

Report

	sim25M.MiniCH
# contigs (>= 0 bp)	23
# contigs (>= 1000 bp)	23
# contigs (>= 5000 bp)	23
# contigs (>= 10000 bp)	23
# contigs (>= 25000 bp)	22
# contigs (>= 50000 bp)	20
Total length (>= 0 bp)	25259994
Total length (>= 1000 bp)	25259994
Total length (>= 5000 bp)	25259994
Total length (>= 10000 bp)	25259994
Total length (>= 25000 bp)	25235600
Total length (>= 50000 bp)	25162144
# contigs	23
Largest contig	4487765
Total length	25259994
Reference length	25000020
GC (%)	43.69
Reference GC (%)	43.69
N50	2347005
NG50	2347005
N75	1189240
NG75	1588793
L50	4
LG50	4
L75	8
LG75	7
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	4532262
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.937
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.77
# indels per 100 kbp	166.48
Largest alignment	4236176
Total aligned length	25259712
NA50	2347005
NGA50	2347005
NA75	1189240
NGA75	1189240
LA50	4
LGA50	4
LA75	8
LGA75	8

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

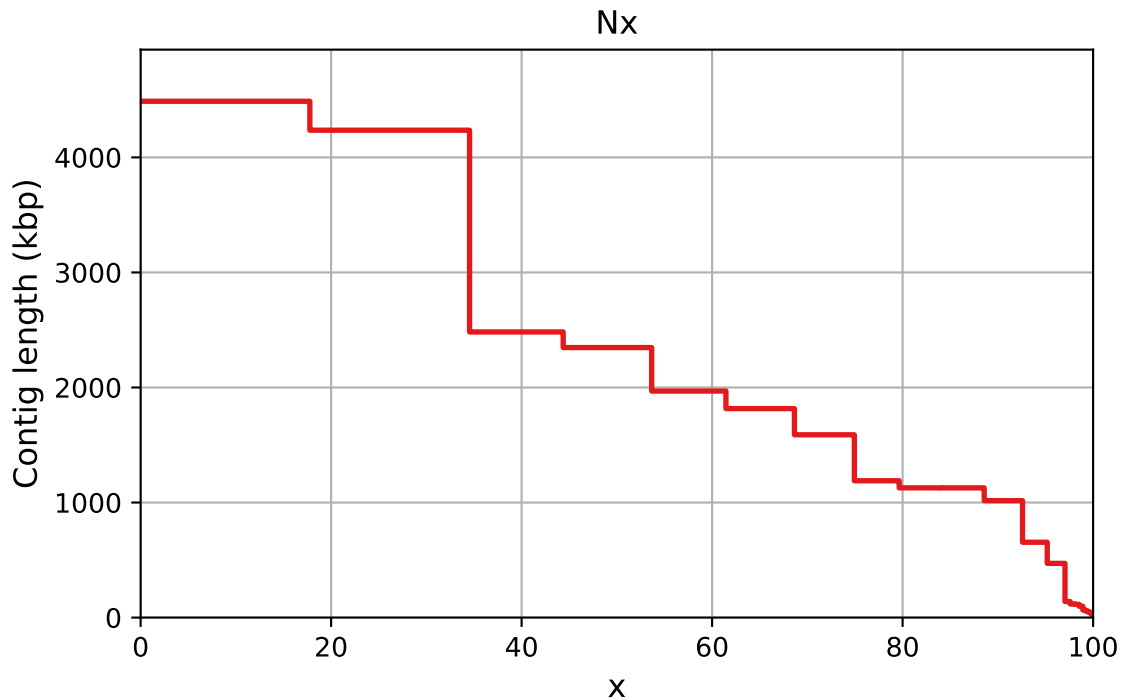
	sim25M.Minich
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	4532262
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	691
# indels	41594
# indels (≤ 5 bp)	41540
# indels (> 5 bp)	54
Indels length	60658

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

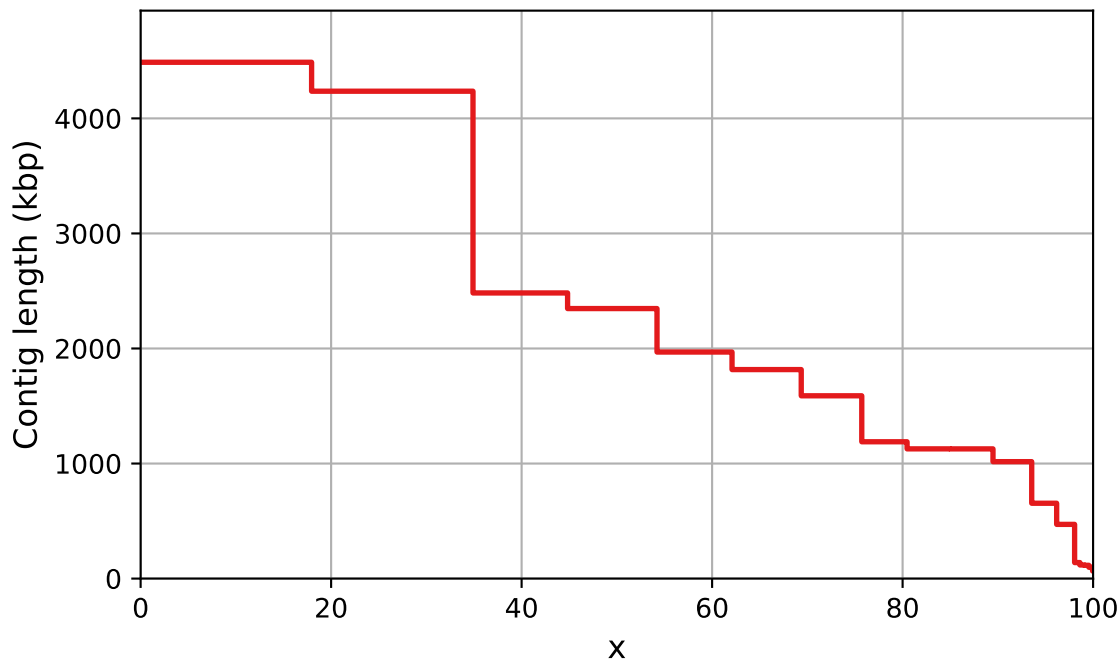
	sim25M.Minich
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).



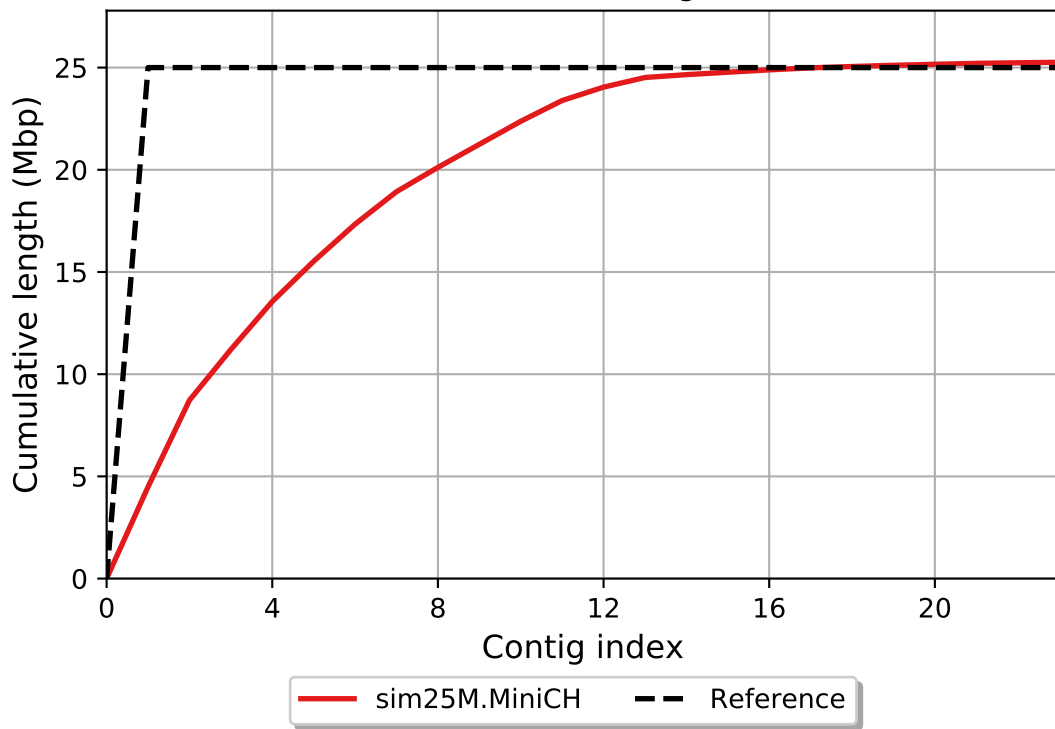
— sim25M.MiniCH

NGx

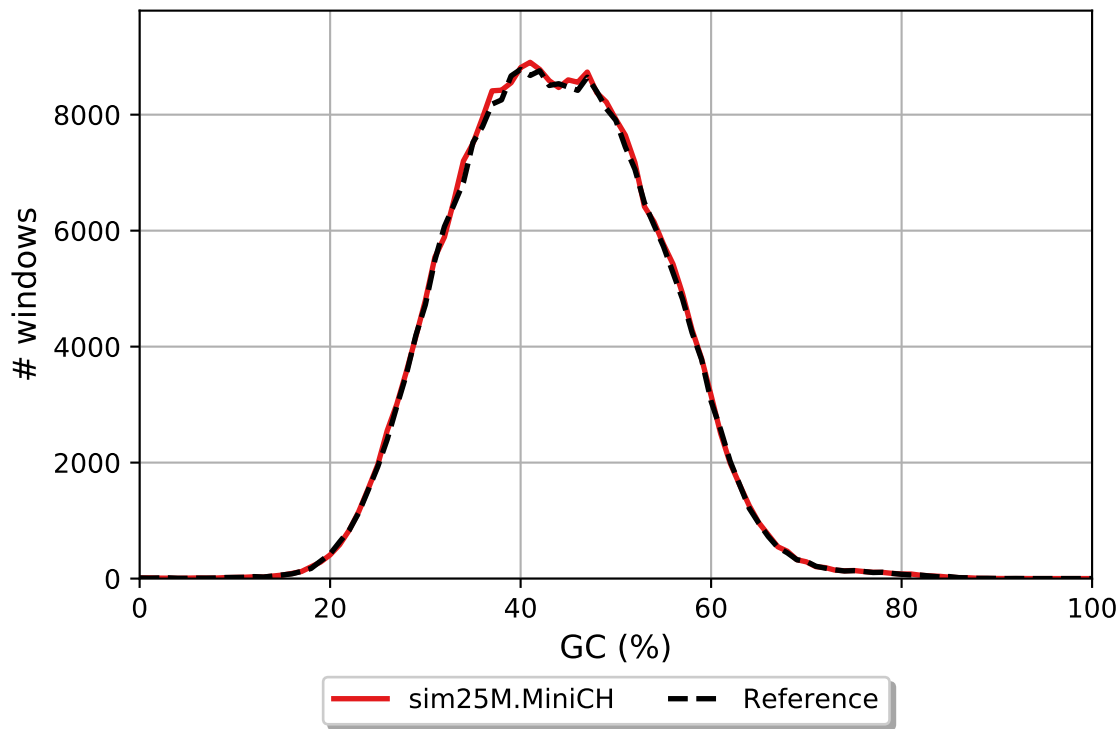


— sim25M.MiniCH

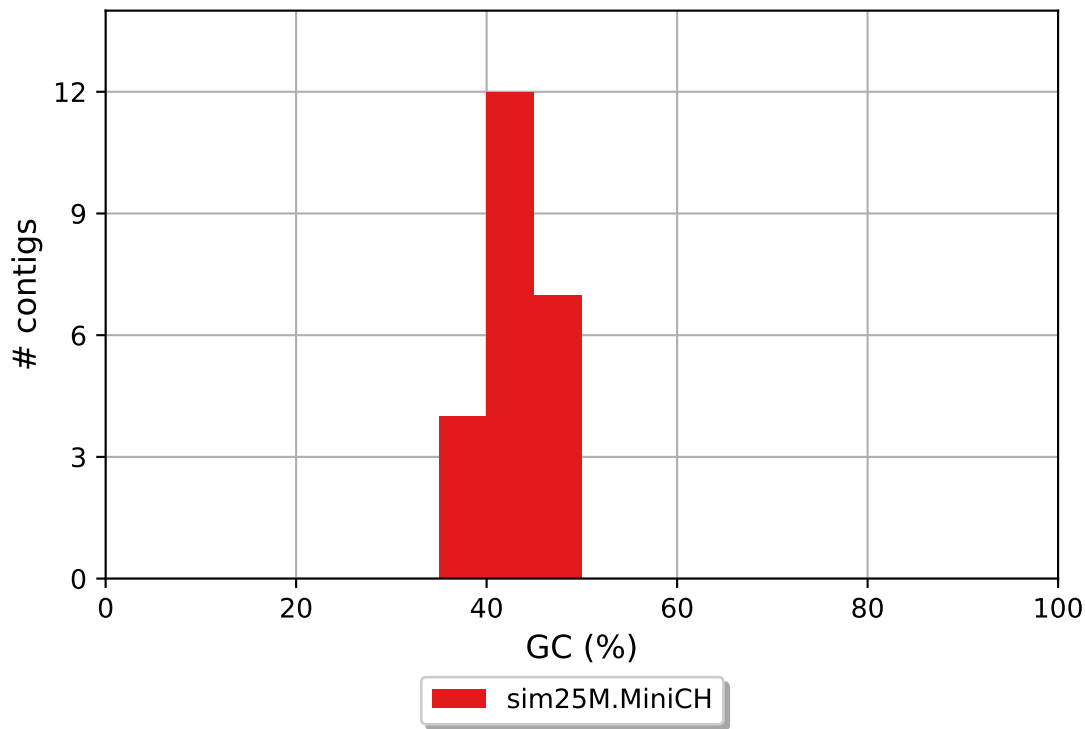
Cumulative length



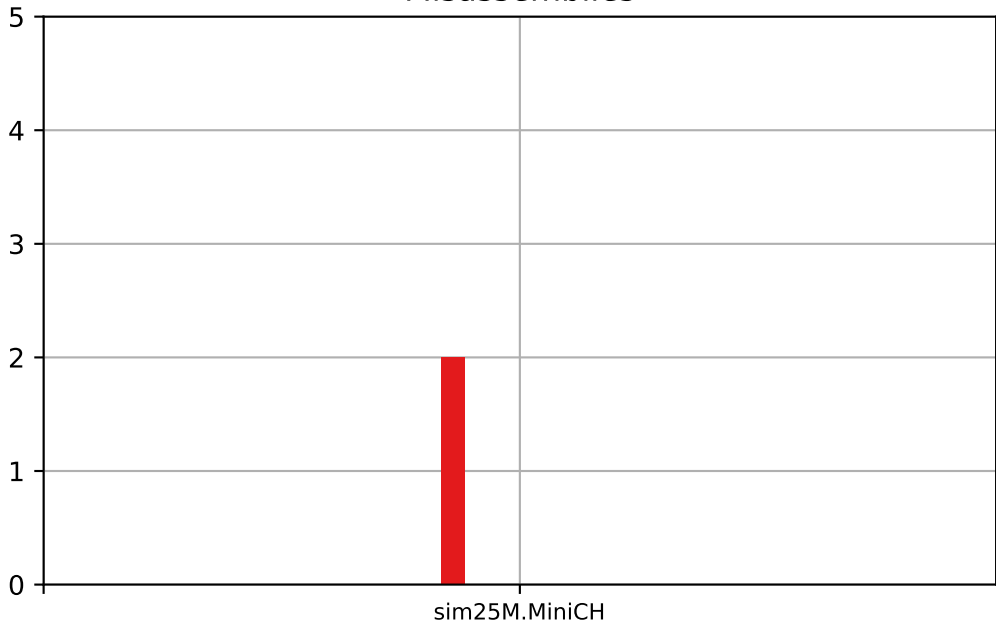
GC content



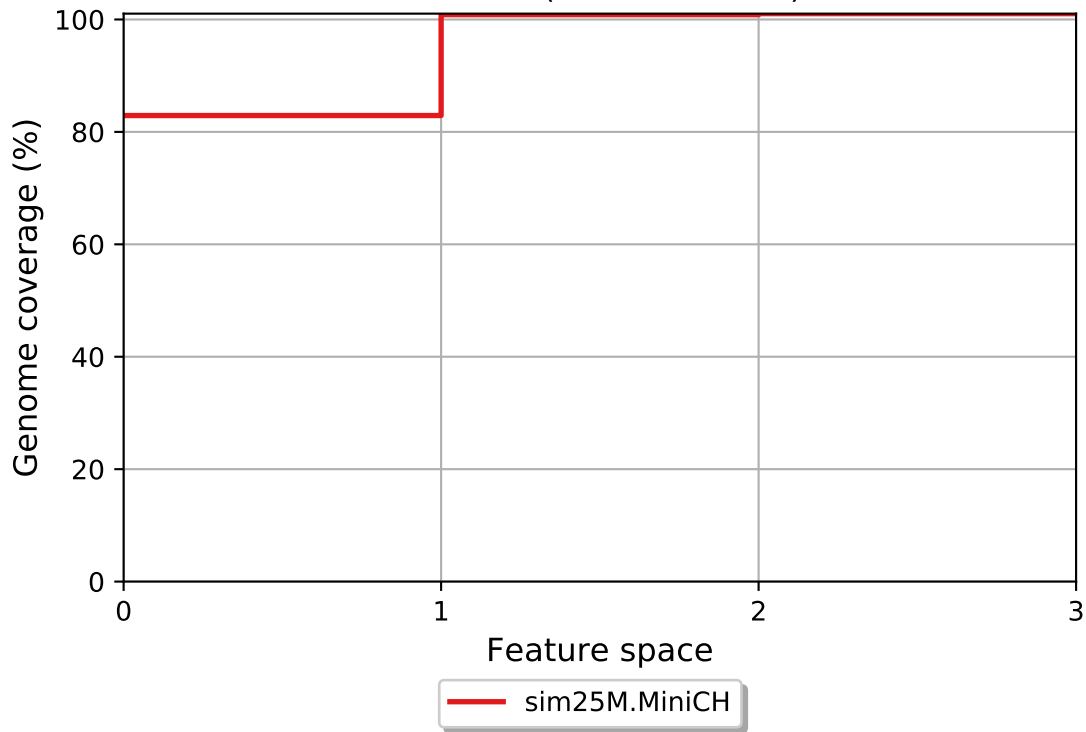
sim25M.Minich GC content



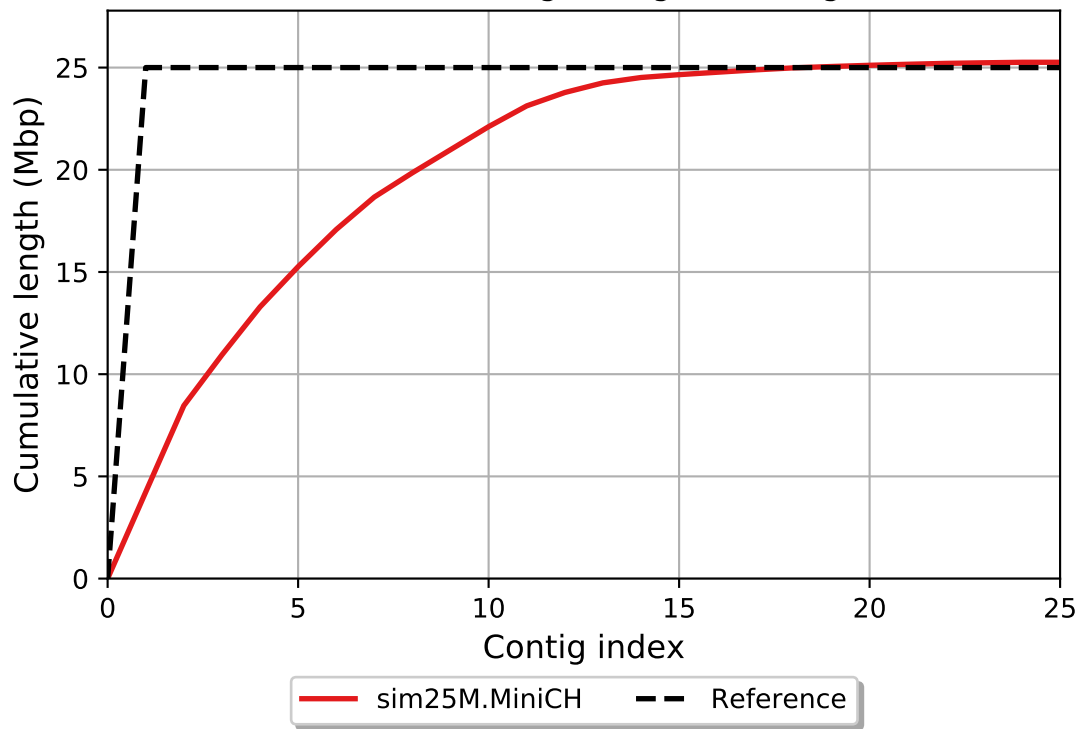
Misassemblies



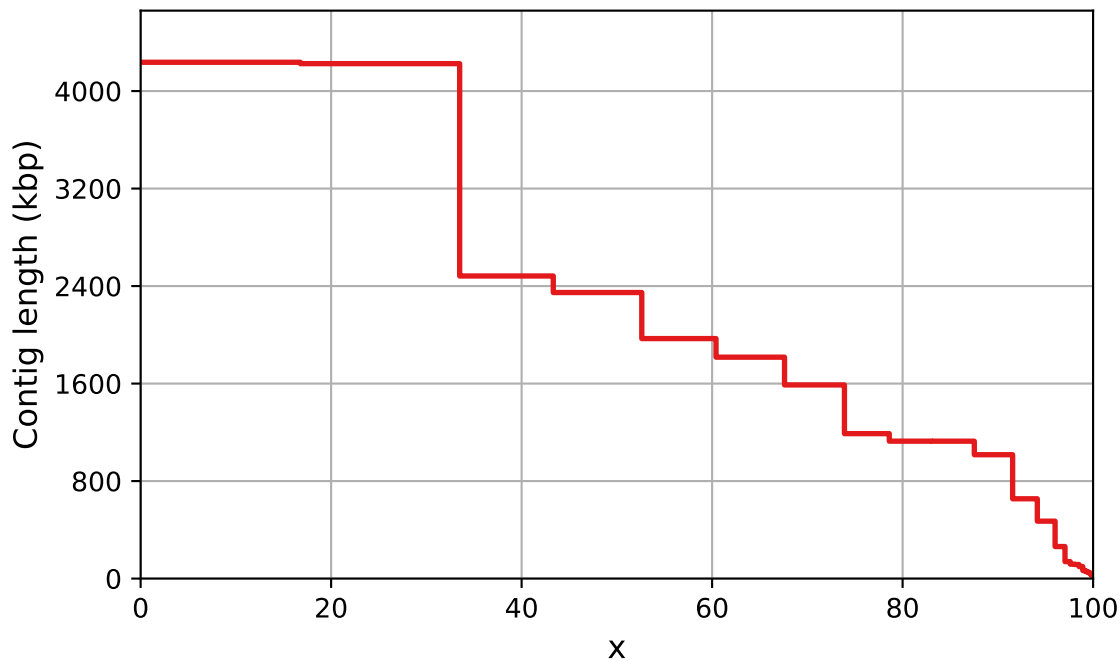
FRCurve (misassemblies)



Cumulative length (aligned contigs)

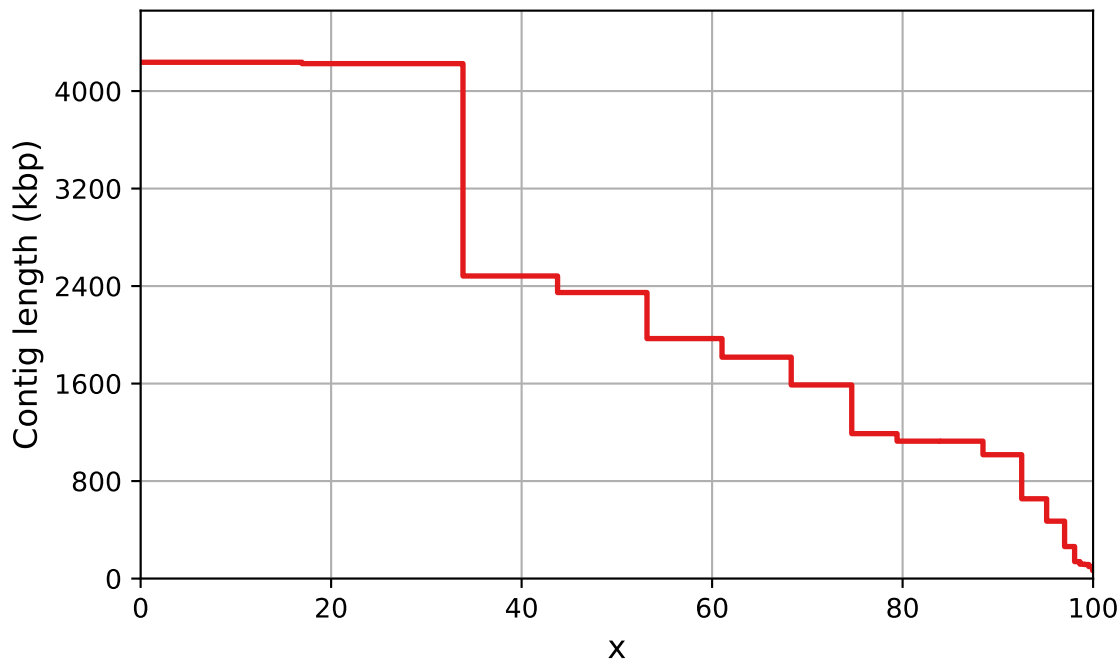


NAx



— sim25M.Minich

NGAx



— sim25M.MiniCH