

Report

	final.contigs
# contigs (>= 0 bp)	579
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	256299
Total length (>= 1000 bp)	14063
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	133
Largest contig	2078
Total length	89926
Reference length	4503108
N50	624
N90	519
auN	765.5
L50	53
L90	116
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	570
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	120 + 0 part
Unaligned length	81997
Genome fraction (%)	0.252
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2268.41
# indels per 100 kbp	139.40
Largest alignment	742
Total aligned length	7891
NA50	-
NA90	-
auNA	52.9
LA50	-
LA90	-

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

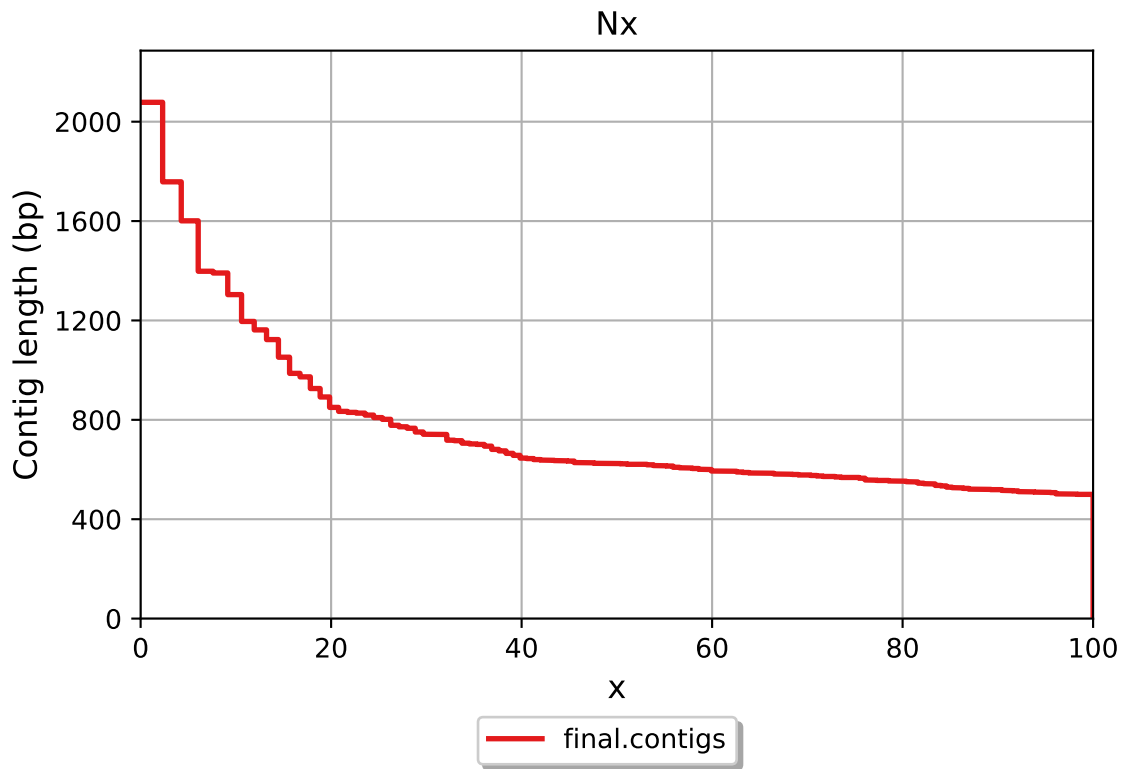
	final.contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	0
# c. inversions	1
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	1
Misassembled contigs length	570
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	179
# indels	11
# indels (<= 5 bp)	8
# indels (> 5 bp)	3
Indels length	49

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).

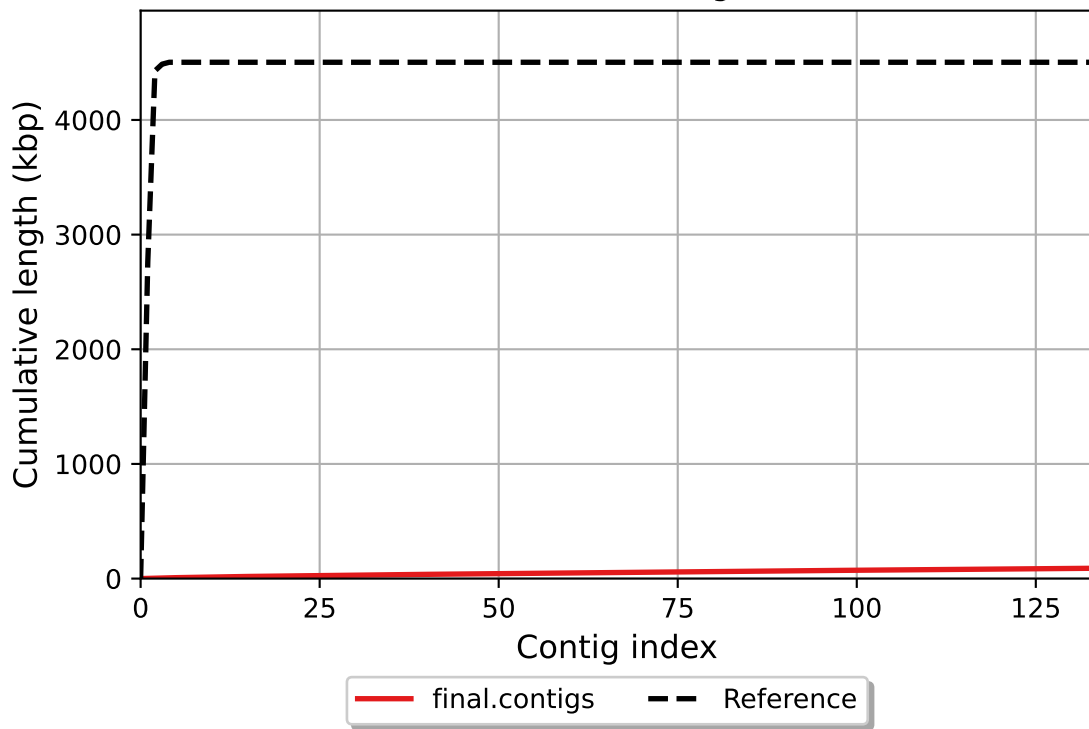
Unaligned report

	final.contigs
# fully unaligned contigs	120
Fully unaligned length	81997
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

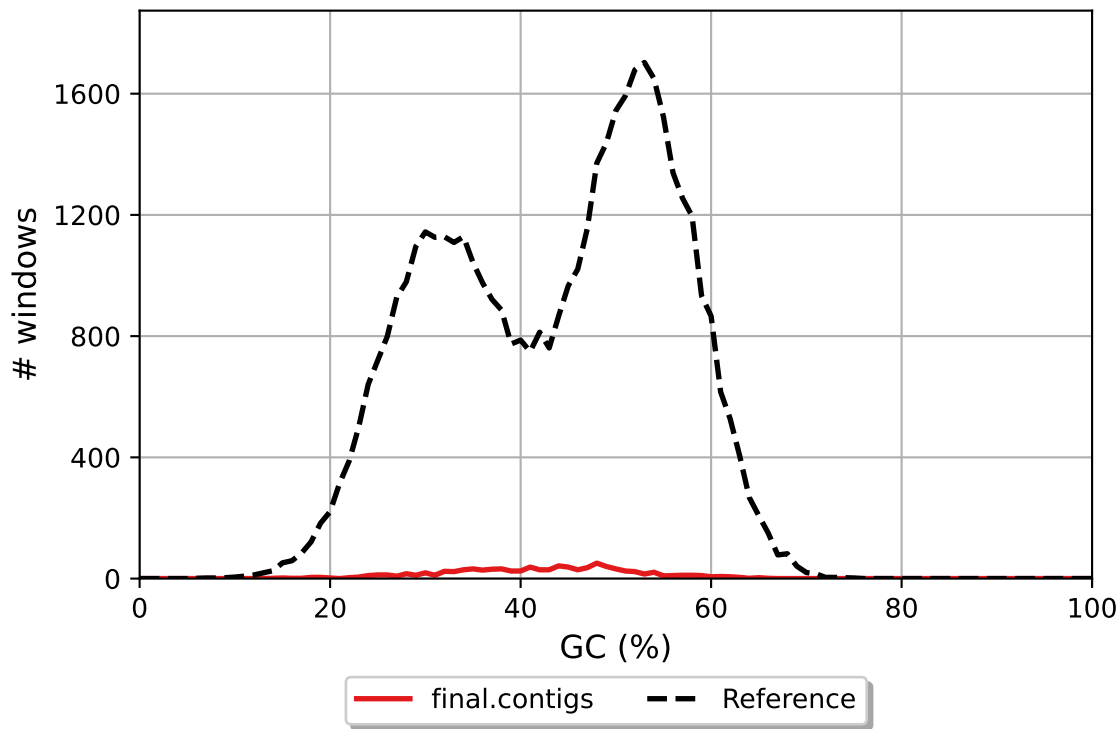
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



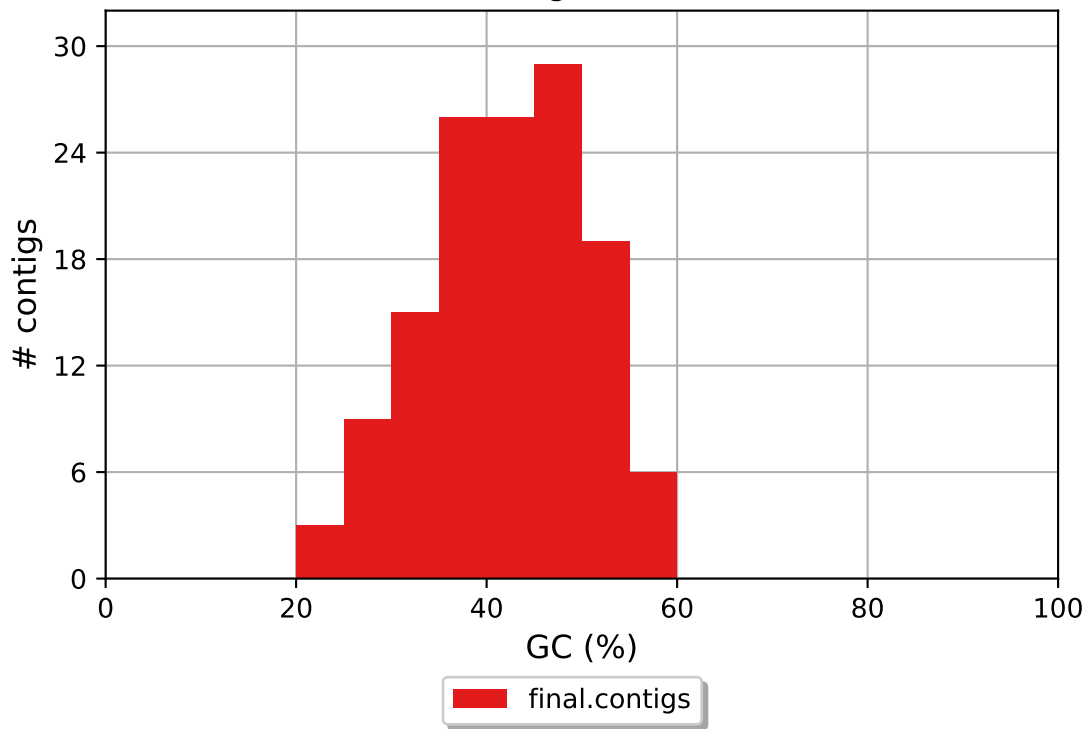
Cumulative length



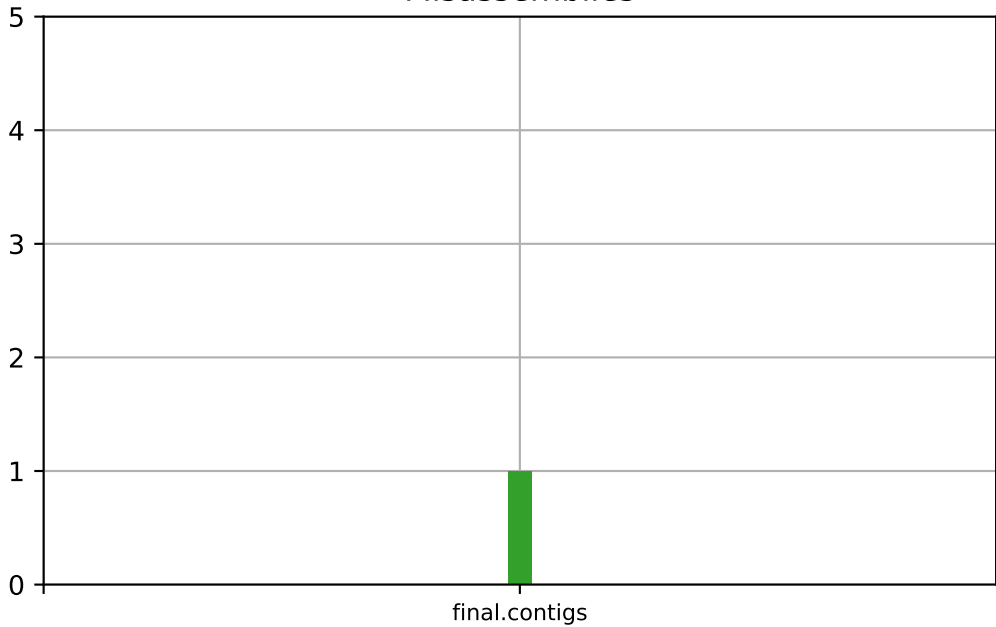
GC content



final.contigs GC content

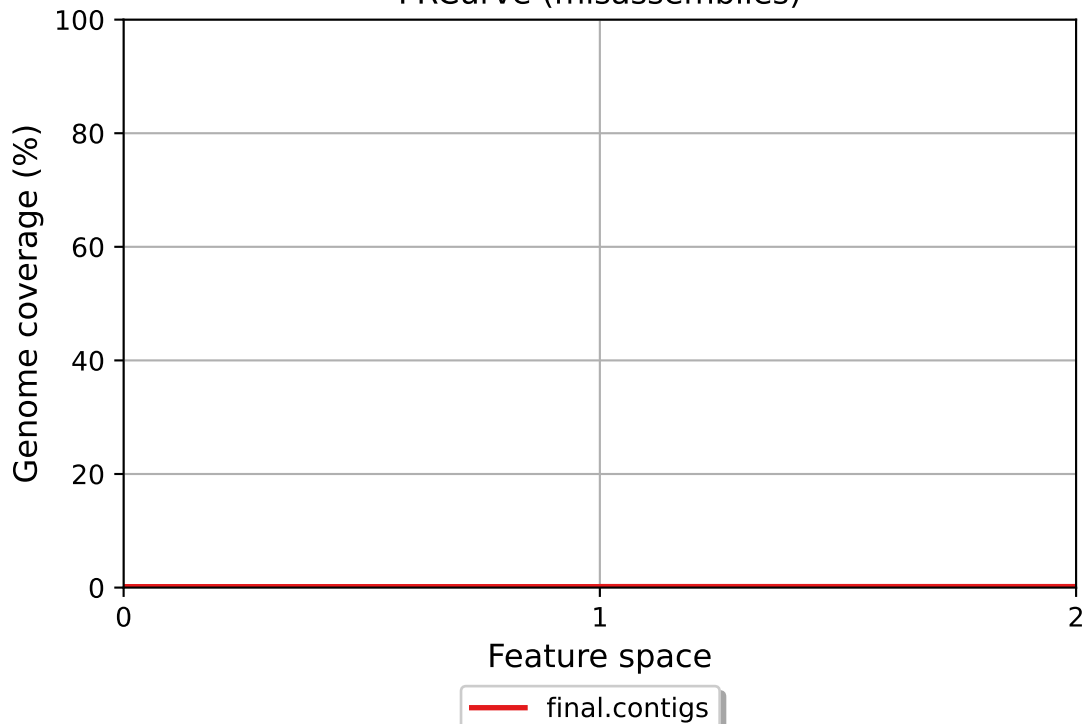


Misassemblies

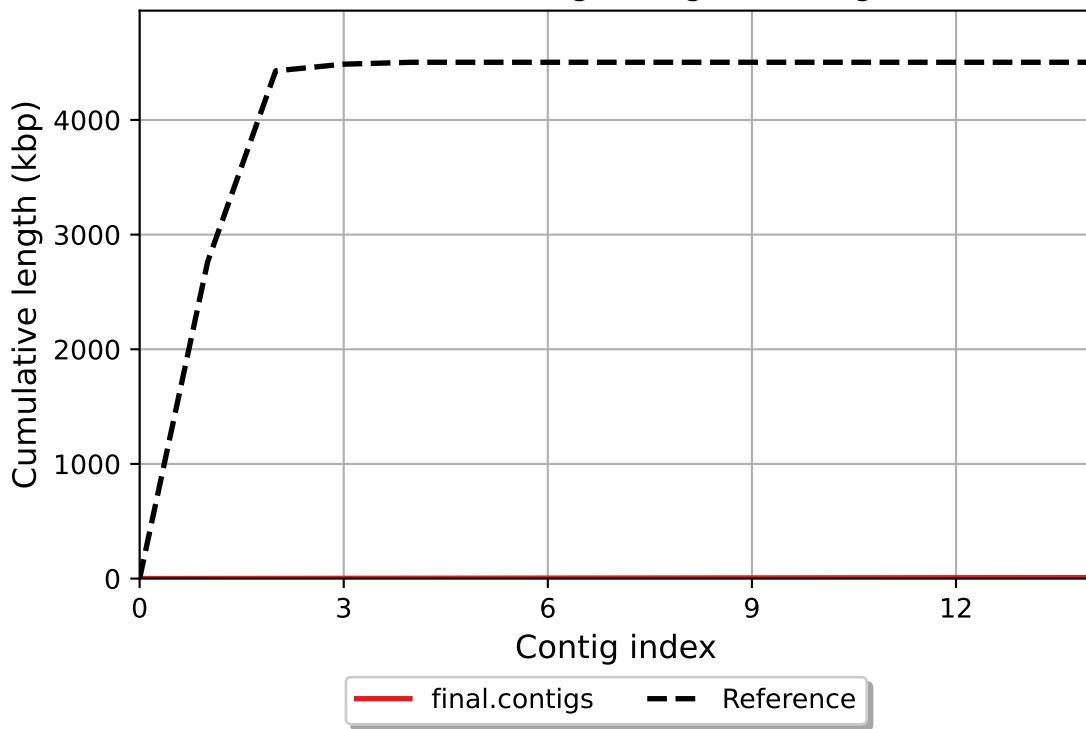


inversions

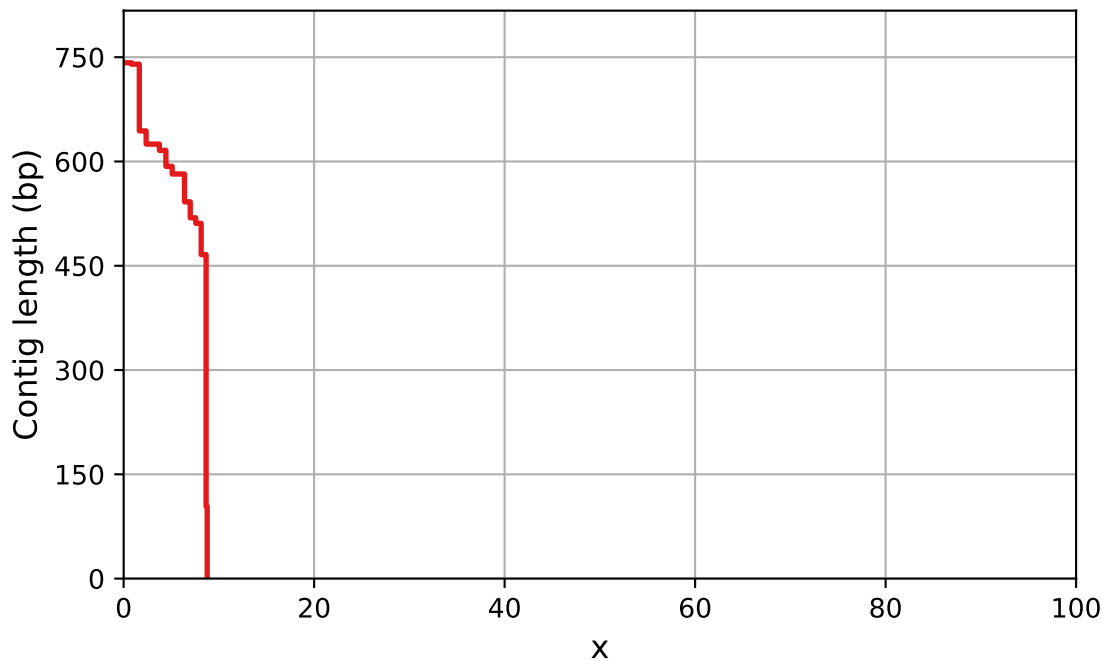
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs