Report

	referencegenome_fna
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
Total length (>= 0 bp)	4951383
Total length (>= 1000 bp)	4951383
# contigs	2
Largest contig	4857450
Total length	4951383
Reference length	4951383
GC (%)	52.24
Reference GC (%)	52.24
N50	4857450
NG50	4857450
N90	4857450
NG90	4857450
auN	4767081.0
auNG	4767081.0
L50	1
LG50	1
L90	1
LG90	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 (%)	100.000
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
# genomic features	14390 + 0 part
Complete BUSCO (%)	98.65
Partial BUSCO (%)	0.00
# predicted rRNA genes	22 + 0 part
Largest alignment	4857450
Total aligned length	4951383
NA50	4857450
NGA50	4857450
NA90	4857450
NGA90	4857450
auNA	4767081.0
auNGA	4767081.0
LA50	1
LGA50	1
LA90	1
LGA90	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

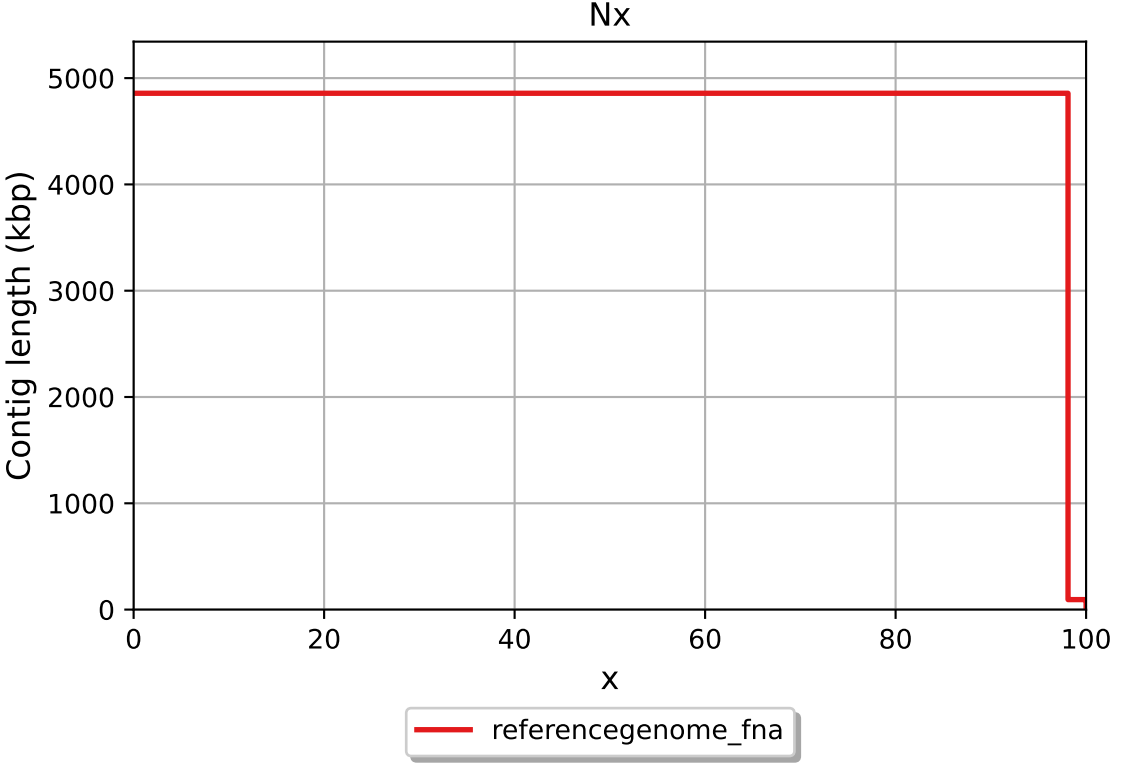
	referencegenome_fna
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

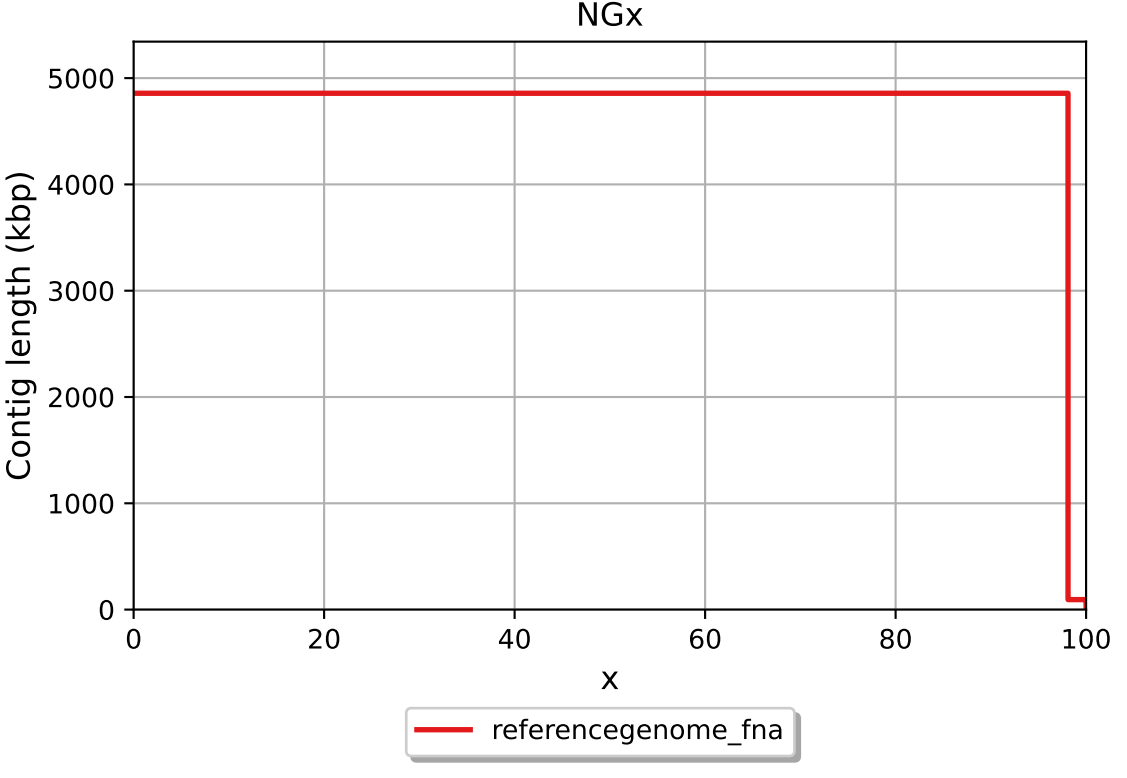
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

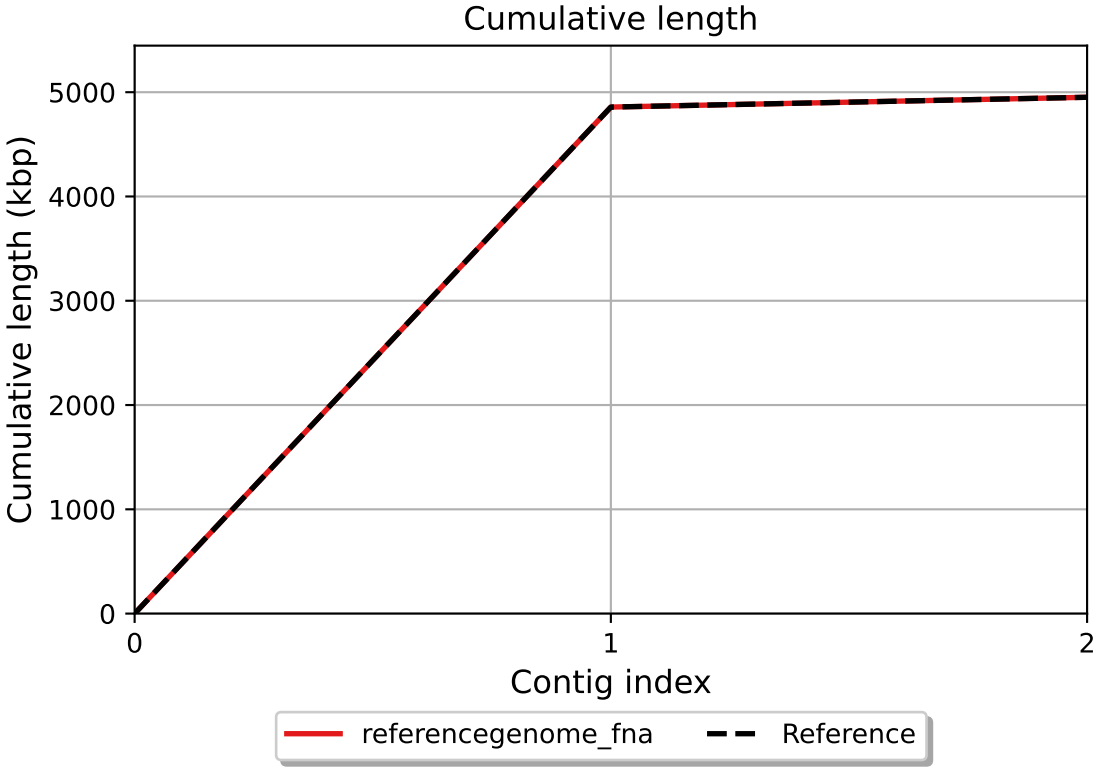
Unaligned report

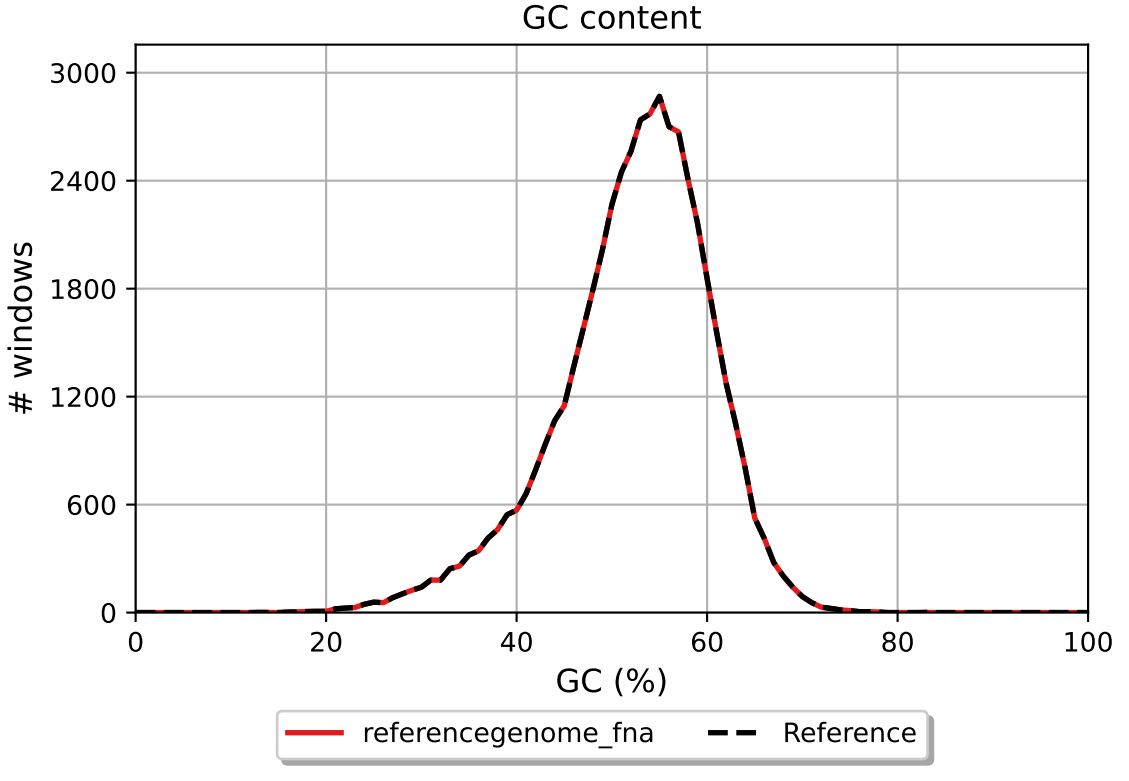
	referencegenome_fna
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

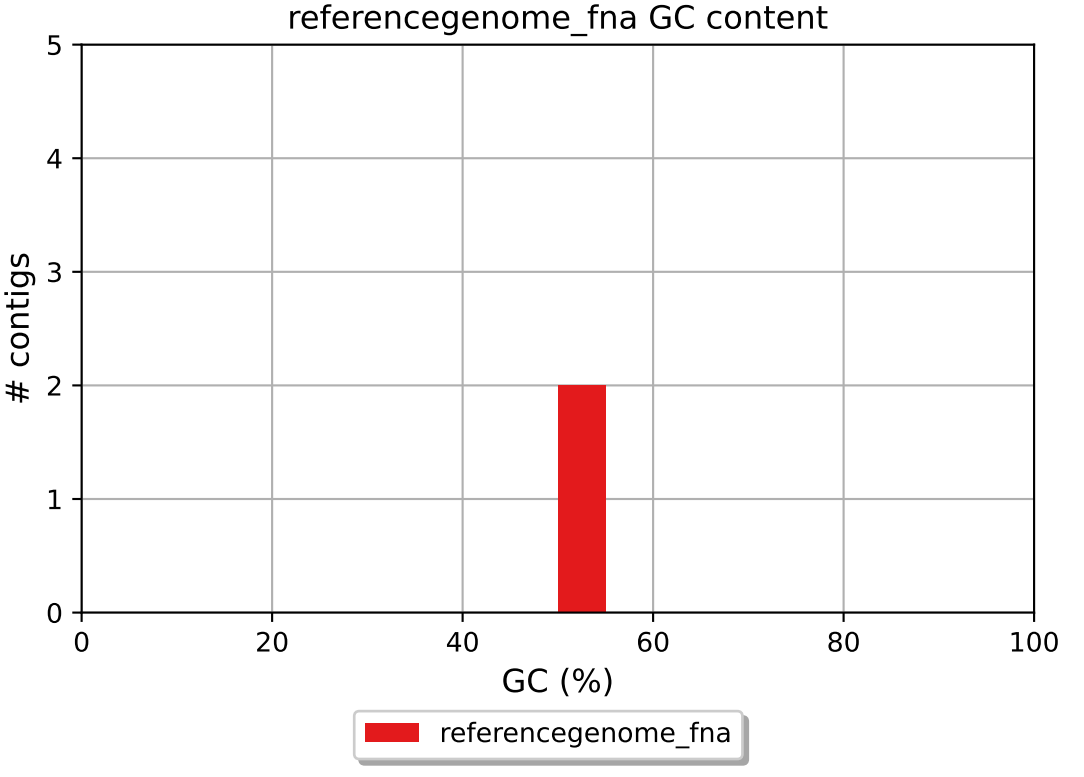
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
referencegenome_fna

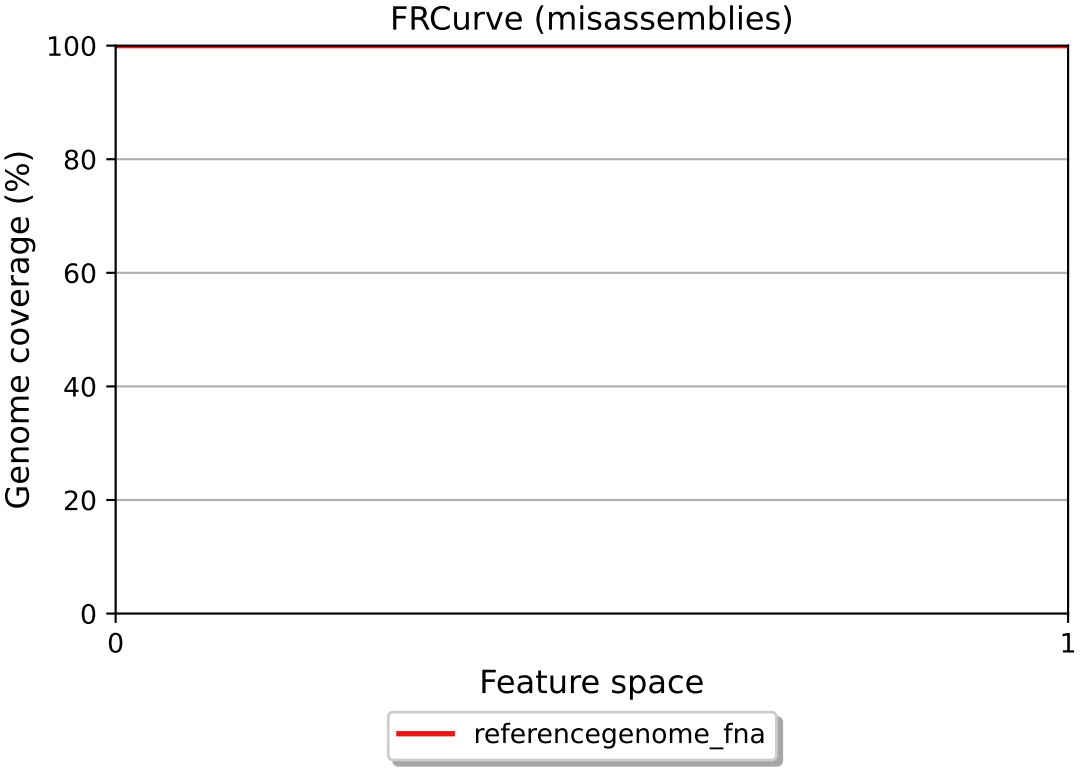

NGx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
referencegenome_fna

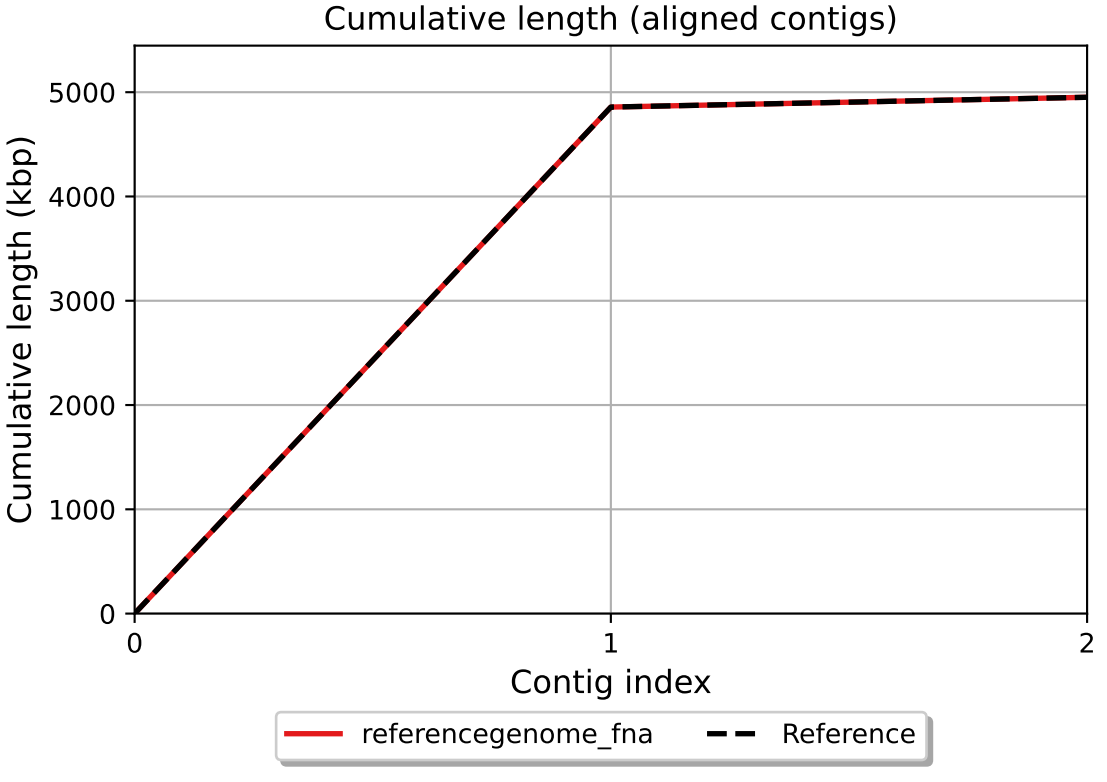

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
Contig index
referencegenome_fna
Reference

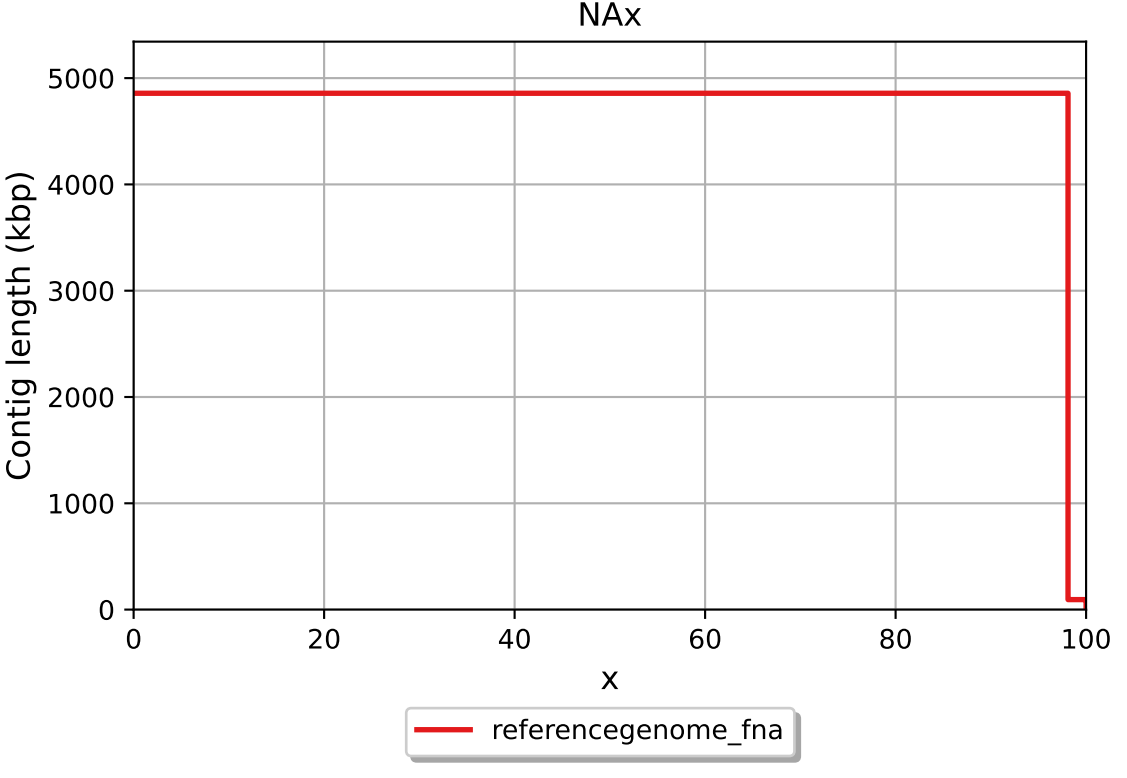

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
referencegenome_fna
Reference

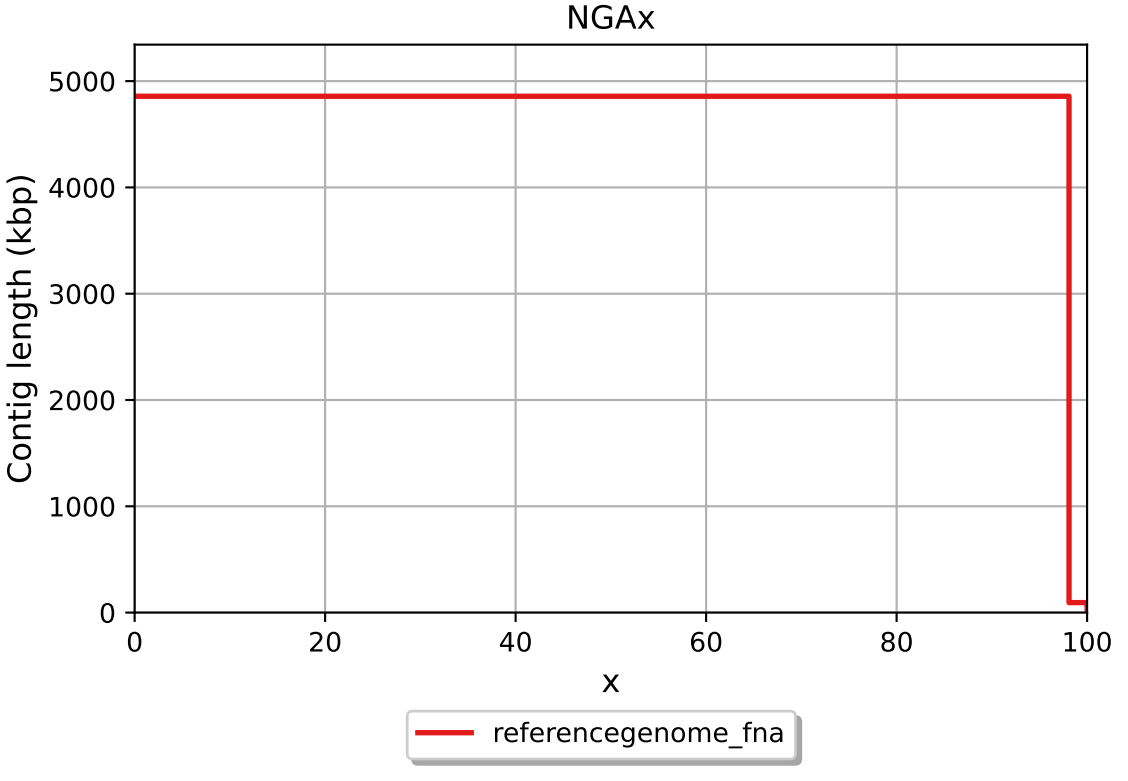

referencegenome_fna GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
referencegenome_fna

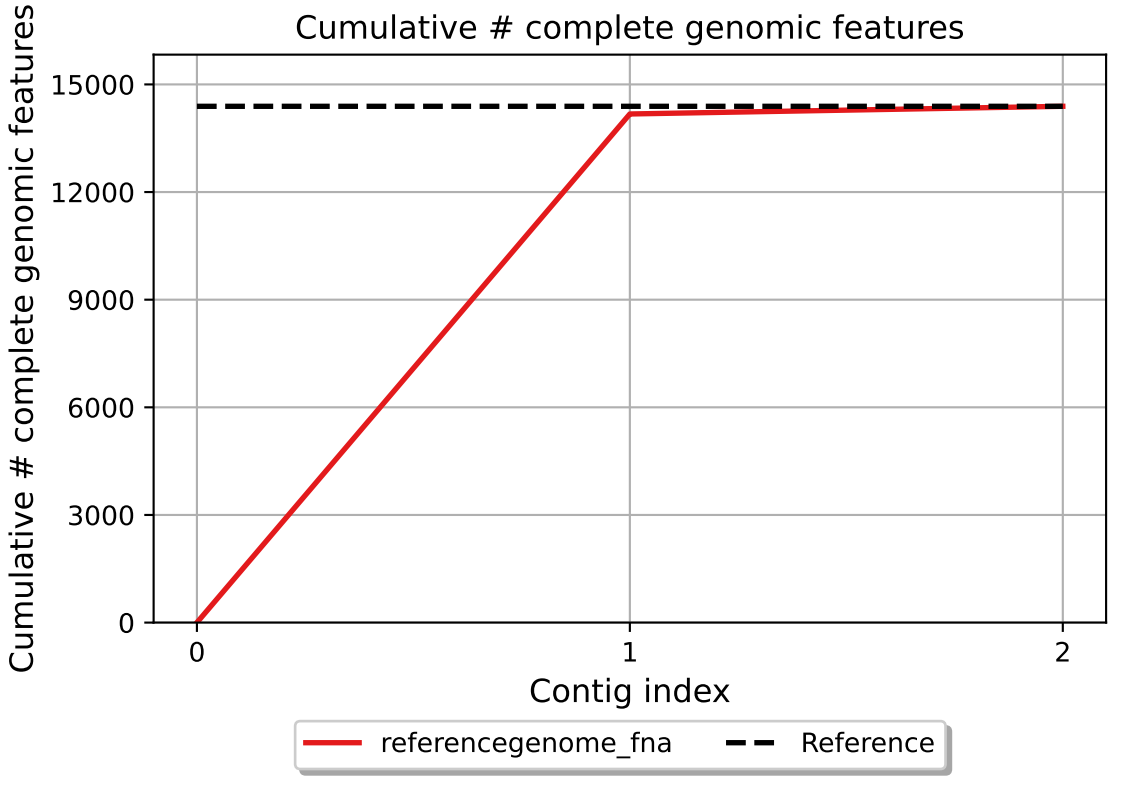
Misassemblies
5
4
3
2
1
0
referencegenome_fna

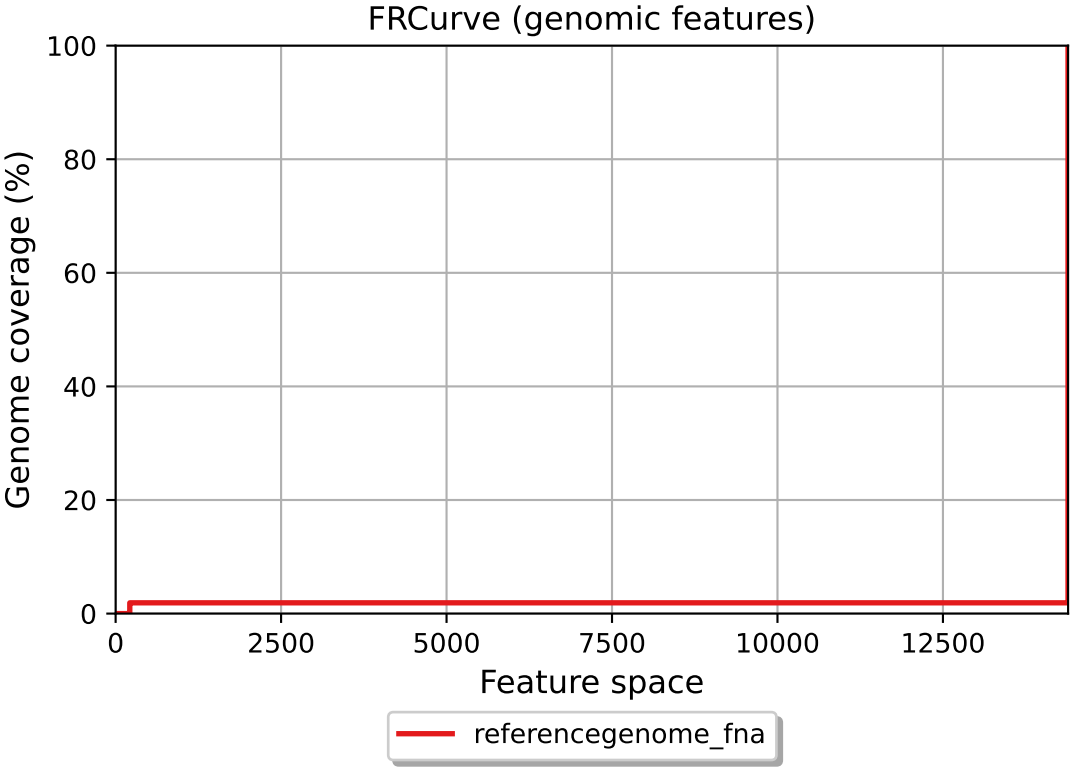

FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
referencegenome_fna


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
Contig index
referencegenome_fna
Reference


NAx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
referencegenome_fna


NGAx
Contig length (kbp)
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
x
referencegenome_fna


Cumulative # complete genomic features
Cumulative # complete genomic features
15000
12000
9000
6000
3000
0
0
1
2
Contig index
referencegenome_fna
Reference


FRCurve (genomic features)
Genome coverage (%)
100
80
60
40
20
0
0
2500
5000
7500
10000
12500
Feature space
referencegenome_fna