**Supplementary File 5.** Assembly metrics for Single Molecule Real-Time sequencing of MT-0080 (‘MT-0080\_PB’), aligned to NC\_000962.3 (H37Rv).

|  |  |
| --- | --- |
|  | **MT-0080\_PB** |
| Number of contigs | 1 |
| Largest contig, length in bp | 4,426,525 |
| GC content, % | 65·61 |
| Genome fraction covered, % | 99·28 |
| Largest alignment, bp | 592,812 |
| Total aligned length, bp | 4,387,983 |
| NG50 | 4,426,525 |
| NA50 | 256,105 |
| Reads mapped, % | 97·48 |
| Average depth of coverage, using filtered reads | 235 |
| Coverage ≥ 10x, % | 100 |
| Number of relocations | 50 |
| Number of inversions | 1 |
| Number of missing bases (‘N’) | 0 |
| Number of CDS | 4,321 |
| Number of RNA | 47 |
| Average nucleotide identity to H37Rv | 99·92% |