

Report

	final.contigs
# contigs (>= 0 bp)	166148
# contigs (>= 1000 bp)	30885
# contigs (>= 5000 bp)	2595
# contigs (>= 10000 bp)	826
# contigs (>= 25000 bp)	156
# contigs (>= 50000 bp)	47
Total length (>= 0 bp)	150487838
Total length (>= 1000 bp)	81750948
Total length (>= 5000 bp)	29811065
Total length (>= 10000 bp)	17866508
Total length (>= 25000 bp)	8108978
Total length (>= 50000 bp)	4319914
# contigs	88129
Largest contig	266140
Total length	120479536
Reference length	147310433
N50	1702
N75	833
L50	13987
L75	40344
# misassemblies	21
# misassembled contigs	13
Misassembled contigs length	10038
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	81
# unaligned contigs	87723 + 239 part
Unaligned length	120327784
Genome fraction (%)	0.077
Duplication ratio	2.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5546.49
# indels per 100 kbp	127.00
Largest alignment	1746
Total aligned length	86305

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

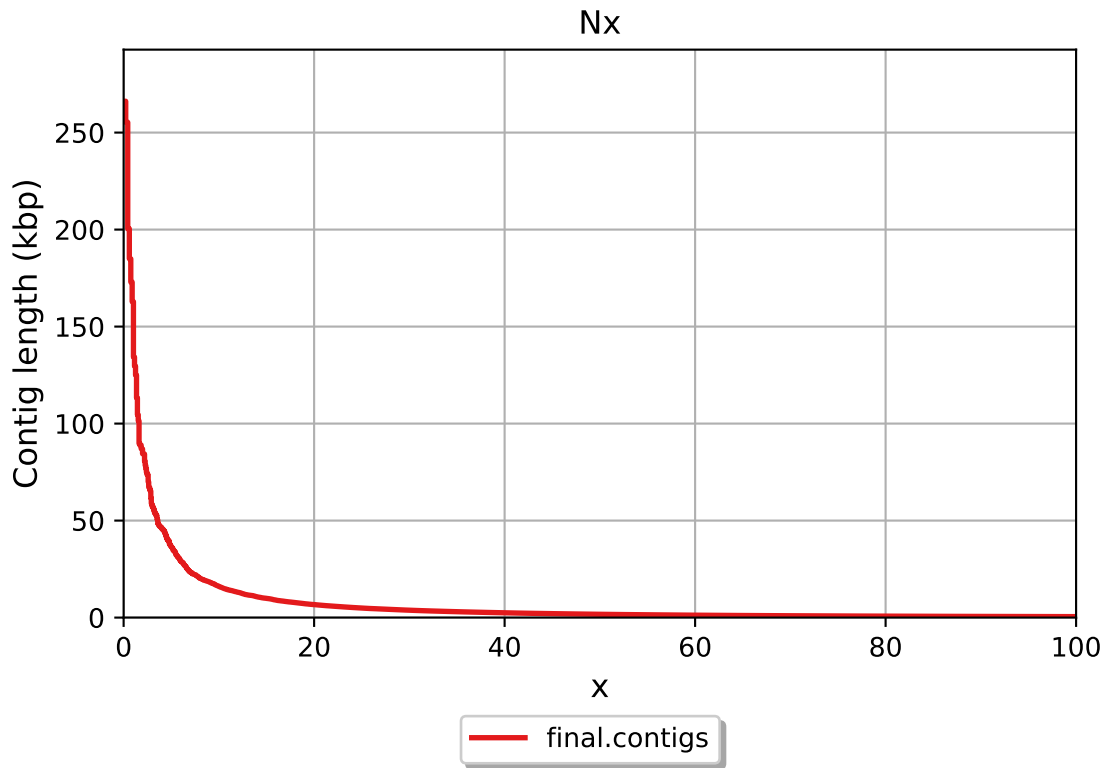
	final.contigs
# misassemblies	21
# contig misassemblies	21
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	21
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	13
Misassembled contigs length	10038
# possibly misassembled contigs	196
# possible misassemblies	262
# local misassemblies	8
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	81
# mismatches	6289
# indels	144
# indels (<= 5 bp)	143
# indels (> 5 bp)	1
Indels length	260

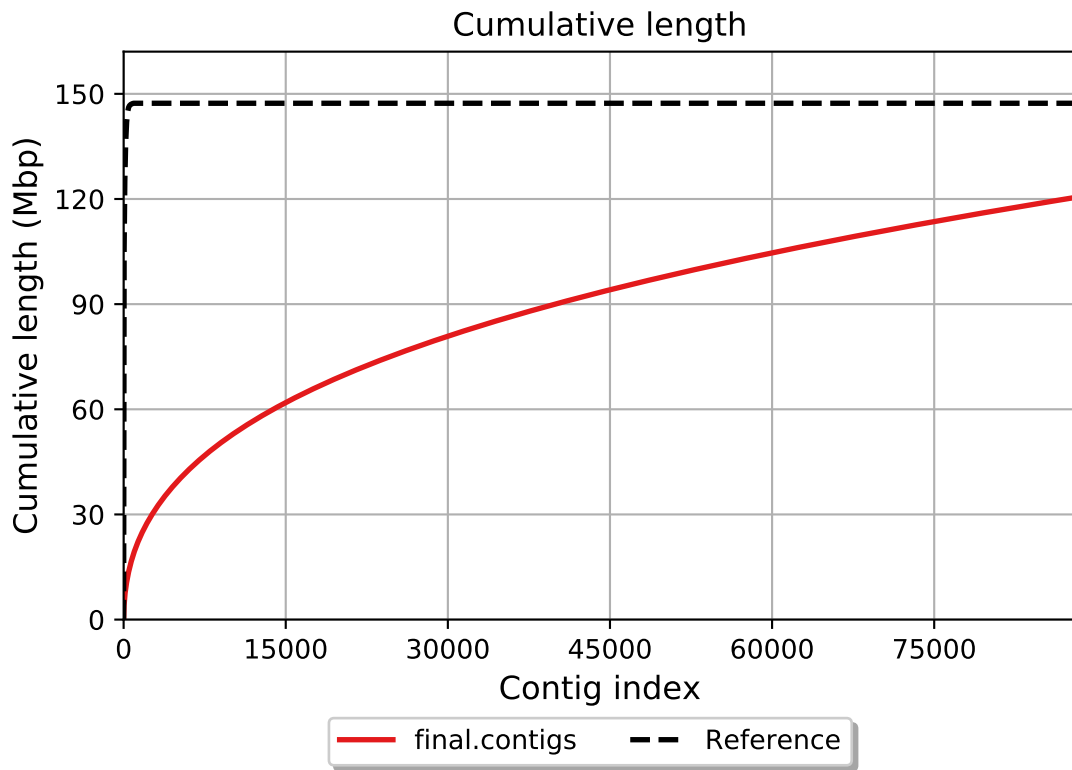
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

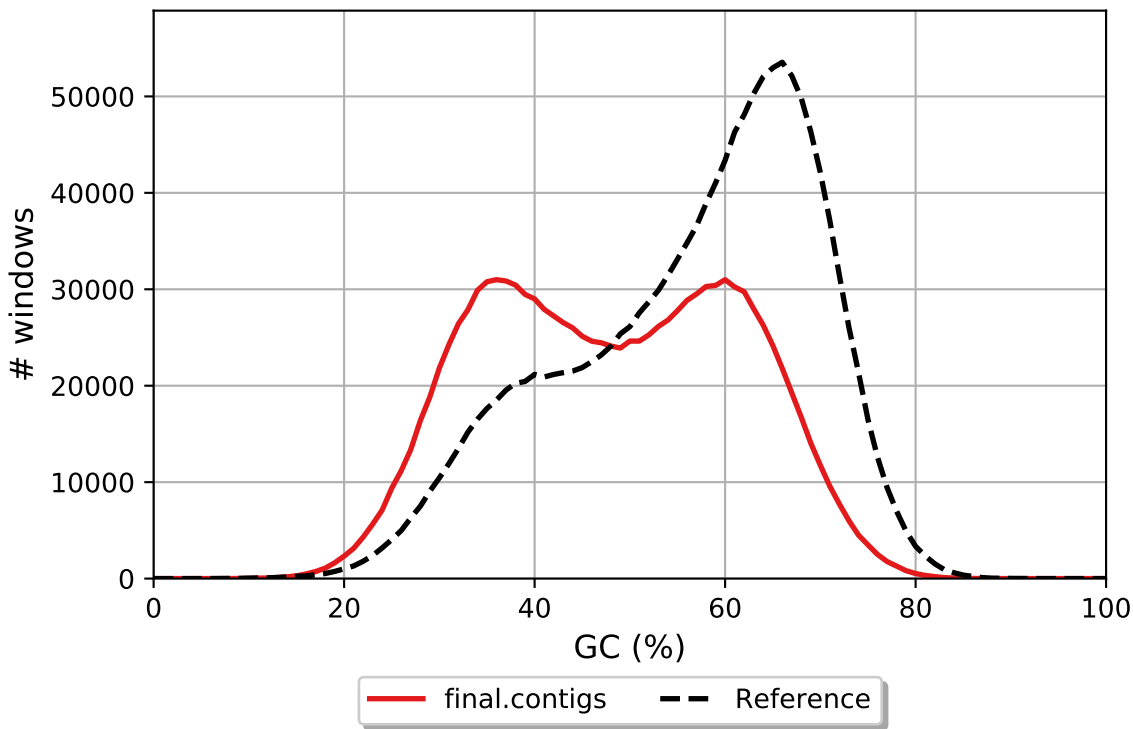
	final.contigs
# fully unaligned contigs	87723
Fully unaligned length	117825195
# partially unaligned contigs	239
Partially unaligned length	2502589
# N's	0

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).

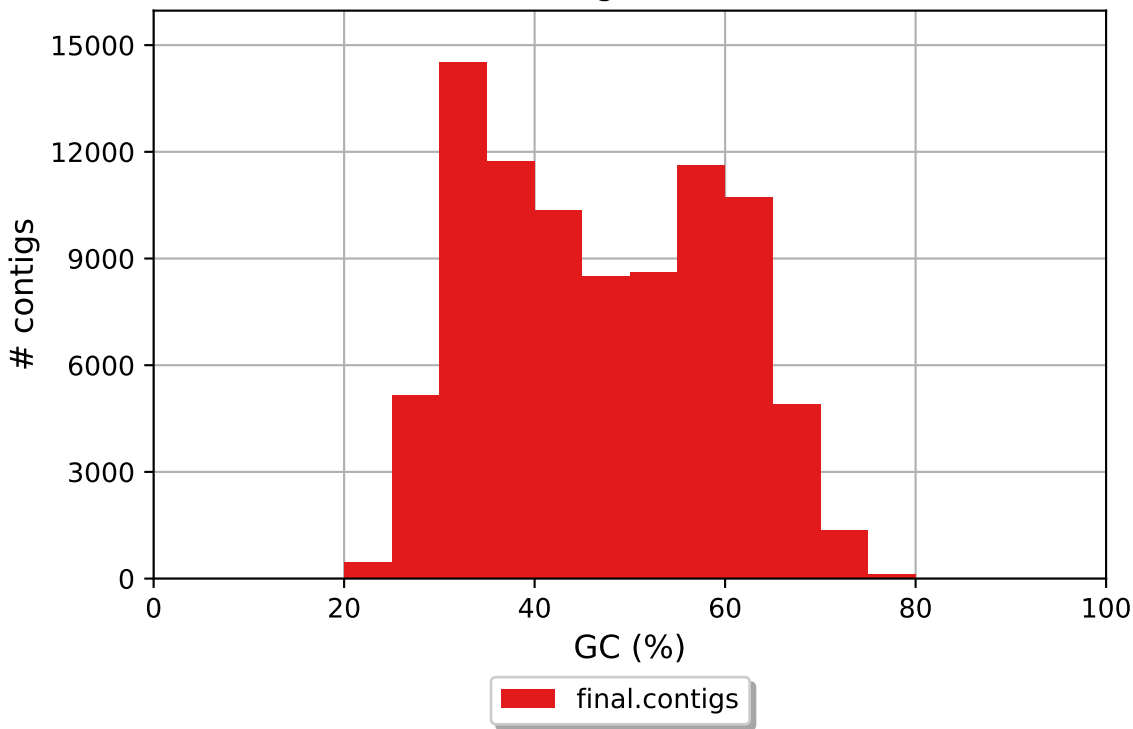




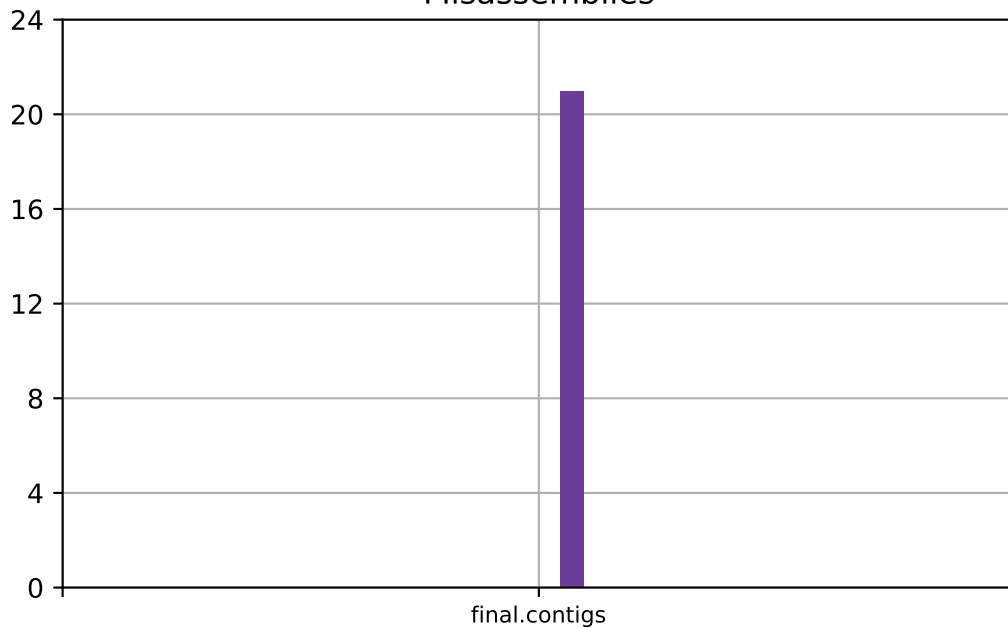
GC content



final.contigs GC content

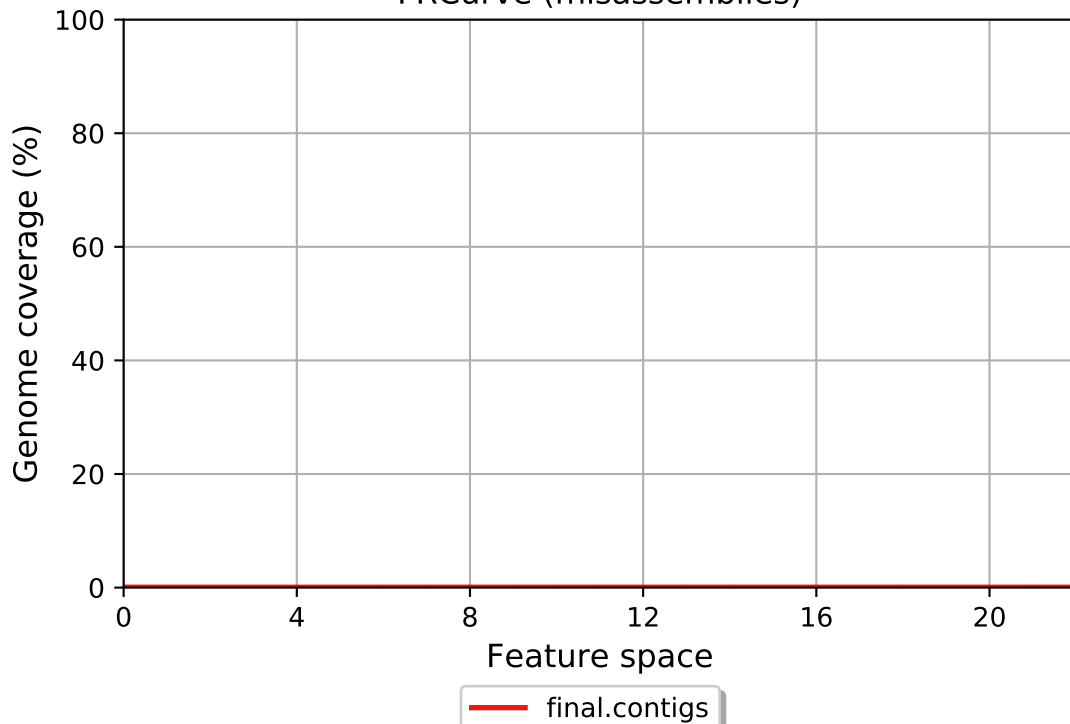


Misassemblies

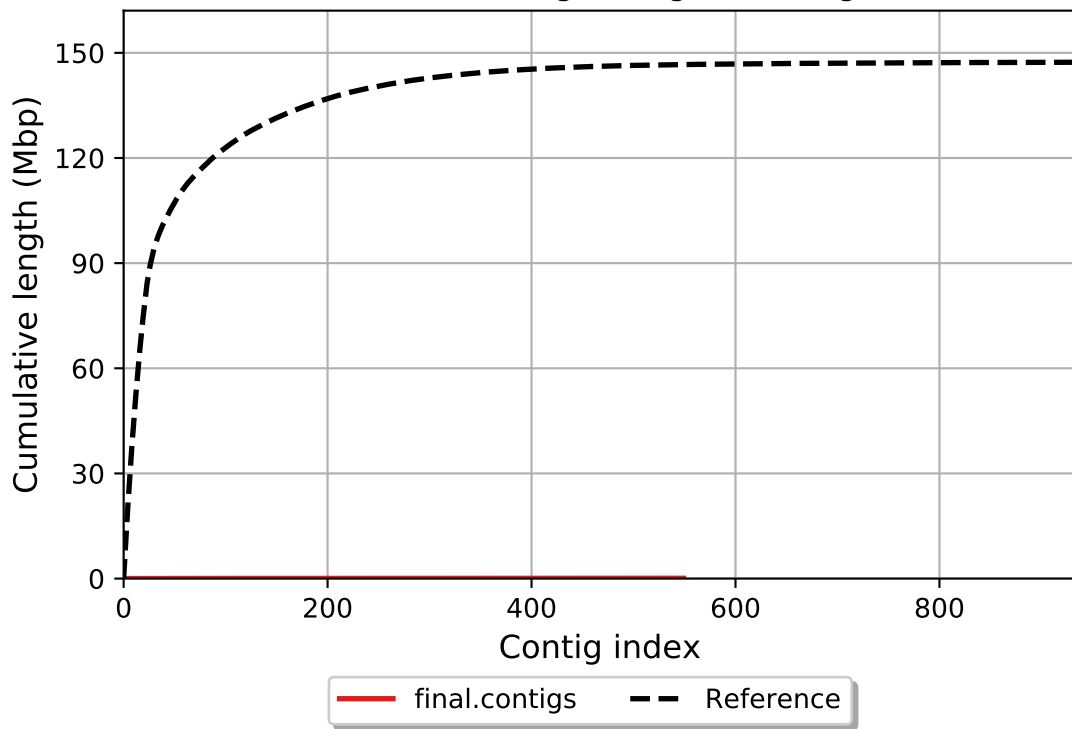


interspecies translocations

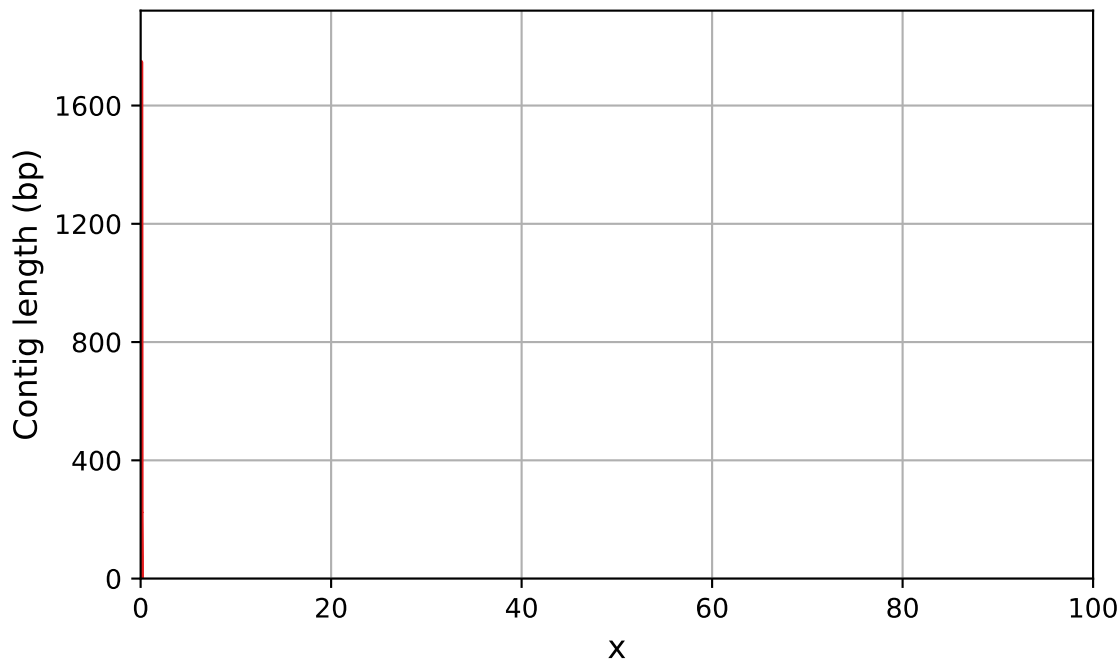
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs