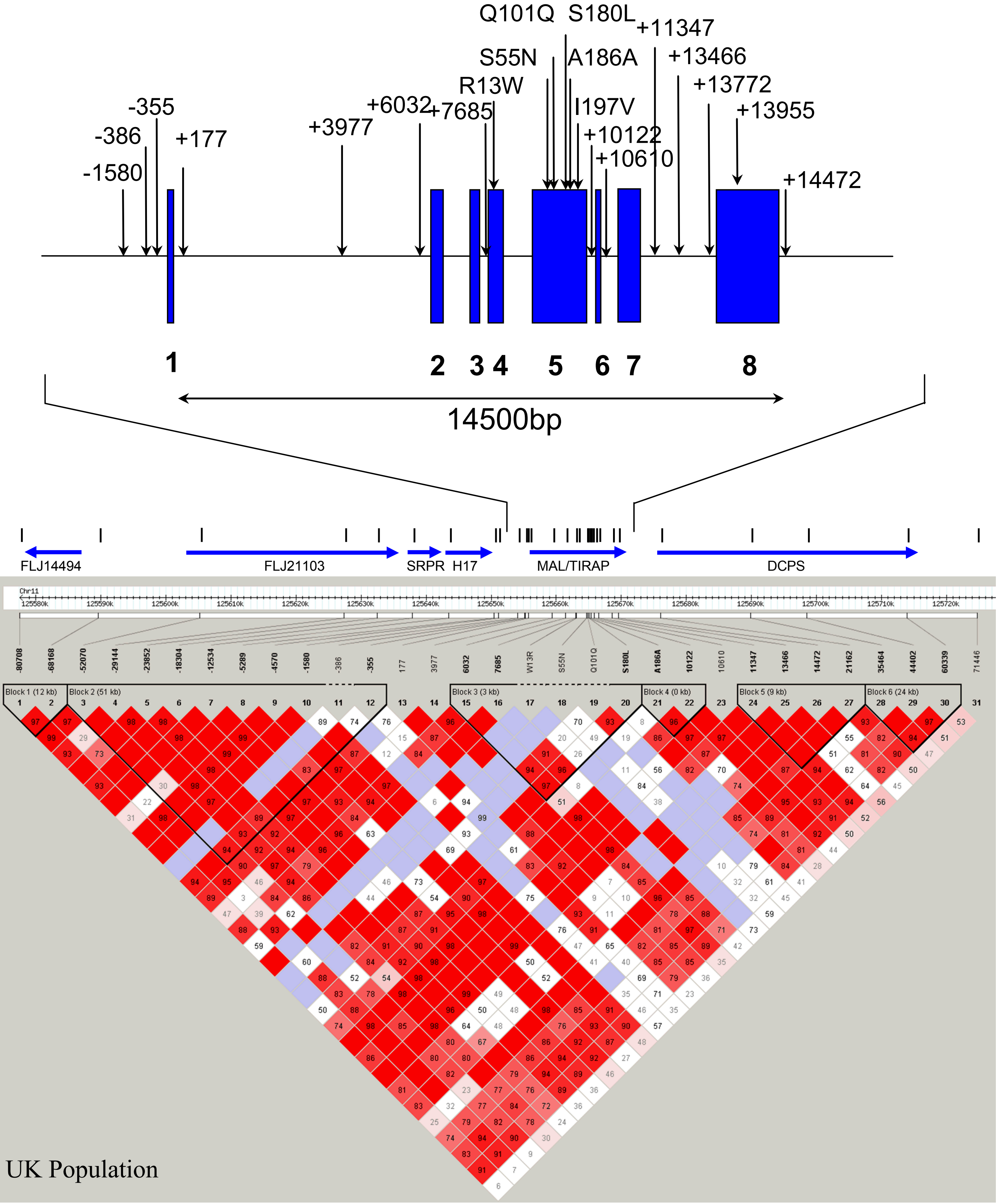
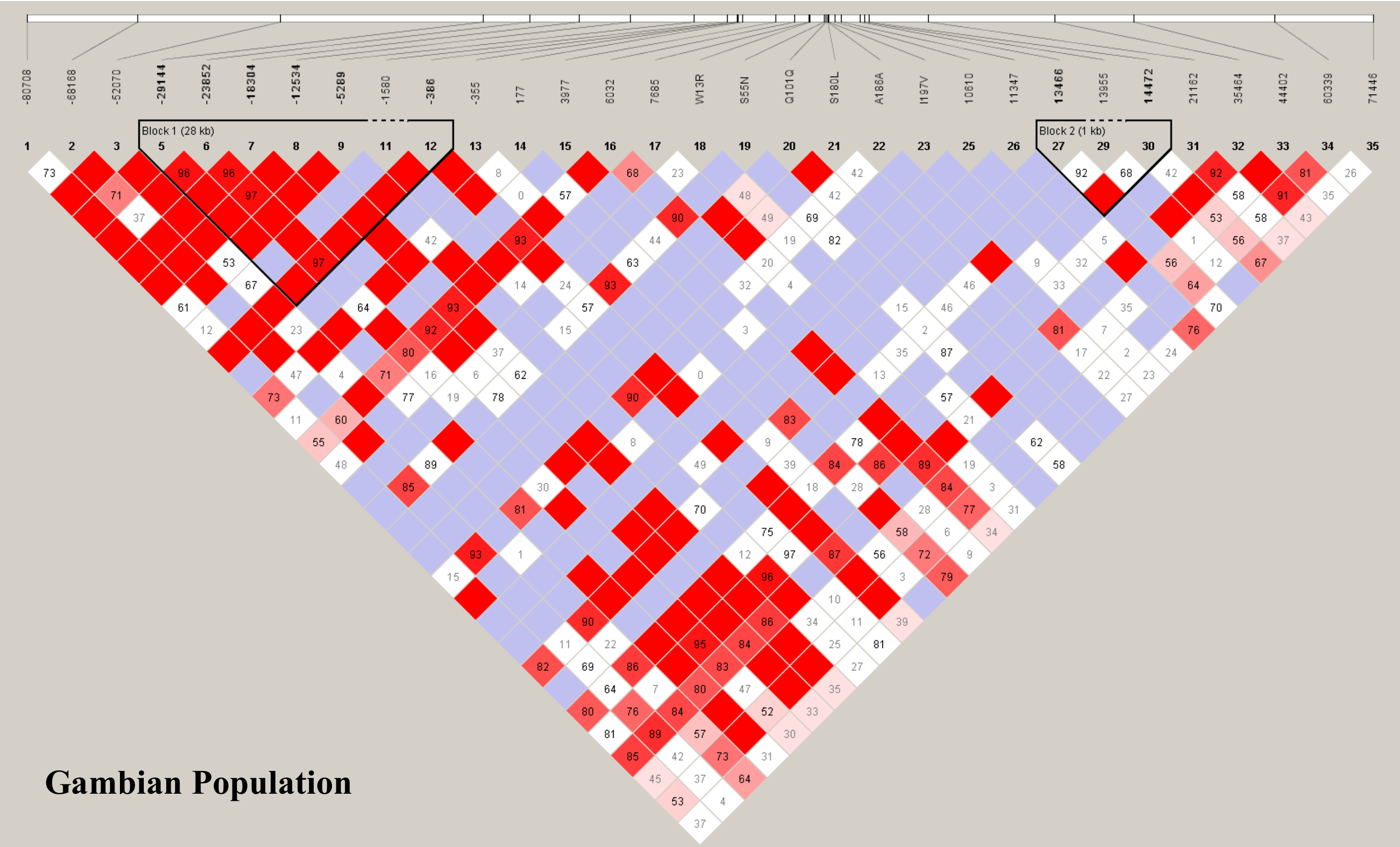
Supplementary Figure 1

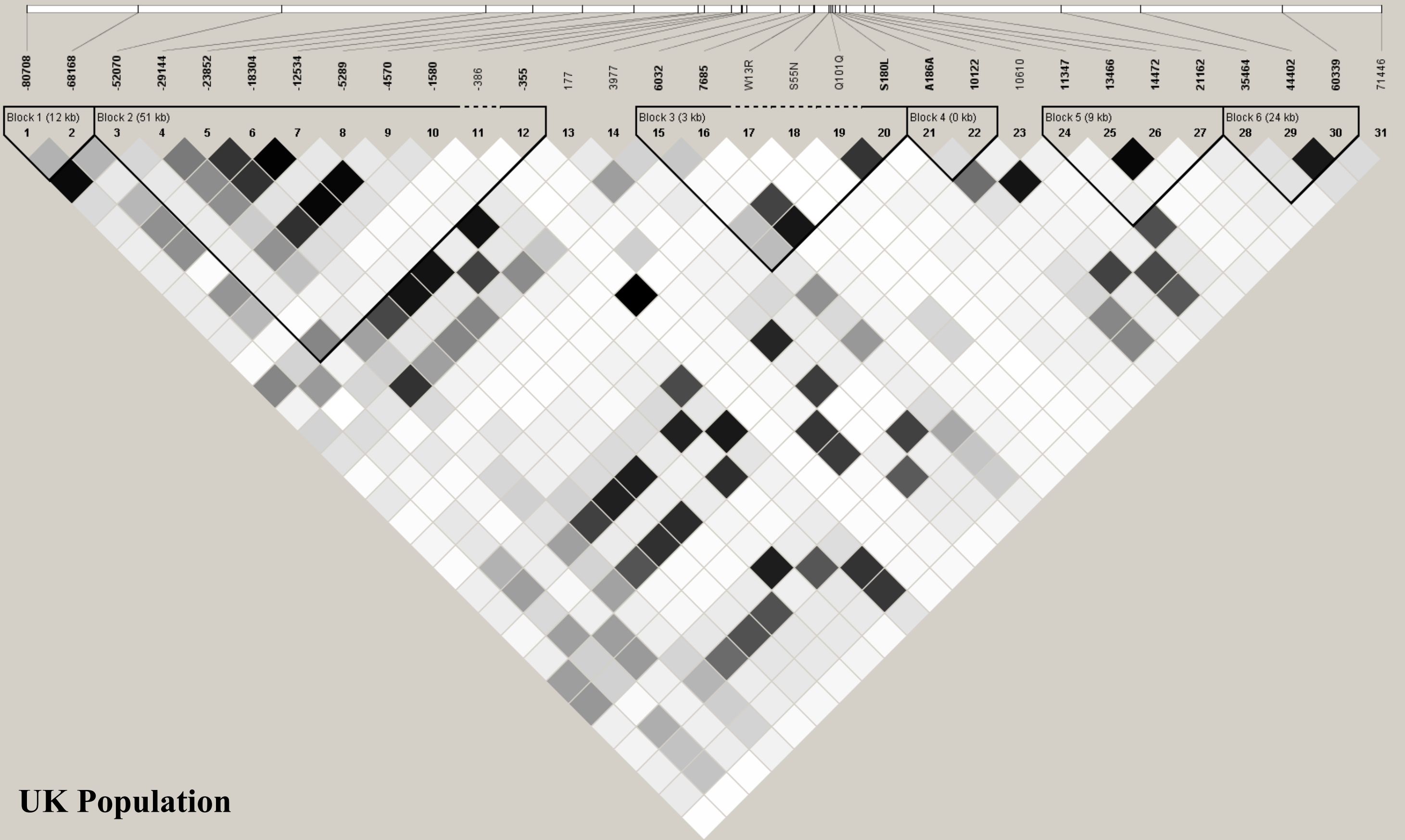
Supplementary Figure 1A. Genomic organisation and linkage disequilibrium (LD) of *TIRAP* and surrounding genomic region.



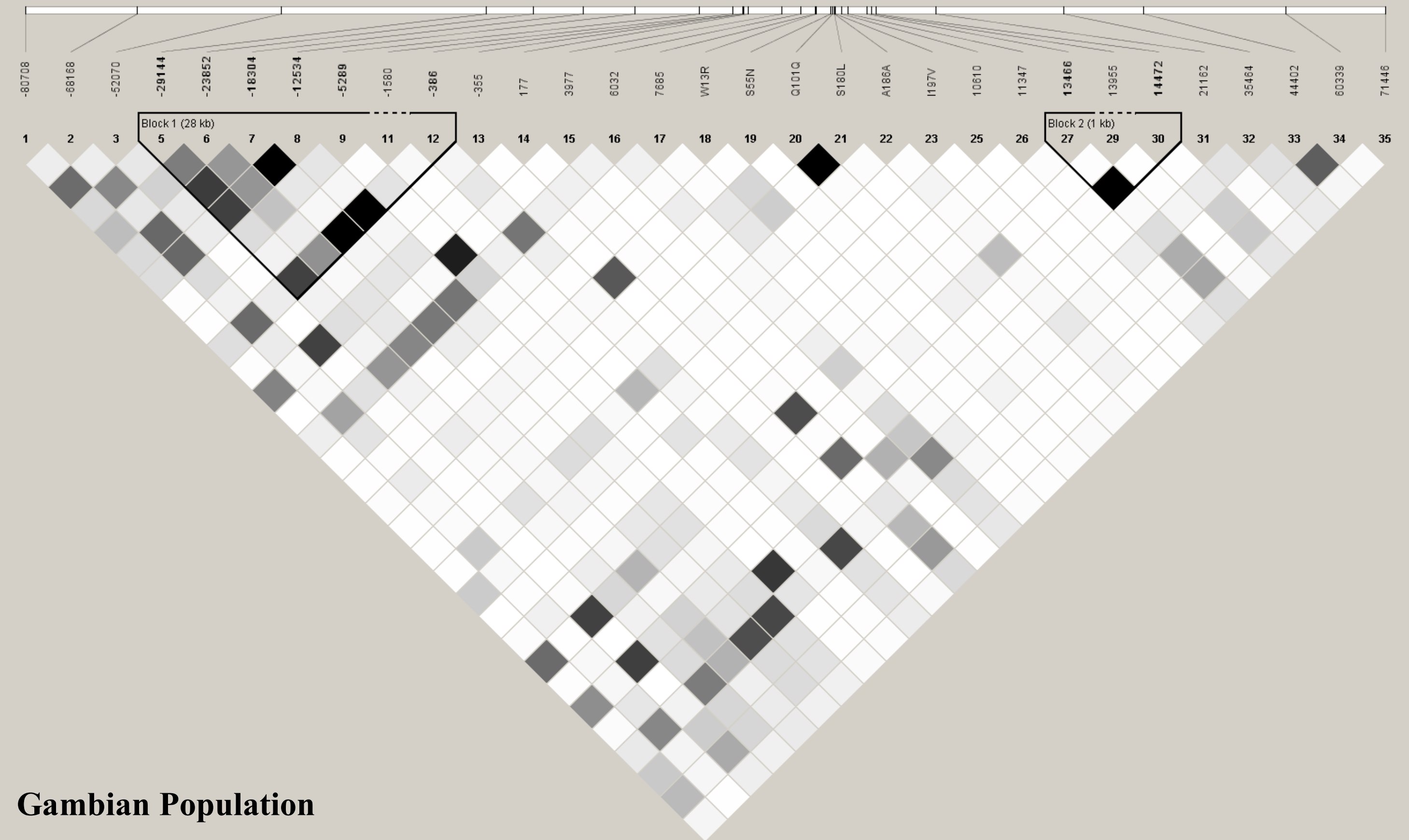


The upper panel illustrates the genomic organization of *TIRAP*. The positions of identified SNPs are marked and exons are numbered. The locations of genotyped SNPs within flanking genes are also shown. HaploView v3.2 plot across *TIRAP* for the UK (upper block) and Gambian (lower block) populations is displayed in the lower panel. Unfilled squares indicate a high degree of LD (LD coefficient D'=1) between pairs of markers. Numbers indicate the D' value expressed as a percentile. Red squares indicate pairs in strong LD with LOD scores for LD≥2, pink squares D'<1 with LOD≥2, blue squares D'=1 with LOD<2, white squares D'<1.0 and LOD<2. The SNPs shown from 5' to 3' are -80708, -68168, -52070, -29144, -23852, -18304, -12534, -5289, -4570, -1580, -386, -355, +177, +3977, +6032, +7685, R13W, S55N, Q101Q, S180L, A186A, V197I, +10122, +10610, +11347, +13466, +13955, +14472, +21162, +35464, +44402, +60339 and +71446. The V197I and +13955 polymorphisms were not present in UK individuals of European ancestry.

Supplementary Figure 1B. HaploView v3.2 plots demonstrating the extent of pairwise LD using the R squared algorithm among the 33 genotyped markers.



UK Population



Gambian Population