

## 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	29859
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 (%)	99.323
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
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	6
# indels	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	8

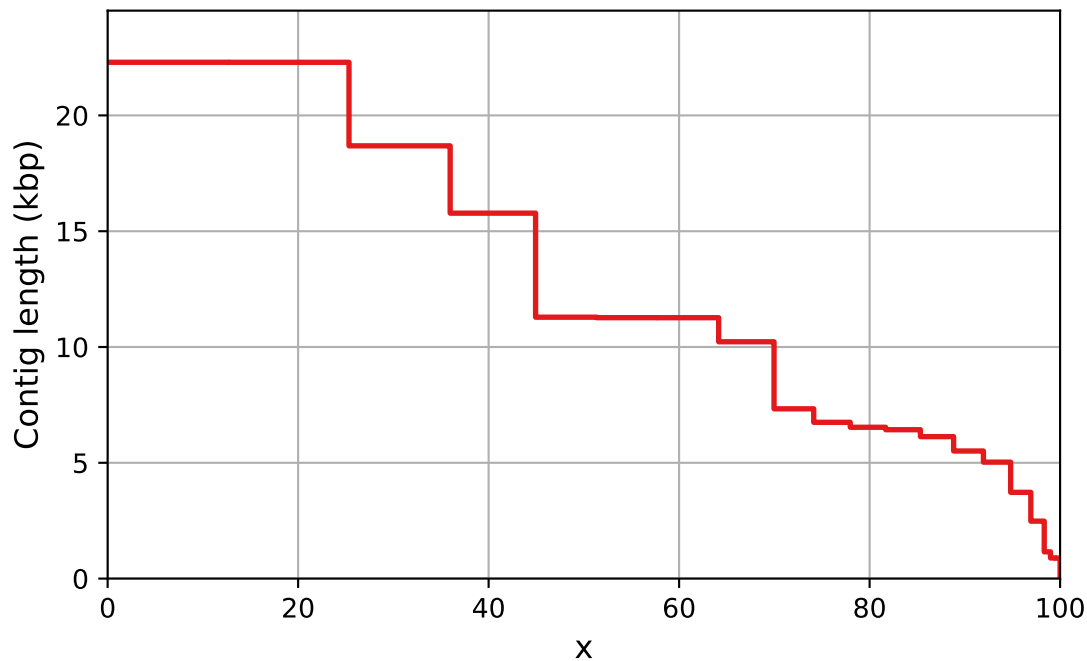
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## 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

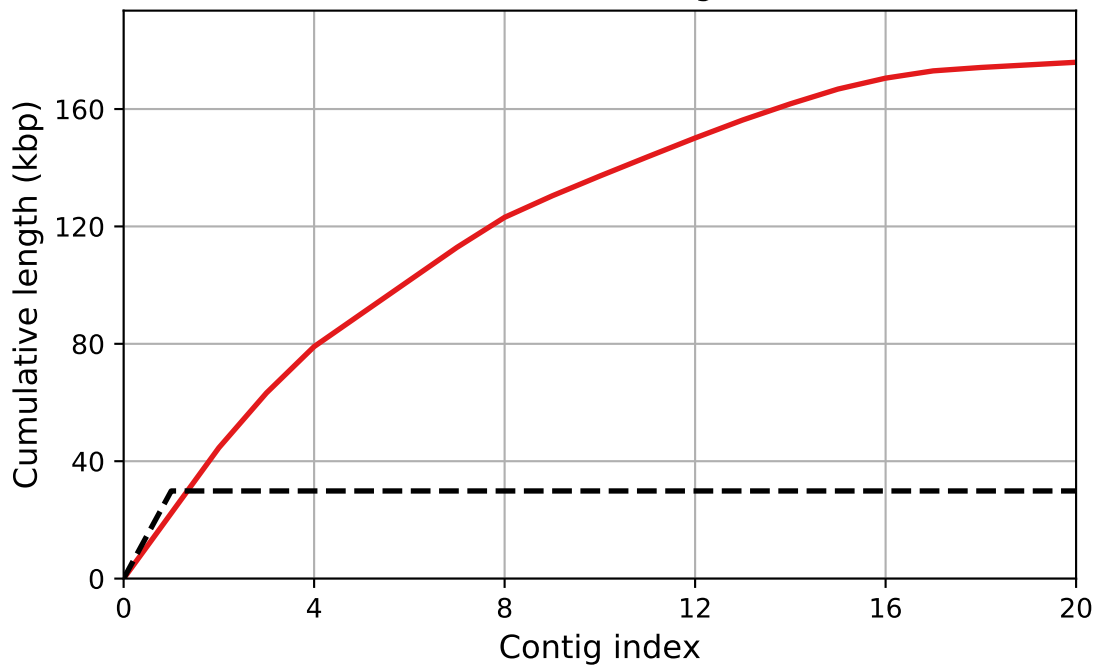
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



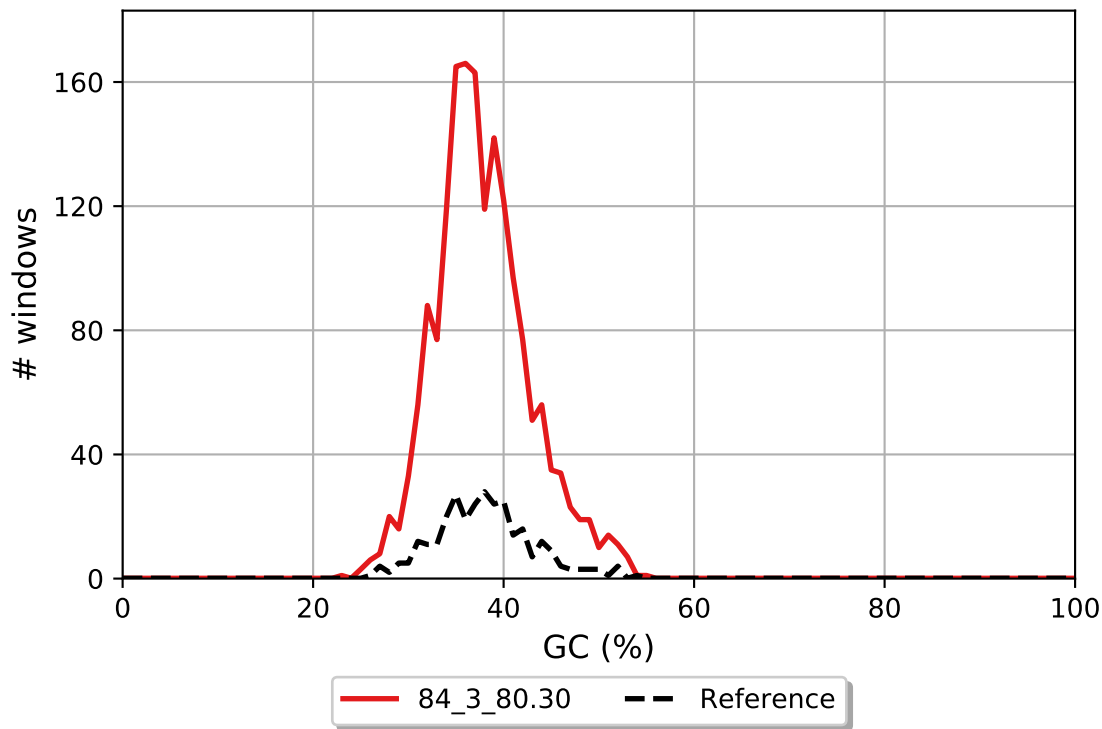
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Cumulative length

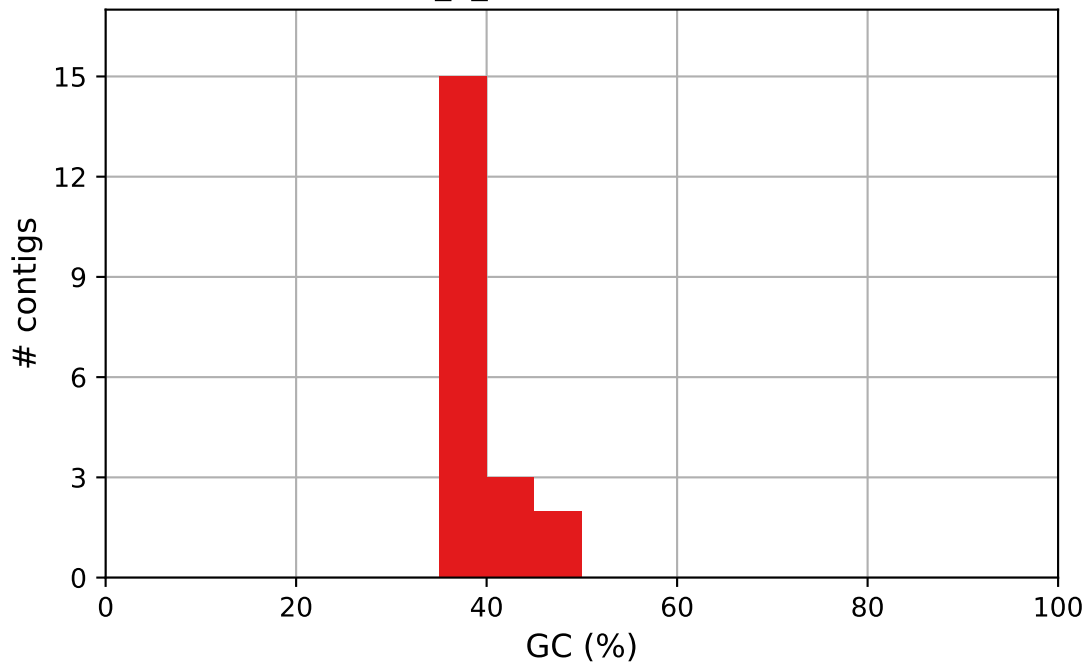


84\_3\_80.30    Reference

## GC content

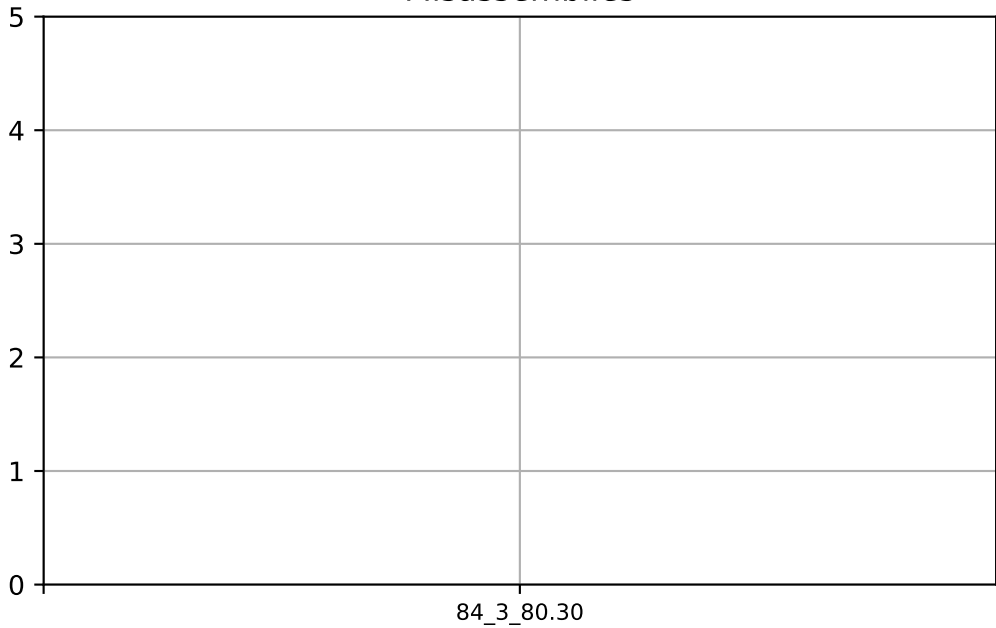


84\_3\_80.30 GC content



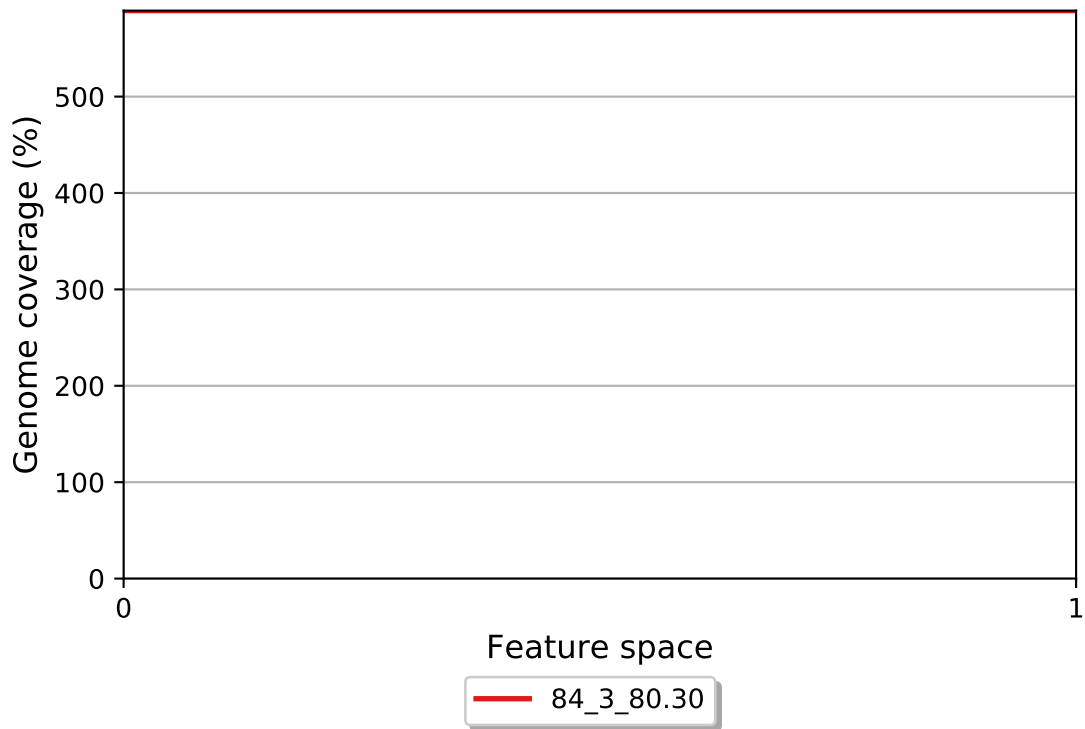
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## Misassemblies

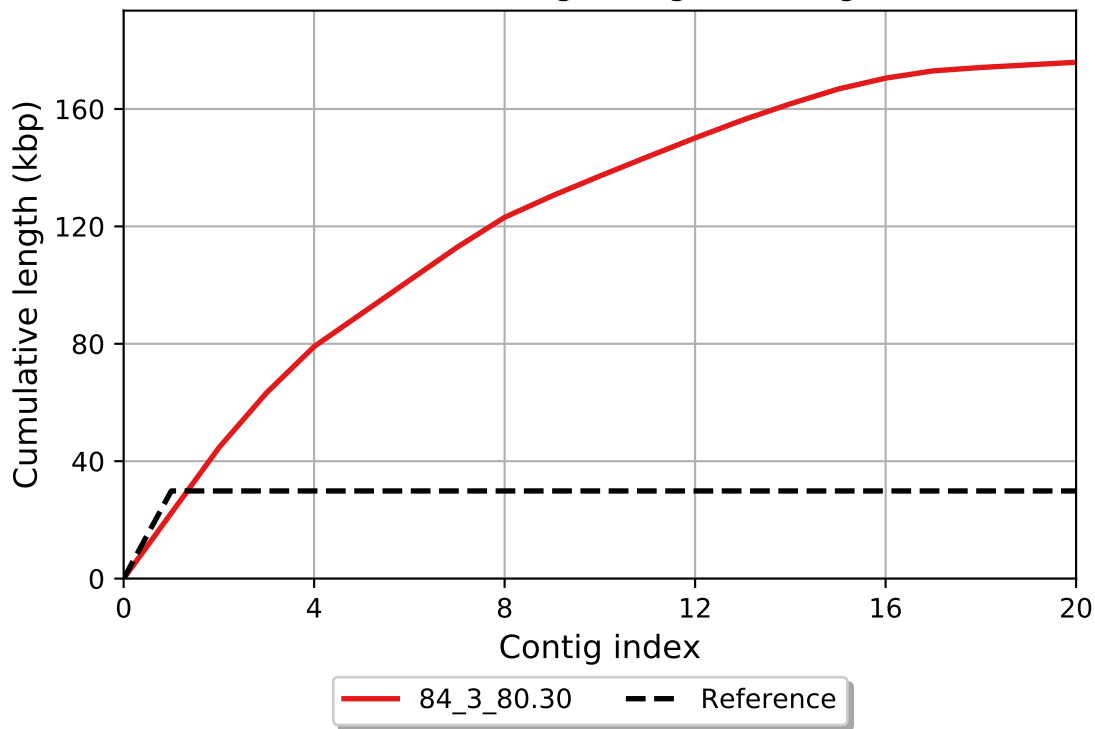




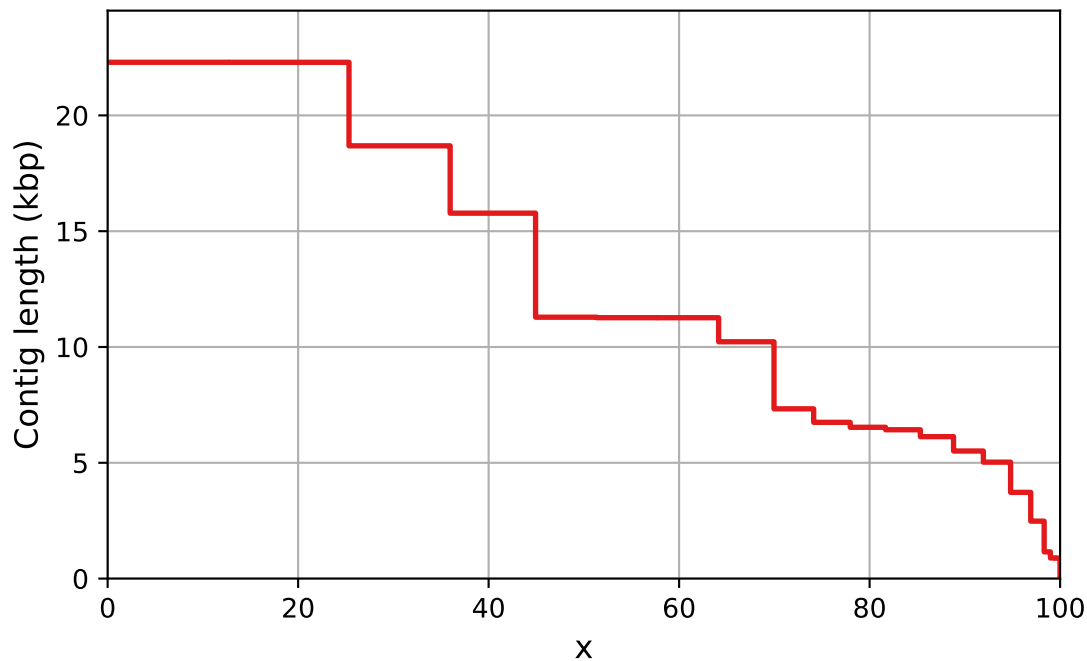
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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