Summary statistic files for TST resistance in HIV positive subjects.

TZ (Tanzania) dominant model with minor allele frequency (MAF) above 5%:

Summary results for analysis of data from Tanzania using a dominant coding. Only SNPs with minor allele frequency above 0.05 were included as per analytical methods.

UG (Uganda)dominant model MAF above 5%:

Summary results for analysis of data from Uganda using a dominant coding. Only SNPs with minor allele frequency above 0.05 were included as per analytical methods.

Combined (TZ and UG) dominant model MAF above 5%:

Summary results for analysis of data from Tanzania and Uganda combined using a dominant coding. Only SNPs with minor allele frequency above 0.05 were included as per analytical methods.

Headings in all files:

CHR Chromosome

SNP SNP identifier (rs number)

BP Physical position (base-pair)

A1 Tested allele (minor allele by default)

TEST Coding for the test

NMISS Number of non-missing individuals included in analysis

OR Odds ratio (--logistic)

SE- standard error of OR

L95 – lower limit of 95% confidence interval

U95 – Upper limit of 95% confidence interval

STAT Coefficient t-statistic

P Asymptotic p-value for t-statistic