

Report

	33_3_80.30
# contigs (>= 0 bp)	35
# contigs (>= 1000 bp)	31
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	228097
Total length (>= 1000 bp)	224694
Total length (>= 5000 bp)	178252
Total length (>= 10000 bp)	117526
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	35
Largest contig	19486
Total length	228097
Reference length	29903
N50	10094
N75	5559
L50	8
L75	15
# 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 (%)	98.993
Duplication ratio	7.705
# N's per 100 kbp	0.00
# mismatches per 100 kbp	131.75
# indels per 100 kbp	64.18
Largest alignment	19486
Total aligned length	228064
NA50	10093
NA75	5558
LA50	8
LA75	15

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_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	39
# indels	19
# indels (<= 5 bp)	19
# indels (> 5 bp)	0
Indels length	19

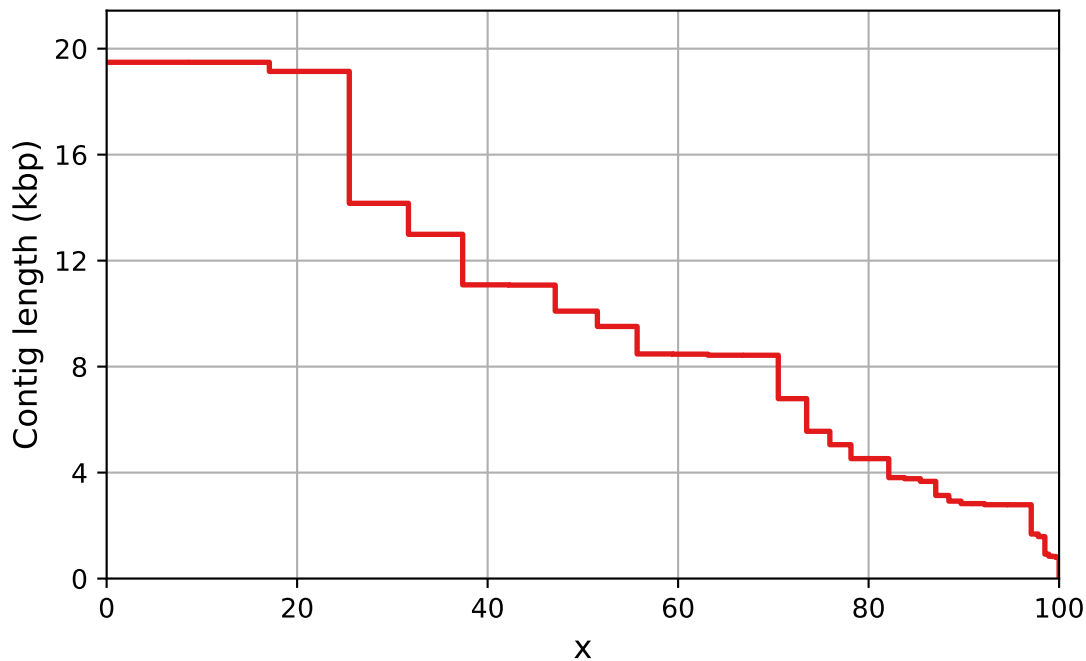
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

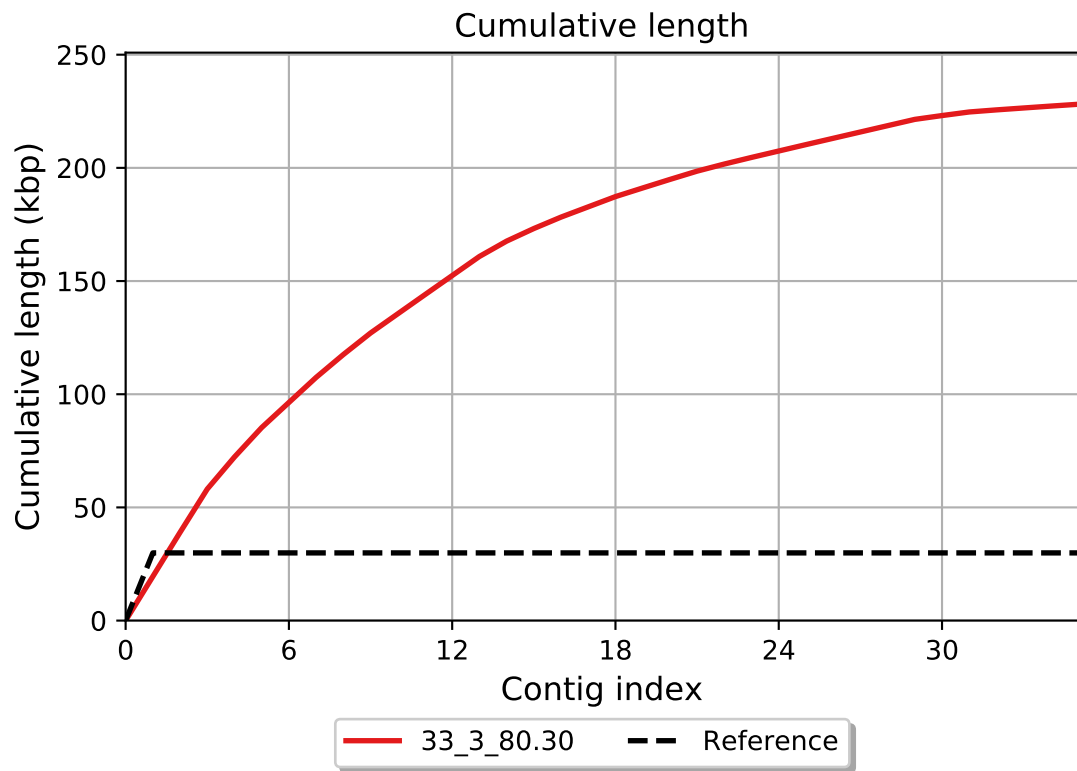
	33_3_80.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

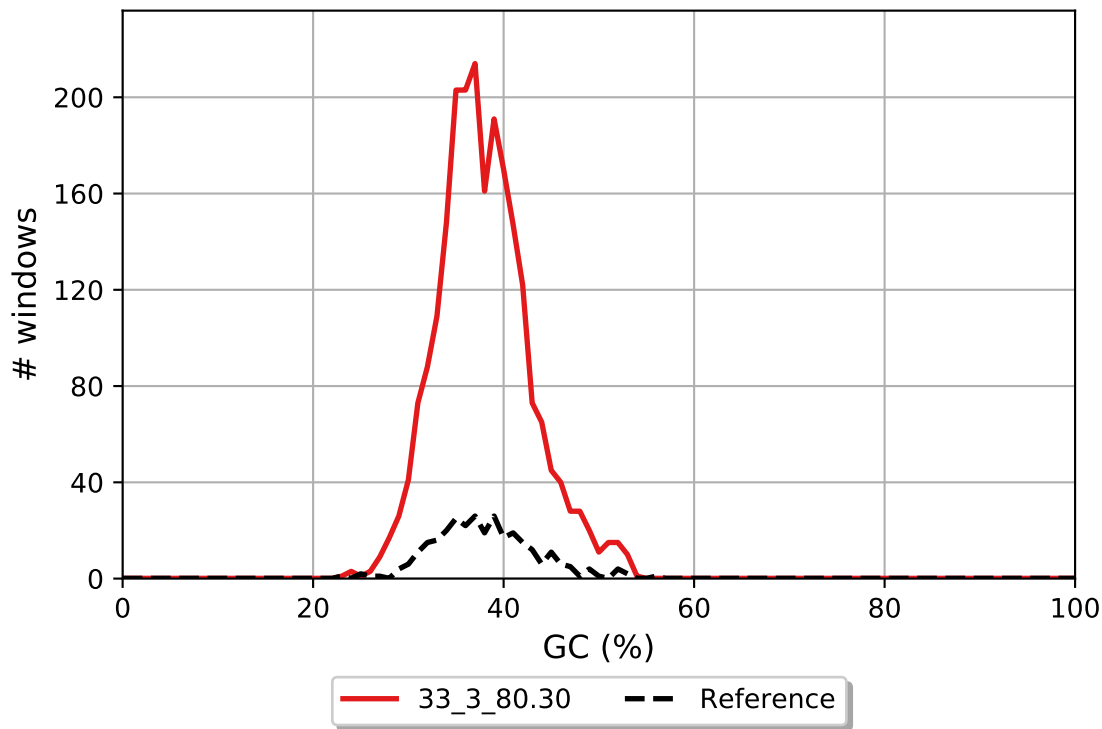
Nx



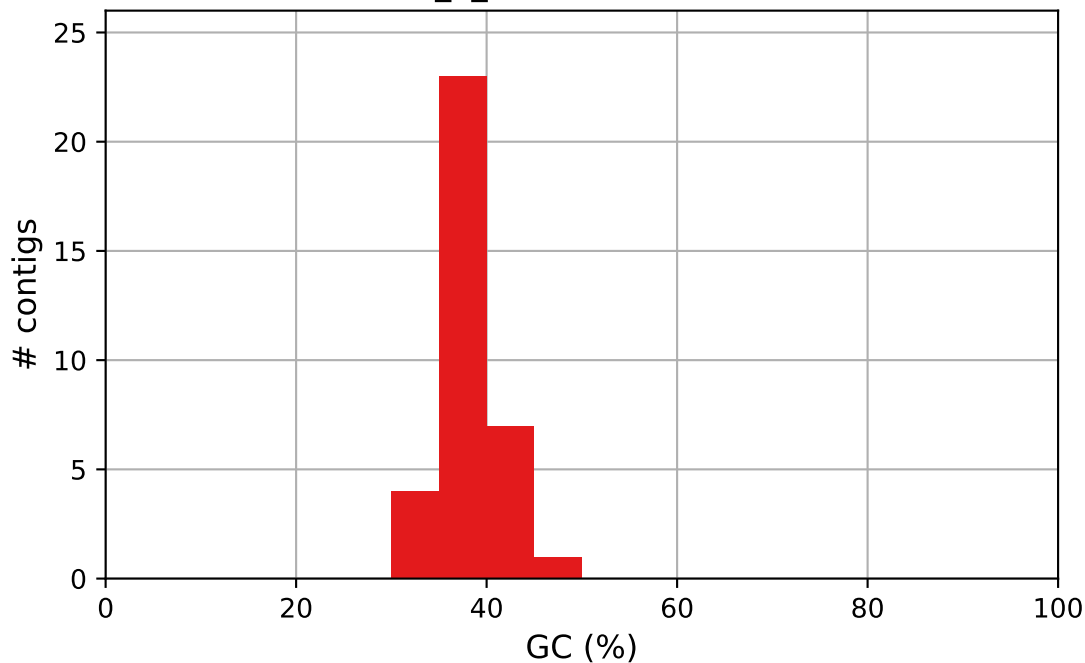
33_3_80.30



GC content

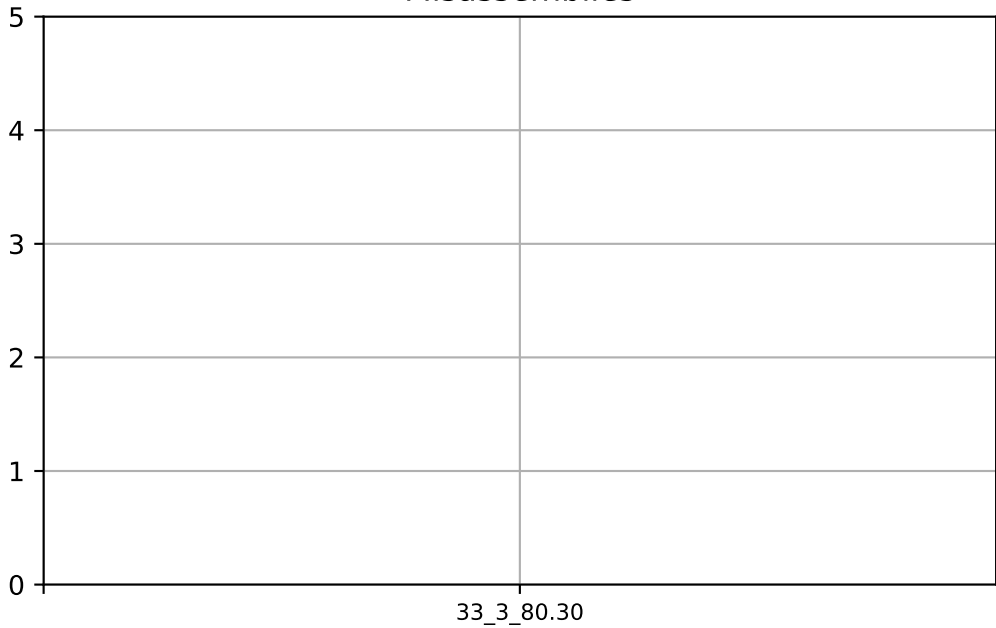


33_3_80.30 GC content

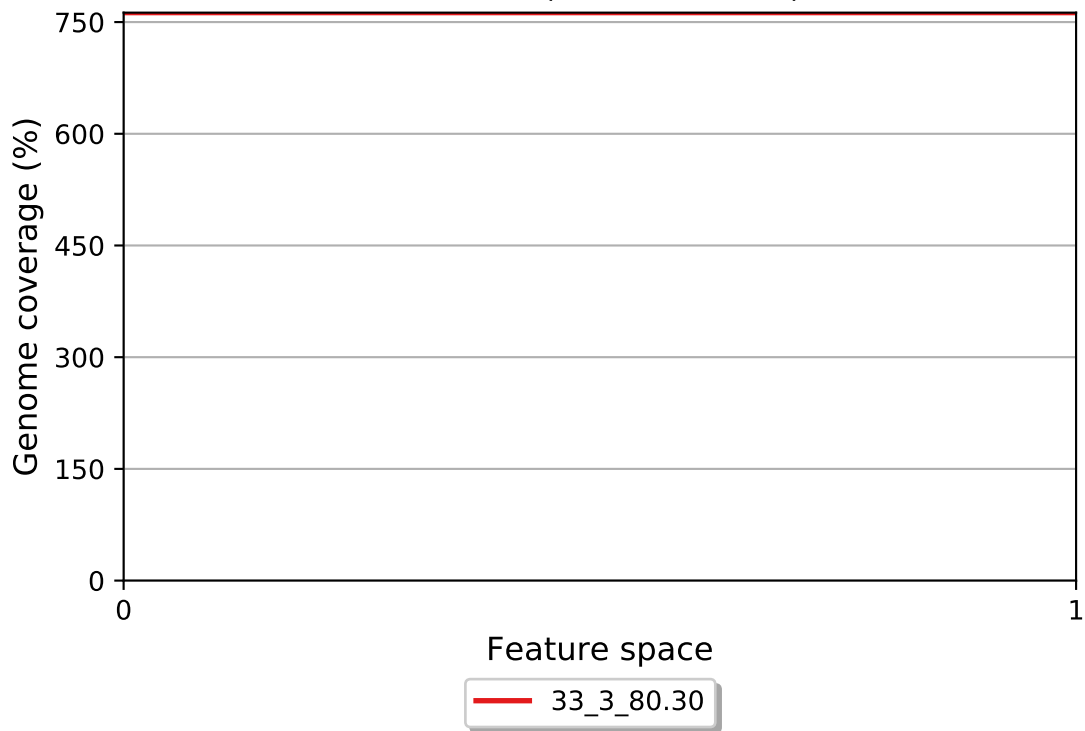


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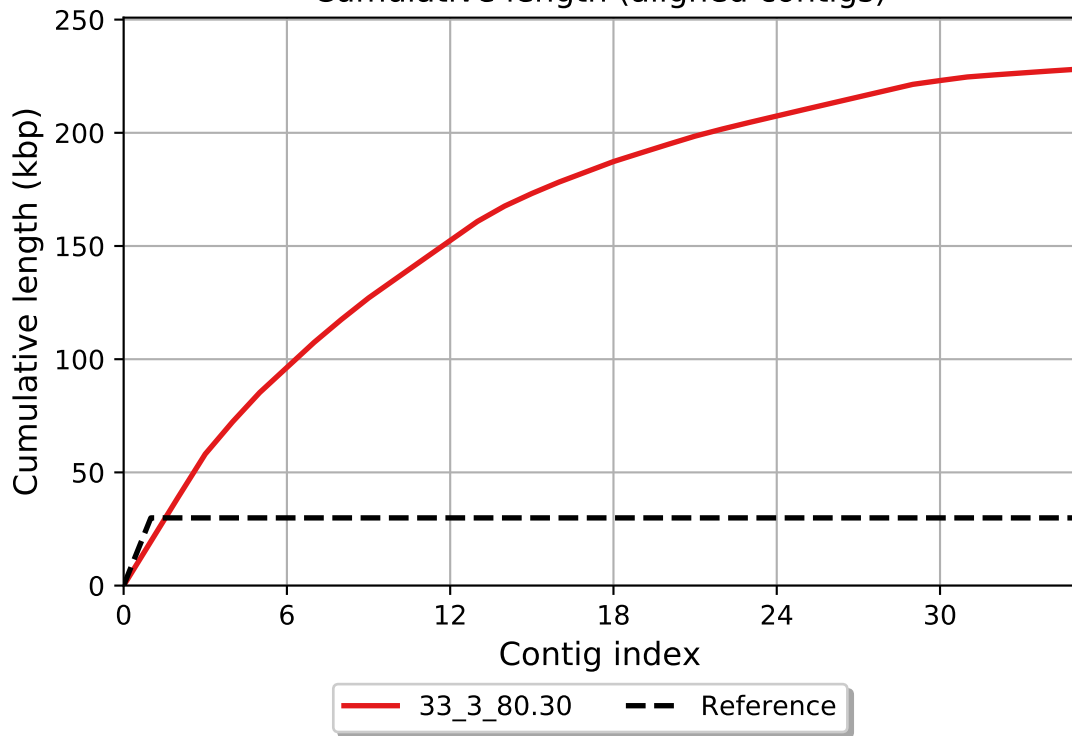
Misassemblies



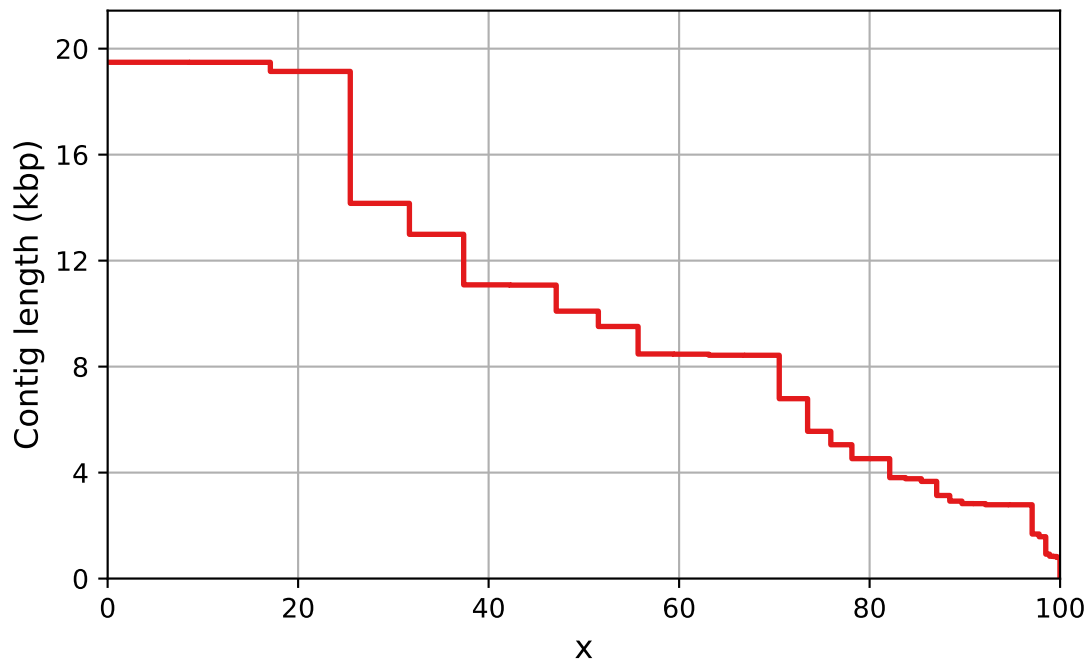
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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