

Supplemental Figure S12. Association test results for coding rare variants (MAF < 5%) in association with LDL around genes *TOMM40*, *APOE*, and *APOC4-APOC2*. Red dots correspond to $-\log_{10}(\text{aSPU p-value})$, and blank dots mark the locations of nonsynonymous rare variants. Dashed line indicates the threshold of genome-wide significance level ($p < 1.56e-7$).

