

## Report

	no_error_ont_hq_50x_dbg_k40
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29703
Total length (>= 1000 bp)	28087
Total length (>= 5000 bp)	23751
Total length (>= 10000 bp)	23751
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5
Largest contig	13183
Total length	29432
Reference length	30119
GC (%)	41.16
Reference GC (%)	41.24
N50	10568
NG50	10568
N90	4336
NG90	4336
auN	10369.7
auNG	10133.1
L50	2
LG50	2
L90	3
LG90	3
# 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 (%)	97.341
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	13183
Total aligned length	29432
NA50	10568
NGA50	10568
NA90	4336
NGA90	4336
auNA	10369.7
auNGA	10133.1
LA50	2
LGA50	2
LA90	3
LGA90	3

All statistics are based on contigs of size >= 300 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	no_error_ont_hq_50x_dbg_k40
# 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

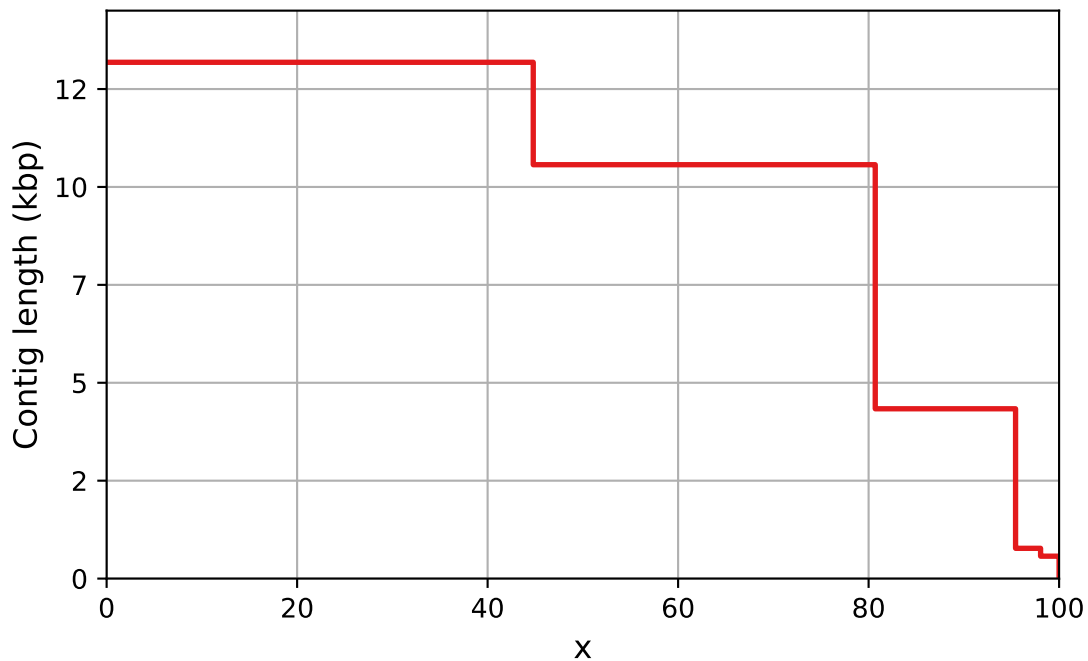
All statistics are based on contigs of size  $\geq 300$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	no_error_ont_hq_50x_dbg_k40
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

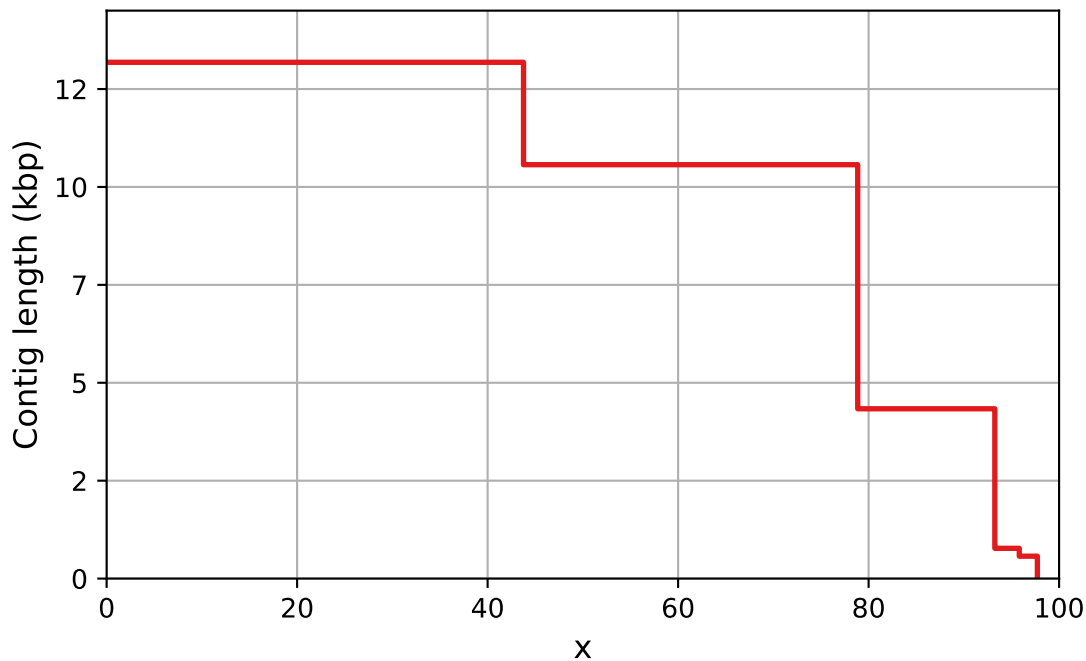
All statistics are based on contigs of size  $\geq 300$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



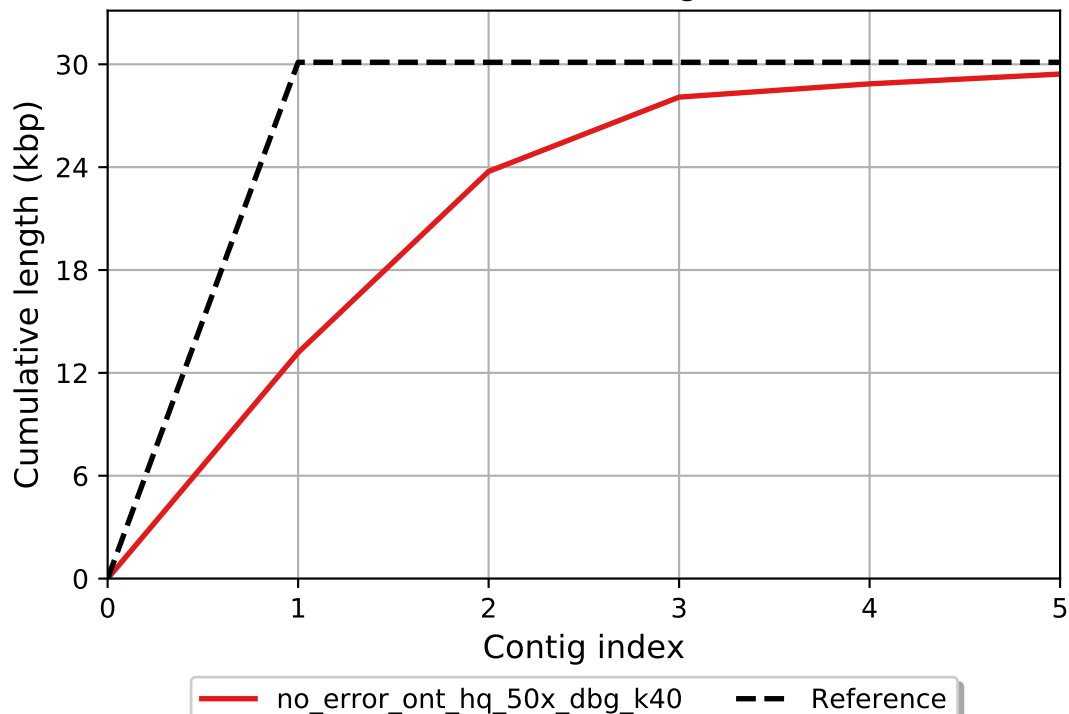
no\_error\_ont\_hq\_50x\_dbg\_k40

NGx

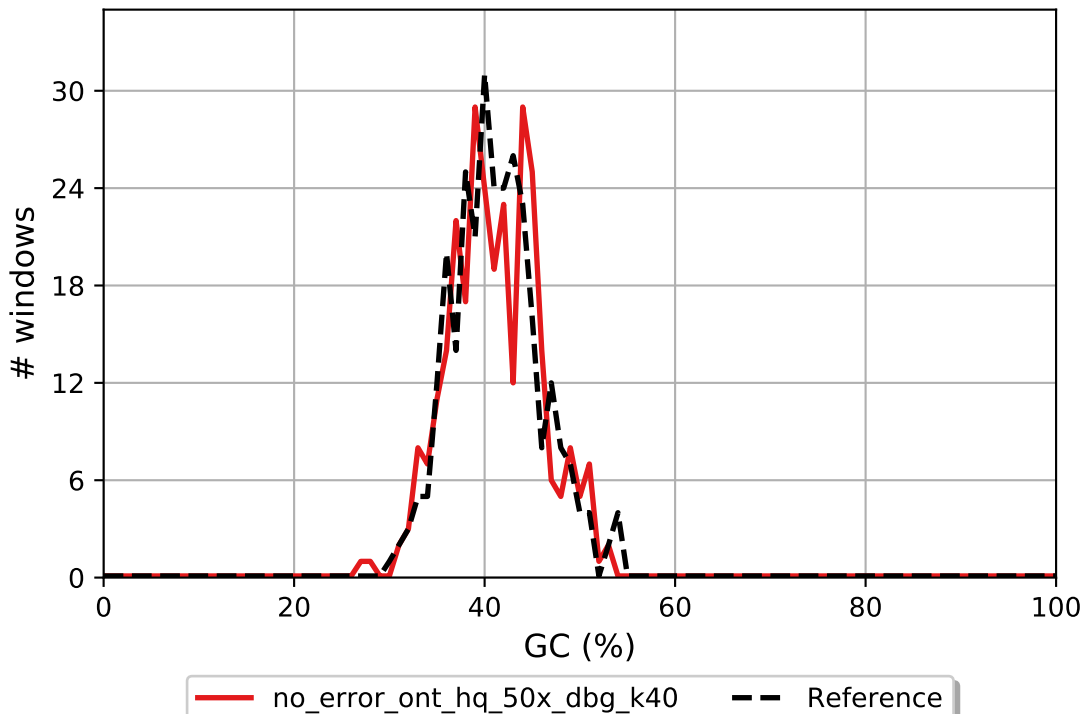


no\_error\_ont\_hq\_50x\_dbg\_k40

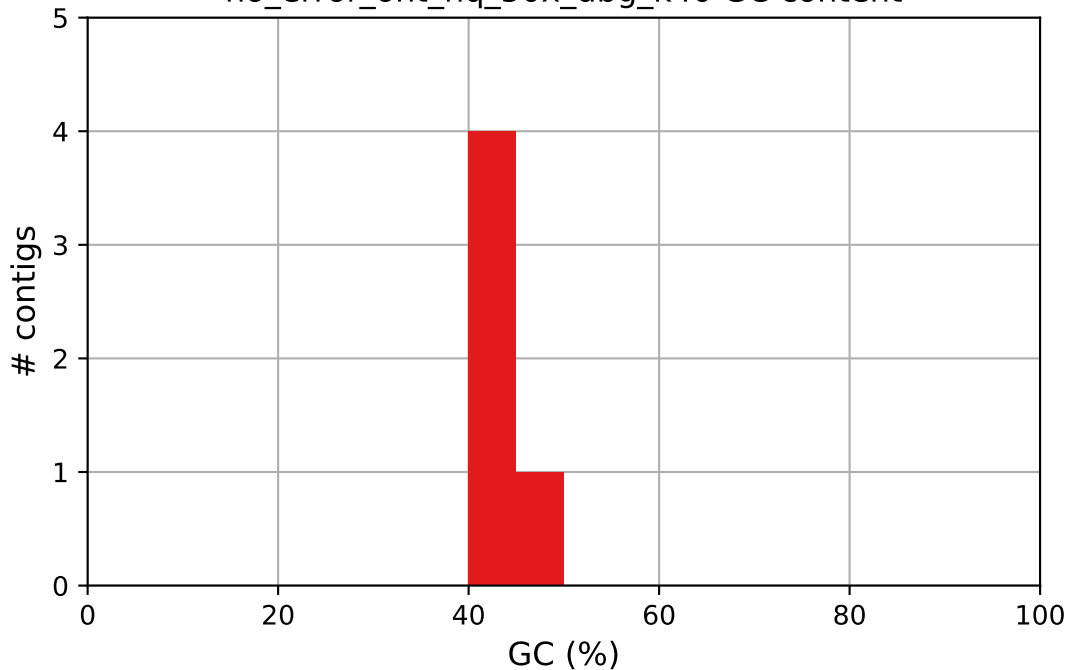
Cumulative length



## GC content



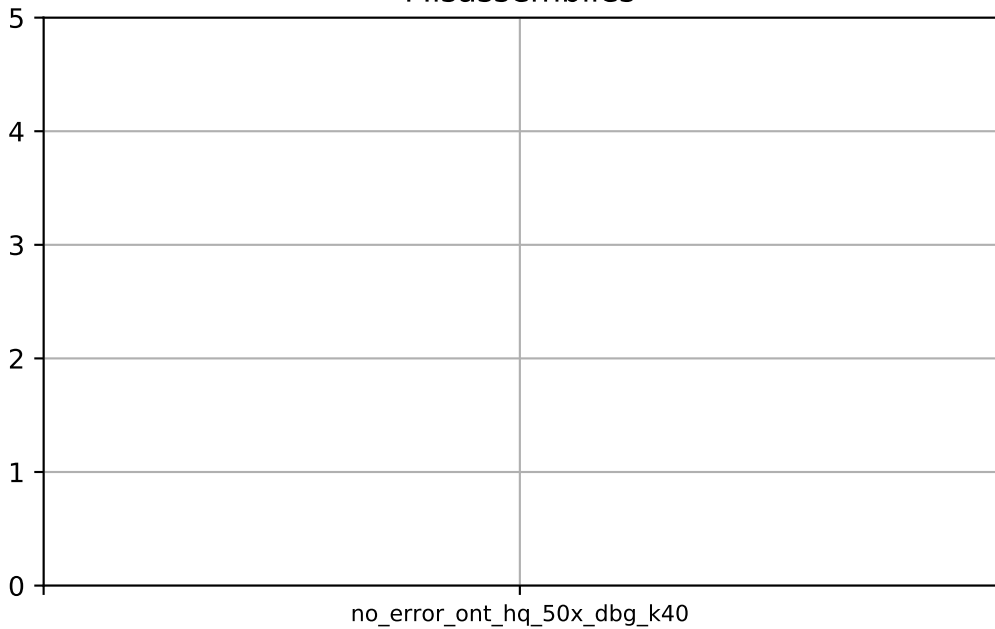
no\_error\_ont\_hq\_50x\_dbg\_k40 GC content



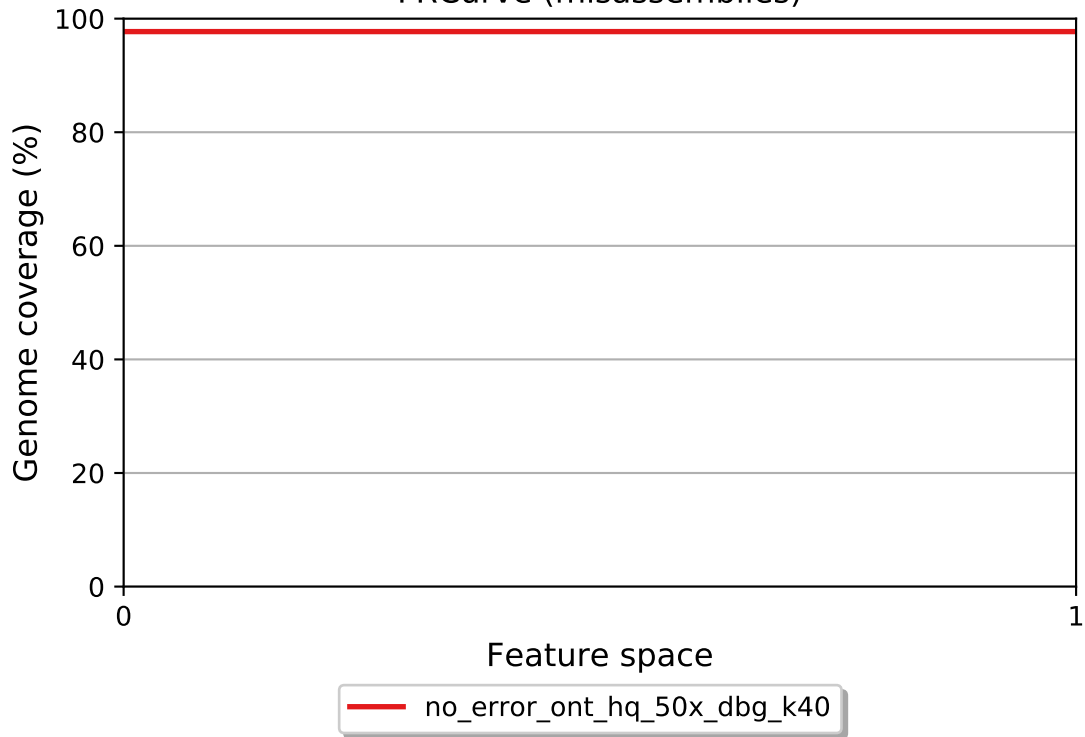
no\_error\_ont\_hq\_50x\_dbg\_k40



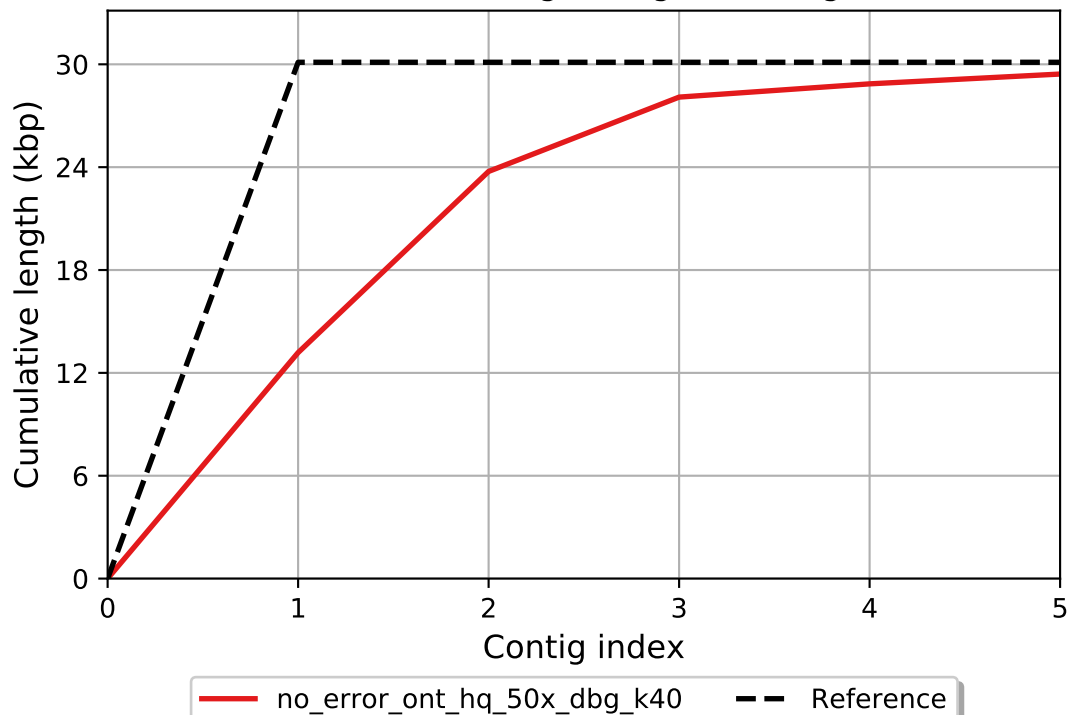
## Misassemblies



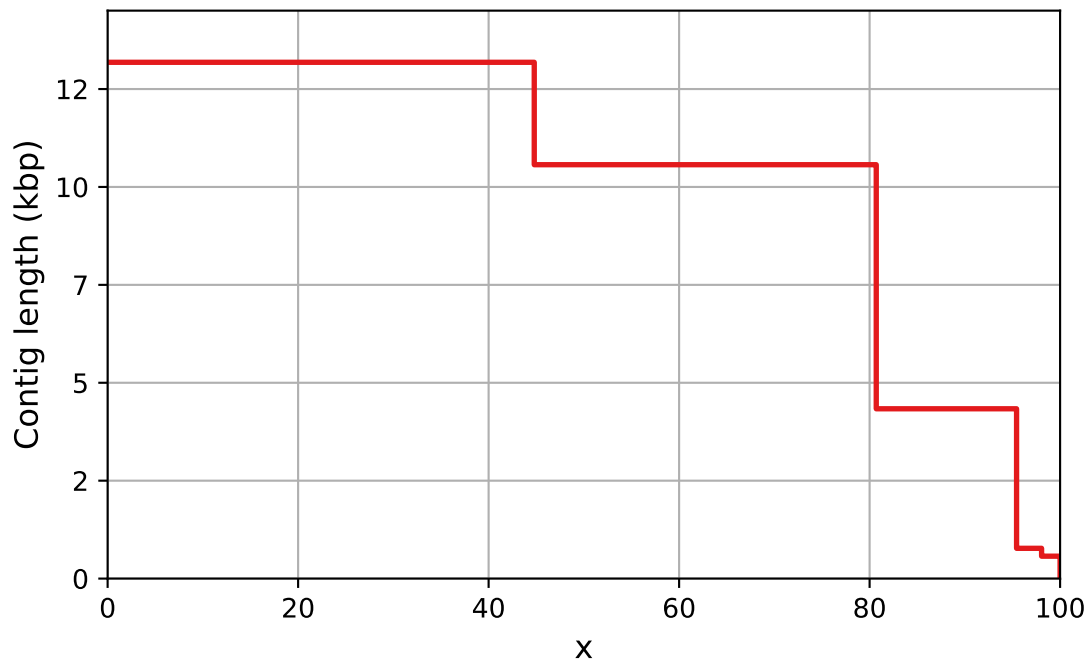
FRCurve (misassemblies)



Cumulative length (aligned contigs)

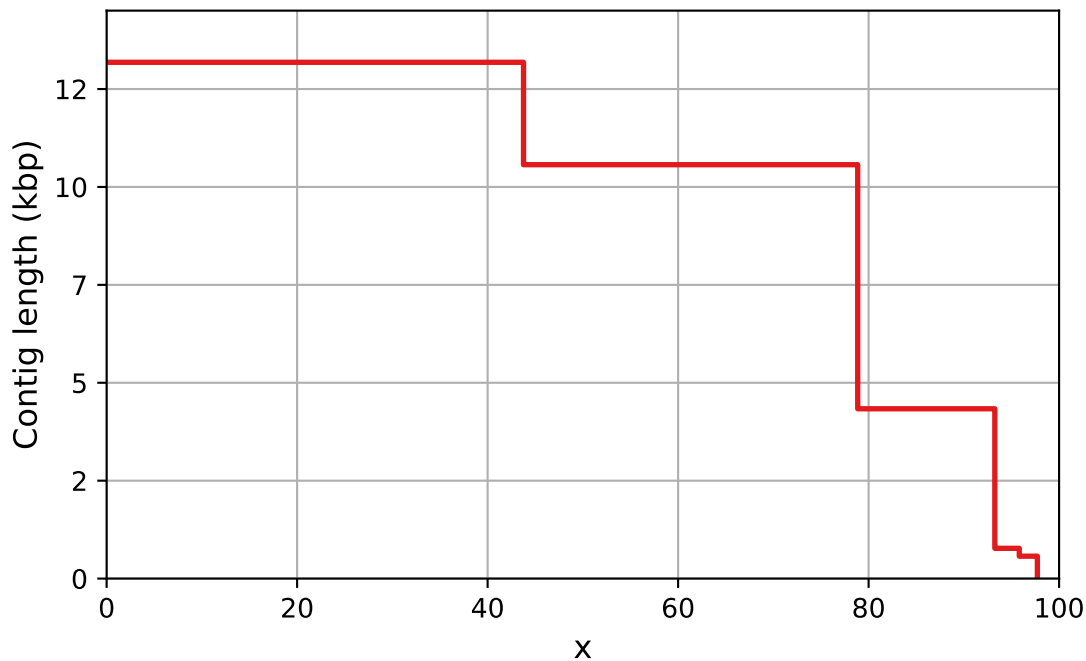


NAx



no\_error\_ont\_hq\_50x\_dbg\_k40

## NGAx



no\_error\_ont\_hq\_50x\_dbg\_k40