

# Report

	sim25M.MiniH.p3
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	11
Total length (>= 0 bp)	25027776
Total length (>= 1000 bp)	25027776
Total length (>= 5000 bp)	25027776
Total length (>= 10000 bp)	25027776
Total length (>= 25000 bp)	25010223
Total length (>= 50000 bp)	24969673
# contigs	13
Largest contig	7646992
Total length	25027776
Reference length	25000020
GC (%)	43.71
Reference GC (%)	43.69
N50	7117838
NG50	7117838
N75	1752972
NG75	1752972
L50	2
LG50	2
L75	4
LG75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	1078
Genome fraction (%)	99.790
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.72
# indels per 100 kbp	7.20
Largest alignment	7645271
Total aligned length	25022685
NA50	7117835
NGA50	7117835
NA75	1752971
NGA75	1752971
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

	sim25M.MiniH.p3
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	428
# indels	1796
# indels ( $\leq 5$ bp)	1795
# indels ( $> 5$ bp)	1
Indels length	2163

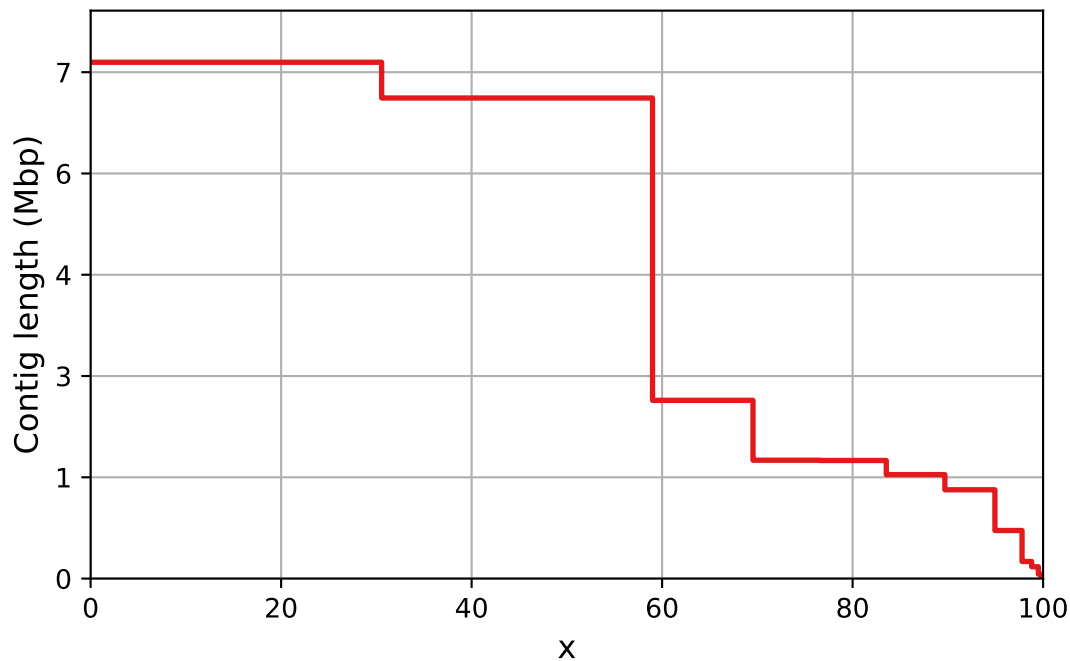
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	sim25M.MiniH.p3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	1078
# N's	0

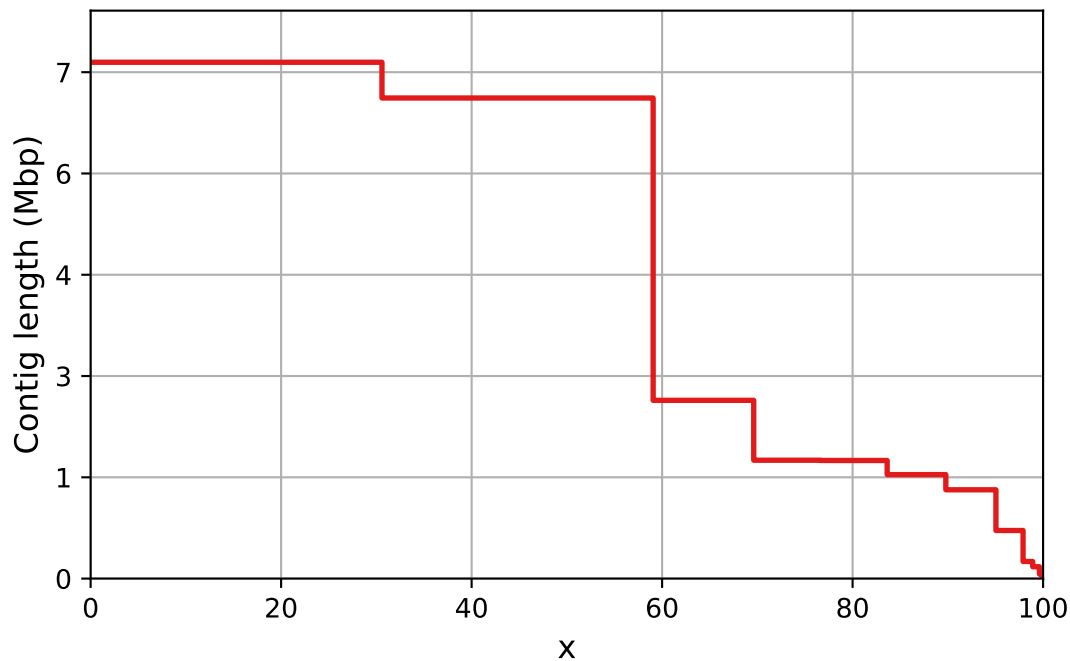
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



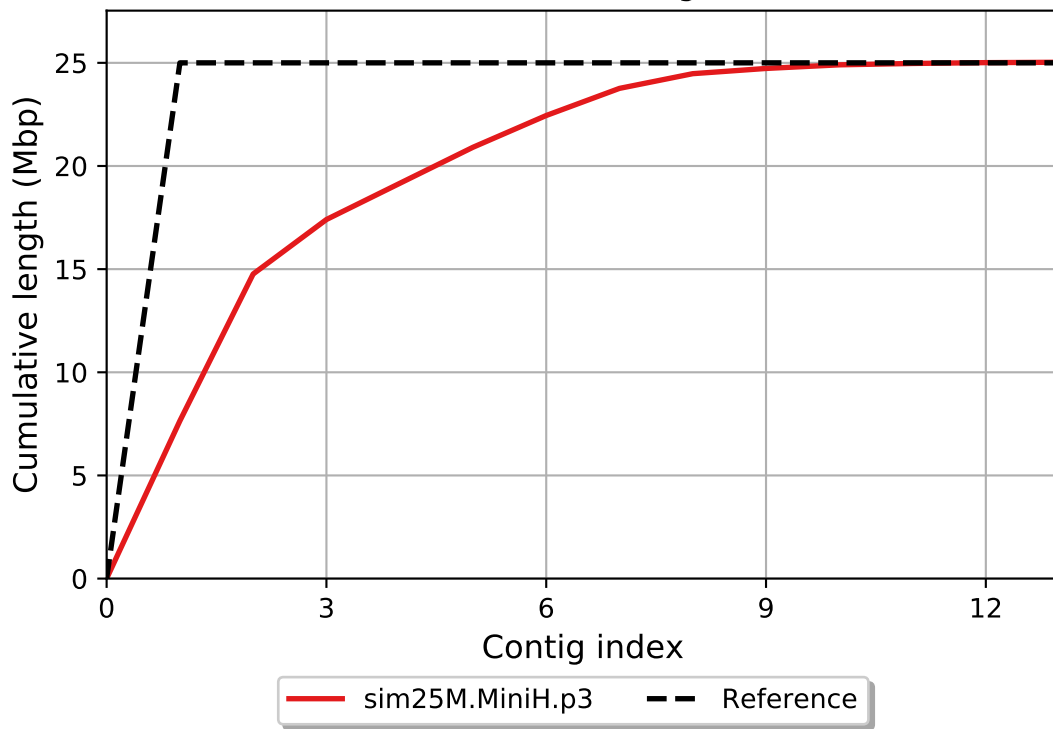
— sim25M.MiniH.p3

NGx

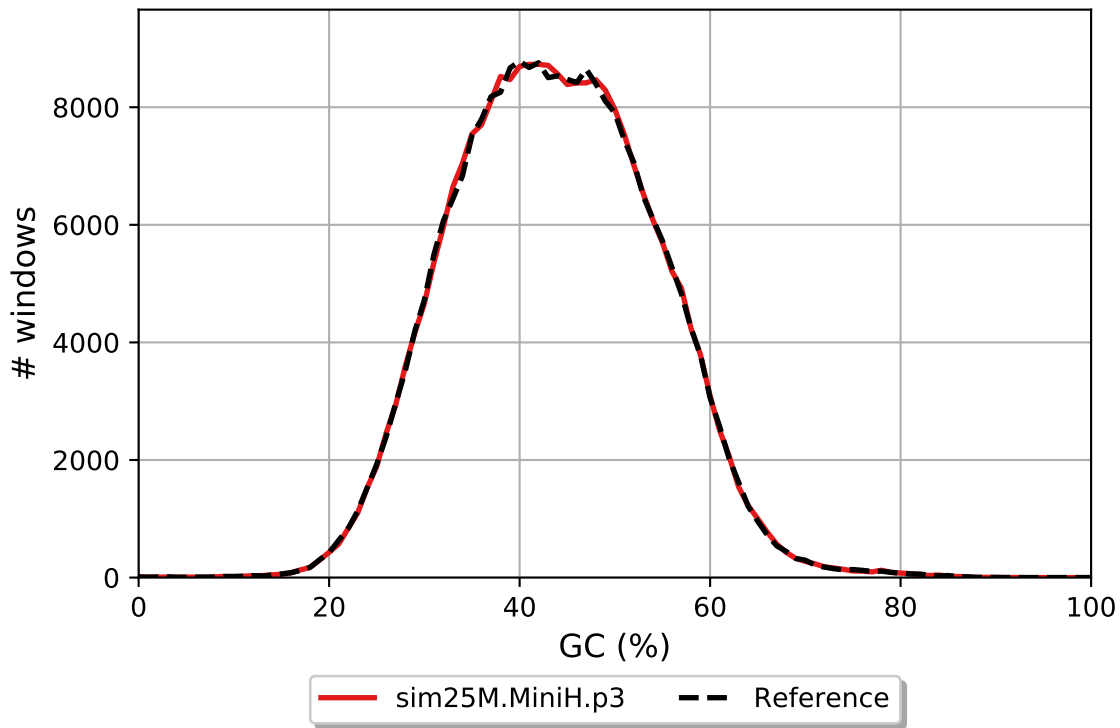


— sim25M.MiniH.p3

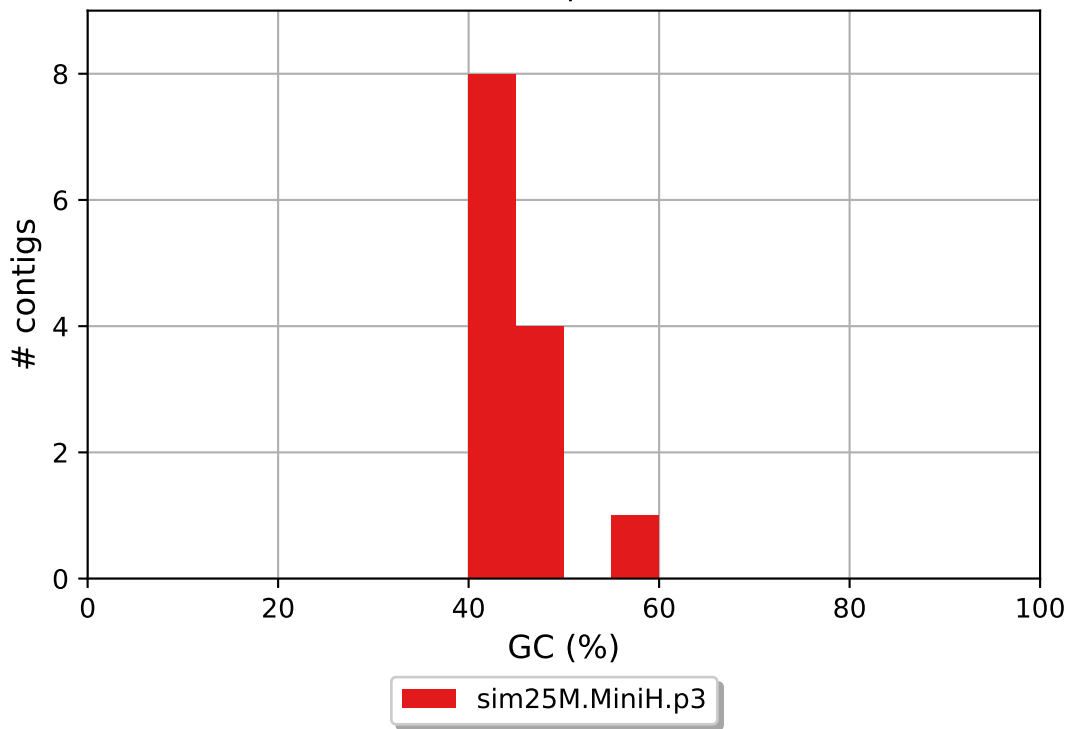
Cumulative length



## GC content

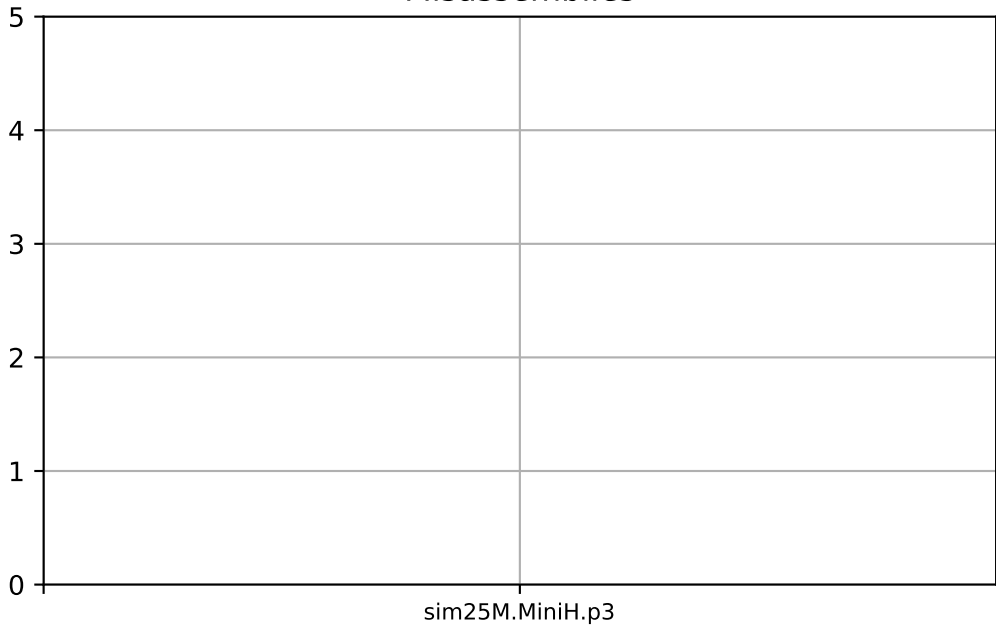


sim25M.MiniH.p3 GC content

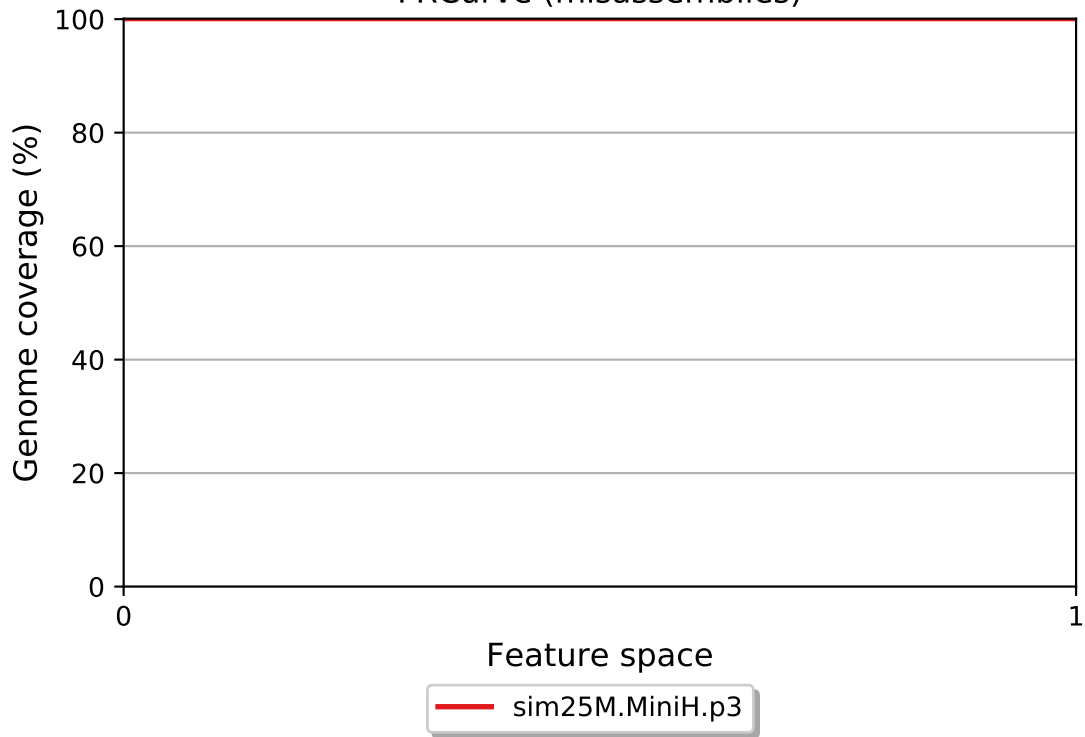




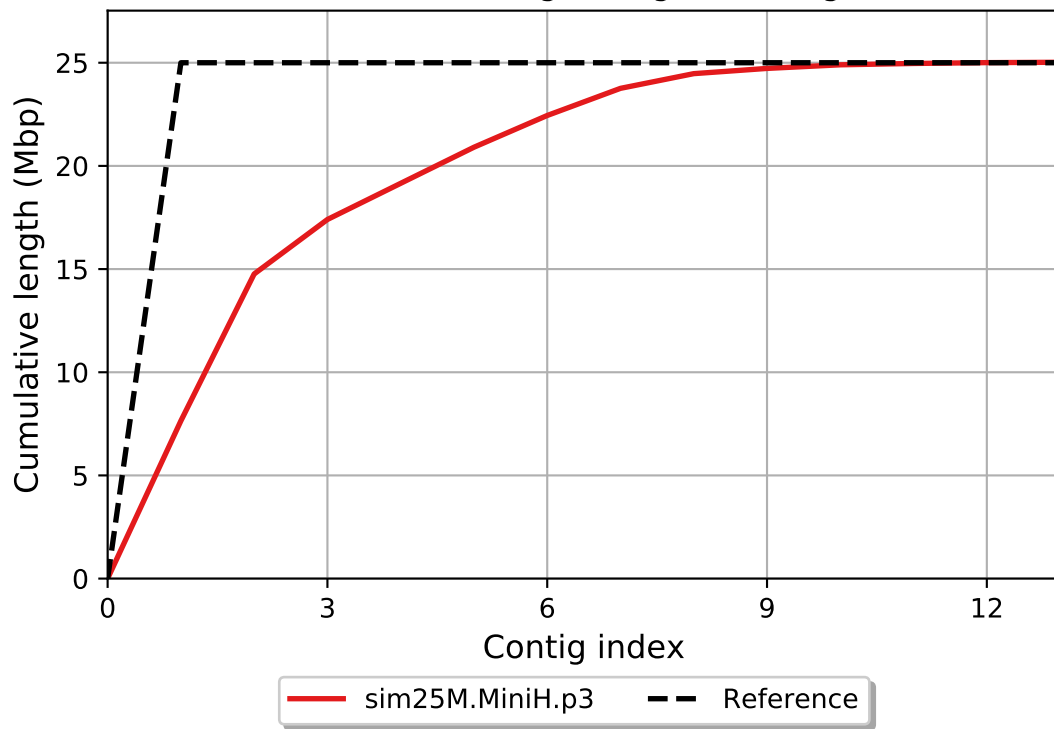
## Misassemblies



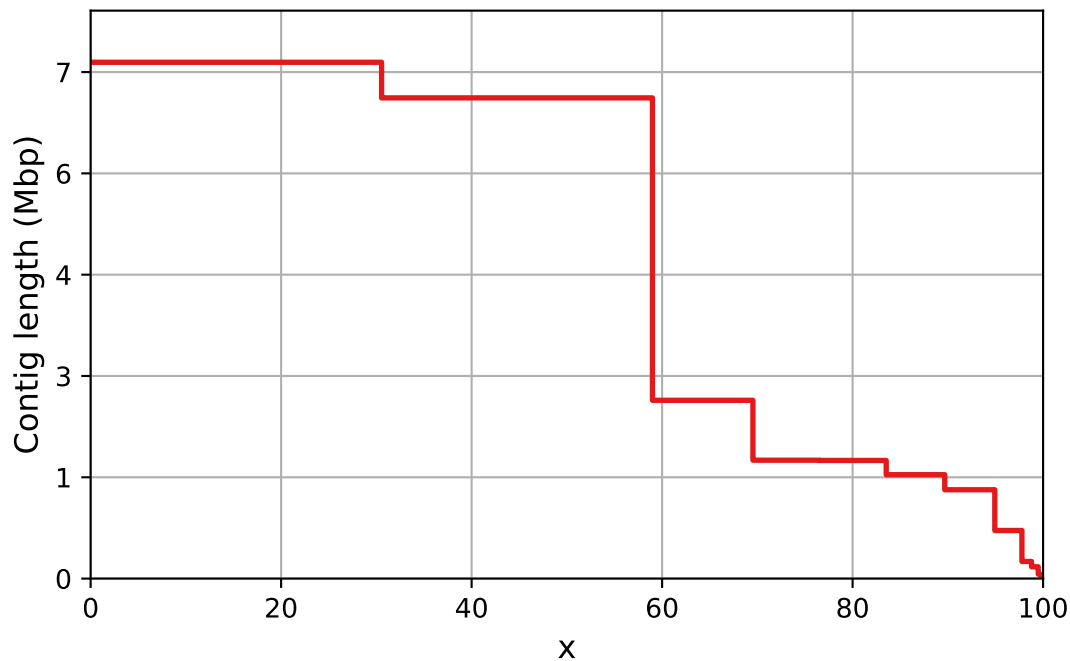
FRCurve (misassemblies)



Cumulative length (aligned contigs)

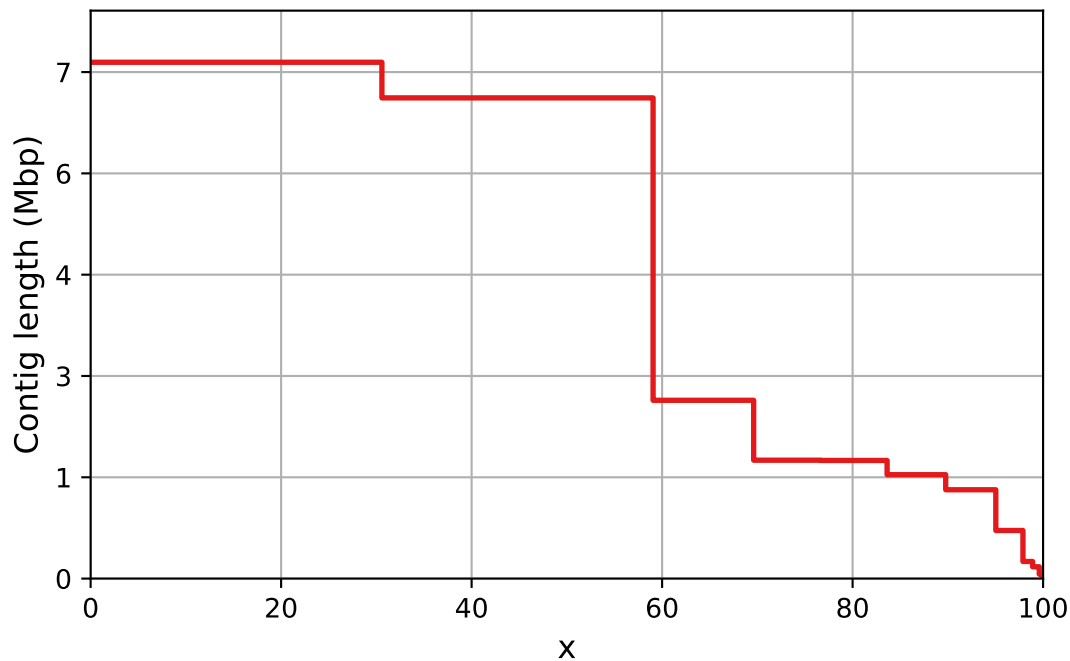


NAx



— sim25M.MinIH.p3

# NGAx



— sim25M.MinIH.p3