

Report

	out_21
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	13725
Total length (>= 1000 bp)	13725
Total length (>= 5000 bp)	13725
Total length (>= 10000 bp)	13725
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	13725
Total length	13725
Reference length	10624
GC (%)	44.26
Reference GC (%)	44.14
N50	13725
NG50	13725
N90	13725
NG90	13725
auN	13725.0
auNG	17731.1
L50	1
LG50	1
L90	1
LG90	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	73.870
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11057.39
# indels per 100 kbp	661.66
Largest alignment	7859
Total aligned length	7859
NA50	7859
NGA50	7859
NA90	-
NGA90	-
auNA	4500.1
auNGA	5813.6
LA50	1
LGA50	1
LA90	-
LGA90	-

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

	out_21
# 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
# local misassemblies	9
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	869
# indels	52
# indels (<= 5 bp)	4
# indels (> 5 bp)	48
Indels length	1975

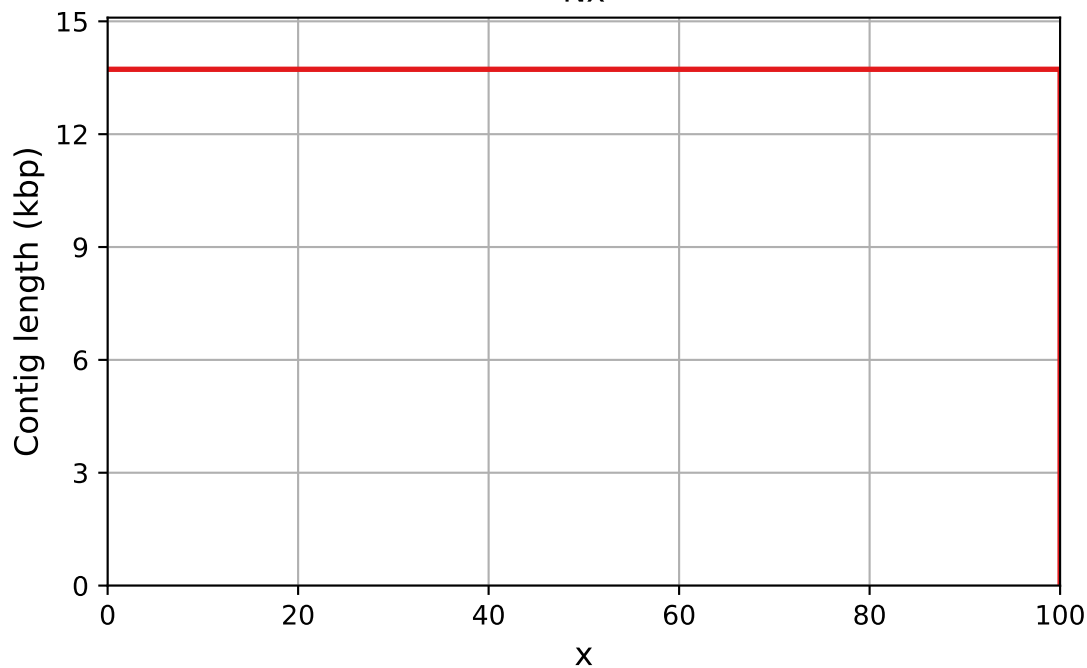
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	out_21
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

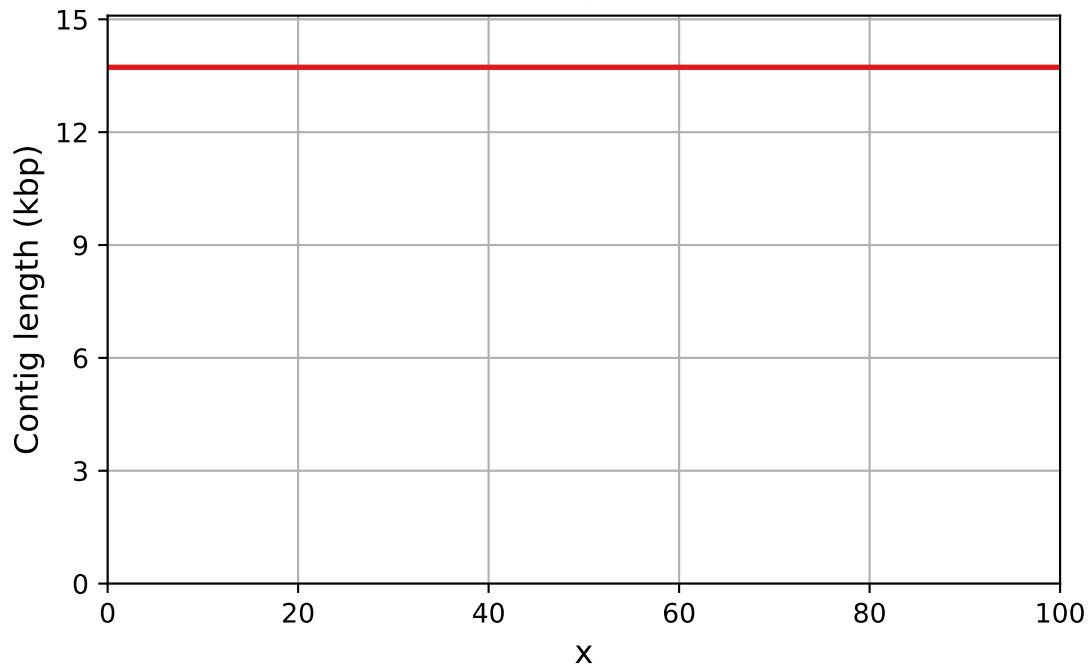
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



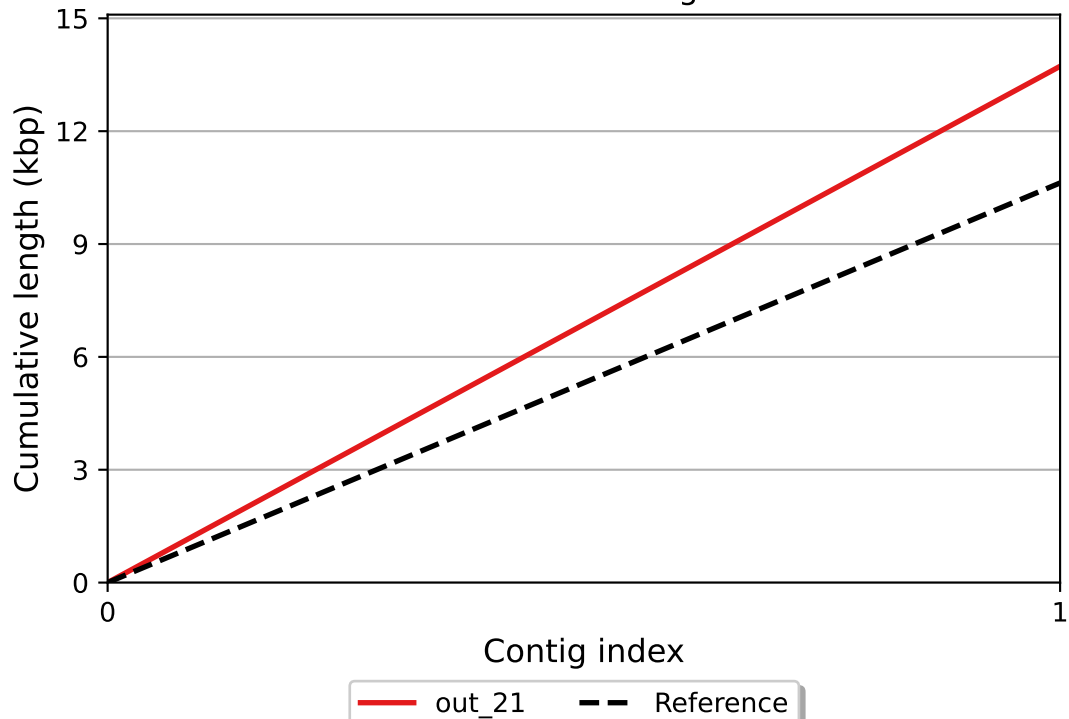
— out\_21

NGx

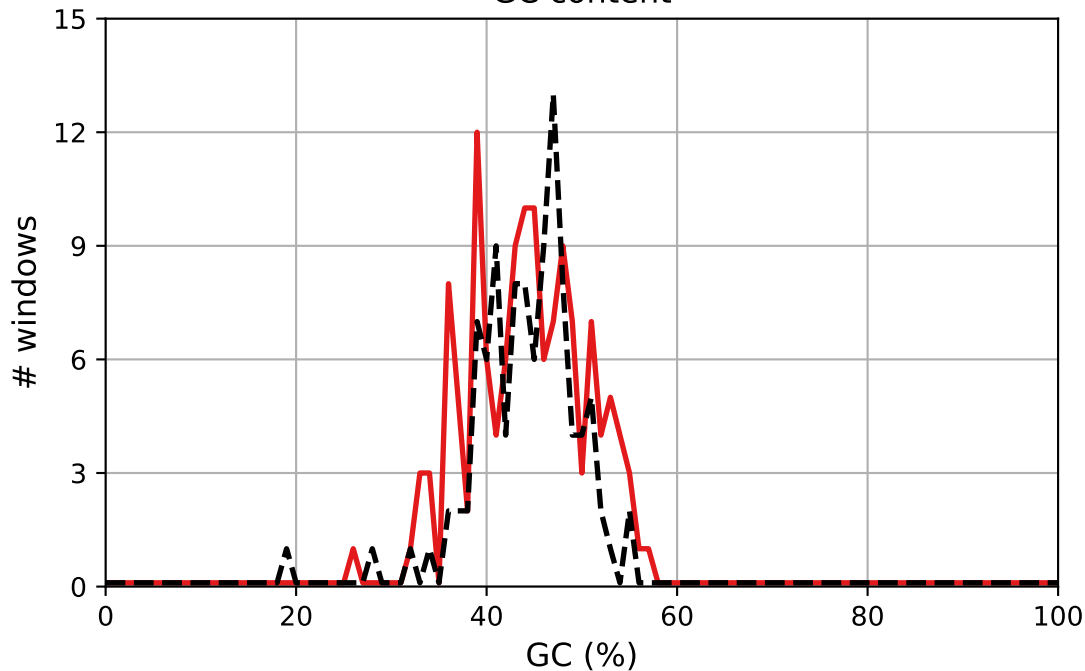


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Cumulative length

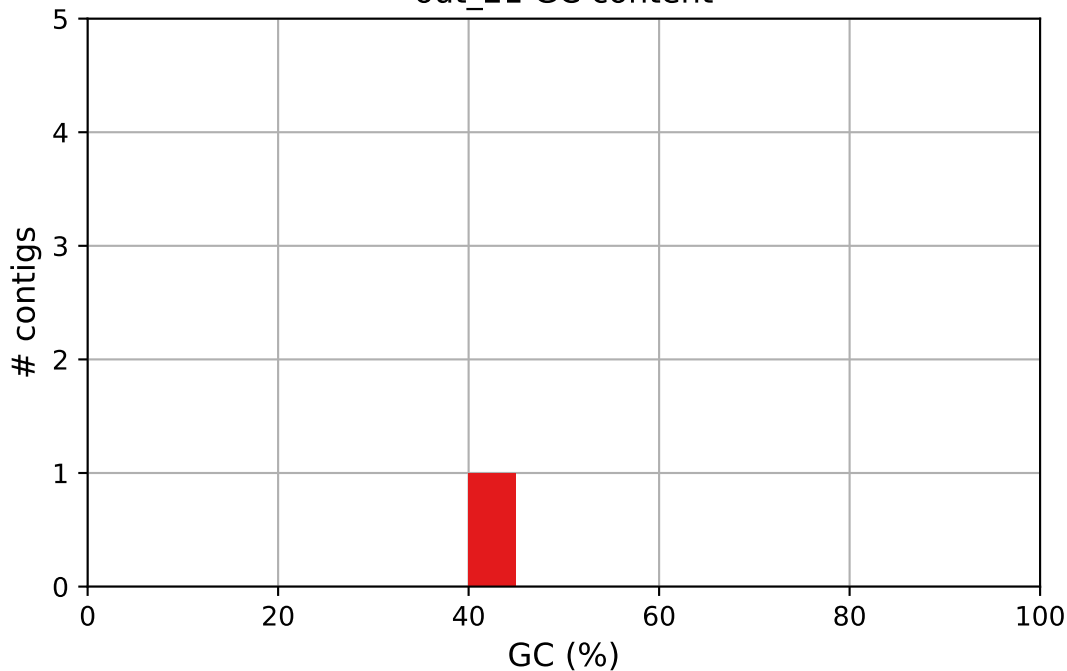


GC content



— out\_21    - - Reference

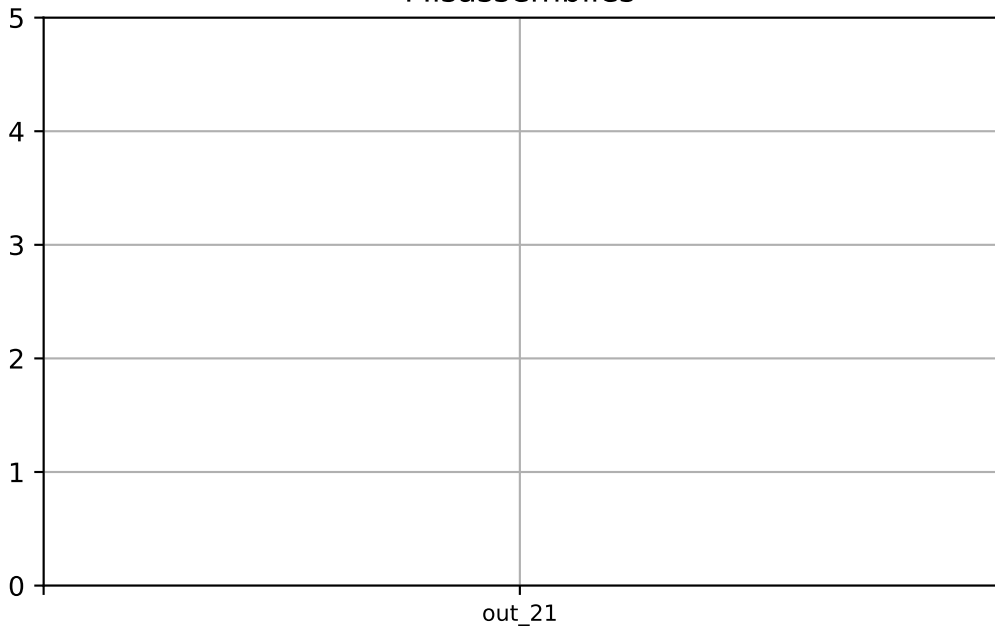
out\_21 GC content



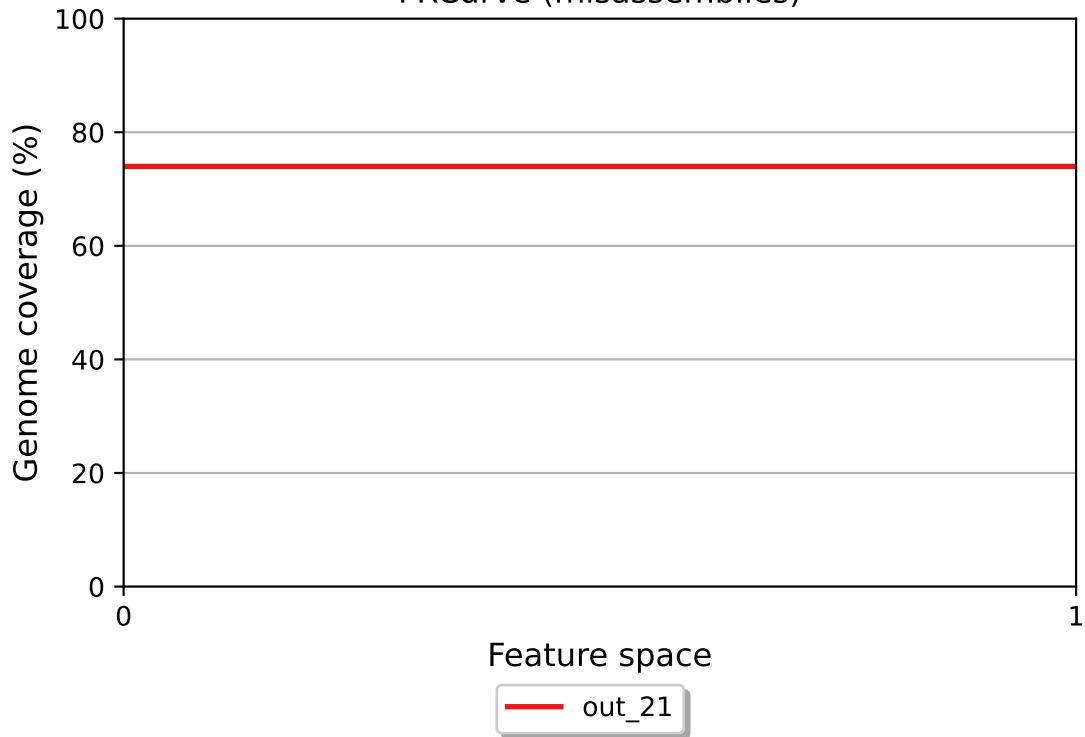
out\_21



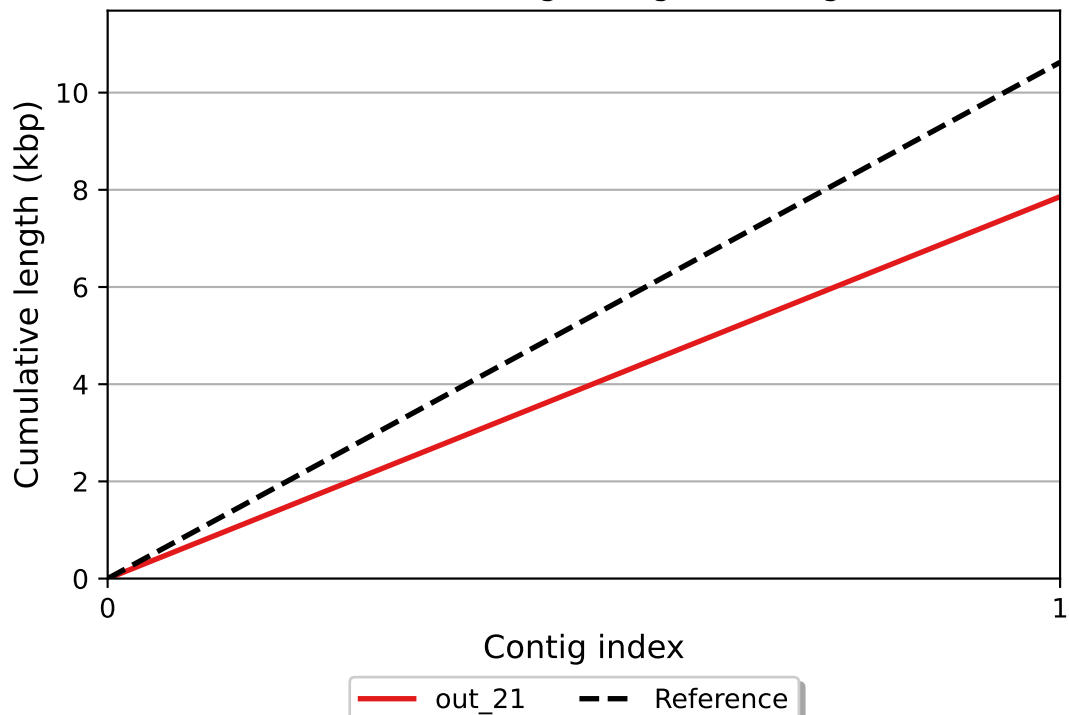
## Misassemblies



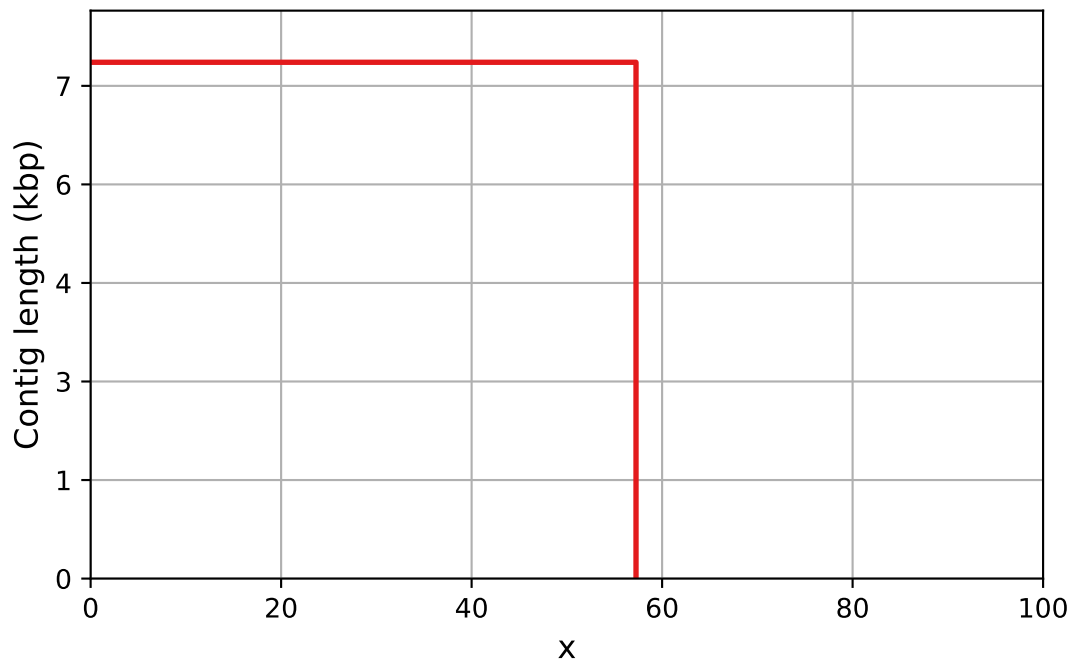
FRCurve (misassemblies)



Cumulative length (aligned contigs)

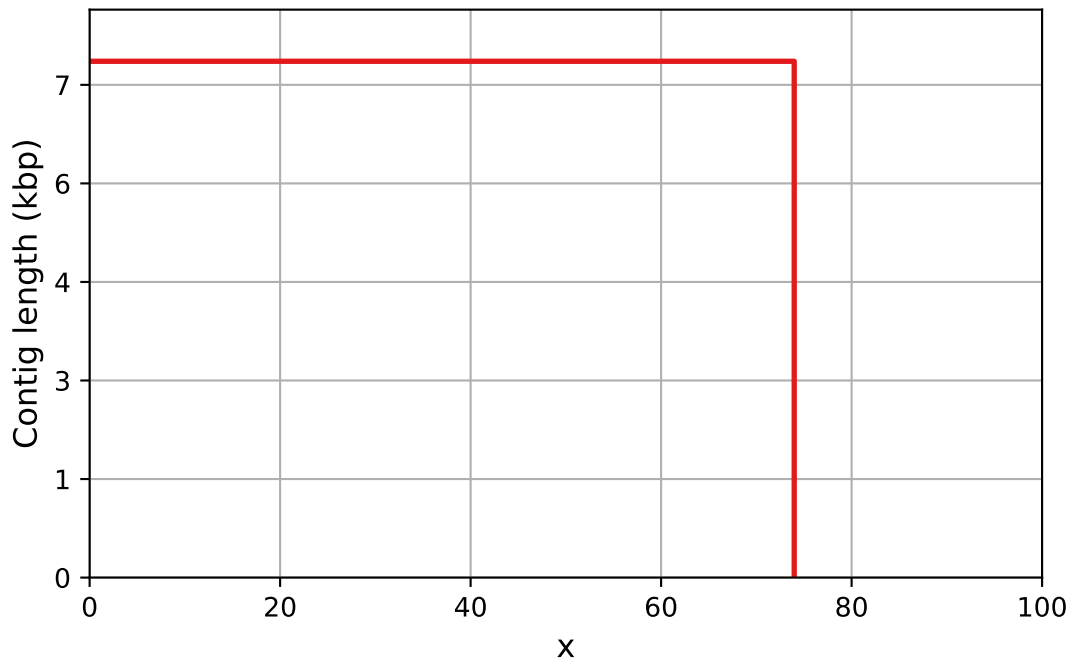


NAx



— out\_21

NGAx



— out\_21