Supplementary Data

Table S1 - Table of assembly statistics for the sequenced genomes: strain name, number of reads, number of contigs, contig N50, genome size, fold coverage, and GenBank assembly ID.

Strain name	**Number of reads**	**Number of contigs**	**Contig N50**	**Genome size (Mb)**	**Fold coverage**	**GenBank accession**
SA43	3,409,873	40	1,536,665 GC%=32.92	2.82	284X	JSBI00000000
A2	4,088,464	66	1,440,939 GC%=33.05	2.82	325X	LELL00000000
A5	675,092	89	1,409,311 GC%=33.01	2.81	46X	LELM00000000
A7	2,263,463	94	1,414,869 GC%=33.09	2.80	177X	LELN00000000
A10	1,971,416	45	1,478,751 GC%=32.92	2.82	145X	LELO00000000
B2	2,860,230	39	1,556,090 GC%=32.92	2.82	209X	LELP00000000
B6	2,982,466	69	1,412,843 GC%=32.93	2.82	219X	LELQ00000000
B7	2,671,694	55	1,432,992 GC%=32.92	2.82	205X	LELR00000000

B10	790,468	45	1,568,876 GC%=32.97	2.82	61X	LELS00000000
C2	1,493,209	80	1,474,449 GC%=33.08	2.79	115X	LELT00000000
C4	254,73	334	1,308,960 GC%=33.49	2.61	17X	LELU00000000
C6	1,534,853	51	1,454,050 GC%32.98	2.82	110X	LELV00000000
C7	1,749,922	53	1,464,338 GC%=32.87	2.82	114X	LELW00000000