

# Report

	sim5M.CanuL
# contigs (>= 0 bp)	35
# contigs (>= 1000 bp)	35
# contigs (>= 5000 bp)	35
# contigs (>= 10000 bp)	33
# contigs (>= 25000 bp)	24
# contigs (>= 50000 bp)	19
Total length (>= 0 bp)	4920161
Total length (>= 1000 bp)	4920161
Total length (>= 5000 bp)	4920161
Total length (>= 10000 bp)	4906506
Total length (>= 25000 bp)	4753145
Total length (>= 50000 bp)	4544034
# contigs	35
Largest contig	663575
Total length	4920161
Reference length	5000040
GC (%)	35.80
Reference GC (%)	35.84
N50	297761
NG50	297761
N75	186935
NG75	182381
L50	6
LG50	6
L75	11
LG75	12
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.454
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.96
# indels per 100 kbp	9.54
Largest alignment	663575
Total aligned length	4920160
NA50	297761
NGA50	297761
NA75	186935
NGA75	182381
LA50	6
LGA50	6
LA75	11
LGA75	12

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

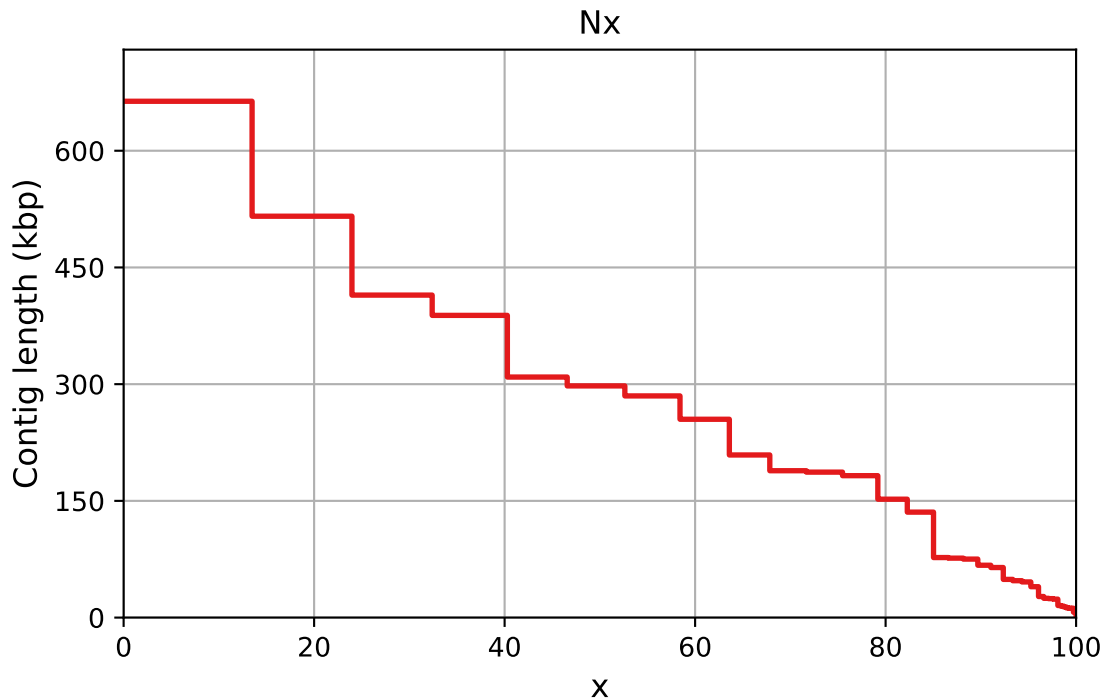
	sim5M.CanuL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	239
# indels	460
# indels ( $\leq 5$ bp)	460
# indels ( $> 5$ bp)	0
Indels length	506

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

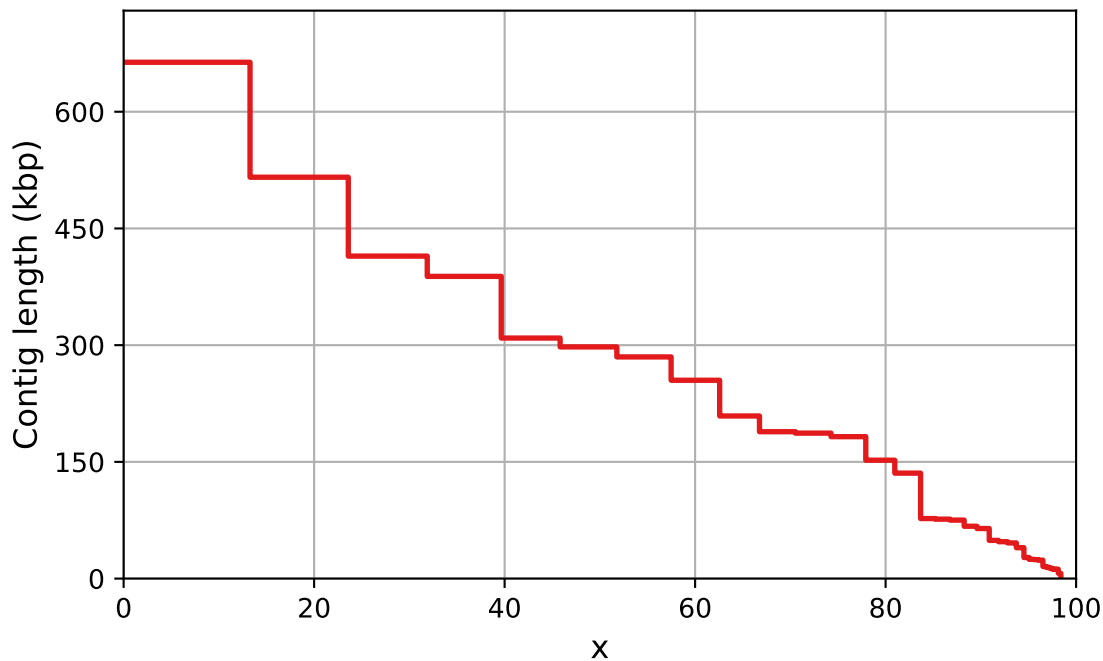
	sim5M.CanuL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



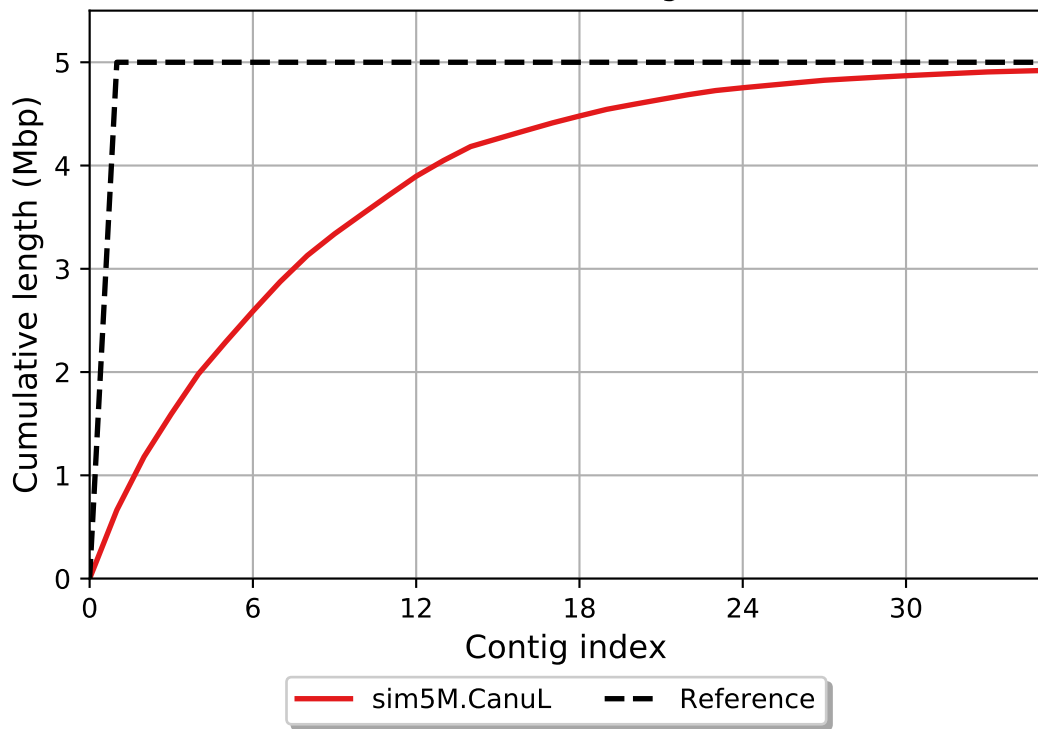
— sim5M.CanuL

# NGx

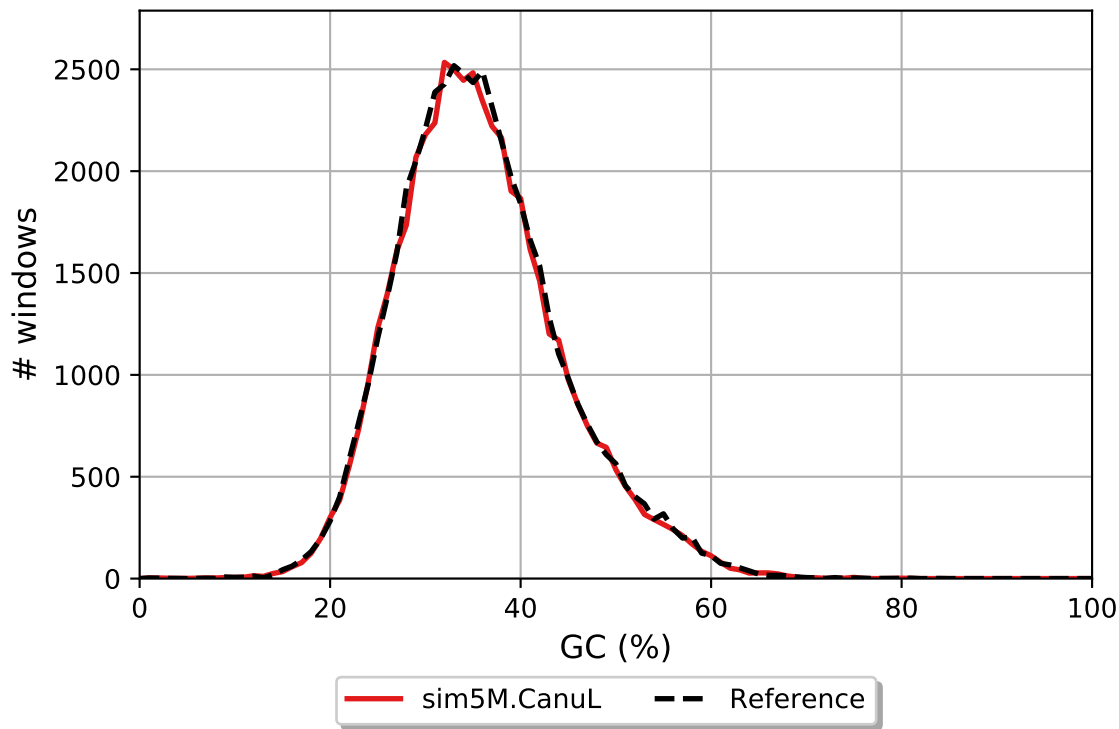


— sim5M.CanuL

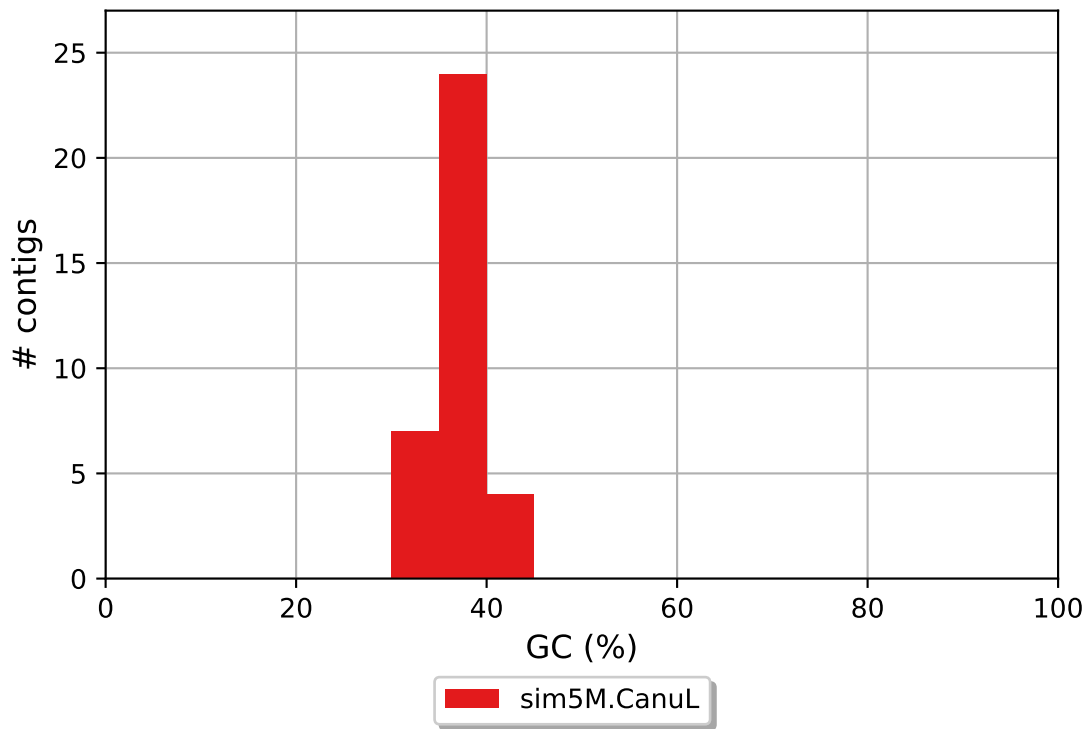
Cumulative length



## GC content

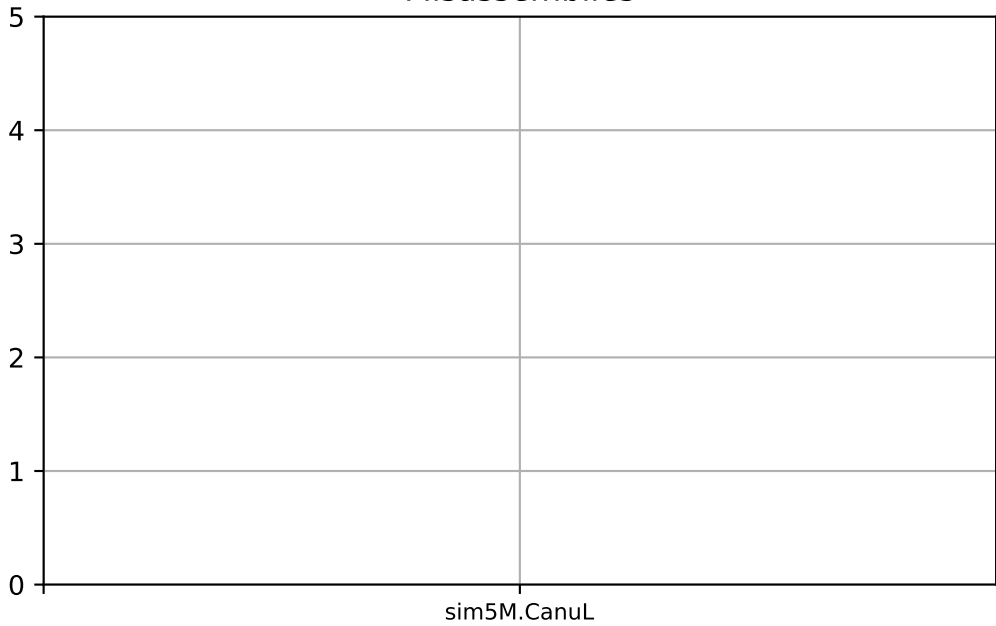


sim5M.CanuL GC content

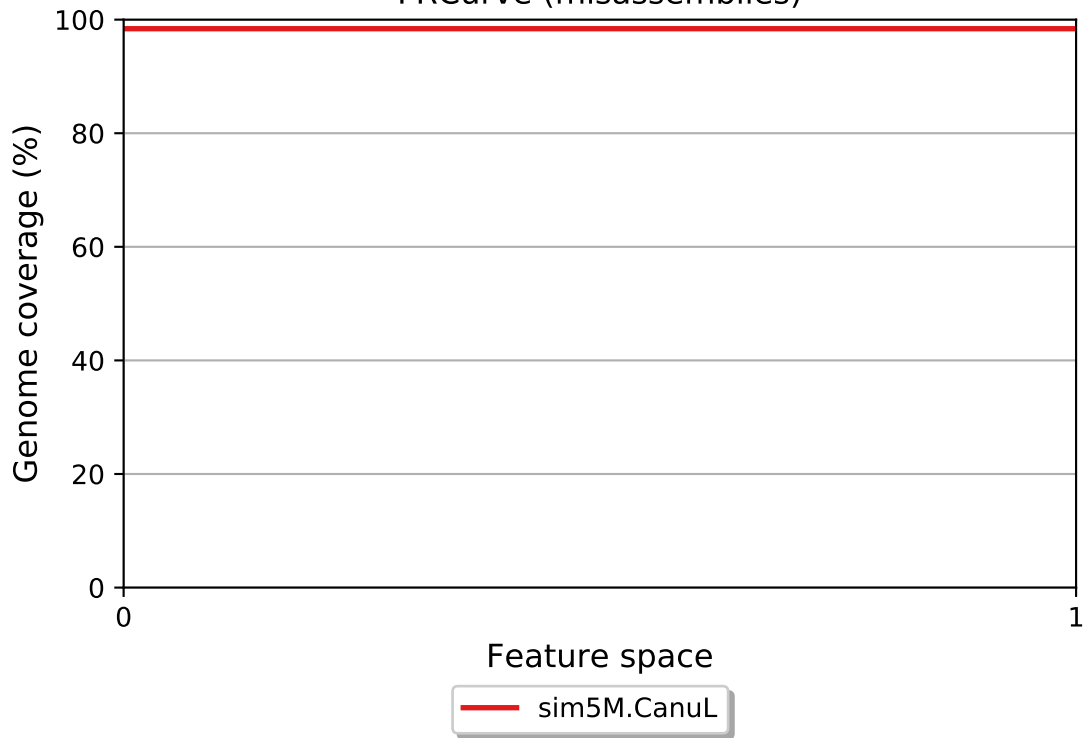




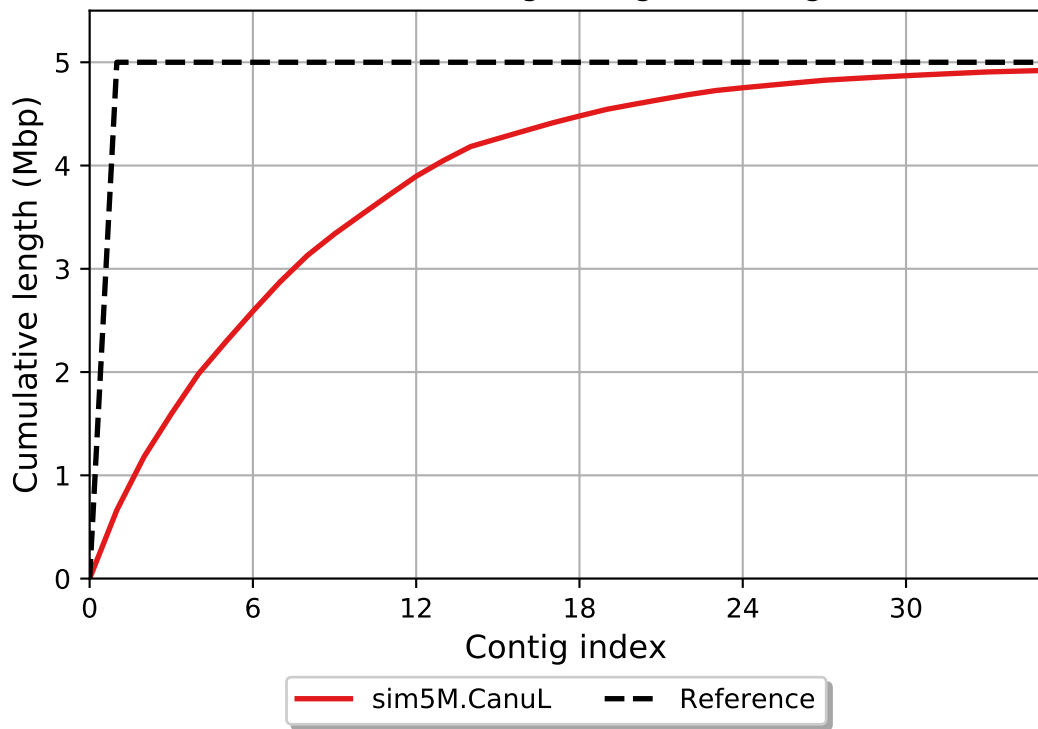
## Misassemblies



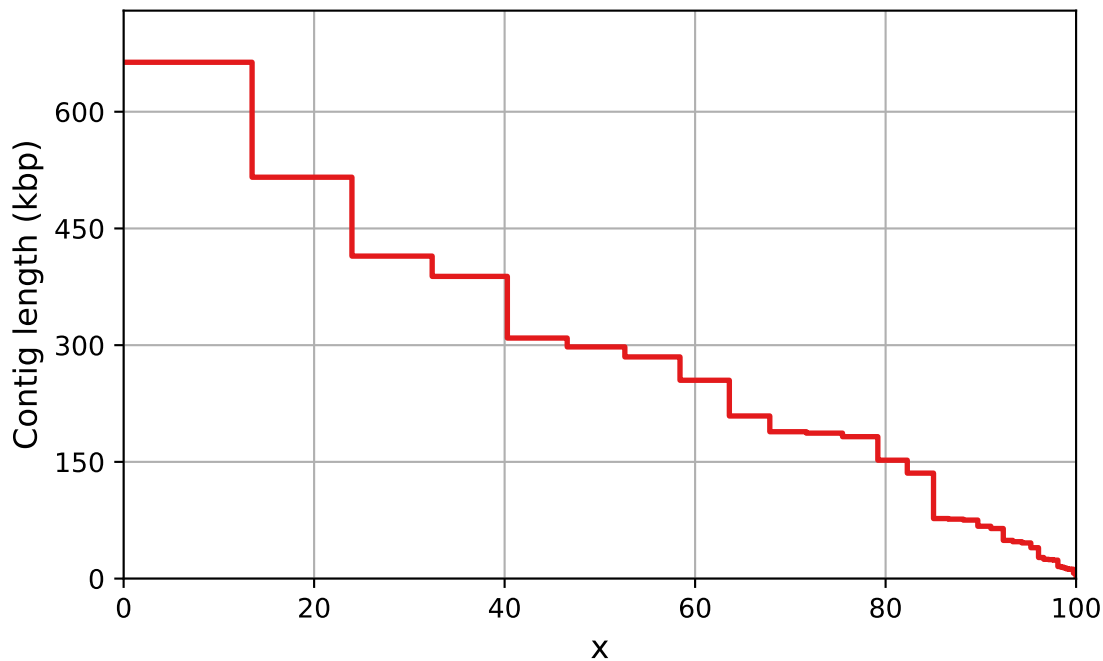
FRCurve (misassemblies)



Cumulative length (aligned contigs)

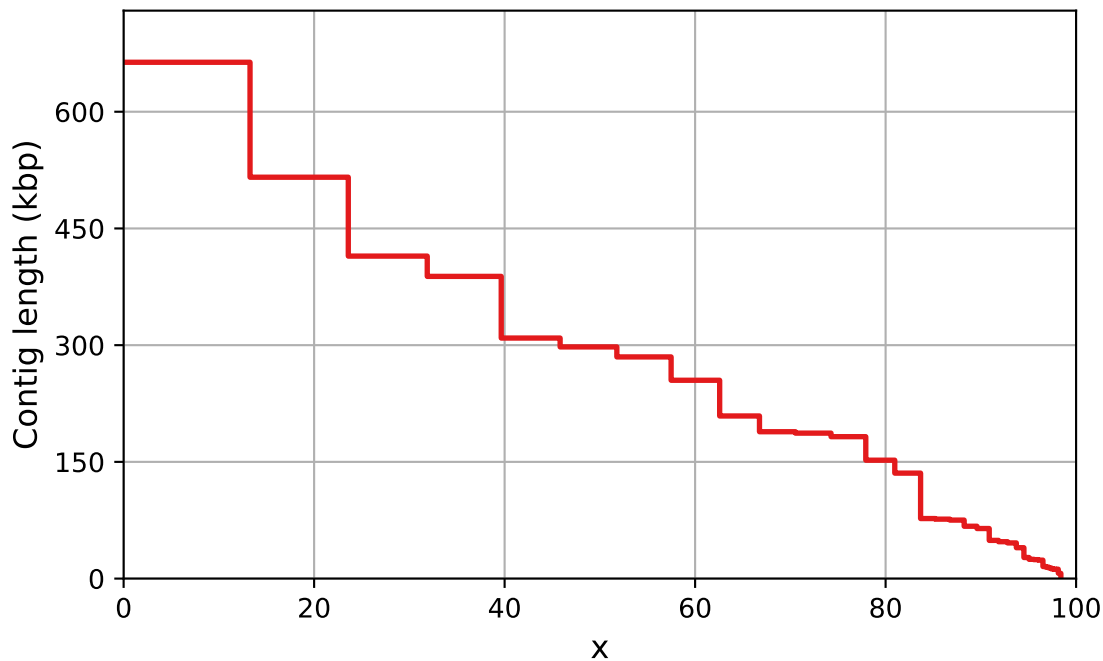


# NAx



— sim5M.CanuL

# NGAx



— sim5M.CanuL