

## Report

	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	48793
Total length (>= 5000 bp)	39648
Total length (>= 10000 bp)	39648
Total length (>= 25000 bp)	39648
Total length (>= 50000 bp)	0
# contigs	10
Largest contig	39648
Total length	51165
Reference length	2789967
GC (%)	49.12
Reference GC (%)	60.77
N50	39648
N75	39648
L50	1
L75	1
# 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	0
# unaligned contigs	1 + 7 part
Unaligned length	49450
Genome fraction (%)	0.016
Duplication ratio	3.745
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4803.49
# indels per 100 kbp	0.00
Largest alignment	121
Total aligned length	760
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	6
# possible misassemblies	7
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	22
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

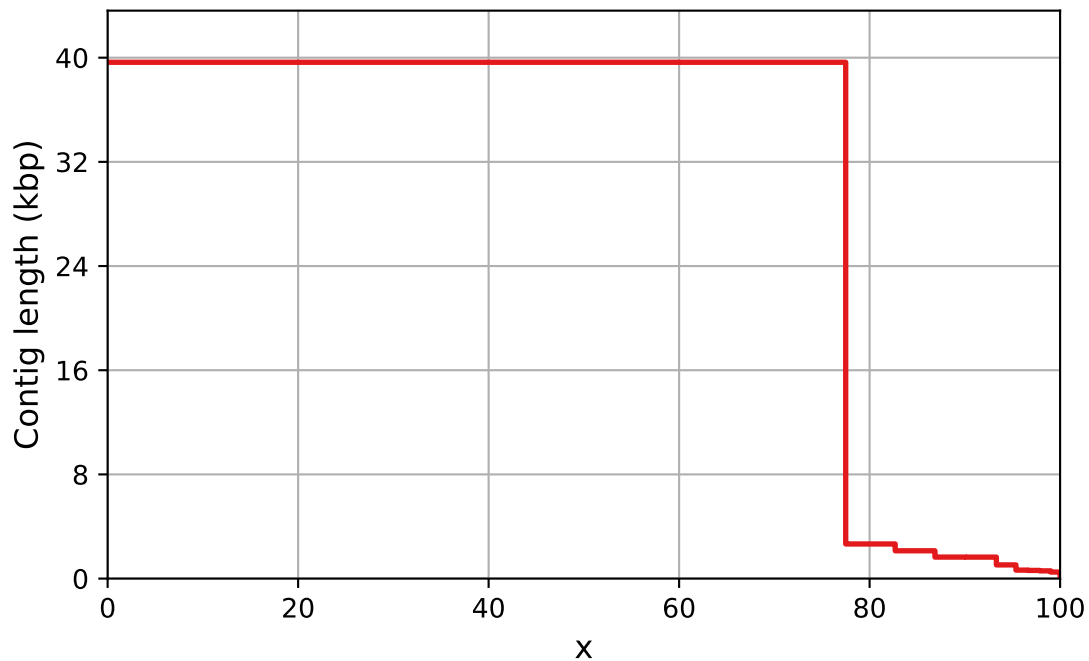
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	2659
# partially unaligned contigs	7
Partially unaligned length	46791
# N's	0

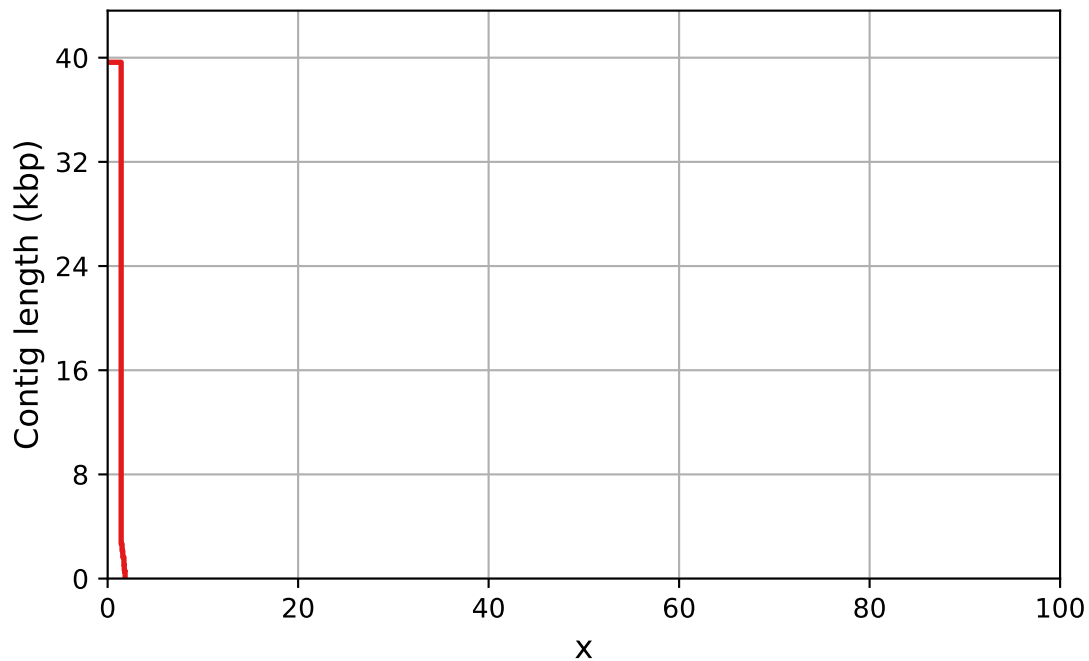
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

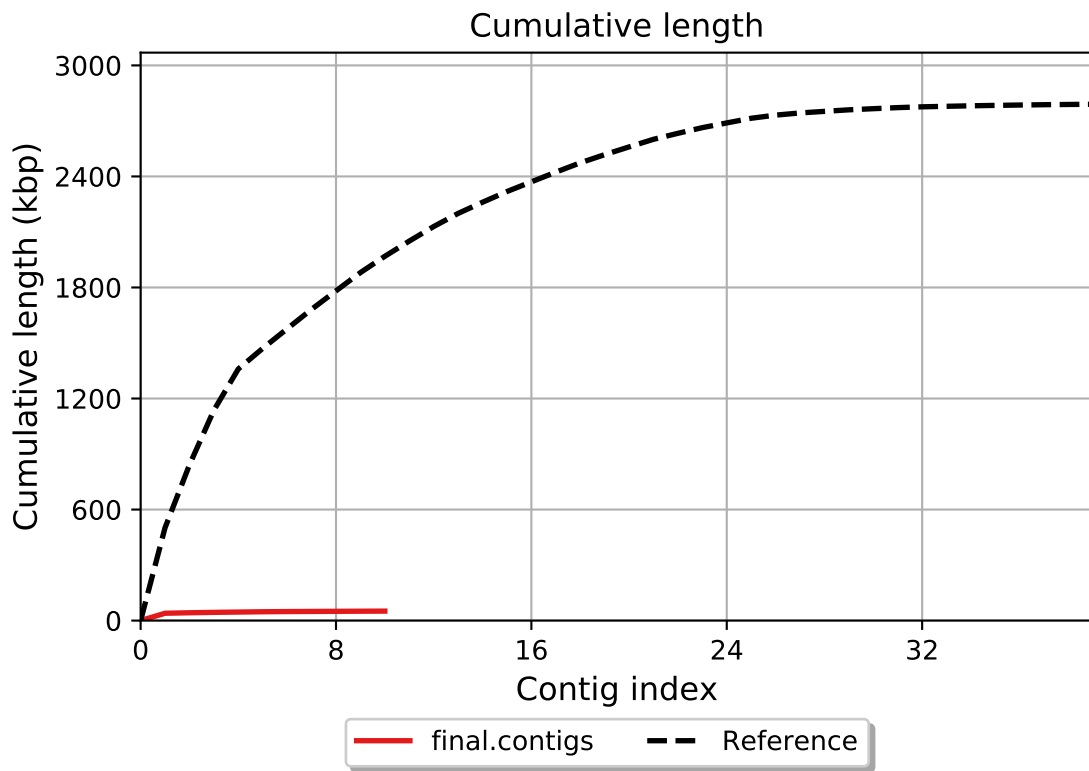


— final.contigs

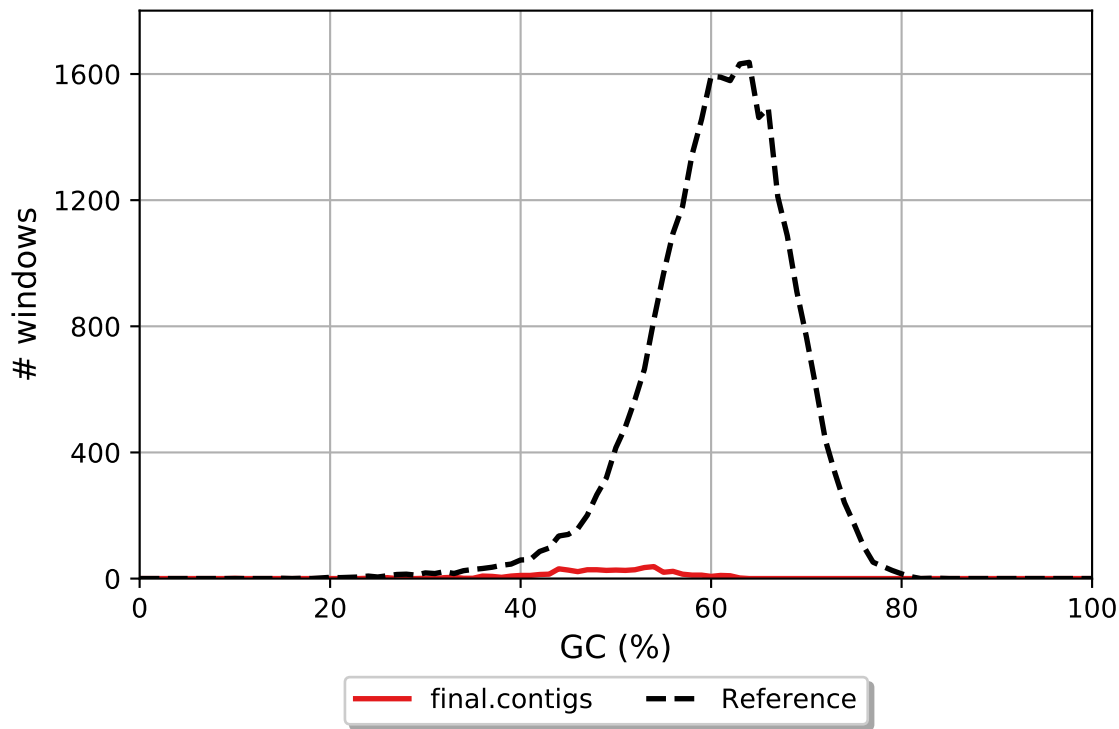
NGx



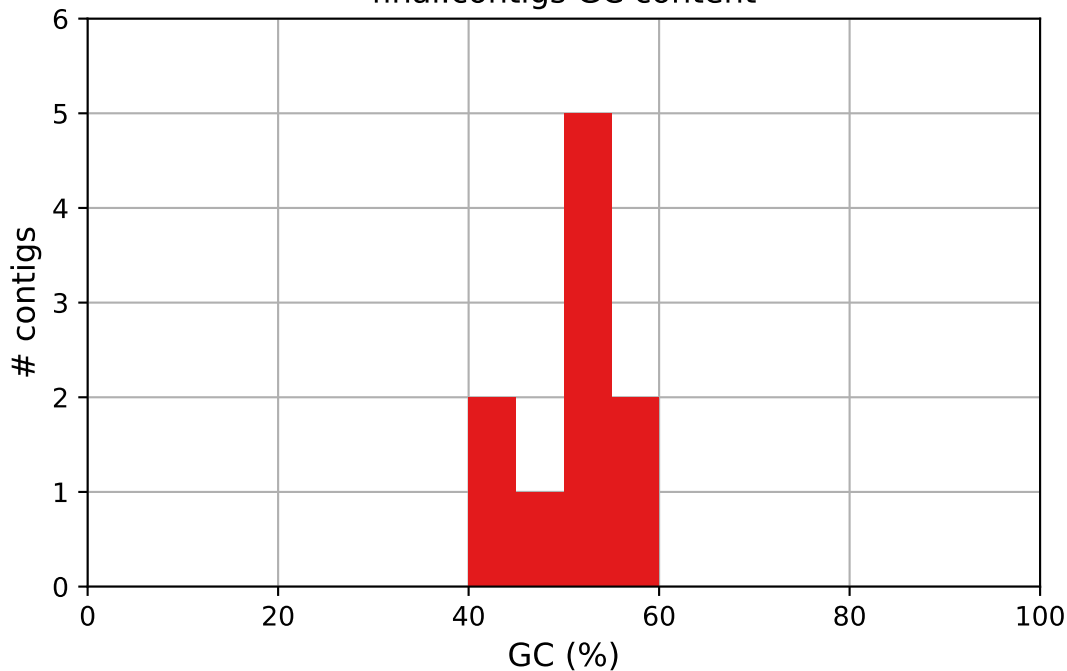
— final.contigs



## GC content



final.contigs GC content



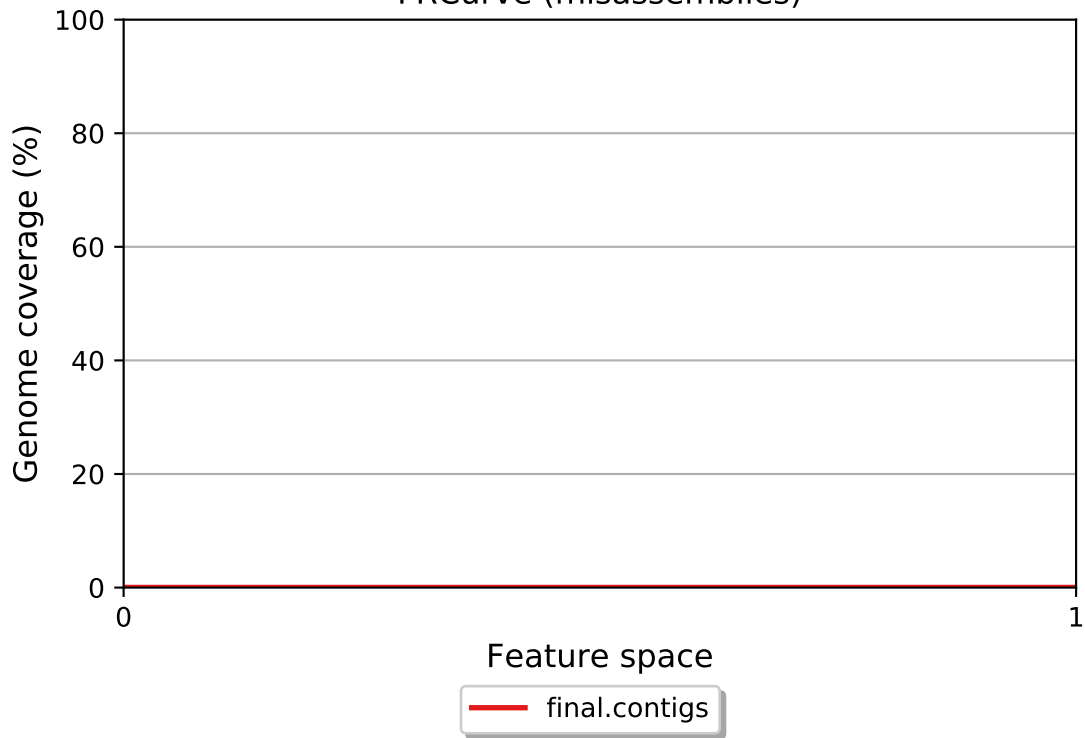
final.contigs



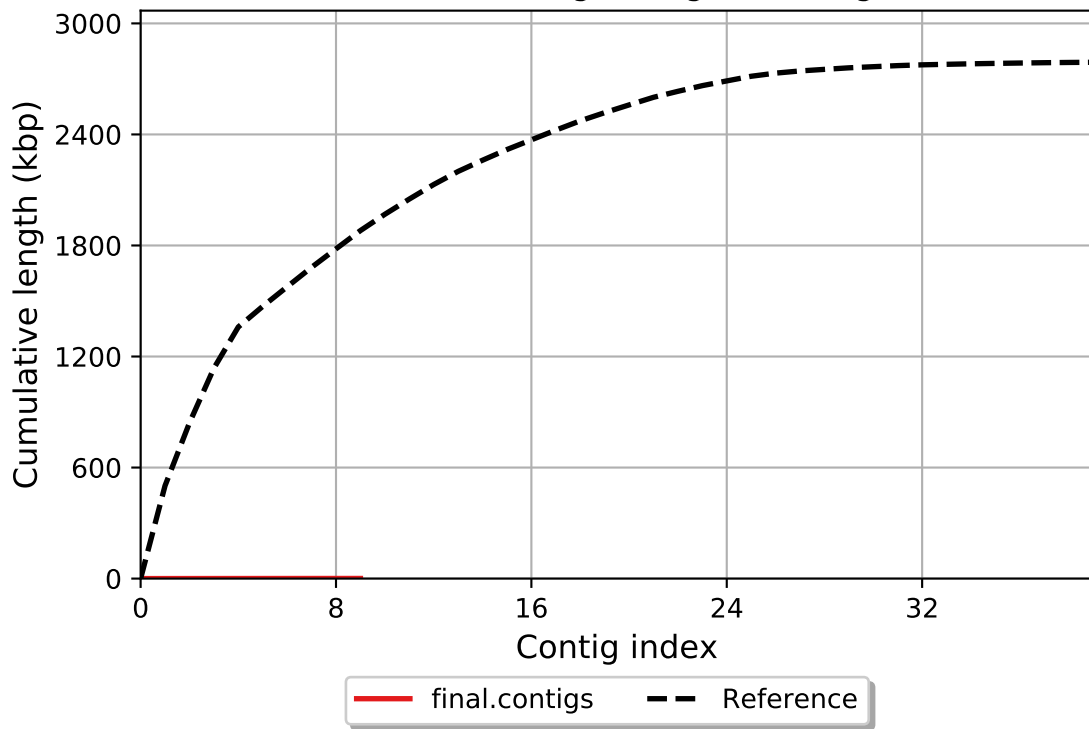
## Misassemblies



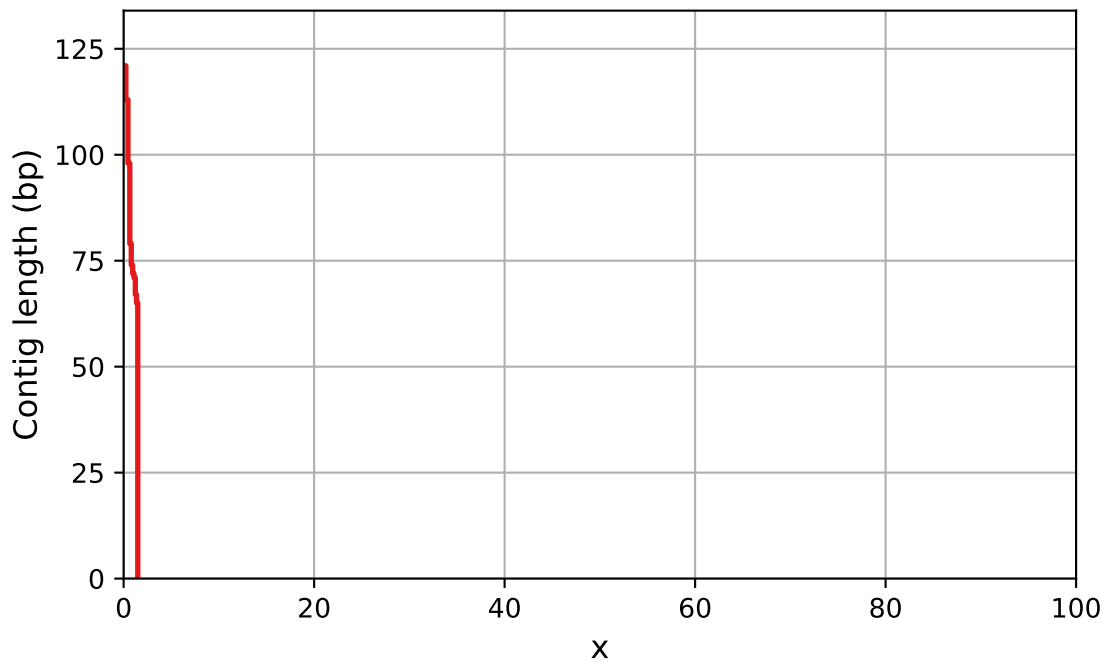
FRCurve (misassemblies)



Cumulative length (aligned contigs)

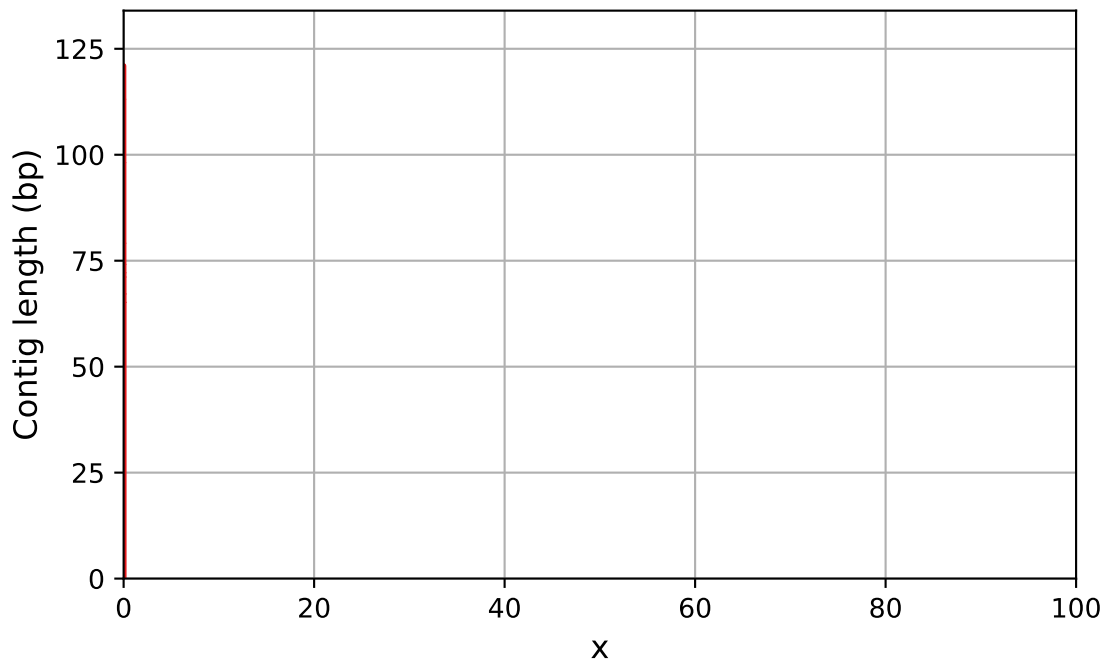


NAx



— final.contigs

# NGAx



— final.contigs