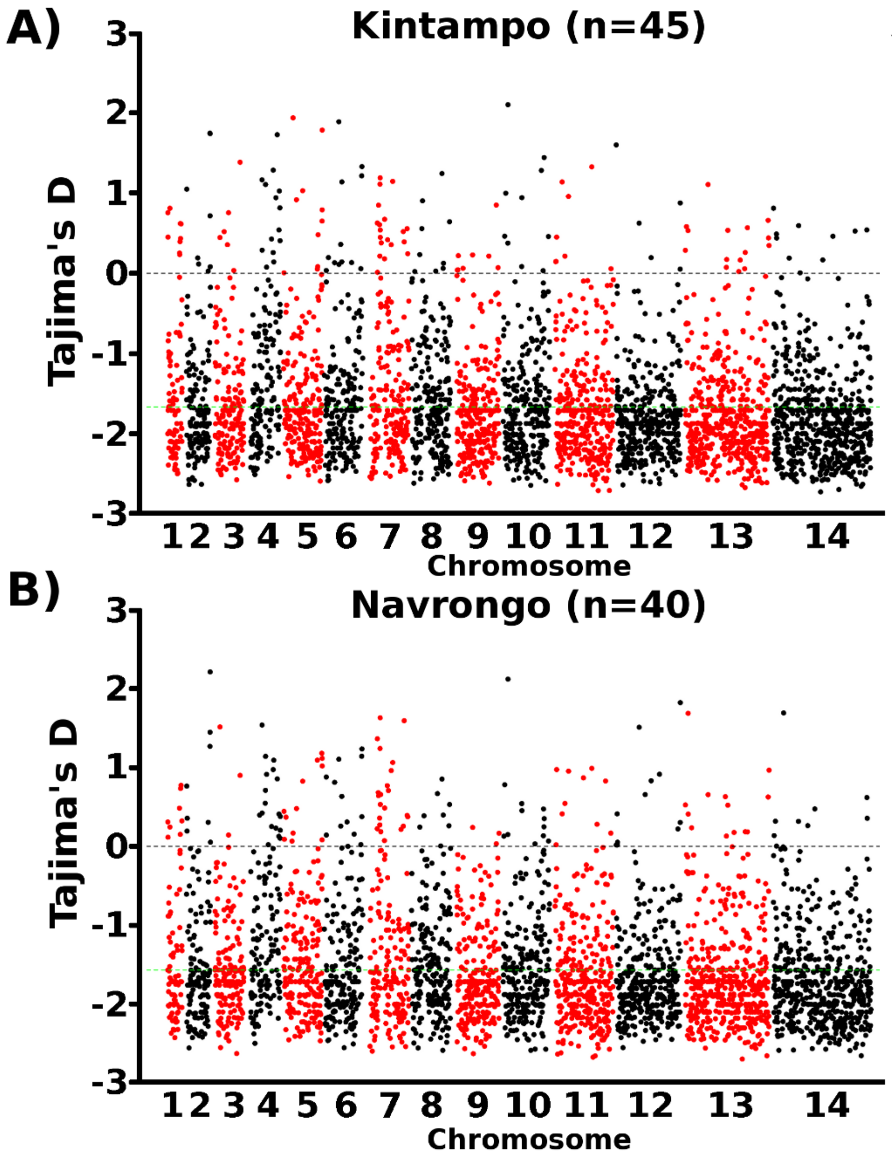
Supplementary Figures

Supplementary Figure S1. Allele frequency distributions of SNPs within genes in each of the two local *P. falciparum* population samples in Ghana. Kintampo population (N = 45), with gene indices plotted according to order in the genome. B. Navrongo population (N = 40), with indices similarly plotted.

Supplementary Figure S2. Principal Component Analysis of genome-wide SNP data (107547 SNPs with no missing data for any of these isolates) shows no difference between *P. falciparum* clinical isolates from the two local populations. Red points show isolates from Kintampo (N = 45) and blue points show isolates from Navrongo (N = 40). The first three principal components respectively account for 1.90%, 1.85%, and 1.83% of the total observed variation among isolates.

Supplementary Figure S1



Supplementary Figure S2