

Report

	SRR1191991_fw_80_complete
# contigs (>= 1000 bp)	43
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
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
GC (%)	41.56
Reference GC (%)	41.12
N50	10392
NG50	14978
N75	5018
NG75	14978
L50	11
LG50	2
L75	21
LG75	2
# 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
NGA50	14977
NA75	5017
NGA75	14977
LA50	11
LGA50	2
LA75	21
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

	SRR1191991_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	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

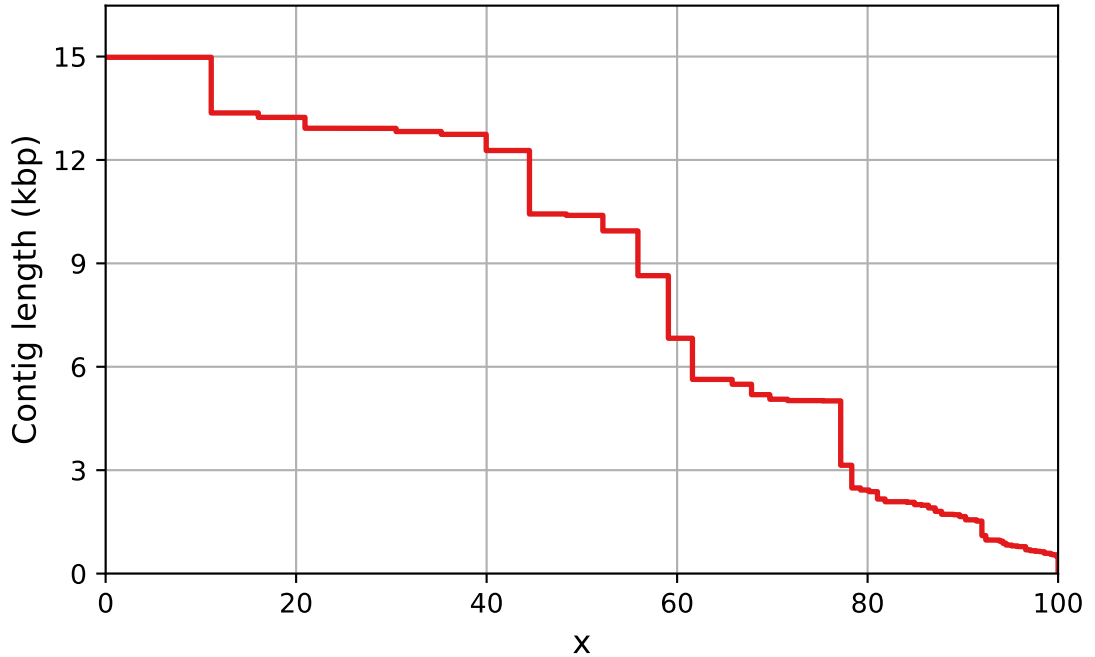
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

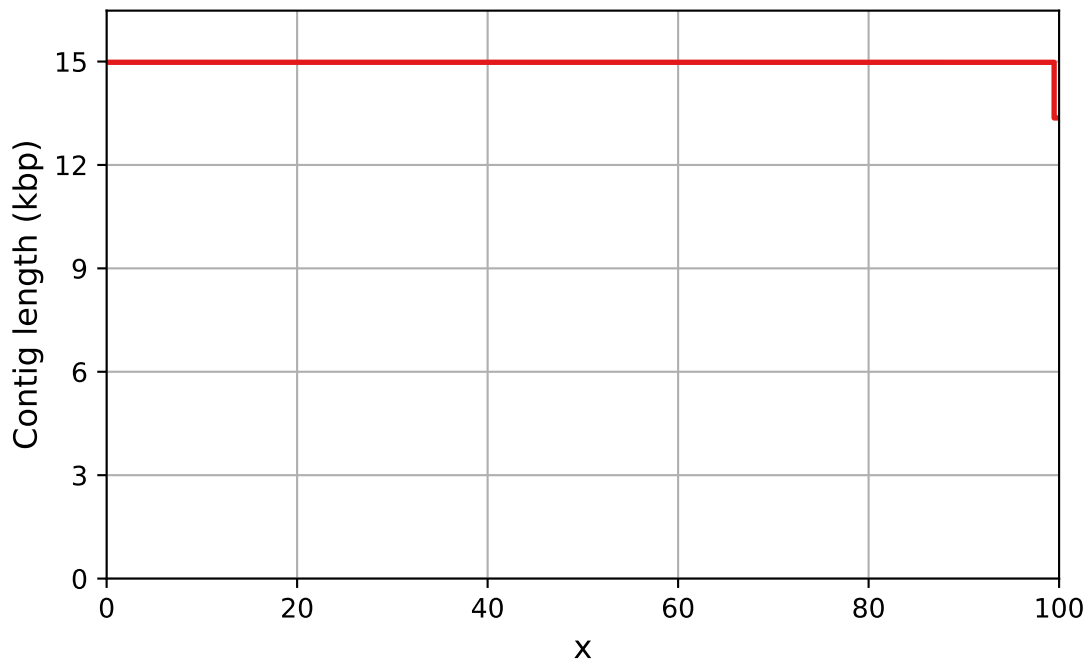
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



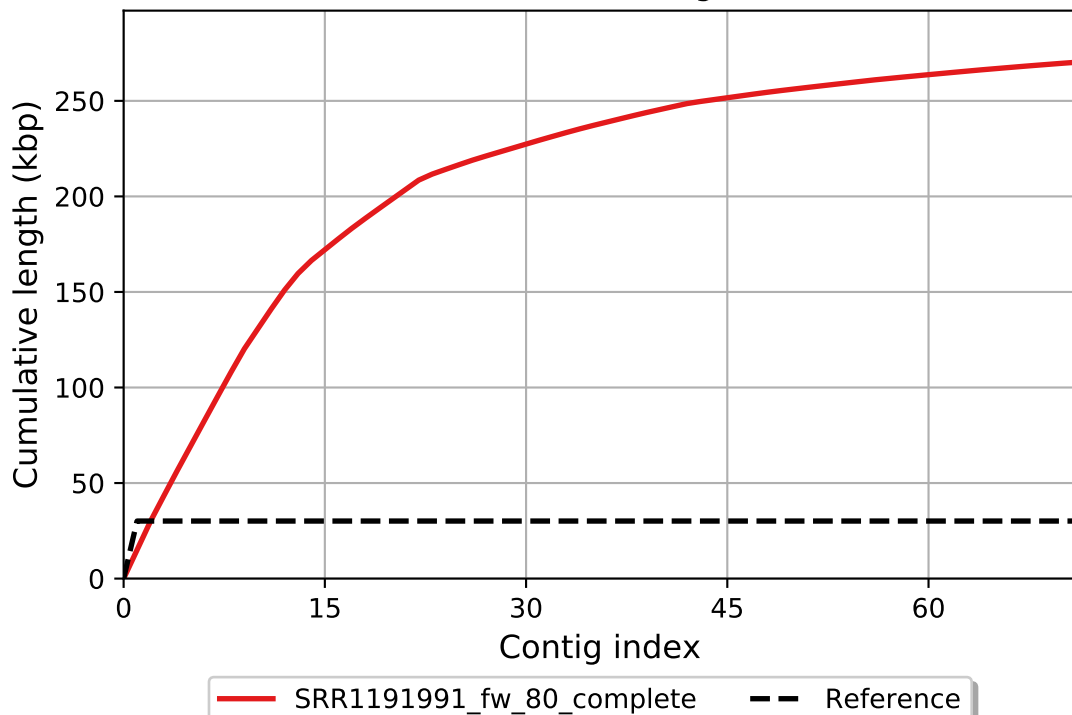
SRR1191991_fw_80_complete

NGx

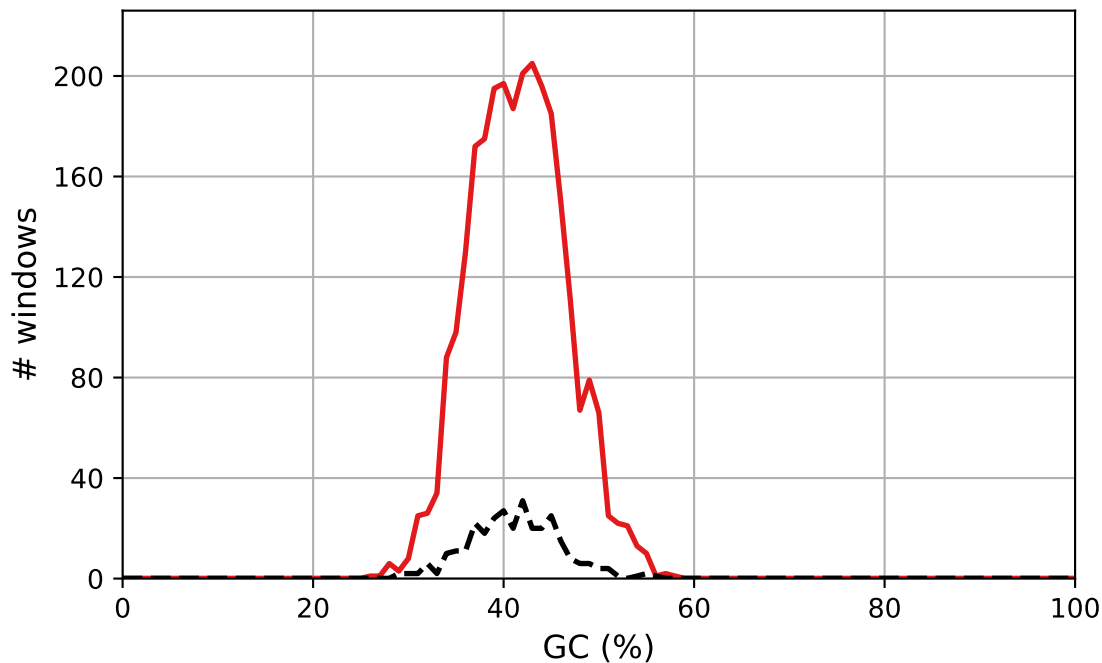


— SRR1191991_fw_80_complete

Cumulative length

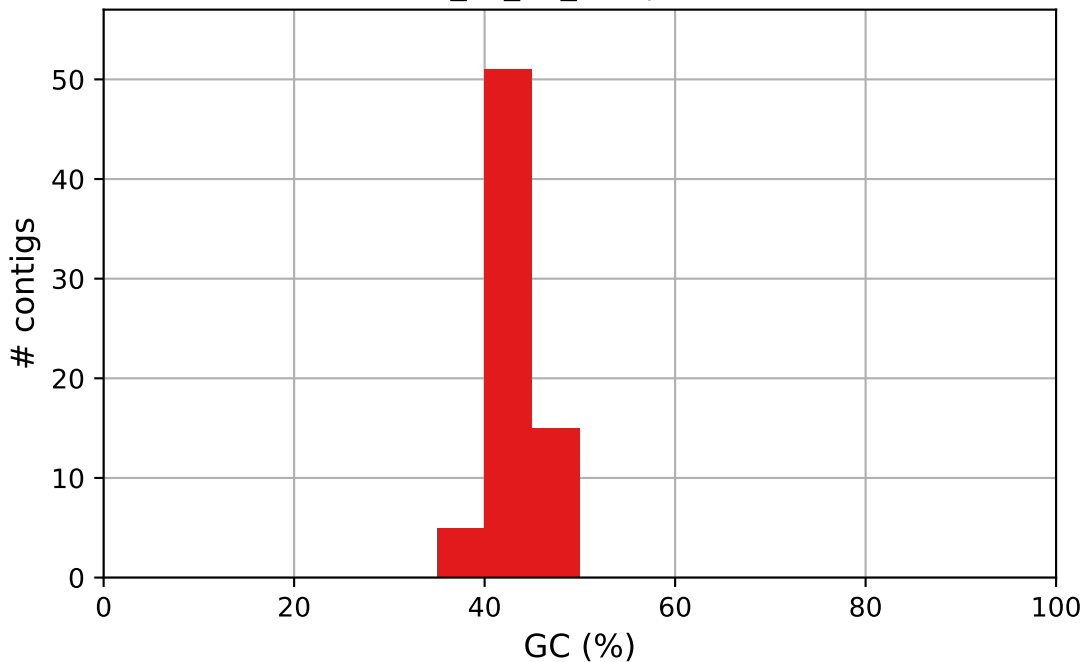


GC content



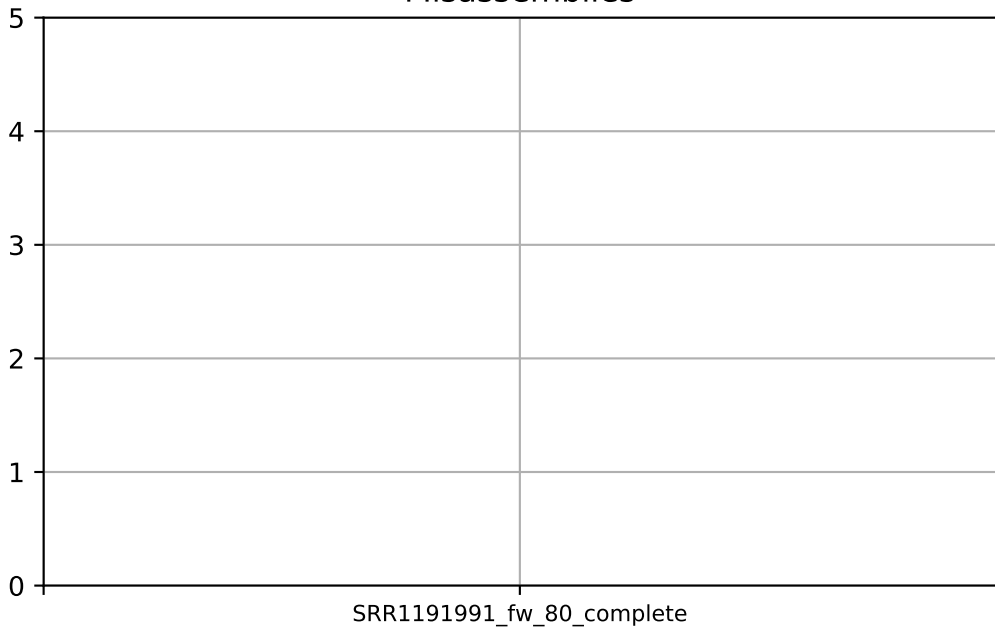
— SRR1191991_fw_80_complete - - Reference

SRR1191991_fw_80_complete GC content

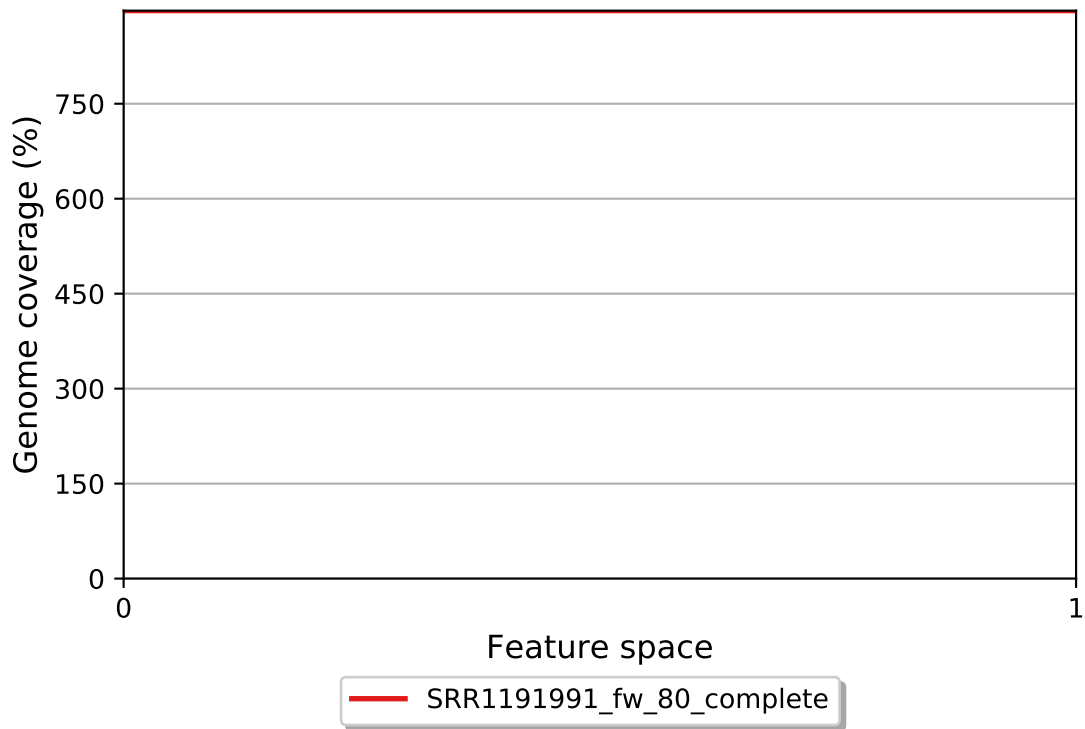


■ SRR1191991_fw_80_complete

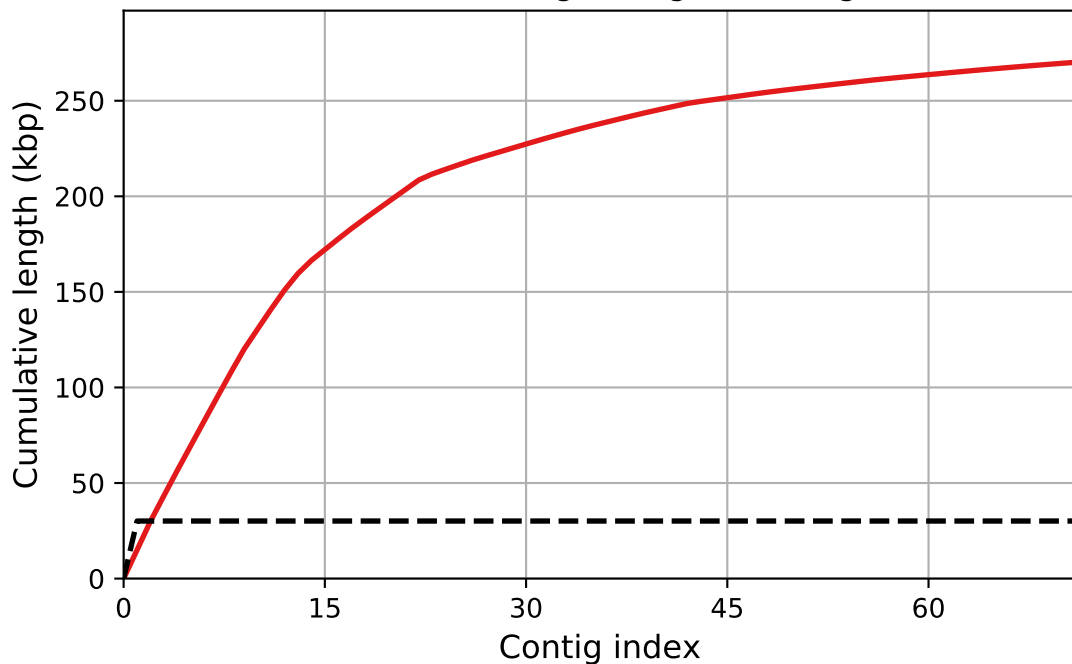
Misassemblies



FRCurve (misassemblies)

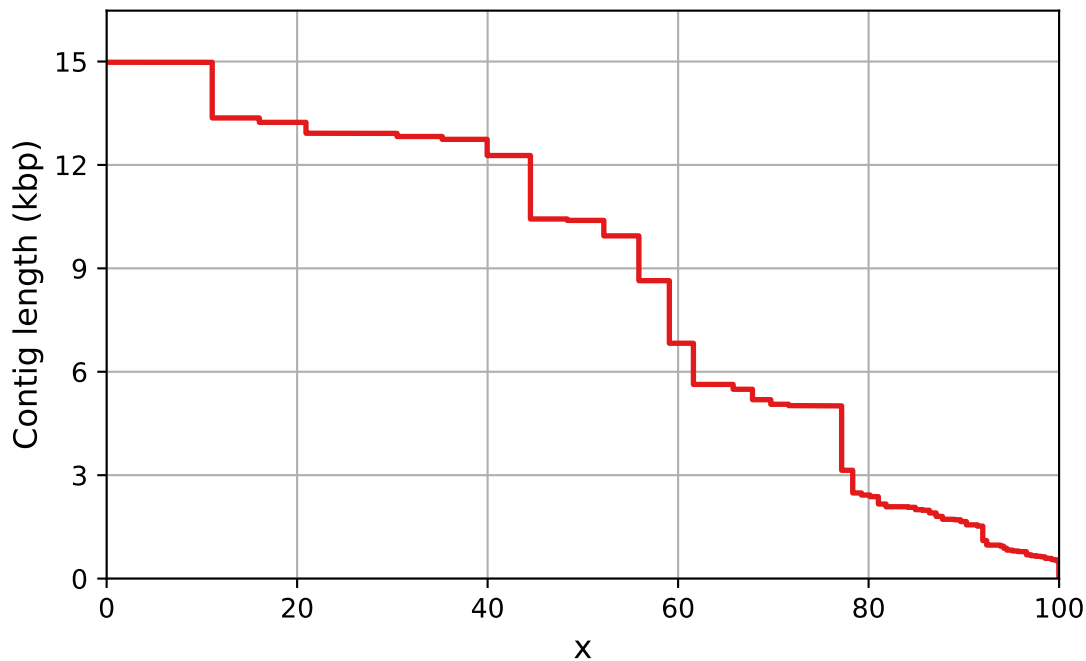


Cumulative length (aligned contigs)



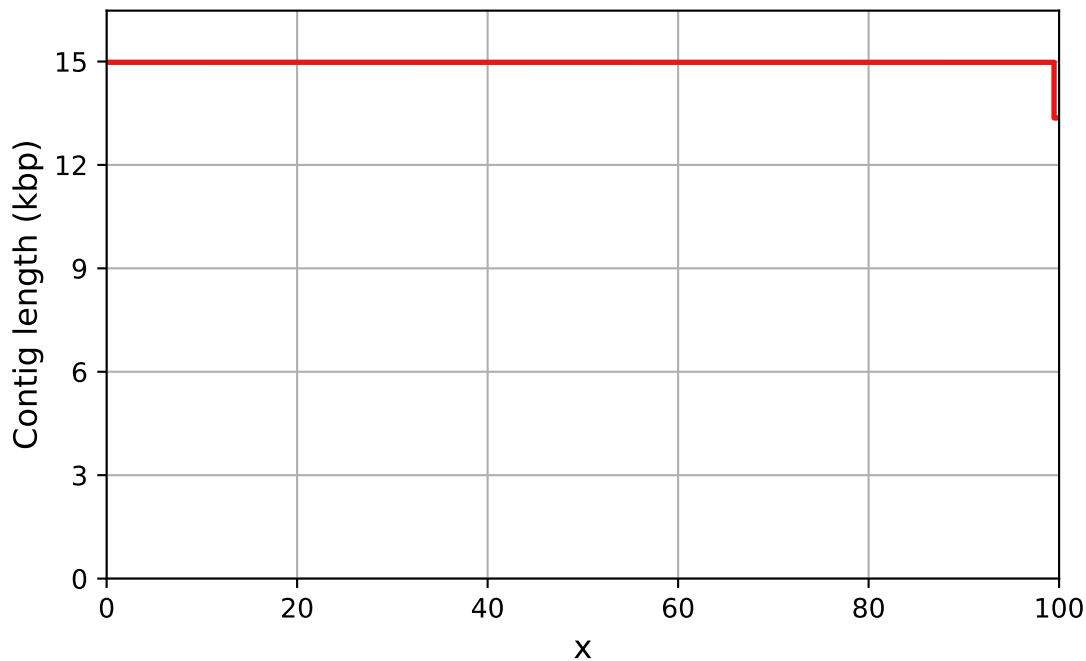
— SRR1191991_fw_80_complete - - Reference

NAx



SRR1191991_fw_80_complete

NGAx



— SRR1191991_fw_80_complete