Report

	contigs
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	936
Total length	936
Reference length	2580418
GC (%)	36.22
Reference GC (%)	37.52
N50	936
NG50	-
N90	936
NG90	-
auN	936.0
auNG	0.3
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 + 0 part
Unaligned length	0
Genome fraction (%)	0.026
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8184.52
# indels per 100 kbp	148.81
Largest alignment	672
Total aligned length	672
NA50	672
NGA50	-
NA90	-
NGA90	-
auNA	482.5
auNGA	0.2
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).

Misassemblies report

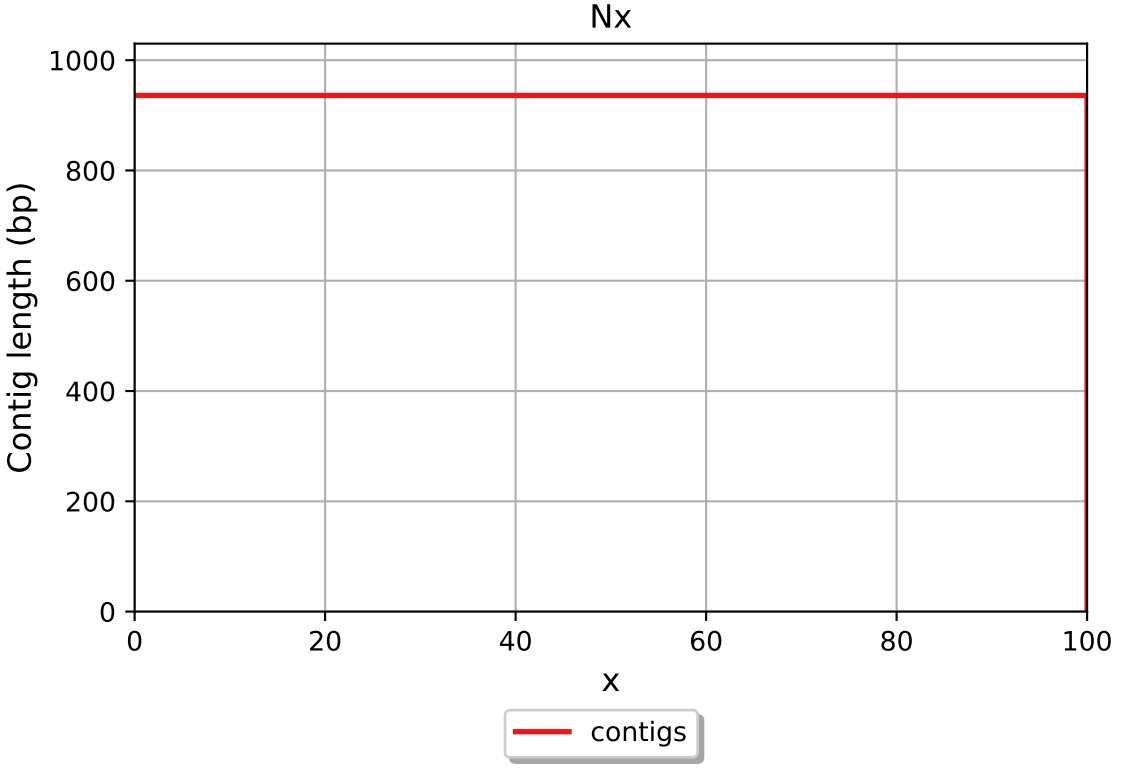
	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	55
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

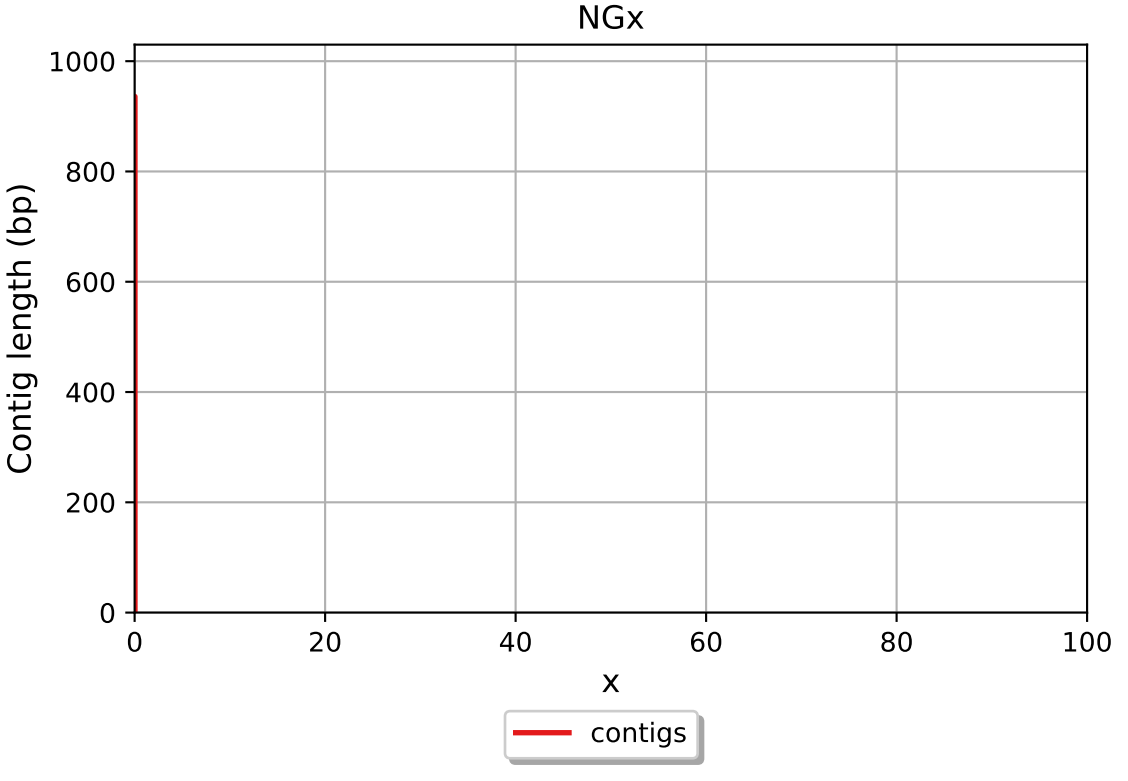
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

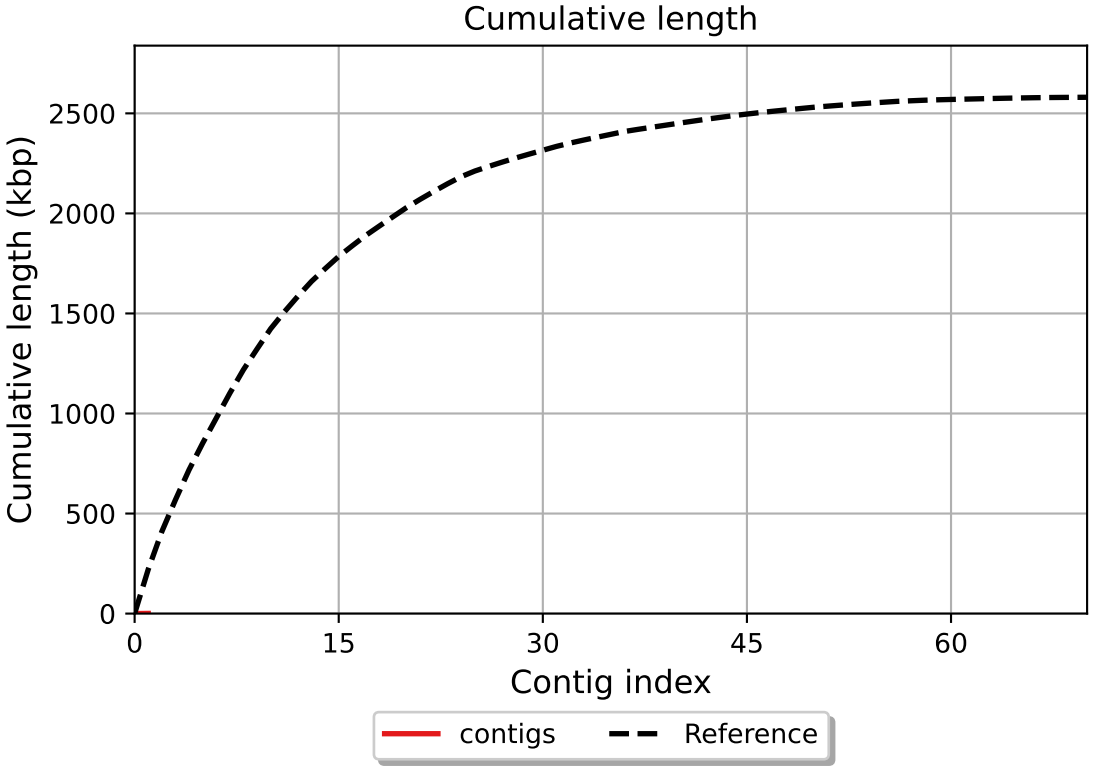
Unaligned report

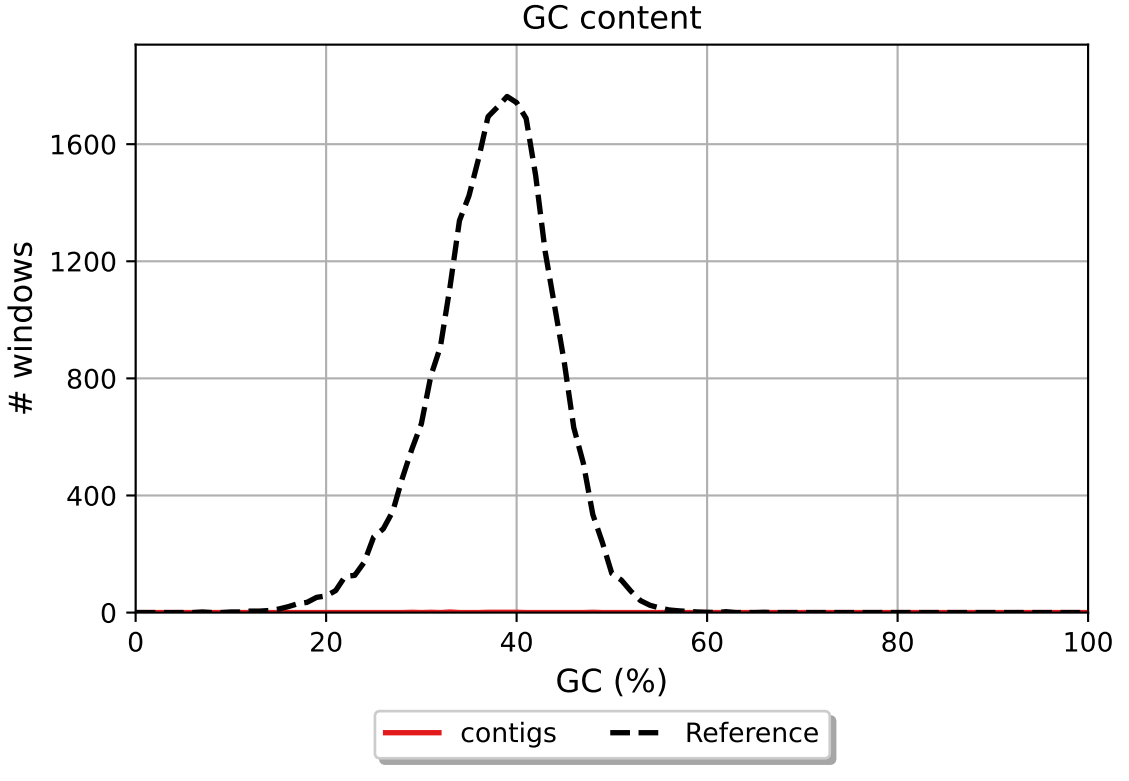
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

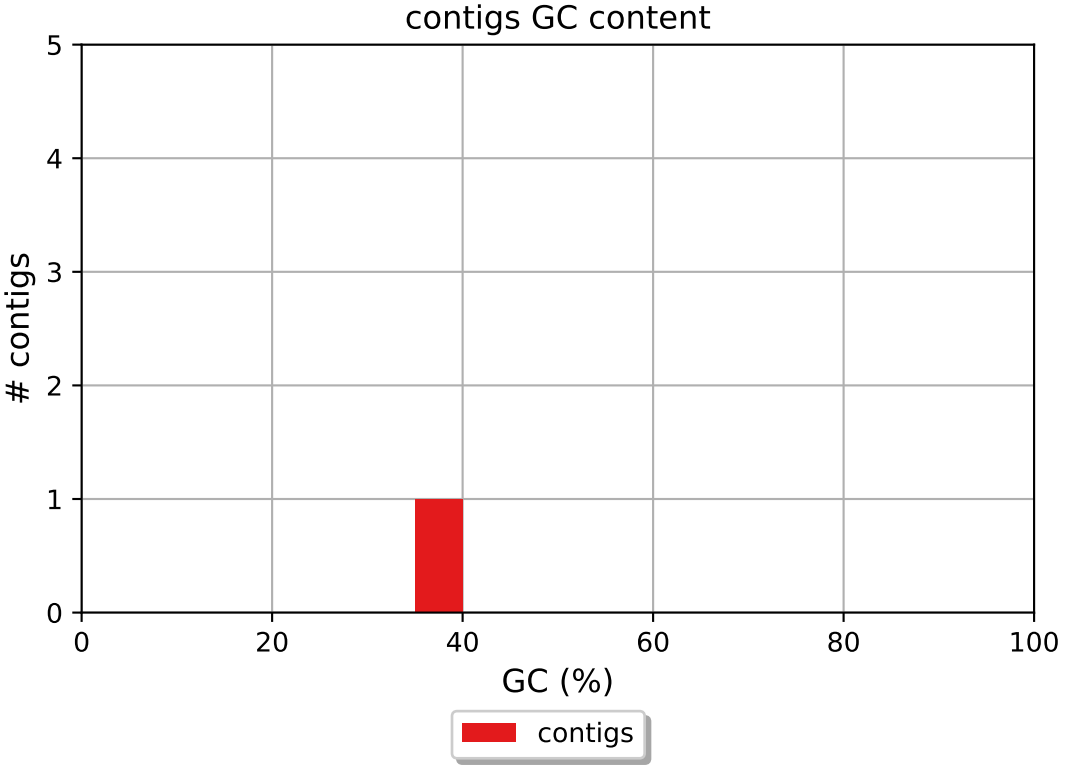
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

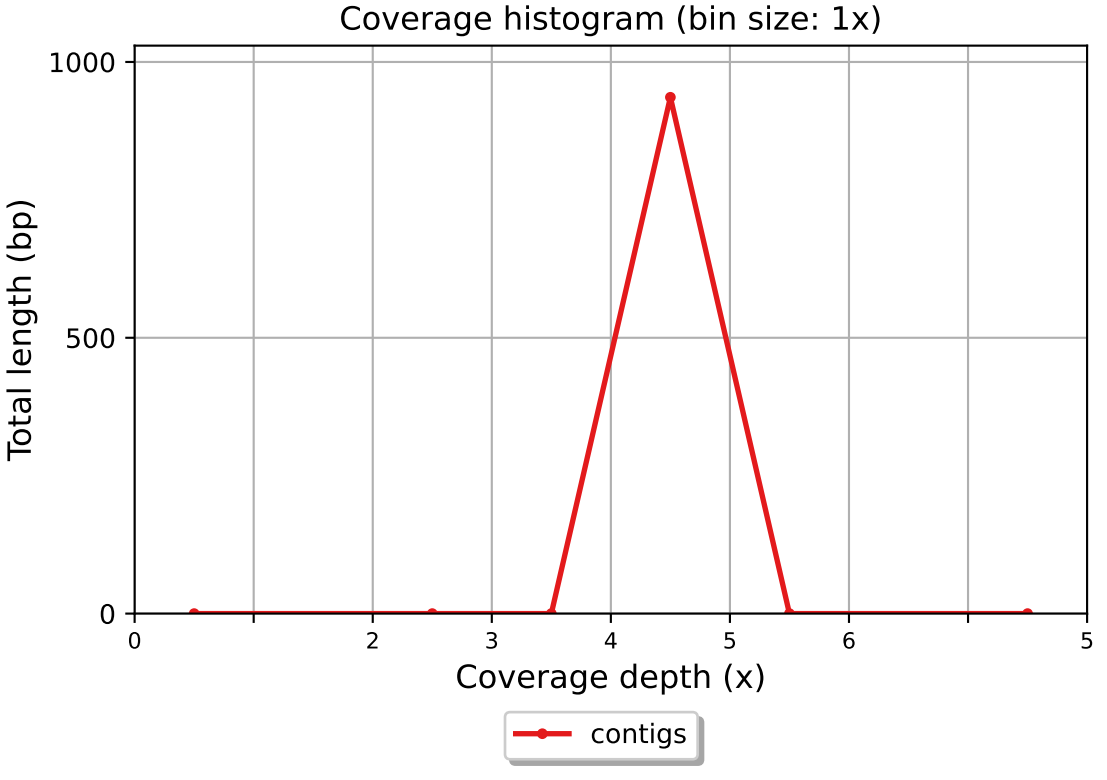

Nx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
contigs

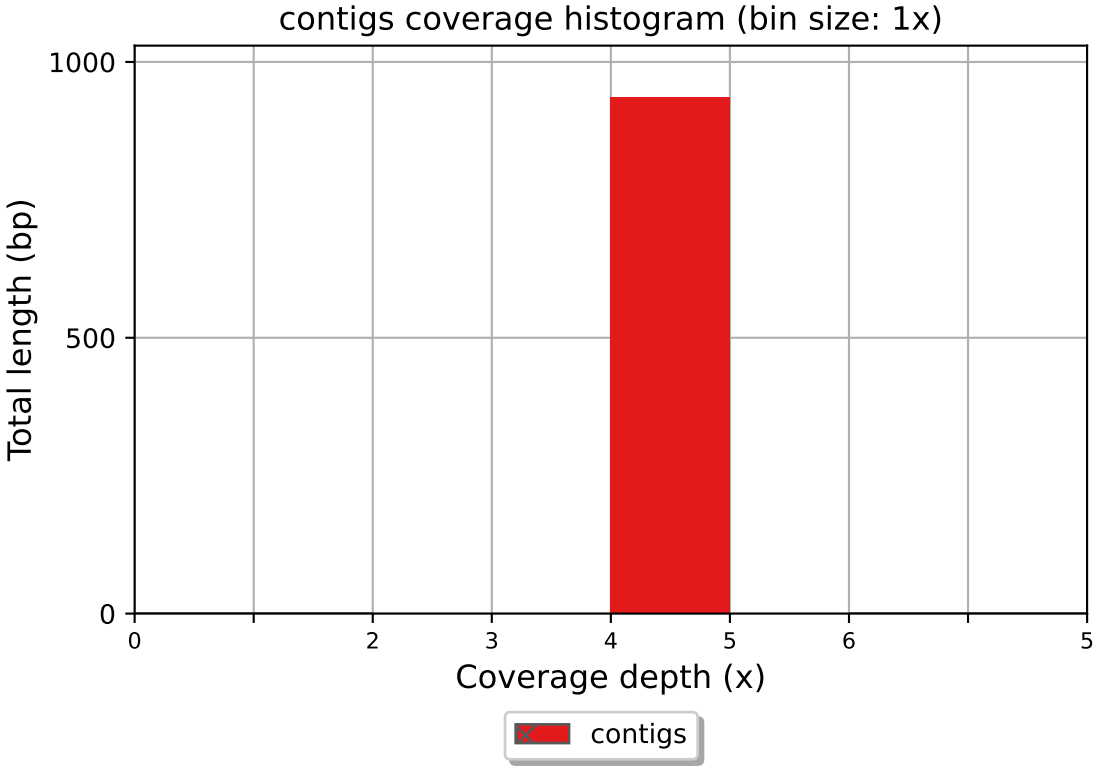

NGx
Contig length (bp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
contigs

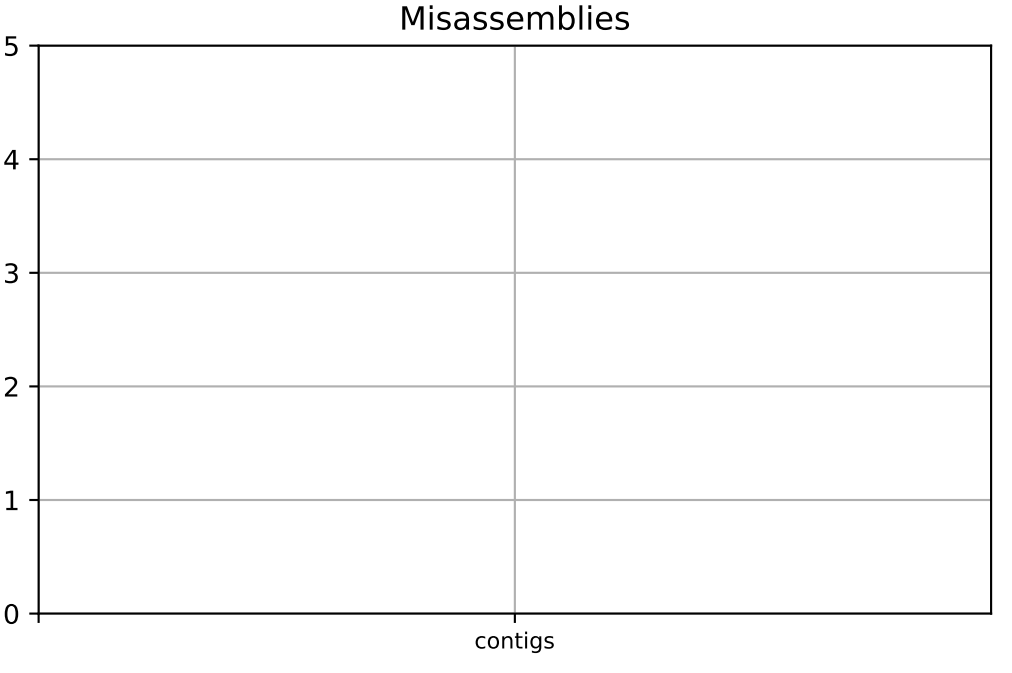

Cumulative length
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
15
30
45
60
Contig index
contigs
Reference

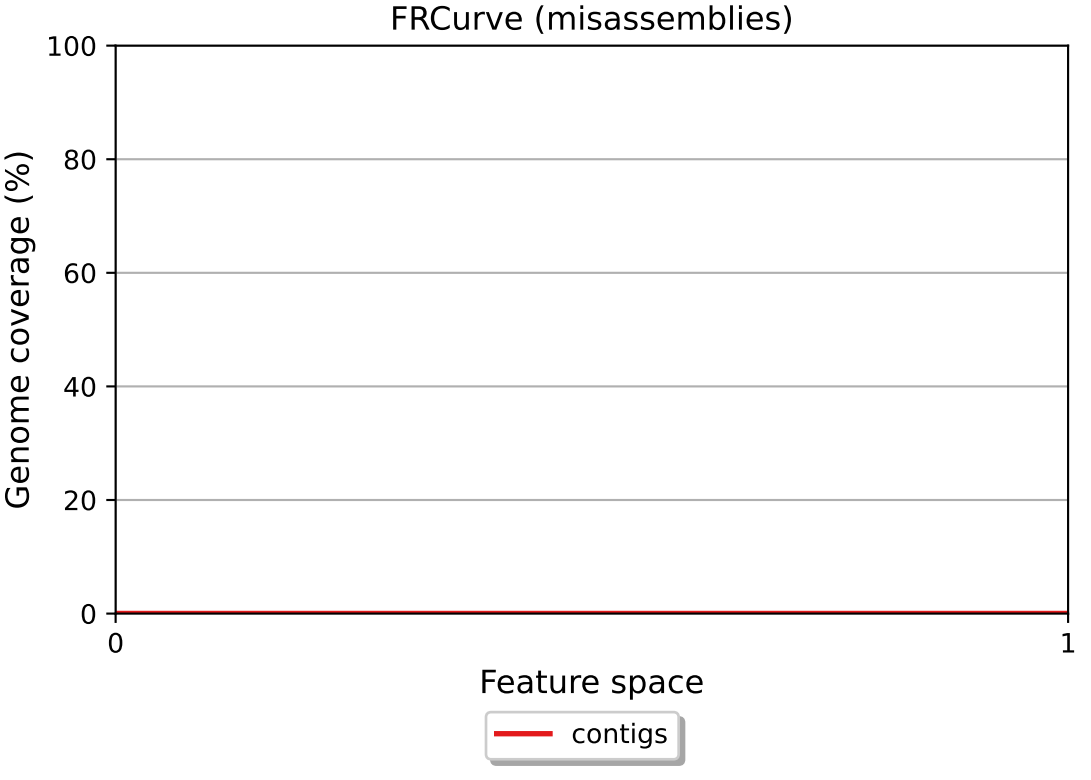

GC content
windows
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
contigs
Reference

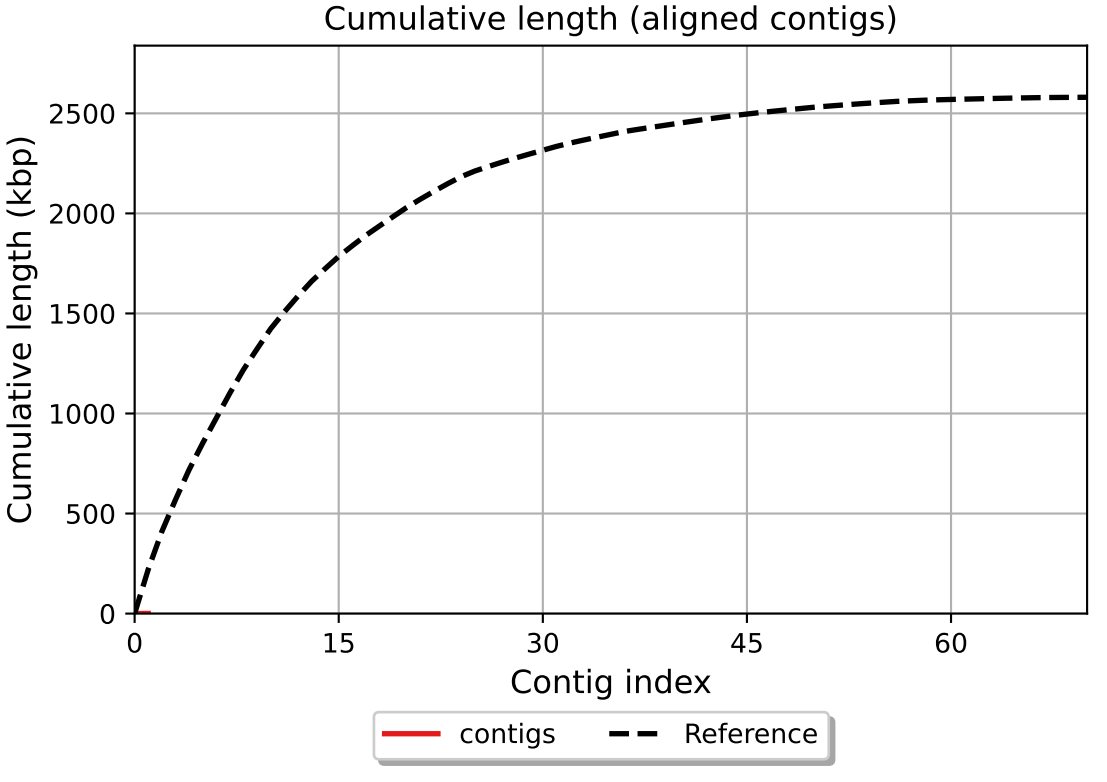

contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs

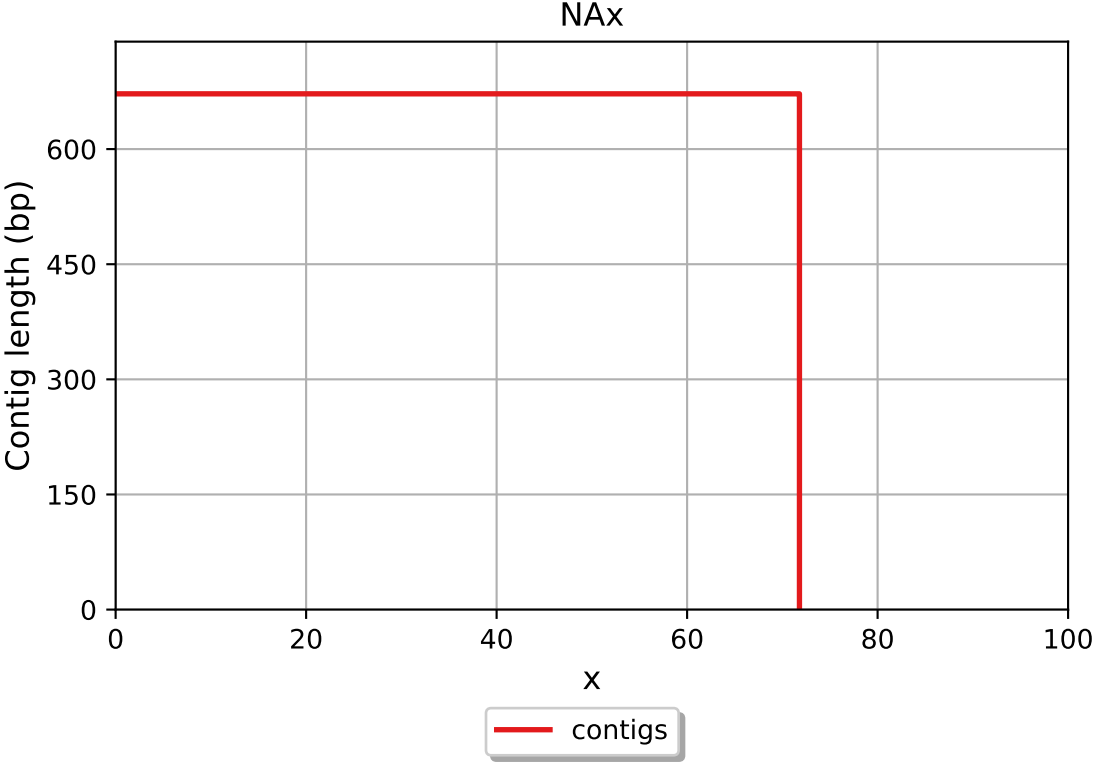

Coverage histogram (bin size: 1x)
Total length (bp)
1000
500
0
0
2
3
4
5
6
5
Coverage depth (x)
contigs

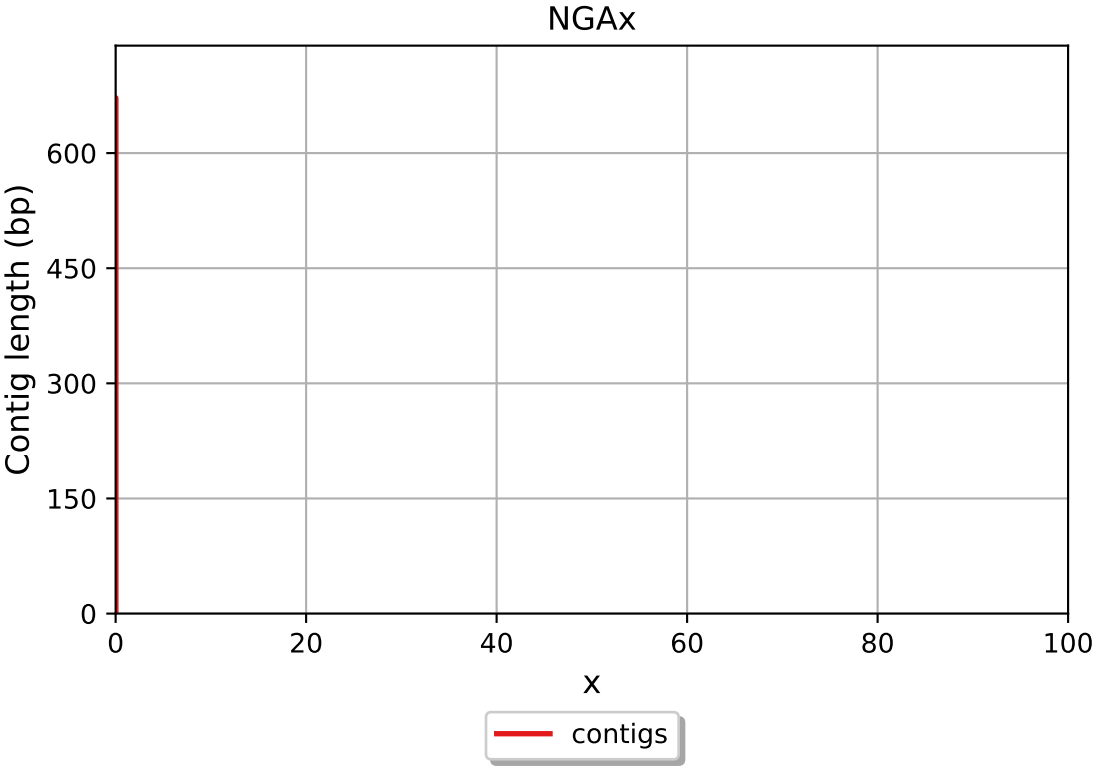

contigs coverage histogram (bin size: 1x)
1000
500
0
Total length (bp)
0
2
3
4
5
6
5
Coverage depth (x)
contigs


Misassemblies
5
4
3
2
1
0
contigs


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
15
30
45
60
Contig index
contigs
Reference


NAx
Contig length (bp)
600
450
300
150
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (bp)
600
450
300
150
0
0
20
40
60
80
100
x
contigs