

Report

	sim5M.MiniL
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	8
# contigs (>= 50000 bp)	8
Total length (>= 0 bp)	4969802
Total length (>= 1000 bp)	4969802
Total length (>= 5000 bp)	4969802
Total length (>= 10000 bp)	4969802
Total length (>= 25000 bp)	4969802
Total length (>= 50000 bp)	4969802
# contigs	8
Largest contig	2070178
Total length	4969802
Reference length	5000040
GC (%)	35.83
Reference GC (%)	35.84
N50	874118
NG50	874118
N75	427859
NG75	427859
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 + 0 part
Unaligned length	0
Genome fraction (%)	98.649
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.64
# indels per 100 kbp	207.08
Largest alignment	2070177
Total aligned length	4969798
NA50	874118
NGA50	874118
NA75	427859
NGA75	427859
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

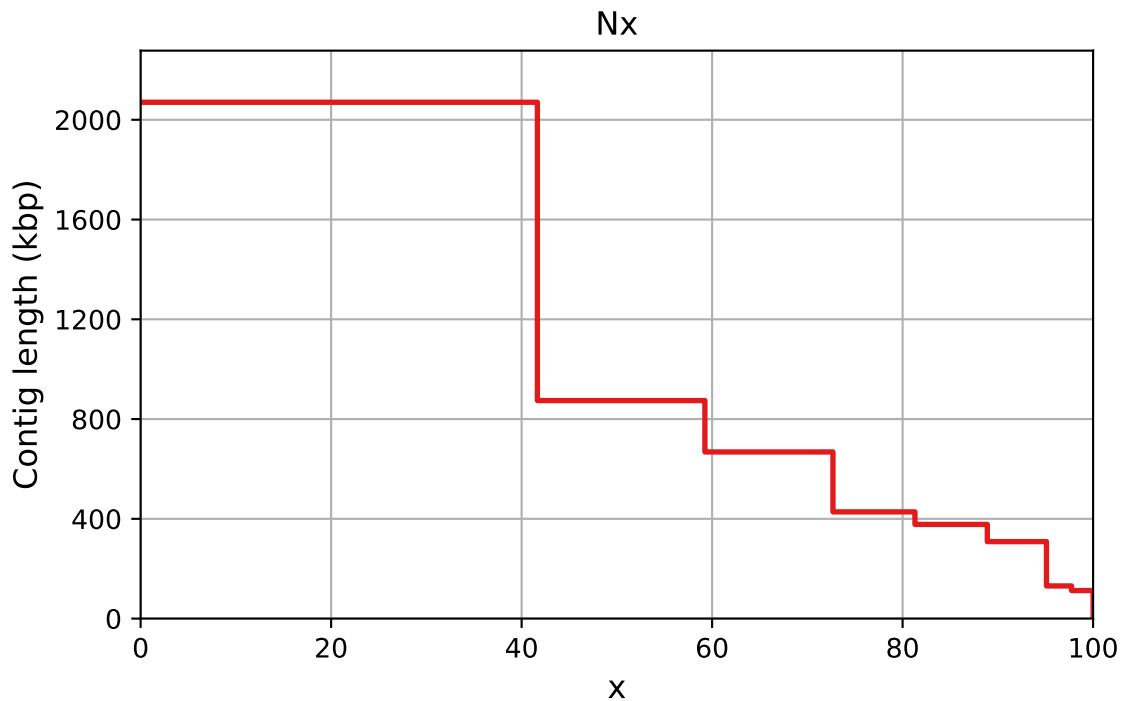
	sim5M.MinilL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	229
# indels	10214
# indels (≤ 5 bp)	10186
# indels (> 5 bp)	28
Indels length	13290

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

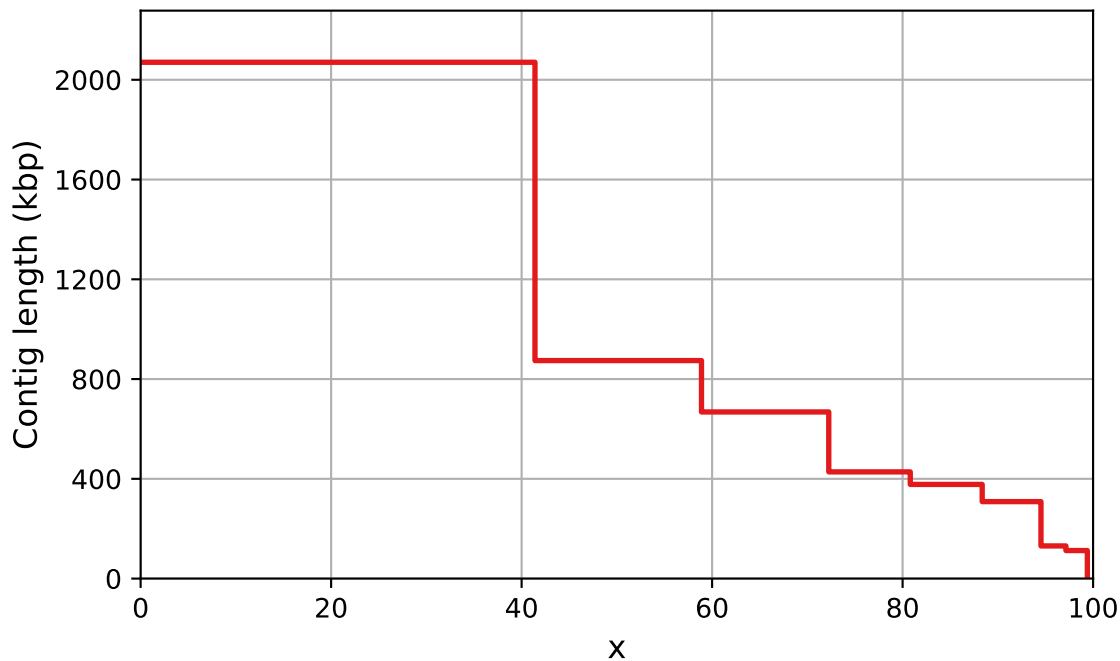
	sim5M.MiniL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).



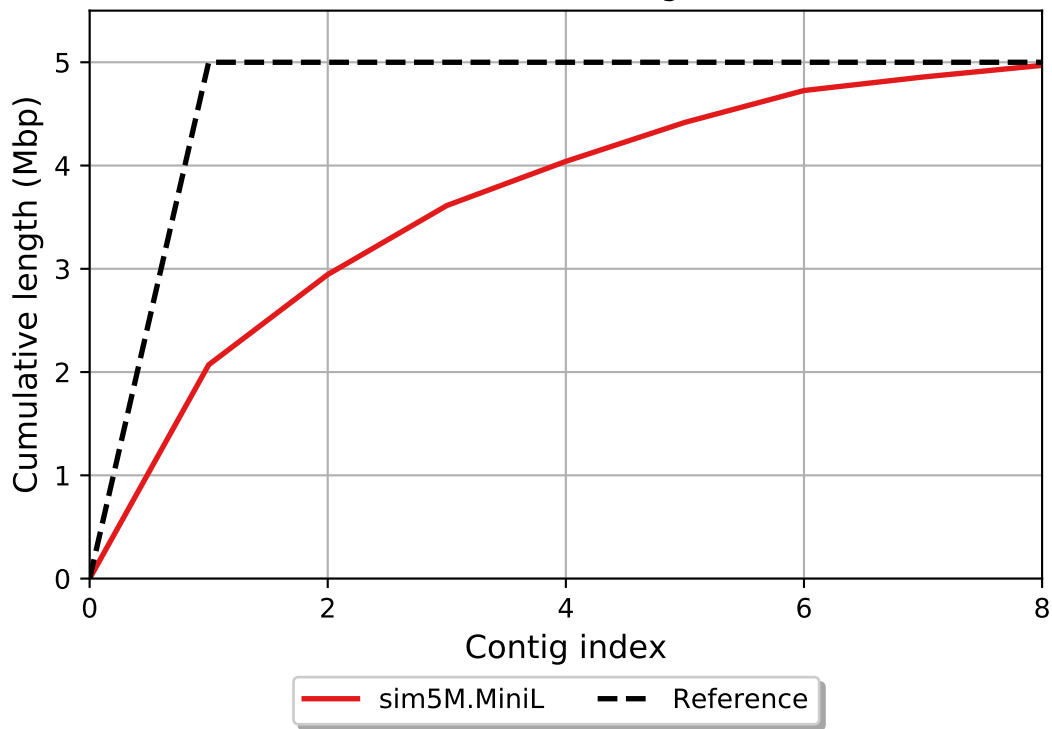
— sim5M.MiniL

NGx

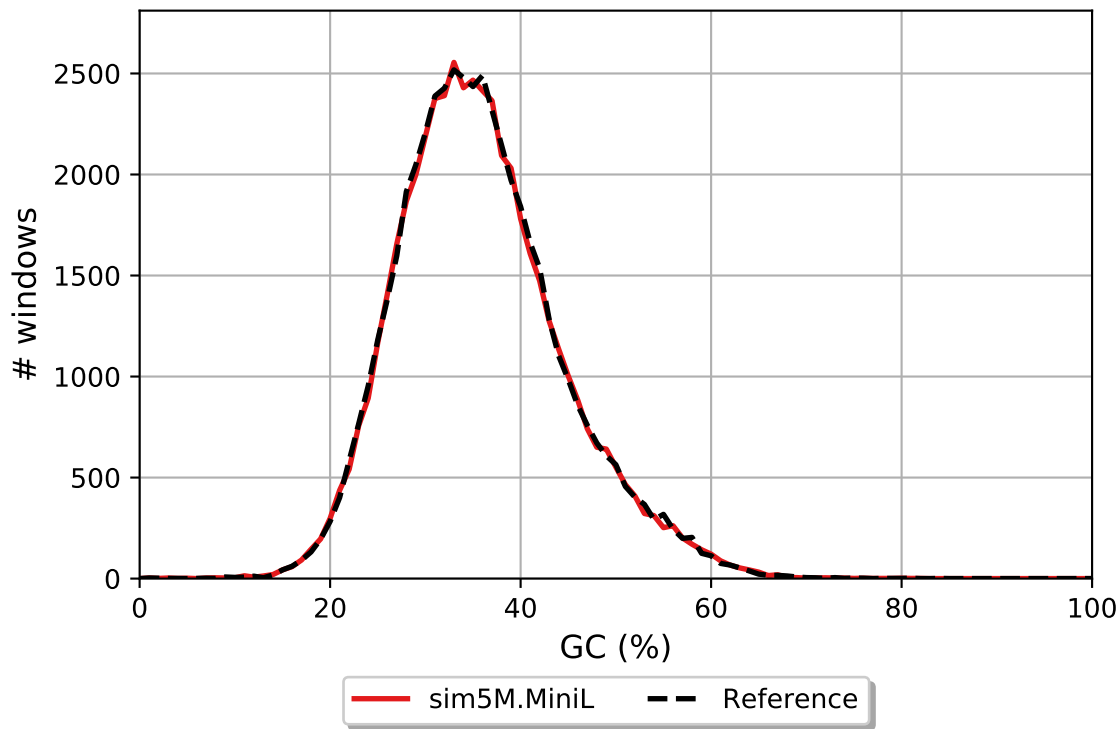


— sim5M.MiniL

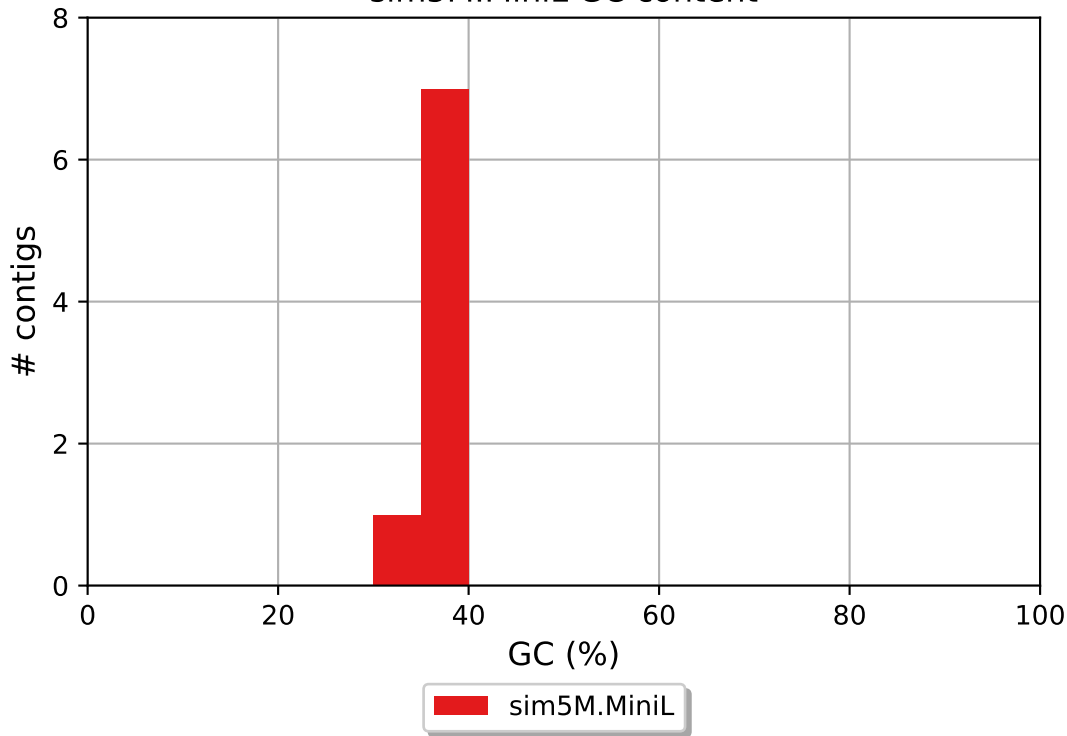
Cumulative length



GC content



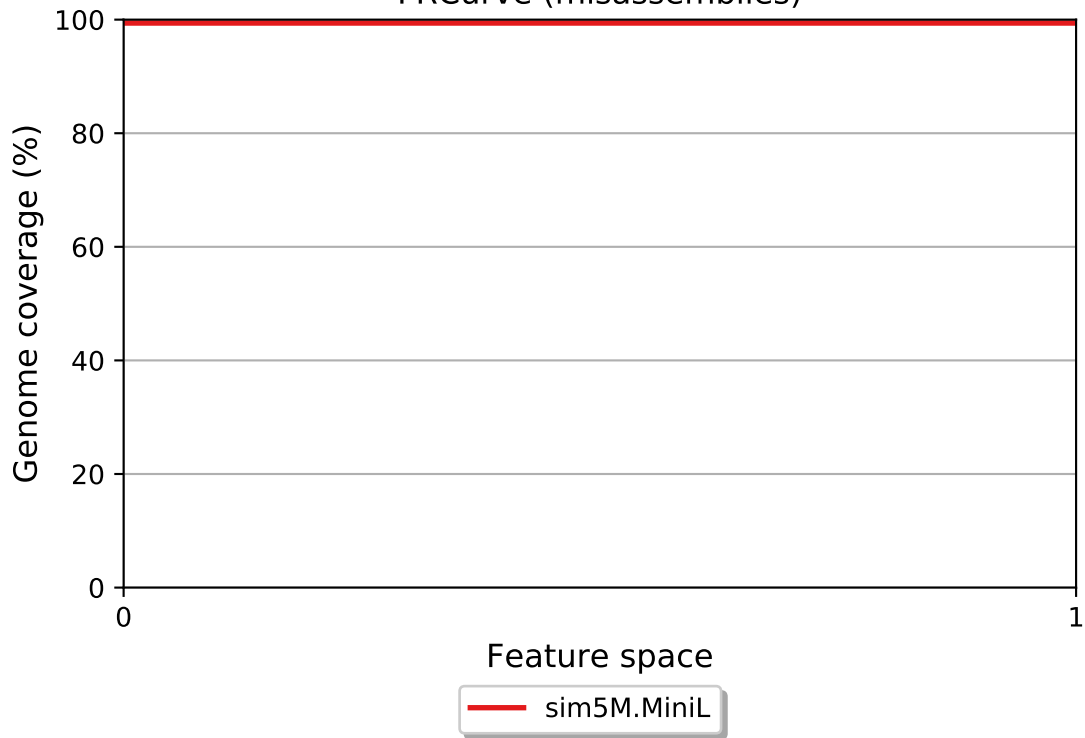
sim5M.MiniL GC content



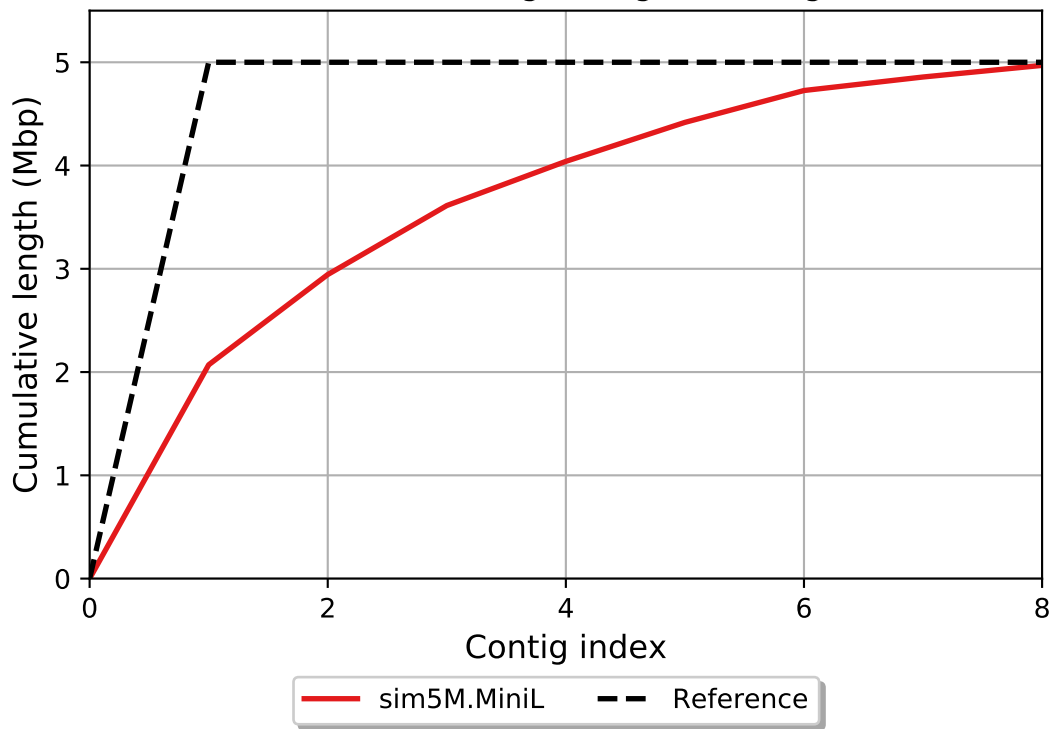
Misassemblies



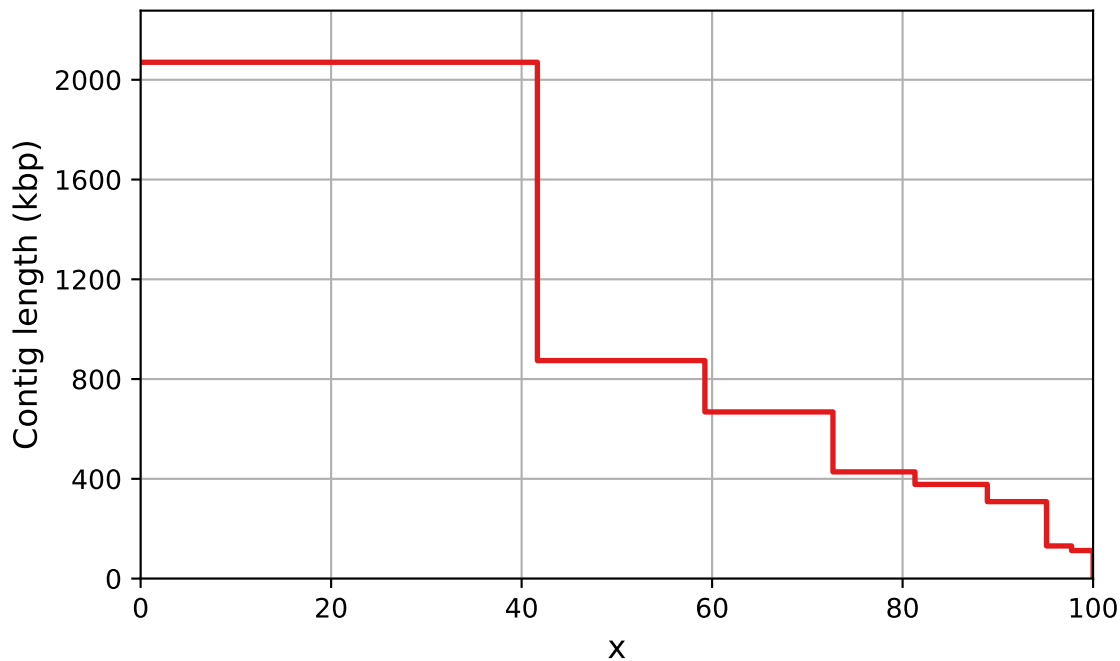
FRCurve (misassemblies)



Cumulative length (aligned contigs)

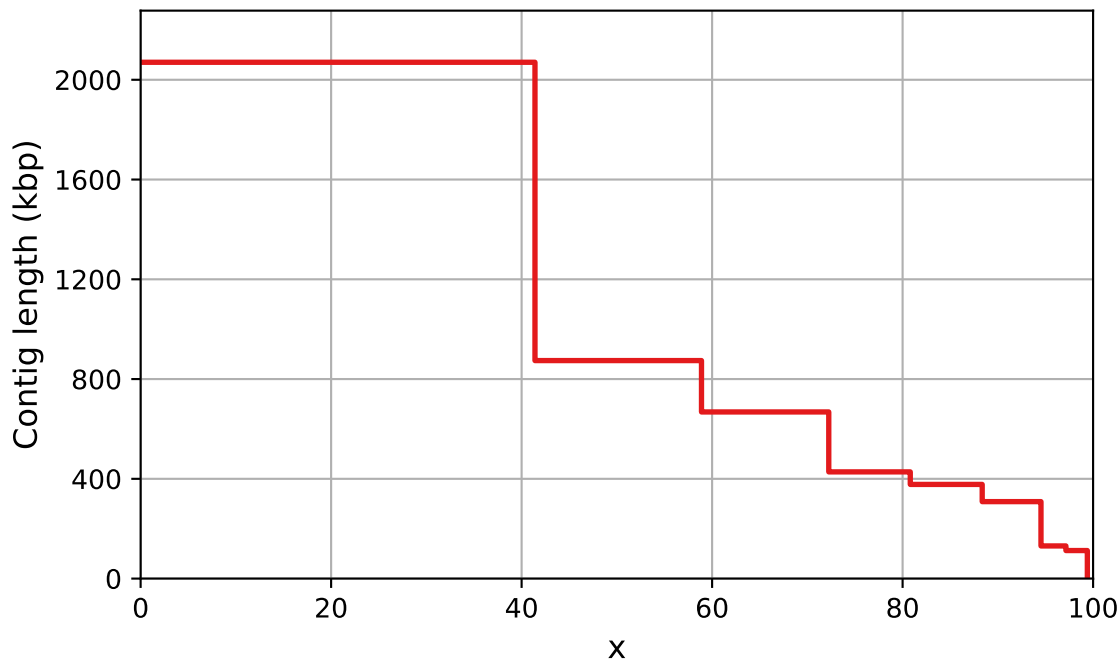


NAx



— sim5M.MiniL

NGAx



— sim5M.MiniL