

Report

	sim5M.CanuH.p1
# contigs (>= 0 bp)	17
# contigs (>= 1000 bp)	17
# contigs (>= 5000 bp)	17
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	6
Total length (>= 0 bp)	5135280
Total length (>= 1000 bp)	5135280
Total length (>= 5000 bp)	5135280
Total length (>= 10000 bp)	5110301
Total length (>= 25000 bp)	4998120
Total length (>= 50000 bp)	4998120
# contigs	17
Largest contig	1474852
Total length	5135280
Reference length	5000040
GC (%)	35.86
Reference GC (%)	35.84
N50	1313777
NG50	1313777
N75	623531
NG75	623531
L50	2
LG50	2
L75	4
LG75	4
# 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 (%)	99.910
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.40
# indels per 100 kbp	0.28
Largest alignment	1474852
Total aligned length	5135272
NA50	1313775
NGA50	1313775
NA75	623528
NGA75	623528
LA50	2
LGA50	2
LA75	4
LGA75	4

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

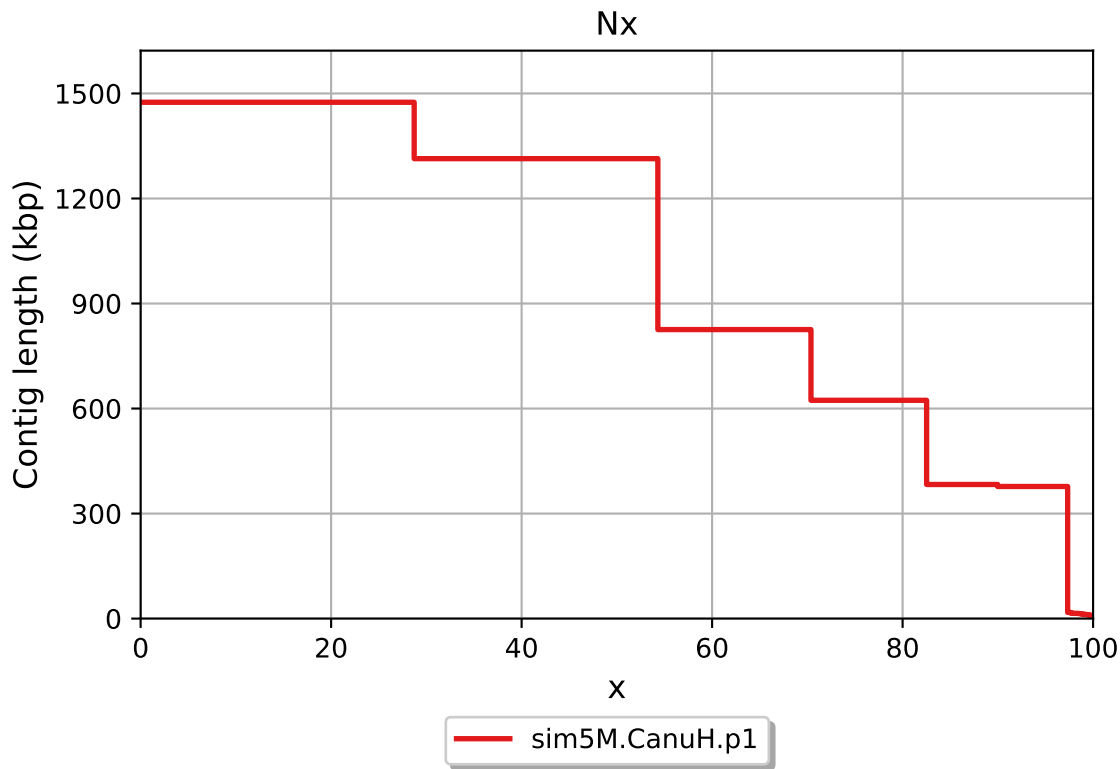
	sim5M.CanuH.p1
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	20
# indels	14
# indels (≤ 5 bp)	14
# indels (> 5 bp)	0
Indels length	17

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).

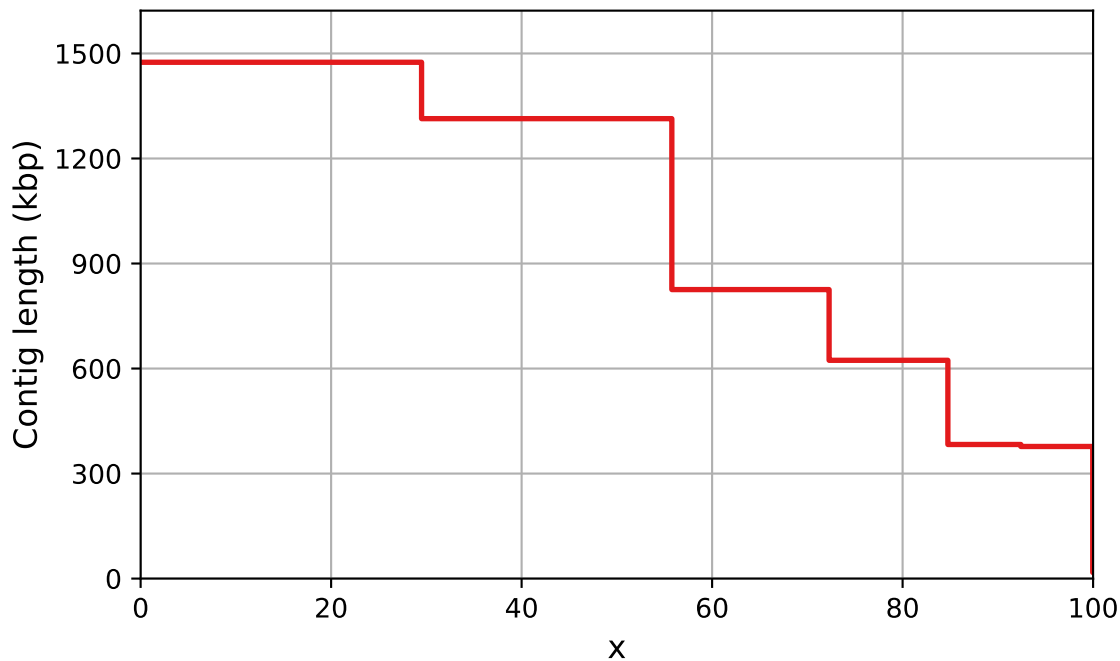
Unaligned report

	sim5M.CanuH.p1
# 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 ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

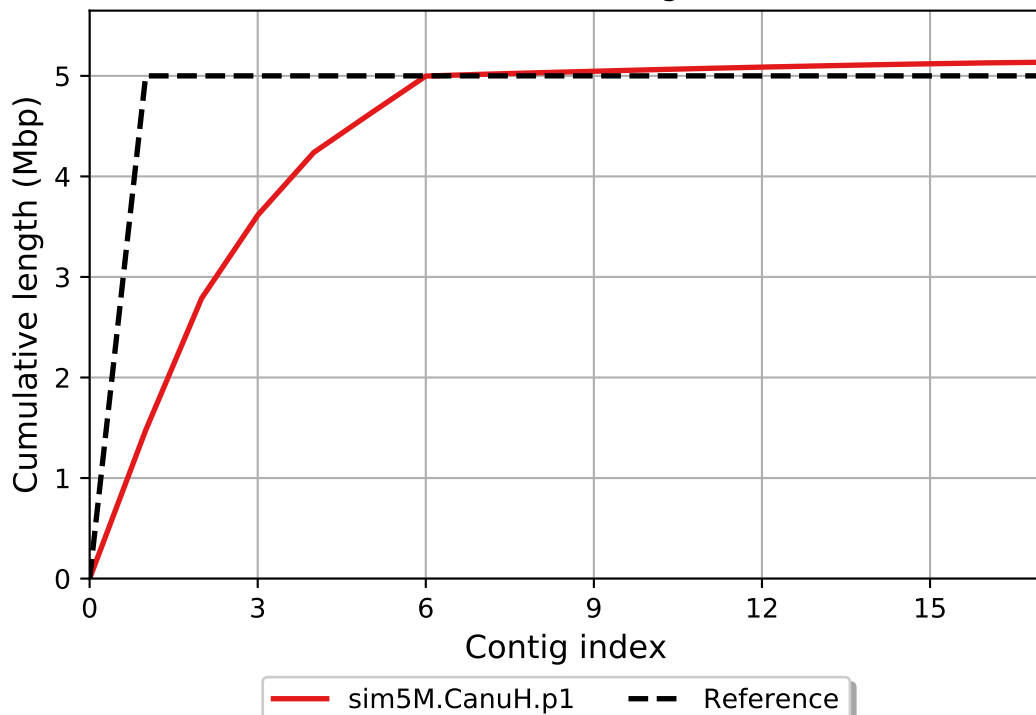


NGx

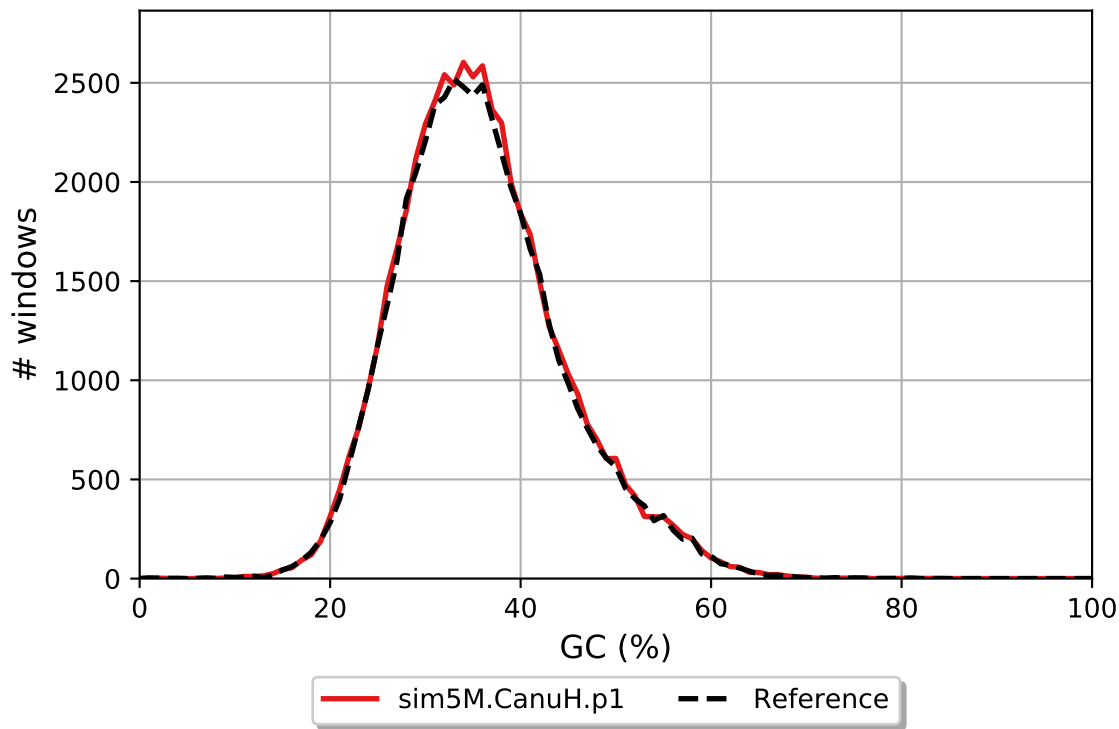


— sim5M.CanuH.p1

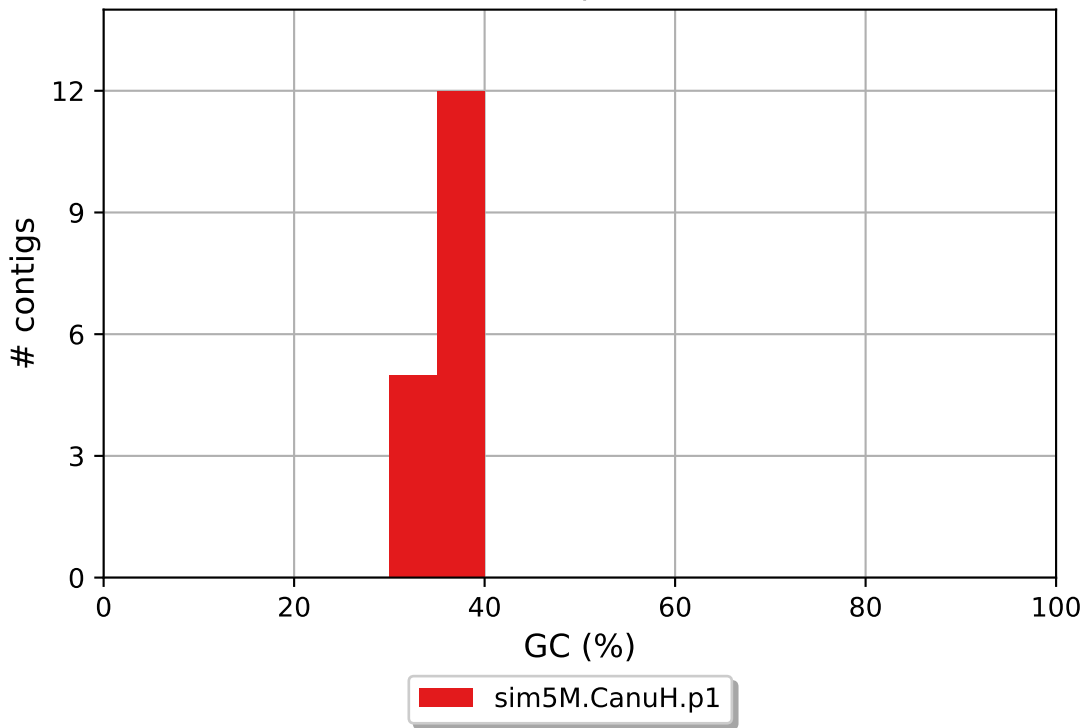
Cumulative length



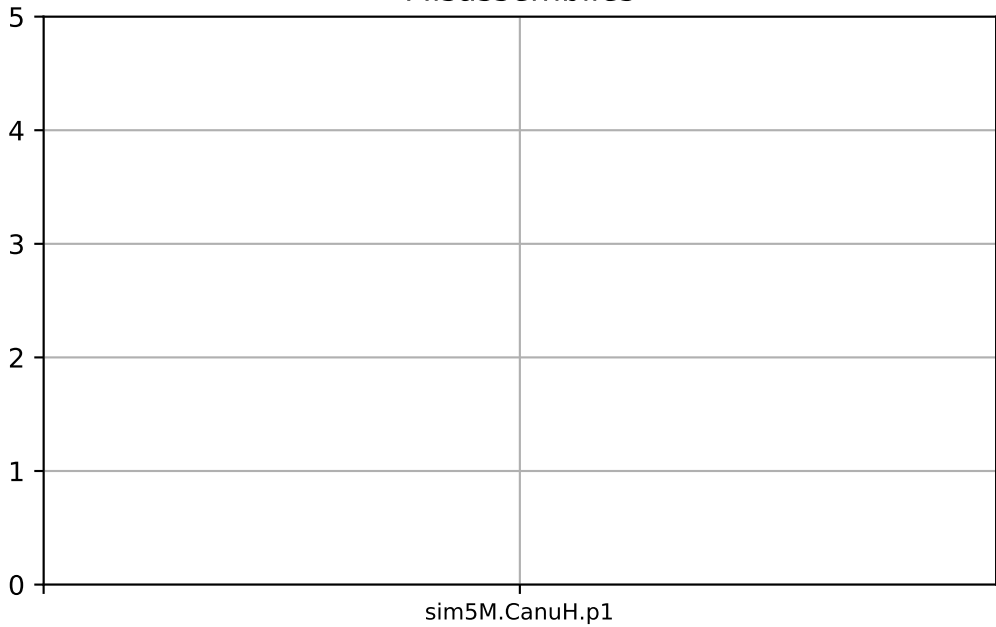
GC content



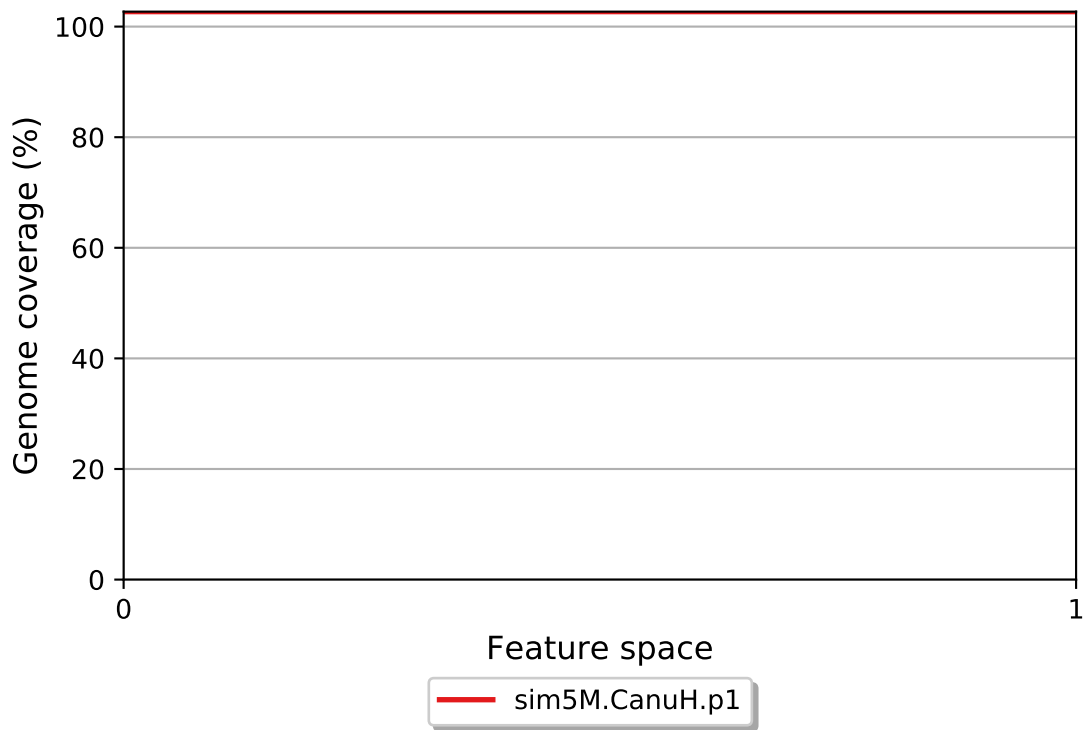
sim5M.CanuH.p1 GC content



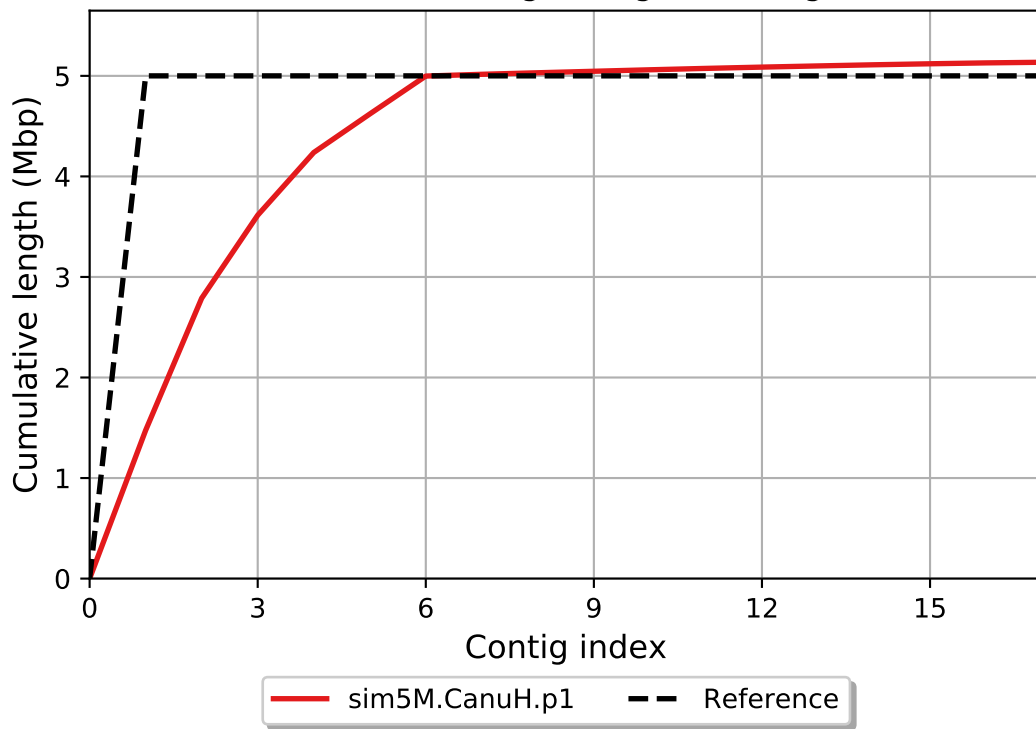
Misassemblies



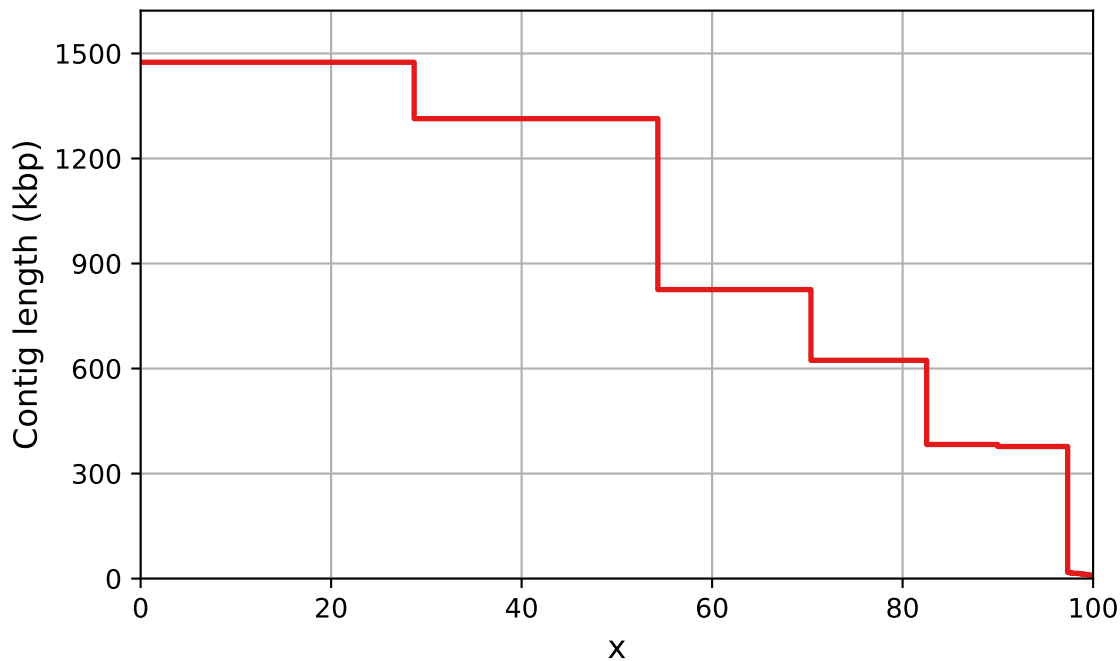
FRCurve (misassemblies)



Cumulative length (aligned contigs)

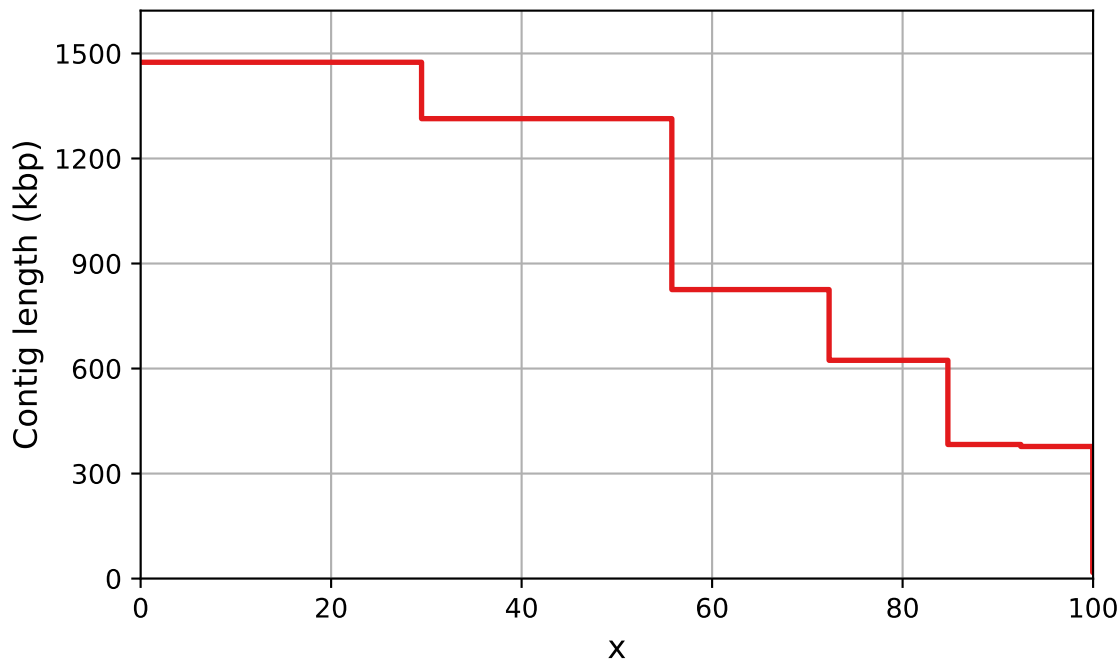


NAx



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NGAx



— sim5M.CanuH.p1