

Supplementary Material

Supplementary definition in the UK Biobank

Definition of Patient Health Questionnaire (PHQ-9)

PHQ-9[1] is a classification algorithm with a total score (0-27) used to screen for and measure depression severity, focusing on nine depressive symptoms and signs (as detailed below: Little interest or pleasure in doing things (UKB: 20514), Feeling down, depressed, or hopeless (UKB:20510, Trouble sleeping(UKB: 20517), Feeling tired (UKB: 20519), Poor appetite or overeating (UKB: 20511), Feeling bad about yourself (UKB: 20507), Trouble concentrating (UKB: 20508), Moving or speaking slowly or fidgety or restless (UKB: 20518), Thoughts that you would be better off dead (UKB: 20513)). In order to meet the 0-3 score for each item of PHQ, the 9 symptom scores (1-4) of our team UK were all reduced by 1 point, which was then added up.

Definition of 7-item Generalized Anxiety Disorder Scale (GAD-7)

GAD-7[1] is a classification algorithm with a total score scale from 0-21 used to screen for and measure anxiety severity, focusing on seven anxious symptoms and signs (as detailed below: Feeling nervous, anxious or on edge (UKB: 20506), Not being able to stop or control worrying (UKB: 20509), Worrying too much about different things (UKB: 20520), Trouble relaxing (UKB: 20515), Being so restless that it is hard to sit still (UKB: 20516), Becoming easily annoyed or irritable (UKB: 20505), Feeling afraid as if something awful might happen (UKB: 20512)). In order to meet the 0-3 score for each item of GAD, the seven symptom scores (1-4) of UKB were all reduced by 1 point, and then were added up to generate GAD-7.

Definition of self-reported depression and anxiety

The criteria for the definition of depression and anxiety were according to the definitions of Davis et al[2]. The case group criteria of depression and anxiety were defined based on self-reports and came from three UK Biobank fields: 20002, 20126 and 20544. The case group of depression was selected based on the code 1286 (UKB: 20002), code 3,4 or 5 (UKB: 20126) and code 11 (UKB: 20544). The case group of anxiety was selected based on the code 1287 (UKB: 20002) and code 15 (UKB: 20544).

The participants who didn't report depressive symptoms and screened negative on PHQ-9

or composite international diagnostic interview short-form (CIDI-SF)[3] were selected as the control group of the self-reported depression, and individuals without self-reported anxiety symptoms didn't screen positive on GAD-7 were defined as control group of self-reported anxiety. The details of the mental disorder definition are shown in supplementary materials.

Definition of single social factors

The definition of a single social factor refers to a recent study published by Zhao et.al [4]. For mental disorders, we selected 13 social factors from three domains (socioeconomic status[SES], neighborhood and living environment, psychosocial factors) for preliminary analysis[5-8]. Briefly, SES include 4 indicators: low household income, low education attainment, poor education quality, and not in paid employment. Social psychological factors include living alone, lack of social support, social inactivity, social isolation and emotional distress. Neighborhood and living environment domain consists of area-level material deprivation, high local crime rate, poor housing quality and instable accommodation. The definition of a single social factor refers to a recent study published by Zhao et.al [4]. All indicators were derived from questionnaire interviews with participants and were defined as binary phenotypes. The responses representing higher social risk were scored as 1, and answers on behalf of lower social risk were scored as 0. The details of the definition are as follows:

Social factors	Original data in UKB		Definition in the present study
	ID(UKB field)	Definition	
Socioeconomic status			
Low household income	Average total household income before tax (738)	1=Less than 18,000; 2=18,000 to 30,999; 3=31,000 to 51,999; 4=52,000 to 100,000; 5=Greater than 100,000	0 = average total household income before tax is more than £31,000; 1 = less than £31,000
Low education attainment	Qualifications (6138)	1=College or University degree; 2=A levels/AS levels or equivalent; 3=O levels/GCSEs or equivalent; 4=CSEs or equivalent; 5=NVQ or HND or HNC or equivalent; 6=Other professional qualifications eg: nursing, teaching	0 = highest education level is college or above; 1 = lower than college
Poor education quality	Education score-England (26414) Education score-Scotland (26431) Education score-Wales (26421)	1=In paid employment or self-employed; 2=Retired; 3=Looking after home and/or family; 4=Unable to work because of sickness or disability; 5=Unemployed; 6=Doing unpaid or voluntary work; 7=Full or part-time student	0 = below the median of education score; 0 = above the median
Not in paid employment	Current employment status (6142)	1=In paid employment or self-employed; 2=Retired; 3=Looking after home and/or family; 4=Unable to work because of sickness or disability; 5=Unemployed; 6=Doing unpaid or voluntary work; 7=Full or part-time student	0 = In paid employment or self-employed; 1 = others
Psychosocial factors			
Living alone	Number in household(709)	Continuous variable	0 = no; 1= yes
Lack of social support	Able to confide (2110)	5=Almost daily; 4=2-4 times a week; 3=About once a week; 2=About once a month; 1=Once every few months; 0=Never or almost never	0 = able to confide in anyone close to you at least once a week; 1 = once a week or less often
Social inactivity	Leisure/social activities (6160)	1=Sports club or gym; 2=Pub or social club; 3=Religious group; 4=Adult education class; 5=Other group activity	0 = attend any group activities once a week or more often; 1 = less often than once a week

Social isolation	Frequency of friend/family visits (1031)	1=Almost daily; 2=2-4 times a week; 3=About once a week; 4=About once a month; 5=Once every few months; 6=Never or almost never; 7=No friends/family outside household	0 = visit friend/family or have them visit you more often than once a week; 1 = once a week or less
Emotional distress	Illness, injury, bereavement, stress in last 2 years (6145)	1=Serious illness, injury or assault to yourself; 2=Serious illness, injury or assault of a close relative; 3=Death of a close relative; 4=Death of a spouse or partner; 5=Marital separation/divorce; 6=Financial difficulties	1 = have experienced illness, injury, bereavement, stress within last 2 years; 0 = none
Neighborhood and living environment			
Area-level material deprivation	Townsend deprivation index at recruitment (189)	Continuous variable	0 = below the median of Townsend deprivation index; 1 = above the median
High local crime rate	Crime score-England (26416) Crime score-Scotland (26434) Crime score-Wales(26425)	Continuous variable	0 = below the median of crime score; 1 = above the median
Poor housing quality	Housing score-England (26415) Housing score-Scotland (26432) Housing score-Wales (26423)	Continuous variable	0 = below the median of housing score; 1 = above the median
Unstable accommodation	Own or rent accommodation lived in (680)	1=Own outright (by you or someone in your household); 2=Own with a mortgage; 3=Rent - from local authority, local council, housing association; 4=Rent - from private landlord or letting agency; 5=Pay part rent and part mortgage (shared ownership); 6=Live in accommodation rent free	0 = own current accommodation outright; 1 = own with mortgage

Reference

- 1 Kroenke K, Spitzer RL, Williams JB, Löwe B. The Patient Health Questionnaire Somatic, Anxiety, and Depressive Symptom Scales: a systematic review. *Gen Hosp Psychiatry*. 2010;32:345-59.
- 2 Davis KAS, Cullen B, Adams M, Brailean A, Breen G, Coleman JRI, et al. Indicators of mental disorders in UK Biobank-A comparison of approaches. *Int J Methods Psychiatr Res*. 2019;28:e1796.
- 3 Gigantesco A, Morosini P. Development, reliability and factor analysis of a self-administered questionnaire which originates from the World Health Organization's Composite International Diagnostic Interview - Short Form (CIDI-SF) for assessing mental disorders. *Clin Pract Epidemiol Ment Health*. 2008;4:8.
- 4 Zhao Y, Li Y, Zhuang Z, Song Z, Wang W, Huang N, et al. Associations of polysocial risk score, lifestyle and genetic factors with incident type 2 diabetes: a prospective cohort study. *Diabetologia*. 2022;65:2056-65.
- 5 Holmberg I, Persson G. Mental disorder at seventy in relation to social factors and attitudes during life. *Acta Psychiatr Scand*. 1986;74:168-77.
- 6 Otte C, Gold SM, Penninx BW, Pariante CM, Etkin A, Fava M, et al. Major depressive disorder. *Nature Reviews Disease Primers*. 2016;2:16065.
- 7 Qi X, Jia Y, Pan C, Li C, Wen Y, Hao J, et al. Index of multiple deprivation contributed to common psychiatric disorders: A systematic review and comprehensive analysis. *Neurosci Biobehav Rev*. 2022;140:104806.
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Supplementary figure

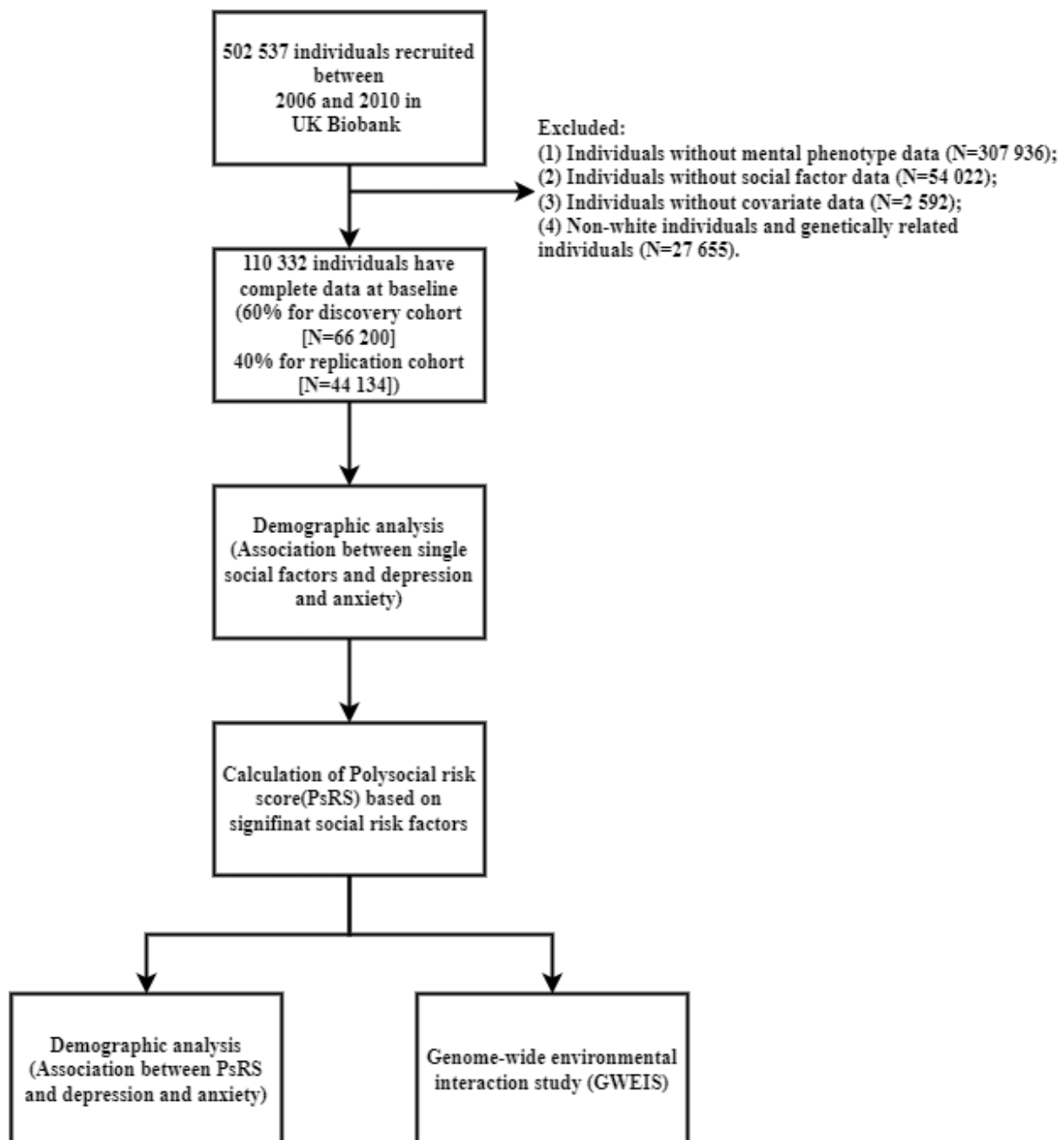


Figure S1. Flow chart of study design.

Supplementary tables

Table S1. Association between single social factor and depression and anxiety (original multivariable regression model).

Table S2. Association between single social risk factor and depression and anxiety (insignificant factors removed).

Table S3. Weights used to calculate PsRS based on multivariable models.

Table S4. The statistical summary of PsRS.

Table S5. The numbers of PsRS-interacted SNPs detected by GWEIS.

Table S6. The PsRS-interacted SNPs for PHQ score in discovery and replication cohort.

Table S7. The PsRS-interacted SNPs for GAD score in discovery and replication cohort.

Table S8. The PsRS-interacted SNPs for self-reported depression in discovery and replication cohort.

Table S9. The PsRS-interacted SNPs for self-reported anxiety in discovery and replication cohort.

Table S10. Functional analysis results for PHQ score candidate genes.

Table S11. Multi-omics-based validation for top candidate genes of mental phenotypes.

Table S1. Association between single social factor and depression and anxiety (original multivariable regression model).

Mental phenotype	Social factor	Discovery cohort			Replication cohort		
		Beta	SE	P	Beta	SE	P
PHQ score	Area-level material deprivation	0.151	0.032	2.31E-06	0.201	0.039	3.35E-07
	Instable accommodation	0.289	0.034	3.39E-17	0.230	0.042	4.11E-08
	Living alone	0.186	0.041	6.69E-06	0.131	0.050	8.97E-03
	Social isolation	0.063	0.030	0.038	0.046	0.037	0.216
	Low household income	0.379	0.035	4.60E-27	0.365	0.043	4.27E-17
	Lack of social support	0.839	0.034	1.27E-132	0.862	0.042	1.37E-93
	Low education attainment	0.159	0.030	8.44E-08	0.209	0.036	1.00E-08
	Not in paid employment	0.359	0.037	5.82E-22	0.339	0.046	1.47E-13
	Social inactivity	0.383	0.032	1.29E-32	0.437	0.040	2.41E-28
	Emotional distress	0.606	0.029	1.36E-95	0.626	0.036	1.98E-68
	High local crime rate	0.025	0.032	0.430	0.033	0.039	0.391
	Poor education quality	0.295	0.032	6.06E-20	0.222	0.039	1.82E-08
	Poor housing quality	0.021	0.029	0.470	0.036	0.035	0.310
GAD score	Area-level material deprivation	0.067	0.030	0.026	0.082	0.037	0.026
	Instable accommodation	0.202	0.032	3.22E-10	0.166	0.039	2.44E-05
	Living alone	-0.118	0.039	2.27E-03	-0.171	0.047	2.86E-04
	Social isolation	0.020	0.028	0.481	0.009	0.035	0.804
	Low household income	0.279	0.033	3.17E-17	0.267	0.041	5.07E-11
	Lack of social support	0.534	0.032	2.80E-62	0.579	0.039	3.65E-49
	Low education attainment	0.082	0.028	3.14E-03	0.119	0.034	5.07E-04
	Not in paid employment	0.213	0.035	1.11E-09	0.185	0.043	1.57E-05
	Social inactivity	0.256	0.030	2.42E-17	0.275	0.037	1.25E-13
	Emotional distress	0.454	0.027	8.31E-62	0.443	0.034	9.47E-40
	High local crime rate	0.029	0.030	0.321	0.026	0.036	0.466
	Poor education quality	0.125	0.030	3.57E-05	0.119	0.037	1.29E-03
	Poor housing quality	-0.008	0.027	0.779	0.021	0.033	0.531
Self-reported depression	Area-level material deprivation	0.151	0.021	1.79E-13	0.129	0.025	2.92E-07
	Instable accommodation	0.315	0.022	4.48E-46	0.299	0.027	1.53E-28
	Living alone	0.248	0.026	2.14E-21	0.202	0.032	2.27E-10
	Social isolation	-0.068	0.019	4.01E-04	-0.080	0.024	7.27E-04
	Low household income	0.485	0.022	1.26E-104	0.456	0.028	1.38E-61
	Lack of social support	0.267	0.022	2.32E-34	0.310	0.027	6.45E-31
	Low education attainment	0.084	0.019	1.35E-05	0.096	0.024	4.30E-05
	Not in paid employment	0.182	0.024	2.62E-14	0.145	0.029	6.75E-07
	Social inactivity	0.146	0.021	1.86E-12	0.205	0.025	7.66E-16
	Emotional distress	0.488	0.019	1.39E-151	0.496	0.023	9.99E-105
	High local crime rate	0.009	0.020	0.644	0.033	0.025	0.188
	Poor education quality	0.196	0.021	1.79E-21	0.173	0.025	6.28E-12
	Poor housing quality	-0.002	0.019	0.933	0.036	0.023	0.117
	Area-level material deprivation	0.043	0.027	0.115	0.016	0.033	0.637
	Instable accommodation	0.160	0.029	2.67E-08	0.160	0.035	6.17E-06
	Living alone	0.034	0.034	0.305	0.035	0.041	0.392

Self-reported anxiety	Social isolation	-0.040	0.025	0.110	-0.051	0.031	0.103
	Low household income	0.271	0.029	1.46E-20	0.254	0.036	1.43E-12
	Lack of social support	0.087	0.029	0.003	0.130	0.035	2.21E-04
	Low education attainment	-0.010	0.025	0.693	0.052	0.031	9.34E-02
	Not in paid employment	0.109	0.032	5.89E-04	0.139	0.039	3.37E-04
	Social inactivity	0.125	0.027	3.26E-06	0.158	0.033	1.56E-06
	Emotional distress	0.342	0.024	4.49E-45	0.308	0.030	5.35E-25
	High local crime rate	0.028	0.027	0.286	-0.001	0.033	0.975
	Poor education quality	0.109	0.027	5.11E-05	0.126	0.033	1.40E-04
	Poor housing quality	-0.107	0.024	1.23E-05	-0.018	0.030	0.553

Table S2. Association between single social risk factor and depression and anxiety (insignificant factors removed).

Mental phenotype	Social risk factor	Discovery cohort				Replication cohort			
		Beta/OR	95% CI Lower	95% CI Upper	<i>P</i>	Beta/OR	95% CI	95% CI Upper	<i>P</i>
PHQ score	Area-level material deprivation	0.16	0.10	0.22	1.18E-07	0.22	0.14	0.29	7.97E-09
	Instable accommodation	0.29	0.22	0.36	2.49E-17	0.23	0.15	0.31	3.78E-08
	Living alone	0.18	0.10	0.26	1.01E-05	0.13	0.03	0.23	9.83E-03
	Low household income	0.38	0.31	0.44	1.08E-26	0.36	0.28	0.45	8.09E-17
	Lack of social support	0.85	0.78	0.91	4.92E-136	0.87	0.78	0.95	1.92E-95
	Low education attainment	0.15	0.10	0.21	2.22E-07	0.20	0.13	0.27	2.23E-08
	Not in paid employment	0.35	0.28	0.42	2.44E-21	0.33	0.24	0.42	2.82E-13
	Social inactivity	0.39	0.32	0.45	1.89E-33	0.44	0.36	0.52	8.25E-29
	Emotional distress	0.60	0.55	0.66	5.12E-95	0.62	0.55	0.70	3.38E-68
	Poor education quality	0.30	0.24	0.36	2.75E-21	0.23	0.15	0.30	4.54E-09
GAD score	Instable accommodation	0.20	0.14	0.26	2.99E-10	0.17	0.09	0.24	2.59E-05
	Low household income	0.26	0.19	0.32	6.32E-16	0.23	0.16	0.31	2.78E-09
	Lack of social support	0.53	0.46	0.59	1.42E-61	0.56	0.49	0.64	1.01E-47
	Low education attainment	0.08	0.03	0.14	3.08E-03	0.12	0.05	0.18	4.57E-04
	Not in paid employment	0.21	0.15	0.28	5.86E-10	0.19	0.11	0.28	6.86E-06
	Social inactivity	0.26	0.20	0.32	7.28E-18	0.28	0.21	0.35	3.80E-14
	Emotional distress	0.45	0.40	0.51	8.40E-62	0.44	0.38	0.51	7.24E-40
	Poor education quality	0.15	0.09	0.20	2.01E-07	0.14	0.07	0.21	4.00E-05
Self-reported depression	Area-level material deprivation	1.17	1.12	1.21	5.25E-15	1.15	1.1	1.21	2.58E-09
	Instable accommodation	1.37	1.31	1.43	6.73E-46	1.35	1.28	1.42	1.66E-28
	Living alone	1.29	1.23	1.36	1.69E-22	1.24	1.16	1.31	2.82E-11
	Low household income	1.63	1.56	1.7	2.58E-106	1.58	1.5	1.67	4.34E-62
	Lack of social support	1.3	1.24	1.35	8.01E-33	1.35	1.28	1.42	1.83E-29
	Low education attainment	1.09	1.05	1.13	4.51E-06	1.1	1.05	1.16	2.27E-05
	Not in paid employment	1.21	1.15	1.27	1.71E-15	1.17	1.1	1.23	1.35E-07
	Social inactivity	1.15	1.11	1.2	7.94E-12	1.22	1.16	1.28	4.12E-15
	Emotional distress	1.63	1.58	1.69	2.15E-153	1.65	1.57	1.72	8.29E-106
	Poor education quality	1.22	1.17	1.27	2.16E-23	1.2	1.14	1.26	2.52E-13
	Instable accommodation	1.18	1.11	1.24	1.70E-08	1.18	1.1	1.26	3.97E-06
	Low household income	1.34	1.27	1.41	1.08E-25	1.32	1.24	1.41	2.64E-16

Self-reported anxiety	Lack of social support	1.09	1.03	1.15	3.18E-03	1.14	1.06	1.22	1.96E-04
	Not in paid employment	1.11	1.05	1.18	6.75E-04	1.15	1.07	1.24	2.13E-04
	Social inactivity	1.13	1.07	1.19	7.00E-06	1.17	1.1	1.25	1.77E-06
	Emotional distress	1.41	1.34	1.48	1.18E-45	1.36	1.29	1.45	1.95E-25
	Poor education quality	1.14	1.09	1.2	1.36E-07	1.15	1.08	1.22	5.21E-06

Table S3. Weights used to calculate PsRS based on multivariable models.

Social risk factor	PHQ score		GAD score		Self-reported		Self-reported	
	Discovery	Replication	Discovery	Replication	Discovery	Replication	Discovery	Replication
Area-level material deprivation	0.162	0.216	0.202	0.165	0.143	0.153	/	/
Instable accommodation	0.290	0.230	/	/	0.299	0.314	0.162	0.163
Living alone	0.181	0.129	/	/	0.211	0.254	/	/
Low household income	0.375	0.361	0.257	0.233	0.457	0.488	0.289	0.278
Lack of social support	0.846	0.866	0.525	0.563	0.300	0.260	0.084	0.130
Low education attainment	0.153	0.203	0.082	0.118	0.099	0.088	/	/
Not in paid employment	0.352	0.334	0.215	0.192	0.153	0.190	0.107	0.142
Social inactivity	0.388	0.440	0.260	0.280	0.199	0.141	0.120	0.157
Emotional distress	0.603	0.625	0.454	0.443	0.498	0.491	0.343	0.310
Poor education quality	0.298	0.226	0.148	0.143	0.180	0.200	0.132	0.140

Table S4. The statistical summary of PsRS.

	Mental Phenotype	Minimum	Quartile 1	Median	Quartile 3	Maximum
Discovery cohort	Self-reported anxiety	0	1.497	2.388	3.253	7.005
	Area-level material deprivation	0	1.613	2.583	3.722	8.000
	Self-reported depression	0	2.105	3.463	4.831	10.000
	PHQ score	0	2.003	3.119	4.461	9.997
Replication cohort	Self-reported anxiety	0	1.497	2.388	3.253	7.005
	GAD score	0	1.590	2.567	3.689	7.996
	Self-reported depression	0	2.170	3.462	4.801	10.000
	PHQ score	0	1.915	3.096	4.493	10.000

Table S5. The numbers of PsRS-interacted SNPs detected by GWEIS.

Mental Phenotype	Discovery cohort		N (<i>P</i> <1.25e-8 in discovery cohort and <i>P</i> <0.05 in replication cohort)
	N (<i>P</i> <5e-8)	N (<i>P</i> <1.25e-8)	
PHQ score	102	62	62
GAD score	30	18	18
Self-reported depression	0	0	0
Self-reported anxiety	1	0	0
Total	133	80	80

Note. N, the number of PsRS-interacted SNPs.

Table S6. The PsRS-interacted SNPs for PHQ score in discovery and replication cohort (Marked in red is significant).

SNP	CHR	Position	Eeference allele	Alternative allele	P discovery	P replication	Overlapped gene
rs141360714	5	16239143	G	T	1.69E-12	0.000659135	ZNF622
rs147165657	5	16274471	G	A	2.10E-12	0.0123691	ZNF622
rs11614439	12	9902857	T	C	2.11E-12	1.41E-08	CD69
rs2689542	7	152542459	A	G	4.69E-11	0.0007633	ACTR3B
rs542946033	7	152543389	C	T	8.34E-11	0.00246084	ACTR3B
rs4591276	19	55029367	C	G	1.35E-10	0.000107614	AC008746.9
rs144469813	4	20274271	T	C	1.75E-10	0.000606422	SLIT2
rs117345247	20	34773553	A	G	3.79E-10	5.85E-06	EPB41L1
rs10518045	4	68710842	C	T	4.50E-10	7.33E-06	TMPRSS11D
rs2860008	4	68710963	C	T	4.51E-10	7.34E-06	TMPRSS11D
rs116587563	4	68710465	A	C	4.51E-10	7.33E-06	TMPRSS11D
rs140314791	4	68709501	T	C	4.53E-10	7.31E-06	TMPRSS11D
rs17088693	4	68709690	C	T	4.53E-10	7.31E-06	TMPRSS11D
rs114006170	4	68704816	T	C	4.81E-10	4.55E-06	TMPRSS11D
rs116531749	3	82128014	C	T	5.12E-10	0.00114896	GBE1
8:41453210_CTCTT C	8	41453210	C	CTCTT	5.20E-10	0.00279471	/
rs111606492	19	55105969	A	C	5.46E-10	2.68E-10	LILRB1
rs148060334	4	68705712	G	A	6.33E-10	7.60E-06	TMPRSS11D
rs1545935	4	68700984	C	G	6.34E-10	6.84E-06	TMPRSS11D
rs17576689	4	68704958	C	T	6.35E-10	7.57E-06	TMPRSS11D
rs115427586	4	68681137	C	T	6.35E-10	9.44E-06	TMPRSS11D
rs76632488	4	68684456	A	G	6.42E-10	9.75E-06	TMPRSS11D
rs150629496	3	82006561	C	G	7.27E-10	0.000285426	GBE1
rs117969745	18	64889618	C	A	9.31E-10	5.54E-06	RPL31P9
rs182485596	6	76667042	T	C	1.32E-09	0.000100584	IMPG1
rs147509787	7	46287804	G	T	1.33E-09	0.0036796	HMGNI1P19
4:68667012_CAAAT C	4	68667012	C	CAAT	1.64E-09	4.48E-05	/
rs112030069	1	213919006	C	G	2.12E-09	0.0141236	PROX1
rs112672202	1	213917791	T	C	2.31E-09	0.0139595	PROX1
rs28529767	1	206300551	T	C	2.33E-09	0.0209615	CTSE
rs183848315	7	152425977	A	G	2.64E-09	0.00429495	XRCC2
rs142221374	3	153568239	G	A	2.93E-09	0.00531383	C3orf79
rs17603507	15	30234960	G	A	3.29E-09	0.000350721	TJP1
rs116107595	3	81624468	C	T	3.34E-09	0.000718239	GBE1
rs118133461	7	152420994	A	G	3.39E-09	0.00362656	XRCC2
rs76722576	7	152421261	A	C	3.86E-09	0.0036653	XRCC2
rs3759812	15	72100019	G	C	3.87E-09	6.21E-05	MYO9A
rs6863037	5	119686074	A	G	4.22E-09	0.000651188	PRR16
rs144501423	5	119670176	G	A	4.53E-09	0.000646586	PRR16
rs144464609	4	108161365	G	T	5.16E-09	0.000152513	DKK2
rs142478061	1	207483392	A	G	5.26E-09	0.0490296	CD55
rs149533016	4	18319183	A	G	5.27E-09	1.43E-06	LCORL
rs142268508	3	81846513	T	C	5.42E-09	0.000118662	GBE1
rs113644415	18	64892371	T	C	5.67E-09	1.42E-05	RPL31P9
rs11661452	18	64893826	T	C	5.79E-09	1.44E-05	RPL31P9
rs79824688	5	141506354	T	C	6.96E-09	0.00419647	NDFIP1
rs148275421	3	194661899	T	G	8.34E-09	0.0056306	XXYL1
rs77140099	1	181391031	A	G	8.84E-09	0.0181991	CACNA1E
rs74594895	16	10839907	G	A	9.45E-09	0.0307412	NUBP1
rs75482345	20	61724045	T	C	9.55E-09	0.0004998	BHLHE23
rs115357900	3	81719118	T	A	9.63E-09	0.000396712	GBE1
rs80029890	7	54449520	T	G	9.98E-09	0.000340082	SLC25A5P3

rs146348447	15	100798747	C	T	1.06E-08	0.0234018	ADAMTS17
rs117918935	15	100798756	A	G	1.08E-08	0.0203625	ADAMTS17
rs117676280	18	58355538	C	T	1.08E-08	1.68E-06	CTBP2P3
rs149137169	8	53343488	A	C	1.08E-08	3.25E-06	ST18
rs62849163	3	58558781	T	A	1.09E-08	0.000577234	FAM107A
rs147753363	4	18381341	C	T	1.13E-08	9.98E-08	LCORL
rs115300689	3	81736535	A	C	1.15E-08	0.000290053	GBE1
rs149469089	3	68327787	G	C	1.21E-08	4.31E-08	FAM19A1
rs370273048	18	62216618	T	G	1.21E-08	0.0313918	CDH7
rs116332061	3	79825415	C	G	1.21E-08	0.00032627	ROBO1
rs112952213	4	18315475	C	G	1.26E-08	1.03E-07	LCORL
rs149965693	3	128248170	T	C	1.48E-08	0.0244584	GATA2
rs117175198	17	7012342	T	C	1.49E-08	9.33E-08	ASGR2
rs72989664	18	76826364	A	T	1.55E-08	0.0105614	ATP9B
rs187269353	2	13670135	C	T	1.69E-08	0.0236091	TRIB2
rs547141653	15	30237979	A	AACACAC ACAC	1.74E-08	0.000348346	/
rs9829418	3	77424153	G	A	1.86E-08	2.94E-05	ROBO2
rs72638373	13	95330457	T	G	1.89E-08	0.00427868	SOX21
rs2086051	4	18478543	A	G	2.06E-08	1.73E-07	LCORL
rs73094392	4	18466752	G	C	2.06E-08	1.96E-07	LCORL
rs148161662	3	81711532	G	A	2.07E-08	0.000264396	GBE1
rs72638377	13	95331826	A	C	2.13E-08	0.00387939	SOX21
rs184710548	7	152535893	G	A	2.21E-08	0.0351477	ACTR3B
rs116638258	3	81869054	A	G	2.26E-08	0.000174517	GBE1
rs78856971	4	68672846	G	T	2.33E-08	8.77E-06	TMPRSS11D
rs41525951	4	68669704	C	T	2.34E-08	8.61E-06	TMPRSS11D
rs114698375	2	106054656	C	G	2.71E-08	0.000602855	FHL2
rs12403496	1	48484051	T	C	2.95E-08	0.00764491	CYP46A4P
rs560272307	18	49267154	A	G	2.99E-08	0.000844276	RPS8P3
rs115594478	3	79701623	A	G	3.04E-08	0.000856885	ROBO1
rs73136325	3	98196626	A	T	3.06E-08	0.0272117	OR5K2
rs116782885	3	82258990	C	T	3.30E-08	0.00495869	GBE1
rs79163829	2	11538351	A	G	3.34E-08	1.36E-06	E2F6
rs74631028	16	12789955	C	T	3.37E-08	0.036485	CPPED1
rs192415402	1	214563395	T	C	3.54E-08	2.10E-07	PTPN14
rs139424815	10	3109286	G	C	3.55E-08	0.000286175	PFKP
rs117793374	18	49313675	C	T	3.62E-08	0.000106258	RPS8P3
rs77814262	3	81865372	G	A	3.62E-08	0.000392649	GBE1
rs11638904	15	37309303	G	C	3.81E-08	0.000109191	MEIS2
rs146398630	11	67997388	T	C	4.08E-08	0.00014852	SUV420H1
rs138004333	6	69596677	C	T	4.13E-08	0.00265024	ADGRB3
rs35381071	4	68694828	T	TG	4.21E-08	0.000316889	TMPRSS11D
rs192290563	11	57619332	C	T	4.24E-08	1.17E-09	CTNND1
4:107007289_C A C	4	107007289	C	CA	4.26E-08	0.00444221	/
rs143089210	8	11401503	A	G	4.27E-08	0.0215525	BLK
rs144173106	15	100793456	GCCTAC ACT	G	4.28E-08	0.0302281	ADAMTS17
rs4938877	11	57629180	A	G	4.39E-08	1.16E-09	OR5BA1P
rs12215234	6	49640046	G	A	4.45E-08	0.00721398	RHAG
rs694158	13	78132151	G	A	4.52E-08	1.22E-05	SCEL
rs117304140	9	102014351	C	A	4.52E-08	0.00163237	SEC61B
rs183917631	14	86791060	A	G	5.06E-08	2.30E-09	FLRT2
rs542897254	7	152534260	CA	C	5.23E-08	0.0350421	ACTR3B
rs36013500	2	152850229	T	C	5.63E-08	7.40E-05	CACNB4
rs71451165	11	29405492	T	C	5.66E-08	0.000854346	RP11-460B17.1
rs180916209	7	152536114	T	C	5.89E-08	0.0434681	ACTR3B

rs114250585	4	68667630	A	G	5.94E-08	1.83E-05	<i>TMPRSS11D</i>
rs115935519	3	19333451	T	C	6.43E-08	1.56E-05	<i>KCNH8</i>
rs79514712	3	81072180	G	C	6.82E-08	0.0126295	<i>RP11-481N16.1</i>
rs115709053	1	37596458	T	G	7.39E-08	0.000278912	<i>GRIK3</i>
rs74440514	15	100794511	A	G	7.63E-08	0.0415094	<i>ADAMTS17</i>
rs76619482	17	69067238	G	A	7.95E-08	0.000236923	<i>LOC124685</i>
rs114069551	4	71335556	G	A	8.00E-08	0.0104434	<i>MUC7</i>
rs78470634	4	162171584	T	C	8.79E-08	0.00106042	<i>FSTL5</i>
rs117827035	15	100792136	A	G	8.80E-08	0.0303534	<i>ADAMTS17</i>
rs74750249	6	5459680	A	C	8.89E-08	4.05E-06	<i>FARS2</i>
rs79749840	4	162169308	T	C	8.95E-08	0.00106522	<i>FSTL5</i>
rs72996103	18	76933689	A	G	8.95E-08	0.00546535	<i>ATP9B</i>
rs76884626	15	100795559	C	G	8.97E-08	0.030336	<i>ADAMTS17</i>
rs75760538	15	100793065	C	T	8.98E-08	0.0303519	<i>ADAMTS17</i>
rs74771048	15	100793128	G	T	8.99E-08	0.0303538	<i>ADAMTS17</i>
rs117053084	15	100794780	C	G	9.00E-08	0.0303164	<i>ADAMTS17</i>
rs117268382	15	100793356	C	A	9.00E-08	0.0302916	<i>ADAMTS17</i>
rs78312362	10	119061917	T	C	9.25E-08	6.57E-06	<i>PDZD8</i>
rs181745281	10	119072662	C	T	9.32E-08	6.64E-06	<i>PDZD8</i>
rs74393558	1	180154806	G	C	9.33E-08	0.00455335	<i>QSOX1</i>
rs113805345	2	199331728	G	T	9.38E-08	0.0311249	<i>PLCL1</i>
rs117669701	15	100796714	T	C	9.39E-08	0.0289186	<i>ADAMTS17</i>
rs76071867	17	10907886	T	G	9.63E-08	0.000257374	<i>SHISA6</i>
rs138580469	15	100787030	G	A	9.65E-08	0.040726	<i>ADAMTS17</i>
rs117098802	15	54221040	G	A	1.04E-07	7.94E-09	<i>UNC13C</i>
rs138332173	15	54215950	T	C	1.10E-07	7.83E-09	<i>UNC13C</i>
rs569519981	3	63749870	G	A	1.14E-07	0.000121297	<i>AC136289.1</i>
rs116138253	21	46675571	T	C	1.17E-07	0.001852	<i>POFUT2</i>
rs6832397	4	190200123	A	G	1.24E-07	0.000380541	<i>RP11-756P10.3</i>
rs140890408	14	36161825	A	G	1.28E-07	0.00133696	<i>RALGAPA1</i>
rs76063481	21	28728691	T	C	1.32E-07	1.09E-06	<i>GPX1P2</i>
rs114501114	3	80278910	A	G	1.33E-07	0.000956861	<i>HNRNPA3P8</i>
rs75057723	20	13156449	C	A	1.35E-07	9.63E-07	<i>ISM1</i>
rs4938874	11	57422341	A	G	1.39E-07	1.92E-09	<i>CLP1</i>
rs147601957	4	190180163	C	T	1.41E-07	0.000399386	<i>RP11-756P10.3</i>
rs138959917	4	190176612	G	A	1.43E-07	0.000402175	<i>RP11-756P10.3</i>
rs150427941	4	107253824	CTATAG A	C	1.43E-07	0.00538083	<i>AIMP1</i>
rs554441230	4	190174901	ATTATT CAAATA TATTGA ATAATA TTAAAA TTATTC AAAAC T	A	1.45E-07	0.000405469	<i>RP11-756P10.3</i>
rs17571316	15	30173956	T	C	1.46E-07	2.19E-05	<i>TJP1</i>
4:190205605_G A G	4	190205605	G	GA	1.47E-07	0.000111851	/
rs7696747	4	107296413	C	A	1.51E-07	0.00198504	<i>AIMP1</i>
rs1971345	3	15400526	A	G	1.53E-07	0.048003	<i>SH3BP5</i>
rs79537527	4	189776630	A	G	1.55E-07	1.05E-05	<i>RP11-756P10.3</i>
rs138345778	4	107092786	GATA	G	1.57E-07	0.00473157	/
rs141135105	4	190228491	T	C	1.59E-07	0.000444298	<i>RP11-756P10.3</i>
rs150173241	4	190227592	A	G	1.59E-07	0.000428428	<i>RP11-756P10.3</i>
rs115329882	4	190230829	G	A	1.60E-07	0.000447357	<i>RP11-756P10.3</i>
rs10019578	4	190233217	A	G	1.60E-07	0.000459188	<i>RP11-756P10.3</i>
rs11097917	4	107096480	T	C	1.61E-07	0.00501066	<i>TBCK</i>

rs12511305	4	107098336	A	G	1.62E-07	0.00502501	TBCK
rs11097919	4	107099131	C	T	1.63E-07	0.00502919	TBCK
rs12499891	4	107097909	G	T	1.63E-07	0.00502661	TBCK
rs7661565	4	107097404	A	G	1.63E-07	0.00502664	TBCK
rs1186457	7	22027745	C	A	1.65E-07	0.00247622	RAPGEF5
rs12498715	4	107146625	T	G	1.69E-07	0.00428228	TBCK
rs7697673	4	107296620	T	G	1.70E-07	0.0016979	AIMP1
rs559768321	4	190174904	CAATTA A	C	1.74E-07	0.000406313	RP11-756P10.3
rs4747620	10	28732111	G	A	1.75E-07	7.04E-07	WAC
rs147733826	1	214921243	A	C	1.76E-07	0.00917917	CENPF
rs368131533	4	190192067	A	G	1.83E-07	0.000424429	RP11-756P10.3
rs373839230	4	190224627	A	G	1.85E-07	0.000289415	RP11-756P10.3
rs201980162	4	107137326	A	G	1.89E-07	0.00431588	TBCK
rs114991996	3	79729232	C	T	1.89E-07	0.0139792	ROBO1
rs34329524	4	179429967	A	G	1.94E-07	0.0176402	RP11-84H6.1
rs117029312	15	30264181	A	G	1.95E-07	0.000615874	TJP1
rs149126506	19	35911133	C	G	1.97E-07	0.000415994	FFAR2
rs72878537	4	107220049	G	A	1.98E-07	0.00440575	TBCK
rs6533245	4	107202935	T	C	2.02E-07	0.00459681	TBCK
rs7786820	7	139006963	A	G	2.06E-07	0.00914387	UBN2
rs7665946	4	107189328	C	T	2.07E-07	0.00446022	TBCK
rs3775090	4	107168520	T	G	2.08E-07	0.00446912	TBCK
rs17274248	4	107205662	T	C	2.08E-07	0.00450787	TBCK
rs17333732	4	107205009	T	C	2.08E-07	0.0045012	TBCK
rs578075416	2	11541938	C	A	2.08E-07	6.39E-08	E2F6
rs11097925	4	107161493	G	A	2.08E-07	0.00448273	TBCK
rs17333879	4	107220426	A	G	2.09E-07	0.00451395	TBCK
rs75055072	4	107201362	A	T	2.09E-07	0.00451168	TBCK
rs113142685	4	107210783	G	A	2.09E-07	0.0045155	TBCK
rs12500775	4	107213501	G	C	2.09E-07	0.0045155	TBCK
rs111450955	4	107215694	A	G	2.09E-07	0.0045155	TBCK
rs72876590	4	107204499	A	T	2.09E-07	0.00451742	TBCK
rs72876592	4	107204776	C	T	2.09E-07	0.00451742	TBCK
rs34899289	4	107194390	G	A	2.10E-07	0.00451098	TBCK
rs12510058	4	107188835	C	T	2.10E-07	0.0045043	TBCK
rs12645698	4	107188432	T	C	2.10E-07	0.0045043	TBCK
rs61544154	4	107189771	T	C	2.10E-07	0.0045043	TBCK
rs75814353	4	107200154	T	C	2.10E-07	0.00451072	TBCK
rs12639869	4	107176104	A	C	2.10E-07	0.00450895	TBCK
rs12642059	4	107173793	A	C	2.10E-07	0.00450895	TBCK
rs56333662	4	107177196	T	A	2.10E-07	0.00450895	TBCK
rs117699451	21	28716047	T	A	2.11E-07	1.28E-06	GPX1P2
rs79468403	4	107074786	C	T	2.11E-07	0.00420242	TBCK
rs80112814	4	107073081	C	A	2.11E-07	0.0042044	TBCK
rs151186466	4	107067567	G	A	2.11E-07	0.00420818	TBCK
rs7688411	4	107189665	T	C	2.11E-07	0.00495156	TBCK
rs12646263	4	107083746	T	C	2.11E-07	0.00420615	TBCK
rs143999404	4	107137621	A	C	2.11E-07	0.00432357	TBCK
rs190663640	4	107135466	A	G	2.11E-07	0.00432357	TBCK
rs4466113	4	107082043	C	T	2.11E-07	0.0042074	TBCK
rs12647078	4	107084333	A	G	2.11E-07	0.00420945	TBCK
rs17273093	4	107086739	C	G	2.11E-07	0.00421077	TBCK
rs78066595	4	107113954	GT	G	2.12E-07	0.00432564	TBCK
rs11097914	4	107070806	C	G	2.12E-07	0.00468405	TBCK
rs59784613	4	107073523	G	A	2.12E-07	0.00467338	TBCK
rs6816043	4	190217278	A	G	2.12E-07	0.000415785	RP11-756P10.3
rs6533246	4	107203084	T	C	2.13E-07	0.00500295	TBCK

rs72876594	4	107207527	T	C	2.13E-07	0.0049956	TBCK
rs7688008	4	107216896	C	G	2.13E-07	0.00501428	TBCK
rs56009469	4	107180715	G	C	2.13E-07	0.0049983	TBCK
rs7662291	4	107185593	A	G	2.13E-07	0.00499607	TBCK
rs7673949	4	107194036	A	G	2.13E-07	0.00499607	TBCK
rs7662395	4	107185855	T	C	2.13E-07	0.00498874	TBCK
rs7669212	4	107186712	A	G	2.13E-07	0.00498874	TBCK
4:107160985_TA A T	4	107160985	T	TAA	2.13E-07	0.00446372	/
rs56231393	4	107180864	T	G	2.14E-07	0.00499383	TBCK
rs7662219	4	107185759	A	C	2.14E-07	0.00499945	TBCK
rs77545165	4	107123821	G	C	2.14E-07	0.00427461	TBCK
rs6818626	4	107123463	C	T	2.14E-07	0.00427835	TBCK
rs12641015	4	107172182	T	C	2.14E-07	0.00497862	TBCK
rs9685018	4	107124824	T	C	2.14E-07	0.00430275	TBCK
rs7667719	4	107186255	C	A	2.15E-07	0.0049974	TBCK
rs72893620	4	107187914	A	G	2.15E-07	0.00500434	TBCK
rs111765566	3	76098110	C	T	2.16E-07	5.97E-05	ROBO2
rs34193646	4	107151929	T	C	2.16E-07	0.00443563	TBCK
rs55634475	4	107067750	C	T	2.16E-07	0.00467777	TBCK
rs79051739	4	107150530	C	T	2.16E-07	0.00443874	TBCK
rs12512966	4	107082411	C	A	2.16E-07	0.00467773	TBCK
rs11097916	4	107087390	T	C	2.16E-07	0.00468093	TBCK
rs12512877	4	107145600	A	G	2.17E-07	0.00443996	TBCK
rs77722499	5	119834179	T	C	2.17E-07	0.0159772	PRR16
rs141144669	4	107086150	AATTT	A	2.17E-07	0.00442988	/
rs140333632	4	107127393	TG	T	2.18E-07	0.0045561	/
rs12641037	4	107142052	A	G	2.18E-07	0.004434	TBCK
rs202205774	4	107136248	C	T	2.18E-07	0.00480009	TBCK
rs12504704	4	107099563	G	A	2.19E-07	0.00482936	TBCK
rs56329826	4	107121031	C	T	2.19E-07	0.00475072	TBCK
rs12506062	4	107115960	G	A	2.19E-07	0.00475101	TBCK
rs12507429	4	107117686	C	A	2.19E-07	0.00475101	TBCK
rs17273445	4	107115665	A	C	2.19E-07	0.00475101	TBCK
rs6818197	4	107123210	C	T	2.19E-07	0.00478205	TBCK
rs535504686	6	151165899	GT	G	2.19E-07	1.03E-06	PLEKHG1
rs6822692	4	107108164	T	C	2.20E-07	0.00474076	TBCK
rs2290607	4	107113299	G	A	2.20E-07	0.00474905	TBCK
rs6533240	4	107112812	C	G	2.20E-07	0.00474929	TBCK
rs147343707	4	107110519	AAAAG	A	2.20E-07	0.00474569	TBCK
rs12503753	4	107068827	G	A	2.20E-07	0.0048254	TBCK
rs117909654	21	32192981	T	C	2.28E-07	0.00040508	KRTAP8-1
rs35317905	4	107199237	ATG	A	2.29E-07	0.00480659	TBCK
rs3840308	4	107254996	GCT	G	2.32E-07	0.00476529	AIMP1
rs769072295	4	107216072	C	CTA	2.32E-07	0.00429284	/
rs6831665	4	107222086	T	C	2.36E-07	0.00490052	TBCK
rs142748972	17	33616733	T	C	2.37E-07	0.00328119	SLFN5
4:107152379_G A G	4	107152379	G	GA	2.37E-07	0.00466463	/
rs56833325	4	107222665	T	C	2.38E-07	0.00491812	TBCK
rs73002025	18	76988674	G	A	2.41E-07	0.039556	ATP9B
rs75511400	2	34919372	A	G	2.44E-07	0.000131167	AC013442.1
rs73154206	7	143086010	T	C	2.45E-07	1.42E-06	ZYX
rs11947335	4	107270658	A	G	2.47E-07	0.00505116	AIMP1
rs17456104	9	131948229	C	T	2.48E-07	3.32E-05	IER5L
rs34622492	8	137328025	G	C	2.54E-07	0.000144385	KHDRBS3
rs78708480	8	137329881	T	C	2.54E-07	0.00015342	KHDRBS3
rs143774502	15	77742598	A	G	2.55E-07	0.00707433	HMG20A

rs62380616	5	150175414	A	G	2.57E-07	7.36E-05	SMIM3
rs7696662	4	107243414	G	A	2.58E-07	0.00654967	AIMP1
rs11940160	4	107247367	G	A	2.59E-07	0.00596038	AIMP1
4:107246676_TA T	4	107246676	T	TA	2.59E-07	0.00511889	/
rs12732933	1	76708130	A	T	2.60E-07	0.000184441	ST6GALNAC3
rs113059611	3	66724521	G	A	2.60E-07	7.70E-05	KBTBD8
rs201062605	4	107215353	CT	C	2.60E-07	0.0102616	TBCK
rs7674796	4	107243261	C	T	2.62E-07	0.00606716	AIMP1
rs147232944	4	107241983	C	T	2.62E-07	0.00665533	AIMP1
rs34144884	8	137322763	C	T	2.63E-07	0.00015305	KHDRBS3
rs35976733	8	137321672	T	C	2.64E-07	0.000153232	KHDRBS3
rs34229749	8	137321701	A	C	2.64E-07	0.000153243	KHDRBS3
rs71530153	8	137322752	A	G	2.64E-07	0.000153006	KHDRBS3
rs34329477	8	137318877	G	A	2.64E-07	0.000152007	KHDRBS3
rs76188442	20	7720259	G	A	2.64E-07	0.00229158	BMP2
rs10433894	4	107251400	G	C	2.66E-07	0.00665007	AIMP1
rs6819224	4	107250658	A	G	2.66E-07	0.00665016	AIMP1
rs35930320	8	137324423	C	T	2.66E-07	0.000153538	KHDRBS3
rs71530154	8	137325505	A	G	2.66E-07	0.000153483	KHDRBS3
rs34545445	8	137326674	T	C	2.66E-07	0.000153489	KHDRBS3
rs3737498	4	107246136	A	C	2.66E-07	0.00665476	AIMP1
rs35667165	8	137337508	T	C	2.68E-07	0.000158183	KHDRBS3
rs35471969	8	137338283	C	T	2.68E-07	0.000158588	KHDRBS3
rs13269261	8	137338230	A	C	2.68E-07	0.000158587	KHDRBS3
rs13261516	8	137346070	G	A	2.71E-07	0.00016745	KHDRBS3
rs34118496	8	137343203	G	T	2.71E-07	0.000167331	KHDRBS3
rs13259351	8	137344523	T	C	2.71E-07	0.000166853	KHDRBS3
rs114021007	5	155373160	T	C	2.71E-07	5.86E-05	SGCD
4:107241814_AT A	4	107241814	A	AT	2.72E-07	0.00590029	/
rs6819742	4	107268016	C	A	2.74E-07	0.00617543	AIMP1
8:137347539_TT TTC T	8	137347539	T	TTTTTC	2.75E-07	0.000420776	/
rs76356450	8	137329763	T	C	2.77E-07	0.000153504	KHDRBS3
rs12642454	4	107266883	G	A	2.78E-07	0.00627394	AIMP1
rs547516699	7	152518557	GAA	G	2.78E-07	0.0128225	/
rs6828660	4	107269794	A	G	2.78E-07	0.00626689	AIMP1
rs3805410	4	107268949	G	A	2.78E-07	0.0062702	AIMP1
rs3805411	4	107269053	G	A	2.78E-07	0.00627042	AIMP1
rs3805409	4	107266401	G	C	2.78E-07	0.00628008	AIMP1
rs532856191	5	37589337	C	T	2.78E-07	0.000249594	WDR70
rs34933283	8	137317058	C	T	2.79E-07	0.000164639	KHDRBS3
rs6858391	4	107261654	A	G	2.79E-07	0.00636521	AIMP1
rs10516534	4	107256703	G	T	2.79E-07	0.00682913	AIMP1
rs970284	20	41280429	G	A	2.79E-07	0.00598651	PTPRT
rs11097928	4	107263868	T	A	2.80E-07	0.00629013	AIMP1
rs55753411	4	107264803	G	A	2.80E-07	0.00629143	AIMP1
rs11097927	4	107262793	C	G	2.80E-07	0.00629839	AIMP1
rs6831032	4	107257696	A	G	2.81E-07	0.00632044	AIMP1
rs55726133	4	107255868	A	G	2.82E-07	0.00633	AIMP1
rs113866132	7	132050334	C	T	2.83E-07	0.00031118	PLXNA4
4:107173543_TT AG T	4	107173543	T	TTAG	2.84E-07	0.00388941	/
rs74509579	8	137316372	A	G	2.85E-07	0.000172328	KHDRBS3
rs35106727	8	137312815	C	T	2.90E-07	0.000176101	KHDRBS3
4:107253771_C AT C	4	107253771	C	CAT	2.99E-07	0.00729124	/

rs113848226	3	66721559	T	G	3.06E-07	7.69E-05	KBTBD8
rs145237635	17	1333895	A	G	3.10E-07	0.00035789	CRK
rs148777093	20	55681131	T	C	3.12E-07	0.000120898	BMP7
rs11461633	4	107227770	TC	T	3.13E-07	0.00389626	TBCK
rs2425506	20	41285430	C	T	3.13E-07	0.00222869	PTPRT
rs144017138	4	107233622	TGAG	T	3.14E-07	0.00456107	TBCK
rs76506384	7	54312950	T	G	3.16E-07	0.00106517	SLC25A5P3
rs6856408	4	107236868	G	A	3.20E-07	0.00623843	AIMP1
rs3762947	4	107236648	G	A	3.20E-07	0.00623901	TBCK
rs117157297	18	49722182	G	A	3.23E-07	1.35E-06	DCC
rs6849341	4	107235750	G	A	3.29E-07	0.0054998	TBCK
rs138663011	11	68106952	G	A	3.29E-07	6.94E-06	LRP5
rs118173208	15	72043489	G	A	3.44E-07	0.0111694	THSD4
rs12693208	2	152875657	C	T	3.44E-07	9.63E-05	CACNB4
rs145040582	1	105661128	AC	A	3.46E-07	0.0157882	RP11-414B7.1
rs59228887	4	107273592	A	G	3.50E-07	0.00618928	AIMP1
rs3762945	4	107235064	C	T	3.50E-07	0.00546816	TBCK
rs7674460	4	107275156	T	A	3.53E-07	0.00621397	AIMP1
rs140904574	8	100798178	T	C	3.55E-07	5.02E-07	VPS13B
rs78685486	20	16731073	A	T	3.63E-07	0.000182559	OTOR
rs11930970	4	107276962	A	G	3.71E-07	0.00634853	AIMP1
rs374289606	15	100763076	A	G	3.71E-07	0.0463478	ADAMTS17
15:100763069_A G A	15	100763069	A	AG	3.73E-07	0.0463477	/
rs142796415	3	194590997	A	C	3.75E-07	0.0106205	XXYL1
rs1014966	6	5452328	T	G	3.75E-07	1.04E-06	FARS2
rs61256759	4	107234345	A	C	3.78E-07	0.00544355	TBCK
rs560375417	4	142366402	A	T	3.81E-07	0.00272159	IL15
rs7678749	4	107278978	C	T	3.82E-07	0.00698302	AIMP1
rs998914	3	112949081	A	G	3.82E-07	3.85E-05	BOC
rs12500295	4	107278166	G	C	3.85E-07	0.00703886	AIMP1
rs147640667	17	29581211	A	G	3.85E-07	0.0221269	NF1
rs10185392	2	143541696	A	G	3.85E-07	1.79E-05	AC092578.1
rs12645490	4	107279482	A	T	3.86E-07	0.00698731	AIMP1
rs189170779	16	50459358	C	A	3.87E-07	0.000135268	NKD1
rs75300145	6	5451845	C	T	3.90E-07	1.09E-06	FARS2
rs73839455	4	107281769	C	T	3.93E-07	0.00624417	AIMP1
rs73839422	4	107233658	C	T	3.93E-07	0.0053879	TBCK
rs6814166	4	107237395	T	C	3.94E-07	0.00568388	TBCK
rs62155760	2	84407782	G	C	3.95E-07	6.55E-06	FUNDC2P2
rs73839456	4	107281995	C	A	3.96E-07	0.0062079	AIMP1
rs7678943	4	107279097	A	T	3.99E-07	0.00656949	AIMP1
rs73719611	6	5457496	C	T	3.99E-07	3.91E-07	FARS2
rs11004662	10	56757641	T	C	4.00E-07	0.000788493	PCDH15
rs11383965	4	107269579	CT	C	4.01E-07	0.0179387	AIMP1
rs116111867	4	106993180	T	C	4.10E-07	0.00601331	TBCK
rs200745531	2	71914197	AC	A	4.11E-07	0.0131143	DYSF
rs57648108	13	95328589	G	T	4.11E-07	0.0198272	SOX21
2:222590580_AT AT A	2	222590580	A	ATAT	4.16E-07	0.000435331	/
rs74154263	10	102778137	A	G	4.23E-07	0.000406954	PDZD7
rs7654865	4	107279450	T	C	4.27E-07	0.00712765	AIMP1
rs11706373	3	75480481	T	C	4.27E-07	0.0259768	FAM86DP
rs17259572	4	106961234	A	G	4.39E-07	0.00744901	TBCK
rs140069950	10	16766411	C	T	4.41E-07	0.000299557	RSU1
rs2425505	20	41284782	C	T	4.51E-07	0.0023241	PTPRT
rs72876575	4	107194607	G	A	4.54E-07	0.0049337	TBCK

4:107226452_G AAT G	4	107226452	G	GAAT	4.56E-07	0.00443467	/
rs34614728	8	137339378	T	C	4.60E-07	0.000363013	KHDRBS3
rs114696892	3	77398283	A	G	4.61E-07	3.37E-06	ROBO2
rs77210717	7	147222039	G	A	4.61E-07	7.25E-05	CNTNAP2
rs76781666	8	137339421	C	T	4.62E-07	0.000323276	KHDRBS3
rs78320450	8	137338984	A	T	4.62E-07	0.000365017	KHDRBS3
rs35677837	8	137339292	A	G	4.62E-07	0.000365018	KHDRBS3
rs115348194	8	137339135	T	G	4.62E-07	0.00036502	KHDRBS3
rs79204859	8	137339420	A	G	4.62E-07	0.000365908	KHDRBS3
rs2425504	20	41284750	C	T	4.62E-07	0.00237814	PTPRT
rs142051800	7	88422978	C	A	4.63E-07	6.12E-07	ZNF804B
rs117997371	11	1724442	T	C	4.63E-07	0.000119652	KRTAP5-6
rs7675728	4	106951814	T	G	4.64E-07	0.0104152	TBCK
rs9684658	4	107182809	T	C	4.69E-07	0.004856	TBCK
rs139856543	14	86806395	C	T	4.70E-07	7.98E-09	FLRT2
rs111887782	3	66716574	C	G	4.72E-07	0.000128699	KBTBD8
rs111702699	7	20287336	T	C	4.74E-07	0.00265207	ITGB8
rs151245473	3	30689332	T	G	4.75E-07	0.0168623	TGFBR2
rs139403898	1	70001210	A	G	4.78E-07	0.00271872	LRRC7
rs372567922	8	13564360	CA	C	4.82E-07	0.00394788	RP11-436P7.1
rs73201271	4	2218685	G	A	4.84E-07	0.00234439	POLN
rs7668477	4	107133452	T	G	4.85E-07	0.00421943	TBCK
rs151147878	11	111676326	G	A	4.88E-07	0.00353711	ALG9
rs144643355	4	190296814	C	T	4.94E-07	0.00236709	RP11-756P10.3
rs114314455	4	190295131	T	C	4.94E-07	0.00236723	RP11-756P10.3
rs17036613	4	107133919	G	A	4.95E-07	0.00469798	TBCK
rs139017098	4	190256885	C	T	4.98E-07	0.00267694	RP11-756P10.3
rs77566898	4	190275760	A	G	4.98E-07	0.00238403	RP11-756P10.3
rs13178893	5	97936747	G	T	5.01E-07	0.00810805	CTBP2P4
rs79869782	3	127687765	G	A	5.01E-07	3.19E-06	KBTBD12
rs150793912	6	134283787	G	A	5.03E-07	1.27E-06	TBPL1
rs117294527	15	100764857	G	C	5.11E-07	0.0279588	ADAMTS17
rs190242095	4	190270325	A	G	5.17E-07	0.00309173	RP11-756P10.3
rs116299110	4	190259853	A	G	5.18E-07	0.00267587	RP11-756P10.3
rs537653234	4	190277007	A	G	5.18E-07	0.00295728	RP11-756P10.3
rs201889407	4	190275002	AT	A	5.18E-07	0.00300007	RP11-756P10.3
rs79022281	4	190280594	T	C	5.18E-07	0.0023854	RP11-756P10.3
rs138320087	4	190248758	A	C	5.19E-07	0.00267872	RP11-756P10.3
rs4926714	1	48512198	A	T	5.20E-07	0.020743	CYP46A4P
rs151144493	6	21731032	G	T	5.22E-07	5.69E-06	RP11-524C21.1
rs4645291	4	107231783	C	T	5.26E-07	0.00546475	TBCK
rs138282012	4	107219776	CA	C	5.28E-07	0.00679005	TBCK
rs145212500	3	80724920	A	G	5.32E-07	0.000312568	RP11-481N16.1
rs9565356	13	78159624	G	A	5.32E-07	2.28E-05	SCEL
4:190302073_C AG C	4	190302073	C	CAG	5.41E-07	0.00246679	/
rs147263165	1	224666974	A	G	5.47E-07	0.00238656	CNIH3
rs10232445	7	26622985	A	G	5.50E-07	0.000220599	KIAA0087
rs760457	21	46329312	C	T	5.52E-07	2.66E-05	ITGB2
4:107202469_TT TG T	4	107202469	T	TTTG	5.53E-07	0.0191777	/
rs12644596	4	107227180	T	C	5.59E-07	0.00531498	TBCK
rs112439126	4	107230534	T	A	5.61E-07	0.0053269	TBCK
rs4607300	4	107228521	C	T	5.71E-07	0.00533085	TBCK
rs6827816	4	107230363	C	T	5.73E-07	0.00534277	TBCK
rs17050261	2	59804348	C	G	5.78E-07	0.0166778	BCL11A
rs74285102	4	107227049	A	G	5.83E-07	0.00590382	TBCK

rs67417943	7	139006581	G	A	5.84E-07	0.0290948	UBN2
rs74132557	1	180134220	A	G	5.86E-07	0.019826	QSOX1
rs184858532	7	44908411	T	C	5.91E-07	0.00313825	H2AFV
rs79747906	18	3967852	C	T	5.98E-07	0.00688738	DLGAP1
rs566087594	8	61840272	G	T	5.99E-07	0.00150988	AC022182.2
rs12507867	4	106947003	G	A	6.00E-07	0.0116351	TBCK
rs62072466	17	18115544	A	T	6.09E-07	0.000206281	ALKBH5
rs73058158	3	36074147	T	A	6.20E-07	0.00227653	AC104308.2
rs77691720	6	5447345	A	G	6.26E-07	1.85E-06	FARS2
rs150011465	4	94502148	T	C	6.27E-07	0.000464064	GRID2
rs73172294	3	179440186	G	A	6.35E-07	0.000184722	USP13
rs62072468	17	18118179	G	A	6.35E-07	0.000221659	ALKBH5
rs115808848	1	117094189	A	G	6.36E-07	7.90E-05	CD58
rs77393553	1	48509897	C	G	6.41E-07	0.0207995	CYP46A4P
rs142664854	21	28083372	C	T	6.49E-07	9.03E-06	ADAMTS1
rs4926713	1	48506768	G	A	6.60E-07	0.0208126	CYP46A4P
rs4927319	1	48507085	A	G	6.63E-07	0.0208076	CYP46A4P
rs1563373	17	18114228	A	G	6.65E-07	0.0002226	ALKBH5
rs62072465	17	18114494	G	C	6.65E-07	0.0002226	ALKBH5
rs538443508	11	8727602	C	G	6.65E-07	1.66E-06	DENND2B
rs73058197	3	36103169	C	T	6.67E-07	0.00506914	AC104308.2
rs183319053	7	44910466	G	A	6.68E-07	0.00359287	H2AFV
rs73113148	7	44891158	G	A	6.69E-07	0.00361557	H2AFV
rs73113154	7	44894986	A	G	6.69E-07	0.00359508	H2AFV
rs7666823	4	163186240	G	A	6.70E-07	0.00468304	FSTL5
rs969262	20	41284395	G	T	6.72E-07	0.00889046	PTPRT
rs117962597	21	45621888	A	G	6.77E-07	7.81E-07	ICOSLG
1:48497395_AA GT_A	1	48497395	A	AAGT	6.89E-07	0.0206076	/
rs9308024	4	162207646	T	C	7.05E-07	0.000300133	FSTL5
rs115244735	4	35817219	G	A	7.07E-07	0.000580064	ARAP2
rs147818180	6	5446302	C	G	7.09E-07	2.14E-06	FARS2
rs4407172	19	55025471	A	C	7.16E-07	0.00620015	LAIR2
rs77029736	1	48493305	A	G	7.20E-07	0.0203021	CYP46A4P
rs35469407	5	26920982	A	G	7.22E-07	0.0210139	CDH9
rs151299022	1	117089537	A	G	7.29E-07	7.27E-05	CD58
rs80273221	6	5446023	G	C	7.30E-07	2.21E-06	FARS2
rs13225744	7	154521619	G	A	7.36E-07	0.0239472	DPP6
rs186678210	7	27335042	T	C	7.39E-07	4.70E-08	RPL35P4
rs144117640	4	162197644	A	G	7.43E-07	0.00311181	FSTL5
rs16960983	17	18104568	A	T	7.43E-07	0.000426292	ALKBH5
rs1891221	1	70006329	T	G	7.44E-07	0.00350854	LRRC7
rs115773911	2	159243289	T	C	7.45E-07	7.12E-07	CCDC148
rs150546162	4	60585598	A	G	7.48E-07	5.40E-06	RP11-593F5.1
rs77900939	15	100761083	G	A	7.51E-07	0.0236248	ADAMTS17
rs78834324	3	129162492	C	T	7.55E-07	0.0191031	IFT122
rs117460909	7	4244193	T	A	7.56E-07	3.36E-07	SDK1
rs631664	20	60940324	G	A	7.56E-07	0.029738	LAMA5
rs16960990	17	18108601	G	A	7.58E-07	0.000417733	ALKBH5
rs111589301	17	18116773	A	G	7.58E-07	0.000221969	ALKBH5
rs11657194	17	18092588	G	T	7.60E-07	0.000447662	ALKBH5
rs11653988	17	18088833	T	C	7.61E-07	0.000454754	ALKBH5
rs79963102	21	16471813	T	G	7.64E-07	0.00192288	NRIP1
rs6121995	20	60940004	T	C	7.70E-07	0.030108	LAMA5
rs8069094	17	18096528	T	C	7.81E-07	0.000439298	ALKBH5
rs72955190	2	59804805	G	T	7.86E-07	0.0078788	BCL11A
rs16960986	17	18108562	A	G	7.87E-07	0.000412427	ALKBH5
rs11655588	17	18107451	G	A	7.88E-07	0.000422895	ALKBH5

rs11655797	17	18107850	T	C	7.88E-07	0.000422895	ALKBH5
rs58441148	17	18106498	A	T	7.88E-07	0.000425809	ALKBH5
rs62072464	17	18108314	C	T	7.89E-07	0.000423241	ALKBH5
rs11868832	17	18105547	G	A	7.90E-07	0.000426066	ALKBH5
rs59602121	2	59805438	G	A	7.90E-07	0.00807529	BCL11A
rs16960980	17	18100858	A	G	7.91E-07	0.000431974	ALKBH5
rs11654177	17	18106214	T	C	7.91E-07	0.000425809	ALKBH5
rs11871491	17	18105656	C	T	7.93E-07	0.000426399	ALKBH5
10:56809968_A GGGTTAGAAG TCCT A	10	56809968	A	AGGGTTA GAAGTCC T	7.94E-07	0.00139368	/
rs11078412	17	18100618	G	A	7.94E-07	0.000432339	ALKBH5
rs729269	7	154512110	A	G	8.00E-07	0.0179532	DPP6
rs77175620	18	69490258	T	C	8.04E-07	0.000364835	RP11-723G8.2
rs66482965	7	139009438	T	C	8.05E-07	0.0146322	UBN2
rs144127908	1	68569437	A	G	8.08E-07	0.00284302	WLS
rs75121681	1	180134075	A	G	8.09E-07	0.0181799	QSOX1
rs62525907	8	61840814	A	G	8.09E-07	0.00327516	AC022182.2
rs3767175	1	180156251	T	C	8.11E-07	0.015045	QSOX1
rs75281874	1	180161444	A	G	8.13E-07	0.0150861	QSOX1
rs62525909	8	61843039	C	A	8.14E-07	0.00350546	AC022182.2
rs769692383	2	152844791	C	CT	8.15E-07	0.00154654	CACNB4
rs3767181	1	180152242	A	G	8.15E-07	0.0150873	QSOX1
rs60285171	17	18110869	T	C	8.18E-07	0.000428779	ALKBH5
rs16960996	17	18110559	G	A	8.18E-07	0.000428749	ALKBH5
rs565395809	21	24722029	G	A	8.19E-07	3.97E-08	EEF1A1P1
rs3088233	17	18112675	T	C	8.20E-07	0.000425951	ALKBH5
rs13284	17	18112130	T	C	8.21E-07	0.000425878	ALKBH5
rs1563371	17	18111793	T	C	8.25E-07	0.000446681	ALKBH5
rs141657748	11	111694888	A	G	8.37E-07	0.00744281	ALG9
rs7249605	19	53485771	G	A	8.40E-07	3.53E-06	ZNF702P
rs140458168	2	106001208	G	A	8.42E-07	0.000228144	FHL2
rs7821208	8	61841372	G	A	8.44E-07	0.00340995	AC022182.2
rs11437627	4	107261439	GT	G	8.51E-07	0.00865221	AIMP1
rs62321990	4	95359772	C	G	8.51E-07	1.60E-06	AC109925.1
rs144331865	18	69482583	C	A	8.56E-07	0.000410314	RP11-723G8.2
rs143517325	5	119738957	G	C	8.58E-07	0.0163052	PRR16
rs73026472	6	170756716	A	T	8.59E-07	0.000415804	PSMB1
rs58023506	8	61841511	A	G	8.70E-07	0.00333771	AC022182.2
rs79569205	4	156760259	T	C	8.80E-07	1.42E-05	ASIC5
rs117116072	18	69562390	C	T	8.95E-07	0.000179982	RP11-723G8.2
rs56370372	17	11472961	T	C	8.98E-07	0.00497619	DNAH9
rs200610784	6	13512060	AT	A	9.01E-07	0.0206782	GFOD1
rs149012815	4	60583109	GT	G	9.10E-07	3.19E-06	RP11-593F5.1
rs143300216	17	21862339	G	T	9.11E-07	0.000101143	RP11-744K17.3
rs77972902	1	180131941	C	G	9.12E-07	0.0173526	QSOX1
rs9951772	18	3982583	T	A	9.17E-07	0.00432944	DLGAP1
rs80349135	3	156772055	A	G	9.20E-07	8.14E-06	CCNL1
rs6689602	1	180132688	G	A	9.21E-07	0.0172975	QSOX1
rs140784679	17	21865262	A	C	9.24E-07	0.00011303	RP11-1109M24.11
rs139211992	17	21868136	G	T	9.33E-07	0.000113498	RP11-1109M24.11
rs6502640	17	18122485	A	G	9.34E-07	0.000217177	ALKBH5
rs139597161	4	60595152	T	C	9.40E-07	5.10E-06	RP11-593F5.1
rs13235929	7	154520810	A	G	9.47E-07	0.0291461	DPP6
rs10015093	4	163190370	T	C	9.56E-07	0.00731326	FSTL5
rs12354230	1	180144240	T	C	9.62E-07	0.016054	QSOX1
rs842451	7	158568522	T	C	9.71E-07	0.0113699	ESYT2
rs13045735	20	60959890	G	A	9.75E-07	0.024939	RPS21

rs145065338	20	56649565	T	C	9.82E-07	9.33E-06	PMEPA1
rs12673237	7	154522065	T	G	9.86E-07	0.029306	DPP6
rs144285214	19	46742869	T	C	9.95E-07	0.0193801	IGFL1
rs76370724	10	92562753	C	CT	1.00E-06	0.00103335	HTR7
rs142964834	21	15231298	A	T	1.00E-06	0.0244121	CYP4F29P
rs78380970	2	59811622	A	C	1.01E-06	0.0103662	BCL11A
rs2460229	8	98446270	G	C	1.01E-06	0.0248176	TSPYL5
rs442140	1	40806933	A	T	1.01E-06	6.15E-06	SMAP2
rs10023120	4	163203871	T	C	1.01E-06	0.00736482	FSTL5
rs140064208	6	34182929	A	G	1.02E-06	0.000769809	CYCSP55
rs67460762	9	139416664	C	T	1.03E-06	2.04E-06	NOTCH1
rs116842049	17	21873326	T	C	1.04E-06	0.000113516	RP11-1109M24.11
rs140612790	17	21876163	T	C	1.04E-06	0.000113519	RP11-1109M24.11
rs138891644	17	21878027	T	A	1.04E-06	0.000113537	RP11-1109M24.11
rs142043739	17	21878585	A	G	1.04E-06	0.000113537	RP11-1109M24.11
rs142385086	17	21882021	A	G	1.04E-06	0.000113579	RP11-1109M24.11
rs151295969	17	21882032	T	G	1.04E-06	0.000113579	RP11-1109M24.11
rs61633784	10	1437844	G	A	1.05E-06	1.81E-05	ADARB2
rs191045897	17	21862107	C	T	1.06E-06	0.000101656	RP11-744K17.3
rs138278949	4	18356145	A	G	1.06E-06	1.07E-05	LCORL
rs184827310	8	100599731	G	A	1.06E-06	2.22E-06	VPS13B
rs145789946	17	21861989	G	C	1.06E-06	0.000101331	RP11-744K17.3
rs149445555	17	21861943	A	T	1.06E-06	0.000101211	RP11-744K17.3
rs116582181	17	21882632	T	C	1.06E-06	0.000113468	RP11-1109M24.11
rs117097386	17	21893125	T	C	1.07E-06	0.000115368	RP11-1109M24.11
rs36058389	17	18123434	T	G	1.07E-06	0.00021167	ALKBH5
rs377112003	17	21908928	T	G	1.07E-06	0.000122241	RP11-1109M24.8
rs570916079	17	21895373	ACTCTCT	A	1.08E-06	0.000124529	RP11-1109M24.11
rs2513390	8	98444949	A	G	1.08E-06	0.0254182	TSPYL5
rs148825205	17	21934763	T	C	1.09E-06	0.00012645	RP11-744K17.7
rs189087245	17	21898510	A	G	1.09E-06	0.000116625	RP11-1109M24.11
rs146041883	5	155013090	T	C	1.09E-06	0.0422103	SGCD
rs146758741	17	21899434	T	C	1.09E-06	0.000116787	RP11-1109M24.11
rs145696529	17	21899207	C	A	1.09E-06	0.000116787	RP11-1109M24.11
rs548446330	1	76046462	A	G	1.09E-06	4.88E-07	SLC44A5
rs118177269	17	21900951	T	C	1.10E-06	0.00011695	RP11-1109M24.11
rs117024651	17	21964839	G	C	1.10E-06	0.000123807	RP11-744K17.8
rs139419939	17	21910161	T	C	1.11E-06	0.000119069	RP11-1109M24.8
rs142641016	18	23651936	C	A	1.11E-06	0.0159521	SS18
rs117260520	17	21908588	A	G	1.11E-06	0.000118695	RP11-1109M24.9
rs56195588	4	162211709	A	T	1.11E-06	0.00108457	FSTL5
rs117979239	17	21910866	T	C	1.11E-06	0.000119265	RP11-1109M24.8
rs765039106	17	21885750	A	AT	1.11E-06	0.000126034	/
rs117055722	17	21909749	C	T	1.11E-06	0.000118892	RP11-1109M24.8
rs140173827	17	21913926	A	G	1.11E-06	0.000119468	RP11-1109M24.7
rs143397338	17	21913600	G	A	1.11E-06	0.000119468	RP11-1109M24.7
rs118133428	7	132063399	A	G	1.11E-06	0.00631105	PLXNA4
rs117524176	17	21968508	A	G	1.12E-06	0.000125666	RP11-744K17.8
rs117582270	17	21920177	G	A	1.12E-06	0.000120104	RP11-744K17.7
rs141023888	17	21918962	T	C	1.12E-06	0.000120104	RP11-744K17.7
rs142815952	17	21921600	T	C	1.12E-06	0.000120104	RP11-744K17.7
rs145410273	17	21929025	G	A	1.12E-06	0.000120103	RP11-744K17.7
rs145771934	17	21924866	C	G	1.12E-06	0.000120543	RP11-744K17.7
rs138179341	17	21948605	T	C	1.13E-06	0.000121169	RP11-744K17.8
rs149680517	17	21965891	A	G	1.13E-06	0.000128097	RP11-744K17.8
rs139195925	17	21939608	T	C	1.13E-06	0.000120812	RP11-744K17.8
rs146915687	17	21939603	G	A	1.13E-06	0.000120812	RP11-744K17.8

rs117645939	17	21934054	A	G	1.13E-06	0.000121533	RP11-744K17.7
rs144677893	17	21932933	A	C	1.13E-06	0.00012012	RP11-744K17.7
rs141378294	17	21944993	A	G	1.13E-06	0.000121166	RP11-744K17.8
rs117953217	17	21944474	T	C	1.13E-06	0.000121167	RP11-744K17.8
rs148021960	17	21948994	A	G	1.13E-06	0.000121169	RP11-744K17.8
rs117763222	17	21951917	A	G	1.13E-06	0.00012117	RP11-744K17.8
rs118119789	17	21953000	T	A	1.13E-06	0.000121174	RP11-744K17.8
rs149652401	17	21956759	C	T	1.13E-06	0.000121176	RP11-744K17.8
rs142644944	17	21959043	T	C	1.13E-06	0.000121177	RP11-744K17.8
rs117640518	17	21960412	A	G	1.13E-06	0.000121177	RP11-744K17.8
rs150081774	17	21961381	T	C	1.13E-06	0.000121179	RP11-744K17.8
1:157753232_G A G	1	157753232	G	GA	1.13E-06	1.72E-07	/
rs183607234	17	21867720	C	G	1.13E-06	0.000126977	RP11-1109M24.11
rs56764036	8	61839895	A	G	1.14E-06	0.00333414	AC022182.2
rs139745416	1	44199508	T	C	1.14E-06	2.72E-06	ST3GAL3
rs3753809	1	180136711	C	T	1.15E-06	0.0193819	QSOX1
rs10808715	8	61849372	G	A	1.16E-06	0.00392194	AC022182.2
rs6536647	4	163200863	G	A	1.16E-06	0.00701847	FSTL5
8:61849486_CT T C	8	61849486	C	CTT	1.16E-06	0.00383708	/
rs72828953	17	55250826	A	G	1.16E-06	0.00445275	AKAP1
rs17759374	7	29348878	T	G	1.17E-06	3.90E-09	CHN2
rs117428532	8	138142037	G	T	1.17E-06	9.99E-05	KHDRBS3
rs115369848	1	38041223	A	G	1.20E-06	0.0241189	GNL2
rs114252768	2	184014965	C	G	1.20E-06	0.00967177	NUP35
rs148387678	3	98381273	G	A	1.20E-06	0.0209398	WWP1P1
rs117736500	17	21964613	T	C	1.22E-06	0.000355207	RP11-744K17.8
rs11004690	10	56795648	T	C	1.22E-06	0.00108559	PCDH15
rs143041513	14	31606308	A	G	1.23E-06	0.00877775	HECTD1
rs551382133	12	20522146	T	C	1.25E-06	0.000131569	PDE3A
rs113612967	17	2717387	A	G	1.27E-06	0.000258631	RAP1GAP2
rs141840545	15	77370159	G	A	1.28E-06	0.0213531	TSPAN3
rs28782783	4	190214359	C	T	1.29E-06	0.000579889	RP11-756P10.3
rs139152084	7	29410546	C	T	1.30E-06	1.26E-07	CHN2
rs11527508	10	56831245	C	A	1.31E-06	0.00100092	PCDH15
rs2527697	7	22030060	T	C	1.33E-06	0.0104297	RAPGEF5
rs186806798	17	21972580	C	G	1.33E-06	0.000129437	RP11-744K17.8
rs28811342	17	18125845	C	T	1.33E-06	0.000233643	LLGL1
rs192117036	17	21972582	G	A	1.34E-06	0.00012815	RP11-744K17.8
rs142118282	4	190332676	A	G	1.35E-06	0.00609923	RP11-756P10.3
rs2107973	7	22029482	A	G	1.35E-06	0.010558	RAPGEF5
rs7802979	7	22030661	T	C	1.35E-06	0.010886	RAPGEF5
rs11371955	8	61840959	TA	T	1.35E-06	0.00425296	AC022182.2
rs62072498	17	18125951	G	C	1.35E-06	0.000238823	LLGL1
rs538446609	17	21853029	C	A	1.36E-06	0.000139803	RP11-1109M24.12
rs184617962	2	209643864	A	G	1.36E-06	1.24E-05	PTH2R
rs115424165	6	11234014	C	T	1.36E-06	1.21E-07	NEDD9
rs7424891	2	92282367	A	G	1.37E-06	4.47E-10	IGKV1OR2-2
rs11967988	6	7607292	T	C	1.37E-06	5.72E-06	SNRNP48
rs2107972	7	22029542	A	C	1.38E-06	0.0105403	RAPGEF5
rs577573266	7	111258850	A	C	1.38E-06	0.0232571	DOCK4
rs74586325	13	23813113	A	G	1.38E-06	0.00236837	SGCG
rs13225062	7	22030483	A	G	1.40E-06	0.0107197	RAPGEF5
rs148275067	17	21854349	T	C	1.42E-06	0.000140302	RP11-744K17.3
rs71636345	5	97982944	A	G	1.44E-06	0.00345832	CTBP2P4
rs9553426	13	25272264	T	C	1.44E-06	0.000168494	ATP12A
rs115549955	3	5678469	A	G	1.45E-06	0.0279164	EDEM1

rs149297758	1	222983281	T	C	1.46E-06	3.78E-05	DISP1
rs7821046	8	61841256	G	A	1.46E-06	0.00480656	AC022182.2
rs77061667	8	60016139	C	T	1.46E-06	0.000146138	TOX
rs79577665	4	134323986	T	G	1.49E-06	0.00992749	PCDH10
rs1224631	15	48123228	T	G	1.49E-06	0.00733633	SEMA6D
rs2853306	8	98435684	G	A	1.51E-06	0.0314457	TSPYL5
rs73022033	3	4403260	T	C	1.51E-06	0.0300118	SUMF1
rs6789501	3	66714241	A	G	1.51E-06	0.000192721	KBTBD8
rs117638454	21	27928148	A	C	1.52E-06	8.84E-06	CYYR1
rs141521629	10	119086303	T	C	1.55E-06	7.60E-05	PDZD8
rs17351328	18	74050217	T	C	1.55E-06	0.0059633	ZNF516
rs544791	15	48124888	G	A	1.56E-06	0.00676497	SEMA6D
rs143973615	17	21852172	A	C	1.56E-06	0.000149747	RP11-1109M24.12
rs11100423	4	163190862	T	G	1.57E-06	0.0112597	FSTL5
rs17363208	2	5913608	A	G	1.57E-06	5.65E-05	SOX11
12:52499485_TG AG T	12	52499485	T	TGAG	1.59E-06	0.000832742	/
rs73182746	3	95069531	G	A	1.62E-06	0.00776803	RPS18P6
rs11057384	12	124370764	A	C	1.63E-06	0.0189107	DNAH10
rs200493526	5	24560457	CA	C	1.63E-06	0.0415834	CDH10
rs200486455	8	61849496	A	T	1.64E-06	0.00604208	AC022182.2
1:104453487_AT CT A	1	104453487	A	ATCT	1.64E-06	9.71E-07	/
rs2513389	8	98436047	T	C	1.66E-06	0.0331334	TSPYL5
rs79058559	5	24553792	T	C	1.67E-06	0.0412992	CDH10
rs757944090	10	28457944	A	AAGG	1.67E-06	2.79E-08	/
rs17457952	5	24512495	A	G	1.68E-06	0.0413372	CDH10
rs182368518	4	161318293	T	C	1.68E-06	2.84E-05	RP11-138A23.1
rs75009488	12	67357682	T	A	1.69E-06	8.47E-08	GRIP1
rs551331	15	48124151	A	G	1.70E-06	0.00623182	SEMA6D
rs111891077	1	66362559	C	T	1.71E-06	0.0328069	PDE4B
rs9876236	3	195771574	A	G	1.72E-06	0.0229263	TFRC
rs142052557	5	24527643	T	C	1.72E-06	0.0413528	CDH10
rs75416251	11	111434033	C	A	1.72E-06	0.00127333	LAYN
rs115141923	4	161322910	C	T	1.74E-06	2.79E-05	RP11-138A23.1
17:21838690_TC T	17	21838690	T	TC	1.75E-06	0.000162541	/
rs11481521	20	36150469	GA	G	1.75E-06	8.43E-06	NNAT
rs75217985	3	66713470	C	G	1.76E-06	0.000192032	KBTBD8
rs139174648	5	24519631	G	C	1.77E-06	0.0364255	CDH10
rs144660835	6	106914943	T	G	1.78E-06	0.00132721	ATG5
rs117183790	6	97236749	A	G	1.79E-06	8.85E-05	GPR63
rs2253994	8	98431841	A	G	1.83E-06	0.0348117	TSPYL5
rs73060169	3	36145416	T	C	1.85E-06	0.0203226	AC104308.2
rs116548736	2	145390250	T	C	1.86E-06	4.94E-06	ZEB2
rs201789575	18	40278396	GTTC	G	1.89E-06	6.57E-07	RIT2
rs115716251	4	35901444	A	T	1.89E-06	0.00446518	ARAP2
rs62073604	17	18065888	C	T	1.89E-06	0.000500125	MYO15A
rs145456621	17	21834777	T	C	1.89E-06	0.000168829	RP11-1109M24.12
rs9877409	3	4372386	G	C	1.89E-06	0.00293235	SUMF1
rs118018177	17	21835517	C	T	1.90E-06	0.000157979	RP11-1109M24.12
rs3753805	1	180138890	A	G	1.90E-06	0.0171298	QSOX1
rs3905359	10	56825358	C	G	1.91E-06	0.00108145	PCDH15
rs117973853	6	150993301	T	C	1.91E-06	1.43E-06	PLEKHG1
rs116928215	17	21834404	T	C	1.91E-06	0.000158774	RP11-1109M24.12
rs62073615	17	18080329	A	T	1.92E-06	0.000724626	MYO15A
rs12660004	5	26919924	T	A	1.92E-06	0.0359669	CDH9
rs117398415	12	124374596	G	A	1.92E-06	0.0308803	DNAH10

rs1996561	8	98425214	G	C	1.92E-06	0.032016	TSPYL5
8:98421668_GC G	8	98421668	G	GC	1.92E-06	0.0328591	/
rs2853300	8	98424479	G	A	1.92E-06	0.0322248	TSPYL5
rs114345502	4	32204514	C	G	1.93E-06	0.000101082	PCDH7
rs4783897	16	55672391	A	G	1.94E-06	5.55E-05	LPCAT2
rs146558436	16	73071025	T	C	1.94E-06	3.88E-07	ZFHX3
rs117282643	12	124371614	T	C	1.95E-06	0.0207071	DNAH10
rs182227893	17	21819095	C	T	1.96E-06	0.000160963	RP11-1109M24.14
rs139297030	17	21818953	A	G	1.97E-06	0.000160252	RP11-1109M24.14
rs149743478	17	21820613	A	G	1.97E-06	0.000160242	RP11-1109M24.14
rs60108251	3	127176185	T	G	1.97E-06	3.24E-05	TPRA1
rs147805212	17	21822004	C	G	1.98E-06	0.00016071	RP11-1109M24.14
rs117212055	17	21822496	G	A	1.98E-06	0.000161107	RP11-1109M24.14
rs117888986	17	21822436	A	C	1.98E-06	0.000161107	RP11-1109M24.14
12:120589817_G TAAAGTTTTT_ G	12	120589817	G	GTAAAGT TTTT	1.98E-06	4.58E-06	/
rs562543261	4	9763318	T	C	2.01E-06	0.0108492	SLC2A9
rs17712413	12	116166767	C	A	2.01E-06	3.35E-05	MED13L
rs75746785	1	237157093	A	C	2.01E-06	0.00519811	RPL35P1
rs77714634	4	32178756	G	A	2.02E-06	0.000115166	PCDH7
rs8077577	17	18064730	T	C	2.03E-06	0.000429073	MYO15A
rs80024556	9	101172602	A	G	2.03E-06	7.10E-06	GABBR2
rs62072500	17	18126918	C	A	2.04E-06	0.000481799	LLGL1
rs141908214	4	32197099	T	C	2.06E-06	0.000108713	PCDH7
rs114020042	12	116171106	A	G	2.06E-06	3.86E-05	MED13L
rs117289863	13	71833628	C	T	2.07E-06	0.0411585	RABEPKP1
rs76938823	12	116164426	T	C	2.07E-06	3.78E-05	MED13L
rs780471355	9	78011618	T	G	2.07E-06	0.011175	OSTF1
rs147887460	16	50487127	G	C	2.09E-06	7.12E-06	NKD1
rs138264396	17	21827916	C	T	2.11E-06	0.000168619	RP11-1109M24.14
rs149859933	15	75294000	G	A	2.11E-06	1.18E-05	SCAMP5
rs34068710	3	150670023	G	A	2.13E-06	1.97E-06	CLRN1
rs735960	17	18057301	A	G	2.13E-06	0.000293739	MYO15A
rs62520285	8	134518585	T	C	2.13E-06	0.0121885	ST3GAL1
4:187589928_C A C	4	187589928	C	CA	2.16E-06	0.000392291	/
rs143129166	12	116173447	G	A	2.18E-06	3.55E-05	MED13L
rs17761602	22	47064075	A	G	2.18E-06	3.23E-06	GRAMD4
rs17058043	6	98251106	A	G	2.20E-06	0.00226571	MMS22L
rs185384447	3	158002973	T	G	2.20E-06	0.00763053	RSRC1
rs185140140	3	39474595	C	T	2.20E-06	0.00273251	RPSA
rs17439972	9	131948849	G	C	2.20E-06	0.000320813	IER5L
rs140256119	4	107135163	C	T	2.24E-06	0.0210615	TBCK
rs542568028	3	118324656	G	T	2.25E-06	1.68E-06	IGSF11
rs62362983	5	75976373	T	G	2.26E-06	2.37E-05	IQGAP2
rs11652964	17	18040404	T	C	2.27E-06	0.00022064	MYO15A
rs147997219	19	49004917	T	C	2.30E-06	0.000143044	LMTK3
rs139036859	13	64886312	C	T	2.31E-06	0.0446888	LGMNP1
rs118139102	12	116156297	A	G	2.31E-06	3.95E-05	MED13L
rs7207276	17	18065737	C	G	2.32E-06	0.000498333	MYO15A
17:18065210_A GG A	17	18065210	A	AGG	2.36E-06	0.000484871	/
rs76682220	2	221127984	A	C	2.39E-06	0.0369252	AC009310.1
rs143302730	9	113985535	G	T	2.39E-06	0.0015425	OR2K2
rs79144486	10	134771136	A	G	2.40E-06	1.26E-08	CFAP46
rs2015336	17	18073610	G	A	2.40E-06	0.000499644	MYO15A

rs77198097	12	124371219	G	A	2.44E-06	0.0243179	DNAH10
rs72842176	2	127914819	A	G	2.44E-06	0.0143276	BIN1
rs62073608	17	18071448	C	T	2.44E-06	0.000517552	MYO15A
rs11044441	12	19322754	A	G	2.45E-06	0.029887	PLEKHA5
rs62073609	17	18071843	C	T	2.45E-06	0.000522881	MYO15A
rs77604835	3	81596421	A	G	2.47E-06	0.000584065	GBE1
rs55918833	17	18072352	C	T	2.50E-06	0.000534446	MYO15A
rs540068909	7	140062755	T	C	2.50E-06	7.59E-06	SLC37A3
rs145246408	17	21844669	G	A	2.51E-06	0.000190231	RP11-1109M24.12
rs139160329	10	22786587	G	A	2.51E-06	0.0169023	SPAG6
rs141719596	1	214641197	T	C	2.53E-06	1.23E-05	PTPN14
rs117668764	17	21842637	T	C	2.56E-06	0.000207169	RP11-1109M24.12
rs17223096	6	133958425	G	T	2.56E-06	1.26E-05	EYA4
rs146671994	6	151138945	A	G	2.56E-06	0.000487158	PLEKHG1
rs75830586	1	91095978	G	A	2.58E-06	0.0302187	BARHL2
rs150309325	9	108170930	A	G	2.61E-06	0.03266	SLC44A1
rs141796363	3	118783696	C	T	2.62E-06	0.000119458	IGSF11
rs997315	17	18085286	G	A	2.66E-06	0.000674196	ALKBH5
rs80221554	16	55098704	T	C	2.66E-06	3.02E-05	IRX6
rs11656035	17	18086025	C	T	2.66E-06	0.000673038	ALKBH5
rs34474249	17	18074525	C	T	2.67E-06	0.000581504	MYO15A
rs746165404	13	95326699	TAT	T	2.68E-06	0.0192944	SOX21
rs62073605	17	18066791	T	C	2.68E-06	0.000748083	MYO15A
rs147989671	14	52856758	A	G	2.68E-06	1.48E-05	TXNDC16
rs62073606	17	18069142	A	G	2.68E-06	0.000729256	MYO15A
rs116997290	8	60308445	C	T	2.69E-06	0.0425618	TOX
rs11654146	17	18076141	C	A	2.71E-06	0.000593178	MYO15A
rs58673429	1	50718961	T	C	2.71E-06	0.010103	ELAVL4
rs113522391	3	120459791	C	T	2.72E-06	4.16E-06	RABL3
rs12136109	1	4243708	T	A	2.72E-06	0.0239634	AJAP1
rs62073649	17	18080522	C	T	2.73E-06	0.000653826	MYO15A
rs10048161	17	18082796	G	C	2.75E-06	0.000608678	MYO15A
21:28071954_A C A	21	28071954	A	AC	2.77E-06	0.00181309	/
rs11658477	17	18044893	A	G	2.81E-06	0.000274115	MYO15A
rs62073603	17	18064316	T	C	2.84E-06	0.000524557	MYO15A
rs13425303	2	221125519	T	C	2.86E-06	0.0329356	AC009310.1
rs17675868	1	200126078	C	T	2.87E-06	0.00184285	NR5A2
rs71893067	10	1509239	ATC	A	2.87E-06	0.00112973	/
rs75157267	9	73018762	C	T	2.87E-06	0.000290478	KLF9
rs116527637	1	5748645	C	G	2.87E-06	0.000122487	NPHP4
rs11655731	17	18107525	T	G	2.89E-06	0.000887826	ALKBH5
rs11868886	17	18105585	A	G	2.90E-06	0.000895193	ALKBH5
rs79500077	13	71840131	G	A	2.91E-06	0.0295434	RABEPKP1
rs111974547	1	8184089	C	T	2.91E-06	0.00457077	RP11-431K24.2
rs76764676	2	145344078	A	G	2.92E-06	4.17E-06	ZEB2
rs1341161	10	96724061	T	C	2.94E-06	0.00831741	CYP2C9
rs149922460	17	21805390	G	A	2.96E-06	0.000179561	RP11-1109M24.15
rs11745250	5	66657771	A	G	2.98E-06	5.73E-06	CD180
rs144849842	1	214613536	T	C	3.01E-06	1.53E-05	PTPN14
rs4839875	6	97268615	A	T	3.01E-06	2.30E-06	GPR63
rs371407211	6	140769067	CT	C	3.02E-06	2.47E-05	/
rs77497601	4	15748053	G	T	3.05E-06	4.26E-07	RP11-442P12.2
rs146166536	4	7156799	G	C	3.05E-06	7.64E-06	GRPEL1
rs62541805	9	36269958	T	C	3.06E-06	0.0163312	GNE
rs142108158	17	21805668	T	C	3.07E-06	0.000184284	RP11-1109M24.15
rs72848807	2	128587108	G	A	3.07E-06	0.000898737	WDR33
rs144326611	9	36257538	T	C	3.07E-06	0.0162578	CLTA

rs185728293	17	21815113	A	G	3.09E-06	0.000159895	RP11-1109M24.14
rs116085930	3	62031671	A	T	3.12E-06	0.00399728	PTPRG
rs78920283	17	10920238	A	G	3.13E-06	0.000101438	SHISA6
rs55951301	1	112326415	ATGT	A	3.13E-06	0.00751377	KCND3
rs56392653	1	112326416	ATC	A	3.13E-06	0.00751377	KCND3
rs745738085	1	112326417	CA	C	3.13E-06	0.00751377	KCND3
rs77162969	17	21831436	T	C	3.14E-06	0.000218831	RP11-1109M24.13
rs71306535	3	150695107	T	C	3.15E-06	1.40E-08	CLRN1
rs62073611	17	18071961	G	C	3.15E-06	0.000788659	MYO15A
rs141712749	17	21831848	T	C	3.16E-06	0.000218568	RP11-1109M24.13
rs11698467	20	60934947	T	C	3.16E-06	0.0227405	LAMA5
rs143380218	3	13369787	T	C	3.18E-06	2.81E-05	NUP210
rs117474622	17	21830267	A	G	3.19E-06	0.000219351	RP11-1109M24.13
8:69312629_TT TCCCCAGCAC TATTTATTGC AAAG_T	8	69312629	T	TTTCCCC AGCACTA TTTATTG CAAAG	3.25E-06	3.65E-06	/
rs145246669	9	38734739	A	G	3.25E-06	1.10E-05	VN2R3P
rs7965360	12	48259382	G	A	3.27E-06	0.000714867	VDR
rs144397327	18	75587176	T	C	3.30E-06	0.0270465	SALL3
rs4847086	1	105641626	A	T	3.31E-06	0.0145274	RP11-414B7.1
rs116561305	5	1554423	G	C	3.32E-06	0.01862	LPCAT1
rs4463677	1	104380531	T	C	3.32E-06	2.51E-06	AMY1C
1:104435616_TA T	1	104435616	T	TA	3.34E-06	1.55E-06	/
rs12190193	6	170757021	T	C	3.35E-06	0.0347419	PSMB1
10:121171354_C TTTTTTTTTT C	10	121171354	C	CTTTTTTTT TT	3.36E-06	0.0226197	/
rs61874594	10	114343260	A	G	3.37E-06	3.72E-05	VTI1A
rs191227827	14	53240085	T	C	3.38E-06	4.32E-06	STYX
rs146547665	3	13377882	T	C	3.38E-06	2.76E-05	NUP210
rs199857577	9	26001632	CT	C	3.40E-06	0.0132073	CAAP1
rs3842814	13	24938062	A	C	3.40E-06	0.00011343	CYCSP33
rs34510512	21	16956149	G	A	3.41E-06	0.000281374	CYCSP42
rs6856	11	62458275	C	T	3.44E-06	5.21E-05	BSCL2
rs7208839	17	21842191	A	G	3.44E-06	0.000204501	RP11-1109M24.12
3:82724068_GT_ G	3	82724068	G	GT	3.44E-06	0.0300637	/
rs80062084	3	157945439	T	C	3.49E-06	0.00638294	RSRC1
rs1499269	4	129218494	G	A	3.51E-06	3.56E-07	JADE1
rs11871039	17	18078904	G	C	3.52E-06	0.000904901	MYO15A
rs1488930	7	154523235	G	A	3.53E-06	0.025134	DPP6
rs189114639	13	70391130	T	A	3.53E-06	0.000396234	KLHL1
rs142666276	15	77398996	G	A	3.54E-06	0.0126655	PEAK1
rs117794975	6	97235850	C	T	3.55E-06	0.000754019	GPR63
rs6544086	2	37729133	A	G	3.57E-06	0.0304477	QPCT
rs111840366	11	40522917	A	G	3.58E-06	6.18E-06	LRRC4C
rs12600694	17	18091019	A	G	3.60E-06	0.0017753	ALKBH5
rs112740591	1	180164132	GGGT	G	3.61E-06	0.0212269	QSOX1
rs112384084	3	195594494	T	C	3.61E-06	4.10E-05	TNK2
rs12034806	1	4239514	T	C	3.61E-06	0.0254369	RP11-374C13.1
rs115899785	1	37668102	T	C	3.62E-06	0.000548945	GRIK3
rs71433207	13	27505413	A	T	3.64E-06	8.76E-07	RPS21P8
rs2714445	7	79878921	T	C	3.65E-06	0.00236308	GNAI1
rs115022648	1	166012729	T	A	3.66E-06	0.00911424	FAM78B
rs145870286	6	134258662	A	G	3.66E-06	3.13E-06	TBPL1
1:156355248_C A C	1	156355248	C	CA	3.70E-06	0.0107871	/

rs12782764	10	1509658	A	G	3.74E-06	0.00207626	ADARB2
rs115454719	4	35813832	T	G	3.75E-06	0.000424804	ARAP2
rs9332235	10	96747905	A	G	3.75E-06	0.00781594	CYP2C9
rs112556211	18	12590378	T	C	3.76E-06	0.0211043	SPIRE1
12:97567137_CT C	12	97567137	C	CT	3.79E-06	6.62E-05	/
rs185728410	7	62199206	C	T	3.80E-06	0.0375257	RP11-196D18.2
rs138552519	17	21838567	A	G	3.81E-06	0.000269981	RP11-1109M24.12
rs115325182	3	19247662	G	A	3.82E-06	0.000389607	KCNH8
rs138576032	3	158058724	C	G	3.85E-06	0.00753425	RSRC1
3:104913189_A C A	3	104913189	A	AC	3.85E-06	0.0216009	/
6:40224564_TC_ T	6	40224564	T	TC	3.86E-06	1.09E-06	/
rs143400353	5	86770691	A	G	3.87E-06	0.000655425	CCNH
rs55894187	3	82700245	A	G	3.89E-06	0.0278531	CYP51A1P1
rs112255063	9	1674294	G	A	3.89E-06	0.0222613	RP11-443B9.1
rs73132167	3	82730257	T	A	3.89E-06	0.028771	CYP51A1P1
rs62072496	17	18124743	A	G	3.91E-06	0.000441702	LLGL1
rs142547867	11	40543645	T	C	3.91E-06	5.53E-06	LRR4C
rs72641981	13	88627047	G	A	3.92E-06	4.51E-07	RPL29P29
rs72929424	11	62462546	G	C	3.93E-06	6.98E-05	BSCL2
12:9458100_TG AG T	12	9458100	T	TGAG	3.93E-06	6.63E-05	/
rs114738411	1	112304164	C	T	3.94E-06	0.00370394	DDX20
rs532147141	12	20756879	T	C	3.95E-06	0.00223463	PDE3A
rs72841922	2	84338670	G	T	3.95E-06	0.000868603	FUNDC2P2
18:9112916_AA T A	18	9112916	A	AAT	3.95E-06	7.24E-05	/
1:104423508_TA T	1	104423508	T	TA	3.97E-06	2.55E-06	/
rs78949801	2	60623902	T	C	3.97E-06	2.02E-05	BCL11A
rs61851649	10	73283718	A	G	3.98E-06	0.00401677	CDH23
rs2192941	2	37718835	C	T	4.00E-06	0.0297967	QPCT
rs61333033	3	36459975	C	T	4.01E-06	0.00162946	STAC
1:104487662_G AGACA G	1	104487662	G	GAGACA	4.01E-06	1.62E-06	/
rs62072497	17	18125877	A	G	4.02E-06	0.000431081	LLGL1
rs56711178	1	105661129	A	T	4.02E-06	0.0166588	RP11-414B7.1
rs61217171	1	105661130	A	T	4.02E-06	0.0166588	RP11-414B7.1
rs41269369	1	239866503	G	A	4.02E-06	0.00574836	CHRM3
rs72694446	1	104396377	G	A	4.02E-06	2.38E-06	AMY1C
rs11231193	11	62466992	C	T	4.03E-06	6.97E-05	BSCL2
rs145898293	10	4517519	C	T	4.03E-06	0.0153189	KLF6
rs58856600	1	104443263	T	G	4.05E-06	1.98E-06	AMY1C
rs72698796	14	101363503	T	C	4.05E-06	1.72E-05	AL117190.3
rs75935513	12	124374598	G	A	4.06E-06	0.0304424	DNAH10
rs34203236	10	1509191	A	G	4.06E-06	0.00219569	ADARB2
rs567644317	2	190781057	A	T	4.08E-06	0.00327691	C2orf88
rs72694443	1	104388206	T	G	4.08E-06	2.40E-06	AMY1C
rs2699462	7	22031326	A	G	4.09E-06	0.0242557	RAPGEF5
rs142627474	2	184080053	C	T	4.10E-06	0.00709418	NUP35
rs17035045	3	36458103	T	C	4.10E-06	0.00178734	STAC
rs532826702	3	84139176	T	C	4.13E-06	7.12E-06	RP11-651J20.1
rs8065026	17	18046290	C	T	4.14E-06	0.000158724	MYO15A
rs146390284	10	96718010	C	T	4.15E-06	0.00542015	CYP2C9
rs150033649	17	72134441	T	A	4.16E-06	2.13E-07	SDK2
rs78254452	2	60629051	G	T	4.18E-06	2.04E-05	BCL11A

rs12031950	1	4236710	T	C	4.18E-06	0.0256174	RP11-374C13.1
rs2527701	7	22031291	T	G	4.18E-06	0.024361	RAPGEF5
1:167211411_C ATTA_C	1	167211411	C	CATTA	4.18E-06	4.93E-06	/
rs12032955	1	4237878	T	C	4.19E-06	0.0255599	RP11-374C13.1
rs7935127	11	62470847	A	G	4.19E-06	7.30E-05	BSCL2
rs61931467	12	115412447	C	T	4.19E-06	0.0122838	TBX3
rs12424638	12	49318800	A	G	4.21E-06	0.0122618	FKBP11
rs34230456	1	4238472	A	G	4.21E-06	0.0254796	RP11-374C13.1
rs112714735	8	117627985	T	C	4.21E-06	3.42E-05	TRPS1
rs11523848	10	82505388	T	C	4.22E-06	0.00147782	RP11-20E23.1
rs2527700	7	22030951	T	C	4.22E-06	0.024071	RAPGEF5
rs1871020	3	82717048	C	T	4.23E-06	0.0292031	CYP51A1P1
rs12032975	1	4238038	T	C	4.25E-06	0.0255404	RP11-374C13.1
rs189554824	3	62047404	C	G	4.25E-06	0.00319999	PTPRG
rs11581912	1	104452251	A	G	4.25E-06	2.46E-06	AMY1C
rs147909535	13	34740757	T	C	4.25E-06	2.69E-07	VDAC1P12
rs12030172	1	4237984	T	G	4.25E-06	0.025581	RP11-374C13.1
rs9628997	1	104453628	T	G	4.26E-06	2.47E-06	AMY1C
rs72679982	1	104451404	A	G	4.26E-06	2.46E-06	AMY1C
rs72694458	1	104412792	G	A	4.26E-06	2.43E-06	AMY1C
rs74732460	1	104412357	T	A	4.26E-06	2.43E-06	AMY1C
rs72694456	1	104405613	A	C	4.26E-06	2.43E-06	AMY1C
rs72694457	1	104409140	A	T	4.26E-06	2.43E-06	AMY1C
rs113991964	7	146109285	G	A	4.26E-06	5.90E-05	CNTNAP2
rs72694451	1	104401791	A	G	4.27E-06	2.44E-06	AMY1C
rs72694454	1	104404783	A	G	4.27E-06	2.43E-06	AMY1C
rs112438207	1	104417312	T	G	4.28E-06	2.44E-06	AMY1C
rs72694461	1	104416516	A	G	4.28E-06	2.44E-06	AMY1C
rs72929434	11	62469929	A	C	4.28E-06	7.00E-05	BSCL2
rs75661393	5	86655947	G	T	4.29E-06	3.36E-06	RASA1
rs113199326	1	104448207	G	A	4.29E-06	2.45E-06	AMY1C
rs41511047	1	104439144	A	G	4.30E-06	2.45E-06	AMY1C
rs72679977	1	104436384	T	C	4.30E-06	2.45E-06	AMY1C
rs72679978	1	104437949	T	C	4.30E-06	2.45E-06	AMY1C
rs72679975	1	104433592	T	C	4.30E-06	2.45E-06	AMY1C
rs13374153	1	104432003	T	C	4.30E-06	2.45E-06	AMY1C
rs13374158	1	104432076	G	C	4.30E-06	2.45E-06	AMY1C
rs75626367	6	97234591	A	G	4.30E-06	0.000971691	GPR63
rs72679979	1	104438156	C	A	4.30E-06	2.45E-06	AMY1C
rs72679976	1	104434536	T	A	4.30E-06	2.45E-06	AMY1C
rs13376648	1	104430434	A	G	4.31E-06	2.45E-06	AMY1C
rs13374076	1	104430099	G	A	4.31E-06	2.45E-06	AMY1C
rs11589939	1	104414029	G	A	4.31E-06	2.45E-06	AMY1C
rs72694464	1	104423351	T	C	4.31E-06	2.45E-06	AMY1C
rs36075516	10	52109311	TC	T	4.33E-06	0.00426559	SGMS1
rs752274458	20	40401611	T	TG	4.34E-06	0.0377987	CHD6
rs72698664	9	12365393	G	T	4.35E-06	0.00470718	TYRP1
rs4678874	3	36457372	G	A	4.37E-06	0.00178524	STAC
rs143564659	20	17884894	A	G	4.38E-06	3.19E-06	SNX5
rs117644056	8	60389355	C	T	4.39E-06	0.02688	TOX
rs2373111	2	37730983	G	C	4.39E-06	0.0323389	QPCT
rs151171352	4	122288378	T	C	4.40E-06	0.00255089	QRFR
rs117180979	12	80090373	C	T	4.40E-06	0.0167102	PPP1R12A
rs150640848	8	138210006	C	A	4.41E-06	0.000114855	KHDRBS3
rs117444449	16	51816056	A	G	4.42E-06	1.82E-06	HNRNPA1P48
rs11762281	7	22031967	T	A	4.43E-06	0.0334935	RAPGEF5
rs72694452	1	104402981	A	G	4.44E-06	2.56E-06	AMY1C

rs12047711	1	105660547	T	C	4.44E-06	0.0226637	RP11-414B7.1
rs6677692	1	105633111	A	C	4.49E-06	0.0140887	RP11-414B7.1
rs11583141	1	105654287	A	G	4.49E-06	0.0227398	RP11-414B7.1
rs12270593	11	62499998	T	C	4.50E-06	7.06E-05	TTC9C
rs7415977	1	105633335	C	T	4.51E-06	0.0140891	RP11-414B7.1
rs56135662	11	62473548	T	C	4.51E-06	7.01E-05	BSCL2
rs11588494	1	104410340	A	G	4.53E-06	2.79E-06	AMY1C
rs73199884	12	111791185	A	G	4.56E-06	0.000123447	CUX2
rs7698238	4	63056880	T	C	4.56E-06	0.0166074	RP11-84A1.1
rs8117723	20	40399442	A	G	4.59E-06	0.0312118	CHD6
rs6692674	1	105632468	A	C	4.61E-06	0.0136162	RP11-414B7.1
rs141146249	12	7882578	G	A	4.65E-06	0.00259754	CLEC4C
rs61744696	9	138664762	T	C	4.66E-06	7.70E-05	KCNT1
rs55707677	11	62506718	G	A	4.67E-06	7.94E-05	TTC9C
rs114678891	6	40231985	C	G	4.67E-06	2.86E-07	LRFN2
rs145342318	4	107135174	A	G	4.67E-06	0.022762	TBCK
rs138826256	9	2025808	A	G	4.68E-06	2.96E-05	SMARCA2
rs56160161	3	112572246	T	C	4.70E-06	2.79E-06	CD200R1
rs7959305	12	80070534	T	C	4.70E-06	0.0168086	PAWR
rs143729540	17	18268113	G	C	4.70E-06	0.0486203	SHMT1
rs59366579	17	18161744	T	C	4.72E-06	0.0256859	FLII
rs139661527	17	21803290	T	C	4.73E-06	0.000217001	RP11-1109M24.15
rs150500972	18	58533335	G	A	4.73E-06	6.31E-05	CDH20
rs11184435	1	105657883	C	A	4.73E-06	0.0237765	RP11-414B7.1
rs139969191	15	27590371	C	T	4.74E-06	0.000139525	GABRG3
rs138554687	3	23113992	C	G	4.74E-06	0.00230906	RPL24P7
rs79058579	2	105819694	A	G	4.75E-06	0.000908501	MRPS9
20:45737915_CT TAAG C	20	45737915	C	CTTAAG	4.81E-06	0.00650115	/
rs140898701	6	106814014	T	C	4.82E-06	3.82E-05	ATG5
rs534521017	4	107215642	CT	C	4.83E-06	0.0424774	/
rs151029329	15	37057383	G	A	4.88E-06	0.00109478	C15orf41
rs143047393	17	21801660	A	C	4.89E-06	0.000251656	RP11-1109M24.15
rs11950678	5	66654519	G	A	4.92E-06	2.82E-06	CD180
rs62073602	17	18057907	G	A	4.92E-06	0.000181584	MYO15A
rs12113414	7	146075680	G	A	4.93E-06	0.000149718	CNTNAP2
rs77091990	7	20264728	A	T	4.93E-06	0.0182866	ITGB8
rs117767075	10	70177061	G	A	4.93E-06	5.58E-09	DNA2
rs56084975	7	22031791	A	G	4.95E-06	0.0339603	RAPGEF5
rs4393145	1	237557302	T	G	4.97E-06	0.0221092	RYR2
rs62414809	6	63011050	C	G	4.99E-06	0.000114156	KHDRBS2
rs12291015	11	62487378	C	T	5.03E-06	7.14E-05	HNRNPUL2
rs138011046	16	3326104	A	G	5.03E-06	6.09E-05	ZNF263
rs114276351	1	224598645	T	C	5.04E-06	0.00806889	WDR26
rs181802249	17	39249357	C	T	5.04E-06	0.000473282	KRTAP4-8
rs6675	11	62505764	T	C	5.05E-06	7.37E-05	TTC9C
rs7104360	11	62503774	A	G	5.06E-06	7.38E-05	TTC9C
rs7949279	11	62502467	T	C	5.07E-06	7.39E-05	TTC9C
rs55894446	2	60617514	G	A	5.08E-06	2.19E-05	BCL11A
rs2576006	10	128330904	G	A	5.08E-06	1.40E-05	C10orf90
rs143917300	16	559760	G	C	5.08E-06	0.0430699	RAB11FIP3
rs11592576	10	1443180	T	A	5.08E-06	1.35E-05	ADARB2
rs7126912	11	62495239	C	A	5.09E-06	7.13E-05	TTC9C
rs6583116	1	105639616	C	G	5.10E-06	0.0211351	RP11-414B7.1
rs6583115	1	105639614	T	C	5.10E-06	0.0211375	RP11-414B7.1
rs11843073	13	95319843	A	T	5.11E-06	0.00104856	SOX21
rs77033618	5	86534291	C	T	5.12E-06	2.44E-05	AC008394.1
rs76972842	2	42493019	A	C	5.12E-06	0.0023505	EML4

rs201302260	13	103324232	CA	C	5.14E-06	0.000100831	TPP2
rs73203802	8	13591904	T	C	5.14E-06	0.0238574	RP11-436P7.2
rs16950006	13	95321913	G	C	5.14E-06	0.00104791	SOX21
rs71306533	3	150666046	T	C	5.15E-06	2.25E-06	CLRN1
rs56323441	11	62506792	G	T	5.15E-06	7.32E-05	TTC9C
rs72776415	16	6272462	A	G	5.16E-06	0.000765103	RBFOX1
rs76202562	12	5458610	C	T	5.20E-06	7.33E-05	KCNA5
rs6925557	6	106791650	C	G	5.21E-06	1.32E-05	ATG5
rs6900767	6	106791545	A	T	5.22E-06	1.33E-05	ATG5
rs10881254	1	105657725	G	A	5.24E-06	0.0237168	RP11-414B7.1
rs556361110	8	22069349	C	A	5.24E-06	0.000272379	BMP1
rs113777195	11	62513643	A	G	5.25E-06	7.05E-05	ZBTB3
rs112132759	7	146125166	A	G	5.26E-06	5.34E-05	CNTNAP2
rs12404997	1	105654091	C	T	5.26E-06	0.0237575	RP11-414B7.1
rs4847087	1	105647075	G	A	5.28E-06	0.0241414	RP11-414B7.1
rs34040681	10	1509044	T	G	5.28E-06	0.00236544	ADARB2
rs115027936	5	173944657	A	G	5.31E-06	0.00363744	GAPDHP71
rs202023115	5	102843177	GA	G	5.31E-06	0.0413828	AC010423.1
rs7936611	11	62492674	G	A	5.32E-06	8.14E-05	HNRNPUL2
rs113687404	3	76029264	C	T	5.32E-06	7.48E-05	ROBO2
rs76858681	17	64707856	T	C	5.33E-06	0.041488	PRKCA
rs72929452	11	62493867	C	T	5.34E-06	7.48E-05	HNRNPUL2
rs142421629	12	19023040	A	G	5.34E-06	2.04E-05	CAPZA3
rs4678876	3	36468079	T	G	5.34E-06	0.00166961	STAC
rs75094269	4	134210050	A	G	5.34E-06	0.00969628	PCDH10
rs144588202	1	239917071	C	T	5.35E-06	0.0143289	CHRM3
rs62072537	17	18216100	A	G	5.35E-06	0.045548	TOP3A
rs16961114	17	18215339	C	G	5.37E-06	0.0455277	TOP3A
rs116151125	1	53642460	T	C	5.37E-06	0.000200487	CPT2
rs6583117	1	105639679	G	A	5.37E-06	0.0223662	RP11-414B7.1
rs13156648	5	26903476	G	A	5.38E-06	0.0252148	CDH9
rs11184421	1	105639051	G	A	5.39E-06	0.0225189	RP11-414B7.1
rs4847092	1	105658443	G	A	5.39E-06	0.0235673	RP11-414B7.1
rs115847948	3	135113957	A	C	5.41E-06	0.000142238	EPHB1
rs73828877	3	36443186	G	C	5.42E-06	0.00164645	STAC
rs138389868	12	79976171	A	G	5.42E-06	0.0186691	PAWR
rs10513698	3	171425654	T	A	5.42E-06	0.00132172	PLD1
rs75793205	12	5478631	T	C	5.43E-06	3.29E-05	KCNA5
rs72712820	4	180023073	C	T	5.43E-06	0.0342635	RP11-774G5.1
rs62072515	17	18213435	G	T	5.45E-06	0.0459529	TOP3A
rs78469001	4	180024718	G	A	5.46E-06	0.0380058	RP11-774G5.1
rs76919197	6	112495348	G	T	5.47E-06	0.0184318	LAMA4
rs3734227	6	144510926	T	C	5.47E-06	0.00101476	STX11
rs752142503	11	62510922	C	CA	5.48E-06	7.17E-05	TTC9C
rs16950001	13	95316946	T	C	5.50E-06	0.0010451	SOX21
rs142047294	3	171422459	G	A	5.54E-06	0.00147148	PLD1
rs35636163	5	98037812	G	A	5.54E-06	0.0186456	RGMB
rs138042840	8	62768126	AT	A	5.54E-06	1.55E-06	ASPH
rs6583123	1	105661518	T	A	5.55E-06	0.0235058	RP11-414B7.1
rs72929471	11	62521475	C	T	5.57E-06	5.99E-05	ZBTB3
rs11184442	1	105662070	C	T	5.57E-06	0.0231664	RP11-414B7.1
rs141799119	16	6084305	T	C	5.58E-06	0.00545981	RBFOX1
12:48261192_TT G T	12	48261192	T	TTG	5.59E-06	0.00148714	/
rs11985417	8	13593700	A	C	5.59E-06	0.0267263	RP11-436P7.2
rs57820954	16	74791827	C	G	5.60E-06	0.0372925	FA2H
rs11670372	19	9110090	A	G	5.61E-06	0.00238307	MUC16
rs111234733	7	146140807	G	T	5.61E-06	5.31E-05	CNTNAP2

rs7112576	11	62511420	A	G	5.62E-06	6.87E-05	TTC9C
rs73063829	3	36475321	A	T	5.62E-06	0.00127319	STAC
rs77648385	3	171413198	T	C	5.63E-06	0.00145532	PLD1
rs12636967	3	36434155	A	G	5.63E-06	0.00110003	STAC
rs77304365	17	69483912	G	A	5.63E-06	0.000708182	LOC124685
rs12631541	3	36434214	G	A	5.63E-06	0.00110092	STAC
rs4847093	1	105658506	G	C	5.67E-06	0.0251447	RP11-414B7.1
rs12039389	1	105659073	A	G	5.68E-06	0.0251291	RP11-414B7.1
rs77943717	3	36431468	A	G	5.68E-06	0.000980244	STAC
13:39919649_C AAAAAAAAAA AAAAAAAAA C	13	39919649	C	CAAAAAA AAAAAA AAAAA	5.68E-06	2.83E-06	/
rs8081155	17	18191948	G	C	5.70E-06	0.0465343	TOP3A
rs62072511	17	18193157	A	G	5.70E-06	0.0465378	TOP3A
rs529628645	12	116172535	CA	C	5.70E-06	8.31E-05	MED13L
rs2885140	3	36454007	T	C	5.71E-06	0.00213202	STAC
rs145121459	10	25431803	A	T	5.72E-06	0.000406538	GPR158
rs3817992	17	18194011	A	C	5.73E-06	0.0465265	TOP3A
rs112389739	6	98216447	TTAAAG	T	5.74E-06	0.00458946	MMS22L
rs117992377	8	142982058	T	C	5.74E-06	2.26E-06	AC138647.1
rs12140941	1	4259253	C	A	5.76E-06	0.0411952	AJAP1
rs116683967	6	66125204	T	C	5.76E-06	4.54E-06	EYS
rs28363367	5	6741558	G	T	5.76E-06	1.96E-05	PAPD7
rs117475996	12	116149843	A	C	5.77E-06	3.17E-05	MED13L
rs1925	17	18177715	A	G	5.78E-06	0.0463377	TOP3A
rs140273457	4	134235478	C	T	5.80E-06	0.00335471	PCDH10
rs115987182	2	105949435	T	C	5.80E-06	0.000633337	TGFBRAP1
rs79782340	7	21301707	C	T	5.86E-06	0.0359604	ASS1P11
rs303736	9	14430737	A	G	5.87E-06	0.034068	NFIB
rs58303436	3	36433205	G	A	5.90E-06	0.00112161	STAC
rs12480992	20	40396754	T	C	5.91E-06	0.0350503	CHD6
rs4810338	20	40397965	T	C	5.94E-06	0.0351803	CHD6
rs760456	21	46329415	C	G	5.95E-06	0.000377306	ITGB2
rs62072509	17	18182393	A	G	5.97E-06	0.0484443	TOP3A
rs59998929	20	40397288	A	T	5.98E-06	0.0351564	CHD6
rs17034995	3	36431080	T	C	6.02E-06	0.00111111	STAC
rs62072507	17	18172335	A	G	6.04E-06	0.048345	TOP3A
rs117353270	18	49132256	A	C	6.04E-06	0.0474289	RSL24D1P9
rs140390274	8	126962162	G	A	6.04E-06	0.000124138	SOD1P3
rs11723971	4	180027296	A	G	6.05E-06	0.0438602	RP11-774G5.1
rs551152882	1	243224687	A	G	6.05E-06	8.50E-05	RP11-261C10.7
rs138424314	3	115147512	A	G	6.05E-06	5.67E-05	GAP43
rs2361038	3	36429578	C	T	6.07E-06	0.00110887	STAC
rs12112484	7	146156390	T	G	6.08E-06	5.27E-05	CNTNAP2
rs2361037	3	36429484	C	T	6.08E-06	0.00110924	STAC
rs78425039	2	42483860	G	C	6.09E-06	0.00201976	EML4
rs4678875	3	36459254	C	T	6.10E-06	0.00183252	STAC
rs145133878	1	17934347	A	C	6.11E-06	0.00129735	ARHGEF10L
rs6583124	1	105661612	A	G	6.12E-06	0.0237999	RP11-414B7.1
rs148492409	3	104931603	C	T	6.13E-06	0.0221239	ALCAM
rs151268864	20	17883163	C	T	6.13E-06	8.08E-06	SNX5
rs77501534	2	95824624	T	G	6.16E-06	2.98E-07	ZNF514
rs11184428	1	105650016	C	A	6.16E-06	0.0279557	RP11-414B7.1
rs6659453	1	105650012	C	G	6.16E-06	0.0279557	RP11-414B7.1
rs147013419	2	144974739	C	T	6.23E-06	0.0106463	GTDC1
rs118108633	11	87439442	A	G	6.23E-06	0.00120447	RP11-665E10.5
rs12128652	1	105642360	A	G	6.24E-06	0.0215483	RP11-414B7.1
rs12311827	12	19256833	T	A	6.24E-06	0.00791829	RP11-282K24.2

rs61954590	12	84241315	C	T	6.24E-06	8.69E-07	RPL6P25
rs950824	7	154528956	G	A	6.25E-06	0.0331468	DPP6
rs28452921	7	26539777	A	G	6.26E-06	0.00987674	SNX10
7:146088842_TT TGTTG T	7	146088842	T	TTTGTTG	6.26E-06	7.50E-05	/
rs12652586	5	26913243	A	G	6.27E-06	0.0302445	CDH9
rs112600086	7	146095320	A	G	6.30E-06	6.07E-05	CNTNAP2
rs10748481	1	105660270	A	G	6.33E-06	0.0264369	RP11-414B7.1
17:18169000_CC CT C	17	18169000	C	CCCT	6.33E-06	0.0492843	/
rs79275841	5	64429122	A	G	6.33E-06	5.22E-05	ADAMTS6
rs77383472	8	22069591	T	C	6.33E-06	0.000882518	BMP1
rs12128596	1	105642215	A	G	6.33E-06	0.0216584	RP11-414B7.1
rs189626704	1	93042999	T	A	6.34E-06	0.00153043	EVI5
rs117062745	12	97572424	T	C	6.34E-06	0.000136497	NEDD1
rs57846685	16	74796162	T	C	6.35E-06	0.0402492	FA2H
rs17034991	3	36426701	C	T	6.38E-06	0.00111598	STAC
1:105648179_AT A	1	105648179	A	AT	6.41E-06	0.0261842	/
rs112883379	7	146101640	T	C	6.42E-06	6.28E-05	CNTNAP2
rs7411599	1	105646216	G	A	6.44E-06	0.0262165	RP11-414B7.1
rs7518450	1	105651502	A	G	6.44E-06	0.026218	RP11-414B7.1
rs10215407	7	26581775	C	T	6.45E-06	0.00496756	KIAA0087
rs6583121	1	105651783	C	T	6.54E-06	0.0264773	RP11-414B7.1
rs118092660	12	10049380	T	C	6.60E-06	5.63E-05	CLEC2A
rs34732465	11	72544977	AT	A	6.61E-06	0.00510486	ATG16L2
rs35314164	5	26899979	TA	T	6.66E-06	0.0167638	CDH9
rs3829248	11	62521663	T	C	6.66E-06	6.72E-05	ZBTB3
rs9438438	1	205884062	C	T	6.66E-06	0.00444891	SLC26A9
rs72929469	11	62521408	T	A	6.67E-06	6.80E-05	ZBTB3
rs147486502	17	49058892	T	A	6.67E-06	4.86E-10	SPAG9
rs10881253	1	105655635	C	T	6.72E-06	0.026006	RP11-414B7.1
rs6676532	1	105656276	G	A	6.72E-06	0.026006	RP11-414B7.1
rs34883409	5	66677647	TA	T	6.73E-06	2.05E-05	CD180
rs10881246	1	105646709	G	A	6.74E-06	0.0264304	RP11-414B7.1
rs11184429	1	105650116	T	A	6.74E-06	0.0260341	RP11-414B7.1
rs10881248	1	105646843	A	T	6.75E-06	0.0264376	RP11-414B7.1
rs7410808	1	105646629	T	C	6.75E-06	0.0264376	RP11-414B7.1
rs588057	5	154578752	T	C	6.75E-06	0.000226384	CTD-2311A18.1
rs113438017	7	146153929	T	C	6.80E-06	5.31E-05	CNTNAP2
rs115029880	1	76025899	C	T	6.83E-06	0.015814	SLC44A5
7:70702497_GA G	7	70702497	G	GA	6.83E-06	0.0218837	/
rs6583122	1	105651943	C	A	6.87E-06	0.0262948	RP11-414B7.1
rs4847088	1	105647513	T	C	6.88E-06	0.0262948	RP11-414B7.1
rs144452076	11	68552827	A	G	6.88E-06	0.000198443	CPT1A
rs10881249	1	105648599	A	T	6.88E-06	0.026355	RP11-414B7.1
rs7415734	1	105652214	G	T	6.88E-06	0.0263409	RP11-414B7.1
rs11184434	1	105655745	T	C	6.89E-06	0.0263359	RP11-414B7.1
rs6964303	7	139009280	C	A	6.89E-06	0.0268395	UBN2
rs11184424	1	105647606	T	C	6.89E-06	0.0263922	RP11-414B7.1
rs11184425	1	105647638	C	A	6.89E-06	0.0263922	RP11-414B7.1
rs7517313	1	105648060	T	C	6.89E-06	0.0263922	RP11-414B7.1
4:122317716_A AAAG A	4	122317716	A	AAAAG	6.89E-06	0.00402034	/
rs11184431	1	105652341	T	C	6.89E-06	0.026378	RP11-414B7.1
rs7412026	1	105656613	T	G	6.90E-06	0.0263798	RP11-414B7.1
rs4847032	1	105654555	T	A	6.90E-06	0.026375	RP11-414B7.1

rs4847091	1	105654850	T	C	6.90E-06	0.026375	RP11-414B7.1
rs11184439	1	105659144	T	C	6.90E-06	0.0258315	RP11-414B7.1
rs7412489	1	105656938	A	G	6.91E-06	0.0263882	RP11-414B7.1
rs62346385	5	26910332	T	C	6.92E-06	0.0307207	CDH9
rs10881250	1	105650446	T	C	6.92E-06	0.0263476	RP11-414B7.1
rs2826177	21	21699226	T	C	6.93E-06	0.00543555	C1QBPP1
rs11184426	1	105647717	G	C	6.94E-06	0.0262709	RP11-414B7.1
rs71174839	1	241898647	GC	G	6.94E-06	0.00241487	WDR64
rs191026992	13	70414224	G	A	7.01E-06	1.14E-05	KLHL1
rs10500688	11	7291369	G	T	7.02E-06	0.035571	SYT9
rs562358754	11	62504167	GA	G	7.07E-06	2.00E-05	TTC9C
rs2826180	21	21702869	G	T	7.08E-06	0.0109784	C1QBPP1
rs148661844	12	111761334	A	G	7.09E-06	7.58E-05	CUX2
rs146777635	12	116151851	G	T	7.09E-06	3.85E-05	MED13L
rs9909104	17	18248021	C	T	7.12E-06	0.0303484	SHMT1
rs76538932	4	134269562	G	C	7.14E-06	0.0032288	PCDH10
rs1297421	17	33120317	T	A	7.15E-06	2.16E-05	CCT6B
rs10158783	1	4263519	A	G	7.15E-06	0.0428611	AJAP1
rs4847089	1	105648916	C	T	7.15E-06	0.0260511	RP11-414B7.1
rs139135933	17	22006015	T	C	7.16E-06	0.000457743	RP11-744K17.8
rs139438716	17	22007042	G	A	7.21E-06	0.000457742	RP11-744K17.8
17:21979313_A G A	17	21979313	A	AG	7.21E-06	0.000458014	/
rs765157457	17	21986388	T	TTGGCAT ATTTTGG GA	7.22E-06	0.000458383	/
17:21997356_G C G	17	21997356	G	GC	7.22E-06	0.000458387	/
rs142742957	22	47766977	G	T	7.22E-06	3.48E-05	TBC1D22A
rs149207264	17	21982057	C	A	7.22E-06	0.000457995	RP11-744K17.8
rs143148863	17	21999976	G	T	7.23E-06	0.000458333	RP11-744K17.8
rs145680787	17	21995997	A	G	7.23E-06	0.00045834	RP11-744K17.8
rs1518051	17	21985976	A	G	7.23E-06	0.00045835	RP11-744K17.8
rs148534077	17	22001104	C	T	7.23E-06	0.000458343	RP11-744K17.8
rs1914613	17	21985742	G	A	7.23E-06	0.000458348	RP11-744K17.8
rs117710326	17	22000374	T	C	7.23E-06	0.000458332	RP11-744K17.8
rs4128942	1	105645726	A	G	7.23E-06	0.0266357	RP11-414B7.1
rs75378953	17	21989903	T	C	7.23E-06	0.000458656	RP11-744K17.8
rs117398458	17	21975033	A	T	7.23E-06	0.000459653	RP11-744K17.8
rs10881245	1	105643320	T	C	7.23E-06	0.0222772	RP11-414B7.1
rs151310017	17	21989917	A	G	7.24E-06	0.000460014	RP11-744K17.8
rs137993192	17	21994809	T	C	7.25E-06	0.000458249	RP11-744K17.8
rs144173214	12	116153585	A	C	7.26E-06	3.89E-05	MED13L
rs10785727	1	105650578	A	G	7.38E-06	0.0264144	RP11-414B7.1
rs115656147	1	25548475	A	G	7.39E-06	3.11E-07	SYF2
rs56722971	3	36424375	A	T	7.39E-06	0.00131129	STAC
rs71306532	3	150666037	A	C	7.41E-06	2.26E-06	CLRN1
rs115557126	7	146145255	A	T	7.43E-06	5.31E-05	CNTNAP2
rs113530263	15	27219750	A	G	7.44E-06	1.54E-05	GABRG3
rs1389538	3	19266335	G	A	7.44E-06	0.00297092	KCNH8
rs10222511	3	131384071	T	G	7.46E-06	0.0374742	CPNE4
rs78001008	4	27485467	A	C	7.46E-06	0.00380524	STIM2
rs10779949	2	62549445	A	C	7.47E-06	0.00249851	B3GNT2
rs138134962	4	47479028	T	C	7.52E-06	0.0129401	ATP10D
rs114664970	6	40127169	C	T	7.55E-06	9.59E-07	LRFN2
rs34336908	5	26909260	CT	C	7.56E-06	0.0195004	CDH9
rs8081343	17	18199150	A	G	7.57E-06	0.0487495	TOP3A
rs78186457	13	26498014	T	G	7.60E-06	0.000168379	ATP8A2

rs80009944	7	31043227	A	G	7.61E-06	0.0307555	ADCYAP1R1
11:62512381_TA T	11	62512381	T	TA	7.62E-06	0.000609825	/
rs59750599	6	98229841	C	A	7.62E-06	0.00397958	MMS22L
rs146726391	8	6982284	G	C	7.63E-06	0.000129234	RPS3AP30
rs11184419	1	105638421	T	C	7.65E-06	0.0313797	RP11-414B7.1
rs62073650	17	18081577	A	G	7.65E-06	0.000581607	MYO15A
rs113139534	7	146147078	T	A	7.66E-06	5.30E-05	CNTNAP2
14:45802643_CT ATTT C	14	45802643	C	CTATTT	7.69E-06	2.00E-08	/
rs11041288	11	7283776	A	G	7.80E-06	0.0415639	SYT9
rs148561464	1	40603479	A	G	7.80E-06	0.00431182	RP11-115D7.3
rs145246068	10	126492394	T	C	7.81E-06	0.000113247	ABRAXAS2
rs8064657	17	55619829	G	A	7.82E-06	1.63E-07	MSI2
rs78301299	11	114965111	T	C	7.84E-06	0.000208301	CADM1
rs146011392	17	22007537	A	G	7.87E-06	0.00049004	RP11-744K17.8
rs144895463	17	22012457	T	C	7.88E-06	0.000489862	RP11-744K17.8
rs141251457	17	22012655	T	C	7.88E-06	0.000489853	RP11-744K17.8
rs143526496	17	22016206	T	A	7.88E-06	0.000489744	RP11-846F4.1
rs62541769	9	36209082	A	G	7.90E-06	0.030138	CLTA
rs2407647	21	21709136	G	A	7.96E-06	0.0185474	C1QBPP1
rs10839755	11	7288018	T	C	7.98E-06	0.0434712	SYT9
rs75497462	9	9202950	T	C	8.00E-06	0.000152885	PTPRD
rs10839754	11	7287818	A	G	8.01E-06	0.0437453	SYT9
rs6720190	2	107106572	T	G	8.04E-06	0.000134539	CD8B2
rs117343657	10	22039230	A	C	8.05E-06	0.009458	MLLT10
rs77590668	3	158116361	A	G	8.07E-06	0.00616839	RSRC1
rs141131066	3	158118893	C	T	8.08E-06	0.00619252	RSRC1
rs191738298	4	86778640	G	A	8.09E-06	8.56E-05	ARHGAP24
rs11029652	11	26646787	G	A	8.10E-06	0.0320052	ANO3
rs140263835	17	39239250	A	T	8.10E-06	0.000414378	KRTAP4-7
rs564284009	8	41648658	GAGA	G	8.11E-06	0.000838626	ANK1
rs117395564	11	104475775	A	G	8.12E-06	4.97E-05	PDGFD
rs56256051	11	12072943	G	A	8.12E-06	2.37E-06	DKK3
rs71640913	1	4257365	G	A	8.13E-06	0.0496778	AJAP1
rs542378728	9	39091561	C	T	8.15E-06	0.00202514	CNTNAP3
rs74653799	6	98226517	AG	A	8.17E-06	0.00418643	MMS22L
rs58726054	4	7560404	T	C	8.25E-06	0.00656238	SORCS2
rs116347716	7	146149451	G	A	8.31E-06	5.29E-05	CNTNAP2
rs17568237	5	75973445	T	C	8.32E-06	0.00926497	IQGAP2
rs111624519	7	146149802	A	T	8.34E-06	5.29E-05	CNTNAP2
rs770944021	22	48118271	G	GA	8.34E-06	0.0024452	FAM19A5
rs2826187	21	21709948	A	T	8.41E-06	0.0178267	C1QBPP1
rs114101428	2	62558951	T	C	8.42E-06	0.00786119	B3GNT2
rs116976804	7	144908420	G	A	8.42E-06	2.86E-06	RPL7P59
rs199568673	22	48112913	CA	C	8.43E-06	0.00145658	FAM19A5
rs138688067	3	132019987	A	G	8.49E-06	2.33E-05	ACP3
rs4877985	9	89124032	T	C	8.49E-06	0.000903378	GAS1
rs112067809	17	31702565	A	G	8.50E-06	1.26E-07	ASIC2
rs12576021	11	7287460	G	T	8.52E-06	0.0429881	SYT9
rs139037368	1	4246346	T	C	8.54E-06	0.0396106	AJAP1
rs2826185	21	21708991	A	G	8.54E-06	0.0202424	C1QBPP1
rs193227825	21	21660115	T	C	8.56E-06	0.00199695	C1QBPP1
rs202120653	19	55168250	ACATTT TCTT	A	8.60E-06	0.00105914	AC009892.9
rs10112791	8	13592517	C	G	8.61E-06	0.0367841	RP11-436P7.2
rs7498	17	18148485	A	G	8.63E-06	0.0426733	FLII
rs181235703	1	93358441	G	C	8.65E-06	0.00151932	DIPK1A

rs71428151	2	125290510	C	G	8.68E-06	3.89E-06	CNTNAP5
rs4860457	4	63051489	T	G	8.71E-06	0.0112383	RP11-84A1.1
rs79037957	16	72831111	C	G	8.78E-06	0.000498034	ZFH3
rs116824245	2	8608228	A	G	8.82E-06	7.63E-07	SNRPEP5
rs12141123	1	239611507	G	A	8.84E-06	0.00389477	CHRM3
6:65986540_AG A	6	65986540	A	AG	8.86E-06	8.07E-06	/
rs118131834	10	96504052	C	T	8.86E-06	0.0117445	CYP2C19
rs117605497	10	70106739	T	C	8.86E-06	8.03E-07	RUFY2
rs146296868	1	30406240	T	C	8.92E-06	5.86E-05	RP3-357I16.1
rs72741940	5	9187580	C	T	8.93E-06	0.0360162	SEMA5A
rs17746486	2	95722609	T	C	8.94E-06	2.32E-07	MAL
rs74670795	17	39071764	G	C	8.94E-06	0.000482467	KRT23
rs188341184	21	28781326	C	T	8.96E-06	1.58E-05	RPL10P1
rs117662606	8	95058960	A	C	8.97E-06	0.000354991	CDH17
rs117509604	6	128894951	G	A	8.98E-06	0.0357672	PTPRK
rs75077451	2	222575807	G	A	8.99E-06	0.000816895	AC079834.1
rs10137097	14	93096228	A	T	9.01E-06	0.00479553	RIN3
rs146468282	12	56768489	T	C	9.01E-06	0.00544062	APOF
rs115580702	2	25126911	G	C	9.04E-06	0.0195961	ADCY3
rs116401620	3	99168125	T	C	9.05E-06	0.00455951	COL8A1
rs141503063	4	111005626	C	A	9.06E-06	0.0342801	ELOVL6
rs2826188	21	21710072	T	G	9.07E-06	0.0179488	C1QBPP1
rs17883670	17	7591722	C	G	9.12E-06	0.0140105	WRAP53
rs74611811	5	55568117	C	T	9.13E-06	8.31E-05	PSMC1P4
rs113783935	6	20531169	A	G	9.13E-06	0.000458928	CDKAL1
rs7113137	11	7289078	C	T	9.17E-06	0.0343274	SYT9
rs9615205	22	48119371	G	T	9.23E-06	0.00225146	FAM19A5
rs61762827	4	149285042	A	G	9.25E-06	0.000941328	NR3C2
5:26916865_CA GAG C	5	26916865	C	CAGAG	9.30E-06	0.0253323	/
rs62417467	6	43007097	G	C	9.35E-06	0.00262302	CUL7
rs17497628	5	26910902	G	C	9.44E-06	0.0293633	CDH9
rs62073607	17	18071338	G	A	9.45E-06	0.00181054	MYO15A
rs115526943	3	99166047	T	G	9.48E-06	0.00453139	COL8A1
rs7730501	5	26900472	C	T	9.49E-06	0.0270911	CDH9
rs9637769	5	52235853	T	C	9.57E-06	0.0453918	ITGA1
rs567959690	13	75152464	T	TTCTATC TATCTAT CTA	9.57E-06	0.00147042	AL355390.1
rs62032667	16	55062315	T	C	9.62E-06	1.44E-05	IRX6
rs317984	5	66666739	G	A	9.64E-06	1.32E-05	CD180
rs139526467	19	29634123	A	G	9.64E-06	0.0406741	UQCRRS1
rs115243416	4	14010108	A	C	9.65E-06	0.0443517	RP11-341G5.2
rs76673557	20	17481097	T	C	9.66E-06	0.0103774	BFSP1
rs143372559	2	235193701	T	C	9.68E-06	0.0232874	SPP2
rs80198879	12	30157579	A	T	9.70E-06	4.13E-06	TMTC1
rs75318837	10	96415549	G	A	9.73E-06	0.0134788	CYP2C18
rs528391640	3	36427899	GAA	G	9.75E-06	0.00229086	/
14:102191282_C TA C	14	102191282	C	CTA	9.75E-06	0.00893158	/
rs61916670	12	29215914	C	T	9.75E-06	0.0382401	FAR2
rs7734956	5	26900903	C	T	9.76E-06	0.0279294	CDH9
rs77397336	2	222587780	A	G	9.80E-06	0.000762878	AC079834.1
rs8073387	17	39391788	G	A	9.80E-06	0.000615809	KRTAP9-8
rs17862370	7	127029562	T	C	9.85E-06	9.70E-05	ZNF800
rs17497167	5	26896286	T	C	9.85E-06	0.0272539	CDH9
rs7524475	1	92982679	T	C	9.86E-06	0.00126878	EVI5

1:105636868_TG T	1	105636868	T	TG	9.88E-06	0.0304069	/
rs6583114	1	105634963	C	T	9.90E-06	0.0209657	<i>RP11-414B7.1</i>
rs149001943	3	99174870	A	C	9.90E-06	0.00480692	<i>COL8A1</i>
rs76358560	15	71511297	G	A	9.92E-06	0.00593428	<i>THSD4</i>
rs1479685	5	26902078	C	T	9.92E-06	0.0285338	<i>CDH9</i>
rs72791324	16	75965325	T	A	9.95E-06	3.35E-05	<i>TERF2IP</i>
rs79063668	7	18994327	G	A	9.99E-06	0.00309456	<i>HDAC9</i>

Table S7. The PsRS-interacted SNPs for GAD score in discovery and replication cohort (Marked in red is significant).

SNP	CHR	Position	Eeference allele	Alternative allele	P discovery	P replication	Overlapped gene
rs146434301	18	24723498	TA	T	2.52E-10	9.04E-09	<i>CHST9</i>
rs140314791	4	68709501	T	C	1.06E-09	0.000101793	<i>TMPRSS11D</i>
rs2860008	4	68710963	C	T	1.06E-09	0.000100573	<i>TMPRSS11D</i>
rs10518045	4	68710842	C	T	1.06E-09	0.000100369	<i>TMPRSS11D</i>
rs116587563	4	68710465	A	C	1.06E-09	0.000100656	<i>TMPRSS11D</i>
rs17088693	4	68709690	C	T	1.06E-09	0.000101659	<i>TMPRSS11D</i>
rs114006170	4	68704816	T	C	1.14E-09	7.36E-05	<i>TMPRSS11D</i>
rs111606492	19	55105969	A	C	1.24E-09	6.54E-07	<i>LILRB1</i>
rs148060334	4	68705712	G	A	1.44E-09	0.00010652	<i>TMPRSS11D</i>
rs17576689	4	68704958	C	T	1.44E-09	0.000107208	<i>TMPRSS11D</i>
rs1545935	4	68700984	C	G	1.69E-09	0.000121113	<i>TMPRSS11D</i>
rs115427586	4	68681137	C	T	1.75E-09	0.000132068	<i>TMPRSS11D</i>
rs76632488	4	68684456	A	G	1.79E-09	0.000146241	<i>TMPRSS11D</i>
rs77927903	10	23161188	C	T	2.40E-09	0.00222043	<i>PIP4K2A</i>
rs184992408	18	41869044	G	T	2.65E-09	1.44E-07	<i>KRT8P5</i>
rs78422940	13	104942046	T	C	3.99E-09	4.94E-05	<i>RPL7P45</i>
rs78286508	6	153802852	G	T	7.07E-09	3.34E-06	<i>AL590867.1</i>
rs80221096	10	23188930	T	C	9.41E-09	0.00148762	<i>PIP4K2A</i>
4:68667012_ CAAT C	4	68667012	C	CAAT	1.49E-08	1.42E-05	/
rs147176127	18	32120008	C	G	1.59E-08	5.35E-07	<i>DTNA</i>
rs11638904	15	37309303	G	C	1.76E-08	0.00588768	<i>MEIS2</i>
rs10924842	1	246969261	C	G	2.26E-08	4.12E-05	<i>KIF28P</i>
rs10924841	1	246968607	C	T	2.34E-08	7.46E-05	<i>KIF28P</i>
rs4926469	1	246969804	T	G	3.12E-08	5.04E-05	<i>KIF28P</i>
rs59378072	2	8744978	T	C	3.23E-08	0.000220711	<i>SNRPEP5</i>
rs61852556	1	246970258	C	T	3.64E-08	5.61E-05	<i>KIF28P</i>
rs719764	6	152522373	A	G	3.89E-08	0.000308436	<i>SYNE1</i>
rs80024556	9	101172602	A	G	4.40E-08	0.000117894	<i>GABBR2</i>
rs80029890	7	54449520	T	G	4.41E-08	0.000423656	<i>SLC25A5P3</i>
rs4591276	19	55029367	C	G	4.54E-08	0.000717896	<i>AC008746.9</i>
rs77483076	6	152523736	C	G	7.86E-08	0.00226792	<i>SYNE1</i>
rs79630665	2	221238702	C	T	8.24E-08	0.0289031	<i>AC009310.1</i>
7:38775121_ GTGTA G	7	38775121	G	GTGTA	8.34E-08	0.0433953	/
rs115967737	1	220260674	A	G	1.05E-07	0.00787438	<i>BPNT1</i>
rs76696574	1	105668020	C	G	1.06E-07	0.000662636	<i>RP11-414B7.1</i>
rs183444862	7	120029186	G	A	1.07E-07	0.000139099	<i>KCND2</i>
rs142221374	3	153568239	G	A	1.14E-07	0.0233329	<i>C3orf79</i>
rs78006154	4	44367358	A	G	1.15E-07	0.0132134	<i>KCTD8</i>
rs147997219	19	49004917	T	C	1.22E-07	2.16E-06	<i>LMTK3</i>
rs73100617	7	32132611	G	C	1.22E-07	4.16E-05	<i>PDE1C</i>
rs11719004	3	100349	C	A	1.24E-07	0.00521654	<i>CHL1</i>
rs142882569	3	45338144	T	G	1.31E-07	0.0135181	<i>LARS2</i>
rs192339362	3	45332746	G	T	1.31E-07	0.0135186	<i>LARS2</i>
rs141360714	5	16239143	G	T	1.39E-07	0.0245929	<i>ZNF622</i>
rs139196868	1	209980595	C	T	1.66E-07	0.00430413	<i>IRF6</i>
rs115549955	3	5678469	A	G	1.80E-07	0.000176873	<i>EDEM1</i>
rs72647054	13	101504370	A	G	1.93E-07	2.28E-06	<i>NALCN</i>
rs17389618	1	209999401	G	A	1.96E-07	0.0075849	<i>DIEXF</i>
rs4926467	1	246968714	T	C	2.13E-07	0.000169522	<i>KIF28P</i>
rs111581301	16	79605807	C	G	2.20E-07	0.000680926	<i>MAF</i>
rs4926468	1	246968746	A	G	2.26E-07	0.000152563	<i>KIF28P</i>

rs188018003	7	131456777	T	C	2.37E-07	2.36E-05	AC009518.2
rs372567922	8	13564360	CA	C	2.38E-07	0.000453999	RP11-436P7.1
rs73702587	8	115472570	T	A	2.63E-07	1.18E-07	RP11-393K19.1
rs73702589	8	115475185	A	T	2.64E-07	1.20E-07	RP11-393K19.1
2:51912409_GTA_G	2	51912409	G	GTA	2.69E-07	6.72E-05	/
rs73702588	8	115472734	C	T	2.71E-07	1.25E-07	RP11-393K19.1
rs77973424	8	115473565	G	A	2.71E-07	1.25E-07	RP11-393K19.1
rs16885943	8	115499823	C	T	2.71E-07	1.26E-07	RP11-393K19.1
rs16885944	8	115499948	A	T	2.71E-07	1.26E-07	RP11-393K19.1
rs73702594	8	115483551	T	A	2.72E-07	1.25E-07	RP11-393K19.1
rs73702593	8	115483517	A	G	2.72E-07	1.25E-07	RP11-393K19.1
rs73702591	8	115483413	A	G	2.72E-07	1.25E-07	RP11-393K19.1
rs746524	8	115496875	T	C	2.82E-07	1.34E-07	RP11-393K19.1
rs73149812	22	17553526	C	T	2.84E-07	0.0045759	IL17RA
rs17653230	10	120201622	A	T	2.88E-07	0.00422966	FAM204A
rs56346559	8	115506657	C	T	2.94E-07	1.39E-07	RP11-393K19.1
rs77359095	6	153866784	C	G	2.99E-07	2.21E-05	AL590867.1
rs72746742	15	85827911	A	G	3.05E-07	0.00900568	ADAMTS7P4
rs16872719	7	21257691	A	G	3.27E-07	0.0380608	ASS1P11
rs77736207	8	115457533	G	A	3.27E-07	5.84E-08	RP11-393K19.1
rs73702585	8	115460709	A	G	3.31E-07	5.96E-08	RP11-393K19.1
rs59630764	8	115461018	A	G	3.31E-07	5.96E-08	RP11-393K19.1
rs60474673	8	115465762	C	A	3.32E-07	5.95E-08	RP11-393K19.1
rs75349344	8	115454607	T	G	3.33E-07	5.95E-08	RP11-393K19.1
rs62374568	5	132733367	T	C	3.39E-07	0.000269633	FSTL4
7:4190210_G T_G	7	4190210	G	GT	3.40E-07	0.0014428	/
rs117025112	11	967944	G	A	3.41E-07	0.021713	AP2A2
rs75123652	8	115459030	C	G	3.44E-07	5.96E-08	RP11-393K19.1
rs16885873	8	115467355	T	C	3.45E-07	1.00E-07	RP11-393K19.1
rs146468282	12	56768489	T	C	3.57E-07	0.00101217	APOF
rs78484020	3	193684005	A	G	3.73E-07	0.00165574	RP11-528A4.3
rs77767147	8	115528006	A	C	3.85E-07	1.88E-07	RP11-393K19.1
rs74803995	3	193677469	T	C	3.88E-07	0.00165759	RP11-528A4.3
rs73705321	8	115532533	C	A	4.07E-07	1.99E-07	RP11-393K19.1
rs189245179	2	84357713	T	C	4.23E-07	0.000235976	FUND2P2
rs114882422	1	188037391	A	T	4.60E-07	3.94E-07	RP11-134C1.1
rs118014449	16	6126384	C	T	4.61E-07	0.0373574	RBFOX1
rs76188550	22	34814862	A	G	4.61E-07	0.00109138	LARGE
rs141065459	8	115537595	G	A	4.80E-07	2.40E-07	RP11-393K19.1
rs568907752	1	188002743	C	G	4.83E-07	2.33E-07	RP11-134C1.1
rs141034234	3	197353587	C	T	5.20E-07	0.0464543	AC024560.3
rs724717	8	115538787	A	G	5.27E-07	2.68E-07	RP11-393K19.1
rs17354902	1	187954825	A	C	5.40E-07	7.67E-07	RP11-134C1.1
rs77458809	3	193672161	T	C	5.48E-07	0.00216756	RP11-528A4.3
rs76456149	8	115542652	T	G	5.55E-07	2.88E-07	RP11-393K19.1
rs76506384	7	54312950	T	G	5.67E-07	0.00523884	SLC25A5P3
rs113921735	12	101935985	T	G	5.77E-07	0.0203551	SPIC
rs73705323	8	115548212	T	C	6.02E-07	3.16E-07	RP11-393K19.1
rs71451165	11	29405492	T	C	6.13E-07	0.000211978	RP11-460B17.1
rs76063481	21	28728691	T	C	6.24E-07	2.16E-06	GPX1P2
rs77412674	8	115554739	T	C	6.26E-07	3.30E-07	RP11-393K19.1
rs553615290	11	46049642	AC	A	6.36E-07	0.000139642	PHF21A
rs185184464	10	25399461	C	G	6.48E-07	5.51E-06	GPR158
rs75820280	3	193676604	T	C	6.62E-07	0.00173851	RP11-528A4.3
rs12215234	6	49640046	G	A	6.64E-07	2.63E-05	RHAG
rs114336979	3	193674845	A	G	6.66E-07	0.00232473	RP11-528A4.3

4:108468503_ ATT A	4	108468503	A	ATT	6.73E-07	0.0346573	/
16:56985739_ CTT C	16	56985739	C	CTT	6.97E-07	0.000247513	/
rs73201271	4	2218685	G	A	7.09E-07	0.000105224	POLN
rs72866387	6	47831141	T	C	7.22E-07	2.90E-05	OPN5
rs182780958	3	31191252	G	A	7.32E-07	0.0328292	GADL1
rs118048058	8	136154777	C	G	7.40E-07	4.85E-07	KHDRBS3
rs146372107	8	136154729	A	C	7.40E-07	4.85E-07	KHDRBS3
rs56338040	4	108467222	T	C	7.41E-07	0.0244046	PAPSS1
rs191452721	3	31191251	T	C	7.42E-07	0.0327462	GADL1
rs149137169	8	53343488	A	C	7.45E-07	2.68E-06	ST18
rs71324488	21	47475825	T	C	7.86E-07	0.000150502	COL6A1
rs140641696	3	31210611	G	A	7.88E-07	0.0212091	GADL1
rs73705324	8	115566786	A	G	7.89E-07	4.37E-07	RP11-393K19.1
4:108467809_ CA C	4	108467809	C	CA	8.02E-07	0.0320653	/
rs73705325	8	115568873	T	G	8.05E-07	4.49E-07	RP11-393K19.1
rs73705326	8	115569591	G	A	8.05E-07	4.49E-07	RP11-393K19.1
rs6854956	4	112901719	A	G	8.12E-07	0.0237034	RP11-255I10.1
rs181518713	3	87071545	A	C	8.20E-07	0.00017019	VGLL3
rs117699451	21	28716047	T	A	8.42E-07	3.03E-06	GPX1P2
rs117223994	15	55002233	T	G	8.52E-07	0.00256556	UNC13C
rs529115038	8	115486745	GA	G	8.62E-07	3.69E-07	/
8:115477078_ AT A	8	115477078	A	AT	8.62E-07	3.66E-07	/
rs114021007	5	155373160	T	C	9.28E-07	0.0063275	SGCD
rs151336847	4	108453589	CA	C	9.49E-07	0.0431094	PAPSS1
rs115709053	1	37596458	T	G	9.50E-07	0.00853536	GRIK3
rs72671489	4	108455800	T	A	9.52E-07	0.0434715	PAPSS1
rs72671488	4	108455798	T	G	9.53E-07	0.0434769	PAPSS1
rs17037828	4	108453123	G	A	9.58E-07	0.043567	PAPSS1
rs72671487	4	108454875	A	G	9.58E-07	0.0435505	PAPSS1
rs60388823	4	108456918	G	A	9.59E-07	0.0435465	PAPSS1
rs17037832	4	108455721	T	A	9.59E-07	0.043548	PAPSS1
rs73837898	4	108457550	A	G	9.59E-07	0.0438824	PAPSS1
rs56837294	4	108456938	A	G	9.61E-07	0.0435526	PAPSS1
rs72682328	4	112901281	G	A	9.64E-07	0.0249584	RP11-255I10.1
rs201571046	8	115500163	TA	T	9.88E-07	4.07E-07	RP11-393K19.1
rs118190018	16	7319648	T	C	9.88E-07	0.000784992	RBFOX1
rs373301858	17	7862593	TA	T	1.00E-06	1.78E-06	/
rs188808988	15	36691902	A	C	1.00E-06	8.24E-08	RP11-702M1.2
rs75124487	4	108468550	C	A	1.07E-06	0.0288982	PAPSS1
rs777812851	1	246973506	A	AAAAGGA TAG	1.11E-06	1.24E-05	KIF28P
rs62344144	5	165301	A	C	1.11E-06	0.000146004	PLEKHG4B
rs6671004	1	246972086	T	A	1.12E-06	3.52E-05	KIF28P
rs6674135	1	246972200	C	T	1.15E-06	3.77E-05	KIF28P
rs1745960	13	113730600	A	T	1.16E-06	0.0223001	MCF2L
rs12124993	1	186284321	C	A	1.20E-06	0.000968027	TPR
rs79481713	3	31237386	C	T	1.23E-06	0.0244613	CNN2P6
rs140457754	3	80497135	C	T	1.25E-06	0.00219471	RP11-481N16.1
rs191883076	6	100439576	C	T	1.26E-06	2.29E-05	MCHR2
rs79282006	9	14789979	C	A	1.29E-06	0.00657357	FREM1
rs141979416	21	28387891	C	G	1.31E-06	0.0433409	ADAMTS5
rs149469089	3	68327787	G	C	1.32E-06	2.38E-05	FAM19A1
rs72682321	4	112894500	G	C	1.34E-06	0.0259013	RP11-255I10.1
rs62331694	4	112896237	C	A	1.39E-06	0.0265303	RP11-255I10.1

rs180786175	8	115517871	A	G	1.39E-06	5.77E-07	RP11-393K19.1
rs186248171	8	115517875	C	T	1.39E-06	5.77E-07	RP11-393K19.1
rs17527759	4	112915030	C	G	1.47E-06	0.044395	RP11-255I10.1
rs78981156	19	55064611	A	G	1.48E-06	0.0021199	AC009892.2
rs548073365	8	115521897	A	G	1.49E-06	6.24E-07	RP11-393K19.1
rs73022033	3	4403260	T	C	1.49E-06	0.00438654	SUMF1
rs115989117	2	215190637	A	G	1.56E-06	1.85E-06	SPAG16
rs138618203	11	9597085	A	G	1.59E-06	0.000414019	WEE1
rs17574963	10	120208008	A	C	1.61E-06	0.0125535	FAM204A
rs73705330	8	115572386	C	G	1.61E-06	1.06E-06	RP11-393K19.1
rs117512829	11	102069135	C	A	1.62E-06	0.0445885	YAP1
rs117969745	18	64889618	C	A	1.64E-06	2.90E-05	RPL31P9
rs143896981	8	115023762	G	T	1.68E-06	1.91E-07	RP11-67H2.1
rs78460917	12	90726337	C	T	1.69E-06	4.31E-05	CCER1
rs150816374	3	130211691	T	G	1.70E-06	2.11E-05	COL6A5
rs138738731	3	164647731	G	A	1.71E-06	2.04E-06	SI
rs575051668	7	31426904	T	C	1.74E-06	0.00064115	NEUROD6
rs116847314	18	61057007	C	A	1.76E-06	0.0011972	VPS4B
rs28529767	1	206300551	T	C	1.77E-06	0.00648047	CTSE
rs145816499	3	124109466	C	T	1.80E-06	1.83E-06	KALRN
rs2714445	7	79878921	T	C	1.81E-06	0.000302076	GNAI1
rs9841038	3	15453986	T	G	1.81E-06	0.0143833	METTL6
rs72685482	8	142539257	T	C	1.82E-06	2.19E-05	AC138647.1
rs4926465	1	246968455	A	G	1.84E-06	0.000394128	KIF28P
rs4912164	1	57887992	T	C	1.84E-06	0.000338405	DAB1
rs544072956	5	156344228	A	T	1.88E-06	2.66E-05	TIMD4
rs201856464	15	56592908	G	A	1.92E-06	0.000660545	TEX9
rs17179857	3	87065282	T	C	1.92E-06	0.000869089	VGLL3
rs1228912	7	84127834	G	C	1.98E-06	0.0212167	SEMA3A
rs116845939	7	88493918	G	T	2.00E-06	1.87E-05	ZNF804B
rs79498666	6	100436719	C	G	2.02E-06	2.38E-05	MCHR2
rs7531476	1	246973530	T	A	2.06E-06	2.88E-05	KIF28P
rs371045168	20	8488417	GAAGAT	G	2.06E-06	0.0484166	/
rs12646388	4	112896102	G	T	2.08E-06	0.0343955	RP11-255I10.1
rs186937865	3	61585601	C	G	2.09E-06	0.0110187	PTPRG
rs117621835	8	79883010	A	G	2.10E-06	0.0429189	IL7
rs74652565	4	79702818	T	C	2.11E-06	3.00E-07	BMP2K
rs7531462	1	246973479	G	A	2.11E-06	1.75E-05	KIF28P
rs78354327	8	115574055	A	G	2.12E-06	1.49E-06	RP11-393K19.1
rs139424815	10	3109286	G	C	2.12E-06	0.00175217	PFKP
rs183917631	14	86791060	A	G	2.15E-06	1.42E-05	FLRT2
rs115073069	20	11069473	G	T	2.15E-06	0.0225578	C20orf187
rs36187401	4	132274569	A	G	2.16E-06	0.000492283	RP11-758B24.1
rs183074991	1	95617626	G	A	2.23E-06	4.55E-07	TMEM56
rs2727729	12	119730802	T	C	2.24E-06	0.0272744	HSPB8
rs386810407	19	52384077	CTTCCAT TA	C	2.24E-06	0.0488628	ZNF577
rs77448671	16	18051633	T	C	2.33E-06	0.0245541	RPL7P47
rs75634755	20	11079395	T	C	2.34E-06	0.0238884	C20orf187
rs17867508	4	118513308	A	G	2.34E-06	0.00556917	NDST3
rs79158798	15	68287324	A	G	2.37E-06	7.55E-05	PIAS1
rs117702508	7	96505432	G	A	2.38E-06	0.0370397	DLX6
rs288794	13	68457521	T	G	2.41E-06	0.00173011	NPM1P22
rs9426273	1	246972266	T	C	2.43E-06	4.50E-05	KIF28P
rs79042120	7	130580396	C	T	2.45E-06	0.0190852	MKLN1
rs112121552	19	52385589	ACC	A	2.47E-06	0.0475311	ZNF577
rs145658929	1	246973875	A	AT	2.50E-06	2.44E-05	KIF28P
rs117929040	7	96514406	T	A	2.51E-06	0.038674	DLX6

rs35020972	3	15460692	TA	T	2.52E-06	0.0323429	METTL6
rs149179325	7	130557425	AGAGAG AAGAGA GAGATA AGAGAG	A	2.53E-06	0.0141583	MKLN1
rs3910751	2	174218857	G	A	2.59E-06	0.00111052	AC092573.2
rs11610071	12	111795257	C	A	2.62E-06	0.000303177	FAM109A
rs41281112	13	100518634	T	C	2.62E-06	0.000559024	CLYBL
rs35381071	4	68694828	T	TG	2.62E-06	0.00105586	TMPRSS11D
rs73705337	8	115574639	C	T	2.63E-06	1.95E-06	RP11-393K19.1
rs190389090	7	124083457	C	T	2.67E-06	0.00722445	SSU72P8
rs11584835	1	246973094	G	A	2.67E-06	2.80E-05	KIF28P
rs112318373	6	124221412	T	C	2.69E-06	0.000105163	NKAIN2
rs115788078	1	82901875	G	C	2.70E-06	0.0436472	ADGRL2
rs586407	11	119994765	A	G	2.75E-06	4.87E-05	TRIM29
rs61831886	10	1517146	T	C	2.78E-06	0.000868704	ADARB2
rs2005398	13	113732347	T	C	2.78E-06	0.0347182	MCF2L
rs288770	13	68454413	T	C	2.80E-06	0.00209107	NPM1P22
rs55948526	1	246973852	A	G	2.87E-06	2.95E-05	KIF28P
rs78947267	7	130555019	G	A	2.88E-06	0.0170972	MKLN1
rs7534538	1	246973700	C	T	2.88E-06	3.05E-05	KIF28P
rs75342732	7	130555355	C	T	2.88E-06	0.0170904	MKLN1
rs35913465	1	246972810	A	G	2.92E-06	3.41E-05	KIF28P
rs113846010	7	130553642	A	G	2.94E-06	0.0174271	MKLN1
rs143125011	19	1959827	C	A	2.96E-06	0.00115097	CSNK1G2
rs9877409	3	4372386	G	C	2.96E-06	0.000350935	SUMF1
rs188313541	15	68298092	T	A	2.98E-06	0.000135128	PIAS1
rs7518032	1	246973638	A	G	2.99E-06	2.93E-05	KIF28P
rs4926466	1	246968469	A	G	2.99E-06	0.000289223	KIF28P
rs17778661	19	52383288	G	C	2.99E-06	0.0495194	ZNF577
rs145121459	10	25431803	A	T	3.03E-06	0.000322188	GPR158
rs8102738	19	52388229	C	T	3.03E-06	0.0467015	ZNF577
rs77458785	19	52384295	G	T	3.03E-06	0.0493072	ZNF577
rs45437201	19	1952850	G	C	3.03E-06	0.00697524	CSNK1G2
rs59911578	19	52385597	C	G	3.04E-06	0.0494317	ZNF577
rs3007292	1	246974010	T	C	3.06E-06	2.97E-05	KIF28P
rs115084606	2	75552159	A	G	3.08E-06	0.000140524	TACR1
1:246974079_ CG C	1	246974079	C	CG	3.10E-06	3.02E-05	/
rs7515707	1	246973374	A	G	3.13E-06	3.16E-05	KIF28P
rs9597939	13	59718113	C	A	3.13E-06	0.000230259	POLR3KP1
rs288795	13	68457437	C	A	3.14E-06	0.00211849	NPM1P22
rs2280277	2	240656525	C	G	3.15E-06	0.0499533	AC079612.1
rs288767	13	68456682	C	T	3.16E-06	0.00199825	NPM1P22
rs74681460	7	130544376	T	C	3.16E-06	0.0195751	MKLN1
rs17574549	10	120195786	T	G	3.19E-06	0.0236217	FAM204A
rs62329971	4	112913171	G	T	3.20E-06	0.0496766	RP11-255I10.1
10:120195780 TA T	10	120195780	T	TA	3.20E-06	0.0236009	/
rs574804956	4	108407751	CA	C	3.21E-06	0.0354429	PAPSS1
15:36754008_ GT G	15	36754008	G	GT	3.21E-06	0.000606651	/
rs2996558	1	246974187	C	T	3.24E-06	3.15E-05	KIF28P
rs75685360	12	43962152	T	C	3.26E-06	0.000662961	RP11-73B8.2
rs9686093	5	154445470	T	C	3.29E-06	3.31E-06	KIF4B
rs3007294	1	246974438	T	C	3.30E-06	3.15E-05	KIF28P
rs78117107	10	23287544	C	T	3.34E-06	0.00137597	ARMC3
rs7524529	1	246973158	T	C	3.35E-06	3.30E-05	KIF28P

rs111605732	10	131331939	G	A	3.35E-06	3.50E-10	MGMT
rs150163576	7	150055084	T	C	3.35E-06	0.0132766	RARRES2
rs142387919	7	150061074	T	C	3.40E-06	0.0117944	REPIN1
rs2996557	1	246974226	A	G	3.46E-06	3.03E-05	KIF28P
rs79525992	7	130555848	G	A	3.48E-06	0.0169657	MKLN1
rs774095435	9	18600715	T	TC	3.55E-06	0.036987	ADAMTSL1
rs188278	13	68453984	C	T	3.58E-06	0.002233	NPM1P22
rs185966	13	68454106	G	T	3.59E-06	0.00224278	NPM1P22
rs595963	6	20175722	A	G	3.59E-06	3.79E-05	MBOAT1
rs158299	13	68453900	T	C	3.61E-06	0.00221728	NPM1P22
rs71522592	8	131744663	A	G	3.62E-06	0.0207949	ASAP1
rs181320539	4	115090495	A	G	3.62E-06	0.00505178	UGT8
rs288769	13	68455565	T	C	3.64E-06	0.00218186	NPM1P22
rs142051800	7	88422978	C	A	3.65E-06	3.59E-05	ZNF804B
rs144631938	6	29476235	T	C	3.69E-06	0.00589618	RPS17P1
rs74146685	10	90032784	G	A	3.70E-06	0.0157932	RNLS
rs12983067	19	46913200	C	G	3.70E-06	0.000972848	CCDC8
rs2099647	19	1948089	T	C	3.73E-06	0.00564361	CSNK1G2
rs7520180	1	246965098	G	A	3.74E-06	0.000532954	KIF28P
rs3007293	1	246974222	A	T	3.75E-06	2.92E-05	KIF28P
rs78033352	7	50183456	C	T	3.77E-06	0.0460568	C7orf72
rs7531852	1	246973283	C	T	3.85E-06	3.28E-05	KIF28P
rs73705340	8	115577768	C	T	3.86E-06	3.02E-06	RP11-393K19.1
rs12882034	14	106519361	T	C	3.94E-06	0.000156342	IGHV3-7
rs7515514	1	246973156	A	G	4.02E-06	3.34E-05	KIF28P
rs7551504	1	246964771	T	G	4.05E-06	0.000529453	KIF28P
rs7186819	16	82706407	C	T	4.10E-06	5.88E-05	CDH13
rs62541805	9	36269958	T	C	4.11E-06	5.76E-06	GNE
rs144326611	9	36257538	T	C	4.12E-06	5.74E-06	CLTA
rs73021652	19	30739969	A	G	4.14E-06	3.46E-05	ZNF536
rs79004974	11	102052263	C	T	4.16E-06	0.00125896	YAP1
rs77215221	2	124004932	C	A	4.19E-06	0.0435129	TSN
rs113644415	18	64892371	T	C	4.23E-06	6.58E-05	RPL31P9
rs6072229	20	39629534	C	T	4.24E-06	2.03E-05	TOP1
rs142052678	13	65218913	A	G	4.24E-06	0.00126709	LGMNP1
rs55779577	19	1950112	A	T	4.25E-06	0.00691164	CSNK1G2
rs17603507	15	30234960	G	A	4.27E-06	0.000598968	TJP1
rs17177765	6	29482797	A	G	4.32E-06	0.00667183	RPS17P1
rs11661452	18	64893826	T	C	4.35E-06	6.67E-05	RPL31P9
rs145608950	1	115205487	T	G	4.35E-06	0.00175383	DENND2C
rs139499380	2	135087890	C	T	4.36E-06	0.000122537	MGAT5
rs6072230	20	39629538	G	A	4.38E-06	1.97E-05	TOP1
rs2996555	1	246974936	C	G	4.43E-06	3.81E-05	KIF28P
rs2996554	1	246975015	A	G	4.51E-06	3.91E-05	KIF28P
rs12127314	1	71472911	A	G	4.60E-06	0.00271486	PTGER3
rs72894982	11	43245078	T	C	4.65E-06	0.0368745	HNRNPKP3
rs138004333	6	69596677	C	T	4.66E-06	9.93E-05	ADGRB3
4:108382777_							
AAT A	4	108382777	A	AAT	4.68E-06	0.0410785	/
rs184134422	7	109990427	T	C	4.69E-06	0.0110573	IMMP2L
rs71426282	2	123945178	A	C	4.70E-06	0.00551093	TSN
rs79782340	7	21301707	C	T	4.73E-06	0.00273808	ASS1P11
rs138663011	11	68106952	G	A	4.74E-06	1.04E-05	LRP5
rs7867475	9	18587204	A	C	4.77E-06	0.0053389	ADAMTSL1
rs73145433	12	100178737	A	G	4.78E-06	2.84E-06	ANKS1B
8:92664237_							
AG A	8	92664237	A	AG	4.79E-06	0.01403	/
rs34694126	4	108411704	CAT	C	4.79E-06	0.0415733	/

rs17037683	4	108376221	T	A	4.80E-06	0.0418939	PAPSS1
rs72671419	4	108378789	G	A	4.80E-06	0.0418937	PAPSS1
rs7690326	4	108381672	G	A	4.80E-06	0.0418926	PAPSS1
rs7690333	4	108381681	G	A	4.80E-06	0.0418926	PAPSS1
rs28415019	4	108380916	T	G	4.80E-06	0.0418926	PAPSS1
rs1835346	6	161162290	G	A	4.82E-06	0.00843778	PLG
rs7867370	9	18587239	C	A	4.83E-06	0.00511207	ADAMTSL1
rs10631015	1	86339511	TAAAA	T	4.87E-06	0.000444197	COL24A1
rs6851675	4	108394219	C	A	4.88E-06	0.0426307	PAPSS1
rs6846065	4	108393857	G	A	4.89E-06	0.0425882	PAPSS1
rs114696892	3	77398283	A	G	4.92E-06	0.000657819	ROBO2
rs140028676	4	108375596	AT	A	4.95E-06	0.0429589	PAPSS1
rs150485043	4	108368293	A	G	4.95E-06	0.0429173	PAPSS1
rs17037768	4	108413114	G	T	4.95E-06	0.0429319	PAPSS1
rs17037762	4	108412908	C	A	4.95E-06	0.0429319	PAPSS1
rs149223968	4	108406552	G	T	4.95E-06	0.0429319	PAPSS1
rs182315905	4	108407203	T	C	4.95E-06	0.0429318	PAPSS1
rs72671459	4	108408109	A	G	4.95E-06	0.0429319	PAPSS1
rs28592707	4	108389952	C	T	4.96E-06	0.0429026	PAPSS1
rs17037711	4	108385102	T	A	4.96E-06	0.0429148	PAPSS1
18:5695961_ TAATA T	18	5695961	T	TAATA	4.98E-06	0.0153961	/
rs116683967	6	66125204	T	C	4.98E-06	8.37E-08	EYS
rs55814949	19	1953166	C	T	4.99E-06	0.00870628	CSNK1G2
4:108402730_ AG A	4	108402730	A	AG	5.10E-06	0.0432957	/
rs72669802	4	108357166	T	C	5.11E-06	0.0436385	PAPSS1
rs148661844	12	111761334	A	G	5.14E-06	0.000324024	CUX2
rs76406875	8	58821337	G	A	5.14E-06	0.0335607	FAM110B
rs149993972	8	79990982	T	C	5.17E-06	0.000934879	IL7
rs12459738	19	1932798	T	C	5.18E-06	0.00434098	CSNK1G2
rs75858231	7	130531946	A	G	5.20E-06	0.0340701	AC016831.6
rs58415489	19	1951647	T	C	5.24E-06	0.0137645	CSNK1G2
rs56256051	11	12072943	G	A	5.25E-06	5.22E-06	DKK3
rs288768	13	68456578	C	T	5.26E-06	0.00201879	NPM1P22
rs75008843	19	31786059	G	A	5.27E-06	4.96E-07	TSHZ3
rs191562832	17	57787529	T	G	5.30E-06	1.18E-05	VMP1
rs72671463	4	108410363	C	G	5.31E-06	0.0432559	PAPSS1
rs77656645	6	128232202	A	G	5.31E-06	4.63E-05	THEMIS
rs60440755	19	31782629	A	G	5.33E-06	4.96E-07	TSHZ3
rs202132012	4	108385870	TA	T	5.37E-06	0.0394987	PAPSS1
rs55965180	11	43262509	C	A	5.40E-06	0.0323695	HNRNPKP3
rs77728351	9	138656634	A	G	5.43E-06	0.00670918	KCNT1
rs77875911	19	31780846	G	C	5.44E-06	5.11E-07	TSHZ3
rs6065299	20	39640568	A	C	5.47E-06	5.64E-05	TOP1
rs73257882	20	39644855	T	C	5.49E-06	5.89E-05	TOP1
rs116205884	7	14825372	C	T	5.51E-06	7.47E-05	DGKB
rs374498896	9	82111472	G	T	5.65E-06	0.000453537	TLE4
rs1006325	20	39633603	T	C	5.65E-06	4.07E-05	TOP1
rs765689265	2	154420705	TTA	T	5.65E-06	0.0237067	/
1:157753232_ GA G	1	157753232	G	GA	5.66E-06	1.42E-07	/
rs1006383	20	39631671	G	A	5.67E-06	3.40E-05	TOP1
rs78639199	19	31779931	T	C	5.71E-06	5.40E-07	TSHZ3
rs72682332	4	112904652	T	C	5.74E-06	0.0377863	RP11-255I10.1
rs76919197	6	112495348	G	T	5.77E-06	0.0124582	LAMA4
rs6072241	20	39641473	A	G	5.78E-06	5.68E-05	TOP1
rs150622554	1	79199296	A	G	5.78E-06	1.27E-07	RP4-641G12.4

rs73257868	20	39634704	A	G	5.82E-06	3.57E-05	TOP1
rs114469298	1	95669553	T	G	5.85E-06	2.14E-06	TMEM56-RWDD3
rs2178804	7	130542828	A	G	5.85E-06	0.0200071	MKLN1
rs181750950	16	51326114	A	G	5.86E-06	4.28E-05	HNRNPA1P48
rs140918174	2	53085705	C	T	5.87E-06	3.41E-09	AC010967.1
rs112363273	20	39645285	C	T	5.87E-06	7.89E-05	TOP1
rs6442522	3	15440556	T	C	5.90E-06	0.0331808	METTL6
rs116918050	12	123610753	C	T	5.92E-06	0.00327818	PITPNM2
rs76843717	19	31798091	T	C	5.94E-06	3.40E-06	TSHZ3
rs6065298	20	39640060	A	G	5.96E-06	5.37E-05	TOP1
rs73257859	20	39630224	T	C	5.98E-06	3.10E-05	TOP1
18:5709882_ TC T	18	5709882	T	TC	6.01E-06	0.0373727	/
rs72671479	4	108435058	T	C	6.03E-06	0.0409166	PAPSS1
rs17037815	4	108444113	A	C	6.06E-06	0.0428984	PAPSS1
rs72671476	4	108430206	A	G	6.06E-06	0.0428547	PAPSS1
rs17037782	4	108421171	C	T	6.07E-06	0.0429079	PAPSS1
rs17037826	4	108449838	C	A	6.08E-06	0.0426746	PAPSS1
rs72671472	4	108426827	A	G	6.08E-06	0.0429434	PAPSS1
rs367692292	4	108448778	T	C	6.08E-06	0.0428897	PAPSS1
rs4276357	4	108446727	A	G	6.10E-06	0.0429225	PAPSS1
rs72671484	4	108442738	A	G	6.10E-06	0.042924	PAPSS1
rs148600869	4	108427635	A	G	6.10E-06	0.0429215	PAPSS1
rs17037810	4	108440616	G	A	6.10E-06	0.0429242	PAPSS1
rs199937856	4	108432358	CA	C	6.11E-06	0.0429244	PAPSS1
rs199857577	9	26001632	CT	C	6.11E-06	0.000187319	CAAP1
rs10488874	4	108420553	G	C	6.11E-06	0.0430312	PAPSS1
rs149531636	4	108425115	G	A	6.12E-06	0.0430066	PAPSS1
rs11944572	4	108435303	T	C	6.12E-06	0.042875	PAPSS1
rs73257865	20	39633163	C	T	6.17E-06	4.66E-05	TOP1
rs17037788	4	108422651	C	T	6.18E-06	0.042898	PAPSS1
rs2383080	9	18586678	G	A	6.20E-06	0.00587471	ADAMTSL1
rs6072223	20	39620847	A	T	6.21E-06	2.39E-05	TOP1
rs11532901	9	18589279	G	A	6.31E-06	0.00516579	ADAMTSL1
rs6065296	20	39629935	A	G	6.35E-06	3.12E-05	TOP1
rs141687852	8	58819162	A	G	6.37E-06	0.0337985	FAM110B
rs151197979	1	245366473	C	T	6.37E-06	3.06E-05	KIF26B
rs567959690	13	75152464	T	TTCTATCT ATCTATCT A	6.37E-06	0.00182757	AL355390.1
rs73064790	7	14822956	A	T	6.40E-06	7.56E-05	DGKB
rs12782764	10	1509658	A	G	6.41E-06	0.00219855	ADARB2
rs150382208	15	25416332	A	C	6.44E-06	0.0136607	TMEM261P1
rs6072233	20	39636872	G	C	6.45E-06	6.02E-05	TOP1
rs6072242	20	39641948	T	C	6.48E-06	6.16E-05	TOP1
18:5708886_ TA T	18	5708886	T	TA	6.49E-06	0.0381117	/
rs72671478	4	108433745	G	A	6.57E-06	0.0431617	PAPSS1
rs574823708	2	38369441	G	T	6.57E-06	0.0093273	CYP1B1
rs184514320	2	85701985	C	A	6.61E-06	0.000194042	SH2D6
rs17313391	8	131691963	T	C	6.72E-06	0.0446692	ASAP1
rs113105757	4	188335074	A	T	6.72E-06	0.00229494	MRPS36P2
rs58481964	18	5708214	A	G	6.73E-06	0.0232618	EPB41L3
rs41525951	4	68669704	C	T	6.74E-06	0.0001025	TMPRSS11D
rs116731467	3	183993361	A	G	6.79E-06	0.0127079	EIF2B5
rs78856971	4	68672846	G	T	6.81E-06	0.000107251	TMPRSS11D
rs188341184	21	28781326	C	T	6.93E-06	1.88E-05	RPL10P1
rs1576897	9	18590952	T	C	6.94E-06	0.00487921	ADAMTSL1

rs117442926	7	95414630	C	G	7.03E-06	0.00920044	DYNC1I1
rs181116195	3	124097352	A	G	7.04E-06	9.83E-07	KALRN
14:48601996_ GT G	14	48601996	G	GT	7.05E-06	0.0498665	/
rs115716922	14	48601998	G	T	7.05E-06	0.0498665	RP11-10A2.1
rs117752475	16	69122402	A	G	7.09E-06	0.0038156	TANGO6
rs4624546	3	15437073	C	T	7.11E-06	0.0405021	METTL6
rs113894469	7	130547967	G	A	7.16E-06	0.0185609	MKLN1
rs1576898	9	18590804	C	T	7.17E-06	0.00475803	ADAMTSL1
rs72874479	11	28015568	T	C	7.19E-06	0.0366406	KIF18A
rs13096970	3	15439902	C	T	7.21E-06	0.041168	METTL6
rs68122973	18	5699240	T	C	7.22E-06	0.0234662	EPB41L3
rs2121545	7	130545517	T	G	7.25E-06	0.0192884	MKLN1
rs34203236	10	1509191	A	G	7.25E-06	0.00234776	ADARB2
rs7196182	16	77841325	G	C	7.26E-06	0.0011884	VAT1L
rs12608096	18	5709890	C	T	7.29E-06	0.02401	EPB41L3
rs111614646	7	130545183	C	T	7.29E-06	0.019394	MKLN1
rs3909916	16	77854848	G	A	7.29E-06	0.00179888	VAT1L
rs12956245	18	5698267	G	T	7.33E-06	0.0235201	EPB41L3
rs6072232	20	39631197	C	A	7.35E-06	4.22E-05	TOP1
rs12605334	18	5697101	T	G	7.43E-06	0.0236251	EPB41L3
rs12437668	15	72094454	C	A	7.50E-06	0.000115761	MYO9A
rs12604811	18	5696608	T	G	7.52E-06	0.0236861	EPB41L3
rs62155760	2	84407782	G	C	7.55E-06	8.62E-06	FUNDC2P2
rs72905696	11	44612648	T	C	7.56E-06	0.000302158	CD82
rs6762167	3	15445037	T	A	7.57E-06	0.0379298	METTL6
rs9855902	3	27727219	T	C	7.58E-06	0.0215725	AC098614.2
rs77393301	7	95404500	A	G	7.58E-06	0.00858374	DYNC1I1
rs12899374	15	36753040	C	A	7.59E-06	0.00116177	RP11-702M1.2
rs2219251	3	15429168	A	G	7.59E-06	0.0421856	METTL6
rs11918807	3	15446277	T	C	7.61E-06	0.0379828	METTL6
rs73372335	10	125922227	A	G	7.62E-06	0.0117411	OAT
rs79924254	3	27729357	T	A	7.62E-06	0.0217215	AC098614.2
rs79707181	7	130540256	G	A	7.64E-06	0.0201685	MKLN1
rs4372704	16	77849042	G	T	7.67E-06	0.00158474	VAT1L
rs142860985	4	165986827	T	C	7.68E-06	0.0482662	TMEM192
rs76623227	3	27731660	G	A	7.70E-06	0.0218696	AC098614.2
rs28420508	3	27724500	G	A	7.71E-06	0.0218187	AC098614.2
rs74446329	17	68876378	A	G	7.78E-06	0.01601	RP11-1058G23.1
rs116471345	3	27741868	T	C	7.79E-06	0.0225435	AC098614.3
rs72794901	5	139214934	G	C	7.79E-06	0.000427864	PSD2
rs76079178	3	27738430	A	G	7.80E-06	0.02232	AC098614.2
rs116375996	3	27739252	A	T	7.83E-06	0.0223952	AC098614.2
rs115944578	3	27734566	A	G	7.85E-06	0.0220964	AC098614.2
rs71453327	12	42371942	A	G	7.85E-06	0.0028036	RP11-2A1.1
rs17571316	15	30173956	T	C	7.88E-06	0.00136367	TJP1
rs17576726	2	130124874	A	G	7.91E-06	1.14E-06	ISCA1P6
10:120178512 GCC G	10	120178512	G	GCC	7.97E-06	0.0443295	/
rs191510703	3	27745770	T	A	7.99E-06	0.0229251	AC098614.3
rs12934135	16	82820866	T	C	8.09E-06	0.025263	CDH13
rs146398630	11	67997388	T	C	8.10E-06	0.00344545	SUV420H1
rs141641643	6	6315590	T	C	8.26E-06	0.0326527	F13A1
18:5698307_ AT A	18	5698307	A	AT	8.29E-06	0.0344667	/
rs560287592	4	79930658	G	C	8.30E-06	3.84E-07	NAA11
rs1377723	15	36762580	G	A	8.32E-06	0.00114899	RP11-702M1.2
rs146293670	1	220268018	A	G	8.37E-06	0.0126806	IARS2

rs28588099	3	27751264	T	C	8.38E-06	0.0239693	<i>EOMES</i>
rs80081239	20	2848083	A	G	8.44E-06	0.00457005	<i>PTPRA</i>
8:115482375_ ATAGT A	8	115482375	A	ATAGT	8.46E-06	8.17E-05	/
rs7179674	15	36756990	G	A	8.47E-06	0.00117574	<i>RP11-702M1.2</i>
rs75819398	4	127643768	C	T	8.52E-06	0.00154475	<i>RBM48P1</i>
rs9847430	3	15449640	T	G	8.52E-06	0.0391651	<i>METTL6</i>
rs182562905	8	3752943	C	T	8.60E-06	1.65E-05	<i>CSMD1</i>
rs533829772	5	176096	T	C	8.62E-06	0.0184653	<i>PLEKHG4B</i>
rs13075694	3	15450400	T	C	8.66E-06	0.0398792	<i>METTL6</i>
rs13075773	3	15450569	T	A	8.68E-06	0.0398921	<i>METTL6</i>
rs72990900	2	211082539	A	G	8.69E-06	0.00108719	<i>ACADL</i>
rs6792128	3	15458857	G	A	8.70E-06	0.0405358	<i>METTL6</i>
rs3861261	16	77854705	G	C	8.75E-06	0.00271466	<i>VAT1L</i>
rs80072402	18	6660730	G	A	8.76E-06	0.000141574	<i>ARHGAP28</i>
rs117618378	7	130538887	C	G	8.92E-06	0.0168143	<i>MKLN1</i>
rs116818000	3	27753310	G	A	8.92E-06	0.0246766	<i>EOMES</i>
rs75404987	8	80026287	A	G	8.92E-06	0.000535667	<i>IL7</i>
rs77082285	19	52387583	A	G	8.95E-06	0.0491307	<i>ZNF577</i>
rs75486749	20	39966771	T	C	8.98E-06	0.00290765	<i>LPIN3</i>
rs1202201	6	20162878	A	G	9.03E-06	0.0174228	<i>MBOAT1</i>
rs79860681	20	39964461	A	G	9.14E-06	0.00281089	<i>RP3-450M14.1</i>
rs72841922	2	84338670	G	T	9.15E-06	0.00011279	<i>FUNDCC2P2</i>
rs10204812	2	236410779	G	A	9.25E-06	0.0169784	<i>AGAP1</i>
rs6065337	20	39966060	A	C	9.31E-06	0.00286039	<i>LPIN3</i>
rs6072343	20	39968188	A	G	9.32E-06	0.00283734	<i>LPIN3</i>
rs56160161	3	112572246	T	C	9.42E-06	1.84E-05	<i>CD200R1</i>
rs113331764	16	77855470	G	A	9.43E-06	0.00279707	<i>VAT1L</i>
rs34040681	10	1509044	T	G	9.48E-06	0.00373332	<i>ADARB2</i>
rs114250585	4	68667630	A	G	9.49E-06	7.17E-05	<i>TMPRSS11D</i>
rs60108251	3	127176185	T	G	9.65E-06	5.73E-05	<i>TPRA1</i>
rs72794900	5	139212839	T	C	9.66E-06	0.000454289	<i>PSD2</i>
rs538443508	11	8727602	C	G	9.71E-06	9.10E-05	<i>DENND2B</i>
rs71309890	3	2401368	A	C	9.80E-06	0.00116016	<i>CNTN4</i>
rs9587342	13	107936790	A	G	9.89E-06	0.00939356	<i>FAM155A</i>
rs74431945	4	79448289	C	T	9.97E-06	6.47E-06	<i>FRAS1</i>

Table S8. The PsRS-interacted SNPs for self-reported depression in discovery and replication

SNP	CHR	Position	Eeference allele	Alternative allele	<i>P</i> discovery	<i>P</i> replication	Overlapped gene
rs13270264	8	15186872	A	G	4.15E-07	0.0495191	<i>RP11-782K4.1</i>
rs112858627	6	21805878	C	T	7.25E-07	0.0465774	<i>RP11-524C21.1</i>
rs59097328	6	21806250	A	G	7.43E-07	0.0432458	<i>RP11-524C21.1</i>
rs759904442	6	21800562	T	TAGTTCAT AAA	9.32E-07	0.0329306	/
6:21799264_ TA T	6	21799264	T	TA	1.04E-06	0.0314449	/
rs7738357	6	21797634	T	C	1.12E-06	0.0346179	<i>RP11-524C21.1</i>
rs34532408	6	21807304	A	T	1.18E-06	0.0425854	<i>RP11-524C21.1</i>
rs7738472	6	21797544	T	G	1.57E-06	0.0359061	<i>RP11-524C21.1</i>
rs6933786	6	21799200	C	T	1.72E-06	0.0359753	<i>RP11-524C21.1</i>
6:21794731_ AAT A	6	21794731	A	AAT	1.72E-06	0.0345461	/
rs9358459	6	21796788	C	G	1.76E-06	0.0374412	<i>RP11-524C21.1</i>
rs9358458	6	21796608	A	C	1.93E-06	0.0467082	<i>RP11-524C21.1</i>
rs9847419	3	61785125	G	A	2.07E-06	0.0133945	<i>PTPRG</i>
rs6935843	6	21796294	T	A	2.29E-06	0.0367143	<i>RP11-524C21.1</i>
rs796820303	6	21793906	G	GT	2.39E-06	0.0410176	/
rs1819685	13	63908772	G	A	2.42E-06	0.0011219	<i>OR7E156P</i>
rs79164741	13	63911387	A	T	2.43E-06	0.0010697	<i>OR7E156P</i>
rs115554083	13	63911397	T	C	2.43E-06	0.0010784	<i>OR7E156P</i>
rs4482153	13	63906500	G	A	2.46E-06	0.0011536	<i>OR7E156P</i>
rs116429100	13	63905839	T	C	2.47E-06	0.0011685	<i>OR7E156P</i>
rs9368349	6	21796583	C	A	2.85E-06	0.0443512	<i>RP11-524C21.1</i>
rs117966702	13	63910539	A	G	2.91E-06	0.0009499	<i>OR7E156P</i>
rs2181361	6	21793962	C	T	3.43E-06	0.039558	<i>RP11-524C21.1</i>
rs2181360	6	21793478	C	T	3.62E-06	0.0360652	<i>RP11-524C21.1</i>
13:63910097 AT A	13	63910097	A	AT	4.71E-06	0.001187	/
rs13212386	6	21795567	G	A	5.94E-06	0.0308483	<i>RP11-524C21.1</i>
rs144588845	11	4330769	G	C	6.60E-06	0.0020052	<i>SSU72P4</i>
6:21752673_ AT A	6	21752673	A	AT	8.69E-06	0.002881	/
rs12002153	9	89300815	A	G	8.87E-06	0.0163041	<i>GAS1</i>
rs142183465	6	21781403	TTGTGT G	T	9.03E-06	0.0200467	<i>RP11-524C21.1</i>

Table S9. The PsRS-interacted SNPs for self-reported anxiety in discovery and replication cohort.

SNP	CHR	Position	Eeference allele	Alternative allele	P discovery	P replication	Overlapped gene
rs199600376	3	141387404	TTTTG	T	2.81E-08	0.0219056	RASA2
rs62484606	8	4629117	C	G	1.29E-07	0.0106378	CSMD1
rs111635254	3	1355796	C	A	1.38E-07	0.00910829	CNTN6
rs1544975	9	78076173	A	T	5.46E-07	0.0238249	RP11-360J12.1
rs4803133	19	53974402	G	C	5.58E-07	0.00133277	ZNF813
rs1359805	9	78080621	C	G	9.17E-07	0.0209027	RP11-360J12.1
rs11780422	8	139916909	G	A	9.42E-07	0.0101858	COL22A1
rs7038910	9	78078806	C	G	9.72E-07	0.0235201	RP11-360J12.1
rs4744749	9	78084484	C	G	9.78E-07	0.0204204	RP11-360J12.1
rs4745404	9	78072761	C	T	1.00E-06	0.0384841	RP11-360J12.1
rs7824825	8	139916826	G	A	1.01E-06	0.00763952	COL22A1
rs7828583	8	139916824	A	T	1.03E-06	0.004864	COL22A1
rs7828568	8	139916797	C	T	1.07E-06	0.00722421	COL22A1
9:78080525_AT_	9	78080525	A	AT	1.19E-06	0.0178178	/
rs1359806	9	78080515	G	A	1.21E-06	0.0237036	RP11-360J12.1
rs1123758	8	139889659	G	A	1.96E-06	0.0315975	COL22A1
rs553504	9	78081291	T	C	2.24E-06	0.00494627	RP11-360J12.1
rs2294845	1	210553523	A	C	2.75E-06	0.0103136	HHAT
rs524314	9	78089799	A	C	2.83E-06	0.00571424	RP11-360J12.1
rs113901498	19	53974835	T	G	3.55E-06	0.00162366	ZNF813
rs524346	9	78089813	G	A	3.68E-06	0.00673008	RP11-360J12.1
rs10124225	9	78069874	T	G	3.70E-06	0.0124595	RP11-360J12.1
rs11144445	9	78110424	A	C	4.09E-06	0.00484006	RP11-360J12.1
8:139916850_AT_A	8	139916850	A	AT	4.33E-06	0.00795844	/
9:78108497_AAA CAATGCTGCAG A	9	78108497	A	AAACAAT GCTGCAG	4.56E-06	0.00578749	/
rs7866499	9	78108533	T	C	4.86E-06	0.00650209	RP11-360J12.1
rs752603387	9	94203050	T	TGCTTAG GA	5.03E-06	0.00500318	/
rs7862507	9	78108367	A	G	5.57E-06	0.0061998	RP11-360J12.1
rs1409933	9	78110916	C	T	5.57E-06	0.00623897	RP11-360J12.1
rs1409932	9	78110868	C	T	5.57E-06	0.00624269	RP11-360J12.1
rs1581881	9	78110317	C	G	5.57E-06	0.00624279	RP11-360J12.1
rs1409931	9	78110775	A	G	5.59E-06	0.0062445	RP11-360J12.1
rs7032347	9	78109702	C	T	5.60E-06	0.006247	RP11-360J12.1
rs1581880	9	78110159	G	T	5.65E-06	0.00626044	RP11-360J12.1
rs1854134	9	78109029	G	A	5.76E-06	0.00631515	RP11-360J12.1
rs1327369	9	78108869	G	A	5.76E-06	0.00631515	RP11-360J12.1
rs1854133	9	78108811	C	T	5.94E-06	0.0066043	RP11-360J12.1
rs528127	9	78111430	G	A	6.27E-06	0.00578447	RP11-360J12.1
rs3094188	6	31142245	A	C	6.33E-06	0.00322051	POU5F1
rs140124660	1	45418936	GA	G	6.73E-06	7.32E-06	EIF2B3
rs12424302	12	94881159	C	T	7.38E-06	0.0496239	CEP83
rs75586365	16	30996363	T	C	7.46E-06	0.00107468	SETD1A
rs777711382	5	96375135	A	AT	7.63E-06	0.0124123	LNPEP
rs13161540	5	96375671	G	A	8.00E-06	0.0148619	LNPEP
rs76611117	3	186738426	A	C	8.00E-06	0.0153969	ST6GAL1
rs13165925	5	96375851	C	T	8.09E-06	0.0129172	LNPEP
rs536195237	4	70816621	CA	C	8.12E-06	0.00389303	/
rs80123179	5	8916500	AAAG	A	8.22E-06	0.0144316	SEMA5A
rs7706943	5	96376766	A	T	8.42E-06	0.0145159	LNPEP
rs3846108	3	10379337	A	G	8.86E-06	0.0106297	ATP2B2
rs115944865	4	138117192	T	C	9.64E-06	0.000309524	TERF1P3

Table S10. Functional analysis results for PHQ score candidate genes.

Category	GeneSet	P	Genes
GO bp	GOBP ROUNDABOUT SIGNALING	1.37E-05	ROBO1:SLIT2
GO bp	GOBP VENTRICULAR SEPTUM MORPHOGENESIS	1.83E-05	PROX1:ROBO1:SLIT2
GO bp	GOBP CEREBRAL CORTEX TANGENTIAL MIGRATION	2.06E-05	ROBO1:SLIT2
GO bp	GOBP NEGATIVE REGULATION OF CHEMOKINE MEDIATED SIGNALING PATHWAY	2.88E-05	ROBO1:SLIT2
GO bp	GOBP OLFACTORY BULB INTERNEURON DEVELOPMENT	3.83E-05	ROBO1:SLIT2
GO bp	GOBP TANGENTIAL MIGRATION FROM THE SUBVENTRICULAR ZONE TO THE OLFACTORY BULB	3.83E-05	ROBO1:SLIT2
GWAScatalog	Adult body size	1.27E-06	ROBO1:GBE1:XXYL T1:LCORL:SLIT2:PR R16:CDH7
Reactome	REACTOME INACTIVATION OF CDC42 AND RAC1	2.88E-05	ROBO1:SLIT2
Reactome	REACTOME ROLE OF ABL IN ROBO SLIT SIGNALING	3.83E-05	ROBO1:SLIT2
Reactome	REACTOME REGULATION OF COMMISSURAL AXON PATHFINDING BY SLIT AND ROBO	6.15E-05	ROBO1:SLIT2
Reactome	REACTOME ACTIVATION OF RAC1	0.000106	ROBO1:SLIT2

Table S11. Multi-omics-based validation for top candidate genes of mental phenotypes.

Phenotype	Candidate Gene	Function confirmation		
		Gene level(GWAS catalog)	Transcript level(TWAS Atlas)	Protein level(UniPort)
PHQ score	<i>CD69</i>	Drinks per week	Lymphocyte Count	
	<i>LCORL</i>	General cognitive	Intelligence	
	<i>CTBP2P3</i>	Depression severity * hours spent watching television interaction		
	<i>ST18</i>	Psychotic experience (distressing)		
	<i>TMPRSS11D</i>	Cognitive performance		
	<i>RPL31P9</i>	Cigarette consumption * hours spent using computers interaction		
	<i>EPB41L1</i>			Intellectual developmental disorder, autosomal dominant 11 (MRD11)
	<i>MYO9A</i>		Neuroimaging Measurement	
	<i>GBE1</i>	Sensitivity to environmental stress and adversity	Attention Deficit Hyperactivity Disorder	
	<i>DKK2</i>	Resting-state electroencephalogram vigilance		
	<i>ROBO1</i>	Facial emotion recognition (fearful faces)	Waist Circumference	Neurooculorenal syndrome (NORS)
	<i>TJP1</i>	Response to antipsychotic treatment		
	<i>SLIT2</i>	Brain morphology (MOSTest)	Body Fat Percentage	
	<i>LILRB1</i>		High-Density Lipoproteins	
GAD score	<i>CHST9</i>	Severe depressive disorders in coronary artery disease	Attention Deficit Hyperactivity Disorder	
	<i>TMPRSS11D</i>	Cognitive performance		
	<i>PIP4K2A</i>	Sensitivity to environmental stress and adversity	Attention Deficit Hyperactivity Disorder	
	<i>RPL7P45</i>	Insomnia		