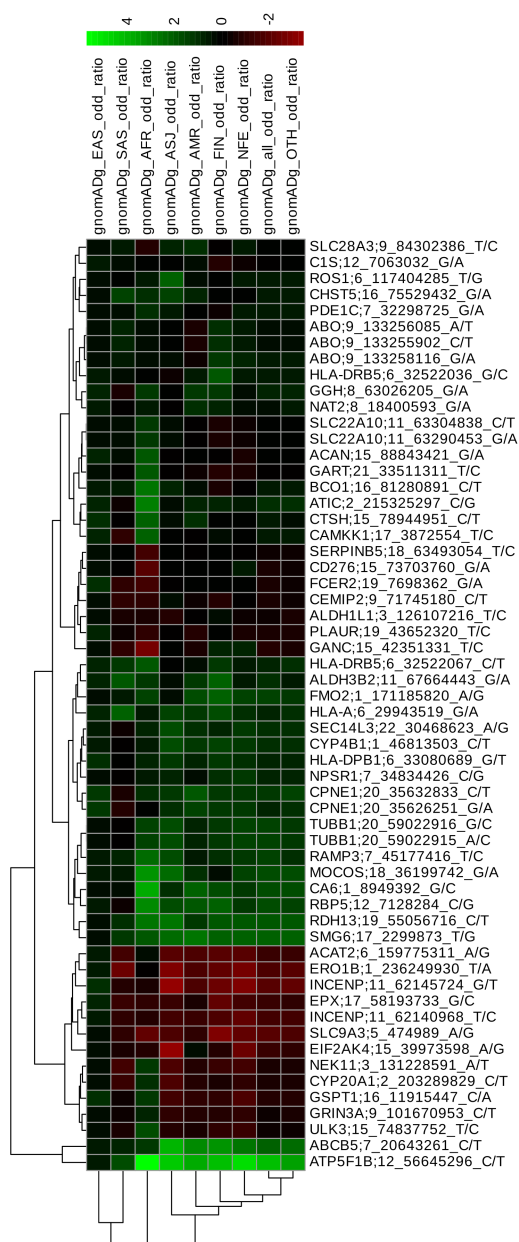
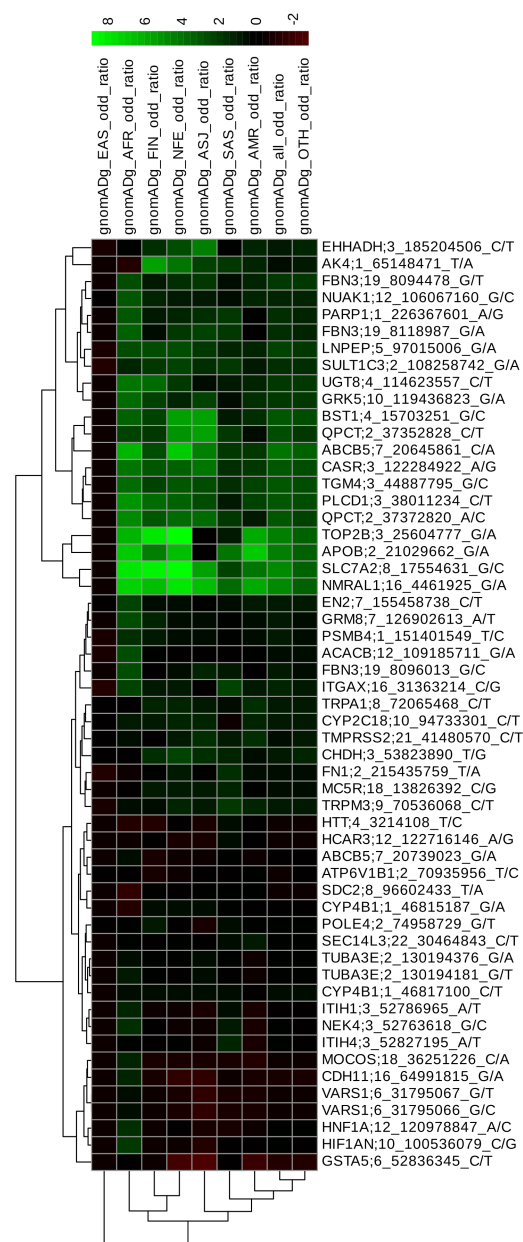


**(a)****(b)**

**Supplementary Figure S6. Heatmaps for the log2 odds ratios of allele frequencies for comparisons between the Thai population and other populations.** The log2 odds ratios of allele frequencies between Thais and nine compared populations from gnomAD genome database were represented by the heatmap colors for 113 common deleterious variants, of which

MAF were greater than 0.1 in Thais and were significantly different from the East Asians.

Heatmaps were separately displayed for (a) 58 variants with  $\log_2$  odds ratio greater than 0 (more frequent in Thais) and (b) 55 variants with the  $\log_2$  odds ratios less than 0 (less frequent in Thais compared to East Asians).