SUPPLEMENTARY ONLINE MATERIAL

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SUPPLEMENTARY NOTE

Supplementary Note 1. REPLICATION COHORTS DESCRIPTIONS

MEC is a population-based prospective cohort study including approximately 215,000 men and women from Hawaii and California [Kolonel, L. N. et al. A multiethnic cohort in Hawaii and Los Angeles: baseline characteristics. Am. J. 869 Epidemiol. 151, 346–357 (2000)]. All participants were 45-75 years of age at baseline, and primarily of five ancestries: Japanese Americans, African Americans, European Americans, Hispanic/Latinos, and Native Hawaiians. MEC was funded by the National Cancer Institute in 1993 to examine lifestyle risk factors and genetic susceptibility to cancer. All eligible cohort members completed baseline and follow-up questionnaires. Participants from the MEC sample in the current analyses included 3,825 women and 3,281 men who self-reported African American background, had measured height and weight available, and had genetic data available. Of these, 4,593 were genotyped on the MEGA chip and 2,513 were genotyped on the Illumina Human1M-Duo chip.

MVP participants were recruited from over 60 Veterans Health Administration medical centers nationwide since 2011. The design of MVP has been previously described [1]. A unique feature of MVP is the linkage of a large biobank to an extensive, national, database from 2003 onward that integrates multiple elements such as diagnosis codes, procedure codes, laboratory values, and imaging reports, which permits detailed phenotyping of this large cohort. MVP has received ethical and study protocol approval by the Veterans Affairs Central Institutional Review Board in accordance with the principles outlined in the Declaration of Helsinki. DNA extracted from participants' blood was genotyped using a customized Affymetrix Axiom® biobank array, the MVP 1.0 Genotyping Array. The array was enriched for both common and rare genetic variants of clinical significance in different ethnic backgrounds. Quality-control procedures used to assign ancestry, remove low-quality samples and variants, and perform genotype imputation were previously described [2]. We excluded: duplicate samples, samples with more heterozygosity than expected an excess (>2.5%) of missing genotype calls, or discordance between genetically inferred sex and phenotypic gender. In addition, one individual from each pair of related individuals (more than second degree relatedness as measured by the KING software) were removed. The MVP participants were assigned to mutually exclusive racial/ethnic groups using HARE (Harmonized Ancestry and Race/Ethnicity), a machine learning algorithm that integrates genetically inferred ancestry with self-identified race/ethnicity [3]. The present study included non-Hispanic African Americans with both genotypic and phenotypic data for genetic association analyses. The phenotyping and analytical details of body mass index in the MVP were previously described [4]. SNP rs111490516 was imputed with quality score of 0.7083.

The UK Biobank is a prospective cohort study with genetic and phenotypic data on more than 500,000 individuals, aged between 39–69 years. Study design, protocols, sample handling and quality control have been described in detail elsewhere (PMID: 25826379 and PMID: 30305743). African ancestry was determined using k-means clustering (PMID: 32692746). Briefly, clustering was performed by projecting the 1000 genomes reference panel dataset based on the PCA loadings from the UK Biobank. We performed k-means clustering with a pre-specified number of 4 clusters. Individuals from the UK Biobank that clustered with the AFR 1000G cluster were assigned African ancestry.

REGARDS: The Reasons for Geographic and Racial Differences in Stroke (REGARDS) project, sponsored by the National Institutes of Health (NIH), is a national study focusing on learning more about the factors that increase a person's risk of having a stroke. REGARDS is an observational study of risk factors for stroke in unrelated adults 45 years or older. 30,239 African American and European American participants were recruited between January 2003 and October 2007. The study design and objectives have been previously described [5]. MEGAEX genotype data is available for 8,837 African American and 1,716 European American REGARDS participants. The study is ongoing and will follow participants

for many years.

BioMe is an ongoing electronic medical record-linked biobank with more than 60,000 patients enrolled through the Mount Sinai Health System in New York. BioMe is a multiethnic biobank comprising individuals of African, Hispanic, European, Asian, and other ancestries [6]. Genotyping data is available on 32,595 individuals and was done using the Global Screening Array (GSA-24v1-0_A1). The data was cleaned for duplicate samples, discordant sex, heterozygosity rate that exceeded 6 SD from the population mean, call rate<95% at the site and individual level, and deviation from Hardy Weinberg equilibrium. Replication was conducted within self-reported African ancestry.

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NHLBI TOPMed: Massachusetts General Hospital Atrial Fibrillation Study (MGH_AF)

NHLBI TOPMed: Outcome Modifying Genes in Sickle Cell Disease (OMG_SCD)
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NHLBI TOPMed: Partners Healthcare Biorepository (Partners)

NHLBI TOPMed: Whole Genome Sequencing to Identify Causal Genetic Variants Influencing CVD Risk - San Antonio Family Studies (SAFS)
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NHLBI TOPMed: Study of African Americans, Asthma, Genes and Environment (SAGE)
The Study of African Americans, Asthma, Genes and Environments (SAGE) was supported by by the National Heart, Lung, and Blood Institute of the National Institute of Health (NIH) grants R01HL117004 and X01HL134589; study enrollment supported by the Sandler Family Foundation, the American Asthma Foundation, the RWJF Amos Medical Faculty Development Program, Harry Wm. and Diana V. Hind Distinguished Professor in Pharmaceutical Sciences II. The SAGE study collaborators include Harold J. Farber, Texas Children's Hospital; Emerita Brigino-Buenaventura, Kaiser Permanente; Michael A. LeNoir, Bay Area Pediatrics; Kelley Meade, UCSF Benioff Children’s Hospital, Oakland; Luisa N. Borrell, City University of New York; Adam Davis, UCSF Benioff Children’s Hospital, Oakland and Fred Lurmann, Sonoma Technologies, Inc. The authors acknowledge the families and patients for their participation and thank the numerous health care providers and community clinics for their support and participation in SAGE. In particular, the authors thank study coordinator Sandra Salazar; the recruiters who obtained the data: Lisa Caine, Elizabeth Castellanos, Brenda Lopez, MD, Shahdad Saeedi; and the lab researcher Celeste Eng who processed the biospecimens.

NHLBI TOPMed: Samoan Adiposity Study (Samoan)
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NHLBI TOPMed: Taiwan Study of Hypertension using Rare Variants (THRV)
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NHLBI TOPMed: Vanderbilt Atrial Fibrillation Ablation Registry (VAFAR)

NHLBI TOPMed: Vanderbilt Genetic Basis of Atrial Fibrillation (VU_AF)

NHLBI TOPMed: Treatment of Pulmonary Hypertension and Sickle Cell Disease with Sildenafil Therapy (walk_PHaSST)
We thank Dr. Mark Gladwin and the investigators of the Walk-PHasst study and the patients who participated in the study. We also thanks the walk-PHaSST clinical site team: Albert Einstein College of Medicine: Jane Little and Verlene Davis; Columbia University: Robyn Barst, Erika Rosenzweig, Margaret Lee and Daniela Brady; UCSF Benioff Children's Hospital Oakland: Claudia Morris, Ward Hagar, Lisa Lavrisha, Howard Rosenfeld, and Elliott Vichinsky; Children's Hospital of Pittsburgh of UPMC: Regina McCollum; Hammersmith Hospital, London: Sally Davies, Gaia Mahalingam, Sharon Meehan, Ofelia Lebanto, and Ines Cabrita; Howard University: Victor Gordeuk, Oswaldo Castro, Onyinye Onyekwere, Vandana Sachdev, Alvin Thomas, Gladys Onojobi, Sharmin Diaz, Margaret Fadojutimi-Akinsiku, and Randa Aladdin; Johns Hopkins University: Reda Girgis, Sophie Lanzkron and Durrant Barasa; NHLBI: Mark Gladwin, Greg Kato, James Taylor, Wynona Coles, Catherine Seamon, Mary Hall, Amy Chi, Cynthia Brenneman, Wen Li, and Erin Smith; University of Colorado: Kathryn Hassell, David Badesch, Deb McCollister and Julie McAfee; University of Illinois at Chicago: Dean Schraufnagel, Robert Molokie, George Kondos, Patricia Cole-Saffold, and Lani Krauz; National Heart & Lung Institute, Imperial College London: Simon Gibbs. Thanks also to the data coordination center team from Rho, Inc.: Nancy Yovetich, Rob Woolson, Jamie Spencer, Christopher Woods, Karen Kesler, Vickie Coble, and Ronald W. Helms. We also thank Dr. Yingze Zhang for directing the Walk-PHasst repository and Dr. Mehdi Nouraie for maintaining the Walk-PHasst database and Dr. Jonathan Goldsmith as a NIH program director for this study. Special thanks to the volunteers who participated in the Walk-PHaSST study. This project was funded with federal funds from the NHLBI, NIH, Department of Health and Human Services, under contract HHSN268200617182C. This study is registered at www.clinicaltrials.gov as NCT00492531. Detail description of the study was published in Blood, 2011 118:855-864, Machado et al "Hospitalization for pain in patients with sickle cell disease treated with sildenafil for elevated TRV and low exercise capacity".

NHLBI TOPMed: Women's Genome Health Study (WGHS)

The WGHS is supported by the National Heart, Lung, and Blood Institute (HL043851 and HL080467) and the National Cancer Institute (CA047988 and UM1CA182913). The most recent cardiovascular endpoints were supported by ARRA funding HL099355.

NHLBI TOPMed: Women's Health Initiative (WHI)
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The Multiethnic Cohort (MEC) is a population-based prospective cohort study including approximately 215,000 men and women from Hawaii and California. All participants were 45-75 years of age at baseline, and primarily of 5 ancestries: Japanese Americans, African Americans, European Americans, Hispanic/Latinos, and Native Hawaiians. (PMIDs: 10695593; 23449381) MEC was funded by the National Cancer Institute in 1993 to examine lifestyle risk factors and genetic susceptibility to cancer. All eligible cohort members completed baseline and follow-up questionnaires. Within the PAGE II investigation, MEC proposes to study: 1) diseases for which we have DNA available for large numbers of cases and controls (breast, prostate, and colorectal cancer, diabetes, and obesity); 2) common traits that are risk factors for these diseases (e.g., body mass index / weight, waist-to-hip ratio, height), and 3) relevant disease-associated biomarkers (e.g., fasting insulin and lipids, steroid hormones). The specific aims are: 1) to determine the population-based epidemiologic profile (allele frequency, main effect, heterogeneity by disease characteristics) of putative causal variants in the five racial/ethnic groups in MEC; 2) for variants displaying effect heterogeneity across ethnic/racial groups, we will utilize differences in LD to identify a more complete spectrum of associated variants at these loci; 3) investigate gene x gene and gene x environment interactions to identify modifiers; 4) examine the associations of putative causal variants with already measured intermediate phenotypes (e.g., plasma insulin, lipids, steroid hormones); and 5) for variants that do not fall within known genes, start to investigate their relationships with gene expression and epigenetic patterns in small genomic studies. The studies listed here are individuals of African and Laitno American ancestry/ethnicity who were part of the breast cancer or prostate cancer case/controls substuides. (dbGaP study accession number: phs000220).

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Baltimore, Maryland, 21218, US; Sandow, Kevin, Lundquist Institute, TGPS, Torrance, California, 90502, US; Sankaran, Vijay G., Harvard University, Division of Hematology/Oncology, Boston, Massachusetts, 02115, US; Santibanez, Jireh, Baylor College of Medicine Human Genome Sequencing Center, Houston, Texas, 77030, US; Schwander, Karen, Washington University in St Louis, St Louis, Missouri, 63130, US; Schwartz, David, University of Colorado at Denver, Denver, Colorado, 80204, US; Sciurba, Frank, University of Pittsburgh, Pittsburgh, Pennsylvania, 15260, US; Seidman, Christine , Harvard Medical School, Genetics, Boston, Massachusetts, 02115, US; Seidman, Jonathan, Harvard Medical School, Boston, Massachusetts, 02115, US; Sériès, Frédéric, Université Laval, Quebec City, G1V 0A6, CA; Sheehan, Vivien, Emory University, Pediatrics, Atlanta, Georgia, 30307, US; Sherman, Stephanie L., Emory University, Human Genetics, Atlanta, Georgia, 30322, US; Shetty, Amol, University of Maryland, Baltimore, Maryland, 21201, US; Shetty, Aniket, University of Colorado at Denver, Denver, Colorado, 80204, US; Sheu, Wayne Hui-Heng, Taichung Veterans General Hospital Taiwan, Taichung City, 407, TW; Shoemaker, M. Benjamin, Vanderbilt University, Medicine/Cardiology, Nashville, Tennessee, 37235, US; Silver, Brian, UMass Memorial Medical Center, Worcester, Massachusetts, 01655, US; Silverman, Edwin, Brigham & Women's Hospital, Boston, Massachusetts, 02115, US; Skomro, Robert, University of Saskatchewan, Saskatoon, SK S7N 5C9, CA; Smith, Albert Vernon, University of Michigan, , ; Smith, Jennifer, University of Michigan, Ann Arbor, Michigan, 48109, US; Smith, Josh, University of Washington, Seattle, Washington, 98195, US; Smith, Nicholas, University of Washington, Epidemiology, Seattle, Washington, 98195, US; Smith, Tanja, New York Genome Center, New York, New York, 10013, US; Smoller, Sylvia, Albert Einstein College of Medicine, New York, New York, 10461, US; Snively, Beverly, Wake Forest Baptist Health, Biostatistical Sciences, Winston-Salem, North Carolina, 27157, US; Snyder, Michael, Stanford University, Stanford, California, 94305, US; Sofer, Tamar, Brigham & Women's Hospital, Boston, Massachusetts, 02115, US; Sotoodehnia, Nona, University of Washington, Seattle, Washington, 98195, US; Stilp, Adrienne M., University of Washington, Seattle, Washington, 98195, US; Storm, Garrett , University of Colorado at Denver, Genomic Cardiology, Aurora, Colorado, 80045, US; Streeten, Elizabeth, University of Maryland, Baltimore, Maryland, 21201, US; Su, Jessica Lasky, Brigham & Women's Hospital, Channing Department of Medicine, Boston, Massachusetts, 02115, US; Sung, Yun Ju, Washington University in St Louis, St Louis, Missouri, 63130, US; Sylvia, Jody, Brigham & Women's Hospital, Boston, Massachusetts, 02115, US; Szpiro, Adam, University of Washington, Seattle, Washington, 98195, US; Taliun, Daniel, University of Michigan, Ann Arbor, Michigan, 48109, US; Tang, Hua, Stanford University, Genetics, Stanford, California, 94305, US; Taub, Margaret, Johns Hopkins University, Baltimore, Maryland, 21218, US; Taylor, Kent D., Lundquist Institute, Institute for Translational Genomics and Populations Sciences, Torrance, California, 90502, US; Taylor, Matthew, University of Colorado Anschutz Medical Campus, Aurora, Colorado, 80045, US; Taylor, Simeon, University of Maryland, Baltimore, Maryland, 21201, US; Telen, Marilyn, Duke University, Durham, North Carolina, 27708, US; Thornton, Timothy A., University of Washington, Seattle, Washington, 98195, US; Threlkeld, Machiko, University of Washington, University of Washington, Department of Genome Sciences, Seattle, Washington, 98195, US; Tinker, Lesley, Fred Hutchinson Cancer Research Center, Cancer Prevention Division of Public Health Sciences, Seattle, Washington, 98109, US; Tirschwell, David, University of Washington, Seattle, Washington, 98195, US; Tishkoff, Sarah, University of Pennsylvania, Genetics, Philadelphia, Pennsylvania, 19104, US; Tiwari, Hemant, University of Alabama, Biostatistics, Birmingham, Alabama, 35487, US; Tong, Catherine, University of Washington, Department of Biostatistics, Seattle, Washington, 98195, US; Tracy, Russell, University of Vermont, Pathology & Laboratory Medicine, Burlington, Vermont, 05405, US; Tsai, Michael, University of Minnesota, Minneapolis, Minnesota, 55455, US; Vaidya, Dhananjay, Johns Hopkins University, Baltimore, Maryland, 21218, US; Van Den Berg, David, University of Southern California, USC Methylation Characterization Center, University of Southern California, California, 90033, US; VandeHaar, Peter, University of Michigan, Ann Arbor, Michigan, 48109, US; Vrieze, Scott, University of Minnesota, Minneapolis, Minnesota, 55455, US; Walker, Tarik, University of Colorado at Denver, Denver, Colorado, 80204, US; Wallace, Robert, University of Iowa, Iowa City, Iowa, 52242, US; Walts, Avram, University

of Colorado at Denver, Denver, Colorado, 80204, US; Wang, Fei Fei, University of Washington, Seattle, Washington, 98195, US; Wang, Heming, Brigham & Women's Hospital, Mass General Brigham, Boston, Massachusetts, 02115, US; Wang, Jiongming, University of Michigan, , US; Watson, Karol, University of California, Los Angeles, Los Angeles, California, 90095, US; Watt, Jennifer, Baylor College of Medicine Human Genome Sequencing Center, Houston, Texas, 77030, US; Weeks, Daniel E., University of Pittsburgh, Pittsburgh, Pennsylvania, 15260, US; Weinstock, Joshua, University of Michigan, Biostatistics, Ann Arbor, Michigan, 48109, US; Weir, Bruce, University of Washington, Seattle, Washington, 98195, US; Weiss, Scott T, Brigham & Women's Hospital, Channing Division of Network Medicine, Department of Medicine, Boston, Massachusetts, 02115, US; Weng, Lu-Chen, Massachusetts General Hospital, Boston, Massachusetts, 02114, US; Wessel, Jennifer, Indiana University, Epidemiology, Indianapolis, Indiana, 46202, US; Willer, Cristen, University of Michigan, Internal Medicine, Ann Arbor, Michigan, 48109, US; Williams, Kayleen, University of Washington, Biostatistics, Seattle, Washington, 98195, US; Williams, L. Keoki, Henry Ford Health System, Detroit, Michigan, 48202, US; Wilson, Carla, Brigham & Women's Hospital, Boston, Massachusetts, 02115, US; Wilson, James, Beth Israel Deaconess Medical Center, Cardiology, Cambridge, Massachusetts, 02139, US; Winterkorn, Lara, New York Genome Center, New York City, New York, 10013, US; Wong, Quenna, University of Washington, Seattle, Washington, 98195, US; Wu, Joseph, Stanford University, Stanford Cardiovascular Institute, Stanford, California, 94305, US; Xu, Huichun, University of Maryland, Baltimore, Maryland, 21201, US; Yanek, Lisa, Johns Hopkins University, Baltimore, Maryland, 21218, US; Yang, Ivana, University of Colorado at Denver, Denver, Colorado, 80204, US; Yu, Ketian, University of Michigan, Ann Arbor, Michigan, 48109, US; Zekavat, Seyedeh Maryam, Broad Institute, Cambridge, Massachusetts, 02142, US; Zhang, Yingze, University of Pittsburgh, Medicine, Pittsburgh, Pennsylvania, 15260, US; Zhao, Snow Xueyan, National Jewish Health, Denver, Colorado, 80206, US; Zhao, Wei, University of Michigan, Department of Epidemiology, Ann Arbor, Michigan, 48109, US; Zhu, Xiaofeng, Case Western Reserve University, Department of Population and Quantitative Health Sciences , Cleveland, Ohio, 44106, US; Zody, Michael, New York Genome Center, New York, New York, 10013, US; Zoellner, Sebastian, University of Michigan, Ann Arbor, Michigan, 48109, US

Supplementary Note 5. REFERENCES

1. Gaziano JM*, et al.* Million Veteran Program: A mega-biobank to study genetic influences on health and disease. *J Clin Epidemiol* **70**, 214-223 (2016).

2. Hunter-Zinck H*, et al.* Genotyping Array Design and Data Quality Control in the Million Veteran Program. *Am J Hum Genet* **106**, 535-548 (2020).

3. Fang H*, et al.* Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. *Am J Hum Genet* **105**, 763-772 (2019).

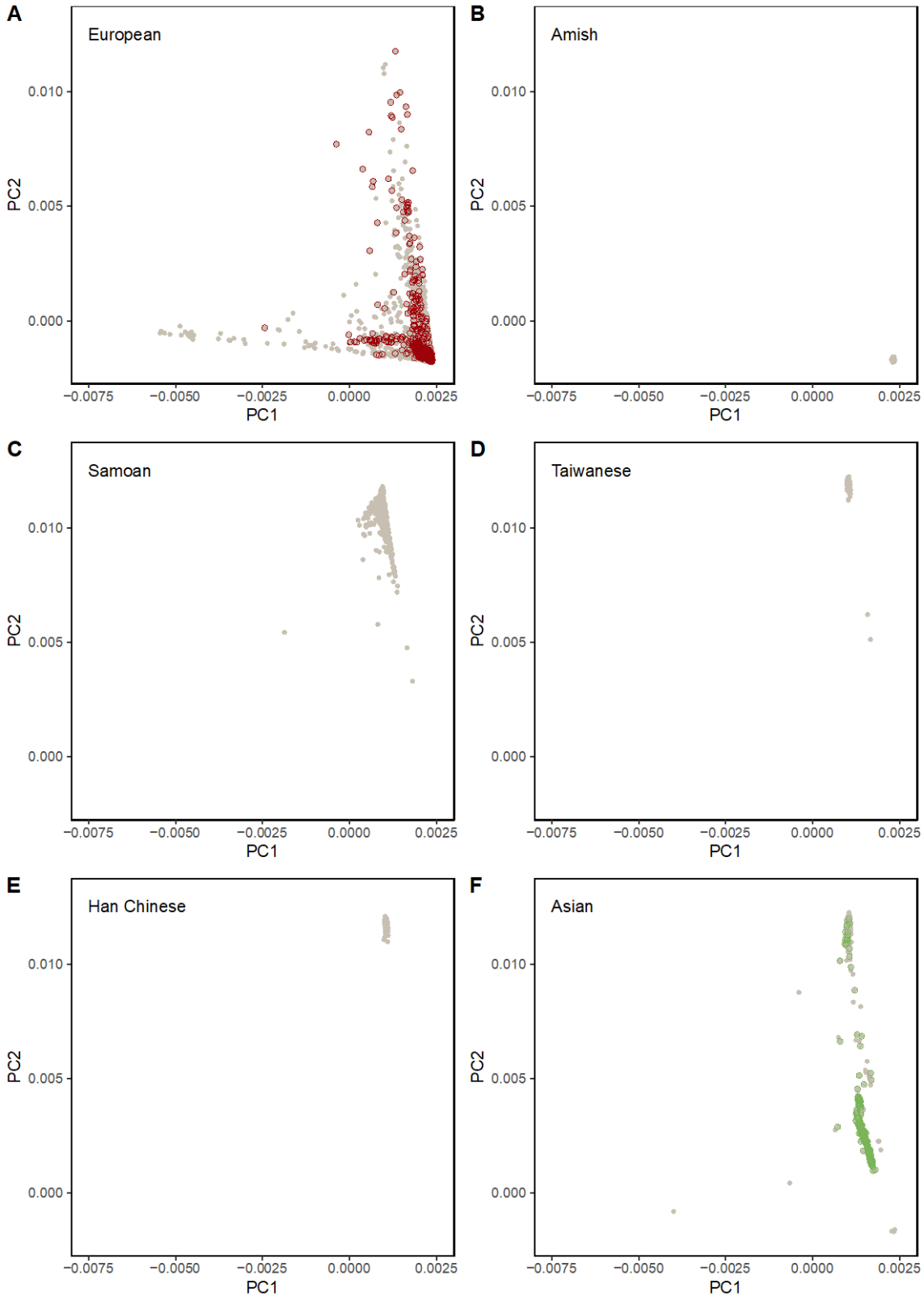
4. Huang J*, et al.* Genomics and phenomics of body mass index reveals a complex disease network. *Nat Commun* **13**, 7973 (2022).

5. Howard VJ*, et al.* The reasons for geographic and racial differences in stroke study: objectives and design. *Neuroepidemiology* **25**, 135-143 (2005).

6. Abul-Husn NS*, et al.* Implementing genomic screening in diverse populations. *Genome Med* **13**, 17 (2021).

Supplementary Figure 1. Scatter plots of PC1 *vs.* PC2 by population group

Individuals with reported population memberships in each population group are denoted by filled circles in grey. Unfilled circles in colors represent inferred population memberships (N = 8,015), using Harmonized Ancestry and Race/Ethnicity (HARE) method (see methods for details). A) European, B) Amish, C) Samoan, D) Taiwanese, E) Han Chinese, F) Asian, G) Puerto Rican, H) Cuban, I) Central American, J) South American, K) Mexican, L) Costa Rican, M) Dominican, N) Barbadian, O) African/African American/Black.



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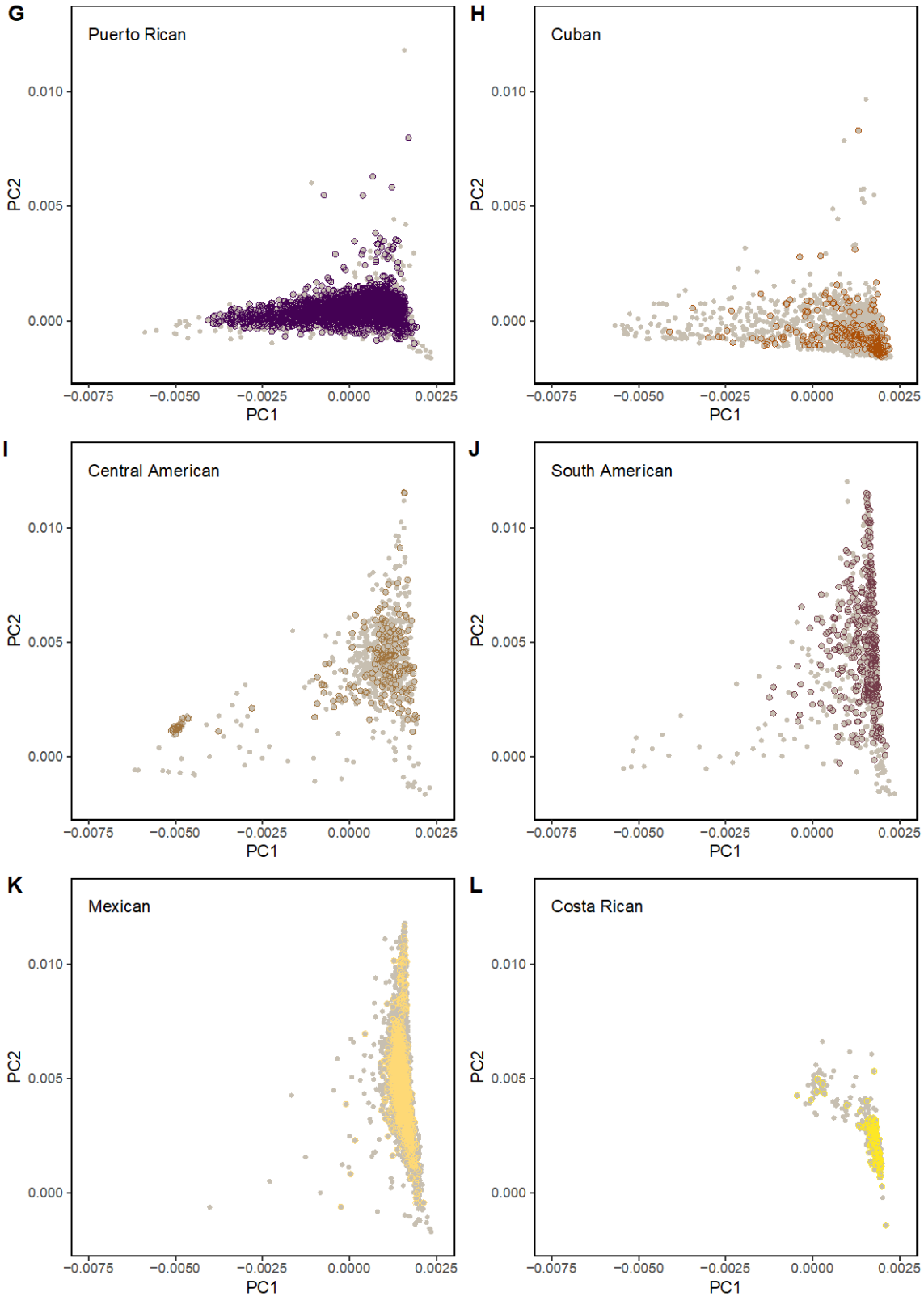

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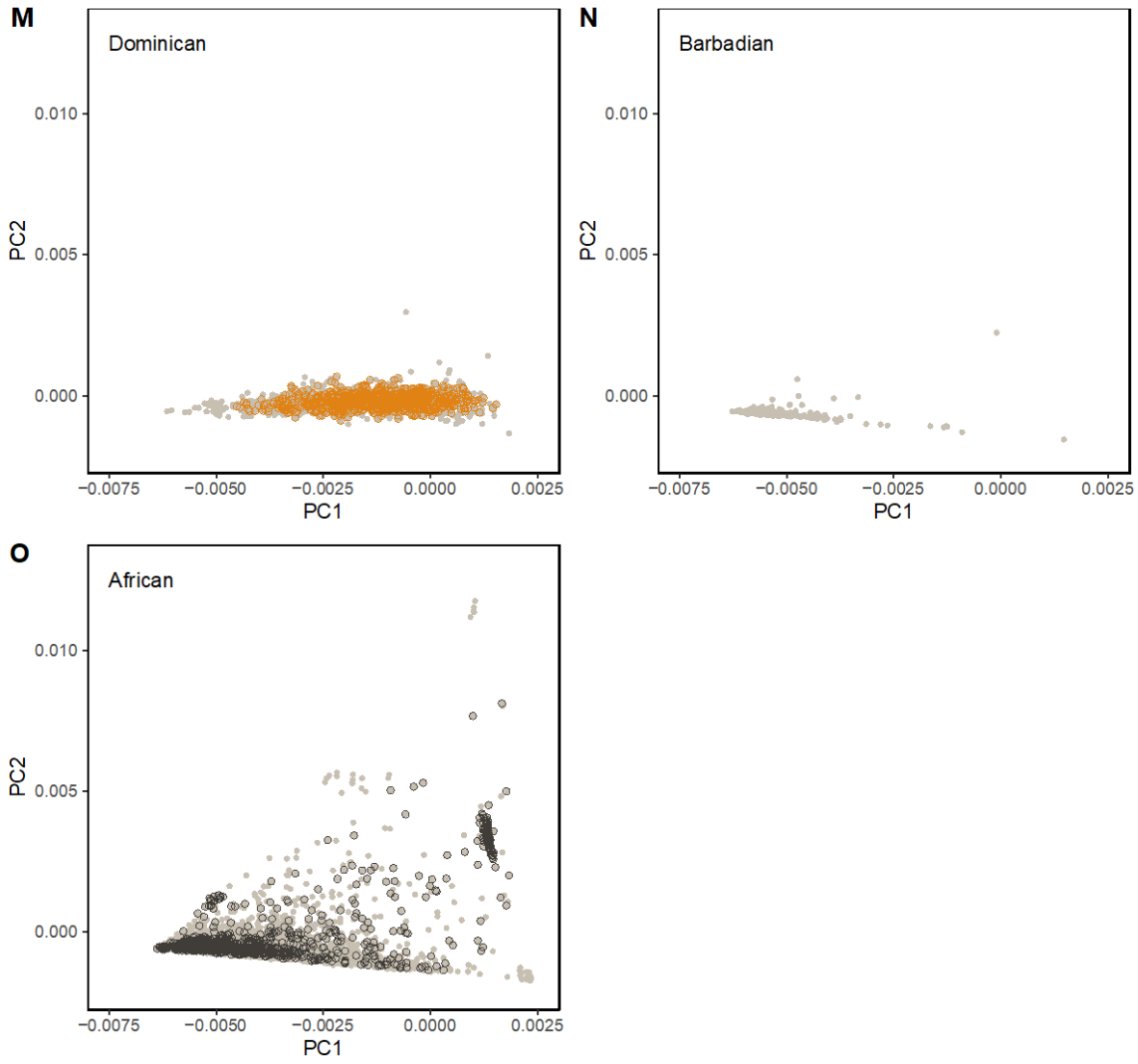
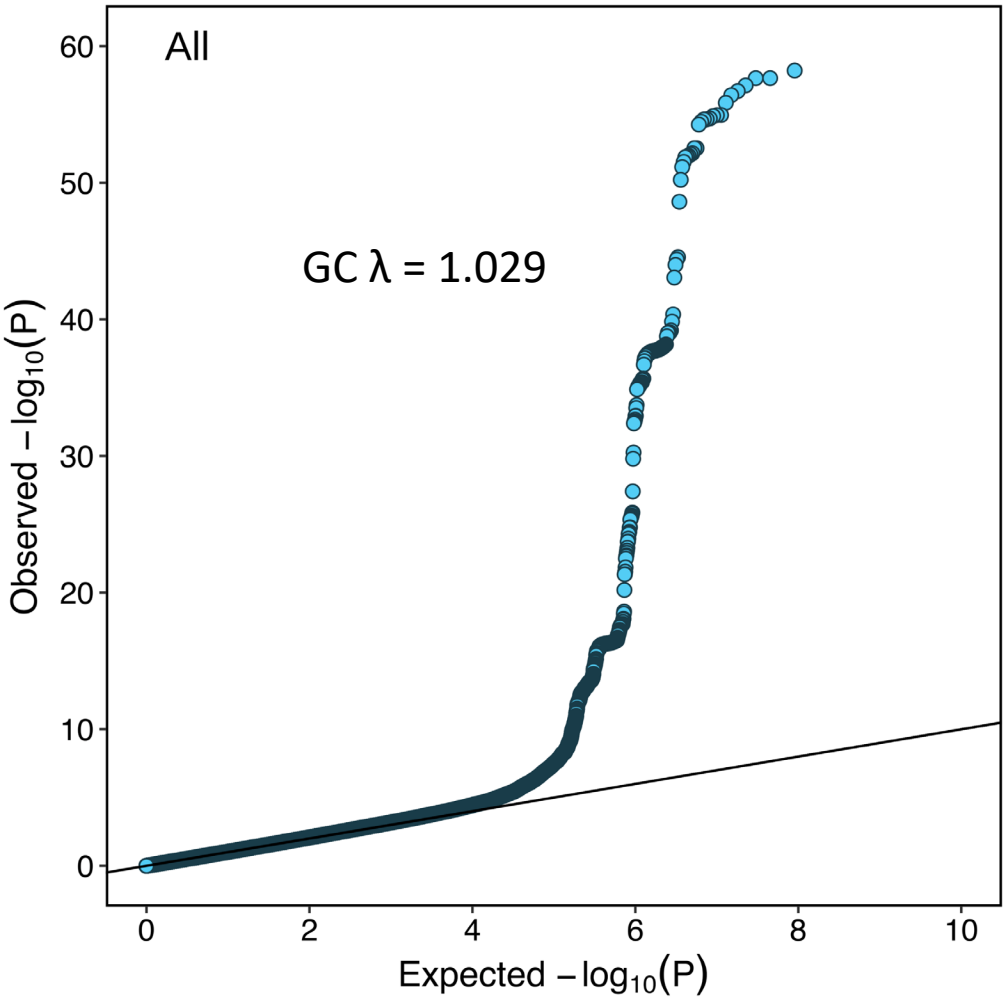


Supplementary Figure 2. QQ plot of primary BMI GWAS

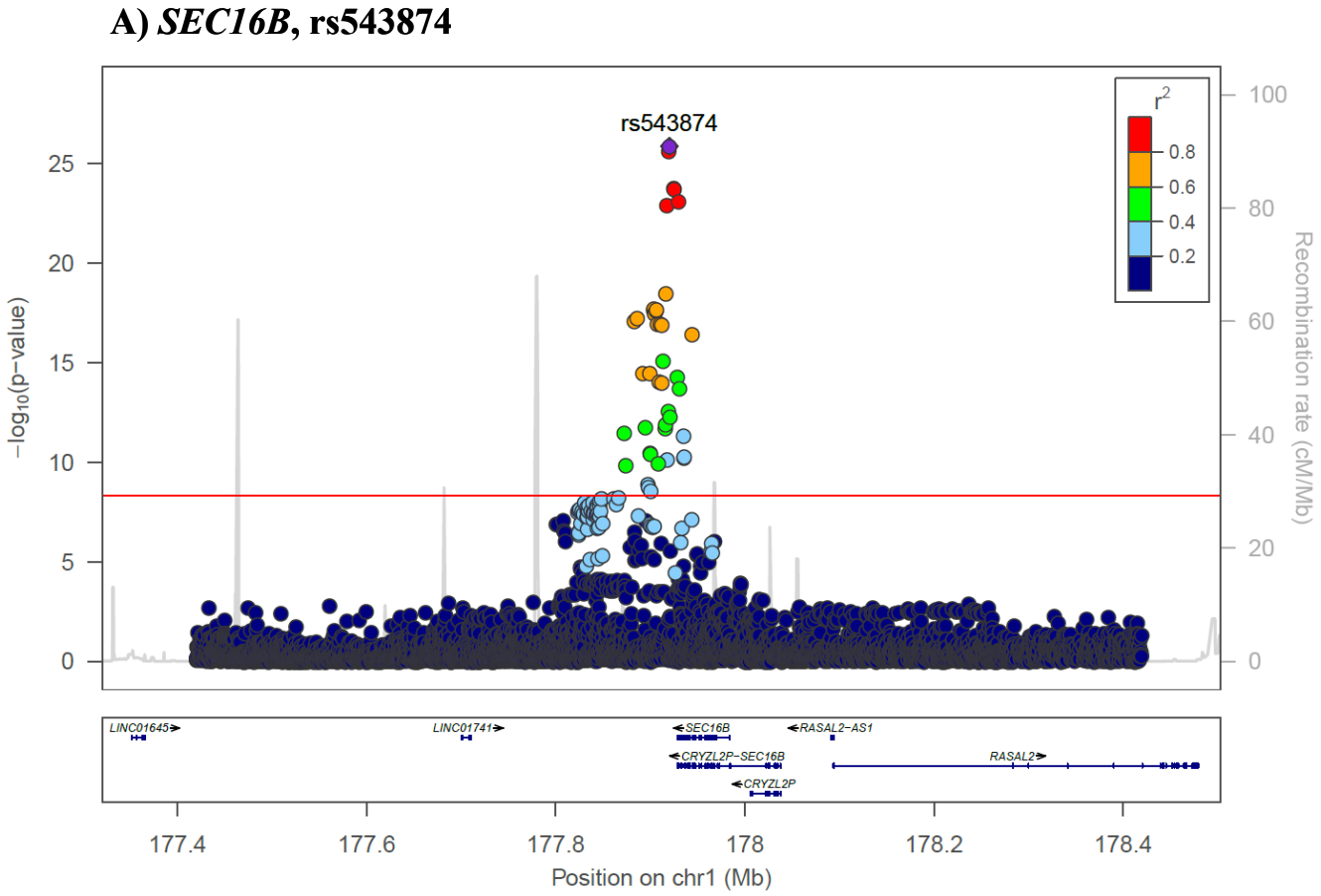
Quantile-quantile plot of multi-population, single variant analysis (N = 88,873 individuals, N = 90,142,062 variants).



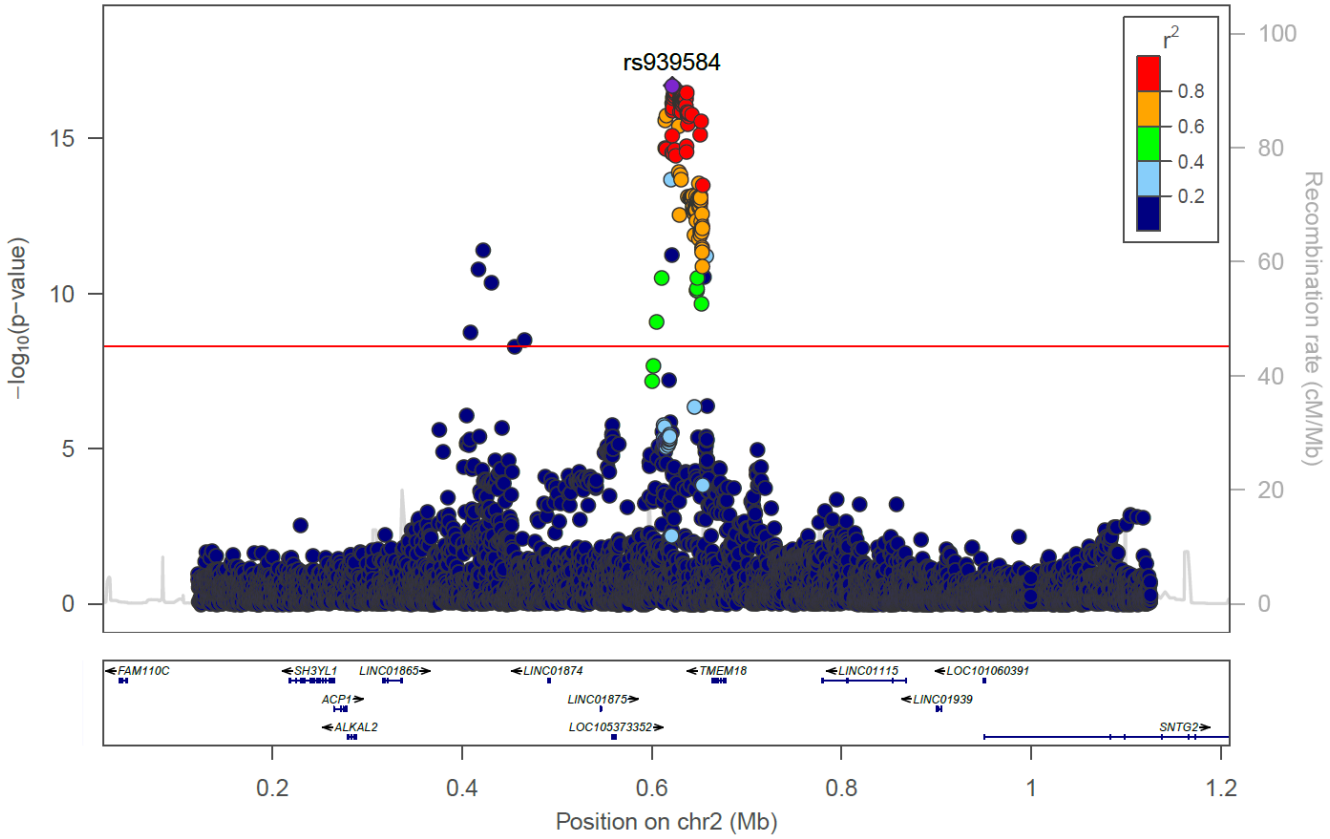
Supplementary Figure 3. Regional association plots

Regional association plots for each significant locus in the multi-population analysis, including all variants ± 500 kb from index variant. The plots appear in order of chromosomal location. TOPMed study populations were used to calculate linkage disequilibrium (LD). The red line indicates genome-wide significance threshold $P = 5 \times 10^{-9}$.

A) *SEC16B*, rs543874; B) *TMEM18*, rs939584; C) *ADCY3*, rs10182181; D) *ETV5*, rs869400; E) *GNPDA2*, rs12507026; F) *POC5*, rs2307111; G) *TFAP2B*, rs2206277; H) *HNF4G*, rs830463; I) *BDNF*, rs3838785; J) *BCDIN3D*, rs7138803; K) *OLFM4*, rs9568868; L) *FTO*, rs1421085; M) *MC4R*, rs6567160; N) *ZC3H4*, rs28590228; O) *MTMR3*, rs111490516; P) *DMD*, rs1379871.



B) *TMEM18*, rs939584



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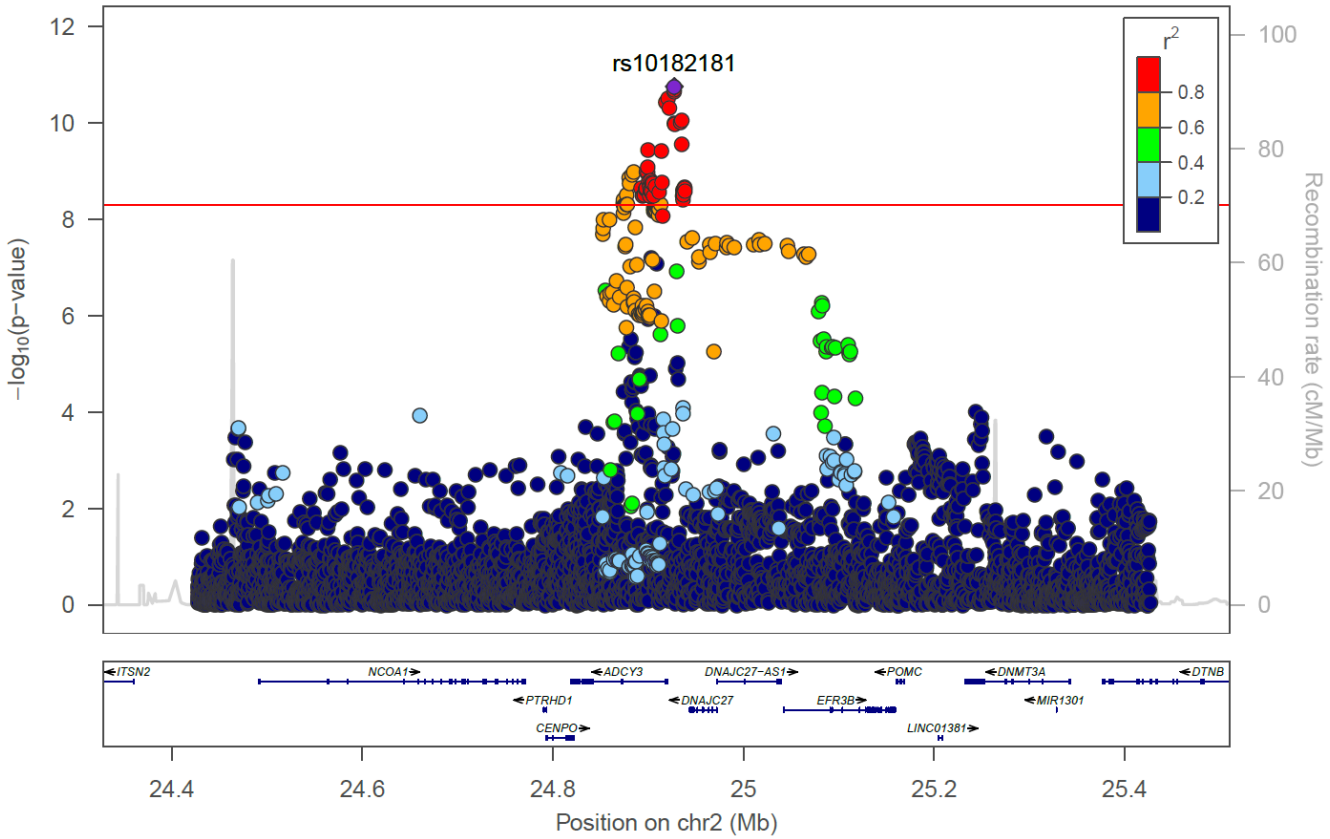

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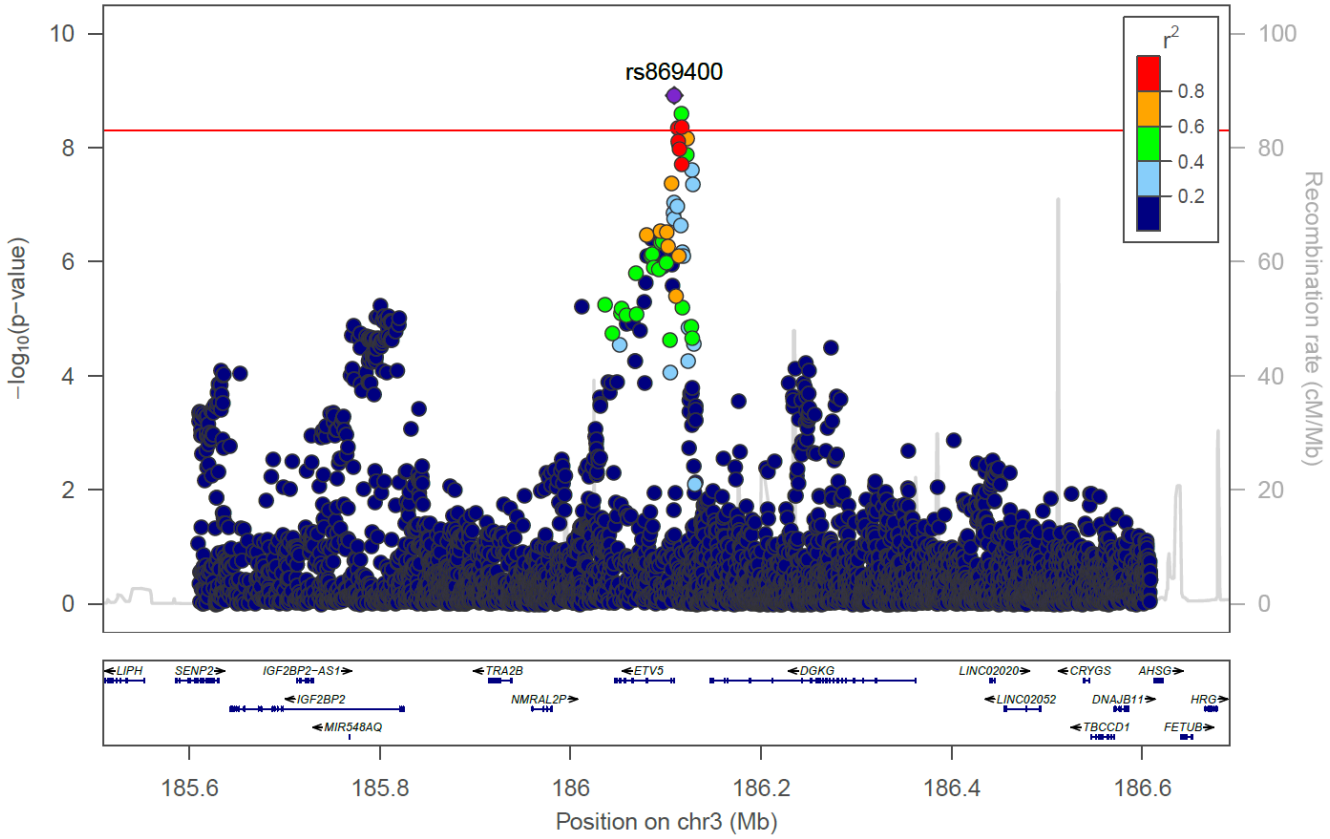

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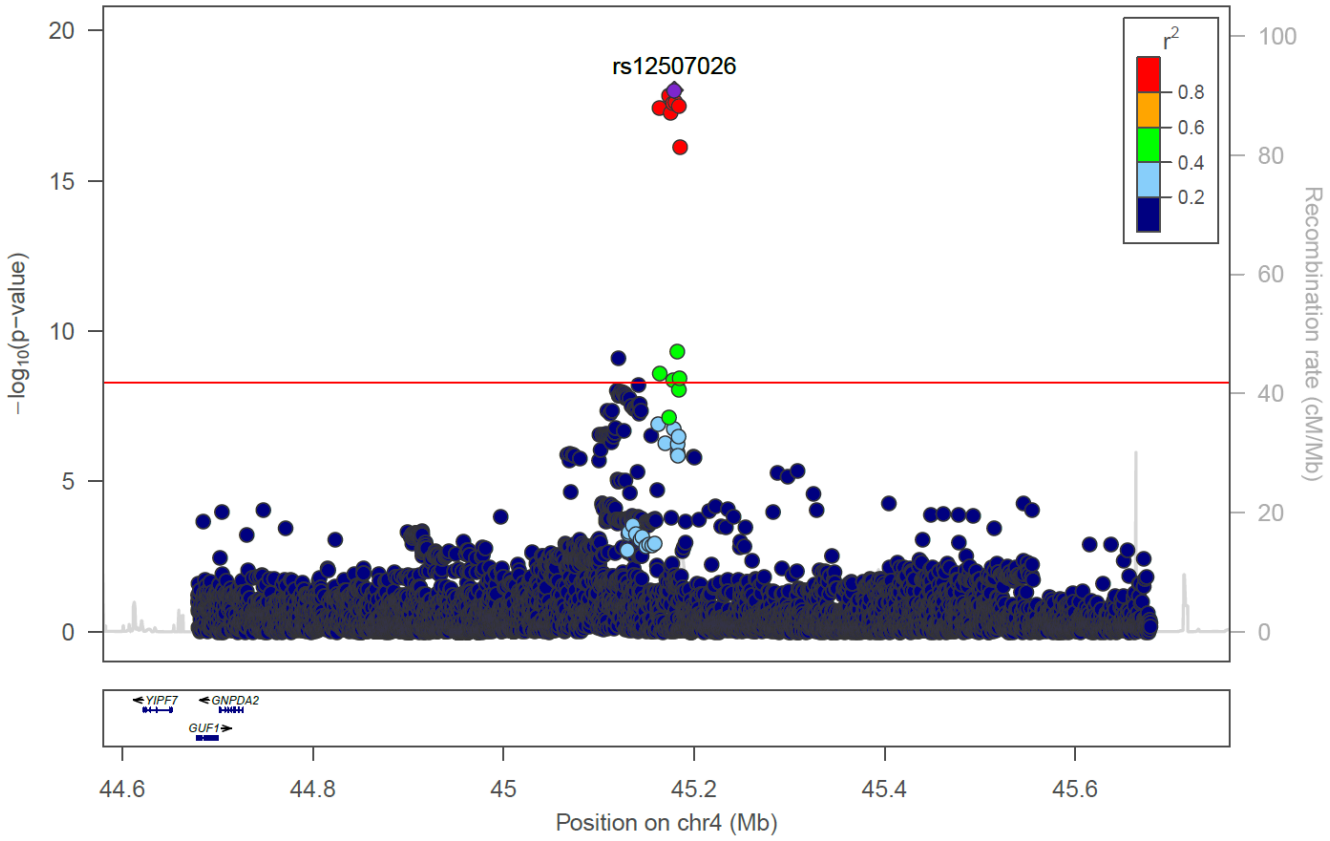
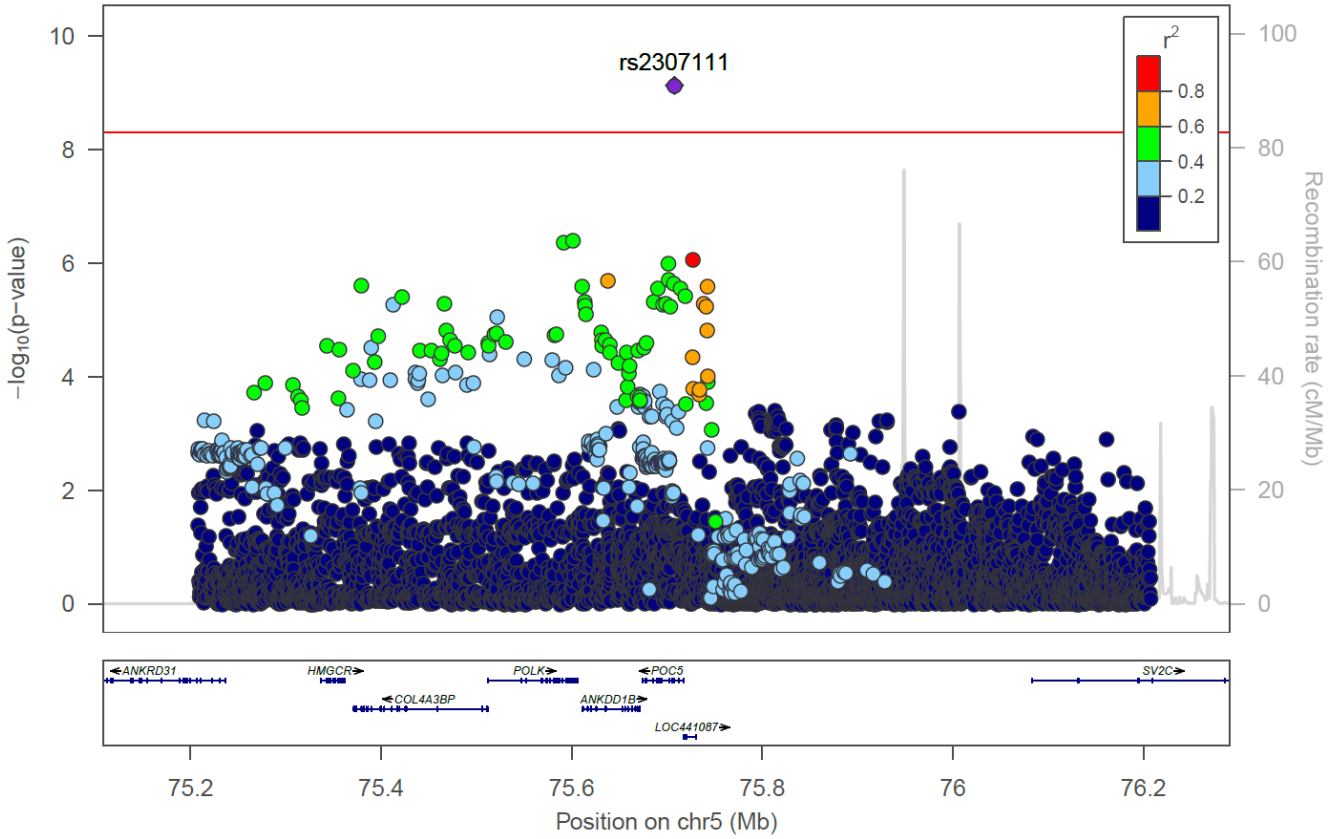
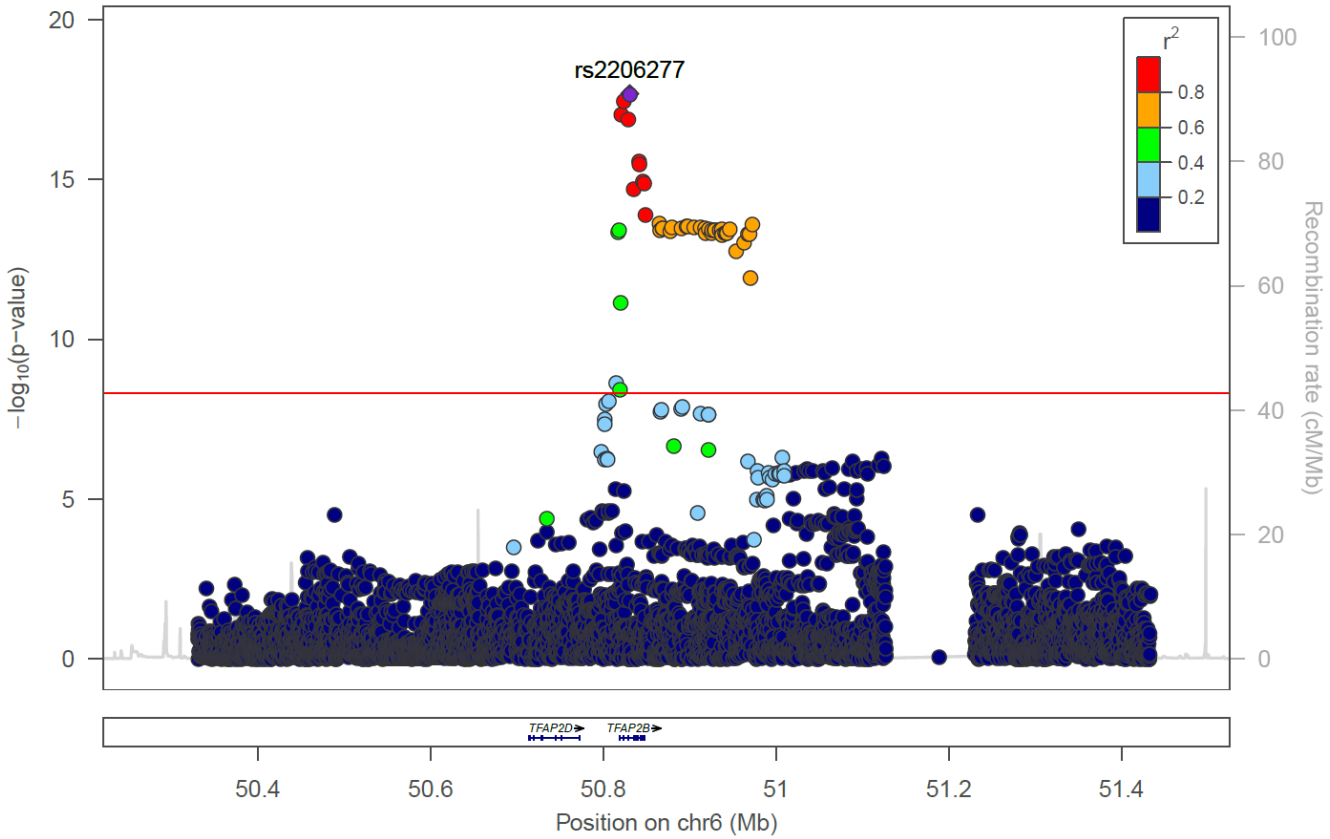


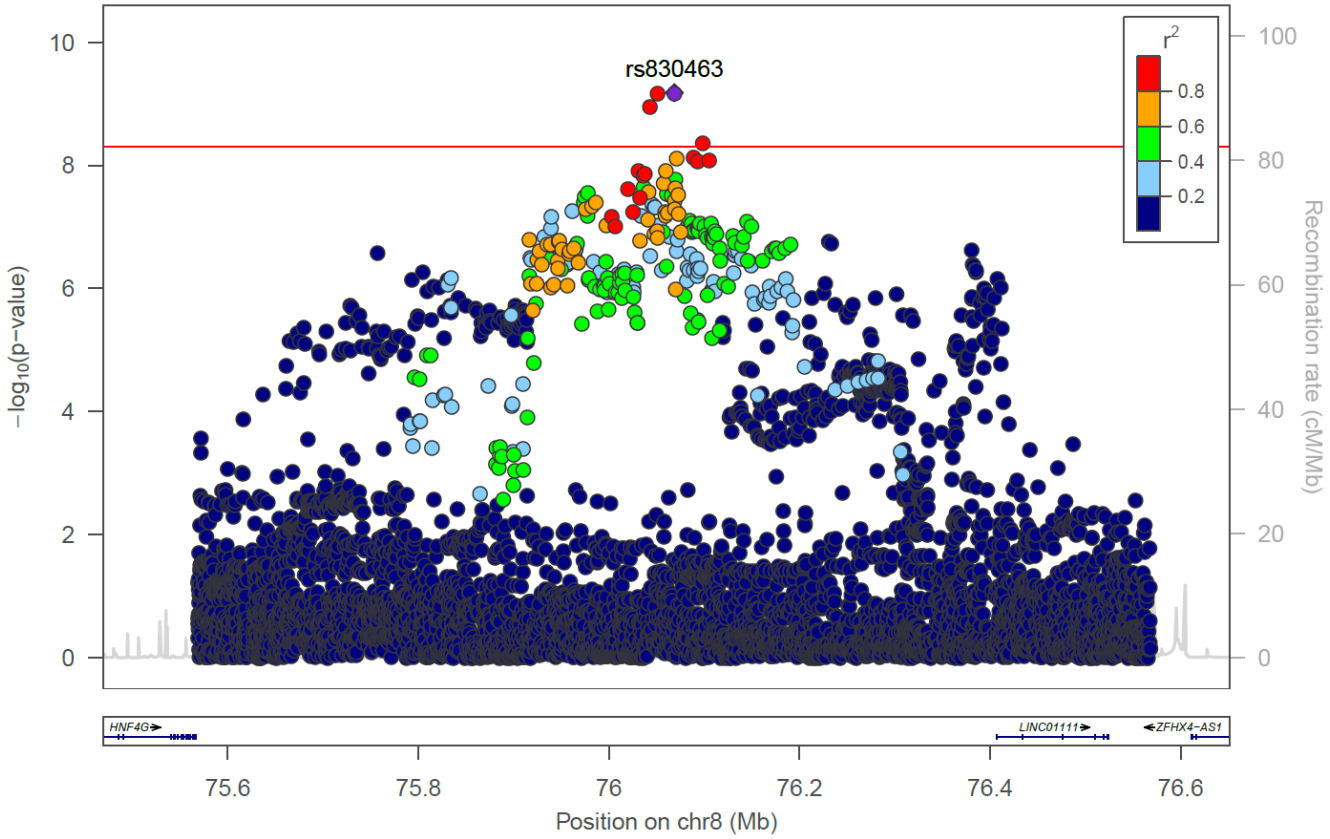
F) *POC5*, rs2307111



G) *TFAP2B*, rs2206277



H) *HNF4G*, rs830463



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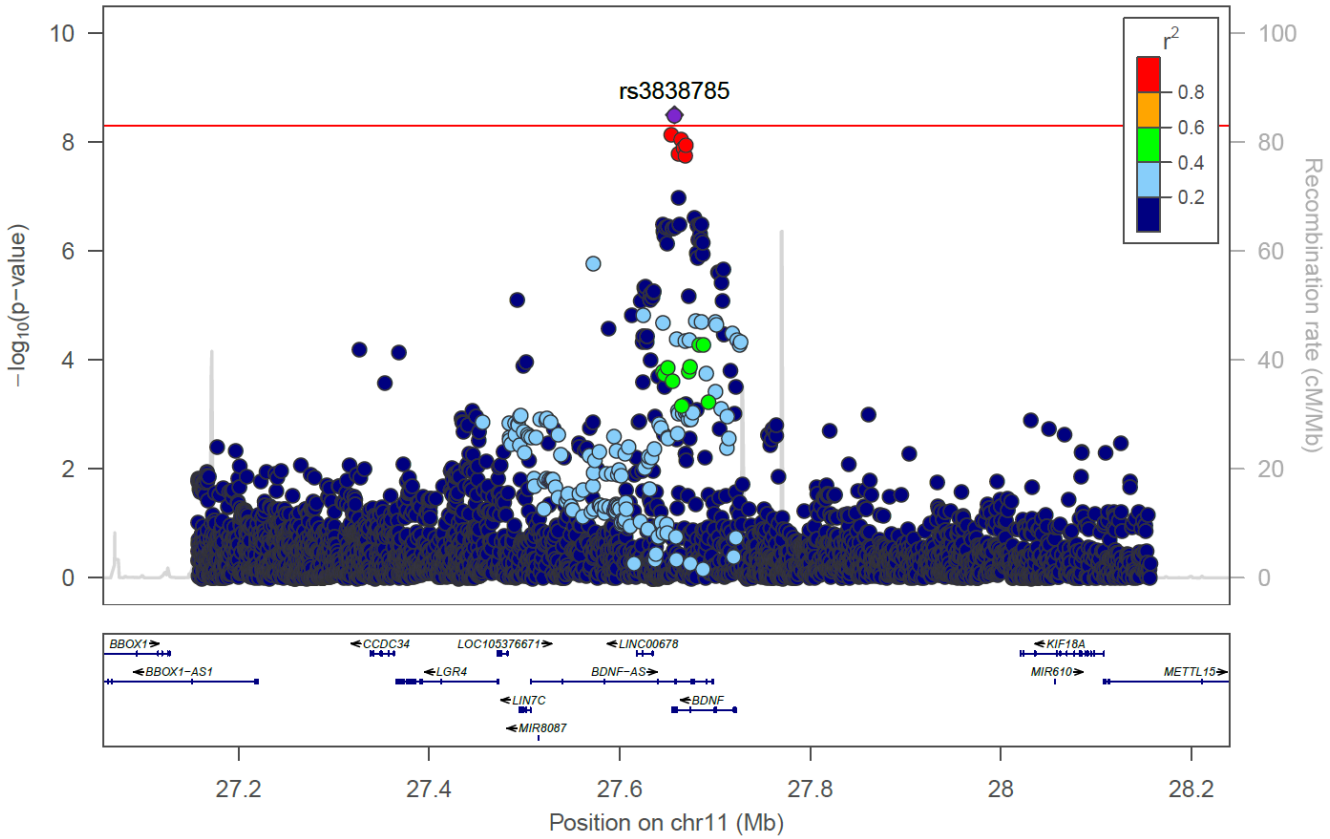

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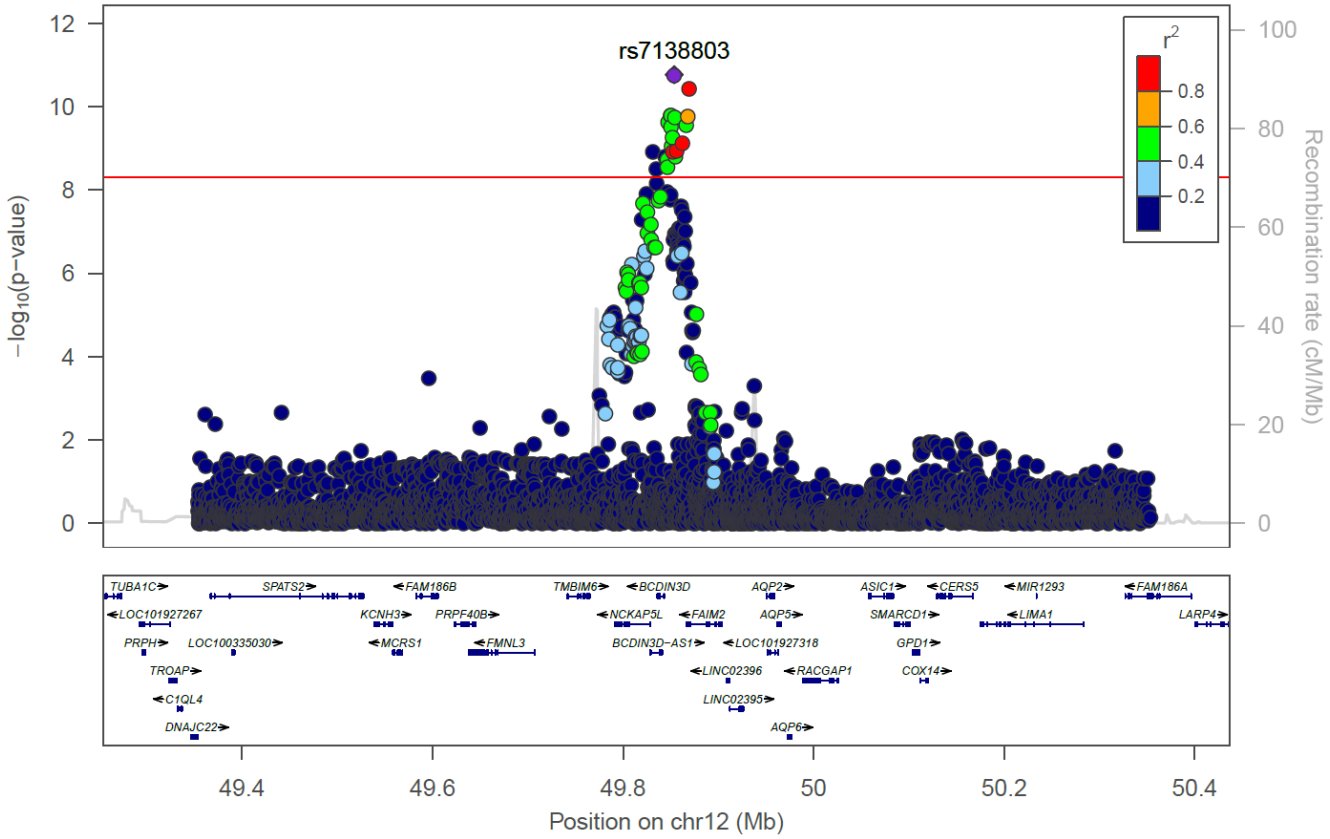

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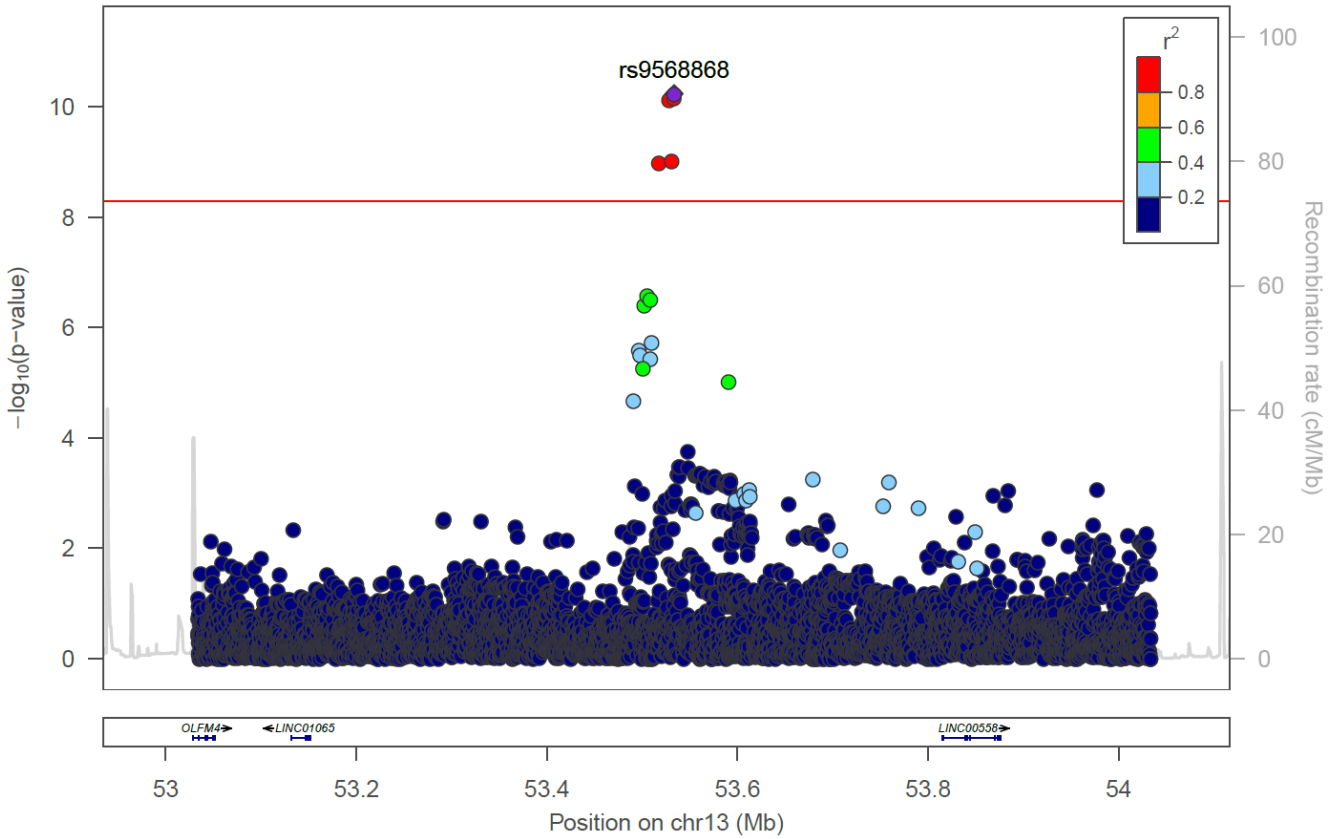
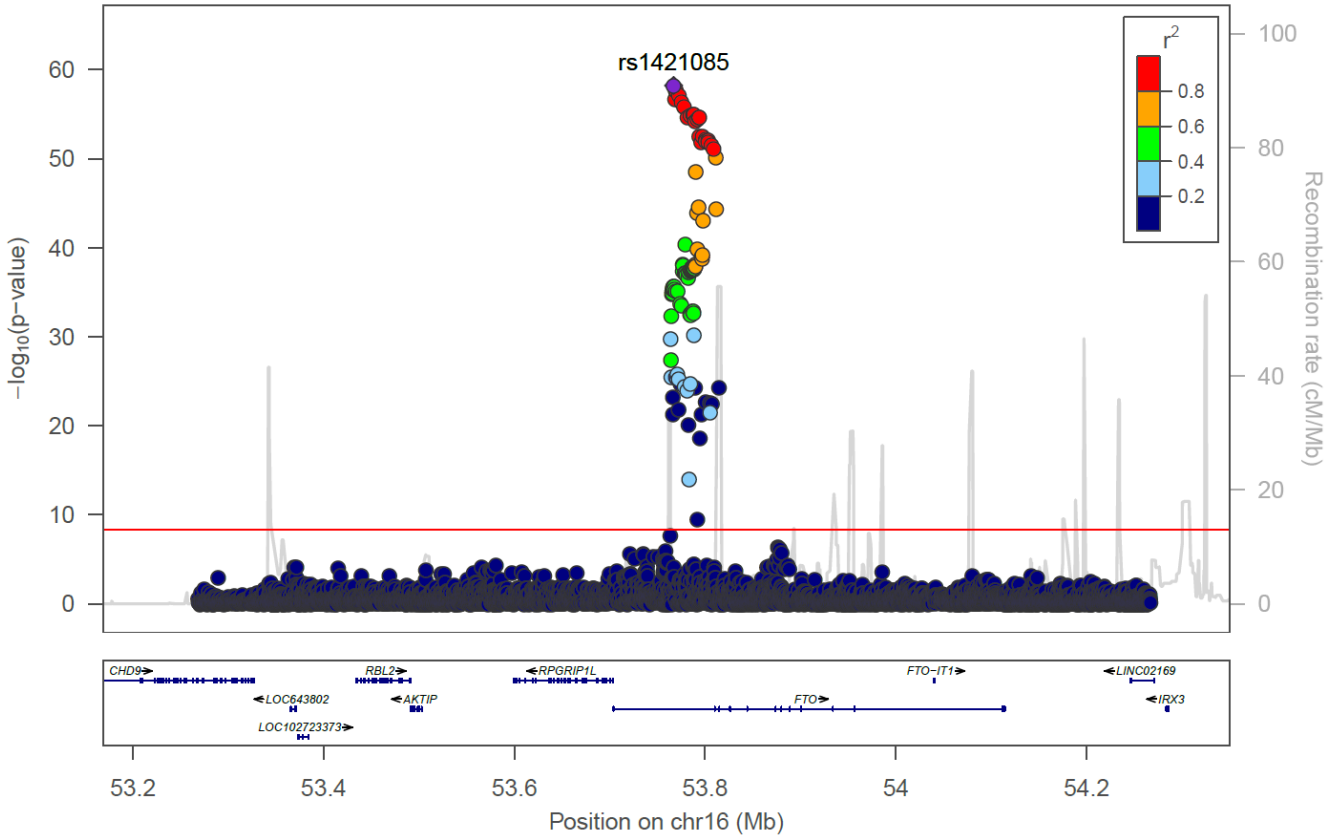


L) *FTO*, rs1421085



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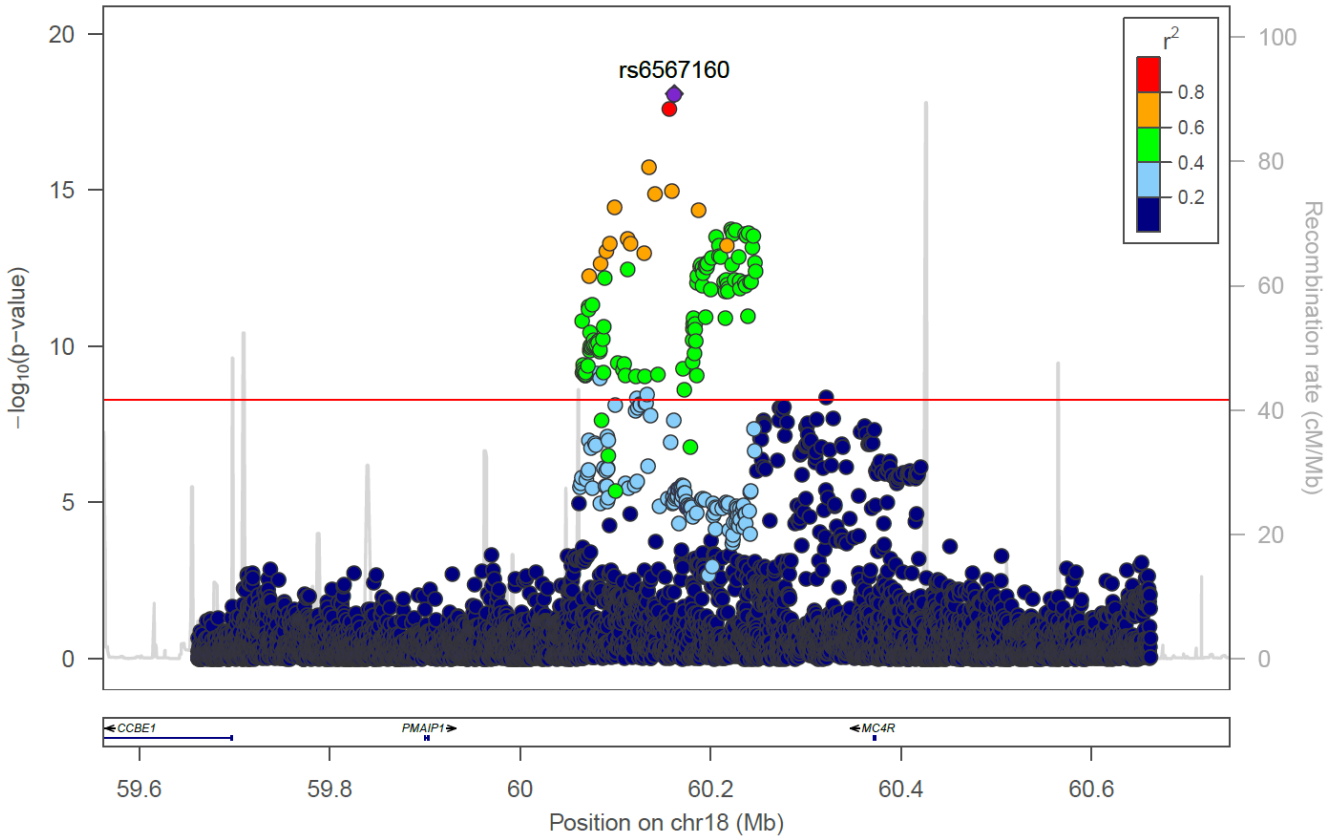

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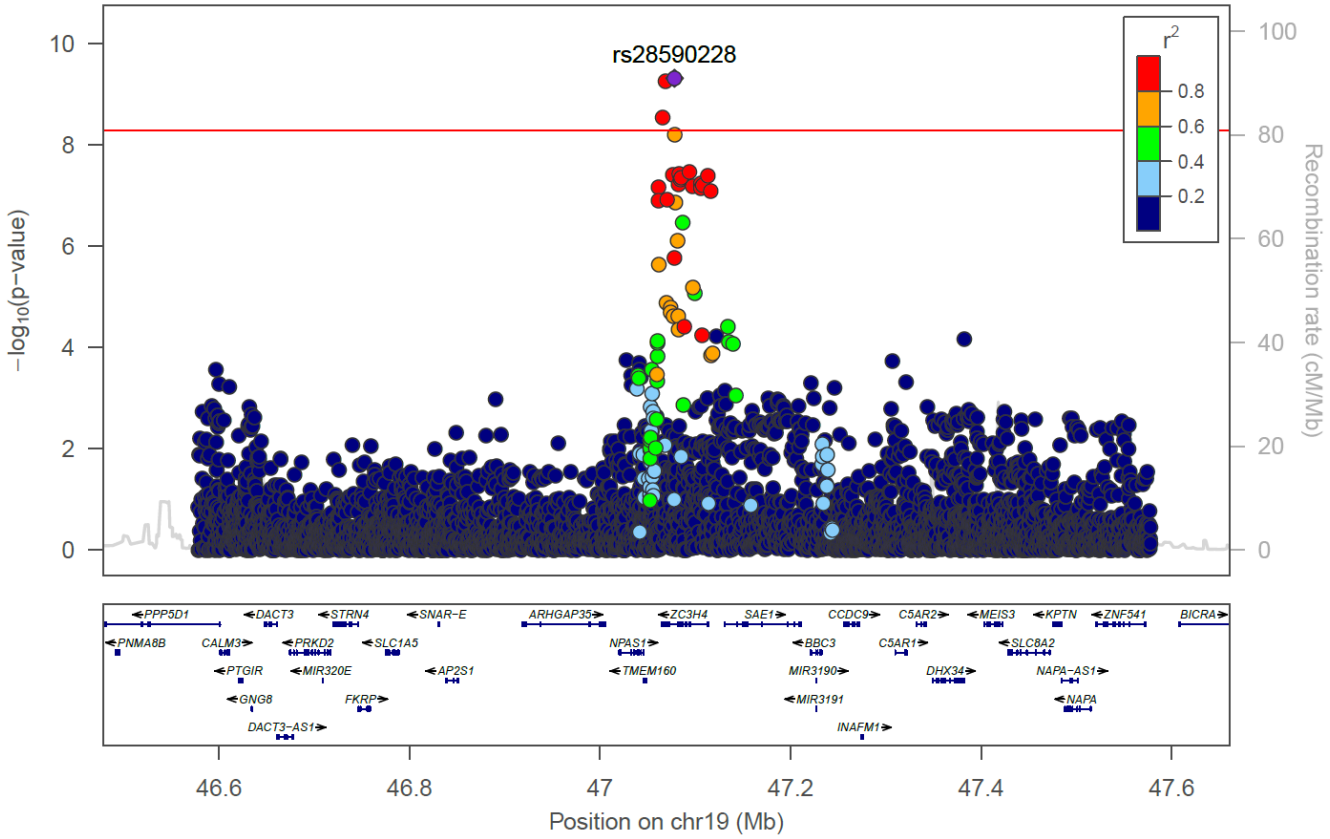
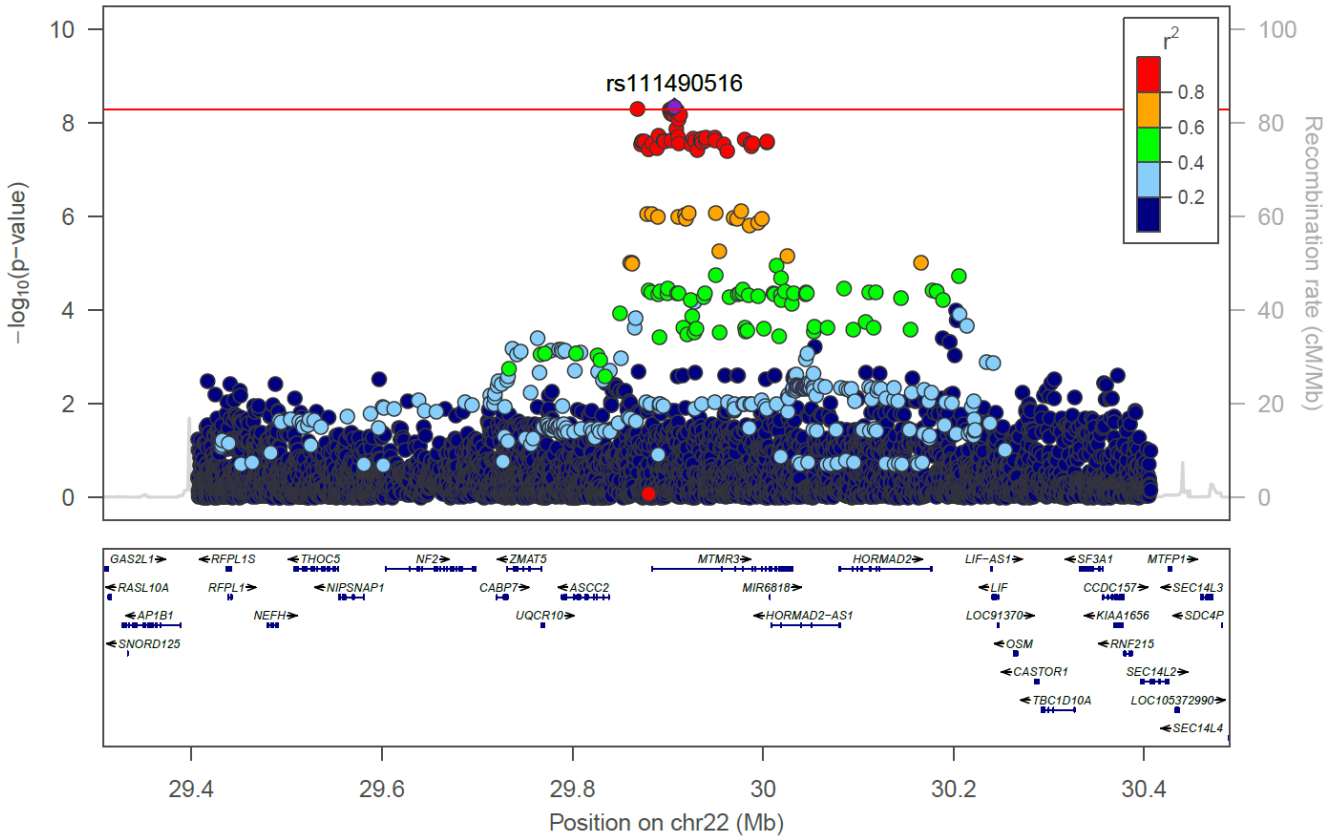
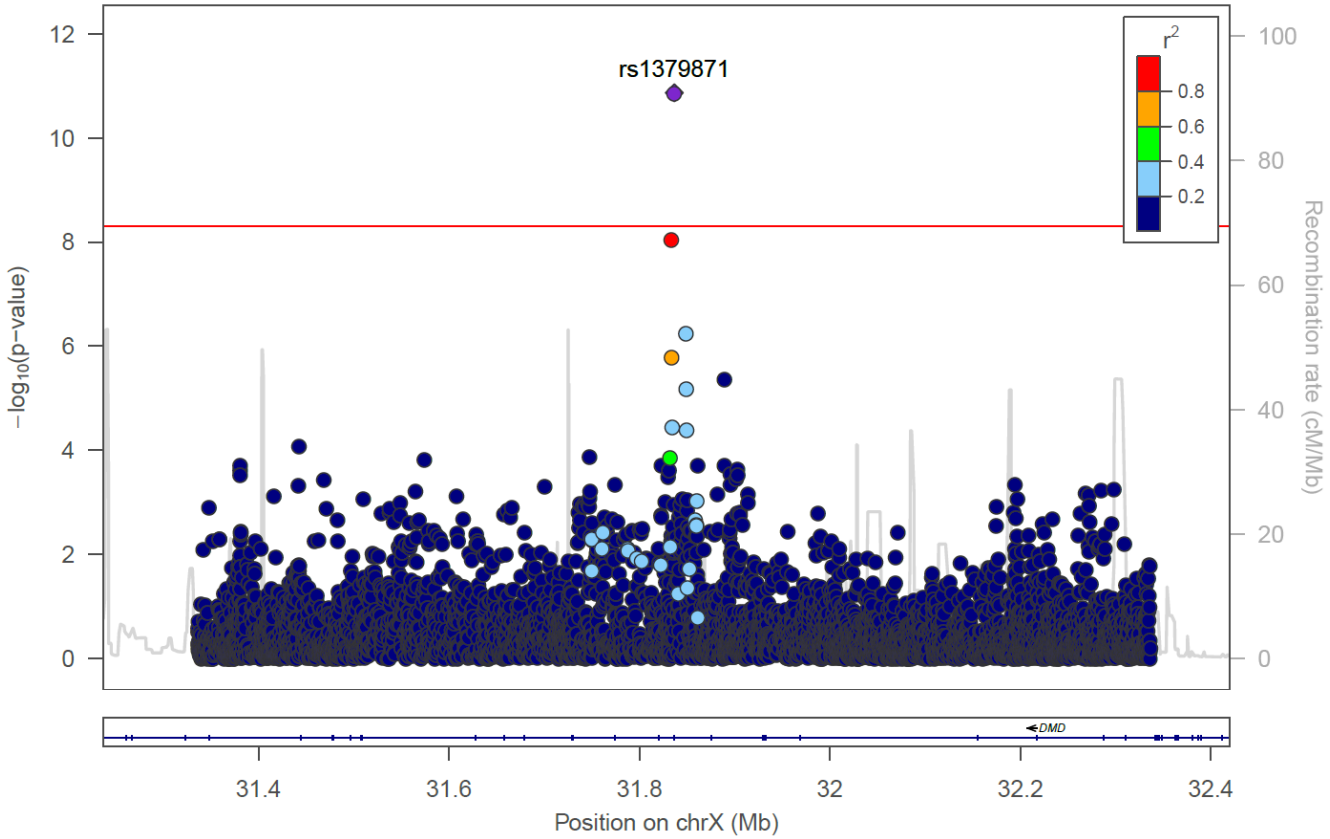


O) *MTMR3*, rs111490516

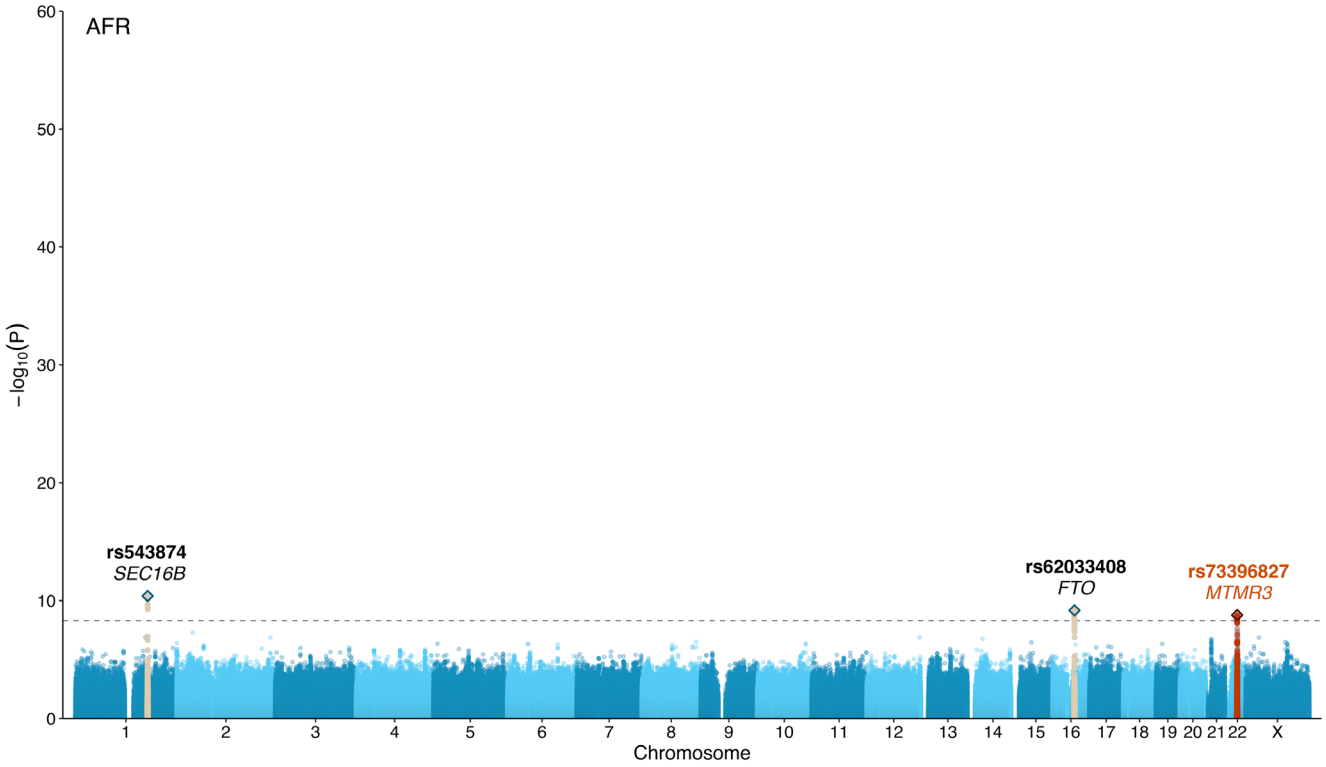


P) *DMD*, rs1379871



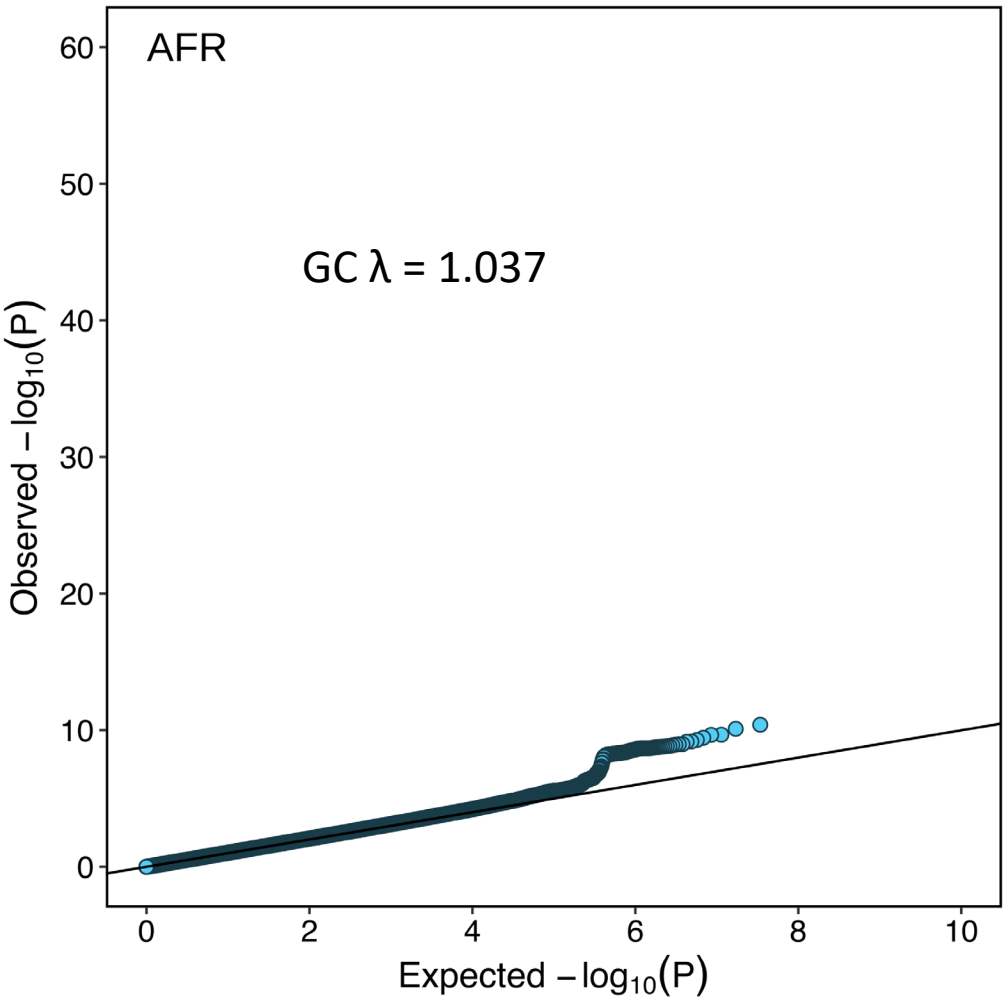
Supplementary Figure 4. Manhattan plot of African population group BMI GWAS

Manhattan plot of African population group, single variant analysis (N = 22,488 individuals). The novel locus *(MTMR3)* is highlighted in red. Previously reported BMI loci are in dark beige. The horizontal dashed line indicates genome-wide significant threshold $P = 5 \times 10^{-9}$.



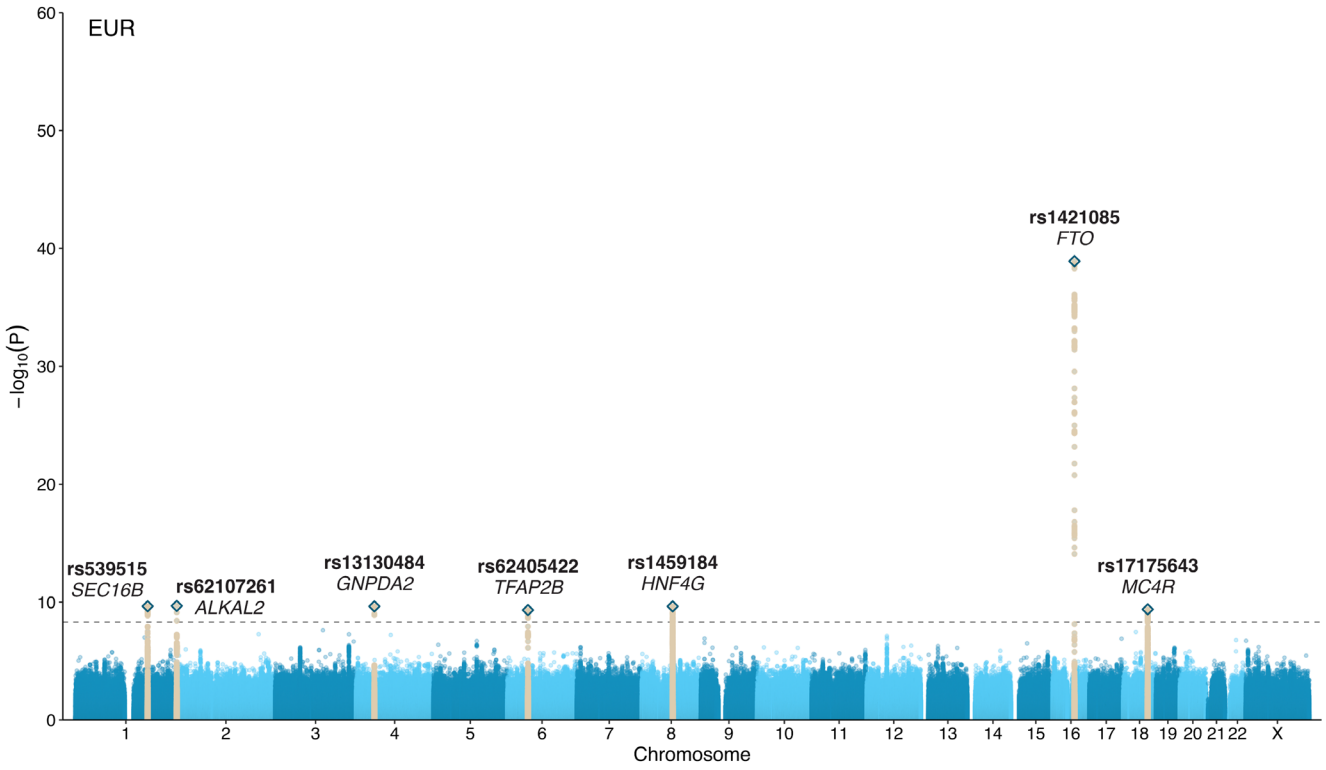
Supplementary Figure 5. QQ plot of African population group BMI GWAS

Quantile-quantile plot of African population group, single variant analysis (N = 22,488 individuals).



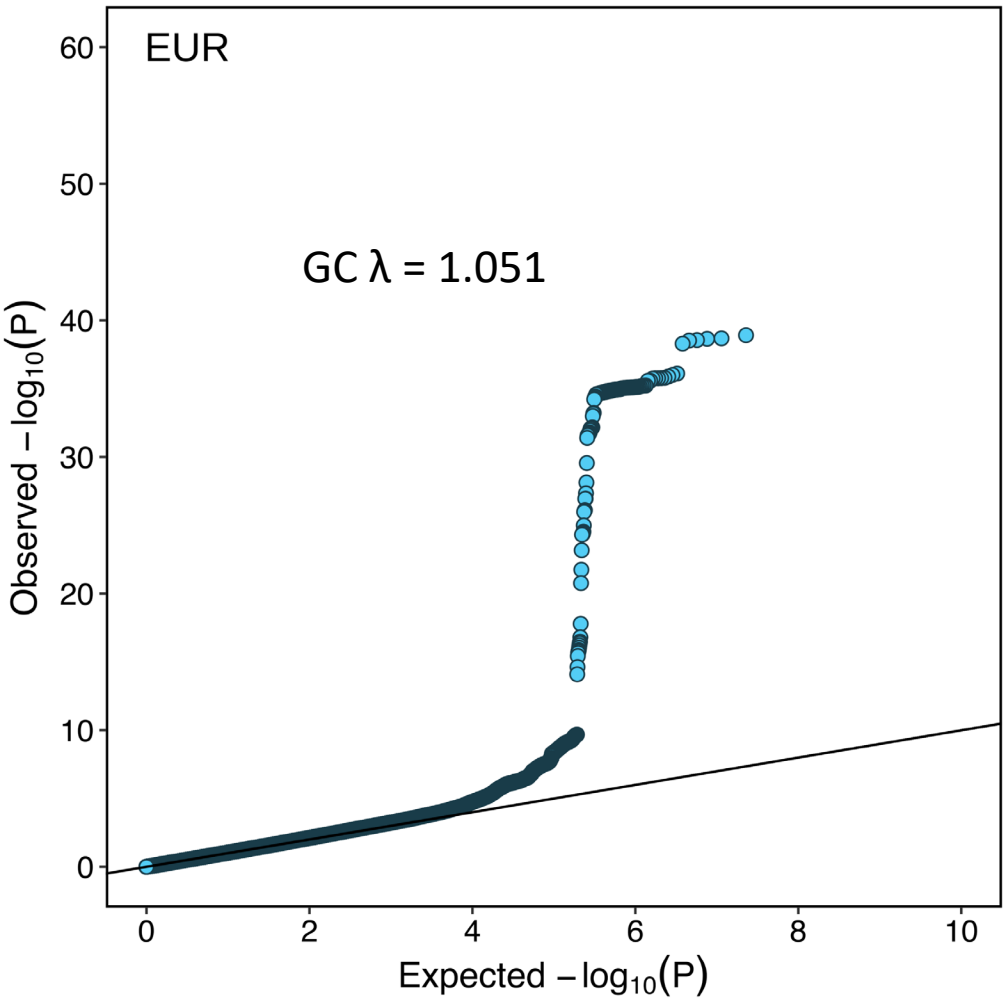
Supplementary Figure 6. Manhattan plot of European population group BMI GWAS

Manhattan plot of European population group, single variant analysis (N = 43,434 individuals). Previously reported BMI loci are in dark beige. The horizontal dashed line indicates genome-wide significant threshold $P = 5 \times 10^{-9}$.



Supplementary Figure 7. QQ plot of European population group BMI GWAS

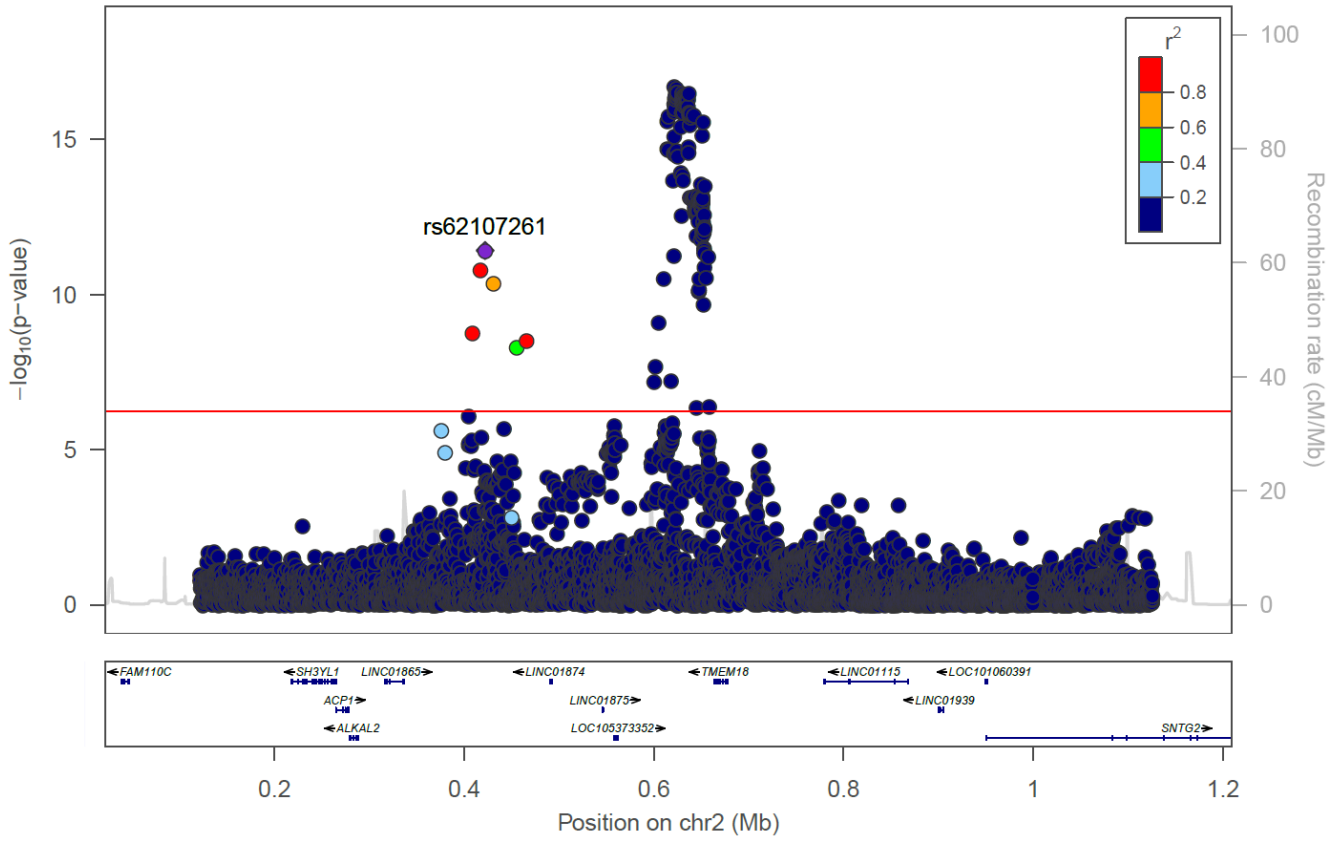
Quantile-quantile plot of European population group, single variant analysis (N = 43,434 individuals).



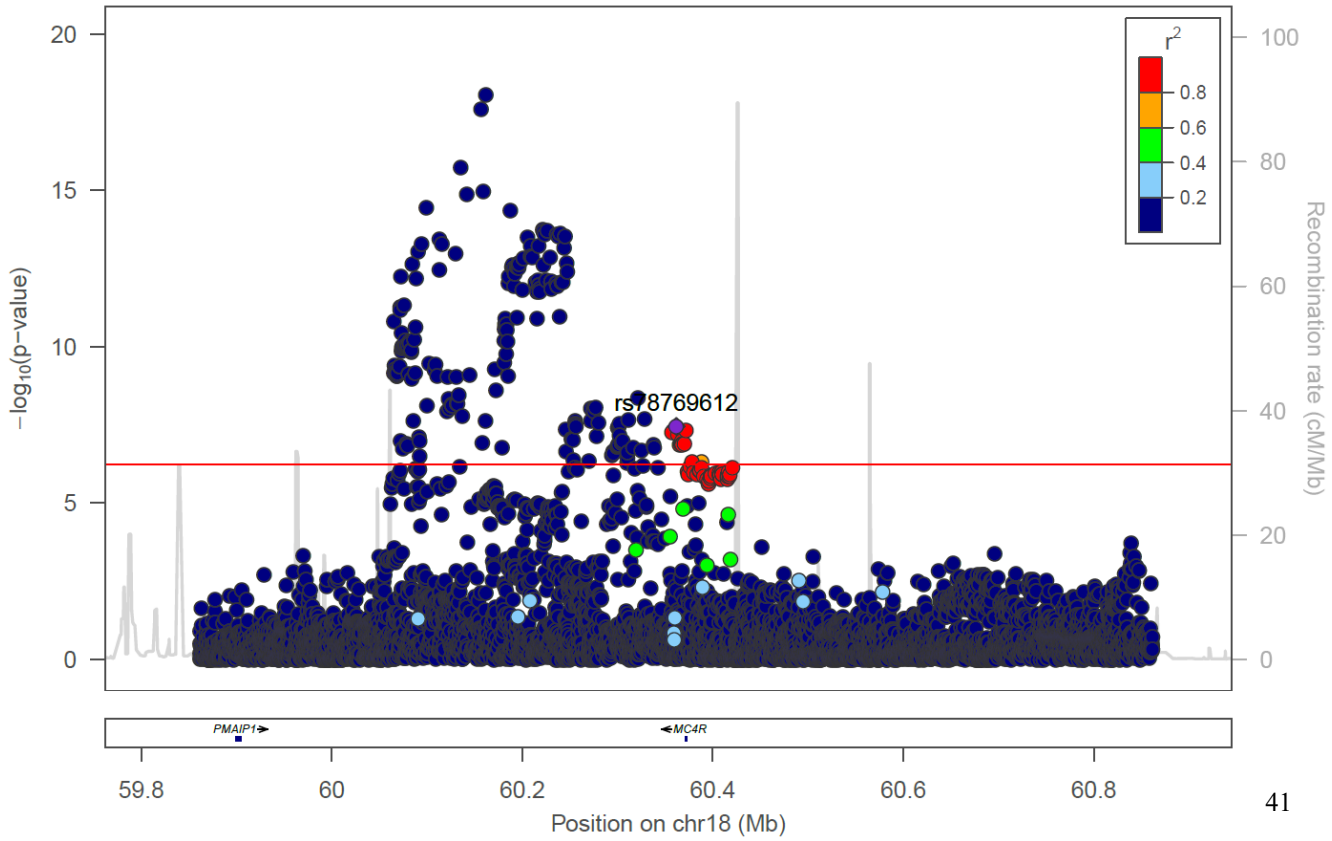
Supplementary Figure 8. Regional association plots of secondary signals

Regional association plots for each significant secondary signal in the multi-population analysis following conditional analysis on top variant, including all variants ± 500 kb from index variant. TOPMed study populations were used to calculate LD. The red line indicates $P = 5.67 \times 10^{-7}$. A) *ALKAL2*, rs62107261; B) *MC4R*, rs78769612.

A) *ALKAL2*, rs62107261

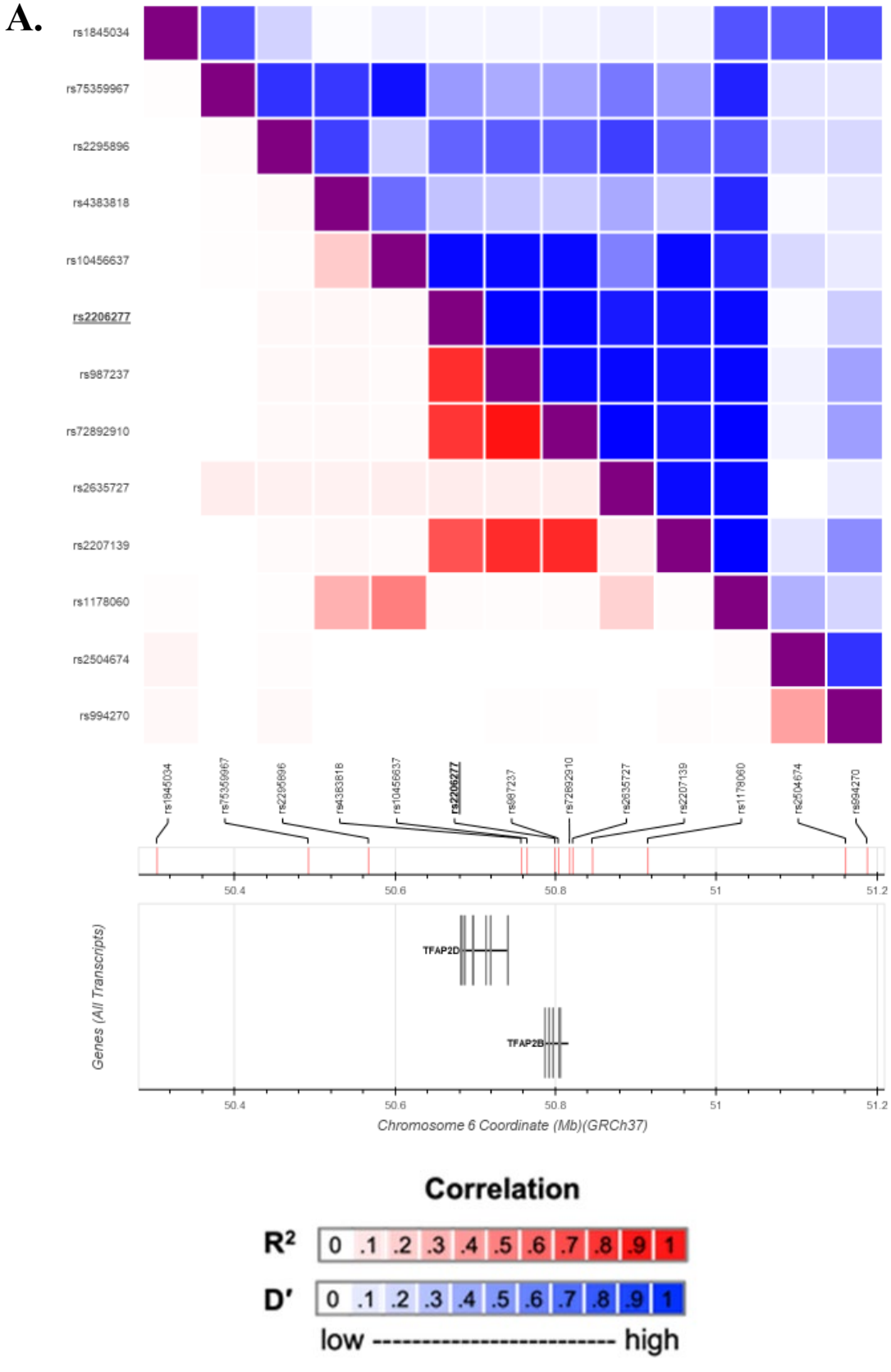


B) *MC4R*, rs78769612



Supplementary Figure 9. LD matrix heatmap for conditionally independent SNPs in known BMI-risk loci

Pairwise LD matrix heatmap for lead index SNP in discovery analyses (bold and underlined) and published BMI GWAS SNPs within 500 kb (+/-) of index SNPs. A) rs2206277 index SNP in *TFAP2B* locus; B) rs3838785 in *BDNF* locus.



Supplementary Figure 9. LD matrix heatmap for conditionally independent SNPs in known BMI-risk loci

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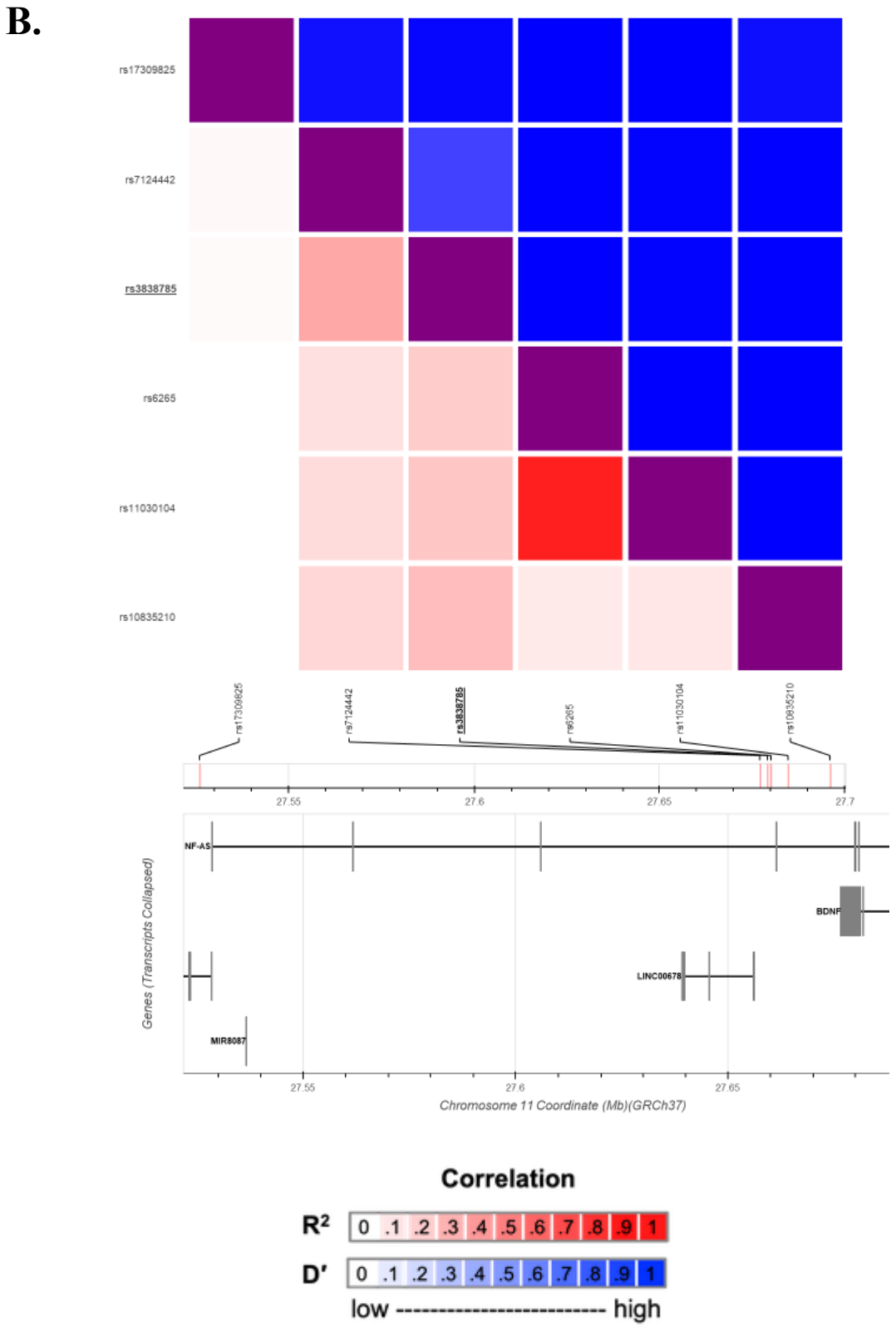
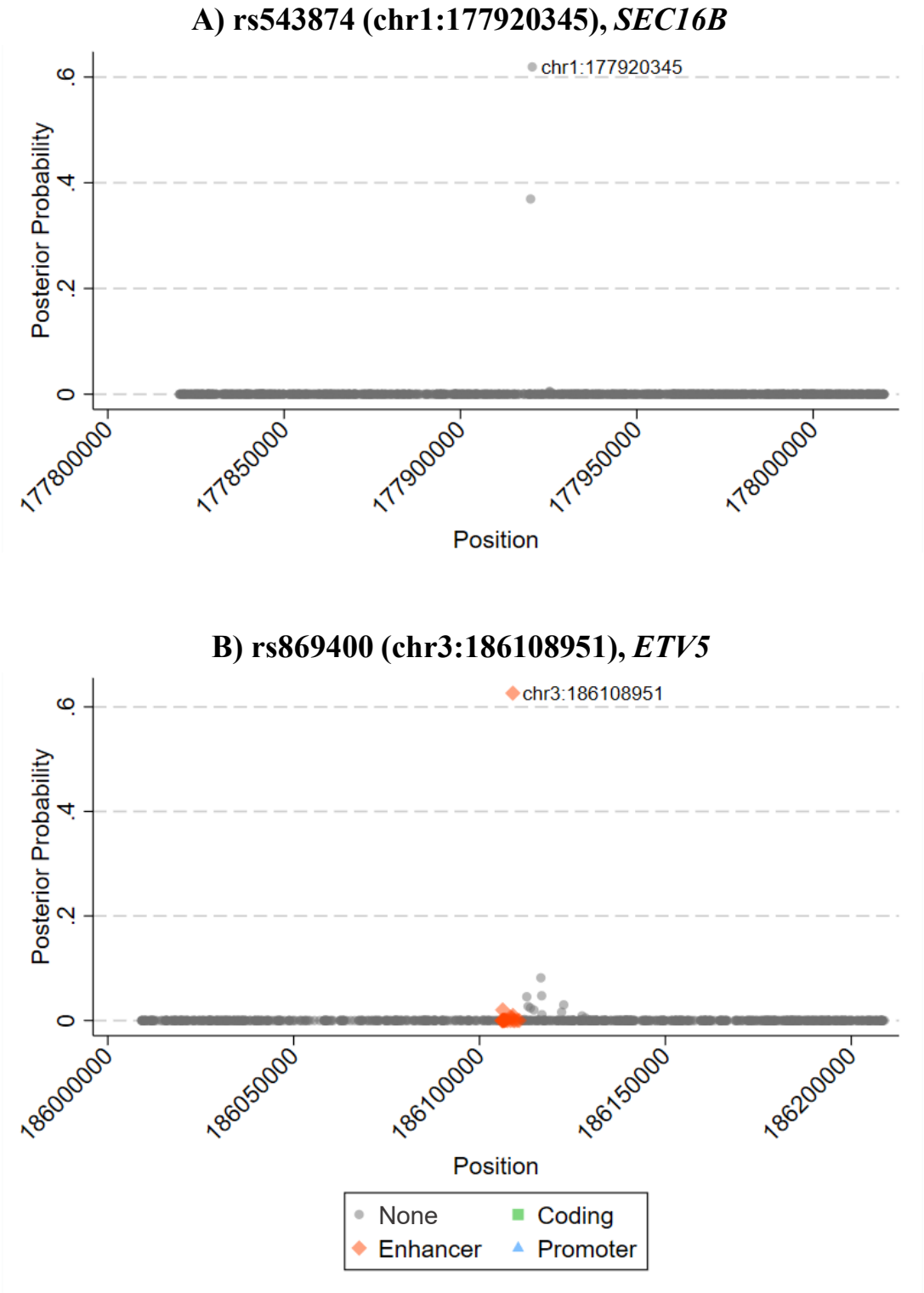


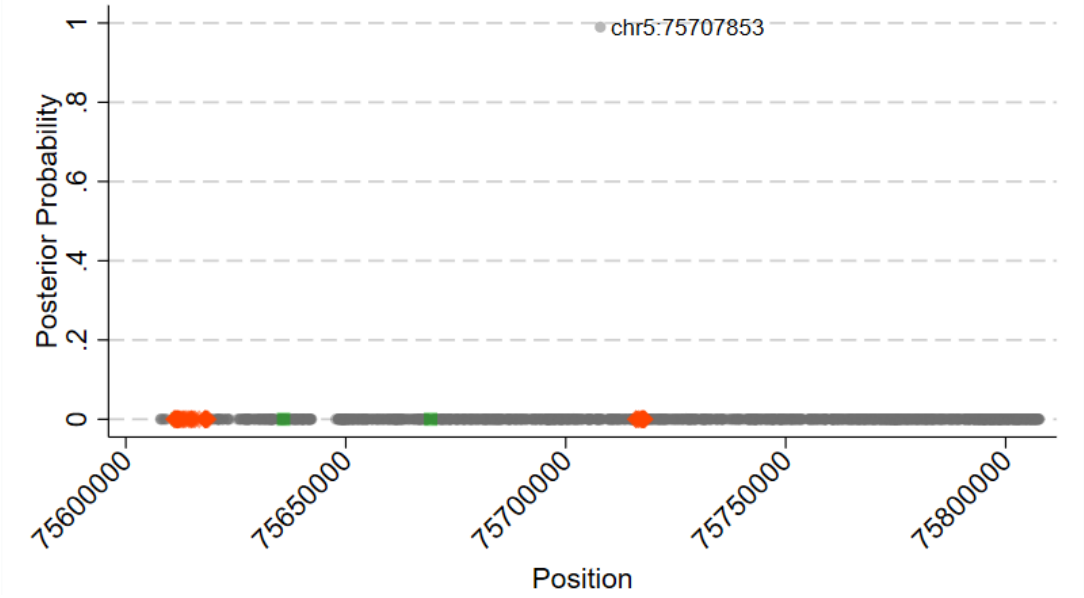
Supplementary Figure 10. Fine-mapping regional plots

Regional plots of posterior probability (PP) from fine-mapping analysis in PAINTOR, including all variants ± 100 kb from index variant for each locus with any variant exhibiting a moderate PP > 0.5. The plots appear in order of chromosomal location. TOPMed study populations were used to calculate LD. Shape and color indicate potential functional consequence of each variant as reported in Variant Effect Prediction (VEP) tool or GeneHancer (see methods for details).

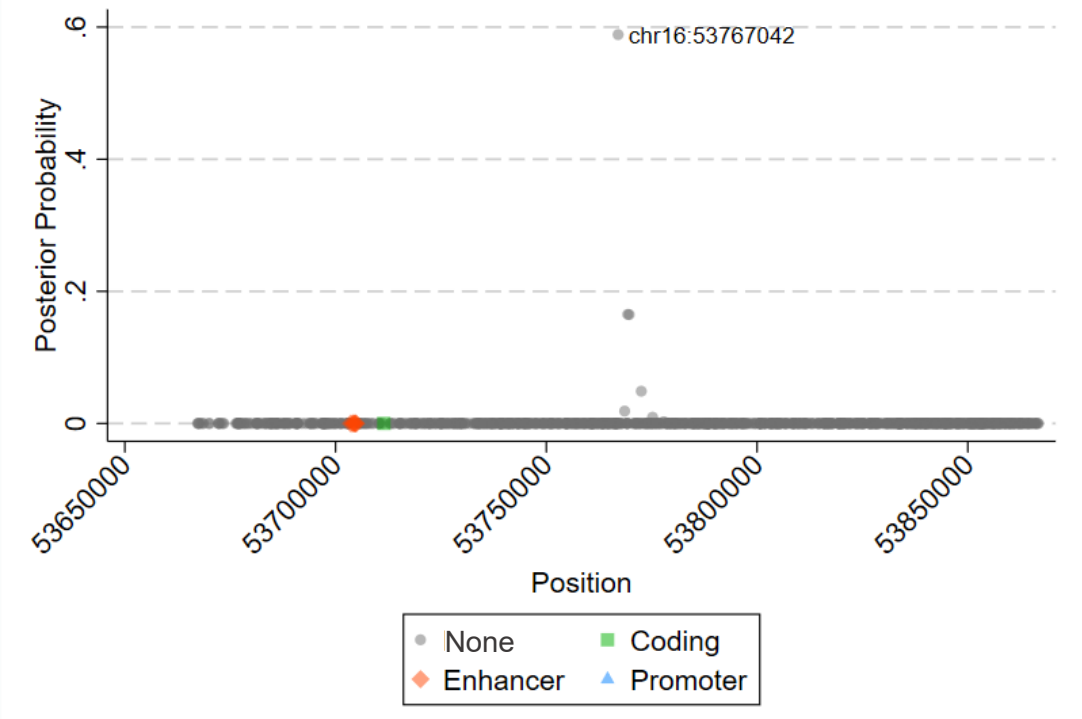
A) rs543874, *SEC16B;* B) rs869400, *ETV5*; C) rs2307111, *POC5*; D) rs1421085, *FTO*; E) rs6567160, *MC4R*; F) rs55731973, *ZC3H4*; G) rs1379871, *DMD*.



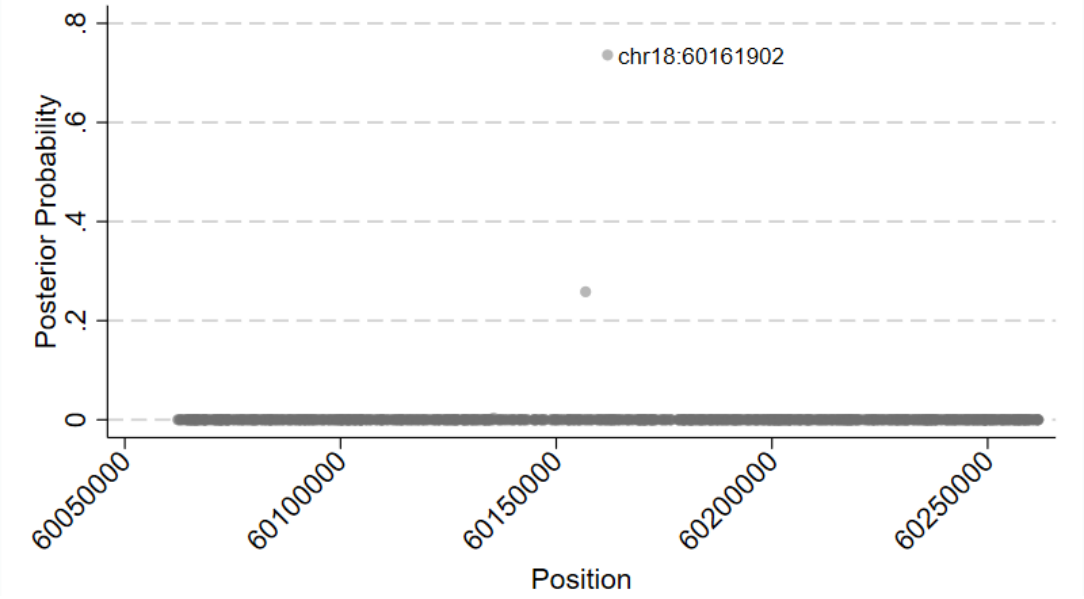
C) rs2307111 (chr5: 75707853), *POC5*



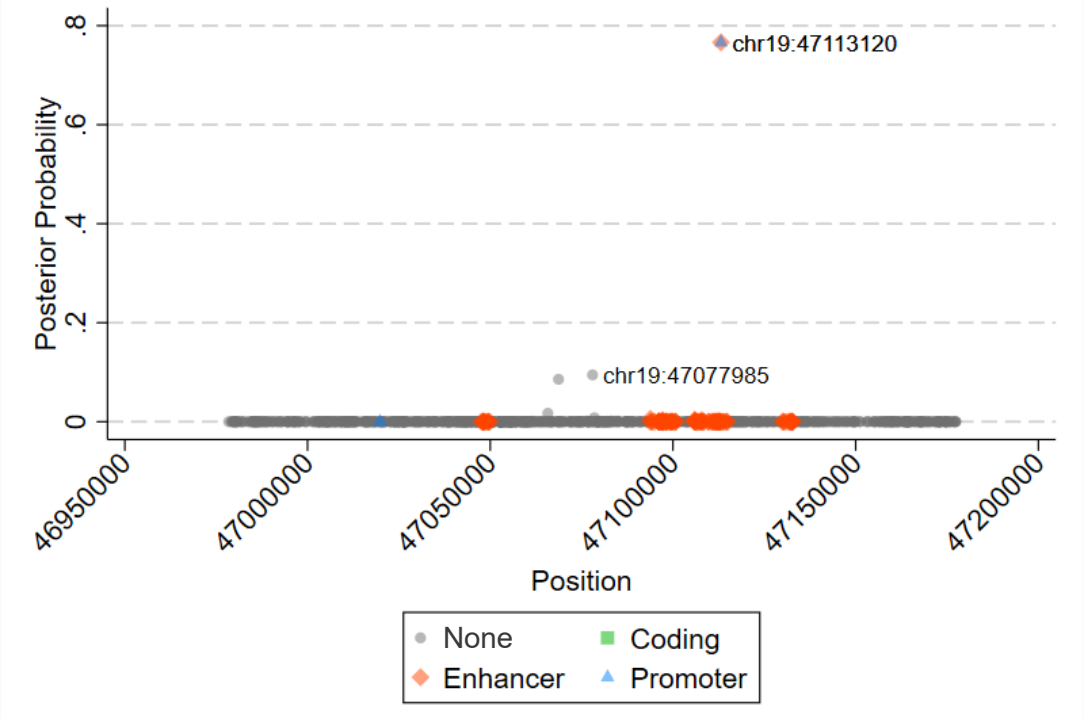
D) rs1421085 (chr16:53767042), *FTO*



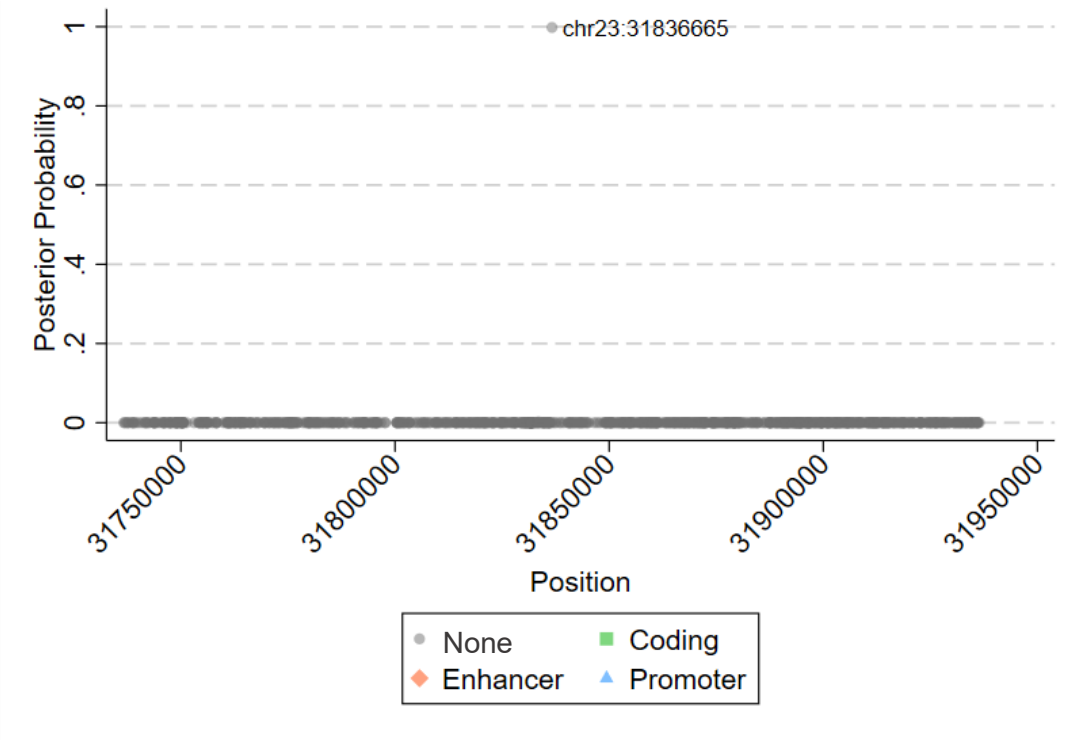
E) rs6567160 (chr18:60161902), *MC4R*



F) rs55731973 (chr19:47113120), *ZC3H4*

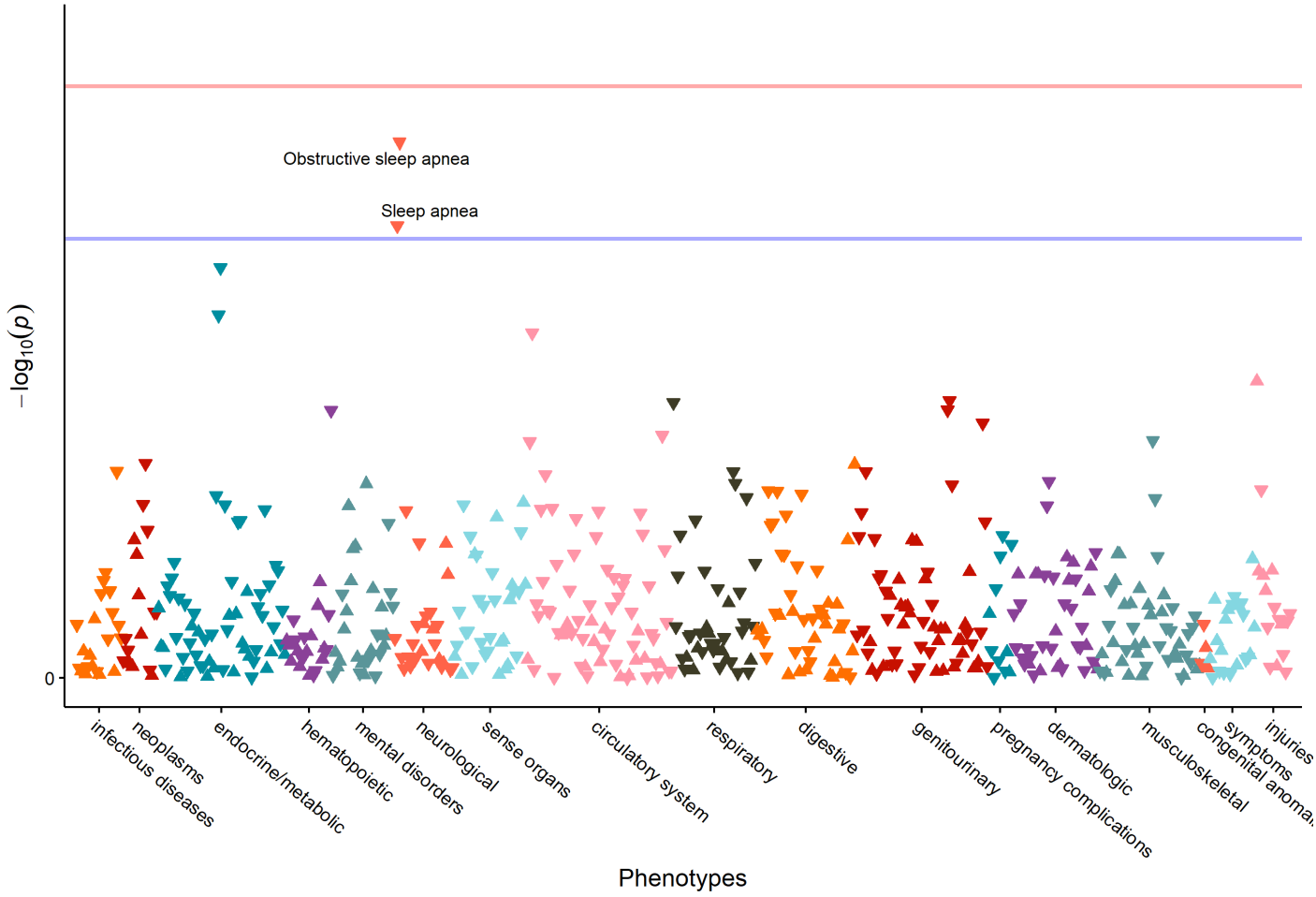


G) rs1379871 (chrX:31836665), *DMD*



Supplementary Figure 11. PheWAS meta-analysis Manhattan plot

Manhattan plot of the PheWAS meta-analysis results. The red line indicates phenome-wide significance threshold ($P < 0.05/538$ PheCodes $= 9.3 \times 10^{-5}$), and the blue line indicates suggestive significance ($P < 0.001$). Only suggestively significant PheCodes are annotate with their phenotype. Arrow indicates direction of effect.



Supplementary Data 1. Participant counts by study and population group

Study	Population groups															Total	Individuals with imputed population membership by study, n (%)
	African	Amish	Asian	Barbadian	Central American	Costa Rican	Cuban	Dominican	European	Han Chinese	Mexican	Puerto Rican	Samoan	South American	Taiwanese		
Amish	0	1106	0	0	0	0	0	0	0	0	0	0	0	0	0	**1106**	0 (0.0%)
ARIC	1503	0	0	0	0	0	0	0	6158	0	0	0	0	0	0	**7661**	0 (0.0%)
BAGS	0	0	0	248	0	0	0	0	0	0	0	0	0	0	0	**248**	0 (0.0%)
BioMe	3138	0	408	0	161	0	149	763	3200	0	101	2595	0	289	0	**10804**	5248 (48.6%)
CARDIA	1379	0	0	0	0	0	0	0	1684	0	0	0	0	0	0	**3063**	0 (0.0%)
CCAF	0	0	0	0	0	0	1	0	360	0	0	0	0	0	0	**361**	4 (1.1%)
CFS	493	0	2	0	0	0	0	0	450	0	1	2	0	0	0	**948**	14 (1.5%)
CHS	711	0	0	0	0	0	0	0	2788	0	12	0	0	0	0	**3511**	53 (1.5%)
COPDGene	3196	0	0	0	0	0	0	0	6661	0	0	0	0	0	0	**9857**	0 (0.0%)
CRA	0	0	0	0	0	341	0	0	0	0	0	0	0	0	0	**341**	123 (36.1%)
DHS (AA CAC)	384	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**384**	0 (0.0%)
FHS	4	0	1	0	0	0	1	0	4092	0	0	0	0	0	0	**4098**	480 (11.7%)
GALAII	0	0	0	0	29	0	3	1	2	0	175	130	0	4	0	**344**	32 (9.3%)
GeneSTAR	777	0	0	0	0	0	0	0	971	0	0	0	0	0	0	**1748**	0 (0.0%)
GENOA	1193	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**1193**	0 (0.0%)
GenSalt	0	0	0	0	0	0	0	0	0	1787	0	0	0	0	0	**1787**	0 (0.0%)
GOLDN	0	0	0	0	0	0	0	0	914	0	0	0	0	0	0	**914**	0 (0.0%)
HCHS/SOL	23	0	0	0	509	0	1899	1124	33	0	1728	2073	0	297	0	**7686**	293 (3.8%)
HVH	26	0	8	0	0	0	0	0	650	0	3	2	0	0	0	**689**	24 (3.5%)
HyperGEN	1838	0	1	0	0	0	0	0	0	0	0	0	0	0	0	**1839**	0 (0.0%)
JHS	3121	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**3121**	0 (0.0%)
LTRC	83	0	4	0	0	0	0	0	1276	0	12	8	0	0	0	**1383**	51 (3.7%)
Mayo_VTE	3	0	0	0	0	0	1	0	920	0	5	1	0	0	0	**930**	54 (5.8%)
MESA	1846	0	603	0	64	0	35	144	1861	0	544	140	0	81	0	**5318**	14 (0.3%)
MGH_AF	1	0	0	0	1	0	3	0	974	0	2	0	0	1	0	**982**	25 (2.5%)
OMG_SCD	443	0	0	0	0	0	0	0	0	0	0	1	0	0	0	**444**	444 (100.0%)
Partners	4	0	1	0	0	0	0	0	117	0	0	0	0	0	0	**122**	2 (1.6%)
SAFS	5	0	2	0	0	0	0	0	23	0	1504	0	0	0	0	**1534**	914 (59.6%)
SAGE	448	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**448**	1 (0.2%)
Samoan	0	0	0	0	0	0	0	0	0	0	0	0	1274	0	0	**1274**	0 (0.0%)
THRV	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2053	**2053**	0 (0.0%)
VAFAR	0	0	0	0	0	0	0	0	173	0	0	0	0	0	0	**173**	0 (0.0%)
VU_AF	46	0	5	0	1	0	1	0	1030	0	2	0	0	1	0	**1086**	6 (0.6%)
walk_PHaSST	373	0	0	0	3	0	1	11	1	0	0	0	0	2	0	**391**	29 (7.4%)
WGHS	0	0	0	0	0	0	0	0	111	0	0	0	0	0	0	**111**	0 (0.0%)
WHI	1450	0	206	0	8	0	34	3	8985	0	176	39	0	20	0	**10921**	204 (1.9%)
Total	**22488**	**1106**	**1241**	**248**	**776**	**341**	**2128**	**2046**	**43434**	**1787**	**4265**	**4991**	**1274**	**695**	**2053**	**88873**	**8015 (9.0%)**
Individuals with imputed population membership by population group, n (%)	1038 (4.6%)	0 (0.0%)	212 (17.1%)	0 (0.0%)	193 (24.9%)	123 (36.1%)	202 (9.5%)	834 (40.8%)	1249 (2.9%)	0 (0.0%)	1128 (26.4%)	2712 (54.3%)	0 (0.0%)	324 (46.6%)	0 (0.0%)	**8015 (9.0%)**	

Supplementary Data 2. BMI and percent female by study

Study	N	Women, N (%)	BMI, mean (SD)
Amish	1106	552 (49.91)	26.97 (4.65)
ARIC	7661	4230 (55.21)	27.35 (5.23)
BAGS	248	141 (56.85)	28.00 (6.87)
BioMe	10804	6242 (57.77)	29.12 (7.01)
CARDIA	3063	1739 (56.77)	24.45 (4.96)
CCAF	361	69 (19.11)	30.42 (6.34)
CFS	948	521 (54.96)	32.27 (8.75)
CHS	3511	2045 (58.25)	26.84 (4.73)
COPDGene	9857	4608 (46.75)	28.82 (6.26)
CRA	341	197 (57.77)	26.39 (4.30)
DHS (AA CAC)	384	220 (57.29)	33.92 (7.79)
FHS	4098	2224 (54.27)	25.82 (4.83)
GALAII	344	226 (65.70)	27.47 (6.90)
GeneSTAR	1748	1037 (59.32)	29.62 (7.17)
GENOA	1193	835 (69.99)	31.08 (6.66)
GenSalt	1787	843 (47.17)	23.44 (3.12)
GOLDN	914	481 (52.63)	28.33 (5.75)
HCHS/SOL	7686	4478 (58.26)	30.11 (6.40)
HVH	689	241 (34.98)	31.86 (7.90)
HyperGEN	1839	1165 (63.35)	32.01 (7.75)
JHS	3121	1952 (62.54)	31.89 (7.31)
LTRC	1383	664 (48.01)	28.32 (5.91)
Mayo_VTE	930	527 (56.67)	31.29 (8.02)
MESA	5318	2801 (52.67)	28.51 (5.48)
MGH_AF	982	202 (20.57)	28.65 (5.56)
OMG_SCD	444	243 (54.73)	25.22 (6.84)
Partners	122	43 (35.25)	30.80 (7.42)
SAFS	1534	899 (58.60)	31.19 (7.41)
SAGE	448	273 (60.94)	28.11 (7.51)
Samoan	1274	772 (60.60)	33.75 (6.84)
THRV	2053	1043 (50.80)	24.76 (3.47)
VAFAR	173	55 (31.79)	32.70 (6.78)
VU_AF	1086	300 (27.62)	31.19 (6.85)
walk_PHaSST	391	210 (53.71)	24.83 (4.86)
WGHS	111	111 (100.00)	28.20 (6.11)
WHI	10921	10920 (99.99)	28.73 (5.97)

Supplementary Data 3. BMI and percent female by population group

Population group	N	Women, N (%)	BMI, mean (SD)
African	22488	13903 (61.82)	30.22 (7.32)
Amish	1106	552 (49.91)	26.97 (4.65)
Asian	1241	711 (57.29)	24.79 (4.42)
Barbadian	248	141 (56.85)	28.00 (6.87)
Central American	776	466 (60.05)	29.98 (6.26)
Costa Rican	341	197 (57.77)	26.39 (4.30)
Cuban	2128	1119 (52.58)	29.20 (5.84)
Dominican	2046	1304 (63.73)	29.05 (5.63)
European	43434	26071 (60.02)	27.76 (5.83)
Han Chinese	1787	843 (47.17)	23.44 (3.12)
Mexican	4265	2555 (59.91)	30.52 (6.72)
Puerto Rican	4991	3027 (60.65)	30.47 (6.95)
Samoan	1274	772 (60.60)	33.75 (6.84)
South American	695	405 (58.27)	28.73 (5.67)
Taiwanese	2053	1043 (50.80)	24.76 (3.47)

Supplementary Data 4. Study-specific descriptive statistics of age and BMI

Study	Population group	Trait	Men						Women					
			N	Mean	SD	Median	Min	Max	N	Mean	SD	Median	Min	Max
Discovery studies														
Amish	Amish	Age (years)	554	49.39	17.29	49	20	90	552	51.63	16.29	53	20	90
		BMI (kg/m²)	554	26.16	3.55	25.93	18.43	43.6	552	27.78	5.42	27.47	16.91	46.85
ARIC	African	Age (years)	608	53.95	6.07	53	44	66	895	53.85	5.89	53	45	65
		BMI (kg/m²)	608	27.7	4.98	27.05	15.65	52.25	895	31.01	6.96	29.6	14.17	65.77
ARIC	European	Age (years)	2823	54.43	5.7	54	44	66	3335	53.71	5.74	53	44	66
		BMI (kg/m²)	2823	27.31	3.91	26.81	16.07	53.75	3335	26.34	5.27	25.26	14.35	54.61
BAGS	Barbadian	Age (years)	107	40.84	12.66	43	18	74	141	38.19	10.83	39	18	72
		BMI (kg/m²)	107	26.34	4.95	25.48	15.86	47.55	141	29.26	7.81	28.69	14.84	59.53
BioMe	Asian	Age (years)	212	53.12	13.47	54	23	81	196	46.77	14.42	44.5	21	91
		BMI (kg/m²)	212	26.59	5.51	25.43	14.35	49.46	196	24.19	4.61	23.27	17.01	43.41
BioMe	African	Age (years)	1074	52.06	12.63	51	19	90	2064	53.05	13.17	53	19	92
		BMI (kg/m²)	1074	28.63	6.36	27.79	15.29	65.61	2064	31.9	8.68	30.42	13.08	78.78
BioMe	Central American	Age (years)	73	52.58	14.4	54	19	77	88	52.45	13.99	55	23	77
		BMI (kg/m²)	73	28.59	5.34	28.19	17.54	45.33	88	30.16	5.51	29	17.95	52.48
BioMe	Cuban	Age (years)	76	59.08	12.92	59	27	84	73	57.96	14.01	58	27	89
		BMI (kg/m²)	76	29.56	5.44	28.32	20.8	44.94	73	27.28	6.45	25.13	17.14	47.26
BioMe	Dominican	Age (years)	290	61.16	13.47	63	24	97	473	54.34	13.31	55	19	89
		BMI (kg/m²)	290	27.92	4.98	27.41	16.17	52.97	473	29.27	5.79	28.26	18.16	58.31
BioMe	Mexican	Age (years)	45	43.87	10.64	42	27	77	56	43.88	10.2	42	31	68
		BMI (kg/m²)	45	28.64	4.28	29.07	21.45	37.48	56	27.89	3.97	27.92	19.31	36.33
BioMe	Puerto Rican	Age (years)	962	55.02	12.5	55	25	87	1633	55.22	13.63	55	19	97
		BMI (kg/m²)	962	29.36	6.65	28.22	13.31	86.81	1633	31.05	7.11	30.17	14.26	68.02
BioMe	South American	Age (years)	137	57.76	13.24	58	25	91	152	54.38	14.54	56.5	24	83
		BMI (kg/m²)	137	28.85	4.99	28.35	19.85	53.11	152	29.42	7	28.23	19.42	70.57
BioMe	European	Age (years)	1693	59.47	14.63	60	19	97	1507	55.31	14.86	56	19	90
		BMI (kg/m²)	1693	27.96	5.33	27.01	15.46	63.11	1507	25.97	6.08	24.57	14.15	57.08
CARDIA	African	Age (years)	550	24.15	3.65	24	18	30	829	24.49	3.82	25	18	31
		BMI (kg/m²)	550	24.63	4.3	23.94	15.76	44.11	829	26.04	6.56	24.31	14.51	53.42
CARDIA	European	Age (years)	774	25.6	3.27	26	18	30	910	25.59	3.32	26	18	30
		BMI (kg/m²)	774	24.35	3.54	23.76	16.81	43.17	910	22.98	4.17	21.96	16.28	46.84
CCAF	Cuban and European*	Age (years)	292	54.34	9.02	56	20	76	69	55.83	10.24	58	22	73
		BMI (kg/m²)	292	30.47	5.96	29.02	20.95	70.17	69	30.24	7.79	28.65	16.48	50.2
CFS	European	Age (years)	216	45.81	14.9	44.5	18	81	234	43.49	14.3	41	18	84
		BMI (kg/m²)	216	31.4	7.24	29.83	19.33	60.95	234	30.3	8.38	29.08	17.52	66.6
CFS	non-Eurpean[1]	Age (years)	211	43.14	14.95	42	18	81	287	44.23	15.13	43	18	86
		BMI (kg/m²)	211	31.83	8.28	30.92	12.71	58.86	287	34.86	9.78	32.72	16.09	84.8
CHS	European	Age (years)	1196	73.06	5.55	72	65	94	1592	72.24	5.17	71	65	98
		BMI (kg/m²)	1196	26.4	3.69	26.05	15.61	46.23	1592	26.31	4.8	25.75	14.65	48.05
CHS	non-European[2]	Age (years)	270	72.42	5.52	71	65	92	453	72.89	5.62	72	65	93
		BMI (kg/m²)	270	27.21	4.27	26.84	16.12	44.17	453	29.64	6.04	29.12	16.34	58.79
COPDGene	African	Age (years)	1765	54.41	6.84	53.1	39.9	80.8	1431	55.13	7.71	53.4	42.4	80.7
		BMI (kg/m²)	1765	27.71	5.71	26.76	14.78	55.27	1431	30.82	7.42	30.12	12.67	64.1
COPDGene	European	Age (years)	3484	62.35	8.83	62.5	45	81	3177	61.64	8.87	62	45	85
		BMI (kg/m²)	3484	28.85	5.52	28.09	13.75	58.65	3177	28.52	6.55	27.51	12.29	56.01
CRA	Costa Rican	Age (years)	144	41.15	15.02	38.91	18.11	91.62	197	39.3	13.53	36.62	18.07	72.07
		BMI (kg/m²)	144	26.02	4.04	25.54	17.25	38.02	197	26.66	4.48	26.43	13.63	40.37
DHS (AA CAC)	African	Age (years)	164	60.01	8.59	60.5	39	79	220	59.42	8.81	60	36	86
		BMI (kg/m²)	164	31.59	6.97	30.85	17.6	63.27	220	35.66	7.93	35.04	20.91	64.82
FHS	African, Cuban, European*	Age (years)	1874	38.97	9.95	38	18	83	2224	38.12	9.74	37	18	79
		BMI (kg/m²)	1874	27.13	4.14	26.62	16.91	52.15	2224	24.72	5.08	23.44	16.34	58.08
GALAII	Mexican	Age (years)	57	19.46	1.04	19	18	22	118	19.83	1.19	19.8	18.01	21.97

GALAII	Mexican	BMI (kg/m²)	57	28.09	7.23	26.5	17.2	52.2	118	27.77	6.93	26.5	17.8	48.1
GALAII	Puerto Rican	Age (years)	48	19.64	0.9	19.79	18	21.21	82	19.34	0.94	19.14	18.02	21.86
		BMI (kg/m²)	48	27.2	6.22	25.9	17.6	44.4	82	26.75	7.3	25	17.5	67.5
GALAII	Other[3]	Age (years)	13	19.67	1.06	19.75	18.21	21.46	26	19.9	1.17	19.75	18.05	21.99
		BMI (kg/m²)	13	27.73	5.41	29.1	19.5	38.51	26	27.44	6.99	27.15	18.7	50.18
GeneSTAR	African	Age (years)	286	40.73	10.78	41	21	66	491	41.06	10.82	41	21	75
		BMI (kg/m²)	286	29.06	6.44	27.87	16.89	53.48	491	32.44	8.4	31.18	16.41	81.19
GeneSTAR	European	Age (years)	425	40.37	10.87	41	21	75	546	43.29	12.32	43	21	79
		BMI (kg/m²)	425	28.72	5.1	27.81	16.5	51.13	546	28.08	7.01	26.35	16.99	61.83
GENOA	African	Age (years)	358	57.37	10.2	56.7	29.4	86.1	835	56.46	10.76	56.7	21	90.3
		BMI (kg/m²)	358	28.4	4.76	28.24	15.24	50.32	835	32.23	7.02	31.52	17.58	61.37
GenSalt	Han Chinese	Age (years)	944	39.75	8.99	39	18	62	843	38.71	8.84	39	18	59
		BMI (kg/m²)	944	23.25	3.08	22.77	16.38	33.82	843	23.66	3.16	23.38	15.87	37.77
GOLDN	European	Age (years)	433	48.42	16.3	48	18	88	481	47.86	16.13	47	18	87
		BMI (kg/m²)	433	28.46	4.9	27.89	17.13	50.73	481	28.2	6.42	27.38	16.6	52.66
HCHS/SOL	Central American	Age (years)	201	43.27	13.95	44	18	74	308	45.69	13.4	47	18	74
		BMI (kg/m²)	201	29.61	5.74	28.89	17.34	47.3	308	30.87	7.06	29.58	16.64	62.37
HCHS/SOL	Cuban	Age (years)	911	49.33	13.19	51	18	74	988	48.91	12.97	50	18	75
		BMI (kg/m²)	911	28.75	5.18	28.33	14.9	50.91	988	29.81	6.37	29.03	14.28	63.78
HCHS/SOL	Dominican	Age (years)	386	45.01	14.78	47	18	75	738	45.74	13.98	47	18	74
		BMI (kg/m²)	386	28.61	4.89	28.61	17.3	55.3	738	29.91	6.15	29.13	15.23	60.57
HCHS/SOL	Mexican	Age (years)	680	42.76	14.26	44	18	74	1048	44.91	13.72	46	18	76
		BMI (kg/m²)	680	29.7	5.5	28.85	16.33	52.94	1048	31.28	7.14	29.86	17.73	70.35
HCHS/SOL	Puerto Rican	Age (years)	884	46.25	14.43	48	18	74	1189	48.4	14.07	50	18	75
		BMI (kg/m²)	884	29.53	6.36	28.56	17.67	55.87	1189	31.8	7.18	30.82	15.62	67.7
HCHS/SOL	South American	Age (years)	116	44.93	12.99	46.5	18	70	181	47.49	13.09	48	18	76
		BMI (kg/m²)	116	28.24	4.76	28	17.12	42.65	181	29.33	6.06	28.52	19.5	49.93
HCHS/SOL	Other[4]	Age (years)	30	47.93	14.36	48.5	21	74	26	45.12	17.59	42	20	74
		BMI (kg/m²)	30	28.75	6.28	27.27	17.65	48.49	26	31.94	8.48	31.39	19.04	61.32
HVH	European	Age (years)	423	61.36	11.1	60	31	89	227	63.86	13.67	64	21	90
		BMI (kg/m²)	423	30.89	6.69	29.53	17.07	74.34	227	33.34	8.99	31.64	18.71	67.49
HVH	non-European[5]	Age (years)	25	60	13.69	59	35	88	14	51.21	12.32	49.5	23	69
		BMI (kg/m²)	25	31.28	10.45	29.6	20.68	76.05	14	38.36	11.28	35.26	23.78	64.73
HyperGEN	African and Asian*	Age (years)	674	46.42	12.43	46	18	85	1165	47.01	13	47	18	84
		BMI (kg/m²)	674	29.6	6.31	28.55	16.51	56.66	1165	33.41	8.15	32.13	16.18	73.68
JHS	African	Age (years)	1169	53.58	12.91	54	21	89	1952	54.69	12.78	55	20	91
		BMI (kg/m²)	1169	30.06	6.31	29.03	16.35	66.09	1952	32.99	7.65	31.92	16.02	91.8
LTRC	European	Age (years)	665	64.09	10.44	65	25	87	611	62.65	10.55	64	21	88
		BMI (kg/m²)	665	28.74	4.97	28.39	16.37	58.63	611	27.74	6.61	27.17	13.28	52.28
LTRC	non-European[6]	Age (years)	54	61.3	9.66	61	40	83	53	56.77	12.25	57	24	80
		BMI (kg/m²)	54	27.17	5.85	26.57	17.37	40	53	30.77	7.16	29.62	19.18	51.01
Mayo_VTE	African, Cuban, European, Mexican, Puerto Rican*	Age (years)	403	58.47	15.33	60	18	91	527	52.42	17.05	53	19	95
		BMI (kg/m²)	403	31.13	6.6	29.94	18.21	70.53	527	31.42	8.95	29.71	17.14	69.63
MESA	Asian	Age (years)	302	61.44	10.2	61	44	84	301	60.95	10.11	60	44	83
		BMI (kg/m²)	302	24.19	3.09	23.86	16.09	33.48	301	23.96	3.31	23.82	16.63	35.35
MESA	African	Age (years)	815	59.43	9.61	58	39	84	1031	60.13	8.98	59	44	91
		BMI (kg/m²)	815	29	4.84	28.61	17.4	52.46	1031	31.07	6.25	30.12	15.68	53.45
MESA	Central American	Age (years)	25	56.2	6.95	56	46	68	39	58.46	8.87	59	46	77
		BMI (kg/m²)	25	28.73	4.73	27.96	23.01	45.64	39	30.33	5.38	30.41	20.44	47.46
MESA	Cuban	Age (years)	17	65.76	11.62	68	45	81	18	70.06	8.13	70	51	82
		BMI (kg/m²)	17	27.87	4.26	26.41	22.02	36.24	18	28.71	6.21	27.36	21.39	46.82
MESA	Dominican	Age (years)	63	57.4	9.65	55	45	80	81	59.33	9.64	59	45	79
		BMI (kg/m²)	63	27.4	3.85	26.89	18.91	39.34	81	28.17	4.47	27.48	19.95	38.5
MESA	Mexican	Age (years)	283	60.7	10.16	60	44	84	261	60.28	9.64	60	44	82
		BMI (kg/m²)	283	29.33	4.46	28.83	17.57	46.28	261	30.98	5.99	30.35	18.84	52.48

MESA	Puerto Rican	Age (years)	63	57.9	8.67	56	45	79	77	59.45	9.37	57	45	81
		BMI (kg/m²)	63	28.8	4.21	28.75	21.89	43.9	77	30.73	6.51	28.67	20.13	51.56
MESA	South American	Age (years)	34	60.68	9.85	60	45	80	47	61.83	11.1	61	45	84
		BMI (kg/m²)	34	27.2	2.87	27.05	22.92	33.95	47	27.93	4.67	27.77	18.3	39.61
MESA	European	Age (years)	915	61.63	9.67	62	45	83	946	61.4	9.95	61	44	84
		BMI (kg/m²)	915	27.98	3.98	27.61	19.01	42.41	946	27.59	5.81	26.52	16.87	48.99
MGH_AF	African, Central American, Cuban, European, Mexican, South American*	Age (years)	780	53.81	10.69	55	19	82	202	56.77	10.27	58	18	80
		BMI (kg/m²)	780	28.8	5.11	27.88	15.2	57.5	202	28.07	7.03	26.56	17.14	54.73
OMG_SCD	African and Puerto Rican*	Age (years)	201	31.68	11.95	29	18	84	243	34.56	12.36	33	18	70
		BMI (kg/m²)	201	24.22	5.88	23.2	13.8	59	243	26.04	7.45	24.3	16	58
Partners	African, Asian, European*	Age (years)	79	48.46	9.47	51	23	60	43	50.16	8.97	53	21	63
		BMI (kg/m²)	79	30.78	7.16	29.29	21.46	59.37	43	30.84	7.96	29.65	19.27	53.59
SAFS	Mexican	Age (years)	620	42.14	17.28	40	18	90	884	44.74	16.74	44	18	97
		BMI (kg/m²)	620	30.32	7.01	29.59	14.36	65.62	884	31.8	7.63	31.07	15.55	70.2
SAFS	non-Mexican[7]	Age (years)	15	38.27	17.51	31	18	75	15	37.8	13.8	32	20	66
		BMI (kg/m²)	15	28.99	6.36	30.02	19.5	39.67	15	33.72	7.68	33	20.81	49.13
SAGE	African	Age (years)	175	20.87	4.45	19.7	18	40.9	273	22.2	5.91	20	18	40.7
		BMI (kg/m²)	175	26.55	6.22	24.5	17.5	49.2	273	29.11	8.09	27	16.26	56.9
Samoan	Samoan	Age (years)	502	45.04	11.54	46.13	24.62	64.96	772	44.2	11.16	43.78	24.53	65
		BMI (kg/m²)	502	31.37	5.83	30.75	18.56	54.06	772	35.3	7	35.04	18.05	61.07
THRV	Taiwanese	Age (years)	1010	52.25	9.95	51	29	86	1043	51.71	9.63	51	18	86
		BMI (kg/m²)	1010	25.35	3.35	25.24	15.87	42.45	1043	24.19	3.49	23.64	15.37	35.82
VAFAR	European	Age (years)	118	57.07	8.63	58.5	32.53	78.21	55	60.49	8.22	61.54	25.68	74.78
		BMI (kg/m²)	118	32.27	6.15	31.41	22.2	56.92	55	33.62	7.94	32.74	21.11	53.26
VU_AF	European	Age (years)	750	53.17	10.69	55	19	80	280	53.72	11.76	56.5	18	81
		BMI (kg/m²)	750	31.1	6.42	30.12	16.81	69.64	280	31.27	7.63	30.1	18.79	55.76
VU_AF	non-European[8]	Age (years)	36	45.47	11.12	48	21	65	20	48.6	10.06	48	29	63
		BMI (kg/m²)	36	31.36	8.36	29.79	20.36	66.29	20	32.75	8.16	30.57	22.08	52.87
walk_PHaSST	African, Central American, Cuban, Domonican, European, South American*	Age (years)	181	35.59	12.23	33.2	18.3	72	210	39.91	13.13	39.5	18.3	84
		BMI (kg/m²)	181	23.77	4.28	22.84	17.09	38.67	210	25.75	5.15	24.97	15.24	45.23
WGHS	European	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	111	49.38	3.46	48	45	59
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	111	28.2	6.11	27.37	18.88	57.61
WHI	Asian	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	206	66.49	7.27	67.24	50	79.04
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	206	25.18	4.5	24.5	16.83	42.33
WHI	African	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	1450	63.58	7.04	63.21	50	80.84
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	1450	31.55	6.19	30.63	17.73	60.91
WHI	Cuban	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	34	64	8.28	64.04	51.05	78.55
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	34	28.78	4.98	28.35	19.35	44.11
WHI	Mexican	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	176	62.62	6.81	62.28	50.02	78.1
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	176	29.07	5.37	28.16	18.63	45.55
WHI	Puerto Rican	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	39	62.74	6.39	63.05	51.09	76.01
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	39	28.78	6.03	27.88	20.53	48.68
WHI	South American	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	20	63.73	7.84	64.53	50.18	75.2
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	20	26.98	3.93	26.36	21.15	38.09
WHI	European[9]	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	8985	67.37	6.54	68.07	49.92	80.07
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	8985	28.36	5.83	27.34	15.59	60.91
WHI	Other[10]	Age (years)	n/a	n/a	n/a	n/a	n/a	n/a	11	63.29	7.99	61.08	52.35	78.09
		BMI (kg/m²)	n/a	n/a	n/a	n/a	n/a	n/a	11	27.02	7.62	24.98	20.84	47.59
TOTAL		**Age (years)**	**35764**	**52.16**	**14.98**	**53**	**18**	**97**	**53109**	**54.47**	**15.16**	**56**	**18**	**98**
		BMI (kg/m²)	**35764**	**28.12**	**5.54**	**27.31**	**12.71**	**86.81**	**53109**	**28.98**	**7.02**	**27.73**	**12.29**	**91.8**
Replication studies														
Study	**Population group**	**Trait**	**Men**						**Women**					
			N	**Mean**	**SD**	**Median**	**Min**	**Max**	**N**	**Mean**	**SD**	**Median**	**Min**	**Max**
MEC		Age (years)	3281	59.72	7.4	61	44	70	3825	57.65	7.61	57	44	70
		BMI (kg/m²)	3281	27.64	4.31	27.18	10.87	54.16	3825	29.5	6.25	28.38	13.42	68.73

MVP	African, African American, Black	Age (years)	69346	58.92	11.65	60	20	103		10543	48.59	11.37	50	20	94
		BMI (kg/m²)	69346	30.06	6.07	29.42	12.21	85.46		10543	31.42	6.32	30.83	14.18	66.8
BioMe		Age (years)	2492	48.63	13.92	49.56	18.01	83.24		4146	48.95	15.1	49.32	18.02	84.04
		BMI (kg/m²)	2492	28.47	6.55	27.46	14.13	69.09		4146	31.89	8.66	30.61	13.08	89.14
UKBB		Age (years)	3718	51.65	8.23	50	39	70		5148	52.05	7.95	51	40	70
		BMI (kg/m²)	3718	28.33	4.29	27.93	16.66	57.48		5148	30.34	5.98	29.59	16.02	68.13
REGARDS		Age (years)	3409	64.03	9.06	63	45	94		5312	63.37	9.27	62	45	96
		BMI (kg/m²)	3409	28.97	5.49	28.43	12.31	51.73		5312	32.02	7.14	31.09	12.16	89.44

BMI, body mass index; SD, standard deviation; n/a, not available

*Combined because when stratified by sex, the number of participant is ≤ 5 in at least one of the population group.

1. CFS non-European: Collapsed African, Asian, Mexican, and Puerto Rican.
2. CHS non-European: Collapsed African and Mexican.
3. GALA II Other: Collapsed Central American, Cuban, Dominican, European, and South American.
4. HCHS_SOL Other: Collapsed African and European.
5. HVH non-European: Collapsed African, Asian, Mexican, and Puerto Rican.
6. LTRC non-European: Collapsed African, Asian, Mexican, and Puerto Rican.
7. SAFS non-Mexican: Collapsed African, Asian, and European.
8. VU_AF non-European: Collapsed African, Asian, South American, Central American, Cuban, and Mexican.
9. WHI European includes 1 participant who is biologically male.
10. WHI Other: Collapsed Central American and Dominican.

Supplementary Data 5. Genome-wide significant variants by locus and ALT frequency by population group

CHR	POS (hg38)	REF	ALT	ALT Freq	rsID	Beta	SE	*P*-value	PVE (%)	Known index variant[a]	OASIS annotaion	Nearest gene	Novel locus[b]	ALT frequency by population group													
														African	Amish	Asian	Barbadian	Central American	Costa Rican	Cuban	Dominican	European	Han Chinese	Mexican	Puerto Rican	Samoan	South American	Taiwanese
1	177920345	A	G	20%	rs543874	0.0639	0.0060	1.38E-26	0.128	Yes	intergenic	*SEC16B*	No	25%	15%	15%	29%	26%	23%	19%	21%	19%	22%	18%	22%	5%	21%	16%
2	621558	C	T	85%	rs939584	0.0576	0.0068	1.99E-17	0.081	No	intergenic	*TMEM18*	No	12%	18%	10%	12%	12%	8%	15%	14%	18%	11%	11%	16%	1%	12%	8%
2	24927427	A	G	56%	rs10182181	0.0350	0.0052	1.76E-11	0.051	Yes	intergenic	*ADCY3*	No	16%	65%	54%	11%	63%	63%	52%	36%	53%	57%	67%	47%	47%	65%	56%
3	186108951	T	G	82%	rs869400	0.0383	0.0063	1.21E-09	0.042	No	UTR5	*ETV5*	No	23%	11%	7%	25%	11%	9%	18%	20%	18%	2%	10%	19%	5%	12%	7%
4	45179317	A	T	36%	rs12507026	0.0449	0.0051	9.55E-19	0.088	Yes	intergenic	*GNPDA2*	No	24%	32%	28%	27%	37%	48%	40%	34%	43%	32%	37%	37%	21%	41%	28%
5	75707853	T	C	55%	rs2307111	-0.0324	0.0053	7.43E-10	0.043	Yes	exonic, missense	*POC5*	No	15%	55%	43%	10%	53%	52%	52%	38%	59%	42%	61%	46%	55%	54%	44%
6	50830813	C	T	19%	rs2206277	0.0543	0.0062	2.05E-18	0.086	Novel	intronic	*TFAP2B*	No	14%	12%	25%	11%	30%	28%	18%	18%	18%	24%	39%	24%	10%	34%	21%
8	76068626	A	G	47%	rs830463	0.0305	0.0049	6.58E-10	0.043	No	intergenic	*HNF4G*	No	33%	60%	37%	30%	46%	50%	49%	43%	56%	35%	51%	48%	24%	48%	36%
11	27657463	GT	G	58%	rs3838785	-0.0303	0.0051	3.14E-09	0.040	Novel	ncRNA_intronic, deletion	*BDNF*	No	63%	21%	27%	63%	57%	55%	38%	52%	31%	26%	52%	48%	32%	53%	24%
12	49853685	G	A	30%	rs7138803	0.0363	0.0054	1.69E-11	0.051	Yes	intergenic	*BCDIN3D*	No	18%	40%	29%	17%	22%	15%	31%	23%	38%	29%	24%	26%	10%	23%	27%
13	53533448	G	T	14%	rs9568868	0.0472	0.0072	5.73E-11	0.048	No	intergenic	*OLFM4*	No	5%	28%	24%	2%	31%	33%	13%	11%	13%	25%	34%	19%	43%	33%	25%
16	53767042	T	C	29%	rs1421085	0.0901	0.0056	6.11E-59	0.295	Yes	intronic	*FTO*	No	11%	50%	19%	9%	21%	30%	35%	25%	42%	10%	22%	27%	20%	23%	14%
18	60161902	T	C	21%	rs6567160	0.0525	0.0059	8.22E-19	0.088	Yes	intergenic	*MC4R*	No	19%	31%	20%	25%	12%	14%	19%	20%	23%	24%	12%	19%	17%	12%	20%
19	47077985	C	T	50%	rs28590228	0.0332	0.0053	4.75E-10	0.044	No	intronic	*ZC3H4*	No	20%	66%	33%	18%	48%	59%	58%	40%	68%	29%	57%	46%	68%	51%	26%
22	29906934	C	T	4%	rs111490516	0.0783	0.0133	4.52E-09	0.039	Novel	intronic	*MTMR3*	Yes	13%	0%	0%	13%	2%	0%	2%	5%	0%	0%	1%	3%	0%	1%	0%
X	31836665	G	C	41%	rs1379871	0.0287	0.0042	1.35E-11	0.052	Yes	intronic	*DMD*	No	45%	18%	63%	52%	62%	53%	40%	42%	33%	70%	62%	47%	48%	64%	67%

CHR, chromosome; POS, position; REF, reference allele; ALT, alternative allele; ALT freq, aternative allele frequency; SE, standard error; PVE, percent variance explained; OASIS, Omics Analysis, Search & Information System

[a] Known index variant 'Yes' indicates previously published index variant from NHGRI-EBI GWAS Catalog; 'No' indicates index variant within 500 kb ± of the published lead variant, not independent of known signal in conditional analysis; 'Novel' indicates new lead variant either not published or conditionally independent.

[b] Novel locus 'Yes' was defined if there is no known index variant within 500 kb ± of the lead variant in current analysis.

Supplementary Data 6. Genome-wide significant variants by locus from African and European population group-specific analyses

Population group	rsID	CHR	POS (hg38)	REF/ALT	ALT Freq	Beta	SE	*P*- value	PVE (%)	Nearest Gene	Known index variant[a]	Novel locus[b]	Index SNP in discovery analysis	Distance from index SNP	R^2
African	rs543874	1	177920345	A/G	25.0%	0.0731	0.0111	4.00E-11	0.194	*SEC16B*	Yes	No	rs543874 (self)	0	-
	rs62033408	16	53794050	A/G	10.6%	0.0982	0.0159	6.72E-10	0.170	*FTO*	No	No	rs1421085	27008	0.951
	rs73396827	22	29906123	C/T	12.6%	0.0873	0.0145	1.66E-09	0.162	*MTMR3*	No	Yes	rs111490516	811	0.997
European	rs539515	1	177919890	A/C	18.9%	0.0556	0.0088	2.22E-10	0.093	*SEC16B*	No	No	rs543874	455	0.997
	rs62107261	2	422144	T/C	4.8%	-0.1015	0.0160	2.08E-10	0.093	*ALKAL2*	Yes	No	rs939584	199414	0.000[c]
	rs13130484	4	45173674	C/T	43.1%	0.0439	0.0069	2.28E-10	0.093	*GNPDA2*	No	No	rs12507026	5643	0.986
	rs62405422	6	50829192	T/C	18.5%	0.0552	0.0089	4.74E-10	0.089	*TFAP2B*	No	No	rs2206277	1621	0.997
	rs1459184	8	76032892	A/T	54.2%	0.0437	0.0069	2.28E-10	0.093	*HNF4G*	No	No	rs830463	35734	0.912
	rs1421085	16	53767042	T/C	41.9%	0.0917	0.0070	1.22E-39	0.400	*FTO*	Yes	No	rs1421085 (self)	0	-
	rs17175643	18	60229509	C/T	26.3%	0.0486	0.0078	4.11E-10	0.090	*MC4R*	No	No	rs6567160	67607	0.751

CHR, chromosome; POS, position; REF, reference allele; ALT, alternative allele; ALT freq, alternative allele frequency; SE, standard error; PVE, percent variance explained; SNP, single nucleotide polymorphism

[a] Known index variant 'Yes' indicates previously published index variant from NHGRI-EBI GWAS Catalog; 'No' indicates index variant within 500 kb ± of the published lead variant, not independent of known signal in conditional analysis; 'Novel' indicates new lead variant either not published or conditionally independent.

[b] Novel locus 'Yes' was defined if there is no known index variant within 500 kb ± of the lead variant in current analysis.

[c] Linkage disequilibrium was calculated using our own data in the total population. All other R^2 values were calculated using TOPLD (http://topld.genetics.unc.edu/).

Supplementary Data 7. Replication of rs111490516

Study	N	Imputation reference panel	Imputation R^2	Freq	Beta	SE	*P*- value
MEC	7,907	1000 Genomes	0.9910	0.113	0.0354	0.0236	0.1325
MVP	79,889	1000 Genomes Project phase 3, version 5	0.7083	0.109	0.0181	0.0090	0.0442
BioMe	4,413	TOPMed	0.9775	0.125	0.0439	0.0311	0.1939
UKBB	8,863	UK10K + HRC	0.9827	0.129	0.0260	0.0222	0.2414
REGARDS	8,676	TOPMed	0.9981	0.125	0.0521	0.0226	0.0213
Meta-analysis	**109,748**			**0.114**	**0.0253**	**0.0072**	**4.76E-04**
Discovery	88,873			0.037	0.0783	0.0133	4.52E-09
Meta-analysis of Discovery + Replication	**198,621**			**0.079**	**0.0372**	**0.0063**	**4.19E-09**

Freq, frequency; SE, standard error

MEC, Multiethnic Cohort Study; MVP, Million Veteran Program; BioMe, BioMe BioBank; UKBB, United Kingdom BioBank; REGARDS, Reasons for Geographic And Racial Differences in Stroke Study

Supplementary Data 8. Variant annotation from Variant Effect Predictor (VEP) for all SNPs in high LD ($R^2 > 0.8$) with top SNP in novel *MTMR3* locus.

Uploaded_variation	Location	Allele	Consequence	IMPACT	Entrez Gene SYMBOL	Feature_type	Feature	BIOTYPE	INTRON	HGVSc	Existing_variation	DISTANCE	STRAND	AF	SOMATIC	PHENO	CADD_PHRED	CADD_RAW	SpliceAI_pred_DS_AG	SpliceAI_pred_DS_AL	SpliceAI_pred_DS_DG	SpliceAI_pred_DS_DL	SpliceAI_pred_SYMBOL
rs111490516	22:29906934-29906934	T	intron_variant	MODIFIER	*MTMR3*	Transcript	ENST00000323630.9	protein_coding	1/18	-	rs111490516	-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	ENST00000333027.7	protein_coding	1/19	-		-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	ENST00000351488.7	protein_coding	1/18	-		-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	ENST00000401950.7	protein_coding	1/19	-		-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant,non_coding_transcript_variant		*MTMR3*	Transcript	ENST00000415511.1	protein_coding_CDS_not_defined	1/5	-		-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	ENST00000445401.5	protein_coding	1/5	-		-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant,non_coding_transcript_variant		*MTMR3*	Transcript	ENST00000495098.5	protein_coding_CDS_not_defined	1/4	-		-	1	0.0397	-	-	0.443	-0.229	0.00	0.00	0.00	0.00	*MTMR3*
rs6006286	22:29868401-29868401	C	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	ENSR00001059241	enhancer	-	-	rs6006286	-	-	0.0421	-	-	1.44	0.0161	-	-	-	-	-
		G	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059241	enhancer	-	-		-	-	-	-	-	1.648	0.0458	-	-	-	-	-
		C	intergenic_variant		-	-	-	-	-	-		-	-	0.0421	-	-	1.44	0.0161	-	-	-	-	-
		G	intergenic_variant		-	-	-	-	-	-		-	-	-	-	-	1.648	0.0458	-	-	-	-	-
rs73394881	22:29871862-29871862	A	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	ENSR00001059243	enhancer	-	-	rs73394881	-	-	0.0351	-	-	**18.25**	1.8692	-	-	-	-	-
		A	intergenic_variant		-	-	-	-	-	-		-	-	0.0351	-	-	**18.25**	1.8692	-	-	-	-	-
rs73394884	22:29872883-29872883	G	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	ENSR00001059243	enhancer	-	-	rs73394884	-	-	0.0353	-	-	5.087	0.3697	-	-	-	-	-
		T	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059243	enhancer	-	-		-	-	-	-	-	5.593	0.4151	-	-	-	-	-
		G	intergenic_variant		-	-	-	-	-	-		-	-	0.0353	-	-	5.087	0.3697	-	-	-	-	-
		T	intergenic_variant		-	-	-	-	-	-		-	-	-	-	-	5.593	0.4151	-	-	-	-	-
rs74832232	22:29873682-29873682	G	regulatory_region_variant	MODIFIER	-	RegulatoryFeature	ENSR00001059243	enhancer	-	-	rs74832232	-	-	0.0353	-	-	**17.07**	1.7057	-	-	-	-	-
		G	intergenic_variant		-	-	-	-	-	-		-	-	0.0353	-	-	**17.07**	1.7057	-	-	-	-	-
rs73394885	22:29875581-29875581	A	intergenic_variant	MODIFIER	-	-	-	-	-	-	rs73394885	-	-	0.0353	-	-	4.218	0.2939	-	-	-	-	-
rs73394892	22:29880062-29880062	A	upstream_gene_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	-	-	rs73394892	3112	1	0.0012	-	-	0.255	-0.341	-	-	-	-	-
		C	upstream_gene_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	-	-		3112	1	-	-	-	0.214	-0.378	-	-	-	-	-
		T	upstream_gene_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	-	-		3112	1	0.0357	-	-	0.202	-0.39	-	-	-	-	-
		A	upstream_gene_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	-	-		3112	1	0.0012	-	-	0.255	-0.341	-	-	-	-	-
		C	upstream_gene_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	-	-		3112	1	-	-	-	0.214	-0.378	-	-	-	-	-
		T	upstream_gene_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	-	-		3112	1	0.0357	-	-	0.202	-0.39	-	-	-	-	-
		A	upstream_gene_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	-	-		3112	1	0.0012	-	-	0.255	-0.341	-	-	-	-	-
		C	upstream_gene_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	-	-		3112	1	-	-	-	0.214	-0.378	-	-	-	-	-
		T	upstream_gene_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	-	-		3112	1	0.0357	-	-	0.202	-0.39	-	-	-	-	-
rs60573683	22:29883670-29883670	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+311G>T	rs60573683	-	1	0.0353	-	-	3.147	0.2021	0.00	0	0	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+311G>T		-	1	0.0353	-	-	3.147	0.2021	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+311G>T		-	1	0.0353	-	-	3.147	0.2021	0.00	0.00	0.00	0.00	*MTMR3*
		T	regulatory_region_variant		-	RegulatoryFeature	ENSR00000145133	promoter	-	-		-	-	0.0353	-	-	3.147	0.2021	-	-	-	-	-
rs73394897	22:29888561-29888561	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+5202T>C	rs73394897, COSV60304704	-	1	0.0353	0,1	0,1	**11.25**	0.9703	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+5202T>C		-	1	0.0353	0,1	0,1	**11.25**	0.9703	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+5202T>C		-	1	0.0353	0,1	0,1	**11.25**	0.9703	0.00	0.00	0.00	0.00	*MTMR3*
rs112565384	22:29890308-29890308	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+6949G>A	rs112565384	-	1	0.0353	-	-	1.965	0.0856	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+6949G>A		-	1	0.0353	-	-	1.965	0.0856	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+6949G>A		-	1	0.0353	-	-	1.965	0.0856	0.00	0.00	0.00	0.00	*MTMR3*
rs73396810	22:29895377-29895377	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+12018G>T	rs73396810	-	1	0.0353	-	-	1.479	0.022	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+12018G>T		-	1	0.0353	-	-	1.479	0.022	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+12018G>T		-	1	0.0353	-	-	1.479	0.022	0.00	0.00	0.00	0.00	*MTMR3*
rs73396811	22:29896358-29896358	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+12999A>G	rs73396811	-	1	0.0353	-	-	5.789	0.4329	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+12999A>G		-	1	0.0353	-	-	5.789	0.4329	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+12999A>G		-	1	0.0353	-	-	5.789	0.4329	0.00	0.00	0.00	0.00	*MTMR3*
rs73396818	22:29902155-29902155	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+18796A>T	rs73396818	-	1	0.0397	-	-	0.366	-0.267	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+18796A>T		-	1	0.0397	-	-	0.366	-0.267	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+18796A>T		-	1	0.0397	-	-	0.366	-0.267	0.00	0.00	0.00	0.00	*MTMR3*
rs113463187	22:29902988-29902988	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+19629C>T	rs113463187	-	1	0.0399	-	-	2.775	0.1688	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+19629C>T		-	1	0.0399	-	-	2.775	0.1688	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+19629C>T		-	1	0.0399	-	-	2.775	0.1688	0.00	0.00	0.00	0.00	*MTMR3*
rs57349783	22:29903544-29903544	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20185T>C	rs57349783	-	1	0.0395	-	-	1.297	-0.006	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20185T>C		-	1	0.0395	-	-	1.297	-0.006	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20185T>C		-	1	0.0395	-	-	1.297	-0.006	0.00	0.00	0.00	0.00	*MTMR3*
rs2158535	22:29903616-29903616	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20257T>C	rs2158535	-	1	0.0395	-	-	1.888	0.0764	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20257T>C		-	1	0.0395	-	-	1.888	0.0764	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20257T>C		-	1	0.0395	-	-	1.888	0.0764	0.00	0.00	0.00	0.00	*MTMR3*
rs2107672	22:29903764-29903764	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20405G>A	rs2107672	-	1	0.0353	-	-	8.09	0.6607	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20405G>A		-	1	0.0353	-	-	8.09	0.6607	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20405G>A		-	1	0.0353	-	-	8.09	0.6607	0.00	0.00	0.00	0.00	*MTMR3*
rs2107673	22:29903808-29903808	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20449T>A	rs2107673	-	1	-	-	-	0.204	-0.387	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20449T>C		-	1	0.0395	-	-	0.258	-0.339	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20449T>A		-	1	-	-	-	0.204	-0.387	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20449T>C		-	1	0.0395	-	-	0.258	-0.339	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20449T>A		-	1	-	-	-	0.204	-0.387	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20449T>C		-	1	0.0395	-	-	0.258	-0.339	0.00	0.00	0.00	0.00	*MTMR3*
rs73396822	22:29904208-29904208	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20849C>A	rs73396822	-	1	-	-	-	5.187	0.3785	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20849C>G		-	1	0.0395	-	-	5.379	0.3957	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20849C>A		-	1	-	-	-	5.187	0.3785	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20849C>G		-	1	0.0395	-	-	5.379	0.3957	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20849C>A		-	1	-	-	-	5.187	0.3785	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20849C>G		-	1	0.0395	-	-	5.379	0.3957	0.00	0.00	0.00	0.00	*MTMR3*
rs73396823	22:29904279-29904279	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20920G>A	rs73396823	-	1	0.0395	-	-	0.683	-0.14	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+20920G>C		-	1	-	-	-	0.572	-0.177	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20920G>A		-	1	0.0395	-	-	0.683	-0.14	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+20920G>C		-	1	-	-	-	0.572	-0.177	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20920G>A		-	1	0.0395	-	-	0.683	-0.14	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+20920G>C		-	1	-	-	-	0.572	-0.177	0.00	0.00	0.00	0.00	*MTMR3*
rs2051858	22:29904422-29904422	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+21063C>T	rs2051858, COSV60307792	-	1	0.0395	0,1	0,1	1.027	-0.055	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+21063C>T		-	1	0.0395	0,1	0,1	1.027	-0.055	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+21063C>T		-	1	0.0395	0,1	0,1	1.027	-0.055	0.00	0.00	0.00	0.00	*MTMR3*
rs2051859	22:29904532-29904532	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+21173G>A	rs2051859	-	1	0.0395	-	-	4.256	0.2972	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+21173G>A		-	1	0.0395	-	-	4.256	0.2972	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+21173G>A		-	1	0.0395	-	-	4.256	0.2972	0.00	0.00	0.00	0.00	*MTMR3*

rs73396826	22:29906042-29906042	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+22683G>A		-	1	0.0395	-	-	0.281	-0.321	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+22683G>A	rs73396826	-	1	0.0395	-	-	0.281	-0.321	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+22683G>A		-	1	0.0395	-	-	0.281	-0.321	0.00	0.00	0.00	0.00	*MTMR3*
rs73396827	22:29906123-29906123	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+22764C>T		-	1	0.0395	-	-	0.952	-0.071	0.00	0.00	0.04	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+22764C>T	rs73396827	-	1	0.0395	-	-	0.952	-0.071	0.00	0.00	0.04	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+22764C>T		-	1	0.0395	-	-	0.952	-0.071	0.00	0.00	0.04	0.00	*MTMR3*
rs73396828	22:29906206-29906206	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+22847T>C		-	1	0.0389	-	-	1.86	0.073	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+22847T>C	rs73396828	-	1	0.0389	-	-	1.86	0.073	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+22847T>C		-	1	0.0389	-	-	1.86	0.073	0.00	0.00	0.00	0.00	*MTMR3*
rs73396830	22:29906213-29906213	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+22854A>G		-	1	0.0389	-	-	0.226	-0.367	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+22854A>G	rs73396830	-	1	0.0389	-	-	0.226	-0.367	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+22854A>G		-	1	0.0389	-	-	0.226	-0.367	0.00	0.00	0.00	0.00	*MTMR3*
rs73396831	22:29906421-29906421	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+23062C>T		-	1	0.0395	-	-	1.009	-0.059	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+23062C>T	rs73396831	-	1	0.0395	-	-	1.009	-0.059	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+23062C>T		-	1	0.0395	-	-	1.009	-0.059	0.00	0.00	0.00	0.00	*MTMR3*
rs112056808	22:29907171-29907171	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+23812C>T		-	1	0.0395	-	-	1.207	-0.021	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+23812C>T	rs112056808	-	1	0.0395	-	-	1.207	-0.021	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+23812C>T		-	1	0.0395	-	-	1.207	-0.021	0.00	0.00	0.00	0.00	*MTMR3*
rs550468632	22:29908987-29908987	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+25628T>C		-	1	0.0375	-	-	0.195	-0.397	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+25628T>C	rs550468632	-	1	0.0375	-	-	0.195	-0.397	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+25628T>C		-	1	0.0375	-	-	0.195	-0.397	0.00	0.00	0.00	0.00	*MTMR3*
rs73396841	22:29909799-29909799	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+26440T>C		-	1	0.0395	-	-	0.02	-0.837	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+26440T>C	rs73396841	-	1	0.0395	-	-	0.02	-0.837	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+26440T>C		-	1	0.0395	-	-	0.02	-0.837	0.00	0.00	0.00	0.00	*MTMR3*
rs73396843	22:29910808-29910808	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+27449T>G		-	1	0.0353	-	-	1.936	0.0822	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+27449T>G	rs73396843	-	1	0.0353	-	-	1.936	0.0822	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+27449T>G		-	1	0.0353	-	-	1.936	0.0822	0.00	0.00	0.00	0.00	*MTMR3*
rs7291683	22:29911218-29911218	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+27859C>T		-	1	0.0395	-	-	3.236	0.2098	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+27859C>T	rs7291683	-	1	0.0395	-	-	3.236	0.2098	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+27859C>T		-	1	0.0395	-	-	3.236	0.2098	0.00	0.00	0.00	0.00	*MTMR3*
rs73396856	22:29911621-29911621	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+28262C>A		-	1	-	-	-	1.996	0.0892	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+28262C>G		-	1	0.0353	-	-	2.149	0.1065	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+28262C>A	rs73396856	-	1	-	-	-	1.996	0.0892	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+28262C>G		-	1	0.0353	-	-	2.149	0.1065	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+28262C>A		-	1	-	-	-	1.996	0.0892	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+28262C>G		-	1	0.0353	-	-	2.149	0.1065	0.00	0.00	0.00	0.00	*MTMR3*
rs73396863	22:29913097-29913097	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-138+29738T>A		-	1	0.0393	-	-	1.817	0.0676	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-138+29738T>A	rs73396863	-	1	0.0393	-	-	1.817	0.0676	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-138+29738T>A		-	1	0.0393	-	-	1.817	0.0676	0.00	0.00	0.00	0.00	*MTMR3*
rs73396885	22:29924436-29924436	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-32600C>A		-	1	0.0353	-	-	1.188	-0.025	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-32600C>A	rs73396885	-	1	0.0353	-	-	1.188	-0.025	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-32600C>A		-	1	0.0353	-	-	1.188	-0.025	0.00	0.00	0.00	0.00	*MTMR3*
		A	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059246	enhancer	-	-		-	-	0.0353	-	-	1.188	-0.025	-	-	-	-	-
rs60098050	22:29926719-29926719	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-30317A>G		-	1	0.0353	-	-	6.904	0.5387	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-30317A>G	rs60098050	-	1	0.0353	-	-	6.904	0.5387	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-30317A>G		-	1	0.0353	-	-	6.904	0.5387	0.00	0.00	0.00	0.00	*MTMR3*
rs111317522	22:29928460-29928460	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-28576C>T		-	1	0.0353	-	-	1.598	0.0389	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-28576C>T	rs111317522	-	1	0.0353	-	-	1.598	0.0389	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-28576C>T		-	1	0.0353	-	-	1.598	0.0389	0.00	0.00	0.00	0.00	*MTMR3*
		T	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059247	enhancer	-	-		-	-	0.0353	-	-	1.598	0.0389	-	-	-	-	-
rs73396896	22:29931253-29931253	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-25783C>A		-	1	0.0353	-	-	**13.9**	1.2343	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-25783C>T		-	1	-	-	-	**14.34**	1.2938	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-25783C>A		-	1	0.0353	-	-	**13.9**	1.2343	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-25783C>T	rs73396896	-	1	-	-	-	**14.34**	1.2938	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-25783C>A		-	1	0.0353	-	-	**13.9**	1.2343	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-25783C>T		-	1	-	-	-	**14.34**	1.2938	0.00	0.00	0.00	0.00	*MTMR3*
		A	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059247	enhancer	-	-		-	-	0.0353	-	-	**13.9**	1.2343	-	-	-	-	-
		T	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059247	enhancer	-	-		-	-	-	-	-	**14.34**	1.2938	-	-	-	-	-
rs113048784	22:29934106-29934106	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-22930G>A		-	1	0.0353	-	-	1.133	-0.035	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-22930G>A	rs113048784	-	1	0.0353	-	-	1.133	-0.035	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-22930G>A		-	1	0.0353	-	-	1.133	-0.035	0.00	0.00	0.00	0.00	*MTMR3*
rs73396902	22:29935150-29935150	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-21886A>G		-	1	0.0355	-	-	8.524	0.7075	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-21886A>G	rs73396902	-	1	0.0355	-	-	8.524	0.7075	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-21886A>G		-	1	0.0355	-	-	8.524	0.7075	0.00	0.00	0.00	0.00	*MTMR3*
rs60751132	22:29935766-29935766	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-21270G>A		-	1	0.0353	0,1	0,1	0.785	-0.112	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-21270G>A	rs60751132,	-	1	0.0353	0,1	0,1	0.785	-0.112	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-21270G>A	COSV60308265	-	1	0.0353	0,1	0,1	0.785	-0.112	0.00	0.00	0.00	0.00	*MTMR3*
		A	regulatory_region_variant		-	RegulatoryFeature	ENSR00000669734	enhancer	-	-		-	-	0.0353	0,1	0,1	0.785	-0.112	-	-	-	-	-
rs112804604	22:29936137-29936138	-	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-20898del		-	1	0.0353	-	-	3.772	0.2558	0.00	0.00	0.00	0.00	*MTMR3*
		-	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-20898del	rs112804604	-	1	0.0353	-	-	3.772	0.2558	0.00	0.00	0.00	0.00	*MTMR3*
		-	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-20898del		-	1	0.0353	-	-	3.772	0.2558	0.00	0.00	0.00	0.00	*MTMR3*
		-	regulatory_region_variant		-	RegulatoryFeature	ENSR00000669734	enhancer	-	-		-	-	0.0353	-	-	3.772	0.2558	-	-	-	-	-
rs111908292	22:29939914-29939914	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-17122A>G		-	1	0.0353	-	-	3.052	0.1937	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-17122A>G	rs111908292	-	1	0.0353	-	-	3.052	0.1937	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-17122A>G		-	1	0.0353	-	-	3.052	0.1937	0.00	0.00	0.00	0.00	*MTMR3*
rs113140876	22:29940180-29940180	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-16856A>G		-	1	0.0353	-	-	4.351	0.3054	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-16856A>G	rs113140876	-	1	0.0353	-	-	4.351	0.3054	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-16856A>G		-	1	0.0353	-	-	4.351	0.3054	0.00	0.00	0.00	0.00	*MTMR3*
rs73398629	22:29949551-29949551	C	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-7485A>C		-	1	0.0353	-	-	4.695	0.3352	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-7485A>C	rs73398629	-	1	0.0353	-	-	4.695	0.3352	0.00	0.00	0.00	0.00	*MTMR3*
		C	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-7485A>C		-	1	0.0353	-	-	4.695	0.3352	0.00	0.00	0.00	0.00	*MTMR3*
		C	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059251	enhancer	-	-		-	-	0.0353	-	-	4.695	0.3352	-	-	-	-	-
rs73398630	22:29949778-29949778	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	1/19	NM_021090.4:c.-137-7258G>A		-	1	0.0355	-	-	0.685	-0.14	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	1/19	NM_153050.3:c.-137-7258G>A	rs73398630	-	1	0.0355	-	-	0.685	-0.14	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	1/18	NM_153051.3:c.-137-7258G>A		-	1	0.0355	-	-	0.685	-0.14	0.00	0.00	0.00	0.00	*MTMR3*
		A	regulatory_region_variant		-	RegulatoryFeature	ENSR00001059251	enhancer	-	-		-	-	0.0355	-	-	0.685	-0.14	-	-	-	-	-
rs60093195	22:29958748-29958748	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	2/19	NM_021090.4:c.-85+1660A>G		-	1	0.0353	-	-	0.783	-0.112	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	2/19	NM_153050.3:c.-85+1660A>G	rs60093195	-	1	0.0353	-	-	0.783	-0.112	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	2/18	NM_153051.3:c.-85+1660A>G		-	1	0.0353	-	-	0.783	-0.112	0.00	0.00	0.00	0.00	*MTMR3*
	22:29962609	T	intron_variant		*MTMR3*	Transcript	NM_021090.4	protein_coding	2/19	NM_021090.4:c.-85+5521C>T		-	1	0.0353	-	-	0.64	-0.154	0.00	0.00	0.00	0.00	*MTMR3*

rs58564057	22:29962009-29962609	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_153050.3	protein_coding	2/19	NM_153050.3:c.-85+5521C>T	rs58564057	-	1	0.0353	-	-	0.64	-0.154	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	2/18	NM_153051.3:c.-85+5521C>T		-	1	0.0353	-	-	0.64	-0.154	0.00	0.00	0.00	0.00	*MTMR3*
rs73398654	22:29980789-29980789	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	5/19	NM_021090.4:c.210+1737C>G	rs73398654	-	1	0.0353	-	-	0.248	-0.347	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	5/19	NM_153050.3:c.210+1737C>G		-	1	0.0353	-	-	0.248	-0.347	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	5/18	NM_153051.3:c.210+1737C>G		-	1	0.0353	-	-	0.248	-0.347	0.00	0.00	0.00	0.00	*MTMR3*
rs73398659	22:29986440-29986440	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	5/19	NM_021090.4:c.211-2040G>A	rs73398659	-	1	0.0353	-	-	0.062	-0.631	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	5/19	NM_153050.3:c.211-2040G>A		-	1	0.0353	-	-	0.062	-0.631	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	5/18	NM_153051.3:c.211-2040G>A		-	1	0.0353	-	-	0.062	-0.631	0.00	0.00	0.00	0.00	*MTMR3*
		A	regulatory_region_variant		-	RegulatoryFeature	ENSR00000669742	enhancer	-	-		-	-	0.0353	-	-	0.062	-0.631	-	-	-	-	-
rs73398662	22:29987780-29987780	G	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	5/19	NM_021090.4:c.211-700C>G	rs73398662	-	1	0.0353	-	-	1.504	0.0256	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	5/19	NM_153050.3:c.211-700C>G		-	1	0.0353	-	-	1.504	0.0256	0.00	0.00	0.00	0.00	*MTMR3*
		G	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	5/18	NM_153051.3:c.211-700C>G		-	1	0.0353	-	-	1.504	0.0256	0.00	0.00	0.00	0.00	*MTMR3*
		G	regulatory_region_variant		-	RegulatoryFeature	ENSR00000669742	enhancer	-	-		-	-	0.0353	-	-	1.504	0.0256	-	-	-	-	-
rs73398664	22:29989196-29989196	T	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	6/19	NM_021090.4:c.293+634G>T	rs73398664	-	1	0.0355	-	-	3.82	0.2599	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	6/19	NM_153050.3:c.293+634G>T		-	1	0.0355	-	-	3.82	0.2599	0.00	0.00	0.00	0.00	*MTMR3*
		T	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	6/18	NM_153051.3:c.293+634G>T		-	1	0.0355	-	-	3.82	0.2599	0.00	0.00	0.00	0.00	*MTMR3*
		T	regulatory_region_variant		-	RegulatoryFeature	ENSR00001238990	enhancer	-	-		-	-	0.0355	-	-	3.82	0.2599	-	-	-	-	-
rs112672347	22:30004075-30004076	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	9/19	NM_021090.4:c.671+1083del	rs112672347	-	1	0.0353	-	-	6.746	0.5233	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	9/19	NM_153050.3:c.671+1083del		-	1	0.0353	-	-	6.746	0.5233	0.00	0.00	0.00	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	9/18	NM_153051.3:c.671+1083del		-	1	0.0353	-	-	6.746	0.5233	0.00	0.00	0.00	0.00	*MTMR3*
		A	upstream_gene_variant		*MIR6818*	Transcript	NR_106876.1	miRNA	-	-		2973	1	0.0353	-	-	6.746	0.5233	-	-	-	-	-
		A	downstream_gene_variant		*HORMAD2-AS1*	Transcript	NR_110541.2	lncRNA	-	-		4670	-1	0.0353	-	-	6.746	0.5233	-	-	-	-	-
rs73398683	22:30004230-30004230	A	intron_variant	MODIFIER	*MTMR3*	Transcript	NM_021090.4	protein_coding	9/19	NM_021090.4:c.671+1237G>A	rs73398683	-	1	0.0353	-	-	9.222	0.7828	0.00	0.00	0.02	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153050.3	protein_coding	9/19	NM_153050.3:c.671+1237G>A		-	1	0.0353	-	-	9.222	0.7828	0.00	0.00	0.02	0.00	*MTMR3*
		A	intron_variant		*MTMR3*	Transcript	NM_153051.3	protein_coding	9/18	NM_153051.3:c.671+1237G>A		-	1	0.0353	-	-	9.222	0.7828	0.00	0.00	0.02	0.00	*MTMR3*
		A	upstream_gene_variant		*MIR6818*	Transcript	NR_106876.1	miRNA	-	-		2819	1	0.0353	-	-	9.222	0.7828	-	-	-	-	-
		A	downstream_gene_variant		*HORMAD2-AS1*	Transcript	NR_110541.2	lncRNA	-	-		4516	-1	0.0353	-	-	9.222	0.7828	-	-	-	-	-

Supplementary Data 9. Summary of per locus association results after conditioning on top index variant

CHR	POS (hg38)	rsID	REF	ALT	ALT Freq	Nearest Gene	Pre-conditioning			N SNPs in region[a]	Post-conditioning			Signif.[b]
							Beta	SE	*P*-value		Beta	SE	*P*-value	
1	178057912	rs111238523	C	T	2%	*RASAL2*	0.058	0.018	1.76E-03	5008	0.065	0.018	4.30E-04	
2	**422144**	**rs62107261**	**T**	**C**	**3%**	***ALKAL2***	**-0.095**	**0.014**	**3.83E-12**	**6640**	**-0.097**	**0.014**	**2.06E-12**	**Yes**
2	24881806	n/a	CCA	C	11%	*ADCY3*	0.042	0.009	2.94E-06	4187	0.038	0.009	2.63E-05	
3	185800743	rs73061097	T	A	32%	*IGF2BP2*	-0.024	0.005	5.70E-06	4848	-0.024	0.005	3.47E-06	
4	45308738	rs80129601	A	G	2%	*GNPDA2*	-0.087	0.019	4.24E-06	6131	-0.081	0.019	2.06E-05	
5	75750228	rs258502	G	T	57%	*POC5*	-0.001	0.005	8.27E-01	6179	-0.019	0.005	6.14E-04	
6	51174169	rs984697642	G	A	3%	*TFAP2B*	-0.072	0.014	3.07E-07	5184	-0.065	0.014	3.97E-06	
8	75725530	rs16939149	A	G	6%	*HNF4G*	-0.039	0.011	4.29E-04	5692	-0.051	0.011	8.10E-06	
11	27647068	rs3838785	A	G	2%	*BDNF*	0.071	0.020	3.06E-04	3667	0.080	0.020	5.76E-05	
12	49831467	rs4391887	A	G	74%	*NCKAP5L*	0.034	0.006	1.18E-09	4264	0.023	0.006	2.79E-04	
13	53367083	rs1036958	T	A	52%	*OLFM4*	-0.014	0.005	4.02E-03	5125	-0.018	0.005	2.70E-04	
16	53730708	rs117502563	G	A	4%	*FTO*	0.031	0.012	7.20E-03	5673	0.054	0.012	4.30E-06	
18	**60361739**	**rs78769612**	**G**	**T**	**2%**	***MC4R***	**-0.106**	**0.019**	**3.53E-08**	**6861**	**-0.100**	**0.019**	**2.17E-07**	**Yes**
19	47321406	rs149173729	C	T	1%	*C5AR1*	0.094	0.027	4.64E-04	4744	0.108	0.027	6.65E-05	
22	30035665	rs73400621	A	G	5%	*MTMR3*	0.029	0.012	1.23E-02	4814	0.042	0.012	4.80E-04	
X	32268401	rs147568648	A	G	11%	*DMD*	-0.023	0.007	6.50E-04	4911	-0.025	0.007	2.19E-04	

CHR, chromosome; POS, position; REF, reference allele; ALT, alternative allele; Freq, frequency; SE, standard error; Signif., significant; n/a, not available

[a] Region was defined as within ± 500kb of each index variant.

[b] Significance threshold for secondary signals ($P < 5.96 \times 10^{-7}$) was determined by Bonferroni correction for the number of variants across all regions

Supplementary Data 10. Summary of association results after conditioning on all known index variants

CHR	POS (hg38)	rsID	Nearest Gene	REF	ALT	ALT Freq	Pre-conditioning			Post-conditioning		
							Beta	SE	*P*-value	Beta	SE	*P*-value
2	621558	rs939584	*TMEM18*	C	T	85%	0.0576	0.0068	1.99E-17	0.0392	0.0282	0.1655
3	186108951	rs869400	*ETV5*	T	G	82%	0.0383	0.0063	1.21E-09	0.0330	0.0225	0.1439
6	**50830813**	**rs2206277**	***TFAP2B***	**C**	**T**	**19%**	**0.0543**	**0.0062**	**2.05E-18**	**0.0687**	**0.0182**	**1.59E-04**
8	76068626	rs830463	*HNF4G*	A	G	47%	0.0305	0.0049	6.58E-10	0.0237	0.0058	4.31E-05
11	**27657463**	**rs3838785**	***BDNF***	**GT**	**G**	**58%**	**-0.0303**	**0.0051**	**3.14E-09**	**-0.0324**	**0.0092**	**4.11E-04**
13	53533448	rs9568868	*OLFM4*	G	T	14%	0.0472	0.0072	5.73E-11	0.1990	0.1881	0.2900
19	47077985	rs28590228	*ZC3H4*	C	T	50%	0.0332	0.0053	4.75E-10	0.0410	0.0219	0.0617
Secondary signal												
18	60361739	rs78769612	*MC4R*	G	T	2%	-0.106	0.019	3.53E-08	-0.0722	0.0945	0.4450

CHR, chromosome; POS, position; REF, reference allele; ALT, alternative allele; Freq, frequency; SE, standard error

Known index variants curated from the following papers (PMIDs): 22344219, 22344221, 23563607, 23583978, 24094743, 24861553, 25673413, 26426971, 28391526, 28430825, 28443625, 28448500, 28552196, 28892062, 29273807, 29381148, 30108127, 30124842, 30595370, 31217584, 35399580

Supplementary Data 11. PAINTOR results for top loci assuming one single causal variant at each locus

Only index variants and those with posterior probability (PP)> 50% are shown. **Bold** identifies variants with > 95% PP.

Locus rsID	CHR	POS (hg38)	rsID	REF	ALT	EAF	MAF	Gene	PAINTOR Annotation	Beta	SE	*P*-value	PVE (%)	PP	Is Index highest PP?
rs543874	1	177920345	rs543874	A	G	0.2043	0.2043	*SEC16B*	-	0.0639	0.0060	1.38E-26	0.128	0.6192	Yes
rs939584	2	621558	rs939584	C	T	0.8518	0.1482	*TMEM18*	-	0.0576	0.0068	1.99E-17	0.081	0.0230	Yes
rs10182181	2	24927427	rs10182181	A	G	0.5608	0.4392	*ADCY3*	-	0.0350	0.0052	1.76E-11	0.051	0.1376	No
		24920780	rs6746013	C	G	0.5629	0.4371		genehancer	0.3462	0.0052	2.99E-11	0.050	0.3163	
rs869400	3	186108951	rs869400	T	G	0.8195	0.1805	*ETV5*	genehancer	0.0383	0.0063	1.21E-09	0.042	0.6263	Yes
rs12507026	4	45179317	rs12507026	A	T	0.3614	0.3614	*GNPDA2*	-	0.0449	0.0051	9.55E-19	0.088	0.3051	Yes
rs2307111	**5**	**75707853**	**rs2307111**	**T**	**C**	**0.5474**	**0.4526**	***POC5***	**-**	**-0.0324**	**0.0053**	**7.43E-10**	**0.043**	**0.9898**	**Yes**
rs2206277	6	50830813	rs2206277	C	T	0.1903	0.1903	*TFAP2B*	-	0.0543	0.0062	2.05E-18	0.086	0.4895	Yes
rs830463	8	76068626	rs830463	A	G	0.4700	0.4700	*HNF4G*	-	0.0305	0.0049	6.58E-10	0.043	0.2278	Yes
rs3838785	11	27657463	rs3838785	GT	G	0.5792	0.4208	*BDNF*	-	-0.0303	0.0051	3.14E-09	0.040	0.3310	Yes
rs7138803	12	49853685	rs7138803	G	A	0.2974	0.2974	*BCDIN3D*	-	0.0363	0.0054	1.69E-11	0.051	0.4231	Yes
rs9568868	13	53533448	rs9568868	G	T	0.1387	0.1387	*OLFM4*	-	0.0472	0.0072	5.74E-11	0.048	0.3631	Yes
rs1421085	16	53767042	rs1421085	T	C	0.2949	0.2949	*FTO*	-	0.0901	0.0056	6.11E-59	0.295	0.5887	Yes
rs6567160	18	60161902	rs6567160	T	C	0.2096	0.2096	*MC4R*	-	0.0525	0.0059	8.22E-19	0.088	0.7360	Yes
rs28590228	19	47077985	rs28590228	C	T	0.5039	0.4961	*ZC3H4*	-	0.0332	0.0053	4.76E-10	0.044	0.0945	No
		47113120	rs55731973	G	T	0.5196	0.4804		promoter, genehancer	0.0297	0.0054	3.91E-08	0.034	0.7664	
rs111490516	22	29906934	rs111490516	C	T	0.0368	0.0368	*MTMR3*	-	0.0783	0.0133	4.52E-09	0.039	0.0407	Yes
rs1379871	**X**	**31836665**	**rs1379871**	**G**	**C**	**0.4131**	**0.4131**	***DMD***	**-**	**0.0287**	**0.0042**	**1.35E-11**	**0.052**	**0.9980**	**Yes**

PAINTOR, Probabilistic Annotation INtegraTOR; CHR, chromosome; POS, position; REF, reference allele; ALT, alternative allele; EAF, effect allele frequency; MAF, minor allele frequency; SE, standard error; PVE, percent variance explained; PP, posterior probability

Supplementary Data 12. Top associations meeting suggestive significance (*P* < 0.001) in PheWAS meta-analysis

			Meta					MyCode					BioMe				
PheCode	**Phenotype Descriptions**	**Category**	**Beta**	**SE**	**OR**	***P***	**N**	**Beta**	**SE**	**OR**	***P***	**N**	**Beta**	**SE**	**OR**	***P***	**N**
327.3	Sleep apnea	neurological	-0.2530	0.0755	0.7765	8.12E-04	7,600	-0.1436	0.1391	0.8663	3.02E-01	1,536	-0.2987	0.0900	0.7418	8.99E-04	6,064
327.32	Obstructive sleep apnea	neurological	-0.2903	0.0785	0.7480	2.19E-04	7,497	-0.1809	0.1455	0.8345	2.14E-01	1,486	-0.3352	0.0933	0.7152	3.26E-04	6,011