

Lineage	Name of SNPs	Name of gene	Nucleotide position	codon	Nucleotide in H37Rv	AA in H37Rv	Nucleotide in Mutant	AA in Mutant
Euro-American (Lineage4)	<i>katG</i> 463	<i>katG</i> or Rv1908c	1389	463	CGG	Arg	CTG	Leu
East-Asian (Lineage2)	Rv2952_0526n	Rv2952	526	176	GGG	Gly	AGG	Arg
Indo-oceanic (Lineage1)	Rv3221c_0085n	TB.3 or Rv3221c	85	29	GTC	Val	ATC	Ile
East-African-Indian (Lineage3)	Rv3804c_0012n	<i>fbpA</i> or Rv3804c	12	4	GTT	Val	GTC	Val
TbD1	<i>gyrA</i> 1842	<i>gyrA</i> or Rv0006	1842	614	ATT	Ile	ATC	Ile
Bovis-Mada	<i>PstS1</i> _1055	<i>PstS1</i> or Rv0934	1055	352	GTT	Val	GCT	Ala

S1 Table. SNPs (n=6) or mutations characteristic of *M. tuberculosis* lineage. AA: Amino-Acids, SNP: Single Nucleotide Polymorphism, H37Rv: reference strain of *M. tuberculosis*, In bold the nucleotide mutated