Report	contigs
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1247
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	11
Largest contig	1247
Total length	7860
Reference length	2754552
GC (%)	38.40
Reference GC (%)	39.34
N50	651
NG50	-
N90	558
NG90	-
auN	773.9
auNG	2.2
L50	5
LG50	-
L90	10
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 (%)	0.285
Duplication ratio	0.999
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1222.46
# indels per 100 kbp	50.94
Largest alignment	1247
Total aligned length	7853
NA50	651
NGA50	-
NA90	558
NGA90	-
auNA	772.9
auNGA	2.2
LA50	5
LGA50	-
LA90	10
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

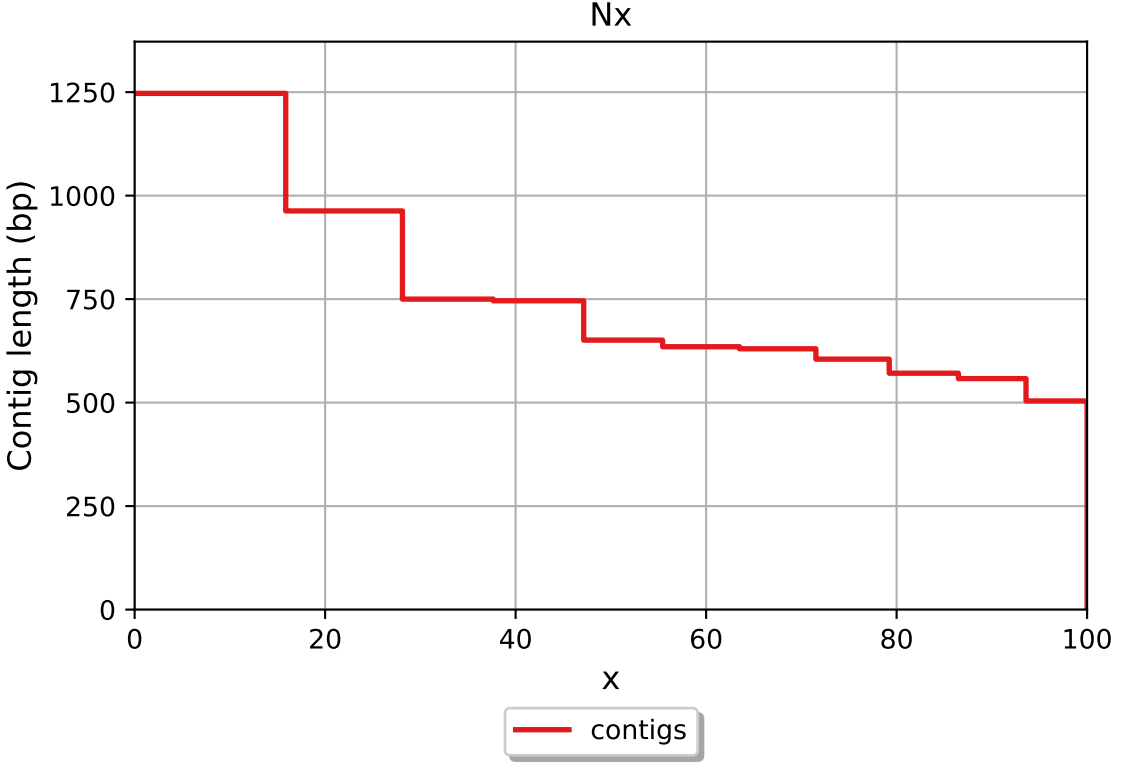
	contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	96
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	10

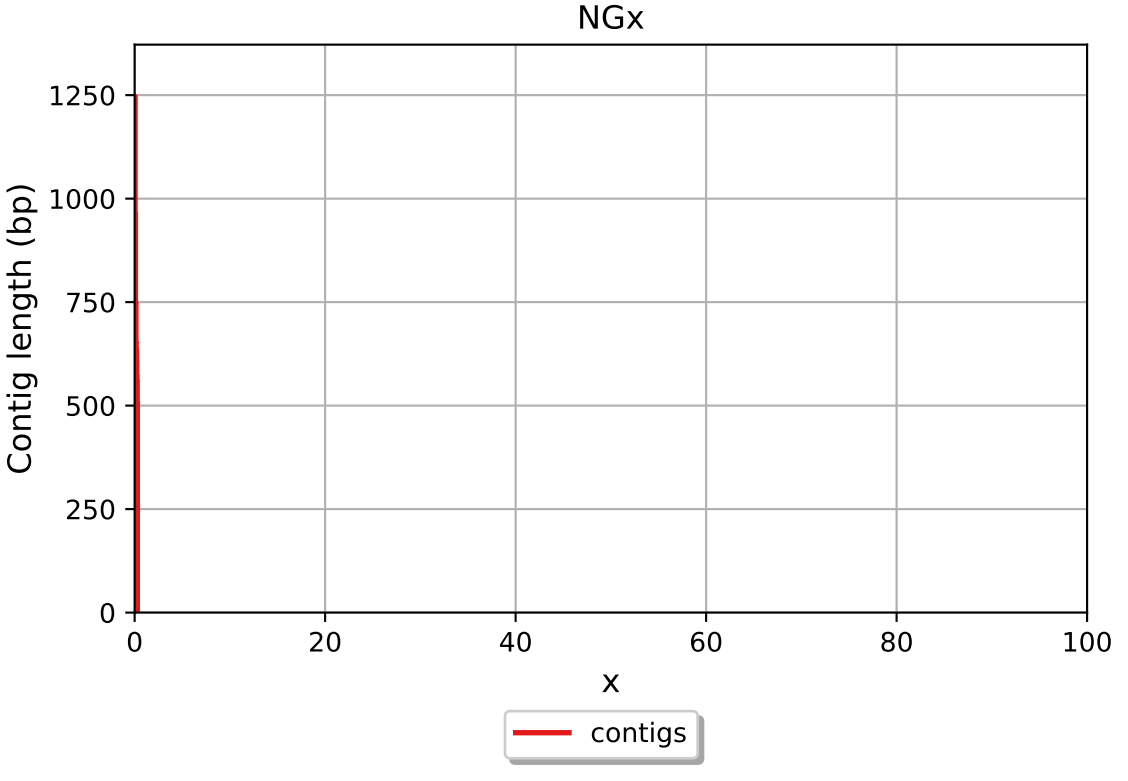
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

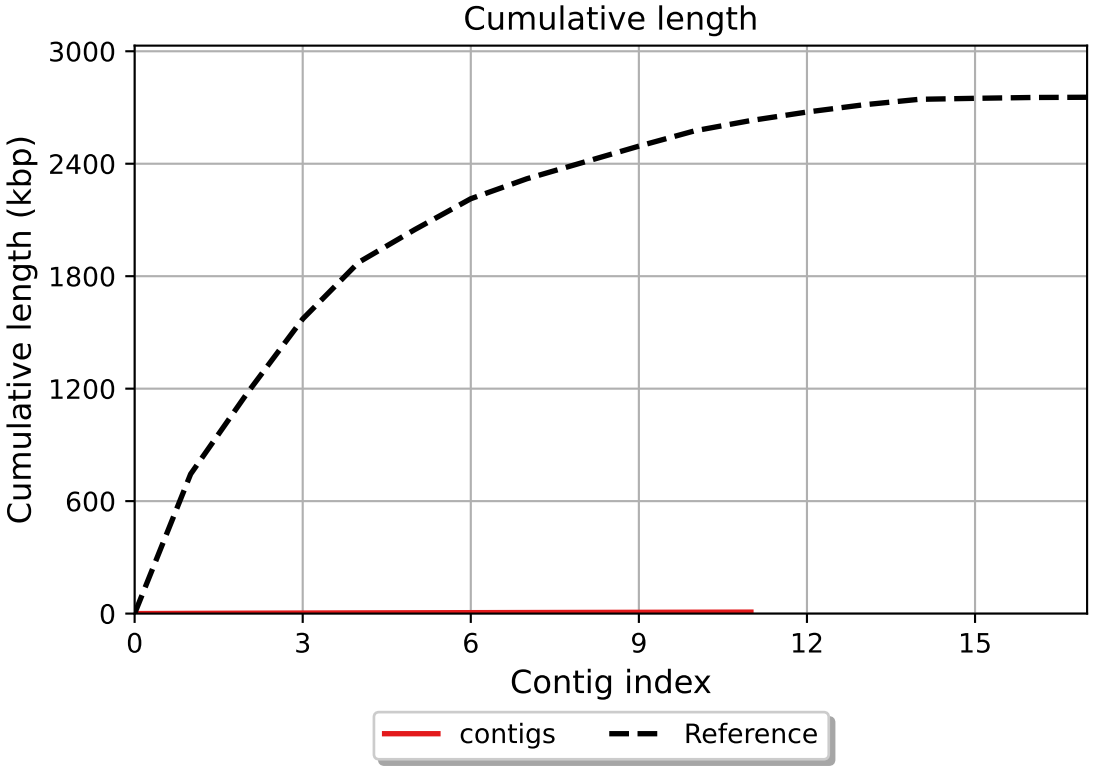
Unaligned report

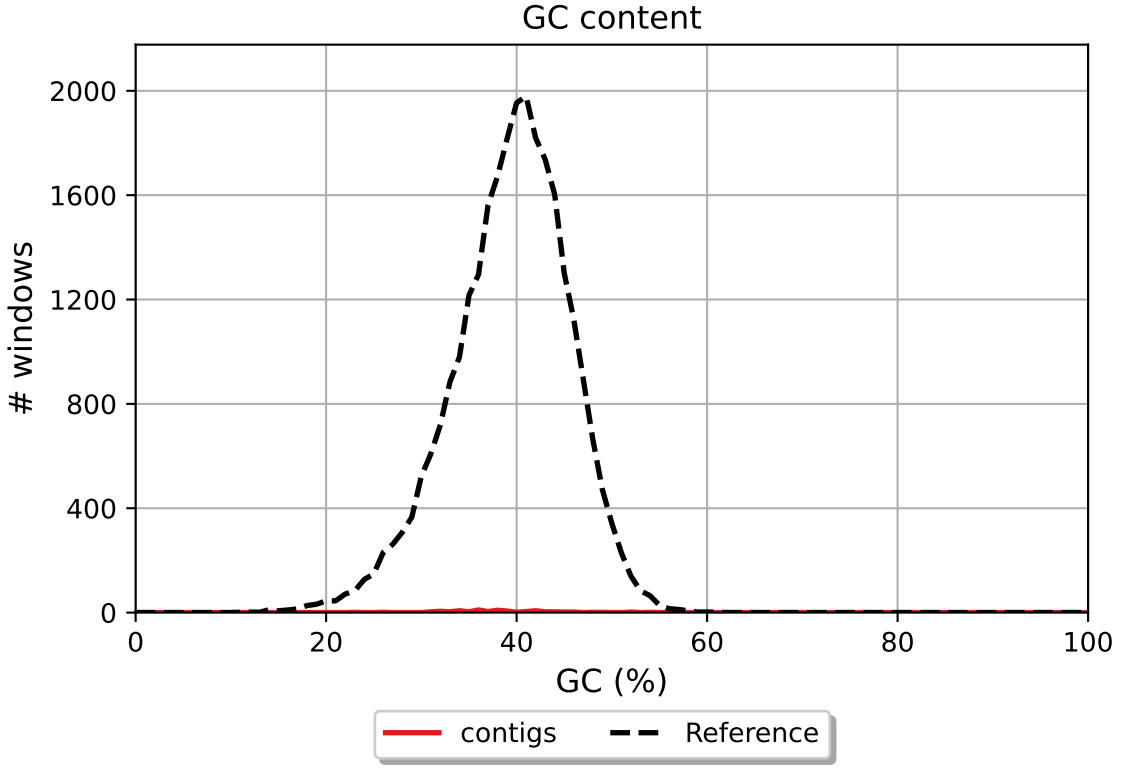
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

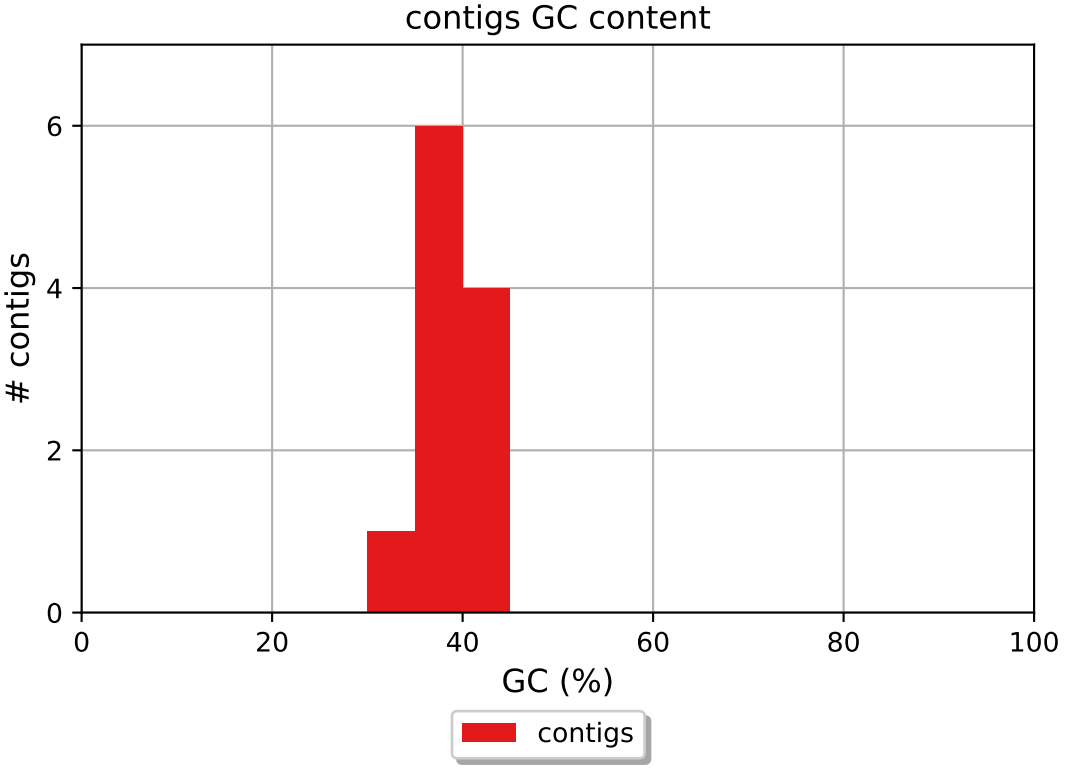
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

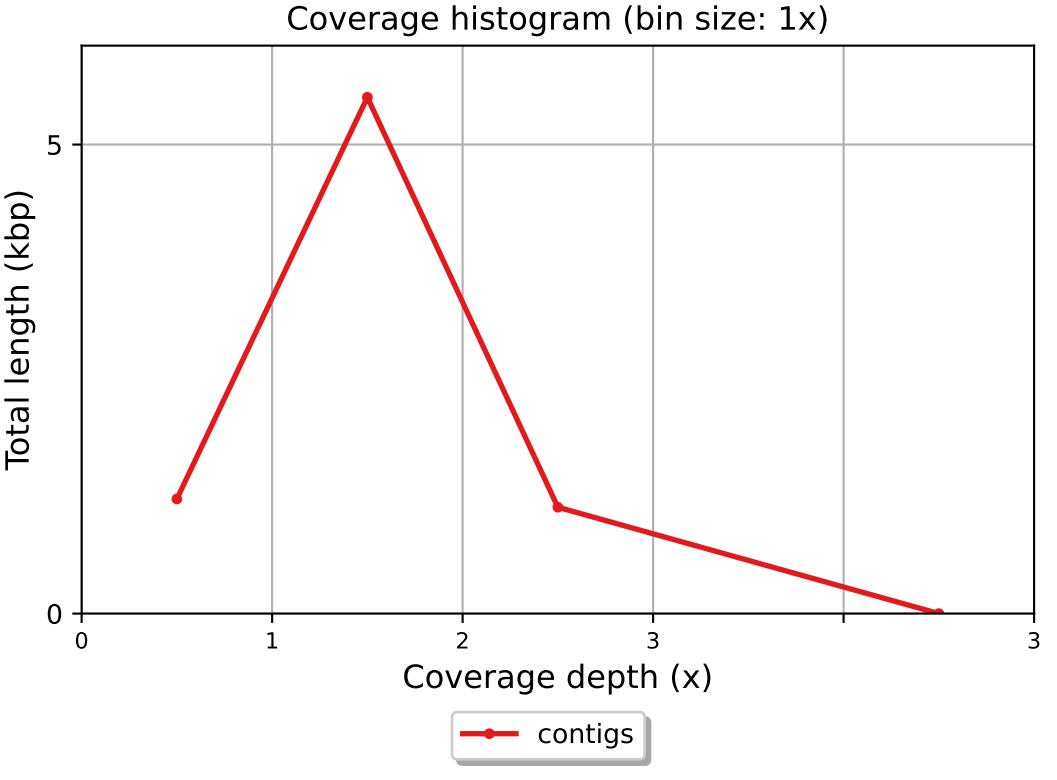

Nx
Contig length (bp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
contigs

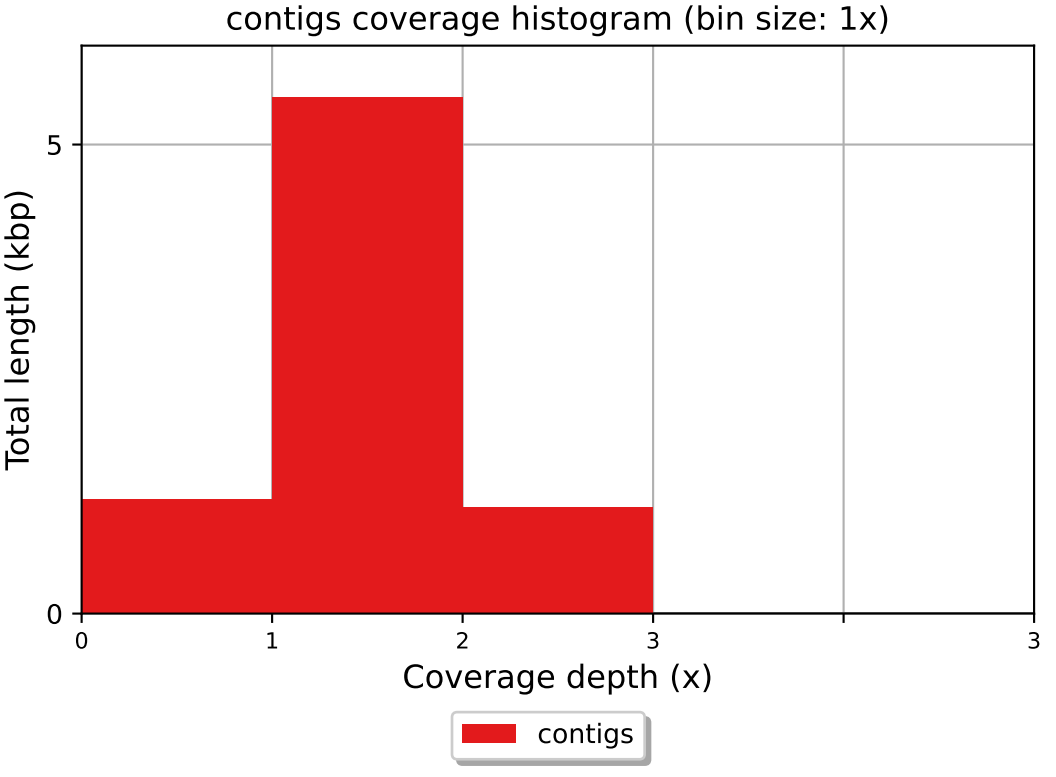

NGx
Contig length (bp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
contigs

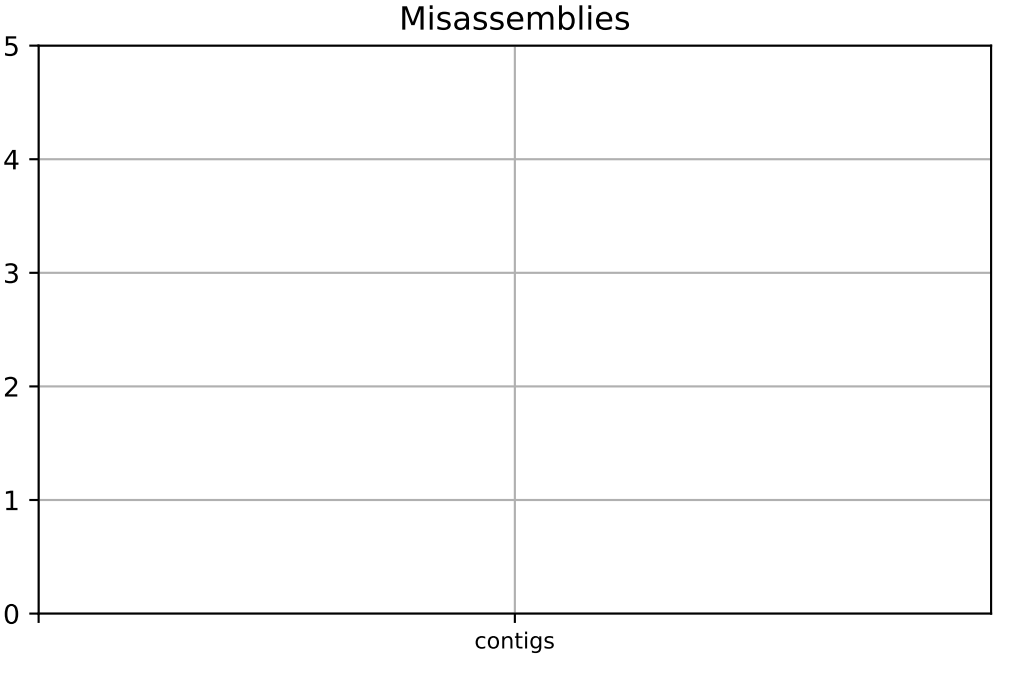

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
3
6
9
12
15
Contig index
contigs
Reference

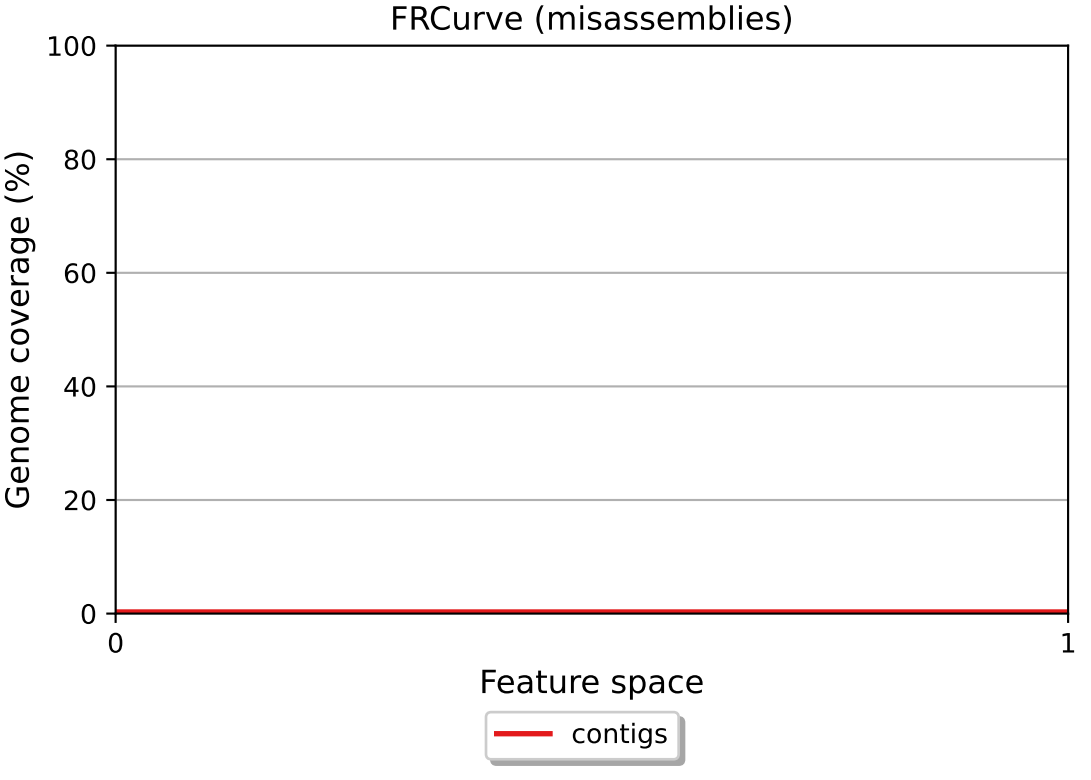

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
contigs
Reference

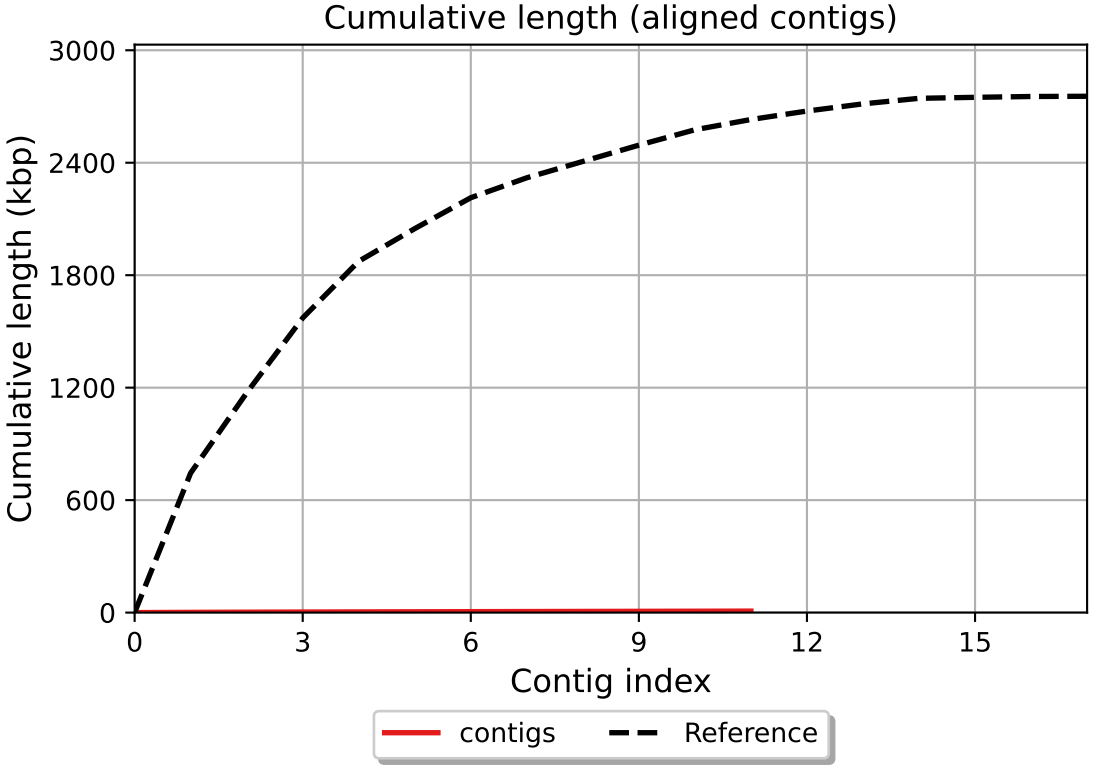

contigs GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
contigs

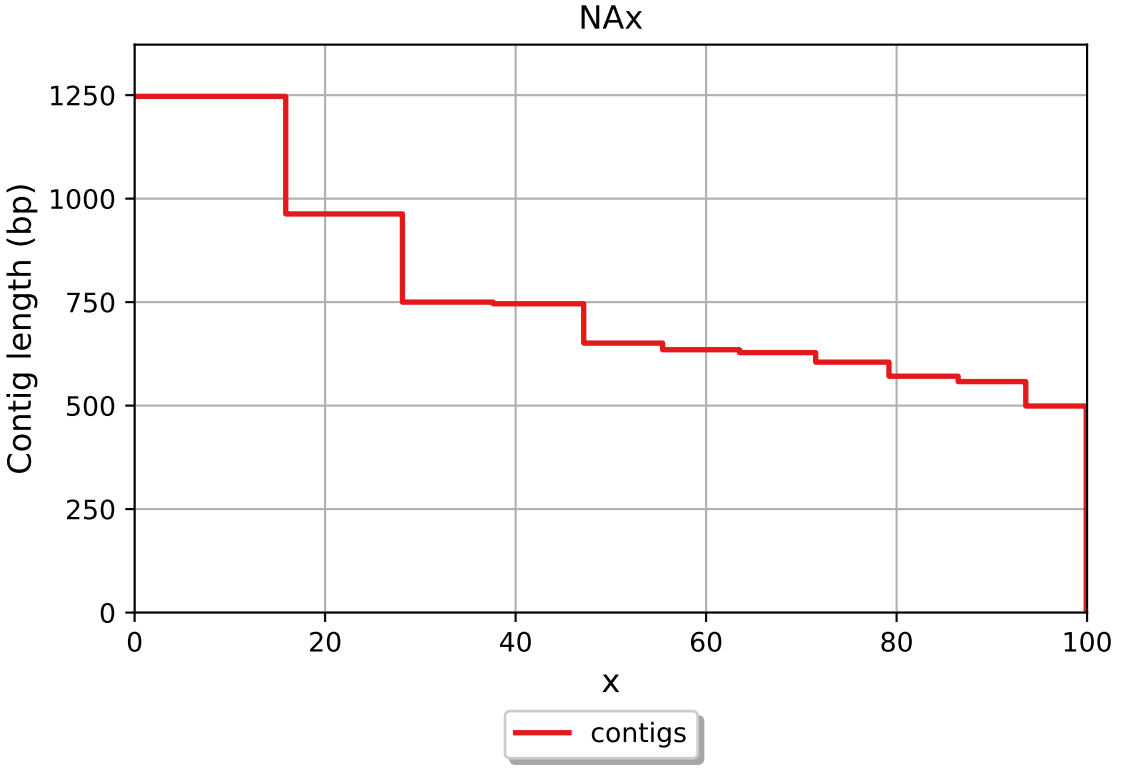

Coverage histogram (bin size: 1x)
Total length (kbp)
5
0
0
1
2
3
3
Coverage depth (x)
contigs

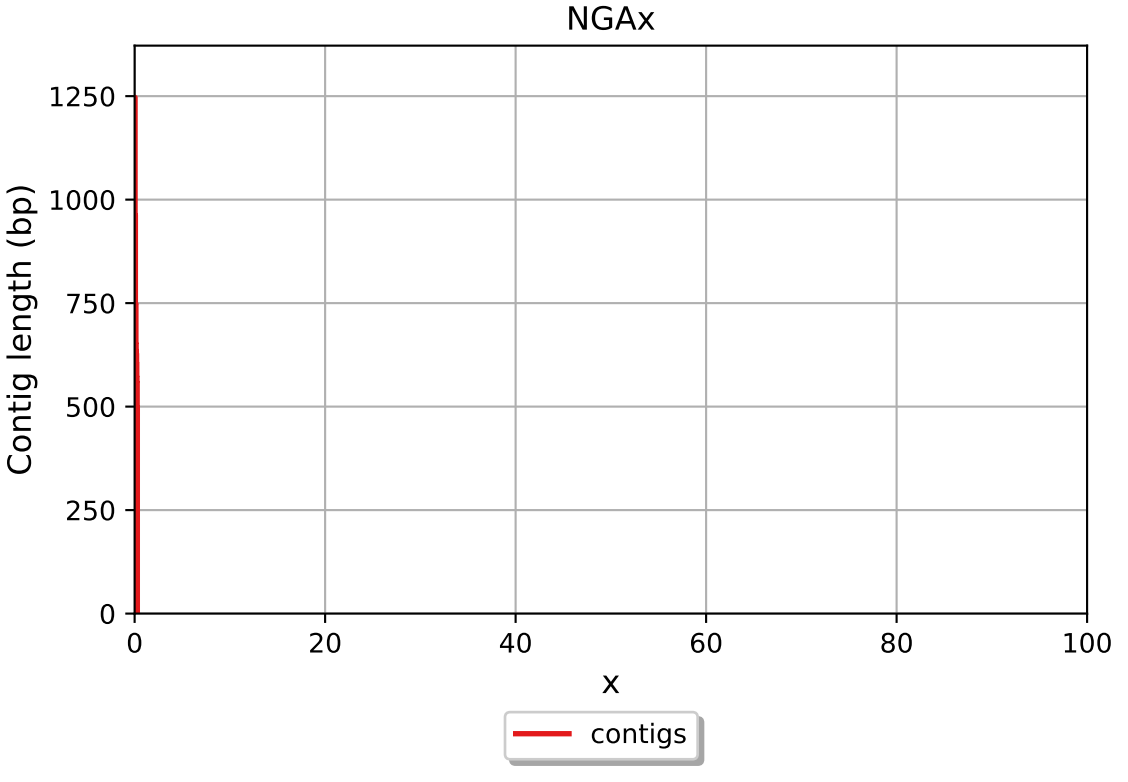

contigs coverage histogram (bin size: 1x)
Total length (kbp)
5
0
0
1
2
3
3
Coverage depth (x)
contigs


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)
3000
2400
1800
1200
600
0
0
3
6
9
12
15
Contig index
contigs
Reference


NAx
Contig length (bp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (bp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
contigs