Report

	CFL_ICFL_R_25_COMB_25
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	4616050
Total length (>= 1000 bp)	4616050
Total length (>= 5000 bp)	4616050
Total length (>= 10000 bp)	4616050
Total length (>= 25000 bp)	4616050
Total length (>= 50000 bp)	4616050
# contigs	3
Largest contig	3945701
Total length	4616050
Reference length	4686137
GC (%)	50.74
Reference GC (%)	50.78
N50	3945701
NG50	3945701
N90	520416
NG90	520416
auN	3436242.9
auNG	3384849.6
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	149933
# 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 (%)	97.834
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	3945701
Total aligned length	4616050
NA50	3945701
NGA50	3945701
NA90	520416
NGA90	520416
auNA	3435626.6
auNGA	3384242.6
LA50	1
LGA50	1
LA90	2
LGA90	2

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

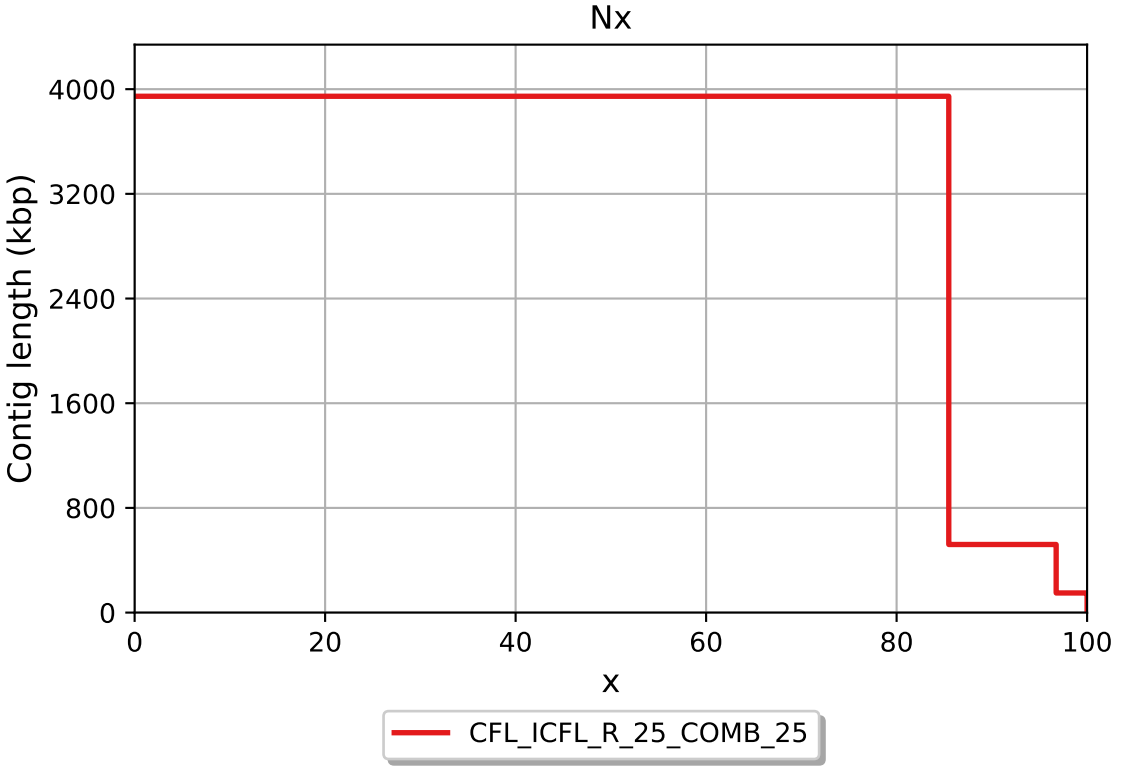
	CFL_ICFL_R_25_COMB_25
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	149933
# local misassemblies	0
# scaffold 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

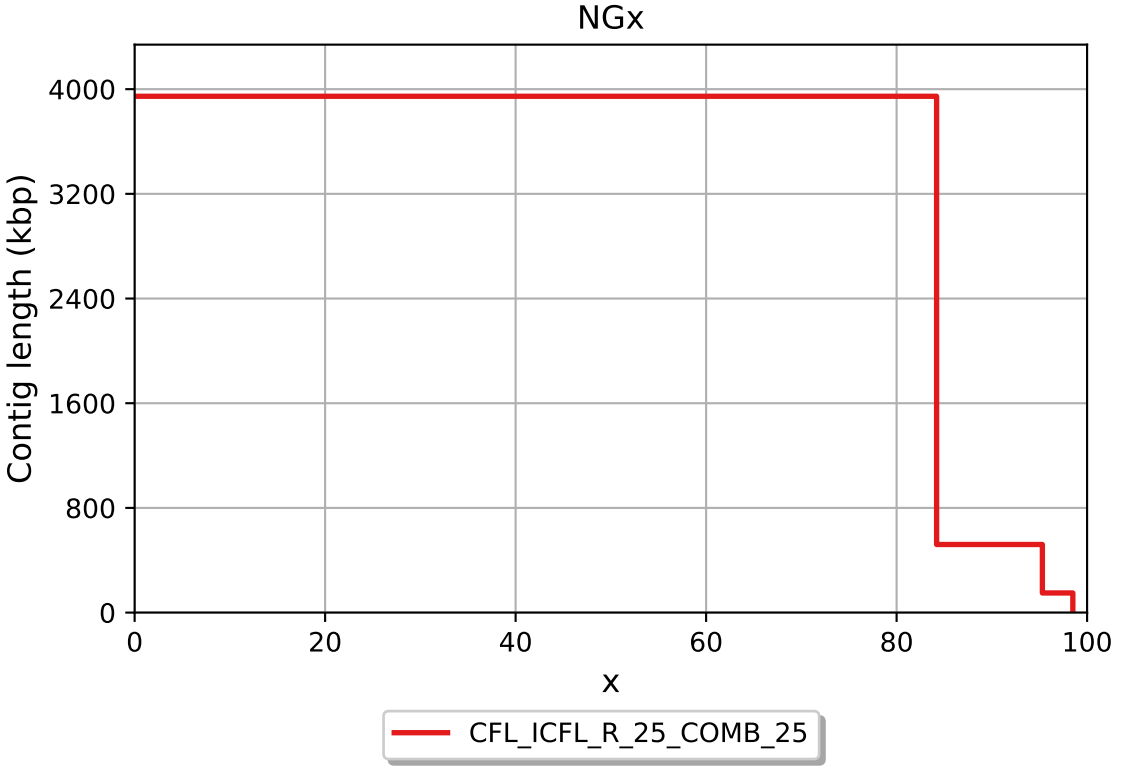
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

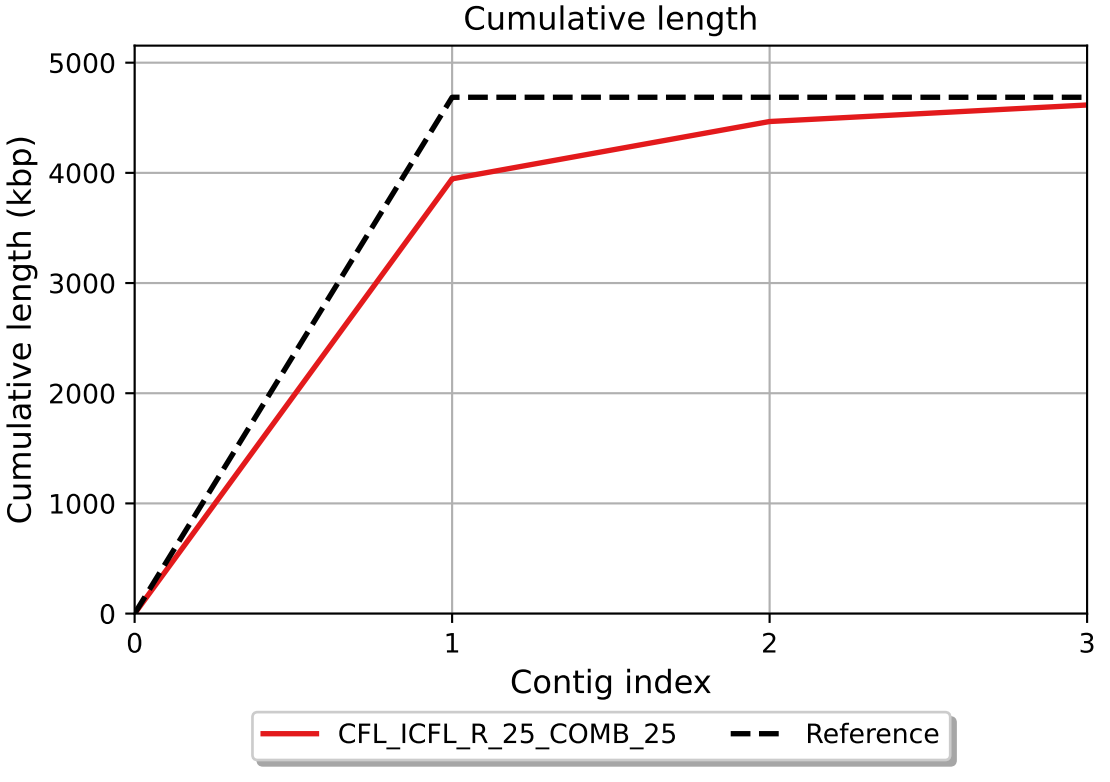
Unaligned report

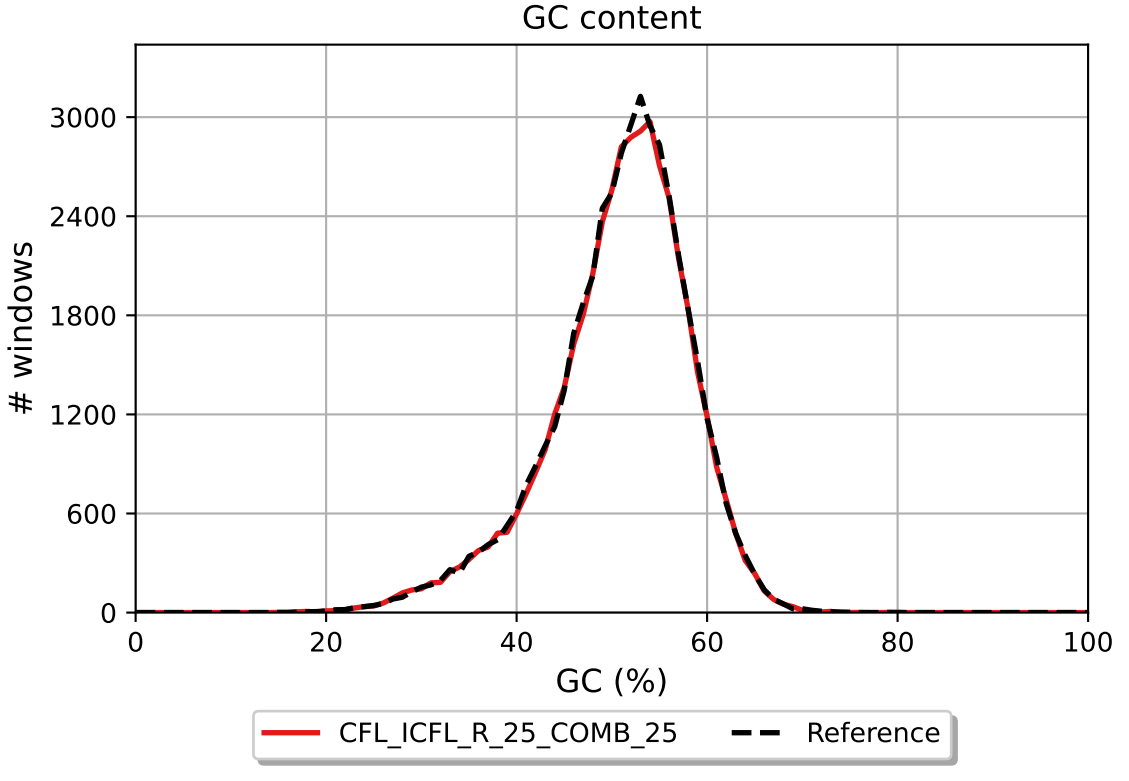
	CFL_ICFL_R_25_COMB_25
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

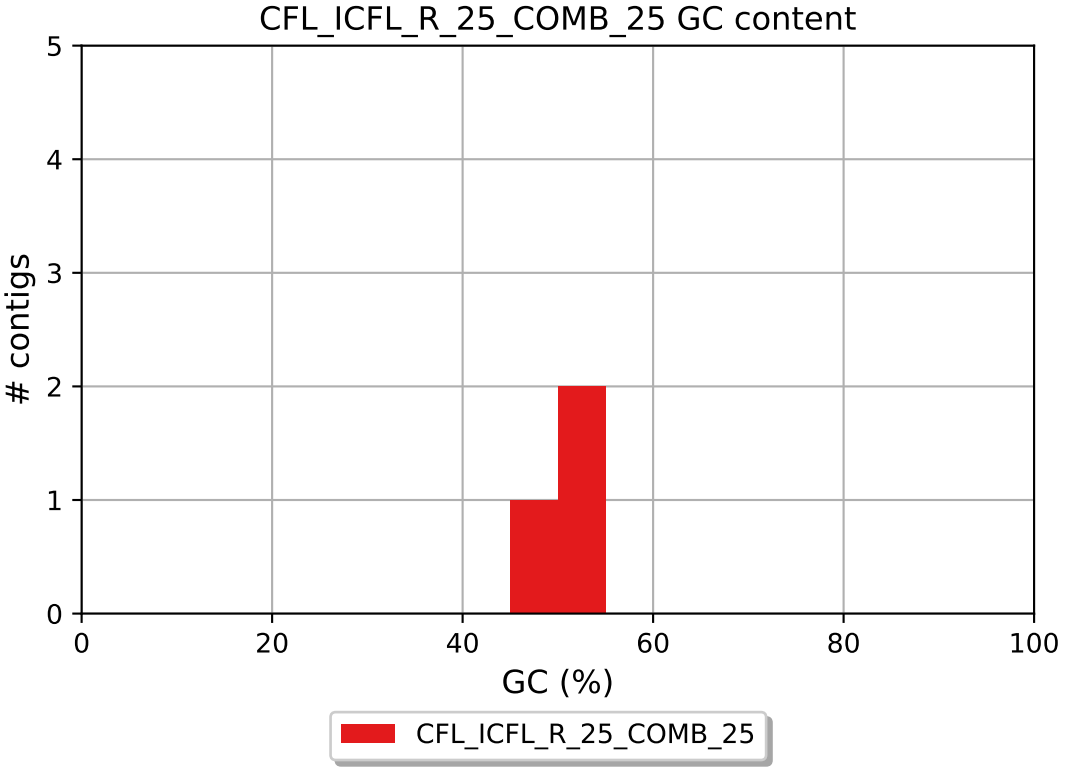
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

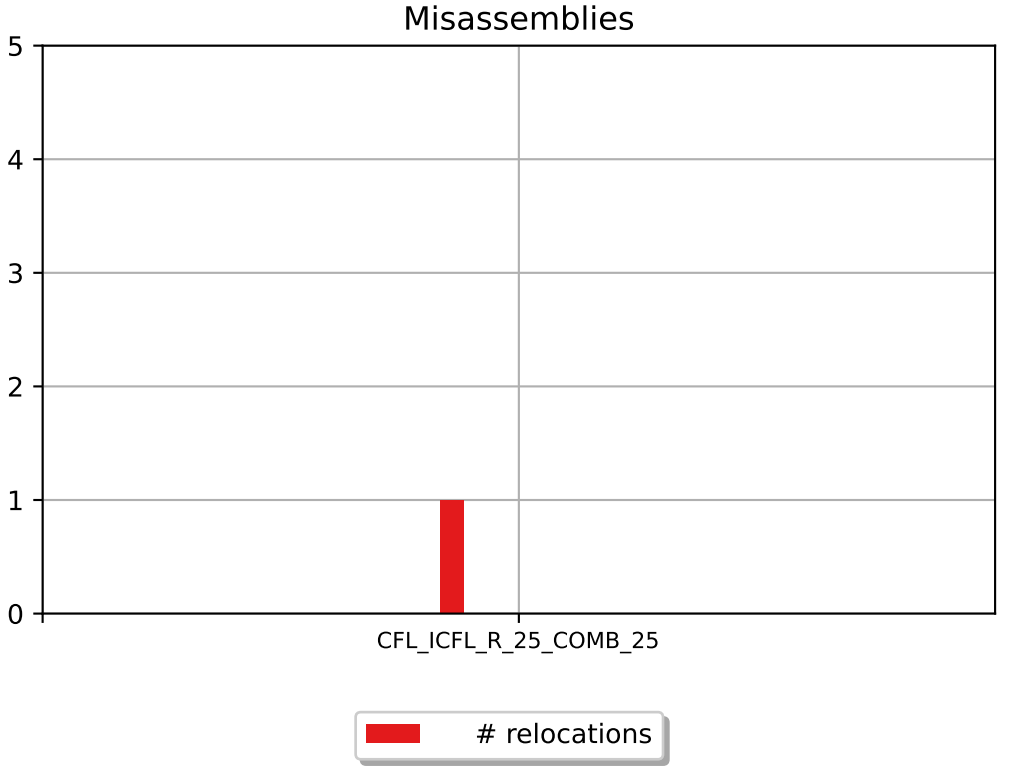

Nx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_25

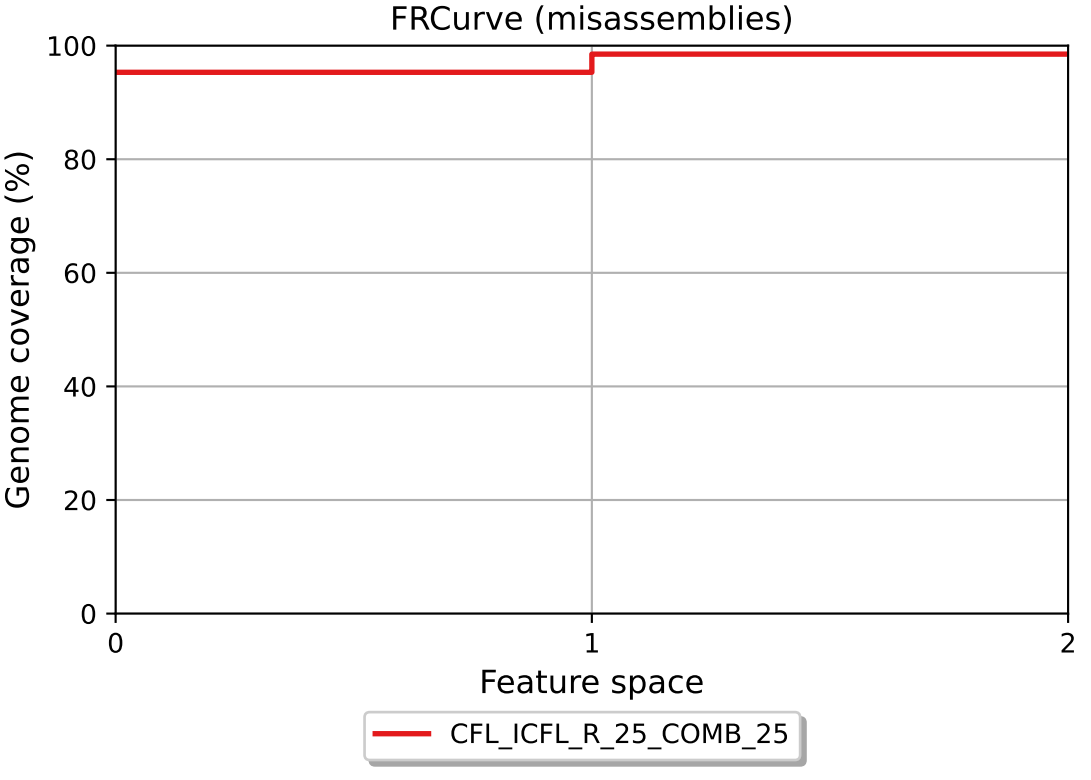

NGx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_25

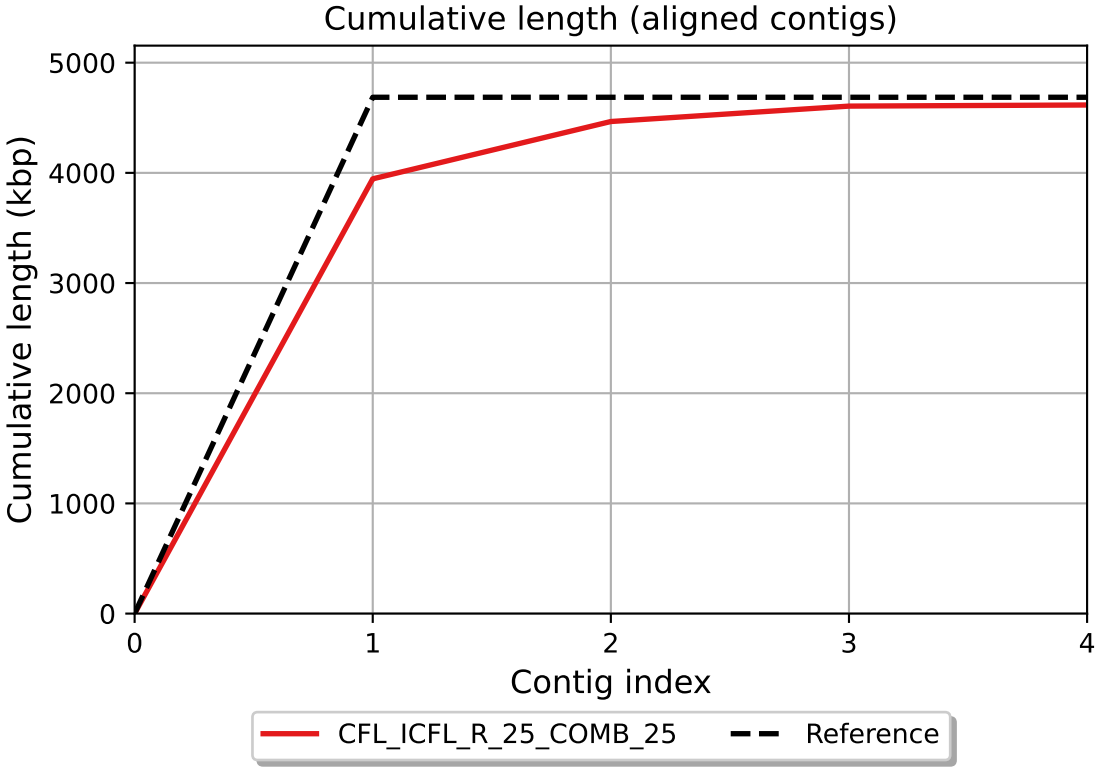

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
Contig index
CFL_ICFL_R_25_COMB_25
Reference

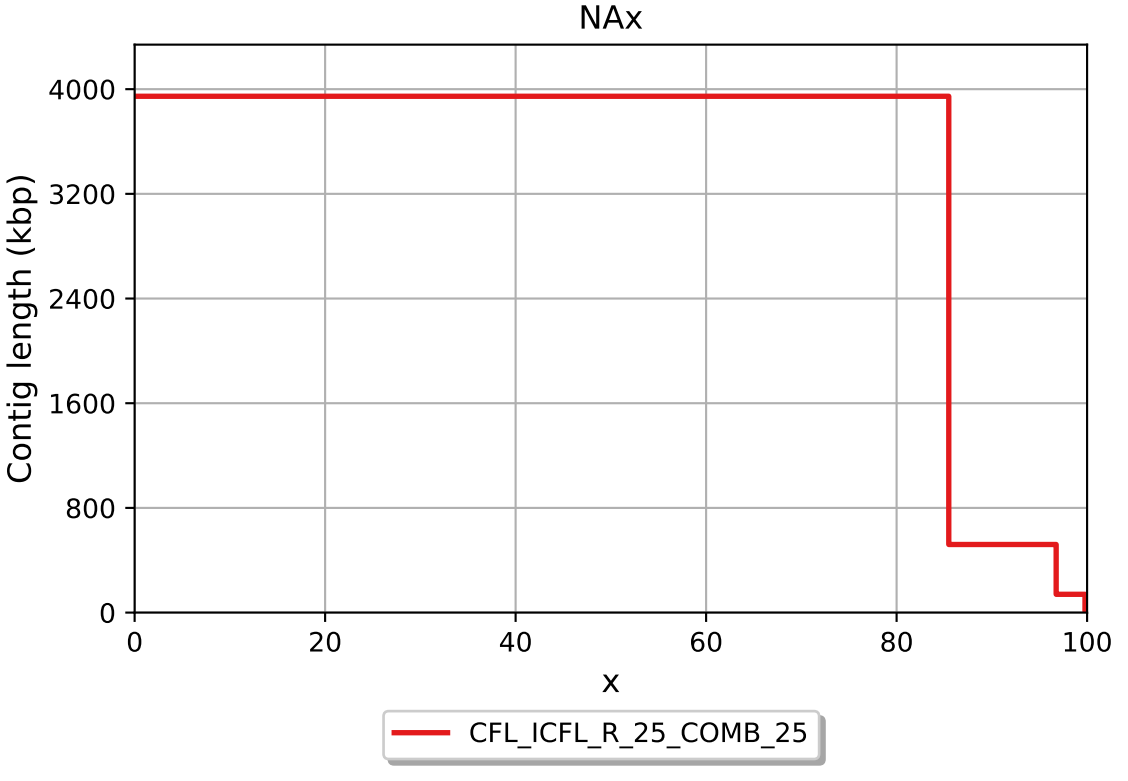

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
CFL_ICFL_R_25_COMB_25
Reference

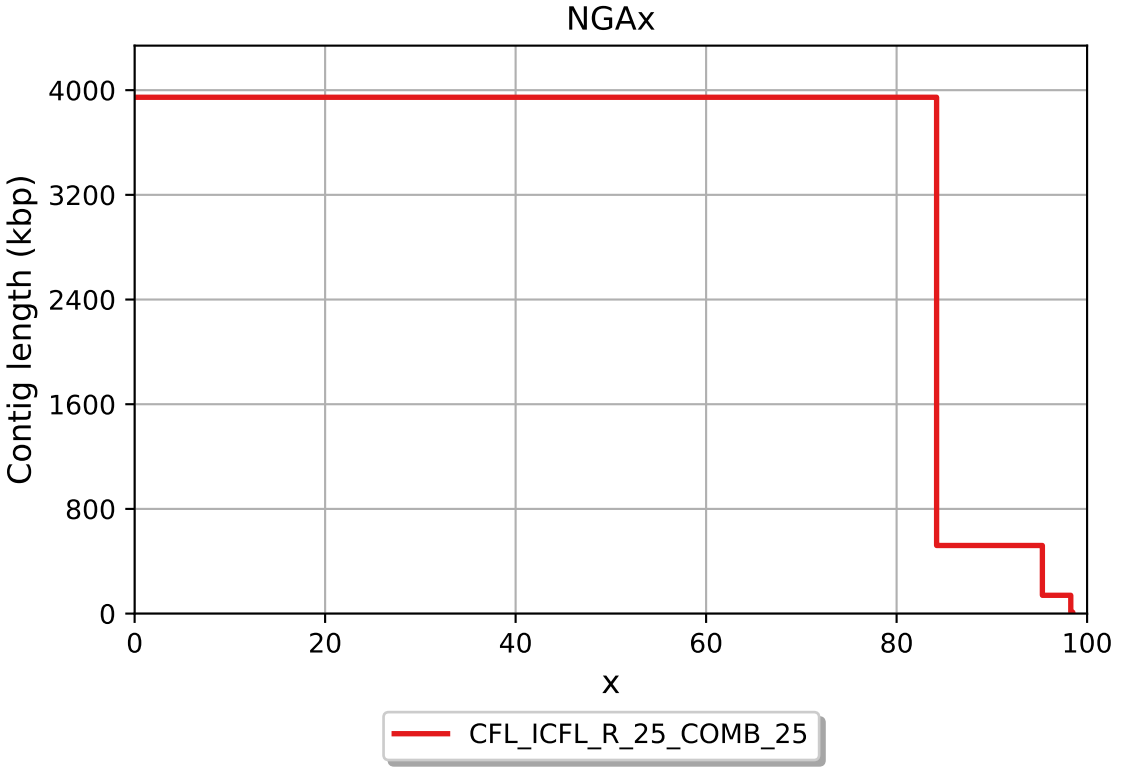

CFL_ICFL_R_25_COMB_25 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
CFL_ICFL_R_25_COMB_25


Misassemblies
5
4
3
2
1
0
CFL_ICFL_R_25_COMB_25
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
CFL_ICFL_R_25_COMB_25


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1
2
3
4
Contig index
CFL_ICFL_R_25_COMB_25
Reference


NAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_25


NGAx
Contig length (kbp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
CFL_ICFL_R_25_COMB_25