

**Supplementary Table S1.** Genomes used for simulated datasets to evaluate error correction.

<b>Entry</b>	<b>Size (bp)</b>	<b>Abundance (%)<sup>1</sup></b>
NC_015189.1	5,178	6.33
NC_010940.1	3,533	1.00
NC_010580.1	181,736	1.78
NC_017867.1	1,938,822	2.71
NC_015052.1	2,400,312	0.45
NC_015920.1	29,448	1.02
NC_009713.1	3,678	4.58
NC_015914.1	6,221,273	4.95
NC_008255.1	4,433,218	0.06
NC_011661.1	1,855,560	0.54
NC_017910.1	4,158,725	2.20
NC_017631.1	5,131,397	5.55
NC_011419.1	100,021	1.27
NC_017642.1	90,868	1.75
NC_014558.2	53560	10.8
NC_013199.1	2968598	5.25
NC_008576.1	4719581	1.51
NC_014002.1	2012424	1.57
NC_010727.1	25164	0.54
NC_014563.1	165693	7.18
NC_016818.1	4861101	2.56
NC_007908.1	4712337	2.84
NC_015729.1	63532	0.90
NC_007954.1	4545906	4.43

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NC_010506.1	5935403	5.19
NC_014009.1	5398	10.0
NC_017098.1	3285855	1.00
NC_015757.1	3551206	4.74
NC_017268.1	1139281	1.69
NC_016842.1	1139330	5.58

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<sup>1</sup> Relative abundance of reads.