

Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Association with Unexpected Common Diseases

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1 Description of participant studies and phenotype definition

Bonn: All cases were recruited by dermatologists at the Department of Dermatology, University of Düsseldorf, Germany. Males who were <30 years of age having AGA of grades IV-VII or <40 years having AGA of grades V-VII[1]. Population-based controls were recruited at the University of Essen for the Heinz Nixdorf Recall cohort (Risk Factors, Evaluation of Coronary Calcium and Lifestyle). All the cases and controls were of German descent and their baldness status were assessed by dermatologist and documented by photographs. The current sample size consists of 582 cases and 347 controls.

CoLaus: Members of this cohort were randomly selected from permanent residents of Lausanne, Switzerland between 2003 and 2006[2,3]. Only individuals with 4 European grandparents were eligible for inclusion in the GWA study. Men were considered to have androgenic alopecia if they experienced Hamilton grade V-VII alopecia between the ages of 35 and 65, while controls were men displaying no hair loss (Hamilton grade I) between ages 45 and 55 or grade II between the ages of 56 and 75. Age of onset was assessed by questionnaire. Participants were recruited and assessed by nurses who had been specifically trained to assess for androgenic alopecia. The current study sample consists of 578 cases and 547 controls.

TwinsUK: The TwinsUK cohort is a population-based sample of Britons, unselected for any disease or trait, which is representative of the UK singleton population[4]. A dermatologist using standardized photographs assessed all subjects. Cases were defined as Hamilton grade V-VII and controls were those without androgenic alopecia (Hamilton grade I). The current study included 162 cases and 210 controls[5].

Nijmegen Biomedical Study. The details of this study were reported previously[6]. Briefly, this is a population-based survey conducted by the Department of Epidemiology and Biostatistics and the Department of Clinical Chemistry of the Radboud University Nijmegen Medical Center (RUNMC), in which 9,371 individuals participated from a total of 22,500 age and sex stratified, randomly selected inhabitants of Nijmegen. Individuals in the Nijmegen Biomedical Study were invited to participate in a study on gene-environment interactions in multifactorial diseases, such as cancer. All participants are of self-reported European descent. In a second phase of this project, participants completed an additional questionnaire and matched their hair pattern at 20 years, 40 years and present age to a Hamilton grading schema[7]. Affected individuals were those reporting Hamilton grade IV-VII by age 40 and controls were those with Hamilton grade I at age 50 years or older, or Hamilton grade II-III at age 60 years or older. A total of 73 cases and 132 controls were included in the current analyses.

23andMe: Participants in this study are unrelated male individuals of predominantly European ancestry, selected from users of the 23andMe Personal Genome Service[8].

Status of male pattern baldness was measured by self assessment through a web based survey. Individuals with Hamilton grade III or higher, age of onset < 40 were defined as cases, and individuals with Hamilton grade I and age ≥ 30 , or Hamilton grade II and age ≥ 50 were considered as controls. In the current study 2,167 cases and 1,753 controls were included.

Iceland: The hair loss of study subjects and the age of onset were identified from questionnaire data. Individuals with considerable hair loss before the age of 50 years were defined as cases. Individuals older than 50 years who reported no hair loss were defined as controls. The current study includes 191 cases and 198 controls.

Australian population based twin study: Measures of hair loss were obtained in the course of an extensive semi-structured telephone interview with respondent booklet, designed to assess physical, psychological and social manifestations of alcoholism and related disorders, conducted with 6265 twins born 1964-71 from the volunteer based Australian Twin Registry. All males (45% of the sample) were asked to rate their degree of hair loss, if any, using the Hamilton-Norwood Baldness scale, which was printed in the respondent booklet). This data collection scheme was validated in a study by Ellis et al.[9]. Individuals with hair loss Hamilton-Norwood type III or greater were classified as cases and population based individuals were recruited as controls. The current analyses consist of 138 unrelated cases and 5728 unrelated controls.

THISEAS: The THISEAS study is a case- control study for coronary artery disease. As part of the study, hair status was assessed in male individuals by trained scientists. The pattern of AGA was determined using the Hamilton and Norwood classification. The controls were those with no hair loss or those with Hamilton grade II at the age of 50 years or older. Participants with Hamilton grade III or higher, age of onset < 50 years were defined as cases. 297 controls and 219 cases were included in the analyses of the current study.

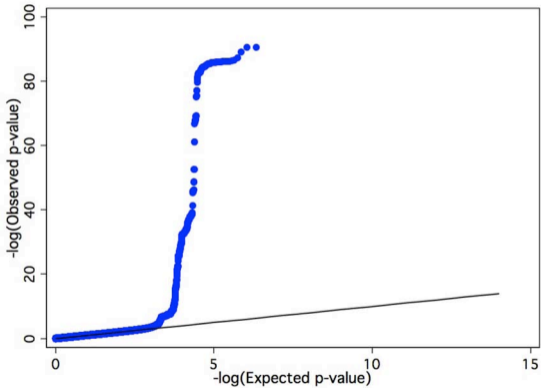
2 Tissue expression analysis

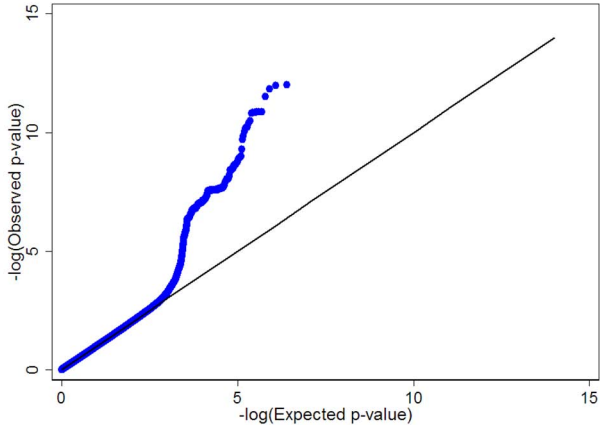
Total RNA from human hair follicles, skin from temple, scalp and whole blood was extracted (RNeasy Micro Kit, Qiagen, Hilden, Germany). Quality and quantity of the RNA was analyzed on a NanoDrop ND-1000 spectrophotometer (Peqlab Biotechnologie, Erlangen, Germany). For quality reasons, each RNA sample was additionally checked for degradation via gel electrophoresis in a BioAnalyzer 2100 (Agilent Technologies, Waldbronn, Germany) with RNA 6000 nano lab chips following manufacturer's instructions. Array-based gene expression analysis of individual tissue samples was performed on Illumina's human HT-12v3 Expression BeadChips using standard protocols (Illumina, San Diego, USA). In brief, 50ng of total RNA was reverse transcribed into cRNA and biotin-UTP labelled using the Illumina TotalPrep 96-RNA Amplification Kit (Ambion/Applied Biosystems, Darmstadt, Germany). Labelled cRNA was hybridized on Illumina HT-12v3 Expression BeadChips.

The obtained fluorescence expression data were background subtracted and quantile normalized using GenomeStudio software (Illumina, San Diego, USA). Supplementary Table3 lists all genes shown in Figure 1 that neighbour the SNP achieving the most significant p-value at the respective identified risk loci for AGA. The average signal (AVG-signal) of identical probes and the detection p-values (which is significant, if a gene is reliably expressed) are shown for each transcript tested. If the expression of a respective gene was detected by more than one Illumina probe, the probe with the best expression values based on all samples tested is presented. The same applies, if several probes detected different transcript variants of a respective gene. Non-present fluorescence intensity after background subtraction was marked as “-“ and defined as not expressed in the corresponding tissue.

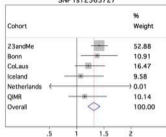
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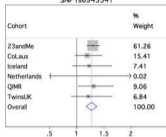




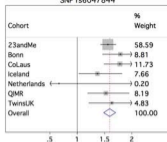
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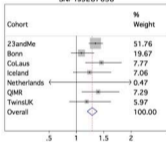
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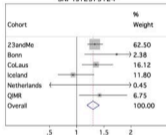
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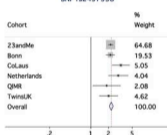
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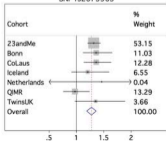
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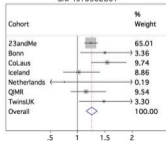


Table S1 Genotyping, imputation and statistical analysis used in the GWA studies

Study	Genotyping		Imputation method	Genome-wide association analysis	
	platforms/chips	calling algorithm		software ^a	λ_{gc}
Bonn	Illumina 317K, 317Kduo, 550K, 610K	Illumina BeadStudio/Genome Studio	IMPUTE[1]	SNPTEST[1]	1.062
CoLaus	Affymetrix GeneChip Human Mapping 500K	BRLMM algorithm	IMPUTE	PLINK[2]	1.024
Iceland	Illumina 317k, 317kduo, CNV370k	Illumina BeadStudio	IMPUTE	SNPTEST	1.022
Nijmegen	Illumina CNV370k	Illumina BeadStudio	IMPUTE	SNPTEST	1.001
TwinsUK	Illumina 610K	Illuminus	IMPUTE	GWAF ^b [3]	1.016
23andMe	Illumina 550+	Illumina GenomeStudio	MACH	R	1.033
Australian	Illumina 317K, CNV370K, 610K	Illumina BeadStudio/Genome Studio	MACH	PLINK	1.016
THISEAS	MetaboChip	GenoSNP	IMPUTE	PLINK	N/A

^a-Association analysis on X chromosome was undertaken by using Clayton's methods[4] implemented in INTERSNP[5]

^b-The relatedness between siblings were corrected by generalized estimating equations[6] implemented in GWAF

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Table S2 Genome-Wide Significant SNPs in fixed-effect model ($p < 5 \times 10^{-8}$)

Chr.	Position	SNP	Effect Allele	Non Effect Allele	Odds Ratio (95% CI)	p-value	Q p-value	r^2
1	10955414	rs2003046	C	A	1.31 (1.21, 1.42)	1.99E-10	0.41	0.02
1	10955669	rs12565727	G	A	0.75 (0.69, 0.82)	9.07E-11	0.43	0
1	10957404	rs9659356	G	A	0.77 (0.71, 0.84)	1.29E-09	0.44	0
1	10960323	rs11576658	T	C	0.77 (0.71, 0.84)	1.06E-09	0.47	0
1	10961063	rs11121667	T	C	0.77 (0.71, 0.84)	1.17E-09	0.44	0
1	10962780	rs7542158	G	A	1.29 (1.19, 1.41)	1.20E-09	0.44	0
1	10966448	rs9430158	G	C	1.29 (1.18, 1.41)	2.43E-08	0.5	0
1	10967416	rs7547568	T	A	1.29 (1.18, 1.42)	2.20E-08	0.51	0
2	239357664	rs4075846	T	A	1.26 (1.17, 1.36)	3.61E-09	0.46	0
2	239359376	rs9287638	C	A	0.77 (0.71, 0.82)	1.01E-12	0.35	0.1
2	239362192	rs9711321	T	C	1.26 (1.18, 1.35)	6.05E-11	0.6	0
2	239362352	rs11683401	T	C	1.26 (1.18, 1.35)	6.02E-11	0.6	0
2	239387248	rs9287645	T	C	1.23 (1.14, 1.31)	1.10E-08	0.65	0
2	239399424	rs9752491	G	A	0.79 (0.73, 0.86)	3.78E-08	0.96	0
2	239400560	rs9751918	G	A	1.27 (1.17, 1.38)	1.71E-08	0.94	0
2	239401104	rs9750952	T	C	1.26 (1.17, 1.37)	2.21E-08	0.97	0
2	239414160	rs12613833	T	C	0.78 (0.72, 0.85)	2.84E-08	0.93	0
7	18833368	rs3852256	G	A	1.26 (1.16, 1.37)	2.16E-08	0.1	0.46
7	18834556	rs17349860	T	C	1.26 (1.16, 1.36)	8.66E-09	0.14	0.39
7	18838216	rs3852257	T	C	1.28 (1.19, 1.37)	6.75E-11	0.15	0.37
7	18840910	rs2016515	T	G	0.79 (0.74, 0.85)	9.75E-10	0.18	0.33
7	18843424	rs13238389	C	A	0.78 (0.72, 0.84)	1.46E-11	0.22	0.28
7	18843932	rs957960	C	A	0.79 (0.74, 0.85)	2.32E-09	0.26	0.23
7	18844140	rs957958	G	A	1.29 (1.2, 1.39)	1.45E-12	0.24	0.25
7	18844400	rs2073963	T	G	0.77 (0.72, 0.83)	1.08E-12	0.42	0
7	18844676	rs2073964	G	A	0.78 (0.72, 0.83)	3.06E-12	0.24	0.24
7	18847600	rs12536836	T	C	1.27 (1.18, 1.36)	4.06E-11	0.32	0.15
7	18850216	rs6461386	G	A	0.8 (0.75, 0.86)	2.19E-09	0.25	0.24
7	18856524	rs756853	G	A	1.27 (1.19, 1.36)	1.40E-11	0.12	0.4
7	18857784	rs13245206	G	A	0.78 (0.73, 0.84)	1.33E-11	0.32	0.15
7	18861422	rs10230371	T	C	0.79 (0.73, 0.84)	1.39E-11	0.19	0.31
7	18862536	rs2249817	G	A	1.27 (1.18, 1.36)	1.56E-11	0.31	0.16
7	18864830	rs6461387	G	A	0.79 (0.74, 0.85)	3.24E-11	0.28	0.2
7	18869540	rs756854	T	C	1.27 (1.18, 1.36)	1.39E-10	0.29	0.19
7	18876756	rs6461390	G	A	1.24 (1.15, 1.33)	2.44E-08	0.4	0.03
7	18878314	rs6951144	G	C	1.24 (1.15, 1.34)	1.95E-08	0.39	0.04
7	18878482	rs6951745	G	A	0.8 (0.75, 0.87)	1.32E-08	0.49	0
7	18879328	rs6461392	G	A	0.8 (0.74, 0.87)	1.24E-08	0.49	0
7	18879340	rs6461393	T	G	0.81 (0.75, 0.87)	2.89E-08	0.22	0.29
7	18879416	rs6461394	G	C	1.25 (1.16, 1.34)	9.54E-09	0.46	0
7	18879904	rs7794241	C	A	0.81 (0.75, 0.87)	2.67E-08	0.29	0.18
7	18880776	rs2286213	G	C	1.24 (1.15, 1.34)	2.60E-08	0.29	0.18
7	18881952	rs10237149	G	A	0.81 (0.75, 0.87)	3.73E-08	0.24	0.26
7	18882084	rs10237366	G	C	0.81 (0.75, 0.87)	4.56E-08	0.39	0.04
7	18882192	rs10237280	T	C	1.24 (1.15, 1.33)	3.49E-08	0.39	0.04
7	18882226	rs13233322	C	A	0.81 (0.75, 0.87)	3.81E-08	0.23	0.27
7	18882400	rs10486314	G	A	1.23 (1.14, 1.33)	4.96E-08	0.15	0.38
7	68245712	rs6947344	T	C	1.27 (1.18, 1.38)	2.14E-09	0.96	0
7	68248320	rs4718865	G	A	0.79 (0.73, 0.85)	1.81E-09	0.94	0
7	68249896	rs6945541	T	C	0.78 (0.73, 0.85)	1.71E-09	0.97	0
7	68249920	rs6965168	G	A	0.79 (0.73, 0.85)	2.41E-09	0.95	0
7	68250480	rs1916029	T	G	0.79 (0.73, 0.85)	2.46E-09	0.95	0
7	68253800	rs1195228	G	A	0.79 (0.72, 0.85)	9.92E-09	0.93	0
17	41255568	rs17762954	T	C	0.76 (0.68, 0.83)	4.87E-08	0.44	0
17	41279432	rs12185233	G	C	1.28 (1.17, 1.39)	3.58E-08	0.46	0
17	41279484	rs12185235	T	C	0.78 (0.72, 0.85)	2.83E-08	0.46	0
17	41279712	rs11079725	T	C	1.28 (1.17, 1.39)	2.66E-08	0.46	0

17	41279852	rs12373123	T	C	1.28 (1.17, 1.39)	2.58E-08	0.46	0
17	41279980	rs12373142	G	C	0.78 (0.72, 0.85)	2.46E-08	0.46	0
17	41280000	rs12373124	T	C	1.33 (1.21, 1.45)	5.07E-10	0.25	0.24
17	41280116	rs12373168	C	A	0.78 (0.72, 0.85)	2.38E-08	0.46	0
17	41280300	rs17690661	G	A	1.28 (1.18, 1.4)	2.12E-08	0.46	0
17	41280584	rs17690679	G	A	0.78 (0.72, 0.85)	2.02E-08	0.46	0
17	41281384	rs17769490	G	A	1.28 (1.18, 1.4)	1.84E-08	0.45	0
17	41283072	rs17769552	G	A	1.29 (1.18, 1.4)	1.32E-08	0.51	0
17	41284392	rs885639	T	G	1.28 (1.18, 1.4)	1.58E-08	0.45	0
17	41286904	rs2873269	T	C	0.78 (0.71, 0.85)	1.68E-08	0.45	0
17	41288960	rs10445368	T	C	0.78 (0.71, 0.85)	2.05E-08	0.43	0
17	41333624	rs1864325	T	C	0.79 (0.73, 0.86)	4.96E-08	0.38	0.07
17	41381748	rs242559	C	A	0.79 (0.73, 0.86)	3.53E-08	0.6	0
17	41388632	rs17571718	T	C	1.27 (1.16, 1.38)	4.51E-08	0.42	0.01
17	41388780	rs17571739	T	C	1.27 (1.17, 1.38)	4.15E-08	0.42	0.01
17	41389668	rs17571781	T	C	1.27 (1.17, 1.38)	3.98E-08	0.41	0.01
17	41390696	rs17571809	G	A	0.79 (0.72, 0.86)	3.93E-08	0.42	0.01
17	41391204	rs17650771	G	A	0.78 (0.71, 0.85)	4.53E-08	0.35	0.11
17	41391544	rs17571857	G	A	0.79 (0.72, 0.86)	3.08E-08	0.41	0.02
17	41392624	rs17650818	T	C	1.27 (1.17, 1.38)	2.96E-08	0.41	0.02
17	41393328	rs17650842	G	A	0.79 (0.72, 0.86)	2.82E-08	0.41	0.02
17	41394844	rs17650860	G	A	1.27 (1.17, 1.38)	2.77E-08	0.41	0.02
17	41395352	rs17650872	T	G	0.79 (0.72, 0.85)	2.55E-08	0.4	0.03
17	41395528	rs17650901	G	A	0.79 (0.72, 0.86)	2.75E-08	0.41	0.02
17	41400056	rs17650973	T	A	0.79 (0.72, 0.86)	2.71E-08	0.42	0.01
17	41400344	rs17650991	C	A	0.77 (0.71, 0.84)	6.85E-09	0.45	0
17	41400820	rs17572147	G	A	0.79 (0.72, 0.86)	2.71E-08	0.42	0.01
17	41401808	rs17572169	T	C	0.79 (0.72, 0.86)	2.71E-08	0.42	0.01
17	41405384	rs17651093	G	A	1.27 (1.17, 1.38)	2.65E-08	0.42	0.01
17	41405704	rs17572248	G	A	0.79 (0.72, 0.86)	2.69E-08	0.42	0.01
17	41406176	rs17651134	G	A	1.27 (1.17, 1.38)	2.77E-08	0.42	0
17	41407680	rs1800547	G	A	0.79 (0.72, 0.86)	2.85E-08	0.42	0
17	41407760	rs17651213	G	A	1.27 (1.17, 1.38)	3.35E-08	0.44	0
17	41407844	rs17572361	T	C	1.27 (1.17, 1.38)	2.84E-08	0.42	0
17	41408120	rs17651243	G	A	1.27 (1.17, 1.38)	2.81E-08	0.42	0
17	41409284	rs2217394	G	A	0.79 (0.72, 0.86)	2.78E-08	0.42	0
17	41410072	rs17651285	G	A	1.27 (1.17, 1.38)	2.78E-08	0.42	0
17	41410224	rs17572467	T	C	1.27 (1.17, 1.38)	2.77E-08	0.42	0
17	41410432	rs17572495	T	G	1.27 (1.17, 1.38)	2.77E-08	0.42	0
17	41411484	rs754512	T	A	0.79 (0.72, 0.86)	2.77E-08	0.42	0
17	41412668	rs1981998	G	A	1.27 (1.17, 1.38)	2.34E-08	0.42	0
17	41413840	rs17572613	G	A	0.79 (0.72, 0.85)	2.33E-08	0.42	0
17	41414464	rs17572627	T	A	1.27 (1.17, 1.38)	2.31E-08	0.42	0
17	41414696	rs17651483	C	A	1.27 (1.17, 1.38)	2.30E-08	0.42	0.01
17	41417116	rs17651549	T	C	0.79 (0.72, 0.85)	2.28E-08	0.42	0
17	41418976	rs1529534	G	A	0.79 (0.72, 0.85)	2.24E-08	0.42	0.01
17	41419232	rs17572795	G	A	1.27 (1.17, 1.38)	2.20E-08	0.42	0.01
17	41419400	rs17572823	T	C	1.27 (1.17, 1.38)	2.21E-08	0.42	0.01
17	41419604	rs17572851	G	A	0.79 (0.72, 0.85)	2.21E-08	0.42	0.01
17	41420044	rs17572893	G	A	1.27 (1.17, 1.38)	2.22E-08	0.42	0.01
17	41420596	rs1529535	C	A	0.79 (0.72, 0.85)	2.22E-08	0.42	0.01
17	41421248	rs10445371	G	A	1.27 (1.17, 1.38)	2.42E-08	0.42	0
17	41533808	rs17660464	C	A	1.29 (1.18, 1.41)	2.60E-08	0.41	0.01
17	41545156	rs17660847	T	C	0.77 (0.7, 0.84)	2.34E-08	0.39	0.04
17	41548344	rs4630591	T	C	0.77 (0.7, 0.84)	3.47E-08	0.34	0.12
17	41577380	rs2696590	G	C	1.3 (1.19, 1.42)	2.61E-08	0.39	0.04
17	41583944	rs1918793	T	C	0.78 (0.71, 0.85)	2.43E-08	0.35	0.1
17	41584304	rs1918792	G	A	1.29 (1.18, 1.41)	2.62E-08	0.43	0
17	41584384	rs1918791	G	C	0.78 (0.71, 0.85)	2.62E-08	0.43	0
17	41584396	rs1918790	T	C	0.78 (0.71, 0.85)	2.62E-08	0.43	0
17	41584548	rs2696576	G	A	0.78 (0.71, 0.85)	2.63E-08	0.43	0
17	41584600	rs2696575	G	A	0.78 (0.71, 0.85)	2.63E-08	0.43	0
17	41585140	rs2532303	T	C	1.29 (1.18, 1.41)	2.63E-08	0.43	0

17	41585192	rs2532302	T	C	1.29 (1.18, 1.41)	2.63E-08	0.43	0
17	41585872	rs2696574	T	C	0.77 (0.7, 0.84)	2.49E-08	0.41	0.02
17	41586424	rs2696573	T	C	0.78 (0.71, 0.85)	2.66E-08	0.43	0
17	41587072	rs2532298	G	A	1.29 (1.18, 1.41)	2.65E-08	0.43	0
17	41587104	rs2532297	G	A	1.29 (1.18, 1.41)	2.65E-08	0.43	0
17	41587392	rs2696572	T	A	0.78 (0.71, 0.85)	2.66E-08	0.43	0
17	41587604	rs2532296	T	C	1.29 (1.18, 1.41)	2.66E-08	0.43	0
17	41588736	rs2109092	G	A	1.29 (1.18, 1.41)	2.66E-08	0.43	0
17	41588768	rs1534456	T	C	1.3 (1.18, 1.42)	2.45E-08	0.5	0
17	41589552	rs17662235	T	C	1.29 (1.18, 1.41)	2.66E-08	0.43	0
17	41589588	rs17585214	T	C	0.78 (0.71, 0.85)	2.67E-08	0.43	0
17	41589836	rs1528074	G	A	0.77 (0.71, 0.84)	2.46E-08	0.5	0
17	41590304	rs1406068	T	C	0.78 (0.71, 0.85)	2.68E-08	0.43	0
17	41592504	rs1528072	C	A	1.29 (1.18, 1.41)	2.98E-08	0.43	0
17	41592844	rs2532292	T	A	0.78 (0.71, 0.85)	2.69E-08	0.43	0
17	41593148	rs2696571	G	C	1.29 (1.18, 1.41)	2.71E-08	0.43	0
17	41594200	rs2532291	G	A	1.29 (1.18, 1.41)	2.75E-08	0.43	0
17	41594268	rs2532290	G	A	1.29 (1.18, 1.41)	2.76E-08	0.43	0
17	41594716	rs17662403	T	C	1.29 (1.18, 1.41)	2.76E-08	0.43	0
17	41594744	rs17585426	T	C	1.29 (1.18, 1.41)	2.77E-08	0.43	0
17	41595736	rs2532288	T	C	0.78 (0.71, 0.85)	2.78E-08	0.43	0
17	41595884	rs1918789	T	C	1.29 (1.18, 1.41)	2.79E-08	0.43	0
17	41596764	rs2141299	C	A	1.29 (1.18, 1.41)	2.79E-08	0.43	0
17	41597080	rs2696567	G	C	0.78 (0.71, 0.85)	2.79E-08	0.43	0
17	41597440	rs2532286	T	C	1.29 (1.18, 1.41)	2.80E-08	0.43	0
17	41598956	rs4792843	G	A	0.78 (0.71, 0.85)	2.80E-08	0.43	0
17	41599756	rs17585608	T	C	0.78 (0.71, 0.85)	2.80E-08	0.43	0
17	41600176	rs2696684	G	A	1.29 (1.18, 1.41)	2.80E-08	0.43	0
17	41600360	rs17585644	T	C	1.29 (1.18, 1.41)	2.82E-08	0.43	0
17	41600672	rs2532282	G	C	0.77 (0.71, 0.84)	2.62E-08	0.41	0.01
17	41600704	rs2696657	T	G	1.29 (1.18, 1.41)	2.86E-08	0.43	0
17	41600948	rs2532281	T	G	0.77 (0.71, 0.84)	2.62E-08	0.41	0.01
17	41601136	rs2532280	G	A	1.3 (1.18, 1.42)	2.64E-08	0.41	0.01
17	41601988	rs2696660	G	A	0.78 (0.71, 0.85)	2.89E-08	0.43	0
17	41602184	rs2532278	C	A	1.29 (1.18, 1.41)	2.89E-08	0.43	0
17	41602304	rs2532277	T	C	1.3 (1.18, 1.42)	2.63E-08	0.41	0.01
17	41602400	rs2532276	C	A	1.29 (1.18, 1.41)	2.78E-08	0.43	0
17	41602776	rs2532275	G	A	1.29 (1.18, 1.41)	2.88E-08	0.43	0
17	41602940	rs2532274	G	A	0.78 (0.71, 0.85)	2.44E-08	0.37	0.08
17	41603092	rs2532273	T	C	0.78 (0.71, 0.85)	2.88E-08	0.43	0
17	41603820	rs2532271	G	A	1.29 (1.18, 1.41)	2.90E-08	0.43	0
17	41604544	rs1881193	T	C	1.29 (1.18, 1.41)	2.89E-08	0.43	0
17	41604592	rs1881194	G	A	1.29 (1.18, 1.41)	2.90E-08	0.43	0
17	41604872	rs17662889	C	A	0.77 (0.7, 0.84)	2.06E-08	0.5	0
17	41605884	rs2532269	T	C	1.3 (1.18, 1.42)	2.73E-08	0.39	0.04
17	41606248	rs2532268	G	C	1.3 (1.18, 1.42)	2.60E-08	0.41	0.02
17	41612072	rs2532253	G	A	1.3 (1.18, 1.42)	2.64E-08	0.41	0.02
17	41615316	rs2732585	C	A	0.77 (0.71, 0.85)	2.71E-08	0.41	0.01
17	41615568	rs2696700	G	A	1.31 (1.19, 1.44)	2.76E-08	0.49	0
17	41621256	rs2696709	G	C	1.29 (1.18, 1.42)	2.82E-08	0.41	0.01
17	41634440	rs2696446	G	A	1.29 (1.18, 1.42)	3.46E-08	0.42	0
18	41043488	rs8083006	T	C	0.78 (0.72, 0.85)	3.25E-09	0.21	0.29
18	41054144	rs10502861	T	C	0.78 (0.72, 0.85)	2.62E-09	0.29	0.18
18	41057328	rs1381556	T	C	1.28 (1.18, 1.38)	3.70E-09	0.3	0.18
18	41058136	rs1350905	G	A	0.78 (0.72, 0.85)	3.74E-09	0.3	0.17
18	41058396	rs1350904	G	A	1.28 (1.18, 1.38)	3.74E-09	0.3	0.17
18	41058524	rs12606816	G	A	0.78 (0.72, 0.85)	3.85E-09	0.31	0.16
18	41061932	rs12959797	G	A	1.28 (1.18, 1.38)	3.40E-09	0.3	0.16
18	41064384	rs8098865	G	A	0.78 (0.72, 0.85)	3.85E-09	0.3	0.17
18	41066892	rs1903647	G	A	0.79 (0.73, 0.86)	9.84E-09	0.26	0.22
18	41066976	rs1903646	T	A	1.27 (1.17, 1.37)	9.40E-09	0.26	0.22
18	41068152	rs8085664	C	A	1.27 (1.17, 1.37)	1.07E-08	0.28	0.19
18	41068488	rs7230186	G	C	0.79 (0.73, 0.86)	9.14E-09	0.27	0.2

18	41072524	rs11082435	T	C	1.27 (1.17, 1.37)	8.27E-09	0.29	0.19
18	41075456	rs11664621	T	C	0.79 (0.73, 0.85)	9.36E-09	0.23	0.26
18	41075696	rs7240906	T	C	1.27 (1.17, 1.38)	8.69E-09	0.23	0.26
18	41075964	rs6507604	T	C	1.27 (1.17, 1.38)	6.06E-09	0.19	0.31
20	21714736	rs972014	T	C	1.51 (1.34, 1.71)	1.50E-11	0.17	0.34
20	21718656	rs1476396	G	C	1.39 (1.29, 1.5)	4.76E-17	0.23	0.27
20	21719760	rs2208309	G	A	0.72 (0.67, 0.78)	4.63E-17	0.23	0.27
20	21719844	rs2208310	T	G	0.66 (0.58, 0.75)	4.31E-10	0.14	0.39
20	21719908	rs2224366	G	C	0.66 (0.58, 0.75)	4.29E-10	0.14	0.39
20	21723784	rs1476398	G	A	1.5 (1.31, 1.71)	6.15E-09	0.1	0.43
20	21724736	rs2208312	T	C	0.74 (0.69, 0.8)	5.15E-14	0.19	0.33
20	21724876	rs2208314	C	A	1.35 (1.25, 1.45)	4.65E-14	0.19	0.33
20	21725916	rs2876622	G	A	1.39 (1.29, 1.5)	4.32E-17	0.24	0.26
20	21728196	rs6047632	T	C	1.35 (1.25, 1.45)	4.83E-14	0.17	0.35
20	21728904	rs6082512	T	C	0.72 (0.67, 0.78)	5.94E-17	0.2	0.32
20	21728972	rs6082513	C	A	1.39 (1.28, 1.49)	6.15E-17	0.2	0.32
20	21729624	rs6047635	T	G	0.66 (0.59, 0.75)	1.57E-11	0.23	0.27
20	21732132	rs873137	C	A	1.53 (1.35, 1.73)	1.08E-11	0.28	0.2
20	21733640	rs6137444	T	C	1.41 (1.31, 1.52)	1.10E-18	0.21	0.3
20	21736176	rs1540930	G	C	1.53 (1.33, 1.76)	2.72E-09	0.12	0.41
20	21736460	rs6075840	T	A	1.53 (1.35, 1.72)	1.24E-11	0.27	0.21
20	21737804	rs6137445	G	A	1.53 (1.35, 1.73)	1.13E-11	0.26	0.22
20	21738076	rs4815066	C	A	1.54 (1.34, 1.77)	2.06E-09	0.12	0.41
20	21738860	rs6137446	G	A	1.53 (1.36, 1.73)	8.77E-12	0.27	0.21
20	21739008	rs6137448	T	A	1.41 (1.31, 1.53)	9.93E-19	0.18	0.34
20	21739854	rs6047641	T	G	0.68 (0.6, 0.77)	3.97E-09	0.97	0
20	21741400	rs6047643	T	A	1.54 (1.34, 1.77)	1.78E-09	0.12	0.41
20	21744856	rs2180700	T	G	1.42 (1.31, 1.53)	8.25E-19	0.19	0.33
20	21745348	rs1540931	C	A	1.5 (1.33, 1.7)	1.06E-10	0.12	0.4
20	21749468	rs6035959	G	A	0.63 (0.56, 0.71)	2.63E-14	0.17	0.34
20	21749500	rs6082519	T	A	0.69 (0.64, 0.74)	3.15E-21	0.28	0.2
20	21751314	rs16983003	T	A	1.3 (1.2, 1.42)	1.13E-09	0.14	0.4
20	21751580	rs4281974	G	A	0.7 (0.64, 0.75)	5.11E-20	0.29	0.19
20	21760118	rs6082520	T	C	1.46 (1.35, 1.57)	4.73E-21	0.27	0.21
20	21762036	rs2224261	T	C	0.69 (0.64, 0.74)	4.98E-21	0.27	0.21
20	21763192	rs6113393	T	C	1.51 (1.4, 1.63)	1.65E-26	0.58	0
20	21766308	rs1535199	G	A	0.66 (0.61, 0.71)	1.83E-26	0.58	0
20	21769148	rs6113394	T	G	0.66 (0.61, 0.71)	1.88E-26	0.58	0
20	21769216	rs6106421	T	C	1.51 (1.4, 1.63)	1.89E-26	0.58	0
20	21769262	rs6113395	G	A	1.51 (1.4, 1.63)	1.89E-26	0.58	0
20	21769910	rs6047663	T	C	1.51 (1.4, 1.63)	1.97E-26	0.58	0
20	21772164	rs4405823	T	A	0.66 (0.62, 0.71)	1.99E-26	0.58	0
20	21772282	rs8122229	G	A	1.51 (1.4, 1.63)	2.05E-26	0.58	0
20	21778508	rs2328647	G	A	1.5 (1.4, 1.62)	3.83E-26	0.6	0
20	21781736	rs2064773	G	A	1.39 (1.29, 1.5)	2.40E-16	0.43	0
20	21781826	rs2144882	T	C	1.87 (1.53, 2.3)	1.89E-09	0.53	0
20	21790888	rs6047676	T	C	1.51 (1.4, 1.63)	1.78E-26	0.58	0
20	21792630	rs1014883	G	A	1.51 (1.4, 1.63)	1.80E-26	0.58	0
20	21792694	rs1014884	T	C	0.66 (0.62, 0.72)	2.11E-26	0.59	0
20	21792828	rs1014885	T	C	1.51 (1.4, 1.63)	1.05E-26	0.56	0
20	21795480	rs6047677	G	C	0.66 (0.62, 0.72)	2.04E-26	0.58	0
20	21798786	rs12479719	G	A	0.74 (0.69, 0.8)	2.80E-13	0.47	0
20	21798850	rs997078	T	A	0.66 (0.62, 0.72)	2.21E-26	0.58	0
20	21800048	rs987050	C	A	1.51 (1.4, 1.62)	2.92E-26	0.53	0
20	21801192	rs6047683	C	A	1.51 (1.4, 1.62)	2.39E-26	0.58	0
20	21801764	rs6047684	G	A	0.66 (0.62, 0.72)	2.39E-26	0.58	0
20	21803904	rs6047685	T	A	1.51 (1.4, 1.62)	2.39E-26	0.58	0
20	21804148	rs6035971	T	A	1.51 (1.4, 1.62)	2.40E-26	0.58	0
20	21811824	rs6113404	T	C	0.65 (0.61, 0.7)	4.21E-30	0.13	0.39
20	21814152	rs6075852	G	A	1.54 (1.44, 1.65)	7.41E-33	0.33	0.14
20	21814376	rs6075854	G	A	0.65 (0.61, 0.7)	3.04E-30	0.15	0.37
20	21814548	rs6075855	T	C	0.65 (0.61, 0.7)	4.64E-30	0.13	0.39
20	21823140	rs6035978	T	C	0.65 (0.6, 0.7)	2.47E-30	0.14	0.37

20	21823172	rs6035979	T	G	1.54 (1.43, 1.65)	2.42E-30	0.14	0.37
20	21823656	rs6047705	T	C	0.65 (0.6, 0.7)	2.34E-30	0.14	0.37
20	21825020	rs4815081	G	A	0.65 (0.6, 0.7)	2.17E-30	0.14	0.37
20	21828044	rs1998076	G	A	1.54 (1.43, 1.65)	1.89E-30	0.14	0.38
20	21832692	rs6137473	G	A	0.66 (0.61, 0.71)	8.18E-28	0.24	0.25
20	21833312	rs4544515	T	C	1.56 (1.45, 1.67)	1.74E-33	0.1	0.43
20	21833500	rs1884588	T	C	1.54 (1.43, 1.65)	2.78E-33	0.22	0.27
20	21833620	rs1884589	C	A	1.54 (1.43, 1.65)	2.94E-33	0.22	0.27
20	21834168	rs6113415	G	A	0.65 (0.61, 0.7)	3.04E-33	0.22	0.27
20	21834362	rs6113416	T	C	1.54 (1.43, 1.65)	3.35E-33	0.22	0.27
20	21835266	rs6047715	T	A	1.54 (1.43, 1.65)	3.47E-33	0.22	0.27
20	21837318	rs6113418	T	A	0.65 (0.61, 0.7)	3.61E-33	0.22	0.27
20	21838690	rs1884592	T	C	1.53 (1.43, 1.64)	3.99E-33	0.26	0.23
20	21838816	rs1884593	C	A	0.65 (0.61, 0.7)	3.75E-33	0.22	0.27
20	21839164	rs6082558	G	A	0.65 (0.61, 0.7)	3.75E-33	0.22	0.27
20	21847028	rs6075858	G	A	0.66 (0.61, 0.71)	3.13E-27	0.17	0.35
20	21847248	rs6047732	G	C	0.65 (0.61, 0.7)	3.70E-33	0.22	0.27
20	21847708	rs2208054	G	A	1.53 (1.43, 1.65)	3.64E-33	0.22	0.27
20	21847864	rs2208055	G	A	1.53 (1.43, 1.65)	3.60E-33	0.22	0.27
20	21848116	rs4390829	G	A	1.54 (1.43, 1.65)	2.74E-33	0.22	0.27
20	21849124	rs3818179	T	C	0.65 (0.61, 0.7)	4.03E-33	0.21	0.29
20	21849398	rs3818182	C	A	1.53 (1.43, 1.64)	4.02E-33	0.21	0.29
20	21853732	rs6515191	T	A	0.65 (0.61, 0.7)	4.43E-33	0.23	0.26
20	21854780	rs6113424	G	A	0.65 (0.61, 0.7)	3.34E-33	0.23	0.27
20	21855562	rs6113425	G	A	0.65 (0.61, 0.7)	2.80E-33	0.23	0.27
20	21856332	rs2281526	G	C	1.53 (1.43, 1.64)	2.52E-33	0.23	0.27
20	21862194	rs927059	T	C	0.65 (0.61, 0.7)	7.56E-33	0.24	0.24
20	21864356	rs6113431	T	A	1.53 (1.43, 1.64)	2.57E-33	0.23	0.26
20	21865392	rs2024885	G	A	1.53 (1.43, 1.64)	2.90E-33	0.24	0.25
20	21866106	rs2328680	T	C	1.53 (1.43, 1.64)	2.52E-33	0.23	0.26
20	21866212	rs2328681	T	C	0.65 (0.61, 0.7)	2.50E-33	0.23	0.26
20	21866288	rs2328682	G	A	0.65 (0.61, 0.7)	2.47E-33	0.23	0.26
20	21866310	rs1007169	T	G	1.53 (1.43, 1.64)	2.39E-33	0.24	0.25
20	21866428	rs2208050	G	A	0.65 (0.61, 0.7)	2.03E-33	0.24	0.25
20	21866472	rs2208051	G	A	1.54 (1.43, 1.65)	1.55E-33	0.24	0.25
20	21866642	rs2328684	T	G	0.65 (0.61, 0.7)	1.43E-33	0.24	0.25
20	21866898	rs6047744	T	G	1.54 (1.43, 1.65)	1.23E-33	0.24	0.25
20	21867054	rs6047745	C	A	0.65 (0.61, 0.7)	1.03E-33	0.24	0.25
20	21868688	rs6113435	G	C	1.54 (1.44, 1.65)	9.32E-34	0.24	0.25
20	21877052	rs2424409	G	C	1.58 (1.41, 1.77)	1.28E-14	0.63	0
20	21877056	rs2424410	C	A	0.65 (0.61, 0.7)	6.08E-34	0.25	0.23
20	21879684	rs6035995	G	A	0.65 (0.61, 0.7)	8.21E-34	0.26	0.23
20	21884484	rs1080275	G	A	0.65 (0.61, 0.7)	5.54E-34	0.25	0.23
20	21886282	rs6047761	C	A	0.65 (0.61, 0.7)	5.11E-34	0.25	0.23
20	21886530	rs4815086	C	A	0.65 (0.61, 0.7)	5.31E-34	0.26	0.23
20	21886604	rs4815087	G	C	1.54 (1.44, 1.65)	4.51E-34	0.25	0.23
20	21891804	rs2424414	T	C	1.84 (1.51, 2.24)	1.56E-09	0.68	0
20	21895184	rs969921	T	A	0.65 (0.61, 0.69)	3.96E-34	0.25	0.23
20	21897592	rs6106434	G	A	1.38 (1.28, 1.49)	1.82E-16	0.34	0.12
20	21899848	rs2207878	G	A	0.66 (0.61, 0.71)	2.99E-28	0.22	0.29
20	21900054	rs970616	C	A	1.38 (1.28, 1.48)	1.37E-16	0.5	0
20	21901648	rs6047768	G	A	0.66 (0.61, 0.71)	3.19E-28	0.24	0.26
20	21906048	rs6047769	G	A	1.54 (1.44, 1.65)	4.35E-34	0.24	0.25
20	21907906	rs2424417	T	A	0.52 (0.43, 0.64)	1.39E-09	0.73	0
20	21909410	rs1555264	G	A	0.66 (0.61, 0.71)	3.98E-28	0.31	0.17
20	21909472	rs1555265	T	C	0.65 (0.61, 0.7)	6.71E-34	0.25	0.23
20	21909964	rs6036003	G	A	1.54 (1.44, 1.65)	5.00E-34	0.25	0.24
20	21910332	rs169311	C	A	1.54 (1.44, 1.66)	2.37E-34	0.23	0.26
20	21911048	rs2424420	T	C	1.58 (1.41, 1.78)	7.59E-15	0.63	0
20	21915950	rs201546	G	A	1.5 (1.31, 1.71)	4.77E-09	0.89	0
20	21916220	rs2424422	C	A	1.59 (1.41, 1.78)	5.93E-15	0.62	0
20	21917512	rs2424424	T	C	1.66 (1.42, 1.93)	1.05E-10	0.28	0.19
20	21920580	rs2009652	T	C	1.54 (1.44, 1.65)	3.74E-34	0.24	0.25

20	21922590	rs6036007	T	C	1.54 (1.44, 1.65)	3.77E-34	0.24	0.25
20	21922836	rs201548	T	C	1.54 (1.44, 1.65)	3.77E-34	0.24	0.25
20	21923026	rs6106438	T	C	1.54 (1.44, 1.66)	3.13E-34	0.23	0.26
20	21925094	rs6113456	T	G	1.55 (1.45, 1.66)	8.92E-35	0.27	0.21
20	21933498	rs6047798	G	A	1.54 (1.44, 1.65)	2.82E-34	0.32	0.14
20	21933780	rs1980551	G	A	0.65 (0.6, 0.69)	1.66E-34	0.29	0.18
20	21934004	rs1980552	T	C	0.65 (0.6, 0.69)	1.53E-34	0.29	0.18
20	21934312	rs6047799	C	A	1.61 (1.5, 1.72)	1.36E-38	0.64	0
20	21935460	rs6047801	T	G	1.61 (1.38, 1.88)	1.46E-09	0.25	0.24
20	21936830	rs127747	G	A	1.6 (1.49, 1.72)	3.14E-39	0.56	0
20	21937972	rs6047804	T	C	0.62 (0.53, 0.73)	5.47E-09	0.16	0.37
20	21945116	rs201559	T	C	0.63 (0.58, 0.67)	3.92E-39	0.58	0
20	21947212	rs201561	G	C	0.63 (0.58, 0.67)	5.37E-39	0.59	0
20	21948174	rs201562	T	G	1.5 (1.39, 1.61)	1.13E-27	0.3	0.16
20	21948280	rs201563	T	C	1.6 (1.49, 1.71)	3.91E-39	0.56	0
20	21955602	rs201564	G	A	1.47 (1.36, 1.58)	9.74E-23	0.9	0
20	21957336	rs201565	T	C	1.6 (1.49, 1.71)	3.65E-39	0.55	0
20	21960862	rs201569	T	C	1.46 (1.36, 1.58)	1.01E-22	0.89	0
20	21961514	rs201571	T	C	1.52 (1.41, 1.64)	9.73E-28	0.79	0
20	21962754	rs201572	T	C	1.52 (1.41, 1.64)	7.83E-28	0.79	0
20	21963564	rs201574	T	C	0.63 (0.58, 0.67)	2.96E-39	0.55	0
20	21975674	rs201587	G	A	0.62 (0.58, 0.67)	2.44E-39	0.56	0
20	21975788	rs4815089	T	C	0.62 (0.53, 0.73)	5.64E-09	0.16	0.38
20	21981560	rs6047837	T	C	1.59 (1.37, 1.85)	1.58E-09	0.23	0.26
20	21981820	rs201593	G	A	0.62 (0.58, 0.67)	1.80E-39	0.57	0
20	21981920	rs6047838	G	A	0.66 (0.58, 0.75)	5.64E-10	0.25	0.25
20	21982672	rs201594	T	C	1.6 (1.49, 1.72)	2.29E-39	0.58	0
20	21983416	rs4815090	T	G	0.67 (0.62, 0.73)	4.43E-21	0.9	0
20	21984524	rs6113483	G	C	1.47 (1.36, 1.58)	4.72E-23	0.9	0
20	21985576	rs6047844	T	C	1.6 (1.49, 1.72)	1.71E-39	0.58	0
20	21986726	rs6137526	T	C	0.68 (0.63, 0.74)	6.63E-23	0.89	0
20	21988422	rs6132477	T	C	0.68 (0.63, 0.74)	4.98E-23	0.89	0
20	21988956	rs16983348	G	A	0.62 (0.53, 0.73)	3.39E-09	0.17	0.36
20	21990418	rs913063	C	A	0.63 (0.59, 0.68)	1.57E-38	0.26	0.22
20	21991920	rs6137527	T	C	0.68 (0.63, 0.74)	4.27E-23	0.89	0
20	21992204	rs6036026	T	C	1.59 (1.48, 1.7)	1.51E-38	0.26	0.22
20	21995176	rs4813445	G	A	1.59 (1.48, 1.7)	1.48E-38	0.26	0.22
20	21997176	rs6036029	T	C	0.63 (0.59, 0.68)	1.48E-38	0.26	0.22
20	21997760	rs4813446	T	C	1.59 (1.48, 1.7)	1.47E-38	0.26	0.22
20	21998504	rs1160312	G	A	0.63 (0.59, 0.68)	1.47E-38	0.26	0.22
20	21999812	rs1887056	C	A	0.63 (0.59, 0.68)	1.39E-38	0.26	0.22
20	22000060	rs16983367	T	G	0.62 (0.53, 0.73)	2.47E-09	0.18	0.35
20	22005176	rs2104504	T	C	1.6 (1.38, 1.86)	6.10E-10	0.26	0.22
20	22005416	rs6113491	C	A	0.63 (0.59, 0.68)	3.10E-37	0.31	0.16
20	22009488	rs6113495	G	A	0.68 (0.63, 0.74)	3.68E-23	0.89	0
20	22009632	rs6113496	T	G	0.63 (0.59, 0.67)	1.02E-38	0.26	0.23
20	22012972	rs6113501	G	A	1.47 (1.36, 1.58)	3.79E-23	0.89	0
20	22013466	rs11698943	G	A	0.68 (0.63, 0.74)	4.50E-23	0.9	0
20	22014992	rs10485628	G	A	1.6 (1.38, 1.86)	5.63E-10	0.26	0.22
20	22018524	rs6036037	C	A	0.63 (0.59, 0.68)	8.62E-37	0.26	0.23
20	22018664	rs6137533	T	C	0.68 (0.63, 0.74)	3.64E-23	0.89	0
20	22022096	rs4813447	G	A	1.6 (1.38, 1.85)	6.48E-10	0.26	0.23
20	22024188	rs6113508	G	A	0.68 (0.63, 0.74)	4.28E-23	0.89	0
20	22025352	rs6113509	G	A	1.47 (1.36, 1.58)	4.22E-23	0.89	0
20	22028540	rs1883751	G	A	1.47 (1.36, 1.58)	4.47E-23	0.89	0
20	22029332	rs4815092	G	C	0.67 (0.62, 0.73)	2.00E-22	0.91	0
20	22030448	rs6036041	G	A	0.65 (0.6, 0.7)	2.04E-28	0.45	0
20	22034416	rs201141	T	C	0.62 (0.53, 0.72)	2.24E-09	0.22	0.29
20	22034860	rs201142	G	A	0.62 (0.53, 0.72)	2.24E-09	0.22	0.29
20	22035538	rs201144	G	A	1.6 (1.38, 1.86)	9.48E-10	0.3	0.18
20	22035670	rs201145	G	A	1.59 (1.48, 1.71)	2.05E-38	0.3	0.17
20	22036650	rs201146	C	A	0.63 (0.59, 0.67)	1.93E-38	0.3	0.17
20	22037084	rs201147	T	A	0.62 (0.53, 0.72)	2.46E-09	0.26	0.24

20	22038388	rs201149	T	A	0.63 (0.59, 0.68)	5.02E-37	0.29	0.19
20	22038580	rs201150	T	A	0.63 (0.59, 0.68)	7.44E-37	0.3	0.17
20	22050152	rs6047915	T	C	0.62 (0.53, 0.72)	2.48E-09	0.26	0.23
20	22052420	rs6047917	G	A	1.59 (1.48, 1.7)	6.03E-37	0.29	0.18
20	22053844	rs2206754	T	C	0.62 (0.53, 0.72)	3.67E-09	0.21	0.29
20	22054230	rs11698068	G	A	1.59 (1.48, 1.7)	7.12E-37	0.29	0.19
20	22055728	rs2328700	T	C	0.62 (0.53, 0.72)	3.60E-09	0.21	0.29
20	22057896	rs6137547	G	A	0.67 (0.62, 0.73)	1.25E-22	0.78	0
20	22059034	rs1303872	T	C	1.56 (1.45, 1.68)	9.58E-33	0.42	0.01
20	22059380	rs1303873	T	C	0.62 (0.53, 0.72)	3.34E-09	0.22	0.29
20	22063728	rs804516	G	A	1.58 (1.47, 1.7)	2.38E-36	0.32	0.15
20	22065778	rs6113534	G	C	0.68 (0.62, 0.73)	4.09E-22	0.84	0
20	22067140	rs804520	G	A	1.56 (1.46, 1.68)	6.82E-35	0.36	0.08
20	22067264	rs804521	G	A	1.61 (1.39, 1.88)	1.05E-09	0.3	0.17
20	22067832	rs973106	G	A	1.48 (1.37, 1.6)	4.95E-22	0.84	0
20	22068288	rs804522	T	C	1.61 (1.39, 1.88)	1.04E-09	0.3	0.17
20	22070158	rs708996	G	C	0.64 (0.6, 0.69)	2.66E-32	0.41	0.01
20	22070810	rs804524	T	C	0.64 (0.6, 0.69)	7.66E-35	0.37	0.08
20	22071128	rs6113539	G	A	1.48 (1.37, 1.6)	4.11E-22	0.85	0
20	22071208	rs804525	C	A	0.61 (0.52, 0.72)	2.48E-09	0.22	0.28
20	22072416	rs804527	T	G	1.62 (1.39, 1.88)	1.01E-09	0.3	0.17
20	22073884	rs804529	C	A	1.62 (1.39, 1.88)	1.01E-09	0.3	0.17
20	22075048	rs708997	C	A	1.62 (1.39, 1.88)	1.01E-09	0.3	0.17
20	22075894	rs708999	T	C	1.61 (1.39, 1.88)	1.04E-09	0.3	0.17
20	22076470	rs804530	T	C	0.61 (0.52, 0.72)	2.58E-09	0.22	0.29
20	22076554	rs804531	G	A	0.65 (0.61, 0.7)	2.89E-29	0.54	0
20	22077324	rs6113543	G	A	0.68 (0.63, 0.73)	5.25E-22	0.86	0
20	22077556	rs804532	G	A	0.61 (0.52, 0.72)	2.72E-09	0.22	0.29
20	22077932	rs804533	G	A	0.64 (0.6, 0.69)	1.09E-34	0.38	0.06
20	22078528	rs1415798	G	C	0.68 (0.63, 0.73)	4.40E-22	0.86	0
20	22079194	rs1415799	T	C	0.68 (0.62, 0.73)	4.07E-22	0.75	0
20	22083308	rs804536	T	C	0.62 (0.53, 0.73)	5.83E-09	0.15	0.39
20	22084000	rs2328701	G	C	0.64 (0.59, 0.69)	1.51E-34	0.32	0.15
20	22084092	rs804537	T	C	1.6 (1.37, 1.86)	3.38E-09	0.22	0.27
20	22084272	rs804538	G	A	0.62 (0.53, 0.73)	1.12E-08	0.15	0.38
20	22084708	rs804539	G	C	0.62 (0.53, 0.73)	1.55E-08	0.15	0.38
20	22084786	rs6047929	G	A	1.49 (1.38, 1.61)	8.13E-25	0.79	0
20	22084840	rs6113548	T	C	1.48 (1.37, 1.61)	4.16E-22	0.53	0
20	22087448	rs1090265	T	C	0.62 (0.53, 0.73)	1.79E-08	0.16	0.38
20	22087934	rs6113551	T	A	1.38 (1.28, 1.49)	3.70E-16	0.28	0.2
20	22092268	rs6137561	G	A	0.71 (0.66, 0.77)	4.69E-19	0.43	0
20	22143064	rs6113583	T	C	1.37 (1.27, 1.48)	3.72E-15	0.17	0.36
20	22144024	rs1159466	G	C	1.37 (1.27, 1.47)	4.87E-17	0.55	0
20	22145212	rs6137582	G	A	0.73 (0.68, 0.79)	3.44E-16	0.13	0.39
20	22145686	rs2876633	T	A	1.37 (1.27, 1.47)	2.29E-16	0.14	0.38
20	22147504	rs742655	T	C	0.74 (0.69, 0.8)	3.89E-17	0.13	0.39
20	22148414	rs804614	G	A	1.35 (1.26, 1.44)	4.29E-17	0.13	0.39
20	22149176	rs804615	T	C	0.74 (0.69, 0.8)	2.82E-17	0.13	0.39
20	22149840	rs804616	T	C	1.35 (1.26, 1.44)	4.16E-17	0.13	0.39
20	22151480	rs804617	T	G	1.35 (1.26, 1.44)	3.61E-17	0.13	0.39
20	22151740	rs709006	T	C	0.74 (0.69, 0.8)	3.60E-17	0.13	0.39
20	22151788	rs709007	G	A	1.35 (1.26, 1.44)	3.54E-17	0.13	0.39
20	22152464	rs804618	G	A	0.74 (0.69, 0.8)	3.60E-17	0.13	0.39
20	22154968	rs1090292	T	C	1.34 (1.26, 1.44)	4.73E-17	0.12	0.41
20	22155156	rs1090293	G	A	0.74 (0.69, 0.8)	4.92E-17	0.12	0.4
20	22157538	rs4815098	G	A	1.37 (1.27, 1.47)	3.23E-16	0.14	0.38
20	22159414	rs1415801	T	G	1.37 (1.27, 1.47)	3.16E-16	0.14	0.38
20	22160946	rs12625314	T	C	0.73 (0.68, 0.79)	3.14E-16	0.14	0.38
20	22160962	rs12625315	T	C	0.74 (0.69, 0.8)	7.69E-14	0.18	0.35
20	22171640	rs6106481	G	A	0.77 (0.71, 0.83)	2.89E-11	0.35	0.1
20	22177504	rs6113592	G	A	0.8 (0.74, 0.86)	2.85E-09	0.36	0.09
20	22187448	rs6047978	C	A	0.8 (0.74, 0.86)	2.96E-09	0.36	0.08
20	22189466	rs1337908	T	A	1.3 (1.2, 1.4)	3.06E-11	0.35	0.11

20	22193868	rs10485630	T	G	1.26 (1.17, 1.36)	1.40E-09	0.41	0
20	22194450	rs6047982	T	G	1.26 (1.17, 1.36)	1.25E-09	0.43	0
20	22200276	rs6113604	T	C	0.77 (0.72, 0.83)	7.35E-11	0.39	0.03
20	22203000	rs4815101	G	C	0.78 (0.72, 0.84)	1.14E-10	0.34	0.12
20	22203172	rs4815102	T	G	0.77 (0.72, 0.83)	7.49E-11	0.4	0.03
20	22204270	rs6113607	T	C	1.29 (1.19, 1.39)	1.14E-10	0.34	0.12
20	22208552	rs200366	G	A	1.35 (1.25, 1.45)	1.97E-15	0.38	0.06
20	22208892	rs6106493	T	C	0.77 (0.72, 0.84)	7.85E-11	0.4	0.03
20	22210264	rs1569781	T	G	0.77 (0.72, 0.84)	7.93E-11	0.4	0.03
20	22210428	rs1569782	G	C	0.78 (0.72, 0.84)	1.20E-10	0.34	0.12
20	22211132	rs2295099	G	A	1.31 (1.22, 1.41)	3.16E-12	0.21	0.29
20	22213098	rs200369	C	A	1.29 (1.2, 1.39)	1.45E-11	0.19	0.33
20	22215058	rs1028444	T	C	1.25 (1.16, 1.34)	2.46E-09	0.5	0
20	22216484	rs6047999	T	C	1.25 (1.16, 1.34)	2.08E-09	0.51	0
20	22219088	rs1832371	G	A	1.25 (1.16, 1.34)	2.22E-09	0.51	0
20	22222860	rs183216	T	A	0.77 (0.72, 0.83)	1.20E-11	0.22	0.29
20	22222930	rs980970	T	C	0.8 (0.74, 0.86)	2.38E-09	0.51	0
20	22223648	rs199780	T	G	0.77 (0.72, 0.83)	1.20E-11	0.22	0.29
20	22224484	rs199781	G	C	0.78 (0.72, 0.83)	1.80E-11	0.16	0.37
20	22224812	rs4813452	T	G	1.25 (1.16, 1.34)	3.67E-09	0.48	0
20	22228604	rs6113622	T	C	1.25 (1.16, 1.34)	2.76E-09	0.51	0
20	22229872	rs17192817	T	C	1.24 (1.16, 1.34)	4.03E-09	0.49	0
20	22230356	rs172036	T	C	0.77 (0.72, 0.83)	9.43E-12	0.2	0.31
20	22231878	rs199790	T	C	1.29 (1.2, 1.39)	1.32E-11	0.17	0.35
20	22235304	rs199793	G	A	0.78 (0.72, 0.83)	7.49E-13	0.32	0.14
20	22238780	rs8124887	G	A	1.23 (1.15, 1.33)	2.57E-08	0.54	0
20	22239220	rs4815103	C	A	1.23 (1.15, 1.33)	2.40E-08	0.53	0
20	22239932	rs199796	T	C	1.28 (1.19, 1.37)	7.59E-11	0.2	0.3
20	22248304	rs169230	G	A	1.25 (1.16, 1.35)	4.30E-09	0.13	0.4
X	65309361	rs7054364	A	C	0.71 (0.67,0.76)	1.33E-25	0.77	0
X	65325170	rs6624875	A	G	0.71 (0.66,0.75)	2.90E-27	0.73	0
X	65331899	rs2206203	C	A	0.71 (0.66,0.75)	1.77E-27	0.66	0
X	65332812	rs1011526	A	G	0.71 (0.66,0.75)	1.77E-27	0.66	0
X	65343765	rs806607	C	T	0.70 (0.65,0.74)	3.11E-29	0.56	0
X	65345254	rs806608	T	G	0.70 (0.66,0.74)	5.05E-29	0.67	0
X	65350264	rs806610	C	T	0.70 (0.65,0.74)	4.82E-29	0.65	0
X	65351982	rs1264216	G	T	0.70 (0.65,0.74)	4.82E-29	0.65	0
X	65356189	rs1091486	T	C	0.70 (0.66,0.74)	5.05E-29	0.67	0
X	65433403	rs5919042	G	A	0.70 (0.65,0.75)	1.84E-26	0.71	0
X	65433624	rs5919043	C	T	0.70 (0.65,0.75)	1.84E-26	0.71	0
X	65448584	rs601552	A	G	0.59 (0.54,0.65)	1.01E-29	0.48	0
X	65448903	rs1463435	C	T	0.78 (0.73,0.83)	5.08E-16	0.55	0
X	65455348	rs6624177	C	T	0.67 (0.63,0.72)	8.23E-31	0.59	0
X	65491314	rs1585131	C	A	0.67 (0.63,0.72)	2.15E-30	0.59	0
X	65521580	rs5964522	T	A	0.66 (0.61,0.70)	1.24E-34	0.66	0
X	65523086	rs1379146	T	A	0.66 (0.61,0.70)	1.32E-34	0.66	0
X	65523281	rs2840240	C	G	0.66 (0.61,0.70)	1.24E-34	0.66	0
X	65528029	rs1926341	C	T	0.66 (0.61,0.70)	7.12E-35	0.66	0
X	65544962	rs5965189	G	A	0.66 (0.61,0.70)	8.97E-35	0.81	0
X	65545588	rs4240047	A	T	0.66 (0.61,0.70)	8.97E-35	0.81	0
X	65546997	rs7888975	G	A	0.65 (0.61,0.70)	6.94E-35	0.77	0
X	65549504	rs5965192	A	G	0.66 (0.61,0.70)	8.15E-35	0.79	0
X	65574614	rs4827479	T	C	0.74 (0.68,0.80)	9.24E-13	0.38	0.05
X	65578623	rs5919100	T	G	0.62 (0.58,0.66)	4.36E-46	0.69	0
X	65586966	rs4361890	C	T	0.62 (0.58,0.66)	2.28E-46	0.69	0
X	65589063	rs4240049	C	T	0.62 (0.58,0.66)	2.28E-46	0.69	0
X	65589137	rs5919108	T	C	0.62 (0.58,0.66)	1.83E-46	0.67	0
X	65589319	rs4357442	A	G	0.62 (0.58,0.66)	1.83E-46	0.67	0
X	65589526	rs5919110	A	T	0.71 (0.65,0.77)	1.14E-16	0.73	0
X	65635063	rs5919135	T	C	0.62 (0.58,0.66)	5.03E-47	0.70	0
X	65640583	rs1331101	A	C	0.62 (0.58,0.66)	9.09E-47	0.74	0
X	65650569	rs5918648	C	T	0.57 (0.52,0.63)	6.21E-31	0.88	0
X	65725320	rs1586315	T	C	0.61 (0.57,0.65)	1.51E-49	0.56	0

X	65730685	rs4827379	T	C	0.71 (0.65,0.77)	1.14E-16	0.73	0
X	65741711	rs1385699	C	T	0.59 (0.55,0.63)	3.00E-53	0.42	0
X	65760568	rs1352015	C	T	0.59 (0.55,0.63)	3.00E-53	0.42	0
X	65831379	rs5919174	G	A	0.46 (0.42,0.50)	7.92E-76	0.83	0
X	65838758	rs5919175	G	A	0.46 (0.42,0.50)	5.23E-76	0.83	0
X	65849574	rs775358	T	C	0.46 (0.42,0.49)	2.33E-81	0.53	0
X	65869018	rs16990143	G	A	0.46 (0.42,0.49)	7.30E-78	0.83	0
X	65895898	rs775362	T	C	0.46 (0.42,0.49)	7.30E-78	0.83	0
X	65933752	rs3843789	T	C	0.48 (0.44,0.54)	5.42E-42	0.98	0
X	65964070	rs5919200	G	A	0.45 (0.42,0.49)	6.37E-83	0.77	0
X	65985316	rs4827384	G	A	0.49 (0.44,0.54)	7.61E-40	0.97	0
X	66002681	rs1041668	G	A	0.45 (0.41,0.49)	1.70E-83	0.62	0
X	66019047	rs7878229	C	T	0.47 (0.42,0.53)	3.24E-36	0.38	0.06
X	66031848	rs4548330	T	G	0.44 (0.41,0.48)	2.57E-86	0.66	0
X	66087225	rs5919235	G	A	0.43 (0.40,0.47)	4.62E-88	0.73	0
X	66138622	rs7057795	C	T	0.44 (0.40,0.47)	2.70E-83	0.75	0
X	66155042	rs471205	T	C	0.67 (0.64,0.72)	5.11E-39	0.64	0
X	66155654	rs476709	T	C	0.44 (0.40,0.47)	2.23E-83	0.74	0
X	66175639	rs505520	C	A	0.42 (0.38,0.46)	4.68E-84	0.72	0
X	66179398	rs574001	C	A	0.42 (0.39,0.46)	1.30E-83	0.59	0
X	66183973	rs532649	G	A	0.42 (0.39,0.46)	7.13E-87	0.75	0
X	66184927	rs485454	G	A	0.42 (0.38,0.46)	1.22E-83	0.70	0
X	66185099	rs489099	C	T	0.42 (0.39,0.46)	9.94E-87	0.75	0
X	66190296	rs531840	T	C	0.42 (0.39,0.46)	4.26E-86	0.76	0
X	66204409	rs5919247	C	T	0.42 (0.39,0.46)	7.68E-87	0.76	0
X	66204780	rs5918688	A	G	0.42 (0.38,0.46)	2.81E-76	0.58	0
X	66214912	rs4827524	A	G	0.42 (0.39,0.46)	6.45E-87	0.76	0
X	66217759	rs989345	G	A	0.42 (0.39,0.46)	2.74E-87	0.75	0
X	66221281	rs5919266	G	T	0.42 (0.39,0.46)	3.39E-86	0.70	0
X	66228526	rs1567524	T	C	0.42 (0.39,0.46)	5.93E-87	0.76	0
X	66232455	rs5919270	G	A	0.42 (0.39,0.46)	5.09E-87	0.76	0
X	66232849	rs1511061	C	T	0.42 (0.38,0.45)	6.82E-90	0.71	0
X	66233156	rs1511060	C	T	0.42 (0.39,0.46)	1.62E-86	0.77	0
X	66235493	rs5918694	T	C	0.42 (0.39,0.46)	1.01E-86	0.76	0
X	66238687	rs4827392	C	A	0.42 (0.39,0.46)	5.77E-87	0.76	0
X	66242222	rs5919272	G	A	0.42 (0.39,0.46)	5.10E-87	0.76	0
X	66242280	rs5918696	T	C	0.42 (0.39,0.46)	3.73E-87	0.74	0
X	66246877	rs4827527	G	A	0.42 (0.39,0.46)	7.97E-87	0.73	0
X	66253452	rs938059	C	A	0.42 (0.39,0.46)	9.42E-87	0.75	0
X	66253825	rs938058	G	A	0.42 (0.39,0.46)	9.42E-87	0.75	0
X	66254894	rs981065	C	T	0.42 (0.39,0.46)	9.07E-87	0.76	0
X	66264409	rs1988995	T	C	0.42 (0.39,0.46)	9.91E-86	0.74	0
X	66265361	rs1511058	C	T	0.42 (0.39,0.46)	7.47E-86	0.76	0
X	66269421	rs1397631	T	C	0.47 (0.41,0.52)	3.37E-36	0.48	0
X	66269660	rs984094	A	G	0.42 (0.39,0.46)	1.17E-86	0.74	0
X	66275691	rs5964588	T	G	0.42 (0.39,0.46)	1.22E-86	0.75	0
X	66275897	rs5919285	G	A	0.42 (0.39,0.46)	1.22E-86	0.75	0
X	66277339	rs5919287	T	C	0.42 (0.39,0.46)	1.22E-86	0.75	0
X	66291862	rs1027970	C	T	0.42 (0.39,0.46)	1.24E-86	0.76	0
X	66293341	rs2221799	G	A	0.42 (0.39,0.46)	1.67E-86	0.76	0
X	66304361	rs4272525	T	C	0.42 (0.39,0.46)	2.82E-86	0.72	0
X	66311578	rs5919309	T	C	0.42 (0.39,0.46)	4.62E-86	0.72	0
X	66322154	rs12007727	A	G	0.43 (0.38,0.48)	2.60E-49	0.96	0
X	66329586	rs5918719	C	T	0.42 (0.39,0.46)	1.75E-86	0.73	0
X	66336675	rs5919321	G	A	0.42 (0.39,0.46)	3.89E-86	0.72	0
X	66347396	rs5919325	A	G	0.42 (0.39,0.46)	2.97E-86	0.73	0
X	66351646	rs2335503	C	T	0.42 (0.39,0.46)	3.27E-86	0.72	0
X	66360222	rs5919335	A	G	0.46 (0.42,0.50)	1.62E-83	0.37	0.07
X	66365693	rs6625150	A	C	0.46 (0.42,0.50)	2.73E-83	0.34	0.12
X	66366212	rs12009759	A	G	0.49 (0.44,0.54)	1.35E-46	0.44	0
X	66393594	rs2335868	T	C	0.46 (0.42,0.50)	2.80E-83	0.35	0.10
X	66398525	rs12558842	C	A	0.46 (0.42,0.49)	4.86E-85	0.38	0.05
X	66398618	rs6625155	C	T	0.46 (0.42,0.49)	4.16E-85	0.38	0.07

X	66414536	rs5918737	T	C	0.46 (0.42,0.50)	5.52E-83	0.34	0.12
X	66428828	rs5919363	G	A	0.46 (0.43,0.50)	9.49E-86	0.11	0.44
X	66436233	rs5965383	G	T	0.46 (0.43,0.50)	2.14E-85	0.12	0.43
X	66436439	rs2335506	G	A	0.46 (0.43,0.50)	4.71E-85	0.13	0.41
X	66437375	rs2335508	A	G	0.46 (0.43,0.50)	4.70E-85	0.12	0.43
X	66447257	rs6625174	G	A	0.46 (0.43,0.50)	1.30E-85	0.13	0.41
X	66455454	rs2878642	A	G	0.46 (0.43,0.50)	1.63E-84	0.13	0.41
X	66456836	rs2336175	A	G	0.46 (0.43,0.50)	2.26E-80	0.13	0.42
X	66457823	rs4484837	G	A	0.48 (0.42,0.54)	6.69E-34	0.14	0.39
X	66471565	rs5918745	T	C	0.45 (0.42,0.49)	3.21E-91	0.21	0.30
X	66475061	rs2497936	T	C	0.48 (0.44,0.52)	1.64E-67	0.60	0
X	66479743	rs2497938	C	T	0.45 (0.42,0.49)	2.40E-91	0.19	0.32
X	66480739	rs2497939	C	A	0.46 (0.42,0.50)	4.01E-82	0.11	0.45
X	66481077	rs2223842	C	A	0.46 (0.43,0.50)	2.42E-85	0.10	0.45
X	66482821	rs2497943	G	T	0.46 (0.43,0.50)	2.51E-84	0.10	0.46
X	66483175	rs2473897	C	T	0.46 (0.43,0.50)	8.34E-85	0.10	0.46
X	66486896	rs2223841	C	T	0.46 (0.43,0.50)	3.90E-85	0.10	0.45
X	66487452	rs2473896	C	T	0.46 (0.43,0.50)	5.01E-85	0.10	0.45
X	66487762	rs2473895	T	C	0.46 (0.43,0.50)	6.85E-85	0.10	0.45
X	66490468	rs2207080	G	A	0.46 (0.43,0.50)	1.47E-84	0.10	0.45
X	66493049	rs721451	G	A	0.46 (0.43,0.50)	7.80E-83	0.12	0.43
X	66493198	rs2473891	T	C	0.46 (0.43,0.50)	5.19E-86	0.11	0.44
X	66529906	rs2473870	G	A	0.46 (0.43,0.50)	2.19E-83	0.11	0.45
X	66544165	rs2497911	A	C	0.46 (0.43,0.50)	2.23E-83	0.10	0.45
X	66549068	rs2497917	A	G	0.46 (0.43,0.50)	1.83E-83	0.10	0.45
X	66564941	rs2497928	C	A	0.46 (0.43,0.50)	1.66E-85	0.13	0.42
X	66569429	rs2497930	C	A	0.46 (0.43,0.50)	2.26E-85	0.12	0.43
X	66580991	rs2497935	G	A	0.46 (0.43,0.50)	2.26E-85	0.12	0.43
X	66624114	rs2207041	A	C	0.50 (0.46,0.54)	4.04E-68	0.23	0.27
X	66662689	rs962458	G	A	0.46 (0.41,0.52)	1.66E-38	0.36	0.08
X	66668280	rs7888856	G	A	0.50 (0.46,0.54)	1.95E-68	0.32	0.15
X	66693791	rs12396249	A	G	0.49 (0.46,0.54)	9.90E-69	0.34	0.12
X	66704950	rs1204038	A	G	0.49 (0.45,0.53)	6.32E-70	0.37	0.07
X	66714836	rs2255702	T	C	0.49 (0.45,0.53)	6.32E-70	0.37	0.07
X	66722755	rs5918757	G	A	0.49 (0.45,0.53)	5.50E-70	0.36	0.09
X	66742082	rs5919393	C	T	0.50 (0.46,0.54)	1.85E-68	0.35	0.10
X	66745110	rs4827545	A	G	0.50 (0.46,0.54)	1.55E-68	0.33	0.13
X	66755476	rs5918760	T	C	0.49 (0.46,0.54)	8.63E-69	0.38	0.06
X	66792481	rs6624304	T	C	0.51 (0.47,0.55)	8.53E-62	0.36	0.08
X	66795644	rs1337080	G	A	0.50 (0.45,0.56)	2.91E-35	0.49	0
X	66831526	rs5918762	T	C	0.51 (0.47,0.55)	8.53E-62	0.36	0.08
X	66854432	rs5918764	T	C	0.50 (0.45,0.56)	2.91E-35	0.49	0
X	66873156	rs5964607	T	C	0.65 (0.61,0.69)	1.09E-37	0.45	0
X	66876367	rs1931542	A	G	0.65 (0.61,0.69)	1.03E-37	0.45	0
X	66881843	rs1572502	C	T	0.65 (0.61,0.69)	1.02E-37	0.45	0
X	66884958	rs1415271	G	T	0.65 (0.61,0.69)	1.00E-37	0.43	0
X	66885326	rs5019585	A	G	0.65 (0.61,0.69)	1.25E-37	0.46	0
X	66895296	rs1931545	G	T	0.65 (0.61,0.69)	1.09E-37	0.45	0
X	66898321	rs3927643	T	C	0.65 (0.61,0.69)	1.09E-37	0.45	0
X	66900243	rs6625208	C	T	0.65 (0.61,0.69)	1.20E-37	0.46	0
X	66904482	rs9699051	T	C	0.50 (0.45,0.56)	2.65E-33	0.71	0
X	66908084	rs7057791	T	C	0.65 (0.61,0.69)	1.44E-37	0.48	0
X	66913866	rs12010636	T	C	0.50 (0.45,0.56)	2.65E-33	0.71	0
X	66920309	rs5919427	G	T	0.65 (0.61,0.69)	1.15E-37	0.45	0
X	66934751	rs4370673	T	G	0.66 (0.61,0.70)	1.02E-35	0.44	0
X	66938275	rs5919432	C	T	0.66 (0.61,0.70)	7.27E-36	0.43	0
X	66944947	rs4456006	C	A	0.65 (0.61,0.69)	2.58E-38	0.34	0.12
X	66950662	rs5964614	T	G	0.65 (0.61,0.70)	8.33E-38	0.38	0.05
X	66979215	rs4827556	C	T	0.65 (0.61,0.70)	3.49E-37	0.41	0.02
X	67005788	rs7885198	A	G	0.67 (0.62,0.71)	1.15E-31	0.83	0
X	67018756	rs2781516	A	G	0.68 (0.63,0.73)	4.66E-23	0.59	0
X	67086147	rs5965478	T	G	0.73 (0.69,0.78)	1.44E-27	0.11	0.45
X	67088023	rs2363785	T	G	0.73 (0.69,0.78)	1.44E-27	0.11	0.45

X	67090057	rs7050236	A	G	0.71 (0.66,0.75)	1.03E-28	0.88	0
X	67090456	rs16989069	T	C	0.71 (0.67,0.75)	2.41E-28	0.87	0
X	67090515	rs16990427	A	G	0.71 (0.66,0.75)	1.41E-28	0.88	0
X	67093330	rs5964632	C	T	0.73 (0.69,0.77)	3.77E-28	0.11	0.45
X	67094419	rs16990434	T	C	0.70 (0.66,0.75)	4.57E-29	0.88	0
X	67094485	rs4562482	C	A	0.73 (0.69,0.77)	3.29E-28	0.11	0.45
X	67094528	rs3898332	G	A	0.70 (0.66,0.75)	5.19E-30	0.82	0
X	67100309	rs5919492	G	T	0.71 (0.67,0.75)	1.18E-29	0.79	0
X	67105253	rs11094062	G	A	0.73 (0.69,0.78)	6.49E-28	0.10	0.45
X	67119659	rs12009526	T	C	0.70 (0.66,0.75)	2.20E-30	0.77	0
X	67125660	rs5918801	T	G	0.70 (0.66,0.75)	2.20E-30	0.77	0
X	67168138	rs12008699	A	G	0.69 (0.65,0.73)	4.00E-33	0.79	0
X	67176649	rs2765950	C	T	0.78 (0.74,0.83)	3.69E-18	0.14	0.40
X	67202792	rs16990499	A	C	0.69 (0.65,0.73)	4.00E-33	0.79	0
X	67204578	rs5918809	G	A	0.71 (0.67,0.75)	1.12E-29	0.65	0
X	67210058	rs17217221	A	G	0.70 (0.66,0.74)	7.21E-30	0.53	0
X	67212853	rs12013576	C	T	0.71 (0.67,0.75)	2.17E-30	0.62	0
X	67281028	rs7881511	A	G	1.27 (1.17,1.38)	1.25E-08	0.15	0.39
X	67288202	rs12011480	T	C	0.72 (0.68,0.76)	3.26E-28	0.45	0
X	67298626	rs12389669	T	G	1.27 (1.17,1.38)	1.25E-08	0.15	0.39
X	67302669	rs12854385	C	A	1.29 (1.18,1.40)	3.20E-09	0.15	0.39

Abbreviation: Chr., chromosome.

Note: the lead SNPs at the genome-wide significant loci are in bold

Table S3 Average Expression Signal for All Genes Shown in Figure 1 across Three Tissue Types and Blood

GENE	Chr.	Illumina PROBE_ID	Hair		Skin		Scalp (temple)		Blood	
			AVG Signal	Detection p value	AVG Signal	Detection p value	AVG Signal	Detection p value	AVG Signal	Detection p value
<i>ANGPTL7</i>	1	ILMN_1813361	562.8	< 10E-03	16.2	9.22E-03	236.9	< 10E-03	-	not significant
<i>C1orf127</i>	1	ILMN_1744089	30.3	9.22E-03	22.5	2.64E-03	10.6	4.87E-02	29.8	not significant
<i>CASZ1</i>	1	ILMN_1655191	285.8	1.32E-03	287.3	< 10E-03	410.6	< 10E-03	122.7	2.64E-03
<i>EXOSC10</i>	1	ILMN_1670796	245.0	1.32E-03	299.6	< 10E-03	346.4	< 10E-03	182.1	< 10E-03
<i>MASP2</i>	1	ILMN_1709408	-	not significant	-	not significant	-	not significant	-	not significant
<i>MTOR</i>	1	ILMN_1769031	90.7	2.64E-03	277.1	< 10E-03	286.4	< 10E-03	115.0	3.95E-03
<i>PEX14</i>	1	ILMN_1763634	60.9	2.64E-03	33.7	< 10E-03	44.6	< 10E-03	28.9	not significant
<i>SRM</i>	1	ILMN_1661337	180.0	2.64E-03	84.4	< 10E-03	79.0	< 10E-03	220.4	< 10E-03
<i>TARDBP</i>	1	ILMN_1677532	4.4	not significant	44.8	< 10E-03	54.9	< 10E-03	70.8	1.32E-02
<i>UBIAD1</i>	1	ILMN_1651872	36.9	6.59E-03	632.1	< 10E-03	390.6	< 10E-03	24.8	not significant
<i>ASB1</i>	2	ILMN_1683096	26.0	1.32E-02	45.8	< 10E-03	60.7	< 10E-03	2.3	not significant
<i>ESPNL</i>	2	ILMN_2115862	-	not significant	-	not significant	-	not significant	-	not significant
<i>HDAC4</i>	2	ILMN_1764396	84.1	2.64E-03	63.5	< 10E-03	102.2	< 10E-03	79.2	1.05E-02
<i>HES6</i>	2	ILMN_1694268	82.4	2.64E-03	19.0	6.59E-03	44.3	< 10E-03	74.2	1.19E-02
<i>KLHL30</i>	2	ILMN_1780663	-	not significant	3.7	not significant	7.8	not significant	-	not significant
<i>MGC16025</i>	2	ILMN_1757561	0.7	not significant	-	not significant	1.1	not significant	-	not significant
<i>PER2</i>	2	ILMN_1738095	93.8	2.64E-03	129.1	< 10E-03	112.4	< 10E-03	50.3	3.43E-02
<i>SCLY</i>	2	ILMN_1722742	1.0	not significant	7.1	not significant	-	not significant	35.5	not significant
<i>TRAF3IP1</i>	2	ILMN_2067032	22.5	2.24E-02	6.7	not significant	17.7	1.19E-02	4.3	not significant
<i>UBE2F</i>	2	ILMN_2164242	257.6	1.32E-03	325.6	< 10E-03	256.3	< 10E-03	584.5	< 10E-03
<i>AUTS2</i>	7	ILMN_1749081	57.3	2.64E-03	331.4	< 10E-03	270.0	< 10E-03	9.5	not significant
<i>FERD3L</i>	7	ILMN_1721475	-	not significant	-	not significant	-	not significant	5.4	not significant

<i>HDAC9</i>	7	ILMN_2408885	33.7	6.59E-03	8.8	not significant	-	not significant	138.4	< 10E-03
<i>PMS2L4</i>	7	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe
<i>STAG3L4</i>	7	ILMN_1669851	3.4	not significant	16.7	7.91E-03	6.8	not significant	4.5	not significant
<i>TWIST1</i>	7	ILMN_1672908	43.7	2.64E-03	129.1	< 10E-03	107.3	< 10E-03	15.9	not significant
<i>TYWI</i>	7	ILMN_1736135	57.4	2.64E-03	22.2	2.64E-03	36.2	< 10E-03	45.1	4.08E-02
<i>WBSCR17</i>	7	ILMN_1701557	1.1	not significant	0.1	not significant	-	not significant	-	not significant
<i>C17orf69</i>	17	ILMN_1743621	14.6	not significant	12.3	3.29E-02	17.7	1.19E-02	-	not significant
<i>CRHR1</i>	17	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe
<i>IMP5</i>	17	ILMN_1744094	4.2	not significant	15.7	1.05E-02	11.9	3.69E-02	83.9	6.59E-03
<i>KIAA1267</i>	17	ILMN_2200636	359.7	< 10E-03	336.7	< 10E-03	388.0	< 10E-03	427.8	< 10E-03
<i>LOC100128977</i>	17	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe
<i>LOC100130148</i>	17	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe
<i>LOC644172</i>	17	ILMN_1772603	8.6	not significant	12.2	3.29E-02	3.1	not significant	14.3	not significant
<i>LRRC37A4</i>	17	ILMN_2393693	3.7	not significant	18.9	6.59E-03	13.1	2.77E-02	20.0	not significant
<i>MAPT</i>	17	ILMN_2298727	29.8	9.22E-03	-	not significant	2.0	not significant	33.4	not significant
<i>MGC57346</i>	17	ILMN_1784428	90.4	2.64E-03	22.4	2.64E-03	44.1	< 10E-03	48.0	3.95E-02
<i>PLEKHM1</i>	17	ILMN_1709549	21.9	2.37E-02	11.8	3.56E-02	34.5	< 10E-03	121.8	2.64E-03
<i>STH</i>	17	ILMN_1665311	9.8	not significant	4.4	not significant	12.9	3.03E-02	0.9	not significant
<i>KIAA1632</i>	18	ILMN_1762608	-	not significant	11.2	4.08E-02	17.9	1.19E-02	-	not significant
<i>PSTPIP2</i>	18	ILMN_1713058	53.7	2.64E-03	50.6	< 10E-03	46.5	< 10E-03	128.7	1.32E-03
<i>SETBP1</i>	18	ILMN_1720513	103.4	2.64E-03	83.2	< 10E-03	124.1	< 10E-03	-	not significant
<i>SIGLEC15</i>	18	ILMN_1797293	-	not significant	-	not significant	-	not significant	-	not significant

<i>SLC14A1</i>	18	ILMN_1805561	-	not significant	27.7	< 10E-03	12.6	3.03E-02	62.2	2.11E-02
<i>SLC14A2</i>	18	ILMN_1664320	-	not significant	6.9	not significant	-	not significant	-	not significant
<i>C20orf56</i>	20	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe
<i>FOXA2</i>	20	ILMN_1668052	-	not significant	-	not significant	-	not significant	6.0	not significant
<i>LOC284788</i>	20	ILMN_1823704	-	not significant	-	not significant	-	not significant	-	not significant
<i>NKX2-2</i>	20	ILMN_1692280	-	not significant	-	not significant	-	not significant	4.4	not significant
<i>NKX2-4</i>	20	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe	no probe
<i>PAX1</i>	20	ILMN_1682096	1.7	not significant	-	not significant	-	not significant	8.7	not significant
<i>PLK1S1</i>	20	ILMN_1779536	20.7	2.50E-02	13.7	2.24E-02	20.8	9.22E-03	11.2	not significant
<i>SSTR4</i>	20	ILMN_1684200	5.4	not significant	-	not significant	-	not significant	0.5	not significant
<i>THBD</i>	20	ILMN_1759787	38.7	3.95E-03	18.5	6.59E-03	15.4	1.98E-02	31.9	not significant
<i>XRN2</i>	20	ILMN_1727617	40.7	3.95E-03	73.2	< 10E-03	33.3	< 10E-03	175.7	< 10E-03

Abbreviations: Chr., chromosome; AVG, average.

Table S4 Summary result for the top SNPs from the genome-wide significant loci using random effect models.

Genetic Variant	Chr.	Position ^a	EA ^b / NEA	EAF	OR (95% CI)	p value	Gene ^c	Number of GW Significant SNPs	Q p value	<i>I</i> ²
rs12565727	1	10955669	A/G	0.789	1.33 (1.22-1.45)	9.07 x 10 ⁻¹¹	<i>TARDBP</i>	8	0.43	< 0.01
rs11683401	2	239362355	T/C	0.447	1.26 (1.18-1.35)	6.02 x 10 ⁻¹¹	<i>HDAC4</i>	9	0.60	< 0.01
rs2073963	7	18844399	G/T	0.530	1.29 (1.20-1.38)	1.27 x 10 ⁻¹²	<i>HDAC9</i>	4	0.42	< 0.01
rs6945541	7	68249896	C/T	0.539	1.27 (1.18-1.38)	1.71 x 10 ⁻⁹	<i>AUTS2</i>	6	0.97	< 0.01
rs17650991	17	41400344	A/C	0.799	1.29 (1.19-1.41)	6.85 x 10 ⁻⁹	17q21.31	88	0.45	< 0.01
rs6047844	20	21985575	T/C	0.460	1.60 (1.49-1.72)	1.71 x 10 ⁻³⁹	<i>PAX1, FOXA2</i>	193	0.58	< 0.01
rs1511061	X	66232849	A/G	0.822	2.40 (2.21-2.62)	6.82 x 10 ⁻⁹⁰	<i>AR</i>	177	0.71	<0.01

Abbreviations: Chr., chromosome; EA, effect allele; NEA, non-effect allele; EAF, effect allele frequency; OR, odds ratio; CI, confidence interval.

^a-Chromosome position located in reference sequence of Genome Build 36.3. ^b-AGA risk increasing allele on forward strand. ^c-Gene harboring the SNP or nearest to the SNP.

Table S5 Interaction results between top SNPs of AR locus and other AGA loci

Chr.	SNP	Interaction OR (95% CI)	Interaction p value	I^2
1	rs12565727	0.99 (0.94-1.05)	0.83	< 0.01
2	rs9287638	1.03 (0.99-1.07)	0.10	< 0.01
7	rs2073963	1.01 (0.98-1.05)	0.42	< 0.01
7	rs6945541 ^a	1.04 (1.00-1.09)	0.07	0.57
17	rs12373124	1.00 (0.92-1.09)	0.97	< 0.01
18	rs10502861	1.01 (0.97-1.04)	0.75	0.38
20	rs6047844	1.02 (0.99-1.05)	0.31	< 0.01

Abbreviations: Chr., chromosome; OR, odds ratio; CI, confidence interval.

^a- I^2 is greater than 50%, meta-analysis was also performed under random effect model with OR (95% CI) = 1.07 (0.98-1.16), P value = 0.14.

Table S6 Association test results for AGA, at Parkinson's disease loci

SNP	chr	position	NEA/ EA	Gt. rate	EAF	HWE p value	p value	Odds Ratio	95% CI	Gene
rs34637584	12	39020469	A/G	1.000	0.998	0.012	0.56	0.769	0.314,1.886	<i>LRRK2</i>
rs356219	4	90856624	A/G	0.974	0.370	0.75	0.86	0.993	0.919,1.073	<i>GPRIN3-SNCA</i>
i4000415	1	153472258	C/T	0.991	0.995	0.59	0.34	0.766	0.441,1.331	<i>GBA</i>
rs12185268	17	41279463	A/G	0.988	0.217	0.32	9.3e-08	0.782	0.714,0.856	<i>IMP5</i>
rs10513789	3	184242767	G/T	1.000	0.796	0.78	0.39	1.041	0.950,1.140	<i>MCCC1</i>
rs6812193	4	77418010	C/T	1.000	0.368	0.93	0.27	0.958	0.887,1.034	<i>FAM47D</i>
rs823156	1	204031263	A/G	0.999	0.180	0.32	0.44	0.963	0.876,1.059	<i>SLC41A1</i>
rs7599054	2	135257016	A/G	1.000	0.462	0.0032	0.27	0.958	0.887,1.034	<i>TMEM163-ACMSD</i>
rs6599389	4	929113	A/G	1.000	0.925	0.56	0.32	0.932	0.810,1.072	<i>TMEM175</i>
rs11868035	17	17655826	A/G	0.999	0.686	0.051	0.23	1.049	0.970,1.134	<i>RAI1-SREBF1</i>
rs10886515	10	121333579	C/T	0.999	0.712	0.60	0.50	0.972	0.897,1.054	<i>TIAL1</i>
rs6475667	9	22598036	A/G	1.000	0.135	0.34	0.72	0.980	0.881,1.091	<i>DMRTA1</i>
rs660895	6	32685358	A/G	1.000	0.191	0.052	0.74	1.016	0.924,1.117	<i>HLA-DRB5-HLA-DQA1</i>
rs2823357	21	15836776	A/G	0.999	0.620	0.19	0.44	0.970	0.899,1.047	<i>NRIP1-USP25</i>
rs11065598	12	120418046	C/T	0.997	0.095	0.73	0.61	0.968	0.853,1.097	<i>FBXL10</i>
rs9379968	6	27352569	A/G	1.000	0.526	0.94	0.56	0.978	0.909,1.053	<i>PRSS16-FKSG83</i>
rs9917256	2	168851281	A/G	0.999	0.875	0.70	0.40	1.049	0.939,1.172	<i>STK39-LASS6</i>
rs10999435	10	72045807	A/G	1.000	0.927	0.23	0.57	0.960	0.833,1.105	<i>PRF1-ADAMTS14</i>
rs4130047	18	38932233	C/T	1.000	0.682	0.89	0.60	0.979	0.905,1.060	<i>RIT2</i>
rs35883	3	29572795	A/G	1.000	0.546	0.95	0.52	0.976	0.907,1.051	<i>RBMS3</i>
rs943914	14	54509818	A/C	0.997	0.705	0.47	0.059	1.080	0.997,1.171	<i>WDHD1</i>
rs7778020	7	48427057	A/G	0.999	0.905	0.94	0.41	0.949	0.837,1.076	<i>ABCA13</i>
rs535586	6	31968316	C/T	0.703	0.309	0.018	0.16	1.072	0.974,1.179	<i>EHMT2</i>
rs17763599	19	2320415	G/T	1.000	0.279	0.38	0.31	1.043	0.962,1.132	<i>SPPL2B-TMPRSS9</i>
rs2414739	15	59781426	A/G	1.000	0.269	0.86	0.59	0.977	0.899,1.062	<i>VPS13C</i>
rs624032	10	28998382	C/T	0.998	0.355	0.85	0.15	1.058	0.980,1.143	<i>WAC-BAMBI</i>
rs182549	2	136333224	C/T	1.000	0.578	2.4e-29	0.89	1.006	0.926,1.092	<i>MCM6</i>
rs6464536	7	142399594	C/T	0.999	0.085	0.92	0.84	1.014	0.888,1.157	<i>KEL-OR9A2</i>
rs7705606	5	39243174	G/T	0.357	0.999	0.93	0.49	0.554	0.099,3.088	<i>FYB</i>
rs17126237	8	18025369	C/T	0.998	0.118	0.57	0.64	1.028	0.916,1.154	<i>ASAHI-NATI</i>

Abbreviation: chr, chromosome; NEA, non-effect allele; EA, effect allele; Gt. rate, genotyping rate; EAF, effect allele frequency.

Note: significant SNP is in bold

Table S7 Association test results for Parkinson's disease, at AGA loci

SNP	chr	position	NEA/ EA	Gt. rate	EAF	HWE p value	p value	Odds Ratio	95% CI	Gene
rs5918696	X	66242280	C/T	0.999	0.148	0.15	0.54	1.020	0.958,1.085	<i>EDA2R-AR</i>
rs6113491	20	22005415	A/C	1.000	0.489	0.037	0.82	1.007	0.952,1.064	<i>PAX1-FOXA2</i>
rs13245206	7	18857784	A/G	1.000	0.608	0.047	0.19	1.039	0.981,1.100	<i>HDAC9</i>
rs9287638	2	239359379	A/C	1.000	0.676	0.12	0.51	0.980	0.924,1.040	<i>ASB1-HDAC4</i>
rs2003046	1	10955414	A/C	1.000	0.772	0.13	0.38	1.030	0.963,1.102	<i>C1orf127-TARDBP</i>
rs6950087	7	68233508	C/T	0.999	0.538	0.046	0.33	0.973	0.921,1.029	<i>AUTS2</i>
rs7349332	2	219464627	C/T	1.000	0.136	0.22	0.79	1.011	0.932,1.097	<i>WNT10A</i>
rs2668692	17	41648797	A/G	0.992	0.784	0.14	2.8e-12	1.283	1.195,1.378	<i>KIAA1267-LRRC37A</i>
rs9668810	12	26317687	C/T	1.000	0.265	0.0010	0.62	1.016	0.954,1.082	<i>SSPN-ITPR2</i>
rs11079281	17	52586786	C/T	1.000	0.539	0.45	0.72	1.010	0.955,1.069	<i>AKAP1-MSI2</i>
rs8085664	18	41068154	A/C	0.999	0.726	0.66	0.65	1.015	0.953,1.081	<i>SETBP1-SLC14A2</i>
rs10850917	12	116801217	C/T	1.000	0.240	0.89	0.58	1.019	0.954,1.088	<i>KSR2</i>
rs10935880	3	153137969	A/G	1.000	0.713	0.86	0.58	1.018	0.957,1.082	<i>SUCNR1-MBNL1</i>
rs7707918	5	158202803	A/C	1.000	0.403	0.029	0.59	1.016	0.960,1.075	<i>EBF1</i>
rs2700482	12	49369532	C/T	1.000	0.349	0.77	0.32	1.030	0.972,1.092	<i>DIP2B</i>
rs12194169	6	9601288	G/T	1.000	0.051	0.034	0.66	1.029	0.906,1.168	<i>OFCC1</i>
rs1907354	10	77882399	A/G	0.998	0.679	0.26	0.31	0.969	0.913,1.029	<i>C10orf11</i>
rs13130633	4	8345096	C/T	0.679	0.226	0.27	0.051	1.073	1.000,1.151	<i>HTRA3</i>
rs803307	1	25331538	A/G	1.000	0.336	0.25	0.37	0.973	0.917,1.033	<i>RUNX3-SYF2</i>
rs10812596	9	27435104	A/G	0.679	0.301	0.67	0.78	0.991	0.929,1.057	<i>MOBK2B</i>
rs4940205	18	43291571	A/G	0.999	0.281	0.19	0.65	1.015	0.954,1.080	<i>CORL2-SMAD2</i>
rs12026324	1	119248233	C/T	1.000	0.709	0.26	0.79	0.992	0.932,1.054	<i>TBX15</i>
rs8053509	16	8769772	G/T	0.999	0.865	0.12	0.98	0.999	0.921,1.084	<i>ABAT</i>
rs2861754	2	67931211	A/G	1.000	0.654	0.74	0.37	1.027	0.968,1.090	<i>ETAA1-CID</i>
rs5762174	22	26195344	A/C	0.998	0.390	0.15	0.49	0.980	0.925,1.038	<i>CRYBA4-MNI</i>
rs4733710	8	130612833	A/C	1.000	0.747	0.96	0.14	1.050	0.985,1.120	<i>GSDMC</i>

Abbreviation: chr, chromosome; NEA, non-effect allele; EA, effect allele; Gt. rate, genotyping rate; EAF, effect allele frequency.