Supplementary Information

A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine

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Supplementary Notes

Supplementary Note 1

Replication of novel migraine candidate associations from CPASSOC

Replication of novel migraine candidate associations from CPASSOC was performed using logistic models adjusting for sex, age, genotype array, recruitment center, and the first 10 genetic principal components (PCs) in an independent data set from UK Biobank (restricted to unrelated European ancestry) for migraine (N_{cases} / $N_{controls}$= 10,005 / 267,330 from data field 20002 with excluding participants with broad headache [defined by data field 6159] in migraine controls to avoid bias due to high correlation and heterogeneity between them) and broad headache (N_{cases} / $N_{controls}$= 67,052 / 269,883, data field: 6159).

Supplementary Note 2

Transcriptome-wide association studies (TWAS)

We performed TWAS to identify genes whose expression pattern across tissues implicates etiology or biological mechanisms shared by migraine and the BP measures. To do this, we first merged the summary statistics for each trait to a subset of SNPs with Hapmap3 SNPs excluding the HLA region [1], and then integrated this pruned GWAS summary data (~1.2 million SNPs) for migraine or each of BP traits (SBP, DBP, and PP) with LD-adjusted weight vector learned from the gene expression data to perform TWASs across 48 tissues from GTEx v.7 [2] using available software and precompiled data resources (see URLs) [1,3]. The strength of association between concordant gene-based genetic influences on gene expression on migraine or BP was given by Z_{TWAS} as described [3]. The number of available gene-based models for gene expression from GTEx ranged from 1,604 for brain substantia nigra to 9,826 for thyroid. We also conducted conditional TWAS analysis among the shared genes by leveraging previous methods for joint/conditional tests of SNPs using summary statistics [4,5] to identify an independent set of TWAS genes. The correlation/LD matrix for this step was computed using Pearson correlation of genetic effects on gene expression predicted for the 1000 genomes genotypes as described[4] across all pairwise genes shared by migraine and the BP measures. With this correlation matrix, we determined separate sets of independent gene-based models of genetic effects for migraine and BP measures separately, deriving a final set of shared gene-based models as the overlap across tissues.

Supplementary Note 3

Mendelian Randomization (MR) sensitivity analyses

We conducted sensitivity analyses for the primary MR analysis using conventional inverse-variance weighted (IVW) MR, weighted median, simple median, MR-egger (Egger regression) implemented in R package “MendelianRandomization” [6]. We also applied MR-Steiger with the R package “TwoSampleMR” to assure that the causal direction between the hypothesized exposure and outcome was correctly assigned [7].

Supplementary Table 1 Genome-wide significant regions from local genetic correlation analysis (*ρ*-HESS) between migraine and blood pressure (*P*<0.05/1703)

Trait 1	Trait 2	chr	start	end	num_snp	local_rhog	var	se	z	*p*
Migraine	DBP	10	95396368	96221243	1073	0.00022339	2.55E-09	5.05E-05	4.42	9.85E-06
	SBP	6	94441175	97093511	4084	0.00022129	2.14E-09	4.63E-05	4.78	1.74E-06
		7	39862670	42001811	2725	-0.0001779	1.77E-09	4.21E-05	-4.23	2.35E-05
		10	95396368	96221243	1073	0.00022985	2.98E-09	5.46E-05	4.21	2.56E-05
	PP	6	94441175	97093511	4084	0.00021535	2.14E-09	4.62E-05	4.66	3.20E-06
		7	39862670	42001811	2725	-0.00025176	2.10E-09	4.58E-05	-5.49	3.98E-08

Abbreviations: chr: chromosome; num_snp: number of SNPs in region; local_rhog: local genetic covariance in the corresponding region; se: standard error; DBP: diastolic blood pressure; SBP: systolic blood pressure; PP: pulse pressure.

Supplementary Table 2 Genome-wide significant regions from local genetic correlation analysis (GWAS-PW) between migraine and blood pressure (PPA_3>0.90)

Trait 1	Trait 2	NSNP	chr	st	sp	PPA_1	PPA_2	PPA_3	PPA_4
Migraine	DBP	4201	1	156336687	158027330	4.79E-09	1.68E-18	0.97	0.03
		5308	1	175089963	177433277	1.48E-10	0.0006	0.96	0.04
		3197	2	95358799	98994973	6.01E-28	0.00022	0.93	0.06
		3876	3	123518258	124935910	1.24E-17	0.00055	0.96	0.04
		6708	6	94441595	97093400	4.02E-11	4.37E-23	0.96	0.04
		1695	10	95397754	96220615	2.31E-56	1.11E-11	0.99	0.01
		4293	10	96222131	97820339	2.39E-26	9.16E-05	0.94	0.06
		849	12	8429979	9031328	1.60E-17	0.00255	0.98	0.01
		4914	13	109815112	111231864	3.33E-11	0.00067	0.95	0.04
		4992	20	18972387	20959637	3.89E-10	5.13E-16	0.98	0.02
	SBP	4201	1	156336687	158027330	1.01E-08	3.26E-22	0.95	0.05
		3876	3	123518258	124935910	7.80E-19	1.14E-07	0.91	0.09
		3426	6	11791351	13209144	3.58E-18	8.69E-23	1.00	0.00
		6708	6	94441595	97093400	2.01E-20	4.02E-27	0.96	0.04
		4050	7	39863558	42001171	2.62E-16	3.54E-16	0.93	0.07
		1695	10	95397754	96220615	8.33E-48	2.43E-15	0.98	0.02
		849	12	8429979	9031328	1.05E-10	7.13E-07	0.95	0.05
	PP	3876	3	123518258	124935910	2.19E-10	0.00112	0.90	0.10
		3426	6	11791351	13209144	2.70E-36	5.29E-19	1.00	0.00
		6708	6	94441595	97093400	1.55E-17	2.31E-23	0.98	0.02
		4050	7	39863558	42001171	8.26E-27	2.29E-12	0.95	0.05
		8343	11	101331132	103958766	5.52E-12	1.80E-05	0.95	0.05
		2853	12	55665948	57548466	1.59E-09	8.35E-45	0.99	0.01
		5202	12	89684199	92065305	1.55E-59	0.00734	0.91	0.08
		4914	13	109815112	111231864	3.49E-08	0.00027	0.98	0.02
		4992	20	18972387	20959637	1.13E-34	2.37E-15	0.91	0.09
		3322	21	35226082	36523905	6.58E-12	9.37E-05	0.94	0.06

Abbreviations: chr: chromosome; NSNP: number of SNPs in region; st:start; ed:end; PPA_1: posterior probability for model 1 (association only to phenotype 1); PPA_2: posterior probability for model 2 (association only to phenotype 2); PPA_3: posterior probability for model 3 (shared association to both phenotypes); PPA_4: posterior probability for model 4 (two distinct associations, one to each phenotype); DBP: diastolic blood pressure; SBP: systolic blood pressure; PP: pulse pressure.

Supplementary Table 3 Genome-wide significant loci shared between migraine and diastolic blood pressure (DBP) from cross-trait meta-analysis using CPASSOC ($P_{\text{meta}} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ	Migraine			DBP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs1271309	12	124820705	chr12:124771217..124843104	A	G	0.17	-0.04	0.01	8.56E-06	-0.20	0.02	1.45E-16	2.04E-20	FAM101A,MIR6880,NCOR2,ZNF664-FAM101A
rs13260	13	110802123	chr13:110788441..110818102	T	G	0.09	0.06	0.01	6.60E-07	-0.20	0.03	1.66E-10	8.69E-15	COL4A1
rs1861881	9	119312256	chr9:119157030..119486923	T	G	0.31	0.03	0.01	6.60E-06	0.12	0.02	6.49E-10	1.67E-13	ASTN2,LOC100128505,PAPPA,PAPPA-AS1,TRIM32
rs2004295	6	39154866	chr6:39093606..39187886	A	G	0.27	-0.04	0.01	4.60E-08	-0.13	0.02	4.79E-11	3.34E-16	KCNK5
rs2052692	11	10667641	chr11:10579687..10736660	A	G	0.33	-0.05	0.01	3.38E-13	0.17	0.02	4.28E-21	4.50E-31	LYVE1,MRVI1,MRVI1-AS1
rs2274319	1	156450873	chr1:156406853..156507670	T	C	0.35	0.07	0.01	1.43E-21	0.10	0.02	1.65E-07	3.64E-21	IQGAP3,MEF2D
rs2500281	1	3220382	chr1:3210950..3229134	A	G	0.28	-0.04	0.01	5.43E-06	0.10	0.02	9.73E-07	6.21E-10	PRDM16
rs28451064	21	35593827	chr21:35593827..35682958	A	G	0.13	-0.06	0.01	2.69E-07	0.13	0.03	1.54E-06	1.96E-10	near MRPS6
rs28455731	6	121846038	chr6:121782750..121848841	T	G	0.16	0.05	0.01	7.29E-09	-0.11	0.02	3.37E-06	7.51E-11	near GJA1
rs2971603	6	97035418	chr6:96732257..97081432	T	C	0.23	0.09	0.01	2.83E-27	0.13	0.02	1.23E-09	5.67E-27	FHL5,UFL1
rs3766694	1	175143207	chr1:175118895..175162805	T	C	0.61	-0.03	0.01	1.26E-06	0.11	0.02	4.07E-10	3.17E-14	KIAA0040
rs3851738	16	75387533	chr16:75305331..75516534	C	G	0.43	-0.04	0.01	1.34E-09	0.13	0.02	7.09E-13	3.12E-19	CFDP1,CHST6,TMEM170A
rs4814864	20	19469817	chr20:19455203..19573475	C	G	0.26	0.07	0.01	2.19E-19	-0.11	0.02	8.04E-09	2.05E-19	SLC24A3
rs57866767	10	96023077	chr10:95952031..96993955	T	C	0.44	0.05	0.01	2.32E-14	0.28	0.02	2.86E-57	7.42E-71	C10orf129,CYP2C8,CYP2C9,CYP2C18,CYP2C19,HELLS,NOC3L,PLCE1,PLCE1-AS1,TBC1D12
rs62155750	2	96491456	chr2:95931218..97428320	A	G	0.31	0.04	0.01	4.42E-07	-0.22	0.02	8.27E-29	5.42E-34	ADRA2B,ARID5A,ASTL,CIAO1,CNNM4,DUSP2,FAHD2A,FAHD2CP,FER1L5,GPAT2,ITPRIPL1,KANSL3,KCNIP3,LINC00342,LMAN2L,NCAPH,NEURL3,PROM2,SNRNP200,STARD7
rs6438857	3	124557643	chr3:124331571..124648820	T	C	0.57	-0.03	0.01	8.92E-07	0.15	0.02	1.50E-17	2.64E-22	ITGB5,KALRN,MUC13,UMPS

rs6881648	5	74991849	chr5:74328643..75146256	A	C	0.37	-0.04	0.01	4.76E-07	-0.17	0.02	5.06E-21	3.43E-26	ANKDD1B,ANKRD31,COL4A3BP,HMGCR,POC5,POLK
rs72663521	1	40005903	chr1:39551488..40088043	A	G	0.19	0.04	0.01	1.94E-06	0.13	0.02	1.42E-08	2.22E-12	BMP8A,KIAA0754,MACF1,PABPC4,PPIEL,SNORA55
rs8008129	14	58829032	chr14:58668484..58853140	T	C	0.34	0.03	0.01	3.91E-06	0.09	0.02	1.37E-06	7.22E-10	ACTR10,ARID4A,FLJ31306,PSMA3
rs978851	10	100660301	chr10:100601902..101139262	T	C	0.29	0.04	0.01	7.76E-06	0.09	0.02	5.50E-06	5.51E-09	CNNM1,HPSE2

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; DBP: diastolic blood pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 4 Genome-wide significant loci shared between migraine and systolic blood pressure (SBP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine			SBP			P_{meta}	Genes within Ranges
							BETA	SE	P	BETA	SE	P		
rs1048483	17	1966457	chr17:1926337..2229067	T	C	0.49	-0.03	0.01	1.31E-06	-0.30	0.03	6.49E-23	9.29E-27	DPH1,HIC1,LOC101927839,MIR132,MIR212,OVCA2,RTN4RL1,SMG6,SRR,TSR1
rs12202891	6	12768218	chr6:12768218..12768218	T	C	0.17	-0.07	0.01	2.16E-10	-0.21	0.04	5.81E-07	2.83E-12	PHACTR1
rs12947578	17	78246734	chr17:78235300..78285371	T	C	0.43	0.05	0.01	1.11E-09	-0.16	0.03	1.01E-06	8.76E-12	RNF213
rs1332844	6	12889004	chr6:12762814..12982423	T	C	0.36	-0.05	0.01	1.48E-13	-0.21	0.03	1.06E-11	1.19E-19	PHACTR1
rs17171710	7	40440233	chr7:40120135..40479852	T	C	0.11	0.09	0.01	4.98E-15	-0.41	0.05	1.13E-16	1.17E-26	CDK13,MPLKIP,SUGCT (C7orf10)
rs2052692	11	10667641	chr11:10579687..10736660	A	G	0.33	-0.05	0.01	3.38E-13	0.19	0.03	2.13E-09	6.23E-17	LYVE1,MRVI1,MRVI1-AS1
rs2274319	1	156450873	chr1:156406853..156507670	T	C	0.35	0.07	0.01	1.43E-21	0.16	0.03	2.47E-07	1.70E-20	IQGAP3,MEF2D
rs2983896	6	97029871	chr6:96682566..97081432	A	G	0.22	0.09	0.01	4.79E-27	0.34	0.04	1.61E-20	1.53E-37	FHL5,UFL1
rs4814864	20	19469817	chr20:19455203..19573475	C	G	0.26	0.07	0.01	2.19E-19	0.18	0.03	1.44E-07	2.36E-18	SLC24A3
rs4888408	16	75432824	chr16:75240935..75516534	A	G	0.43	-0.04	0.01	3.02E-09	0.37	0.03	1.42E-32	4.24E-39	BCAR1,CFDP1,CHST6,CTRB1,CTRB2,LOC100506281,TMEM170A
rs546240	11	30533622	chr11:30493671..30570681	T	C	0.38	-0.03	0.01	3.55E-06	0.15	0.03	5.76E-07	3.84E-10	MPPED2
rs57866767	10	96023077	chr10:95952031..96797500	T	C	0.44	0.05	0.01	2.32E-14	0.45	0.03	1.14E-49	2.82E-60	CYP2C8,CYP2C9,CYP2C18,CYP2C19,HELLS,NOC3L,PLCE1,PLCE1-AS1,TBC1D12
rs6438857	3	124557643	chr3:124331571..124648820	T	C	0.57	-0.03	0.01	8.92E-07	0.27	0.03	3.13E-19	1.77E-23	ITGB5,KALRN,MUC13,UMPS
rs733701	6	39171862	chr6:39115413..39187886	T	C	0.26	0.06	0.01	1.26E-12	0.19	0.03	3.70E-08	7.53E-15	KCNK5
rs8080108	17	47513711	chr17:47289566..47516523	T	C	0.30	-0.03	0.01	3.74E-06	-0.30	0.03	3.15E-20	1.22E-23	ABI3,FLJ40194,LOC102724596,MIR6129,PHB,PHOSPHO1,ZNF652
rs978851	10	100660301	chr10:100601902..101139262	T	C	0.29	0.04	0.01	7.76E-06	0.15	0.03	8.10E-06	1.53E-08	CNNM1,HPSE2

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; SBP: systolic blood pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 5 Genome-wide significant loci shared between migraine and pulse pressure (PP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine			PP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs1048483	17	1966457	chr17:1926337..2229067	T	C	0.49	-0.03	0.01	1.31E-06	-0.20	0.02	1.47E-22	5.13E-28	DPH1,HIC1,LOC101927839,MIR132,MIR212,OVCA2,RTN4RL1,SMG6,SRR,TSR1
rs11172113	12	57527283	chr12:57256380..57545756	T	C	0.42	0.10	0.01	5.64E-49	-0.12	0.02	3.02E-08	1.71E-50	GPR182,LRP1,MYO1A,NAB2,RDH16,SDR9C7,STAT6,TAC3,TMEM194A,ZBTB39
rs12202891	6	12768218	chr6:12768218..13022728	T	C	0.17	-0.07	0.01	2.16E-10	-0.21	0.03	5.19E-14	9.87E-22	PHACTR1
rs12875271	13	110792743	chr13:110788441..110804809	A	G	0.09	-0.06	0.01	5.15E-07	-0.19	0.04	1.18E-07	6.29E-12	COL4A1
rs1332844	6	12889004	chr6:12762814..13098302	T	C	0.36	-0.05	0.01	1.48E-13	-0.20	0.02	6.95E-22	3.11E-33	PHACTR1
rs17171710	7	40440233	chr7:40000089..40479852	T	C	0.11	0.09	0.01	4.98E-15	-0.37	0.03	7.39E-28	3.10E-41	CDK13,MPLKIP,SUGCT (C7orf10)
rs1800470	19	41858921	chr19:41851509..41946095	A	G	0.40	0.04	0.01	4.97E-07	-0.15	0.02	1.76E-12	1.49E-17	ATP5SL,B3GNT8,B9D2,BCKDHA,EXOSC5,TGFB1,TMEM91
rs2282652	11	102097315	chr11:101915105..102125714	T	C	0.33	-0.04	0.01	6.47E-08	0.15	0.02	1.17E-11	2.46E-17	C11orf70,YAP1
rs28577186	16	4488191	chr16:4399075..4687695	A	G	0.35	-0.04	0.01	1.44E-06	-0.14	0.02	8.39E-10	3.77E-14	C16orf96,CDIP1,CORO7,CORO7-PAM16,DNAJA3,HMOX2,MGRN1,NMRAL1,PAM16,UBALD1,VASN
rs2983896	6	97029871	chr6:96732257..97081432	A	G	0.22	0.09	0.01	4.79E-27	0.21	0.02	1.26E-17	2.74E-36	FHL5,UFL1
rs4888408	16	75432824	chr16:75242729..75516534	A	G	0.43	-0.04	0.01	3.02E-09	0.25	0.02	1.01E-32	1.31E-41	BCAR1,CFDP1,CHST6,CTRB1,LOC100506281,TMEM170A
rs546240	11	30533622	chr11:30449319..30570681	T	C	0.38	-0.03	0.01	3.55E-06	0.13	0.02	4.47E-10	3.07E-14	MPPED2
rs57866767	10	96023077	chr10:95973747..96784778	T	C	0.44	0.05	0.01	2.32E-14	0.18	0.02	4.88E-18	2.35E-29	CYP2C9,CYP2C18,CYP2C19,HELLS,NOC3L,PLCE1,PLCE1-AS1,TBC1D12
rs6035355	20	19465089	chr20:19455203..19614751	A	T	0.28	0.07	0.01	4.86E-18	0.29	0.02	1.25E-36	9.26E-54	SLC24A3
rs6438857	3	124557643	chr3:124441501..124648820	T	C	0.57	-0.03	0.01	8.92E-07	0.13	0.02	9.00E-10	2.55E-14	ITGB5,MUC13,UMPS
rs6515020	20	19504904	chr20:19460032..19587337	T	C	0.09	-0.06	0.01	1.12E-07	-0.21	0.03	5.79E-10	4.03E-15	SLC24A3

rs6693567	1	150510660	chr1:150250534..150832108	T	C	0.27	-0.04	0.01	1.21E-08	0.14	0.02	4.09E-09	8.51E-15	ADAMTSL4,ADAMTSL4-AS1,ARNT,C1orf54,CIART,CTSK,CTSS,ECM1,ENSA,GOLPH3L,HORMAD1,LINC00568,MCL1,MIR4257,MIR6878,MRPS21,PRPF3,RPRD2,TARS2
rs934287	2	203708307	chr2:203320423..204367311	A	G	0.17	-0.04	0.01	3.66E-06	0.16	0.03	1.18E-09	1.01E-13	ABI2,BMPR2,CARF,CYP20A1,FAM117B,ICA1L,NBEAL1,RAPH1,WDR12
rs974819	11	103660567	chr11:103599717..103718660	T	C	0.29	-0.03	0.01	1.00E-05	0.11	0.02	4.15E-07	1.67E-10	Intergenic
rs9982601	21	35599128	chr21:35566316..35716371	T	C	0.13	-0.05	0.01	1.78E-07	-0.21	0.03	7.51E-12	3.38E-17	Intergenic

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; PP: pulse pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 6 replication of migraine novel loci from CPASSOC meta-analysis by using logistic regression in UK Biobank

Chr	SNP	BP	A1	A2	MAF	Migraine (N=277,335)			Headache (N=336,935)		
						BETA	SE	*P*	BETA	SE	*P*
1	rs72663521	40005903	G	A	0.18	0.004	0.019	0.82	-0.020	0.008	0.01
1	rs3766694	175143207	T	C	0.38	-0.041	0.015	6.07E-03	-0.028	0.006	1.54E-05
2	rs62155750	96491456	A	G	0.31	0.036	0.016	0.02	0.004	0.007	0.55
3	rs6438857	124557643	T	C	0.42	-0.028	0.015	0.05	-0.015	0.006	0.02
5	rs6881648	74991849	A	C	0.37	-0.066	0.015	9.39E-06	-0.029	0.006	6.86E-06
11	rs974819	103660567	T	C	0.29	-0.009	0.016	0.56	0.008	0.007	0.23
12	rs1271309	124820705	A	G	0.16	-0.062	0.020	1.78E-03	-0.030	0.008	3.27E-04
13	rs12875271	110792743	A	G	0.09	-0.064	0.024	8.59E-03	-0.024	0.011	0.02
13	rs13260	110802123	G	T	0.09	-0.063	0.025	0.01	-0.022	0.011	0.04
14	rs8008129	58829032	T	C	0.36	0.041	0.015	6.93E-03	0.011	0.006	0.08
16	rs28577186	4488191	G	A	0.33	0.028	0.015	0.07	-0.005	0.007	0.44
17	rs1048483	1966457	C	T	0.49	0.019	0.015	0.20	0.014	0.006	0.03
17	rs8080108	47513711	T	C	0.31	-0.054	0.016	6.43E-04	-0.030	0.007	9.98E-06
19	rs1800470	41858921	G	A	0.37	-0.049	0.015	1.19E-03	-0.024	0.006	1.59E-04
21	rs28451064	35593827	G	A	0.13	0.117	0.023	2.96E-07	0.032	0.009	6.37E-04
21	rs9982601	35599128	C	T	0.13	0.092	0.022	3.82E-05	0.025	0.009	6.14E-03

Abbreviations: Chr: chromosome; BP: physical position; MAF: minor allele frequency; SE: standard error.

Position is under build 37/hg19.

Model adjusted for sex, age, genotype array, recruitment center, and 10 PCs.

Supplementary Table 7 eQTL results for rs62155750 at *ADRA2B* from GTEx (version 7 release)

Gencode Id	Gene Symbol	Variant Id	SNP Id	P-Value	NES	Tissue
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	1.40E-14	0.46	Thyroid
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	7.90E-11	0.41	Nerve - Tibial
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	2.10E-08	0.33	Colon - Transverse
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	2.90E-08	0.29	Adipose - Subcutaneous
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	3.30E-08	0.34	Stomach
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	4.1E-06	0.31	Adipose - Visceral (Omentum)
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	4.8E-06	0.26	Esophagus - Muscularis
ENSG00000222040.3	ADRA2B	2_96491456_A_G_b37	rs62155750	0.000038	0.22	Muscle - Skeletal

Abbreviations: NES=normalized effect size.

Supplementary Table 8 **eQTL results for rs1048483 from GTEx (version 7 release)**

Gencode Id	Gene Symbol	Variant Id	SNP Id	*P*-Value	NES	Tissue
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.30E-17	-0.45	Artery - Tibial
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	4.20E-17	-0.41	Muscle - Skeletal
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	5.50E-16	-0.46	Esophagus - Mucosa
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.10E-14	-0.34	Lung
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.70E-14	-0.36	Thyroid
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	6.00E-14	-0.43	Skin - Sun Exposed (Lower leg)
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.10E-13	-0.35	Esophagus - Muscularis
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	3.40E-12	-0.37	Adipose - Subcutaneous
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	9.90E-12	-0.4	Heart - Atrial Appendage
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.40E-11	-0.37	Adipose - Visceral (Omentum)
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.40E-10	-0.4	Colon - Transverse
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.60E-10	-0.44	Colon - Sigmoid
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	3.60E-10	-0.36	Whole Blood
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.00E-09	-0.36	Skin - Not Sun Exposed (Suprapubic)
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.20E-09	-0.46	Stomach
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	2.80E-09	-0.38	Breast - Mammary Tissue
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	3.50E-09	-0.36	Nerve - Tibial
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.20E-08	-0.33	Esophagus - Gastroesophageal Junction
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.20E-07	-0.29	Artery - Aorta
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.60E-07	-0.46	Pancreas
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	1.70E-07	-0.28	Cells - Transformed fibroblasts
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	3.60E-07	-0.45	Brain - Cerebellum
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	4.60E-07	-0.29	Heart - Left Ventricle
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	5.00E-07	-0.34	Adrenal Gland
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	8.20E-07	-0.49	Brain - Anterior cingulate cortex (BA24)
ENSG00000167720.8	SRR	17_1966457_C_T_b37	rs1048483	9.70E-07	-0.47	Brain - Cortex
ENSG00000185924.6	RTN4RL1	17_1966457_C_T_b37	rs1048483	0.0000013	0.17	Adipose - Visceral (Omentum)

Abbreviations: NES=normalized effect size.

Supplementary Table 9 Genome-wide significant loci shared between migraine with aura and diastolic blood pressure (DBP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine with aura			SBP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs3798293	6	97033370	chr6:96841762..97067047	A	G	0.22	-0.12	0.03	6.63E-07	-0.13	0.02	2.70E-10	1.04E-12	[**FHL5**,UFL1]
rs2052692	11	10667641	chr11:10579687..10736660	A	G	0.65	-0.11	0.02	3.09E-06	0.17	0.02	4.28E-21	1.09E-24	[LYVE1,**MRVI1**, MRVI1-AS1]

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; DBP: dystolic blood pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 10 Genome-wide significant loci shared between migraine with aura and systolic blood pressure (SBP) from cross-trait meta-analysis using CPASSOC ($P_{\text{meta}} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine with aura			SBP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs2983896	6	97029871	chr6:96767685..97081432	A	G	0.22	0.12	0.03	8.85E-07	0.34	0.04	1.61E-20	2.72E-26	[**FHL5**,UFL1]
rs2052692	11	10667641	chr11:10579687..10736660	A	G	0.65	-0.11	0.02	3.09E-06	0.19	0.03	2.13E-09	3.02E-12	[LYVE1,**MRVI1**,MRVI1-AS1]

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; SBP: systolic blood pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 11 Genome-wide significant loci shared between migraine with aura and pulse pressure (PP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine with aura			PP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs2983896	6	97029871	chr6:96767685..97070190	A	G	0.22	0.12	0.03	8.85E-07	0.21	0.02	1.26E-17	8.11E-22	[**FHL5**,UFL1]
rs11172113	12	57527283	chr12:57502981..57540751	T	C	0.45	0.10	0.02	1.11E-06	-0.12	0.02	3.02E-08	1.58E-10	[**LRP1**,STAT6]

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; PP: pulse pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 12 Genome-wide significant loci shared between migraine without aura and diastolic blood pressure (DBP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine without aura			DBP			P_{meta}	Genes within Ranges
							BETA	SE	P	BETA	SE	P		
rs2274319	1	156450873	chr1:156450873..156500604	T	C	0.64	0.09	0.02	2.45E-06	0.10	0.02	1.65E-07	7.57E-10	[IQGAP3,**MEF2D**]
rs4141663	3	124551967	chr3:124331571..124648820	T	C	0.44	0.08	0.02	8.18E-06	-0.15	0.02	1.41E-17	5.36E-22	[**ITGB5**,KALRN,MUC13,UMPS]
rs34995334	6	121845679	chr6:121782750..121848841	A	G	0.17	-0.12	0.03	1.44E-06	0.11	0.02	3.27E-06	3.96E-08	Intergenic
rs3798293	6	97033370	chr6:96786215..97067047	A	G	0.22	-0.15	0.02	5.99E-12	-0.13	0.02	2.70E-10	8.21E-15	[**FHL5**,UFL1]
rs78378222	17	7571752	chr17:7417640..7700063	T	G	0.02	-0.34	0.07	2.91E-06	-0.61	0.08	1.71E-14	1.80E-18	[ATP1B2,CD68,DNAH2,EFNB3,EIF4A1,FXR2,MPDU1,POLR2A,RPL29P2,SAT2,SENP3,SENP3-EIF4A1,SHBG,SNORA48,SNORA67,SNORD10,SOX15,TNFSF12,TNFSF12-TNFSF13,TNFSF13,**TP53**,WRAP53]

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; DBP: diastolic blood pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 13 Genome-wide significant loci shared between migraine without aura and systolic blood pressure (SBP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine without aura			SBP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs2274319	1	156450873	chr1:156439000..156474119	T	C	0.64	0.09	0.02	2.45E-06	0.16	0.03	2.47E-07	1.14E-08	[**MEF2D**]
rs2983896	6	97029871	chr6:96767685..97081432	A	G	0.22	0.15	0.02	5.82E-12	0.34	0.04	1.61E-20	1.45E-24	[**FHL5**,UFL1]
rs7454157	6	12909874	chr6:12764286..12948388	A	G	0.35	0.11	0.02	8.20E-08	0.21	0.03	1.31E-11	9.53E-14	[**PHACTR1**]

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; SBP: systolic blood pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 14 Genome-wide significant loci shared between migraine without aura and pulse pressure (PP) from cross-trait meta-analysis using CPASSOC ($P_{meta} \leq 5\times10^{-08}$)

SNP	CHR	BP	POS	A1	A2	A1FREQ1	Migraine without aura			PP			P_{meta}	Genes within Ranges
							BETA	SE	*P*	BETA	SE	*P*		
rs11172113	12	57527283	chr12:57362422..57540751	T	C	0.45	0.16	0.02	4.27E-16	-0.12	0.02	3.02E-08	1.68E-17	[GPR182,**LRP1**,MYO1A,NAB2,STAT6,TAC3,TMEM194A,ZBTB39]
rs12631961	3	124561848	chr3:124450321..124648336	T	C	0.42	0.09	0.02	5.16E-06	-0.13	0.02	6.51E-10	8.23E-13	[**ITGB5**,MUC13,UMPS]
rs1332844	6	12889004	chr6:12762814..13052693	T	C	0.65	-0.10	0.02	1.95E-07	-0.20	0.02	6.95E-22	2.84E-28	[**PHACTR1**]
rs2983896	6	97029871	chr6:96767685..97070190	A	G	0.22	0.15	0.02	5.82E-12	0.21	0.02	1.26E-17	1.52E-24	[**FHL5,**UFL1]
rs78378222	17	7571752	chr17:7417640..7700063	T	G	0.02	-0.34	0.07	2.91E-06	1.05	0.09	1.28E-28	7.32E-36	[ATP1B2,CD68,DNAH2,EFNB3,EIF4A1,FXR2,MPDU1,POLR2A,RPL29P2,SAT2,SENP3,SENP3-EIF4A1,SHBG,SNORA48,SNORA67,SNORD10,SOX15,TNFSF12,TNFSF12-TNFSF13,TNFSF13,**TP53**,WRAP53]
rs80080721	17	47777540	chr17:47661137..47964202	T	G	0.11	0.13	0.03	8.98E-06	-0.18	0.03	9.88E-09	2.70E-11	[FAM117A,FLJ45513,KAT7,NXPH3,**SLC35B1**,SPOP,TAC4]

Abbreviations: CHR: chromosome; BP: physical position; POS: position; A1FREQ: A1 allele frequency; PP: pulse pressure.

Position is under build 37/hg19.

All these loci were genome-wide significant ($P<5\times10^{-8}$) for cross-trait meta-analysis (using heterogonous version of CPASSOC, SHet) and $P<1\times10^{-5}$ for single trait GWAS.

Supplementary Table 15 The conditional/joint significant shared TWAS genes between migraine and diastolic blood pressure (DBP)

ID	CHR	Migraine				DBP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\mathrm{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\mathrm{Bonferroni}}$
KIAA0040	1	Artery_Tibial	rs2272784	5.00	4.75E-03	Skin_Sun_Exposed_Lower_leg	rs2272784	6.08	1.02E-05
						Skin_Not_Sun_Exposed_Suprapubic	rs2272784	5.95	2.00E-05
TSPAN2	1	Artery_Aorta	rs2078371	9.72	1.54E-18	Minor_Salivary_Gland	rs11466111	-4.19	0.05
		Artery_Tibial	rs2078371	7.20	5.01E-09				
ADRA2B	2	Skin_Sun_Exposed_Lower_leg	rs11695514	-5.07	3.45E-03	Esophagus_Gastroesophageal_Junction	rs1813381	11.21	1.82E-25
						Skin_Not_Sun_Exposed_Suprapubic	rs1813381	11.06	1.42E-24
						Adipose_Visceral_Omentum	rs1813381	10.95	4.18E-24
						Thyroid	rs1813381	10.80	3.30E-23
						Adipose_Subcutaneous	rs1813381	10.68	9.83E-23
						Stomach	rs1813381	10.52	2.92E-22
						Colon_Transverse	rs1813381	10.52	3.67E-22
						Skin_Sun_Exposed_Lower_leg	rs1813381	10.31	5.77E-21
						Spleen	rs1813381	10.24	5.73E-21
						Nerve_Tibial	rs1813381	10.23	1.36E-20
						Breast_Mammary_Tissue	rs1813381	10.20	1.01E-20
						Esophagus_Muscularis	rs1813381	10.18	1.88E-20
						Heart_Left_Ventricle	rs1813381	10.11	2.41E-20
						Muscle_Skeletal	rs1813381	9.86	4.52E-19
						Heart_Atrial_Appendage	rs1813381	9.78	7.52E-19
						Testis	rs1813381	-6.44	1.06E-06
						Lung	rs1813381	6.31	2.11E-06
						Brain_Cerebellum	rs1813381	-5.81	3.69E-05
						Artery_Aorta	rs1813381	-5.02	3.34E-03
ITGB5	3	Artery_Coronary	rs4141663	4.58	0.01	Artery_Coronary	rs4141663	-9.09	3.15E-16
		Artery_Tibial	rs4141663	4.77	0.01	Artery_Tibial	rs4141663	-8.46	2.14E-13
		Cells_Transformed_fibroblasts	rs4141663	-5.27	9.99E-04	Colon_Sigmoid	rs4141663	-8.35	3.31E-13
		Esophagus_Mucosa	rs4141663	-5.35	6.86E-04	Esophagus_Muscularis	rs4141663	-8.27	9.94E-13

		Nerve_Tibial	rs4141663	5.08	3.54E-03	Nerve_Tibial	rs4141663	-8.27	1.26E-12
						Esophagus_Gastroesophageal_Junction	rs4141663	-8.20	1.15E-12
						Artery_Aorta	rs4141663	-8.09	3.77E-12
						Esophagus_Mucosa	rs4141663	7.77	6.21E-11
						Brain_Hypothalamus	rs4141663	-6.57	1.14E-07
						Muscle_Skeletal	rs4141663	-4.52	0.05
RP11-71H17.9	3	Brain_Cerebellum	rs4141663	-4.81	0.01	Brain_Cerebellum	rs4141663	5.14	1.60E-03
		Brain_Nucleus_accumbens_basal_ganglia	rs4141663	-4.50	0.02	Ovary	rs4141663	4.39	0.03
CISD2	4	Artery_Tibial	rs7694724	4.61	0.03	Ovary	rs13116385	8.31	2.53E-13
						Colon_Sigmoid	rs13116385	7.87	1.64E-11
						Esophagus_Mucosa	rs13116385	7.87	2.86E-11
						Nerve_Tibial	rs13116385	7.63	2.28E-10
						Skin_Sun_Exposed_Lower_leg	rs13116385	7.39	1.24E-09
						Breast_Mammary_Tissue	rs13116385	7.28	1.64E-09
						Cells_Transformed_fibroblasts	rs13116385	7.16	5.83E-09
						Esophagus_Muscularis	rs13116385	7.02	1.68E-08
						Thyroid	rs13116385	6.90	4.99E-08
						Brain_Hippocampus	rs13116385	6.70	4.53E-08
						Uterus	rs13116385	6.56	1.11E-07
						Brain_Cerebellar_Hemisphere	rs13116385	6.44	5.24E-07
						Adipose_Visceral_Omentum	rs13116385	6.33	1.53E-06
						Artery_Tibial	rs13116385	5.84	4.11E-05
						Adipose_Subcutaneous	rs13116385	5.76	6.59E-05
						Lung	rs13116385	5.48	3.25E-04
						Skin_Not_Sun_Exposed_Suprapubic	rs13116385	4.83	0.01
ANKDD1B	5	Esophagus_Mucosa	rs34358	-4.85	0.01	Esophagus_Mucosa	rs2307111	-9.47	2.19E-17
		Nerve_Tibial	rs34358	-4.65	0.03	Thyroid	rs2307111	-8.99	2.41E-15
					0.03	Nerve_Tibial	rs2307111	-8.72	2.61E-14
					0.03	Brain_Cerebellum	rs2307111	-8.06	4.50E-12
					0.03	Skin_Not_Sun_Exposed_Suprapubic	rs2307111	-8.01	8.52E-12

					0.03	Colon_Sigmoid	rs2307111	-7.97	7.66E-12
					0.03	Esophagus_Muscularis	rs2307111	-7.39	1.12E-09
					0.03	Skin_Sun_Exposed_Lower_leg	rs2307111	-6.64	2.81E-07
					0.03	Cells_Transformed_fibroblasts	rs2307111	-6.28	2.51E-06
					0.03	Brain_Cerebellar_Hemisphere	rs2307111	-6.16	3.17E-06
GJA1	6	Artery_Tibial	rs9320821	5.33	7.94E-04	Artery_Aorta	rs6932373	-8.78	1.08E-14
UFL1	6	Adipose_Subcutaneous	rs2983896	9.95	2.01E-19	Spleen	rs11756315	6.17	2.97E-06
		Artery_Tibial	rs2983896	10.14	2.99E-20	Nerve_Tibial	rs11756315	6.09	1.09E-05
		Brain_Cerebellum	rs2983896	9.49	1.32E-17	Pancreas	rs11756315	5.74	4.64E-05
		Nerve_Tibial	rs2983896	9.81	1.02E-18	Whole_Blood	rs11756315	5.68	8.01E-05
		Pancreas	rs2983896	10.44	8.56E-22	Stomach	rs11756315	5.55	1.24E-04
		Spleen	rs2983896	9.18	1.87E-16	Artery_Tibial	rs11756315	5.52	2.69E-04
		Stomach	rs2983896	8.98	1.20E-15	Adipose_Subcutaneous	rs11756315	5.47	3.59E-04
		Vagina	rs2983896	7.52	1.06E-10				
		Whole_Blood	rs2983896	7.16	4.85E-09				
ABO	9	Vagina	rs495828	4.42	0.02	Artery_Aorta	rs579459	-8.28	7.86E-13
						Adrenal_Gland	rs579459	-7.83	2.21E-11
						Whole_Blood	rs579459	7.82	3.07E-11
						Artery_Tibial	rs579459	-7.26	3.15E-09
						Artery_Coronary	rs579459	-7.23	1.48E-09
						Breast_Mammary_Tissue	rs579459	-6.95	1.84E-08
						Colon_Sigmoid	rs579459	-6.72	9.00E-08
						Pituitary	rs579459	-6.56	2.25E-07
						Heart_Atrial_Appendage	rs579459	-6.48	5.13E-07
						Vagina	rs579459	-6.46	2.11E-07
						Adipose_Subcutaneous	rs579459	-6.13	6.89E-06
						Adipose_Visceral_Omentum	rs579459	-6.05	8.67E-06
						Muscle_Skeletal	rs579459	-5.67	1.06E-04
						Colon_Transverse	rs579459	-5.64	8.65E-05
						Esophagus_Mucosa	rs579459	-5.59	1.80E-04

						Brain_Cerebellar_Hemisphere	rs579459	-5.36	3.52E-04
						Heart_Left_Ventricle	rs579459	-5.34	4.55E-04
						Pancreas	rs579459	-4.97	3.35E-03
						Uterus	rs579459	-4.53	0.01
CYP2C9	10	Skin_Not_Sun_Exposed_Suprapubic	rs7078478	-5.73	7.42E-05	Skin_Sun_Exposed_Lower_leg	rs11187960	-8.69	3.11E-14
		Skin_Sun_Exposed_Lower_leg	rs7078478	-4.56	0.04	Skin_Not_Sun_Exposed_Suprapubic	rs11187960	-8.25	1.16E-12
MRVI1	11	Artery_Tibial	rs4909945	6.95	2.99E-08	Artery_Tibial	rs10840378	-6.59	3.50E-07
						Esophagus_Muscularis	rs10840378	6.54	4.75E-07
						Brain_Substantia_nigra	rs10840378	6.51	1.19E-07
						Brain_Cerebellum	rs10840378	6.04	8.92E-06
						Brain_Cortex	rs10840378	5.76	3.32E-05
C12orf5	12	Artery_Tibial	rs2160875	5.44	4.28E-04	Nerve_Tibial	rs3217926	5.05	4.28E-03
		Stomach	rs2160875	4.45	0.04				
CFDP1	16	Adipose_Subcutaneous	rs4888378	5.24	1.29E-03	Brain_Hippocampus	rs766521	-7.20	1.37E-09
		Adipose_Visceral_Omentum	rs4888378	4.52	0.04	Cells_Transformed_fibroblasts	rs766521	-6.84	5.70E-08
		Adrenal_Gland	rs4888378	4.40	0.05	Nerve_Tibial	rs766521	-6.15	7.32E-06
		Artery_Coronary	rs4888378	4.64	0.01	Brain_Cerebellum	rs766521	-5.56	1.58E-04
		Brain_Cortex	rs4888378	4.86	4.61E-03	Muscle_Skeletal	rs766521	-4.95	0.01
		Brain_Hippocampus	rs4888378	6.02	3.97E-06	Breast_Mammary_Tissue	rs766521	-4.78	0.01
		Breast_Mammary_Tissue	rs4888378	5.49	2.01E-04	Artery_Coronary	rs766521	-4.75	0.01
		Cells_EBV-transformed_lymphocytes	rs4888378	5.00	1.57E-03	Adipose_Subcutaneous	rs766521	-4.73	0.02
		Cells_Transformed_fibroblasts	rs4888378	6.34	1.69E-06	Brain_Cortex	rs766521	-4.64	0.01
		Colon_Sigmoid	rs4888378	4.84	0.01	Esophagus_Gastroesophageal_Junction	rs766521	-4.64	0.02
		Esophagus_Gastroesophageal_Junction	rs4888378	4.82	0.01	Pancreas	rs766521	-4.45	0.04
		Esophagus_Muscularis	rs4888378	4.73	0.02	Colon_Sigmoid	rs766521	-4.44	0.04
		Lung	rs4888378	4.60	0.03	Cells_EBV-transformed_lymphocytes	rs766521	-4.43	0.03
		Muscle_Skeletal	rs4888378	5.44	3.82E-04				
		Nerve_Tibial	rs4888378	5.97	2.32E-05				
		Pancreas	rs4888378	5.39	3.55E-04				
		Skin_Not_Sun_Exposed_Suprapubic	rs4888378	5.17	1.67E-03				

		Stomach	rs4888378	4.55	0.02				
SLC24A3	20	Artery_Aorta	rs4814863	-7.38	9.77E-10	Artery_Aorta	rs4814858	5.32	6.53E-04
		Artery_Coronary	rs4814863	-6.75	4.76E-08	Artery_Coronary	rs4814858	5.19	6.72E-04
		Artery_Tibial	rs4814863	-8.43	2.77E-13				

Abbreviations: CHR: chromosome; DBP: diastolic blood pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}<0.05$) for both migraine and blood pressure in at least one GTEx tissues, and significant from TWAS conditional/joint analysis for both traits.

Supplementary Table 16 The conditional/joint significant shared TWAS genes between migraine and systolic blood pressure (SBP)

ID	CHR	Migraine				SBP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$
ITGB5	3	Artery_Coronary	rs4141663	4.58	0.01	Artery_Coronary	rs4141663	-9.27	5.71E-17
		Artery_Tibial	rs4141663	4.77	0.01	Artery_Tibial	rs4141663	-8.88	5.18E-15
		Cells_Transformed_fibroblasts	rs4141663	-5.27	9.99E-04	Esophagus_Muscularis	rs4141663	-8.64	4.31E-14
		Esophagus_Mucosa	rs4141663	-5.35	6.86E-04	Nerve_Tibial	rs4141663	-8.65	4.85E-14
		Nerve_Tibial	rs4141663	5.08	3.54E-03	Artery_Aorta	rs4141663	-8.56	7.23E-14
						Esophagus_Gastroesophageal_Junction	rs4141663	-8.52	7.42E-14
						Colon_Sigmoid	rs4141663	-8.25	7.56E-13
						Esophagus_Mucosa	rs4141663	7.77	6.42E-11
						Brain_Hypothalamus	rs4141663	-7.13	2.19E-09
SNX24	5	Artery_Aorta	rs13172078	-4.91	0.01	Adrenal_Gland	rs1644318	-6.69	9.60E-08
						Skin_Sun_Exposed_Lower_leg	rs1644318	-5.54	2.58E-04
						Artery_Aorta	rs1644318	-5.12	1.91E-03
RP1-257A7.5	6	Artery_Aorta	rs9349379	9.61	4.61E-18	Artery_Tibial	rs9349379	8.60	6.28E-14
		Artery_Coronary	rs9349379	7.62	7.96E-11	Artery_Aorta	rs9349379	8.54	8.50E-14
		Artery_Tibial	rs9349379	9.72	2.10E-18	Artery_Coronary	rs9349379	7.12	3.36E-09
UFL1	6	Adipose_Subcutaneous	rs2983896	9.95	2.01E-19	Spleen	rs2983896	9.17	1.99E-16
		Artery_Tibial	rs2983896	10.14	2.99E-20	Nerve_Tibial	rs2983896	9.15	5.60E-16
		Brain_Cerebellum	rs2983896	9.49	1.32E-17	Pancreas	rs2983896	9.00	1.16E-15
		Nerve_Tibial	rs2983896	9.81	1.02E-18	Whole_Blood	rs2983896	8.51	1.05E-13
		Pancreas	rs2983896	10.44	8.56E-22	Stomach	rs2983896	8.10	2.43E-12
		Spleen	rs2983896	9.18	1.87E-16	Artery_Tibial	rs2983896	7.69	1.16E-10
		Stomach	rs2983896	8.98	1.20E-15	Adipose_Subcutaneous	rs2983896	7.57	2.98E-10
		Vagina	rs2983896	7.52	1.06E-10	Brain_Cerebellum	rs2983896	6.46	5.92E-07
		Whole_Blood	rs2983896	7.16	4.85E-09	Vagina	rs2983896	4.68	0.01
C7orf10	7	Artery_Aorta	rs12533531	-7.76	5.35E-11	Artery_Aorta	rs17171710	8.21	1.37E-12
RBM20	10	Brain_Cortex	rs10885035	4.46	0.03	Artery_Tibial	rs2419577	-4.92	0.01
						Brain_Substantia_nigra	rs2419577	-4.39	0.02

MRVI1	11	Artery_Tibial	rs4909945	6.95	2.99E-08	Esophagus_Muscularis	rs1470260	7.17	5.68E-09
						Brain_Substantia_nigra	rs1470260	5.39	1.12E-04
						Brain_Cerebellum	rs1470260	5.27	7.65E-04
						Brain_Cortex	rs1470260	5.12	1.20E-03
SMG6	17	Esophagus_Mucosa	rs2236375	-4.63	0.03	Esophagus_Mucosa	rs8069947	-7.84	3.60E-11
						Brain_Cerebellum	rs8069947	-6.64	1.85E-07
						Brain_Cortex	rs8069947	-6.12	3.71E-06
						Testis	rs8069947	-5.13	2.57E-03
						Skin_Sun_Exposed_Lower_leg	rs8069947	-4.87	0.01
DMPK	19	Pancreas	rs1548029	4.45	0.04	Pancreas	rs7256192	7.19	3.17E-09
						Artery_Tibial	rs7256192	6.56	4.49E-07
						Artery_Aorta	rs7256192	6.20	3.49E-06
						Adipose_Subcutaneous	rs7256192	6.24	3.62E-06
						Thyroid	rs7256192	5.61	1.97E-04
						Esophagus_Mucosa	rs7256192	5.57	2.06E-04
						Prostate	rs7256192	5.35	2.37E-04
						Nerve_Tibial	rs7256192	5.02	4.84E-03
						Skin_Sun_Exposed_Lower_leg	rs7256192	5.00	0.01
						Breast_Mammary_Tissue	rs7256192	4.69	0.01
						Whole_Blood	rs7256192	4.67	0.02
						Lung	rs7256192	4.71	0.02
						Skin_Not_Sun_Exposed_Suprapubic	rs7256192	4.56	0.04
						Adipose_Visceral_Omentum	rs7256192	4.49	0.04
SLC24A3	20	Artery_Aorta	rs4814863	-7.38	9.77E-10	Artery_Tibial	rs17812022	-6.31	2.26E-06
		Artery_Coronary	rs4814863	-6.75	4.76E-08	Artery_Aorta	rs17812022	-4.57	0.03
		Artery_Tibial	rs4814863	-8.43	2.77E-13				
ASCC2	22	Cells_EBV-transformed_lymphocytes	rs5752933	-4.81	4.11E-03	Brain_Nucleus_accumbens_basal_ganglia	rs12627866	6.18	2.01E-06
						Artery_Tibial	rs12627866	6.01	1.46E-05
						Esophagus_Muscularis	rs12627866	5.95	2.06E-05
						Artery_Aorta	rs12627866	5.92	2.08E-05

Muscle_Skeletal	rs12627866	5.56	1.95E-04
Nerve_Tibial	rs12627866	5.50	3.66E-04
Brain_Cortex	rs12627866	5.08	1.52E-03
Heart_Atrial_Appendage	rs12627866	5.10	1.93E-03
Lung	rs12627866	4.91	0.01
Brain_Cerebellar_Hemisphere	rs12627866	4.47	0.03

Abbreviations: CHR: chromosome; SBP: systolic blood pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}<0.05$) for both migraine and blood pressure in at least one GTEx tissues, and significant from TWAS conditional/joint analysis for both traits.

Supplementary Table 17 **The conditional/joint significant shared TWAS genes between migraine and pulse pressure (PP)**

ID	CHR	Migraine				PP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$
MEF2D	1	Artery_Tibial	rs1925950	7.56	3.25E-10	Artery_Tibial	rs1185700	5.03	3.91E-03
ITGB5	3	Artery_Coronary	rs4141663	4.58	0.01	Artery_Coronary	rs4141663	-6.17	2.16E-06
		Artery_Tibial	rs4141663	4.77	0.01	Artery_Tibial	rs4141663	-6.20	4.62E-06
		Cells_Transformed_fibroblasts	rs4141663	-5.27	9.99E-04	Artery_Aorta	rs4141663	-5.97	1.50E-05
		Esophagus_Mucosa	rs4141663	-5.35	6.86E-04	Esophagus_Muscularis	rs4141663	-5.93	2.30E-05
		Nerve_Tibial	rs4141663	5.08	3.54E-03	Esophagus_Gastroesophageal_Junction	rs4141663	-5.78	3.61E-05
						Nerve_Tibial	rs4141663	-5.82	5.61E-05
						Colon_Sigmoid	rs4141663	-5.38	3.53E-04
						Brain_Hypothalamus	rs4141663	-5.05	1.00E-03
						Esophagus_Mucosa	rs4141663	4.92	0.01
SNX24	5	Artery_Aorta	rs13172078	-4.91	0.01	Adrenal_Gland	rs1644318	-9.30	6.33E-17
						Muscle_Skeletal	rs1644318	-6.76	1.04E-07
						Skin_Sun_Exposed_Lower_leg	rs1644318	-5.67	1.24E-04
						Artery_Aorta	rs1644318	-5.29	7.80E-04
						Brain_Frontal_Cortex_BA9	rs1644318	-4.69	0.01
GJA1	6	Artery_Tibial	rs9320821	5.33	7.94E-04	Adipose_Visceral_Omentum	rs9401457	-6.28	2.06E-06
						Nerve_Tibial	rs9401457	-6.00	1.88E-05
						Artery_Aorta	rs9401457	5.38	4.69E-04
RP1-257A7.5	6	Artery_Aorta	rs9349379	9.61	4.61E-18	Artery_Aorta	rs9349379	12.64	7.74E-33
		Artery_Coronary	rs9349379	7.62	7.96E-11	Artery_Tibial	rs9349379	12.65	9.06E-33
		Artery_Tibial	rs9349379	9.72	2.10E-18	Artery_Coronary	rs9349379	10.83	8.12E-24
UFL1	6	Adipose_Subcutaneous	rs2983896	9.95	2.01E-19	Pancreas	rs2983896	8.42	1.82E-13
		Artery_Tibial	rs2983896	10.14	2.99E-20	Spleen	rs2983896	8.28	5.29E-13
		Brain_Cerebellum	rs2983896	9.49	1.32E-17	Nerve_Tibial	rs2983896	8.28	1.15E-12
		Nerve_Tibial	rs2983896	9.81	1.02E-18	Whole_Blood	rs2983896	7.84	2.71E-11
		Pancreas	rs2983896	10.44	8.56E-22	Stomach	rs2983896	6.99	1.20E-08
		Spleen	rs2983896	9.18	1.87E-16	Artery_Tibial	rs2983896	6.69	1.87E-07
		Stomach	rs2983896	8.98	1.20E-15	Adipose_Subcutaneous	rs2983896	6.56	4.30E-07
		Vagina	rs2983896	7.52	1.06E-10	Brain_Cerebellum	rs2983896	6.03	9.43E-06
		Whole_Blood	rs2983896	7.16	4.85E-09	Vagina	rs2983896	4.40	0.02

C7orf10	7	Artery_Aorta	rs12533531	-7.76	5.35E-11	Artery_Aorta	rs17171710	10.78	2.77E-23
RBM20	10	Brain_Cortex	rs10885035	4.46	0.03	Brain_Substantia_nigra	rs4918582	-5.52	5.33E-05
						Artery_Aorta	rs4918582	-4.56	0.03
SMG6	17	Esophagus_Mucosa	rs2236375	-4.63	0.03	Esophagus_Mucosa	rs1048483	-8.25	1.23E-12
						Brain_Cortex	rs1048483	-6.81	3.86E-08
						Brain_Cerebellum	rs1048483	-5.11	1.89E-03
						Cells_Transformed_fibroblasts	rs1048483	-5.12	2.26E-03
						Adipose_Subcutaneous	rs1048483	-4.57	0.04
DMPK	19	Pancreas	rs1548029	4.45	0.04	Pancreas	rs11672660	7.58	1.70E-10
						Artery_Tibial	rs11672660	7.30	2.39E-09
						Artery_Aorta	rs11672660	7.15	5.68E-09
						Adipose_Subcutaneous	rs11672660	6.99	2.22E-08
						Esophagus_Mucosa	rs11672660	6.46	8.33E-07
						Thyroid	rs11672660	6.28	3.22E-06
						Prostate	rs11672660	5.96	7.02E-06
						Skin_Sun_Exposed_Lower_leg	rs11672660	5.59	1.96E-04
						Nerve_Tibial	rs11672660	5.58	2.33E-04
						Breast_Mammary_Tissue	rs11672660	5.26	7.08E-04
						Lung	rs11672660	5.30	8.72E-04
						Whole_Blood	rs11672660	5.18	1.31E-03
						Skin_Not_Sun_Exposed_Suprapubic	rs11672660	5.13	2.12E-03
						Adipose_Visceral_Omentum	rs11672660	5.06	2.54E-03
						Spleen	rs11672660	4.69	0.01
SLC24A3	20	Artery_Aorta	rs4814863	-7.38	9.77E-10	Artery_Tibial	rs3790228	-12.25	1.32E-30
		Artery_Coronary	rs4814863	-6.75	4.76E-08	Artery_Aorta	rs3790228	-10.88	8.94E-24
		Artery_Tibial	rs4814863	-8.43	2.77E-13	Artery_Coronary	rs3790228	-7.29	9.64E-10
						Cells_Transformed_fibroblasts	rs3790228	-7.37	1.25E-09
						Adipose_Subcutaneous	rs3790228	-6.01	1.47E-05
ASCC2	22	Cells_EBV-transformed_lymphocytes	rs5752933	-4.81	4.11E-03	Brain_Nucleus_accumbens_basal_ganglia	rs16988381	6.38	5.55E-07
						Esophagus_Muscularis	rs16988381	6.44	9.18E-07
						Artery_Aorta	rs16988381	6.20	3.51E-06
						Artery_Tibial	rs16988381	6.21	4.41E-06
						Nerve_Tibial	rs16988381	5.68	1.27E-04
						Brain_Cortex	rs16988381	5.29	4.89E-04

Brain_Cerebellar_Hemisphere	rs16988381	4.67	0.01
Lung	rs16988381	4.75	0.02
Brain_Cerebellum	rs16988381	4.63	0.02
Muscle_Skeletal	rs16988381	4.65	0.02

Abbreviations: CHR: chromosome; PP: pulse pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}$<0.05) for both migraine and blood pressure in at least one GTEx tissues, and significant from TWAS conditional/joint analysis for both traits.

Supplementary Table 18 **The shared TWAS genes between migraine with aura and diastolic blood pressure (DBP)**

ID	CHR	Migraine with aura				DBP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$
MST1	3	Brain_Anterior_cingulate_cortex_BA24	rs4855881	4.31	0.04	Spleen	rs11130216	-7.17	3.27E-09
						Skin_Sun_Exposed_Lower_leg	rs11130216	-7.08	1.23E-08
						Heart_Left_Ventricle	rs11130216	-6.48	4.44E-07
						Stomach	rs11130216	-6.39	7.30E-07
						Lung	rs11130216	-6.33	1.89E-06
						Cells_Transformed_fibroblasts	rs11130216	-6.21	3.83E-06
						Thyroid	rs11130216	-6.17	6.70E-06
						Esophagus_Mucosa	rs11130216	-5.66	1.20E-04
						Brain_Cerebellum	rs11130216	-5.65	9.09E-05
						Brain_Hypothalamus	rs11130216	-5.45	1.15E-04
						Adipose_Subcutaneous	rs11130216	-5.43	4.51E-04
						Artery_Coronary	rs11130216	-4.77	0.01
						Brain_Anterior_cingulate_cortex_BA24	rs11130216	-4.55	0.01
						Brain_Hippocampus	rs11130216	-4.28	0.04
RP11-624M8.1	6	Brain_Amygdala	rs1832937	-4.22	0.04	Lung	rs6919947	-5.19	1.58E-03
UFL1	6	Brain_Cerebellum	rs13208321	4.46	0.05	Spleen	rs11756315	6.17	2.97E-06
						Nerve_Tibial	rs11756315	6.09	1.09E-05
						Pancreas	rs11756315	5.74	4.64E-05
						Whole_Blood	rs11756315	5.68	8.01E-05
						Stomach	rs11756315	5.55	1.24E-04
						Artery_Tibial	rs11756315	5.52	2.69E-04
						Adipose_Subcutaneous	rs11756315	5.47	3.59E-04
RHOF	12	Minor_Salivary_Gland	rs34395322	4.49	0.01	Minor_Salivary_Gland	rs11059094	4.55	0.01
HMOX2	16	Artery_Tibial	rs2304634	4.88	0.01	Spleen	rs12446456	6.91	2.13E-08
PDE6G	17	Muscle_Skeletal	rs1122424	5.10	2.43E-03	Testis	rs11150782	-4.73	0.02

Brain_Cerebellum	rs11150782	-4.60	0.02

Abbreviations: CHR: chromosome; DBP: diastolic blood pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}<0.05$) for both migraine and blood pressure in at least one GTEx tissues.

Supplementary Table 19 The shared TWAS genes between migraine with aura and systolic blood pressure (SBP)

ID	CHR	Migraine with aura				SBP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$
MST1	3	Brain_Anterior_cingulate_cortex_BA24	rs4855881	4.31	0.04	Spleen	rs13100791	-5.74	4.22E-05
						Skin_Sun_Exposed_Lower_leg	rs13100791	-5.57	2.28E-04
						Brain_Hypothalamus	rs13100791	-4.95	1.64E-03
						Brain_Cerebellum	rs13100791	-5.09	2.06E-03
						Thyroid	rs13100791	-5.04	4.45E-03
						Heart_Left_Ventricle	rs13100791	-4.87	0.01
						Stomach	rs13100791	-4.70	0.01
						Esophagus_Mucosa	rs13100791	-4.70	0.02
						Lung	rs13100791	-4.59	0.03
RP11-624M8.1	6	Brain_Amygdala	rs1832937	-4.22	0.04	Lung	rs6900852	-6.92	3.40E-08
						Brain_Hippocampus	rs6900852	-5.36	1.85E-04
						Brain_Spinal_cord_cervical_c-1	rs6900852	-5.06	8.17E-04
						Ovary	rs6900852	-5.00	1.56E-03
						Brain_Cerebellar_Hemisphere	rs6900852	-4.96	3.01E-03
						Brain_Anterior_cingulate_cortex_BA24	rs6900852	-4.82	3.85E-03
						Brain_Hypothalamus	rs6900852	-4.62	0.01
						Pancreas	rs6900852	-4.75	0.01
						Brain_Amygdala	rs6900852	-4.52	0.01
						Nerve_Tibial	rs6900852	-4.85	0.01
						Thyroid	rs6900852	-4.79	0.02
						Esophagus_Gastroesophageal_Junction	rs6900852	-4.65	0.02
UFL1	6	Brain_Cerebellum	rs13208321	4.46	0.05	Spleen	rs2983896	9.17	1.99E-16
						Nerve_Tibial	rs2983896	9.15	5.60E-16
						Pancreas	rs2983896	9.00	1.16E-15
						Whole_Blood	rs2983896	8.51	1.05E-13
						Stomach	rs2983896	8.10	2.43E-12

						Artery_Tibial	rs2983896	7.69	1.16E-10
						Adipose_Subcutaneous	rs2983896	7.57	2.98E-10
						Brain_Cerebellum	rs2983896	6.46	5.92E-07
						Vagina	rs2983896	4.68	0.01
RHOF	12	Minor_Salivary_Gland	rs34395322	4.49	0.01	Minor_Salivary_Gland	rs4069666	4.51	0.01
NMRAL1	16	Adrenal_Gland	rs2304634	4.42	0.04	Brain_Anterior_cingulate_cortex_BA24	rs12446456	4.41	0.03
HMOX2	16	Artery_Tibial	rs2304634	4.88	0.01	Spleen	rs12446456	9.22	1.26E-16
						Adipose_Visceral_Omentum	rs12446456	6.16	4.33E-06
						Brain_Cerebellum	rs12446456	4.96	4.16E-03
						Thyroid	rs12446456	4.63	0.04
NMRAL1	16	Muscle_Skeletal	rs2304634	4.58	0.03	Brain_Anterior_cingulate_cortex_BA24	rs12446456	4.41	0.03
		Prostate	rs2304634	4.42	0.03				
		Thyroid	rs2304634	4.77	0.02				
PAM16	16	Whole_Blood	rs2304634	-4.47	0.05	Spleen	rs9935080	-4.73	0.01
						Stomach	rs9935080	-4.61	0.02
						Heart_Left_Ventricle	rs9935080	4.48	0.04

Abbreviations: CHR: chromosome; SBP: systolic blood pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}<0.05$) for both migraine and blood pressure in at least one GTEx tissues.

Supplementary Table 20 The shared TWAS genes between migraine with aura and pulse pressure (PP)

ID	CHR	Migraine with aura				PP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\mathrm{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\mathrm{Bonferroni}}$
RP11-624M8.1	6	Brain_Amygdala	rs1832937	-4.22	0.04	Lung	rs4897160	-5.43	4.28E-04
						Brain_Hippocampus	rs4897160	-4.87	2.49E-03
UFL1	6	Brain_Cerebellum	rs13208321	4.46	0.05	Pancreas	rs2983896	8.42	1.82E-13
						Spleen	rs2983896	8.28	5.29E-13
						Nerve_Tibial	rs2983896	8.28	1.15E-12
						Whole_Blood	rs2983896	7.84	2.71E-11
						Stomach	rs2983896	6.99	1.20E-08
						Artery_Tibial	rs2983896	6.69	1.87E-07
						Adipose_Subcutaneous	rs2983896	6.56	4.30E-07
						Brain_Cerebellum	rs2983896	6.03	9.43E-06
						Vagina	rs2983896	4.40	0.02
LRP1	12	Artery_Tibial	rs11172113	4.87	0.01	Skin_Sun_Exposed_Lower_leg	rs11172113	-5.75	7.71E-05
						Artery_Tibial	rs11172113	-5.54	2.44E-04
NMRAL1	16	Adrenal_Gland	rs2304634	4.42	0.04	Brain_Anterior_cingulate_cortex_BA24	rs4785955	5.52	8.94E-05
		Muscle_Skeletal	rs2304634	4.58	0.03	Skin_Sun_Exposed_Lower_leg	rs4785955	5.69	1.08E-04
		Prostate	rs2304634	4.42	0.03	Esophagus_Gastroesophageal_Junction	rs4785955	5.56	1.31E-04
		Thyroid	rs2304634	4.77	0.02	Brain_Putamen_basal_ganglia	rs4785955	5.27	3.84E-04
						Brain_Cortex	rs4785955	5.22	7.02E-04
						Lung	rs4785955	5.27	1.06E-03
						Ovary	rs4785955	5.04	1.27E-03
						Cells_Transformed_fibroblasts	rs4785955	5.21	1.40E-03
						Heart_Left_Ventricle	rs4785955	5.06	2.06E-03
						Stomach	rs4785955	5.04	2.08E-03
						Liver	rs4785955	4.95	2.15E-03
						Pancreas	rs4785955	5.05	2.18E-03
						Esophagus_Muscularis	rs4785955	5.13	2.23E-03
						Breast_Mammary_Tissue	rs4785955	5.03	2.37E-03

						Esophagus_Mucosa	rs4785955	5.11	2.53E-03
						Pituitary	rs4785955	4.97	2.85E-03
						Colon_Sigmoid	rs4785955	4.99	2.94E-03
						Nerve_Tibial	rs4785955	5.12	2.94E-03
						Brain_Cerebellar_Hemisphere	rs4785955	4.95	3.14E-03
						Whole_Blood	rs4785955	5.00	3.41E-03
						Artery_Tibial	rs4785955	5.02	4.08E-03
						Brain_Hippocampus	rs4785955	4.65	0.01
						Brain_Cerebellum	rs4785955	4.74	0.01
						Heart_Atrial_Appendage	rs4785955	4.73	0.01
						Adipose_Visceral_Omentum	rs4785955	4.69	0.02
						Skin_Not_Sun_Exposed_Suprapubic	rs4785955	4.72	0.02
						Brain_Nucleus_accumbens_basal_ganglia	rs4785955	4.50	0.02
HMOX2	16	Artery_Tibial	rs2304634	4.88	0.01	Spleen	rs4785955	7.49	2.94E-10
						Brain_Cerebellum	rs4785955	6.11	5.69E-06
						Adipose_Visceral_Omentum	rs4785955	5.94	1.75E-05
						Thyroid	rs4785955	5.67	1.37E-04
						Brain_Nucleus_accumbens_basal_ganglia	rs4785955	-5.10	1.06E-03
						Breast_Mammary_Tissue	rs4785955	4.90	4.71E-03
						Brain_Caudate_basal_ganglia	rs4785955	-4.79	0.01
						Lung	rs4785955	4.83	0.01
						Nerve_Tibial	rs4785955	4.72	0.02
PAM16	16	Whole_Blood	rs2304634	-4.47	0.05	Stomach	rs4785955	-5.18	9.88E-04

Abbreviations: CHR: chromosome; PP: pulse pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}<0.05$) for both migraine and blood pressure in at least one GTEx tissues.

Supplementary Table 21 The shared TWAS genes between migraine without aura and diastolic blood pressure (DBP)

ID	CHR	Migraine without aura				DBP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$
TSPAN2	1	Artery_Aorta	rs2078371	5.66	9.45E-05	Minor_Salivary_Gland	rs11466111	-4.19	0.05
ITGB5	3	Esophagus_Mucosa	rs1265646	-4.87	0.01	Artery_Coronary	rs4141663	-9.09	3.15E-16
		Nerve_Tibial	rs1265646	4.80	0.02	Artery_Tibial	rs4141663	-8.46	2.14E-13
						Colon_Sigmoid	rs4141663	-8.35	3.31E-13
						Esophagus_Muscularis	rs4141663	-8.27	9.94E-13
						Nerve_Tibial	rs4141663	-8.27	1.26E-12
						Esophagus_Gastroesophageal_Junction	rs4141663	-8.20	1.15E-12
						Artery_Aorta	rs4141663	-8.09	3.77E-12
						Esophagus_Mucosa	rs4141663	7.77	6.21E-11
						Brain_Hypothalamus	rs4141663	-6.57	1.14E-07
						Muscle_Skeletal	rs4141663	-4.52	0.05
MANBA	4	Small_Intestine_Terminal_Ileum	rs228614	4.39	0.03	Artery_Aorta	rs13107325	-8.82	6.98E-15
						Breast_Mammary_Tissue	rs13107325	-8.40	2.31E-13
						Cells_Transformed_fibroblasts	rs13107325	-8.39	3.49E-13
						Adrenal_Gland	rs13107325	-7.80	2.67E-11
						Brain_Cerebellar_Hemisphere	rs13107325	7.15	3.78E-09
						Spleen	rs13107325	6.55	2.52E-07
						Brain_Hippocampus	rs13107325	6.18	1.41E-06
						Small_Intestine_Terminal_Ileum	rs13107325	5.81	1.76E-05
						Testis	rs13107325	5.23	1.56E-03
U91328.19	6	Brain_Putamen_basal_ganglia	rs17531978	4.32	0.04	Brain_Cerebellum	rs198846	-10.43	1.08E-21
						Brain_Cerebellar_Hemisphere	rs198846	-8.54	5.84E-14
						Brain_Spinal_cord_cervical_c-1	rs198846	-7.42	2.25E-10
						Brain_Nucleus_accumbens_basal_ganglia	rs198846	-6.71	6.25E-08
						Colon_Sigmoid	rs198846	-5.11	1.57E-03
						Brain_Caudate_basal_ganglia	rs198846	-4.94	2.75E-03
						Brain_Hippocampus	rs198846	-4.75	4.53E-03
						Brain_Putamen_basal_ganglia	rs198846	-4.55	0.01
UFL1	6	Adipose_Subcutaneous	rs2273621	5.89	3.05E-05	Spleen	rs11756315	6.17	2.97E-06

		Artery_Tibial	rs2273621	6.13	7.34E-06	Nerve_Tibial	rs11756315	6.09	1.09E-05
		Brain_Cerebellum	rs2273621	6.62	2.06E-07	Pancreas	rs11756315	5.74	4.64E-05
		Nerve_Tibial	rs2273621	5.81	5.92E-05	Whole_Blood	rs11756315	5.68	8.01E-05
		Pancreas	rs2273621	6.67	1.33E-07	Stomach	rs11756315	5.55	1.24E-04
		Spleen	rs2273621	5.11	1.42E-03	Artery_Tibial	rs11756315	5.52	2.69E-04
		Stomach	rs2273621	5.19	9.44E-04	Adipose_Subcutaneous	rs11756315	5.47	3.59E-04
		Vagina	rs2273621	5.88	7.83E-06				
		Whole_Blood	rs2273621	4.86	0.01				
HVCN1	12	Brain_Hippocampus	rs17619763	5.36	1.87E-04	Brain_Hippocampus	rs11065822	-9.04	3.61E-16
						Whole_Blood	rs11065822	6.39	9.77E-07

Abbreviations: CHR: chromosome; DBP: diastolic blood pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}<0.05$) for both migraine and blood pressure in at least one GTEx tissues.

Supplementary Table 22 **The shared TWAS genes between migraine without aura and systolic blood pressure (SBP)**

ID	CHR	Migraine without aura				SBP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\text{Bonferroni}}$
ITGB5	3	Esophagus_Mucosa	rs1265646	-4.87	0.01	Artery_Coronary	rs4141663	-9.27	5.71E-17
		Nerve_Tibial	rs1265646	4.80	0.02	Artery_Tibial	rs4141663	-8.88	5.18E-15
						Esophagus_Muscularis	rs4141663	-8.64	4.31E-14
						Nerve_Tibial	rs4141663	-8.65	4.85E-14
						Artery_Aorta	rs4141663	-8.56	7.23E-14
						Esophagus_Gastroesophageal_Junction	rs4141663	-8.52	7.42E-14
						Colon_Sigmoid	rs4141663	-8.25	7.56E-13
						Esophagus_Mucosa	rs4141663	7.77	6.42E-11
						Brain_Hypothalamus	rs4141663	-7.13	2.19E-09
FHL5	6	Artery_Tibial	rs2273621	-5.05	3.55E-03	Artery_Tibial	rs2983896	-6.00	1.64E-05
PHACTR1	6	Artery_Aorta	rs9349379	6.29	2.03E-06	Artery_Aorta	rs9349379	8.50	1.24E-13
		Artery_Tibial	rs9349379	5.77	6.34E-05	Artery_Tibial	rs9349379	7.31	2.23E-09
		Brain_Spinal_cord_cervical_c-1	rs9349379	4.62	0.01				
RP1-257A7.5	6	Artery_Aorta	rs9349379	6.01	1.19E-05	Artery_Tibial	rs9349379	8.60	6.28E-14
		Artery_Coronary	rs9349379	6.20	1.84E-06	Artery_Aorta	rs9349379	8.54	8.50E-14
		Artery_Tibial	rs9349379	6.22	3.90E-06	Artery_Coronary	rs9349379	7.12	3.36E-09
U91328.19	6	Brain_Putamen_basal_ganglia	rs17531978	4.32	0.04	Brain_Cerebellum	rs198846	-6.40	9.15E-07
						Brain_Cerebellar_Hemisphere	rs198846	-5.11	1.40E-03
UFL1	6	Adipose_Subcutaneous	rs2273621	5.89	3.05E-05	Spleen	rs2983896	9.17	1.99E-16
		Artery_Tibial	rs2273621	6.13	7.34E-06	Nerve_Tibial	rs2983896	9.15	5.60E-16
		Brain_Cerebellum	rs2273621	6.62	2.06E-07	Pancreas	rs2983896	9.00	1.16E-15
		Nerve_Tibial	rs2273621	5.81	5.92E-05	Whole_Blood	rs2983896	8.51	1.05E-13
		Pancreas	rs2273621	6.67	1.33E-07	Stomach	rs2983896	8.10	2.43E-12
		Spleen	rs2273621	5.11	1.42E-03	Artery_Tibial	rs2983896	7.69	1.16E-10
		Stomach	rs2273621	5.19	9.44E-04	Adipose_Subcutaneous	rs2983896	7.57	2.98E-10
		Vagina	rs2273621	5.88	7.83E-06	Brain_Cerebellum	rs2983896	6.46	5.92E-07
		Whole_Blood	rs2273621	4.86	0.01	Vagina	rs2983896	4.68	0.01
HVCN1	12	Brain_Hippocampus	rs17619763	5.36	1.87E-04	Brain_Hippocampus	rs11065822	-4.93	1.86E-03
						Whole_Blood	rs11065822	4.94	4.59E-03

Abbreviations: CHR: chromosome; SBP: systolic blood pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}$<0.05) for both migraine and blood pressure in at least one GTEx tissues.

Supplementary Table 23 The shared TWAS genes between migraine without aura and pulse pressure (PP)

ID	CHR	Migraine without aura				PP			
		Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\mathrm{Bonferroni}}$	Tissue	BEST.GWAS.ID	TWAS.Z	$P_{\mathrm{Bonferroni}}$
ITGB5	3	Esophagus_Mucosa	rs1265646	-4.87	0.01	Artery_Coronary	rs4141663	-6.17	2.16E-06
		Nerve_Tibial	rs1265646	4.80	0.02	Artery_Tibial	rs4141663	-6.20	4.62E-06
						Artery_Aorta	rs4141663	-5.97	1.50E-05
						Esophagus_Muscularis	rs4141663	-5.93	2.30E-05
						Esophagus_Gastroesophageal_Junction	rs4141663	-5.78	3.61E-05
						Nerve_Tibial	rs4141663	-5.82	5.61E-05
						Colon_Sigmoid	rs4141663	-5.38	3.53E-04
						Brain_Hypothalamus	rs4141663	-5.05	1.00E-03
						Esophagus_Mucosa	rs4141663	4.92	0.01
MANBA	4	Small_Intestine_Terminal_Ileum	rs228614	4.39	0.03	Brain_Cerebellum	rs13107325	-6.56	3.19E-07
						Artery_Aorta	rs13107325	5.50	2.38E-04
						Breast_Mammary_Tissue	rs13107325	5.26	7.08E-04
						Adrenal_Gland	rs13107325	5.03	2.13E-03
						Spleen	rs13107325	-4.96	3.05E-03
						Brain_Cerebellar_Hemisphere	rs13107325	-4.85	0.01
						Cells_Transformed_fibroblasts	rs13107325	4.89	0.01
FHL5	6	Artery_Tibial	rs2273621	-5.05	3.55E-03	Artery_Tibial	rs2983896	-6.12	7.64E-06
PHACTR1	6	Artery_Aorta	rs9349379	6.29	2.03E-06	Artery_Aorta	rs9349379	12.39	1.83E-31
		Artery_Tibial	rs9349379	5.77	6.34E-05	Artery_Tibial	rs9349379	11.13	6.97E-25
		Brain_Spinal_cord_cervical_c-1	rs9349379	4.62	0.01	Breast_Mammary_Tissue	rs9349379	5.46	2.40E-04
						Cells_Transformed_fibroblasts	rs9349379	5.19	1.53E-03
RP1-257A7.5	6	Artery_Aorta	rs9349379	6.01	1.19E-05	Artery_Aorta	rs9349379	12.64	7.74E-33
		Artery_Coronary	rs9349379	6.20	1.84E-06	Artery_Tibial	rs9349379	12.65	9.06E-33
		Artery_Tibial	rs9349379	6.22	3.90E-06	Artery_Coronary	rs9349379	10.83	8.12E-24
U91328.19	6	Brain_Putamen_basal_ganglia	rs17531978	4.32	0.04	Whole_Blood	rs13161	6.27	2.12E-06
						Uterus	rs13161	4.33	0.03
UFL1	6	Adipose_Subcutaneous	rs2273621	5.89	3.05E-05	Pancreas	rs2983896	8.42	1.82E-13
		Artery_Tibial	rs2273621	6.13	7.34E-06	Spleen	rs2983896	8.28	5.29E-13
		Brain_Cerebellum	rs2273621	6.62	2.06E-07	Nerve_Tibial	rs2983896	8.28	1.15E-12
		Nerve_Tibial	rs2273621	5.81	5.92E-05	Whole_Blood	rs2983896	7.84	2.71E-11

		Pancreas	rs2273621	6.67	1.33E-07	Stomach	rs2983896	6.99	1.20E-08
		Spleen	rs2273621	5.11	1.42E-03	Artery_Tibial	rs2983896	6.69	1.87E-07
		Stomach	rs2273621	5.19	9.44E-04	Adipose_Subcutaneous	rs2983896	6.56	4.30E-07
		Vagina	rs2273621	5.88	7.83E-06	Brain_Cerebellum	rs2983896	6.03	9.43E-06
		Whole_Blood	rs2273621	4.86	0.01	Vagina	rs2983896	4.40	0.02
HBCBP	12	Adrenal_Gland	rs11172113	4.85	0.01	Adrenal_Gland	rs11172113	-7.59	1.44E-10
LRP1	12	Artery_Tibial	rs11172113	8.13	3.45E-12	Skin_Sun_Exposed_Lower_leg	rs11172113	-5.75	7.71E-05
						Artery_Tibial	rs11172113	-5.54	2.44E-04
TMEM194A	12	Heart_Atrial_Appendage	rs11172113	-4.93	4.57E-03	Heart_Atrial_Appendage	rs11172113	5.10	1.87E-03
ATP5SL	19	Brain_Cortex	rs3810174	4.48	0.03	Brain_Caudate_basal_ganglia	rs4803457	-4.71	0.01
C19orf69	19	Lung	rs3810174	4.62	0.03	Lung	rs4803457	-5.15	2.03E-03
						Nerve_Tibial	rs4803457	-5.09	3.48E-03
						Esophagus_Mucosa	rs4803457	-4.81	0.01
						Muscle_Skeletal	rs4803457	-4.53	0.04
						Adipose_Subcutaneous	rs4803457	-4.53	0.05

Abbreviations: CHR: chromosome; PP: pulse pressure.

All these loci were TWAS significant ($P_{\text{Bonferroni}}$<0.05) for both migraine and blood pressure in at least one GTEx tissues.

Supplementary Table 24 Sensitivity analysis for mendelian randomization using IVW, weighted median, simple median, and MR-egger

Method	Exposure	Outcome	Beta	SE	P
IVW	β_{DBP}	$\beta_{Migraine}$	0.16	0.02	<0.001
	β_{SBP}		0.05	0.01	<0.001
	β_{PP}		-0.05	0.03	0.04
	β_{DBP}	β_{MA}	0.14	0.05	0.01
	β_{SBP}		0.07	0.03	0.03
	β_{PP}		-0.06	0.05	0.24
	β_{DBP}	β_{MO}	0.30	0.05	<0.001
	β_{SBP}		0.07	0.03	0.03
	β_{PP}		-0.18	0.05	0.001
Weighted Median	β_{DBP}	$\beta_{Migraine}$	0.15	0.03	<0.001
	β_{SBP}		0.03	0.02	0.07
	β_{PP}		-0.09	0.03	<0.001
	β_{DBP}	β_{MA}	0.06	0.08	0.45
	β_{SBP}		0.01	0.05	0.81
	β_{PP}		-0.11	0.08	0.16
	β_{DBP}	β_{MO}	0.30	0.07	<0.001
	β_{SBP}		0.08	0.04	0.06
	β_{PP}		-0.15	0.07	0.04
Simple Median	β_{DBP}	$\beta_{Migraine}$	0.18	0.03	<0.001
	β_{SBP}		0.03	0.02	0.04
	β_{PP}		-0.07	0.03	0.01
	β_{DBP}	β_{MA}	0.10	0.08	0.19
	β_{SBP}		0.02	0.05	0.71
	β_{PP}		-0.05	0.07	0.51
	β_{DBP}	β_{MO}	0.30	0.07	<0.001
	β_{SBP}		0.08	0.04	0.06
	β_{PP}		-0.09	0.07	0.18
MR-Egger	β_{DBP}	$\beta_{Migraine}$	0.14	0.06	0.02
	β_{SBP}		0.06	0.04	0.11
	β_{PP}		-0.08	0.07	0.25
	β_{DBP}	β_{MA}	0.14	0.14	0.34
	β_{SBP}		0.06	0.09	0.51
	β_{PP}		-0.19	0.14	0.18

β_{DBP}	β_{MO}	0.30	0.1	0.01
β_{SBP}		0.10	0.08	0.16
β_{PP}		-0.21	0.15	0.16

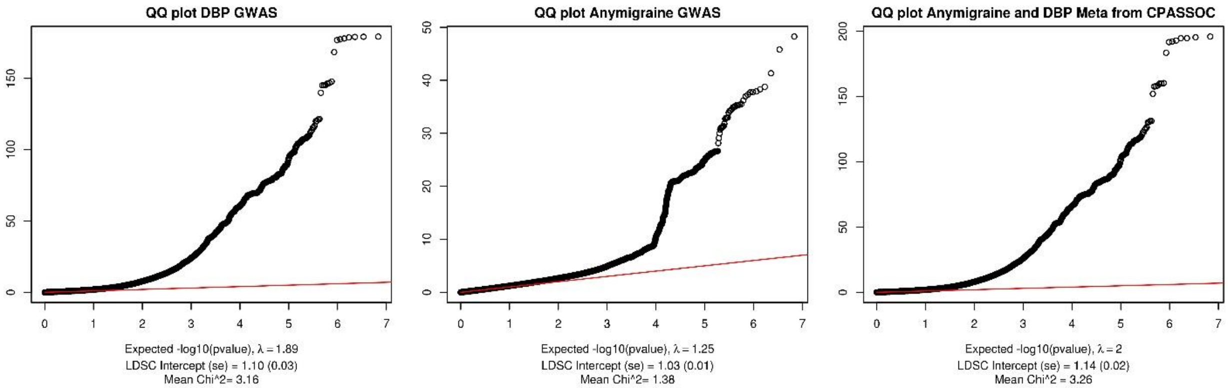
Abbreviations: SE: standard error; IVW: inverse-variance weighted; MR-Egger: Egger regression; DBP: diastolic blood pressure; SBP: systolic blood pressure; PP: pulse pressure; MA: migraine with aura; MO: migraine without aura.

All sensitivity analyses were conducted using the corresponding models implemented in R package “MendelianRandomization”.

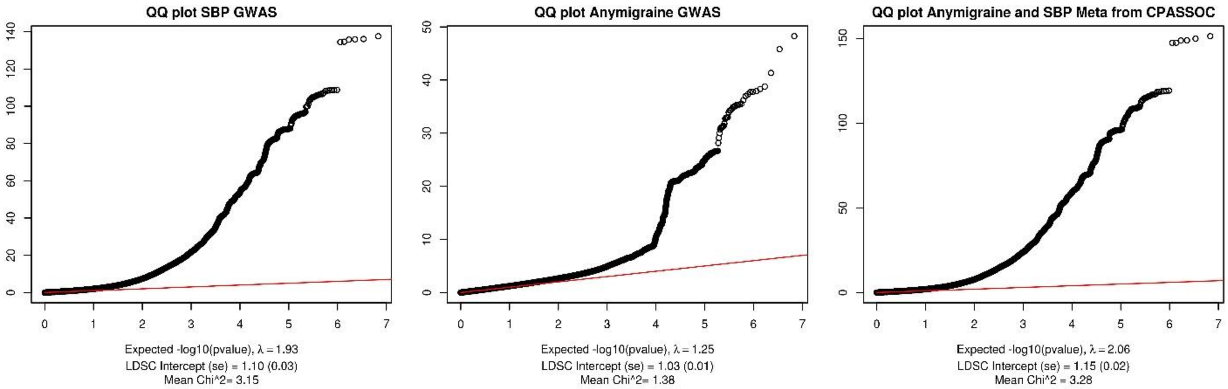
Supplementary Table 25 Mendelian randomization (MR) analysis for five instruments from antihypertensive medications genetic targets with migraine and MR power calculation

Exposure	Outcome	SNP	CHR	effect	MAF	*R2*	*R2*.TOTAL	MR.effect	*P*	MR.POWER
DBP	Anymigraine	rs8077276	17	-0.02	0.38	0.0001	0.0008	0.20	0.98	0.25
		rs2484294	10	0.03	0.27	0.0003				
		rs1888693	10	0.02	0.34	0.0002				
		rs3821843	3	0.02	0.32	0.0001				
		rs2239046	12	0.01	0.32	0.0000				
SBP		rs8077276	17	-0.02	0.38	0.0002	0.0011	0.08	0.89	0.1
		rs2484294	10	0.03	0.27	0.0004				
		rs1888693	10	0.03	0.34	0.0003				
		rs3821843	3	0.02	0.32	0.0002				
		rs2239046	12	0.01	0.32	0.0001				
PP		rs8077276	17	-0.01	0.38	0.0000	0.0003	-0.11	0.68	0.07
		rs2484294	10	0.01	0.27	0.0000				
		rs1888693	10	0.01	0.34	0.0001				
		rs3821843	3	0.01	0.32	0.0001				
		rs2239046	12	0.01	0.32	0.0000				

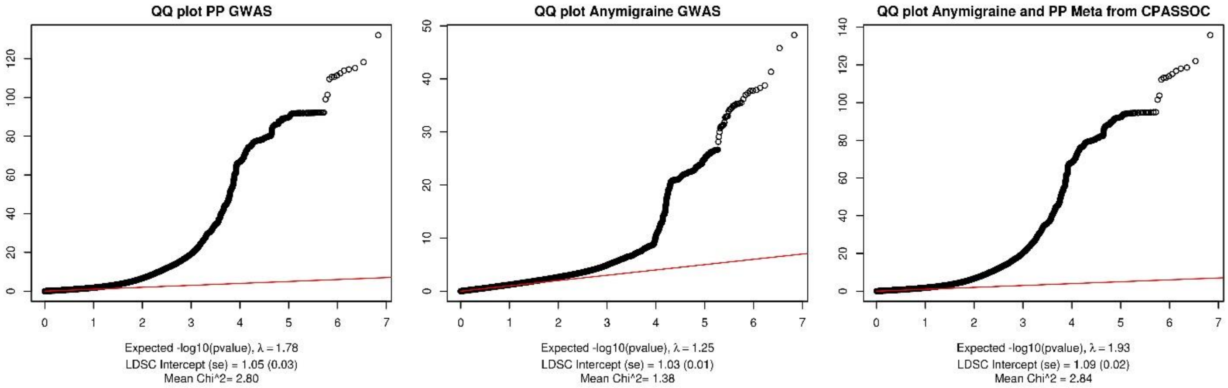
Abbreviations: SNP: single nucleotide polymorphisms; CHR: chromosome; MAF: minor allele frequency; R2: proportion of variance explained for the association between the corresponding SNP and the exposure variable; R2.TOTAL: proportion of variance explained for the association between all the five SNPs and the exposure variable; DBP: diastolic blood pressure; MR.POWER: estimated power in mendelian randomization; SBP: systolic blood pressure; PP: pulse pressure; MA: migraine with aura; MO: migraine without aura.



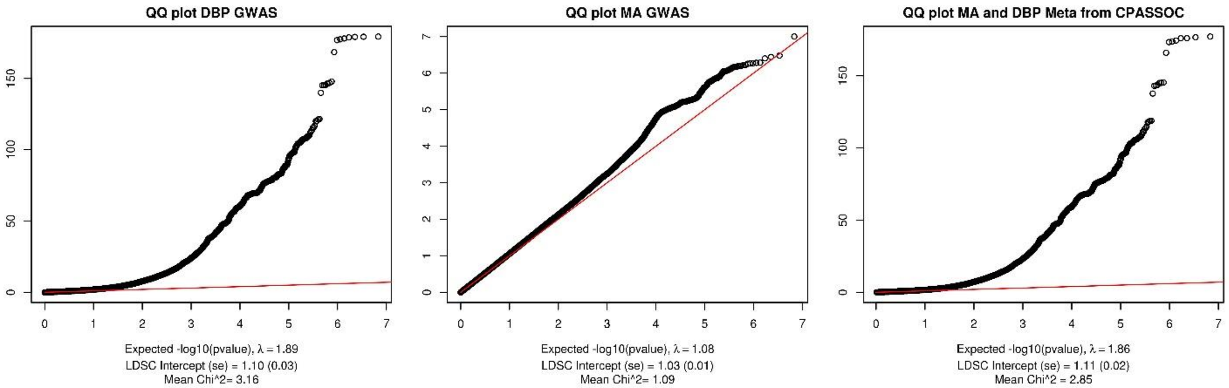
Supplementary Figure 1 Quantile-quantile (QQ) plot for diastolic blood pressure (DBP), migraine, and cross-trait meta-analysis between DBP and migraine.



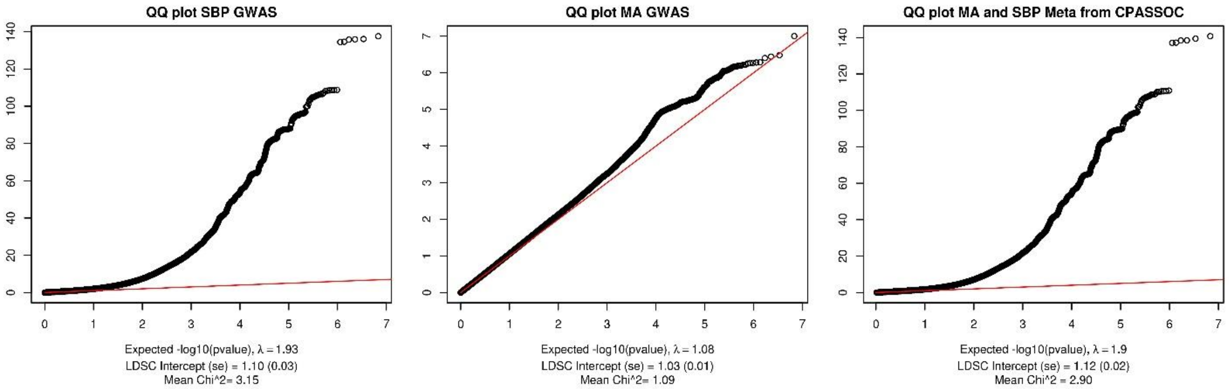
Supplementary Figure 2 Quantile-quantile (QQ) plot for systolic blood pressure (SBP), migraine, and cross-trait meta-analysis between SBP and migraine.



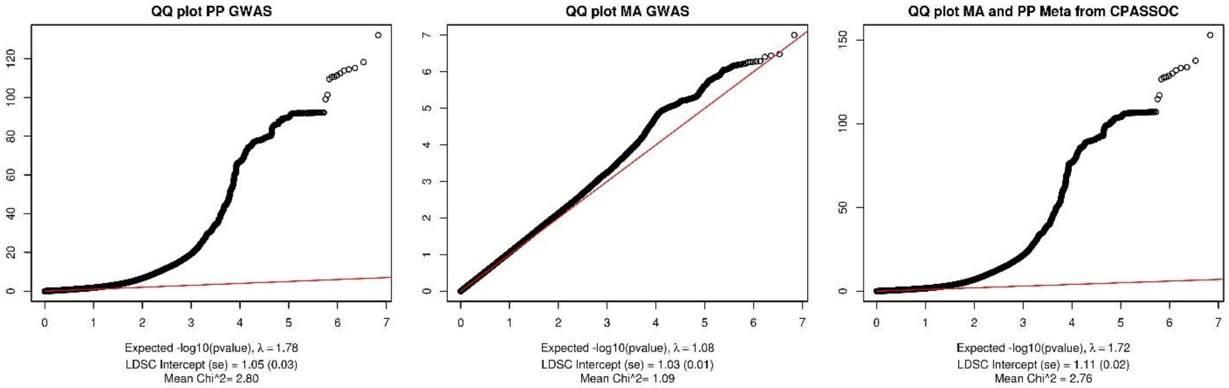
Supplementary Figure 3 Quantile-quantile (QQ) plot for pulse pressure (PP), migraine, and cross-trait meta-analysis between SBP and migraine.



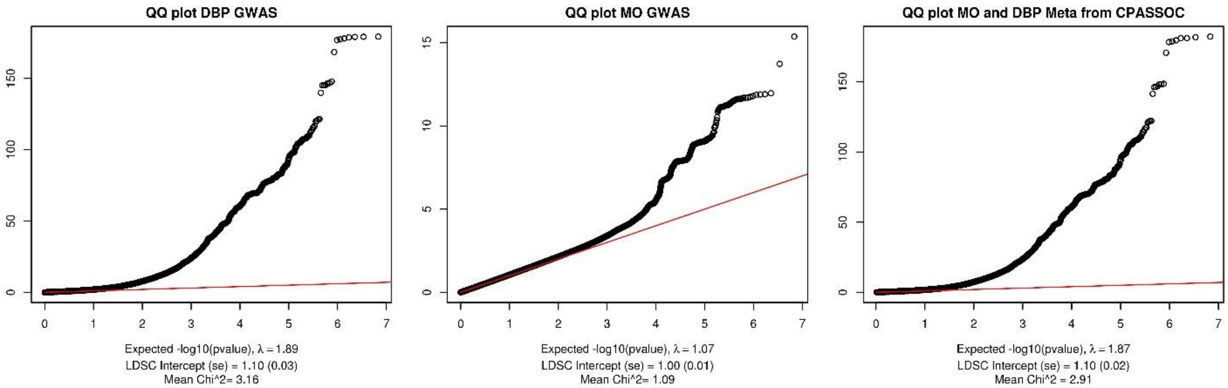
Supplementary Figure 4 **Quantile-quantile (QQ) plot for diastolic blood pressure (DBP), migraine with aura (MA), and cross-trait meta-analysis between DBP and MA.**



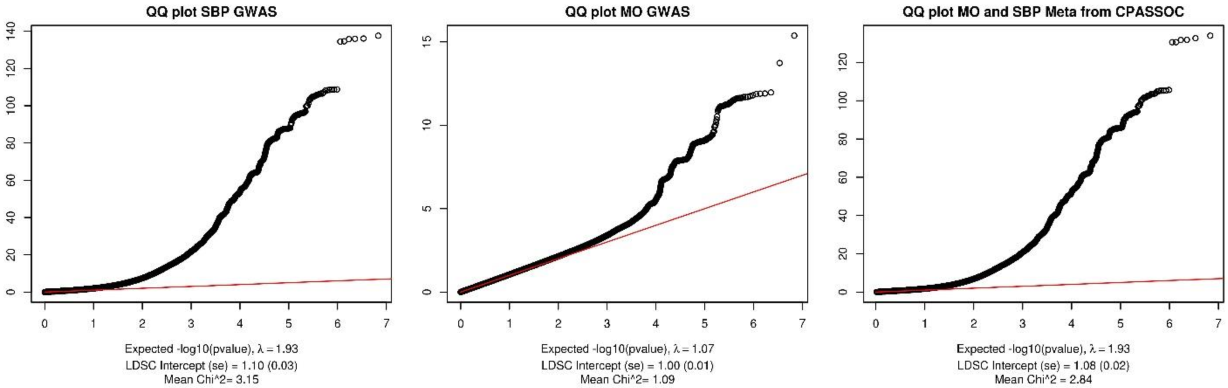
Supplementary Figure 5 **Quantile-quantile (QQ) plot for systolic blood pressure (SBP), migraine with aura (MA), and cross-trait meta-analysis between SBP and MA.**



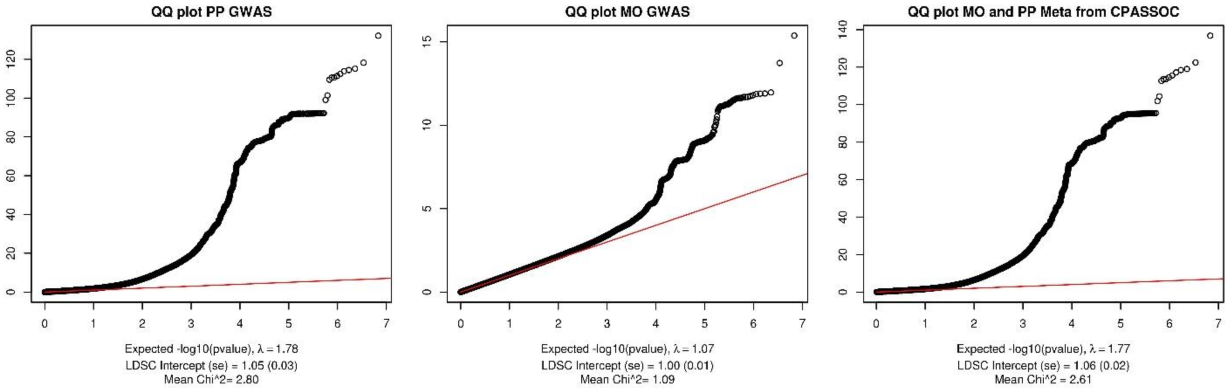
Supplementary Figure 6 **Quantile-quantile (QQ) plot for pulse pressure (PP), migraine with aura (MA), and cross-trait meta-analysis between PP and MA.**



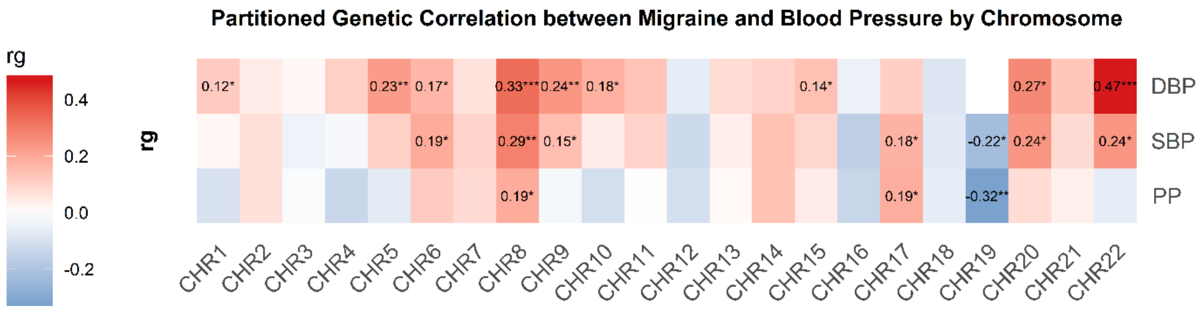
Supplementary Figure 7 **Quantile-quantile (QQ) plot for diastolic blood pressure (DBP), migraine without aura (MO), and cross-trait meta-analysis between DBP and MO.**



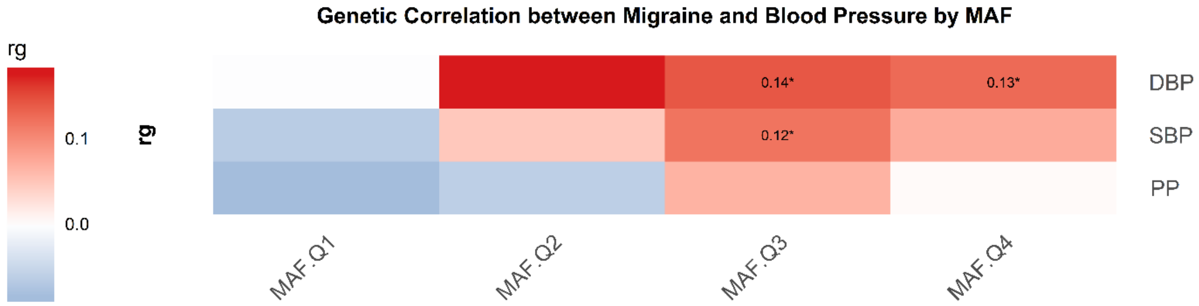
Supplementary Figure 8 **Quantile-quantile (QQ) plot for systolic blood pressure (SBP), migraine without aura (MO), and cross-trait meta-analysis between SBP and MO.**



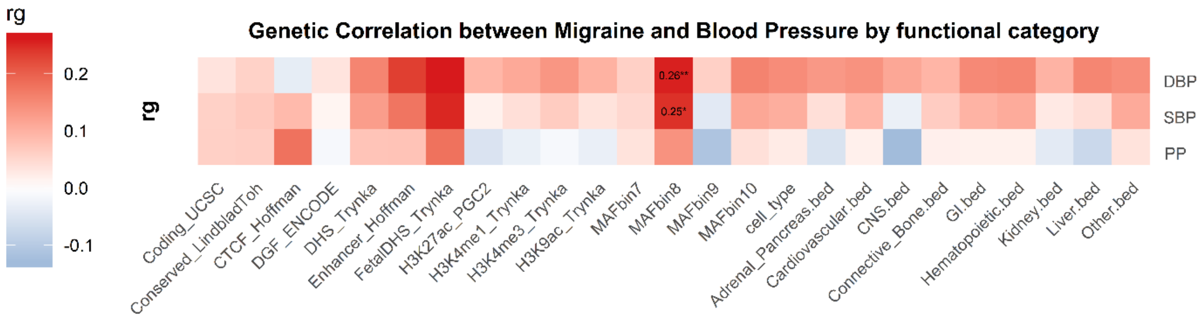
Supplementary Figure 9 **Quantile-quantile (QQ) plot for pulse pressure (PP), migraine without aura (MO), and cross-trait meta-analysis between PP and MO.**


Partitioned Genetic Correlation between Migraine and Blood Pressure by Chromosome

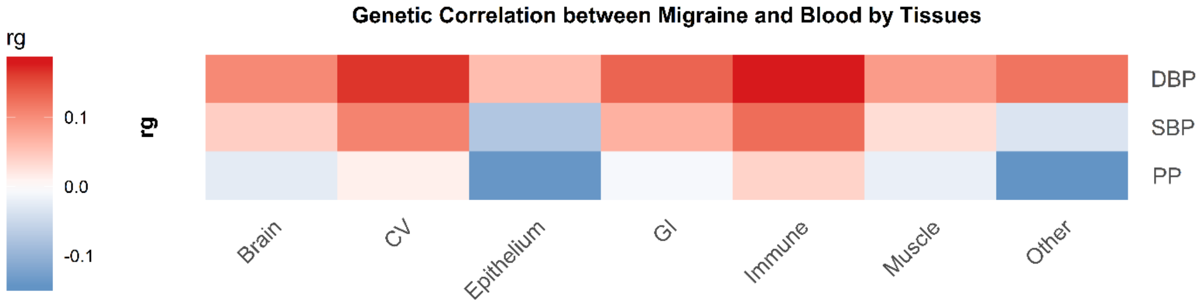
Supplementary Figure 10 Partitioned genetic correlation between migraine and blood pressure by different chromosomes. Colors represent the estimated annotation specific genetic correlation between migraine and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (P<0.05) are labeled with r_g. The nominally significant effects are labeled with “*” ($P < 0.05$), “**” ($P < 0.01$), and “***” ($P < 0.001$).


Genetic Correlation between Migraine and Blood Pressure by MAF

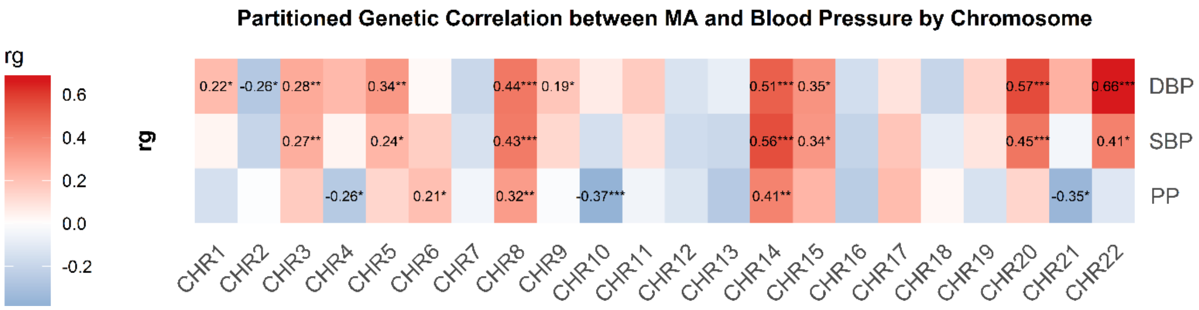
Supplementary Figure 11 Partitioned genetic correlation between migraine and blood pressure by minor allele frequency (MAF) quartiles. Colors represent the estimated annotation specific genetic correlation between migraine and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (P<0.05) are labeled with r_g. The nominally significant effects are labeled with “*” ($P < 0.05$), “**” ($P < 0.01$), and “***” ($P < 0.001$).



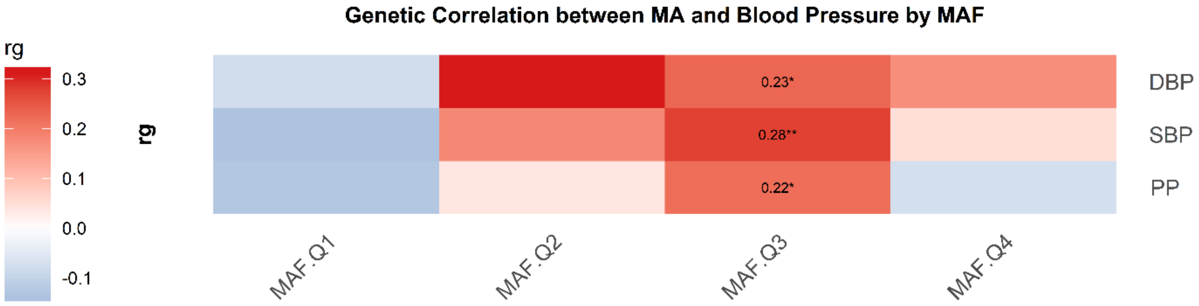
Supplementary Figure 12 **Partitioned genetic correlation between migraine and blood pressure by different functional categories.** Colors represent the estimated annotation specific genetic correlation between migraine and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (*P*<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" (*P* < 0.05), "**" (*P* < 0.01), and "***" (*P* < 0.001).



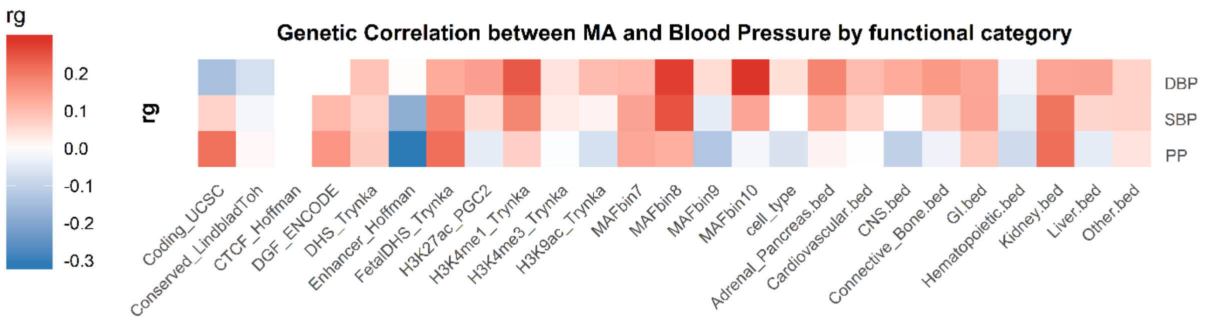
Supplementary Figure 13 **Partitioned genetic correlation between migraine and blood pressure by seven tissues based on GenoSkyline-Plus annotations.** Colors represent the estimated annotation specific genetic correlation between migraine and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (*P*<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" (*P* < 0.05), "**" (*P* < 0.01), and "***" (*P* < 0.001).



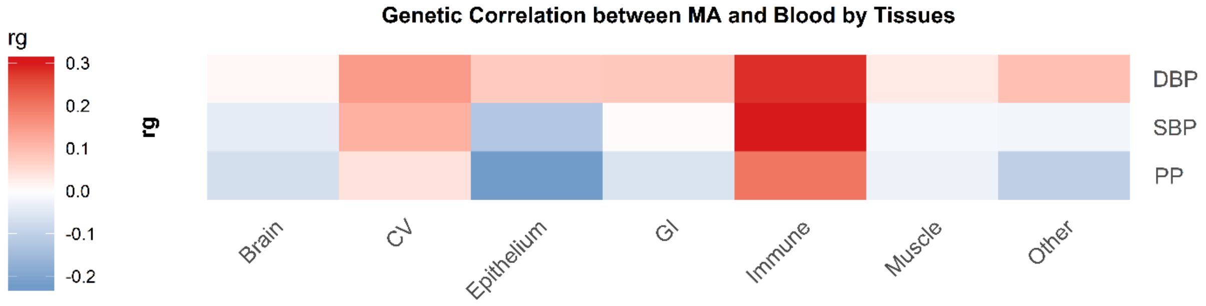
Supplementary Figure 14 Partitioned genetic correlation between migraine with aura (MA) and blood pressure by different chromosomes. Colors represent the estimated annotation specific genetic correlation between migraine with aura (MA) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (*P*<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" ($P < 0.05$), "**" ($P < 0.01$), and "***" ($P < 0.001$).



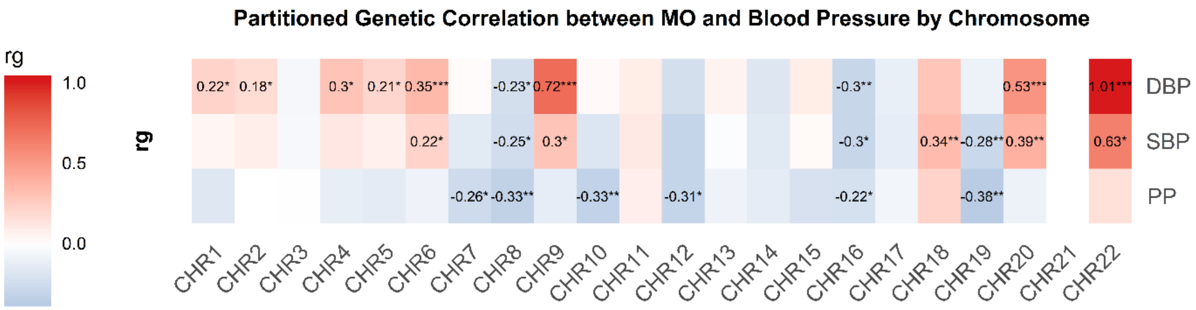
Supplementary Figure 15 Partitioned genetic correlation between migraine with aura (MA) and blood pressure by minor allele frequency (MAF) quartiles. Colors represent the estimated annotation specific genetic correlation between migraine with aura (MA) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (*P*<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" ($P < 0.05$), "**" ($P < 0.01$), and "***" ($P < 0.001$).



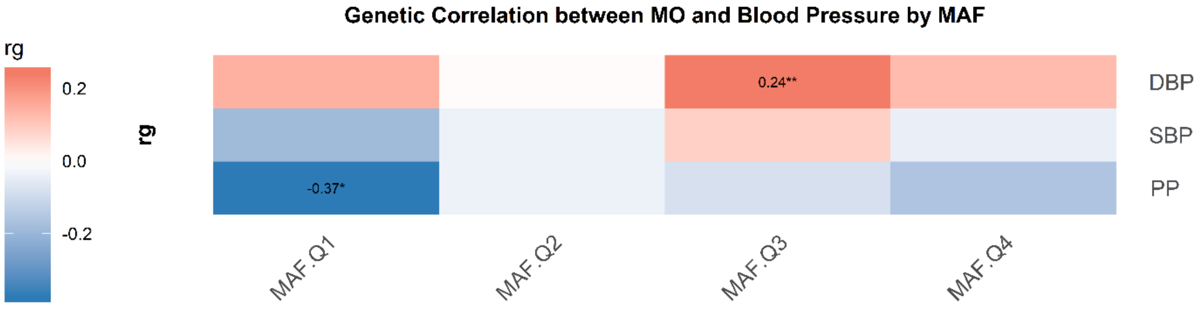
Supplementary Figure 16 Partitioned genetic correlation between migraine with aura (MA) and blood pressure by different functional categories. Colors represent the estimated annotation specific genetic correlation between migraine with aura (MA) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (P<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" ($P < 0.05$), "**" ($P < 0.01$), and "***" ($P < 0.001$).



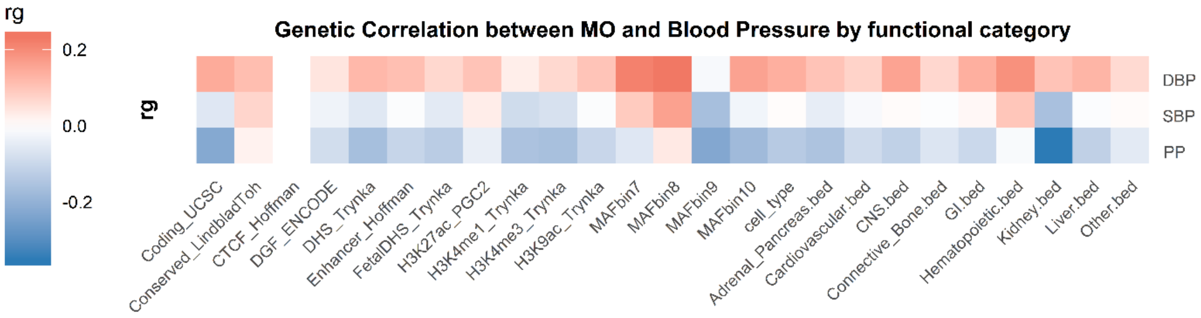
Supplementary Figure 17 Partitioned genetic correlation between migraine with aura (MA) and blood pressure by seven tissues based on GenoSkyline-Plus annotations. Colors represent the estimated annotation specific genetic correlation between migraine with aura (MA) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (P<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" ($P < 0.05$), "**" ($P < 0.01$), and "***" ($P < 0.001$).



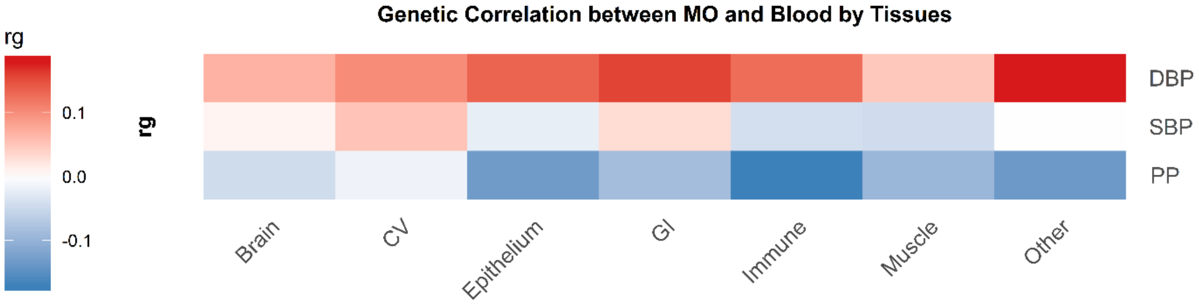
Supplementary Figure 18 Partitioned genetic correlation between migraine without aura (MO) and blood pressure by different chromosomes. Colors represent the estimated annotation specific genetic correlation between migraine without aura (MO) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (*P*<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" ($P < 0.05$), "**" ($P < 0.01$), and "***" ($P < 0.001$).



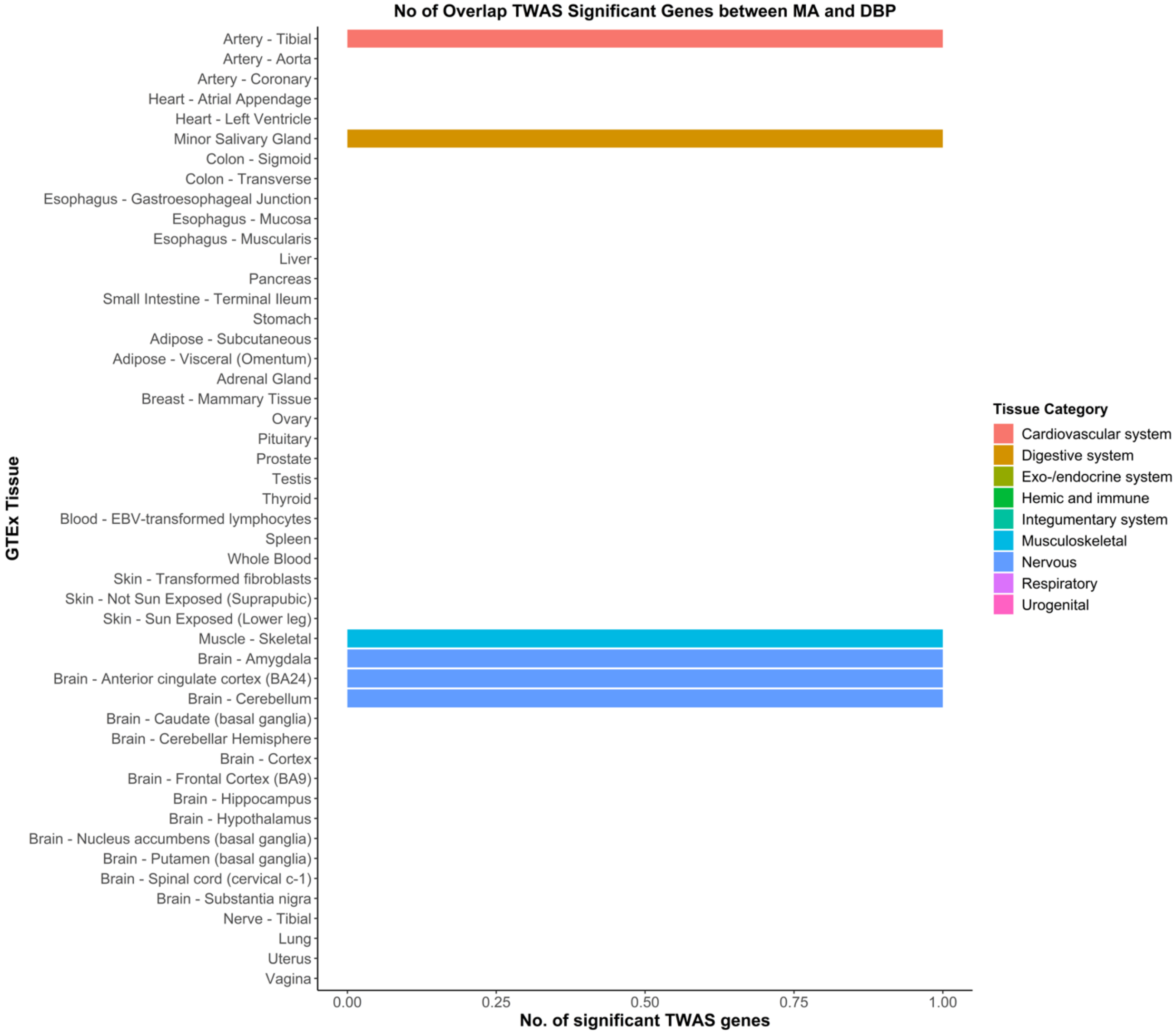
Supplementary Figure 19 Partitioned genetic correlation between migraine without aura (MO) and blood pressure by minor allele frequency (MAF) quartiles. Colors represent the estimated annotation specific genetic correlation between migraine without aura (MO) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects (*P*<0.05) are labeled with r_g. The nominally significant effects are labeled with "*" ($P < 0.05$), "**" ($P < 0.01$), and "***" ($P < 0.001$).



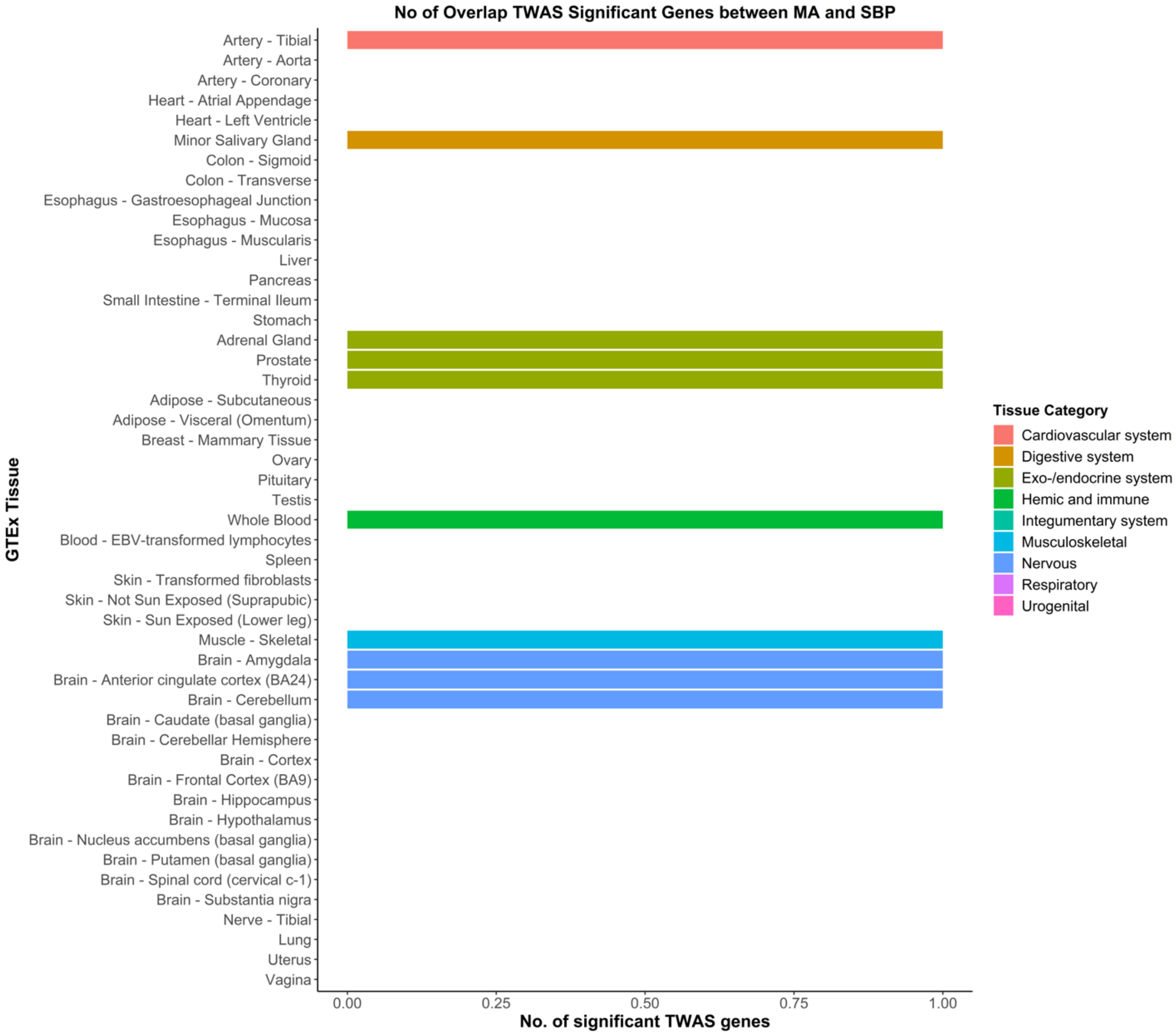
Supplementary Figure 20 Partitioned genetic correlation between migraine without aura (MO) and blood pressure by different functional categories. Colors represent the estimated annotation specific genetic correlation between migraine without aura (MO) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects ($P<0.05$) are labeled with r_g. The nominally significant effects are labeled with “*” ($P < 0.05$), “**” ($P < 0.01$), and “***” ($P < 0.001$).



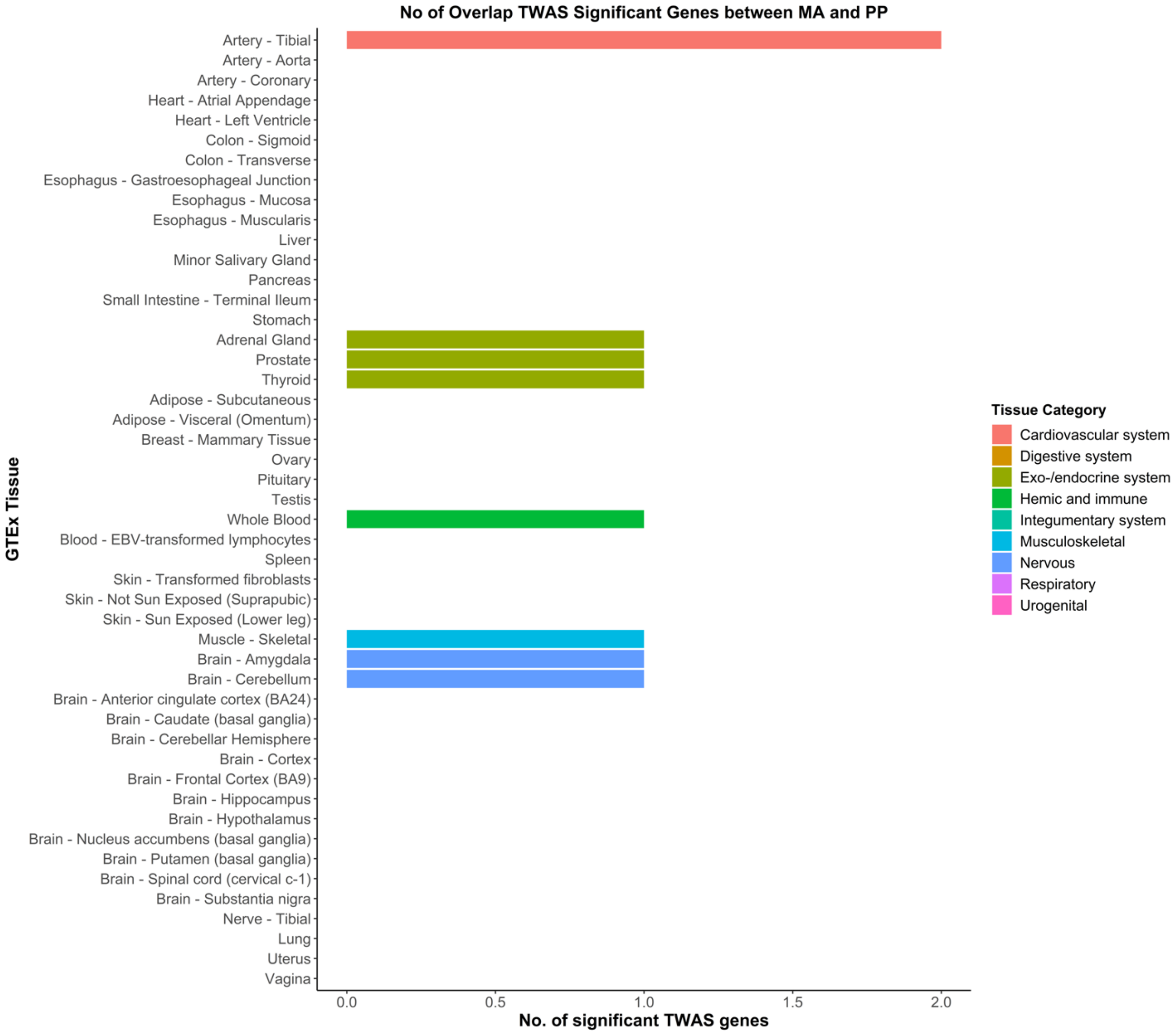
Supplementary Figure 21 Partitioned genetic correlation between migraine without aura (MO) and blood pressure by seven tissues based on GenoSkyline-Plus annotations. Colors represent the estimated annotation specific genetic correlation between migraine without aura (MO) and BP traits (DBP, SBP, and PP) using GNOVA, red for positive genetic correlation and blue for negative genetic correlation at the corresponding annotation. The significant effects ($P<0.05$) are labeled with r_g. The nominally significant effects are labeled with “*” ($P < 0.05$), “**” ($P < 0.01$), and “***” ($P < 0.001$).



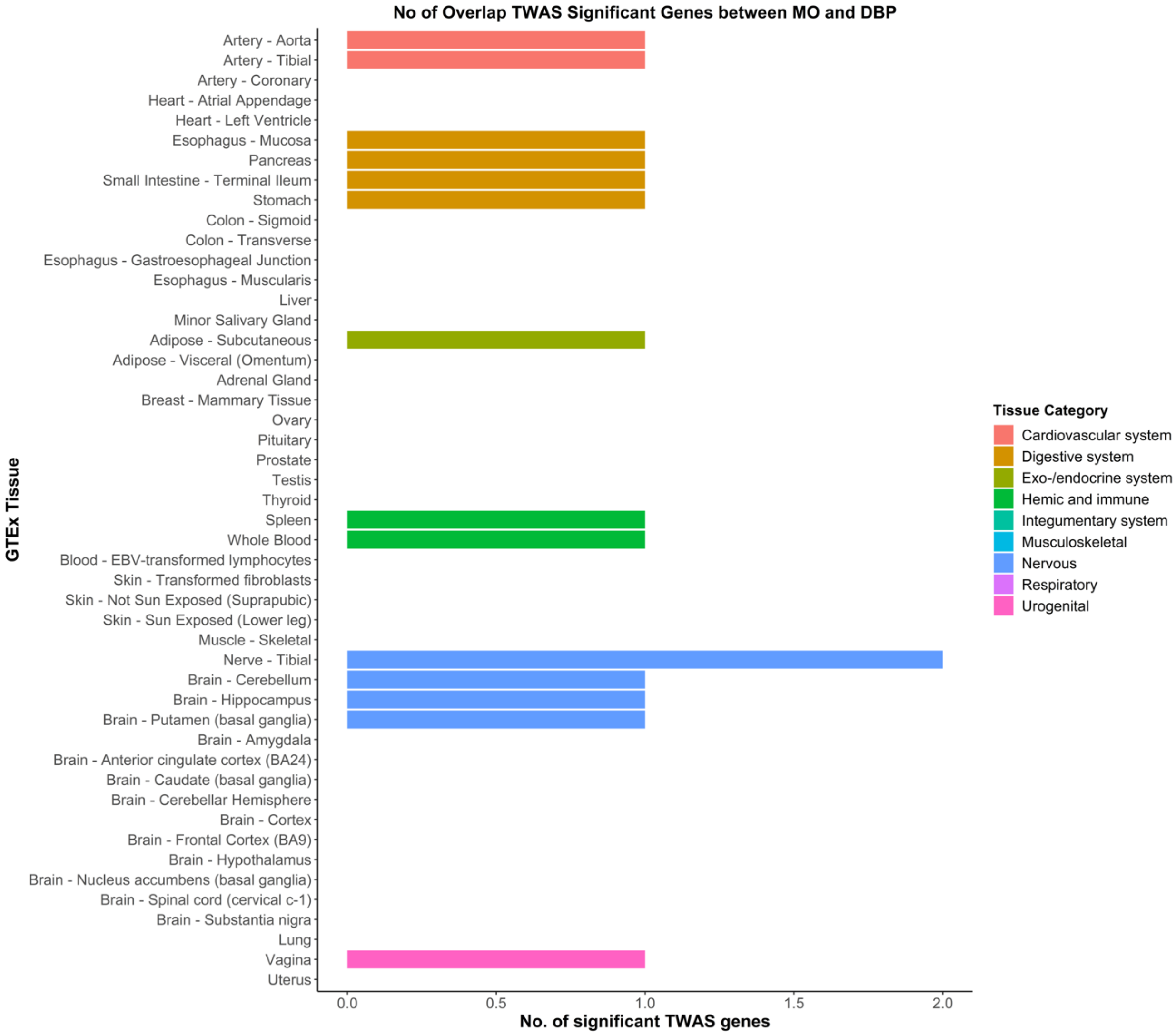
Supplementary Figure 22 The number of shared TWAS significant genes between migraine with aura (MA) and diastolic blood pressure (DBP) across 48 GTEx tissues. Colors represent different tissue categories.



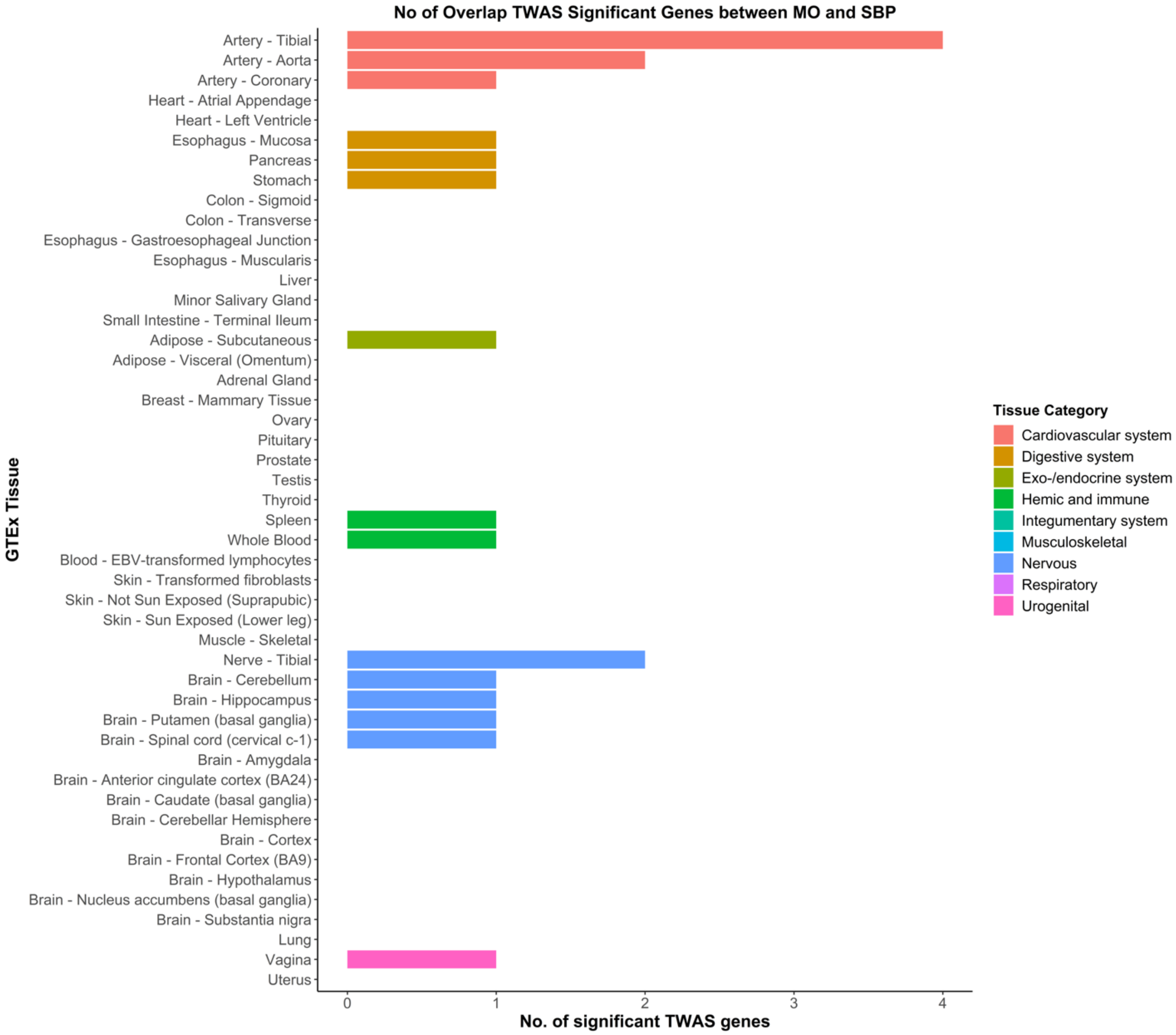
Supplementary Figure 23 The number of shared TWAS significant genes between migraine with aura (MA) and systolic blood pressure (SBP) across 48 GTEx tissues. Colors represent different tissue categories.



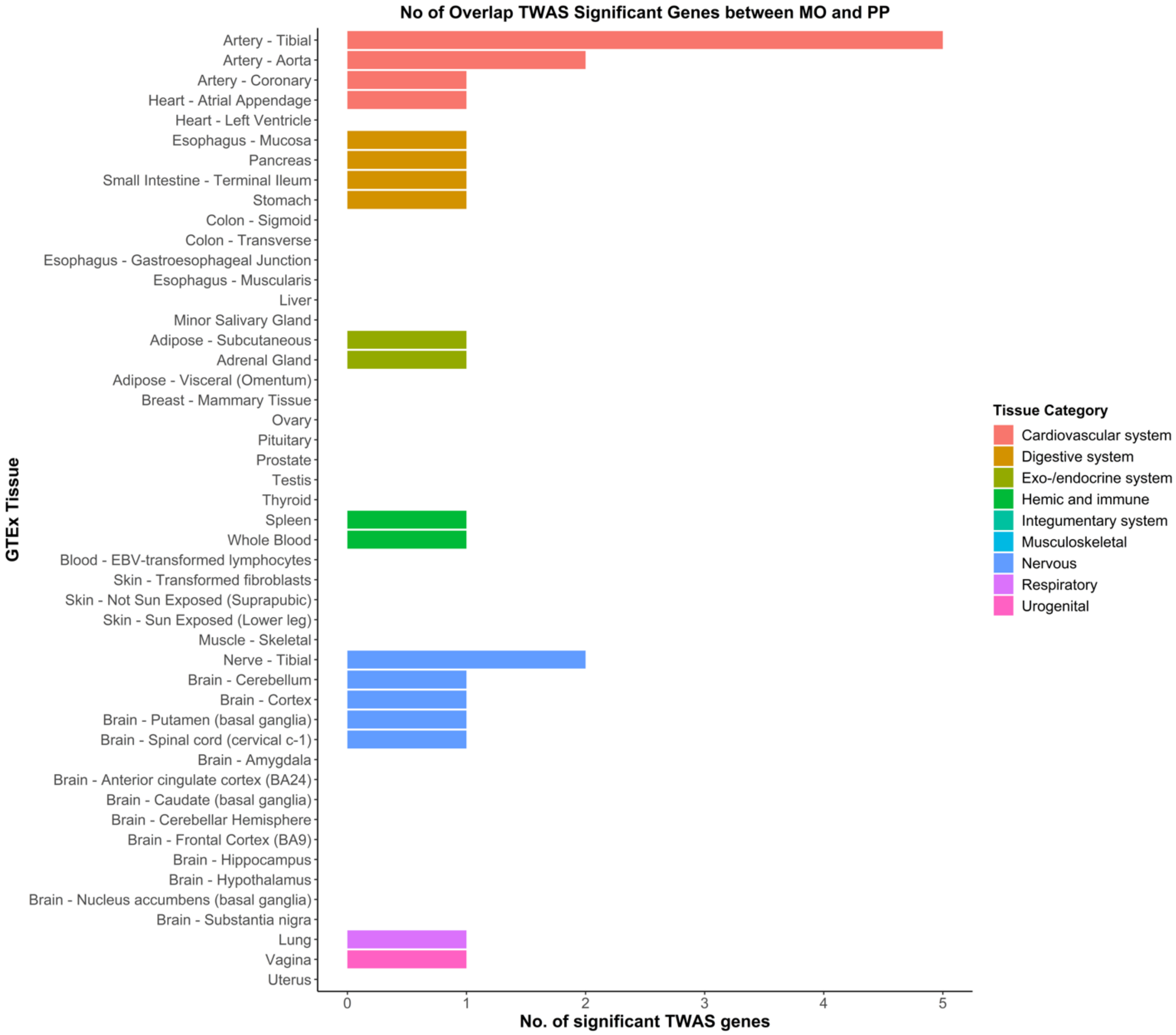
Supplementary Figure 24 **The number of shared TWAS significant genes between migraine with aura (MA) and pulse pressure (PP) across 48 GTEx tissues.** Colors represent different tissue categories.



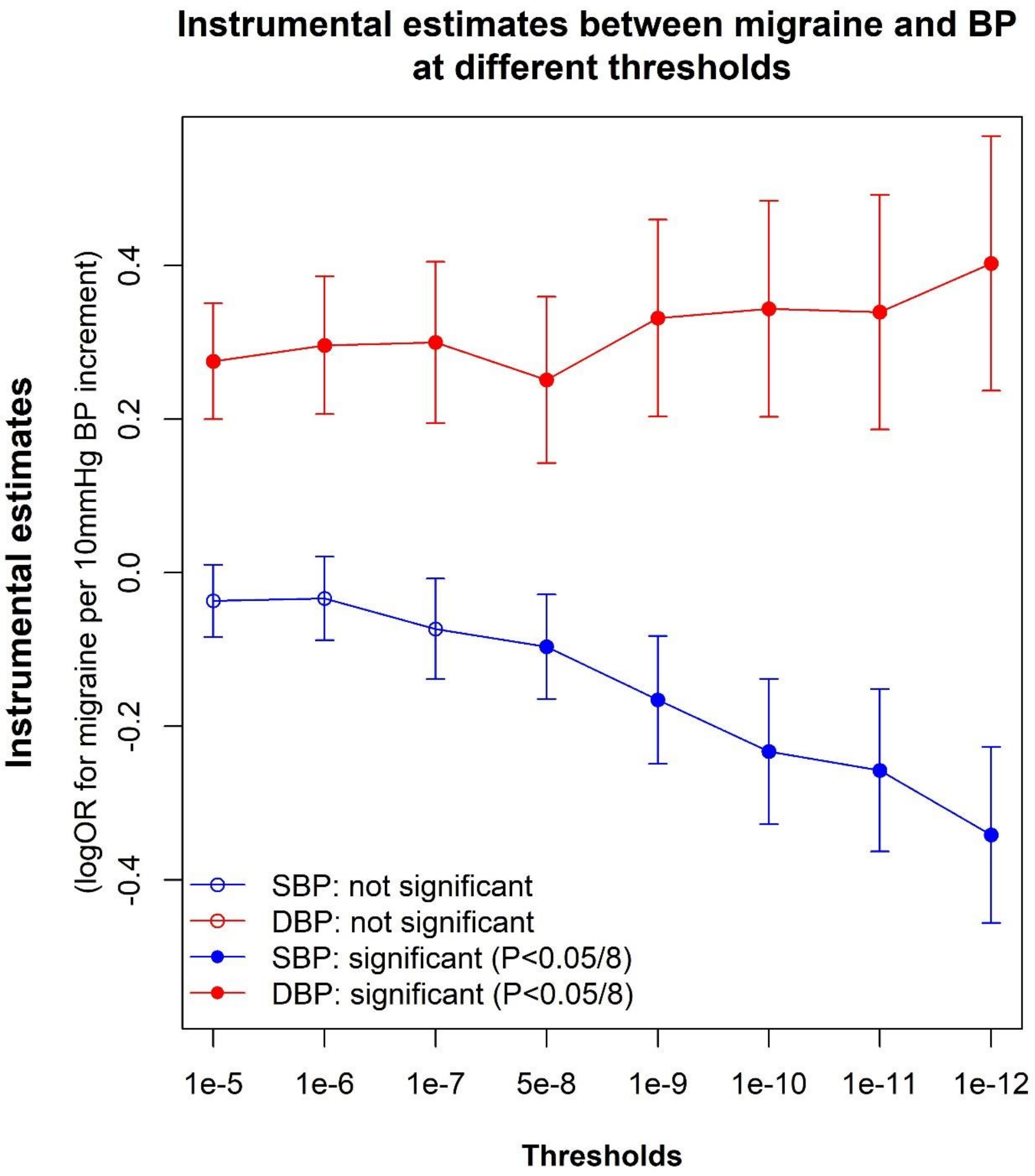
Supplementary Figure 25 **The number of shared TWAS significant genes between migraine without aura (MO) and diastolic blood pressure (DBP) across 48 GTEx tissues.** Colors represent different tissue categories.



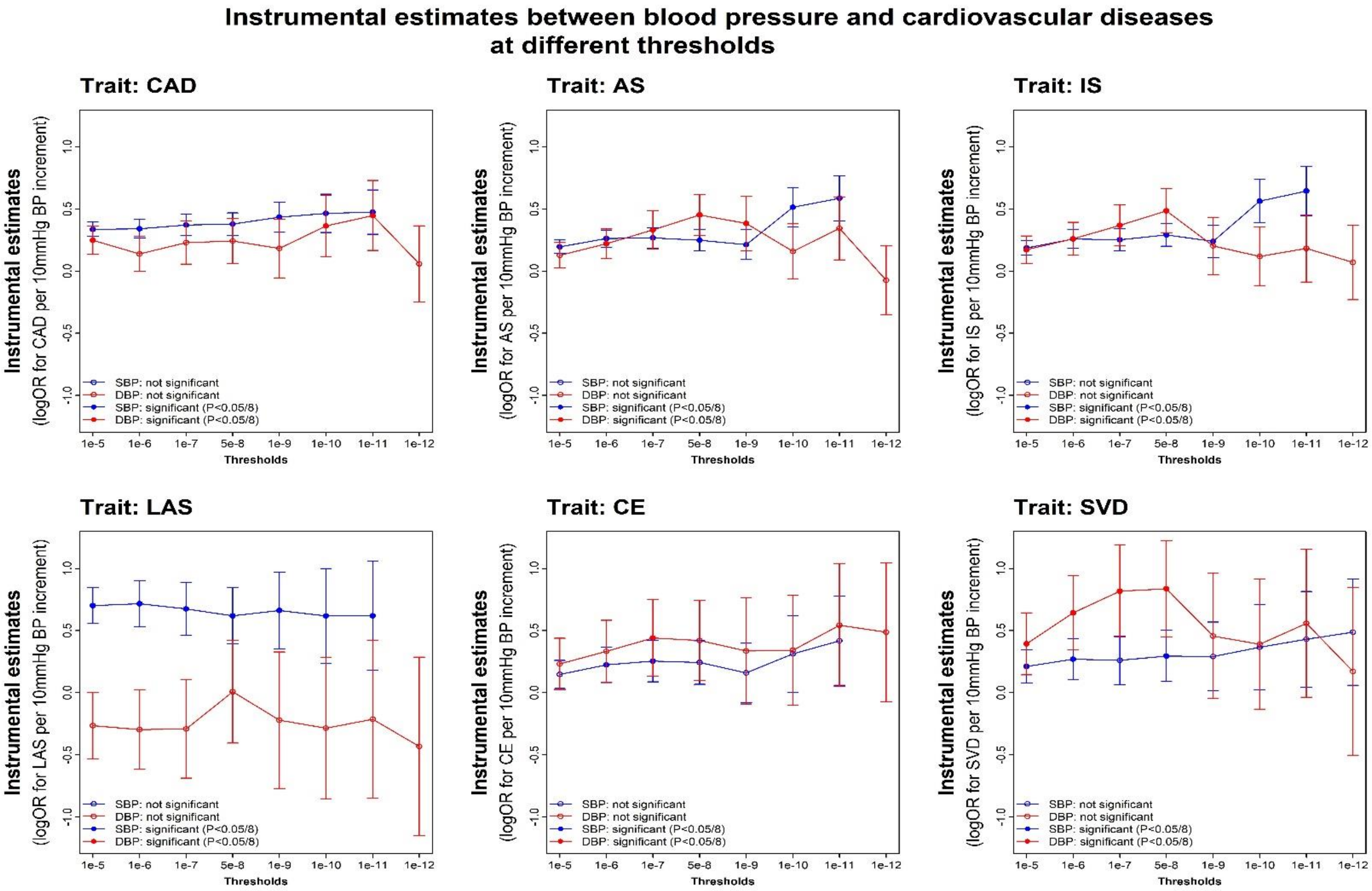
Supplementary Figure 26 **The number of shared TWAS significant genes between migraine without aura (MO) and systolic blood pressure (SBP) across 48 GTEx tissues.** Colors represent different tissue categories.



Supplementary Figure 27 **The number of shared TWAS significant genes between migraine without aura (MO) and pulse pressure (PP) across 48 GTEx tissues.** Colors represent different tissue categories.



Supplementary Figure 28 Instrumental estimates for migraine per 10mmHg increment of SBP and DBP by restricting SNPs that are not associated with DBP and SBP (*P*>0.05). For SBP, SNPs that were related with DBP (P_{GWAS} for DBP≤0.05) were removed and then used the summary statistics for the remaining SNPs to run GSMR at eight different thresholds (1e-5, 1e-6, 1e-7, 5e-8, 1e-9, 1e-10, 1e-11, and 1e-12). For DBP, SNPs that were related with SBP (P_{GWAS} for SBP≤0.05) were removed and conducted GSMR for DBP.



Supplementary Figure 29 **Instrumental estimates for cardiovascular comorbidities of migraine per 10mmHg increment of SBP and DBP by restricting SNPs that are not associated with DBP and SBP (*P*>0.05).** For SBP, SNPs that were related with DBP (P_{GWAS} for DBP≤0.05) were removed and then used the summary statistics for the remaining SNPs to run GSMR at eight different thresholds (1e-5, 1e-6, 1e-7, 5e-8, 1e-9, 1e-10, 1e-11, and 1e-12). For DBP, SNPs that were related with SBP (P_{GWAS} for SBP≤0.05) were removed and conducted GSMR for DBP. CAD: coronary artery disease; AS: any stroke; IS: ischemic stroke; LAS: large artery stroke; CE: cardioembolic stroke; SVD: small vessel stroke.

Author list for International Headache Genetics Consortium (IHGC) on paper "Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine", Nature Genetics, 2016, 48(8):856-66. doi: 10.1038/ng.3598. [PubMed ID: 27322543].

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