

Genome-wide association analysis identifies a meningioma risk locus at 11p15.5

Elizabeth B. Claus^{1,2,*†}, Alex J. Cornish^{3,*}, Peter Broderick^{3,*}, Joellen M. Schildkraut^{4,*}, Sara E. Dobbins³, Amy Holroyd³, Lisa Calvocoressi¹, Lingeng Lu¹, Helen M. Hansen⁵, Ivan Smirnov⁵, Kyle M. Walsh⁵, Johannes Schramm⁶, Per Hoffmann^{7,8}, Markus M. Nöthen^{8,9}, Karl-Heinz Jöckel¹⁰, Anthony Swerdlow^{3,11}, Signe Benzon Larsen¹², Christoffer Johansen¹², Matthias Simon^{6,13**}, Melissa Bondy^{14,**}, Margaret Wrensch^{5,15,**}, Richard Houlston^{3,**†}, Joseph L. Wiemels^{5,15,16,**}

1. School of Public Health, Yale University, New Haven, Connecticut, USA.
2. Department of Neurosurgery, Brigham and Women's Hospital, Boston, Massachusetts, USA.
3. Division of Genetics and Epidemiology, The Institute of Cancer Research, London, UK.
4. Department of Public Health Sciences, University of Virginia, Charlottesville, Virginia, USA.
5. Division of Neuroepidemiology, Department of Neurological Surgery, University of California San Francisco, San Francisco, California, USA.
6. University of Bonn Medical School, Bonn, Germany.
7. Human Genomics Research Group, Department of Biomedicine, University of Basel, Basel, Switzerland.
8. Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany.
9. Institute of Human Genetics, University of Bonn School of Medicine & University Hospital Bonn, Bonn, Germany.
10. Institute for Medical Informatics, Biometry and Epidemiology, University Hospital Essen, University of Duisburg-Essen, Essen, Germany.

11. Division of Breast Cancer Research, The Institute of Cancer Research, London, UK.
12. Unit of Survivorship, The Danish Cancer Society Research Center, Copenhagen, Denmark.
13. Department of Neurosurgery, Bethel Clinic, Bielefeld, Germany.
14. Section of Epidemiology and Population Sciences, Department of Medicine and Dan L. Duncan Comprehensive Cancer Center, Baylor College of Medicine, Houston, Texas, USA.
15. Institute for Human Genetics, University of California San Francisco, San Francisco, California, USA.
16. Department of Epidemiology and Biostatistics, University of California San Francisco, San Francisco, California, USA.

*. These authors contributed equally to this work.

**. These authors jointly supervised the work.

†. Correspondence to: Elizabeth B. Claus, Laboratory of Epidemiology and Public Health, 60 College Street, Ste 205, New Haven, Connecticut, USA, 06510. Tel: 203.785.6415; Fax: 203.785.6912; Email: elizabeth.claus@yale.edu. Richard S Houlston, Division of Genetics and Epidemiology, The Institute of Cancer Research, 15 Cotswold Road, London, UK, SM2 5NG. Tel: +44 (0) 208 722 4175; Fax: +44 (0) 722 4365; E-mail: richard.houlston@icr.ac.uk.

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CONFLICT OF INTEREST

The authors declare no competing financial interests.

AUTHORSHIP

R.H. and E.B.C. developed the project and provided overall project management; A.J.C., S.E.D., and R.H. drafted the manuscript. A.J.C. and S.E.D. performed bioinformatic and statistical analyses; P.B. performed project management and supervised genotyping; A.H. performed genotyping. Within the United States, E.B.C. obtained funding and managed the overall project; E.B.C., J.L.W., M.W., M.B., and J.M.S. oversaw IRB approval, patient recruitment and sample acquisition; L.C. supervised data collection and project management; L.L. and H.M.H. oversaw specimen storage and DNA isolation; J.L.W. and H.M.H. performed all genotyping; I.S. and K.M.W. performed bioinformatic and statistical analyses. Within Germany, M.S., J.S. and A.S. obtained funding, and were responsible for patient recruitment and sample acquisition, P.H. and M.M.N. oversaw DNA isolation and genotyping of the HNR controls and obtained funding for this, K.-H.J. provided samples. Within Denmark, S.B.L. and C.J. conducted subject recruitment and sample collection. All authors contributed to the final manuscript.

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ABSTRACT

BACKGROUND: Meningioma are adult brain tumors originating in the meningeal coverings of the brain and spinal cord, with significant heritable basis. Genome-wide association studies (GWAS) have previously identified only a single risk locus for meningioma, at 10p12.31.

METHODS: To identify a susceptibility locus for meningioma, we conducted a meta-analysis of two GWAS, imputed using a merged reference panel of 1,000 Genomes and UK10K data, with validation in two independent sample series totaling 2,138 cases and 12,081 controls.

RESULTS: We identified a new susceptibility locus for meningioma at 11p15.5 (rs2686876, odds ratio = 1.44, $P = 9.86 \times 10^{-9}$). A number of genes localize to the region of linkage disequilibrium encompassing rs2686876, including *RIC8A*, which plays a central role in the development of neural crest-derived structures, such as the meninges.

CONCLUSIONS: This finding advances our understanding of the genetic basis of meningioma development and provides additional support for a polygenic model of meningioma.

KEYWORDS: Genome-wide association study; Meningioma; Risk; Single-nucleotide polymorphism; Polygenic

IMPORTANCE OF STUDY

Meningioma are adult tumors arising in the meninges and account for around a third of all primary brain tumors. Evidence for common genetic variation contributing to meningioma predisposition has been provided by a genome-wide association study, which identified a risk locus at chromosome 10p12.31. To gain further insight into the inherited susceptibility of meningioma, we performed a meta-analysis of two genome-wide association studies and two independent validation series comprising 2,138 cases and 12,081 controls, and report the identification of a new risk locus for meningioma at 11p15.5. A number of genes localize to this locus, including *RIC8A*, which plays a central role in the development of neural crest-derived structures, such as the meninges. This is only the second study, and the largest, to robustly associate common genetic variation as a risk factor for meningioma.

INTRODUCTION

Meningioma are adult tumors arising in the membranous layers surrounding the brain and spinal cord and account for around a third of all primary brain tumors ¹⁻³. The incidence of meningioma is two-fold higher in females than in males, and the disease is more common in individuals with African ancestry ¹. Although mortality rates are relatively low, meningioma is associated with substantial morbidity.

Compared with malignant glial tumors, meningioma has been relatively understudied with regard to etiologic risk factors. Indeed, excluding exposure to ionizing radiation, no environmental factor has consistently been associated with tumor risk ^{2,3}. Evidence for an inherited predisposition to meningioma is provided by the elevated risk seen in neurofibromatosis ⁴ and Gorlin syndrome ⁵. While the risk of meningioma associated with these disorders is high, they are rare and collectively contribute little to the three-fold increased risk of the tumor in the relatives of meningioma patients ^{6,7}. Evidence for common genetic variation contributing to meningioma predisposition has been provided by a genome-wide association study (GWAS) ^{8,9}, which identified a risk locus at chromosome 10p12.31 ^{10,11}.

To gain a further insight into inherited susceptibility to meningioma, we performed a meta-analysis of a previously published GWAS ¹⁰ and a new unpublished GWAS, thereby providing increased study power to identify new risk loci and reduce the likelihood of false-positives ¹². Following replication genotyping in two additional independent series we report the identification of a new risk locus for meningioma mapping to chromosome 11p15.5.

METHODS

Ethics

Collection of patient samples and associated clinicopathological information in this study was completed with written informed consent and relevant ethical review board approval at the respective centers in accordance with the tenets of the Declaration of Helsinki. Specifically, these centers are for the German-GWAS: the ethics committees of the Medical Faculty of the University of Bonn and University Hospital Essen; USA-GWAS: the institutional review boards at Yale University School of Medicine, Brigham and Women's Hospital, University of California at San Francisco, MD Anderson Cancer Center, Duke University School of Medicine, the Kaiser Foundation Research Institute and the State of Connecticut Department of Public Health Human Investigation Committee; UK-replication: the South East Multicentre Research Ethics Committee and the Scottish Multicentre Research Ethics Committee; Danish-replication: the Danish ethical committee system, the Danish Data Protection Board and the Danish Ministry of Justice.

Genome-wide association studies

This meta-analysis was completed based on two GWAS data sets (**Supplementary Table 1**). The diagnosis of meningioma (ICD-10 D32/C70) was established in accordance with World Health Organization (WHO) guidelines.

The German-GWAS comprised 834 cases (250 male) and 2,103 controls (1,047 male). The German-GWAS case-control study has been described previously¹⁰. Cases subjects were patients who underwent surgery for meningioma at the University of Bonn Medical Center between 1996 and 2008. Controls subjects were healthy individuals with no past history of

malignancy from the Heinz Nixdorf Recall (HNR) study¹³. DNA was extracted from samples using conventional methodologies and quantified using PicoGreen (Invitrogen, Carlsbad, USA). Genotyping of cases and controls was conducted using either Illumina Infinium HD Human660w-Quad or OmniExpress Beadchips according to the manufacturer's protocols (Illumina, San Diego, USA).

The USA-GWAS comprised 772 cases (217 male) and 7,720 controls (2,966 male). Case patients eligible for the study included all persons diagnosed between 2006 and 2013 with a histologically confirmed intracranial meningioma among residents of the states of California, Connecticut, Massachusetts, North Carolina and Texas. Case patients were diagnosed between the ages of 20-79 and were identified through the Rapid Care Ascertainment systems and state tumor registries at their respective study site. Controls were obtained through random-digit dialing performed by an outside consulting firm (Kreider Research and Consulting) ($n=689$) or are from The Resource for Genetic Epidemiology Research on Aging (GERA) cohort ($n=7,031$)^{14,15}. Controls obtained through random-digit dialing were frequency matched with case patients by 5-year age interval, sex, and state of residence. Patients with a prior history of meningioma and/or a brain lesion of unknown pathology were not eligible for inclusion. The GERA cohort is comprised of 110,266 adult members of the Kaiser Permanente Medical Care Plan, Northern California Region (KPNC). Participants were enrolled through participation in a mailed study conducted in 2007 of all KPNC adult members who had been members for more than two years. Respondents who completed consent forms were mailed saliva collection kits (Oragene). We sampled 7,031 individuals from 56,848 non-Hispanic white individuals whose data passed quality control for inclusion in the control group, to ensure 1:10 matching between cases and controls in the USA-GWAS thereby optimizing study power, since there is little benefit of additional controls thereafter

¹⁶. Genotyping of cases and controls of all USA-GWAS subjects was completed using Affymetrix Axiom EUR arrays according to the manufacturer's protocols (Santa Clara, California, USA).

Statistical analysis

The quality control procedure described by Anderson *et al.* ¹⁷ was applied to each of the GWAS individually (**Supplementary Table 1**). To identify samples with discordant sex information, the mean homozygosity rate across X-chromosome markers was computed and samples were excluded if this rate contradicted the reported sex or was inconclusive (a rate between 0.2 and 0.8). We next excluded individuals if they exhibited an elevated genotype failure rate (>3%) or an outlying heterozygosity rate (± 3 standard deviations from the mean). To identify duplicated or related individuals, the degree of shared ancestry between pairs of individuals was computed (using identity by descent, IBD). If a pair of individuals had an IBD score >0.185, then the individual with the lowest variant call rate was excluded. Individuals with a non-European ancestry were identified by merging data from three HapMap version II populations (CEU, JPT/CHB and YRI) and conducting principal component analysis on the merged individuals. Individuals with a second principal component score less than 0.072 were excluded. Variants were excluded if they had a high missing data rate (>5%), if the genotyping call rates differed between the cases and the controls ($P < 10^{-5}$ using Fisher's exact test), if they had a minor allele frequency (MAF) <0.01 or if they deviated significantly from Hardy-Weinberg equilibrium (HWE, $P < 10^{-5}$). Individuals were phased using SHAPEIT version 2.r837 software ¹⁸ and a merged reference panel (EGAD00001000776, the European Genome-phenome Archive) containing data from the 1000 Genomes Project ¹⁹ (Phase 3) and the UK10K ²⁰. GWAS data were imputed to more than 10 million single nucleotide polymorphisms (SNPs) using IMPUTE version 2.3.0 ²¹ and

the same reference panel. Imputation was conducted separately for each of the studies. In each data set, the data were pruned to the set of variants common to the cases and controls before imputation. Tests of association between the directly genotyped and imputed SNPs and meningioma were performed using logistic regression under an additive genetics model using SNPTEST version 2.5.2²². Poorly imputed SNPs (information measure <0.8), SNPs with a low MAF (<0.005) and SNPs that deviated from HWE ($P < 10^{-5}$) were excluded. To evaluate the possibility of differential genotyping of cases and controls and the adequacy of the case-control matching, quantile-quantile (Q-Q) plots of the test statistics were generated (**Supplementary Fig. 1**). The computed inflation factor λ is based on the 90% least significant SNPs²³. In each study, the effects of population stratification were limited by including in the analysis the first two and three principal components for the German and USA series respectively. Eigenvectors for each of the GWAS data sets were computed using EIGENSOFT version 4.2²⁴.

Meta-analyses of the individual GWAS were completed using the β estimates and standard errors from each study and the fixed-effects inverse-variance method implemented in META version 1.7²⁵. Cochran's Q -statistic and the I^2 statistic were used to test for heterogeneity and estimate the proportion of the total variation that is due to heterogeneity²⁶. Meta-analysis was only completed for a SNP if it passed the quality thresholds in all considered GWAS. SNPTEST was used to perform conditional association analysis. SNP associations at $P < 5 \times 10^{-8}$ in the meta-analyses are considered genome-wide significant²⁷. Despite imposing a stringent significance threshold of $P < 5 \times 10^{-8}$ for declaring a GWAS association as being significant it is possible that some such associations might still be false positives. To further assess the robustness of an association, Wakefield has proposed the application of an

approximate Bayes factor to calculate the Bayes false discovery probability (BFDP)²⁸. We estimated the BFDP based on a plausible OR of 1.2 and a prior probability of 0.0001²⁹.

Replication studies

Ten promising SNP associations from the meta-analysis of the two GWAS were taken forward for *de novo* replication (**Supplementary Table 2**). Promising associations were pre-specified as loci with SNP association P -values $<10^{-5}$, which also had support from additional correlated SNPs mapping to the same genetic region (i.e. $r^2 >0.5$ and $P <10^{-3}$). The UK-replication series comprised 439 cases (ICD10 D32/C70) from the INTERPHONE study³⁰ and 1,865 population-based controls with no past history of any malignancy, ascertained through the National Study of Colorectal Cancer Genetics³¹. The Danish-replication series comprised 115 cases (ICD-O 9530-9537) from the INTERPHONE study and 411 controls with no past history of cancer, ascertained through the Danish Central Population Registry. Replication genotyping of UK and Danish samples was performed using allele-specific PCR KASP chemistry (LGC, UK). Primers are detailed in **Supplementary Table 3**. 34 samples were excluded from the UK-replication series for having three or more failed calls. Call rates for each genotyped SNP were $>98\%$ in the remaining UK samples. Six samples were excluded from the Danish-replication series due to the failed call of the genotyped SNP.

Sequencing

To assess the fidelity of imputation of rs7124615, a subset of 126 cases and 56 controls from the German-GWAS series, selected to be enriched for the presumptive T allele, were sequenced using BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, MA, USA) in conjunction with ABI 3700xl semi-automated sequencers (Applied Biosystems). We did not detect the presence of the T allele in any of the samples. rs7124615 maps to a highly

repetitive region, suggesting this SNP may be incorrectly annotated to this region. Primer sequences are detailed in **Supplementary Table 3**.

Heritability analysis

We used Genome-wide Complex Trait Analysis (GCTA) to estimate the heritability ascribed to the genotyped SNPs across all autosomes and each individual autosome³². SNPs were excluded based on high missing rate (>5%), low MAF (MAF <0.01) or evidence of deviation from HWE ($P < 0.05$). Individuals identified as being closely related were also excluded. Restricted maximum likelihood analysis was run using a genetic relationship matrix for each pair of samples. The lifetime risk of meningioma was used to transform the estimated heritability to the liability scale, as previously advocated when calculating the heritability of common lethal diseases such as cancer³³. The lifetime risk of brain and nervous system tumors is 0.62%³⁴ and meningioma account for 36% of primary brain tumors³⁵ and we therefore estimated the lifetime risk of meningioma to be 0.224%. We followed the methodology of Yang *et al.*³⁶ to adjust for incomplete linkage disequilibrium between the genotyped and causal SNPs at a range of MAF thresholds between 0.1 and 0.5. Heritability was estimated for the German and USA series individually and a meta-analysis of the results completed under a fixed-effects model. We additionally used the phenotype correlation-genotype correlation (PCGC) regression method to estimate the heritability ascribed to the genotyped SNPs across all autosomes³⁷, using the genetic relationship matrix and lifetime risk estimate that was used with GCTA. We adjusted for population structure when estimating heritability using the GCTA and PCGC regression approaches by including as covariates the first two and three principal components for the German and USA series respectively. Estimates of individual variance in risk associated with meningioma risk SNPs was carried out using the method described in Pharoah *et al.*³⁸.

Expression quantitative trait loci analysis

Publicly available data from 47 tissues from the Genotype-Tissue Expression (GTEx) project³⁹ v7 release were used to examine the relationship between SNP genotype and gene expression. We set a significance threshold for the expression quantitative trait loci (eQTL) analysis of $P < 2.01 \times 10^{-5}$, corresponding to a Bonferroni correction for 2,491 tests (53 genes across 47 tissues).

Summary-level Mendelian randomization analysis

To examine the relationship between meningioma risk loci and gene expression we performed a summary-level Mendelian randomization (SMR) analysis, as per Zhu *et al.*⁴⁰. Briefly, GWAS summary statistics files were generated from the meta-analysis. Reference files were generated using data from the 1000 Genomes Project (Phase 3) and UK10K. As previously advocated, only probes with at least one eQTL P -value of $< 5.0 \times 10^{-8}$ were considered for SMR analysis. We set a threshold for the SMR test of $P_{\text{SMR}} < 1.01 \times 10^{-4}$, corresponding to a Bonferroni correction for 496 tests (496 probes with a top eQTL $P < 5.0 \times 10^{-8}$ across 47 tissues). HEIDI test P -values < 0.05 were taken to indicate significant heterogeneity.

Data availability

Genotype data from GERA are available from dbGaP (accession phs000674.v2.p2). 1000 Genomes Project and UK10K imputation panel data are available from EGA (accession EGAD00001000776). Remaining data are available from the authors upon request.

RESULTS

Association analysis

We analyzed GWAS SNP data passing quality control for 1,606 cases and 9,823 controls of European ancestry from two studies: a previously reported GWAS of 834 cases and 2,103 controls (German-GWAS) ¹⁰ and a new GWAS of 772 cases and 7,720 controls (USA-GWAS) from Yale University, Brigham and Women's Hospital, MD Anderson Cancer Center, Duke University School of Medicine, and The University of California, San Francisco (**Supplementary Tables 1 and 4**). To increase genomic resolution, we used data from the 1000 Genomes Project and UK10K to impute >9 million SNPs. Q-Q plots for SNPs with a MAF >1% post imputation did not show evidence of substantive over-dispersion (λ between 0.99 and 1.04; **Supplementary Fig. 1**). We computed joint odds ratios (ORs) and 95% confidence intervals (CIs) under a fixed-effects model for each SNP and associated per allele principal component corrected *P*-values for all cases versus controls from the two series (**Fig. 1, Supplementary Fig. 2**).

The strongest association was provided by SNP rs530000334 ($P = 1.41 \times 10^{-11}$), which maps to the previously identified risk locus at 10p12.31 (**Fig. 1**). Excluding the poorly imputed SNP rs7124615 at 11p15.5 no other association was genome-wide significant. We sought independent validation of promising associations (i.e. $P < 10^{-5}$) at ten loci where support was provided by SNPs in linkage disequilibrium ($r^2 > 0.5$ and $P < 10^{-3}$) by genotyping additional case-control series from the UK and Denmark (**Supplementary Table 2**). In a combined analysis of the GWAS and replication datasets for these select SNPs the only genome-wide association was shown by rs2686876, also at 11p15.5 ($P = 9.86 \times 10^{-9}$; **Table 1; Fig. 2; Supplementary Table 2**). The BFDP for this association was 1.8%, thereby supporting the

robustness of the association. At both 11p15.5 and 10p12.31, a conditional analysis of SNP genotypes provided no evidence for additional independent signals at either risk locus.

Most meningioma (>80%) are WHO grade I tumors with the remainder grade II (atypical, 15%) and grade III (anaplastic) meningioma ⁴¹; males are more likely than females to have atypical or aggressive lesions. We assessed the relationship between 11p15.5 genotype and WHO grade, sex and age at diagnosis by case-only analysis. WHO grade was not available for all USA-GWAS, UK-replication and Danish-replication cases and therefore the WHO grade case-only analysis was restricted to the German-GWAS cases. Case-only analyses of sex and age at diagnosis were conducted in all series. These analyses provided no evidence for association between rs2686876 and WHO grade, sex or age at diagnosis, consistent with a generic effect of genotype on meningioma risk (**Supplementary Table 5**).

A number of genes localize to the region of linkage disequilibrium encompassing rs2686876 (**Fig. 3**). They include *RIC8A*, a homolog of *C. elegans Ric8/synembryn* that encodes a highly conserved G protein regulator. Intriguingly *RIC8A* plays a central role in the development of neural crest-derived structures including the meninges ⁴². To gain insight into the biological basis underlying the 11p15.5 association we first evaluated each of the risk SNPs as well as the correlated variants ($r^2 > 0.8$) using the online resources HaploReg v4 ⁴³, RegulomeDB ⁴⁴ and SeattleSeq ⁴⁵ for evidence of functional effects (**Supplementary Table 6**). These data revealed active chromatin states overlapping SNPs correlated with rs2686876.

We explored whether there were any associations between rs2686876 genotype and the transcript levels of genes within 1Mb using eQTL data on 47 tissues generated by the GTEx project ³⁹ (**Supplementary Table 7**). After accounting for multiple testing (53 genes across

47 tissues; $P < 2.01 \times 10^{-5}$), significant eQTL for *ANO9* were observed in brain caudate basal ganglia ($P = 8.30 \times 10^{-7}$) and brain putamen basal ganglia ($P = 2.58 \times 10^{-6}$), for *BETIL* in esophagus mucosa ($P = 9.03 \times 10^{-6}$) and for *PSMD13* in brain anterior cingulate cortex ($P = 1.36 \times 10^{-5}$). *ANO9* upregulation has been observed in colorectal cancer ⁴⁶ and has been associated with poor prognosis in pancreatic cancer ⁴⁷. The rs2686876 meningioma risk allele was however conversely associated with lower *ANO9* expression at the two eQTLs. Whilst the risk allele of rs2686876 is associated with higher *RIC8A* expression at nominal significance levels ($P < 0.05$) in 15 of the 47 tissues, the associations were not significant after correction for multiple testing.

We used SMR analysis to test for a concordance between signals from GWAS and *cis* eQTL for genes within 1 Mb of the sentinel and correlated SNPs ($r^2 > 0.8$) at the 11p15.5 locus and derived b_{XY} statistics, which estimate the effect of gene expression on meningioma risk (**Supplementary Table 8**). After accounting for multiple testing, the SMR analysis failed to provide overwhelming evidence to implicate a specific gene.

DISCUSSION

We have provided the first evidence that implicates variation at 11p15.5 as a determinant of meningioma risk. To our knowledge this is only the second study, and the largest, to robustly associate common genetic variation as a risk factor for meningioma.

Although functional studies will be required, dysregulation of *RIC8A* provides an attractive basis of the 11p15.5 association *a priori*. *RIC8A* has an essential role in the development of the mammalian central nervous system, maintaining the integrity of pial basement membrane and modulating cell division ⁴². Intriguingly, conditional *Ric8a* knockout mice have been reported to exhibit defects in meningeal layer formation ⁴².

Thus far, variation at only two loci have been robustly shown to affect meningioma risk ¹⁰. To estimate the potential heritability of meningioma attributable to all common variation we applied GCTA ³² and PCGC regression ³⁷ to the GWAS datasets (**Supplementary Table 9**). Combining data from the two GWAS indicates that the heritability associated with common variation is 27.9% ($\pm 4.4\%$).

The identification of risk variants at 11p15.5 provides further evidence for common genetic variation influencing meningioma risk and suggests the involvement of specific genes in tumor development. Since variation at 10p12.31 and 11p15.5 only account for approximately 4% of the familial risk of meningioma (**Supplementary Table 10**) it is likely that further risk variants for meningioma will be identified through additional and larger GWAS.

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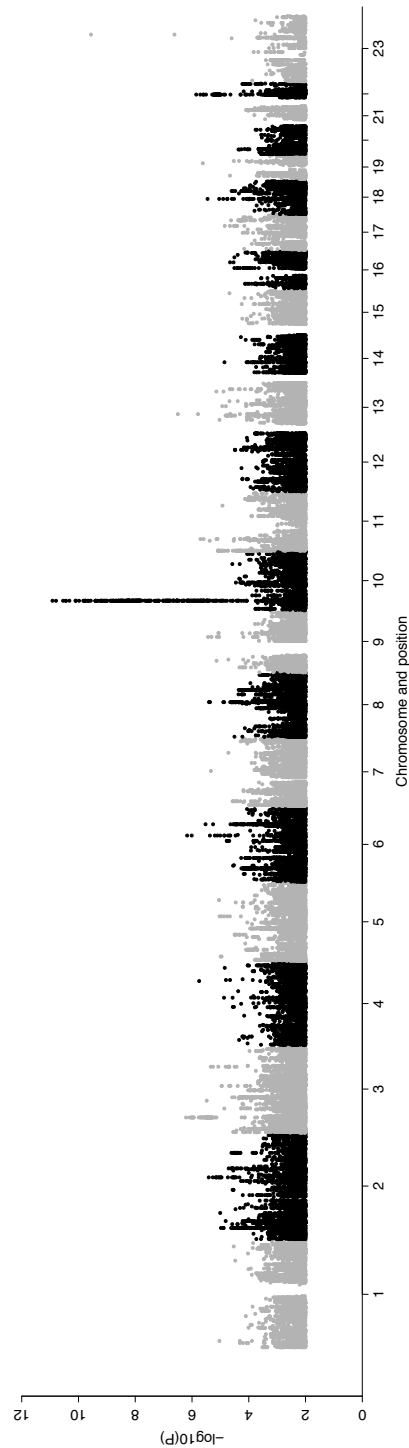


Figure 1: Manhattan plot of association P values. Shown are the genome-wide P values (two-sided) of >9 million successfully imputed single nucleotide polymorphisms (SNPs) in 1,606 cases and 9,823 controls. Text labeled in red are previously identified risk loci and text labeled in blue are newly identified risk loci. Imputation of rs7124615 was not supported by sequencing and this SNP is therefore not represented.

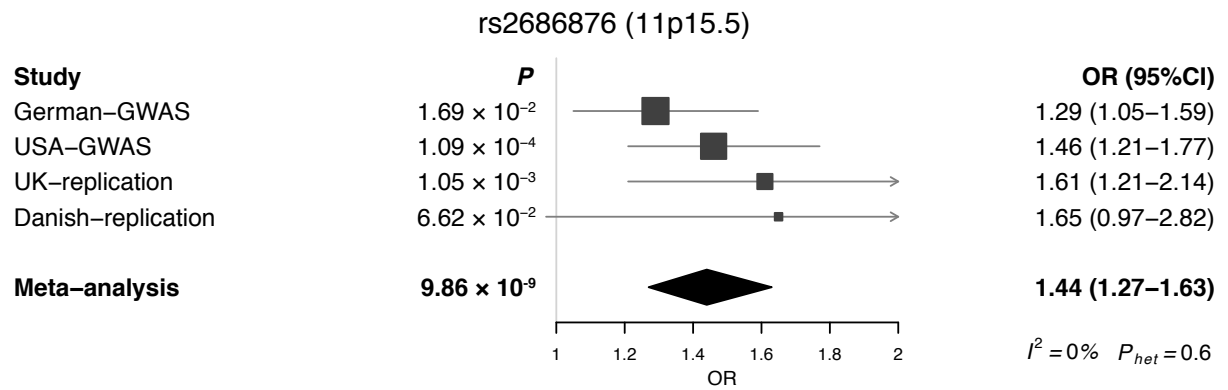


Figure 2: Forest plot of effect size and direction for the single nucleotide polymorphism (SNP) from the newly reported locus associated with meningioma risk.

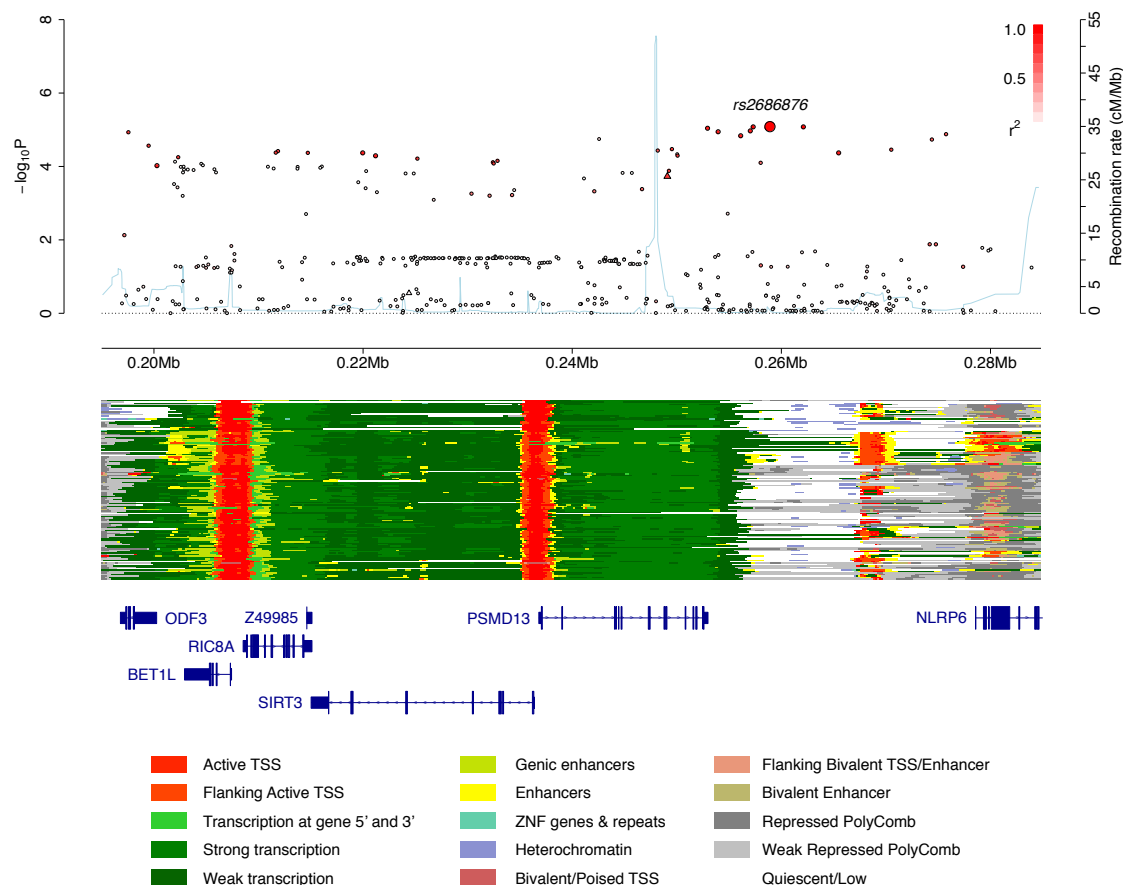


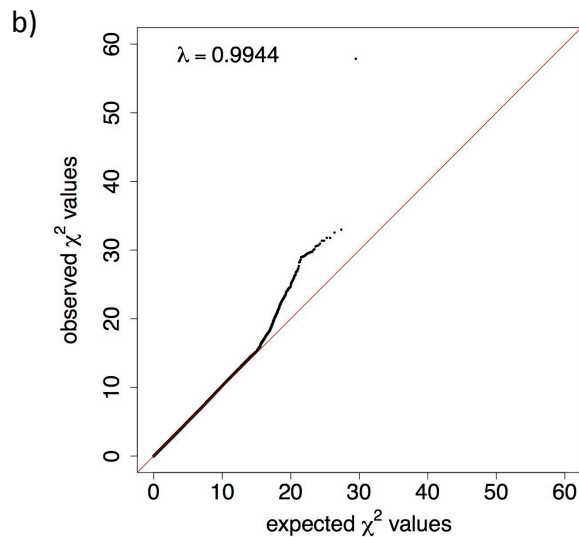
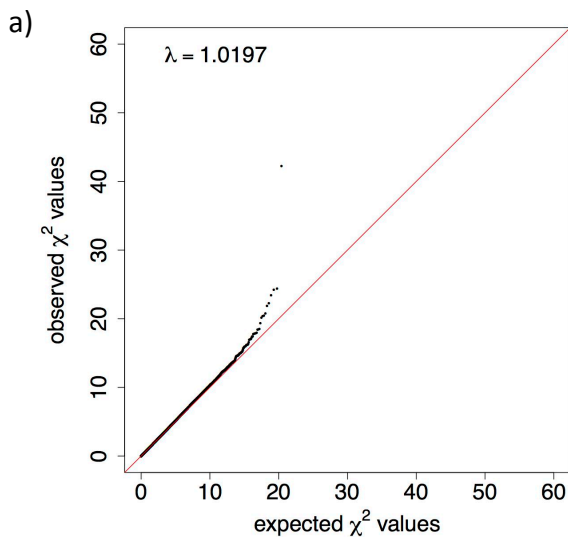
Figure 3: Regional plot of the 11p15.5 association. Plot (drawn using visPig⁴⁸) shows association results of both genotyped (triangles) and imputed (circles) single nucleotide polymorphisms (SNPs) in the genome-wide association study (GWAS) samples and recombination rates. $-\log_{10} P$ values (y axes) of the SNPs are shown according to their chromosomal positions (x axes). The sentinel SNP is shown as a large circle and is labeled by its rsID. The color intensity of each symbol reflects the extent of linkage disequilibrium with the top genotyped SNP, white ($r^2=0$) through to dark red ($r^2=1.0$). Genetic recombination rates, estimated using 1000 Genomes Project samples¹⁹, are shown with a light blue line. Physical positions are based on NCBI build 37 of the human genome. Also shown are the chromatin-state segmentation tracks for 127 cell types and tissues from ENCODE and the Roadmap Epigenomics Consortium⁴⁹, generated using ChromHMM⁵⁰ and the Wash U Epigenome Browser⁵¹, and the positions of genes and transcripts mapping to the region of association. *ANO9* is located 128 kb centromeric of the plotted region.

Table 1: Summary results for the single nucleotide polymorphism (SNP) from the newly reported locus associated with meningioma risk.

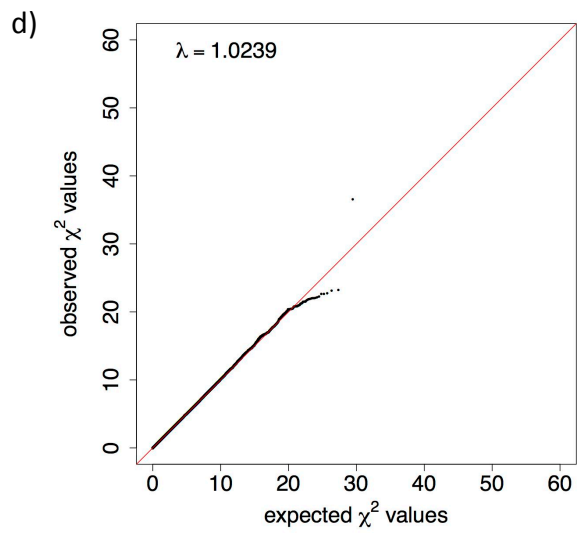
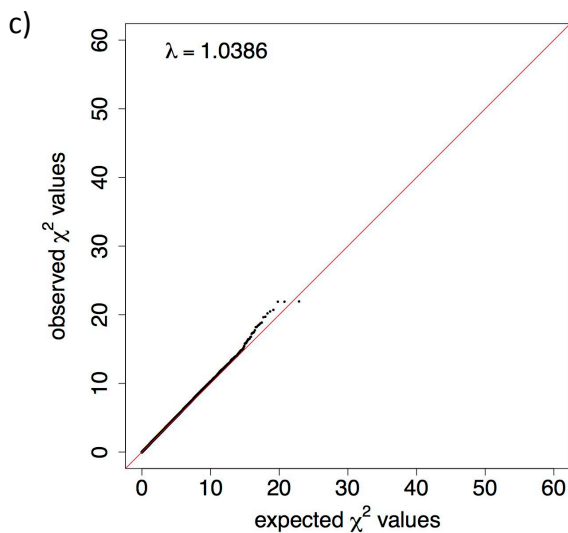
SNP	Locus	Position	Risk	Study	Control			P value
		(bp) *	allele		Case RAF	RAF	OR (95% CI)	
rs2686876	11p15.5	258909	T	German-GWAS	0.927	0.902	1.29 (1.05-1.59)	1.69×10^{-3}
				USA-GWAS	0.938	0.910	1.46 (1.21-1.77)	1.09×10^{-4}
				GWAS phase meta-analysis			1.38 (1.20-1.59)	8.19×10^{-6}
				UK-replication	0.955	0.921	1.61 (1.21-2.14)	1.05×10^{-3}
				Danish-replication	0.943	0.905	1.65 (0.97-2.82)	6.62×10^{-2}
				Replication phase meta-analysis			1.62 (1.26-2.08)	1.73×10^{-4}
			Combined GWAS/replication phase meta-analysis			1.44 (1.27-1.63)	9.86×10^{-9}	

RAF, risk allele frequency; OR, odds ratio; CI, confidence interval; * Position is based on NCBI build 37.

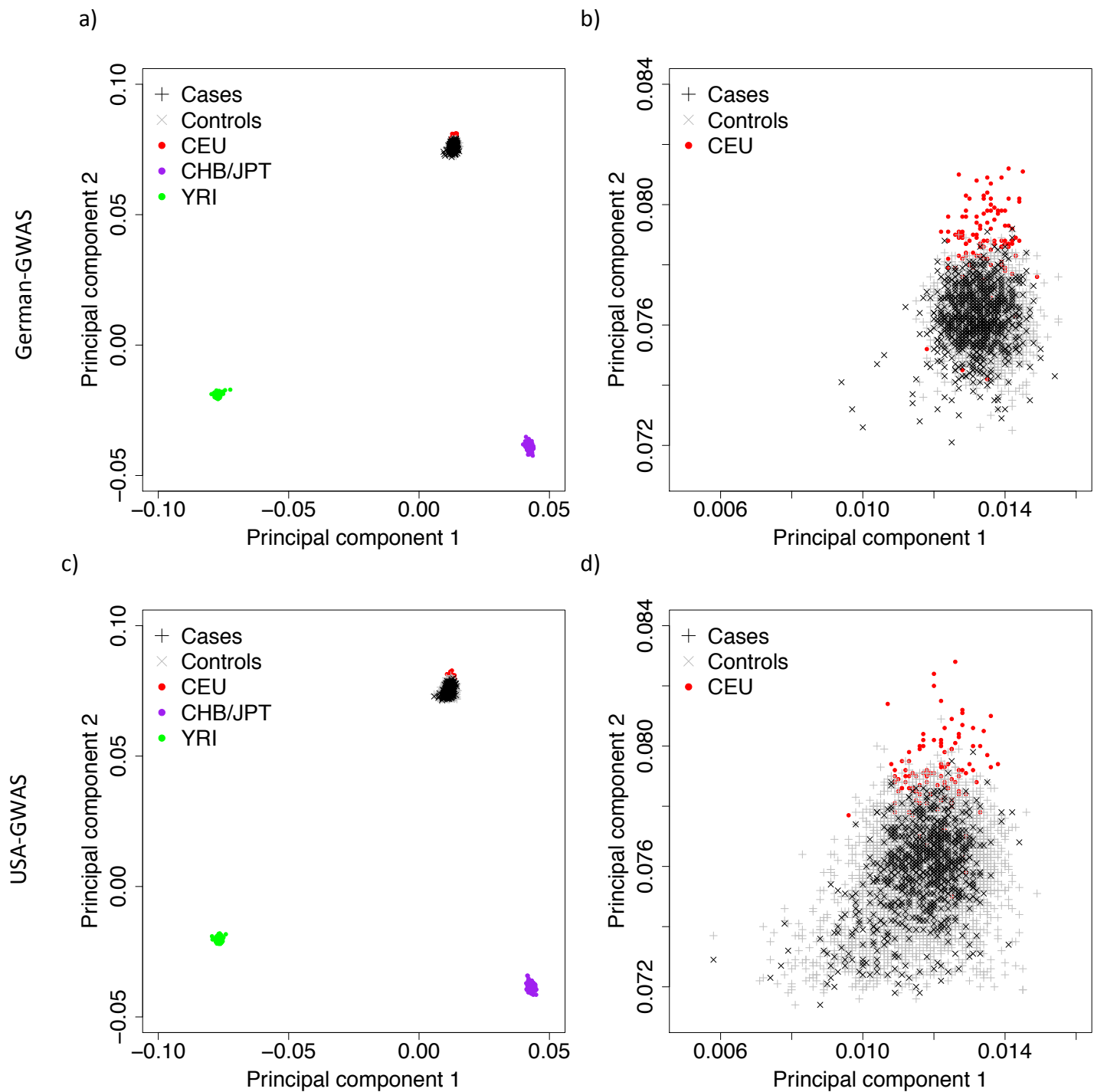
German-GWAS



USA-GWAS



Supplementary Figure 1: Quantile-Quantile (Q-Q) plots of observed and expected χ^2 values of association between meningioma risk and SNP genotype. German-GWAS (adjustment carried out on first two principle components): a) genotyped and b) imputed SNPs. USA-GWAS (adjustment carried out on the first three principle components): c) genotyped and d) imputed SNPs. Red line represents the null hypothesis of no true association.



Supplementary Figure 2: PCA plots of the GWAS data sets. Cases and controls from each series were merged with three HapMap version II populations and PCA was conducted on the merged individuals. German-GWAS showing a) cases, controls and three HapMap populations and b) cases, controls and only the CEU HapMap population. USA-GWAS showing c) cases, controls and three HapMap populations and d) cases, controls and only the CEU HapMap population.

Supplementary Table 1: Details of the quality control (QC) filters applied at the sample-level and SNP-level.

Study	Status	Sample-level QC							SNP-level QC (completed on cases and controls combined)				
		Sample numbers pre-QC	Sample numbers removed by filtering stages				Sample numbers post-QC	Platform	SNP numbers removed by filtering stages			SNPs post-QC	
			Sex discordance	Missing rate	Heterozygosity rate	Relatedness			Divergent ancestry	Case/control call rate ^b	Call rate		MAF & HWE <i>P</i> values
German-GWAS	Cases	961	24	15	13	11	64	834	Illumina 660w-Quad and Illumina OmniExpress	1,979	2	11,752	291,378
	Controls	2,132	2	3	15	4	5	2,103					
USA-GWAS	Cases	935	0	4	12	0	147	772	Affymetrix Axiom Western European Panel	15,170	0	7,866	395,907
	Controls	57,646	31	188	894	526	6,512	7,720 ^a					

^a 7,720 controls were sampled at random from 49,495 post-QC controls to ensure 1:10 case-control ratio

^b SNPs excluded if call rate differs between cases and controls ($P < 10^{-5}$)

^c SNPs excluded if call rate < 95%

Supplementary Table 2: Summary statistics from all data sets for SNPs taken forward to the replication phase.

SNP details					German-GWAS				
SNP	Locus	Position (bp)	Risk allele	Other allele	Case RAF	Control RAF	OR (95% CI)	P value	Case RAF
rs749917	1p36.13	18503402	C	T	0.745	0.720	1.17 (1.02-1.34)	2.51E-02	0.767
rs62248541	3p22.3	34365349	T	G	0.067	0.050	1.54 (1.16-2.05)	2.82E-03	0.072
rs2105297	6q21	105668048	G	C	0.296	0.256	1.30 (1.13-1.49)	2.14E-04	0.303
rs117837262	9p21.2	26564699	A	C	0.085	0.067	1.34 (1.06-1.68)	1.34E-02	0.096
rs2686876	11p15.5	258909	T	A	0.927	0.902	1.29 (1.05-1.59)	1.69E-02	0.938
rs2240941	11p14.3	22881687	A	C	0.140	0.111	1.43 (1.18-1.73)	3.00E-04	0.147
rs1017602	11p14.2	26792264	T	G	0.939	0.909	1.46 (1.18-1.82)	5.79E-04	0.929
rs12428241	13q14.11	42127834	A	G	0.082	0.065	1.35 (1.07-1.71)	1.18E-02	0.101
rs1941941	18q12.2	35097335	A	T	0.229	0.210	1.19 (1.03-1.37)	2.03E-02	0.250
rs11090280	22q11.23	24028412	C	T	0.519	0.486	1.21 (1.07-1.36)	2.10E-03	0.556

Positions are reported for hg19. RAF: risk allele frequency; OR: odds ratio derived with respect to the risk allele.

USA-GWAS			Meta analysis prior to replication				UK-replicat	
Control RAF	OR (95% CI)	P value	OR (95% CI)	P value	I ²	P _{het}	Case RAF	Control RAF
0.722	1.28 (1.13-1.45)	7.30E-05	1.23 (1.12-1.35)	9.24E-06	2.98	3.10E-01	0.734	0.736
0.049	1.64 (1.29-2.08)	5.73E-05	1.60 (1.33-1.92)	6.19E-07	0.00	7.50E-01	0.070	0.071
0.264	1.23 (1.09-1.39)	6.71E-04	1.26 (1.15-1.38)	6.74E-07	0.00	5.90E-01	0.262	0.276
0.070	1.50 (1.22-1.84)	1.34E-04	1.43 (1.22-1.66)	7.33E-06	0.00	4.77E-01	0.074	0.073
0.910	1.46 (1.21-1.77)	1.09E-04	1.38 (1.20-1.59)	8.19E-06	0.00	4.01E-01	0.955	0.921
0.121	1.29 (1.09-1.52)	2.69E-03	1.35 (1.19-1.53)	4.21E-06	0.00	4.32E-01	0.131	0.132
0.906	1.32 (1.10-1.59)	2.83E-03	1.38 (1.20-1.58)	7.76E-06	0.00	4.80E-01	0.893	0.913
0.069	1.64 (1.33-2.03)	3.92E-06	1.51 (1.29-1.77)	3.17E-07	30.08	2.32E-01	0.050	0.055
0.205	1.32 (1.16-1.50)	3.19E-05	1.26 (1.14-1.38)	3.53E-06	10.44	2.91E-01	0.241	0.225
0.505	1.23 (1.10-1.37)	1.80E-04	1.22 (1.12-1.32)	1.41E-06	0.00	8.41E-01	0.541	0.522

Supplementary Table 3: Primers used for replication genotyping and sequencing.

Primers used for replication genotyping.

SNP	Allele 1 primer ^a	Allele 2 primer ^b	Common primer
rs749917	TGTGCTATTAGTAGCCTTGCCAC	AGTGCTATTAGTAGCCTTGCCAT	CATCCAGAAAAATTATAGGAAGCGCTGTA
rs62248541	CATACATAAAGCACCAAAAGTATGATGG	ACATACATAAAGCACCAAAAGTATGATGT	TTTCTCAGCATGTGATCCAACATTGGAAT
rs2105297	TTTGTCATAATCTGATTCAGAGAGACG	TGTCATAATCTGATTCAGAGAGACC	GGACCAATGTGATATATTGTGGAAGTGAA
rs117837262	TTTCTTCTCTGCCTGGAGTAAAG	CTTCTCTGCCTGGAGTAAAG	TCCTTACCCTCAAGATCTGAAATAGCTAT
rs2686876	CCTGTGCGACAGAGCAAGACA	CCTGTGCGACAGAGCAAGACT	GTTTTTATGTGACATGAAGATGGTATTCAA
rs2240941	TGTCAGGTACATCACCTGTATGTTG	GGTCAGGTACATCACCTGTATGTTT	CTTCTGTAATTTCCACTCCACCTCCTA
rs1017602	TAGTGAGATTCTTTGACAGACCTACAT	GTGAGATTCTTTGACAGACCTACA	AATAATTCCTTCTACTTCTTTTTCTCTT
rs12428241	TGGCACCAGACCTGGCCAGTT	GCACCAGACCTGGCCAGTC	AACTTACATCGTGGGACATCCCAAATTTT
rs1941941	TGTCTTGCAAGCAGGTGTTTGGC	GTCTTGCAAGCAGGTGTTTGGC	TGCCAAAAGCCACCCTGGGAA
rs11090280	TTCCTATGACTTATTTGTAGTCCTTT	ACTTCCTATGACTTATTTGTAGTCCTTT	CCCACAGAGAGGGTCTGTAGAAAT

^a Allele 1 primers have a 5' FAM label - GAAGGTGACCAAGTTCATGC. ^b Allele 2 primers have a 5' VIC label - GAAGGTGCGAGTCAACGGATT.

Primers used for sequencing.

SNP	Left primer	Right primer
rs7124615	TGATGTGTTGAGACCGAAA	CCATTCTGATTTGCCTGCT

Supplementary Table 4: Details of each GWAS and replication data set.

Stage	Study	Final sample numbers		% Male		Imputed SNPs
		Cases	Controls	Cases	Controls	
Discovery	German-GWAS	834	2,103	29.98	49.79	9,213,034
	USA-GWAS	772	7,720	28.11	38.42	9,084,775
Replication	UK-replication	418	1,852	27.03	36.88	NA
	Danish-replication	114	406	30.70	59.85	NA

Successfully imputed SNPs in each discovery series GWAS were those with info score ≥ 0.80 , case and control MAF > 0.01 and $P_{HWE} > 1 \times 10^{-5}$.

Supplementary Table 5: Association between SNP genotype and tumor grade, sex and age at diagnosis in meningioma cases.

Tumor grade													
SNP details					German-GWAS				USA-GWAS				
SNP	Locus	Position (bp)	Risk allele	Genotypes	Grade I	Grade II/III	OR (95% CI)	P value					
rs2686876	11p15.5	258909	T	T T	532	148	0.81 (0.49-1.31)	3.79E-01	Tumor WHO grade data unavailable				
				T A	87	19							
				A A	4	1							

Sex													
SNP details					German-GWAS				USA-GWAS				
SNP	Locus	Position (bp)	Risk allele	Genotypes	Male	Female	OR (95% CI)	P value	Male	Female	OR (95% CI)	P value	Male
rs2686876	11p15.5	258909	T	T T	216	501	1.12 (0.74-1.68)	5.96E-01	182	482	0.76 (0.51-1.14)	1.77E-01	102
				T A	34	78			32	70			7
				A A	0	5			3	3			0

Age at diagnosis													
SNP details					German-GWAS				USA-GWAS				
SNP	Locus	Position (bp)	Risk allele	Genotypes	< 57 years	≥ 57 years	OR (95% CI)	P value	< 57 years	≥ 57 years	OR (95% CI)	P value	< 57 years
rs2686876	11p15.5	258909	T	T T	266	449	0.76 (0.52-1.10)	1.32E-01	281	376	0.86 (0.58-1.26)	4.01E-01	120
				T A	50	61			48	51			8
				A A	2	3			2	4			0

Positions are reported for hg19. OR: odds ratio derived with respect to the risk allele.

UK-replication	Danish-replication
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Tumor WHO grade data unavailable

Tumor WHO grade data unavailable

UK-replication			Danish-replication				Meta analysis			
Female	OR (95% CI)	P value	Male	Female	OR (95% CI)	P value	OR (95% CI)	P value	I ²	P _{het}
273			33	68						
26	1.58 (0.68-3.65)	2.95E-01	2	11	2.54 (0.55-11.79)	2.03E-01	1.03 (0.78-1.34)	8.57E-01	37.25	1.89E-01
2			0	0						

UK-replication			Danish-replication				Meta analysis			
≥ 57 years	OR (95% CI)	P value	< 57 years	≥ 57 years	OR (95% CI)	P value	OR (95% CI)	P value	I ²	P _{het}
255			37	64						
25	1.68 (0.76-3.73)	2.12E-01	5	8	0.93 (0.29-2.94)	8.98E-01	0.87 (0.68-1.12)	2.84E-01	10.36	3.41E-01
2			0	0						

Supplementary Table 6: Genomic annotation of new meningioma risk locus.

SNP	Position	r^2 (rs2686876)	D' (rs2686876)	Gene	Annotation	RegulomeDB	GERP	CADD
rs1045502	252818	0.97	0.99	<i>PSMD13</i>	3'-UTR	5	4.28	10.55
rs1045577	252942	0.97	0.99	<i>PSMD13</i>	3'-UTR	6	-0.66	5.03
rs2686878	253958	0.97	0.99			4	0.21	1.37
rs143265326	256110	0.96	0.99			No data	-1.28	0.69
rs532483	257030	1.00	1.00			5	1.34	5.64
rs939924	257308	0.99	1.00			4	-1.03	10.75
rs2734242	258646	1.00	1.00			No data	0.47	1.12
rs200015280	258741	1.00	1.00			No data	0.50	1.94
rs2686876	258909	1.00	1.00			6	0.14	1.34
rs151035694	262106	0.97	0.99			6	NA	0.74

Data are shown for the sentinel SNP (in bold) and its proxies ($r^2 > 0.8$ in 1000 Genomes EUR Phase 1 data) with RegulomeDB scores reflecting evidence of histone marks, DNase hypersensitivity sites or transcription factor occupancy. Also indicated are genomic evolutionary rate profiling (GERP) scores and combined annotation dependent depletion (CADD) scores. RegulomeDB scores: 4: TF binding + DNase peak; 5: TF binding or DNase peak; 6: other binding or DNase peak.

Supplementary Table 7: eQTL results for rs2686876, using data on 47 tissues from GTEx. Shown are all genes within 1Mb of rs2686876

Tissue	Number of samples	<i>ANOG</i>	<i>AP2A2</i>	<i>B4GALNT4</i>	<i>BET1L</i>	<i>CD151</i>	<i>CDHR5</i>	<i>CEND1</i>	<i>CHID1</i>	<i>CICP23</i>	<i>CRACR2B</i>	<i>DEAF1</i>	<i>DRD4</i>	<i>EPS8L2</i>	<i>GATD1</i>	<i>HRAS</i>
Adipose Subcutaneous	385	3.50E-01	9.85E-01	3.78E-03	6.60E-01	8.67E-01	2.74E-02	1.34E-01	4.13E-01	NA	2.68E-01	3.80E-02	4.68E-01	4.70E-01	6.95E-01	5.63E-01
Adipose Visceral Omentum	313	8.25E-01	6.48E-01	8.80E-02	3.20E-01	6.79E-03	3.37E-01	2.98E-01	8.48E-01	NA	2.53E-01	6.27E-01	4.28E-01	4.12E-01	3.18E-01	1.56E-01
Adrenal Gland	175	7.19E-01	6.13E-01	9.75E-02	7.95E-01	7.63E-01	1.02E-01	4.17E-01	4.85E-01	NA	4.34E-01	5.20E-01	4.72E-03	6.01E-03	4.16E-01	2.66E-01
Artery Aorta	267	7.01E-01	9.30E-01	1.71E-01	7.21E-01	5.04E-01	4.17E-01	6.09E-01	2.64E-01	NA	7.14E-01	5.05E-01	7.89E-01	8.60E-01	5.19E-01	1.48E-01
Artery Coronary	152	2.60E-01	8.05E-01	6.68E-01	4.49E-04	3.45E-01	4.00E-02	6.88E-01	8.85E-01	NA	1.19E-01	7.01E-01	5.25E-01	4.58E-01	2.08E-01	8.32E-01
Artery Tibial	388	9.52E-02	7.45E-01	7.38E-01	6.48E-02	8.30E-02	3.37E-01	2.16E-01	9.47E-01	NA	2.28E-01	8.79E-01	4.02E-01	6.95E-01	3.40E-02	1.87E-01
Brain Amygdala	88	9.15E-01	1.80E-02	5.72E-03	2.50E-02	7.19E-01	6.27E-01	8.36E-01	3.95E-01	NA	4.84E-01	1.69E-01	3.58E-01	4.61E-01	9.98E-01	8.80E-01
Brain Anterior Cingulate Cortex BA24	109	8.07E-01	3.79E-01	7.98E-01	1.40E-03	2.66E-01	6.74E-01	4.86E-01	8.48E-01	NA	5.99E-01	7.69E-01	8.45E-01	1.55E-03	1.68E-01	1.76E-01
Brain Caudate Basal Ganglia	144	8.30E-07	6.56E-01	7.93E-01	2.58E-02	7.60E-01	2.92E-02	6.96E-01	2.21E-01	NA	7.47E-01	5.62E-02	4.40E-01	8.90E-01	2.22E-01	6.25E-01
Brain Cerebellar Hemisphere	125	4.91E-01	2.22E-01	5.90E-01	7.87E-01	3.13E-01	3.04E-01	7.45E-01	4.16E-01	NA	7.50E-01	3.66E-02	3.39E-01	4.79E-01	4.14E-01	7.63E-01
Brain Cortex	136	3.70E-01	3.30E-01	2.92E-01	6.08E-03	3.59E-01	2.51E-01	1.33E-01	4.35E-01	NA	4.28E-01	1.46E-01	8.29E-01	2.37E-01	3.48E-01	8.32E-01
Brain Frontal Cortex BA9	118	3.08E-01	1.84E-01	6.01E-01	1.01E-02	6.31E-01	3.49E-01	9.43E-02	6.83E-01	NA	5.73E-01	2.29E-02	7.99E-01	3.25E-01	7.13E-01	3.62E-01
Brain Hippocampus	111	6.86E-01	9.82E-01	7.21E-01	5.96E-01	6.70E-01	9.54E-02	1.78E-01	6.25E-01	NA	8.54E-01	4.77E-02	6.77E-01	8.44E-01	9.69E-01	8.58E-01
Brain Hypothalamus	108	9.41E-01	3.19E-01	4.61E-01	7.19E-01	6.25E-01	6.00E-01	4.70E-01	1.31E-01	NA	7.11E-01	8.02E-01	8.20E-01	6.89E-01	7.33E-01	1.72E-01
Brain Nucleus Accumbens Basal Ganglia	130	3.68E-01	1.02E-01	9.10E-01	1.12E-02	2.25E-01	2.96E-01	6.45E-01	7.46E-02	NA	8.10E-01	8.69E-01	7.69E-01	9.92E-01	1.76E-01	7.15E-01
Brain Putamen Basal Ganglia	111	2.58E-06	7.04E-01	2.42E-01	6.22E-03	6.89E-01	8.40E-01	1.50E-01	3.59E-01	NA	2.18E-01	8.90E-01	3.58E-01	5.16E-01	5.01E-01	9.46E-01
Brain Spinal Cord Cervical c-1	83	7.59E-01	7.22E-01	1.40E-01	3.46E-01	8.90E-01	5.30E-01	2.83E-02	9.65E-01	NA	1.79E-01	1.63E-01	8.32E-01	6.08E-01	5.74E-01	8.62E-02
Brain Substantia Nigra	80	1.09E-01	6.03E-02	6.10E-01	6.93E-01	6.59E-01	1.80E-01	7.28E-01	5.23E-01	NA	9.86E-01	4.89E-01	7.87E-01	3.20E-01	2.82E-01	5.15E-01
Breast Mammary Tissue	251	6.74E-01	7.99E-01	1.74E-01	2.22E-01	5.09E-01	3.51E-01	4.70E-01	6.30E-01	NA	6.67E-01	4.37E-02	9.58E-01	3.47E-02	9.60E-01	9.77E-01
Cells EBV Transformed Lymphocytes	117	8.98E-01	5.79E-01	6.23E-01	7.39E-01	9.05E-01	5.82E-01	5.19E-01	2.49E-01	NA	9.27E-01	2.69E-01	6.14E-01	8.20E-01	1.73E-01	8.56E-01
Cells Transformed Fibroblasts	300	9.44E-01	5.76E-01	3.06E-01	1.53E-01	1.01E-02	4.63E-01	6.79E-01	5.79E-01	NA	3.01E-02	4.15E-01	7.19E-01	9.63E-02	1.23E-01	1.40E-02
Colon Sigmoid	203	3.78E-01	2.05E-01	5.90E-01	2.71E-01	9.05E-01	8.04E-01	2.56E-01	8.19E-01	NA	7.34E-01	2.77E-01	7.82E-01	1.80E-01	6.40E-02	5.10E-01
Colon Transverse	246	1.71E-01	5.35E-01	9.93E-01	1.05E-01	6.30E-01	8.72E-01	9.86E-03	9.47E-01	NA	3.78E-01	5.57E-02	5.54E-01	2.02E-01	5.74E-01	6.59E-01
Esophagus Gastroesophageal Junction	213	8.63E-02	4.48E-01	1.09E-01	3.18E-01	6.02E-01	1.01E-01	2.32E-01	4.67E-01	NA	8.57E-01	6.63E-01	8.60E-01	8.88E-01	8.69E-01	3.77E-01
Esophagus Mucosa	358	6.10E-01	1.71E-01	5.43E-01	2.95E-02	8.78E-01	2.95E-01	1.78E-02	6.17E-02	NA	7.87E-01	4.73E-01	4.55E-02	3.84E-01	9.54E-01	5.20E-01
Esophagus Muscularis	335	5.42E-01	8.79E-01	7.83E-01	9.03E-06	6.34E-01	7.99E-01	6.51E-01	7.02E-01	NA	7.10E-01	1.69E-01	3.56E-01	6.55E-02	3.13E-01	4.96E-01
Heart Atrial Appendage	264	7.10E-03	7.67E-01	3.35E-01	2.04E-02	1.88E-01	7.17E-01	5.57E-01	8.28E-01	NA	8.85E-01	2.99E-01	3.75E-02	7.90E-01	2.92E-01	6.43E-02
Heart Left Ventricle	272	6.89E-02	4.73E-01	1.66E-01	2.69E-01	6.09E-01	NA	2.96E-01	7.85E-01	NA	8.26E-01	6.22E-01	5.28E-01	7.27E-01	1.09E-01	5.33E-01
Liver	153	6.84E-01	6.41E-01	5.09E-01	7.49E-01	5.18E-01	1.88E-01	3.09E-01	2.33E-01	NA	5.99E-01	2.61E-01	2.37E-01	4.23E-02	1.82E-01	7.83E-01
Lung	383	2.71E-01	7.07E-02	3.15E-01	7.30E-01	2.27E-01	4.05E-01	1.18E-01	9.17E-01	NA	8.62E-01	1.71E-01	1.25E-01	9.17E-01	6.46E-01	1.45E-01
Minor Salivary Gland	85	6.40E-01	4.78E-01	2.54E-01	7.00E-01	9.84E-01	8.20E-01	4.36E-01	4.85E-01	NA	5.48E-01	5.16E-02	6.88E-01	3.93E-01	2.98E-01	2.13E-01
Muscle Skeletal	491	7.18E-01	2.52E-01	9.85E-01	2.64E-03	4.15E-01	1.85E-01	9.11E-01	5.17E-01	NA	9.47E-01	1.58E-01	7.41E-01	7.78E-01	7.08E-01	4.36E-01
Nerve Tibial	361	9.54E-01	4.68E-01	1.54E-01	3.48E-01	9.75E-01	6.13E-01	3.77E-01	6.32E-01	NA	6.21E-01	6.64E-01	9.48E-01	9.86E-01	6.91E-01	9.96E-02
Ovary	122	3.07E-01	2.67E-01	3.07E-01	6.38E-02	2.81E-01	2.49E-01	9.81E-01	5.85E-01	NA	3.06E-01	7.47E-01	4.28E-01	5.24E-01	9.56E-01	3.85E-01
Pancreas	220	2.33E-01	1.72E-01	5.21E-01	1.49E-01	2.44E-01	4.04E-01	5.93E-01	3.63E-02	NA	7.30E-01	6.80E-01	7.41E-01	3.32E-01	8.02E-01	9.29E-02
Pituitary	157	5.55E-02	6.32E-01	1.38E-01	3.78E-01	3.05E-01	9.20E-01	4.56E-01	3.56E-01	NA	5.55E-01	7.13E-01	8.36E-01	2.54E-02	5.65E-01	5.80E-02
Prostate	132	7.29E-03	4.76E-01	1.65E-01	9.96E-01	6.58E-01	7.04E-01	8.42E-01	8.82E-01	NA	8.16E-01	3.47E-01	1.96E-01	7.05E-01	5.24E-01	4.41E-01
Skin not Sun Exposed Suprapubic	335	8.75E-01	5.86E-02	4.66E-01	6.27E-01	1.18E-01	6.47E-01	3.16E-02	5.69E-01	NA	1.62E-01	7.06E-01	1.01E-01	5.77E-01	6.86E-01	5.41E-01
Skin Sun Exposed Lower Leg	414	9.81E-01	6.58E-01	2.19E-01	3.08E-01	6.43E-01	7.01E-01	1.13E-01	5.31E-01	NA	5.98E-01	1.64E-01	1.64E-01	7.37E-01	8.42E-01	1.49E-01
Small Intestine Terminal Ileum	122	3.91E-01	5.06E-01	2.61E-01	4.57E-01	1.73E-01	8.81E-02	5.23E-01	2.82E-03	NA	5.72E-01	1.40E-01	5.99E-02	7.69E-03	7.79E-02	6.69E-01

Spleen	146	7.92E-02	1.02E-01	9.69E-01	8.44E-01	1.55E-01	1.05E-01	6.32E-02	5.25E-02	NA	1.11E-01	2.89E-01	2.09E-01	8.68E-02	8.31E-01	2.19E-01
Stomach	237	1.15E-01	2.98E-02	4.30E-01	8.36E-01	3.20E-01	6.77E-01	1.15E-01	8.85E-01	NA	7.43E-01	3.73E-01	3.28E-01	8.19E-01	9.29E-01	7.34E-01
Testis	225	9.63E-01	2.04E-01	8.60E-01	5.14E-01	8.21E-01	4.38E-02	2.26E-01	2.36E-01	7.23E-03	3.69E-01	6.63E-01	7.93E-01	4.86E-02	1.52E-01	8.36E-01
Thyroid	399	8.48E-01	4.41E-01	6.07E-02	9.65E-01	6.09E-01	5.54E-01	7.79E-01	8.32E-01	NA	1.42E-01	1.86E-01	4.47E-01	4.47E-01	4.47E-01	4.66E-01
Uterus	101	8.83E-01	5.76E-01	6.58E-01	8.50E-01	8.97E-01	8.97E-01	2.30E-01	1.04E-01	NA	9.54E-01	1.38E-01	3.31E-01	1.33E-01	4.96E-01	8.70E-01
Vagina	106	8.69E-01	7.64E-01	5.73E-01	4.73E-01	1.31E-01	1.62E-02	2.58E-01	9.27E-01	NA	1.46E-01	3.17E-01	8.86E-01	9.01E-01	7.18E-02	2.41E-01
Whole Blood	369	8.22E-01	2.82E-01	2.43E-01	1.02E-01	3.26E-01	1.61E-01	8.72E-03	5.85E-01	9.65E-01	3.95E-01	2.72E-01	5.45E-01	1.00E+00	5.81E-01	2.71E-01

Highlighted cells correspond to $P < 2.01 \times 10^{-5}$, corresponding to $P < 0.05$ with a Bonferroni correction for 2,491 tests (53 genes across 47 tissues).

Cells marked NA if data not available

7.46E-01	8.63E-01	3.53E-01	6.01E-01	7.58E-02	6.09E-01	7.40E-01	1.28E-01	NA	8.22E-01	5.89E-01	1.33E-01	NA	6.96E-01	3.95E-01	NA	6.39E-01	9.84E-01	5.29E-01	9.36E-01	4.18E-01
3.54E-01	1.58E-01	9.56E-01	NA	8.67E-01	3.66E-02	2.75E-01	6.17E-01	NA	5.33E-01	5.90E-01	6.05E-01	7.55E-01	9.71E-02	6.27E-01	NA	7.57E-01	4.99E-01	6.83E-01	6.85E-01	7.51E-01
4.88E-01	2.39E-01	8.08E-01	7.54E-02	5.67E-01	4.02E-04	4.20E-01	8.51E-01	NA	9.66E-01	6.66E-02	9.51E-01	7.56E-01	8.65E-01	9.70E-02	9.35E-02	6.73E-01	3.82E-01	2.04E-01	5.38E-01	6.66E-01
5.05E-01	1.65E-01	8.05E-02	2.71E-01	3.77E-01	2.72E-01	3.53E-01	7.89E-01	NA	6.46E-01	3.97E-01	NA	NA	6.88E-01	5.26E-01	NA	1.78E-02	7.60E-01	4.94E-01	4.06E-02	8.85E-01
6.86E-01	2.86E-01	8.19E-01	NA	8.41E-01	1.17E-01	2.41E-01	3.13E-01	NA	2.11E-01	4.62E-01	2.36E-01	3.30E-01	3.37E-01	3.31E-01	NA	9.88E-02	1.14E-01	8.58E-01	9.29E-01	5.03E-01
1.29E-01	1.94E-01	4.13E-01	NA	4.19E-01	5.90E-01	6.87E-01	8.64E-01	7.82E-01	9.85E-01	7.00E-02	7.94E-02	8.65E-01	2.56E-02	4.12E-02	NA	4.58E-01	5.27E-01	3.59E-01	9.77E-01	5.82E-01
5.57E-01	4.26E-02	6.82E-01	2.05E-01	2.08E-01	5.49E-01	8.83E-01	6.41E-01	NA	8.90E-01	NA	NA	NA	2.97E-01	3.10E-01	NA	6.99E-01	6.04E-01	9.39E-01	6.55E-01	8.72E-01

<i>POLR2L</i>	<i>PSMD13</i>	<i>PTDSS2</i>	<i>RASSF7</i>	<i>RIC8A</i>	<i>RN7SL838P</i>	<i>RNH1</i>	<i>RPLP2</i>	<i>SCGB1C1</i>	<i>SCT</i>	<i>SIGIRR</i>	<i>SIRT3</i>	<i>SLC25A22</i>	<i>SNORA52</i>	<i>TALDO1</i>	<i>TMEM80</i>	<i>TSPAN4</i>
9.39E-01	1.11E-01	8.58E-01	5.91E-02	3.65E-03	NA	3.54E-03	5.56E-01	NA	NA	4.31E-03	6.76E-01	1.51E-01	6.41E-01	1.52E-01	9.38E-01	6.75E-01
6.86E-01	3.25E-01	3.49E-01	6.99E-01	1.80E-02	NA	9.50E-01	1.83E-01	NA	NA	1.28E-01	4.07E-01	3.33E-01	1.96E-01	1.44E-02	9.54E-01	6.39E-01
3.83E-01	6.61E-01	5.78E-01	2.61E-02	1.28E-02	NA	1.48E-01	5.94E-01	NA	NA	6.77E-01	2.04E-01	2.63E-02	6.29E-01	7.69E-01	8.58E-01	3.61E-01
7.05E-01	2.81E-01	7.34E-01	3.30E-03	9.00E-01	NA	5.34E-01	8.13E-01	NA	NA	1.20E-01	6.09E-01	1.14E-01	1.98E-01	8.95E-01	8.93E-01	2.13E-01
9.59E-01	3.05E-01	7.84E-01	6.21E-01	7.11E-02	NA	5.57E-02	5.77E-01	NA	NA	3.80E-01	3.36E-01	8.68E-01	1.51E-01	1.74E-01	9.84E-01	3.25E-02
7.89E-01	3.17E-02	2.73E-02	9.90E-02	6.23E-03	NA	8.84E-01	9.76E-01	NA	NA	5.63E-04	6.49E-01	8.15E-01	1.28E-01	4.21E-01	1.87E-01	9.07E-01
6.03E-01	5.33E-02	1.13E-01	4.31E-01	1.09E-03	NA	9.39E-02	2.41E-01	NA	NA	9.36E-01	7.84E-01	2.44E-02	3.92E-01	8.62E-01	2.82E-01	4.97E-02
9.53E-01	1.36E-05	4.97E-02	4.24E-01	8.88E-03	NA	2.00E-02	4.42E-01	NA	7.66E-01	3.63E-02	9.61E-01	3.69E-01	9.92E-01	4.80E-01	4.93E-01	1.16E-02
8.06E-01	2.52E-02	5.02E-01	6.15E-01	2.16E-02	NA	2.80E-01	1.83E-01	NA	8.03E-01	4.16E-01	3.62E-01	5.52E-01	8.25E-01	8.69E-01	9.18E-01	4.21E-02
1.47E-01	1.75E-01	2.25E-01	7.88E-01	1.62E-02	NA	5.96E-01	5.53E-01	1.91E-01	4.08E-01	5.81E-01	1.00E+00	7.93E-01	7.41E-01	4.79E-01	4.11E-01	7.03E-01
1.00E+00	5.16E-03	9.62E-01	3.19E-01	1.62E-01	NA	9.96E-01	9.29E-01	NA	NA	3.84E-01	7.82E-01	7.03E-01	3.98E-01	8.65E-01	1.33E-01	2.51E-01
6.91E-01	2.32E-02	1.23E-01	9.68E-01	5.08E-01	NA	6.64E-01	2.19E-01	NA	NA	1.60E-01	5.19E-01	3.62E-01	5.76E-01	1.53E-01	4.53E-01	1.97E-01
6.13E-01	5.10E-03	6.57E-01	8.80E-01	8.03E-03	NA	8.53E-01	3.84E-01	NA	2.96E-01	8.68E-02	7.52E-02	8.53E-01	6.25E-01	9.53E-01	6.56E-01	5.66E-01
9.22E-01	7.06E-03	4.75E-01	4.35E-01	3.19E-01	NA	2.53E-01	3.45E-01	NA	7.27E-01	2.62E-01	3.46E-01	2.33E-01	1.34E-01	5.28E-01	4.97E-01	5.45E-01
4.89E-01	5.78E-05	9.27E-01	9.47E-01	1.92E-04	5.46E-01	3.98E-01	8.93E-01	NA	NA	1.46E-01	6.65E-01	5.70E-01	1.06E-01	2.26E-01	4.78E-01	1.18E-01
1.78E-01	4.22E-03	2.15E-01	7.81E-01	4.13E-01	NA	1.01E-01	4.75E-02	NA	NA	2.20E-01	3.05E-01	4.45E-01	2.97E-01	7.87E-01	2.10E-01	2.15E-02
4.59E-01	1.35E-01	4.15E-01	7.23E-01	4.78E-02	NA	7.84E-01	7.32E-01	NA	8.09E-01	3.07E-01	2.97E-02	2.65E-01	4.98E-01	2.78E-01	7.65E-02	4.57E-01
5.93E-01	9.37E-02	2.08E-01	7.40E-01	2.51E-01	NA	4.80E-01	5.32E-01	NA	NA	9.53E-01	9.25E-01	8.37E-01	8.71E-01	8.07E-01	9.65E-01	6.80E-01
7.13E-01	7.31E-01	1.17E-01	3.38E-01	2.49E-01	3.89E-01	9.93E-01	7.01E-01	NA	NA	6.63E-01	3.82E-01	9.13E-01	9.83E-01	2.73E-01	6.00E-01	8.91E-01
2.31E-01	2.53E-01	5.75E-01	2.32E-02	5.81E-01	NA	8.69E-01	3.61E-01	NA	1.34E-01	7.94E-01	4.84E-01	8.65E-01	1.06E-01	1.36E-01	6.46E-01	9.67E-01
3.56E-01	6.04E-02	2.81E-01	2.20E-02	3.74E-01	NA	4.08E-01	3.61E-01	NA	NA	7.85E-02	9.81E-01	8.31E-01	7.71E-01	1.61E-01	4.81E-01	6.87E-01
1.95E-02	5.83E-01	4.27E-01	5.81E-02	3.05E-04	NA	8.14E-01	1.82E-01	NA	5.97E-01	5.81E-01	4.19E-01	8.02E-01	7.68E-01	9.65E-01	9.54E-01	8.58E-02
3.82E-01	6.31E-01	7.69E-01	9.28E-01	3.25E-01	NA	2.42E-02	3.61E-01	NA	1.15E-01	9.32E-01	9.08E-03	4.16E-01	3.17E-02	7.39E-01	3.32E-01	3.89E-01
7.58E-01	8.28E-02	8.30E-01	1.28E-01	2.62E-01	NA	9.76E-01	7.50E-01	NA	4.15E-01	1.15E-01	8.26E-01	5.67E-01	2.99E-01	6.04E-02	3.53E-01	5.29E-01
5.03E-01	1.25E-01	1.84E-01	8.24E-01	5.72E-02	NA	9.65E-01	1.75E-01	NA	7.85E-01	8.17E-01	4.00E-01	3.47E-01	6.27E-01	3.06E-01	2.87E-01	6.44E-01
7.60E-01	3.93E-01	6.70E-01	4.56E-01	4.14E-02	NA	5.34E-01	4.77E-01	NA	3.14E-01	1.22E-01	9.43E-01	9.16E-01	8.12E-02	8.80E-01	3.87E-01	5.64E-01
6.10E-01	1.87E-01	4.49E-02	4.54E-02	5.58E-03	NA	6.63E-01	2.65E-01	NA	6.86E-01	3.25E-01	1.55E-01	5.75E-01	5.52E-01	5.15E-02	2.66E-01	8.67E-01
2.22E-01	6.56E-01	6.81E-02	4.88E-01	9.40E-02	NA	4.74E-01	3.53E-01	NA	NA	1.92E-01	8.91E-01	8.44E-01	1.37E-01	4.12E-01	8.35E-01	9.43E-01
1.48E-01	5.08E-01	1.23E-01	3.81E-01	1.35E-01	NA	8.31E-01	5.44E-01	NA	2.62E-01	9.75E-01	1.69E-01	6.78E-01	5.38E-01	7.77E-01	4.03E-01	6.38E-01
5.22E-01	6.29E-01	4.33E-01	1.69E-01	1.78E-01	4.66E-02	4.15E-01	1.39E-01	NA	4.39E-02	6.31E-02	3.25E-01	2.88E-02	6.97E-01	5.86E-01	5.22E-01	6.29E-01
7.19E-01	8.28E-01	2.11E-01	6.91E-01	5.18E-01	NA	4.38E-01	7.40E-01	NA	NA	7.70E-01	4.20E-01	5.59E-01	1.20E-02	2.16E-01	1.82E-01	3.76E-03
2.17E-01	6.25E-03	6.70E-02	7.00E-01	2.30E-01	NA	5.71E-01	1.43E-01	NA	8.46E-01	2.31E-01	5.62E-01	9.74E-01	8.95E-01	5.36E-01	9.95E-01	8.90E-01
5.67E-01	4.31E-01	1.24E-02	4.75E-02	8.86E-02	3.55E-01	2.41E-01	6.53E-01	NA	NA	3.29E-02	3.90E-01	1.89E-02	3.40E-02	5.81E-01	6.83E-01	3.49E-01
7.75E-01	7.11E-02	9.79E-01	6.99E-01	5.39E-02	NA	7.46E-01	6.32E-01	NA	9.13E-01	1.89E-01	6.24E-01	2.56E-01	4.88E-01	7.19E-01	8.22E-01	7.24E-01
8.65E-01	6.22E-03	8.16E-01	3.85E-01	9.59E-02	NA	4.00E-01	9.95E-01	5.91E-03	NA	1.54E-04	4.91E-02	6.07E-01	9.50E-01	5.00E-01	1.67E-01	7.43E-01
1.95E-01	2.95E-01	9.26E-01	7.76E-01	6.44E-02	NA	6.66E-02	9.88E-01	NA	1.80E-01	1.93E-01	5.95E-01	2.84E-01	9.97E-01	8.06E-01	1.31E-01	1.95E-01
7.04E-01	2.41E-01	5.55E-01	8.64E-01	2.23E-01	1.07E-01	3.89E-01	5.21E-01	NA	1.24E-02	4.38E-01	1.39E-01	9.86E-01	2.12E-01	3.01E-01	7.85E-01	1.07E-01
5.37E-01	7.85E-03	6.52E-01	9.64E-01	6.34E-01	NA	4.97E-01	2.84E-01	NA	NA	2.12E-01	2.83E-01	6.41E-01	1.94E-01	1.67E-01	9.44E-01	2.15E-02
2.67E-02	3.40E-03	7.79E-01	8.72E-01	2.22E-01	NA	7.37E-02	2.67E-01	NA	NA	1.01E-01	7.69E-01	8.45E-01	9.29E-01	2.51E-02	8.07E-01	8.34E-01
1.79E-01	4.13E-01	8.33E-01	1.28E-01	7.34E-01	9.06E-01	7.23E-01	1.04E-02	NA	1.92E-01	5.03E-01	6.73E-01	9.03E-01	4.80E-01	6.82E-01	1.18E-01	4.80E-01

1.99E-01	2.40E-01	1.11E-01	2.88E-01	3.90E-02	7.89E-01	1.10E-01	2.54E-01	1.52E-01	5.83E-01	3.40E-01	2.97E-01	6.51E-01	9.03E-01	4.19E-01	7.30E-01	7.36E-01
4.17E-01	3.72E-03	4.67E-01	7.96E-01	2.42E-01	NA	5.36E-01	9.06E-01	NA	7.29E-01	9.61E-01	2.64E-01	8.24E-01	2.26E-02	5.54E-01	8.74E-01	8.92E-01
5.07E-01	9.82E-01	2.26E-01	1.73E-01	2.65E-01	7.06E-01	7.58E-01	6.58E-01	7.91E-01	9.89E-01	9.85E-01	1.52E-02	2.89E-01	5.56E-01	4.29E-02	8.81E-01	9.57E-01
9.98E-01	5.81E-01	1.59E-02	2.79E-02	8.56E-01	4.88E-01	8.49E-01	2.59E-01	NA	5.79E-01	3.63E-01	7.37E-01	8.84E-01	2.53E-01	3.58E-01	4.40E-01	2.76E-01
8.69E-02	1.20E-01	4.26E-01	3.82E-01	7.32E-01	NA	6.18E-01	2.03E-01	NA	9.91E-01	7.86E-01	5.20E-01	4.88E-01	2.19E-01	1.33E-01	1.01E-01	9.59E-01
7.88E-01	9.16E-01	2.81E-01	3.46E-01	5.60E-01	NA	8.72E-01	9.23E-02	NA	9.36E-01	6.26E-01	5.28E-01	9.79E-01	9.71E-01	6.35E-01	8.16E-01	1.40E-01
5.30E-01	7.64E-01	5.97E-01	7.74E-01	9.50E-01	NA	2.00E-01	1.20E-01	3.74E-01	NA	1.00E-02	8.71E-01	9.46E-01	9.90E-02	6.41E-01	4.60E-01	9.07E-01

Supplementary Table 8: SMR analysis.

Tissue	Gene	SNP	SNP bp	A1	A2	Freq (A1)	b_{GWAS}	SE_{GWAS}	P_{GWAS}	strongest associated <i>cis</i> -eQTL			SMR analysis			
										b_{eQTL}	SE_{eQTL}	P_{eQTL}	b_{SMR}	SE_{SMR}	P_{SMR}	P_{HEIDI}
Muscle Skeletal	<i>BET1L</i>	rs12226698	213740	T	C	0.041	-0.424	0.109	1.02E-04	0.727	0.082	5.52E-19	-0.584	0.164	3.70E-04	1.59E-05
Adipose Subcutaneous	<i>SIRT3</i>	rs4758633	219538	G	A	0.524	-0.148	0.041	2.68E-04	0.393	0.037	1.14E-25	-0.377	0.109	5.78E-04	1.60E-02
Esophagus Mucosa	<i>SIRT3</i>	rs4758633	219538	G	A	0.524	-0.148	0.041	2.68E-04	0.318	0.036	4.62E-19	-0.464	0.138	7.42E-04	1.60E-02
Skin Sun Exposed Lower leg	<i>SIRT3</i>	rs4758633	219538	G	A	0.524	-0.148	0.041	2.68E-04	0.266	0.036	8.53E-14	-0.557	0.170	1.06E-03	4.04E-02
Artery Aorta	<i>BET1L</i>	rs79902640	202835	G	A	0.041	-0.428	0.110	1.01E-04	0.703	0.119	3.49E-09	-0.608	0.187	1.16E-03	8.34E-01
Lung	<i>SIRT3</i>	rs10902106	220243	C	T	0.537	-0.143	0.040	3.91E-04	0.191	0.025	9.29E-15	-0.753	0.233	1.26E-03	5.47E-02
Cells Transformed fibroblasts	<i>SIRT3</i>	rs4758633	219538	G	A	0.524	-0.148	0.041	2.68E-04	0.230	0.034	1.27E-11	-0.642	0.200	1.33E-03	2.96E-02
Skin Not Sun Exposed Suprapubic	<i>SIRT3</i>	rs4758633	219538	G	A	0.524	-0.148	0.041	2.68E-04	0.267	0.040	2.00E-11	-0.554	0.173	1.37E-03	2.94E-01
Adipose Visceral Omentum	<i>SIRT3</i>	rs4980325	234451	T	G	0.525	-0.142	0.040	4.39E-04	0.245	0.032	3.53E-14	-0.579	0.182	1.43E-03	1.03E-01
Nerve Tibial	<i>SIRT3</i>	rs4980325	234451	T	G	0.525	-0.142	0.040	4.39E-04	0.267	0.037	8.40E-13	-0.533	0.169	1.60E-03	5.80E-02
Heart Atrial Appendage	<i>PSMD13</i>	rs10902106	220243	C	T	0.537	-0.143	0.040	3.91E-04	-0.253	0.042	2.22E-09	0.567	0.186	2.28E-03	1.93E-01
Thyroid	<i>SIRT3</i>	rs4758633	219538	G	A	0.524	-0.148	0.041	2.68E-04	0.193	0.035	3.71E-08	-0.767	0.253	2.38E-03	1.33E-01
Colon Sigmoid	<i>RIC8A</i>	rs4980325	234451	T	G	0.525	-0.142	0.040	4.39E-04	-0.221	0.039	1.51E-08	0.642	0.215	2.82E-03	1.32E-01
Nerve Tibial	<i>LRRC56</i>	rs72841204	519077	T	C	0.180	0.133	0.054	1.41E-02	-0.752	0.066	2.99E-30	-0.176	0.073	1.63E-02	5.49E-01
Testis	<i>RNH1</i>	rs176939	496073	G	C	0.211	0.135	0.052	9.08E-03	-0.385	0.066	4.91E-09	-0.351	0.147	1.72E-02	5.74E-01
Skin Not Sun Exposed Suprapubic	<i>RNH1</i>	rs57195489	522022	T	A	0.184	0.132	0.054	1.42E-02	0.238	0.028	1.31E-17	0.554	0.235	1.85E-02	8.28E-01
Adipose Subcutaneous	<i>LRRC56</i>	rs55983230	521954	A	T	0.185	0.133	0.054	1.27E-02	-0.517	0.078	2.49E-11	-0.258	0.111	1.96E-02	5.47E-01
Adipose Visceral Omentum	<i>LRRC56</i>	rs55983230	521954	A	T	0.185	0.133	0.054	1.27E-02	-0.476	0.074	1.12E-10	-0.280	0.121	2.01E-02	4.55E-01
Skin Sun Exposed Lower leg	<i>RNH1</i>	rs55983230	521954	A	T	0.185	0.133	0.054	1.27E-02	0.153	0.025	1.93E-09	0.875	0.380	2.14E-02	6.96E-01
Esophagus Gastroesophageal Junction	<i>LRRC56</i>	rs55983230	521954	A	T	0.185	0.133	0.054	1.27E-02	-0.504	0.088	8.90E-09	-0.265	0.116	2.23E-02	3.87E-01
Adrenal Gland	<i>RIC8A</i>	rs760058	279214	C	G	0.292	-0.116	0.048	1.65E-02	-0.343	0.057	1.95E-09	0.338	0.152	2.59E-02	6.95E-03
Artery Tibial	<i>AP2A2</i>	rs12798548	1021099	T	C	0.087	0.268	0.113	1.79E-02	-0.334	0.056	2.74E-09	-0.801	0.364	2.78E-02	3.59E-01
Artery Aorta	<i>RIC8A</i>	rs56186913	207698	T	C	0.583	0.094	0.042	2.42E-02	-0.337	0.038	6.33E-19	-0.279	0.128	2.89E-02	1.21E-04
Esophagus Mucosa	<i>PTDSS2</i>	rs61876346	499583	A	G	0.233	0.118	0.051	2.20E-02	-0.270	0.040	1.44E-11	-0.436	0.201	3.01E-02	3.17E-01
Heart Atrial Appendage	<i>SIRT3</i>	rs7934919	224832	C	T	0.205	0.108	0.050	3.06E-02	0.796	0.058	1.50E-43	0.136	0.063	3.26E-02	1.92E-01
Cells Transformed fibroblasts	<i>BET1L</i>	rs3830001	247200	T	G	0.580	-0.091	0.041	2.68E-02	0.301	0.038	2.16E-15	-0.303	0.142	3.30E-02	9.97E-02
Esophagus Muscularis	<i>SIRT3</i>	rs34046183	231087	T	C	0.205	0.107	0.050	3.16E-02	0.899	0.062	6.13E-47	0.119	0.056	3.35E-02	1.21E-02
Esophagus Muscularis	<i>RIC8A</i>	rs35993711	220223	A	G	0.205	0.107	0.050	3.25E-02	0.618	0.042	2.75E-49	0.173	0.082	3.44E-02	4.08E-01
Heart Atrial Appendage	<i>RIC8A</i>	rs34046183	231087	T	C	0.205	0.107	0.050	3.16E-02	0.673	0.066	3.13E-24	0.159	0.076	3.55E-02	4.65E-01
Esophagus Muscularis	<i>PSMD13</i>	rs6598066	243185	G	A	0.731	-0.101	0.046	3.03E-02	-0.293	0.034	9.57E-18	0.344	0.164	3.57E-02	7.49E-02
Heart Left Ventricle	<i>SIRT3</i>	rs7930599	228834	G	C	0.205	0.107	0.050	3.13E-02	0.343	0.038	7.21E-20	0.313	0.149	3.61E-02	1.38E-01
Skin Sun Exposed Lower leg	<i>PSMD13</i>	rs6598066	243185	G	A	0.731	-0.101	0.046	3.03E-02	-0.225	0.027	1.32E-16	0.448	0.214	3.61E-02	2.16E-02
Esophagus Gastroesophageal Junction	<i>RIC8A</i>	rs34046183	231087	T	C	0.205	0.107	0.050	3.16E-02	0.484	0.056	5.20E-18	0.222	0.106	3.70E-02	4.51E-01
Esophagus Gastroesophageal Junction	<i>SIRT3</i>	rs34046183	231087	T	C	0.205	0.107	0.050	3.16E-02	0.650	0.077	2.43E-17	0.165	0.079	3.72E-02	4.09E-03
Heart Left Ventricle	<i>RIC8A</i>	rs12805487	229376	T	C	0.205	0.107	0.050	3.17E-02	0.379	0.046	7.66E-17	0.283	0.136	3.75E-02	5.75E-01
Colon Sigmoid	<i>LRRC56</i>	rs67092853	510980	G	A	0.184	0.118	0.053	2.62E-02	-0.530	0.093	1.12E-08	-0.223	0.108	3.83E-02	3.46E-01
Brain Caudate basal ganglia	<i>SIRT3</i>	rs3216	214421	C	G	0.205	0.109	0.050	3.05E-02	-0.468	0.068	4.57E-12	-0.232	0.112	3.89E-02	4.82E-03
Brain Nucleus accumbens basal ganglia	<i>SIRT3</i>	rs7930599	228834	G	C	0.205	0.107	0.050	3.13E-02	-0.400	0.058	3.91E-12	-0.269	0.131	3.97E-02	4.96E-03
Adipose Visceral Omentum	<i>PSMD13</i>	rs7124022	244964	A	G	0.738	-0.100	0.047	3.37E-02	-0.326	0.041	9.12E-16	0.305	0.149	4.00E-02	4.30E-01
Brain Cerebellar Hemisphere	<i>PSMD13</i>	rs1128322	244197	C	T	0.739	-0.099	0.047	3.40E-02	-0.477	0.059	4.52E-16	0.207	0.101	4.03E-02	4.33E-02

Testis	<i>PSMD13</i>	rs6598063	243672	A	G	0.731	-0.097	0.046	3.71E-02	-0.573	0.051	5.65E-29	0.169	0.082	4.04E-02	1.14E-02
Artery Tibial	<i>SIRT3</i>	rs6598071	219800	C	T	0.729	-0.097	0.046	3.63E-02	0.410	0.046	2.50E-19	-0.236	0.116	4.14E-02	1.23E-01
Adipose Subcutaneous	<i>PSMD13</i>	rs6598070	225466	C	T	0.730	-0.099	0.046	3.23E-02	-0.249	0.038	3.92E-11	0.398	0.195	4.17E-02	9.91E-02
Pancreas	<i>PSMD13</i>	rs7116130	244129	T	C	0.731	-0.097	0.046	3.58E-02	-0.436	0.058	5.04E-14	0.223	0.110	4.32E-02	2.38E-01
Stomach	<i>PSMD13</i>	rs6598071	219800	C	T	0.729	-0.097	0.046	3.63E-02	-0.305	0.041	6.85E-14	0.317	0.157	4.38E-02	9.83E-02
Esophagus Mucosa	<i>RNH1</i>	rs11246164	488877	T	C	0.185	0.110	0.053	3.80E-02	0.310	0.037	3.59E-17	0.355	0.176	4.40E-02	1.36E-01
Artery Aorta	<i>SIRT3</i>	rs6598059	244961	C	G	0.739	-0.099	0.047	3.47E-02	0.399	0.060	2.12E-11	-0.248	0.123	4.40E-02	4.32E-01
Lung	<i>PSMD13</i>	rs1533825	214163	A	G	0.269	0.095	0.046	4.05E-02	0.274	0.027	9.92E-24	0.346	0.172	4.47E-02	3.40E-02
Brain Spinal cord cervical c-1	<i>PSMD13</i>	rs6598071	219800	C	T	0.729	-0.097	0.046	3.63E-02	-0.693	0.100	4.03E-12	0.140	0.070	4.50E-02	3.07E-02
Colon Transverse	<i>SIRT3</i>	rs7481993	237875	T	C	0.731	-0.095	0.046	4.08E-02	0.390	0.041	9.39E-22	-0.244	0.122	4.54E-02	9.50E-02
Whole Blood	<i>RIC8A</i>	rs1533825	214163	A	G	0.269	0.095	0.046	4.05E-02	0.234	0.026	1.48E-19	0.405	0.203	4.57E-02	4.31E-02
Skin Sun Exposed Lower leg	<i>PTDSS2</i>	rs72851107	450987	C	G	0.185	0.111	0.054	3.92E-02	-0.284	0.038	4.84E-14	-0.391	0.196	4.67E-02	1.29E-01
Liver	<i>PSMD13</i>	rs7124022	244964	A	G	0.738	-0.100	0.047	3.37E-02	-0.356	0.063	1.77E-08	0.280	0.141	4.69E-02	1.67E-01
Nerve Tibial	<i>RIC8A</i>	rs6421986	221659	G	A	0.729	-0.093	0.046	4.39E-02	-0.416	0.036	8.06E-31	0.223	0.113	4.71E-02	1.01E-02
Brain Nucleus accumbens basal ganglia	<i>PSMD13</i>	rs10400248	247029	T	C	0.730	-0.095	0.047	4.21E-02	-0.751	0.082	3.38E-20	0.126	0.064	4.71E-02	3.53E-01
Brain Cortex	<i>PSMD13</i>	rs10400248	247029	T	C	0.730	-0.095	0.047	4.21E-02	-0.780	0.088	7.01E-19	0.121	0.061	4.75E-02	7.29E-02
Esophagus Mucosa	<i>PSMD13</i>	rs7481993	237875	T	C	0.731	-0.095	0.046	4.08E-02	-0.210	0.027	5.36E-15	0.453	0.229	4.78E-02	1.21E-01
Pituitary	<i>PSMD13</i>	rs10400248	247029	T	C	0.730	-0.095	0.047	4.21E-02	-0.534	0.064	5.94E-17	0.177	0.090	4.82E-02	3.70E-02
Esophagus Gastroesophageal Junction	<i>PSMD13</i>	rs7128044	244115	A	G	0.731	-0.097	0.046	3.71E-02	-0.233	0.040	5.64E-09	0.415	0.212	4.96E-02	3.02E-01
Lung	<i>LRRCS6</i>	rs55768561	450763	G	T	0.185	0.110	0.054	4.14E-02	-0.281	0.039	6.13E-13	-0.391	0.199	4.98E-02	1.82E-01
Brain Caudate basal ganglia	<i>PSMD13</i>	rs511744	219089	C	T	0.702	-0.090	0.045	4.55E-02	-0.660	0.068	3.67E-22	0.136	0.069	5.02E-02	3.11E-01
Artery Tibial	<i>PSMD13</i>	rs1045288	237087	G	A	0.732	-0.094	0.046	4.24E-02	-0.187	0.026	6.00E-13	0.504	0.258	5.08E-02	2.56E-02
Artery Aorta	<i>PSMD13</i>	rs10400248	247029	T	C	0.730	-0.095	0.047	4.21E-02	-0.216	0.031	4.00E-12	0.438	0.224	5.11E-02	3.89E-02
Esophagus Muscularis	<i>LRRCS6</i>	rs55768561	450763	G	T	0.185	0.110	0.054	4.14E-02	-0.518	0.077	2.35E-11	-0.212	0.109	5.11E-02	1.51E-01
Whole Blood	<i>PSMD13</i>	rs3829998	230751	G	A	0.730	-0.092	0.046	4.55E-02	-0.211	0.024	3.93E-18	0.439	0.225	5.13E-02	3.24E-02
Esophagus Mucosa	<i>B4GALNT4</i>	rs34084668	362872	A	G	0.284	-0.143	0.071	4.36E-02	0.397	0.053	1.18E-13	-0.360	0.185	5.15E-02	2.95E-01
Whole Blood	<i>IFITM1</i>	rs6598043	324630	C	G	0.694	-0.148	0.073	4.38E-02	0.200	0.028	9.41E-13	-0.742	0.382	5.24E-02	7.90E-01
Brain Frontal Cortex BA9	<i>RIC8A</i>	rs7395328	242624	A	T	0.731	-0.095	0.046	4.01E-02	-0.455	0.078	5.95E-09	0.209	0.108	5.29E-02	4.42E-02
Adipose Subcutaneous	<i>RIC8A</i>	rs511744	219089	C	T	0.702	-0.090	0.045	4.55E-02	-0.256	0.034	3.52E-14	0.350	0.181	5.32E-02	7.61E-02
Brain Hippocampus	<i>PSMD13</i>	rs10794304	246456	A	G	0.730	-0.093	0.047	4.58E-02	-0.459	0.062	1.41E-13	0.203	0.105	5.38E-02	2.84E-01
Cells Transformed fibroblasts	<i>RIC8A</i>	rs3825075	217140	C	T	0.709	-0.091	0.045	4.36E-02	-0.131	0.021	2.54E-10	0.696	0.362	5.45E-02	6.54E-02
Brain Amygdala	<i>PSMD13</i>	rs10400248	247029	T	C	0.730	-0.095	0.047	4.21E-02	-0.541	0.091	3.42E-09	0.175	0.091	5.46E-02	3.29E-01
Brain Substantia nigra	<i>PSMD13</i>	rs6421986	221659	G	A	0.729	-0.093	0.046	4.39E-02	-0.454	0.071	1.55E-10	0.205	0.106	5.46E-02	5.21E-01
Whole Blood	<i>IFITM2</i>	rs6598043	324630	C	G	0.694	-0.148	0.073	4.38E-02	0.091	0.016	5.02E-09	-1.633	0.857	5.67E-02	3.49E-01
Thyroid	<i>PSMD13</i>	rs12574034	212262	C	T	0.293	0.086	0.045	5.54E-02	0.318	0.026	1.62E-34	0.272	0.144	5.84E-02	4.63E-02
Nerve Tibial	<i>PSMD13</i>	rs3782120	206089	A	G	0.272	0.089	0.046	5.56E-02	0.396	0.033	1.40E-33	0.224	0.118	5.87E-02	2.44E-02
Heart Atrial Appendage	<i>BET1L</i>	rs3782123	205198	A	C	0.726	0.090	0.045	4.67E-02	0.362	0.062	5.18E-09	0.250	0.133	5.97E-02	3.51E-02
Brain Cortex	<i>RIC8A</i>	rs511744	219089	C	T	0.702	-0.090	0.045	4.55E-02	-0.438	0.079	3.03E-08	0.205	0.109	6.00E-02	1.70E-01
Brain Cerebellar Hemisphere	<i>LRRCS6</i>	rs113339519	492034	T	C	0.176	0.108	0.054	4.81E-02	-0.668	0.111	1.52E-09	-0.161	0.086	6.03E-02	1.01E-01
Nerve Tibial	<i>AP2A2</i>	rs67927955	1034755	T	C	0.084	0.224	0.113	4.71E-02	-0.336	0.058	8.17E-09	-0.666	0.355	6.05E-02	4.26E-01
Cells Transformed fibroblasts	<i>LRRCS6</i>	rs146730949	435463	T	A	0.184	0.108	0.055	5.15E-02	-0.417	0.062	1.74E-11	-0.258	0.138	6.14E-02	1.34E-01
Esophagus Mucosa	<i>BET1L</i>	rs12574034	212262	C	T	0.293	0.086	0.045	5.54E-02	-0.371	0.043	9.78E-18	-0.233	0.125	6.15E-02	8.24E-03
Brain Frontal Cortex BA9	<i>PSMD13</i>	rs3782120	206089	A	G	0.272	0.089	0.046	5.56E-02	0.619	0.076	5.77E-16	0.143	0.077	6.25E-02	4.06E-01
Brain Hypothalamus	<i>PSMD13</i>	rs12574034	212262	C	T	0.293	0.086	0.045	5.54E-02	0.488	0.062	3.00E-15	0.177	0.095	6.27E-02	4.26E-01

Skin Not Sun Exposed Suprapubic	<i>PSMD13</i>	rs12574034	212262	C	T	0.293	0.086	0.045	5.54E-02	0.211	0.027	4.00E-15	0.409	0.220	6.27E-02	9.64E-02
Brain Anterior cingulate cortex BA24	<i>PSMD13</i>	rs519592	236811	A	G	0.731	-0.089	0.047	5.64E-02	-0.610	0.072	2.80E-17	0.146	0.079	6.28E-02	3.34E-01
Breast Mammary Tissue	<i>PSMD13</i>	rs1045454	204228	A	G	0.272	0.090	0.046	5.15E-02	0.188	0.033	2.14E-08	0.481	0.261	6.58E-02	5.96E-02
Breast Mammary Tissue	<i>RIC8A</i>	rs3782120	206089	A	G	0.272	0.089	0.046	5.56E-02	0.228	0.038	2.37E-09	0.388	0.213	6.83E-02	6.69E-02
Muscle Skeletal	<i>HRAS</i>	rs4963198	551753	A	G	0.642	-0.123	0.068	7.10E-02	0.145	0.023	6.70E-10	-0.852	0.492	8.31E-02	2.05E-01
Testis	<i>BET1L</i>	rs58692051	207410	T	C	0.272	0.082	0.046	7.77E-02	-0.524	0.059	6.06E-19	-0.156	0.090	8.36E-02	5.53E-02
Colon Transverse	<i>PSMD13</i>	rs6598075	207275	G	C	0.272	0.082	0.046	7.77E-02	0.306	0.041	1.07E-13	0.267	0.156	8.60E-02	1.01E-01
Colon Sigmoid	<i>PSMD13</i>	rs6598075	207275	G	C	0.272	0.082	0.046	7.77E-02	0.319	0.046	2.57E-12	0.257	0.150	8.71E-02	2.32E-01
Minor Salivary Gland	<i>PSMD13</i>	rs58692051	207410	T	C	0.272	0.082	0.046	7.77E-02	0.382	0.069	3.33E-08	0.214	0.127	9.29E-02	5.49E-02
Thyroid	<i>LRRC56</i>	rs45453193	536052	C	G	0.218	0.131	0.077	8.95E-02	-0.328	0.046	9.83E-13	-0.401	0.242	9.85E-02	9.79E-01
Whole Blood	<i>EPS8L2</i>	rs10736901	737969	A	G	0.238	0.129	0.076	9.09E-02	-0.319	0.054	3.29E-09	-0.404	0.249	1.04E-01	6.12E-01
Artery Tibial	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.689	0.046	1.14E-51	0.201	0.126	1.10E-01	9.83E-01
Testis	<i>HRAS</i>	rs12576769	535026	T	C	0.115	0.155	0.096	1.06E-01	0.947	0.093	1.52E-24	0.164	0.103	1.10E-01	3.57E-01
Esophagus Muscularis	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.539	0.042	2.85E-37	0.257	0.161	1.11E-01	9.46E-01
Artery Aorta	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.777	0.062	1.38E-35	0.178	0.112	1.11E-01	8.34E-01
Nerve Tibial	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.542	0.044	2.40E-35	0.256	0.160	1.11E-01	7.07E-01
Adipose Subcutaneous	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.467	0.042	5.14E-29	0.296	0.186	1.12E-01	7.81E-01
Muscle Skeletal	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.479	0.048	7.35E-24	0.289	0.182	1.12E-01	8.82E-01
Cells Transformed fibroblasts	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.505	0.053	3.32E-21	0.274	0.173	1.13E-01	4.29E-01
Adipose Subcutaneous	<i>PKP3</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.584	0.068	6.95E-18	0.237	0.150	1.14E-01	3.61E-01
Adipose Visceral Omentum	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.313	0.036	7.30E-18	0.442	0.280	1.14E-01	9.04E-01
Brain Frontal Cortex BA9	<i>LRRC56</i>	rs112687793	537469	C	T	0.117	0.159	0.097	1.00E-01	-0.694	0.121	8.78E-09	-0.229	0.145	1.14E-01	5.40E-01
Colon Sigmoid	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.602	0.071	2.04E-17	0.230	0.146	1.14E-01	9.98E-01
Brain Cortex	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.557	0.067	1.45E-16	0.249	0.158	1.15E-01	5.65E-01
Esophagus Gastroesophageal Junction	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.462	0.056	1.89E-16	0.300	0.190	1.15E-01	9.98E-01
Heart Left Ventricle	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.292	0.040	4.29E-13	0.475	0.302	1.17E-01	6.25E-01
Breast Mammary Tissue	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.314	0.046	8.34E-12	0.441	0.282	1.18E-01	5.28E-01
Brain Frontal Cortex BA9	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.489	0.072	1.47E-11	0.283	0.181	1.18E-01	4.13E-01
Nerve Tibial	<i>PKP3</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.512	0.076	1.47E-11	0.271	0.173	1.18E-01	7.84E-01
Heart Atrial Appendage	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.328	0.049	3.07E-11	0.422	0.270	1.18E-01	7.06E-01
Brain Hypothalamus	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.720	0.110	5.20E-11	0.192	0.123	1.18E-01	8.22E-01
Brain Caudate basal ganglia	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.515	0.082	2.88E-10	0.269	0.173	1.19E-01	9.92E-01
Colon Sigmoid	<i>HRAS</i>	rs4963176	538532	C	G	0.342	0.106	0.067	1.11E-01	-0.252	0.036	3.73E-12	-0.421	0.271	1.20E-01	1.03E-01
Brain Nucleus accumbens basal ganglia	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.536	0.097	2.89E-08	0.258	0.167	1.23E-01	5.49E-01
Brain Putamen basal ganglia	<i>SIGIRR</i>	rs35828848	403545	T	C	0.202	-0.138	0.086	1.08E-01	-0.521	0.094	2.89E-08	0.266	0.172	1.23E-01	3.41E-01
Brain Putamen basal ganglia	<i>PSMD13</i>	rs1533824	214169	C	T	0.322	0.072	0.046	1.21E-01	0.452	0.067	1.48E-11	0.158	0.105	1.31E-01	6.55E-01
Cells Transformed fibroblasts	<i>PSMD13</i>	rs1533824	214169	C	T	0.322	0.072	0.046	1.21E-01	0.154	0.024	1.16E-10	0.463	0.307	1.32E-01	7.84E-02
Pancreas	<i>TSPAN4</i>	rs10902229	897692	T	C	0.160	-0.140	0.091	1.23E-01	0.579	0.091	2.37E-10	-0.242	0.161	1.34E-01	6.50E-01
Ovary	<i>LRRC56</i>	rs113966858	527759	G	T	0.211	0.118	0.077	1.26E-01	-0.807	0.111	3.73E-13	-0.146	0.098	1.34E-01	7.80E-01
Brain Substantia nigra	<i>TMEM80</i>	rs28575104	643109	G	T	0.589	-0.098	0.065	1.27E-01	-0.894	0.134	2.64E-11	0.110	0.074	1.37E-01	4.67E-01
Artery Coronary	<i>SIGIRR</i>	rs4074794	409815	A	G	0.168	-0.142	0.094	1.29E-01	-0.467	0.073	1.60E-10	0.305	0.207	1.40E-01	6.45E-01
Skin Sun Exposed Lower leg	<i>C11orf35</i>	rs145270051	539826	A	G	0.055	-0.228	0.151	1.32E-01	0.416	0.062	1.54E-11	-0.547	0.372	1.41E-01	3.16E-01
Artery Tibial	<i>HRAS</i>	rs12628	534242	G	A	0.340	0.098	0.066	1.39E-01	-0.248	0.023	1.00E-26	-0.396	0.271	1.43E-01	2.96E-01
Pancreas	<i>IFITM5</i>	rs11600194	287959	A	G	0.386	0.095	0.065	1.43E-01	0.698	0.085	1.52E-16	0.136	0.095	1.50E-01	6.61E-01

Testis	<i>LRRCS6</i>	rs117967265	439699	T	C	0.043	0.222	0.152	1.45E-01	-0.554	0.081	1.08E-11	-0.401	0.281	1.54E-01	6.56E-01
Testis	<i>CDHR5</i>	rs12360820	620927	C	A	0.825	-0.116	0.080	1.47E-01	0.503	0.084	2.39E-09	-0.231	0.164	1.59E-01	1.55E-01
Testis	<i>IFITM3</i>	rs9666598	325386	G	C	0.840	-0.124	0.087	1.53E-01	-0.280	0.045	3.80E-10	0.445	0.319	1.63E-01	8.49E-01
Esophagus Muscularis	<i>HRAS</i>	rs12785860	531224	G	A	0.339	0.094	0.066	1.59E-01	-0.301	0.031	1.30E-22	-0.311	0.223	1.64E-01	2.61E-01
Adrenal Gland	<i>SIGIRR</i>	rs7935145	382480	A	G	0.205	-0.123	0.087	1.56E-01	-0.436	0.074	3.44E-09	0.283	0.205	1.68E-01	9.76E-01
Esophagus Mucosa	<i>SIGIRR</i>	rs7935145	382480	A	G	0.205	-0.123	0.087	1.56E-01	-0.187	0.033	1.23E-08	0.661	0.480	1.69E-01	2.54E-01
Pancreas	<i>NLRP6</i>	rs10902119	288115	C	T	0.393	0.087	0.064	1.77E-01	0.682	0.091	8.65E-14	0.127	0.096	1.84E-01	6.60E-01
Heart Atrial Appendage	<i>LRRCS6</i>	rs12576389	433554	T	C	0.198	0.075	0.055	1.79E-01	-0.474	0.085	2.39E-08	-0.157	0.120	1.92E-01	1.67E-01
Whole Blood	<i>BET1L</i>	rs4980320	198986	C	T	0.461	-0.056	0.043	1.88E-01	0.374	0.040	6.06E-21	-0.151	0.116	1.93E-01	1.45E-01
Artery Aorta	<i>HRAS</i>	rs1870727	539744	G	A	0.347	0.087	0.066	1.93E-01	-0.367	0.040	6.38E-20	-0.236	0.183	1.97E-01	5.03E-01
Artery Aorta	<i>PTDSS2</i>	rs112828724	512899	G	A	0.039	0.219	0.171	2.02E-01	-0.530	0.090	4.08E-09	-0.412	0.331	2.13E-01	2.02E-01
Nerve Tibial	<i>B4GALNT4</i>	rs7481525	378188	C	T	0.406	-0.078	0.063	2.19E-01	-0.265	0.038	2.29E-12	0.294	0.243	2.26E-01	2.34E-01
Thyroid	<i>TSPAN4</i>	rs10492	866920	G	T	0.191	-0.100	0.083	2.27E-01	0.440	0.045	7.24E-23	-0.228	0.190	2.31E-01	8.07E-01
Cells Transformed fibroblasts	<i>TSPAN4</i>	rs10492	866920	G	T	0.191	-0.100	0.083	2.27E-01	0.408	0.054	3.72E-14	-0.246	0.206	2.33E-01	2.43E-01
Lung	<i>TSPAN4</i>	rs10492	866920	G	T	0.191	-0.100	0.083	2.27E-01	0.298	0.046	1.09E-10	-0.337	0.284	2.35E-01	9.60E-01
Skin Not Sun Exposed Suprapubic	<i>TSPAN4</i>	rs10492	866920	G	T	0.191	-0.100	0.083	2.27E-01	0.180	0.032	2.00E-08	-0.559	0.474	2.38E-01	8.66E-01
Brain Caudate basal ganglia	<i>LRRCS6</i>	rs12574052	548603	G	A	0.673	-0.077	0.066	2.49E-01	-0.304	0.053	1.09E-08	0.252	0.223	2.59E-01	9.88E-01
Testis	<i>B4GALNT4</i>	rs11246141	387204	G	A	0.521	0.075	0.065	2.50E-01	-0.306	0.055	2.39E-08	-0.246	0.218	2.60E-01	7.48E-01
Thyroid	<i>C11orf35</i>	rs10736899	579256	A	C	0.063	-0.155	0.139	2.65E-01	0.362	0.049	9.81E-14	-0.429	0.389	2.70E-01	5.98E-01
Skin Not Sun Exposed Suprapubic	<i>C11orf35</i>	rs10736899	579256	A	C	0.063	-0.155	0.139	2.65E-01	0.453	0.078	6.08E-09	-0.343	0.313	2.73E-01	6.62E-01
Breast Mammary Tissue	<i>ATHL1</i>	rs11246057	295808	G	A	0.370	-0.074	0.067	2.71E-01	0.405	0.048	3.43E-17	-0.183	0.168	2.75E-01	2.41E-01
Esophagus Mucosa	<i>C11orf35</i>	rs11246203	590605	G	C	0.063	-0.152	0.138	2.70E-01	0.372	0.054	6.23E-12	-0.409	0.376	2.76E-01	3.05E-01
Pancreas	<i>CHID1</i>	rs12806927	852855	T	C	0.060	0.165	0.149	2.71E-01	-0.936	0.137	7.76E-12	-0.176	0.162	2.77E-01	5.34E-01
Nerve Tibial	<i>TSPAN4</i>	rs4074344	872529	T	C	0.298	0.081	0.074	2.71E-01	-0.243	0.035	5.50E-12	-0.334	0.308	2.77E-01	6.24E-01
Cells Transformed fibroblasts	<i>IFITM2</i>	rs9666295	323222	T	C	0.850	-0.102	0.093	2.76E-01	0.417	0.064	1.04E-10	-0.244	0.228	2.83E-01	3.43E-01
Skin Sun Exposed Lower leg	<i>BET1L</i>	rs1023430	224393	G	A	0.197	-0.054	0.051	2.81E-01	0.332	0.038	4.67E-18	-0.164	0.153	2.85E-01	8.04E-04
Artery Tibial	<i>BET1L</i>	rs1023430	224393	G	A	0.197	-0.054	0.051	2.81E-01	0.277	0.034	6.42E-16	-0.197	0.184	2.85E-01	1.04E-03
Esophagus Muscularis	<i>BET1L</i>	rs1023430	224393	G	A	0.197	-0.054	0.051	2.81E-01	0.295	0.046	1.72E-10	-0.185	0.174	2.88E-01	4.23E-05
Pituitary	<i>BET1L</i>	rs10902108	225256	T	C	0.197	-0.054	0.051	2.86E-01	-0.425	0.056	2.16E-14	0.127	0.120	2.90E-01	7.03E-04
Skin Not Sun Exposed Suprapubic	<i>BET1L</i>	rs10902108	225256	T	C	0.197	-0.054	0.051	2.86E-01	0.288	0.045	2.39E-10	-0.188	0.178	2.93E-01	1.38E-02
Stomach	<i>TMEM80</i>	rs10902182	651768	G	C	0.451	-0.064	0.062	3.01E-01	-0.522	0.061	9.78E-18	0.123	0.120	3.04E-01	9.94E-01
Liver	<i>EPS8L2</i>	rs11246280	707424	T	C	0.519	0.063	0.061	3.01E-01	0.534	0.069	7.79E-15	0.118	0.115	3.05E-01	1.00E+00
Nerve Tibial	<i>HRAS</i>	rs11246177	539080	T	G	0.324	0.067	0.068	3.22E-01	-0.248	0.028	7.34E-19	-0.272	0.277	3.25E-01	8.92E-01
Artery Aorta	<i>EPS8L2</i>	rs28364668	705297	C	G	0.547	0.060	0.061	3.27E-01	-0.465	0.055	1.93E-17	-0.129	0.132	3.30E-01	9.90E-01
Ovary	<i>SIGIRR</i>	rs10902157	394005	C	T	0.558	0.065	0.067	3.31E-01	0.779	0.102	2.09E-14	0.083	0.086	3.35E-01	9.41E-01
Testis	<i>PKP3</i>	rs10902157	394005	C	T	0.558	0.065	0.067	3.31E-01	-0.561	0.085	4.64E-11	-0.115	0.120	3.36E-01	8.44E-01
Nerve Tibial	<i>TALDO1</i>	rs186605450	729806	G	C	0.016	-0.230	0.253	3.65E-01	-0.485	0.088	3.39E-08	0.473	0.529	3.71E-01	8.50E-01
Esophagus Mucosa	<i>RIC8A</i>	rs61876177	199813	G	A	0.137	0.050	0.060	4.05E-01	0.384	0.052	1.79E-13	0.130	0.157	4.08E-01	2.68E-01
Artery Coronary	<i>HRAS</i>	rs12797431	521119	A	G	0.302	0.056	0.069	4.12E-01	-0.325	0.050	9.84E-11	-0.173	0.213	4.16E-01	4.78E-01
Thyroid	<i>ATHL1</i>	rs11246055	291694	G	A	0.685	0.056	0.069	4.16E-01	0.569	0.043	2.20E-40	0.099	0.122	4.17E-01	4.97E-01
Pancreas	<i>ATHL1</i>	rs11246055	291694	G	A	0.685	0.056	0.069	4.16E-01	0.749	0.080	5.66E-21	0.075	0.093	4.18E-01	6.21E-01
Artery Tibial	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.668	0.044	8.92E-52	-0.080	0.101	4.28E-01	2.86E-01
Nerve Tibial	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.610	0.047	3.64E-39	-0.088	0.111	4.28E-01	1.67E-01
Heart Left Ventricle	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.441	0.038	8.77E-32	-0.122	0.154	4.28E-01	3.87E-01

Esophagus Gastroesophageal Junction	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.652	0.061	2.04E-26	-0.082	0.104	4.28E-01	1.51E-01
Brain Cortex	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.509	0.064	1.20E-15	-0.106	0.134	4.29E-01	1.87E-01
Brain Amygdala	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.542	0.081	2.00E-11	-0.099	0.126	4.30E-01	5.54E-01
Brain Putamen basal ganglia	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.602	0.094	1.24E-10	-0.089	0.113	4.31E-01	7.09E-01
Brain Frontal Cortex BA9	<i>ATHL1</i>	rs2242566	295876	T	C	0.338	-0.054	0.068	4.27E-01	0.396	0.069	8.55E-09	-0.136	0.172	4.31E-01	1.71E-01
Pituitary	<i>RIC8A</i>	rs3782116	223119	C	T	0.685	-0.035	0.044	4.31E-01	-0.511	0.075	7.61E-12	0.068	0.086	4.34E-01	4.86E-02
Skin Not Sun Exposed Suprapubic	<i>HRAS</i>	rs7394514	547210	C	T	0.382	0.051	0.065	4.34E-01	-0.133	0.023	1.35E-08	-0.385	0.497	4.38E-01	5.46E-01
Skin Not Sun Exposed Suprapubic	<i>DRD4</i>	rs79820513	558165	G	T	0.086	0.093	0.121	4.42E-01	-0.570	0.081	2.10E-12	-0.163	0.213	4.45E-01	8.94E-01
Esophagus Mucosa	<i>ANO9</i>	rs7481614	438662	G	A	0.676	0.052	0.068	4.45E-01	-0.330	0.040	2.69E-16	-0.157	0.207	4.47E-01	2.51E-01
Adipose Subcutaneous	<i>TMEM80</i>	rs11246262	680647	C	A	0.469	-0.032	0.043	4.59E-01	-0.667	0.041	7.75E-59	0.048	0.064	4.60E-01	9.57E-01
Muscle Skeletal	<i>TMEM80</i>	rs11246262	680647	C	A	0.469	-0.032	0.043	4.59E-01	-0.637	0.040	2.72E-58	0.050	0.067	4.60E-01	9.26E-01
Cells Transformed fibroblasts	<i>TMEM80</i>	rs11246262	680647	C	A	0.469	-0.032	0.043	4.59E-01	-0.571	0.043	8.75E-41	0.056	0.075	4.60E-01	9.49E-01
Breast Mammary Tissue	<i>TMEM80</i>	rs11246262	680647	C	A	0.469	-0.032	0.043	4.59E-01	-0.568	0.048	6.08E-32	0.056	0.076	4.60E-01	8.71E-01
Pancreas	<i>HRAS</i>	rs4963184	524397	C	T	0.299	0.051	0.069	4.57E-01	-0.323	0.055	3.73E-09	-0.158	0.214	4.61E-01	9.01E-01
Vagina	<i>ATHL1</i>	rs12801980	293188	C	T	0.359	-0.050	0.068	4.66E-01	0.563	0.091	7.32E-10	-0.088	0.122	4.69E-01	6.75E-01
Uterus	<i>ATHL1</i>	rs12801980	293188	C	T	0.359	-0.050	0.068	4.66E-01	0.418	0.075	3.01E-08	-0.119	0.164	4.70E-01	2.75E-01
Skin Sun Exposed Lower leg	<i>HRAS</i>	rs111226498	522480	G	A	0.092	0.084	0.116	4.70E-01	-0.261	0.038	1.06E-11	-0.321	0.447	4.73E-01	2.50E-01
Skin Sun Exposed Lower leg	<i>DRD4</i>	rs140942386	583158	A	G	0.059	-0.109	0.153	4.78E-01	-0.367	0.067	4.21E-08	0.296	0.420	4.81E-01	4.84E-01
Thyroid	<i>PKP3</i>	rs4077477	390320	T	C	0.548	0.046	0.066	4.84E-01	-0.230	0.032	6.04E-13	-0.201	0.289	4.86E-01	8.57E-01
Brain Cerebellar Hemisphere	<i>TMEM80</i>	rs6597995	677200	A	G	0.467	-0.030	0.043	4.85E-01	-0.804	0.086	5.84E-21	0.037	0.054	4.86E-01	8.57E-01
Brain Hypothalamus	<i>TMEM80</i>	rs6597995	677200	A	G	0.467	-0.030	0.043	4.85E-01	-0.814	0.105	1.03E-14	0.037	0.053	4.87E-01	4.21E-01
Adipose Visceral Omentum	<i>PIDD</i>	rs6597979	815323	T	G	0.495	-0.043	0.063	4.87E-01	0.286	0.034	2.91E-17	-0.152	0.220	4.89E-01	7.25E-01
Esophagus Gastroesophageal Junction	<i>PIDD</i>	rs6597979	815323	T	G	0.495	-0.043	0.063	4.87E-01	0.269	0.041	6.32E-11	-0.161	0.234	4.89E-01	5.87E-01
Thyroid	<i>TMEM80</i>	rs7118663	684489	T	C	0.468	-0.029	0.043	4.95E-01	-0.653	0.035	9.30E-77	0.045	0.066	4.95E-01	8.24E-01
Testis	<i>TMEM80</i>	rs7118663	684489	T	C	0.468	-0.029	0.043	4.95E-01	-0.870	0.065	8.97E-41	0.034	0.050	4.95E-01	9.39E-01
Cells EBV-transformed lymphocytes	<i>CDHR5</i>	rs35134589	625695	A	G	0.229	0.052	0.076	4.94E-01	0.886	0.147	1.90E-09	0.059	0.086	4.97E-01	7.51E-01
Esophagus Muscularis	<i>TMEM80</i>	rs12291981	681502	G	C	0.492	-0.029	0.043	4.98E-01	-0.750	0.047	3.09E-56	0.039	0.058	4.98E-01	9.43E-01
Skin Not Sun Exposed Suprapubic	<i>TMEM80</i>	rs12291981	681502	G	C	0.492	-0.029	0.043	4.98E-01	-0.666	0.051	5.54E-39	0.044	0.065	4.98E-01	9.50E-01
Esophagus Gastroesophageal Junction	<i>TMEM80</i>	rs12291981	681502	G	C	0.492	-0.029	0.043	4.98E-01	-0.739	0.059	1.89E-35	0.039	0.058	4.98E-01	9.52E-01
Colon Sigmoid	<i>TMEM80</i>	rs12291981	681502	G	C	0.492	-0.029	0.043	4.98E-01	-0.768	0.062	2.07E-35	0.038	0.056	4.98E-01	8.78E-01
Small Intestine Terminal Ileum	<i>TMEM80</i>	rs12291981	681502	G	C	0.492	-0.029	0.043	4.98E-01	-0.746	0.096	1.03E-14	0.039	0.058	4.99E-01	9.60E-01
Vagina	<i>TMEM80</i>	rs12291981	681502	G	C	0.492	-0.029	0.043	4.98E-01	-0.699	0.107	7.49E-11	0.042	0.062	5.00E-01	7.63E-01
Adrenal Gland	<i>PDDC1</i>	rs7948539	775651	A	T	0.483	-0.043	0.064	5.00E-01	0.566	0.061	1.51E-20	-0.076	0.113	5.01E-01	2.32E-01
Pituitary	<i>PDDC1</i>	rs12223324	772701	G	A	0.483	-0.042	0.064	5.05E-01	0.526	0.059	5.52E-19	-0.081	0.121	5.06E-01	3.33E-01
Heart Left Ventricle	<i>CEND1</i>	rs12223324	772701	G	A	0.483	-0.042	0.064	5.05E-01	0.540	0.070	1.02E-14	-0.079	0.118	5.07E-01	3.42E-01
Brain Caudate basal ganglia	<i>ATHL1</i>	rs12286628	297057	C	A	0.305	-0.047	0.071	5.06E-01	0.587	0.066	3.73E-19	-0.080	0.121	5.07E-01	2.53E-01
Brain Anterior cingulate cortex BA24	<i>ATHL1</i>	rs12286628	297057	C	A	0.305	-0.047	0.071	5.06E-01	0.558	0.079	1.42E-12	-0.084	0.127	5.08E-01	5.02E-01
Skin Sun Exposed Lower leg	<i>PDDC1</i>	rs10902219	758446	A	G	0.665	0.031	0.047	5.10E-01	-0.208	0.035	4.07E-09	-0.150	0.228	5.12E-01	9.92E-01
Adrenal Gland	<i>TMEM80</i>	rs11246253	670493	A	T	0.468	-0.028	0.043	5.12E-01	-0.710	0.066	4.65E-27	0.040	0.061	5.13E-01	8.91E-01
Ovary	<i>TMEM80</i>	rs11246253	670493	A	T	0.468	-0.028	0.043	5.12E-01	-0.558	0.074	3.81E-14	0.050	0.077	5.14E-01	8.65E-01
Artery Coronary	<i>PIDD</i>	rs7122416	807149	A	G	0.492	-0.041	0.063	5.13E-01	0.241	0.041	5.53E-09	-0.170	0.262	5.15E-01	7.65E-01
Nerve Tibial	<i>NLRP6</i>	rs11603524	268628	A	G	0.238	-0.032	0.049	5.14E-01	-0.329	0.050	3.35E-11	0.097	0.150	5.16E-01	1.01E-01
Adipose Subcutaneous	<i>NLRP6</i>	rs11602372	266957	T	G	0.239	-0.032	0.049	5.19E-01	-0.283	0.048	5.06E-09	0.111	0.174	5.22E-01	3.53E-01
Esophagus Mucosa	<i>TMEM80</i>	rs6598006	659266	T	C	0.449	-0.040	0.062	5.25E-01	-0.302	0.039	4.15E-15	0.131	0.207	5.26E-01	9.70E-01

Nerve Tibial	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.711	0.041	3.10E-67	0.038	0.061	5.27E-01	9.05E-01
Artery Tibial	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.711	0.044	7.30E-60	0.038	0.061	5.27E-01	9.50E-01
Skin Sun Exposed Lower leg	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.650	0.041	6.43E-57	0.042	0.066	5.27E-01	9.62E-01
Lung	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.472	0.032	3.25E-49	0.058	0.091	5.27E-01	9.73E-01
Heart Left Ventricle	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.655	0.046	8.09E-46	0.042	0.066	5.27E-01	8.55E-01
Artery Aorta	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.599	0.046	7.21E-39	0.046	0.072	5.27E-01	8.84E-01
Heart Atrial Appendage	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.671	0.054	1.65E-35	0.041	0.064	5.27E-01	8.26E-01
Artery Coronary	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.625	0.066	2.32E-21	0.044	0.069	5.28E-01	9.27E-01
Brain Spinal cord cervical c-1	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.861	0.121	1.07E-12	0.032	0.050	5.28E-01	8.21E-01
Pituitary	<i>TMEM80</i>	rs12277188	688091	T	C	0.469	-0.027	0.043	5.27E-01	-0.473	0.068	4.14E-12	0.058	0.092	5.28E-01	8.97E-01
Thyroid	<i>RIC8A</i>	rs11604127	196944	T	C	0.231	-0.032	0.051	5.36E-01	-0.275	0.035	1.92E-15	0.115	0.187	5.37E-01	2.84E-01
Lung	<i>NLRP6</i>	rs58807415	268718	G	A	0.238	-0.030	0.049	5.35E-01	-0.272	0.045	2.02E-09	0.112	0.181	5.37E-01	8.24E-02
Whole Blood	<i>SCGB1C1</i>	rs11604127	196944	T	C	0.231	-0.032	0.051	5.36E-01	0.395	0.062	2.23E-10	-0.080	0.131	5.38E-01	2.37E-01
Thyroid	<i>EPS8L2</i>	rs7107522	703175	G	A	0.159	0.054	0.088	5.38E-01	-0.203	0.029	4.28E-12	-0.267	0.435	5.39E-01	6.10E-01
Brain Caudate basal ganglia	<i>EPS8L2</i>	rs7107522	703175	G	A	0.159	0.054	0.088	5.38E-01	0.609	0.107	1.18E-08	0.089	0.145	5.40E-01	7.79E-01
Skin Not Sun Exposed Suprapubic	<i>RIC8A</i>	rs72865316	247028	A	G	0.214	-0.030	0.049	5.40E-01	-0.287	0.034	2.33E-17	0.106	0.173	5.41E-01	2.26E-01
Heart Atrial Appendage	<i>CEND1</i>	rs7936322	745884	T	C	0.486	-0.039	0.064	5.44E-01	0.511	0.078	4.38E-11	-0.075	0.125	5.46E-01	2.07E-01
Skin Sun Exposed Lower leg	<i>MUC5B</i>	rs2735709	1252708	C	G	0.498	-0.037	0.062	5.44E-01	-0.285	0.049	8.23E-09	0.131	0.217	5.47E-01	9.61E-01
Testis	<i>DRD4</i>	rs11539530	609353	A	G	0.228	0.045	0.075	5.48E-01	-0.400	0.065	5.65E-10	-0.113	0.189	5.50E-01	7.31E-01
Pancreas	<i>EFCAB4A</i>	rs1138714	825110	G	A	0.555	-0.038	0.063	5.50E-01	0.543	0.054	7.27E-24	-0.069	0.116	5.50E-01	8.62E-01
Adipose Visceral Omentum	<i>HRAS</i>	rs12420875	603776	C	T	0.229	0.043	0.075	5.71E-01	-0.225	0.038	2.28E-09	-0.189	0.335	5.72E-01	8.94E-01
Heart Left Ventricle	<i>PKP3</i>	rs11246147	396701	T	C	0.548	0.037	0.066	5.75E-01	-0.555	0.079	1.64E-12	-0.067	0.119	5.76E-01	8.42E-01
Whole Blood	<i>NLRP6</i>	rs521922	254421	G	A	0.273	-0.026	0.047	5.77E-01	-0.180	0.031	9.31E-09	0.146	0.263	5.79E-01	5.41E-02
Heart Left Ventricle	<i>EFCAB4A</i>	rs4963120	825777	T	C	0.553	-0.035	0.063	5.83E-01	0.296	0.048	7.82E-10	-0.117	0.215	5.85E-01	9.18E-01
Whole Blood	<i>EFCAB4A</i>	rs4963120	825777	T	C	0.553	-0.035	0.063	5.83E-01	0.253	0.046	3.49E-08	-0.137	0.251	5.85E-01	9.49E-01
Brain Frontal Cortex BA9	<i>MUC5B</i>	rs4963050	1249536	T	G	0.305	0.037	0.068	5.84E-01	0.832	0.127	4.84E-11	0.045	0.082	5.85E-01	6.68E-01
Brain Cortex	<i>MUC5B</i>	rs4963059	1272858	T	C	0.303	0.037	0.068	5.89E-01	1.060	0.117	1.62E-19	0.035	0.064	5.90E-01	8.49E-01
Skin Not Sun Exposed Suprapubic	<i>PDDC1</i>	rs11606152	767750	T	C	0.724	0.025	0.047	5.91E-01	-0.206	0.038	4.67E-08	-0.124	0.231	5.92E-01	7.53E-01
Esophagus Muscularis	<i>EPS8L2</i>	rs7108216	702097	C	T	0.611	-0.034	0.063	5.95E-01	0.648	0.048	1.98E-41	-0.052	0.097	5.95E-01	9.96E-01
Artery Tibial	<i>EPS8L2</i>	rs7108216	702097	C	T	0.611	-0.034	0.063	5.95E-01	0.452	0.037	1.40E-34	-0.074	0.140	5.95E-01	9.83E-01
Esophagus Gastroesophageal Junction	<i>EPS8L2</i>	rs7108216	702097	C	T	0.611	-0.034	0.063	5.95E-01	0.588	0.066	7.84E-19	-0.057	0.107	5.96E-01	9.77E-01
Colon Sigmoid	<i>EPS8L2</i>	rs7108216	702097	C	T	0.611	-0.034	0.063	5.95E-01	0.430	0.054	1.74E-15	-0.078	0.147	5.96E-01	9.90E-01
Adrenal Gland	<i>EPS8L2</i>	rs7108216	702097	C	T	0.611	-0.034	0.063	5.95E-01	0.527	0.091	7.51E-09	-0.064	0.120	5.97E-01	9.93E-01
Lung	<i>PTDSS2</i>	rs34690033	492677	C	G	0.136	-0.047	0.090	5.97E-01	-0.382	0.058	3.66E-11	0.124	0.236	5.98E-01	1.95E-01
Artery Aorta	<i>RNH1</i>	rs34690033	492677	C	G	0.136	-0.047	0.090	5.97E-01	-0.359	0.062	6.35E-09	0.132	0.251	5.98E-01	3.56E-01
Esophagus Muscularis	<i>B4GALNT4</i>	rs67542097	364795	A	G	0.504	0.035	0.066	5.98E-01	0.344	0.044	4.99E-15	0.101	0.192	5.99E-01	1.41E-01
Heart Left Ventricle	<i>EPS8L2</i>	rs73407148	707152	C	G	0.131	0.050	0.094	5.99E-01	0.948	0.081	9.27E-32	0.052	0.099	5.99E-01	9.66E-01
Esophagus Gastroesophageal Junction	<i>B4GALNT4</i>	rs67542097	364795	A	G	0.504	0.035	0.066	5.98E-01	0.348	0.055	2.68E-10	0.100	0.190	5.99E-01	3.41E-01
Cells EBV-transformed lymphocytes	<i>TMEM80</i>	rs73407148	707152	C	G	0.131	0.050	0.094	5.99E-01	0.748	0.095	2.58E-15	0.066	0.126	6.00E-01	9.64E-01
Heart Atrial Appendage	<i>EPS8L2</i>	rs73407148	707152	C	G	0.131	0.050	0.094	5.99E-01	0.449	0.067	1.42E-11	0.110	0.210	6.00E-01	9.56E-01
Testis	<i>MUC2</i>	rs12225760	1090101	T	C	0.086	0.056	0.110	6.13E-01	-0.552	0.094	3.69E-09	-0.101	0.200	6.14E-01	9.49E-01
Esophagus Muscularis	<i>CEND1</i>	rs6597984	780410	G	T	0.496	-0.032	0.064	6.22E-01	-0.259	0.041	2.36E-10	0.122	0.249	6.23E-01	5.65E-01
Skin Sun Exposed Lower leg	<i>ANO9</i>	rs59379217	439039	A	G	0.612	0.031	0.063	6.25E-01	-0.162	0.027	1.30E-09	-0.191	0.393	6.26E-01	3.08E-01
Artery Tibial	<i>RIC8A</i>	rs3782118	222620	C	T	0.697	-0.021	0.044	6.31E-01	-0.381	0.030	7.03E-36	0.056	0.116	6.32E-01	2.83E-02

Brain Cerebellar Hemisphere	<i>PIDD</i>	rs7484123	805234	A	G	0.503	-0.030	0.063	6.31E-01	0.701	0.070	9.00E-24	-0.043	0.090	6.32E-01	8.51E-01
Nerve Tibial	<i>IFITM5</i>	rs1060819	295527	C	T	0.744	0.034	0.070	6.32E-01	-0.881	0.072	2.17E-34	-0.038	0.080	6.32E-01	4.47E-01
Artery Tibial	<i>PIDD</i>	rs7484123	805234	A	G	0.503	-0.030	0.063	6.31E-01	0.213	0.027	9.07E-16	-0.141	0.295	6.32E-01	8.88E-01
Thyroid	<i>HRAS</i>	rs12421239	545276	T	G	0.223	0.037	0.077	6.31E-01	-0.334	0.037	6.60E-20	-0.111	0.231	6.32E-01	7.86E-01
Whole Blood	<i>IFITM5</i>	rs1060819	295527	C	T	0.744	0.034	0.070	6.32E-01	-0.573	0.069	7.38E-17	-0.059	0.123	6.32E-01	3.56E-01
Artery Coronary	<i>RIC8A</i>	rs3782118	222620	C	T	0.697	-0.021	0.044	6.31E-01	-0.350	0.052	1.20E-11	0.061	0.127	6.32E-01	5.95E-02
Esophagus Gastroesophageal Junction	<i>HRAS</i>	rs12421239	545276	T	G	0.223	0.037	0.077	6.31E-01	-0.315	0.044	5.85E-13	-0.117	0.245	6.32E-01	6.26E-01
Adipose Subcutaneous	<i>HRAS</i>	rs12421239	545276	T	G	0.223	0.037	0.077	6.31E-01	-0.243	0.034	8.17E-13	-0.152	0.318	6.32E-01	5.18E-01
Prostate	<i>ATHL1</i>	rs1060819	295527	C	T	0.744	0.034	0.070	6.32E-01	0.638	0.091	1.96E-12	0.053	0.111	6.32E-01	5.80E-01
Brain Cerebellar Hemisphere	<i>EPS8L2</i>	rs11246277	706310	A	G	0.158	0.042	0.088	6.32E-01	1.024	0.127	7.78E-16	0.041	0.087	6.32E-01	9.57E-01
Colon Sigmoid	<i>SIRT3</i>	rs3782118	222620	C	T	0.697	-0.021	0.044	6.31E-01	0.385	0.066	5.86E-09	-0.055	0.115	6.33E-01	4.48E-02
Muscle Skeletal	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.697	0.044	1.96E-55	0.046	0.100	6.46E-01	2.38E-01
Adipose Subcutaneous	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.914	0.062	2.24E-49	0.035	0.077	6.46E-01	1.67E-01
Esophagus Mucosa	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.597	0.041	5.75E-49	0.054	0.117	6.46E-01	5.26E-01
Skin Sun Exposed Lower leg	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.516	0.037	9.61E-45	0.062	0.136	6.46E-01	1.64E-01
Esophagus Muscularis	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.708	0.053	1.03E-40	0.045	0.099	6.46E-01	2.64E-01
Adipose Visceral Omentum	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.615	0.048	3.85E-38	0.052	0.114	6.46E-01	2.56E-01
Lung	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.615	0.049	3.90E-36	0.052	0.114	6.46E-01	3.80E-01
Colon Transverse	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.692	0.056	7.07E-35	0.047	0.101	6.46E-01	4.06E-01
Breast Mammary Tissue	<i>IFITM5</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	-0.956	0.080	5.61E-33	-0.034	0.073	6.46E-01	4.64E-01
Artery Aorta	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.797	0.068	9.97E-32	0.040	0.088	6.46E-01	2.52E-01
Lung	<i>IFITM5</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	-0.759	0.066	2.53E-30	-0.042	0.092	6.46E-01	5.09E-01
Stomach	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.615	0.058	4.66E-26	0.052	0.114	6.46E-01	3.94E-01
Colon Sigmoid	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.620	0.059	1.56E-25	0.052	0.113	6.46E-01	4.71E-01
Artery Coronary	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.566	0.078	3.36E-13	0.057	0.124	6.46E-01	2.20E-01
Brain Cerebellar Hemisphere	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.655	0.090	3.89E-13	0.049	0.107	6.46E-01	2.24E-01
Adrenal Gland	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.488	0.068	8.53E-13	0.066	0.144	6.46E-01	4.09E-01
Brain Nucleus accumbens basal ganglia	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.512	0.072	1.14E-12	0.063	0.137	6.46E-01	4.15E-01
Whole Blood	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.263	0.040	5.85E-11	0.122	0.267	6.46E-01	6.95E-01
Ovary	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.656	0.100	6.44E-11	0.049	0.107	6.46E-01	5.01E-01
Liver	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.689	0.109	2.52E-10	0.047	0.102	6.46E-01	5.35E-01
Brain Hypothalamus	<i>ATHL1</i>	rs7104019	295670	A	G	0.741	0.032	0.070	6.46E-01	0.538	0.085	2.90E-10	0.060	0.130	6.46E-01	3.81E-01
Adipose Visceral Omentum	<i>RIC8A</i>	rs3782115	223272	G	A	0.698	-0.020	0.045	6.49E-01	-0.269	0.033	9.45E-16	0.075	0.166	6.50E-01	3.00E-02
Testis	<i>ATHL1</i>	rs7924483	297638	A	T	0.740	0.032	0.071	6.54E-01	0.755	0.063	7.04E-33	0.042	0.094	6.55E-01	2.17E-01
Esophagus Muscularis	<i>PIDD</i>	rs11246314	805589	A	G	0.501	-0.028	0.063	6.54E-01	0.239	0.025	3.42E-21	-0.117	0.262	6.55E-01	8.32E-01
Adipose Subcutaneous	<i>IFITM5</i>	rs7924483	297638	A	T	0.740	0.032	0.071	6.54E-01	-0.811	0.077	4.56E-26	-0.039	0.087	6.55E-01	4.82E-01
Breast Mammary Tissue	<i>PIDD</i>	rs11246314	805589	A	G	0.501	-0.028	0.063	6.54E-01	0.395	0.043	4.76E-20	-0.071	0.159	6.55E-01	7.01E-01
Nerve Tibial	<i>PIDD</i>	rs11246314	805589	A	G	0.501	-0.028	0.063	6.54E-01	0.227	0.028	5.60E-16	-0.124	0.277	6.55E-01	7.26E-01
Artery Aorta	<i>IFITM5</i>	rs7924483	297638	A	T	0.740	0.032	0.071	6.54E-01	-0.726	0.093	8.08E-15	-0.044	0.098	6.55E-01	5.84E-01
Minor Salivary Gland	<i>IFITM5</i>	rs7924483	297638	A	T	0.740	0.032	0.071	6.54E-01	-1.209	0.162	8.00E-14	-0.026	0.059	6.55E-01	4.73E-01
Brain Hippocampus	<i>ATHL1</i>	rs7924483	297638	A	T	0.740	0.032	0.071	6.54E-01	0.619	0.095	7.55E-11	0.051	0.114	6.55E-01	2.58E-01
Brain Spinal cord cervical c-1	<i>ATHL1</i>	rs7924483	297638	A	T	0.740	0.032	0.071	6.54E-01	0.478	0.084	1.35E-08	0.066	0.148	6.55E-01	4.81E-01
Artery Aorta	<i>PIDD</i>	rs11246316	805712	G	A	0.503	-0.027	0.063	6.65E-01	0.355	0.033	6.44E-27	-0.077	0.177	6.65E-01	7.06E-01
Spleen	<i>PIDD</i>	rs11246316	805712	G	A	0.503	-0.027	0.063	6.65E-01	0.462	0.057	2.79E-16	-0.059	0.136	6.65E-01	6.99E-01

Esophagus Muscularis	<i>IFITM2</i>	rs1058873	308178	C	T	0.244	0.033	0.078	6.73E-01	-0.258	0.036	7.62E-13	-0.128	0.303	6.74E-01	5.63E-01
Colon Sigmoid	<i>IFITM2</i>	rs1058873	308178	C	T	0.244	0.033	0.078	6.73E-01	-0.311	0.051	7.54E-10	-0.106	0.252	6.74E-01	NA
Artery Tibial	<i>IFITM2</i>	rs1058873	308178	C	T	0.244	0.033	0.078	6.73E-01	-0.216	0.039	3.16E-08	-0.153	0.363	6.74E-01	6.62E-01
Skin Sun Exposed Lower leg	<i>SIGIRR</i>	rs7396263	412867	G	A	0.767	0.031	0.074	6.75E-01	-0.233	0.030	1.71E-14	-0.133	0.316	6.75E-01	3.31E-01
Muscle Skeletal	<i>IRF7</i>	rs11246217	623765	G	A	0.274	0.029	0.070	6.83E-01	0.295	0.046	2.10E-10	0.097	0.239	6.84E-01	2.87E-01
Brain Caudate basal ganglia	<i>CD151</i>	rs6597977	834802	G	A	0.701	-0.028	0.069	6.84E-01	0.564	0.064	1.90E-18	-0.050	0.123	6.85E-01	9.84E-01
Lung	<i>HRAS</i>	rs1870726	539648	A	G	0.223	0.031	0.077	6.90E-01	-0.311	0.034	1.32E-19	-0.099	0.248	6.90E-01	5.95E-01
Colon Transverse	<i>HRAS</i>	rs1870726	539648	A	G	0.223	0.031	0.077	6.90E-01	-0.376	0.054	3.20E-12	-0.082	0.205	6.90E-01	7.95E-01
Esophagus Mucosa	<i>HRAS</i>	rs1870726	539648	A	G	0.223	0.031	0.077	6.90E-01	-0.198	0.029	1.12E-11	-0.155	0.389	6.90E-01	8.79E-01
Stomach	<i>HRAS</i>	rs1870726	539648	A	G	0.223	0.031	0.077	6.90E-01	-0.422	0.062	1.15E-11	-0.073	0.183	6.90E-01	8.19E-01
Brain Putamen basal ganglia	<i>TMEM80</i>	rs10794333	693787	G	A	0.555	-0.017	0.042	6.93E-01	-0.954	0.103	2.59E-20	0.017	0.044	6.93E-01	6.36E-01
Brain Frontal Cortex BA9	<i>TMEM80</i>	rs10794333	693787	G	A	0.555	-0.017	0.042	6.93E-01	-0.789	0.091	3.14E-18	0.021	0.053	6.93E-01	6.45E-01
Esophagus Muscularis	<i>CHID1</i>	rs28439945	855318	C	T	0.749	0.030	0.077	6.95E-01	-0.237	0.038	3.56E-10	-0.127	0.324	6.96E-01	9.23E-01
Lung	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.352	0.028	2.52E-37	-0.069	0.179	7.00E-01	8.72E-01
Thyroid	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.301	0.025	1.48E-32	-0.081	0.209	7.00E-01	8.66E-01
Adipose Subcutaneous	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.375	0.032	1.99E-31	-0.065	0.168	7.00E-01	8.31E-01
Skin Sun Exposed Lower leg	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.266	0.023	1.82E-30	-0.091	0.237	7.00E-01	7.73E-01
Esophagus Mucosa	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.283	0.027	5.42E-25	-0.086	0.223	7.00E-01	7.24E-01
Skin Not Sun Exposed Suprapubic	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.259	0.029	9.76E-20	-0.094	0.243	7.00E-01	8.20E-01
Whole Blood	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.157	0.017	1.53E-19	-0.154	0.401	7.00E-01	9.43E-01
Cells Transformed fibroblasts	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.248	0.034	2.80E-13	-0.098	0.254	7.00E-01	7.39E-01
Muscle Skeletal	<i>CHID1</i>	rs111904243	857345	A	G	0.119	-0.042	0.109	7.00E-01	0.324	0.044	2.22E-13	-0.130	0.338	7.00E-01	9.81E-01
Heart Atrial Appendage	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.272	0.038	1.25E-12	-0.089	0.232	7.00E-01	7.79E-01
Stomach	<i>PIDD</i>	rs6597981	803017	G	A	0.510	-0.024	0.063	7.00E-01	0.211	0.036	5.16E-09	-0.115	0.300	7.01E-01	8.57E-01
Thyroid	<i>IFITM5</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	-0.834	0.067	2.01E-35	-0.032	0.085	7.04E-01	5.10E-01
Skin Not Sun Exposed Suprapubic	<i>ATHL1</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	0.463	0.042	8.57E-29	0.058	0.152	7.04E-01	2.77E-01
Cells Transformed fibroblasts	<i>ATHL1</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	0.304	0.032	1.23E-21	0.088	0.232	7.04E-01	2.77E-01
Small Intestine Terminal Ileum	<i>IFITM5</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	-1.124	0.128	1.38E-18	-0.024	0.063	7.04E-01	6.73E-01
Spleen	<i>IFITM5</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	-0.997	0.119	4.26E-17	-0.027	0.071	7.04E-01	5.54E-01
Artery Coronary	<i>IFITM5</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	-0.987	0.119	1.46E-16	-0.027	0.072	7.04E-01	5.82E-01
Small Intestine Terminal Ileum	<i>ATHL1</i>	rs7110174	296203	G	A	0.732	0.027	0.071	7.04E-01	0.404	0.065	5.59E-10	0.066	0.175	7.04E-01	7.87E-01
Heart Atrial Appendage	<i>ATHL1</i>	rs2242565	295343	A	G	0.741	0.026	0.070	7.08E-01	0.492	0.049	4.10E-24	0.053	0.142	7.09E-01	2.77E-01
Spleen	<i>ATHL1</i>	rs2242565	295343	A	G	0.741	0.026	0.070	7.08E-01	0.644	0.093	3.80E-12	0.040	0.108	7.09E-01	4.40E-01
Skin Not Sun Exposed Suprapubic	<i>ANO9</i>	rs7394572	432436	A	G	0.604	0.023	0.063	7.11E-01	-0.205	0.032	7.91E-11	-0.113	0.307	7.12E-01	4.93E-01
Minor Salivary Gland	<i>TMEM80</i>	rs12287651	676668	G	C	0.550	-0.015	0.041	7.14E-01	-0.572	0.087	5.06E-11	0.026	0.072	7.14E-01	4.25E-01
Thyroid	<i>RNH1</i>	rs1044707	491334	C	A	0.131	-0.033	0.091	7.15E-01	-0.287	0.044	7.01E-11	0.116	0.318	7.15E-01	7.95E-01
Nerve Tibial	<i>RPLP2</i>	rs7479101	802115	G	A	0.672	-0.024	0.066	7.19E-01	0.155	0.020	2.44E-14	-0.154	0.427	7.19E-01	4.44E-01
Adipose Subcutaneous	<i>RPLP2</i>	rs7479101	802115	G	A	0.672	-0.024	0.066	7.19E-01	0.139	0.023	1.18E-09	-0.172	0.480	7.19E-01	7.61E-01
Cells Transformed fibroblasts	<i>HRAS</i>	rs79808876	465763	A	C	0.130	-0.031	0.091	7.32E-01	-0.221	0.036	1.02E-09	0.141	0.412	7.32E-01	4.07E-01
Adipose Visceral Omentum	<i>PTDSS2</i>	rs79808876	465763	A	C	0.130	-0.031	0.091	7.32E-01	-0.347	0.057	1.48E-09	0.090	0.262	7.32E-01	6.49E-01
Adipose Subcutaneous	<i>RNH1</i>	rs79808876	465763	A	C	0.130	-0.031	0.091	7.32E-01	-0.232	0.040	4.61E-09	0.134	0.392	7.32E-01	8.47E-01
Brain Anterior cingulate cortex BA24	<i>TMEM80</i>	rs4963169	672934	G	A	0.550	-0.014	0.041	7.36E-01	-0.827	0.096	7.61E-18	0.017	0.050	7.36E-01	6.86E-01
Brain Caudate basal ganglia	<i>TMEM80</i>	rs4963169	672934	G	A	0.550	-0.014	0.041	7.36E-01	-0.747	0.088	2.54E-17	0.019	0.055	7.36E-01	6.08E-01
Brain Amygdala	<i>TMEM80</i>	rs4963169	672934	G	A	0.550	-0.014	0.041	7.36E-01	-0.820	0.110	7.06E-14	0.017	0.050	7.36E-01	2.86E-01

Lung	<i>RIC8A</i>	rs72878027	205021	G	C	0.220	-0.017	0.050	7.36E-01	-0.279	0.030	3.56E-20	0.060	0.180	7.36E-01	9.37E-03
Skin Sun Exposed Lower leg	<i>CD151</i>	rs72847212	834389	C	T	0.212	0.026	0.078	7.40E-01	-0.343	0.031	2.12E-28	-0.076	0.228	7.40E-01	1.00E+00
Skin Not Sun Exposed Suprapubic	<i>CD151</i>	rs72847212	834389	C	T	0.212	0.026	0.078	7.40E-01	-0.302	0.034	9.75E-19	-0.086	0.260	7.40E-01	9.99E-01
Adipose Subcutaneous	<i>CD151</i>	rs72847212	834389	C	T	0.212	0.026	0.078	7.40E-01	-0.228	0.026	5.55E-18	-0.114	0.344	7.40E-01	9.95E-01
Esophagus Mucosa	<i>LRRC56</i>	rs7131513	500278	T	C	0.300	0.023	0.070	7.42E-01	-0.253	0.041	8.63E-10	-0.091	0.278	7.43E-01	1.82E-01
Stomach	<i>RNH1</i>	rs35811812	498442	A	G	0.127	-0.029	0.091	7.52E-01	-0.334	0.059	1.16E-08	0.087	0.274	7.52E-01	5.55E-01
Brain Cerebellar Hemisphere	<i>RNH1</i>	rs3868122	493068	G	A	0.480	-0.021	0.067	7.55E-01	-0.496	0.077	1.43E-10	0.042	0.134	7.55E-01	7.12E-01
Pancreas	<i>IRF7</i>	rs1061502	614318	C	T	0.273	0.022	0.070	7.56E-01	0.451	0.066	8.23E-12	0.048	0.155	7.56E-01	4.62E-01
Esophagus Muscularis	<i>TSPAN4</i>	rs12577104	843927	G	A	0.818	-0.027	0.088	7.61E-01	-0.305	0.042	2.97E-13	0.088	0.289	7.61E-01	9.61E-01
Artery Tibial	<i>TSPAN4</i>	rs12577104	843927	G	A	0.818	-0.027	0.088	7.61E-01	-0.227	0.033	5.31E-12	0.118	0.388	7.61E-01	9.26E-01
Whole Blood	<i>TSPAN4</i>	rs12577104	843927	G	A	0.818	-0.027	0.088	7.61E-01	-0.304	0.047	6.90E-11	0.088	0.290	7.61E-01	9.98E-01
Heart Left Ventricle	<i>TSPAN4</i>	rs12577104	843927	G	A	0.818	-0.027	0.088	7.61E-01	-0.219	0.036	7.55E-10	0.123	0.403	7.61E-01	9.57E-01
Artery Tibial	<i>RPLP2</i>	rs28710291	805302	A	G	0.677	-0.019	0.066	7.70E-01	0.151	0.020	7.63E-14	-0.128	0.439	7.70E-01	5.55E-01
Esophagus Mucosa	<i>RPLP2</i>	rs28710291	805302	A	G	0.677	-0.019	0.066	7.70E-01	0.168	0.025	4.01E-11	-0.115	0.396	7.71E-01	6.74E-01
Skin Sun Exposed Lower leg	<i>RPLP2</i>	rs28710291	805302	A	G	0.677	-0.019	0.066	7.70E-01	0.113	0.018	5.29E-10	-0.172	0.588	7.71E-01	4.77E-01
Whole Blood	<i>RNH1</i>	rs71487293	486414	A	G	0.127	-0.026	0.091	7.78E-01	-0.210	0.035	2.74E-09	0.122	0.434	7.78E-01	6.74E-01
Nerve Tibial	<i>PTDSS2</i>	rs116101630	506826	C	G	0.127	-0.026	0.091	7.79E-01	-0.411	0.048	1.56E-17	0.063	0.223	7.79E-01	3.96E-01
Brain Cerebellar Hemisphere	<i>PTDSS2</i>	rs116101630	506826	C	G	0.127	-0.026	0.091	7.79E-01	-0.562	0.081	3.13E-12	0.046	0.163	7.79E-01	5.73E-01
Spleen	<i>RNH1</i>	rs116101630	506826	C	G	0.127	-0.026	0.091	7.79E-01	-0.435	0.067	8.74E-11	0.059	0.210	7.79E-01	4.78E-01
Adipose Visceral Omentum	<i>RNH1</i>	rs116101630	506826	C	G	0.127	-0.026	0.091	7.79E-01	-0.330	0.052	2.70E-10	0.078	0.277	7.79E-01	7.48E-01
Thyroid	<i>DEAF1</i>	rs10902192	690462	C	A	0.676	-0.012	0.044	7.83E-01	-0.187	0.025	1.07E-13	0.065	0.237	7.83E-01	7.10E-01
Esophagus Gastroesophageal Junction	<i>PTDSS2</i>	rs34590039	517348	T	G	0.094	-0.025	0.091	7.85E-01	-0.646	0.080	7.84E-16	0.039	0.142	7.85E-01	8.80E-01
Adipose Subcutaneous	<i>TSPAN4</i>	rs12577118	844057	G	C	0.694	0.020	0.073	7.86E-01	-0.236	0.033	1.16E-12	-0.084	0.309	7.86E-01	9.80E-01
Brain Cortex	<i>PNPLA2</i>	rs7925131	820268	G	A	0.731	-0.019	0.072	7.87E-01	-0.670	0.068	7.60E-23	0.029	0.107	7.88E-01	7.58E-01
Brain Frontal Cortex BA9	<i>PNPLA2</i>	rs7925131	820268	G	A	0.731	-0.019	0.072	7.87E-01	-0.826	0.098	4.13E-17	0.023	0.087	7.88E-01	8.54E-01
Heart Left Ventricle	<i>PNPLA2</i>	rs7925131	820268	G	A	0.731	-0.019	0.072	7.87E-01	-0.207	0.038	3.85E-08	0.094	0.348	7.88E-01	8.26E-01
Colon Sigmoid	<i>PTDSS2</i>	rs112273746	517369	C	T	0.127	-0.024	0.092	7.93E-01	-0.534	0.076	1.48E-12	0.045	0.172	7.93E-01	6.77E-01
Colon Transverse	<i>RNH1</i>	rs112273746	517369	C	T	0.127	-0.024	0.092	7.93E-01	-0.396	0.057	3.08E-12	0.061	0.232	7.93E-01	8.05E-01
Adipose Subcutaneous	<i>PTDSS2</i>	rs112273746	517369	C	T	0.127	-0.024	0.092	7.93E-01	-0.313	0.050	2.83E-10	0.077	0.294	7.93E-01	6.87E-01
Artery Coronary	<i>PTDSS2</i>	rs112273746	517369	C	T	0.127	-0.024	0.092	7.93E-01	-0.487	0.077	2.82E-10	0.050	0.189	7.93E-01	6.40E-01
Skin Sun Exposed Lower leg	<i>LRRC56</i>	rs61876335	488878	C	T	0.128	-0.023	0.091	7.96E-01	0.458	0.057	8.55E-16	-0.051	0.198	7.96E-01	1.87E-01
Skin Sun Exposed Lower leg	<i>POLR2L</i>	rs28404903	841763	C	G	0.688	0.017	0.067	7.98E-01	0.127	0.020	3.21E-10	0.136	0.529	7.98E-01	9.16E-01
Skin Not Sun Exposed Suprapubic	<i>LRRC56</i>	rs34834607	526707	C	T	0.120	0.025	0.097	7.98E-01	0.650	0.073	3.28E-19	0.038	0.149	7.98E-01	2.85E-01
Brain Cortex	<i>HRAS</i>	rs12421457	505780	C	T	0.127	-0.023	0.091	8.00E-01	-0.483	0.070	5.17E-12	0.048	0.189	8.00E-01	4.58E-01
Brain Cortex	<i>TMEM80</i>	rs9667500	683761	A	G	0.549	-0.010	0.041	8.01E-01	-0.852	0.087	1.32E-22	0.012	0.048	8.01E-01	4.00E-01
Pancreas	<i>DEAF1</i>	rs9667500	683761	A	G	0.549	-0.010	0.041	8.01E-01	-0.707	0.073	4.05E-22	0.015	0.058	8.01E-01	5.79E-01
Brain Nucleus accumbens basal ganglia	<i>TMEM80</i>	rs9667500	683761	A	G	0.549	-0.010	0.041	8.01E-01	-0.894	0.094	1.18E-21	0.012	0.046	8.01E-01	3.54E-01
Colon Transverse	<i>TMEM80</i>	rs9667500	683761	A	G	0.549	-0.010	0.041	8.01E-01	-0.472	0.053	2.76E-19	0.022	0.087	8.01E-01	7.06E-01
Brain Hippocampus	<i>TMEM80</i>	rs9667500	683761	A	G	0.549	-0.010	0.041	8.01E-01	-0.887	0.102	2.83E-18	0.012	0.046	8.01E-01	5.40E-01
Prostate	<i>TMEM80</i>	rs9667500	683761	A	G	0.549	-0.010	0.041	8.01E-01	-0.657	0.083	1.88E-15	0.016	0.063	8.01E-01	4.99E-01
Nerve Tibial	<i>RNH1</i>	rs34300336	509648	C	A	0.308	0.016	0.066	8.03E-01	-0.235	0.028	1.57E-17	-0.070	0.281	8.03E-01	9.53E-01
Esophagus Gastroesophageal Junction	<i>CD151</i>	rs28681202	834098	T	C	0.691	-0.017	0.069	8.07E-01	0.629	0.051	2.58E-35	-0.027	0.109	8.07E-01	1.00E+00
Colon Sigmoid	<i>CD151</i>	rs28681202	834098	T	C	0.691	-0.017	0.069	8.07E-01	0.663	0.056	7.78E-33	-0.025	0.104	8.07E-01	1.00E+00
Minor Salivary Gland	<i>CD151</i>	rs28681202	834098	T	C	0.691	-0.017	0.069	8.07E-01	0.422	0.068	4.47E-10	-0.040	0.163	8.07E-01	1.00E+00

Vagina	<i>CD151</i>	rs28681202	834098	T	C	0.691	-0.017	0.069	8.07E-01	0.436	0.075	5.09E-09	-0.039	0.158	8.07E-01	1.00E+00
Liver	<i>CD151</i>	rs1130680	838424	T	C	0.662	0.016	0.068	8.11E-01	0.628	0.067	8.01E-21	0.026	0.108	8.12E-01	9.60E-01
Adrenal Gland	<i>PTDSS2</i>	rs34612778	458441	C	G	0.097	-0.021	0.091	8.21E-01	-0.625	0.104	1.86E-09	0.033	0.146	8.21E-01	8.79E-01
Thyroid	<i>ANO9</i>	rs10794325	441806	A	C	0.613	-0.014	0.064	8.26E-01	-0.340	0.033	2.99E-25	0.042	0.190	8.26E-01	7.23E-01
Spleen	<i>ANO9</i>	rs10794325	441806	A	C	0.613	-0.014	0.064	8.26E-01	-0.415	0.066	3.13E-10	0.034	0.155	8.26E-01	7.31E-01
Minor Salivary Gland	<i>ANO9</i>	rs10794325	441806	A	C	0.613	-0.014	0.064	8.26E-01	-0.598	0.098	1.02E-09	0.024	0.108	8.26E-01	6.73E-01
Whole Blood	<i>C11orf35</i>	rs28650290	559964	T	C	0.072	-0.026	0.117	8.26E-01	0.429	0.075	1.20E-08	-0.060	0.273	8.27E-01	9.11E-01
Esophagus Mucosa	<i>DRD4</i>	rs12272314	590648	G	A	0.273	0.015	0.070	8.29E-01	-0.329	0.044	6.72E-14	-0.046	0.213	8.29E-01	5.44E-01
Whole Blood	<i>ANO9</i>	rs7482616	449811	G	A	0.614	-0.014	0.064	8.30E-01	-0.114	0.020	2.44E-08	0.121	0.565	8.30E-01	1.70E-01
Cells Transformed fibroblasts	<i>IFITM1</i>	rs61876261	356080	C	T	0.417	-0.014	0.066	8.33E-01	-0.311	0.034	6.90E-20	0.044	0.211	8.33E-01	4.85E-01
Nerve Tibial	<i>IFITM1</i>	rs61876261	356080	C	T	0.417	-0.014	0.066	8.33E-01	-0.193	0.030	7.25E-11	0.072	0.340	8.33E-01	5.95E-01
Cells Transformed fibroblasts	<i>IFITM3</i>	rs61876261	356080	C	T	0.417	-0.014	0.066	8.33E-01	-0.172	0.027	1.41E-10	0.081	0.382	8.33E-01	6.52E-01
Skin Not Sun Exposed Suprapubic	<i>PHRF1</i>	rs7101726	599313	C	T	0.272	0.015	0.070	8.33E-01	-0.191	0.034	2.25E-08	-0.077	0.367	8.33E-01	3.25E-01
Nerve Tibial	<i>POLR2L</i>	rs1130719	838760	A	T	0.687	0.014	0.067	8.37E-01	-0.131	0.020	1.09E-10	-0.106	0.513	8.37E-01	9.24E-01
Lung	<i>RPLP2</i>	rs1135628	823809	G	C	0.236	0.015	0.076	8.40E-01	-0.203	0.025	9.27E-16	-0.075	0.373	8.40E-01	6.56E-01
Thyroid	<i>RPLP2</i>	rs1135628	823809	G	C	0.236	0.015	0.076	8.40E-01	-0.170	0.025	7.08E-12	-0.090	0.446	8.41E-01	6.91E-01
Adipose Visceral Omentum	<i>CD151</i>	rs7114218	831122	T	C	0.693	-0.014	0.069	8.43E-01	0.291	0.035	8.62E-17	-0.047	0.236	8.43E-01	8.42E-01
Thyroid	<i>IRF7</i>	rs7933436	658511	T	C	0.551	-0.008	0.041	8.45E-01	-0.232	0.036	9.84E-11	0.035	0.178	8.45E-01	6.34E-01
Brain Putamen basal ganglia	<i>RIC8A</i>	rs7930823	206767	A	G	0.307	0.009	0.045	8.46E-01	0.377	0.067	1.99E-08	0.023	0.119	8.46E-01	1.38E-02
Pancreas	<i>ANO9</i>	rs7102822	439879	A	G	0.395	-0.012	0.064	8.49E-01	-0.463	0.064	3.96E-13	0.026	0.139	8.49E-01	8.28E-01
Muscle Skeletal	<i>CD151</i>	rs4075290	830487	T	C	0.694	-0.013	0.069	8.52E-01	0.499	0.036	6.84E-44	-0.026	0.138	8.52E-01	1.00E+00
Pituitary	<i>HRAS</i>	rs35068485	466032	T	A	0.128	-0.017	0.091	8.53E-01	-0.663	0.091	2.53E-13	0.025	0.137	8.54E-01	4.54E-01
Esophagus Muscularis	<i>RNH1</i>	rs35068485	466032	T	A	0.128	-0.017	0.091	8.53E-01	-0.310	0.044	1.79E-12	0.054	0.293	8.54E-01	7.63E-01
Whole Blood	<i>TMEM80</i>	rs7928943	698253	T	A	0.172	0.016	0.085	8.54E-01	0.371	0.033	5.24E-30	0.042	0.230	8.54E-01	9.92E-01
Pancreas	<i>TMEM80</i>	rs7928943	698253	T	A	0.172	0.016	0.085	8.54E-01	0.771	0.076	5.00E-24	0.020	0.111	8.54E-01	9.85E-01
Cells Transformed fibroblasts	<i>RNH1</i>	rs7480899	438459	C	T	0.801	0.014	0.078	8.59E-01	0.306	0.040	2.75E-14	0.045	0.256	8.59E-01	3.61E-01
Heart Atrial Appendage	<i>HRAS</i>	rs71487291	486027	C	T	0.116	-0.016	0.093	8.60E-01	-0.388	0.057	1.13E-11	0.042	0.241	8.60E-01	4.27E-01
Colon Transverse	<i>PTDSS2</i>	rs71487291	486027	C	T	0.116	-0.016	0.093	8.60E-01	-0.455	0.071	1.17E-10	0.036	0.205	8.60E-01	8.82E-01
Ovary	<i>PNPLA2</i>	rs12574605	885330	A	C	0.495	0.011	0.063	8.60E-01	-0.473	0.085	2.77E-08	-0.023	0.134	8.60E-01	9.09E-01
Esophagus Mucosa	<i>PHRF1</i>	rs7936397	577534	A	G	0.268	0.012	0.071	8.61E-01	-0.283	0.039	4.04E-13	-0.044	0.250	8.61E-01	3.10E-01
Uterus	<i>TMEM80</i>	rs11246269	698626	T	C	0.172	0.014	0.085	8.66E-01	0.918	0.127	4.87E-13	0.016	0.093	8.66E-01	9.49E-01
Esophagus Muscularis	<i>PTDSS2</i>	rs35996687	458595	A	G	0.116	-0.015	0.094	8.69E-01	-0.609	0.064	1.20E-21	0.025	0.154	8.69E-01	7.77E-01
Brain Putamen basal ganglia	<i>HRAS</i>	rs35996687	458595	A	G	0.116	-0.015	0.094	8.69E-01	-0.474	0.082	6.23E-09	0.033	0.197	8.69E-01	8.00E-01
Adrenal Gland	<i>TSPAN4</i>	rs9704922	842775	A	G	0.205	-0.013	0.081	8.69E-01	0.855	0.094	8.48E-20	-0.016	0.094	8.69E-01	9.99E-01
Artery Aorta	<i>NLRP6</i>	rs77447196	280464	G	C	0.219	-0.008	0.053	8.74E-01	-0.422	0.069	1.12E-09	0.020	0.127	8.74E-01	6.89E-02
Whole Blood	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.778	0.039	1.13E-86	-0.014	0.092	8.75E-01	9.99E-01
Lung	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.518	0.034	1.68E-51	-0.022	0.138	8.75E-01	9.99E-01
Testis	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.574	0.039	3.56E-49	-0.020	0.124	8.75E-01	9.99E-01
Nerve Tibial	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.498	0.034	4.00E-48	-0.023	0.143	8.75E-01	9.97E-01
Cells Transformed fibroblasts	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.471	0.037	3.89E-37	-0.024	0.152	8.75E-01	9.99E-01
Ovary	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.633	0.083	2.90E-14	-0.018	0.113	8.75E-01	9.99E-01
Brain Nucleus accumbens basal ganglia	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.504	0.081	5.56E-10	-0.022	0.142	8.75E-01	9.88E-01
Artery Coronary	<i>CD151</i>	rs28648546	833327	G	A	0.738	-0.011	0.071	8.75E-01	0.279	0.050	2.44E-08	-0.040	0.256	8.75E-01	9.91E-01
Esophagus Muscularis	<i>RPLP2</i>	rs28360884	802902	G	T	0.677	-0.010	0.067	8.77E-01	0.186	0.028	2.43E-11	-0.055	0.358	8.77E-01	5.65E-01

Heart Atrial Appendage	<i>RPLP2</i>	rs28360884	802902	G	T	0.677	-0.010	0.067	8.77E-01	0.228	0.038	1.56E-09	-0.045	0.292	8.77E-01	5.31E-01
Whole Blood	<i>PTDSS2</i>	rs12419157	494141	C	T	0.123	-0.014	0.093	8.80E-01	-0.245	0.042	7.57E-09	0.057	0.378	8.80E-01	7.99E-01
Artery Tibial	<i>CHID1</i>	rs10794339	900929	G	C	0.546	-0.009	0.066	8.87E-01	0.173	0.025	3.01E-12	-0.054	0.382	8.87E-01	9.93E-01
Artery Aorta	<i>CD151</i>	rs28507856	833975	T	G	0.694	-0.009	0.069	8.91E-01	0.356	0.051	4.74E-12	-0.027	0.193	8.91E-01	9.98E-01
Uterus	<i>CD151</i>	rs28507856	833975	T	G	0.694	-0.009	0.069	8.91E-01	0.373	0.063	3.48E-09	-0.025	0.184	8.91E-01	1.00E+00
Colon Transverse	<i>CD151</i>	rs7127272	835719	G	A	0.259	0.010	0.071	8.93E-01	-0.646	0.054	1.37E-33	-0.015	0.110	8.93E-01	1.00E+00
Stomach	<i>ANO9</i>	rs11246166	496924	C	G	0.617	0.008	0.066	8.99E-01	-0.262	0.039	2.51E-11	-0.032	0.250	8.99E-01	6.33E-01
Lung	<i>ANO9</i>	rs11246166	496924	C	G	0.617	0.008	0.066	8.99E-01	-0.233	0.035	5.07E-11	-0.036	0.282	8.99E-01	2.70E-01
Thyroid	<i>PTDSS2</i>	rs12419209	494510	C	T	0.131	-0.011	0.090	9.05E-01	-0.363	0.045	7.12E-16	0.030	0.248	9.05E-01	7.43E-01
Cells Transformed fibroblasts	<i>CHID1</i>	rs12799446	877869	C	T	0.515	-0.007	0.063	9.05E-01	-0.321	0.045	8.22E-13	0.023	0.196	9.05E-01	9.80E-01
Lung	<i>CHID1</i>	rs12799446	877869	C	T	0.515	-0.007	0.063	9.05E-01	-0.199	0.028	1.09E-12	0.038	0.315	9.05E-01	9.10E-01
Colon Transverse	<i>CHID1</i>	rs12799446	877869	C	T	0.515	-0.007	0.063	9.05E-01	-0.269	0.049	3.44E-08	0.028	0.234	9.05E-01	9.96E-01
Esophagus Gastroesophageal Junction	<i>CHID1</i>	rs72479392	897981	T	C	0.093	0.014	0.115	9.05E-01	0.532	0.094	1.45E-08	0.026	0.215	9.05E-01	9.98E-01
Brain Cortex	<i>PIDD</i>	rs6597978	817286	C	G	0.565	0.008	0.064	9.06E-01	0.294	0.053	3.67E-08	0.026	0.219	9.06E-01	6.40E-01
Artery Tibial	<i>CD151</i>	rs28454516	833828	A	G	0.686	-0.008	0.070	9.07E-01	0.384	0.029	4.30E-40	-0.021	0.183	9.07E-01	9.94E-01
Prostate	<i>CD151</i>	rs28454516	833828	A	G	0.686	-0.008	0.070	9.07E-01	0.744	0.089	4.66E-17	-0.011	0.095	9.07E-01	1.00E+00
Pituitary	<i>CHID1</i>	rs12420667	888533	T	G	0.505	-0.007	0.063	9.07E-01	0.396	0.055	6.01E-13	-0.019	0.160	9.07E-01	9.87E-01
Adrenal Gland	<i>CD151</i>	rs7924806	833668	T	C	0.688	-0.008	0.069	9.07E-01	0.811	0.065	1.18E-35	-0.010	0.085	9.07E-01	9.99E-01
Spleen	<i>CD151</i>	rs7924806	833668	T	C	0.688	-0.008	0.069	9.07E-01	0.679	0.066	7.32E-25	-0.012	0.101	9.07E-01	1.00E+00
Small Intestine Terminal Ileum	<i>CD151</i>	rs7924806	833668	T	C	0.688	-0.008	0.069	9.07E-01	0.407	0.047	8.63E-18	-0.020	0.169	9.07E-01	1.00E+00
Muscle Skeletal	<i>POLR2L</i>	rs6591	840363	T	C	0.533	0.007	0.064	9.11E-01	-0.196	0.026	3.34E-14	-0.037	0.329	9.11E-01	9.99E-01
Heart Atrial Appendage	<i>CHID1</i>	rs7125550	883479	C	G	0.495	0.007	0.063	9.11E-01	-0.244	0.044	2.96E-08	-0.029	0.259	9.11E-01	6.82E-01
Pancreas	<i>RNH1</i>	rs10751659	437559	T	C	0.799	-0.008	0.077	9.14E-01	0.369	0.062	2.40E-09	-0.023	0.209	9.14E-01	6.28E-01
Esophagus Mucosa	<i>POLR2L</i>	rs7117701	835622	G	A	0.690	-0.007	0.068	9.14E-01	0.333	0.030	2.63E-29	-0.022	0.205	9.14E-01	9.99E-01
Esophagus Mucosa	<i>CD151</i>	rs1130276	831809	G	T	0.743	-0.007	0.071	9.25E-01	0.790	0.052	2.85E-52	-0.009	0.090	9.25E-01	9.96E-01
Heart Left Ventricle	<i>CD151</i>	rs1130276	831809	G	T	0.743	-0.007	0.071	9.25E-01	0.501	0.043	7.05E-31	-0.013	0.142	9.25E-01	9.98E-01
Cells EBV-transformed lymphocytes	<i>CD151</i>	rs1130276	831809	G	T	0.743	-0.007	0.071	9.25E-01	0.894	0.102	2.25E-18	-0.008	0.080	9.25E-01	9.98E-01
Breast Mammary Tissue	<i>CD151</i>	rs1130276	831809	G	T	0.743	-0.007	0.071	9.25E-01	0.259	0.033	6.06E-15	-0.026	0.276	9.25E-01	9.97E-01
Brain Spinal cord cervical c-1	<i>CD151</i>	rs1130276	831809	G	T	0.743	-0.007	0.071	9.25E-01	0.640	0.088	3.73E-13	-0.011	0.112	9.25E-01	9.76E-01
Brain Hippocampus	<i>CD151</i>	rs1130276	831809	G	T	0.743	-0.007	0.071	9.25E-01	0.522	0.075	4.06E-12	-0.013	0.137	9.25E-01	9.70E-01
Skin Not Sun Exposed Suprapubic	<i>POLR2L</i>	rs5030778	836008	C	T	0.691	0.006	0.068	9.27E-01	0.191	0.028	1.01E-11	0.032	0.353	9.27E-01	9.69E-01
Heart Atrial Appendage	<i>PTDSS2</i>	rs12418264	524371	T	C	0.124	0.008	0.094	9.28E-01	-0.435	0.067	1.06E-10	-0.019	0.217	9.28E-01	7.34E-01
Esophagus Mucosa	<i>CHID1</i>	rs7479057	879081	C	T	0.485	0.006	0.063	9.30E-01	0.333	0.038	1.62E-18	0.017	0.189	9.30E-01	9.23E-01
Lung	<i>RNH1</i>	rs12421266	537120	T	C	0.129	0.008	0.094	9.30E-01	-0.320	0.039	1.71E-16	-0.026	0.295	9.30E-01	8.11E-01
Brain Putamen basal ganglia	<i>CD151</i>	rs61876748	833262	G	T	0.736	-0.006	0.071	9.32E-01	0.762	0.083	5.97E-20	-0.008	0.094	9.32E-01	9.99E-01
Cells Transformed fibroblasts	<i>EFCAB4A</i>	rs61876748	833262	G	T	0.736	-0.006	0.071	9.32E-01	0.515	0.066	7.18E-15	-0.012	0.139	9.32E-01	9.96E-01
Heart Left Ventricle	<i>PTDSS2</i>	rs61877780	531165	C	A	0.098	0.007	0.094	9.43E-01	-0.410	0.073	1.83E-08	-0.016	0.229	9.43E-01	9.08E-01
Stomach	<i>CD151</i>	rs6762	838722	C	T	0.258	0.005	0.071	9.47E-01	-0.496	0.053	6.73E-21	-0.010	0.144	9.47E-01	9.98E-01
Muscle Skeletal	<i>PTDSS2</i>	rs61877795	537502	T	C	0.129	0.006	0.094	9.47E-01	-0.287	0.053	4.86E-08	-0.022	0.329	9.47E-01	6.92E-01
Thyroid	<i>CD151</i>	rs7947543	833728	G	A	0.688	-0.004	0.069	9.55E-01	0.820	0.038	5.64E-105	-0.005	0.084	9.55E-01	1.00E+00
Esophagus Muscularis	<i>CD151</i>	rs7947543	833728	G	A	0.688	-0.004	0.069	9.55E-01	0.589	0.035	6.52E-65	-0.007	0.117	9.55E-01	1.00E+00
Small Intestine Terminal Ileum	<i>CHID1</i>	rs36002505	859915	T	C	0.506	-0.003	0.063	9.63E-01	0.414	0.074	1.87E-08	-0.007	0.153	9.63E-01	9.67E-01
Colon Transverse	<i>PIDD</i>	rs7121646	800485	A	T	0.542	-0.003	0.064	9.64E-01	0.231	0.037	2.84E-10	-0.013	0.279	9.64E-01	8.39E-01
Heart Atrial Appendage	<i>CD151</i>	rs28448654	833898	C	T	0.689	-0.003	0.069	9.67E-01	0.642	0.051	1.16E-36	-0.004	0.107	9.67E-01	9.98E-01

Pituitary	<i>CD151</i>	rs28448654	833898	C	T	0.689	-0.003	0.069	9.67E-01	0.803	0.072	3.74E-29	-0.003	0.086	9.67E-01	9.99E-01
Adipose Subcutaneous	<i>POLR2L</i>	rs28448654	833898	C	T	0.689	-0.003	0.069	9.67E-01	-0.163	0.021	1.88E-15	0.017	0.421	9.67E-01	1.00E+00
Brain Cerebellar Hemisphere	<i>CD151</i>	rs28448654	833898	C	T	0.689	-0.003	0.069	9.67E-01	0.498	0.075	2.43E-11	-0.006	0.138	9.67E-01	9.53E-01
Brain Substantia nigra	<i>CD151</i>	rs28448654	833898	C	T	0.689	-0.003	0.069	9.67E-01	0.791	0.120	4.79E-11	-0.004	0.087	9.67E-01	7.92E-01
Whole Blood	<i>POLR2L</i>	rs28448654	833898	C	T	0.689	-0.003	0.069	9.67E-01	-0.159	0.024	4.04E-11	0.018	0.432	9.67E-01	1.00E+00
Whole Blood	<i>IFITM3</i>	rs10398	308180	G	A	0.193	0.003	0.080	9.70E-01	0.525	0.064	1.74E-16	0.006	0.153	9.70E-01	8.50E-01
Adrenal Gland	<i>PIDD</i>	rs7117921	800486	T	C	0.542	-0.002	0.065	9.76E-01	0.323	0.044	1.69E-13	-0.006	0.200	9.76E-01	7.22E-01
Heart Left Ventricle	<i>PIDD</i>	rs7117921	800486	T	C	0.542	-0.002	0.065	9.76E-01	0.244	0.037	4.44E-11	-0.008	0.265	9.76E-01	8.61E-01
Breast Mammary Tissue	<i>RPLP2</i>	rs7117921	800486	T	C	0.542	-0.002	0.065	9.76E-01	0.127	0.023	1.86E-08	-0.015	0.507	9.76E-01	7.96E-01
Brain Hypothalamus	<i>CD151</i>	rs74194353	833138	T	C	0.687	0.002	0.069	9.76E-01	0.536	0.091	4.35E-09	0.004	0.128	9.76E-01	9.38E-01
Adipose Visceral Omentum	<i>TMEM80</i>	rs7928305	695842	A	G	0.175	-0.001	0.060	9.82E-01	0.697	0.054	3.08E-38	-0.002	0.086	9.82E-01	9.49E-01
Spleen	<i>TMEM80</i>	rs7928305	695842	A	G	0.175	-0.001	0.060	9.82E-01	0.926	0.086	9.14E-27	-0.001	0.065	9.82E-01	9.12E-01
Brain Nucleus accumbens basal ganglia	<i>EPS8L2</i>	rs76431003	707025	A	G	0.204	0.002	0.082	9.84E-01	0.632	0.104	1.24E-09	0.003	0.130	9.84E-01	9.35E-01
Cells Transformed fibroblasts	<i>DRD4</i>	rs72844713	606770	T	C	0.079	0.002	0.126	9.90E-01	-0.617	0.101	8.78E-10	-0.002	0.203	9.90E-01	6.62E-01
Nerve Tibial	<i>DRD4</i>	rs72844713	606770	T	C	0.079	0.002	0.126	9.90E-01	-0.453	0.073	4.92E-10	-0.003	0.277	9.90E-01	6.05E-01
Skin Sun Exposed Lower leg	<i>RIC8A</i>	rs1976848	201584	A	T	0.214	-0.001	0.052	9.90E-01	-0.236	0.033	8.46E-13	0.003	0.221	9.90E-01	1.75E-02

GWAS and eQTL betas (b) are with respect to allele A1. SE: standard error. The SMR method calculates eQTL *P*-values from betas and standard errors and therefore reported eQTL *P*-values may not coincide exactly with those reported

Supplementary Table 9: Heritability estimates computed using GCTA and PCGC.

GCTA estimate of heritability ascribed to common variation across all autosomes

Chromosomes	German-GWAS		USA-GWAS		Meta-analysis			
	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	I^2	P_{het}
Autosomes	0.336 (\pm 0.058)	3.30E-09	0.237 (\pm 0.054)	4.94E-06	0.279 (\pm 0.044)	3.14E-10	20.68	2.62E-01

S.E., standard error.

GCTA estimate of heritability ascribed to common variation across all autosomes adjusted for incomplete LD between causal SNPs and those used to compute I^2

MAF threshold	German-GWAS		USA-GWAS		Meta-analysis			
	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	I^2	P_{het}
0.5	0.326 (\pm 0.058)	4.94E-06	0.237 (\pm 0.054)	4.94E-06	0.279 (\pm 0.044)	3.06E-10	20.58	2.62E-01
0.4	0.308 (\pm 0.058)	4.74E-06	0.241 (\pm 0.054)	4.74E-06	0.273 (\pm 0.040)	5.34E-12	0.00	3.98E-01
0.3	0.301 (\pm 0.056)	7.46E-06	0.232 (\pm 0.053)	7.46E-06	0.265 (\pm 0.039)	6.56E-12	0.00	3.71E-01
0.2	0.294 (\pm 0.051)	1.31E-06	0.238 (\pm 0.050)	1.31E-06	0.265 (\pm 0.036)	1.53E-13	0.00	4.36E-01
0.1	0.217 (\pm 0.040)	1.65E-03	0.118 (\pm 0.040)	1.65E-03	0.168 (\pm 0.049)	6.92E-04	67.45	7.96E-02

S.E., standard error.

GCTA estimate of heritability ascribed to common variation on each autosome

Chromosome	German-GWAS		USA-GWAS		Meta-analysis			
	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	I^2	P_{het}
1	0.035 (\pm 0.018)	NA	0.000 (\pm 0.015)	NA	0.016 (\pm 0.018)	3.53E-01	57.14	1.27E-01
2	0.021 (\pm 0.018)	NA	0.041 (\pm 0.017)	NA	0.031 (\pm 0.012)	9.67E-03	0.00	4.06E-01
3	0.035 (\pm 0.017)	NA	0.026 (\pm 0.015)	NA	0.030 (\pm 0.011)	7.62E-03	0.00	6.84E-01
4	0.010 (\pm 0.015)	NA	0.009 (\pm 0.014)	NA	0.009 (\pm 0.010)	3.52E-01	0.00	9.37E-01
5	0.000 (\pm 0.014)	NA	0.020 (\pm 0.014)	NA	0.010 (\pm 0.010)	3.31E-01	0.00	3.30E-01
6	0.036 (\pm 0.016)	NA	0.000 (\pm 0.008)	NA	0.016 (\pm 0.018)	3.73E-01	75.10	4.51E-02
7	0.051 (\pm 0.016)	NA	0.001 (\pm 0.013)	NA	0.026 (\pm 0.025)	3.08E-01	83.49	1.39E-02
8	0.000 (\pm 0.012)	NA	0.025 (\pm 0.014)	NA	0.012 (\pm 0.012)	3.40E-01	45.99	1.74E-01
9	0.005 (\pm 0.013)	NA	0.011 (\pm 0.012)	NA	0.008 (\pm 0.009)	3.60E-01	0.00	7.49E-01
10	0.024 (\pm 0.015)	NA	0.000 (\pm 0.012)	NA	0.010 (\pm 0.012)	3.73E-01	35.66	2.13E-01
11	0.001 (\pm 0.013)	NA	0.018 (\pm 0.012)	NA	0.009 (\pm 0.009)	2.88E-01	0.00	3.33E-01
12	0.023 (\pm 0.014)	NA	0.002 (\pm 0.012)	NA	0.011 (\pm 0.010)	2.92E-01	22.09	2.57E-01
13	0.015 (\pm 0.012)	NA	0.009 (\pm 0.011)	NA	0.012 (\pm 0.008)	1.54E-01	0.00	7.21E-01
14	0.008 (\pm 0.012)	NA	0.013 (\pm 0.010)	NA	0.011 (\pm 0.008)	1.64E-01	0.00	7.21E-01
15	0.014 (\pm 0.011)	NA	0.004 (\pm 0.010)	NA	0.009 (\pm 0.007)	2.29E-01	0.00	4.92E-01
16	0.031 (\pm 0.012)	NA	0.016 (\pm 0.010)	NA	0.022 (\pm 0.008)	6.02E-03	0.00	3.61E-01
17	0.001 (\pm 0.011)	NA	0.014 (\pm 0.009)	NA	0.008 (\pm 0.007)	2.38E-01	0.00	3.37E-01
18	0.013 (\pm 0.011)	NA	0.022 (\pm 0.011)	NA	0.017 (\pm 0.008)	3.31E-02	0.00	5.63E-01
19	0.000 (\pm 0.009)	NA	0.004 (\pm 0.008)	NA	0.002 (\pm 0.006)	7.08E-01	0.00	7.52E-01
20	0.000 (\pm 0.010)	NA	0.000 (\pm 0.009)	NA	0.000 (\pm 0.007)	9.79E-01	0.00	9.82E-01
21	0.007 (\pm 0.008)	NA	0.006 (\pm 0.007)	NA	0.007 (\pm 0.005)	2.08E-01	0.00	9.26E-01
22	0.002 (\pm 0.008)	NA	0.005 (\pm 0.007)	NA	0.004 (\pm 0.005)	4.61E-01	0.00	8.20E-01

S.E., standard error. GCTA does not compute *P*-values for individual chromosomes.

PCGC estimate of heritability ascribed to common variation across all autosomes

Chromosomes	German-GWAS		USA-GWAS		Meta-analysis			
	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	h^2 (\pm S.E.)	<i>P</i> value	I^2	P_{het}
Autosomes	0.349 (\pm 0.070)	NA	0.185 (\pm 0.061)	NA	0.263 (\pm 0.082)	1.32E-03	68.03	7.69E-02

S.E., standard error. PCGC does not compute *P*-values.

Supplementary Table 10: Individual variance in risk associated with meningioma SNPs.

SNP	Reported	Locus	RAF	OR	% risk
rs11012732	Previously reported	10p12.31	0.35	1.31	2.68
rs2686876	First reported in this study	11p15.5	0.90	1.44	1.74
Total					4.42

RAF, risk allele frequency; OR, odds ratio derived with respect to the risk allele.