Report

	CFL_ICFL_R_35_COMB_100
# 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)	4672180
Total length (>= 1000 bp)	4672180
Total length (>= 5000 bp)	4672180
Total length (>= 10000 bp)	4672180
Total length (>= 25000 bp)	4672180
Total length (>= 50000 bp)	4672180
# contigs	3
Largest contig	3980974
Total length	4672180
Reference length	4686137
GC (%)	50.73
Reference GC (%)	50.78
N50	3980974
NG50	3980974
N90	529247
NG90	529247
auN	3457590.9
auNG	3447293.0
L50	1
LG50	1
L90	2
LG90	2
# 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 (%)	98.742
Duplication ratio	1.010
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.04
# indels per 100 kbp	0.00
Largest alignment	3980974
Total aligned length	4672038
NA50	3980974
NGA50	3980974
NA90	529247
NGA90	529247
auNA	3457581.1
auNGA	3447283.1
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).
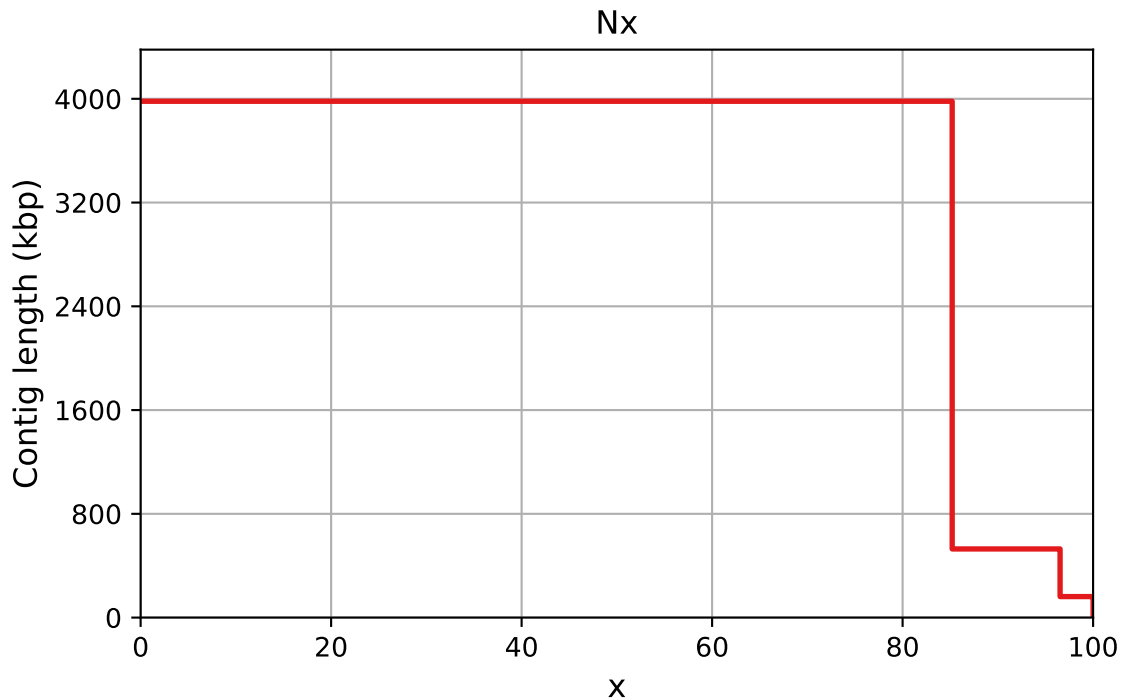
Misassemblies report
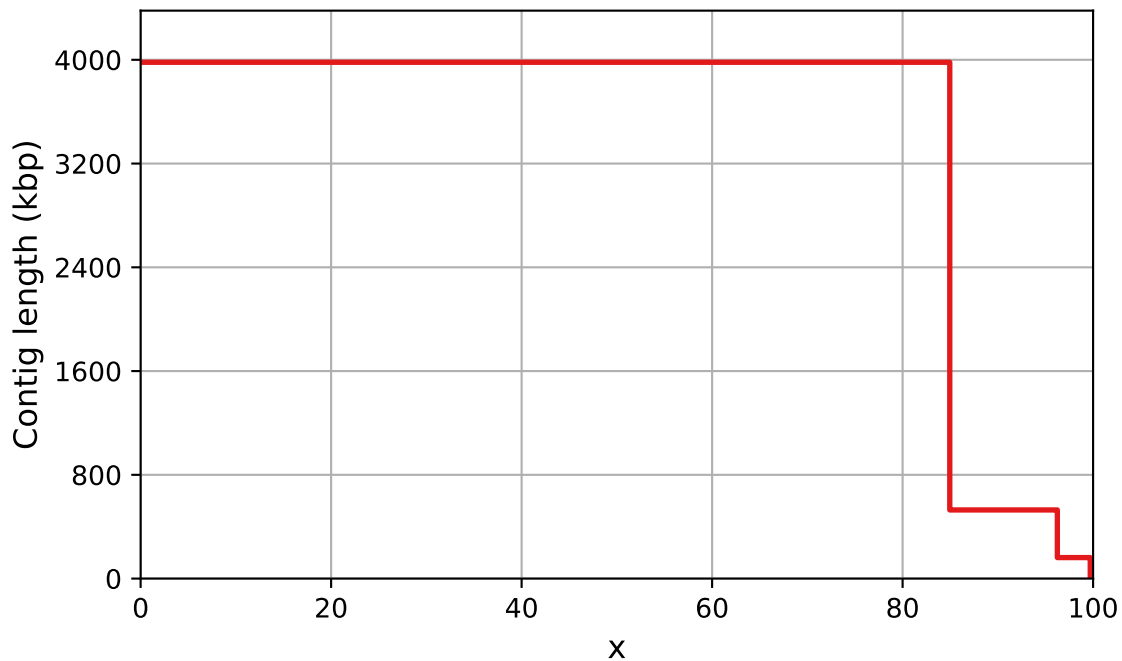
	CFL_ICFL_R_35_COMB_100
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	142
# 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).
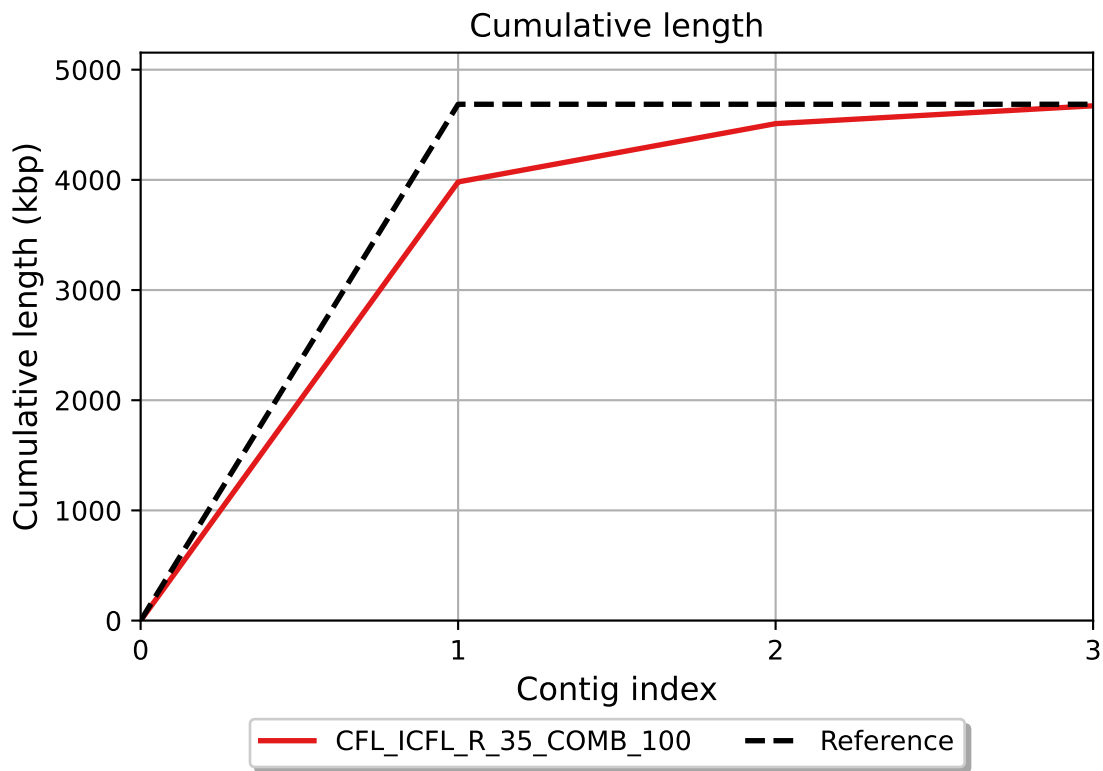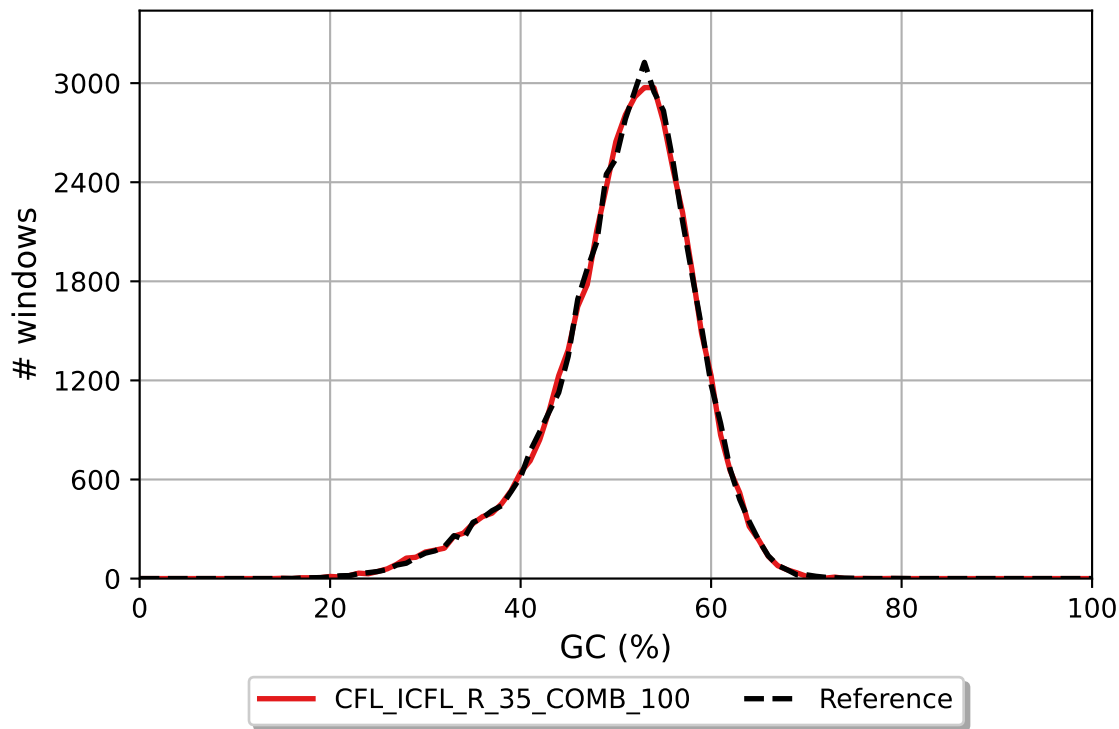
Unaligned report

	CFL_ICFL_R_35_COMB_100
# 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).
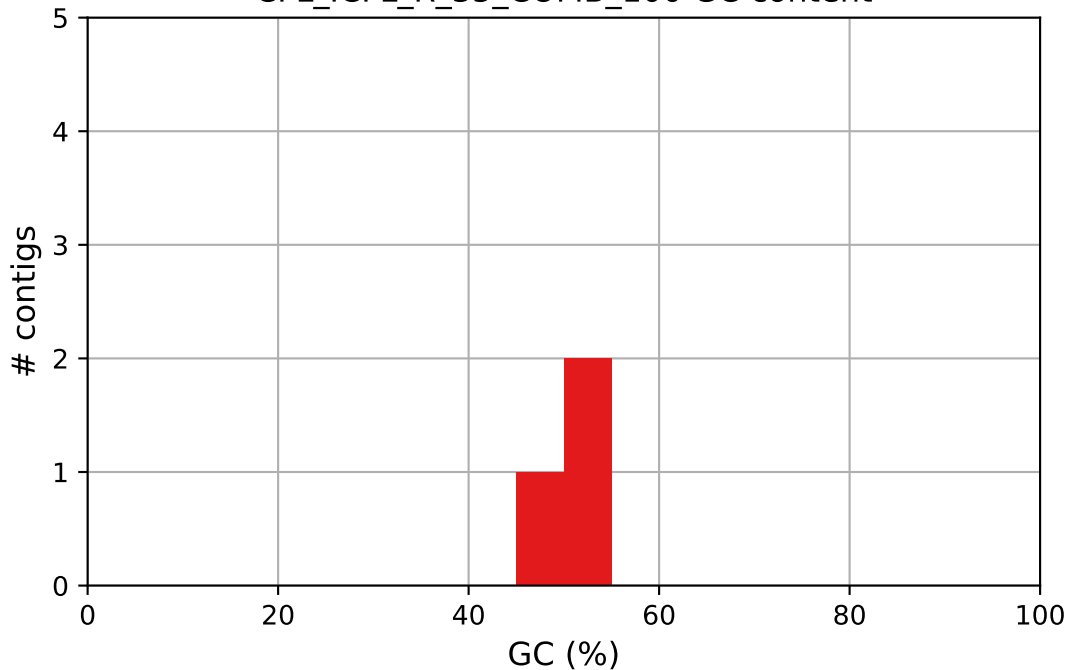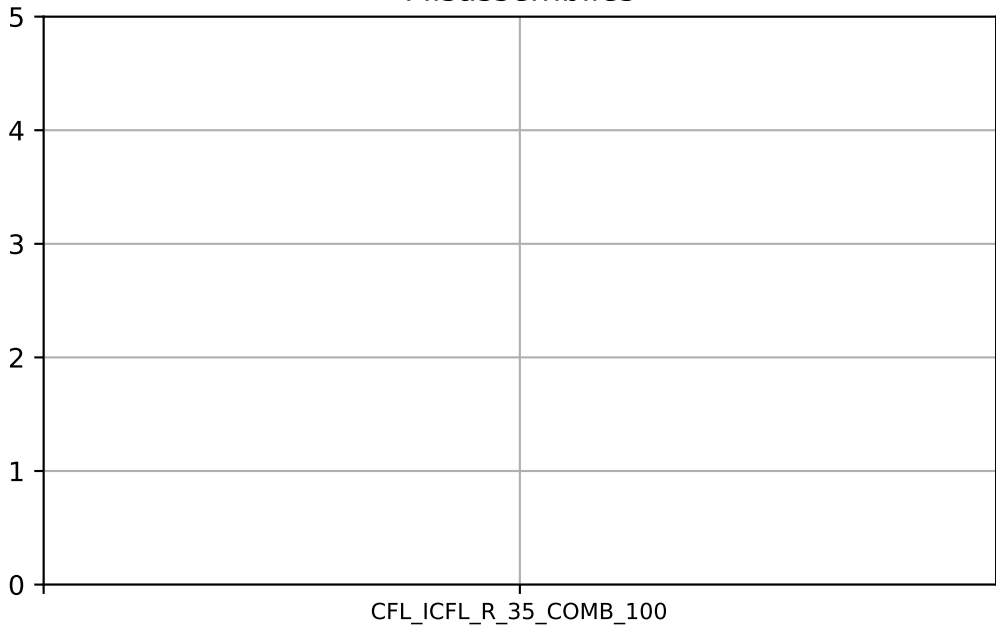
Nx

CFL_ICFL_R_35_COMB_100

NGx

CFL_ICFL_R_35_COMB_100

Cumulative length

GC content

CFL_ICFL_R_35_COMB_100 GC content
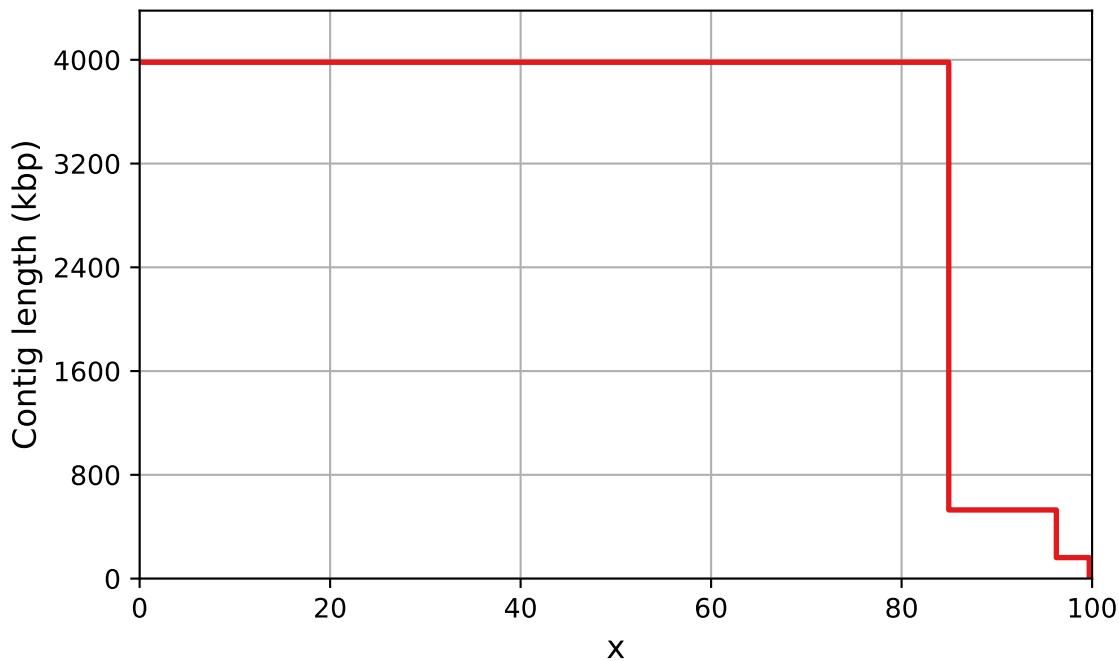
Misassemblies

CFL_ICFL_R_35_COMB_100

FRCurve (misassemblies)

Genome coverage (%)

Feature space

CFL_ICFL_R_35_COMB_100
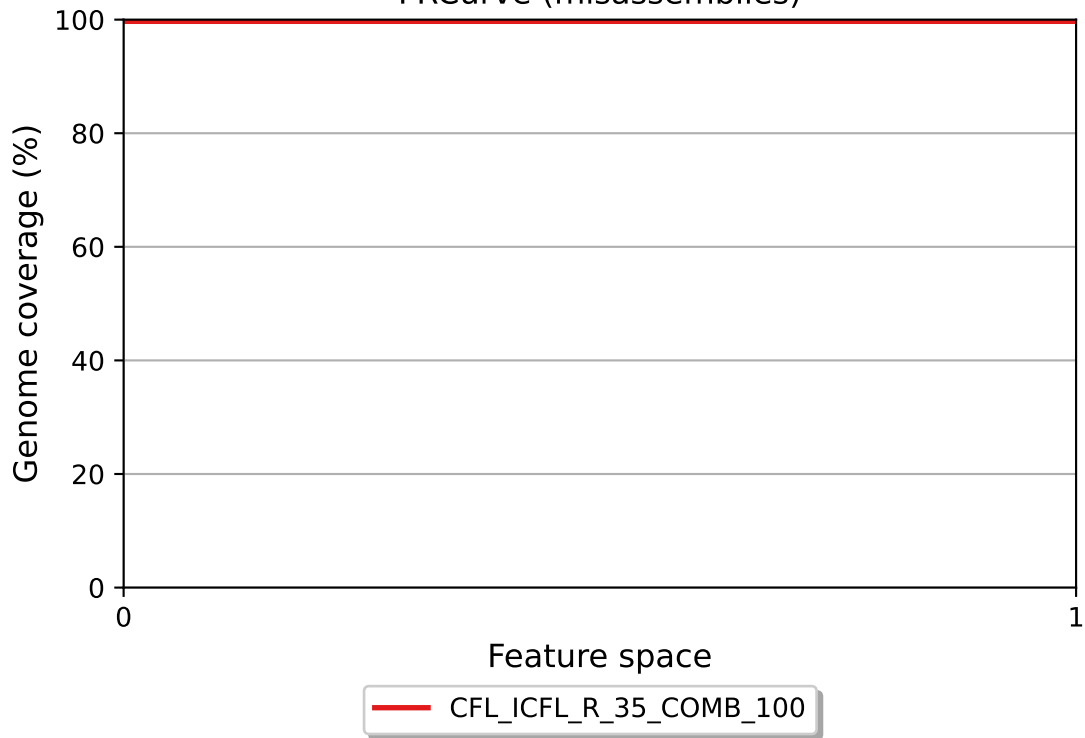
Cumulative length (aligned contigs)

NAx

NGAx