

Report

	AJ055.MiniH.p2
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	5671342
Total length (>= 1000 bp)	5671342
Total length (>= 5000 bp)	5671342
Total length (>= 10000 bp)	5671342
Total length (>= 25000 bp)	5671342
Total length (>= 50000 bp)	5671342
# contigs	2
Largest contig	5505584
Total length	5671342
Reference length	5504133
GC (%)	57.23
Reference GC (%)	57.38
N50	5505584
NG50	5505584
N75	5505584
NG75	5505584
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	169061
Genome fraction (%)	99.939
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.69
# indels per 100 kbp	8.05
Largest alignment	5501187
Total aligned length	5502281
NA50	5501187
NGA50	5501187
NA75	5501187
NGA75	5501187
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.MiniH.p2
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	38
# indels	443
# indels (≤ 5 bp)	438
# indels (> 5 bp)	5
Indels length	658

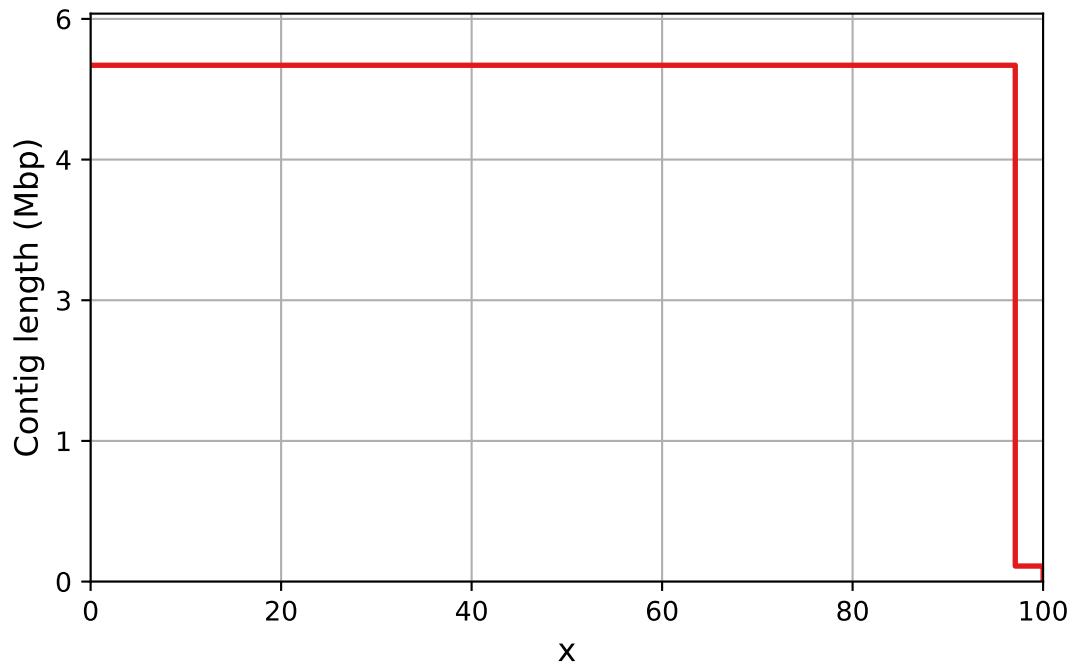
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ055.MiniH.p2
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	169061
# N's	0

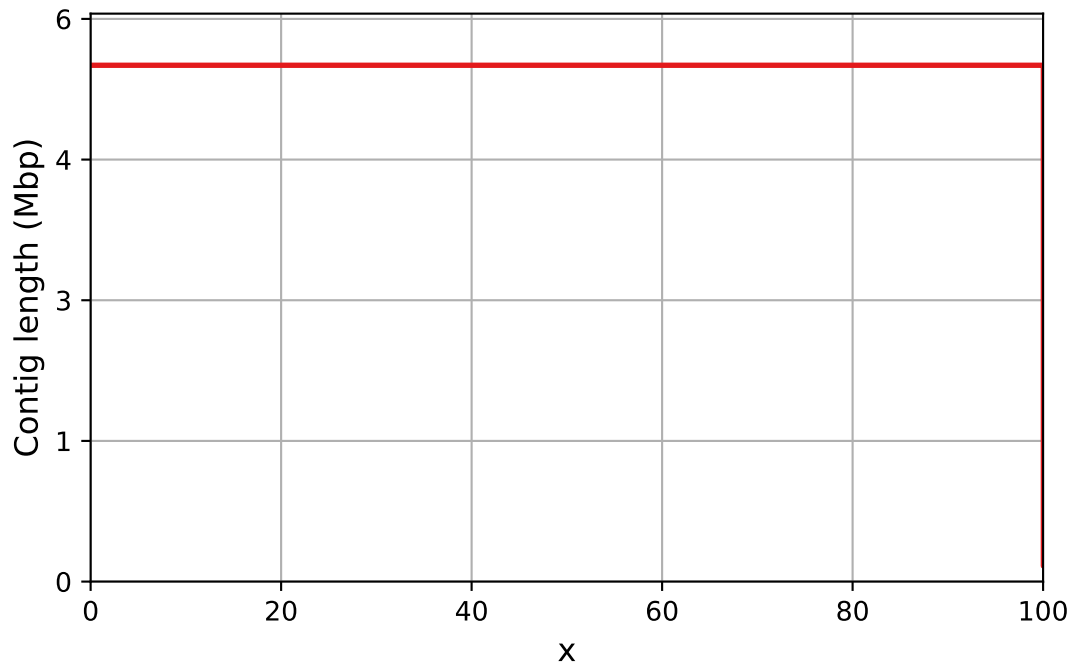
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

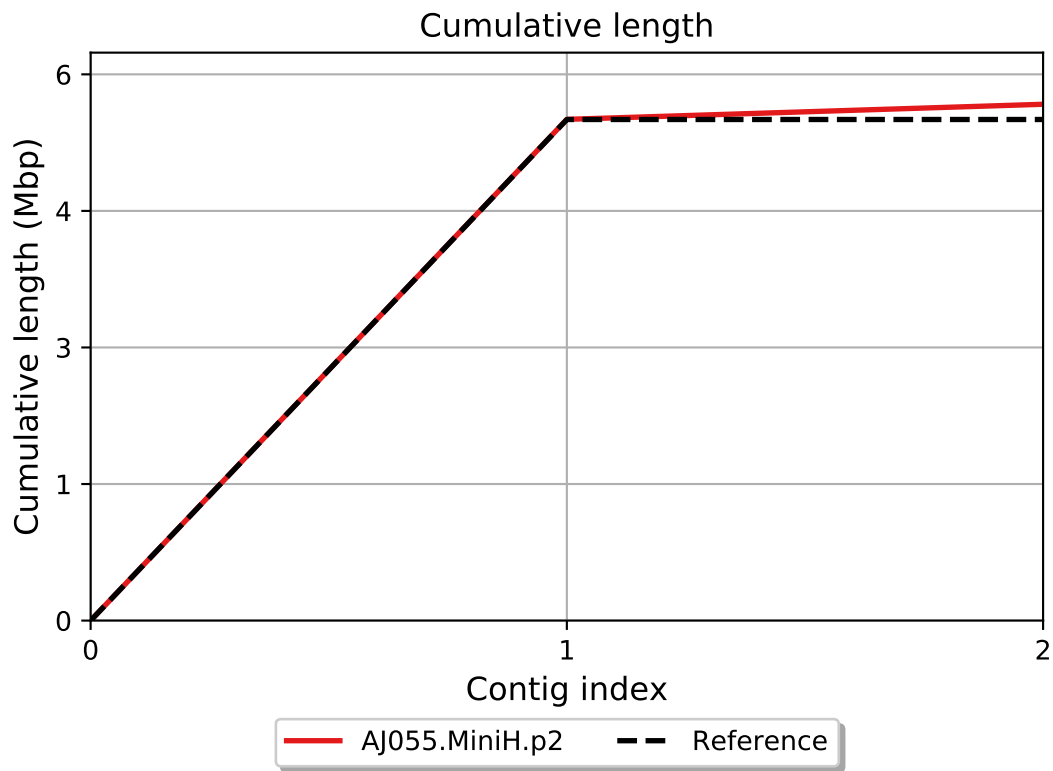


AJ055.MiniH.p2

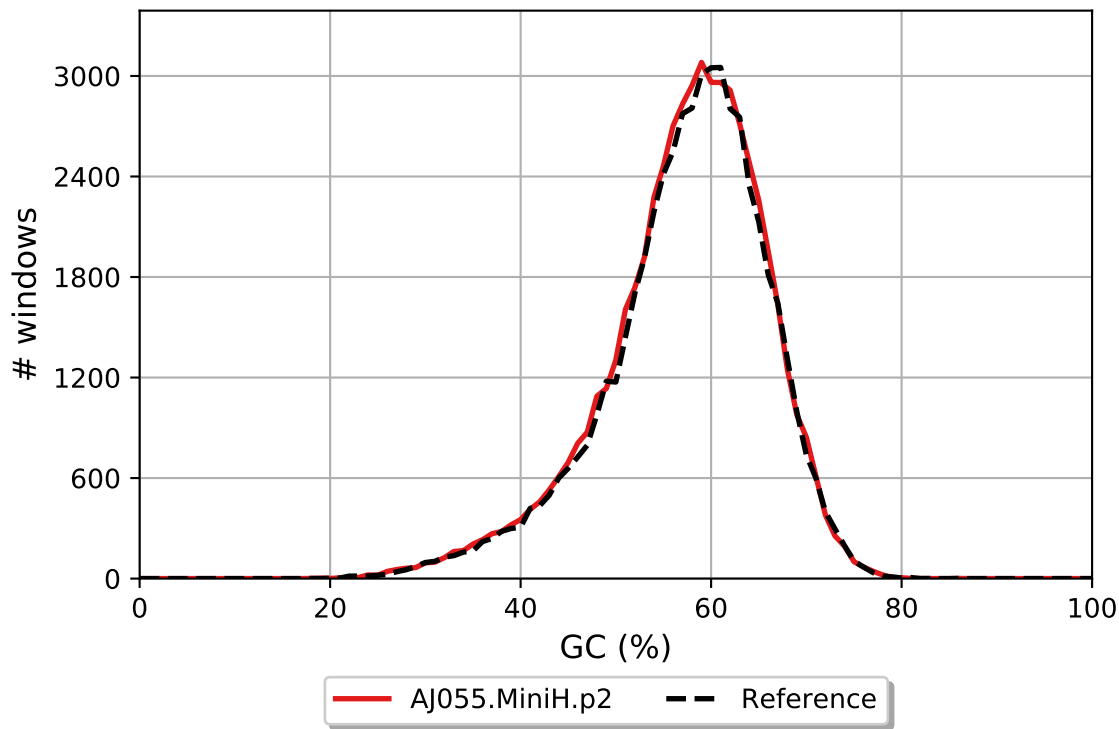
NGx



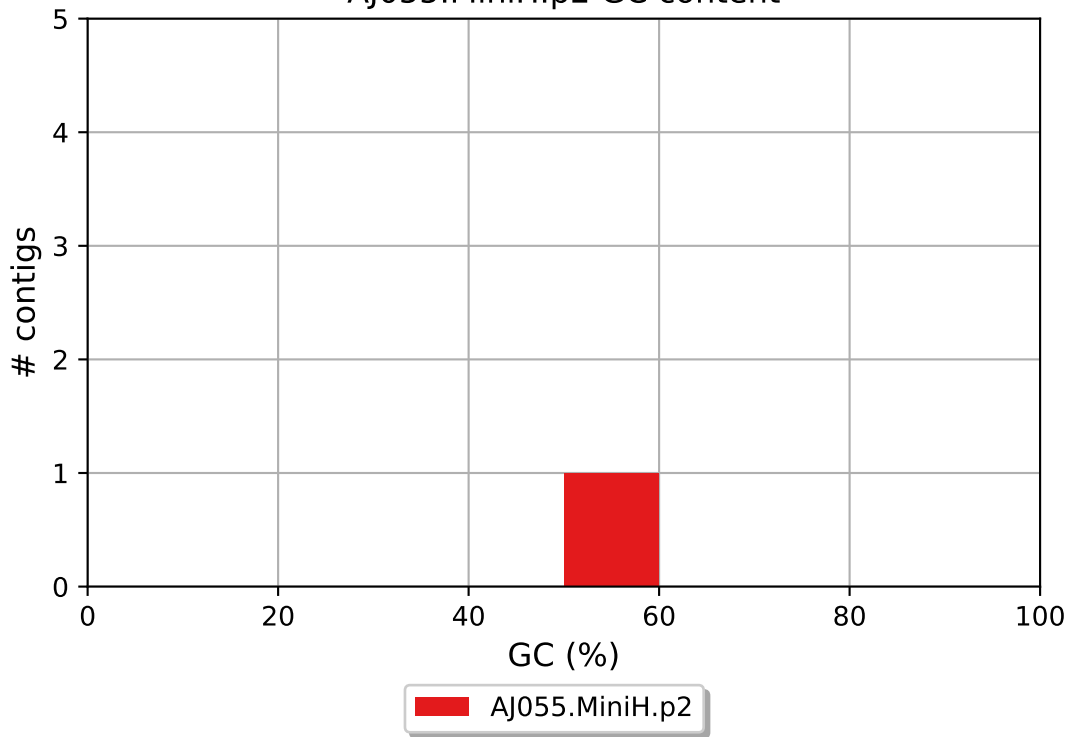
AJ055.MiniH.p2



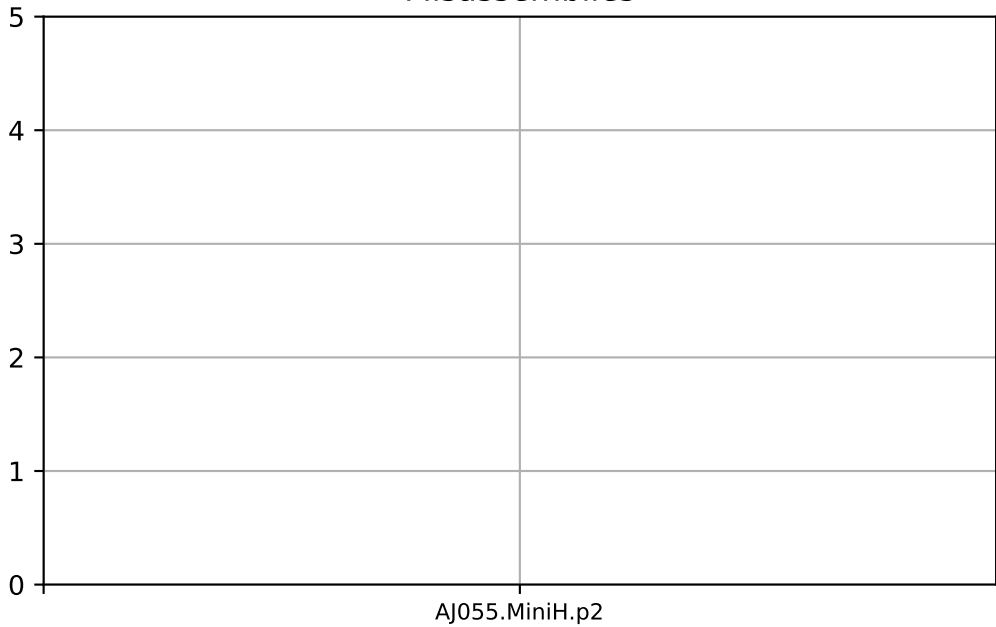
GC content



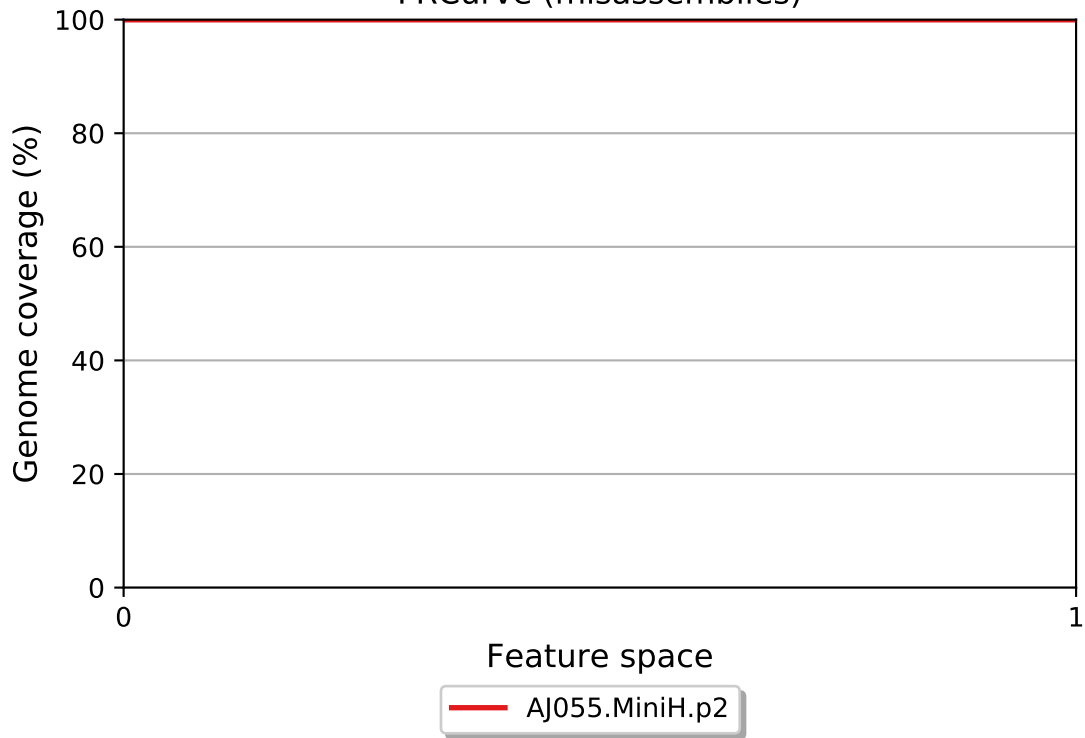
AJ055.MiniH.p2 GC content



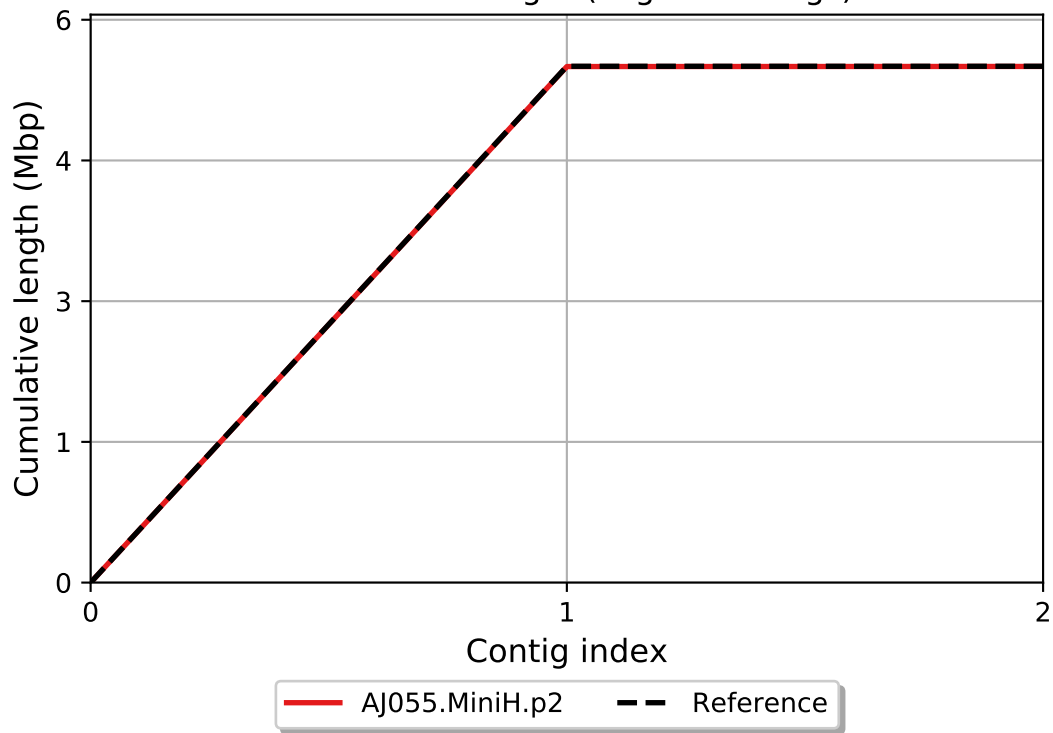
Misassemblies



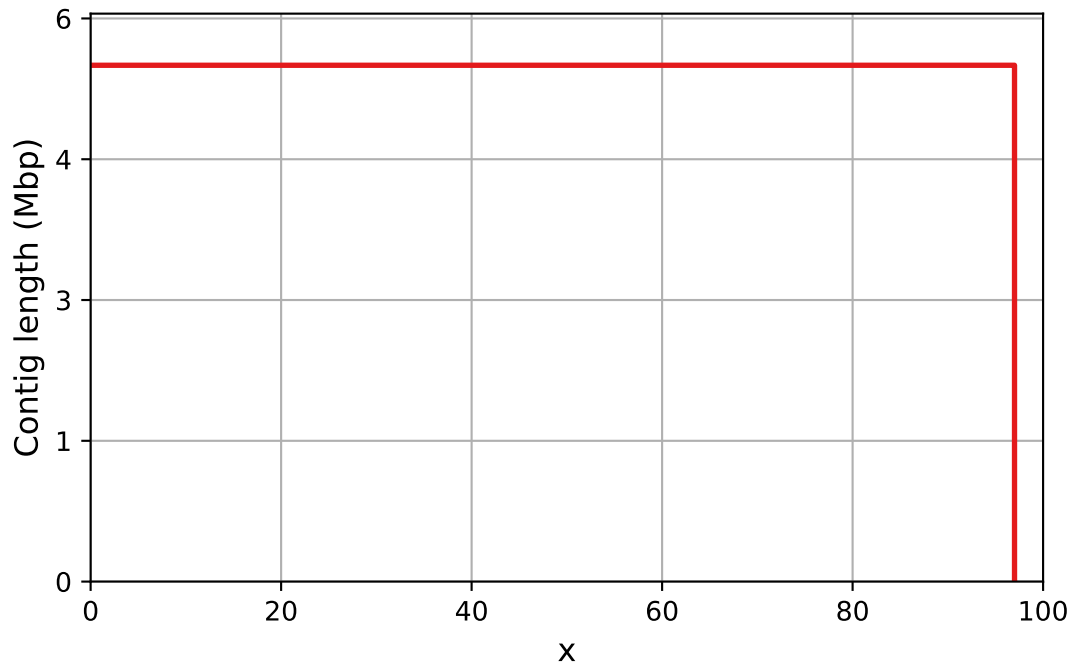
FRCurve (misassemblies)



Cumulative length (aligned contigs)

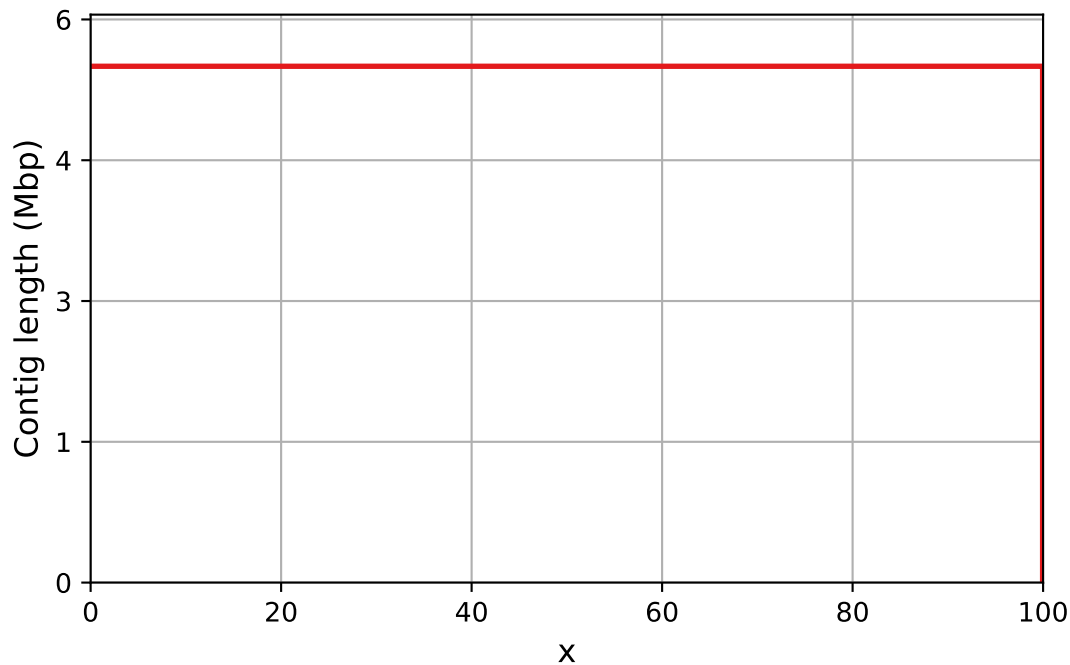


NAx



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NGAx



AJ055.MiniH.p2