Report

	min5_CFL_ICFL_10
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	18
Total length (>= 0 bp)	3667354
Total length (>= 1000 bp)	3667354
Total length (>= 5000 bp)	3667354
Total length (>= 10000 bp)	3667354
Total length (>= 25000 bp)	3667354
Total length (>= 50000 bp)	3667354
# contigs	18
Largest contig	629320
Total length	3667354
Reference length	4686137
GC (%)	50.86
Reference GC (%)	50.78
N50	205600
NG50	165097
N90	106944
NG90	-
auN	312210.1
auNG	244334.5
L50	5
LG50	8
L90	14
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	629320
# 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 (%)	78.233
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	554159
Total aligned length	3667354
NA50	205600
NGA50	165097
NA90	106944
NGA90	-
auNA	261166.7
auNGA	204388.1
LA50	6
LGA50	9
LA90	15
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

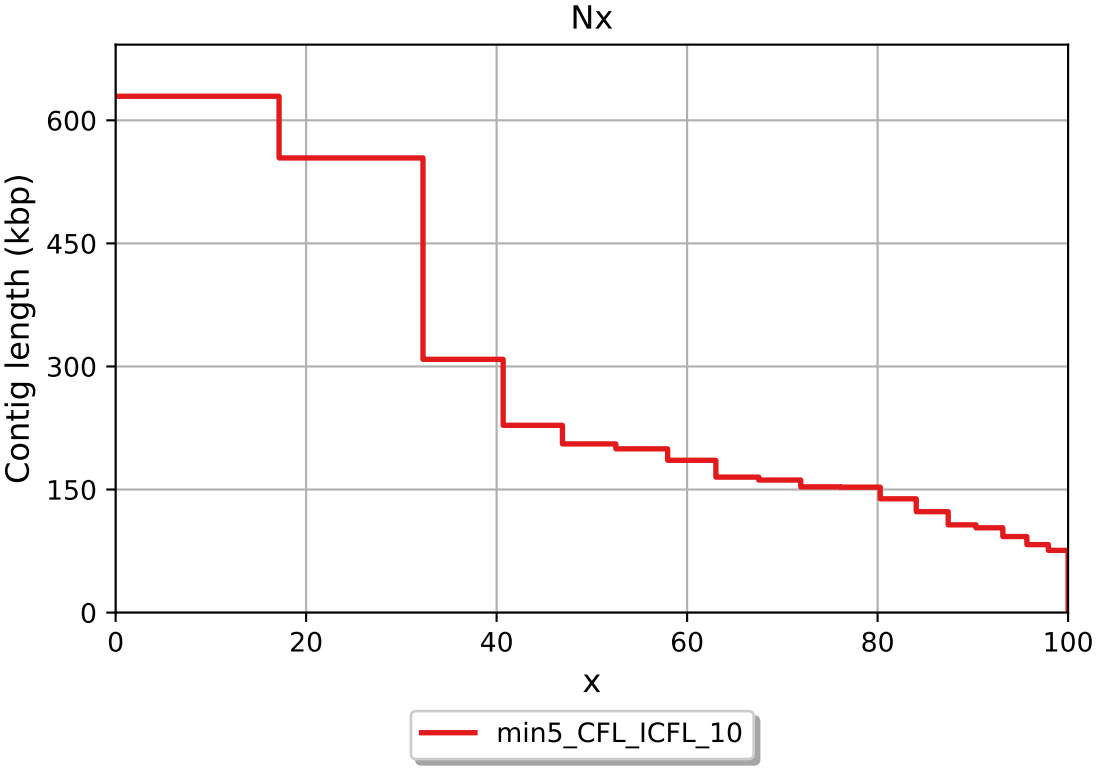
	min5_CFL_ICFL_10
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	629320
# local misassemblies	0
# scaffold gap 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

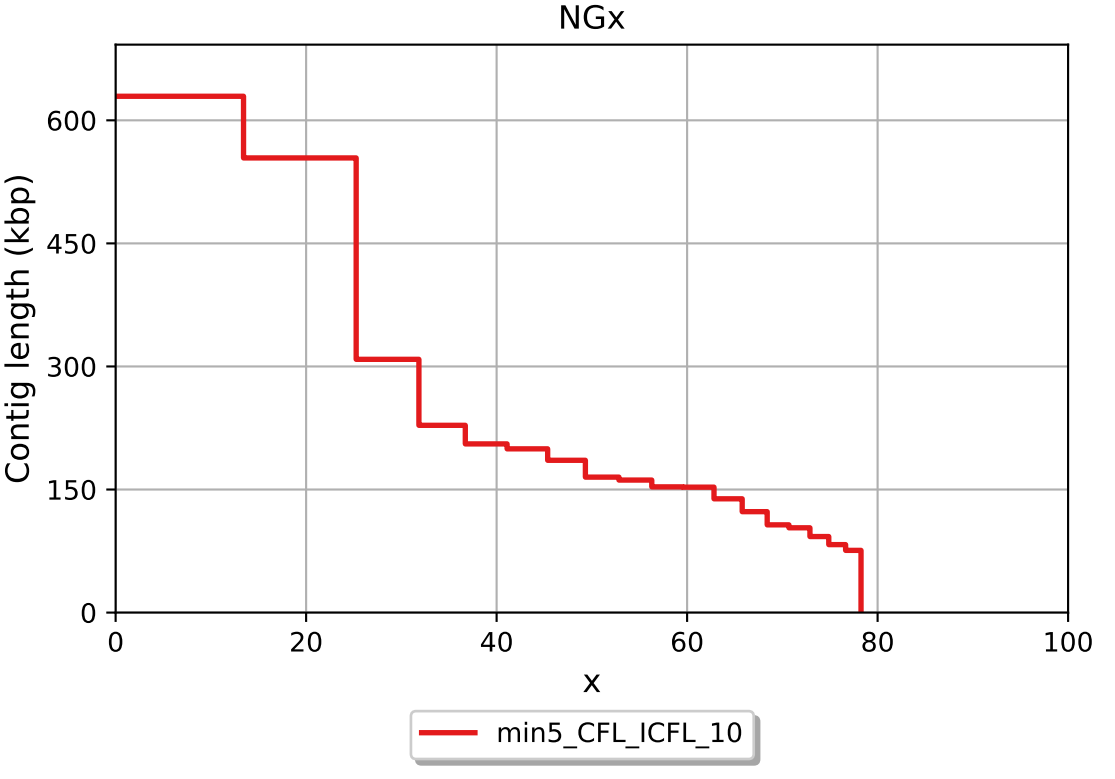
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

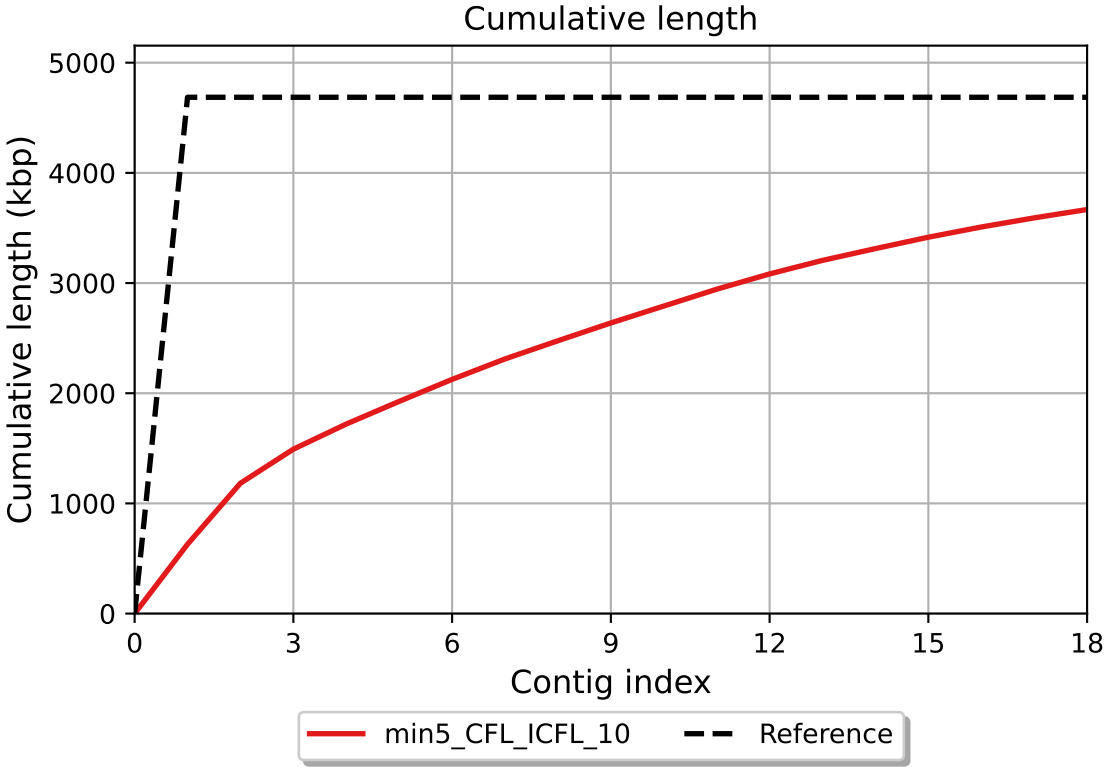
Unaligned report

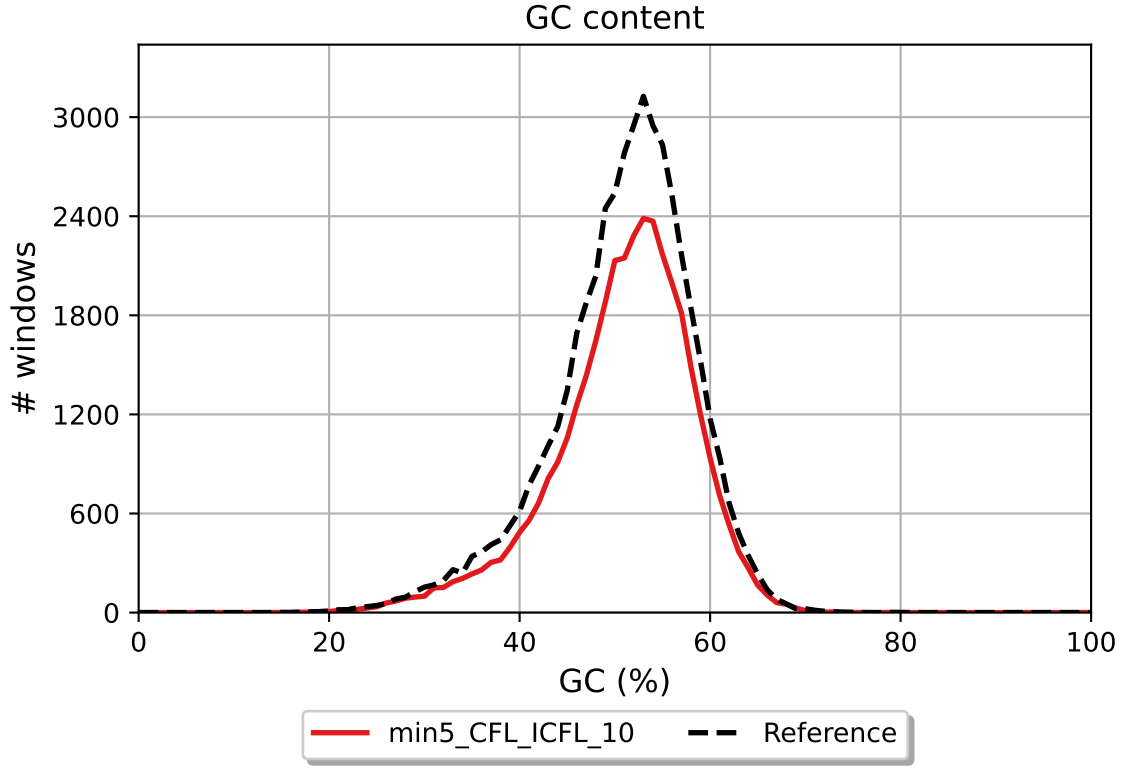
	min5_CFL_ICFL_10
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

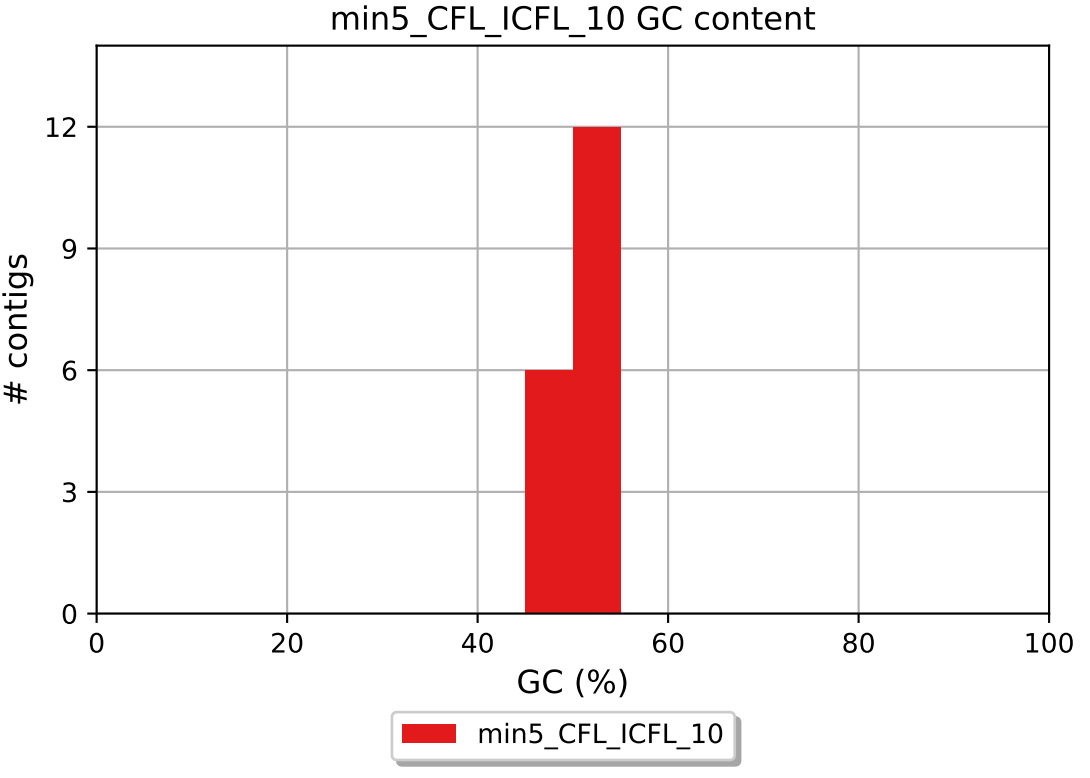
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

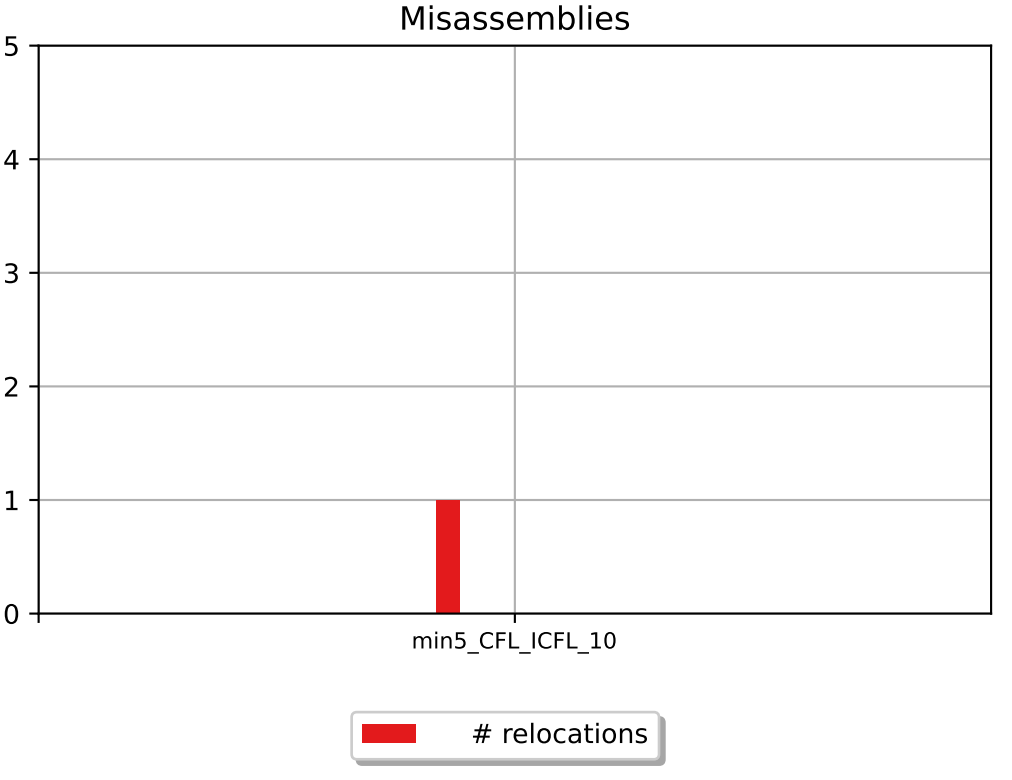

Nx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
min5_CFL_ICFL_10

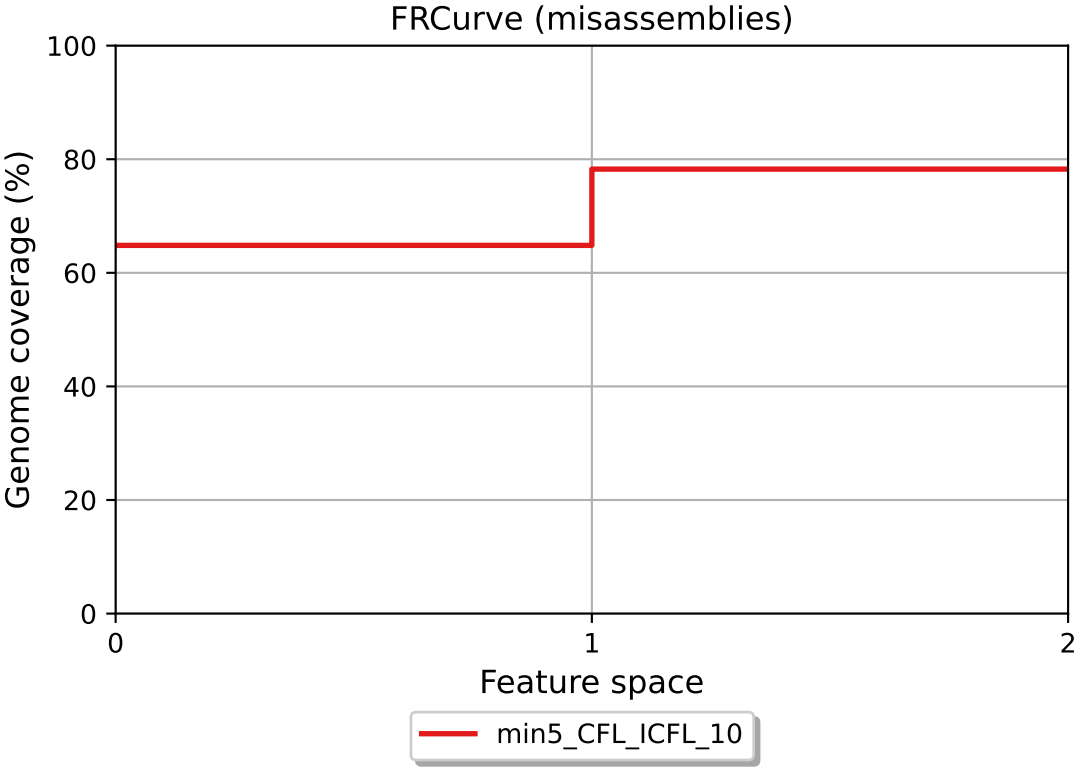

NGx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
min5_CFL_ICFL_10

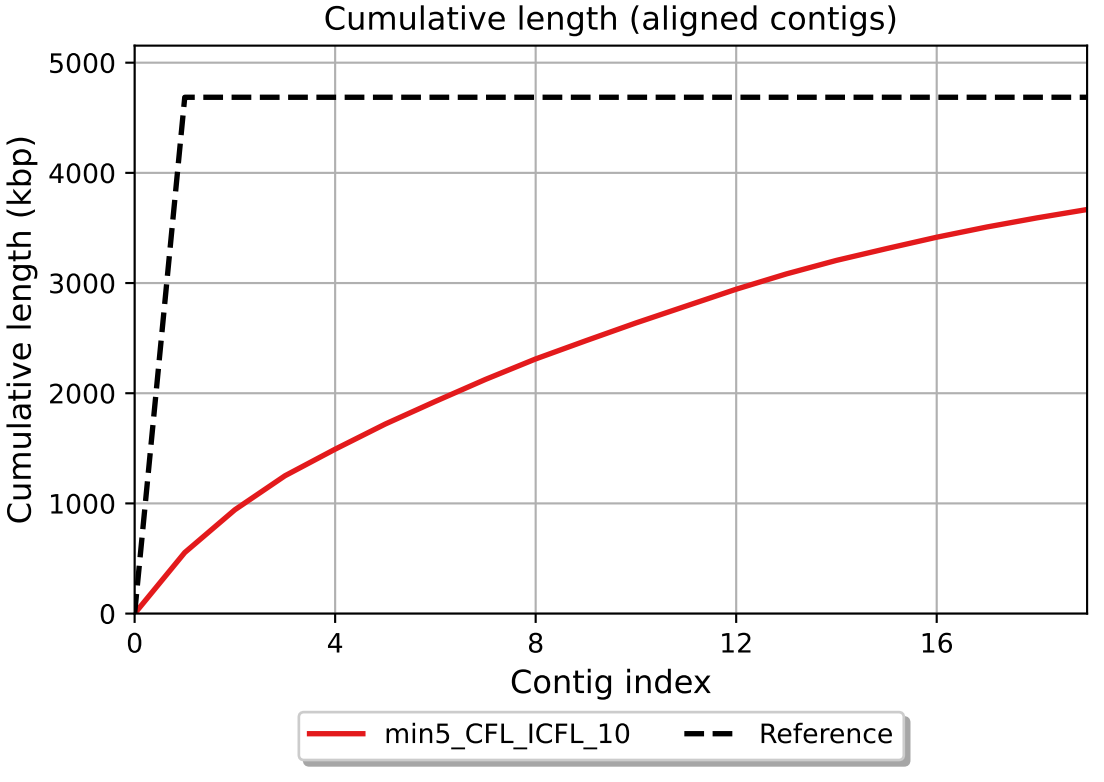

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
18
Contig index
min5_CFL_ICFL_10
Reference

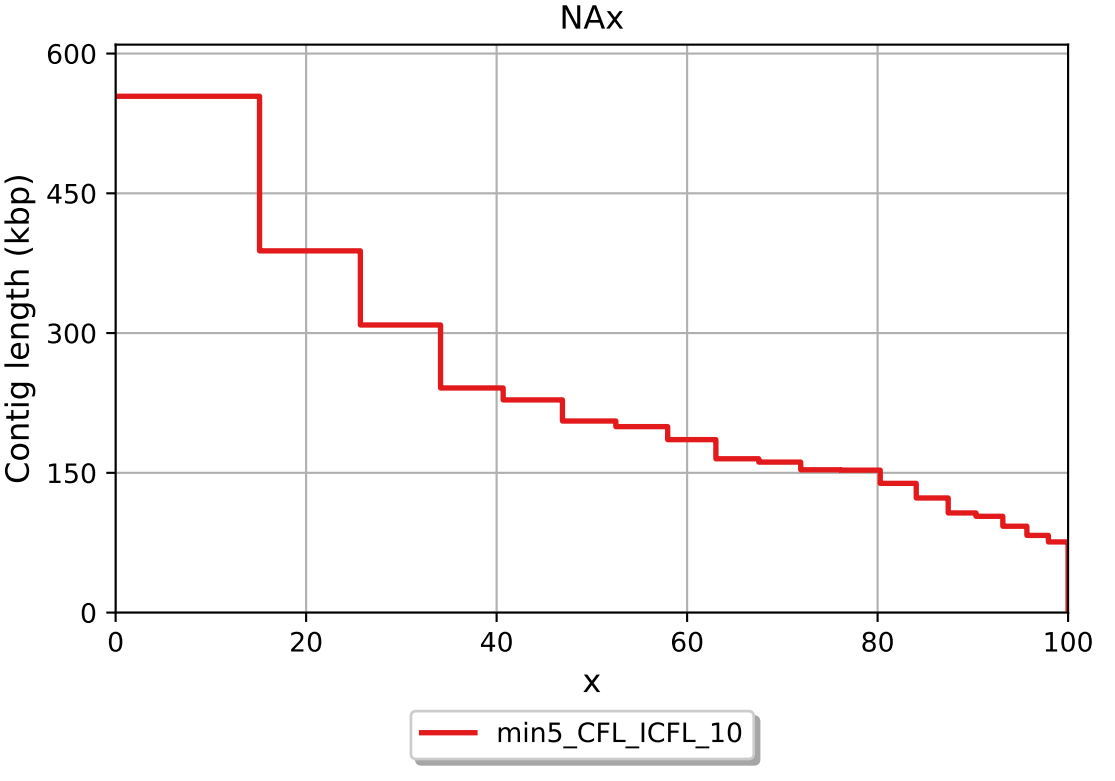

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
min5_CFL_ICFL_10
Reference

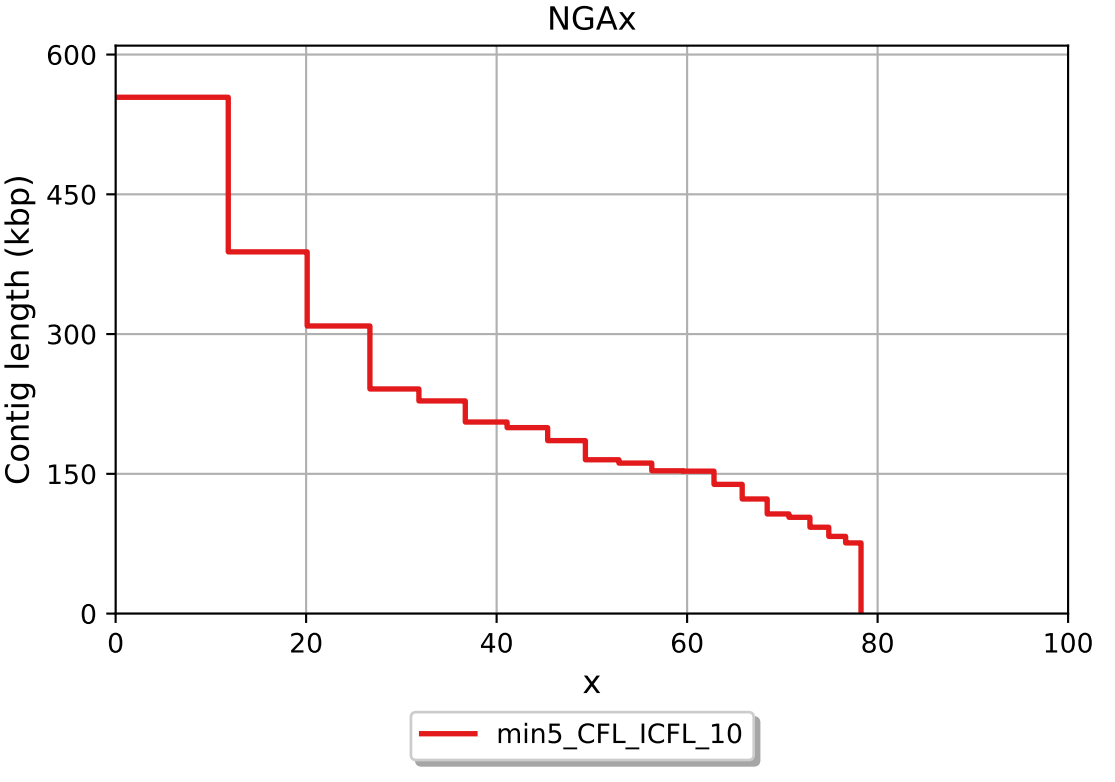

min5_CFL_ICFL_10 GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
min5_CFL_ICFL_10


Misassemblies
5
4
3
2
1
0
min5_CFL_ICFL_10
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
min5_CFL_ICFL_10


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
Contig index
min5_CFL_ICFL_10
Reference


NAx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
min5_CFL_ICFL_10


NGAx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
min5_CFL_ICFL_10