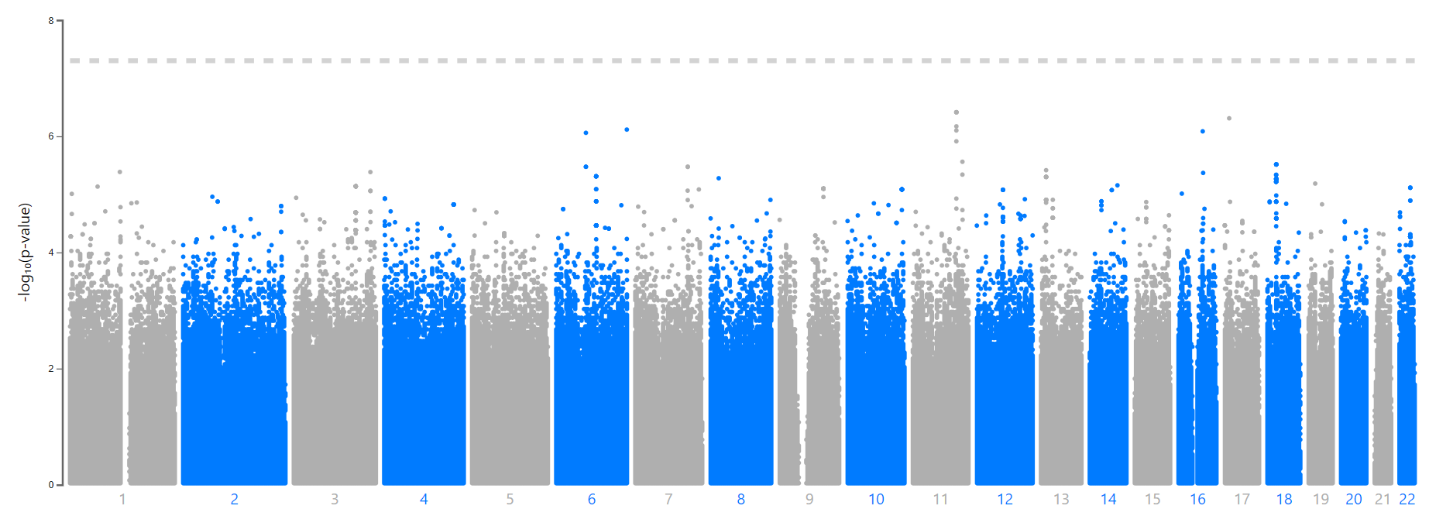
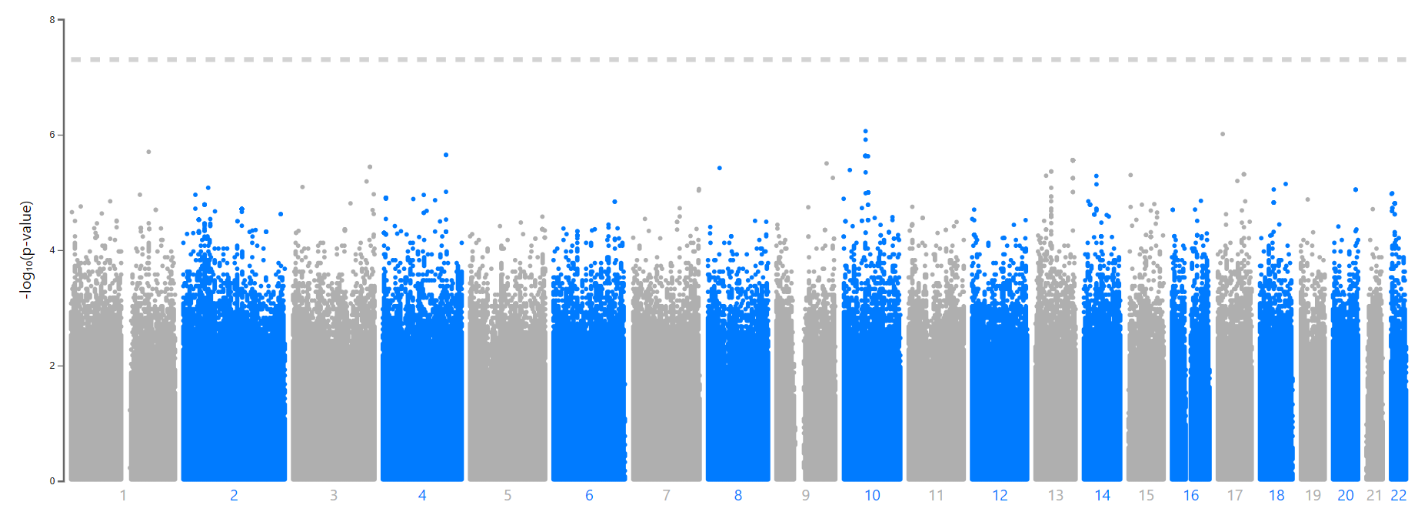
**Supplemental Figure 1. Manhattan Plot for Interaction Between SNP and L4.6/Ugandan Lineage in Cohort 1**

****

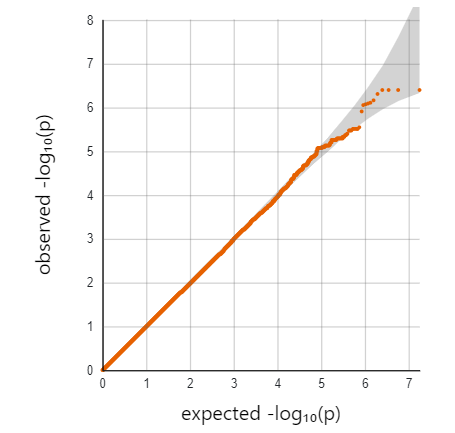
The Manhattan plot shows the inverse log(10) of the p-values for the association between interaction of each SNP and the L4.6/Ugandan lineage and TBscore on the y-axis and the x-axis represent the physical location of each SNP on the chromosomes, which are in order from 1-22.

**Supplemental Figure 2. Manhattan Plot for Interaction Between SNP and L4.6/Ugandan Lineage in Cohort 2**

****

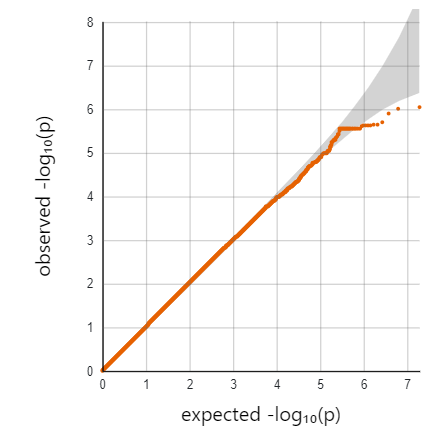
The Manhattan plot shows the inverse log(10) of the p-values for the association between interaction of each SNP and the L4.6/Ugandan lineage and TBscore on the y-axis and the x-axis represent the physical location of each SNP on the chromosomes, which are in order from 1-22.

**Supplemental Figure 3. Quantile-Quantile Plot for Interaction Between SNP and L4.6/Ugandan Lineage in Cohort 1**

****

The quantile-quantile (Q-Q) plot shows the inverse log(10) of the observed p-values on the Y-axis relative to what is expected if there was no association on the x-axis. Deviations above the line indicate an association with the outcome. If the line deviates at the low quantiles, then this is considered evidence to suggest genome-wide inflation of the test statistics, which typically indicates unmeasured confounding.

**Supplemental Figure 4. Quantile-Quantile Plot for Interaction Between SNP and L4.6/Ugandan Lineage in Cohort 2**

****

The quantile-quantile (Q-Q) plot shows the inverse log(10) of the observed p-values on the Y-axis relative to what is expected if there was no association on the x-axis. Deviations above the line indicate an association with the outcome. If the line deviates at the low quantiles, then this is considered evidence to suggest genome-wide inflation of the test statistics, which typically indicates unmeasured confounding.