

Report

	AJ055.CanuH.p1
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	5727525
Total length (>= 1000 bp)	5727525
Total length (>= 5000 bp)	5727525
Total length (>= 10000 bp)	5727525
Total length (>= 25000 bp)	5703410
Total length (>= 50000 bp)	5675539
# contigs	4
Largest contig	5497403
Total length	5727525
Reference length	5504133
GC (%)	57.19
Reference GC (%)	57.38
N50	5497403
NG50	5497403
N75	5497403
NG75	5497403
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	2 + 1 part
Unaligned length	229028
Genome fraction (%)	99.877
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	2.58
Largest alignment	5497400
Total aligned length	5498494
NA50	5497400
NGA50	5497400
NA75	5497400
NGA75	5497400
LA50	1
LGA50	1
LA75	1
LGA75	1

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

	AJ055.CanuH.p1
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	142
# indels (≤ 5 bp)	142
# indels (> 5 bp)	0
Indels length	146

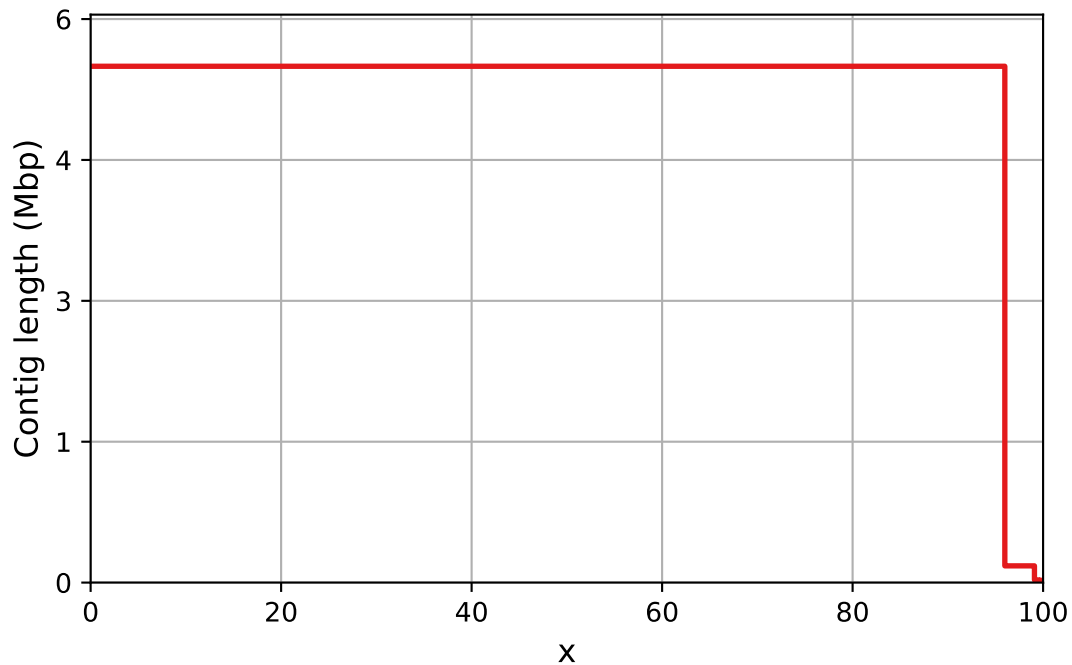
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ055.CanuH.p1
# fully unaligned contigs	2
Fully unaligned length	51986
# partially unaligned contigs	1
Partially unaligned length	177042
# N's	0

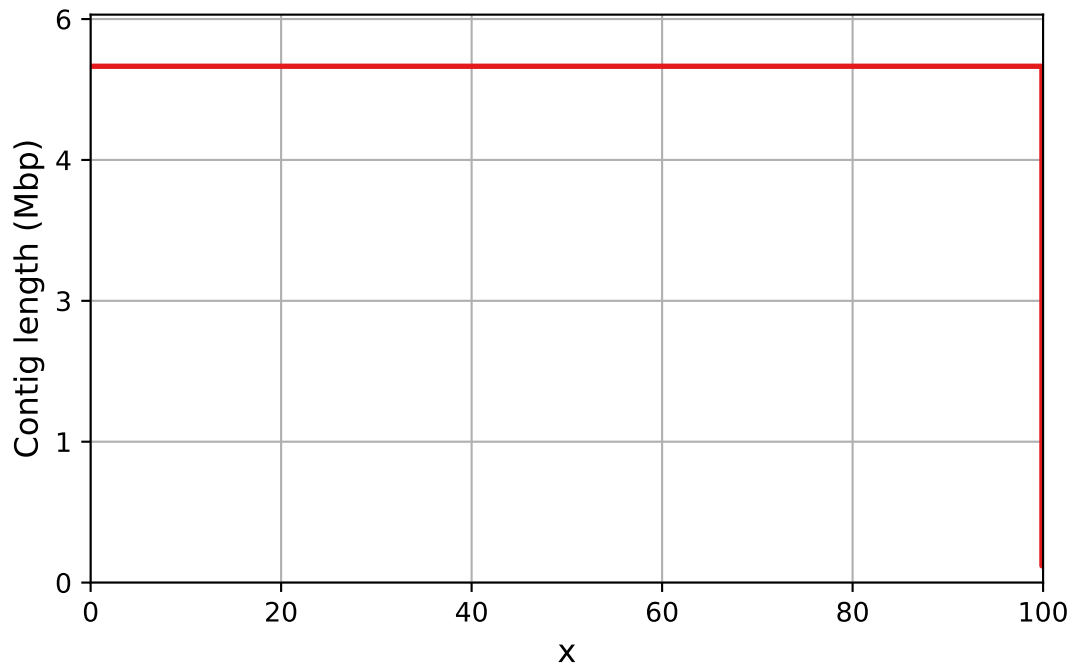
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



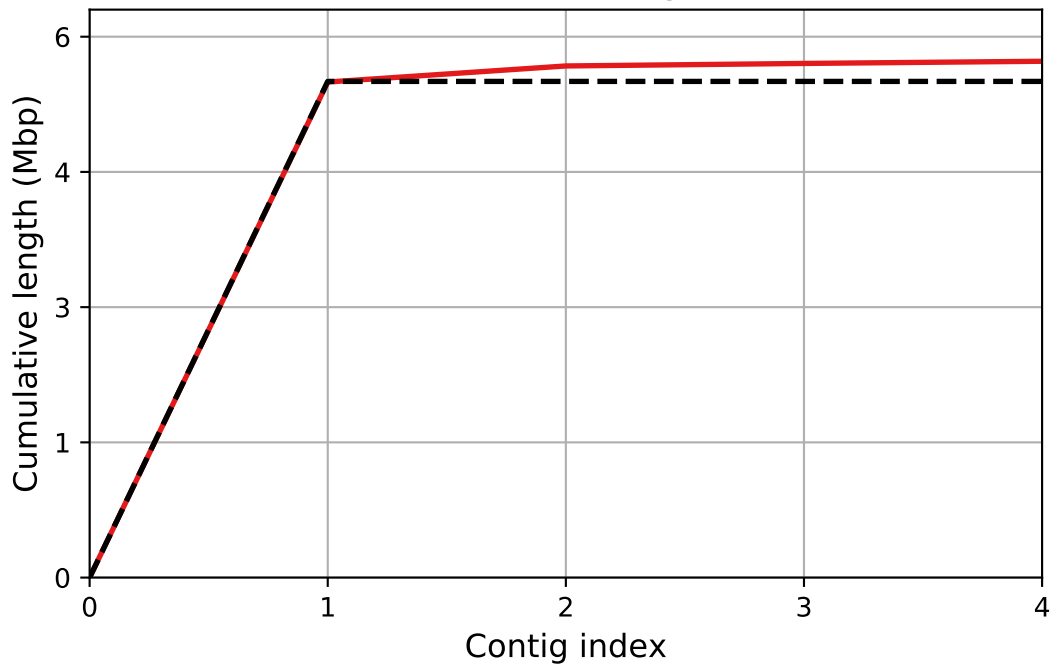
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NGx



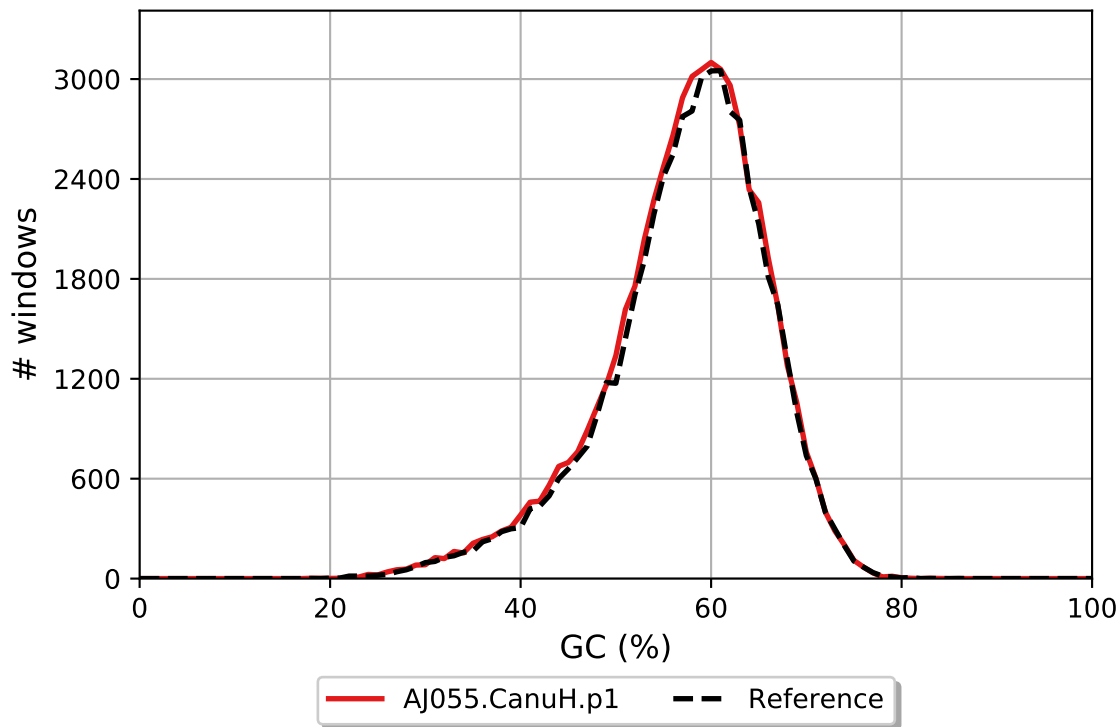
Aj055.CanuH.p1

Cumulative length

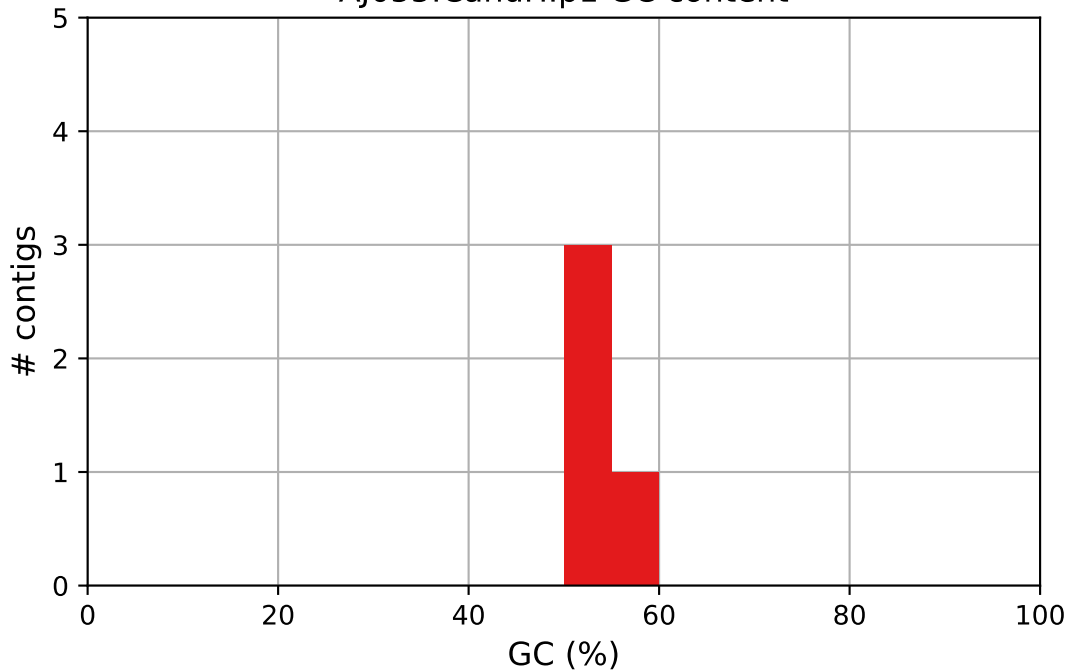


AJ055.CanuH.p1 Reference

GC content

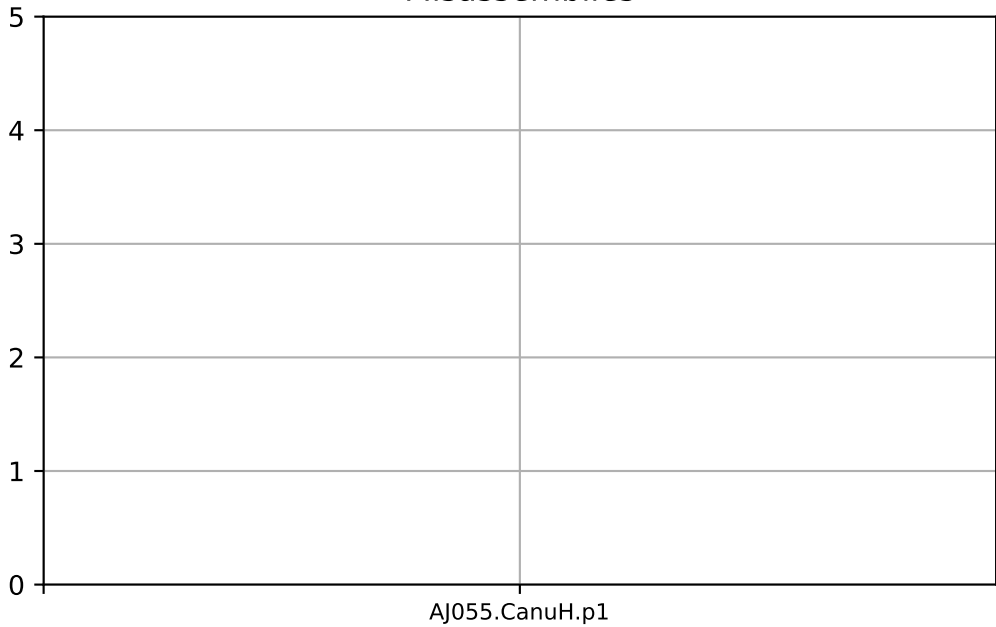


AJ055.CanuH.p1 GC content

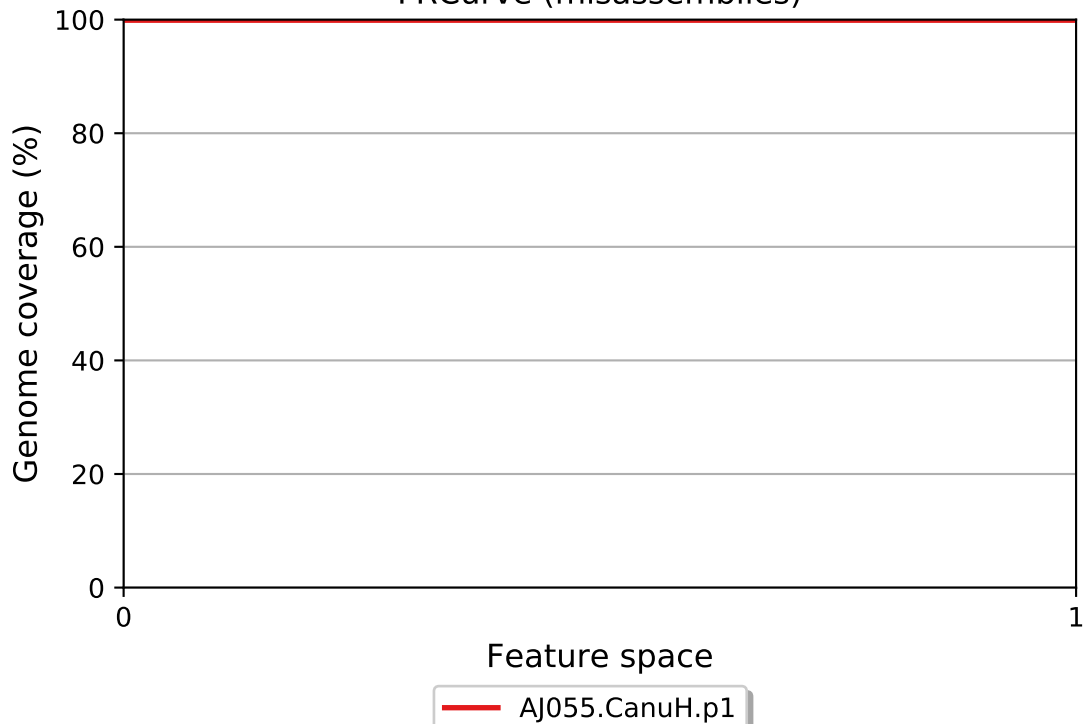


AJ055.CanuH.p1

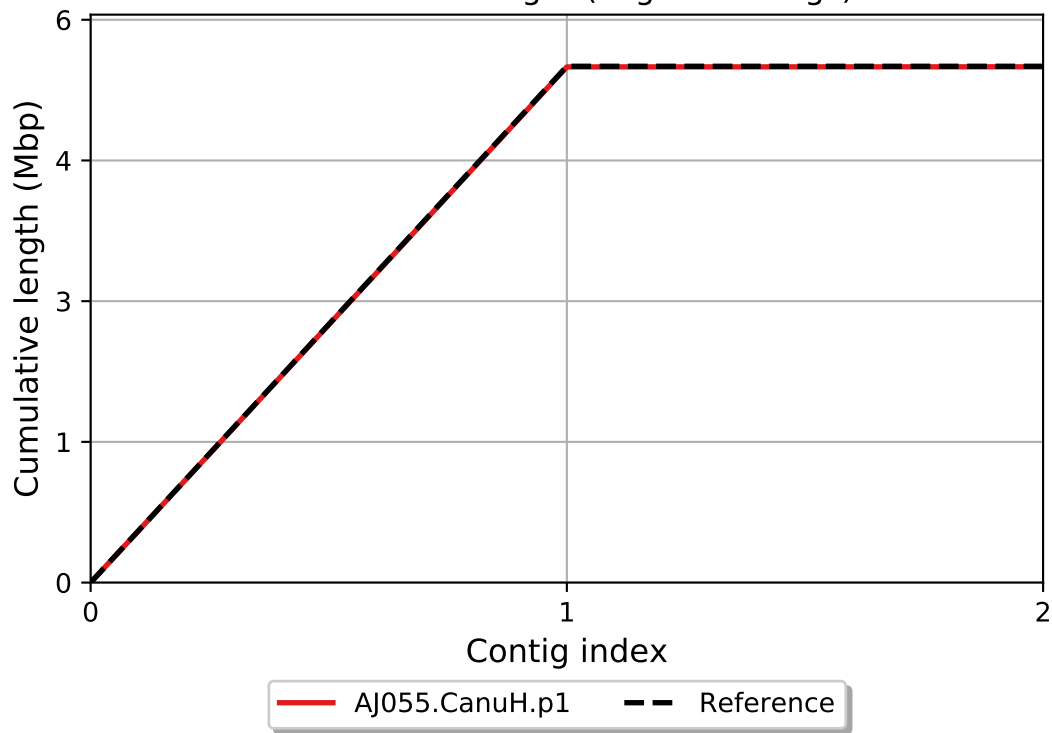
Misassemblies



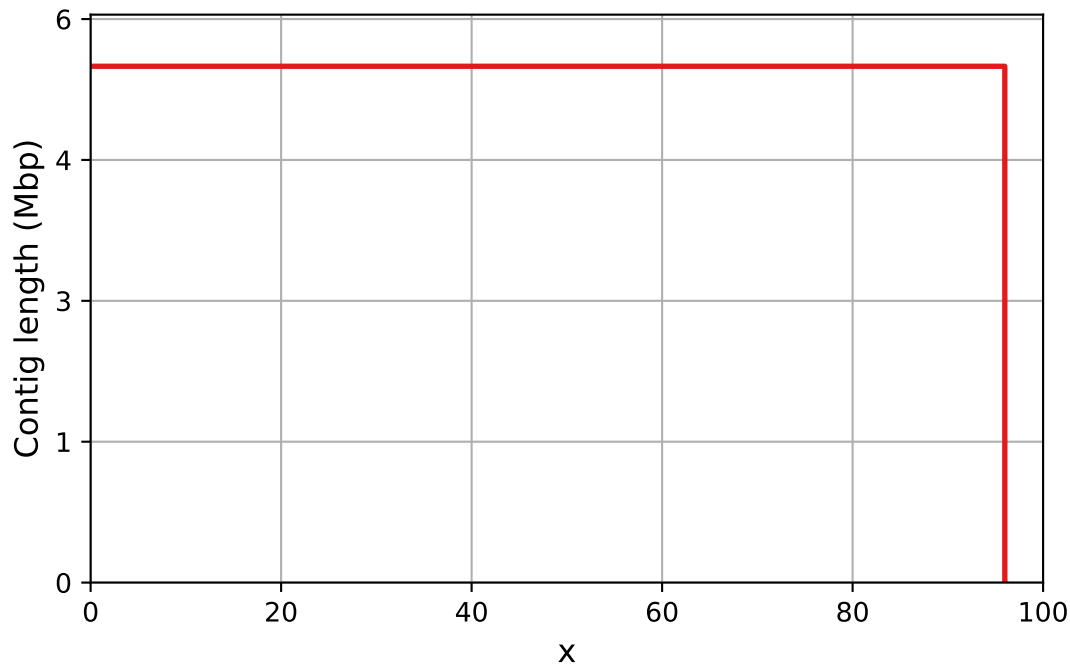
FRCurve (misassemblies)



Cumulative length (aligned contigs)

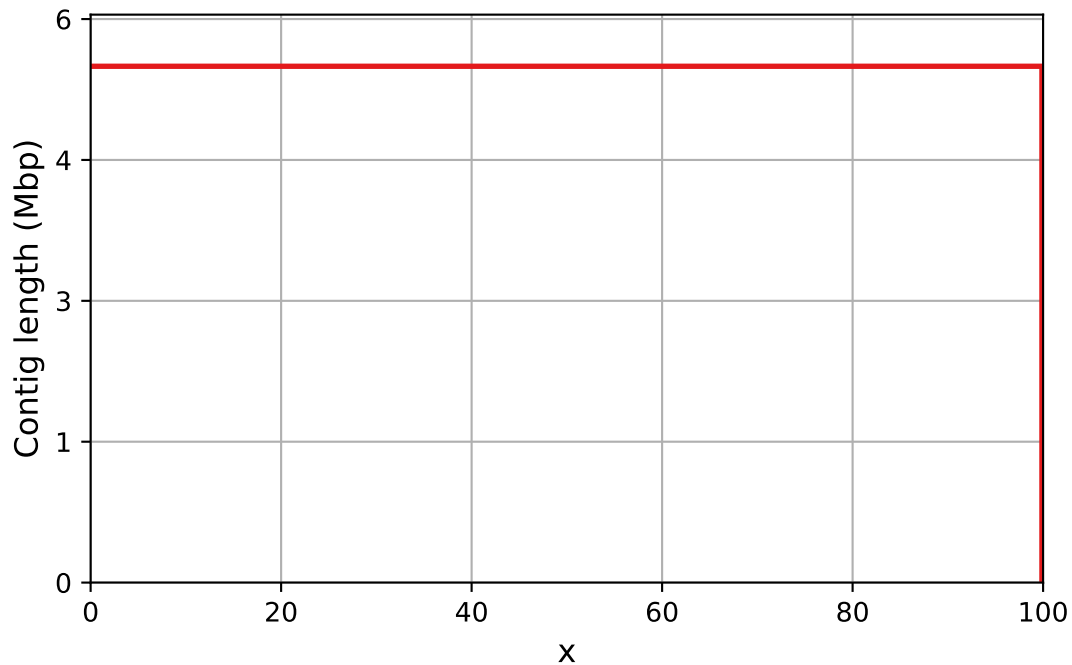


NAx



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NGAx



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