

**Supplemental Table S1. Comparison of Racon consensus with overlapping windows (ovl) and the default Racon consensus with non-overlapping windows.** In the default version windows are of length 500bp. For the overlap version, every window is extended by 10% on each of its ends, causing a 100bp overlap with the previous/next window.

		Miniasm+Racon 1 iteration	Miniasm+Racon 2 iterations	Miniasm+Racon ovl. 1 iteration	Miniasm+Racon ovl. 2 iterations	
<i>Lambda</i>	Ref. genome size [bp]	48502	48502	48502	48502	
	Total bases [bp]	47916	47872	47852	47856	
	Ref. chromosomes [#]	1	1	1	1	
	ONT	Contigs [#]	1	1	1	1
	30×	Aln. bases ref. [bp]	48438 (99.87%)	48434 (99.86%)	48438 (99.87%)	48434 (99.86%)
		Aln. bases query [bp]	47916 (100.00%)	47872 (100.00%)	47852 (100.00%)	47856 (100%)
		Avg. Identity	97.59	97.97	97.60	98.02
<i>E. coli</i> K-12	Ref. genome size [bp]	4641652	4641652	4641652	4641652	
	Total bases [bp]	4637173	4632058	4634190	4630935	
	Ref. chromosomes [#]	1	1	1	1	
	ONT	Contigs [#]	1	1	1	1
	R7.3	Aln. bases ref. [bp]	4640867 (99.98%)	4641323 (99.99%)	4641016 (99.99%)	4641323 (99.99%)
	54×	Aln. bases query [bp]	4636689 (99.99%)	4632055 (100.00%)	4634187 (100.00%)	4630932 (100.00%)
		Avg. Identity	99.13	99.32	99.18	99.34
<i>S. cerevisiae</i> S288C	Ref. genome size [bp]	12157105	12157105	12157105	12157105	
	Total bases [bp]	12172019	12167797	12164303	12163261	
	Ref. chromosomes [#]	17	17	17	17	
	ONT	Contigs [#]	42	42	42	42
	R9	Aln. bases ref. [bp]	12104541 (99.57%)	12110095 (99.61%)	12104999 (99.57%)	12111938 (99.63%)
	59×	Aln. bases query [bp]	12108082 (99.48%)	12115796 (99.57%)	12101200 (99.48%)	12113024 (99.59%)
		Avg. Identity	97.88	98.04	97.89	98.02
<i>E. coli</i> K-12	Ref. genome size [bp]	4641652	4641652	4641652	4641652	
	Total bases [bp]	4653199	4645508	4650598	4644089	
	Ref. chromosomes [#]	1	1	1	1	
	PacBio	Contigs [#]	1	1	1	1
	P6C4	Aln. bases ref. [bp]	4641501 (100.00%)	4641439 (100.00%)	4641501 (100.00%)	4641439 (100.00%)
	160×	Aln. bases query [bp]	4653111 (100.00%)	4645508 (100.00%)	4650536 (100.00%)	4644089 (100.00%)
		Avg. Identity	99.63	99.90	99.69	99.94
<i>S. cerevisiae</i> W303	Ref. genome size [bp]	12157105	12157105	12157105	12157105	
	Total bases [bp]	12071278	12051573	12065231	12047858	
	Ref. chromosomes [#]	17	17	17	17	
	PacBio	Contigs [#]	30	30	30	30
	P4C2	Aln. bases ref. [bp]	12023607 (98.90%)	12025677 (98.92%)	12022784 (98.90%)	12023956 (98.90%)
	127×	Aln. bases query [bp]	12046299 (99.79%)	12027338 (99.80%)	12040526 (99.80%)	12024239 (99.80%)
		Avg. Identity	99.43	99.72	99.48	99.74
<i>C. elegans</i>	Ref. genome size [bp]	100272607	100272607	100272607	100272607	
	Total bases [bp]	106353704	106392402	106246733	106276277	
	Ref. chromosomes [#]	6	6	6	6	
	PacBio	Contigs [#]	77	77	77	76
	P6C4	Aln. bases ref. [bp]	100017898 (99.75%)	99979140 (99.71%)	100017956 (99.75%)	99990098 (99.72%)
	81×	Aln. bases query [bp]	101711974 (95.64%)	101741297 (95.63%)	101608070 (95.63%)	101638862 (95.64%)
		Avg. Identity	99.44	99.73	99.47	99.77