Report

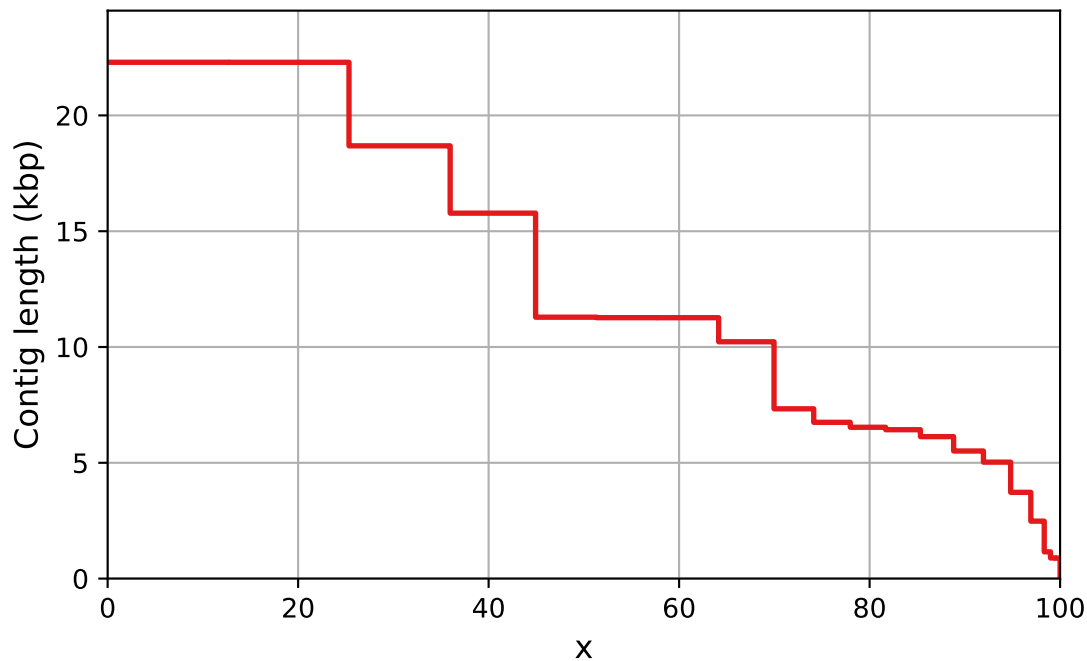|	84_3_80.30
# contigs (>= 0 bp)	20
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	175937
Total length (>= 1000 bp)	174163
Total length (>= 5000 bp)	166803
Total length (>= 10000 bp)	123096
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	20
Largest contig	22294
Total length	175937
Reference length	29903
N50	11287
N75	6748
L50	5
L75	10
# 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 (%)	99.064
Duplication ratio	5.939
# N's per 100 kbp	0.00
# mismatches per 100 kbp	195.79
# indels per 100 kbp	27.01
Largest alignment	22293
Total aligned length	175922
NA50	11286
NA75	6747
LA50	5
LA75	10

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

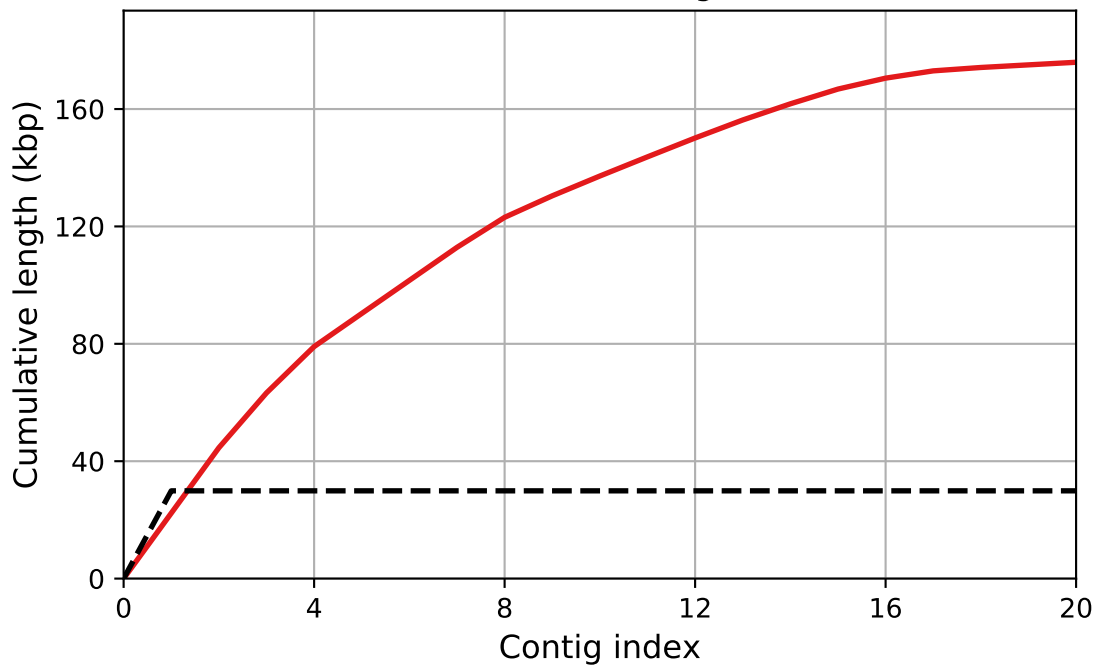|	84_3_80.30
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# c. interspecies translocations	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# s. interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	58
# indels	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	8

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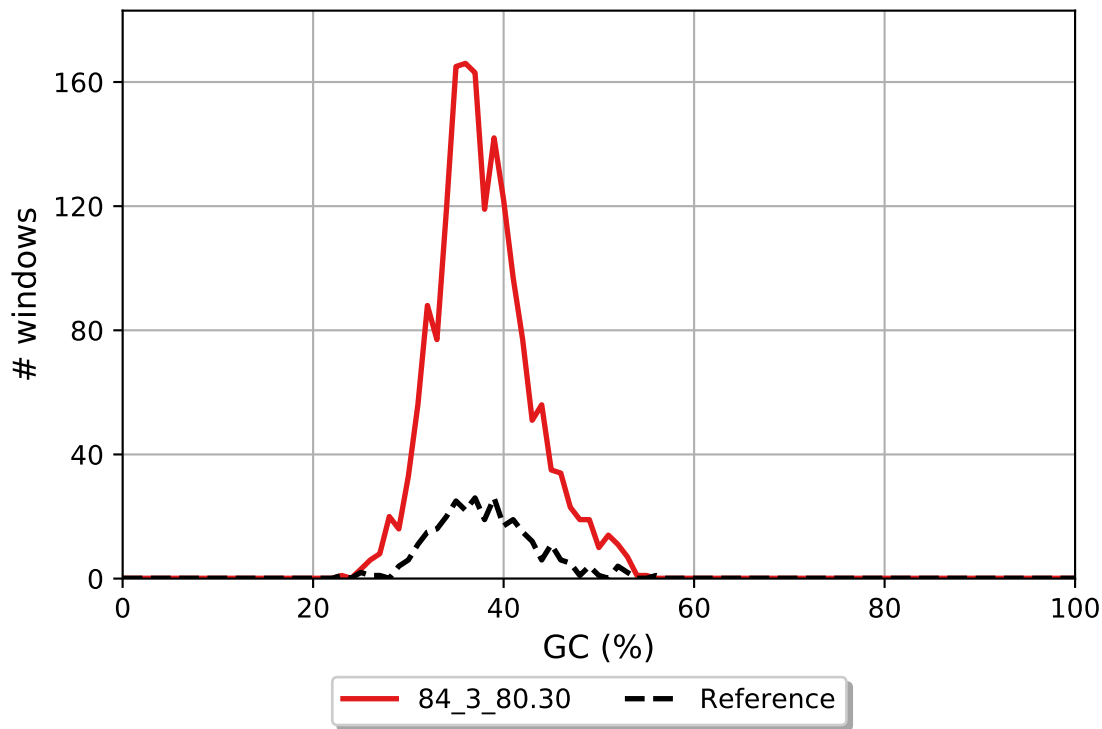(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	84_3_80.30
# 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

Cumulative length

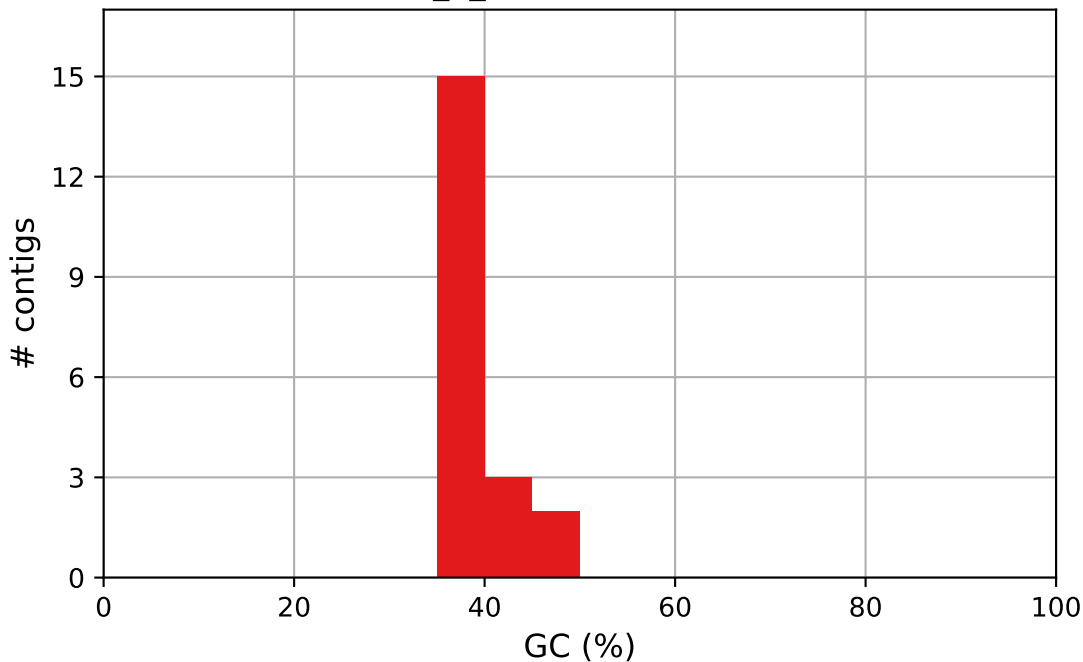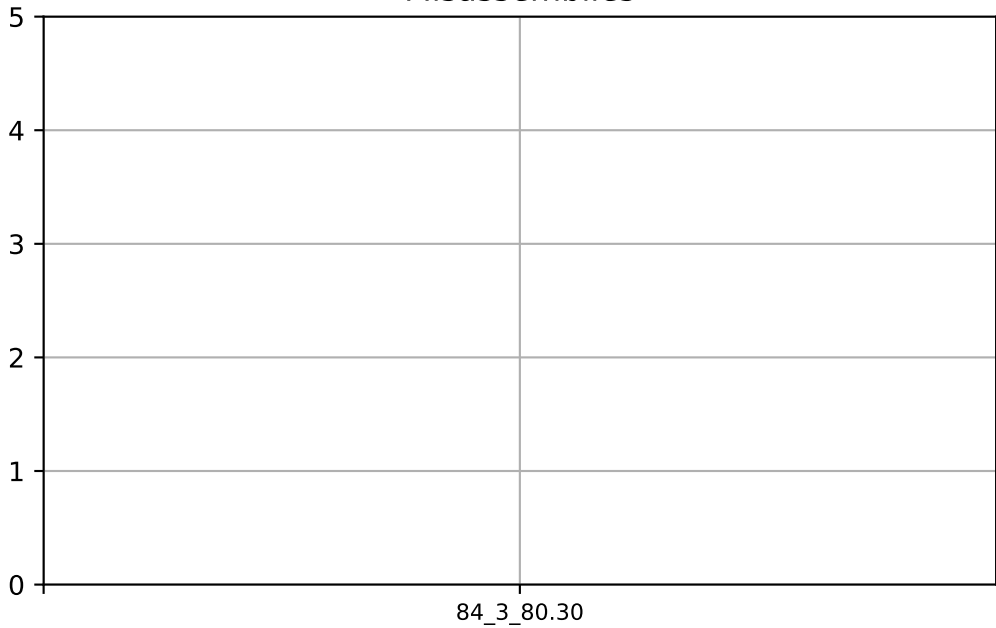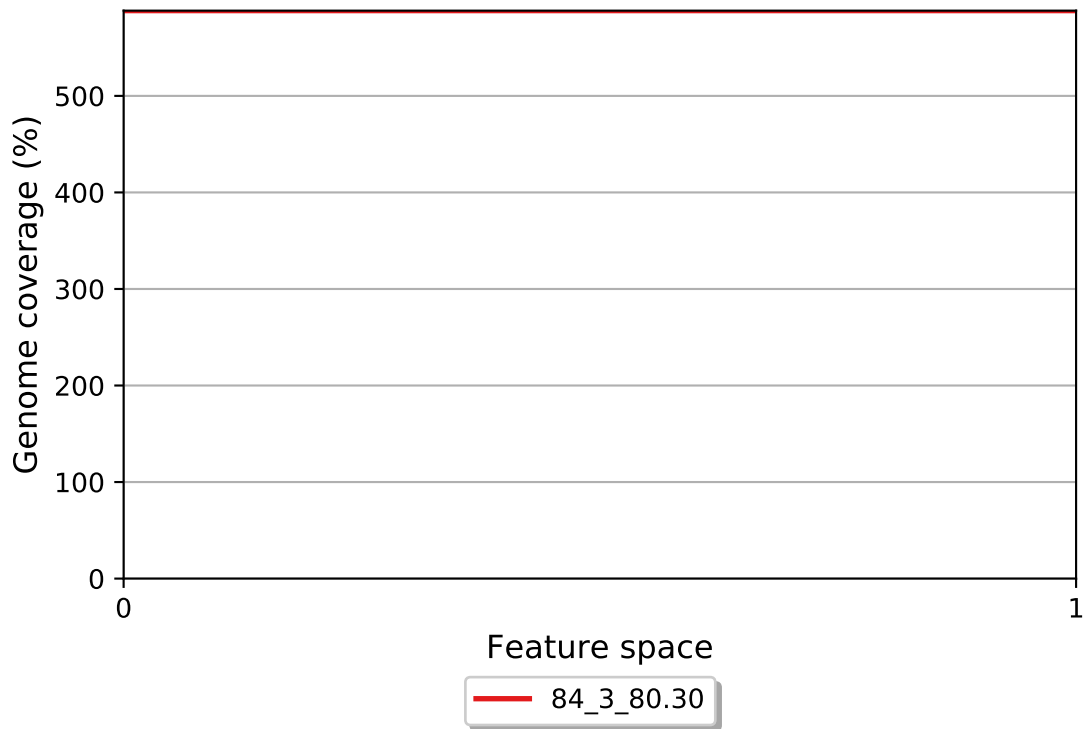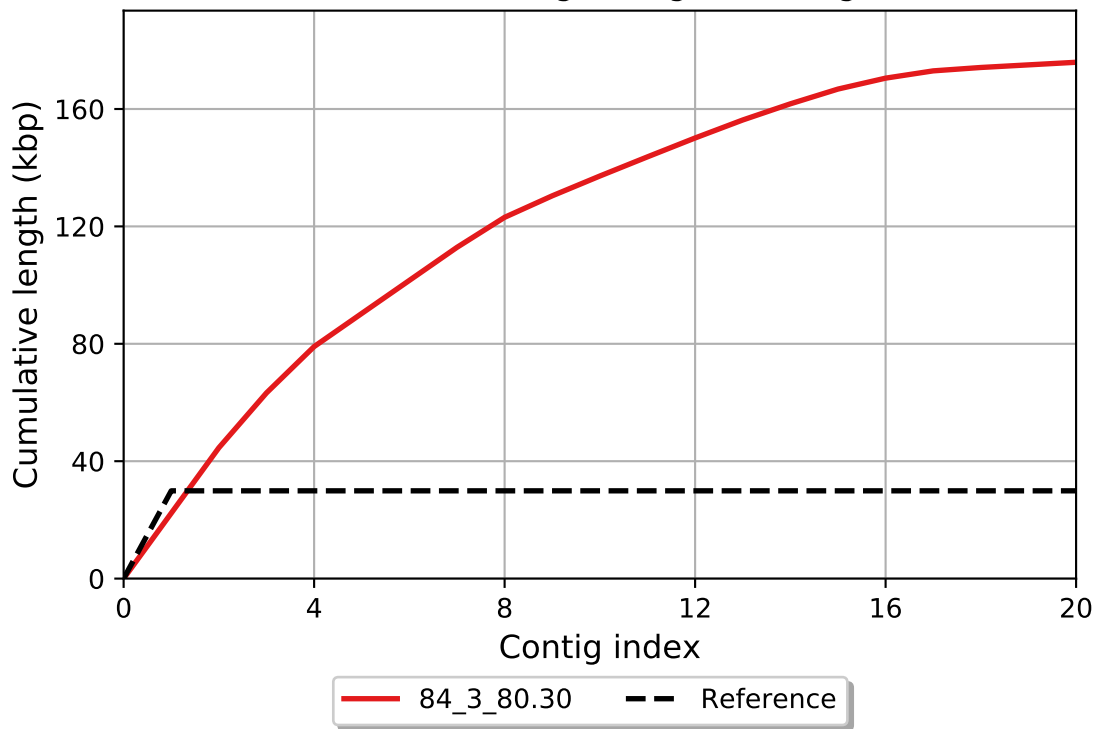GC content

84_3_80.30 GC content

Misassemblies
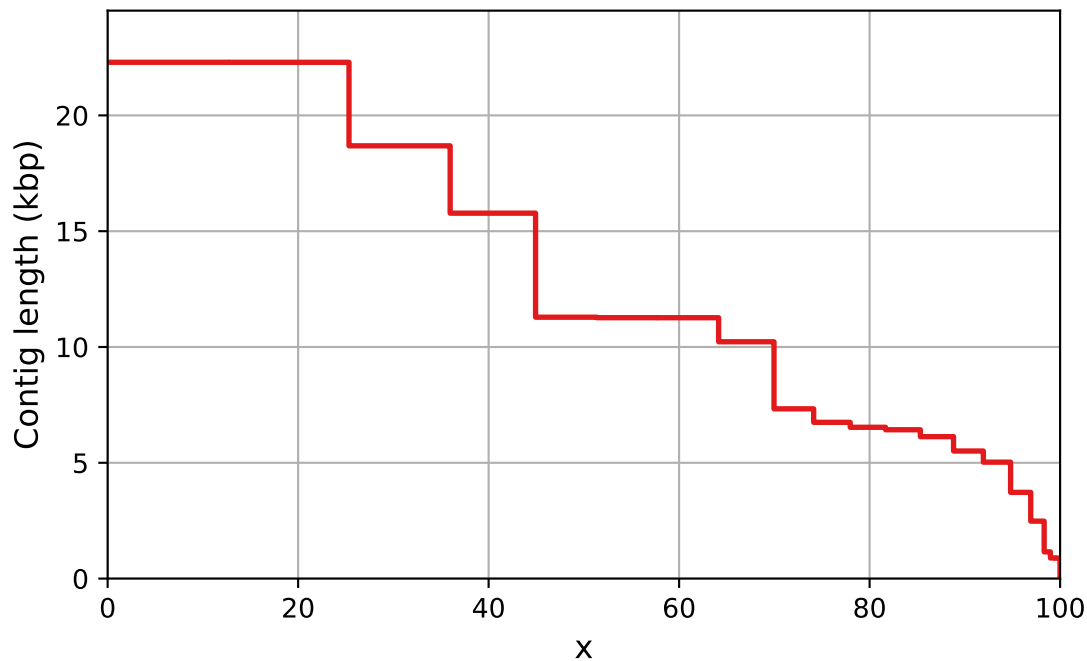
FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

Contig length (kbp)

x

84_3_80.30