Report

	contigs_olc_min20
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	310
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	2
Largest contig	178
Total length	310
Reference length	30119
GC (%)	41.61
Reference GC (%)	41.24
N50	178
NG50	-
N90	132
NG90	-
auN	158.4
auNG	1.6
L50	1
LG50	-
L90	2
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 (%)	1.029
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	178
Total aligned length	310
NA50	178
NGA50	-
NA90	132
NGA90	-
auNA	158.4
auNGA	1.6
LA50	1
LGA50	-
LA90	2
LGA90	-

All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

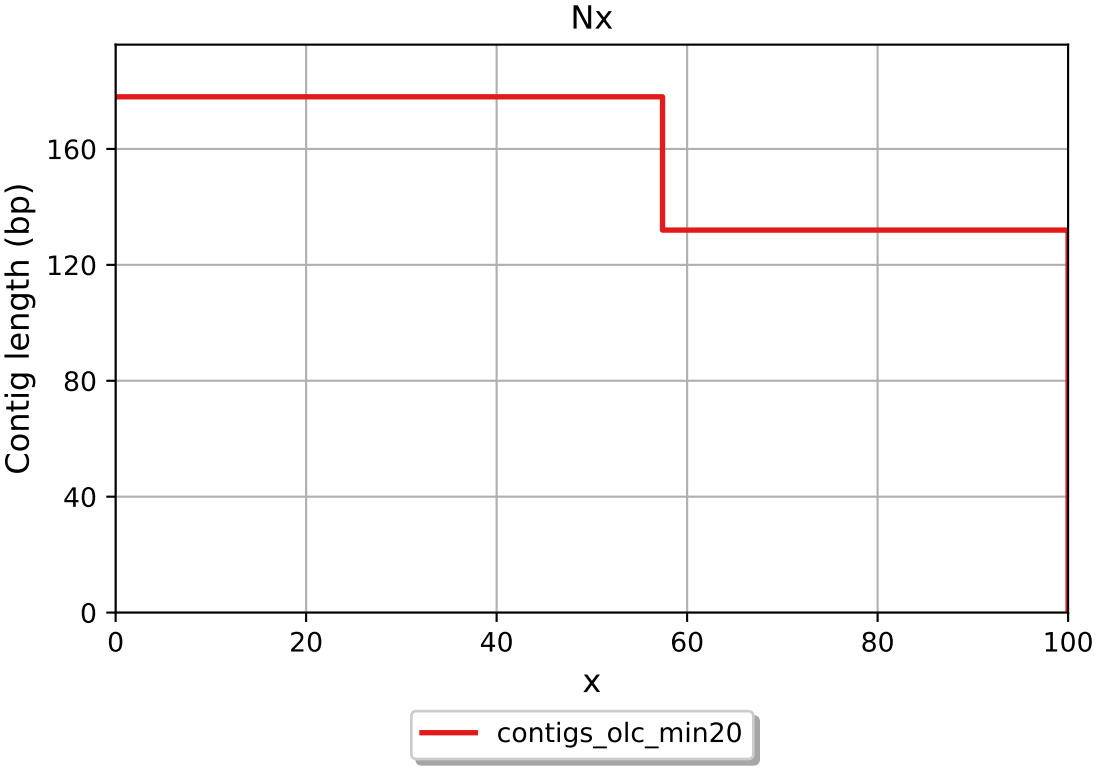
	contigs_olc_min20
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. 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

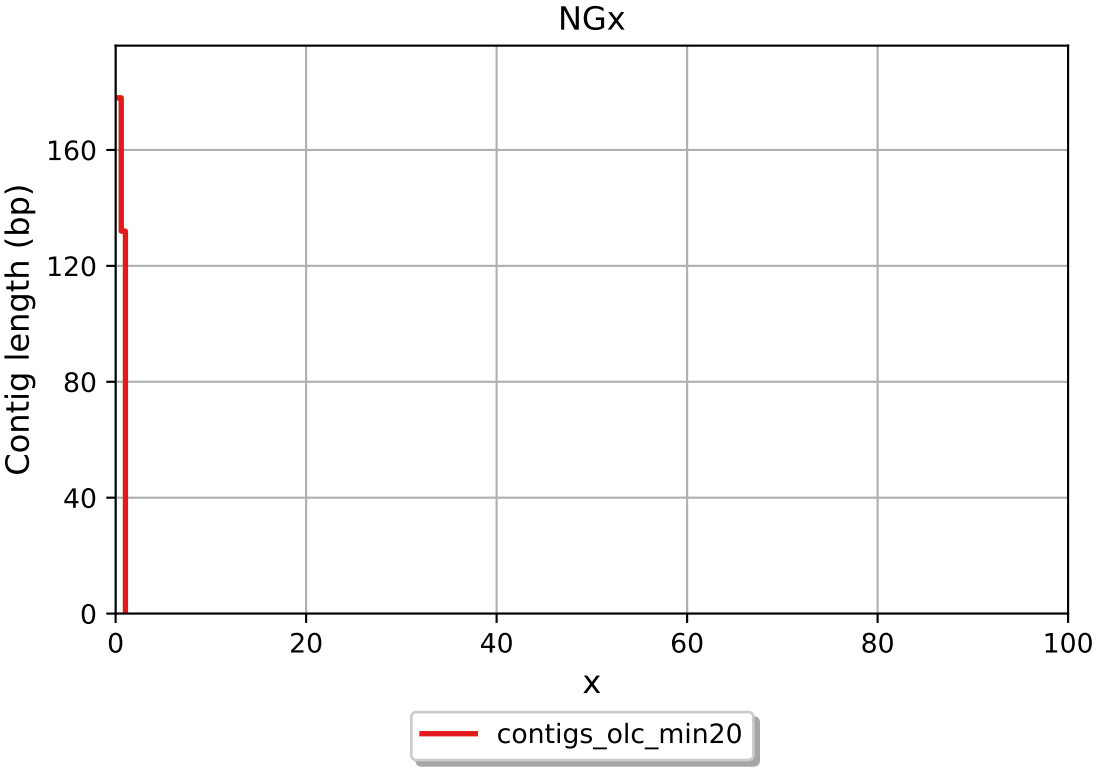
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

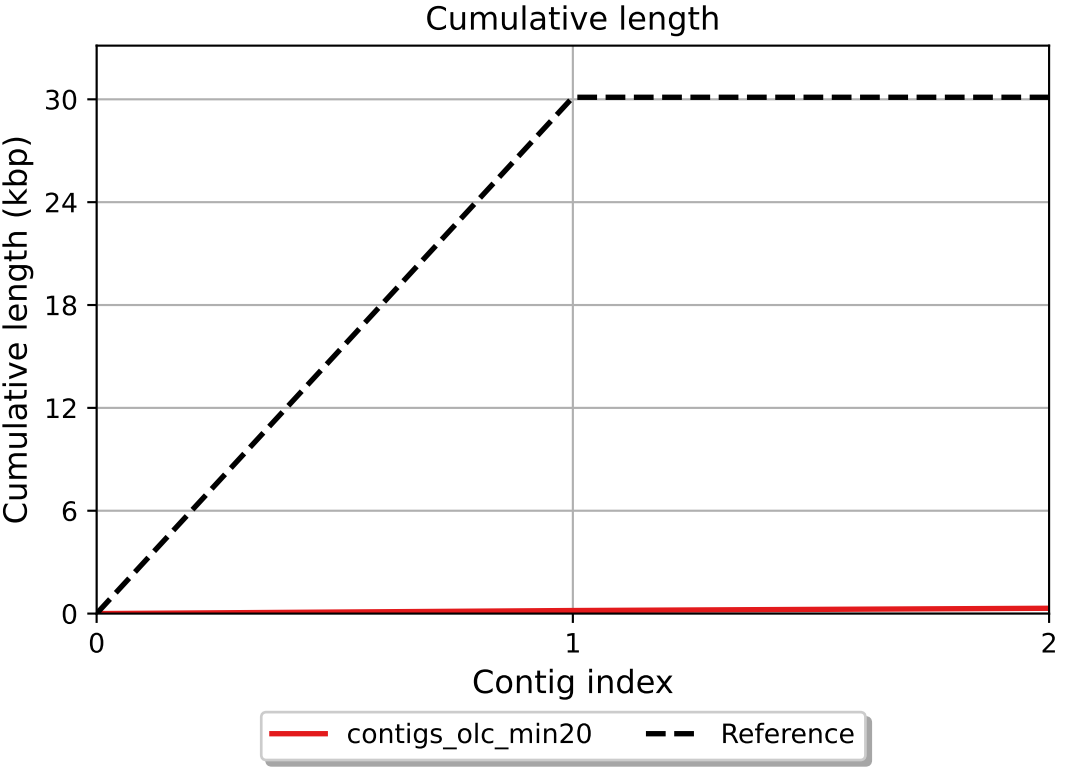
Unaligned report

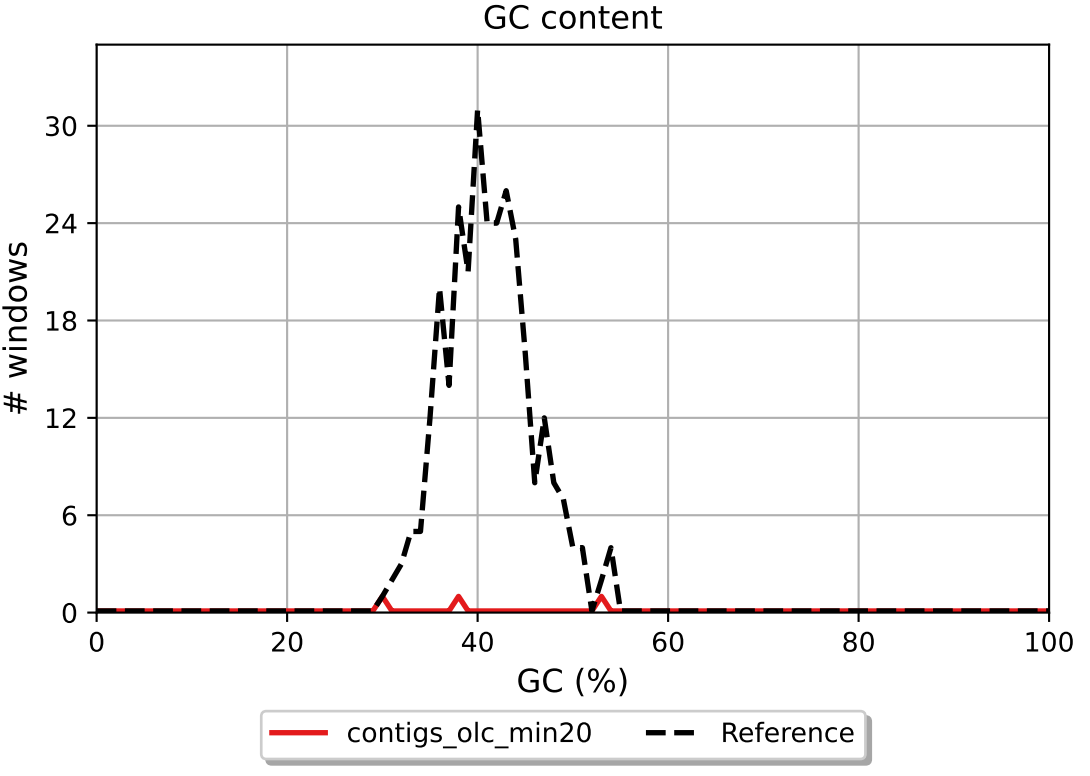
	contigs_olc_min20
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

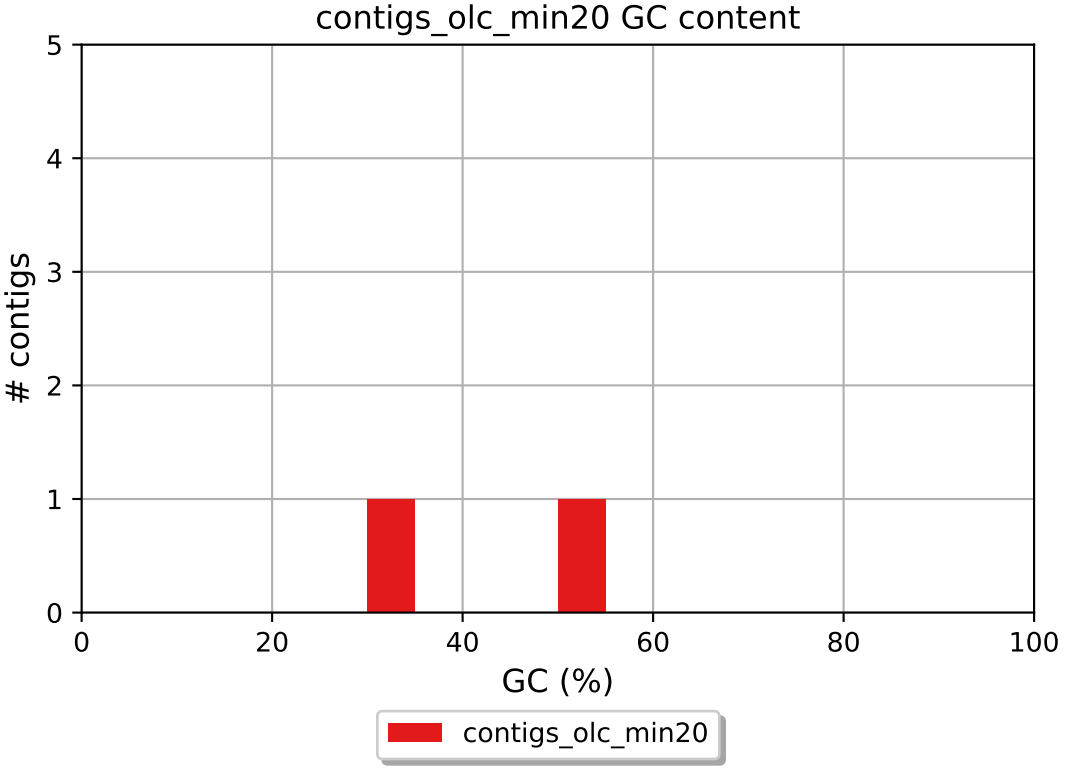
All statistics are based on contigs of size >= 100 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

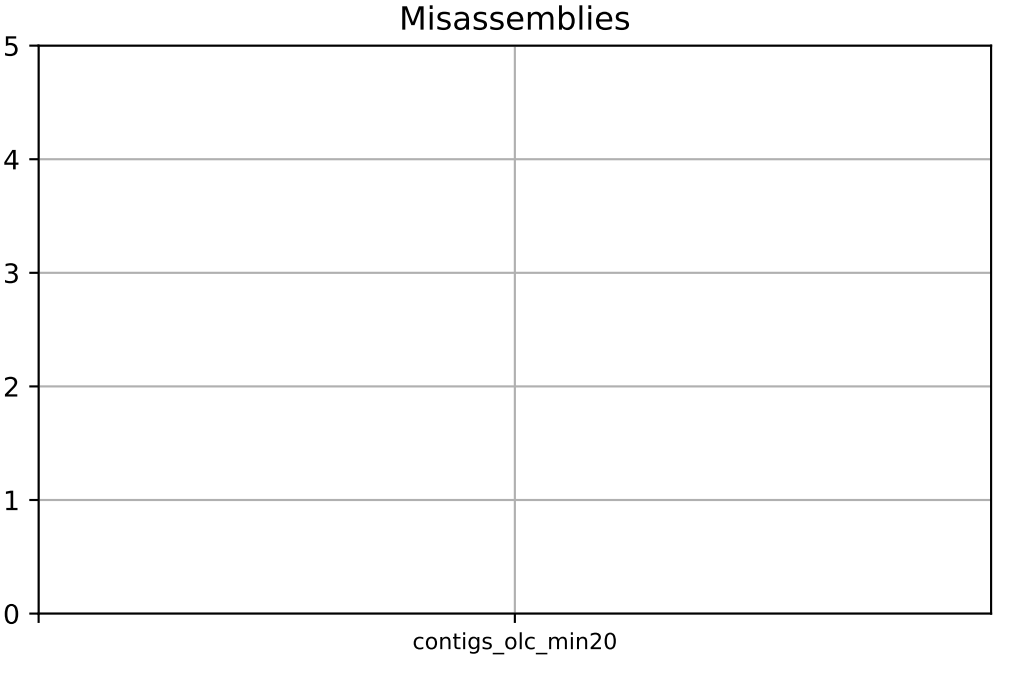

Nx
Contig length (bp)
0
40
80
120
160
0
20
40
60
80
100
x
contigs_olc_min20

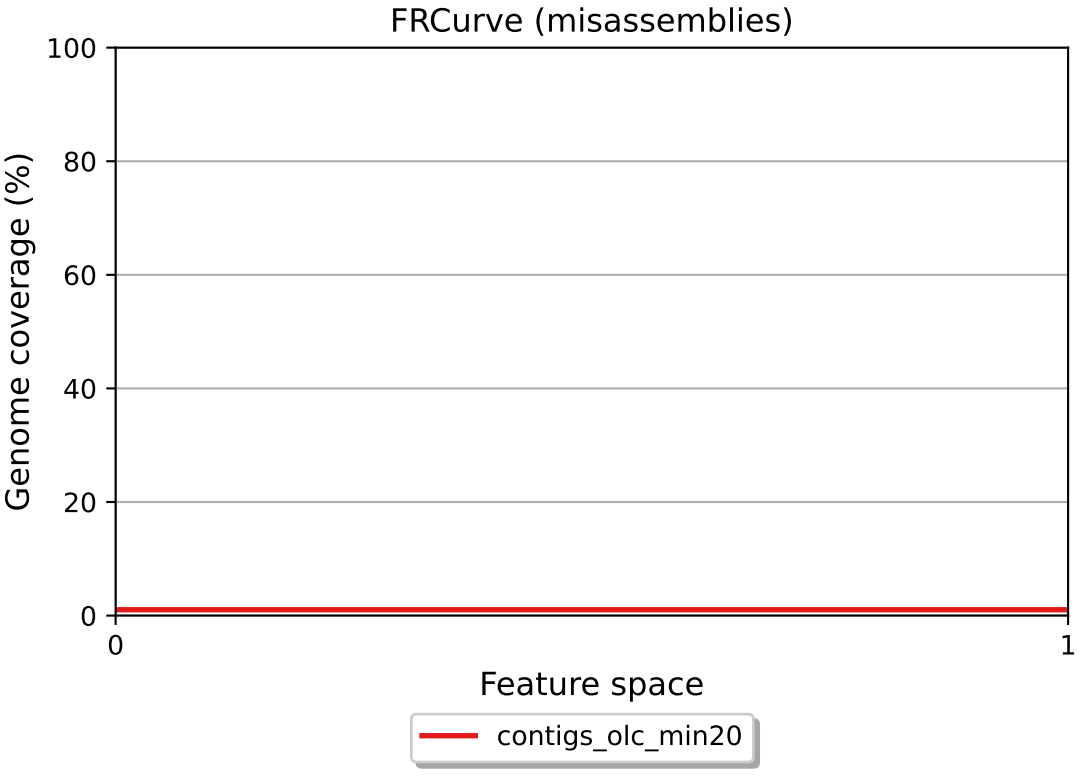

NGx
Contig length (bp)
0
40
80
120
160
0
20
40
60
80
100
x
contigs_olc_min20

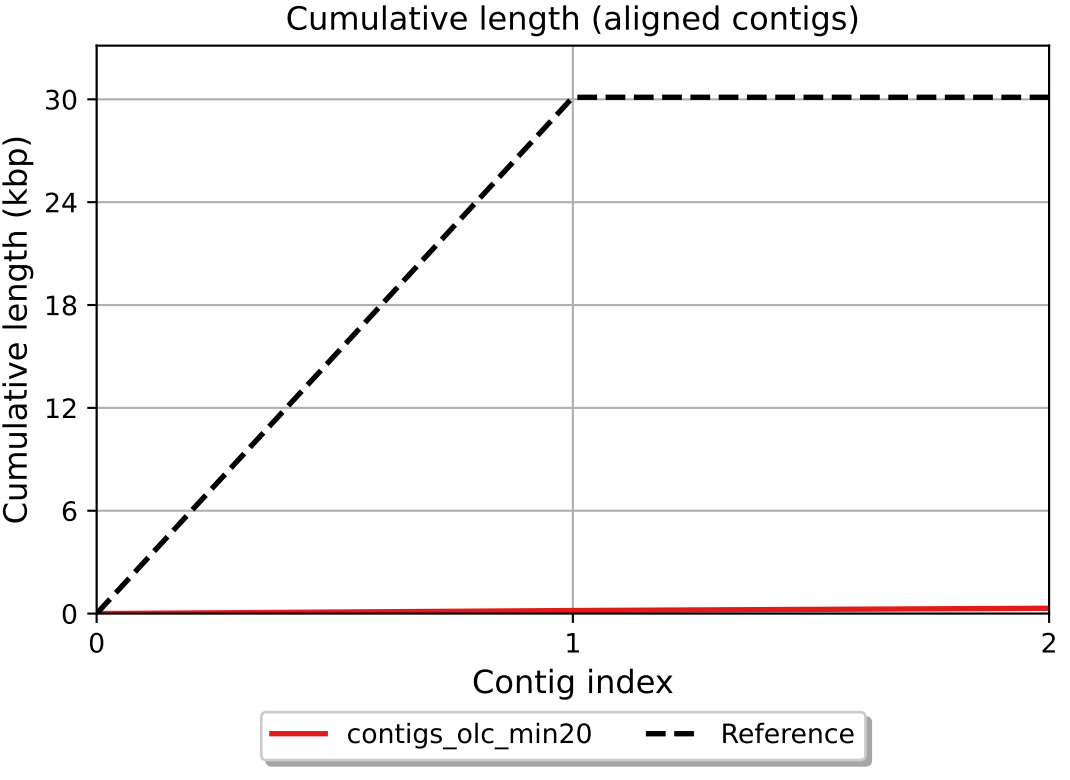

Cumulative length
Cumulative length (kbp)
30
24
18
12
6
0
0
1
2
Contig index
contigs_olc_min20
Reference

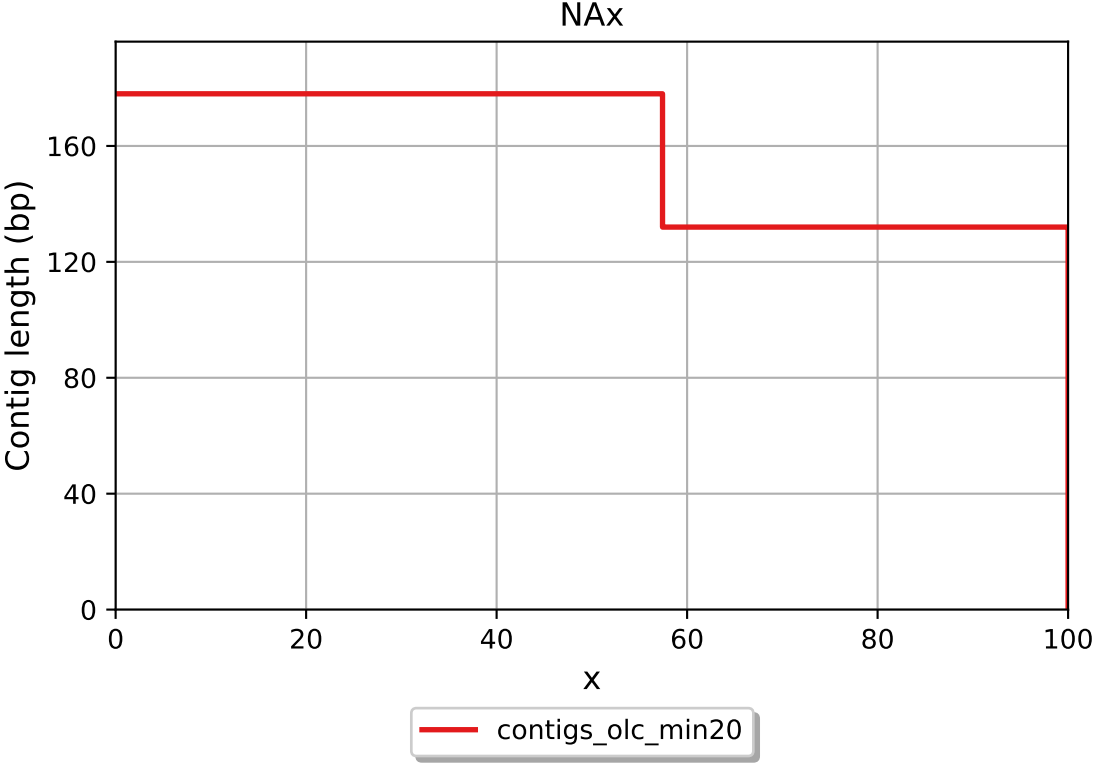

GC content
windows
GC (%)
0
6
12
18
24
30
0
20
40
60
80
100
contigs_olc_min20
Reference

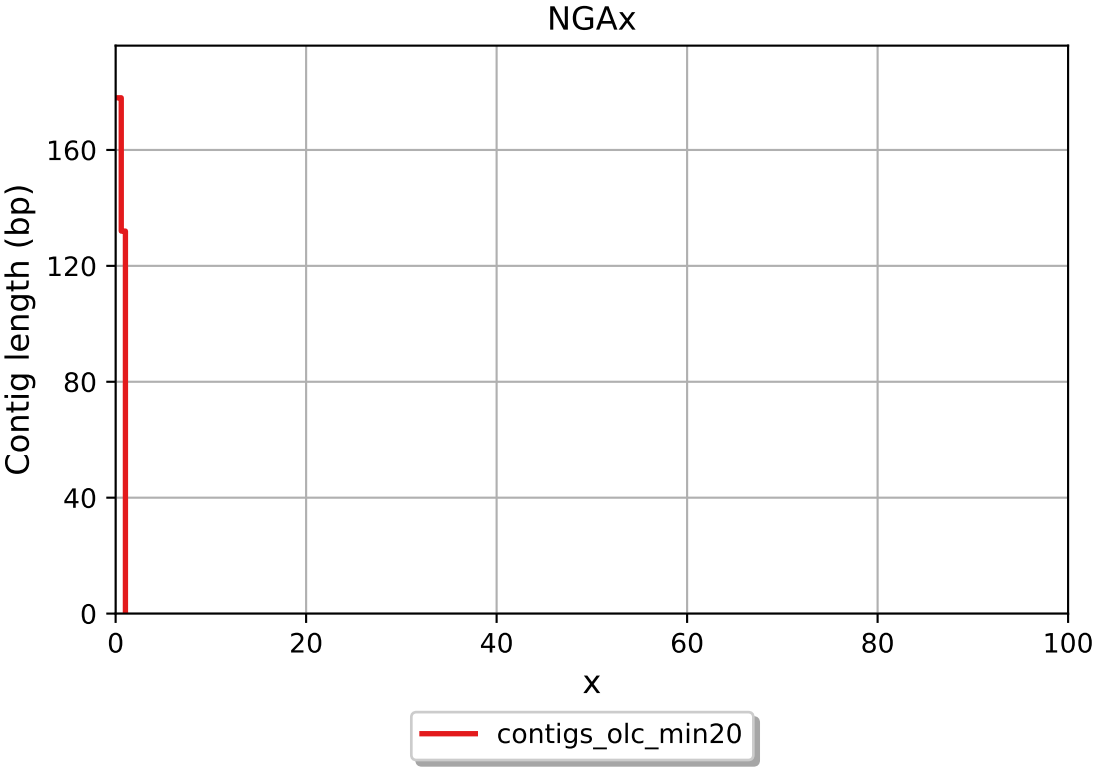

contigs_olc_min20 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
contigs_olc_min20


Misassemblies
5
4
3
2
1
0
contigs_olc_min20


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
contigs_olc_min20


Cumulative length (aligned contigs)
Cumulative length (kbp)
30
24
18
12
6
0
0
1
2
Contig index
contigs_olc_min20
Reference


NAx
Contig length (bp)
0
40
80
120
160
0
20
40
60
80
100
x
contigs_olc_min20


NGAx
Contig length (bp)
0
40
80
120
160
0
20
40
60
80
100
x
contigs_olc_min20