

Report

	contigs
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	25447
Total length (>= 5000 bp)	25447
Total length (>= 10000 bp)	25447
Total length (>= 25000 bp)	25447
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	25447
Total length	25447
Reference length	4171062
GC (%)	47.22
Reference GC (%)	0.00
N50	25447
NG50	-
N90	25447
NG90	-
auN	25447.0
auNG	155.2
L50	1
LG50	-
L90	1
LG90	-
# 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 + 1 part
Unaligned length	25330
Genome fraction (%)	0.003
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5128.21
# indels per 100 kbp	0.00
Largest alignment	117
Total aligned length	117
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	0.5
auNGA	0.0
LA50	-
LGA50	-
LA90	-
LGA90	-

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
# possibly misassembled contigs	1
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	6
# indels	0
# indels ( $\leq 5$ bp)	0
# indels ( $> 5$ bp)	0
Indels length	0

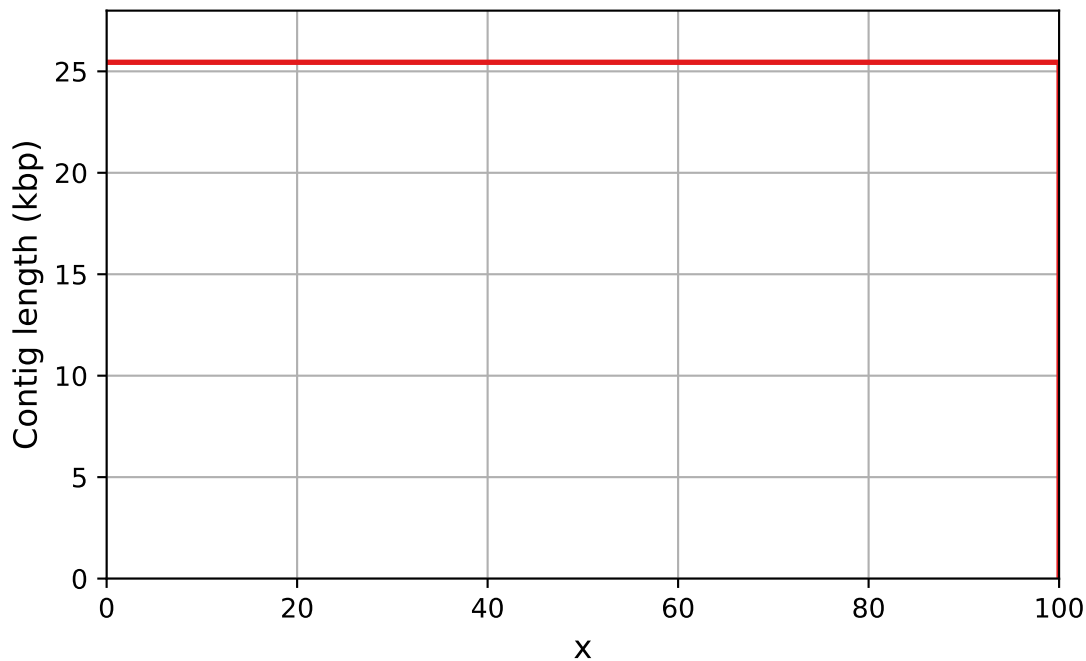
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	25330
# N's	0

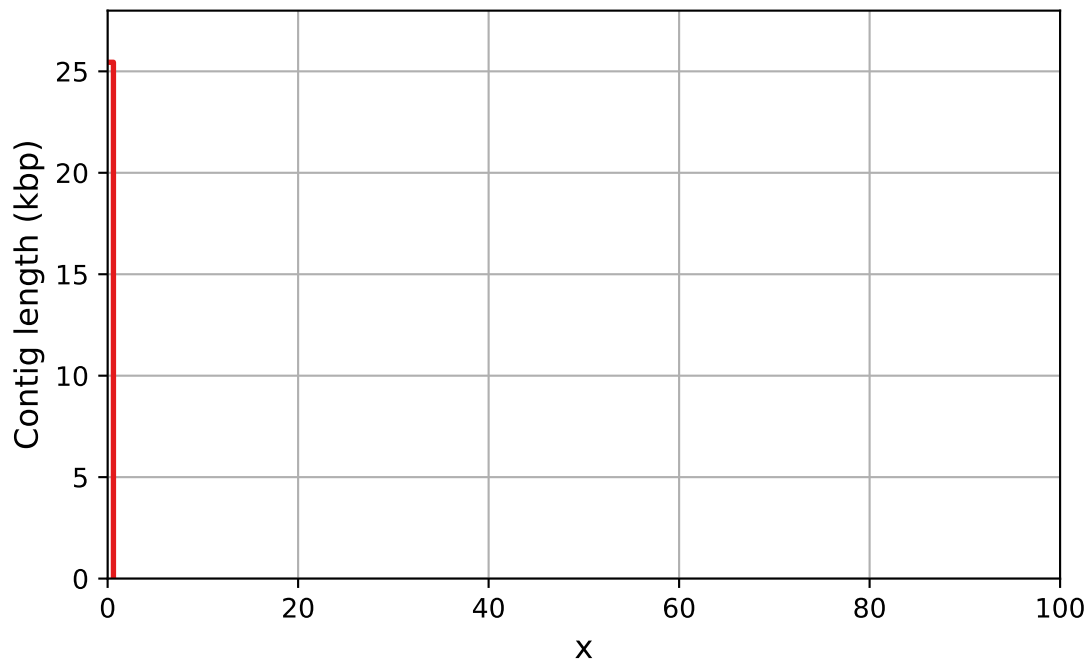
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



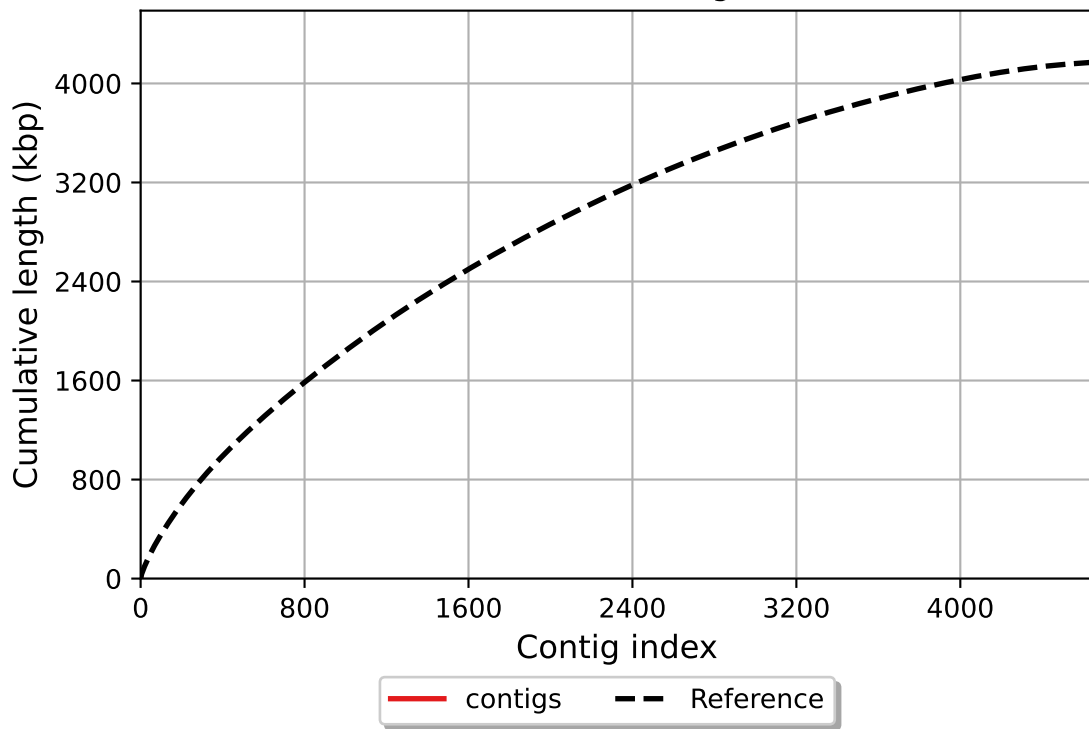
— contigs

NGx

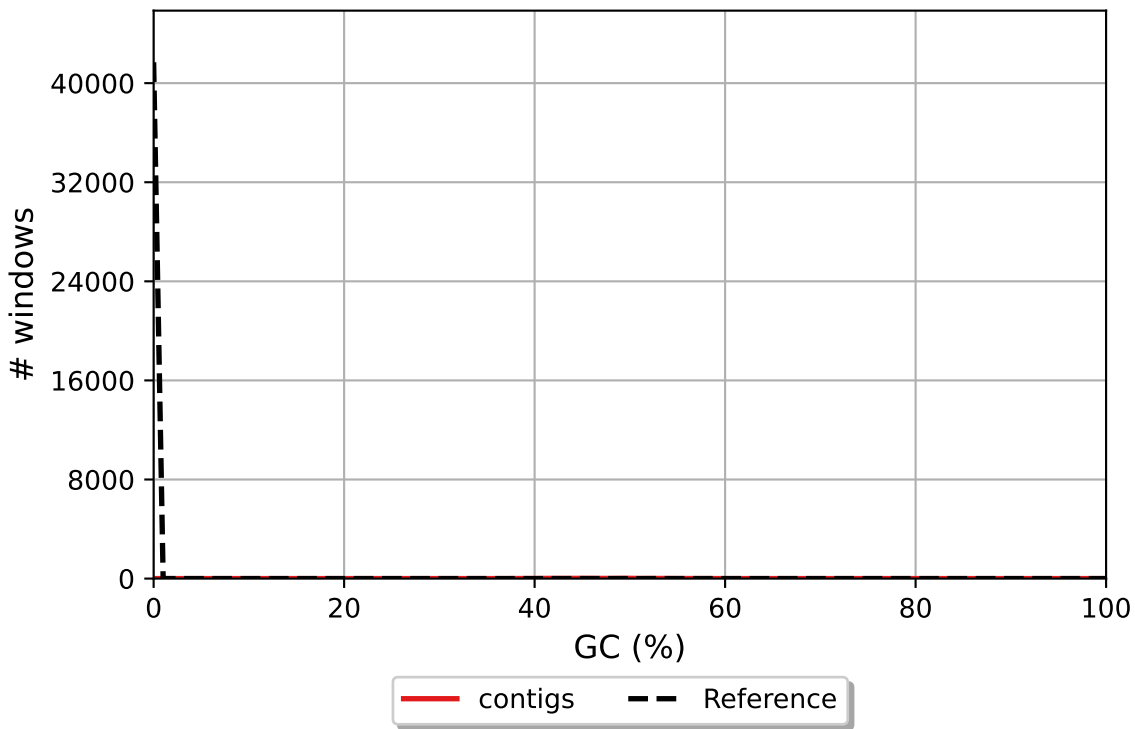


contigs

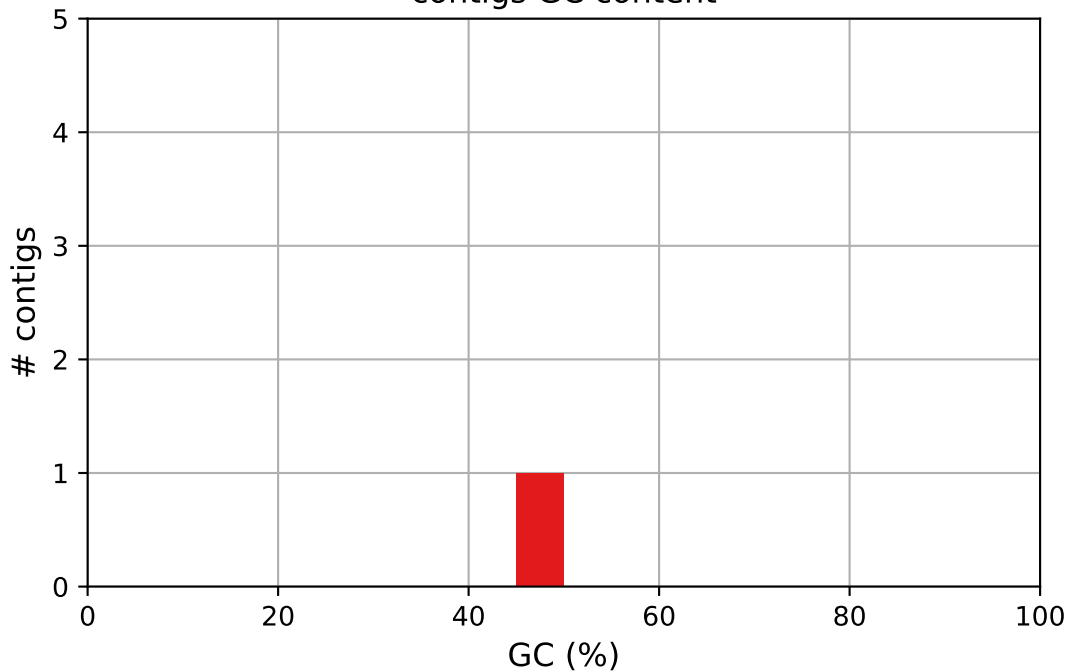
Cumulative length



# GC content



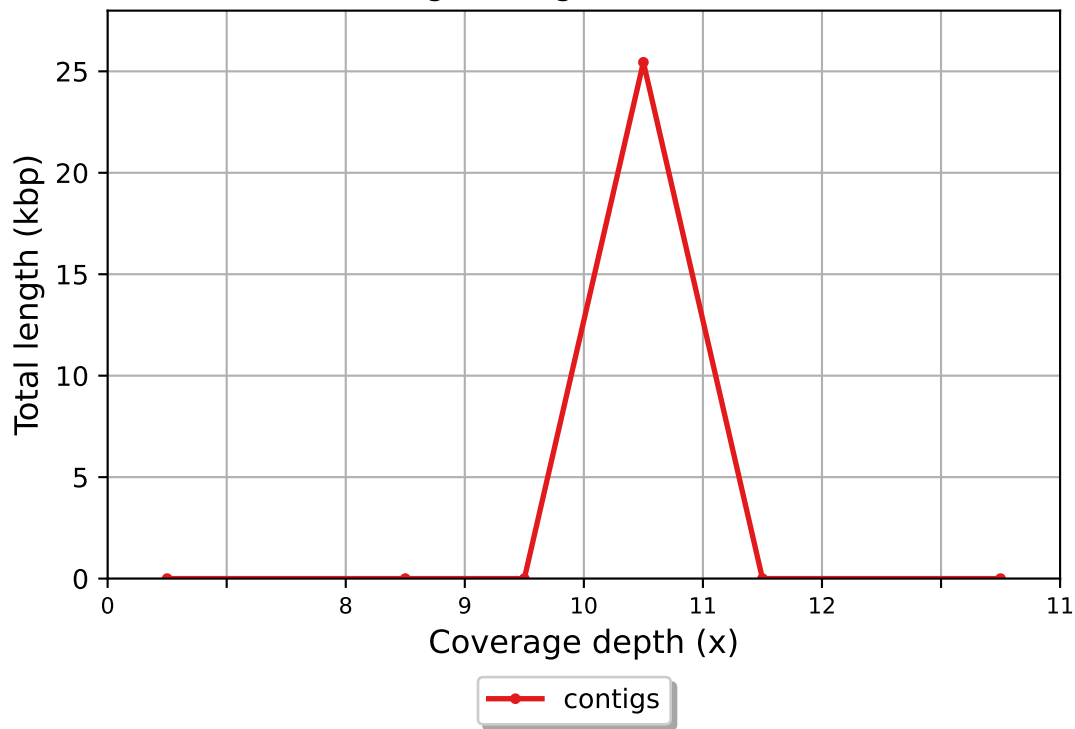
contigs GC content



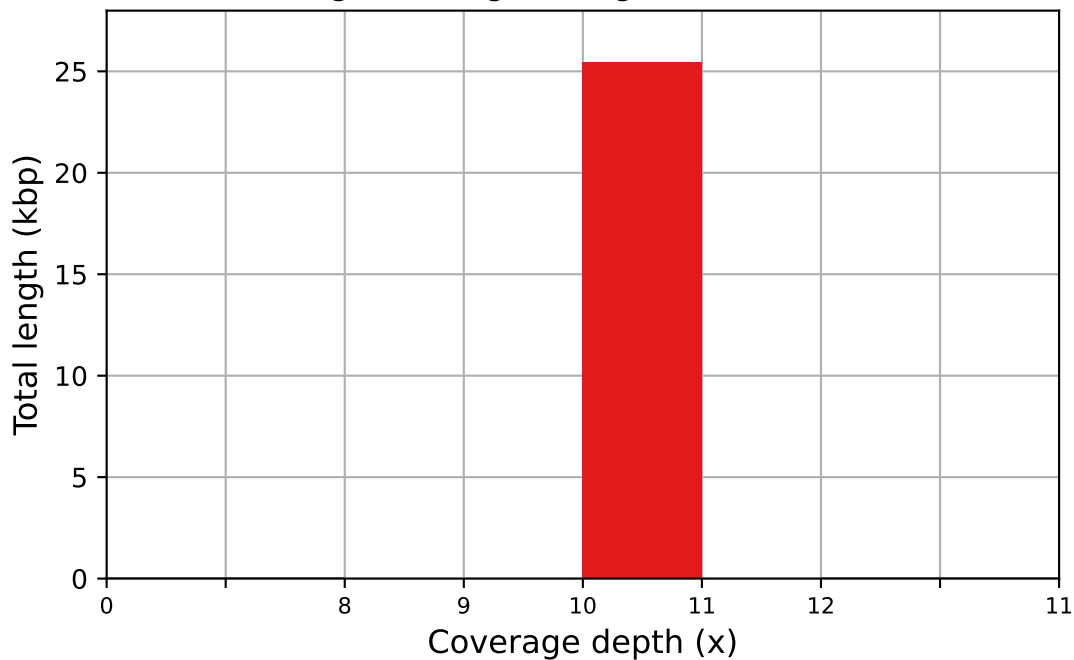
contigs



Coverage histogram (bin size: 1x)

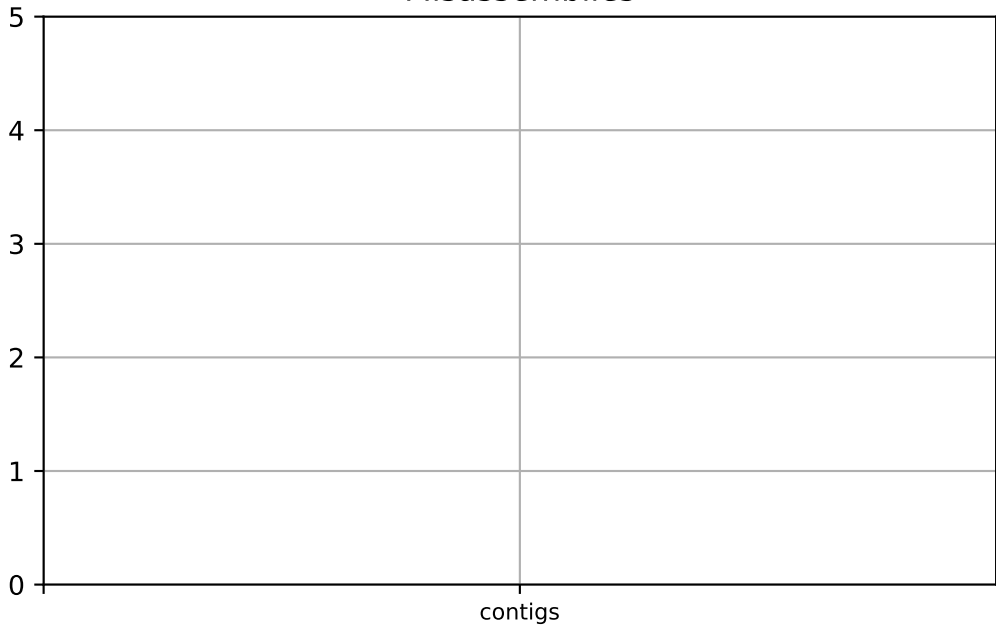


contigs coverage histogram (bin size: 1x)

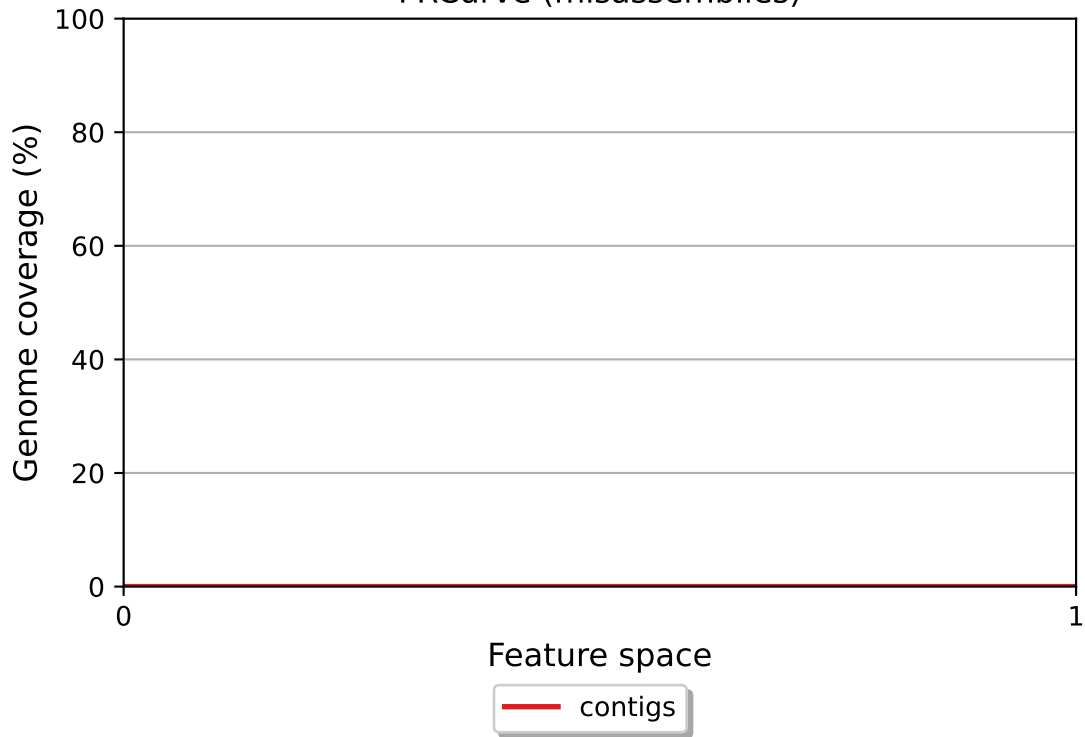


contigs

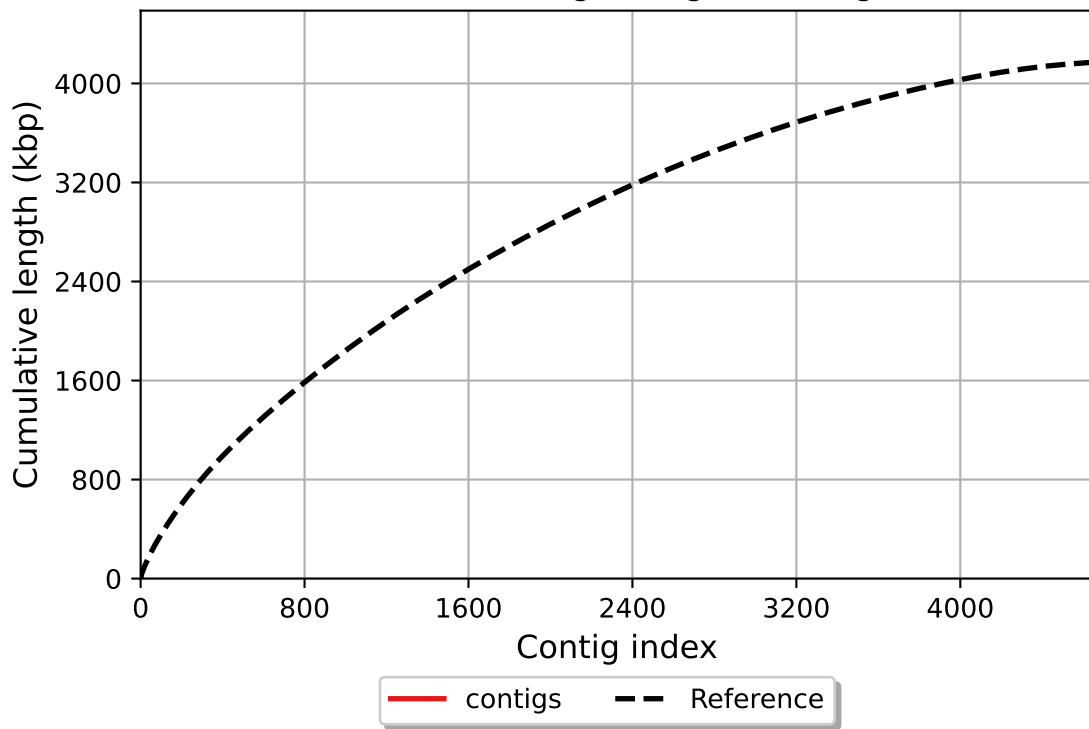
# Misassemblies



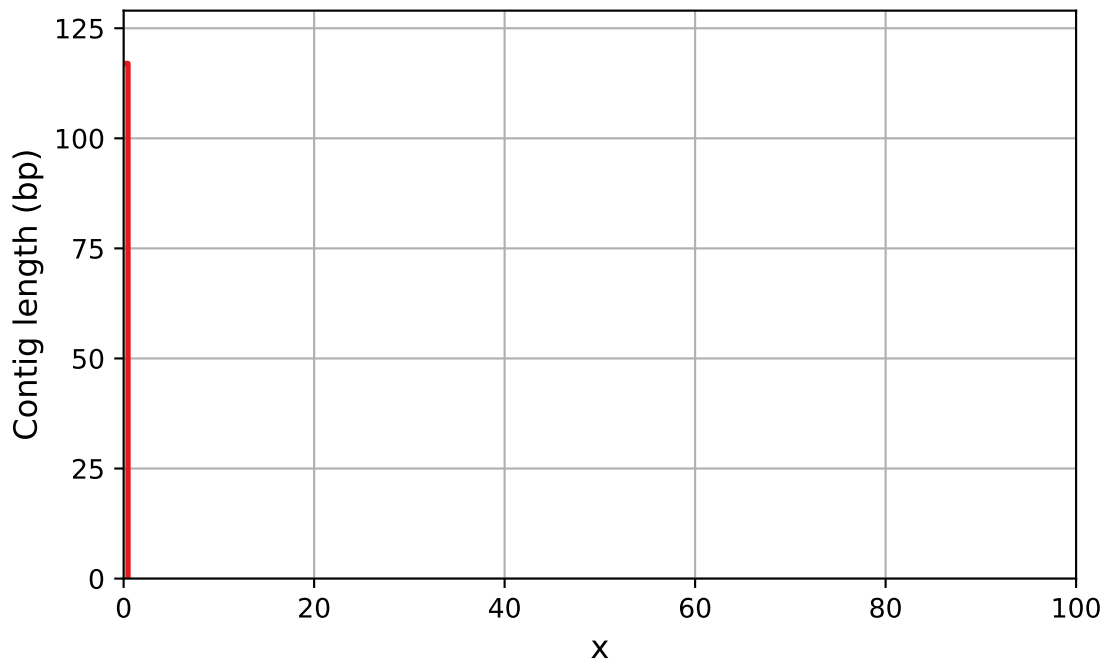
FRCurve (misassemblies)



Cumulative length (aligned contigs)

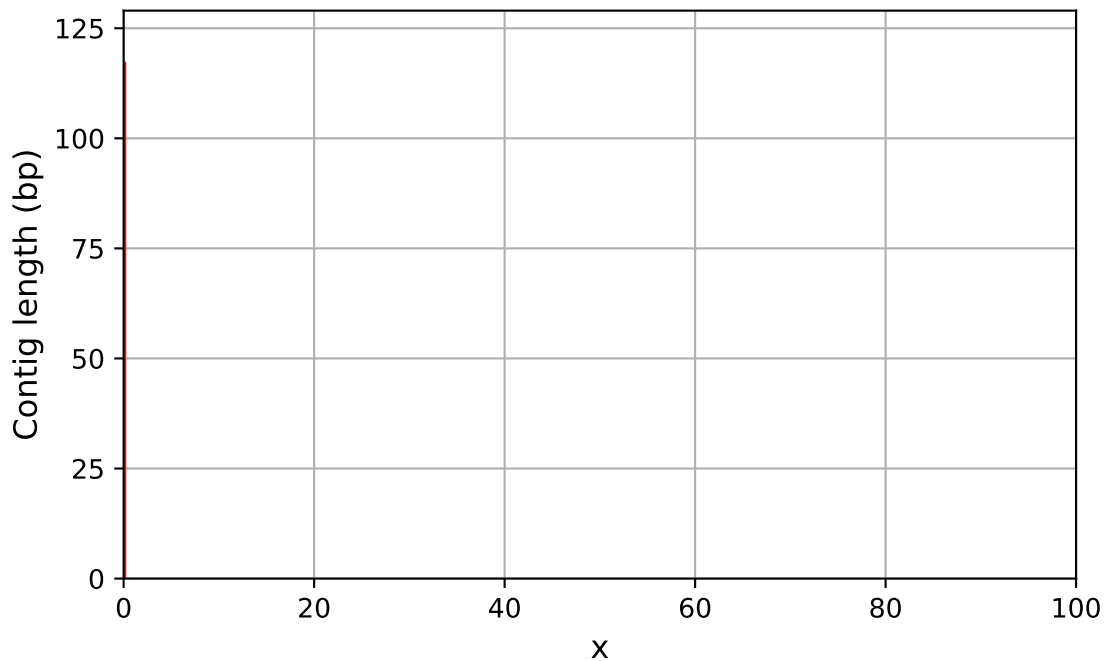


NAx



contigs

# NGAx



contigs