Report

	CFL_ICFL_R_25_COMB_10
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	13
Total length (>= 0 bp)	4008961
Total length (>= 1000 bp)	4008961
Total length (>= 5000 bp)	4008961
Total length (>= 10000 bp)	4008961
Total length (>= 25000 bp)	4008961
Total length (>= 50000 bp)	4008961
# contigs	13
Largest contig	966909
Total length	4008961
Reference length	4686137
GC (%)	50.81
Reference GC (%)	50.78
N50	614695
NG50	423213
N90	144184
NG90	-
auN	536226.3
auNG	458738.3
L50	3
LG50	4
L90	9
LG90	-
# misassemblies	3
# misassembled contigs	2
Misassembled contigs length	1601893
# 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 (%)	85.549
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	859729
Total aligned length	4008961
NA50	382868
NGA50	257519
NA90	134689
NGA90	-
auNA	440962.1
auNGA	377240.3
LA50	4
LGA50	5
LA90	11
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

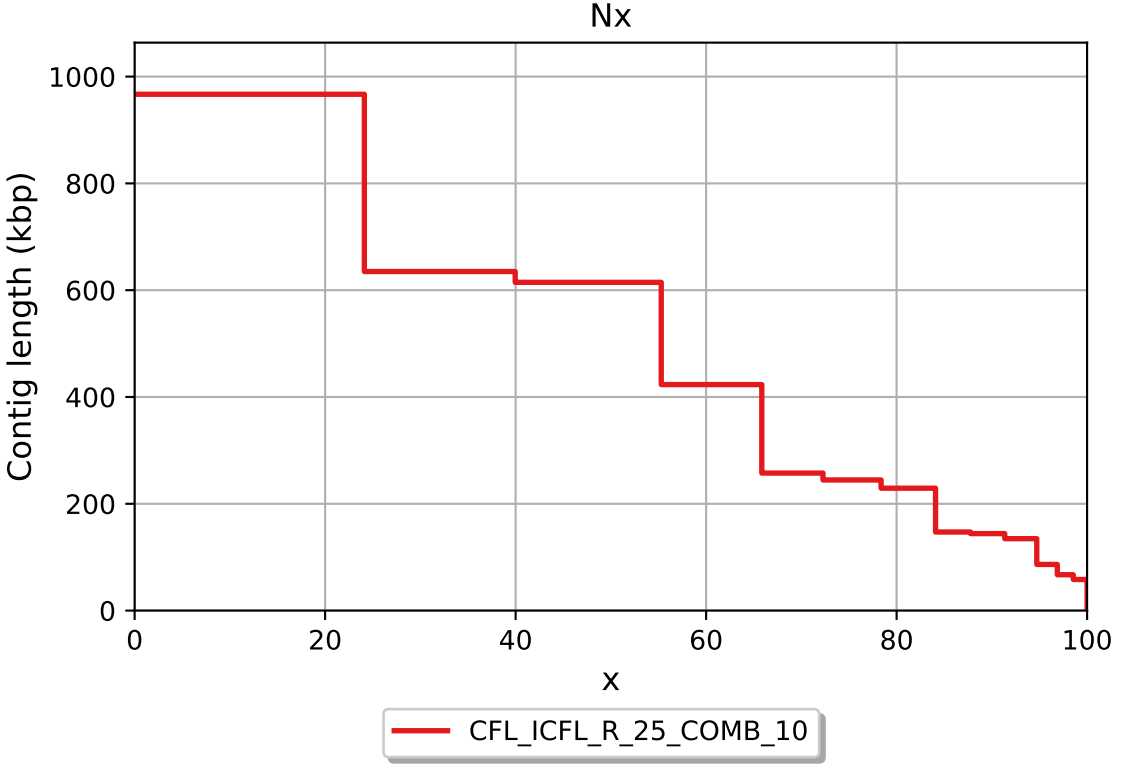
	CFL_ICFL_R_25_COMB_10
# misassemblies	3
# contig misassemblies	3
# c. relocations	3
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	1601893
# local misassemblies	0
# scaffold 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

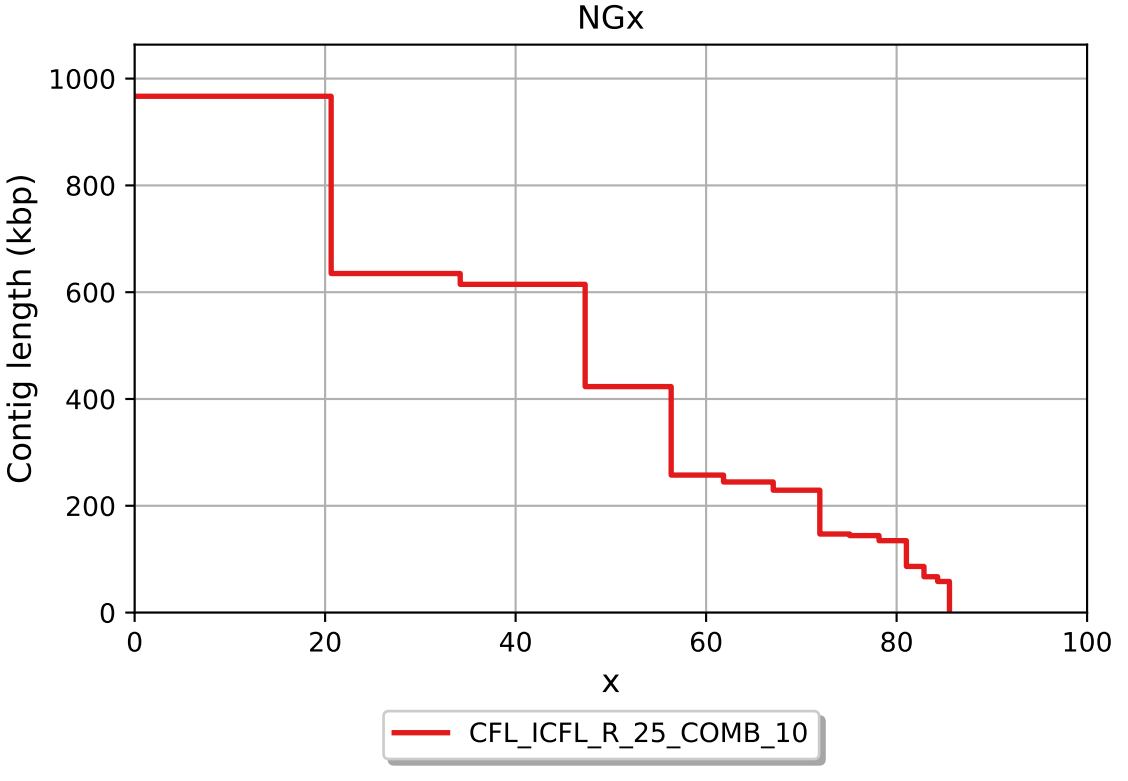
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

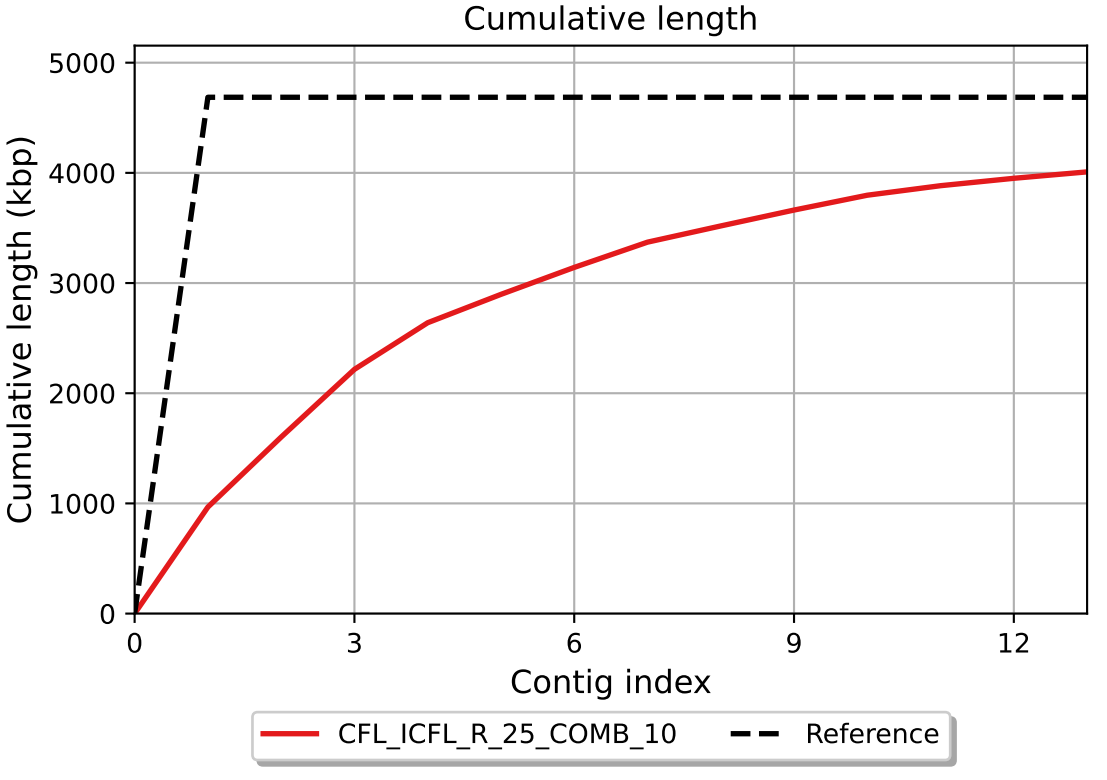
Unaligned report

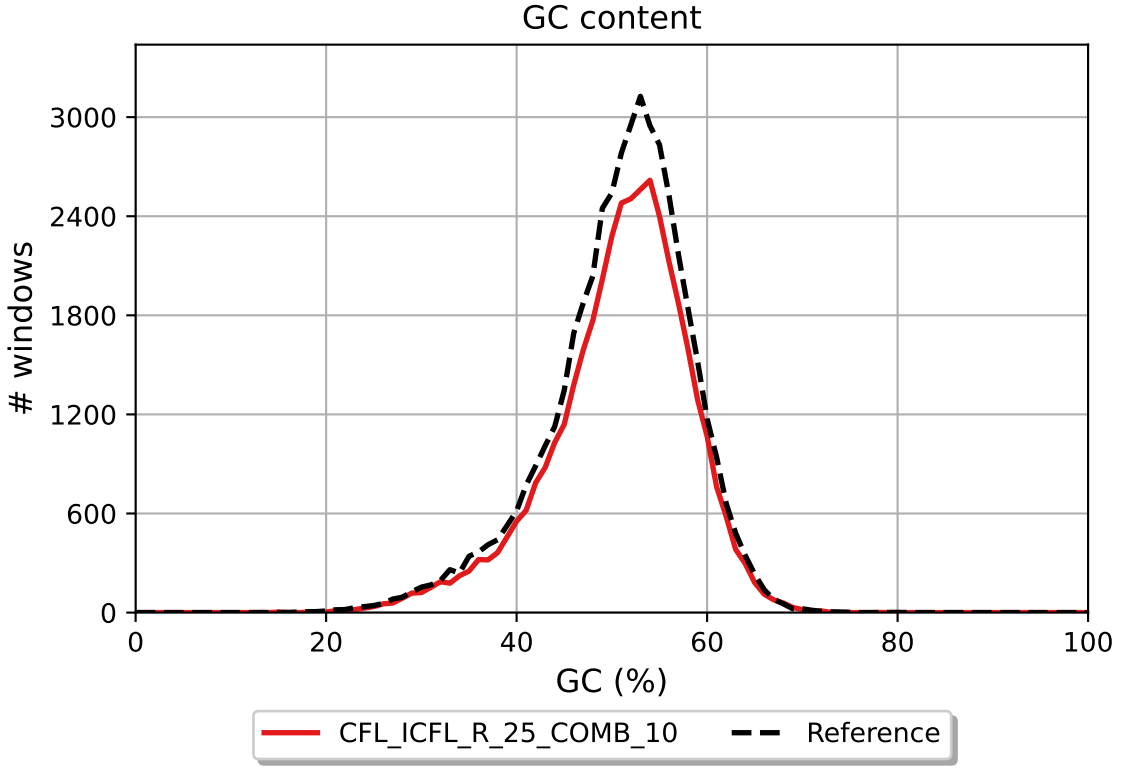
	CFL_ICFL_R_25_COMB_10
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

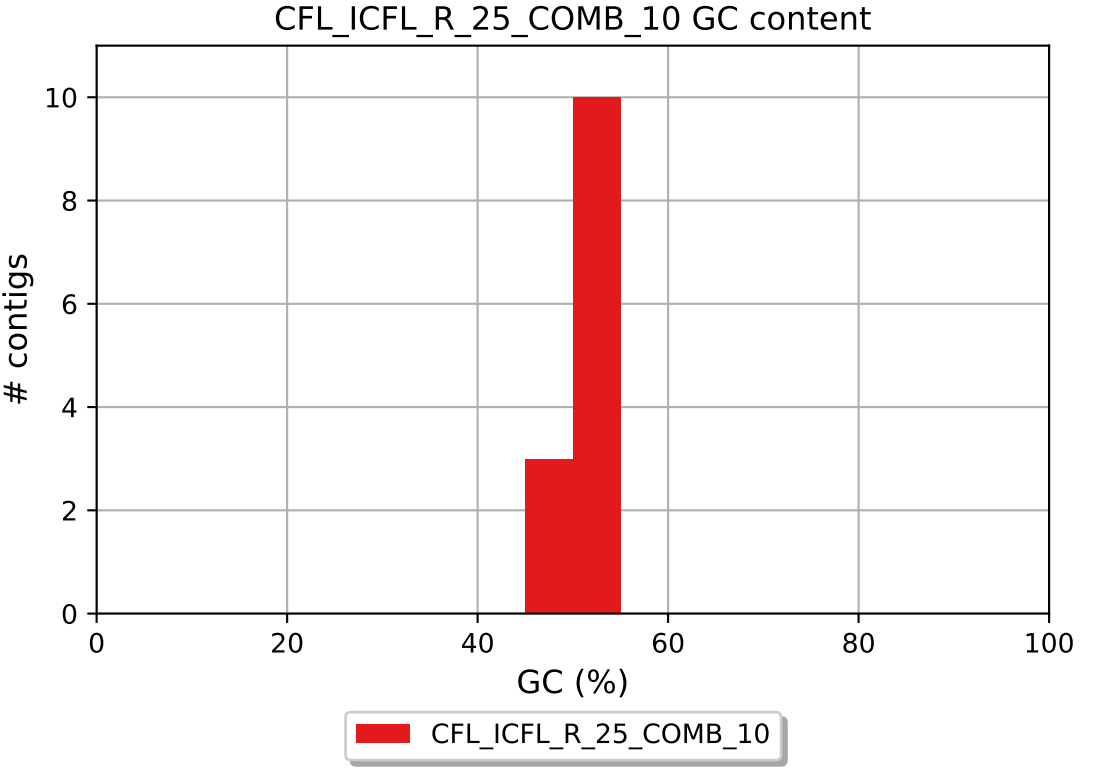
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

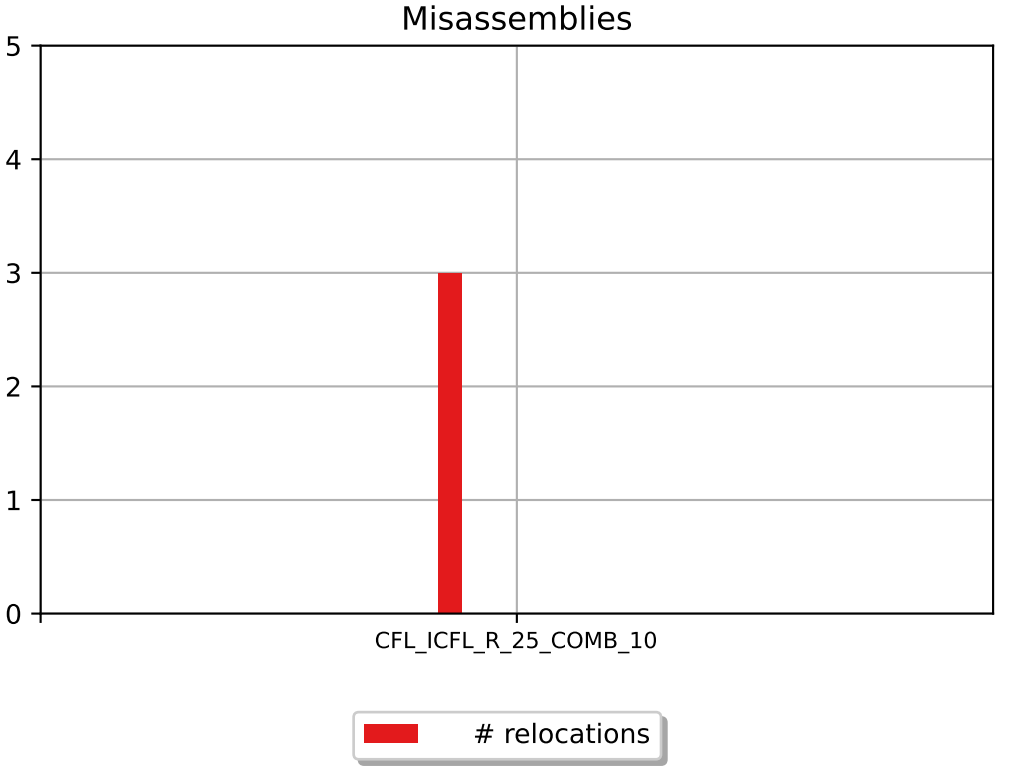

Nx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_10

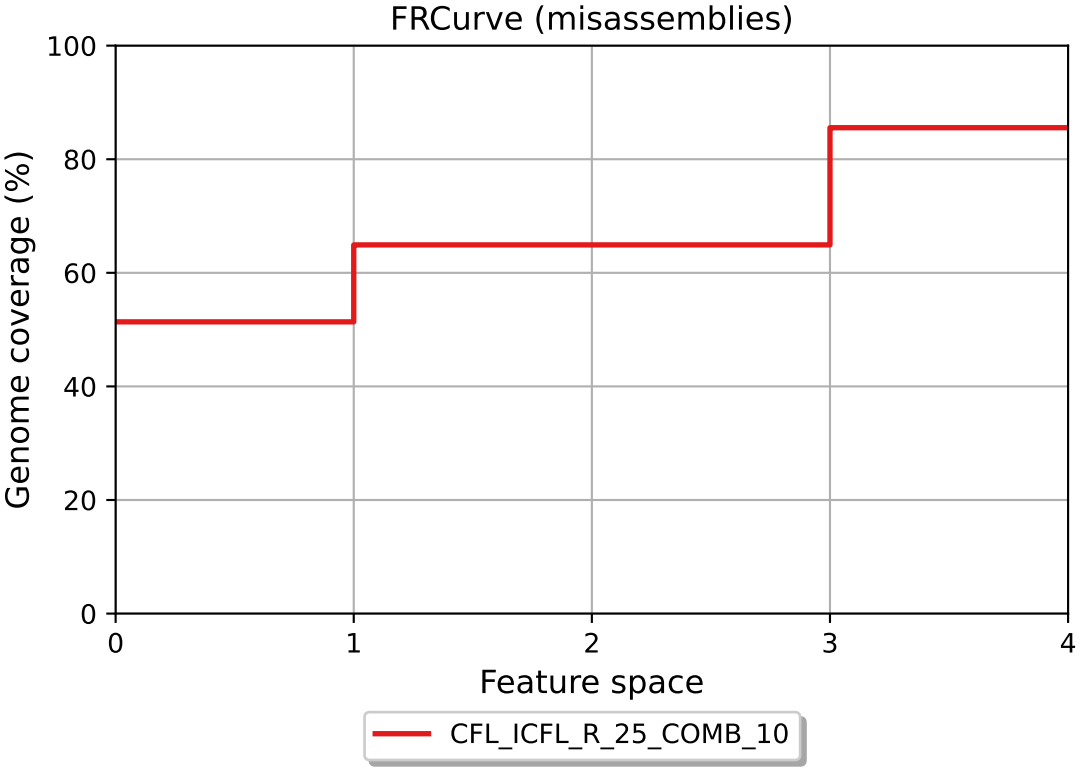

NGx
Contig length (kbp)
1000
800
600
400
200
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_10

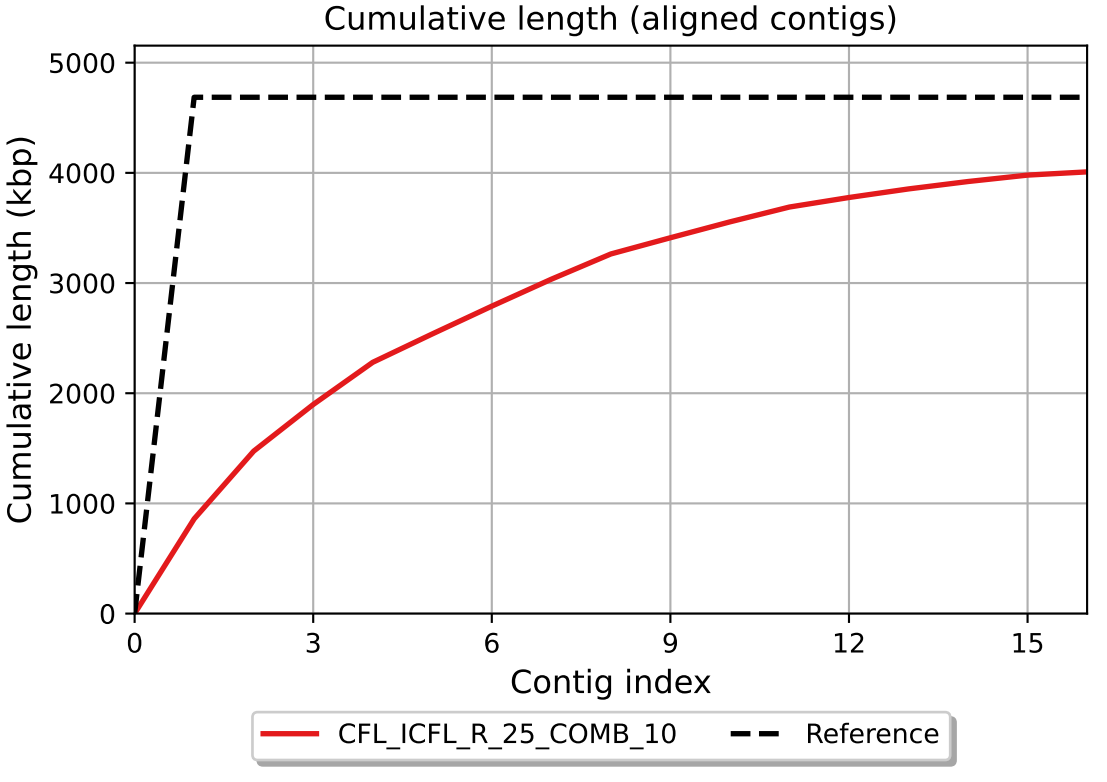

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
Contig index
CFL_ICFL_R_25_COMB_10
Reference

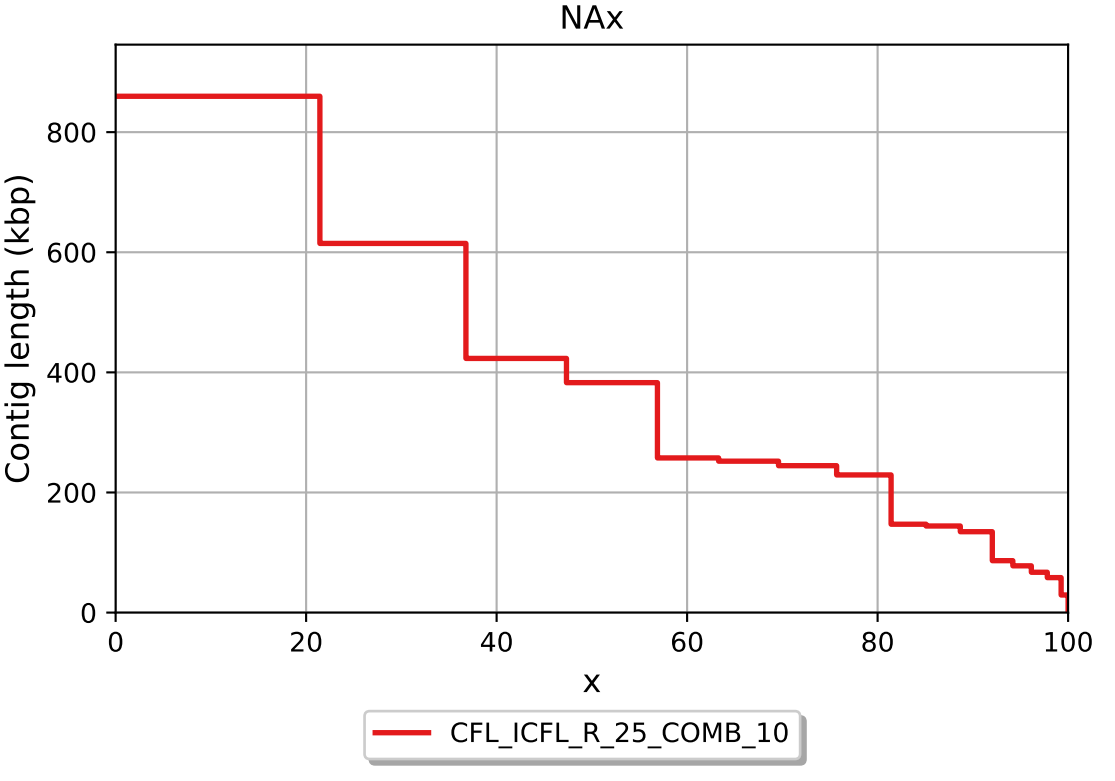

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
CFL_ICFL_R_25_COMB_10
Reference

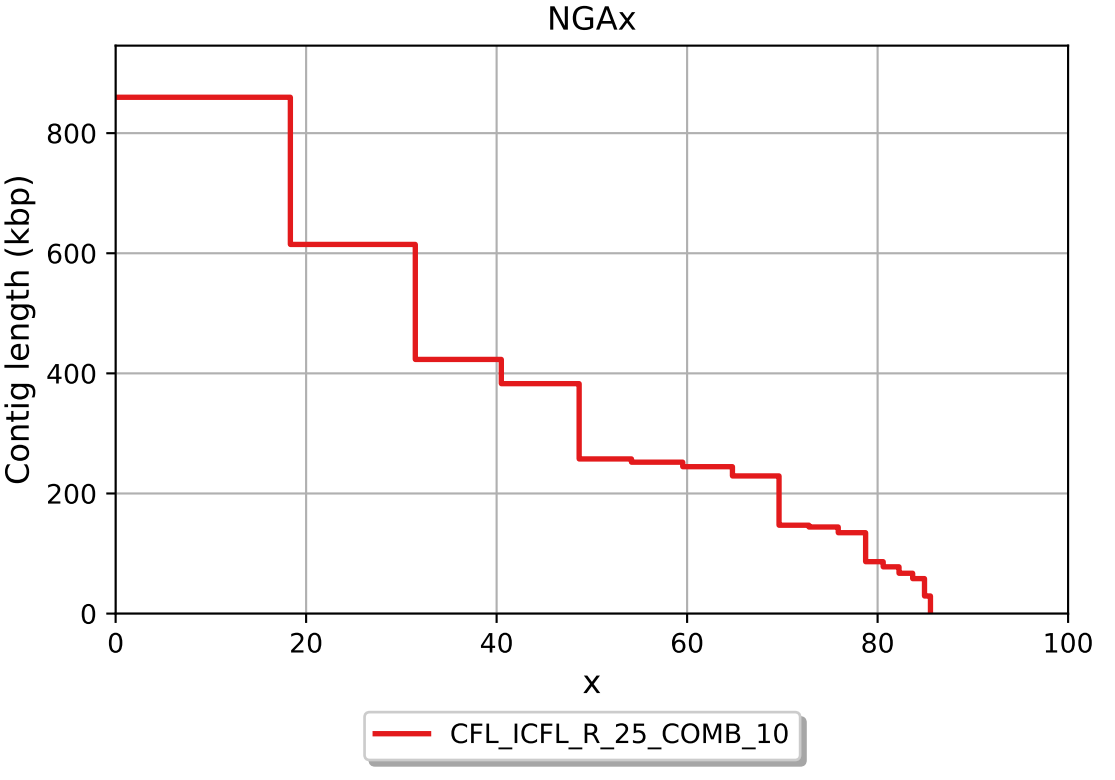

CFL_ICFL_R_25_COMB_10 GC content
contigs
0
2
4
6
8
10
0
20
40
60
80
100
GC (%)
CFL_ICFL_R_25_COMB_10


Misassemblies
5
4
3
2
1
0
CFL_ICFL_R_25_COMB_10
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
3
4
Feature space
CFL_ICFL_R_25_COMB_10


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
3
6
9
12
15
Contig index
CFL_ICFL_R_25_COMB_10
Reference


NAx
Contig length (kbp)
800
600
400
200
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_10


NGAx
Contig length (kbp)
0
200
400
600
800
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_10