

Report

	final.contigs
# contigs (>= 0 bp)	160996
# contigs (>= 1000 bp)	25023
# contigs (>= 5000 bp)	1191
# contigs (>= 10000 bp)	278
# contigs (>= 25000 bp)	34
# contigs (>= 50000 bp)	9
Total length (>= 0 bp)	123162917
Total length (>= 1000 bp)	51570041
Total length (>= 5000 bp)	10974398
Total length (>= 10000 bp)	4853961
Total length (>= 25000 bp)	1460584
Total length (>= 50000 bp)	650955
# contigs	89318
Largest contig	131335
Total length	95113204
Reference length	2224914
N50	1093
N75	703
L50	21182
L75	48971
# misassemblies	6
# misassembled contigs	6
Misassembled contigs length	6938
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	87957 + 47 part
Unaligned length	93826347
Genome fraction (%)	55.430
Duplication ratio	1.044
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1151.00
# indels per 100 kbp	7.70
Largest alignment	3896
Total aligned length	1270523

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

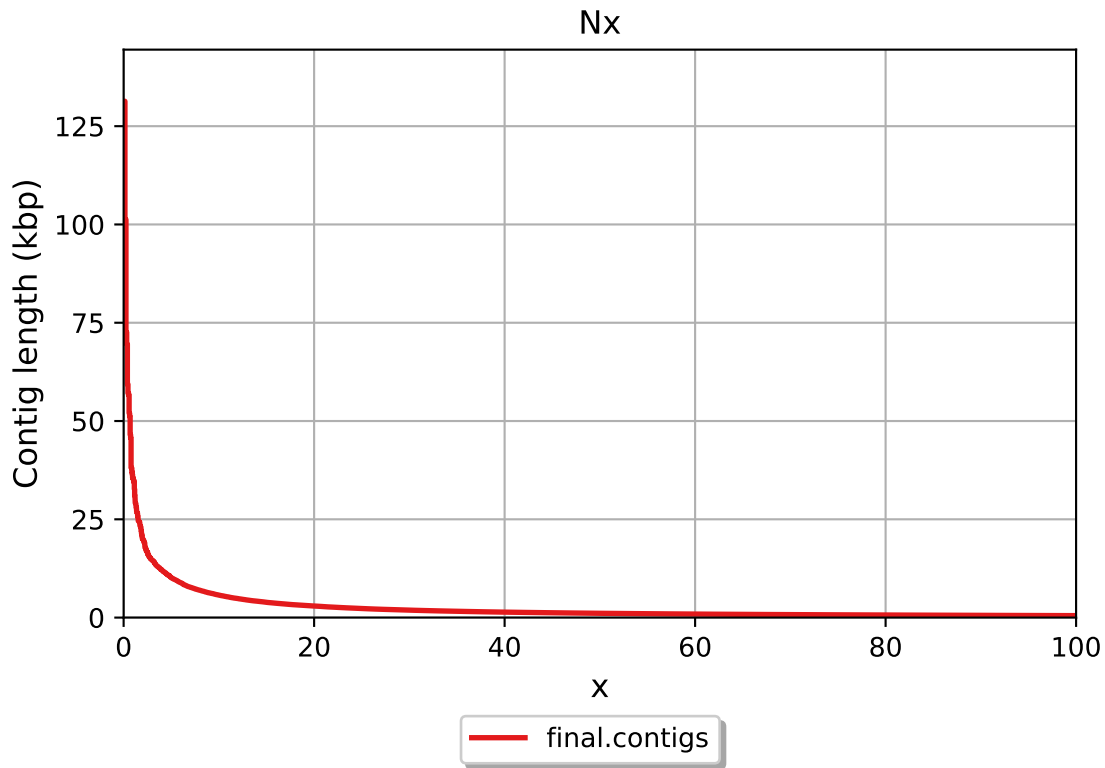
	final.contigs
# misassemblies	6
# contig misassemblies	6
# c. relocations	6
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	6
Misassembled contigs length	6938
# possibly misassembled contigs	47
# possible misassemblies	55
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	14195
# indels	95
# indels (<= 5 bp)	86
# indels (> 5 bp)	9
Indels length	347

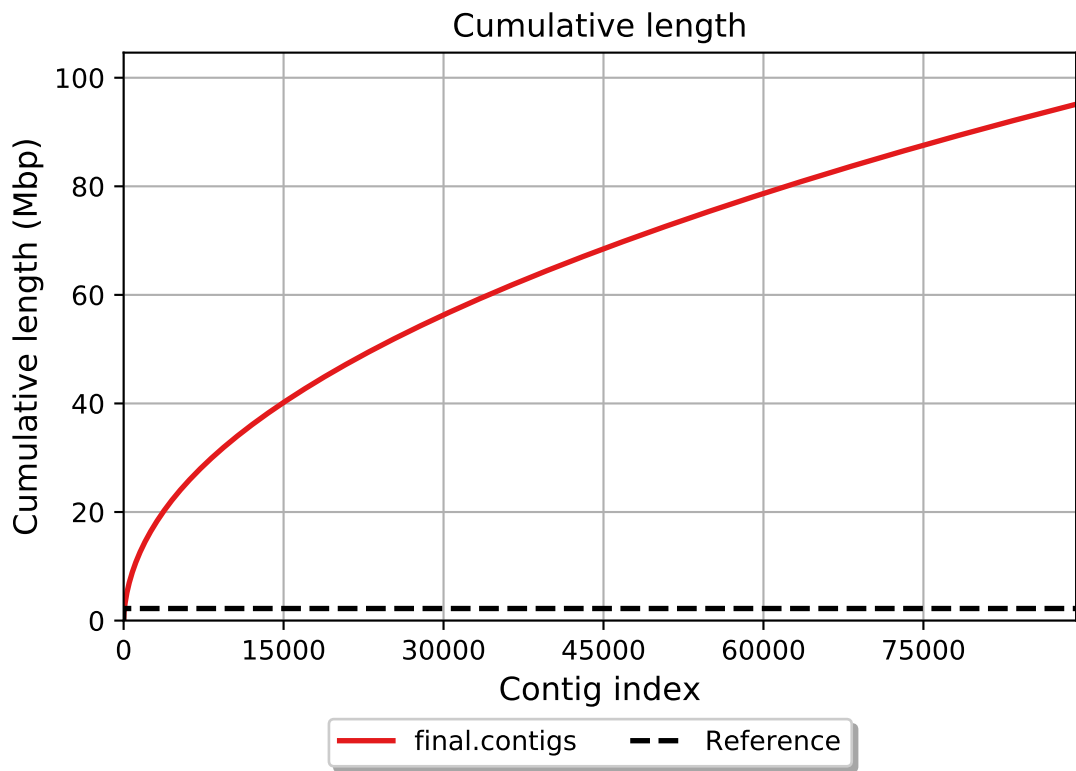
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

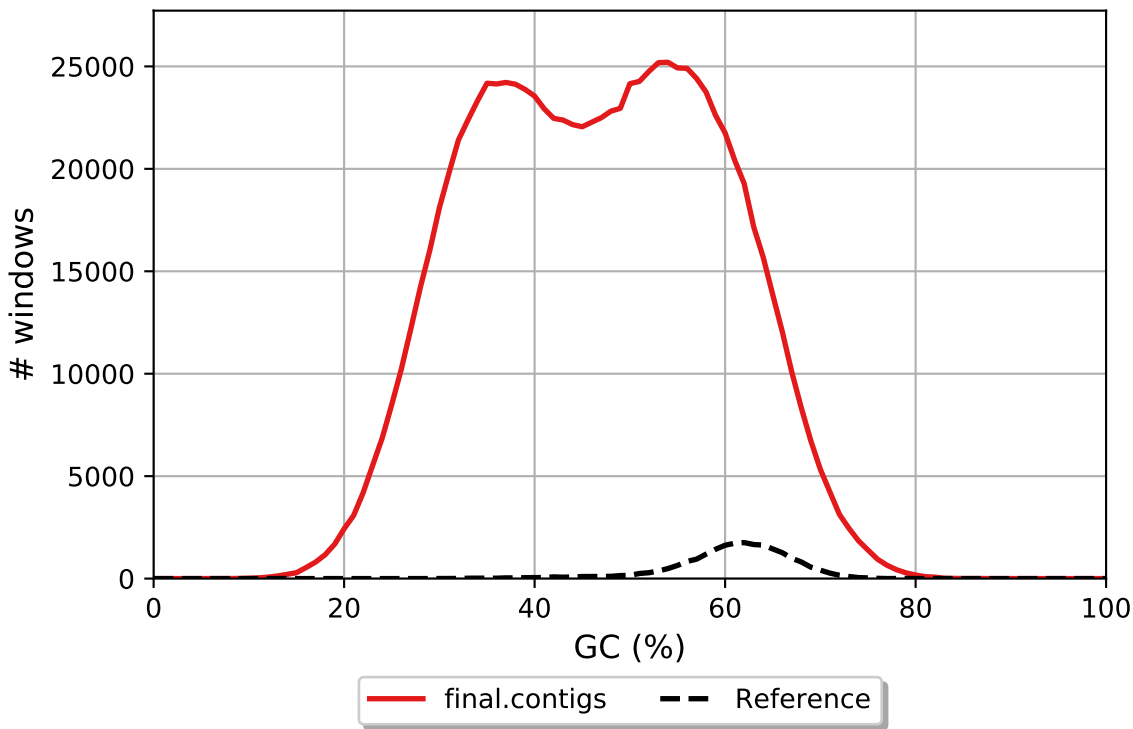
	final.contigs
# fully unaligned contigs	87957
Fully unaligned length	93763776
# partially unaligned contigs	47
Partially unaligned length	62571
# N's	0

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).

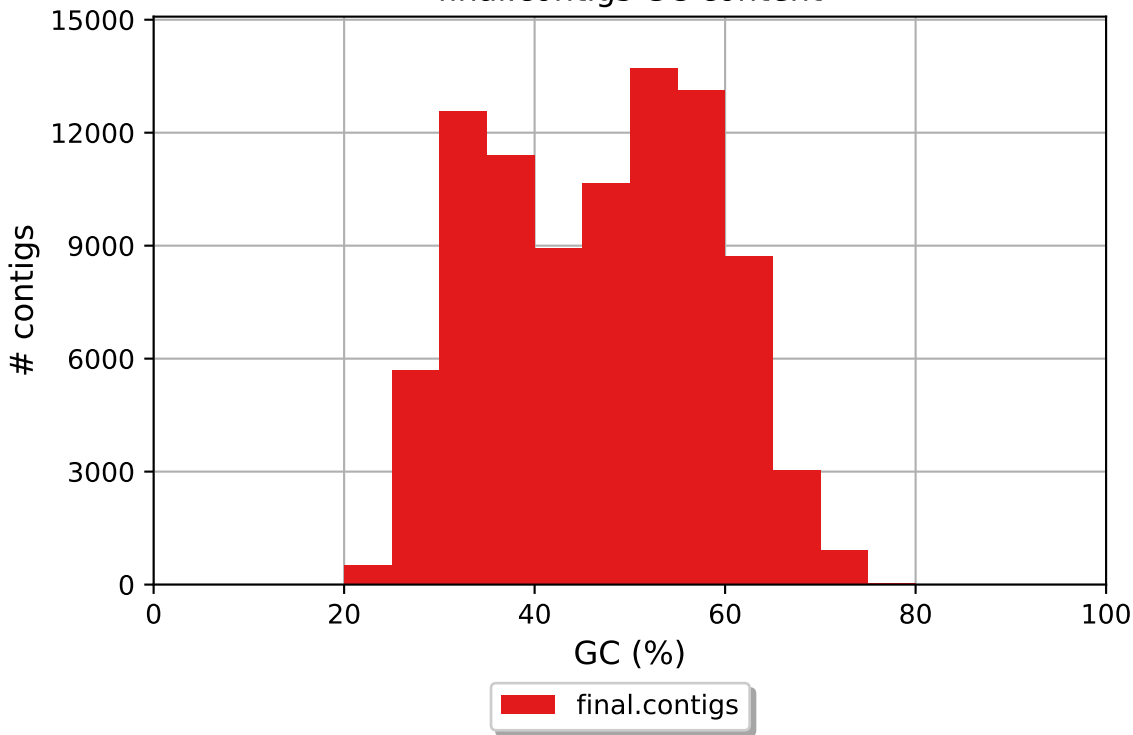




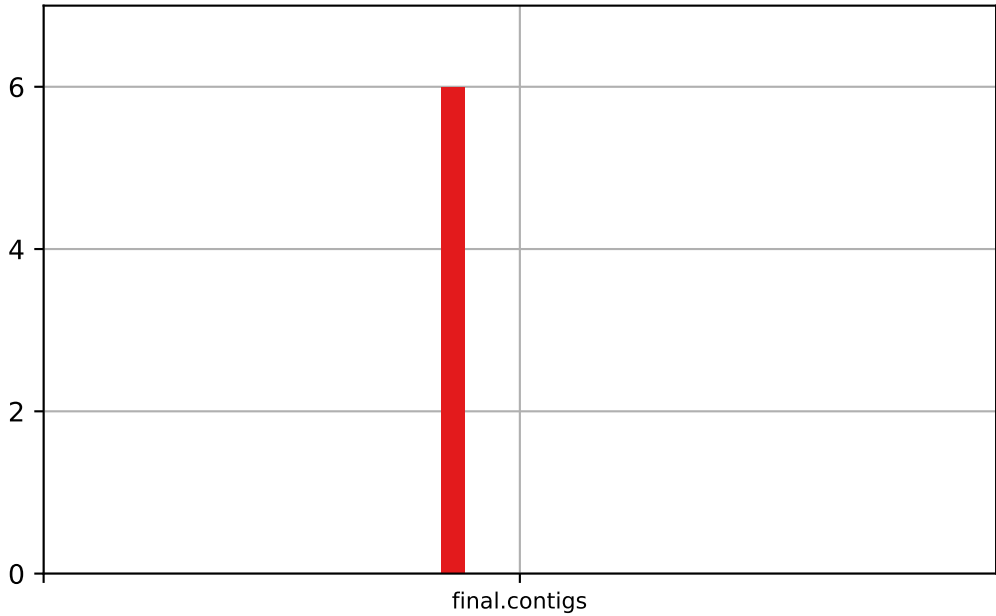
GC content



final.contigs GC content

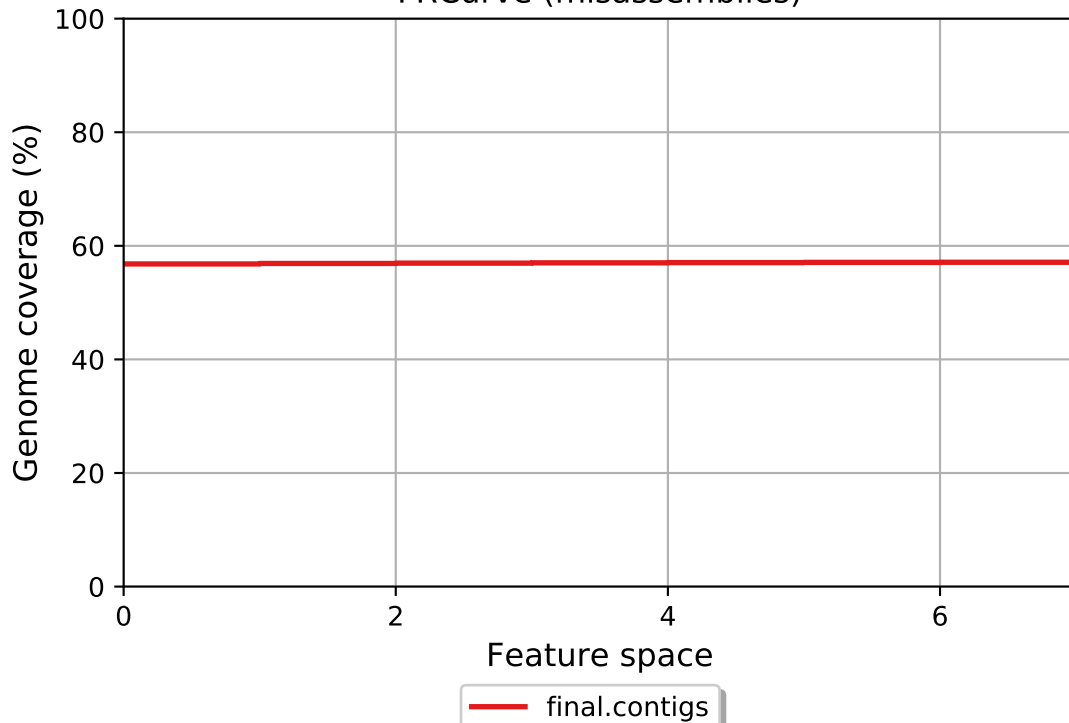


Misassemblies

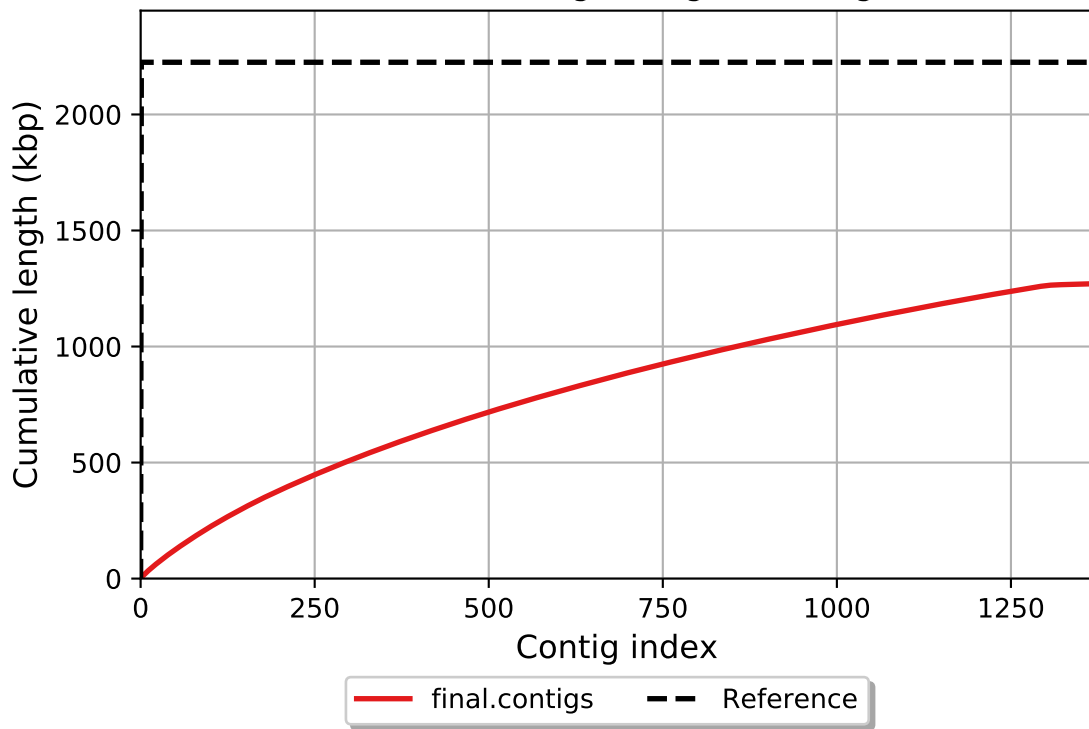


 # relocations

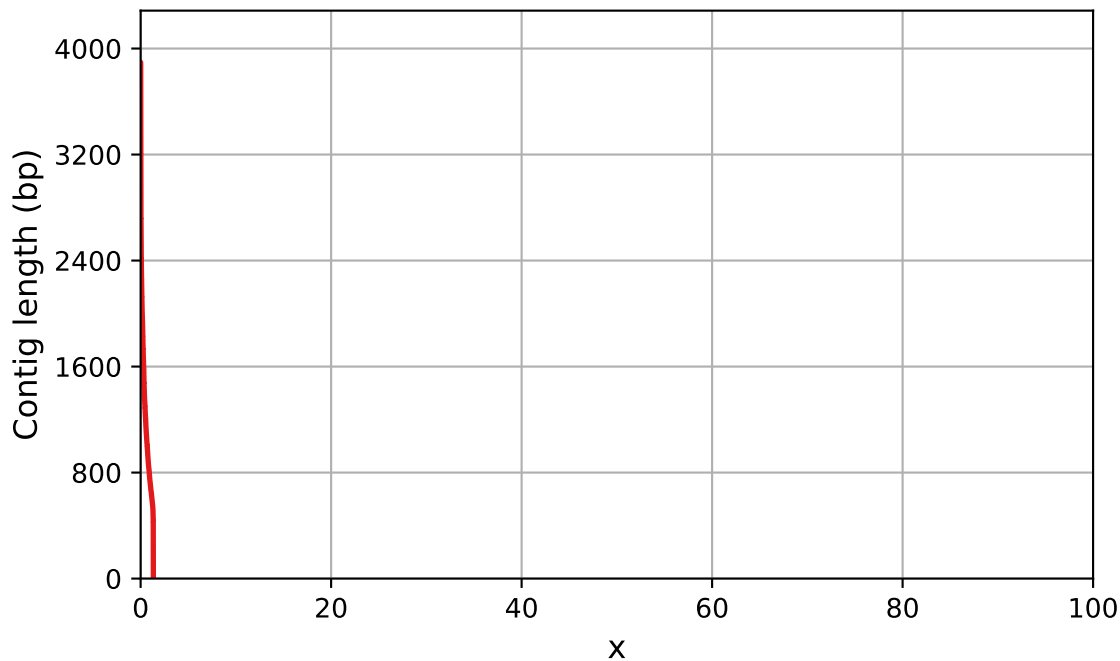
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs