Report

	contigs_k31
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29748
Total length (>= 1000 bp)	29748
Total length (>= 5000 bp)	29748
Total length (>= 10000 bp)	29748
Total length (>= 25000 bp)	29748
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29748
Total length	29748
Reference length	30119
GC (%)	41.27
Reference GC (%)	41.24
N50	29748
NG50	29748
N90	29748
NG90	29748
auN	29748.0
auNG	29381.6
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 (%)	98.768
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	29748
Total aligned length	29748
NA50	29748
NGA50	29748
NA90	29748
NGA90	29748
auNA	29748.0
auNGA	29381.6
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

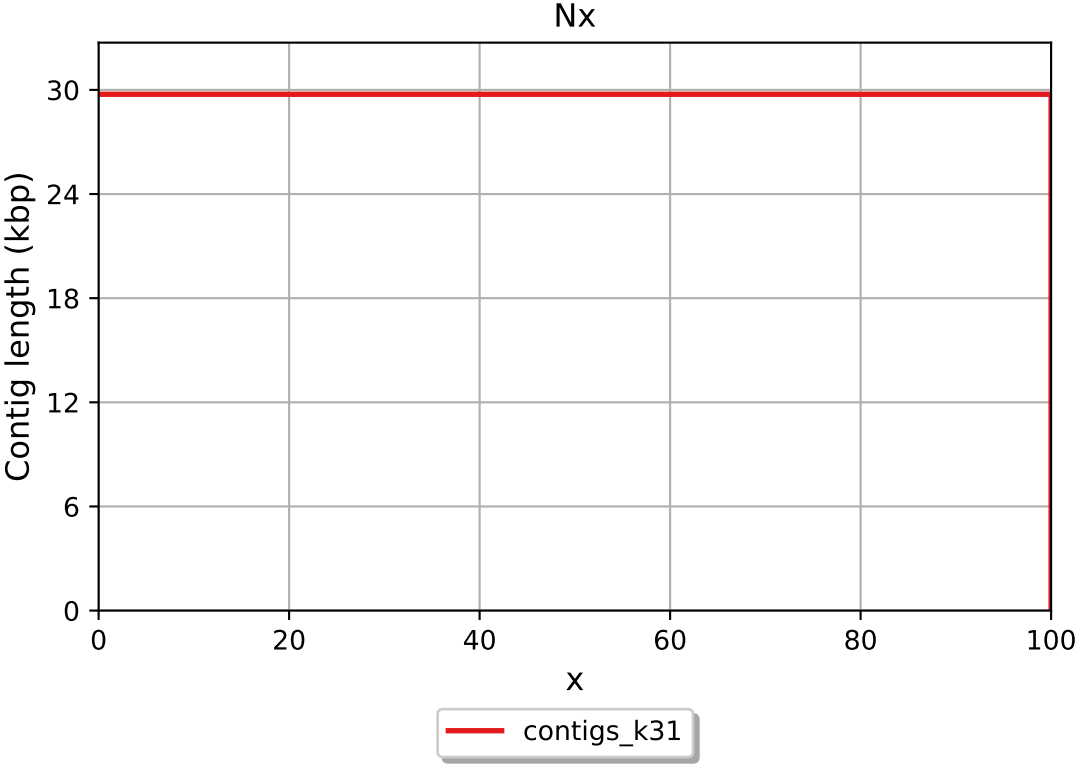
	contigs_k31
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	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

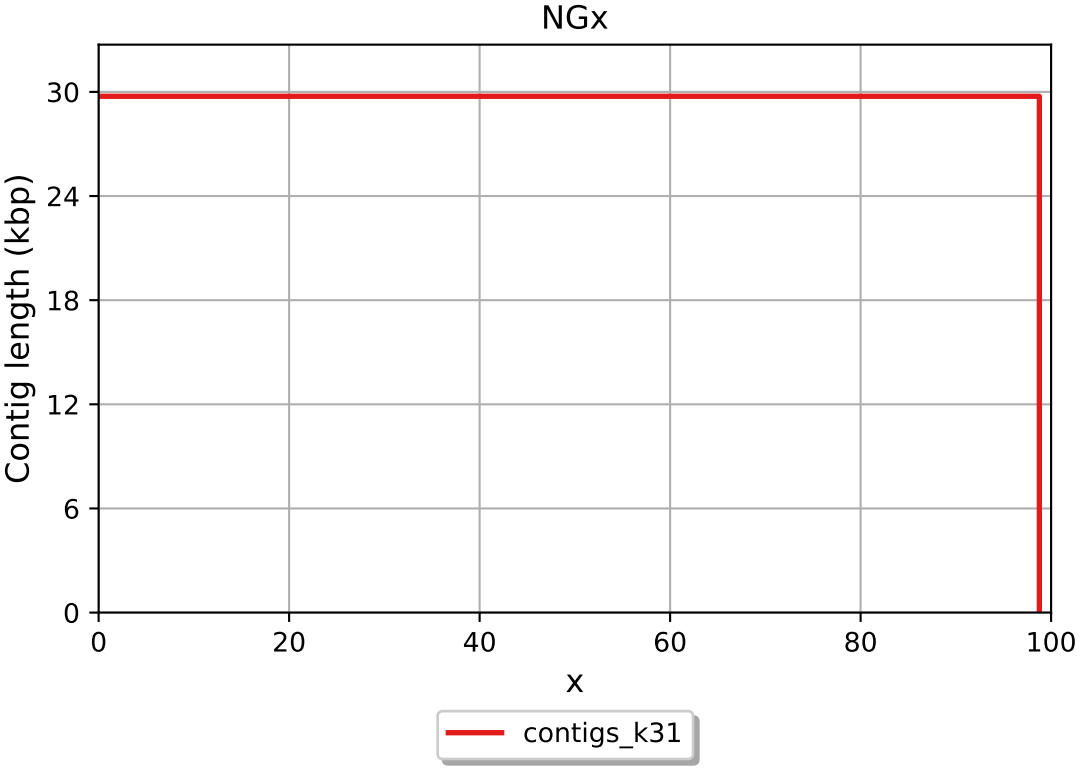
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

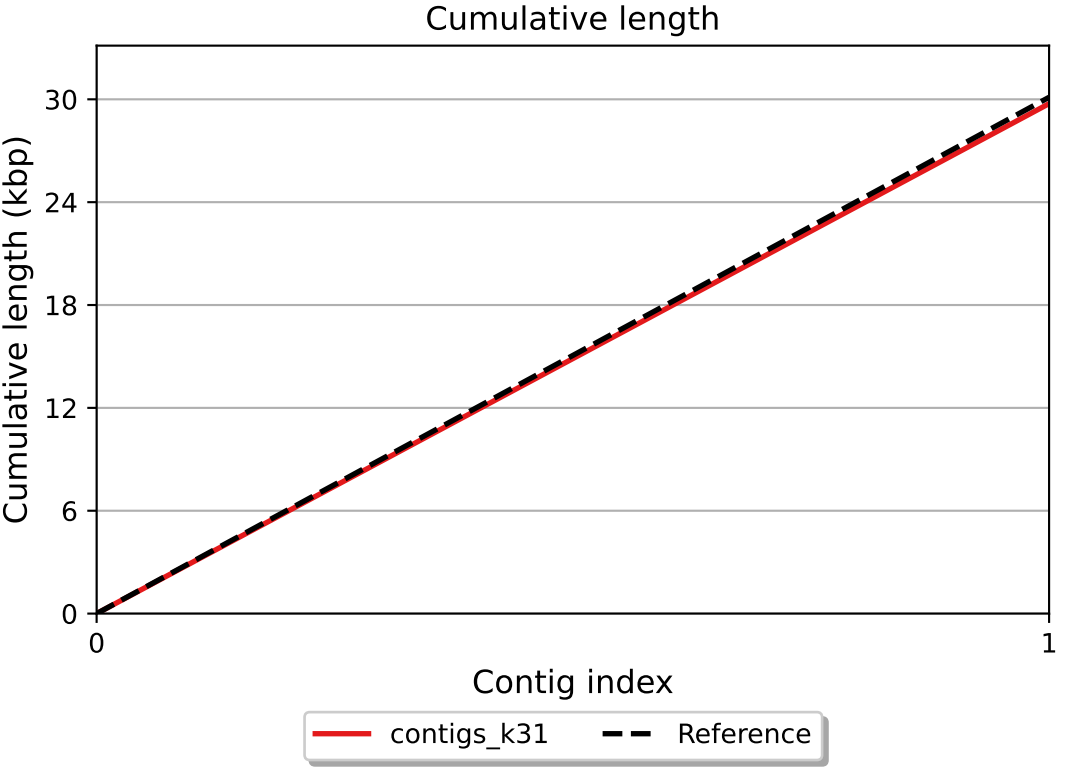
Unaligned report

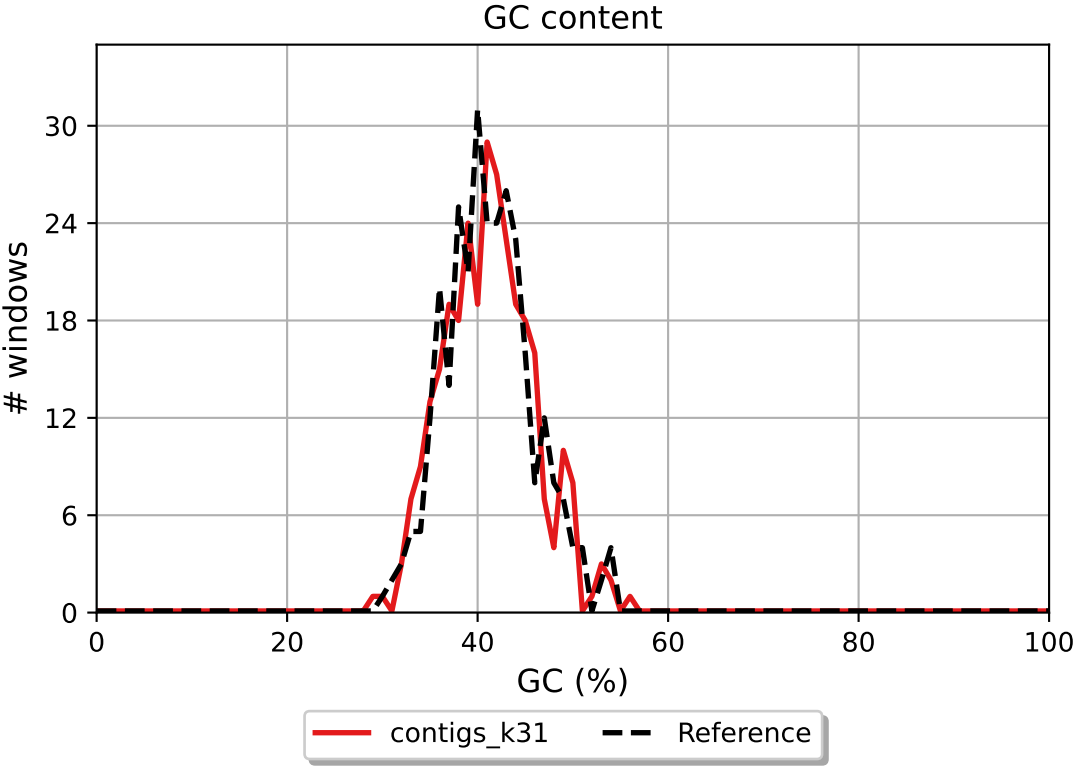
	contigs_k31
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

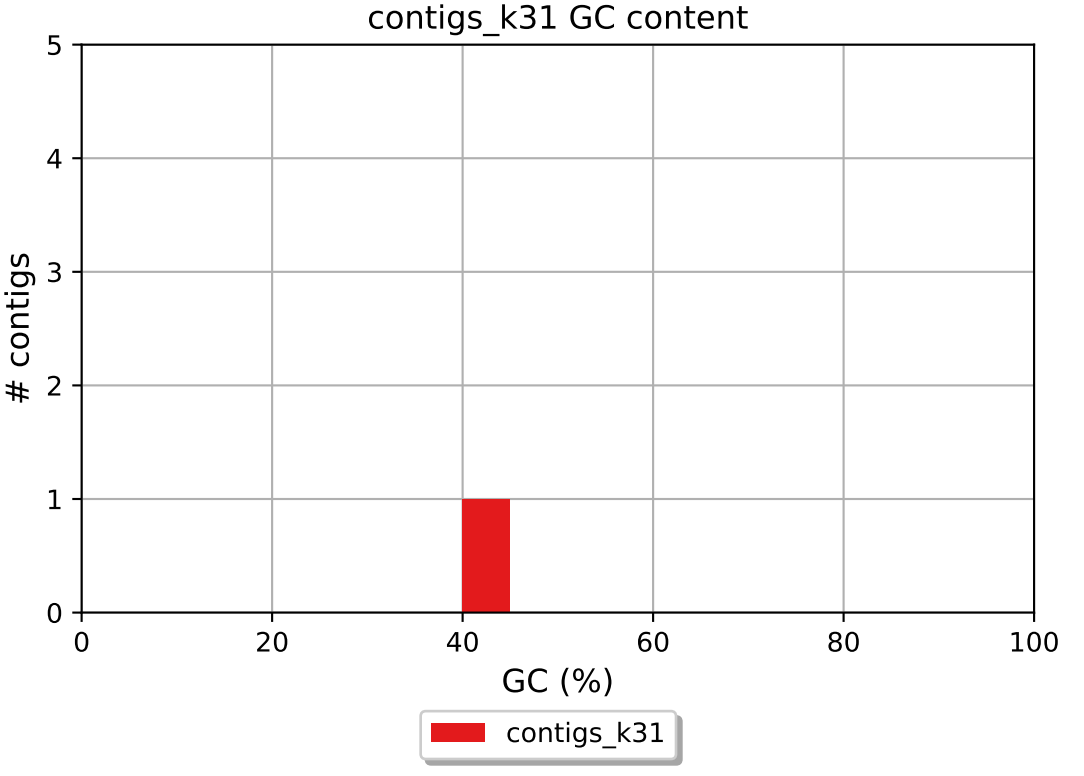
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

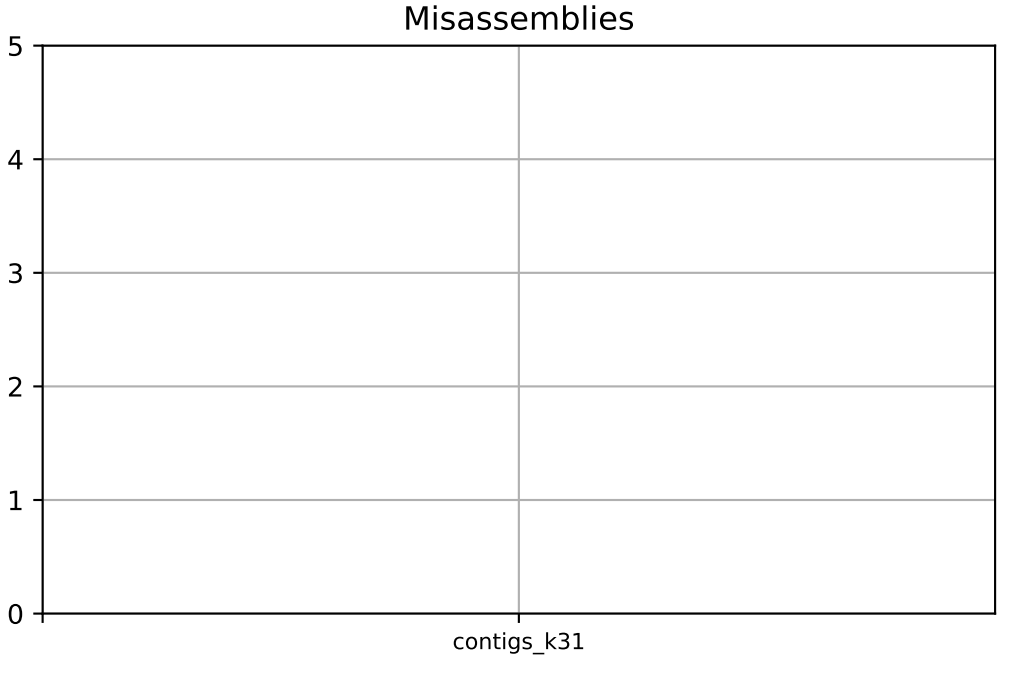

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs_k31

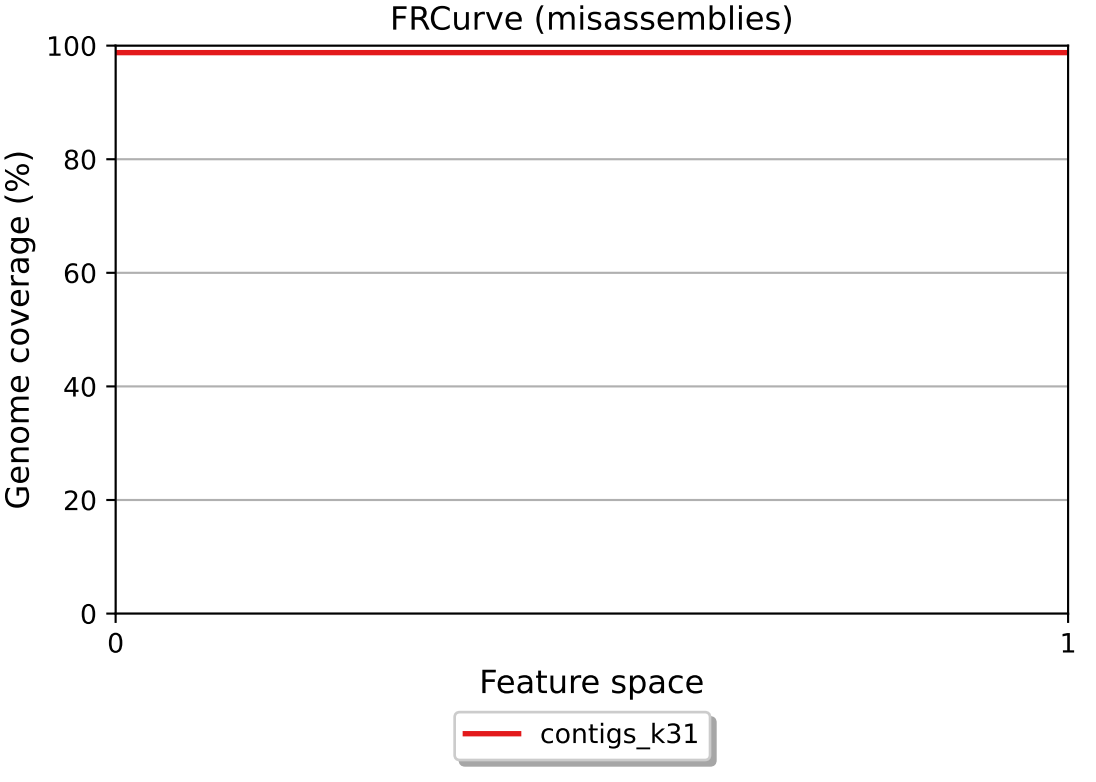

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs_k31

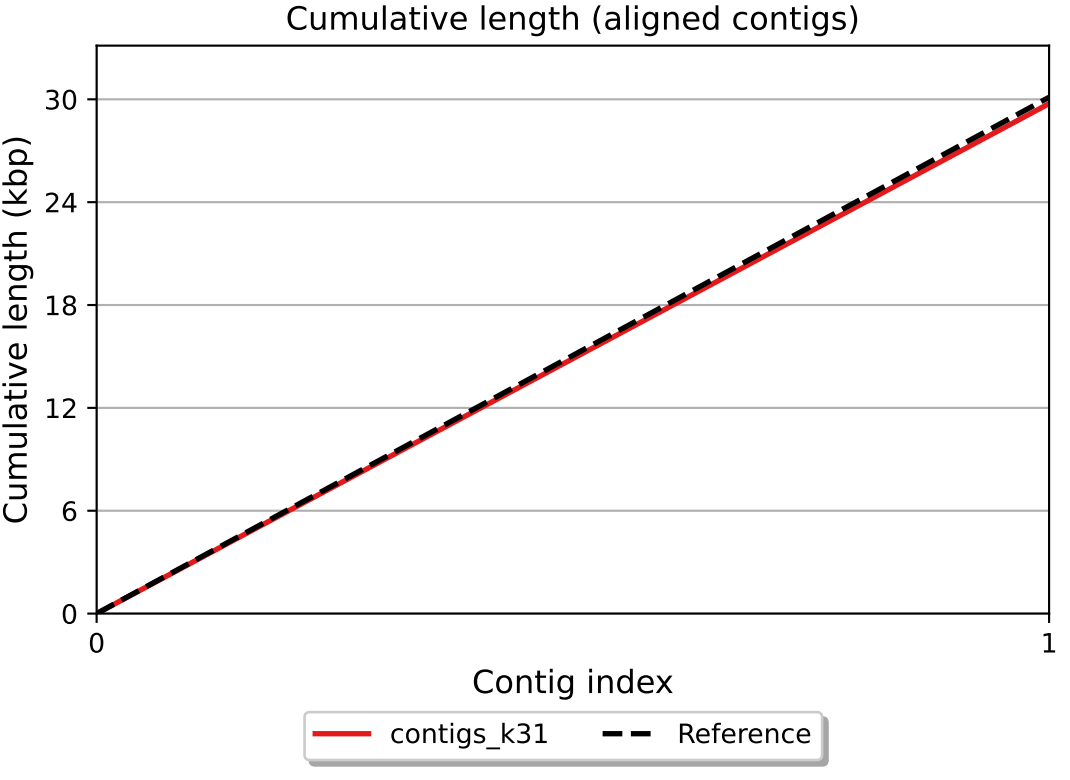

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
contigs_k31
Reference

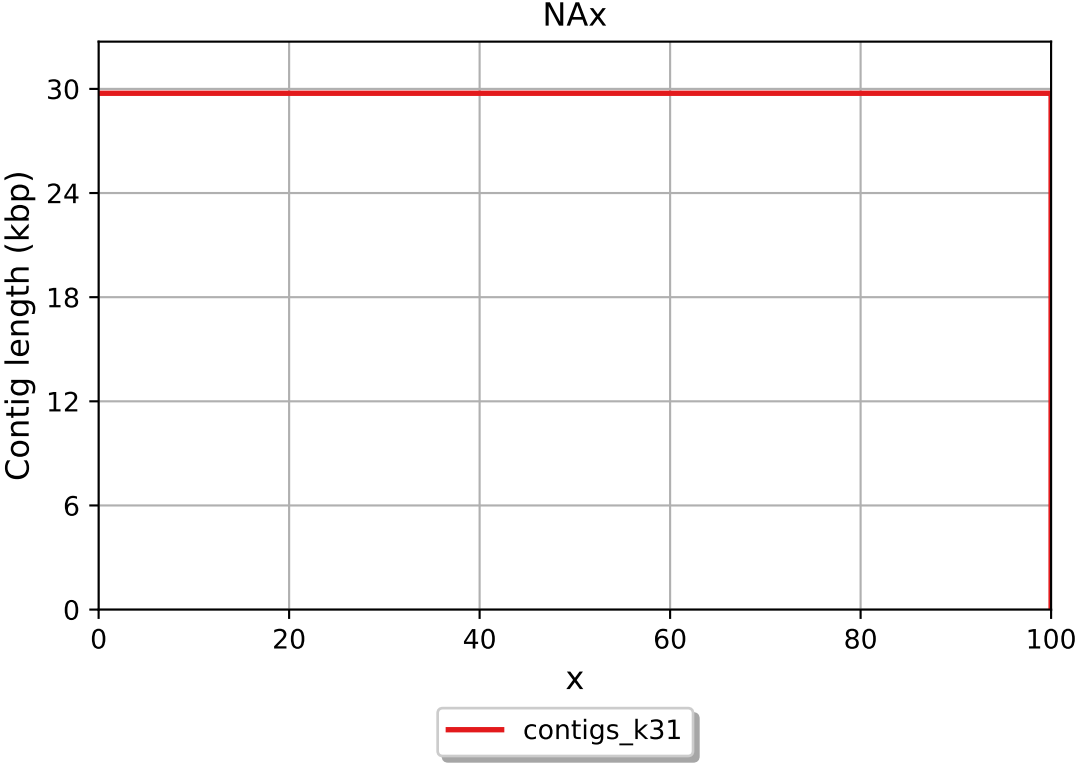

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
contigs_k31
Reference

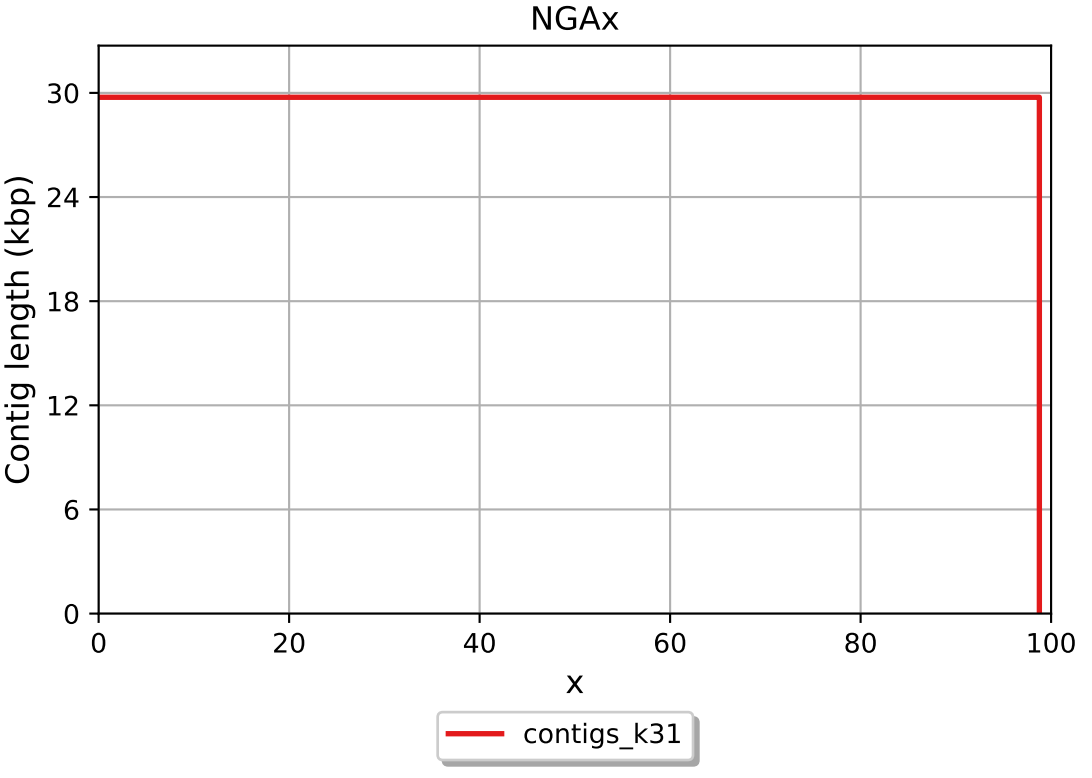

contigs_k31 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs_k31


Misassemblies
5
4
3
2
1
0
contigs_k31


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
contigs_k31


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
Contig index
contigs_k31
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs_k31


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
contigs_k31