

Report

	sim5M.Metasm
# contigs (≥ 0 bp)	1
# contigs (≥ 1000 bp)	1
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	1
Total length (≥ 0 bp)	5794912
Total length (≥ 1000 bp)	5794912
Total length (≥ 5000 bp)	5794912
Total length (≥ 10000 bp)	5794912
Total length (≥ 25000 bp)	5794912
Total length (≥ 50000 bp)	5794912
# contigs	1
Largest contig	5794912
Total length	5794912
Reference length	5000040
GC (%)	35.03
Reference GC (%)	35.84
N50	5794912
NG50	5794912
N75	5794912
NG75	5794912
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	4
# misassembled contigs	1
Misassembled contigs length	5794912
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	28.685
Duplication ratio	4.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.21
Largest alignment	1429727
Total aligned length	5794912
NA50	1137402
NGA50	1137942
NA75	1045178
NGA75	1045178
LA50	3
LGA50	2
LA75	4
LGA75	4

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.Metasm
# misassemblies	4
# relocations	4
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	5794912
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

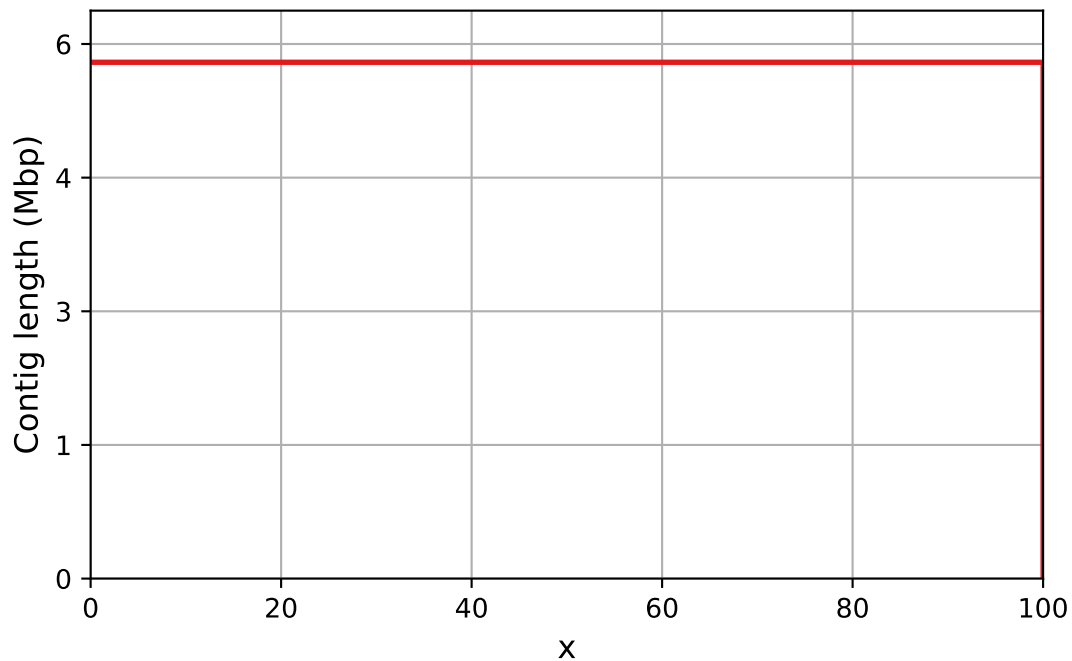
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim5M.Metasm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

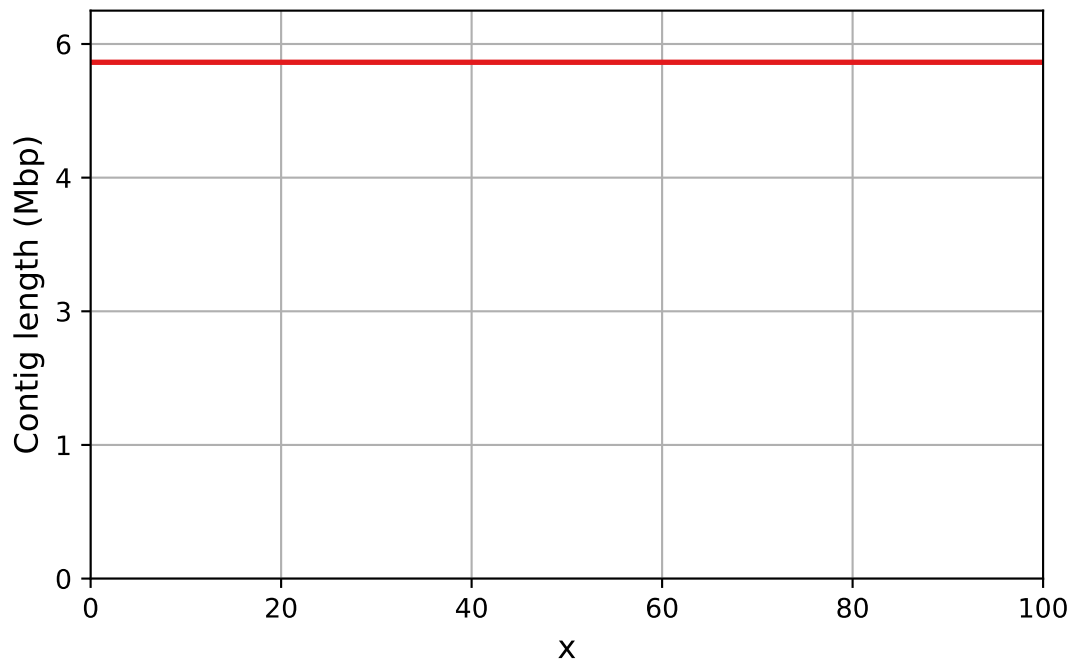
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

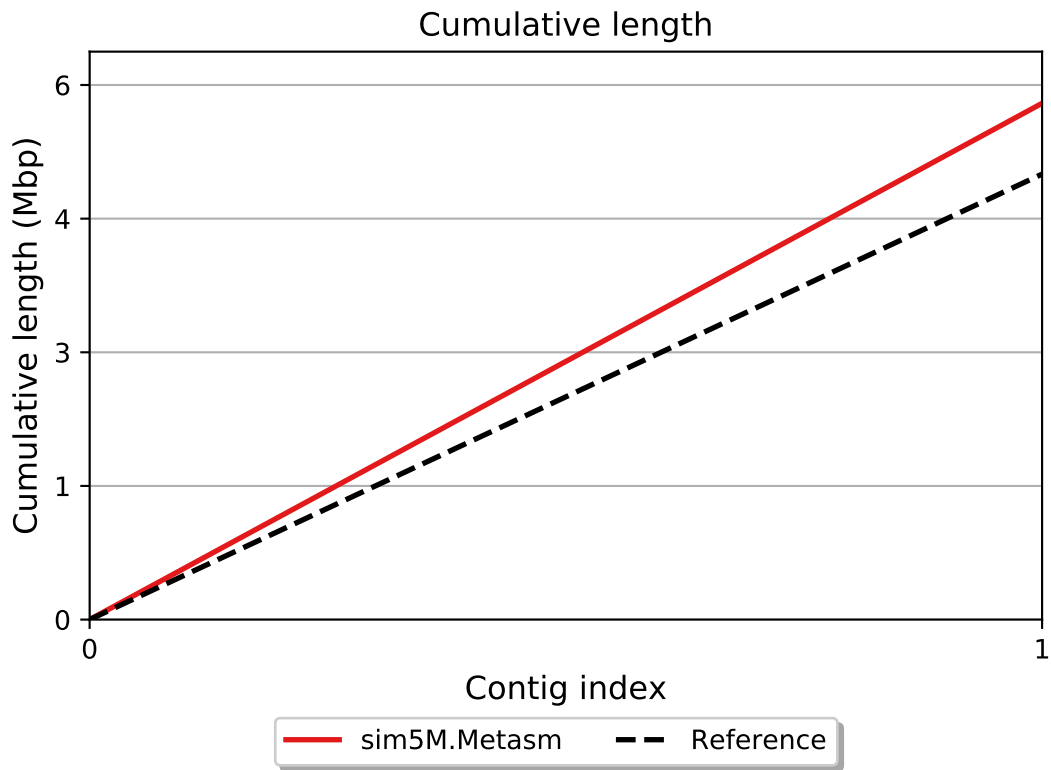


— sim5M.Metasm

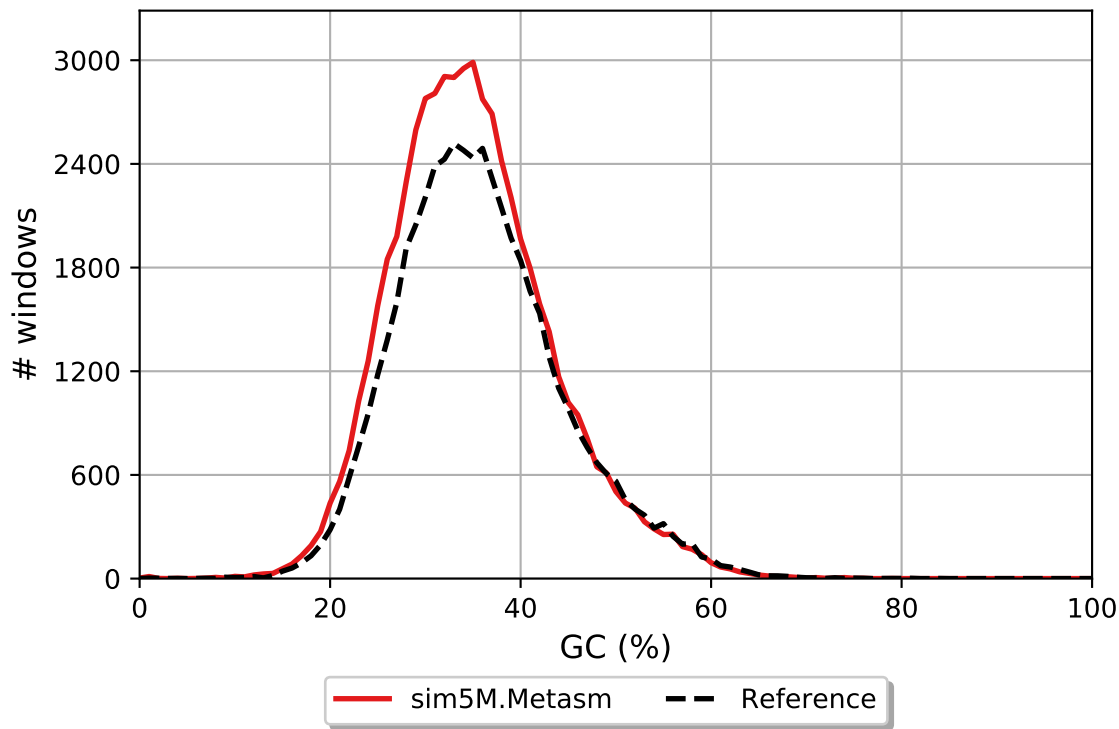
NGx



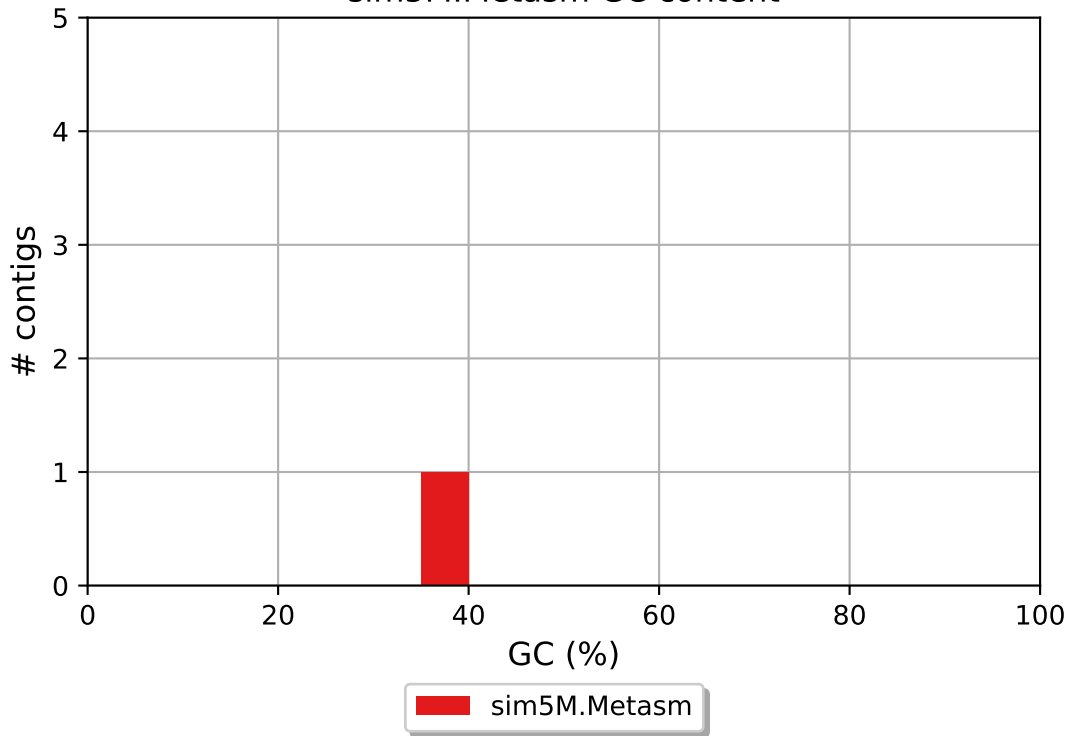
— sim5M.Metasm



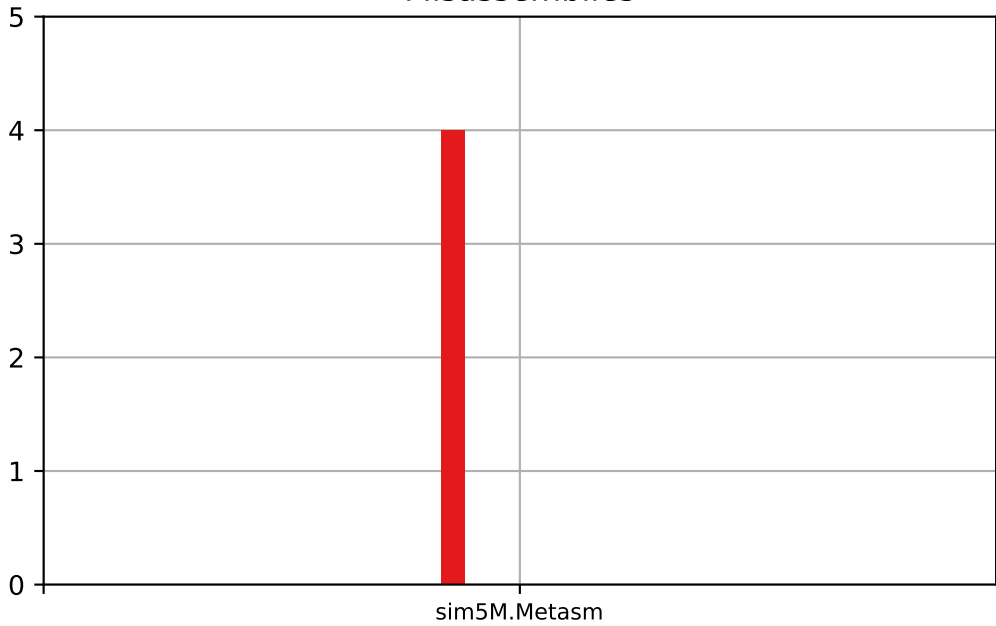
GC content



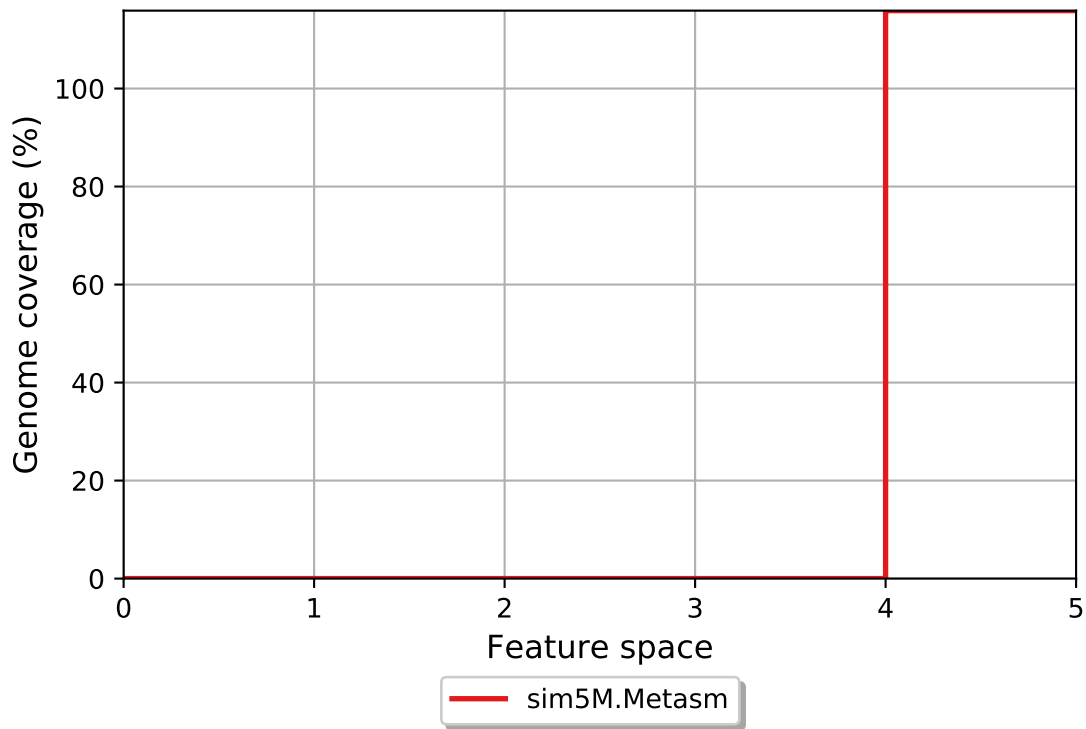
sim5M.Metasm GC content



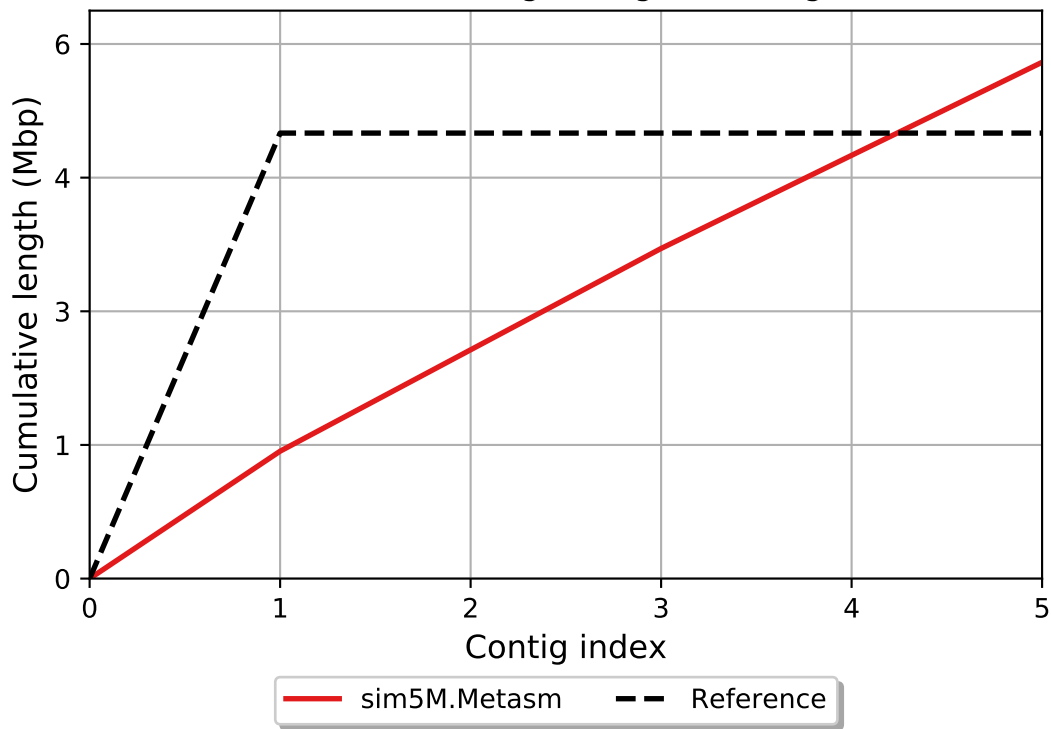
Misassemblies



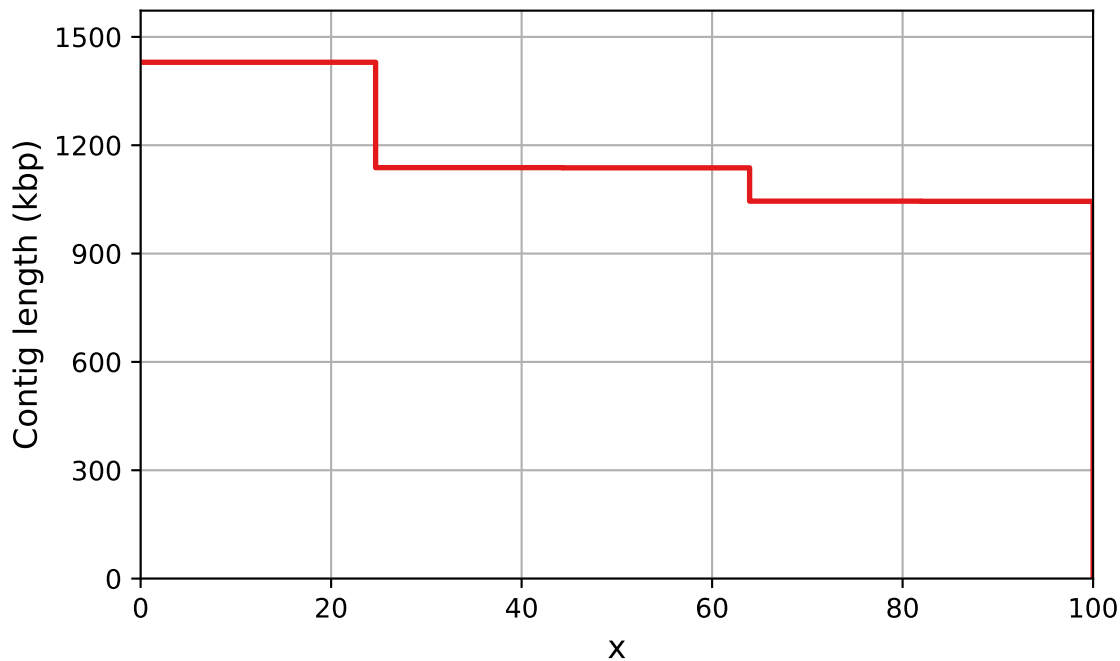
FRCurve (misassemblies)



Cumulative length (aligned contigs)

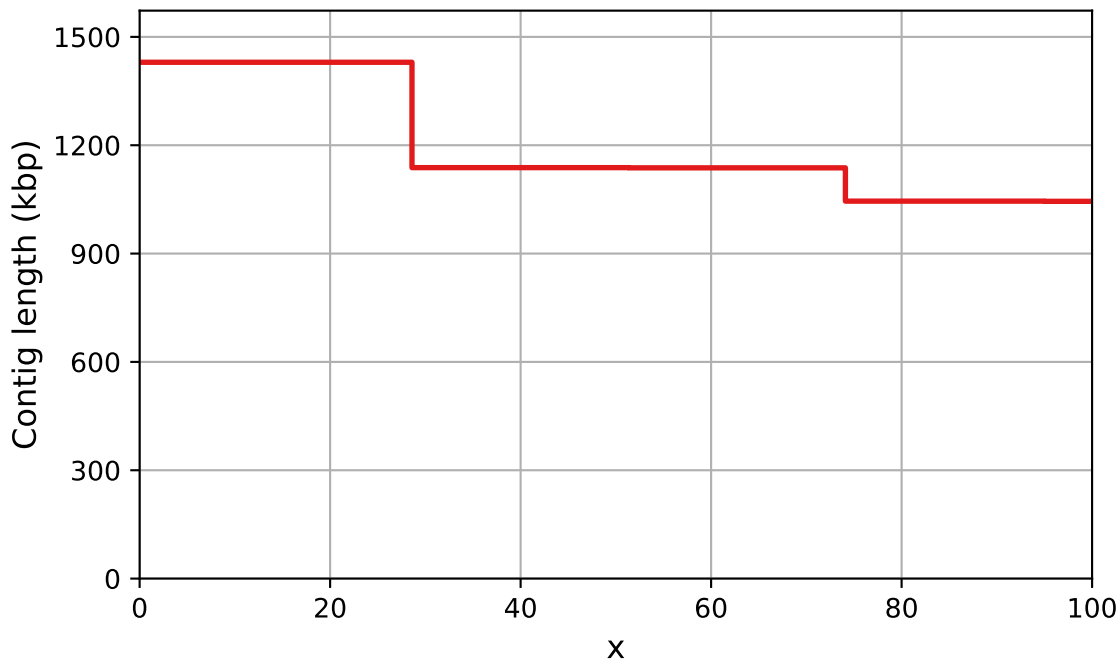


NAx



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NGAx



— sim5M.Metasm