

Report

	yeast_1d.guppy_213.canu	polished_genome	polished_genome_racon
# contigs (>= 0 bp)	28	28	28
# contigs (>= 1000 bp)	28	28	28
# contigs (>= 5000 bp)	27	27	27
# contigs (>= 10000 bp)	27	27	27
# contigs (>= 25000 bp)	23	23	23
# contigs (>= 50000 bp)	19	19	19
Total length (>= 0 bp)	12396504	12445256	12444850
Total length (>= 1000 bp)	12396504	12445256	12444850
Total length (>= 5000 bp)	12393564	12442316	12441903
Total length (>= 10000 bp)	12393564	12442316	12441903
Total length (>= 25000 bp)	12315344	12363598	12363166
Total length (>= 50000 bp)	12187661	12235859	12235915
# contigs	28	28	28
Largest contig	1095012	1099417	1099192
Total length	12396504	12445256	12444850
Reference length	12157105	12157105	12157105
GC (%)	38.18	38.12	38.12
Reference GC (%)	38.15	38.15	38.15
N50	822302	825460	825513
NG50	906352	909870	909841
N75	542910	545057	545086
NG75	542910	669406	669437
L50	7	7	7
LG50	6	6	6
L75	11	11	11
LG75	11	10	10
# misassemblies	109	110	108
# misassembled contigs	22	22	22
Misassembled contigs length	12281598	12330013	12329731
# local misassemblies	87	86	94
# unaligned mis. contigs	0	1	0
# unaligned contigs	4 + 16 part	4 + 15 part	4 + 17 part
Unaligned length	144181	179178	152923
Genome fraction (%)	97.565	97.380	97.626
Duplication ratio	1.033	1.036	1.036
# N's per 100 kbp	0.00	0.00	0.02
# mismatches per 100 kbp	212.37	207.85	205.12
# indels per 100 kbp	343.76	73.09	25.04
Largest alignment	793752	796529	796503
Total aligned length	12248096	12260835	12289078
NA50	328144	329389	329272
NGA50	328144	329389	329272
NA75	180039	180725	180756
NGA75	184613	185295	185303
LA50	12	12	12
LGA50	12	12	12
LA75	26	26	26
LGA75	25	25	25

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

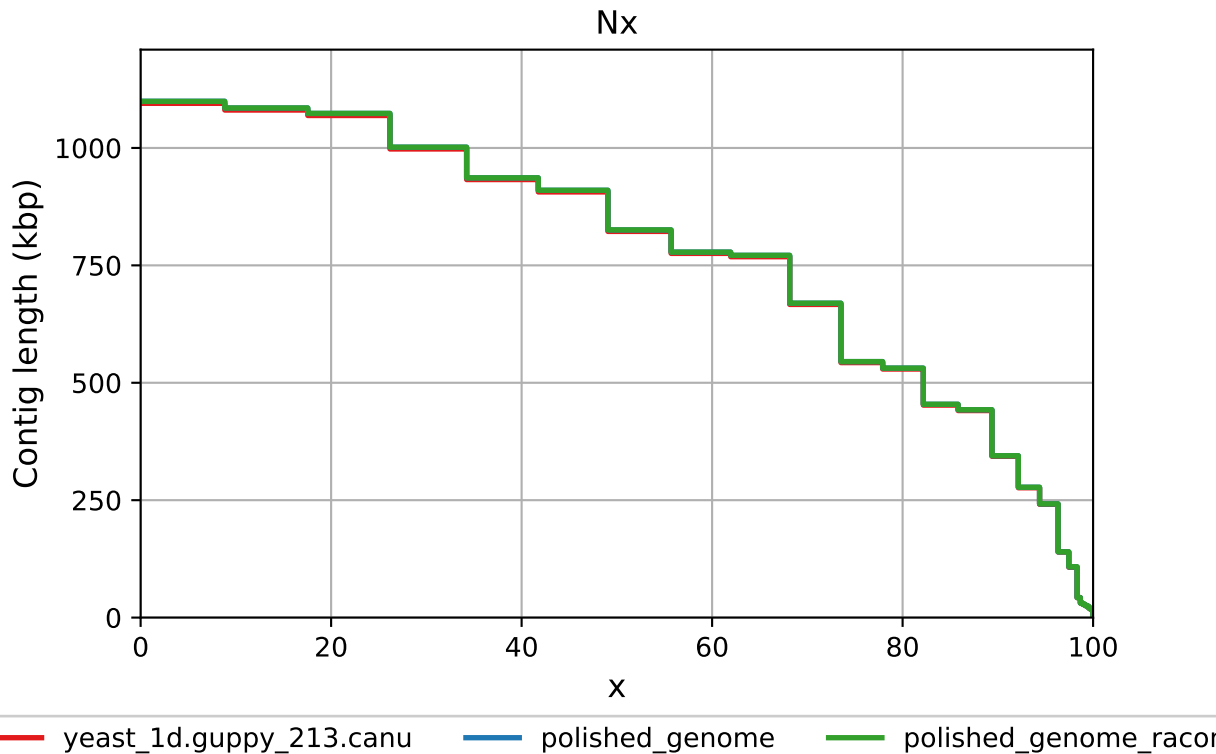
	yeast_1d.guppy_213.canu	polished_genome	polished_genome_racon
# misassemblies	109	110	108
# relocations	47	46	44
# translocations	62	64	64
# inversions	0	0	0
# misassembled contigs	22	22	22
Misassembled contigs length	12281598	12330013	12329731
# local misassemblies	87	86	94
# unaligned mis. contigs	0	1	0
# mismatches	25189	24607	24345
# indels	40773	8653	2972
# indels (<= 5 bp)	40158	8308	2611
# indels (> 5 bp)	615	345	361
Indels length	55736	15539	10350

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

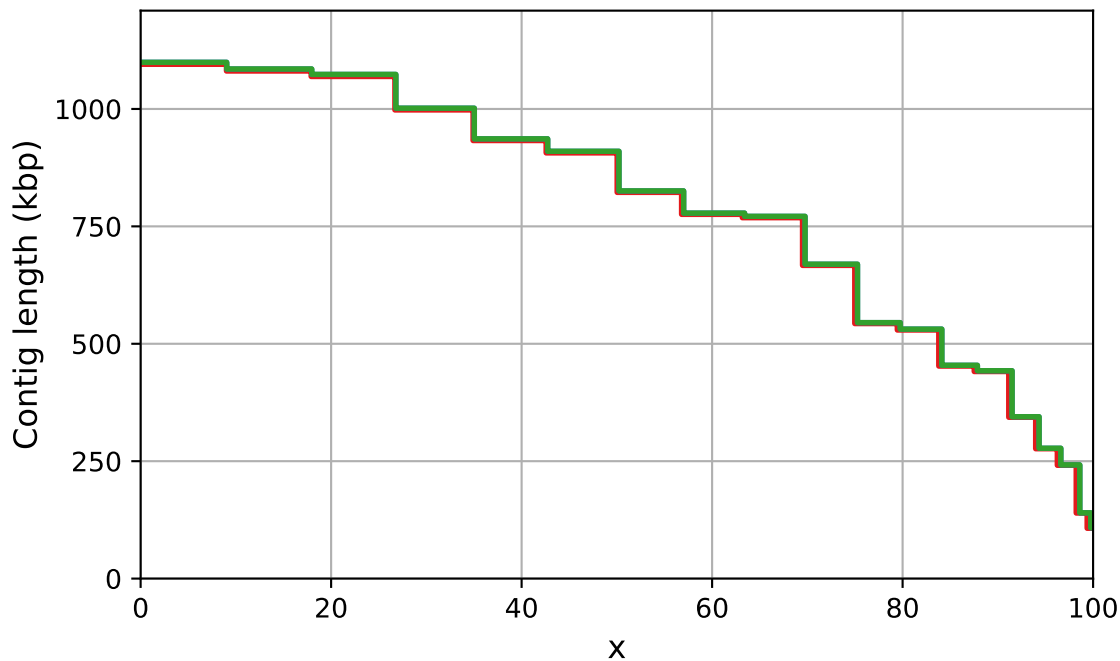
Unaligned report

	yeast_1d.guppy_213.canu	polished_genome	polished_genome_racon
# fully unaligned contigs	4	4	4
Fully unaligned length	72834	73392	73266
# partially unaligned contigs	16	15	17
Partially unaligned length	71347	105786	79657
# N's	0	0	3

All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

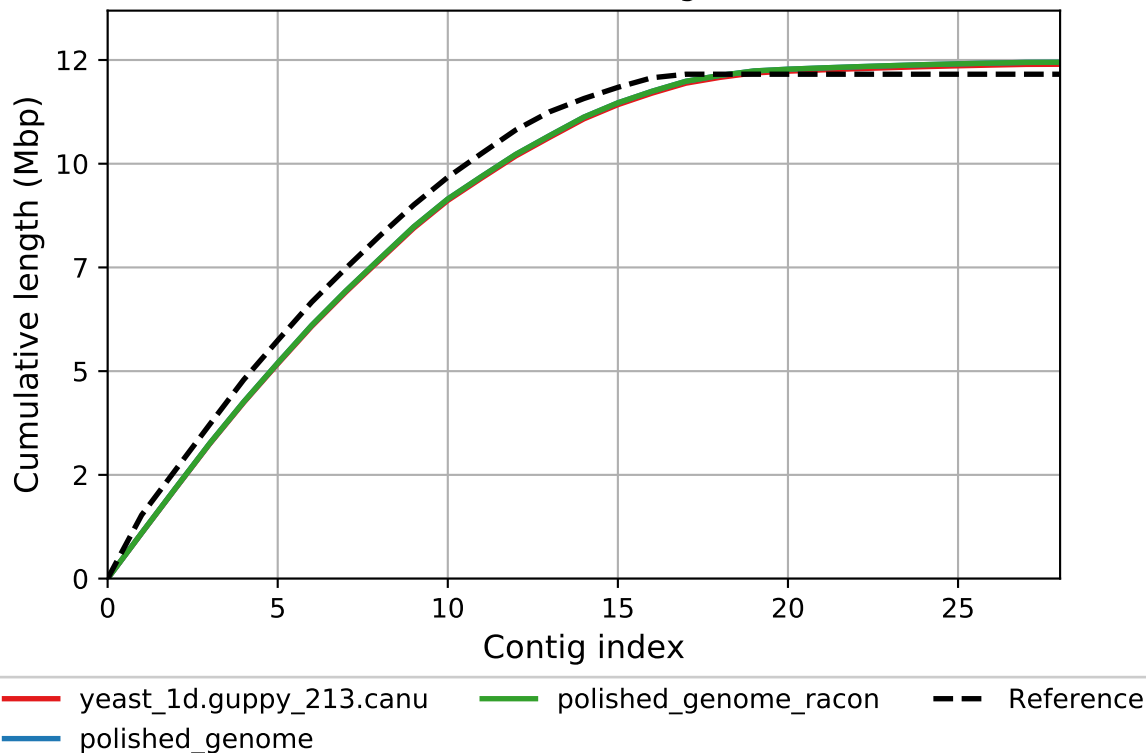


NGx

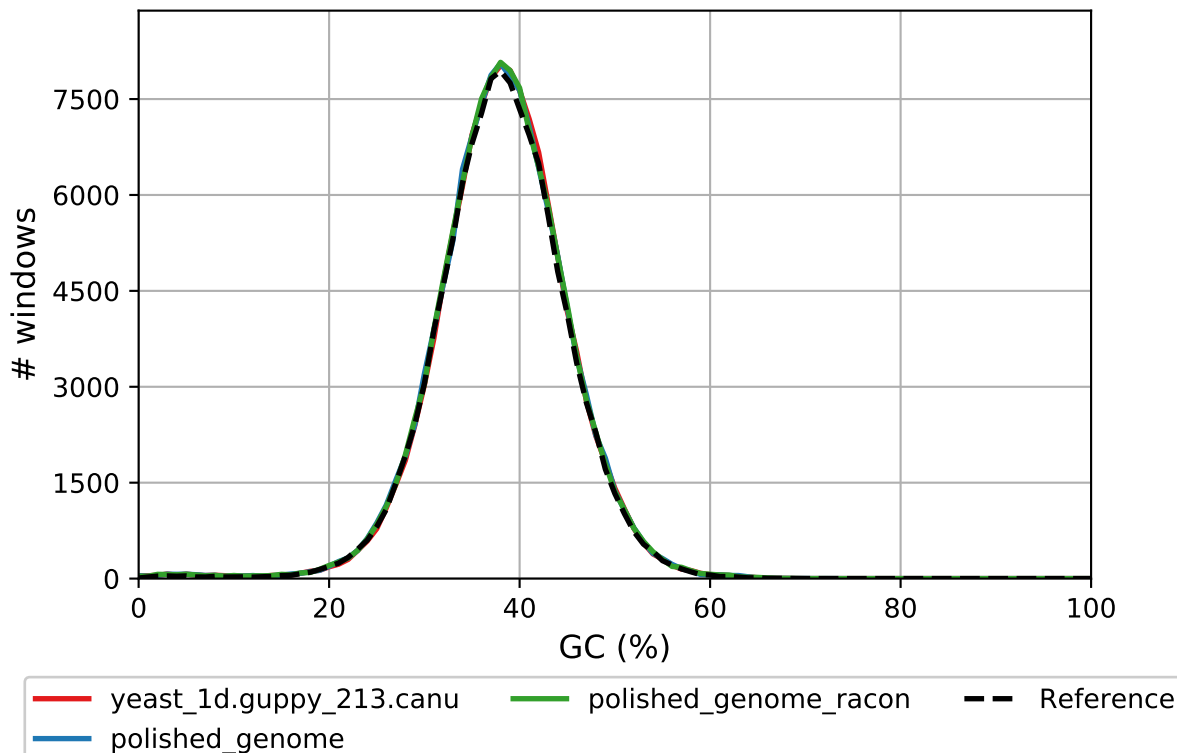


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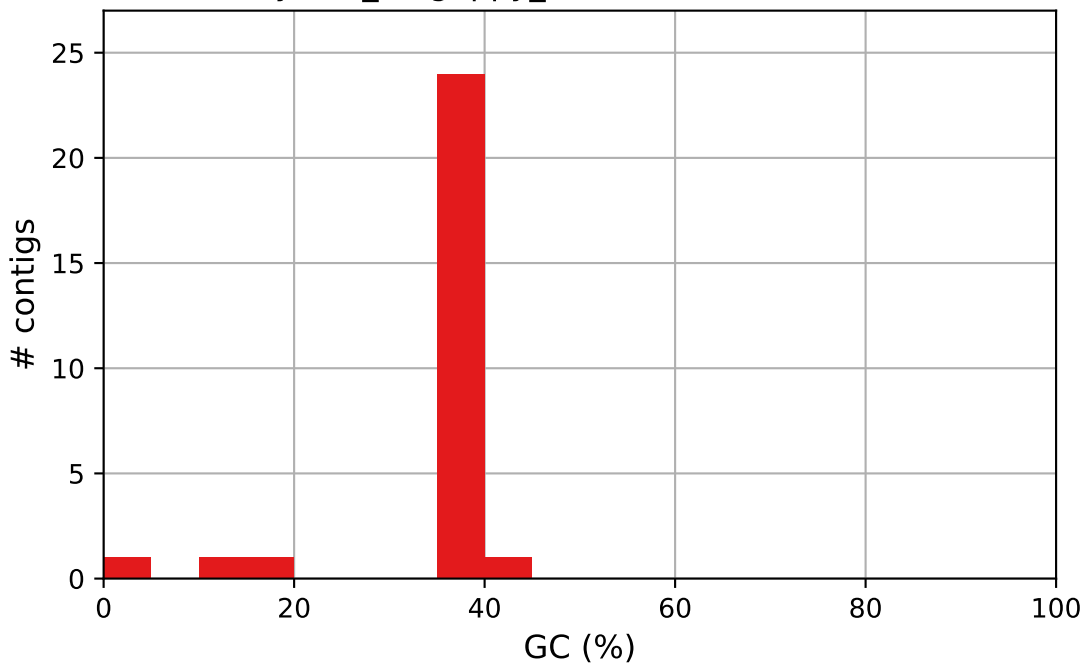
Cumulative length



GC content

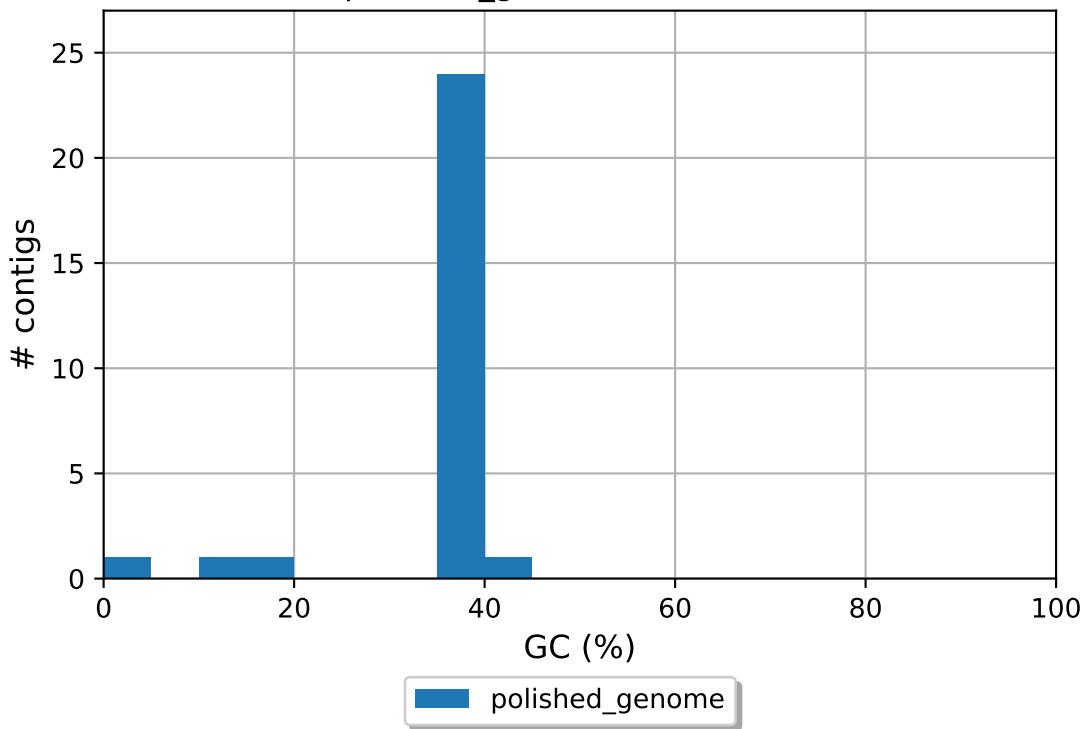


yeast_1d.guppy_213.canu GC content

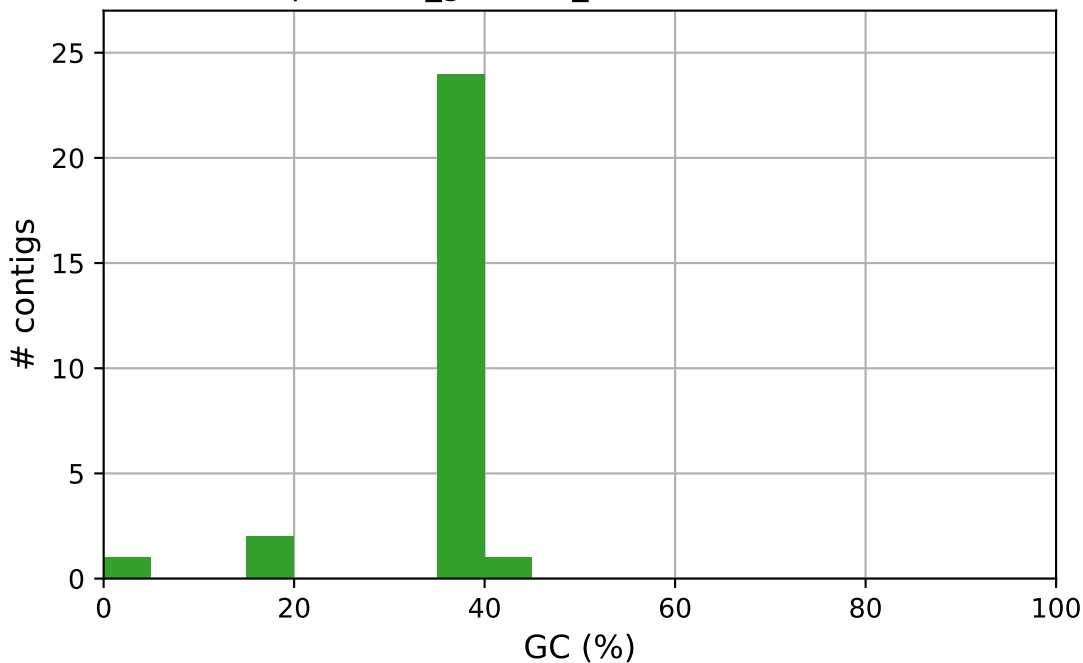


yeast_1d.guppy_213.canu

polished_genome GC content

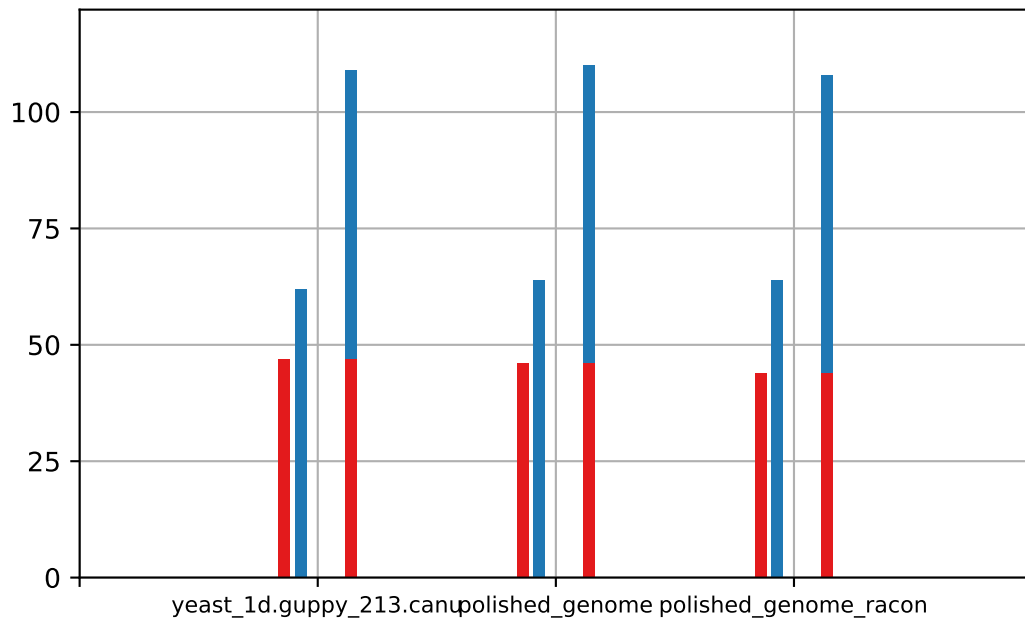


polished_genome_racon GC content



polished_genome_racon

Misassemblies

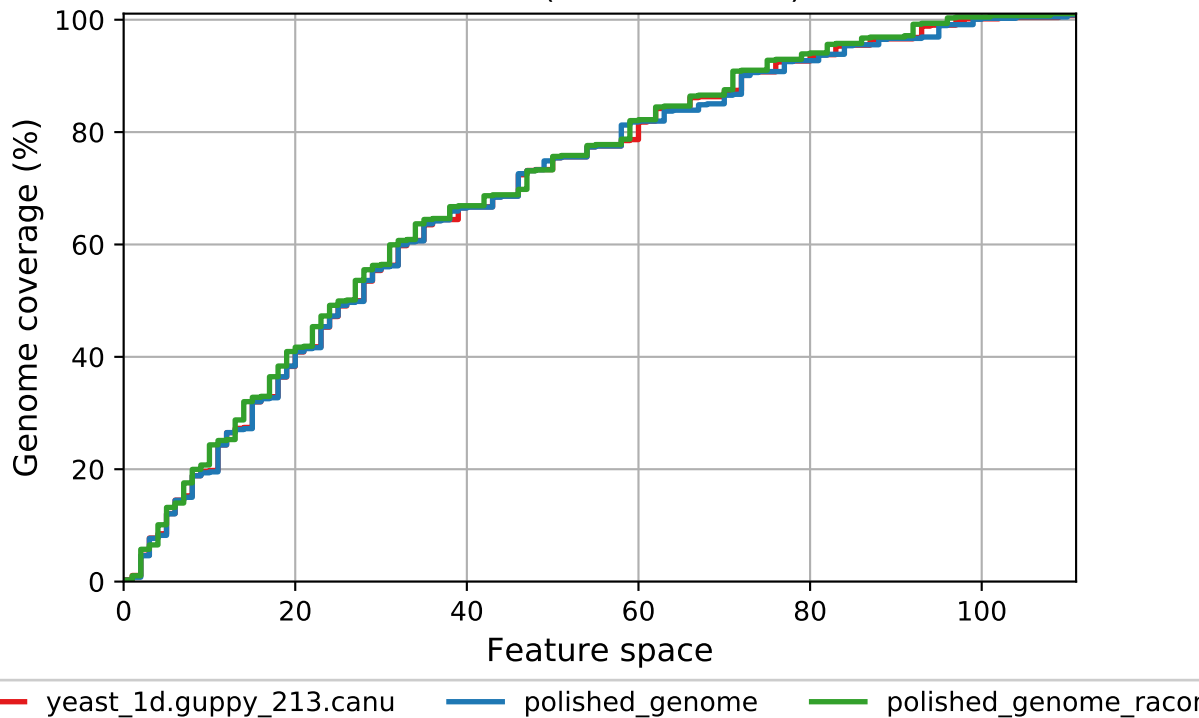


relocations

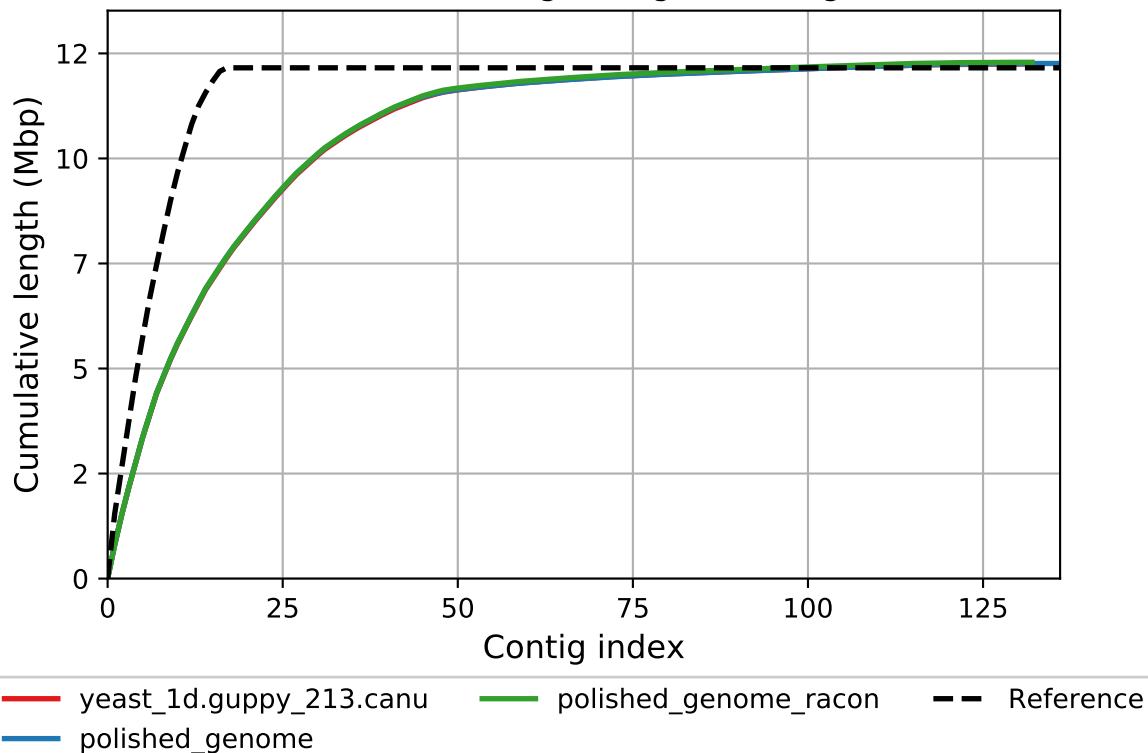


translocations

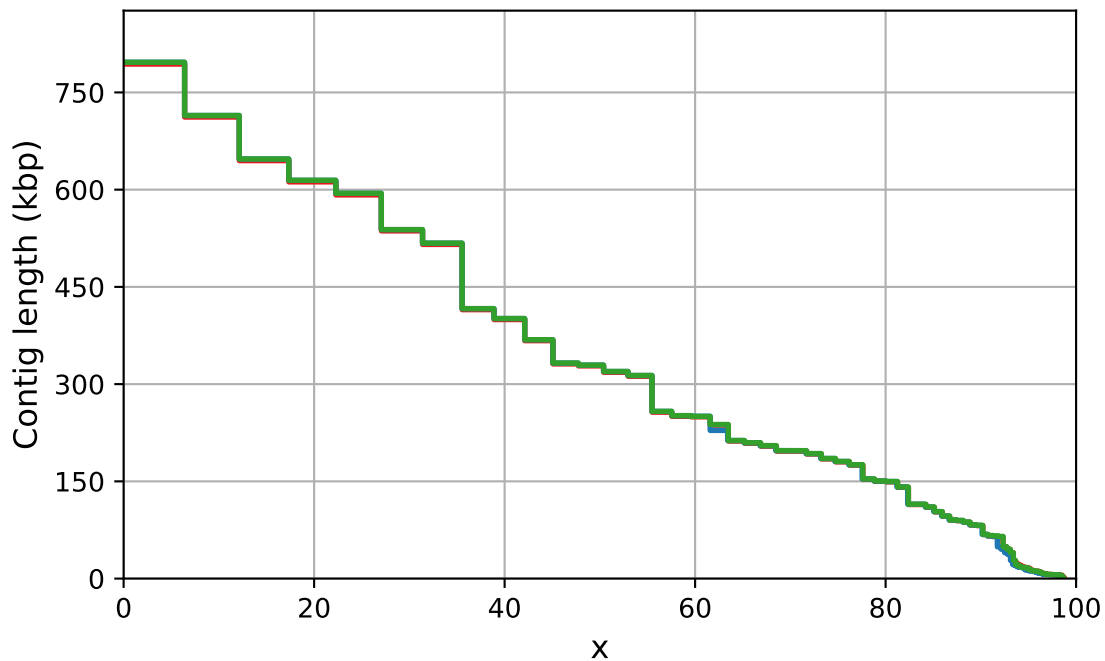
FRCurve (misassemblies)



Cumulative length (aligned contigs)

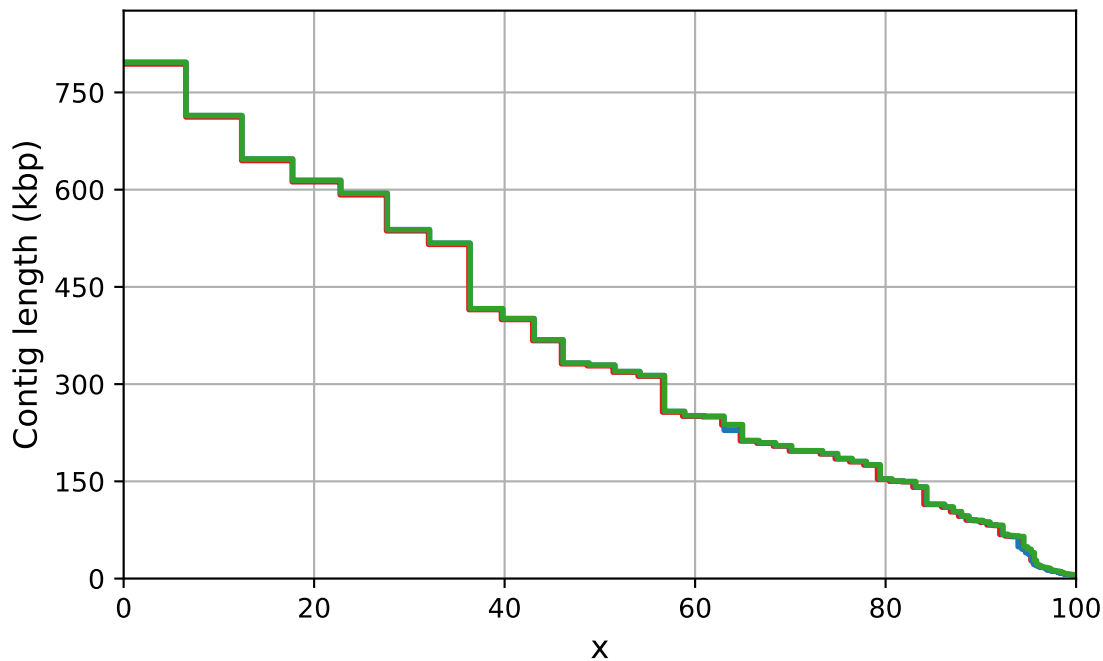


NAx



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NGAx



— yeast_1d.guppy_213.canu — polished_genome — polished_genome_racon

Genome fraction, %

100

99

98

97

■ yeast_1d.guppy_213.canu ■ polished_genome ■ polished_genome_racon

