

Report

	final.contigs
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	50597
Total length (>= 5000 bp)	41132
Total length (>= 10000 bp)	41132
Total length (>= 25000 bp)	26811
Total length (>= 50000 bp)	0
# contigs	15
Largest contig	26811
Total length	55291
Reference length	4168427
GC (%)	50.57
Reference GC (%)	62.60
N50	14321
N75	2448
L50	2
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	0 + 12 part
Unaligned length	52204
Genome fraction (%)	0.033
Duplication ratio	2.262
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2930.40
# indels per 100 kbp	146.52
Largest alignment	176
Total aligned length	1755
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	7
# possible misassemblies	9
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	40
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

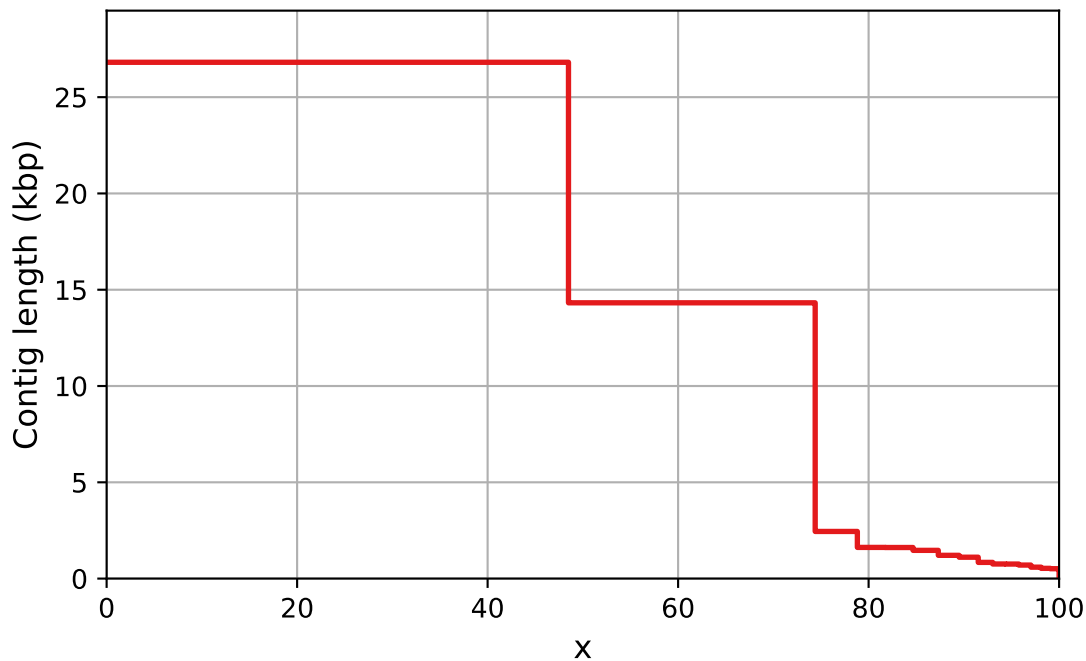
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
Partially unaligned length	52204
# N's	0

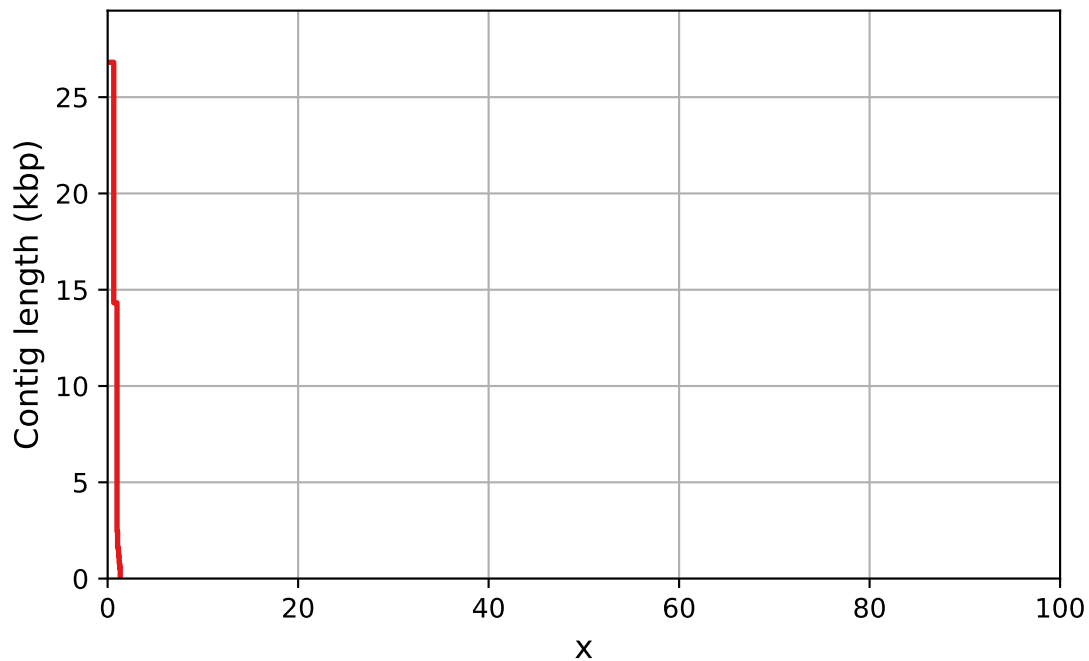
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



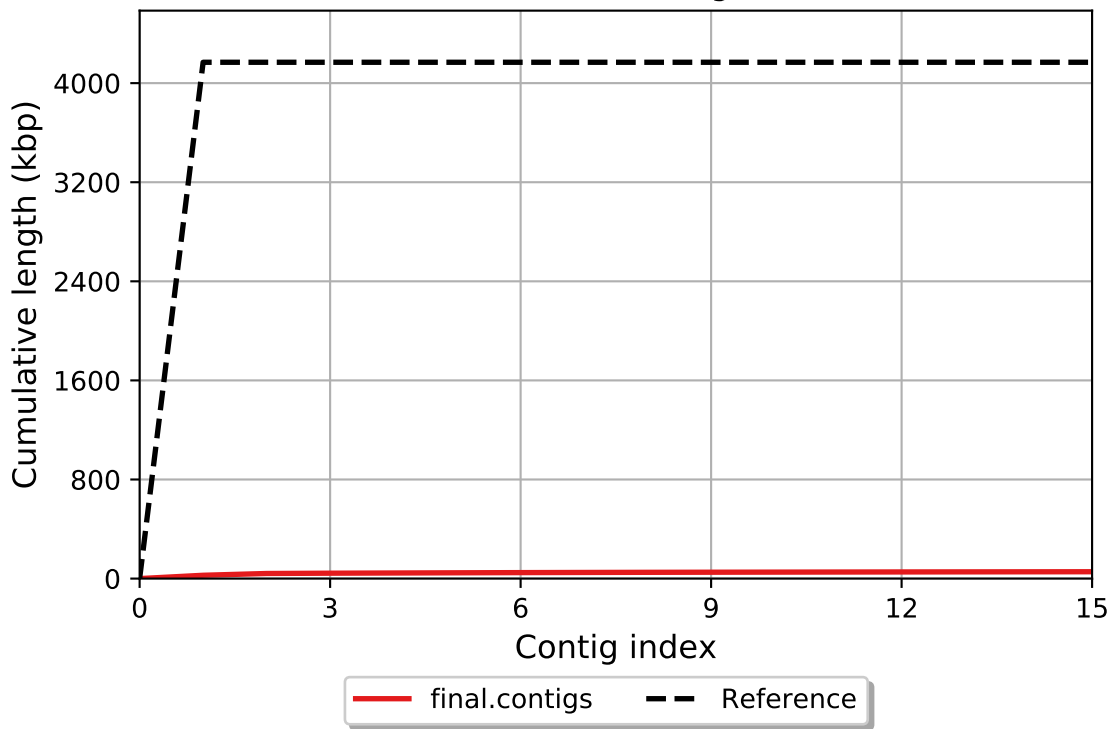
— final.contigs

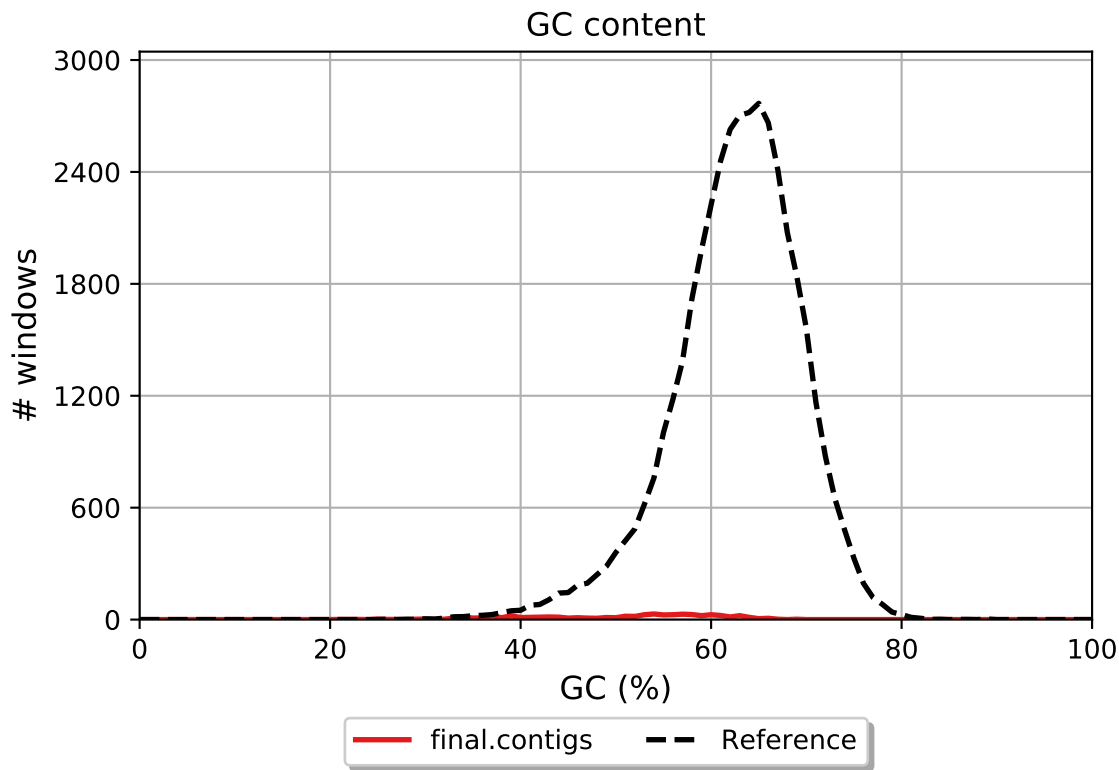
NGx



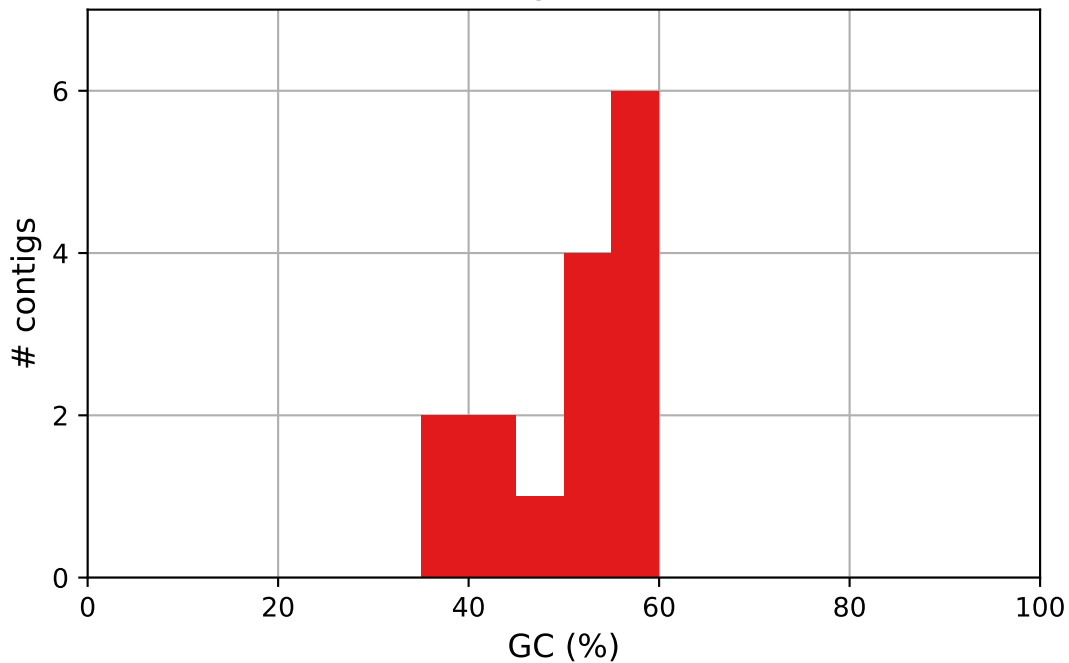
— final.contigs

Cumulative length





final.contigs GC content

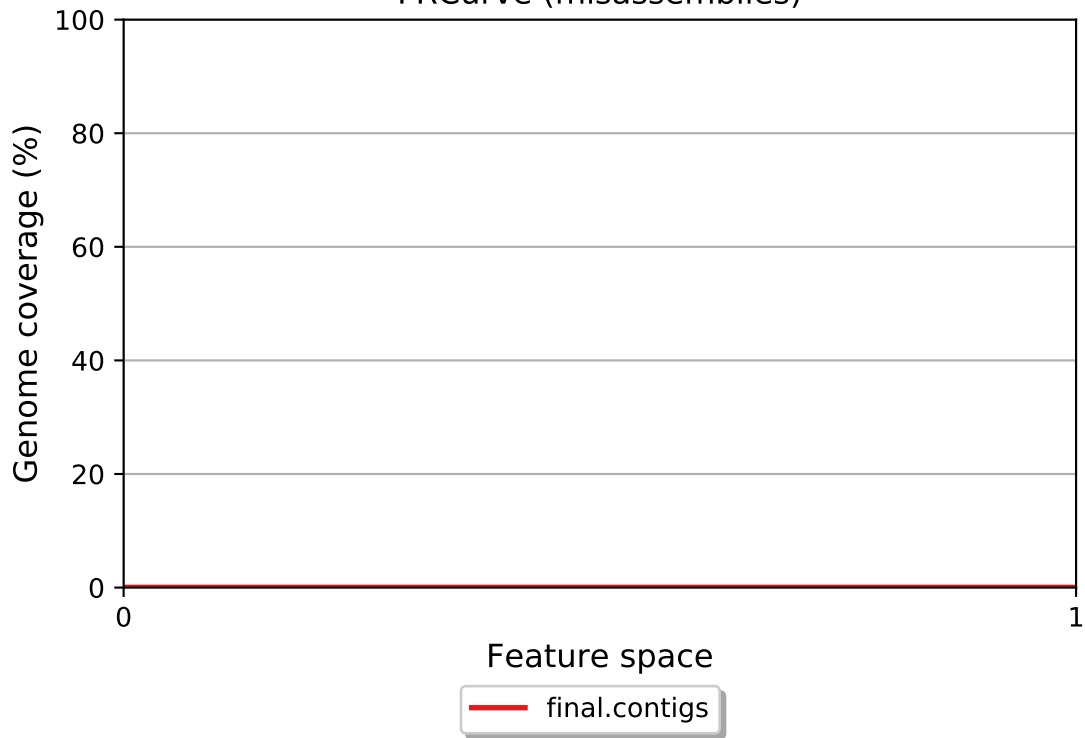


final.contigs

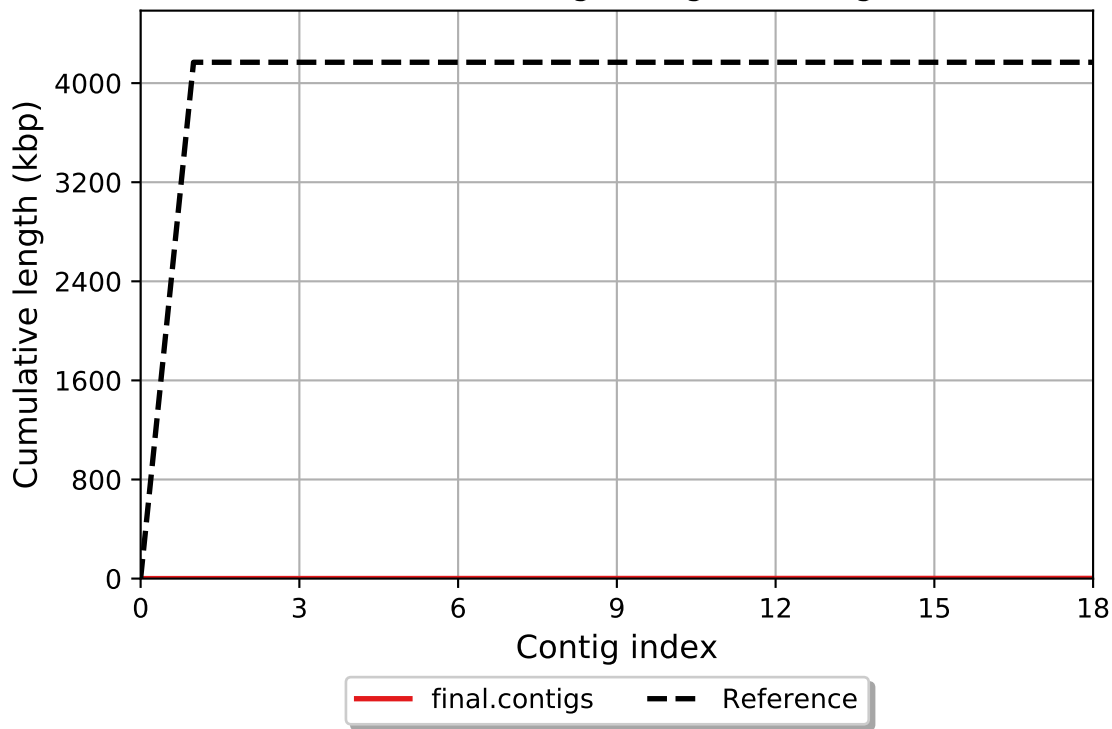
Misassemblies



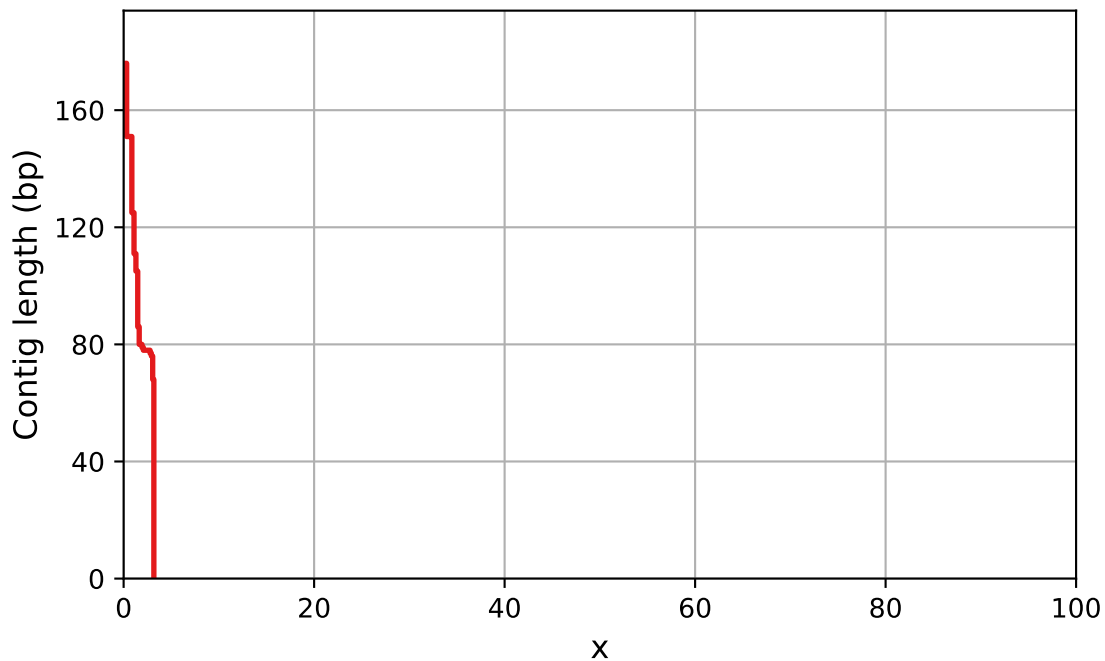
FRCurve (misassemblies)



Cumulative length (aligned contigs)

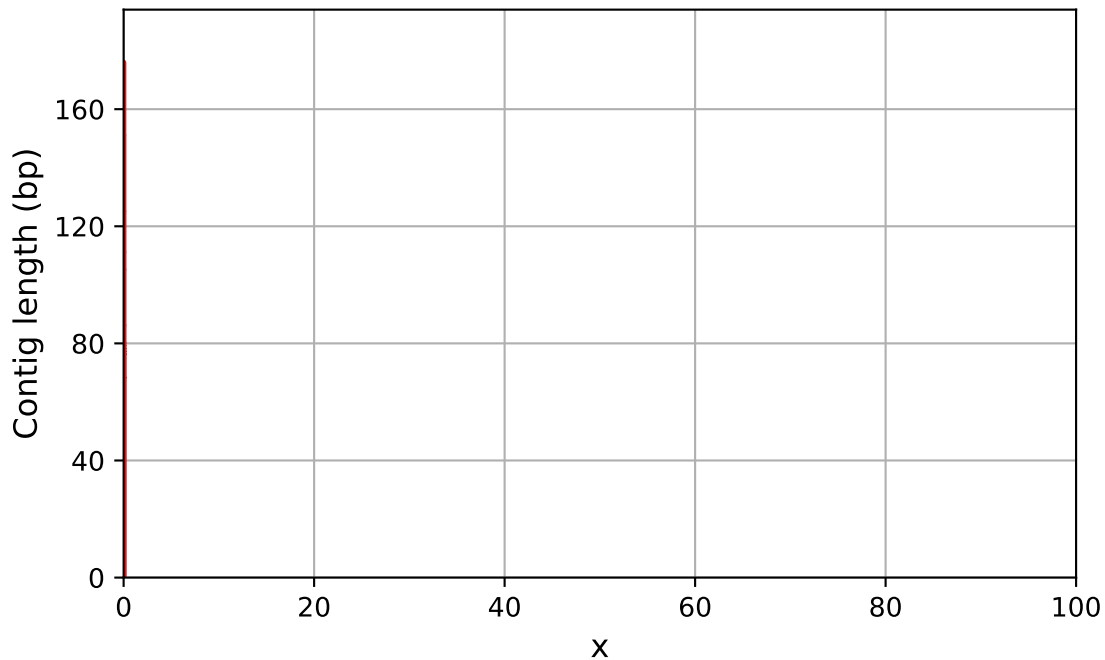


NAx



— final.contigs

NGAx



— final.contigs