

Report

	sim5M.MiniCL
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	13
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	11
Total length (>= 0 bp)	5087756
Total length (>= 1000 bp)	5087756
Total length (>= 5000 bp)	5087756
Total length (>= 10000 bp)	5087756
Total length (>= 25000 bp)	5050633
Total length (>= 50000 bp)	5050633
# contigs	13
Largest contig	1348395
Total length	5087756
Reference length	5000040
GC (%)	35.84
Reference GC (%)	35.84
N50	704173
NG50	704173
N75	413350
NG75	413350
L50	3
LG50	3
L75	5
LG75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	3719
Genome fraction (%)	99.556
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.75
# indels per 100 kbp	207.88
Largest alignment	1341548
Total aligned length	5077176
NA50	704169
NGA50	704169
NA75	413350
NGA75	413350
LA50	3
LGA50	3
LA75	5
LGA75	5

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.MinicL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	286
# indels	10348
# indels (≤ 5 bp)	10339
# indels (> 5 bp)	9
Indels length	13385

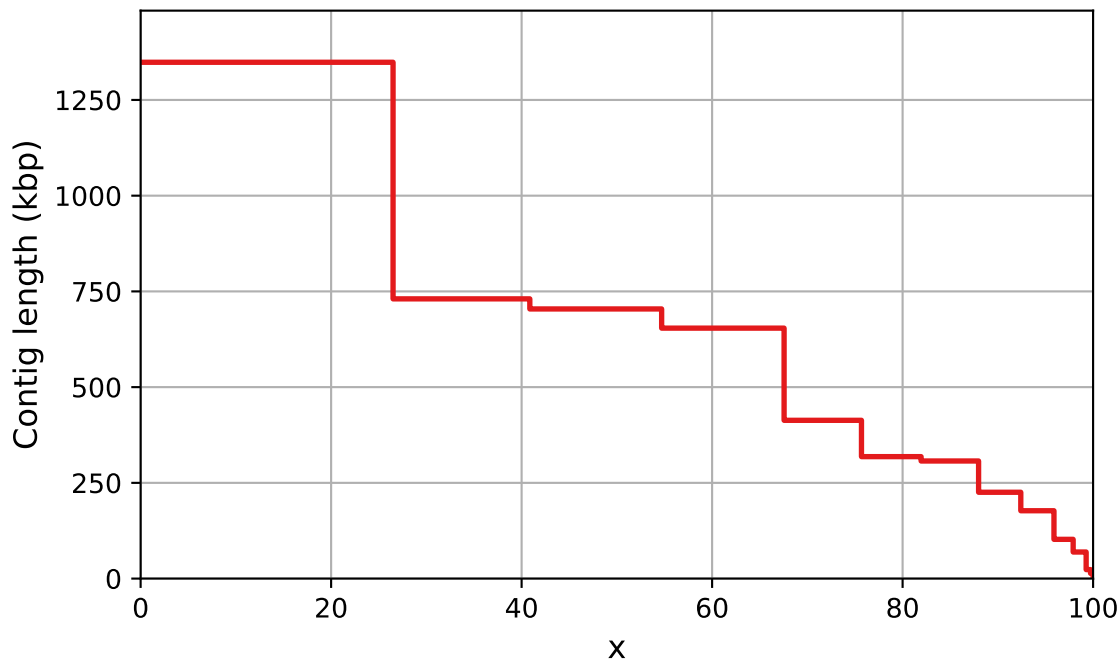
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim5M.MinicL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	3719
# N's	0

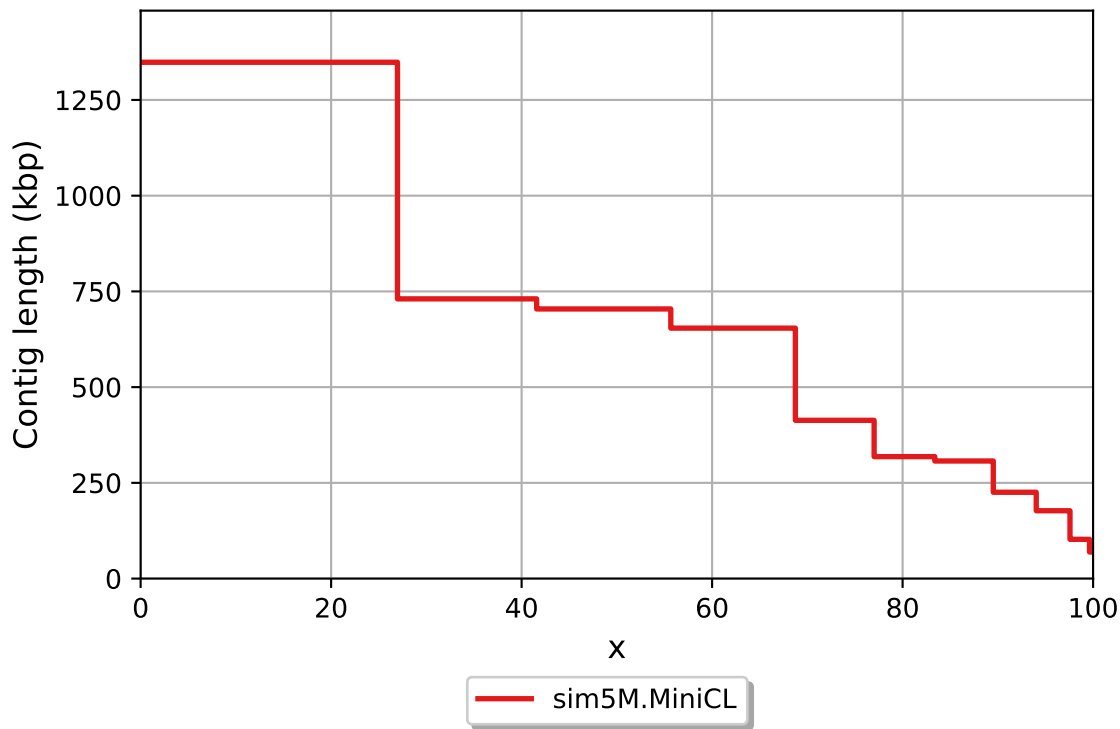
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

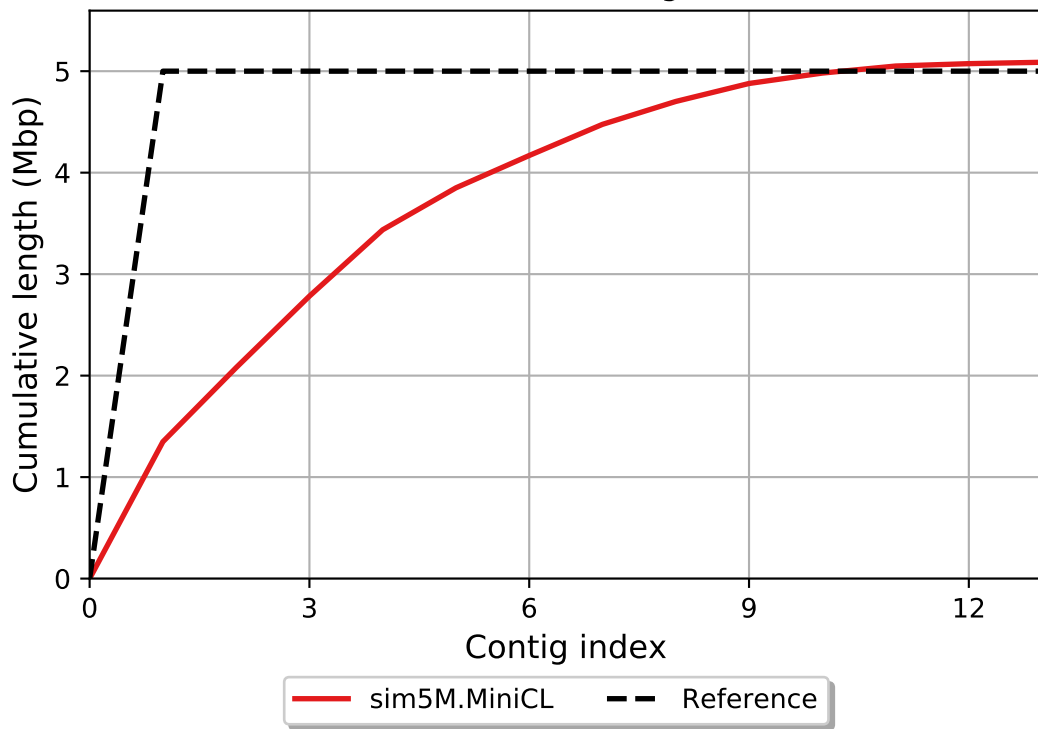


sim5M.MiniCL

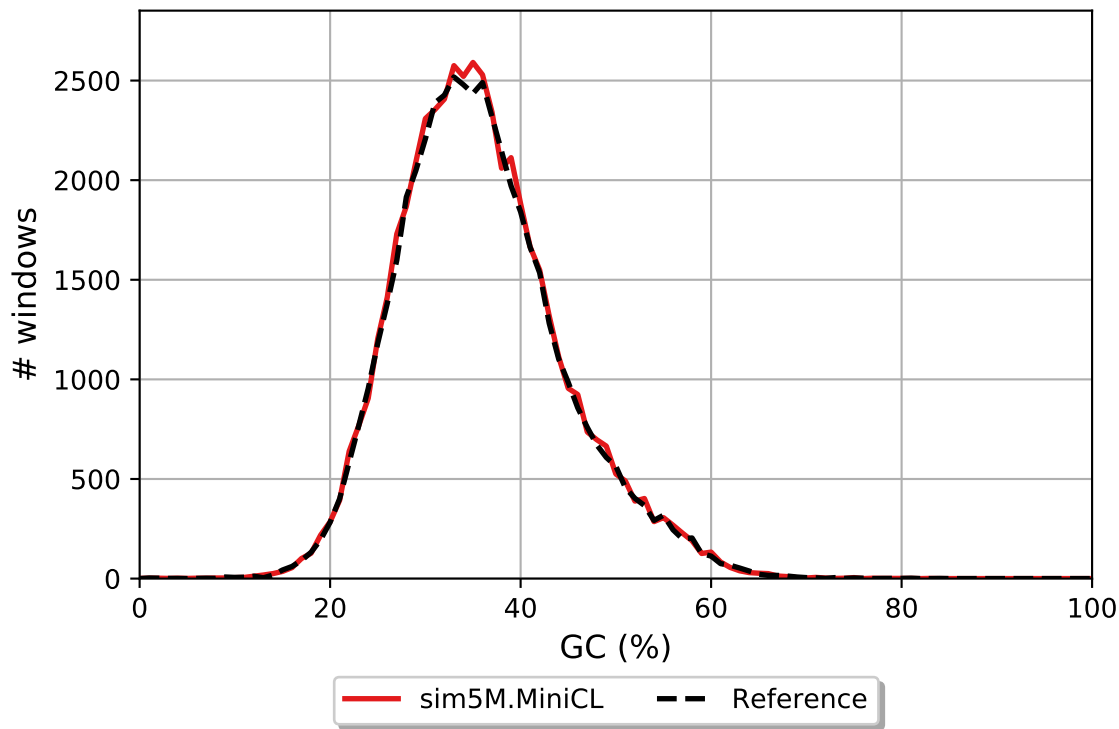
NGx



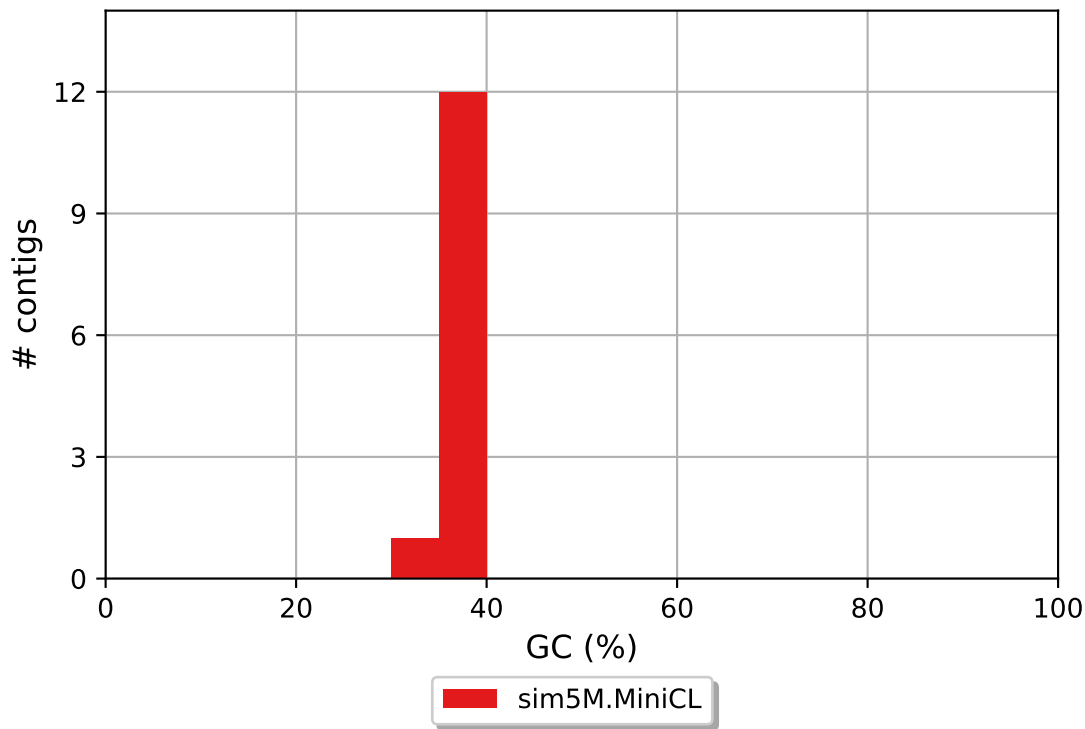
Cumulative length



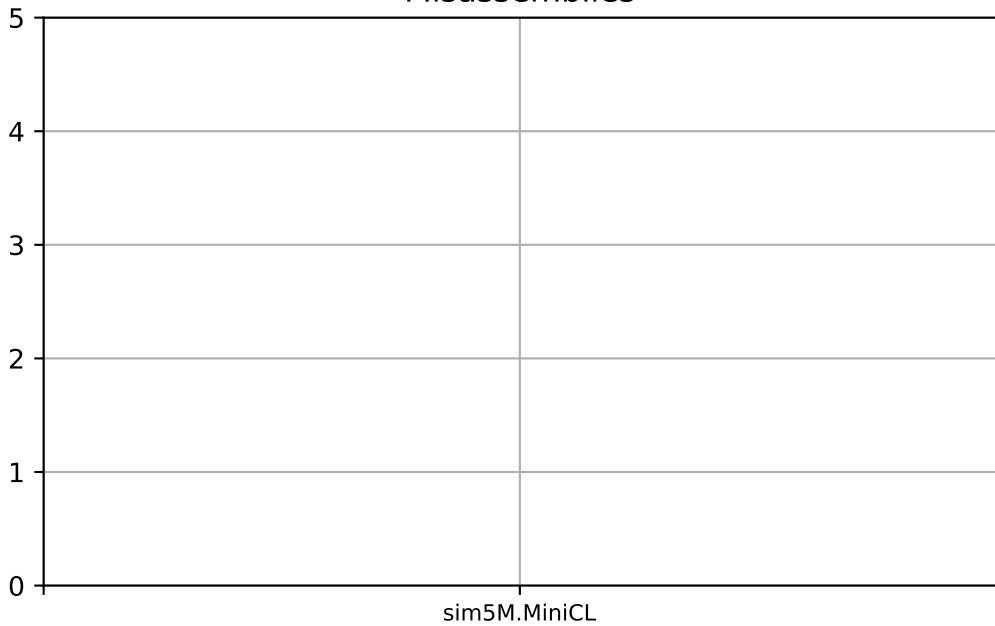
GC content



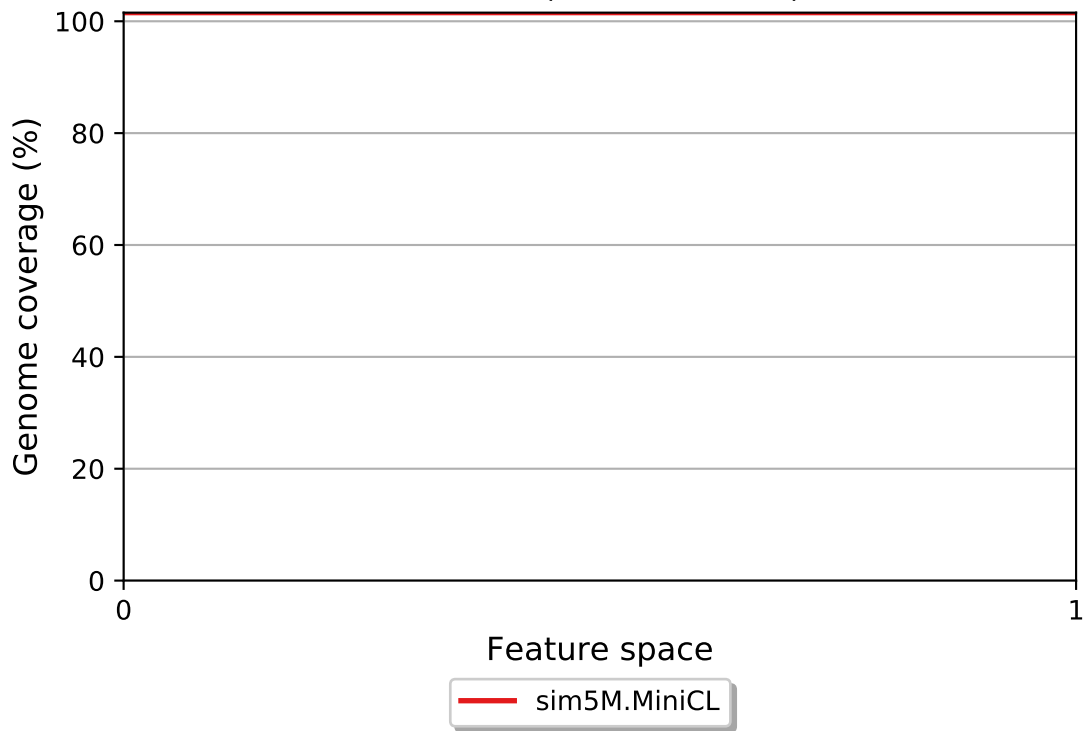
sim5M.MiniCL GC content



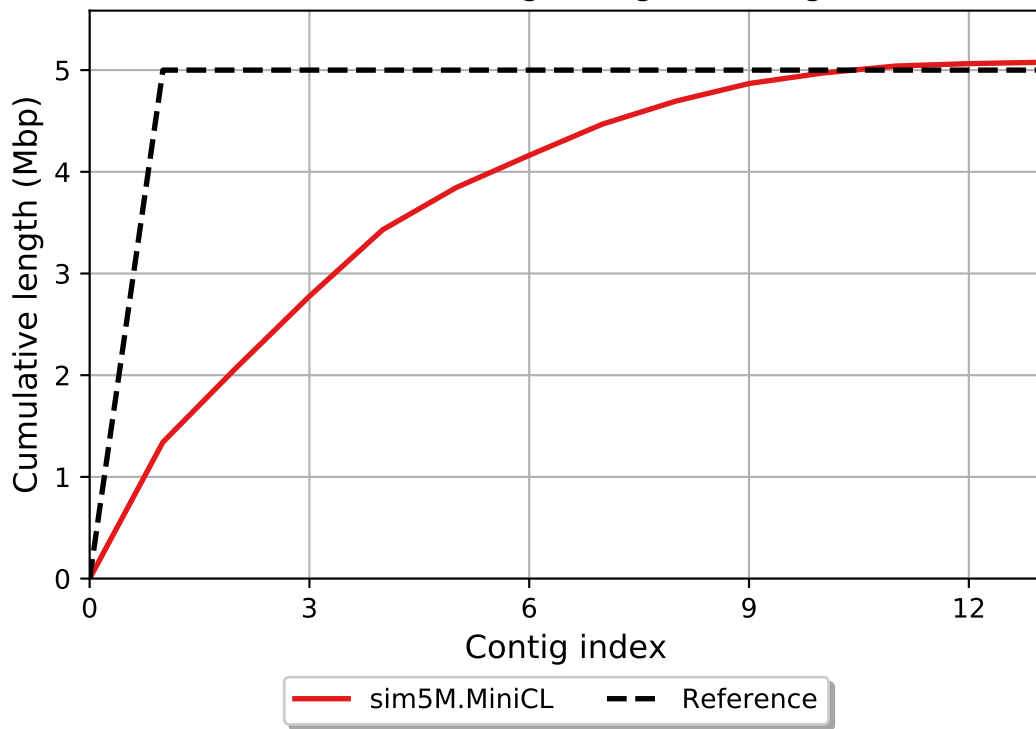
Misassemblies



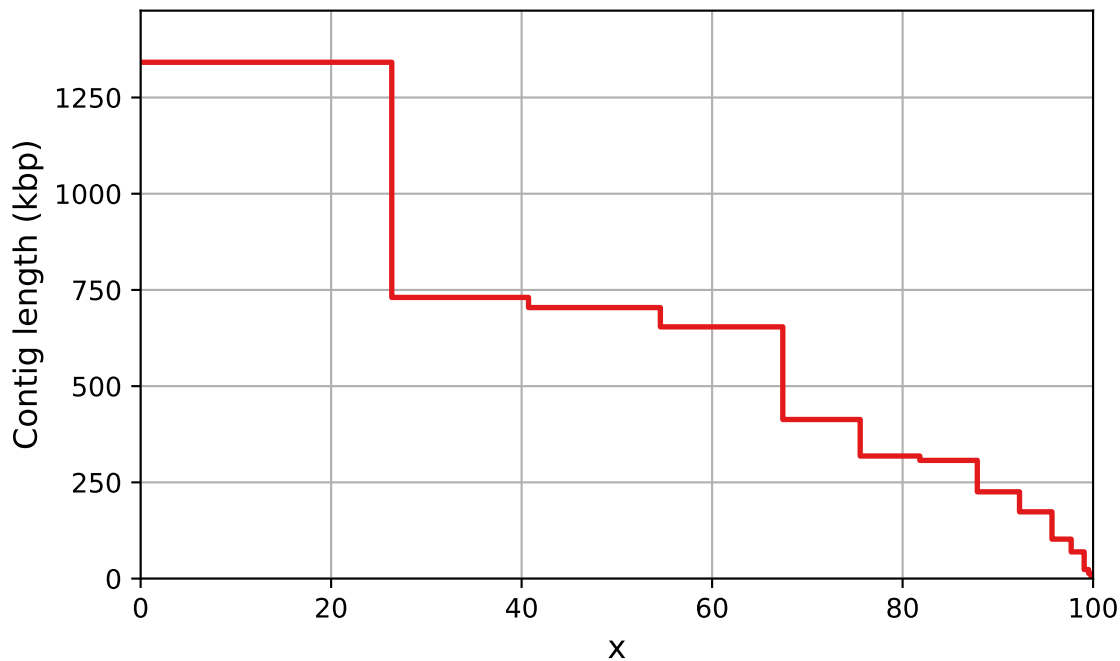
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



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NGAx

