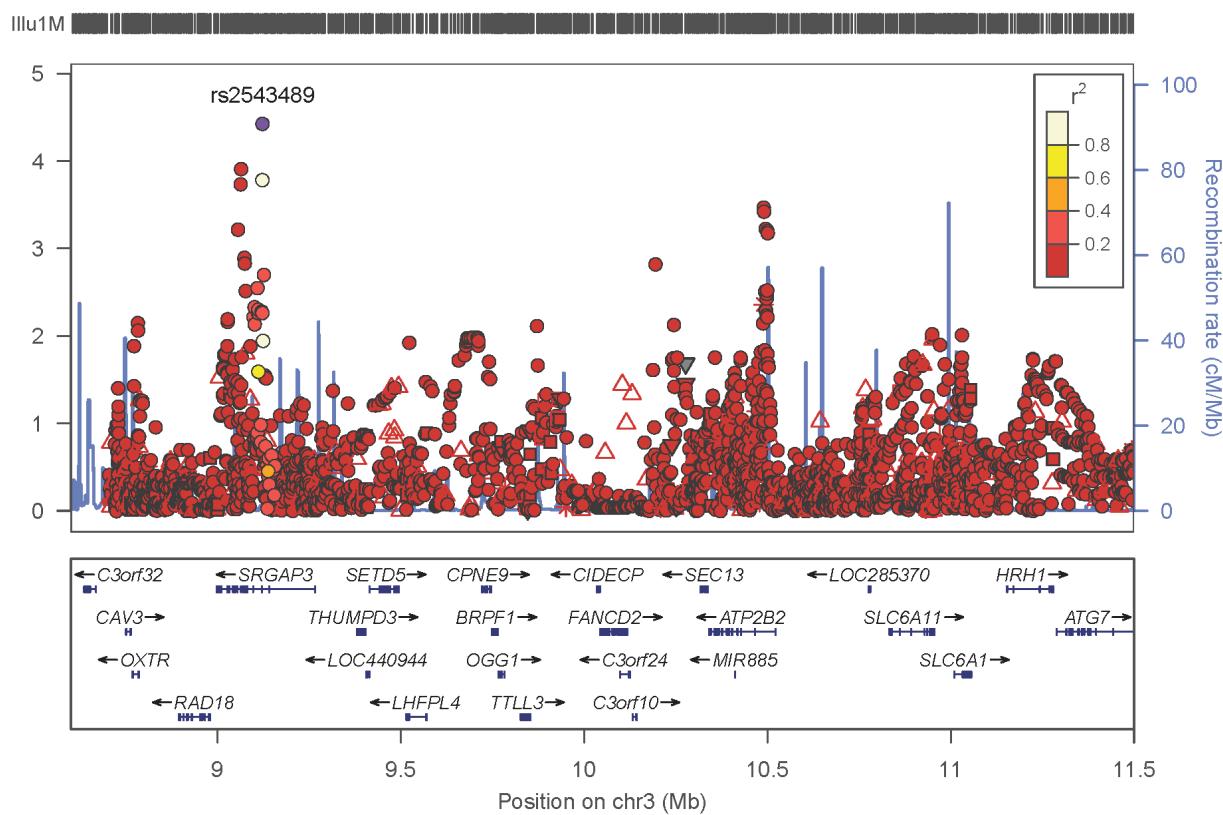
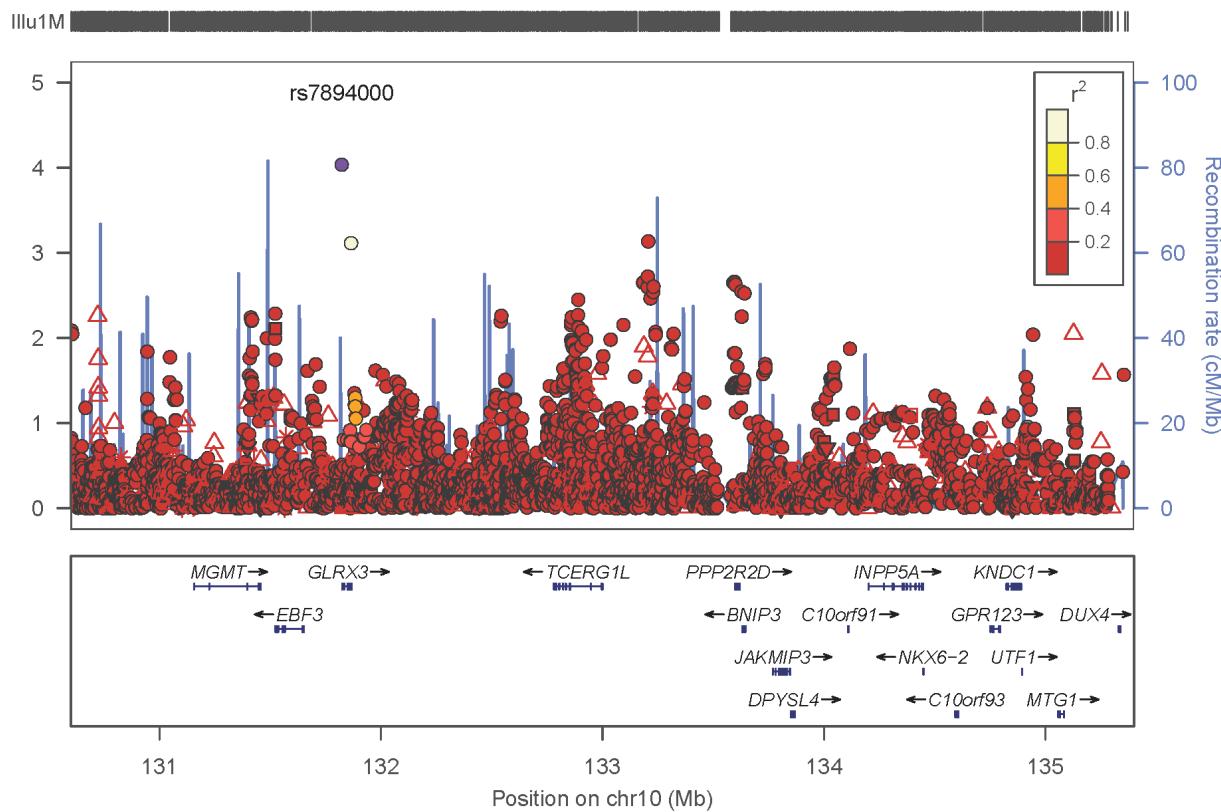
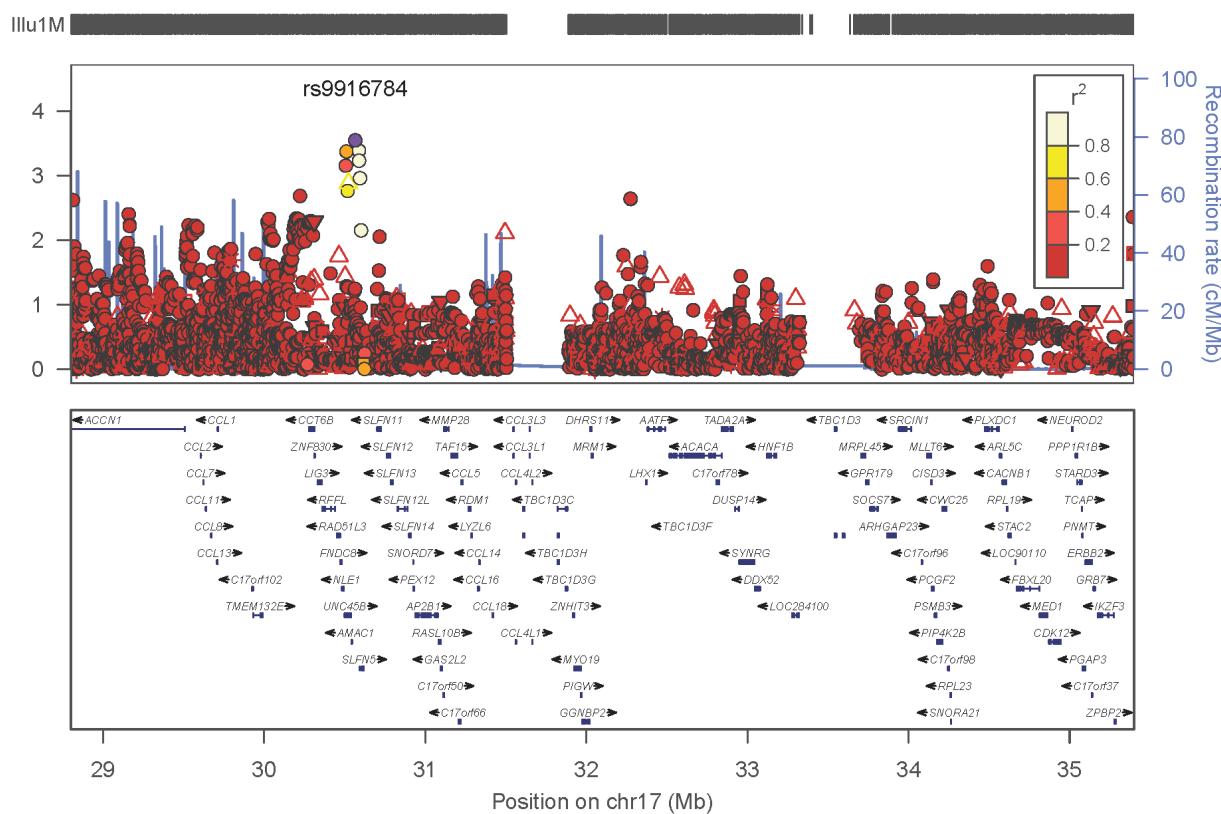


Figure S2: Regional LocusZoom plots of association in the full imputed dataset across three genomic regions previously linked to OM susceptibility: (A) the 3p25.3 region [8] adjusted for PCs; (B) the 10q26.3 region (linkage peak microsatellite D10S212, [8]) adjusted for PCs; (C) the 17q12 region [9] adjusted for PCs, and (D) a smaller region of the 17q12 plot to highlight the gene position for the top SNPs. The top associated SNPs are represented by purple circles with the colour of all other SNPs representative of the pairwise r^2 value relative to the top SNP using patterns of LD from the CEU HapMap populations. Recombination rates are shown by the solid blue line. Physical positions and gene designations are based on NCBI Build 36 of the human genome.

(A)



(B)**(C)**

(D)

