

# Report

	AJ055.MiniH.p1
# 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)	5670982
Total length (>= 1000 bp)	5670982
Total length (>= 5000 bp)	5670982
Total length (>= 10000 bp)	5670982
Total length (>= 25000 bp)	5670982
Total length (>= 50000 bp)	5670982
# contigs	2
Largest contig	5505273
Total length	5670982
Reference length	5504133
GC (%)	57.24
Reference GC (%)	57.38
N50	5505273
NG50	5505273
N75	5505273
NG75	5505273
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	169027
Genome fraction (%)	99.939
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.04
# indels per 100 kbp	55.57
Largest alignment	5500863
Total aligned length	5501955
NA50	5500863
NGA50	5500863
NA75	5500863
NGA75	5500863
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.p1
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	57
# indels	3057
# indels ( $\leq 5$ bp)	3036
# indels ( $> 5$ bp)	21
Indels length	4705

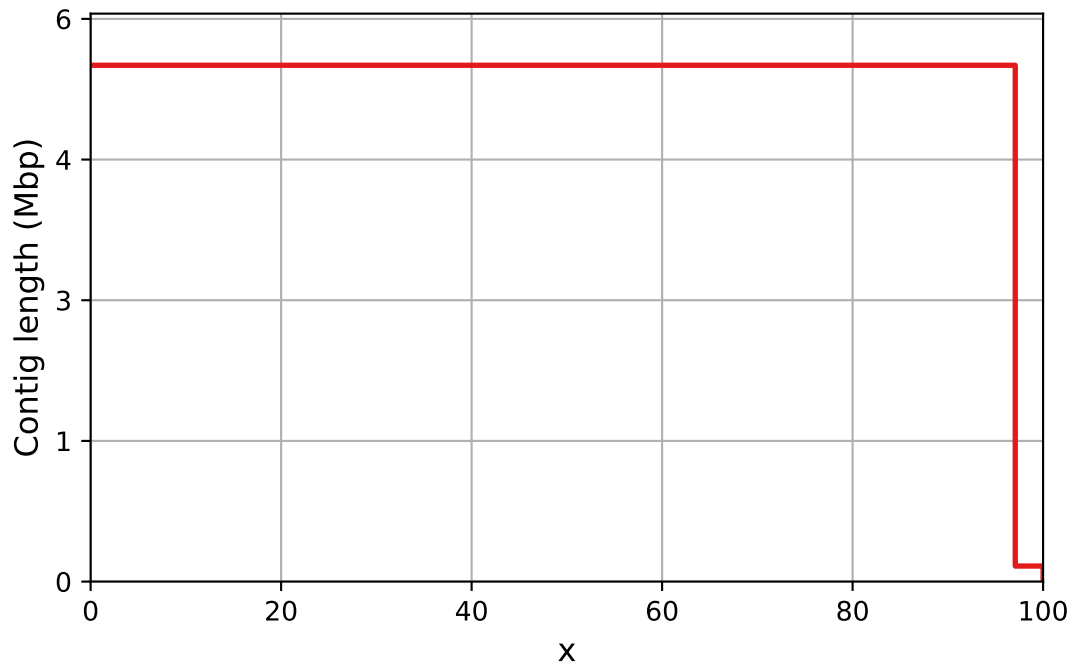
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ055.MiniH.p1
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	169027
# N's	0

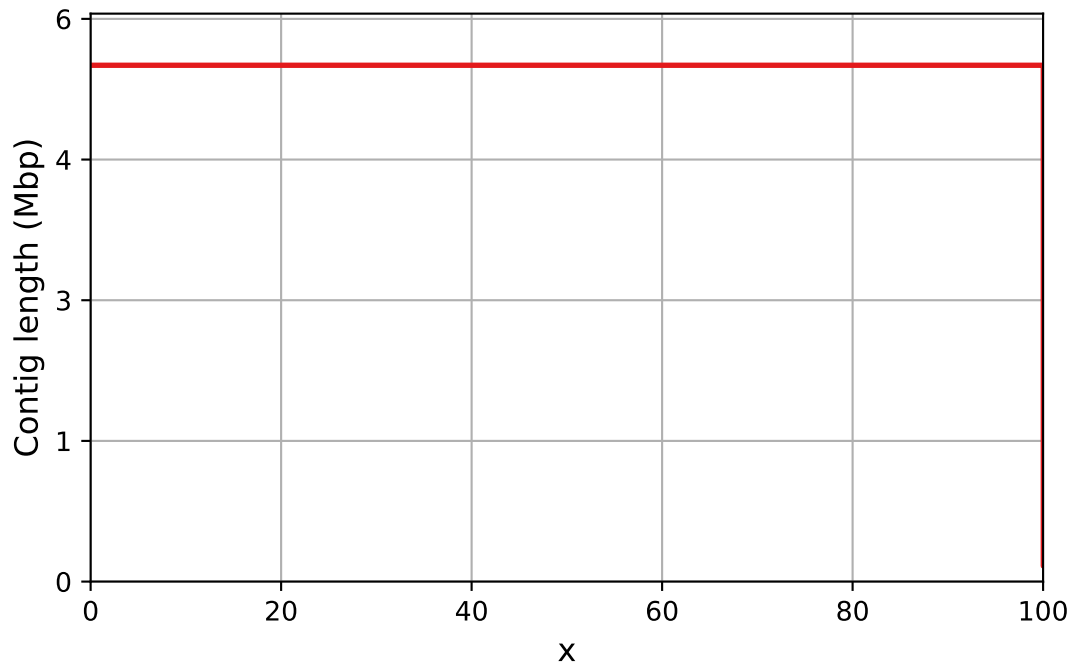
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

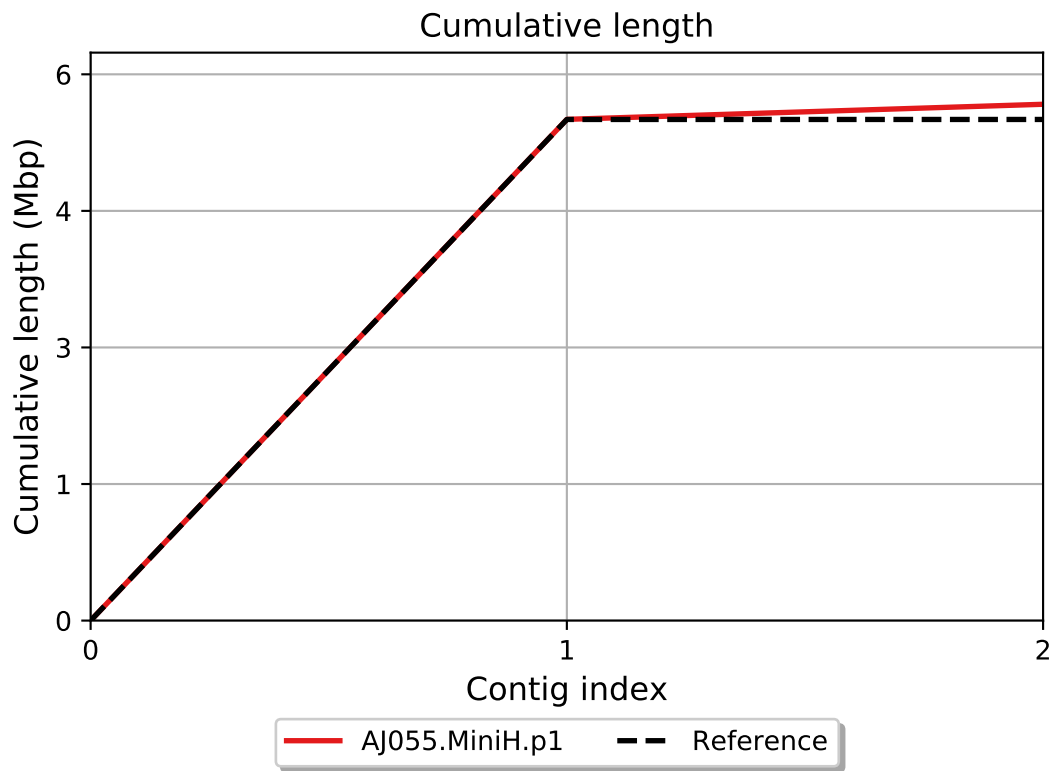


AJ055.MiniH.p1

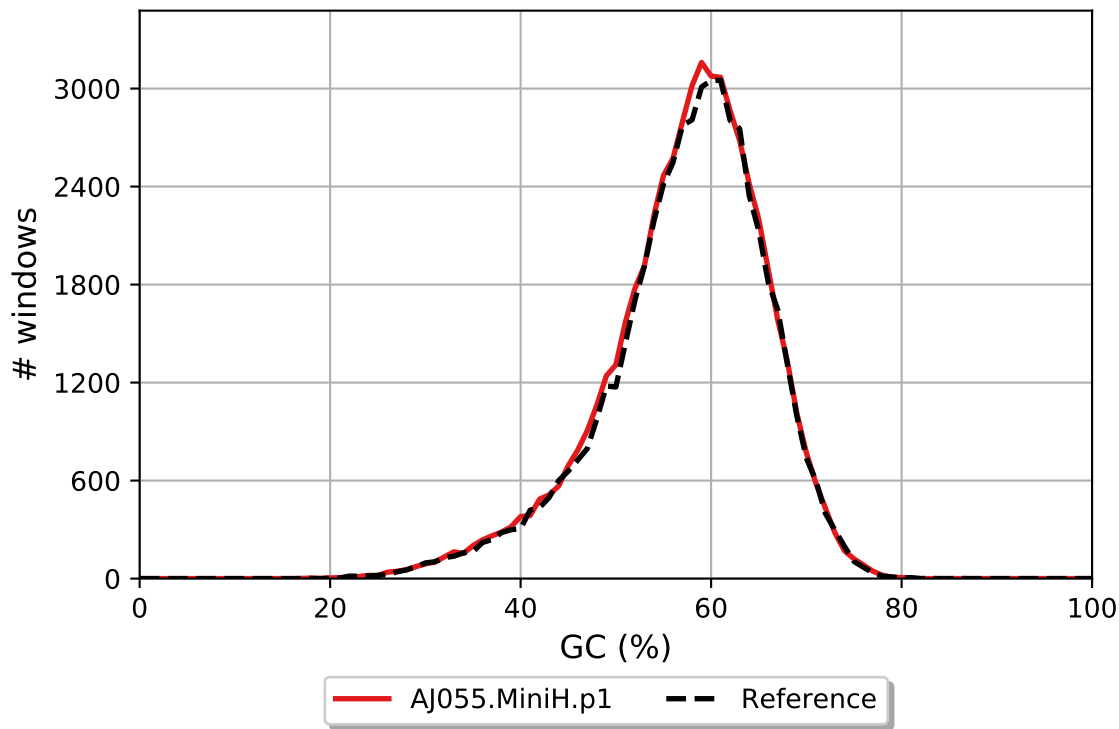
NGx



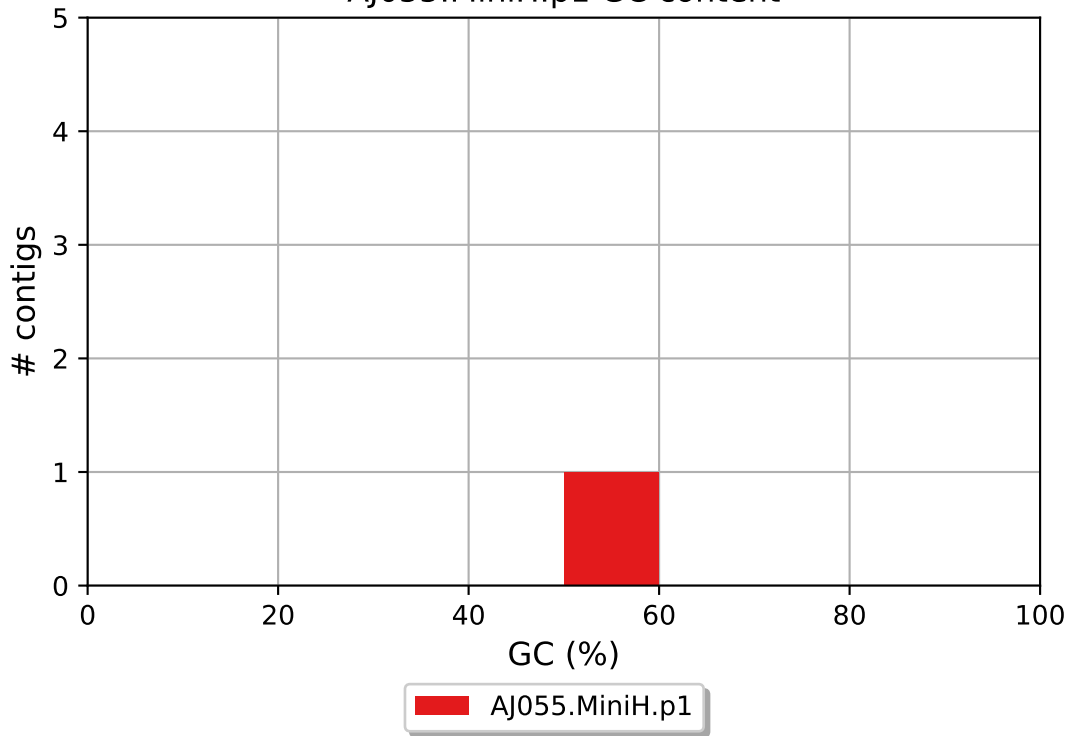
AJ055.MiniH.p1



# GC content

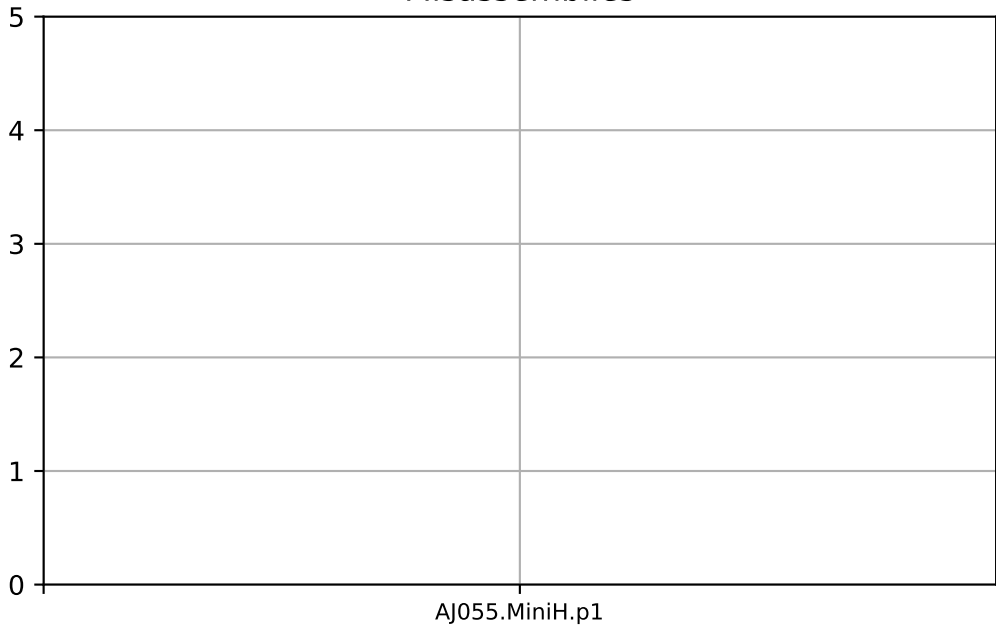


AJ055.MiniH.p1 GC content

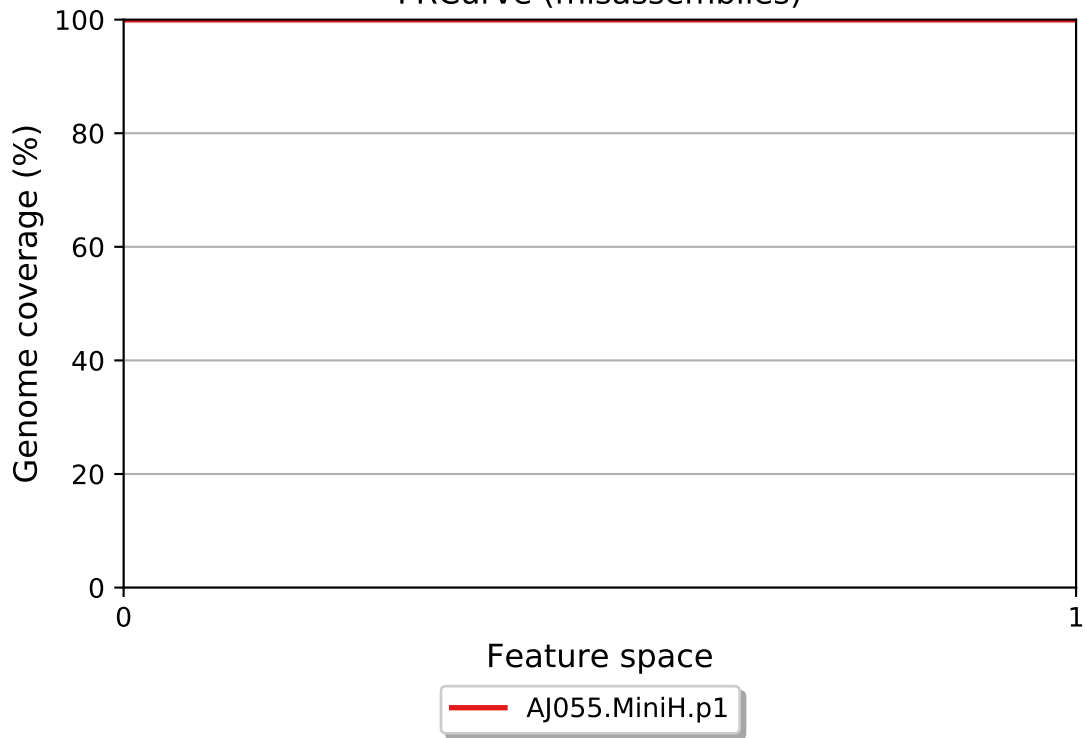




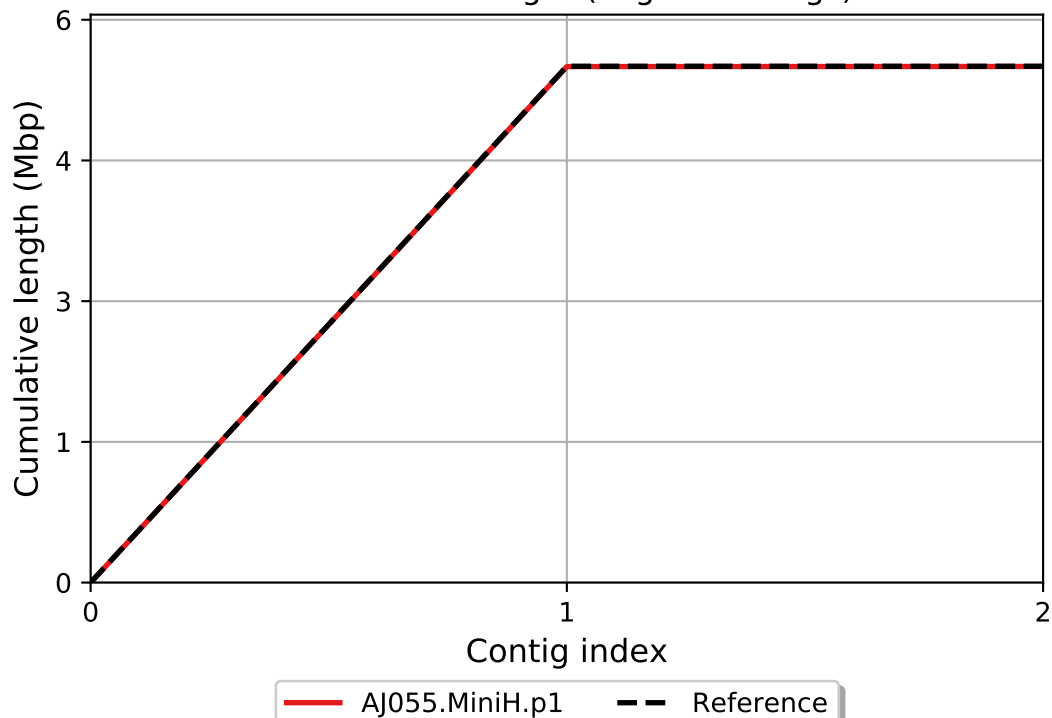
## Misassemblies



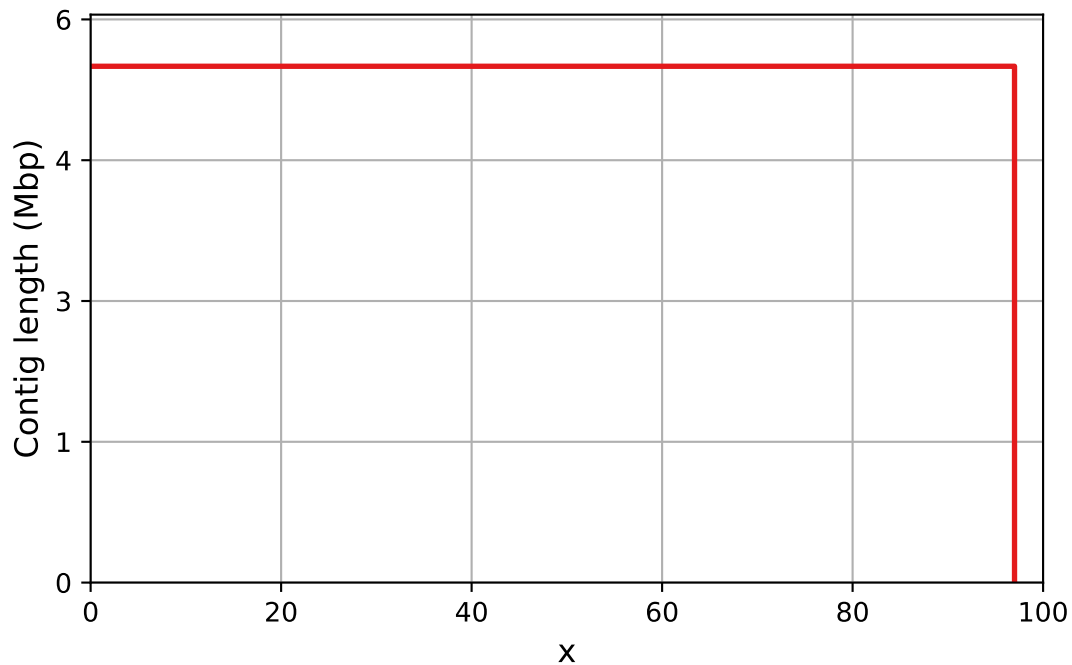
FRCurve (misassemblies)



Cumulative length (aligned contigs)

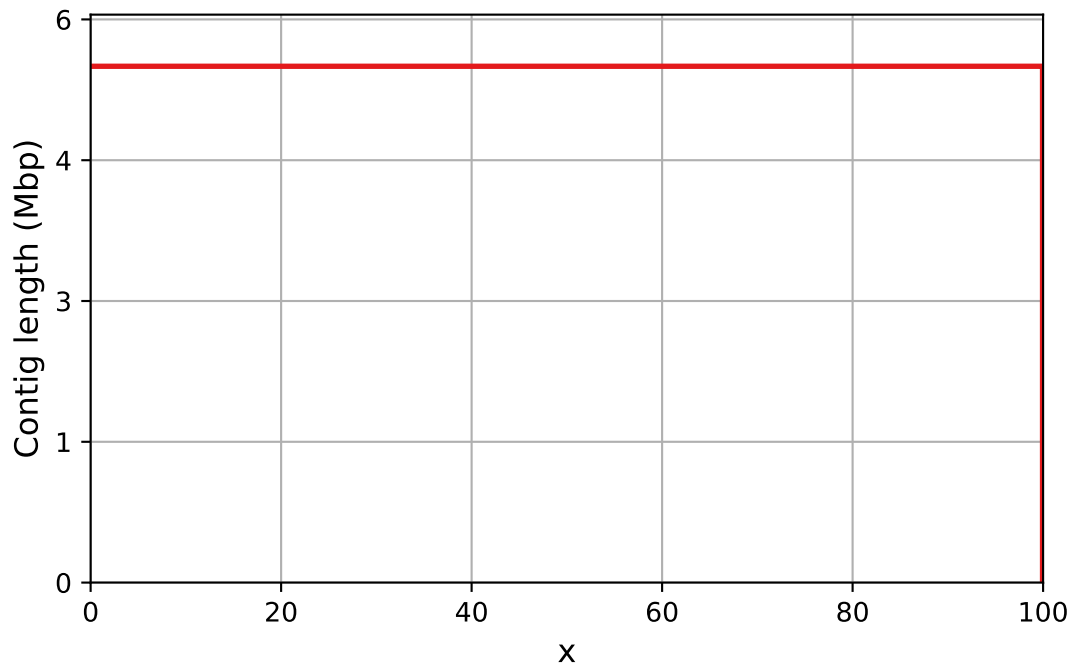


NAx



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NGAx



AJ055.MiniH.p1