

## Report

	contigs
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	30000
Total length (>= 1000 bp)	30000
Total length (>= 5000 bp)	30000
Total length (>= 10000 bp)	30000
Total length (>= 25000 bp)	30000
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	30000
Total length	30000
Reference length	3315175
GC (%)	55.57
Reference GC (%)	57.25
N50	30000
N75	30000
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	0 + 0 part
Unaligned length	0
Genome fraction (%)	0.905
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.33
# indels per 100 kbp	0.00
Largest alignment	30000
Total aligned length	30000
NA50	30000
NGA50	-
NA75	30000
LA50	1
LA75	1

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

	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
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

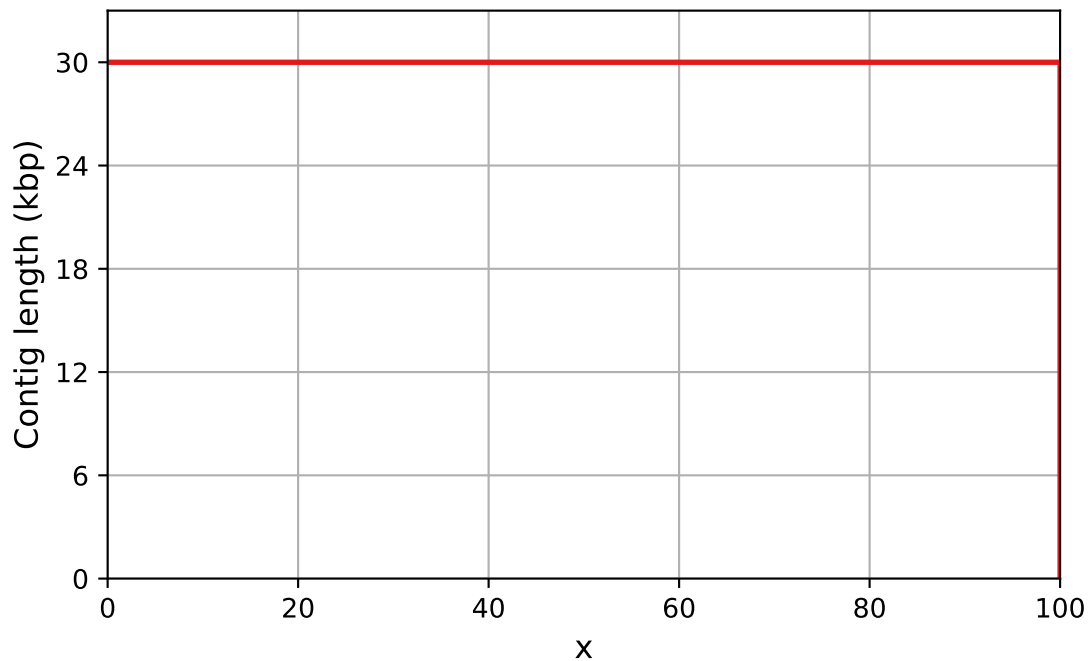
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

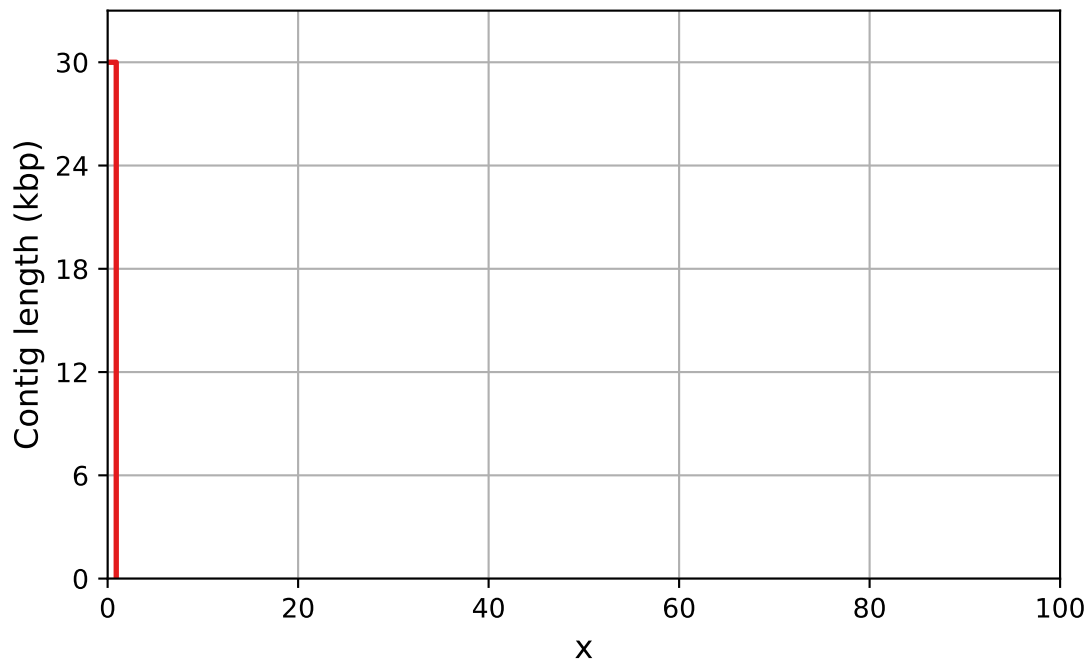
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

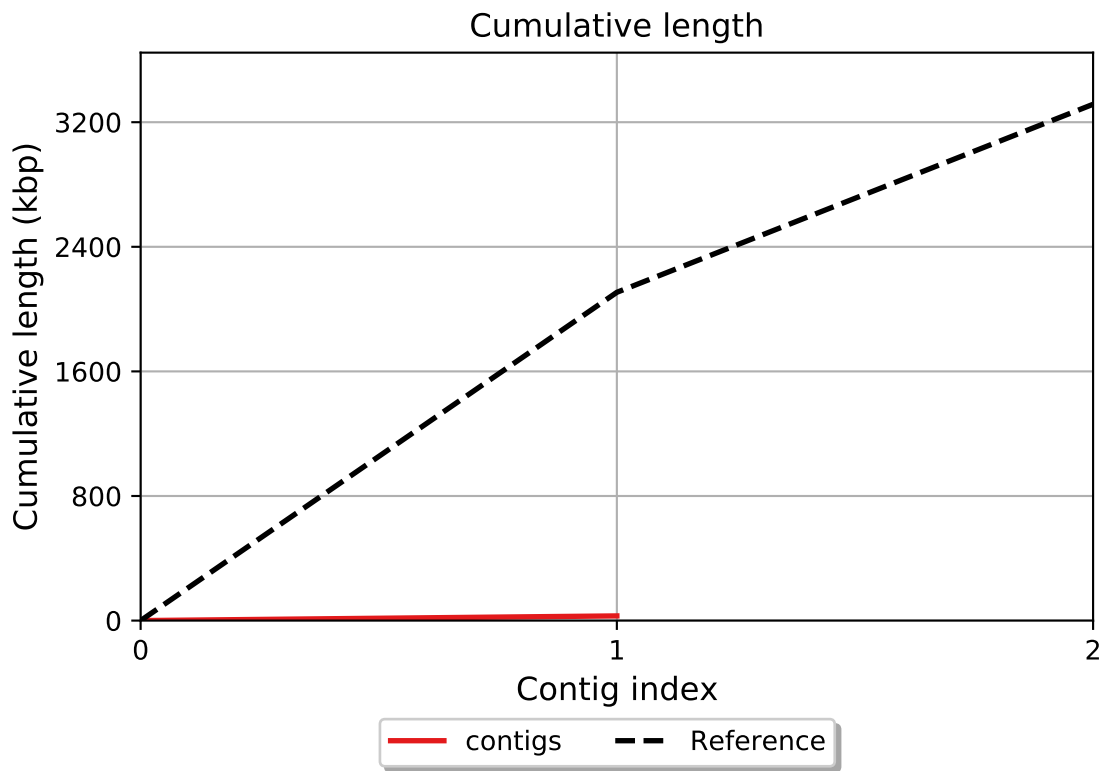


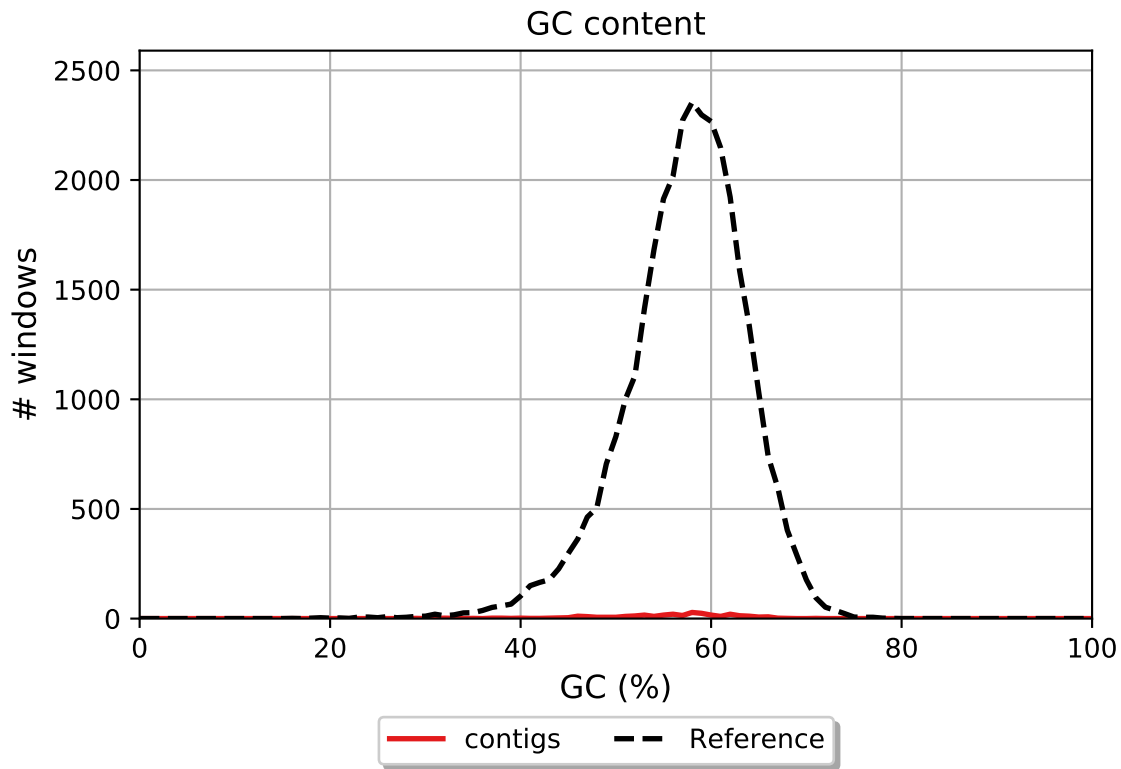
— contigs

NGx

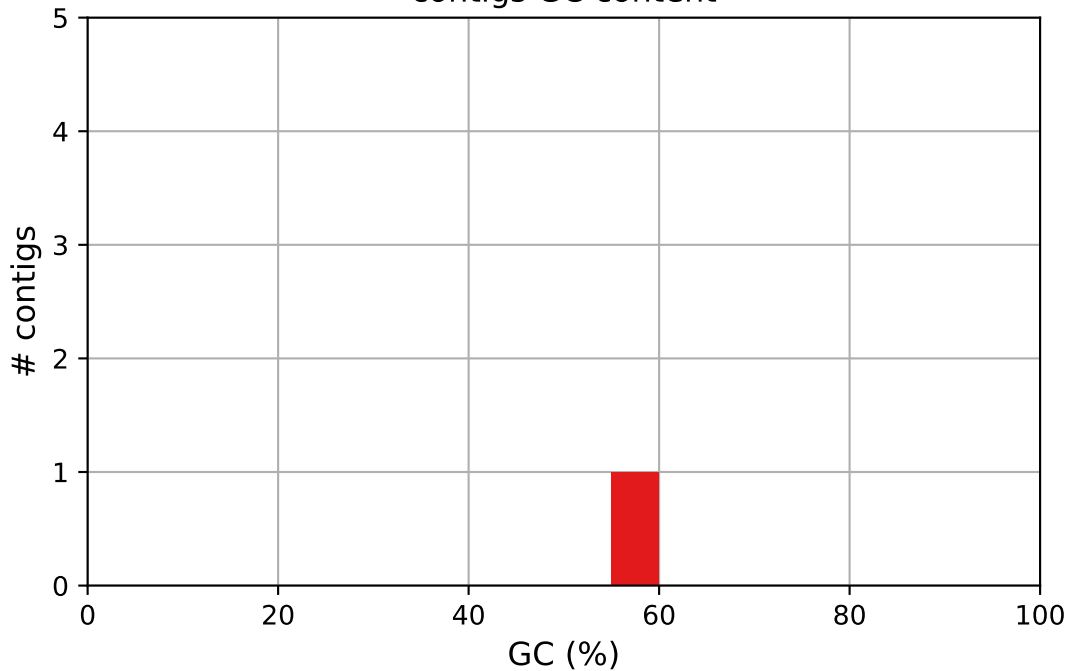


— contigs





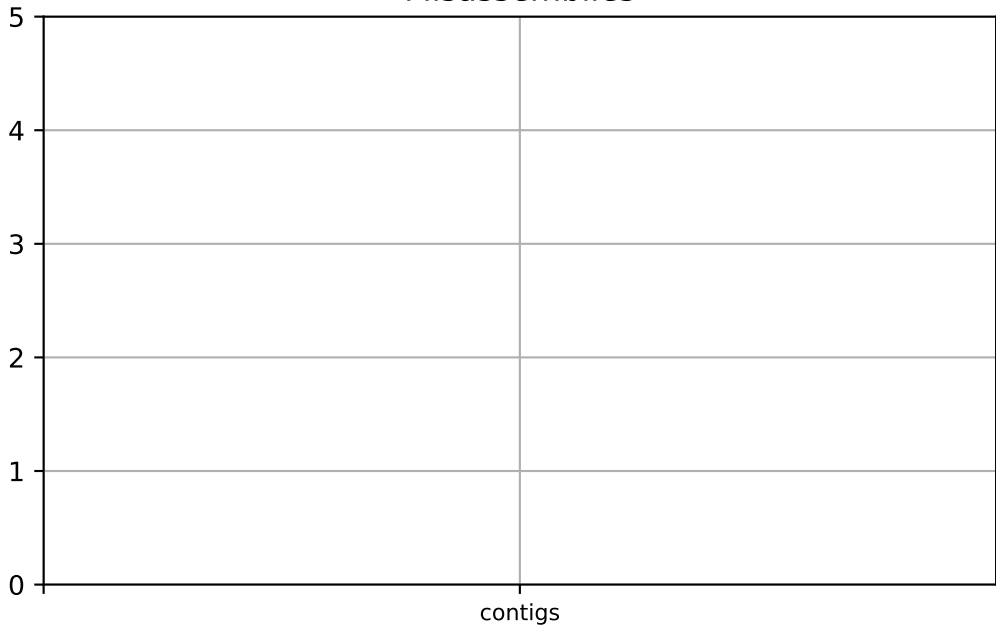
contigs GC content



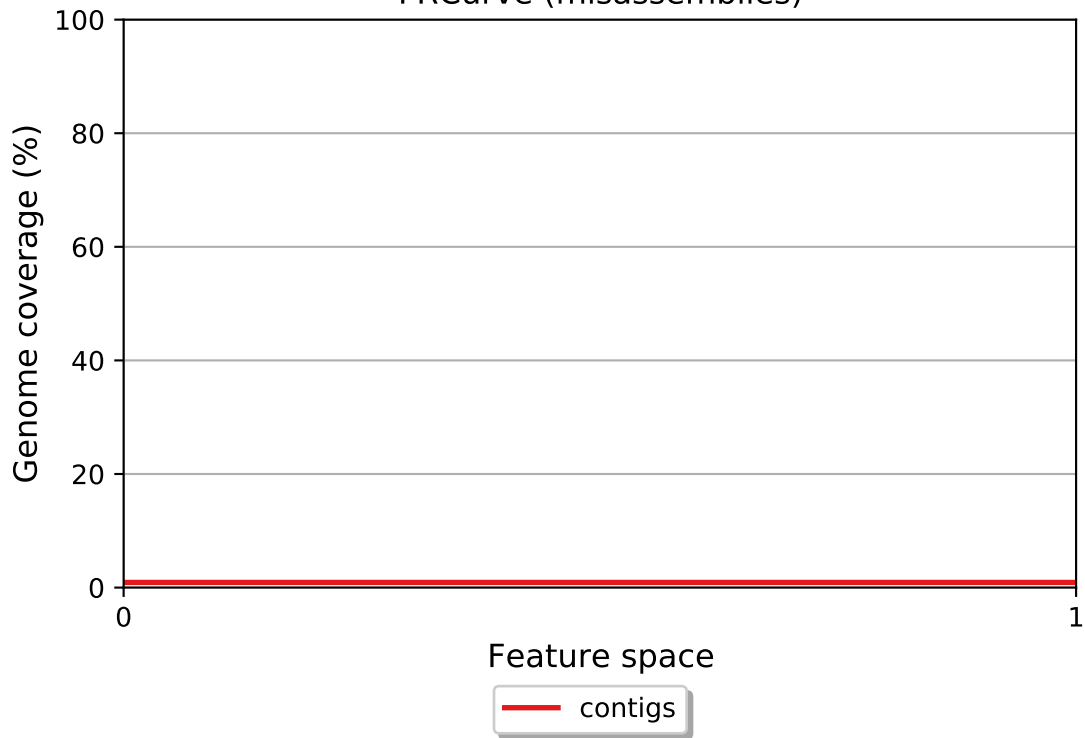
contigs



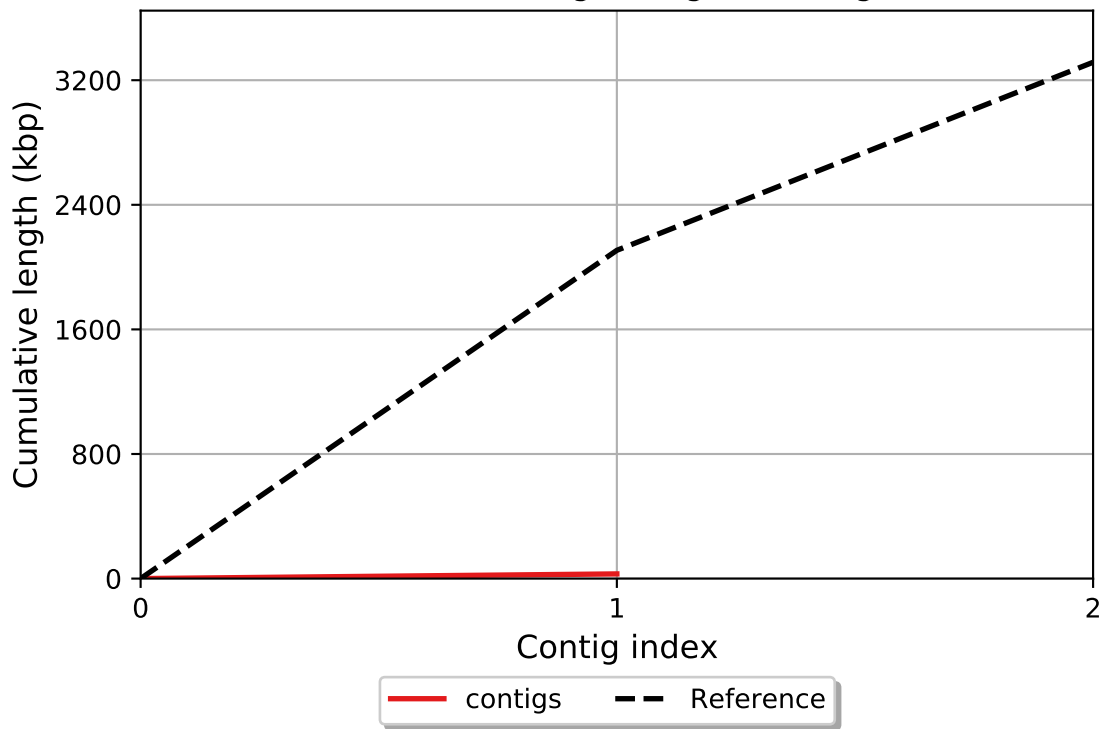
# Misassemblies



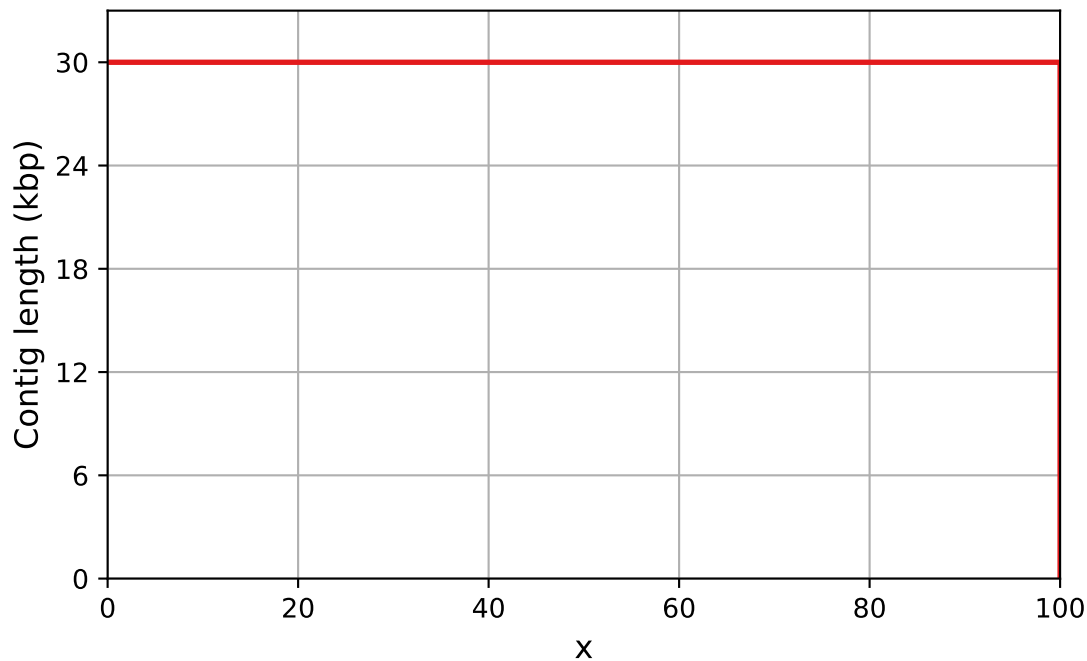
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— contigs

# NGAx

