

Supplementary Table 1. Summary of single nucleotide variants identified in 47 efflux pump genes studied

Definition of dataset	Susceptible MTB (n=1432)	MDR-TB (n=200)	Pre-XDR-TB (n=172)	XDR-TB (n=417)
<i>Total no. of variants</i>	1436 [#]	170	222	284
Non-Coding Variants	89	107	3	12
Synonymous Variants	446	12	60	87
Frameshift variants	63	30	22	26
Missense Variants	814	11	129	151
Stop-gain Variants	21	9	8	8
Stop-loss Variants	0	1	0	0
Start Loss	3	0	0	0
Unique Variants		91* (53.5%)	153 *(68.9)	174* (61.3)

[#], identified by comparison of genomes from susceptible strains with H37Rv; *, identified by comparison of MDR, pre-XDR or XDR genomes as compared with susceptible strains