

Report

	33_0.30
# contigs (>= 0 bp)	23
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	99383
Total length (>= 1000 bp)	96900
Total length (>= 5000 bp)	68306
Total length (>= 10000 bp)	44523
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	23
Largest contig	11289
Total length	99383
Reference length	29903
N50	6577
N75	2932
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 (%)	97.820
Duplication ratio	3.398
# N's per 100 kbp	0.00
# mismatches per 100 kbp	61.54
# indels per 100 kbp	34.19
Largest alignment	11289
Total aligned length	99368
NA50	6576
NA75	2932
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

	33_0.30
# 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	18
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	10

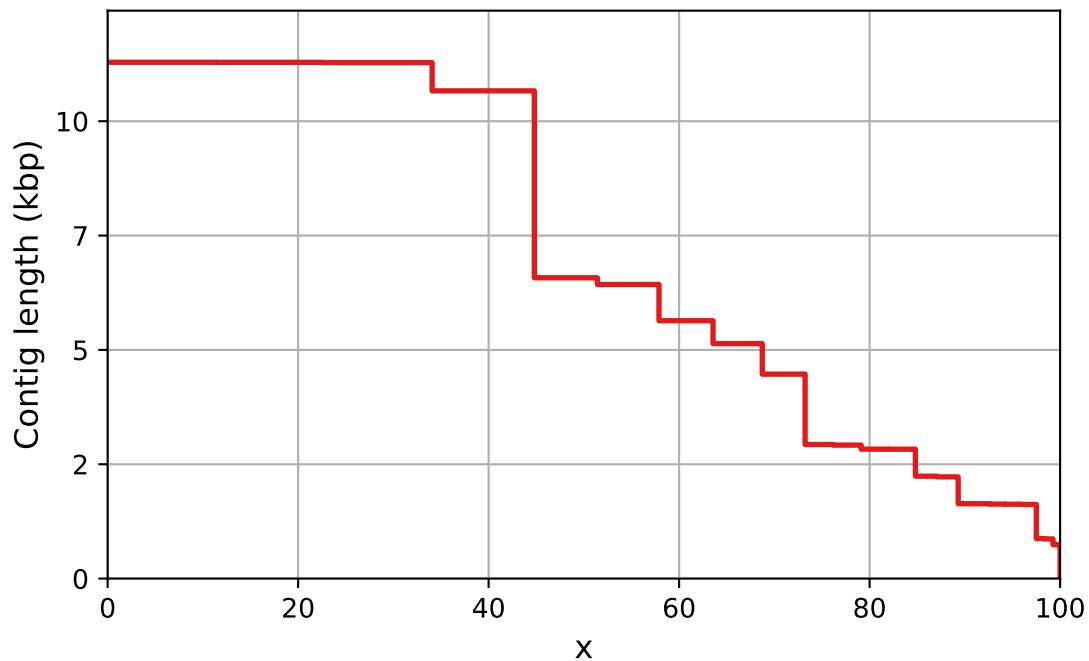
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

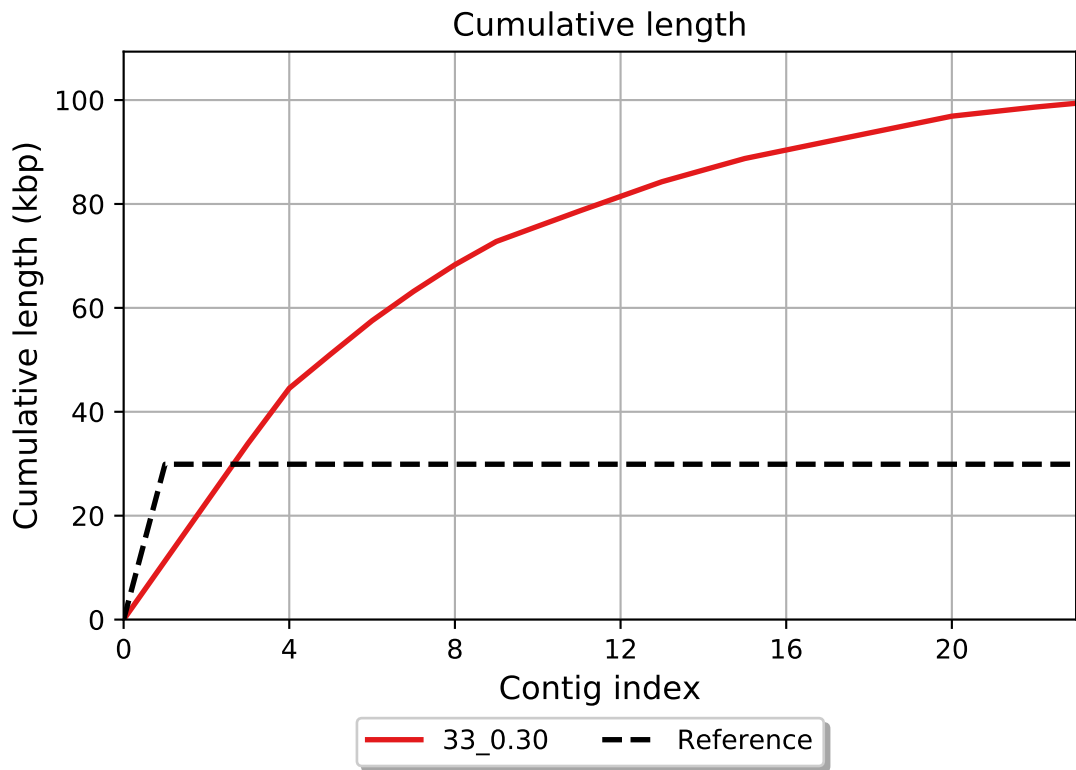
	33_0.30
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

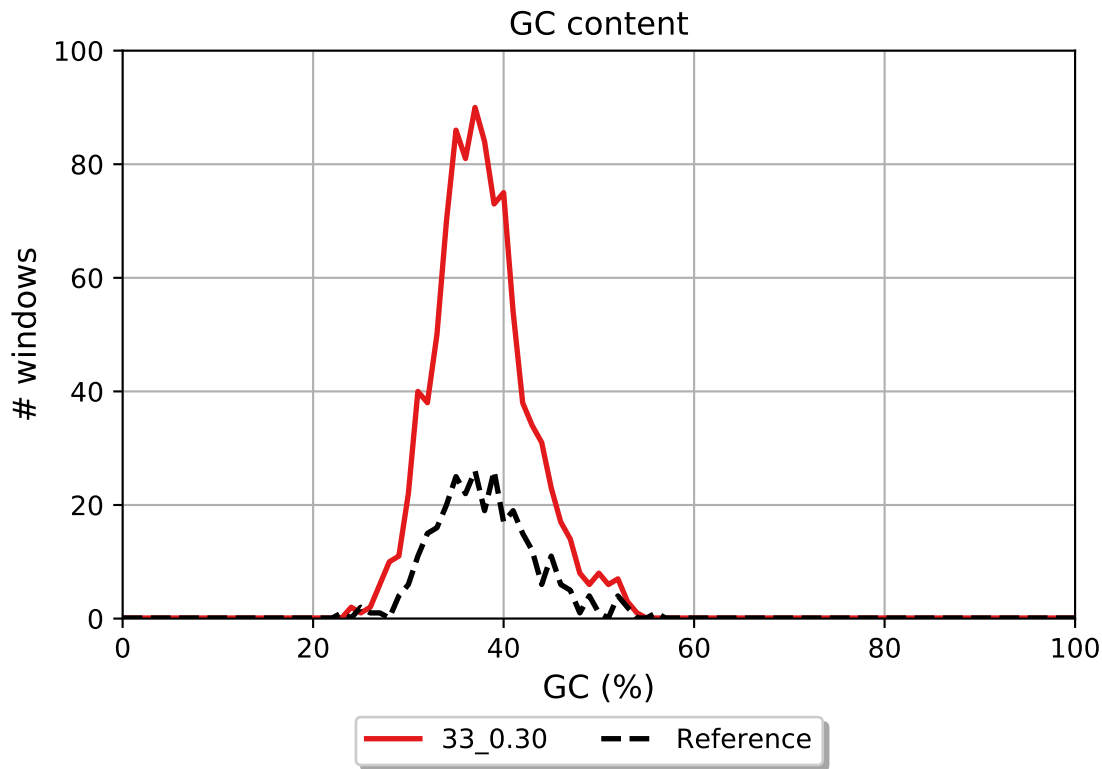
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

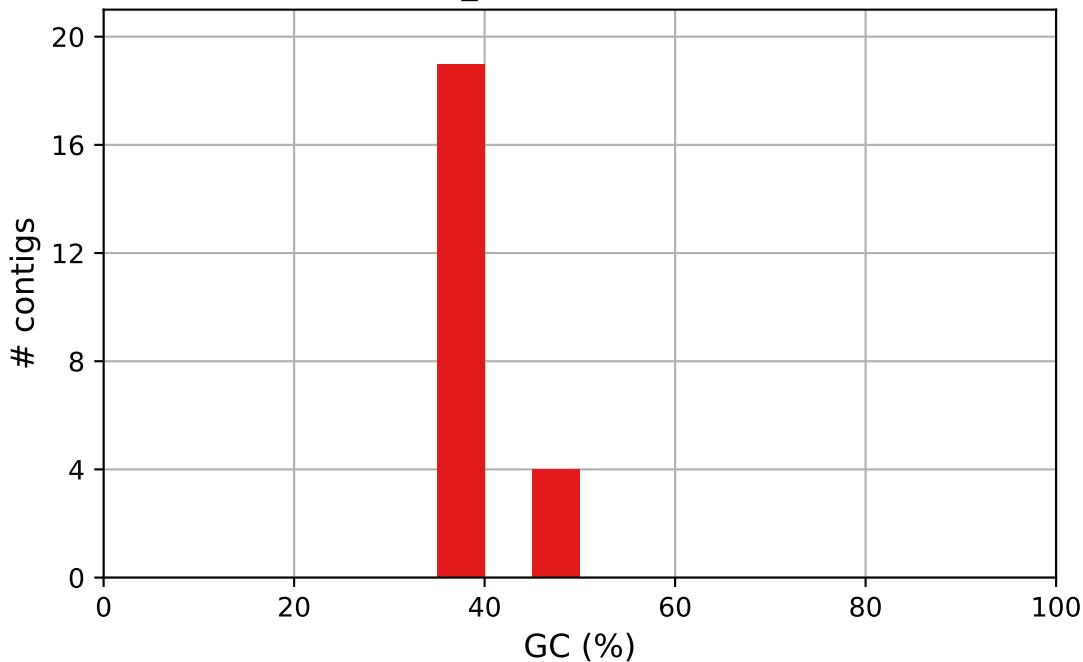


33_0.30



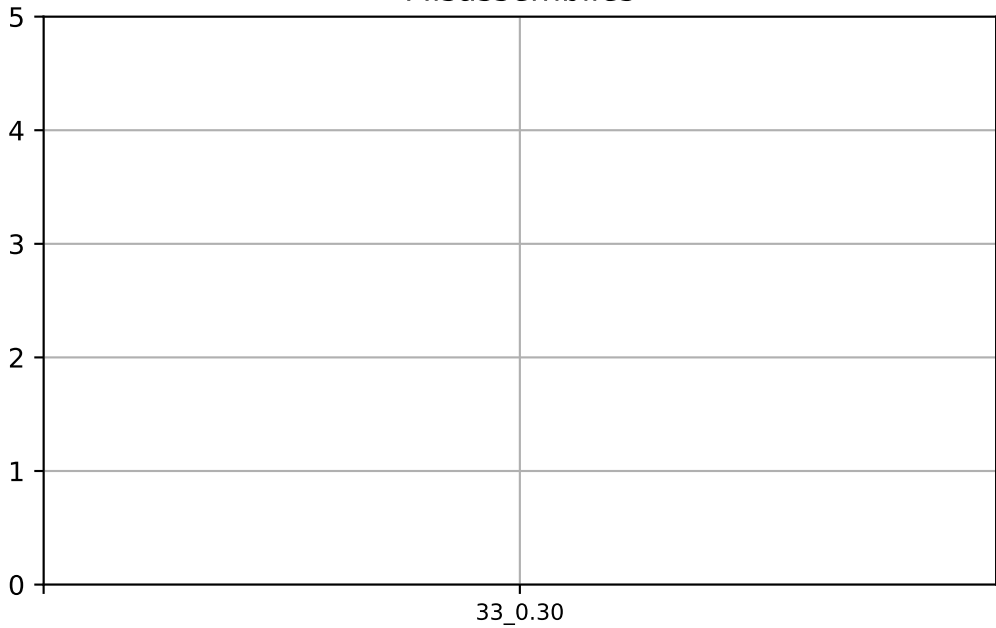


33_0.30 GC content

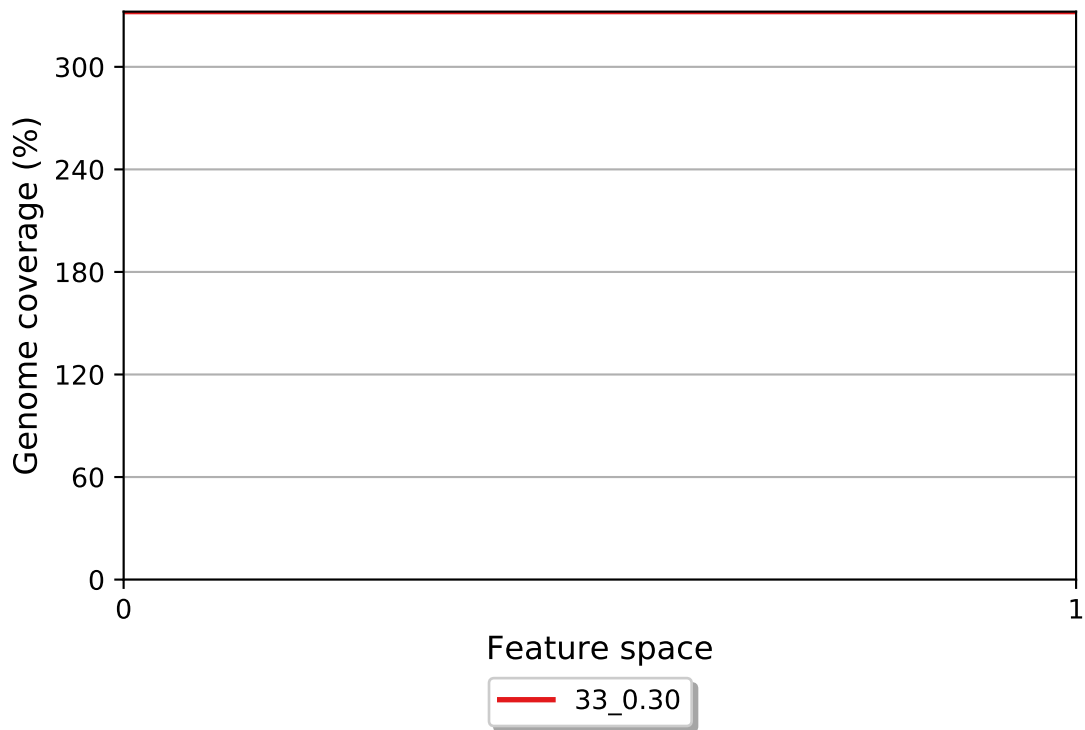


33_0.30

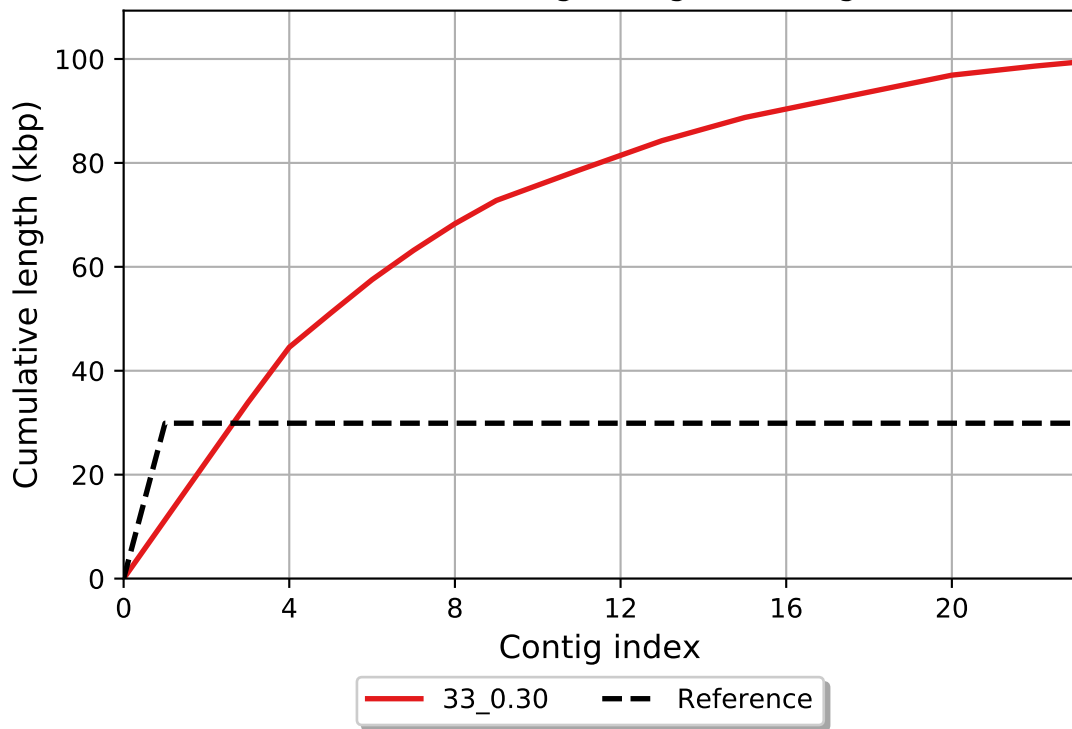
Misassemblies



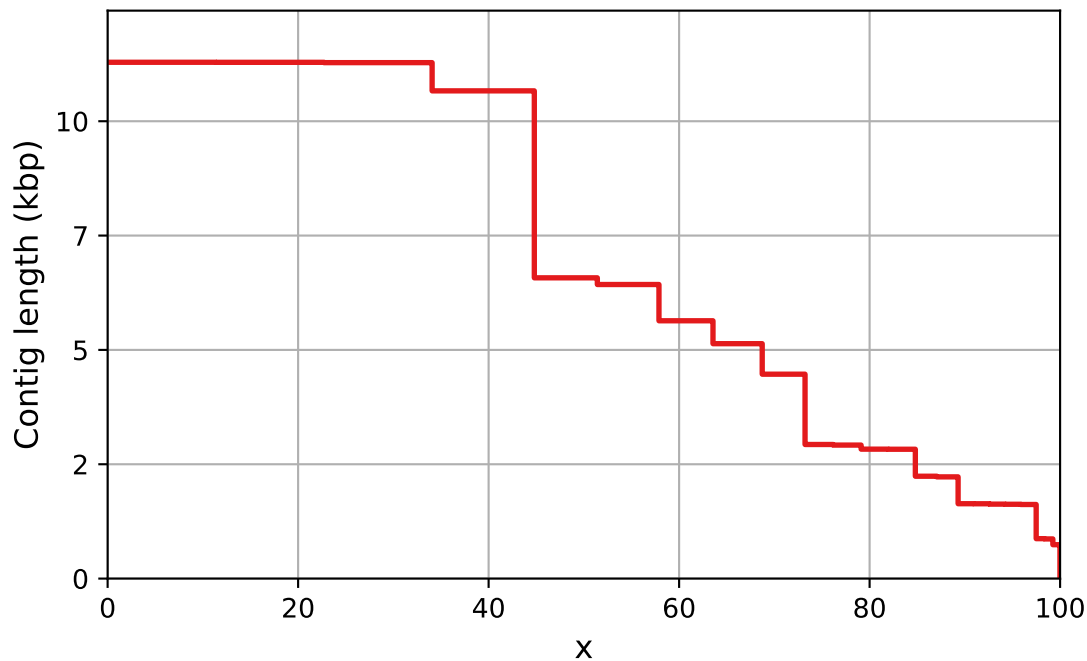
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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