

## Report

	final.contigs
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	75000
Total length (>= 5000 bp)	55134
Total length (>= 10000 bp)	49812
Total length (>= 25000 bp)	36020
Total length (>= 50000 bp)	0
# contigs	20
Largest contig	36020
Total length	81210
Reference length	2077614
GC (%)	43.16
Reference GC (%)	39.47
N50	13792
N75	4124
L50	2
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	2 + 13 part
Unaligned length	76691
Genome fraction (%)	0.088
Duplication ratio	2.468
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4096.12
# indels per 100 kbp	600.76
Largest alignment	558
Total aligned length	3000
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	11
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	75
# indels	11
# indels (<= 5 bp)	11
# indels (> 5 bp)	0
Indels length	12

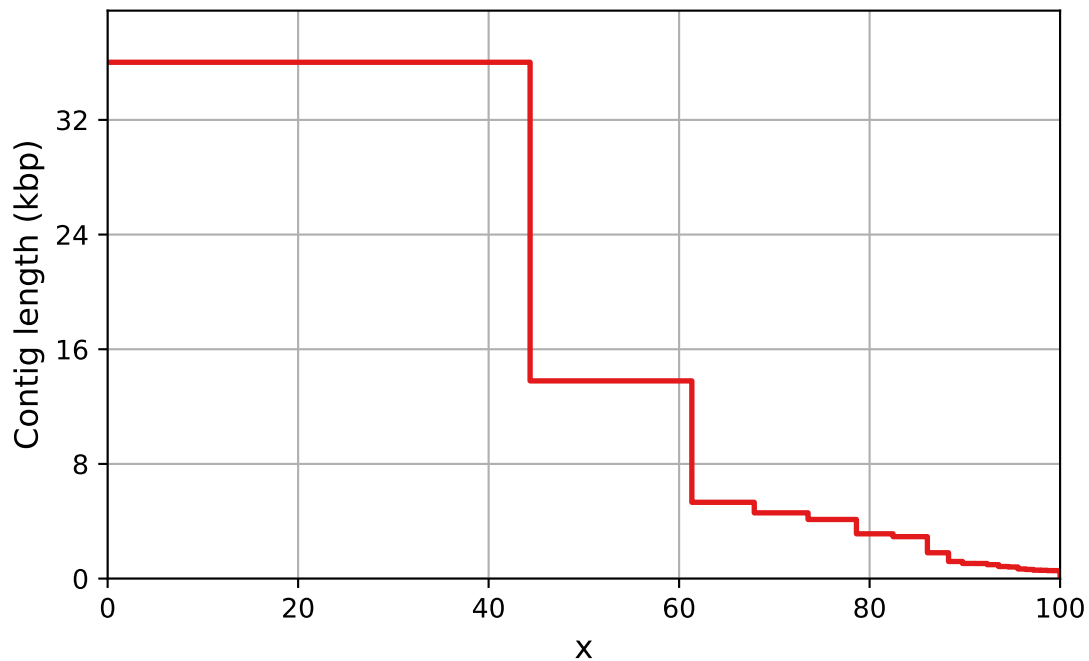
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1645
# partially unaligned contigs	13
Partially unaligned length	75046
# N's	0

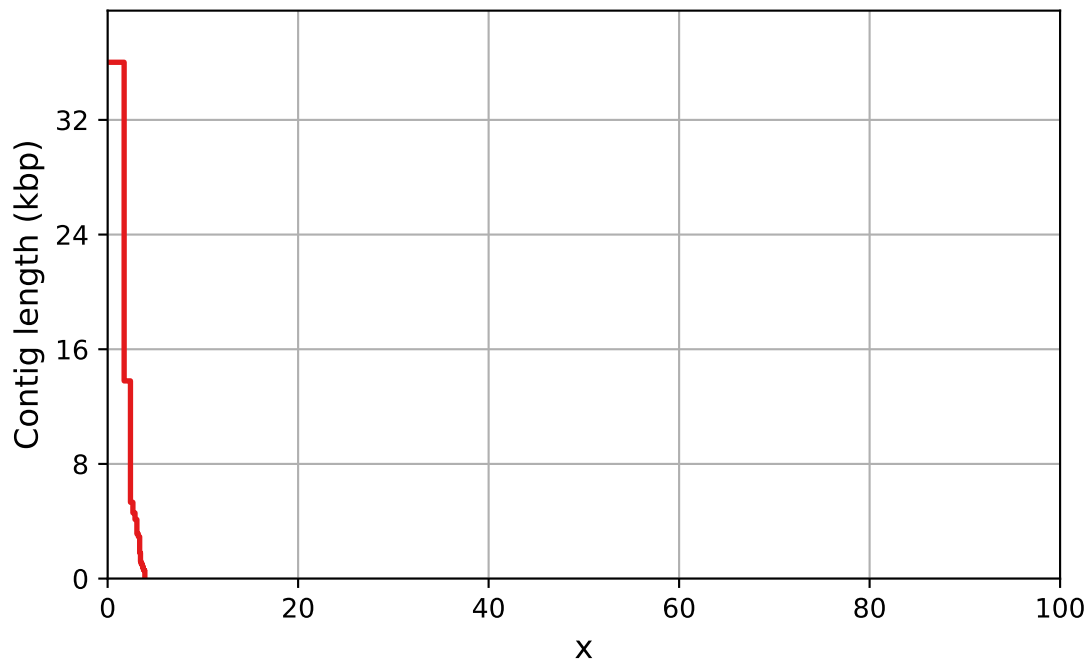
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

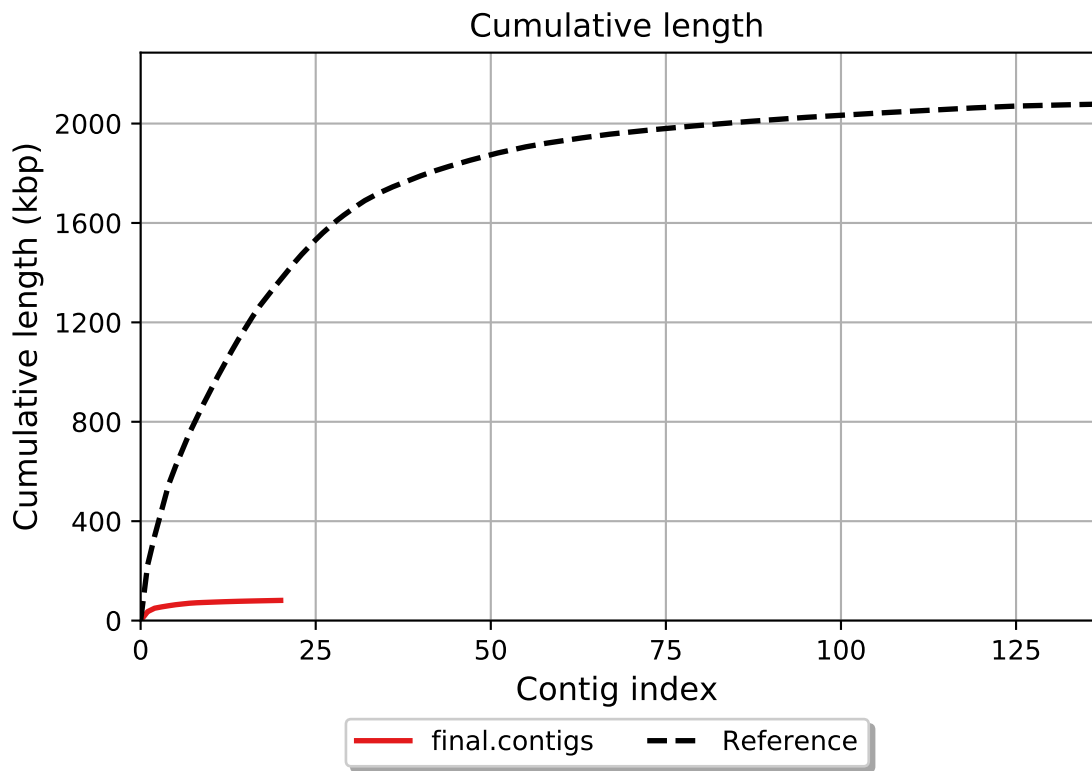


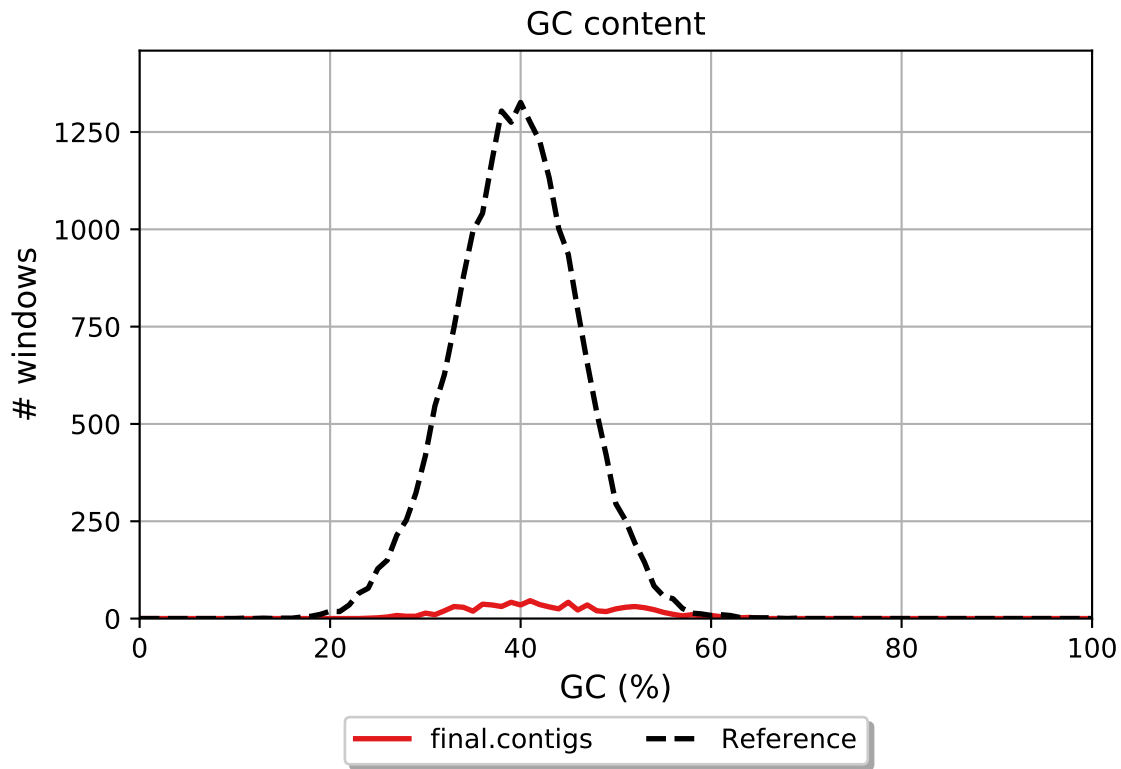
— final.contigs

NGx

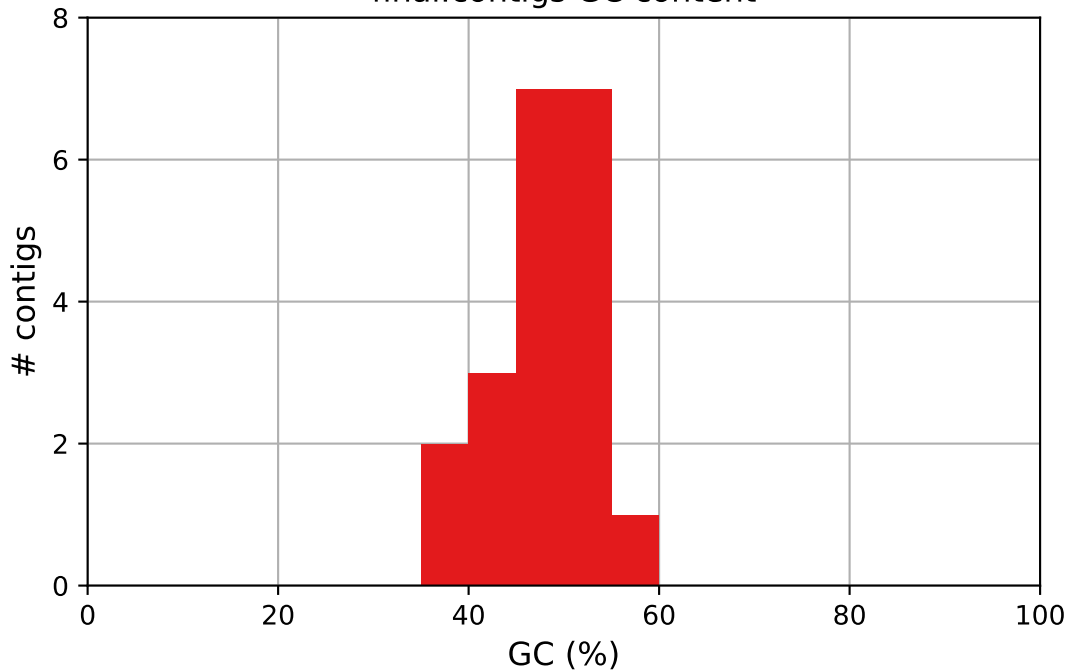


— final.contigs





final.contigs GC content



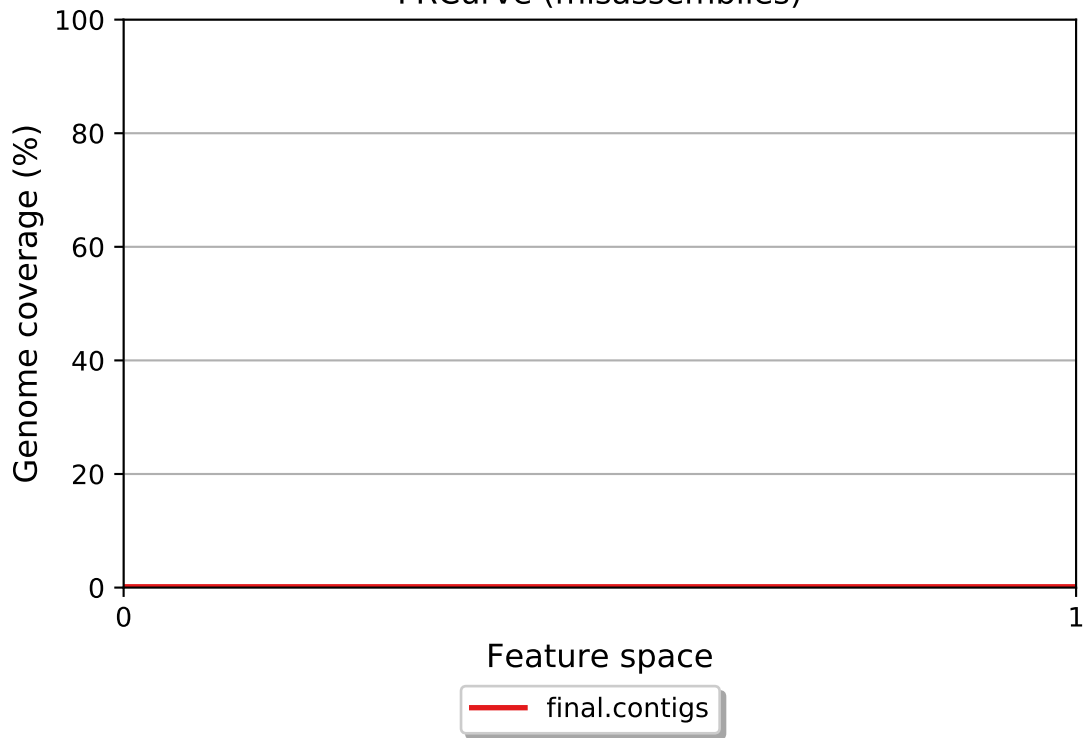
final.contigs



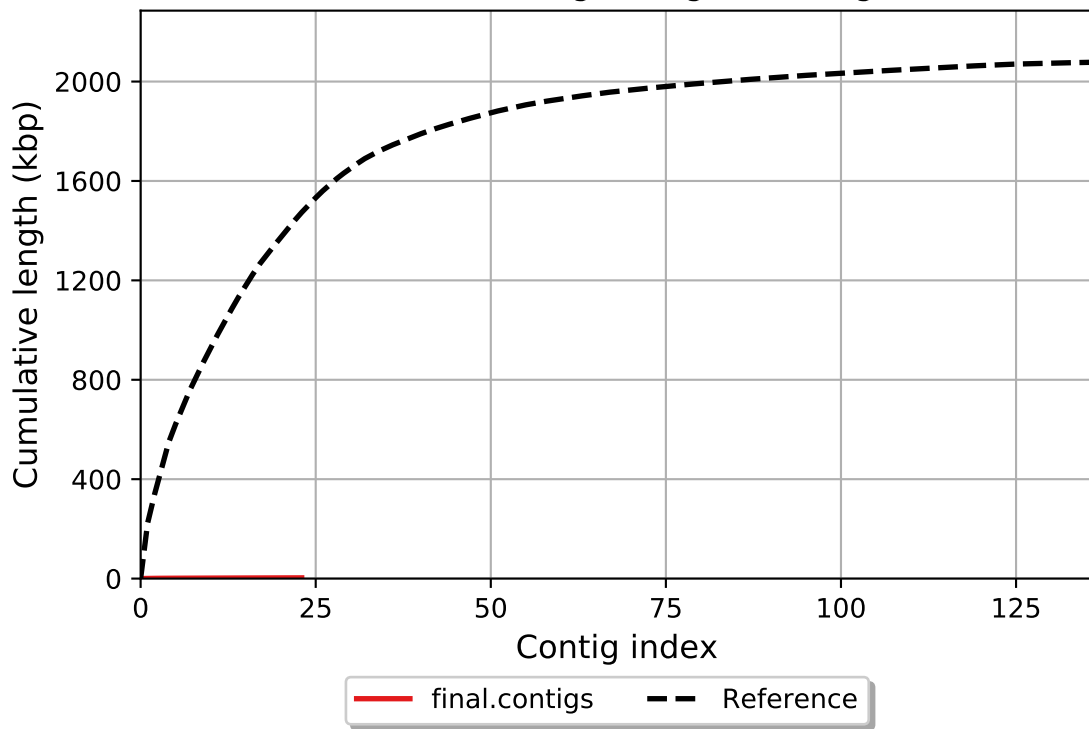
## Misassemblies



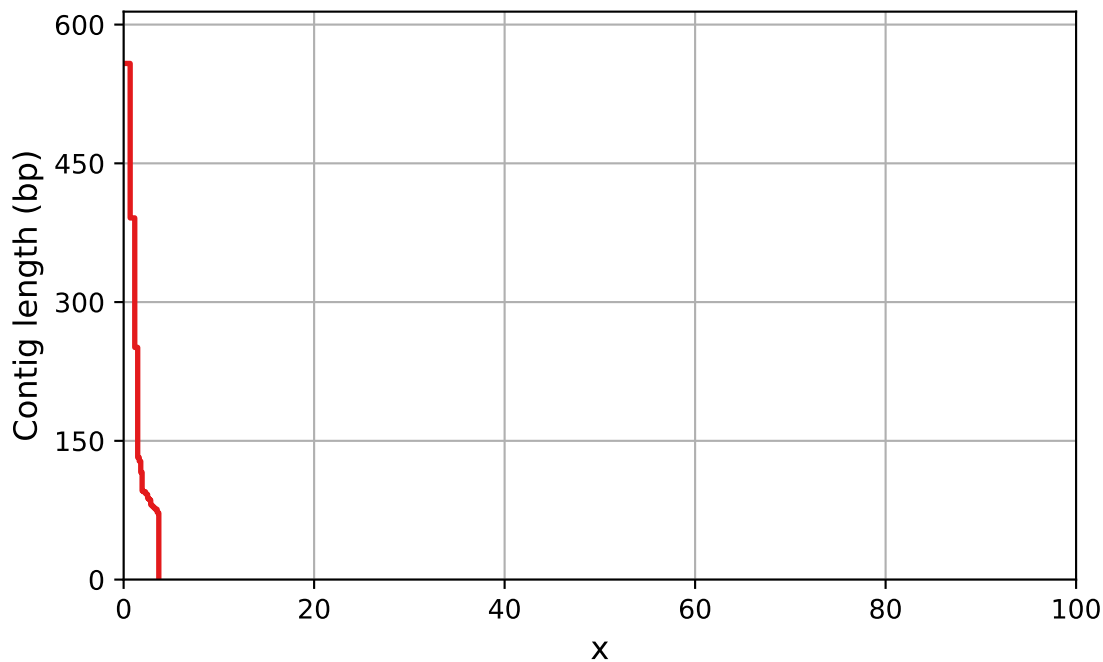
FRCurve (misassemblies)



Cumulative length (aligned contigs)

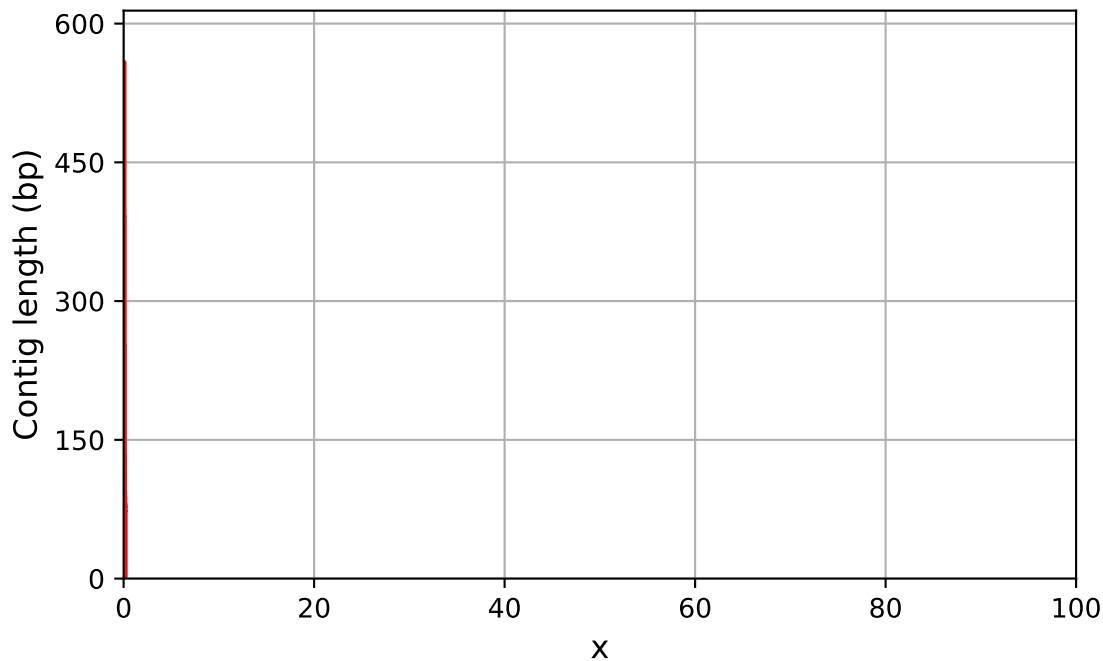


NAx



— final.contigs

# NGAx



— final.contigs