

# Report

	sim5M.MiniH.p2
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	4983309
Total length (>= 1000 bp)	4983309
Total length (>= 5000 bp)	4983309
Total length (>= 10000 bp)	4983309
Total length (>= 25000 bp)	4983309
Total length (>= 50000 bp)	4983309
# contigs	3
Largest contig	2861752
Total length	4983309
Reference length	5000040
GC (%)	35.83
Reference GC (%)	35.84
N50	2861752
NG50	2861752
N75	1154416
NG75	1154416
L50	1
LG50	1
L75	2
LG75	2
# 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 (%)	99.632
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.72
# indels per 100 kbp	2.69
Largest alignment	2861746
Total aligned length	4983302
NA50	2861746
NGA50	2861746
NA75	1154415
NGA75	1154415
LA50	1
LGA50	1
LA75	2
LGA75	2

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

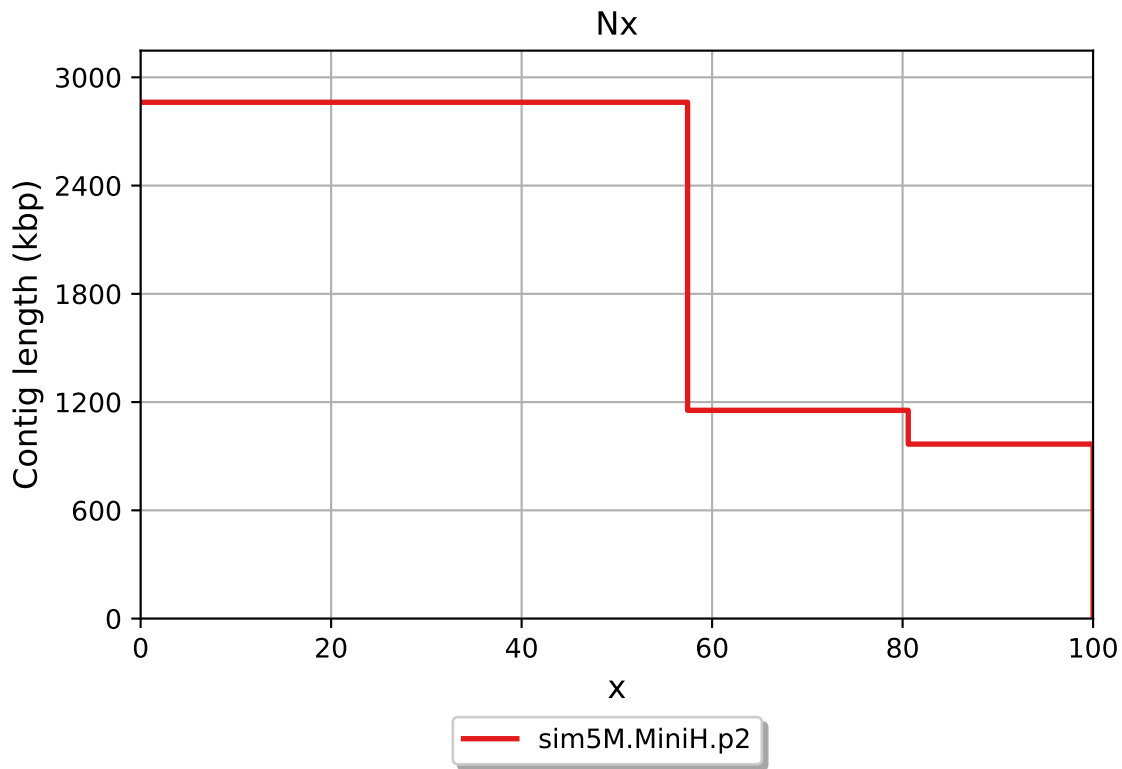
	sim5M.MiniH.p2
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	36
# indels	134
# indels ( $\leq 5$ bp)	134
# indels ( $> 5$ bp)	0
Indels length	159

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).

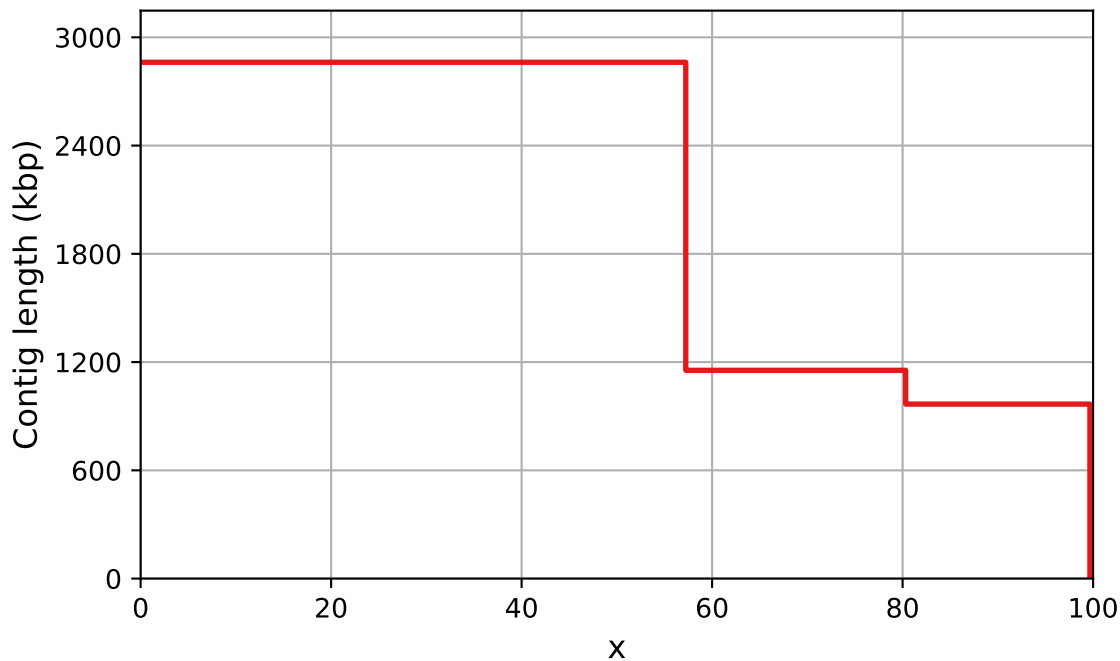
## Unaligned report

	sim5M.MinIH.p2
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

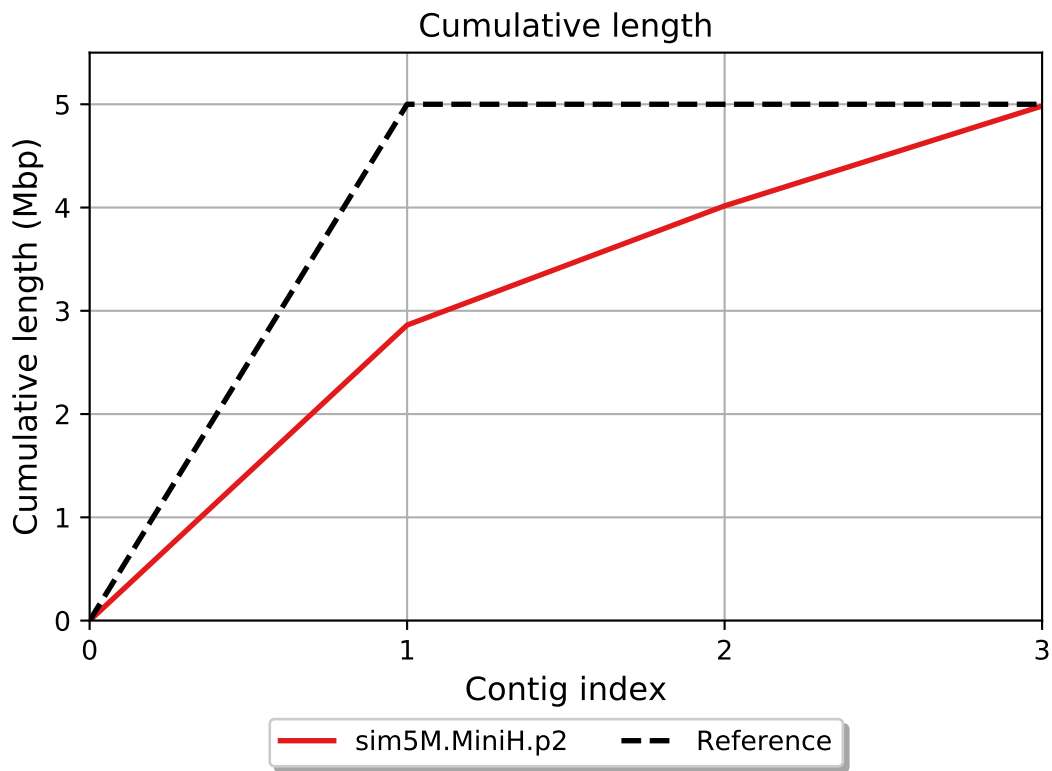
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



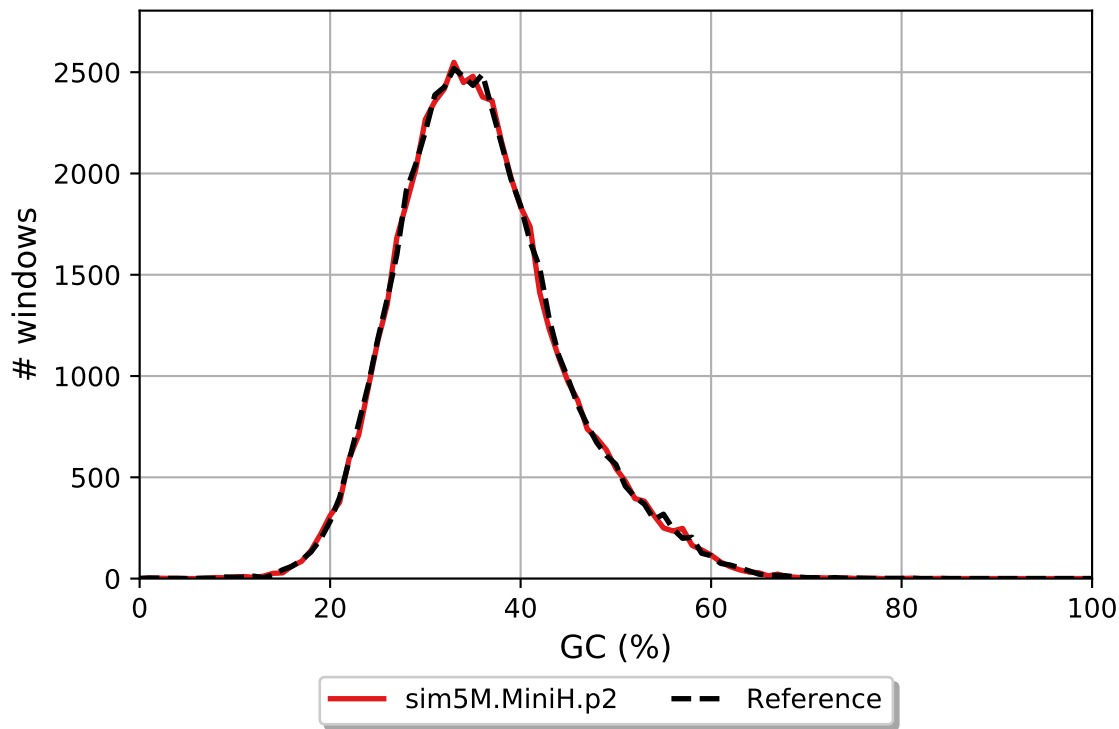
NGx



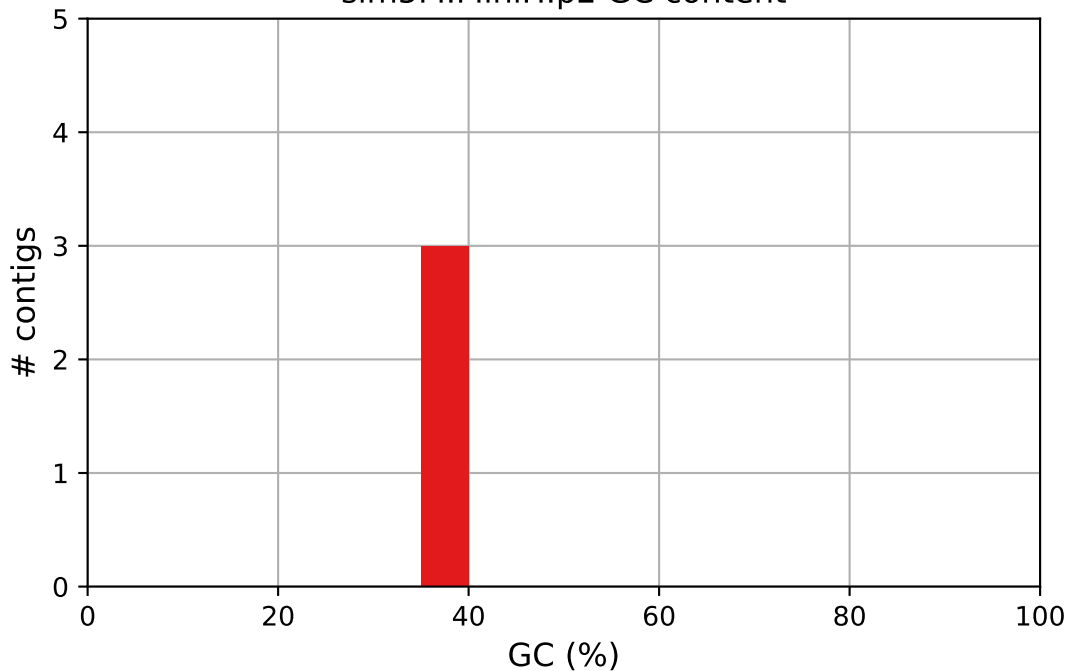
— sim5M.MiniH.p2



## GC content



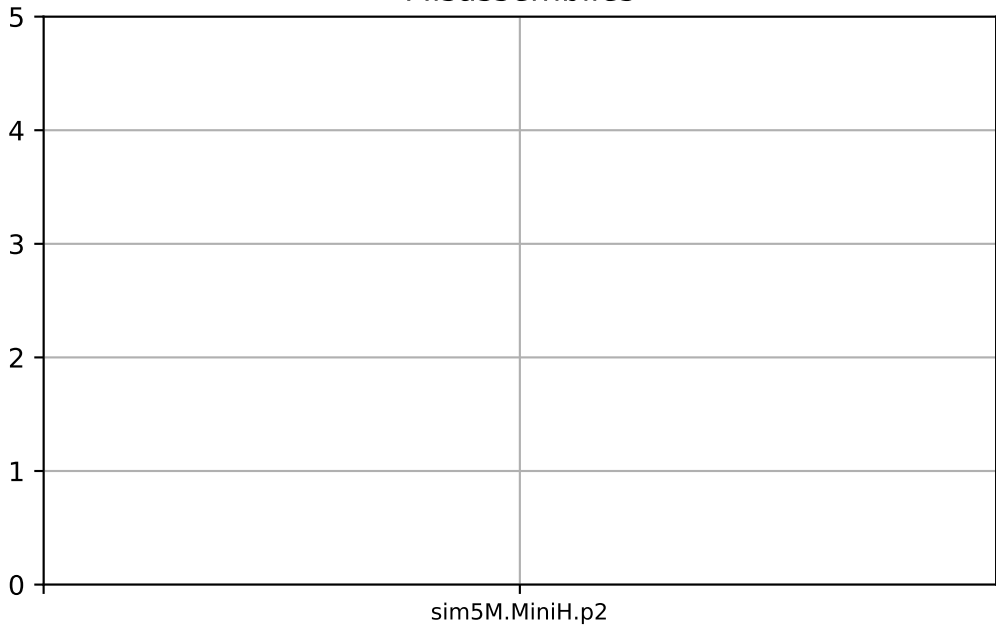
sim5M.MiniH.p2 GC content



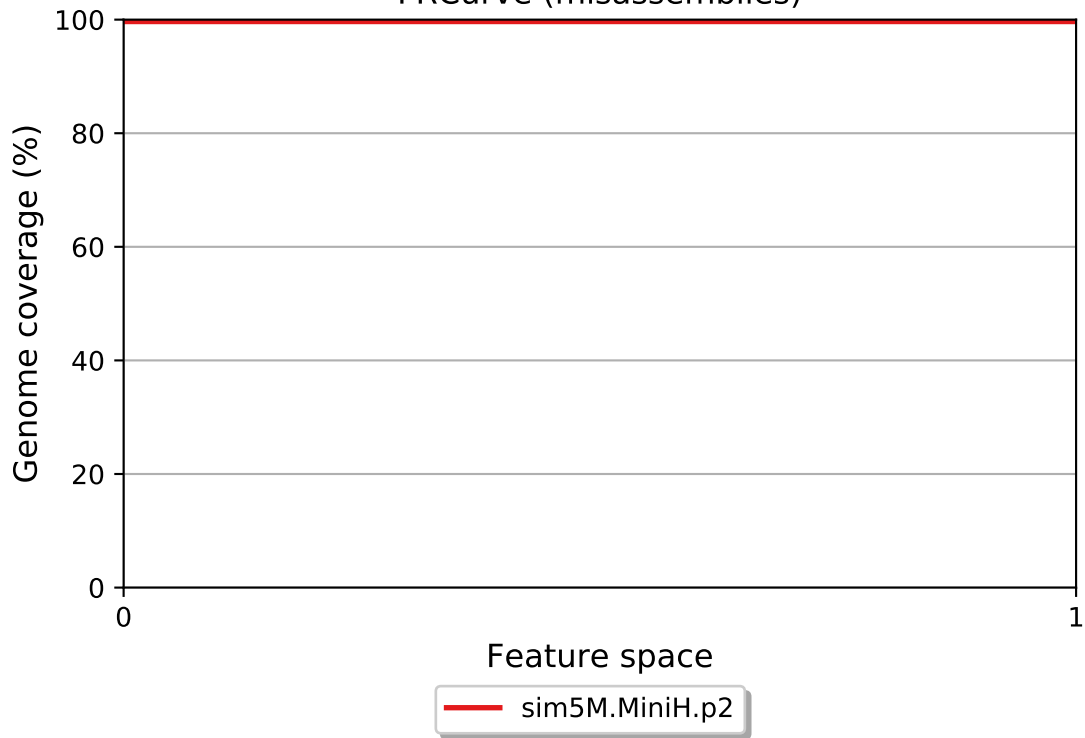
sim5M.MiniH.p2



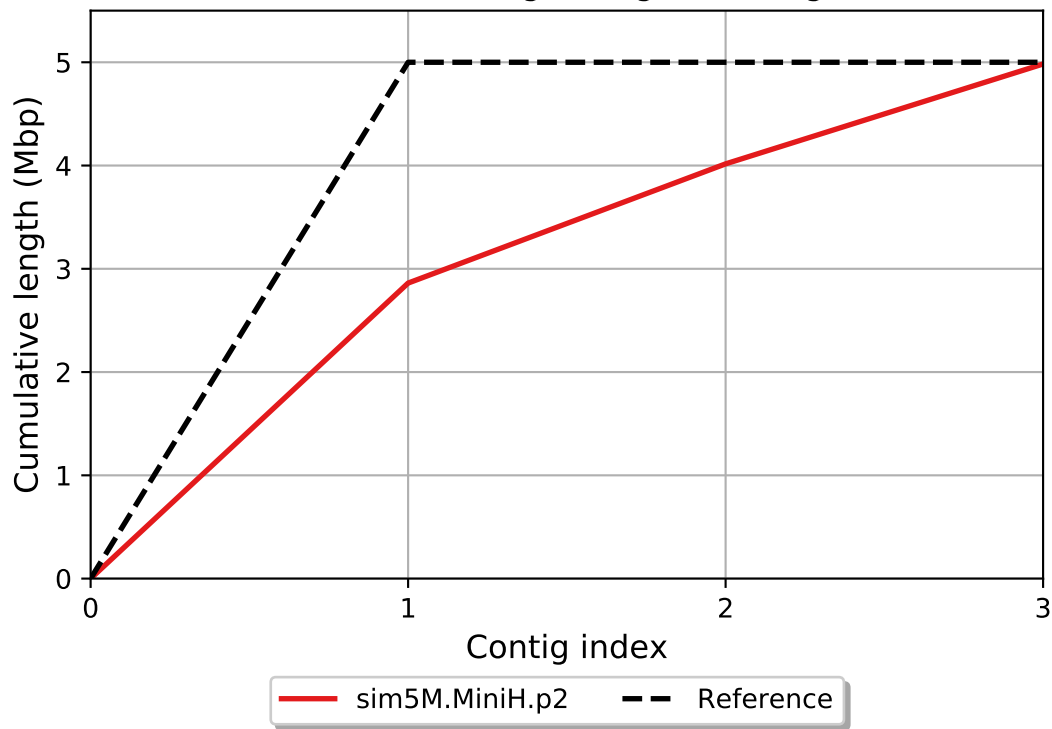
## Misassemblies



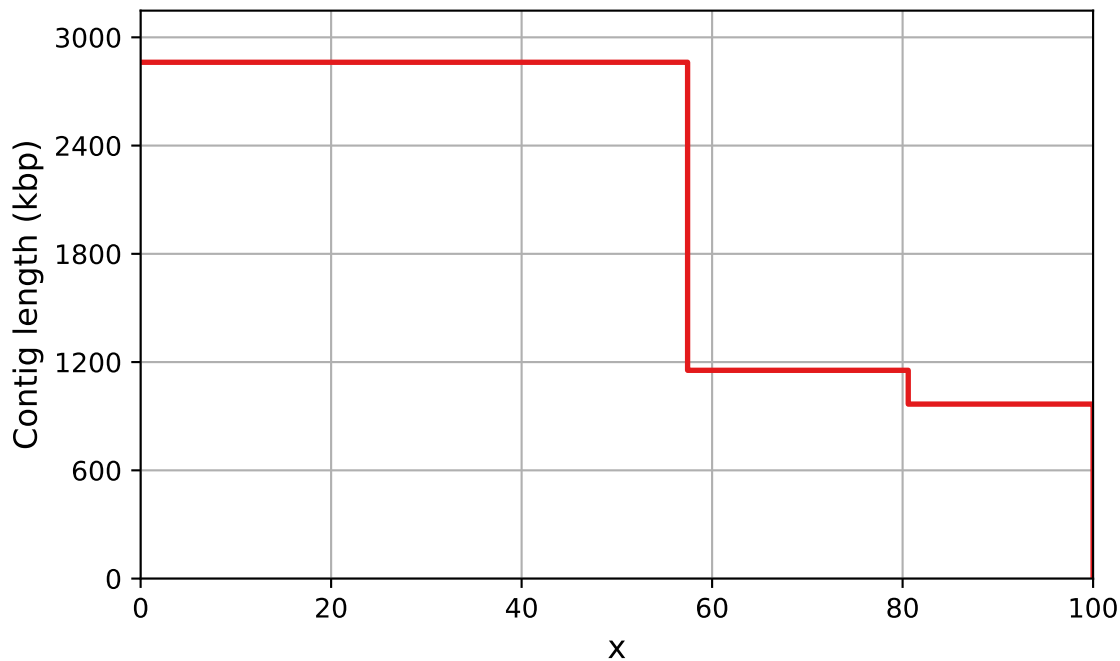
FRCurve (misassemblies)



Cumulative length (aligned contigs)

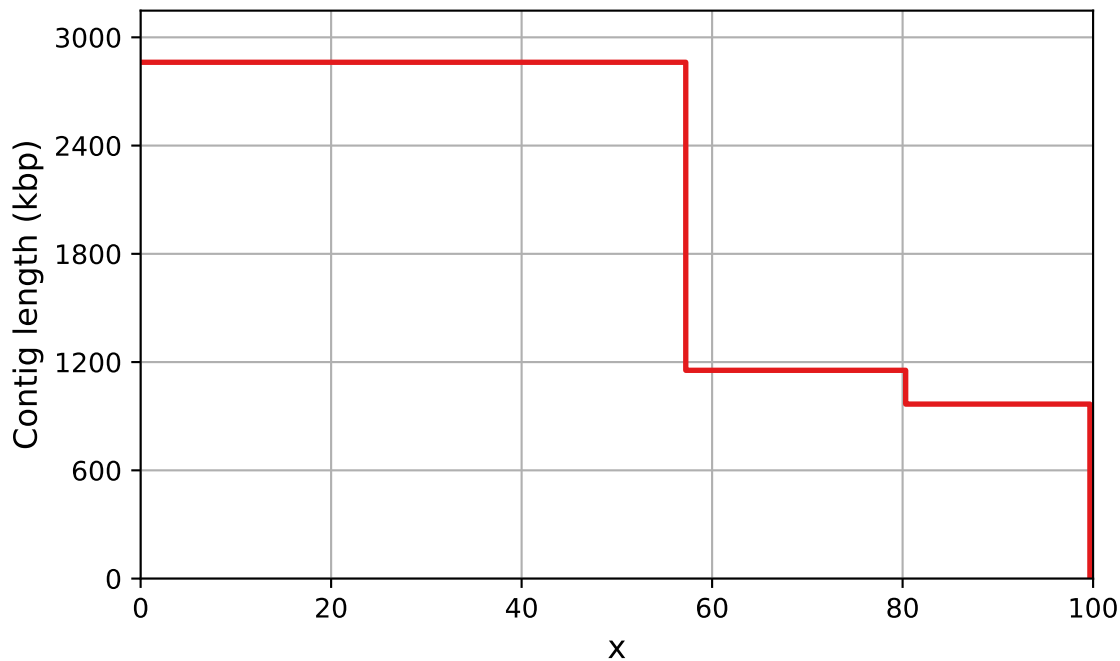


NAx



— sim5M.MiniH.p2

# NGAx



— sim5M.MiniH.p2