

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)	150487812
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	88130
Largest contig	266140
Total length	120479996
Reference length	153504479
N50	1702
N75	833
L50	13987
L75	40344
# misassemblies	22
# misassembled contigs	15
Misassembled contigs length	11753
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	81
# unaligned contigs	87758 + 220 part
Unaligned length	120340232
Genome fraction (%)	0.078
Duplication ratio	1.945
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5410.32
# indels per 100 kbp	142.44
Largest alignment	1746
Total aligned length	78871

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

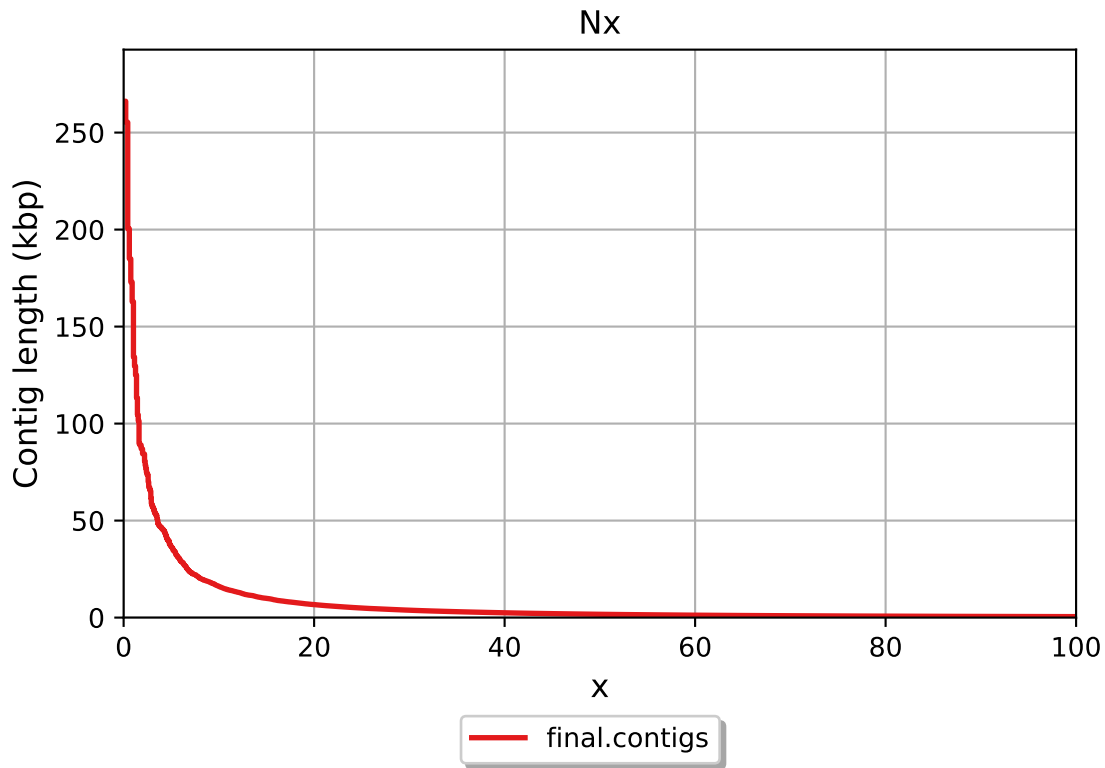
	final.contigs
# misassemblies	22
# contig misassemblies	22
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	22
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	15
Misassembled contigs length	11753
# possibly misassembled contigs	178
# possible misassemblies	239
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	81
# mismatches	6457
# indels	170
# indels (<= 5 bp)	169
# indels (> 5 bp)	1
Indels length	289

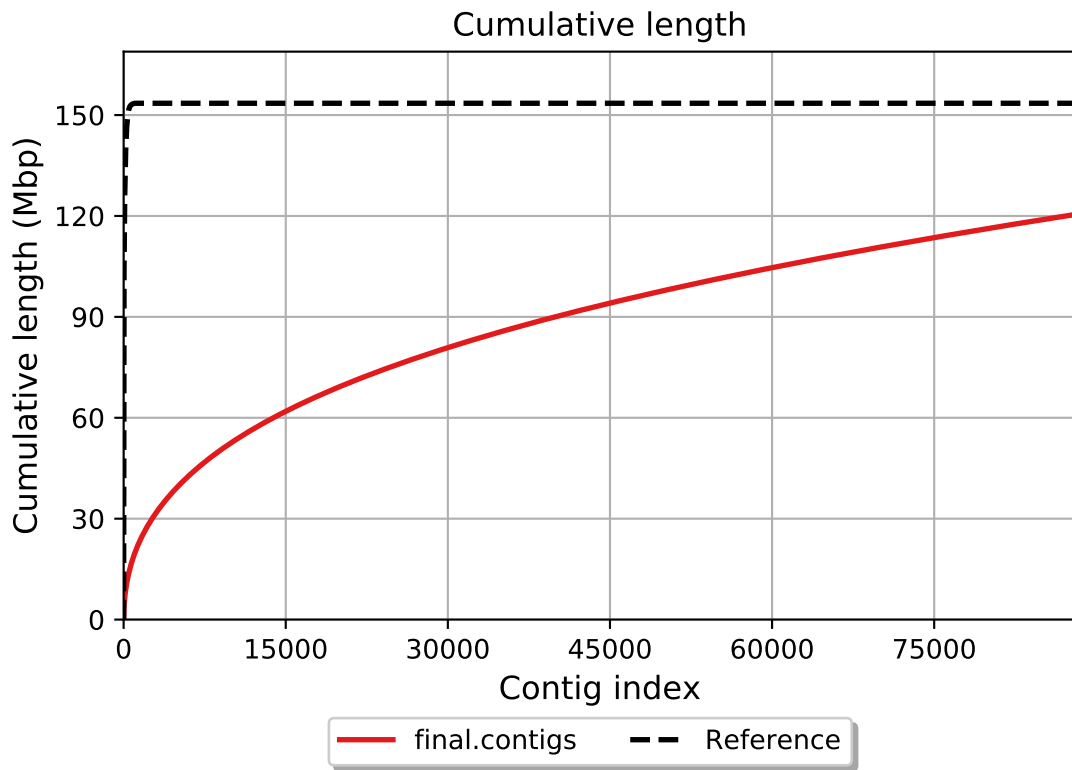
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

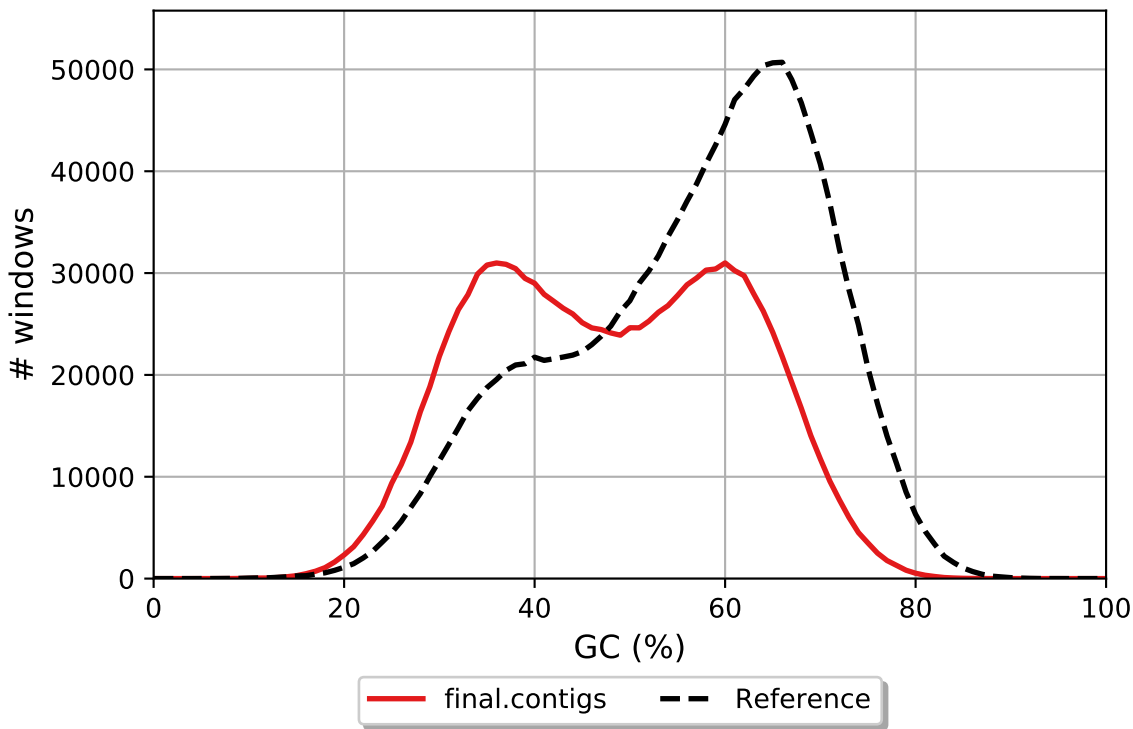
	final.contigs
# fully unaligned contigs	87758
Fully unaligned length	117886582
# partially unaligned contigs	220
Partially unaligned length	2453650
# N's	0

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).

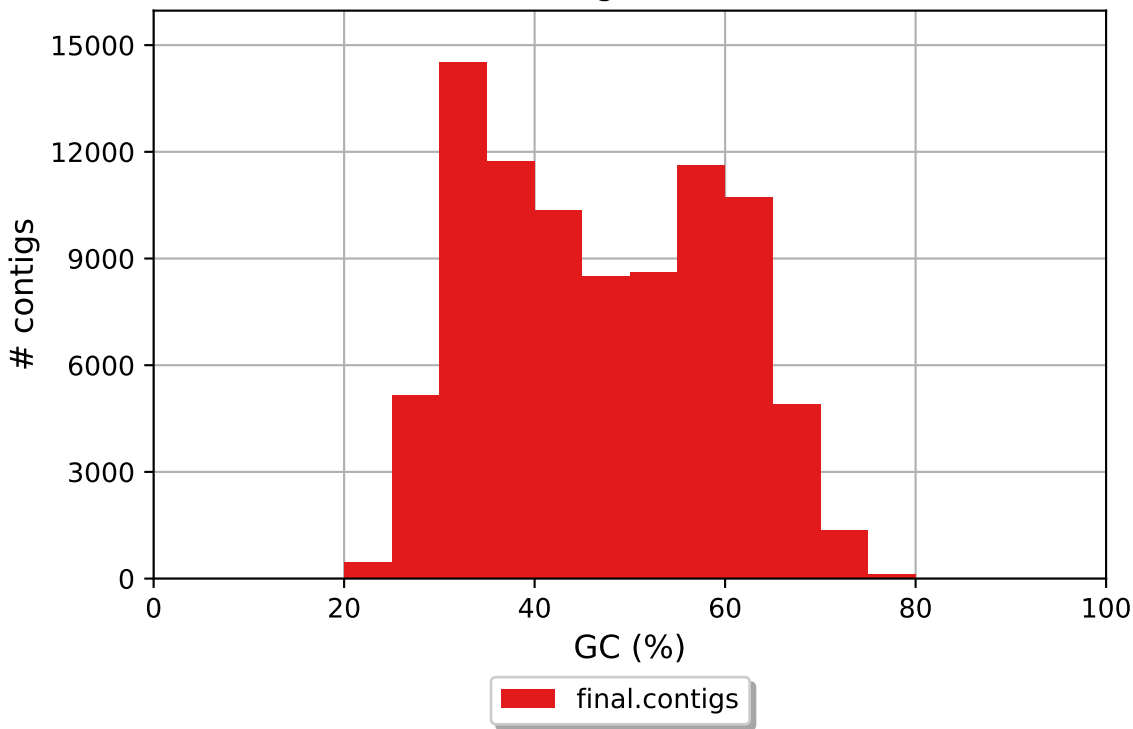




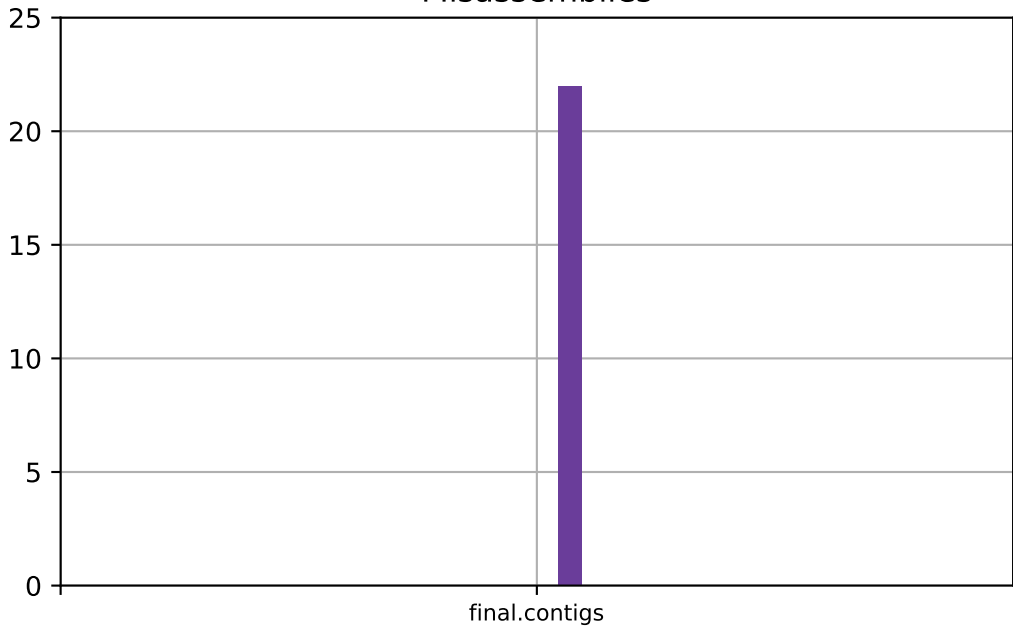
GC content



final.contigs GC content

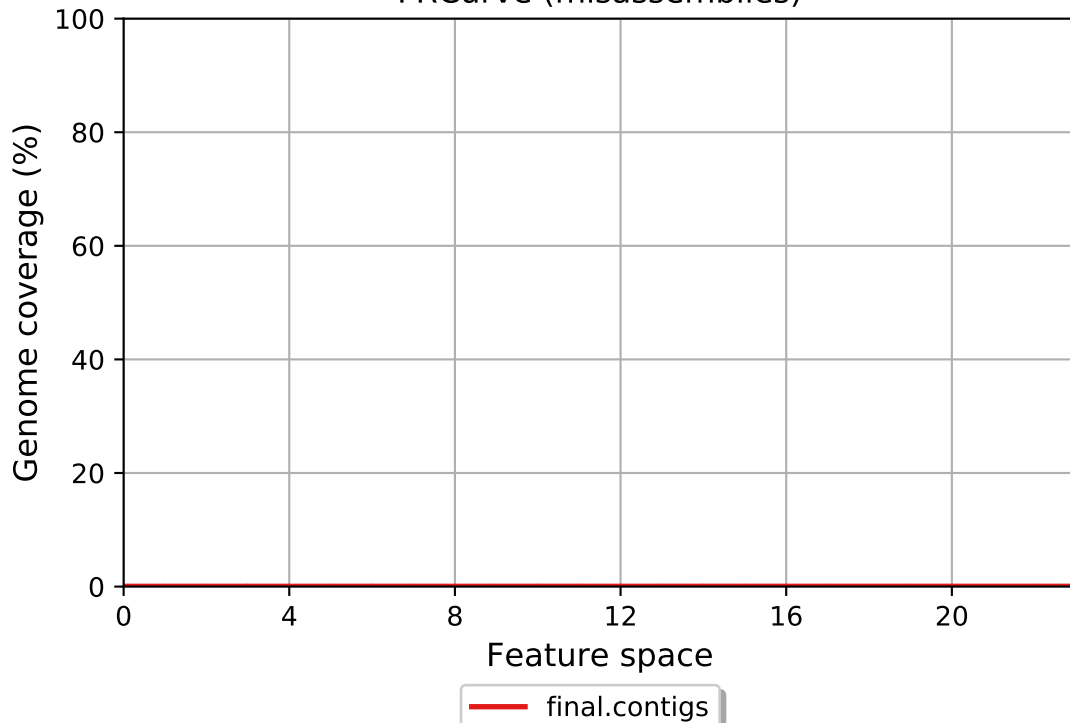


Misassemblies

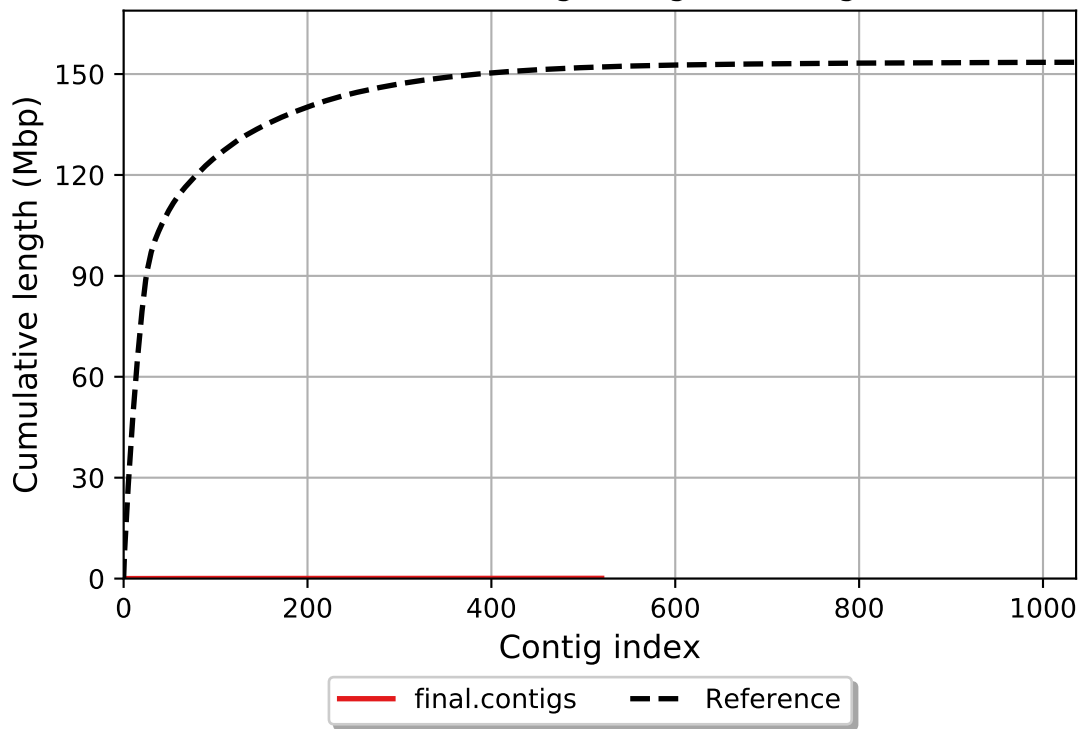


interspecies translocations

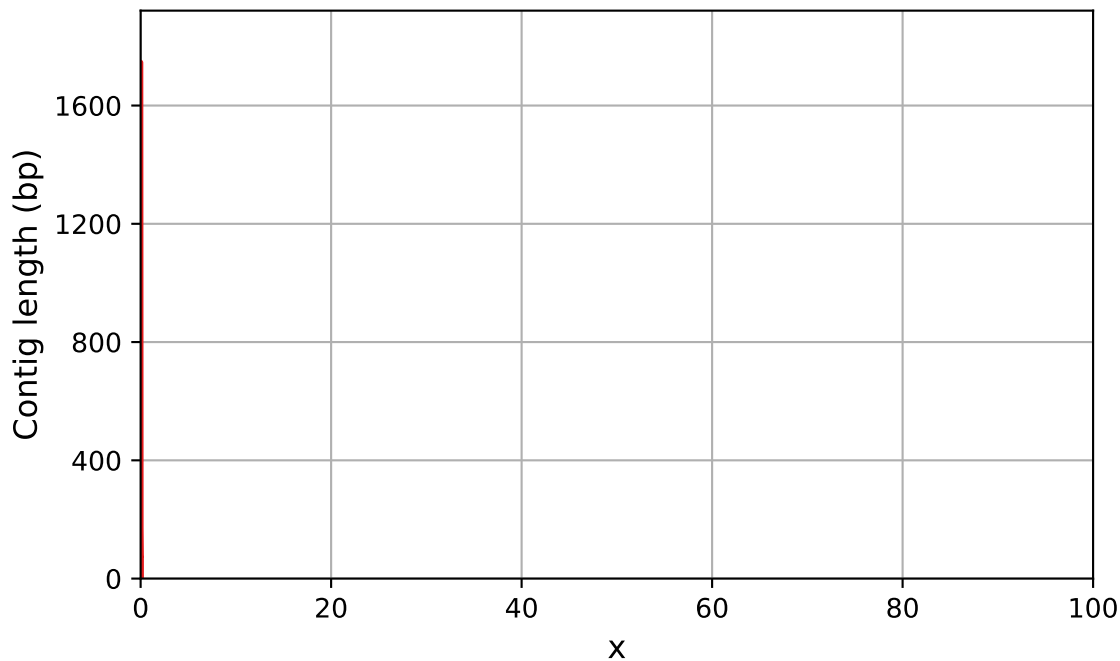
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs