

# Report

	sim25M.MiniCL
# contigs (>= 0 bp)	43
# contigs (>= 1000 bp)	43
# contigs (>= 5000 bp)	43
# contigs (>= 10000 bp)	42
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	39
Total length (>= 0 bp)	25176816
Total length (>= 1000 bp)	25176816
Total length (>= 5000 bp)	25176816
Total length (>= 10000 bp)	25168743
Total length (>= 25000 bp)	25147836
Total length (>= 50000 bp)	25053997
# contigs	43
Largest contig	2343337
Total length	25176816
Reference length	25000020
GC (%)	43.69
Reference GC (%)	43.69
N50	1073552
NG50	1073552
N75	761653
NG75	761653
L50	8
LG50	8
L75	15
LG75	15
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	76745
# local misassemblies	6
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.536
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.92
# indels per 100 kbp	198.90
Largest alignment	2343337
Total aligned length	25170834
NA50	1073551
NGA50	1073551
NA75	758216
NGA75	758216
LA50	8
LGA50	8
LA75	15
LGA75	15

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

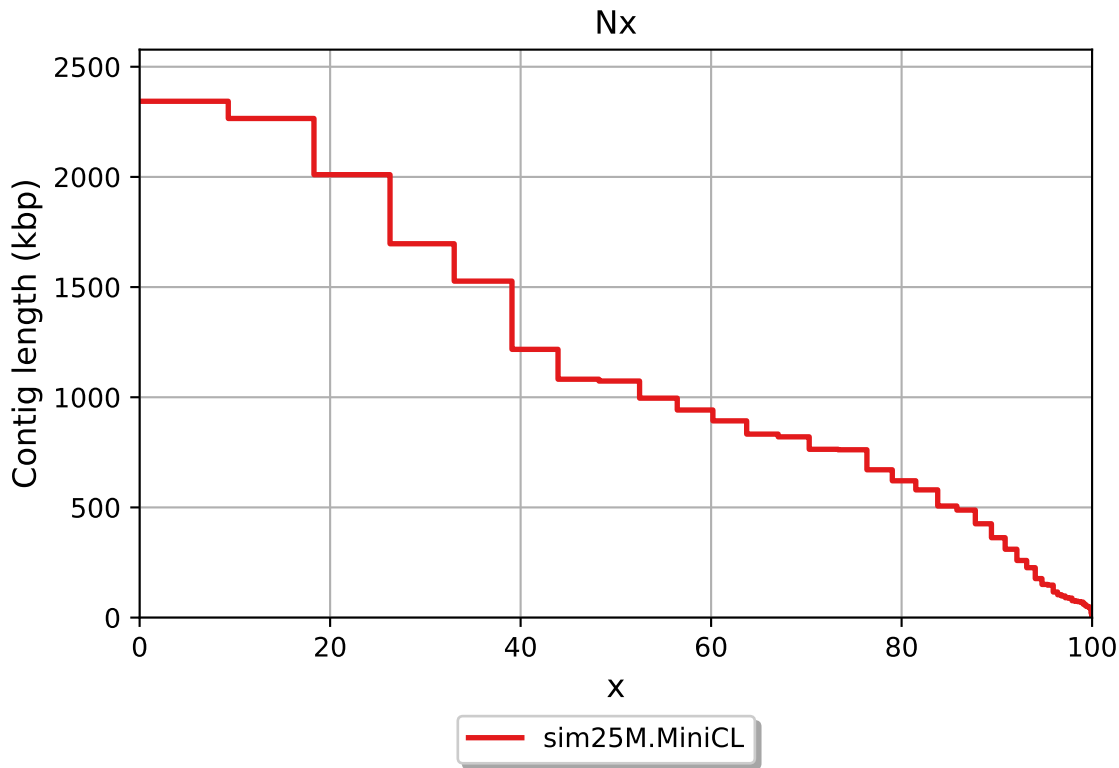
	sim25M.MinicL
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	76745
# local misassemblies	6
# unaligned mis. contigs	0
# mismatches	2219
# indels	49493
# indels ( $\leq 5$ bp)	49423
# indels ( $> 5$ bp)	70
Indels length	65636

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).

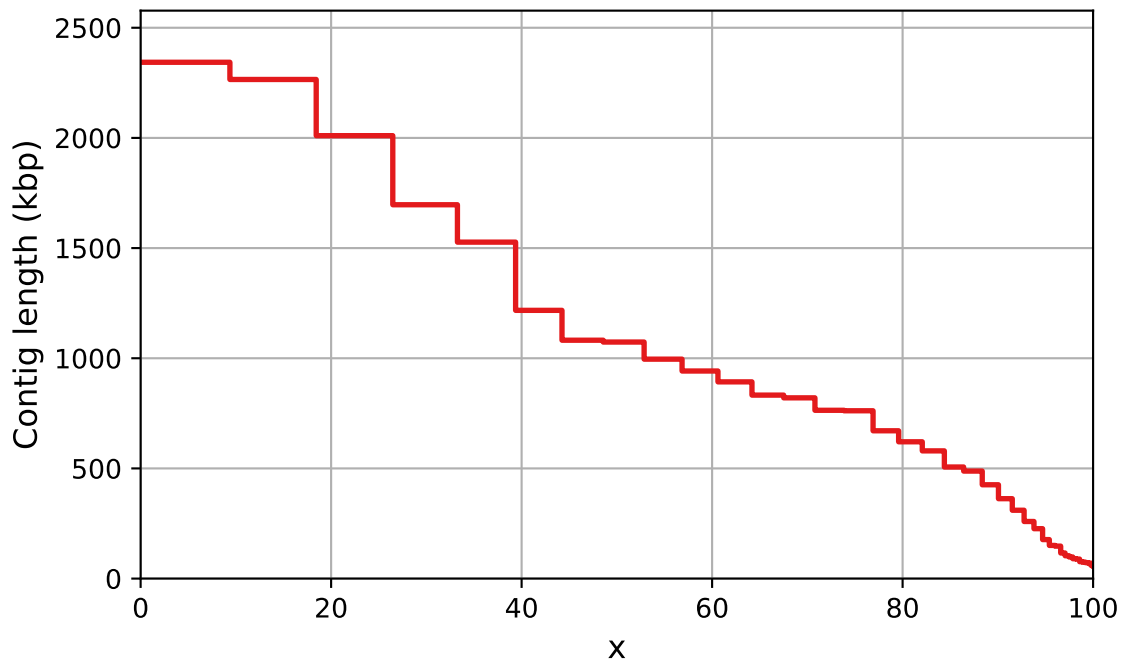
## Unaligned report

	sim25M.MinicL
# 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).

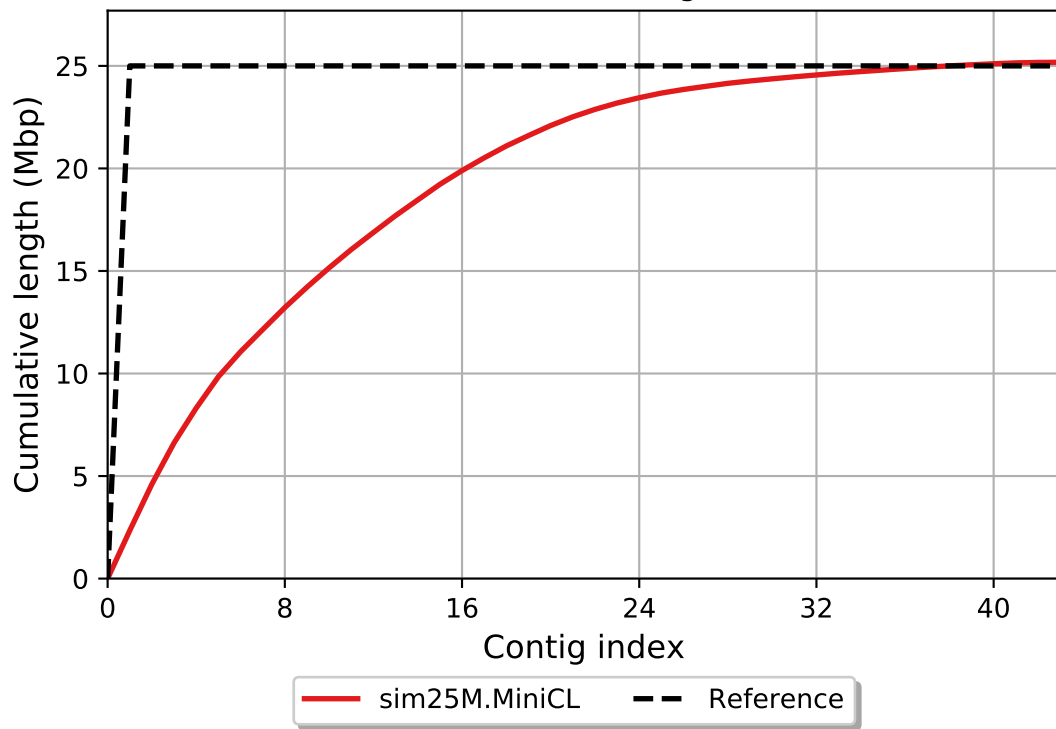


NGx

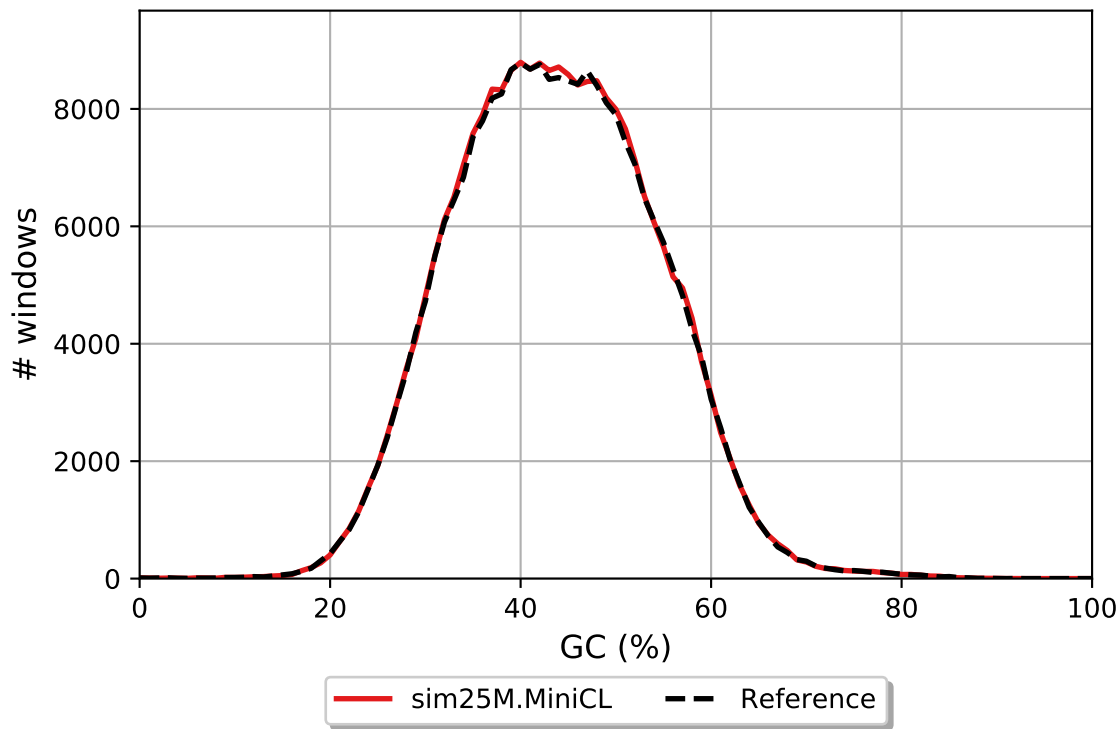


— sim25M.MiniCL

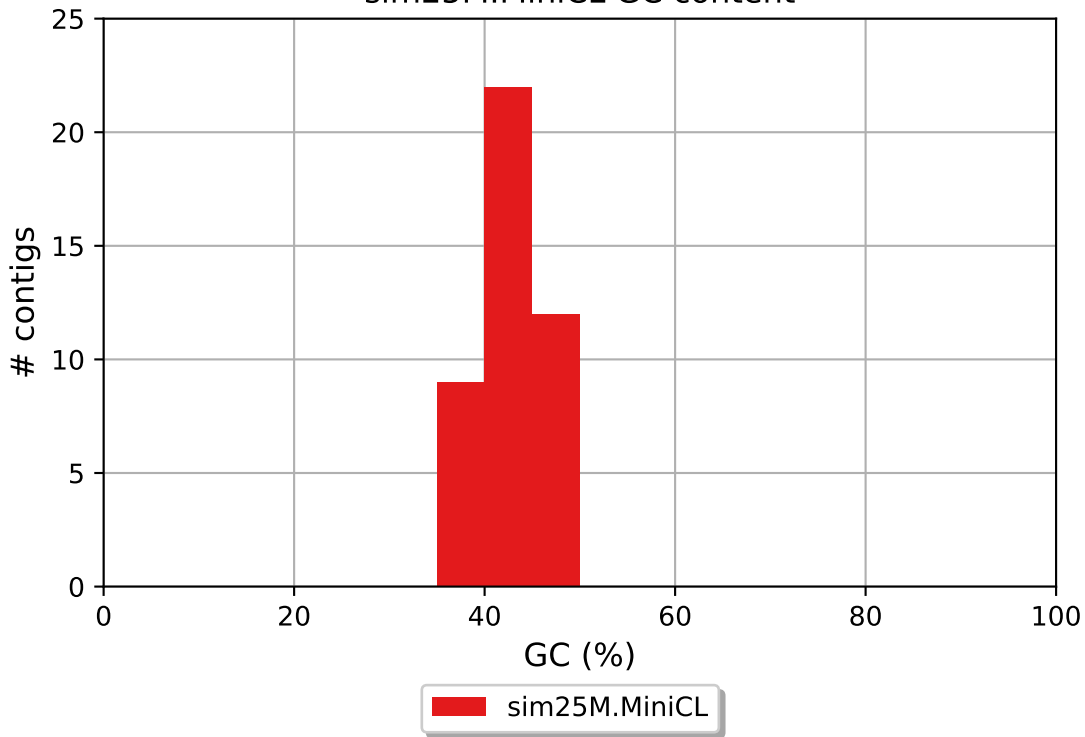
Cumulative length



GC content

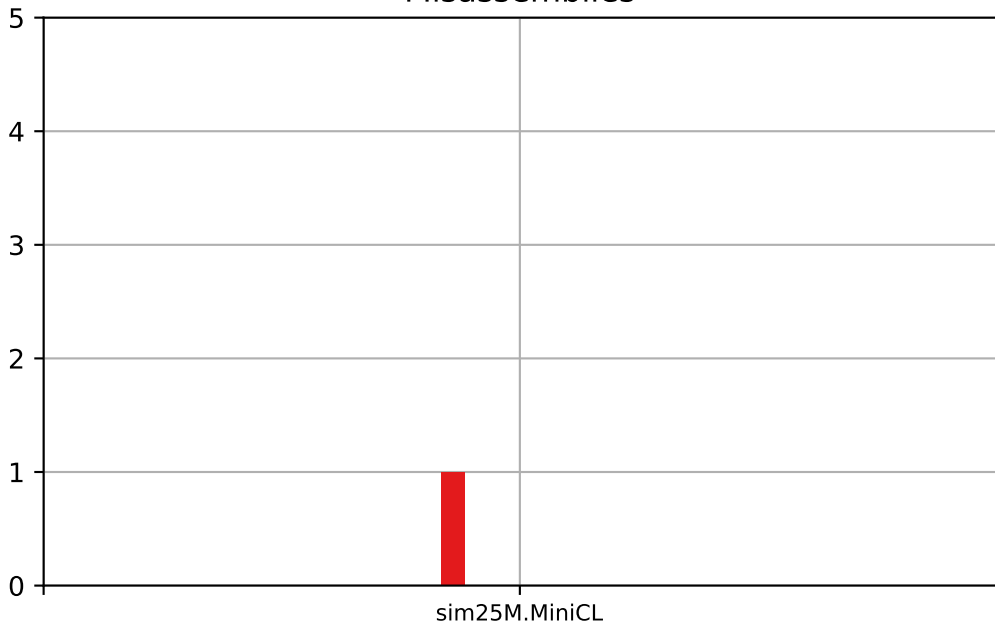


sim25M.MinicL GC content

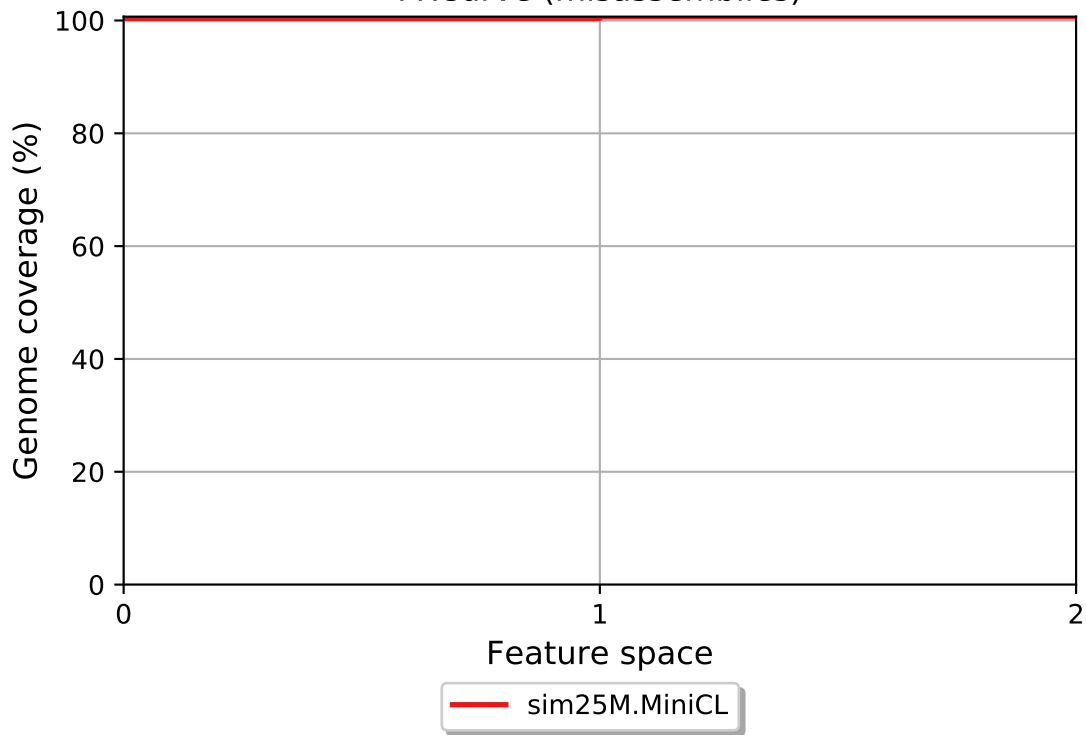




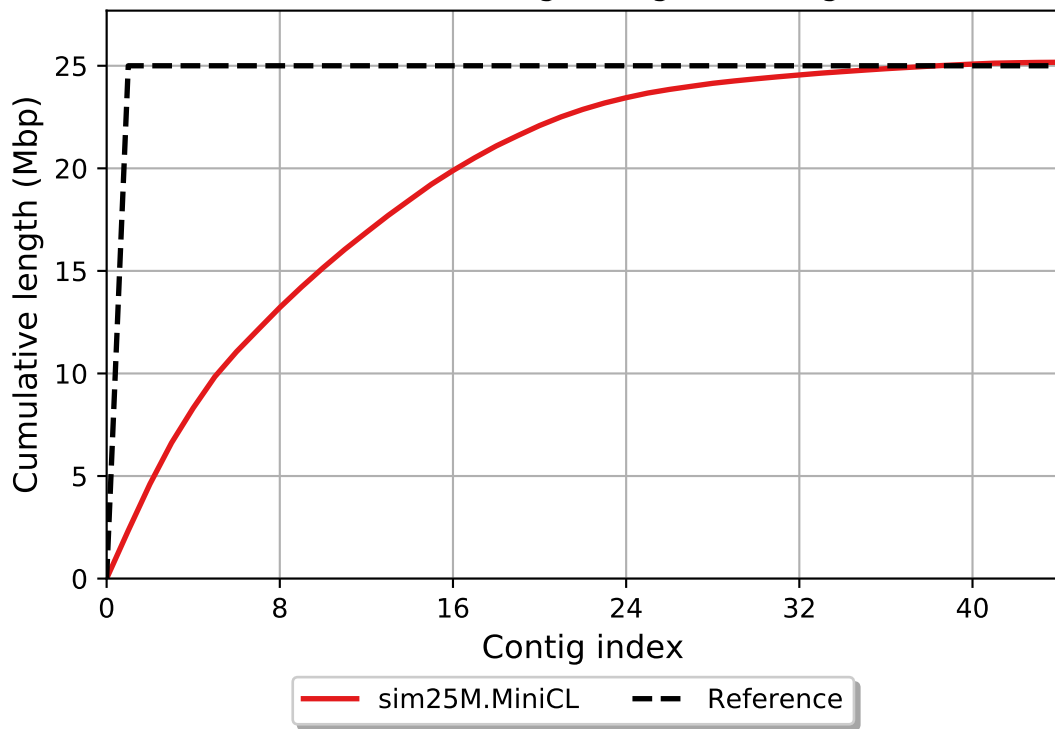
## Misassemblies



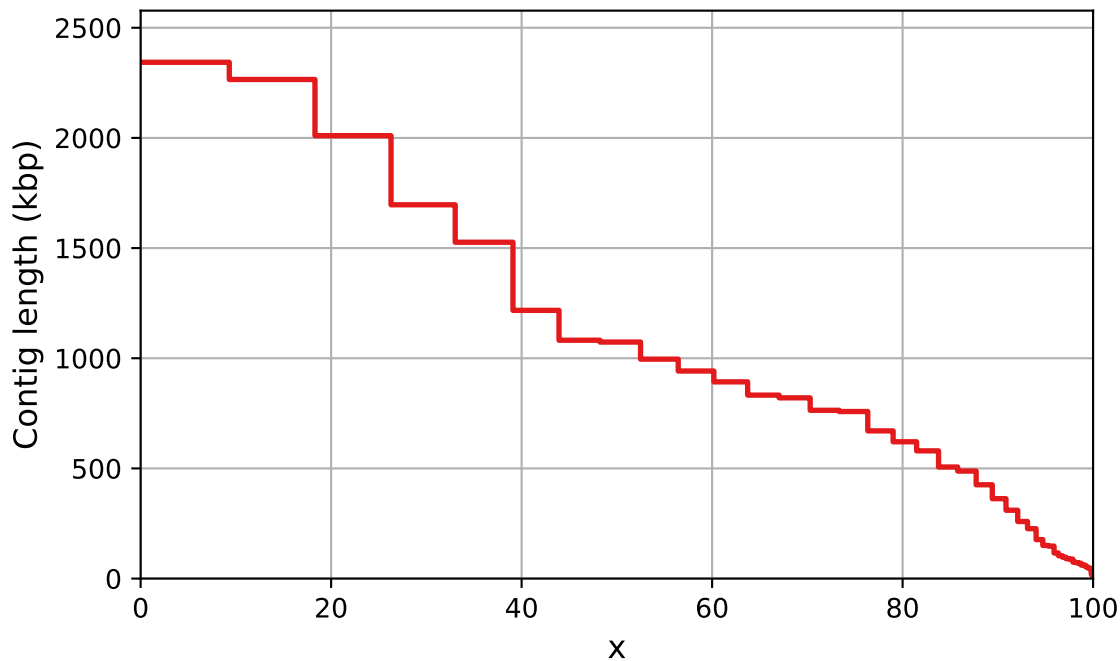
FRCurve (misassemblies)



Cumulative length (aligned contigs)

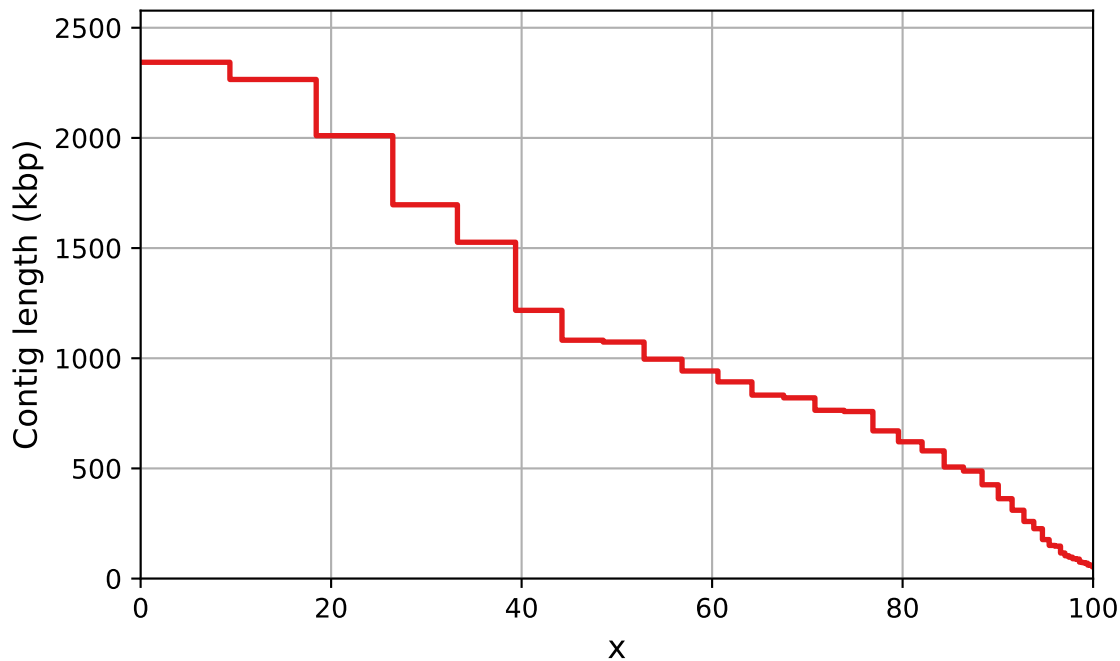


NAx



— sim25M.MiniCL

# NGAx



— sim25M.MiniCL