MAF	HWE P-value	Call rate	Other	Software	Build	Software	Adjustment*
AGES-RS	Illumina 370 K	BeadStudio	<95%	sex mismatch, sample failure, genotype mismatch with reference panel	>1%	>10 ⁻⁶	>97%		MACH	HapMap release 22 CEU (build 36)	ProbABEL	
ARIC1	Affymetrix 6.0	Birdseed	<95%	sex mismatch, 1st degree relatives, cryptic relatedness, genotype discordance, outliers in PCA	>1%	>10 ⁻⁶	>95%	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	study site
ARIC2	Affymetrix 6.0	Birdseed	<95%	sex mismatch, 1st degree relatives, cryptic relatedness, genotype discordance, outliers in PCA	>1%	>10 ⁻⁶	>95%	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	study site
ARIC3	Affymetrix 6.0	Birdseed	<95%	sex mismatch, 1st degree relatives, cryptic relatedness, genotype discordance, outliers in PCA	>1%	>10 ⁻⁶	>95%	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	study site
BLSA	Illumina HumanHap 550K	BeadStudio	<98.5%	Non-European, sex mismatch	≥1%	≥10 ⁻⁴	>99%	-	MACH	HapMap release 22 CEU (build 36)	Merlin-offline, mach2dat	PCA
CHS	Illumina 370 CNV	BeadStudio	<95%	sex mismatch, sample failure	≥1%	≥10 ⁻⁵	>97%	>2 replicate errors or Mendelian inconsistencies (for reference CEPH trios), heterozygote frequency=0, not in HapMap	BimBam10	HapMap release 21A CEU (build36)	R	site
ERF	Illumina 6k, Illumina 318K, Illumina 370K and Affymetrix 250K	BeadStudio, BRLMM	-	-	>1%	>10 ⁻⁶	>98%	-	MACH	HapMap release 22 CEU (build 36)	Probable, R	Relatedness
FHS	Affymetrix 500K and MIPS 50K combined	BRLMM	<97%	subject heterozygosity >5 SD away from the mean, large Mendelian error rate	>1%	>10 ⁻⁶	>97%	SNPs: mishap $p > 10^{-9}$, <100 Mendelian errors SD from the mean	MACH	HapMap release 22 CEU (build 36)	R packages kinship, GEE	Relatedness
HABC	Illumina Infinium Human1M-Duo BeadChip	BeadStudio	-	-	≥ 1%	≥10 ⁻⁶	≥97%	-	MACH	HapMap release 22 CEU (build 36)	R	none
HBCS	Illumina Infinium 610K Quad (Custom modified)	BeadStudio	-	HWE > 10 ⁻⁵	>1%	>10 ⁻⁶	>95%	-	MACH	HapMap release 22 CEU (build 36)	PLINK & ProbABEL	none

Cohort	Platform	Calling algorithm	Sample QC		Imputation QC			Imputation		Analysis		
			Call rate	Other exclusions	MAF	HWE P-value	Call rate	Other	Software	Build	Software	Adjustment*
InCHIANTI	Illumina HumanHap 550K	BeadStudio	-	gender mismatch, IBD analysis to exclude related individuals	>1%	>10 ⁻⁴	>98%	-	MACH	HapMap release 22 CEU (build 36)	Mach2qtl & Mach2dat	none
MESA	Affymetrix Genome-Wide Human SNP Array 6.0	Birdseed	<95%	Sample Level: gender mismatches, cryptic duplicates, and SNP level: monomorphic SNPs, SNPs with observed heterozygosity > 53%, and SNPs with missing rate > 5%	>1%	>10 ⁻⁴	>95%	-	IMPUTE	NCBI Build 36	SNPTest	first 10 PCs
MKF3	Affymetrix 500K	BRLMM	<93%	sex mismatch	-	-	-	-	MACH	HapMap release 21 CEU (build 35)	ProbABEL	none
MKF4	Affymetrix 6.0 (1000K)	Birdseed2	<93%	sex mismatch	-	-	>93%	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	none
NHSBrC	Illumina 550K	BeadStudio	<90%	SNP QC: MAF <0.01; Sample QC: call rate <90%, -duplicates and first/second degree relatives -ancestry outliers	-	-	-	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	disease status, top 4 EVs
NHSchd	Affymetrix 6.0	Birdseed	<98%	SNP QC: pHWE<10E-4, MAF <0.02 ; Sample QC: call rate <98%, --sex discrepancy with genetic data from X-linked markers -duplicates and first/second degree relatives -ancestry outliers -heterozygosity -missing phenotype information	-	-	-	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	disease status, top 3 EVs
NHSkid	Illumina 610Q	BeadStudio	<95%	SNP QC: MAF <0.01, pHWE<10E-5; Sample QC: call rate <95%, -duplicates and first/second degree relatives -ancestry outliers	-	-	-	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	disease status, top 4 EVs

Cohort	Platform	Calling algorithm	Sample QC		Imputation QC				Imputation		Analysis	
			Call rate	Other exclusions	MAF	HWE P-value	Call rate	Other	Software	Build	Software	Adjustment*
NHSt2d	Affymetrix 6.0	Birdseed	<98%	SNP QC, pHWE<10E-4, MAF <0.02, >1 discordance/12 replicates, significant plate associations; Sample QC: call rate <98%, -sex discrepancy with genetic data from X-linked markers -duplicates and first/second degree relatives -ancestry outliers -heterozygosity -autosomal chromosome aberrations	-	-	-	-	MACH	HapMap release 22 CEU (build 36)	ProbABEL	disease status, top 3 EVs
RS1	Version 3 Illumina Infinium II HumanHap 550 SNP chip array	BeadStudio	<98%	sex mismatch, excess autosomal heterozygosity >0,336, outliers identified by IBS clustering analysis	≥1%	>10-6	≥98%	-	MACH	HapMap release 22 CEU (build 36)	SPSS, ProbABEL, GRIMP, R	none
RS2	Version 3 Illumina Infinium II HumanHap 550 SNP chip array	BeadStudio	<98%	sex mismatch, excess autosomal heterozygosity >0,336, outliers identified by IBS clustering analysis	≥1%	>10-6	≥98%	-	MACH	HapMap release 22 CEU (build 36)	SPSS, ProbABEL, GRIMP, R	none
RS3	Version 3 Illumina Infinium II HumanHap 550 SNP chip array	BeadStudio	<98%	sex mismatch, excess autosomal heterozygosity >0,336, outliers identified by IBS clustering analysis	≥1%	>10-6	≥98%	-	MACH	HapMap release 22 CEU (build 36)	SPSS, ProbABEL, GRIMP, R	none
RUSH (MAP)	Affymetrix 6.0	Birdsuite	<95%	genotype-derived gender discordant with reported gender, inbreeding coefficient $F>0.04$	≥1%	>10-6	>95%	Exclusion: mishap test <10-9	MACH	HapMap release 22 CEU (build 36)	SAS, ProbABEL, R	First 3 principal components of eigenstrat
RUSH (ROS)	Affymetrix 6.0	Birdsuite	<95%	genotype-derived gender discordant with reported gender, inbreeding coefficient $F>0.04$	≥1%	>10-6	>95%	Exclusion: mishap test <10-9	MACH	HapMap release 22 CEU (build 36)	SAS, ProbABEL, R	First 3 principal components of eigenstrat
SardiNIA	Affymetrix 10K, 500K, 1000K	BRLMM	<95%	sex mismatch, Mendelian error	>1%	>10-6	>90%	-	MACH	HapMap CEU (build 36)	MERLIN	dummy variable: self-report vs. tester read and reported answers
SHIP	Affymetrix Human SNP Array 6.0	Birdseed V2	<92%	duplicate samples (by IBS), reported/genotyped gender mismatch	-	-	-	-	IMPUTE	HapMap release 22 CEU (Build 36)	SNPTEST, QUICKTES, R, PLINK	none

EV, Eigenvector ; HWE, Hardy-Weinberg equilibrium; IBD, identity by descent; IBS, identity by state; MAF, minor allele frequency; PCA, principal component analysis; QC, quality control; SNP, single nucleotide polymorphism.

*Adjustment additional to age and sex.

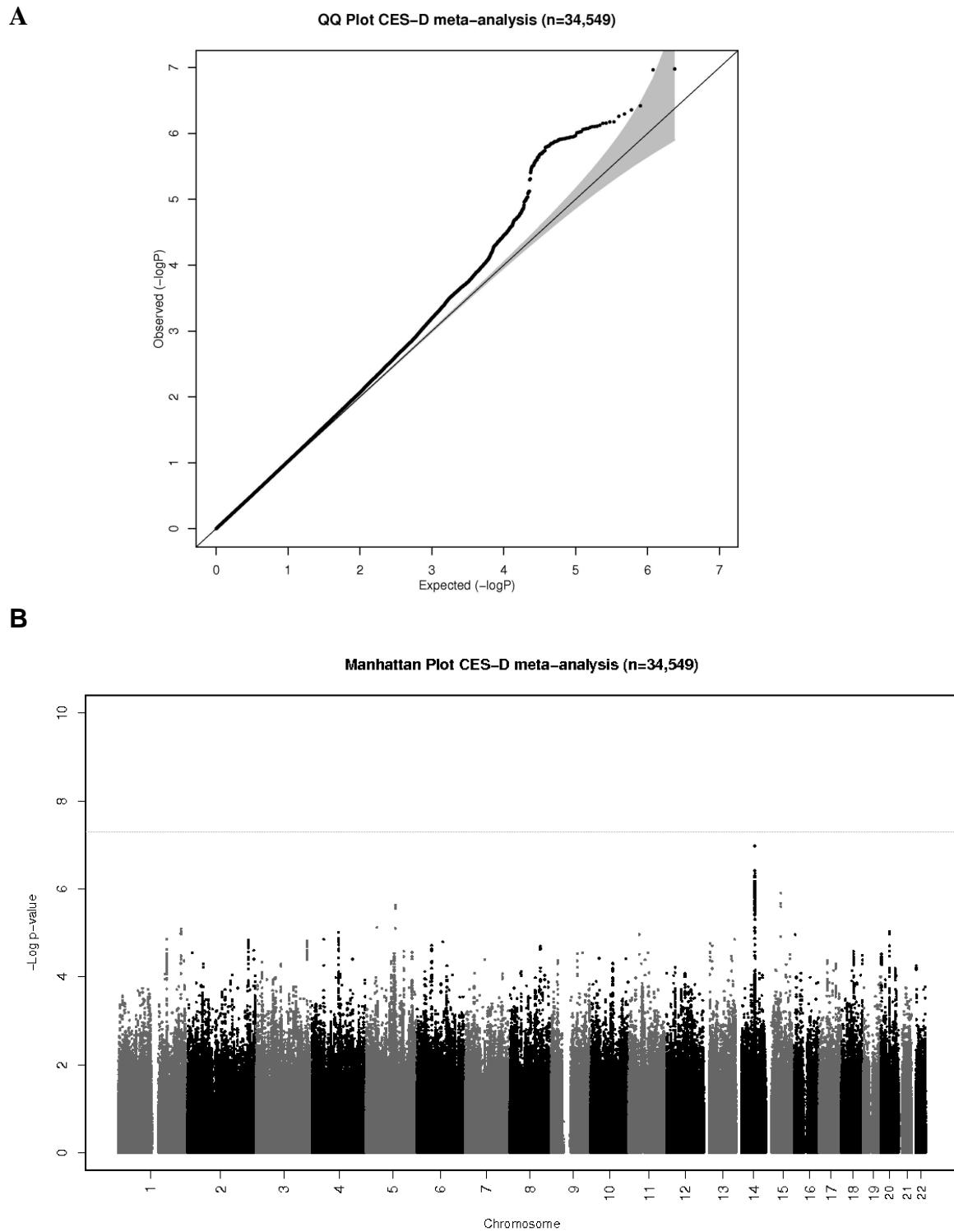


Figure S1. Genome-wide association study results for depressive symptoms in the discovery sample. Quantile-Quantile (**A**) and Manhattan (**B**) plot of total depressive symptoms score meta-analysis of discovery samples ($n = 34,549$). CES-D, Center for Epidemiologic Studies Depression scale.

Table S2. Additional top SNP information

SNP	# genotyped*	# imputed**	r ^{2***}
rs13137117	1	24	0.91
rs161645	0	24	0.97
rs357282	12	13	0.93
rs40465	1	23	0.93
rs4594522	9	16	0.97
rs4653635	1	24	0.99
rs8020095	9	14	0.91
rs8038316	0	24	0.98

SNP, single nucleotide polymorphism.

* Number of cohorts that genotyped this SNP

** Number of cohorts that did not genotype this SNP

*** Observed versus expected variance ratio (measure of imputation quality) r² is based on SNPs that had not been genotyped.

Table S3. Single nucleotide polymorphisms (SNPs) with a p -value $<10^{-4}$ from the overall meta-analysis (discovery + replication, $n = 51,258$).

SNP	Allele1	Allele2	Freq1	Weight	Zscore	P-value	Direction	HetISq	HetPVal
rs40465	t	g	0,652	49820	-5,459	4,78E-08	-----+?-----	0	0,601
rs161645	a	g	0,337	49820	5,359	8,39E-08	+++++++-----+?++++	0	0,752
rs6421926	t	c	0,338	49820	5,327	9,96E-08	+++++++-----+?++++	0	0,739
rs60271	a	c	0,339	51258	5,155	2,54E-07	+++++++-----+?++++	0	0,652
rs1383605	a	t	0,206	51258	4,766	1,88E-06	+-----+-----+-----	0	0,723
rs10279132	t	g	0,715	51256	4,735	2,19E-06	+++++++-----+-----	0	0,514
rs2242277	t	c	0,793	51258	-4,727	2,28E-06	-+-----+-----+-----	0	0,732
rs12679544	t	c	0,793	51258	-4,685	2,80E-06	-+-----+-----+-----	0	0,688
rs8020095	a	g	0,161	40902	4,668	3,04E-06	+++-----+-----+?---+	33,5	0,069
rs7152001	c	g	0,839	40902	-4,665	3,08E-06	---+-----+-----+?+?++	33,1	0,072
rs11914750	t	c	0,671	51258	-4,542	5,58E-06	---+-----+-----+-----	0	0,527
rs1008813	a	g	0,519	51255	4,535	5,77E-06	++++-----+-----+-----	15,1	0,256
rs1008812	a	g	0,482	51257	-4,534	5,80E-06	-----+-----+-----	15,5	0,250
rs1976423	a	c	0,502	47397	-4,533	5,82E-06	-----+---+?---+---+?-----	10,6	0,321
rs17026230	a	g	0,330	51258	4,531	5,86E-06	+++-----+-----+-----	0	0,495
rs1873213	t	g	0,969	45537	-4,525	6,05E-06	---??---?---?+?---+-----?	25,1	0,165
rs8072065	a	g	0,829	51257	-4,523	6,10E-06	-----+-----+-----	0	0,679
rs1008814	a	t	0,519	51257	4,521	6,16E-06	++++-----+-----+-----	15,3	0,253
rs8000066	t	c	0,519	51257	4,506	6,60E-06	++++-----+-----+-----	14,5	0,263
rs7587554	t	c	0,474	51258	4,498	6,85E-06	+++-----+-----+-----	0,9	0,447
rs10958604	t	g	0,786	51258	-4,497	6,88E-06	-+-----+-----+-----	0	0,736
rs7339176	a	g	0,518	51257	4,493	7,01E-06	++++-----+-----+-----	15	0,257
rs12452091	c	g	0,830	51257	-4,492	7,07E-06	-----+-----+-----	0	0,677
rs12451111	t	c	0,169	51257	4,473	7,72E-06	++++-----+-----+-----	0	0,750
rs12793618	a	g	0,043	41709	-4,469	7,86E-06	??---+-----+-----?---+?	0	0,883
rs9900677	a	g	0,830	51257	-4,467	7,94E-06	-----+-----+-----	0	0,694
rs17488749	a	g	0,145	49818	-4,461	8,16E-06	-----+-----+-----?-----	39	0,033
rs17488784	a	t	0,145	49818	-4,458	8,28E-06	-----+-----+-----?-----	38,9	0,033
rs9468252	a	g	0,969	45537	-4,454	8,42E-06	---??---?---?+?---+-----?	18,7	0,235
rs11784532	t	c	0,785	51258	-4,45	8,58E-06	-+-----+-----+-----	0	0,656
rs12451588	c	g	0,832	51257	-4,44	8,98E-06	-----+-----+-----	0	0,753
rs8038316	a	g	0,050	48103	-4,425	9,64E-06	-?-----+-----+-----	19,4	0,204
rs1592757	c	g	0,364	51258	4,406	1,05E-05	++++-----+-----+-----	28,7	0,099
rs1503389	t	c	0,931	48099	4,405	1,06E-05	+?++++-----+-----+-----	0	0,631
rs12452510	a	t	0,166	51257	4,402	1,07E-05	++++-----+-----+-----	0	0,813
rs10091355	t	c	0,846	51258	-4,386	1,16E-05	-+-----+-----+-----	0	0,679
rs6900413	a	g	0,031	47317	4,382	1,18E-05	---+?+?+?+?+---?+-----?	23	0,182
rs12449501	a	g	0,167	51253	4,371	1,24E-05	++++-----+-----+-----	0	0,815
rs2409064	a	g	0,932	48103	4,36	1,30E-05	+?++++-----+-----+-----	0	0,640
rs16966168	a	g	0,150	50250	4,359	1,31E-05	+++?+?+-----+-----+-----	0	0,551
rs7485858	t	c	0,369	50251	-4,349	1,37E-05	---??-----+-----+-----	0	0,728
rs1421669	c	g	0,628	51258	-4,334	1,47E-05	-----+-----+-----+-----	28,8	0,098
rs2168312	a	g	0,261	51258	4,333	1,47E-05	++++-----+-----+-----	11,2	0,309
rs7978337	a	t	0,369	50250	-4,329	1,50E-05	---??-----+-----+-----	0	0,730
rs2139680	a	t	0,369	50251	-4,316	1,59E-05	---??-----+-----+-----	0	0,722
rs2447838	t	c	0,436	51258	4,311	1,63E-05	++++-----+-----+-----	29,3	0,094
rs9535050	a	g	0,478	51257	4,299	1,72E-05	+++-----+-----+-----	0	0,827
rs2312971	c	g	0,516	51257	-4,293	1,76E-05	---+-----+-----+-----	0	0,683
rs9959343	t	c	0,261	51258	4,293	1,77E-05	+-----+-----+-----+-----	13,4	0,278
rs10101533	a	g	0,151	51258	4,292	1,77E-05	+-----+-----+-----+-----	0	0,691
rs4942783	c	g	0,522	51257	-4,282	1,85E-05	---+-----+-----+-----	0	0,836
rs4754128	a	g	0,932	48102	4,282	1,86E-05	+?++++-----+-----+-----	0	0,617
rs7004479	t	c	0,154	51258	4,28	1,87E-05	+-----+-----+-----+-----	0	0,670
rs6493686	c	g	0,950	48103	4,278	1,89E-05	+?++++-----+-----+-----	22,6	0,167

SNP	Allele1	Allele2	Freq1	Weight	Zscore	P-value	Direction	HetISq	HetPVal
rs8033074	a	c	0,950	48103	4,276	1,90E-05	+?+++++-----+-----	22,4	0,169
rs7107383	a	t	0,072	48103	-4,276	1,91E-05	-?-----+-----	0	0,730
rs937055	t	c	0,919	51258	-4,267	1,99E-05	-----+-----+-----	11,9	0,298
rs254035	a	t	0,437	51258	4,264	2,01E-05	+++++-----+-----	31,1	0,079
rs12453488	a	g	0,173	51254	4,262	2,02E-05	+++++-----+-----	0	0,670
rs2447832	t	c	0,437	51258	4,259	2,05E-05	+++++-----+-----	30,9	0,080
rs323105	c	g	0,965	43679	-4,247	2,17E-05	-?-----?-----?+---	27,4	0,136
rs2312972	t	c	0,521	51257	-4,245	2,18E-05	-----+-----+-----	0	0,845
rs1520550	a	g	0,631	51258	4,24	2,23E-05	-----+-----+-----	0	0,762
rs7833452	a	g	0,847	51258	-4,236	2,27E-05	-----+-----+-----	0	0,702
rs10785027	a	t	0,369	51258	-4,234	2,30E-05	-----+-----+-----	0	0,757
rs2077781	t	g	0,261	51258	4,228	2,36E-05	-----+-----+-----	11,9	0,298
rs33817	a	g	0,437	51258	4,226	2,38E-05	+++++-----+-----	27,1	0,115
rs8030855	c	g	0,056	51258	4,221	2,43E-05	+++++-----+-----	0	0,599
rs16870152	t	c	0,843	51256	4,219	2,46E-05	+++++-----+-----	31,7	0,074
rs2276203	a	g	0,261	51258	4,214	2,51E-05	-----+-----+-----	12,7	0,288
rs7182991	t	g	0,055	51258	4,208	2,58E-05	+++++-----+-----	0	0,684
rs4636213	a	g	0,200	51258	4,207	2,59E-05	+++++-----+-----	0	0,966
rs7182611	c	g	0,055	51258	4,2	2,67E-05	+++++-----+-----	0	0,679
rs185260	a	c	0,563	51258	-4,197	2,71E-05	-----+-----+-----	26,7	0,118
rs4489949	a	g	0,944	51258	-4,194	2,74E-05	-----+-----+-----	0	0,605
rs2414196	c	g	0,738	51258	4,191	2,78E-05	-----+-----+-----	35,7	0,047
rs1356893	t	c	0,605	51258	4,185	2,85E-05	-----+-----+-----	0	0,603
rs254025	c	g	0,563	51258	-4,184	2,87E-05	-----+-----+-----	27,8	0,107
rs7177816	a	g	0,054	51258	4,183	2,88E-05	+++++-----+-----	0	0,679
rs11664693	c	g	0,262	51258	4,183	2,88E-05	-----+-----+-----	6,7	0,369
rs12667152	t	g	0,156	49818	-4,182	2,88E-05	-----+-----+-----	37,3	0,041
rs4941210	t	c	0,262	51258	4,179	2,92E-05	-----+-----+-----	8,5	0,346
rs254020	t	c	0,438	51258	4,178	2,94E-05	+++++-----+-----	27,6	0,110
rs1073839	t	g	0,850	51257	-4,176	2,96E-05	-----+-----+-----	0	0,613
rs1353416	a	g	0,355	51258	4,176	2,97E-05	-----+-----+-----	0	0,480
rs2414195	a	g	0,738	51258	4,175	2,98E-05	-----+-----+-----	36,9	0,040
rs11927424	a	g	0,644	51258	-4,172	3,02E-05	-----+-----+-----	0	0,522
rs9596054	a	g	0,478	51257	4,17	3,04E-05	-----+-----+-----	0	0,768
rs3111816	a	g	0,352	51239	-4,17	3,04E-05	-----+-----+-----	0	0,964
rs4073665	a	g	0,873	51258	-4,169	3,05E-05	-----+-----+-----	26,1	0,124
rs1397164	a	c	0,637	49820	4,168	3,08E-05	-----+-----+-----	22,3	0,170
rs7170422	t	c	0,945	51258	-4,167	3,08E-05	-----+-----+-----	0	0,664
rs10851526	t	c	0,261	51258	-4,167	3,09E-05	-----+-----+-----	35,1	0,050
rs11977246	t	c	0,844	49818	4,166	3,10E-05	+++++-----+-----	37,4	0,041
rs254023	t	c	0,563	51258	-4,166	3,11E-05	-----+-----+-----	27,6	0,109
rs2919955	a	g	0,352	51257	4,165	3,12E-05	+++++-----+-----	0	0,660
rs7641985	a	c	0,644	51258	-4,163	3,14E-05	-----+-----+-----	0	0,476
rs13155692	t	c	0,748	49820	-4,161	3,18E-05	-----+-----+-----	17,1	0,233
rs9554349	t	c	0,033	38528	4,16	3,18E-05	+?+-----+-----+?+?+?	0	0,517
rs11147450	t	c	0,521	51257	-4,16	3,18E-05	-----+-----+-----	0	0,795
rs2125659	t	c	0,946	51258	-4,158	3,21E-05	-----+-----+-----	0	0,698
rs10505424	a	c	0,199	51258	4,156	3,24E-05	+++++-----+-----	0	0,977
rs17750582	a	c	0,055	51258	4,155	3,25E-05	+++++-----+-----	0	0,659
rs17553281	a	t	0,822	51257	-4,155	3,25E-05	-----+-----+-----	23,5	0,152
rs1442111	t	g	0,352	51258	4,155	3,26E-05	+++++-----+-----	0	0,721
rs10879604	a	t	0,374	50251	-4,155	3,26E-05	-----+-----+-----	0	0,670
rs1587150	a	t	0,355	51258	4,154	3,27E-05	+++++-----+-----	0	0,481
rs12955929	t	g	0,958	46834	-4,153	3,28E-05	-----+-----+-----	16	0,258
rs8026763	t	c	0,262	51239	-4,152	3,30E-05	-----+-----+-----	35,5	0,048
rs7308693	t	c	0,631	51258	4,149	3,33E-05	-----+-----+-----	0	0,724
rs1011947	a	g	0,262	51258	4,148	3,36E-05	-----+-----+-----	5	0,393

SNP	Allele1	Allele2	Freq1	Weight	Zscore	P-value	Direction	HetISq	HetPVal
rs10785028	t	g	0,631	51258	4,147	3,38E-05	---+-----+-----+-----	0	0,723
rs7137885	t	c	0,368	51258	-4,144	3,42E-05	+---+-----+-----+-----	0	0,735
rs2161097	t	c	0,438	51258	4,143	3,43E-05	+++++---+-----+-----	29,4	0,093
rs7555997	a	c	0,101	50232	-4,141	3,46E-05	---??-+-----+-----	0	0,808
rs2447828	t	c	0,438	51258	4,138	3,51E-05	+++++---+-----+-----	29,9	0,088
rs11927001	a	g	0,869	51258	4,131	3,62E-05	---+-----+-----+-----	27,2	0,113
rs2125657	t	c	0,054	51258	4,131	3,62E-05	+++++---+-----+-----	0	0,695
rs2112163	t	c	0,438	51258	4,13	3,62E-05	+++++---+-----+-----	30,2	0,086
rs6551366	c	g	0,355	51258	4,128	3,66E-05	+++---+-----+-----	0	0,487
rs1589595	t	c	0,738	51258	-4,128	3,66E-05	---+-----+-----+-----	5,8	0,382
rs1522116	t	c	0,441	51257	4,126	3,69E-05	+++++---+-----+-----	0	0,791
rs920623	a	g	0,352	51258	4,125	3,71E-05	+++++---+-----+-----	0	0,649
rs7205464	t	g	0,097	51256	4,122	3,75E-05	+++++---+-----+-----	0	0,945
rs7295470	t	c	0,372	51258	-4,122	3,75E-05	+---+-----+-----+-----	0	0,723
rs1426134	c	g	0,353	51258	-4,12	3,78E-05	-----+-----+-----	0	0,915
rs16893023	a	c	0,194	51258	4,119	3,80E-05	+++++---+-----+-----	0	0,952
rs12050204	t	g	0,080	51252	-4,119	3,81E-05	-----+-----+-----	0	0,759
rs9903859	a	g	0,160	51257	4,118	3,82E-05	+++++---+-----+-----	0	0,495
rs1045301	t	g	0,082	51258	-4,111	3,94E-05	-----+-----+-----	0	0,810
rs2337127	a	c	0,946	51258	-4,11	3,95E-05	-----+-----+-----	0	0,698
rs1687128	t	g	0,081	51258	4,105	4,05E-05	+++++---+-----+-----	9	0,339
rs9303295	a	g	0,850	51257	-4,103	4,09E-05	---+-----+-----+-----	0	0,654
rs4776080	t	c	0,269	51258	-4,101	4,12E-05	+-----+-----+-----	34,6	0,053
rs10879605	t	c	0,374	51258	-4,1	4,13E-05	+-----+-----+-----	0	0,744
rs2414218	t	c	0,276	51257	-4,1	4,13E-05	+-----+-----+-----	31,8	0,073
rs325501	c	g	0,587	51258	-4,097	4,19E-05	-----+-----+-----	17,3	0,227
rs2414217	t	c	0,276	51258	-4,093	4,26E-05	+-----+-----+-----	30,6	0,083
rs325481	a	g	0,586	51258	-4,092	4,27E-05	-----+-----+-----	19,4	0,200
rs1583953	t	c	0,353	51258	4,087	4,37E-05	+++++---+-----+-----	0	0,858
rs988542	a	g	0,628	51258	4,086	4,39E-05	---+-----+-----+-----	0	0,759
rs1106420	a	t	0,318	51258	-4,086	4,39E-05	+-----+-----+-----	1,4	0,442
rs8079016	t	c	0,161	51257	4,086	4,40E-05	+++++---+-----+-----	0	0,494
rs7953276	a	c	0,377	51258	-4,084	4,43E-05	---+-----+-----+-----	0	0,868
rs12955292	a	g	0,036	46834	4,083	4,44E-05	+++++---+-----+-----	22,3	0,184
rs768792	a	g	0,647	51258	-4,083	4,45E-05	-----+-----+-----	0	0,868
rs1687119	a	g	0,919	51258	-4,08	4,51E-05	-----+-----+-----	8,9	0,339
rs9535127	t	c	0,481	51257	4,076	4,59E-05	+++---+-----+-----	0	0,864
rs10748226	t	g	0,628	51258	4,075	4,60E-05	---+-----+-----+-----	0	0,778
rs4760780	t	c	0,629	51258	4,075	4,60E-05	---+-----+-----+-----	0	0,740
rs6445194	t	g	0,489	51258	-4,075	4,61E-05	+-----+-----+-----	5,9	0,381
rs12441046	t	g	0,724	51258	4,072	4,65E-05	+-----+-----+-----	30,9	0,080
rs13177473	a	g	0,647	51258	-4,068	4,75E-05	-----+-----+-----	0	0,852
rs1542727	a	g	0,174	51258	4,065	4,81E-05	+++++---+-----+-----	0	0,536
rs2203976	t	c	0,628	51258	4,062	4,87E-05	---+-----+-----+-----	0	0,738
rs6582151	t	c	0,371	51258	-4,06	4,91E-05	+-----+-----+-----	0	0,728
rs2139675	t	g	0,628	51258	4,059	4,93E-05	---+-----+-----+-----	0	0,737
rs13250310	a	t	0,732	48103	-4,056	4,99E-05	+?-----+-----+-----	8,7	0,344
rs1394309	a	g	0,932	48437	-4,053	5,05E-05	---+-----+-----+-----	38,6	0,038
rs139265	a	g	0,833	51256	-4,049	5,15E-05	+-----+-----+-----	0,4	0,454
rs16955611	a	g	0,949	51258	-4,044	5,25E-05	-----+-----+-----	0	0,773
rs7899547	t	g	0,360	51258	4,043	5,27E-05	+-----+-----+-----	0	0,918
rs2028526	t	c	0,648	51251	-4,042	5,31E-05	-----+-----+-----	0	0,748
rs9645898	a	c	0,706	50250	-4,041	5,33E-05	---??-----+-----	0	0,784
rs3922857	t	c	0,097	51256	4,039	5,36E-05	+++++---+-----+-----	0	0,921
rs2363065	t	c	0,628	51258	4,039	5,37E-05	---+-----+-----+-----	0	0,744
rs7976937	t	c	0,361	51258	-4,039	5,38E-05	+-----+-----+-----	0	0,862
rs325485	a	g	0,388	51257	4,037	5,42E-05	+++++---+-----+-----	12,8	0,287

SNP	Allele1	Allele2	Freq1	Weight	Zscore	P-value	Direction	HetISq	HetPVal
rs6964185	a	g	0,126	51256	-4,032	5,53E-05	-+-----+-----+-----+-----	0	0,675
rs2836021	t	c	0,836	51256	4,03	5,59E-05	+-----+-----+-----+-----	0	0,788
rs11179680	a	g	0,362	51258	-4,027	5,64E-05	+-----+-----+-----+-----	0	0,864
rs10984257	t	c	0,869	51258	-4,024	5,72E-05	-----+-----+-----+-----	37,6	0,037
rs11683777	t	c	0,151	44606	4,022	5,77E-05	?+++++++--+-----+-----?	0	0,823
rs12824659	a	g	0,333	51258	-4,021	5,79E-05	-----+-----+-----+-----	0	0,954
rs4889796	t	c	0,781	49819	4,02	5,83E-05	-+-----+-----+-----+-----	26,8	0,121
rs11611073	a	g	0,362	51258	-4,018	5,86E-05	+-----+-----+-----+-----	0	0,865
rs508760	t	g	0,070	48103	-4,018	5,87E-05	-?-----+-----+-----+-----	0	0,631
rs7975033	a	t	0,372	51258	-4,015	5,94E-05	+-----+-----+-----+-----	0	0,704
rs6875442	a	c	0,625	51258	4,012	6,01E-05	+++++++--+-----+-----+-----	0	0,958
rs9365900	a	g	0,071	40276	4,011	6,05E-05	??+-----+-----+-----+-----	23,5	0,171
rs2211846	a	g	0,165	50250	-4,01	6,08E-05	-+-----+-----+-----+-----	0	0,769
rs10742719	a	c	0,525	50249	-4,008	6,13E-05	-+-----+-----+-----+-----	0	0,590
rs2043475	t	c	0,168	51257	4,007	6,14E-05	+++++++--+-----+-----+-----	0	0,604
rs2995807	t	c	0,140	51256	-4,007	6,15E-05	+-----+-----+-----+-----	0	0,948
rs7964705	t	c	0,629	51258	4,006	6,17E-05	-+-----+-----+-----+-----	0	0,697
rs7199995	t	c	0,140	51256	4,005	6,20E-05	+++++++--+-----+-----+-----	0	0,964
rs2836012	a	t	0,165	51255	-4,005	6,21E-05	-+-----+-----+-----+-----	0	0,833
rs2296561	a	t	0,879	49820	-4,005	6,22E-05	-----+-----+-----+-----?	32,9	0,069
rs2084919	t	c	0,515	51258	4,004	6,23E-05	+-----+-----+-----+-----	1,6	0,439
rs1915293	t	c	0,629	51258	4,004	6,24E-05	-+-----+-----+-----+-----	0	0,699
rs12367407	a	t	0,637	51258	4,002	6,27E-05	-+-----+-----+-----+-----	0	0,858
rs10942087	t	c	0,637	51258	4	6,33E-05	+++++++--+-----+-----+-----	0	0,832
rs323097	a	c	0,959	46834	-4	6,33E-05	-----+-----+-----+-----?	13,7	0,286
rs2047268	a	c	0,363	51258	-3,999	6,36E-05	-----+-----+-----+-----	0	0,826
rs13157155	c	g	0,626	51258	3,998	6,38E-05	+++++++--+-----+-----+-----	0	0,958
rs2148473	a	g	0,869	51258	-3,998	6,39E-05	-----+-----+-----+-----	39,2	0,029
rs11917572	t	c	0,959	47020	3,997	6,42E-05	+++++++--+-----+-----+-----	0	0,605
rs4627955	a	g	0,625	51258	3,996	6,43E-05	+++++++--+-----+-----+-----	0	0,955
rs12654558	t	c	0,636	51258	3,996	6,45E-05	+++++++--+-----+-----+-----	0	0,830
rs2836014	a	c	0,165	51257	-3,995	6,48E-05	-+-----+-----+-----+-----	0	0,806
rs1472763	c	g	0,318	50246	3,994	6,49E-05	+++?+++++--+-----+-----+-----	0	0,684
rs12657561	t	c	0,364	51258	-3,992	6,55E-05	-----+-----+-----+-----	0	0,831
rs10984272	a	t	0,870	51258	-3,991	6,57E-05	-----+-----+-----+-----	40,5	0,024
rs10984285	t	c	0,124	51258	3,99	6,61E-05	+++++--+-----+-----+-----	39,9	0,026
rs9516233	t	c	0,648	51257	3,987	6,69E-05	+++++--+-----+-----+-----	31,1	0,078
rs1443737	a	t	0,363	51258	-3,987	6,70E-05	+-----+-----+-----+-----	0	0,860
rs13013073	c	g	0,388	43950	-3,986	6,73E-05	-?-----+-----+-----+-----	0	0,552
rs7825010	a	g	0,842	51258	-3,985	6,74E-05	-+-----+-----+-----+-----	0	0,689
rs11179697	a	g	0,363	51258	-3,985	6,74E-05	+-----+-----+-----+-----	0	0,851
rs13163964	a	g	0,625	51258	3,983	6,80E-05	+++++++--+-----+-----+-----	0	0,953
rs325506	c	g	0,433	49820	3,983	6,81E-05	+++++++--+-----+-----+-----	10,5	0,320
rs6551361	t	c	0,645	51258	-3,981	6,87E-05	-----+-----+-----+-----	0	0,541
rs11038193	a	t	0,529	50250	-3,979	6,91E-05	-+-----+-----+-----+-----	0,6	0,450
rs9524069	a	c	0,648	51257	3,978	6,94E-05	+++++--+-----+-----+-----	31,5	0,075
rs13339086	a	g	0,097	51256	3,977	6,99E-05	+++++++--+-----+-----+-----	0	0,930
rs995431	a	t	0,637	51258	3,976	7,00E-05	+++++--+-----+-----+-----	0	0,831
rs9949310	t	c	0,959	46834	-3,976	7,02E-05	-----+-----+-----+-----?	13,4	0,291
rs4072224	a	g	0,903	51256	-3,975	7,05E-05	-----+-----+-----+-----	0	0,860
rs139263	a	g	0,166	51256	3,972	7,13E-05	-+-----+-----+-----+-----	0	0,465
rs10413178	t	c	0,094	51258	-3,972	7,14E-05	-----+-----+-----+-----	0	0,921
rs11179681	a	g	0,638	51258	3,972	7,14E-05	-+-----+-----+-----+-----	0	0,867
rs13181679	a	g	0,352	51258	3,971	7,15E-05	+++++--+-----+-----+-----	0	0,896
rs1443738	t	g	0,363	51258	-3,97	7,18E-05	+-----+-----+-----+-----	0	0,863
rs7467375	t	g	0,125	51258	3,97	7,20E-05	+++++--+-----+-----+-----	39,7	0,027
rs7177989	t	c	0,726	51258	3,968	7,26E-05	-+-----+-----+-----+-----	36,2	0,044

SNP	Allele1	Allele2	Freq1	Weight	Zscore	P-value	Direction	HetISq	HetPVal
rs973303	t	g	0,353	51257	-3,966	7,31E-05	-----+-----+-----	29,5	0,092
rs6881764	a	g	0,482	51258	3,961	7,48E-05	++++++-+-----+-----	22,7	0,161
rs8008773	a	t	0,873	51258	-3,96	7,48E-05	-----+-----+-----	46,6	0,008
rs12541821	a	g	0,139	51258	3,96	7,51E-05	+-----+-----+-----	0	0,573
rs12134580	t	c	0,971	35673	-3,959	7,52E-05	----??+?-?????-----	50,7	0,022
rs12368237	a	g	0,375	51258	-3,956	7,61E-05	+-----+-----+-----	0	0,856
rs6421241	t	c	0,609	51258	3,955	7,65E-05	-+-----+-----+-----	0	0,740
rs1443742	t	c	0,362	51258	-3,955	7,66E-05	+-----+-----+-----	0	0,863
rs4297682	a	g	0,904	51256	-3,955	7,67E-05	-----+-----+-----	0	0,867
rs2049103	a	g	0,958	47020	3,954	7,68E-05	++++-+--+?+-----+-----	0	0,687
rs11923274	a	g	0,958	47020	3,953	7,73E-05	++++-+--+?+-----+-----	0	0,656
rs10180695	t	c	0,424	51258	3,951	7,78E-05	+++++-----+-----+-----	0	0,940
rs4971723	t	c	0,435	51258	3,951	7,79E-05	+++++-----+-----+-----	0	0,904
rs11783005	t	c	0,284	48103	3,951	7,79E-05	+?+-----+-----+-----	10,3	0,322
rs2414188	t	c	0,267	51258	-3,951	7,80E-05	-+-----+-----+-----	33,7	0,059
rs11618590	t	c	0,837	51257	-3,95	7,81E-05	-----+-----+-----	0	0,613
rs1545292	a	g	0,625	51258	3,95	7,83E-05	-+-----+-----+-----	0	0,855
rs4412846	a	t	0,353	51257	-3,949	7,84E-05	-----+-----+-----	30	0,088
rs7974278	c	g	0,624	51258	3,948	7,87E-05	-+-----+-----+-----	0	0,855
rs12521551	a	g	0,364	51258	-3,947	7,90E-05	-----+-----+-----	0	0,831
rs7651475	t	c	0,042	47020	-3,947	7,93E-05	-----+-----+-----	0	0,664
rs2881577	a	g	0,958	47020	3,946	7,94E-05	++++-+--+?+-----+-----	0	0,664
rs4738700	t	c	0,662	51258	-3,945	7,98E-05	-----+-----+-----	16,2	0,241
rs1373834	a	g	0,648	51257	3,944	8,01E-05	++++-+--+?+-----+-----	33,1	0,064
rs13162928	t	c	0,648	51258	-3,943	8,04E-05	-----+-----+-----	0	0,894
rs1363179	t	g	0,583	51258	-3,943	8,05E-05	-----+-----+-----	30,4	0,085
rs6582152	c	g	0,368	51258	-3,941	8,11E-05	+-----+-----+-----	0	0,667
rs8091788	a	g	0,829	51258	-3,94	8,14E-05	-+-----+-----+-----	0	0,585
rs7628116	c	g	0,042	47020	-3,938	8,23E-05	-----+-----+-----	0	0,699
rs1421908	t	c	0,417	51258	3,937	8,25E-05	++++-+--+?+-----+-----	30,8	0,081
rs7907283	a	g	0,087	51258	3,936	8,30E-05	+++++-----+-----+-----	19,3	0,202
rs3787851	t	c	0,165	51257	-3,935	8,32E-05	-+-----+-----+-----	0	0,791
rs12452350	a	g	0,833	51257	-3,932	8,41E-05	-----+-----+-----	0	0,601
rs10769092	t	g	0,497	51258	-3,932	8,42E-05	-+-----+-----+-----	0	0,555
rs6895949	a	g	0,279	51258	3,93	8,50E-05	+++-----+-----+-----	27,2	0,114
rs10101647	a	g	0,160	51258	3,93	8,51E-05	+-----+-----+-----	0	0,662
rs731428	t	c	0,936	49819	-3,929	8,53E-05	-----+-----+-----	0	0,560
rs4077278	c	g	0,475	51257	-3,928	8,56E-05	-----+-----+-----	0	0,939
rs7317531	t	g	0,457	51256	-3,927	8,59E-05	-+-----+-----+-----	0	0,804
rs12519063	t	c	0,637	51258	3,926	8,64E-05	++++-+--+?+-----+-----	0	0,836
rs2111380	a	t	0,435	51258	3,926	8,65E-05	+++++-----+-----+-----	0	0,908
rs7822661	t	c	0,140	51258	3,925	8,66E-05	+-----+-----+-----	0	0,595
rs12209628	t	c	0,800	51258	-3,925	8,67E-05	-----+-----+-----	0	0,970
rs1530303	t	c	0,350	51258	3,925	8,68E-05	+++++-----+-----+-----	0	0,924
rs7620638	a	g	0,958	47020	3,924	8,70E-05	++++-+--+?+-----+-----	0	0,661
rs12205387	t	c	0,200	51258	3,924	8,72E-05	++++-+--+?+-----+-----	0	0,971
rs1501192	t	c	0,701	51258	-3,924	8,72E-05	-----+-----+-----	0	0,478
rs9898999	t	c	0,167	51257	3,922	8,80E-05	+++++-----+-----+-----	0	0,598
rs13248919	a	g	0,264	48103	3,918	8,92E-05	-?+-----+-----+-----	6,7	0,371
rs10742718	c	g	0,525	51258	-3,916	9,00E-05	-+-----+-----+-----	0,3	0,456
rs10742725	t	c	0,475	50243	3,914	9,07E-05	+--+?+-----+-----+-----	0	0,574
rs926300	a	t	0,828	51258	3,913	9,12E-05	+++++-----+-----+-----	0	0,703
rs6545190	t	g	0,564	51258	-3,91	9,25E-05	-----+-----+-----	0	0,915
rs7631883	a	g	0,042	47020	-3,909	9,27E-05	-----+-----+-----	0	0,657
rs2352545	t	c	0,565	51258	-3,908	9,33E-05	-----+-----+-----	0	0,912
rs7930681	t	c	0,498	51258	3,904	9,45E-05	+-----+-----+-----	9,6	0,330
rs2139686	a	c	0,957	47020	3,902	9,53E-05	++++-+--+?+-----+-----	0	0,673

SNP	Allele1	Allele2	Freq1	Weight	Zscore	P-value	Direction	HetISq	HetPVal
rs2163946	a	g	0,529	48818	-3,901	9,57E-05	--+??--+++++-----+---?+-	0	0,464
rs1738819	t	c	0,133	51258	3,901	9,57E-05	-++++-+-----+-----+-----	0	0,738
rs4901754	a	g	0,654	51257	-3,9	9,62E-05	+-----+-----+-----+-----	0	0,581
rs1395268	a	c	0,173	51258	3,899	9,66E-05	+---+---+-----+-----+-----	0	0,588
rs2836007	t	c	0,165	51257	-3,899	9,68E-05	-+---+-----+-----+-----	0	0,834
rs7713437	a	g	0,720	51258	-3,898	9,68E-05	---+---+-----+-----+-----	25	0,136
rs2762089	a	t	0,355	51257	-3,898	9,69E-05	-----+-----+-----+-----	31,2	0,078
rs11179688	t	g	0,377	51258	-3,898	9,70E-05	+-----+-----+-----+-----	0	0,846
rs11746102	a	g	0,363	51258	-3,897	9,74E-05	-----+-----+-----+-----	0	0,837
rs11179690	a	g	0,623	51258	3,897	9,75E-05	-+++--+-----+-----+-----	0	0,843
rs7316126	a	t	0,624	51258	3,893	9,88E-05	-+++--+-----+-----+-----	0	0,834
rs4736893	a	g	0,231	51258	-3,893	9,91E-05	-----+-----+-----+-----	0	0,942
rs7728789	t	c	0,637	51258	3,891	9,97E-05	++++-+-----+-----+-----	0	0,835

Table S4. Replication of top SNPs (p -value $<10^{-5}$) from previous genome-wide association studies.

Study	SNP	Chr	Effective allele	Original study		Current study - Discovery set ($n = 34,549$)		Current study - Overall meta-analysis ($n = 51,258$)	
				Direction of effect	P -value	Direction of effect	P -value	Direction of effect	P -value
Sullivan 2009 (1738 ca, 1802 co) (1)	rs2522833*	7	C	+	1.2e-06	+	0.26	+	0.83
Wray 2012 (5763 ca, 6901 co)** (2)	rs11579964	1	T	-	4.4e-06	+	0.19	+	0.19
	rs7647854	3	G	+	4.6e-06	+	0.61	+	0.57
	rs12446956	16	C	+	1.1e-06	+	0.94	-	0.77
	rs12457996	18	C	-	5.7e-06	-	0.79	+	0.68
Terracciano 2010 ($n = 4,811$)*** (3)	rs12912233	15	T	+	6.3e-07	-	0.85	-	0.37
	rs8070473	17	T	-	1.5e-06	+	0.94	+	0.26
	rs349475	5	T	+	2.4e-06	+	0.72	+	0.28
	rs12420464	11	T	-	3.3e-06	+	0.17	+	0.51
	rs1927745	13	A	-	4.7e-06	-	0.69	+	0.78
	rs10514585	16	A	+	4.9e-06	-	0.053	-	0.011
	rs11009175	10	A	+	5.4e-06	-	0.067	-	0.17
	rs17864092	7	T	-	5.5e-06	-	0.60	-	0.33
	rs1449984	2	A	-	6.6e-06	+	0.90	-	0.76
	rs1924397	13	A	+	7.6e-06	+	0.66	+	0.21
rs10744304	12	A	-	8.7e-06	+	0.31	-	0.80	
rs2017305	10	A	-	9.0e-06	-	0.99	-	0.63	

ca, cases; co, controls; Chr, chromosome; SNP, single nucleotide polymorphism.

*This SNP was tested for association in the current study as it was replicated previously.

** Largest meta-analysis of major depressive disorder.

*** Meta-analysis of trait depression, only independent top SNPs were tested here.

Supplemental References

1. Sullivan PF, de Geus EJ, Willemsen G, James MR, Smit JH, Zandbelt T, *et al.* (2009): Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. *Mol Psychiatry* 14: 359-375.
2. Wray NR, Pergadia ML, Blackwood DH, Penninx BW, Gordon SD, Nyholt DR, *et al.* (2012): Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. *Mol Psychiatry* 17:36-48.
3. Terracciano A, Tanaka T, Sutin AR, Sanna S, Deiana B, Lai S, *et al.* (2010): Genome-wide association scan of trait depression. *Biol Psychiatry* 68: 811-817.