

Report

	SRR1191991_fw_80_complete
# contigs (≥ 0 bp)	71
# contigs (≥ 1000 bp)	43
# contigs (≥ 5000 bp)	22
# contigs (≥ 10000 bp)	11
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	270199
Total length (≥ 1000 bp)	249684
Total length (≥ 5000 bp)	208527
Total length (≥ 10000 bp)	141059
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	71
Largest contig	14979
Total length	270199
Reference length	30114
N50	10392
N75	5018
L50	11
L75	21
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	82.782
Duplication ratio	10.839
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4849.77
# indels per 100 kbp	20.06
Largest alignment	14978
Total aligned length	270133
NA50	10391
NA75	5017
LA50	11
LA75	21

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

	SRR1191991_fw_80_complete
# 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	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1209
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	14

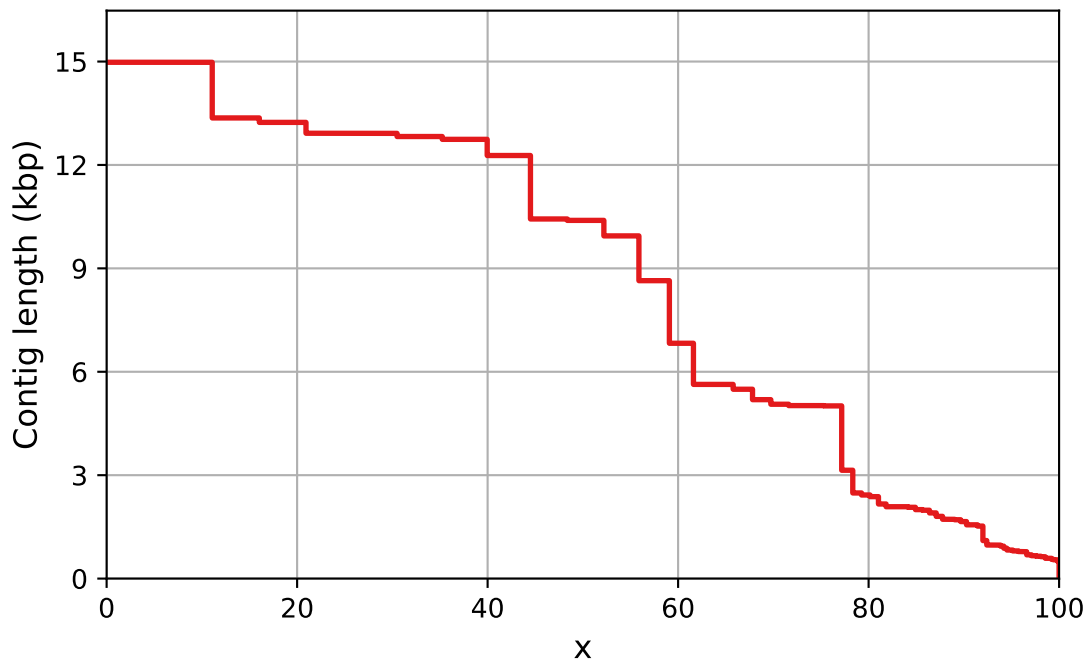
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR1191991_fw_80_complete
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

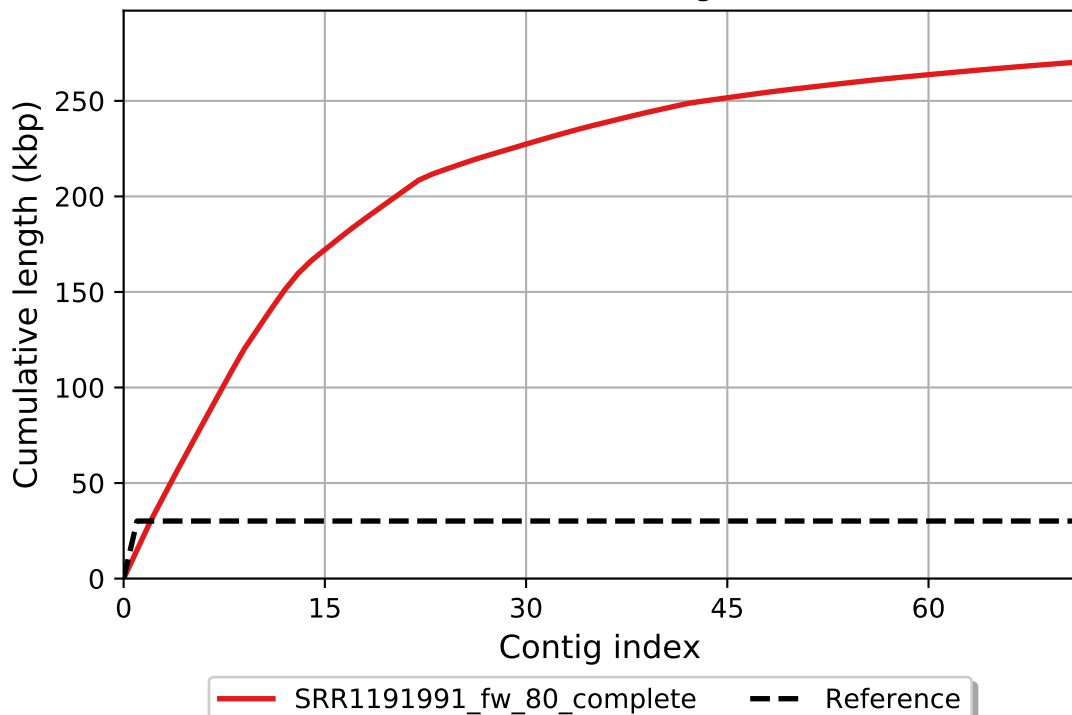
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

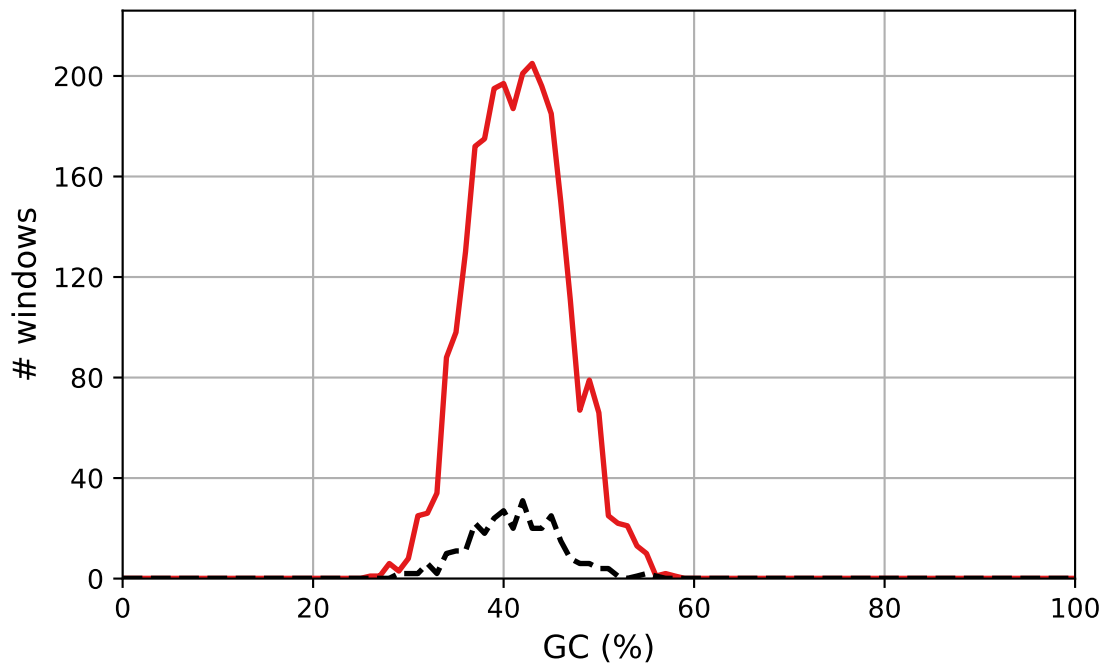


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Cumulative length

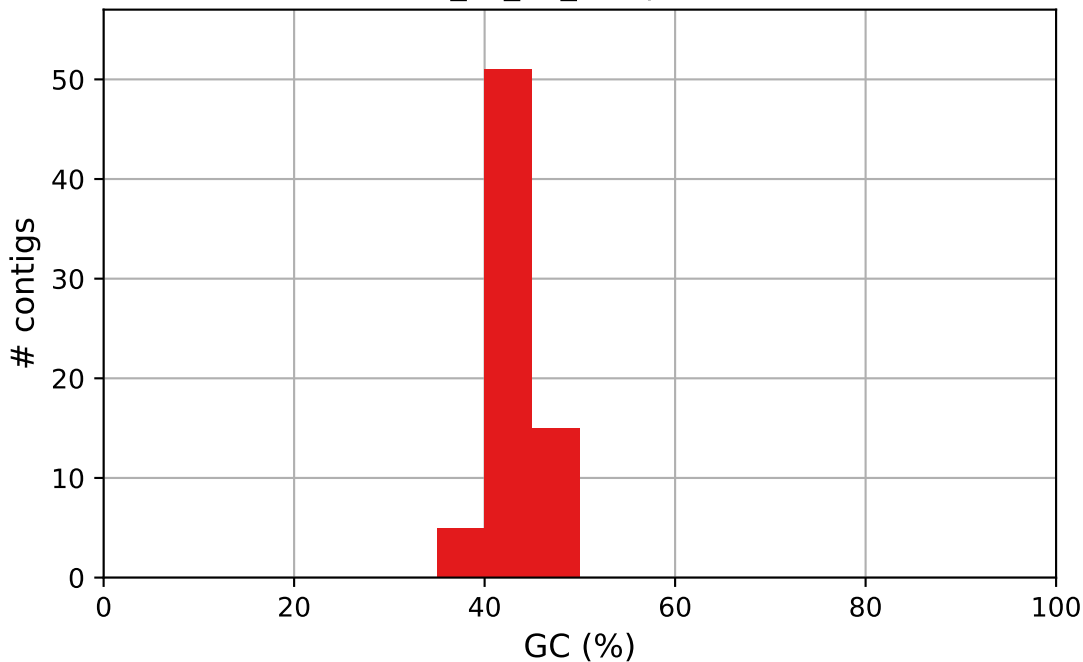


GC content



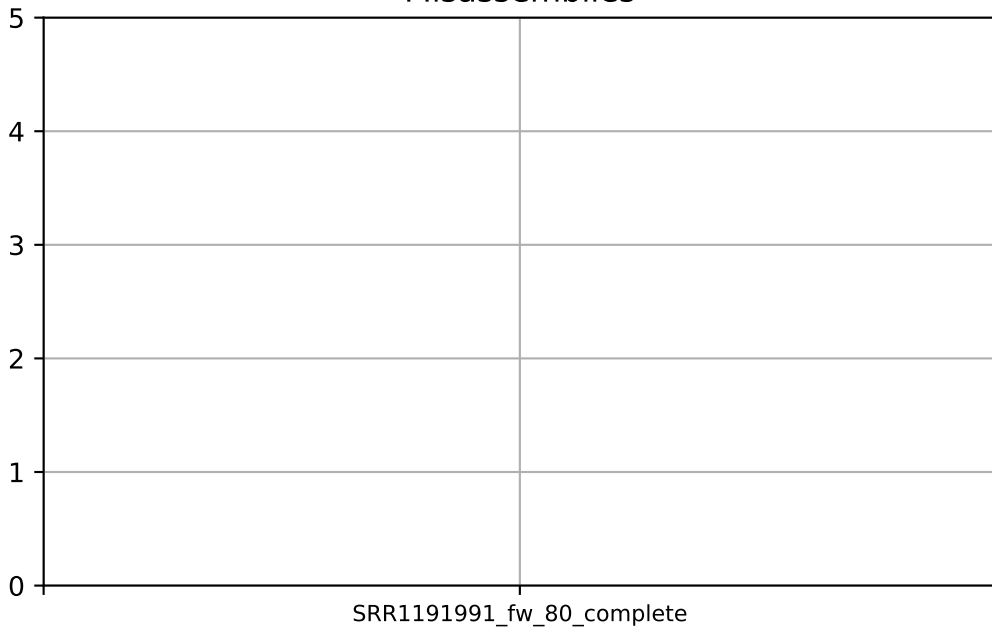
— SRR1191991_fw_80_complete - - Reference

SRR1191991_fw_80_complete GC content

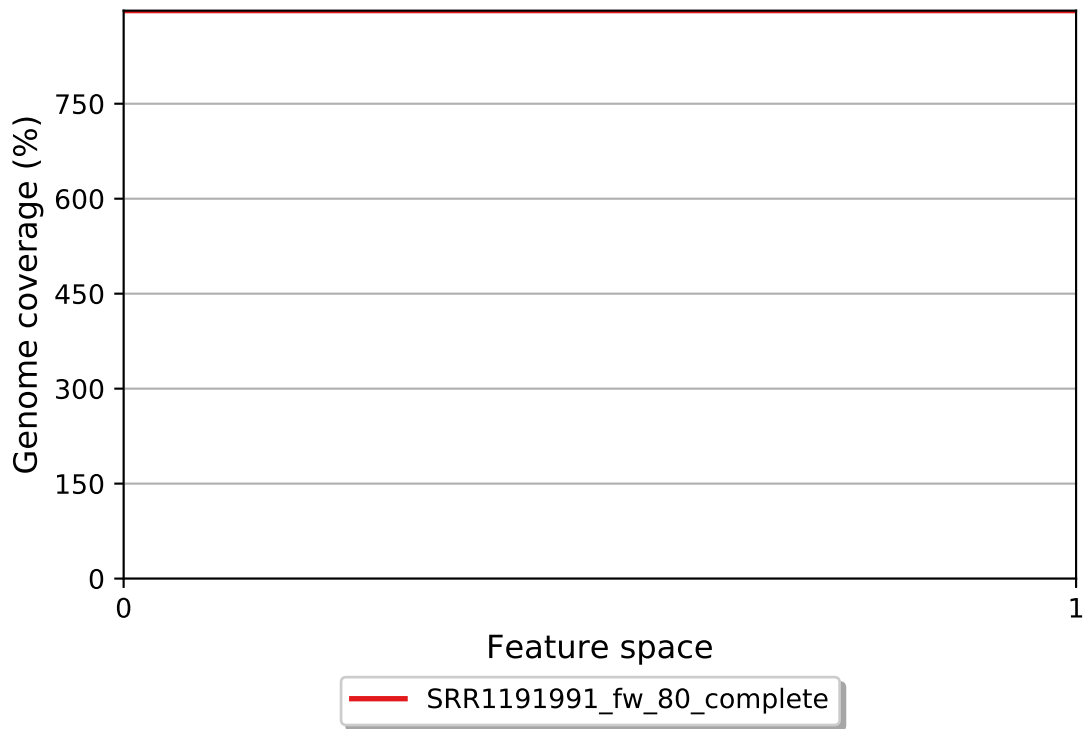


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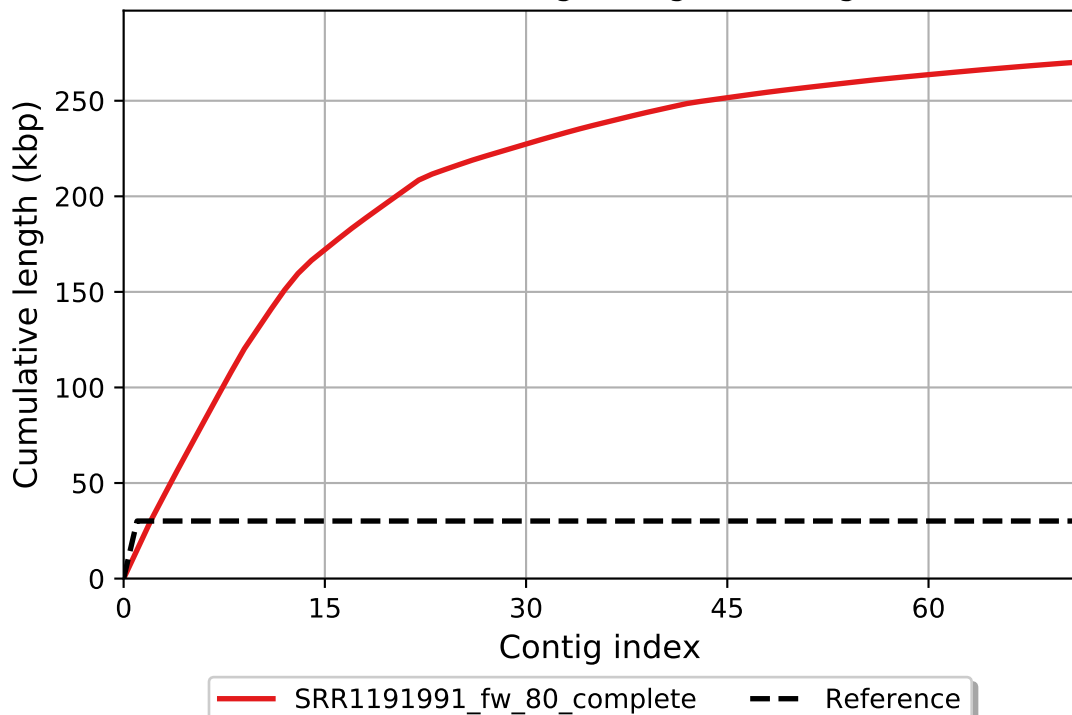
Misassemblies



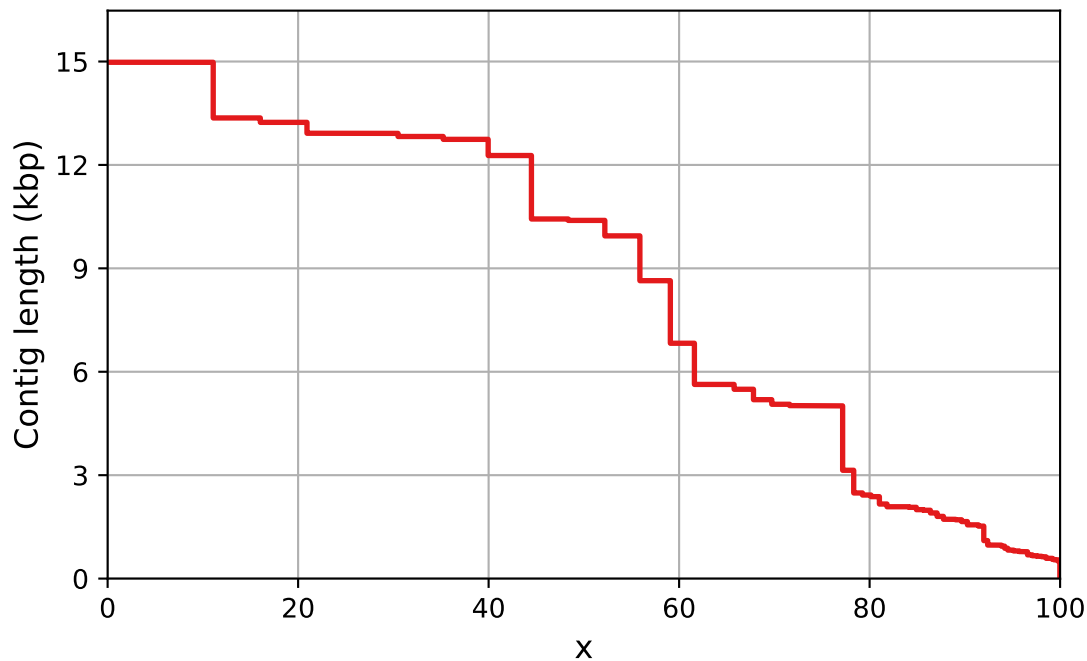
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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