Supporting Information for:

Choice of reference sequence and assembler for alignment of *Listeria monocytogenes* short-read sequence data greatly influences rates of error in SNP analyses

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Table S3: Summary statistics describing three sequencing runs of four *Listeria monocytogenes* strain 08-5578 genomic DNA samples on an Illumina MiSeq benchtop sequencer. Genomic DNA was extracted from an *L. monocytogenes* strain 08-5578 culture grown from a single colony. The sample was then divided into four subsamples that were indexed and sequenced three times.

Run	Yield	Average Cluster Density (k/mm2)	Total Reads	Reads Passing Filter
1	3.96GB	478.5	9,357,411	8,506,127
2	1.16GB	178.5	5,077,244	2,302,912
3	7.76GB	1075.0	19,068,628	16,320,666