

Report

	sim25M.CanuL
# contigs (>= 0 bp)	447
# contigs (>= 1000 bp)	447
# contigs (>= 5000 bp)	432
# contigs (>= 10000 bp)	379
# contigs (>= 25000 bp)	198
# contigs (>= 50000 bp)	105
Total length (>= 0 bp)	22820914
Total length (>= 1000 bp)	22820914
Total length (>= 5000 bp)	22787727
Total length (>= 10000 bp)	22365556
Total length (>= 25000 bp)	19518340
Total length (>= 50000 bp)	16260769
# contigs	447
Largest contig	738962
Total length	22820914
Reference length	25000020
GC (%)	43.69
Reference GC (%)	43.69
N50	109830
NG50	90296
N75	42805
NG75	30178
L50	40
LG50	51
L75	124
LG75	170
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	12658
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	85.629
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.86
# indels per 100 kbp	76.13
Largest alignment	738962
Total aligned length	22820813
NA50	109830
NGA50	90296
NA75	42805
NGA75	30178
LA50	40
LGA50	51
LA75	124
LGA75	170

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

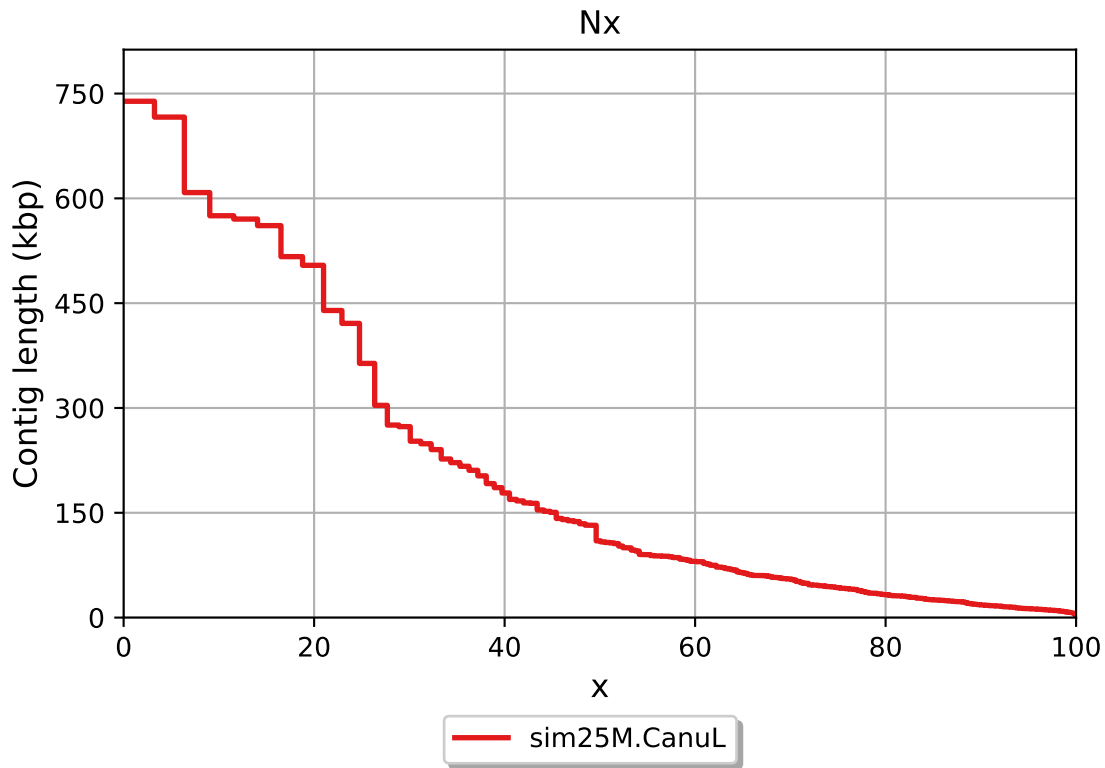
	sim25M.CanuL
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	12658
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	4894
# indels	16298
# indels (≤ 5 bp)	16293
# indels (> 5 bp)	5
Indels length	17730

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).

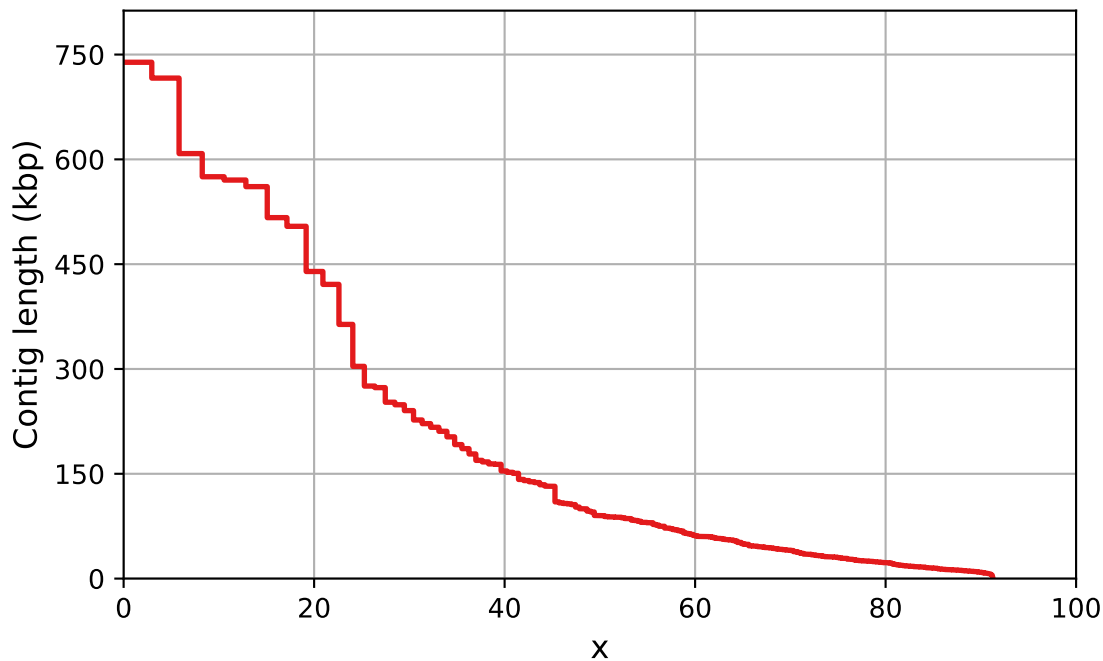
Unaligned report

	sim25M.CanuL
# 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).

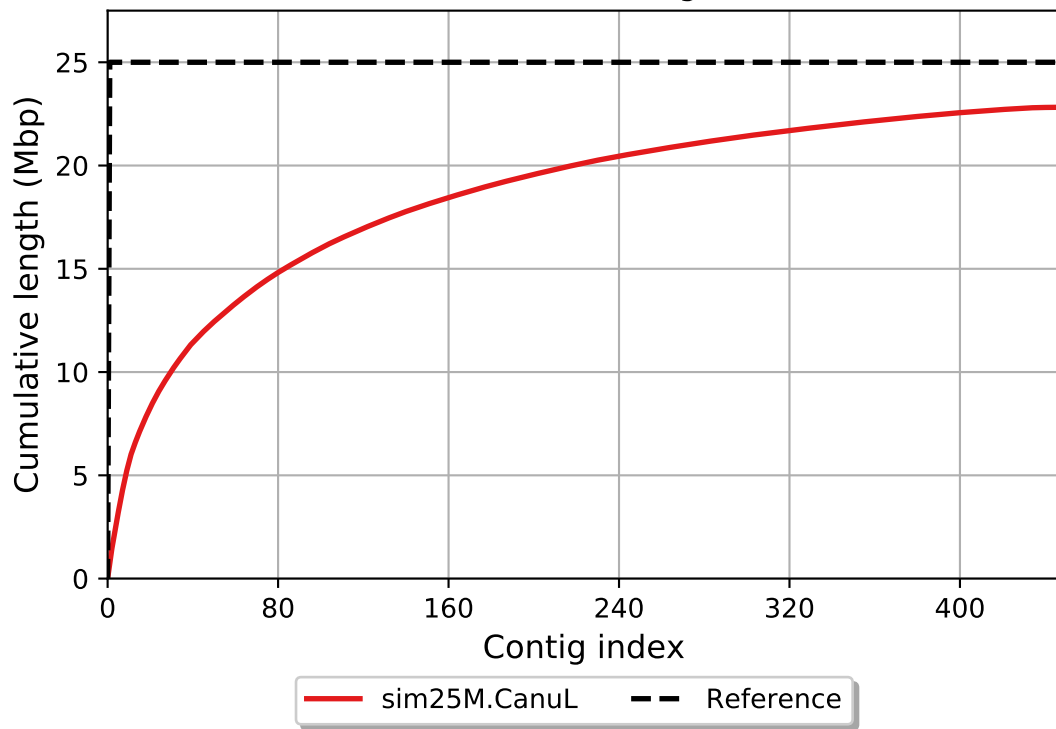


NGx

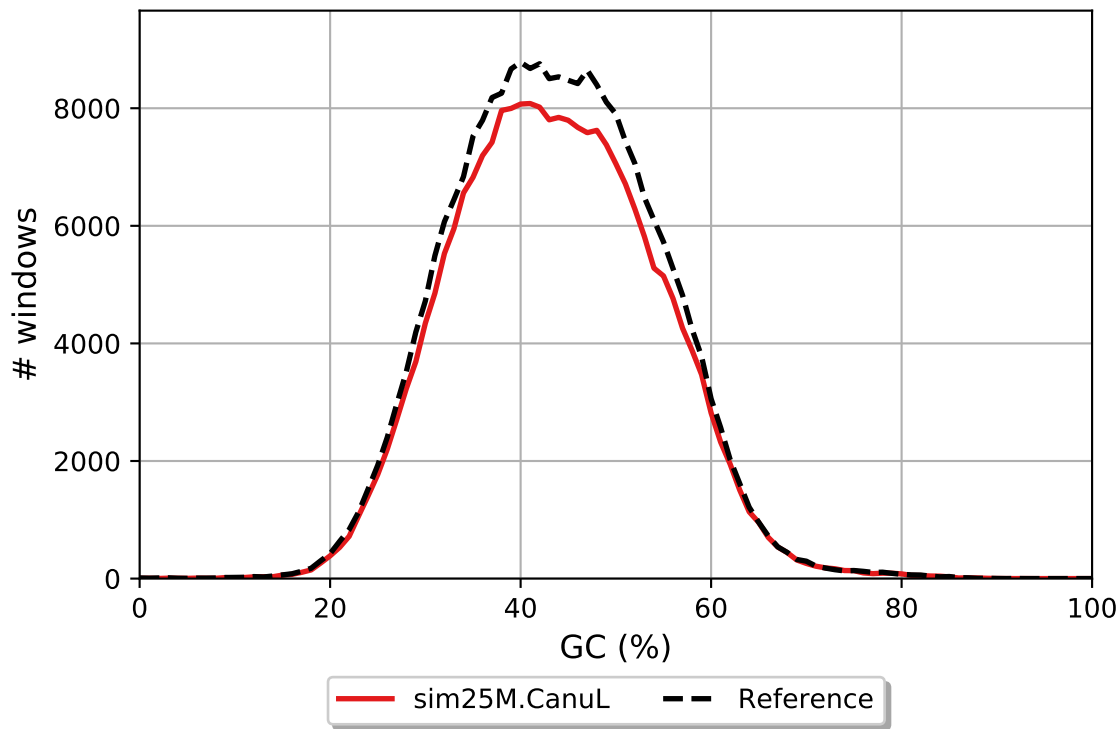


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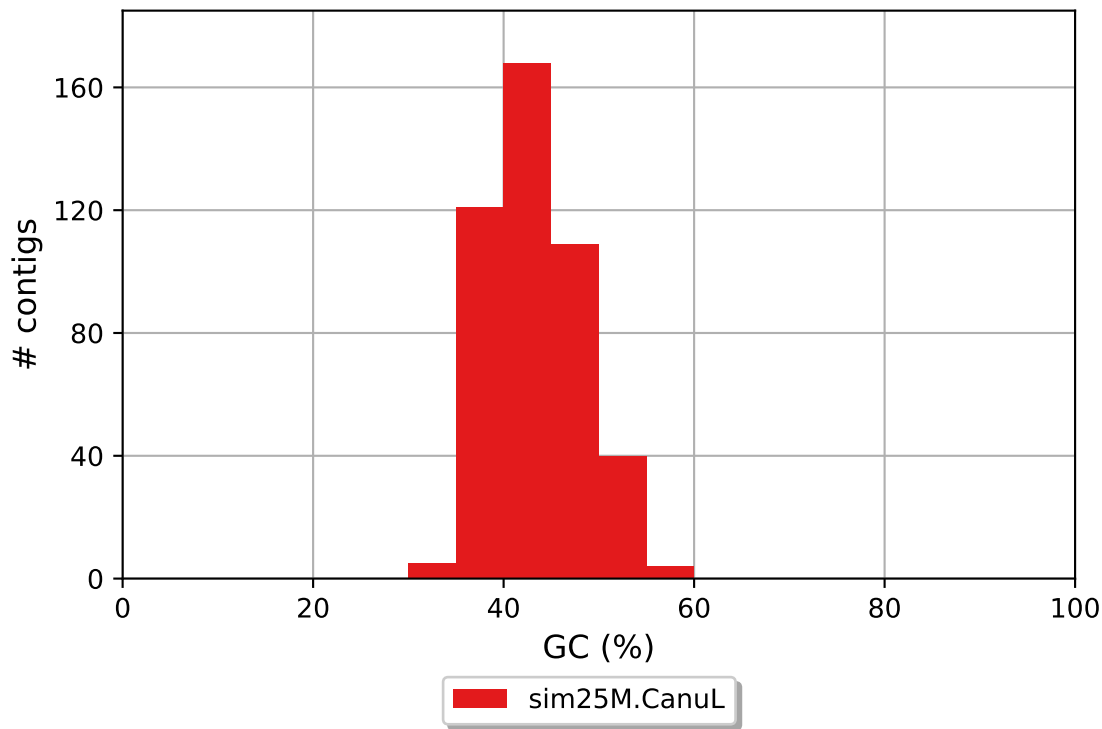
Cumulative length



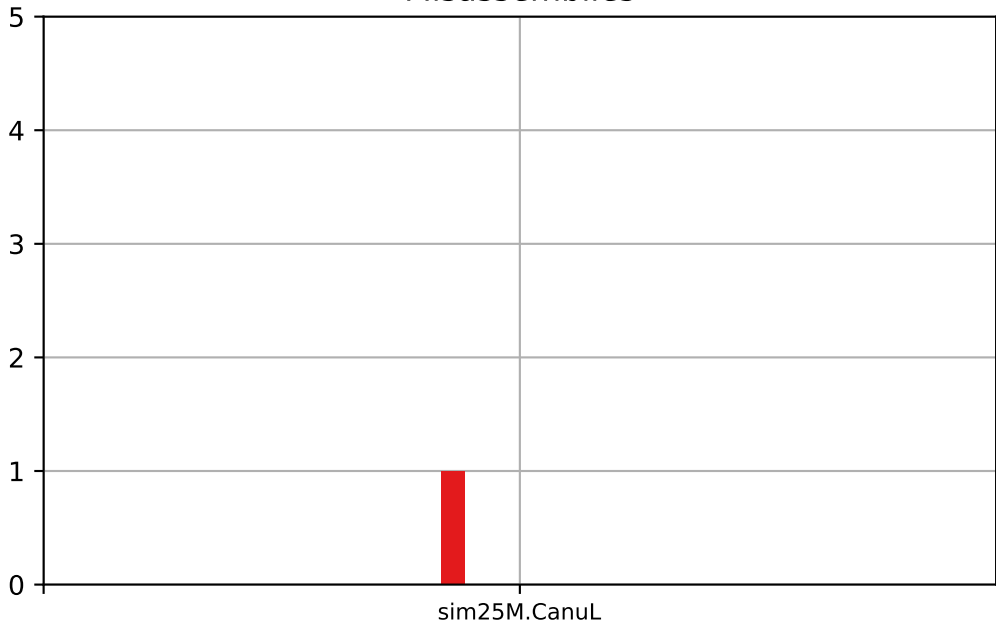
GC content



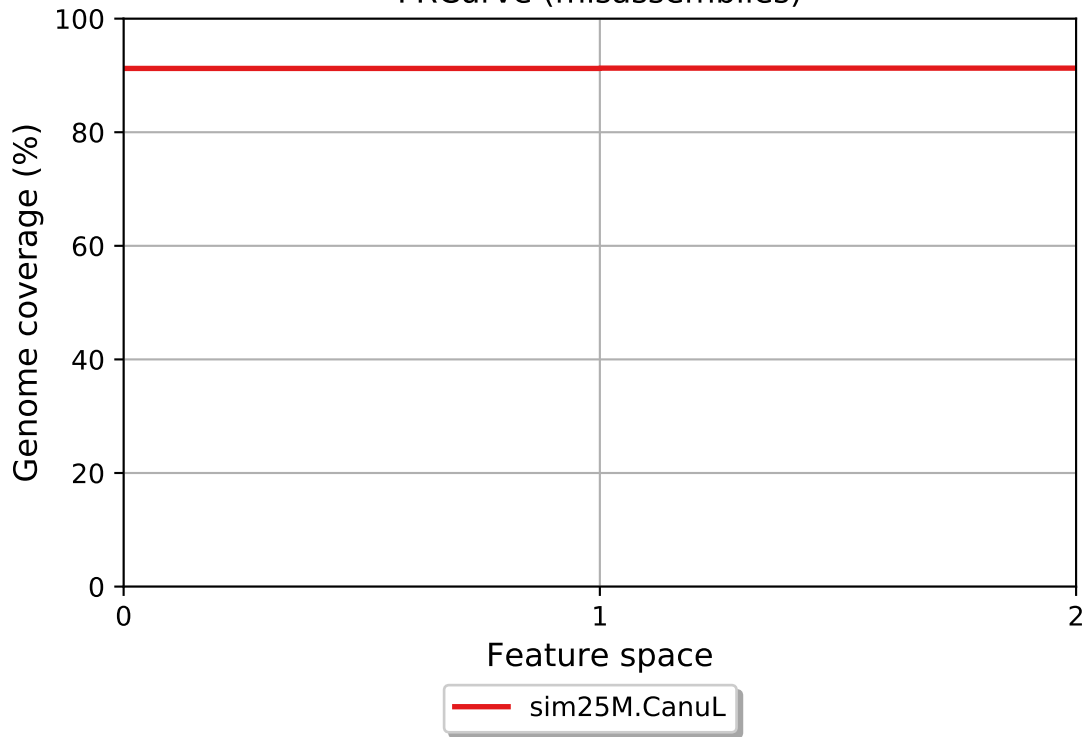
sim25M.CanuL GC content



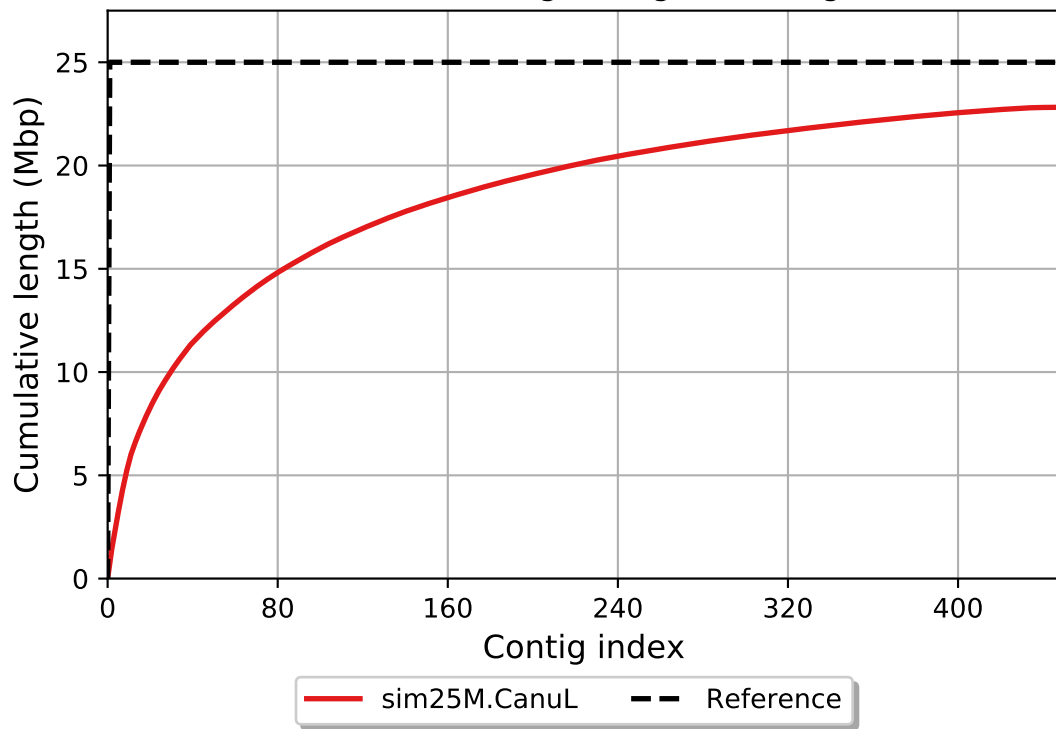
Misassemblies



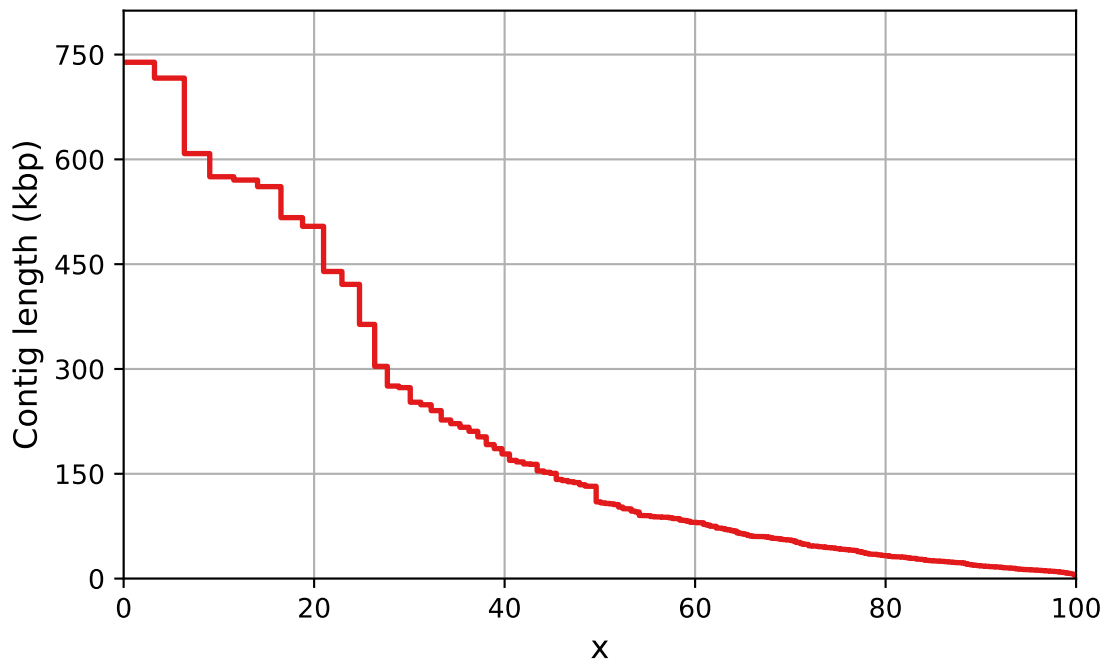
FRCurve (misassemblies)



Cumulative length (aligned contigs)

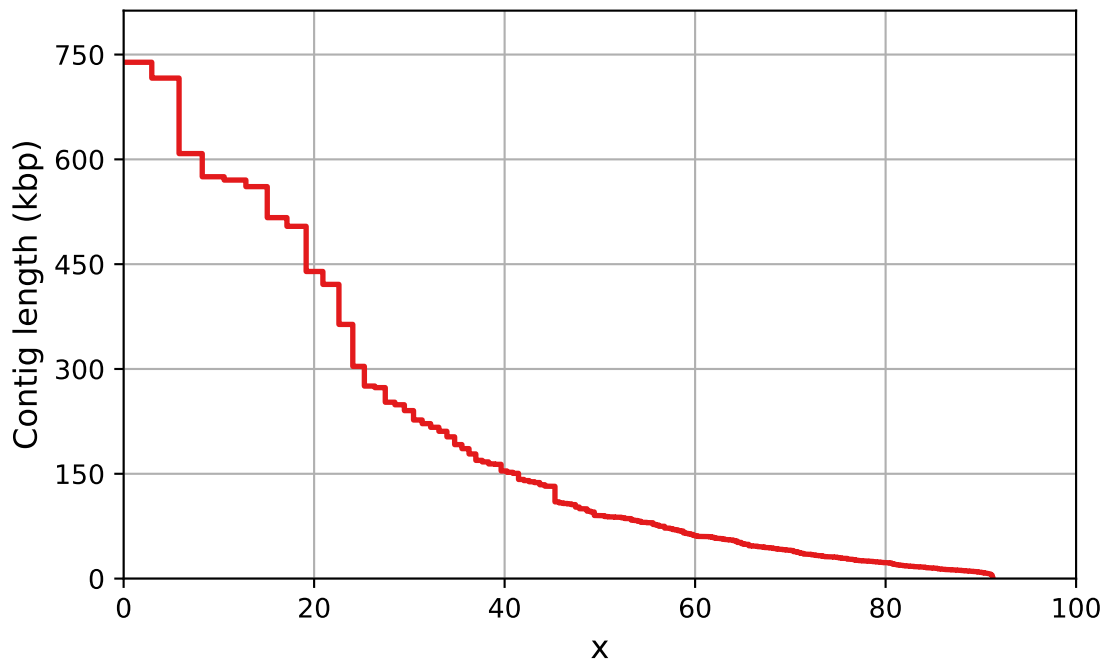


NAx



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NGAx



— sim25M.CanuL