

Report

	lv3_k800_kf3
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	115439
Total length (>= 1000 bp)	115439
Total length (>= 5000 bp)	115439
Total length (>= 10000 bp)	115439
Total length (>= 25000 bp)	115439
Total length (>= 50000 bp)	0
# contigs	4
Largest contig	29134
Total length	115439
Reference length	29903
GC (%)	39.49
Reference GC (%)	37.97
N50	28909
NG50	29134
N90	28563
NG90	29134
auN	28861.2
auNG	111417.2
L50	2
LG50	1
L90	4
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	3 + 0 part
Unaligned length	86606
Genome fraction (%)	96.422
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	28833
Total aligned length	28833
NA50	-
NGA50	28833
NA90	-
NGA90	28833
auNA	7201.6
auNGA	27801.3
LA50	-
LGA50	1
LA90	-
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

	lv3_k800_kf3
# 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

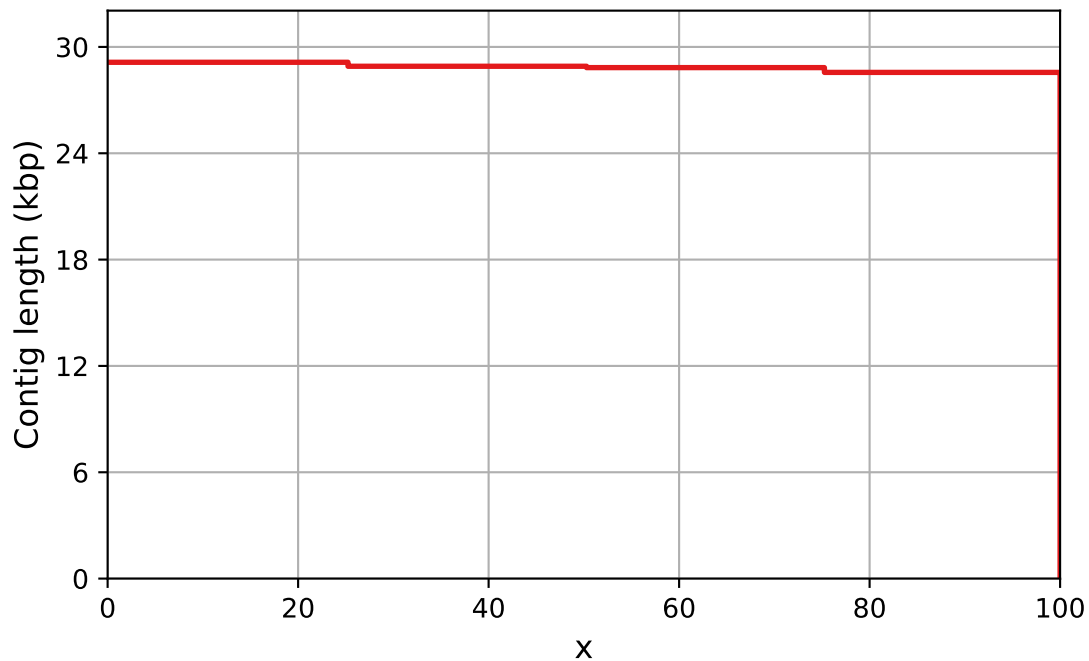
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	lv3_k800_kf3
# fully unaligned contigs	3
Fully unaligned length	86606
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

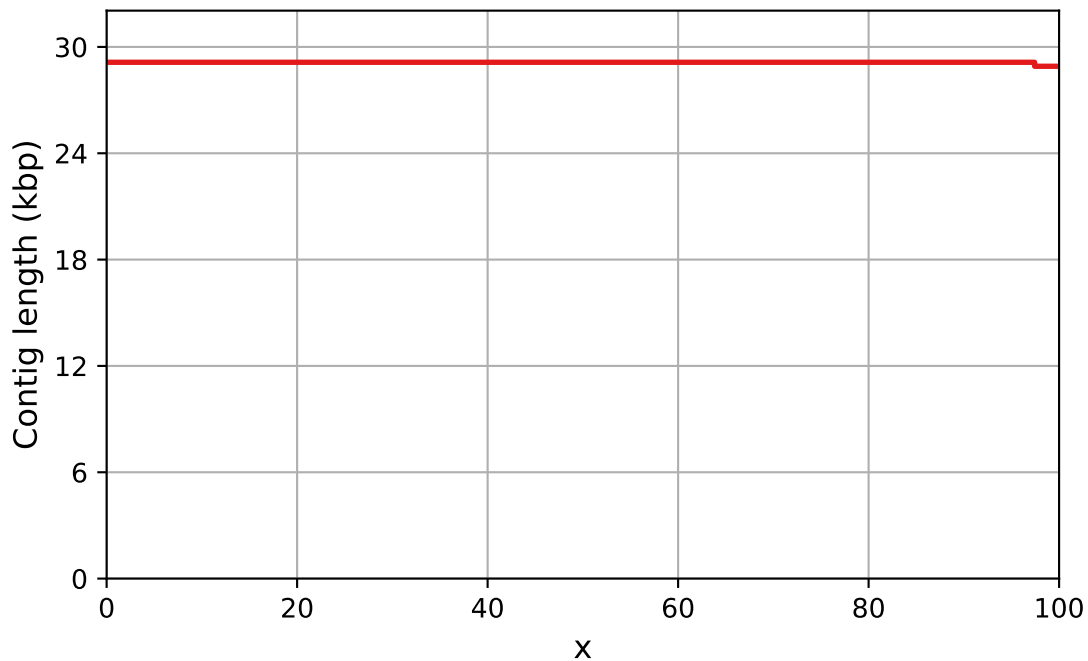
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

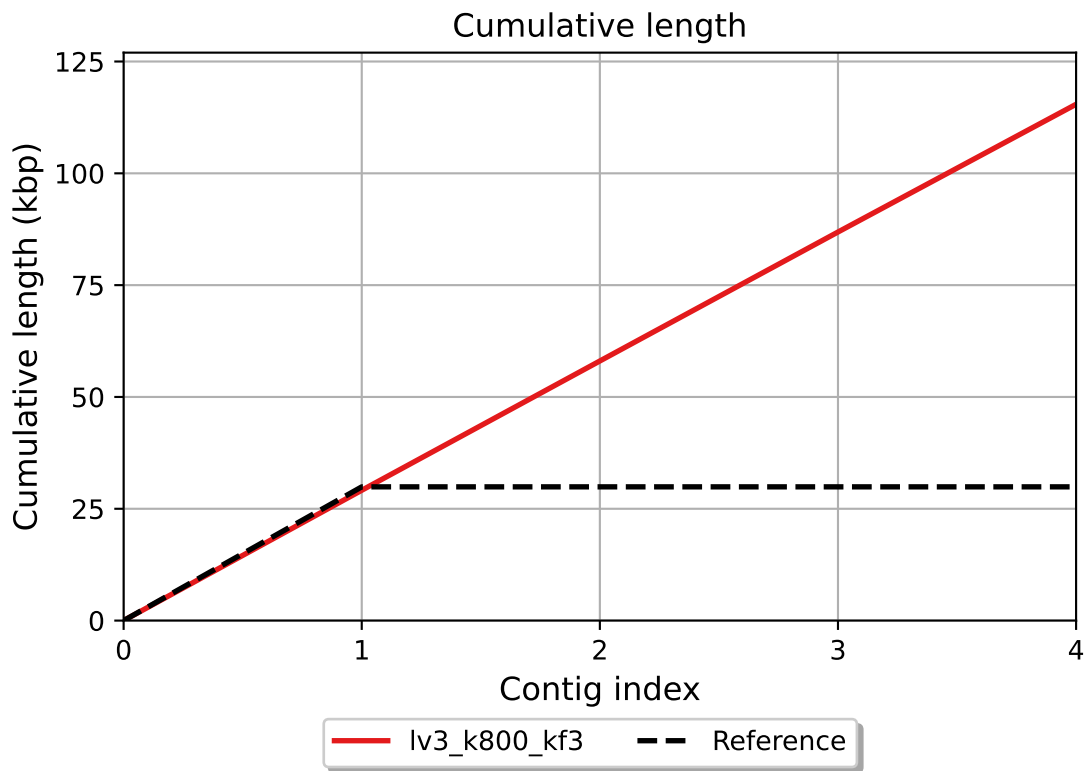


lv3_k800_kf3

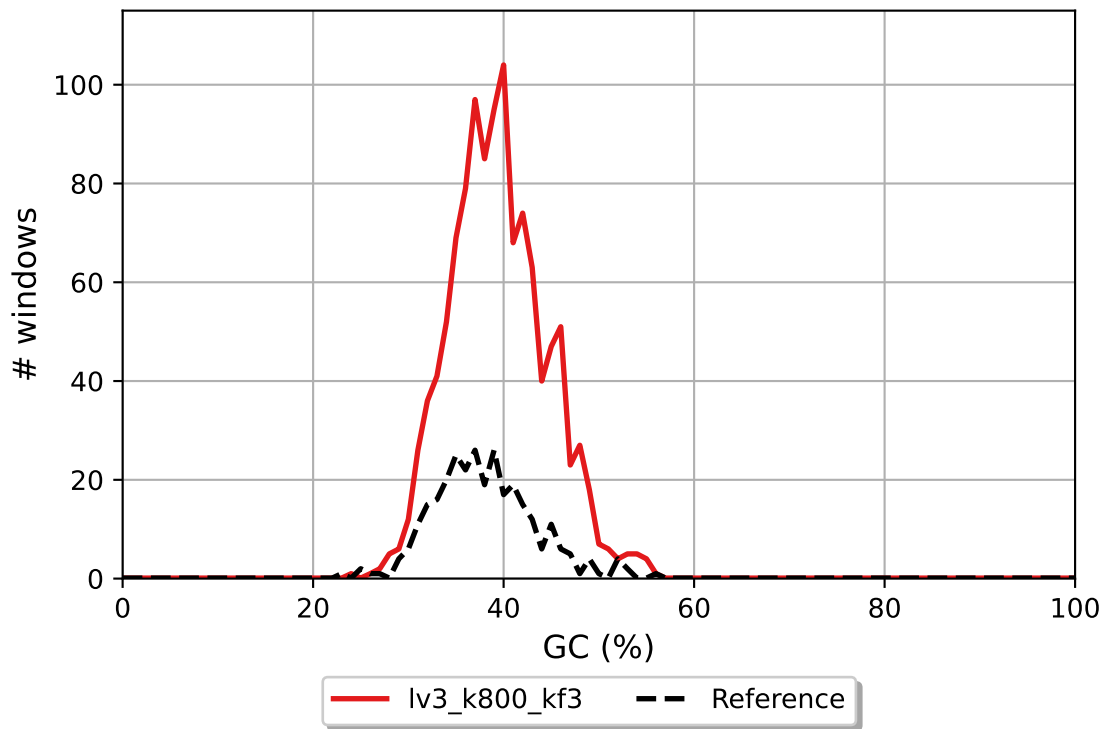
NGx



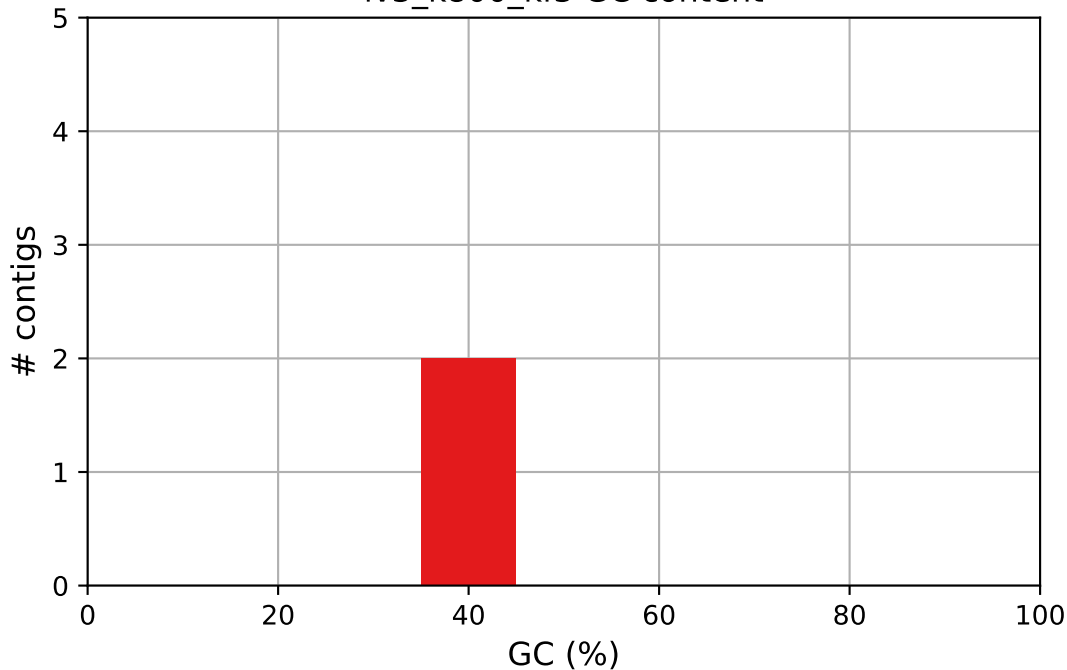
lv3_k800_kf3



GC content

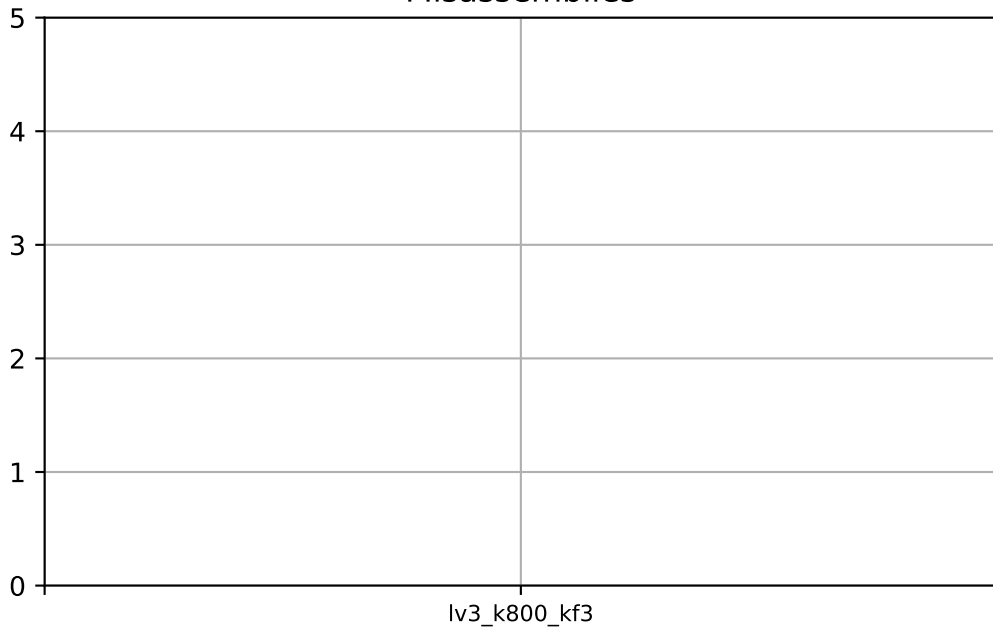


lv3_k800_kf3 GC content

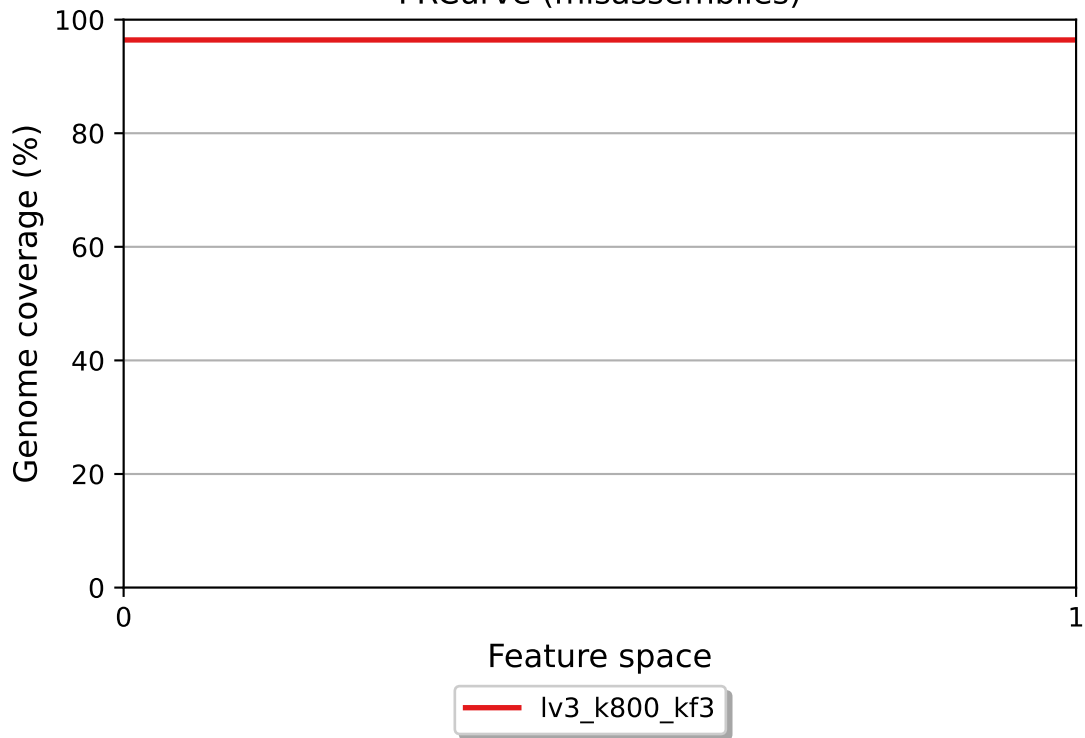


lv3_k800_kf3

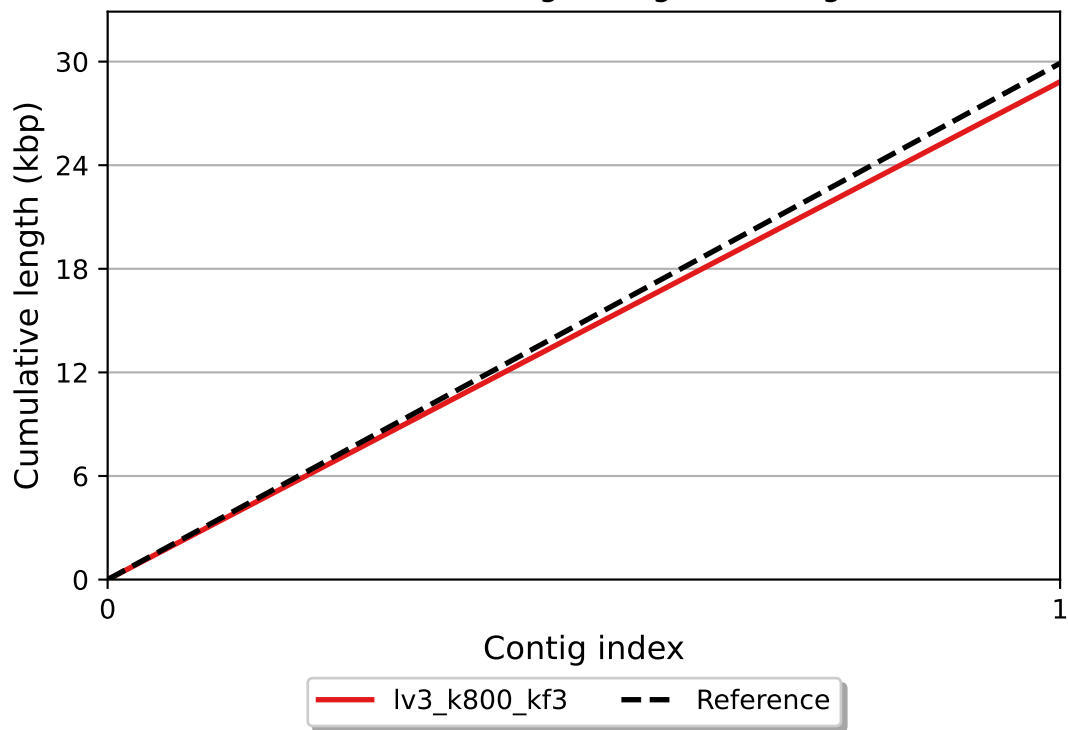
Misassemblies



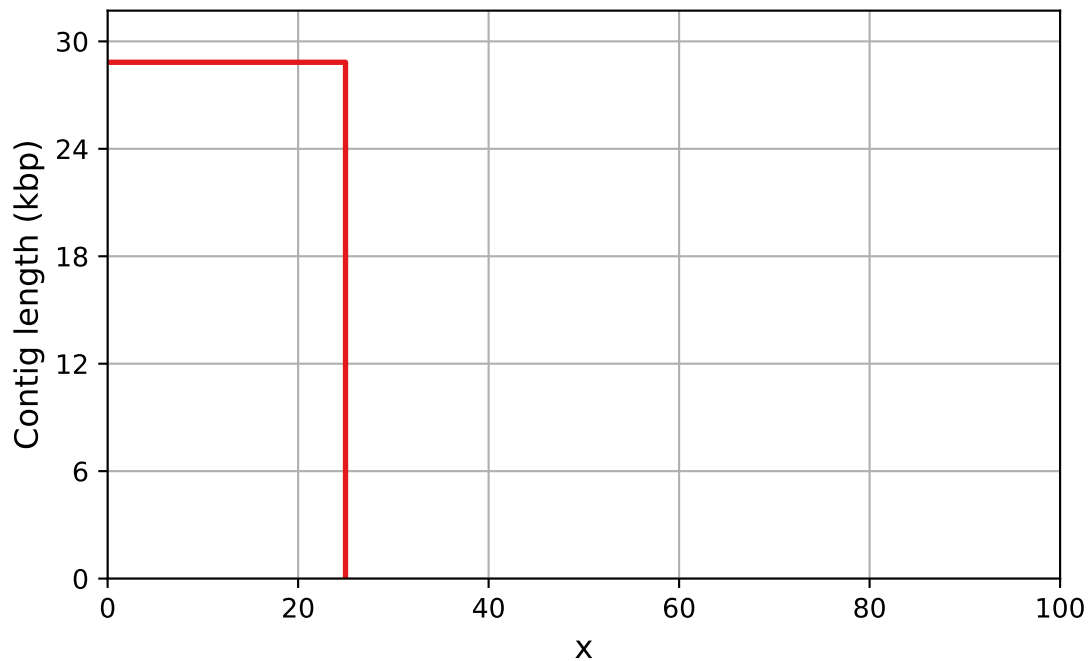
FRCurve (misassemblies)



Cumulative length (aligned contigs)

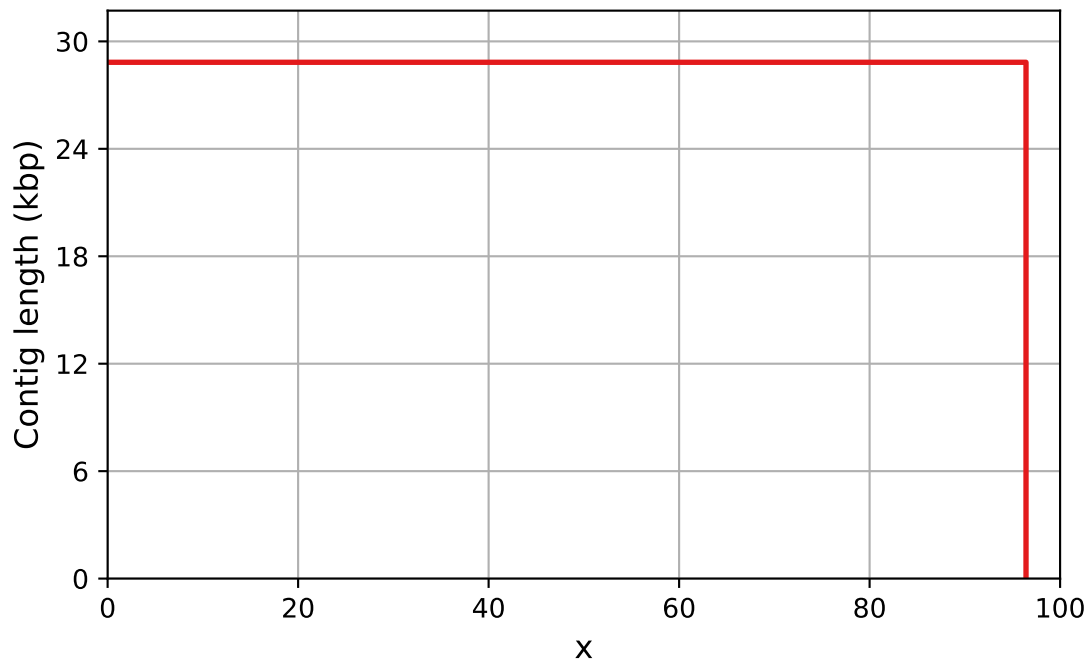


NAx



lv3_k800_kf3

NGAx



lv3_k800_kf3