



Supplementary Figure 2. The regional association plots of five independent SNPs in the cholesterol-related genes SNPs in the region of 50 kilobases up or downstream of **(A)** *APOB* rs1801701_T C>T, **(B)** *CDH13* rs35859010_T C>T, **(C)** *CDH13* rs1833970_A T>A, **(D)** *CDH13* rs254315_C T>C, **(E)** *CDH13* rs425904_C T>C. Data points are colored according to the level of linkage disequilibrium of each pair of SNPs based on the hg19/1000 Genomes European population. The left-hand y-axis shows the association P-value of individual SNPs in the discovery dataset, which is plotted as $-\log_{10}(P)$ against chromosomal base-pair position. The right-hand y-axis shows the recombination rate estimated from HapMap Data Rel 22/phase II European population. **(F)** Linkage disequilibrium block of four SNPs on *CDH13*. The values of R square in the block present the linkage disequilibrium levels of four SNPs on *CDH13*.