Report	contigs
# contigs (>= 0 bp)	7
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	179607
Total length (>= 1000 bp)	177919
Total length (>= 5000 bp)	173211
Total length (>= 10000 bp)	167264
Total length (>= 25000 bp)	167264
Total length (>= 50000 bp)	132140
# contigs	6
Largest contig	132140
Total length	179288
Reference length	197394
GC (%)	33.59
Reference GC (%)	33.43
N50	132140
NG50	132140
N90	35124
NG90	4708
auN	104598.0
auNG	95003.7
L50	1
LG50	1
L90	2
LG90	4
# misassemblies	4
# misassembled contigs	2
Misassembled contigs length	138087
# 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 (%)	90.751
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.81
# indels per 100 kbp	3.90
Largest alignment	59758
Total aligned length	179288
NA50	35879
NGA50	35124
NA90	34011
NGA90	790
auNA	40771.8
auNGA	37032.0
LA50	2
LGA50	3
LA90	4
LGA90	8

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

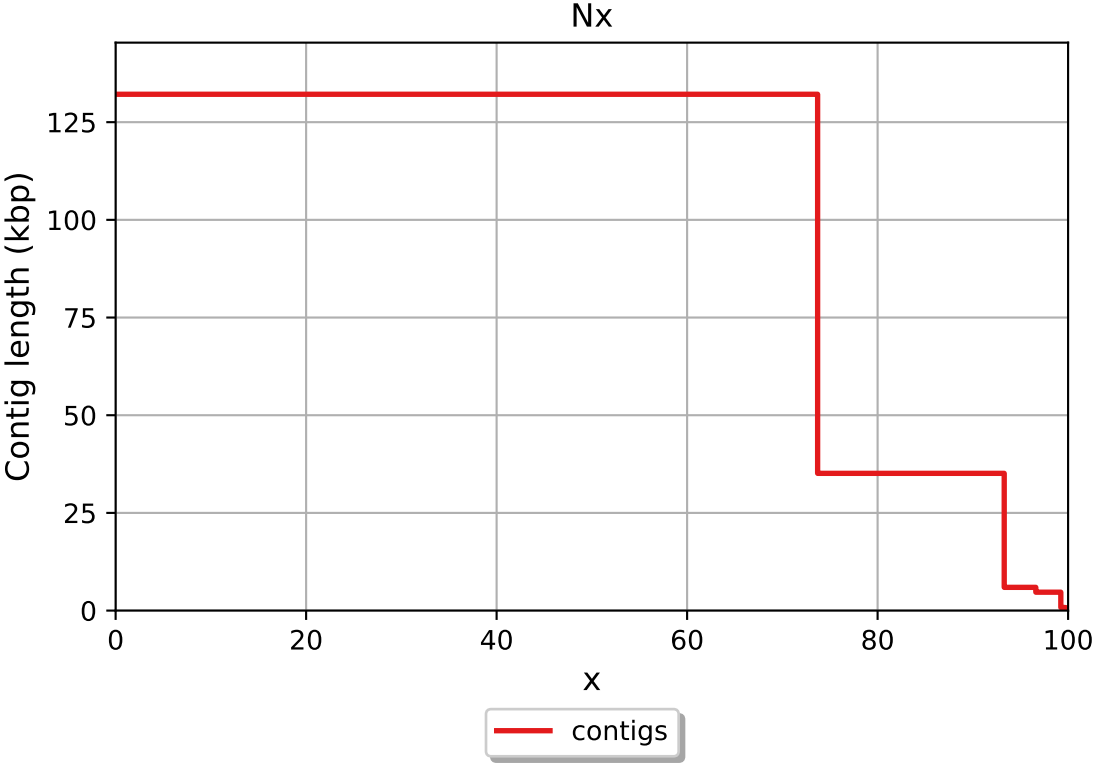
	contigs
# misassemblies	4
# contig misassemblies	4
# c. relocations	2
# c. translocations	0
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	138087
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	14
# indels	7
# indels (<= 5 bp)	7
# indels (> 5 bp)	0
Indels length	9

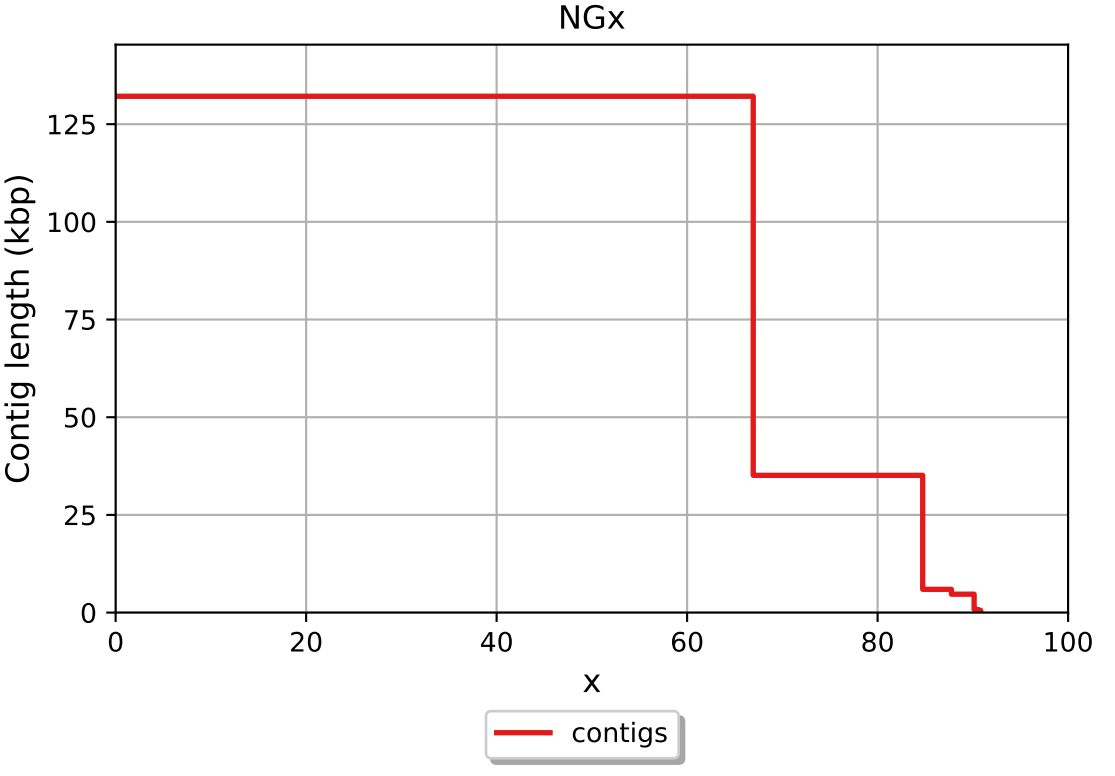
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

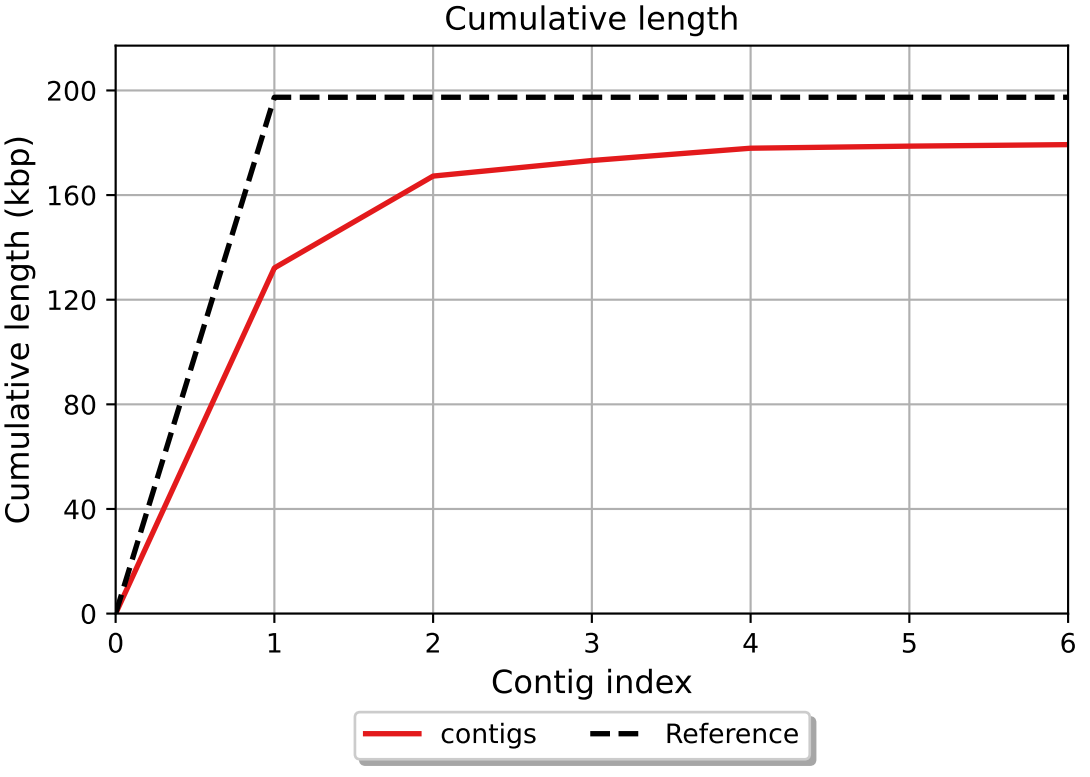
Unaligned report

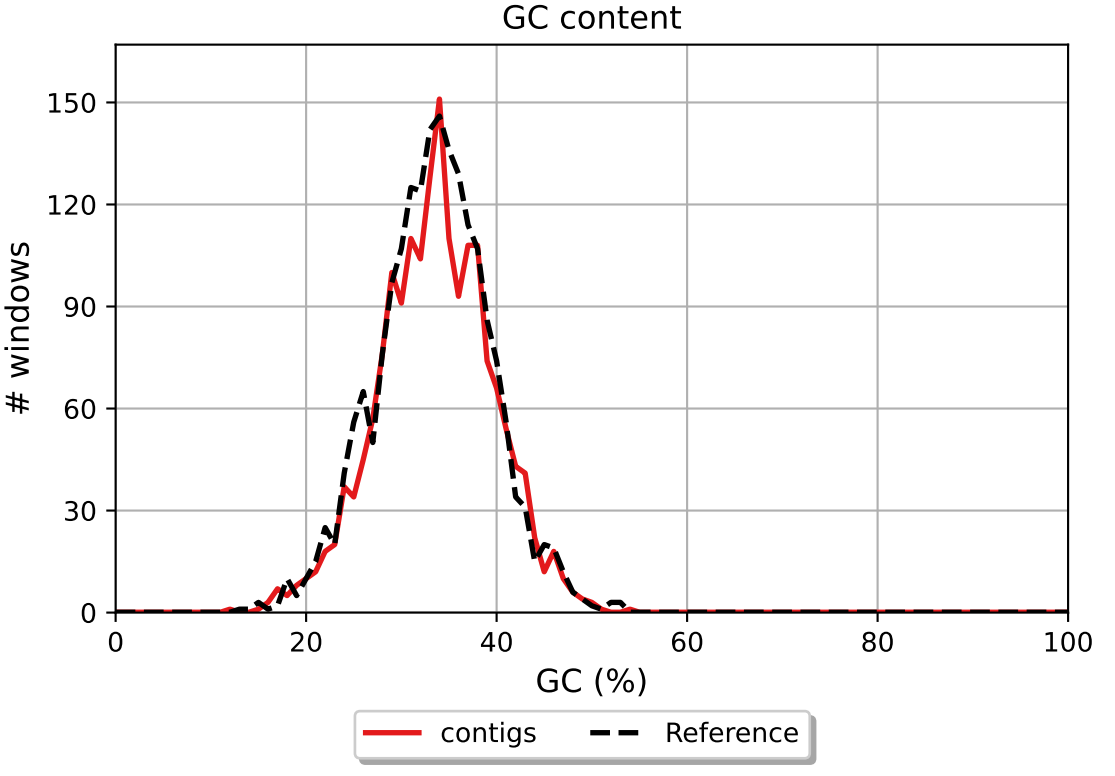
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

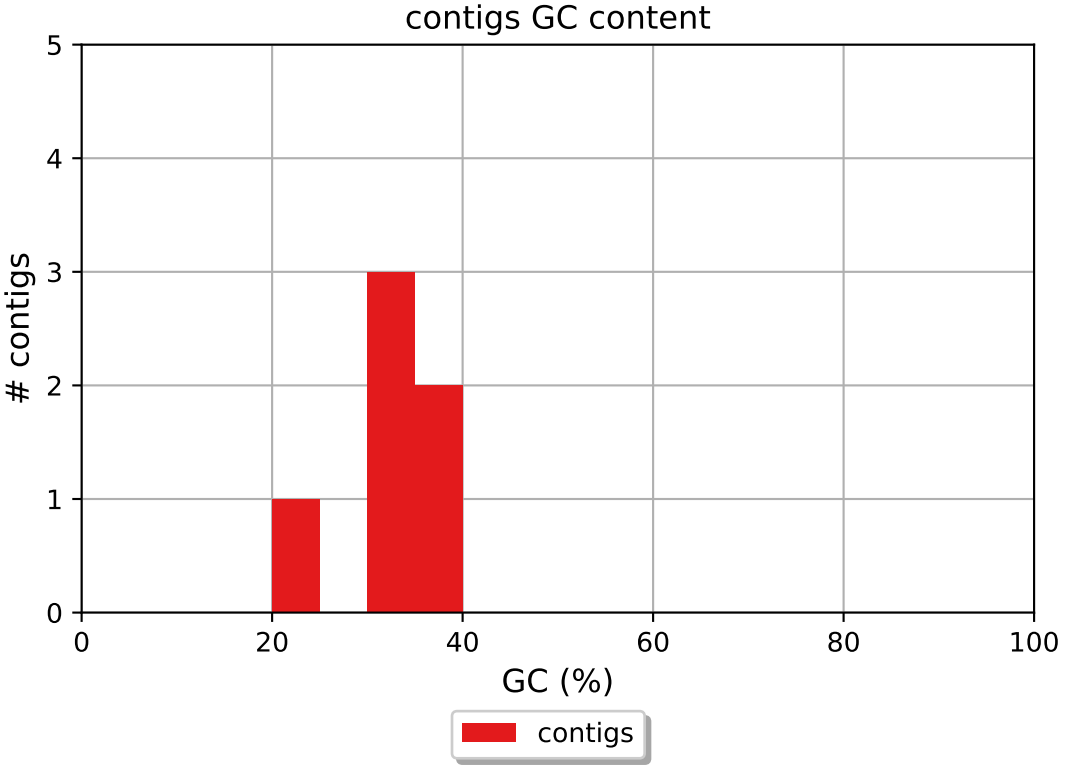
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

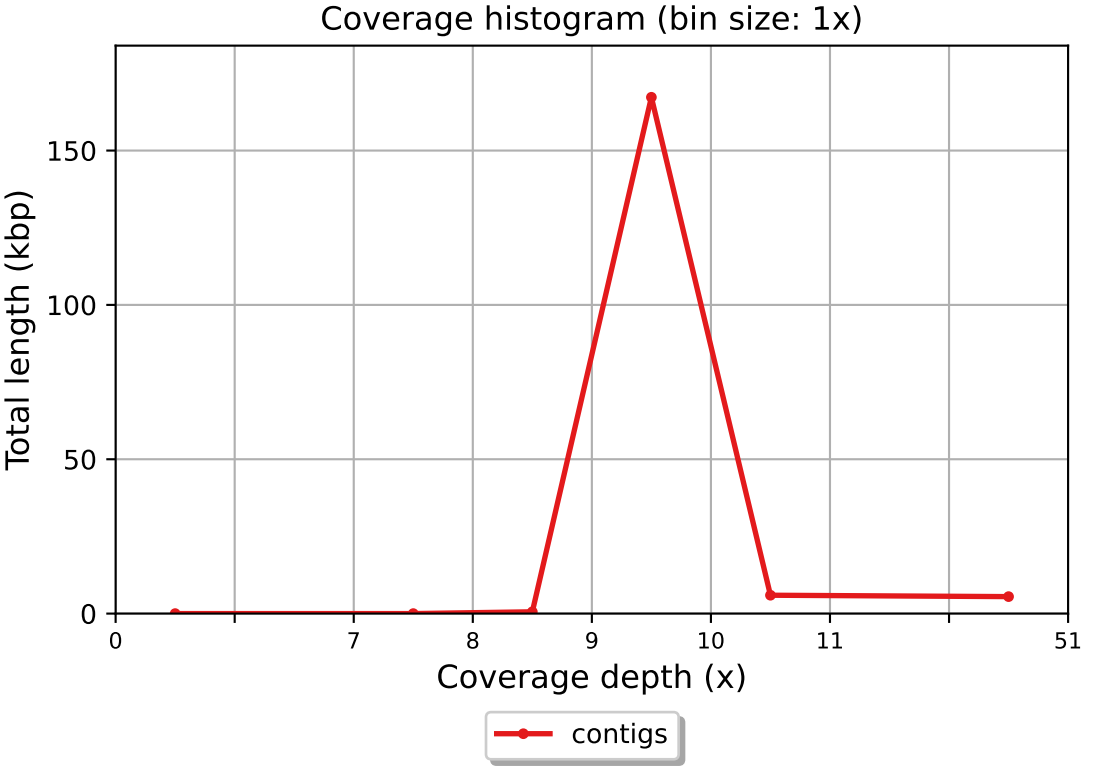

Nx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
contigs

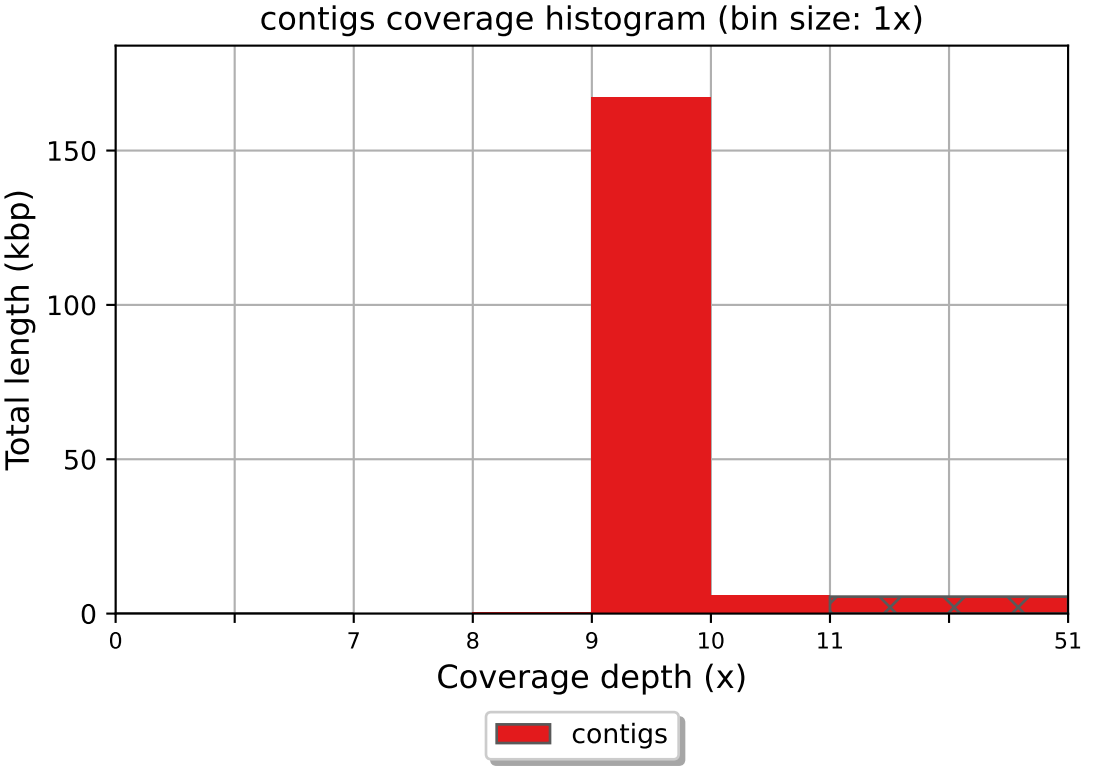

NGx
Contig length (kbp)
125
100
75
50
25
0
0
20
40
60
80
100
x
contigs


Cumulative length
Cumulative length (kbp)
200
160
120
80
40
0
0
1
2
3
4
5
6
Contig index
contigs
Reference

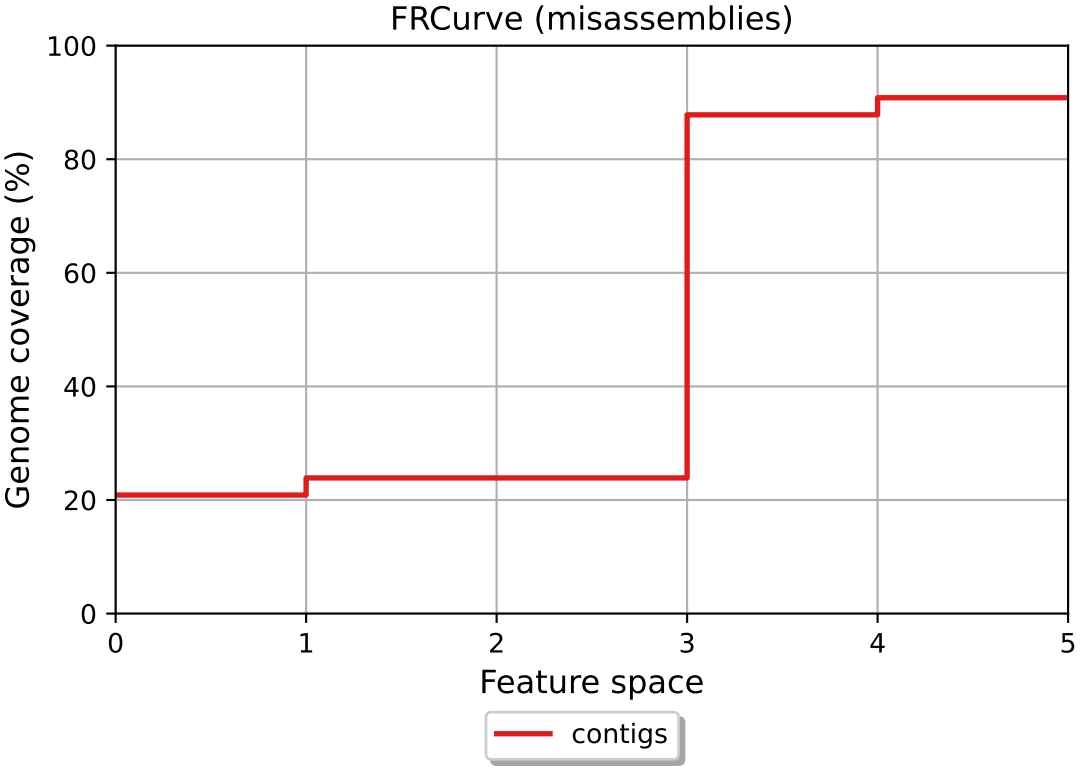

GC content
windows
150
120
90
60
30
0
0
20
40
60
80
100
GC (%)
contigs
Reference

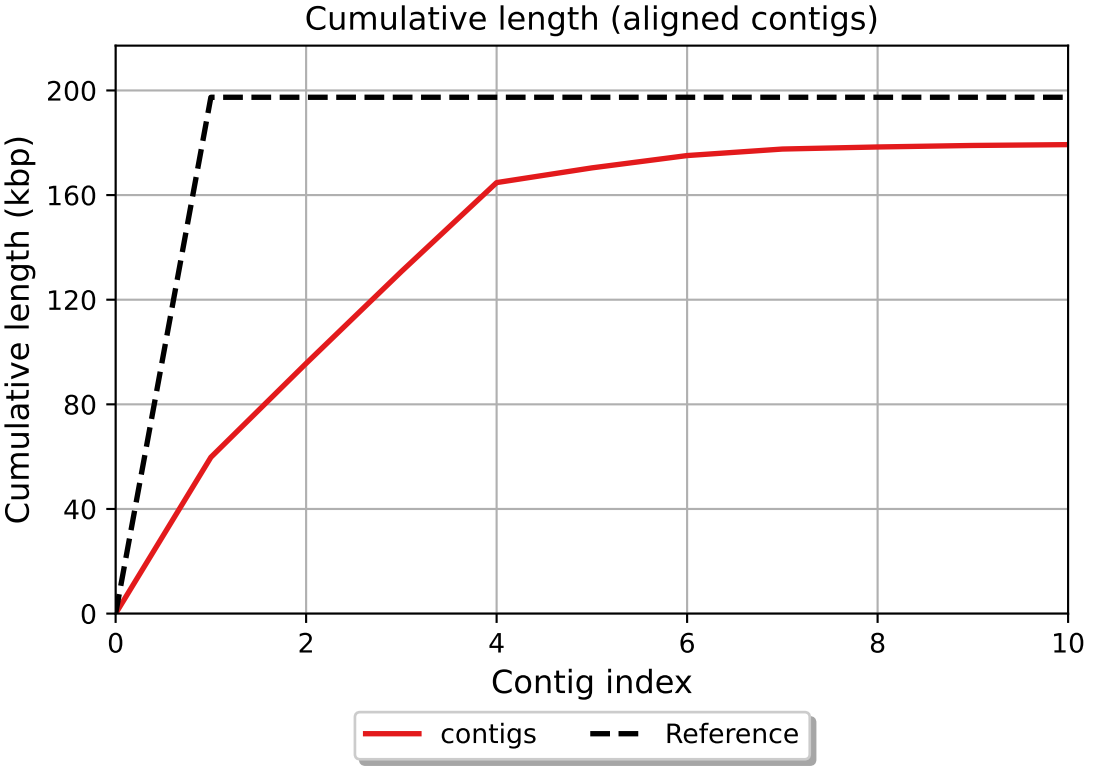

contigs GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs

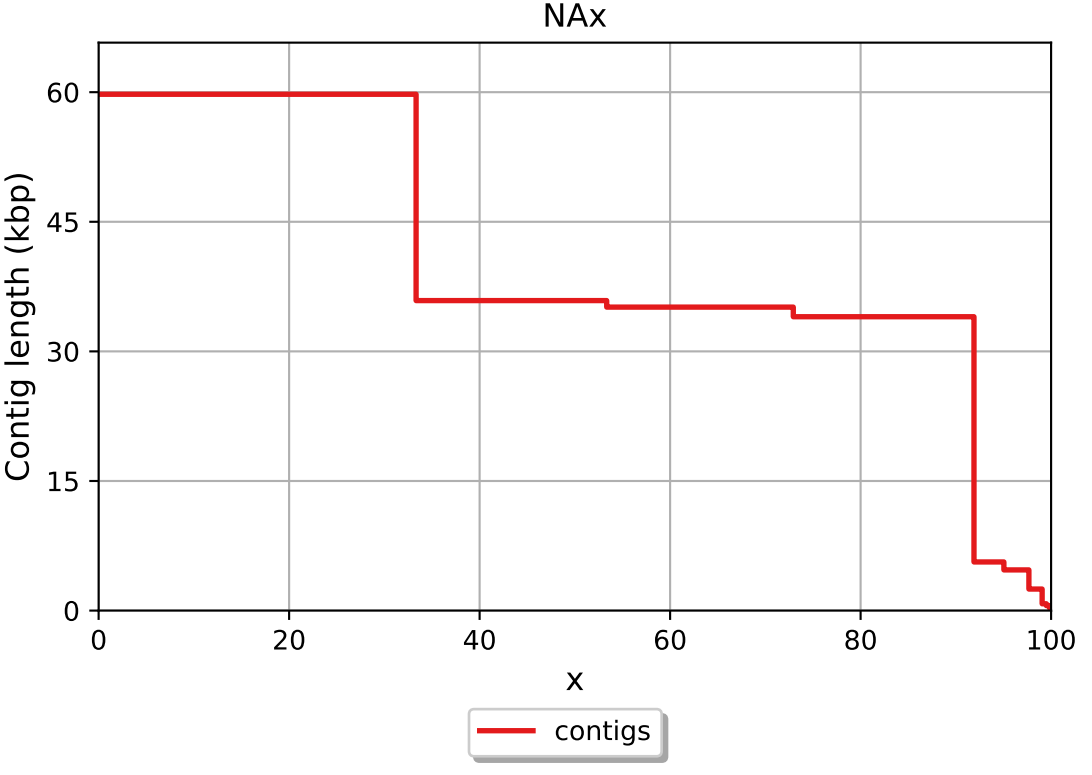

Coverage histogram (bin size: 1x)
Total length (kbp)
150
100
50
0
0
7
8
9
10
11
51
Coverage depth (x)
contigs

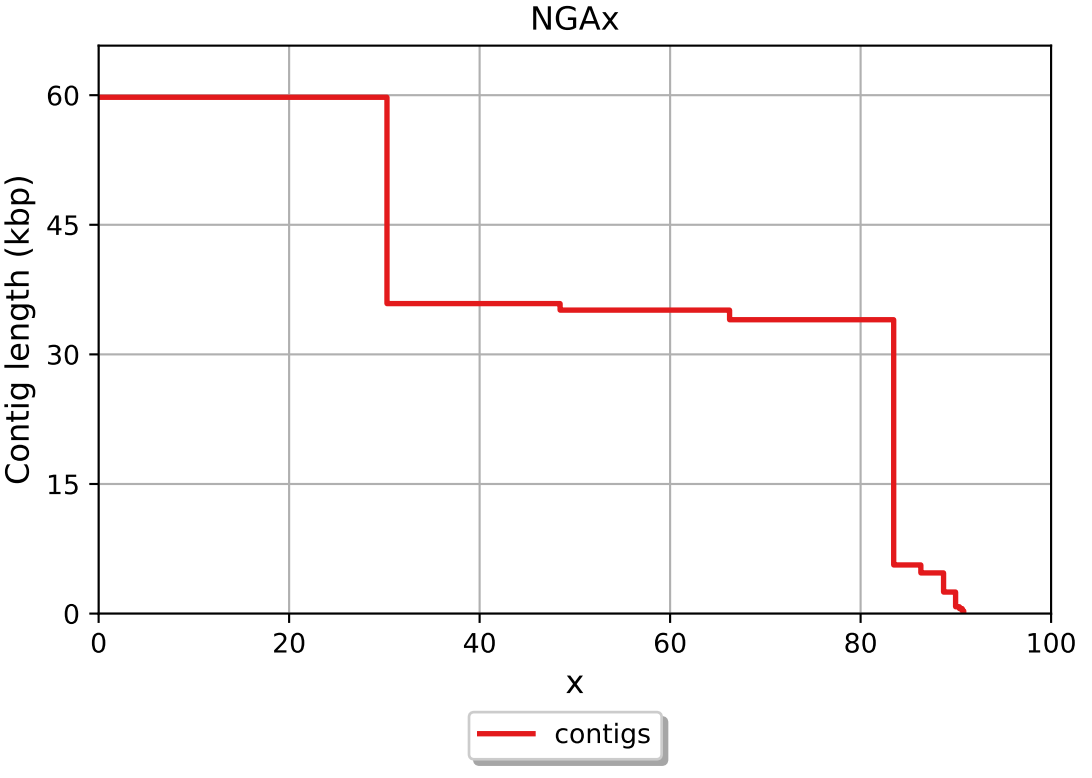

contigs coverage histogram (bin size: 1x)
Total length (kbp)
150
100
50
0
0
7
8
9
10
11
51
Coverage depth (x)
contigs

Misassemblies
5
4
3
2
1
0
contigs
relocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
5
Feature space
contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
200
160
120
80
40
0
0
2
4
6
8
10
Contig index
contigs
Reference


NAx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
60
45
30
15
0
0
20
40
60
80
100
x
contigs