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GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN

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Background: *Genome-wide association studies (GWAS) have made little progress in identifying variants linked to depression. We hypothesized that examining depressive symptoms and considering gene–environment interaction (GxE) might improve efficiency for gene discovery. We therefore conducted a GWAS and genome-wide by environment interaction study (GWEIS) of depressive symptoms.* **Methods:** *Using data from the SHARe cohort of the Women's Health Initiative, comprising African Americans (n = 7,179) and Hispanics/Latinas (n = 3,138), we examined genetic main effects and GxE with stressful life events and social support. We also conducted a heritability analysis using genome-wide complex trait analysis (GCTA). Replication was attempted in four independent cohorts.* **Results:** *No SNPs achieved genome-wide significance for main effects in either discovery sample. The top signals in African Americans were rs73531535 (located 20 kb from GPR139, $P = 5.75 \times 10^{-8}$) and rs75407252 (intronic to CACNA2D3, $P = 6.99 \times 10^{-7}$). In Hispanics/Latinas, the top signals were rs2532087 (located 27 kb from CD38, $P = 2.44 \times 10^{-7}$) and rs4542757 (intronic to DCC, $P = 7.31 \times 10^{-7}$). In the GEWIS with stressful life events, one interaction signal was genome-wide significant in African Americans (rs4652467; $P = 4.10 \times 10^{-10}$; located 14 kb from CEP350). This interaction was not observed in a smaller replication cohort. Although heritability estimates for depressive symptoms and stressful life events were each less than 10%, they were strongly genetically correlated (rG = 0.95), suggesting that common variation underlying self-reported depressive symptoms and stressful life event exposure, though modest on their own, were highly overlapping in this sample.* **Conclusions:** *Our results underscore the need for larger samples, more GEWIS, and greater investigation into genetic and environmental determinants of depressive symptoms in minorities.*

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Key words: *genome-wide association study; gene-environment interaction; depression; stressful life events; social support*

INTRODUCTION

Although family and twin studies show that depression is driven partly by genetic variation,[1] until just recently,[2] genome-wide association studies (GWAS) have made little progress in identifying specific loci linked to depression.[3] Several factors could explain the lack of success, including the complex genetic architecture of depression, small samples, and heterogeneity in the "depression" phenotype.[4,5] Moreover, with the exception of two studies,[6,7] including a large meta-analysis,[6] most prior GWAS have examined diagnoses, rather than quantitative traits (e.g., depressive symptoms). In light of evidence suggesting the diagnostic categories have been artificially imposed on a continuum of depression risk,[8] such case-control analyses may have limitations. For example, simulations studies demonstrate that for common phenotypes (i.e., with prevalence greater than 10%), the quantitative trait approach may have power advantages under certain conditions in population-based samples.[9] GWAS have also neglected the role of gene-environment interaction (GxE),[10] which many believe contributes to the etiology of depression.[11,12] Previous GxE studies have been limited to candidate genes; these results have been highly controversial.[13–16] Studies of GxE in the context of GWAS for psychiatric phenotypes are needed and may be informative for identifying novel genomic loci.[17,18] Indeed, GxE studies using genome-wide data for other complex phenotypes have revealed genotype–phenotype associations not apparent in genetic main effect analyses.[19–21]

Further, genetic studies of depression and other psychiatric phenotypes have almost exclusively comprised samples of European ancestry, leaving racial/ethnic minorities underrepresented in psychiatric genetics research. Extending genetic association studies to more diverse racial/ethnic populations—especially of women—is therefore needed. These studies are likely to be informative, as depression appears at least as heritable (around 40%) among African Americans[22,23] and Hispanics [24] compared to European Americans.[1] Such extensions are also important given known racial/ethnic (as well as sex) disparities. For example, epidemiological studies have observed lower lifetime prevalence estimates for major depressive disorder (MDD) among non-Whites,[25] despite a higher burden of social-environmental adversity from stressful life events,[26] discrimination,[27,28] and lower socioeconomic status.[29] Epidemiological studies have also consistently showed a twofold elevated risk of MDD in women compared to men.[30]

Here, we aimed to address these limitations by conducting a GWAS of depressive symptoms and performing a genome-wide by environment interaction study (GWEIS), sometimes referred to as genomewide interaction scans, using data from a large population-based epidemiological sample of African American and Hispanic/Latina women drawn from the Women's Health Initiative (WHI).

METHODS AND MATERIALS

OVERVIEW

As described elsewhere[31,32] (www.whi.org), the WHI consists of an observational study (WHI-OS) and randomized clinical trial (WHI-CT). The WHI-OS prospectively followed 93,676 postmenopausal women ages 50–79 recruited from 40 clinical centers in the United States between 1993 and 1998. The WHI-CT enrolled 68,132 postmenopausal women of the same age and between the same time period to participate in one of three prevention trials: (1) hormone therapy; (2) dietary modification; and (3) calcium/vitamin D supplementation. We analyzed data from women genotyped as part of the WHI SNP Health Association Resource (SHARe), a sub-study of self-reported minority women in WHI ($n = 7{,}480$ African American and 3,352 Hispanic/Latina women). All participants consented to be included in studies for general research use. Data were downloaded from the database of Genotypes and Phenotypes (dbGaP; accession #phs000200.v9.p3).

PHENOTYPE DEFINITION

Depressive symptoms were assessed at enrollment using total scores from a six-item version of the Center for Epidemiological Studies of Depression Scale (CES-D),[33] a widely-used measure of depressive symptoms in epidemiological studies. The six-item CES-D captured core symptoms of depression in the past week, including anhedonia, depressed mood, and behavioral symptoms (e.g., felt depressed; sleep was restless; enjoyed life; had crying spells; felt sad; felt people disliked you). The six-item scale correlates highly with the full 20-item CES-D ($r = 0.88$).[32] Brief versions of the CES-D correlate highly in older adults with diagnoses of MDD obtained from structured interviews.[34]

As CES-D scores in this population-based sample could have been influenced by antidepressant medication use, we used a nonparametric imputation algorithm developed in a previous GWAS of depressive symptoms[6] to adjust the CES-D score of women taking antidepressants (as determined by pill bottles women brought to the baseline interview). This algorithm, which increased the CES-D score for all antidepressant users, was based on one used to adjust blood pressure for persons on antihypertensive medications[35] (see Supporting Information).

We tested for statistical GxE interaction with two environmental exposures—stressful life events and social support—both of which were shown to correlate with depressive symptoms in WHI[32] and numerous other studies.[36] These two social–environmental exposures were measured at enrollment, concurrently with depressive symptoms. Stressful life events were assessed using a scale modified from the Almeida County Study,[37,38] which asked women to indicate whether they had experienced 11 different major losses or traumatic events in the past year (see Supporting Information for specific items). Items were summed to create a total count of the number of past-year stressors among those with complete data on all stressors (ranging from 0 to 11). Social support was assessed using nine items from the 19-item Medical Outcome Survey.[39] We summed across these items to obtain a measure for level of perceived social support.

SNP GENOTYPING AND IMPUTATION

All participants were genotyped using the Affymetrix 6.0 chip designed to human genome build 36. Genotyping, on all samples plus 2% blinded duplicates, was performed at Affymetrix, Inc., Santa Clara, CA. A total of 720,101 (African Americans) and 709,042 (Hispanics/Latinas) SNPs passed preimputation filters.

Quality control procedures were performed at the Fred Hutchinson Cancer Research Center (FHCRC) in Seattle, WA. As described elsewhere (refer to[40] and Supporting Information), the WHI GARNET Coordinating Center (www.garnetstudy.org) performed the imputation using the 1000 Genomes Interim reference panel (release December 2010) and BEAGLE software version 3.3.1.[41]

QUALITY CONTROL (QC) OF SNPS AND SAMPLES

In addition to the QC standards imposed by WHI, we additionally excluded SNPs with a MAF of $\leq 2\%$ or imputation quality score $< r^2 = 0.80$. Population stratification was assessed by WHI investigators using a principal components analysis estimated by the program EIGENSTRAT.[42] A total of 61 genetic outliers were removed from the African American analysis based on their PCA scores. After QC, 10,771 women (7,419 African American and 3,352 Hispanic/Latina women) were available for analysis. Allele dosages (meaning the probability of the three possible genotypes), rather than hard-called or "best guess" genotypes, were used for both the GWAS and GWEIS analyses.

STATISTICAL ANALYSES

GWAS Analysis. We performed a GWAS, using PLINK version 1.07,[43] separately for African Americans and Hispanics/Latinas. We used linear regression for all analyses, modeled each SNP additively, and used the standard 5×10^{-8} as our threshold for statistical significance. After obtaining GWAS results, SNPs were clumped according to linkage disequilibrium (LD) to identify independent loci represented by a single best SNP.[43] This clump procedure used the following thresholds to identify independent SNPs: (1) SNPs that had LD $r^2 \geq 0.25$; and (2) SNPs that were within 250 kb. We also analyzed SNPs on the X chromosome.

Both GWAS analyses (and the GWEIS, described below) adjusted for the following covariates, measured at baseline: age, income, education, marital status, and four principal components adjusting for population structure.[40] These covariates were included because each was associated with depressive symptoms in either the SHARe or larger WHI cohort,[32] and prior studies have suggested inclusion of covariates in GWAS of common phenotypes may increase power.[44] Quantile-quantile (QQ) and Manhattan plots were generated using R.[45] Regional association plots were generated using Locus Zoom.[46] Inverse variance weighted fixed-effect meta-analyses were conducted using METAL (http://www.sph.umich.edu/csg/abecasis/metal/;[47]).

GWEIS Analysis. We performed the GWEIS using probABEL.[48] Both stressful life events and social support were modeled separately using a categorical variable derived by taking quartiles of the total score distribution (0 = first quartile; 1 = second quartile; 2 = third quartile; 3 = fourth quartile). The lowest quartile group (0) indicated the lowest social-environmental risk group, whereas the highest quartile group (3) indicated the highest social-environmental risk group. We used quartiles to facilitate interpretation and address the skewed distribution of these variables; categorization (into four or more categories) does not result in the loss of information (and power) that occurs when continuous variables are dichotomized.[49] We tested for GxE by including dummy variables for quartile group as well as a SNP by quartile-group (treated as ordinal) interaction term in the model. We used a Bonferroni correction to establish a significance threshold accounting for multiple testing of two environmental exposures ($\alpha = 2.5 \times 10^{-8}$). To reduce the likelihood of spurious GxE findings, we used model-robust estimates of standard errors (also known as sandwich standard errors)[50] in all tests of GxE. Robust variance estimates can reduce the possibility of inflated Type I errors found for GxE effects if the environmental main effect is misspecified or if there is departure from the presumed linear model.[51–53] *P*-values corresponding to the interaction term (in the multiple regression model) were calculated in R based on a Wald chi-square test.

REPLICATION

We sought replication of top GWAS findings ($P < 1 \times 10^{-6}$) in each sample using data from four independent cohorts (see Supporting Information); two cohorts (HRS and HCHS/SOL) were also used to replicate the GWEIS results. For the African American replication, we analyzed data from African American women in the Health and Retirement Study (HRS; $n = 1{,}231$; mean age 62.09),[54,55] where depressive symptoms were measured using an 8-item version of the CES-D, social support was measured through three items asking about support received from a spouse, children, family, and friends, and stressful life events were measured through a composite measure developed to most closely approximate the discovery analysis. We also analyzed data from African Americans in the Grady Trauma Project (GTP; $n = 2{,}010$ women ages 18–65),[56] where depressive symptoms were assessed using the Beck Depression Inventory.[57] For the Hispanic/Latino replication, we analyzed data from the Hispanic Community Health Study/Study of Latinos (HCHS/SOL; $n = 3{,}371$ women ages 50–76), where depressive symptoms were measured by a 10-item CES-D, social support was measured through the 12-item version of the Interpersonal Support Evaluation List,[58] and stressful life events was assessed through a composite measure designed to match the discovery sample. We also assessed top GWAS findings for both Hispanics and African Americans in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE Consortium), which performed the largest meta-analysis GWAS of depressive symptoms to date using 17 European-ancestry population-based studies ($n = 51{,}258$ individuals) of older adults where depressive symptoms were measured through the CES-D.[6]

SECONDARY ANALYSES

We performed four secondary analyses. First, we conducted two sets of meta analyses to determine the degree to which the top GWAS SNPs ($P < 10^{-5}$) obtained in African Americans also showed evidence of nominal association in Hispanics/Latinas and vice versa. Second, we reran the GWAS in each sample after additionally adjusting for both environmental exposures, as both stressful life events and social support were found to make large and unique contributions to the variance in depressive symptoms. Third, we performed an analysis using genome-wide complex trait analysis (GCTA), which uses restricted maximum likelihood (REML) to obtain an estimation of the additive effect of common variants or "SNP-chip heritability."[59] We conducted these analyses, focusing on depressive symptoms, stressful life events, and social support separately, to evaluate the unique genetic contribution to these phenotypes and the potential presence of gene–environment correlation. We also examined the genetic contribution to depressive symptoms after adjusting for each of these environmental exposures individually. These analyses were performed only in African Americans, as a power calculation indicated the Hispanic/Latino sample would be underpowered to detect SNP heritability estimates in the range reported in previous studies of European Americans (ranging from 21[60] to 32%[61] for major depressive disorder; MDD). We also performed a bivariate REML analysis to determine the genetic correlation between depressive symptoms and these two environmental exposures.[62] Finally, to evaluate the strength of our findings given the skewed distribution of our outcome, we repeated the top GWAS ($P < 1 \times 10^{-5}$) and GWEIS ($P < 1 \times 10^{-6}$) tests of association using a nonparametric bootstrap. For the top GWAS SNPs, we fit a linear regression on 1,000 bootstrap samples using the boot package in R[63,64] and compared the effective sizes (betas) from the bootstrap samples to the betas obtained in the original analysis for each top SNP. For the top GWEIS SNPs, we fit linear regressions to 5,000 datasets simulated under the null hypothesis[65] and generated *P*-values for each top SNP. These *P*-values represent the number of betas that were more extreme than the beta obtained in the original analysis divided by 5,000 replicates. A significant *P*-value therefore indicates that the GxE interaction is significant at that level.

RESULTS

DISCOVERY SAMPLE: GWAS

There were 7,179 African American and 3,138 Hispanic/Latina women in the analysis. See Supporting Information Table S1 for sample demographic characteristics. Depressive symptoms scores were slightly higher in Hispanics/Latinas (mean = 3.27; sd = 3.20) and skewed toward lower values (skew = 1.22; kurtosis = 1.24), particularly in African Americans (mean = 2.52; sd = 2.71; skew = 1.55; kurtosis = 2.97). However, as linear regression is robust to minor violations of normality[66] and tests of GxE are sensitive to changing the scale of the phenotype,[67] we did not perform any transformations.

Manhattan and QQ plots are shown in Supporting Information Fig. S1. As shown in the QQ plot, there was no evidence of inflation in either the African American ($\lambda = 1.004$, median = 0.458) or Hispanic/Latina ($\lambda = 0.998$, median = 0.455) GWAS.

No SNPs achieved genome-wide significance in either sample (Table 1). The peak signal in African Americans ($P = 5.75 \times 10^{-8}$) was for an imputed SNP rs73531535 located 20 kb from *GPR139* (the G protein coupled receptor 139), although several other SNPs in the region that also showed support were genotyped (Supporting Information Fig. S2). The second strongest association signal in African Americans was observed at rs75407252 ($P = 6.99 \times 10^{-7}$), in an intron of *CACNA2D3*, which encodes a voltage-dependent calcium channel subunit (Supporting Information Fig. S3).

In Hispanics/Latinas, the peak signal ($P = 2.44 \times 10^{-7}$) was for an imputed SNP rs2532087 located approximately 27 kb away from *CD38* (Supporting Information Fig. S4). The second strongest association signal was for the imputed SNP rs4542757 ($P = 7.31 \times 10^{-7}$) located in an intron of *DCC* (deleted in colorectal cancer; Supporting Information Fig. S5). All GWAS results at $P < 1 \times 10^{-4}$ are shown for African Americans (Supporting Information Table S2) and Hispanics/Latinas (Supporting Information Table S3). No SNPs achieved genome-wide significance on the X chromosome for either sample (Supporting Information Table S4).

TABLE 1. Genome-wide association study (GWAS) results for the top loci ($p<1\times10^{-5}$) in African Americans and Hispanics/Latinos

SNP	chr	position	A1	A2	MAF	G/I	Info	Beta	SE	P-value	Location	Closest Gene (<20kb)
African Americans												
rs73531535	16	20105038	C	T	0.229	I	0.938	-0.297	0.055	5.75E-08		*GPR139*
rs75407252	3	54241886	C	T	0.053	I	0.813	-0.548	0.110	6.99E-07	intron variant	*CACNA2D3*
rs11233283	11	82415904	A	G	0.016	I	0.986	-0.298	0.062	1.41E-06		
rs34257140	17	42675053	G	T	0.149	I	0.999	-0.313	0.065	1.59E-06		
rs580112	3	177289895	A	G	0.184	I	0.945	0.279	0.060	2.84E-06	intron variant	*LINC00578*
rs1413154	13	83240729	G	T	0.205	I	0.825	-0.283	0.061	3.54E-06		
rs1893586	21	43286918	A	G	0.483	I	0.947	0.211	0.046	4.19E-06	intron variant	*PRDM15*
rs10777901	12	98492992	A	C	0.481	I	0.993	0.206	0.045	4.27E-06		
rs10125319	9	133426729	C	T	0.491	I	0.920	-0.214	0.047	4.27E-06		
rs10221121	16	56840328	A	G	0.229	G	0.986	-0.241	0.053	5.98E-06	intron variant	*NUP93*
rs210329	14	54059800	G	T	0.332	I	0.989	0.217	0.048	6.35E-06		*RPS3AP46*
rs28493952	3	95747804	C	T	0.320	I	0.850	0.234	0.052	6.41E-06		
rs7312307	12	106441333	C	G	0.087	I	0.904	0.376	0.084	6.92E-06		*NUAK1*
rs17030391	2	43353504	A	G	0.143	I	0.808	0.316	0.071	7.84E-06		
rs4866976	5	45579793	A	G	0.086	G	0.996	-0.361	0.081	8.04E-06	intron variant	*HCN1*
rs418207	3	9225376	A	G	0.477	I	0.811	-0.219	0.050	9.59E-06	intron variant	*SRGAP3*
Hispanics/Latinos												
rs2532087	4	15878327	C	G	0.231	I	0.8154	0.5379	0.104	2.44E-07		
rs4542757	18	50198724	C	T	0.418	I	0.9304	-0.4135	0.0833	7.31E-07	intron variant	*DCC*
rs10249677	7	50650831	G	T	0.042	I	0.8816	1.0497	0.2157	1.20E-06		*GRB10*
rs1129411	2	231077725	A	G	0.085	I	0.9941	0.6637	0.1417	2.94E-06	missense/intron variant	*SP110*
rs11738766	5	8214282	A	G	0.279	G	1.0253	-0.4134	0.0885	3.11E-06		
rs34359572	1	194036781	A	G	0.072	I	0.8899	-0.7471	0.1619	4.10E-06		
rs609508	20	54167720	C	G	0.214	I	0.9752	0.4429	0.097	5.21E-06		
rs16823787	2	183692791	A	G	0.084	G	0.9823	0.6591	0.1444	5.21E-06		*FRZB*
rs17345417	4	95948486	A	G	0.111	G	0.9949	-0.574	0.1259	5.30E-06	intron variant	*BMPR1B*
rs2822657	21	15774729	C	T	0.457	I	0.9875	-0.3657	0.0802	5.35E-06		*HSPA13*
rs13033587	2	52857818	C	T	0.475	I	0.9342	0.376	0.0828	5.85E-06		
rs9601962	13	83312889	G	T	0.185	I	0.8544	0.4945	0.1098	6.91E-06		
rs2282123	6	89907561	C	G	0.255	G	1.0034	0.4114	0.0915	7.19E-06	intron variant	*GABRR1*
rs10886733	10	122402887	C	T	0.117	I	0.9766	0.556	0.1237	7.23E-06		*MIR5694*
rs61848143	10	24746704	C	G	0.177	I	0.8403	-0.5023	0.1122	7.85E-06	intron variant	*KIAA1217*
rs10166852	2	183450923	C	G	0.474	I	0.9666	-0.3752	0.0838	7.85E-06		
rs6736484	2	45146524	G	T	0.075	G	0.8556	-0.7206	0.1621	9.05E-06		
rs2912513	8	69968166	A	T	0.033	I	0.9774	-0.996	0.2243	9.33E-06	intron variant	*LINC01592*

The table lists all LD-pruned SNPs associated with depressive symptoms at $p<1\times10^{-5}$. A1 is the tested allele using an additive model, where allele dosages were analyzed. The closest gene within 20kb upstream/downstream of the SNP is provided. All SNPs are on the positive (5′ to 3′) strand. Chr: chromosome; position: base pair position, G/I: genotyped or imputed.

REPLICATION SAMPLES: GWAS

Sixteen SNPs from the African American analysis and 18 SNPs from the Hispanic/Latina analysis with $P < 1 \times 10^{-5}$ were evaluated in four independent samples. For the African American replication (Table 2), one SNP was nominally significant in the HRS (rs418207; $P = 0.015$), though was not statistically associated after correction for multiple testing ($\alpha = 0.003$). This SNP showed the same direction and magnitude of effect in WHI and HRS and is intronic to *SRGAP3*, the gene that encodes the enzyme SLIT-ROBO Rho GTPase-activating 3.

In the Hispanic/Latina replication (Table 3), the peak WHI signal (rs2532087) also had the lowest *P*-value of the 18 SNPs in HCHS/SOL ($P = 0.00964$), though this result was not significantly associated after multiple testing correction ($\alpha = 0.003$). However, the direction and effect size were nearly identical in both the discovery and replication samples (WHI $\beta = 0.54$; HCHS/SOL $\beta = 0.56$). The Hispanic/Latina discovery and HCHS/SOL replication results were also highly concordant, with 72% of linear regression β coefficients (13 out of 18 SNPs) yielding the same direction of effect (sign test $P = 0.05$). None of the top GWAS findings in African Americans or Hispanics/Latinas were significantly associated with depressive symptoms in the CHARGE consortium of European Americans (refer to Supporting Information Table S5).

DISCOVERY SAMPLE: GWEIS

Women in each sample reported a similar number of stressful life events (African American mean = 2.15, sd = 1.57; Hispanic/Latina mean = 2.13, sd = 1.68) and levels of social support (African American mean = 35.29, sd = 7.63; Hispanic/Latina mean = 34.27, sd = 8.92). The number of stressful life events and depressive symptoms were *positively* associated in both African Americans ($r^2 = 0.10$; $P < 0.001$) and Hispanics/Latinas ($r^2 = 0.10$; $P < 0.001$). Social support was *negatively* associated with depressive symptoms in both African Americans ($r^2 = 0.09$; $P < 0.001$) and Hispanics/Latinas ($r^2 = 0.15$; $P < 0.001$).

There was no evidence of genomic inflation for the African American stressful life events ($\lambda = 0.99$) and social support analyses ($\lambda = 1.02$) or the Hispanic/Latina stressful life events ($\lambda = 1.01$) and social support analyses ($\lambda = 1.03$) (Supporting Information Figs. S6 and S7).

One association signal was genome-wide significant (rs4652467; $P = 4.10 \times 10^{-10}$) in African Americans for the stressful life events GWEIS (Table 4). This SNP, located within 20 kb of *CEP350*, was imputed, as were other SNPs in the region with $P < 2.4 \times 10^{-8}$ (Fig. 1). The second strongest signal in African Americans was rs7275997 ($P = 1.22 \times 10^{-7}$), a genotyped intronic SNP located in *TMPRSS15* (transmembrane protease, serine 15; Supporting Information Fig. S8). The GWEIS of social support in African Americans did not yield any genome-wide significant results (Table 4). The top two loci were rs77966298 ($P = 2.43 \times 10^{-7}$; Supporting Information Fig. S9) and rs6419121 ($P = 3.98 \times 10^{-7}$; Supporting Information Fig. S10).

In Hispanics/Latinas, we did not find any genome-wide significant association signals for either GWEIS (Table 5). The top two loci in the GWEIS of stressful life events were rs58707171 ($P = 3.02 \times 10^{-7}$) and rs6579218 ($P = 4.94 \times 10^{-7}$) (Supporting Information Fig. S11). The top two loci in the GWEIS of social support were rs35612712 ($P = 3.42 \times 10^{-7}$) and rs61973969 ($P = 9.41 \times 10^{-7}$) (Supporting Information Fig. S12).

REPLICATION SAMPLES: GWEIS

No top variants were significant in any replication sample (Table 6).

SECONDARY ANALYSES

The top loci in African Americans did not have similarly low *P*-values in Hispanics/Latinas and vice versa (see Supporting Information). Rerunning the GWAS after including the environmental exposures did not systematically change the results (see Supporting Information). SNP heritability estimates for depressive symptoms and the environmental exposures were low (less than 10%) when each was examined on its own and only significant for stressful life events, after adjusting for covariates (Table 7). The numerically largest and statistically significant estimate was found for stressful life events (8%). Interestingly, a very large genetic correlation was detected in the bivariate REML for depressive symptoms and stressful life events (rG = 0.95; $P = 0.04$) after adjusting for covariates, suggesting that the genetic influences on depressive symptoms and stressful life events are largely shared. Indeed, after adjusting for each environmental measure in the REML analysis, no significant heritable signal for depressive symptoms remained. The GWAS and GWEIS results using a nonparametric bootstrap were similar to our original findings (see Supporting Information), suggesting our results were not sensitive to distributional assumptions.

DISCUSSION

This study involved two major innovations in efforts to identify the genetic basis of depression. First, to our knowledge, this was the first genome-wide GxE analysis of depression. Prior GxE studies have focused on a relatively limited set of candidate gene polymorphisms, many of which have showed mixed results.[10,68] Second, our study was also the largest GWAS of depressive symptoms conducted specifically in African Americans and Hispanics/Latinas. To our knowledge, only one prior GWAS was conducted among these groups; this study had a much smaller sample (African Americans $n = 1{,}603$; Hispanics $n = 1{,}443$) and did not examine GxE.[69]

We highlight three findings. First, although no genome-wide significant loci were detected in our

TABLE 2. Replication of genome-wide association study (GWAS) results for the top loci ($P < 1 \times 10^{-5}$) in African Americans

			WHI		HRS					GTP					Discovery: WHI ($n = 7{,}179$)			Replication: HRS ($n = 1{,}231$)			Replication: GTP ($n = 2{,}010$)		
SNP	Chr	Position	A1	A2	G/I	Info	MAF	A1	A2	G/I	Info	MAF	A1	A2	β	SE	*P*-value	β	SE	*P*-value	β	SE	*P*-value
rs73531535	16	20105038	C	T	I	0.995	0.245	C	T	I	0.973	0.246	T	C	−0.297	0.055	5.75×10^{-8}	0.060	0.106	0.573	−0.325	0.452	0.472
rs75407252	3	54241886	C	T	I	0.922	0.051	C	T	I	0.868	0.048	T	C	−0.548	0.110	6.99×10^{-7}	0.285	0.208	0.171	0.241	0.969	0.804
rs11233283	11	82415904	A	G	I	0.999	0.192	A	G	I	0.968	0.185	A	G	−0.298	0.062	1.41×10^{-6}	0.194	0.117	0.098	−0.015	0.504	0.976
rs34257140	17	42675053	G	T	G	1	0.102	G	T	I	0.971	0.106	T	G	−0.313	0.065	1.59×10^{-6}	0.112	0.152	0.461	−0.131	0.639	0.838
rs580112	3	177289895	A	G	I	0.999	0.158	A	G	I	0.985	0.152	A	G	0.279	0.060	2.84×10^{-6}	−0.130	0.123	0.290	0.120	0.539	0.824
rs1413154	13	83240729	G	T	G	1	0.219	G	T	G	0.987	0.223	T	G	−0.283	0.061	3.54×10^{-6}	0.141	0.105	0.181	−0.024	0.465	0.959
rs1893586	21	43286918	A	G	I	0.999	0.462	A	G	I	0.993	0.478	A	G	0.211	0.046	4.19×10^{-6}	−0.046	0.094	0.626	−0.281	0.385	0.465
rs10777901	12	98492992	A	C	G	1	0.498	A	C	G	1.018	0.476	A	C	0.206	0.045	4.27×10^{-6}	0.155	0.090	0.085	0.220	0.381	0.563
rs10125319	9	133426729	C	T	I	0.996	0.495	C	T	I	1.008	0.487	T	C	−0.214	0.047	4.27×10^{-6}	−0.039	0.089	0.664	−0.408	0.382	0.286
rs10221121	16	56840328	A	G	G	1	0.230	A	G	G	1.001	0.210	A	G	−0.241	0.053	5.98×10^{-6}	−0.020	0.109	0.857	−0.448	0.472	0.343
rs210329	14	54059800	G	T	I	0.996	0.303	G	T	I	0.970	0.283	T	G	0.217	0.048	6.35×10^{-6}	−0.018	0.101	0.856	0.346	0.436	0.427
rs28493952	3	95747804	C	T	I	0.979	0.291	C	T	I	0.936	0.295	T	C	0.234	0.052	6.41×10^{-6}	0.065	0.104	0.530	0.736	0.435	0.091
rs7312307	12	106441333	C	G	I	0.982	0.090	C	G	I	0.927	0.091	C	G	0.376	0.084	6.92×10^{-6}	0.124	0.162	0.447	−0.674	0.694	0.331
rs17030391	2	43353504	A	G	I	0.998	0.122	A	G	I	0.961	0.132	A	G	0.316	0.071	7.84×10^{-6}	−0.009	0.143	0.947	−0.142	0.579	0.806
rs4866976	5	45579793	A	G	I	0.989	0.076	A	G	I	0.943	0.082	A	G	−0.361	0.081	8.04×10^{-6}	0.205	0.171	0.230	−1.304	0.719	0.070
rs418207	3	9225376	A	G	G	1	0.486	A	G	G	1.029	0.494	A	G	−0.219	0.050	9.59×10^{-6}	−0.228	0.093	0.015	0.030	0.378	0.938

HRS, Health and Retirement Study. These models were estimated using R 3.0.1. Covariates in HRS were age, income, education, marital status and the top 10 principal components. Imputation was conducted using IMPUTE2.

GTP, Grady Trauma Project. In these analyses with dosage data, PLINK models A1 as the tested allele. SNPs were analyzed using additive coding, where allele dosages were analyzed. Covariates in the GTP were age, income per month, education, marital status, and five principal components. In the GTP, quality control and imputation were performed by the PGC Statistical Analysis Group. Methods for imputation are described in the Supporting Information.

The Bonferroni adjusted α level in these analyses was $0.05/16 = 0.003$.

TABLE 3. Replication of genome-wide association study (GWAS) results for the top loci ($P < 1 \times 10^{-5}$) in Hispanics

			WHI		HCHS/SOL					Discovery: WHI ($n = 3{,}138$)			Replication: HCHS/SOL ($n = 3{,}371$)		
SNP	Chr	Position	A1	A2	G/I	Info	MAF	A1	A2	β	SE	P-value	β	SE	P-value
rs2532087	4	15878327	C	G	I	0.926	0.210	C	G	0.538	0.104	2.44×10^{-7}	0.556	0.215	0.00964
rs4542757	18	50198724	C	T	G	1.000	0.415	C	T	−0.413	0.083	7.31×10^{-7}	−0.072	0.174	0.68
rs10249677	7	50650831	G	T	I	0.979	0.065	T	G	1.050	0.216	1.20×10^{-6}	−0.582	0.354	0.1
rs1129411	2	231077725	A	G	G	1.000	0.084	A	G	0.664	0.142	2.94×10^{-6}	0.262	0.305	0.39
rs11738766	5	8214282	A	G	G	1.000	0.286	A	G	−0.413	0.089	3.11×10^{-6}	−0.277	0.191	0.147
rs34359572	1	194036781	A	G	I	0.999	0.083	A	G	−0.747	0.162	4.10×10^{-6}	−0.019	0.311	0.951
rs609508	20	54167720	C	G	I	0.998	0.215	C	G	0.443	0.097	5.21×10^{-6}	0.069	0.208	0.738
rs16823787	2	183692791	A	G	I	0.987	0.091	A	G	0.659	0.144	5.21×10^{-6}	−0.099	0.297	0.739
rs17345417	4	95948486	A	G	I	0.996	0.102	A	G	−0.574	0.126	5.30×10^{-6}	0.194	0.284	0.495
rs2822657	21	15774729	C	T	G	1.000	0.436	T	C	−0.366	0.080	5.35×10^{-6}	−0.098	0.171	0.569
rs13033587	2	52857818	C	T	I	0.997	0.489	T	C	0.376	0.083	5.85×10^{-6}	0.298	0.174	0.0869
rs9601962	13	83312889	G	T	I	0.973	0.210	T	G	0.494	0.110	6.91×10^{-6}	0.098	0.211	0.644
rs2282123	6	89907561	C	G	I	0.995	0.238	C	G	0.411	0.092	7.19×10^{-6}	0.049	0.202	0.808
rs10886733	10	122402887	C	T	I	0.989	0.106	T	C	0.556	0.124	7.23×10^{-6}	0.054	0.272	0.843
rs61848143	10	24746704	C	G	I	0.985	0.175	G	C	−0.502	0.112	7.85×10^{-6}	0.410	0.223	0.0662
rs10166852	2	183450923	C	G	I	0.989	0.471	C	G	−0.375	0.084	7.85×10^{-6}	0.141	0.176	0.423
rs6736484	2	45146524	G	T	I	0.948	0.068	G	T	−0.721	0.162	9.05×10^{-6}	−0.285	0.338	0.399
rs2912513	8	69968166	A	T	I	0.999	0.035	A	T	−0.996	0.224	9.33×10^{-6}	−0.119	0.472	0.8

HCHS/SOL, Hispanic Community Health Study/Study of Latinos. These models were estimated using a linear mixed model fit by maximum likelihood with age, education, study center, five principal components, and covariates adjusting for the sampling design. Imputation was conducted using IMPUTE2. In HCHS/SOL, A1 was the tested allele. The Bonferroni adjusted α level in these analyses was $0.05/18 = 0.003$.

TABLE 4. Genome-wide by environment interaction study (GWEIS) results for the top loci ($P < 1 \times 10^{-6}$) in African Americans

									SNP main effect			SNP × environment interaction term				
SNP	Chr	Position	G/I	Info	MAF	A1	A2	Freq1	β	SE	*P*-value	β	SE	*P*-value	Location	Closest gene (<20 kb)
Stressful Life Event Results ($n = 6{,}982$)																
rs4652467	1	180097705	I	0.945	0.026	A	G	0.026	−0.662	0.167	1	0.691	0.111	4.10×10^{-10}		*CEP350*
rs7275997	21	19663487	G	0.993	0.180	A	G	0.820	0.264	0.069	1	−0.278	0.053	1.22×10^{-7}	Intron variant	*TMPRSS15*
rs28377528	7	153884444	I	0.874	0.420	A	G	0.580	−0.212	0.058	1	0.237	0.046	3.23×10^{-7}	Intron variant	*DPP6*
rs2852310	18	43093004	I	0.996	0.027	A	G	0.027	−0.560	0.183	1	0.617	0.123	4.66×10^{-7}	Intron variant	*SLC14A2*
rs12183135	6	151353805	G	0.996	0.024	C	G	0.024	−0.137	0.155	1	0.491	0.100	8.01×10^{-7}		*MTHFD1L*
Social Support Results ($n = 6{,}908$)																
rs77966298	2	10984514	I	0.891	0.034	A	G	0.966	0.796	0.223	1	−0.592	0.115	2.43×10^{-7}		*PDIA6*
rs6419121	4	88490040	I	0.921	0.178	C	G	0.178	−0.375	0.096	1	0.280	0.055	3.98×10^{-7}		
rs10836421	11	35581792	I	0.971	0.315	A	G	0.315	−0.184	0.071	1	0.217	0.043	4.34×10^{-7}		
rs78012311	21	33634345	I	0.981	0.104	C	G	0.104	0.468	0.094	1	−0.321	0.065	8.23×10^{-7}		*MIS18A*

Robust (sandwich) standard errors are presented. In these tests of statistical interaction (on the additive scale and using allele dosages), probABEL uses A2 as the tested (nonreference) allele. The β coefficients in these models can be interpreted as follows. For stressful life events, for example, the SNP main effect β coefficient indicates the average difference in levels of depressive symptoms for women with a zero value on all covariates, who have 1 copy of the tested allele, and who are in the lowest quartile of stressful life events. The GxE interaction term indicates the average estimated difference in the effect of each tested allele on depressive symptoms associated with a one-unit different in stressful life events, adjusting for covariates. The Bonferroni adjusted α level in these analyses was 2.5×10^{-8}.

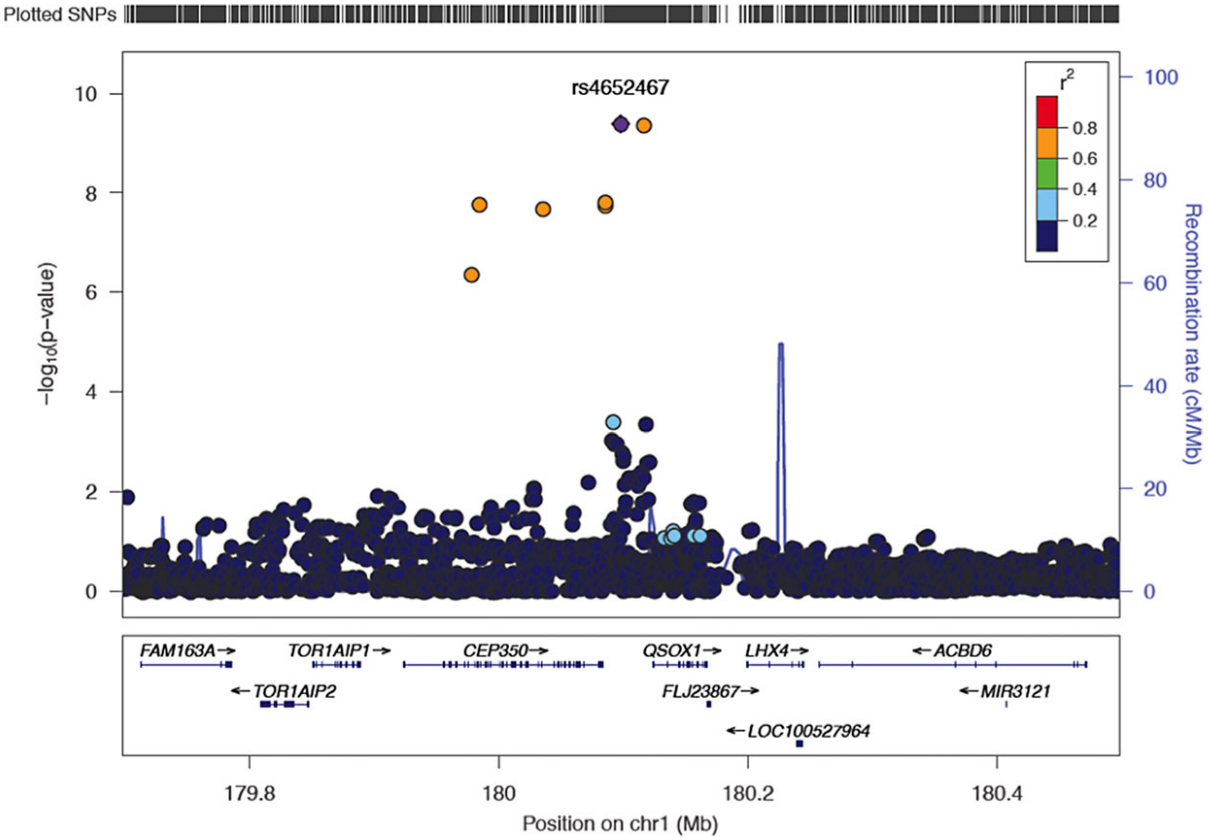

Figure 1. Regional association plot for the top SNP (rs4652467) identified in the African American genome-wide by environment interaction study (GWEIS) of stressful life events. The regional association plot was generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for the African American reference panel only as the SNP was monomorphic in Europeans (100% G allele). The left-side *y*-axis refers to the log of the *P*-value corresponding to the test of association between each SNP (denoted as a colored dot) and stressful life events (in the test of GxE) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The index SNP (rs4652467, purple diamond) and its closest neighbors (shown in orange) are imputed.

GWAS, three of the strongest signals were in genes previously implicated in depression-related phenotypes. In African Americans, our top SNP was located 20 kb from *GPR139*. Recent studies show that GPR139 encodes a highly conserved G-protein-coupled receptor whose ligands are tryptophan and phenylalanine.[70] Expression of GPR139 appears to be restricted to the central system and evidence from mouse studies suggests that it is specifically expressed in the lateral habenula and septum, two regions previously implicated in the pathophysiology of depression.[71] Based on these results, Bonaventure and colleagues suggested that GRP139 may mediate the well-established depressogenic effects of tryptophan depletion.[70] Our second best SNP in African Americans was located in a calcium channel gene (*CACNA2D3*). Variants in calcium channel signaling genes have been associated with MDD and other psychiatric disorders in large-scale genome-wide association studies.[72,73] However, the *CACNA2D3* variant did not show evidence of association in either the GTP or HRS replication samples. In the analysis of Hispanics/Latinas, the second strongest signal was located in *DCC* (deleted in colorectal cancer), which encodes the netrin-1 receptor.[74] *DCC* regulates transmembrane signaling receptor activity and is mutated or downregulated in colorectal cancer and esophageal carcinoma. Manitt and colleagues recently found *DCC* signaling aids in establishing medial prefrontal cortex dopamine synaptic connectivity and that higher expression of DCC may be linked to suicide.[75] The *DCC* variant, however, was not associated with depressive symptoms in our replication sample. However, the *DCC* variant (as well as other top loci) showed similar directions of effect across the discovery and replication results, suggesting that our study may have been underpowered. Indeed, a post-hoc power calculation suggested we had poor power among the top results ($P < 1 \times 10^{-5}$) to detect the effect sizes observed given our discovery sample sizes (African Americans = 7,179; Hispanics = 3,138). Specifically, the average power among the top SNPs was 0.26 in the African American GWAS and 0.23 in the Hispanic discovery GWAS. Thus, it appears that even larger samples sizes

TABLE 5. Genome-wide by environment interaction study (GWEIS) results for the top loci ($P < 1 \times 10^{-6}$) in Hispanics

									SNP main effect			SNP × environment interaction term				
SNP	Chr	Position	G/I	Info	MAF	A1	A2	Freq1	β	SE	*P*-value	β	SE	*P*-value	Location	Closest gene (<20 kb)
Stressful Life Event Results (*n* = 2,989)																
rs58707171	4	36317832	I	0.921	0.037	A	C	0.963	0.649	0.254	1	−0.778	0.152	3.02×10^{-7}	Intron variant	*DTHD1*
rs6579218	20	33709846	I	0.989	0.156	C	G	0.844	0.425	0.142	1	−0.505	0.100	4.94×10^{-7}	Intron variant	*EDEM2*
rs10227305	7	3272267	I	0.849	0.207	A	C	0.793	0.308	0.133	1	−0.454	0.093	9.36×10^{-7}		
Social Support Results (*n* = 3,012)																
rs35612712	4	187347203	I	0.941	0.416	C	T	0.416	−0.375	0.119	1	0.376	0.074	3.42×10^{-7}	Intron variant	*F11-AS1*
rs61973969	13	96689182	I	0.985	0.032	C	T	0.032	−0.979	0.317	1	0.839	0.171	9.41×10^{-7}	Intron variant	*UGGT2*

Robust (sandwich) standard errors are presented. In these tests of statistical interaction (on the additive scale and using allele dosages), probABEL uses A2 as the tested (nonreference) allele. The β coefficients in these models can be interpreted as follows. For stressful life events, for example, the SNP main effect β coefficient indicates the average difference in levels of depressive symptoms for women with a zero value on all covariates, who have 1 copy of the tested allele, and who are in the lowest quartile of stressful life events. The GxE interaction term indicates the average estimated difference in the effect of each tested allele on depressive symptoms associated with a one-unit different in stressful life events, adjusting for covariates. The Bonferroni adjusted α level in these analyses was 2.5×10^{-8}.

are needed to detect SNPs associated with depressive symptoms.

Second, in the African American sample, we observed a genome-wide significant interaction between rs4652467, a variant 14 kb away from *CEP350*, and stressful life events. This interaction suggested depressive symptoms were highest among those with more exposure to stressful life events who also had more copies of the major allele. However, this GxE was not observed in the HRS replication. Whether this lack of replication indicates a spurious GxE result or is due to the differences in WHI and HRS phenotype definitions is unclear. Of note, only three of the six depressive symptoms assessed in WHI were also assessed in HRS; the stressful life events measures also had limited overlap (see Supporting Information for comparisons). The failure to identify more genome-wide significant GxE loci or replicate the one genome-wide significant finding may also be due to the small discovery sample size or smaller size of the HRS sample. Our discovery GWEIS analysis could have been underpowered, especially since GxE studies are known to require even larger samples than primary genetic association studies, perhaps as much as four times the size.[76,77] However, a post-hoc power calculation we ran suggested our discovery GWEIS had high power (>90%) to detect the effect estimates we observed. This power estimate is likely inflated due to Winner's Curse (or the phenomena by which detected effects are larger than they really are)[78] and also does not take into account measurement error. Future studies are needed to identify optimal methods to estimate Winner's curse adjusted effect sizes for GxE interaction effects that also address measurement error.

Third, we were able to estimate the SNP heritability of depressive symptoms as well as the two social-environmental exposures in African Americans. SNP heritability estimates were low (less than 10%) for all three phenotypes. The SNP heritability for depressive symptoms (5%) was numerically the lowest and about one-quarter the size of estimates that have been observed in case-control studies of MDD with European-ancestry samples.[60,61] SNP-chip heritability estimates of other psychiatric and behavioral symptoms have also been shown elsewhere[79,80] to produce similarly lower heritability estimates than those obtained from studies examining disorders. Moreover, the largest and only statistically significant estimate observed was for stressful life events (8%), suggesting there may be some degree of gene-environment correlation. Our SNP heritability estimate for stressful life events was lower than a previous study, which found that SNPs explained 29% of the variance in stressful life events.[81] That study, however, was of European ancestry adults and focused on 6-month, rather than past-year stressors and was drawn from a case-control sample of adults with recurrent MDD. Interestingly, we also found a very large genetic correlation for depressive symptoms with stressful life events (rG = 0.95), suggesting that common variation underlying depressive symptoms and stressful life event

TABLE 6. Replication of genome-wide by environment interaction study (GWEIS) results for the top loci ($P < 1 \times 10^{-6}$) in African Americans and Hispanics

									SNP main effect			SNP × environment interaction term		
SNP	Chr	Position	G/I	Info	MAF	A1	A2	Freq1	β	SE	*P*-value	β	SE	*P*-value
African Americans														
Stressful Life Event Results ($n = 952$)														
rs4652467	1	180097705	I	0.919	0.029	A	G	0.971	0.143	0.310	0.645	−1.227	0.765	0.109
rs7275997	21	19663487	I	0.999	0.176	A	G	0.176	−0.242	0.151	0.109	0.124	0.279	0.655
rs28377528	7	153884444	I	0.960	0.439	A	G	0.439	−0.018	0.116	0.878	0.074	0.206	0.718
rs2852310	18	43093004	I	0.961	0.028	A	G	0.972	0.192	0.273	0.483	0.660	0.422	0.118
rs12183135	6	151353805	I	0.953	0.025	C	G	0.975	−0.693	0.374	0.064	−0.035	0.889	0.969
Social Support Results ($n = 952$)														
rs77966298	2	10984514	I	0.995	0.027	A	G	0.027	0.177	0.686	0.796	−0.073	0.319	0.820
rs6419121	4	88490040	I	0.994	0.177	C	G	0.823	−0.136	0.259	0.598	0.105	0.131	0.422
rs10836421	11	35581792	I	0.998	0.284	A	G	0.716	0.325	0.193	0.092	−0.166	0.100	0.098
rs78012311	21	33634345	I	0.995	0.082	C	G	0.918	0.470	0.343	0.171	−0.243	0.176	0.167
Hispanics														
Stressful Life Event Results ($n = 1{,}117$)														
rs58707171	4	36317832	I	0.992	0.040	A	C	0.960	0.374	0.413	0.365	−0.771	0.788	0.328
rs6579218	20	33709846	I	0.997	0.141	G	C	0.141	0.554	0.241	0.022	0.210	0.411	0.609
rs10227305	7	3272267	G	1	0.196	A	C	0.804	0.115	0.211	0.586	0.233	0.362	0.521
Social Support Results ($n = 1{,}117$)														
rs35612712	4	187347203	I	0.999	0.401	T	C	0.401	−0.026	0.174	0.883	−0.170	0.268	0.525
rs61973969	13	96689182	I	0.998	0.035	T	C	0.035	−0.118	0.458	0.797	0.467	0.706	0.509

The African American replication was performed in HRS, Health and Retirement Study. The Hispanic/Latino replication was performed in HCHS/SOL, Hispanic Community Health Study/Study of Latinos. The Bonferroni adjusted α level in these analyses was $0.05/9 = 0.006$. Robust (sandwich) standard errors were used.

exposure, though modest on their own, were highly overlapping in this sample. This finding could be an artifact of the correlated nature of these variables when assessed in cross-sectional studies. Indeed, stressful life events ($r = 0.32$) and social support ($r = 0.30$) were modestly correlated with depressive symptoms, and thus these GCTA results could reflect shared genetic contribution to self-reported measures. Future studies are needed to replicate these findings and determine the impact of this degree of gene-environment correlation (as well as environment-depression correlation) for studying GxE.

Another area for future research relates to whether and how to adjust for use of antidepressant medications in studies of depressive symptoms. In the current study, we followed the precedent set by the CHARGE consortium,[6] which conducted the largest meta-analysis of depressive symptoms to date, and used an algorithm to modify our depressive symptom score

TABLE 7. Results of genome-wide complex trait analysis based on the GREML method

	Model 1			Model 2		
	V(G)/Vp	SE	*P*	V(G)/Vp	SE	*P*
Depressive symptoms	0.05	0.04	0.07	0.04	0.04	0.16
Stressful life events	0.08	0.04	0.02	0.06	0.04	0.06
Social support	0.04	0.04	0.13	0.03	0.04	0.25
Depressive symptoms, controlling for stress	0.03	0.04	0.18	0.02	0.04	0.29
Depressive symptoms, controlling for support	0.04	0.04	0.11	0.03	0.04	0.19
	rG	SE	*P*	rG	SE	*P*
Depressive symptoms and stressful life events	0.95	0.32	0.01	0.97	0.48	0.04
Depressive symptoms and social support	−0.80	0.45	0.08	−0.79	0.76	0.21

V(G)/Vp = SNP heritability estimate.
rG = bivariate REML analysis.
Model 1: Adjusted for age, principal components, and imputation group.
Model 2: Adjusted for Model 1 covariates and income, education, marital status.
All phenotypes were treated as continuous measures.
P-values for the bivariate REML analysis are one-sided and test whether the genetic correlation between depressive symptoms and each of the two environmental exposures is significantly different from zero.

to account for medication use. By harmonizing our depressive symptoms phenotype to theirs, we aimed to facilitate future replication efforts and increase interpretation of results across individual studies. However, there are certainly many alternative approaches, such as conducting the GWAS and GWEIS analyses after excluding medication users, or accounting for medication use using alternative adjustment algorithms (of note, including antidepressant medication use would not have been appropriate, for reasons outlined in the Supporting Information). Simulation studies are needed to fully evaluate the strengths and drawbacks of alternative approaches. Such studies could evaluate the extent to which different conditions (e.g., the percentage of the sample taking medications, the shape of the distribution of the outcome, the average effect sizes for the efficacy of medications, and differences in the distribution of outcome by medication use) produce different GWAS and GWEIS effect estimates.

As noted, future studies pursuing genome-wide environment interaction will require large samples. In the absence of a large sample, researchers can use several alternative approaches to GWEIS including: (1) testing for GxE with replicable variants identified from GWAS; (2) pursuing two-stage genome-wide GxE[82]; and (3) conducting gene pathway-by-environment interaction analyses [83] or polygenic risk score-by-environment interaction analyses.[84–86]

Several limitations should be noted. First, the outcome was based on a brief inventory of depressive symptoms during the past week, rather than levels of depressive symptoms captured over a longer period of time. Thus, it is unclear how long these symptoms lasted. However, the CES-D has demonstrated excellent psychometric properties, including in predicting DSM-IV diagnoses,[33,34] and its widespread use in epidemiological studies enabled us to conduct discovery and replication analyses. Future studies of trait or diagnostic measures of depressive symptoms in minority populations are needed. Second, the social-environmental exposures included in our GxE analyses were based on retrospective reporting and in the case of stressful life events, only captured the prior year. Thus, our study was not designed to capture whether genetic variation interacted with stressors experienced earlier in the lifespan. Prospective studies examining GxE at different stages of the lifespan are needed. Moreover, stressful life events and social support were assessed concurrently with depressive symptoms in the discovery sample as well as both replications. This may not be ideal, especially when studying the effects of stress, as prior work suggests the odds of depression is greatest in the same month of the stressor.[87] Longitudinal, prospective studies measuring social-environmental exposures antecedent to and close in time to depressive symptoms are necessary. These study designs are particularly important, as prior work suggests support for the 5-HTTLPR G×E, for example, is more consistent when structured interviews of stressful life events are used instead of self-report questionnaires.[88,89] Finally, our replication samples were smaller and more phenotypically heterogeneous than the discovery sample. For example, the WHI and HRS samples were of older adults, GTP comprised mostly middle-aged adults, and HCHS/SOL comprised a broader age range. The phenotypic measures also varied across these samples. Unfortunately, these limitations reflect the state of the field. Harmonizing data for GWAS and GxE analyses on a large scale in racial/ethnic minority populations is challenging. Whether our failure to replicate reflects Type I error in the discovery sample or Type II error in the replication is unknown. By undertaking these analyses, we hope to spark more large-scale epidemiological studies to incorporate such measures and to study the genetic determinants of depression in women, who are more burdened by the disorder than men.

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REFERENCES

1. Sullivan PF, Neale MC, Kendler KS. Genetic epidemiology of major depression: review and meta analysis. Am J Psychiatry 2000;157:1552–1562.
2. CONVERGE Consortium. Sparse whole-genome sequencing identifies two loci for major depressive disorder. Nature 2015;523(7562):588–591.

3. Major Depressive Disorder Working Group of the Psychiatric GWAS Consortium, Ripke S, Wray NR, et al. A mega-analysis of genome-wide association studies for major depressive disorder. Mol Psychiatry 2013;18(4):497–511.
4. Levinson DF, Mostafavi S, Milaneschi Y, et al. Genetic studies of major depressive disorder: why are there no genome-wide association study findings and what can we do about it? Biol Psychiatry 2014;76(7):510–512.
5. Flint J, Kendler KS. The genetics of major depression. Neuron 2014;81:484–503.
6. Hek K, Demirkan A, Lahti J, et al. A genome-wide association study of depressive symptoms. Biol Psychiatry 2013;73(7):667–678.
7. Terracciano A, Tanaka T, Sutin AR, et al. Genome-wide association scan of trait depression. Biol Psychiatry 2010;68(9):811–817.
8. Kendler KS, Gardner CO. Boundaries of major depression: an evaluation of DSM-IV criteria. Am J Psychiatry 1998;155:172–177.
9. Yang J, Wray NR, Visscher PM. Comparing apples and oranges: equating the power of case-control and quantitative trait association studies. Genet Epidemiol 2010;34:254–257.
10. Dunn EC, Brown RC, Dai Y, et al. Genetic determinants of depression: recent findings and future directions. Harv Rev Psychiatry 2015;23(1):1–18.
11. Caspi A, Sugden K, Moffitt TE, et al. Influence of life stress on depression: moderation by a polymorphism in the 5- HTT gene. Science 2003;301:386–389.
12. Dunn EC, Uddin M, Subramanian SV, Smoller JW, Galea S, Koenen KC. Gene-environment interaction (GxE) research in youth depression: a systematic review with recommendations for future research. J Child Psychol Psychiatry 2011;52(12):1223–1238.
13. Risch N, Herrell R, Lehner T, et al. Interaction between the serotonin transporter gene (5-HTTLPR), stressful life events, and risk of depression: a meta analysis. J Am Med Assoc 2009;301(23):2462–2471.
14. Munafo MR, Durrant C, Lewis G, Flint J. Gene X environment interactions at the serotonin transporter locus. Biol Psychiatry 2009;65:211–219.
15. Karg K, Burmeister M, Shedden K, Sen S. The serotonin transporter promoter variant (5-HTTLPR), stress, and depression meta analysis revisited: evidence of genetic moderation. Archives Gen Psychiatry 2011;68(5):444–454.
16. Duncan LE, Pollastri AR, Smoller JW. Mind the gap: why many geneticists and psychological scientists have discrepant views about gene-environment interaction (GxE) research. American Psychologist 2014;69(3):249–268.
17. van Os J, Rutten BP. Gene-environment-wide interaction studies in psychiatry. Am J Psychiatry 2009;166(9):964–966.
18. Winham SJ, Biernacka JM. Gene-environment interactions in genome-wide association studies: current approaches and new directions. J Child Psychol Psychiatry 2013;54(10):1120–1134.
19. Wu C, Kraft P, Zhai K, et al. Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nat Genet 2012;44(10):1090–1097.
20. Seigert S, Hampe J, Schafmayer C, et al. Genome-wide investigation of gene-environment interactions in colorectal cancer. Hum Genet 2013;132(2):219–231.
21. Manning AK, Hivert MF, Scott RA, et al. A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nat Genet 2012;44:659–669.
22. Whitfield KE, Edwards CL, Brandon D, McDougald C. Genetic and environmental influences on depressive symptoms by age and gender in African American twins. Aging Ment Health 2008;12(2):221–227.
23. Duncan AE, Munn-Chernoff MA, Hudson DL, et al. Genetic and environmental risk for major depression in African-American and European-American women. Twin Res Hum Genet 2014;17(4):244–253.
24. Olvera RL, Bearden CE, Velligan DI, et al. Common genetic influences on depression, alcohol, and substance use disorders in Mexican-American families. Am J Med Genet B Neuropsychiatr Genet 2011;156B(5):561–568.
25. Kessler RC, Berglund P, Demler O, Jin R, Koretz D, et al. The epidemiology of major depressive disorder: results from the National Comorbidity Survey Replication (NCS-R). J Am Med Assoc 2003;289:3095–3015.
26. Hatch SL, Dohrenwend BP. Distribution of traumatic and other stressful life events by race/ethnicity, gender, SES, and age: a review of the research. Am J Community Psychol 2007;40: 313–332.
27. Williams DR, Mohammed SA. Discrimination and racial disparities in health: evidence and needed research. J Behav Med 2009;32:20–47.
28. Mays VM, Cochran SD, Barnes NW. Race, race-based discrimination, and health outcomes among African Americans. Ann Rev Psychology 2007;58:201–225.
29. Crimmins EM, Hayward MD, Seeman TE. Race/ethnicity, socioeconomic status, and health. In: Anderson NB, Bulatao RA, Cohen B, editors. Critical Perspectives on Racial and Ethnic Differences in Health in Late Life. Washington, DC: The National Academies Press; 2004.
30. Kessler RC, Berglund P, Demler O, Jin R, Merikangas KR, Walters EE. Lifetime prevalence and age-of-onset distributions of DSM-IV disorders in the National Comorbidity Survey Replication. Archives Gen Psychiatry 2005;62(6):593–602.
31. Design of the Women's Health Initiative clinical trial and observational study. The Women's Health Initiative Study Group. Control Clinical Trials 1998;19:61–109. http://www.ncbi.nlm.nih.gov/pubmed/9492970
32. Wassertheil-Smoller S, Shumaker S, Ockene J, et al. Depression and cardiovascular sequela in postmenopausal women: The Women's Health Initiative (WHI). Archives Intern Med 2004;164:289–298.
33. Radloff LS. The CES-D scale: a self-report depression scale for research in the general population. Appl Psychol Measure 1977;1:385–401.
34. Irwin M, Artin KH, Oxman MN. Screening for depression in the older adult: criterion validity of the 10-item Center for Epidemiological Studies Depression Scale (CES-D). Arch Intern Med 1999;159(15):1701–1704.
35. Levy D, DeStefano AL, Larson MG, et al. Evidence for a gene influencing blood pressure on chromosome 17: genome scan linkage results for longitudinal blood pressure phenotypes in subjects from the Framingham Heart Study. Hypertension 2000;36(4):477–483.
36. Wade TD, Kendler KS. The relationship between social support and major depression: cross-sectional, longitudinal, and genetic perspectives. J Nerv Ment Dis 2000;188(5):251–258.
37. Berkman LF, Syme SL. Social networks, host resistance, and mortality: a nine-year follow-up study of Alameda County residents. Am J Epidemiol 1979;109(2):186–204.
38. Smoller JW, Pollack MH, Wassertheil-Smoller S, et al. Panic attacks, daily life ischemia, and chest pain in postmenopausal women. Psychosom Med 2006;68(6):824–832.
39. Sherbourne CD, Stewart AL. The MOS social support survey. Soc Sci Med 1991;32(6):705–714.

40. Women's Health Initiative SHARe Project. Imputation Report - 1000 Genomes Project Reference Panel; 2011. Available at: https://www.garnetstudy.org/sites/www/content/files/dataflow-cleaning/WHI_SHARe_qc_report_1000G_final.pdf.
41. Browning B, Browning SA. A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. Am J Human Genet 2009;84:210–223.
42. Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis corrects for stratification in genome-wide association studies. Nat Genet 2006;38:904–909.
43. Purcell S, Neale B, Todd-Brown K, et al. PLINK: a toolset for whole-genome association and population-based linkage analysis. Am J Human Genet 2007;81(3):559–575.
44. Pirinen M, Donnelly P, Spencer CCA. Including known covariates can reduce power to detect genetic effects in case-control studies. Nat Genet 2012;44(8):848–851.
45. R Development Core Team. R: A Language and Environment for Statistical Computing. Vienna, Austria: R Foundation for Statistical Computing; 2011.
46. Pruim RJ, Welch RP, Sanna S, et al. LocusZoom: regional visualization of genome-wide association scan results. Bioinformatics 2010;26(18):2336–2337.
47. Willer CJ, Li Y, Abecasis GR. METAL: fast and efficient meta-analysis of genomewide association scans. Bioinformatics 2010;26(17):2190–2191.
48. Aulchenko YS, Struchalin MV, vanDuijn CM. probABEL package for genome-wide association analysis of imputed data. BMC Bioinformatics 2010;11:134.
49. Altman DG, Royston P. The cost of dichotomising continuous variables. Brit Med J 2006;332(7549):1080.
50. White H. A heteroskedasticity-consistent covariance-matrix estimator and a direct test for heterodkedasticity. Econometrica 1980;48:817–838.
51. Voorman A, Lumley T, McKnight B, Rice K. Behavior of qq-plots and genomic control in studies of gene-environment interaction. Plos One 2011;65(5):e19416.
52. Cornelis MC, Tchetgen EJ, Liang L, et al. Gene-environment interactions in genome-wide association studies: a comparative study of tests applied to empirical studies of type 2 diabetes. Am J Epidemiol 2012;175(3):191–202.
53. Almli LM, Duncan R, Feng H, et al. Correcting systematic inflation in genetic association tests that consider interaction effects: application to a genome-wide association study of posttraumatic stress disorder. J Am Med Assoc Psychiatry 2014;71(12):1392–1399.
54. Juster FT, Suzman R. An overview of the health and retirement study. J Human Res 1995;30:S7–S56.
55. Sonnega A, Faul JD, Ofstedal MB, Langa KM, Phillips JWR, Weir DR. Cohort profile: the health and retirement study (HRS). Int J Epidemiol 2014;43(2):576–585.
56. Gillespie CF, Bradley B, Mercer K, et al. Trauma exposure and stress-related disorders in inner city primary care patients. Gen Hosp Psychiatry 2009;31(6):505–514.
57. Beck AT, Ward CH, Mendelson M, Mock J, Erbaugh J. An inventory for measuring depression. Archives Gen Psychiatry 1961;4:561–571.
58. Cohen S, Mermelstein R, Kamarck T, Hoberman H. Measuring the functional components of social support. In: Sarason IG, Sarason B, editors. Social Support: Theory, Research, and Application. Netherlands: Springer; 1985:73–94.
59. Yang J, Lee SH, Goddard ME, Visscher PM. GCTA: a tool for genome-wide complex trait analysis. Am J Human Genet 2011;88:76–82.
60. Lee SH, Ripke S, Neale BM, et al. Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nat Genet 2013;45(9):984–994.
61. Lubke GH, Hottenga JJ, Walters R, et al. Estimating the genetic variance of major depressive disorder due to all single nucleotide polymorphisms. Biol Psychiatry 2012;72(8):707–709.
62. Lee SH, Yang J, Goddard ME, Visscher PM, Wray NR. Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. Bioinformatics 2012;28(19):2540–2542.
63. Canty A, Ripley B. boot: Boostrap R (S-Plus) Functions. R package version 1.3-17. 2015. https://cran.r-project.org/web/packages/boot/citation.html
64. Davison AC, Hinkley DV. Bootstrap Methods and Their Applications. Cambridge: Cambridge University Press; 1997.
65. Buzkova P, Lumley T, Rice K. Permutation and parametric bootstrap tests for gene-gene and gene-environment interactions. Ann Hum Genet 2011;75(1):36–45.
66. van Belle G. STRUTS: Statistical Rules of Thumb. New York, NY: John Wiley and Sons; 2002.
67. Kraft P, Hunter DJ. The challenge of assessing complex gene-environment and gene-gene interactions. In: Khoury MJ, Bedrosian SR, Gwinn M, Higgins JPT, Ioannidis JPA, Little J, editors. Human Genome Epidemiology: Building the Evidence for Using Genetic Information to Improve Health and Prevent Disease. 2nd ed. New York, NY: Oxford University Press; 2009.
68. Duncan LE, Keller MC. A critical review of the first 10 years of candidate gene-by-environment interaction research in psychiatry. Am J Psychiatry 2011;168(10):1041–1049.
69. Ware EB, Mukherjee B, Sun YV, Diez-Roux AV, Kardia SL, Smith JA. Comparative genome-wide association studies of a depressive symptom phenotype in a repeated measures setting by race/ethnicity in the Multi-Ethnic Study of Atherosclerosis. BMC Genet 2015;16:118.
70. Bonaventure P, Liu C, Lee G, et al. GPR139, an Orphan Receptor Highly Enriched in the Habenula and Septum, is Activated by the Essential Amino Acids L-Tryptophan and L-Phenylalanine. Poster presented at: American College of Neuropsychopharmacology. Hollywood, FL; 2015.
71. Li K, Zhou T, Liao L, et al. betaCaMKII in lateral habenula mediates core symptoms of depression. Science- 2013;341(6149):1016–1020.
72. Cross-Disorder Group of the Psychiatric Genomics Consortium. Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. Lancet 2013;381(9875):1371–1379.
73. Schizophrenia Working Group of the Psychiatric Genomics C. Biological insights from 108 schizophrenia-associated genetic loci. Nature 2014;511(7510):421–427.
74. Manitt C, Labelle-Dumais C, Eng C, et al. Peri-pubertal emergence of UNC-5 homologue expression by dopamine neurons in rodents. PLoS One 2010;5(7):e11463.
75. Manitt C, Eng C, Pokinko M, et al. dcc orchestrates the development of the prefrontal cortex during adolescence and is altered in psychiatric patients. Transl Psychiatry 2013;3:e338.
76. Luan JA, Wong MY, Day NE, Wareham NJ. Sample size determination for studies of gene-environment interaction. Int J Epidemiol 2001;30(5):1035–1040.

77. Thomas D. Methods for investigating gene-environment interactions in candidate pathway and genome-wide association studies. Annu Rev Publ Health 2010;31:21–36.
78. Hardy J, Low NC. Genes and environment in psychiatry: winner's curse or cure? Archives Gen Psychiatry 2011;68(5):455–456.
79. Trzaskowski M, Dale PS, Plomin R. No genetic influence for childhood behavior problems from DNA analysis. J Am Acad Child Adolesc Psychiatry 2013;52(10):1048–1056 e1043.
80. Sieradzka D, Power RA, Freeman D, Cardno AG, Dudbridge F, Ronald A. Heritability of Individual Psychotic Experiences Captured by Common Genetic Variants in a Community Sample of Adolescents. Behav Genet 2015;45(5):493–502.
81. Power RA, Wingenbach T, Cohen-Woods S, et al. Estimating the heritability of reporting stressful life events captured by common genetic variants. Psychol Med 2013;43(9):1965–1971.
82. Gauderman WJ, Zhang P, Morrison JL, Lewinger JP. Finding novel genes by testing GxE interactions in a genome-wide association study. Genet Epidemiol 2013;37:603–613.
83. Sharafeldin N, Slattery ML, Liu Q, et al. A candidate-pathway approach to identify gene-environment interactions: analyses of colon cancer risk and survival. J Natl Cancer Inst 2015;107(9). pii: djv160. http://www.ncbi.nlm.nih.gov/pubmed/26072521
84. Musliner KL, Seifuddin F, Judy JA, Pirooznia M, Goes FS, Zandi PP. Polygenic risk, stressful life events and depressive symptoms in older adults: a polygenic score analysis. Psychol Med 2015;45(8):1709–1720.
85. Peyrot WJ, Milaneschi Y, Abdellaoui A, et al. Effect of polygenic risk scores on depression in childhood trauma. Brit J Psychiatry 2014;205(2):113–119.
86. Mullins N, Power RA, Fisher HL, et al. Polygenic interactions with environmental adversity in the aetiology of major depressive disorder. Psychol Med 2015:1–12.
87. Kendler KS, Karkowski LM, Prescott CA. Causal relationship between stressful life events and the onset of major depression. Am J Psychiatry 1999;156(6):837–841.
88. Uher R, McGuffin P. The moderation by the serotonin transporter gene of environmental adversity in the aetiology of mental illness: review and methodological analysis. Mol Psychiatry 2008;13:131–146.
89. Caspi A, Hariri AR, Holmes A, Uher R, Moffitt TE. Genetic sensitivity to the environment: Rhe case of the serotonin transporter gene and its implications for studying complex diseases and traits. Am J Psychiatry 2010;167(5): 1–19.

Supplemental Materials

Genome-Wide Association Study (GWAS) and Genome-Wide by Environment Interaction Study (GWEIS) of Depressive Symptoms in African American and Hispanic/Latina Women

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Description of Discovery and Replication Samples: Sampling, Genotyping, and Statistical Analyses

A. Women's Health Initiative (WHI) SNP Health Association Resource (SHARe)

As described elsewhere [1; 2] (www.whi.org), the WHI consists of an observational study (WHI-OS) and randomized clinical trial (WHI-CT). The WHI-OS has prospectively followed 93,676 postmenopausal women ages 50-79 recruited from 40 clinical centers in the United States between October 1 1993 and December 31 1998. The WHI-CT enrolled 68,132 postmenopausal women of the same age and between the same time period to participate in one of three prevention trials: (1) hormone therapy; (2) dietary modification; and (3) calcium/vitamin D. We analyzed data from 7,480 African American and 3,352 Hispanic women who were genotyped as part of the WHI SNP Health Association Resource (SHARe), a sub-study of self-reported minority women in WHI.

From the WHI cohort, 12,500 African American or Hispanic women were chosen based on appropriate consent and available DNA to make up the SHARe sample. Participants in both the WHI-OS and WHI-CT components were included. An initial cohort included 12,156 African American or Hispanic women, divided nearly equally between WHI-OS (African American N=3869, 45%; Hispanic N=1753, 48%) and WHI-CT (African American N=4646, 55%; Hispanic N=1888, 52%) components. Of these 12,156 women, there were 99 could not be genotyped. In addition subjects with call rate<95% (N=16), who were duplicates (N=34) or had a Y chromosome (N=1) were removed, leaving a cohort of 12,008 women. Only data from the 10,832 (7,480 African American and 3,352 Hispanic/Latina women) consented to be included in studies for general research use are included in this analysis; data from these women were included in the database of Genotypes and Phenotypes (dbGaP).

Of note, the inclusion criteria are quite different between observational and clinical trial studies. Indeed, subjects included in the observational study (OS) are primarily those who did not want to participate in the clinical trial portion (CT), or who did not meet eligibility criteria. Though in some cases subjects were recruited directly for the observational study. This distinction is somewhat diluted by the fact that the clinical trial component is made up of three different clinical trials, each with distinct inclusion criteria, including diet modification, Vitamin D supplementation, and hormone therapy. Given the significant variation within the clinical trial cohort, it is less likely that there is a consistent bias introduced because of differences in inclusion criteria. The difference in inclusion criteria between CT and OS will likely lead to overall differences between those two groups as a whole. However, in the SHARe cohort, which is split nearly equally between the two groups (OS and CT), the distinction may contribute to a more representative sample, since subjects who would meet inclusion criteria are not over represented as they would be if the observational study was a population cohort.

All participants were genotyped using the Affymetrix 6.0 chip designed to human genome build 36. Genotyping, on all samples plus 2% blinded duplicates, was performed at Affymetrix, Inc., Santa Clara, CA. A total of 720,101 (African Americans) and 709,042 (Hispanics) SNPs passed pre-imputation filters. Data cleaning and harmonization were performed at the Fred Hutchinson Cancer Research Center (FHCRC) in Seattle, WA. As described elsewhere [3], the WHI GARNET Coordinating Center (www.garnetstudy.org) imputed additional SNPs using the 1000 Genomes reference panel build 37 (release December 2010 interim) and BEAGLE software version 3.3.1 [4]. SNPs were selected for imputation based on mapping to build 37 and meeting several quality filters. Specifically, SNPs with low concordance rates (<98% ascertained from duplicate samples), and low call rates (<95%) were excluded from imputation and SNPs with minor allele frequency (MAF) of ≥ 1% and Hardy-Weinberg equilibrium p-values > 0.0001 were included. Imputation was performed in three groups (two African American groups and one Hispanic/Latina group). Imputation for the African American group was randomly divided into two groups of roughly equal size to minimize computation time. A combined African and European panel was used to impute the African American samples. A combined panel of Asian, European, African, and American samples was used to impute the Hispanic/Latina sample.

Allele dosages (the probability of each of the three genotypes, reflecting the level of certainty in the genotype prediction) were imputed for autosomes (7,500,448 imputed SNPs in Hispanics; 8,731,206 imputed SNPs in African Americans); and the X chromosome. After filtering, the total number of SNPs passing our filters was similar for African American (5,489,102) and Hispanic/Latina women (5,297,172).

Both GWAS analyses (and the GWEIS) adjusted for the following covariates, measured at baseline: age (ages 50-59- referent; ages 60-69; ages 70-79), income (1=less than 19,000-referent; 2=20,000-49,000; 3=50,000 and above; 4=missing), education (1=less than high school-referent; 2=high school/vocational technical training; 3=some college or Associates degree; 4=college degree; 5=graduate school or degree; 6=missing), marital status (1=never married-referent; 2=divorced/separated; 3=widowed; 4=married/married like relationship; 5=missing), and four principal components generated by the WHI GARNET Coordinating Center using EIGENSTRAT [5] to adjust for population structure [3]. In the analyses with African Americans, we also adjusted for imputation group (group 1 versus group 2) as the imputation was conducted in two groups.

B. Grady Trauma Project (GTP)

The Grady Trauma Project (GTP) is a cross-sectional study that has genotyped approximately 4000 individuals and collected phenotype data on multiple psychiatric disorders, including post-traumatic stress disorder, Major Depressive Disorder, as well as exposure to child trauma [6]. GTP participants are predominately urban, low socioeconomic status adults (mean age 40 years) of African American ancestry with high rates of current PTSD (estimated at 30%). Participants were recruited from waiting rooms in the gynecology and primary care medical (non-psychiatric) clinics at Grady Memorial Hospital, a publicly funded hospital in Atlanta, Georgia. To be eligible for participation, participants had to be between 18-65 years of age, not actively psychotic, and able to give informed consent. After signing an informed consent approved by the Emory Institutional Review Board, trained research assistants administered the interview consisting of questionnaires. The interview took 45-75 minutes to complete. Additional details about the cohort are available here: http://gradytraumaproject.com

GTP participants provided a blood and/or saliva sample (Oragene saliva kits; DNAGenotek, Ottawa, Ontario, Canada). DNA was extracted from saliva using the Agencourt DNAdvance Nucleic Acid Isolation Kit (Beckman Coulter, Inc., Brea, CA), or from blood using either the E.Z.N.A. Mag-Bind Blood DNA Kit (Omega Bio-Tek, Inc., Norcross, GA) or ArchivePure DNA Blood Kit (5 Prime, Inc, Gaithersburg, MD). Genome-wide genotyping was conducted using Illumina's Omni1-Quad BeadChip, which captures 1,011,219 individual SNPs. Genotypes were then called using Illumina's GenomeStudio software. The quality control parameters for retaining SNPs and subjects were: SNP missingness < 0.05 (before sample removal); subject missingness < 0.02; autosomal heterozygosity deviation (imbreeding coefficient:| Fhet | < 0.2); SNP missingness < 0.02 (after sample removal); differential missingness between cases and controls < 0.02; and Hardy-Weinberg equilibrium (P > 10−6 in controls or P > 10−10 in cases).

Genotype imputation was performed using the pre-phasing/imputation stepwise approach implemented in SHAPEIT / IMPUTE2 (imputing chromosomal chunk size of 3 Mb using default parameters). The imputation reference set consisted of 2,186 phased haplotypes from the full 1000 Genomes Project dataset (August 2012, 30,069,288 variants, release "v3.macGT1" http://mathgen.stats.ox.ac.uk/impute/data_download_1000G_phase1_integrated.html). After imputation, SNPs with high imputation quality (INFO >0.8) and low missingness (<1%) were identified for further quality control. After linkage disequilibrium pruning ($r^2 > 0.02$) and frequency filtering (MAF > 0.05), there were 100,151 autosomal SNPs. This SNP set was used for robust relatedness testing and population structure analysis. Relatedness testing was done with PLINK, and among pairs of subjects with PI_HAT > 0.2, one member of each pair was removed at random after preferentially retaining post-traumatic stress disorder (PTSD, the original study phenotype) cases over controls. Principal component analysis was done with the same collection of autosomal SNPs. Further quality control of the imputed data included INFO > 0.1 and MAF > 0.005.

In the female GTP sample, we sought to replicate top findings from the GWAS ($p<1x10^{-6}$) using linear regression under an additive model. After removing individuals receiving treatment for schizophrenia (N=127), the GTP GWAS analyses adjusted for the following covariates: age (quartiles: ages 18-25- referent; ages 26-37; ages 38-50, ages 51-65), income per month (1=less than 499-referent; 2=500-999; 3=1000-1999; 4=2000 or more), education (1=less than high school-referent; 2=high school graduate/GED; 3=some college/technical school graduate;4=college graduate; 5=graduate school or degree), marital status (1=single or never married-referent; 2=married; 3=divorced/separated; 4=widowed; 5=domestic partner). In addition, the top 5 principal components were included as covariates to adjust for population structure.

C. Hispanic Community Health Study/Study of Latinos (HCHS/SOL)

The Hispanic Community Health Study (HCHS)/Study of Latinos (SOL) is a community-based prospective cohort study of 16,415 self-identified Hispanic/Latino persons (aged 18-74 at screening) from randomly selected households in four U.S. field centers (Chicago, IL; Miami, FL; Bronx, NY; San Diego, CA) with baseline examination (2008 to 2011) and yearly follow-up by telephone for at least three years. The HCHS/SOL cohort includes participants who self-identified as having Hispanic/Latino background, the largest groups being Central American (n=1,730), Cuban (n=2,348), Dominican (n=1,460), Mexican (n=6,471), Puerto-Rican (n=2,728), and South American (n=1,068). The goals of the HCHS/SOL are to describe the prevalence of risk and protective factors for chronic conditions (such as diabetes, pulmonary disease, and cardiovascular disease), and to quantify mortality and disease exacerbation over time. The baseline clinical examination [7] included comprehensive biological (e.g., anthropometrics, blood draw, oral glucose tolerance test, ankle brachial pressure index, electrocardiogram), behavioral (e.g. dietary intake, physical activity, overnight sleep exam, tobacco and alcohol use), and socio-demographic (e.g., socioeconomic status, migration history) assessments.

The sample design and cohort selection has been previously described [8]. Briefly, a stratified two-stage area probability sample of household addresses was selected in each of the four field centers. The first sampling stage selected census block groups, and the second stage selected households within each block group. Both stages oversampled certain strata to increase the likelihood that a selected address yielded a Hispanic/Latino household. Households were screened for eligibility, and the 45-74 age group was oversampled. The unequal probabilities of selection in the HCHS/SOL cohort are taken into account by including a trimmed and calibrated sampling weight as a covariate in the association tests.

HCHS/SOL subjects who consented to have their DNA extracted for genetic studies had blood samples sent to Illumina Microarray Services for genotyping on the Illumina SOL HCHS Custom 15041502 B3 array. This array comprised the Illumina Omni 2.5M array (HumanOmni2.5-8v1-1) and additional custom content selected for HCHS/SOL, including ancestry-informative markers, variants characteristic of Amerindian populations, known GWAS hits, and other candidate gene markers. Quality assurance/quality control (QA/QC) was performed by Illumina, LA Biomed, and the HCHS/SOL Genetic Analysis Center (GAC) according to recommended methods [9] to generate recommended SNP and sample-level quality filters. In brief, samples were checked for annotated versus genetic sex, gross chromosomal anomalies [10], call rates, batch effects, duplicate sample discordance, Mendelian errors, relatedness, and population structure. 12,803 unique study samples passed these criteria and were used for association testing. SNPs that passed the Illumina/LA Biomed assay failure indicator were further checked for Hardy-Weinberg equilibrium, MAF, duplicate probe discordance, and missing call rate. A total of 2,232,944 SNPs passed both quality and informativeness filters (unduplicated on the array and polymorphic)

Genome-wide imputation was carried out on all 12,803 samples together using the 1000 Genomes Project phase 1 reference panel [11] and IMPUTE2 software [12; 13]. Genotypes were first pre-phased with SHAPEIT2 (v2.r644) and then imputed with IMPUTE2 (v2.3.0). Only variants with at least two copies of the minor allele present in any of the four 1000 Genomes continental panels were imputed, yielding a total of 25,568,744 imputed variants. Overall imputation quality was assessed both by looking at the distribution of imputed quality metrics by different MAF levels and by examining results from the IMPUTE2 internal masking experiments (as some genotyped variants were "masked", meaning removed from the imputation basis).

The following approach was used to simultaneously characterize population structure and relatedness between individuals within sub-populations, in the presence of admixed individuals.

1. Estimate relatedness using KING-robust [14], which is robust to discrete population structure but not to admixture or departures from HWE within sub-populations.
2. Use PC-AiR[15] to find ancestry-representative principal components with the following steps:
    a) Partition the sample into a mutually unrelated set and the remaining (relatives of the unrelated set)
    b) Perform standard principal components analysis (PCA) on the set of unrelated individuals
    c) Predict sample eigenvectors for the set of related individuals based on genetic similarity
3. Re-estimate relatedness using PC-Relate [16], which uses sample eigenvectors to provide unbiased kinship coefficients in the presence of population structure, admixture and HWE departures.
4. Repeat steps 2-3 to obtain final sets of sample eigenvectors and kinship coefficients .

This procedure identified 19 individuals with primarily East Asian ancestry, who were excluded from analysis and the above procedure was repeated for the remaining 12,784 samples.

From the HCHS/SOL sample set, 3,371 females aged at least 50 were selected to match the demographics of the WHI sample set. The GWAS analyses used a linear mixed-effect model to account for the correlations between individuals due to genetic relatedness (kinship), shared household, and block group. These correlation matrices were modeled as random effects. The analyses also adjusted for the following covariates as fixed effects: log(sampling weight), field center, age (decades: ages 50-59- referent; ages 60-69; ages 70-76), education (1=no high school diploma or GED- referent, 2=at most a High school diploma or GED, 3=greater than high school (or GED) education, 4=bachelors degree, 5=masters, professional, or doctorate degree), marital status (1=single- referent, 2=married or partnered, 3=divorced or separated, 4=widowed). In addition, the top 5 principal components were included as covariates to adjust for population stratification. Income was not included due to high levels of missing data.

D. Health and Retirement Study (HRS)

The Health and Retirement Study (HRS) is a longitudinal panel study that surveys a representative sample of approximately 20,000 Americans over the age of 50 every two years. The study collects information about income and wealth, health and use of health services, cognition and physical functioning, work and retirement, and family connections [17; 18]. DNA was extracted from buccal swabs or saliva collected during a face-to-face interview in the respondents' homes. These data represent respondents who provided DNA samples and signed consent forms in 2006 (Phase 1), 2008 (Phase 2), and 2010 (Phase 3).

Respondents were excluded from this analysis if they were male, less than 40 years of age, had a low cognitive score (equivalent of MMSE < 22), or had missing genotype or phenotype data. A total of 1231 African Americans were included in the GWAS analysis. Average age at assessment was 62.09 years (sd=7.84). A total of 129 (10.48%) were using antidepressant medications, which were assessed from self-reported use of medications for depression. The GWEIS analysis included 952 respondents, where mean age was 62.60 (sd=7.71) and 95 (9.98%) were using antidepressant medication.

DNA was collected either from buccal swabs and extracted using the Qiagen Autopure method (Phase 1 samples), or from saliva samples extracted with Oragene (Phase 2 and Phase 3 samples). The DNA samples were genotyped at the Center for Inherited Disease Research (CIDR) using the Illumina HumanOmni2.5 array. DNA samples from Phases 1 and 2 were called together, and DNA samples from Phase 3 were called subsequently. GenomeStudio version 2011.2, Genotyping Module 1.9.4, and GenTrain version 1.0 were used for all genotype calling. A total of 12,507 subjects from Phase 1-2 and 3,175 subjects from Phase 3 were successfully genotyped by CIDR. The Genetics Coordinating Center of the University of Washington subsequently applied quality assurance / quality control methods [9] to generate recommended SNP and sample level quality filters. In brief, samples were checked for annotated versus genetic sex, gross chromosomal anomalies [10], relatedness and population structure, missing call rates, batch effects, duplicate sample discordance, and Mendelian errors. At the SNP level, checks were performed for Hardy-Weinberg equilibrium (separately within subsamples of non-Hispanic whites and African Americans), MAF, duplicate probe discordance, and missing call rate.

Genome-wide imputation was carried out using the 1000 Genomes Project phase 1 reference panel [11] and IMPUTE2 software [12; 13]. A total of 15,620 samples were imputed together (12,505 Phase 1-2 samples and 3,115 Phase 3 samples) using genotyped SNPs passing the quality filter and representing unique genomic positions. Genotypes were first pre-phased with SHAPEIT2 and then imputed with IMPUTE2 (v2.3.0). Only variants with at least four copies of the minor allele present in any of the four 1000 Genomes continental panels were imputed, yielding a total of 23,070,889 imputed variants. Overall imputation quality was assessed both by looking at the distribution of imputed quality metrics across the MAF spectrum and by examining results from the IMPUTE2 internal masking experiments.

The GWAS and GWEIS analyses adjusted for the following covariates: income (1=<19,000; 2=20,000-49,000; 3=50,000+; 4=missing), age (1=50-60, 2=60-70, 3=70-80), education (1=less than high school, 2=high school/GED, 3=some college or two year college degree, 4=college degree, 5=graduate degree, 6=missing), marital status (1=never married, 2=divorced/separated, 3=widowed, 4=married/partnered, 5=missing), and the top 10 PCs. Income, age, education and marital status were treated as categorical variables and PCs were treated as continuous variables. Both the GWAS and GWEIS replications were conducted using R 3.0.1, where A1 was the tested allele for GWAS and A2 was the tested allele for GWEIS replication.

E. Adjustment for Antidepressant Medications

As CES-D scores in this population-based sample could have been influenced by antidepressant medication use, we used a nonparametric imputation algorithm developed in a previous GWAS of depressive symptoms[19] to adjust the CES-D score of women taking antidepressants (as determined by pill bottles women brought to the baseline interview). This algorithm made two assumptions: (1) the CES-D score of a woman taking antidepressants is *lower* (i.e., indicating fewer depressive symptoms) than would be expected if she were not taking antidepressants; (2) women with high CES-D scores, on average, respond less to their antidepressant than women with lower CES-D scores. We therefore replaced the CES-D score of women on antidepressants (n=429) with the mean depressive symptom score of all persons using antidepressants that had the same or a higher CES-D score. For example, an antidepressant user with an observed CES-D score of 4 would have a revised score of 7.11 (derived by taking the average CES-D scores of antidepressant users with a CES-D value of 4 or greater). Thus, CES-D scores for all antidepressant users were increased through this algorithm (average difference=2.21). This algorithm was based on one used to adjust blood pressure for persons on antihypertensive medications [20].

As described in the Discussion section of the paper, there are certainly many alternative approaches. Of note, we decided not to treat antidepressant medication use as a covariate for the following reasons. There are two reasons to treat a given variable as a covariate. The first is because it is a precision variable, meaning a variable that improves the model's prediction of the trait. Thus, by including the precision variable in the analysis, we are able to reduce the variance in the outcome and increase power (to capture the predictive ability of other variables in the model). The second is because the variable is a confounder, which in this case would be a variable that is associated with both the genotype and depressive symptoms. Whether medication use is a precision variable or a confounder, inclusion of medication use as a covariate means that we then estimate its association with depressive symptoms conditioned on all other variables in the model. However, the effect of medication use on depressive symptoms cannot be estimated by the model in this way, since a woman who uses medications has a reduced depressive symptom score compared to what it would actually be had she not been using medication.

F. Conduct of the GWEIS Analysis

We performed the GWEIS using probABEL [21]. Both stressful life events and social support were modeled separately using a categorical variable derived by taking quartiles of the total score distribution (0=first quartile; 1=second quartile; 2=third quartile; 3=fourth quartile). The lowest quartile group (0) was used to indicate the lowest social-environmental risk group, whereas the highest quartile group (3) indicated the highest social-environmental risk group. We tested for GxE by including dummy variables for quartile group as well as a SNP by quartile-group (treated as ordinal) interaction term in the model. Thus, the GxE analysis included the SNP main effect, the environmental main effect (i.e., 3 of the categorical variables, with the omitted group being the 0 quartile group), and a cross-product interaction term corresponding to the test for interaction between the SNP and an interval variable corresponding to level of quartile group (0,1,2, or 3).

We used a Bonferroni correction to establish a significance threshold accounting for multiple testing of two environmental exposures (alpha=2.5×10^{-8}). To reduce the likelihood of spurious GxE findings, we used model-robust estimates of standard errors (also known as sandwich standard errors) [22] in all tests of GxE. Prior work suggests robust variance estimates can reduce the possibility of inflated Type I errors found for GxE effects if the environmental main effect is misspecified or if there is departure from the presumed linear model [23-25]. P-values corresponding to the interaction term (in the multiple regression model) were calculated in R based on a Wald chi-square test.

Description of Phenotypes in Each Sample

A. Depressive Symptoms

Table 1 below summarizes the individual items used to capture depressive symptoms across each of the studies. The table is organized by the WHI indicators to show where similar items were assessed across each study.

WHI. Depressive symptoms were assessed at enrollment using total scores from a six-item version of the Center for Epidemiological Studies of Depression Scale (CES-D) [26], which is arguably the most widely-used measure of depressive symptoms in epidemiological studies. The six item CES-D captured core symptoms of major depressive disorder (MDD) in the past week, including anhedonia, depressed mood, and behavioral symptoms (e.g., felt depressed; sleep was restless; enjoyed life; had crying spells; felt sad; felt people disliked you). These items were combined into a total score, derived by summing the individual items (after reverse coding item 3); higher scores indicated higher depressive symptoms. The six item scale has been found to correlate highly with the full 20 item scale (r=0.88) [2].

GTP. Depressive symptoms were measured using the Beck Depression Inventory, Second Edition (BDI-II) [27], which is a 21-item psychometrically validated, widely used, continuous measure of current depressive symptoms The self-report measure contains items assessing the presence and severity of depressive symptoms over the past two weeks rated on a scale of 0 to 3. Responses are summed to yield a total BDI score, with raw scores indicating minimal depression (0-13), mild depression (14-19), moderate depression (20-28), and severe depression (29-63). Evidence for the BDI's reliability and validity has been shown across different populations and cultural groups in individuals ranging from 13 to 80 years of age [28; 29].

The original BDI was revised in 1996 to be more consistent with Major Depressive Disorder criteria in the Diagnostic and Statistical Manual of Mental Disorders, Fourth Edition (DSM-IV).

HCHS/SOL. Depressive symptoms were measured using a 10-item CES-D, which asked respondents to report how often in the past week they experienced each symptom. Response options ranged from 0=rarely or none of the time (<1 day) to 3=all of the time (5-7 days).

HRS. Depressive symptoms were measured in the HRS using an 8-item CES-D, which asked respondents whether they experienced each symptom much of the time during the past. Response options were yes/no. Positive items were reverse scored.

Table 1. Summary of depressive symptoms indicators used across each study

WHI (6-item CES-D)	**GTP (21 item Beck)**	**HCHS/SOL (10-item CES-D)**	**HRS (8-item CES-D)**
You felt depressed		I felt depressed.	You felt depressed.
Your sleep was restless	Changes in Sleeping Patterns	My sleep was restless.	Your sleep was restless
You enjoyed life	Loss of Pleasure Loss of Interest		
You had crying spells	Crying		
You felt sad	Sadness		You felt sad
You felt that people disliked you	Self-Dislike		
	Pessimism		
	Past Failure		
	Guilty Feelings		
	Punishment Feelings		
	Tiredness or fatigue	I could not “get going”.	You could not get going.
	Self-Criticalness		
	Suicidal Thoughts or Wishes		
	Lost of interest in sex		
	Indecisiveness		
	Worthlessness		
	Loss of Energy	I felt that everything I did was an effort.	You felt that everything you did was an effort.
	Irritability		
	Changes in Appetite		
	Concentration difficulty	I had trouble keeping my mind on what I was doing.	
	Agitation	I was bothered by things that usually don’t bother me.	
		I felt hopeful about the future.	
		I felt fearful.	
		I was happy.	You were happy.
		I felt lonely.	You felt lonely.
			You enjoyed life.

B. Social Support

WHI. Social support was assessed using nine items from the 19-item Medical Outcome Survey [30]. Women rated how often they experienced social support (1=none of the time to 4=all of the time). These nine items were: (1) Someone you can count on to listen to you when you need to talk; (2) someone to give you good advice about a problem; (3) someone to take you to the doctor if you need it; (4) someone to have a good time with; (5) someone to help you understand a problem when you need it; (6) someone to help with daily chores if you are sick; (7) someone to share your most private worries and fears; (8) someone to do something fun with; and (9) someone to love you and make you feel wanted. We summed across items to obtain a measure for levels of perceived social support. We then used quartiles in this distribution of level of social support to create a set of categorical variables (0=highest levels of social support; 3=lowest levels of social support) for use in the GxE analysis.

HCHS/SOL. Social support was assessed using the 12-item Interpersonal Support Evaluation List (ISEL-12), which asks respondents to indicate the different types of social support they have available [31]. Sample items include: If I were sick, I could easily find someone to help me with me daily chores; I don't often get invited to do things with others; When I need suggestions on how to deal with a personal problem, I know someone I can turn to. Response options are: 0 = Definitely False; 1 = Probably False; 2 = Probably True; 3 = Definitely True. Total scores were derived by summing across all individual items.

HRS. Social support was assessed using three positive social support questions that asked about relationships the respondent has with their spouse/partner, children, family, and friends. A social support score was created by combining the mean score of positive social support items across each relationship category (score range 0-16). Scores were included if there were fewer than two missing items in each category, otherwise they were set to missing. Positive social support items included: (1) How much do they really understand the way you feel about things; (2) How much you can rely on them if you have a serious problem; and (3) How much can you open up to them if you need to talk about your worries. Response options range from 1= A lot to 4=Not at all. Items were reverse scored so that higher scores indicate higher social support.

Table 2. Summary of social support indicators used across each study

WHI	HCHS/SOL	HRS
Someone you can count on to listen to you when you need to talk		How much do they really understand the way you feel about things
Someone to give you good advice about a problem	There is someone I can turn to for advice about handling problems with my family. If a family crisis arose, it would be difficult to find someone who could give me good advice about how to handle it.	
Someone to take you to the doctor if you need it		
Someone to have a good time with		
Someone to help you understand a problem when you need it	When I need suggestions on how to deal with a personal problem, I know someone I can turn to.	How much you can rely on them if you have a serious problem
Someone to help with daily chores if you are sick	If I were sick, I could easily find someone to help me with my daily chores.	
Someone to share your most private worries and fears	I feel that there is no one I can share my most private worries and fears with.	How much can you open up to them if you need to talk about your worries
Someone to do something fun with	If I wanted to go on a trip for a day (for example to the beach, the country or mountains), I would have a hard time finding someone to go with me.	

	If I decide one afternoon that I would like to go to a movie that evening, I could easily find someone to go with me. If I wanted to have lunch with someone, I could easily find someone to join me.
Someone to love you and make you feel wanted	
	I don't often get invited to do things with others.
	If I had to go out of town for a few weeks, it would be difficult to find someone who would look after my house or apartment (the plants, pets, garden, etc.).
	If I was stranded 10 miles from home, there is someone I could call who could come and get me.
	If I needed some help in moving to a new house or apartment, I would have a hard time finding someone to help me.

C. Stressful Life Events

WHI. Stressful life events were assessed using a scale modified from the Almeida County Study [32; 33]. Women indicated whether each event occurred in the past year: (1) spouse or partner died; (2) close friend or family member died or had a serious illness; (3) major problems with money; (4) divorce or break-up with a spouse or partner; (5) family member or close friend had a divorce or break-up; (6) major conflict with children or grandchildren; (7) major accidents, disasters, mugging, unwanted sexual experiences, robberies, or similar events; (8) you or family member lost job or retired; (9) physically abused by being hit, slapped, pushed, shoved, punched, or threatened with a weapon by a family member or close friend; (10) verbally abused by being made fun of, severely criticized, told you were stupid or worthless person, or threatened with harm to yourself, your possessions, or your pets, by a family member or close friend; and (11) pet died. Items were summed to create a total count of the number of past-year stressors among those with complete data on all stressors (ranging from 0-11). We then used quartiles in this distribution of number of stressful life events to create a set of categorical variables (0=highest levels of stressful life events; 3=lowest levels of stressful life events).

HCHS/SOL. Exposure to stressful life events was assessed using 13-items (selected to most closely approximate the measure used in WHI), which asked participants to report whether they had been exposed to the following events in the past year: (1) Close friend or family member ever die because of an accident, homicide, or suicide; (2) Experienced ongoing financial strain; (3) Had ongoing difficulties in a relationship with someone close to you; (4) Take something from you by force or threat, such as in a robbery, mugging, or hold up); (5) Beat you up or attack you; (6) Make you have sex by using force of threatening to harm you? This includes any type of unwanted sexual activity; (7) Suffer injury or property damage because of fire; (8) Suffer injury or property damage because of severe weather or either a natural or manmade disaster; (9) Forced to evacuate from your home or did you otherwise learn of an imminent hazard or danger in your environment; (10) In a motor vehicle accident serious enough to cause injury to one or more passengers; (11) Have some other terrifying or shocking experience, something I haven't mentioned yet; (12) Had ongoing difficulties with your job or ability to work; (13) Had another ongoing problem not listed here.

HRS. Stress was assessed using five items that assessed recent stressful life events, seven questions that asked about lifetime traumas, and information about whether and when a spouse/partner died. In each case, respondents were asked to provide the year in which the event occurred. Only events that occurred in the previous year were scored as recent exposures. Stressful life events included: (1) Loss of a job (other than retirement); (2) Being unemployed and looking for work for longer than three months; (3) Having an unemployed household member look for work for longer than three months; (4) Moving to a worse residence or neighborhood; and (5) Being robbed or having a home burglarized. Lifetime traumas included: (1) Having a child die; (2) Experiencing a major fire, flood, earthquake or natural disaster; (3) Firing a weapon in combat or being fired upon; (4) Having a spouse, partner or child addicted to alcohol; (5) Being the victim of a serious physical attack or assault; (6) Having a life-threatening illness or accident; and (7) Having a spouse or child or a life-threatening illness or accident. Items were summed to create a combined score ranging from 0-13.

Table 3. Summary of stressful life events indicators used across each study

WHI	HCHS/SOL	HRS
spouse or partner died	Close friend or family member ever die because of an accident, homicide, or suicide	
close friend or family member died or had a serious illness		Having a child die Having a spouse, partner or child addicted to alcohol Having a spouse or child or a life-threatening illness or accident
major problems with money	Experienced ongoing financial strain	
divorce or break-up with a spouse or partner		
family member or close friend had a divorce or break-up		
major conflict with children or grandchildren	Had ongoing difficulties in a relationship with someone close to you	
major accidents, disasters, mugging, unwanted sexual experiences, robberies, or similar events	Take something from you by force or threat, such as in a robbery, mugging, or hold up Make you have sex by using force of threatening to harm you (This includes any type of unwanted sexual activity) Suffer injury or property damage because of fire In a motor vehicle accident serious enough to cause injury to one or more passengers	Being robbed or having a home burglarized Being the victim of a serious physical attack or assault
you or family member lost job or retired		Loss of a job (other than retirement) Being unemployed and looking for work for longer than three months Having an unemployed household member look for work for longer than three months
physically abused by being hit, slapped, pushed, shoved, punched, or threatened with a weapon by a family member or close friend	Beat you up or attack you	
verbally abused by being made fun of, severely criticized, told you were stupid or worthless person, or threatened with harm to yourself, your possessions, or		

your pets, by a family member or close friend		
pet died		
	Suffer injury or property damage because of severe weather or either a natural or manmade disaster	Experiencing a major fire, flood, earthquake or natural disaster
	Forced to evacuate from your home or did you otherwise learn of an imminent hazard or danger in your environment	
	Have some other terrifying or shocking experience, something I haven’t mentioned yet;	
	Had ongoing difficulties with your job or ability to work	
	Had another ongoing problem not listed here.	
		Moving to a worse residence or neighborhood
		Firing a weapon in combat or being fired upon
		Having a life-threatening illness or accident

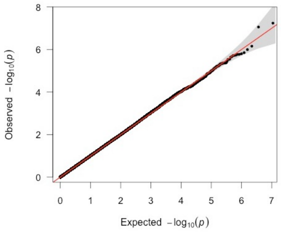
D. Antidepressant Medication Adjustment

As noted, we used a nonparametric imputation algorithm developed in a previous GWAS of depressive symptoms [19] to adjust the CES-D score of women taking antidepressant medications (as determined by pill bottles women brought to the baseline interview). This algorithm made two assumptions: (1) the CES-D score of a woman taking antidepressants is *lower* (i.e., indicating fewer depressive symptoms) than would be expected if she were not taking antidepressants; (2) women with high CES-D scores, on average, respond less to their antidepressant than women with lower CES-D scores. We therefore replaced the CES-D score of women on antidepressants (n=429) with the mean depressive symptom score of all persons using antidepressants that had the same or a higher CES-D score. For example, an antidepressant user with an observed CES-D score of 4 would have a revised score of 7.11 (derived by taking the average CES-D scores of antidepressant users with a CES-D value of 4 or greater). Thus, CES-D scores for all antidepressant users were increased through this algorithm (average difference=2.21). This algorithm was based on one used to adjust blood pressure for persons on antihypertensive medications [20].

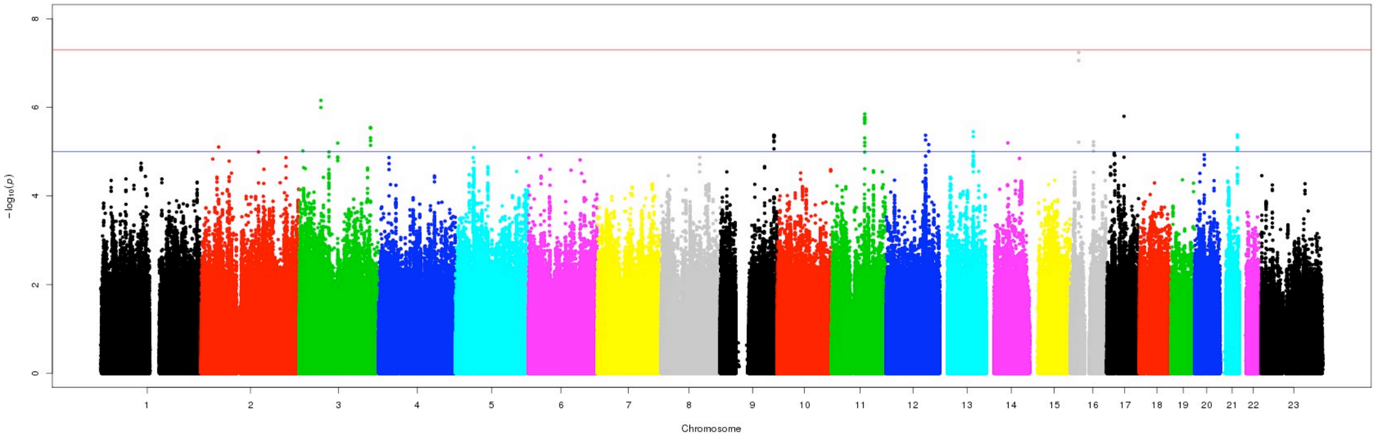
Supplementary Figures for Primary Analyses

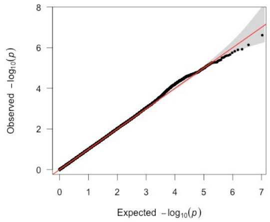
All supplementary figures for the primary analyses are presented in the subsequent pages.

Supplemental Figure 1. Quantile-quantile (QQ) plots and Manhattan plots for depressive symptoms in African Americans and Hispanics/Latinos

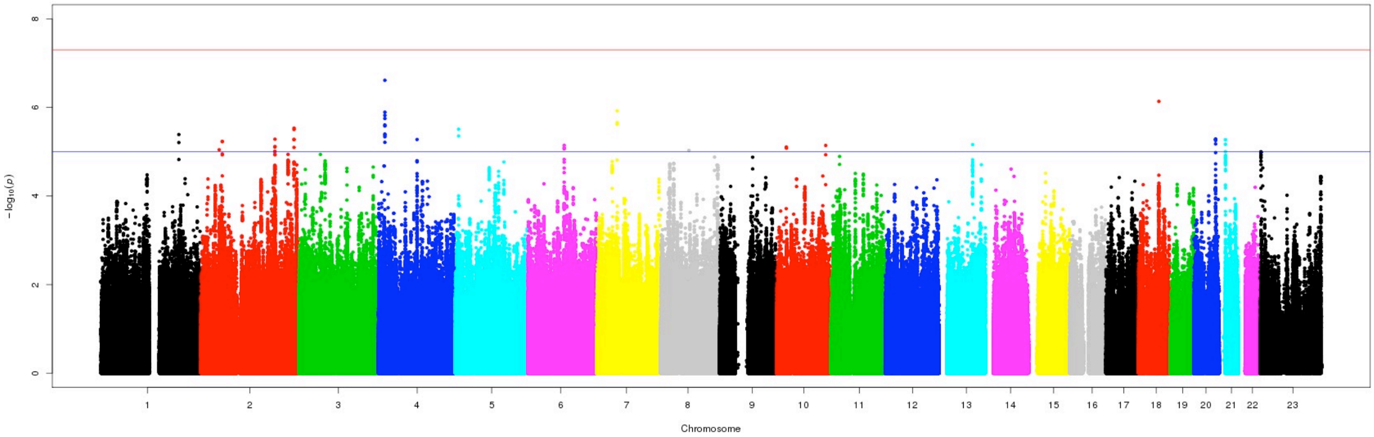


Panel A. African American sample – depressive symptoms





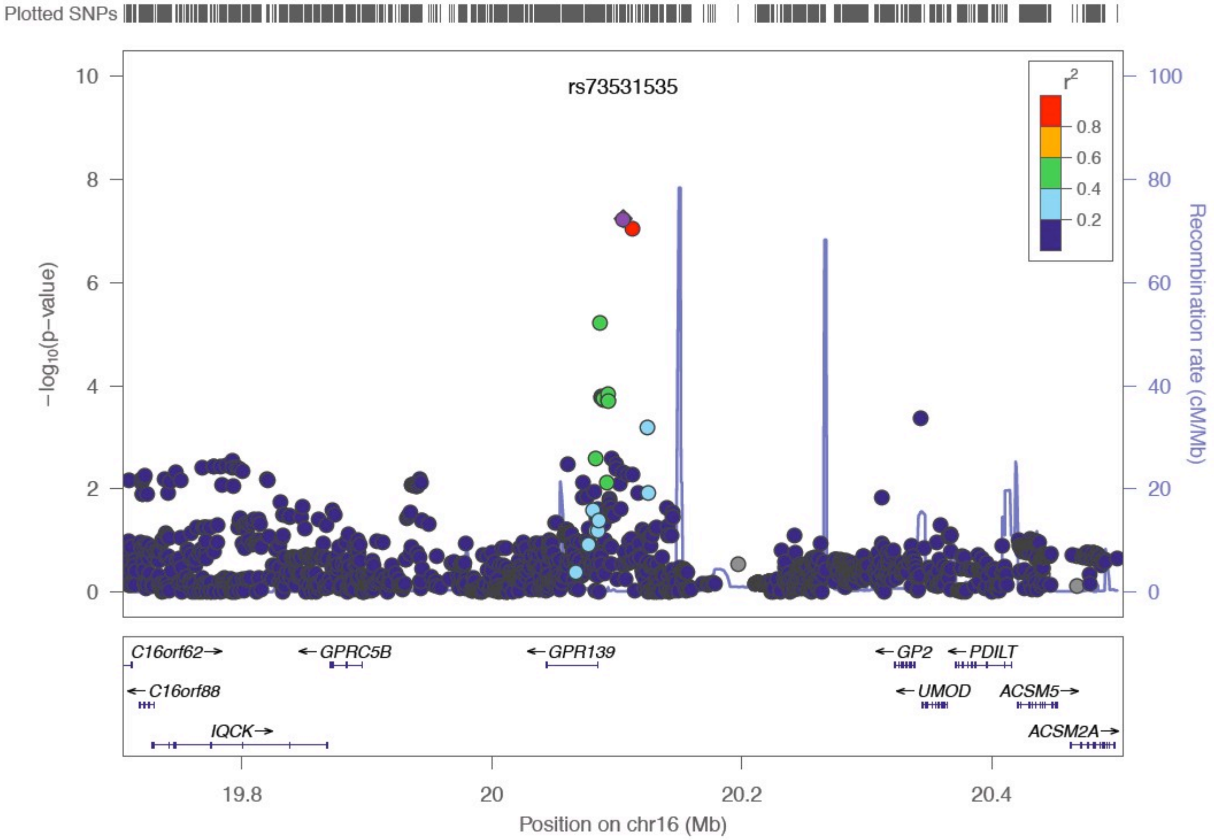
Panel B. Hispanic/Latino sample – depressive symptoms



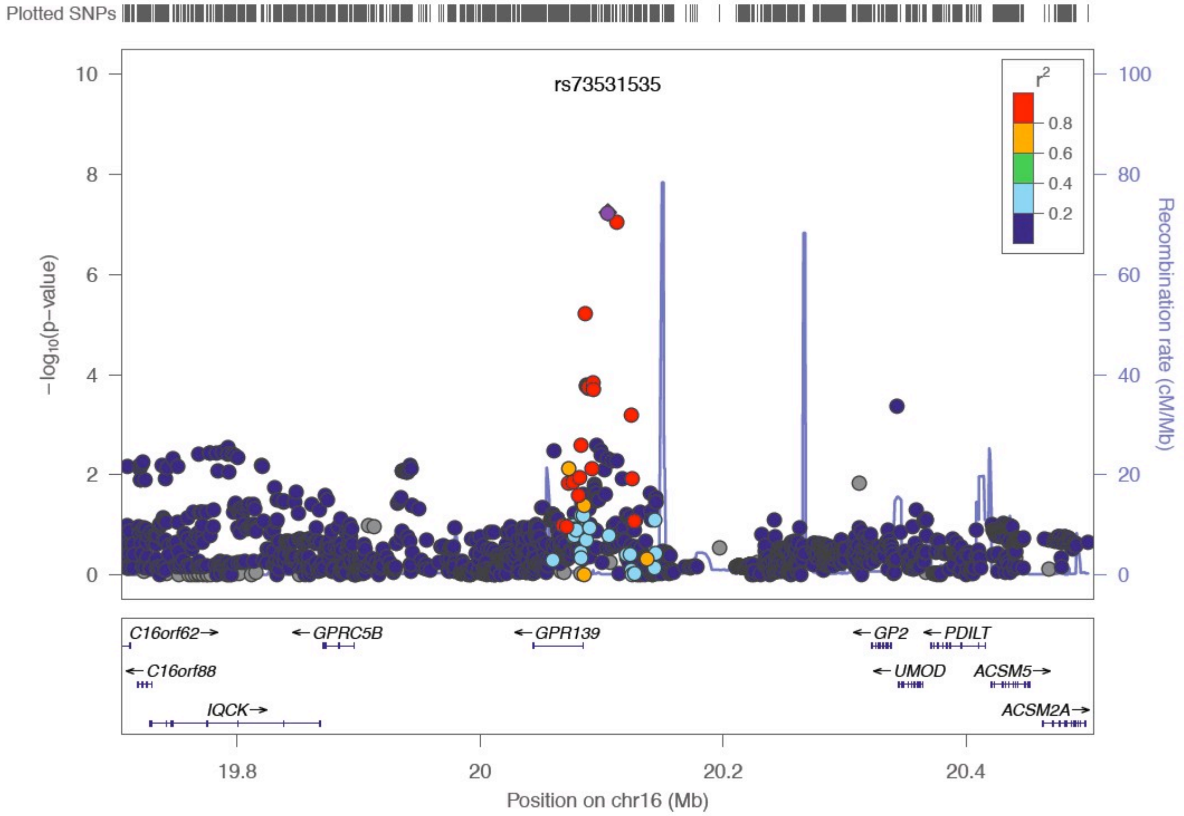
The quantile–quantile plot ("QQ-plot"), which presents the observed by expected P-values on the -log10 scale), indicates conformity of the observed results to what would be expected under the null. In the Manhattan plot, the x-axis is the chromosomal position and the y-axis is the log10 p-value for the association between each SNP and depressive symptoms derived from the linear regression model. The red line shows the genome-wide significance level ($5x10^{-8}$).

Supplemental Figure 2. Regional association plots for the top SNP (rs73531535) identified in the African American GWAS

Panel A. Plot generated using African reference panel



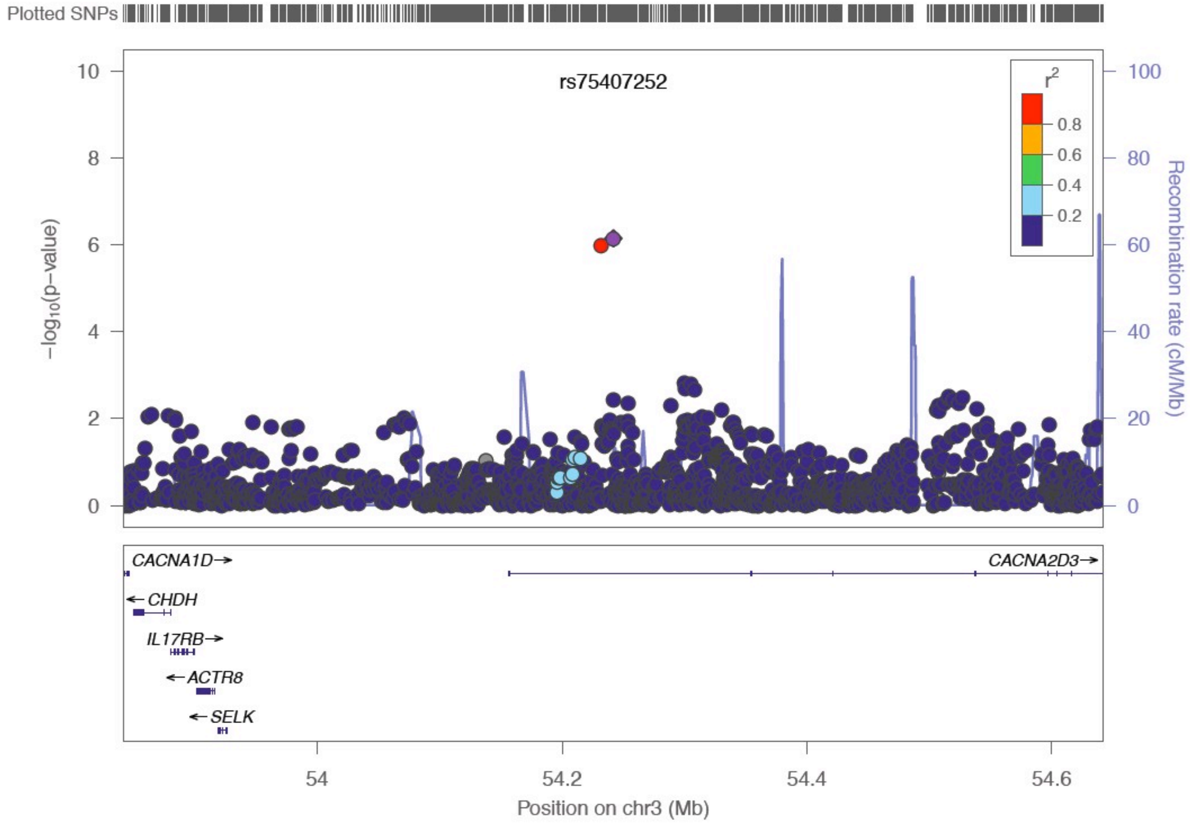
Panel B. Plot generated using European reference panel



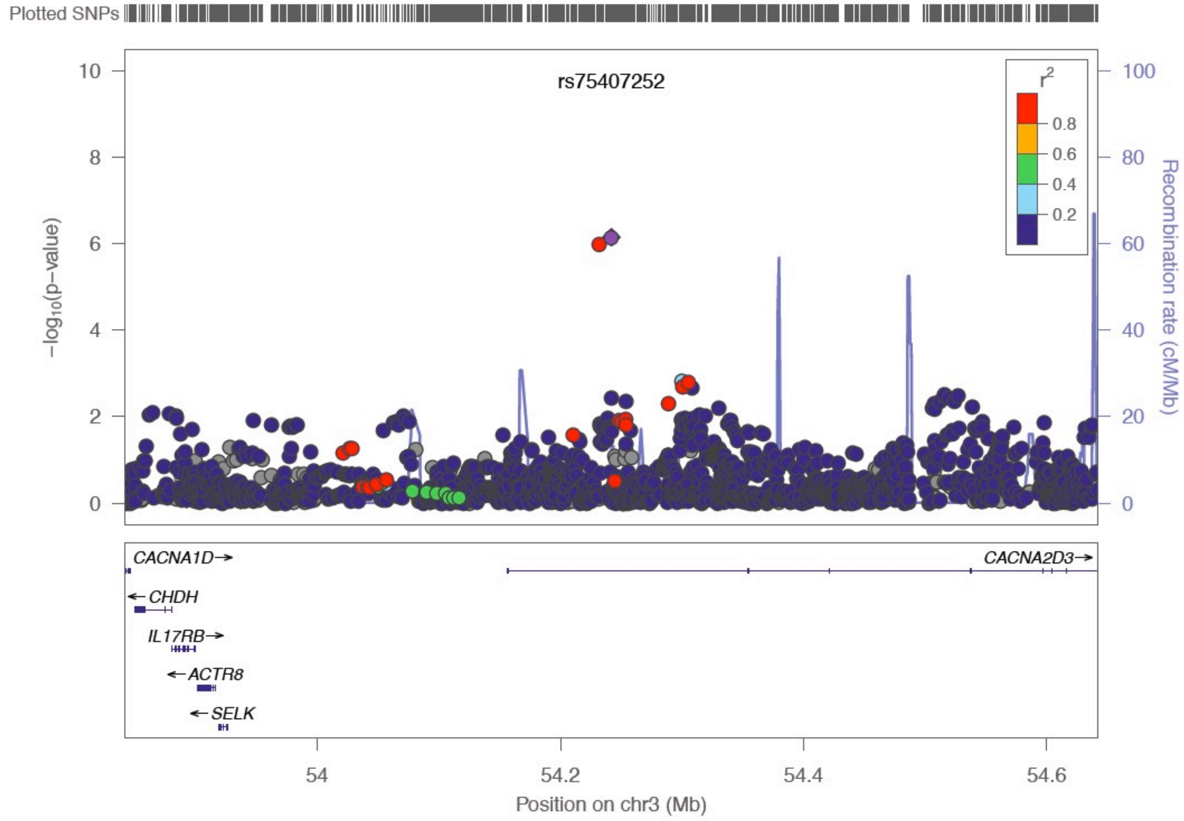
Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for both African American and European reference panels as the WHI analysis with African American used both reference groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The SNP (rs73531535) is located 20kb upstream from *GPR139* (the G protein-coupled receptor 139). Both the index SNP (shown in purple diamond) and its closest neighbor (shown in red) are imputed. Several other SNPs in this region were genotyped (rs10221121; $p=5.976\times10^{-6}$; rs4784727; $p= 9.645\times10^{-6}$).

Supplemental Figure 3. Regional association plots for the second best SNP (rs75407252) identified in the African American GWAS

Panel A. Plot generated using African reference panel

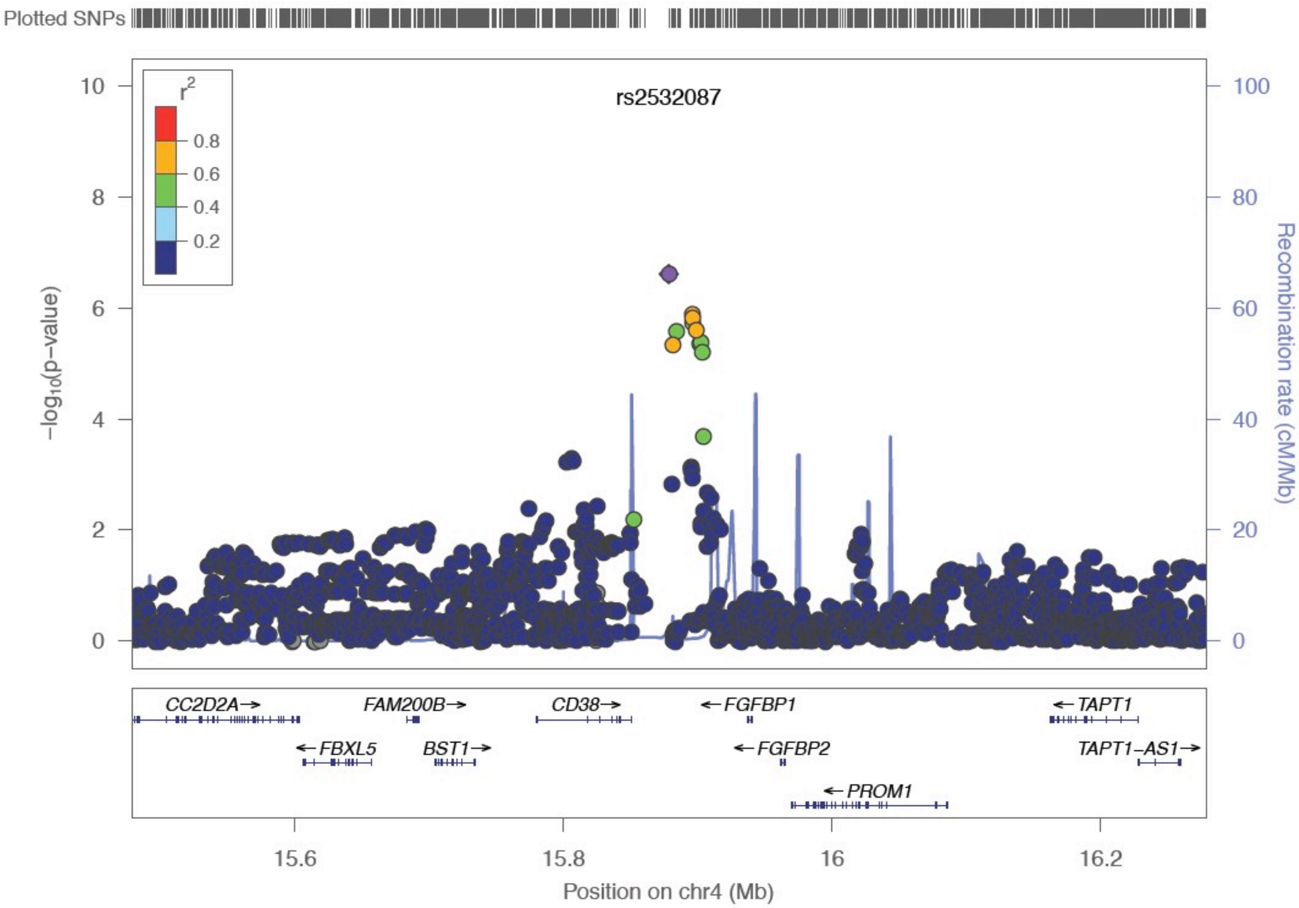


Panel B. Plot generated using European reference panel



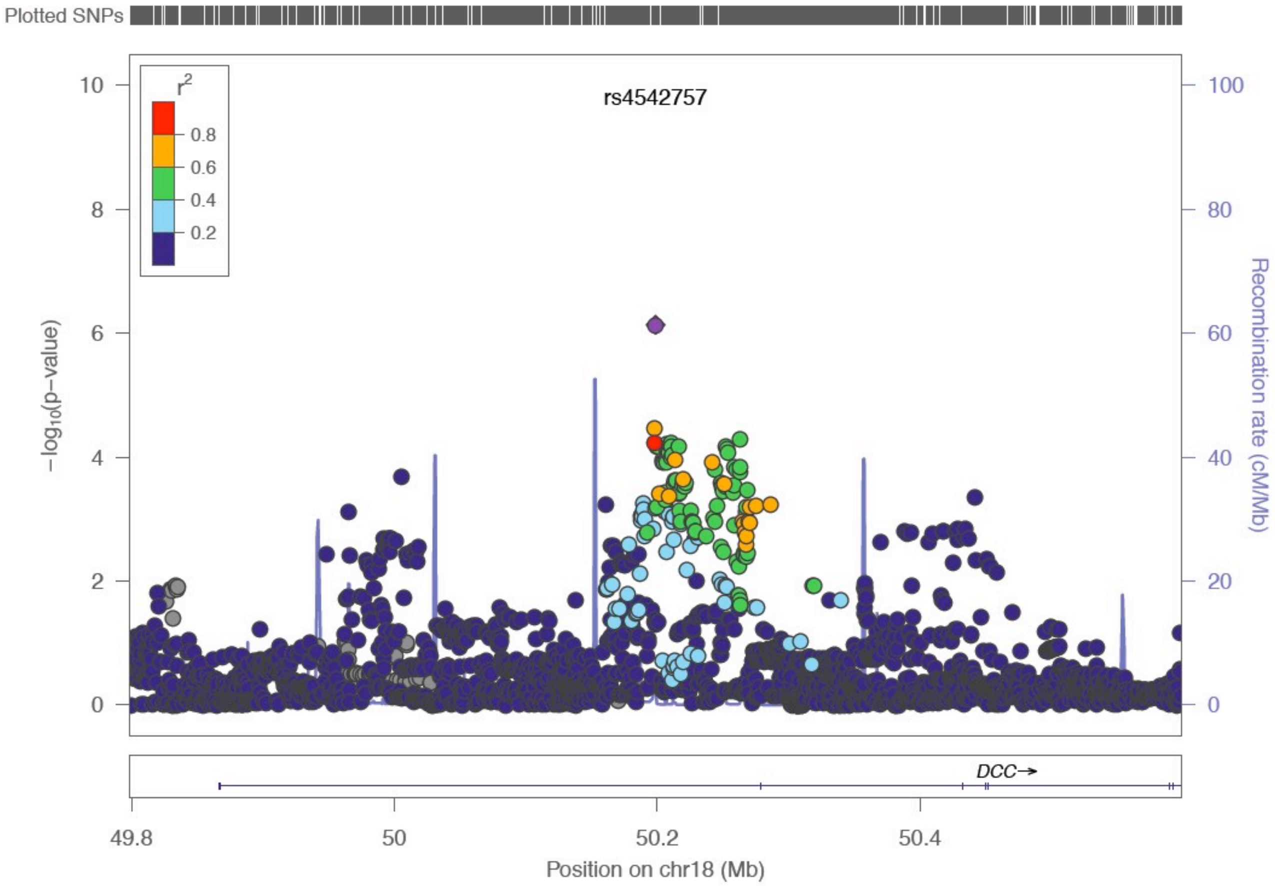
Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for both African American and European reference panels as the WHI analysis with African American used both reference groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The intronic SNP (rs75407252) is located in *CACNA2D3*. Both the index SNP (shown in purple) and its closest neighbor (shown in red) are imputed.

Supplemental Figure 4. Regional association plot for the top SNP (rs2532087) identified in the Hispanic/Latina GWAS



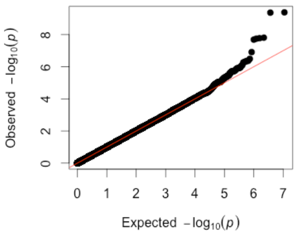
The regional association plot was generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for the European 1000 Genomes reference panel only as the WHI analysis with Hispanics used all reference groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The SNP rs2532087 is an imputed SNP located 27kb away from *CD38*. Of note, while the index SNP (rs2532087) is imputed, other SNPs in moderate to high LD in this region, including rs6845349 ($p=1.775\times10^{-6}$) and rs1860234 (p=2.622x10-6) were genotyped.

Supplemental Figure 5. Regional association plot for the second best SNP (rs4542757) identified in the Hispanic/Latina GWAS

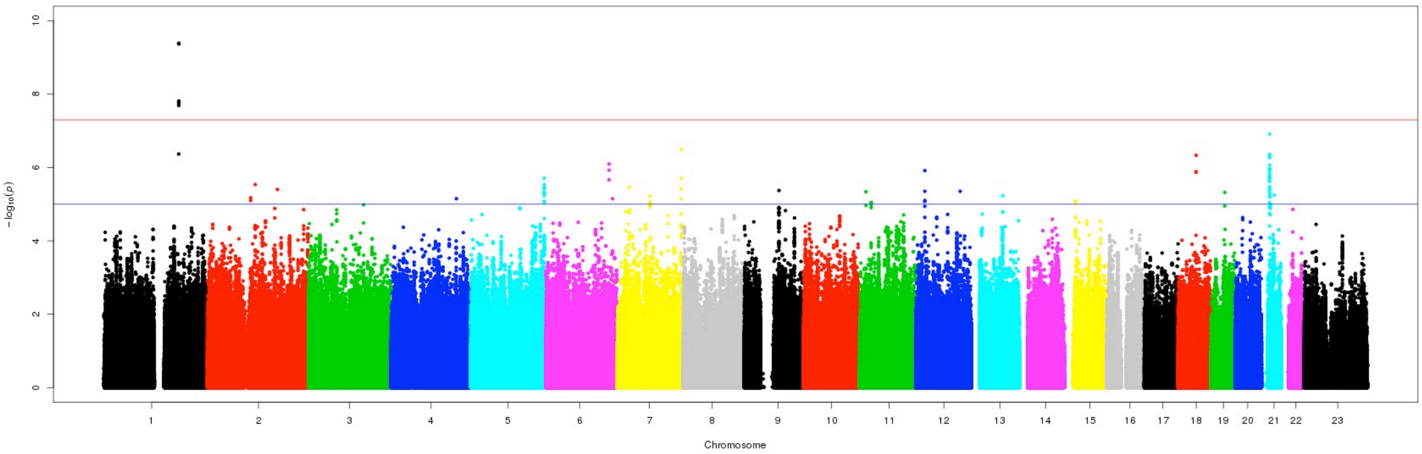


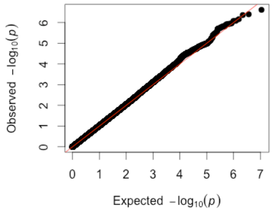
The regional association plot was generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for the European 1000 Genomes reference panel only as the WHI analysis with Hispanics used all reference groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The intronic SNP (rs4542757), which was imputed, is located in *DCC* (deleted in colorectal cancer).

Supplemental Figure 6. Quantile-quantile (QQ) plots and Manhattan plots for gene-environment interaction (GxE) results in African Americans for stressful life events and social support

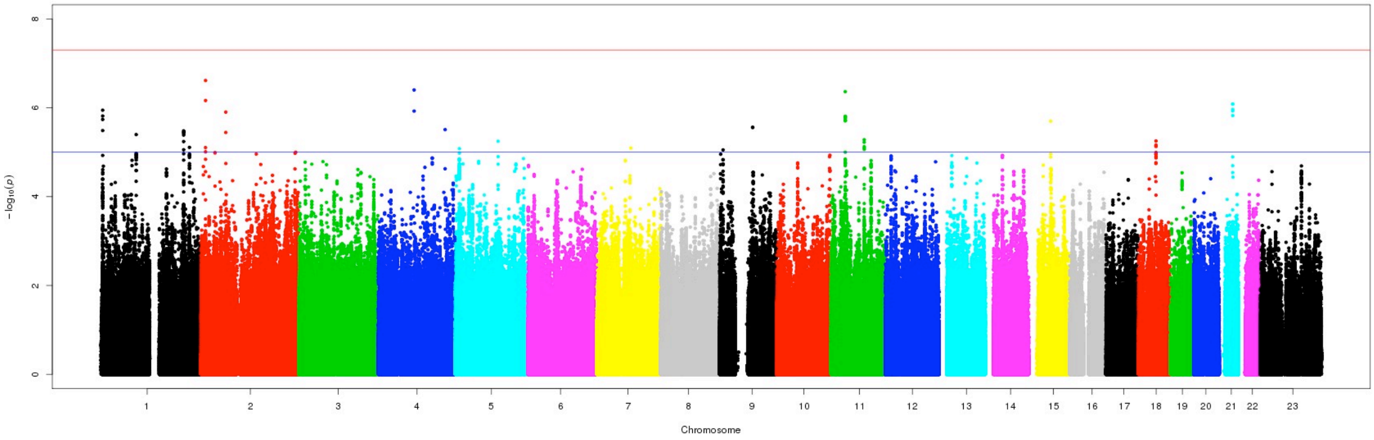


Panel A. African American sample – stressful life events (n=6,982)



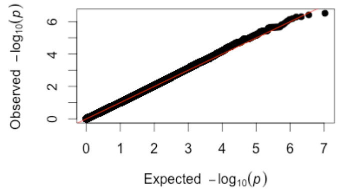


Panel B. African American sample – social support (n=6,908)

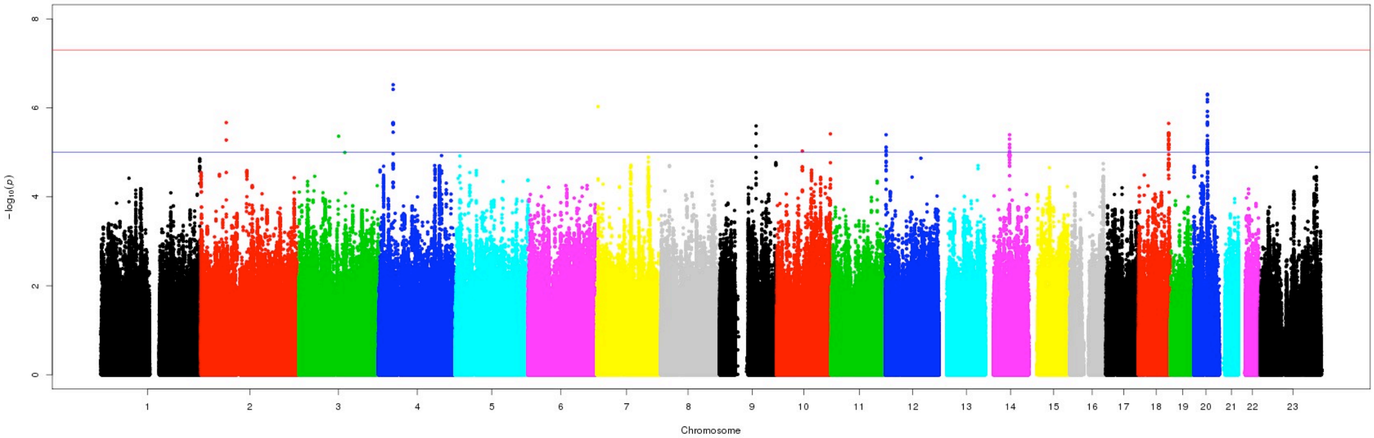


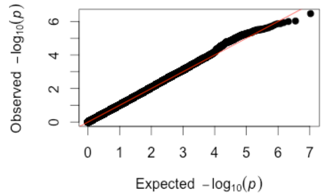
The quantile–quantile plot ("QQ-plot"), which presents the observed by expected P-values on the -log10 scale), indicates conformity of the observed results to what would be expected under the null. In the Manhattan plot, the x-axis is the chromosomal position and the y-axis is the log10 p-value for the association between each SNP and depressive symptoms derived from the linear regression model. The red line shows the genome-wide significance level ($5x10^{-8}$).

Supplemental Figure 7. Quantile-quantile (QQ) plots and Manhattan plots for gene-environment interaction (GxE) results in Hispanics/Latinos for stressful life events and social support

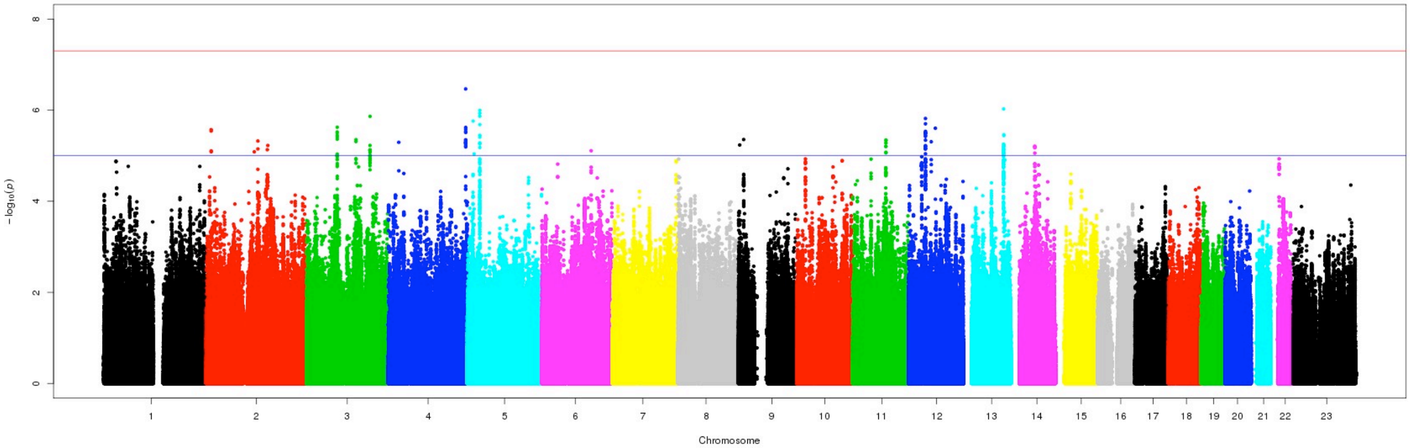


Panel A. Hispanics/Latinos sample – stressful life events (n=2,989)





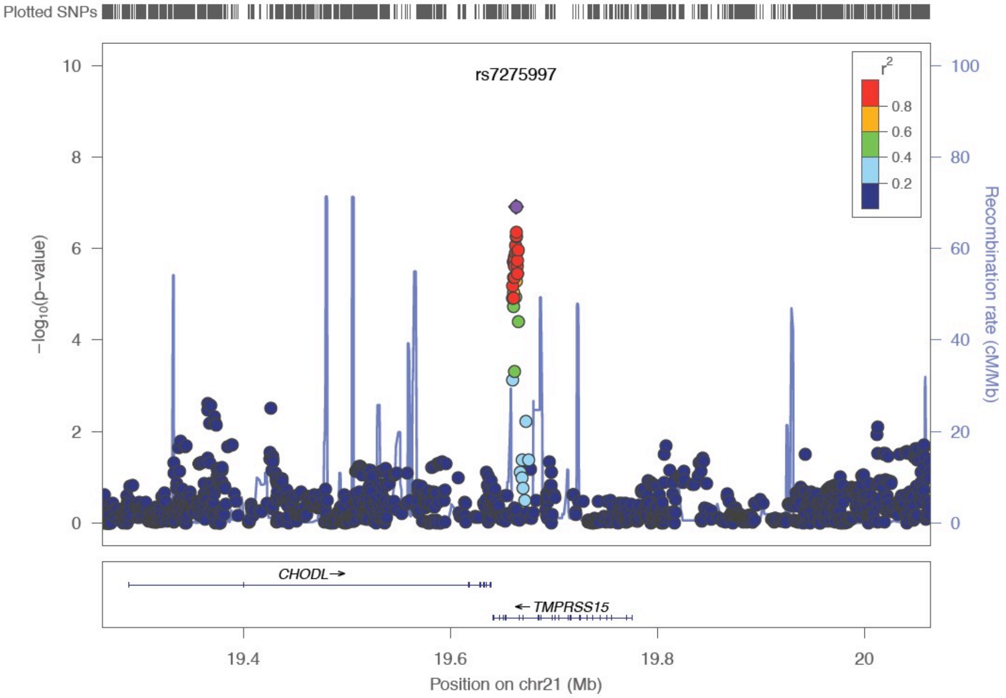
Panel B. Hispanics/Latinos sample – social support (n=3,012)



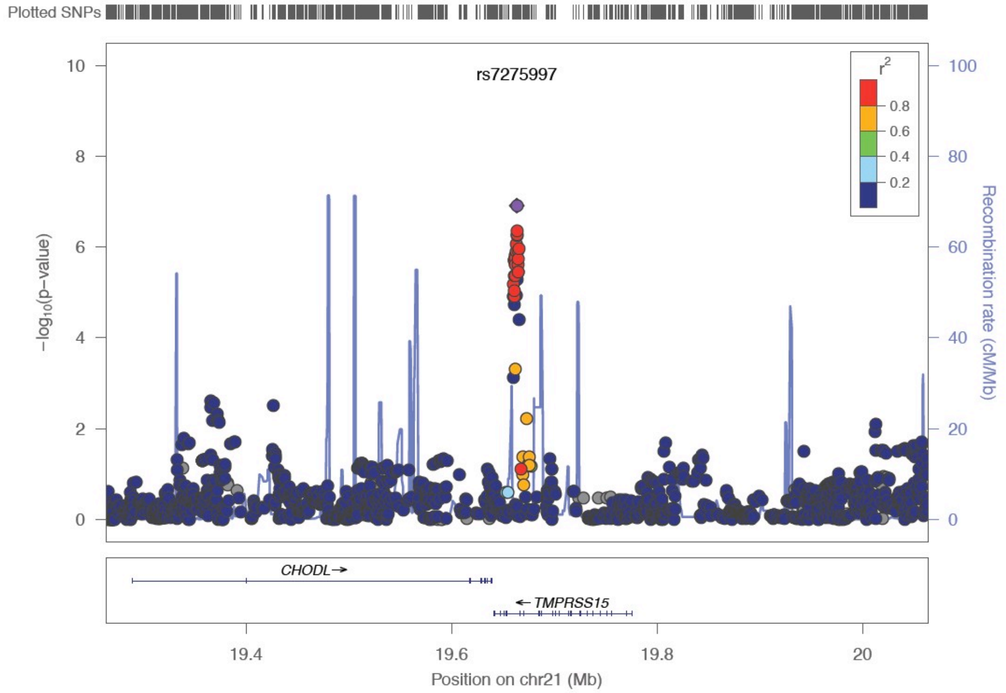
The quantile–quantile plot ("QQ-plot"), which presents the observed by expected P-values on the -log10 scale), indicates conformity of the observed results to what would be expected under the null. In the Manhattan plot, the x-axis is the chromosomal position and the y-axis is the log10 p-value for the association between each SNP and depressive symptoms derived from the linear regression model. The red line shows the genome-wide significance level (5x10^{-8}).

Supplemental Figure 8. Regional association plots for the second top SNP (rs7275997) identified in the African American GWEIS of stressful life events

Panel A. Plot generated using African reference panel



Panel B. Plot generated using European reference panel

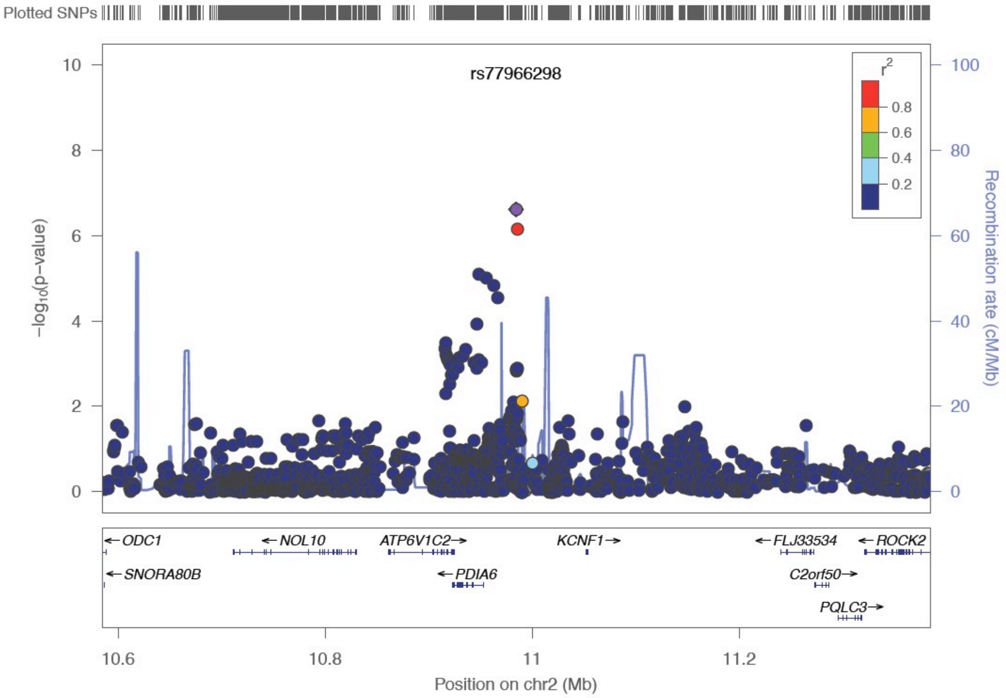


Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for both African American and European reference panels as the WHI analysis with African American used both reference

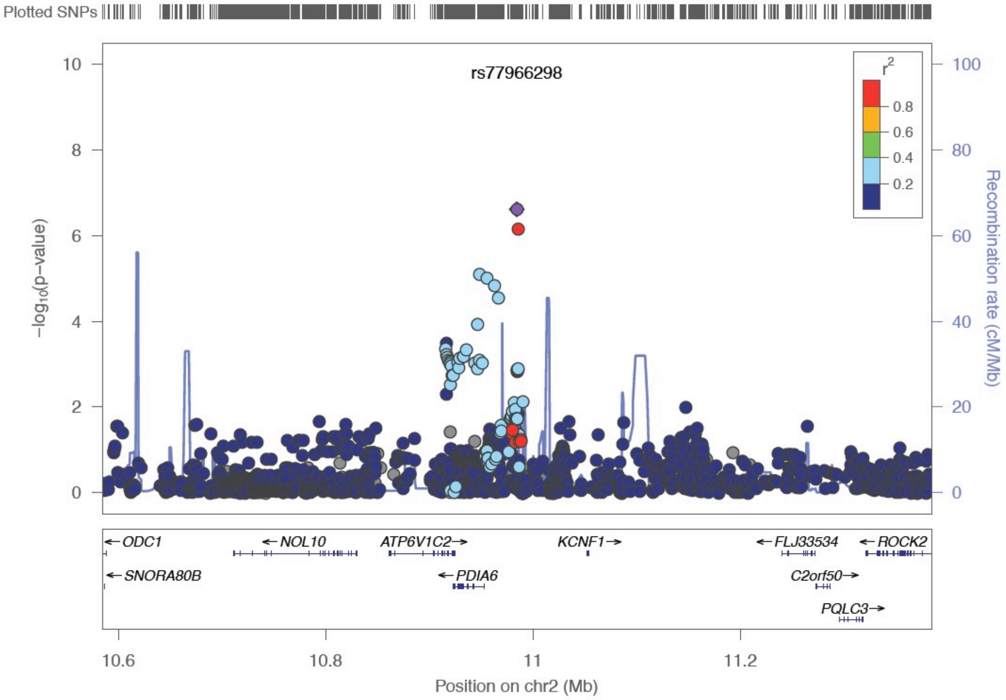
groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The intronic SNP (rs7275997) is located in *TMPRSS15*. Both the top SNP (shown in purple) and several of its closest neighbors (shown in red) are genotyped (rs7277468; 5.37×10^{-7} and rs1040634; 1.078×10^{-6}).

Supplemental Figure 9. Regional association plots for the top SNP (rs77966298) identified in the African American GWEIS of social support

Panel A. Plot generated using African reference panel



Panel B. Plot generated using European reference panel

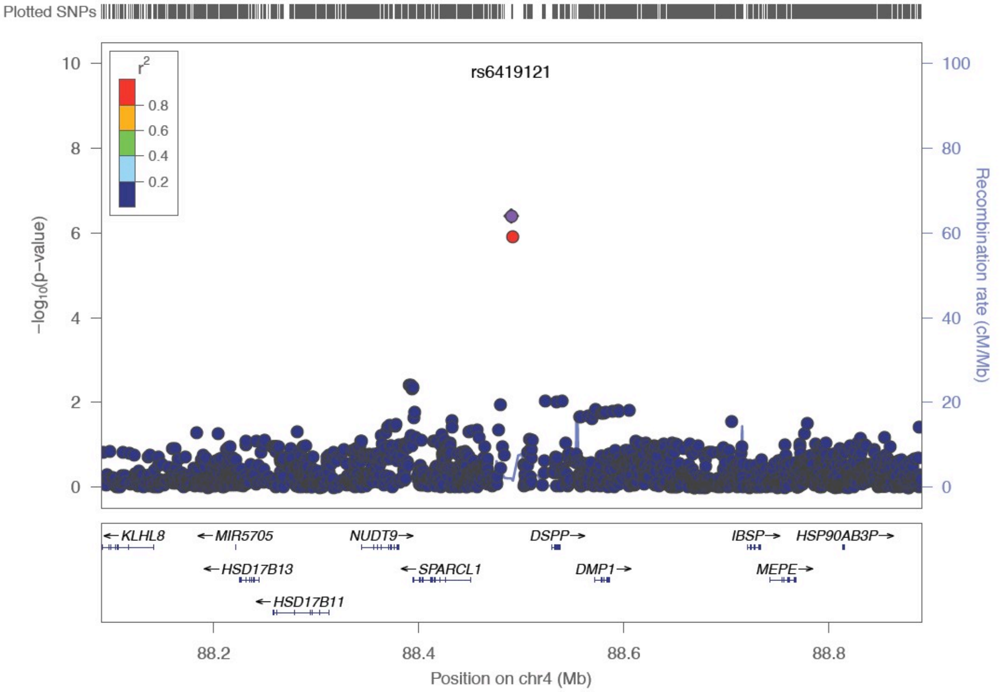


Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for both African American and European reference panels as the WHI analysis with African American used both reference

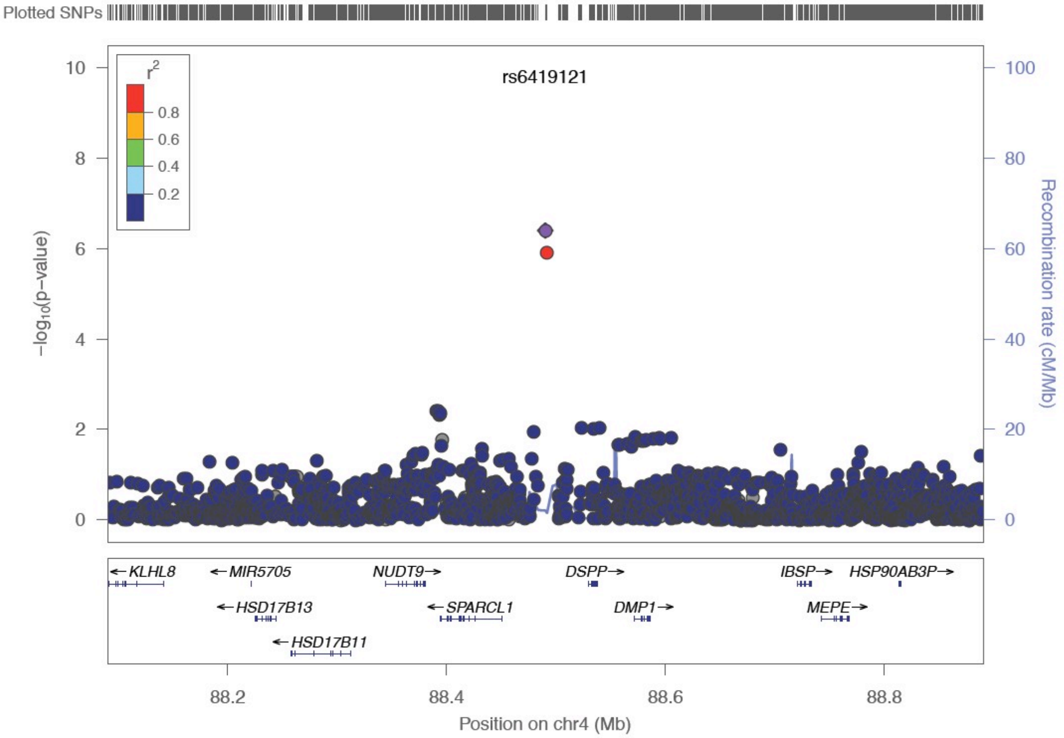
groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The top SNP, located within 20kb of *PDIA6* was imputed, as were most other SNPs in this region. However, its closest neighbor (in red; rs1040634p=6.87x10^{-7}) and at least one other SNP in this region (rs1665272; p=1.25x10^{-6}) were genotyped.

Supplemental Figure 10. Regional association plots for the second best SNP (rs6419121) identified in the African American GWEIS of social support

Panel A. Plot generated using African reference panel



Panel B. Plot generated using European reference panel

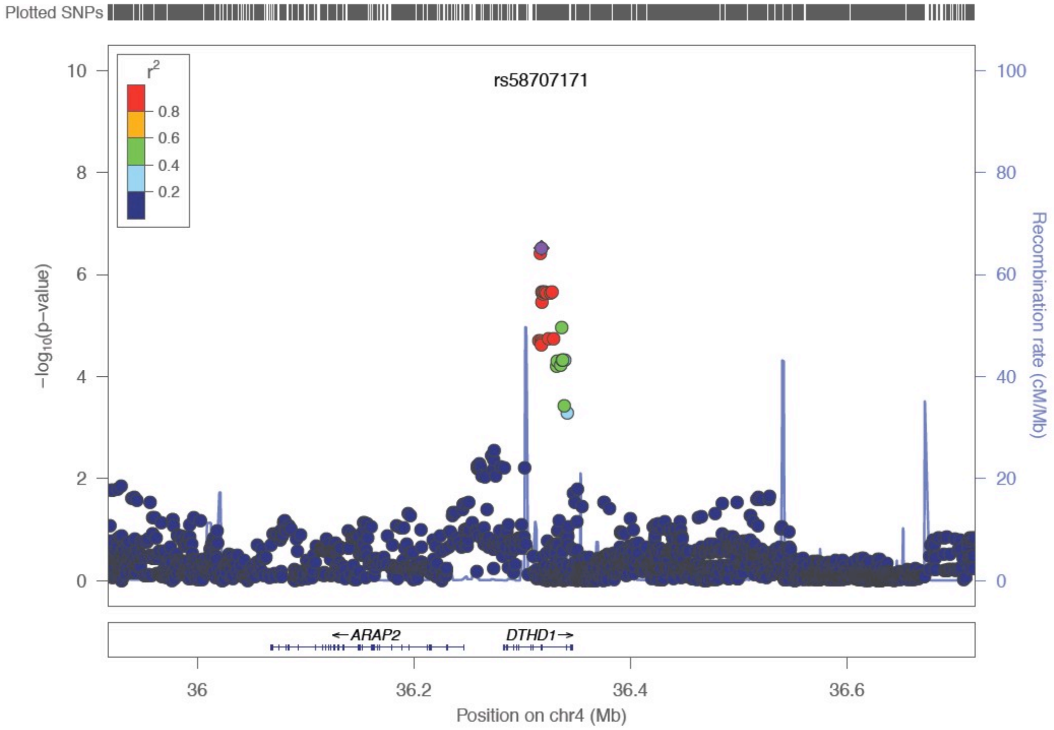


Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for both African American and European reference panels as the WHI analysis with African American used both reference

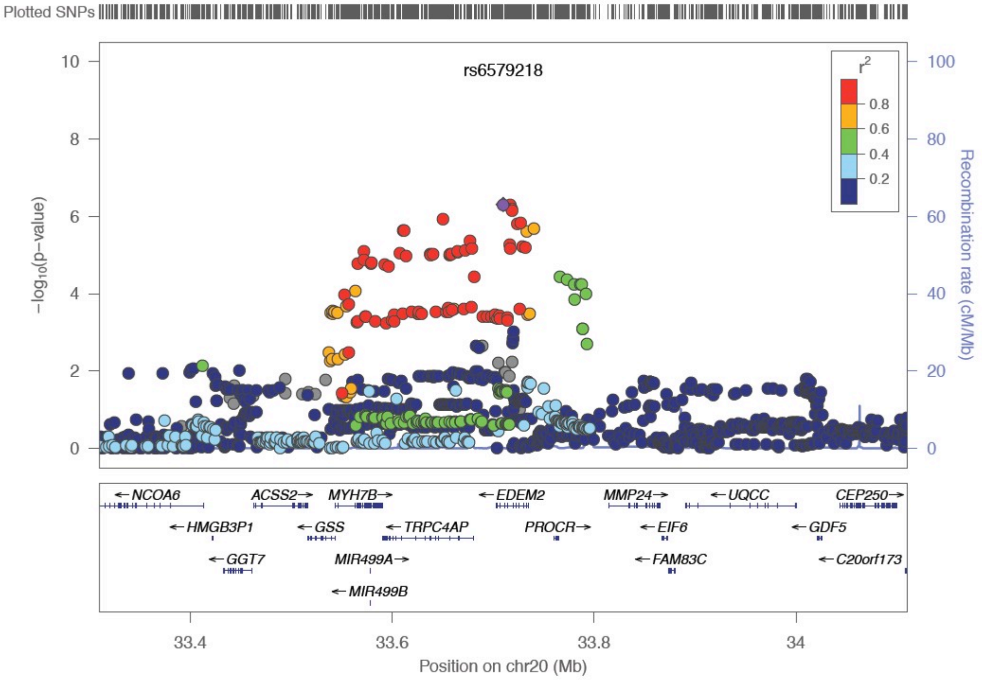
groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The top SNP (shown in purple) is imputed, though its closest neighbor (in red; rs2199458; $p=1.19\times10^{-6}$) was genotyped.

Supplemental Figure 11. Regional association plots for the top SNP (rs58707171) and second best SNP (rs6579218) identified in the Hispanic/Latina GWEIS of stressful life events

Panel A. Plot for the top SNP generated using European reference panel



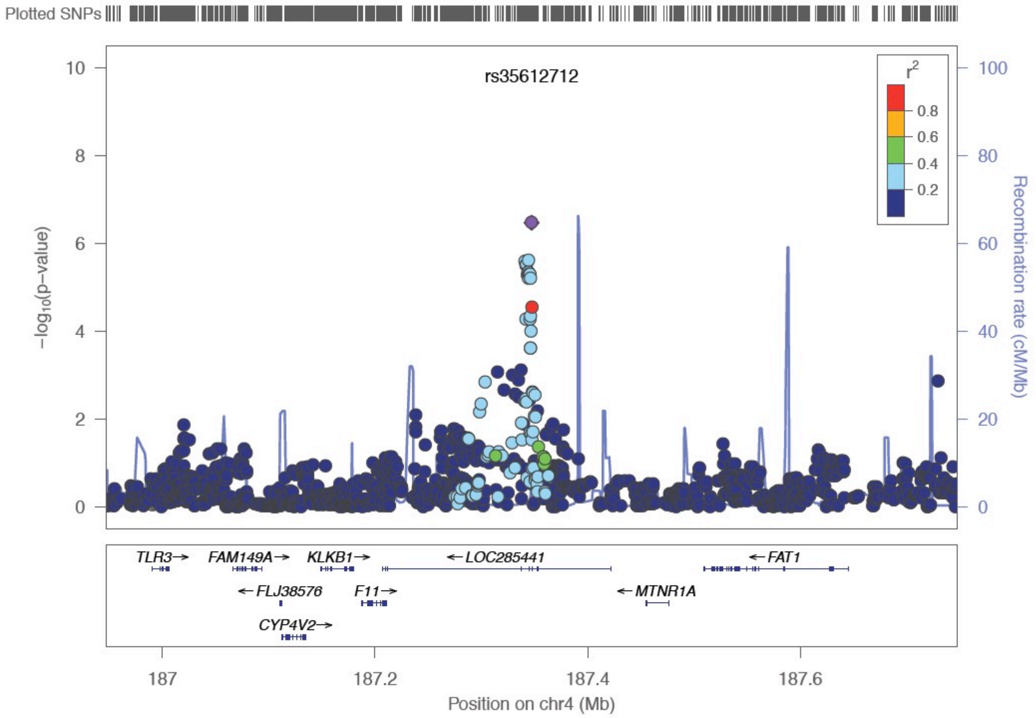
Panel B. Plot for the second best SNP generated using European reference panel



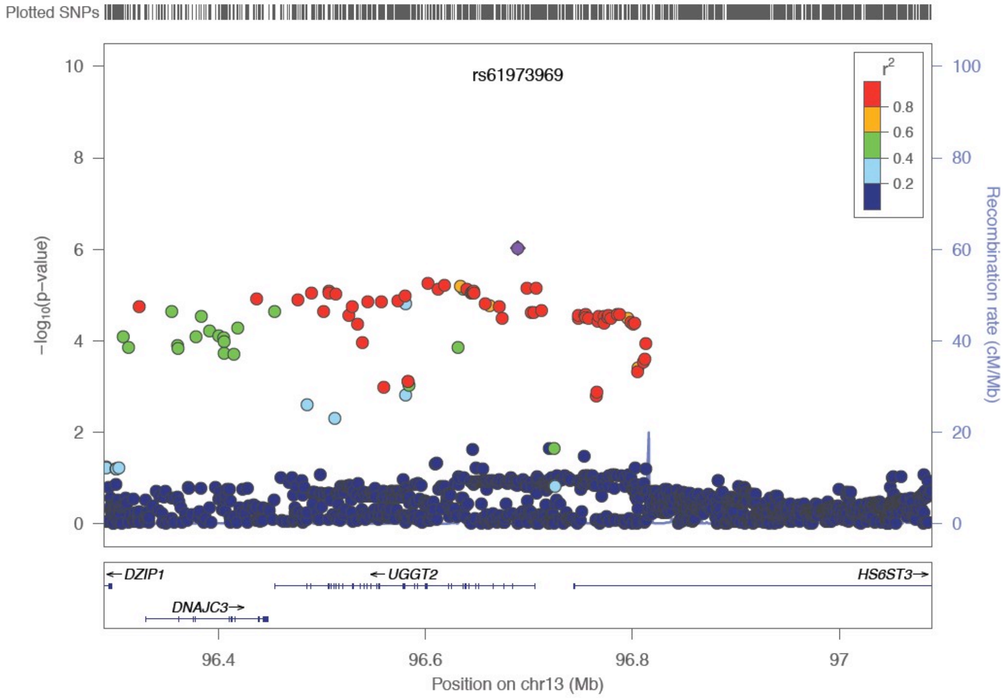
Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for the European 1000 Genomes reference panel only as the WHI analysis with Hispanics used all reference groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The intronic SNP rs58707171 is located in *DTHD1* and was imputed, as were many other SNPs in the region, though with some exception (e.g., rs17518487 was genotyped; $p=2.16x10^{-6}$). The intronic SNP rs6579218 is located in *EDEM2* and was imputed, as were many other SNPs in the region, though with some exception (e.g., rs1535466; $p=7.32x10^{-7}$).

Supplemental Figure 12. Regional association plots for the top SNP (rs35612712) and second best SNP (rs61973969) identified in the Hispanic/Latina GWEIS of social support

Panel A. Plot for the top SNP generated using European reference panel



Panel B. Plot for the second best SNP generated using European reference panel



Regional association plots were generated using LocusZoom (http://csg.sph.umich.edu/locuszoom/). We present results for the European 1000 Genomes reference panel only as the WHI analysis with Hispanics used all reference groups for imputation. The left-side y-axis refers to the log of the p-value corresponding to the test of association between each SNP (denoted as a colored dot) and levels of depressive symptoms. SNPs are colored based on the level of linkage disequilibrium (LD) between each SNP and the index SNP. r^2 values are determined based on the HG19/1000 Genomes (March 2012 build) data. The intronic SNP rs35612712 is located in *F11-AS1* and was imputed, as were most other SNPs in the region. The intronic SNP rs61973969 is located in *UGGT2* and was imputed, as were most other SNPs in the region.

Supplementary Tables for Primary Analyses

Supplementary tables for the primary analyses are presented in the subsequent pages.

Supplemental Table 1. Descriptive statistics on analytic sample derived from the Women's Health Initiative (WHI) SNP Health Association Resource (WHI SHARe) Sample

			Depressive Symptoms		
	N	%	Mean	SD	p-value
African American Sample (n=7,179)					
Age					p<0.001
50-59 (referent)	3169	44.14	2.69	-2.91	
60-69	3088	43.01	2.39	-2.58	
70-79	922	12.84	2.37	-2.38	
Income					p<0.001
Less than 19,000 (referent)	1706	23.76	3.18	-3.15	
20,000 – 49,000	2949	41.08	2.40	-2.56	
50,000 +	2105	29.32	2.10	-2.33	
Missing	419	5.84	2.80	-3.03	
Education					p<0.001
Less than high school (referent)	605	8.43	3.45	-3.43	
High school/vocational	1825	25.42	2.70	-2.78	
Some college/Associates	1897	26.42	2.57	-2.70	
College degree	658	9.17	2.17	-2.46	
Graduate school or degree	2112	29.42	2.15	-2.40	
Missing	82	1.14	2.73	-2.62	
Marital Status					p=0.015
Never married (referent)	426	5.93	2.43	-2.59	
Divorced/separated	2132	29.70	2.67	-2.90	
Widowed	1482	20.64	2.59	-2.69	
Married/Married-like relationship	3078	42.88	2.38	-2.60	
Missing	61	0.85	2.93	-2.73	
Hispanic/Latina Sample (n=3,138)					
Age					p=0.003
50-59 (referent)	1625	51.78	3.42	-3.30	
60-69	1238	39.45	3.19	-3.14	
70-79	275	8.76	2.76	-2.76	
Income					p<0.001
Less than 19,000 (referent)	956	30.47	3.88	-3.46	
20,000 – 49,000	1175	37.44	2.97	-2.89	
50,000 +	755	24.06	2.67	-2.91	
Missing	252	8.03	4.14	-3.69	
Education					p<0.001
Less than high school (referent)	629	20.04	4.14	-3.52	
High school/vocational	917	29.22	3.30	-3.18	
Some college/Associates	808	25.75	3.04	-3.05	
College degree	248	7.90	2.87	-2.94	
Graduate school or degree	495	15.77	2.62	-2.86	

Missing	41	1.31	4.09	-3.49	
Marital Status					p<0.001
Never married (referent)	136	4.33	3.73	-3.48	
Divorced/separated	656	20.91	3.75	-3.35	
Widowed	388	12.36	3.56	-3.53	
Married/Married-like relationship	1925	61.34	3.00	-3.01	
Missing	33	1.05	4.02	-3.31	

Depressive symptom results are based on the transformed version of the CES-D score that takes into account antidepressant medication use.

Supplemental Table 2. Genome-wide association study (GWAS) results for the top loci (p<1x10-4) in African Americans

Chr	SNP	Base Pair	A1	A2	Freq of A1	MAF	Genotyping	Info	Beta	SE	P-value	Genes in Region (±300kb)
16	rs73531535	20105038	C	T	0.771	0.229	imputed	0.938	-0.297	0.055	5.75E-08	IQCK, GPRC5B, GPR139, GP2, UMOD, PDILT
3	rs75407252	54241886	C	T	0.947	0.053	imputed	0.813	-0.548	0.110	6.99E-07	CACNA2D3
11	rs11233283	82415904	A	G	0.842	0.016	imputed	0.986	-0.298	0.062	1.41E-06	FAM181B, PRCP, DDIAS, RAB30
17	rs34257140	42675053	G	T	0.852	0.149	imputed	0.999	-0.313	0.065	1.59E-06	LOC101926996, RUNDC3A, SLC25A39, GRN, FAM171A2, ITGA2B, GPATCH8, FZD2, LINC01180, C17orf104, CCDC43, DBF4B, ADAM11, GJC1, HIGD1B, EFTUD2
3	rs580112	177289895	A	G	0.184	0.184	imputed	0.945	0.279	0.060	2.84E-06	LINC00501, LINC00578, LOC102724550
13	rs1413154	83240729	G	T	0.205	0.205	imputed	0.825	-0.283	0.061	3.54E-06	-
21	rs1893586	43286918	A	G	0.483	0.483	imputed	0.947	0.211	0.046	4.19E-06	LINC00111, LINC00479, LINC00112, RIPK4, MIR6814, PRDM15, C2CD2, ZBTB21, ZNF295
12	rs10777901	98492992	A	C	0.481	0.481	imputed	0.993	0.206	0.045	4.27E-06	MIR4303
9	rs10125319	133426729	C	T	0.491	0.491	imputed	0.920	-0.214	0.047	4.27E-06	HMCN2, ASS1, LOC100272217, FUBP3, MIR6856, PRDM12, EXOSC2, ABL1
16	rs10221121	56840328	A	G	0.229	0.229	genotyped	0.986	-0.241	0.053	5.98E-06	BBS2, MT4, MT3, MT2A, MT1L, MT1E, MT1M, MT1JP, MT1A, MT1DP, MT1B, MT1F, MT1G, MT1H, MT1IP, MT1X, NUP93, MIR138
14	rs210329	54059800	G	T	0.668	0.332	imputed	0.989	0.217	0.048	6.35E-06	-
3	rs28493952	95747804	C	T	0.320	0.320	imputed	0.850	0.234	0.052	6.41E-06	-
12	rs7312307	106441333	C	G	0.913	0.087	imputed	0.904	0.376	0.084	6.92E-06	NUAK1, CKAP4, TCP11L2
2	rs17030391	43353504	A	G	0.143	0.143	imputed	0.808	0.316	0.071	7.84E-06	LOC102723854, ZFP36L2, LINC01126, THADA
5	rs4866976	45579793	A	G	0.914	0.086	genotyped	0.996	-0.361	0.081	8.04E-06	HCN1
3	rs418207	9225376	A	G	0.477	0.477	imputed	0.811	-0.219	0.050	9.59E-06	RAD18, SRGAP3, LOC101927416, THUMPD3, SETD5

2	rs9287319	142244994	A	G	0.619	0.381	imputed	0.998	-0.206	0.047	1.01E-05	LRP1B
3	rs1526725	74069839	A	G	0.535	0.465	imputed	0.989	-0.198	0.045	1.01E-05	CNTN3
17	rs7215491	18236042	C	T	0.252	0.252	imputed	1.000	-0.229	0.052	1.07E-05	ATPAF2, GID4, DRG2, MYO15A, ALKBH5, LLGL1, FLII, MIEF2, TOP3A, SMCR8, SHMT1, MIR6778, EVPLL, FLJ35934, KRT17P5, KRT16P1, LGALS9C, USP32P2, FAM106A, CCDC144B
20	rs2071443	23859753	C	T	0.307	0.307	genotyped	1.003	0.216	0.049	1.18E-05	CST9, CST3, CST4, CST1, CST2, CST5, GGTLC1
6	rs115166133	31440669	C	G	0.716	0.285	imputed	0.997	-0.218	0.050	1.21E-05	PSORS1C3, HCG27, HLA
17	rs205108	19678308	A	C	0.324	0.324	imputed	0.945	-0.217	0.050	1.22E-05	SLC47A1, SNORA59A, SNORA59B, ALDH3A2, SLC47A2, ALDH3A1, ULK2, AKAP10, SPECC1
8	rs145045265	95134018	A	G	0.112	0.112	imputed	0.970	0.312	0.072	1.35E-05	MIR378D2, PDP1, CDH17, GEM, RAD54B
4	rs1002221	25427515	A	T	0.912	0.088	imputed	0.963	0.349	0.080	1.36E-05	SEPSECS, PI4K2B, ZCCHC4, ANAPC4, SLC34A2, SEPP1, FLJ32255, LOC648987, ANXA2R, LOC153684, LOC100132356, LOC100506639, ZNF131, NIM1K, HMGCS1, CCL28
5	rs13171192	43102668	C	T	0.964	0.036	imputed	0.940	-0.538	0.124	1.36E-05	SEPP1, FLJ32255, LOC648987, ANXA2R, LOC153684, LOC100132356, LOC100506639, ZNF131, NIM1K, HMGCS1, CCL28
2	rs12992342	210467771	A	G	0.717	0.283	imputed	0.990	0.230	0.053	1.37E-05	MAP2, UNC80
6	rs28687292	932203	C	T	0.865	0.135	imputed	0.913	-0.297	0.068	1.38E-05	EXOC2, HUS1B, LOC101927691, LOC285768
14	rs12050244	82938678	A	T	0.105	0.105	imputed	0.950	-0.324	0.075	1.42E-05	-
2	rs4666058	28563402	G	T	0.065	0.065	imputed	0.904	0.412	0.095	1.46E-05	BRE, LOC100505736, LOC100505716, FLJ31356, FOSL2, PLB1
6	rs7763054	128274667	A	G	0.145	0.145	imputed	0.915	-0.286	0.066	1.54E-05	THEMIS, PTPPRK, LOC101928140
2	rs10195019	69370660	A	C	0.421	0.421	imputed	0.909	0.208	0.048	1.63E-05	BMP10, GKN2, GKN1, ANTXR`, MIR3126, GFPT1, NFU1, LPPR5, LPPR4, LOC100129620, LOC101928270
1	rs75783244	99708843	A	T	0.081	0.081	imputed	0.951	0.359	0.084	1.82E-05	LPPR5, LOC100129620, LPPR4, LOC101928270
9	rs7040936	110273259	G	T	0.855	0.145	imputed	0.817	0.312	0.074	2.17E-05	RAD23B, LINC01509, KLF4

17	rs2108944	9196576	C	T	0.449	0.449	genotyped	1.003	0.190	0.045	2.19E-05	NTN1, LOC101928266, STX8, WDR16
5	rs863221	80042275	G	T	0.209	0.209	imputed	0.985	0.236	0.056	2.19E-05	ZFYVE16, FAM151B, ANKRD34B, LINC01337, DHFR, MTRNR2L2, MSH3, RASGRF2
3	rs729327	11174324	A	G	0.129	0.129	genotyped	1.014	0.280	0.066	2.29E-05	SLC6A11, SLC6A1, HRH1, ATG7
3	rs112051974	169946115	C	T	0.095	0.095	imputed	0.807	0.358	0.085	2.35E-05	SAMD7, LOC100128164, SEC62, GPR160, PHC3, PRKCI, SKIL, CLDN11, MIR6828, SLC7A14
3	rs75395973	15517208	C	T	0.949	0.051	imputed	0.989	-0.429	0.102	2.42E-05	COL6A4P1, CAPN7, SH3BP5, METTL6, EAF1, COLQ, MIR4270, HACL1, BTD, ANKRD28
2	rs2017678	155610942	A	C	0.367	0.367	imputed	0.965	-0.208	0.049	2.50E-05	LOC100144595, KCNJ3
6	rs56092544	53563543	C	T	0.738	0.262	imputed	0.880	0.230	0.055	2.51E-05	GCLC, LOC101927136, LOC101927171, KLHL31, LRRC1, LOC101927189
10	rs11594412	133143956	C	T	0.033	0.033	genotyped	1.049	0.512	0.122	2.54E-05	TCERG1L
12	rs768526	98634060	A	G	0.021	0.021	imputed	0.860	0.710	0.169	2.60E-05	MIR4303, SLC9A7P1, LOC643770, TMPO
6	rs9480568	105952546	C	T	0.306	0.306	imputed	1.003	0.206	0.049	2.62E-05	PREP
11	rs11226214	104046825	A	T	0.935	0.065	genotyped	1.002	0.379	0.090	2.69E-05	PDGFD, DDI1
13	rs9562023	96729741	G	T	0.972	0.028	genotyped	1.017	-0.562	0.134	2.78E-05	DNAJC3, UGGT2, HS6ST3
5	rs256151	151481425	A	G	0.596	0.404	imputed	0.959	0.196	0.047	2.81E-05	G3BP1, GLRA1, NMUR2
11	rs3133084	126027473	A	G	0.399	0.399	imputed	0.987	0.194	0.046	2.85E-05	HYLS1PUS3, DDX25, CDON, RPUSD4, FAM118B, SRPR, FOXRED1, TIRAP, DCPS, ST3GAL4, KIRREL3
9	rs12339503	16394621	A	G	0.390	0.390	imputed	0.879	-0.205	0.049	2.86E-05	C9orf92, BNC2
16	rs72774171	10177152	A	G	0.154	0.154	imputed	0.917	0.270	0.064	2.91E-05	GRIN2A
10	rs114512949	58633476	C	T	0.023	0.023	imputed	0.878	0.664	0.159	3.02E-05	-
2	rs681900	75074967	C	T	0.310	0.310	genotyped	0.995	-0.201	0.048	3.05E-05	LOXL3, DOK1, M1AP, SEMA4F, HK2, LINC01291, POLE4, TACR1, MIR5000
20	rs1413019	12804159	A	C	0.410	0.410	genotyped	1.021	0.189	0.045	3.08E-05	LOC101929486, LOC102606466, LOC100505515, SPTLC3
6	rs365475	132055621	C	T	0.163	0.163	genotyped	0.995	-0.260	0.062	3.09E-05	ARG1, MED23, ENPP3, OR2A4, CTAGE9, ENPP1, CTGF
21	rs17766531	43285830	C	T	0.023	0.023	imputed	0.862	0.674	0.162	3.29E-05	LINC00111, LINC00479, LINC00112, RIPK4, MIR6814, PRDM15, C2CD2, ZBTB21, UMODL1, C21orf128
5	rs256649	33579193	A	G	0.828	0.172	imputed	0.883	-0.261	0.063	3.29E-05	TARS, ADAMTS12

8	rs11203866	17357690	C	T	0.463	0.463	imputed	0.968	0.189	0.046	3.49E-05	ZDHHC2, CNOT7, VPS37A, MTMR7, SLC7A2, PDGFRL, MTUS1
4	rs4864419	138329927	A	T	0.341	0.341	genotyped	1.021	-0.193	0.047	3.54E-05	PCDH18
1	rs7522243	110362858	A	G	0.688	0.312	imputed	0.852	-0.216	0.052	3.62E-05	GPR61, GNAI3, MIR197, GNAT2, AMPD2, GSTM4, GSTM2, GSTM1, GSTM5, GSTM3, EPS8L3, CSF1, AHCYL1, STRIP1, ALX3, UBL4B
2	rs61736780	39107750	A	G	0.121	0.121	imputed	1.002	0.282	0.068	3.75E-05	HNRNPLL, GALM, SRSF7, GEMIN6, DHX57, MORN2, ARHGEF33, LOC375196, SOS1, CDKL4
13	rs9553645	26252082	A	G	0.101	0.101	imputed	1.007	-0.303	0.074	3.76E-05	ATP8A2
3	rs241693	60408404	C	T	0.829	0.171	genotyped	1.019	0.250	0.061	3.82E-05	FHIT
13	rs2892059	28021642	A	G	0.068	0.068	imputed	0.967	-0.371	0.090	3.98E-05	USP12, LINC00412, RPL21, RPL21P28, SNORD102, SNORA27RASL11A, GTF3A, MTIF3, LNX3, POLR1D
1	rs12120264	62141104	C	T	0.453	0.453	imputed	0.932	0.191	0.047	4.12E-05	NFIA, MGC34796, TM2D1, INADL
1	rs2025900	151331304	A	T	0.228	0.228	genotyped	1.002	0.217	0.053	4.14E-05	CDC42SE1, MLLT11, GABPB2, SEMA6C, TNFAIP8L2, LYSMD1, SCNM1, TMOD4, VPS72, PIP5K1A, PSMD4, ZNF687, PI4KB, RFX5, SELENBP1, PSMB4, POGZ, CGN, TUFT1, MIR554, SNX27
19	rs10425058	28769519	G	T	0.334	0.334	genotyped	0.997	0.193	0.047	4.33E-05	LOC100420587
12	rs11045834	21341096	C	T	0.640	0.360	genotyped	0.992	-0.190	0.047	4.41E-05	SLCO1B3, SLCO1B7, SLCO1B1, SLCO1A2, IAPP, PYROXD1, RECQL
15	rs12902838	62859627	A	T	0.143	0.143	imputed	0.896	-0.275	0.067	4.41E-05	MIR8067, MIR6085, TLN2, MIR190A
1	rs12028403	25430696	C	T	0.572	0.428	imputed	0.804	0.206	0.050	4.46E-05	CLIC4, RUNX3, MIR6731, SYF2, RSRP1, RHD, TMEM50A, RHCE
16	rs875528	85966710	A	G	0.190	0.190	imputed	0.972	0.236	0.058	4.48E-05	GSE1, MIR7851, GINS2, C16orf74, MIR1910, EMC8, COX4I1, IRF8, MIR6774, LINC01082, LINC01081
20	rs3787319	48060879	A	G	0.068	0.068	imputed	0.891	0.384	0.094	4.52E-05	STAU1, DDX27, ZNFX1, ZFAS1, SNORD12C, SNORD12B, SNORD12, KCNB1, PTGIS, B4GALT5
14	rs2239223	72849509	A	C	0.777	0.223	imputed	0.870	0.238	0.058	4.59E-05	RGS6, MIR7843, DPF3
14	rs55885638	87406442	C	T	0.828	0.172	imputed	0.949	0.248	0.061	4.60E-05	LOC283585
21	rs9653742	19260617	C	T	0.057	0.057	imputed	1.043	-0.385	0.094	4.62E-05	CXADR, BTG3, C21orf91, CHODL
6	rs6926204	138778360	C	T	0.161	0.161	imputed	0.816	0.273	0.067	4.68E-05	KIAA1244, PBOV1, HEBP2, NHSL1,

												MIR3145, FLJ46906, LOC100507462
12	rs7309339	92307434	A	T	0.887	0.113	imputed	0.950	0.294	0.072	4.78E-05	C12orf79, BTG1
1	rs73109935	238956229	A	G	0.940	0.060	imputed	0.804	0.423	0.104	4.89E-05	-
2	rs777728	195987493	C	T	0.457	0.457	genotyped	0.986	0.185	0.046	5.03E-05	-
2	rs72849648	142243655	A	G	0.261	0.261	imputed	0.956	-0.211	0.052	5.07E-05	LRP1B
18	rs1355829	37442877	G	T	0.489	0.489	genotyped	0.995	-0.181	0.045	5.08E-05	LINC00669, MIR5583
19	rs7255520	56252087	A	G	0.450	0.450	genotyped	0.981	-0.183	0.045	5.14E-05	SHISA7, ISOC2, ZNF628, NAT14, SSC5D, SBK2, SBK3, ZNF579, FIZ1, ZNF524, ZNF865, ZNF784, ZNF580, ZNF581, CCDC106, U2AF2, EPN1, NLRP9, RFPL4A, RFPL4AL1, NLRP11, NLRP4, NLRP13, NLRP8, NLRP5
2	rs2113477	155107307	A	G	0.400	0.400	imputed	1.005	-0.184	0.046	5.23E-05	GALNT13, LOC100144595
8	rs73701495	117825857	C	T	0.217	0.217	imputed	0.963	0.225	0.056	5.36E-05	EIF3H, UTP23, RAD21, MIR3610, AARD, SLC30A8
7	rs114504975	136790449	A	C	0.882	0.118	imputed	0.935	-0.288	0.071	5.37E-05	CHRM2, LOC349160, MIR490, PTN, DGKI
7	rs28811691	136781852	A	T	0.916	0.084	imputed	0.935	-0.337	0.083	5.42E-05	-
9	rs114185697	85885752	A	G	0.965	0.035	imputed	0.863	-0.526	0.130	5.46E-05	RASEF, FRMD3
11	rs621803	81764637	C	T	0.130	0.130	imputed	0.999	-0.267	0.066	5.48E-05	LOC101928989, MIR4300
15	rs1797230	47834003	A	T	0.706	0.294	genotyped	1.014	-0.199	0.049	5.52E-05	SEMA6D, LINC01491
4	rs141747386	29224802	A	G	0.026	0.026	imputed	0.845	-0.615	0.152	5.52E-05	-
11	rs10893883	128374713	C	T	0.841	0.159	genotyped	0.986	0.247	0.061	5.53E-05	ETS1, MIR6090, LOC101929517, FLI1
14	rs3783447	53191647	A	G	0.178	0.178	imputed	0.927	0.244	0.061	5.60E-05	TXNDC16, GPR137C, ERO1L, PSMC6, STYX, GNPNAT1, FERMT2
4	rs6855873	42539270	C	T	0.669	0.331	imputed	0.871	-0.204	0.051	5.74E-05	SHISA3, ATP8A1
17	rs11868357	28681477	A	G	0.845	0.155	imputed	0.974	0.252	0.063	5.75E-05	EFCAB5, NSRP1, MIR423, MIR3184, SLC6A4, BLMH, TMIGD1, CPD, GOSR1, TBC1D29, LRRC37BP1, SH3GL1P2
1	rs4650557	81947833	A	G	0.219	0.219	imputed	0.872	-0.232	0.058	5.76E-05	LOC101927434, LPHN2
8	rs72671011	110955107	C	G	0.894	0.106	imputed	0.845	0.317	0.079	5.86E-05	SYBU, KCNV1
11	rs58295558	13400278	C	G	0.856	0.144	imputed	0.865	-0.273	0.068	5.93E-05	ARNTL, BTBD10, PTH, FAR1
10	rs34657340	63385565	C	T	0.799	0.201	imputed	0.901	-0.236	0.059	6.13E-05	TMEM26, C10orf107, ARID5B
11	rs79672112	35568512	A	G	0.059	0.059	imputed	0.954	-0.387	0.097	6.16E-05	SLC1A2, PAMR1, FJX1, TRIM44

7	rs74809298	86791242	A	G	0.112	0.112	imputed	0.844	-0.308	0.077	6.30E-05	GRM3, KIAA1324L, DMTF1, TMEM243, TP53TG1, CROT, ABCB4
21	rs117310959	21875197	C	T	0.887	0.113	imputed	0.974	0.285	0.071	6.42E-05	LINC00320
1	rs59020993	111311509	C	T	0.801	0.199	imputed	0.973	0.225	0.057	6.93E-05	CYMP, LOC440602, KCNA10, KCNA2, KCNA3, CD53, LRIF1
10	rs12769766	72646785	A	T	0.052	0.052	imputed	0.972	-0.409	0.103	6.98E-05	PRF1, ADAMTS14, TBATA, SGPL1, PCBD1
9	rs10756752	16389209	G	T	0.668	0.332	imputed	1.001	-0.188	0.047	6.99E-05	C9orf92, BNC2
2	rs2074822	241974289	A	G	0.796	0.204	imputed	0.956	0.229	0.058	7.00E-05	KIF1A, AGXT, C2orf54, LOC200772, SNED1, MTERF4, PASK, PPP1R7, ANO7, HDLBP, SEPT2
14	rs1875286	33744179	C	T	0.652	0.348	genotyped	1.010	-0.186	0.047	7.06E-05	NPAS3
8	rs62509955	61098543	A	C	0.963	0.037	imputed	0.951	0.478	0.120	7.08E-05	LINC01301, CA8
5	rs1428221	79137674	A	G	0.942	0.058	imputed	0.972	0.385	0.097	7.14E-05	PAPD4, CMYA5, MTX3, THBS4, SERINC5
2	rs7607006	64608793	A	T	0.657	0.343	genotyped	1.004	0.186	0.047	7.16E-05	PELI1, LINC00309, LOC100507006, LGALSL, AFTPH, MIR4434, LOC339807, SERTAD2
8	rs73631040	20804931	A	G	0.221	0.221	imputed	0.933	0.222	0.056	7.20E-05	LOC286114
9	rs9410127	140629940	C	T	0.692	0.308	genotyped	0.990	-0.194	0.049	7.22E-05	ENTPD8, NSMF, MIR7114, PNPLA7, MRPL41, PNPLA7, DPH7, ZMYND19, ARRDC1, EHMT1, MIR602, LOC100133077, CACNA1B
3	rs1153484	2350800	C	G	0.708	0.292	imputed	0.942	-0.200	0.050	7.26E-05	CNTN4
5	rs7706435	173375673	C	G	0.100	0.100	imputed	0.990	0.297	0.075	7.30E-05	LINC01484, LINC01485, CPEB4, C5orf47, HMP19
11	rs1187173	91992044	A	G	0.128	0.128	genotyped	0.995	0.265	0.067	7.39E-05	FAT3
5	rs10071186	178329095	C	T	0.568	0.432	imputed	0.870	0.191	0.048	7.43E-05	CLK4, ZNF354A, AACSP1, ZNF354B, ZFP2, ZNF454, GRM6, ZNF879, ZNF354C, ADAMTS2
11	rs10834936	26300060	C	T	0.389	0.389	genotyped	0.980	-0.184	0.046	7.45E-05	MAN1C1, SEPN1, MTFR1L, LOC646471, AUNIP, PAQR7, STMN1, MIR3917, PAFAH2, EXTL1, SLC30A2, TRIM63, PDIK1L, FAM110D, ZNF593, CNKSR1, CATSPER4, LOC101928303, CEP85
13	rs78739594	68844332	A	C	0.147	0.147	imputed	0.974	-0.254	0.064	7.52E-05	C1QTNF9B, ANKRD20A19P, SPATA13, MIR2276, C1QTNF9, PARP4
14	rs74462728	83358277	A	G	0.043	0.043	imputed	0.890	-0.460	0.116	7.53E-05	-

13	rs9318386	24771101	C	T	0.756	0.244	genotyped	1.010	0.207	0.052	7.57E-05	-
5	rs10074285	58153360	A	C	0.980	0.020	imputed	0.959	-0.642	0.162	7.72E-05	LOC101928600, RAB3C, PDE4D
13	rs7997918	58090211	A	C	0.855	0.145	imputed	0.949	-0.257	0.065	7.89E-05	PCDH17
12	rs12827379	11971623	C	G	0.746	0.255	genotyped	1.012	0.200	0.051	8.19E-05	LINC01252, ETV6, BCL2L14, MIR1244
3	rs56897773	36788497	A	G	0.234	0.234	imputed	0.843	0.228	0.058	8.20E-05	STAC, DCLK3, TRANK1, EPM2AIP1, MLH1
8	rs1976289	15345669	A	C	0.305	0.305	genotyped	1.011	-0.190	0.048	8.35E-05	SGCZ, TUSC3
2	rs1996412	206612585	C	T	0.121	0.121	genotyped	1.015	-0.279	0.071	8.48E-05	PARD3B, NRP2, INO80D
17	rs8073794	19627229	C	G	0.485	0.485	imputed	0.947	0.180	0.046	8.51E-05	SLC47A1, SNORA59A, SNORA59B, ALDH3A2, SLC47A2, ALDH3A1, ULK2, AKAP10, SPECC1
10	rs9731275	45188487	C	T	0.117	0.117	imputed	0.822	0.302	0.077	8.54E-05	TMEM72, RASSF4, C10orf10
3	rs1865713	24658565	C	T	0.412	0.412	genotyped	0.991	0.180	0.046	8.66E-05	THRB, MIR4792
7	rs13237603	82514138	C	T	0.196	0.196	imputed	0.815	0.244	0.062	8.75E-05	PCLO
2	rs2727897	52579178	C	T	0.174	0.174	imputed	0.963	-0.236	0.060	8.82E-05	-
1	rs58729818	114743061	A	G	0.708	0.292	imputed	0.842	0.210	0.054	8.95E-05	AP4B1, DCLRE1B, HIPK1, OLFML3, SYT6, TRIM33
13	rs111725321	50902466	A	T	0.028	0.028	imputed	0.977	0.536	0.137	8.98E-05	DLEU1, DLEU2, MIR16
11	rs7952680	81757217	C	T	0.045	0.045	imputed	0.908	-0.443	0.113	9.16E-05	LOC101927434
6	rs9383498	169977075	C	T	0.601	0.399	imputed	0.987	0.181	0.046	9.25E-05	WDR27, C6orf120, PHF10, TCTE3, ERMARD, LINC00242, LINC00574
18	rs568405	26452104	C	T	0.899	0.101	imputed	0.897	0.306	0.078	9.28E-05	-
8	rs1112005	18255876	C	T	0.792	0.208	genotyped	1.014	0.213	0.055	9.30E-05	NAT1, NAT2, PSD3
3	rs233143	21573315	A	T	0.836	0.165	imputed	0.897	-0.247	0.063	9.41E-05	VENTXP7, ZNF385D
13	rs61955768	112908035	C	G	0.789	0.211	imputed	0.856	-0.237	0.061	9.45E-05	LINC00403, SOX1, LINC01070, LOC101928730, SPACA7, TUBGCP3
6	rs71552133	2659056	A	G	0.027	0.027	imputed	0.806	0.601	0.154	9.57E-05	C6orf195, MYLK4, WRNIP1, SERPINB1, MIR4645, SERPINB9P1, SERPINB9, SERPINB6
12	rs2219791	21476113	A	T	0.386	0.386	imputed	0.840	-0.196	0.050	9.70E-05	SLCO1B7, SLCO1B1, SLCO1A2, IAPP, PYROXD1, RECQL, GOLT1B, SPX, GYS2
13	13_68849762	68849762	A	G	0.126	0.126	imputed	0.988	-0.264	0.068	9.76E-05	C1QTNF9B, ANKRD20A19P, SPATA13, MIR2276, C1QTNF9, PARP4
5	rs6865183	169479733	A	T	0.198	0.198	imputed	0.959	-0.224	0.057	9.78E-05	DOCK2, FAM196B, MIR378E, FOXI1, LINC01187, C5orf58, LCP2, LINC01366

5	rs6869301	141454199	A	T	0.325	0.325	genotyped	0.989	0.186	0.048	9.78E-05	PCDH1, LOC729080, KIAA0141, PCDH12, RNF14, GNPDA1, NDFIP1, SPRY4, LOC101926941
10	rs2480345	25701341	C	G	0.523	0.477	genotyped	0.993	-0.176	0.045	9.81E-05	LINC01516, GPR158, LINC00836
16	rs4843365	86409396	A	C	0.792	0.208	genotyped	1.016	-0.212	0.054	9.89E-05	LINC01082, LINC01081, LOC146513, FENDRR, FOXF1, MTHFSD, FLJ30679, FOXC2, FOXL1
2	rs1402712	212865774	C	T	0.307	0.307	imputed	0.944	-0.201	0.052	9.93E-05	ERBB4
7	rs4252499	142609749	C	T	0.911	0.090	imputed	0.981	-0.308	0.079	9.98E-05	MTRNR2L6, PRSS1, PRSS3P2, PRSS2, EPHB6, TRPV6, TRPV5, C7orf34, KEL, OR9A2, OR6V1, OR6W1P, PIP, TAS2R39

In these genetic main effect analyses with dosage data, PLINK models A1 as the reference allele. All genes within the region of the SNP are listed (±300kb). The orientation of all SNPs is on the positive (5’ to 3’) strand. SNPs were analyzed using additive coding.

Supplemental Table 3. Genome-wide association study (GWAS) results for the top loci (p<1x10-4) in Hispanics

Chr	SNP	Base Pair	A1	A2	Freq of A1	MAF	Genotyping	Info	Beta	SE	P-value	Genes in Region (±300kb)
4	rs2532087	15878327	C	G	0.231	0.231	imputed	0.815	0.538	0.104	2.44E-07	CC2D2A, FBXL5, FAM200B, BST1, CD38, FGFBP1, FGFBP2, PROM1, TAPT1
18	rs4542757	50198724	C	T	0.418	0.418	imputed	0.930	-0.414	0.083	7.31E-07	DCC
7	rs10249677	50650831	G	T	0.042	0.042	imputed	0.882	1.050	0.216	1.20E-06	IKZF1, FIGNL1, DDC, GRB10
2	rs1129411	231077725	A	G	0.085	0.085	imputed	0.994	0.664	0.142	2.94E-06	TRIP12, FBXO36, SLC16A14, SP110, SP140, SP140L, SP100
5	rs11738766	8214282	A	G	0.279	0.279	genotyped	1.025	-0.413	0.089	3.11E-06	LOC729506, MIR4458HG, MIR4458
1	rs34359572	194036781	A	G	0.928	0.072	imputed	0.890	-0.747	0.162	4.10E-06	-
20	rs609508	54167720	C	G	0.786	0.214	imputed	0.975	0.443	0.097	5.21E-06	LINC01441, LINC01440
2	rs16823787	183692791	A	G	0.916	0.084	genotyped	0.982	0.659	0.144	5.21E-06	DNAJC10, FRZB, NCKAP1, DUSP19, NUP35
4	rs17345417	95948486	A	G	0.889	0.111	genotyped	0.995	-0.574	0.126	5.30E-06	BMPR1B, UNC5C
21	rs2822657	15774729	C	T	0.457	0.457	imputed	0.988	-0.366	0.080	5.35E-06	LIPI, RBM11, ABCC13, HSPA13, SAMSN1, LOC388813
2	rs13033587	52857818	C	T	0.525	0.475	imputed	0.934	0.376	0.083	5.85E-06	-
13	rs9601962	83312889	G	T	0.185	0.185	imputed	0.854	0.495	0.110	6.91E-06	-
6	rs2282123	89907561	C	G	0.745	0.255	genotyped	1.003	0.411	0.092	7.19E-06	RNGTT, PNRC1, SRSF12, PM20D2, GABRR1, GABRR2, UBE2J1, RRAGD, ANKRD6
10	rs10886733	122402887	C	T	0.117	0.117	imputed	0.977	0.556	0.124	7.23E-06	PPAPDC1A, MIR5694, LINC01561, WDR11, KIAA1217, MIR603, ARHGAP21
10	rs61848143	24746704	C	G	0.177	0.177	imputed	0.840	-0.502	0.112	7.85E-06	-
2	rs10166852	183450923	C	G	0.474	0.474	imputed	0.967	-0.375	0.084	7.85E-06	PDE1A, DNAJC10, FRZB, CAMKMT, SIX3SIX2, LINC01121
2	rs6736484	45146524	G	T	0.925	0.075	genotyped	0.856	-0.721	0.162	9.05E-06	-
8	rs2912513	69968166	A	T	0.033	0.033	imputed	0.977	-0.996	0.224	9.33E-06	C8orf34, LOC100505718

2	rs2692223	216264859	C	T	0.388	0.388	imputed	0.946	-0.366	0.083	1.15E-05	ABCA12, ATIC, FN1, LOC102724849, LINC00607
3	rs10452033	53441376	A	G	0.207	0.207	genotyped	1.007	0.425	0.097	1.15E-05	RFT1, PRKCD, TKT, DCP1A, CACNA1D
11	rs6483772	21502994	C	G	0.891	0.109	genotyped	1.005	-0.553	0.127	1.28E-05	NELL1
8	rs2597346	133472489	A	T	0.214	0.214	genotyped	1.037	-0.419	0.096	1.32E-05	KCNQ3, HPYR1, LRRC6, TMEM71
9	rs11138151	81964981	A	G	0.370	0.370	genotyped	1.002	-0.359	0.082	1.33E-05	LOC101927450, TLE4
3	rs2046062	65221301	C	T	0.911	0.089	imputed	0.983	-0.603	0.140	1.61E-05	MIR548A2, MAGI1
7	rs10260904	38265035	C	G	0.724	0.276	imputed	0.993	-0.383	0.089	1.65E-05	EPDR1, STARD3NL, TARP, AMPH
5	rs4895304	120760466	A	G	0.875	0.125	imputed	0.903	-0.545	0.126	1.71E-05	LOC102467226
8	rs77426031	32032495	C	T	0.611	0.389	imputed	1.010	-0.352	0.082	1.82E-05	NRG1
8	rs4871995	22233726	A	C	0.466	0.466	imputed	0.974	0.344	0.080	1.95E-05	DMTN, FAM160B2, NUDT18, HR, REEP4, LGI3, SFTPC, BMP1, PHYHIP, MIR320A, POLR3D, PIWIL2, SLC39A14, PPP3CC, SORBS3, PDLIM2, C8orf58, CCAR2, BIN3
13	rs9558277	105026227	A	G	0.636	0.365	imputed	0.917	-0.366	0.086	1.97E-05	-
2	rs30102	237817538	C	G	0.312	0.312	genotyped	1.015	-0.362	0.085	1.98E-05	COPS8
8	rs2318345	139901178	C	T	0.080	0.080	genotyped	1.066	-0.613	0.144	2.00E-05	COL22A1, TRAPPC9, CHRAC1, AGO2, PTK2
8	rs55879311	141628219	A	G	0.249	0.249	imputed	0.916	0.412	0.097	2.02E-05	-
4	rs3909663	14150004	G	T	0.559	0.441	genotyped	0.981	-0.350	0.082	2.10E-05	LINC01182, LINC01085
3	rs1043435	184797765	C	T	0.851	0.149	imputed	0.896	0.505	0.119	2.22E-05	VPS8, C3orf70, EHHADH, MIR5588, MAP3K13
5	rs6873646	84333373	C	G	0.712	0.288	genotyped	0.973	-0.375	0.088	2.29E-05	-
3	rs1523129	119499608	A	G	0.036	0.036	genotyped	1.091	0.917	0.217	2.37E-05	POGLUT1, TIMMDC1, CD80, ADPRH, PLA1A, POPDC2, COX17, MAATS1, NR1I2, GSK3B
14	rs4902222	63766103	A	G	0.961	0.039	imputed	0.833	-1.012	0.240	2.46E-05	KCNH5, RHOJ, GPHB5, PPP2R5E, WDR89
3	rs61000450	16114030	C	T	0.040	0.040	imputed	0.933	0.918	0.218	2.51E-05	ANKRD28, MIR563, GALNT15, DPH3, OXNAD1, RFTN1
5	rs7726195	107595562	G	T	0.977	0.023	imputed	0.929	-1.214	0.289	2.78E-05	FBXL17

15	rs4924625	42422649	A	G	0.450	0.450	imputed	0.979	-0.342	0.082	3.07E-05	JMJD7, PLA2G4B, SPTBN5, MIR4310, EHD4, LOC101928363, LOC101928388, PLA2G4E, PLA2G4D, PLA2G4F, VPS39, MIR627, TMEM87A, GANC, CAPN3, ZNF106
11	rs568349	60585901	A	G	0.748	0.252	genotyped	1.016	0.380	0.091	3.09E-05	MS4A13, LINC00301, MS4A8, MS4A15, MS4A10, CCDC86, PTGDR2, ZP1, PRPF19, TMEM109, TMEM132A, SLC15A3, CD6
11	rs10792508	80493214	A	C	0.577	0.423	imputed	0.947	-0.351	0.084	3.21E-05	LOC101928944
1	rs72696094	115067229	C	T	0.186	0.186	imputed	0.993	0.424	0.102	3.33E-05	TRIM33, BCAS2, DENND2C, AMPD1, NRAS, CSDE1
2	rs1905469	52897160	A	C	0.607	0.393	genotyped	0.993	-0.336	0.081	3.52E-05	-
10	rs4532958	115214154	A	C	0.729	0.271	imputed	1.016	0.373	0.090	3.54E-05	TCF7L2, HABP2, NRAP, CASP7, PLEKHS1
4	rs17023119	96089692	C	G	0.049	0.049	imputed	1.004	0.764	0.185	3.60E-05	BMPR1B, UNC5C
14	rs7158271	71077857	G	T	0.968	0.032	genotyped	0.997	-0.953	0.230	3.61E-05	COX16, SYNJ2BP, ADAM21, ADAM20P1, ADAM20, MED6, LOC101928075, MAP3K9, PCNX
9	rs10981121	114618482	C	T	0.777	0.224	imputed	1.023	0.390	0.095	3.83E-05	ZNF483, PTGR1, LRRC37A5P, DNAJC25, GNG10, C9orf84, UGCG, MIR4668, MIR3134, SUSD1
17	rs10853165	32878962	C	T	0.303	0.303	genotyped	0.992	0.356	0.086	3.84E-05	CCL2, CCL7, CCL11, CCL8, CCL13, CCL1, C17orf102, TMEM132E
2	rs12471790	179196233	A	G	0.320	0.320	imputed	1.007	0.365	0.089	3.92E-05	PDE11A, RBM45, OSBPL6, MIR548N, LOC101927027, PRKRA, DFNB59, FKBP7, PLEKHA3, TTN
1	rs12025086	209462140	A	G	0.407	0.407	imputed	0.859	-0.359	0.087	4.08E-05	MIR205HG, MIR205, CAMK1G
10	rs41283275	50022040	A	G	0.145	0.145	imputed	1.009	0.458	0.112	4.12E-05	ARHGAP22, WDFY4, LRRC18, MIR4294, VSTM4
2	rs11096713	17142461	G	T	0.169	0.169	imputed	0.970	0.443	0.108	4.13E-05	FAM49A
2	rs28669108	237782083	C	T	0.535	0.465	imputed	0.849	-0.354	0.086	4.15E-05	ACKR3, COPS8
7	rs73728223	154533714	A	G	0.040	0.040	imputed	0.857	0.910	0.222	4.17E-05	DPP6, PAXIP1
2	rs13032996	149016812	A	C	0.634	0.366	imputed	0.958	0.345	0.084	4.22E-05	ORC4, MBD5
12	rs77124177	128446865	A	G	0.886	0.114	imputed	0.960	-0.518	0.126	4.31E-05	FLJ37505, LINC00507, LOC100996679, LOC101927694
4	rs80240587	121622918	A	T	0.977	0.023	imputed	0.868	-1.157	0.284	4.62E-05	PRDM5

17	rs78138611	71705874	A	T	0.906	0.094	imputed	0.936	0.582	0.143	4.63E-05	SDK2, LOC100134391, LINC00469, LOC400620
4	rs1024601	109266380	C	T	0.938	0.062	imputed	0.971	-0.677	0.166	4.70E-05	LEF1, RPL34
4	rs11736272	8064899	G	T	0.229	0.229	imputed	0.920	0.399	0.098	4.73E-05	AFAP1, ABLIM2, SH3TC1, HTRA3
2	rs12052844	237846639	A	G	0.590	0.410	imputed	0.967	-0.331	0.081	4.83E-05	COPS8
18	rs4305172	50262705	C	T	0.583	0.417	imputed	0.935	-0.340	0.084	5.12E-05	DCC
3	rs6770011	56519128	A	T	0.728	0.272	imputed	1.002	-0.366	0.090	5.14E-05	ERC2, CCDC66, FAM208A, ARHGEF3
6	rs2446649	39588118	A	G	0.798	0.202	imputed	0.926	-0.421	0.104	5.29E-05	KCNK16, KIF6, DAAM2, LOC100505635, MOCS1
3	rs1400159	6826053	C	T	0.927	0.073	genotyped	1.000	-0.611	0.151	5.40E-05	GRM7
19	rs12151017	17774512	C	T	0.834	0.167	imputed	0.820	-0.478	0.118	5.47E-05	PLVAP, BST2, MVB12A, TMEM221, NXNL1, SLC27A1, PGLS, FAM129C, COLGAT1, UNC13A, MAP1S, FCHO1, B3GNT3, INSL3, JAK3, RPL18A, SNORA68, SLC5A5, CCDC124, KCNN1
12	rs10842115	23253062	C	G	0.264	0.264	imputed	1.012	-0.368	0.091	5.49E-05	LOC101928441
18	rs73401026	11258947	A	G	0.770	0.231	imputed	1.024	0.380	0.094	5.56E-05	PIEZO2, LINC01255
11	rs1176746	113802601	A	G	0.259	0.259	imputed	0.967	0.371	0.092	5.66E-05	TMPRSS5, ZW10, CLDN25, USP28, HTR3B, HTR3A, ZBTB16
2	rs7599310	49232729	A	G	0.796	0.204	imputed	0.913	-0.419	0.104	5.67E-05	STON1-GTF2A1L, LHCGR, FSHR
5	rs984465	99613735	C	T	0.422	0.422	imputed	0.941	0.335	0.083	5.71E-05	LOC100133050, FAM174A
2	rs17016152	35326045	A	T	0.073	0.073	imputed	0.991	0.614	0.153	5.77E-05	IFT74, LRRC19, TEK, LINC00032, EQTN, MOB3B, IFNK, C9orf72
9	rs57352266	27248138	G	T	0.882	0.119	imputed	0.991	-0.491	0.122	6.06E-05	TET1, CCAR1, SNORD98, STOX1, DDX50, DDX21, KIAA1279, SRGN, VPS26A, SUPV3L1, LOC101928994, HKDC1, HK1
10	rs7907661	70740091	A	G	0.186	0.186	genotyped	1.013	0.411	0.103	6.19E-05	MYOCD, LOC100128006, ARHGAP44, ELAC2
17	rs72815168	12950555	A	C	0.205	0.205	imputed	0.903	-0.414	0.103	6.29E-05	LINC01213, LINC01214, TSC22D2, SERP1, EIF2A, SELT
3	rs9845738	150062028	A	G	0.329	0.329	imputed	0.992	0.339	0.085	6.32E-05	ST13, XPNPEP3, DNAJB7, RBX1, MIR1281, EP300, L3MBTL2, CHADL, RANGAP1, MIR6889, ZC3H7B, TEF

22	rs11912447	41528577	C	T	0.034	0.034	imputed	0.957	0.943	0.235	6.37E-05	NRXN1, FAM49A
2	rs10197605	49930153	A	C	0.500	0.500	imputed	0.978	0.319	0.080	6.39E-05	-
2	rs12466757	17132189	C	T	0.452	0.452	genotyped	1.010	0.325	0.081	6.42E-05	-
12	rs10777158	77835446	G	T	0.310	0.310	genotyped	1.035	-0.337	0.084	6.47E-05	-
6	rs11153331	112368342	C	T	0.567	0.433	imputed	0.859	-0.344	0.086	6.50E-05	FYN, WISP3, TUBE1, FAM229B, LAMA4, LOC101927640
12	rs4767925	121085949	A	G	0.907	0.093	imputed	0.833	-0.595	0.149	6.61E-05	MSI1, COX6A1, TRIAP1, GATC, SRSF9, DYNLL1, COQ5, RNF10, POP5, CABP1, MLEC, UNC119B, MIR4700, ACADS, SPPL3
19	rs2269816	58064287	C	T	0.255	0.255	imputed	1.012	0.360	0.090	6.68E-05	ZNF805, ZNF460, ZNF543, ZNF304, TRAPPC2B, ZNF547, ZNF548, ZNF17, ZNF749, VN1R1, ZNF772, ZNF419, ZNF773, ZNF549, ZNF550, ZNF416, ZIK1, ZNF530, ZNF134, ZNF211, ZSCAN4, ZNF551, ZNF154, ZNF671, ZNF776, ZNF586, ZNF552, FKBP1AP1, ZNF587B, ZNF587
2	rs2056788	180973167	C	T	0.032	0.032	imputed	1.034	-0.938	0.235	6.69E-05	ZNF385B, MIR1258, CWC22
9	rs7862935	112375372	C	T	0.148	0.148	imputed	1.002	-0.452	0.114	6.97E-05	EPB41L4B, PTPN3, PALM2
11	rs10768049	34193779	C	T	0.554	0.447	imputed	0.931	-0.326	0.082	7.22E-05	LMO2, CAPRIN1, NAT10, ABTB2, CAT, LOC102724957, SOX6, MIR6073
14	rs35612540	26083442	C	T	0.549	0.451	imputed	0.926	-0.325	0.082	7.39E-05	-
2	rs13425598	35230677	A	G	0.905	0.095	imputed	0.924	-0.571	0.144	7.45E-05	-
11	rs11023812	16006615	A	G	0.076	0.076	imputed	0.864	0.637	0.161	7.58E-05	-
15	rs12908653	62994928	A	G	0.370	0.370	imputed	0.911	0.343	0.087	7.58E-05	MGC15885, TLN2, MIR190A
2	rs842560	184288853	C	T	0.967	0.033	imputed	1.066	0.920	0.233	7.75E-05	NUP35
4	rs12500262	66669547	A	T	0.693	0.307	genotyped	0.990	0.341	0.086	8.06E-05	EPHA5
11	rs1482747	23224830	C	G	0.667	0.333	imputed	1.020	-0.331	0.084	8.08E-05	MIR8054
2	rs17244632	165551404	A	G	0.081	0.081	genotyped	1.033	0.568	0.144	8.08E-05	GRB14, COBLL1, SNORA70F, LOC101929633, SLC38A11
6	rs13203167	96228904	A	G	0.530	0.470	imputed	0.915	-0.328	0.083	8.24E-05	FUT9, MANEA

8	rs73199978	18623251	C	G	0.874	0.126	imputed	0.931	-0.498	0.127	8.35E-05	PSD3
17	rs16959526	64525885	A	G	0.210	0.210	genotyped	1.070	0.370	0.094	8.42E-05	PRKCA, MIR634
8	rs10101909	22277040	A	G	0.352	0.352	imputed	0.829	-0.360	0.092	8.46E-05	HR, REEP4, LGI3, SFTPC, BMP1, PHYHIP, MIR320A, POLR3D, PIWIL2, SLC39A14, PPP3CC, SORBS3, PDLIM2, C8orf58, CCAR2, BIN3, EGR3, PEBP4
12	rs2596756	95857121	C	G	0.852	0.148	imputed	0.924	0.454	0.115	8.47E-05	FGD6, VEZT, MIR331, MIR3685, METAP2, USP44, PGAM1P5, NTN4
5	rs2112145	97969137	A	G	0.144	0.144	genotyped	1.012	0.443	0.113	8.62E-05	RGMB, CHD1, LOC100289230
19	rs56127833	48146967	A	G	0.081	0.081	imputed	0.970	0.578	0.147	8.91E-05	DHX34, MEIS3, SLC8A2, KPTN, NAPA, ZNF541, GLTSCR1, EHD2, GLTSCR2, SNORD23, SEPW1, TPRX1, CRX, SULT2A1, SNAR-A13, SNAR-A12, SNAR-C1, SNAR-C2, SNAR-C5, SNAR-A2, SNAR-A1, SNAR-A3, SNAR-A9, SNAR-A4, SNAR-A8, SNAR-A6, SNAR-A5, SNAR-A7, SNAR-A14, SNAR-A11, SNAR-A10, SNAR-C5, SNAR-C1, SNAR-C2, SNAR-C4
4	rs4697429	23937074	C	T	0.357	0.357	genotyped	1.055	-0.334	0.085	9.03E-05	PPARGC1A
8	rs34919099	89722463	G	T	0.221	0.221	imputed	0.971	0.378	0.097	9.15E-05	-
18	rs3894011	48167352	C	T	0.030	0.030	imputed	0.880	0.965	0.247	9.27E-05	SKA1, MAPK4, MRO, ME2
1	rs1981228	216056210	A	T	0.432	0.432	imputed	0.913	0.328	0.084	9.33E-05	KCTD3, USH2A
9	rs10820820	93731198	C	T	0.879	0.121	genotyped	1.012	0.472	0.121	9.51E-05	SYK, LOC100129316, AUH
11	rs11219892	124953354	C	T	0.839	0.161	imputed	0.940	0.434	0.111	9.74E-05	MSANTD2, LOC100507283, ROBO3, ROBO4, HEPN1, HEPACAM, CCDC15, SLC37A2, TMEM218, PKNOX2
20	rs78384127	36960439	A	G	0.955	0.045	imputed	0.806	0.826	0.212	9.91E-05	TTI1, RPRD1B, TGM2, KIAA1755, LOC149684, BPI, LBP, SNHG17, SNORA71B, SNORA71A, SNORA71C, SNORA71D, SNHG11, SNORA71E, NORA60, RALGAPB, ADIG, ARHGAP40
9	rs11144241	77737899	A	G	0.940	0.060	imputed	0.917	-0.673	0.173	9.99E-05	TRPM6, C9orf40, C9orf41, NMRK1, OSTF1

In these genetic main effect analyses with dosage data, PLINK models A1 as the reference allele. All genes within the region of the SNP are listed (±300kb). The orientation of all SNPs is on the positive (5’ to 3’) strand. SNPs were analyzed using additive coding.

Supplemental Table 4. Genome-wide association study (GWAS) results for the top loci (p<1x10-4) for the X chromosome in African Americans and Hispanics

African Americans

CHR	BP	A1	A2	FRQ A1	INFO	BETA	SE	P
23	4508701	A	G	0.254	0.999	-0.214	0.052	3.48E-05
23	111748128	C	G	0.346	0.936	-0.200	0.049	5.29E-05
23	30633161	A	G	0.104	1.006	0.297	0.074	5.66E-05
23	30632452	A	C	0.106	0.977	0.294	0.074	7.07E-05
23	111712678	A	C	0.347	0.990	-0.189	0.048	7.50E-05
23	30618423	C	T	0.107	0.948	0.297	0.075	7.52E-05
23	111715262	C	T	0.652	0.981	0.190	0.048	7.67E-05
23	111717346	C	T	0.338	0.965	-0.191	0.049	8.95E-05

Hispanics

CHR	BP	A1	A2	FRQ A1	INFO	BETA	SE	P
23	4633635	C	G	0.535	1.013	-0.347	0.079	1.00E-05
23	4633714	G	T	0.535	1.015	-0.347	0.078	1.02E-05
23	4634014	C	T	0.465	1.015	0.347	0.078	1.02E-05
23	4634601	C	T	0.465	1.015	0.346	0.078	1.04E-05
23	4634120	C	T	0.465	1.015	0.346	0.078	1.04E-05
23	4631296	A	C	0.544	1.020	-0.344	0.078	1.18E-05
23	4632372	A	G	0.533	1.002	-0.346	0.079	1.19E-05
23	4633322	C	T	0.546	0.942	-0.356	0.082	1.31E-05
23	4632073	G	T	0.460	0.982	0.348	0.080	1.38E-05
23	4631907	A	G	0.462	1.027	0.337	0.078	1.62E-05
23	4631254	C	T	0.544	1.017	-0.339	0.079	1.64E-05
23	4632561	C	T	0.475	0.983	0.340	0.080	1.95E-05
23	8956544	A	G	0.046	1.009	0.793	0.187	2.32E-05
23	4643304	A	G	0.535	0.922	-0.348	0.083	2.60E-05
23	4643144	A	G	0.534	0.921	-0.343	0.083	3.49E-05
23	4643018	C	T	0.467	0.921	0.343	0.083	3.57E-05
23	153211538	A	G	0.433	1.039	0.350	0.085	3.62E-05
23	153247722	C	T	0.589	0.981	-0.363	0.088	3.64E-05
23	153247954	C	T	0.582	1.005	-0.357	0.086	3.65E-05
23	153219665	C	T	0.568	1.049	-0.347	0.084	3.80E-05
23	153227770	A	G	0.433	1.066	0.344	0.083	3.80E-05
23	153225634	C	G	0.434	1.049	0.346	0.084	3.93E-05
23	153246018	A	G	0.571	1.051	-0.346	0.084	3.94E-05
23	153241386	G	T	0.566	1.073	-0.339	0.083	4.46E-05
23	153245128	C	G	0.566	1.070	-0.339	0.083	4.48E-05
23	153254605	C	G	0.563	1.014	-0.348	0.085	4.54E-05
23	153239720	A	G	0.435	1.082	0.337	0.083	4.64E-05
23	153245217	A	G	0.446	1.013	0.344	0.085	5.15E-05
23	8954586	C	T	0.958	0.903	-0.829	0.206	5.91E-05

23	4642016	C	T	0.424	1.005	0.317	0.079	6.66E-05
23	153207925	A	G	0.485	0.977	0.338	0.086	8.09E-05
23	153252908	C	T	0.468	0.936	0.343	0.088	9.17E-05
23	153252147	C	T	0.469	0.932	0.344	0.088	9.18E-05
23	153247745	A	G	0.536	0.899	-0.350	0.090	9.36E-05
23	69401419	C	T	0.466	0.889	-0.335	0.086	9.59E-05

In these genetic main effect analyses, PLINK models A1 as the tested allele. The orientation of all SNPs is on the positive (5' to 3') strand. SNPS were analyzed using additive coding and allele dosages.

Supplemental Table 5. Results from look-ups of top SNPs in each sample with the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE Consortium) meta analysis of depressive symptoms (n=51,258)

Top SNPs from African American Analysis

SNP	A1	A2	Freq A1	FreqSE	MinFreq	MaxFre	Weight	Z-score	p-value	Direction	Het Isq	Het Chisquare	Het DF	Het p-value
rs580112	A	G	0.376	0.021	0.336	0.443	34549	2.144	0.0321	+++-++++-++++++---	0	13.949	17	0.6707
rs1413154	T	G	0.940	0.016	0.869	0.951	33165	0.269	0.7882	--+-+++++?--++---+	16.7	19.204	16	0.2582
rs1893586	A	G	0.374	0.021	0.308	0.396	34548	-1.140	0.2544	---++++--+-+-+-++-	0	16.656	17	0.4779
rs10777901	A	C	0.508	0.016	0.470	0.558	33111	-0.963	0.3357	++++-----++----+-?	14.2	18.656	16	0.2869
rs10125319	T	C	0.609	0.027	0.526	0.649	34549	-0.462	0.6440	-+-+-++--+----+-+-	18.2	20.790	17	0.2358
rs10221121	A	G	0.291	0.020	0.255	0.345	34547	-2.132	0.0330	-+--+------+----+-	0	8.962	17	0.9415
rs210329	T	G	0.622	0.034	0.464	0.639	34549	-0.067	0.9467	+--++---++--+-+++-	0	10.885	17	0.8625
rs17030391	A	G	0.165	0.007	0.151	0.184	34549	-0.329	0.7420	++-+----+-+++--+--	0	11.286	17	0.8413
rs4866976	A	G	0.947	0.007	0.927	0.962	28949	0.573	0.5667	+?+??---+-+-+++--?	0	12.606	13	0.4787
rs418207	A	G	0.401	0.027	0.347	0.497	34549	-0.370	0.7118	--+++-+++--+++-+--	0	9.819	17	0.9110

Top SNPs from Hispanic Analysis

SNP	A1	A2	Freq A1	FreqSE	MinFreq	MaxFre	Weight	Z-score	p-value	Direction	Het Isq	Het Chisquare	Het DF	Het p-value
rs2532087	C	G	0.201	0.017	0.176	0.243	33111	-0.383	0.7018	-+--++-+---++++--?	0	13.122	16	0.664
rs4542757	T	C	0.653	0.026	0.604	0.713	34549	0.934	0.3503	+-+-+--++++-+++-+-	35.2	26.253	17	0.070
rs11738766	A	G	0.130	0.014	0.093	0.144	33541	-0.326	0.7443	+--??-+---++--+--+	0	5.741	15	0.984
rs609508	C	G	0.784	0.017	0.765	0.830	34548	-0.339	0.7348	-++--++++++-+-+---	0	12.576	17	0.764
rs16823787	A	G	0.909	0.015	0.875	0.943	31394	-0.984	0.3252	-?-+++---++----+-+	0	14.222	16	0.582
rs17345417	A	G	0.877	0.019	0.817	0.898	34549	0.010	0.9921	-+-+--++++---+-+-+	0	15.891	17	0.532
rs2822657	T	C	0.407	0.020	0.328	0.440	34548	-1.204	0.2285	---++---++-+-++--+	0	16.098	17	0.517
rs2282123	C	G	0.834	0.020	0.754	0.861	34548	0.476	0.6337	+-++-+-+--+-+---++	0	8.883	17	0.944

These results are based on the CHARGE Consortium meta-analysis GWAS of depressive symptoms using 17 population-based studies (n=51,258 individuals) of White older adults where depressive symptoms were measured through the CESD. Meta analysis was performed using p-value based method, weighted by sample size, and adjusting for age, sex, and principal components. Analyses were performed in METAL, where A2 was the tested allele.

Supplemental Table 6. Top loci from African American GWAS (10x10-5) in Hispanics and results from meta analysis of WHI participants

		African American GWAS Results				Hispanic GWAS Results				Meta Analysis Results								
Chr	SNP	A1	A2	A1 Freq	p-value	A1	A2	Freq A1	p-value	A1	A2	Effect	SE	p-value	Direction	HetISq	HetChiSq	HetPVal
16	chr16:20105038	C	T	0.771	5.75E-08	C	T	0.910	0.7615	T	C	0.264	0.051	2.27E-07	++	64.1	2.787	0.095
11	rs58295558	C	G	0.856	0.00005935	C	G	0.893	0.0007189	C	G	-0.309	0.060	2.86E-07	--	21.2	1.269	0.260
17	rs2108944	C	T	0.449	0.00002194	C	T	0.506	0.03635	T	C	-0.183	0.039	2.29E-06	--	0	0.095	0.758
13	rs1413154	G	T	0.205	3.54E-06	G	T	0.059	0.3315	T	G	0.271	0.058	2.53E-06	++	0	0.362	0.547
3	rs1526725	A	G	0.535	0.00001014	A	G	0.614	0.09321	A	G	-0.185	0.039	2.87E-06	--	0	0.408	0.523
2	rs1402712	C	T	0.307	0.00009931	C	T	0.633	0.01409	T	C	0.203	0.044	4.16E-06	++	0	0.007	0.934
16	chr16:10177152	A	G	0.154	0.00002908	A	G	0.057	0.05652	A	G	0.276	0.060	4.43E-06	++	0	0.083	0.773
21	rs1893586	A	G	0.483	4.19E-06	A	G	0.350	0.2741	A	G	0.184	0.040	5.00E-06	++	35.9	1.561	0.212
6	rs6926204	C	T	0.161	0.00004677	C	T	0.129	0.04335	T	C	-0.266	0.059	5.58E-06	--	0	0.049	0.826
11	rs11233283	A	G	0.842	1.41E-06	A	G	0.959	0.758	A	G	-0.268	0.059	5.79E-06	-+	64.6	2.822	0.093
17	rs205108	A	C	0.324	0.00001216	A	C	0.106	0.246	A	C	-0.209	0.047	6.72E-06	--	0	0.198	0.656
17	rs11868357	A	G	0.845	0.00005747	A	G	0.959	0.02885	A	G	0.269	0.060	7.48E-06	++	0	0.933	0.334
12	rs12827379	C	G	0.746	0.00008193	C	G	0.828	0.03342	C	G	0.204	0.046	7.59E-06	++	0	0.039	0.843
6	rs3828890	C	G	0.716	0.00001214	C	G	0.869	0.2929	C	G	-0.203	0.046	8.96E-06	--	0	0.536	0.464
12	rs7309339	A	T	0.887	0.00004777	A	T	0.944	0.1141	A	T	0.293	0.067	0.00001271	++	0	0.002	0.962
11	rs10893883	C	T	0.841	0.00005529	C	T	0.789	0.08682	T	C	-0.223	0.052	0.00001521	--	0	0.522	0.470
5	rs256151	A	G	0.596	0.00002808	A	G	0.294	0.222	A	G	0.178	0.042	0.00001841	++	0	0.7	0.403
9	rs10756752	G	T	0.668	0.00006987	G	T	0.499	0.1012	T	G	0.174	0.041	0.00002022	++	0	0.367	0.545
2	chr2:142243655	A	G	0.261	0.0000507	A	G	0.393	0.1182	A	G	-0.187	0.044	0.00002077	--	0	0.773	0.379
8	rs2446816	A	G	0.112	0.00001346	A	G	0.103	0.4835	A	G	0.262	0.063	0.000032	++	53.6	2.155	0.142
3	rs729327	A	G	0.129	0.00002295	A	G	0.083	0.484	A	G	0.248	0.060	0.00003496	++	24.2	1.319	0.251
3	rs580112	A	G	0.184	2.84E-06	A	G	0.332	0.6064	A	G	0.201	0.049	0.00003724	++	80.8	5.204	0.023
9	rs12339503	A	G	0.390	0.00002857	A	G	0.175	0.5027	A	G	-0.183	0.045	0.00004193	--	16.1	1.191	0.275
4	rs6855873	C	T	0.669	0.00005738	C	T	0.731	0.24	T	C	0.182	0.045	0.00004216	++	0	0.815	0.367
2	rs61736780	A	G	0.121	0.00003755	A	G	0.026	0.6905	A	G	0.270	0.066	0.00004345	++	0	0.443	0.506
3	rs1153484	C	G	0.708	0.00007256	C	G	0.731	0.2222	C	G	-0.179	0.044	0.00004815	--	0	0.765	0.382

1	chr1:238956229	A	G	0.940	0.00004887	A	G	0.973	0.4282	A	G	0.389	0.096	0.00005057	++	0	0.728	0.394
2	rs9287319	A	G	0.619	0.00001014	A	G	0.879	0.7287	A	G	-0.175	0.044	0.00006166	-+	72.2	3.592	0.058
20	rs2071443	C	T	0.307	0.00001179	C	T	0.549	0.6305	T	C	-0.167	0.042	0.00006628	--	72	3.574	0.059
8	rs11203866	C	T	0.463	0.00003494	C	T	0.247	0.5635	T	C	-0.163	0.041	0.00007035	--	40.8	1.69	0.194
2	rs2113477	A	G	0.400	0.00005226	A	G	0.578	0.3802	A	G	-0.159	0.040	0.0000712	--	27.5	1.38	0.240
15	rs1797230	A	T	0.706	0.00005516	A	T	0.500	0.3172	A	T	-0.165	0.042	0.0000782	--	39.8	1.661	0.197
6	rs365475	C	T	0.163	0.0000309	C	T	0.456	0.2884	T	C	0.194	0.049	0.00007913	++	66.1	2.953	0.086
13	rs7997918	A	C	0.855	0.00007888	A	C	0.904	0.3908	A	C	-0.231	0.059	0.00008226	--	0	0.852	0.356
5	rs13171192	C	T	0.964	0.00001364	C	T	0.909	0.3127	T	C	0.364	0.093	0.00008559	++	77.9	4.534	0.033
12	rs11045834	C	T	0.640	0.00004406	C	T	0.682	0.4806	T	C	0.160	0.041	0.00008799	++	44.9	1.816	0.178
14	rs3783447	A	G	0.178	0.00005597	A	G	0.075	0.6228	A	G	0.220	0.056	0.00008822	++	9.7	1.107	0.293
3	rs418207	A	G	0.477	9.59E-06	A	G	0.345	0.9905	A	G	-0.171	0.044	0.00008987	--	76.6	4.271	0.039
3	rs241693	C	T	0.829	0.0000382	C	T	0.649	0.3502	T	C	-0.191	0.049	0.0001009	--	63.7	2.757	0.097
13	rs2892059	A	G	0.068	0.0000398	A	G	0.029	0.9055	A	G	-0.327	0.084	0.0001025	--	45.4	1.833	0.176
7	rs4252499	C	T	0.911	0.00009979	C	T	0.954	0.4691	T	C	0.284	0.073	0.0001057	++	0	0.664	0.415
14	chr14:83358277	A	G	0.043	0.0000753	A	G	0.046	0.3639	A	G	-0.383	0.099	0.0001134	--	38.1	1.616	0.204
16	rs4843365	A	C	0.792	0.00009889	A	C	0.845	0.4124	A	C	-0.188	0.049	0.0001154	--	0	0.965	0.326
6	rs28687292	C	T	0.865	0.00001376	C	T	0.975	0.135	T	C	0.255	0.066	0.0001182	+-	84.2	6.319	0.012
3	rs1865713	C	T	0.412	0.00008664	C	T	0.167	0.5558	T	C	-0.163	0.042	0.0001188	--	0	0.983	0.322
12	rs2219791	A	T	0.386	0.00009697	A	T	0.166	0.4682	A	T	-0.176	0.046	0.000119	--	0	0.933	0.334
9	rs10125319	C	T	0.491	4.27E-06	C	T	0.413	0.7499	T	C	0.156	0.041	0.0001206	+-	84.5	6.458	0.011
5	rs6865183	A	T	0.198	0.00009782	A	T	0.039	0.737	A	T	-0.213	0.055	0.0001207	--	0	0.505	0.477
5	rs6869301	A	T	0.325	0.00009779	A	T	0.281	0.3987	A	T	0.160	0.042	0.0001283	++	21.1	1.268	0.260
21	chr21:21875197	C	T	0.887	0.00006419	C	T	0.904	0.5454	T	C	-0.240	0.063	0.0001351	--	44.3	1.796	0.180
15	rs12902838	A	T	0.143	0.00004414	A	T	0.292	0.3497	A	T	-0.202	0.053	0.0001432	--	68	3.124	0.077
16	rs875528	A	G	0.190	0.00004485	A	G	0.110	0.8931	A	G	0.199	0.053	0.0001538	++	58.2	2.394	0.122
21	rs9653742	C	T	0.057	0.00004618	C	T	0.020	0.6998	T	C	0.334	0.089	0.0001845	+-	64.3	2.8	0.094
3	rs56897773	A	G	0.234	0.00008197	A	G	0.052	0.8136	A	G	0.207	0.056	0.0001977	+-	42	1.723	0.189
11	rs7952680	C	T	0.045	0.00009155	C	T	0.027	0.7109	T	C	0.383	0.103	0.0002021	++	39.5	1.654	0.198

14	rs12050244	A	T	0.105	0.00001421	A	T	0.082	0.7667	A	T	-0.245	0.066	0.0002094	-+	80.8	5.206	0.023
8	chr8:117825857	C	T	0.217	0.00005355	C	T	0.029	0.2443	T	C	-0.202	0.054	0.0002117	-+	74.9	3.978	0.046
20	rs3787319	A	G	0.068	0.00004519	A	G	0.025	0.6497	A	G	0.328	0.089	0.0002119	+-	68.4	3.164	0.075
6	rs56092544	C	T	0.738	0.00002514	C	T	0.609	0.7671	T	C	-0.166	0.045	0.0002487	--	77.6	4.46	0.035
8	chr8:110955107	C	G	0.894	0.00005861	C	G	0.938	0.9775	C	G	0.261	0.072	0.0002686	+-	65.5	2.897	0.089
2	rs2017678	A	C	0.367	0.00002498	A	C	0.810	0.6456	A	C	-0.163	0.045	0.0002729	-+	78.9	4.748	0.029
16	rs10221121	A	G	0.229	5.98E-06	A	G	0.257	0.5831	A	G	-0.167	0.046	0.0002773	-+	86.9	7.621	0.006
19	rs7255520	A	G	0.450	0.0000514	A	G	0.367	0.9529	A	G	-0.142	0.040	0.0003503	--	72.5	3.633	0.057
3	rs28493952	C	T	0.320	6.41E-06	C	T	0.153	0.1674	T	C	-0.169	0.047	0.0003551	-+	89.6	9.577	0.002
7	rs10228919	A	C	0.882	0.00005374	A	C	0.890	0.9889	A	C	-0.223	0.063	0.0003806	--	72.9	3.69	0.055
2	rs681900	C	T	0.310	0.00003052	C	T	0.188	0.6055	T	C	0.154	0.044	0.0003889	+-	80.4	5.106	0.024
7	rs13237603	C	T	0.196	0.00008753	C	T	0.263	0.6474	T	C	-0.186	0.052	0.0003889	--	67.1	3.038	0.081
14	rs210329	G	T	0.668	6.35E-06	G	T	0.435	0.4922	T	G	-0.146	0.041	0.0004022	-+	88.1	8.389	0.004
3	chr3:15517208	C	T	0.949	0.00002418	C	T	0.966	0.3872	T	C	0.326	0.093	0.0004529	+-	84.1	6.293	0.012
10	rs34657340	C	T	0.799	0.00006128	C	T	0.842	0.9214	T	C	0.180	0.052	0.0004983	+-	74.9	3.983	0.046
2	rs17030391	A	G	0.143	7.84E-06	A	G	0.098	0.2951	A	G	0.215	0.062	0.0005475	+-	89.1	9.158	0.002
1	rs59020993	C	T	0.801	0.00006926	C	T	0.851	0.8026	T	C	-0.173	0.050	0.0005885	-+	75.5	4.081	0.043
20	rs1413019	A	C	0.410	0.00003081	A	C	0.680	0.5824	A	C	0.137	0.040	0.0006152	+-	83.2	5.958	0.015
8	rs1112005	C	T	0.792	0.00009302	C	T	0.796	0.9998	T	C	-0.162	0.048	0.0006422	0	72.4	3.625	0.057
2	rs777728	C	T	0.457	0.00005032	C	T	0.237	0.5707	T	C	-0.140	0.041	0.0006606	-+	80.7	5.184	0.023
11	rs11226214	A	T	0.935	0.00002692	A	T	0.855	0.8503	A	T	0.238	0.070	0.0007085	++	83.9	6.212	0.013
2	rs12992342	A	G	0.717	0.00001367	A	G	0.221	0.3105	A	G	0.158	0.047	0.0007126	+-	88.2	8.483	0.004
17	rs8073794	C	G	0.485	0.00008511	C	G	0.530	0.8057	C	G	0.137	0.041	0.000749	+-	75.8	4.126	0.042
14	rs1875286	C	T	0.652	0.00007057	C	T	0.657	0.7778	T	C	0.138	0.041	0.0007752	+-	78.3	4.609	0.032
1	rs12028403	C	T	0.572	0.0000446	C	T	0.575	0.7643	T	C	-0.143	0.043	0.0008706	-+	82.4	5.679	0.017
10	rs2480345	C	G	0.523	0.00009812	C	G	0.432	0.8624	C	G	-0.131	0.040	0.0008729	-+	75.9	4.145	0.042
19	rs10425058	G	T	0.334	0.00004326	G	T	0.304	0.6001	T	G	-0.138	0.041	0.0008869	-+	83.2	5.943	0.015
11	chr11:35568512	A	G	0.059	0.00006155	A	G	0.120	0.7912	A	G	-0.251	0.076	0.0009263	--	80.7	5.175	0.023
11	rs3133084	A	G	0.399	0.00002853	A	G	0.633	0.4727	A	G	0.134	0.041	0.0009406	+-	85.9	7.109	0.008

2	rs10195019	A	C	0.421	0.00001634	A	C	0.639	0.3795	A	C	0.139	0.042	0.0009464	+-	88.1	8.424	0.004
14	rs55885638	C	T	0.828	0.00004602	C	T	0.750	0.8402	T	C	-0.167	0.051	0.0009987	-+	82.9	5.848	0.016
18	rs568405	C	T	0.899	0.00009283	C	T	0.827	0.789	T	C	-0.206	0.063	0.001013	--	78	4.55	0.033
13	chr13:68844332	A	C	0.147	0.00007518	A	C	0.024	0.01146	A	C	-0.204	0.062	0.001052	-+	91.2	11.371	0.001
5	rs10071186	C	T	0.568	0.00007434	C	T	0.508	0.7221	T	C	-0.137	0.042	0.001059	-+	80.5	5.125	0.024
1	rs12120264	C	T	0.453	0.00004125	C	T	0.290	0.3659	T	C	-0.136	0.042	0.001067	-+	85.6	6.949	0.008
11	rs621803	C	T	0.130	0.00005475	C	T	0.202	0.7911	T	C	0.176	0.055	0.00132	+-	83.5	6.073	0.014
10	rs12769766	A	T	0.052	0.00006981	A	T	0.118	0.8125	A	T	-0.253	0.079	0.001347	--	82.2	5.625	0.018
1	rs2025900	A	T	0.228	0.00004142	A	T	0.245	0.4922	A	T	0.147	0.046	0.001354	+-	85.7	6.999	0.008
10	rs11594412	C	T	0.033	0.00002542	C	T	0.053	0.637	T	C	-0.318	0.100	0.001432	-+	87.2	7.809	0.005
12	rs10777901	A	C	0.481	4.27E-06	A	C	0.494	0.07619	A	C	0.125	0.039	0.001482	+-	92.9	14.178	0.000
21	rs17766531	C	T	0.023	0.00003294	C	T	0.052	0.9132	T	C	-0.383	0.121	0.001534	--	86.2	7.232	0.007
6	rs7763054	A	G	0.145	0.0000154	A	G	0.263	0.5018	A	G	-0.171	0.054	0.001615	-+	89.2	9.229	0.002
5	rs863221	G	T	0.209	0.00002188	G	T	0.336	0.4579	T	G	-0.146	0.047	0.001675	-+	88.5	8.723	0.003
13	rs61955768	C	G	0.789	0.00009449	C	G	0.586	0.9923	C	G	-0.153	0.049	0.001742	-+	81.7	5.455	0.020
11	rs10834936	C	T	0.389	0.00007448	C	T	0.175	0.1689	T	C	0.131	0.042	0.002042	+-	87.6	8.091	0.004
13	rs9562023	G	T	0.972	0.00002785	G	T	0.931	0.8529	T	G	0.313	0.102	0.002166	+-	87.8	8.207	0.004
10	chr10:58633476	C	T	0.023	0.00003024	C	T	0.023	0.2866	T	C	-0.418	0.137	0.00228	-+	89.2	9.246	0.002
1	rs4650557	A	G	0.219	0.00005763	A	G	0.253	0.4774	A	G	-0.148	0.049	0.00247	-+	86.7	7.524	0.006
13	rs9318386	C	T	0.756	0.0000757	C	T	0.614	0.537	T	C	-0.134	0.044	0.002502	-+	85.5	6.892	0.009
6	rs9383498	C	T	0.601	0.00009254	C	T	0.547	0.3592	T	C	-0.120	0.040	0.003004	-+	86.3	7.318	0.007
8	rs62509955	A	C	0.963	0.00007084	A	C	0.968	0.2488	A	C	0.314	0.106	0.003051	+-	88	8.355	0.004
3	rs233143	A	T	0.836	0.00009406	A	T	0.776	0.4837	A	T	-0.158	0.054	0.003286	-+	85.9	7.112	0.008
10	rs9731275	C	T	0.117	0.0000854	C	T	0.336	0.8451	T	C	-0.169	0.059	0.003991	-+	86.1	7.214	0.007
5	rs4866976	A	G	0.914	8.04E-06	A	G	0.875	0.1138	A	G	-0.193	0.067	0.004264	-+	93	14.283	0.000
14	rs2239223	A	C	0.777	0.00004591	A	C	0.492	0.3886	A	C	0.133	0.047	0.005051	+-	89.5	9.518	0.002
5	rs7706435	C	G	0.100	0.00007297	C	G	0.135	0.3085	C	G	0.176	0.063	0.005258	+-	88.9	8.994	0.003
17	rs34257140	G	T	0.852	1.59E-06	G	T	0.503	0.1259	T	G	0.141	0.051	0.005379	+-	94.3	17.635	0.000
4	rs4864419	A	T	0.341	0.00003544	A	T	0.483	0.1198	A	T	-0.110	0.040	0.00573	-+	91.6	11.927	0.001

5	rs256649	A	G	0.828	0.00003294	A	G	0.796	0.1127	A	G	-0.147	0.054	0.00622	-+	91.9	12.306	0.000
18	rs1355829	G	T	0.489	0.00005076	G	T	0.647	0.06537	T	G	0.107	0.039	0.006708	+-	92	12.5	0.000
6	chr6:2659056	A	G	0.027	0.00009574	A	G	0.035	0.3646	A	G	0.344	0.127	0.006723	+-	88.5	8.721	0.003
2	rs2727897	C	T	0.174	0.00008819	C	T	0.141	0.0624	T	C	0.144	0.054	0.007462	+-	91.5	11.725	0.001
2	rs7607006	A	T	0.657	0.00007164	A	T	0.742	0.06752	A	T	0.111	0.042	0.007526	+-	91.6	11.963	0.001
13	rs9553645	A	G	0.101	0.00003756	A	G	0.193	0.206	A	G	-0.156	0.060	0.009089	-+	91.5	11.79	0.001
9	rs7040936	G	T	0.855	0.00002166	G	T	0.578	0.33	T	G	-0.143	0.056	0.01021	-+	91.9	12.404	0.000
1	rs7522243	A	G	0.688	0.00003619	A	G	0.665	0.05934	A	G	-0.114	0.045	0.01101	-+	92.9	14.153	0.000
2	rs2074822	A	G	0.796	0.00006995	A	G	0.597	0.2194	A	G	0.119	0.047	0.01118	+-	90.8	10.918	0.001
12	rs768526	A	G	0.021	0.00002602	A	G	0.197	0.8105	A	G	0.211	0.088	0.01649	++	91.7	12.021	0.001
1	rs58729818	A	G	0.708	0.00008947	A	G	0.480	0.0398	A	G	0.102	0.045	0.02475	+-	93.1	14.568	0.000
5	rs10074285	A	C	0.980	0.00007715	A	C	0.938	0.4232	A	C	-0.258	0.115	0.02499	-+	91.1	11.254	0.001
8	rs1976289	A	C	0.305	0.00008347	A	C	0.381	0.01181	A	C	-0.086	0.042	0.0377	-+	94.3	17.49	0.000
2	rs1996412	C	T	0.121	0.00008477	C	T	0.391	0.1642	T	C	0.107	0.053	0.04323	+-	92.5	13.337	0.000

Meta analysis results were obtained using METAL. Results are sorted by p-value corresponding to the meta analysis. Columns for the meta analysis refer to the overall estimated effect size for allele 1 (effect), the overall standard error for the effect size estimate (SE), the meta analysis p-value (p-value), summary of effect direction for each study, with one + or - per study (direction), I2 statistic of heterogeneity, on a scale of 0-100% (hetisq), chi-squared statistic in simple test of heterogeneity (hetchisq), degrees of freedom for heterogeneity statistic (df), and p-value for heterogeneity statistic (hetpval). The zero in column “direction” is due to a beta estimate of exactly 0 for Hispanics.

Supplemental Table 7. Top loci from Hispanic/Latina GWAS (10x10-5) in African Americans and results from meta analysis of WHI participants

		Hispanic GWAS Results				African American GWAS Results				Meta Analysis Results								
Chr	SNP	A1	A2	A1 Freq	p-value	A1	A2	A1 Freq	p-value	A1	A2	Effect	SE	p-value	Direction	HetISq	HetChiSq	HetPVal
8	rs34919099	G	T	0.2213	0.0000915	G	T	0.251	0.02158	T	G	-0.177	0.046	0.0001054	--	82.1	5.574	0.01823
14	rs35612540	C	T	0.5493	0.00007394	C	T	0.4626	0.05258	T	C	0.152	0.041	0.0002357	++	83.2	5.967	0.01458
10	rs7907661	A	G	0.1861	0.0000619	A	G	0.0344	0.4124	A	G	0.286	0.079	0.0002989	++	73	3.697	0.0545
3	rs10452033	A	G	0.2068	0.00001153	A	G	0.3348	0.06447	A	G	0.151	0.042	0.0003445	++	89.9	9.909	0.001644
2	rs1905469	A	C	0.6066	0.00003518	A	C	0.5187	0.07277	A	C	-0.139	0.039	0.0003677	--	87	7.716	0.005472
8	rs2597346	A	T	0.2137	0.00001322	A	T	0.0857	0.3459	A	T	-0.219	0.062	0.0004028	--	86.5	7.411	0.006481
10	rs10886733	C	T	0.1167	7.23E-06	C	T	0.1013	0.2476	T	C	-0.228	0.067	0.0006571	--	89.9	9.934	0.001622
6	rs2282123	C	G	0.7451	7.19E-06	C	G	0.9442	0.8651	C	G	0.228	0.067	0.0006606	++	88.4	8.647	0.003275
9	rs10981121	C	T	0.7765	0.0000383	C	T	0.7871	0.143	T	C	-0.156	0.047	0.0009044	--	87.7	8.119	0.004381
17	rs10853165	C	T	0.3031	0.00003837	C	T	0.1611	0.2526	T	C	-0.163	0.050	0.0009646	--	86.5	7.403	0.006513
17	rs16959526	A	G	0.2096	0.00008417	A	G	0.0697	0.4509	A	G	0.208	0.064	0.001207	++	82.1	5.581	0.01816
2	rs30102	C	G	0.3118	0.00001981	C	G	0.0759	0.8383	C	G	-0.191	0.060	0.001503	--	87.8	8.223	0.004137
18	chr18:11258947	A	G	0.7695	0.00005557	A	G	0.6194	0.1438	A	G	0.132	0.042	0.001791	++	88.5	8.673	0.003229
13	rs9601962	G	T	0.1849	6.91E-06	G	T	0.1549	0.3585	T	G	-0.166	0.055	0.002389	--	91.6	11.901	0.0005612
21	rs2822657	C	T	0.4574	5.35E-06	C	T	0.3725	0.5173	T	C	0.117	0.041	0.004057	++	92.3	12.953	0.0003194
4	rs3909663	G	T	0.5591	0.00002102	G	T	0.4565	0.3529	T	G	0.112	0.039	0.004368	++	90.8	10.874	0.0009752
3	rs6770011	A	T	0.7276	0.00005138	A	T	0.6564	0.3278	A	T	-0.122	0.044	0.004944	--	89.5	9.497	0.002058
8	rs4871995	A	C	0.4656	0.00001949	A	C	0.2677	0.6383	A	C	0.124	0.045	0.005612	++	90.8	10.846	0.0009899
11	rs1176746	A	G	0.2586	0.00005659	A	G	0.1538	0.6114	A	G	0.146	0.053	0.006057	++	88.9	8.969	0.002746
5	rs4895304	A	G	0.8753	0.00001706	A	G	0.9571	0.7364	A	G	-0.229	0.086	0.00749	-+	91.3	11.525	0.0006867
2	rs17016152	A	T	0.0726	0.00005772	A	T	0.1488	0.2374	A	T	0.156	0.059	0.008177	++	90.6	10.624	0.001117
9	rs57352266	G	T	0.8815	0.00006063	G	T	0.9503	0.9414	T	G	0.208	0.081	0.009619	+-	89.4	9.419	0.002147
2	rs13425598	A	G	0.9051	0.00007455	A	G	0.6183	0.171	A	G	-0.121	0.047	0.009811	--	90.8	10.925	0.0009487
15	rs4924625	A	G	0.4495	0.00003068	A	G	0.2373	0.7433	A	G	-0.116	0.045	0.01009	--	90.8	10.924	0.000949
4	rs4697429	C	T	0.3565	0.00009033	C	T	0.0884	0.8994	T	C	0.149	0.058	0.0102	+-	88.6	8.766	0.00307
2	rs10166852	C	G	0.4737	7.85E-06	C	G	0.774	0.9587	C	G	-0.118	0.047	0.01277	-+	92.8	13.848	0.0001982

2	rs7599310	A	G	0.796	0.00005674	A	G	0.6348	0.4052	A	G	-0.110	0.045	0.01321	--	90.7	10.798	0.001016
12	rs10777158	G	T	0.31	0.00006473	G	T	0.3695	0.5364	T	G	0.101	0.041	0.01336	++	90.3	10.26	0.001359
20	rs609508	C	G	0.7863	5.21E-06	C	G	0.7323	0.6989	C	G	0.111	0.045	0.01389	++	93.3	14.945	0.0001107
2	rs11096713	G	T	0.1688	0.00004126	G	T	0.2571	0.4483	T	G	-0.114	0.046	0.01424	--	91.3	11.432	0.000722
4	rs11736272	G	T	0.2293	0.00004728	G	T	0.226	0.6939	T	G	-0.123	0.050	0.01487	--	90.8	10.817	0.001006
2	rs1129411	A	G	0.085	2.94E-06	A	G	0.0307	0.2371	A	G	0.229	0.097	0.0187	+-	94.4	17.806	0.00002446
3	rs1400159	C	T	0.927	0.000054	C	T	0.9384	0.7907	T	C	0.182	0.078	0.02017	++	90.9	11.025	0.000899
19	rs56127833	A	G	0.0806	0.00008907	A	G	0.1881	0.343	A	G	0.123	0.053	0.02119	++	90.9	10.974	0.0009238
9	rs11144241	A	G	0.9397	0.00009992	A	G	0.9374	0.7195	A	G	-0.200	0.088	0.02246	--	90.1	10.087	0.001494
1	chr1:115067229	C	T	0.1863	0.00003325	C	T	0.0376	0.1708	T	C	-0.176	0.078	0.02319	-+	92.9	14.011	0.0001817
9	rs10820820	C	T	0.8789	0.00009515	C	T	0.8504	0.6002	T	C	-0.125	0.055	0.02394	--	90.4	10.436	0.001236
5	rs11738766	A	G	0.2788	3.11E-06	A	G	0.3053	0.9765	A	G	-0.094	0.043	0.02645	-+	94.1	16.894	0.00003952
5	rs6873646	C	G	0.7123	0.00002291	C	G	0.5671	0.7406	C	G	-0.089	0.040	0.02673	--	92.4	13.169	0.0002847
11	rs10792508	A	C	0.5768	0.00003212	A	C	0.3021	0.9274	A	C	-0.096	0.043	0.02697	--	92	12.452	0.0004176
2	rs13032996	A	C	0.6338	0.0000422	A	C	0.8044	0.907	A	C	0.104	0.047	0.02755	+-	91.7	11.977	0.0005387
6	rs2446649	A	G	0.7978	0.00005294	A	G	0.5211	0.6106	A	G	-0.092	0.043	0.03289	--	91.7	12.08	0.0005098
14	rs7158271	G	T	0.9678	0.00003607	G	T	0.8216	0.248	T	G	0.120	0.056	0.03303	++	92.8	13.902	0.0001925
11	rs568349	A	G	0.7478	0.00003093	A	G	0.7931	0.901	A	G	0.097	0.047	0.04039	+-	92.4	13.212	0.0002782
11	rs11219892	C	T	0.8387	0.00009736	C	T	0.6836	0.6717	T	C	-0.090	0.046	0.04729	--	91.3	11.465	0.0007093
4	rs17345417	A	G	0.8891	5.30E-06	A	G	0.9446	0.2606	A	G	-0.147	0.077	0.05689	-+	94.6	18.426	0.00001767
12	rs10842115	C	G	0.2636	0.0000549	C	G	0.6468	0.9987	C	G	-0.081	0.043	0.05807	--	92.1	12.718	0.0003622
12	rs2596756	C	G	0.8516	0.00008466	C	G	0.7809	0.9048	C	G	0.093	0.051	0.06673	++	91.8	12.136	0.0004945
7	rs10260904	C	G	0.7244	0.00001655	C	G	0.5559	0.885	C	G	-0.073	0.040	0.06814	-+	93.5	15.286	0.00009238
4	chr4:121622918	A	T	0.9769	0.00004623	A	T	0.8929	0.4806	A	T	-0.127	0.073	0.0829	--	92.9	14.137	0.0001699
4	rs17023119	C	G	0.0489	0.00003601	C	G	0.1723	0.6992	C	G	0.093	0.057	0.1005	++	93.1	14.563	0.0001356
8	rs2318345	C	T	0.0797	0.00001995	C	T	0.3117	0.8009	T	C	0.073	0.046	0.1099	++	93.7	15.768	0.00007162
2	rs12471790	A	G	0.3198	0.00003922	A	G	0.1069	0.134	A	G	0.089	0.058	0.1237	+-	94.1	16.846	0.0000405

3

2	rs16823787	A	G	0.9157	5.21E-06	A	G	0.7876	0.9203	A	G	0.080	0.052	0.1237	+-	94.6	18.474	0.00001723
3	rs2046062	C	T	0.911	0.00001608	C	T	0.7972	0.8952	T	C	0.081	0.053	0.1276	+-	93.9	16.35	0.00005267
2	rs2692223	C	T	0.3876	0.00001148	C	T	0.5074	0.4166	T	C	0.063	0.042	0.1311	+-	94.4	17.706	0.00002578
2	rs12466757	C	T	0.4517	0.00006417	C	T	0.5358	0.602	T	C	-0.060	0.040	0.1341	-+	92.9	14.049	0.0001782
13	rs9558277	A	G	0.6355	0.00001974	A	G	0.6924	0.3851	A	G	-0.066	0.045	0.1379	-+	94.1	16.837	0.00004073
2	rs10197605	A	C	0.5	0.00006392	A	C	0.5568	0.5343	A	C	0.059	0.040	0.1414	+-	93	14.244	0.0001606
4	rs12500262	A	T	0.693	0.00008065	A	T	0.9145	0.09103	A	T	0.086	0.059	0.1442	+-	93.9	16.294	0.00005425
19	rs2269816	C	T	0.255	0.00006676	C	T	0.2162	0.3184	T	C	-0.061	0.048	0.2031	-+	93.5	15.328	0.00009034
18	rs4305172	C	T	0.5834	0.00005124	C	T	0.7355	0.2989	T	C	0.056	0.044	0.2096	+-	93.7	15.94	0.00006538
22	rs11912447	C	T	0.0336	0.00006372	C	T	0.2984	0.6956	T	C	-0.061	0.050	0.2206	--	93.2	14.686	0.000127
3	rs61000450	C	T	0.0398	0.00002511	C	T	0.2779	0.8211	T	C	-0.060	0.050	0.2342	--	93.9	16.438	0.00005028
5	rs984465	C	T	0.4215	0.0000571	C	T	0.649	0.344	T	C	-0.049	0.041	0.2346	-+	93.6	15.737	0.00007279
9	rs11138151	A	G	0.37	0.00001332	A	G	0.3144	0.205	A	G	-0.046	0.042	0.2651	-+	94.8	19.381	0.00001071
1	rs1981228	A	T	0.4322	0.00009325	A	T	0.4048	0.3339	A	T	0.045	0.041	0.275	+-	93.4	15.043	0.0001051
9	rs7862935	C	T	0.1476	0.00006971	C	T	0.4071	0.6689	T	C	0.046	0.042	0.2792	+-	93.3	14.858	0.0001159
2	rs17244632	A	G	0.0814	0.00008076	A	G	0.0423	0.06621	A	G	0.088	0.089	0.3222	+-	94.4	17.98	0.00002232
7	rs10249677	G	T	0.0423	1.20E-06	G	T	0.2154	0.7593	T	G	-0.056	0.057	0.3248	-+	95.6	22.807	1.79E-06
2	rs2056788	C	T	0.0323	0.00006687	C	T	0.2999	0.9339	T	C	0.045	0.049	0.3601	++	93.4	15.115	0.0001012
11	rs6483772	C	G	0.8907	0.00001281	C	G	0.7712	0.384	C	G	-0.043	0.049	0.3752	-+	94.8	19.074	0.00001258
1	rs34359572	A	G	0.928	4.10E-06	A	G	0.8463	0.3772	A	G	-0.052	0.060	0.3801	-+	95.3	21.304	3.92E-06
2	rs842560	C	T	0.9672	0.00007752	C	T	0.6736	0.09064	T	C	0.040	0.048	0.4007	-+	94.4	17.818	0.0000243
10	rs4532958	A	C	0.7287	0.00003538	A	C	0.7145	0.1458	A	C	0.034	0.044	0.4388	+-	94.6	18.681	0.00001545

14	rs4902222	A	G	0.9609	0.00002463	A	G	0.6387	0.09007	A	G	0.039	0.051	0.4466	-+	95	20.149	7.17E-06
3	rs1523129	A	G	0.036	0.00002369	A	G	0.316	0.09381	A	G	-0.034	0.047	0.4706	+-	95.1	20.212	6.93E-06
5	rs7726195	G	T	0.9772	0.00002775	G	T	0.8014	0.9328	T	G	0.040	0.056	0.4708	+-	94.2	17.108	0.00003532
6	rs11153331	C	T	0.5666	0.000065	C	T	0.3844	0.1209	T	C	0.030	0.044	0.4929	+-	94.4	17.925	0.00002298
17	chr17:71705874	A	T	0.9062	0.00004632	A	T	0.8913	0.1487	A	T	0.045	0.068	0.5069	+-	94.5	18.301	0.00001887
5	rs2112145	A	G	0.1442	0.00008618	A	G	0.3605	0.3112	A	G	0.025	0.044	0.5608	+-	93.8	16.145	0.00005866
3	rs9845738	A	G	0.3292	0.00006315	A	G	0.2132	0.05236	A	G	0.026	0.046	0.5696	+-	94.9	19.491	0.00001011
11	rs1482747	C	G	0.6671	0.00008082	C	G	0.6803	0.1034	C	G	-0.023	0.042	0.5754	-+	94.4	17.898	0.0000233
11	rs10768049	C	T	0.5535	0.00007225	C	T	0.7042	0.04254	T	C	0.023	0.045	0.6144	+-	94.9	19.653	9.28E-06
4	rs1024601	C	T	0.9377	0.00004701	C	T	0.7948	0.2289	T	C	0.009	0.053	0.8654	+-	94.5	18.03	0.00002175
10	rs41283275	A	G	0.145	0.00004119	A	G	0.2293	0.06076	A	G	0.004	0.048	0.9332	+-	95.1	20.365	6.40E-06

Meta analysis results were obtained using METAL. Results are sorted by p-value corresponding to the meta analysis. Columns for the meta analysis refer to the overall estimated effect size for allele 1 (effect), the overall standard error for the effect size estimate (SE), the meta analysis p-value (p-value), summary of effect direction for each study, with one + or - per study (direction), I2 statistic of heterogeneity, on a scale of 0-100% (hetisq), chi-squared statistic in simple test of heterogeneity (hetchisq), degrees of freedom for heterogeneity statistic (df), and p-value for heterogeneity statistic (hetpval)

Supplemental Table 8. Genome-wide by environment interaction study (GWEIS) of stressful life events results for the top loci (p<1x10-4) in African Americans

Stressful Life Event Results (n=6,982)

									SNP Main Effect			SNP*Stressful Life Events Interaction Term			
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq A1	Beta	SE	p-value	Beta	SE	p-value	Genes in region (±300kb)
rs4652467	1	180097705	imputed	0.945	0.026	A	G	0.026	-0.662	0.167	1.0	0.691	0.111	4.1E-10	RP11-12M5.4, TOR1AIP2, IFRG15, RP11-533E19.7, TOR1AIP1, RN7SL230P, RP11-533E19.2, RP11-533E19.5, CEP350, RP11-502H18.2, QSOX1, LHX4, RP5-1180C10.2, ACBD6
rs7275997	21	19663487	genotyped	0.993	0.180	A	G	0.820	0.264	0.069	1.0	-0.278	0.053	1.2E-07	CHODL, AP000998.2, TMPRSS15, AL109763.1, AL109763.2
rs28377528	7	153884444	imputed	0.874	0.420	A	G	0.580	-0.212	0.058	1.0	0.237	0.046	3.2E-07	DPP6, RP5-1048B16.1, AC006019.3, AC006019.4
rs2852310	18	43093004	imputed	0.996	0.027	A	G	0.027	-0.560	0.183	1.0	0.617	0.123	4.7E-07	SLC14A2, RP11-309E23.2, RP11-749H17.1, RP11-749H17.2, RP11-116O18.1, RP11-116O18.3, SLC14A1
rs12183135	6	151353805	genotyped	0.996	0.024	C	G	0.024	-0.137	0.155	0.6	0.491	0.100	8.0E-07	PLEKHG1, MTHFD1L, RNU6-302P, AL133260.1, RP1-292B18.3, RP1-292B18.4, RP1-297M16.2, RNU6-300P, AKAP12, RNU6-1247P, RNY4P20, RN7SKP268
rs74067201	12	21630449	imputed	0.872	0.077	C	T	0.077	-0.346	0.116	1.0	0.382	0.079	1.2E-06	SLCO1B1, SLCO1A2, IAPP, PYROXD1, RECQL, GOLT1B, C12orf39, GYS2, LDHB, RP11-59N23.3, RP11-59N23.1, KCNJ8
rs184784	5	176440229	imputed	0.981	0.364	G	T	0.636	-0.151	0.056	1.0	0.214	0.045	2.0E-06	RP11-375B1.1, RP11-375B1.2, RP11-375B1.3, UNC5A, HK3, UIMC1, ZNF346, ZNF346-IT1, FGFR4, NSD1, RAB24, MXD3, PRELID1

rs11688799	2	114459729	imputed	0.951	0.355	G	T	0.645	-0.120	0.057	1.0	0.213	0.046	2.9E-06	IGKV1OR2-108, AC016745.3, RP11-480C16.1, CBWD2, AC016745.1, FOXD4L1, RP11-395L14.3, RP11-395L14.4, FAM138B, MIR1302-3, WASH2P, RPL23AP7, RABL2A, AC017074.1, AC017074.2, RNU6-744P, SLC35F5, MIR4782, AC024704.2, AC104653.1, snoU13, RP11-141B14.1, ACTR3, AC010982.1, AC110769.3, AC110769.1
rs11975583	7	29351383	genotyped	1.026	0.089	A	G	0.911	0.276	0.094	1.0	-0.316	0.068	3.5E-06	CTB-113D17.1, CPVL, AC005162.4, AC007096.1, CHN2, AC004593.3, AC007255.8, PRR15, ZNRF2P2
rs13383024	2	167674990	imputed	0.813	0.028	A	G	0.028	-0.338	0.180	0.9	0.552	0.120	4.0E-06	XIRP2
rs74801432	9	82829143	imputed	0.851	0.101	G	T	0.900	0.194	0.094	1.0	-0.316	0.069	4.3E-06	RP11-394O9.1
rs17041572	12	106438975	genotyped	1.015	0.147	A	G	0.147	0.141	0.076	0.9	-0.288	0.063	4.5E-06	RP11-114F10.2, NUAK1, RP11-114F10.3, CKAP4, RP11-651L5.2, RNU7-94P, TCP11L2
rs1714354	11	15170644	imputed	0.820	0.208	C	T	0.792	0.142	0.073	1.0	-0.250	0.055	4.6E-06	PDE3B, CYP2R1, CALCB, CALCA, INSC
rs117085128	19	33957024	imputed	0.843	0.023	C	T	0.023	-0.133	0.176	0.6	0.506	0.111	4.8E-06	WDR88, AC008738.2, LRP3, CTD-2540B15.10, CTD-2540B15.13, SLC7A10, CTD-2540B15.6, CTD-2540B15.12, CEBPA, CTD-2540B15.11, CTD-2540B15.7, CEBPA-AS1, CTD-2540B15.9, CEBPG, PEPD, CTD-2329C7.2, CHST8
rs7277215	21	19663563	genotyped	0.990	0.317	C	T	0.317	-0.193	0.058	1.0	0.209	0.046	5.1E-06	CHODL, AP000998.2, TMPRSS15, AL109763.1, AL109763.2
rs114623838	21	30827502	imputed	0.854	0.094	C	G	0.906	0.389	0.108	1.0	-0.338	0.074	5.7E-06	MAP3K7CL, U3, AF124730.4, LINC00189, BACH1, BACH1-IT1, AP000240.9, BACH1-AS1, BACH1-IT2, snoU13, BACH1-IT3, GRIK1, GRIK1-AS2,

															RP11-313P22.1, GRIK1-AS1
rs76817427	13	74640343	imputed	0.983	0.031	C	T	0.969	0.548	0.172	1.0	-0.512	0.113	5.9E-06	KLF12, LINC00402, RNY1P5
rs10225940	7	78662986	imputed	0.828	0.201	C	T	0.799	0.247	0.077	1.0	-0.251	0.055	6.1E-06	MAGI2, MAGI2-IT1, MAGI2-AS1, MAGI2-AS2, RNU6-337P
rs9983799	21	20894396	imputed	0.954	0.440	A	C	0.561	0.134	0.055	1.0	-0.193	0.043	6.2E-06	AP000855.4, RNU1-139P
rs60988535	2	103577636	imputed	0.882	0.022	A	G	0.978	0.514	0.218	1.0	-0.614	0.136	6.7E-06	SLC9A2, MFSD9, TMEM182, AC007251.2, AC108051.1, AC108051.2, AC108051.3, AC073987.1
rs4709327	6	159866758	genotyped	1.022	0.187	A	T	0.813	0.177	0.067	1.0	-0.221	0.049	7.1E-06	RP11-13P5.2, FNDC1, FNDC1-IT1, RP11-125D12.1, RP11-125D12.2, RP3-393E18.2, SOD2, RNU4ATAC18P, WTAP
rs4691056	4	156619547	imputed	0.910	0.097	G	T	0.097	-0.332	0.098	1.0	0.315	0.070	7.1E-06	RP13-487K5.1, GUCY1A3, RP11-588K22.2, GUCY1B3, ASIC5, TDO2, CTSO
rs7175250	15	27340121	imputed	0.994	0.354	C	T	0.354	0.159	0.056	1.0	-0.202	0.045	8.2E-06	GABRB3, GABRA5, GABRG3, AC136896.1, RNA5SP391, AC144833.1
rs11030112	11	27705188	imputed	0.978	0.241	A	G	0.241	-0.168	0.067	1.0	0.217	0.049	9.0E-06	LGR4, RP11-159H22.2, LIN7C, BDNF-AS, RNA5SP339, LINC00678, BDNF, RP11-587D21.4, RP11-406D1.2
rs4854855	3	131612826	imputed	0.950	0.403	C	T	0.403	-0.157	0.058	1.0	0.194	0.044	1.0E-05	CPNE4, MIR5704
rs2826622	21	22334139	genotyped	1.002	0.053	A	G	0.053	-0.206	0.115	0.9	0.366	0.083	1.1E-05	LINC00320, NCAM2, AP001136.2
rs73243407	5	117610995	imputed	0.966	0.200	C	T	0.800	0.241	0.069	1.0	-0.231	0.053	1.3E-05	CTD-3179P9.1, CTD-3179P9.2, CTD-2281M20.1
rs6432630	2	161437078	genotyped	1.017	0.064	C	T	0.936	0.407	0.112	1.0	-0.347	0.080	1.3E-05	RBMS1, RMRPP3, MIR4785, RN7SL423P
rs79504848	22	27424724	imputed	0.884	0.147	A	T	0.147	-0.218	0.083	1.0	0.255	0.059	1.4E-05	CTA-211A9.5, RP1-90L6.2, RP1-90L6.3, RNU6-1066P, CTA-992D9.6, CTA-992D9.7, CTA-503F6.2, RP5-1172A22.1, CTA-929C8.5, CTA-929C8.7, CTA-929C8.6

rs76573392	2	230694795	imputed	0.859	0.178	C	T	0.822	0.221	0.079	1.0	-0.247	0.057	1.4E-05	DNER, RNU7-9P, TRIP12, RNU6-613P, FBXO36, RNU6-964P, FBXO36-IT1, RNU6-1027P, SLC16A14, RNY4P19, AC009950.2
rs13433731	3	66873257	genotyped	0.990	0.046	C	T	0.046	-0.378	0.140	1.0	0.406	0.093	1.4E-05	KBTBD8
rs12682870	9	98453245	imputed	0.906	0.170	C	T	0.170	0.118	0.075	0.9	-0.260	0.060	1.5E-05	RP11-435O5.7, RP11-435O5.2, PTCH1, RP11-435O5.6, RP11-435O5.5, RP11-435O5.4, RP11-332M4.1, RP11-180I4.2, LINC00476, DKFZP434H0512, RNU2-46P, ERCC6L2, RNA5SP289
rs3757725	7	20395354	imputed	0.965	0.168	C	G	0.168	-0.170	0.073	1.0	0.237	0.055	1.6E-05	AC005062.2, RP11-486P11.1, MACC1, MACC1-AS1, AC005083.1, AC099342.1, CTA-293F17.1, ITGB8, SNORD56, ABCB5
rs2994880	13	25661296	imputed	0.973	0.447	A	G	0.553	0.154	0.055	1.0	-0.178	0.041	1.9E-05	RNF17, CENPJ, TPTE2P1, LSP1, PABPC3, AMER2, AMER2-AS1, LINC01053, LINC01076, MTMR6, AL590787.1, RP11-271M24.2, NUPL1, ATP8A2
rs7979685	12	76404890	imputed	0.856	0.354	C	T	0.354	-0.144	0.061	1.0	0.198	0.046	1.9E-05	RP11-114H23.1, AC131012.1, RN7SL734P, RP11-290L1.5, PHLDA1, RP11-290L1.3, RP11-290L1.2, NAP1L1, RNU6-1271P, RP11-54A9.1
rs73078178	5	27078202	imputed	0.838	0.034	A	G	0.034	-0.199	0.153	0.8	0.462	0.108	1.9E-05	CDH9, RNU6-738P
rs10895877	11	105690604	genotyped	0.994	0.199	A	G	0.199	0.196	0.066	1.0	-0.229	0.054	2.0E-05	RP11-94P11.4, GRIA4, RNU4-55P, AP000673.1, RNU6-277P, MSANTD4, KBTBD3, AASDHPPT, RP11-677I18.3, RP11-677I18.4
rs4871103	8	121729507	imputed	1.001	0.060	A	G	0.060	0.373	0.111	1.0	-0.377	0.088	2.0E-05	MRPL13, MTBP, SNTB1, RP11-713M15.1, RP11-713M15.2, RP11-369K17.1
rs76915987	7	121666511	imputed	0.881	0.032	C	G	0.968	0.585	0.190	1.0	-0.552	0.130	2.1E-05	RN7SKP277, PTPRZ1, AASS, RNU7-154P, RP11-560I19.1,

															FEZF1, FEZF1-AS1, CADPS2
rs72842947	10	87658570	imputed	0.962	0.074	C	T	0.926	-0.354	0.102	1.0	0.332	0.078	2.1E-05	GRID1, RP11-93H12.2, RP11-93H12.4, RN7SKP238, RNA5SP322
rs1470907	12	50186069	imputed	0.912	0.199	G	T	0.801	0.222	0.074	1.0	-0.234	0.055	2.3E-05	SPATS2, KCNH3, MCRS1, PRPF40B, RP11-133N21.10, FAM186B, RNU6-834P, FMNL3, TMBIM6, NCKAP5L, BCDIN3D-AS1, BCDIN3D, RP11-70F11.7, FAIM2, RP11-70F11.11, RP11-70F11.8, AQP2, RP11-469H8.6, RP11-469H8.8, AQP5, AQP6, RACGAP1, ASIC1, SMARCD1
rs2618644	20	17879539	imputed	0.979	0.144	G	T	0.856	0.173	0.081	1.0	-0.248	0.059	2.3E-05	DSTN, RRBP1, BANF2, AL035045.1, RP5-905G11.3, RNU6-192P, SNX5, OVOL2, SNORD17, MGME1, RP4-726N1.2, RNU7-137P, Y_RNA, PET117, CSRP2BP, AL050321.1
rs61142485	9	120279081	imputed	0.837	0.088	A	T	0.088	0.164	0.102	0.9	-0.334	0.079	2.4E-05	ASTN2, RN7SKP125, RP11-388N2.1, RP11-500B12.1, TLR4, RNU6-1082P, snoZ13_snr52, RP11-281A20.2
rs2205165	14	78786133	imputed	0.849	0.032	A	G	0.968	0.561	0.173	1.0	-0.514	0.122	2.6E-05	RNA5SP388, NRXN3, RP11-332E19.2, AC007056.1, AC008045.1
rs10956832	8	93346831	genotyped	0.999	0.267	C	T	0.267	0.260	0.059	1.0	-0.202	0.048	2.6E-05	RUNX1T1, RP11-700E23.2, RP11-700E23.1, RP11-587H10.1, RP11-587H10.2
rs2353591	5	1764750	imputed	0.860	0.279	A	G	0.722	0.182	0.067	1.0	-0.204	0.049	2.7E-05	LPCAT1, CTD-2245E15.3, SDHAP3, CTD-2012J19.3, RP11-43F13.1, MIR4277, CTD-2587M23.1, MRPL36, NDUFS6, CTD-2194D22.1, CTD-2194D22.2, IRX4, CTD-2194D22.3, CTD-2194D22.4, RP11-259O2.1, RP11-259O2.2, RP11-259O2.3

rs4907471	13	112610478	imputed	0.951	0.114	A	G	0.114	-0.213	0.089	1.0	0.264	0.063	2.8E-05	RP11-65D24.2, LINC00354, AL136302.1, SNORD44, SOX1, RP11-450H6.3, LINC00404, LINC00403, LINC01070
rs12614360	2	139062633	imputed	0.987	0.122	C	T	0.878	0.318	0.084	1.0	-0.246	0.059	2.8E-05	HNMT, AC069394.1, AC097721.2, AC114763.1, SPOPL, AC092620.2, RP11-231E19.1, AC092620.3
rs111373030	15	54262361	imputed	0.950	0.085	A	G	0.085	-0.202	0.107	0.9	0.312	0.075	2.9E-05	WDR72, RNU6-449P, RP11-643A5.2, UNC13C
rs28434174	15	87229083	imputed	0.985	0.089	A	G	0.089	-0.233	0.104	1.0	0.314	0.075	2.9E-05	AGBL1, RP11-182L7.1, RP11-133L19.2, RP11-133L19.1
rs71474509	11	99001236	imputed	0.969	0.030	G	T	0.970	-0.526	0.145	1.0	0.596	0.143	3.0E-05	RP11-99C10.1, CNTN5, RN7SKP53, AP003558.1
rs115048050	9	22526738	imputed	0.869	0.022	A	G	0.022	-0.647	0.222	1.0	0.558	0.134	3.0E-05	DMRTA1, RP11-399D6.2, RP11-370B11.3
rs6012567	20	36208012	imputed	0.953	0.391	C	T	0.391	-0.200	0.058	1.0	0.184	0.044	3.1E-05	MANBAL, SRC, BLCAP, NNAT, LINC00489, RP4-640H8.2, CTNNBL1
rs2589529	15	35530030	imputed	0.974	0.115	G	T	0.115	0.222	0.080	1.0	-0.292	0.070	3.1E-05	AQR, ZNF770, AC114546.1, RP11-463I20.3, RP11-463I20.2, RP11-323I15.5, ANP32AP1, DPH6, MIR3942
rs66875495	6	77417930	imputed	0.917	0.060	G	T	0.940	0.459	0.127	1.0	-0.364	0.087	3.1E-05	RNU6-261P, RP11-35J1.1, U6, RP11-354K4.2
rs9828857	3	131599228	imputed	0.988	0.499	A	G	0.499	-0.182	0.055	1.0	0.178	0.043	3.2E-05	CPNE4, MIR5704
rs35581782	6	133518764	imputed	0.907	0.023	C	T	0.023	-0.407	0.171	1.0	0.466	0.112	3.3E-05	LINC00326, EYA4, RP1-283K11.3, RP1-283K11.2
rs138313363	6	32990000	imputed	0.912	0.028	C	G	0.972	0.351	0.176	1.0	-0.425	0.102	3.3E-05	HLA-DQA2, MIR3135B, HLA-DQB2, HLA-DOB, TAP2, PSMB8, TAPSAR1, PSMB9, TAP1, PPP1R2P1, HLA-DMB, AL645941.1, XXbac-BPG181M17.5, HLA-DMA, BRD2, BRD2-IT1, XXbac-BPG181M17.6, HLA-DOA, HLA-DPA1, HLA-DPB1, HLA-DPB2, HCG24, COL11A2, RXRB, RNY4P10, SLC39A7, HSD17B8, MIR219-1, RING1,

															XXbac-BPG157A10.21, HCG25, VPS52, RPS18, B3GALT4, WDR46, PFDN6, RGL2, TAPBP, ZBTB22, DAXX
rs6926443	6	17096354	genotyped	1.007	0.158	C	T	0.842	0.210	0.074	1.0	-0.224	0.054	3.3E-05	STMND1, RBM24, CAP2
rs2122993	3	1495223	imputed	0.943	0.419	A	G	0.581	-0.258	0.053	1.0	0.176	0.043	3.4E-05	CNTN6
rs3995545	10	15038205	imputed	0.862	0.069	C	G	0.069	0.276	0.107	1.0	-0.385	0.093	3.4E-05	FAM107B, CDNF, HSPA14, RP11-398C13.6, SUV39H2, DCLRE1C, MEIG1, OLAH, ACBD7, C10orf111, RPP38, NMT2, FAM171A1, RP11-25G10.2
rs2391284	7	26572971	imputed	0.995	0.077	A	G	0.924	-0.377	0.094	1.0	0.345	0.083	3.4E-05	SNX10, AC004540.4, AC004540.5, KIAA0087, AC004947.2, C7orf71, SKAP2
rs73365577	5	166941146	imputed	0.943	0.069	C	T	0.931	0.219	0.114	1.0	-0.335	0.081	3.5E-05	TENM2, CTB-180C19.1, CTC-286N12.1, CTB-105L4.2, CTB-78F1.1, CTB-78F1.2
rs62115662	2	12507370	imputed	1.000	0.051	A	G	0.949	0.300	0.128	1.0	-0.348	0.084	3.5E-05	AC096559.1, MIR3681, RNU6-843P, AC096559.2
rs75285234	3	55482495	imputed	0.904	0.020	A	G	0.020	-0.434	0.203	1.0	0.557	0.135	3.6E-05	RP11-889D3.1, RP11-889D3.2, RP11-64C1.1, RP11-875H7.1, RP11-875H7.2, WNT5A, WNT5A-AS1, RP11-875H7.5, ERC2, RP11-58O15.1
rs10251762	7	68335032	imputed	0.895	0.140	G	T	0.860	0.190	0.082	1.0	-0.253	0.061	3.6E-05	RNA5SP231, RP11-123O1.1, RNU6-832P
rs72946702	2	114543890	imputed	0.973	0.179	C	T	0.821	-0.216	0.070	1.0	0.230	0.056	3.8E-05	CBWD2, FOXD4L1, RP11-395L14.3, RP11-395L14.4, FAM138B, MIR1302-3, WASH2P, RPL23AP7, RABL2A, AC017074.1, AC017074.2, RNU6-744P, SLC35F5, MIR4782, AC024704.2, AC104653.1, snoU13, RP11-141B14.1, ACTR3, AC010982.1,

															AC110769.3, AC110769.1, U3
rs72829191	5	148297036	imputed	0.954	0.024	C	T	0.976	0.372	0.188	1.0	-0.540	0.131	3.9E-05	HTR4, HTR4-IT1, ADRB2, SH3TC2, RP11-44B19.1, RNU6-732P, MIR584, CTC-529P8.1, RN7SKP145, ABLIM3, RP11-331K21.1, AC012613.2
rs2786767	1	168742357	genotyped	0.974	0.433	C	T	0.433	0.167	0.055	1.0	-0.182	0.044	4.0E-05	RP5-968D22.3, XCL2, XCL1, DPT, AL049798.1, RP1-10C16.1, LINC00626, LINC00970, RNA5SP66
rs4880701	10	5085182	imputed	0.831	0.227	C	T	0.773	-0.194	0.068	1.0	0.233	0.057	4.0E-05	AKR1E2, AKR1C1, U8, AKR1C2, RP11-499O7.7, AKR1C3, AKR1CL1, AKR1C4, RP11-445P17.3, RP11-445P17.8, AKR1C7P
rs75343055	11	88905268	imputed	0.817	0.082	A	G	0.918	-0.320	0.107	1.0	0.348	0.085	4.1E-05	GRM5, AP001482.1, TYR, NOX4
rs10491684	9	449798	genotyped	1.005	0.147	A	G	0.147	0.270	0.076	1.0	-0.255	0.062	4.1E-05	CBWD1, C9orf66, DOCK8, RP11-59O6.3, RP11-165F24.3, KANK1, RP11-165F24.2, RP11-165F24.5, RN7SL412P, RP11-31F19.1, RNU6-1327P, RP11-130C19.3
rs1936544	13	81137320	genotyped	1.006	0.036	G	T	0.036	-0.635	0.161	1.0	0.441	0.107	4.1E-05	SPRY2, RNU6-61P
rs75573806	2	119841767	imputed	0.890	0.033	A	G	0.967	0.342	0.172	1.0	-0.442	0.108	4.1E-05	RP11-19E11.1, EN1, MARCO, RP11-77A13.1, C1QL2, RN7SL468P, STEAP3, STEAP3-AS1, C2orf76, DBI
rs12542772	8	2100441	imputed	1.020	0.140	A	C	0.140	-0.181	0.076	1.0	0.233	0.057	4.2E-05	ARHGEF10, KBTBD11-OT1, RP11-439C15.4, KBTBD11, RP11-439C15.5, RP11-1049H7.2, MYOM2, AC133633.2, AC133633.1

rs11227134	11	64926057	imputed	0.806	0.212	C	T	0.788	-0.259	0.072	1.0	0.233	0.057	4.2E-05	EHD1, RP11-665N17.4, MIR192, MIR194-2, ATG2A, PPP2R5B, GPHA2, C11orf85, BATF2, ARL2, RP11-399J13.3, SNX15, SAC3D1, NAALADL1, RN7SL114P, CDCA5, ZFPL1, AP003068.6, VPS51, AP003068.9, TM7SF2, ZNHIT2, AP003068.12, FAU, SYVN1, MRPL49, RNU2-23P, SPDYC, AP003068.18, AP003068.23, CAPN1, SLC22A20, POLA2, CDC42EP2, DPF2, TIGD3, RP11-867O8.5, SLC25A45, FRMD8, NEAT1, AP000769.1
rs78000700	5	155759387	imputed	0.944	0.213	C	G	0.213	-0.131	0.069	0.9	0.212	0.052	4.2E-05	SGCD
rs12414101	10	66493783	imputed	1.010	0.160	A	G	0.841	0.236	0.079	1.0	-0.236	0.058	4.2E-05	RP11-179K3.2
rs4971800	2	52509039	imputed	0.924	0.036	A	C	0.036	-0.459	0.166	1.0	0.464	0.113	4.3E-05	AC007682.1, Y_RNA, AC087073.1, AC139712.4
rs141747386	4	29224802	imputed	0.845	0.026	A	G	0.026	0.097	0.156	0.5	0.460	0.113	4.3E-05	RP11-292B1.2, RP11-769N22.1, RP11-472K22.1, RP11-472K22.2, RNU6-1221P
rs17175405	13	73194036	imputed	0.970	0.049	A	C	0.951	0.078	0.114	0.5	-0.356	0.087	4.3E-05	SNORD37, SNORA68, SNORA9, RNU6-80P, MZT1, BORA, DIS3, PIBF1, AL391384.1, RNU6-79P
rs10047482	11	68231843	imputed	0.883	0.213	C	T	0.787	0.200	0.073	1.0	-0.218	0.053	4.4E-05	SUV420H1, C11orf24, LRP5, PPP6R3, AP000807.2, AP000807.1, CTD-2007L18.5, AP003096.1, GAL, MTL5, CPT1A
rs113562433	1	210854780	imputed	0.917	0.042	A	G	0.958	0.208	0.151	0.8	-0.409	0.100	4.5E-05	HHAT, KCNH1
rs7146816	14	86182567	genotyped	1.014	0.410	G	T	0.590	0.112	0.056	1.0	-0.171	0.042	4.5E-05	CTD-2128A3.2, LINC00911, RP11-497E19.1, RP11-497E19.2, FLRT2, CTD-2341M24.1, RP11-1079H9.1
rs4411726	2	240864044	imputed	0.974	0.391	A	G	0.609	-0.116	0.056	1.0	0.180	0.044	4.5E-05	RP11-315F22.1, AC093802.1, NDUFA10, MIR4786, OR6B2,

															PRR21, OR6B3, AC013469.1, MYEOV2, OTOS
rs7852300	9	119850589	imputed	1.014	0.122	C	T	0.878	0.182	0.084	1.0	-0.237	0.058	4.7E-05	ASTN2, AL354981.1, SNORA70C, RN7SKP128, RN7SKP125
rs58154819	8	66079444	imputed	0.949	0.156	A	G	0.156	0.266	0.073	1.0	-0.248	0.061	4.7E-05	
rs2460057	11	93684902	genotyped	0.943	0.146	A	G	0.854	0.184	0.082	1.0	-0.243	0.060	4.9E-05	KIAA1731, Y_RNA, SCARNA9, TAF1D, SNORA25, SNORA32, SNORD6, SNORA1, SNORA8, SNORD5, SNORA18, MIR1304, SNORA40, C11orf54, MED17, snoU13, RN7SL195P, VSTM5, HEPHL1, PANX1, RP11-680H20.2
rs9676754	19	34575610	imputed	0.814	0.067	A	G	0.933	0.310	0.127	1.0	-0.362	0.089	4.9E-05	KCTD15, RN7SL150P, LSM14A, KIAA0355, AC010504.2, GPI
rs10923429	1	118345406	imputed	1.021	0.086	A	G	0.086	-0.224	0.096	1.0	0.278	0.069	4.9E-05	MAN1A2, AL157902.3, FAM46C, SNORA40, GDAP2, WDR3, SPAG17
rs11002875	10	80976472	imputed	0.824	0.066	A	G	0.066	-0.266	0.124	1.0	0.352	0.087	4.9E-05	ZMIZ1-AS1, RP11-481G8.2, ZMIZ1, PPIF, ZCCHC24, RP11-342M3.5, RP11-342M3.1, AL133481.1, EIF5AL1
rs112793369	6	119051014	imputed	0.940	0.037	C	T	0.963	0.159	0.150	0.7	-0.387	0.095	4.9E-05	CEP85L, PLN, RP11-210H10 A.1, MCM9, ASF1A, RP11-351A11.1, FAM184A
rs74453505	7	55139715	imputed	0.986	0.095	A	G	0.905	0.273	0.100	1.0	-0.275	0.068	5.0E-05	RP11-745C15.2, SNORA73, EGFR, EGFR-AS1, LANCL2
rs77809368	21	41348328	imputed	0.877	0.100	A	G	0.100	0.198	0.096	1.0	-0.312	0.077	5.0E-05	AF064860.5, AF064860.7, IGSF5, PCP4, DSCAM, MIR4760
rs59071566	4	113821674	imputed	0.876	0.207	C	G	0.207	-0.132	0.071	0.9	0.213	0.053	5.0E-05	C4orf21, LARP7, MIR302B, MIR367, MIR302D, MIR302A, MIR302C, RP11-148B6.2, Y_RNA, ANK2, RP11-119H12.6, RP11-650J17.1,

															RP11-650J17.2
rs605730	11	87829489	imputed	0.951	0.417	C	T	0.417	-0.159	0.057	1.0	0.175	0.043	5.2E-05	RP11-164N3.1, RP11-164N3.2, RP11-164N3.3, Y_RNA, RAB38, MIR3166, CTSC
rs745069	13	24291972	imputed	0.824	0.240	C	T	0.240	-0.174	0.072	1.0	0.229	0.057	5.2E-05	SACS, SACS-AS1, LINC00327, LINC00352, TNFRSF19, MIPEP, AL139080.1, C1QTNF9B-AS1, C1QTNF9B, ANKRD20A19P, RP11-307N16.6, SPATA13, RP11-309I15.1
rs66475911	16	59574268	imputed	0.898	0.424	C	T	0.577	-0.176	0.057	1.0	0.183	0.045	5.2E-05	AC040163.1, RNU4-58P, RP11-105C20.2
rs1570739	13	74625691	imputed	0.965	0.465	C	T	0.535	-0.105	0.056	0.9	0.178	0.044	5.2E-05	KLF12, LINC00402, RNY1P5
rs17745017	14	55978825	imputed	0.926	0.042	A	G	0.042	-0.387	0.137	1.0	0.388	0.096	5.3E-05	RP11-665C16.6, FBXO34, RP11-665C16.5, ATG14, TBPL2, KTN1-AS1, KTN1, Y_RNA, RP11-813I20.2, RPL13AP3, LINC00520
rs2085746	11	61924407	imputed	1.001	0.377	C	T	0.377	0.136	0.056	1.0	-0.180	0.045	5.4E-05	FADS2, FADS3, RAB3IL1, RNU6-1243P, BEST1, FTH1, AP003733.1, RP11-810P12.5, INCENP, SCGB1D1, SCGB2A1, RP11-703H8.9, SCGB1D2, SCGB2A2, SCGB1D4, RP11-703H8.7, ASRGL1, AP003064.2, CTD-2531D15.5, SCGB1A1, CTD-2531D15.4, AHNAK
rs2283826	22	26924995	genotyped	0.982	0.279	A	G	0.721	0.214	0.062	1.0	-0.189	0.047	5.7E-05	SEZ6L, RP11-259P1.1, RNA5SP495, ASPHD2, HPS4, SRRD, TFIP11, CTA-445C9.14, CTA-445C9.15, TPST2, MIR548J, CRYBB1, CRYBA4, MIAT, CTA-373H7.7, CTA-211A9.5
rs4660660	1	39459072	imputed	0.958	0.075	A	G	0.925	0.297	0.110	1.0	-0.316	0.079	5.7E-05	RRAGC, RP5-864K19.4, MYCBP, GJA9, RHBDL2,

															RNU6-605P, Y_RNA, AKIRIN1, NDUFS5, MACF1, RNU6-608P, RNA5SP44, RP11-416A14.1, RP11-420K8.1
rs272138	2	131566140	genotyped	0.975	0.192	C	T	0.808	-0.083	0.068	0.8	0.224	0.056	5.8E-05	POTEI, AC013269.3, CFC1B, AC013269.4, AC013269.5, AC140481.2, AC140481.4, CFC1, POTEJ, RNU6-848P, CYP4F30P, AC140481.7, GPR148, AC140481.8, AMER3, AC133785.1, ARHGEF4, SCARNA4, FAM168B, PLEKHB2
rs6424087	1	3538835	imputed	0.948	0.483	C	G	0.517	-0.175	0.054	1.0	0.171	0.043	5.9E-05	PRDM16, ARHGEF16, RP11-168F9.2, MEGF6, MIR551A, RP11-46F15.2, TPRG1L, WRAP73, TP73, RP5-1092A11.5, RP5-1092A11.2, TP73-AS1, CCDC27, SMIM1, LRRC47, RN7SL574P, RP1-286D6.5, CEP104, DFFB, AL691523.1, C1orf174, RP13-15E13.1
rs143152600	11	76286995	imputed	0.942	0.036	C	T	0.964	0.390	0.167	1.0	-0.457	0.114	5.9E-05	PRKRIR, RP11-111M22.2, RP11-111M22.4, RP11-111M22.5, Y_RNA, RP11-111M22.3, C11orf30, RP11-672A2.6, RP11-672A2.5, RP11-672A2.4, AP001189.4, LRRC32, RP11-672A2.3, GUCY2EP, RP11-672A2.1, RP11-21L23.4, TSKU, RP11-21L23.3, RP11-21L23.2, ACER3
rs7808815	7	29390463	imputed	0.949	0.230	C	T	0.770	-0.192	0.065	1.0	0.211	0.052	6.0E-05	CPVL, AC005162.4, AC007096.1, CHN2, AC004593.3, AC007255.8, PRR15, ZNRF2P2
rs1097438	4	173139186	imputed	0.944	0.344	C	T	0.344	-0.116	0.058	1.0	0.186	0.046	6.0E-05	GALNTL6
rs17216006	13	74516103	imputed	0.992	0.028	C	T	0.972	0.545	0.171	1.0	-0.469	0.117	6.1E-05	LINC00393, KLF12,

															LINC00402
rs7300788	12	98398951	imputed	0.984	0.346	C	T	0.654	-0.041	0.058	0.5	0.186	0.046	6.1E-05	RP11-1016B18.1, RNU6-36P, MIR4495, MIR4303, RP11-690J15.1
rs58520099	5	155785692	imputed	1.003	0.130	A	G	0.870	0.266	0.086	1.0	-0.244	0.061	6.1E-05	SGCD
rs16835033	3	123691294	genotyped	1.007	0.057	C	T	0.943	0.305	0.124	1.0	-0.330	0.082	6.1E-05	MYLK, MYLK-AS2, RP11-9N20.3, SNORA5, CCDC14, ROPN1, AC117401.1, KALRN, MIR5002
rs11738275	5	154711844	imputed	0.941	0.211	A	G	0.211	-0.206	0.072	1.0	0.207	0.052	6.2E-05	
rs79199846	1	214426896	imputed	0.834	0.031	A	G	0.969	0.708	0.188	1.0	-0.480	0.120	6.4E-05	PROX1-AS1, PROX1, RP11-53A1.2, SMYD2, RP11-176D17.3, PTPN14
rs77199818	20	40922738	imputed	0.895	0.036	A	G	0.964	0.520	0.158	1.0	-0.438	0.110	6.4E-05	RP5-1121H13.4, RP5-1121H13.3, PTPRT
rs72971175	2	127663827	imputed	0.825	0.022	C	T	0.978	0.368	0.206	0.9	-0.522	0.130	6.4E-05	GYPC, RNU6-675P, AC114783.1, RNU7-182P, RP11-521O16.1, RP11-521O16.2, BIN1, CYP27C1
rs4525771	21	28108219	imputed	0.940	0.193	A	G	0.193	-0.175	0.076	1.0	0.217	0.054	6.7E-05	AP001596.6, AP001597.1, KB-1466C5.1, CYYR1, ADAMTS1, AP001601.2, ADAMTS5, MIR4759
rs10431149	11	69904105	imputed	0.910	0.334	G	T	0.334	-0.159	0.062	1.0	0.188	0.047	6.7E-05	FGF3, RP11-626H12.1, RP11-626H12.2, RP11-626H12.3, ANO1-AS2, RNU6-1175P, ANO1, RP11-805J14.3, ANO1-AS1, FADD, RP11-805J14.5, PPFIA1, AP000487.6, MIR548K, CTA-797E19.1, CTA-797E19.2
rs10886165	10	119633104	imputed	0.944	0.370	C	T	0.370	-0.215	0.057	1.0	0.181	0.045	6.8E-05	RP11-328K15.1, RP11-355F22.1, RAB11FIP2, RP11-354M20.3, CASC2
rs116497593	16	79175180	imputed	0.853	0.034	A	G	0.034	-0.182	0.164	0.7	0.435	0.109	6.9E-05	WWOX, RP11-319G9.3, PIH1, RP11-319G9.5, RP11-556H2.4, RP11-556H2.3, RP11-556H2.2, WWOX, RP11-679B19.2, RNA5SP431

rs77688048	12	41990321	imputed	0.871	0.041	A	G	0.041	-0.467	0.167	1.0	0.431	0.108	6.9E-05	PDZRN4, RP11-413B19.2, RNA5SP360, RP11-630C16.1, RP11-630C16.2
rs4298160	4	78171898	genotyped	0.997	0.178	C	T	0.178	-0.118	0.073	0.9	0.209	0.053	6.9E-05	SEPT11, CCNI, RNU6-1187P, CCNG2, RP11-625I7.1, CXCL13
rs16941975	15	60245758	imputed	0.958	0.156	A	G	0.844	0.159	0.076	1.0	-0.225	0.057	7.0E-05	GTF2A2, AC092755.4, BNIP2, RP11-361D15.2, FOXB1, RP11-82L7.4
rs77890769	14	89758384	imputed	0.882	0.189	G	T	0.811	-0.147	0.074	1.0	0.243	0.061	7.0E-05	FOXN3, RP11-356K23.1, RP11-356K23.2, RP11-33N16.2, RP11-33N16.3, FOXN3-AS1, FOXN3-AS2, Y_RNA
rs11745703	5	38755640	genotyped	1.004	0.319	G	T	0.319	0.109	0.056	1.0	-0.176	0.044	7.0E-05	EGFLAM, CTD-2263F21.1, LIFR, LIFR-AS1, MIR3650, CTD-2196P11.2, RP11-122C5.1, CTD-2127H9.1, RP11-122C5.3, OSMR, RICTOR
rs4528898	3	26612385	imputed	0.827	0.120	A	G	0.880	-0.275	0.086	1.0	0.285	0.072	7.0E-05	AC099754.1, LRRC3B, AC114877.3, AC114877.1
rs79444675	9	1898387	imputed	0.832	0.217	G	T	0.217	0.165	0.071	1.0	-0.226	0.057	7.0E-05	SMARCA2, RP11-264I13.2, RNU2-25P
rs2705394	18	43119600	imputed	0.938	0.154	C	T	0.846	0.221	0.081	1.0	-0.232	0.058	7.1E-05	SLC14A2, RP11-309E23.2, RP11-749H17.1, RP11-749H17.2, RP11-116O18.1, RP11-116O18.3, SLC14A1, SIGLEC15
rs73109935	1	238956229	imputed	0.804	0.060	A	G	0.940	0.012	0.120	0.08	-0.335	0.084	7.1E-05	RP11-177F15.1
rs79859091	16	6710645	imputed	0.864	0.119	G	T	0.119	0.188	0.085	1.0	-0.288	0.073	7.1E-05	RP11-420N3.2, RBFOX1, RP11-468I15.1, RNU7-99P, RNU6-457P
rs76094576	3	5196770	imputed	0.913	0.031	C	T	0.031	-0.435	0.168	1.0	0.406	0.102	7.2E-05	AC018816.3, snoU13, BHLHE40-AS1, BHLHE40, Y_RNA, ARL8B, AC026202.3, AC026202.1, EDEM1, MIR4790, RN7SL553P, AC026202.5

rs17170824	7	37039593	imputed	0.959	0.417	C	T	0.417	-0.089	0.057	0.9	0.172	0.043	7.2E-05	AOAH, RP11-85E16.1, AC007349.4, AC007349.5, AC007349.7, ELMO1, MIR1200, ELMO1-AS1, AC009196.1, snoU13
rs2808221	1	237488563	imputed	0.822	0.282	A	T	0.282	-0.170	0.068	1.0	0.208	0.052	7.2E-05	RYR2, RN7SKP195, MIR4428, SNORA25
rs7557842	2	197005195	imputed	0.964	0.415	G	T	0.585	-0.152	0.055	1.0	0.174	0.044	7.3E-05	DNAH7, STK17B, RP11-347P5.1, HECW2, snoU13, AC020571.3, RN7SL820P
rs114245032	12	117352098	imputed	0.911	0.055	C	T	0.055	-0.179	0.129	0.8	0.340	0.086	7.4E-05	RP11-497G19.1, RP11-497G19.2, C12orf49, RNFT2, RNU6-558P, HRK, FBXW8, RP11-231I16.1, TESC, RP11-103B5.2, FBXO21, NOS1
rs1284762	3	102271342	imputed	0.807	0.411	C	G	0.411	0.140	0.061	0.4	-0.188	0.047	7.4E-05	ZPLD1, RP11-280H21.1, RNU6-461P
rs6687996	1	31079246	imputed	0.975	0.386	C	T	0.386	-0.122	0.057	1.0	0.175	0.044	7.5E-05	RP4-591L5.1, RP4-591L5.2, MATN1, MATN1-AS1, LAPTM5, MIR4420, RP5-1125N11.1, RP1-65J11.1, RN7SKP91, RP1-65J11.5, SDC3
rs10994058	10	61618789	imputed	0.976	0.348	G	T	0.348	0.187	0.058	1.0	-0.178	0.045	7.6E-05	RP11-135D11.2, SLC16A9, LINC00948, CCDC6, C10orf40, ANK3, RP11-388P9.2, Y_RNA
rs67647967	7	29490769	imputed	0.914	0.205	A	G	0.205	0.153	0.069	1.0	-0.218	0.055	7.6E-05	CPVL, CHN2, AC004593.3, AC007255.8, PRR15, ZNRF2P2, MIR550A3, AC007276.5
rs7724315	5	73380475	imputed	0.910	0.212	C	T	0.212	0.205	0.066	1.0	-0.209	0.053	7.7E-05	ARHGEF28, CTC-575I10.1, RNU7-196P, RP11-428C6.2, CTD-2292M14.1, AC106732.1, CTD-2275D24.4, RN7SL814P, CTD-2275D24.1, CTD-2275D24.2, CTD-2275D24.3, CTC-419K13.1
rs79754532	11	106145488	imputed	0.934	0.027	C	T	0.973	0.228	0.183	0.8	-0.461	0.117	7.7E-05	GRIA4, RNU6-277P, MSANTD4, KBTBD3, AASDHPPT, RP11-677I18.3,

															RP11-677I18.4, RP11-680E19.1
rs211745	1	76005942	imputed	1.004	0.393	C	T	0.607	0.095	0.056	0.9	-0.167	0.042	7.7E-05	SLC44A5, RNU6-503P, RP4-682C21.5, ACADM, RABGGTB, SNORD45C, SNORD45A, SNORD45B, MSH4
rs6949733	7	80671050	imputed	0.805	0.300	A	G	0.300	-0.148	0.066	1.0	0.193	0.049	8.0E-05	SEMA3C, AC005008.2
rs2291347	11	130286766	genotyped	0.987	0.300	A	G	0.300	0.059	0.059	0.7	-0.190	0.048	8.0E-05	APLP2, ST14, ZBTB44, Metazoa_SRP, RP11-121M22.1, ADAMTS8, ADAMTS15, C11orf44
rs76940324	6	51385308	imputed	0.889	0.021	C	T	0.980	0.808	0.227	1.0	-0.582	0.148	8.1E-05	SNORD66, RP3-335N17.2, PKHD1
rs3746754	20	61579666	genotyped	1.004	0.123	C	T	0.123	0.252	0.081	1.0	-0.274	0.070	8.2E-05	SLCO4A1, RP11-93B14.5, LINC00686, NTSR1, RP11-93B14.4, LINC00659, MRGBP, OGFR-AS1, OGFR, COL9A3, TCFL5, DIDO1, GID8, SLC17A9, BHLHE23, RP11-305P22.9, LINC00029, LINC01056, HAR1B, HAR1A, RP5-963E22.5, RP5-963E22.4, MIR124-3, YTHDF1, BIRC7, MIR3196, NKAIN4
rs12693083	2	176728443	imputed	0.811	0.451	G	T	0.451	0.124	0.060	1.0	-0.182	0.046	8.3E-05	AC016751.3, AC016751.2, KIAA1715, EVX2, HOXD13, HOXD12, HOXD11, AC009336.1, HOXD10, HOXD-AS2, HOXD9, HOXD8, HOXD3, MIR10B, HOXD4
rs79245726	21	20104348	imputed	0.947	0.078	C	T	0.078	0.316	0.103	1.0	-0.352	0.089	8.3E-05	TMPRSS15, AL109763.1, AL109763.2, AF240627.2, MIR548X, AP001537.1, AL157359.4, AL157359.3
rs753197	11	45754874	imputed	0.894	0.113	C	T	0.887	-0.252	0.088	1.0	0.292	0.074	8.3E-05	RP11-430H10.4, RP11-958J22.1, RP11-958J22.3, CHST1, RP11-495O11.1, CTD-2210P24.1, CTD-2210P24.2,

															CTD-2210P24.3, CTD-2210P24.4, SLC35C1, CTD-2210P24.6, CRY2, MAPK8IP1, RP11-618K13.2, C11orf94, PEX16, GYLTL1B, PHF21A
rs1157329	18	64645270	imputed	0.818	0.486	A	C	0.514	-0.135	0.059	1.0	0.182	0.046	8.3E-05	RNU6-1037P, AC113195.1, MIR5011
rs131058	22	47910533	imputed	0.841	0.117	A	G	0.117	-0.264	0.091	1.0	0.262	0.067	8.5E-05	CITF22-49D8.1, LL22NC03-75H12.2, LINC00898, RP11-191L9.4
rs73898758	20	16436683	imputed	0.980	0.035	C	T	0.965	-0.476	0.130	1.0	0.504	0.128	8.7E-05	KIF16B, AL118509.1, Y_RNA, RP4-705D16.3, SNRPB2, OTOR
rs7011265	8	25914928	imputed	1.000	0.118	C	T	0.882	-0.214	0.081	1.0	0.260	0.066	8.7E-05	RP11-219J21.2, RP11-299D14.2, EBF2, RNA5SP258, PPP2R2A
rs9324750	5	152916029	imputed	0.974	0.473	A	C	0.527	-0.182	0.056	1.0	0.170	0.043	8.7E-05	GRIA1, RN7SL177P
rs62240227	3	18064255	imputed	0.871	0.280	A	G	0.280	0.096	0.063	0.9	-0.201	0.051	8.7E-05	TBC1D5, AC132807.1
rs113230270	3	151716036	imputed	0.896	0.139	A	G	0.139	0.194	0.083	1.0	-0.257	0.065	8.7E-05	AADACL2, RP11-454C18.2, RP11-64D22.2, RP11-64D22.5, AADAC, SUCNR1, RP11-246A10.1, MBNL1, MBNL1-AS1
rs12477554	2	75402065	genotyped	0.998	0.393	A	G	0.393	-0.188	0.058	1.0	0.168	0.043	8.8E-05	HK2, AC104135.3, AC104135.2, AC104135.4, POLE4, TACR1, MIR5000, RP11-355F16.1, snoU13, EVA1A, AC007099.2
rs396997	1	26893067	imputed	0.923	0.384	C	T	0.384	-0.098	0.058	0.9	0.172	0.044	8.8E-05	CEP85, SH3BGRL3, UBXN11, CD52, AIM1L, RN7SL490P, ZNF683, LIN28A, DHDDS, RP3-476K8.3, HMGN2, RPS6KA1, MIR1976, RN7SL679P, Y_RNA, snoU13, RP5-968P14.2, ARID1A, RN7SL501P, PIGV, RN7SL165P, ZDHHC18, SFN
rs524839	11	128660208	imputed	0.955	0.122	A	G	0.878	-0.203	0.081	1.0	0.287	0.073	8.9E-05	ETS1, RP11-1007G5.2, RP11-264E20.2, RP11-264E20.1, RP11-744N12.3, FLI1, FLI1-

															AS1, KCNJ1, KCNJ5, C11orf45, TP53AIP1, ARHGAP32, RNU6-876P, Y_RNA
rs2175472	16	78509562	imputed	0.999	0.271	A	G	0.271	0.084	0.061	0.8	-0.183	0.047	8.9E-05	WWOX, RP11-190D6.2, RP11-264L1.4, RP11-264L1.3
rs12056433	8	12891872	imputed	0.964	0.335	C	G	0.665	-0.154	0.059	1.0	0.177	0.045	8.9E-05	LONRF1, RP11-252C15.1, LINC00681, AC090133.1, KIAA1456, RNU6-842P, DLC1, Y_RNA
rs79130661	3	152182300	imputed	0.929	0.020	C	T	0.020	-0.359	0.208	0.9	0.497	0.127	9.0E-05	MBNL1, MBNL1-AS1, TMEM14E, Y_RNA, RP11-362A9.3, RP11-788A4.1
rs780873	12	116195781	genotyped	0.977	0.112	A	G	0.888	-0.148	0.089	0.9	0.267	0.068	9.1E-05	RP11-1028N23.3, RP11-1028N23.2, RP11-1028N23.4, RN7SL865P, RP11-110L15.1, RP11-110L15.2, SNORD56, MED13L, RP11-493P1.2
rs12195349	6	18658219	imputed	0.846	0.042	A	G	0.042	-0.348	0.145	1.0	0.373	0.095	9.1E-05	RNF144B, snoU13, MIR548A1
rs4145578	10	52656373	imputed	0.938	0.121	A	G	0.121	0.215	0.082	1.0	-0.270	0.069	9.1E-05	SGMS1, RP11-50E11.3, RP11-564C4.6, ASAH2B, A1CF, RP11-449O16.2, RP11-96B5.4, PRKG1, RP11-96B5.3
rs11100921	4	139329501	imputed	0.931	0.083	C	T	0.917	0.310	0.099	1.0	-0.275	0.070	9.2E-05	LINC00616, SLC7A11-AS1, SLC7A11, RP11-733C7.1, LINC00498, LINC00499, LINC00500, RP11-173E2.2
rs28642088	16	6730845	imputed	0.912	0.162	G	T	0.838	0.139	0.077	0.9	-0.216	0.055	9.2E-05	RP11-420N3.2, RBFOX1, RP11-468I15.1, RNU7-99P, RNU6-457P
rs28608542	9	98466364	imputed	0.993	0.059	A	G	0.941	0.229	0.121	0.9	-0.317	0.081	9.2E-05	RP11-435O5.7, RP11-435O5.2, PTCH1, RP11-435O5.6, RP11-435O5.5, RP11-435O5.4, RP11-332M4.1, RP11-180I4.2, LINC00476, DKFZP434H0512, RNU2-46P, ERCC6L2, RNA5SP289
rs13265104	8	15571142	imputed	0.928	0.395	A	G	0.605	-0.206	0.056	1.0	0.171	0.044	9.2E-05	TUSC3, AC091559.1, RP11-77B22.2
rs35819675	2	230603117	imputed	0.941	0.361	C	G	0.361	-0.118	0.058	1.0	0.173	0.044	9.3E-05	DNER, RNU7-9P, TRIP12,

															RNU6-613P, FBXO36, RNU6-964P, FBXO36-IT1, RNU6-1027P, SLC16A14
rs61844533	10	6778842	imputed	0.825	0.073	A	C	0.927	-0.353	0.105	1.0	0.363	0.093	9.3E-05	PRKCQ, PRKCQ-AS1, RP11-554I8.1, RP11-554I8.2, LINC00707, RP11-799O21.2
rs6063436	20	36294785	imputed	0.938	0.151	A	G	0.849	-0.220	0.075	1.0	0.239	0.061	9.3E-05	SRC, BLCAP, NNAT, LINC00489, RP4-640H8.2, CTNNBL1, VSTM2L
rs10072728	5	4919906	genotyped	0.986	0.061	G	T	0.939	0.314	0.109	1.0	-0.307	0.078	9.3E-05	RP11-445O3.2, CTD-2318H23.1, CTD-2161F6.3, CTD-2161F6.2, CTD-2161F6.1, CTD-2046I8.1, CTD-2247C11.2, CTD-2247C11.1, LINC01020, CTD-2247C11.4, CTD-2247C11.5, RN7SKP73, CTD-2297D10.2, ADAMTS16, CTD-2297D10.1
rs1481103	4	73649117	genotyped	0.972	0.220	C	T	0.781	-0.164	0.064	1.0	0.204	0.052	9.4E-05	ADAMTS3, RNU4ATAC9P, RNU6ATAC5P, RP11-352E8.2, COX18, ANKRD17
rs11776881	8	131805603	imputed	0.869	0.466	A	C	0.534	-0.094	0.058	0.9	0.179	0.046	9.4E-05	KB-1568E2.1, ADCY8, RP11-737F9.2, RP11-737F9.1
rs10425998	19	31957139	genotyped	1.022	0.204	C	T	0.796	0.128	0.067	1.0	-0.196	0.050	9.5E-05	CTC-439O9.3, TSHZ3, AC007796.1, AC008992.1, CTD-2050I18.2, CTD-2050I18.1, AC011525.2, AC011525.4, RNA5SP471
rs17253044	6	25503735	genotyped	1.016	0.143	C	T	0.857	0.175	0.081	1.0	-0.227	0.058	9.5E-05	RP3-522P13.3, LRRC16A, Y_RNA, RNU6-987P, AL160037.1, snoU13, SCGN, HIST1H2AA, HIST1H2BA, SLC17A4, SLC17A1
rs6715792	2	217175528	imputed	0.926	0.165	A	G	0.835	-0.169	0.076	1.0	0.239	0.061	9.5E-05	MREG, PECR, TMEM169, XRCC5, RP11-566E18.3, MARCH4, AC012513.6, AC069155.1, Y_RNA, AC098820.2, SMARCAL1, AC098820.3, AC098820.4, RPL37A, AC073321.3,

															AC073321.4
rs72984613	11	103702299	imputed	0.925	0.090	A	G	0.090	0.156	0.095	0.9	-0.318	0.081	9.5E-05	RP11-563P16.1, MIR4693, PDGFD, RP11-617B3.2, DDI1
rs13339093	16	78619484	imputed	0.813	0.143	C	T	0.143	-0.206	0.087	1.0	0.252	0.065	9.6E-05	WWOX, RP11-264L1.4, RP11-264L1.3
rs73579711	6	125552553	imputed	0.966	0.021	A	G	0.021	0.472	0.171	1.0	-0.559	0.143	9.6E-05	RP11-510H23.1, RNF217, TPD52L1, HDDC2, RP11-735G4.1, RP11-138M12.1
rs77692718	18	9160940	imputed	0.909	0.037	C	T	0.037	0.168	0.140	0.8	-0.487	0.125	9.7E-05	NDUFV2, RP11-21J18.1, RP11-143J12.3, RP11-143J12.2, ANKRD12, Y_RNA, RP11-888D10.4, snoU13, RP11-888D10.3, TWSG1
rs2793447	6	24360149	imputed	0.806	0.115	A	G	0.886	-0.163	0.093	0.9	0.317	0.081	9.7E-05	NRSN1, SNORD46, DCDC2, KAAG1, RNU6-391P, MRS2, GPLD1, ALDH5A1, KIAA0319, TDP2
rs6573843	14	69067164	imputed	0.985	0.185	C	G	0.815	0.205	0.070	1.0	-0.199	0.051	9.8E-05	RAD51B, CTD-2325P2.4, CTD-2325P2.3, RNU6-921P, ZFP36L1, RN7SL224P, ACTN1
rs7190816	16	13935499	imputed	0.969	0.214	A	G	0.214	0.147	0.066	1.0	-0.210	0.054	1.0E-04	U91319.1, U95743.1, ERCC4, CTD-2135D7.2, CTD-2135D7.3, CTD-2135D7.5, CTD-2135D7.4, MKL

All genes within the region of the SNP are listed (±300kb). Robust (sandwich) standard errors are presented. In these tests of statistical interaction (on the additive scale), probABEL uses A2 as the tested (non-reference) allele, consistent with MACH. The beta coefficients in these models can be interpreted as follows. The SNP main effect beta coefficient indicates the average difference in levels of depressive symptoms for every additional tested allele for women with a zero value on all covariates and who are in the lowest quartile of stressful life events. The GxE interaction term indicates the average estimated difference in the effect of each tested allele on depressive symptoms associated with a one-unit different in stressful life events, adjusting for covariates. Our Bonferroni adjusted alpha level in these analyses was $2.5x10^{-8}$.

Supplemental Table 9. Genome-wide by environment interaction study (GWEIS) of social support results for the top loci (p<1x10-4) in African Americans

Social Support Results (n=6,908)

									SNP Main Effect			SNP*Social Support Interaction Term			
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value	Genes in region (±300kb)
rs77966298	2	10984514	imputed	0.891	0.034	A	G	0.966	0.796	0.223	1.0	-0.592	0.115	2.4E-07	NOL10, AC092687.5, RN7SL832P, AC092687.3, ATP6V1C2, RNU7-138P, RP11-791G15.2, PDIA6, RNU7-176P, AC092687.4, RP11-245G13.2, KCNF1, AC062028.1, C2orf50
rs6419121	4	88490040	imputed	0.921	0.178	C	G	0.178	-0.375	0.096	1.0	0.280	0.055	4.0E-07	MIR5705, HSD17B13, RP11-529H2.2, HSD17B11, RN7SL681P, Y_RNA, NUDT9, RP11-710E1.2, SPARCL1, RP11-742B18.1, DSPP, DMP1, snoU13, IBSP, MEPE
rs10836421	11	35581792	imputed	0.971	0.315	A	G	0.315	-0.184	0.071	1.0	0.217	0.043	4.3E-07	SLC1A2, RP1-68D18.3, RP4-683L5.1, PAMR1, RP5-945I17.2, FJX1, RP1-276E15.1, TRIM44, RP11-698N11.4
rs78012311	21	33634345	imputed	0.981	0.104	C	G	0.104	0.468	0.094	1.0	-0.321	0.065	8.2E-07	HUNK, HUNK-AS1, LINC00159, AP000261.1, AP000265.1, MIS18A, MIS18A-AS1, MRAP, AP000266.7, URB1, RN7SL109P, SNORA80, C21orf119, EVA1C, SNORA33
rs350182	1	4548292	imputed	0.827	0.038	A	G	0.038	-0.696	0.201	1.0	0.489	0.101	1.1E-06	RP5-1166F10.1, RP1-37J18.1, RP1-37J18.2, AJAP1

rs1665272	2	61379286	genotyped	1.032	0.361	G	T	0.639	-0.281	0.065	1.0	0.202	0.042	1.3E-06	AC010733.4, REL, RNU4-51P, RP11-373L24.1, PUS10, RNA5SP95, PEX13, KIAA1841, AC016747.3, C2orf74, RP11-493E12.1, AHSA2, USP34, RP11-493E12.2, SNORA70B
rs2414325	15	54888537	imputed	0.947	0.309	C	T	0.691	0.279	0.074	1.0	-0.214	0.045	2.0E-06	UNC13C
rs12346228	9	81929337	imputed	0.995	0.116	C	G	0.116	0.196	0.098	1.0	-0.303	0.065	2.8E-06	RP11-165H23.1, RP11-375O18.2, TLE4
rs13120623	4	165634055	genotyped	0.986	0.025	A	C	0.025	-0.743	0.212	1.0	0.553	0.119	3.1E-06	RNU6-284P, RP11-294O2.2, RNU6-668P, RP11-366M4.3, TRIM61, FAM218A, RP11-366M4.13
rs823067	1	205771704	imputed	1.003	0.307	C	T	0.693	0.247	0.069	1.0	-0.198	0.043	3.3E-06	CDK18, RNU2-19P, MFSD4, RNU6-418P, ELK4, SLC45A3, NUCKS1, AC119673.1, SNORA72, RAB7L1, SLC41A1, PM20D1, SLC26A9, RP4-681L3.2
rs746191	1	87849215	imputed	0.996	0.431	A	G	0.431	0.265	0.064	1.0	-0.190	0.041	4.0E-06	HS2ST1, RP5-1052I5.2, RP5-1052I5.1, AL139139.1, LMO4, RP4-544H6.2, RNA5SP52
rs7924546	11	82574706	imputed	0.998	0.461	A	G	0.461	-0.194	0.065	1.0	0.185	0.041	5.2E-06	RP11-179A16.1, SNORD112, RP11-179A16.2, FAM181B, RP11-718B12.2, PRCP, snoU13, C11orf82, RP11-659G9.3, RAB30, SNORA70E, RAB30-AS1, RP11-113K21.4, PCF11

rs41358246	18	43065571	genotyped	0.989	0.026	C	G	0.026	-0.672	0.240	1.0	0.551	0.121	5.6E-06	SLC14A2, RP11-309E23.2, RP11-749H17.1, RP11-749H17.2, RP11-116O18.1, RP11-116O18.3, SLC14A1
rs7734621	5	106282604	imputed	0.834	0.321	A	G	0.321	0.282	0.073	1.0	-0.211	0.046	5.7E-06	CTC-254B4.1
rs61830370	1	220168022	imputed	0.922	0.336	A	T	0.336	0.281	0.071	1.0	-0.201	0.045	7.8E-06	SLC30A10, RNA5SP76, U3, EPRS, snoU13, BPNT1, IARS2, MIR215, MIR194-1, RAB3GAP2, SNORA36B
rs41458545	7	84858778	genotyped	0.982	0.058	C	T	0.942	0.406	0.147	1.0	-0.371	0.083	8.1E-06	AC074183.4, SEMA3D, LINC00972
rs2520676	5	10020652	genotyped	1.016	0.124	C	T	0.876	-0.226	0.095	1.0	0.276	0.062	8.3E-06	CTD-2143L24.1, RNA5SP177, RP11-447B18.1, CTD-2199O4.1, CTD-2199O4.3, CTD-2199O4.7, CTD-2199O4.6, FAM173B, CTD-2256P15.1, CCT5, CTD-2256P15.4, CTD-2256P15.5, CMBL, Y_RNA
rs7860514	9	8354775	imputed	0.955	0.160	C	T	0.160	0.249	0.089	1.0	-0.253	0.057	8.9E-06	PTPRD
rs17866612	2	234956006	imputed	0.947	0.028	G	T	0.973	0.634	0.225	1.0	-0.536	0.121	1.0E-05	UGT1A1, UGT1A10, UGT1A9, UGT1A7, UGT1A6, UGT1A5, UGT1A4, UGT1A3, AC114812.5, UGT1A8, MROH2A, HJURP, MSL3P1, TRPM8, AC005538.5, SPP2, AC006037.2, RP11-309M7.1
rs144773402	2	34629564	imputed	0.832	0.055	A	T	0.055	-0.368	0.163	1.0	0.393	0.089	1.0E-05	AC009499.1, AC073218.1, AC011748.1, AC073218.2, RP11-529E15.1

rs17297115	2	233510979	genotyped	1.008	0.134	C	T	0.134	-0.343	0.095	1.0	0.243	0.055	1.1E-05	ALPP, AC068134.8, ECEL1P2, ALPPL2, AC068134.6, ALPI, ECEL1, PRSS56, CHRND, CHRNG, TIGD1, EIF4E2, MIR5001, AC073254.1, EFHD1, RN7SL359P, snoU13, GIGYF2, AC064852.4, KCNJ13, RNU6-107P, Y_RNA, C2orf82, NGEF
rs16833775	2	137110579	genotyped	0.982	0.308	G	T	0.692	-0.285	0.069	1.0	0.189	0.043	1.1E-05	AC068492.1, CXCR4, RN7SKP141, AC010146.2, AC092786.1
rs7028393	9	2366509	imputed	0.962	0.458	C	T	0.543	-0.252	0.065	1.0	0.178	0.040	1.1E-05	SMARCA2, RNU2-25P, RN7SL592P, RP11-125B21.2, RP11-91N2.3, VLDLR
rs1036270	10	132690651	imputed	0.898	0.409	A	G	0.409	0.241	0.066	1.0	-0.186	0.042	1.2E-05	MIR378C, AL607076.1, TCERG1L, RP11-462G8.3
rs61947610	13	31528027	imputed	0.985	0.039	A	C	0.961	-0.516	0.140	1.0	0.448	0.102	1.2E-05	USPL1, ALOX5AP, LINC00398, TEX26-AS1, LINC00545, MEDAG, TEX26, RP11-252M21.6, LINC01066, HSPH1, B3GALTL
rs8012822	14	42255054	imputed	0.992	0.239	C	T	0.239	-0.236	0.075	1.0	0.202	0.046	1.2E-05	CTD-2298J14.2, SNORA31, LRFN5, AL138498.1
rs10845985	12	14511348	imputed	0.940	0.305	A	G	0.305	-0.273	0.073	1.0	0.193	0.044	1.2E-05	RN7SL46P, RP11-134N1.2, RNU6-491P, RN7SL676P, RPL30P11, ATF7IP, PLBD1, RP11-502N13.2, RN7SKP134, RP11-695J4.2, GUCY2C
rs10141304	14	42169439	imputed	0.978	0.142	A	G	0.142	-0.248	0.093	1.0	0.254	0.058	1.2E-05	CTD-2298J14.2, SNORA31, LRFN5, AL138498.1

rs147700557	10	131917420	imputed	0.920	0.147	A	G	0.147	-0.342	0.105	1.0	0.262	0.060	1.3E-05	EBF3, MIR4297, LINC00959, GLRX3
rs10006642	4	133522032	imputed	0.910	0.263	G	T	0.737	0.201	0.078	1.0	-0.206	0.047	1.4E-05	RP11-62N21.1, RP11-149A7.2, RP11-404I7.2
rs74960061	13	68326936	imputed	0.854	0.098	A	G	0.902	0.275	0.122	1.0	-0.298	0.069	1.4E-05	
rs6879798	5	169506954	imputed	0.886	0.389	C	G	0.389	-0.217	0.070	1.0	0.187	0.043	1.4E-05	DOCK2, FAM196B, MIR378E, FOXI1, CTB-27N1.1, C5orf58, LCP2, CTB-114C7.4, CTB-114C7.3, KCNIP1, KCNMB1
rs79672112	11	35568512	imputed	0.954	0.059	A	G	0.059	-0.097	0.125	0.6	0.318	0.073	1.4E-05	SLC1A2, RP1-68D18.3, RP4-683L5.1, PAMR1, RP5-945I17.2, FJX1, RP1-276E15.1, TRIM44, RP11-698N11.4
rs7520919	1	77485632	imputed	0.885	0.090	A	G	0.910	-0.261	0.109	1.0	0.330	0.076	1.5E-05	RNU6-161P, RP11-415A20.1, ST6GALNAC5, AC096951.1, RP4-564M11.2, PIGK, AK5
rs113758196	7	70807394	imputed	0.969	0.101	C	T	0.899	0.374	0.112	1.0	-0.275	0.063	1.5E-05	WBSCR17, MIR3914-1, AC079398.1
rs2845945	11	99656514	imputed	0.925	0.414	A	G	0.586	-0.248	0.066	1.0	0.178	0.041	1.6E-05	CNTN5
rs7712698	5	58043255	genotyped	1.000	0.057	A	G	0.057	-0.462	0.147	1.0	0.357	0.083	1.6E-05	PLK2, GAPT, MIR548AE2, CTD-2117L12.1, RAB3C, RP11-479O16.1, CTD-2176I21.2, PDE4D, RP11-266N13.2
rs78267647	3	59721074	imputed	0.818	0.084	C	T	0.916	-0.381	0.115	1.0	0.319	0.074	1.6E-05	RP11-719N22.2, FHIT, NPCDR1
rs941179	12	124985028	genotyped	1.017	0.107	A	G	0.107	0.407	0.101	1.0	-0.285	0.066	1.7E-05	FAM101A, RP11-522N14.2, NCOR2, RP11-83B20.1, SCARB1

rs75395973	3	15517208	imputed	0.989	0.051	C	T	0.949	-0.275	0.162	0.9	0.446	0.104	1.7E-05	COL6A4P1, CAPN7, Y_RNA, SH3BP5-AS1, SH3BP5, snoU13, RNU6-454P, METTL6, EAF1, RNU6-1024P, EAF1-AS1, COLQ, MIR4270, RN7SL110P, HACL1, BTD, ANKRD28, MIR3134, RP11-44D5.1, RN7SL4P
rs10822045	10	52746151	imputed	0.980	0.409	C	G	0.409	0.207	0.063	1.0	-0.175	0.041	1.8E-05	ASAH2B, A1CF, RP11-449O16.2, RP11-96B5.4, PRKG1, RP11-96B5.3, RP11-40C11.2, AC022537.1
rs2762109	13	94051889	imputed	0.975	0.249	A	G	0.751	0.262	0.079	1.0	-0.198	0.046	1.8E-05	GPC6, SNORD22
rs73059143	5	19289230	imputed	0.958	0.037	A	G	0.037	-0.767	0.193	0.9	0.454	0.106	1.8E-05	RP11-124N3.3, RP11-124N3.2, CDH18
rs76956521	5	150464641	imputed	0.836	0.031	A	C	0.969	0.341	0.194	1.0	-0.483	0.113	1.8E-05	SMIM3, AC010441.1, IRGM, ZNF300, ZNF300P1, GPX3, TNIP1, ANXA6, CTB-17P3.4, CCDC69, GM2A, SLC36A3, SLC36A2, AC034205.1
rs4600849	3	32027672	imputed	0.924	0.347	C	T	0.653	0.141	0.069	1.0	-0.180	0.042	1.9E-05	OSBPL10, OSBPL10-AS1, ZNF860, SNORA25, Y_RNA, GPD1L, snoU13, RP11-384L8.1, CMTM8, AC097639.1
rs76634298	2	148339129	imputed	0.957	0.339	C	T	0.339	0.162	0.070	1.0	-0.189	0.044	1.9E-05	snoU13, RNU6-692P, AC013406.1, Y_RNA, RNU6-715P, RNA5SP106, ACVR2A, RNU6-1275P
rs7037884	9	2213818	genotyped	1.015	0.140	G	T	0.140	0.295	0.086	1.0	-0.249	0.058	1.9E-05	SMARCA2, RP11-264I13.2, RNU2-25P, RN7SL592P, RP11-125B21.2

rs9817234	3	68707641	imputed	0.980	0.232	C	T	0.768	0.296	0.075	1.0	-0.194	0.045	1.9E-05	FAM19A1, AC096922.1, FAM19A4, RNA5SP135
rs11073147	15	36392562	genotyped	0.991	0.221	A	G	0.221	-0.254	0.080	1.0	0.203	0.048	2.0E-05	DPH6-AS1, MIR4510, RP11-184D12.1, RP11-684B21.1, RP11-475A13.2
rs164266	6	1202299	imputed	0.920	0.066	C	T	0.066	-0.303	0.135	1.0	0.339	0.079	2.0E-05	RP5-1077H22.2, RP5-1077H22.1, RP5-856G1.1, AL033381.1, snoU13, FOXQ1, RP4-668J24.2, FOXF2
rs9435067	1	6193084	imputed	0.802	0.054	C	T	0.946	0.114	0.147	0.6	-0.365	0.086	2.1E-05	MIR4689, NPHP4, AL356261.1, KCNAB2, AL035406.1, CHD5, RPL22, RP1-120G22.11, RNF207, ICMT, LINC00337, HES3, GPR153, ACOT7, RP1-202O8.3, HES2, ESPN, MIR4252
rs792052	2	5560650	imputed	0.889	0.430	A	G	0.570	-0.211	0.066	1.0	0.180	0.042	2.1E-05	AC107057.1, AC107057.2, AC108025.2, SOX11, AC010729.1
rs77620255	4	115263602	imputed	0.875	0.044	A	G	0.044	0.523	0.154	1.0	-0.478	0.113	2.2E-05	UGT8
rs12906291	15	55846059	imputed	0.968	0.088	A	G	0.912	0.393	0.118	1.0	-0.291	0.069	2.3E-05	RAB27A, RP11-139H15.1, PIGB, CCPG1, DYX1C1-CCPG1, MIR628, C15orf65, DYX1C1, PYGO1, PRTG, RP11-420M1.2, AC009997.1, NEDD4
rs75441182	5	171222776	imputed	0.949	0.034	A	G	0.966	-0.666	0.167	1.0	0.508	0.120	2.3E-05	AC011410.1, CTB-78H18.1, C5orf50, FBXW11, STK10, AC113342.1

rs10917676	1	163089736	imputed	0.959	0.245	C	T	0.245	-0.150	0.079	0.9	0.204	0.048	2.4E-05	C1orf110, RGS4, RGS5, RP11-267N12.1, RP11-267N12.3, RP11-77M5.1, NUF2, SNORD112
rs4640379	2	233141377	genotyped	0.904	0.330	C	T	0.330	-0.225	0.074	1.0	0.186	0.044	2.4E-05	DIS3L2, AC105461.1, MIR562, ALPP, AC068134.8, ECEL1P2, ALPPL2, AC068134.6, ALPI, ECEL1, PRSS56, CHRND, CHRNG, TIGD1, EIF4E2, MIR5001
rs1040637	6	134823919	genotyped	1.001	0.161	A	G	0.161	-0.186	0.087	1.0	0.217	0.051	2.4E-05	SGK1, snoU13, RNA5SP218, Y_RNA, RP11-557H15.3, LINC01010, RP11-557H15.4, RP11-557H15.5, CTA-31J9.2, RP1-287H17.1
rs7612233	3	16223445	imputed	0.933	0.045	C	T	0.045	-0.396	0.162	1.0	0.382	0.090	2.5E-05	GALNT15, DPH3, OXNAD1, RFTN1, RP11-415F23.2, RP11-415F23.3, RP11-415F23.4
rs9289733	3	146527585	imputed	0.912	0.040	A	T	0.040	-0.578	0.181	1.0	0.432	0.102	2.5E-05	PLSCR1, RNU6-428P, PLSCR5, PLSCR5-AS1, RP11-649A16.1, RP11-232M24.1, U3, RNU6-505P
rs7142399	14	95145579	imputed	0.969	0.321	A	G	0.321	-0.148	0.069	1.0	0.177	0.042	2.6E-05	SERPINA1, RP11-349I1.2, SERPINA11, SERPINA9, SERPINA12, SERPINA4, SERPINA5, RP11-986E7.7, SERPINA3, SERPINA13P, GSC, RP11-991C1.1

rs76817598	15	55933969	imputed	0.953	0.043	A	T	0.958	0.404	0.159	1.0	-0.393	0.093	2.6E-05	PIGB, CCPG1, DYX1C1-CCPG1, MIR628, C15orf65, DYX1C1, PYGO1, PRTG, RP11-420M1.2, AC009997.1, NEDD4
rs115074218	12	23859564	imputed	0.808	0.051	C	T	0.051	0.419	0.131	1.0	-0.441	0.105	2.6E-05	SOX5, RP11-437F6.1
rs1383743	11	38669677	imputed	0.954	0.124	A	G	0.877	0.400	0.112	1.0	-0.264	0.063	2.7E-05	RP11-63D14.1, RP11-277K23.1, RP11-64I17.1
rs6891892	5	147497871	imputed	0.952	0.063	C	T	0.937	0.519	0.143	1.0	-0.346	0.082	2.7E-05	SPINK1, SCGB3A2, C5orf46, CTC-327F10.5, CTC-327F10.4, SPINK5, SPINK14, SPINK6, CTC-295J13.3, SPINK13, RP11-373N22.3, SPINK7, AC091948.1, SPINK9, FBXO38
rs78358474	14	70596552	imputed	0.902	0.023	C	G	0.977	0.806	0.245	1.0	-0.540	0.129	2.7E-05	SMOC1, SLC8A3, RP11-486O13.2, ADAM21P1, RP11-718G2.5, COX16, SYNJ2BP-COX16, RNU2-51P, SYNJ2BP, RP11-486O13.4
rs34698110	12	26104829	imputed	0.918	0.106	G	T	0.894	-0.350	0.104	1.0	0.301	0.072	2.8E-05	RN7SKP262, RP11-443N24.2, RP11-443N24.3, RP11-443N24.4, RASSF8-AS1, RASSF8, BHLHE41, SSPN, RP11-283G6.3, RP11-283G6.4, RP11-283G6.5
rs9487750	6	112233400	imputed	0.907	0.280	C	G	0.280	0.224	0.070	1.0	-0.192	0.046	2.8E-05	snoU13, FYN, RP1-97J1.2, WISP3, TUBE1, FAM229B, LAMA4, RP1-142L7.5, RNU6-1226P

rs9923066	16	85021693	imputed	0.913	0.200	A	G	0.800	0.289	0.084	1.0	-0.215	0.051	2.8E-05	USP10, CRISPLD2, RP11-254F19.2, AC025280.1, RP11-254F19.3, ZDHHC7, KIAA0513, FAM92B, CTC-786C10.1, LINC00311
rs10735548	9	83153980	imputed	0.973	0.169	C	G	0.169	0.300	0.085	1.0	-0.237	0.057	2.8E-05	AL353707.1
rs78312281	3	154045191	imputed	0.973	0.134	A	G	0.866	0.255	0.096	1.0	-0.243	0.058	2.9E-05	ARHGEF26-AS1, ARHGEF26, DHX36, snoU13, GPR149, RP11-656A15.1
rs11776881	8	131805603	imputed	0.869	0.466	A	C	0.534	-0.186	0.070	1.0	0.183	0.044	3.1E-05	KB-1568E2.1, ADCY8, RP11-737F9.2, RP11-737F9.1
rs6935115	6	15170802	genotyped	0.895	0.256	C	T	0.256	-0.238	0.079	1.0	0.201	0.048	3.2E-05	RP11-146I2.1, RN7SL332P, AL050335.1, RP11-560J1.2, JARID2, JARID2-AS1, RNU6-522P, RNU6-645P
rs843184	9	105878269	imputed	0.929	0.275	G	T	0.275	-0.154	0.073	1.0	0.184	0.044	3.3E-05	CYLC2, RP11-341A22.2, RP11-436F21.1
rs2922310	2	177482095	imputed	0.995	0.338	A	C	0.338	-0.220	0.070	1.0	0.179	0.043	3.3E-05	MTX2, AC068706.2, AC068706.1, AC017048.1, AC017048.2, RP11-324L17.1, AC017048.3, AC017048.4, RNU6ATAC14P, AC092162.1, AC073636.1
rs74326443	5	10007500	imputed	0.824	0.146	C	T	0.854	-0.207	0.100	1.0	0.268	0.065	3.4E-05	TAS2R1, CTD-2143L24.1, RNA5SP177, RP11-447B18.1, CTD-2199O4.1, CTD-2199O4.3, CTD-2199O4.7, CTD-2199O4.6, FAM173B, CTD-2256P15.1, CCT5, CTD-2256P15.4, CTD-2256P15.5, CMBL, Y_RNA
rs11980441	7	82422080	imputed	0.984	0.413	C	T	0.587	0.257	0.068	1.0	-0.174	0.042	3.4E-05	PCLO, RNA5SP235

rs11748913	5	2535215	genotyped	1.013	0.400	C	T	0.400	-0.220	0.067	1.0	0.167	0.040	3.4E-05	RP11-129I19.2, IRX2, C5orf38, RP11-468D11.1
rs138223394	4	110696258	imputed	0.810	0.249	A	G	0.249	0.306	0.079	1.0	-0.215	0.052	3.5E-05	SEC24B, MIR576, CCDC109B, CASP6, AC004067.5, PLA2G12A, CFI, RP11-602N24.3, GAR1, RRH, LRIT3, EGF, RNU6-35P, ELOVL6
rs4019308	12	76126019	imputed	0.854	0.424	A	G	0.576	0.313	0.071	1.0	-0.185	0.045	3.5E-05	GLIPR1L2, GLIPR1, RP11-585P4.5, KRR1, RP11-114H23.1, SNORA70, RP11-114H23.2, AC131012.1, RN7SL734P, RP11-290L1.5, PHLDA1, RP11-290L1.3
rs11780706	8	123759570	imputed	0.985	0.170	C	T	0.170	-0.288	0.086	1.0	0.217	0.052	3.5E-05	RP11-96B2.1, RP11-973F15.1, snoU13, RP11-973F15.2, RP11-44N11.2, RP11-44N11.3, ZHX2, RP11-44N11.1, AC016405.2, RP11-557C18.4, RP11-557C18.3, DERL1, TBC1D31, RNY4P5
rs112880493	18	41654470	imputed	0.845	0.029	C	T	0.029	-0.858	0.251	1.0	0.529	0.128	3.5E-05	RNU6-443P, RNA5SP455, CTC-782O7.1
rs57579228	2	19950737	imputed	0.938	0.261	A	C	0.261	-0.265	0.076	1.0	0.191	0.046	3.6E-05	AC010096.1, AC010096.2, AC019055.1, LINC00954, TTC32, RP11-79O8.1, WDR35, AC079145.4, MATN3, LAPTM4A
rs936700	3	176672512	genotyped	1.012	0.186	G	T	0.186	-0.307	0.089	1.0	0.208	0.050	3.6E-05	RP11-644C3.1, RNA5SP147, RP11-255G21.1, TBL1XR1, TBL1XR1-AS1, Y_RNA, RNU6-681P

rs148152391	6	131300443	imputed	0.995	0.053	G	T	0.053	0.450	0.135	1.0	-0.375	0.091	3.6E-05	RP11-102N11.1, SMLR1, EPB41L2, AKAP7
rs2834005	21	34291708	imputed	0.968	0.437	C	T	0.437	0.199	0.065	1.0	-0.173	0.042	3.7E-05	SYNJ1, PAXBP1-AS1, PAXBP1, C21orf49, C21orf62, SNORA70, AP000281.2, AP000282.2, AP000282.3, OLIG2, LINC00945, OLIG1, AP000289.6, AP000290.7, C21orf54
rs1495941	11	61390368	genotyped	0.982	0.048	C	T	0.952	0.348	0.148	1.0	-0.343	0.083	3.7E-05	DDB1, DAK, CYB561A3, TMEM138, TMEM216, CPSF7, RP11-286N22.8, SDHAF2, RN7SL23P, PPP1R32, RP11-286N22.10, MIR4488, LRRC10B, SYT7, RP11-794G24.1, RP11-855O10.2, RPLP0P2, RP11-855O10.3, DAGLA, RP11-467L20.10, MYRF, TMEM258, MIR611, FEN1, FADS2, FADS1, MIR1908, FADS3, RAB3IL1
rs6072996	20	41769928	imputed	0.990	0.276	C	T	0.276	-0.216	0.073	1.0	0.181	0.044	4.0E-05	PTPRT, RP4-753D4.2, RN7SKP100, RP1-269M15.3, RN7SL666P, SCARNA15, RNU6-743P
rs11083297	18	26244923	imputed	0.989	0.210	C	T	0.790	-0.275	0.075	1.0	0.199	0.048	4.0E-05	RP11-510D21.1

rs1007462	17	55203315	genotyped	1.011	0.249	C	T	0.751	-0.139	0.073	0.9	0.191	0.047	4.2E-05	C17orf67, DGKE, RP11-670E13.2, RNU6-1158P, TRIM25, RP11-670E13.5, MIR3614, COIL, RP5-1107A17.3, SCPEP1, RP5-1107A17.4, AC007114.1, RNF126P1, RP11-166P13.3, AKAP1, RP11-166P13.4, MSI2, RN7SL437P
rs4686780	3	186208238	imputed	1.008	0.473	A	T	0.527	-0.205	0.064	1.0	0.163	0.040	4.2E-05	DGKG, RP11-78H24.1, RP11-48F14.1, RP11-48F14.2, CRYGS, TBCCD1, DNAJB11, AHSG, FETUB, RP11-134F2.2, HRG, RP11-573D15.8, KNG1, RNU6-1105P, RP11-573D15.9, EIF4A2, SNORD2, SNORA63, SNORA81, SNORA4, RFC4
rs2185875	6	72591049	imputed	0.988	0.151	A	G	0.151	0.273	0.087	1.0	-0.234	0.057	4.3E-05	AL354933.1, RNU4-66P, RIMS1
rs5770654	22	50079641	imputed	0.880	0.315	G	T	0.685	0.213	0.077	1.0	-0.189	0.046	4.3E-05	C22orf34, MIR3667, RP1-29C18.10, RP1-29C18.9, RP1-29C18.8, RP5-983L19.2, RN7SKP252, BRD1, RP3-522J7.6, ZBED4, ALG12, CITF22-1A6.3, CRELD2, PIM3
rs957165	19	29882525	imputed	0.952	0.343	G	T	0.657	0.255	0.071	1.0	-0.177	0.043	4.4E-05	UQCRFS1, CTB-32O4.2, RN7SL340P, CTC-525D6.1, CTC-525D6.5, CTC-525D6.2, VSTM2B, POP4, PLEKHF1
rs75901505	2	78207763	imputed	0.810	0.075	C	T	0.925	0.382	0.137	1.0	-0.321	0.079	4.4E-05	AC105399.2, AC073628.1, AC012494.1

rs7132867	12	68171916	genotyped	0.994	0.474	G	T	0.474	0.214	0.065	1.0	-0.166	0.041	4.4E-05	RP11-542B15.1, RP11-335O4.1, DYRK2, RP11-335O4.3, RP11-43N5.1, GS1-410F4.4, IFNG-AS1
rs9557793	13	102697015	genotyped	1.013	0.458	G	T	0.458	0.197	0.062	1.0	-0.162	0.040	4.4E-05	FGF14, RNU1-24P, MIR2681, RNY1P2, MIR4705, FGF14-IT1
rs3772077	2	216189825	imputed	0.927	0.206	A	G	0.794	-0.296	0.079	1.0	0.213	0.052	4.4E-05	ABCA12, AC072062.3, AC073284.4, snoU13, ATIC, FN1, AC012462.1, AC012462.2, AC012462.3, AC012668.1, AC012668.2, AC012668.3, LINC00607
rs2310770	3	94785192	imputed	0.960	0.462	A	T	0.538	-0.165	0.065	1.0	0.167	0.041	4.5E-05	LINC00879
rs2046427	3	3560195	imputed	0.850	0.343	A	G	0.343	0.234	0.072	1.0	-0.185	0.045	4.5E-05	AC026188.1, AC024158.1, SUMF1, LRRN1
rs11801833	1	87698626	genotyped	1.017	0.191	C	T	0.809	-0.229	0.078	1.0	0.208	0.051	4.5E-05	HS2ST1, RP4-604K5.3, RP4-604K5.2, RP5-1052I5.2, RP5-1052I5.1, AL139139.1, LMO4, RP4-544H6.2, RNA5SP52
rs76109323	2	46804120	imputed	0.868	0.083	A	G	0.917	-0.329	0.125	1.0	0.338	0.083	4.7E-05	EPAS1, AC016912.3, TMEM247, RN7SL817P, ATP6V1E2, RP11-417F21.2, RHOQ, RP11-417F21.1, PIGF, CRIPT, SOCS5, RP11-333I13.1, AC016722.1, AC016722.2, AC016722.3
rs6655923	1	221627469	imputed	0.905	0.192	A	G	0.192	-0.332	0.086	1.0	0.214	0.053	4.8E-05	RP11-421L10.1, RP11-103C3.1, DUSP10

rs11264150	1	35854802	genotyped	1.020	0.039	A	T	0.039	0.739	0.151	1.0	-0.462	0.114	4.8E-05	ZMYM1, SFPQ, Y_RNA, RN7SL136P, ZMYM4, RN7SL503P, SNORA62, ZMYM4-AS1, RNY5P1, KIAA0319L, NCDN, RP4-728D4.2, TFAP2E, PSMB2
rs78025358	2	159772439	imputed	0.899	0.325	C	T	0.325	0.173	0.072	1.0	-0.183	0.045	4.9E-05	PKP4, AC005042.4, AC005042.5, DAPL1, RNU2-21P, TANC1, RNU6-580P
rs4653747	1	226681827	imputed	0.902	0.292	A	G	0.708	-0.145	0.071	1.0	0.191	0.047	5.0E-05	MIXL1, LIN9, snoU13, PARP1, RN7SKP165, C1orf95, ITPKB, ITPKB-IT1, ITPKB-AS1
rs11936313	4	185642174	imputed	0.988	0.095	C	T	0.095	-0.277	0.122	1.0	0.280	0.069	5.0E-05	IRF2, SNORD79, RP11-326I11.5, RP11-326I11.3, RP11-326I11.4, RP11-242J7.1, CASP3, PRIMPOL, MLF1IP, ACSL1, RP11-701P16.1, RP11-701P16.2, RP11-701P16.5, MIR3945, RP11-701P16.4, MIR4455, RP11-386B13.4, HELT
rs272392	13	64618428	imputed	0.988	0.487	A	G	0.487	-0.270	0.064	1.0	0.160	0.040	5.1E-05	AL445989.1, RP11-473M10.3, RNU6-81P, RP11-394A14.2, RP11-394A14.4, LINC00355
rs12062024	1	4089259	genotyped	1.012	0.474	A	T	0.526	0.202	0.065	1.0	-0.159	0.039	5.2E-05	DFFB, AL691523.1, C1orf174, RP13-15E13.1, RP13-614K11.1, RP13-614K11.2
rs112865975	16	25969777	imputed	0.839	0.066	A	G	0.066	0.436	0.128	1.0	-0.353	0.087	5.2E-05	HS3ST4, MIR548W, RNA5SP405

rs12037513	1	26224633	genotyped	1.003	0.449	A	G	0.551	0.210	0.064	1.0	-0.161	0.040	5.3E-05	MAN1C1, RP1-187B23.1, SEPN1, RP1-317E23.6, RP1-317E23.3, MTFR1L, AL020996.1, RP1-317E23.7, AUNIP, RP1-125I3.2, PAQR7, Y_RNA, STMN1, MIR3917, AL033528.1, PAFAH2, RNU6-110P, SCARNA17, SCARNA18, EXTL1, SLC30A2, TRIM63, AL391650.1, PDIK1L, FAM110D, ZNF593, RP11-96L14.7, CNKSR1, CATSPER4
rs7905870	10	17050313	imputed	0.983	0.251	C	T	0.749	0.180	0.075	1.0	-0.180	0.045	5.3E-05	RSU1, RP11-197M22.2, CUBN, RP11-406H21.2, TRDMT1, VIM-AS1, VIM, RP11-124N14.3
rs7709181	5	43004195	genotyped	1.009	0.175	A	G	0.175	0.264	0.080	1.0	-0.203	0.050	5.3E-05	GHR, CCDC152, SEPP1, CTD-2325A15.5, CTD-2201E18.5, CTD-2201E18.3, CTD-2035E11.3, CTD-2035E11.4, ANXA2R, AC025171.1, CTD-2035E11.5, ZNF131, NIM1, CTD-2636A23.2, HMGCS1
rs9579645	13	31310506	imputed	0.934	0.417	A	C	0.583	-0.207	0.064	1.0	0.166	0.041	5.4E-05	HMGB1, USPL1, ALOX5AP, LINC00398, TEX26-AS1, LINC00545, MEDAG, TEX26, RP11-252M21.6, LINC01066
rs2201354	14	43926576	imputed	0.957	0.463	A	T	0.463	-0.158	0.065	1.0	0.163	0.040	5.5E-05	
rs10849297	12	5682600	imputed	0.903	0.257	C	T	0.257	-0.245	0.079	1.0	0.197	0.049	5.6E-05	RP11-1038A11.3, RP11-319E16.2, RP11-1038A11.2, RP11-1038A11.1, NTF3, ANO2
rs1392479	5	106246797	imputed	0.875	0.414	A	C	0.414	-0.230	0.070	1.0	0.175	0.043	5.6E-05	CTC-254B4.1

rs10084370	2	213091799	imputed	0.980	0.268	C	T	0.732	-0.206	0.069	1.0	0.181	0.045	5.7E-05	ERBB4, MIR548F2
rs2419607	10	113978499	imputed	0.874	0.274	G	T	0.726	0.268	0.076	1.0	-0.187	0.046	5.7E-05	GPAM, TECTB, GUCY2GP, ACSL5, RP11-324O2.3, RP11-324O2.6, ZDHHC6, VTI1A
rs6773797	3	14745465	imputed	0.896	0.078	C	G	0.078	-0.330	0.127	1.0	0.300	0.075	5.9E-05	SLC6A6, GRIP2, RNU6-905P, AC090952.5, CCDC174, C3orf20, AC090957.2, RP11-95M5.1, FGD5, FGD5-AS1, NR2C2
rs870382	11	24666837	imputed	0.917	0.306	C	G	0.306	-0.248	0.074	1.0	0.180	0.045	6.0E-05	Y_RNA, LUZP2
rs7152412	14	95129029	imputed	0.871	0.490	G	T	0.510	-0.235	0.070	1.0	0.175	0.044	6.1E-05	SERPINA1, RP11-349I1.2, SERPINA11, SERPINA9, SERPINA12, SERPINA4, SERPINA5, RP11-986E7.7, SERPINA3, SERPINA13P, GSC, RP11-991C1.1
rs4024642	3	23911262	imputed	0.929	0.070	A	C	0.070	-0.415	0.139	1.0	0.302	0.075	6.1E-05	UBE2E2, RNU6-922P, RNU6-788P, AC020626.1, UBE2E1-AS1, UBE2E1, NKIRAS1, RPL15, NR1D2, LINC00691, THRB
rs11719519	3	186104558	genotyped	1.001	0.387	C	T	0.613	-0.150	0.063	1.0	0.166	0.041	6.1E-05	ETV5, DGKG, RP11-78H24.1, RP11-48F14.1, RP11-48F14.2, CRYGS, TBCCD1, DNAJB11, AHSG, FETUB, RP11-134F2.2, HRG

rs4761794	12	52819181	imputed	0.962	0.213	C	G	0.213	0.235	0.076	1.0	-0.201	0.050	6.3E-05	KRT80, C12orf80, LINC00592, KRT7, RP3-416H24.1, KRT86, KRT121P, RP11-845M18.7, KRT81, RP11-845M18.6, KRT83, AC121757.1, KRT85, KRT84, RP3-416H24.4, KRT82, RP11-1020M18.10, KRT75, KRT6B, KRT6C, KRT6A, KRT5, AC055736.1, KRT71, KRT74, KRT72, RP11-641A6.2, KRT73, KRT2, KRT1, KRT77, RP11-641A6.3
rs60127739	6	95154047	imputed	0.824	0.169	G	T	0.832	-0.180	0.089	0.4	0.236	0.059	6.4E-05	RP3-463P15.1
rs73686997	7	36232724	imputed	0.879	0.104	C	T	0.897	0.046	0.100	1.0	-0.245	0.061	6.4E-05	SEPT7, RNU6-1085P, AC083864.3, PP13004, RP11-196O2.1, EEPD1, AC007327.5, RP11-182J23.1, KIAA0895, Y_RNA, ANLN, AC006960.7
rs6577956	8	139863048	genotyped	0.994	0.425	C	T	0.576	0.149	0.066	1.0	-0.160	0.040	6.5E-05	COL22A1, RP11-324F11.1, SNORA25, CTD-2534J5.1
rs10488069	7	156380932	imputed	0.820	0.421	C	G	0.421	0.189	0.072	1.0	-0.184	0.046	6.6E-05	AC073133.2, AC073133.1, LINC01006, C7orf13, RNF32, AC005534.8, LMBR1, RNU4-31P
rs2251308	10	131062816	genotyped	1.007	0.055	A	G	0.946	-0.488	0.125	1.0	0.344	0.086	6.7E-05	RP11-168C9.1, MGMT, AL355531.1, AL355531.2
rs116083225	10	78007558	imputed	0.878	0.024	C	T	0.024	0.799	0.201	1.0	-0.633	0.159	6.7E-05	C10orf11, AC012047.1, RN7SL518P, RNU6-673P, RP11-369F10.2

rs397280	9	4655278	imputed	0.854	0.159	G	T	0.842	0.334	0.102	1.0	-0.238	0.060	6.7E-05	AL162419.1, RNU6-694P, SLC1A1, SPATA6L, PPAPDC2, RP11-6J24.6, CDC37L1, AK3, RCL1, MIR101-2, RP11-125K10.5, AL158147.2
rs1290100	2	49260542	imputed	0.942	0.422	C	G	0.422	0.206	0.067	1.0	-0.167	0.042	6.8E-05	STON1-GTF2A1L, LHCGR, FSHR, RNU6-439P
rs7310727	12	116844713	genotyped	1.000	0.430	G	T	0.570	-0.223	0.063	1.0	0.160	0.040	6.9E-05	MED13L, MIR620, RP11-115H15.2, AC060226.1, RP11-148B3.2, MIR4472-2, RP11-148B3.1, LINC00173, RP11-809C9.2, MAP1LC3B2, RP11-497G19.3, RP11-497G19.1, RP11-497G19.2
rs72751005	9	83293176	imputed	0.816	0.059	A	G	0.941	-0.531	0.141	1.0	0.371	0.093	6.9E-05	AL353707.1, RP11-289F5.1
rs41271491	1	230399307	imputed	0.932	0.083	A	C	0.917	0.333	0.125	1.0	-0.287	0.072	7.0E-05	RP11-552D4.1, BX323860.1, GALNT2, RP5-956O18.2, RP5-956O18.3, PGBD5
rs12311356	12	26063733	genotyped	0.835	0.425	C	T	0.575	-0.242	0.068	1.0	0.168	0.042	7.0E-05	IFLTD1, RN7SKP262, RP11-443N24.2, RP11-443N24.3, RP11-443N24.4, RASSF8-AS1, RASSF8, BHLHE41, SSPN, RP11-283G6.3
rs4861972	4	182411425	imputed	0.909	0.481	C	G	0.481	-0.145	0.068	1.0	0.171	0.043	7.1E-05	RP11-665C14.2
rs1156513	3	55929848	genotyped	0.995	0.054	A	G	0.946	0.282	0.145	0.9	-0.337	0.085	7.1E-05	ERC2, RP11-58O15.1, MIR3938, RN7SKP45, RNA5SP133
rs12513577	5	34285666	imputed	0.951	0.492	A	C	0.508	0.225	0.067	1.0	-0.164	0.041	7.2E-05	AMACR, RP11-1084J3.4, C1QTNF3, RP11-1250I15.3, RP11-1023L17.1

rs4787133	16	8179165	imputed	0.980	0.232	A	T	0.768	0.319	0.079	1.0	-0.189	0.048	7.3E-05	CTD-2535I10.1, AC093515.1, RP11-279O17.2, RP11-279O17.1, AC018767.1, RP11-279O17.3, RP11-568A19.1
rs17777147	2	196084339	genotyped	1.013	0.053	A	C	0.053	-0.341	0.147	1.0	0.320	0.081	7.3E-05	AC010983.1, AC064834.1, RP11-762E8.1, RNU6-169P
rs16884125	4	30821987	imputed	0.939	0.103	A	G	0.897	0.256	0.110	1.0	-0.265	0.067	7.3E-05	PCDH7, RP11-619J20.1
rs35896491	5	158537278	imputed	0.939	0.059	A	G	0.059	-0.412	0.141	1.0	0.320	0.081	7.5E-05	EBF1, CTD-2363C16.1, CTD-2363C16.2, RP11-175K6.1, RNF145, CTB-11I22.1, CTB-11I22.2, SNORA68, UBLCP1, AC008697.1, IL12B, RNU4ATAC2P
rs1545942	16	48427306	imputed	0.842	0.351	C	G	0.649	-0.274	0.074	1.0	0.184	0.046	7.5E-05	ABCC12, RP11-3M1.1, ABCC11, LONP2, SIAH1, RN7SL54P, AC023818.1, RP11-44I10.6, snoU13, N4BP1, RP11-44I10.3, CTC-527H23.2, RP11-42I10.1, CTC-527H23.3, CTC-527H23.4, AC007611.1
rs75028708	6	69713044	imputed	0.974	0.028	A	G	0.028	0.469	0.153	1.0	-0.445	0.112	7.5E-05	BAI3, AL158051.1
rs11992998	8	1126263	imputed	0.843	0.276	C	T	0.724	0.151	0.076	1.0	-0.185	0.047	7.8E-05	ERICH1-AS1, CTD-2281E23.2, CTD-2281E23.3, CTD-2281E23.1, AF067845.1
rs12290821	11	21165620	genotyped	1.005	0.274	C	T	0.726	0.179	0.070	1.0	-0.177	0.045	7.9E-05	NELL1, RNA5SP336, RP11-670N15.1, RNA5SP337
rs7640232	3	87449493	imputed	0.950	0.357	A	G	0.644	-0.181	0.070	1.0	0.173	0.044	7.9E-05	MIR4795, CHMP2B, POU1F1
rs12695006	2	241052837	imputed	1.012	0.135	A	G	0.865	0.292	0.097	1.0	-0.219	0.056	8.0E-05	NDUFA10, MIR4786, OR6B2, PRR21, OR6B3, AC013469.1, MYEOV2, OTOS, AC124861.1, AC124861.2

rs4504281	4	78954098	imputed	0.941	0.111	A	G	0.889	-0.387	0.101	1.0	0.265	0.067	8.0E-05	CNOT6L, MRPL1, FRAS1, AC093897.1
rs5010472	4	162235785	genotyped	1.015	0.404	A	G	0.404	-0.219	0.066	1.0	0.161	0.041	8.0E-05	RP11-234O6.2, FSTL5
rs7573170	2	130429895	genotyped	0.994	0.175	A	G	0.175	-0.205	0.081	1.0	0.199	0.051	8.1E-05	snoU13, AC079776.1, AC079776.2, AC079776.3, AC079776.7
rs9459530	6	166333758	imputed	1.011	0.264	A	T	0.736	-0.220	0.068	1.0	0.177	0.045	8.1E-05	PDE10A, RNU6-730P, RP11-252P19.1, RP11-252P19.2, SDIM1, LINC00473, AL590482.1, SNORD45, T, RNU6-153P
rs6049835	20	24636401	imputed	0.973	0.209	A	G	0.791	-0.203	0.079	1.0	0.197	0.050	8.3E-05	SYNDIG1, RP11-526K17.2, RP5-860P4.2, CST7
rs10475881	5	167882953	genotyped	0.906	0.456	C	G	0.545	0.102	0.068	0.9	-0.160	0.041	8.3E-05	TENM2, CTB-178M22.1, CTB-178M22.2, WWC1, RARS, FBLL1, PANK3, MIR103A1, CTC-558O2.2, SLIT3, CTC-558O2.1
rs3912421	8	13539846	genotyped	1.007	0.141	C	T	0.141	0.385	0.085	1.0	-0.228	0.058	8.3E-05	DLC1, RNA5SP255, RP11-145O15.3, C8orf48, RP11-480O10.1
rs11145246	9	79671228	imputed	0.982	0.470	A	G	0.530	-0.233	0.062	1.0	0.160	0.041	8.3E-05	PRUNE2, PCA3, FOXB2, VPS13A-AS1, VPS13A

rs10818729	9	125371916	imputed	0.891	0.406	C	T	0.594	-0.337	0.068	1.0	0.172	0.044	8.3E-05	MRRF, RP11-498E2.7, RP11-498E2.8, PTGS1, RP11-498E2.9, AL162424.1, RP11-542K23.10, RP11-542K23.7, RP11-542K23.9, OR1J1, OR1J2, OR1J4, OR1N1, OR1N2, OR1L8, RP11-64P14.7, OR1Q1, OR1B1, OR1L1, OR1L3, OR1L4, OR1L6, OR5C1, PDCL, OR1K1, RC3H2, SNORD90, ZBTB6
rs1221129	9	122052177	genotyped	1.001	0.223	A	T	0.223	-0.251	0.080	1.0	0.189	0.048	8.4E-05	BRINP1, RP11-295D22.1
rs75525627	2	178443625	imputed	0.882	0.043	C	G	0.043	0.626	0.147	1.0	-0.397	0.101	8.4E-05	NFE2L2, AC074286.1, RP11-337N6.2, RP11-337N6.1, snoU13, AGPS, TTC30B, AC073834.3, TTC30A, PDE11A, AC012499.1
rs2762107	13	94052346	imputed	0.951	0.136	A	C	0.864	0.212	0.098	1.0	-0.228	0.058	8.5E-05	GPC6, SNORD22
rs3812312	7	158930775	imputed	1.005	0.095	A	G	0.095	-0.446	0.112	1.0	0.263	0.067	8.5E-05	WDR60, LINC00689, VIPR2
rs12426427	12	23829883	genotyped	0.978	0.038	A	T	0.038	-0.364	0.179	1.0	0.378	0.096	8.6E-05	SOX5, RP11-437F6.1
rs35895337	7	16027952	imputed	0.953	0.054	C	T	0.946	0.421	0.155	1.0	-0.329	0.084	8.6E-05	AC005550.4, AC005550.5, AC006041.1, RP11-196O16.1, ISPD, ISPD-AS1
rs17053010	5	155359809	imputed	1.010	0.074	C	G	0.074	-0.267	0.125	1.0	0.283	0.072	8.7E-05	RNA5SP199, SGCD
rs17470444	8	14808002	genotyped	0.986	0.230	A	G	0.770	0.138	0.077	0.9	-0.179	0.046	8.7E-05	SGCZ, MIR383, CTD-2023J5.1
rs2838308	21	44877881	imputed	0.828	0.240	A	G	0.761	-0.165	0.080	1.0	0.210	0.053	8.8E-05	AP001631.10, CRYAA, LINC00322, AP001046.5, AP001046.6, SIK1, LINC00319, LINC00313, AP001048.4, HSF2BP, RRP1B, PDXK

rs16825066	2	213950049	genotyped	1.007	0.071	C	G	0.071	0.317	0.111	1.0	-0.297	0.076	8.8E-05	AC079610.1, AC093381.2, AC108066.1, MIR4776-2, IKZF2, RP11-105N14.1, RP11-105N14.3, RP11-105N14.2, AC079610.2, SPAG16
rs1598293	8	15631108	genotyped	1.004	0.207	A	G	0.207	0.241	0.076	1.0	-0.201	0.051	8.9E-05	TUSC3, AC091559.1, RP11-77B22.2
rs508486	2	239339712	imputed	0.885	0.330	A	C	0.330	-0.116	0.072	0.9	0.174	0.044	8.9E-05	ESPNL, KLHL30, FAM132B, ILKAP, AC016757.3, AC096574.4, HES6, PER2, AC012485.1, AC012485.2, TRAF3IP1, RNU6-234P, ASB1, AC016999.2, AC092619.1, AC113618.1
rs8067602	17	31421139	imputed	0.812	0.076	C	T	0.076	0.438	0.137	1.0	-0.354	0.090	8.9E-05	MYO1D, Y_RNA, AC084809.2, AC084809.3, TMEM98, SPACA3, ASIC2, RP1-29G21.1, RP11-40A13.1
rs12318425	12	97571404	imputed	0.977	0.062	C	T	0.062	-0.482	0.146	1.0	0.332	0.085	9.0E-05	NEDD1, Y_RNA, RP11-541G9.1, RP11-397H6.1, RP11-541G9.2, RMST
rs7522882	1	75442994	imputed	0.955	0.250	A	T	0.750	0.304	0.083	1.0	-0.190	0.049	9.0E-05	RP11-17E13.2, CRYZ, TYW3, RP11-93N20.1, RP11-510C10.4, RP11-510C10.2, LHX8, RP11-510C10.3, RNU6-622P, SLC44A5

rs522200	22	26795840	imputed	0.812	0.303	A	G	0.303	-0.225	0.083	1.0	0.190	0.048	9.0E-05	CTA-796E4.3, CTA-796E4.4, SEZ6L, RP11-259P1.1, RNA5SP495, ASPHD2, HPS4, SRRD, TFIP11, CTA-445C9.14, CTA-445C9.15, TPST2, MIR548J, CRYBB1, CRYBA4, MIAT, CTA-373H7.7, CTA-211A9.5
rs732672	21	44464034	imputed	0.854	0.277	C	G	0.723	0.196	0.079	1.0	-0.189	0.048	9.1E-05	PDE9A, AP001628.7, AP001628.6, WDR4, NDUFV3, ERVH48-1, MIR5692B, AP001630.5, PKNOX1, CBS, U2AF1, AP001631.1, AP001631.9, AP001631.10, CRYAA, LINC00322
rs4262962	16	7202020	imputed	0.987	0.113	G	T	0.113	-0.200	0.101	1.0	0.228	0.058	9.1E-05	RBFOX1, RNU6-457P, RNU6-328P, snoMe28S-Am2634
rs162681	1	59643864	imputed	0.951	0.406	A	G	0.594	0.249	0.066	1.0	-0.159	0.041	9.1E-05	RP4-794H19.2, RP4-794H19.1, RP4-794H19.4, RP11-145M4.1, RP11-145M4.2, RP11-145M4.3, RP11-470E16.1, RP11-467C18.1, FGGY
rs12328200	2	62644651	imputed	0.910	0.179	A	G	0.179	0.312	0.082	1.0	-0.211	0.054	9.1E-05	COMMD1, AC018462.2, B3GNT2, MIR5192, RN7SL51P, snoU13, AC093159.1, RN7SL18P, TMEM17, AC092155.4, EHBP1
rs6550857	3	24358906	genotyped	0.990	0.331	A	G	0.331	0.182	0.069	1.0	-0.172	0.044	9.1E-05	LINC00691, THRB, THRB-IT1, THRB-AS1, RP11-317L10.1, MIR4792

rs7286517	22	48417543	imputed	0.917	0.279	A	G	0.721	0.228	0.074	1.0	-0.180	0.046	9.2E-05	RP11-191L9.4, RP13-455A7.1, CTA-280A3 B.2, LL22NC03-121E8.4, LL22NC03-121E8.3, MIR3201
rs964036	10	9711702	imputed	0.970	0.394	C	T	0.606	0.164	0.063	1.0	-0.157	0.040	9.2E-05	RP5-1051H14.2
rs112437369	5	71821469	imputed	0.949	0.033	C	T	0.967	-0.725	0.179	1.0	0.443	0.113	9.2E-05	MRPS27, RN7SL153P, PTCD2, CTC-365E16.1, RP11-389C8.3, RP11-389C8.2, ZNF366, CTC-347C20.2, CTC-347C20.1, Y_RNA, CTD-2631K10.1, TNPO1
rs16841175	4	7775099	imputed	0.966	0.286	C	T	0.714	0.252	0.072	1.0	-0.172	0.044	9.3E-05	SORCS2, AFAP1-AS1, AFAP1, AC097381.1, ABLIM2, MIR95, RP11-338K13.1, RP11-1258F18.1
rs61510063	14	30649449	imputed	0.942	0.127	A	G	0.874	0.261	0.101	1.0	-0.239	0.061	9.3E-05	PRKD1, RP11-269C4.2, CTD-2251F13.1, RP11-1103G16.1
rs11256679	10	10611797	imputed	0.985	0.392	A	C	0.608	-0.213	0.067	1.0	0.163	0.042	9.3E-05	RP11-271F18.1, RP11-271F18.4, SFTA1P
rs17116089	1	58051878	genotyped	0.992	0.028	A	C	0.028	-0.694	0.243	0.9	0.519	0.133	9.3E-05	DAB1, RP6-102O10.1, AL137855.1, RP4-737A23.2
rs78571373	5	155762951	imputed	0.954	0.205	C	T	0.795	0.143	0.083	1.0	-0.193	0.049	9.3E-05	SGCD

rs11156650	14	21213607	imputed	0.944	0.302	C	G	0.698	0.107	0.069	0.9	-0.164	0.042	9.4E-05	OSGEP, RP11-203M5.7, APEX1, TMEM55B, PNP, RP11-203M5.8, RNASE10, RNASE9, RNASE11, RP11-14J7.6, RNASE12, OR6S1, Y_RNA, RNASE4, ANG, AL163636.6, RP11-903H12.3, EDDM3A, EDDM3B, RNASE6, RP11-219E7.1, RNASE1, RP11-219E7.3, RP11-219E7.2, RNASE3, RP11-219E7.4, RP11-84C10.3, RP11-84C10.2, RNASE2, RN7SL189P, METTL17, RP11-84C10.4, SLC39A2, NDRG2, TPPP2, AL161668.5, RP11-998D10.1, RNASE13, RNASE7
rs11605726	11	4178374	imputed	0.978	0.275	C	G	0.725	-0.199	0.070	1.0	0.176	0.045	9.4E-05	STIM1, SNORA7, RRM1, RRM1-AS1, RP11-23F23.2, OR52B4, TRIM21, AC010930.1, OR52K2
rs17577994	8	20885995	genotyped	1.015	0.131	A	G	0.131	-0.355	0.095	1.0	0.214	0.055	9.5E-05	RP11-369E15.1, RP11-369E15.3, RP11-369E15.4, RP11-369E15.2, RP11-421P23.1, RP11-421P23.2, AC021613.1, RP11-24P4.1
rs12145920	1	176772883	genotyped	1.019	0.040	C	T	0.040	-0.536	0.177	1.0	0.357	0.091	9.5E-05	PAPPA2, ASTN1, MIR488
rs10497114	2	153582724	imputed	0.931	0.178	C	T	0.178	0.273	0.085	1.0	-0.211	0.054	9.6E-05	FMNL2, PRPF40A, ARL6IP6

rs6439279	3	131009133	genotyped	1.019	0.245	C	T	0.755	-0.202	0.071	1.0	0.182	0.047	9.7E-05	ATP2C1, ASTE1, NEK11, RP11-265F19.1, RNU6-726P, AC121332.1, AC083908.1, RP11-933H2.4, NUDT16P, NUDT16, RP11-517B11.7, MRPL3, SNORA58, RP11-517B11.4, CPNE4
rs13414359	2	227677593	genotyped	1.018	0.261	A	G	0.739	-0.242	0.072	1.0	0.185	0.047	9.7E-05	MIR5702, IRS1, RP11-395N3.2, RP11-395N3.1, RHBDD1, SNORA48, COL4A4
rs10842618	12	25969413	imputed	1.005	0.252	A	T	0.252	0.207	0.071	1.0	-0.183	0.047	9.7E-05	IFLTD1, RP11-685B13.2, RN7SKP262, RP11-443N24.2, RP11-443N24.3, RP11-443N24.4, RASSF8-AS1, RASSF8
rs4149018	12	21291561	imputed	0.909	0.072	G	T	0.072	-0.527	0.145	1.0	0.300	0.077	9.8E-05	SLCO1B3, LST3, SLCO1B7, RP11-125O5.2, SLCO1B1, SLCO1A2, IAPP, PYROXD1
rs67949532	8	51856198	imputed	0.993	0.238	C	T	0.762	-0.236	0.075	1.0	0.185	0.047	9.8E-05	SNTG1, SNORA

Supplemental Table 10. Genome-wide by environment interaction study (GWEIS) of stressful life events results for the top loci (p<1x10-4) in Hispanics

Stressful Life Event Results (n=2,989)

									SNP Main Effect			SNP*Stressful Life Events Interaction			
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value	Genes in region (±300kb)
rs58707171	4	36317832	imputed	0.921	0.037	A	C	0.963	0.649	0.254	1.0	-0.778	0.152	3.0E-07	ARAP2, RP11-431M7.3, DTHD1, RP11-431M7.2, RP11-722M1.1
rs6579218	20	33709846	imputed	0.989	0.156	C	G	0.844	0.425	0.142	1.0	-0.505	0.100	4.9E-07	NCOA6, GGT7, ACSS2, GSS, MYH7B, MIR499A, TRPC4AP, RNU6-407P, EDEM2, SNORD56, PROCR, RNA5SP483, RP4-614O4.12, AL121753.1, MMP24-AS1, MMP24, RP4-614O4.11, EIF6, FAM83C-AS1, FAM83C, UQCC1
rs10227305	7	3272267	imputed	0.849	0.207	A	C	0.793	0.308	0.133	1.0	-0.454	0.093	9.4E-07	CARD11, AC004906.3, RN7SKP130, AC024028.1, AC091801.1, AC073316.2, AC073316.1, SDK1, RP11-30B1.1, AC069286.1
rs35332487	2	62510388	imputed	0.831	0.275	A	C	0.275	0.323	0.116	1.0	-0.406	0.086	2.2E-06	COMMD1, AC018462.2, B3GNT2, MIR5192, RN7SL51P, snoU13, AC093159.1, RN7SL18P, TMEM17
rs150902333	18	74523543	imputed	0.855	0.021	G	T	0.021	-0.418	0.336	0.8	1.015	0.215	2.2E-06	LINC00908, LINC00683, RP11-111H3.3, AC034110.1, RP11-162A12.2, RNU6-346P, ZNF236, RP11-862L9.3, MBP
rs7021957	9	90404921	imputed	0.983	0.021	C	T	0.979	-1.069	0.291	1.0	1.005	0.214	2.6E-06	DAPK1, DAPK1-IT1, CTSL, AL160279.1, CTSL3P, XXyac-YM21GA2.6, XXyac-YM21GA2.3, XXyac-YM21GA2.7, XXyac-YM21GA2.4, SPATA31E1, SPATA31C1, CDK20, U6
rs61159401	10	134122841	imputed	0.945	0.277	A	G	0.277	0.472	0.111	1.0	-0.365	0.079	3.9E-06	JAKMIP3, RP11-140A10.3, DPYSL4, STK32C, LRRC27, PWWP2B, RP11-432J24.2, RP11-432J24.3, C10orf91, RP11-432J24.5, RP11-432J24.6, INPP5A
rs2429123	12	2113147	imputed	0.953	0.314	C	T	0.686	0.324	0.114	0.9	-0.358	0.078	4.0E-06	ADIPOR2, CACNA2D4, LRTM2, RP5-1096D14.3, LINC00940,

															DCP1B, CACNA1C, RP5-1096D14.6, CACNA1C-IT1, CACNA1C-IT2, CACNA1C-AS4, CACNA1C-IT3
rs112528192	14	60065024	imputed	0.941	0.048	A	G	0.048	-0.498	0.259	1.0	0.723	0.157	4.0E-06	DAAM1, AL159140.1, GPR135, L3HYPDH, RP11-701B16.2, JKAMP, CCDC175, RTN1, MIR5586
rs2690231	3	98774813	genotyped	1.018	0.022	G	T	0.022	0.633	0.285	1.0	-1.112	0.242	4.4E-06	ST3GAL6, DCBLD2, RNU6-26P, CTD-2021J15.1, RNU6-1263P, LINC00973
rs73282658	10	64236716	imputed	1.012	0.039	G	T	0.039	0.399	0.217	0.9	-0.775	0.175	9.4E-06	RTKN2, RP11-120C12.3, RN7SL591P, ZNF365, AC067751.1
rs1949618	3	114101705	imputed	0.882	0.028	A	C	0.028	0.864	0.257	1.0	-1.104	0.250	1.0E-05	QTRTD1, DRD3, RP11-553L6.2, ZNF80, TIGIT, RP11-553L6.5, MIR568, ZBTB20, ZBTB20-AS1, RP11-197K3.1
rs6810864	4	156733002	imputed	0.850	0.407	G	T	0.593	0.308	0.107	1.0	-0.337	0.077	1.2E-05	RP13-487K5.1, GUCY1A3, RP11-588K22.2, GUCY1B3, ASIC5, TDO2, CTSO
rs55806466	5	11357930	imputed	0.936	0.289	A	C	0.289	-0.472	0.116	1.0	0.363	0.083	1.2E-05	CTNND2
rs2732394	7	128096678	genotyped	1.010	0.211	C	T	0.789	-0.348	0.114	1.0	0.393	0.090	1.3E-05	MIR129-1, LEP, RP11-62J1.4, AC018635.1, RBM28, RNU7-27P, PRRT4, IMPDH1, RNU7-54P, RP11-212P7.3, HILPDA, RP11-155G14.6, METTL2B, RP11-212P7.2, RP11-274B21.1, RNU6-177P, RP11-274B21.10, FAM71F2, RP11-274B21.8, RP11-274B21.9, RNA5SP242, RNA5SP243, FAM71F1, CALU
rs11104732	12	88477988	imputed	0.935	0.073	C	T	0.073	0.660	0.173	1.0	-0.604	0.139	1.4E-05	RP11-248E9.5, RP11-248E9.6, C12orf50, C12orf29, CEP290, RNA5SP364, TMTC3
rs12025688	1	245795851	imputed	0.936	0.158	C	T	0.842	0.220	0.138	0.9	-0.410	0.094	1.4E-05	KIF26B, AL359983.1, RP11-522M21.2, RP11-522M21.3, SMYD3

rs7854133	9	139517144	imputed	0.879	0.444	A	G	0.444	-0.252	0.103	1.0	0.314	0.073	1.7E-05	DKFZP434A062, GPSM1, DNLZ, CARD9, SNAPC4, SDCCAG3, PMPCA, INPP5E, SEC16A, C9orf163, NOTCH1, MIR4673, RP11-413M3.4, MIR4674, RP11-611D20.2, U3, RP11-251M1.1, EGFL7, MIR126, AGPAT2, AL590226.1, FAM69B, SNHG7, LCN10, LCN6, LCN8, LCN15, TMEM141, RP11-216L13.17, KIAA1984, RP11-216L13.19, RP11-216L13.18, KIAA1984-AS1, RABL6, MIR4292, C9orf172, PHPT1, MAMDC4, EDF1, TRAF2, MIR4479
rs8063680	16	83104307	imputed	0.924	0.111	A	C	0.889	0.515	0.170	1.0	-0.493	0.115	1.8E-05	CDH13, RP11-22H5.2, AC099506.1, RN7SL134P, CTD-3253I12.1
rs10258747	7	84873729	genotyped	1.007	0.373	C	T	0.373	-0.263	0.100	1.0	0.316	0.074	1.9E-05	SEMA3D, LINC00972
rs61967961	13	96765381	imputed	0.934	0.035	A	G	0.035	-0.476	0.255	1.0	0.585	0.137	2.0E-05	UGGT2, HS6ST3, RN7SL164P
rs299120	4	139434076	genotyped	1.000	0.340	C	T	0.340	-0.297	0.103	0.9	0.320	0.075	2.0E-05	SLC7A11, RP11-733C7.1, LINC00498, LINC00499, LINC00500, RP11-173E2.2, RP11-98O2.1, AC093766.1
rs28627384	8	21324221	imputed	0.957	0.077	C	T	0.923	-0.614	0.161	1.0	0.565	0.133	2.0E-05	RP11-24P4.1, AC009695.1, AC022716.1, GFRA2
rs7673991	4	152019760	imputed	0.821	0.339	A	G	0.339	-0.170	0.114	1.0	0.344	0.081	2.0E-05	LRBA, RNA5SP168, RPS3A, SNORD73, SH3D19, SNORD73A, RP11-372K14.2, PRSS48, RNU6-1282P, RP11-731D1.4
rs9993229	4	151502267	imputed	0.976	0.445	A	G	0.555	0.322	0.100	0.9	-0.311	0.073	2.0E-05	LRBA, RP11-1336O20.2, MAB21L2, AC110813.1
rs36001788	7	84853807	imputed	0.914	0.421	A	T	0.421	0.261	0.105	1.0	-0.326	0.076	2.0E-05	AC074183.4, SEMA3D, LINC00972
rs525861	20	792182	imputed	0.983	0.496	A	G	0.496	0.235	0.099	0.8	-0.312	0.073	2.1E-05	CSNK2A1, TCF15, SRXN1, RP5-850E9.3, SCRT2, SLC52A3, FAM110A, ANGPT4, RSPO4
rs71607662	4	12682800	imputed	0.937	0.033	C	T	0.033	-0.329	0.266	1.0	0.708	0.166	2.1E-05	RP11-22A3.2, RP11-22A3.1
rs797652	7	83462196	imputed	0.998	0.197	A	G	0.803	0.320	0.130	1.0	-0.374	0.088	2.2E-05	SEMA3E, AC006322.1, SEMA3A

rs3751585	15	51741056	genotyped	1.001	0.150	A	G	0.150	0.480	0.129	1.0	-0.422	0.099	2.2E-05	RP11-108K3.1, CYP19A1, MIR4713, RP11-108K3.3, RP11-108K3.2, GLDN, RP11-108K3.4, RP11-707P17.1, DMXL2, RP11-707P17.2, AC020892.1, SCG3, RP11-313P18.2, RP11-313P18.1, LYSMD2
rs11944754	4	140559737	imputed	0.998	0.463	C	T	0.537	-0.249	0.095	1.0	0.299	0.071	2.4E-05	NAA15, RP11-83A24.2, RP11-83A24.1, ACA64, RAB33B, SETD7, RP11-342I1.2, RP11-308D13.3, MGST2, RN7SKP237, MAML3, RN7SKP253
rs4782770	16	83362689	imputed	0.983	0.434	C	G	0.566	0.309	0.098	0.9	-0.294	0.070	2.4E-05	CDH13, RP11-543N12.1, AC009142.1, MIR3182
rs17058669	18	73700808	imputed	0.994	0.062	C	T	0.938	-0.333	0.202	1.0	0.658	0.156	2.4E-05	RP11-704C2.1, RP11-173L6.1, RP11-357H3.1, RP11-1O2.1, RP11-94B19.6, RP11-94B19.1, RP11-94B19.5, RP11-94B19.2, RP11-94B19.7, RP11-94B19.3, RP11-94B19.4
rs2351336	10	87141582	imputed	0.978	0.405	C	T	0.405	0.223	0.098	1.0	-0.311	0.074	2.5E-05	RP11-181F12.1, RP11-475D12.1, RP11-475D12.2, RP11-113E21.1, RNU6-325P, RN7SKP84, GRID1, RP11-93H12.2, RP11-93H12.4, RN7SKP238
rs9291157	4	3754853	imputed	0.967	0.225	C	T	0.225	0.434	0.110	1.0	-0.360	0.085	2.5E-05	DOK7, RP11-529E10.6, LRPAP1, AL590235.1, RP11-529E10.7, LINC00955, RP3-368B9.2, RP3-513G18.2, AC141928.1, ADRA2C, AC226119.5, FAM86EP, AC116562.2
rs116705011	2	113840150	imputed	1.048	0.020	A	T	0.020	-0.865	0.397	1.0	0.849	0.202	2.6E-05	IL1A, IL1B, AC079753.1, IL37, IL36G, IL36A, IL36B, IL36RN, IL1F10, RNU6-1180P, IL1RN, PSD4, AC016683.5, AC016683.6, PAX8, RP11-65I12.1
rs73102276	5	52149891	imputed	0.979	0.040	A	C	0.040	-0.644	0.295	1.0	0.785	0.186	2.6E-05	CTD-2288O8.1, ITGA1, PELO, CTD-2175A23.1, ITGA2, CTD-2366F13.2, MOCS2, CTD-2366F13.1

rs2425157	20	34419083	imputed	0.852	0.169	C	T	0.169	0.450	0.133	1.0	-0.447	0.107	2.7E-05	ERGIC3, FER1L4, SPAG4, CPNE1, RP1-309K20.6, RN7SKP271, RNU6-759P, RBM12, NFS1, ROMO1, RBM39, snoU13, RNU6-1166P, PHF20, Y_RNA, RNU4-40P, RNU6-937P, SCAND1, CNBD2, LINC00657, RP4-550H1.4, RP4-550H1.5, EPB41L1
rs7709291	5	35848563	imputed	0.991	0.471	C	G	0.471	-0.234	0.102	1.0	0.294	0.070	2.9E-05	SPEF2, RNU7-130P, CTD-2113L7.1, IL7R, CAPSL, RP11-79C6.3, UGT3A1, UGT3A2, LMBRD2, MIR580
4_140550169	4	140550169	imputed	0.922	0.485	A	T	0.485	0.294	0.099	1.0	-0.305	0.073	2.9E-05	NAA15, RP11-83A24.2, RP11-83A24.1, ACA64, RAB33B, SETD7, RP11-342I1.2, RP11-308D13.3, MGST2, RN7SKP237, MAML3, RN7SKP253
rs300773	2	115035	genotyped	1.036	0.290	C	T	0.290	0.217	0.104	1.0	-0.339	0.081	2.9E-05	FAM110C, AC079779.7, SH3YL1, ACP1, FAM150B, AC079779.4, AC079779.5, AC079779.6, AC105393.1
rs7597602	2	45533630	genotyped	0.995	0.127	C	T	0.873	0.255	0.146	0.9	-0.411	0.099	3.1E-05	SIX2, AC093702.1, AC009236.1, AC009236.2, SRBD1, RN7SL414P
rs117662659	18	13839112	imputed	0.992	0.029	C	G	0.971	0.329	0.283	0.8	-0.693	0.167	3.3E-05	LDLRAD4, RP11-53B2.4, MIR4526, RP11-701H16.4, FAM210A, AP001010.1, RN7SL362P, RNMT, AP001525.1, MC5R, MC2R, ZNF519, RP11-411B10.2, RP11-411B10.3, AC006557.1
rs2424292	20	20199115	imputed	1.007	0.087	A	G	0.087	-0.675	0.172	1.0	0.529	0.128	3.4E-05	RIN2, NAA20, CRNKL1, C20orf26, RP5-1002M8.4, RP5-1178H5.2, RP5-1096J16.1, RN7SL690P, INSM1, RALGAPA2
rs4676613	3	39248253	imputed	0.933	0.235	C	G	0.235	0.304	0.111	1.0	-0.360	0.087	3.5E-05	SCN11A, AC116038.1, RNU6-1227P, WDR48, GORASP1, TTC21A, CSRNP1, XIRP1, CX3CR1, CCR8, SLC25A38, RPSA, SNORA6, SNORA62, AC099332.1, MOBP
rs11176109	12	66656567	imputed	0.974	0.068	A	G	0.932	-0.397	0.171	1.0	0.604	0.146	3.6E-05	HMGA2, RP11-366L20.4, RNA5SP362, LLPH, TMBIM4, RP11-

															745O10.2, IRAK3, AC078889.1, RP11-335I12.2, RN7SKP166, HELB, snoU13, GRIP1
rs80025189	10	109729242	imputed	0.994	0.070	A	G	0.930	0.373	0.192	0.9	-0.508	0.123	3.7E-05	RP11-215N21.1
rs1649907	2	231411563	imputed	1.000	0.229	C	T	0.771	-0.307	0.113	1.0	0.339	0.082	3.7E-05	SP140, SP140L, SP100, RN7SL834P, AC010149.4, RNU6-451P, AC098823.3, CAB39, RNU6-268P
rs2901318	1	69991677	imputed	0.955	0.403	C	T	0.403	0.338	0.098	1.0	-0.307	0.075	3.8E-05	RP11-74K19.1, RP3-380B4.1, LRRC7
rs10080121	5	6873628	imputed	1.036	0.129	A	C	0.871	-0.259	0.134	0.9	0.421	0.102	3.9E-05	LINC01018, NSUN2, SRD5A1, CTD-2044J15.2, CTD-2044J15.1, PAPD7, RP11-332J15.3, RP11-332J15.4, RP11-332J15.1, RN7SKP79, RP11-332J15.2, RP11-122F24.1, RNA5SP176
rs10068763	5	180486785	imputed	0.868	0.317	C	G	0.683	0.252	0.113	1.0	-0.328	0.080	4.2E-05	CTC-205M6.5, MGAT1, LINC00847, ZFP62, BTNL8, Y_RNA, BTNL3, RNU6-1036P, BTNL9, OR2V1, OR2V2, CTC-338M12.2, CTC-338M12.5, TRIM7, CTC-338M12.6, CTC-338M12.1, TRIM41, MIR4638, CTC-338M12.7, GNB2L1, SNORD96A, SNORD95, CTC-338M12.4, TRIM52, AC008443.1, TRIM52-AS1, CTC-338M12.9, RNU6-705P, AC138035.2, AC138035.1
rs72728750	4	140562751	imputed	0.939	0.030	C	T	0.970	0.722	0.279	1.0	-0.815	0.199	4.2E-05	NAA15, RP11-83A24.2, RP11-83A24.1, ACA64, RAB33B, SETD7, RP11-342I1.2, RP11-308D13.3, MGST2, RN7SKP237, MAML3, RN7SKP253
rs4888151	16	81559009	imputed	0.842	0.333	A	C	0.333	0.299	0.109	1.0	-0.344	0.084	4.2E-05	BCMO1, RP11-55K13.1, GAN, MIR4720, RP11-391L3.1, CMIP, RP11-960L18.1, PLCG2
rs2513689	11	114995252	imputed	0.977	0.187	C	T	0.813	-0.353	0.118	1.0	0.373	0.091	4.5E-05	ACA59, CADM1, AP000462.3, AP000462.2, AP000462.1
rs56284064	8	127239496	imputed	0.964	0.100	C	T	0.900	0.481	0.179	1.0	-0.490	0.120	4.5E-05	LINC00861, RP11-622O11.4, AC090573.1, RP11-65D17.1, RP11-103H7.1, RP11-103H7.2, RNU6-869P, RP11-103H7.3

rs13172000	5	118614132	imputed	0.928	0.292	C	G	0.292	-0.366	0.110	1.0	0.325	0.080	4.5E-05	DTWD2, CTB-161M19.4, RNU6-373P, DMXL1, snoU13, RNU6-701P, MIR5706, AC027320.1, TNFAIP8, RN7SL174P, RNA5SP190, HSD17B4
rs1320292	3	21701712	imputed	0.965	0.228	A	G	0.228	-0.158	0.113	0.8	0.338	0.083	4.5E-05	AC104183.1, RP11-180N14.1, ZNF385D, ZNF385D-AS1, AC023798.1, ZNF385D-AS2
rs6553778	4	168351130	imputed	0.967	0.257	C	T	0.743	0.364	0.121	1.0	-0.331	0.082	4.9E-05	SPOCK3, RP11-436A7.1, RN7SL776P, RN7SKP188
rs1505	10	96750759	imputed	0.962	0.293	C	G	0.293	-0.224	0.110	1.0	0.312	0.077	5.2E-05	CYP2C18, CYP2C19, CYP2C9, CYP2C8, RP11-310E22.5, C10orf129, RP11-310E22.4, PDLIM1
rs73680417	7	15749895	imputed	0.942	0.024	C	G	0.976	-0.945	0.270	1.0	0.964	0.238	5.2E-05	AGMO, MEOX2, AC005550.3, AC005550.4, AC005550.5, AC006041.1
rs362835	6	146662958	imputed	0.823	0.256	A	G	0.744	-0.264	0.118	1.0	0.386	0.096	5.6E-05	GRM1, RNA5SP222, RAB32, RP11-715G15.1, ADGB, RNU6-734P
rs1484456	2	126978134	genotyped	1.020	0.121	C	T	0.121	0.450	0.138	1.0	-0.439	0.109	5.6E-05	AC114813.1, AC023347.1
rs164547	6	94071318	genotyped	0.974	0.363	A	T	0.637	0.430	0.101	1.0	-0.301	0.075	5.6E-05	RP1-23E21.2, EPHA7
rs2277765	20	23425163	imputed	0.978	0.105	C	T	0.895	0.312	0.151	1.0	-0.442	0.110	5.6E-05	RNA5SP478, RP4-737E23.2, RP3-322G13.7, AL096677.1, NXT1, RP3-322G13.5, GZF1, NAPB, RNA5SP479, CSTL1, CST11, Y_RNA, CST8, RP3-333B15.4, CST13P, CST9L, CST9, CST3, RP11-218C14.8, RP11-218C14.5, CST4
rs74344410	3	194707501	imputed	0.889	0.098	C	T	0.098	-0.361	0.178	1.0	0.482	0.120	5.6E-05	FAM43A, AC106706.1, AC090505.6, AC090505.4, AC090505.1, XXYLT1, XXYLT1-AS1, MIR3137, RN7SL36P, XXYLT1-AS2, RNU6-25P, ACAP2, ACAP2-IT1
rs1840434	18	23254626	genotyped	1.001	0.439	C	G	0.561	-0.310	0.099	1.0	0.292	0.072	5.7E-05	RN7SL97P
rs35974919	20	16609653	imputed	0.946	0.138	G	T	0.138	-0.153	0.138	0.7	0.405	0.101	5.7E-05	KIF16B, AL118509.1, Y_RNA, RP4-705D16.3, SNRPB2, OTOR, RP5-1195D24.1
rs13128851	4	12667311	imputed	0.936	0.035	C	T	0.035	-0.312	0.257	0.8	0.653	0.162	5.8E-05	RP11-22A3.2, RP11-22A3.1
rs6945284	7	131753164	imputed	0.998	0.346	G	T	0.654	0.219	0.098	1.0	-0.286	0.071	5.8E-05	AC008085.1, AC009518.4, snosnR60_Z15, PLXNA4, AC018643.4, AC011625.1

rs28508377	15	96180740	imputed	0.835	0.208	C	T	0.792	-0.287	0.127	0.9	0.398	0.099	5.9E-05	LINC00924, RP11-398J10.2, RNU2-3P
rs79561885	7	56294018	imputed	0.936	0.038	C	T	0.962	0.492	0.269	1.0	-0.678	0.169	5.9E-05	MRPS17, ZNF713, GBAS, PSPH, CCT6A, SNORA22, SNORA15, SUMF2, PHKG1, snoU13, CHCHD2, NUPR1L, AC073136.1, RNU6-1335P, RNU6-1052P, RP13-492C18.2, RP11-760D2.1, RP11-760D2.11
rs11199041	10	121365398	imputed	0.997	0.268	C	T	0.268	-0.449	0.109	1.0	0.316	0.079	6.1E-05	GRK5, RP11-79M19.2, MIR4681, RGS10, TIAL1, BAG3, INPP5F, RN7SL846P, MCMBP, SEC23IP
rs2263340	6	51100751	imputed	0.808	0.246	A	G	0.246	-0.209	0.123	0.9	0.354	0.088	6.1E-05	TFAP2B, SNORD66
rs7856247	9	71426664	imputed	0.964	0.375	C	T	0.625	0.248	0.100	1.0	-0.283	0.071	6.2E-05	PGM5, TMEM252, RP11-274B18.4, RP11-274B18.2, PIP5K1B, FAM122A, RP11-203L2.4, RNU6-820P, PRKACG, FXN
rs9950008	18	1592549	imputed	1.003	0.363	A	T	0.363	0.373	0.100	1.0	-0.299	0.075	6.2E-05	LINC00470, RN7SKP72, RP11-476K15.1, CTD-2015H3.2, CTD-2015H3.1, RP11-161I6.2
rs1484180	6	134375588	imputed	0.947	0.227	A	G	0.227	-0.431	0.119	1.0	0.334	0.083	6.2E-05	RP3-323P13.2, RP4-662A9.2, TCF21, TBPL1, SLC2A12, RN7SL408P, SGK1, snoU13, RNA5SP218, Y_RNA
rs2492645	10	134113934	imputed	0.954	0.447	G	T	0.554	-0.295	0.103	1.0	0.285	0.071	6.2E-05	JAKMIP3, RP11-140A10.3, DPYSL4, STK32C, LRRC27, PWWP2B, RP11-432J24.2, RP11-432J24.3, C10orf91, RP11-432J24.5, RP11-432J24.6, INPP5A
rs72830064	17	39633610	imputed	0.939	0.043	C	G	0.043	-0.321	0.255	0.8	0.642	0.160	6.3E-05	KRTAP4-2, KRTAP4-1, KRTAP9-1, KRTAP9-2, KRTAP9-3, KRTAP9-8, KRTAP9-4, KRTAP9-9, KRTAP9-6, KRTAP9-7, KRTAP29-1, KRTAP16-1, KRTAP17-1, KRT33A, KRT33B, KRT34, KRT31, AC003958.2, KRT37, KRT38, KRT32, RNU2-32P, KRT35, KRT36, KRT13, AC019349.5, KRT15, KRT19, LINC00974, KRT9, KRT14, KRT16, KRT17, JUP, KRT42P, EIF1, GAST, HAP1, RNA5SP442, RN7SL399P
rs58312048	10	132641192	imputed	0.810	0.020	C	T	0.980	-1.189	0.372	1.0	0.995	0.249	6.3E-05	MIR378C, AL607076.1, TCERG1L,

															RP11-462G8.3
rs577723	9	79099667	imputed	0.977	0.328	A	G	0.672	-0.254	0.106	1.0	0.311	0.078	6.4E-05	PCSK5, RFK, GCNT1, AL161626.1, PRUNE2, AL359314.1, PCA3
rs4702010	5	14051338	imputed	0.966	0.456	A	T	0.544	-0.257	0.099	1.0	0.289	0.072	6.5E-05	DNAH5, CTB-51A17.1, TRIO
rs745157	10	86017365	genotyped	1.004	0.214	C	T	0.786	-0.314	0.115	1.0	0.361	0.091	6.5E-05	RNU1-65P, RP11-338I21.1, GHITM, C10orf99, CDHR1, LRIT2, LRIT1, RGR, LINC00858, CCSER2
rs55905003	1	99221582	imputed	0.991	0.121	A	G	0.879	0.406	0.163	1.0	-0.424	0.106	6.6E-05	SNX7, LPPR5, RP5-896L10.1
rs9624565	22	25101796	imputed	0.860	0.129	C	T	0.871	-0.425	0.138	1.0	0.454	0.114	6.7E-05	SPECC1L, SPECC1L-ADORA2A, ADORA2A, ADORA2A-AS1, UPB1, AP000355.2, GUCD1, SNRPD3, GGT1, FAM211B, AP000356.2, PIWIL3, SGSM1, SNORD56, TMEM211, KIAA1671
rs12192132	6	96425480	imputed	0.899	0.046	C	T	0.954	-0.644	0.243	1.0	0.768	0.193	6.8E-05	FUT9
rs13331416	16	79491599	imputed	0.982	0.023	C	T	0.977	0.502	0.339	0.9	-0.756	0.190	7.0E-05	WWOX, RP11-679B19.2, RNA5SP431, RP11-467I17.1, MAF, AC009159.1, RP11-345M22.1, RP11-345M22.2
rs611059	1	86796060	imputed	0.853	0.323	A	C	0.323	-0.308	0.111	1.0	0.316	0.079	7.1E-05	COL24A1, ODF2L, CLCA2, CLCA1, CLCA4, RP4-651E10.4, AL356270.1
rs183197	3	37514459	imputed	0.935	0.228	A	G	0.228	0.262	0.120	1.0	-0.359	0.091	7.4E-05	LRRFIP2, RP11-285J16.1, snoU13, RP11-259K5.1, RP11-259K5.2, GOLGA4, RNA5SP129, C3orf35, ITGA9, RNU7-73P, AC093415.2
rs10086950	8	10355378	genotyped	1.009	0.291	A	C	0.291	-0.256	0.104	1.0	0.305	0.077	7.4E-05	MSRA, RP11-981G7.1, RP11-981G7.2, RNU6-729P, RP11-981G7.3, PRSS51, RP11-981G7.6, PRSS55, RP1L1, MIR4286, C8orf74, RNA5SP252, SOX7, CTD-2135J3.3, PINX1, SNORD112
rs36111117	12	12484604	imputed	0.835	0.467	A	C	0.533	0.348	0.107	1.0	-0.306	0.077	7.7E-05	BCL2L14, LRP6, RNU6-545P, RNU6-1295P, MANSC1, LOH12CR2, LOH12CR1, DUSP16, RP11-253I19.3, CREBL2
rs62105720	2	959461	imputed	0.895	0.244	A	G	0.244	-0.250	0.128	0.9	0.347	0.088	7.7E-05	TMEM18, AC092159.2, AC092159.3, AC116609.1, RP13-539J13.1, AC116609.3, AC116609.2, AC113607.1, AC113607.2,

															AC113607.3, AC116614.1, SNTG2, AC114808.3, AC114808.2
rs11186443	10	92888749	imputed	0.916	0.411	C	G	0.411	-0.147	0.103	0.8	0.299	0.076	7.7E-05	HTR7, RPP30, Y_RNA, ANKRD1, RNU6-740P, RP11-236B18.2, RP11-236B18.5, LINC00502, PCGF5, HECTD2
rs34510188	3	961138	imputed	0.906	0.151	A	C	0.849	0.085	0.135	0.5	-0.385	0.097	7.8E-05	AC090044.1, AC090044.2, AC087430.1, RN7SL120P, CNTN6
rs58807708	18	75917063	imputed	0.912	0.081	C	T	0.081	-0.386	0.185	1.0	0.491	0.124	7.9E-05	LINC01029, RP11-671C19.2, RNU6-655P, RP11-100K18.1
rs7239940	18	56488872	imputed	0.949	0.235	C	T	0.765	0.454	0.128	1.0	-0.356	0.090	8.0E-05	ALPK2, RP11-1151B14.4, RP11-126O1.2, SNORD28, RP11-126O1.5, MALT1, RP11-126O1.4, RP11-108P20.1, RP11-108P20.3, RP11-108P20.2, RN7SL112P, RNU6-219P, RP11-108P20.4, U8, ZNF532, RNU2-69P, OACYLP, RP11-685A21.1
rs673870	3	59770221	imputed	0.955	0.115	C	T	0.885	0.470	0.163	1.0	-0.430	0.109	8.1E-05	RP11-719N22.2, FHIT, NPCDR1
rs12078824	1	173820365	imputed	0.987	0.308	C	T	0.308	-0.121	0.105	0.8	0.304	0.077	8.1E-05	SLC9C2, RP3-436N22.3, ANKRD45, RP11-360D2.1, snoU13, KLHL20, RN7SKP160, CENPL, Y_RNA, DARS2, GAS5-AS1, GAS5, SNORD78, ZBTB37, SERPINC1, RNA5SP67, RC3H1, RNA5SP68, RC3H1-IT1, RP11-160H22.3, RP11-160H22.5
rs76132822	8	77679194	imputed	0.974	0.068	C	T	0.933	0.374	0.186	1.0	-0.513	0.130	8.3E-05	RP11-706J10.1, ZFHX4-AS1, RP11-115I9.1, ZFHX4, RP11-48D4.2, hsa-mir-3149, PEX2
rs11918028	3	115722224	genotyped	0.993	0.439	A	T	0.561	-0.315	0.099	1.0	0.293	0.074	8.3E-05	GAP43, LSAMP, RN7SL815P
rs1541809	16	12692429	imputed	1.039	0.110	A	T	0.110	0.280	0.131	1.0	-0.431	0.110	8.4E-05	SNX29, RP11-165M1.3, RP11-165M1.2, RP11-552C15.1, CTD-3037G24.4, CTD-3037G24.3, CPPED1, MIR4718, CTD-2583P5.1, CTD-2583P5.3, SNORA27
rs16828277	2	151367141	genotyped	0.985	0.067	C	G	0.934	0.454	0.191	1.0	-0.528	0.134	8.6E-05	AC016682.1, AC113610.1, RND3, AC104777.2, AC104777.3, AC104777.1, AC104777.4

rs3893887	10	24421223	genotyped	1.039	0.410	G	T	0.591	0.096	0.094	0.7	-0.277	0.070	8.6E-05	KIAA1217, MIR603
rs10014219	4	180195744	imputed	0.943	0.029	A	G	0.971	-0.267	0.256	0.7	0.741	0.189	8.7E-05	RP11-404J23.1
rs4430832	18	40578249	imputed	0.928	0.022	C	T	0.022	0.796	0.277	1.0	-0.776	0.198	8.7E-05	RIT2, SYT4
rs76091677	1	239567316	imputed	0.827	0.171	A	G	0.829	0.276	0.136	1.0	-0.381	0.097	8.7E-05	RP11-544D21.2, RP11-544D21.1, CHRM3, CHRM3-AS2
rs1571093	9	121546987	imputed	0.966	0.472	A	T	0.528	-0.274	0.097	1.0	0.287	0.073	8.8E-05	RP11-349E4.1, RP11-127L21.1
rs12507255	4	151630959	imputed	0.972	0.343	C	T	0.343	-0.253	0.104	1.0	0.286	0.073	8.8E-05	LRBA, RP11-1336O20.2, MAB21L2, AC110813.1, RNA5SP168
rs61869288	10	87018325	imputed	0.948	0.124	C	G	0.876	0.359	0.167	1.0	-0.427	0.109	8.8E-05	RP11-181F12.1, RP11-475D12.1, RP11-475D12.2, RP11-113E21.1, RNU6-325P
rs9905095	17	20849769	genotyped	1.015	0.171	G	T	0.829	-0.310	0.123	1.0	0.364	0.093	8.8E-05	AC126365.1, RP11-283C24.1, CCDC144NL, RP11-344E13.4, RP11-344E13.3, RNU6-1178P, RP11-381P6.1, USP22, RP11-746M1.1, AC087393.1, DHRS7B, TMEM11, AC087294.2, RN7SL426P, C17orf103
rs11969052	6	5747351	imputed	0.964	0.198	C	T	0.198	0.256	0.121	1.0	-0.365	0.093	8.9E-05	FARS2, RP1-232P20.1, RP1-256G22.2, RP3-380B8.4, RN7SL221P, NRN1, AL157775.1
rs113203864	14	102058409	imputed	0.802	0.025	A	G	0.976	0.981	0.383	1.0	-0.901	0.230	8.9E-05	RP11-168L7.1, LINC00524, RP11-168L7.3, RP11-1029J19.2, DIO3OS, DIO3, RP11-1029J19.4, RP11-1029J19.5, RP11-796G6.2, PPP2R5C, CTD-2017C7.2, RNU6-790P, CTD-2017C7.1
rs141956143	15	22935366	imputed	0.863	0.191	C	T	0.810	0.333	0.137	1.0	-0.370	0.094	8.9E-05	MIR4509-2, GOLGA8DP, AC116165.1, RN7SL545P, GOLGA6L1, RP11-566K19.3, TUBGCP5, CYFIP1, NIPA2, NIPA1, RP11-566K19.6, RP11-566K19.5, RP11-26F2.1, WHAMMP3
rs6121187	20	34846320	genotyped	0.849	0.214	G	T	0.214	0.266	0.128	1.0	-0.367	0.094	9.1E-05	SCAND1, CNBD2, LINC00657, RP4-550H1.4, RP4-550H1.5, EPB41L1, snoU13, RP11-234K24.3, AL121895.1, AAR2, DLGAP4, RP5-977B1.7
rs10092170	8	62157882	imputed	1.033	0.051	C	T	0.051	-0.458	0.217	1.0	0.509	0.130	9.1E-05	AC022182.1, AC022182.3, CLVS1, RP11-787D18.2, RP11-787D18.1,

														ASPH
rs12649929	4	152217433	imputed	0.998	0.458	C	T	0.458	0.176	0.098	0.9	-0.272	0.070	9.4E-05	LRBA, RPS3A, SNORD73, SH3D19, SNORD73A, RP11-372K14.2, PRSS48, RNU6-1282P, RP11-731D1.4, RP11-610P16.1, FAM160A1, AC097455.1, RN7SKP35
rs17102539	14	21674364	genotyped	1.032	0.185	A	G	0.185	-0.546	0.131	1.0	0.362	0.093	9.5E-05	RP11-219E7.4, RP11-84C10.3, RP11-84C10.2, RNASE2, RN7SL189P, METTL17, RP11-84C10.4, SLC39A2, NDRG2, TPPP2, AL161668.5, RP11-998D10.1, RNASE13, RNASE7, RNASE8, ARHGEF40, ZNF219, RP11-998D10.7, TMEM253, RP11-998D10.4, RNU6-252P, OR5AU1, LINC00641, HNRNPC, RPGRIP1, SUPT16H, RP11-524O1.4, CHD8, SNORD9, SNORD8, RN7SL650P, RAB2B, TOX4, METTL3
rs4907999	1	99207578	genotyped	0.986	0.499	A	G	0.499	0.172	0.096	0.9	-0.279	0.071	9.5E-05	SNX7, LPPR5, RP5-896L10.1
rs10773498	12	128657480	genotyped	0.995	0.391	A	G	0.609	0.284	0.096	1.0	-0.272	0.070	9.6E-05	RP11-749H20.4, LINC00507, LINC00508, RP11-349K16.1, RP13-653N12.1, RP13-653N12.2, MIR4419B, TMEM132C, MIR3612, snoU13, RP11-553N19.1
rs17277101	13	62692800	imputed	0.956	0.056	C	T	0.944	-0.605	0.200	1.0	0.676	0.173	9.8E-05	LINC00358, LINC01075, LINC01074, LINC00459
rs926052	19	44952236	imputed	0.890	0.420	A	T	0.580	0.340	0.106	1.0	-0.284	0.073	9.8E-05	ZNF234, ZNF226, ZNF227, ZNF235, ZNF233, ZNF112, CTC-512J12.6, ZNF285, CTC-512J12.4, ZNF229, AC069278.4, ZNF180, CEACAM20, AC138472.6, CEACAM22P, IGSF23, CTB-171A8.1, PVR, CEACAM19, CEACAM16, snoZ6, BCL3

rs114860038	6	32966363	imputed	0.856	0.025	A	G	0.025	-0.395	0.365	0.7	0.771	0.198	9.8E-05	XXbac-BPG254F23.7, HLA-DQA2, MIR3135B, HLA-DQB2, HLA-DOB, TAP2, PSMB8, TAPSAR1, PSMB9, TAP1, PPP1R2P1, HLA-DMB, AL645941.1, XXbac-BPG181M17.5, HLA-DMA, BRD2, BRD2-IT1, XXbac-BPG181M17.6, HLA-DOA, HLA-DPA1, HLA-DPB1, HLA-DPB2, HCG24, COL11A2, RXRB, RNY4P10, SLC39A7, HSD17B8, MIR219-1, RING1, XXbac-BPG157A10.21, HCG25, VPS52, RPS18, B3GALT4, WDR46, PFDN6, RGL

Supplemental Table 11. Genome-wide by environment interaction study (GWEIS) of social support results for the top loci (p<1x10-4) in Hispanics

Social Support Results (n=3,012)

									SNP Main Effect			SNP*Social Support Interaction Term			
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value	**Genes in region (±300kb)**
rs35612712	4	187347203	imputed	0.941	0.416	C	T	0.416	-0.375	0.119	1.0	0.376	0.074	3.4E-07	FAM149A, SNORA31, AC110771.1, CYP4V2, KLKB1, F11, F11-AS1, RP11-215A19.2, RNU6-1055P, MTNR1A, FAT1
rs61973969	13	96689182	imputed	0.985	0.032	C	T	0.032	-0.979	0.317	1.0	0.839	0.171	9.4E-07	DNAJC3, UGGT2, HS6ST3, RN7SL164P
rs10055256	5	30594814	genotyped	0.808	0.074	A	C	0.927	-0.894	0.213	1.0	0.779	0.159	1.0E-06	
rs56233800	3	153523918	imputed	0.805	0.045	G	T	0.955	-1.270	0.264	1.0	0.986	0.204	1.4E-06	RP11-23D24.2, Y_RNA, RP11-217E22.5, U8, ARHGEF26-AS1
rs7980104	12	41226934	imputed	0.976	0.465	C	G	0.535	-0.382	0.117	1.0	0.339	0.070	1.5E-06	MUC19, RNU6-713P, CNTN1
rs7708252	5	14279073	imputed	1.083	0.024	C	T	0.024	0.952	0.363	1.0	-1.093	0.229	1.7E-06	TRIO
rs4677373	3	74097623	genotyped	1.032	0.351	A	G	0.351	-0.513	0.128	1.0	0.363	0.077	2.4E-06	RP11-20B7.1, RP11-508O18.1, Y_RNA, CNTN3
rs269803	12	65324099	imputed	0.983	0.341	C	T	0.660	-0.393	0.114	1.0	0.350	0.074	2.5E-06	RASSF3, RP11-338E21.3, AC025262.1, GNS, RP11-629N8.3, snoU13, TBC1D30, RP11-766N7.3, RP11-766N7.4, RNU6ATAC42P, RP11-168J19.2, WIF1, RNU6-166P, LEMD3
rs73177473	2	11814010	imputed	0.996	0.058	A	T	0.942	-1.007	0.235	1.0	0.732	0.156	2.7E-06	AC099344.3, LINC00570, E2F6, AC099344.1, RNA5SP84, GREB1, MIR4429, RNU2-13P, RNA5SP85, RN7SL674P, AC011994.1, NTSR2, LPIN1, AC106875.1, AC012456.3, AC012456.4, MIR548S, MIR4262, AC096559.1
rs61968178	13	97390691	imputed	0.880	0.023	C	G	0.023	-1.002	0.420	1.0	1.040	0.224	3.5E-06	HS6ST3, LINC00359, RP11-65L19.4, RN7SKP7, SNORD112, OXGR1
rs7724344	5	30464915	imputed	0.872	0.038	A	G	0.038	1.221	0.322	1.0	-0.991	0.215	3.9E-06	
rs11787999	9	12693732	genotyped	1.025	0.051	C	T	0.949	-0.741	0.233	1.0	0.715	0.156	4.4E-06	TYRP1, RP11-3L8.3, RN7SL849P, LURAP1L, Y_RNA

rs4688038	3	119498808	imputed	0.995	0.045	C	T	0.045	0.654	0.281	1.0	-0.750	0.163	4.4E-06	POGLUT1, RP11-190C22.8, TIMMDC1, CD80, RP11-190C22.9, ADPRH, PLA1A, POPDC2, COX17, MAATS1, RP11-169N13.4, NR1I2, GSK3B
rs10897679	11	80535639	imputed	0.905	0.469	C	T	0.531	0.296	0.123	1.0	-0.349	0.076	4.5E-06	RNU6-544P, RP11-686G23.2
rs56115267	2	124863880	imputed	1.010	0.215	C	G	0.785	-0.488	0.129	1.0	0.409	0.089	4.8E-06	RN7SKP102, AC079154.1, CNTNAP5
rs4759123	12	55335999	genotyped	0.998	0.444	A	G	0.556	0.536	0.118	1.0	-0.339	0.074	4.9E-06	DCD, RP11-850F7.7, MUCL1, TESPA1, RP11-616L12.1, NEUROD4, OR9K2, OR10A7
rs6813290	4	25306302	imputed	0.992	0.157	A	C	0.157	-0.491	0.160	1.0	0.439	0.096	5.1E-06	LGI2, SEPSECS, PI4K2B, RP11-660M5.1, ZCCHC4, AC108218.1, ANAPC4, RNU7-126P
rs10217474	9	2945905	imputed	0.962	0.026	A	T	0.974	-1.083	0.374	1.0	1.036	0.228	5.8E-06	VLDLR, KCNV2, KIAA0020, CARM1P1, AL589675.1, RP11-32F11.2, RFX3
rs13389636	2	148966451	imputed	0.961	0.144	A	C	0.856	-0.636	0.161	1.0	0.469	0.104	6.0E-06	ACVR2A, ORC4, AC009480.1, MBD5, SNORA48
rs1952587	14	57161217	imputed	1.018	0.348	A	T	0.652	0.566	0.122	1.0	-0.335	0.074	6.2E-06	TMEM260, RP11-624J12.1, RP11-1085N6.2, RP11-1085N6.3, RP11-1085N6.4, RP11-1085N6.6, OTX2, OTX2-AS1, RP11-1085N6.5, RN7SL461P, RNU6-1204P
rs12786450	11	80117619	imputed	0.914	0.438	C	T	0.438	0.226	0.117	0.9	-0.342	0.076	6.2E-06	CTD-2555I5.1, RNU6-544P
rs57253120	2	147690048	imputed	0.883	0.377	G	T	0.377	-0.456	0.129	1.0	0.357	0.080	7.4E-06	AC103881.1, AC062032.1
rs1150132	6	119484162	imputed	0.974	0.408	C	T	0.408	0.518	0.114	1.0	-0.338	0.076	7.8E-06	MCM9, ASF1A, RP11-351A11.1, FAM184A, Y_RNA, MIR548B, MAN1A1, RNU6-194P
rs1550987	2	116309137	genotyped	0.971	0.029	C	T	0.971	-1.471	0.325	1.0	0.972	0.218	8.2E-06	DPP10
rs6882539	5	16880120	imputed	0.927	0.100	C	T	0.900	-0.464	0.187	1.0	0.534	0.120	9.1E-06	FAM134B, RP11-260E18.1, CTC-461F20.1, Y_RNA, MYO10, RNA5SP179, RNU6-660P, BASP1, CTD-2228A4.1, AC091878.1, RNA5SP180
rs1673864	12	32268544	imputed	1.006	0.415	A	T	0.585	0.284	0.119	1.0	-0.317	0.072	1.1E-05	RP11-428G5.5, AC023050.1, KIAA1551, RP11-843B15.2, BICD1, Y_RNA, FGD4
rs4748708	10	21017303	genotyped	0.993	0.398	A	G	0.602	-0.387	0.117	1.0	0.329	0.075	1.2E-05	MIR4675, NEBL

rs5748470	22	19907118	imputed	0.842	0.394	A	G	0.606	-0.231	0.124	0.9	0.345	0.079	1.2E-05	AC000067.1, SEPT5, GP1BB, TBX1, GNB1L, C22orf29, TXNRD2, COMT, MIR4761, ARVCF, TANGO2, MIR185, AC006547.13, AC006547.15, DGCR8, MIR3618, MIR1306, AC006547.8, TRMT2A, RANBP1, SNORA77, ZDHHC8, AC006547.14, XXbac-B444P24.8, LINC00896
rs7928750	11	44503937	imputed	0.924	0.151	C	G	0.849	0.680	0.169	1.0	-0.447	0.102	1.2E-05	EXT2, ALX4, RP11-58K22.1, CD82, RP11-58K22.5, RP11-58K22.4, RP11-45A12.1, RP11-45A12.2, TSPAN18
rs741806	8	1233646	imputed	0.861	0.238	A	G	0.762	0.317	0.139	1.0	-0.378	0.086	1.2E-05	ERICH1-AS1, CTD-2281E23.2, CTD-2281E23.3, CTD-2281E23.1, AF067845.1, DLGAP2, RP11-666I19.2
rs111498404	13	100071142	imputed	0.835	0.033	A	G	0.968	1.355	0.392	1.0	-0.909	0.208	1.2E-05	UBAC2-AS1, UBAC2, RN7SKP9, GPR18, GPR183, MIR623, AL583784.1, LINC00449, TM9SF2, RNY3P6, LINC01039, CLYBL, MIR4306, CLYBL-AS2
rs117402539	13	96436428	imputed	0.955	0.028	A	G	0.973	1.073	0.359	1.0	-0.863	0.197	1.2E-05	CLDN10, CLDN10-AS1, DZIP1, DNAJC3-AS1, DNAJC3, snR65, UGGT2
rs61865293	10	109975933	imputed	0.823	0.043	C	T	0.043	1.277	0.249	1.0	-0.841	0.193	1.3E-05	RP11-215N21.1
rs10229990	7	154516331	imputed	0.853	0.056	A	G	0.944	-0.445	0.285	0.9	0.794	0.182	1.3E-05	DPP6, RP11-476H24.1, PAXIP1-AS2, PAXIP1, RP11-5C23.1, RP11-5C23.2, PAXIP1-AS1
rs12027950	1	30527553	genotyped	1.011	0.324	A	G	0.677	-0.375	0.116	1.0	0.323	0.074	1.3E-05	AL645944.1, RP11-111I12.1, RP5-893G23.1
rs11012272	10	20978879	imputed	0.964	0.162	G	T	0.838	0.588	0.167	1.0	-0.424	0.098	1.4E-05	MIR4675, NEBL
rs6789681	3	74263894	imputed	0.853	0.488	A	G	0.512	-0.521	0.124	1.0	0.335	0.077	1.5E-05	RP11-508O18.1, Y_RNA, CNTN3
rs6867405	5	30645525	imputed	0.921	0.067	C	G	0.067	0.677	0.205	1.0	-0.658	0.152	1.5E-05	
rs9525089	13	96580664	imputed	0.856	0.052	C	T	0.948	0.960	0.273	1.0	-0.689	0.159	1.5E-05	DZIP1, DNAJC3-AS1, DNAJC3, snR65, UGGT2, HS6ST3, RN7SL164P

rs4711550	6	38474793	genotyped	1.001	0.261	C	T	0.261	-0.272	0.127	1.0	0.339	0.079	1.5E-05	BTBD9, SNORD45, AL031905.1, BTBD9-AS1, Y_RNA, GLO1, RP3-503A6.2, DNAH8, RN7SL465P
rs11158614	14	66300707	genotyped	1.032	0.280	C	T	0.721	-0.439	0.120	1.0	0.338	0.078	1.6E-05	FUT8, CTD-2014B16.3, AL391261.1, RP11-783L4.1
rs1294336	1	233442583	imputed	0.881	0.479	A	G	0.479	0.542	0.116	1.0	-0.322	0.075	1.7E-05	PCNXL2, MLK4, RNU4-77P
rs9436185	1	60199591	genotyped	0.993	0.072	C	T	0.072	0.586	0.205	1.0	-0.562	0.131	1.7E-05	FGGY, MIR4711, RP4-782L23.2, RP4-782L23.1, HOOK1, CYP2J2, RN7SL475P, C1orf87
rs6792028	3	125836673	imputed	0.849	0.363	A	G	0.363	0.472	0.125	1.0	-0.342	0.080	1.8E-05	RP11-379B18.5, AC092902.1, RP11-666A20.4, FAM86JP, ALG1L, ROPN1B, SLC41A3, RP11-158I23.1, AC117422.1, RP11-124N2.1, ALDH1L1, ALDH1L1-AS1, U1, ALDH1L1-AS2, RP11-71E19.1, RP11-71E19.2, KLF15, RP11-71E19.5, CCDC37
rs17106202	10	87799496	imputed	0.962	0.053	C	G	0.947	-0.971	0.243	1.0	0.683	0.159	1.8E-05	GRID1, RNA5SP322, MIR346, AL732479.1
rs2448270	11	80100774	imputed	0.978	0.279	A	C	0.721	0.430	0.130	1.0	-0.338	0.079	1.8E-05	CTD-2555I5.1, RNU6-544P
rs7021312	9	119573882	genotyped	0.999	0.038	C	T	0.962	-1.099	0.242	1.0	0.792	0.185	1.9E-05	ASTN2, RP11-264C15.2, RP11-67K19.3, TRIM32, AL354981.1
rs489307	12	41492180	imputed	0.910	0.483	C	T	0.483	0.254	0.124	1.0	-0.316	0.074	2.1E-05	CNTN1, PDZRN4
rs41263965	1	32110574	imputed	0.969	0.036	A	G	0.036	-0.858	0.326	1.0	0.745	0.176	2.3E-05	ZCCHC17, RP11-266K22.2, FABP3, SERINC2, AC114494.1, RNU6-40P, RP11-439L8.3, RP11-439L8.4, RP11-73M7.1, TINAGL1, HCRTR1, PEF1, RP11-73M7.6, RP11-73M7.9, COL16A1, BAI2, MIR4254, RP11-84A19.3, SPOCD1, RP11-84A19.2, RP11-84A19.4, PTP4A2, AL136115.1, RP4-534N18.2
rs2973241	4	37479364	imputed	0.971	0.412	A	G	0.588	-0.314	0.114	1.0	0.299	0.071	2.5E-05	MIR4801, KIAA1239, C4orf19, RP11-36B15.1, RELL1, Y_RNA
rs16964375	15	37238599	genotyped	0.983	0.083	C	T	0.917	-0.913	0.218	1.0	0.588	0.140	2.5E-05	C15orf41, RP11-16L14.2, CSNK1A1P1, U3, RP11-122D10.1, MEIS2, Y_RNA, RP11-128A17.1

rs2236232	14	68038779	imputed	0.924	0.362	G	T	0.638	0.316	0.119	1.0	-0.312	0.074	2.6E-05	MPP5, ATP6V1D, Y_RNA, EIF2S1, PLEK2, MIR5694, TMEM229B, PLEKHH1, PIGH, RP11-643G16.4, ARG2, VTI1B, 5S_rRNA, RP11-1012A1.4, RDH11, RDH12, RN7SL369P, ZFYVE26, U3, RN7SL213P, RAD51B
rs163831	5	14052118	imputed	0.986	0.132	A	G	0.132	0.386	0.180	1.0	-0.452	0.108	2.8E-05	DNAH5, CTB-51A17.1, TRIO
rs55772025	3	74118286	imputed	0.838	0.332	A	T	0.668	-0.515	0.130	1.0	0.354	0.085	2.8E-05	RP11-20B7.1, RP11-508O18.1, Y_RNA, CNTN3
rs11621396	14	59554597	genotyped	1.032	0.442	C	T	0.442	0.338	0.112	1.0	-0.297	0.071	2.8E-05	RP11-112J1.2, DAAM1
rs72777250	2	8083198	imputed	0.949	0.100	C	T	0.900	-0.711	0.195	1.0	0.553	0.132	2.9E-05	AC092580.3, AC092580.4, AC007463.2, AC007464.1, LINC00299, U91324.1
rs61278300	5	148853051	imputed	0.897	0.067	A	G	0.067	-0.607	0.232	1.0	0.583	0.140	3.0E-05	ABLIM3, RP11-331K21.1, AC012613.2, AFAP1L1, GRPEL2, GRPEL2-AS1, PCYOX1L, IL17B, RP11-394O4.3, MIR143HG, AC131025.8, MIR143, MIR145, CSNK1A1, CTB-89H12.4, ARHGEF37, AC021078.1, RNU6-588P, U3, RN7SL868P, PPARGC1B, MIR378A
rs2623695	8	3588767	genotyped	0.849	0.129	C	T	0.871	0.549	0.202	1.0	-0.470	0.113	3.0E-05	CSMD1, RNA5SP251
rs79626217	9	109449544	imputed	0.853	0.090	C	T	0.090	0.682	0.208	1.0	-0.591	0.142	3.1E-05	RP11-308N19.1, RP11-540H22.2, RP11-308N19.3, RP11-308N19.4, RN7SKP77, RNA5SP292, ZNF462, RP11-508N12.4, RP11-508N12.2
rs228855	6	134248060	imputed	0.879	0.491	A	G	0.509	0.383	0.121	1.0	-0.330	0.079	3.1E-05	RP3-323P13.2, RP4-662A9.2, TCF21, TBPL1, SLC2A12, RN7SL408P, SGK1, snoU13
rs7609571	3	74128405	imputed	1.022	0.382	A	T	0.382	0.483	0.112	1.0	-0.296	0.071	3.2E-05	RP11-20B7.1, RP11-508O18.1, Y_RNA, CNTN3
rs7930030	11	44504804	imputed	0.952	0.436	A	G	0.436	0.401	0.112	1.0	-0.295	0.071	3.2E-05	EXT2, ALX4, RP11-58K22.1, CD82, RP11-58K22.5, RP11-58K22.4, RP11-45A12.1, RP11-45A12.2, TSPAN18
rs112771839	12	91830185	imputed	0.932	0.072	A	G	0.072	0.614	0.217	1.0	-0.600	0.145	3.3E-05	DCN, RP11-121E16.1, RP11-1041F24.1

rs10831562	11	11288590	genotyped	0.995	0.216	A	G	0.784	0.418	0.134	1.0	-0.349	0.084	3.5E-05	RP11-179A10.1, CTD-3224I3.3, GALNT18, CSNK2A3, RP11-567I13.1
rs353219	5	148857630	imputed	0.930	0.063	C	G	0.063	-0.614	0.241	1.0	0.599	0.145	3.5E-05	ABLIM3, RP11-331K21.1, AC012613.2, AFAP1L1, GRPEL2, GRPEL2-AS1, PCYOX1L, IL17B, RP11-394O4.3, MIR143HG, AC131025.8, MIR143, MIR145, CSNK1A1, CTB-89H12.4, ARHGEF37, AC021078.1, RNU6-588P, U3, RN7SL868P, PPARGC1B, MIR378A
rs12813179	12	132302228	imputed	0.906	0.356	C	G	0.644	-0.452	0.121	1.0	0.331	0.080	3.7E-05	RP11-495K9.9, RP11-495K9.7, RNA5SP377, RP11-495K9.6, SFSWAP, RP11-495K9.5, RNA5SP378, RNU6-1017P, MMP17, RP11-417L19.2, ULK1, RP11-417L19.4, PUS1, EP400, AC137590.1, SNORA49, RP13-820C6.2, EP400NL
rs112079519	14	88420230	imputed	0.939	0.026	A	G	0.026	1.258	0.334	1.0	-0.989	0.240	3.8E-05	CTD-2007A10.1, RP11-1152H15.1, RP11-804L24.2, GALC, RNU6-835P, GPR65, RP11-300J18.2, RP11-300J18.1, RP11-300J18.3, RP11-753D20.1, RP11-753D20.4, RP11-753D20.3, KCNK10
rs2488067	10	94506738	genotyped	1.026	0.029	C	T	0.029	-1.167	0.382	1.0	0.841	0.204	3.8E-05	IDE, KIF11, RN7SL644P, HHEX, Y_RNA, EXOC6
rs9571671	13	67361647	imputed	0.978	0.392	C	T	0.392	0.351	0.119	1.0	-0.312	0.076	3.9E-05	PCDH9, RNU7-87P, PCDH9-AS2, PCDH9-AS3, PCDH9-AS4
rs11959113	5	148228496	imputed	0.843	0.251	A	G	0.251	-0.502	0.146	1.0	0.367	0.089	4.1E-05	HTR4, HTR4-IT1, ADRB2, SH3TC2, RP11-44B19.1, RNU6-732P, MIR584, CTC-529P8.1, RN7SKP145, ABLIM3
rs11041079	11	6909271	imputed	0.822	0.023	C	T	0.977	-1.237	0.296	1.0	0.873	0.213	4.3E-05	DNHD1, RRP8, RP11-732A19.8, ILK, TAF10, RP11-732A19.2, TPP1, RP11-732A19.9, DCHS1, RP11-732A19.5, RP11-732A19.6, MRPL17, GVINP1, OR2AG2, OR2AG1, OR6A2, OR10A5,

															OR10A2, OR10A4, OR2D2, OR2D3, ZNF215, ZNF214, NLRP14, RBMXL2
rs1492349	12	88854647	genotyped	0.889	0.061	A	G	0.939	-0.758	0.237	1.0	0.620	0.152	4.5E-05	TMTC3, Y_RNA, KITLG, RNU1-117P
rs895073	3	122825311	imputed	0.944	0.107	A	T	0.893	0.755	0.207	1.0	-0.473	0.116	4.5E-05	DIRC2, RP11-67L2.2, SEMA5B, AC078794.1, PDIA5, SEC22A, RP11-797D24.3, ADCY5, RP11-797D24.4
rs17528171	12	32338115	imputed	0.994	0.457	A	G	0.457	-0.479	0.122	1.0	0.303	0.074	4.5E-05	RP11-428G5.5, AC023050.1, KIAA1551, RP11-843B15.2, BICD1, Y_RNA, FGD4, RNU6-494P
rs7134785	12	2649890	imputed	0.956	0.065	A	G	0.065	-0.611	0.246	1.0	0.584	0.143	4.5E-05	CACNA1C, CACNA1C-IT3, CACNA1C-AS3, CACNA1C-AS2, CACNA1C-AS1, RP11-885B4.1, RP11-885B4.2, CBX3P4, FKBP4, RP4-816N1.6, RP4-816N1.7, ITFG2, NRIP2
rs17254816	12	78992140	genotyped	0.972	0.194	C	T	0.806	-0.360	0.141	1.0	0.367	0.090	4.5E-05	RP11-38F22.1, RP11-754N21.1, RP11-90C1.1, RP11-171L9.1, RP11-123M21.1, SYT1
rs7651537	3	130017439	imputed	0.943	0.458	A	G	0.458	-0.350	0.123	1.0	0.300	0.074	4.5E-05	AC083906.1, ALG1L2, RP11-93K22.13, AC083906.2, FAM86HP, RP11-77P16.4, AC130888.1, COL6A4P2, COL6A5, AC093004.1, COL6A6
rs34364349	17	73485707	imputed	0.888	0.049	A	G	0.049	-0.962	0.282	1.0	0.689	0.169	4.8E-05	NUP85, GGA3, MRPS7, MIF4GD, RP11-649A18.12, SLC25A19, GRB2, RP11-16C1.3, RP11-16C1.2, RP11-16C1.1, MIR3678, RNU6-938P, Y_RNA, KIAA0195, AC100787.1, CASKIN2, TSEN54, LLGL2, MYO15B, RECQL5, SMIM5, SMIM6, SAP30BP, RP11-474I11.8, RP11-474I11.7, ITGB4, GALK1, H3F3B, MIR4738, UNK
rs12454002	18	73834343	genotyped	0.995	0.277	A	G	0.277	0.361	0.131	1.0	-0.342	0.084	5.0E-05	RP11-173L6.1, RP11-357H3.1, RP11-1O2.1, RP11-94B19.6, RP11-

															94B19.1, RP11-94B19.5, RP11-94B19.2, RP11-94B19.7, RP11-94B19.3, RP11-94B19.4, ZNF516, RP11-504I13.3
rs56116608	2	20579309	imputed	0.884	0.113	C	T	0.887	-0.625	0.177	1.0	0.502	0.124	5.1E-05	AC098828.2, RN7SL140P, RNU6-961P, SDC1, RNU7-113P, PUM2, AC007041.1, RNA5SP86, RHOB, AC023137.2, Y_RNA, AC012065.4, HS1BP3, RP11-130L8.2, HS1BP3-IT1, GDF7, AC012065.7, RP11-130L8.1
rs10161651	13	30780458	imputed	0.851	0.434	A	C	0.566	0.288	0.123	1.0	-0.314	0.078	5.2E-05	LINC00572, LINC00544, RP11-629E24.2, LINC00365, LINC00384, LINC00385, KATNAL1, AL356750.1, RNU6-64P, LINC00427, LINC00426, LINC01058, HMGB1
rs2440430	8	6283772	genotyped	1.011	0.054	A	G	0.946	0.564	0.223	1.0	-0.565	0.140	5.2E-05	RP11-124B13.1, RP11-115C21.2, MCPH1, ANGPT2, CTD-2541M15.3, CTD-2541M15.1, CTD-2541M15.4, AGPAT5
rs9328385	6	728418	genotyped	1.018	0.326	A	G	0.326	0.333	0.113	1.0	-0.291	0.072	5.4E-05	EXOC2, RP1-20B11.2, HUS1B, RP11-532F6.3, RP11-532F6.4, RP11-532F6.5, RP11-284J1.1, RP5-1077H22.2, RP5-1077H22.1, RP5-856G1.1
rs13023244	2	144267567	imputed	0.853	0.419	A	G	0.419	-0.445	0.128	1.0	0.319	0.079	5.4E-05	ARHGAP15, AC096558.1, RP11-570L15.2, RP11-570L15.1, AC092652.1, RP11-434H14.1, CTD-2252P21.1, AC079584.2
rs7227575	18	65922901	genotyped	1.008	0.254	A	C	0.254	-0.504	0.132	1.0	0.335	0.083	5.6E-05	RP11-659F24.1, RP11-526H11.1, RP11-421N8.2, RP11-128D14.1
rs57672995	15	63313588	imputed	0.824	0.085	C	T	0.085	-0.428	0.213	1.0	0.522	0.130	5.7E-05	TLN2, AC103740.1, MIR190A, RP11-1069G10.1, RP11-1069G10.2, TPM1, RP11-244F12.3, RP11-244F12.2, RP11-69G7.1, LACTB, RPS27L, RAB8B, APH1B, CA12
rs7739129	6	169736925	imputed	0.921	0.101	A	G	0.101	-0.629	0.211	1.0	0.487	0.121	5.9E-05	RP3-495K2.1, RP11-417E7.1, RP11-417E7.2, XXyac-YX65C7_A.2, THBS2, XXyac-YX65C7_A.3, RP1-

															137D17.1, RP1-137D17.2, WDR27
rs2426931	20	59447834	genotyped	1.004	0.404	A	G	0.404	0.387	0.110	1.0	-0.290	0.072	6.0E-05	RP11-151E14.1, RP5-827L5.2, RP5-827L5.1
rs73013006	6	148306353	imputed	0.973	0.302	C	T	0.698	-0.516	0.122	1.0	0.319	0.079	6.0E-05	SAMD5, RP11-307P5.1, RP11-307P5.2, RP11-242F11.2, RP11-631F7.2, RP11-631F7.1, SASH1, RNU6-1222P
rs4775501	15	62725025	imputed	0.823	0.135	C	T	0.865	0.626	0.197	1.0	-0.457	0.114	6.1E-05	C2CD4B, RP11-299H22.1, hsa-mir-7162, RP11-1O10.1, AC126323.1, RP11-299H22.5, RP11-299H22.6, RP11-299H22.7, TLN2, RP11-625H11.1, RP11-625H11.2
rs10950028	7	65634168	imputed	0.973	0.234	A	G	0.234	-0.395	0.138	1.0	0.335	0.084	6.1E-05	VKORC1L1, GUSB, AC068533.1, ASL, AC068533.7, CRCP, RP5-1132H15.1, TPST1, RNU6-313P, LINC00174, RNU6-96P, GS1-124K5.2, snoU13
rs34060969	4	126753635	imputed	0.957	0.100	C	T	0.900	-0.820	0.183	1.0	0.482	0.120	6.1E-05	RP11-399F2.2, RP11-318I4.1
rs17026901	2	102890386	genotyped	0.974	0.061	C	T	0.061	-0.943	0.242	1.0	0.569	0.142	6.1E-05	IL1R2, IL1R1, AC007271.3, IL1RL2, IL1RL1, IL18R1, IL18RAP, MIR4772, AC007278.2, AC007278.3, SLC9A4
rs7036143	9	91425294	genotyped	1.014	0.313	A	G	0.687	0.393	0.129	1.0	-0.308	0.077	6.3E-05	NXNL2, RP13-60M5.2, MIR4289, RP11-791O21.5, C9orf47, S1PR3, RP11-82L18.4, SHC3, RP11-82L18.2
rs8016889	14	38246440	imputed	0.946	0.367	A	G	0.367	0.404	0.124	1.0	-0.312	0.078	6.7E-05	MIPOL1, RP11-356O9.2, RP11-356O9.1, FOXA1, TTC6, SNORA42, RNU6-1277P, LINC00517, CTD-2058B24.3, CTD-2058B24.2
rs749269	14	68052983	genotyped	0.989	0.083	A	G	0.083	-0.801	0.231	1.0	0.524	0.132	6.9E-05	MPP5, ATP6V1D, Y_RNA, EIF2S1, PLEK2, MIR5694, TMEM229B, PLEKHH1, PIGH, RP11-643G16.4, ARG2, VTI1B, 5S_rRNA, RP11-1012A1.4, RDH11, RDH12, RN7SL369P, ZFYVE26, U3, RN7SL213P, RAD51B

rs12629612	3	169178006	imputed	0.961	0.242	A	G	0.758	0.549	0.139	1.0	-0.346	0.087	6.9E-05	MECOM, RP11-641D5.2, RP11-3K16.2, RNU6-637P
rs7563897	2	127398038	imputed	0.964	0.462	C	T	0.462	0.207	0.120	0.9	-0.299	0.075	7.0E-05	AC023347.1, GYPC, RNU6-675P, AC114783.1
rs262641	1	2104981	genotyped	0.997	0.340	A	G	0.660	0.308	0.120	1.0	-0.299	0.075	7.1E-05	GNB1, RP1-140A9.1, CALML6, TMEM52, C1orf222, RP11-547D24.1, GABRD, RP11-547D24.3, PRKCZ, RP5-892K4.1, RP11-181G12.2, C1orf86, AL590822.2, AL590822.1, RP11-181G12.5, RP11-181G12.4, SKI, MORN1, RP4-713A8.1, AL589739.1, RP4-740C4.6, RP4-740C4.7, RP4-740C4.9, RP4-740C4.8, RER1, PEX10, PLCH2
rs2101761	5	180108234	imputed	0.805	0.438	A	G	0.438	-0.306	0.127	1.0	0.313	0.079	7.1E-05	CTC-573N18.1, RNU6-525P, CNOT6, AC122714.1, SCGB3A1, FLT4, RP11-451H23.3, RNU1-17P, OR2Y1, CTC-205M6.5, MGAT1, LINC00847, ZFP62, BTNL8, Y_RNA
rs12498635	4	17269825	imputed	0.949	0.279	G	T	0.721	0.461	0.139	1.0	-0.328	0.083	7.3E-05	RP11-141E13.1, RP11-576E20.1, SNORA75, QDPR, CLRN2, snoU13
rs4378808	2	215361240	genotyped	0.999	0.248	A	C	0.248	0.528	0.123	1.0	-0.323	0.081	7.3E-05	SPAG16, AC107218.3, VWC2L, VWC2L-IT1, BARD1
rs76920500	10	132002936	imputed	0.975	0.087	A	G	0.087	-0.727	0.216	1.0	0.498	0.126	7.4E-05	EBF3, LINC00959, GLRX3, RP11-540N6.1
rs74905609	9	76318042	imputed	0.801	0.030	A	G	0.030	1.185	0.434	1.0	-1.079	0.272	7.5E-05	RP11-128I7.1, RNA5SP286
rs2985941	13	46153600	genotyped	1.010	0.378	C	G	0.622	-0.384	0.118	1.0	0.303	0.077	7.6E-05	GTF2F2, AL138963.1, SNORA31, TPT1, RP11-290D2.6, TPT1-AS1, RP11-290D2.3, SLC25A30, SLC25A30-AS1, COG3, FAM194B, RNA5SP27, LINC01055, SPERT, SIAH3
rs34442243	3	68535882	imputed	0.969	0.167	A	T	0.167	0.588	0.149	1.0	-0.383	0.097	7.6E-05	FAM19A1, AC096922.1, FAM19A4
rs12676122	8	40557679	genotyped	1.015	0.227	A	G	0.227	-0.298	0.140	1.0	0.340	0.086	7.7E-05	CTA-392C11.2, RP11-301G7.1, ZMAT4, RP11-465K16.1
rs1553501	14	57462169	imputed	1.061	0.125	A	G	0.875	0.605	0.177	1.0	-0.391	0.099	7.8E-05	RP11-1085N6.3, RP11-1085N6.4, RP11-1085N6.6, OTX2, OTX2-AS1, RP11-1085N6.5, RN7SL461P,

															RNU6-1204P, RP11-108M12.3, EXOC5, AL391152.1, AP5M1
rs80128717	3	161036712	imputed	0.841	0.032	G	T	0.968	1.134	0.353	1.0	-0.773	0.196	7.9E-05	PPM1L, B3GALNT1, NMD3, SPTSSB, RP11-3P17.4, RP11-3P17.5, OTOL1
rs943317	10	92018838	imputed	1.019	0.166	A	C	0.166	0.527	0.137	1.0	-0.354	0.090	7.9E-05	RN7SKP143, RP11-15K3.1, RP11-94M14.2, RP11-94M14.3
rs9830144	3	116333667	imputed	0.911	0.168	C	T	0.168	0.459	0.146	1.0	-0.403	0.102	8.0E-05	LSAMP, LSAMP-AS1, LINC00903, RN7SL582P, TUSC7, MIR4447
rs7997324	13	96307645	imputed	0.900	0.050	C	T	0.050	-0.838	0.274	1.0	0.625	0.159	8.0E-05	CLDN10, CLDN10-AS1, DZIP1, DNAJC3-AS1, DNAJC3, snR65, UGGT2
rs12124900	1	63971756	imputed	0.911	0.121	C	T	0.879	0.605	0.209	1.0	-0.464	0.118	8.0E-05	LINC00466, RP11-335E6.3, RP4-792G4.2, FOXD3, Y_RNA, ALG6, ITGB3BP, EFCAB7, RN7SL488P, RNU7-123P, DLEU2L, PGM1, RN7SL130P, ROR1
rs9795353	11	341256	imputed	0.973	0.122	A	C	0.879	-0.567	0.159	1.0	0.419	0.106	8.1E-05	RP11-304M2.6, LINC01001, RP11-304M2.3, RNU6-447P, BET1L, SCGB1C1, ODF3, RP11-304M2.5, RIC8A, SIRT3, PSMD13, NLRP6, RP11-326C3.2, ATHL1, IFITM5, IFITM2, RP11-326C3.7, IFITM1, RP11-326C3.11, IFITM3, RP11-326C3.10, RP11-326C3.14, RP11-326C3.13, RP11-326C3.12, RP11-326C3.15, B4GALNT4, PKP3, SIGIRR, ANO9, RN7SL838P, PTDSS2, RP13-317D12.3, RNH1, RP13-46H24.1, HRAS, LRRC56, C11orf35, RP11-496I9.1, RASSF7, MIR210HG, MIR210, PHRF1, IRF7, CDHR5, SCT, DRD4
rs6566579	18	69561921	genotyped	0.967	0.178	G	T	0.178	-0.366	0.154	1.0	0.365	0.093	8.1E-05	RP11-723G8.2, RP11-723G8.1, RP11-736G13.1
rs3439	2	233450937	imputed	0.962	0.456	G	T	0.544	-0.337	0.117	1.0	0.299	0.076	8.2E-05	DIS3L2, ALPP, AC068134.8, ECEL1P2, ALPPL2, AC068134.6, ALPI, ECEL1, PRSS56, CHRND, CHRNG, TIGD1, EIF4E2, MIR5001, AC073254.1, EFHD1,

															RN7SL359P, snoU13, GIGYF2, AC064852.4, KCNJ13, RNU6-107P, Y_RNA, C2orf82, NGEF
rs7072648	10	54340976	imputed	0.974	0.262	A	G	0.738	0.570	0.139	1.0	-0.333	0.085	8.3E-05	PRKG1, PRKG1-AS1, DKK1, RP11-346D6.6, RP11-556E13.1, MBL2, Y_RNA
rs17016135	3	25318290	imputed	0.980	0.044	C	T	0.956	-0.683	0.303	1.0	0.743	0.189	8.3E-05	AC133680.1, RN7SL216P, RNA5SP125, RARB, RNA5SP126, SNORD5
rs35094093	10	61251890	imputed	0.963	0.065	A	G	0.936	0.635	0.226	1.0	-0.525	0.133	8.3E-05	PHYHIPL, FAM13C, RP11-443O13.3, RP11-135D11.2, SLC16A9, LINC00948, CCDC6
rs12081726	1	185465254	imputed	0.932	0.055	A	G	0.055	0.863	0.248	1.0	-0.679	0.173	8.3E-05	SWT1, Y_RNA, IVNS1ABP, GS1-279B7.2, GS1-279B7.1, RNU7-183P, GS1-204I12.1, GS1-204I12.4, HMCN1
rs9487940	6	112968423	imputed	0.946	0.104	C	T	0.104	0.479	0.213	1.0	-0.512	0.130	8.5E-05	RP11-506B6.6, RFPL4B, AL365214.1, RP1-105O18.1, snoU13, AL357514.1
rs12174377	6	103971216	imputed	0.800	0.122	C	G	0.878	0.204	0.195	0.7	-0.459	0.117	8.7E-05	SNORA33
rs12986546	2	155939607	imputed	0.986	0.243	A	G	0.243	-0.332	0.144	1.0	0.334	0.085	8.8E-05	KCNJ3, AC092625.1, RNU6-1001P, RNU6-546P
rs2645766	2	238257896	imputed	0.979	0.221	G	T	0.779	-0.442	0.130	1.0	0.344	0.088	8.8E-05	AC105760.3, AC105760.2, COPS8, AC107079.1, AC112715.2, COL6A3, AC112721.1, AC112721.2, MLPH, RNU6-1140P, PRLH, RAB17, AC104667.3, AC096574.5, LRRFIP1
rs2720597	8	30693016	imputed	1.015	0.342	A	G	0.658	-0.324	0.120	1.0	0.294	0.075	8.9E-05	RBPMS, GTF2E2, CTD-2373N4.5, SMIM18, RNU5A-3P, GSR, UBXN8, PPP2CB, TEX15, PURG, WRN
rs916807	22	30400381	imputed	0.983	0.102	C	T	0.102	-0.668	0.200	1.0	0.445	0.114	8.9E-05	RP1-76B20.11, RP1-76B20.12, CABP7, ZMAT5, Y_RNA, UQCR10, ASCC2, MTMR3, RNU6-331P, AC003681.1, CTA-85E5.10, HORMAD2, RP3-438O4.4, RP1-102K2.6, LIF, RP1-102K2.8, OSM, GATSL3, RP1-130H16.18,

																TBC1D10A
rs76297944	3	167170991	imputed	1.005	0.020	C	T	0.980	0.956	0.404	1.0		-0.847	0.216	9.1E-05	ZBBX, RP11-576M8.2, SERPINI2, WDR49, PDCD10, SERPINI1
rs75741192	11	82046467	imputed	0.844	0.046	A	C	0.954	-0.846	0.278	1.0		0.795	0.204	9.5E-05	RP11-179A16.1, SNORD112, RP11-179A16.2
rs7771679	6	138465030	imputed	1.004	0.415	A	G	0.585	0.370	0.111	1.0		-0.277	0.071	9.8E-05	RP11-356I2.4, TNFAIP3, RP11-10J5.1, RP11-240M16.1, PERP, KIAA1244, PBOV1, RP3-422G23.4, HEBP2, NHSL1, MIR3145
rs73129261	1	244295486	imputed	0.980	0.049	C	T	0.951	-1.090	0.246	1.0		0.680	0.174	9.8E-05	AKT3, RP11-278H7.1, ZBTB18, AL590483.1, RP11-278H7.4, RN7SL148P, RP11-278H7.3, C1orf100, RP11-518L10.5, ADS

Results of Secondary Analyses

Here, we present the results for the two sets of secondary analyses performed. First, we examined whether SNPs with association $p<1x10^{-5}$ in either sample (African American or Hispanics) showed similar direction or statistical evidence of association in the other sample. Second, we performed a second GWAS in each sample after additionally adjusting for the two environmental exposures, as both stressful life events and social support were found to make large and unique contributions to the variance in depressive symptoms.

A. Comparison of GWAS Results Between Racial/Ethnic Groups

We conducted two sets of meta analyses to determine the degree to which the top GWAS SNPs ($p<10x10^{-5}$) obtained in African Americans were also the top SNPs in Hispanics and vice versa. Slightly less than half of the African American top SNPs (59 of the 127 SNPs tested) had effects in the same direction among Hispanics (Supplemental Table 5; sign test p=0.24). The strongest signal from a meta analysis of these 127 SNPs in both samples was for rs73531535 ($p=2.27x10^{-7}$), which was the top hit in the African American GWAS. Examination of I^2 values (which indicate the amount of heterogeneity not due to chance) suggested a large degree of heterogeneity across samples (average $I^2 = 60.22$). Filtering out rare variants (SNPs with frequencies ≤ 5% in either African Americans or Hispanics) had no major impact on the results (49 of 104 SNPs in the same direction; sign test p=0.31).

About half of the Hispanic/Latina top SNPs (44 of the 86 SNPs tested) had effects in the same direction among African Americans (Supplemental Table 6; sign test p=0.46). The best SNP in this meta analysis was for rs34919099 ($p=1.05x10^{-4}$). We were unable to meta analyze results for our two top Hispanic SNPs (rs2532087 and rs4542757) as these were filtered out due to imputation quality in the African American GWAS. There was a very large degree of heterogeneity across samples (average $I^2 = 91.75$). Filtering out rare variants (SNPs with frequencies ≤ 5% in either African Americans or Hispanics) had no major impact on the results (37 of 69 SNPs in the same direction; sign test p=0.32).

B. GWAS Results After Adjusting for Social Support and Stressful Life Events

We performed a second GWAS in each sample that additionally adjusted for quartiles of stressful life events and social support in addition to the other covariates described previously. We conducted this second GWAS because these two exposures were found, in both population groups, to make large and unique contributions to the variance in depressive symptoms beyond the other covariates (see Table 4 below). In addition, previous studies have also noted the potential gains in power that could arise by accounting for the role of environmental exposures as a means to reduce sample heterogeneity [34]. We included both exposures simultaneously in the model for this second GWAS, as the exposures were only modestly correlated with each other (African American r=0.20; Hispanic/Latina r=0.23). This secondary GWAS contained slightly fewer respondents due to missingness on both environmental exposures (n=6888 African Americans and n=3004 Hispanics).

Table 4. Percent of variance in the adjusted CES-D score explained in each model

	Model 1	Model 2	Model 3	Model 4	Model 5
African Americans	0.04	3.25	10.58	10.02	15.55
Hispanics	0.52	4.65	13.15	13.43	19.32

Model 1: Model with genetic covariates (i.e., principal components and imputation group for African Americans)
Model 2: Model with genetic and demographic covariates (age, income, education, marital status)
Model 3: Model with genetic and demographic covariates and stressful life events
Model 4: Model with genetic and demographic covariates and social support
Model 5: Model with all covariates
Cell entries are based on adjusted r^2 values, which account for the number of parameters in the model.

Results of the secondary GWAS in each sample are shown in Figure 13 below. There was no evidence of genomic inflation in this secondary GWAS of African Americans ($\lambda = 1.006$). In African Americans, we found that results of the GWAS including environmental covariates were attenuated relative to the original

GWAS that did not include covariates for the two environmental exposures (stressful life events and social support). For example, while the direction of effect of the top result (rs73531535) was similar between the primary GWAS (beta= -0.297; p=5.75E-08) and secondary GWAS (beta=-0.2537; p=1.496e-06), the magnitude of effect was slightly reduced. A similar attenuation in the magnitude of effect was also detected for the second top result (rs75407252) when comparing the primary GWAS (beta= -0.548; p=6.99E-07) to the secondary GWAS (beta=-0.4942; p=6.99E-07).

We found an opposite pattern of results in Hispanics. Among Hispanics, inclusion of environmental covariates led to a slight strengthening of the magnitude of association for the top SNPs. For instance, the top result in the secondary GWAS, rs4542757 (beta=-0.4276; p=6.882e-08), had a modestly larger effect in the secondary GWAS compared to the primary GWAS, where it was the second best result (beta=-0.4135; p=7.31E-07). Similarly, the second best result in the secondary GWAS, rs34359572 (beta=-0.8158; p=1.88e-07), had a larger association in the secondary GWAS compared to the primary GWAS, where it was the sixth best result (beta=-0.7471; p=4.10E-06). There was no evidence of genomic inflation in this secondary GWAS of Hispanics (λ =1.005).

Taken together, these results suggest including known social-environmental covariates could help strengthen results from GWAS. However, in some cases, and as demonstrated in a recent paper [35], co-varying out the effect of environment may be an over-adjustment as it could reduce observed genetic differences between individuals in the sample and may lead to biased results.

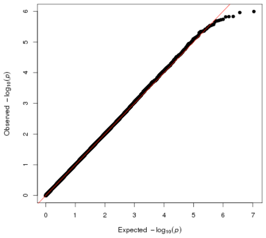
C. GWAS and GWEIS Results Using Non-Parametric Bootstrap

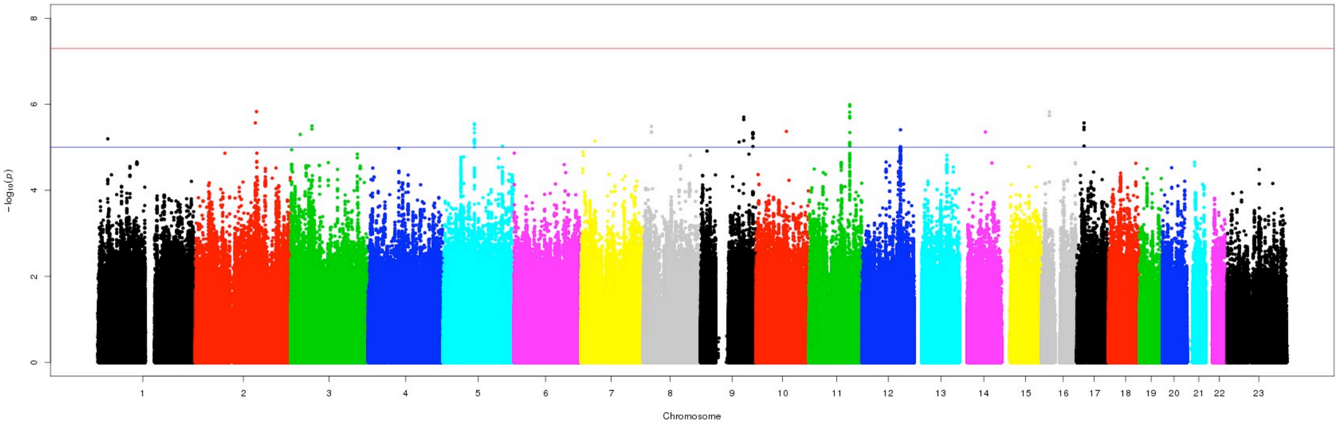
To evaluate the strength of our findings given the skewed distribution of our outcome, we repeated the top GWAS ($p<1x10^{-5}$) and GWEIS ($p<1x10^{-6}$) tests of association using a non-parametric bootstrap. For the top GWAS SNPs, we fit a linear regression on 1000 bootstrap samples using the boot package in R[36; 37] and compared the effective sizes (betas) from the bootstrap samples to the beta obtained in the original analysis for each top SNP. For the top GWEIS SNPs, we fit linear regressions to 5000 datasets simulated under the null hypothesis[38] and generated p-values for each top SNP. These p-values represent the number of betas that were more extreme than the beta obtained in the original analysis divided by 5000 replicates. A significant p-value therefore indicates that the GxE interaction is significant at that level.

As shown in Supplemental Table 12, the GWAS results using a non-parametric bootstrap were similar to our original findings. As shown in Supplemental Tables 13 and 14, the GWEIS results were also highly significant, in that no betas were more extreme in the bootstrap analyses for any SNP relative to the original analysis (e.g., 0/5000 corresponds to p<0.0002). Both sets of findings suggest our results were not sensitive to distributional assumptions of the outcome.

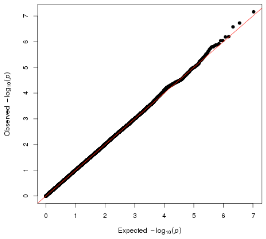
Supplemental Figure 13. Manhattan plot depicting results of GWAS including stressful life events and social support

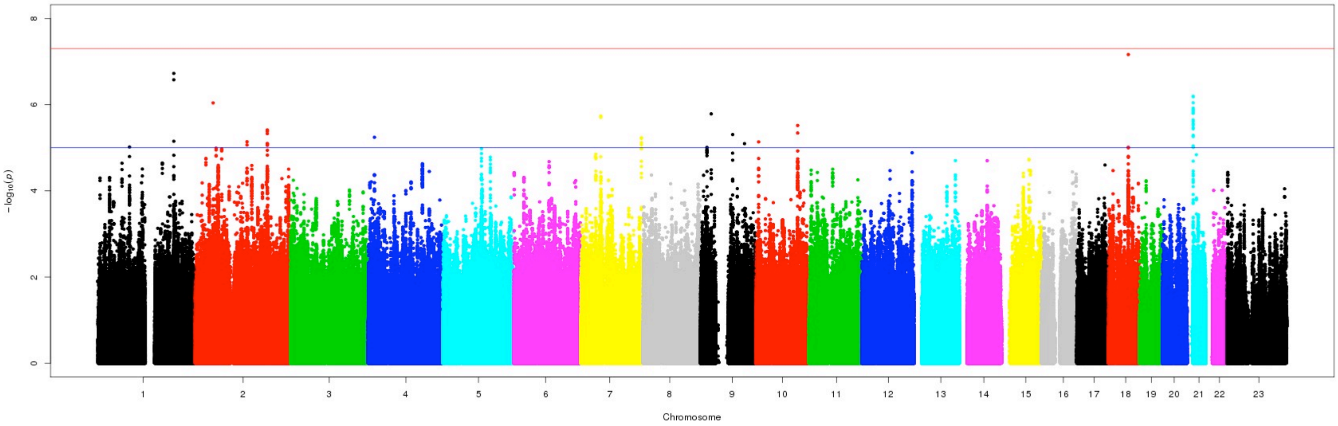
African American





Hispanic/Latina





Supplemental Table 12. Bootstrap results for genome-wide association study (GWAS) top loci (p<1x10-5) in African Americans and Hispanics/Latinos

SNP	chr	position	A1	A2	MAF	G/I	Info	Beta	SE	P-value	Location	Closest Gene (<20kb)	Bootstrap analysis		
													Mean Beta	Upper 95% CI	Lower 95% CI
African Americans															
rs73531535	16	20105038	C	T	0.229	I	0.938	-0.297	0.055	5.75E-08		*GPR139*	-0.298	-0.182	-0.406
rs75407252	3	54241886	C	T	0.053	I	0.813	-0.548	0.11	6.99E-07	intron variant	*CACNA2D3*	-0.546	-0.309	-0.781
rs11233283	11	82415904	A	G	0.016	I	0.986	-0.298	0.062	1.41E-06			-0.303	-0.179	-0.429
rs34257140	17	42675053	G	T	0.149	I	0.999	-0.313	0.065	1.59E-06			-0.309	-0.175	-0.450
rs580112	3	177289895	A	G	0.184	I	0.945	0.279	0.06	2.84E-06	intron variant	*LINC00578*	0.279	0.397	0.163
rs1413154	13	83240729	G	T	0.205	I	0.825	-0.283	0.061	3.54E-06			-0.284	-0.172	-0.401
rs1893586	21	43286918	A	G	0.483	I	0.947	0.211	0.046	4.19E-06	intron variant	*PRDM15*	0.210	0.303	0.116
rs10777901	12	98492992	A	C	0.481	I	0.993	0.206	0.045	4.27E-06			0.206	0.292	0.119
rs10125319	9	133426729	C	T	0.491	I	0.92	-0.214	0.047	4.27E-06			-0.214	-0.126	-0.305
rs10221121	16	56840328	A	G	0.229	G	0.986	-0.241	0.053	5.98E-06	intron variant	*NUP93*	-0.242	-0.144	-0.341
rs210329	14	54059800	G	T	0.332	I	0.989	0.217	0.048	6.35E-06		*RPS3AP46*	0.215	0.318	0.121
rs28493952	3	95747804	C	T	0.32	I	0.85	0.234	0.052	6.41E-06			0.237	0.343	0.130
rs7312307	12	106441333	C	G	0.087	I	0.904	0.376	0.084	6.92E-06		*NUAK1*	0.376	0.515	0.222
rs17030391	2	43353504	A	G	0.143	I	0.808	0.316	0.071	7.84E-06			0.310	0.459	0.168
rs4866976	5	45579793	A	G	0.086	G	0.996	-0.361	0.081	8.04E-06	intron variant	*HCN1*	-0.361	-0.194	-0.535
rs418207	3	9225376	A	G	0.477	I	0.811	-0.219	0.05	9.59E-06	intron variant	*SRGAP3*	-0.220	-0.122	-0.324
Hispanics/Latinos															
rs2532087	4	15878327	C	G	0.231	I	0.8154	0.5379	0.104	2.44E-07			0.544	0.759	0.339
rs4542757	18	50198724	C	T	0.418	I	0.9304	-0.4135	0.0833	7.31E-07	intron variant	*DCC*	-0.411	-0.264	-0.559
rs10249677	7	50650831	G	T	0.042	I	0.8816	1.0497	0.2157	1.20E-06		*GRB10*	1.042	1.553	0.552

rs1129411	2	231077725	A	G	0.085	I	0.9941	0.6637	0.1417	2.94E-06	missense/intron variant	*SP110*	0.666	0.986	0.349
rs11738766	5	8214282	A	G	0.279	G	1.0253	-0.4134	0.0885	3.11E-06			-0.408	-0.234	-0.565
rs34359572	1	194036781	A	G	0.072	I	0.8899	-0.7471	0.1619	4.10E-06			-0.749	-0.355	-1.166
rs609508	20	54167720	C	G	0.214	I	0.9752	0.4429	0.097	5.21E-06			0.445	0.618	0.254
rs16823787	2	183692791	A	G	0.084	G	0.9823	0.6591	0.1444	5.21E-06		*FRZB*	0.662	0.926	0.415
rs17345417	4	95948486	A	G	0.111	G	0.9949	-0.574	0.1259	5.30E-06	intron variant	*BMPR1B*	-0.574	-0.334	-0.837
rs2822657	21	15774729	C	T	0.457	I	0.9875	-0.3657	0.0802	5.35E-06		*HSPA13*	-0.365	-0.203	-0.514
rs13033587	2	52857818	C	T	0.475	I	0.9342	0.376	0.0828	5.85E-06			0.379	0.533	0.221
rs9601962	13	83312889	G	T	0.185	I	0.8544	0.4945	0.1098	6.91E-06			0.491	0.723	0.257
rs2282123	6	89907561	C	G	0.255	G	1.0034	0.4114	0.0915	7.19E-06	intron variant	*GABRR1*	0.411	0.588	0.246
rs10886733	10	122402887	C	T	0.117	I	0.9766	0.556	0.1237	7.23E-06		*MIR5694*	0.550	0.816	0.302
rs61848143	10	24746704	C	G	0.177	I	0.8403	-0.5023	0.1122	7.85E-06	intron variant	*KIAA1217*	-0.497	-0.286	-0.701
rs10166852	2	183450923	C	G	0.474	I	0.9666	-0.3752	0.0838	7.85E-06			-0.373	-0.210	-0.532
rs6736484	2	45146524	G	T	0.075	G	0.8556	-0.7206	0.1621	9.05E-06			-0.722	-0.382	-1.058
rs2912513	8	69968166	A	T	0.033	I	0.9774	-0.996	0.2243	9.33E-06	intron variant	*LINC01592*	-1.007	-0.632	-1.368

The table lists all LD-pruned SNPs associated with depressive symptoms at p<1x10-5. A1 is the tested allele using an additive model, where alleles were analyzed as dosages. The closest gene within 20kb upstream/downstream of the SNP is provided. All SNPs are on the positive (5' to 3') strand. Chr: chromosome; position: base pair position, G/I: genotyped or imputed. Bootstrap analysis: Mean and upper and lower limit of 95% confidence interval of betas obtained from 1000 replicates.

Supplemental Table 13. Bootstrap results for genome-environment wide interaction study (GEWIS) top loci ($p<1x10^{-6}$) in African Americans

Stressful Life Event Results (n=6,982)

									SNP Main Effect			SNP*Stressful Life Events Interaction Term			Location	Closest Gene (<20kb)	Bootstrap analysis
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value			p-value
rs4652467	1	180097705	I	0.945	0.026	A	G	0.026	-0.662	0.167	1	0.691	0.111	4.10E-10		*CEP350*	< 0.0002
rs7275997	21	19663487	G	0.993	0.18	A	G	0.82	0.264	0.069	1	-0.278	0.053	1.22E-07	intron variant	*TMPRSS15*	< 0.0002
rs28377528	7	153884444	I	0.874	0.42	A	G	0.58	-0.212	0.058	1	0.237	0.046	3.23E-07	intron variant	*DPP6*	< 0.0002
rs2852310	18	43093004	I	0.996	0.027	A	G	0.027	-0.56	0.183	1	0.617	0.123	4.66E-07	intron variant	*SLC14A2*	< 0.0002
rs12183135	6	151353805	G	0.996	0.024	C	G	0.024	-0.137	0.155	1	0.491	0.1	8.01E-07		*MTHFD1L*	< 0.0002

Social Support Results (n=6,908)

									SNP Main Effect			SNP*Social Support Interaction Term			Location	Closest Gene (<20kb)	Bootstrap analysis
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value			p-value
rs77966298	2	10984514	I	0.891	0.034	A	G	0.966	0.796	0.223	1	-0.592	0.115	2.43E-07		*PDIA6*	< 0.0002
rs6419121	4	88490040	I	0.921	0.178	C	G	0.178	-0.375	0.096	1	0.28	0.055	3.98E-07			< 0.0002
rs10836421	11	35581792	I	0.971	0.315	A	G	0.315	-0.184	0.071	1	0.217	0.043	4.34E-07			< 0.0002
rs78012311	21	33634345	I	0.981	0.104	C	G	0.104	0.468	0.094	1	-0.321	0.065	8.23E-07		*MIS18A*	< 0.0002

Robust (sandwich) standard errors are presented. In these tests of statistical interaction (on the additive scale and using allele dosages), probABEL uses A2 as the tested (non-reference) allele. The beta coefficients in these models can be interpreted as follows. The SNP main effect beta coefficient indicates the average difference in levels of depressive symptoms for women with a zero value on all covariates, who have 1 copy of the tested allele, and who are in the lowest quartile of stressful life events. The GxE interaction term indicates the average estimated difference in the effect of each tested allele on depressive symptoms associated with a one-unit different in stressful life events, adjusting for covariates. The Bonferroni adjusted alpha level in these analyses was 2.5x10-8. For the Bootstrap analysis, p-values are presented, which represent the number of betas that were more extreme than the beta obtained in the original analysis divided by 5000 replicates. A significant p-value therefore indicates that the GxE interaction is significant at that level (e.g. 0/5000 corresponds to $p < 0.0002$).

Supplemental Table 14. Bootstrap results for genome-environment wide interaction study (GEWIS) top top loci ($p<1x10^{-6}$) in Hispanics

Stressful Life Event Results (n=2,989)

									SNP Main Effect			**SNP*Stressful Life Events Interaction Term**			**Location**	**Closest Gene (<20kb)**	**Bootstrap analysis**
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value			p-value
rs58707171	4	36317832	I	0.921	0.037	A	C	0.963	0.649	0.254	1	-0.778	0.152	3.02E-07	intron variant	*DTHD1*	< 0.0002
rs6579218	20	33709846	I	0.989	0.156	C	G	0.844	0.425	0.142	1	-0.505	0.1	4.94E-07	intron variant	*EDEM2*	< 0.0002
rs10227305	7	3272267	I	0.849	0.207	A	C	0.793	0.308	0.133	1	-0.454	0.093	9.36E-07			< 0.0002

Social Support Results (n=3,012)

									SNP Main Effect			**SNP*Social Support Interaction Term**			**Location**	**Closest Gene (<20kb)**	**Bootstrap analysis**
SNP	chr	position	G/I	Info	MAF	A1	A2	Freq1	Beta	SE	p-value	Beta	SE	p-value			p-value
rs35612712	4	187347203	I	0.941	0.416	C	T	0.416	-0.375	0.119	1	0.376	0.074	3.42E-07	intron variant	*F11-AS1*	< 0.0002
rs61973969	13	96689182	I	0.985	0.032	C	T	0.032	-0.979	0.317	1	0.839	0.171	9.41E-07	intron variant	*UGGT2*	< 0.0002

Robust (sandwich) standard errors are presented. In these tests of statistical interaction (on the additive scale and using allele dosages), probABEL uses A2 as the tested (non-reference) allele. The beta coefficients in these models can be interpreted as follows. The SNP main effect beta coefficient indicates the average difference in levels of depressive symptoms for women with a zero value on all covariates, who have 1 copy of the tested allele, and who are in the lowest quartile of stressful life events. The GxE interaction term indicates the average estimated difference in the effect of each tested allele on depressive symptoms associated with a one-unit different in stressful life events, adjusting for covariates. The Bonferroni adjusted alpha level in these analyses was 2.5x10-8. Mean and standard deviation (SD) for the distribution of betas for the GxE interaction in the bootstrap analyses are presented. For the Bootstrap analysis, p-values are presented, which represent the number of betas that were more extreme than the beta obtained in the original analysis divided by 5000 replicates. A significant p-value therefore indicates that the GxE interaction is significant at that level (e.g. 0/5000 corresponds to $p < 0.0002$).

References

1 1998. Design of the Women's Health Initiative clinical trial and observational study. The Women's Health Initiative Study Group. Control and Clinical Trials 19:61-109.

2 Wassertheil-Smoller S, Shumaker S, Ockene J, Talavera GA, Greenland P, Cochrane B, Robbins J, Aragaki A, Dunbar-Jacob J. 2004. Depression and cardiovascular sequela in postmenopausal women: The Women's Health Initiative (WHI). Archives of Internal Medicine 164:289-298.

3 Women's Health Initiative SHARe Project. 2011. Imputation Report - 1000 Genomes Project reference panel.

4 Browning B, Browning SA. 2009. A unified approach to genotype imputation and haplotype-phase inference for large data sets of trios and unrelated individuals. American Journal of Human Genetics 84:210-223.

5 Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. 2006. Principal components analysis corrects for stratification in genome-wide association studies. Nature Genetics 38:904-909.

6 Gillespie CF, Bradley B, Mercer K, Smith AK, Conneely K, Gapen M, Weiss T, Schwartz AC, Cubells JF, Ressler KJ. 2009. Trauma exposure and stress-related disorders in inner city primary care patients. Gen Hosp Psychiatry 31(6):505-14.

7 Sorlie PD, Aviles-Santa LM, Wassertheil-Smoller S, Kaplan RC, Daviglus ML, Giachello AL, Schneiderman N, Raij L, Talavera G, Allison M and others. 2010. Design and implementation of the Hispanic Community Health Study/Study of Latinos. Ann Epidemiol 20(8):629-41.

8 Lavange LM, Kalsbeek WD, Sorlie PD, Aviles-Santa LM, Kaplan RC, Barnhart J, Liu K, Giachello A, Lee DJ, Ryan J and others. 2010. Sample design and cohort selection in the Hispanic Community Health Study/Study of Latinos. Annals of Epidemiology 20(8):642-9.

9 Laurie CC, Doheny KF, Mirel DB, Pugh EW, Bierut LJ, Bhangale T, Boehm F, Caporaso NE, Cornelis MC, Edenberg HJ and others. 2010. Quality control and quality assurance in genotypic data for genome-wide association studies. Genet Epidemiol 34(6):591-602.

10 Laurie CC, Laurie CA, Rice K, Doheny KF, Zelnick LR, McHugh CP, Ling H, Hetrick KN, Pugh EW, Amos C and others. 2012. Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nat Genet 44(6):642-50.

11 Genomes Project C, Abecasis GR, Auton A, Brooks LD, DePristo MA, Durbin RM, Handsaker RE, Kang HM, Marth GT, McVean GA. 2012. An integrated map of genetic variation from 1,092 human genomes. Nature 491(7422):56-65.

12 Howie BN, Donnelly P, Marchini J. 2009. A flexible and accurate genotype imputation method for the next generation of genome-wide association studies. PLoS Genet 5(6):e1000529.

13 Howie BN, Marchini J, Stephens M. 2011. Genotype imputation with thousands of genomes. G3: Genes, Genomics, Genetics 1:457-470.

14 Manichaikul A, Mychaleckyj JC, Rich SS, Daly K, Sale M, Chen WM. 2010. Robust relationship inference in genome-wide association studies. Bioinformatics 26(22):2867-73.

15 Thornton T, Tang H, Hoffmann TJ, Ochs-Balcom HM, Caan BJ, Risch N. 2012. Estimating kinship in admixed populations. Am J Hum Genet 91(1):122-38.

16 Conomos MP, Miller MB, Thorton TA. 2015. Robust inference of population structure for ancestry prediction and correction of stratification in the presence of relatedness. Genetic Epidemiology.

17 Juster FT, Suzman R. 1995. An overview of the health and retirement study. Journal of Human Resources 30.

18 Sonnega A, Faul JD, Ofstedal MB, Langa KM, Phillips JWR, Weir DR. 2014. Cohort profile: the health and retirement study (HRS). International Journal of Epidemiology 43(2):576-585.

19 Hek K, Demirkan A, Lahti J, Terracciano A, Teumer A, Cornelis MC, Amin N, Bakshis E, Baumert J, Ding J and others. 2013. A genome-wide association study of depressive symptoms. Biological Psychiatry 73(7):667-78.

20 Levy D, DeStefano AL, Larson MG, O'Donnell CJ, Lifton RP, Gavras H, Cupples LA, Myers RH. 2000. Evidence for a gene influencing blood pressure on chromosome 17: Genome scan linkage results for

longitudinal blood pressure phenotypes in subjects from the Framingham Heart Study. Hypertension 36(4):477-483.

21 Aulchenko YS, Struchalin MV, vanDuijn CM. 2010. probABEL package for genome-wide association analysis of imputed data. BMC Bioinformatics 11:134.

22 White H. 1980. A heteroskedasticity-consistent covariance-matrix estimator and a direct test for heterodkedasticity. Econometrica 48:817-838.

23 Voorman A, Lumley T, McKnight B, Rice K. 2011. Behavior of qq-plots and genomic control in studies of gene-environment interaction. Plos One 65(5):e19416.

24 Cornelis MC, Tchetgen EJ, Liang L, Qui L, Chatterjee N, Hu FB, Kraft P. 2012. Gene-environment interactions in genome-wide association studies: A comparative study of tests applied to empirical studies of type 2 diabetes. American Journal of Epidemiology 175(3):191-202.

25 Almli LM, Duncan R, Feng H, Ghosh D, Binder EB, Bradley B, Ressler KJ, Conneely KN, Epstein MP. 2014. Correcting systematic inflation in genetic association tests that consider interaction effects: application to a genome-wide association study of posttraumatic stress disorder. JAMA Psychiatry 71(12):1392-9.

26 Radloff LS. 1977. The CES-D scale: A self-report depression scale for research in the general population. Applied Psychological Measurement 1:385-401.

27 Beck AT, Steer RA, Brown GK. 1996. Manual for the Beck Depression Inventory-II. San Antonio, Texas: Psychological Corporation.

28 Wang YP, Gorenstein C. 2013. Psychometric properties of the Beck Depression Inventory-II: a comprehensive review. Rev Bras Psiquiatr 35(4):416-31.

29 Beck AT, Steer RA, Carbin MG. 1988. Psychometric properties of the Beck Depression Inventory: Twenty-five years of evaluation. Clinical psychology review 8(1):77-100.

30 Sherbourne CD, Stewart AL. 1991. The MOS social support survey. Soc Sci Med 32(6):705-14.

31 Cohen S, Mermelstein R, Kamarck T, Hoberman H. 1985. Measuring the functional components of social support. In: Sarason IG, Sarason B, editors. Social support: Theory, research, and application. Netherlands: Springer. p 73-94.

32 Berkman LF, Syme SL. 1979. Social networks, host resistance, and mortality: a nine-year follow-up study of Alameda County residents. Am J Epidemiol 109(2):186-204.

33 Smoller JW, Pollack MH, Wassertheil-Smoller S, Brunner R, Curb D, Torner J, Oberman A, Hendrix SL, Hsia J, Sheps DS. 2006. Panic attacks, daily life ischemia, and chest pain in postmenopausal women. Psychosom Med 68(6):824-32.

34 Power RA, Cohen-Woods S, Ng MY, Butler AW, Craddock N, Korszun A, Jones L, Jones I, Gill M, Rice JP and others. 2013. Genome-wide association analysis accounting for environmental factors through propensity-score matching: application to stressful life events in major depressive disorder. Am J Med Genet B Neuropsychiatr Genet 162B(6):521-9.

35 Aschard H, Vihjalmsson BJ, Joshi AD, Price AL, Kraft P. 2015. Adjusting for heritable covariates can bias effect estimates in genome-wide association studies. American Journal of Human Genetics 96:329-339.

36 Canty A, Ripley B. 2015. boot: Boostrap R (S-Plus) Functions. R package version 1.3-17.

37 Davison AC, Hinkley DV. 1997. Bootstrap Methods and TheirApplications. Cambridge: Cambridge University Press.

38 Buzkova P, Lumley T, Rice K. 2011. Permutation and parametric bootstrap tests for gene-gene and gene-environment interactions. Ann Hum Genet 75(1):36-45.