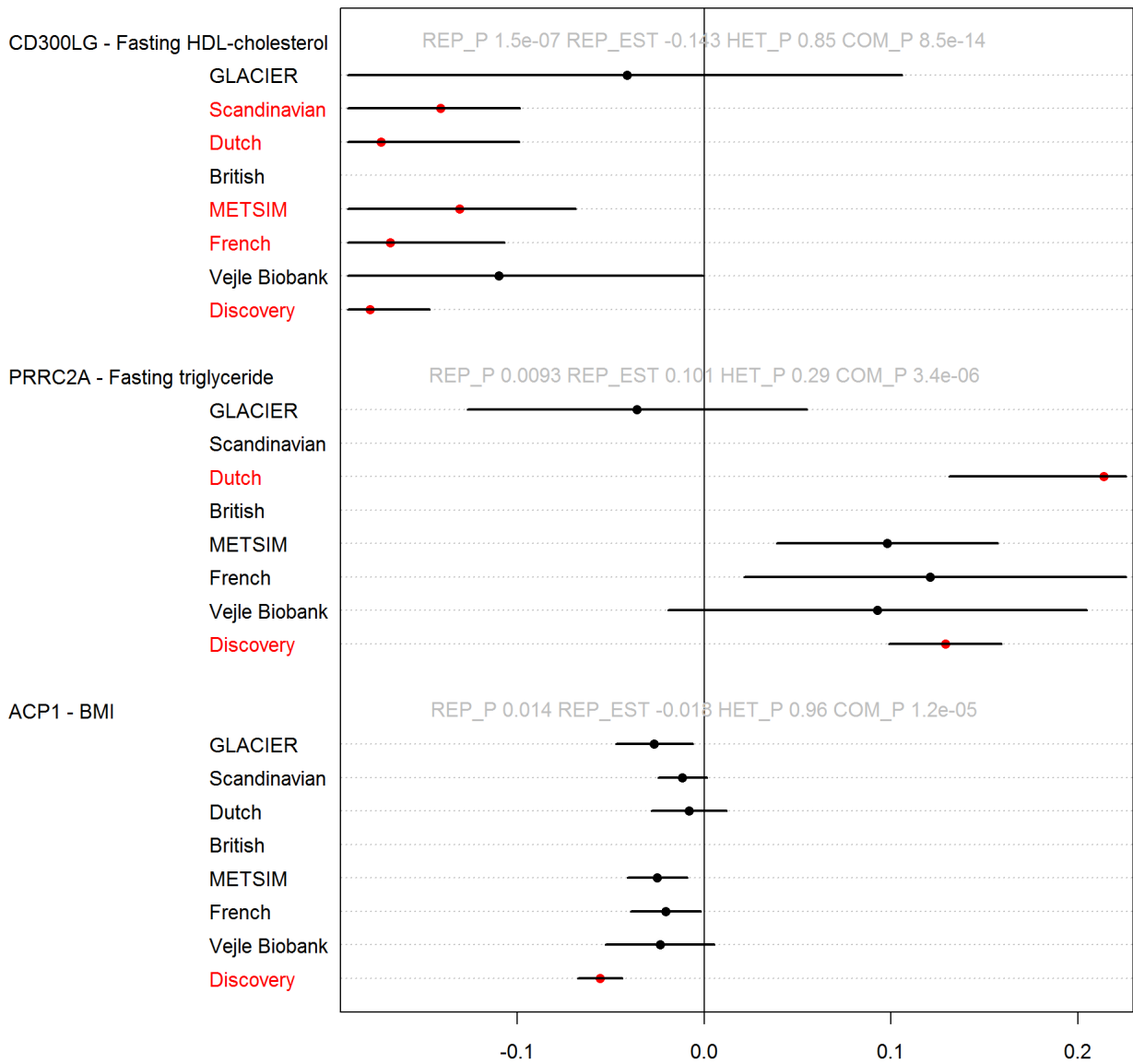


Quantitative traits



ESM Figure 15 Replication of selected coding SNPs with quantitative metabolic phenotypes in stage 3 European samples.

For each association is shown the effect in discovery (stage 2) samples and the cohort-specific replication effect. In red are studies with a nominally significant association ($P < 0.05$). Data are effect and SE on a rank normalized scale. REP_P: P -value in replication samples, REP_EST: Effect size (on rank normalized scale) in replication samples, HET_P: P -value for heterogeneity in replication samples, COM_P: Combined P -value.