

Report	test
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	683296
Total length (>= 1000 bp)	683296
Total length (>= 5000 bp)	683296
Total length (>= 10000 bp)	677242
Total length (>= 25000 bp)	677242
Total length (>= 50000 bp)	642993
# contigs	3
Largest contig	642993
Total length	683296
Reference length	21282515
GC (%)	20.27
Reference GC (%)	18.70
N50	642993
NG50	-
N90	642993
NG90	-
auN	606837.5
auNG	19483.1
L50	1
LG50	-
L90	1
LG90	-
# total reads	29208
# left	13777
# right	13751
Mapped (%)	113.21
Reference mapped (%)	129.63
Properly paired (%)	63.15
Reference properly paired (%)	51.6
Avg. coverage depth	27
Reference avg. coverage depth	0
Coverage >= 1x (%)	98.11
Reference coverage >= 1x (%)	4.86
# misassemblies	5
# misassembled contigs	3
Misassembled contigs length	683296
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	145975
Genome fraction (%)	2.519
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	227.98
# indels per 100 kbp	234.68
# genomic features	1247 + 26 part
Largest alignment	477214
Total aligned length	537321
NA50	477214
NGA50	-
NA90	-
NGA90	-
auNA	334803.9
auNGA	10749.2
LA50	1
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).

## Reads report

	test
# total reads	29208
# left	13777
# right	13751
# mapped	33066
Mapped (%)	113.21
# properly paired	18444
Properly paired (%)	63.15
# singletons	1345
Singletons (%)	4.6
# misjoint mates	1176
Misjoint mates (%)	4.03
Avg. coverage depth	27
Coverage >= 1x (%)	98.11
Coverage >= 5x (%)	91.9
Coverage >= 10x (%)	89.92
# reference mapped	37871
Reference mapped (%)	129.63
# reference properly paired	15074
Reference properly paired (%)	51.6
# reference singletons	1181
Reference singletons (%)	4.04
# reference misjoint mates	8990
Reference misjoint mates (%)	30.77
Reference avg. coverage depth	0
Reference coverage >= 1x (%)	4.86
Reference coverage >= 5x (%)	2.79
Reference coverage >= 10x (%)	2.67

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

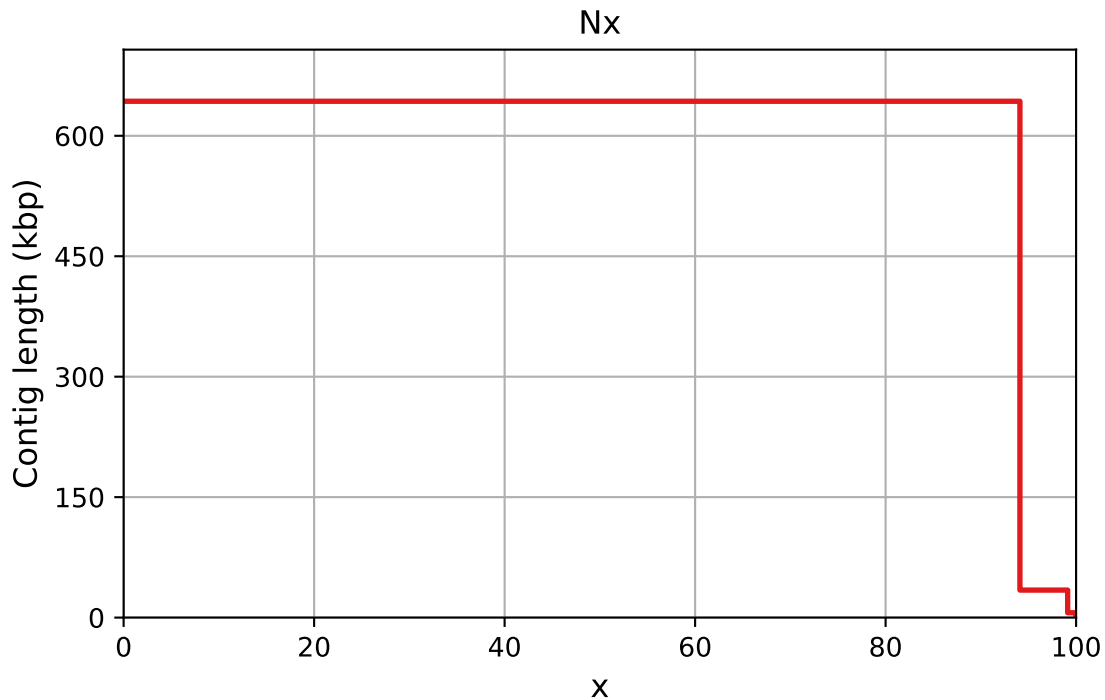
	test
# misassemblies	5
# contig misassemblies	5
# c. relocations	3
# c. translocations	2
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	683296
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	1225
# indels	1261
# indels (<= 5 bp)	754
# indels (> 5 bp)	507
Indels length	10564

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

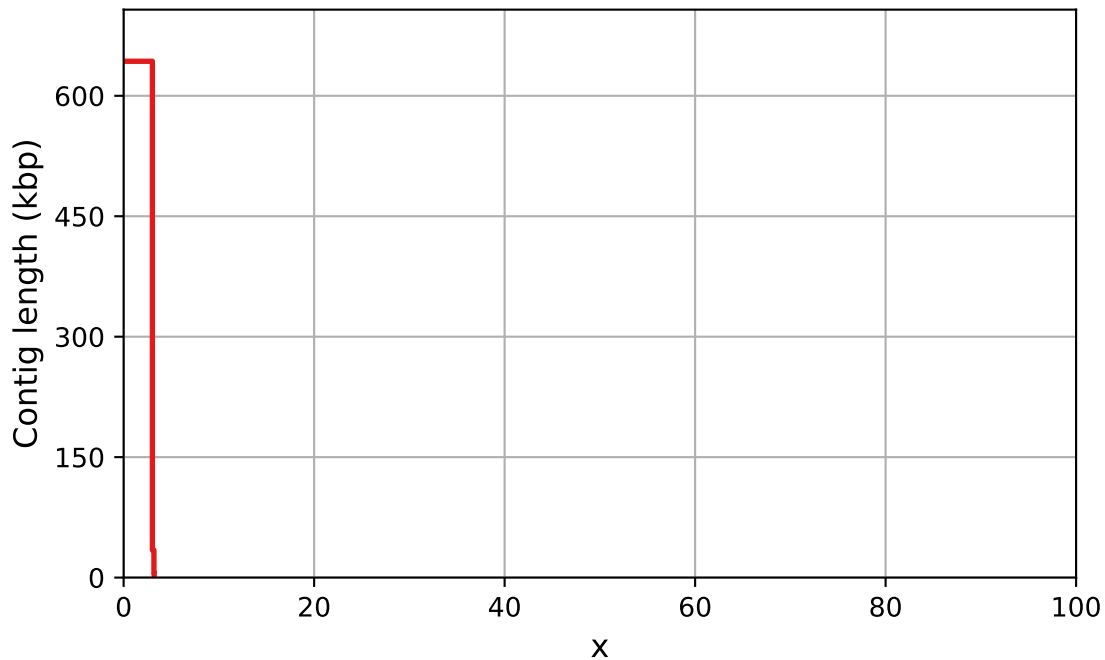
	test
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	145975
# N's	0

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).



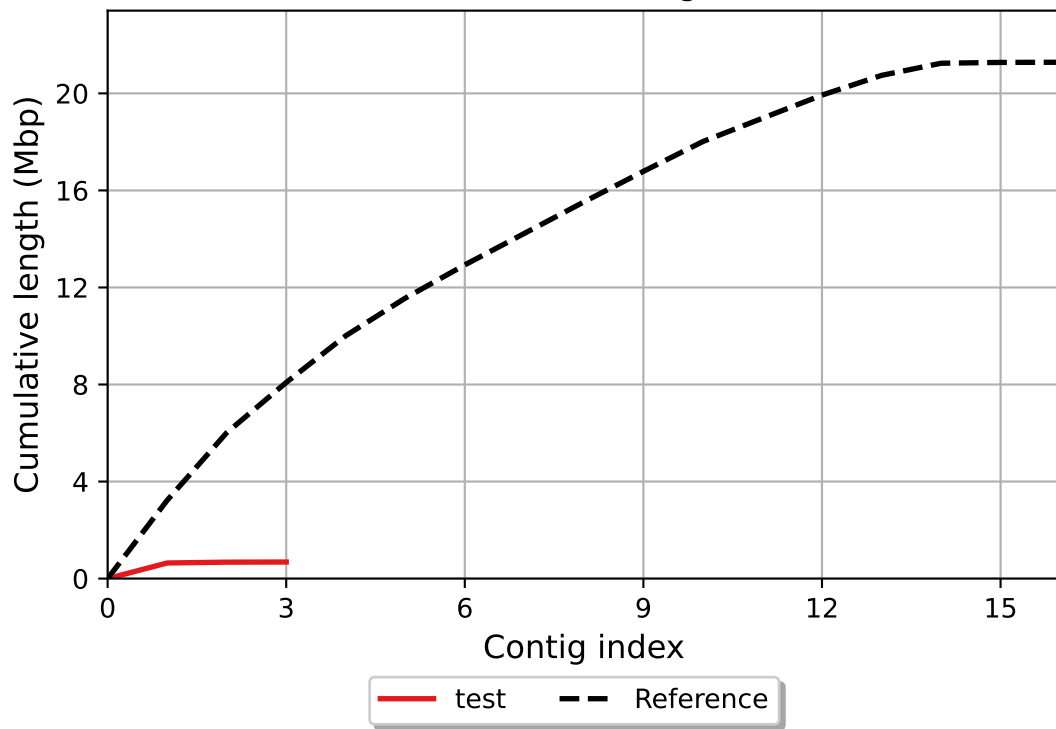
test

NGx

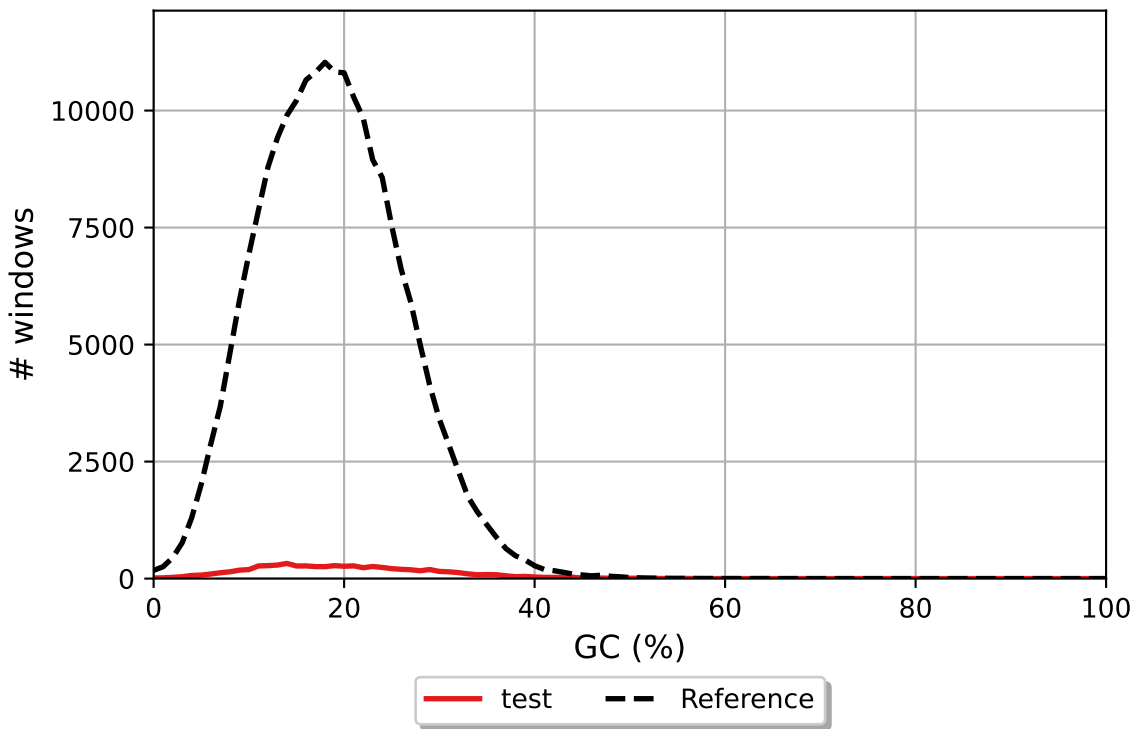


test

Cumulative length

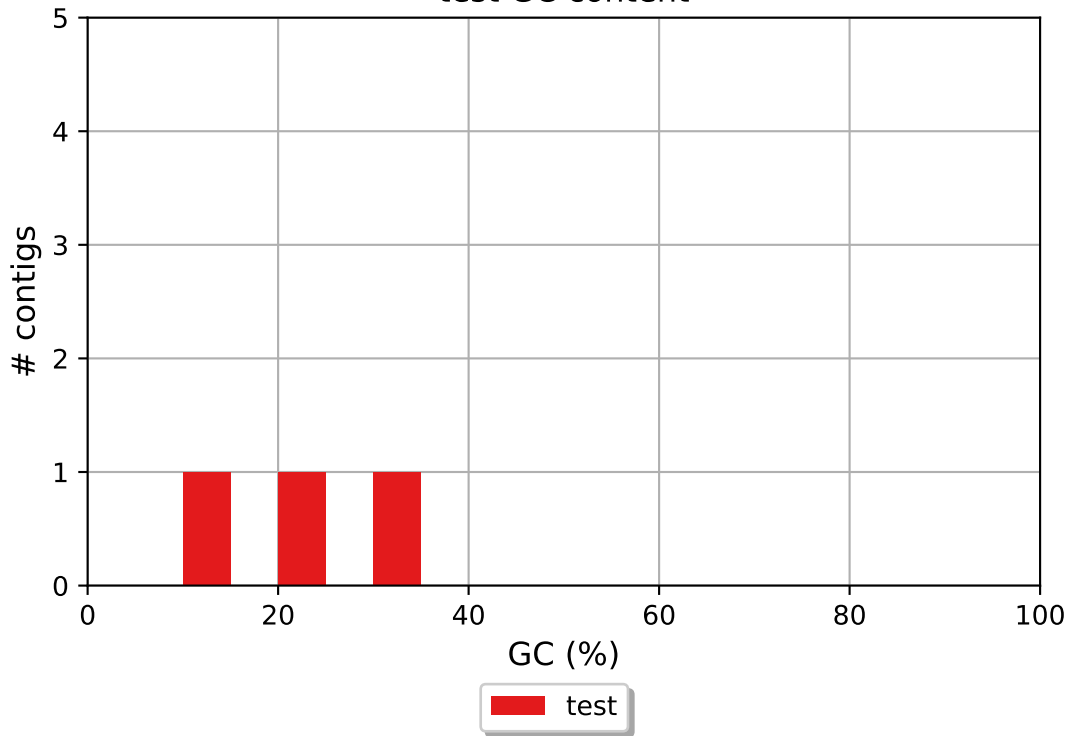


GC content

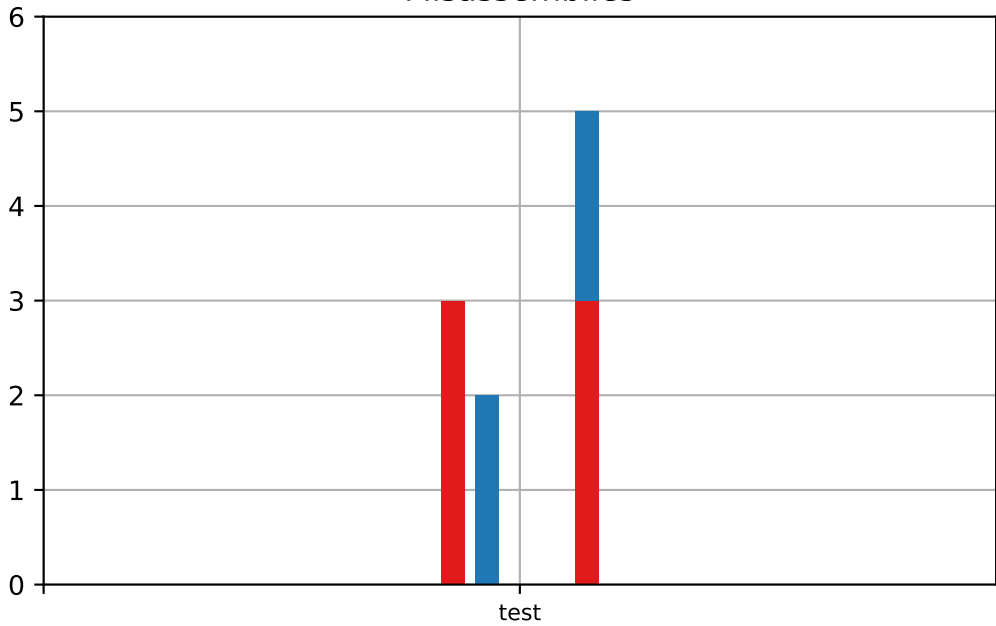




test GC content



## Misassemblies

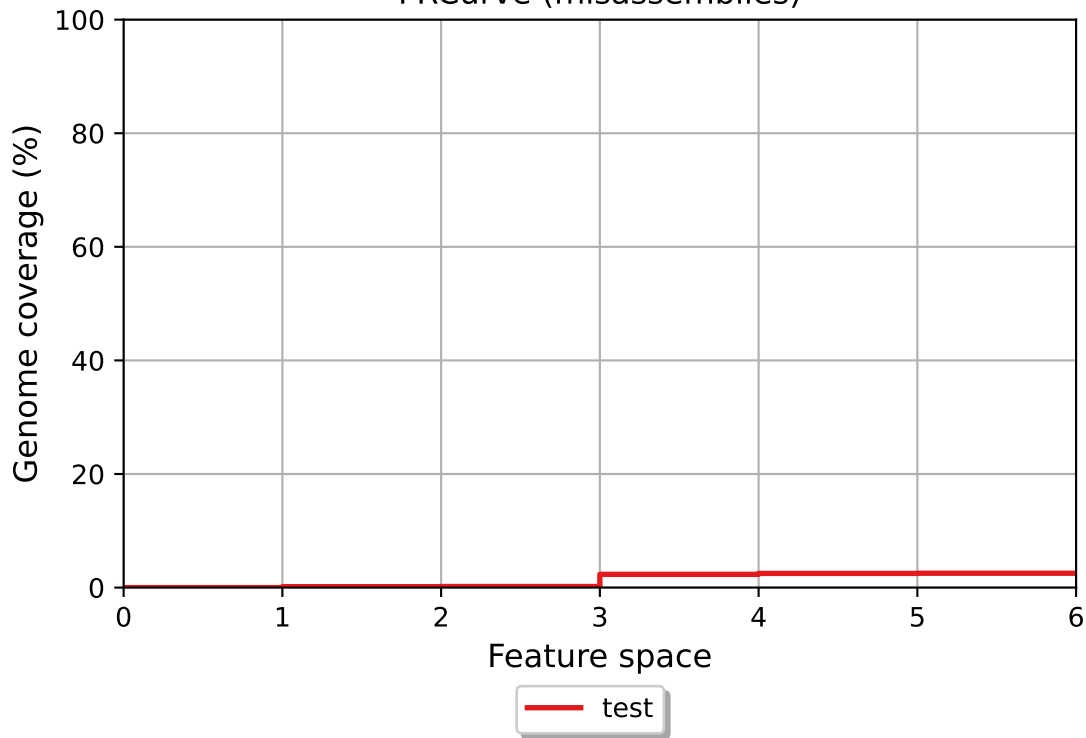


# relocations

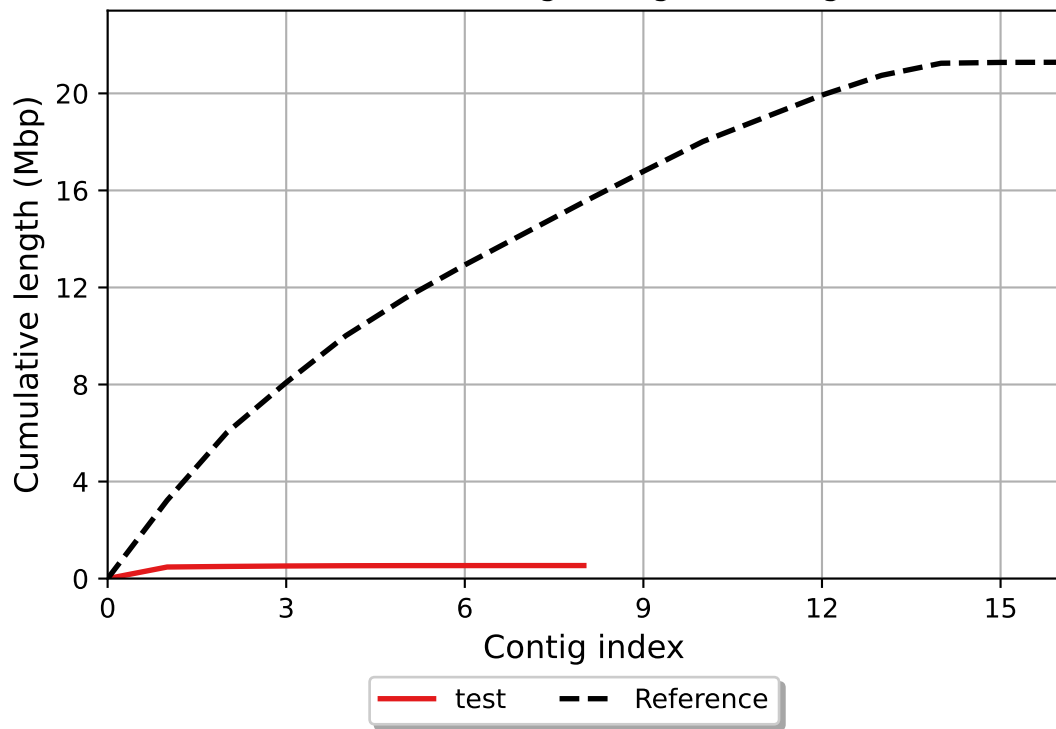


# translocations

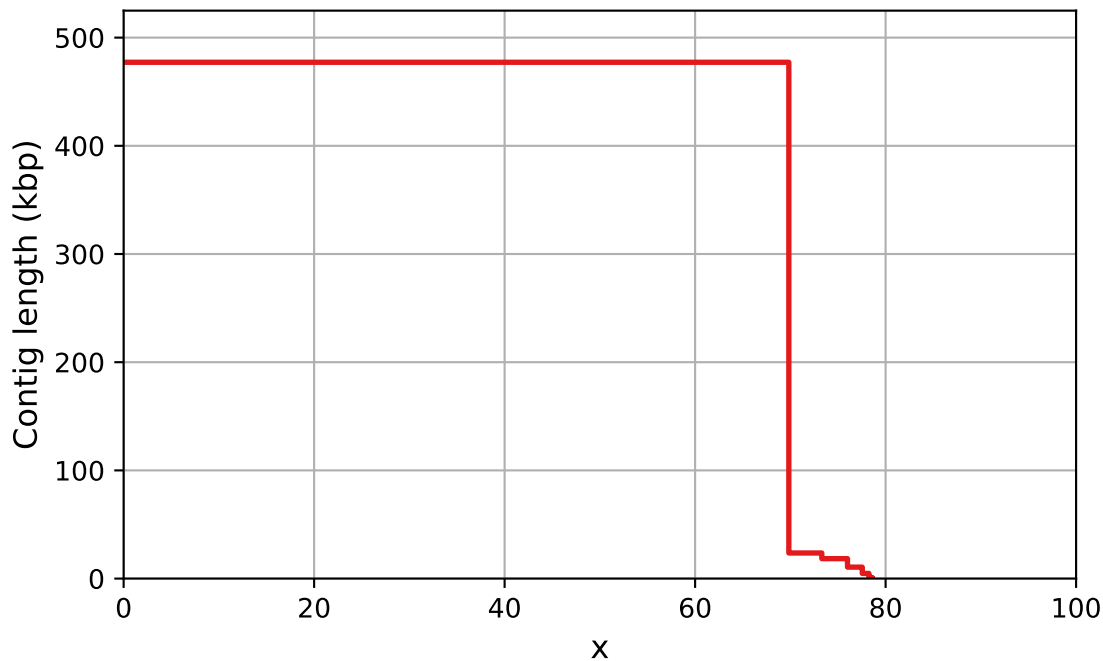
FRCurve (misassemblies)



Cumulative length (aligned contigs)

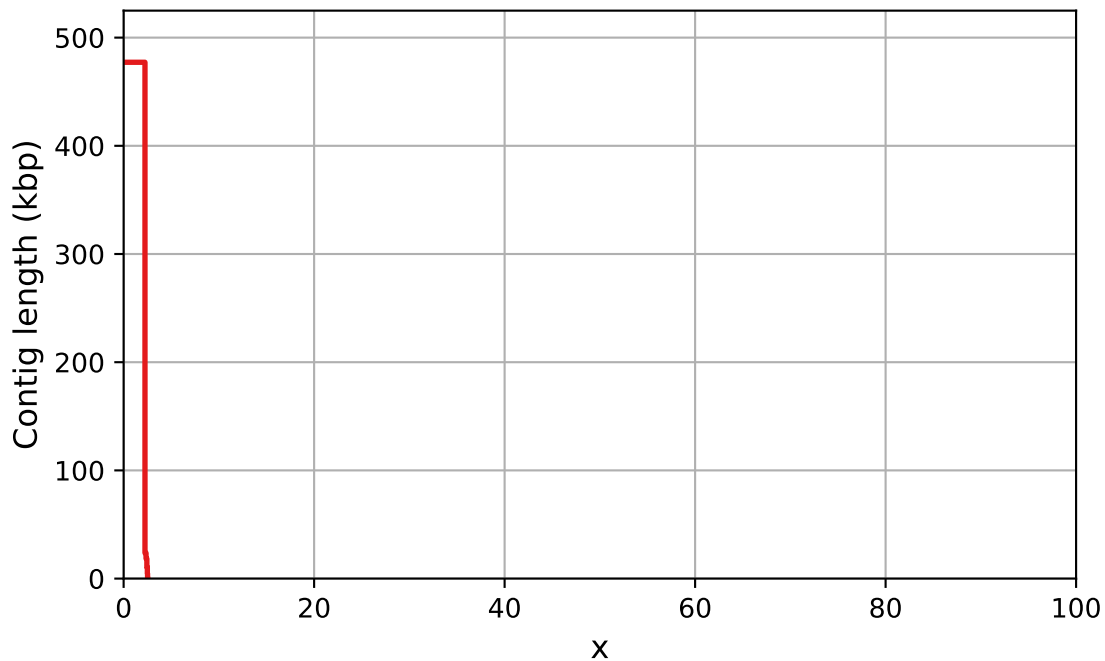


NAx



test

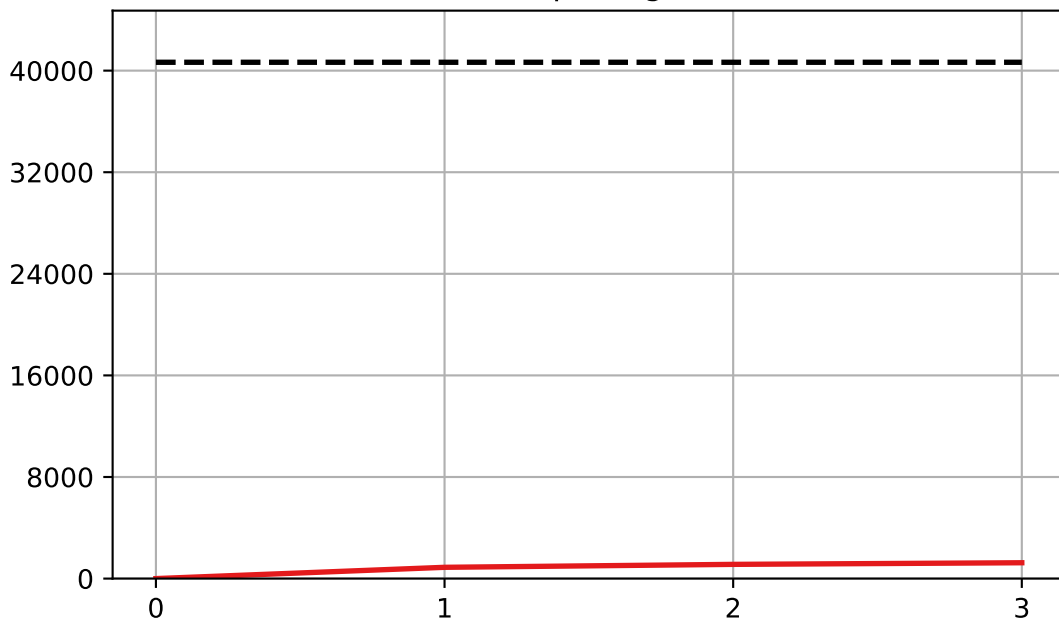
# NGAx



test

Cumulative # complete genomic features

Cumulative # complete genomic features



Contig index

— test    - - Reference

FRCurve (genomic features)

