

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	3
Largest contig	25447
Total length	26910
Reference length	3040590
GC (%)	46.27
Reference GC (%)	0.00
N50	25447
NG50	-
N90	25447
NG90	-
auN	24103.3
auNG	213.3
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	25328
Genome fraction (%)	0.033
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6458.12
# indels per 100 kbp	0.00
Largest alignment	617
Total aligned length	991
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	17.1
auNGA	0.2
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	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	64
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

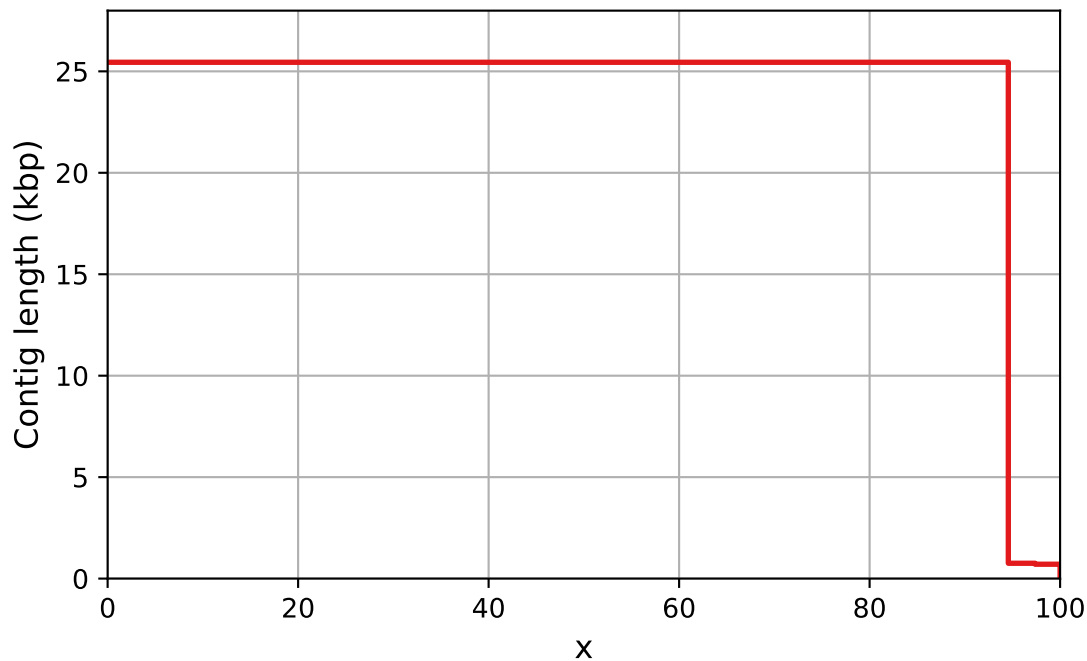
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	25328
# N's	0

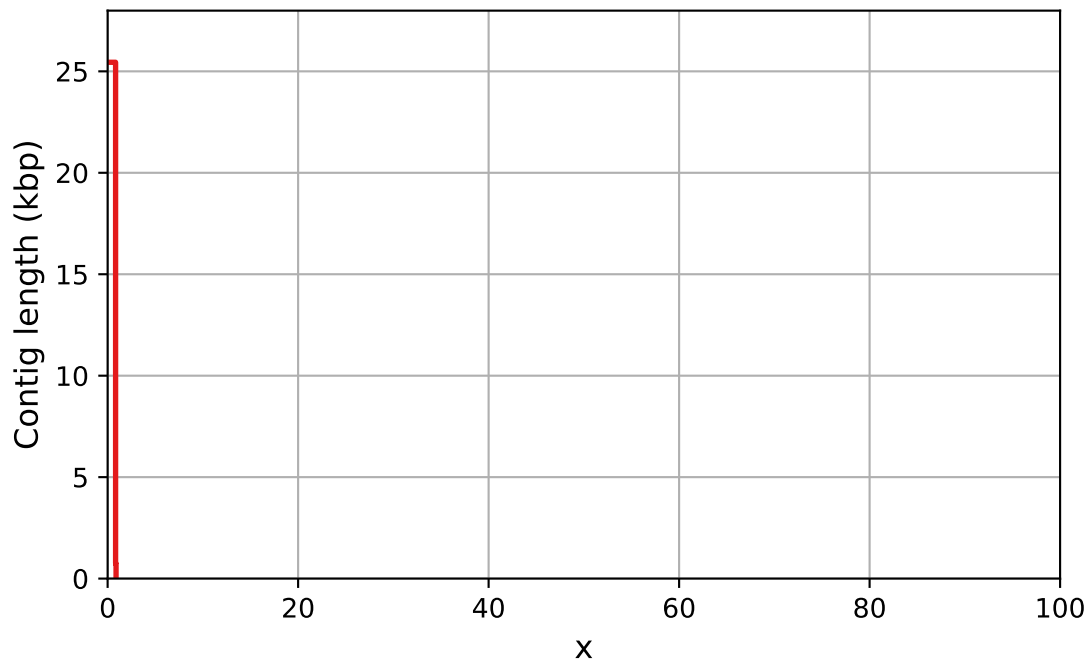
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



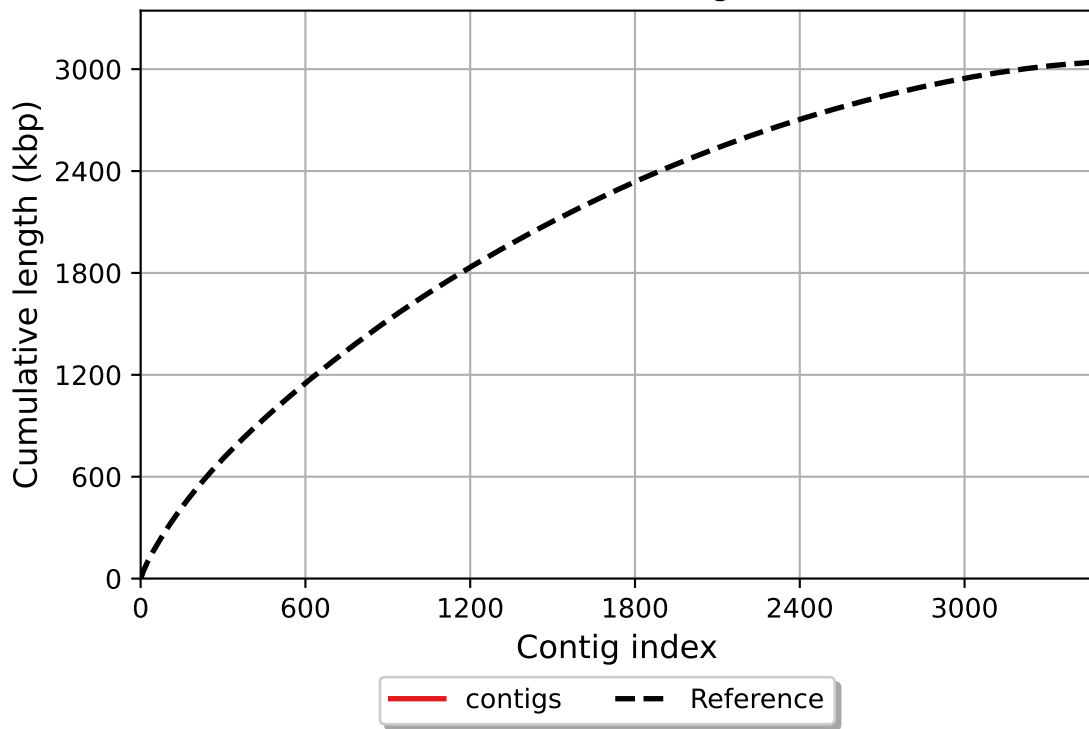
contigs

NGx

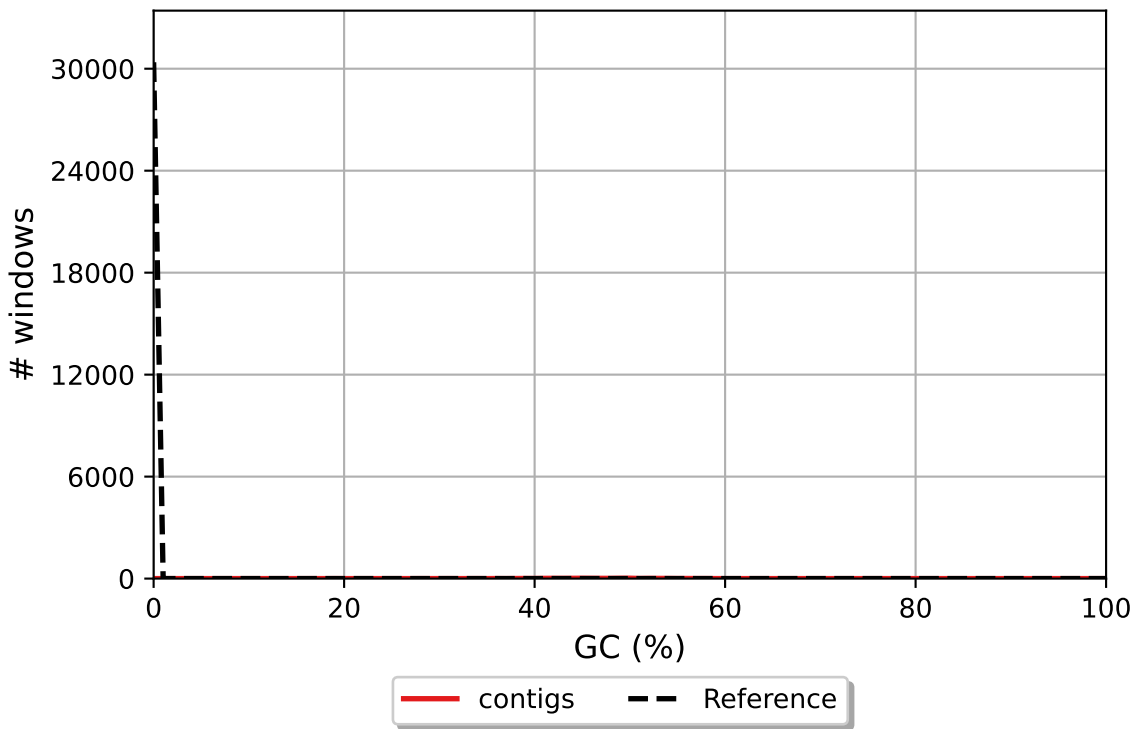


— contigs

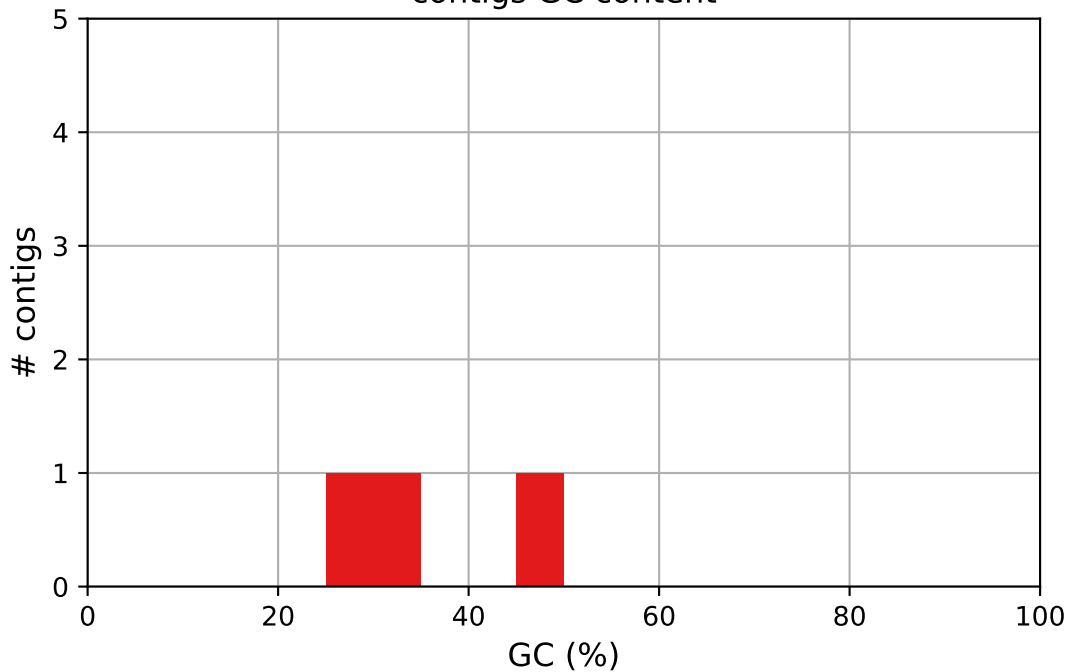
Cumulative length



# GC content



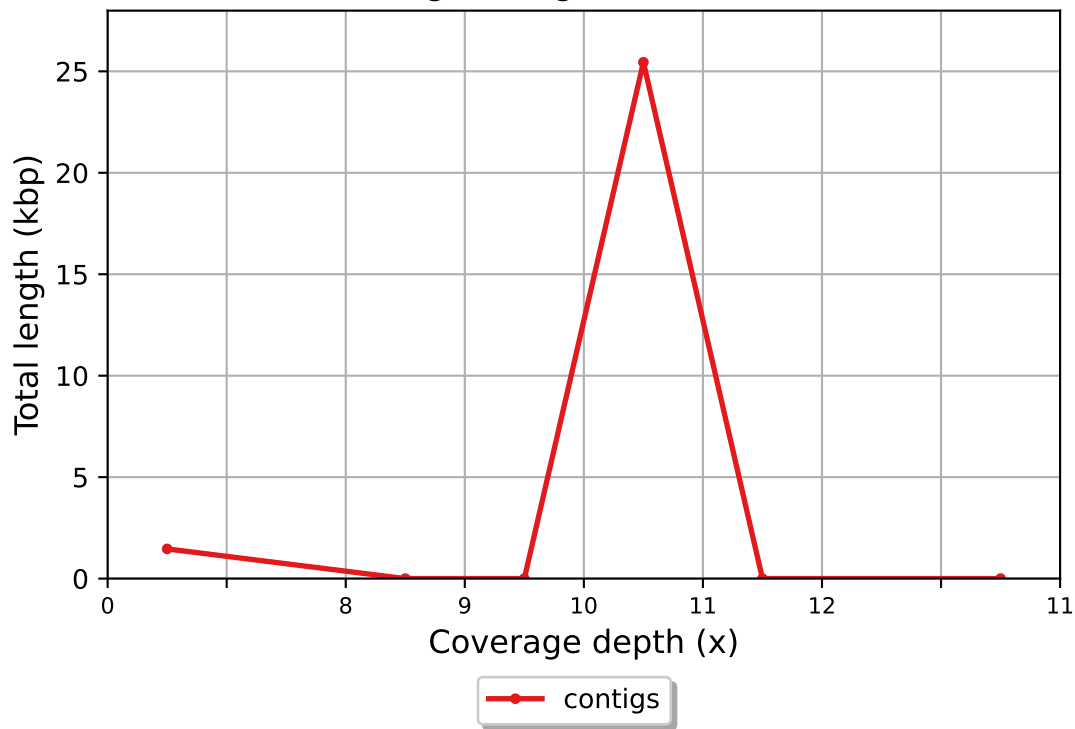
contigs GC content



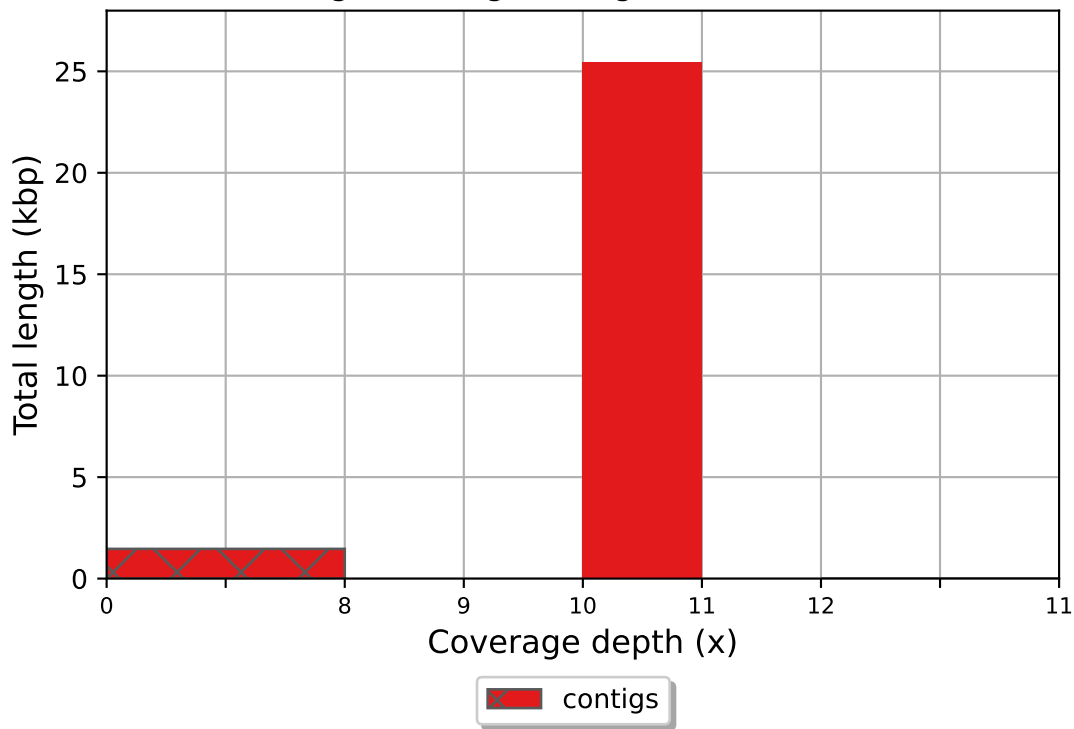
contigs



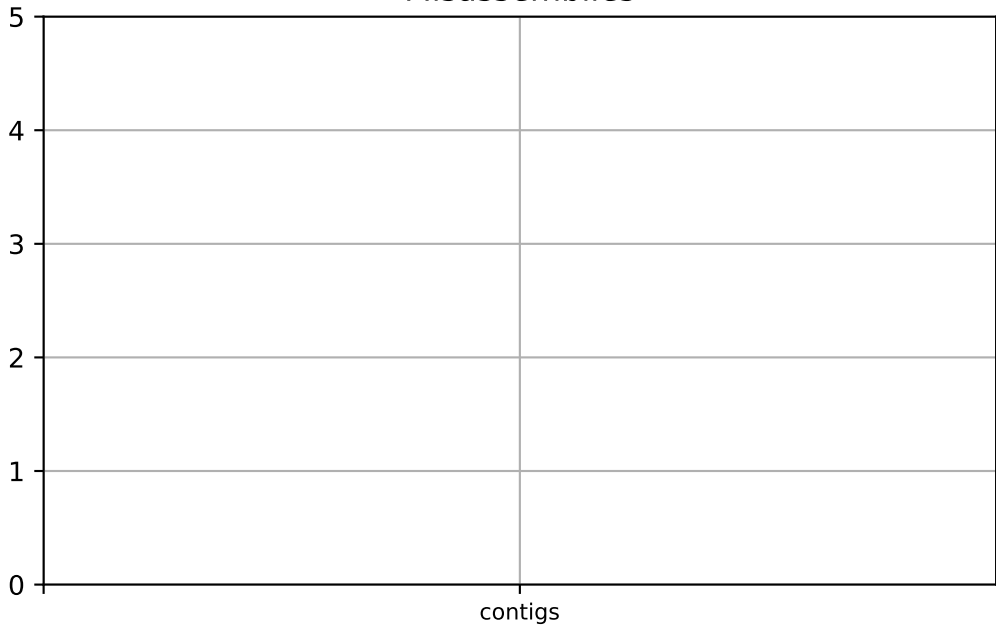
Coverage histogram (bin size: 1x)



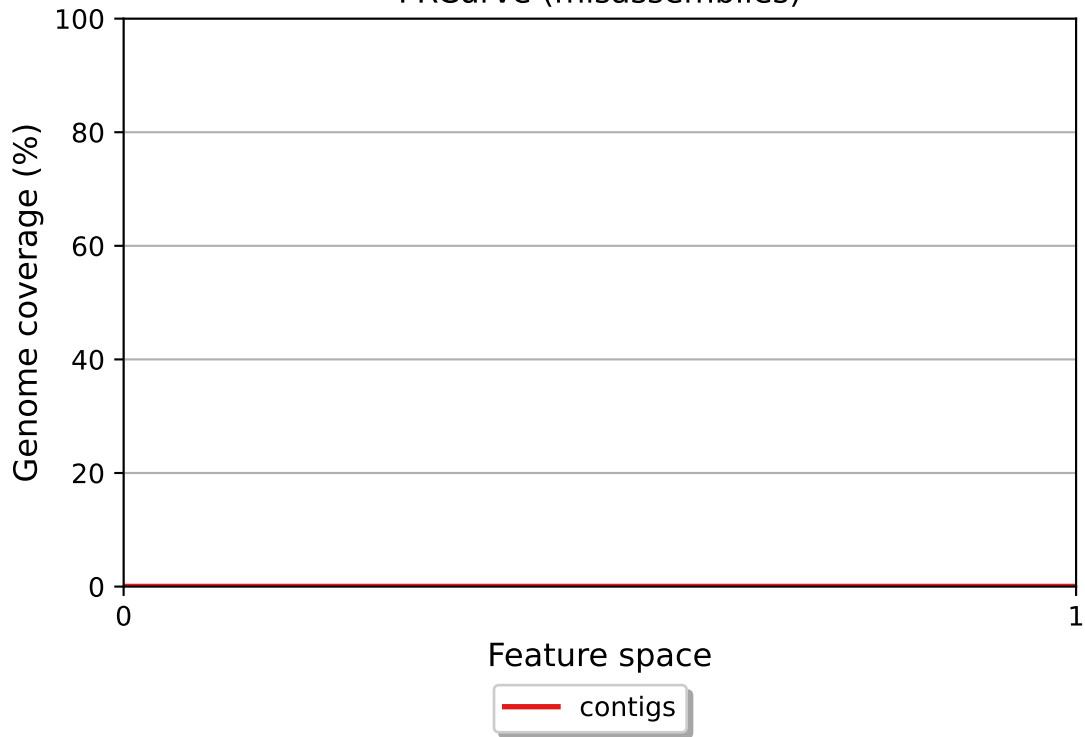
contigs coverage histogram (bin size: 1x)



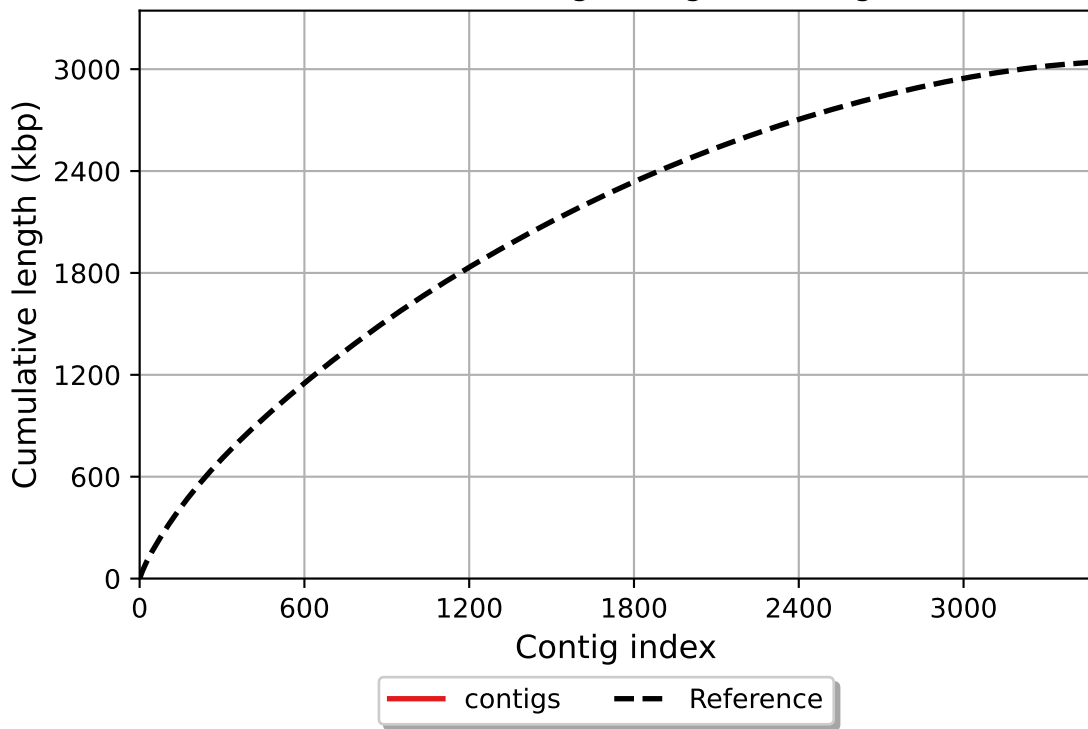
# Misassemblies



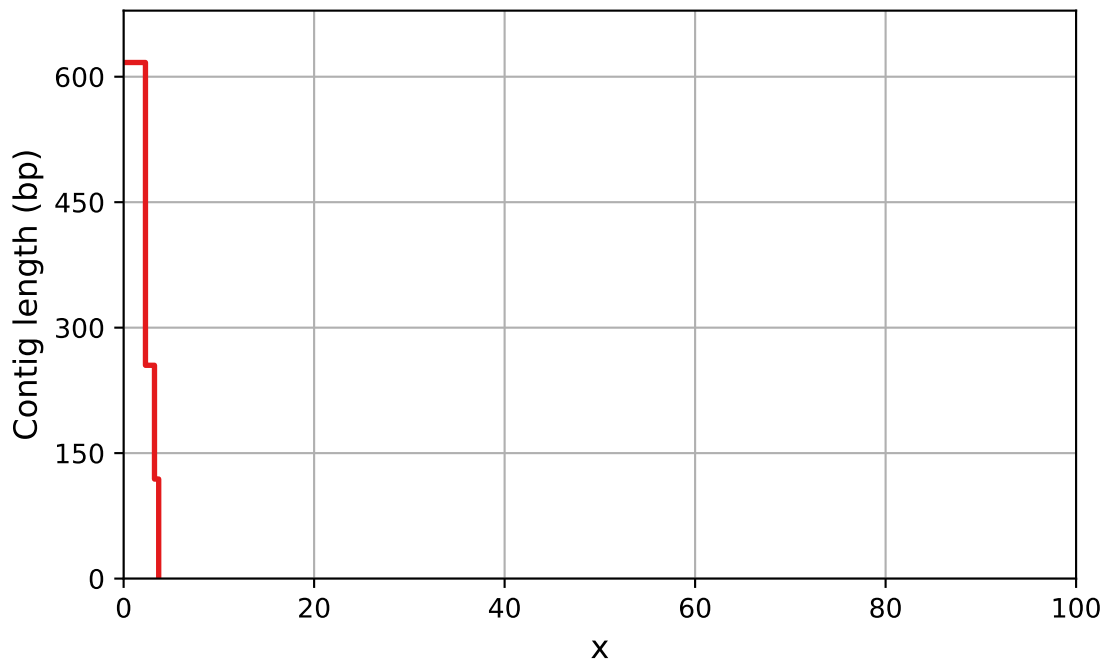
FRCurve (misassemblies)



Cumulative length (aligned contigs)

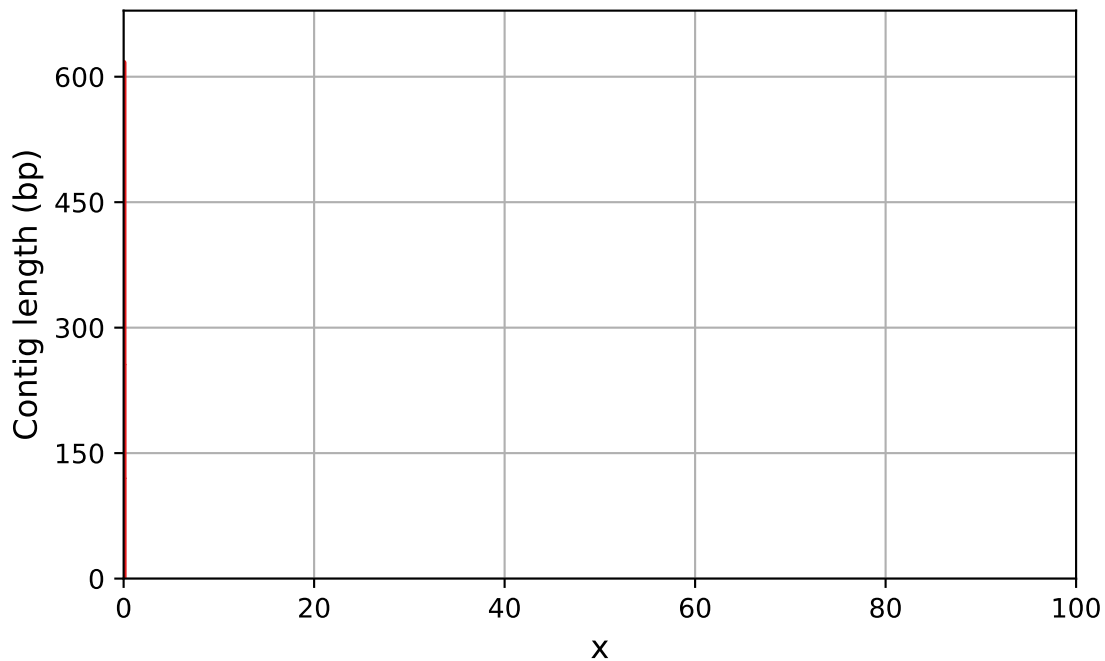


NAx



— contigs

# NGAx



— contigs