Report

	CFL_ICFL_COMB_10
# contigs (>= 0 bp)	20
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	20
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	20
Total length (>= 0 bp)	3682715
Total length (>= 1000 bp)	3682715
Total length (>= 5000 bp)	3682715
Total length (>= 10000 bp)	3682715
Total length (>= 25000 bp)	3682715
Total length (>= 50000 bp)	3682715
# contigs	20
Largest contig	631919
Total length	3682715
Reference length	4686137
GC (%)	50.87
Reference GC (%)	50.78
N50	207671
NG50	165097
N90	99608
NG90	-
auN	268101.6
auNG	210694.2
L50	6
LG50	9
L90	16
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	631919
# 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 (%)	78.560
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	388239
Total aligned length	3682715
NA50	207671
NGA50	165097
NA90	99608
NGA90	-
auNA	216723.2
auNGA	170317.2
LA50	7
LGA50	10
LA90	17
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

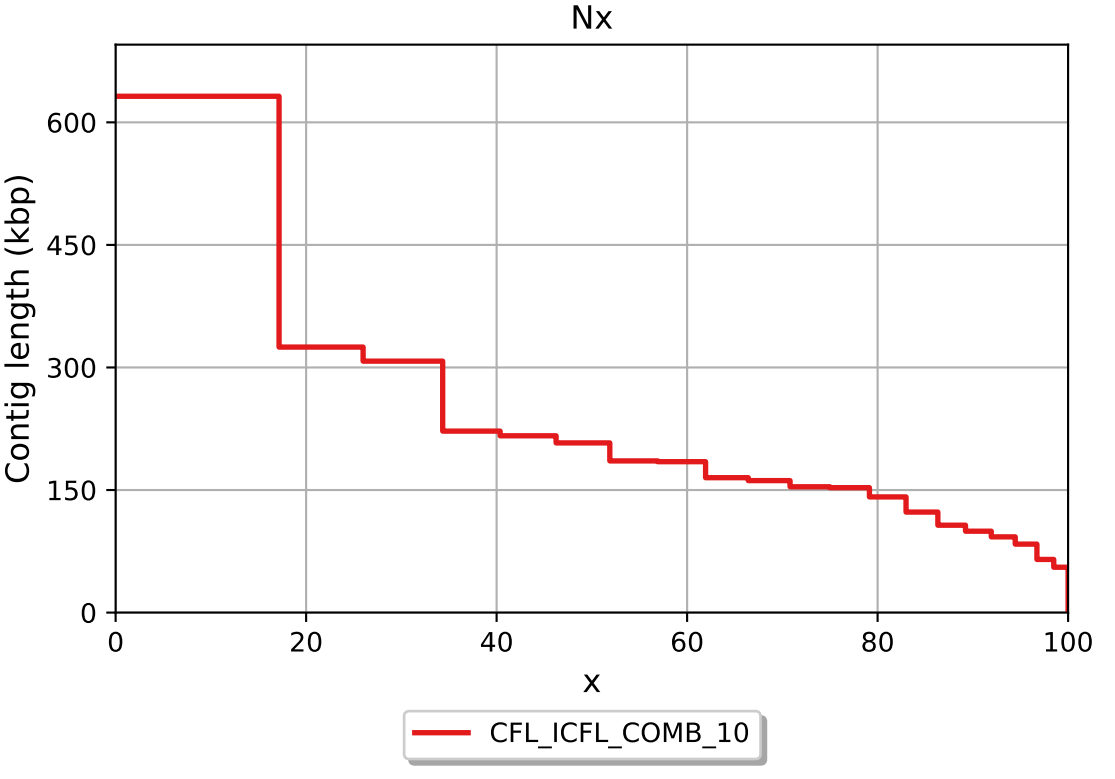
	CFL_ICFL_COMB_10
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	631919
# local misassemblies	0
# scaffold gap 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

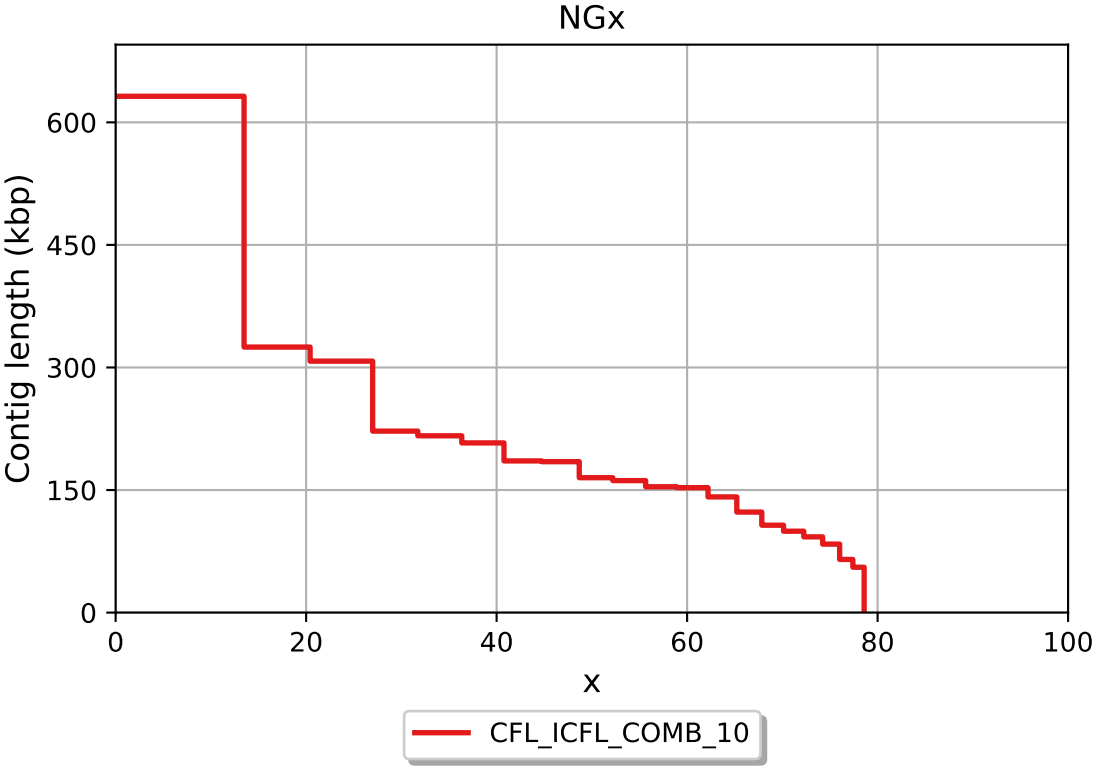
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

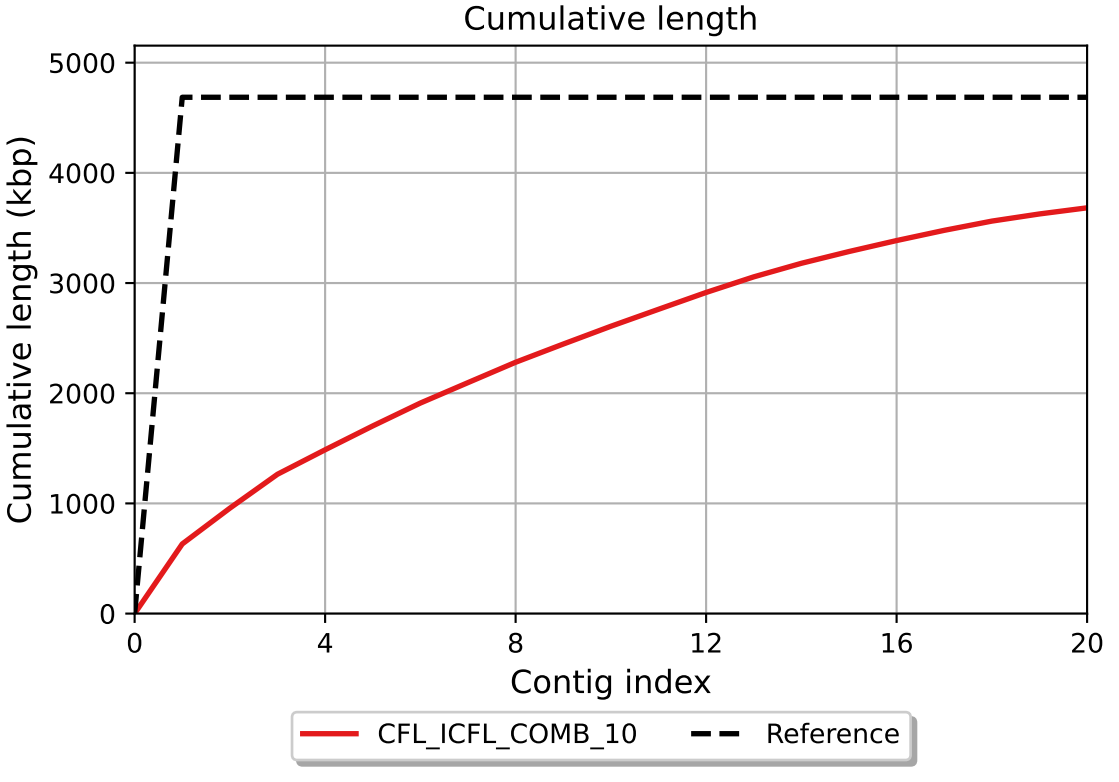
Unaligned report

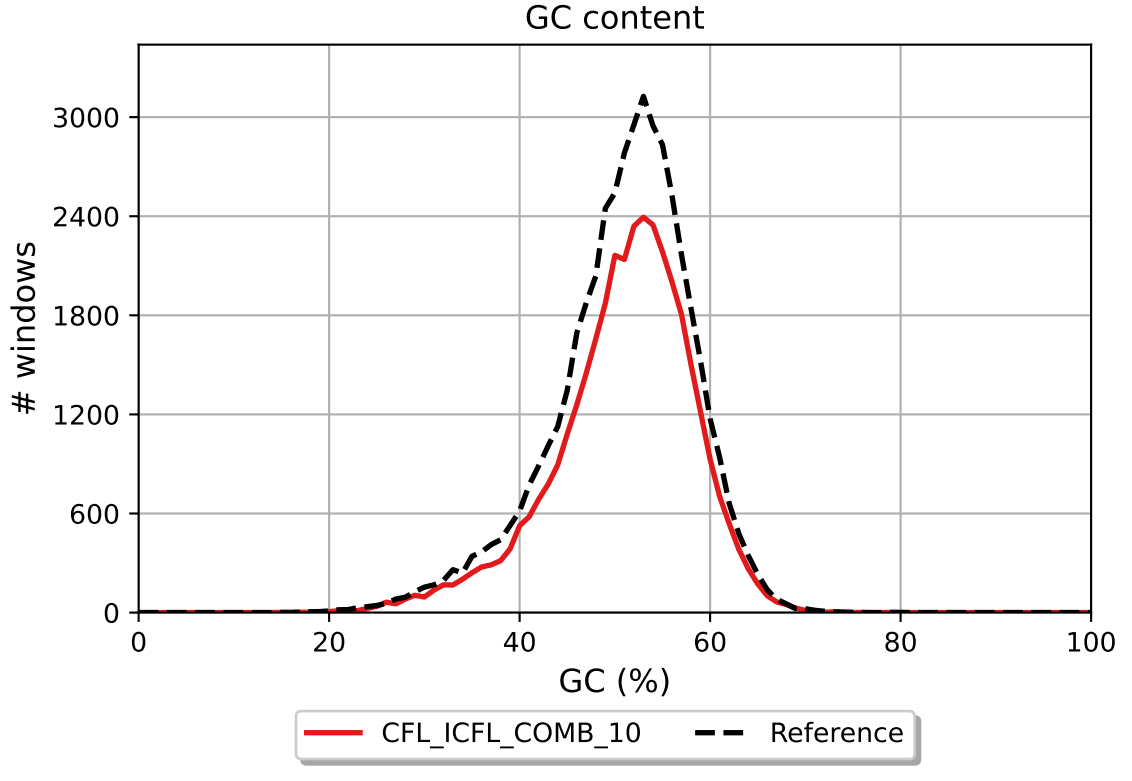
	CFL_ICFL_COMB_10
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

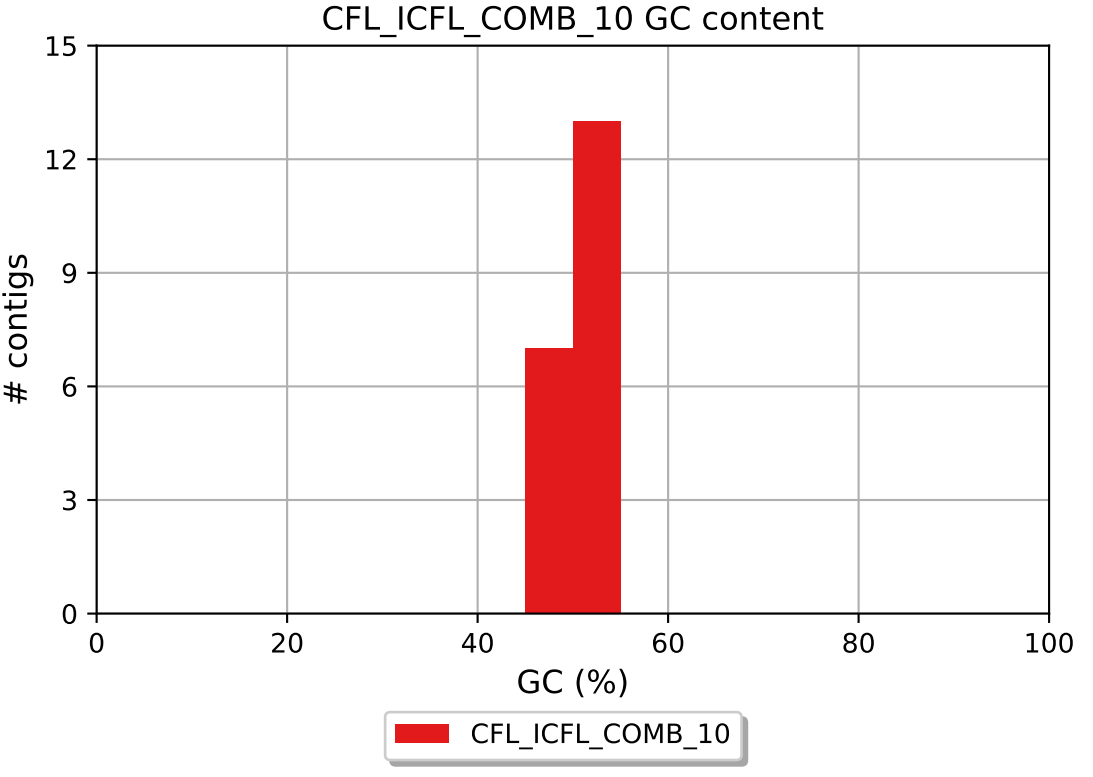
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
CFL_ICFL_COMB_10

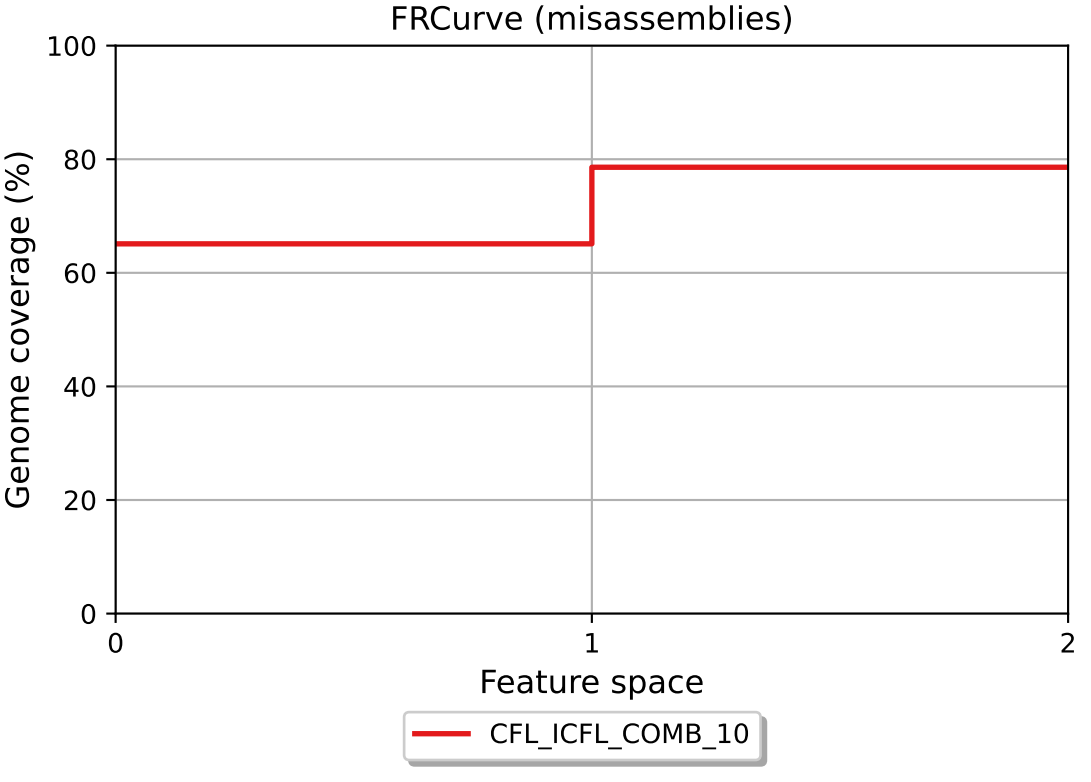

NGx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
CFL_ICFL_COMB_10

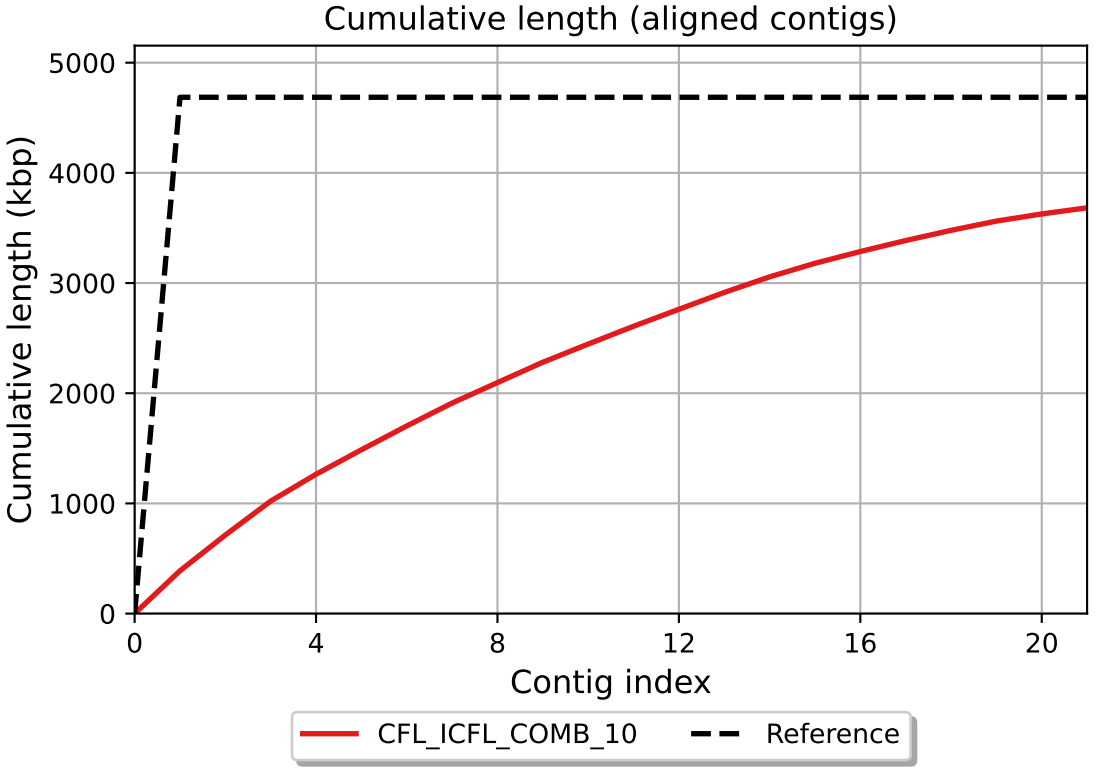

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
CFL_ICFL_COMB_10
Reference

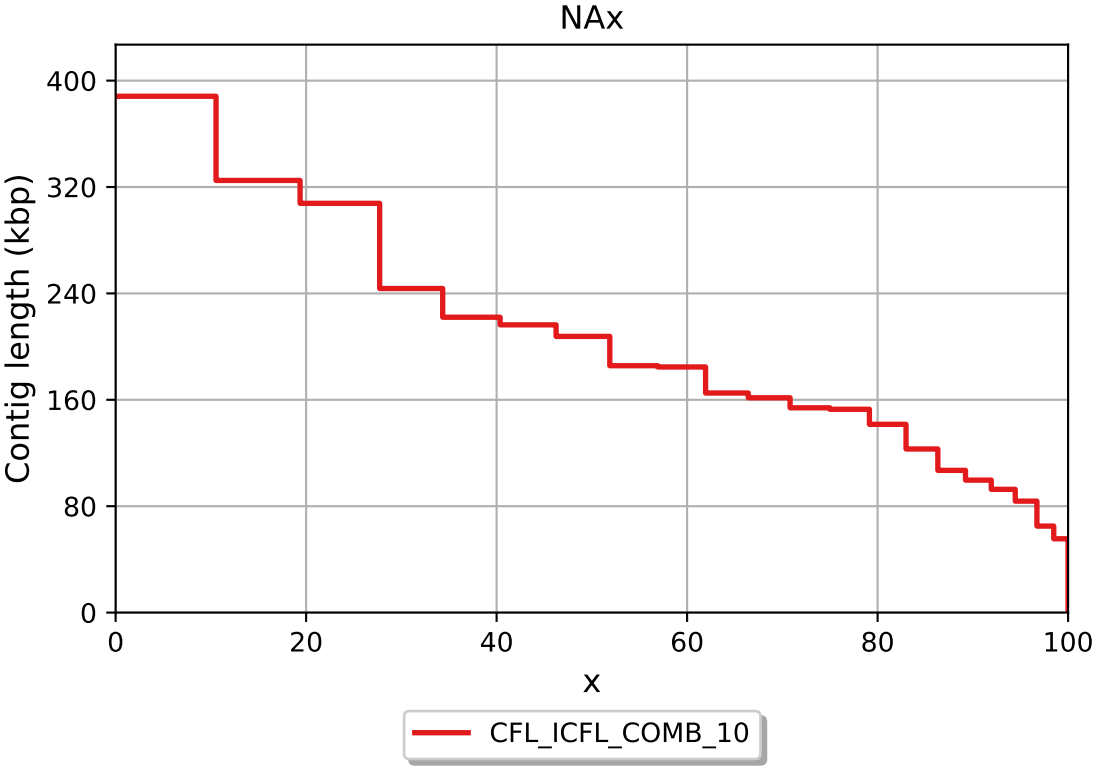

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
CFL_ICFL_COMB_10
Reference

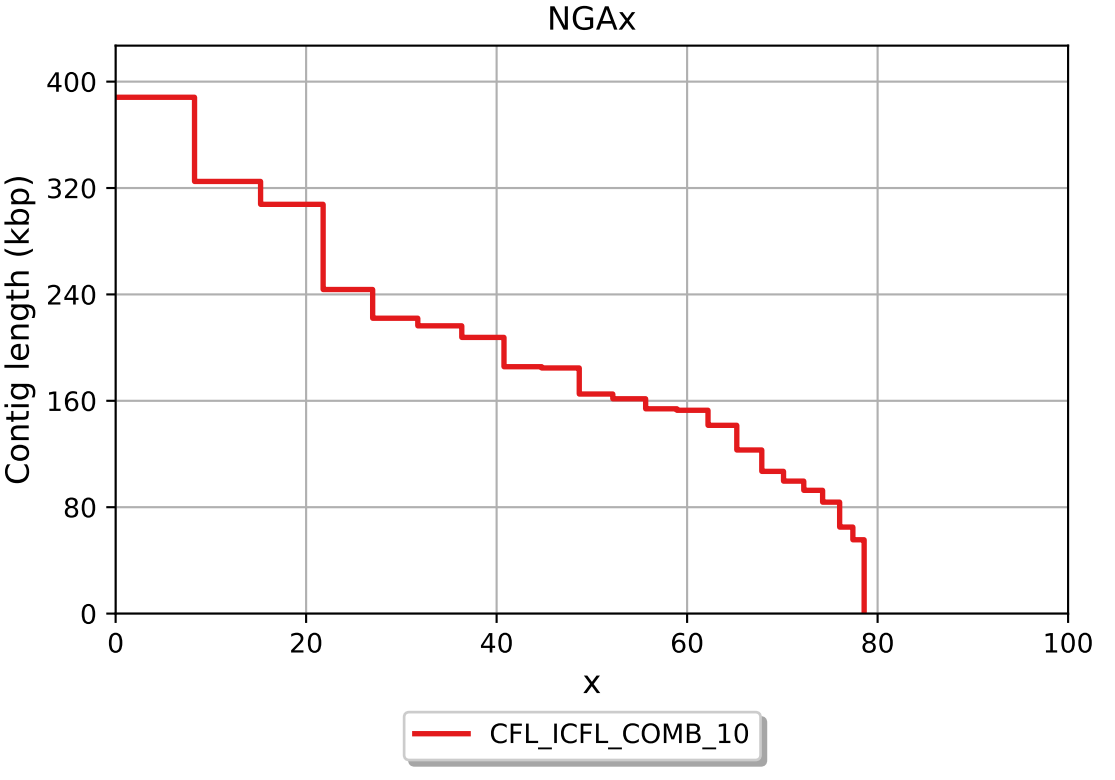

CFL_ICFL_COMB_10 GC content
contigs
GC (%)
0
3
6
9
12
15
0
20
40
60
80
100
CFL_ICFL_COMB_10

Misassemblies
5
4
3
2
1
0
CFL_ICFL_COMB_10
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
CFL_ICFL_COMB_10


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
4
8
12
16
20
Contig index
CFL_ICFL_COMB_10
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
CFL_ICFL_COMB_10


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
CFL_ICFL_COMB_10