

Report

	sim25M.CanuH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1970
# contigs (>= 5000 bp)	1618
# contigs (>= 10000 bp)	525
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16040850
Total length (>= 1000 bp)	16030450
Total length (>= 5000 bp)	14707258
Total length (>= 10000 bp)	6510036
Total length (>= 25000 bp)	25036
Total length (>= 50000 bp)	0
# contigs	1975
Largest contig	25036
Total length	16034390
Reference length	25000020
GC (%)	43.89
Reference GC (%)	43.69
N50	9228
NG50	6788
N75	7082
L50	682
LG50	1243
L75	1175
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	47.354
Duplication ratio	1.354
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.68
# indels per 100 kbp	45.18
Largest alignment	25036
Total aligned length	16030637
NA50	9219
NGA50	6781
NA75	7082
LA50	682
LGA50	1244
LA75	1175

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.CanuH.cr
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	1856
# indels	5349
# indels (≤ 5 bp)	5331
# indels (> 5 bp)	18
Indels length	6146

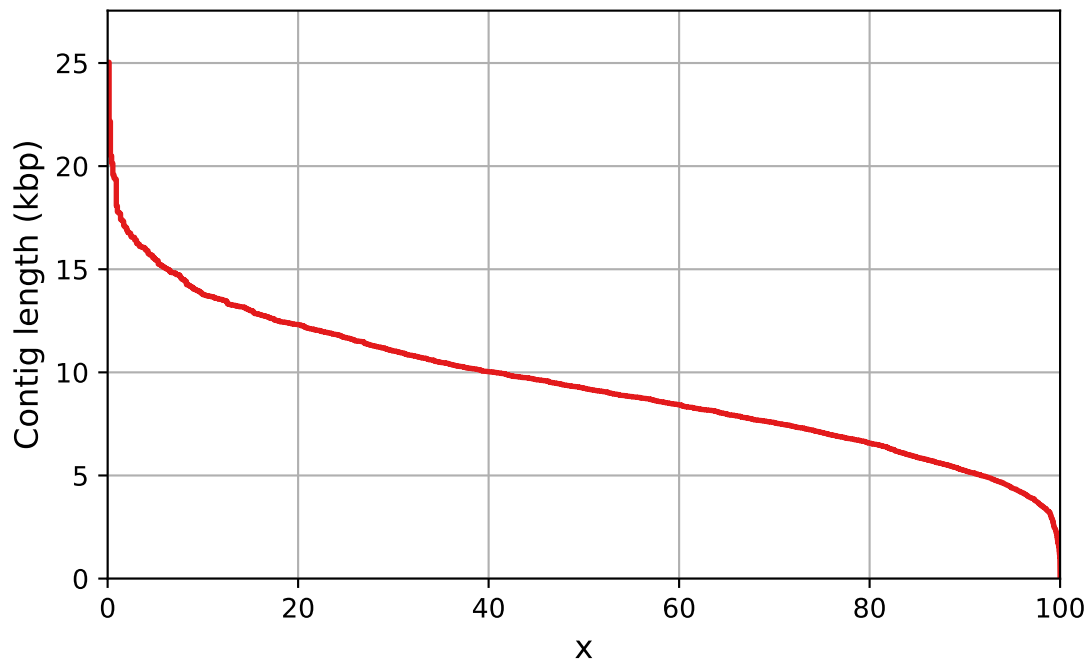
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim25M.CanuH.cr
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

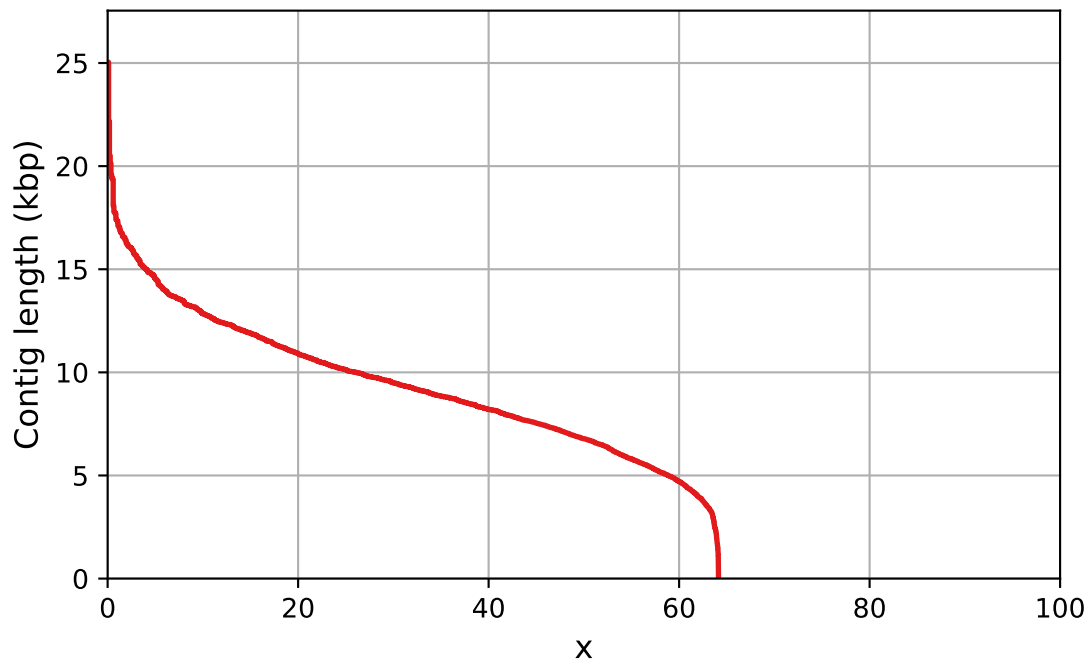
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



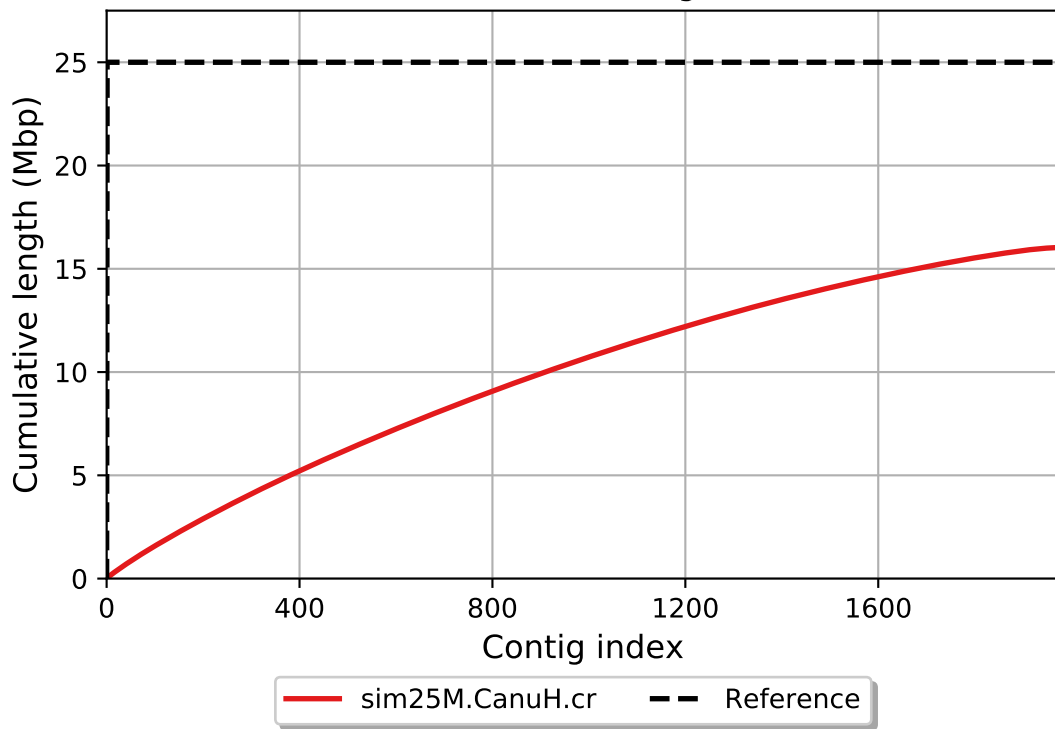
— sim25M.CanuH.cr

NGx

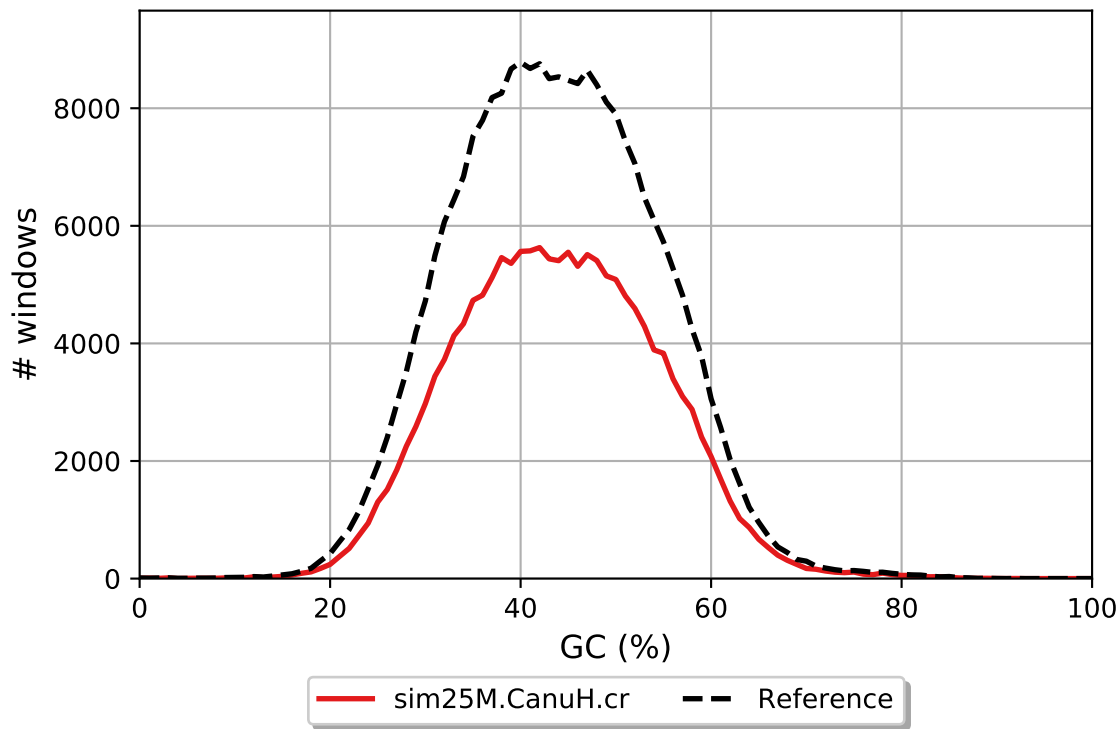


— sim25M.CanuH.cr

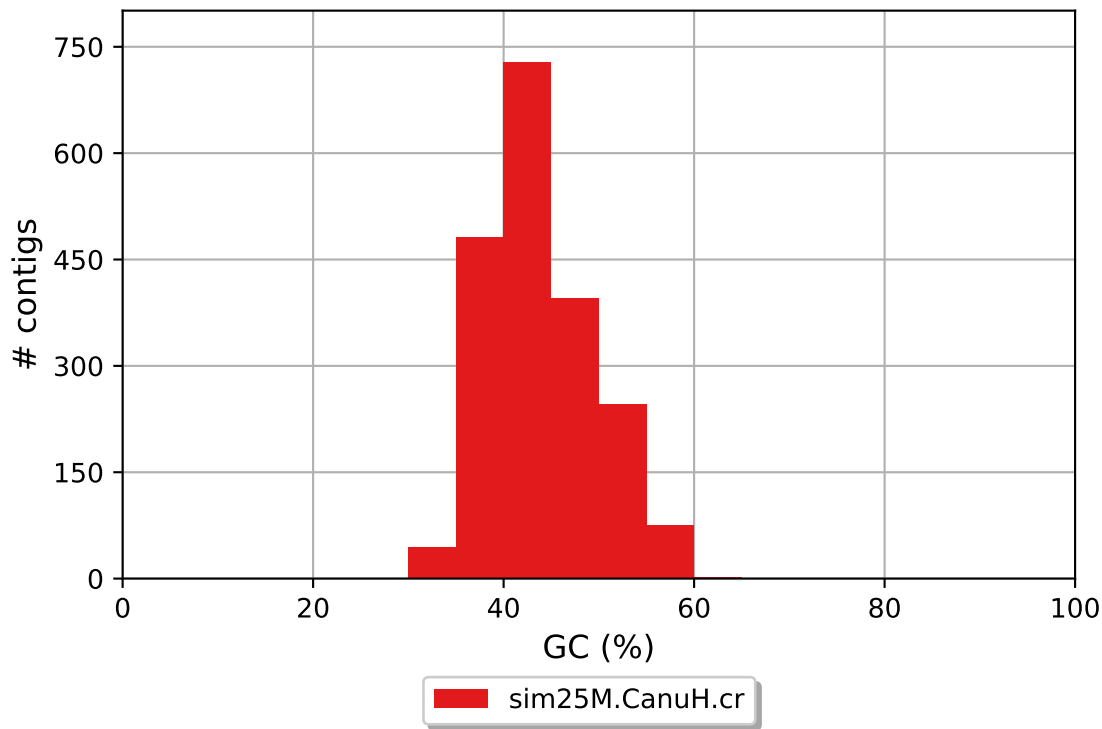
Cumulative length



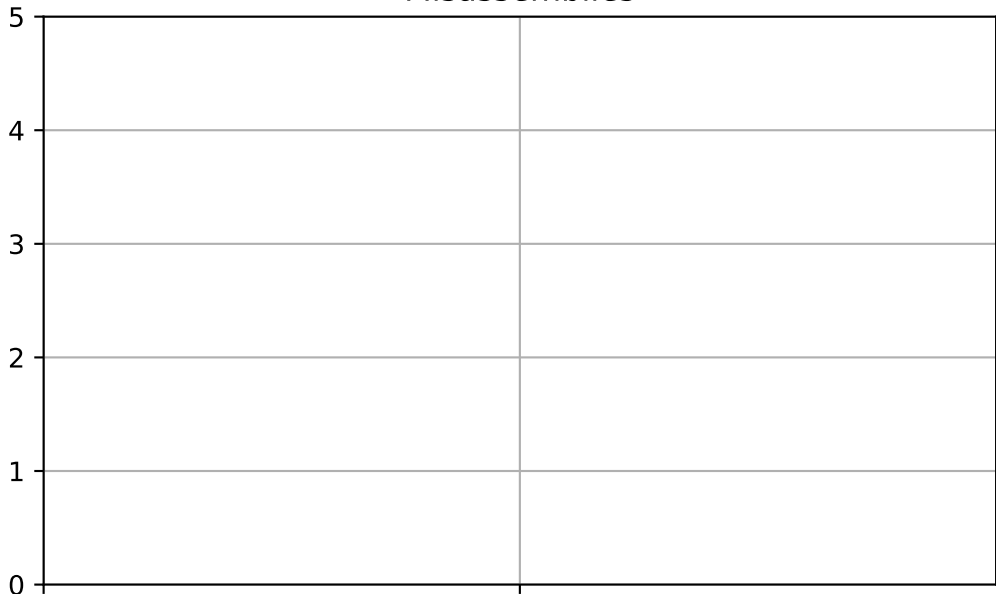
GC content



sim25M.CanuH.cr GC content

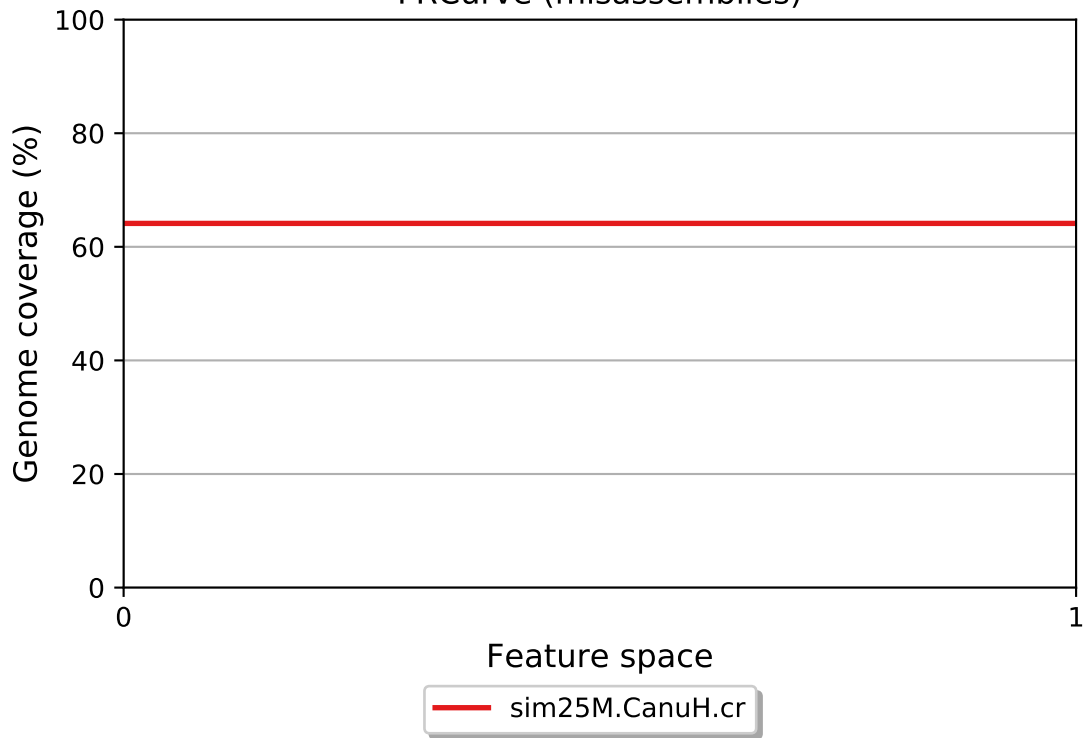


Misassemblies

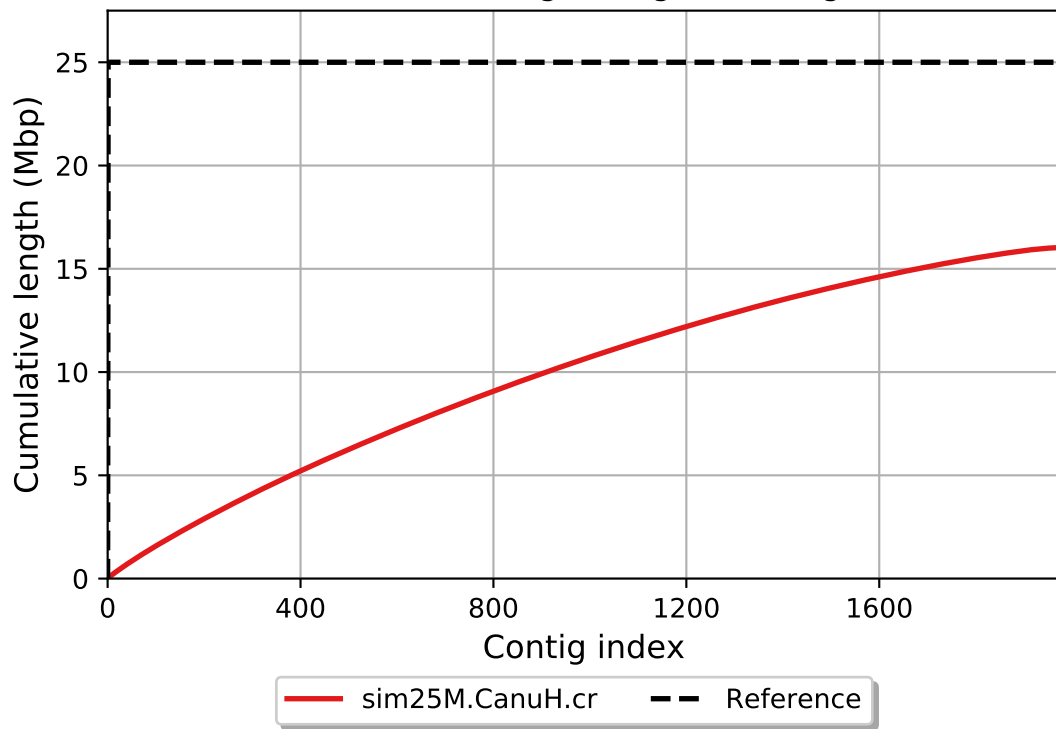


sim25M.CanuH.cr

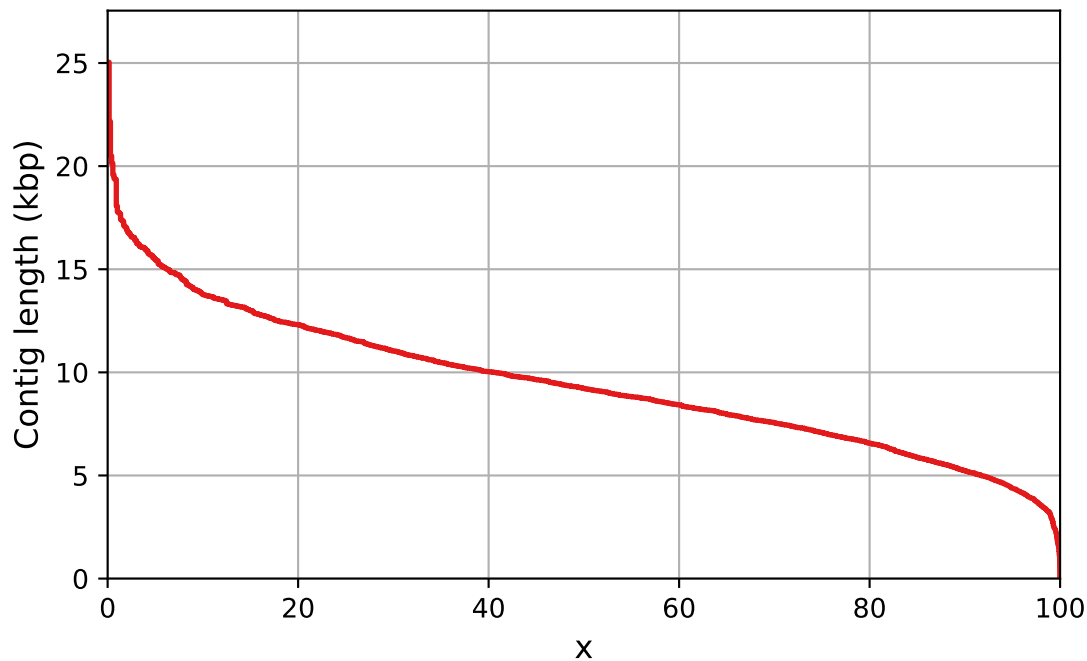
FRCurve (misassemblies)



Cumulative length (aligned contigs)

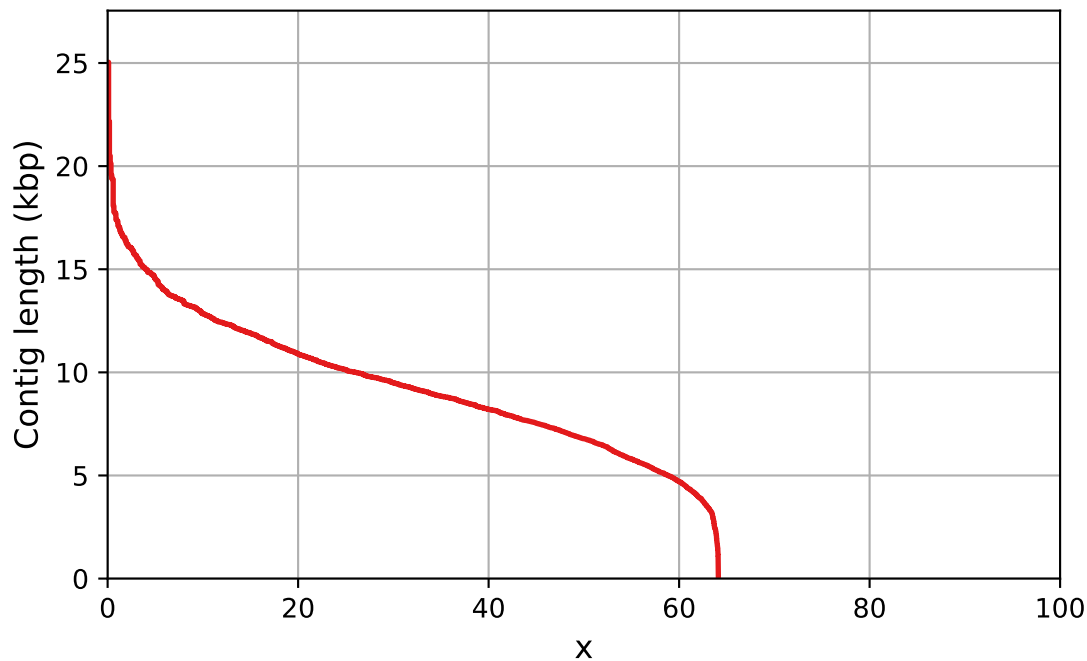


NAx



— sim25M.CanuH.cr

NGAx



— sim25M.CanuH.cr