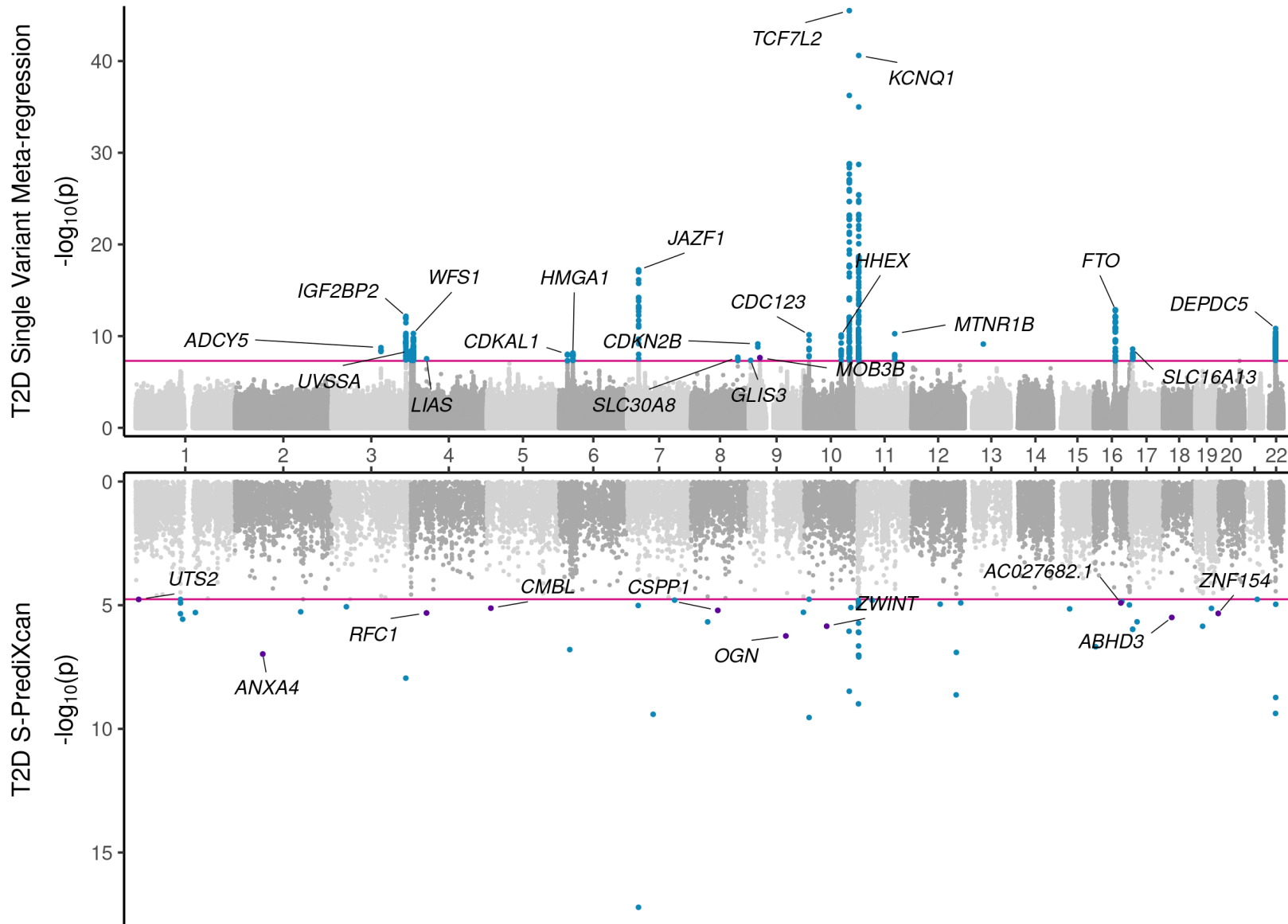
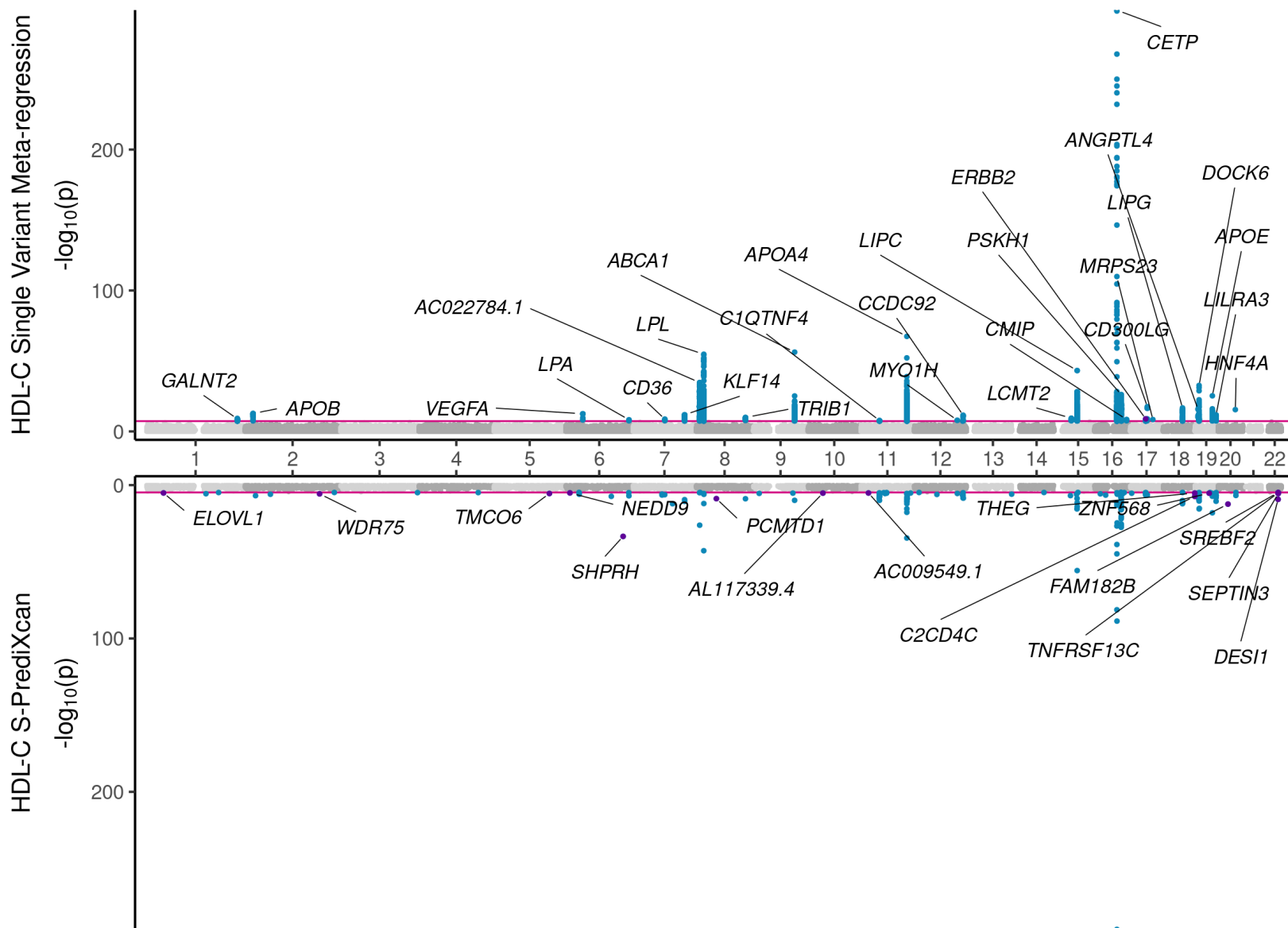


Supplementary Figure 1. Meta-regression results for A) Type 2 Diabetes, B) HDL cholesterol, C) LDL cholesterol, D) total cholesterol, and E) triglycerides. Miami plot showing findings for single variant meta-regression analyses using MR-MEGA on top and S-PrediXcan results (for all tissues) on the bottom, S-PrediXcan p-values were adjusted for multiple testing using an experiment-wide Benjamini-Hochberg false discovery rate (FDR) approach, results shown in blue are genome-wide significant for single variant results ($p < 5 \times 10^{-8}$) and significant after FDR adjustment for S-PrediXcan results, results shown in purple are novel loci.

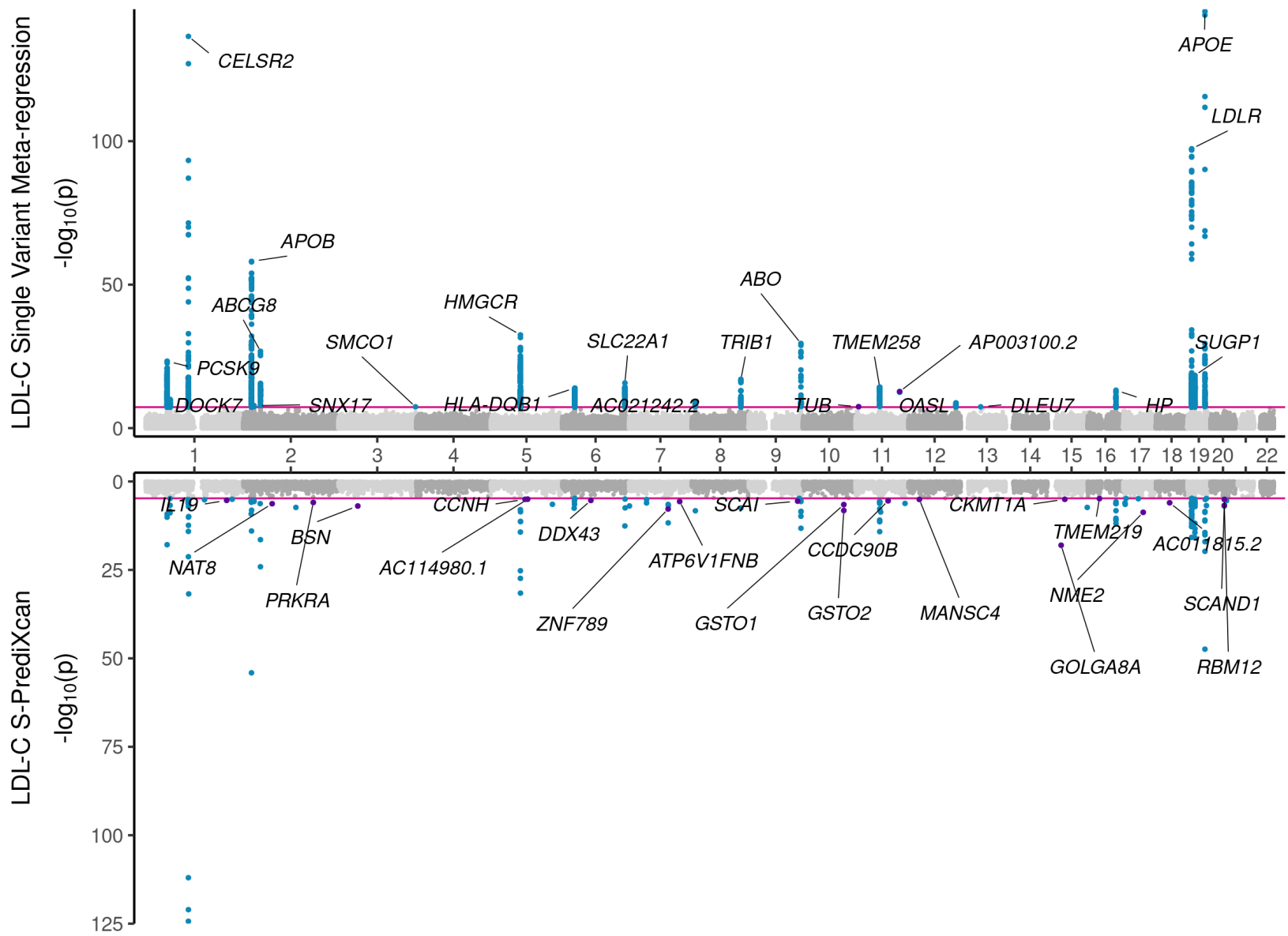
1A.



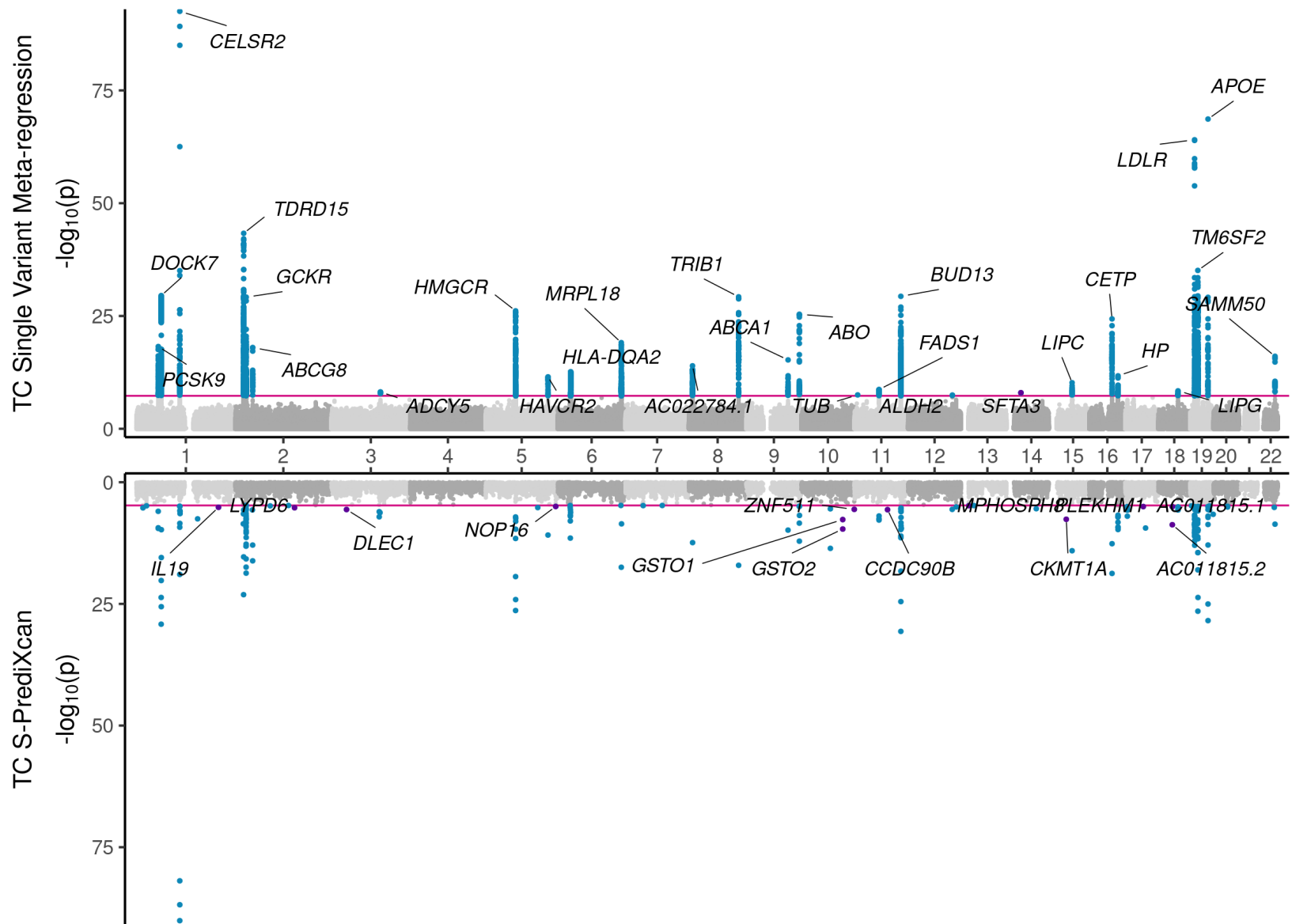
1B.



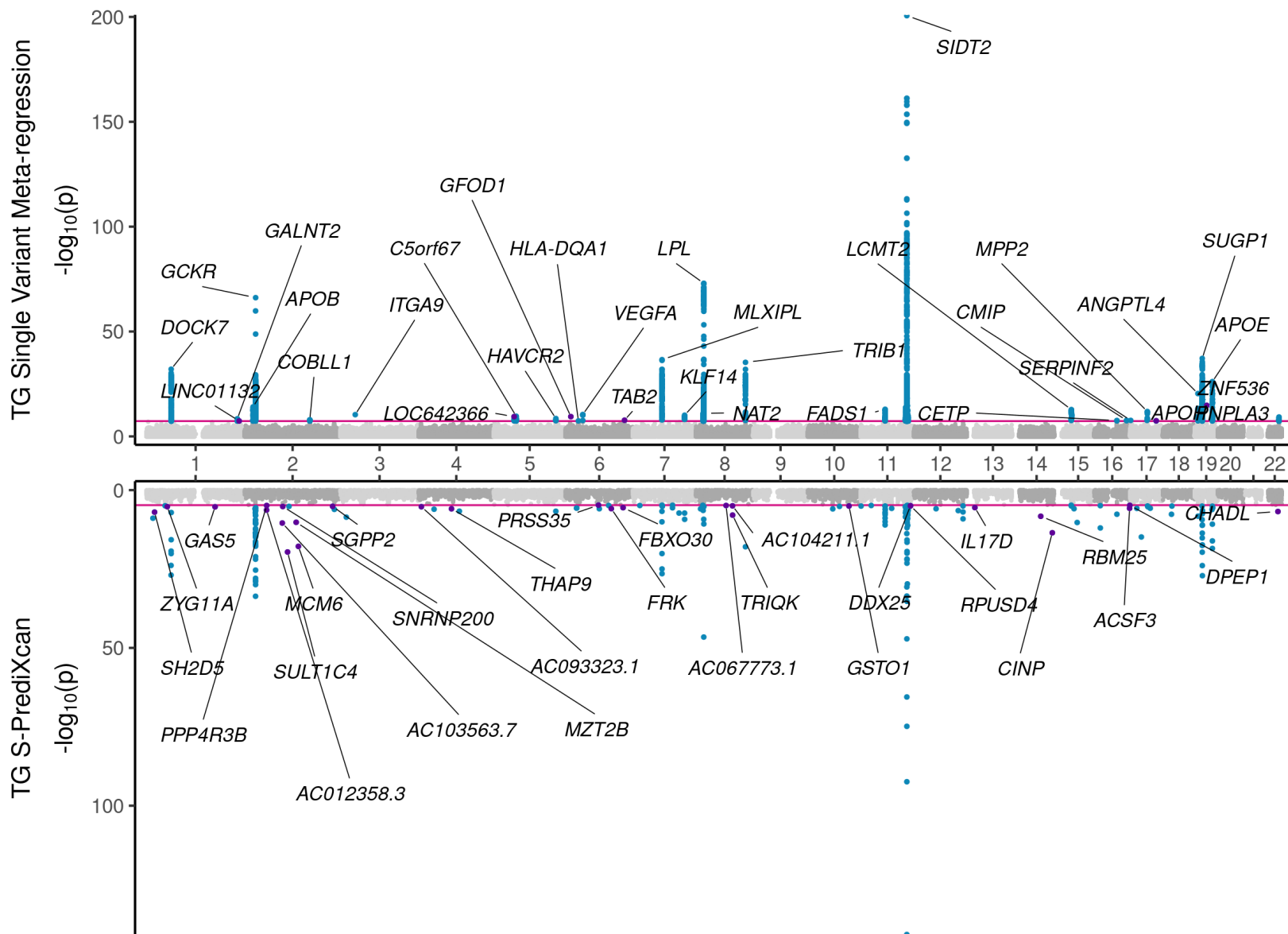
1C.



1D.



1E

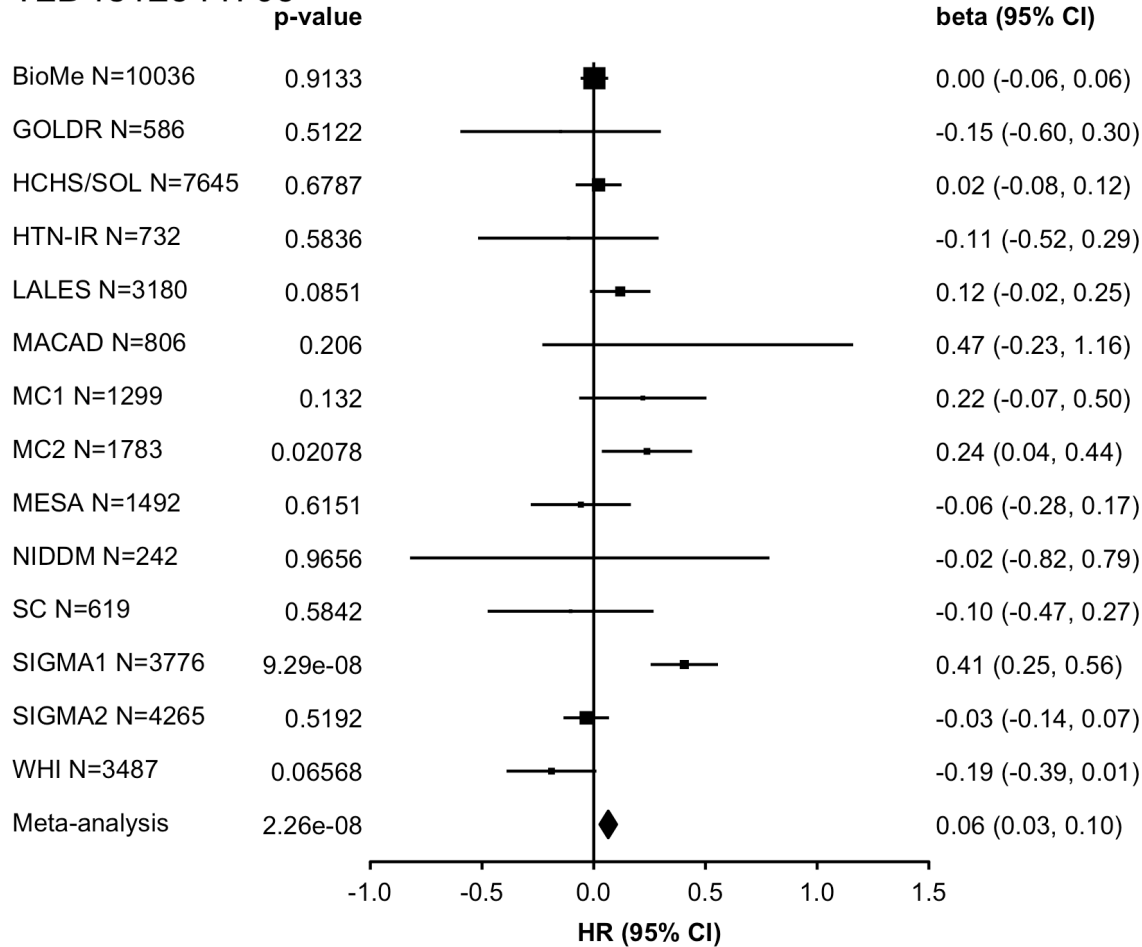


Supplementary Figure 2. Study-level results for A) rs12344703 for type 2 diabetes, B) rs9850922 for LDL cholesterol C) rs75594955 for LDL cholesterol, D) rs186143467 for LDL cholesterol, E) rs75594955 for total cholesterol F) rs564036749 for total cholesterol, G) rs143891608 for triglycerides H) rs186560848 for triglycerides, I) rs181676594 for triglycerides J) rs552736307 for triglycerides, and K) rs557199842 for triglycerides.

Forest plot showing results by study for novel top variants. Study-specific p-values and effect estimates were generated using the GWAS software indicated in Supplementary Data 1. Meta-analysis p-values and effect estimates were generated using MR-MEGA; the beta and 95% confidence interval (CI) correspond to beta_0 from MR-MEGA

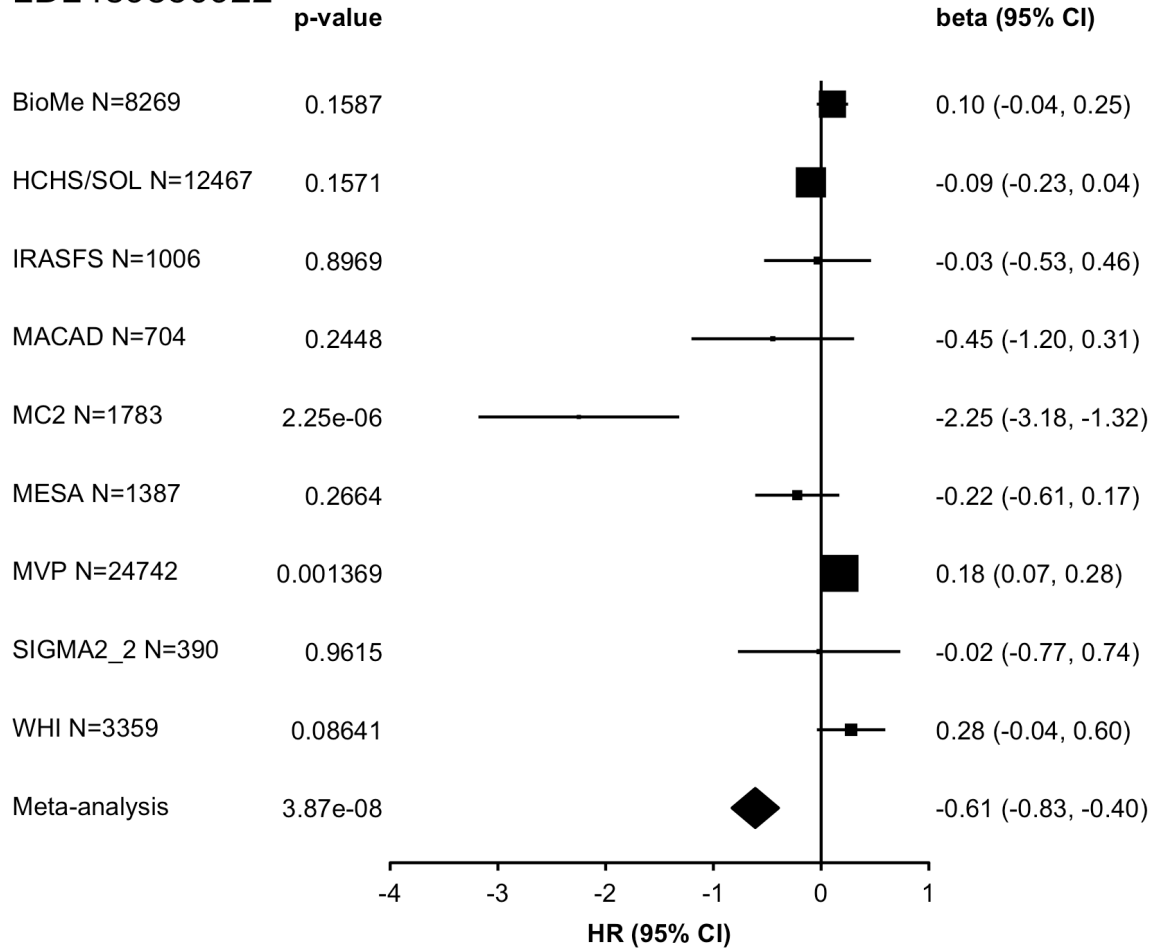
2A.

T2D rs12344703



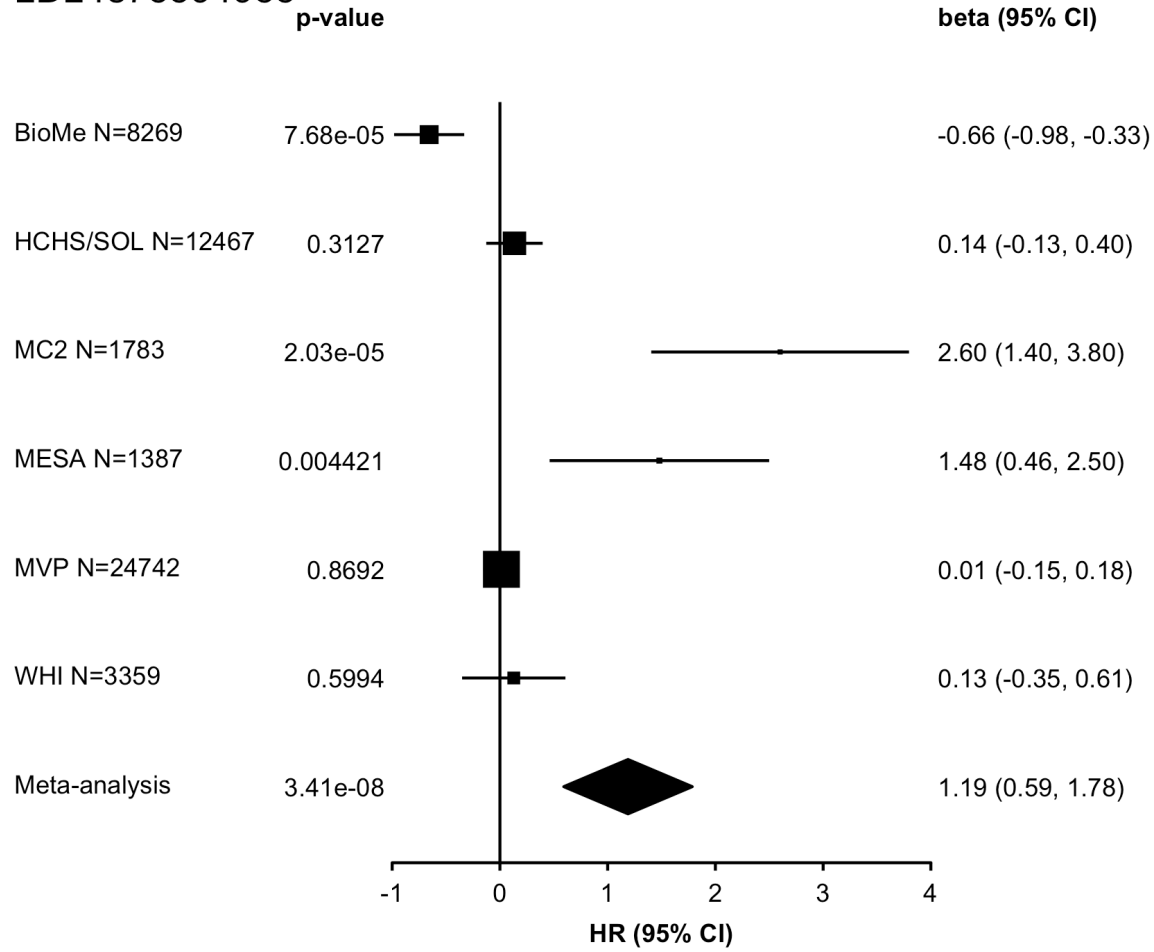
2B.

LDL rs9850922



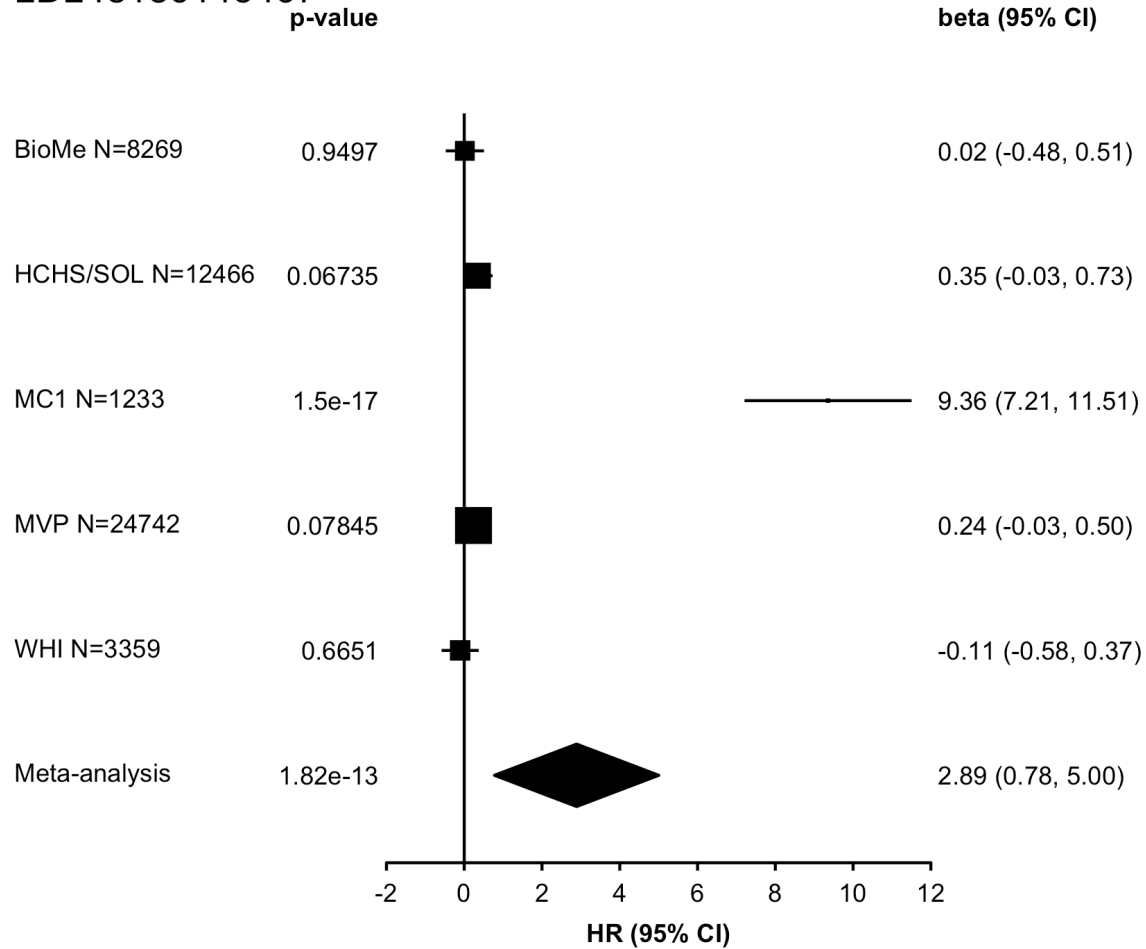
2C.

LDL rs75594955



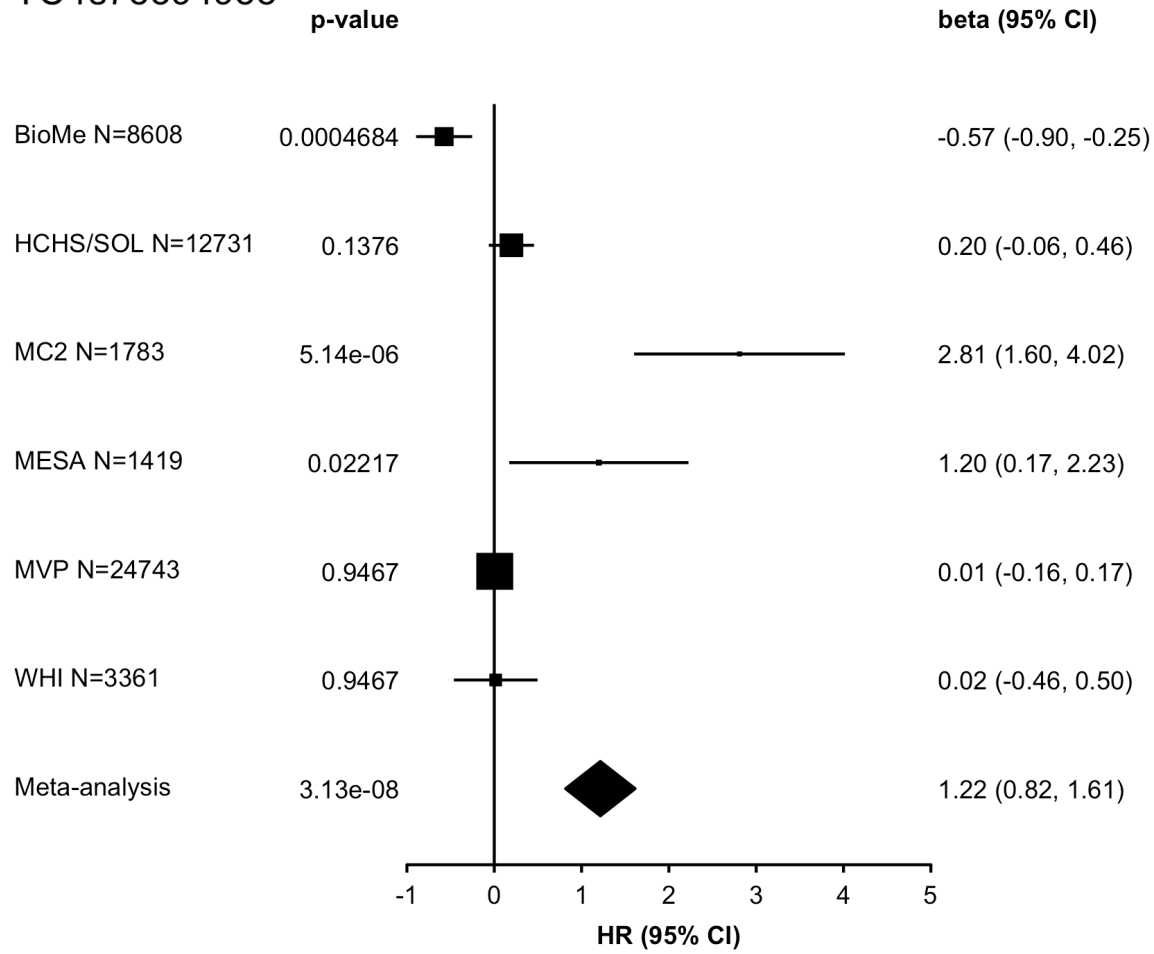
2D.

LDL rs186143467



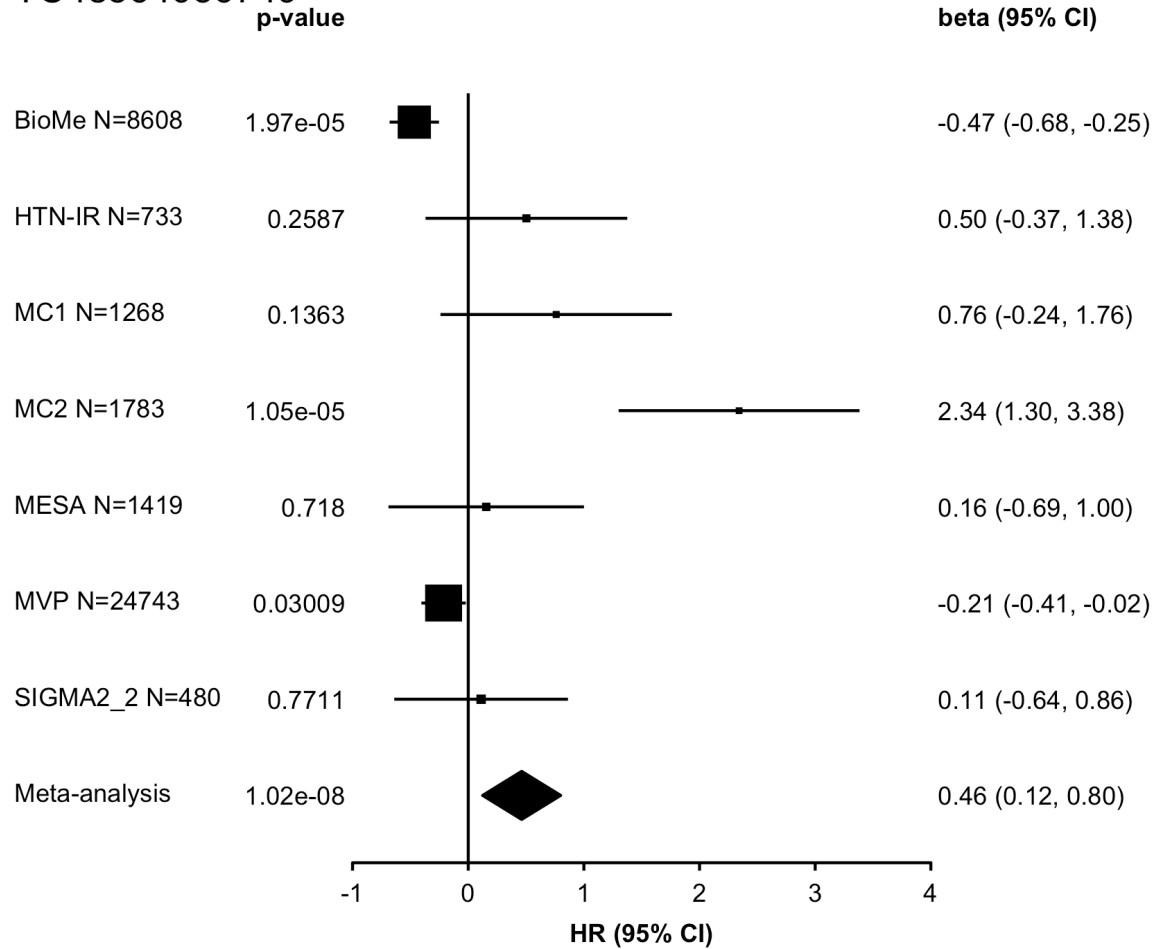
2E.

TC rs75594955



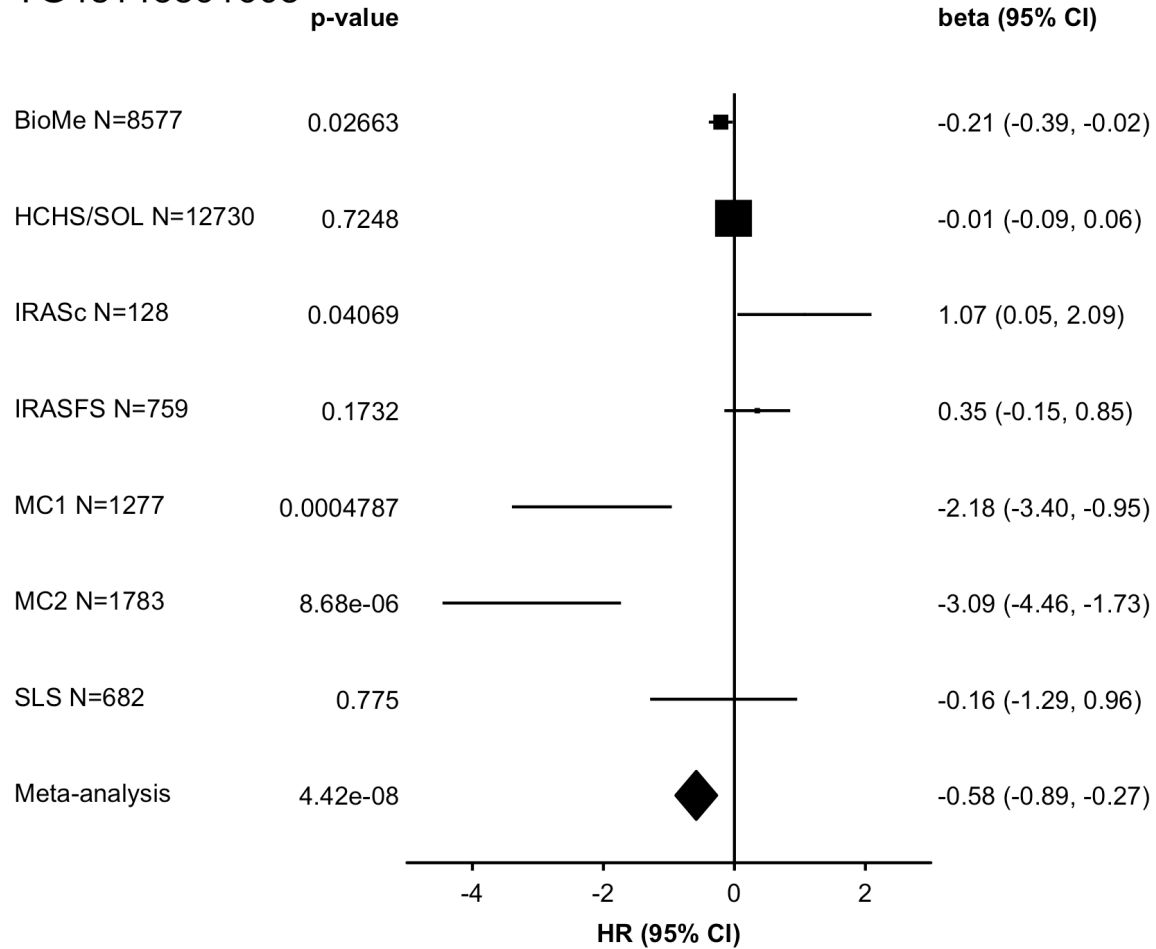
2F.

TC rs564036749



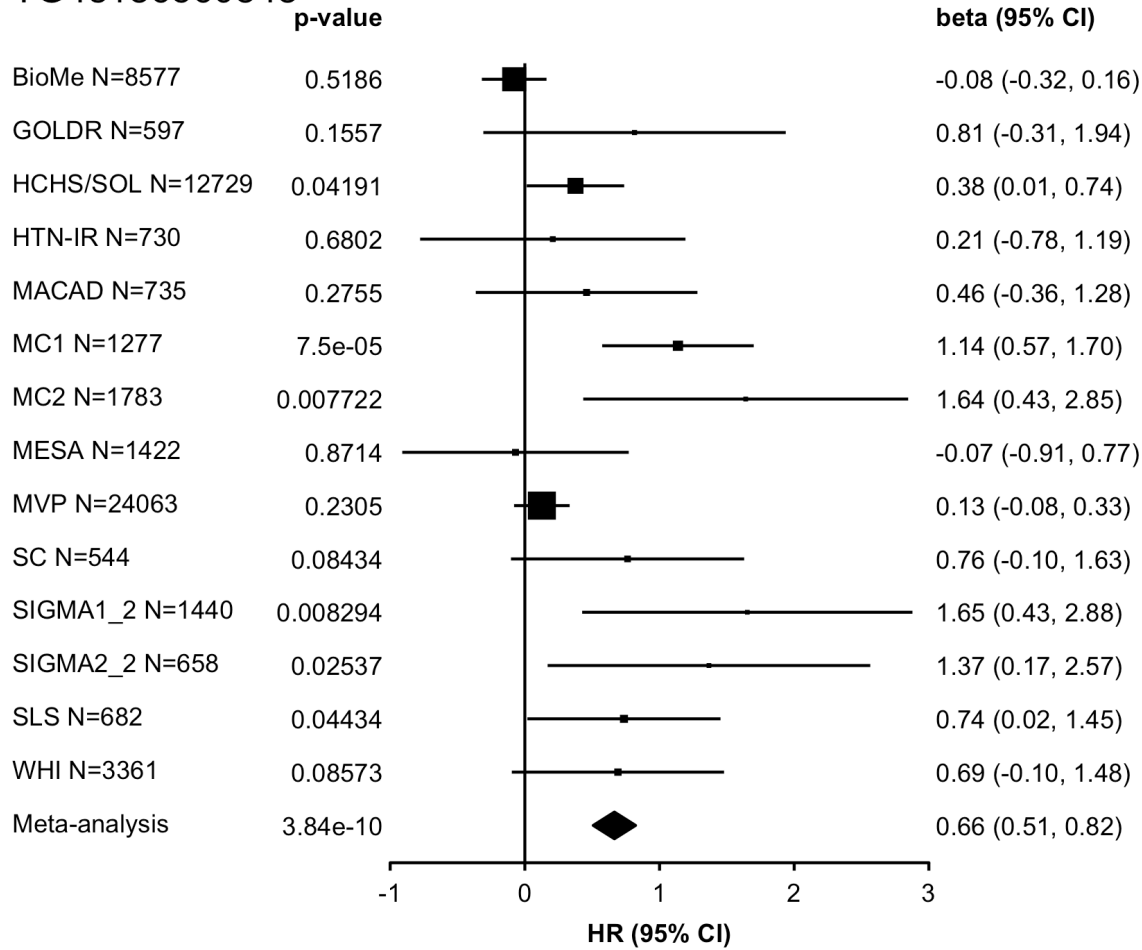
2G.

TG rs143891608



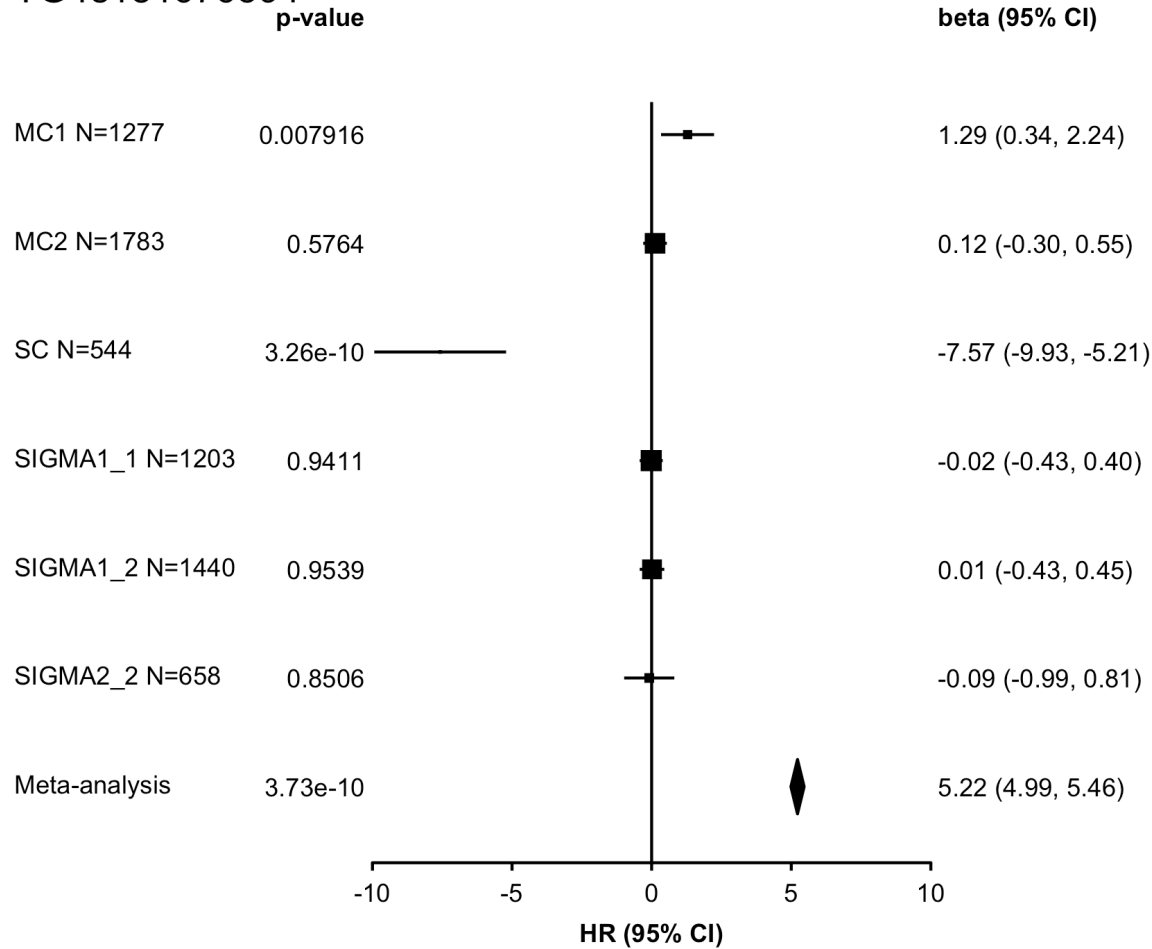
2H.

TG rs186560848



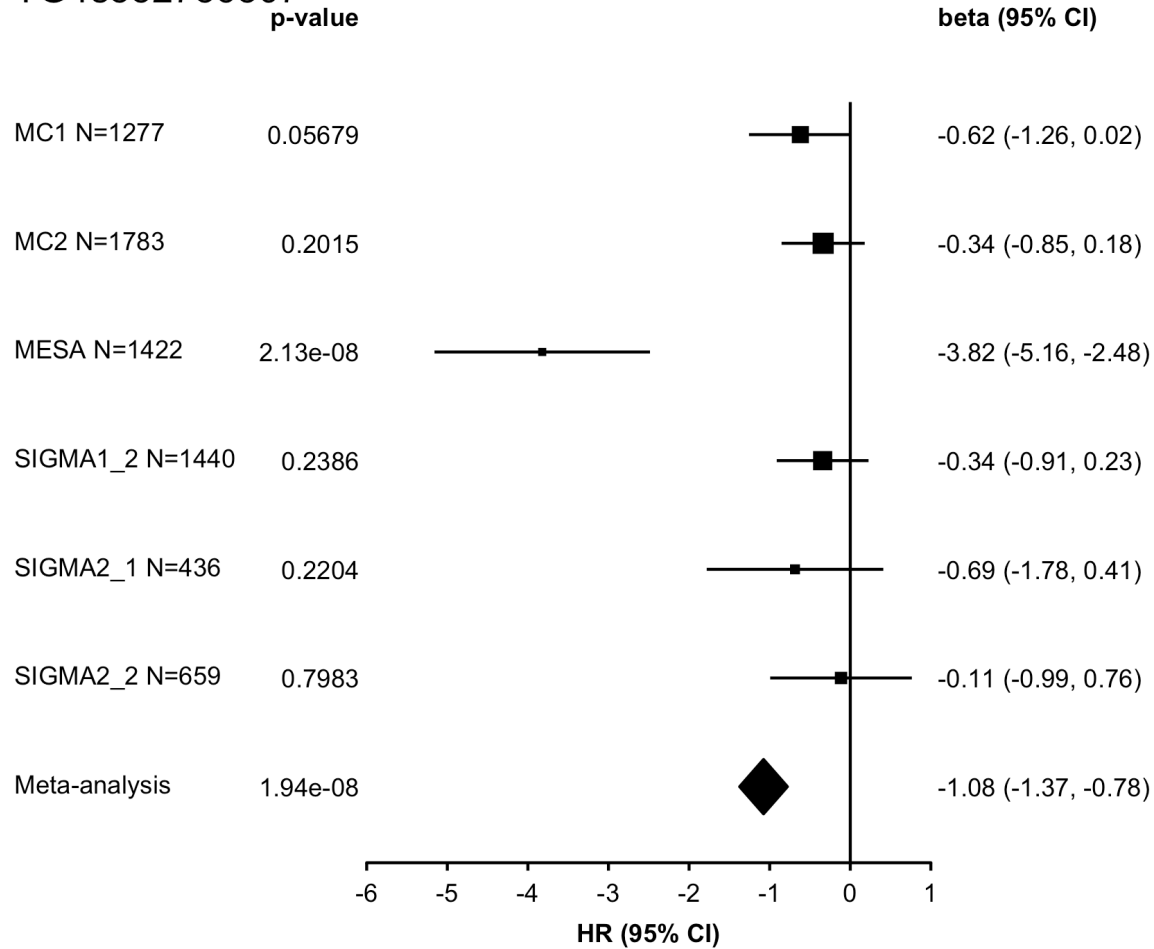
21.

TG rs181676594



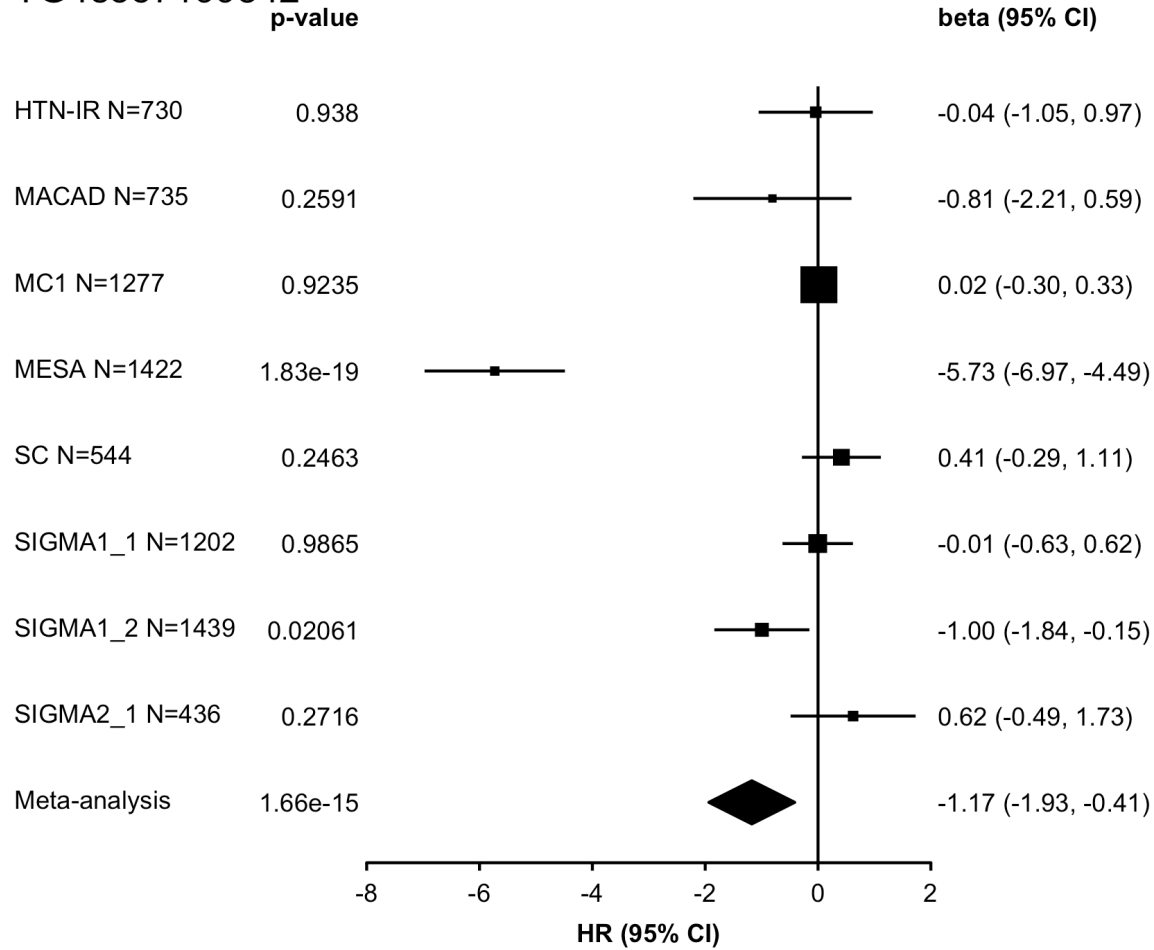
2J.

TG rs552736307



2K.

TG rs557199842



Supplementary Figure 3. Correlation of measured gene expression for S-PrediXcan-identified islet cell model results in InsPIRE Consortium pancreatic islet cell data. Heatmap depicting correlation of measured gene expression for each of our S-PrediXcan-identified islet cell model findings, and *INS*, which is in close proximity but was not significant using S-PrediXcan, in InsPIRE Consortium pancreatic islet gene expression data. Correlation represents Pearson correlation coefficient for gene expression for each gene-gene pair. Positive correlation values are shades of blue, negative correlation values are shades of red.

