

Report

	final.contigs
# contigs (>= 0 bp)	1016
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	433449
Total length (>= 1000 bp)	23564
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	185
Largest contig	2468
Total length	128230
Reference length	17285411
N50	646
N75	556
L50	71
L75	125
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	1426
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	112 + 3 part
Unaligned length	82058
Genome fraction (%)	0.265
Duplication ratio	1.120
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2715.06
# indels per 100 kbp	153.15
Largest alignment	1369
Total aligned length	40935

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

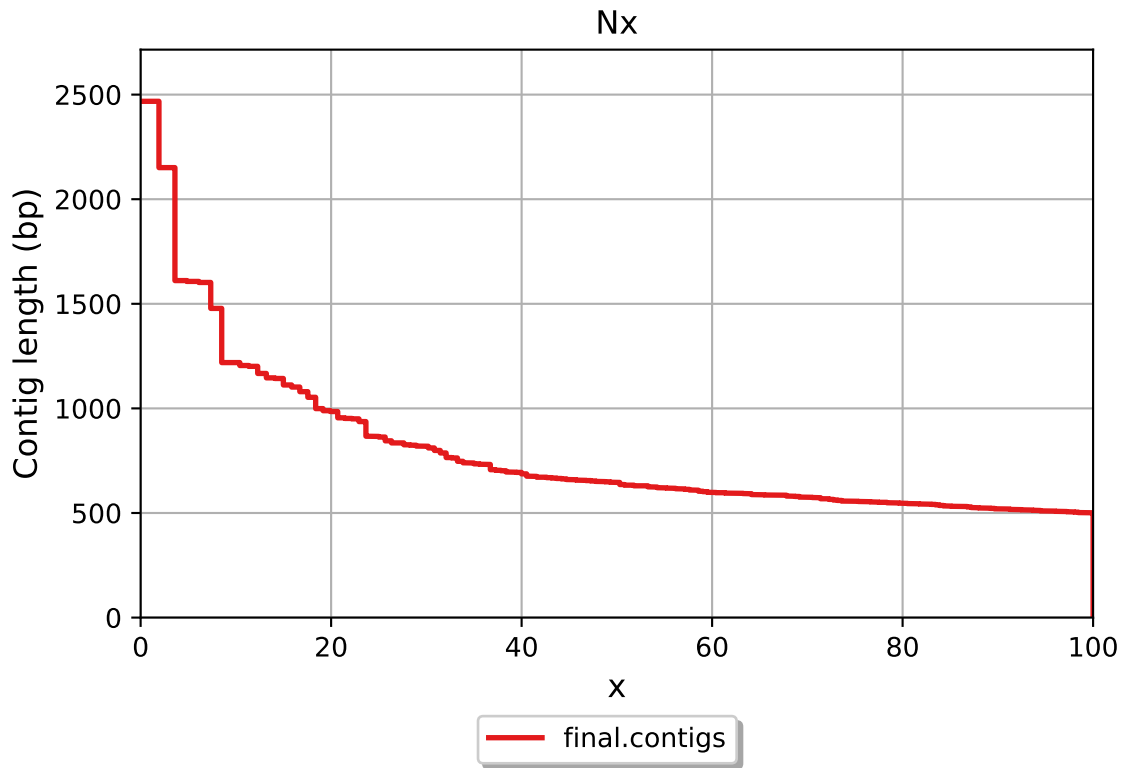
	final.contigs
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	2
Misassembled contigs length	1426
# possibly misassembled contigs	3
# possible misassemblies	3
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1241
# indels	70
# indels (<= 5 bp)	65
# indels (> 5 bp)	5
Indels length	189

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).

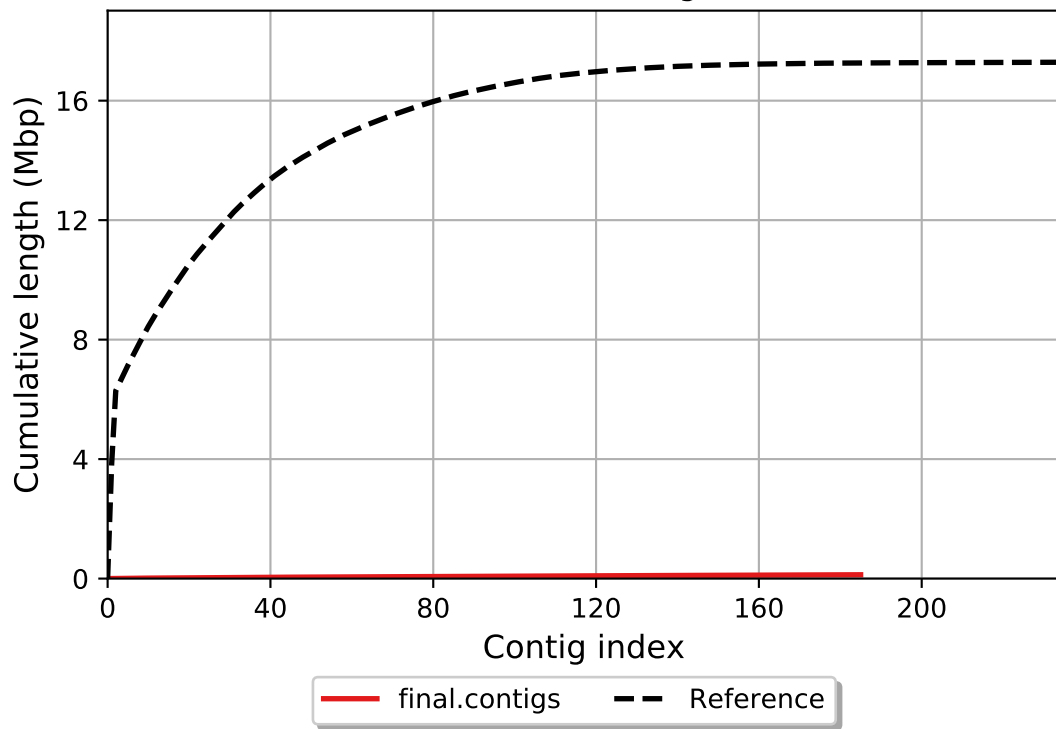
Unaligned report

	final.contigs
# fully unaligned contigs	112
Fully unaligned length	78917
# partially unaligned contigs	3
Partially unaligned length	3141
# N's	0

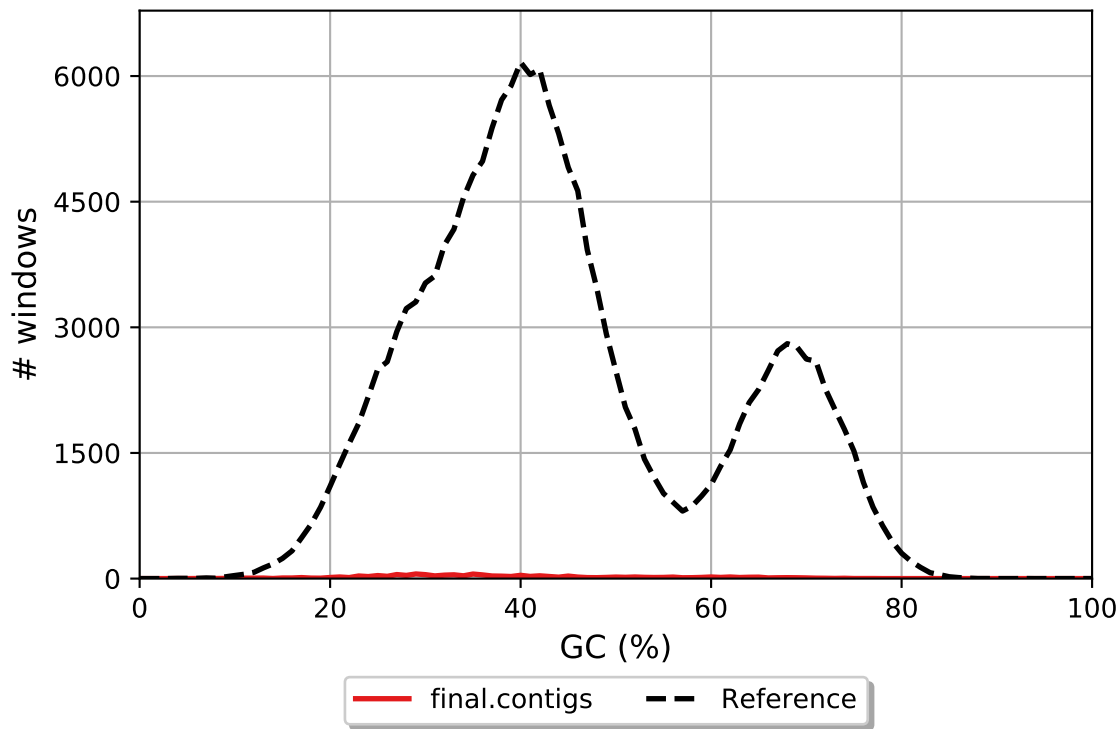
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



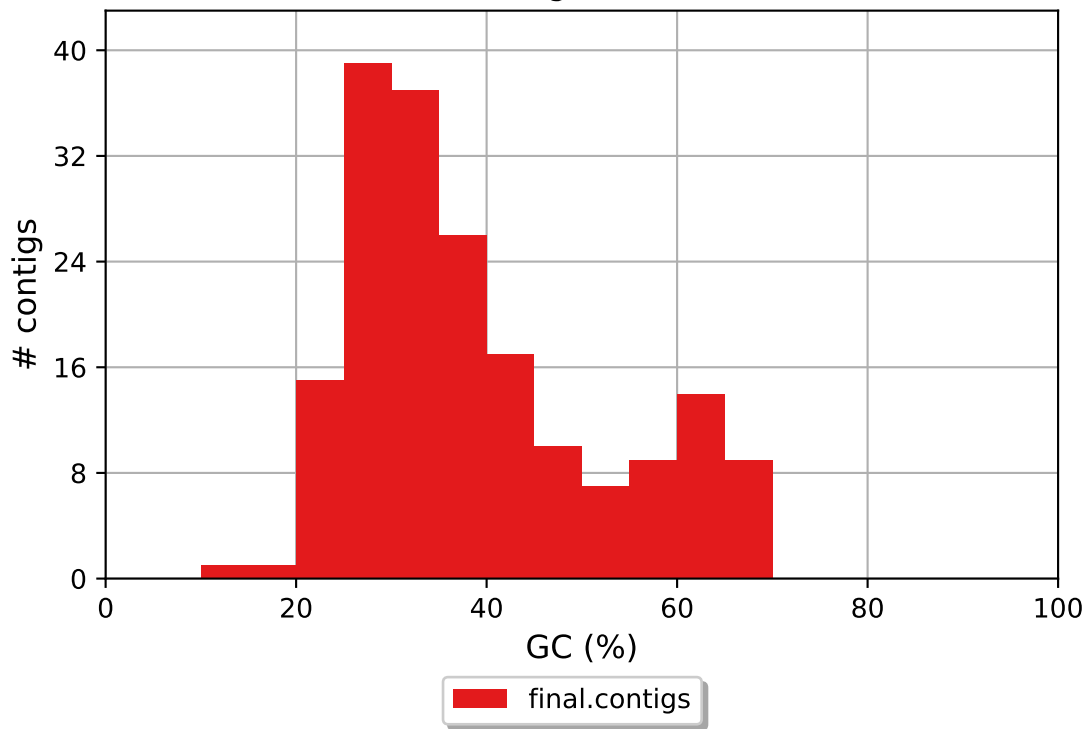
Cumulative length



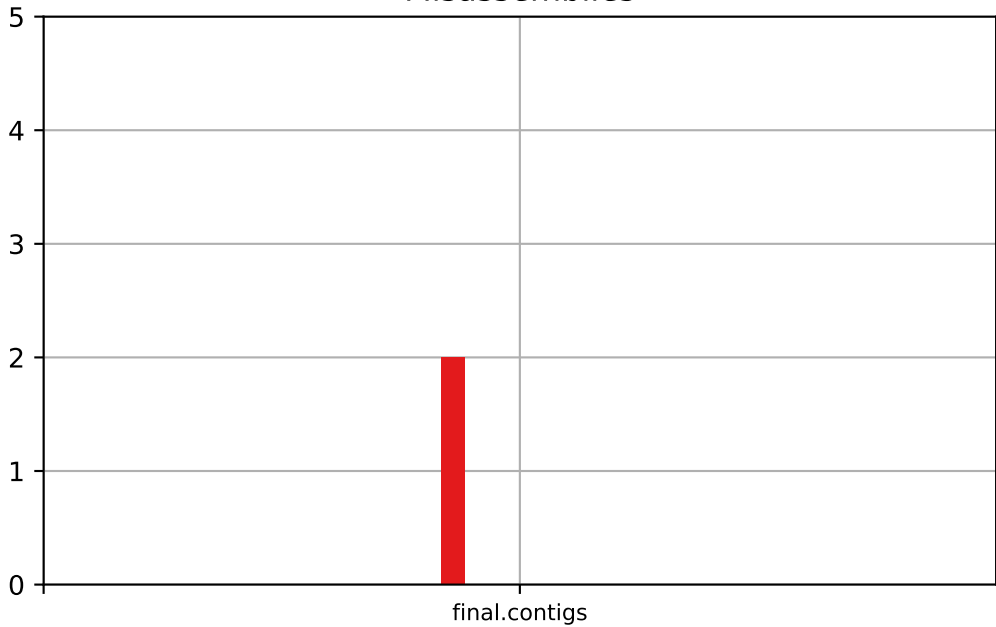
GC content



final.contigs GC content

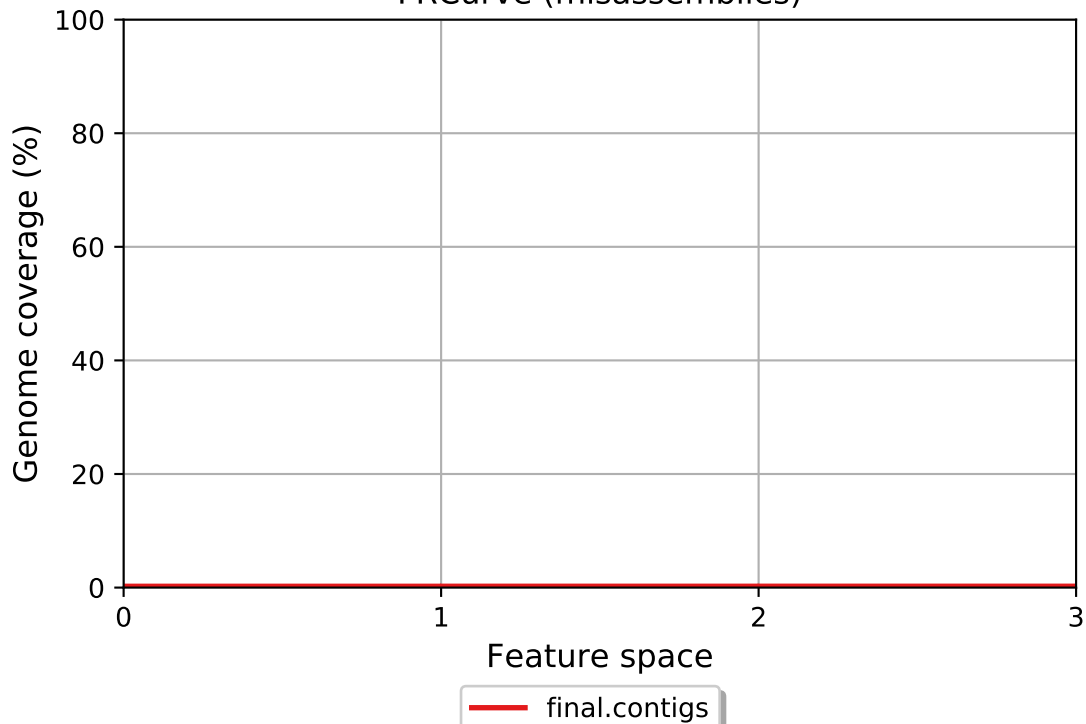


Misassemblies

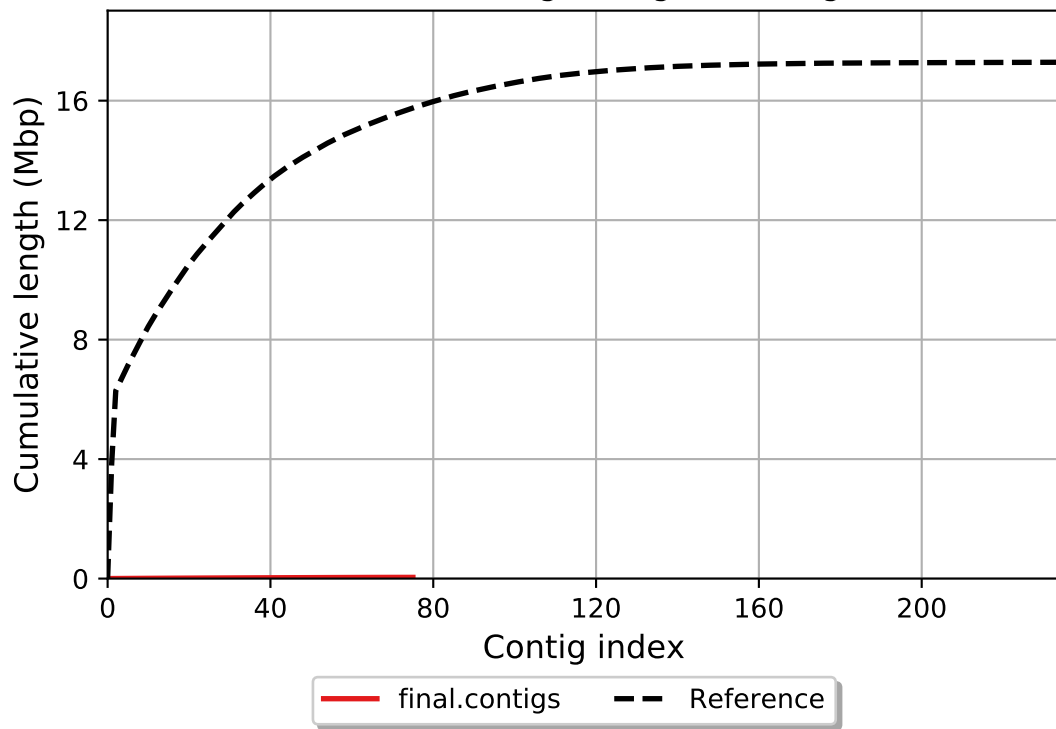


 # relocations

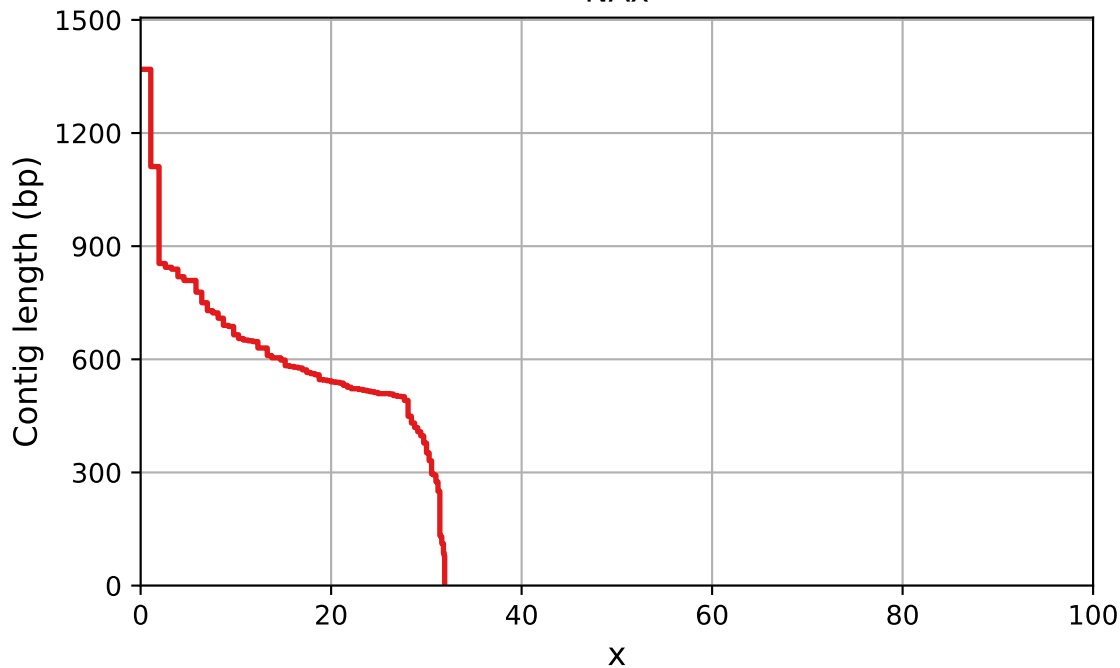
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs