

**Table S1.** Scaffolding of Illumina assemblies (CLC) using SSPACE and Ion Torrent PGM mate-pair library reads. SSPACE used bowtie as the aligner. Expected insert size between paired reads, minimum allowed error, and the orientation of paired reads were set to 3000, 0.5, and RR, which were estimated after initial mapping using CLC Genomics Workbench. Parameters for SSPACE running were -k 5 -a 0.7 -o 20 -T 24.

Strains	Before scaffolding	After scaffolding	% changes
<i>Shigella boydii</i> ATCC 9210	417 contigs	89 scaffolds	No. of contigs: 21.3%
	Sum = 4319423	Sum = 4544256	N50: 1057.9%
	Max = 104473	Max = 629220	
	N50 = 22487	N50 = 237891	
<i>Pseudomonas syringae</i> pv. <i>syringae</i> KCTC 12500	90 contigs	59 scaffolds	No. of contigs: 65.6%
	Sum = 6092296	Sum = 6106646	N50: 386.1%
	Max = 667266	Max = 1561385	
	N50 = 393565	N50 = 1519549	
<i>Pseudomonas amygdali</i> pv. <i>lachrymans</i> 98A-744	260 contigs	96 scaffolds	No. of contigs: 36.9%
	Sum = 6154729	Sum = 6280482	N50: 525.9%
	Max = 266682	Max = 794048	
	N50 = 83802	N50 = 440720	
	N's = 3249	N's = 130436	

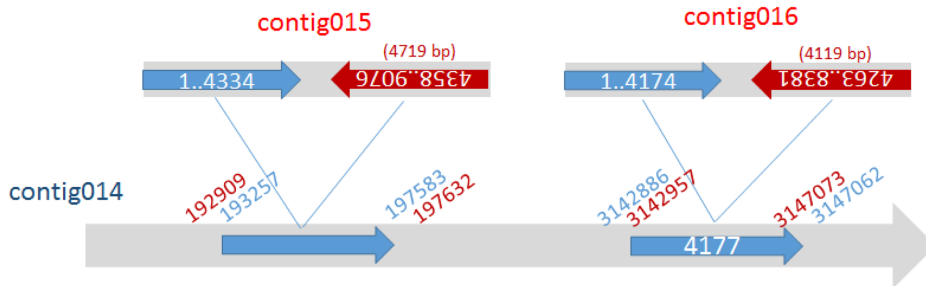
**Table S2.** Error correction of PacBio HGAP assemblies using Illumina data.

Strains	No. of variants after 1 <sup>st</sup> round	No. of variants after 2 <sup>nd</sup> round	No. of variants after 3 <sup>rd</sup> round
<i>Shigella boydii</i> ATCC 9210	16	133	181
<i>Pseudomonas syringae</i> pv. <i>syringae</i> KCTC 12500	8	0	0
<i>Pseudomonas amygdali</i> pv. <i>lachrymans</i> 98A-744	15	0	0

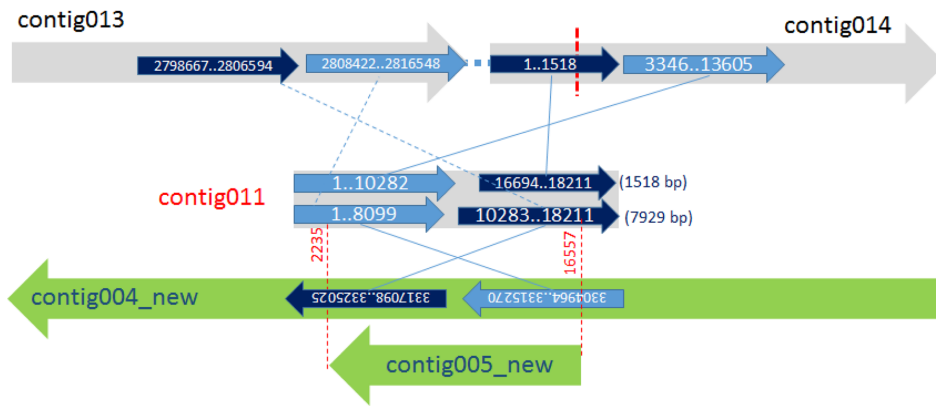
**Table S3.** Mapping and scaffold statistics for Ion Torrent mate-pair reads on A5-miseq and CLC assemblies. Bowtie and SSPACE Premium v2.3 were used read mapping and evaluation of mapping results, respectively.

Strains	A5-miseq	CLC Genomics Workbench
<i>Shigella boydii</i> ATCC 9210 (201991 read pairs)	Mapped pairs = 44273 Consistent pairs = 37663 96 scaffolds Sum = 4512631 Max = 336538 N50 = 136335	Mapped pairs = 54606 Consistent pairs = 50591 89 scaffolds Sum = 4544256 Max = 629220 N50 = 237891
<i>Pseudomonas syringae</i> pv. <i>syringae</i> KCTC 12500 (156759 read pairs)	Mapped pairs = 3123 Consistent pairs = 2392 64 scaffolds Sum = 6119547 Max = 1435830 N50 = 1121134	Mapped reads = 4123 Consistent pairs = 3947 59 scaffolds Sum = 6106646 Max = 1561385 N50 = 1519549
<i>Pseudomonas amygdali</i> pv. <i>lachrymans</i> 98A-744 (144293 read pairs)	Mapped pairs = 13646 Consistent pairs = 11146 69 scaffolds Sum = 6277105 Max = 1044266 N50 = 346807	Mapped reads = 22027 Consistent pairs = 20933 96 scaffolds Sum = 6280482 Max = 794048 N50 = 440720

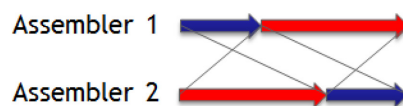
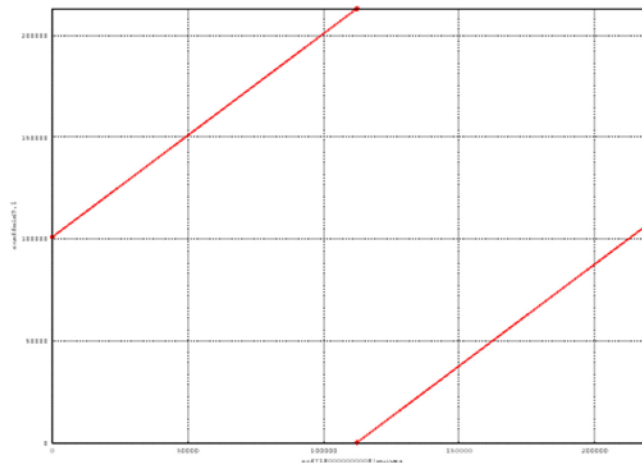
*Shigella boydii* ATCC 9210



*Pseudomonas syringae* pv. *syringae*



**Fig. S1.** Examples of small HGAP contigs that are completely contained in the main contig.



**Fig. S2.** MUMmer-based alignment of contig sequence from a putative plasmid from HS311 (211 kb), produced from two different sequencing results suggest its circular topology. Horizontal axis, PacBio HGAP-assembly; vertical axis, Illumina a5-miseq assembly.

**Table S#.** Mapping and scaffold statistics for Ion Torrent mate-pair reads on A5-miseq and CLC assemblies. Bowtie and SSPACE Premium v2.3 were used read mapping and evaluation of mapping results, respectively.

Strains	A5-miseq	CLC Genomics Workbench
<i>Shigella boydii</i> ATCC 9210 (201991 read pairs)	Mapped pairs = 44273 Consistent pairs = 37663 96 scaffolds Sum = 4512631 Max = 336538 N50 = 136335	Mapped pairs = 54606 Consistent pairs = 50591 89 scaffolds Sum = 4544256 Max = 629220 N50 = 237891
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