

S4 Table: Statistics of *M. leprae* whole genome sequences

	Alignment rate (%)¹	Average read depth coverage¹
1126-2007	38.98	6.27
1126-2011	23.47	11.21
3208-2007	42.33	37.19
3208-2015	66.41	31.38
2188-2007	72.36	123.86
2188-2014	16.74	58.25

¹ Fraction of total reads that aligned to the reference genome TN.