

Report

	lv7_k1000_kf3_tt1000
# contigs (>= 0 bp)	380
# contigs (>= 1000 bp)	380
# contigs (>= 5000 bp)	160
# contigs (>= 10000 bp)	80
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	2631824
Total length (>= 1000 bp)	2631824
Total length (>= 5000 bp)	2138134
Total length (>= 10000 bp)	1590436
Total length (>= 25000 bp)	512901
Total length (>= 50000 bp)	0
# contigs	380
Largest contig	28485
Total length	2631824
Reference length	29903
GC (%)	39.74
Reference GC (%)	37.97
N50	15994
NG50	28485
N90	2644
NG90	28485
auN	14806.5
auNG	1303147.9
L50	60
LG50	1
L90	228
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	258 + 0 part
Unaligned length	1903681
Genome fraction (%)	98.947
Duplication ratio	24.605
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2222.89
# indels per 100 kbp	0.00
Largest alignment	27392
Total aligned length	728017
NA50	-
NGA50	27392
NA90	-
NGA90	27392
auNA	3347.9
auNGA	294657.3
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

	lv7_k1000_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	16183
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

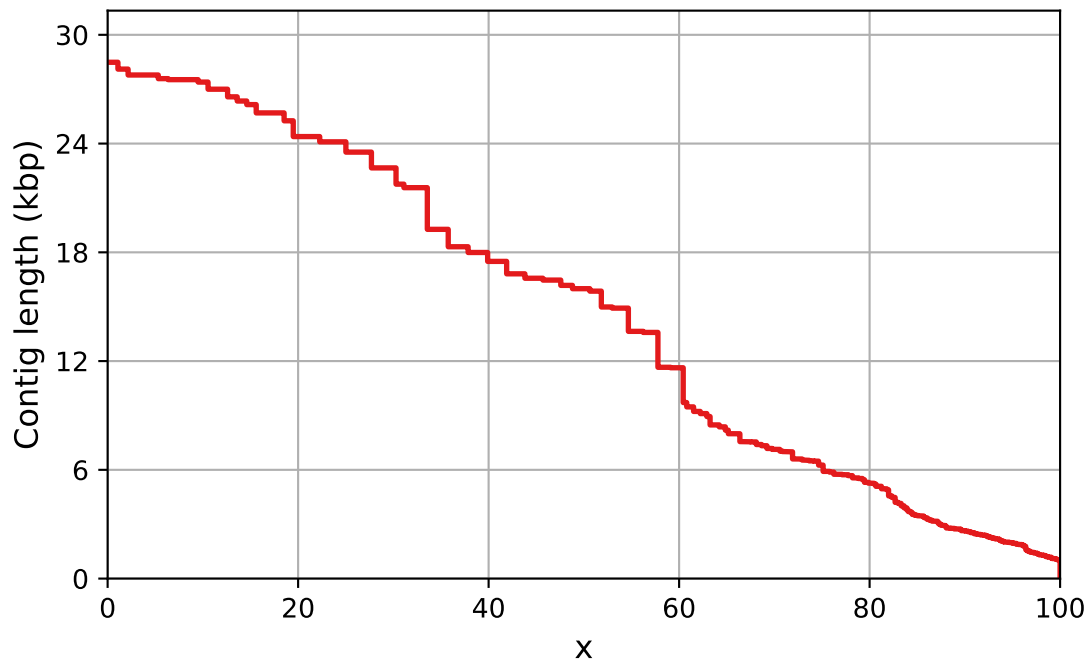
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	lv7_k1000_kf3_tt1000
# fully unaligned contigs	258
Fully unaligned length	1903681
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

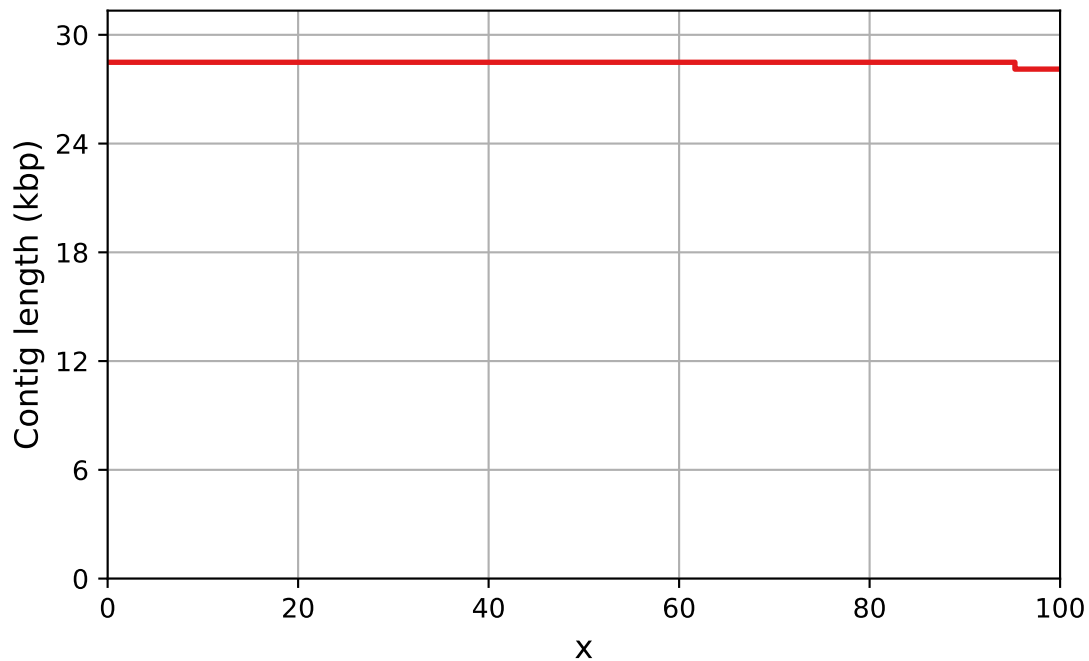
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



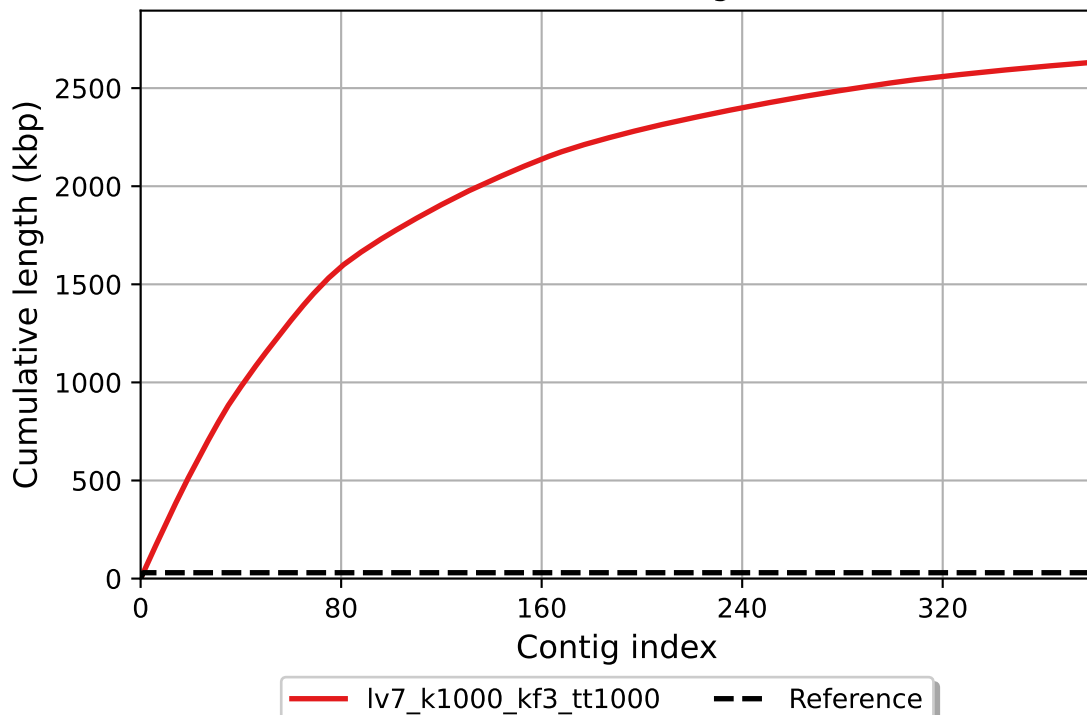
lv7_k1000_kf3_tt1000

NGx

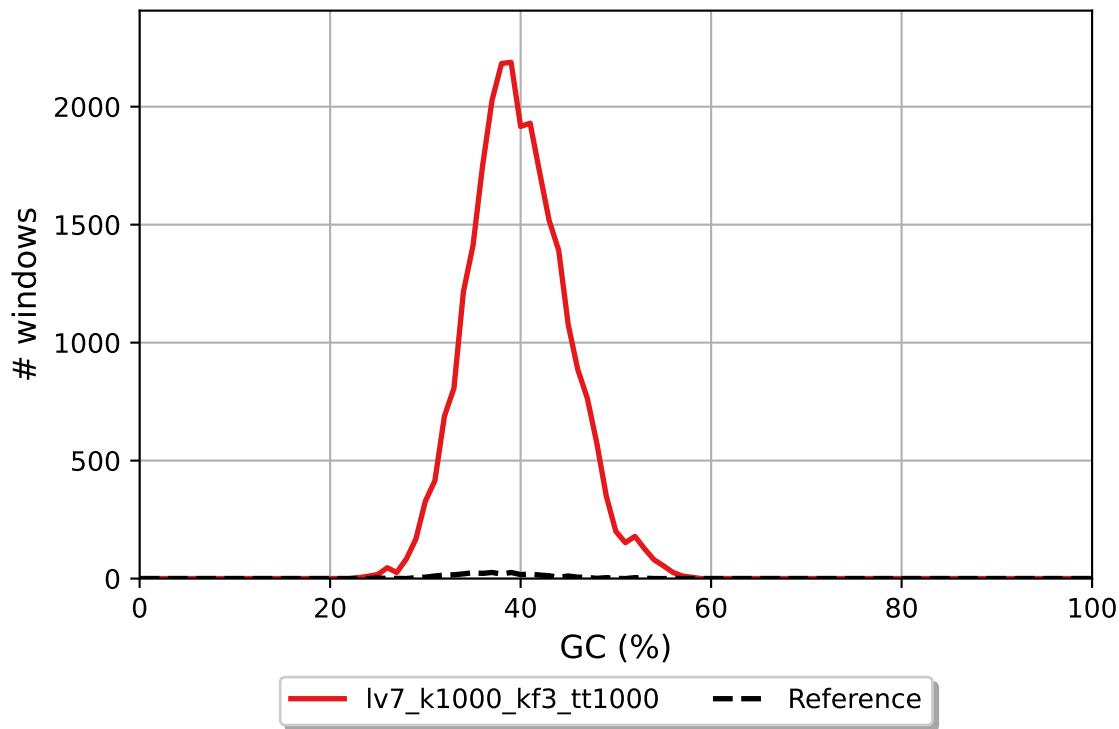


lv7_k1000_kf3_tt1000

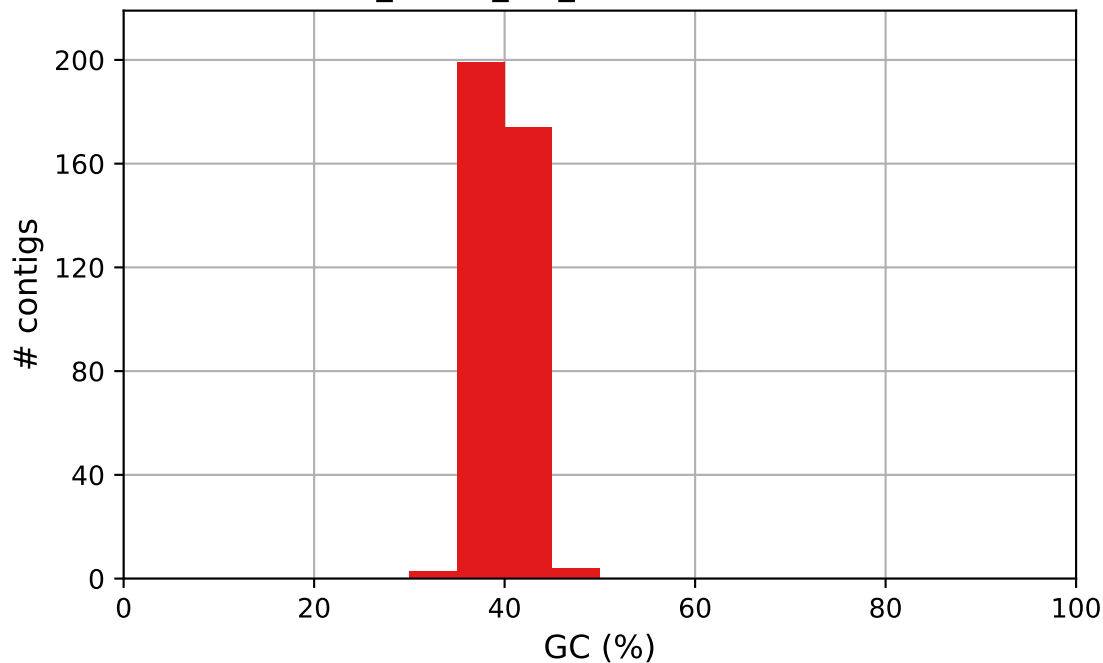
Cumulative length



GC content

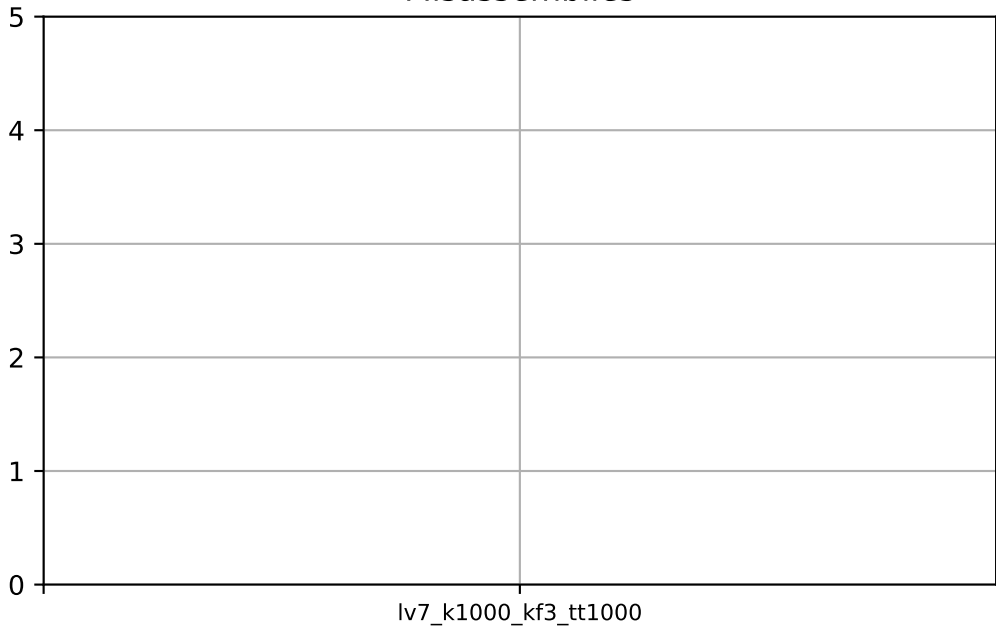


lv7_k1000_kf3_tt1000 GC content

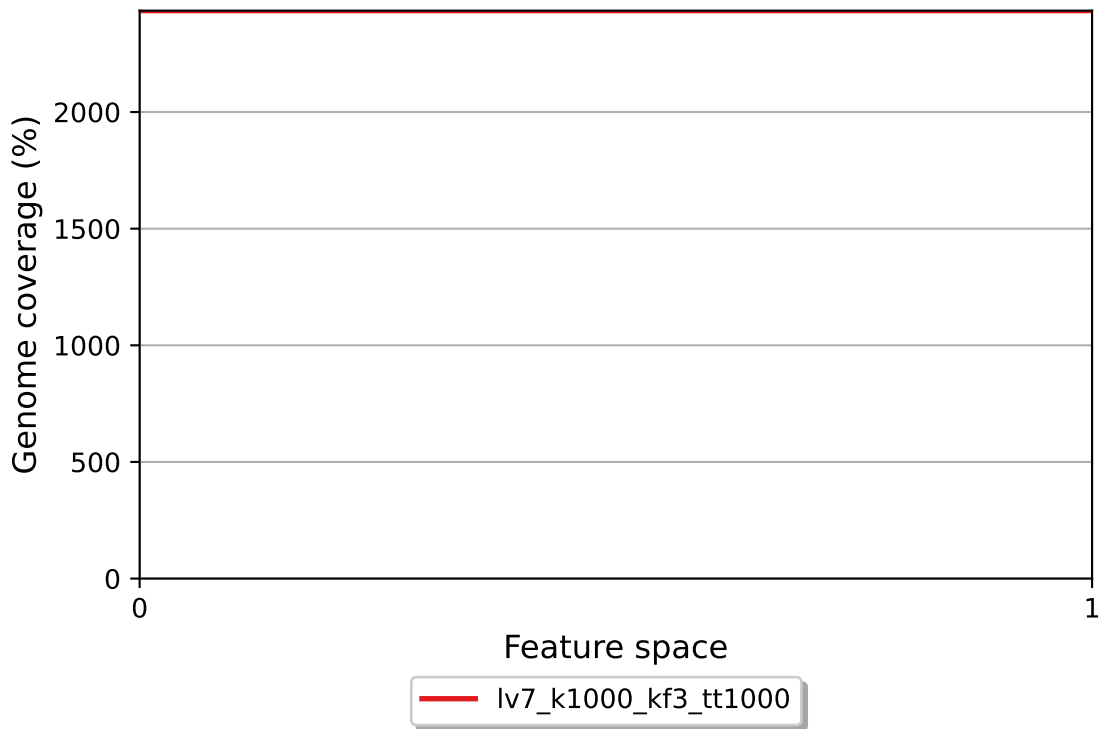


lv7_k1000_kf3_tt1000

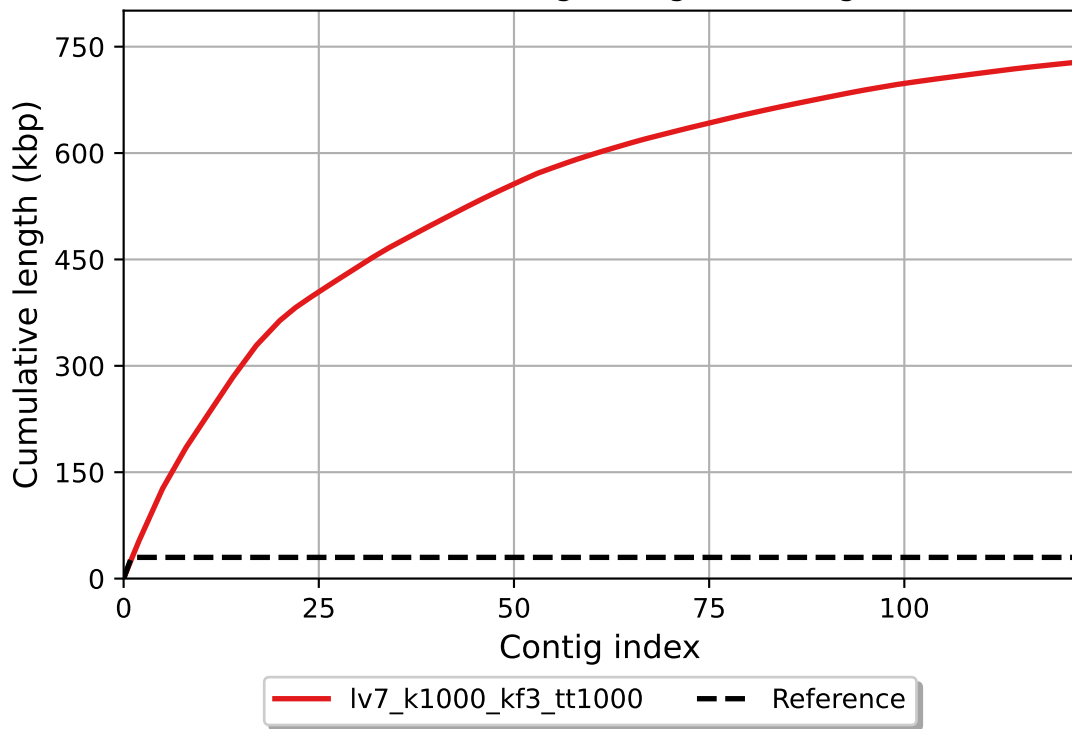
Misassemblies



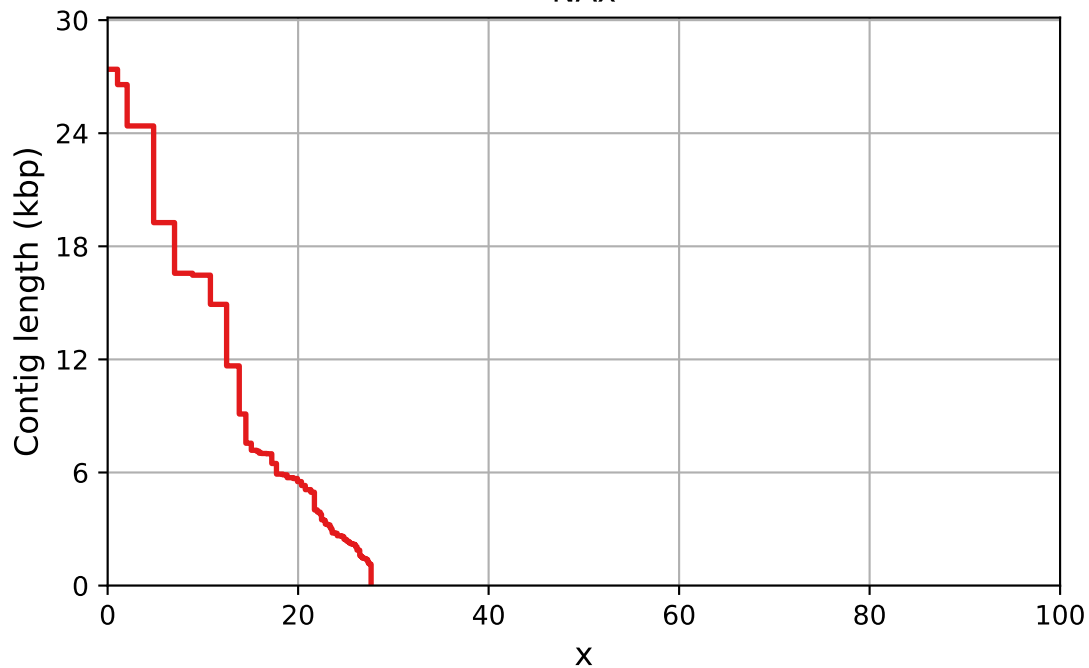
FRCurve (misassemblies)



Cumulative length (aligned contigs)

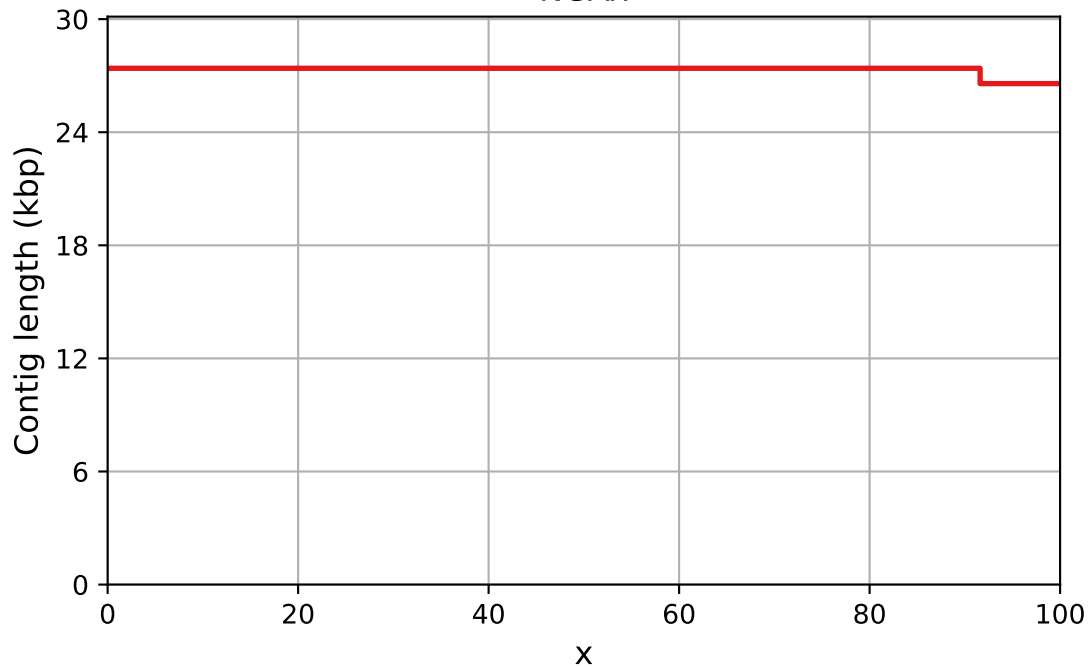


NAx



lv7_k1000_kf3_tt1000

NGAx



lv7_k1000_kf3_tt1000