

Report

	final.contigs
# contigs (>= 0 bp)	161952
# contigs (>= 1000 bp)	25167
# contigs (>= 5000 bp)	1190
# contigs (>= 10000 bp)	282
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	9
Total length (>= 0 bp)	123859441
Total length (>= 1000 bp)	51904151
Total length (>= 5000 bp)	11009046
Total length (>= 10000 bp)	4897402
Total length (>= 25000 bp)	1486506
Total length (>= 50000 bp)	650797
# contigs	89614
Largest contig	131335
Total length	95542768
Reference length	2224914
N50	1095
N75	703
L50	21215
L75	49092
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	7945
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	88245 + 46 part
Unaligned length	94245108
Genome fraction (%)	55.854
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1154.42
# indels per 100 kbp	7.73
Largest alignment	3896
Total aligned length	1280524

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

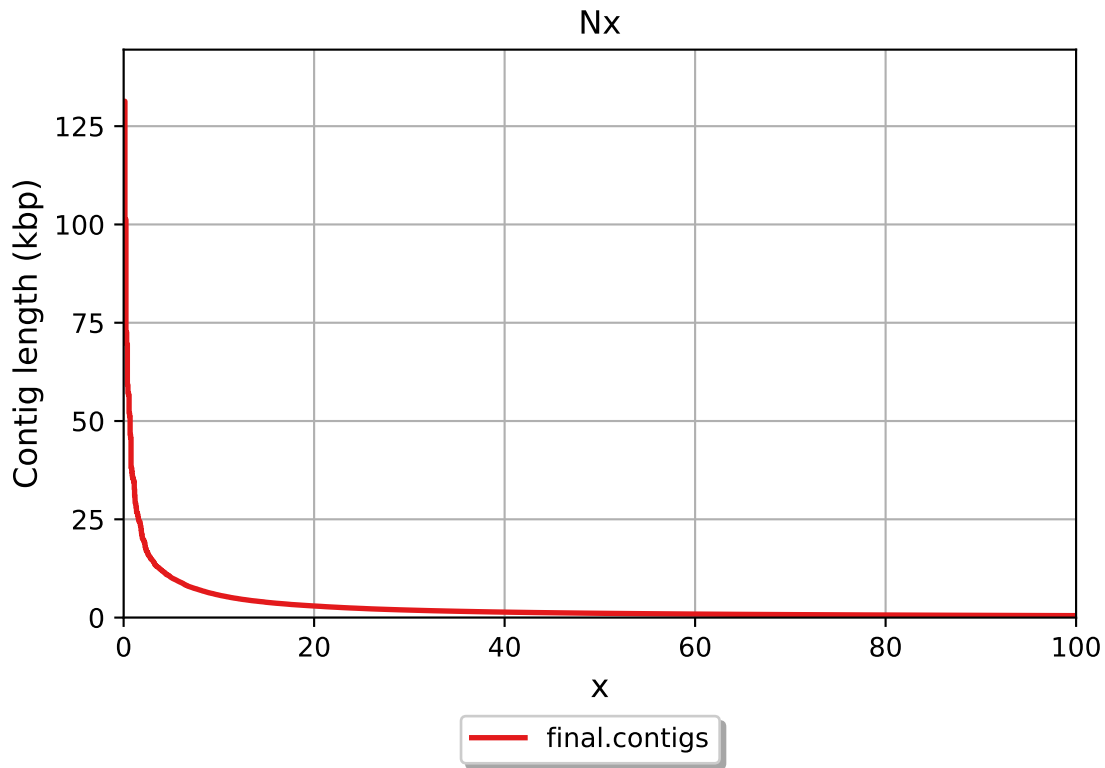
	final.contigs
# misassemblies	7
# contig misassemblies	7
# c. relocations	7
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	7
Misassembled contigs length	7945
# possibly misassembled contigs	46
# possible misassemblies	55
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	14346
# indels	96
# indels (<= 5 bp)	88
# indels (> 5 bp)	8
Indels length	334

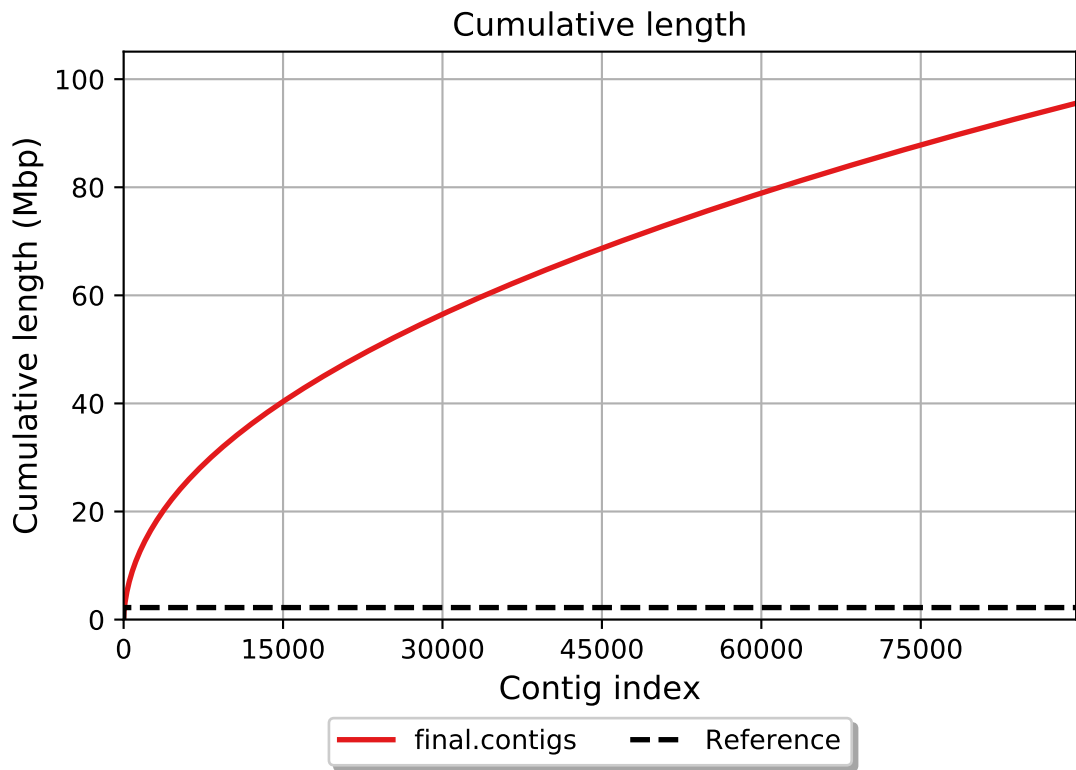
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

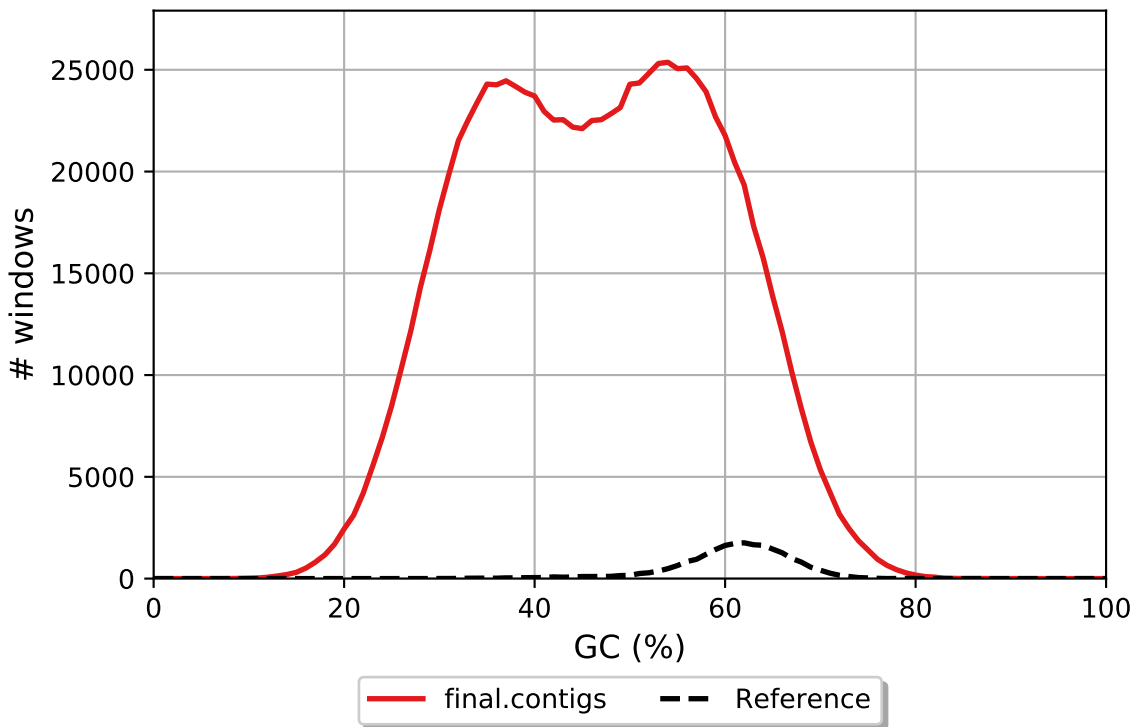
	final.contigs
# fully unaligned contigs	88245
Fully unaligned length	94184447
# partially unaligned contigs	46
Partially unaligned length	60661
# N's	0

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).

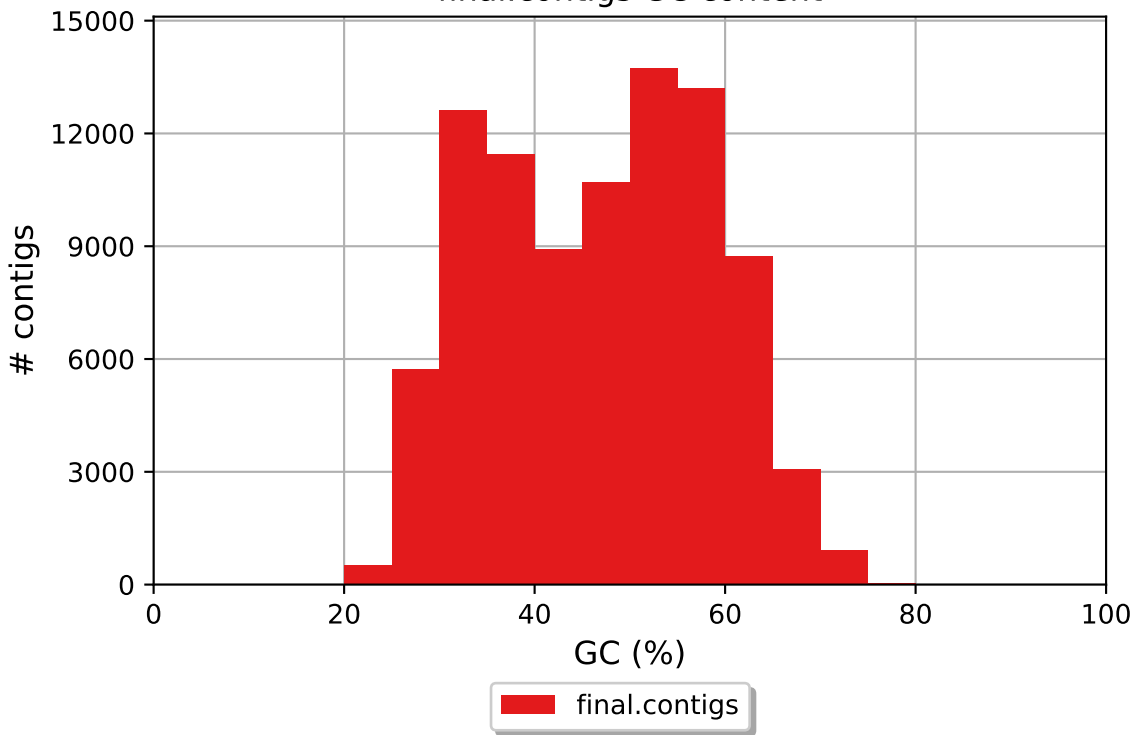




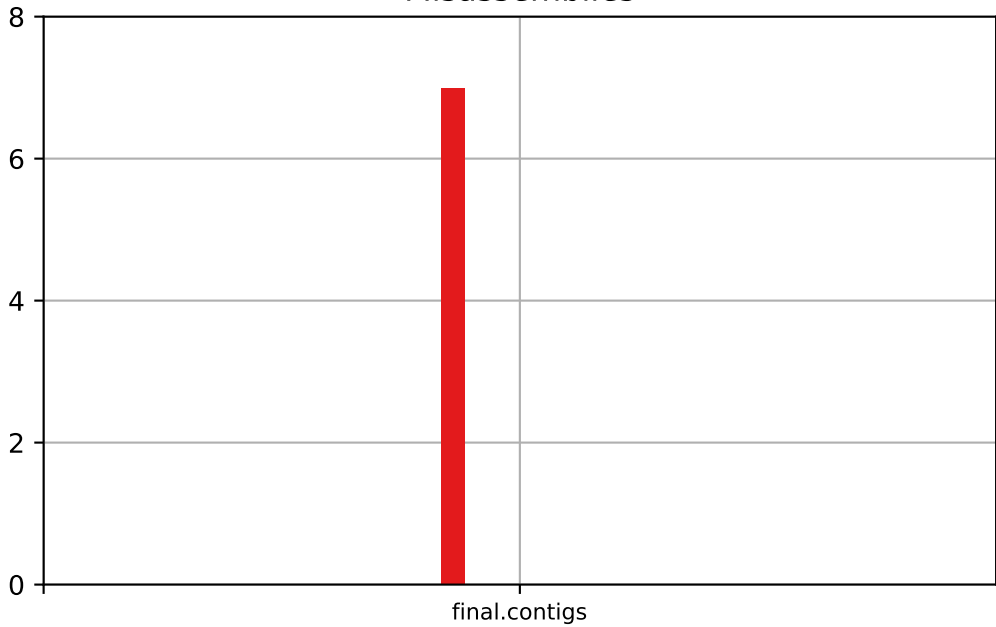
GC content



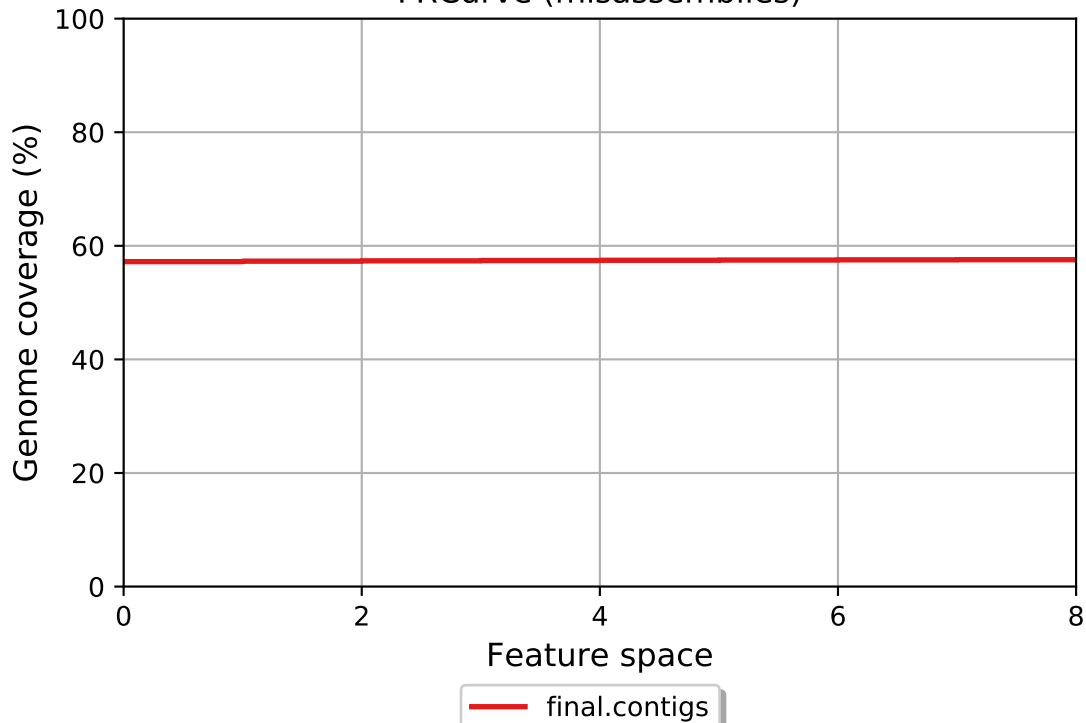
final.contigs GC content



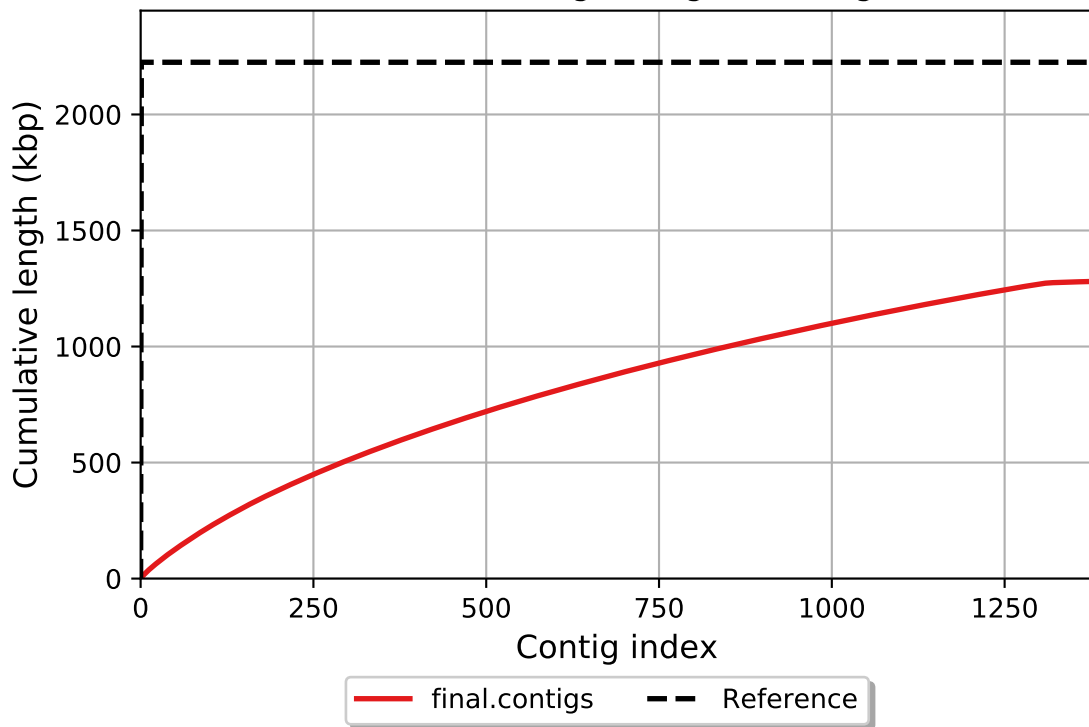
Misassemblies



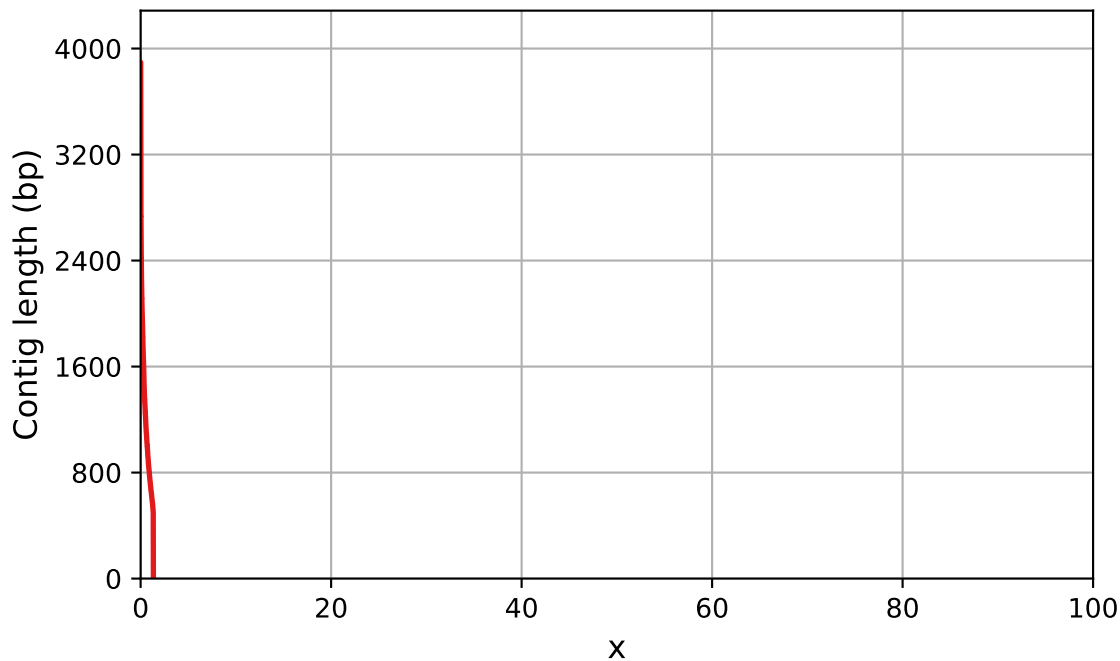
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs