

Report

	lv6_k1000_kf3_tt1000
# contigs (>= 0 bp)	94
# contigs (>= 1000 bp)	94
# contigs (>= 5000 bp)	60
# contigs (>= 10000 bp)	43
# contigs (>= 25000 bp)	22
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	1190238
Total length (>= 1000 bp)	1190238
Total length (>= 5000 bp)	1132857
Total length (>= 10000 bp)	998119
Total length (>= 25000 bp)	620511
Total length (>= 50000 bp)	0
# contigs	94
Largest contig	29309
Total length	1190238
Reference length	29903
GC (%)	39.57
Reference GC (%)	37.97
N50	25959
NG50	29309
N90	9334
NG90	29309
auN	21772.5
auNG	866616.5
L50	22
LG50	1
L90	51
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	60 + 0 part
Unaligned length	797289
Genome fraction (%)	99.324
Duplication ratio	13.228
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2018.97
# indels per 100 kbp	0.00
Largest alignment	28574
Total aligned length	392874
NA50	-
NGA50	28574
NA90	-
NGA90	28574
auNA	6725.1
auNGA	267681.6
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

	lv6_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	7932
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

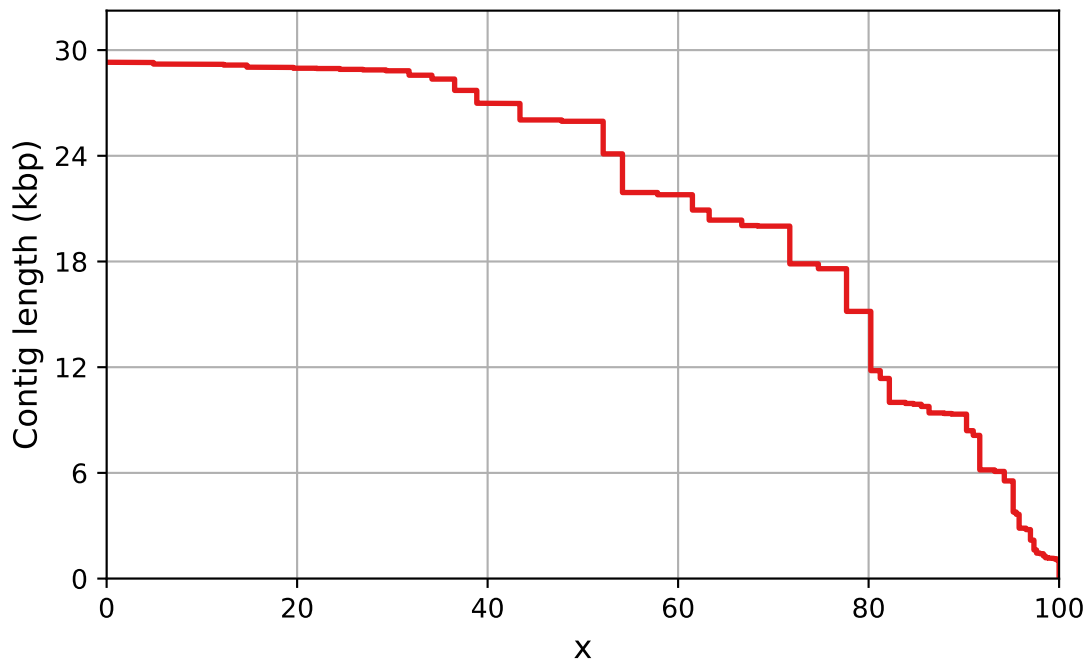
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	lv6_k1000_kf3_tt1000
# fully unaligned contigs	60
Fully unaligned length	797289
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

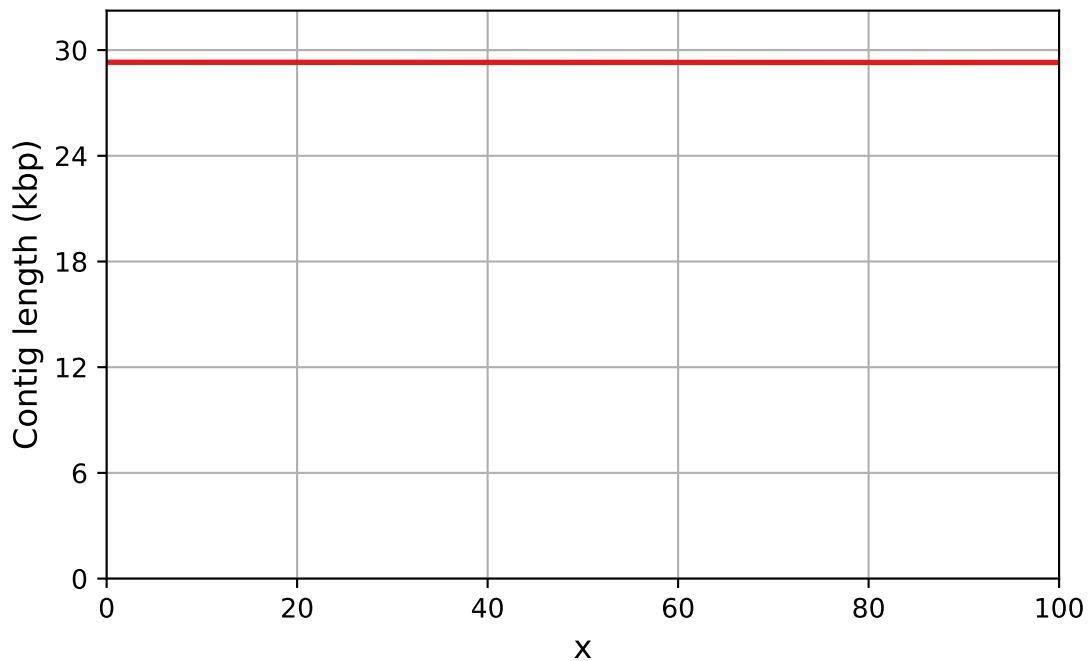
All statistics are based on contigs of size ≥ 50 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

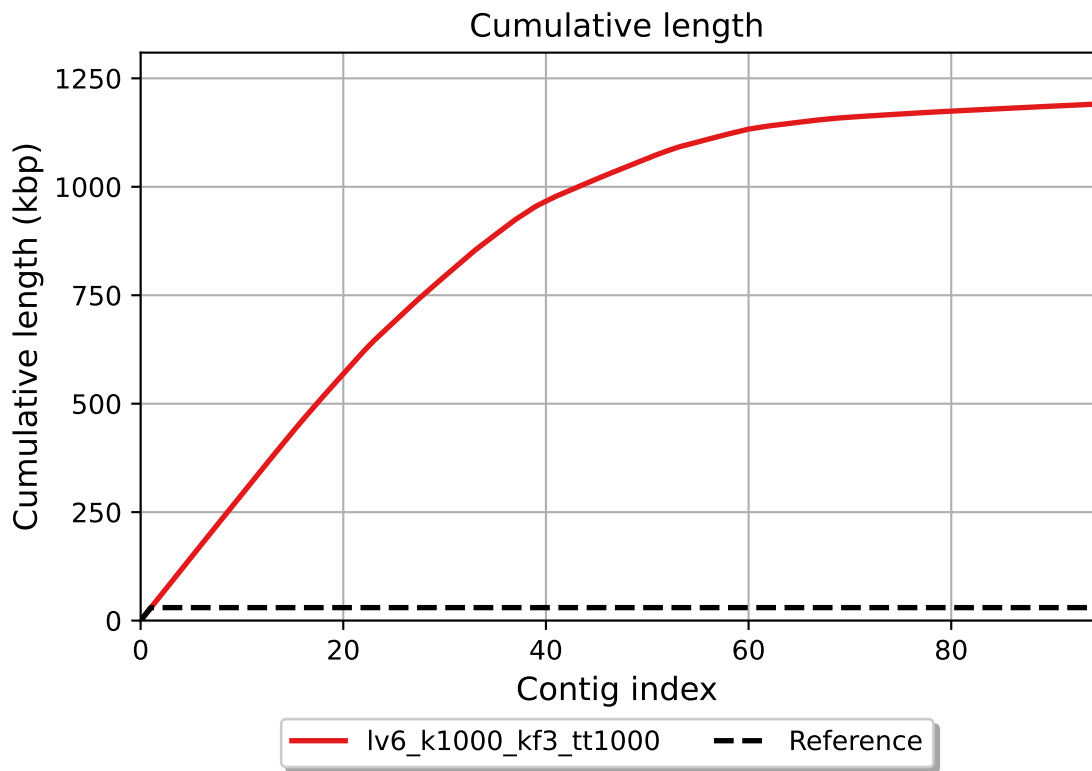


lv6_k1000_kf3_tt1000

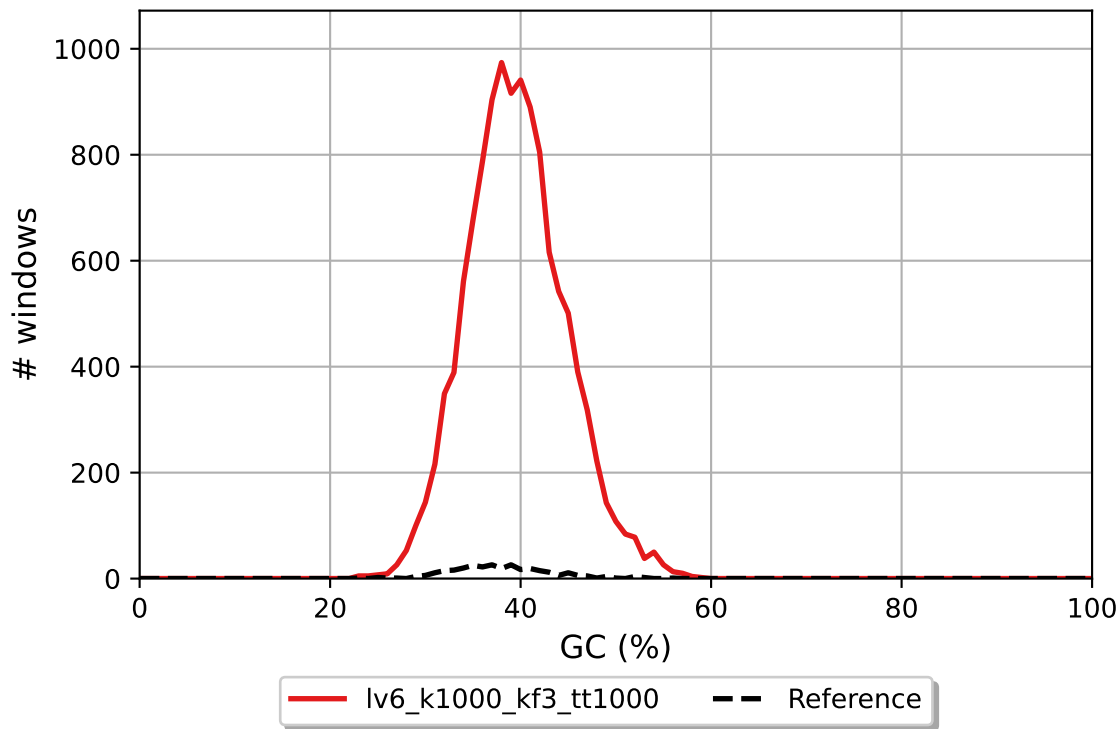
NGx



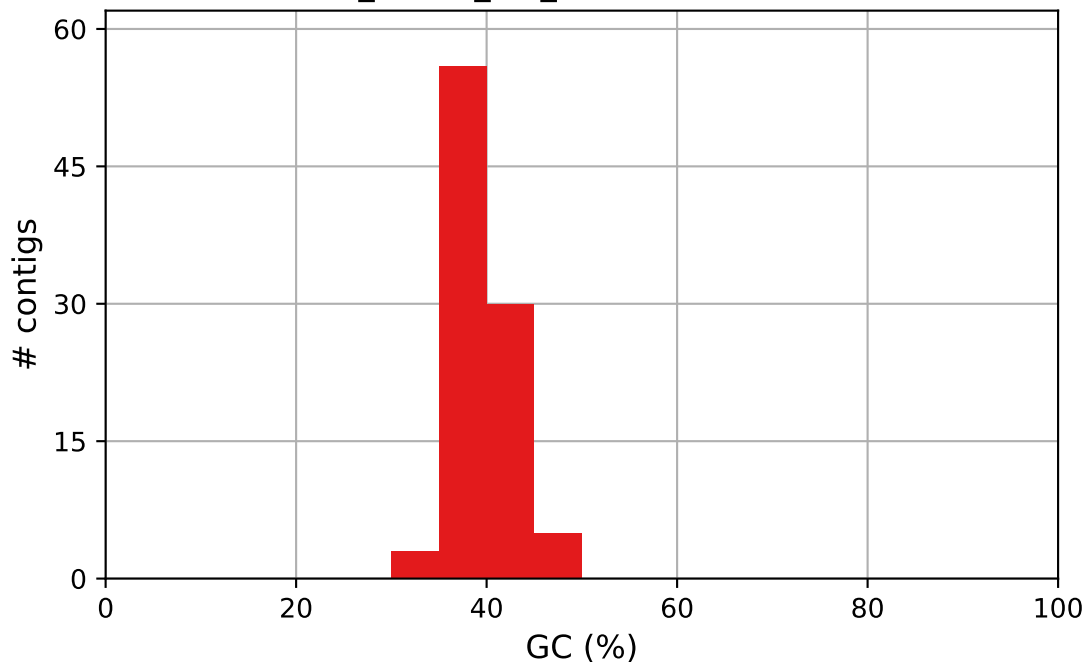
lv6_k1000_kf3_tt1000



GC content

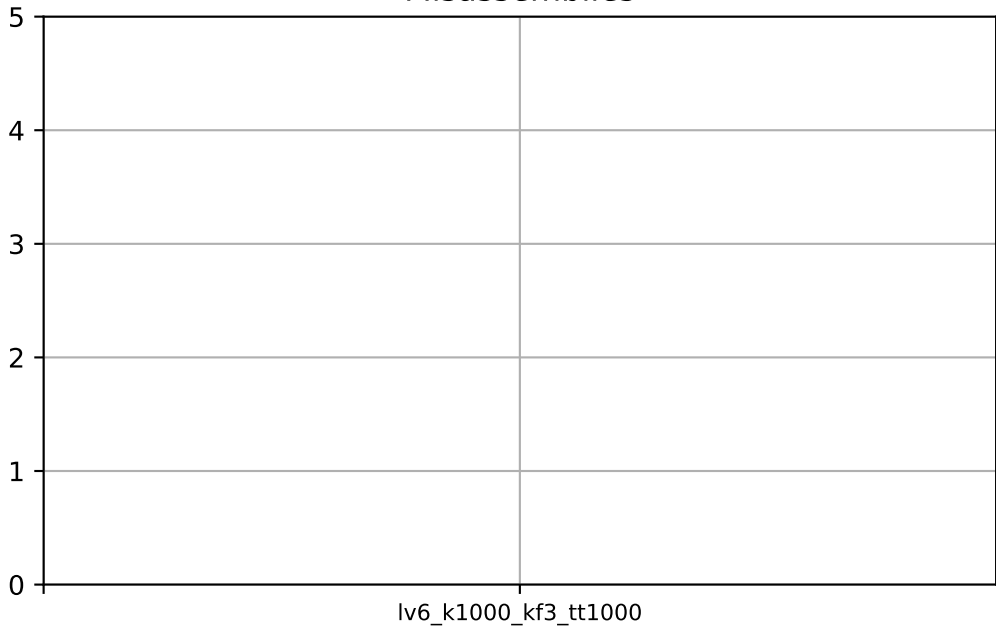


lv6_k1000_kf3_tt1000 GC content

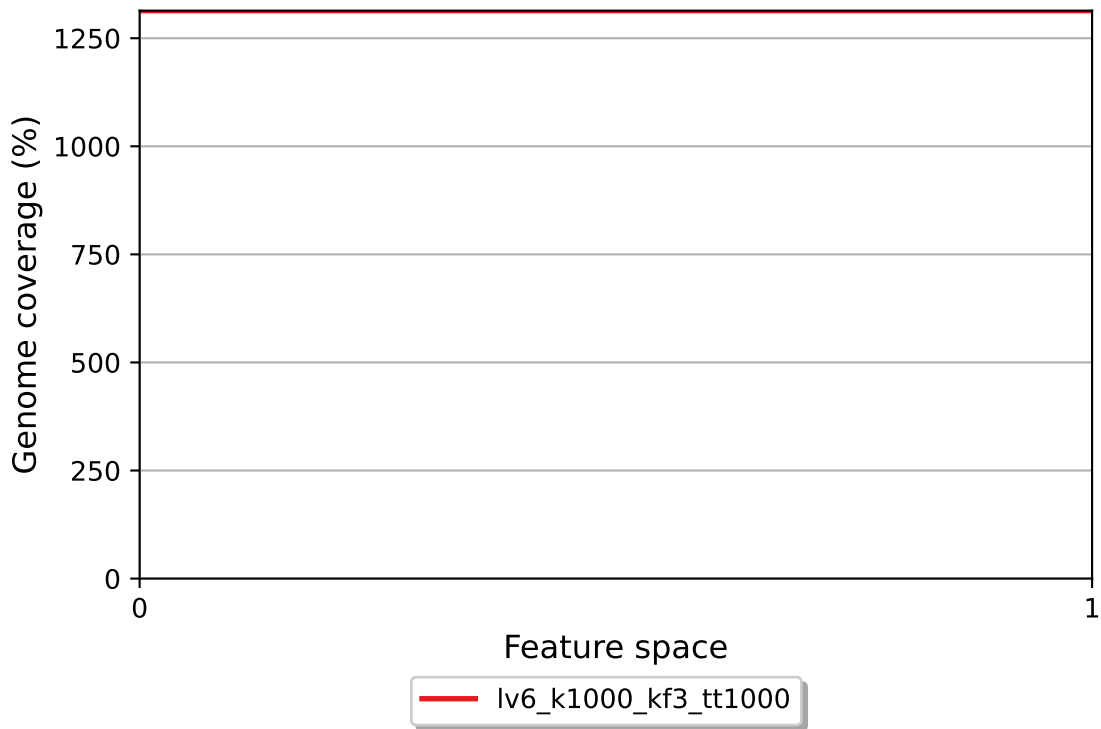


lv6_k1000_kf3_tt1000

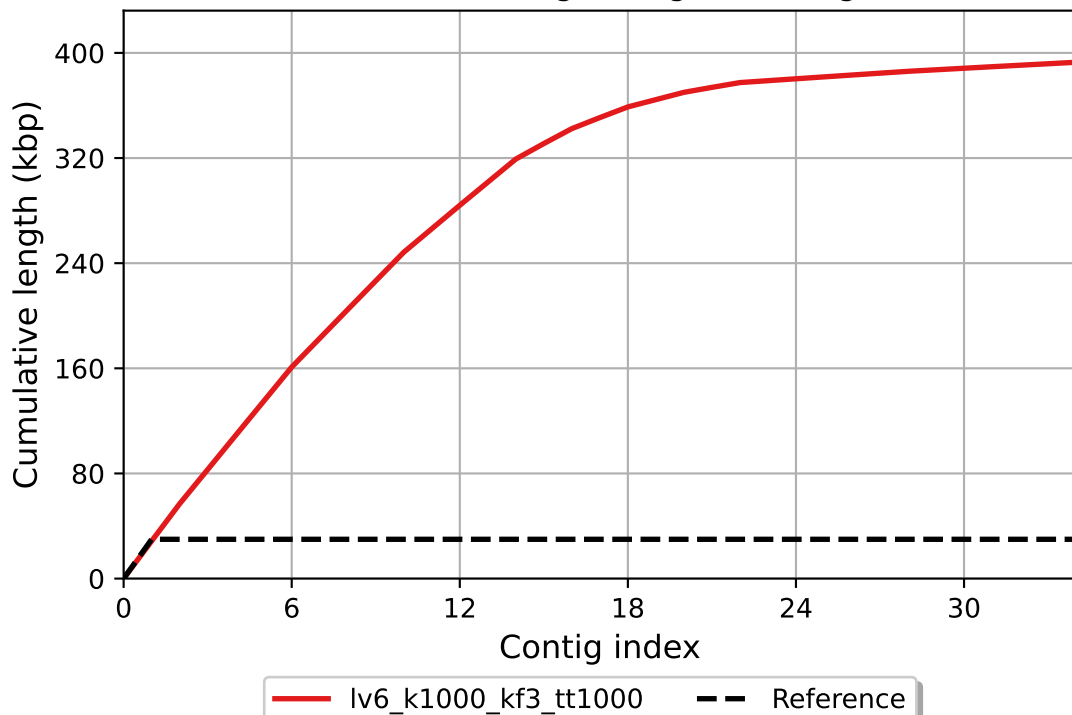
Misassemblies



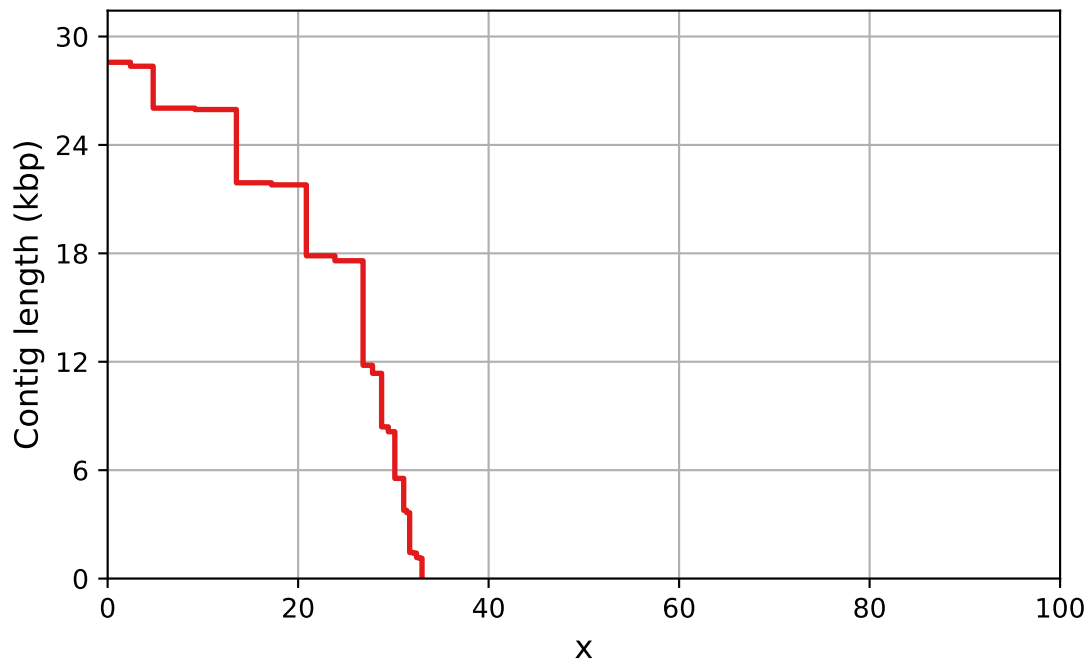
FRCurve (misassemblies)



Cumulative length (aligned contigs)

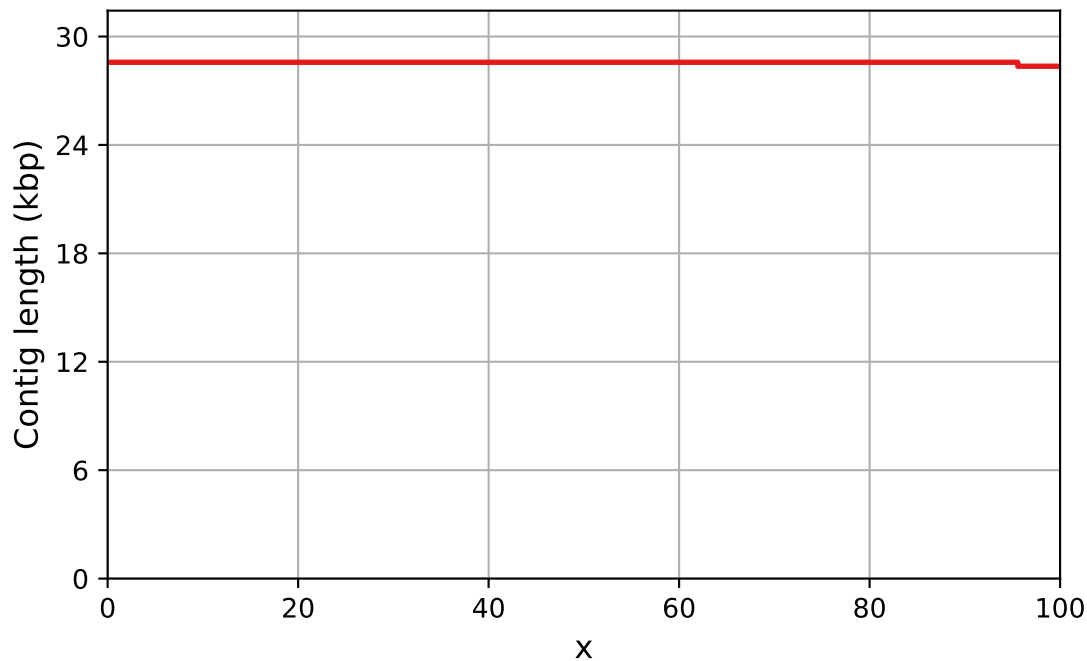


NAx



lv6_k1000_kf3_tt1000

NGAx



lv6_k1000_kf3_tt1000