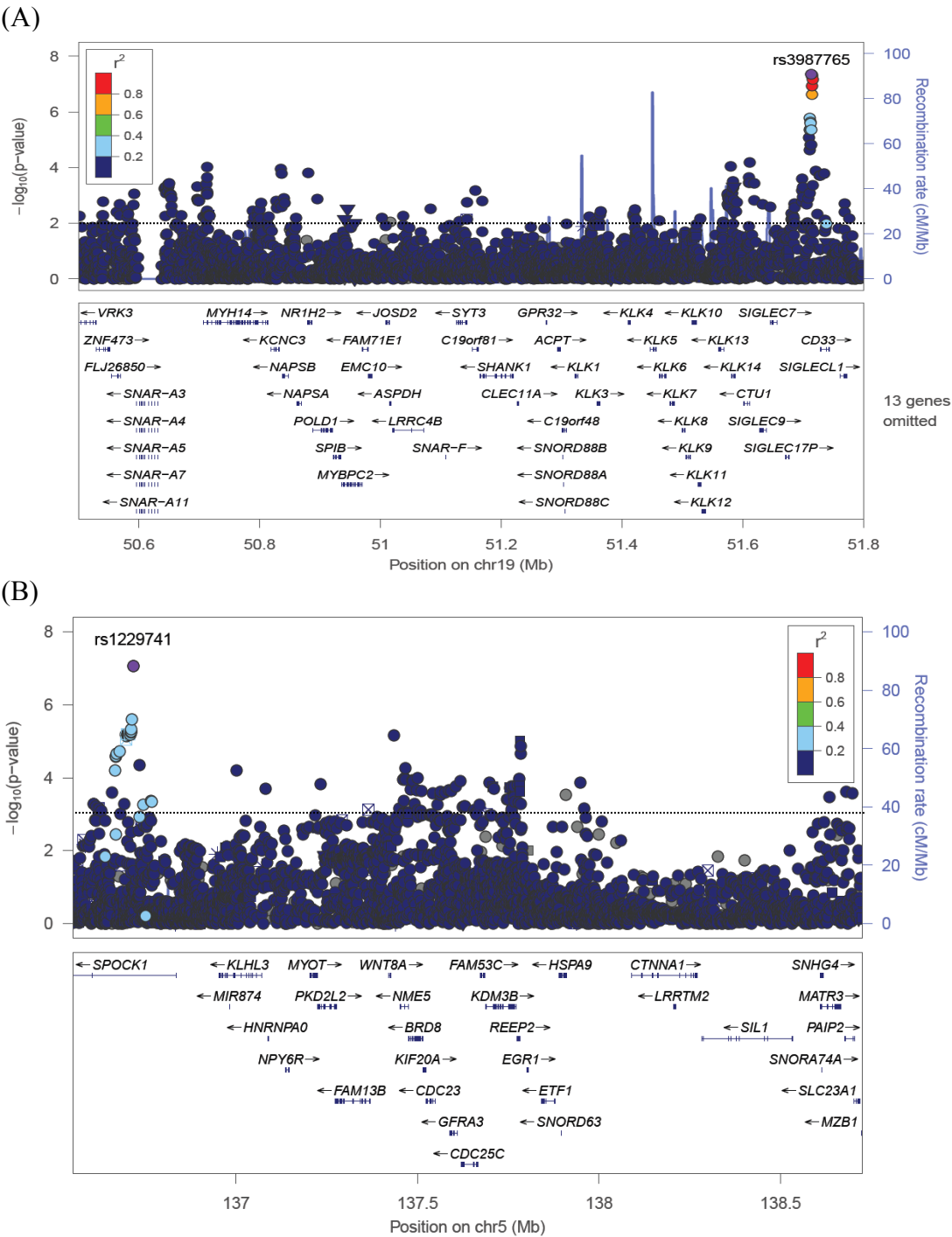
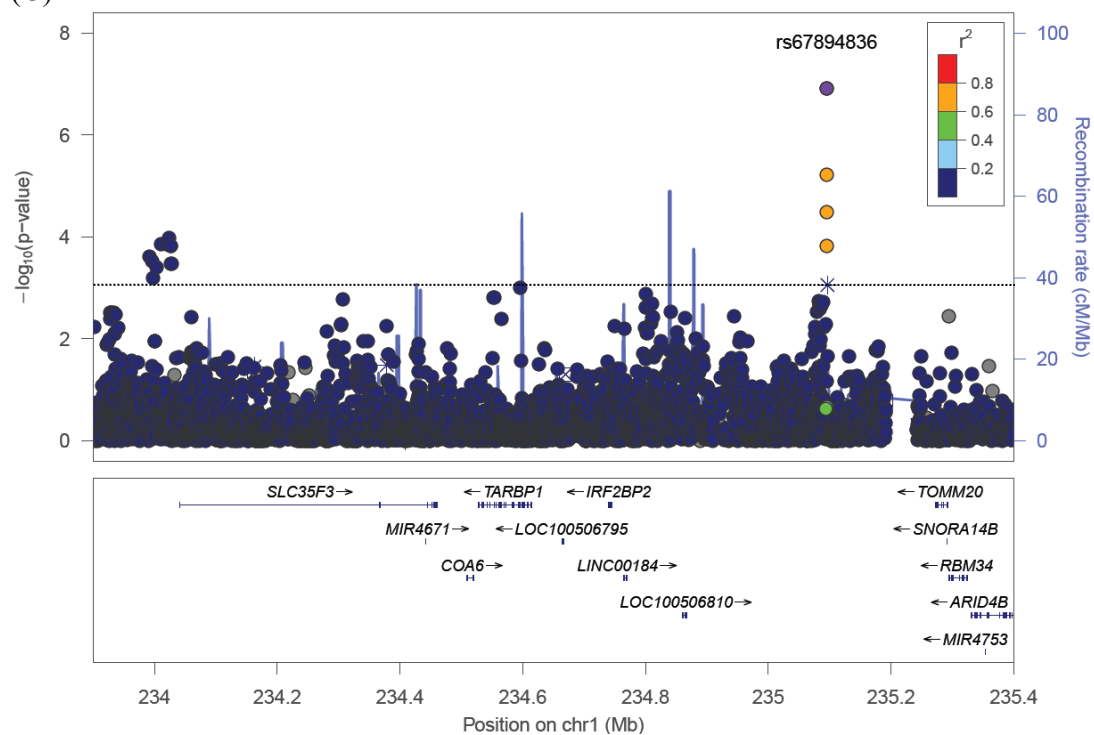


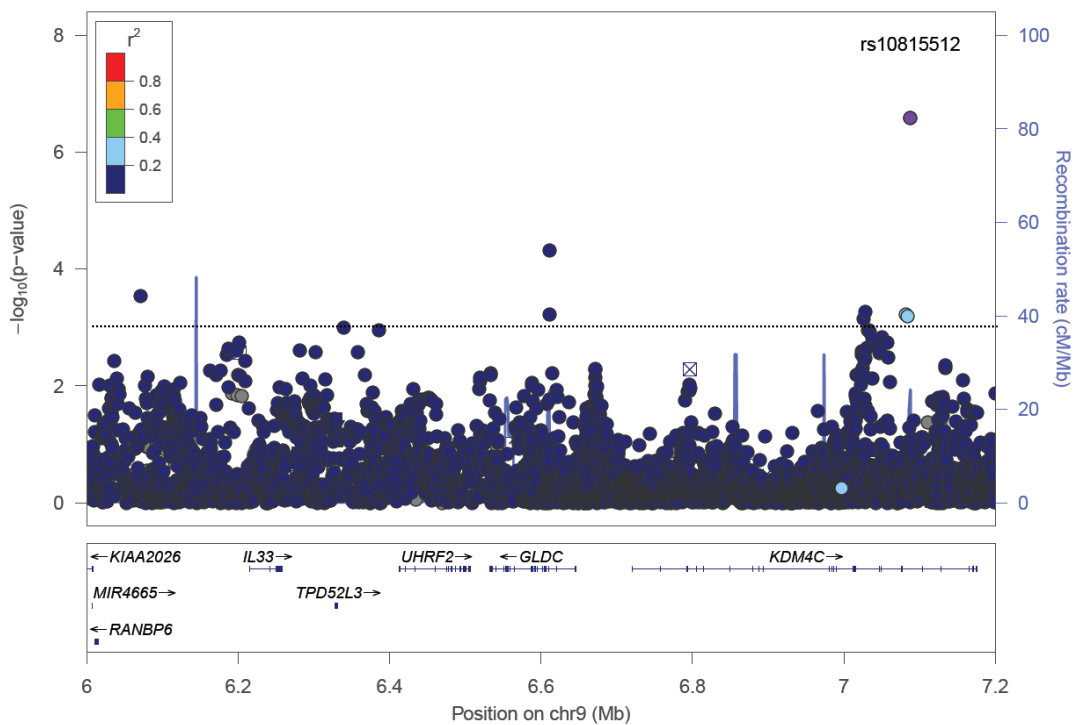
Figure S6. Regional association results from the GWAS meta-analysis in the Urban Health Study and their linkage disequilibrium patterns with reference to the 1000 Genomes AFR panel. The r^2 correlations between the SNP with the lowest meta-analysis P value (shown in purple) and its surrounding SNPs selected for replication testing (meta-analysis $P < 1 \times 10^{-3}$) are shown for each of the following 8 regions: (A) *SIGLEC17P* / *CD33*, (B) *SPOCK1*, (C) *IRF2BP2* / *TOMM20*, (D) *KDM4C*, (E) *IFFO2* / *UBR4*, (F) *HLA-DQA1* / *HLA-DQB1*, (G) *KIAA1671*, and (H) *PAX5* / *ZCCHC7*. The blue horizontal dotted line indicates the meta-analysis $P < 1 \times 10^{-3}$ threshold for selecting SNPs for replication testing. Plots are oriented to capture the SNPs selected for replication within each 3MB region examined rather than being centered on the highest association peak. SNPs are intergenic or intronic (solid circles), coding (nonsynonymous SNPs shown as inverted triangles and untranslated or synonymous SNPs shown as squares), located in a conserved transcription factor binding site (stars), or highly conserved in placental mammals (known as MCS44 Placental, squares with diagonal lines). Gene locations and their orientations are shown along with recombination peaks in light blue. SNPs with missing r^2 values are shown in grey.



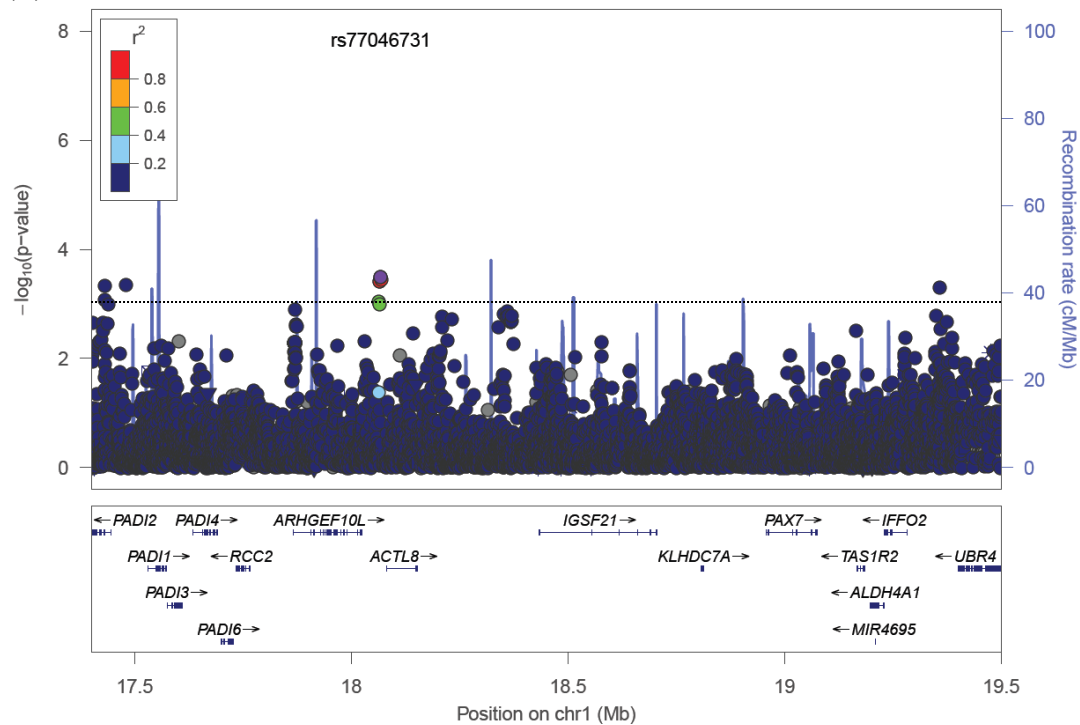
(C)



(D)

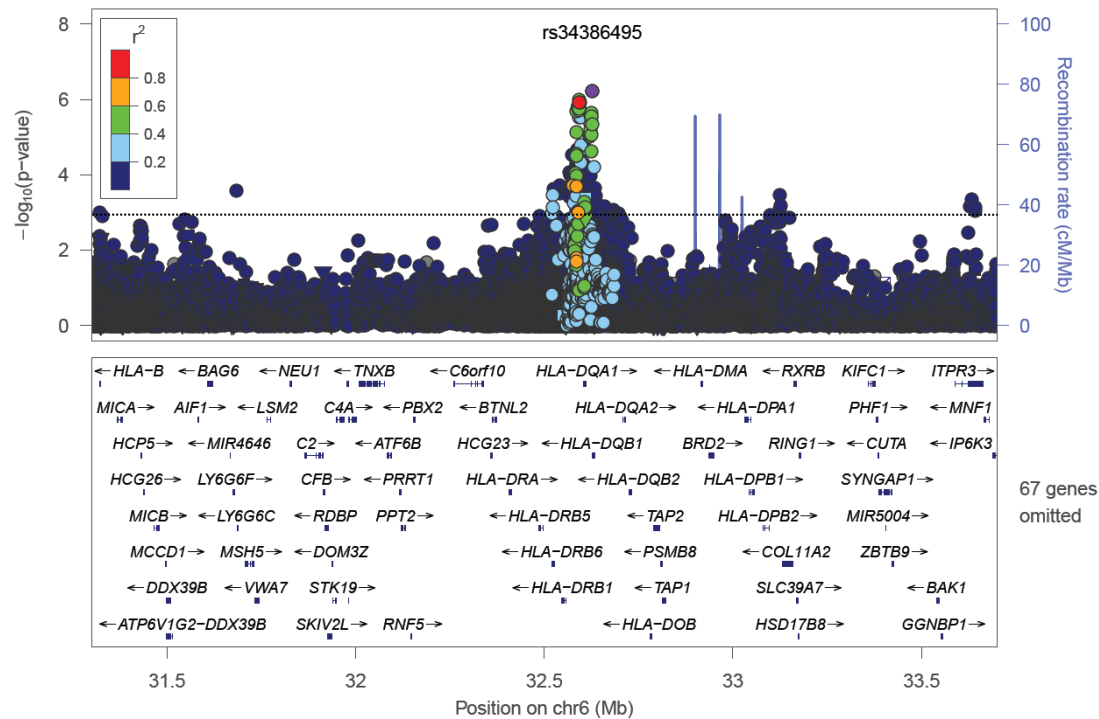


(E)

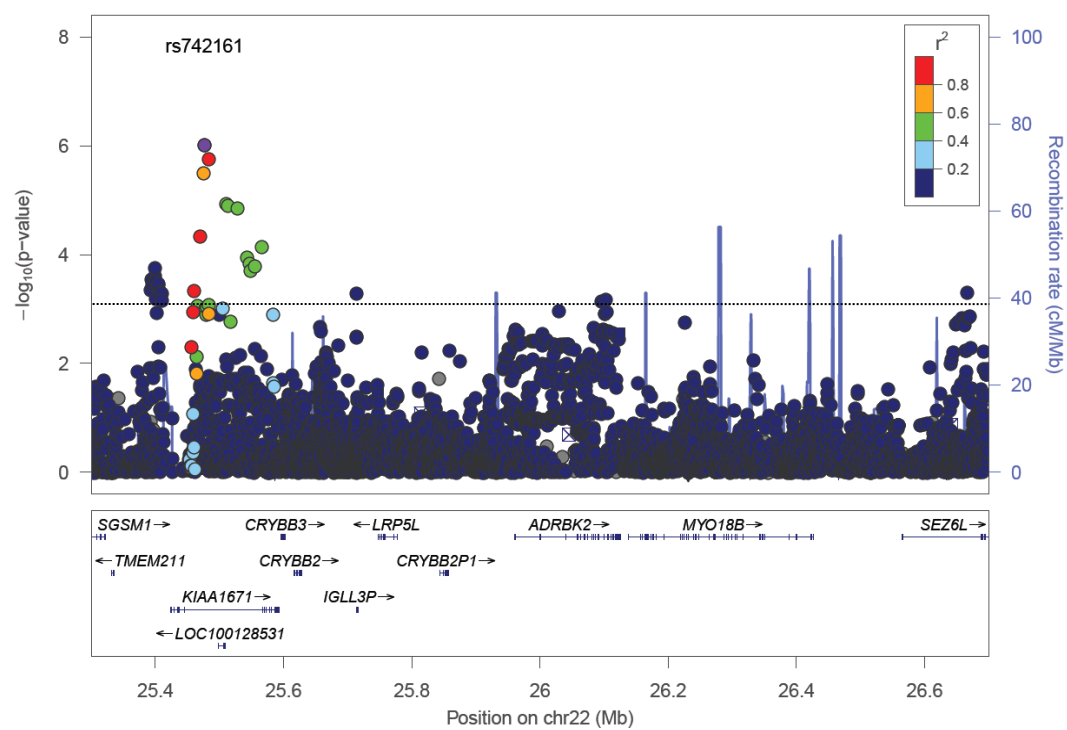


The top associated indel (chr1:19357344:D, not shown) is intergenic between *IFFO2* and *UBR4*.

(F)



(G)



(H)

