Report	contigs
# contigs (>= 0 bp)	205
# contigs (>= 1000 bp)	118
# contigs (>= 5000 bp)	83
# contigs (>= 10000 bp)	75
# contigs (>= 25000 bp)	58
# contigs (>= 50000 bp)	37
Total length (>= 0 bp)	4559356
Total length (>= 1000 bp)	4540236
Total length (>= 5000 bp)	4462702
Total length (>= 10000 bp)	4406717
Total length (>= 25000 bp)	4140684
Total length (>= 50000 bp)	3413284
# contigs	124
Largest contig	221601
Total length	4544603
Reference length	4639675
GC (%)	50.72
Reference GC (%)	50.79
N50	71324
NG50	69051
N90	26205
NG90	21591
auN	94028.9
auNG	92102.2
L50	18
LG50	19
L90	57
LG90	60
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	182275
# 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 (%)	97.937
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.34
# indels per 100 kbp	0.22
Largest alignment	221546
Total aligned length	4543859
NA50	71324
NGA50	69051
NA90	26205
NGA90	21324
auNA	93196.4
auNGA	91286.7
LA50	18
LGA50	19
LA90	57
LGA90	61

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

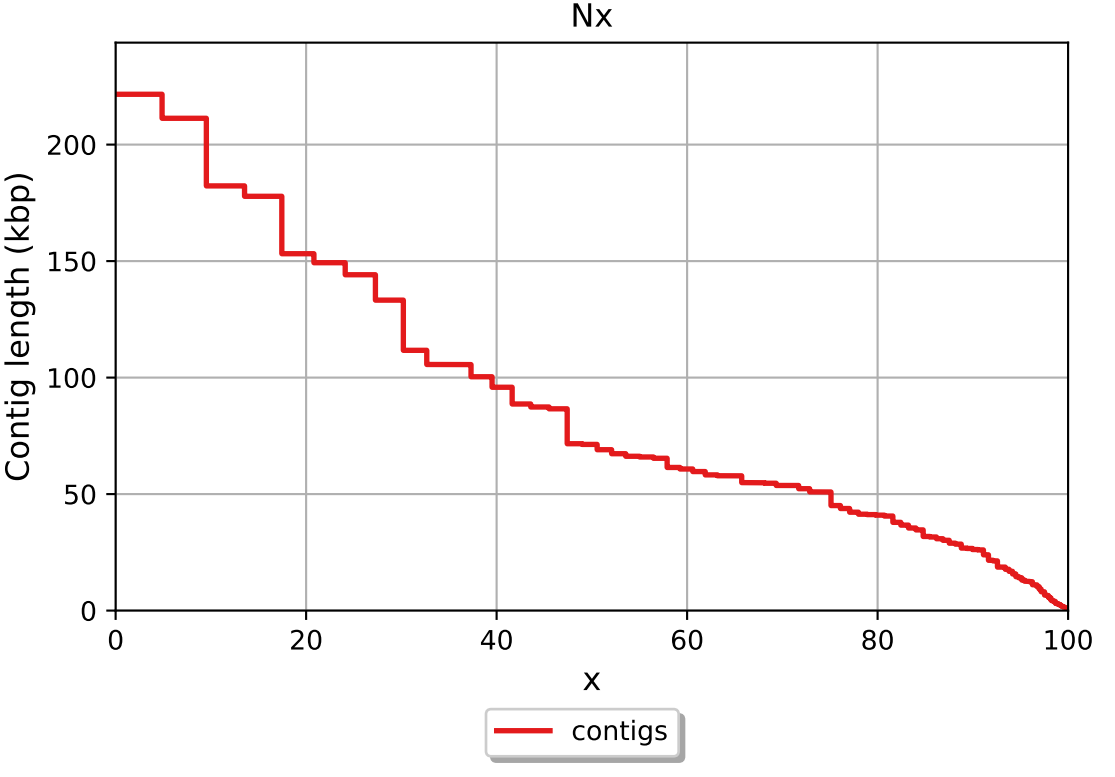
	contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	182275
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	61
# indels	10
# indels (<= 5 bp)	4
# indels (> 5 bp)	6
Indels length	1059

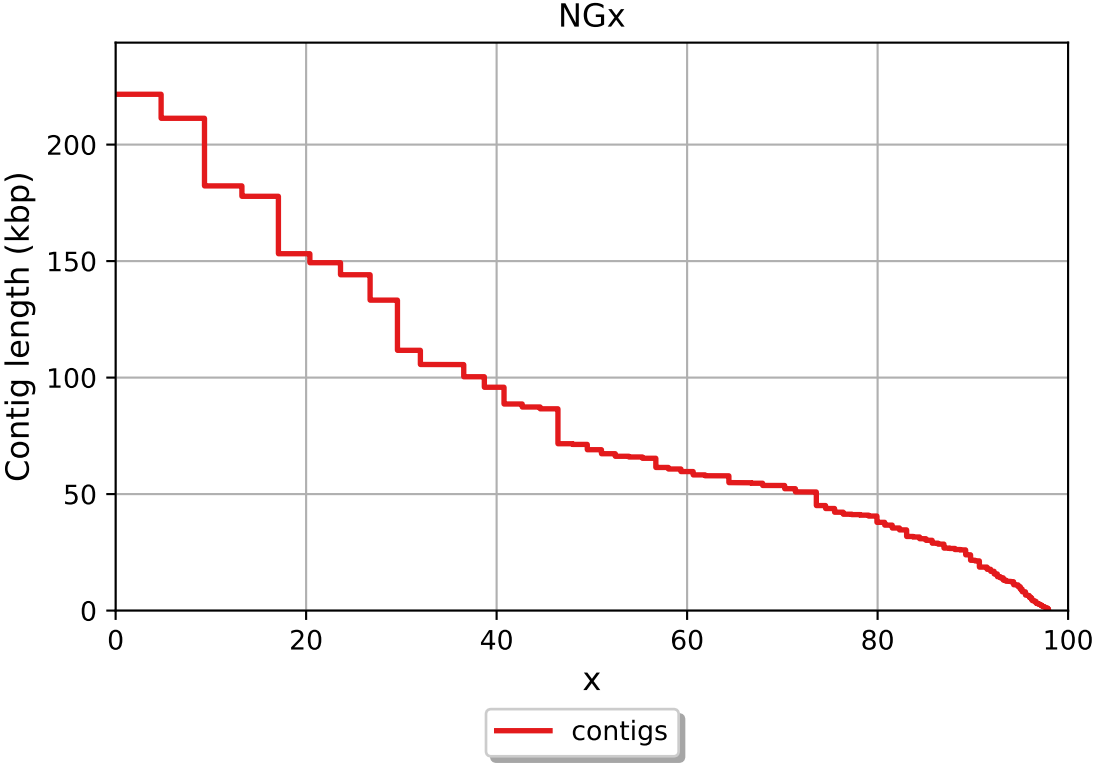
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

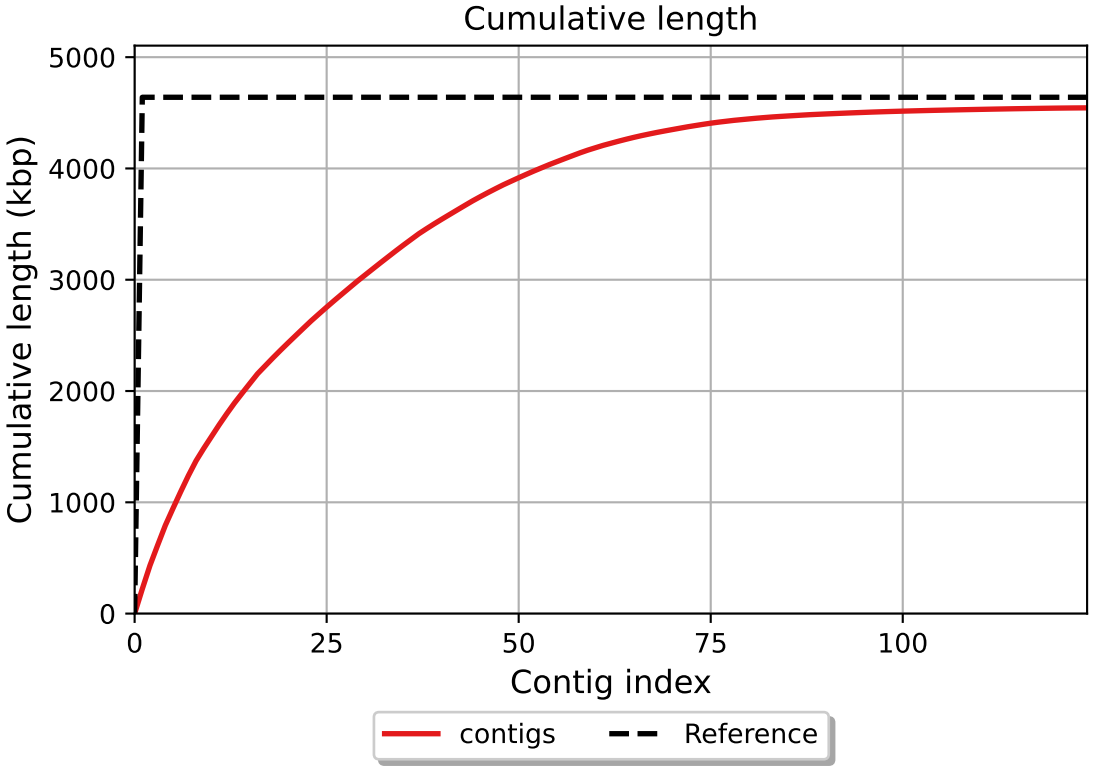
Unaligned report

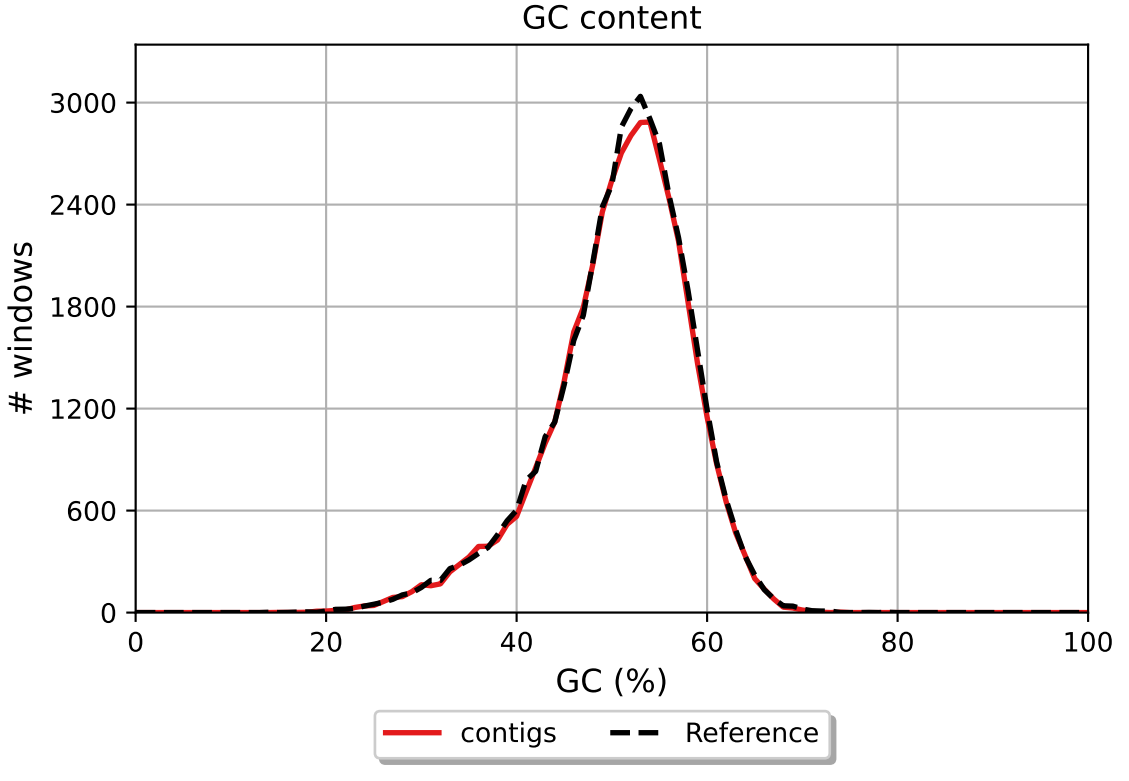
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

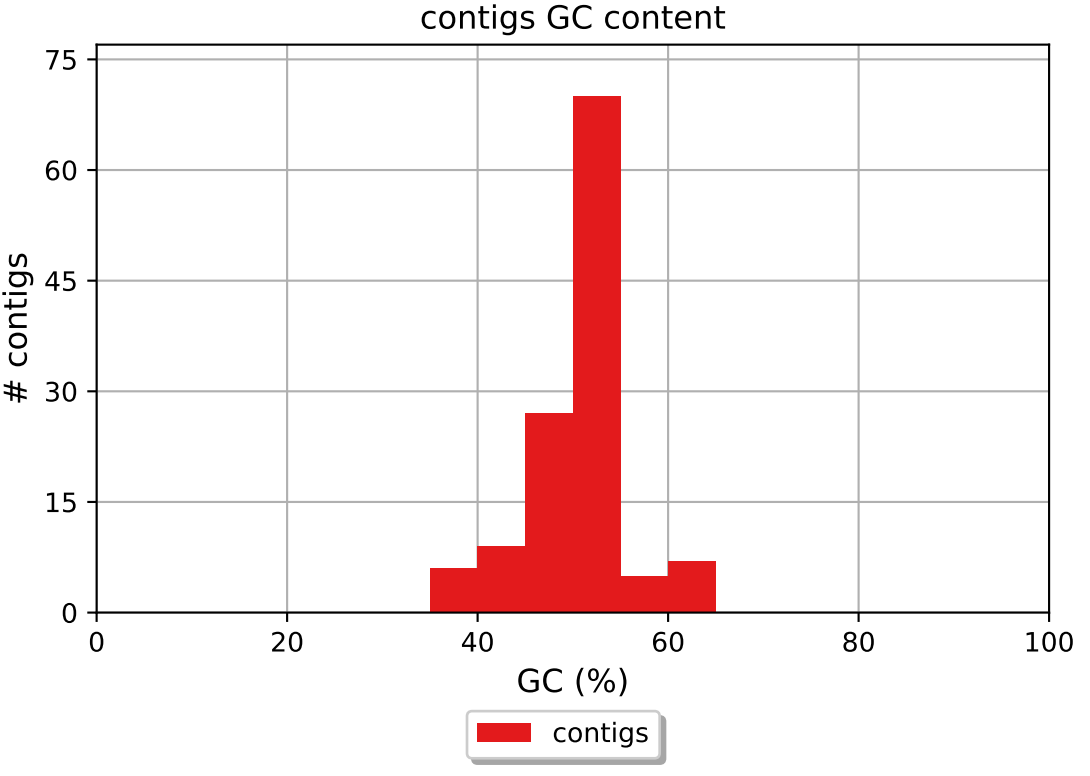
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

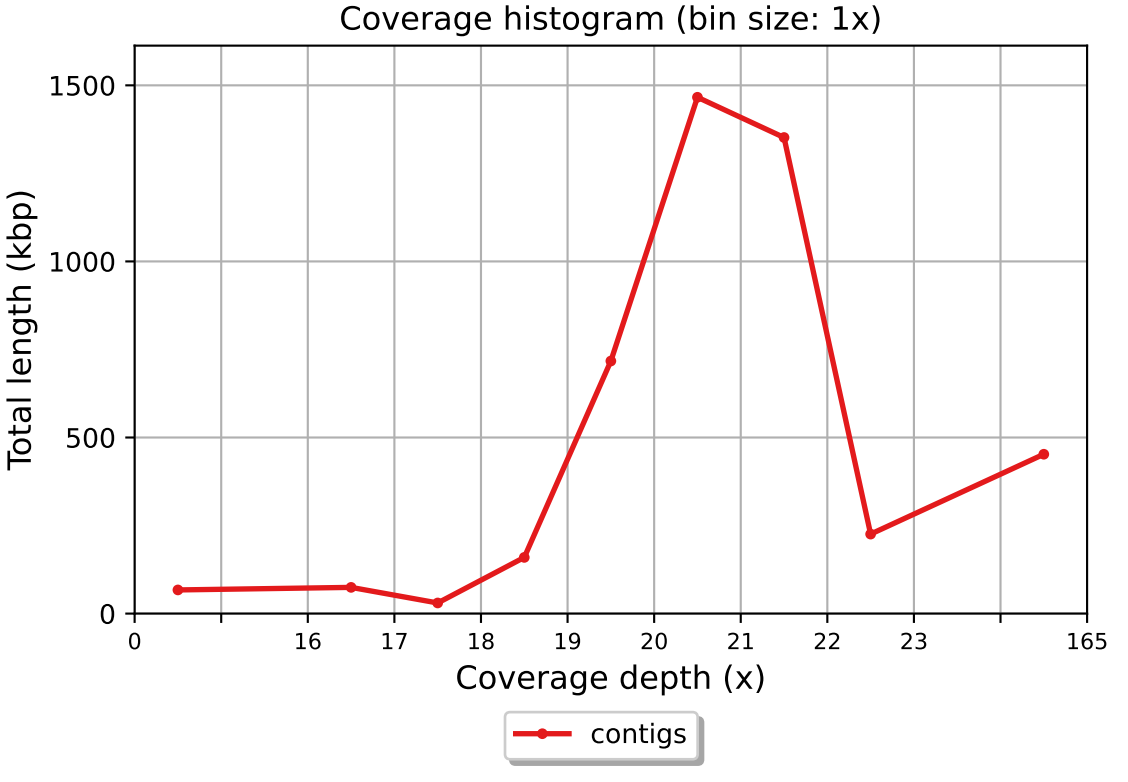

Nx
Contig length (kbp)
200
150
100
50
0
0
20
40
60
80
100
x
contigs

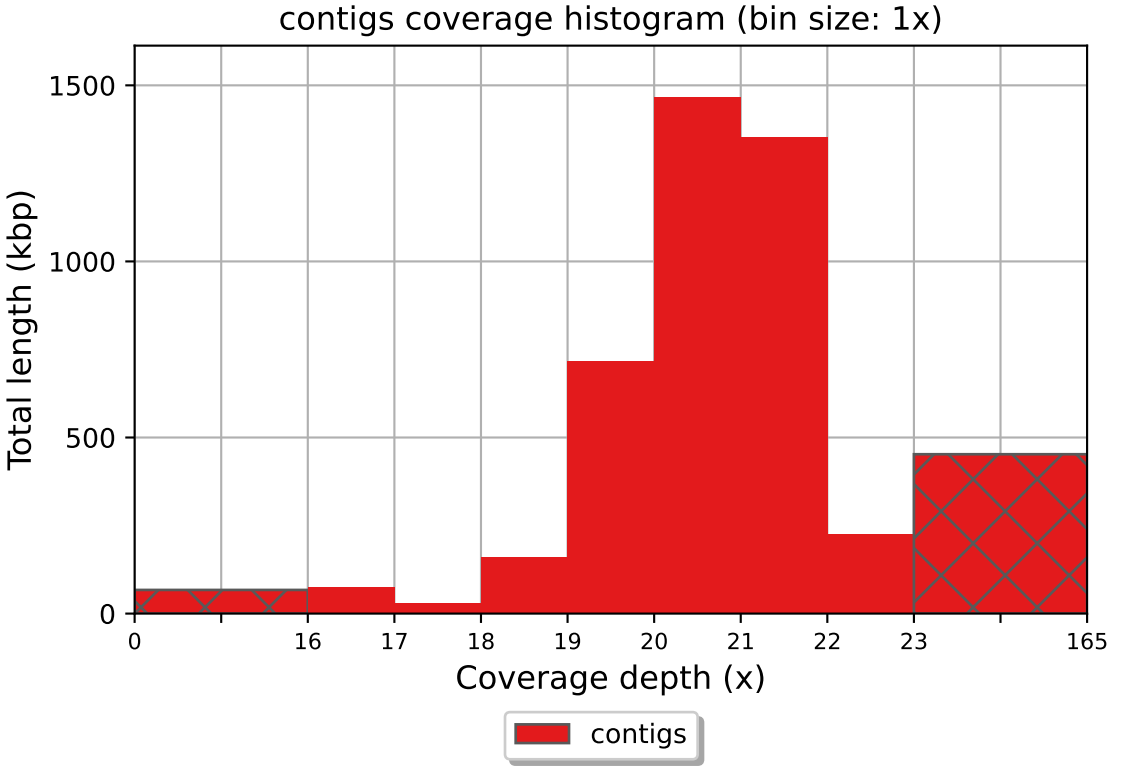

NGx
Contig length (kbp)
0
50
100
150
200
0
20
40
60
80
100
x
contigs

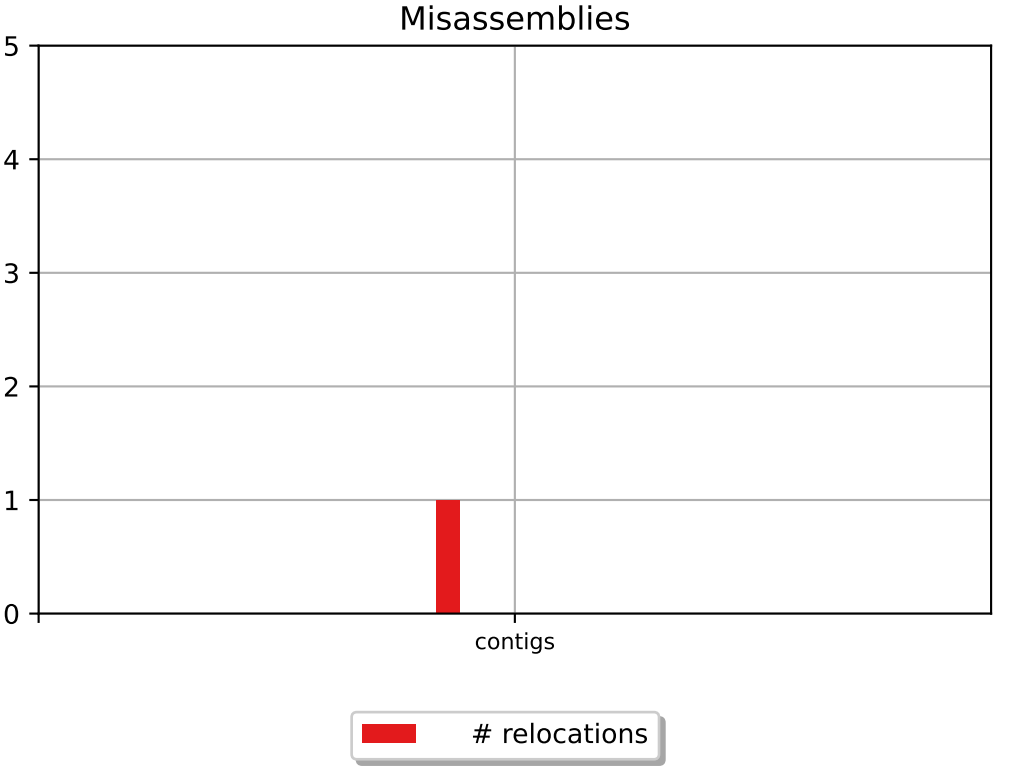

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
25
50
75
100
Contig index
contigs
Reference

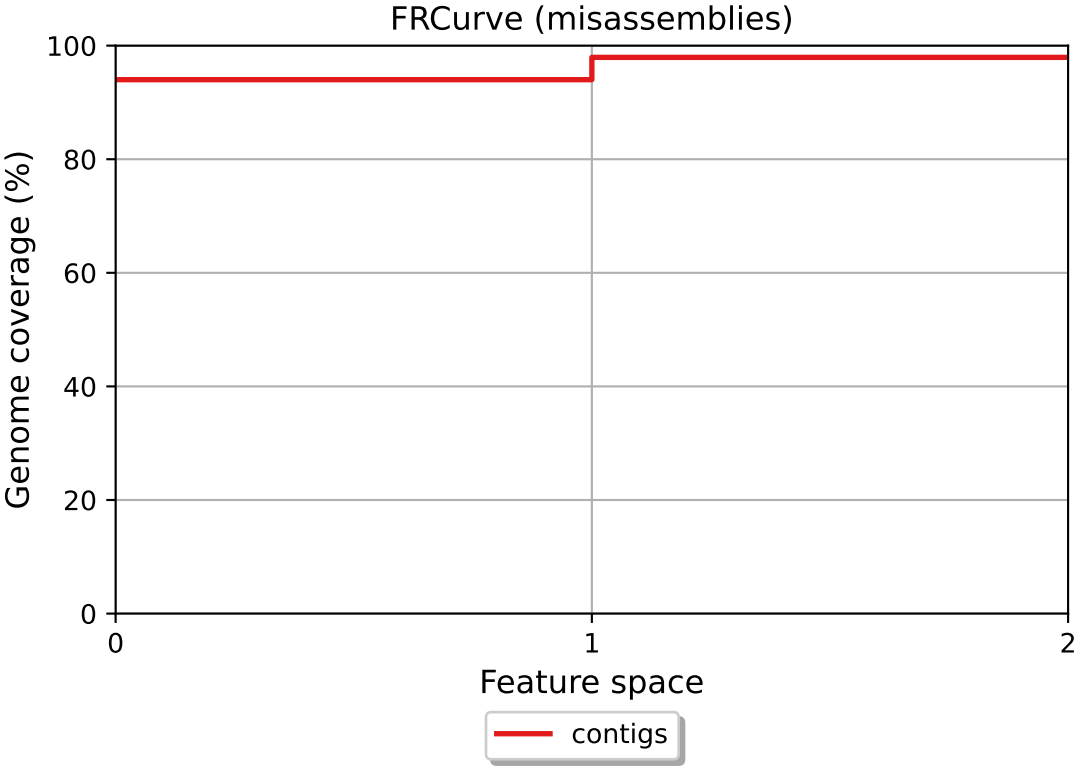

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
contigs
Reference

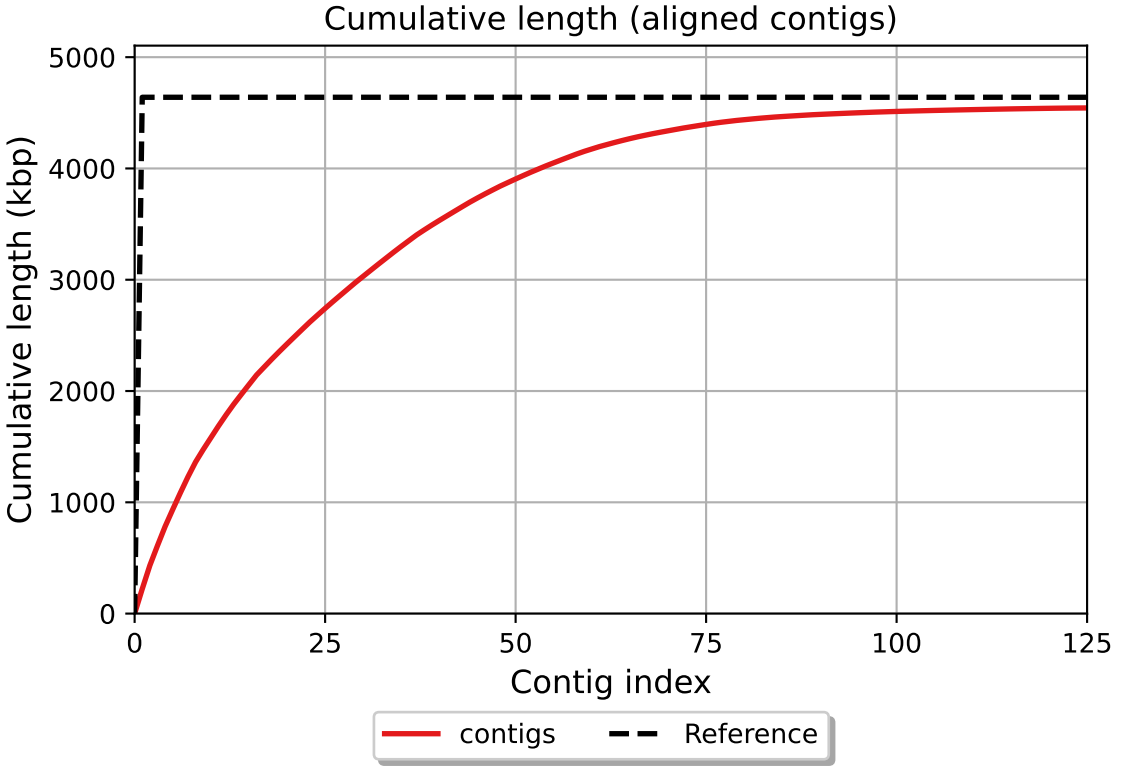

contigs GC content
contigs
GC (%)
0
15
30
45
60
75
0
20
40
60
80
100
contigs

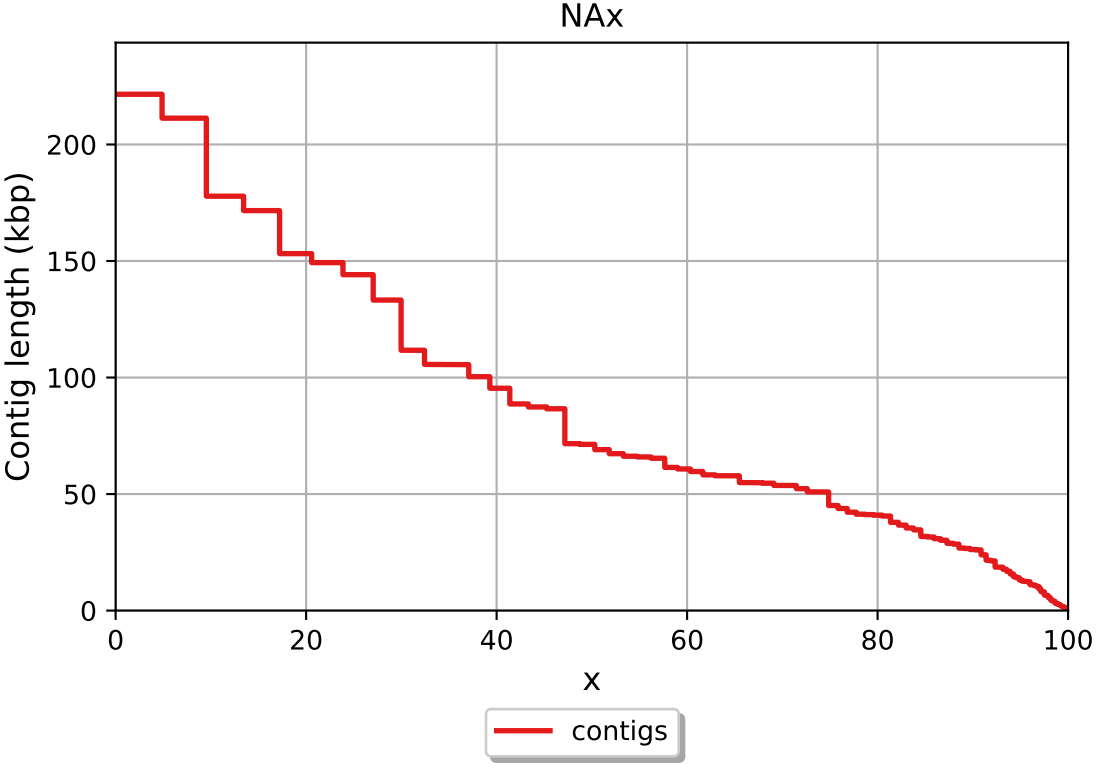

Coverage histogram (bin size: 1x)
Total length (kbp)
1500
1000
500
0
0
16
17
18
19
20
21
22
23
165
Coverage depth (x)
contigs

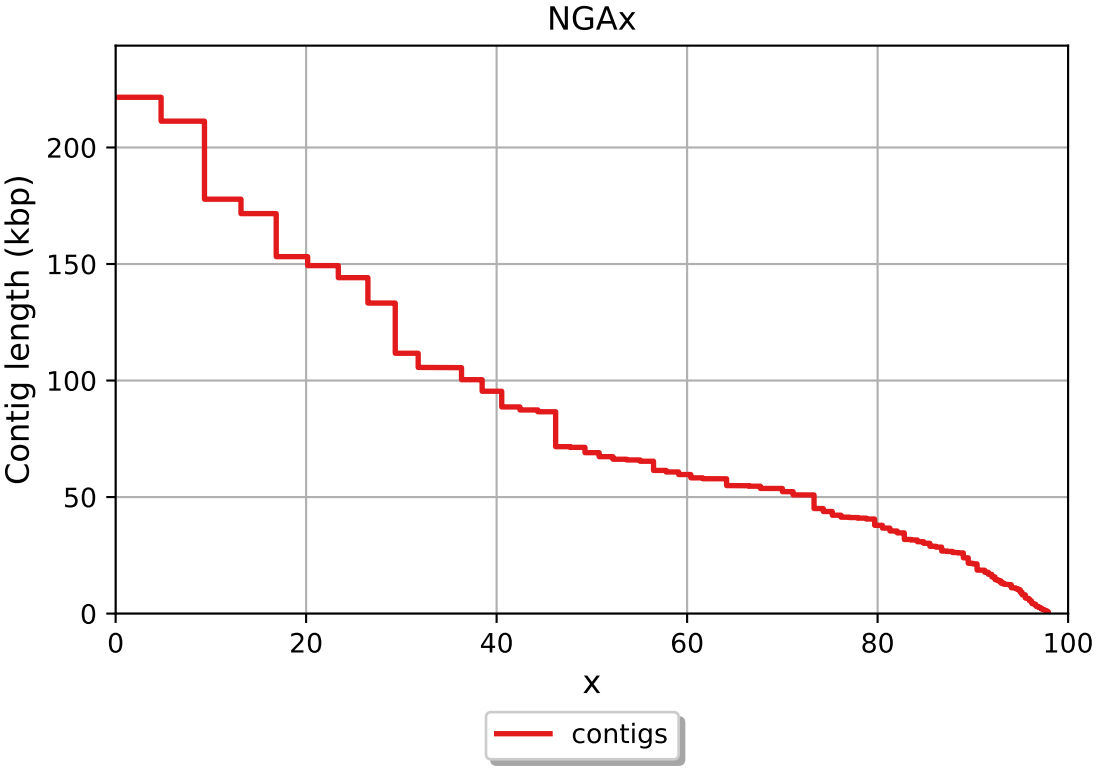

contigs coverage histogram (bin size: 1x)
Total length (kbp)
1500
1000
500
0
0
16
17
18
19
20
21
22
23
165
Coverage depth (x)
contigs


Misassemblies
5
4
3
2
1
0
contigs
relocations


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


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
25
50
75
100
125
Contig index
contigs
Reference


NAx
Contig length (kbp)
0
50
100
150
200
0
20
40
60
80
100
x
contigs


NGAx
Contig length (kbp)
0
50
100
150
200
0
20
40
60
80
100
x
contigs