

Report

	sim25M.MiniCL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1988
# contigs (>= 5000 bp)	1604
# contigs (>= 10000 bp)	538
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16137699
Total length (>= 1000 bp)	16130858
Total length (>= 5000 bp)	14722734
Total length (>= 10000 bp)	6765125
Total length (>= 25000 bp)	53068
Total length (>= 50000 bp)	0
# contigs	1995
Largest contig	27394
Total length	16135811
Reference length	25000020
GC (%)	43.96
Reference GC (%)	43.69
N50	9229
NG50	6747
N75	6955
L50	674
LG50	1232
L75	1174
# misassemblies	12
# misassembled contigs	10
Misassembled contigs length	68879
# local misassemblies	40
# unaligned mis. contigs	5
# unaligned contigs	494 + 60 part
Unaligned length	5245791
Genome fraction (%)	34.622
Duplication ratio	1.258
# N's per 100 kbp	0.00
# mismatches per 100 kbp	192.40
# indels per 100 kbp	1327.84
Largest alignment	27391
Total aligned length	10884419
NA50	6383
NGA50	-
LA50	849

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.cr
# misassemblies	12
# relocations	12
# translocations	0
# inversions	0
# misassembled contigs	10
Misassembled contigs length	68879
# local misassemblies	40
# unaligned mis. contigs	5
# mismatches	16653
# indels	114932
# indels (≤ 5 bp)	114838
# indels (> 5 bp)	94
Indels length	127254

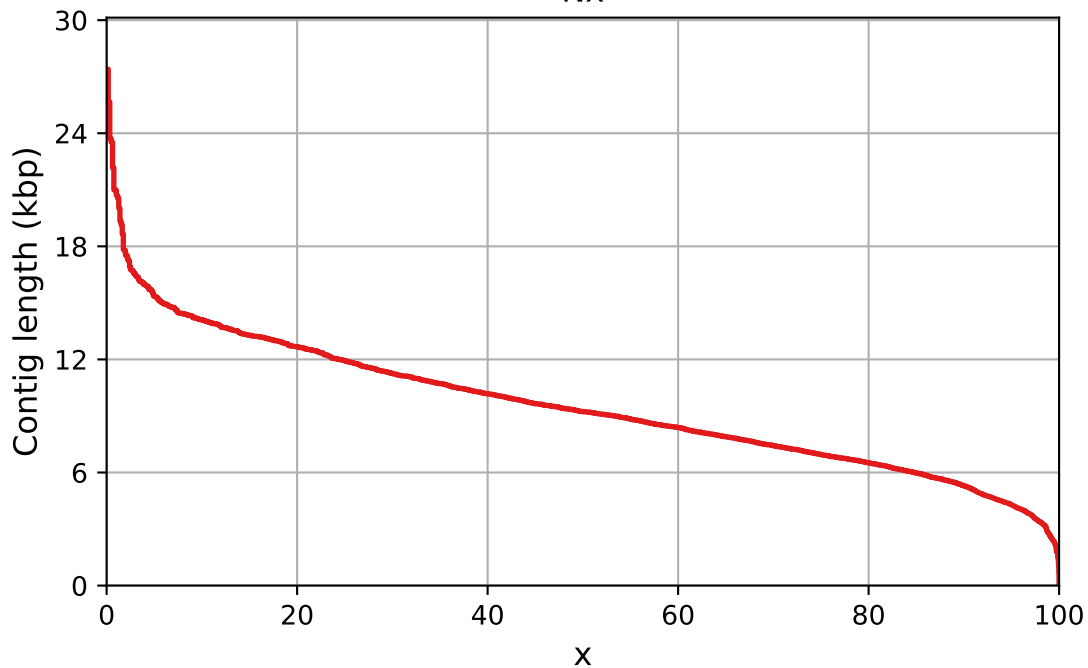
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim25M.MinicL.cr
# fully unaligned contigs	494
Fully unaligned length	4923025
# partially unaligned contigs	60
Partially unaligned length	322766
# N's	0

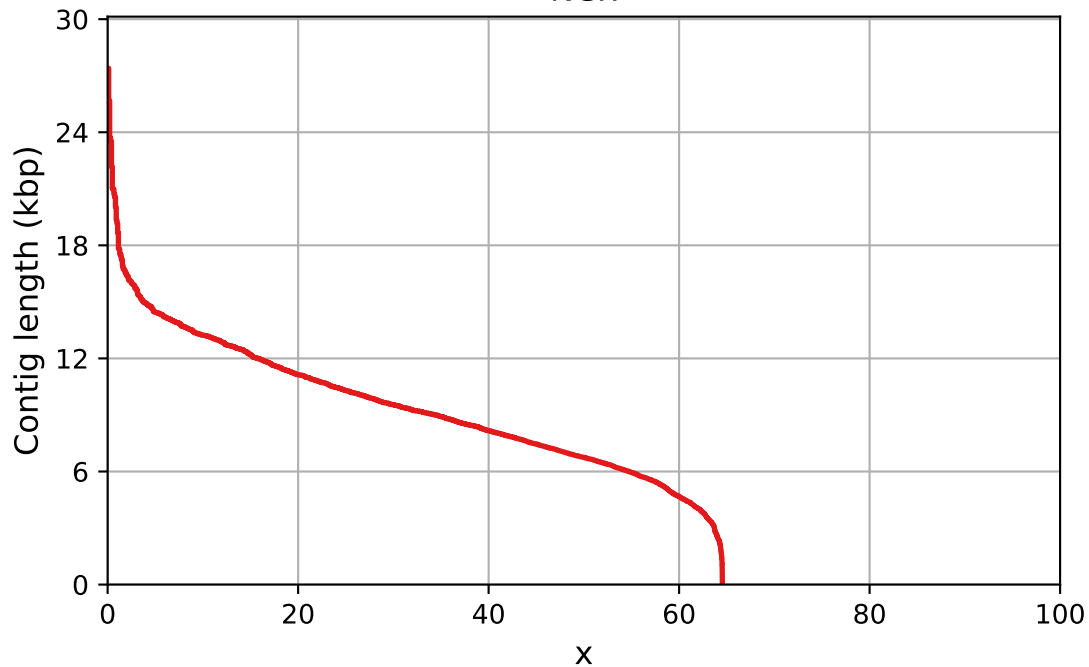
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



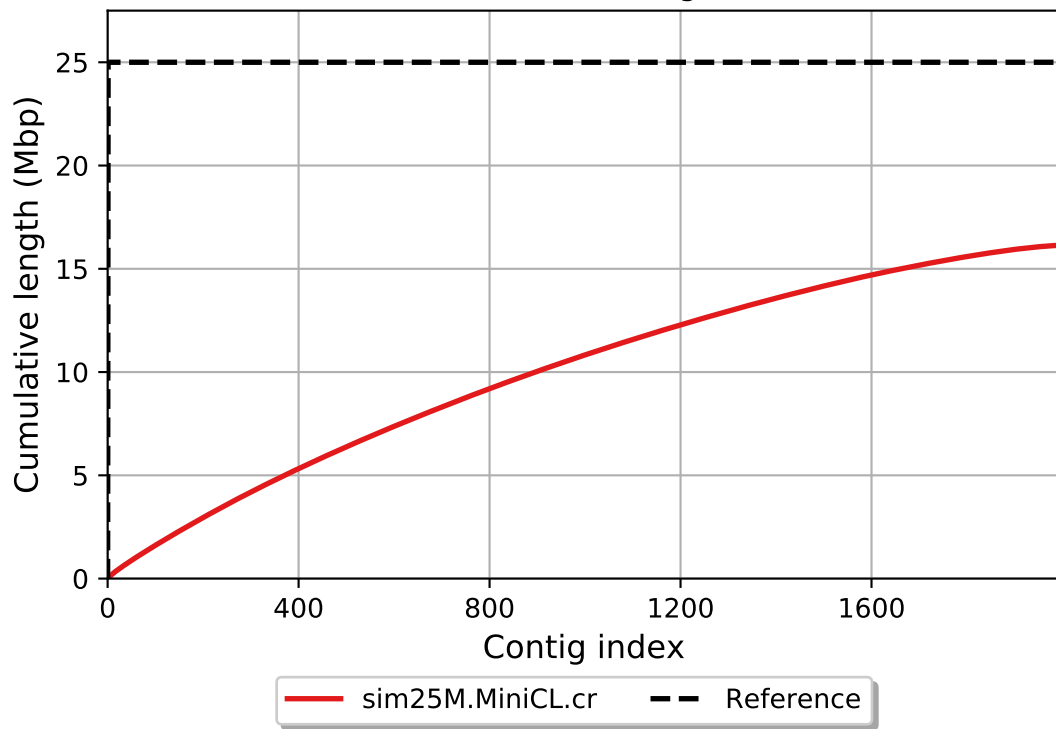
— sim25M.MiniCL.cr

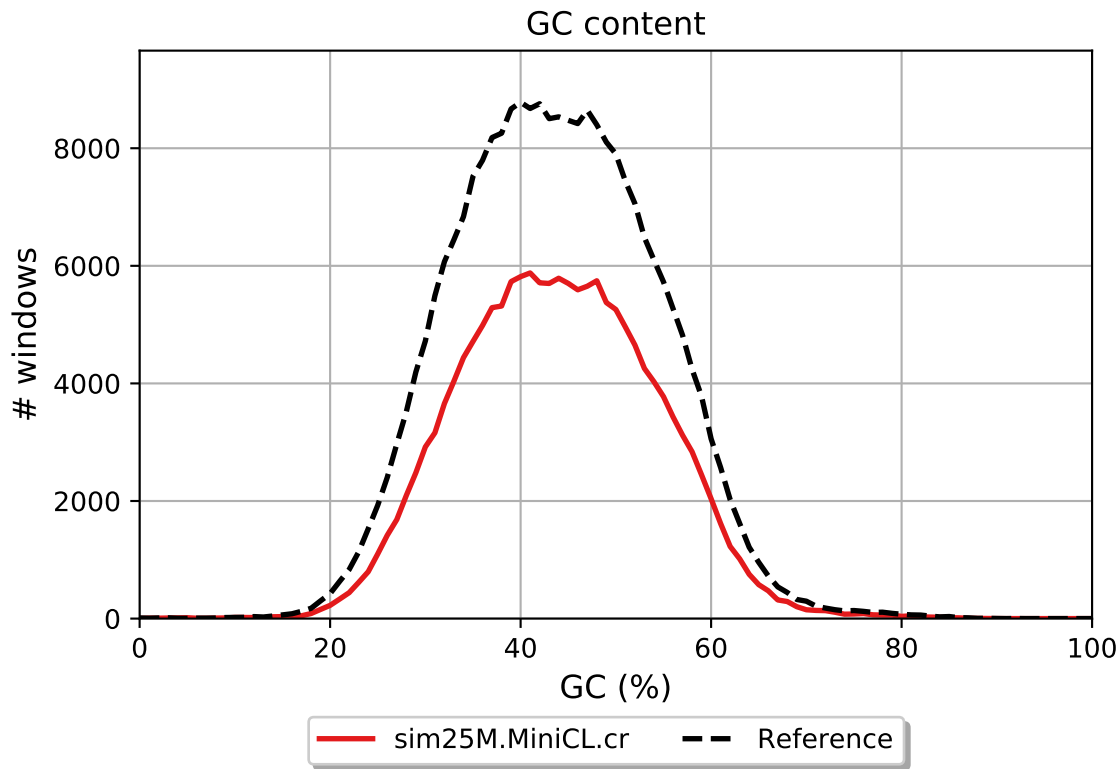
NGx



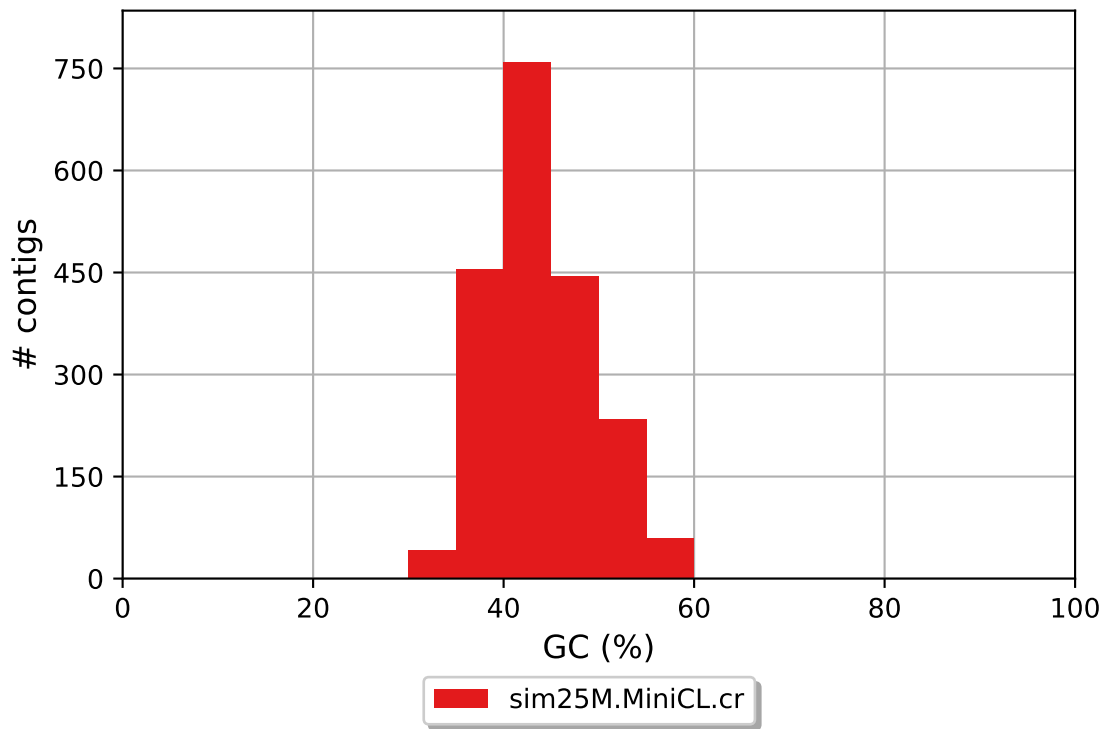
— sim25M.MiniCL.cr

Cumulative length

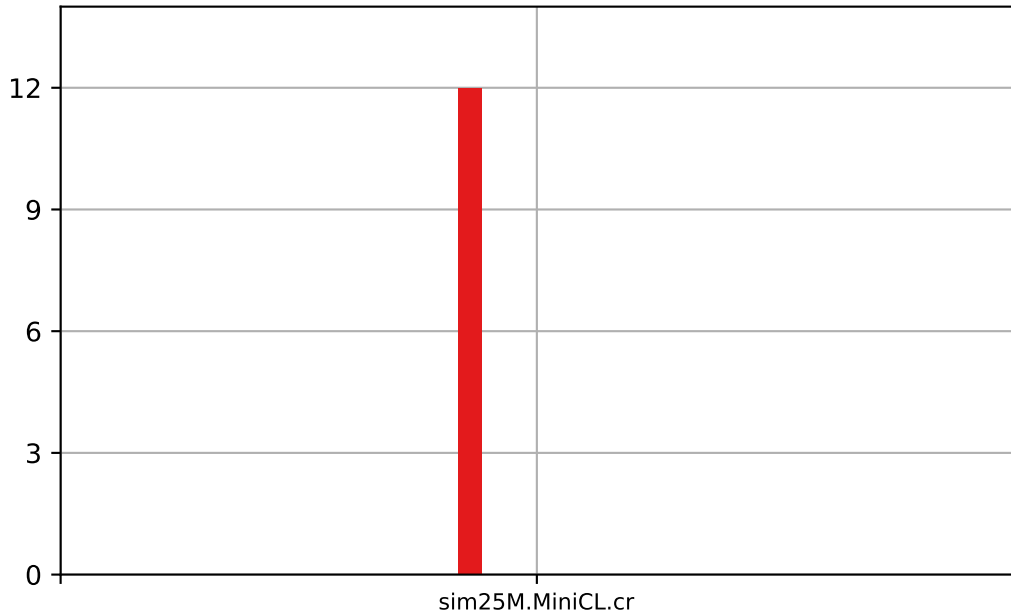




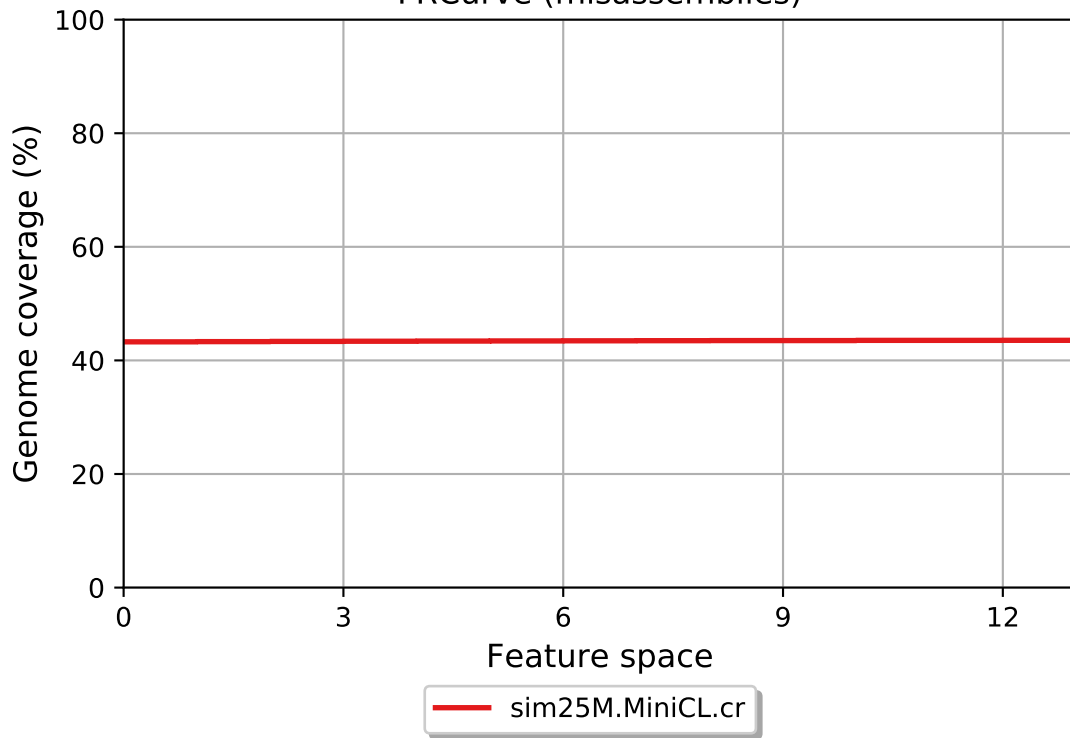
sim25M.MinicL.cr GC content



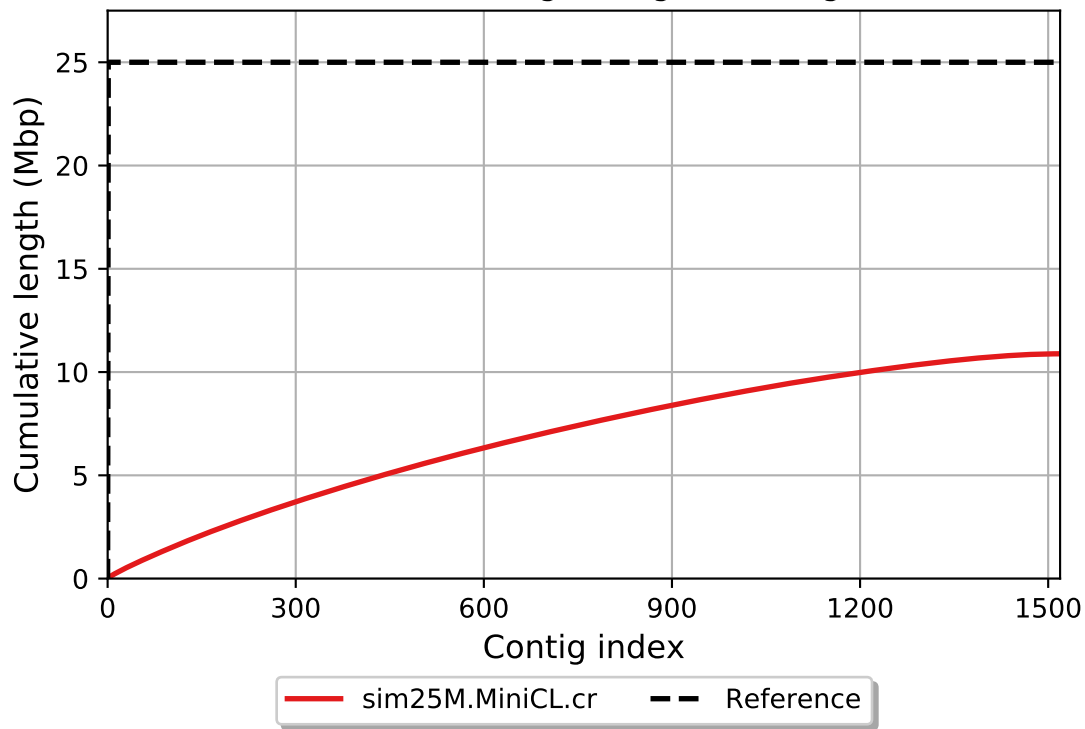
Misassemblies



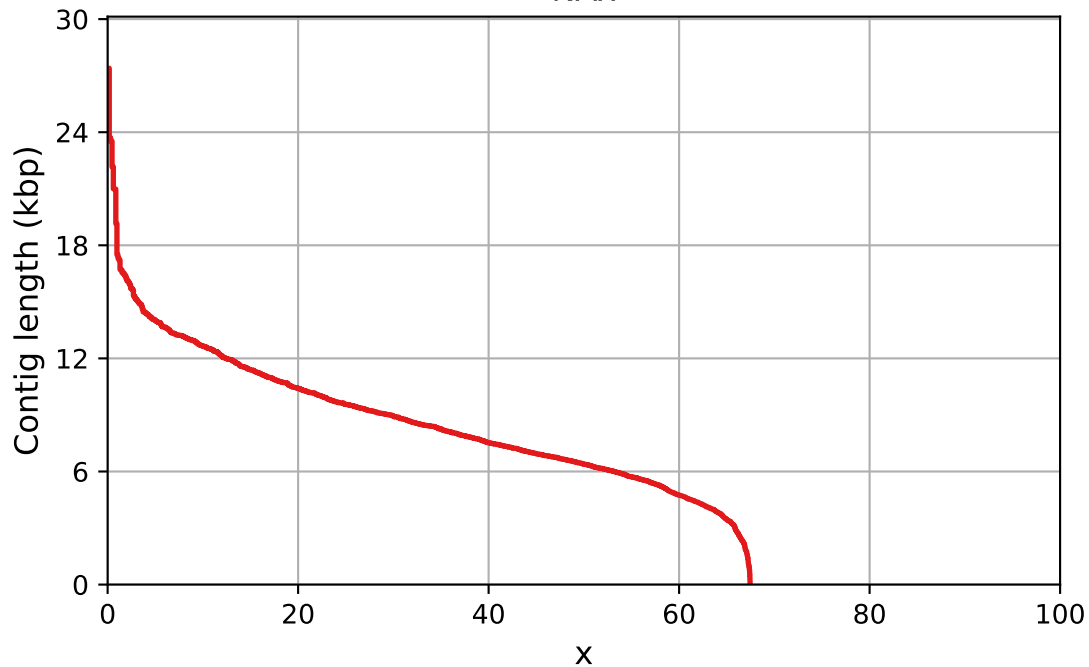
FRCurve (misassemblies)



Cumulative length (aligned contigs)

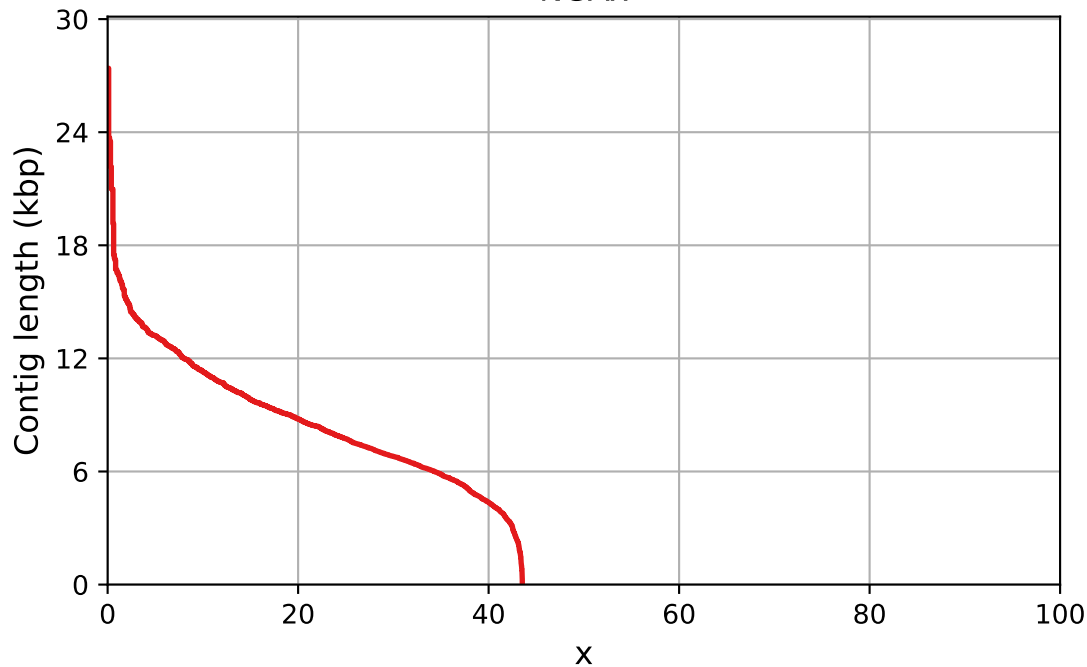


NAx



— sim25M.MinicL.cr

NGAx



— sim25M.MiniCL.cr