

Report

	flye_error
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29456
Total length (>= 1000 bp)	29456
Total length (>= 5000 bp)	29456
Total length (>= 10000 bp)	29456
Total length (>= 25000 bp)	29456
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29456
Total length	29456
Reference length	30119
GC (%)	41.20
Reference GC (%)	41.24
N50	29456
NG50	29456
N90	29456
NG90	29456
auN	29456.0
auNG	28807.6
L50	1
LG50	1
L90	1
LG90	1
# 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 (%)	97.683
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	13.58
# indels per 100 kbp	71.32
Largest alignment	29446
Total aligned length	29446
NA50	29446
NGA50	29446
NA90	29446
NGA90	29446
auNA	29436.0
auNGA	28788.0
LA50	1
LGA50	1
LA90	1
LGA90	1

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

	flye_error
# 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	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	4
# indels	21
# indels (<= 5 bp)	21
# indels (> 5 bp)	0
Indels length	25

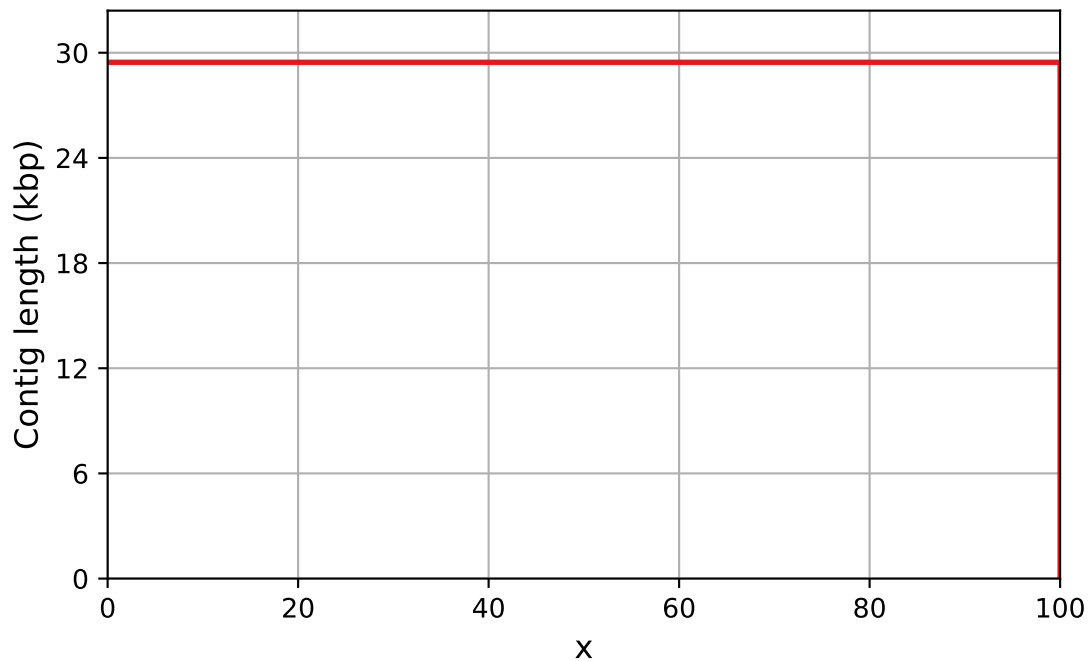
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

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

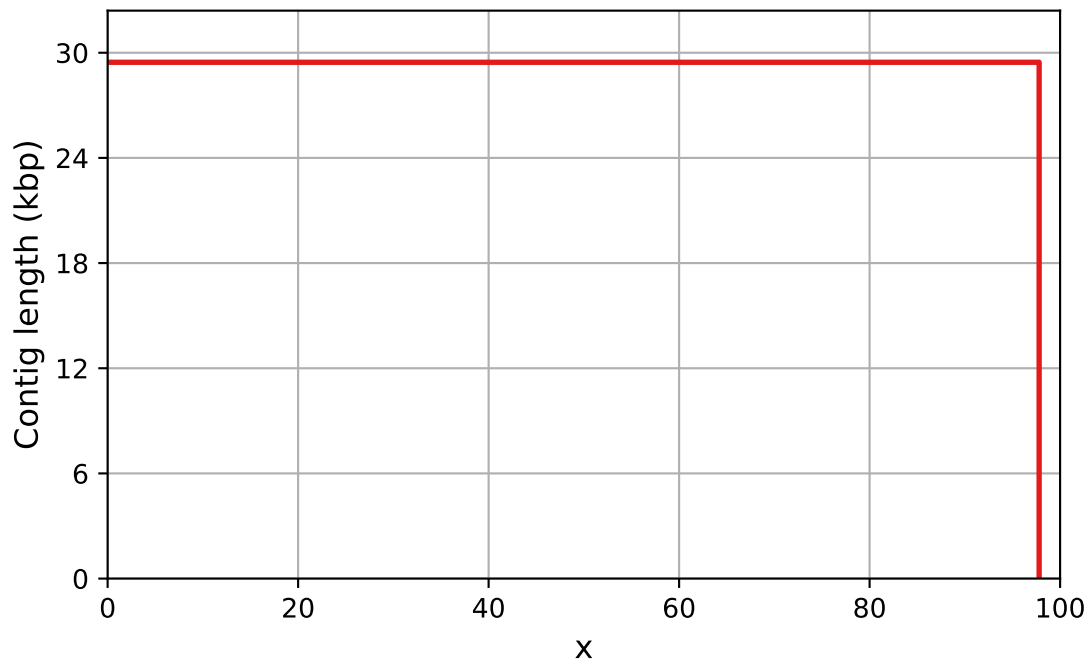
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



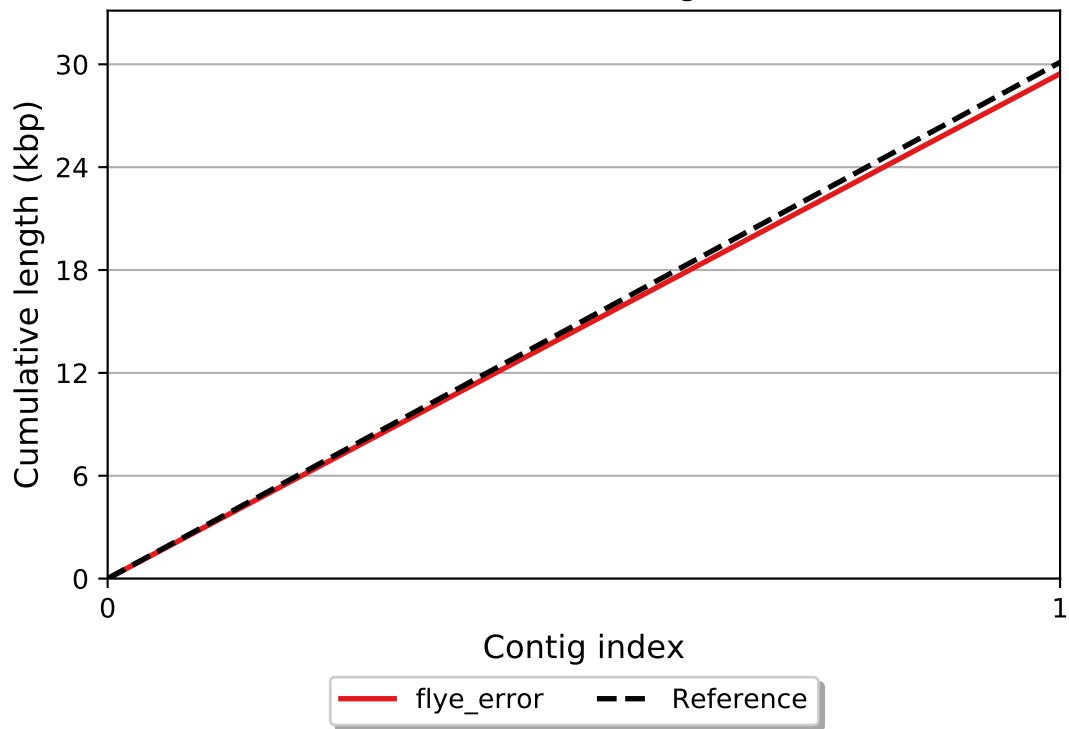
flye_error

NGx

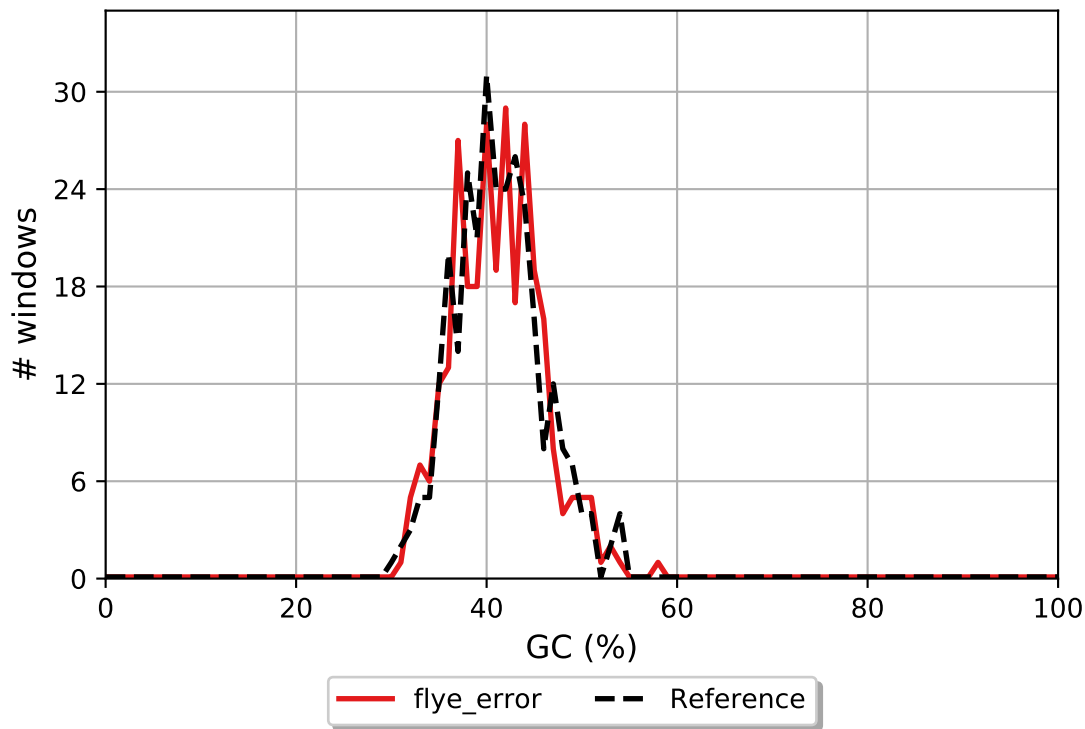


flye_error

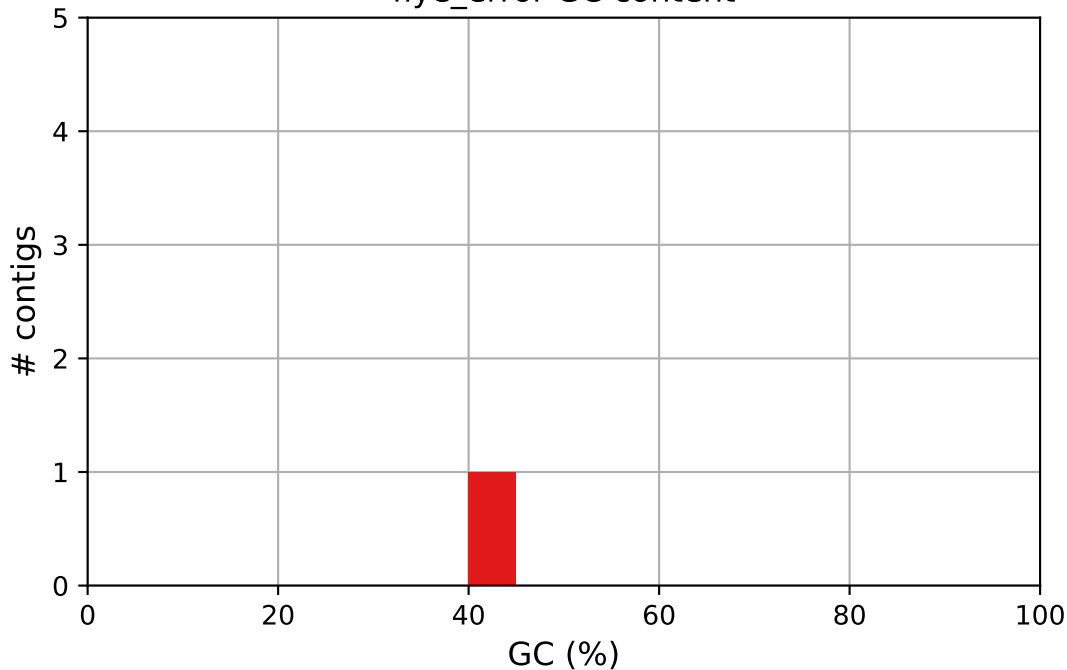
Cumulative length



GC content

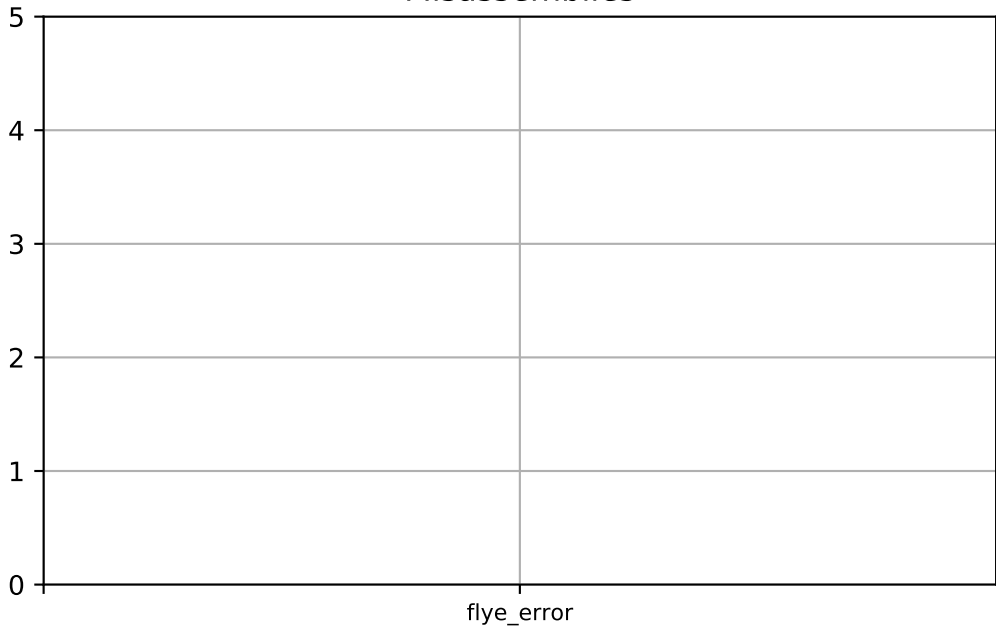


flye_error GC content

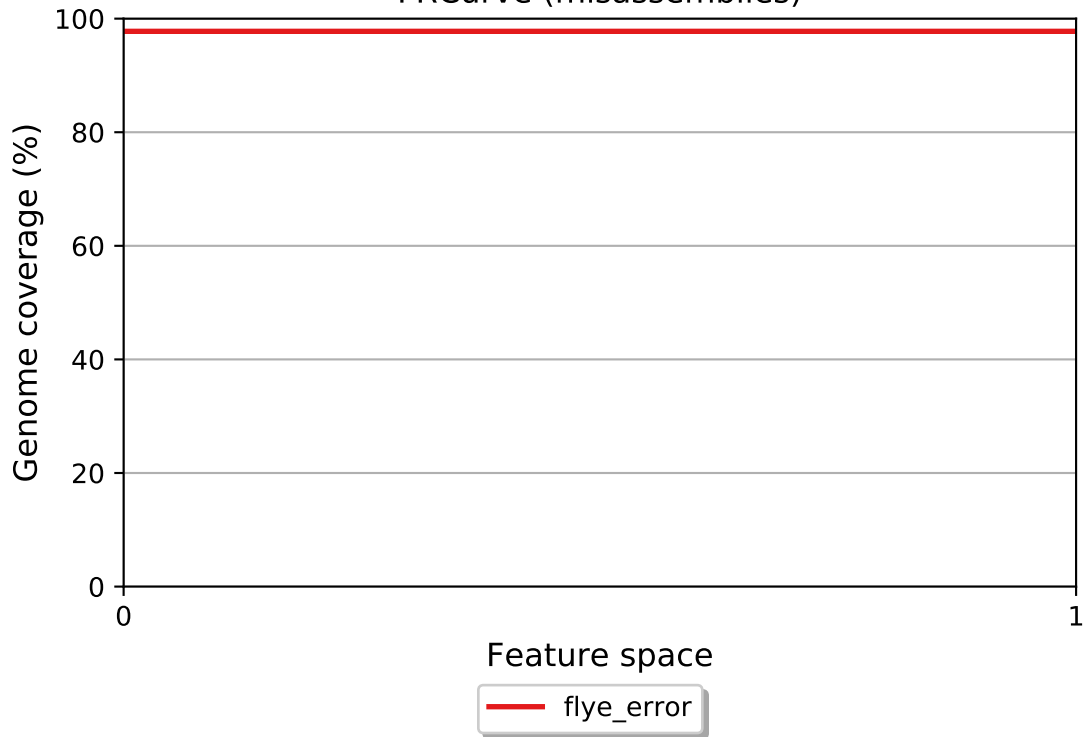


flye_error

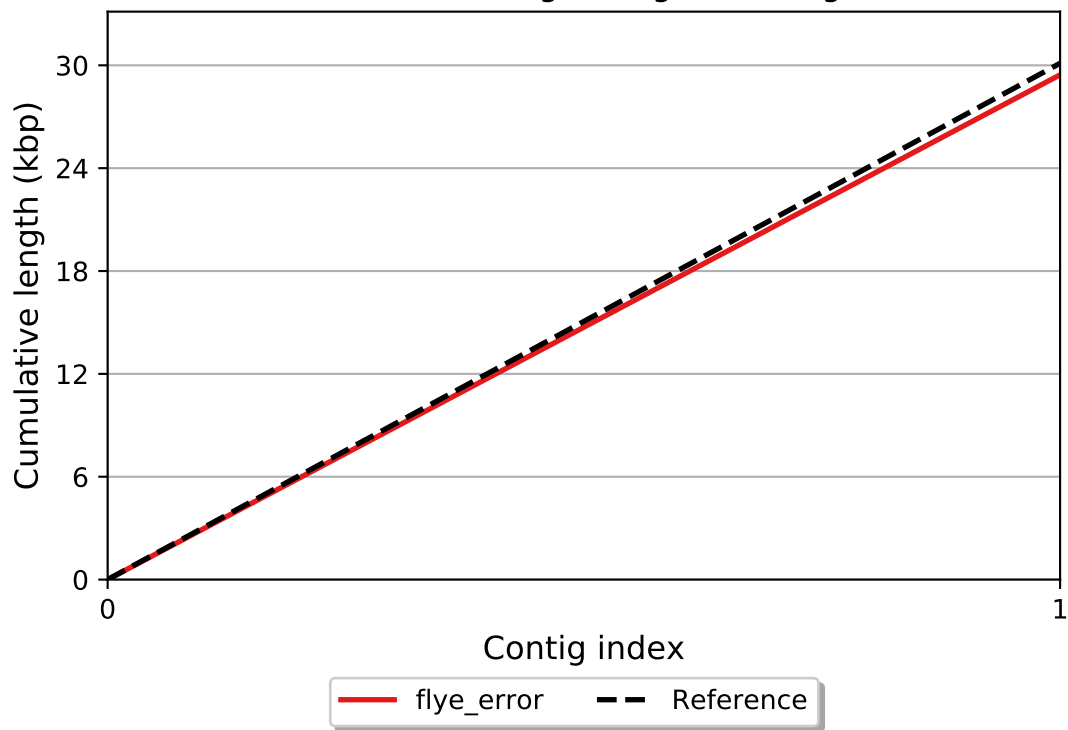
Misassemblies



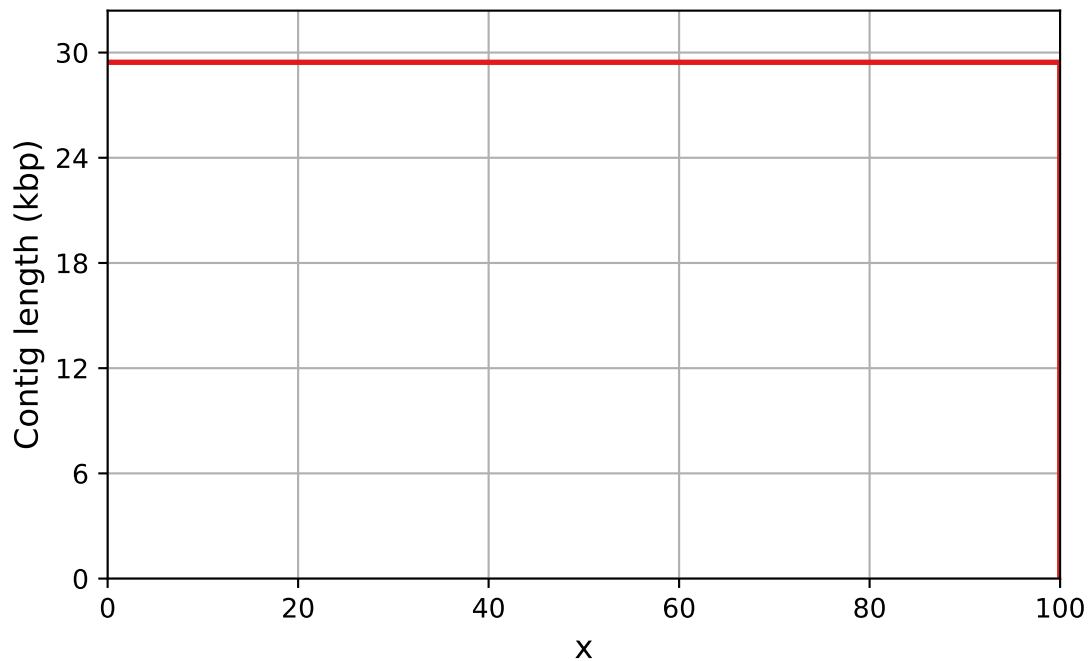
FRCurve (misassemblies)



Cumulative length (aligned contigs)

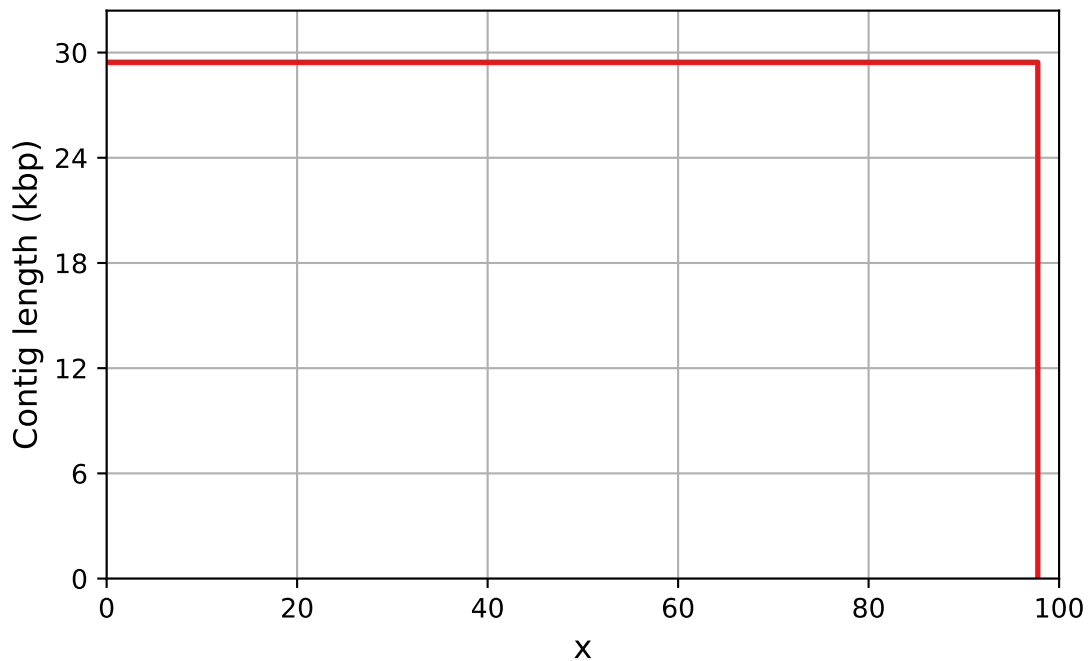


NAx



flye_error

NGAx



flye_error