

Supplemental Table 1. SNP differences between the *in vitro* selected LZD resistant mutant (9679/00 1.1.2) and the reference sequence H37Rv.

Position	Reference	SNP	Frequency	Count	Coverage	Substitution	Annotation
55553	C	T	100	34	34	Pro -> Ser	Gene: ponA1. CDS: ponA1*
234477	T	G	100	8	8	Tyr -> Stp	Gene: Rv0197. CDS: oxidoreductase*
333892	G	C	100	6	6	Arg -> Gly	Gene: PE_PGRS3. CDS: PE_PGRS3
338100	T	C	100	12	12	Asn -> Ser	Gene: PE_PGRS4. CDS: PE_PGRS4
467516	G	C	100	15	15		Gene: PPE9. CDS: PPE9
623472	A	G	100	7	7	Asp -> Gly	Gene: PE_PGRS6. CDS: PE_PGRS6
635633	C	T	100	116	116		Gene: Rv0543c. CDS: hypothetical protein*
801268	T	C	100	69	69	Cys -> Arg	Gene: rplC. CDS: rplC
836272	A	G	100	14	14	Glu -> Gly	Gene: PE_PGRS9. CDS: PE_PGRS9
836291	A	G	100	11	11		Gene: PE_PGRS9. CDS: PE_PGRS9
836454	A	G	100	18	18	Thr -> Ala	Gene: PE_PGRS9. CDS: PE_PGRS9
836538	A	G	100	14	14	Asn -> Asp	Gene: PE_PGRS9. CDS: PE_PGRS9
838990	C	G	100	4	4		Gene: PE_PGRS10. CDS: PE_PGRS10
839334	A	G	100	7	7	Lys -> Arg	Gene: PE_PGRS10. CDS: PE_PGRS10
839348	A	G	100	4	4	Ser -> Gly	Gene: PE_PGRS10. CDS: PE_PGRS10
840496	C	G	100	6	6		Gene: PE_PGRS10. CDS: PE_PGRS10

958922	C	A	100	119	119		Gene: ercc3. CDS: ercc3*
1244700	G	C	100	107	107	Val -> Leu	Gene: zwf1. CDS: zwf1*
1313338	A	C	100	37	37		n.n.
1711627	C	T	100	119	119		Gene: Rv1520. CDS: sugar transferase*
1823438	C	T	100	108	108	Trp -> Stp	Gene: cydB. CDS: cydB*
2006032	A	G	98	130	132	Gln -> Arg	Gene: Rv1771. CDS: oxidoreductase*
2153410	A	G	100	148	148	Val -> Ala	Gene: Rv1907c. CDS: hypothetical protein*
2219929	T	C	100	53	53	Leu -> Pro	Gene: Rv1977. CDS: hypothetical protein*
2473038	C	A	100	45	45		Gene: cobS. CDS: cobS*
3105736	G	C	100	60	60	Asn -> Lys	Gene: Rv2797c. CDS: hypothetical protein*
3379718	T	C	100	12	12		Gene: PPE47. CDS: PPE47
3379757	A	C	100	7	7		Gene: PPE47. CDS: PPE47
3379763	G	A	100	14	14		Gene: PPE47. CDS: PPE47
3748105	C	G	100	87	87	Asp -> His	Gene: PPE55. CDS: PPE55

*denotes genes that were also present in the genomes of three further H37Rv variants selected *in vitro* for resistance to other antibiotics (possible failures in the H37Rv reference sequence).