

# Report

	lv1_k70_kf2
# 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)	29403
Total length (>= 1000 bp)	29403
Total length (>= 5000 bp)	29403
Total length (>= 10000 bp)	29403
Total length (>= 25000 bp)	29403
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	29403
Total length	29403
Reference length	29903
GC (%)	37.95
Reference GC (%)	37.97
N50	29403
NG50	29403
N90	29403
NG90	29403
auN	29403.0
auNG	28911.4
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 (%)	98.328
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	29403
Total aligned length	29403
NA50	29403
NGA50	29403
NA90	29403
NGA90	29403
auNA	29403.0
auNGA	28911.4
LA50	1
LGA50	1
LA90	1
LGA90	1

All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	lv1_k70_kf2
# 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

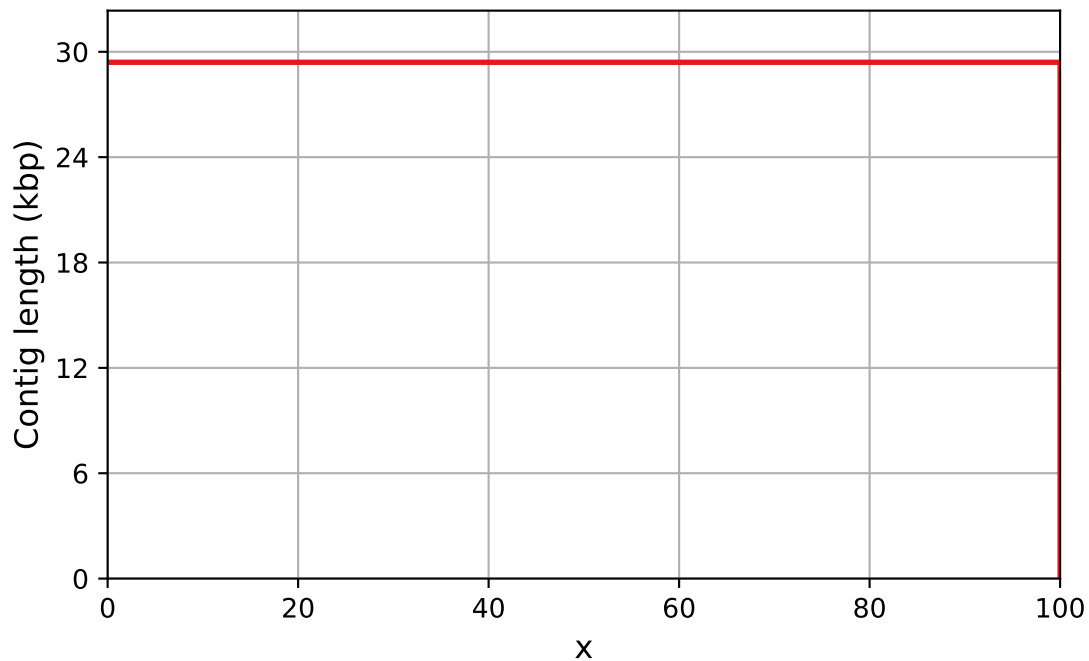
All statistics are based on contigs of size  $\geq 50$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	lv1_k70_kf2
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

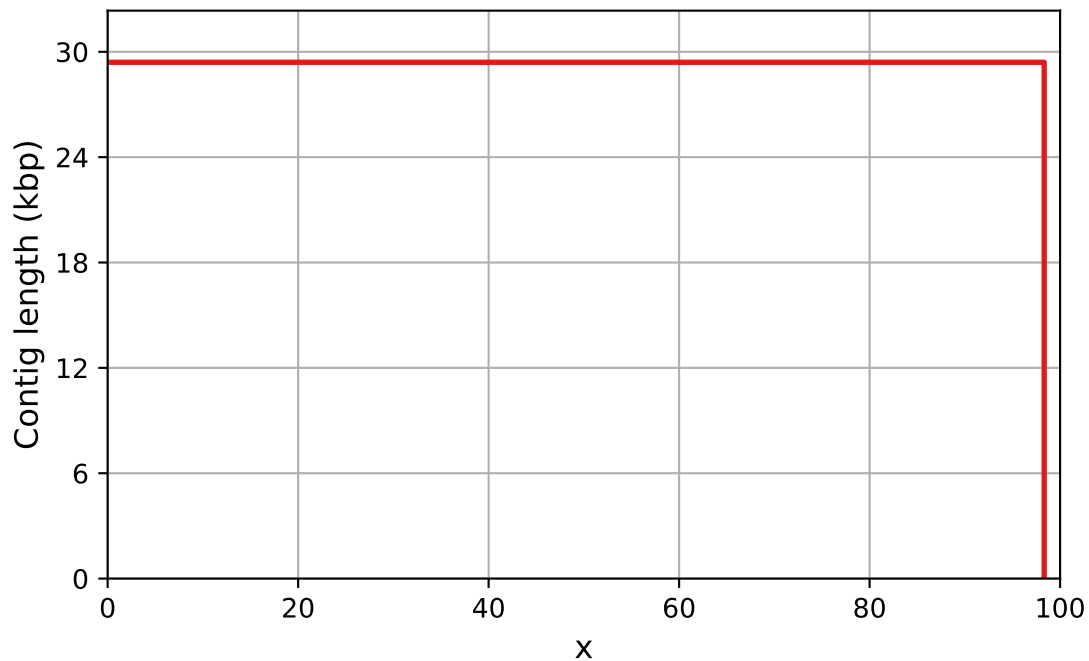
All statistics are based on contigs of size  $\geq 50$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



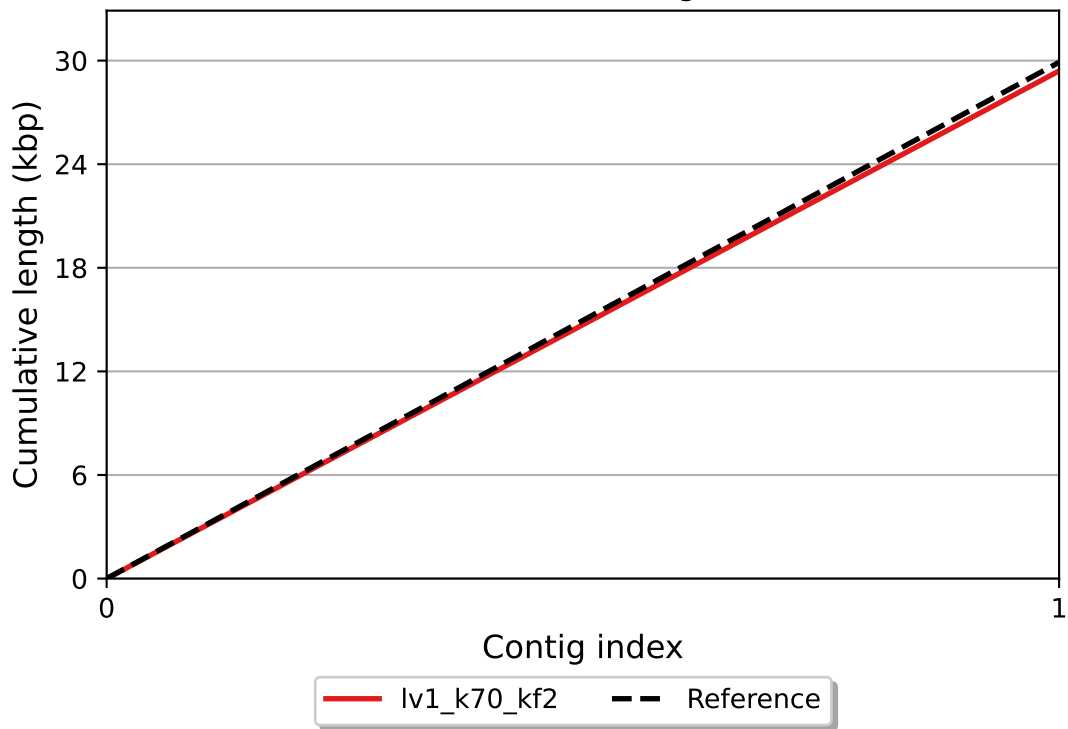
lv1\_k70\_kf2

NGx

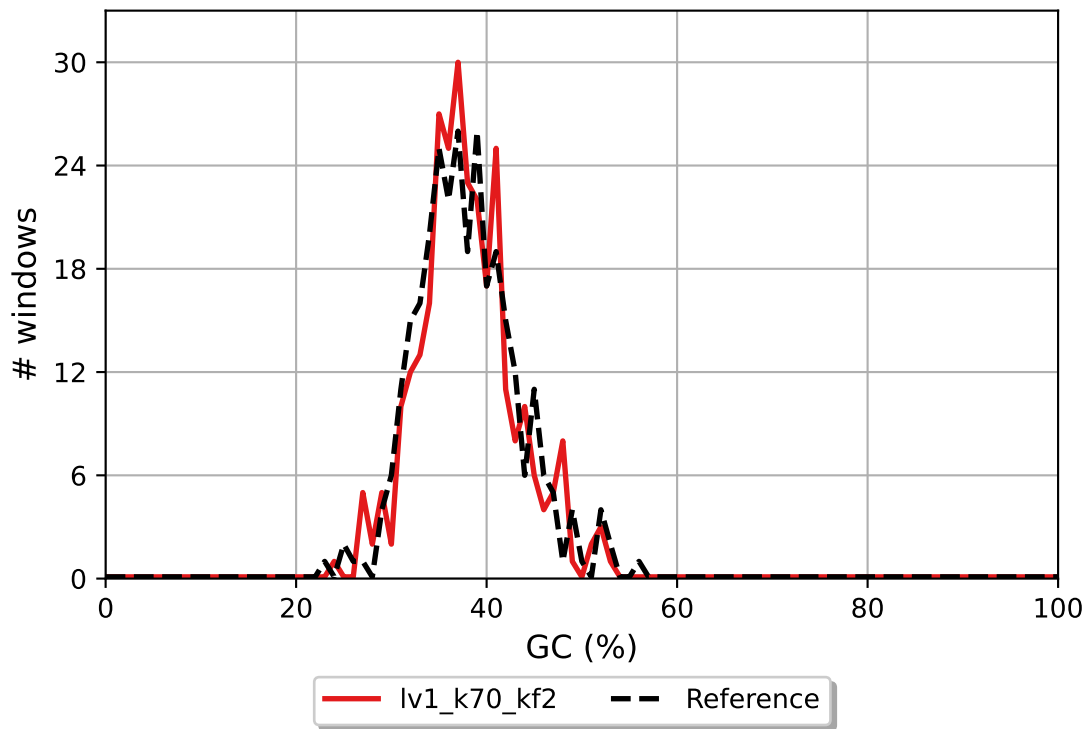


lv1\_k70\_kf2

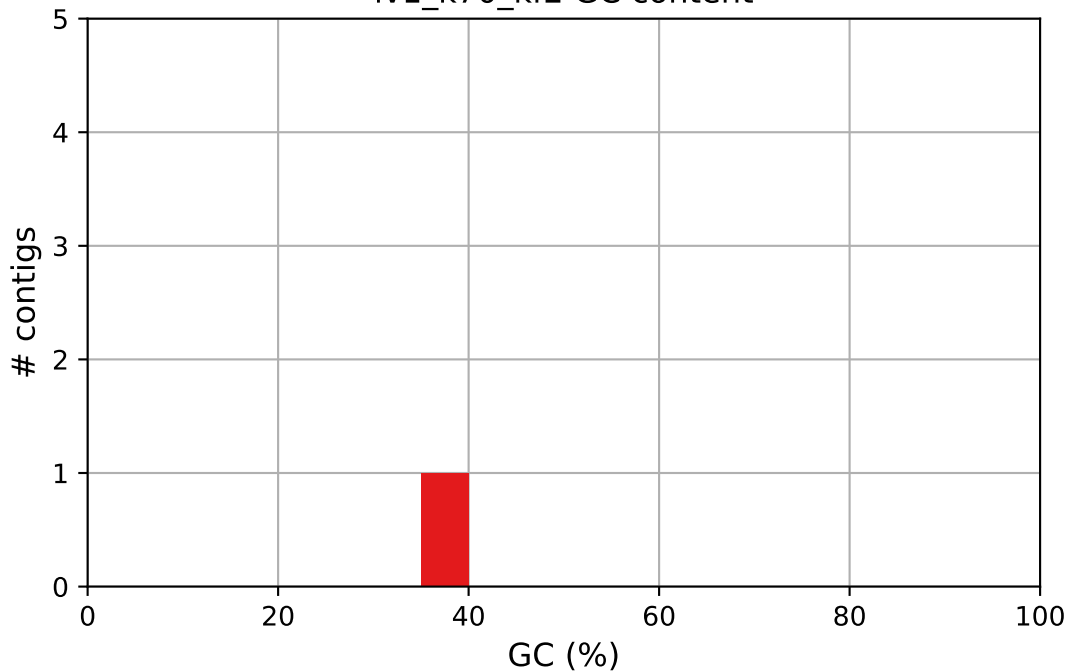
Cumulative length



GC content



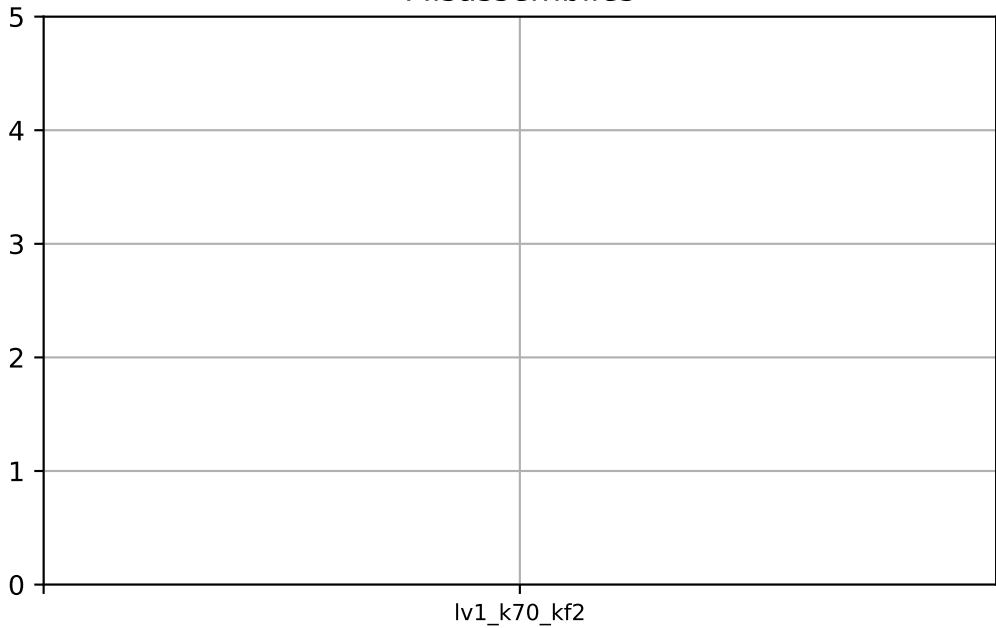
lv1\_k70\_kf2 GC content



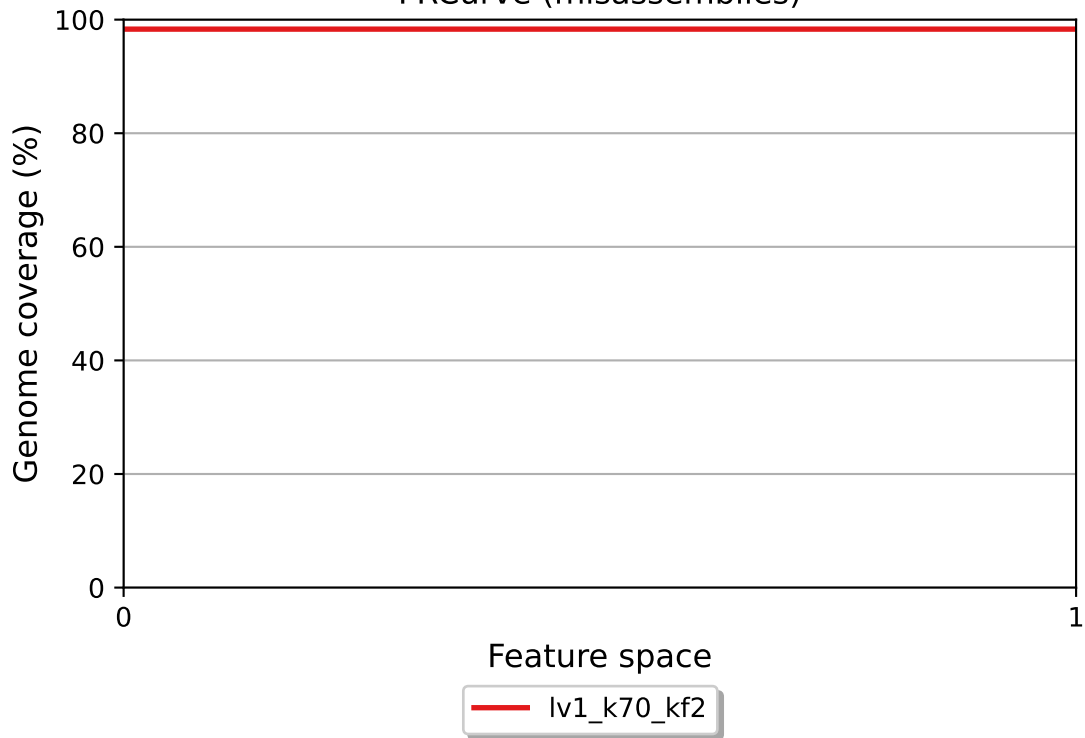
lv1\_k70\_kf2



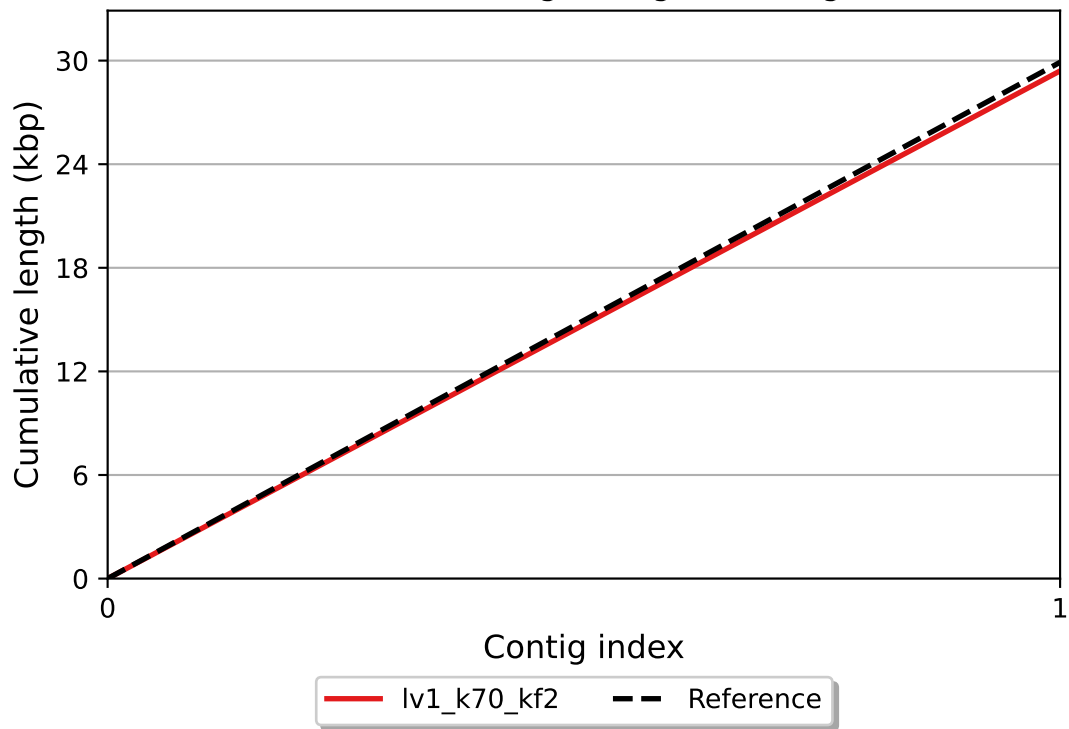
## Misassemblies



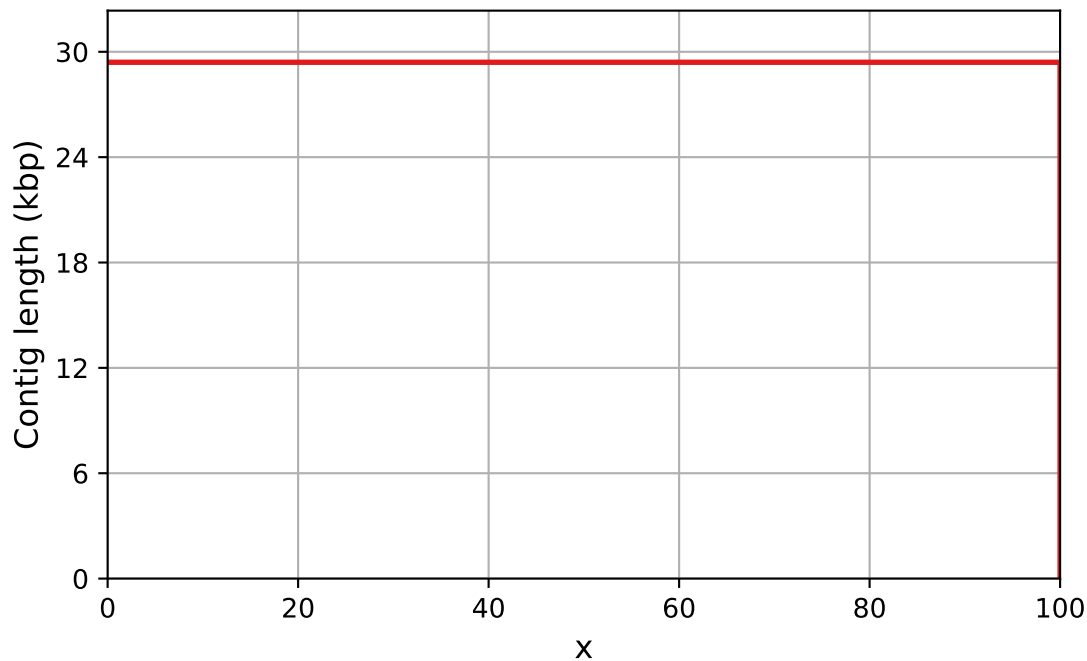
FRCurve (misassemblies)



Cumulative length (aligned contigs)

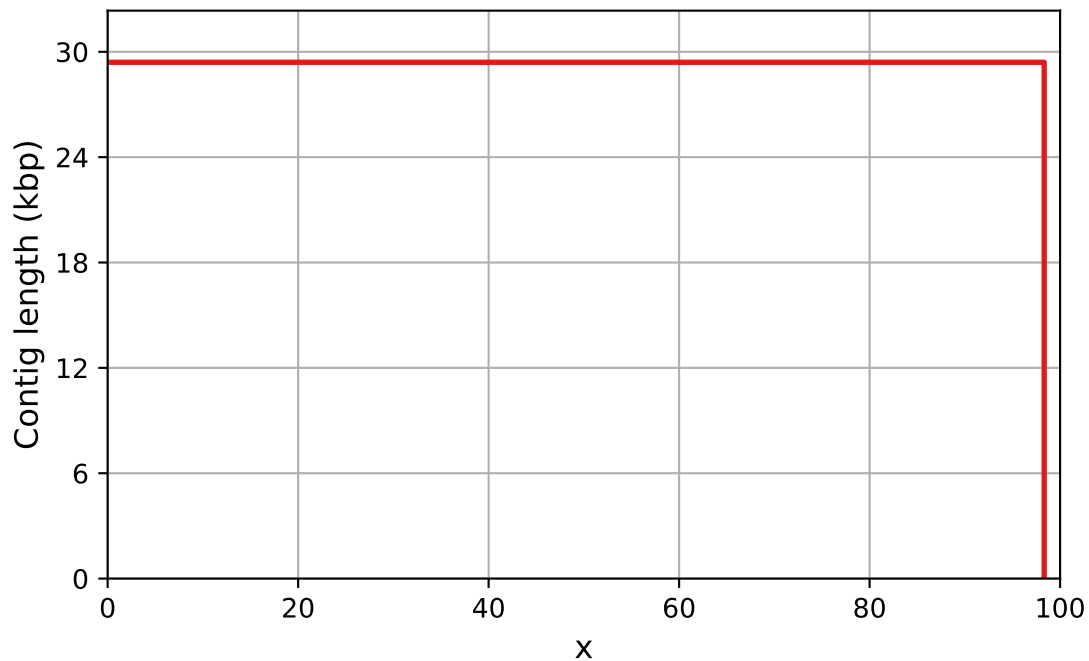


NAx



lv1\_k70\_kf2

# NGAx



lv1\_k70\_kf2