

Report

	SRR1191915_fw_80_complete
# contigs (>= 1000 bp)	41
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	9
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	217532
Total length (>= 5000 bp)	154474
Total length (>= 10000 bp)	132020
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	61
Largest contig	16104
Total length	232126
Reference length	30114
GC (%)	41.68
Reference GC (%)	41.12
N50	13281
NG50	16104
N75	2818
NG75	15967
L50	8
LG50	1
L75	20
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	91.854
Duplication ratio	8.392
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3503.13
# indels per 100 kbp	14.46
Largest alignment	16102
Total aligned length	231917
NA50	13280
NGA50	16102
NA75	2817
NGA75	15871
LA50	8
LGA50	1
LA75	20
LGA75	2

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

	SRR1191915_fw_80_complete
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	969
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	10

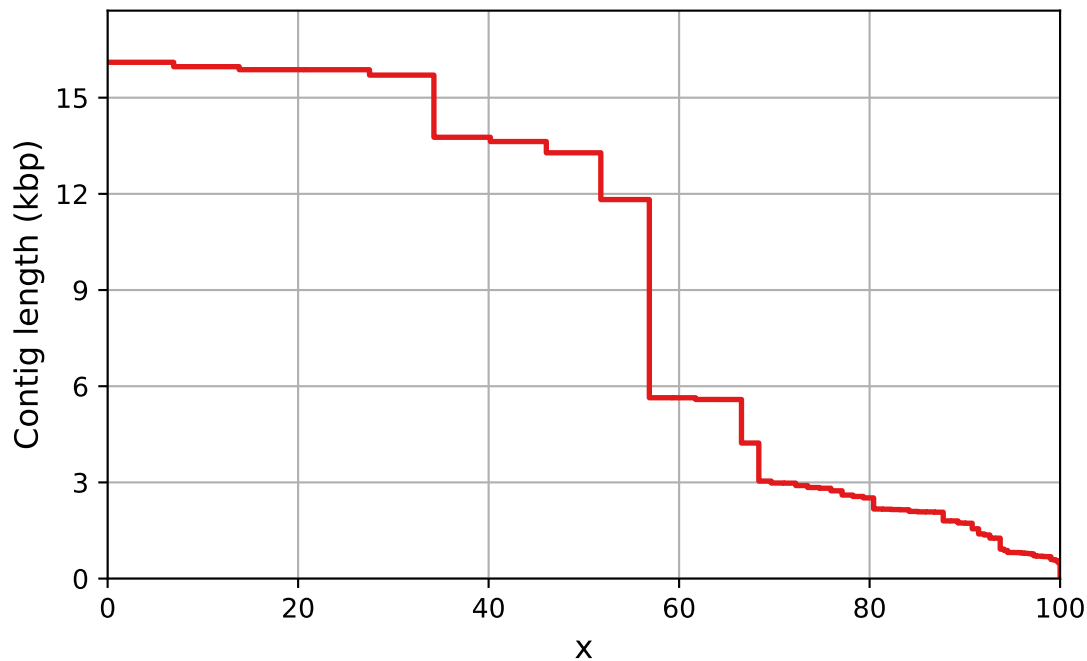
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR1191915_fw_80_complete
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

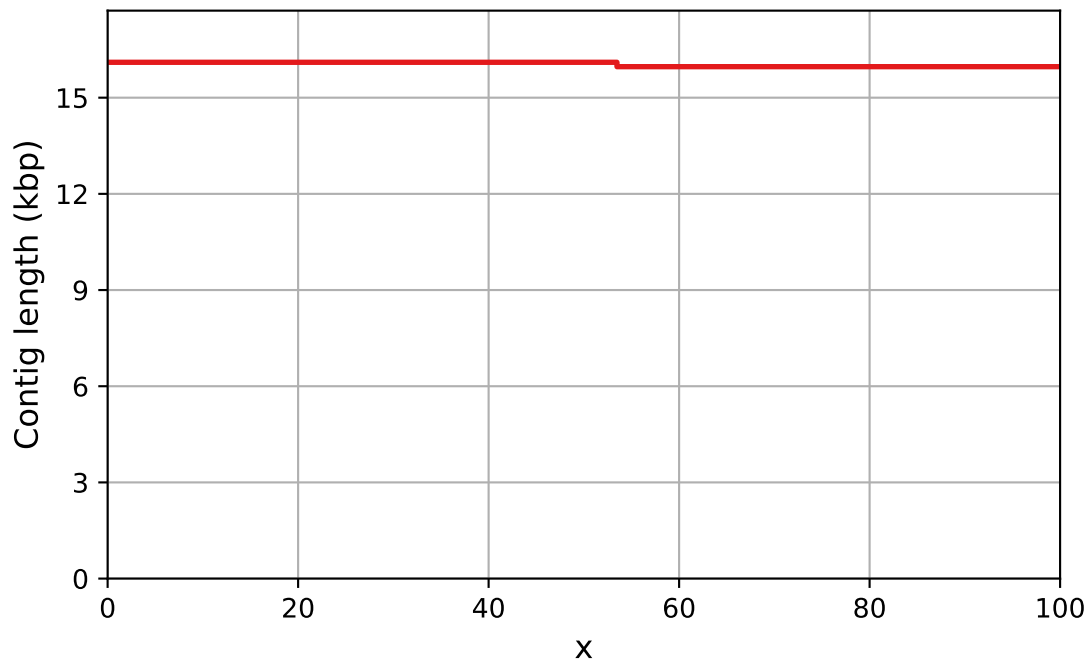
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

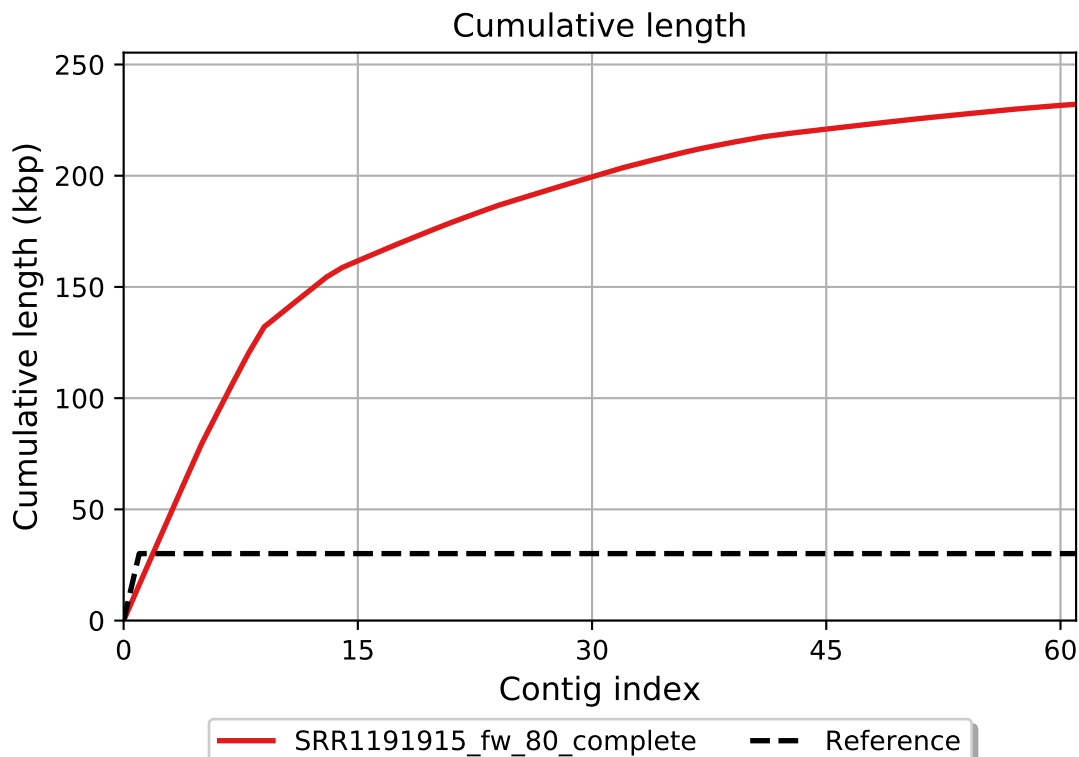


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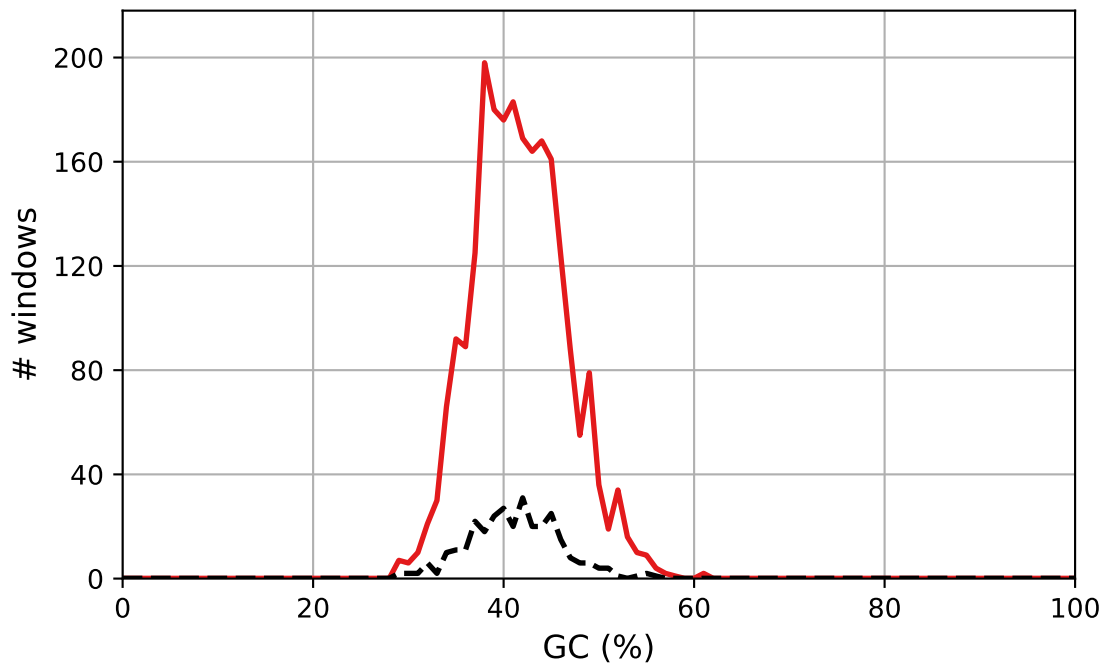
NGx



— SRR1191915_fw_80_complete

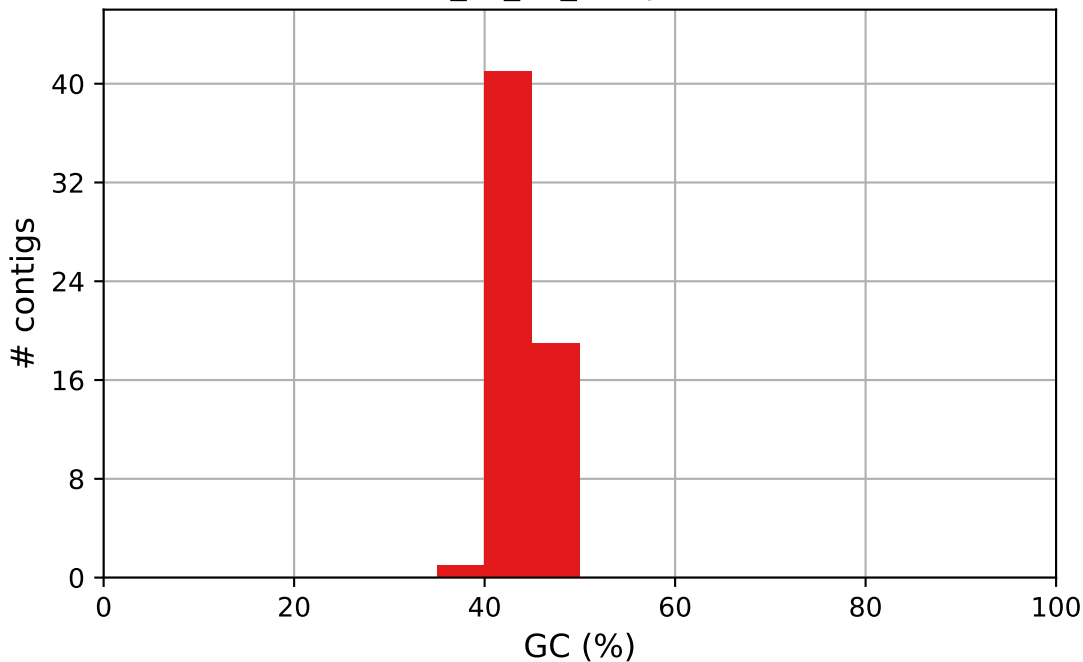


GC content



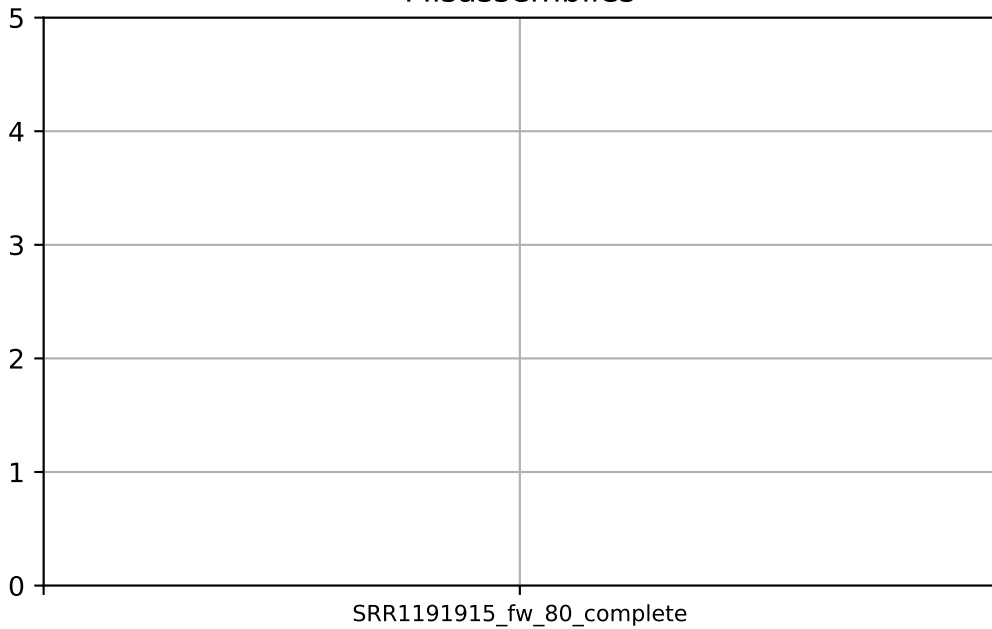
— SRR1191915_fw_80_complete - - Reference

SRR1191915_fw_80_complete GC content

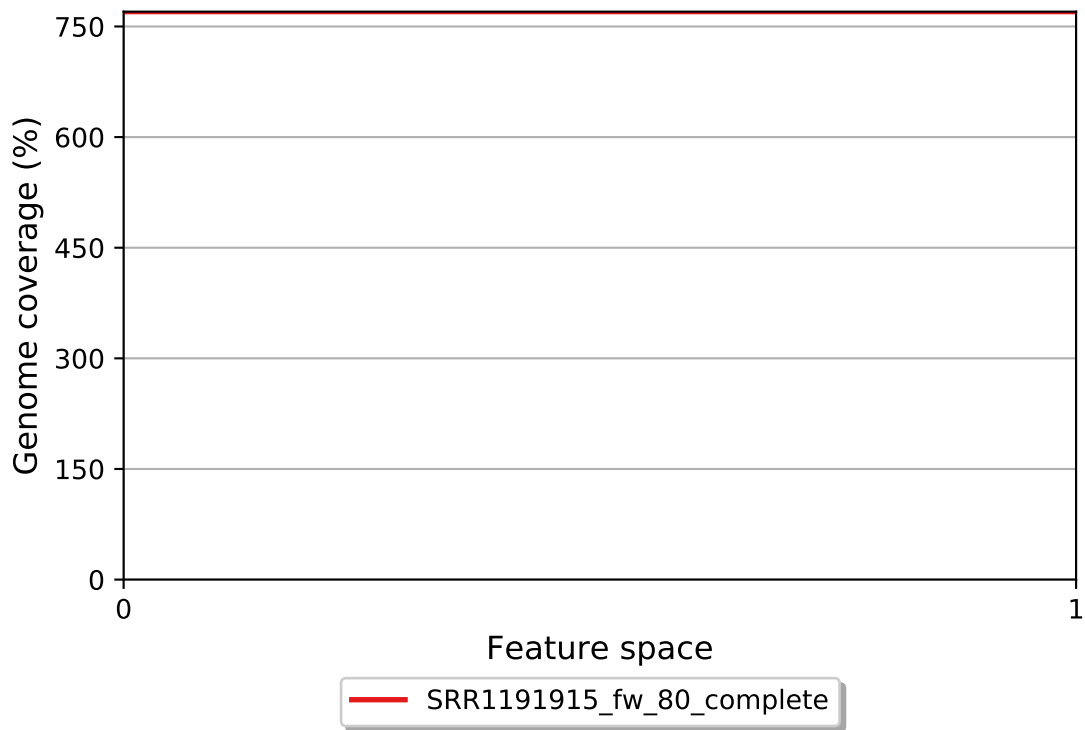


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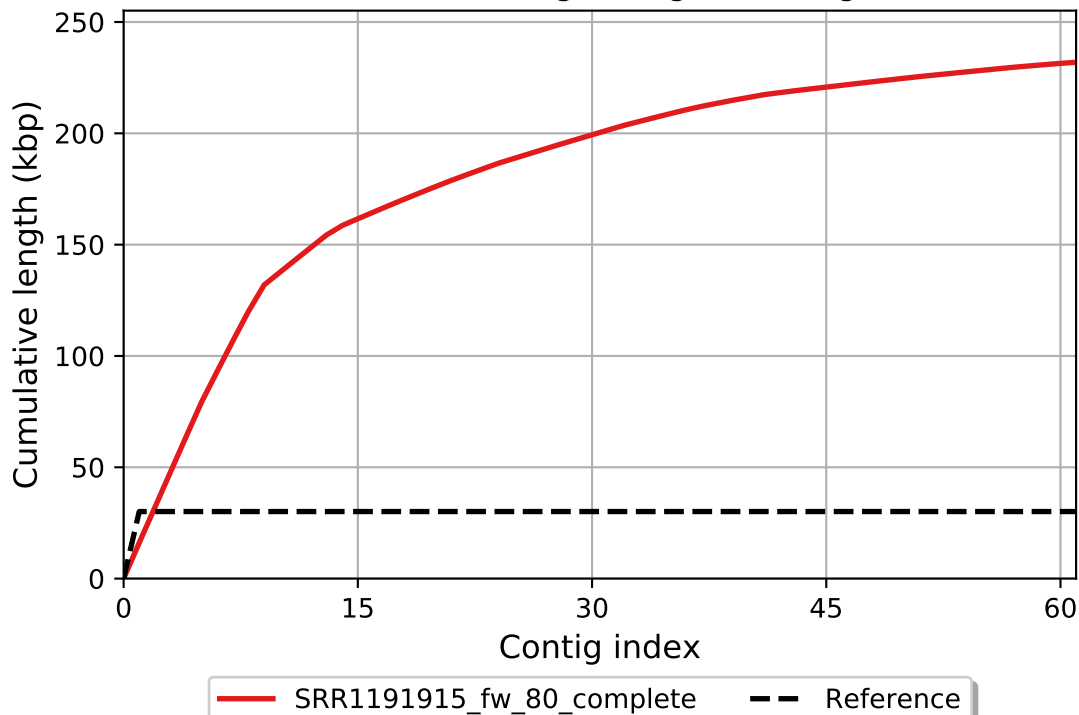
Misassemblies

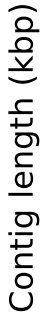


FRCurve (misassemblies)



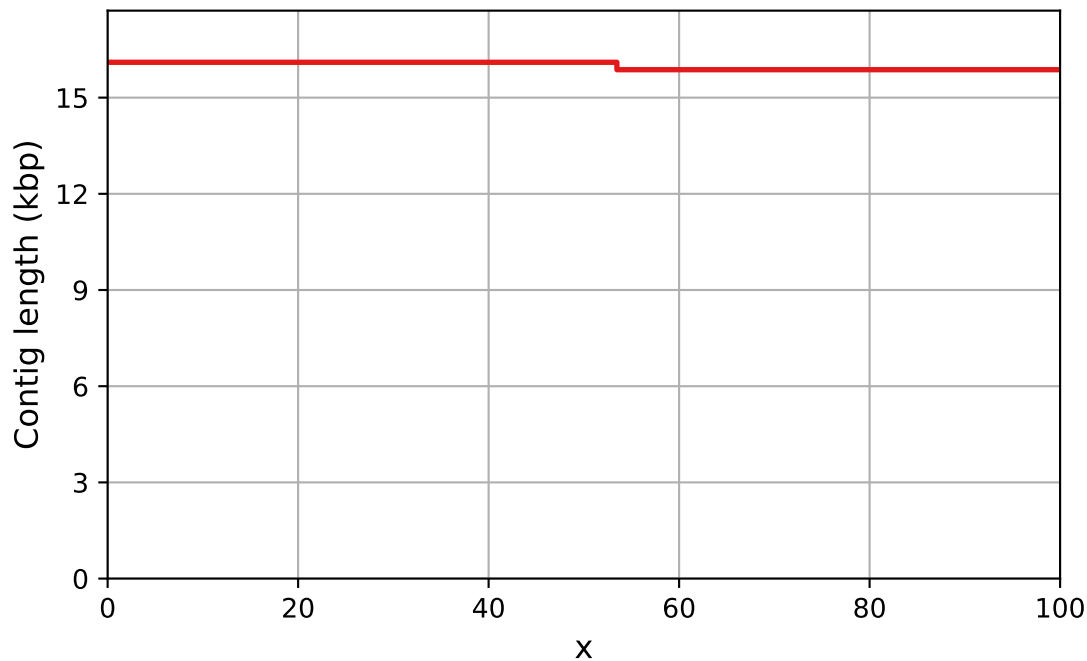
Cumulative length (aligned contigs)



Na^x 

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NGAx



— SRR1191915_fw_80_complete