

Report

	flye_noerror
# 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)	29430
Total length (>= 1000 bp)	29430
Total length (>= 5000 bp)	29430
Total length (>= 10000 bp)	29430
Total length (>= 25000 bp)	29430
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29430
Total length	29430
Reference length	30119
GC (%)	41.17
Reference GC (%)	41.24
N50	29430
NG50	29430
N90	29430
NG90	29430
auN	29430.0
auNG	28756.8
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 (%)	97.712
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	29430
Total aligned length	29430
NA50	29430
NGA50	29430
NA90	29430
NGA90	29430
auNA	29430.0
auNGA	28756.8
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_noerror
# 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	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

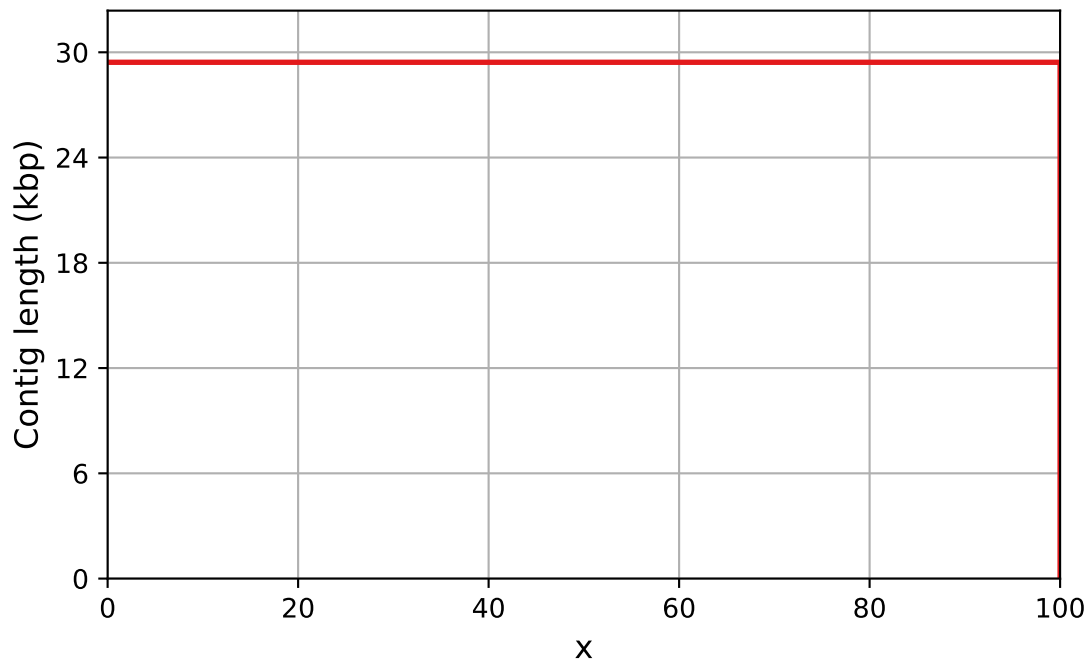
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

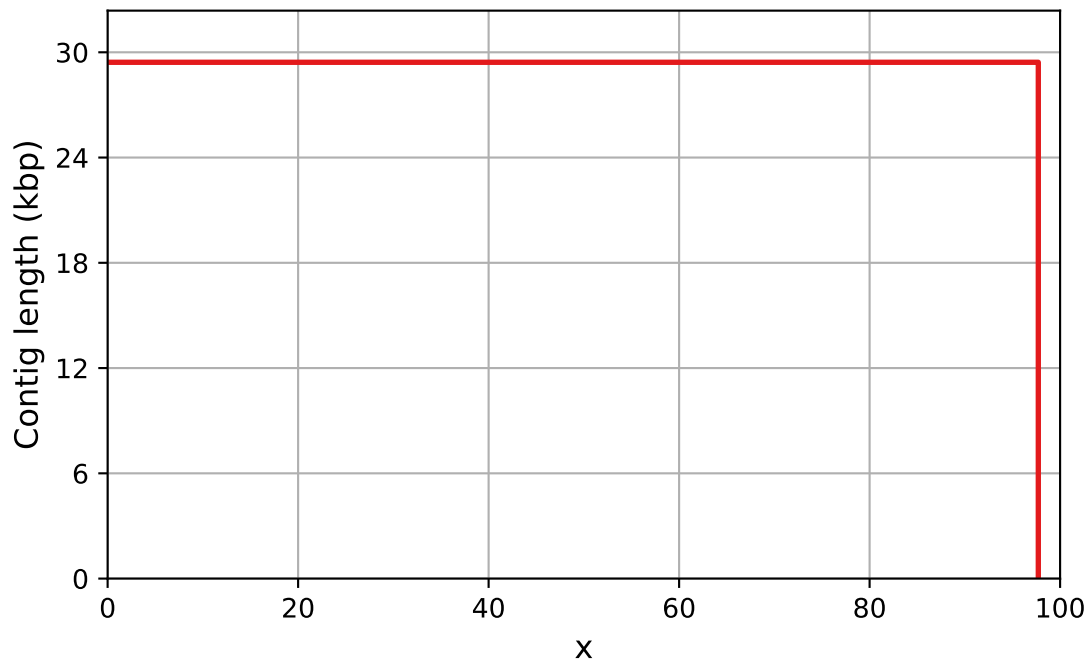
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



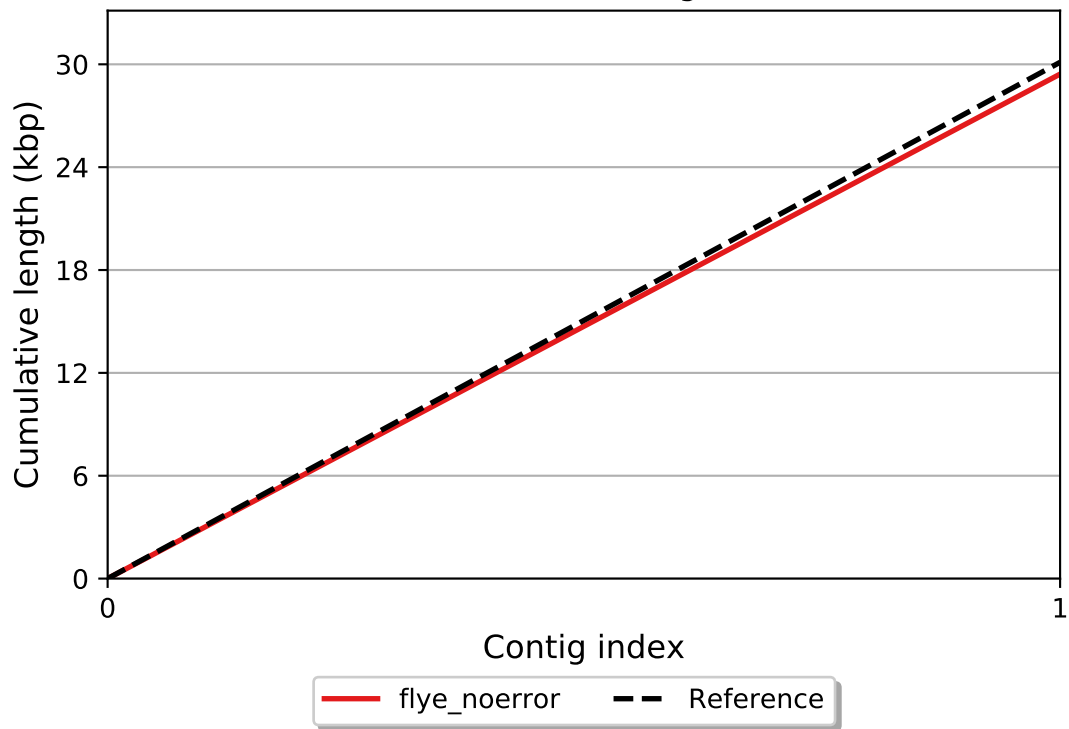
flye\_noerror

NGx

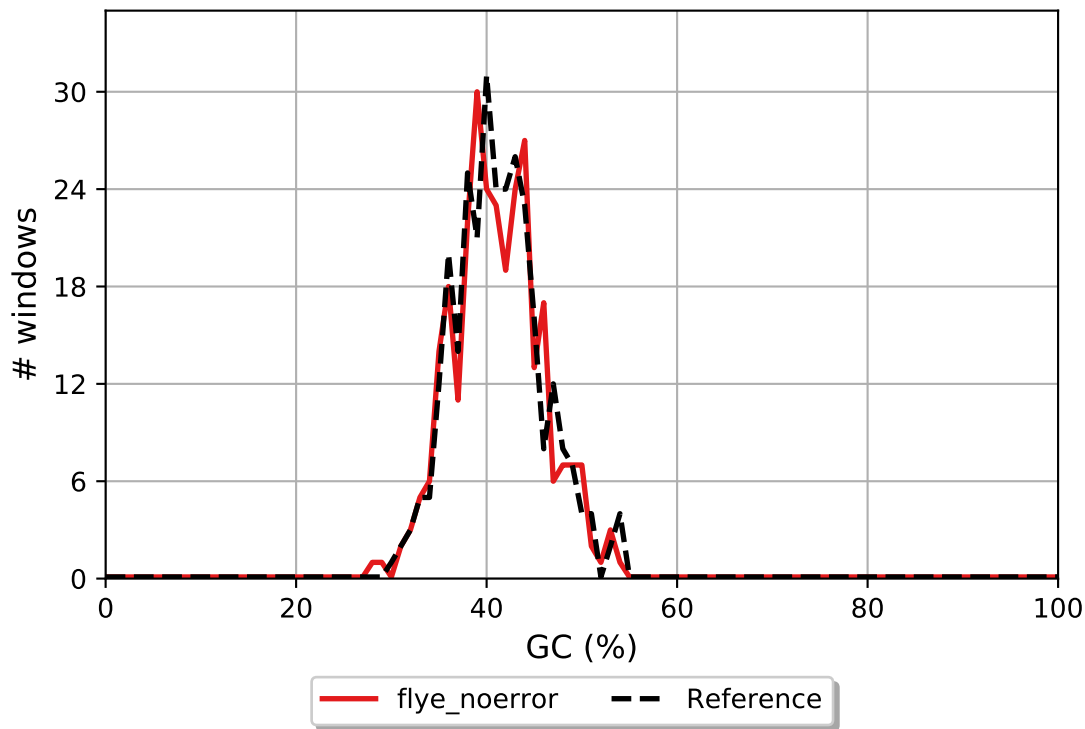


flye\_noerror

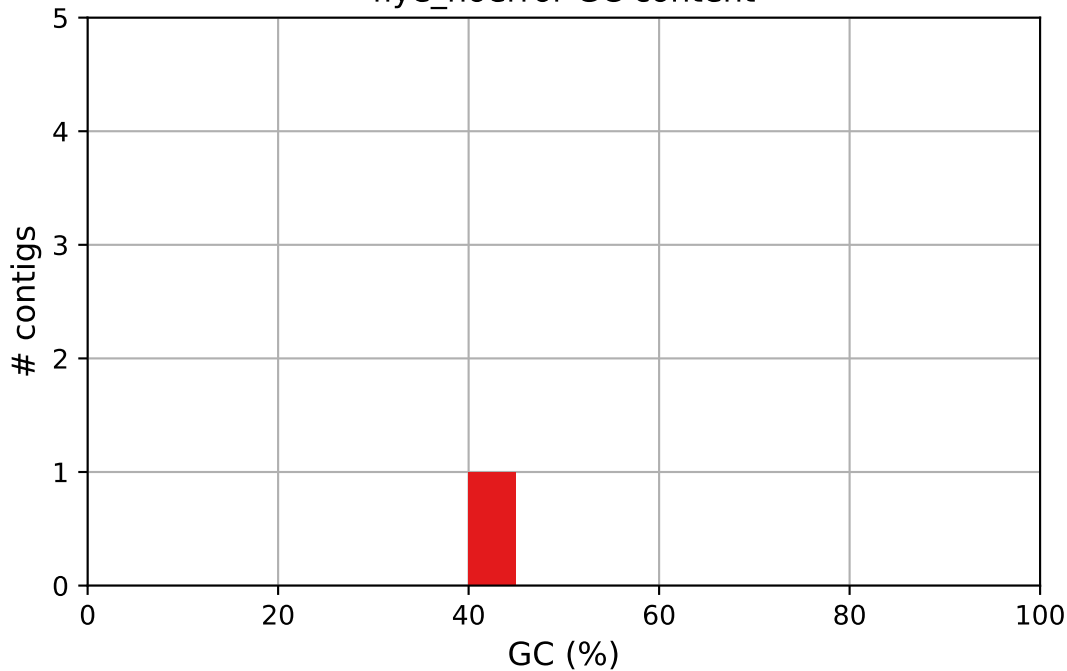
Cumulative length



## GC content



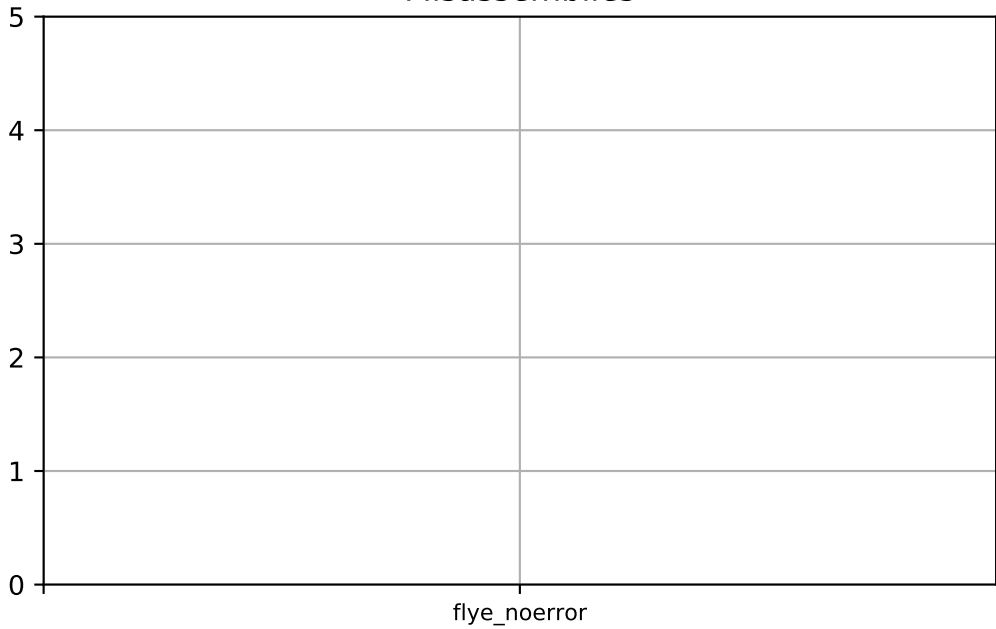
flye\_noerror GC content



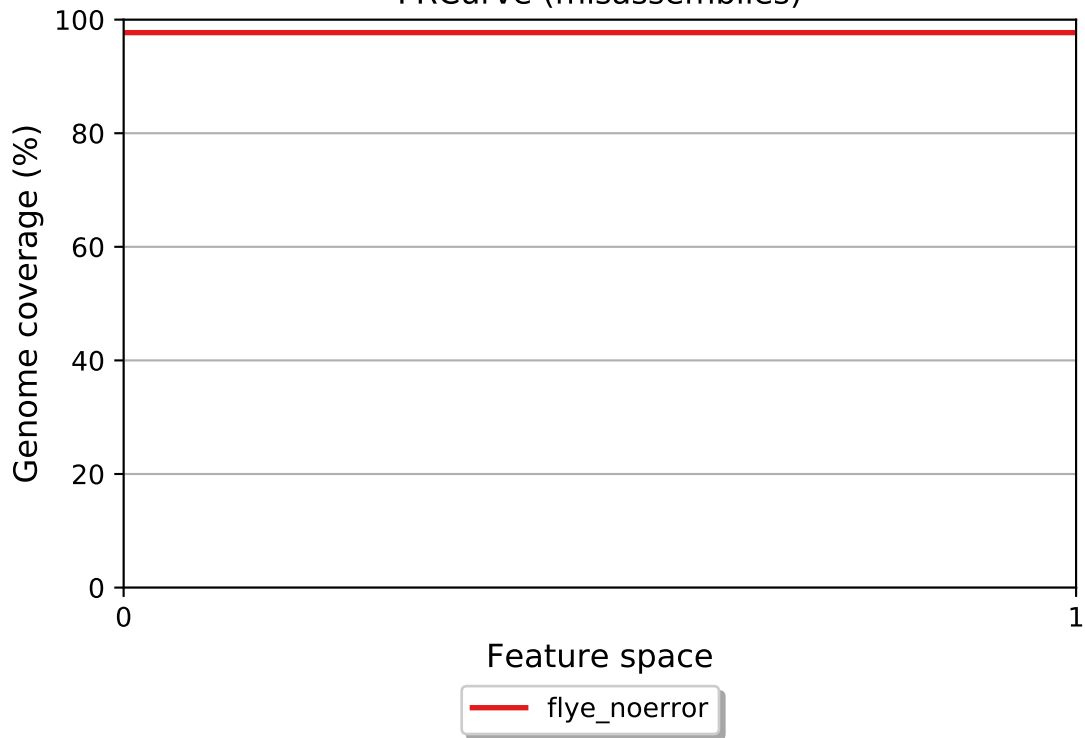
flye\_noerror



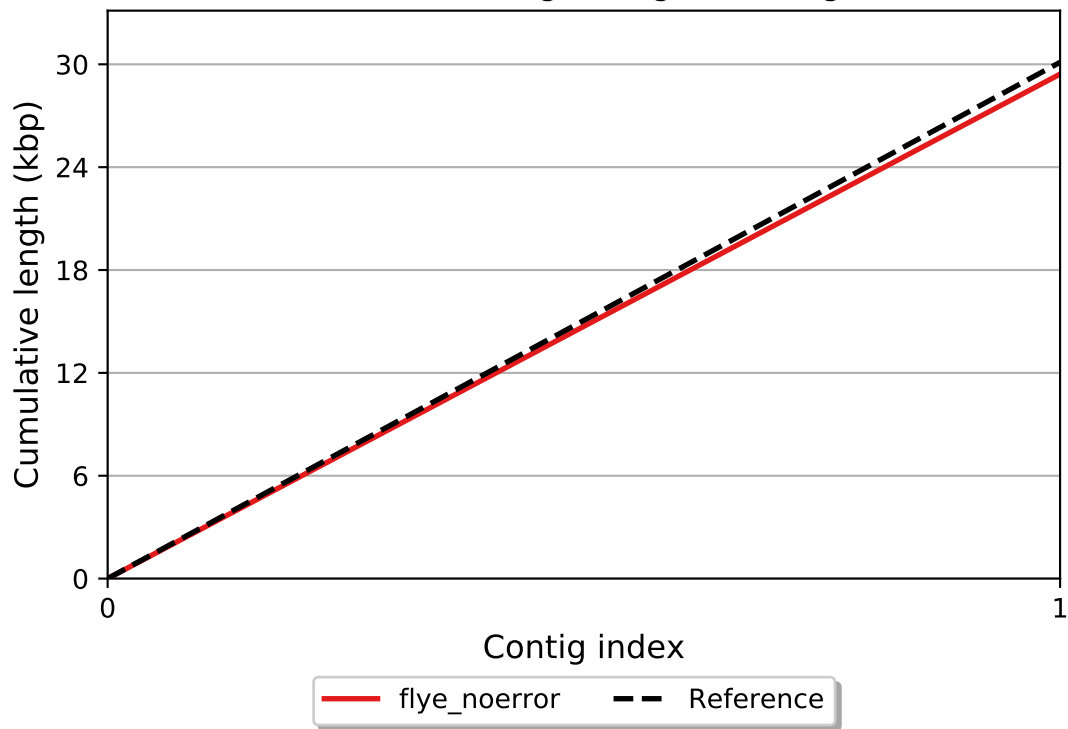
## Misassemblies



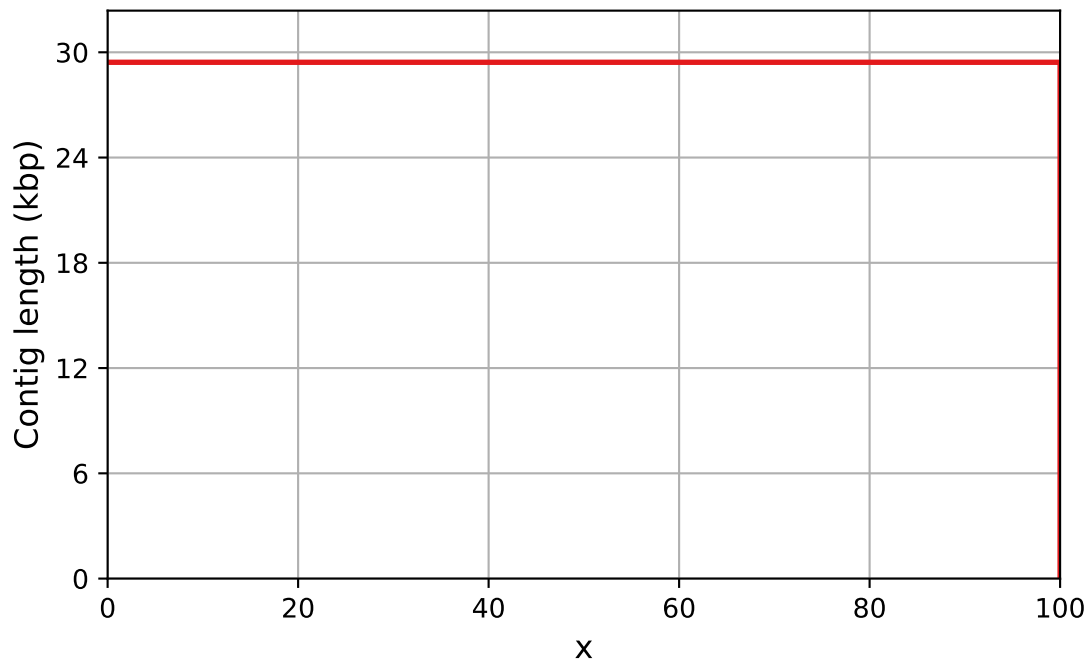
FRCurve (misassemblies)



Cumulative length (aligned contigs)

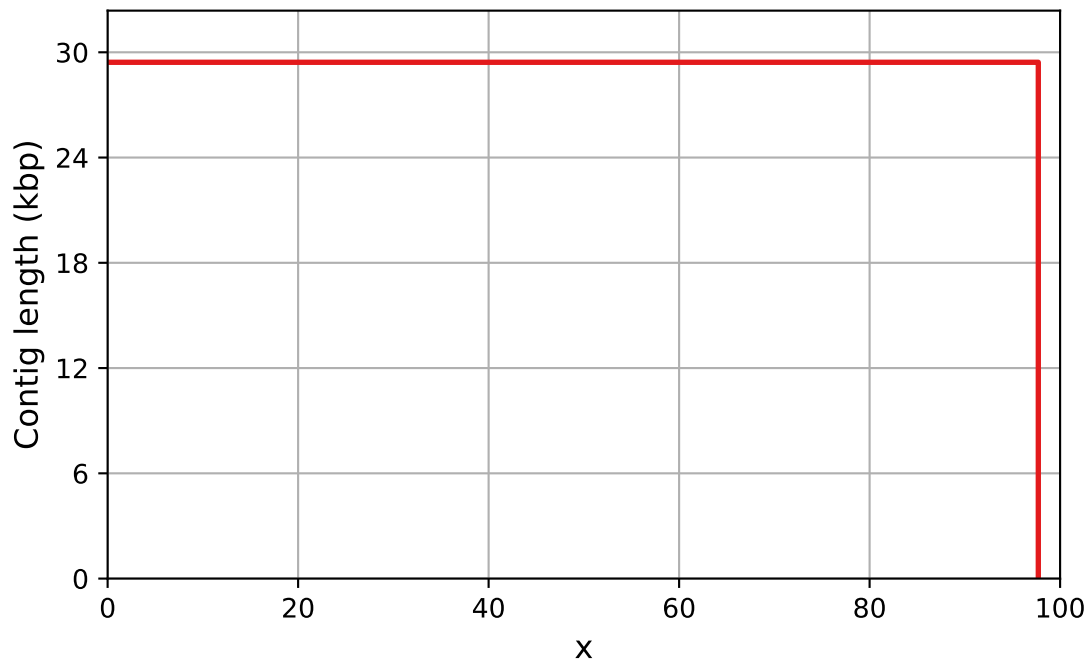


NAx



flye\_noerror

# NGAx



— flye\_noerror