Table S1. Quality of Illumina MiSeq genome sequence data.

Strain	Total sequence bases	Number of paired reads (2x)	Number of mapped reads (1x)	Percentage of reference sequenced	Percentage of reference with ≥ 5 reads	Mean coverage ± SD	Mean mapping quality
PL1	1,695,850,781	6,253,736	3,165,344	96.17%	94.07%	73 ± 40	58.22
PL2	1,840,022,251	6,843,040	3,462,925	96.37%	93.92%	79 ± 46	58.13
PL5	1,898,391,977	7,052,785	3,572,673	95.73%	94.64%	82 ± 39	58.10
PL7	1,811,579,470	6,710,022	3,393,759	95.85%	94.37%	78 ± 38	58.14