Report

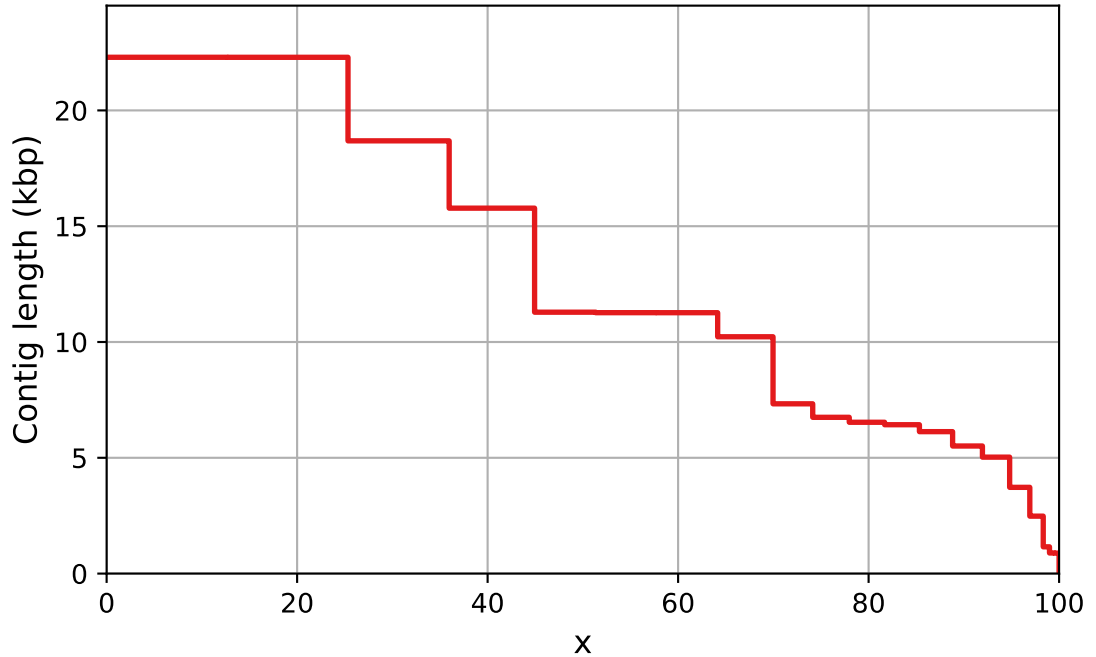|	84_3_80.30
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	174163
Total length (>= 5000 bp)	166803
Total length (>= 10000 bp)	123096
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	20
Largest contig	22294
Total length	175937
Reference length	29859
GC (%)	37.84
Reference GC (%)	38.00
N50	11287
NG50	22294
N75	6748
NG75	22293
L50	5
LG50	1
L75	10
LG75	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 (%)	99.323
Duplication ratio	5.939
# N's per 100 kbp	0.00
# mismatches per 100 kbp	20.25
# indels per 100 kbp	27.01
Largest alignment	22293
Total aligned length	175922
NA50	11286
NGA50	22293
NA75	6747
NGA75	22292
LA50	5
LGA50	1
LA75	10
LGA75	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

	84_3_80.30
# 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
# 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	6
# 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).
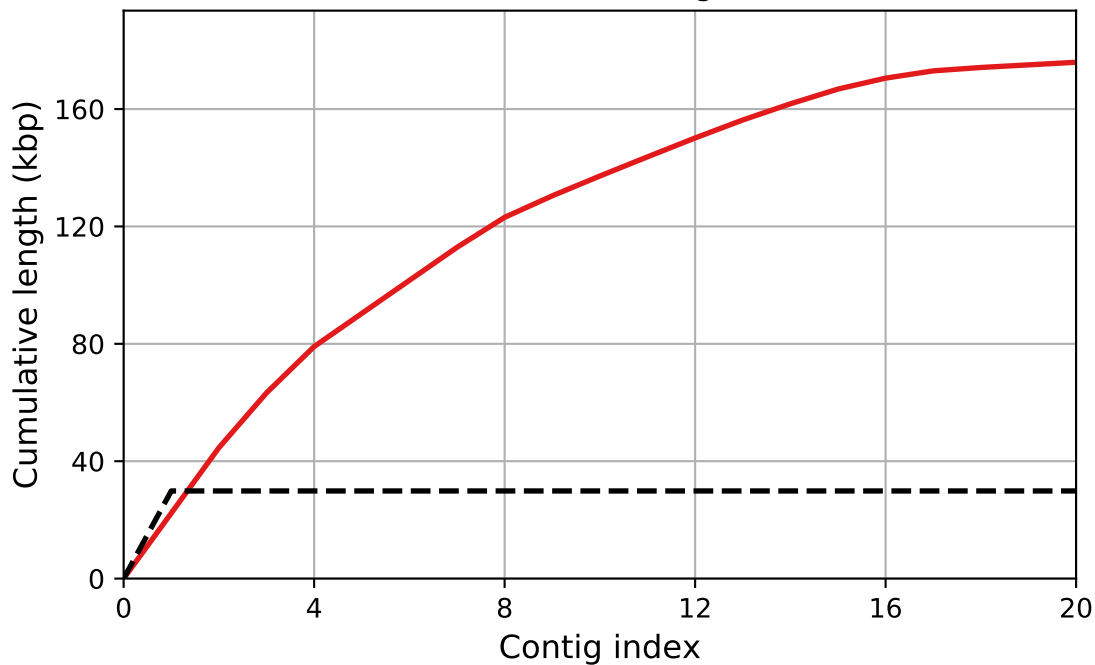
Unaligned report

	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

NGx

Contig length (kbp)

x
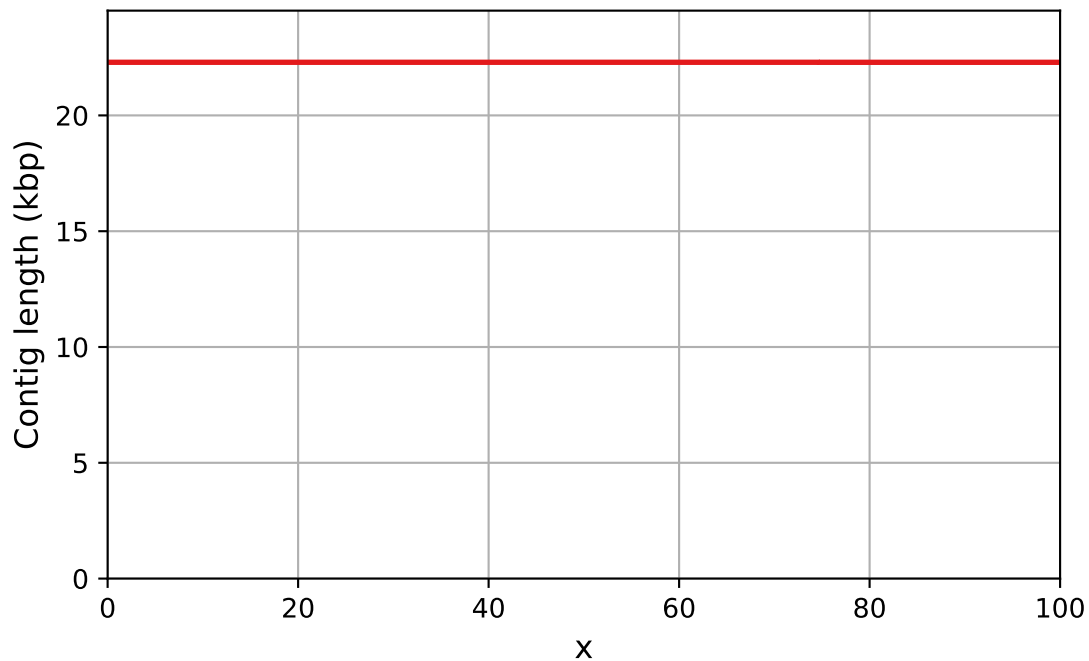
84_3_80.30

Cumulative length

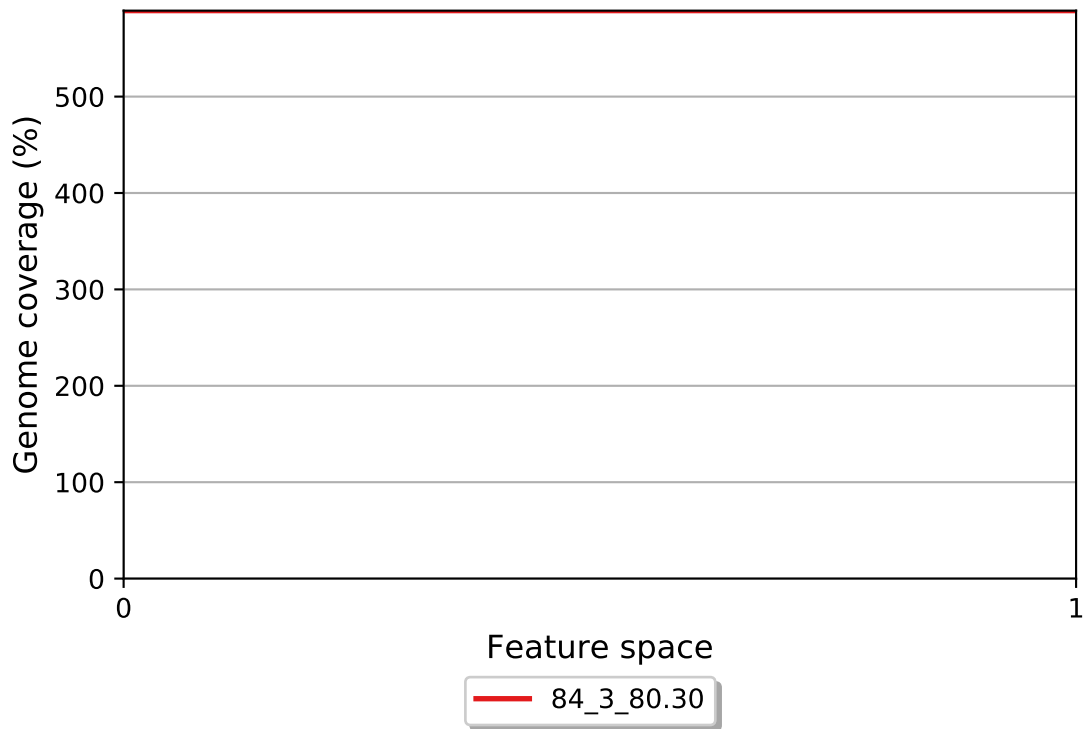|	
84_3_80.30	Reference

GC content
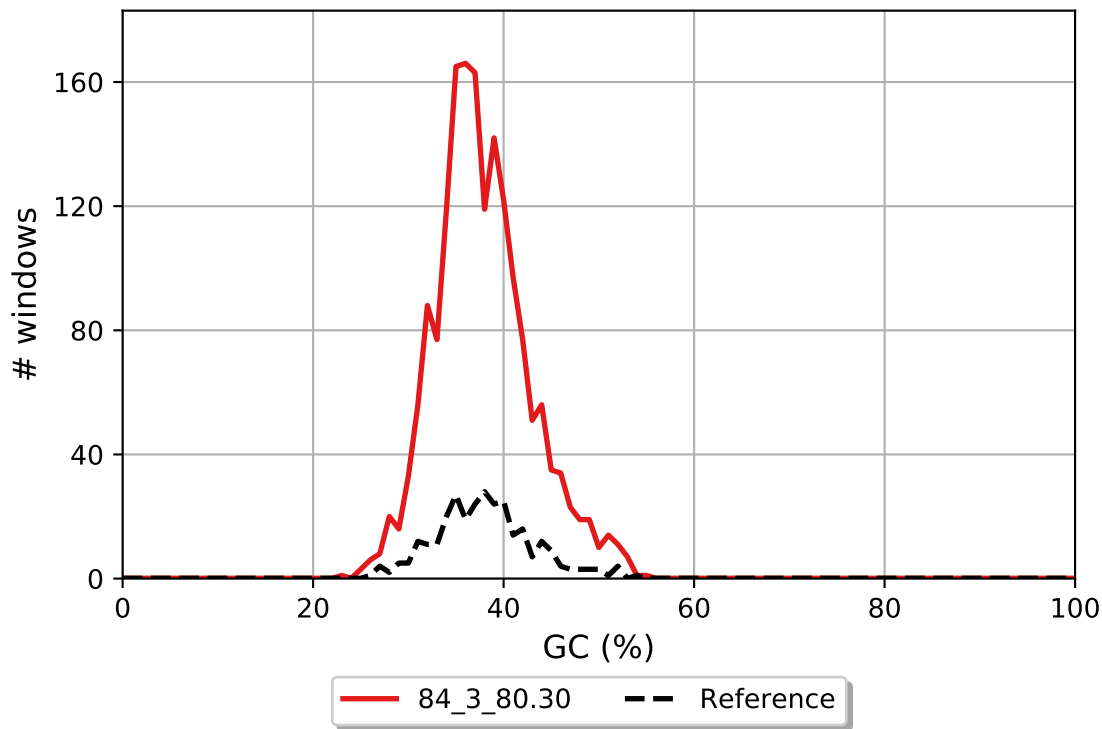
84_3_80.30 GC content
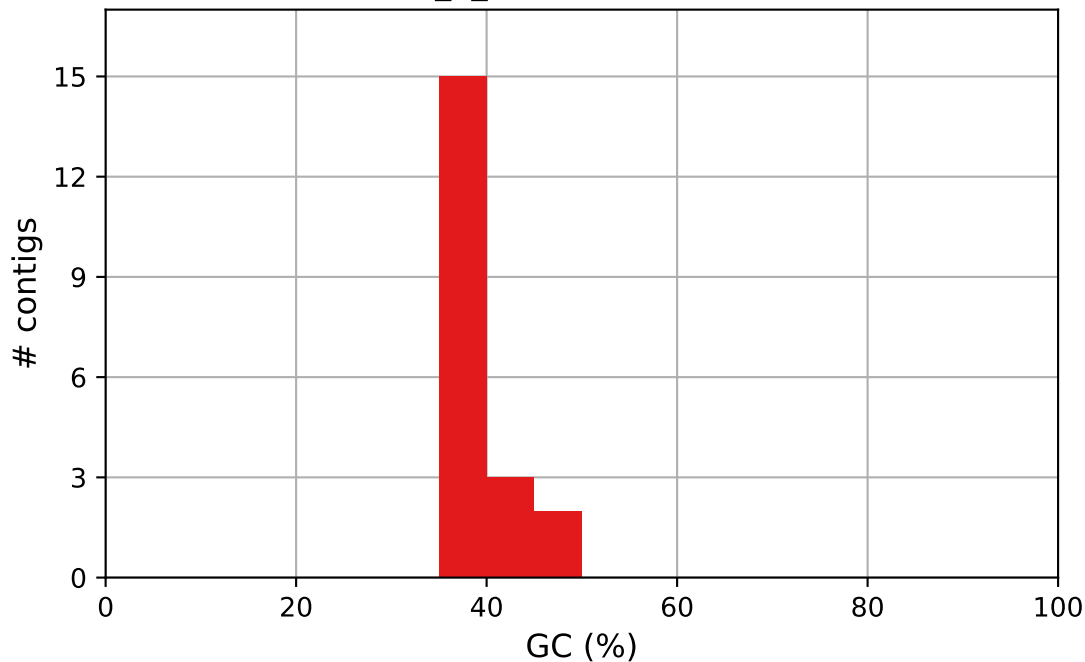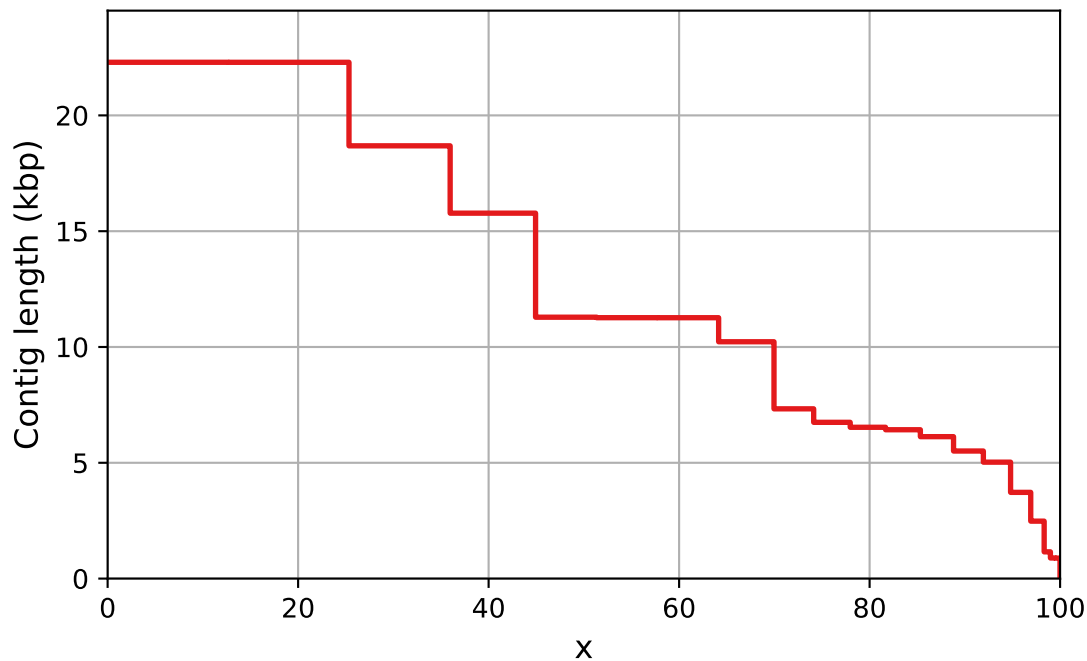
Misassemblies

84_3_80.30

FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

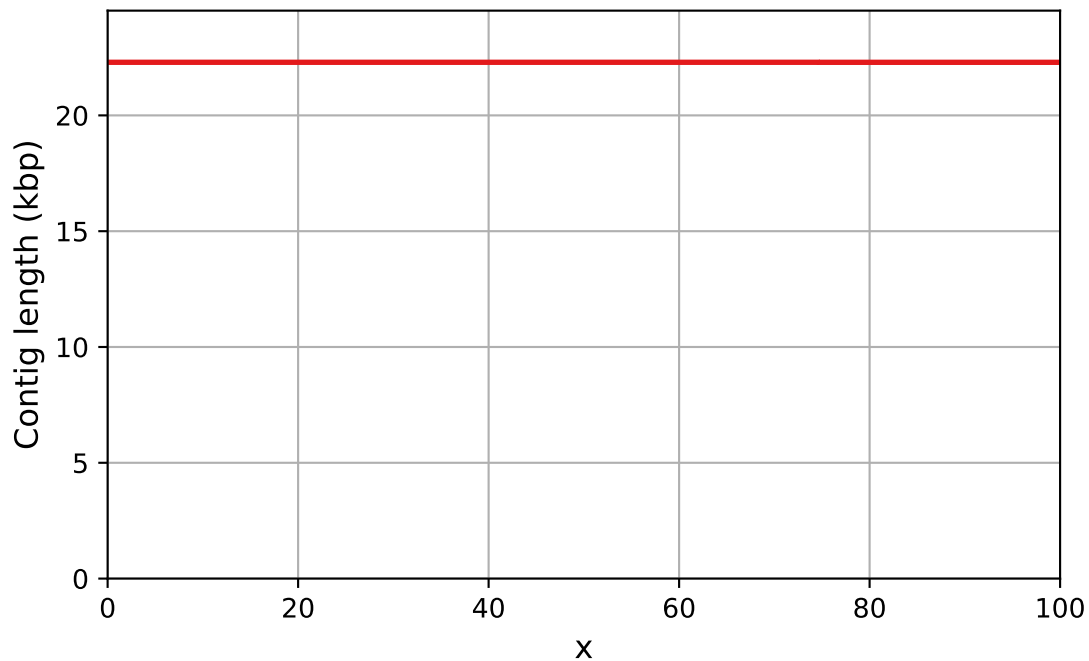Contig length (kbp) vs x

84_3_80.30

NGAx

Contig length (kbp)

x

84_3_80.30