

Report

	final.contigs
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	59964
Total length (>= 5000 bp)	49430
Total length (>= 10000 bp)	36014
Total length (>= 25000 bp)	36014
Total length (>= 50000 bp)	0
# contigs	18
Largest contig	36014
Total length	65246
Reference length	5695417
GC (%)	48.15
Reference GC (%)	72.40
N50	36014
N75	5845
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	7 + 9 part
Unaligned length	63205
Genome fraction (%)	0.011
Duplication ratio	3.324
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6351.79
# indels per 100 kbp	0.00
Largest alignment	105
Total aligned length	1183
NGA50	-

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	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	8
# possible misassemblies	9
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	39
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

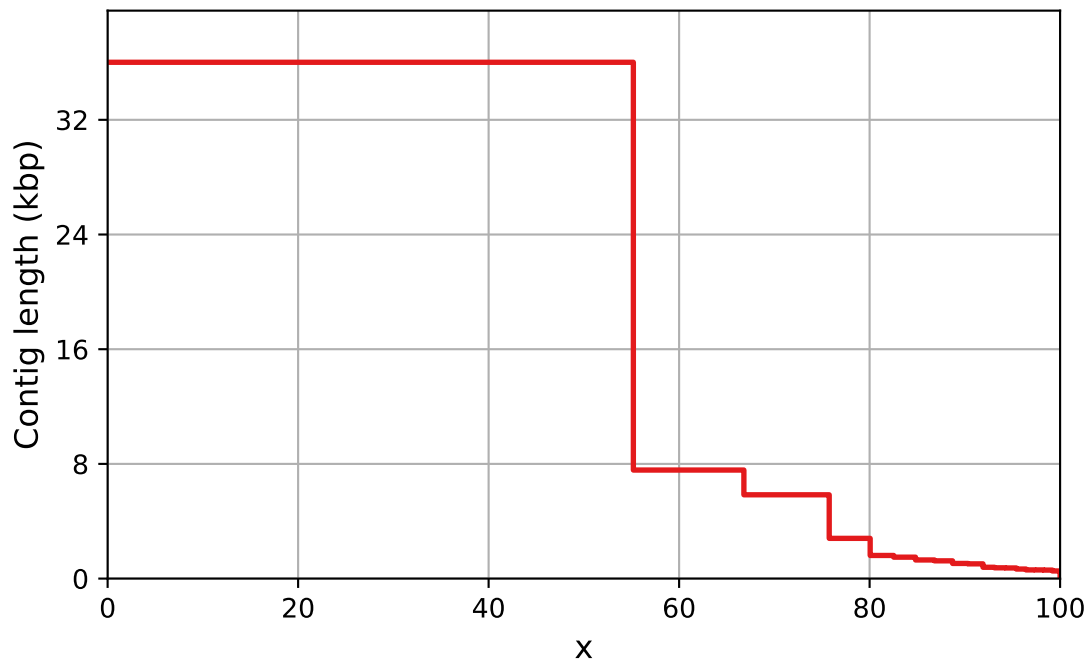
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	7
Fully unaligned length	53735
# partially unaligned contigs	9
Partially unaligned length	9470
# N's	0

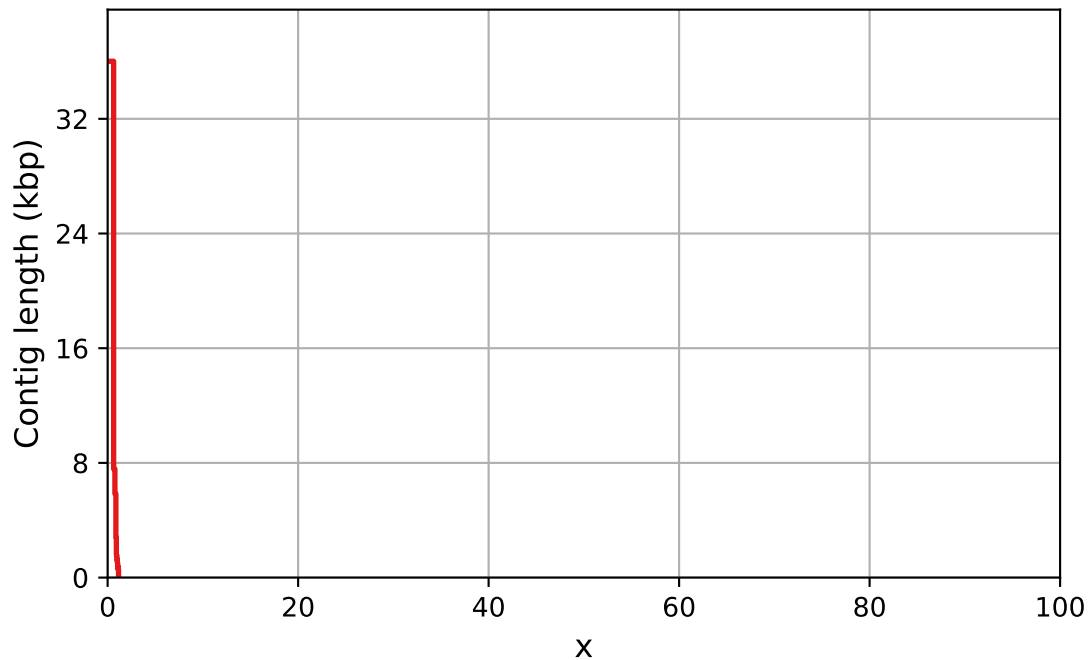
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

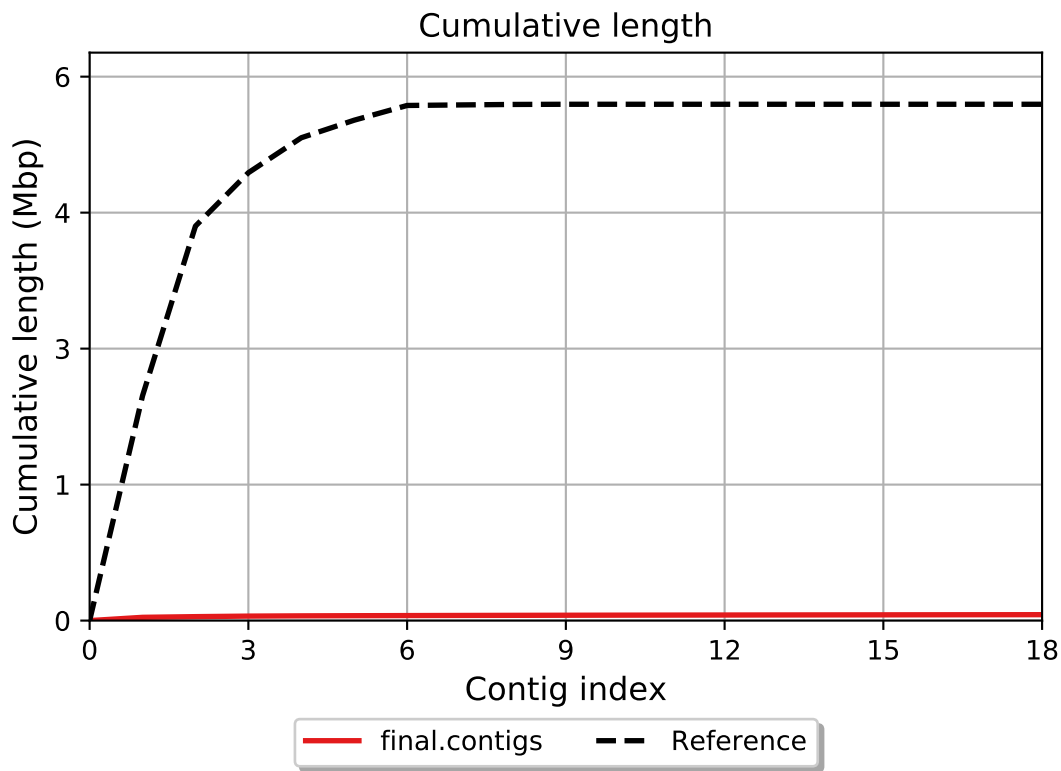


— final.contigs

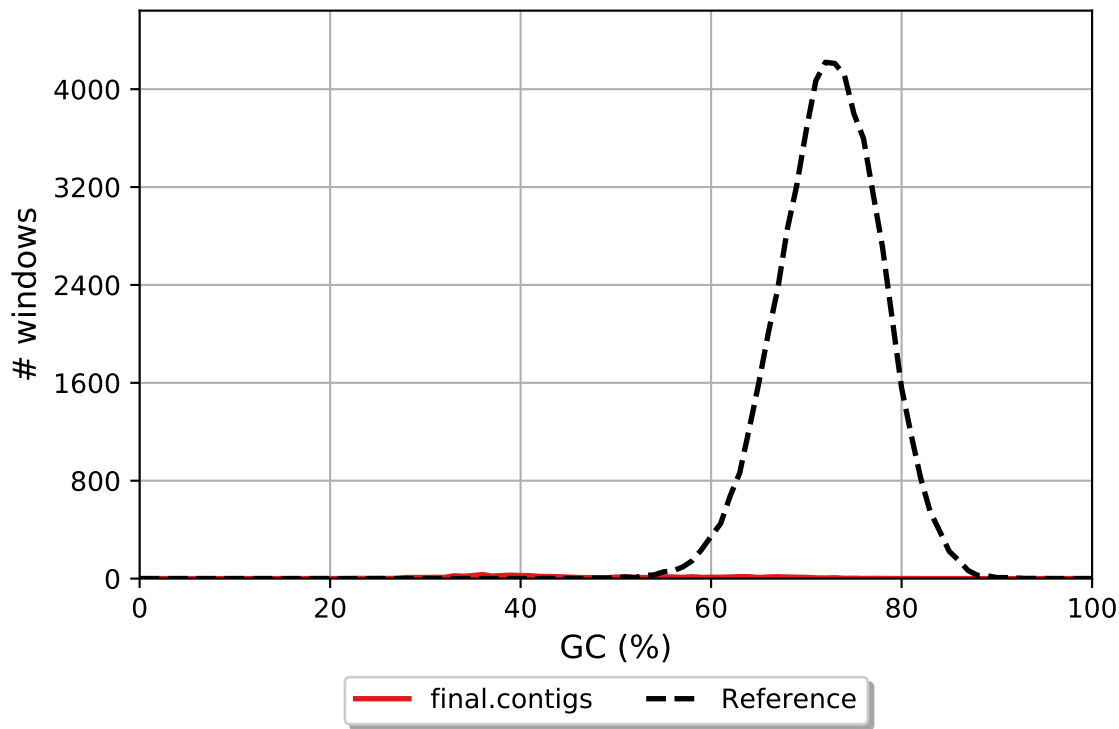
NGx



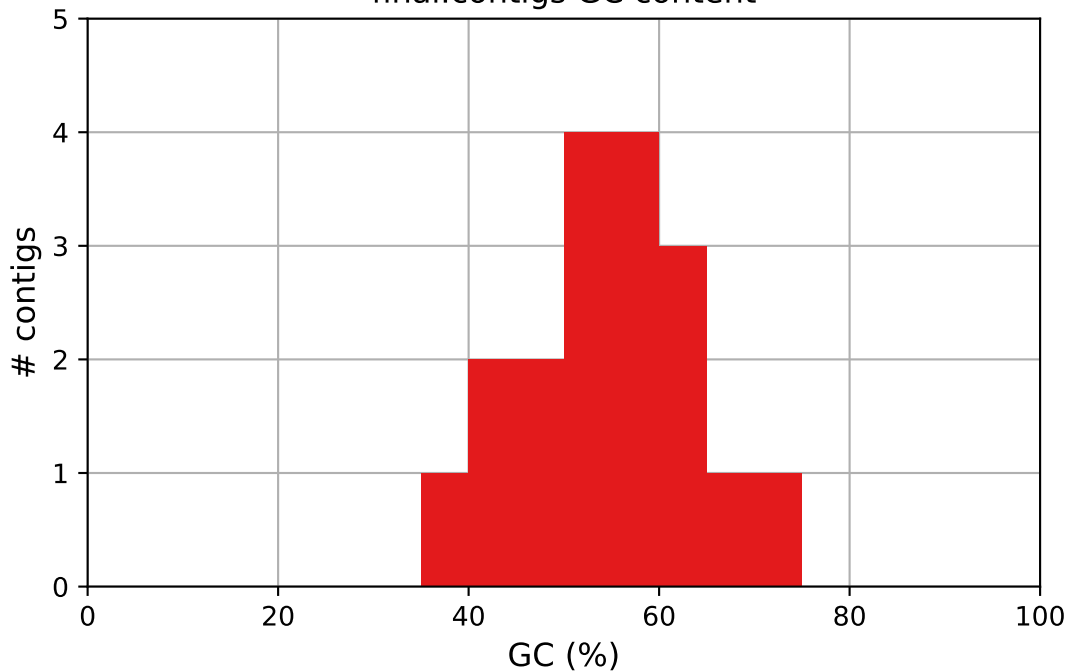
— final.contigs



GC content



final.contigs GC content

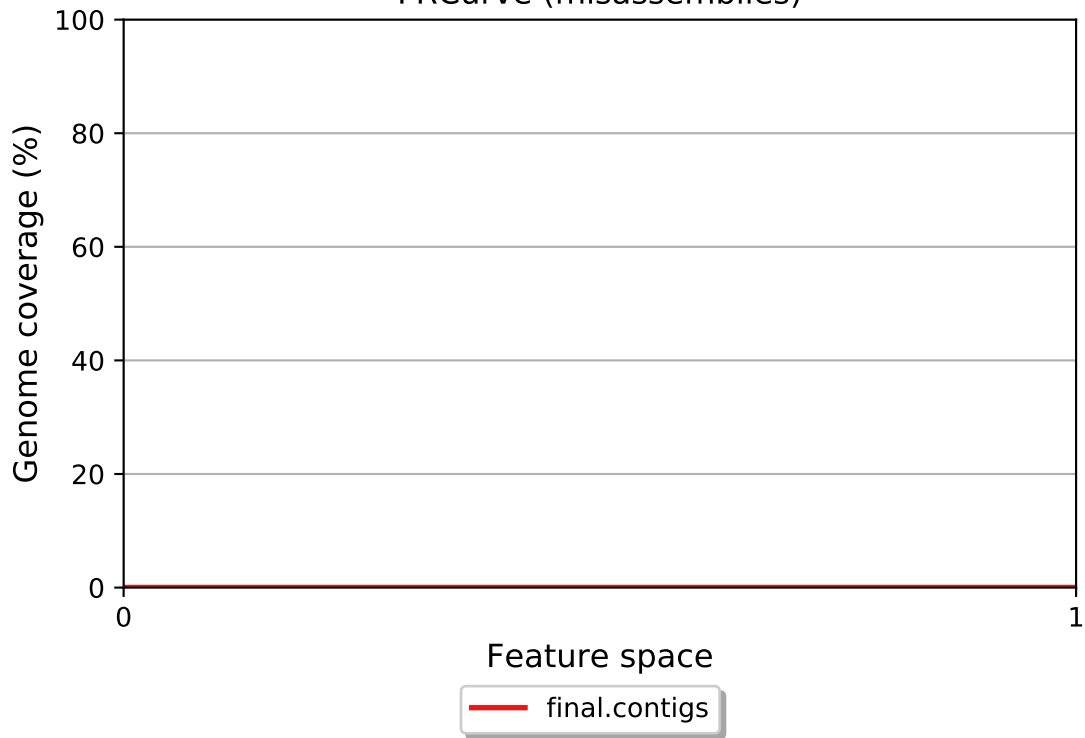


final.contigs

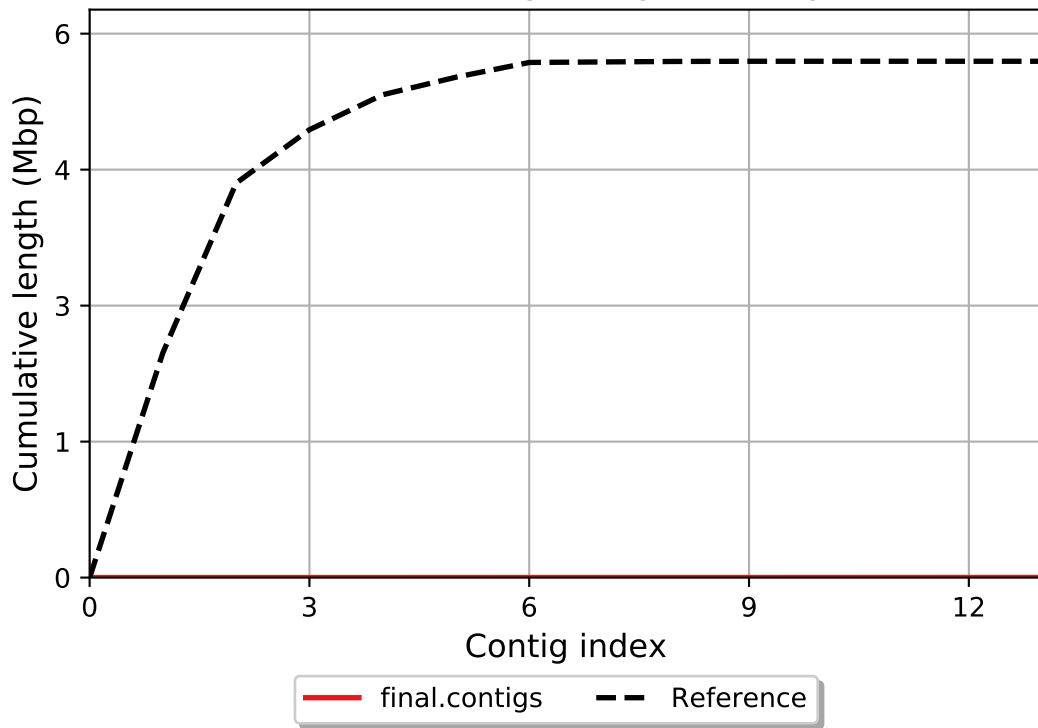
Misassemblies



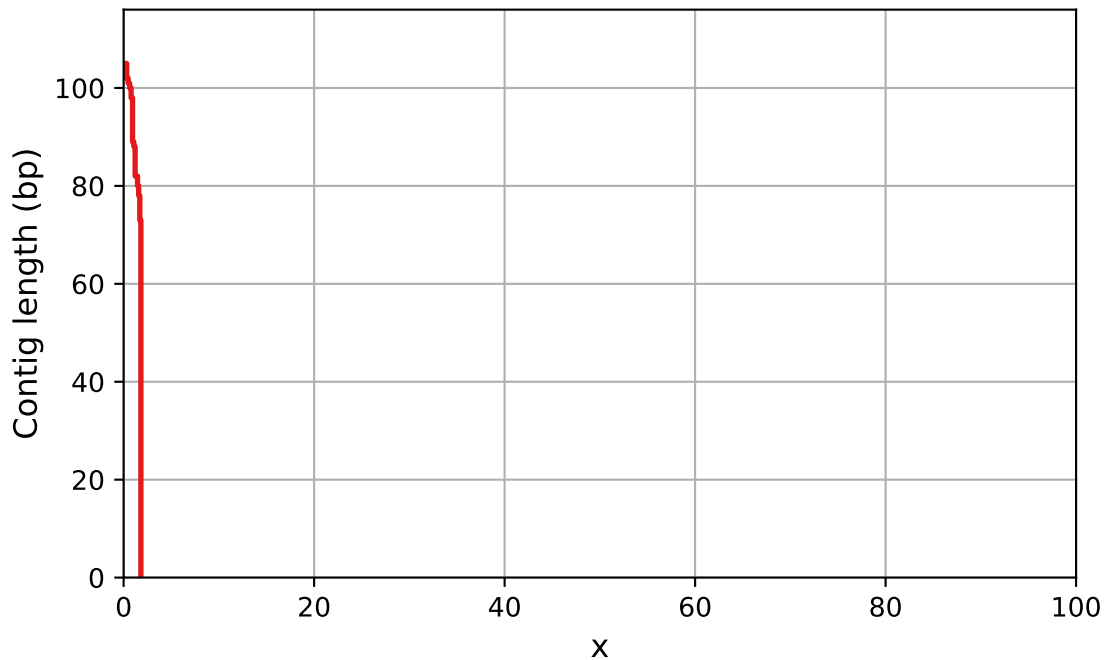
FRCurve (misassemblies)



Cumulative length (aligned contigs)

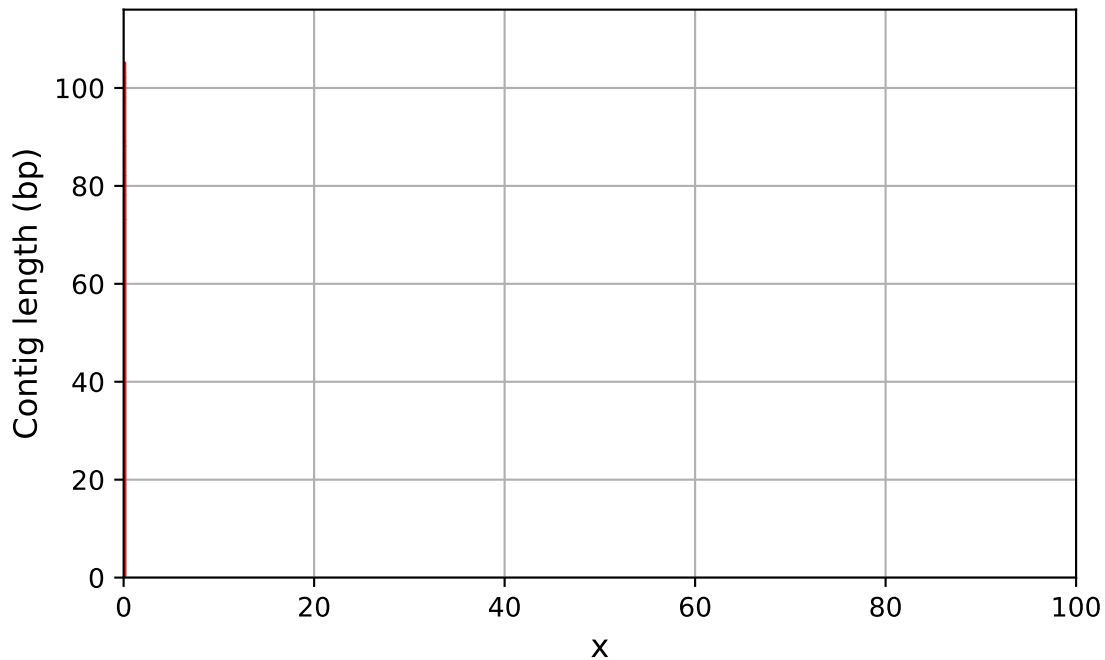


NAx



— final.contigs

NGAx



— final.contigs