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Supplementary information

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Genomic, phenomic and geographic associations of leukocyte telomere length in the United States

In the format provided by the authors and unedited

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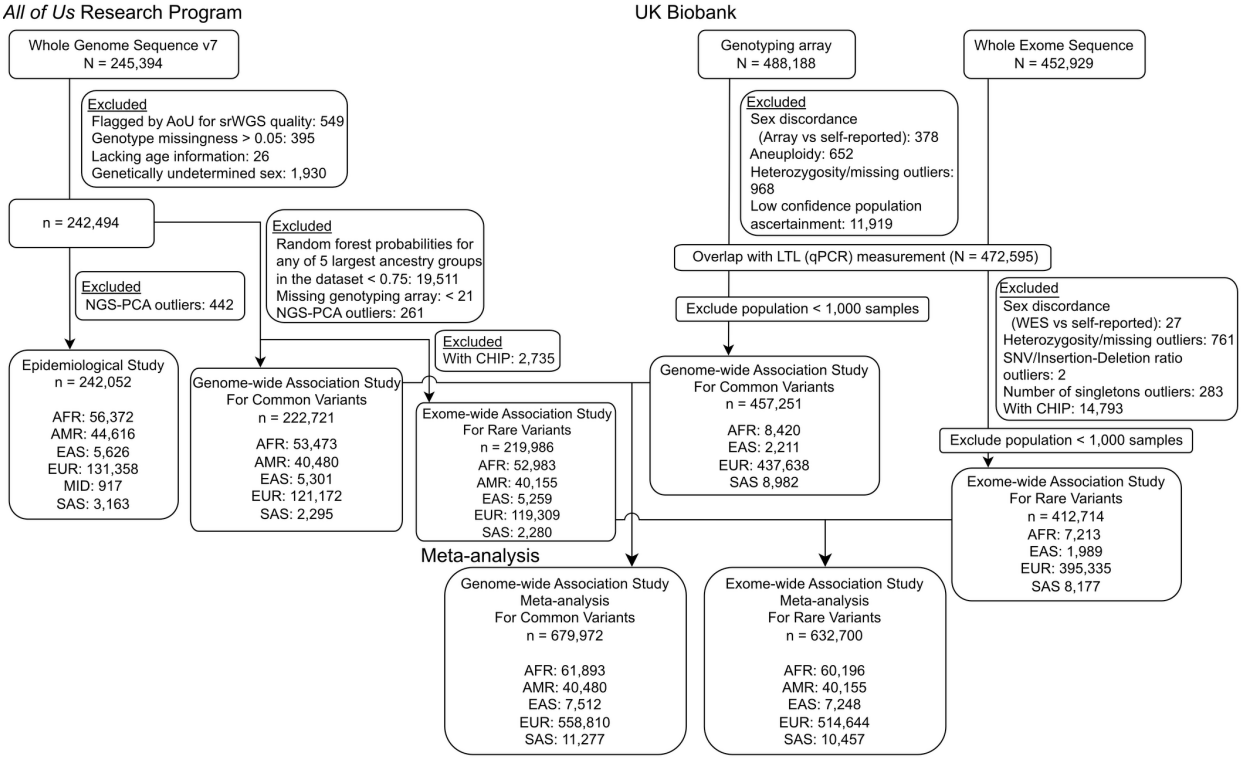
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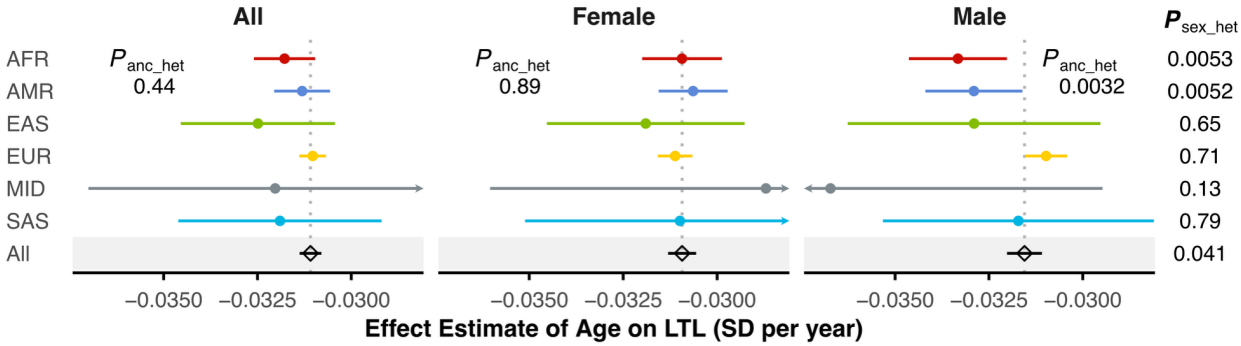
Supplementary Fig. 8: Locuszoom plots with FINEMAP and PoPS annotations for significant loci in meta-analysis of common variant genome-wide association studies. (Figures only) 21

Supplementary Fig. 1: Sample selection within the *All of Us* Research Program.



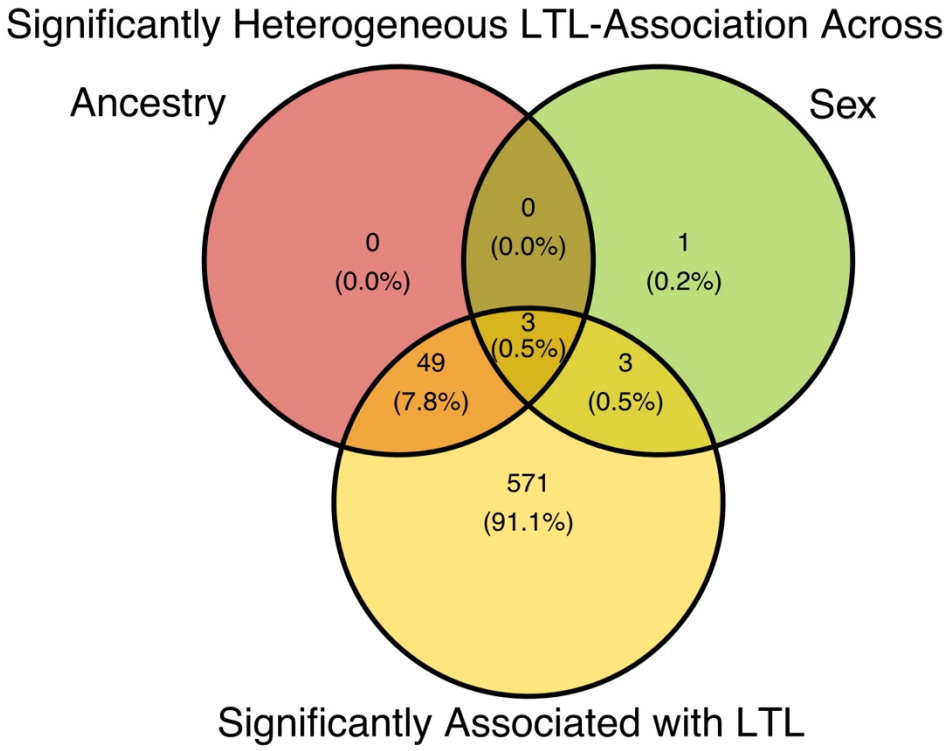
The *All of Us* Research Program (AoU) version 7 released 245,394 WGS data. We excluded flagged samples for sequencing quality by AoU (n = 549), genotyping missingness > 0.01 (n = 395), lacking age information (n = 26), and genetically undetermined sex (n = 1,930) to construct a cohort of 242,494 participants included in our analysis. For epidemiology, we further excluded outliers (> 20 median absolute deviations) for NGS-PCs (n = 442). For genomic studies, we further excluded < 0.75 for random forest probabilities for the largest 5 genetic ancestries [African-like population (AFR), Admixed American-like population (AMR), East Asian-like population (EAS), European-like population (EUR), Middle Eastern-like population (MID), and South Asian-like population (SAS)] in AoU (n = 19,511), missing genotyping array information (n < 21, According to AoU publishing policy, numbers below 21 cannot be published. Precise counts are not calculable due to overlapping samples across multiple QC metrics.), and outliers (> 20 median absolute deviation) for NGS-PCs (n = 261). We re-analyzed UK Biobank (UKB) for genome-wide association study (GWAS) for common variants and exome-wide rare variant association study (RVAS) for meta-analyses. We used genotyping array data (N = 488,188) for GWAS and whole exome sequence data (N = 452,929) for RVAS in UKB. Individuals with clonal hematopoiesis of indeterminate potential (CHIP) were excluded from RVAS in both AoU (n = 2,735) and UKB (n = 14,793).

Supplementary Fig. 2: Associations between leukocyte telomere length (LTL) and age and their heterogeneity in the *All of Us* Research Program.



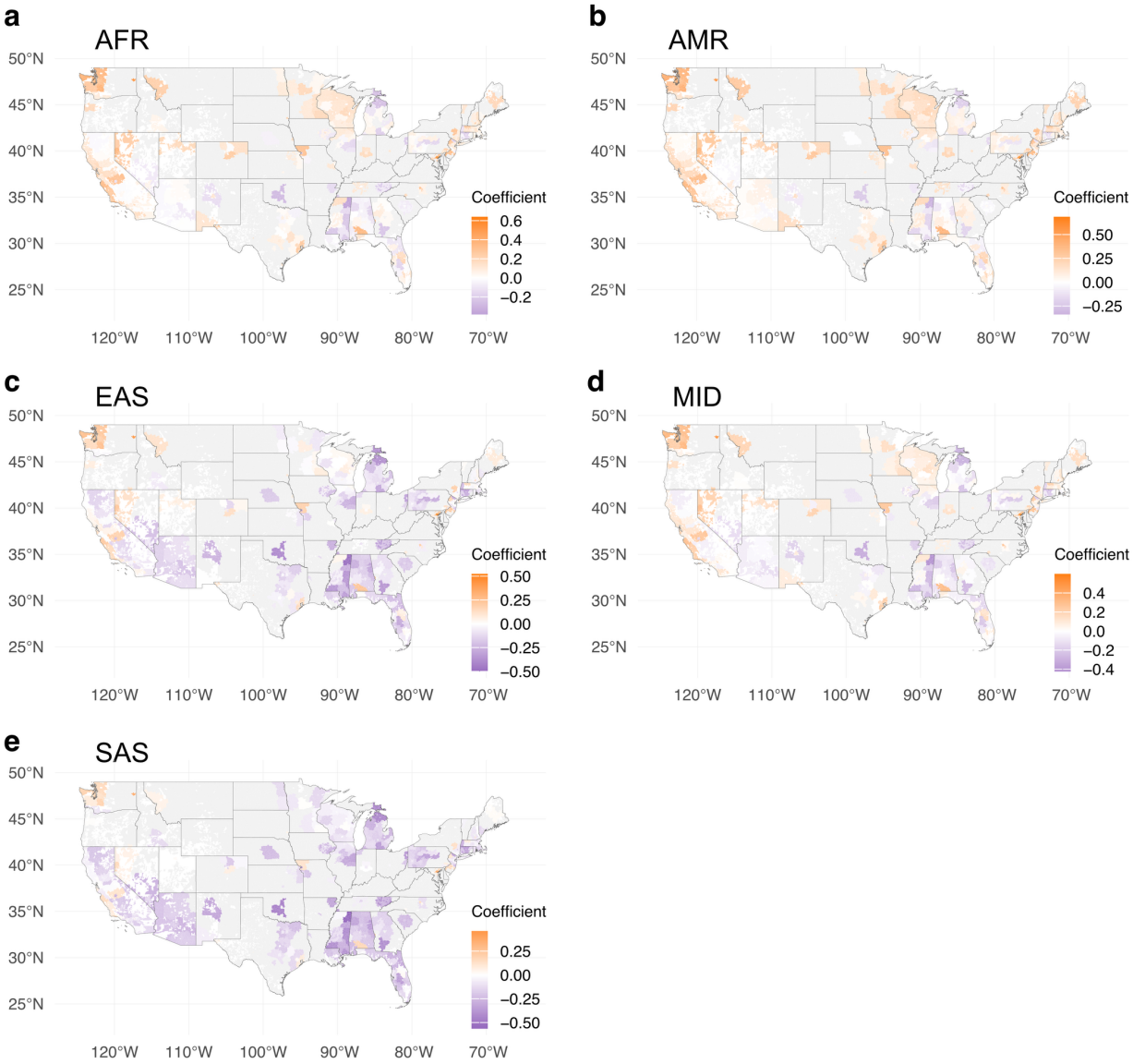
Analysis of the heterogeneity in the effect of age on leukocyte telomere length (LTL), stratified by genetic ancestry and sex. Effect estimates are presented with 95% confidence intervals. The linear regression model was adjusted for sex, the first 10 genetic principal components, sequencing site, socioeconomic factors (unemployment for over a year, housing instability, annual income, educational attainment, living alone, health insurance status, and neighborhood deprivation index), lifestyle (smoking status and alcohol consumption), and anthropometric traits (height and weight). Heterogeneity *P*-values for genetic ancestry (P_{anc_het}) and sex (P_{sex_het}) were derived by Cochran's Q test, which are distinct from the P-values for each association. The vertical dotted lines represent the overall effect size in each sex group rather than 0. AFR: African-like population, AMR: Admixed American-like population, EAS: East Asian-like population, EUR: European-like population, MID: Middle Eastern-like population, SAS: South Asian-like population, SD: standard deviation.

Supplementary Fig. 3: Associations between leukocyte telomere length (LTL) and phecodes and their heterogeneity in the *All of Us* Research Program.



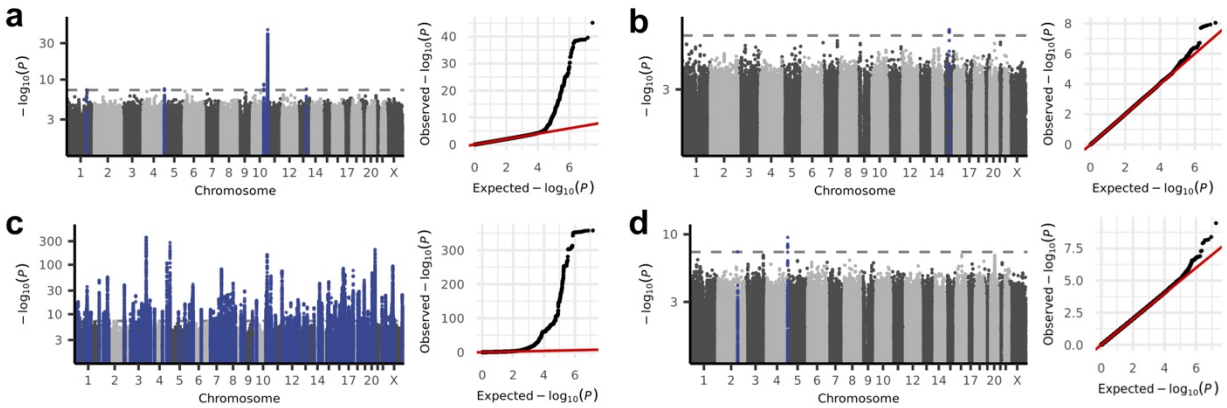
The Venn diagram for the phecodes that was significantly associated with leukocyte telomere length (LTL) (yellow) and those associations were significantly heterogeneous across genetic ancestries (red) and sexes (green) by Cochran's Q test with Bonferroni correction.

Supplementary Fig. 4: Ancestry-wise analyses of geographic heterogeneity for leukocyte telomere length (LTL) in the United States.



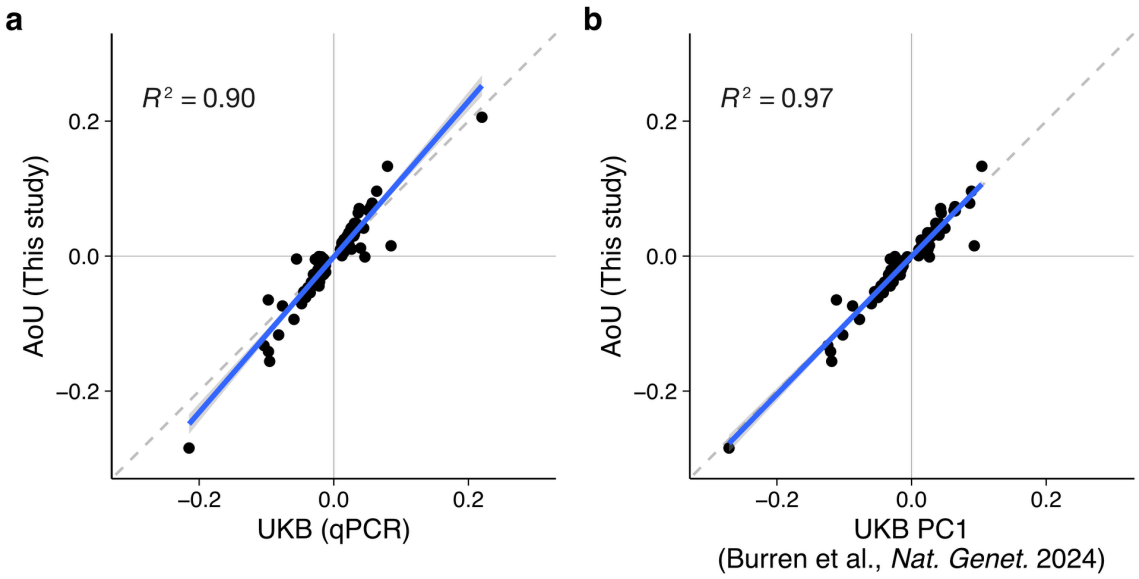
Geographical heterogeneity by 3-digit ZIP code prefix was tested with linear regression model adjusted for age, sex, the first 10 genetic principal components (PCs), and sequencing site within each genetic ancestry. The figure for the European-like population is shown in Extended Data Fig. 4f. Geographic boundary information for ZIP Code Tabulation Areas, states, and the U.S. nation were obtained from the U.S. Census Bureau TIGER/Line shape files. AFR: African-like population, AMR: Admixed American-like population, EAS: East Asian-like population, MID: Middle Eastern-like population, SAS: South Asian-like population.

Supplementary Fig. 5: Genome-wide association study for leukocyte telomere length (LTL) in the UK Biobank.



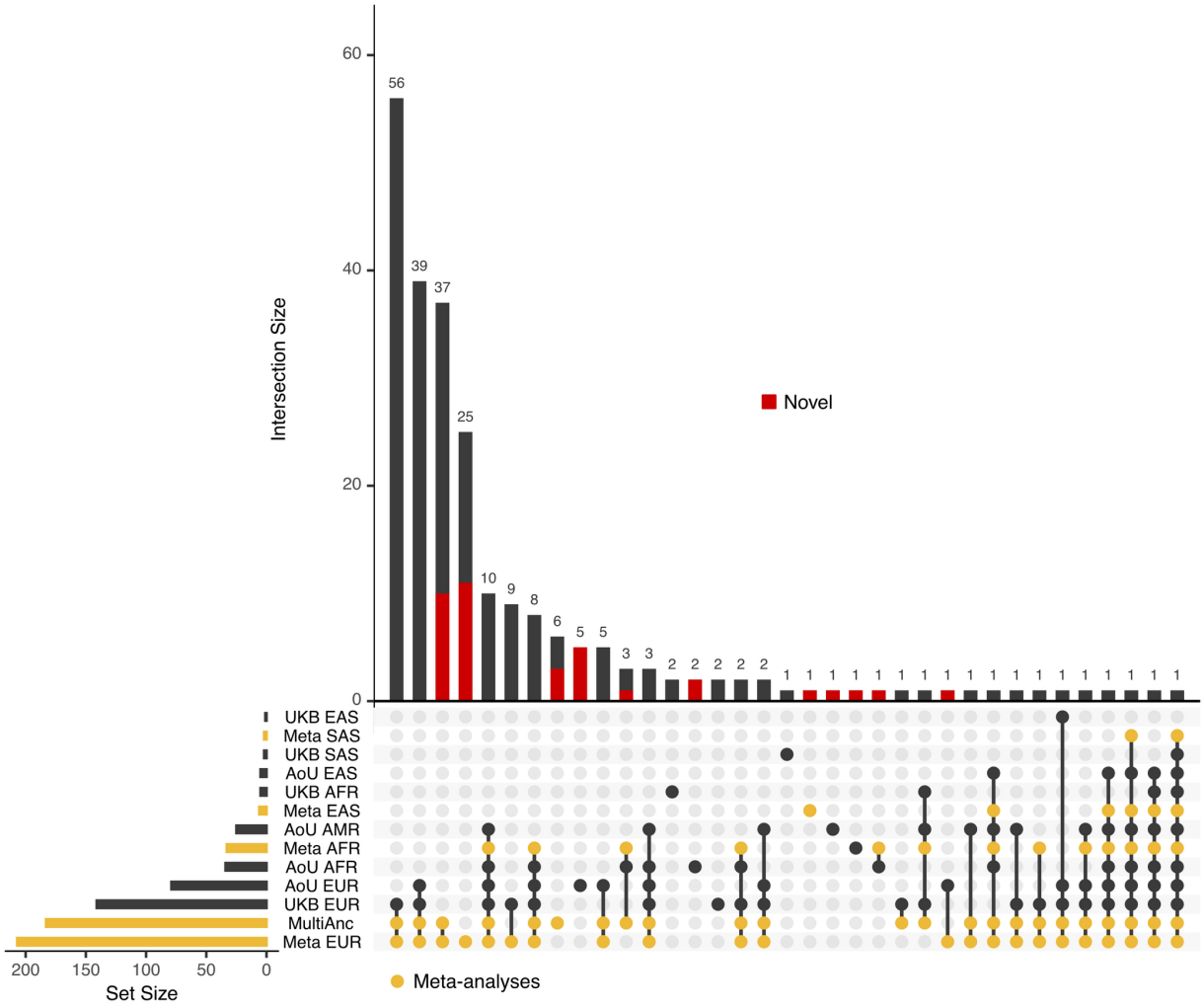
Genome-wide association studies for common variants were performed in the UK Biobank using previously published qPCR measurement of leukocyte telomere length[1] separately for African-like population (AFR) (**a**), East Asian-like population (EAS) (**b**), European-like population (EUR) (**c**), and South Asian-like population (SAS) (**d**). Genomic control with LD Score regression intercept was applied. Blue points in Manhattan plots represent significant loci ($P < 5 \times 10^{-8}$).

Supplementary Fig. 6: Effect estimate comparison for leukocyte telomere length (LTL) between cohorts.



a, Effect estimates of lead variants from significant loci in our revised GWAS using qPCR-based leukocyte telomere length (LTL) measurements in the UK Biobank (UKB; 129 variants) were compared with those from the *All of Us* Research Program (AoU) in individuals of the European-like population (EUR). **b**, Effect estimates for the same set of variants were compared between PC1 (an integrated measure combining qPCR and TelSeq published previously[2]) in UKB and AoU, based on loci present in both EUR summary statistics (125 variants).

Supplementary Fig. 7: Overlap of the significant loci in various GWAS performed in this study.



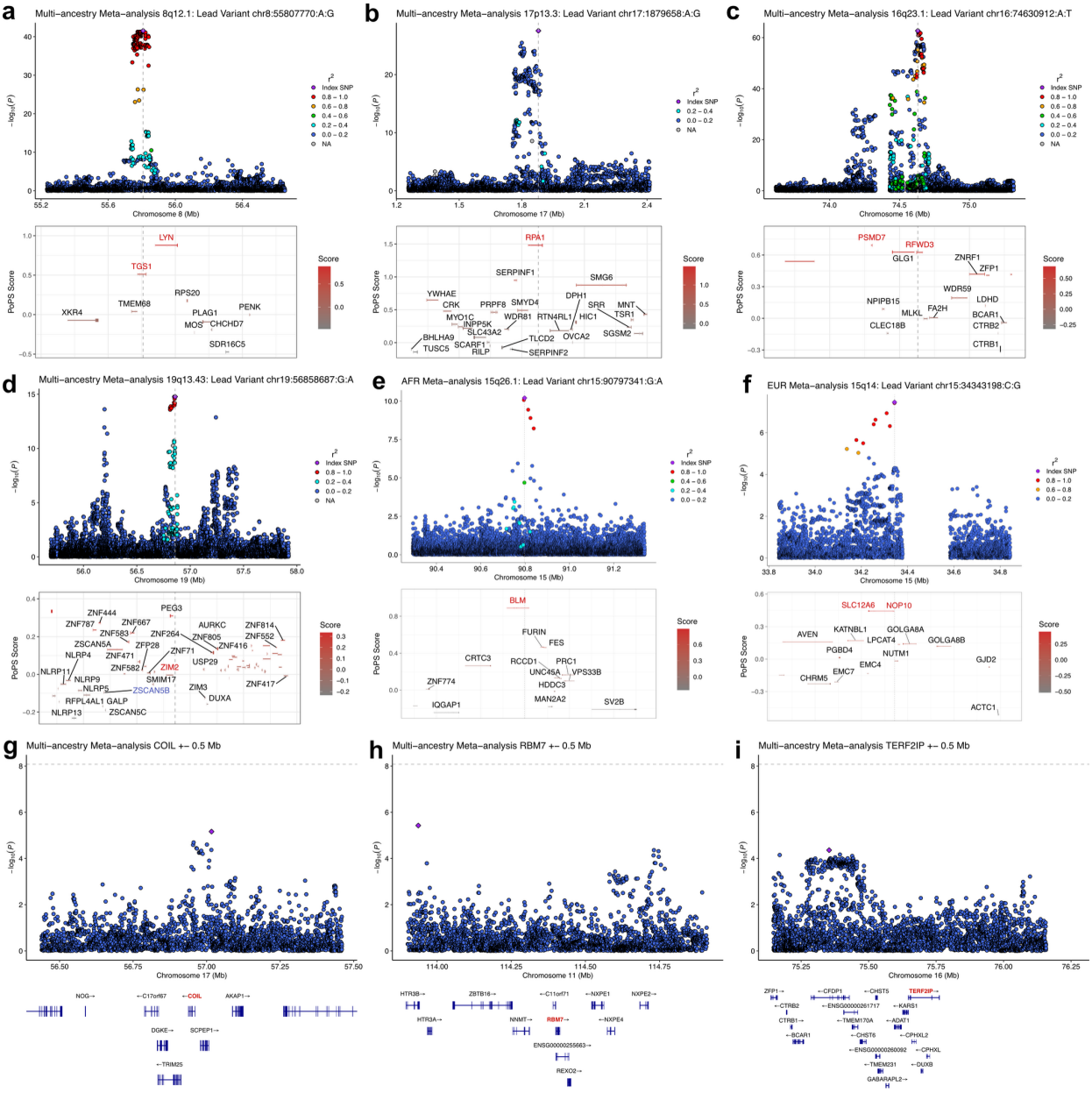
The overlap of the significant loci in all performed genome-wide association studies for common variants in this study. Overlap was defined by less than 1 Mb distance between significant variants. AFR: African-like population, AoU: the *All of Us* Research Program, EAS: East Asian-like population, EUR: European-like population, SAS: South Asian-like population, UKB: the UK Biobank.

Supplementary Fig. 8: Locuszoom plots with FINEMAP and PoPS annotations for significant loci in meta-analysis of common variant genome-wide association studies. (Legends only)

Figures are provided at the last of this PDF due to large size.

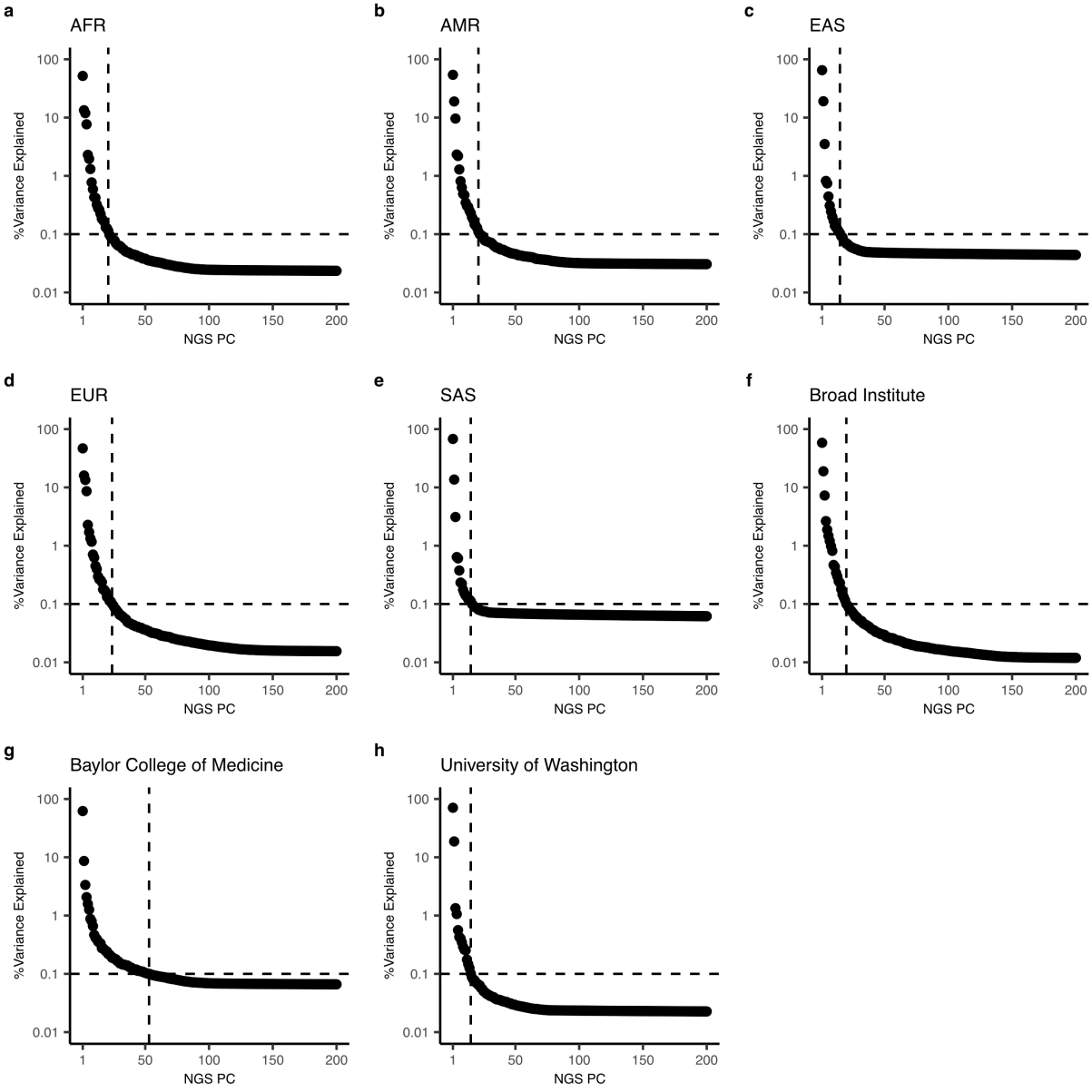
The locuszoom plots for significant loci in meta-analyses for the *All of Us* Research Program and UK Biobank common variant genome-wide association studies were plotted with FINEMAP[3] and PoPS[4] annotations if available. Red texts indicate the nearest and PoPS prioritized genes.

Supplementary Fig. 9: Locuszoom plots for common variant genome-wide association study near the novel genes found in the rare variant association study.



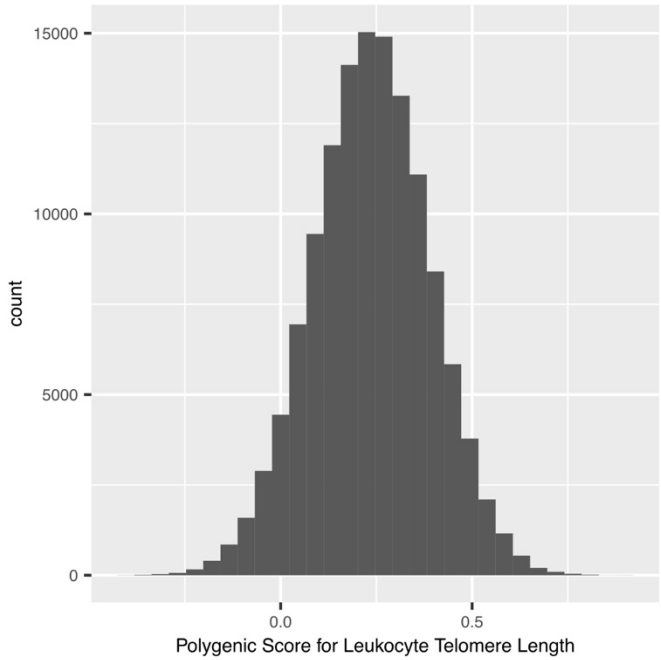
The locuszoom plots for common variant GWAS around the novel genes found in rare variant gene aggregation tests. If the locus overlaps with GWAS locus (**a**-**f**), PoPS[4] scores were plotted below, and red texts indicate the nearest and PoPS prioritized genes.

Supplementary Fig. 10: Number of NGS-derived principal components used to adjust the estimated leukocyte telomere length.



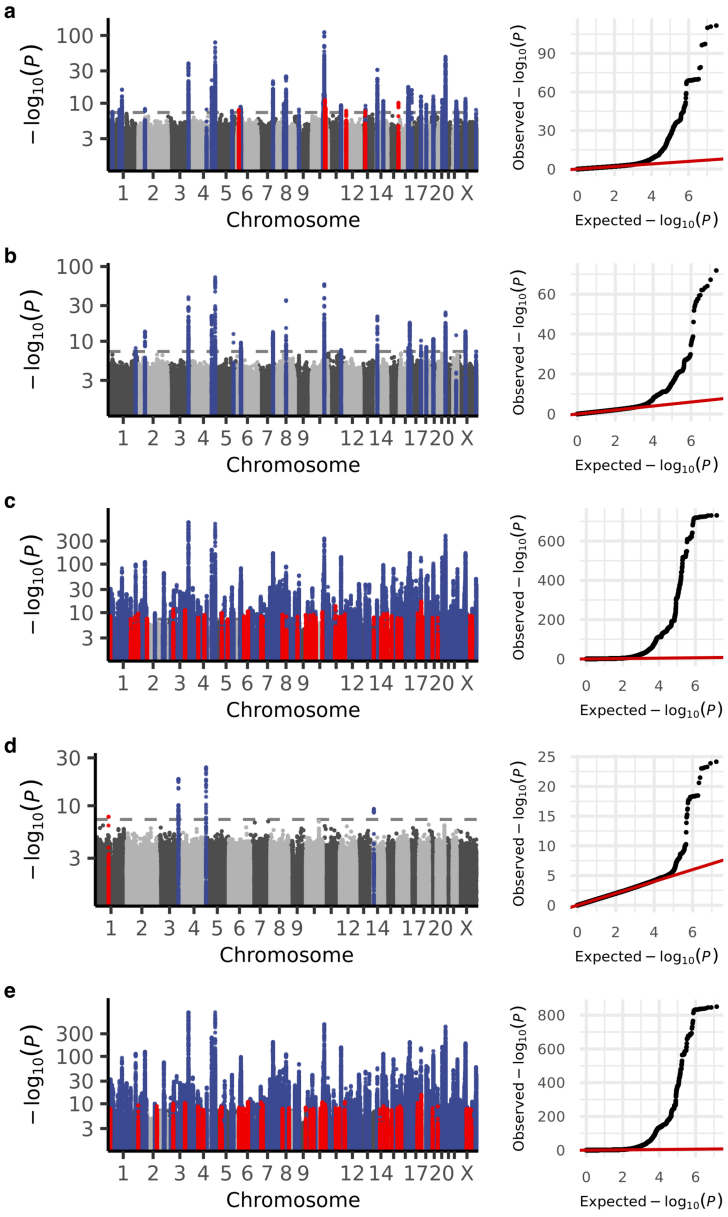
We calculated principal components (PCs) by modified NGS-PCA software[5] using sequencing depth for every 1,000 base-pairs across the genome calculated by mosdepth[6]. Calculations were separately done for sequencing center (for epidemiology) and genetic ancestry (for genomic studies) to reduce computational burden. PCs explaining over 0.1 % of the calculated total variance were used to adjust the leukocyte telomere length estimated by TelSeq[7].

Supplementary Fig. 11: Distribution of polygenic score for leukocyte telomere length.



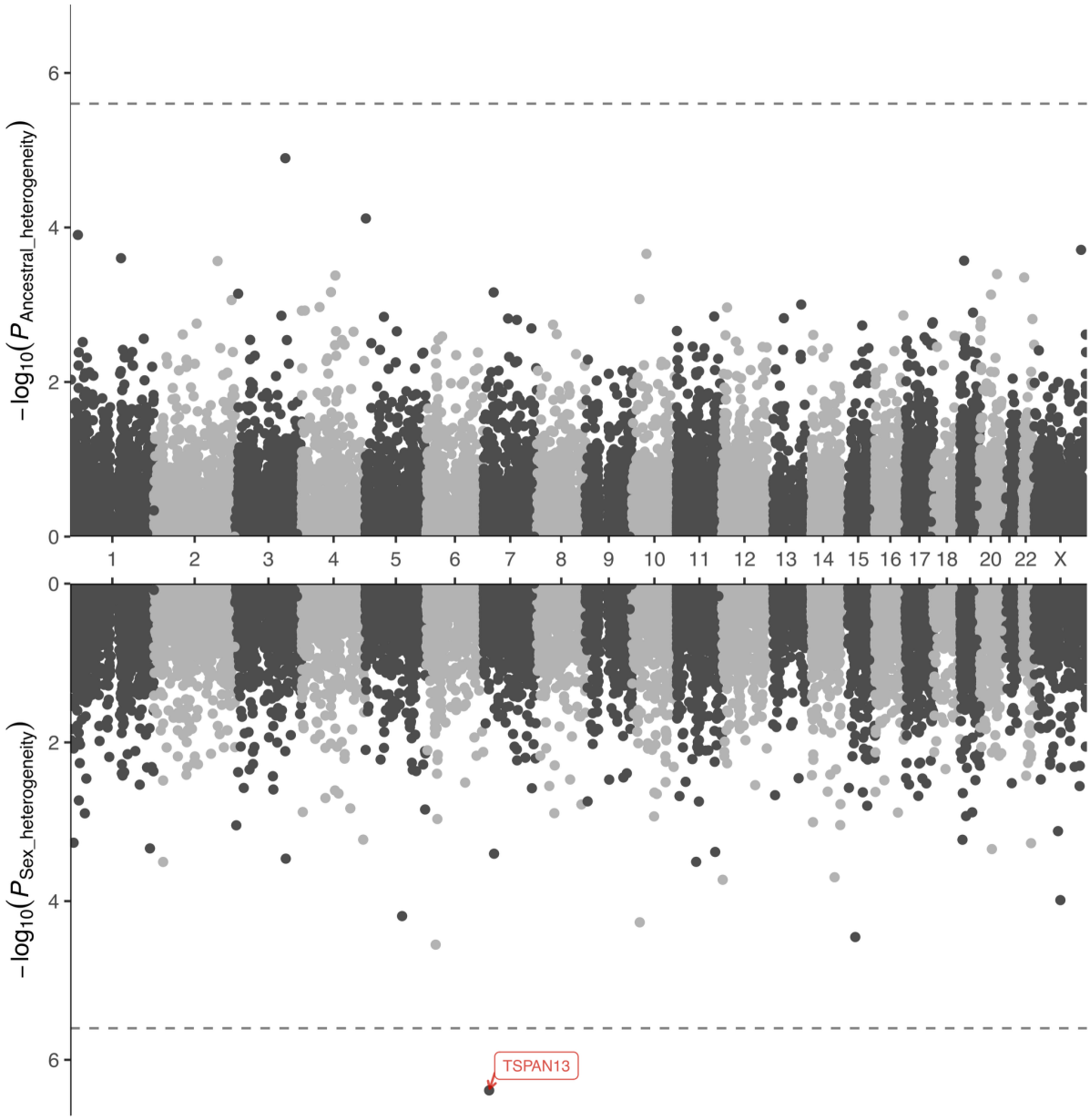
The distribution of the original polygenic score for leukocyte telomere length before standardization was plotted for European-like population in the *All of Us* Research Program.

Supplementary Fig. 12: Meta-analysis of genome-wide association studies using all available summary statistics.



a-d, Fixed effect meta-analyses for common variant (minor allele frequency > 0.1%) genome-wide association studies (GWASs) were performed for the All of Us Research Program, the UK Biobank, and the NHLBI Trans-Omics for Precision Medicine (TOPMed), leveraging all available most updated summary statistics. We performed fixed-effect meta-analyses separately for African-like population (AFR) (**a**), Admixed American-like population (AMR) (**b**), European-like population (EUR) (**c**), and South Asian-like population (SAS) (**d**) using GWAMA[8]. **e**, Multi-ancestry meta-analysis was performed with MR-MEGA[9] leveraging all available summary statistics shown in Supplementary Table 22. We only included variants found in 2 or more cohorts. Blue represents previously known significant loci ($P < 5\times10^{-8}$), and red represents novel significant loci.

Supplementary Fig. 13: Ancestral and sex heterogeneity in rare variant association study.



We performed meta-analysis of genome-wide rare variant aggregation tests for leukocyte telomere length (LTL) in the *All of Us* Research Program and UK Biobank, separately for each ancestry and sex. Ancestral and sex heterogeneity *P*-values were then calculated using GWAMA[8]. The dashed lines represent the significance thresholds (heterogeneity $P < 2.5 \times 10^{-6}$).

Supplementary Note 1: Additional epidemiological associations between LTL and traits

We specifically curated (Methods) and tested the associations for the following conditions: non-hematologic neoplasms and hematologic neoplasms; clonal hematopoiesis of indeterminate potential (CHIP), a precancerous condition defined by the presence of expanded leukemogenic mutations that we previously showed to be associated with LTL[10]; and CAD. Non-hematologic neoplasms were associated with longer LTL [odds ratio (OR) = 1.07, $P = 5.2\times10^{-7}$] with additional adjustment for total cholesterol, smoking, blood pressure, BMI, and blood glucose (n = 82,371). In comparison, hematologic neoplasms were associated with shorter LTL (OR = 0.80, $P = 1.8\times10^{-14}$). Both non-hematologic and hematologic neoplasms were associated with longer LTL-PGS in EUR (non-hematologic: OR = 1.03, $P = 0.01$; hematologic: OR = 1.08, $P = 3.8\times10^{-3}$; n = 52,685). CHIP was associated with shorter LTL ($\beta = -0.24$, $P = 4.1\times10^{-14}$), as we and others reported before in other datasets[2,10], with heterogeneity across driver genes (Extended Data Fig. 10). Greater variant allele fraction of CHIP was robustly associated with shorter LTL ($\beta = -0.014$, $P = 1.9\times10^{-11}$). Increased risk of CAD was associated with both measured shorter LTL (OR = 0.85, $P = 6.1\times10^{-27}$) and shorter LTL-PGS (OR = 0.95, $P = 1.3\times10^{-3}$ in EUR) with the same additional adjustment.

Here, we observed that both longer measured LTL and higher LTL-PGS were associated with increased risk of non-hematologic malignancies. In contrast, for hematologic malignancies, we found a discordant pattern: higher LTL-PGS was associated with increased risk, while longer measured LTL was associated with decreased risk. These findings were consistent with prior UKB results[1], which reported that (1) longer measured LTL is linked to lower leukemia risk while generally linked to higher risk for other cancers, and (2) genetically longer LTL is associated with increased risk of both hematologic and non-hematologic cancers. This supports the model we previously proposed[10], in which genetically longer telomeres increase the likelihood of acquiring somatic mutations, including those that lead to CHIP or leukemia, possibly by enabling more cell divisions. Once clonal expansion begins, however, the elevated proliferation of hematopoietic cells accelerates telomere attrition in hematologic cells, leading to shorter measured LTL. In contrast, non-hematologic cancers do not affect leukocyte turnover and thus do not influence measured LTL. Given that telomere length is well correlated across tissues[11], this results in a consistent association between longer LTL (both measured and genetically inferred) and increased risk of non-hematologic cancers.

Supplementary Note 2: Additional details in common variant GWAS loci

Among the PoPS-prioritized genes, *GFI1B*, a master transcription factor that is necessary for maintaining hematopoietic stem cell quiescence[12], was prioritized by PoPS at the 9q34.13 locus (Extended Data Fig. 7c). The lead variant chr9:133018743:C:T (nearest gene *GTF3C5*, $AF_{EUR} = 0.186$, $\beta_{EUR} = -0.015$, $P_{EUR} = 2.5\times10^{-10}$) is in linkage disequilibrium (LD) with chr9:133004155:C:T (rs524137, $R^2_{EUR} = 0.52$), a functionally validated causal variant identified in GWAS for myeloproliferative neoplasms[13]. Chr9:133004155:C:T accelerates the cell cycles

of hematopoietic stem cells via GFI1B suppression, consistent with its association with shorter LTL.

Among the novel loci that were both closest to the lead variant and had the highest PoPS scores at the locus, *PTEN* was prioritized by PoPS at 10q23.31 and nearest to the lead variant (chr10:87957355:G:T, $AF_{EUR} = 0.0394$, $\beta_{EUR} = 0.028$, $P_{EUR} = 2.1\times10^{-9}$, Extended Data Fig. 7d); it has been shown to negatively regulate telomerase expression[14]. *EXOSC7* at 3p21.31 locus (lead variant: chr3:44976290:A:G, $AF_{EUR} = 0.0917$, $\beta_{EUR} = -0.019$, $P_{EUR} = 1.4\times10^{-9}$, Extended Data Fig. 7e) was another gene that meets this criterion; it is a component of the RNA exosome complex, which is involved in the processing of the telomerase RNA template[15]. Notably, other members of the EXOSC gene family have also been implicated in prior and in the present LTL GWASs.

Supplementary Note 3: Additional details in sex-stratified GWAS and sex-specific locus
We found 76 genome-wide significant loci in male specific EUR meta-analysis, of which 68 loci (89.5%) overlapped with female-specific EUR meta-analysis loci defined by significant variants within 1 Mb. Female specific EUR meta-analysis found 94 significant loci, of which 67 (71.3%) overlapped with male specific EUR meta-analysis loci.

The lead variant at the female-specific locus was chrX:152767196:C:A ($AF_{Female} = 0.15$, $\beta_{Female} = 0.066$, $P_{Female} = 4.1\times10^{-80}$; $AF_{Male} = 0.15$, $\beta_{Male} = 0.0046$, $P_{Male} = 0.093$; $P_{Sex\text{-}heterogeneity} = 2.4\times10^{-43}$), a missense variant in *MAGEA6*. Phenome-wide association study for chrX:152767196:C:A in AoU showed no significantly associated phecode in overall, female-, and male-specific analyses, with no significant sex heterogeneity after Bonferroni correction ($P < 2.9\times10^{-5}$; Supplementary Table 22).

Supplementary Note 4: Additional discussion on subtelomeric GWAS loci
While we observed many subtelomeric signals, the specific downstream molecular mediators remain undefined. TERRA[16] is an appealing candidate given its origin from subtelomeres and role in telomere biology. However, further functional work will be required to validate whether subtelomeric variants influence telomere length via TERRA along with other possible mechanisms. We also note that this enrichment of subtelomeric associations may, in part, reflect analytic or structural biases (e.g., variant detection near chromosome ends) and thus the subtelomeric enrichment should be interpreted with caution.

Supplementary Note 5: Additional GWAS meta-analysis leveraging all available summary statistics
Burren et al. (*Nature Genetics*, 2024) estimated leukocyte telomere length (LTL) in the UK Biobank (UKB) using whole-genome sequencing and TelSeq (Ding et al., *Nucleic Acids Res*., 2014). Subsequent integration of TelSeq and qPCR-based measurements had improved sensitivity for detecting genetic associations through genome-wide association studies (GWAS). However, because TelSeq-based LTL estimates from UKB were not made publicly available at

the time of our analysis, we conducted GWAS meta-analyses using the qPCR-derived LTL measurements in UKB.

To maximize power and fully leverage all available data, we then incorporated publicly available GWAS summary statistics from the combined TelSeq + qPCR LTL measurement in UKB (Burren et al., *Nature Genetics*, 2024, available only for European ancestry [EUR]) and from the NHLBI Trans-Omics for Precision Medicine (TOPMed) program using TelSeq (Taub et al., *Cell Genomics*, 2022), together with the results from the present study based on the *All of U*s Research Program (AoU) using TelSeq. We also performed ancestry-wise meta-analysis for other ancestries [African-like population (AFR), Admixed American-like population (AMR), and South Asian-like population (SAS)] using corresponding summary statistics in AoU and UKB (qPCR) and TOPMed (African, Hispanic/Latino, and Asian). Since ancestry definition doesn't perfectly match between TOPMed and AoU/UKB, we performed ancestry-stratified meta-analyses for SAS by combining summary statistics for SAS in UKB and AoU, and summary statistics for Asian in TOPMed, where the majority of Asian participants are of South Asian (Supplementary Table 23).

In ancestry-specific meta-analyses, we identified 45 (7 novel) independent loci in AFR, 23 (0) in AMR, 253 (47) in EUR, and 4 (1) in SAS. Multi-ancestry meta-analysis yielded 242 independent loci, of which 46 were novel. Thirteen out of 46 novel loci were unique to this multi-ancestry meta-analysis. In total, we identified 274 non-overlapping independent loci, including 69 novel loci. We found 23 out of 274 non-overlapping common variant GWAS loci had RVAS genes within 500 Kb (Supplementary Table 24).

Lead variants from each significant locus are listed in Supplementary Table 24 and corresponding Manhattan and Q-Q plots are shown in Supplementary Fig. 12. Full details of each meta-analysis, including contributing cohorts and linkage disequilibrium score regression (LDSC) metrics, are provided in Supplementary Table 23.

All meta-analyses were performed using the same statistical framework as described in the Methods section.

Supplementary Note 6: Additional details on RVAS findings

Six novel genes identified in our RVAS all had evidence of involvement in telomere biology. TGS1 forms the 2,2,7-trimethylguanosine cap structure at the 5′ end of human telomerase RNA, which recruits telomerase to telomeres and engages Cajal bodies in telomere maintenance[17]. RPA1 binds to telomeres, and gain-of-function mutations in RPA1 cause short telomeres[18]. Consistently, rare deleterious variants in RPA1 were associated with longer LTL in our RVAS (Fig. 4b). RFWD3 and ZSCAN5B play roles in DNA damage response[19,20]. NOP10 is a component of telomerase RNA-protein complex[21].

For the five RVAS genes which did not align with PoPS prioritization: *RTEL1* was nearest but PoPS prioritized a smaller secondary peak, *NOP10* was nearest while PoPS instead prioritized the adjacent gene likely in another credible set with a similar score, *DCLRE1B* was the second nearest gene whereas PoPS prioritized in another credible set, *WRAP53* had other genes in the locus with established roles in telomere biology (*TP53* and *CTC1*) which PoPS prioritized, *ZSCAN5B* was nearest to the secondary peak in the locus while PoPS prioritized a gene linked to the largest peak, and *ZSWIM3* was ranked 3rd by PoPS in the locus among multiple credible sets.

We performed genetic ancestry- and sex-specific RVAS and assessed the heterogeneity (Supplementary Fig. 13). No significant heterogeneity was observed across ancestries. However, we identified that the association with *TSPAN13* was significantly heterogeneous between sexes. *TSPAN13* was nominally associated with LTL in both sexes but with opposite directions (β_{Female} = -0.33, $P_{Female} = 5.7\times10^{-4}$; β_{Male} = 0.44, $P_{Male} = 2.0\times10^{-4}$; $P_{Sex\text{-}heterogeneity} = 4.1\times10^{-7}$, Supplementary Table 25). A link between *TSPAN13* and telomere biology has not been previously reported.

Supplementary Note 7: Additional discussion about observed heterogeneity in epidemiology

The associations between shorter LTL and indicators of socioeconomic disadvantage and poor lifestyle reinforce prior mechanistic evidence that chronic stress (e.g., inflammatory, oxidative, or psychosocial stress) can accelerate telomere attrition[22,23]. Patterns of stress exposure and its biological consequences are known to differ by sex and ancestry. For instance, studies have reported higher allostatic load among some minoritized racial and ethnic groups[24,25], potentially reflecting cumulative social and environmental stressors that have also been linked to shorter LTL. Accordingly, part of the heterogeneity observed by genetic ancestry in our study could reflect underlying social and environmental differences correlated with ancestry, rather than ancestry itself. Likewise, sex differences in both biological and psychosocial stress exposure[26,27], as well as in telomere maintenance mechanisms, may contribute to the distinct LTL associations observed in our ancestry- and sex-stratified analyses. While our findings are consistent with these prior observations, we note that our analyses cannot directly disentangle genetic, biological, and social factors.

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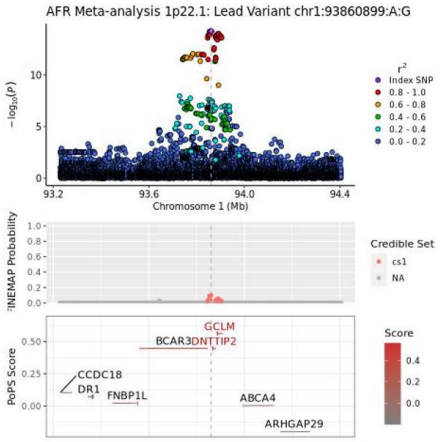
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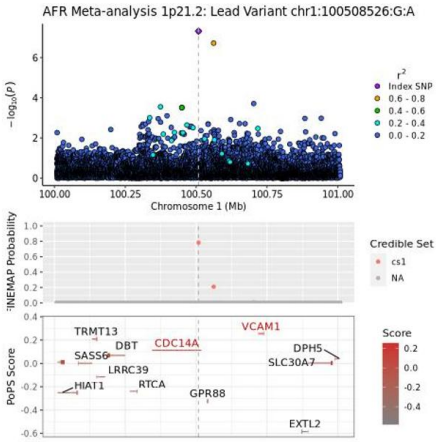
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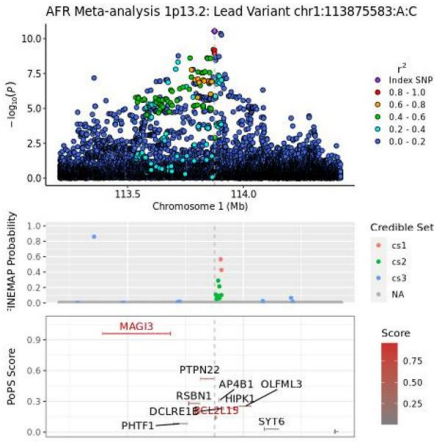
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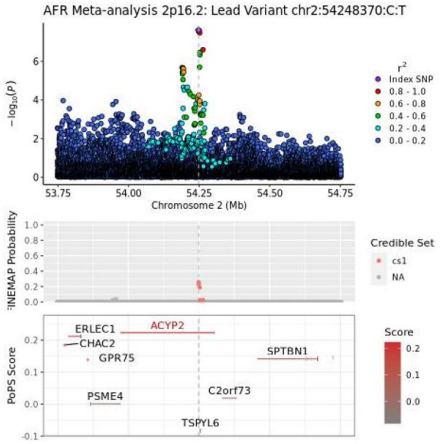
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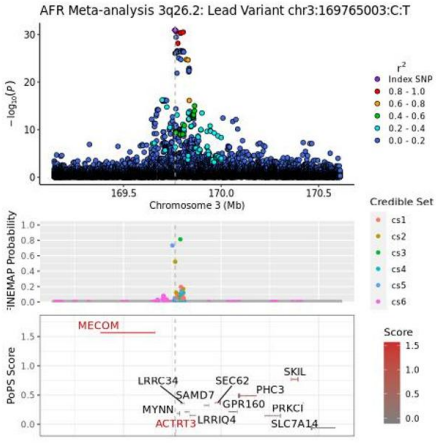
Supplementary Fig. 8:
Locuszoom plots with FINEMAP and PoPS annotations for significant loci in meta-analysis of common variant genome-wide association studies.
(Figures only)

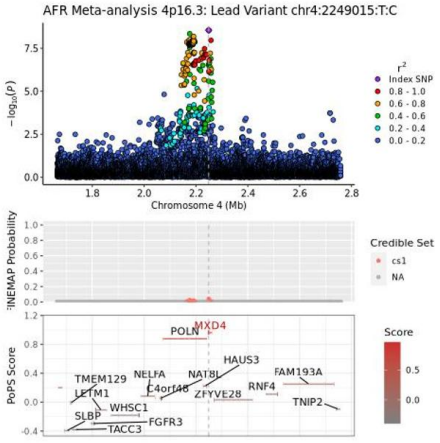

AFR Meta-analysis 1p22.1: Lead Variant chr1:93860899:A:G
Chromosome 1 (Mb)
FINEMAP Probability
PoPS Score
GCLM
BCAR3
DNTTIP2
CCDC18
DR1
FNBP1L
ABCA4
ARHGAP29

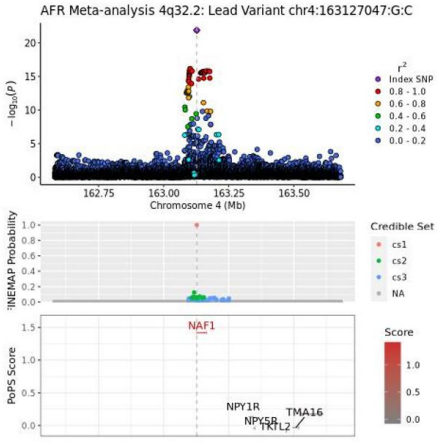

AFR Meta-analysis 1p21.2: Lead Variant chr1:100508526:G:A
Chromosome 1 (Mb)
FINEMAP Probability
PoPS Score
TRMT13
VCAM1
DBT
CDC14A
DPH5
SASS6
SLC30A7
LRRC39
HIAT1
RTCA
GPR88
EXTL2

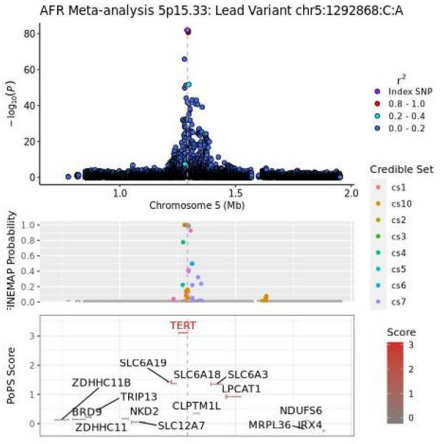

AFR Meta-analysis 1p13.2: Lead Variant chr1:113875583:A:C
Chromosome 1 (Mb)
FINEMAP Probability
PoPS Score
MAGI3
PTPN22
AP4B1
OLFML3
RSBN1
HIPK1
DCLRE1B
CELF2L19
PHTF1
SYT6

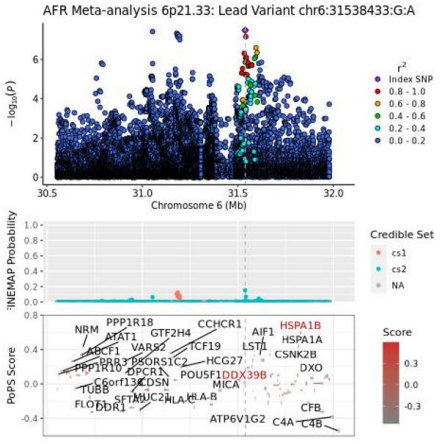

AFR Meta-analysis 2p16.2: Lead Variant chr2:54248370:C:T
Chromosome 2 (Mb)
FINEMAP Probability
PoPS Score
ERLEC1
ACYP2
CHAC2
GPR75
SPTBN1
PSME4
C2orf73
TSPYL6

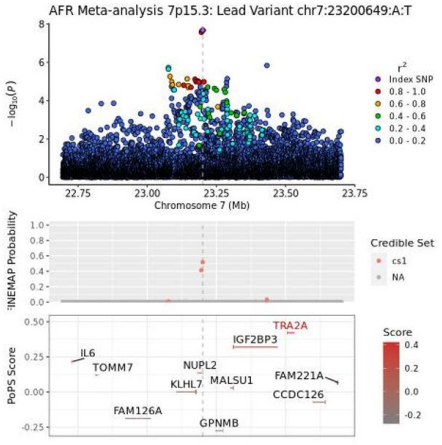

AFR Meta-analysis 3q26.2: Lead Variant chr3:169765003:C:T
Chromosome 3 (Mb)
FINEMAP Probability
PoPS Score
MECOM
LRRC34
SEC62
SKIL
SAMD7
PHC3
GPR160
MYNN
PRKCI
ACTRT3
LRRIQ4
SLC7A14

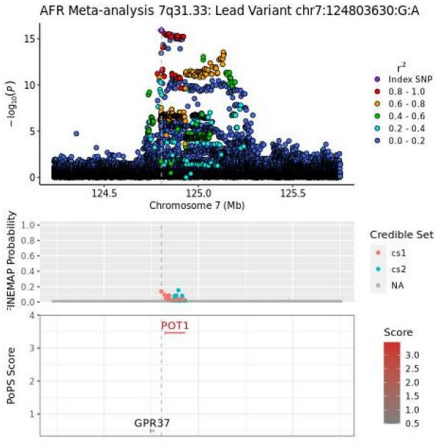

AFR Meta-analysis 4p16.3: Lead Variant chr4:2249015:T:C
Chromosome 4 (Mb)
FINEMAP Probability
PoPS Score
POLN
MXD4
HAUS3
TMEM129
NELFA
NAT8L
FAM193A
LETM1
C4orf48
RNF4
ZFYVE28
TNIP2
SLBP
WHSC1
TACC3
FGFR3

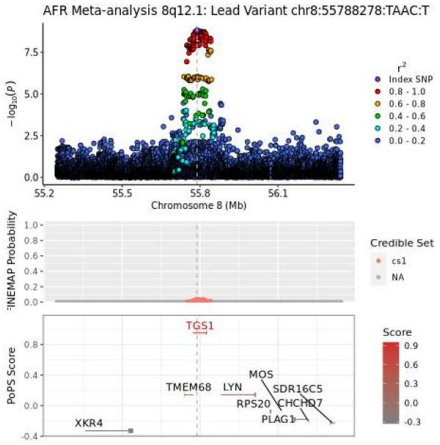

AFR Meta-analysis 4q32.2: Lead Variant chr4:163127047:G:C
Chromosome 4 (Mb)
FINEMAP Probability
PoPS Score
NAF1
NPY1R
NPY5R
TMA16
TKTL2

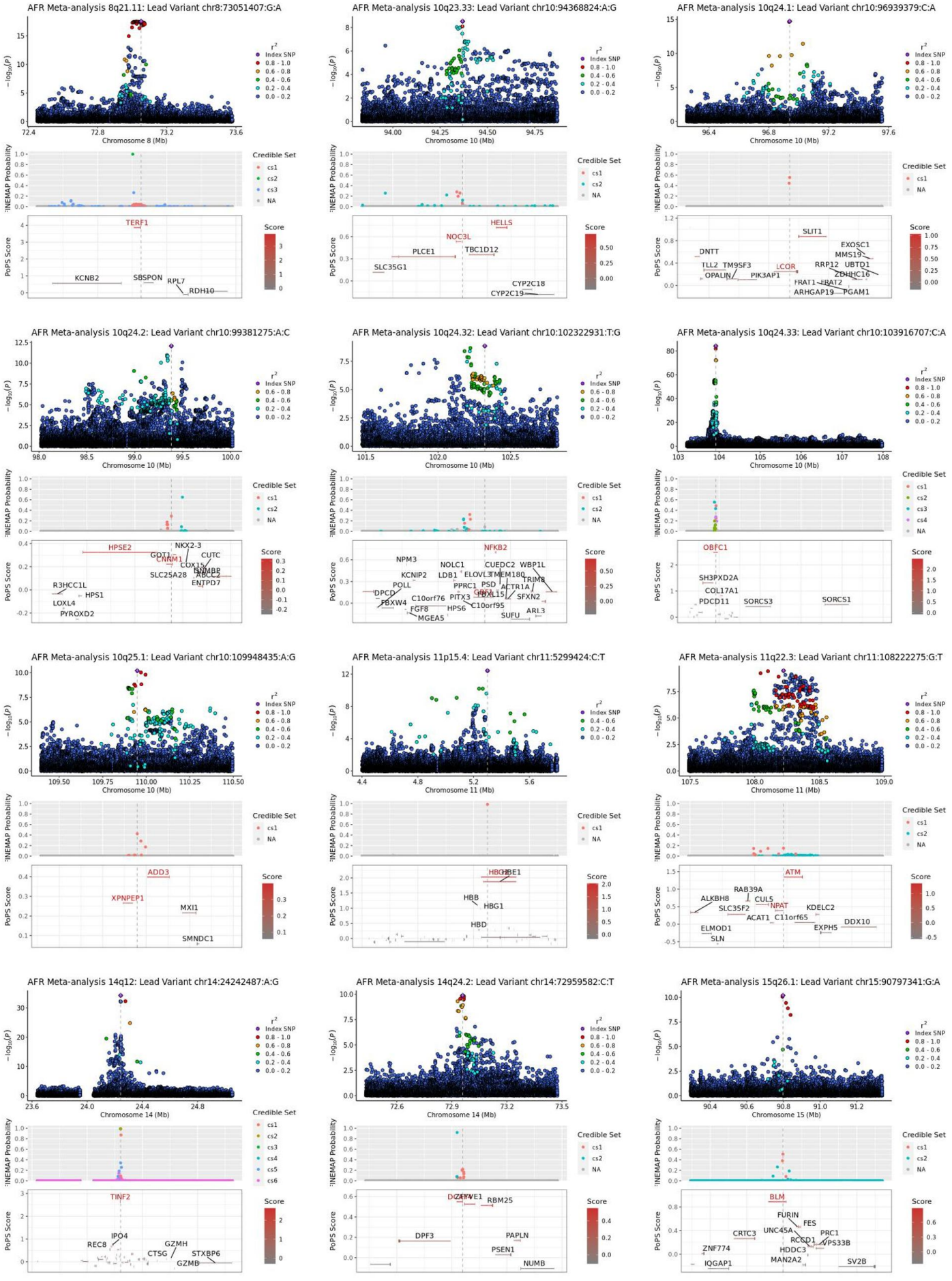

AFR Meta-analysis 5p15.33: Lead Variant chr5:1292868:C:A
Chromosome 5 (Mb)
FINEMAP Probability
PoPS Score
TERT
SLC6A19
ZDHHC11B
SLC6A18
SLC6A3
LPCAT1
TRIP13
BRD9
NKD2
CLPTM1L
NDUFS6
ZDHHC11
SLC12A7
MRPL36
IRX4

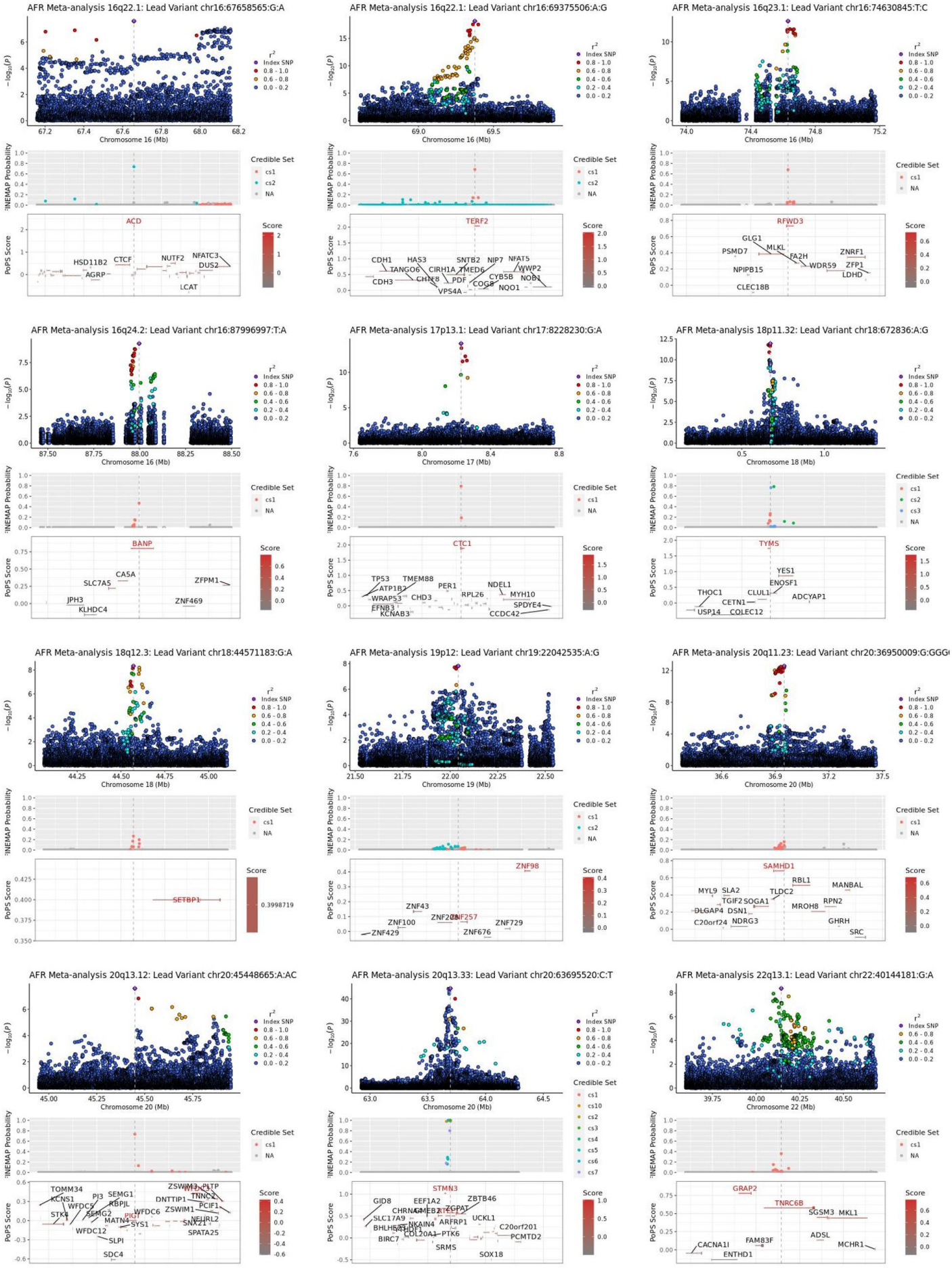

AFR Meta-analysis 6p21.33: Lead Variant chr6:31538433:G:A
Chromosome 6 (Mb)
FINEMAP Probability
PoPS Score
NRM
PPP1R18
CCHCR1
HSPA1B
ATAT1
GTF2H4
AIF1
HSPA1A
ABCF1
VARS2
TCF19
LST1
CSNK2B
PRR3
PSORS1C2
HCG27
PPP1R10
DPCR1
POU5F1
DDX39B
DXO
C6orf136
CDSN
MICA
TUBB
MUC22
HLA-B
FLOT1
SFTA2
DDR1
CFB
ATP6V1G2
C4A
C4B

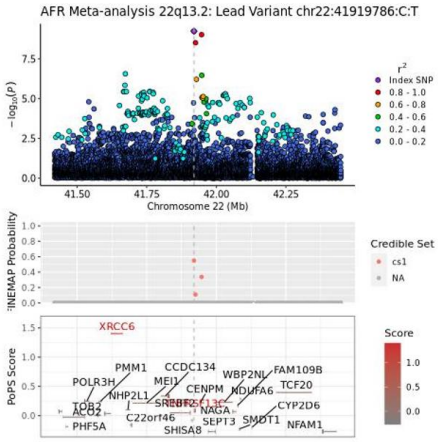

AFR Meta-analysis 7p15.3: Lead Variant chr7:23200649:A:T
Chromosome 7 (Mb)
FINEMAP Probability
PoPS Score
TRA2A
IGF2BP3
IL6
TOMM7
NUPL2
KLHL7
MALSU1
FAM221A
CCDC126
FAM126A
GPNMB

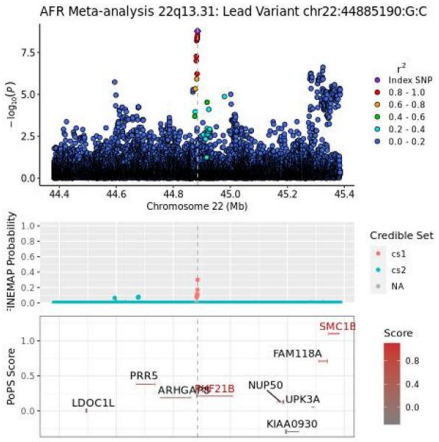

AFR Meta-analysis 7q31.33: Lead Variant chr7:124803630:G:A
Chromosome 7 (Mb)
FINEMAP Probability
PoPS Score
POT1
GPR37

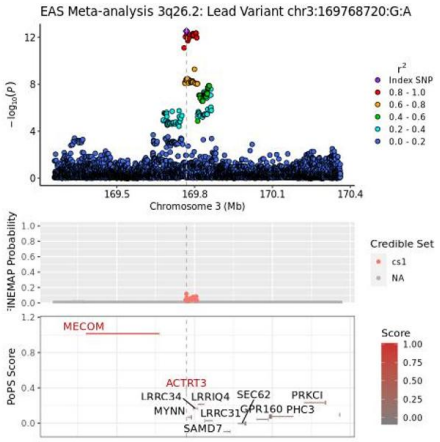

AFR Meta-analysis 8q12.1: Lead Variant chr8:55788278:TAAC:T
Chromosome 8 (Mb)
FINEMAP Probability
PoPS Score
TGS1
MOS
TMEM68
LYN
SDR16C5
RPS20
CHCHD7
PLAG1
XKR4

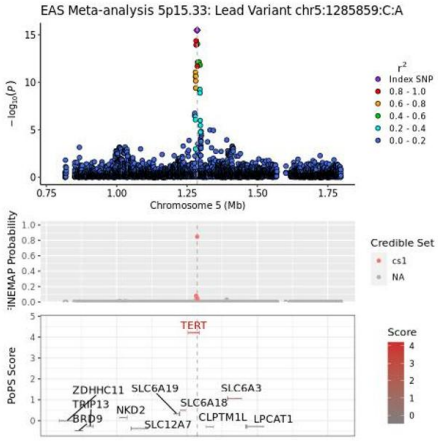

AFR Meta-analysis 8q21.11: Lead Variant chr8:73051407:G:A
Chromosome 8 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
TERF1
KCNB2
SBSPON
RPL7
RDH10
AFR Meta-analysis 10q23.33: Lead Variant chr10:94368824:A:G
Chromosome 10 (Mb)
HELLS
NOC3L
PLCE1
TBC1D12
SLC35G1
CYP2C18
CYP2C19
AFR Meta-analysis 10q24.1: Lead Variant chr10:96939379:C:A
Chromosome 10 (Mb)
SLIT1
EXOSC1
MMS19
DNTT
TLL2
TM9SF3
LCOR
RRP12
UBTD1
OPALIN
PIK3AP1
ZDHHC16
FRAT1
FRAT2
ARHGAP19
PGAM1
AFR Meta-analysis 10q24.2: Lead Variant chr10:99381275:A:C
Chromosome 10 (Mb)
HPSE2
NKX2-3
GOT1
CUTC
CNNM1
COX15
SLC25A28
ABCC2
ENTPD7
R3HCC1L
HPS1
LOXL4
PYROXD2
AFR Meta-analysis 10q24.32: Lead Variant chr10:102322931:T:G
Chromosome 10 (Mb)
NFKB2
NPM3
NOLC1
CUEDC2
WBP1L
KCNIP2
LDB1
ELOVL3
TMEM180
TRIM8
POLL
PPRC1
PSD
ACTR1A
DPCD
C10orf76
PITX3
GRID1
ZDHHC15
SFXN2
FBXW4
FGF8
HPS6
C10orf95
MGEA5
SUFU
ARL3
AFR Meta-analysis 10q24.33: Lead Variant chr10:103916707:C:A
Chromosome 10 (Mb)
OBFC1
SH3PXD2A
COL17A1
PDCD11
SORCS3
SORCS1
AFR Meta-analysis 10q25.1: Lead Variant chr10:109948435:A:G
Chromosome 10 (Mb)
ADD3
XPNPEP1
MXI1
SMNDC1
AFR Meta-analysis 11p15.4: Lead Variant chr11:5299424:C:T
Chromosome 11 (Mb)
HBG2
HBE1
HBB
HBG1
HBD
AFR Meta-analysis 11q22.3: Lead Variant chr11:108222275:G:T
Chromosome 11 (Mb)
ATM
RAB39A
ALKBH8
CUL5
SLC35F2
NPAT
KDELC2
ACAT1
C11orf65
DDX10
ELMOD1
EXPH5
SLN
AFR Meta-analysis 14q12: Lead Variant chr14:24242487:A:G
Chromosome 14 (Mb)
TINF2
IPO4
REC8
GZMH
CTSG
STXBP6
GZMB
AFR Meta-analysis 14q24.2: Lead Variant chr14:72959582:C:T
Chromosome 14 (Mb)
DCAF4
ZFYVE1
RBM25
DPF3
PAPLN
PSEN1
NUMB
AFR Meta-analysis 15q26.1: Lead Variant chr15:90797341:G:A
Chromosome 15 (Mb)
BLM
FURIN
FES
CRTC3
UNC45A
PRC1
RCSD1
VPS33B
HDDC3
ZNF774
MAN2A2
IQGAP1
SV2B

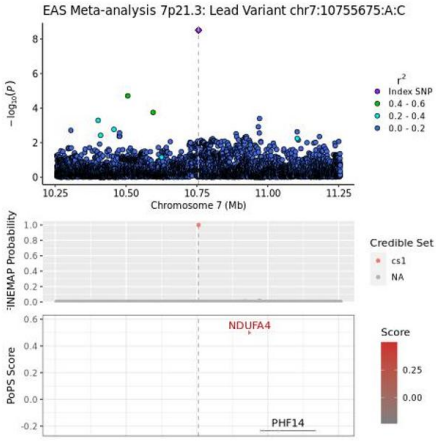

AFR Meta-analysis 16q22.1: Lead Variant chr16:67658565:G:A
AFR Meta-analysis 16q22.1: Lead Variant chr16:69375506:A:G
AFR Meta-analysis 16q23.1: Lead Variant chr16:74630845:T:C
AFR Meta-analysis 16q24.2: Lead Variant chr16:87996997:T:A
AFR Meta-analysis 17p13.1: Lead Variant chr17:8228230:G:A
AFR Meta-analysis 18p11.32: Lead Variant chr18:672836:A:G
AFR Meta-analysis 18q12.3: Lead Variant chr18:44571183:G:A
AFR Meta-analysis 19p12: Lead Variant chr19:22042535:A:G
AFR Meta-analysis 20q11.23: Lead Variant chr20:36950009:G:GGG
AFR Meta-analysis 20q13.12: Lead Variant chr20:45448665:A:AC
AFR Meta-analysis 20q13.33: Lead Variant chr20:63695520:C:T
AFR Meta-analysis 22q13.1: Lead Variant chr22:40144181:G:A
Chromosome 16 (Mb)
Chromosome 17 (Mb)
Chromosome 18 (Mb)
Chromosome 19 (Mb)
Chromosome 20 (Mb)
Chromosome 22 (Mb)
−log10(p)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
cs4
cs5
cs6
cs7
cs10
NA
PoPS Score
Score
ACD
HSD11B2
CTCF
NUTF2
NFATC3
DUS2
AGRP
LCAT
TERF2
CDH1
HAS3
TANGO6
CIRH1A
7MED6
SNTB2
NIP7
NFAT5
WWP2
CYB5B
NOB1
CDH3
CHTF8
PDF
COG8
NQO1
VPS4A
RFWD3
GLG1
PSMD7
MLKL
FA2H
ZNRF1
WDR59
ZFP1
LDHD
NPIPB15
CLEC18B
BANP
CA5A
SLC7A5
ZFPM1
JPH3
KLHDC4
ZNF469
CTC1
TP53
TMEM88
ATP1B2
PER1
NDEL1
WRAP53
CHD3
RPL26
MYH10
SPDYE4
KCNAB3
CCDC42
TYMS
YES1
ENOSF1
THOC1
CLUL1
ADCYAP1
CETN1
USP14
COLEC12
SETBP1
0.3998719
ZNF98
ZNF43
ZNF208
ZNF257
ZNF100
ZNF729
ZNF429
ZNF676
SAMHD1
RBL1
MANBAL
MYL9
SLA2
TLDC2
TGIF2
SOGA1
RPN2
DLGAP4
DSN1
MROH8
C20orf24
NDRG3
GHRH
SRC
TOMM34
KCNS1
PI3
SEMG1
WFDC5
RBPJL
STK4
SEMG2
PIGT
WFDC6
ZSWIM1
MATN4
SYS1
WFDC12
SLPI
SDC4
ZSWIM3
PLTP
TNNC2
DNTTIP1
PCIF1
SNX21
NEURL2
SPATA25
STMN3
GID8
EEF1A2
ZBTB46
CHRNA7
GMEB2
ATP5L2
CPPAT
SLC17A9
NKAIN4
ARFRP1
UCKL1
BHLHB5
RHOF
COL20A1
PTK6
C20orf201
PCMTD2
BIRC7
SRMS
SOX18
GRAP2
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SGSM3
MKL1
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MCHR1
CACNA1I
FAM83F
ENTHD1

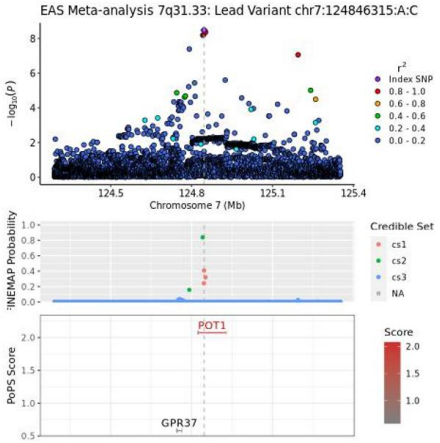

AFR Meta-analysis 22q13.2: Lead Variant chr22:41919786:C:T
Chromosome 22 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
XRCC6
PMM1
CCDC134
WBP2NL
FAM109B
POLR3H
MEI1
CENPM
NDUFA6
TCF20
NHP2L1
TOB2
ACO2
C2orf46
NAGA
SEPT3
SMDT1
NFAM1
CYP2D6
PHF5A
SHISA8

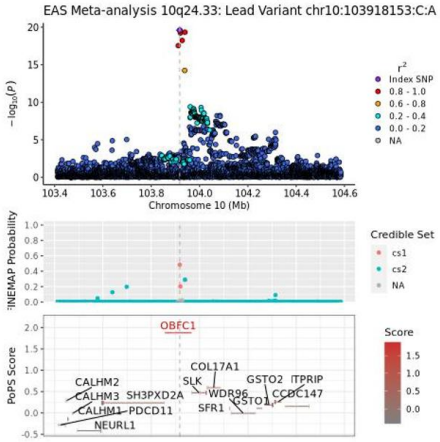

AFR Meta-analysis 22q13.31: Lead Variant chr22:44885190:G:C
Chromosome 22 (Mb)
FINEMAP Probability
Credible Set
cs1
cs2
NA
PoPS Score
Score
SMC1B
FAM118A
PRR5
ARHGAP21B
NUP50
LDOC1L
UPK3A
KIAA0930

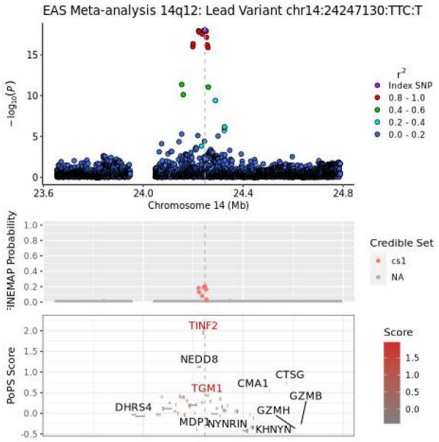

EAS Meta-analysis 3q26.2: Lead Variant chr3:169768720:G:A
Chromosome 3 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
MECOM
ACTRT3
LRRC34
LRRIQ4
SEC62
PRKCI
MYNN
LRRC31
GPR160
PHC3
SAMD7

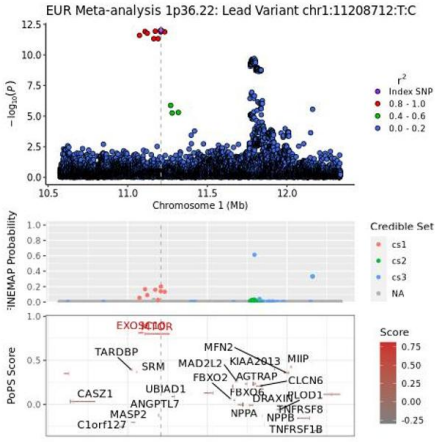

EAS Meta-analysis 5p15.33: Lead Variant chr5:1285859:C:A
Chromosome 5 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
TERT
ZDHHC11
SLC6A19
SLC6A3
TRIP13
SLC6A18
NKD2
CLPTM1L
LPCAT1
BRD9
SLC12A7

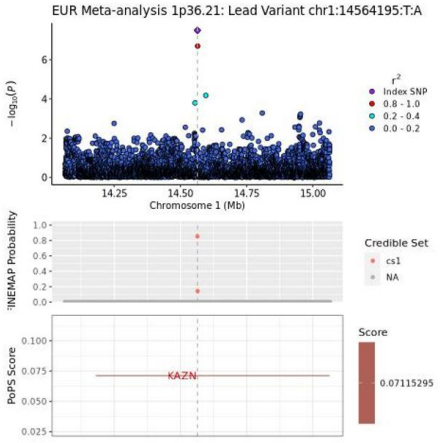

EAS Meta-analysis 7p21.3: Lead Variant chr7:10755675:A:C
Chromosome 7 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
NDUFA4
PHF14

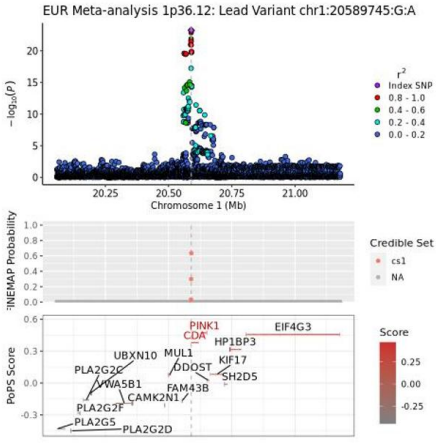

EAS Meta-analysis 7q31.33: Lead Variant chr7:124846315:A:C
Chromosome 7 (Mb)
FINEMAP Probability
Credible Set
cs1
cs2
cs3
NA
PoPS Score
Score
POT1
GPR37

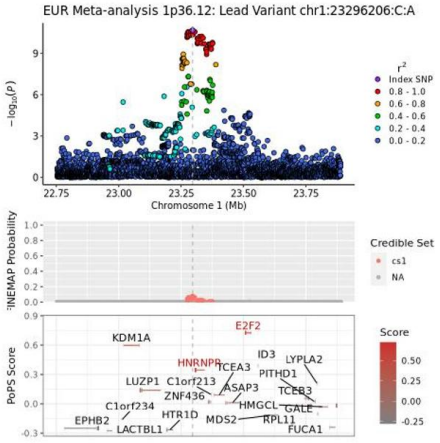

EAS Meta-analysis 10q24.33: Lead Variant chr10:103918153:C:A
Chromosome 10 (Mb)
FINEMAP Probability
Credible Set
cs1
cs2
NA
PoPS Score
Score
OBFC1
COL17A1
CALHM2
SLK
GSTO2
ITPRIP
CALHM3
SH3PXD2A
WDR96
GSTO1
CCDC147
CALHM1
PDCD11
SFR1
NEURL1

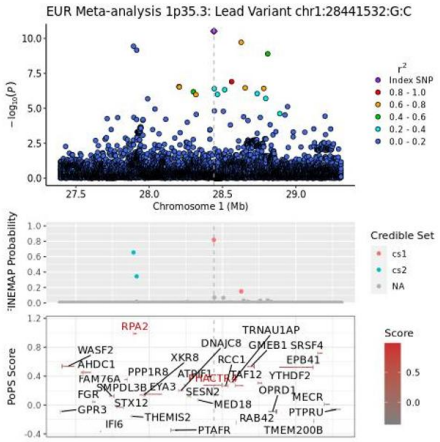

EAS Meta-analysis 14q12: Lead Variant chr14:24247130:TTC:T
Chromosome 14 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
TINF2
NEDD8
CMA1
CTSG
TGM1
GZMB
DHRS4
GZMH
MDP1
NYNRIN
KHNYN

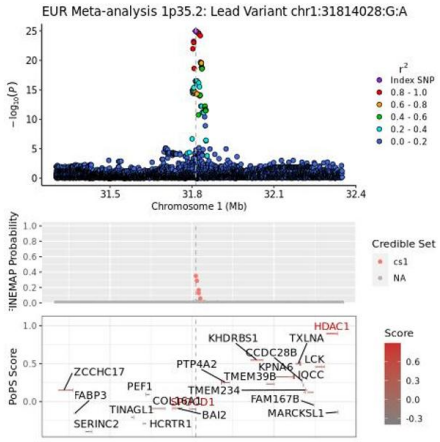

EUR Meta-analysis 1p36.22: Lead Variant chr1:11208712:T:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
cs1
cs2
cs3
NA
PoPS Score
Score
EXOSC10
MTOR
TARDBP
MFN2
SRM
MAD2L2
KIAA2013
MIIP
FBXO2
AGTRAP
CLCN6
CASZ1
UBIAD1
FBXO6
DRAXIN
NLOD1
ANGPTL7
MFRSF8
MASP2
NPPA
NPPB
C1orf127
TNFRSF18

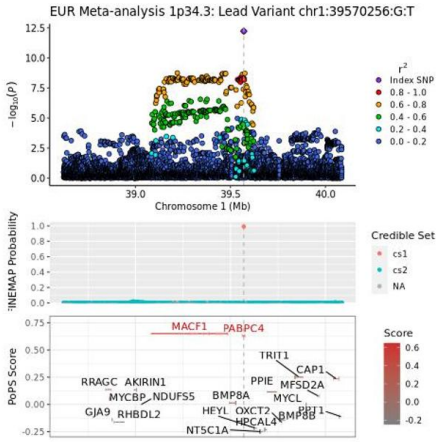

EUR Meta-analysis 1p36.21: Lead Variant chr1:14564195:T:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
KAZN
0.07115295

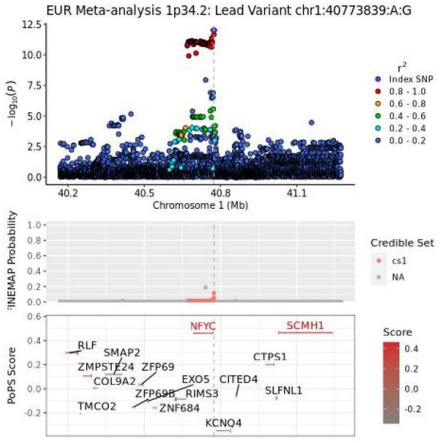

EUR Meta-analysis 1p36.12: Lead Variant chr1:20589745:G:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
PINK1
EIF4G3
CDK
HP1BP3
UBXN10
MUL1
KIF17
PLA2G2C
ODDOST
SH2D5
VWA5B1
FAM43B
CAMK2N1
PLA2G2F
PLA2G5
PLA2G2D

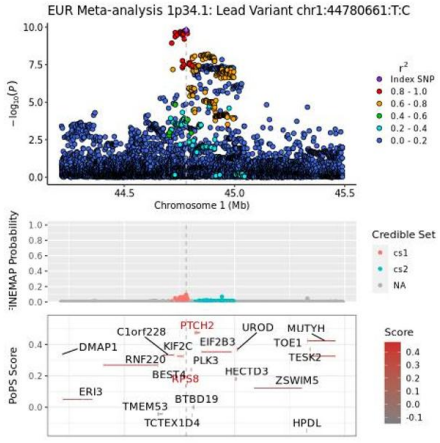

EUR Meta-analysis 1p36.12: Lead Variant chr1:23296206:C:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
cs1
NA
PoPS Score
Score
E2F2
KDM1A
ID3
LYPLA2
HNRNPR
TCEA3
PITHD1
LUZP1
C1orf213
ASAP3
TCEB3
ZNF436
C1orf234
HMGCL
GALE
HTR1D
EPHB2
MDS2
RPL11
LACTBL1
FUCA1

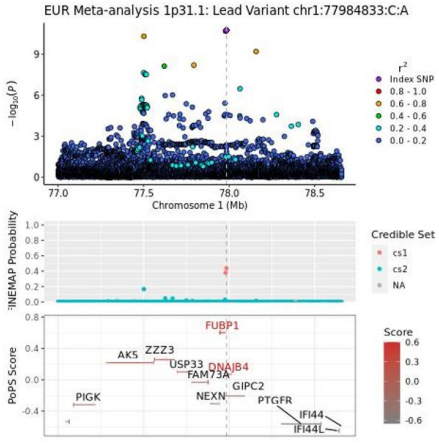

EUR Meta-analysis 1p35.3: Lead Variant chr1:28441532:G:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

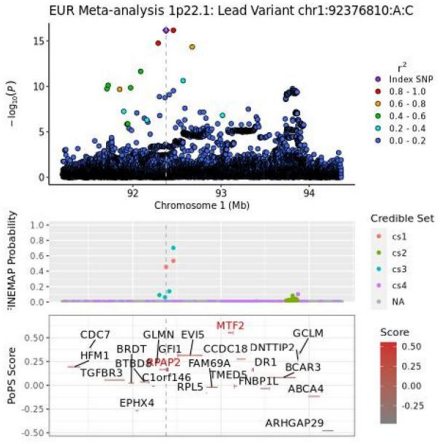

EUR Meta-analysis 1p35.2: Lead Variant chr1:31814028:G:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

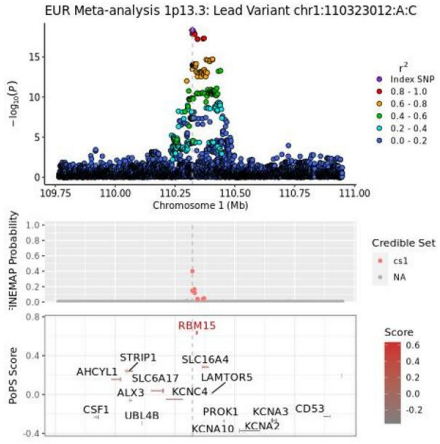

EUR Meta-analysis 1p34.3: Lead Variant chr1:39570256:G:T
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

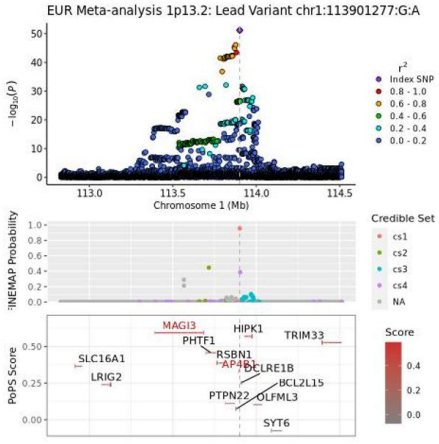

EUR Meta-analysis 1p34.2: Lead Variant chr1:40773839:A:G
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

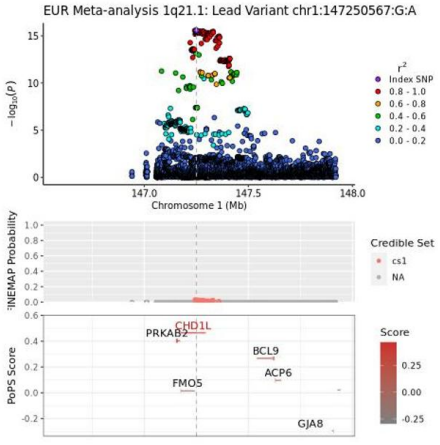

EUR Meta-analysis 1p34.1: Lead Variant chr1:44780661:T:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

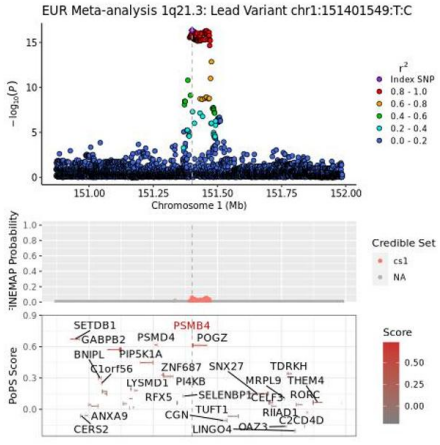

EUR Meta-analysis 1p31.1: Lead Variant chr1:77984833:C:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

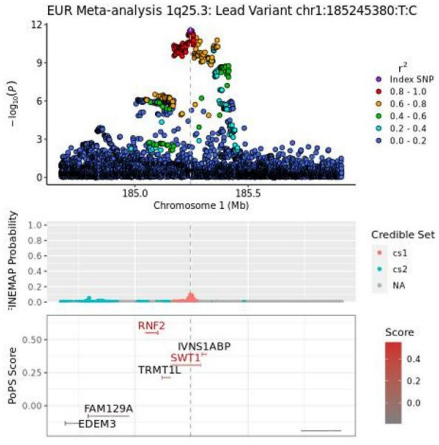

EUR Meta-analysis 1p22.1: Lead Variant chr1:92376810:A:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

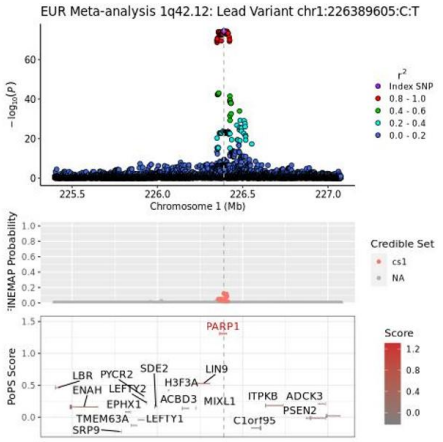

EUR Meta-analysis 1p13.3: Lead Variant chr1:110323012:A:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

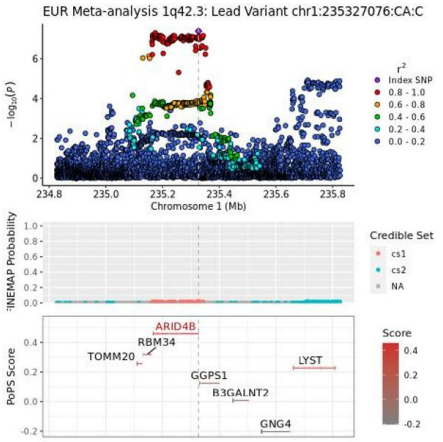

EUR Meta-analysis 1p13.2: Lead Variant chr1:113901277:G:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

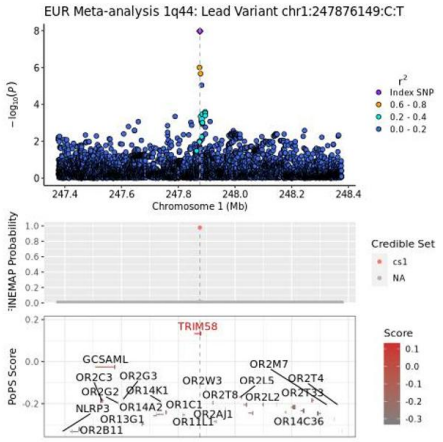

EUR Meta-analysis 1q21.1: Lead Variant chr1:147250567:G:A
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

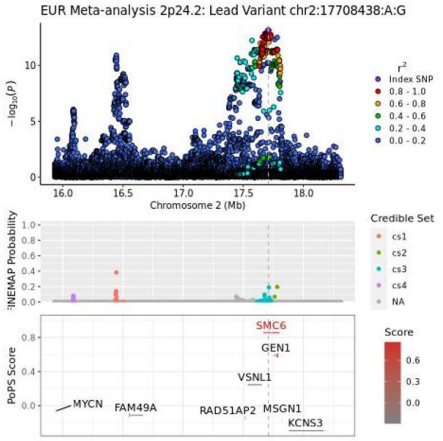

EUR Meta-analysis 1q21.3: Lead Variant chr1:151401549:T:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

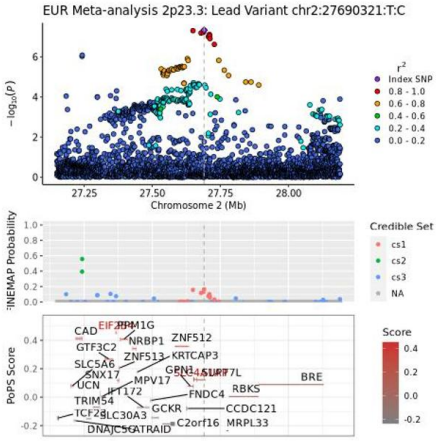

EUR Meta-analysis 1q25.3: Lead Variant chr1:185245380:T:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

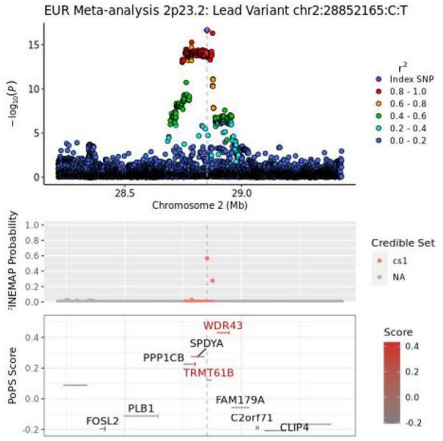

EUR Meta-analysis 1q42.12: Lead Variant chr1:226389605:C:T
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
PARP1
Score

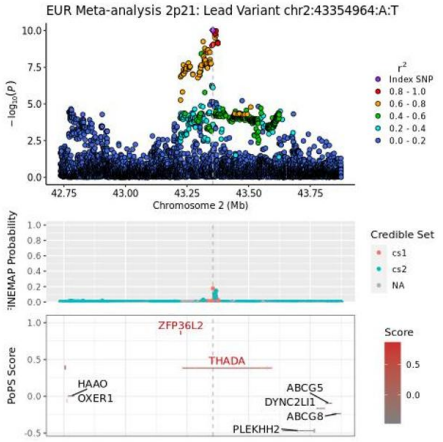

EUR Meta-analysis 1q42.3: Lead Variant chr1:235327076:CA:C
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
ARID4B
Score

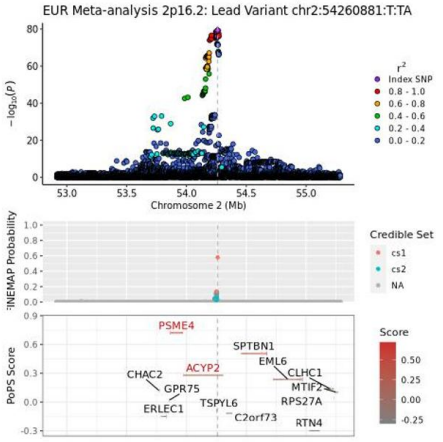

EUR Meta-analysis 1q44: Lead Variant chr1:247876149:C:T
Chromosome 1 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
TRIM58
Score

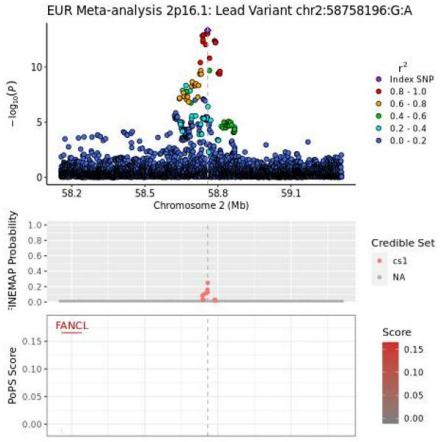

EUR Meta-analysis 2p24.2: Lead Variant chr2:17708438:A:G
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
SMC6
Score

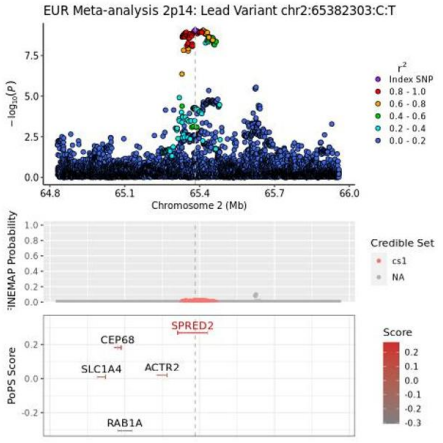

EUR Meta-analysis 2p23.3: Lead Variant chr2:27690321:T:C
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score

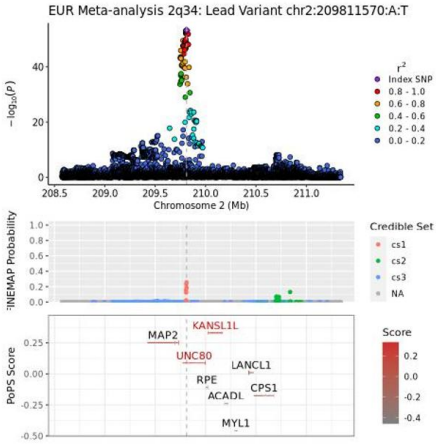

EUR Meta-analysis 2p23.2: Lead Variant chr2:28852165:C:T
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
WDR43
Score

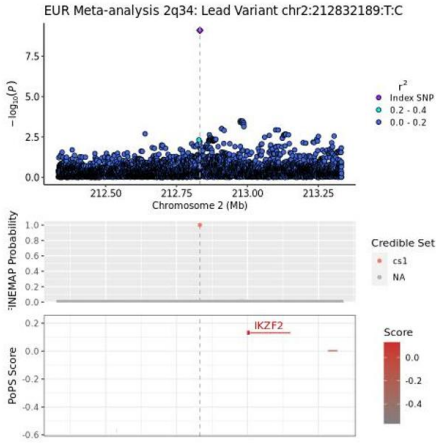

EUR Meta-analysis 2p21: Lead Variant chr2:43354964:A:T
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
ZFP36L2
Score

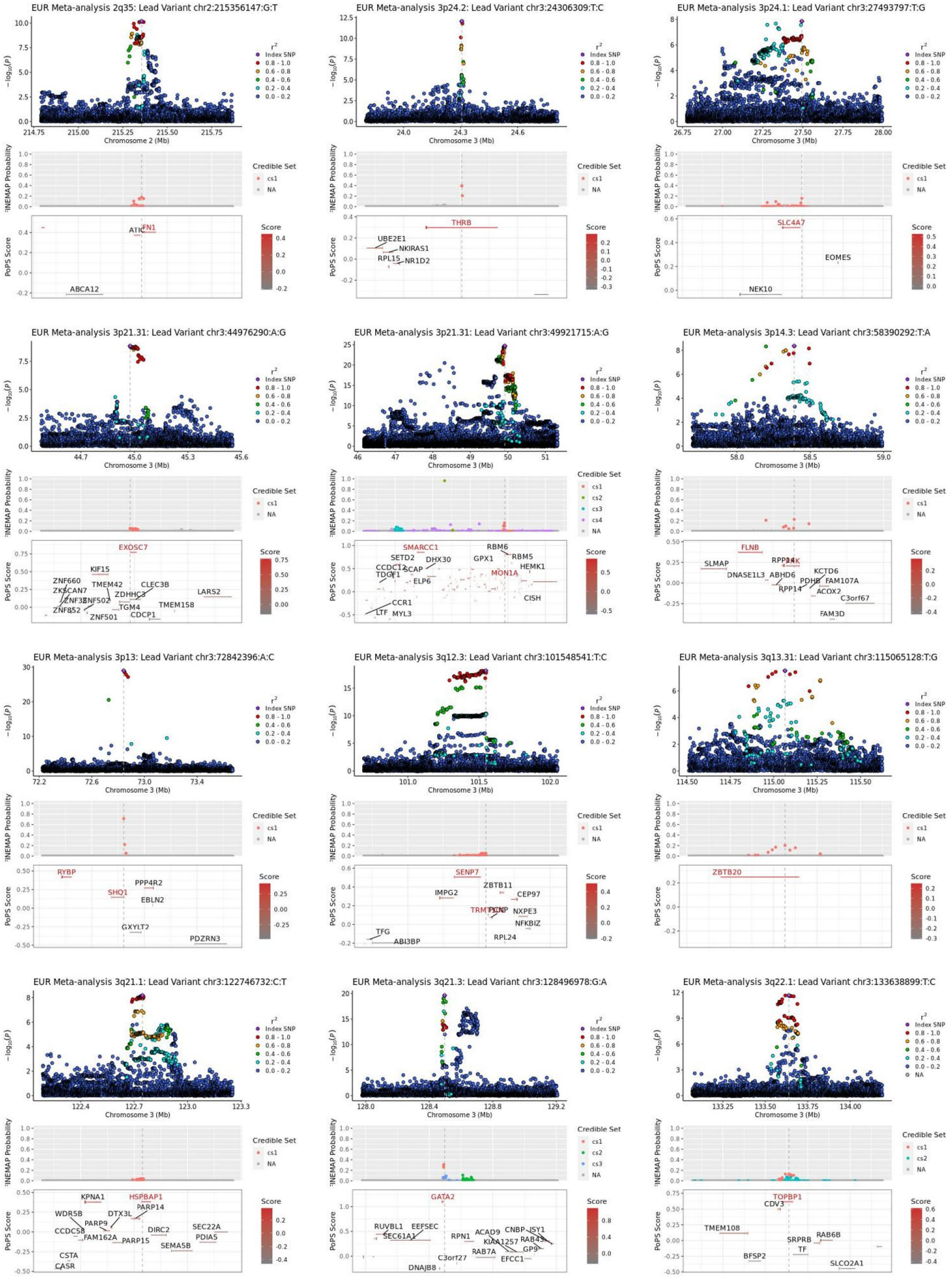

EUR Meta-analysis 2p16.2: Lead Variant chr2:54260881:T:TA
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
PSME4
Score

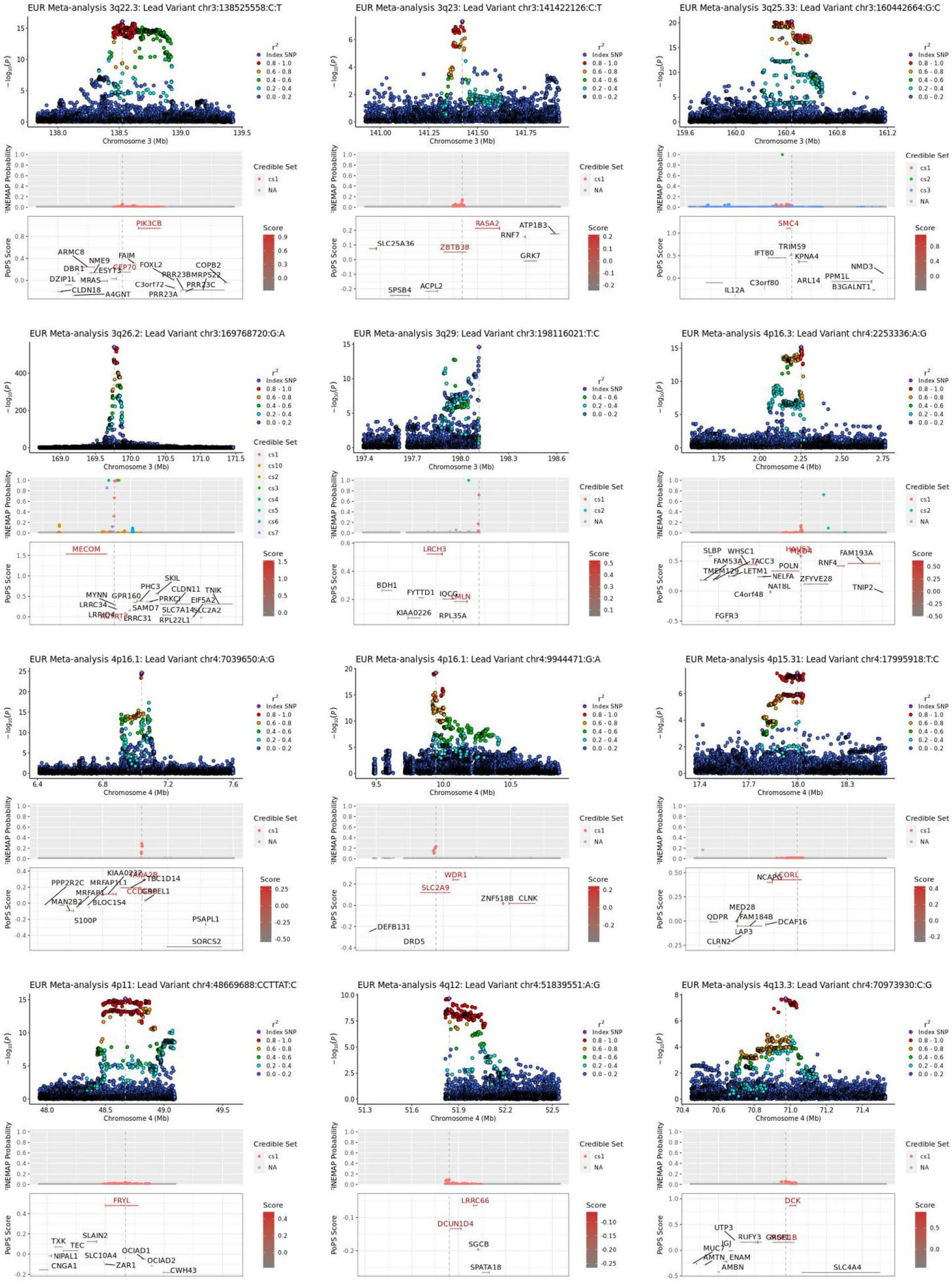

EUR Meta-analysis 2p16.1: Lead Variant chr2:58758196:G:A
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
FANCL
Score

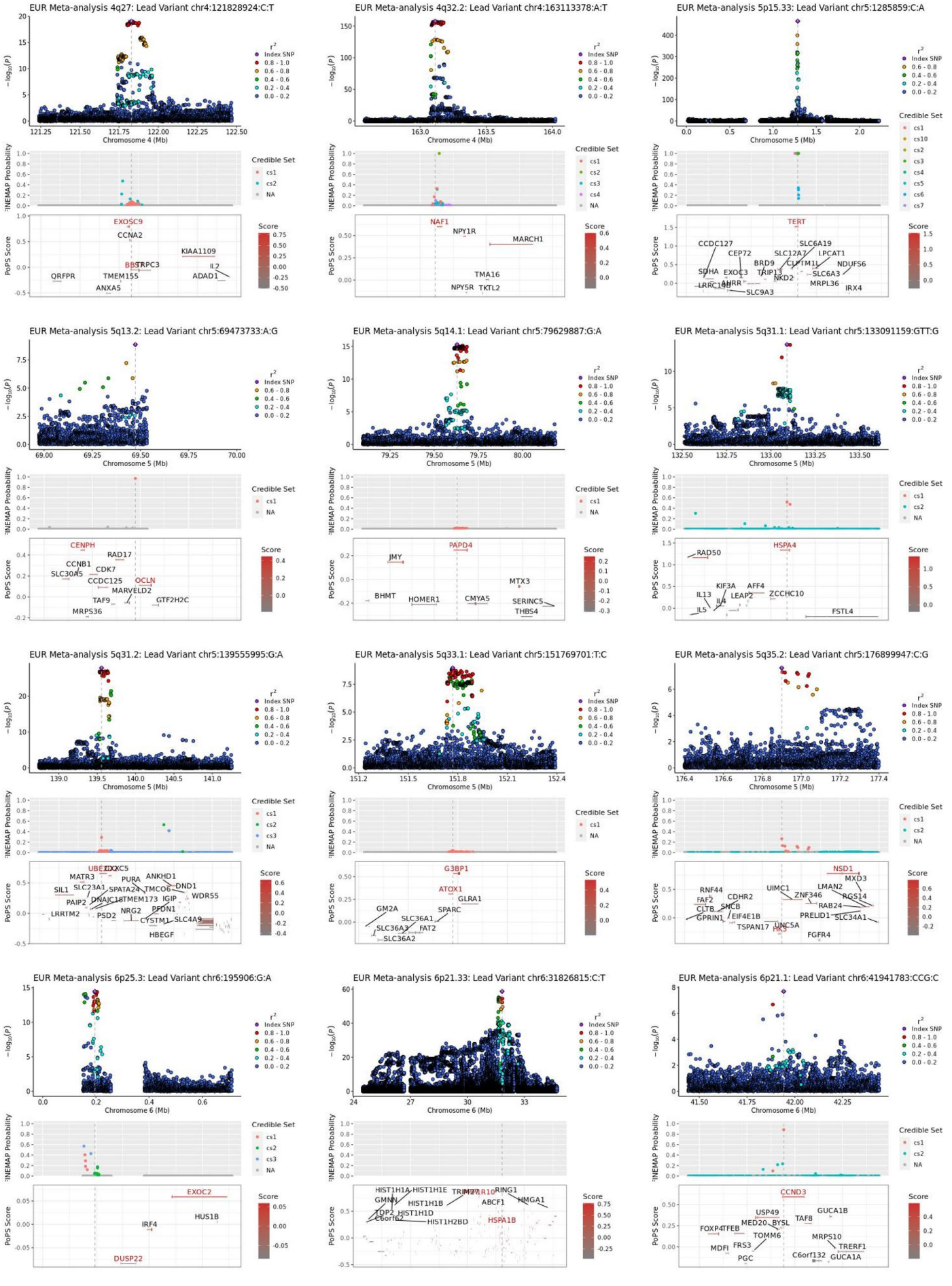

EUR Meta-analysis 2p14: Lead Variant chr2:65382303:C:T
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
SPRED2
Score

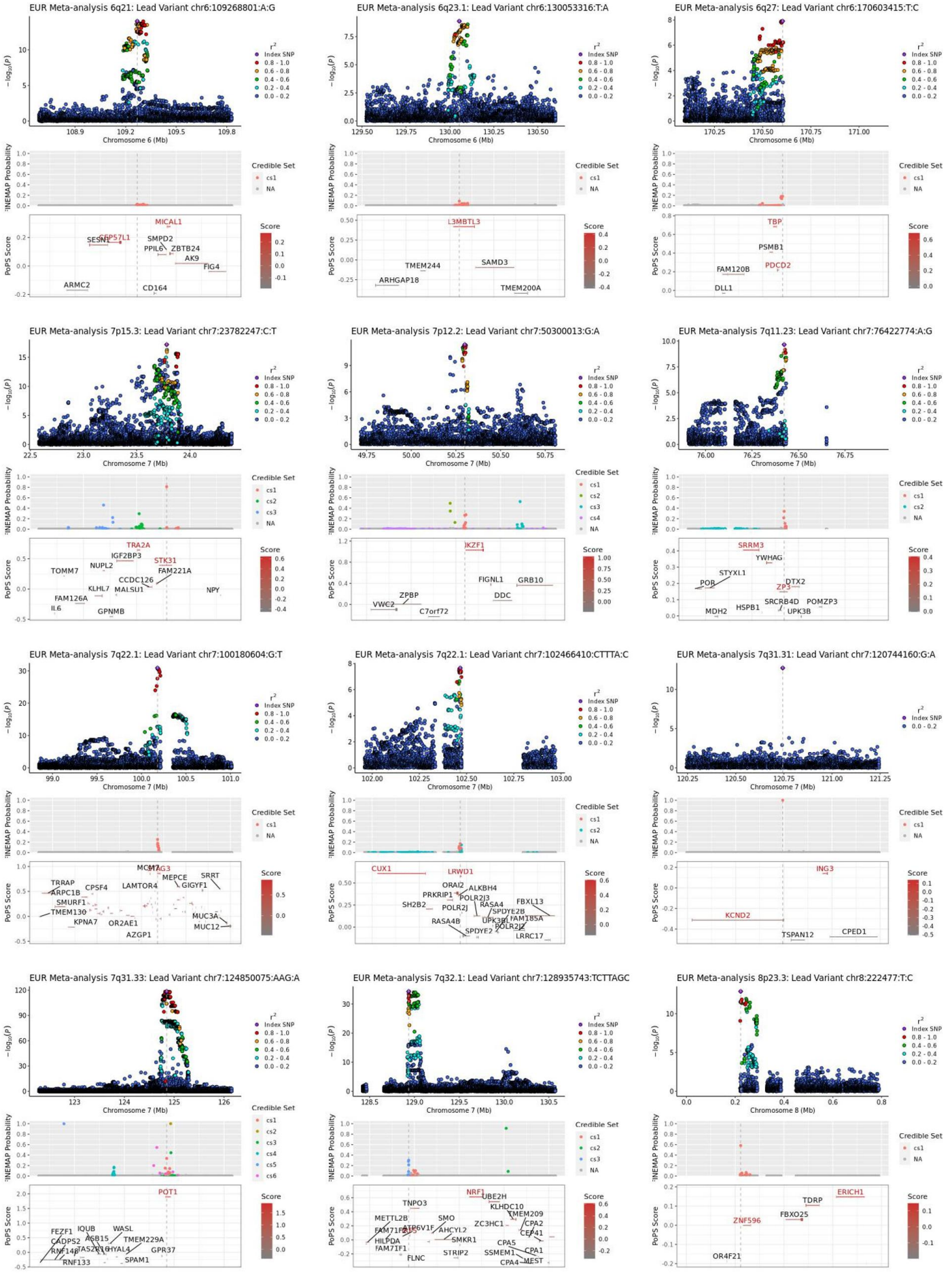

EUR Meta-analysis 2q34: Lead Variant chr2:209811570:A:T
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
KANSL1L
Score

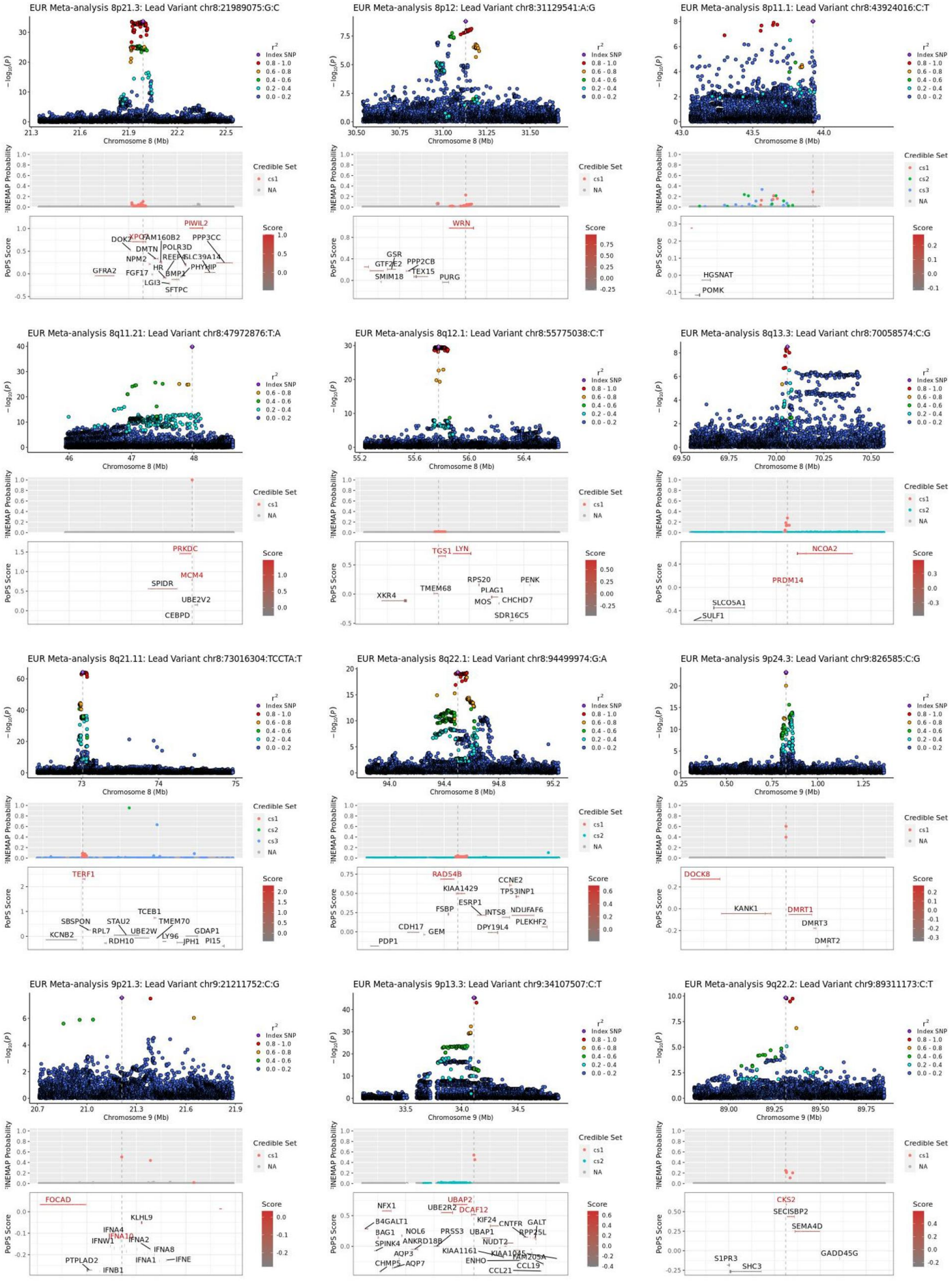

EUR Meta-analysis 2q34: Lead Variant chr2:212832189:T:C
Chromosome 2 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
IKZF2
Score

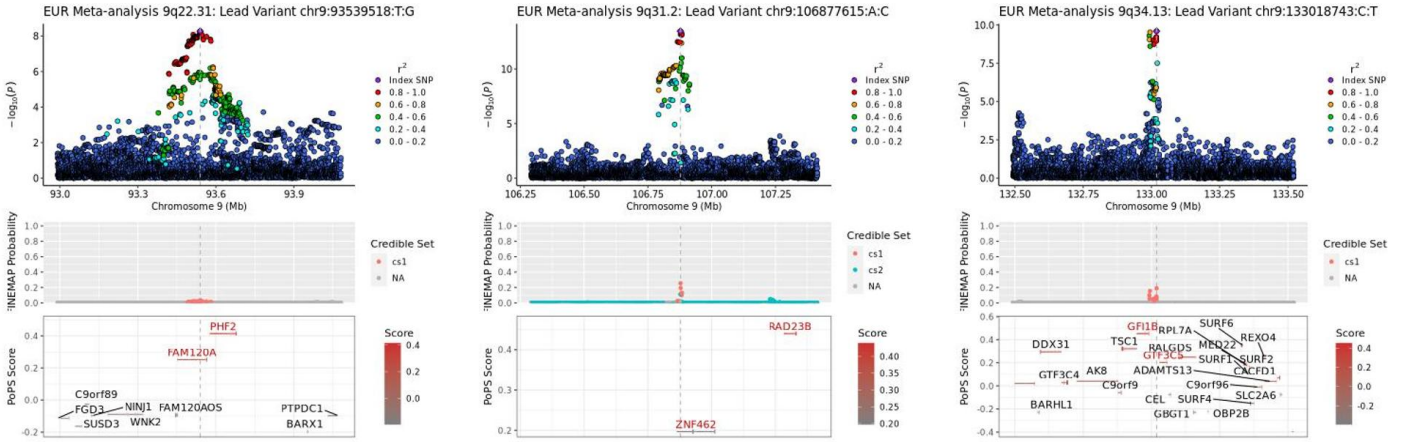

EUR Meta-analysis 2q35: Lead Variant chr2:215356147:G:T
EUR Meta-analysis 3p24.2: Lead Variant chr3:24306309:T:C
EUR Meta-analysis 3p24.1: Lead Variant chr3:27493797:T:G
EUR Meta-analysis 3p21.31: Lead Variant chr3:44976290:A:G
EUR Meta-analysis 3p21.31: Lead Variant chr3:49921715:A:G
EUR Meta-analysis 3p14.3: Lead Variant chr3:58390292:T:A
EUR Meta-analysis 3p13: Lead Variant chr3:72842396:A:C
EUR Meta-analysis 3q12.3: Lead Variant chr3:101548541:T:C
EUR Meta-analysis 3q13.31: Lead Variant chr3:115065128:T:G
EUR Meta-analysis 3q21.1: Lead Variant chr3:122746732:C:T
EUR Meta-analysis 3q21.3: Lead Variant chr3:128496978:G:A
EUR Meta-analysis 3q22.1: Lead Variant chr3:133638899:T:C
−log10(p)
Chromosome 2 (Mb)
Chromosome 3 (Mb)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
cs4
NA
PoPS Score
Score
ATIC
FN1
ABCA12
THRB
UBE2E1
NKIRAS1
RPL15
NR1D2
SLC4A7
EOMES
NEK10
EXOSC7
KIF15
ZNF660
TMEM42
CLEC3B
ZKSCAN7
ZDHHC3
ZNF32
ZNF502
LARS2
ZNF852
TGM4
TMEM158
ZNF501
CDCP1
SMARCC1
RBM6
SETD2
DHX30
GPX1
RBM5
CCDC12
SCAP
HEMK1
TDGF1
ELP6
MON1A
CCR1
CISH
LTF
MYL3
FLNB
SLMAP
RPP14
KCTD6
DNASE1L3
ABHD6
PDHB
FAM107A
ACOX2
C3orf67
FAM3D
RYBP
PPP4R2
SHQ1
EBLN2
GXYLT2
PDZRN3
SENP7
ZBTB11
IMPG2
CEP97
TRMT1
NXPE3
NFKBIZ
RPL24
TFG
ABI3BP
ZBTB20
KPNA1
HSPBAP1
PARP14
WDR5B
DTX3L
PARP9
CCDC58
FAM162A
DIRC2
PARP15
SEC22A
PDIA5
SEMA5B
CSTA
CASR
GATA2
RUVBL1
EEFSEC
SEC61A1
RPN1
ACAD9
CNBP
ISY1
KIAA1257
RAB43
GP9
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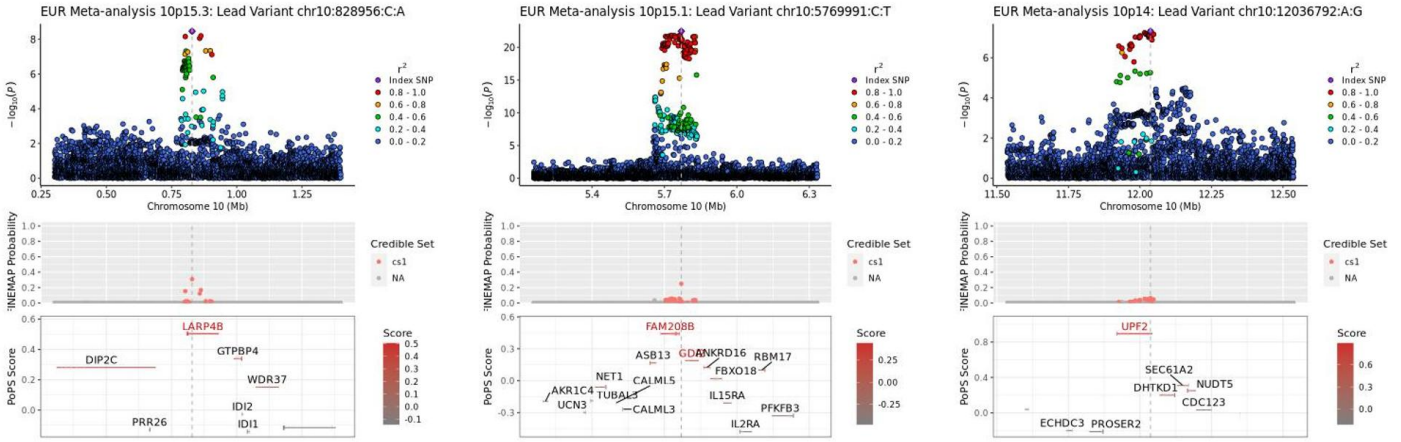

EUR Meta-analysis 3q22.3: Lead Variant chr3:138525558:C:T
EUR Meta-analysis 3q23: Lead Variant chr3:141422126:C:T
EUR Meta-analysis 3q25.33: Lead Variant chr3:160442664:G:C
EUR Meta-analysis 3q26.2: Lead Variant chr3:169768720:G:A
EUR Meta-analysis 3q29: Lead Variant chr3:198116021:T:C
EUR Meta-analysis 4p16.3: Lead Variant chr4:2253336:A:G
EUR Meta-analysis 4p16.1: Lead Variant chr4:7039650:A:G
EUR Meta-analysis 4p16.1: Lead Variant chr4:9944471:G:A
EUR Meta-analysis 4p15.31: Lead Variant chr4:17995918:T:C
EUR Meta-analysis 4p11: Lead Variant chr4:48669688:CCTTAT:C
EUR Meta-analysis 4q12: Lead Variant chr4:51839551:A:G
EUR Meta-analysis 4q13.3: Lead Variant chr4:70973930:C:G
−log10(p)
Chromosome 3 (Mb)
Chromosome 4 (Mb)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
cs4
cs5
cs6
cs7
cs10
NA
PoPS Score
Score
PIK3CB
ARMC8
NME9
FAIM
DBR1
ESYT3
CEP70
FOXL2
COPB2
PRR23B
MRPS22
DZIP1L
MRAS
C3orf72
PRR23C
CLDN18
A4GNT
PRR23A
RASA2
ATP1B3
RNF7
SLC25A36
ZBTB38
GRK7
SPSB4
ACPL2
SMC4
TRIM59
IFT80
KPNA4
NMD3
C3orf80
ARL14
PPM1L
IL12A
B3GALNT1
MECOM
SKIL
PHC3
CLDN11
TNIK
MYNN
GPR160
PRKCI
EIF5A2
LRRC34
SAMD7
SLC7A14
SLC2A2
LRRIQ4
ARRC31
RPL22L1
LRCH3
BDH1
FYTTD1
IQCG
LMLN
KIAA0226
RPL35A
SLBP
WHSC1
HMSD
FAM193A
FAM53A
TACC3
RNF4
POLN
TMEM129
LETM1
NELFA
ZFYVE28
NAT8L
TNIP2
C4orf48
FGFR3
KIAA0232
TADA2B
TBC1D14
PPP2R2C
MRFAP1L1
MRFAP1
CCDC88B
PEL1
MAN2B2
BLOC1S4
S100P
PSAPL1
SORCS2
WDR1
SLC2A9
ZNF518B
CLNK
DEFB131
DRD5
NCAPG
LCORL
MED28
QDPR
FAM184B
DCAF16
LAP3
CLRN2
FRYL
SLAIN2
TXK
TEC
SLC10A4
OCIAD1
OCIAD2
NIPAL1
ZAR1
CNGA1
CWH43
LRRC66
DCUN1D4
SGCB
SPATA18
DCK
UTP3
RUFY3
GRSF1
MUC7
IGJ
AMTN
ENAM
AMBN
SLC4A4

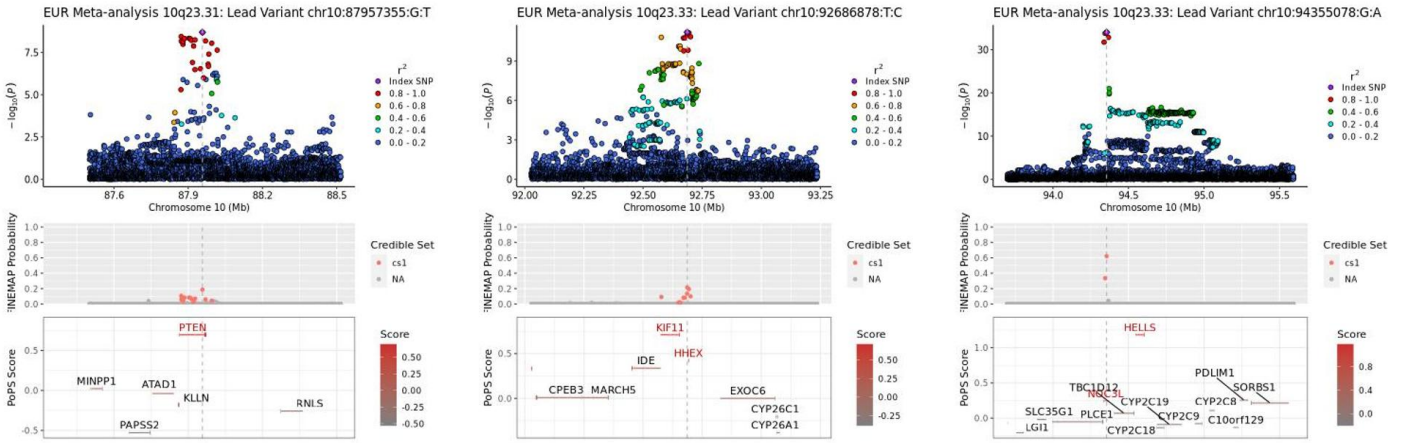

EUR Meta-analysis 4q27: Lead Variant chr4:121828924:C:T
EUR Meta-analysis 4q32.2: Lead Variant chr4:163113378:A:T
EUR Meta-analysis 5p15.33: Lead Variant chr5:1285859:C:A
EUR Meta-analysis 5q13.2: Lead Variant chr5:69473733:A:G
EUR Meta-analysis 5q14.1: Lead Variant chr5:79629887:G:A
EUR Meta-analysis 5q31.1: Lead Variant chr5:133091159:GTT:G
EUR Meta-analysis 5q31.2: Lead Variant chr5:139555995:G:A
EUR Meta-analysis 5q33.1: Lead Variant chr5:151769701:T:C
EUR Meta-analysis 5q35.2: Lead Variant chr5:176899947:C:G
EUR Meta-analysis 6p25.3: Lead Variant chr6:195906:G:A
EUR Meta-analysis 6p21.33: Lead Variant chr6:31826815:C:T
EUR Meta-analysis 6p21.1: Lead Variant chr6:41941783:CCG:C
−log10(p)
Chromosome 4 (Mb)
Chromosome 5 (Mb)
Chromosome 6 (Mb)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
cs4
cs5
cs6
cs7
cs10
NA
PoPS Score
Score
EXOSC9
CCNA2
KIAA1109
TRPC3
IL2
ADAD1
QRFPR
TMEM155
ANXA5
NAF1
NPY1R
MARCH1
TMA16
NPY5R
TKTL2
TERT
CCDC127
SLC6A19
CEP72
SLC12A7
LPCAT1
BRD9
CLPTM1L
NDUFS6
SDHA
EXOC3
TRIP13
SLC6A3
NKD2
AHRR
MRPL36
LRRC18
SLC9A3
IRX4
CENPH
RAD17
CCNB1
CDK7
SLC30A5
CDC125
OCLN
MARVELD2
TAF9
GTF2H2C
MRPS36
PAPD4
JMY
MTX3
BHMT
HOMER1
CMYA5
SERINC5
THBS4
HSPA4
RAD50
KIF3A
AFF4
IL13
LEAP2
ZCCHC10
IL4
IL5
FSTL4
UBE2D3
MATR3
PURA
ANKHD1
SIL1
SLC23A1
SPATA24
TMCO6
DND1
WDR55
PAIP2
DNAJC18
TMEM173
IGIP
LRRTM2
PSD2
NRG2
PFDN1
CYSTM1
SLC4A9
HBEGF
G3BP1
ATOX1
GLRA1
GM2A
SLC36A1
SPARC
SLC36A3
FAT2
SLC36A2
NSD1
MXD3
RNF44
UIMC1
LMAN2
FAF2
CDHR2
ZNF346
RGS14
CLTB
SMCB
RAB24
GPRIN1
EIF4E1B
PRELID1
SLC34A1
TSPAN17
UNC5A
FGFR4
EXOC2
HUS1B
IRF4
DUSP22
HIST1H1A
HIST1H1E
TRIM27
TAR10
RING1
GMNN
HIST1H1B
ABCF1
HMGA1
TDP2
HIST1H1D
C6orf62
HIST1H2BD
HSPA1B
CCND3
USP49
GUCA1B
TAF8
FOXP4
TFEB
MED20
BYSL
TOMM6
MRPS10
MDFI
FRS3
TRERF1
PGC
C6orf132
GUCA1A

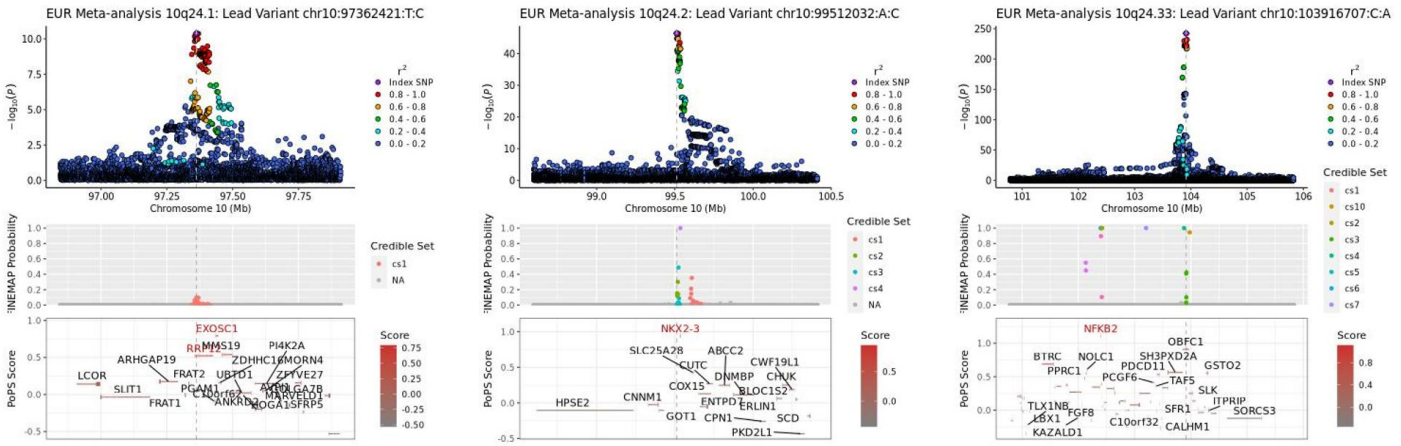

EUR Meta-analysis 6q21: Lead Variant chr6:109268801:A:G
EUR Meta-analysis 6q23.1: Lead Variant chr6:130053316:T:A
EUR Meta-analysis 6q27: Lead Variant chr6:170603415:T:C
EUR Meta-analysis 7p15.3: Lead Variant chr7:23782247:C:T
EUR Meta-analysis 7p12.2: Lead Variant chr7:50300013:G:A
EUR Meta-analysis 7q11.23: Lead Variant chr7:76422774:A:G
EUR Meta-analysis 7q22.1: Lead Variant chr7:100180604:G:T
EUR Meta-analysis 7q22.1: Lead Variant chr7:102466410:CTTTA:C
EUR Meta-analysis 7q31.31: Lead Variant chr7:120744160:G:A
EUR Meta-analysis 7q31.33: Lead Variant chr7:124850075:AAG:A
EUR Meta-analysis 7q32.1: Lead Variant chr7:128935743:TCTTAGC
EUR Meta-analysis 8p23.3: Lead Variant chr8:222477:T:C
−log10(p)
Chromosome 6 (Mb)
Chromosome 7 (Mb)
Chromosome 8 (Mb)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
cs4
cs5
cs6
NA
PoPS Score
Score
MICAL1
SESN1
GPS7L1
SMPD2
PPIL6
ZBTB24
AK9
FIG4
ARMC2
CD164
L3MBTL3
TMEM244
SAMD3
ARHGAP18
TMEM200A
TBP
PSMB1
FAM120B
PDCD2
DLL1
TRA2A
IGF2BP3
STK31
TOMM7
NUPL2
FAM221A
CCDC126
KLHL7
MALSU1
NPY
FAM126A
IL6
GPNMB
IKZF1
FIGNL1
GRB10
ZPBP
DDC
VWC2
C7orf72
SRRM3
YWHAG
STYXL1
POR
DTX2
ZP3
SRCRB4D
POMZP3
MDH2
HSPB1
UPK3B
MCM7
DAG3
TRRAP
MEPCE
SRRT
ARPC1B
CPSF4
LAMTOR4
GIGYF1
SMURF1
TMEM130
KPNA7
OR2AE1
AZGP1
MUC3A
MUC12
CUX1
LRWD1
ORAI2
ALKBH4
PRKRIP1
POLR2J3
SH2B2
POLR2J
RASA4
SPDYE2B
FBXL13
RASA4B
UPK3B
FAM185A
POLR2J2
SPDYE2
LRRC17
ING3
KCND2
TSPAN12
CPED1
POT1
FEZF1
IQUB
WASL
ACSBG1
CADPS2
TMEM229A
RNF148
TAS2R16
HYAL4
GPR37
SPAM1
RNF133
NRF1
UBE2H
TNPO3
KLHDC10
METTL2B
TMEM209
SMO
ZC3HC1
CPA2
FAM71F2
ATP6V1F
AHCYL2
CEP41
HILPDA
SMKR1
CPA5
FAM71F1
STRIP2
SSMEM1
CPA1
FLNC
CPA4
MEST
ERICH1
TDRP
FBXO25
ZNF596
OR4F21

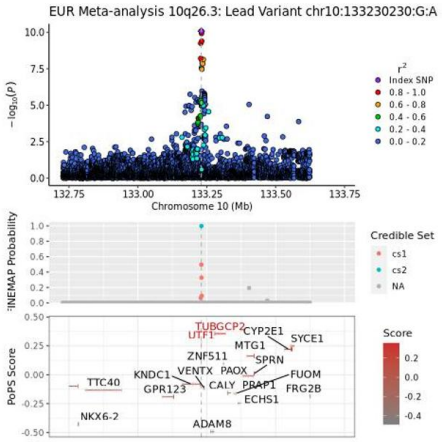

EUR Meta-analysis 8p21.3: Lead Variant chr8:21989075:G:C
EUR Meta-analysis 8p12: Lead Variant chr8:31129541:A:G
EUR Meta-analysis 8p11.1: Lead Variant chr8:43924016:C:T
EUR Meta-analysis 8q11.21: Lead Variant chr8:47972876:T:A
EUR Meta-analysis 8q12.1: Lead Variant chr8:55775038:C:T
EUR Meta-analysis 8q13.3: Lead Variant chr8:70058574:C:G
EUR Meta-analysis 8q21.11: Lead Variant chr8:73016304:TCCTA:T
EUR Meta-analysis 8q22.1: Lead Variant chr8:94499974:G:A
EUR Meta-analysis 9p24.3: Lead Variant chr9:826585:C:G
EUR Meta-analysis 9p21.3: Lead Variant chr9:21211752:C:G
EUR Meta-analysis 9p13.3: Lead Variant chr9:34107507:C:T
EUR Meta-analysis 9q22.2: Lead Variant chr9:89311173:C:T
Chromosome 8 (Mb)
Chromosome 9 (Mb)
−log10(p)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
NA
PoPS Score
Score
PIWIL2
XPC
DOK2
FAM160B2
PPP3CC
DMTN
POLR3D
NPM2
REEP4
SLC39A14
HR
PHYKPL
GFRA2
FGF17
BMP1
LGI3
SFTPC
WRN
GSR
GTF2E2
PPP2CB
TEX15
SMIM18
PURG
HGSNAT
POMK
PRKDC
MCM4
SPIDR
UBE2V2
CEBPD
TGS1
LYN
RPS20
PENK
TMEM68
PLAG1
XKR4
MOS
CHCHD7
SDR16C5
NCOA2
PRDM14
SLCO5A1
SULF1
TERF1
TCEB1
SBSPON
STAU2
TMEM70
RPL7
UBE2W
GDAP1
KCNB2
LY96
RDH10
JPH1
PI15
RAD54B
CCNE2
KIAA1429
TP53INP1
ESRP1
FSBP
INTS8
NDUFAF6
PLEKHF2
CDH17
DPY19L4
GEM
PDP1
DOCK8
KANK1
DMRT1
DMRT3
DMRT2
FOCAD
KLHL9
IFNA4
IFNA10
IFNW1
IFNA2
IFNA8
PTPLAD2
IFNA1
IFNE
IFNB1
NFX1
UBAP2
UBE2R2
DCAF12
KIF24
CNTFR
GALT
B4GALT1
BAG1
NOL6
PRSS3
UBAP1
RPP25L
SPINK4
ANKRD18B
NUDT2
AQP3
KIAA1161
KIAA1045
FAM205A
CHMP5
AQP7
ENHO
CCL21
CCL19
CKS2
SECISBP2
SEMA4D
GADD45G
S1PR3
SHC3

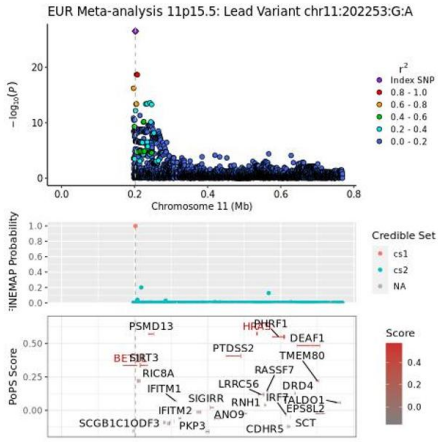

EUR Meta-analysis 9q22.31: Lead Variant chr9:93539518:T:G
EUR Meta-analysis 9q31.2: Lead Variant chr9:106877615:A:C
EUR Meta-analysis 9q34.13: Lead Variant chr9:133018743:C:T
Chromosome 9 (Mb)
PHF2
FAM120A
C9orf89
FGD3
NINJ1
FAM120AOS
SUSD3
WNK2
PTPDC1
BARX1
RAD23B
ZNF462
GFI1B
RPL7A
SURF6
REXO4
DDX31
TSC1
RALGDS
MED22
GTF3C5
SURF1
SURF2
GTF3C4
AK8
ADAMTS13
CACFD1
C9orf9
C9orf96
SLC2A6
BARHL1
CEL
SURF4
GBGT1
OBP2B
Index SNP
Credible Set
Score
PoPS Score
FINEMAP Probability

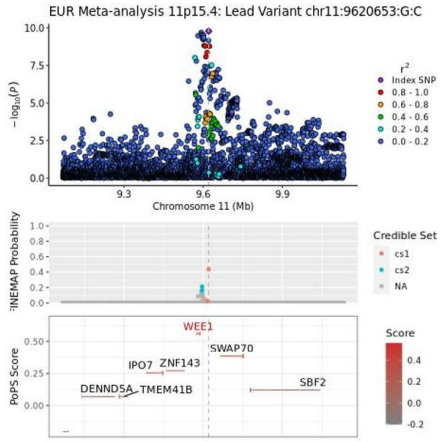

EUR Meta-analysis 10p15.3: Lead Variant chr10:828956:C:A
EUR Meta-analysis 10p15.1: Lead Variant chr10:5769991:C:T
EUR Meta-analysis 10p14: Lead Variant chr10:12036792:A:G
Chromosome 10 (Mb)
LARP4B
DIP2C
GTPBP4
WDR37
IDI2
PRR26
IDI1
FAM208B
ASB13
GDA
ANKRD16
RBM17
FBXO18
NET1
CALML5
AKR1C4
TUBAL3
IL15RA
UCN3
CALML3
PFKFB3
IL2RA
UPF2
SEC61A2
DHTKD1
NUDT5
CDC123
ECHDC3
PROSER2
Index SNP
Credible Set
Score
PoPS Score
FINEMAP Probability

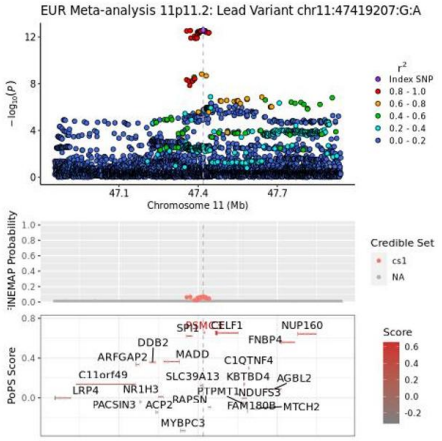

EUR Meta-analysis 10q23.31: Lead Variant chr10:87957355:G:T
EUR Meta-analysis 10q23.33: Lead Variant chr10:92686878:T:C
EUR Meta-analysis 10q23.33: Lead Variant chr10:94355078:G:A
Chromosome 10 (Mb)
PTEN
MINPP1
ATAD1
KLLN
RNLS
PAPSS2
KIF11
HHEX
IDE
CPEB3
MARCH5
EXOC6
CYP26C1
CYP26A1
HELLS
PDLIM1
SORBS1
TBC1D12
NSG2
CYP2C19
CYP2C8
SLC35G1
PLCE1
CYP2C9
C10orf129
LGI1
CYP2C18
Index SNP
Credible Set
Score
PoPS Score
FINEMAP Probability

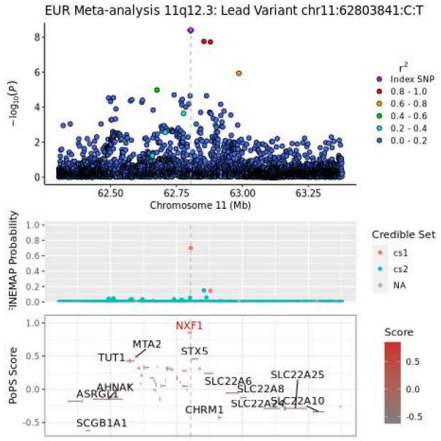

EUR Meta-analysis 10q24.1: Lead Variant chr10:97362421:T:C
EUR Meta-analysis 10q24.2: Lead Variant chr10:99512032:A:C
EUR Meta-analysis 10q24.33: Lead Variant chr10:103916707:C:A
Chromosome 10 (Mb)
EXOSC1
RRP12
MMS19
PI4K2A
ARHGAP19
ZDHHC18
MORN4
LCOR
FRAT2
UBTD1
ZFYVE27
SLIT1
PGAM1
AVEN
GAZB
C10orf62
MARVELD1
FRAT1
ANKRD22
BOGA1
SFRP5
NKX2-3
SLC25A28
ABCC2
CUTC
CWF19L1
DNMBP
CHUK
COX15
BLOC1S2
HPSE2
CNNM1
ENTPD1
ERLIN1
GOT1
CPN1
SCD
PKD2L1
NFKB2
OBFC1
BTRC
NOLC1
SH3PXD2A
PDCD11
GSTO2
PPRC1
PCGF6
TAF5
SLK
ITPRIP
TLX1NB
FGF8
SFR1
SORCS3
LBX1
C10orf32
CALHM1
KAZALD1
Index SNP
Credible Set
Score
PoPS Score
FINEMAP Probability

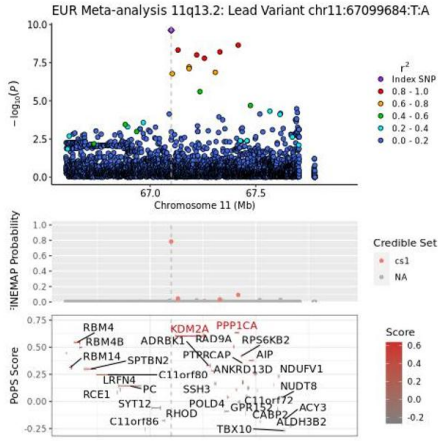

EUR Meta-analysis 10q26.3: Lead Variant chr10:133230230:G:A
Chromosome 10 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
TUBGCP2
CYP2E1
SYCE1
MTG1
ZNF511
SPRN
KNDC1
VENTX
PAOX
FUOM
TTC40
GPR123
CALY
PRAP1
FRG2B
ECHS1
NKX6-2
ADAM8

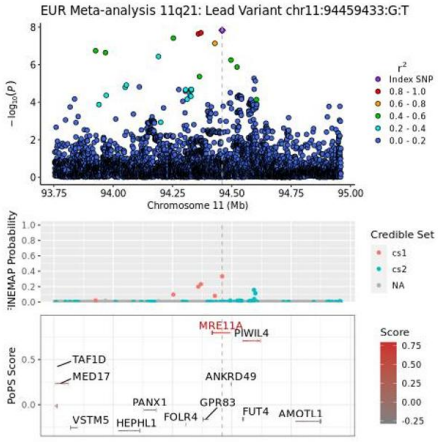

EUR Meta-analysis 11p15.5: Lead Variant chr11:202253:G:A
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
PSMD13
HMBS
DHRF1
DEAF1
PTDSS2
TMEM80
SIRT3
RASSF7
RIC8A
IFITM1
LRRC56
DRD4
SIGIRR
RNH1
ALDO1
IFITM2
ANO9
EPS8L2
SCGB1C1
ODF3
PKP3
CDHR5
SCT

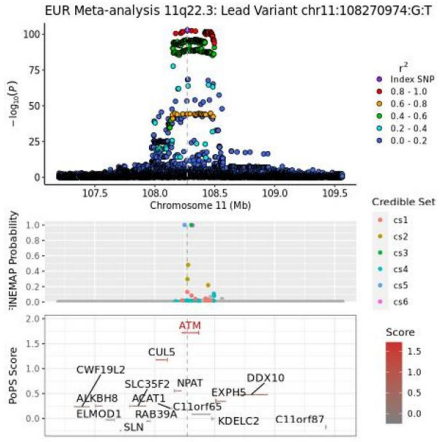

EUR Meta-analysis 11p15.4: Lead Variant chr11:9620653:G:C
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
WEE1
SWAP70
IPO7
ZNF143
SBF2
DENND5A
TMEM41B

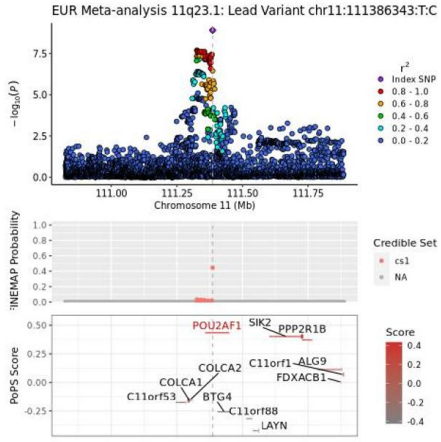

EUR Meta-analysis 11p11.2: Lead Variant chr11:47419207:G:A
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
SPI1
CELF1
NUP160
FNBP4
DDB2
MADD
ARFGAP2
C1QTNF4
C11orf49
SLC39A13
KBTBD4
AGBL2
LRP4
NR1H3
PTPMT1
INDUFS3
PACSIN3
ACP2
RAPSN
FAM180B
MTCH2
MYBPC3

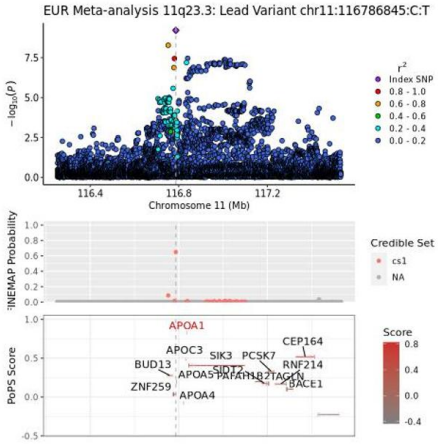

EUR Meta-analysis 11q12.3: Lead Variant chr11:62803841:C:T
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
NXF1
MTA2
STX5
TUT1
SLC22A25
SLC22A6
SLC22A8
AHNAK
ASRGL1
SLC22A5
SLC22A10
CHRM1
SCGB1A1

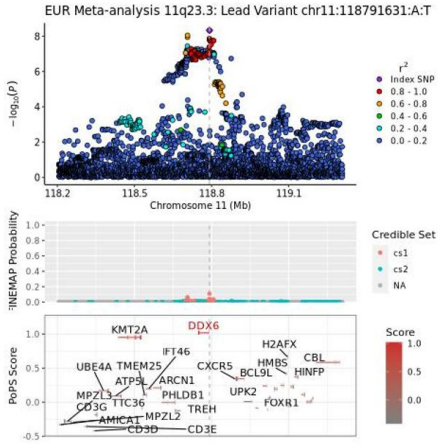

EUR Meta-analysis 11q13.2: Lead Variant chr11:67099684:T:A
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
RBM4
KDM2A
PPP1CA
RBM4B
ADRBK1
RAD9A
RPS6KB2
RBM14
SPTBN2
PTPRCAP
AIP
LRFN4
C11orf80
ANKRD13D
NDUFV1
RCE1
PC
SSH3
NUDT8
SYT12
POLD4
GPR15
C11orf72
ACY3
RHOD
CABP2
C11orf86
ALDH3B2
TBX10

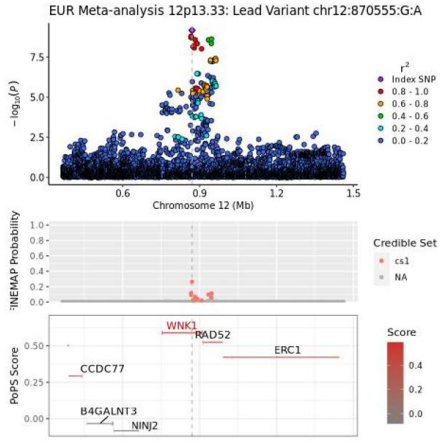

EUR Meta-analysis 11q21: Lead Variant chr11:94459433:G:T
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
MRE11A
PIWIL4
TAF1D
MED17
ANKRD49
PANX1
GPR83
VSTM5
HEPHL1
FOLR4
FUT4
AMOTL1

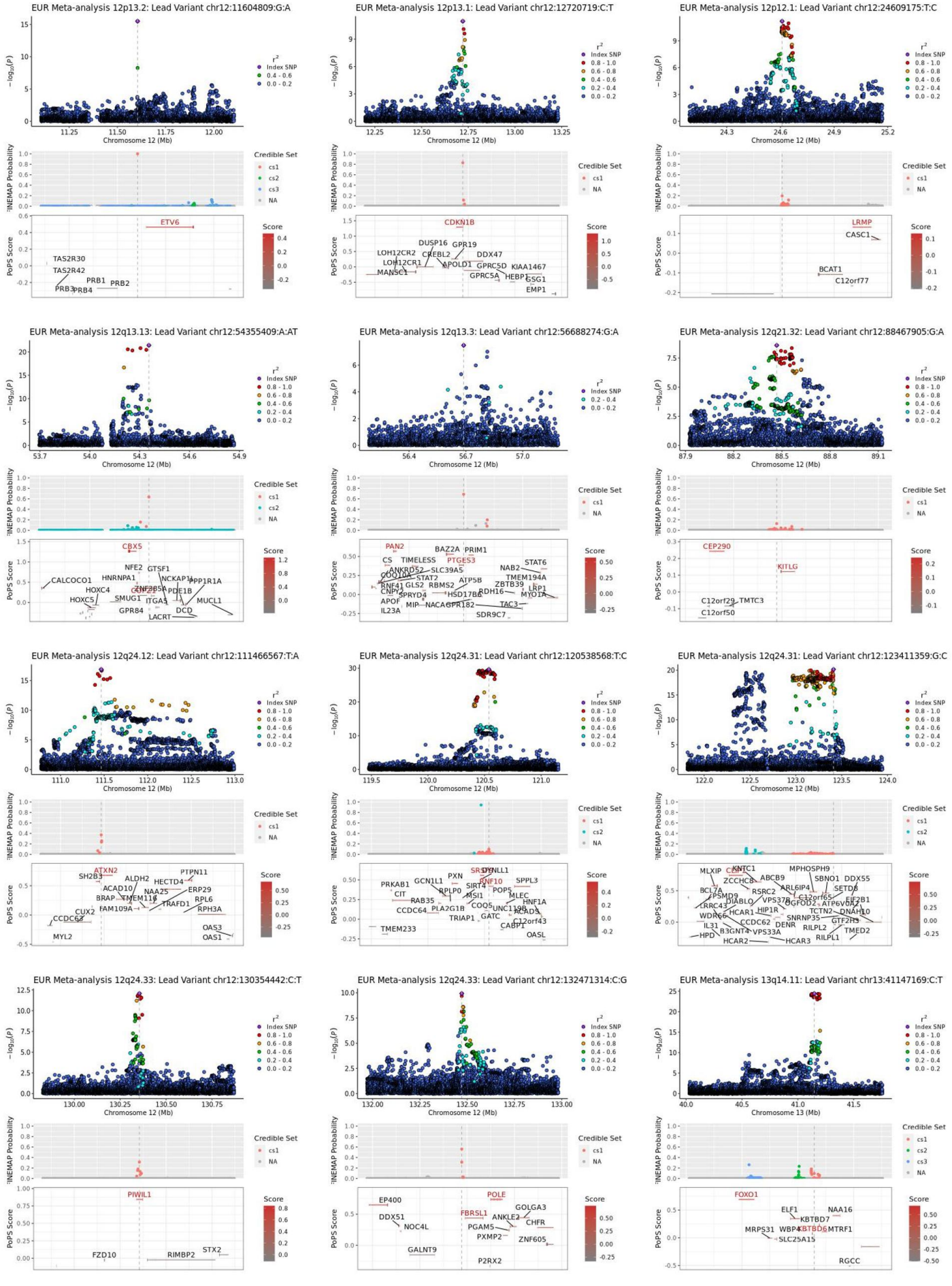

EUR Meta-analysis 11q22.3: Lead Variant chr11:108270974:G:T
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
ATM
CUL5
CWF19L2
SLC35F2
NPAT
DDX10
EXPH5
AKAP8
ACAT1
C11orf65
ELMOD1
RAB39A
KDELC2
C11orf87
SLN

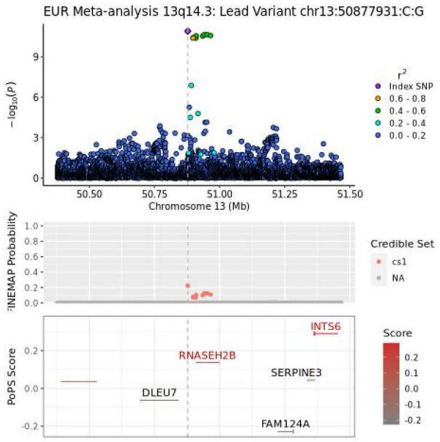

EUR Meta-analysis 11q23.1: Lead Variant chr11:111386343:T:C
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
POU2AF1
SIK2
PPP2R1B
COLCA2
C11orf1
ALG9
FDXACB1
COLCA1
C11orf53
BTG4
C11orf88
LAYN

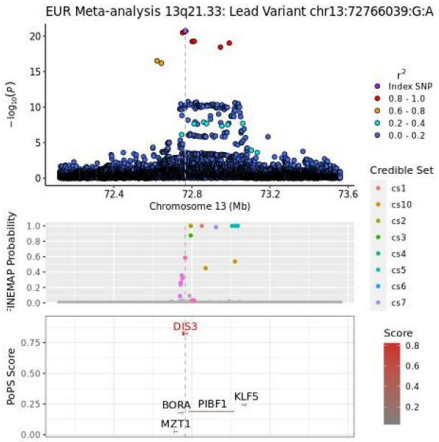

EUR Meta-analysis 11q23.3: Lead Variant chr11:116786845:C:T
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
APOA1
CEP164
APOC3
SIK3
PCSK7
BUD13
RNF214
SIDT2
APOA5
PAFAH1B2
TAGLN
BACE1
ZNF259
APOA4

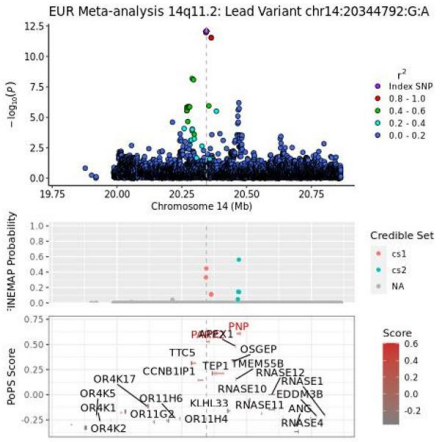

EUR Meta-analysis 11q23.3: Lead Variant chr11:118791631:A:T
Chromosome 11 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
KMT2A
DDX6
IFT46
H2AFX
CBL
UBE4A
TMEM25
CXCR5
HMBS
HINFP
ATP9L
ARCN1
BCL9L
MPZL3
PHLDB1
UPK2
CD3G
TTC36
TREH
FOXR1
AMICA1
MPZL2
CD3D
CD3E

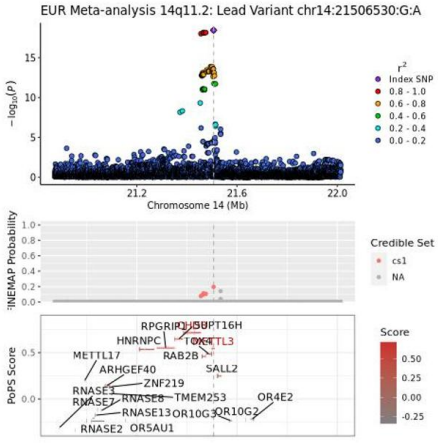

EUR Meta-analysis 12p13.33: Lead Variant chr12:870555:G:A
Chromosome 12 (Mb)
FINEMAP Probability
Credible Set
PoPS Score
Score
WNK1
RAD52
ERC1
CCDC77
B4GALNT3
NINJ2

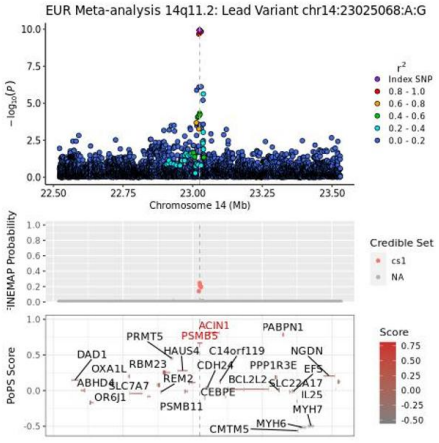

EUR Meta-analysis 12p13.2: Lead Variant chr12:11604809:G:A
EUR Meta-analysis 12p13.1: Lead Variant chr12:12720719:C:T
EUR Meta-analysis 12p12.1: Lead Variant chr12:24609175:T:C
EUR Meta-analysis 12q13.13: Lead Variant chr12:54355409:A:AT
EUR Meta-analysis 12q13.3: Lead Variant chr12:56688274:G:A
EUR Meta-analysis 12q21.32: Lead Variant chr12:88467905:G:A
EUR Meta-analysis 12q24.12: Lead Variant chr12:111466567:T:A
EUR Meta-analysis 12q24.31: Lead Variant chr12:120538568:T:C
EUR Meta-analysis 12q24.31: Lead Variant chr12:123411359:G:C
EUR Meta-analysis 12q24.33: Lead Variant chr12:130354442:C:T
EUR Meta-analysis 12q24.33: Lead Variant chr12:132471314:C:G
EUR Meta-analysis 13q14.11: Lead Variant chr13:41147169:C:T
Chromosome 12 (Mb)
Chromosome 13 (Mb)
−log10(p)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
NA
PoPS Score
Score
ETV6
TAS2R30
TAS2R42
PRB1
PRB2
PRB3
PRB4
CDKN1B
DUSP16
GPR19
CREBL2
DDX47
APOLD1
GPRC5D
KIAA1467
GPRC5A
HEBP1
GSG1
EMP1
LOH12CR2
LOH12CR1
MANSC1
LRMP
CASC1
BCAT1
C12orf77
CBX5
NFE2
GTSF1
CALCOCO1
HNRNPA1
NCKAP1
PPP1R1A
HOXC4
ZNF285A
PDE1B
HOXC5
SMUG1
ITGA5
MUCL1
GPR84
DCD
LACRT
PAN2
BAZ2A
PRIM1
CS
TIMELESS
PTGES3
STAT6
ANKRD52
SLC39A5
NAB2
COQ10A
STAT2
ATP5B
TMEM194A
RNF41
GLS2
RBMS2
ZBTB39
CNPY2
SPRYD4
HSD17B6
RDH16
LRP1
MYO1A
APOF
MIP
NACA
GPR182
TAC3
IL23A
SDR9C7
CEP290
KITLG
C12orf29
TMTC3
C12orf50
ATXN2
SH2B3
ALDH2
PTPN11
HECTD4
ACAD10
NAA25
ERP29
BRAP
TMEM116
TRAFD1
RPL6
FAM109A
RPH3A
CUX2
CCDC62
OAS3
OAS1
MYL2
SRSF7
PNLLP1
PRKAB1
GCN1L1
PXN
RNF10
SPPL3
CIT
RPLP0
SIRT4
POP5
MSI1
MLEC
RAB35
HNF1A
CCDC64
PLA2G1B
COQ5
UNC119B
RCAD5
TRIAP1
GATC
C12orf43
CABP1
TMEM233
OASL
MLXIP
CHN1
KNTC1
MPHOSPH9
ZCCHC8
ABCB9
SBNO1
DDX55
BCL7A
PSMD9
RSRC2
ARL6IP4
SETD8
DIABLO
VPS37B
C12orf65
GTF2B1
LRRC43
OGFOD2
ATP6V0A2
HCAR1
HIP1R
TCTN2
DNAH10
WDR66
SNRNP35
IL31
CCDC62
DENR
RILPL2
GTF2H3
B3GNT4
VPS33A
TMED2
HPD
HCAR2
HCAR3
RILPL1
PIWIL1
FZD10
RIMBP2
STX2
EP400
POLE
GOLGA3
DDX51
FBRSL1
ANKLE2
CHFR
NOC4L
PGAM5
PXMP2
ZNF605
GALNT9
P2RX2
FOXO1
ELF1
NAA16
KBTBD7
MRPS31
WBP4
KBTBD6
MTRF1
SLC25A15
RGCC

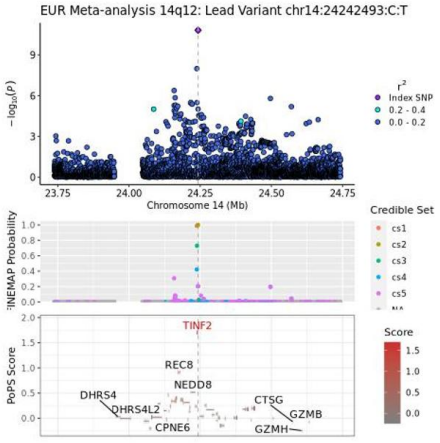

EUR Meta-analysis 13q14.3: Lead Variant chr13:50877931:C:G
Chromosome 13 (Mb)
FINEMAP Probability
PoPS Score
INTS6
RNASEH2B
SERPINE3
DLEU7
FAM124A

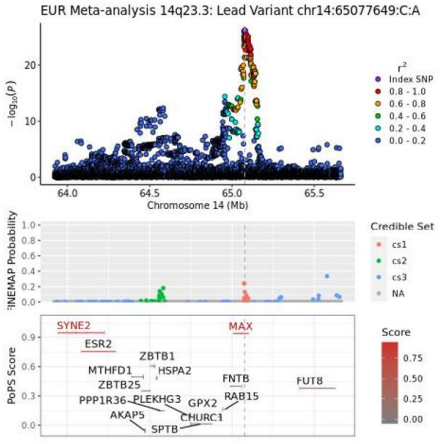

EUR Meta-analysis 13q21.33: Lead Variant chr13:72766039:G:A
Chromosome 13 (Mb)
FINEMAP Probability
PoPS Score
DIS3
BORA
PIBF1
KLF5
MZT1

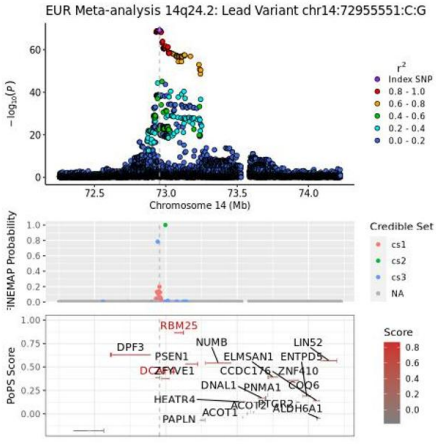

EUR Meta-analysis 14q11.2: Lead Variant chr14:20344792:G:A
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
PNP
APEX1
OSGEP
TTC5
TEP1
TMEM55B
CCNB1IP1
RNASE12
OR4K17
RNASE1
OR4K5
RNASE10
EDDM3B
OR11H6
KLHL33
OR4K1
OR11G2
RNASE11
ANG
OR11H4
OR4K2
RNASE4

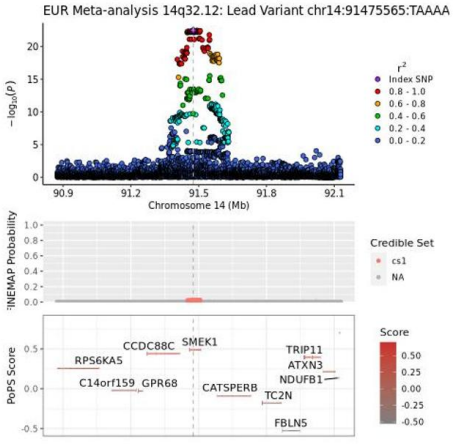

EUR Meta-analysis 14q11.2: Lead Variant chr14:21506530:G:A
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
RPGRIP1L
SUPT16H
HNRNPC
TOX4
TTL3
METTL17
RAB2B
ARHGEF40
SALL2
ZNF219
RNASE1
RNASE7
RNASE8
TMEM253
OR4E2
RNASE13
OR10G3
OR10G2
RNASE2
OR5AU1

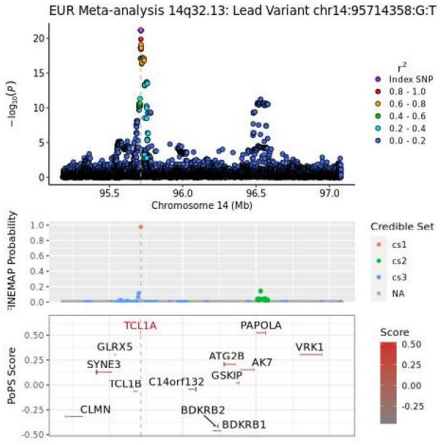

EUR Meta-analysis 14q11.2: Lead Variant chr14:23025068:A:G
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
ACIN1
PSMB5
PRMT5
PABPN1
HAUS4
C14orf119
NGDN
DAD1
OXA1L
RBM23
CDH24
PPP1R3E
EFS
ABHD4
SLC7A7
REM2
BCL2L2
SLC22A17
OR6J1
CEBPE
IL25
PSMB11
MYH7
CMTM5
MYH6

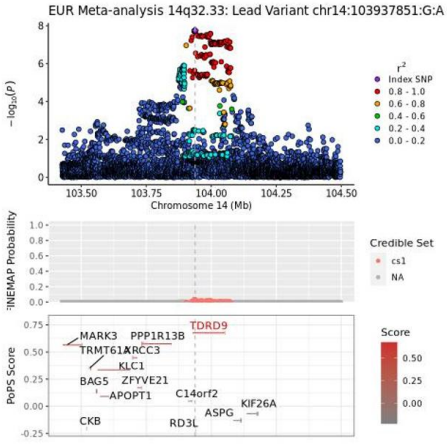

EUR Meta-analysis 14q12: Lead Variant chr14:24242493:C:T
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
TINF2
REC8
NEDD8
DHRS4
DHRS4L2
CTSG
GZMB
CPNE6
GZMH

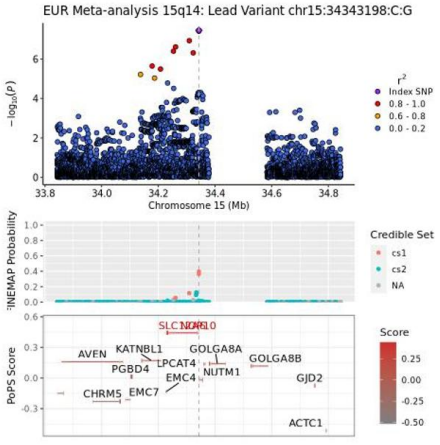

EUR Meta-analysis 14q23.3: Lead Variant chr14:65077649:C:A
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
SYNE2
MAX
ESR2
ZBTB1
MTHFD1
HSPA2
ZBTB25
FNTB
FUT8
PPP1R36
PLEKHG3
GPX2
RAB15
AKAP5
CHURC1
SPTB

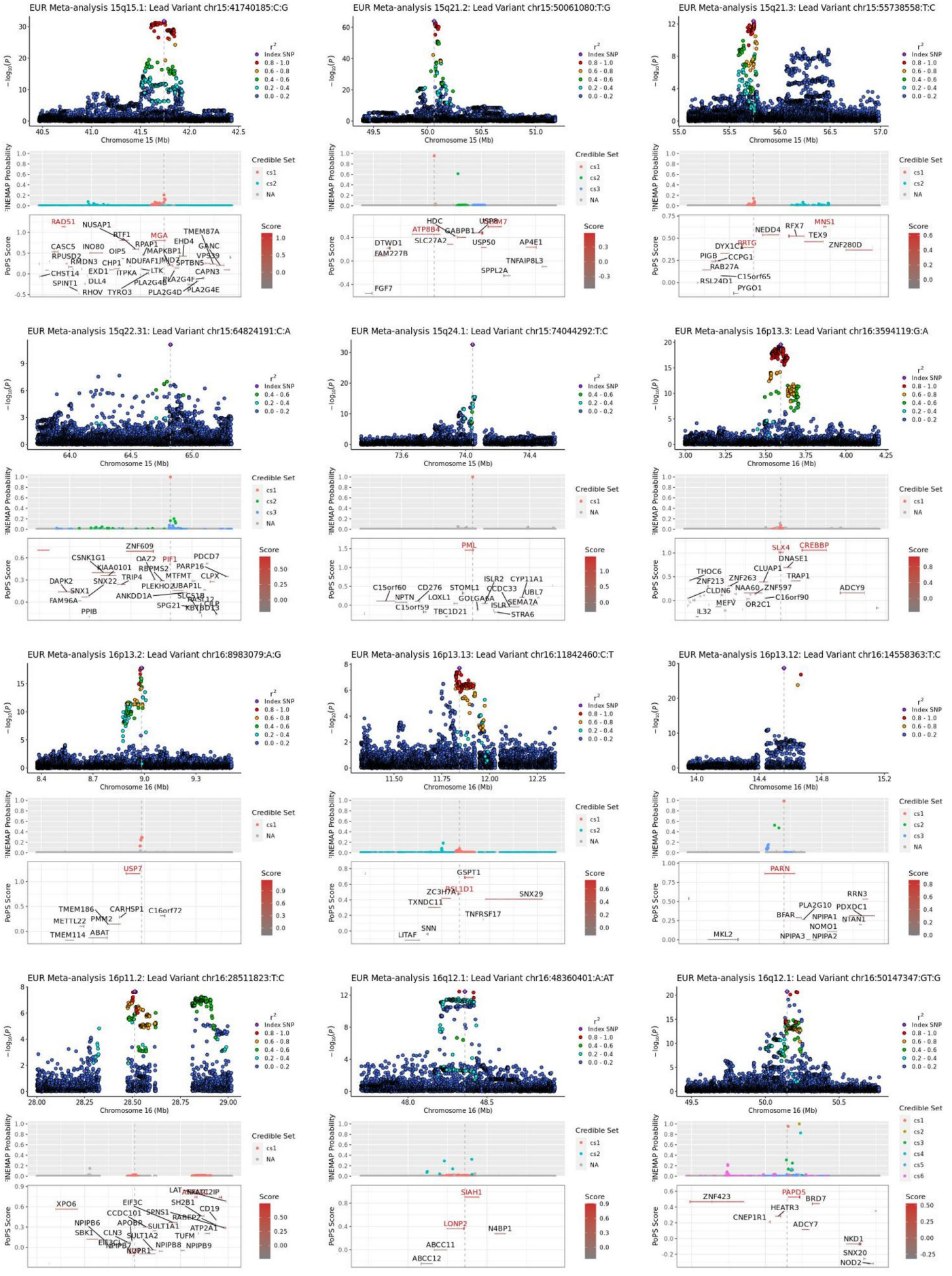

EUR Meta-analysis 14q24.2: Lead Variant chr14:72955551:C:G
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
RBM25
DPF3
NUMB
LIN52
PSEN1
ELMSAN1
ENTPD5
DCAF5
VVE1
CCDC176
ZNF410
DNAL1
PNMA1
SOD2
HEATR4
ACOT7
PTGR2
ALDH6A1
PAPLN
ACOT1

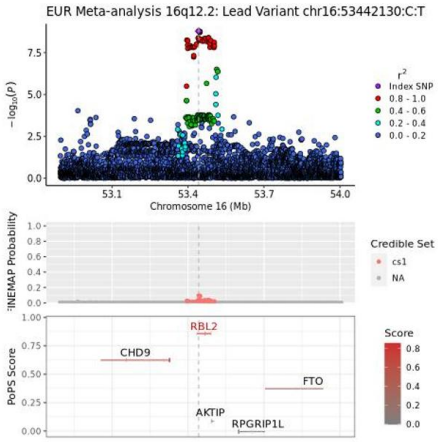

EUR Meta-analysis 14q32.12: Lead Variant chr14:91475565:TAAAA
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
CCDC88C
SMEK1
RPS6KA5
TRIP11
ATXN3
NDUFB1
C14orf159
GPR68
CATSPERB
TC2N
FBLN5

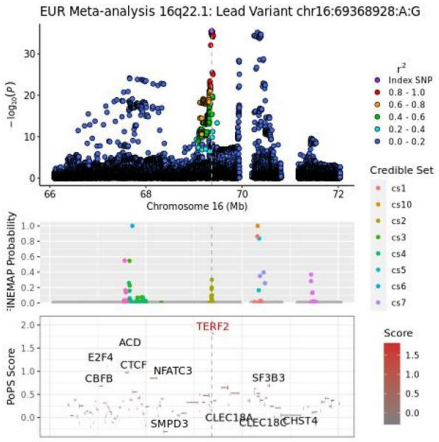

EUR Meta-analysis 14q32.13: Lead Variant chr14:95714358:G:T
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
TCL1A
PAPOLA
GLRX5
VRK1
SYNE3
ATG2B
AK7
GSKIP
TCL1B
C14orf132
CLMN
BDKRB2
BDKRB1

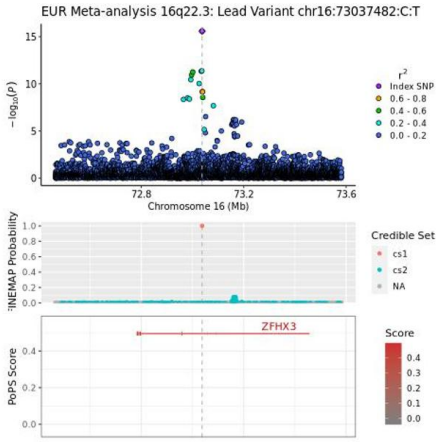

EUR Meta-analysis 14q32.33: Lead Variant chr14:103937851:G:A
Chromosome 14 (Mb)
FINEMAP Probability
PoPS Score
TDRD9
MARK3
PPP1R13B
TRMT61A
RCC3
KLC1
BAG5
ZFYVE21
APOPT1
C14orf2
KIF26A
ASPG
CKB
RD3L

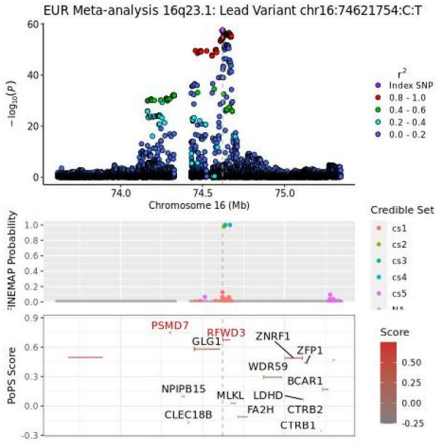

EUR Meta-analysis 15q14: Lead Variant chr15:34343198:C:G
Chromosome 15 (Mb)
FINEMAP Probability
PoPS Score
AVEN
KATNBL1
GOLGA8A
LPCAT4
GOLGA8B
PGBD4
NUTM1
EMC4
GJD2
CHRM5
EMC7
ACTC1

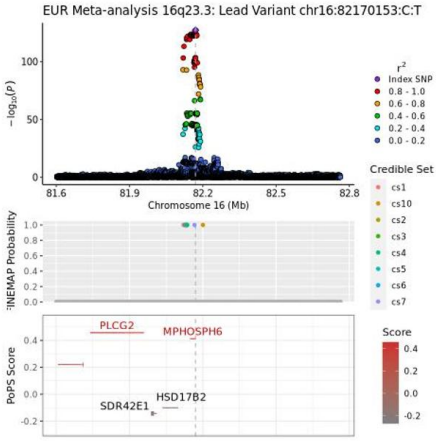

EUR Meta-analysis 15q15.1: Lead Variant chr15:41740185:C:G
EUR Meta-analysis 15q21.2: Lead Variant chr15:50061080:T:G
EUR Meta-analysis 15q21.3: Lead Variant chr15:55738558:T:C
EUR Meta-analysis 15q22.31: Lead Variant chr15:64824191:C:A
EUR Meta-analysis 15q24.1: Lead Variant chr15:74044292:T:C
EUR Meta-analysis 16p13.3: Lead Variant chr16:3594119:G:A
EUR Meta-analysis 16p13.2: Lead Variant chr16:8983079:A:G
EUR Meta-analysis 16p13.13: Lead Variant chr16:11842460:C:T
EUR Meta-analysis 16p13.12: Lead Variant chr16:14558363:T:C
EUR Meta-analysis 16p11.2: Lead Variant chr16:28511823:T:C
EUR Meta-analysis 16q12.1: Lead Variant chr16:48360401:A:AT
EUR Meta-analysis 16q12.1: Lead Variant chr16:50147347:GT:G
−log10(p)
Chromosome 15 (Mb)
Chromosome 16 (Mb)
r²
Index SNP
0.8 - 1.0
0.6 - 0.8
0.4 - 0.6
0.2 - 0.4
0.0 - 0.2
FINEMAP Probability
Credible Set
cs1
cs2
cs3
cs4
cs5
cs6
NA
PoPS Score
Score

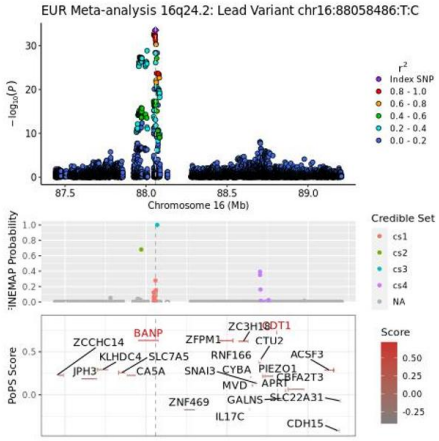

EUR Meta-analysis 16q12.2: Lead Variant chr16:53442130:C:T
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
RBL2
CHD9
FTO
AKTIP
RPGRIP1L

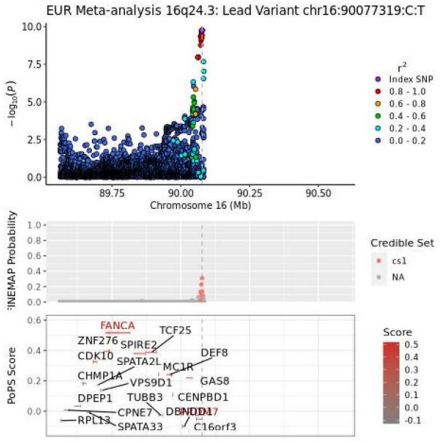

EUR Meta-analysis 16q22.1: Lead Variant chr16:69368928:A:G
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
TERF2
ACD
E2F4
CTCF
NFATC3
CBFB
SF3B3
SMPD3
CLEC18A
CLEC18C
CHST4

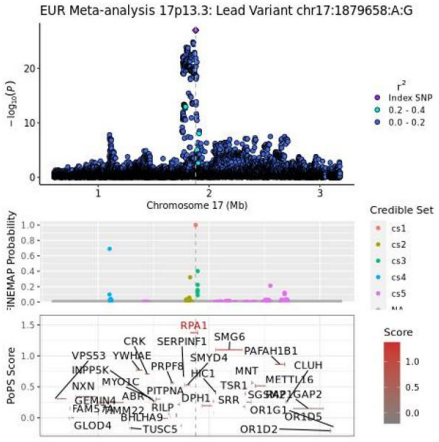

EUR Meta-analysis 16q22.3: Lead Variant chr16:73037482:C:T
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
ZFHX3

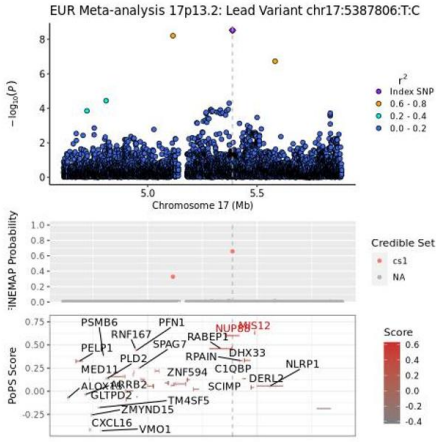

EUR Meta-analysis 16q23.1: Lead Variant chr16:74621754:C:T
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
PSMD7
RFWD3
ZNRF1
GLG1
ZFP1
WDR59
BCAR1
NPIPB15
MLKL
LDHD
FA2H
CTRB2
CLEC18B
CTRB1

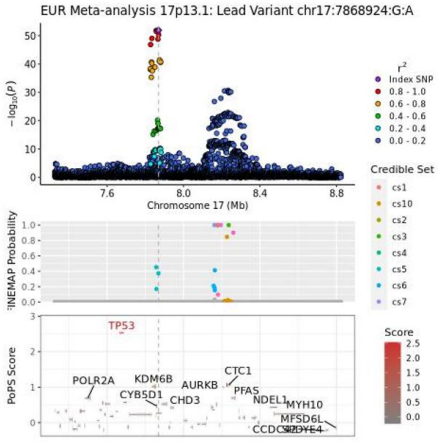

EUR Meta-analysis 16q23.3: Lead Variant chr16:82170153:C:T
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
PLCG2
MPHOSPH6
SDR42E1
HSD17B2

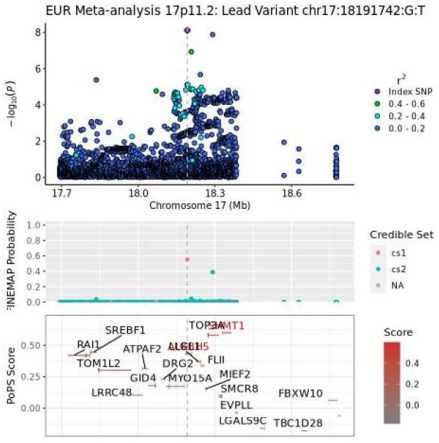

EUR Meta-analysis 16q24.2: Lead Variant chr16:88058486:T:C
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
BANP
ZC3H18
SDT1
ZCCHC14
ZFPM1
CTU2
KLHDC4
SLC7A5
RNF166
AC5F3
JPH3
CA5A
SNAI3
CYBA
PIEZO1
CBFA2T3
MVD
APRT
ZNF469
GALNS
SLC22A31
IL17C
CDH15

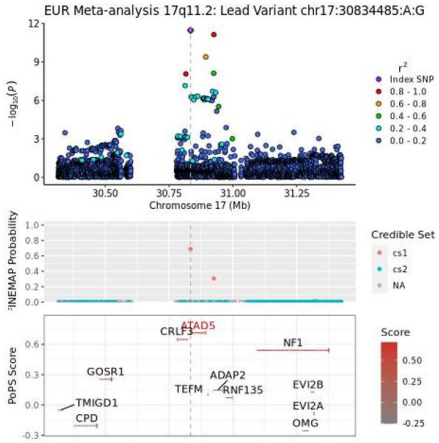

EUR Meta-analysis 16q24.3: Lead Variant chr16:90077319:C:T
Chromosome 16 (Mb)
FINEMAP Probability
PoPS Score
FANCA
TCF25
ZNF276
SPIRE2
CDK10
SPATA2L
DEF8
MC1R
CHMP1A
VPS9D1
GAS8
DPEP1
TUBB3
CENPBD1
CPNE7
RPL13
SPATA33
C16orf3

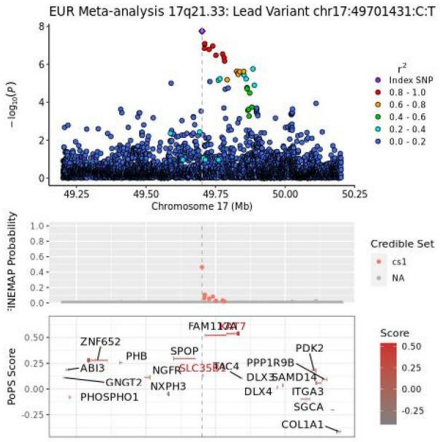

EUR Meta-analysis 17p13.3: Lead Variant chr17:1879658:A:G
Chromosome 17 (Mb)
FINEMAP Probability
PoPS Score
RPA1
SMG6
CRK
SERPINF1
VPS53
YWHAE
PAFAH1B1
SMYD4
INPP5K
PRPF8
CLUH
HIC1
MNT
MYO1C
TSR1
METTL16
NXN
ABR
PITPNA
DPH1
SRR
SGSM2
RAP2GAP2
GEMIN4
RILP
OR1G1
FAM57A
BHLHA9
GLOD4
TUSC5
OR1D2
OR1D5

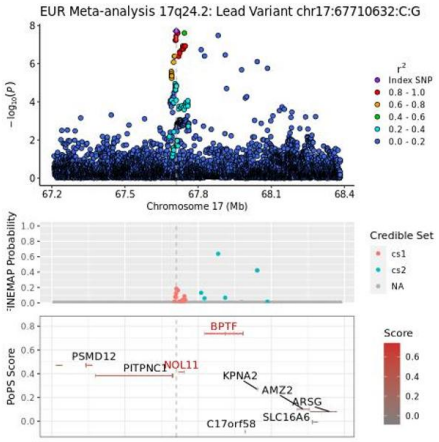

EUR Meta-analysis 17p13.2: Lead Variant chr17:5387806:T:C
Chromosome 17 (Mb)
FINEMAP Probability
PoPS Score
PSMB6
PFN1
RNF167
NUP88
NUP43
RABEP1
SPAG7
PELP1
PLD2
RPAIN
DHX33
MED11
ZNF594
C1QBP
NLRP1
DERL2
ALOX15B
NRBP2
SCIMP
GLTPD2
TM4SF5
ZMYND15
CXCL16
VMO1

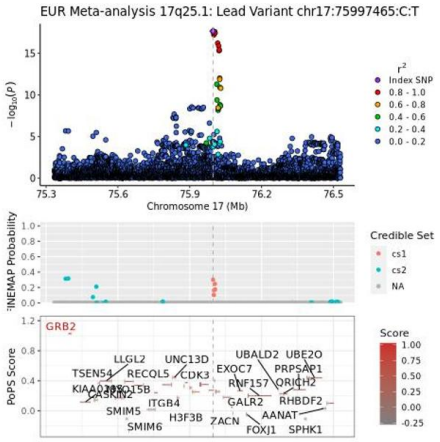

EUR Meta-analysis 17p13.1: Lead Variant chr17:7868924:G:A
Chromosome 17 (Mb)
FINEMAP Probability
PoPS Score
TP53
POLR2A
KDM6B
AURKB
CTC1
CYB5D1
CHD3
PFAS
NDEL1
MYH10
MFSD6L
CCDC57

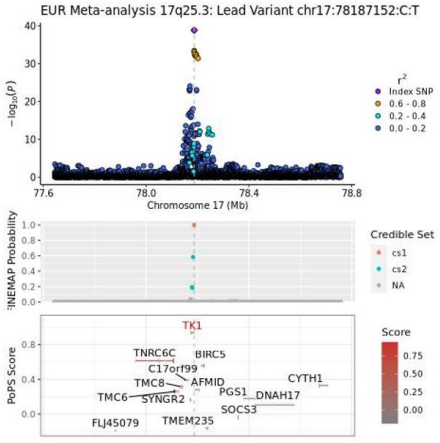

EUR Meta-analysis 17p11.2: Lead Variant chr17:18191742:G:T
Chromosome 17 (Mb)
FINEMAP Probability
PoPS Score
SREBF1
TOP3A
AMT1
RAI1
ATAD5
ATPAF2
FLII
TOM1L2
DRG2
GID4
MYO15A
MIEF2
LRRC48
SMCR8
FBXW10
EVPLL
LGALS9C
TBC1D28

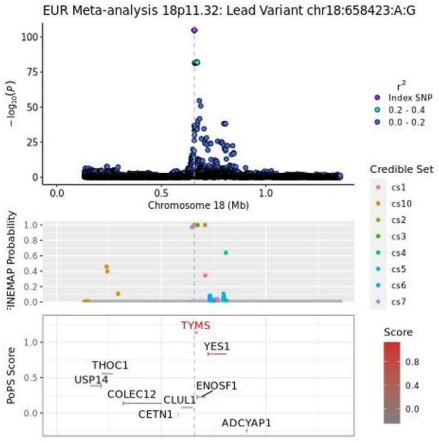

EUR Meta-analysis 17q11.2: Lead Variant chr17:30834485:A:G
Chromosome 17 (Mb)
FINEMAP Probability
PoPS Score
CRLF3
NF1
GOSR1
ADAP2
TEFM
RNF135
EVI2B
TMIGD1
EVI2A
CPD
OMG

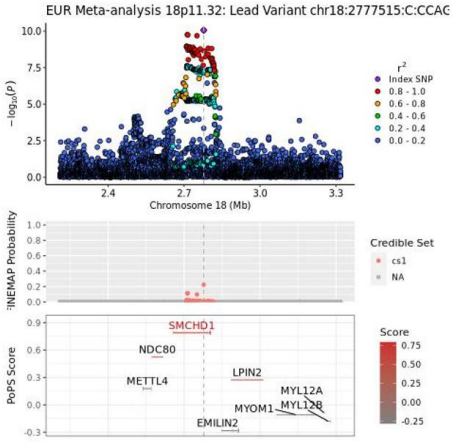

EUR Meta-analysis 17q21.33: Lead Variant chr17:49701431:C:T
Chromosome 17 (Mb)
FAM117A
KAT7
ZNF652
PHB
SPOP
ABI3
NGFR
SLC35A5
TAC4
PPP1R9B
PDK2
GNGT2
NXPH3
DLX5
AMD14
DLX4
ITGA3
PHOSPHO1
SGCA
COL1A1
Index SNP
Credible Set
cs1
NA
Score

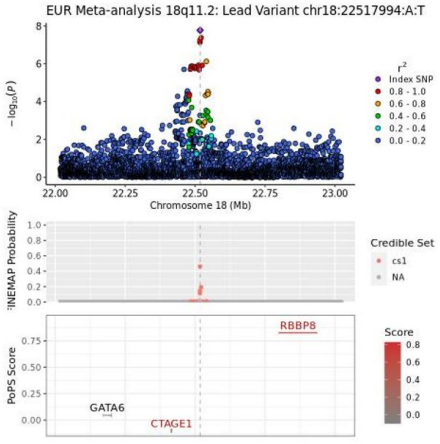

EUR Meta-analysis 17q24.2: Lead Variant chr17:67710632:C:G
Chromosome 17 (Mb)
BPTF
PSMD12
PITPNC1
NOL11
KPNA2
AMZ2
ARSG
SLC16A6
C17orf58
Index SNP
Credible Set
cs1
cs2
NA
Score

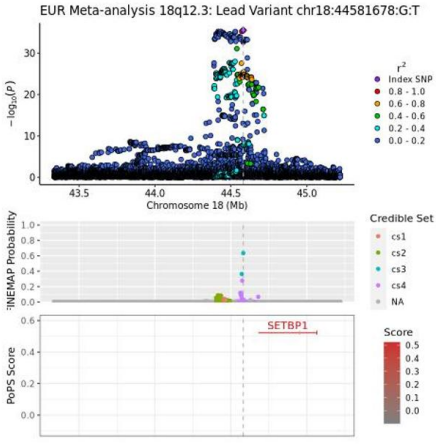

EUR Meta-analysis 17q25.1: Lead Variant chr17:75997465:C:T
Chromosome 17 (Mb)
GRB2
LLGL2
UNC13D
UBALD2
UBE2O
TSEN54
RECQL5
CDK3
EXOC7
PRPSAP1
RNF157
ORICH2
ITGB4
GALR2
RHBDF2
SMIM5
H3F3B
ZACN
AANAT
SMIM6
FOXJ1
SPHK1
Index SNP
Credible Set
cs1
cs2
NA
Score

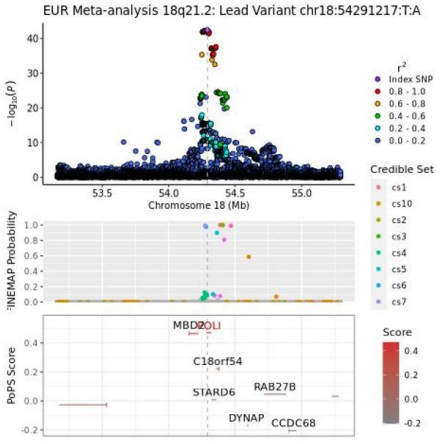

EUR Meta-analysis 17q25.3: Lead Variant chr17:78187152:C:T
Chromosome 17 (Mb)
TK1
TNRC6C
BIRC5
C17orf99
AFMID
TMC8
CYTH1
TMC6
SYNGR2
PGS1
DNAH17
SOCS3
FLJ45079
TMEM235
Index SNP
Credible Set
cs1
cs2
NA
Score

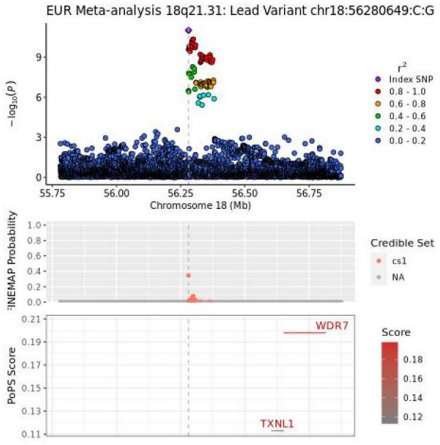

EUR Meta-analysis 18p11.32: Lead Variant chr18:658423:A:G
Chromosome 18 (Mb)
TYMS
YES1
THOC1
USP14
COLEC12
CLUL1
ENOSF1
CETN1
ADCYAP1
Index SNP
Credible Set
cs1
cs10
cs2
cs3
cs4
cs5
cs6
cs7
Score

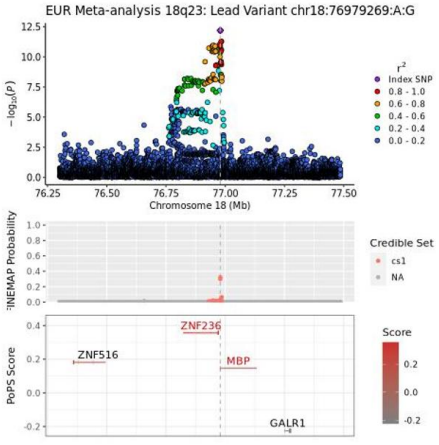

EUR Meta-analysis 18p11.32: Lead Variant chr18:2777515:C:CCAC
Chromosome 18 (Mb)
SMCHD1
NDC80
LPIN2
METTL4
MYL12A
MYL12B
MYOM1
EMILIN2
Index SNP
Credible Set
cs1
NA
Score

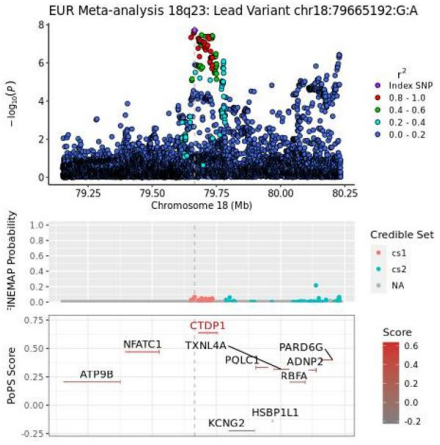

EUR Meta-analysis 18q11.2: Lead Variant chr18:22517994:A:T
Chromosome 18 (Mb)
RBBP8
GATA6
CTAGE1
Index SNP
Credible Set
cs1
NA
Score

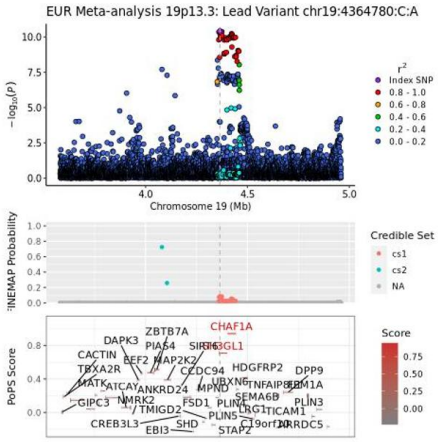

EUR Meta-analysis 18q12.3: Lead Variant chr18:44581678:G:T
Chromosome 18 (Mb)
SETBP1
Index SNP
Credible Set
cs1
cs2
cs3
cs4
NA
Score

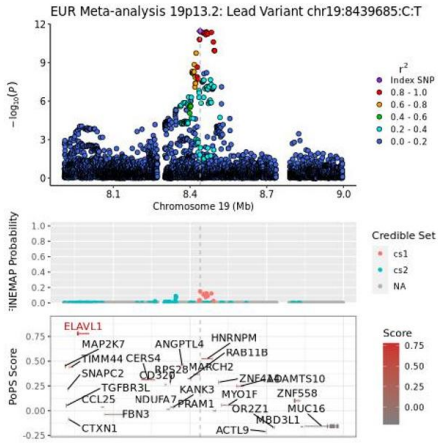

EUR Meta-analysis 18q21.2: Lead Variant chr18:54291217:T:A
Chromosome 18 (Mb)
MBD2
OLI
C18orf54
STARD6
RAB27B
DYNAP
CCDC68
Index SNP
Credible Set
cs1
cs10
cs2
cs3
cs4
cs5
cs6
cs7
Score

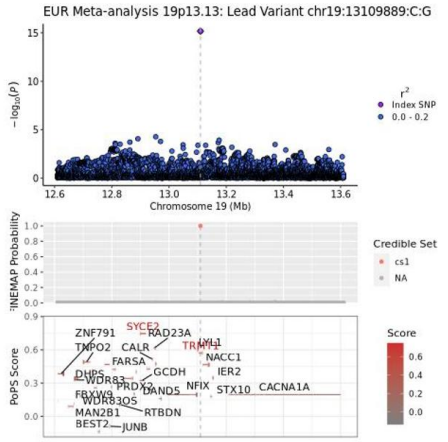

EUR Meta-analysis 18q21.31: Lead Variant chr18:56280649:C:G
Chromosome 18 (Mb)
WDR7
TXNL1
Index SNP
Credible Set
cs1
NA
Score

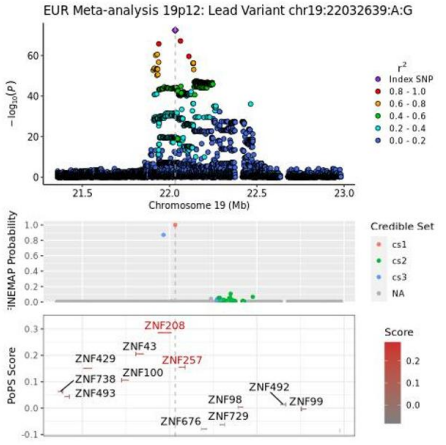

EUR Meta-analysis 18q23: Lead Variant chr18:76979269:A:G
Chromosome 18 (Mb)
ZNF236
ZNF516
MBP
GALR1
Index SNP
Credible Set
cs1
NA
Score

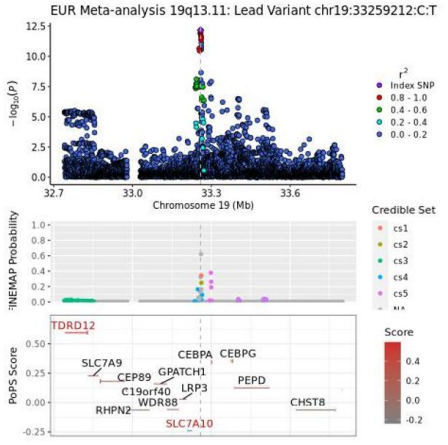

EUR Meta-analysis 18q23: Lead Variant chr18:79665192:G:A
Chromosome 18 (Mb)
CTDP1
NFATC1
TXNL4A
PARD6G
POLC1
ADNP2
ATP9B
RBFA
HSBP1L1
KCNG2
Index SNP
Credible Set
cs1
cs2
NA
Score

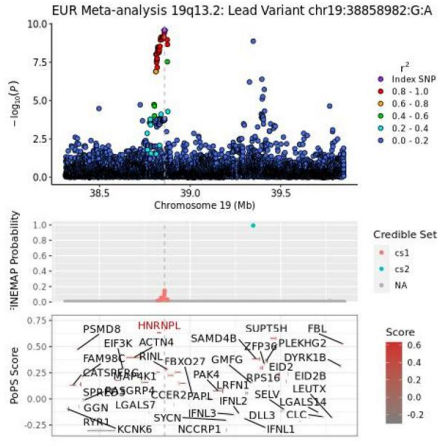

EUR Meta-analysis 19p13.3: Lead Variant chr19:4364780:C:A
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
CHAF1A
ZBTB7A
DAPK3
PIAS4
SIRT6
GGL1
CACTIN
EEF2
MAP2K2
TBXA2R
CCDC94
HDGFRP2
DPP9
MATK
ATCAY
ANKRD24
MPND
HBXN6
TNFAIP8L1
EIF4A1
GIPC3
NMRK2
FSD1
PLIN4
SEMA6D
LRG1
TICAM1
PLIN3
TMIGD2
PLIN5
CREB3L3
EBI3
SHD
STAP2
C19orf24
ARRDC5

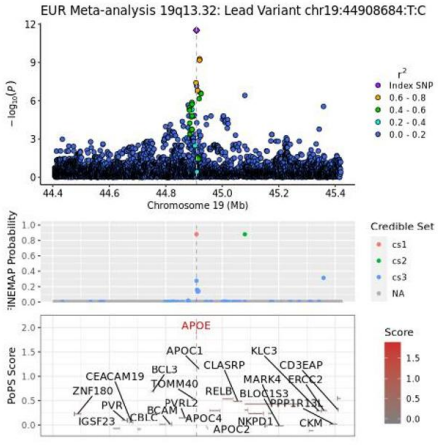

EUR Meta-analysis 19p13.2: Lead Variant chr19:8439685:C:T
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
ELAVL1
MAP2K7
ANGPTL4
HNRNPM
TIMM44
CERS4
RAB11B
SNAPC2
BPS2
MARCH2
CD320
ZNF444
ADAMTS10
TGFBR3L
KANK3
MYO1F
ZNF558
CCL25
NDUFA7
PRAM1
OR2Z1
MUC16
FBN3
MBD3L1
CTXN1
ACTL9

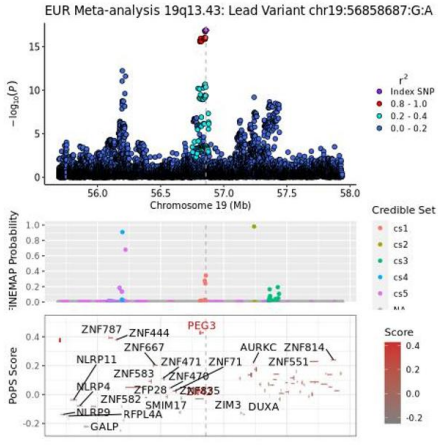

EUR Meta-analysis 19p13.13: Lead Variant chr19:13109889:C:G
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
ZNF791
SYCE2
RAD23A
TMPO2
CALR
TRMT1
KYL1
NACC1
FARSA
DHPS
GCDH
IER2
WDR83
PRDX2
NFIX
STX10
CACNA1A
FBXW9
WDR83OS
DAND5
MAN2B1
RTBDN
BEST2
JUNB

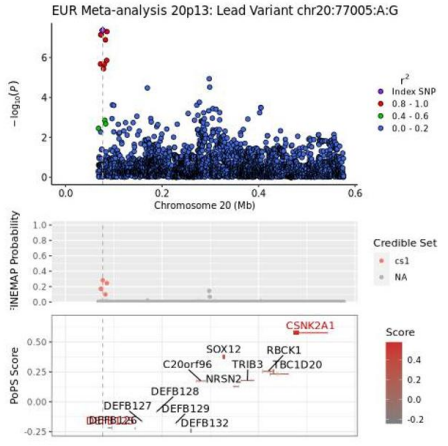

EUR Meta-analysis 19p12: Lead Variant chr19:22032639:A:G
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
ZNF208
ZNF43
ZNF429
ZNF257
ZNF738
ZNF100
ZNF493
ZNF492
ZNF98
ZNF99
ZNF729
ZNF676

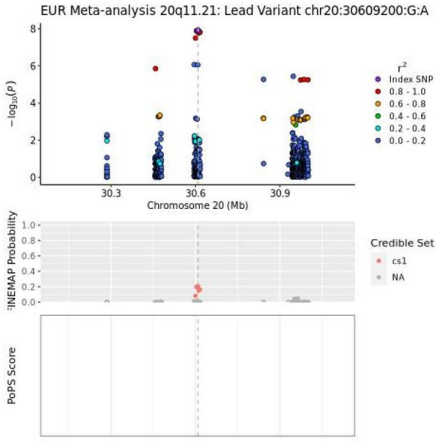

EUR Meta-analysis 19q13.11: Lead Variant chr19:33259212:C:T
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
TDRD12
CEBPA
CEBPG
SLC7A9
CEP89
GPATCH1
PEPD
C19orf40
LRP3
WDR88
CHST8
RHPN2
SLC7A10

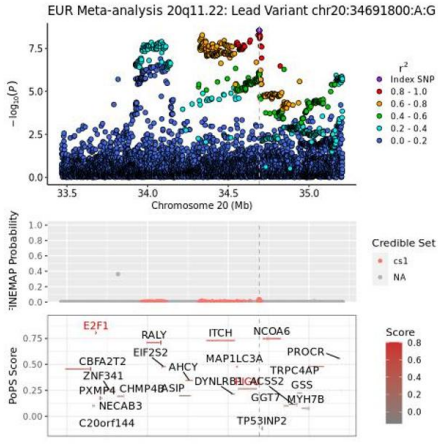

EUR Meta-analysis 19q13.2: Lead Variant chr19:38858982:G:A
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
PSMD8
HNRNPL
SUPT5H
FBL
EIF3K
ACTN4
SAMD4B
ZFP36
PLEKHG2
FAM98C
RINL
FBXO27
GMFG
DYRK1B
EID2
CATSPERG
PAK4
EID2B
RPS16
LRFN1
SELV
LEUTX
IFNL2
LGALS14
GGN
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CCER2
PAPL
DLL3
CLC
SYCN
IFNL3
RYR1
KCNK6
NCCRP1
IFNL1

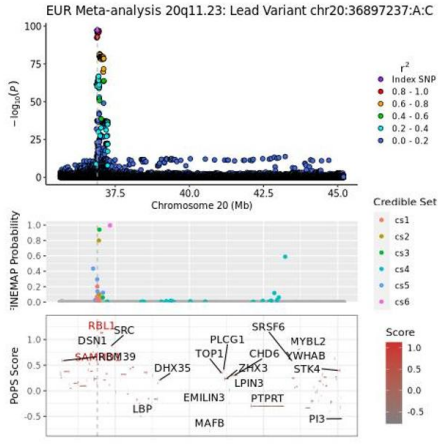

EUR Meta-analysis 19q13.32: Lead Variant chr19:44908684:T:C
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
APOE
APOC1
KLC3
CLASRP
CD3EAP
CEACAM19
BCL3
TOMM40
MARK4
ERCC2
ZNF180
RELB
BLOC1S3
PVR
PVRL2
PPP1R13L
BCAM
CBLC
APOC4
NKPD1
CKM
IGSF23
APOC2

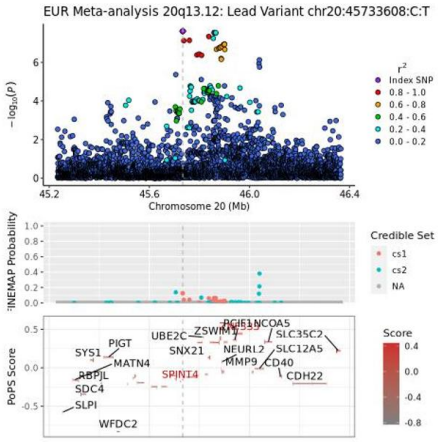

EUR Meta-analysis 19q13.43: Lead Variant chr19:56858687:G:A
Chromosome 19 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
ZNF787
ZNF444
PEG3
ZNF667
AURKC
ZNF814
NLRP11
ZNF471
ZNF71
ZNF551
ZNF583
ZNF470
NLRP4
ZNF28
ZNF835
ZNF582
SMIM17
ZIM3
DUXA
NLRP9
RFPL4A
GALP

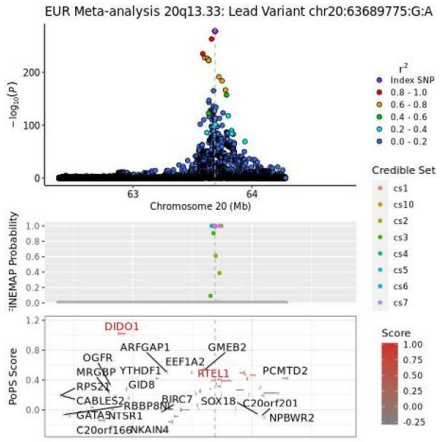

EUR Meta-analysis 20p13: Lead Variant chr20:77005:A:G
Chromosome 20 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
CSNK2A1
SOX12
RBCK1
C20orf96
TRIB3
TBC1D20
NRSN2
DEFB128
DEFB127
DEFB129
DEFB126
DEFB132

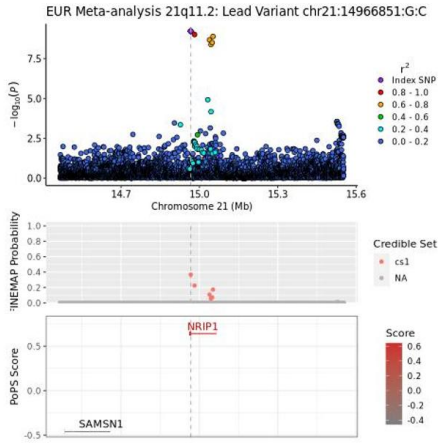

EUR Meta-analysis 20q11.21: Lead Variant chr20:30609200:G:A
Chromosome 20 (Mb)
FINEMAP Probability
PoPS Score
Credible Set

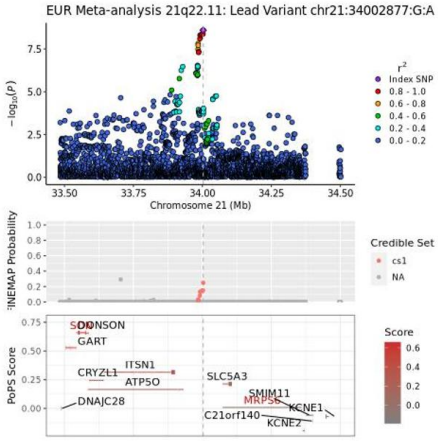

EUR Meta-analysis 20q11.22: Lead Variant chr20:34691800:A:G
Chromosome 20 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
E2F1
RALY
ITCH
NCOA6
EIF252
PROCR
CBFA2T2
AHCY
MAP1LC3A
ZNF341
TRPC4AP
PXMP4
CHMP4B
PASIP
DYNLRB1
CAC552
GSS
GGT7
MYH7B
NECAB3
C20orf144
TP53INP2

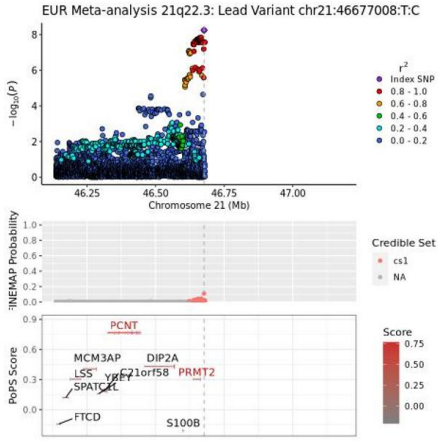

EUR Meta-analysis 20q11.23: Lead Variant chr20:36897237:A:C
Chromosome 20 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
RBL1
SRC
SRSF6
DSN1
PLCG1
MYBL2
SAMD9L
TOP1
CHD6
YWHAB
DHX35
ZHX3
STK4
LPIN3
EMILIN3
PTPRT
LBP
MAFB
PI3

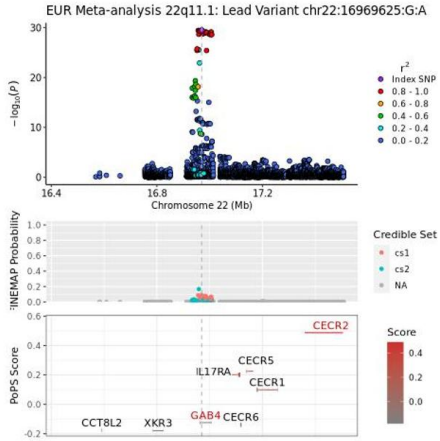

EUR Meta-analysis 20q13.12: Lead Variant chr20:45733608:C:T
Chromosome 20 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
SPINT4
CDH22
SLPI
WFDC2

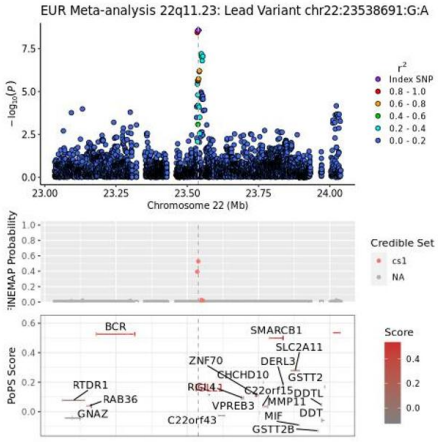

EUR Meta-analysis 20q13.33: Lead Variant chr20:63689775:G:A
Chromosome 20 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
DIDO1
ARFGAP1
GMEB2
EEF1A2
RTEL1
PCMTD2
SOX18
C20orf201
NPBWR2
C20orf166NKAIN4

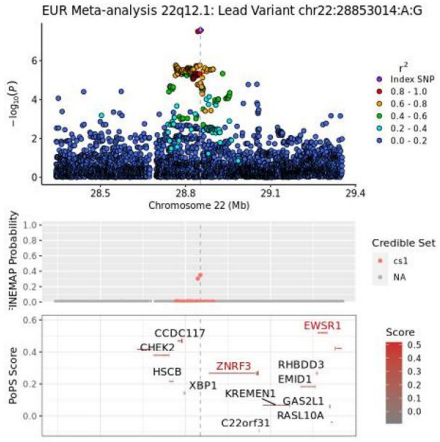

EUR Meta-analysis 21q11.2: Lead Variant chr21:14966851:G:C
Chromosome 21 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
NRIP1
SAMSN1

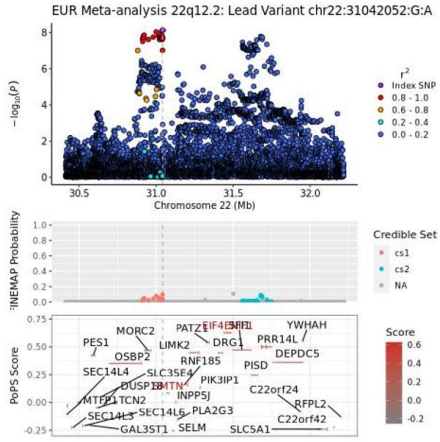

EUR Meta-analysis 21q22.11: Lead Variant chr21:34002877:G:A
Chromosome 21 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
SOD1
GART
ITSN1
CRYZL1
ATP5O
SLC5A3
SMIM11
MRPS6
KCNE1
C21orf140
KCNE2
DNAJC28

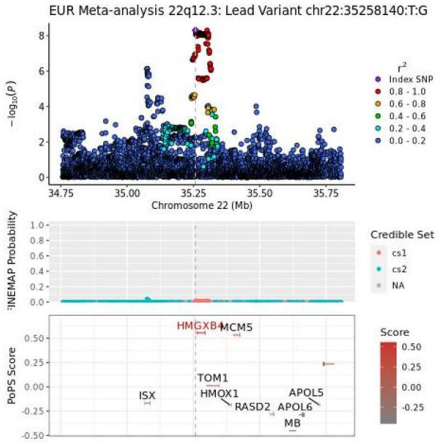

EUR Meta-analysis 21q22.3: Lead Variant chr21:46677008:T:C
Chromosome 21 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
PCNT
MCM3AP
DIP2A
LSS
C21orf58
PRMT2
SPATC1L
FTCD
S100B

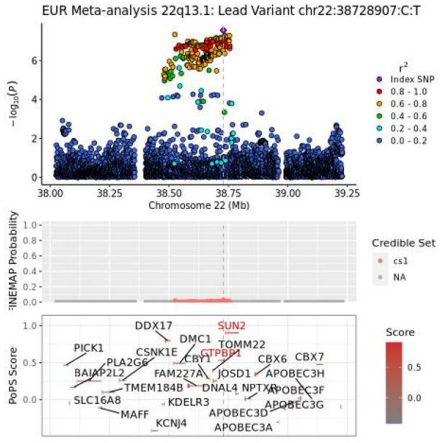

EUR Meta-analysis 22q11.1: Lead Variant chr22:16969625:G:A
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
CECR2
CECR5
IL17RA
CECR1
CCT8L2
XKR3
GAB4
CECR6

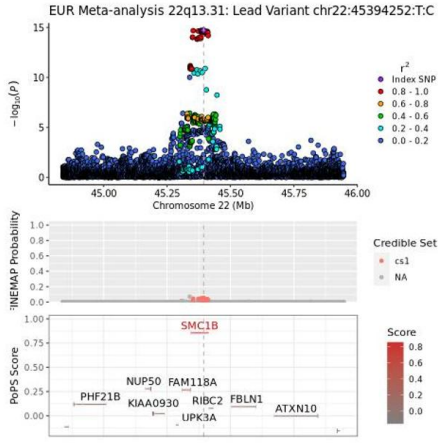

EUR Meta-analysis 22q11.23: Lead Variant chr22:23538691:G:A
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
BCR
SMARCB1
SLC2A11
ZNF70
DERL3
CHCHD10
GSTT2
RTDR1
RAB36
GNAZ
VPREB3
MMP11
DDT
C22orf43
MIF
GSTT2B

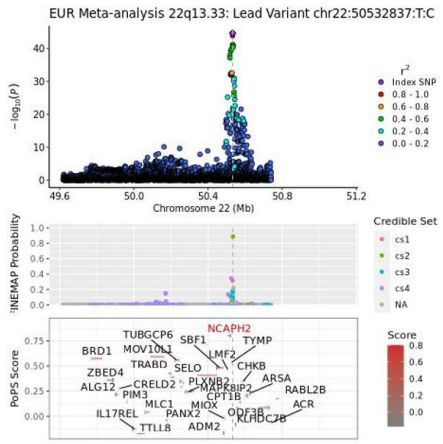

EUR Meta-analysis 22q12.1: Lead Variant chr22:28853014:A:G
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
CCDC117
EWSR1
CHEK2
HSCB
ZNRF3
RHBDD3
EMID1
XBP1
KREMEN1
GAS2L1
C22orf31
RASL10A

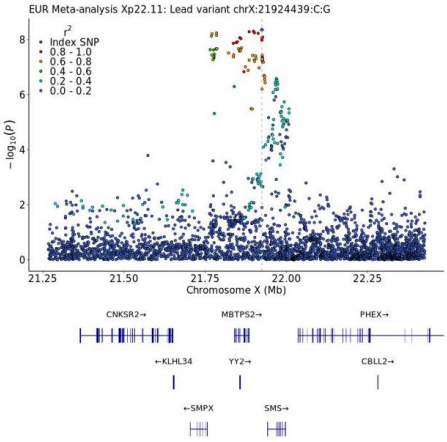

EUR Meta-analysis 22q12.2: Lead Variant chr22:31042052:G:A
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
MORC2
YWHAH
PES1
LIMK2
DRG1
PRR14L
OSBP2
RNF185
DEPDC5
PISD
SEC14L4
SLC35F4
PIK3IP1
C22orf24
INPP5J
RFPL2
SEC14L3
SEC14L6
PLA2G3
C22orf42
GAL3ST1
SELM
SLC5A1

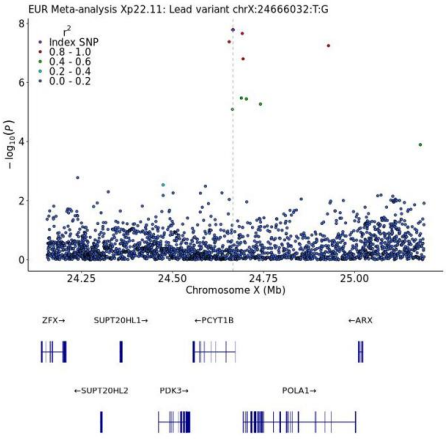

EUR Meta-analysis 22q12.3: Lead Variant chr22:35258140:T:G
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
HMGXB4
MCM5
TOM1
ISX
HMOX1
APOL5
RASD2
APOL6
MB

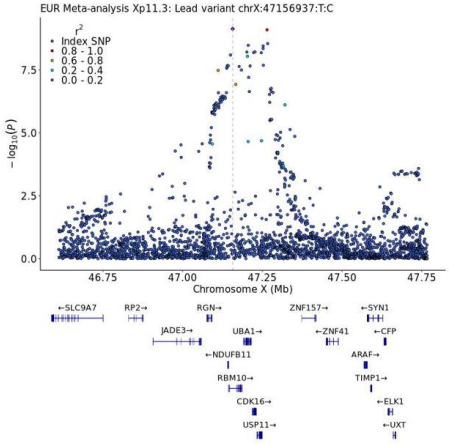

EUR Meta-analysis 22q13.1: Lead Variant chr22:38728907:C:T
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
DDX17
SUN2
DMC1
PICK1
CSNK1E
TOMM22
CTPBP1
PLA2G6
CBY1
CBX6
CBX7
BAIAP2L2
FAM227A
JOSD1
APOBEC3H
TMEM184B
DNAL4
NPTXR
APOBEC3F
SLC16A8
KDELR3
APOBEC3G
MAFF
KCNJ4
APOBEC3D
APOBEC3A

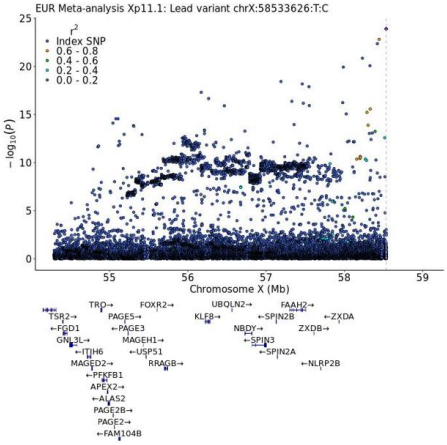

EUR Meta-analysis 22q13.31: Lead Variant chr22:45394252:T:C
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
SMC1B
NUP50
FAM118A
PHF21B
KIAA0930
RIBC2
FBLN1
ATXN10
UPK3A

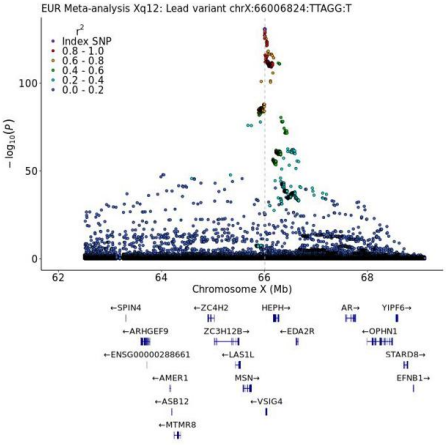

EUR Meta-analysis 22q13.33: Lead Variant chr22:50532837:T:C
Chromosome 22 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
NCAPH2
TUBGCP6
SBF1
TYMP
BRD1
MOV10L1
LMF2
TRABD
SELO
CHKB
ZBED4
CRELD2
PLXNB2
ARSA
ALG12
MAPK8IP2
PIM3
CPT1B
RABL2B
MLC1
MIOX
ACR
IL17REL
PANX2
QDPR
KLHDC7B
TTLL8
ADM2

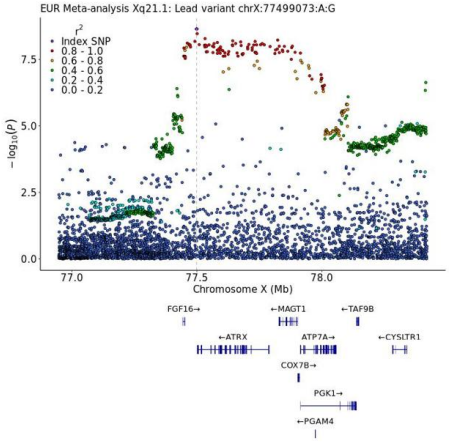

EUR Meta-analysis Xp22.11: Lead variant chrX:21924439:C:G
Chromosome X (Mb)
CNKSR2→
MBTPS2→
PHEX→
←KLHL34
YY2→
CBLL2→
←SMPX
SMS→

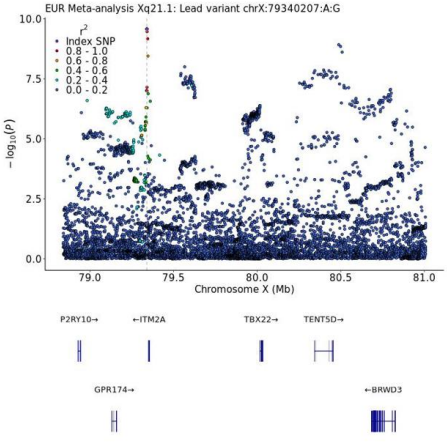

EUR Meta-analysis Xp22.11: Lead variant chrX:24666032:T:G
Chromosome X (Mb)
ZFX→
SUPT20HL1→
←PCYT1B
←ARX
←SUPT20HL2
PDK3→
POLA1→

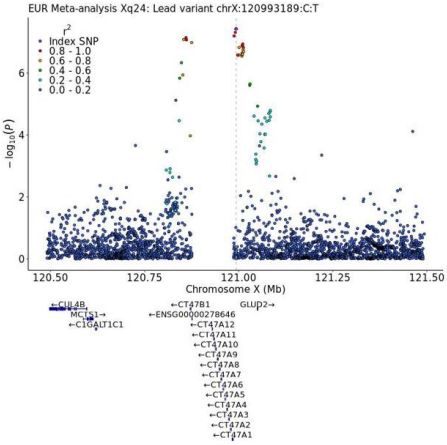

EUR Meta-analysis Xp11.3: Lead variant chrX:47156937:T:C
Chromosome X (Mb)
←SLC9A7
RP2→
RGN→
ZNF157→
←SYN1
JADE3→
UBA1→
←ZNF41
←CFP
←NDUFB11
ARAF→
RBM10→
TIMP1→
CDK16→
←ELK1
USP11→
←UXT

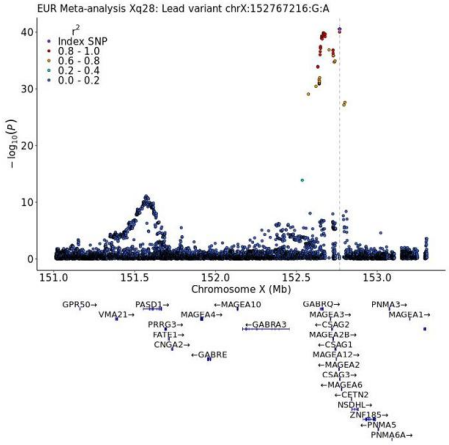

EUR Meta-analysis Xp11.1: Lead variant chrX:58533626:T:C
Chromosome X (Mb)
TRO→
FOXR2→
UBQLN2→
FAAH2→
TSR2→
PAGE5→
KLF8→
←SPIN2B
←ZXDA
←FGD1
←PAGE3
NBDY→
ZXDB→
GNL3L→
MAGEH1→
←SPIN3
←ITIH6
←USP51
←SPIN2A
MAGED2→
RRAGB→
←NLRP2B
←PFKFB1
APEX2→
←ALAS2
PAGE2B→
PAGE2→
←FAM104B

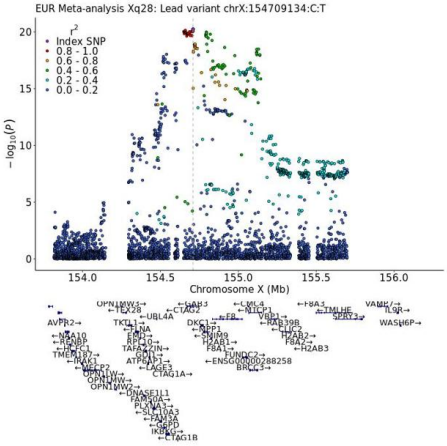

EUR Meta-analysis Xq12: Lead variant chrX:66006824:TTAGG:T
Chromosome X (Mb)
←SPIN4
←ZC4H2
HEPH→
AR→
YIPF6→
←ARHGEF9
ZC3H12B→
←EDA2R
←OPHN1
←ENSG00000288661
←LAS1L
STARD8→
←AMER1
MSN→
EFNB1→
←ASB12
←VSIG4
←MTMR8

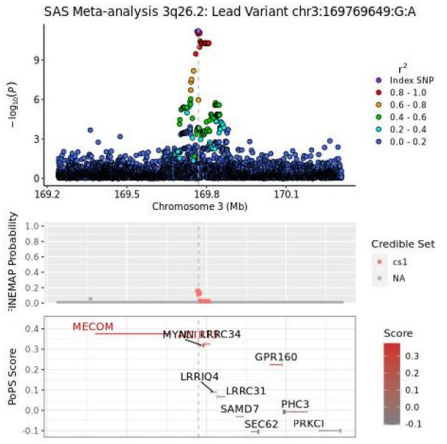

EUR Meta-analysis Xq21.1: Lead variant chrX:77499073:A:G
Chromosome X (Mb)
FGF16→
←MAGT1
←TAF9B
←ATRX
ATP7A→
←CYSLTR1
COX7B→
PGK1→
←PGAM4

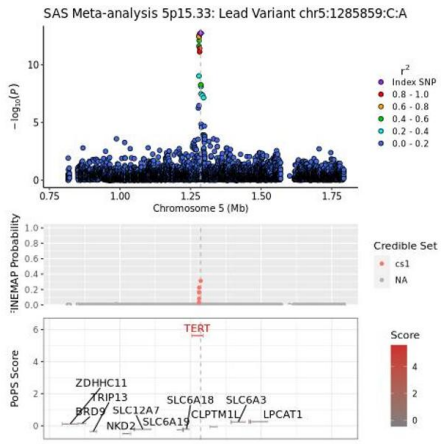

EUR Meta-analysis Xq21.1: Lead variant chrX:79340207:A:G
Chromosome X (Mb)
P2RY10→
←ITM2A
TBX22→
TENT5D→
GPR174→
←BRWD3

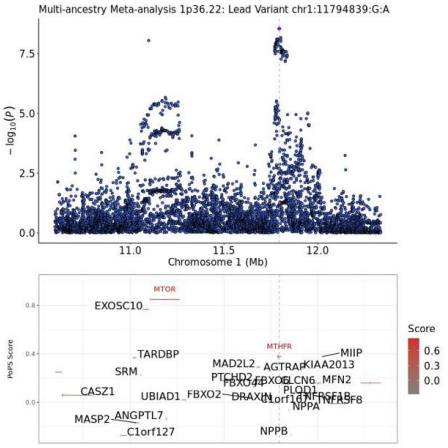

EUR Meta-analysis Xq24: Lead variant chrX:120993189:C:T
Chromosome X (Mb)
←CUL4B
MCTS1→
←C1GALT1C1
←CT47B1
GLUD2→
←ENSG00000278646
←CT47A12
←CT47A11
←CT47A10
←CT47A9
←CT47A8
←CT47A7
←CT47A6
←CT47A5
←CT47A4
←CT47A3
←CT47A2
←CT47A1

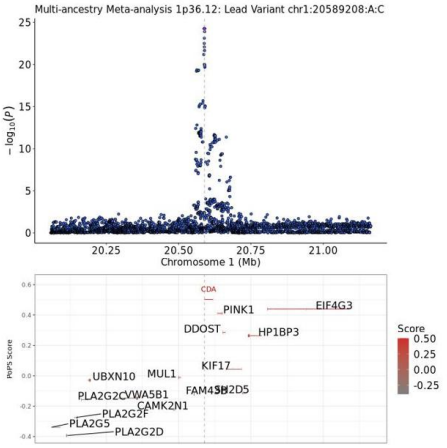

EUR Meta-analysis Xq28: Lead variant chrX:152767216:G:A
Chromosome X (Mb)
GPR50→
PASD1→
←MAGEA10
GABRQ→
PNMA3→
VMA21→
MAGEA4→
MAGEA3→
MAGEA1→
PRRG3→
←CSAG2
←GABRA3
FATE1→
MAGEA2B→
CNGA2→
←CSAG1
←GABRE
MAGEA12→
←MAGEA2
CSAG3→
←MAGEA6
←CETN2
NSUHL→
ZNF185→
←PNMA5
PNMA6A→

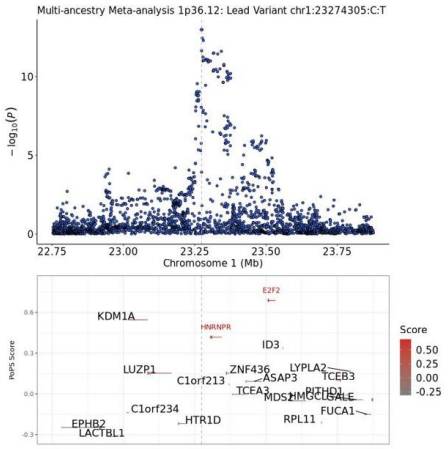

EUR Meta-analysis Xq28: Lead variant chrX:154709134:C:T
Chromosome X (Mb)
OPN1MW3→
←TEX28
←CTAG2
←GAB3
←LAL4
←NTCP1
←F8A3
←TMLHE
SPRY3→
VAMP7→
IL9R→
AVPR2→
TKTL1→
←UBL4A
←DKC1
←RAB39B
WAS↓6P→
←NSA10
←RBM41
←SMIM9
←F8A2→
←F8A1
←F8A3
←MTRF1
←TMEM187
←TAFAZ
←ENSG00000288258
←MAGEA5
←CTAG1A→
OPN1MW2→
←CMTM5E11
←FAM30A→
←PLXNA1→
←SLC10A3
←FAM30B
←IKBKG
←CTAG1B

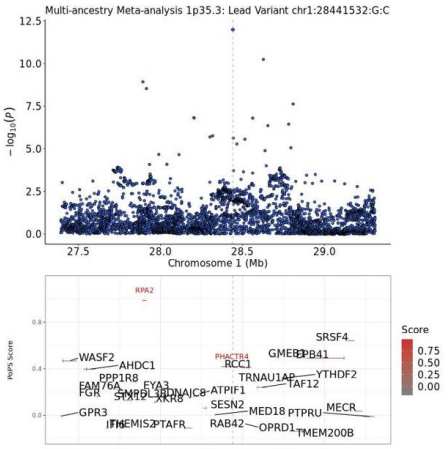

SAS Meta-analysis 3q26.2: Lead Variant chr3:169769649:G:A
Chromosome 3 (Mb)
FINEMAP Probability
PoPS Score
Credible Set
Score
MECOM
MYNN
LRRC34
GPR160
LRRIQ4
LRRC31
SAMD7
PHC3
SEC62
PRKCI

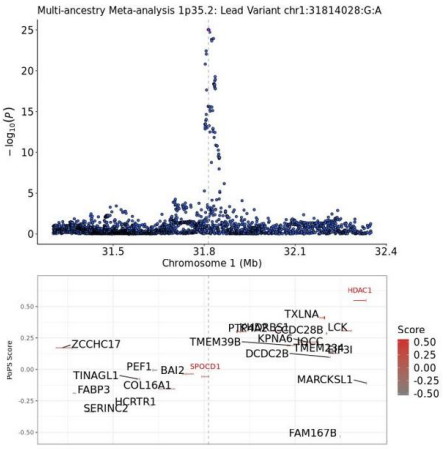

SAS Meta-analysis 5p15.33: Lead Variant chr5:1285859:C:A
Chromosome 5 (Mb)
Credible Set
cs1
NA
Score
TERT
ZDHHC11
TRIP13
BRD9
SLC12A7
NKD2
SLC6A19
SLC6A18
SLC6A3
CLPTM1L
LPCAT1

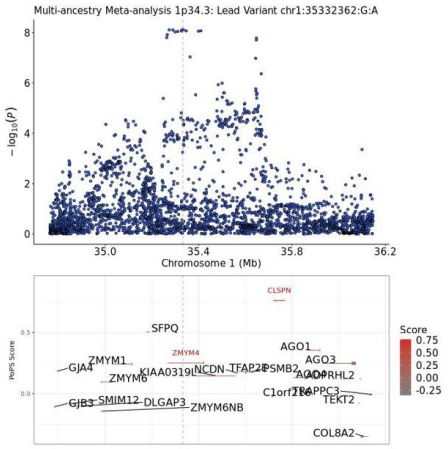

Multi-ancestry Meta-analysis 1p36.22: Lead Variant chr1:11794839:G:A
Chromosome 1 (Mb)
Score
MTOR
EXOSC10
TARDBP
SRM
CASZ1
UBIAD1
FBXO2
MTHFR
MAD2L2
AGTRAP
PTCHD2
FBXO6
GLCN6
MFN2
PLOD1
DRAXIN
C1orf127
NPPA
NPPB
MIIP
KIAA2013

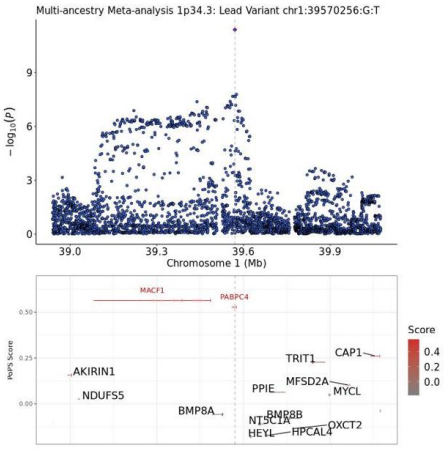

Multi-ancestry Meta-analysis 1p36.12: Lead Variant chr1:20589208:A:C
Chromosome 1 (Mb)
Score
CDA
PINK1
EIF4G3
DDOST
HP1BP3
KIF17
UBXN10
MUL1
PLA2G2C
VWA5B1
FAM43B
CAMK2N1
PLA2G2F
PLA2G5
PLA2G2D

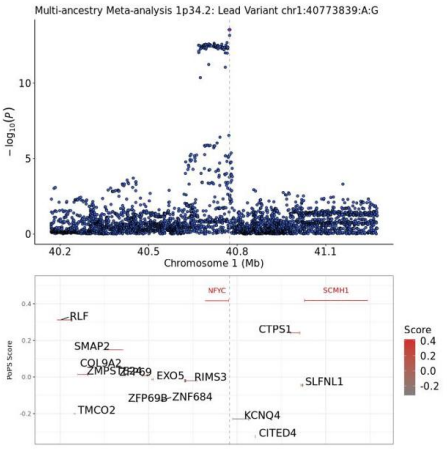

Multi-ancestry Meta-analysis 1p36.12: Lead Variant chr1:23274305:C:T
Chromosome 1 (Mb)
Score
E2F2
KDM1A
HNRNPR
ID3
LUZP1
C1orf213
ZNF436
LYPLA2
ASAP3
TCEB3
TCEA3
MDS2
PITHD1
C1orf234
HTR1D
RPL11
FUCA1
EPHB2
LACTBL1

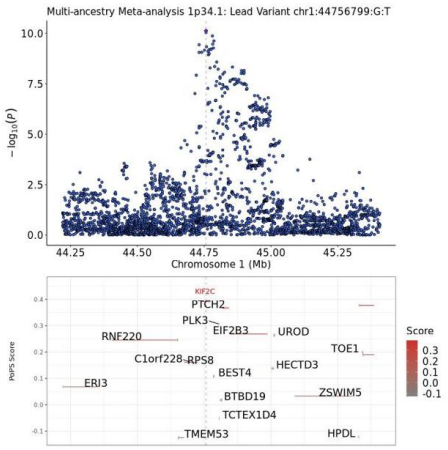

Multi-ancestry Meta-analysis 1p35.3: Lead Variant chr1:28441532:G:C
Chromosome 1 (Mb)
Score
RPA2
WASF2
AHDC1
PPP1R8
FAM76A
FCR
EYA3
PHACTR4
RCC1
GMEB2
PPB41
YTHDF2
TAF12
TRNAU1AP
ATPIF1
SESN2
MED18
PTPRU
MECR
GPR3
PTAFR
RAB42
OPRD1
TMEM200B
SRSF4

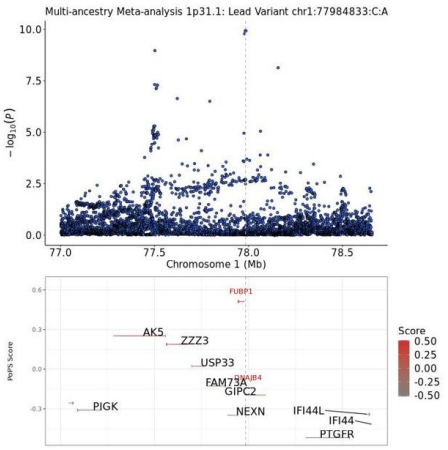

Multi-ancestry Meta-analysis 1p35.2: Lead Variant chr1:31814028:G:A
Chromosome 1 (Mb)
Score
HDAC1
TXLNA
ZCCHC17
TMEM39B
DCDC2B
KPNA6
HCFC1
TMEM234
TINAGL1
PEF1
BAI2
SPOCD1
FABP3
COL16A1
HCRTR1
SERINC2
MARCKSL1
FAM167B

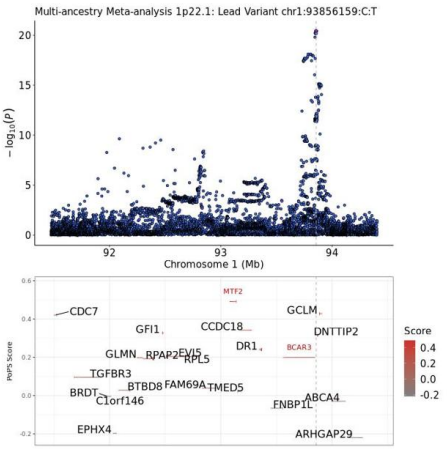

Multi-ancestry Meta-analysis 1p34.3: Lead Variant chr1:35332362:G:A
Chromosome 1 (Mb)
Score
CLSPN
SFPQ
AGO1
AGO3
ZMYM1
ZMYM4
GJA4
KIAA0319L
NCDN
TFAP2E
PSMB2
ZMYM6
C1orf174
APPC3
TEKT2
GJB3
SMIM12
DLGAP3
ZMYM6NB
COL8A2

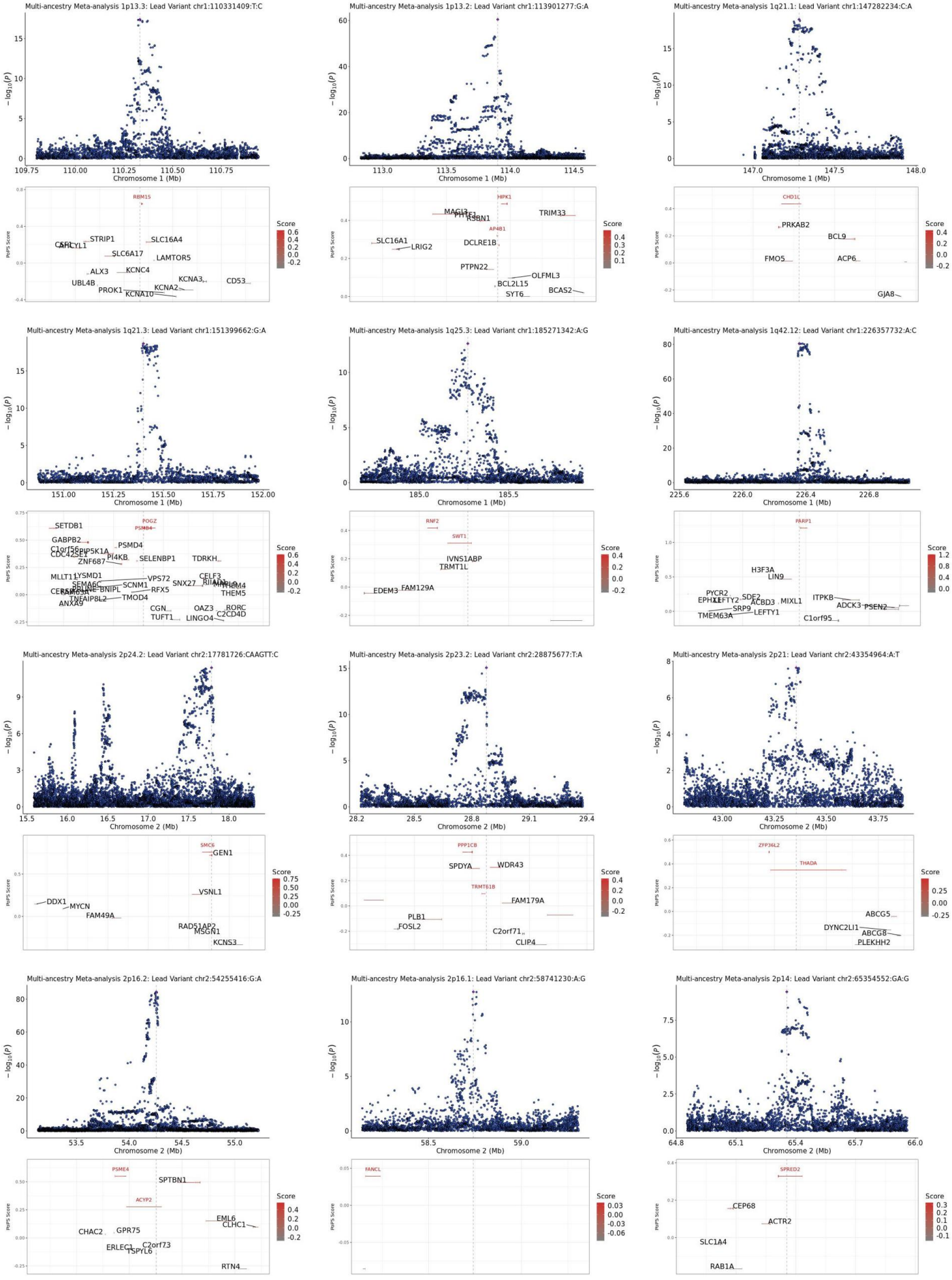

Multi-ancestry Meta-analysis 1p34.3: Lead Variant chr1:39570256:G:T
Chromosome 1 (Mb)
Score
MACF1
PABPC4
AKIRIN1
NDUFS5
BMP8A
TRIT1
CAP1
PPIE
MFSD2A
MYCL
NT5C1A
BMP8B
HEYL
HPCAL4
OXCT2

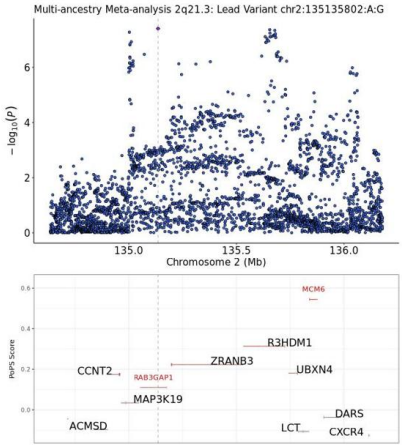

Multi-ancestry Meta-analysis 1p34.2: Lead Variant chr1:40773839:A:G
Chromosome 1 (Mb)
Score
NFYC
SCMH1
RLF
CTPS1
SMAP2
COL9A2
ZMPSTE24
EXO5
RIMS3
SLFNL1
ZFP69B
ZNF684
TMCO2
KCNQ4
CITED4

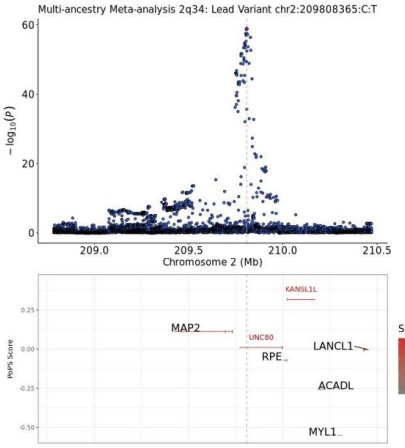

Multi-ancestry Meta-analysis 1p34.1: Lead Variant chr1:44756799:G:T
Chromosome 1 (Mb)
Score
KIF2C
PTCH2
PLK3
EIF2B3
UROD
RNF220
TOE1
C1orf228
RPS8
HECTD3
BEST4
ERI3
BTBD19
ZSWIM5
TCTEX1D4
TMEM53
HPDL

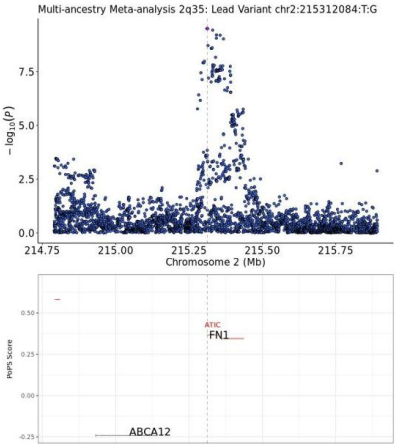

Multi-ancestry Meta-analysis 1p31.1: Lead Variant chr1:77984833:C:A
Chromosome 1 (Mb)
Score
FUBP1
AK5
ZZZ3
USP33
FAM73A
SNAP4
GIPC2
PIGK
NEXN
IFI44L
IFI44
PTGFR

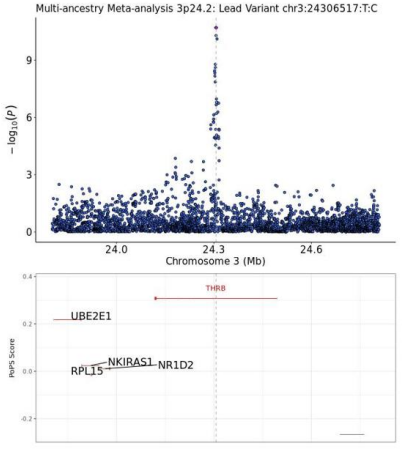

Multi-ancestry Meta-analysis 1p22.1: Lead Variant chr1:93856159:C:T
Chromosome 1 (Mb)
Score
MTF2
CDC7
GCLM
GFI1
CCDC18
DNTTIP2
DR1
BCAR3
GLMN
RPAP2
EVI5
RPL5
TGFBR3
BRDT
BTBD8
FAM69A
TMED5
C1orf146
ABCA4
FNBP1L
EPHX4
ARHGAP29

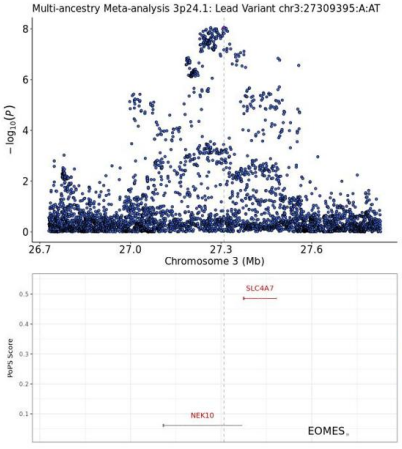

Multi-ancestry Meta-analysis 1p13.3: Lead Variant chr1:110331409:T:C
Multi-ancestry Meta-analysis 1p13.2: Lead Variant chr1:113901277:G:A
Multi-ancestry Meta-analysis 1q21.1: Lead Variant chr1:147282234:C:A
Multi-ancestry Meta-analysis 1q21.3: Lead Variant chr1:151399662:G:A
Multi-ancestry Meta-analysis 1q25.3: Lead Variant chr1:185271342:A:G
Multi-ancestry Meta-analysis 1q42.12: Lead Variant chr1:226357732:A:C
Multi-ancestry Meta-analysis 2p24.2: Lead Variant chr2:17781726:CAAGTT:C
Multi-ancestry Meta-analysis 2p23.2: Lead Variant chr2:28875677:T:A
Multi-ancestry Meta-analysis 2p21: Lead Variant chr2:43354964:A:T
Multi-ancestry Meta-analysis 2p16.2: Lead Variant chr2:54255416:G:A
Multi-ancestry Meta-analysis 2p16.1: Lead Variant chr2:58741230:A:G
Multi-ancestry Meta-analysis 2p14: Lead Variant chr2:65354552:GA:G
Chromosome 1 (Mb)
Chromosome 2 (Mb)
PwPS Score
Score

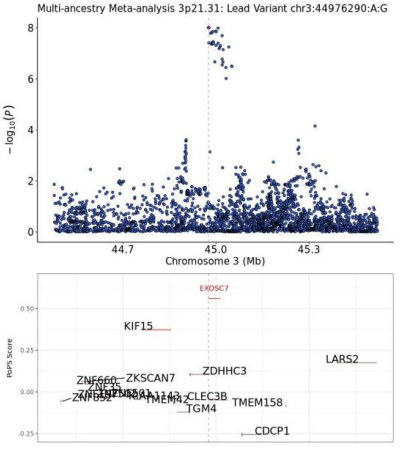

Multi-ancestry Meta-analysis 2q21.3: Lead Variant chr2:135135802:A:G
Chromosome 2 (Mb)
PheWAS Score
Score
MCM6
R3HDM1
ZRANB3
CCNT2
RAB3GAP1
UBXN4
MAP3K19
ACMSD
LCT
DARS
CXCR4

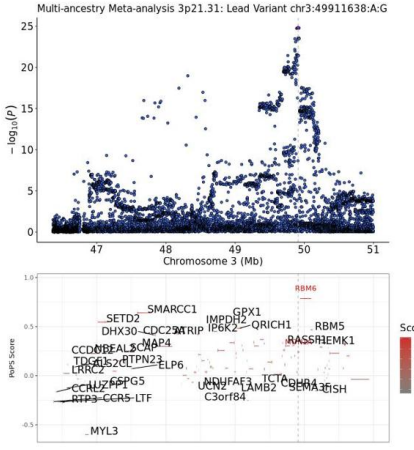

Multi-ancestry Meta-analysis 2q34: Lead Variant chr2:209808365:C:T
Chromosome 2 (Mb)
PheWAS Score
Score
KANSL1L
MAP2
UNC80
LANCL1
RPE
ACADL
MYL1

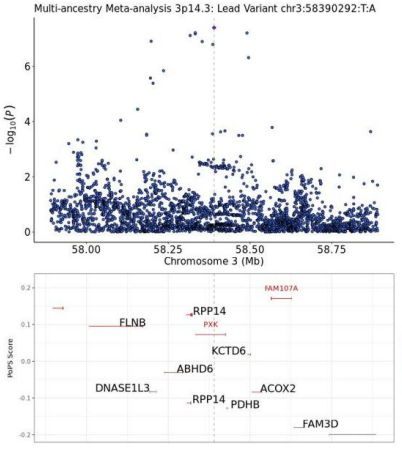

Multi-ancestry Meta-analysis 2q35: Lead Variant chr2:215312084:T:G
Chromosome 2 (Mb)
PheWAS Score
Score
ATIC
FN1
ABCA12

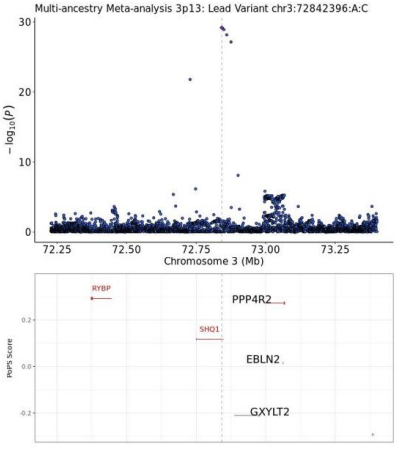

Multi-ancestry Meta-analysis 3p24.2: Lead Variant chr3:24306517:T:C
Chromosome 3 (Mb)
PheWAS Score
Score
THRB
UBE2E1
NKIRAS1
NR1D2
RPL15

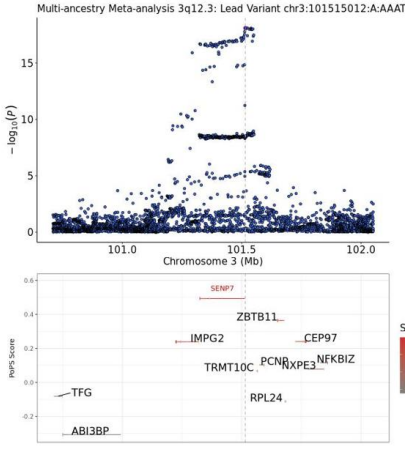

Multi-ancestry Meta-analysis 3p24.1: Lead Variant chr3:27309395:A:AT
Chromosome 3 (Mb)
PheWAS Score
Score
SLC4A7
NEK10
EOMES

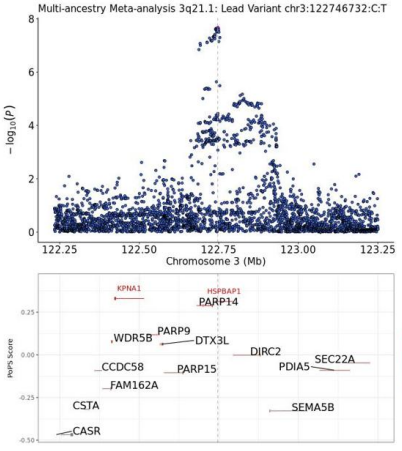

Multi-ancestry Meta-analysis 3p21.31: Lead Variant chr3:44976290:A:G
Chromosome 3 (Mb)
PheWAS Score
Score
EXOSC7
KIF15
ZDHHC3
ZKSCAN7
CLEC3B
TMEM158
TGM4
LARS2
CDCP1

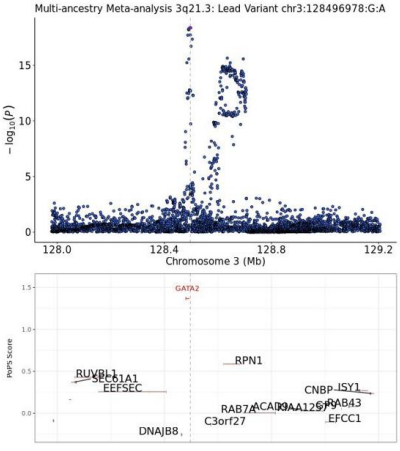

Multi-ancestry Meta-analysis 3p21.31: Lead Variant chr3:49911638:A:G
Chromosome 3 (Mb)
PheWAS Score
Score
RBM6
SMARCC1
SETD2
DHX30
CDC25A
MAP4
IMPDH2
MTRIP
IP6K2
GPX1
QRICH1
RBM5
RASSF1
EMK1
ELP6
CSPG5
UCN2
LAMB2
C3orf84
SEMA3G
ISH
LTF
MYL3

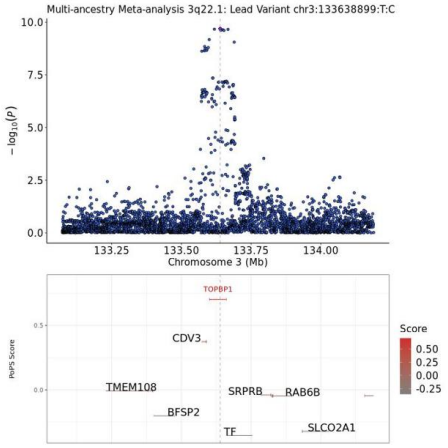

Multi-ancestry Meta-analysis 3p14.3: Lead Variant chr3:58390292:T:A
Chromosome 3 (Mb)
PheWAS Score
Score
FAM107A
FLNB
RPP14
FXK
KCTD6
ABHD6
DNASE1L3
ACOX2
PDHB
FAM3D

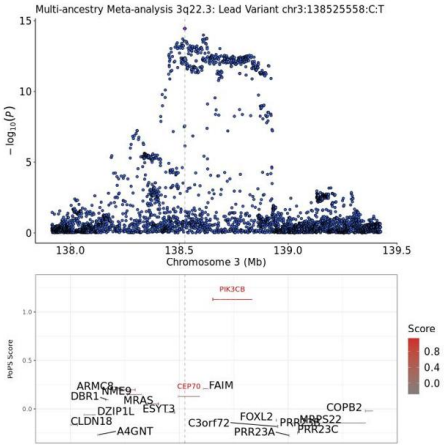

Multi-ancestry Meta-analysis 3p13: Lead Variant chr3:72842396:A:C
Chromosome 3 (Mb)
PheWAS Score
Score
RYBP
PPP4R2
SHQ1
EBLN2
GXYLT2

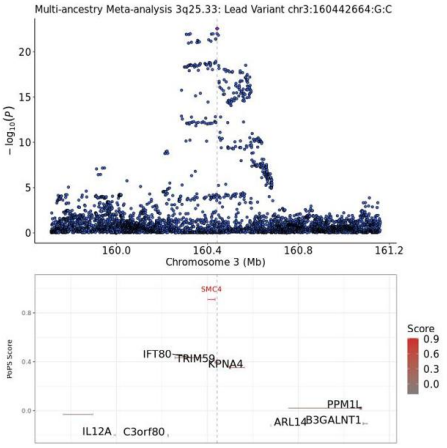

Multi-ancestry Meta-analysis 3q12.3: Lead Variant chr3:101515012:A:AAATT
Chromosome 3 (Mb)
PheWAS Score
Score
SENP7
ZBTB11
IMPG2
CEP97
TRMT10C
PCNP
NXPE3
NFKBIZ
TFG
RPL24
ABI3BP

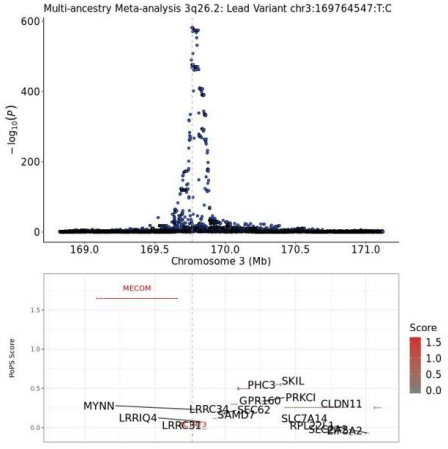

Multi-ancestry Meta-analysis 3q21.1: Lead Variant chr3:122746732:C:T
Chromosome 3 (Mb)
PheWAS Score
Score
KPNA1
HSPBAP1
PARP14
WDR5B
PARP9
DTX3L
DIRC2
CCDC58
PARP15
PDIAS
SEC22A
FAM162A
CSTA
SEMA5B
CASR

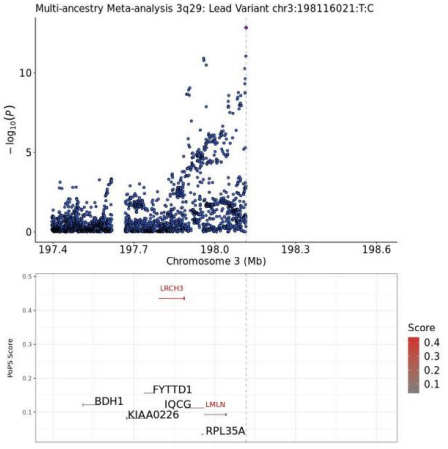

Multi-ancestry Meta-analysis 3q21.3: Lead Variant chr3:128496978:G:A
Chromosome 3 (Mb)
PheWAS Score
Score
GATA2
RPN1
RUVBL1
SEC61A1
EEFSEC
CNBP
ISY1
RAB7A
ACAD9
RAB43
C3orf27
EFCC1
DNAJB8

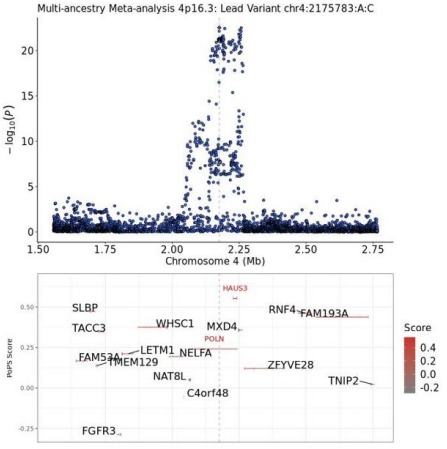

Multi-ancestry Meta-analysis 3q22.1: Lead Variant chr3:133638899:T:C
Chromosome 3 (Mb)
PWPS Score
Score
TOPBP1
CDV3
TMEM108
SRPRB
RAB6B
BFSP2
TF
SLCO2A1

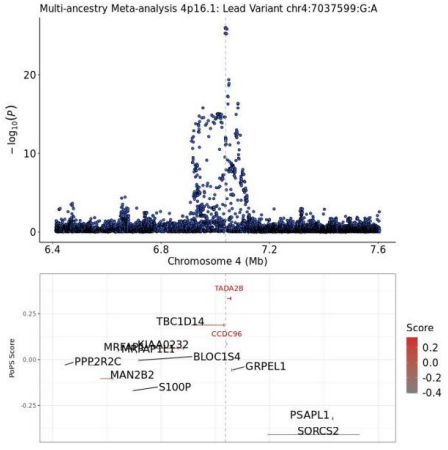

Multi-ancestry Meta-analysis 3q22.3: Lead Variant chr3:138525558:C:T
Chromosome 3 (Mb)
PWPS Score
Score
PIK3CB
ARMC8
DBR1
NME9
MRAS
CEP70
FAIM
DZIP1L
ESYT3
COPB2
CLDN18
A4GNT
C3orf72
FOXL2
PRR23A
MRPS22
PRR23C

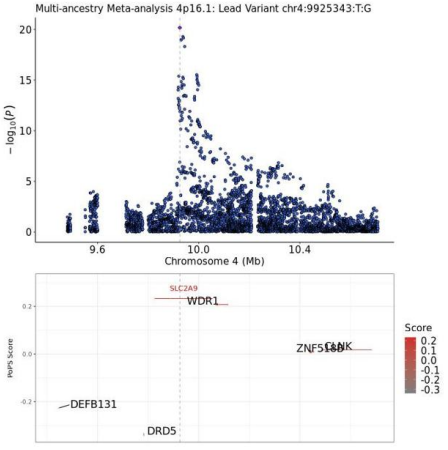

Multi-ancestry Meta-analysis 3q25.33: Lead Variant chr3:160442664:G:C
Chromosome 3 (Mb)
PWPS Score
Score
SMC4
IFT80
TRIM59
KPNA4
PPM1L
ARL14
B3GALNT1
IL12A
C3orf80

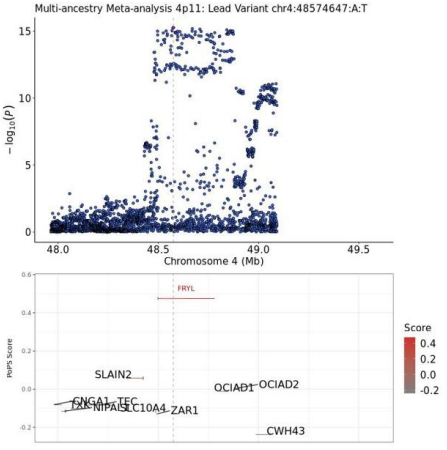

Multi-ancestry Meta-analysis 3q26.2: Lead Variant chr3:169764547:T:C
Chromosome 3 (Mb)
PWPS Score
Score
MECOM
PHC3
SKIL
GPR160
PRKCI
CLDN11
MYNN
LRRC34
SEC62
SAMD7
SLC7A14
LRRIQ4
LRRC37B

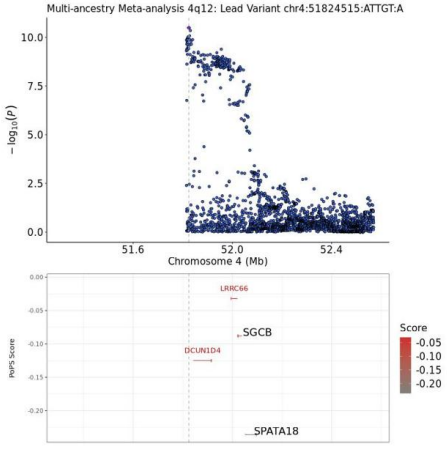

Multi-ancestry Meta-analysis 3q29: Lead Variant chr3:198116021:T:C
Chromosome 3 (Mb)
PWPS Score
Score
LRCH3
FYTTD1
BDH1
IQCG
LMLN
KIAA0226
RPL35A

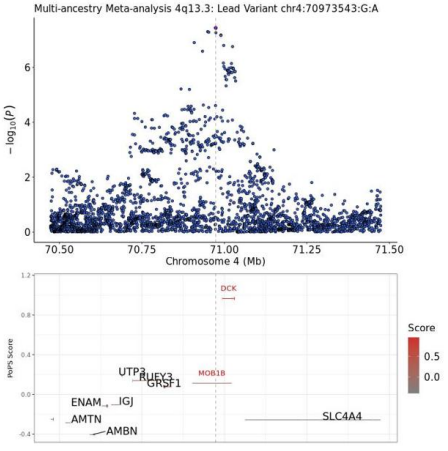

Multi-ancestry Meta-analysis 4p16.3: Lead Variant chr4:2175783:A:C
Chromosome 4 (Mb)
PWPS Score
Score
HAUS3
SLBP
RNF4
FAM193A
TACC3
WHSC1
MXD4
POLN
FAM53A
LETM1
NELFA
TMEM129
ZFYVE28
NAT8L
TNIP2
C4orf48
FGFR3

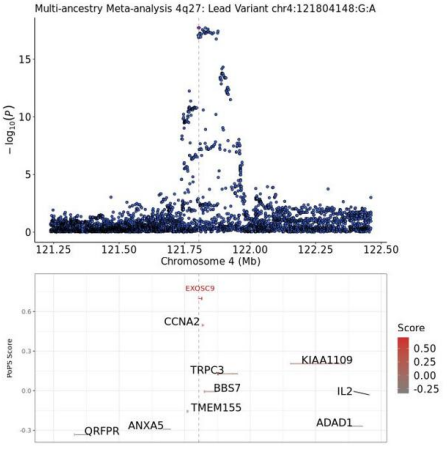

Multi-ancestry Meta-analysis 4p16.1: Lead Variant chr4:7037599:G:A
Chromosome 4 (Mb)
PWPS Score
Score
TADA2B
TBC1D14
MRPL4
KIAA0232
CCDC96
PPP2R2C
BLOC1S4
GRPEL1
MAN2B2
S100P
PSAPL1
SORCS2

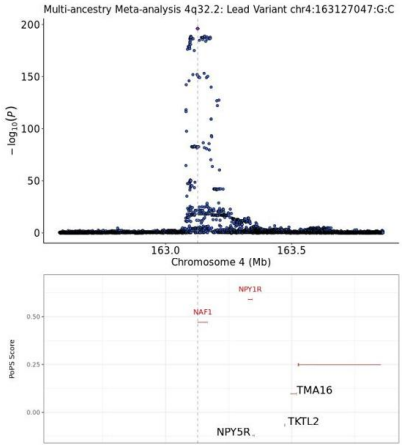

Multi-ancestry Meta-analysis 4p16.1: Lead Variant chr4:9925343:T:G
Chromosome 4 (Mb)
PWPS Score
Score
SLC2A9
WDR1
ZNF518B
DEFB131
DRD5

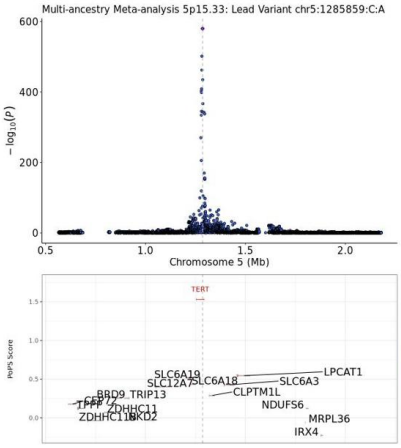

Multi-ancestry Meta-analysis 4p11: Lead Variant chr4:48574647:A:T
Chromosome 4 (Mb)
PWPS Score
Score
FRYL
SLAIN2
OCIAD1
OCIAD2
CNGA1
TEC
ZAR1
CWH43

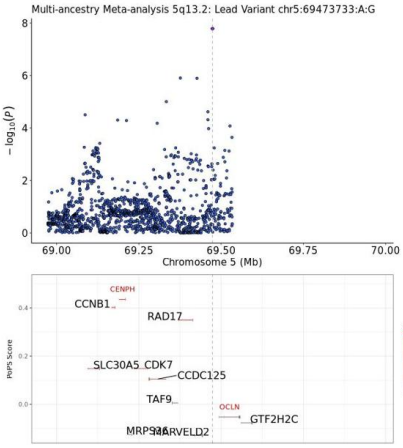

Multi-ancestry Meta-analysis 4q12: Lead Variant chr4:51824515:ATTGT:A
Chromosome 4 (Mb)
PWPS Score
Score
LRRC66
SGCB
DCUN1D4
SPATA18

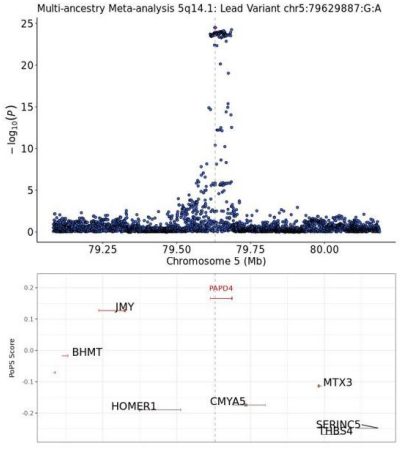

Multi-ancestry Meta-analysis 4q13.3: Lead Variant chr4:70973543:G:A
Chromosome 4 (Mb)
PWPS Score
Score
DCK
UTP3
RUVY3
GRSF1
MOB1B
ENAM
IGJ
AMTN
AMBN
SLC4A4

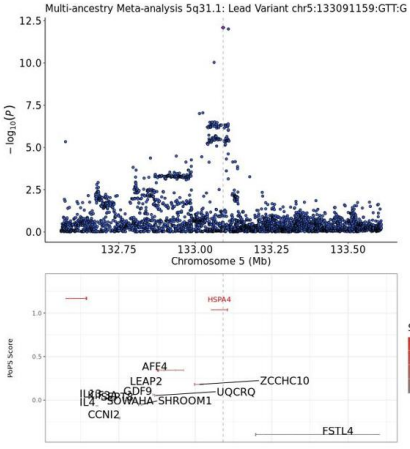

Multi-ancestry Meta-analysis 4q27: Lead Variant chr4:121804148:G:A
Chromosome 4 (Mb)
PWPS Score
Score
EXOSC9
CCNA2
KIAA1109
TRPC3
BBS7
IL2
TMEM155
ADAD1
QRFPR
ANXA5

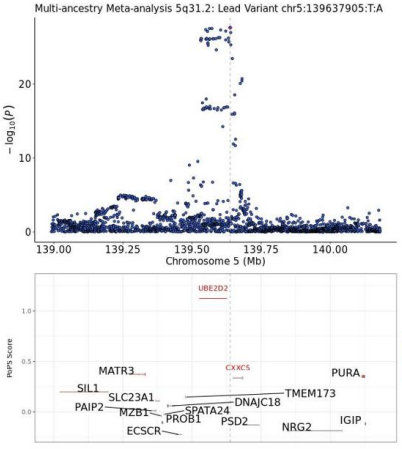

Multi-ancestry Meta-analysis 4q32.2: Lead Variant chr4:163127047:G:C
Chromosome 4 (Mb)
PWPS Score
Score
NPY1R
NAF1
TMA16
TKTL2
NPY5R

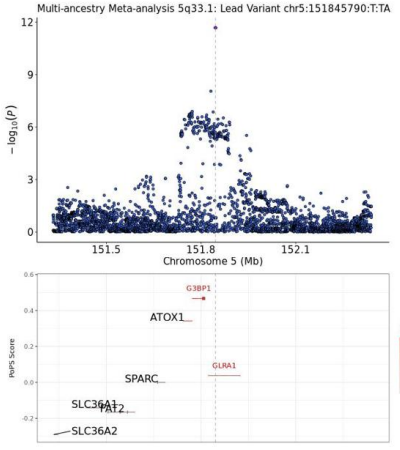

Multi-ancestry Meta-analysis 5p15.33: Lead Variant chr5:1285859:C:A
Chromosome 5 (Mb)
PWPS Score
Score
TERT
SLC6A19
SLC12A5
SLC6A18
SLC6A3
LPCAT1
CLPTM1L
NDUFS6
MRPL36
IRX4

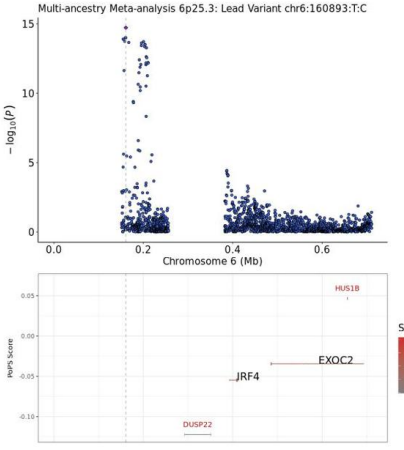

Multi-ancestry Meta-analysis 5q13.2: Lead Variant chr5:69473733:A:G
Chromosome 5 (Mb)
PWPS Score
Score
CENPH
CCNB1
RAD17
SLC30A5
CDK7
CCDC125
TAF9
OCLN
GTF2H2C
MRPS36
HARVELD2

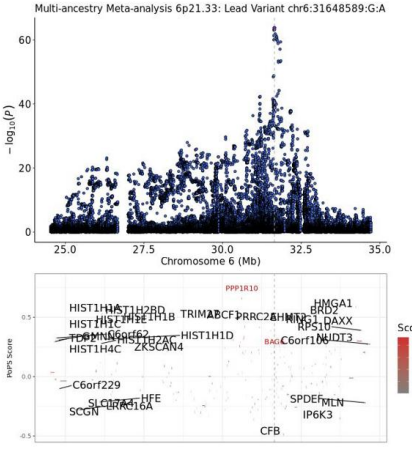

Multi-ancestry Meta-analysis 5q14.1: Lead Variant chr5:79629887:G:A
Chromosome 5 (Mb)
PWPS Score
Score
PAPD4
JMY
BHMT
MTX3
HOMER1
CMYA5
SERINC5
THBS4

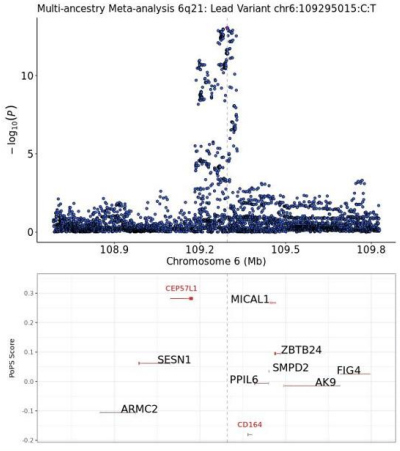

Multi-ancestry Meta-analysis 5q31.1: Lead Variant chr5:133091159:GTT:G
Chromosome 5 (Mb)
PWPS Score
Score
HSPA4
AFF4
LEAP2
ZCCHC10
GDF9
UQCRQ
SHROOM1
CCNI2
FSTL4

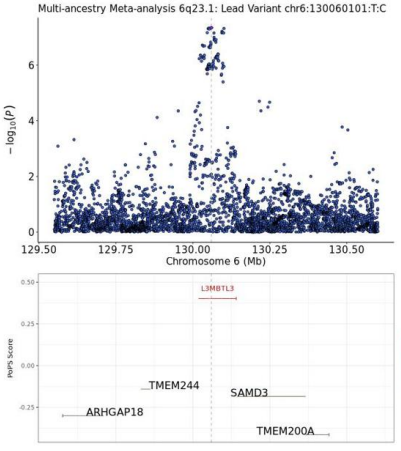

Multi-ancestry Meta-analysis 5q31.2: Lead Variant chr5:139637905:T:A
Chromosome 5 (Mb)
PWPS Score
Score
UBE2D2
CXXC5
MATR3
PURA
SIL1
SLC23A1
TMEM173
PAIP2
MZB1
SPATA24
DNAJC18
PROB1
PSD2
NRG2
IGIP
ECSCR

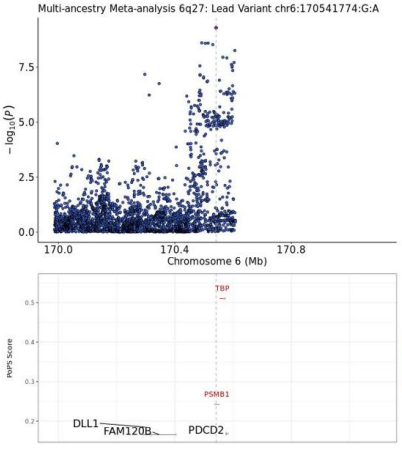

Multi-ancestry Meta-analysis 5q33.1: Lead Variant chr5:151845790:T:TA
Chromosome 5 (Mb)
PWPS Score
Score
G3BP1
ATOX1
GLRA1
SPARC
SLC36A1
PAT2
SLC36A2

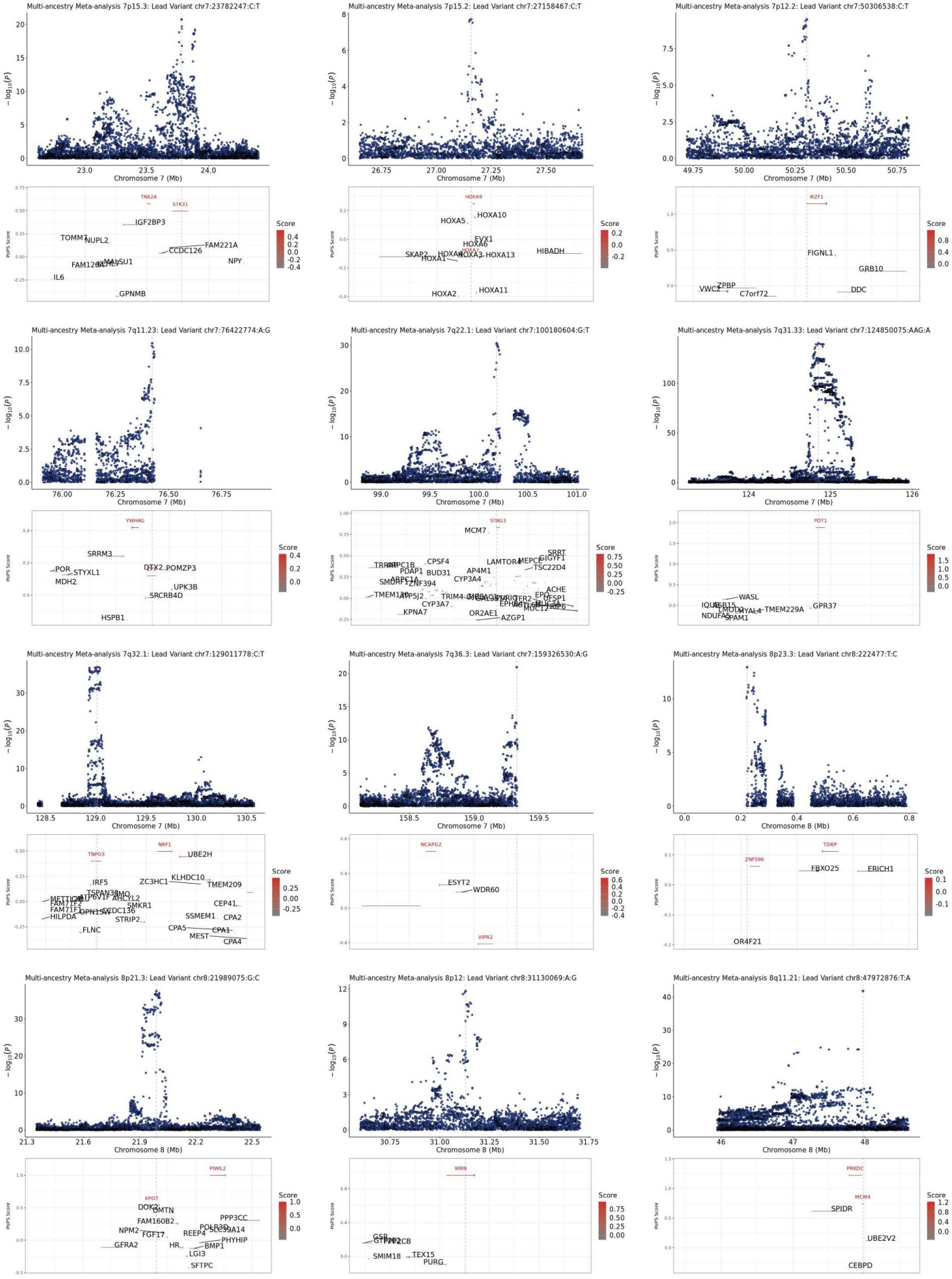

Multi-ancestry Meta-analysis 6p25.3: Lead Variant chr6:160893:T:C
Chromosome 6 (Mb)
PWPS Score
Score
HUS1B
EXOC2
JRF4
DUSP22

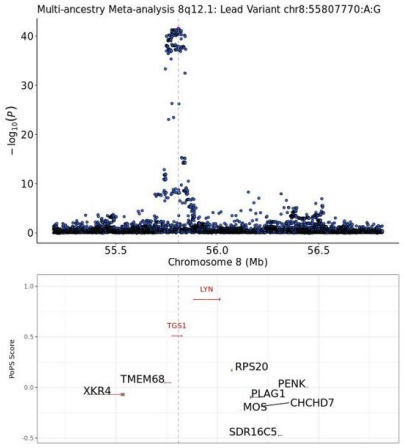

Multi-ancestry Meta-analysis 6p21.33: Lead Variant chr6:31648589:G:A
Chromosome 6 (Mb)
PWPS Score
Score
PPP1R10
HMGA1
BRD2
DAXX
RPS10
NUDT3
C6orf106
HIST1H1D
ZKSCAN4
C6orf229
HFE
SCGN
SPDEF
MLN
IP6K3
CFB

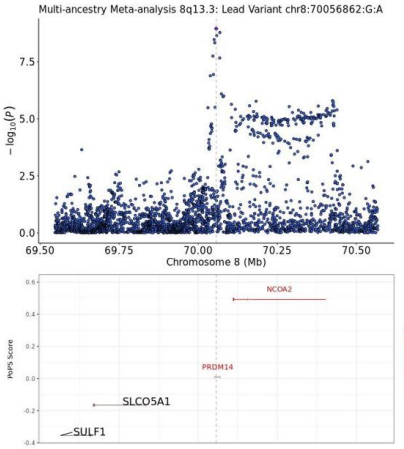

Multi-ancestry Meta-analysis 6q21: Lead Variant chr6:109295015:C:T
Chromosome 6 (Mb)
PWPS Score
Score
CEP57L1
MICAL1
ZBTB24
SESN1
SMPD2
FIG4
PPIL6
AK9
ARMC2
CD164

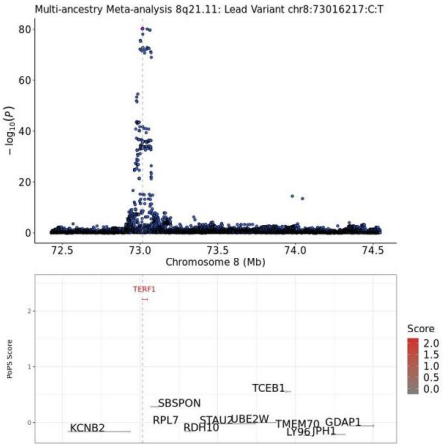

Multi-ancestry Meta-analysis 6q23.1: Lead Variant chr6:130060101:T:C
Chromosome 6 (Mb)
PWPS Score
Score
L3MBTL3
TMEM244
SAMD3
ARHGAP18
TMEM200A

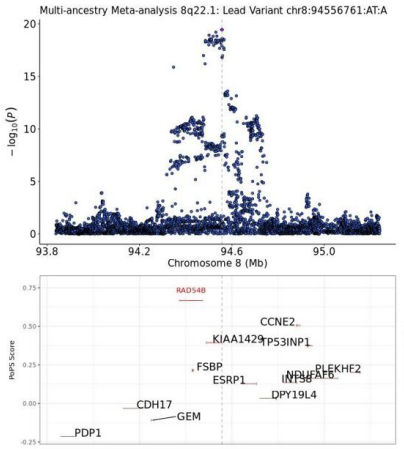

Multi-ancestry Meta-analysis 6q27: Lead Variant chr6:170541774:G:A
Chromosome 6 (Mb)
PWPS Score
Score
TBP
PSMB1
DLL1
FAM120B
PDCD2

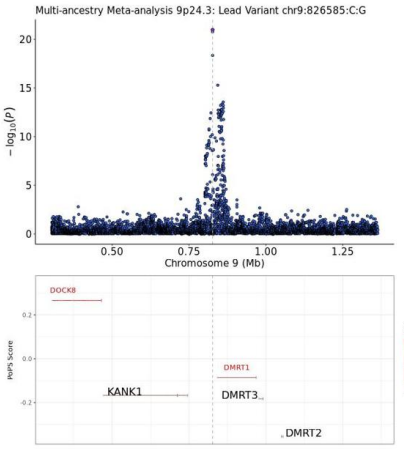

Multi-ancestry Meta-analysis 7p15.3: Lead Variant chr7:23782247:C:T
Multi-ancestry Meta-analysis 7p15.2: Lead Variant chr7:27158467:C:T
Multi-ancestry Meta-analysis 7p12.2: Lead Variant chr7:50306538:C:T
Multi-ancestry Meta-analysis 7q11.23: Lead Variant chr7:76422774:A:G
Multi-ancestry Meta-analysis 7q22.1: Lead Variant chr7:100180604:G:T
Multi-ancestry Meta-analysis 7q31.33: Lead Variant chr7:124850075:AAG:A
Multi-ancestry Meta-analysis 7q32.1: Lead Variant chr7:129011778:C:T
Multi-ancestry Meta-analysis 7q36.3: Lead Variant chr7:159326530:A:G
Multi-ancestry Meta-analysis 8p23.3: Lead Variant chr8:222477:T:C
Multi-ancestry Meta-analysis 8p21.3: Lead Variant chr8:21989075:G:C
Multi-ancestry Meta-analysis 8p12: Lead Variant chr8:31130069:A:G
Multi-ancestry Meta-analysis 8q11.21: Lead Variant chr8:47972876:T:A
− log10(P)
Chromosome 7 (Mb)
Chromosome 8 (Mb)
PoPS Score
Score

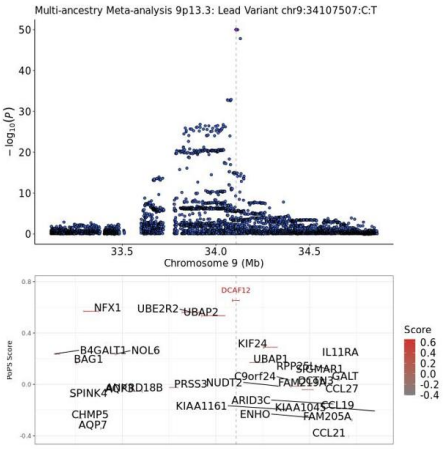

Multi-ancestry Meta-analysis 8q12.1: Lead Variant chr8:55807770:A:G
Chromosome 8 (Mb)
PoPS Score
Score
LYN
TGS1
RPS20
PENK
TMEM68
XKR4
PLAG1
CHCHD7
MOS
SDR16C5

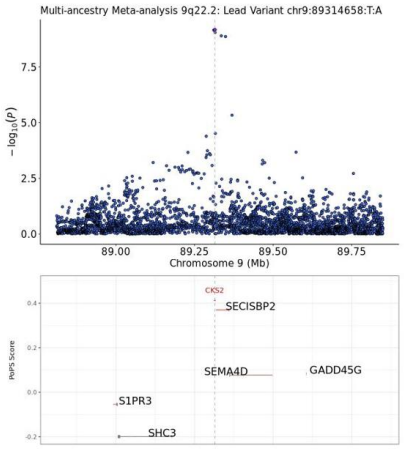

Multi-ancestry Meta-analysis 8q13.3: Lead Variant chr8:70056862:G:A
Chromosome 8 (Mb)
PoPS Score
Score
NCOA2
PRDM14
SLCO5A1
SULF1

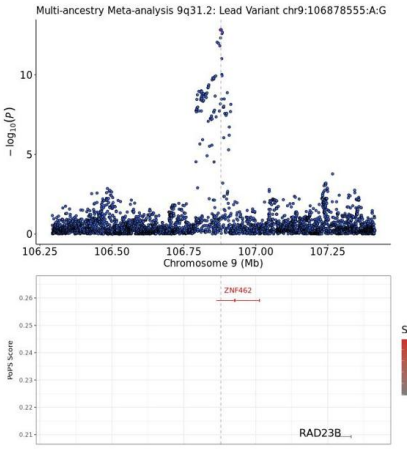

Multi-ancestry Meta-analysis 8q21.11: Lead Variant chr8:73016217:C:T
Chromosome 8 (Mb)
PoPS Score
Score
TERF1
TCEB1
SBSPON
RPL7
STAU2
UBE2W
TMEM70
GDAP1
KCNB2
RDH10
LY96
PH1

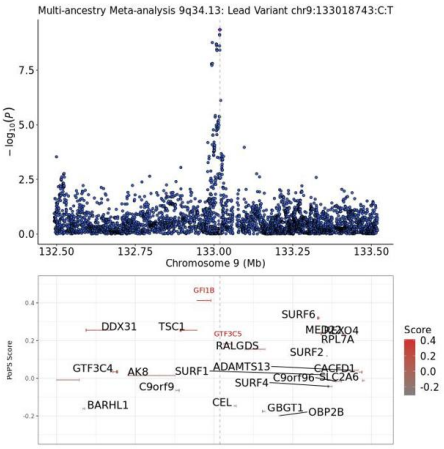

Multi-ancestry Meta-analysis 8q22.1: Lead Variant chr8:94556761:AT:A
Chromosome 8 (Mb)
PoPS Score
Score
RAD54B
CCNE2
KIAA1429
TP53INP1
FSBP
PLEKHF2
ESRP1
NPLOC4
AFAP6
INTS8
DPY19L4
CDH17
GEM
PDP1

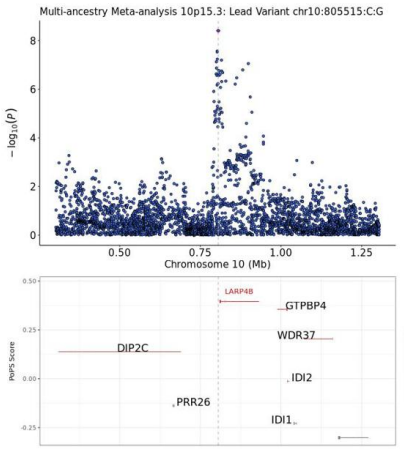

Multi-ancestry Meta-analysis 9p24.3: Lead Variant chr9:826585:C:G
Chromosome 9 (Mb)
PoPS Score
Score
DOCK8
DMRT1
KANK1
DMRT3
DMRT2

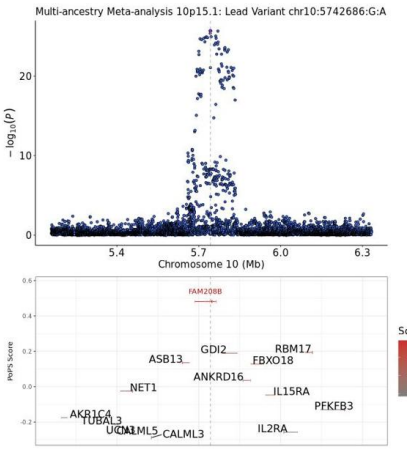

Multi-ancestry Meta-analysis 9p13.3: Lead Variant chr9:34107507:C:T
Chromosome 9 (Mb)
PoPS Score
Score
DCAF12
NFX1
UBE2R2
UBAP2
KIF24
B4GALT1
NOL6
BAG1
UBAP1
IL11RA
C9orf24
SPINK4
PRSS3
NUDT2
CCL27
ARID3C
KIAA1161
ENHO
CCL19
FAM205A
CHMP5
AQP7
CCL21

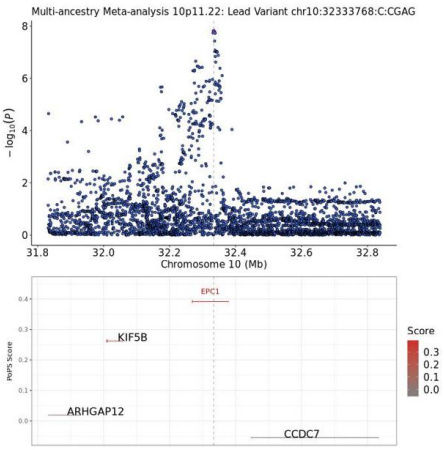

Multi-ancestry Meta-analysis 9q22.2: Lead Variant chr9:89314658:T:A
Chromosome 9 (Mb)
PoPS Score
Score
CKS2
SECISBP2
SEMA4D
GADD45G
S1PR3
SHC3

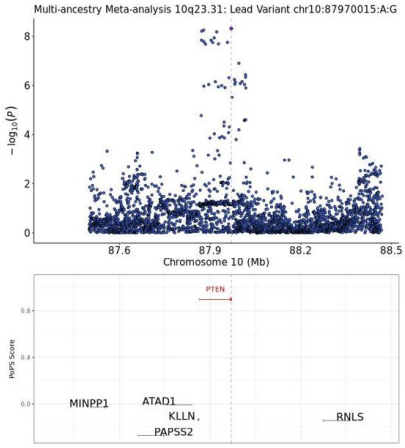

Multi-ancestry Meta-analysis 9q31.2: Lead Variant chr9:106878555:A:G
Chromosome 9 (Mb)
PoPS Score
Score
ZNF462
RAD23B

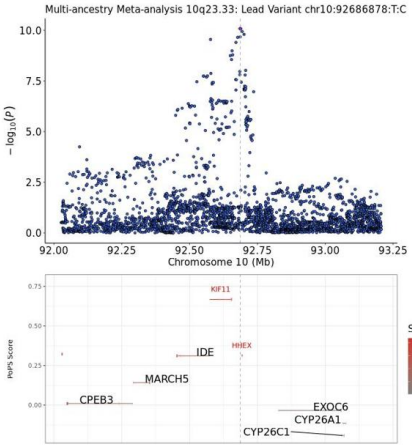

Multi-ancestry Meta-analysis 9q34.13: Lead Variant chr9:133018743:C:T
Chromosome 9 (Mb)
PoPS Score
Score
GFI1B
SURF6
DDX31
TSC1
GTF3C5
RALGDS
SURF2
GTF3C4
AK8
SURF1
ADAMTS13
CACFD1
C9orf9
SURF4
C9orf96
SLC2A6
BARHL1
CEL
GBGT1
OBP2B

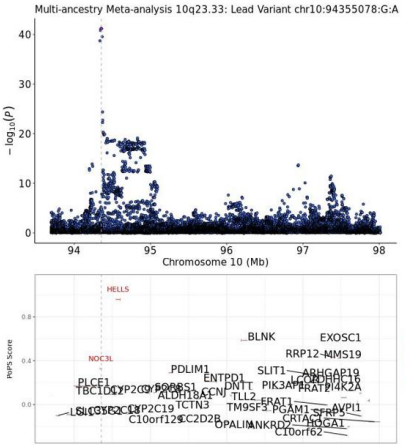

Multi-ancestry Meta-analysis 10p15.3: Lead Variant chr10:805515:C:G
Chromosome 10 (Mb)
PoPS Score
Score
LARP4B
GTPBP4
WDR37
DIP2C
IDI2
PRR26
IDI1

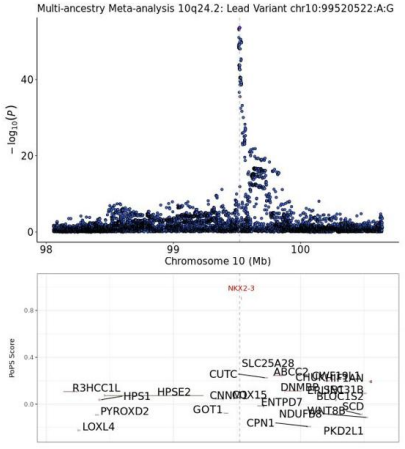

Multi-ancestry Meta-analysis 10p15.1: Lead Variant chr10:5742686:G:A
Chromosome 10 (Mb)
PoPS Score
Score
FAM208B
ASB13
GDI2
RBM17
FBXO18
ANKRD16
NET1
IL15RA
PFKFB3
AKR1C4
TUBAL3
CALML5
CALML3
IL2RA

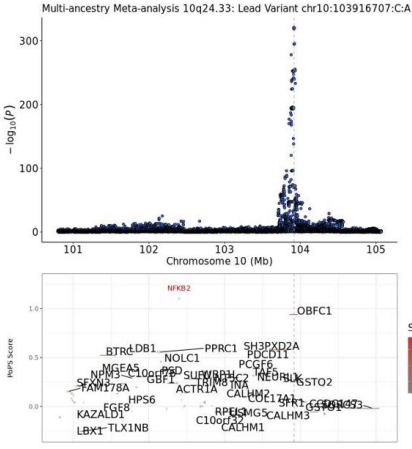

Multi-ancestry Meta-analysis 10p11.22: Lead Variant chr10:32333768:C:CGAG
Chromosome 10 (Mb)
PoPS Score
Score
EPC1
KIF5B
ARHGAP12
CCDC7

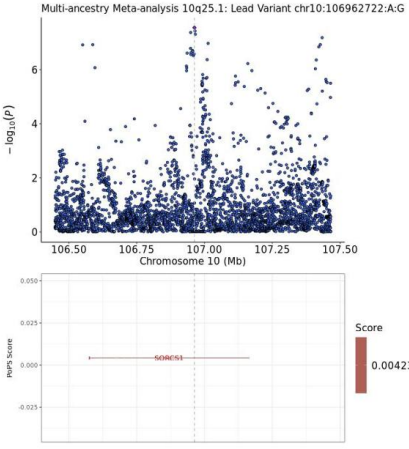

Multi-ancestry Meta-analysis 10q23.31: Lead Variant chr10:87970015:A:G
Chromosome 10 (Mb)
PtrPS Score
Score
PTEN
MINPP1
ATAD1
KLLN
PAPSS2
RNLS

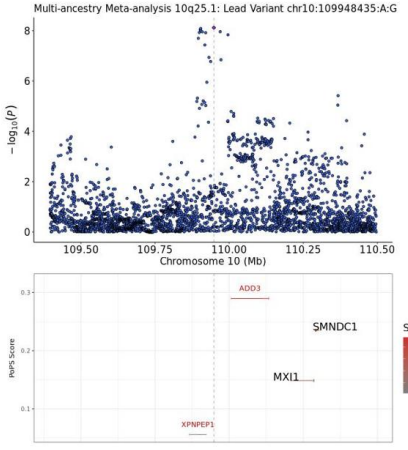

Multi-ancestry Meta-analysis 10q23.33: Lead Variant chr10:92686878:T:C
Chromosome 10 (Mb)
PtrPS Score
Score
KIF11
IDE
HHEX
MARCH5
CPEB3
EXOC6
CYP26A1
CYP26C1

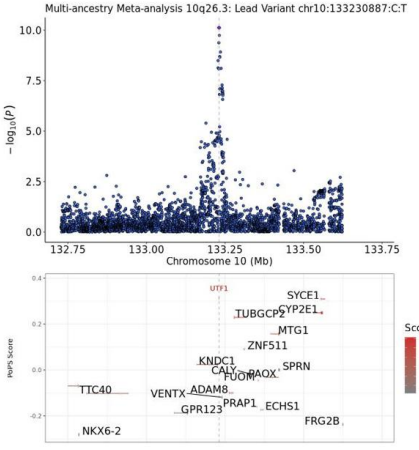

Multi-ancestry Meta-analysis 10q23.33: Lead Variant chr10:94355078:G:A
Chromosome 10 (Mb)
PtrPS Score
Score
HELLS
NOC3L
BLNK
EXOSC1
RRP12
MMS19
PDLIM1
SLIT1
ARHGAP19
PLCE1
ENTPD1
DNTT
PIK3AP1
TBC1D12
ALDH18A1
TLL2
ERAL1
TCTN3
TM9SF3
PGAM1
AVPI1
C10orf125
SCC2D2B
OPALIN
ANKRD2
C10orf62

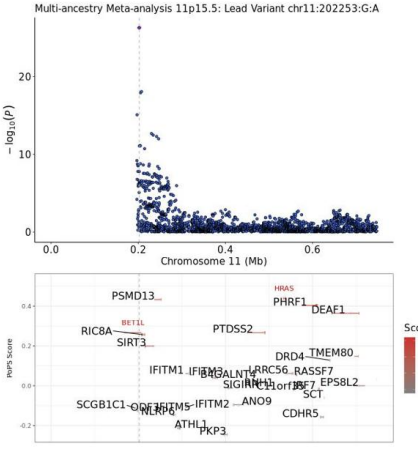

Multi-ancestry Meta-analysis 10q24.2: Lead Variant chr10:99520522:A:G
Chromosome 10 (Mb)
PtrPS Score
Score
NKX2-3
SLC25A28
CUTC
R3HCC1L
HPS1
HPSE2
CNNM2
GDX15
ENTPD7
PYROXD2
GOT1
NDUFB8
LOXL4
CPN1
PKD2L1

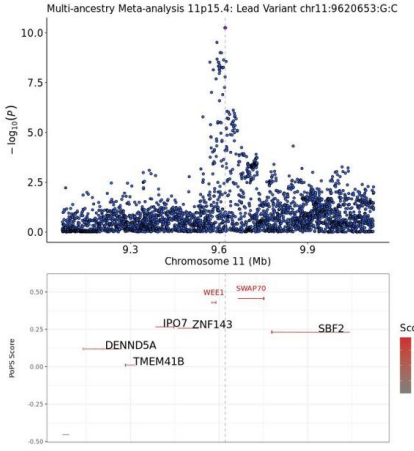

Multi-ancestry Meta-analysis 10q24.33: Lead Variant chr10:103916707:C:A
Chromosome 10 (Mb)
PtrPS Score
Score
NFKB2
OBFC1
BTRC
LDB1
PPRC1
SH3PXD2A
NOLC1
PCGF6
MGEA5
GBF1
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TLX1NB
CALHM1
CALHM3

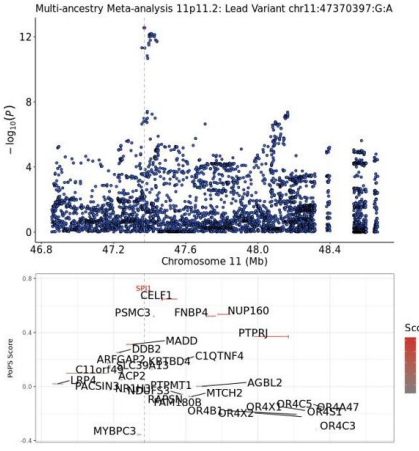

Multi-ancestry Meta-analysis 10q25.1: Lead Variant chr10:106962722:A:G
Chromosome 10 (Mb)
PtrPS Score
Score
SORCS1
0.004230036

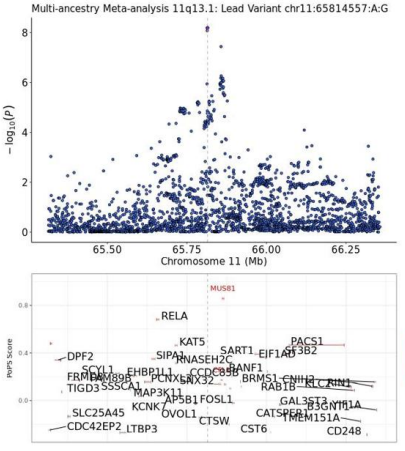

Multi-ancestry Meta-analysis 10q25.1: Lead Variant chr10:109948435:A:G
Chromosome 10 (Mb)
PtrPS Score
Score
ADD3
SMNDC1
MXI1
XPNPEP1

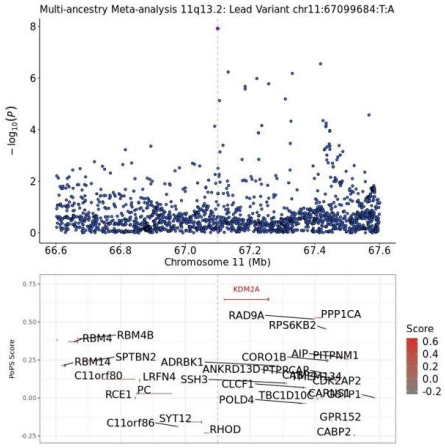

Multi-ancestry Meta-analysis 10q26.3: Lead Variant chr10:133230887:C:T
Chromosome 10 (Mb)
PtrPS Score
Score
UTF1
SYCE1
TUBGCP2
CYP2E1
MTG1
ZNF511
KNDC1
CALU
RAOX
SPRN
FUOM
TTC40
VENTX
ADAM8
PRAP1
ECHS1
GPR123
FRG2B
NKX6-2

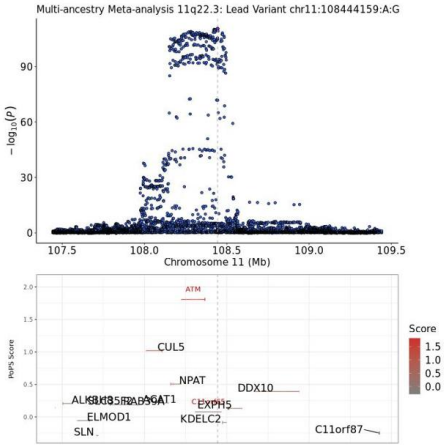

Multi-ancestry Meta-analysis 11p15.5: Lead Variant chr11:202253:G:A
Chromosome 11 (Mb)
PtrPS Score
Score
HRAS
PSMD13
PHRF1
DEAF1
BET1L
RIC8A
PTDSS2
SIRT3
DRD4
TMEM80
IFITM1
IFITM3
LRRC56
RASSF7
SIGIRR
EPS8L2
SCT
SCGB1C1
IFITM2
ANO9
CDHR5
NLRP6
ATHL1
TKP3

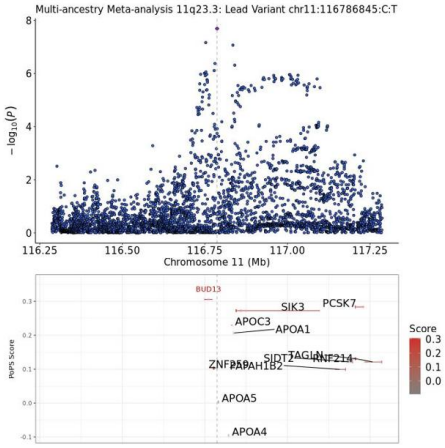

Multi-ancestry Meta-analysis 11p15.4: Lead Variant chr11:9620653:G:C
Chromosome 11 (Mb)
PtrPS Score
Score
WEE1
SWAP70
IPO7
ZNF143
SBF2
DENND5A
TMEM41B

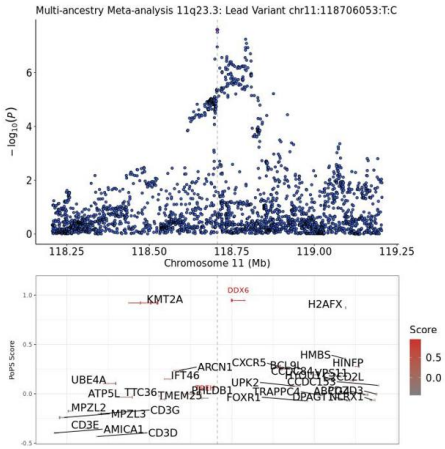

Multi-ancestry Meta-analysis 11p11.2: Lead Variant chr11:47370397:G:A
Chromosome 11 (Mb)
PtrPS Score
Score
SPI1
CELF1
PSMC3
FNBP4
NUP160
PTPRJ
MADD
DDB2
ARFGAP2
KBTBD4
C1QTNF4
C11orf49
ZNF259
ACP2
LRP4
PACSIN3
PPTMT1
AGBL2
MTCH2
OR4X1
OR4C5
OR4A47
OR4B1
OR4X2
OR4S1
OR4C3
MYBPC3

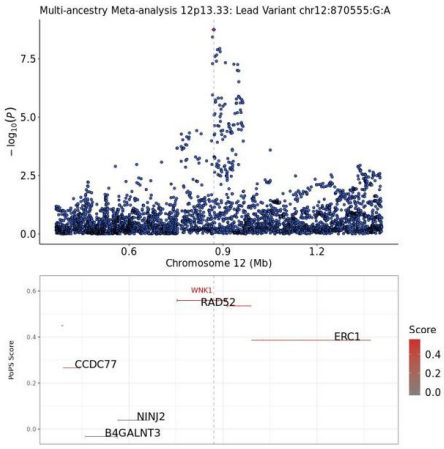

Multi-ancestry Meta-analysis 11q13.1: Lead Variant chr11:65814557:A:G
Chromosome 11 (Mb)
PtrPS Score
Score
MUS81
RELA
KAT5
PACS1
SART1
SIPA1
RNASEH2C
EIF1AD
DPF2
SCYL1
RANBP9
RANBP10
RANBP2
RANF1
TIGD3
SSSCA1
MAP3K11
AP5B1
FOSL1
GAL3ST3
KCNK7
OVOL1
CATSPER3
SLC25A45
CTSW
CST6
TMEM151A
CDC42EP2
LTBP3
CD248

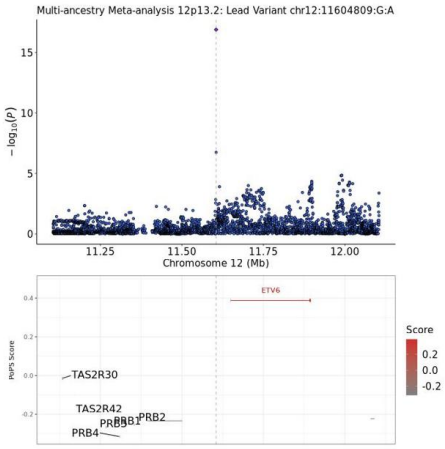

Multi-ancestry Meta-analysis 11q13.2: Lead Variant chr11:67099684:T:A
Chromosome 11 (Mb)
PoPS Score
Score

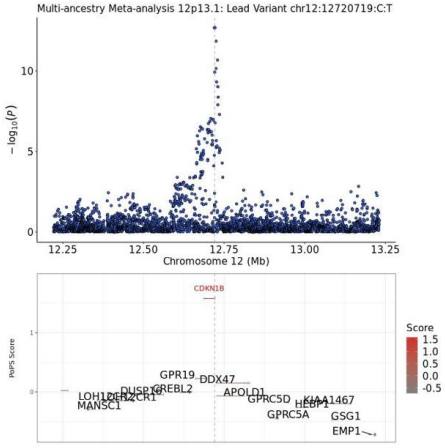

Multi-ancestry Meta-analysis 11q22.3: Lead Variant chr11:108444159:A:G
Chromosome 11 (Mb)
PoPS Score
Score

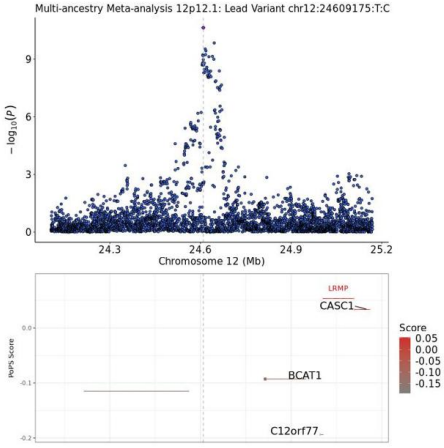

Multi-ancestry Meta-analysis 11q23.3: Lead Variant chr11:116786845:C:T
Chromosome 11 (Mb)
PoPS Score
Score

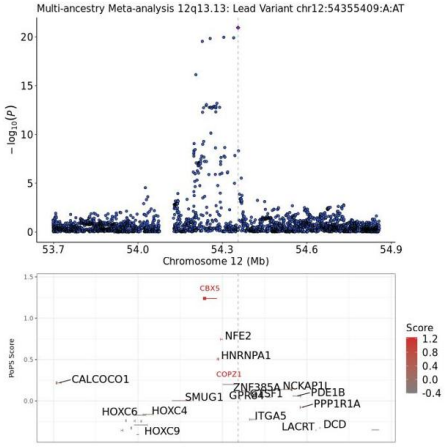

Multi-ancestry Meta-analysis 11q23.3: Lead Variant chr11:118706053:T:C
Chromosome 11 (Mb)
PoPS Score
Score

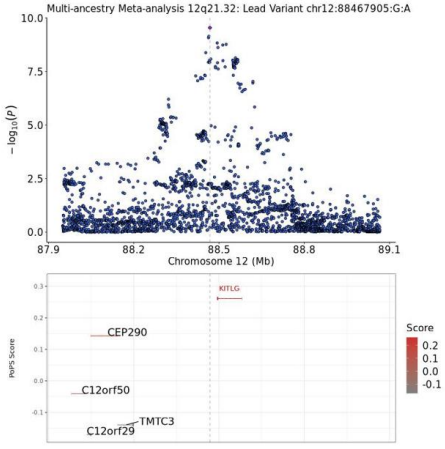

Multi-ancestry Meta-analysis 12p13.33: Lead Variant chr12:870555:G:A
Chromosome 12 (Mb)
PoPS Score
Score

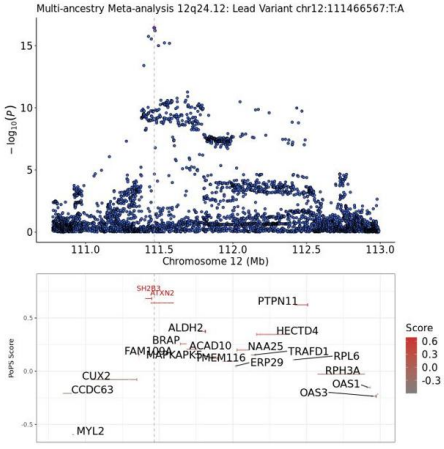

Multi-ancestry Meta-analysis 12p13.2: Lead Variant chr12:11604809:G:A
Chromosome 12 (Mb)
PoPS Score
Score

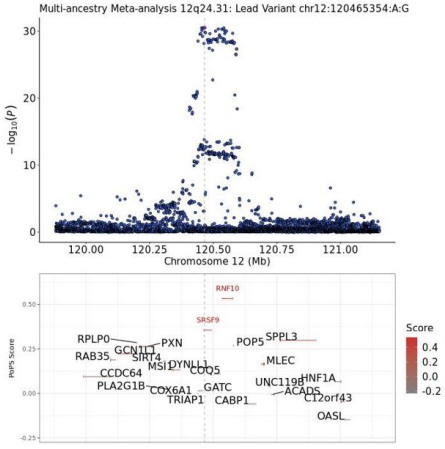

Multi-ancestry Meta-analysis 12p13.1: Lead Variant chr12:12720719:C:T
Chromosome 12 (Mb)
PoPS Score
Score

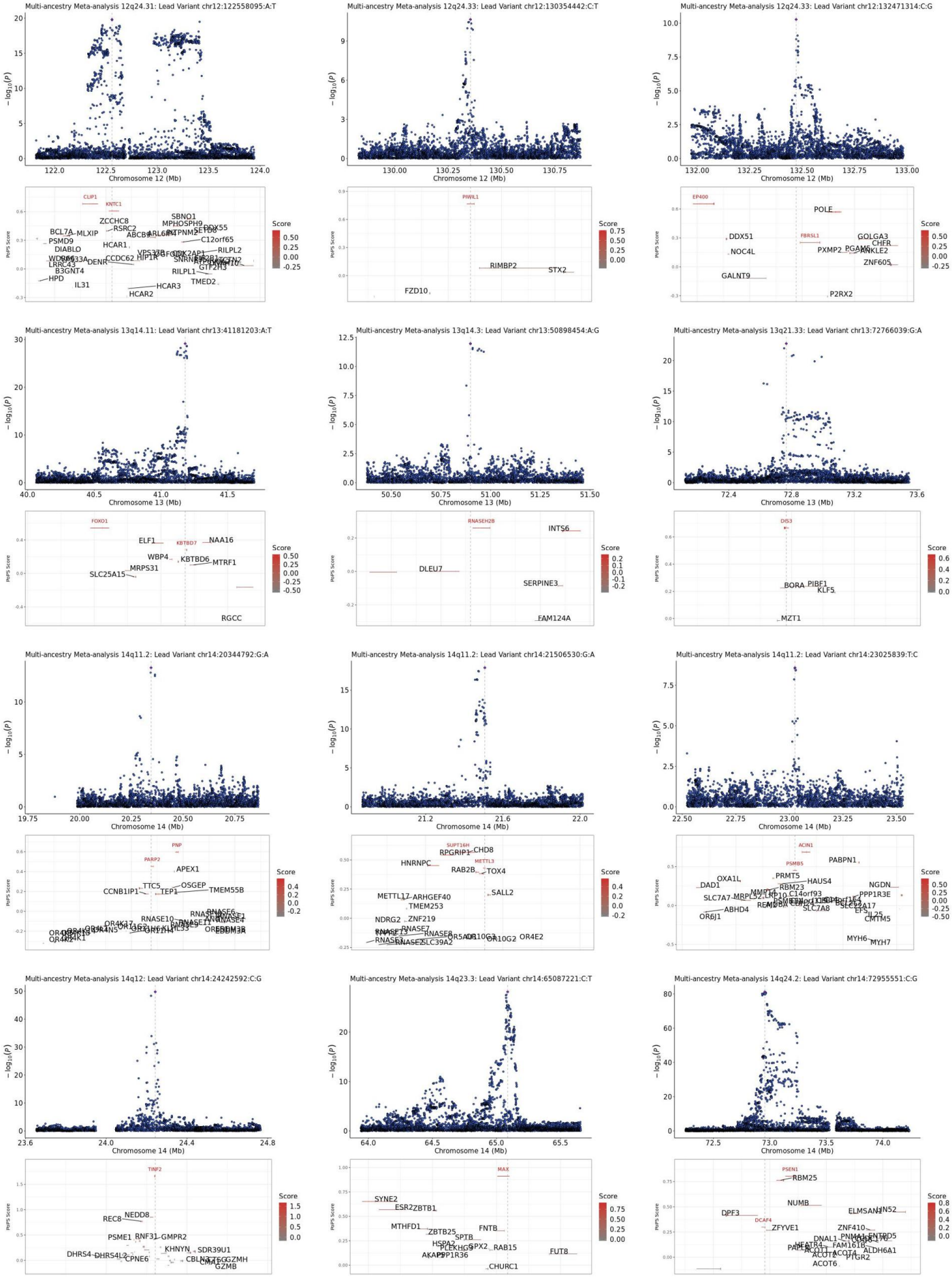

Multi-ancestry Meta-analysis 12p12.1: Lead Variant chr12:24609175:T:C
Chromosome 12 (Mb)
PoPS Score
Score

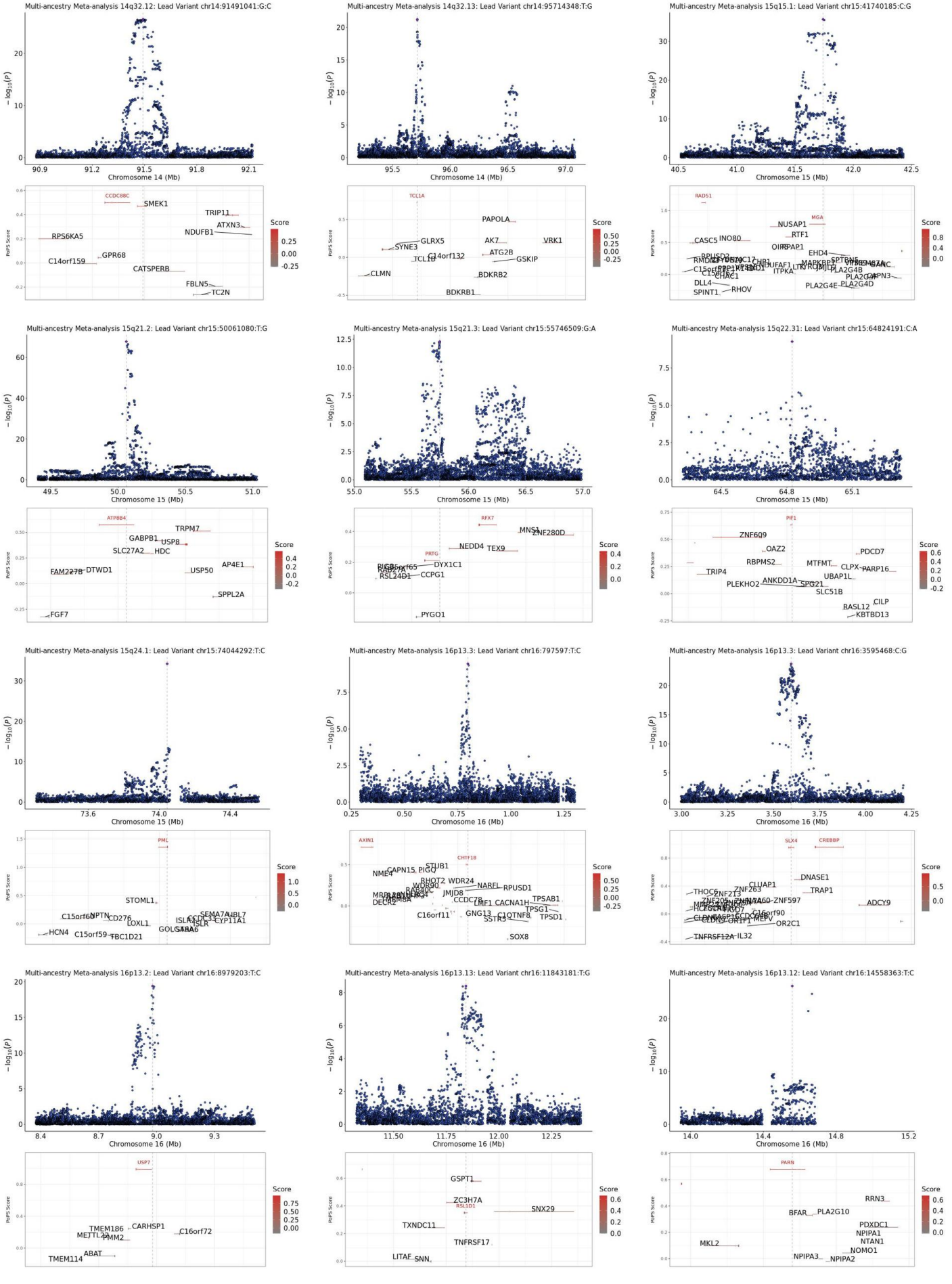

Multi-ancestry Meta-analysis 12q13.13: Lead Variant chr12:54355409:A:AT
Chromosome 12 (Mb)
PoPS Score
Score

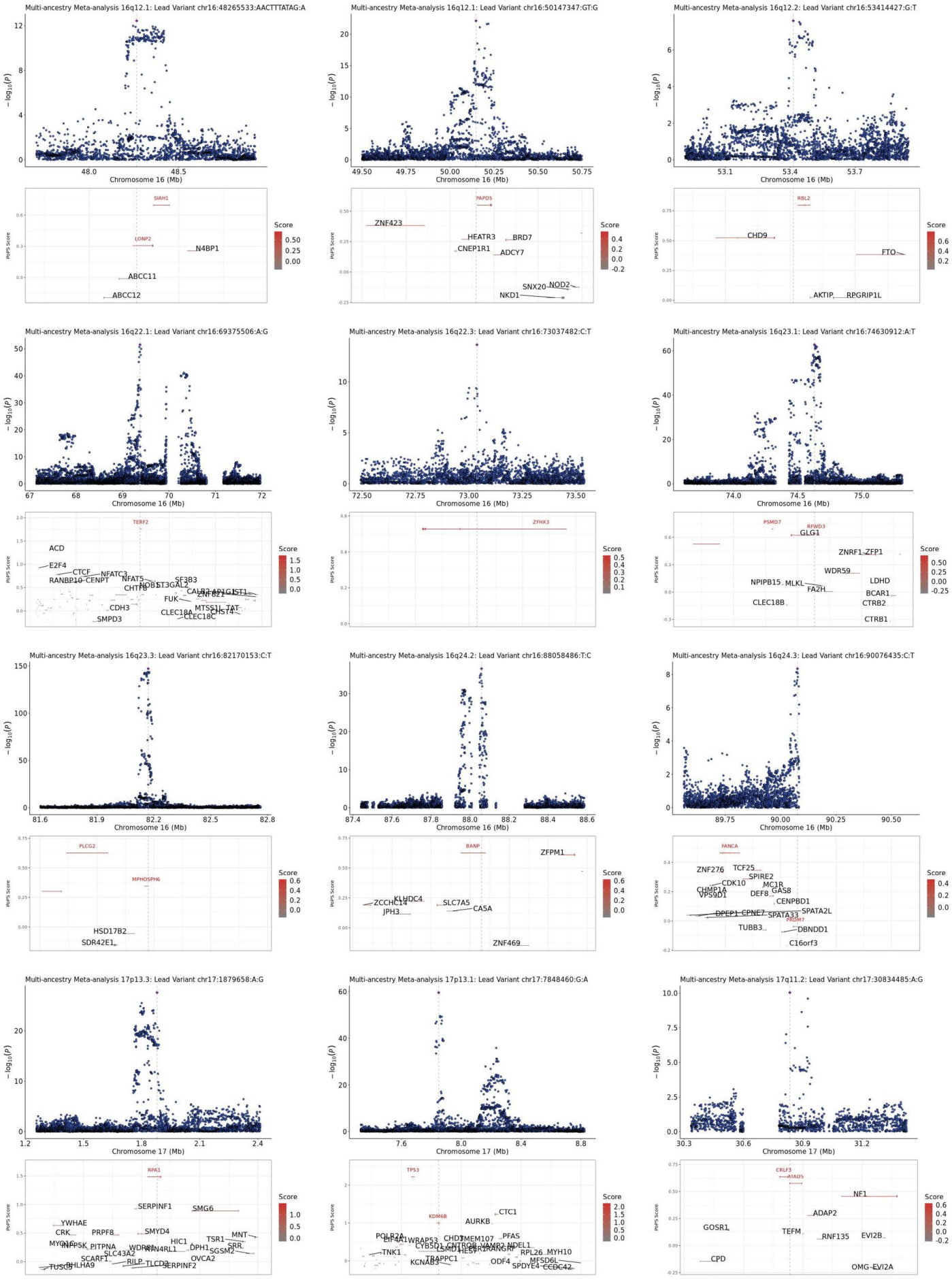

Multi-ancestry Meta-analysis 12q21.32: Lead Variant chr12:88467905:G:A
Chromosome 12 (Mb)
PoPS Score
Score

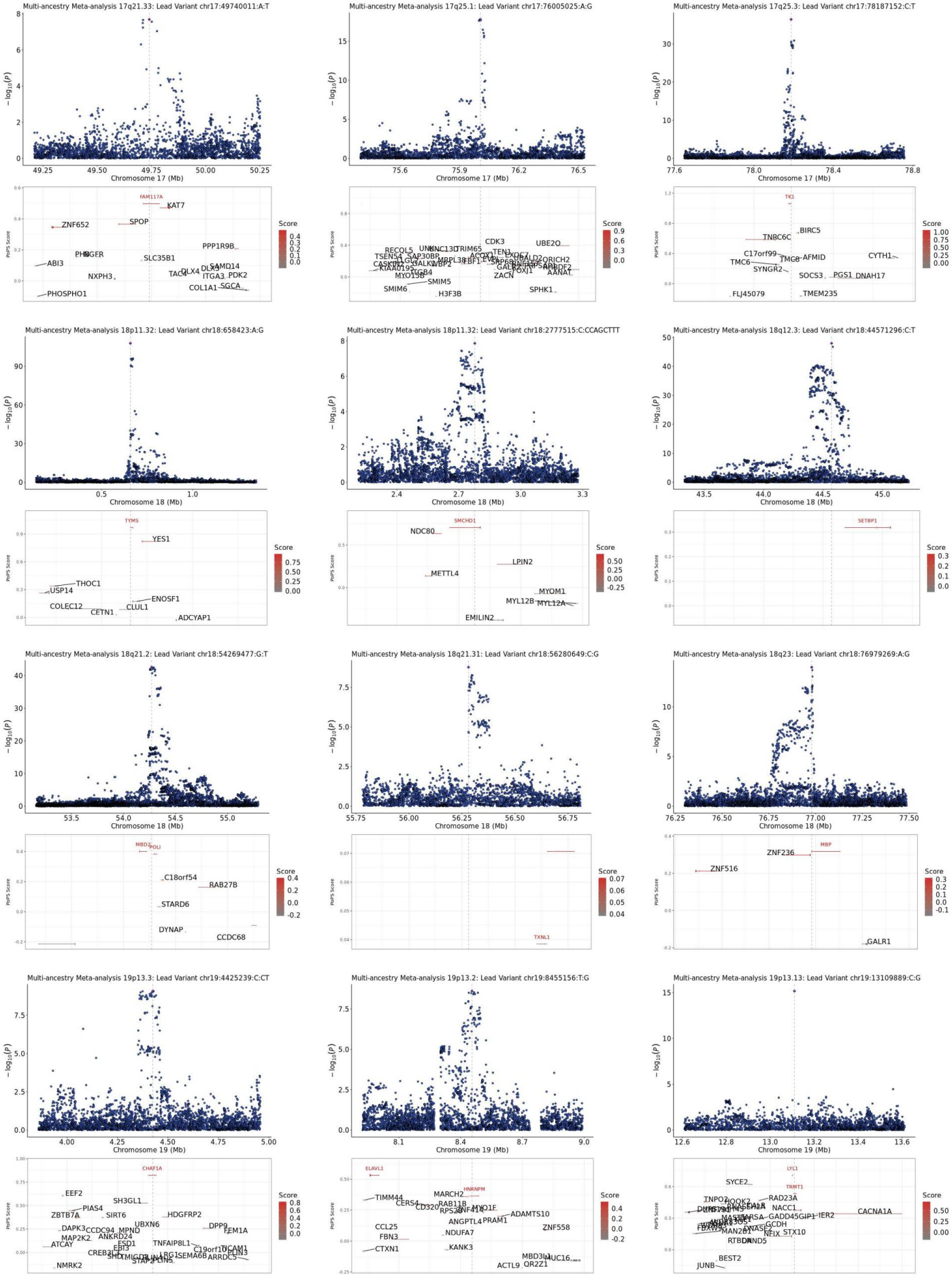

Multi-ancestry Meta-analysis 12q24.12: Lead Variant chr12:111466567:T:A
Chromosome 12 (Mb)
PoPS Score
Score

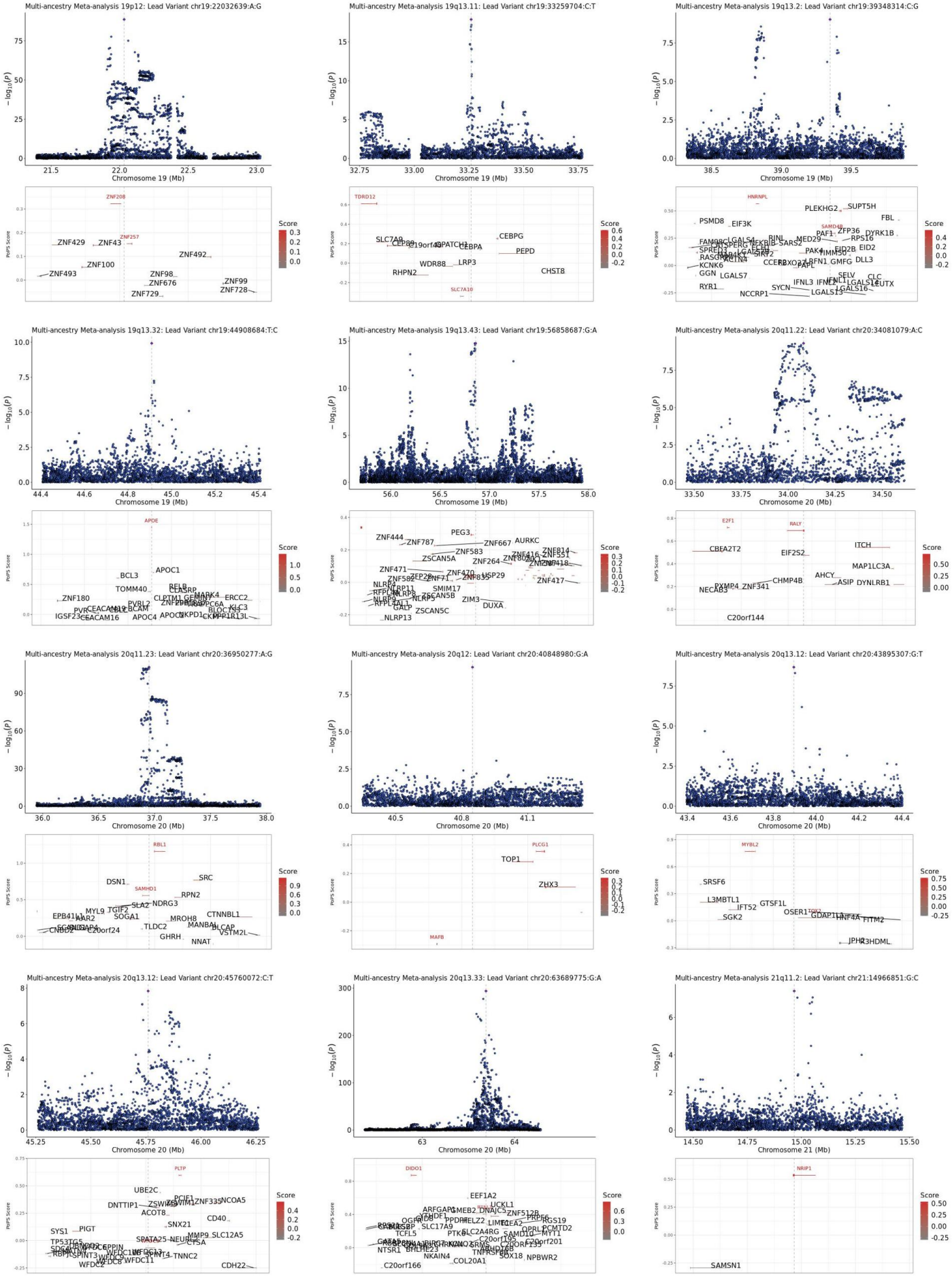

Multi-ancestry Meta-analysis 12q24.31: Lead Variant chr12:120465354:A:G
Chromosome 12 (Mb)
PoPS Score
Score

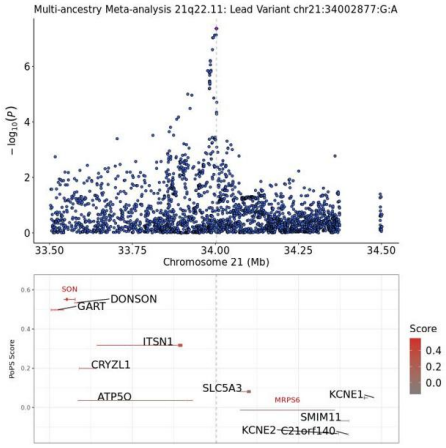

Multi-ancestry Meta-analysis 12q24.31: Lead Variant chr12:122558095:A:T
Multi-ancestry Meta-analysis 12q24.33: Lead Variant chr12:130354442:C:T
Multi-ancestry Meta-analysis 12q24.33: Lead Variant chr12:132471314:C:G
Multi-ancestry Meta-analysis 13q14.11: Lead Variant chr13:41181203:A:T
Multi-ancestry Meta-analysis 13q14.3: Lead Variant chr13:50898454:A:G
Multi-ancestry Meta-analysis 13q21.33: Lead Variant chr13:72766039:G:A
Multi-ancestry Meta-analysis 14q11.2: Lead Variant chr14:20344792:G:A
Multi-ancestry Meta-analysis 14q11.2: Lead Variant chr14:21506530:G:A
Multi-ancestry Meta-analysis 14q11.2: Lead Variant chr14:23025839:T:C
Multi-ancestry Meta-analysis 14q12: Lead Variant chr14:24242592:C:G
Multi-ancestry Meta-analysis 14q23.3: Lead Variant chr14:65087221:C:T
Multi-ancestry Meta-analysis 14q24.2: Lead Variant chr14:72955551:C:G
− log10(P)
Chromosome 12 (Mb)
Chromosome 13 (Mb)
Chromosome 14 (Mb)
PoPS Score
Score

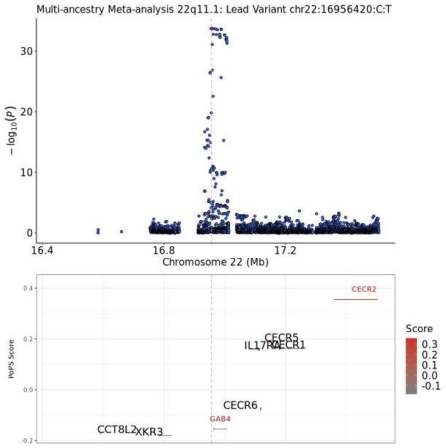

Multi-ancestry Meta-analysis 14q32.12: Lead Variant chr14:91491041:G:C
Multi-ancestry Meta-analysis 14q32.13: Lead Variant chr14:95714348:T:G
Multi-ancestry Meta-analysis 15q15.1: Lead Variant chr15:41740185:C:G
Multi-ancestry Meta-analysis 15q21.2: Lead Variant chr15:50061080:T:G
Multi-ancestry Meta-analysis 15q21.3: Lead Variant chr15:55746509:G:A
Multi-ancestry Meta-analysis 15q22.31: Lead Variant chr15:64824191:C:A
Multi-ancestry Meta-analysis 15q24.1: Lead Variant chr15:74044292:T:C
Multi-ancestry Meta-analysis 16p13.3: Lead Variant chr16:797597:T:C
Multi-ancestry Meta-analysis 16p13.3: Lead Variant chr16:3595468:C:G
Multi-ancestry Meta-analysis 16p13.2: Lead Variant chr16:8979203:T:C
Multi-ancestry Meta-analysis 16p13.13: Lead Variant chr16:11843181:T:G
Multi-ancestry Meta-analysis 16p13.12: Lead Variant chr16:14558363:T:C
Chromosome 14 (Mb)
Chromosome 15 (Mb)
Chromosome 16 (Mb)
PoPS Score
Score

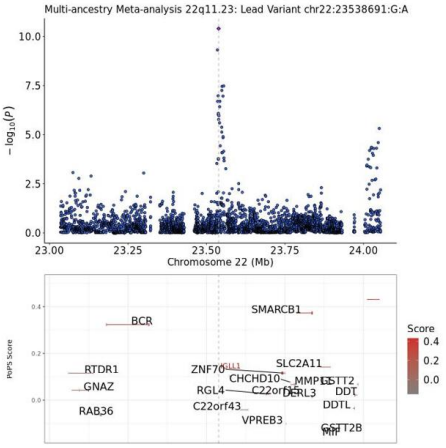

Multi-ancestry Meta-analysis 16q12.1: Lead Variant chr16:48265533:AACTTTATAG:A
Multi-ancestry Meta-analysis 16q12.1: Lead Variant chr16:50147347:GT:G
Multi-ancestry Meta-analysis 16q12.2: Lead Variant chr16:53414427:G:T
Multi-ancestry Meta-analysis 16q22.1: Lead Variant chr16:69375506:A:G
Multi-ancestry Meta-analysis 16q22.3: Lead Variant chr16:73037482:C:T
Multi-ancestry Meta-analysis 16q23.1: Lead Variant chr16:74630912:A:T
Multi-ancestry Meta-analysis 16q23.3: Lead Variant chr16:82170153:C:T
Multi-ancestry Meta-analysis 16q24.2: Lead Variant chr16:88058486:T:C
Multi-ancestry Meta-analysis 16q24.3: Lead Variant chr16:90076435:C:T
Multi-ancestry Meta-analysis 17p13.3: Lead Variant chr17:1879658:A:G
Multi-ancestry Meta-analysis 17p13.1: Lead Variant chr17:7848460:G:A
Multi-ancestry Meta-analysis 17q11.2: Lead Variant chr17:30834485:A:G
Chromosome 16 (Mb)
Chromosome 17 (Mb)
PoPS Score
Score

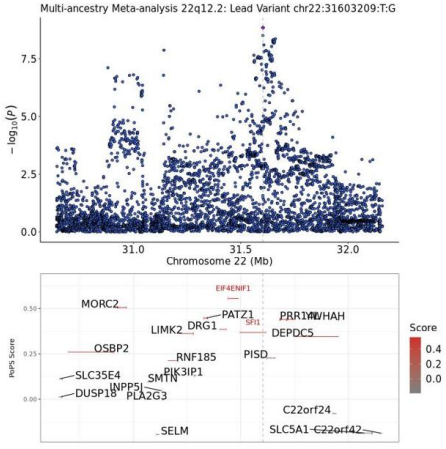

Multi-ancestry Meta-analysis 17q21.33: Lead Variant chr17:49740011:A:T
Chromosome 17 (Mb)
FAM117A
KAT7
ZNF652
SPOP
PPP1R9B
PHOSPHO1
ABI3
SLC35B1
NXPH3
DLX4
SAMD14
ITGA3
PDK2
COL1A1
SGCA
Score
Multi-ancestry Meta-analysis 17q25.1: Lead Variant chr17:76005025:A:G
Chromosome 17 (Mb)
CDK3
UBE2Q
SMIM6
H3F3B
SPHK1
ZACN
Score
Multi-ancestry Meta-analysis 17q25.3: Lead Variant chr17:78187152:C:T
Chromosome 17 (Mb)
TK1
BIRC5
TNRC6C
C17orf99
AFMID
CYTH1
TMC6
TMC8
SYNGR2
SOCS3
PGS1
DNAH17
FLJ45079
TMEM235
Score
Multi-ancestry Meta-analysis 18p11.32: Lead Variant chr18:658423:A:G
Chromosome 18 (Mb)
TYMS
YES1
THOC1
USP14
ENOSF1
COLEC12
CETN1
CLUL1
ADCYAP1
Score
Multi-ancestry Meta-analysis 18p11.32: Lead Variant chr18:2777515:C:CCAGCTTT
Chromosome 18 (Mb)
SMCHD1
NDC80
LPIN2
METTL4
MYOM1
MYL12B
MYL12A
EMILIN2
Score
Multi-ancestry Meta-analysis 18q12.3: Lead Variant chr18:44571296:C:T
Chromosome 18 (Mb)
SETBP1
Score
Multi-ancestry Meta-analysis 18q21.2: Lead Variant chr18:54269477:G:T
Chromosome 18 (Mb)
MBD2
POLI
C18orf54
RAB27B
STARD6
DYNAP
CCDC68
Score
Multi-ancestry Meta-analysis 18q21.31: Lead Variant chr18:56280649:C:G
Chromosome 18 (Mb)
TXNL1
Score
Multi-ancestry Meta-analysis 18q23: Lead Variant chr18:76979269:A:G
Chromosome 18 (Mb)
MBP
ZNF236
ZNF516
GALR1
Score
Multi-ancestry Meta-analysis 19p13.3: Lead Variant chr19:4425239:C:CT
Chromosome 19 (Mb)
CHAF1A
EEF2
SH3GL1
PIAS4
ZBTB7A
SIRT6
HDGFRP2
UBXN6
DAPK3
CCDC94
MPND
DPP9
FEM1A
MAP2K2
ANKRD24
ATCAY
ESD1
EPI3
TNFAIP8L1
C19orf10
ICAM1
CREB3L3
SEMA6B
ARRDC3
NMRK2
Score
Multi-ancestry Meta-analysis 19p13.2: Lead Variant chr19:8455156:T:G
Chromosome 19 (Mb)
ELAVL1
HNRNPM
TIMM44
MARCH2
CERS4
RAB11B
CD320
RPS26
MYO1F
ADAMTS10
ANGPTL4
PRAM1
ZNF558
CCL25
NDUFA7
FBN3
CTXN1
KANK3
MBD3L1
UC16
ACTL9
QR2Z1
Score
Multi-ancestry Meta-analysis 19p13.13: Lead Variant chr19:13109889:C:G
Chromosome 19 (Mb)
LYL1
TRMT1
SYCE2
TNPO2
HOOK2
RAD23A
NACC1
CACNA1A
IER2
GADD45GIP1
GCDH
NFIX
STX10
RTBDN
DND5
BEST2
JUNB
Score

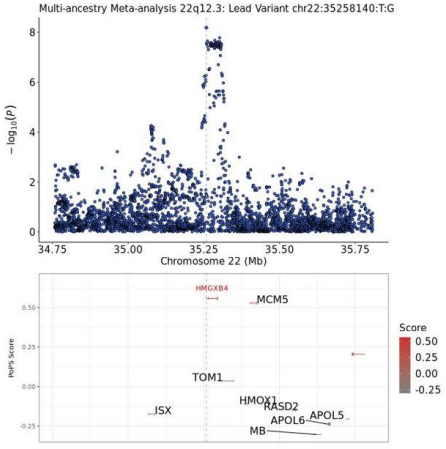

Multi-ancestry Meta-analysis 19p12: Lead Variant chr19:22032639:A:G
Multi-ancestry Meta-analysis 19q13.11: Lead Variant chr19:33259704:C:T
Multi-ancestry Meta-analysis 19q13.2: Lead Variant chr19:39348314:C:G
Multi-ancestry Meta-analysis 19q13.32: Lead Variant chr19:44908684:T:C
Multi-ancestry Meta-analysis 19q13.43: Lead Variant chr19:56858687:G:A
Multi-ancestry Meta-analysis 20q11.22: Lead Variant chr20:34081079:A:C
Multi-ancestry Meta-analysis 20q11.23: Lead Variant chr20:36950277:A:G
Multi-ancestry Meta-analysis 20q12: Lead Variant chr20:40848980:G:A
Multi-ancestry Meta-analysis 20q13.12: Lead Variant chr20:43895307:G:T
Multi-ancestry Meta-analysis 20q13.12: Lead Variant chr20:45760072:C:T
Multi-ancestry Meta-analysis 20q13.33: Lead Variant chr20:63689775:G:A
Multi-ancestry Meta-analysis 21q11.2: Lead Variant chr21:14966851:G:C
− log10(P)
Chromosome 19 (Mb)
Chromosome 20 (Mb)
Chromosome 21 (Mb)
PheWAS Score
Score

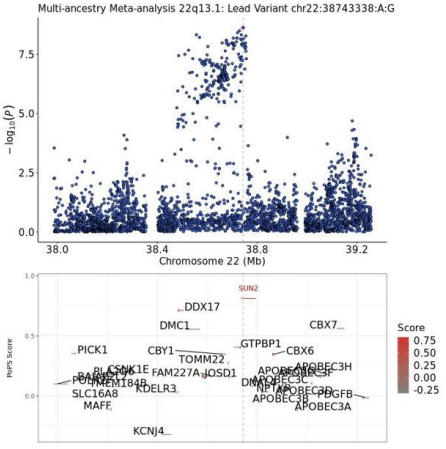

Multi-ancestry Meta-analysis 21q22.11: Lead Variant chr21:34002877:G:A
Chromosome 21 (Mb)
SON
GART
DONSON
ITSN1
CRYZL1
SLC5A3
ATP5O
MRPS6
KCNE1
SMIM11
KCNE2
C21orf140
Score

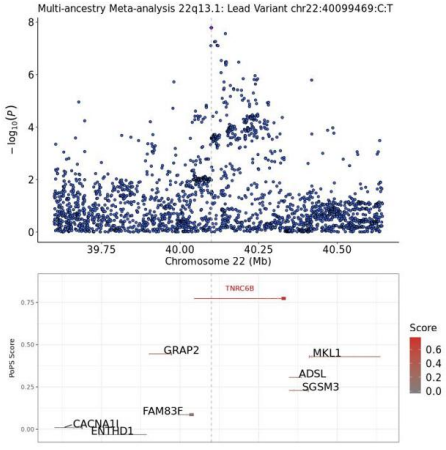

Multi-ancestry Meta-analysis 22q11.1: Lead Variant chr22:16956420:C:T
Chromosome 22 (Mb)
CECR2
CECR5
IL17RA
CECR1
CECR6
GAB4
CCT8L2
KKR3
Score

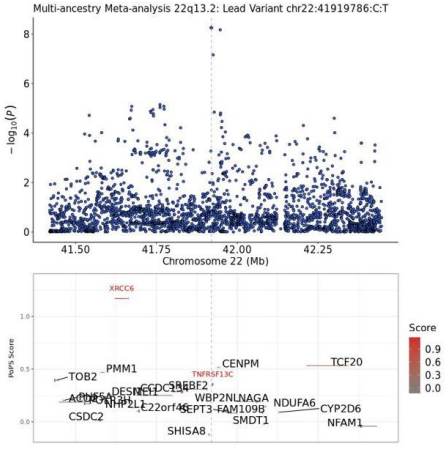

Multi-ancestry Meta-analysis 22q11.23: Lead Variant chr22:23538691:G:A
Chromosome 22 (Mb)
SMARCB1
BCR
RTDR1
GNAZ
RAB36
ZNF70
SLC2A11
CHCHD10
MMP11
C22orf43
VPREB3
DDT
DDTL
GSTT2B
Score

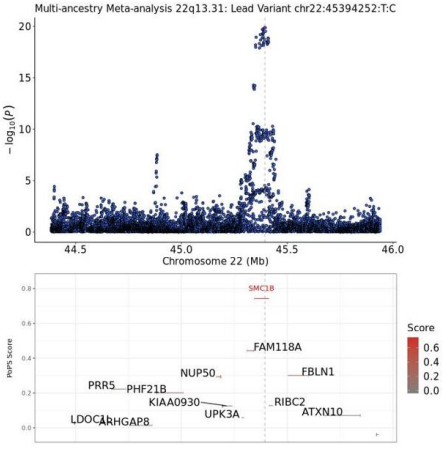

Multi-ancestry Meta-analysis 22q12.2: Lead Variant chr22:31603209:T:G
Chromosome 22 (Mb)
EIF4ENIF1
MORC2
PATZ1
LIMK2
DRG1
SF1
DEPDC5
OSBP2
RNF185
PISD
SLC35E4
PIK3IP1
SMTN
DUSP18
PLA2G3
C22orf24
SELM
SLC5A1
C22orf42
Score

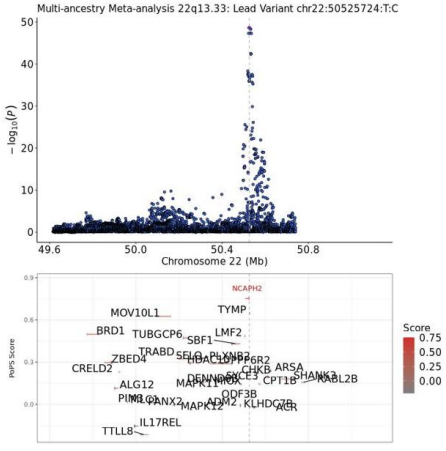

Multi-ancestry Meta-analysis 22q12.3: Lead Variant chr22:35258140:T:G
Chromosome 22 (Mb)
HMGXB4
MCM5
TOM1
ISX
HMOX1
RASD2
APOL6
APOL5
MB
Score

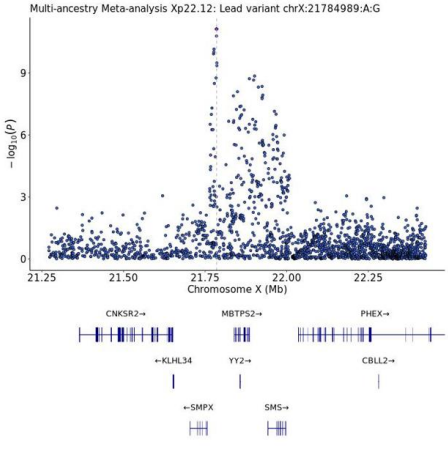

Multi-ancestry Meta-analysis 22q13.1: Lead Variant chr22:38743338:A:G
Chromosome 22 (Mb)
SUN2
DDX17
DMC1
CBX7
PICK1
CBY1
GTPBP1
CBX6
TOMM22
FAM227A
LOSD1
SLC16A8
MAFF
KCNJ4
Score

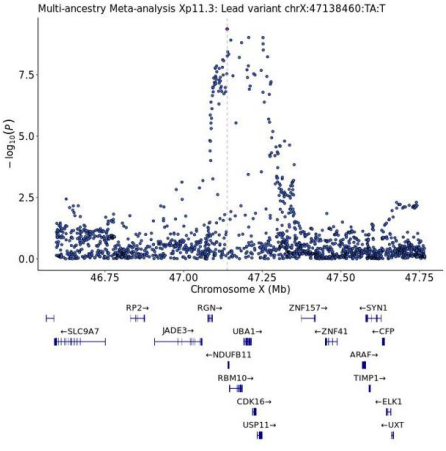

Multi-ancestry Meta-analysis 22q13.1: Lead Variant chr22:40099469:C:T
Chromosome 22 (Mb)
TNRC6B
GRAP2
MKL1
ADSL
SGSM3
FAM83F
CACNA1I
EN1HD1
Score

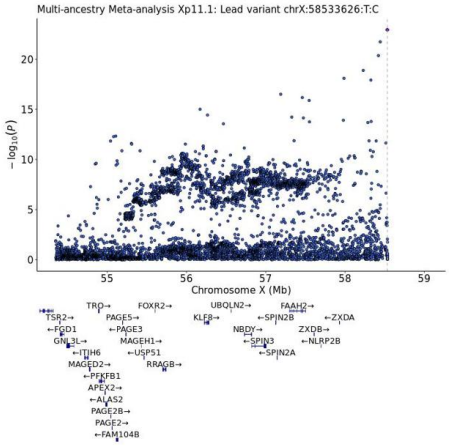

Multi-ancestry Meta-analysis 22q13.2: Lead Variant chr22:41919786:C:T
Chromosome 22 (Mb)
XRCC6
TOB2
PMM1
CENPM
TCF20
TNFRSF13C
CSDC2
SHISA8
SMDT1
NFAM1
Score

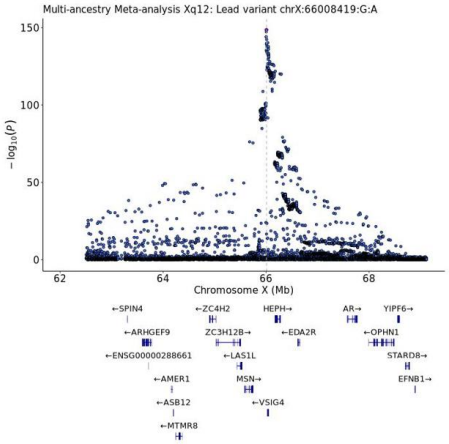

Multi-ancestry Meta-analysis 22q13.31: Lead Variant chr22:45394252:T:C
Chromosome 22 (Mb)
SMC1B
FAM118A
FBLN1
NUP50
PRR5
PHF21B
KIAA0930
RIBC2
ATXN10
UPK3A
LDOC1
ARHGAP8
Score

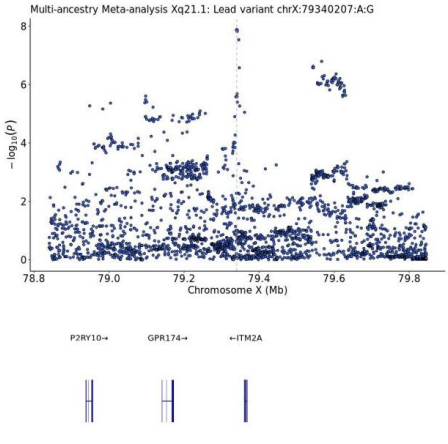

Multi-ancestry Meta-analysis 22q13.33: Lead Variant chr22:50525724:T:C
Chromosome 22 (Mb)
NCAPH2
MOV10L1
TYMP
BRD1
TUBGCP6
LMF2
SBF1
TRABD
ZBED4
CRELD2
ALG12
TTLL8
IL17REL
Score

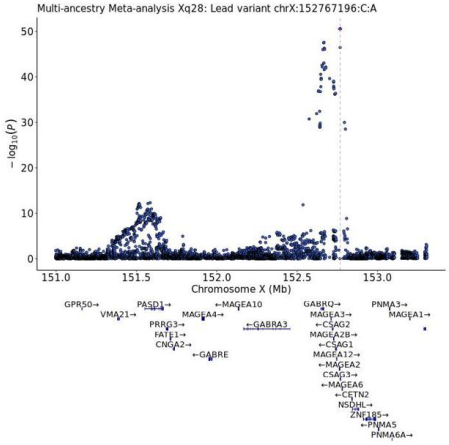

Multi-ancestry Meta-analysis Xp22.12: Lead variant chrX:21784989:A:G
Chromosome X (Mb)
CNKSR2→
MBTPS2→
PHEX→
←KLHL34
YY2→
CBLL2→
←SMPX
SMS→

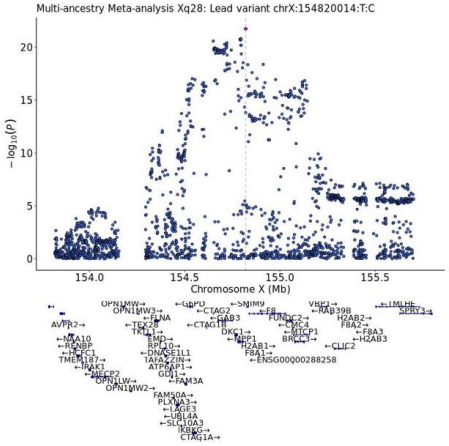

Multi-ancestry Meta-analysis Xp11.3: Lead variant chrX:47138460:TA:T
Chromosome X (Mb)
RP2→
RGN→
ZNF157→
←SYN1
←SLC9A7
JADE3→
UBA1→
←ZNF41
←CFP
←NDUFB11
ARAF→
RBM10→
TIMP1→
CDK16→
←ELK1
USP11→
←UXT


Multi-ancestry Meta-analysis Xp11.1: Lead variant chrX:58533626:T:C
$-\log_{10}(P)$
Chromosome X (Mb)
TRO→
FOXR2→
UBQLN2→
FAAH2→
TSR2→
PAGE5→
KLF8→
←SPIN2B
←ZXDA
←FGD1
←PAGE3
NBDY→
ZXDB→
GNL3L→
MAGEH1→
←SPIN3
←NLRP2B
←TIMM8
←USP51
←SPIN2A
MAGED2→
RRAGB→
←PFKFB1
APEX2→
←ALAS2
PAGE2B→
PAGE2→
←FAM104B


Multi-ancestry Meta-analysis Xq12: Lead variant chrX:66008419:G:A
$-\log_{10}(P)$
Chromosome X (Mb)
←SPIN4
←ZC4H2
HEPH→
AR→
YIPF6→
←ARHGEF9
ZC3H12B→
←EDA2R
←OPHN1
←ENSG00000288661
←LAS1L
STARD8→
←AMER1
MSN→
EFNB1→
←ASB12
←VSIG4
←MTMR8


Multi-ancestry Meta-analysis Xq21.1: Lead variant chrX:79340207:A:G
$-\log_{10}(P)$
Chromosome X (Mb)
P2RY10→
GPR174→
←ITM2A


Multi-ancestry Meta-analysis Xq28: Lead variant chrX:152767196:C:A
$-\log_{10}(P)$
Chromosome X (Mb)
GPR50→
PASD1→
←MAGEA10
GABRQ→
PNMA3→
VMA21→
MAGEA4→
MAGEA3→
MAGEA1→
←GABRA3
←CSAG2
PRRG3→
FATE1→
MAGEA2B→
CNGA2→
←CSAG1
←GABRE
MAGEA12→
←MAGEA2
CSAG3→
←MAGEA6
←CETN2
NSDHL→
ZNF185→
←PNMA5
PNMA6A→


Multi-ancestry Meta-analysis Xq28: Lead variant chrX:154820014:T:C
$-\log_{10}(P)$
Chromosome X (Mb)
OPN1MW→
←GPD1
←SMIM9
VBP1→
←TMLHE
OPN1MW3→
←CTAG2
←F8
←RAB39B
SPRY3→
←FLNA
←GAB3
FUNDC2→
H2AB2→
AVPR2→
←TEX28
←CTAG1B
←MMGT1
F8A2→
←NAA10
TKTL1→
DKC1→
←MPP1
←MTCP1
←F8A3
←RENBP
EMD→
BRCC3→
←H2AB3
←HCFC1
RPL10→
H2AB1→
←CLIC2
TMEM187→
←DNASE1L1
FBA1→
←PAK1
TAPBP→
←ENSG00000288258
←MECP2
ATP6AP1→
OPN1LW→
GDI1→
←FAM3A
OPN1MW2→
FAM50A→
PLXNA3→
←LAGE3
←UBL4A
←SLC10A3
←KBTBD→
CTAG1A→