

## Report

	final.contigs
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	76593
Total length (>= 5000 bp)	68596
Total length (>= 10000 bp)	55180
Total length (>= 25000 bp)	36014
Total length (>= 50000 bp)	0
# contigs	16
Largest contig	36014
Total length	81343
Reference length	5695417
GC (%)	51.49
Reference GC (%)	72.40
N50	19166
N75	7571
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	0
# unaligned contigs	6 + 9 part
Unaligned length	79954
Genome fraction (%)	0.009
Duplication ratio	2.718
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5479.45
# indels per 100 kbp	0.00
Largest alignment	105
Total aligned length	869
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	9
# possible misassemblies	11
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	28
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

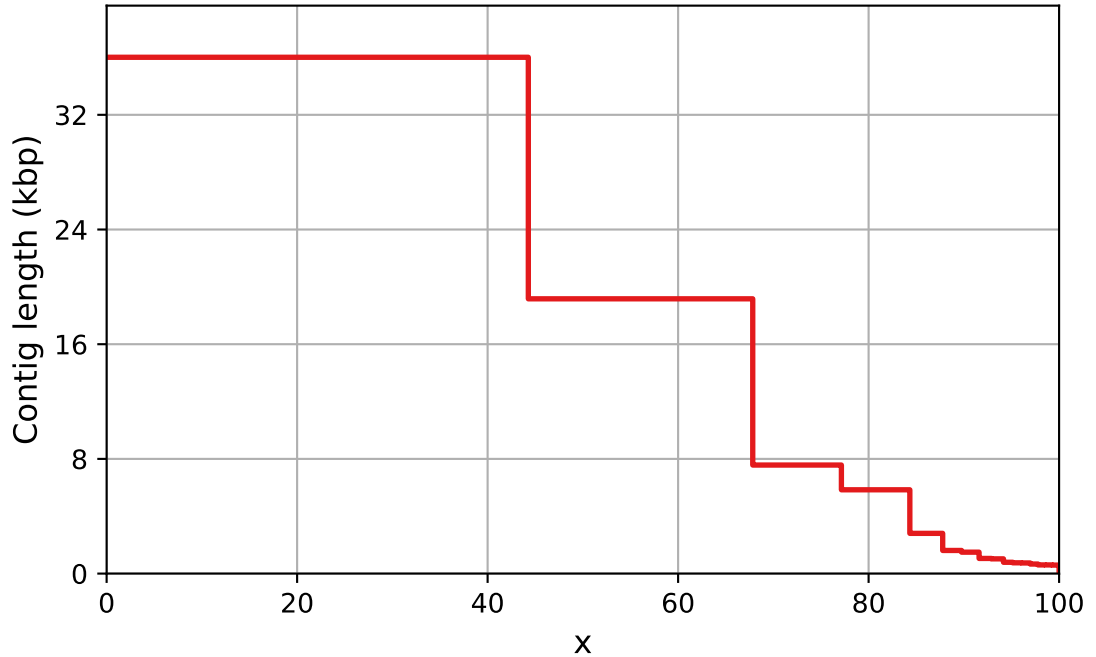
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	6
Fully unaligned length	52436
# partially unaligned contigs	9
Partially unaligned length	27518
# N's	0

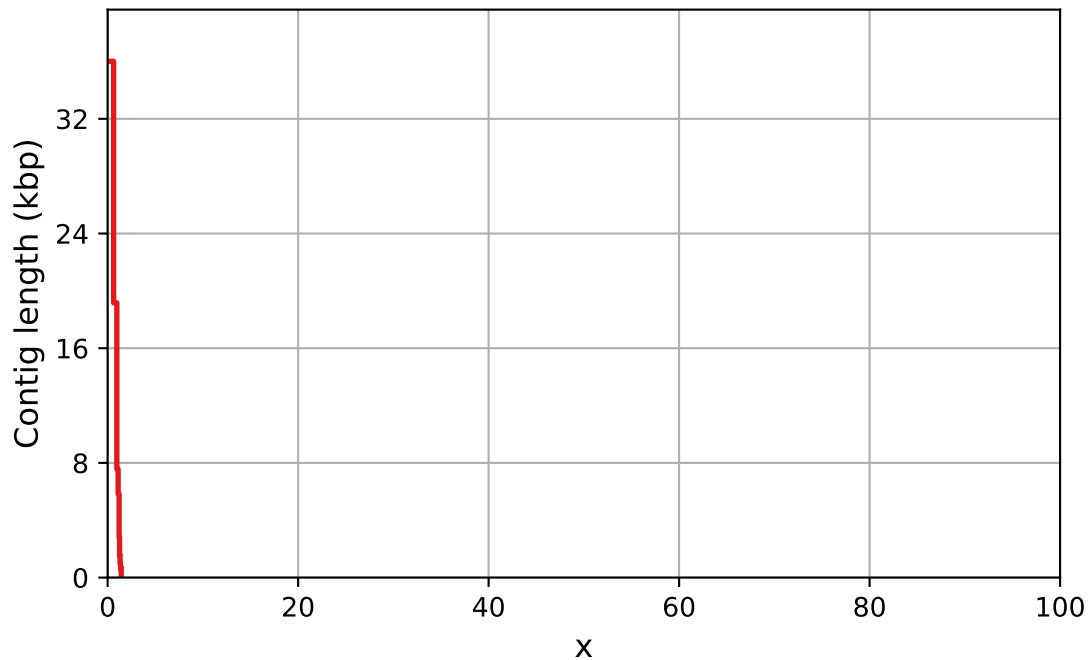
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

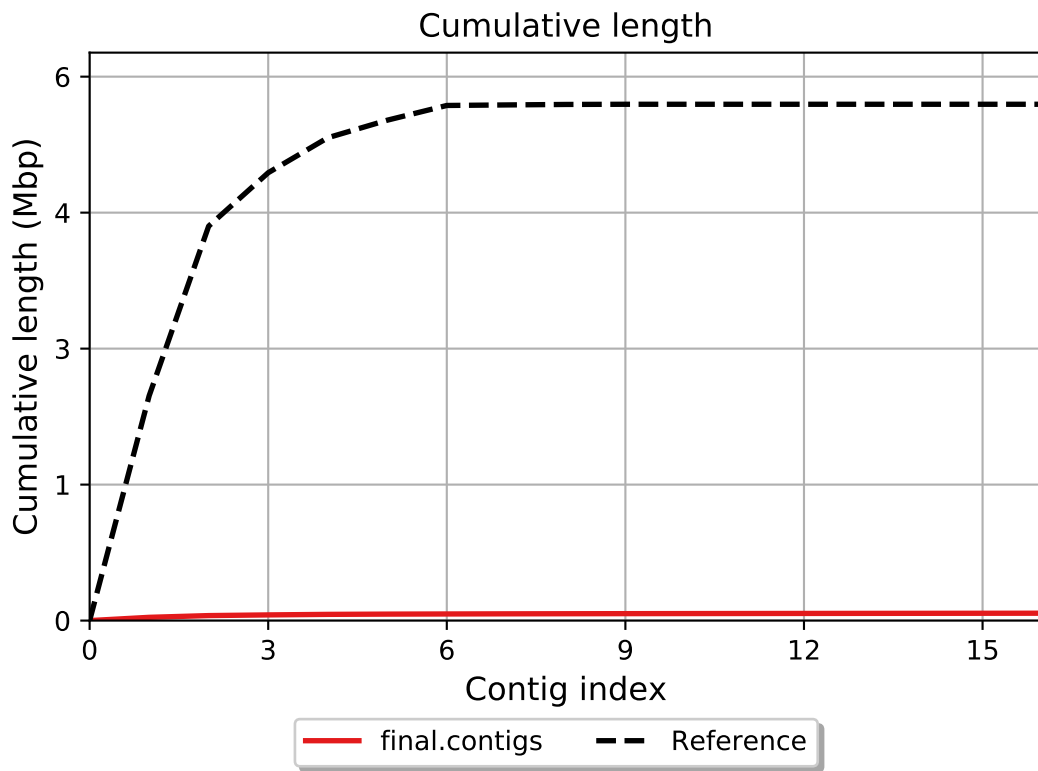


— final.contigs

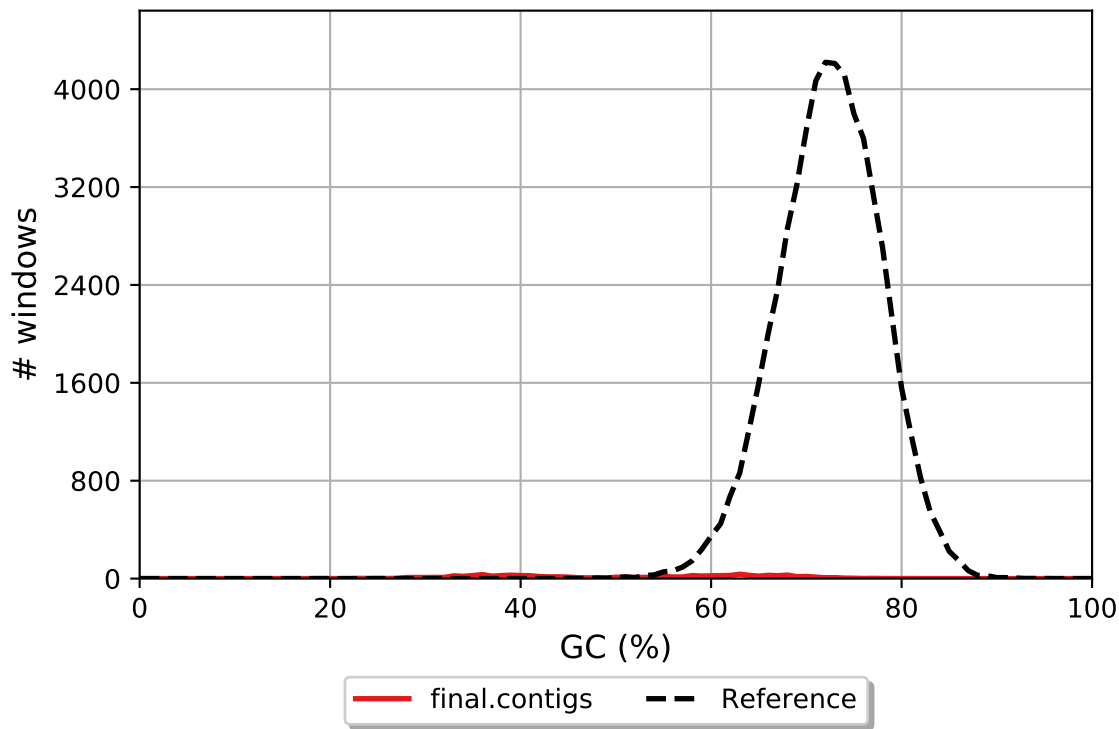
NGx



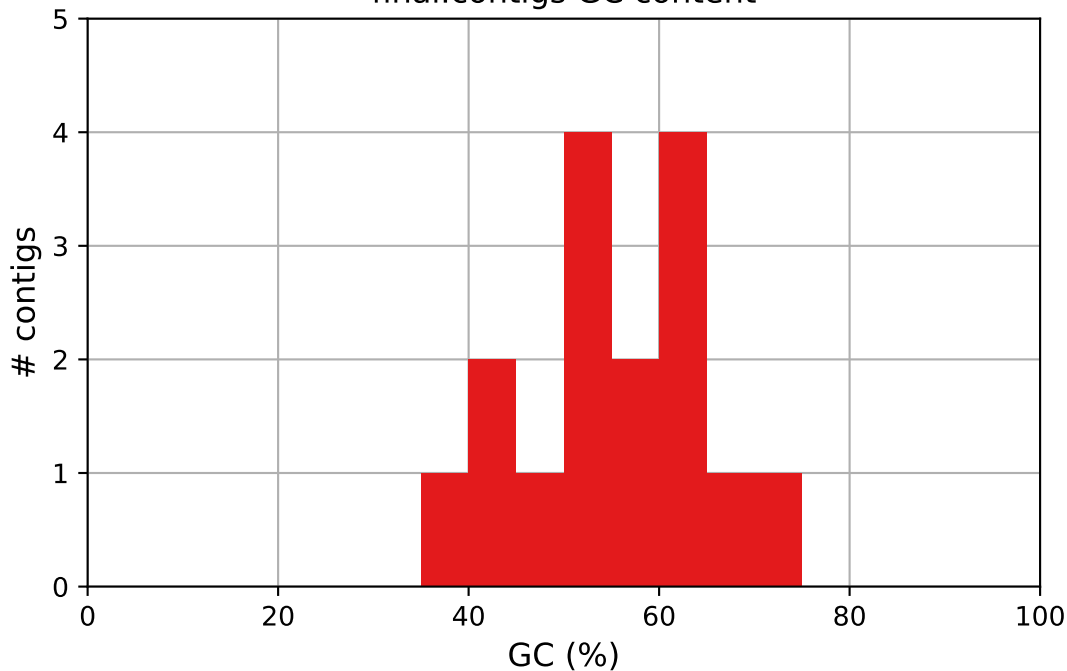
— final.contigs



## GC content



final.contigs GC content



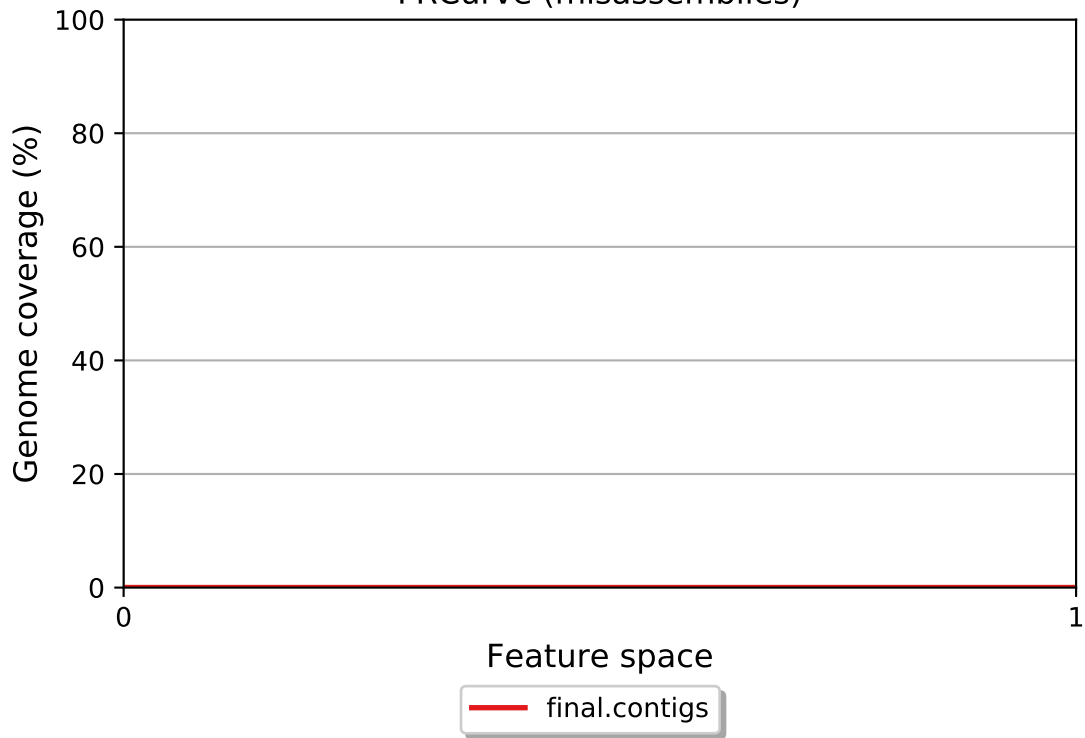
final.contigs



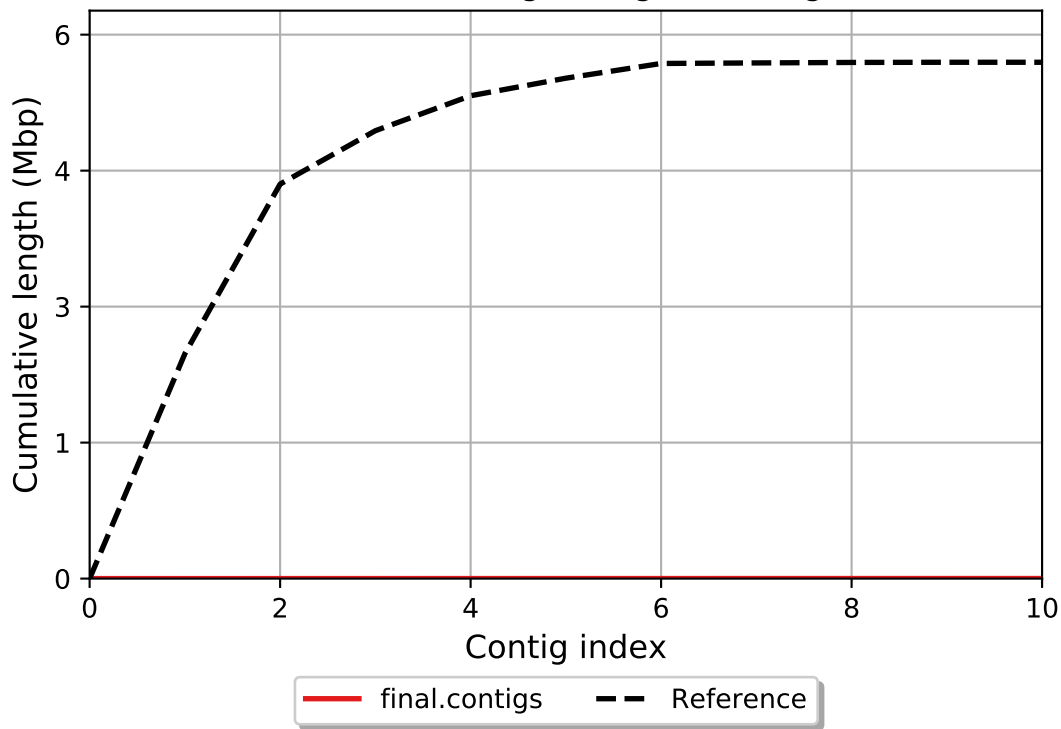
## Misassemblies



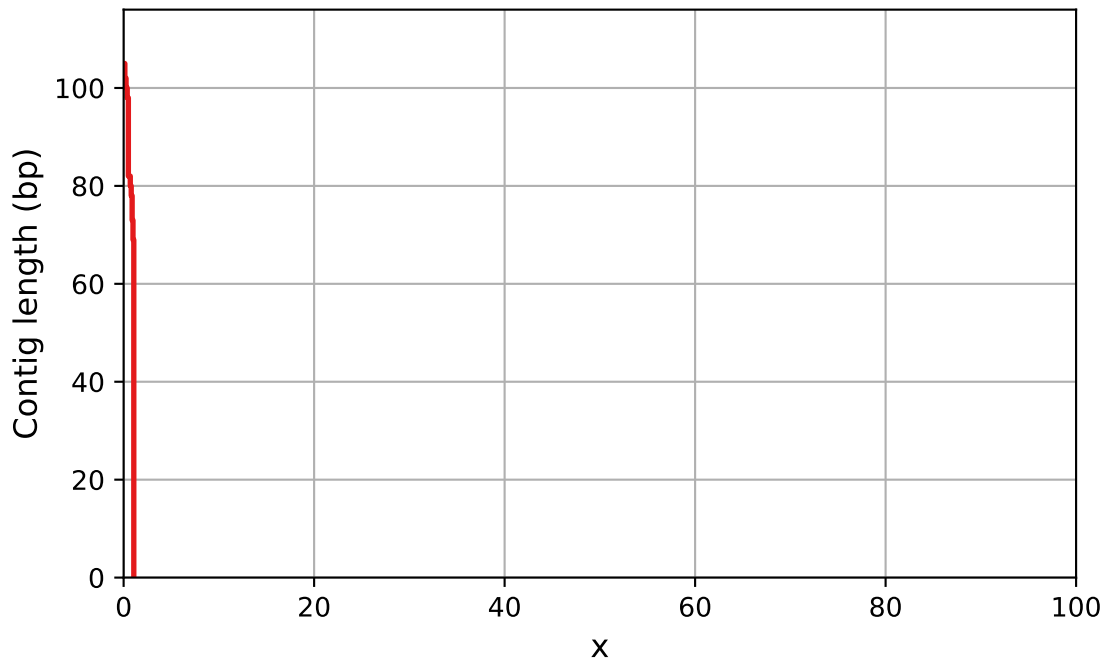
FRCurve (misassemblies)



Cumulative length (aligned contigs)

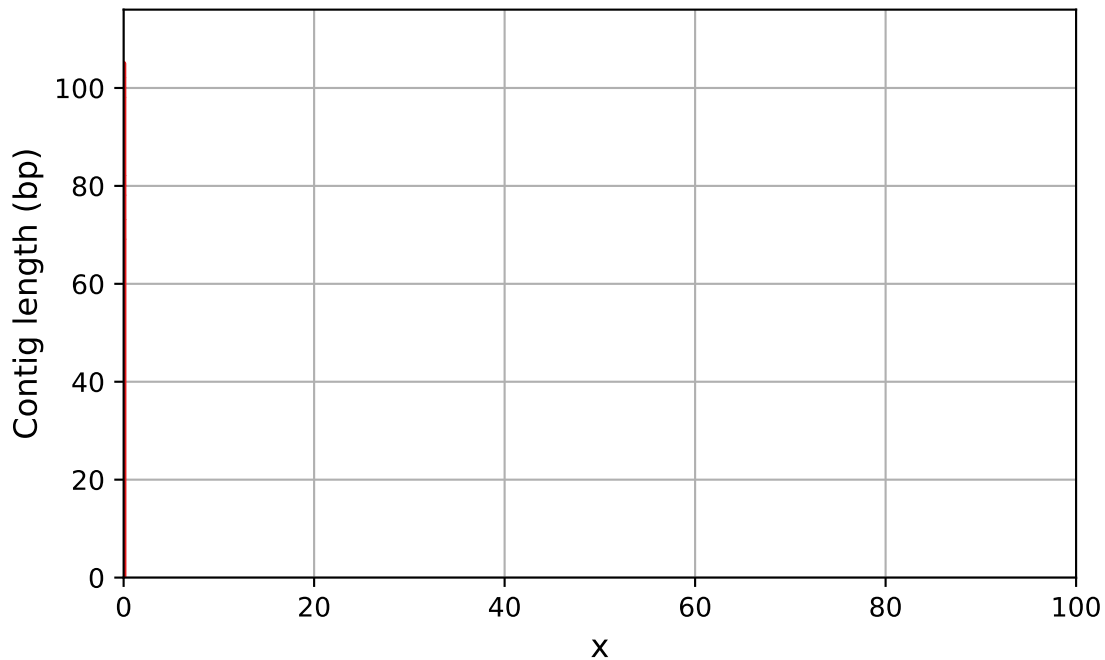


NAx



— final.contigs

# NGAx



— final.contigs