

## Report

	33_38.30
# contigs (>= 0 bp)	30
# contigs (>= 1000 bp)	27
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	165907
Total length (>= 1000 bp)	163613
Total length (>= 5000 bp)	115471
Total length (>= 10000 bp)	83631
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	30
Largest contig	18870
Total length	165907
Reference length	29835
N50	10622
N75	4527
L50	6
L75	12
# 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 (%)	98.478
Duplication ratio	5.649
# N's per 100 kbp	0.00
# mismatches per 100 kbp	23.84
# indels per 100 kbp	40.86
Largest alignment	18870
Total aligned length	165885
NA50	10621
NA75	4526
LA50	6
LA75	12

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

	33_38.30
# 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	7
# indels	12
# indels (<= 5 bp)	12
# indels (> 5 bp)	0
Indels length	12

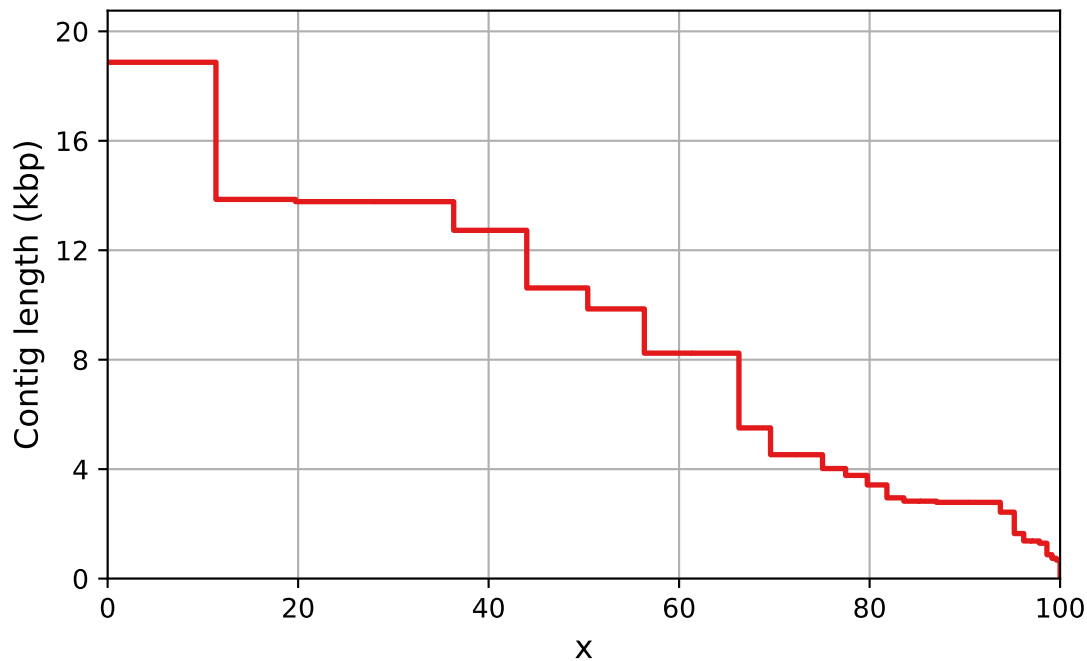
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	33_38.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

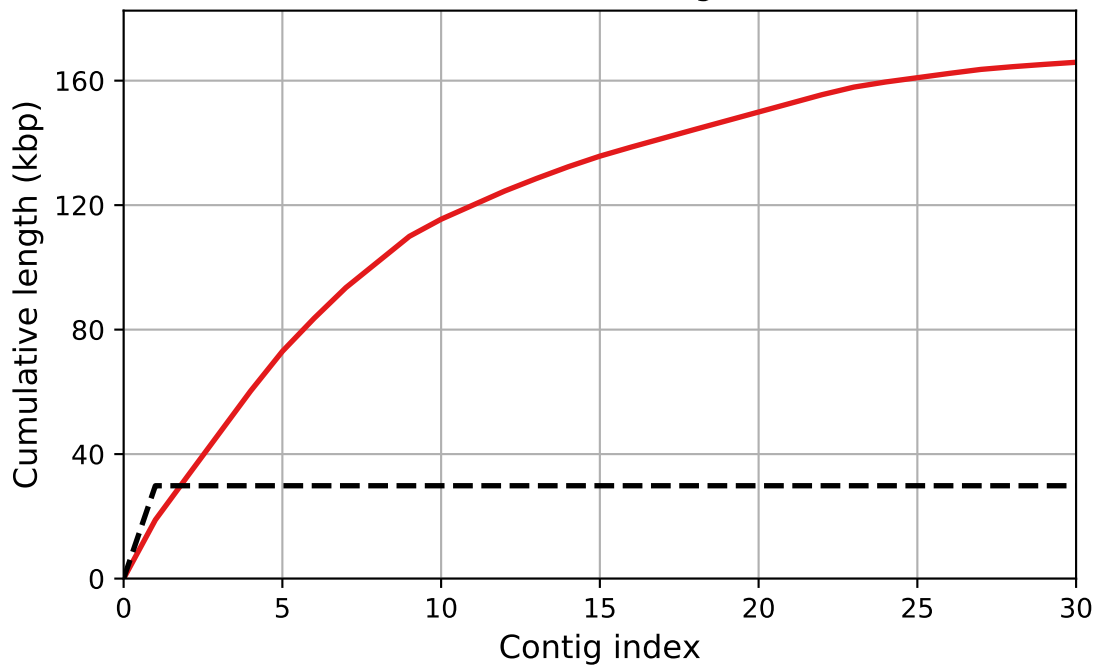
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



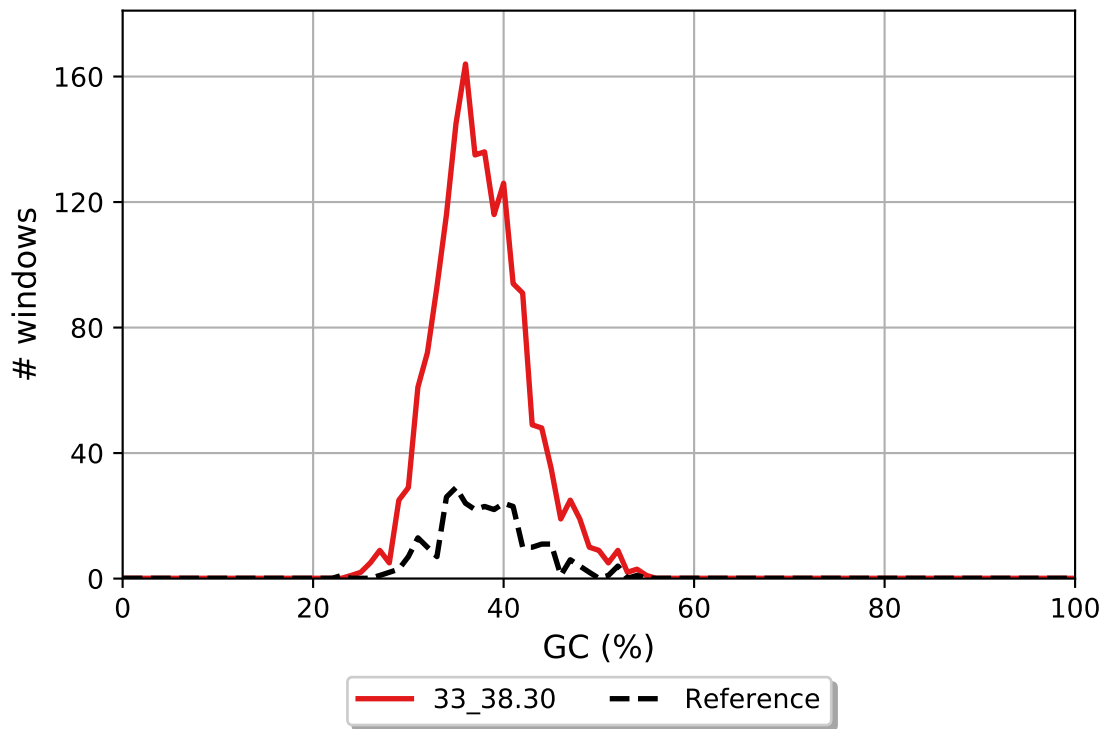
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Cumulative length

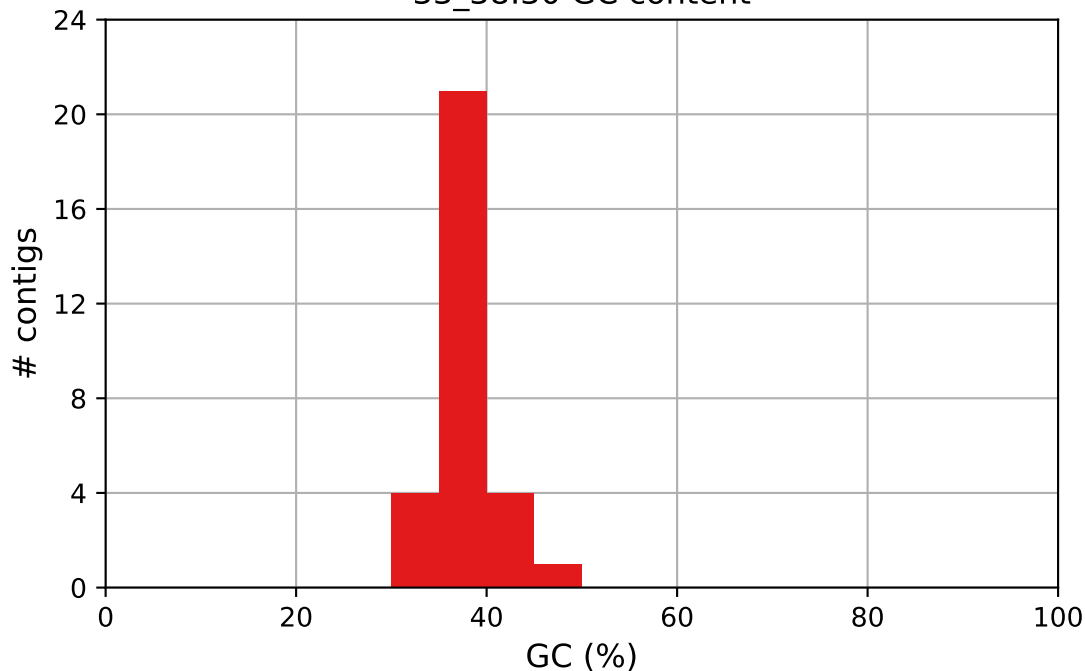


— 33\_38.30    - - Reference

## GC content

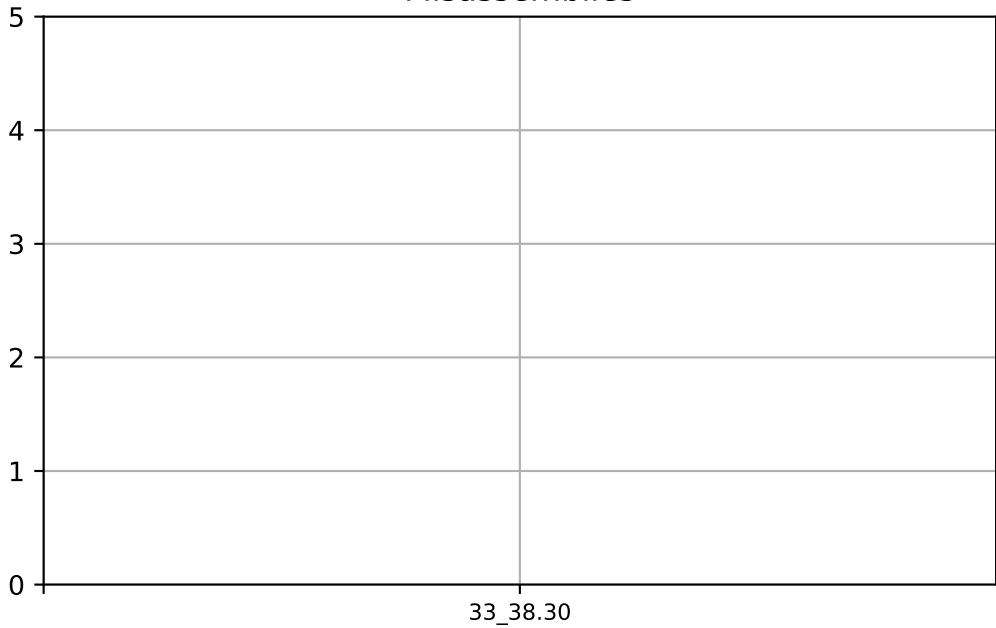


33\_38.30 GC content



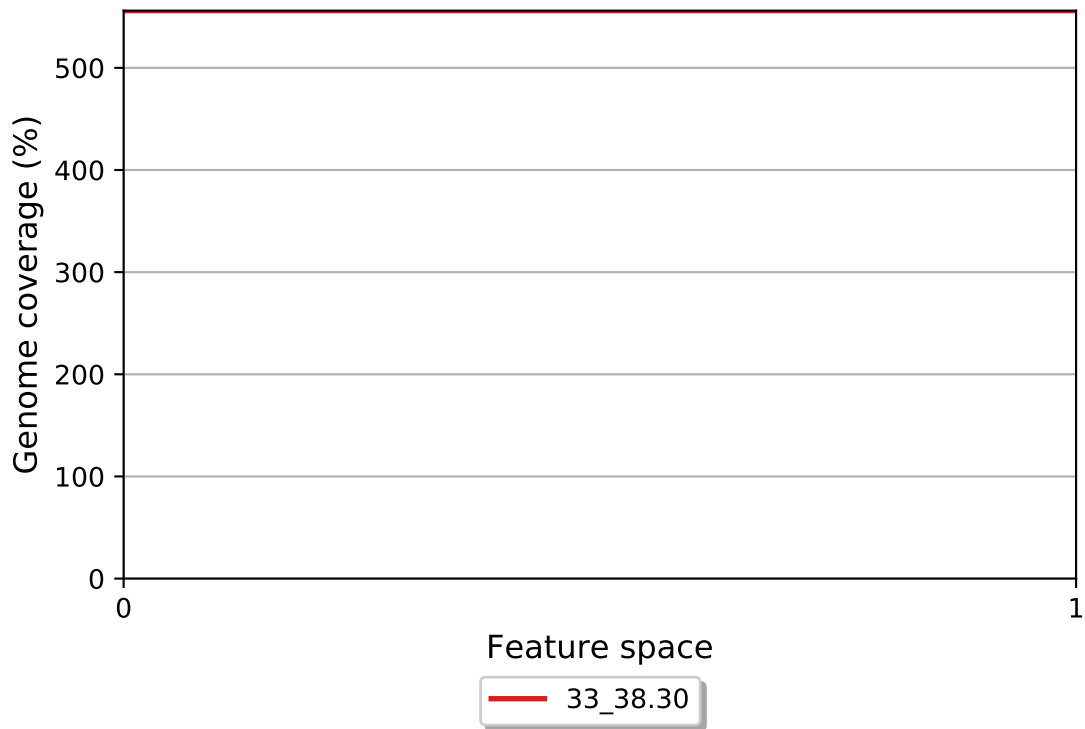
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# Misassemblies

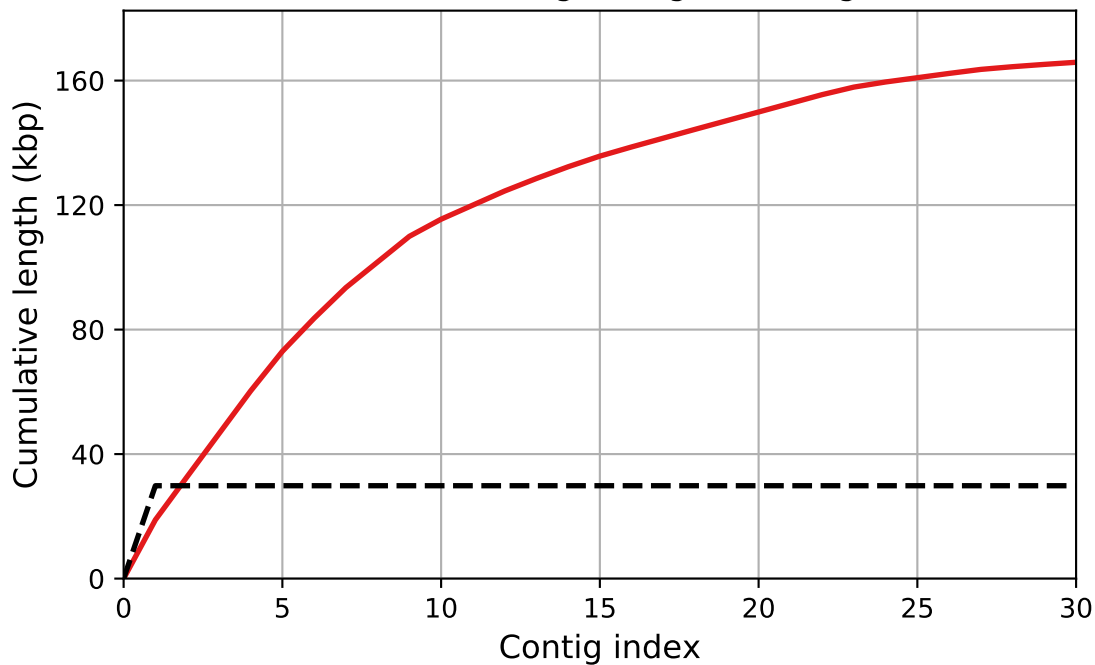




FRCurve (misassemblies)

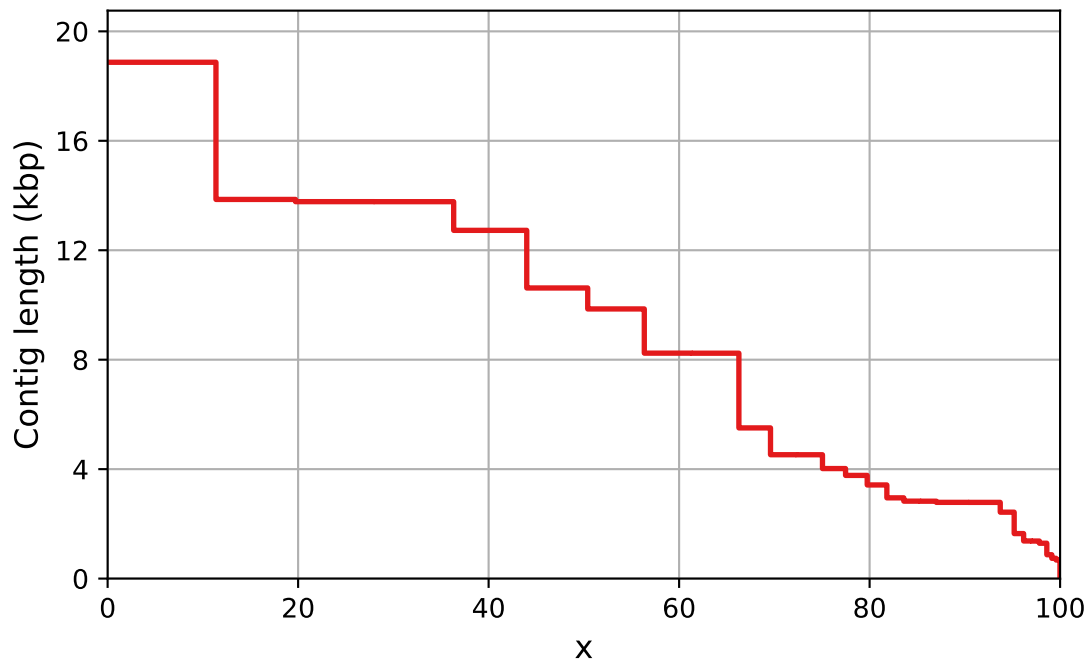


Cumulative length (aligned contigs)



— 33\_38.30    - - Reference

NAx



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