

Report

	sim5M.CanuL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1977
# contigs (>= 5000 bp)	1589
# contigs (>= 10000 bp)	468
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	15637868
Total length (>= 1000 bp)	15630960
Total length (>= 5000 bp)	14249824
Total length (>= 10000 bp)	5858862
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1979
Largest contig	23710
Total length	15632480
Reference length	5000040
GC (%)	35.82
Reference GC (%)	35.84
N50	8964
NG50	12650
N75	6886
NG75	11418
L50	675
LG50	168
L75	1168
LG75	272
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 1 part
Unaligned length	4866
Genome fraction (%)	95.001
Duplication ratio	3.290
# N's per 100 kbp	0.00
# mismatches per 100 kbp	42.74
# indels per 100 kbp	96.29
Largest alignment	23710
Total aligned length	15621678
NA50	8954
NGA50	12649
NA75	6885
NGA75	11418
LA50	676
LGA50	168
LA75	1168
LGA75	272

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.CanuL.cr
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	2030
# indels	4574
# indels (≤ 5 bp)	4571
# indels (> 5 bp)	3
Indels length	4968

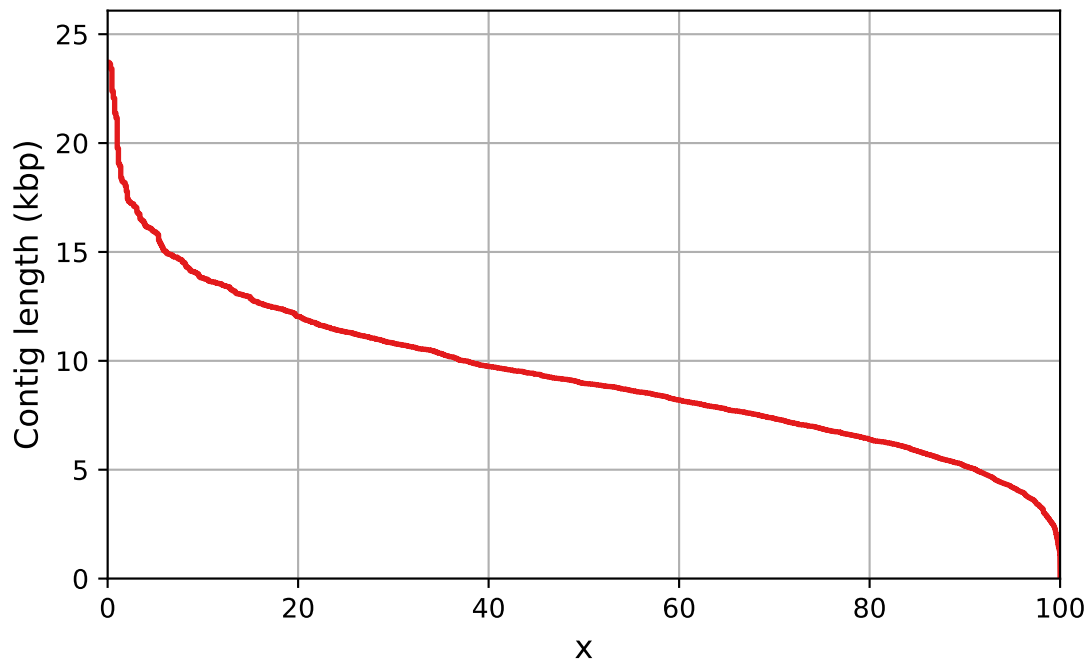
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim5M.CanuL.cr
# fully unaligned contigs	1
Fully unaligned length	3524
# partially unaligned contigs	1
Partially unaligned length	1342
# N's	0

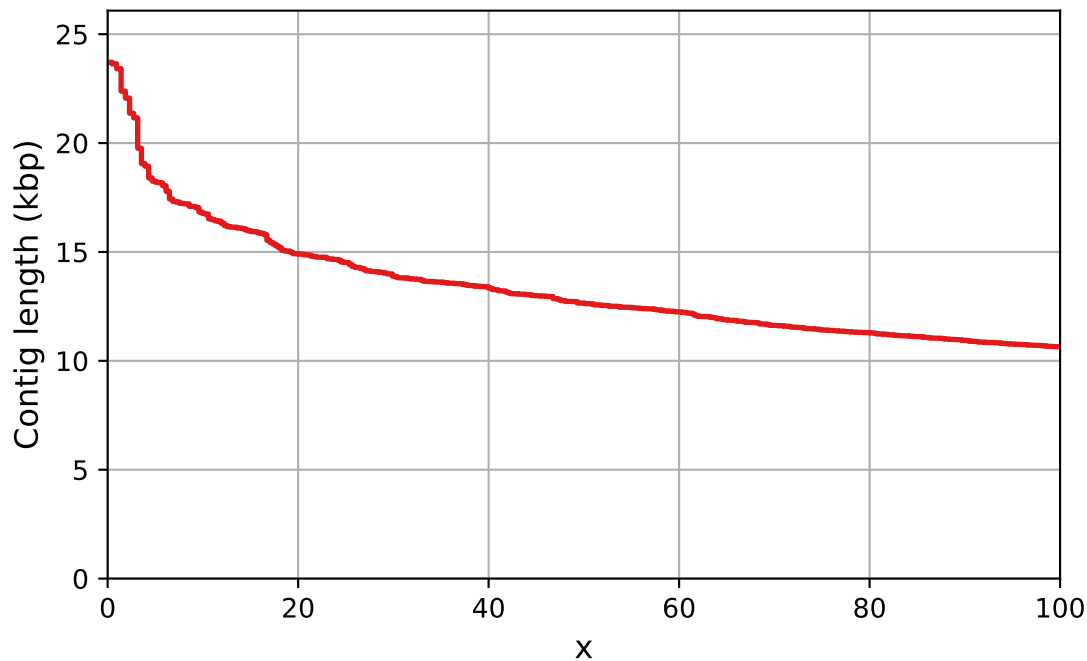
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



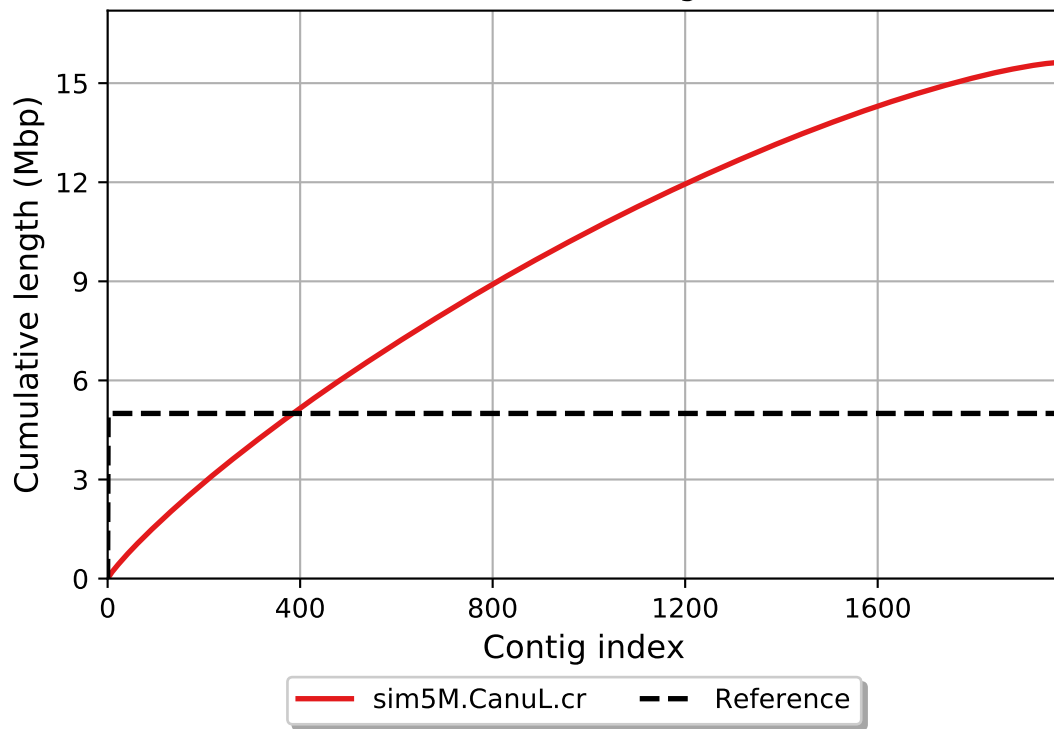
— sim5M.CanuL.cr

NGx

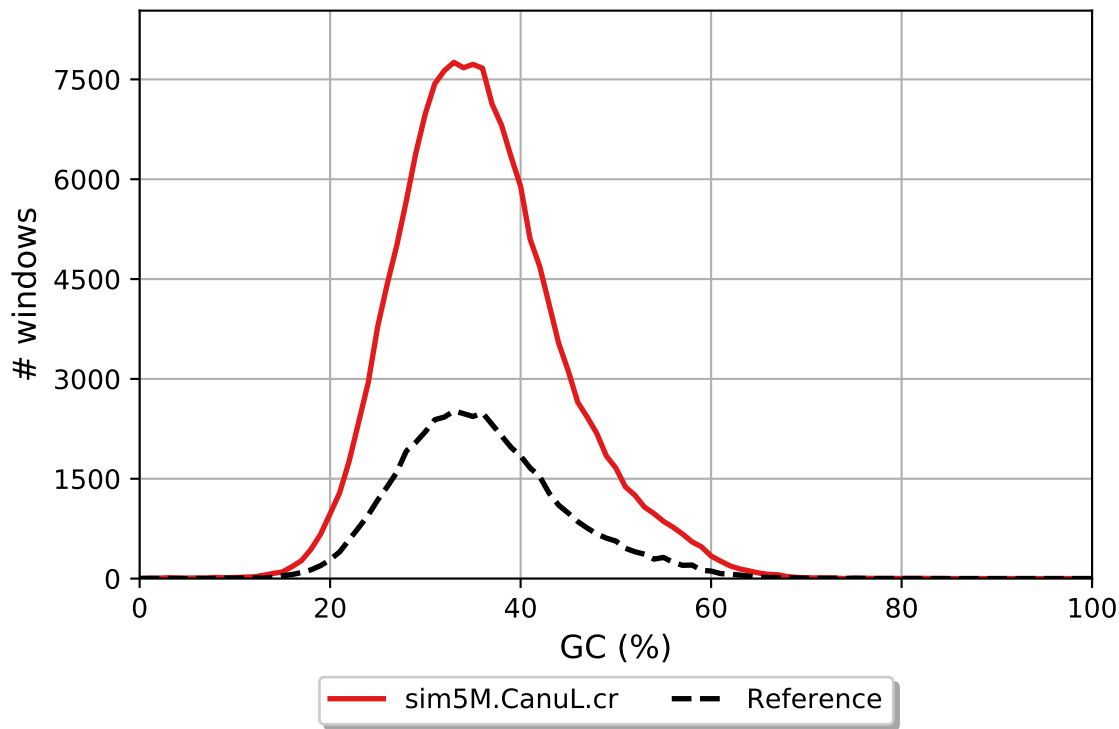


— sim5M.CanuL.cr

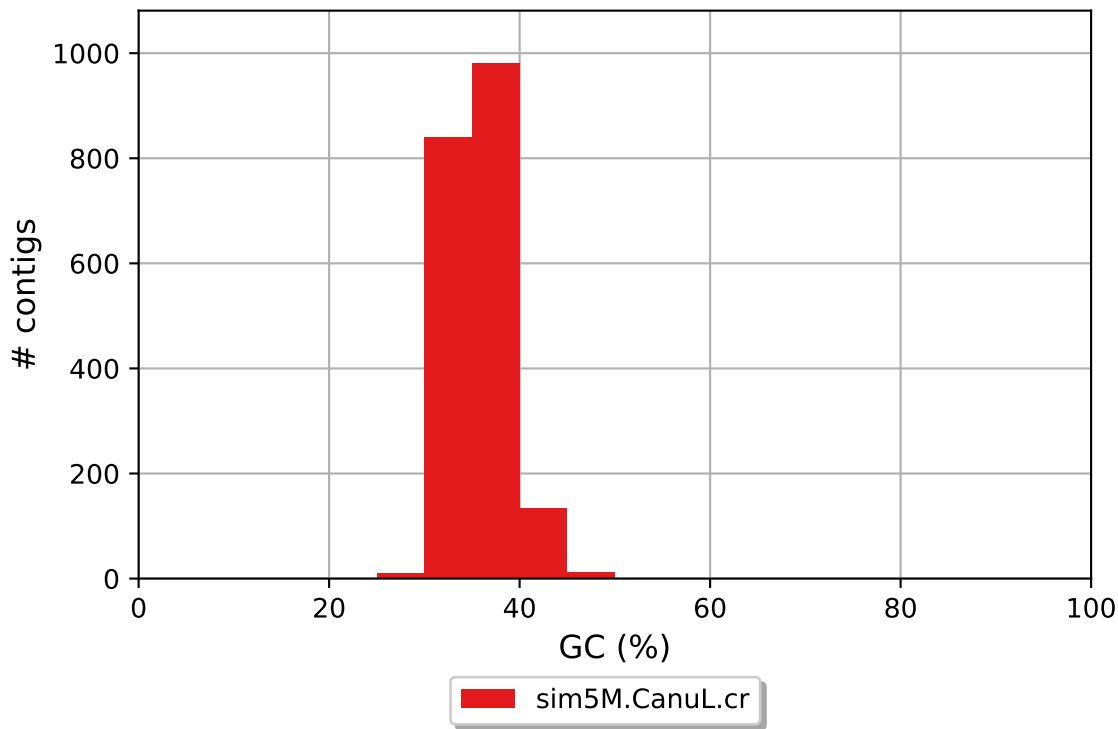
Cumulative length



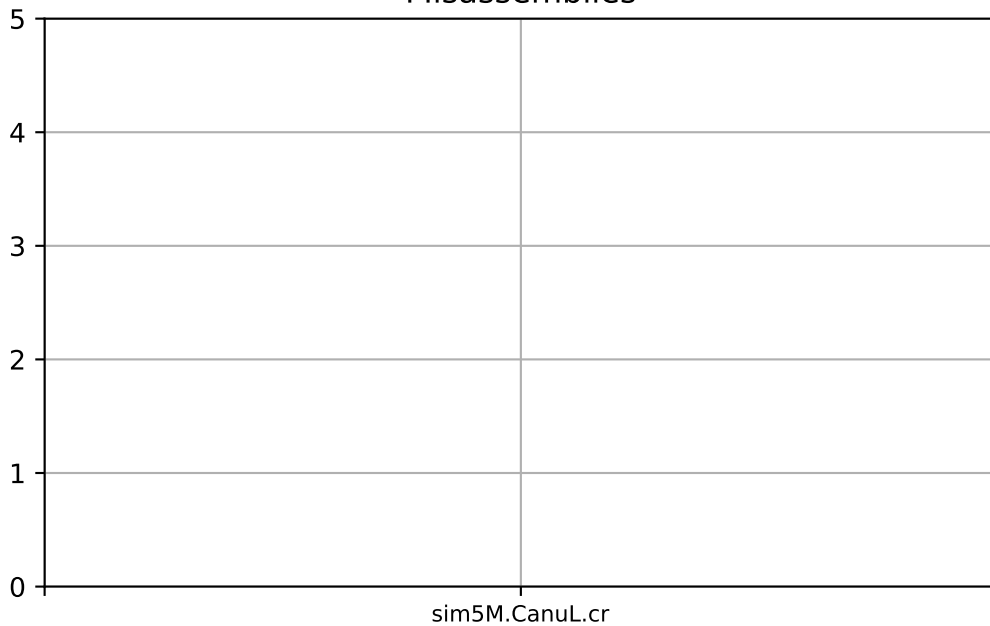
GC content



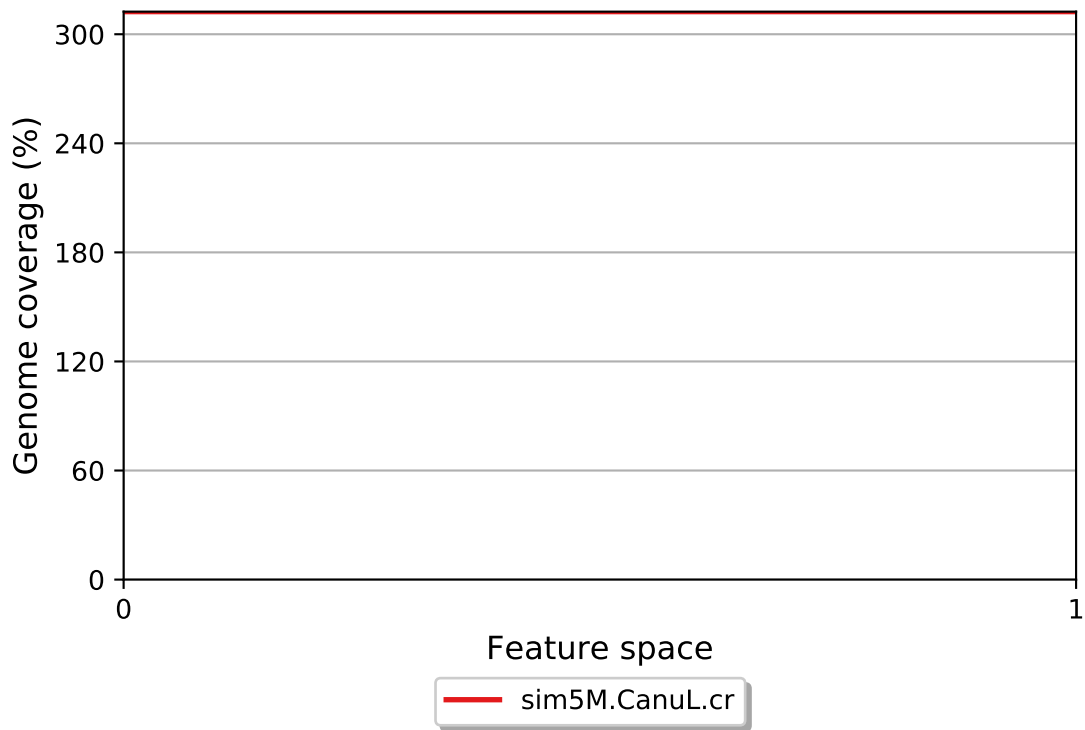
sim5M.CanuL.cr GC content



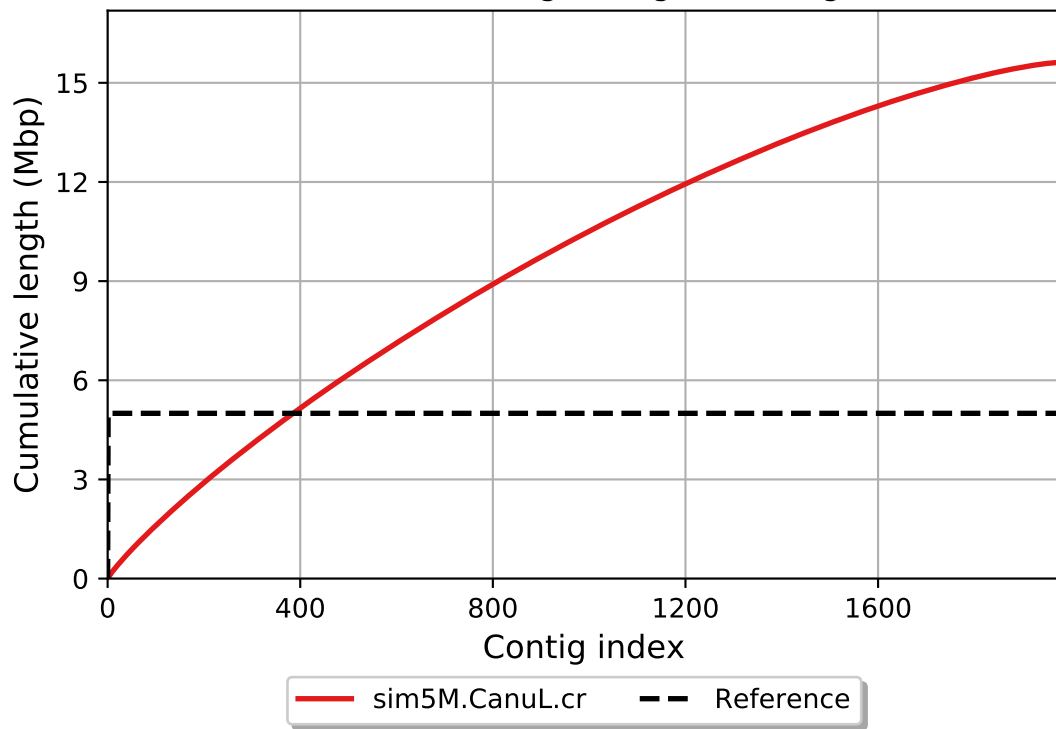
Misassemblies



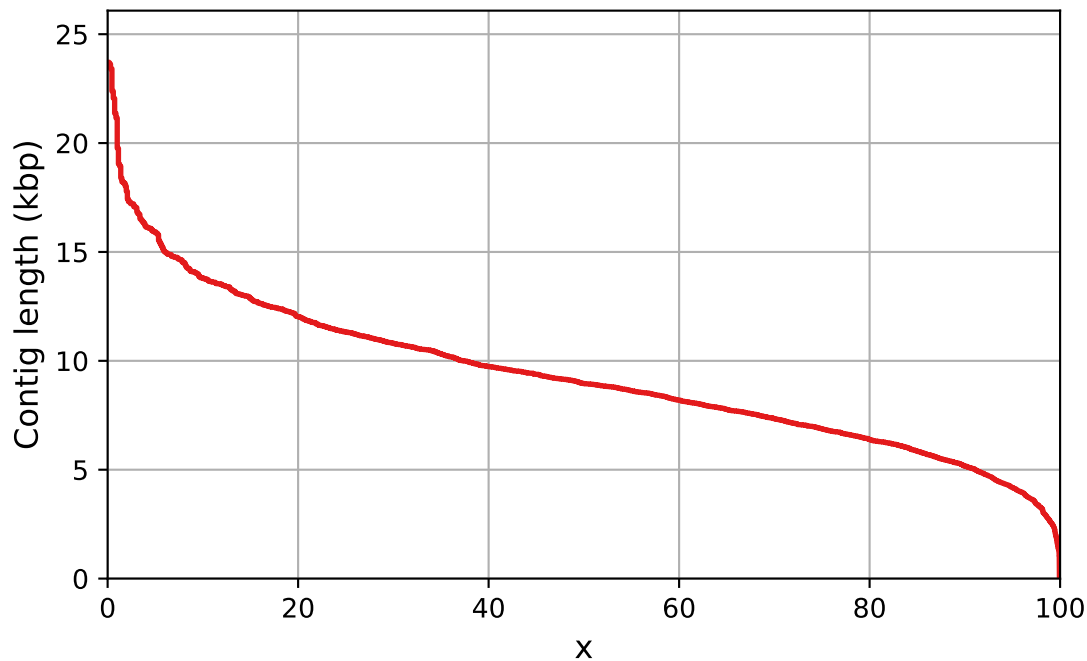
FRCurve (misassemblies)



Cumulative length (aligned contigs)

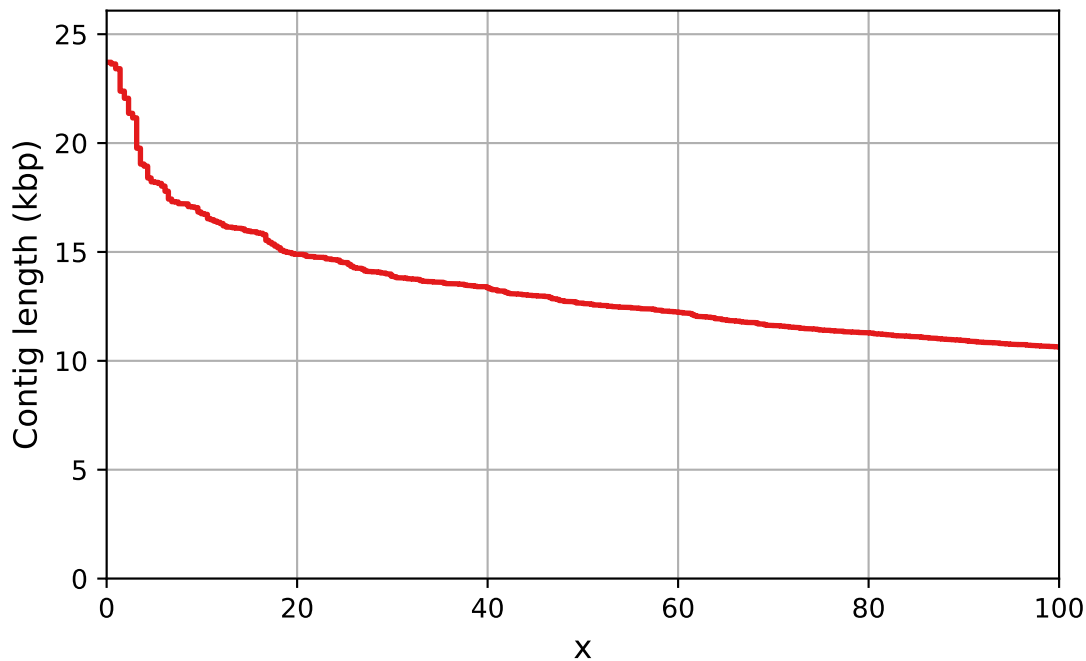


NAx



— sim5M.CanuL.cr

NGAx



— sim5M.CanuL.cr