

Report

	lv5_k2000_kf3_tt1000
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	455375
Total length (>= 1000 bp)	455375
Total length (>= 5000 bp)	455375
Total length (>= 10000 bp)	455375
Total length (>= 25000 bp)	455375
Total length (>= 50000 bp)	0
# contigs	16
Largest contig	29372
Total length	455375
Reference length	29903
GC (%)	39.67
Reference GC (%)	37.97
N50	28547
NG50	29372
N90	27620
NG90	29372
auN	28475.4
auNG	433634.5
L50	8
LG50	1
L90	15
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	12 + 0 part
Unaligned length	342543
Genome fraction (%)	97.495
Duplication ratio	3.870
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1537.68
# indels per 100 kbp	0.00
Largest alignment	29154
Total aligned length	112832
NA50	-
NGA50	29154
NA90	-
NGA90	29154
auNA	6994.7
auNGA	106518.6
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

	lv5_k2000_kf3_tt1000
# 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	1735
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

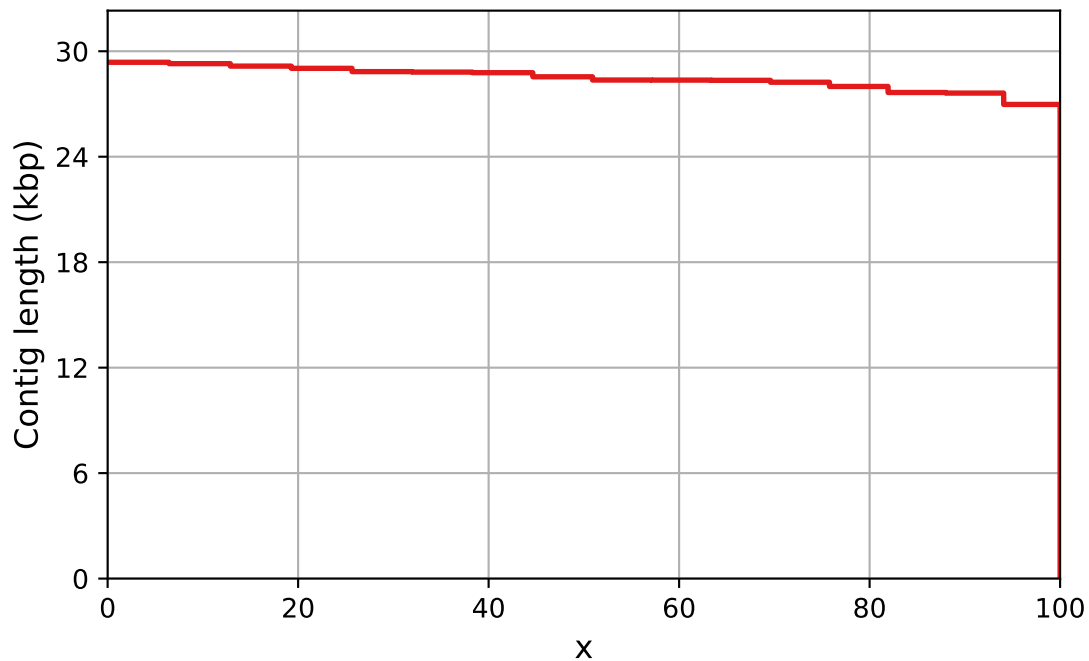
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	lv5_k2000_kf3_tt1000
# fully unaligned contigs	12
Fully unaligned length	342543
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

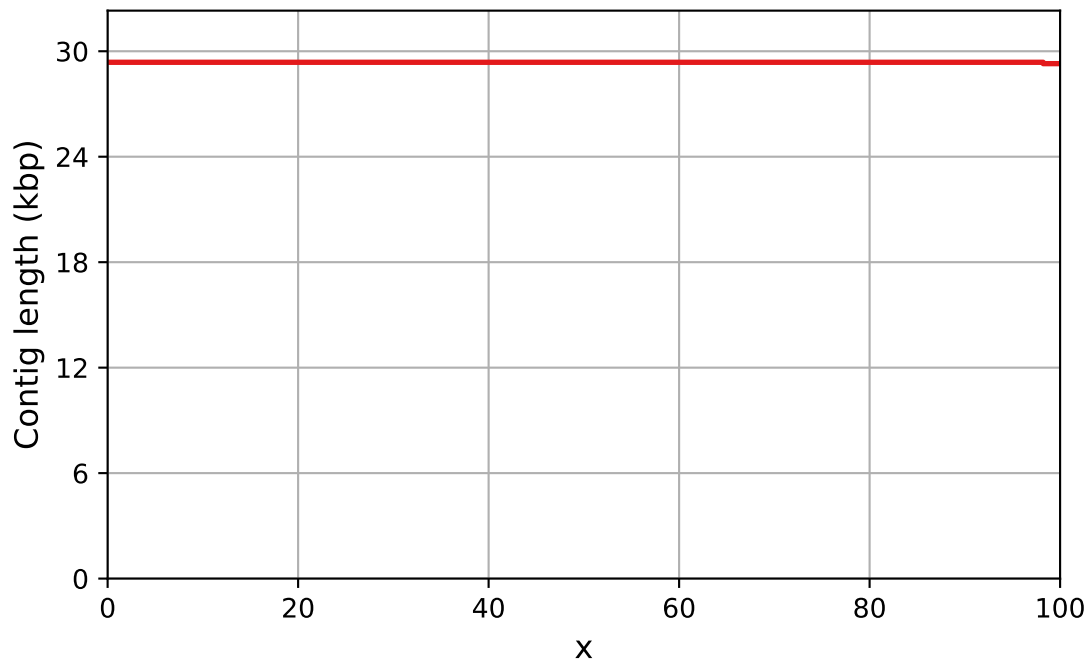
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

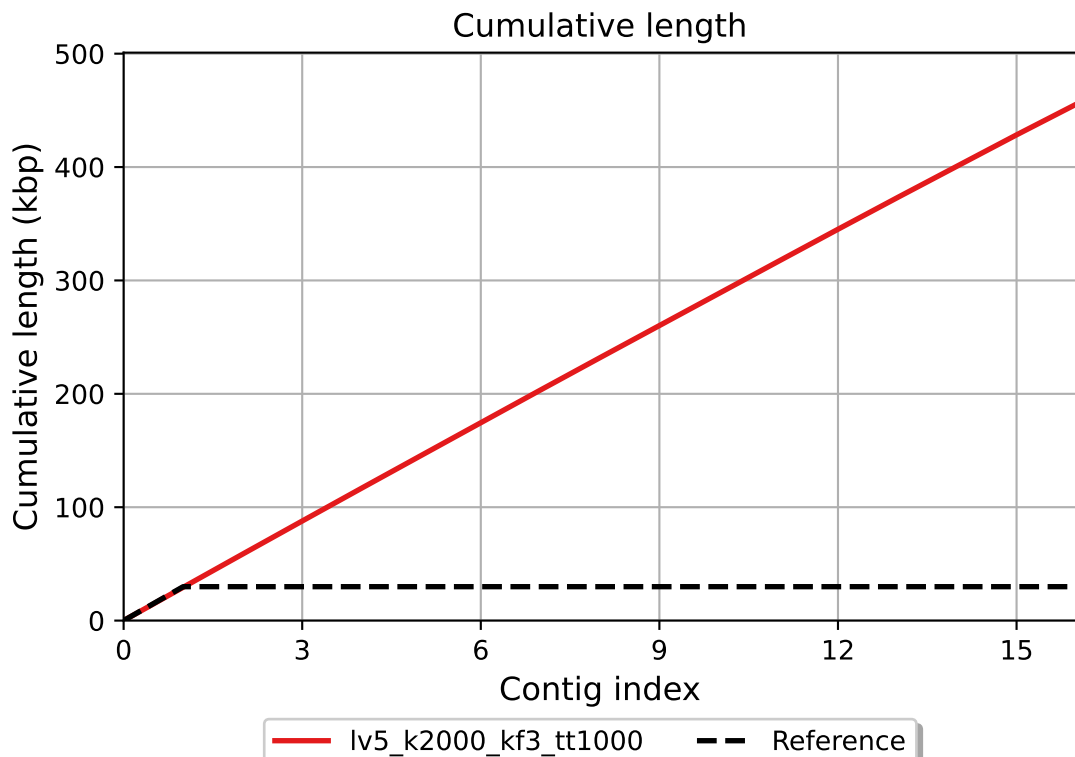


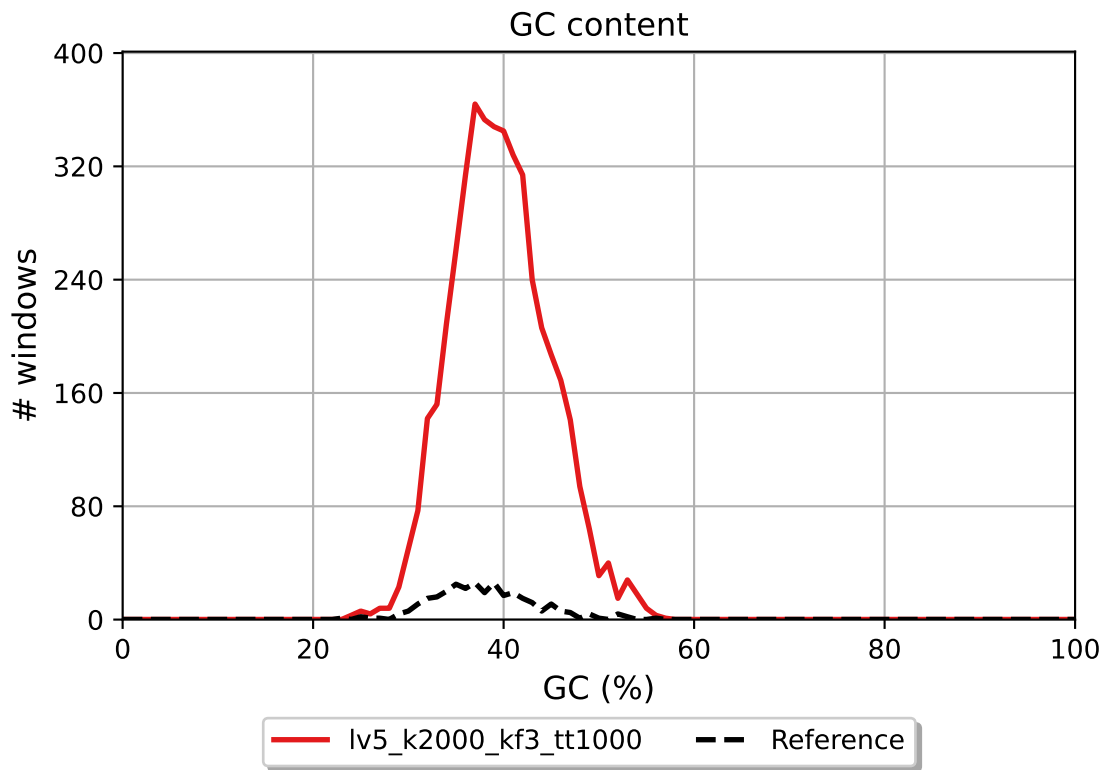
lv5_k2000_kf3_tt1000

NGx

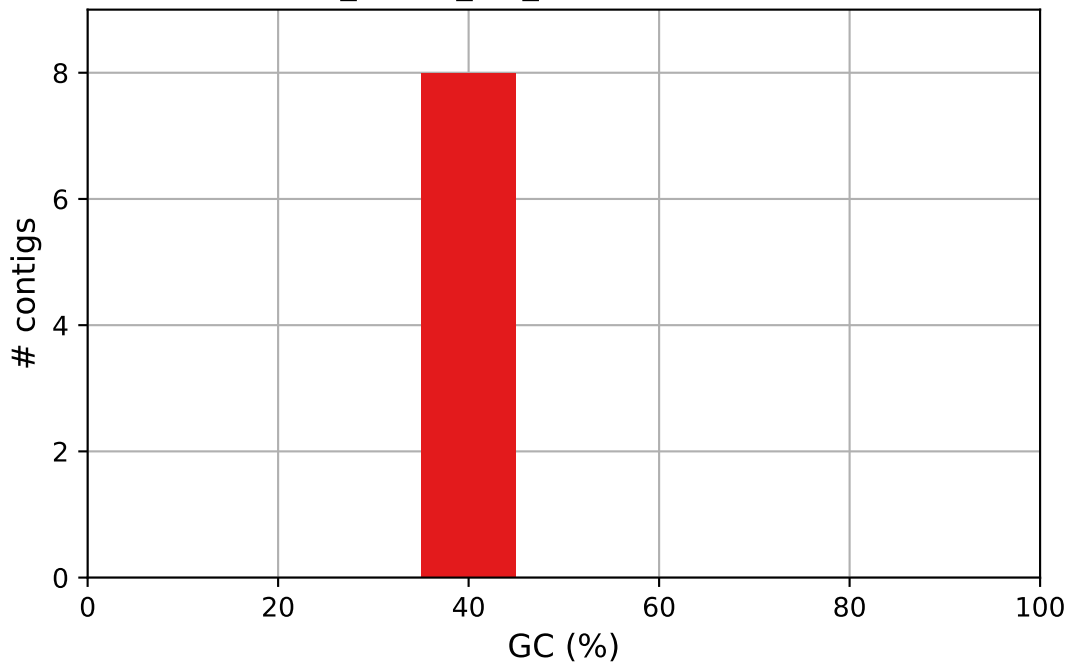


lv5_k2000_kf3_tt1000



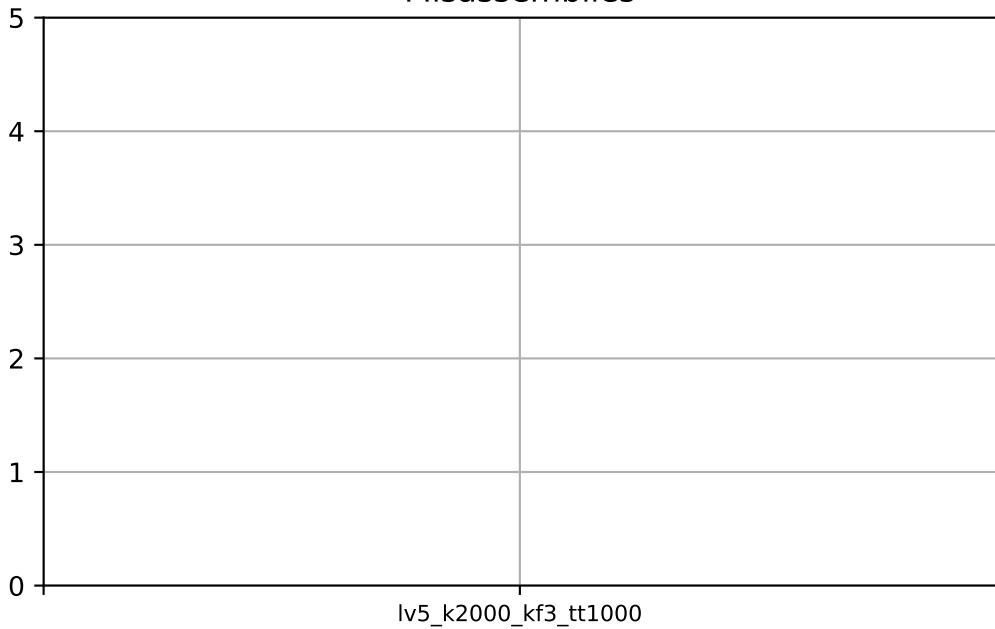


lv5_k2000_kf3_tt1000 GC content

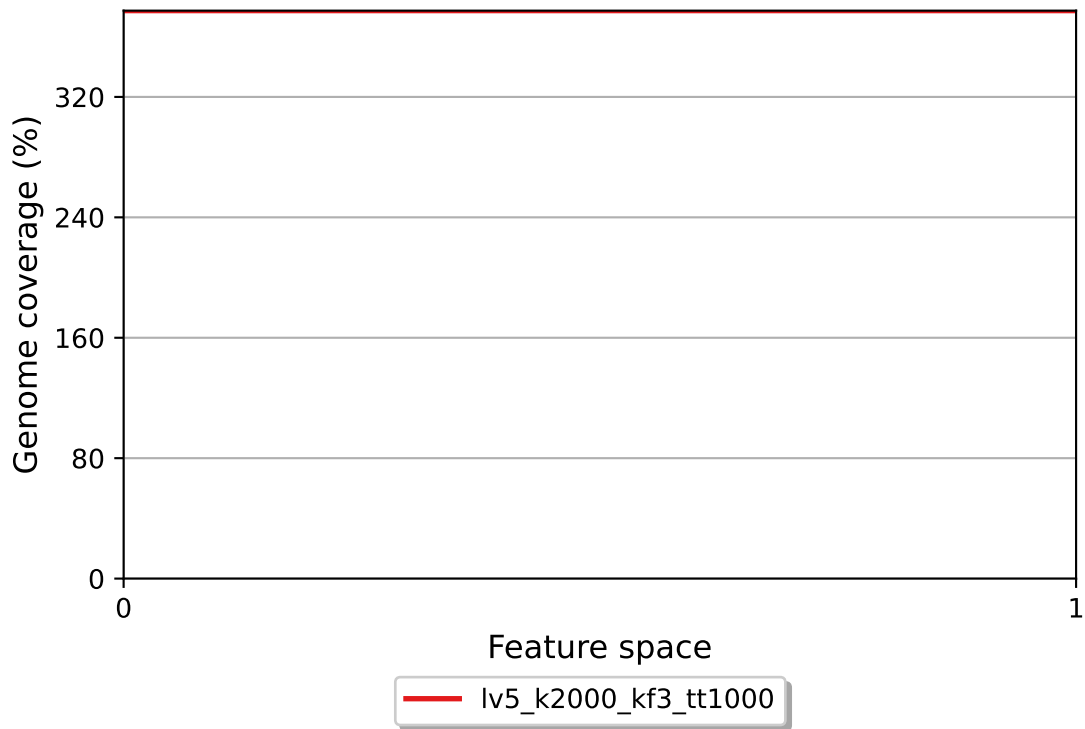


lv5_k2000_kf3_tt1000

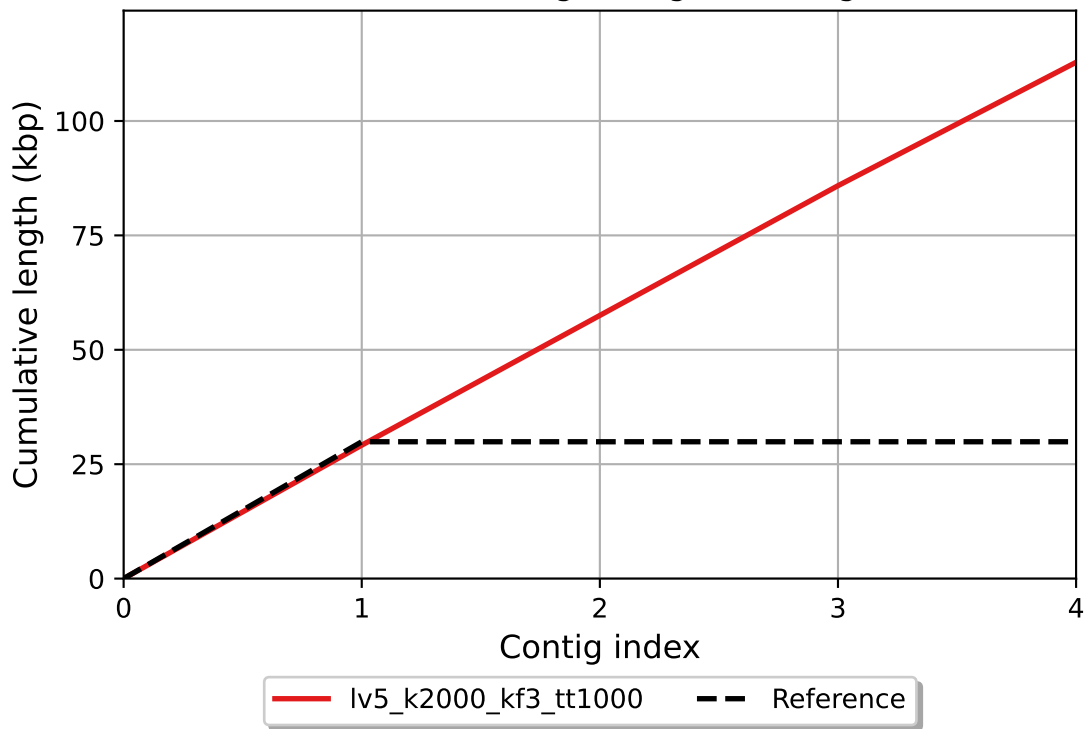
Misassemblies



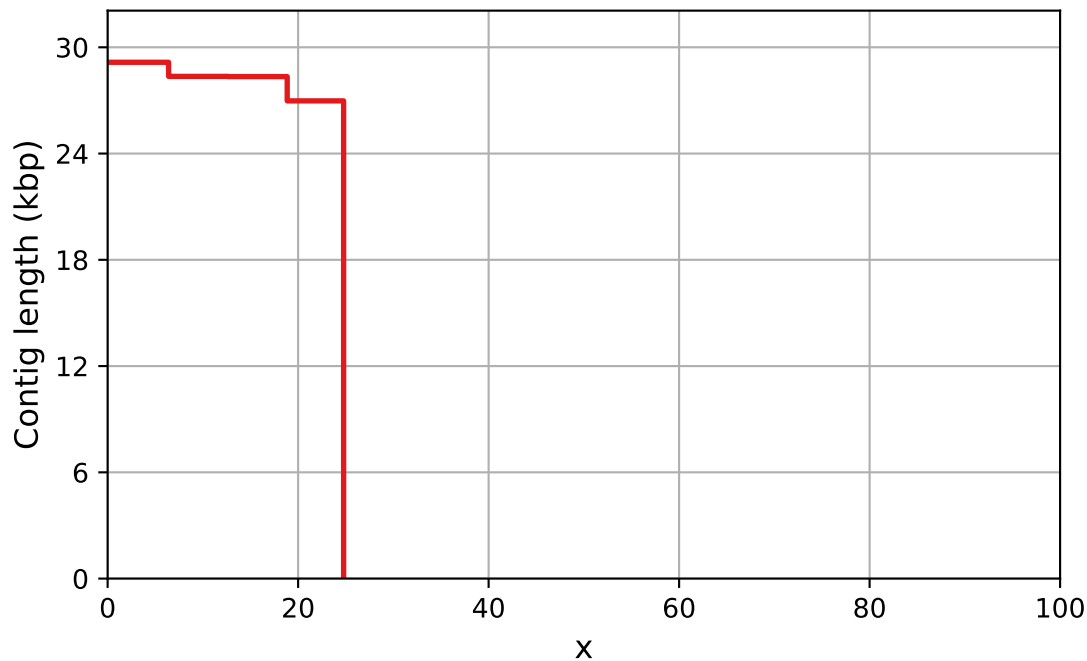
FRCurve (misassemblies)



Cumulative length (aligned contigs)

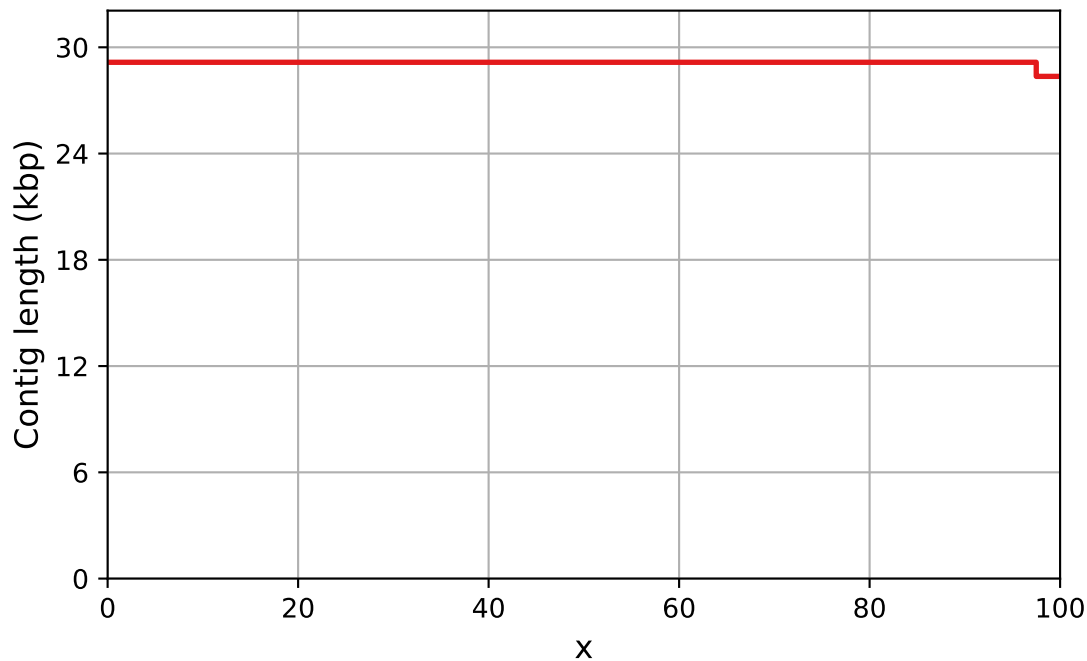


NAx



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NGAx



lv5_k2000_kf3_tt1000