

# Report

	AJ292.MiniH.p2
# 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)	5445266
Total length (>= 1000 bp)	5445266
Total length (>= 5000 bp)	5445266
Total length (>= 10000 bp)	5445266
Total length (>= 25000 bp)	5445266
Total length (>= 50000 bp)	5445266
# contigs	1
Largest contig	5445266
Total length	5445266
Reference length	5445112
GC (%)	57.62
Reference GC (%)	57.62
N50	5445266
NG50	5445266
N75	5445266
NG75	5445266
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	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.999
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.24
# indels per 100 kbp	5.20
Largest alignment	5445266
Total aligned length	5445266
NA50	5445266
NGA50	5445266
NA75	5445266
NGA75	5445266
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

	AJ292.MiniH.p2
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	13
# indels	283
# indels ( $\leq 5$ bp)	282
# indels ( $> 5$ bp)	1
Indels length	398

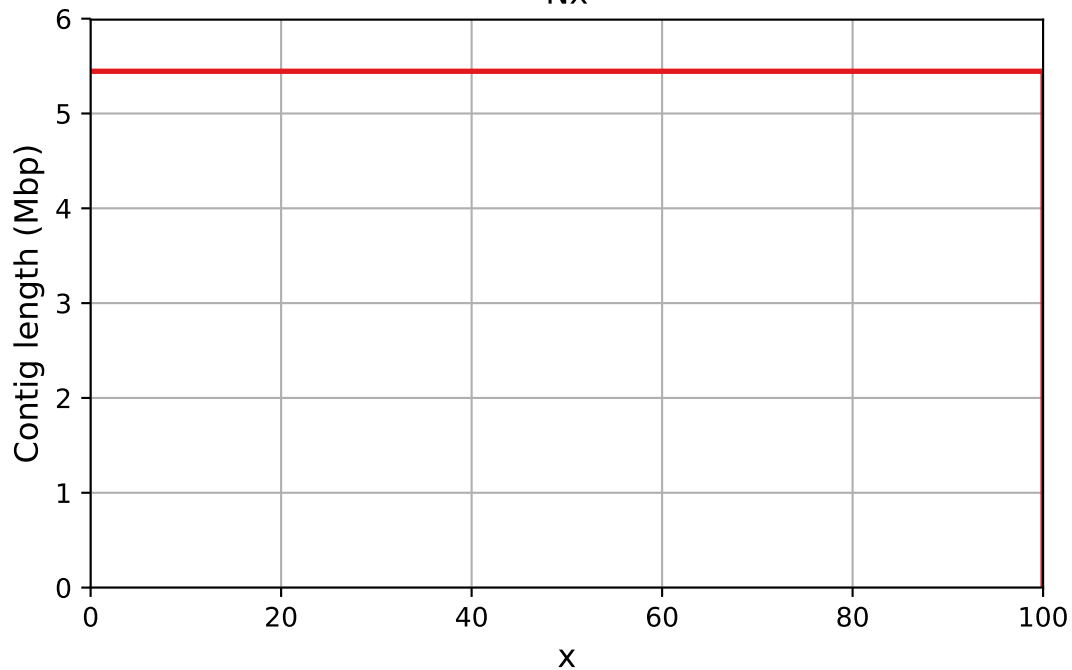
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ292.MiniH.p2
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

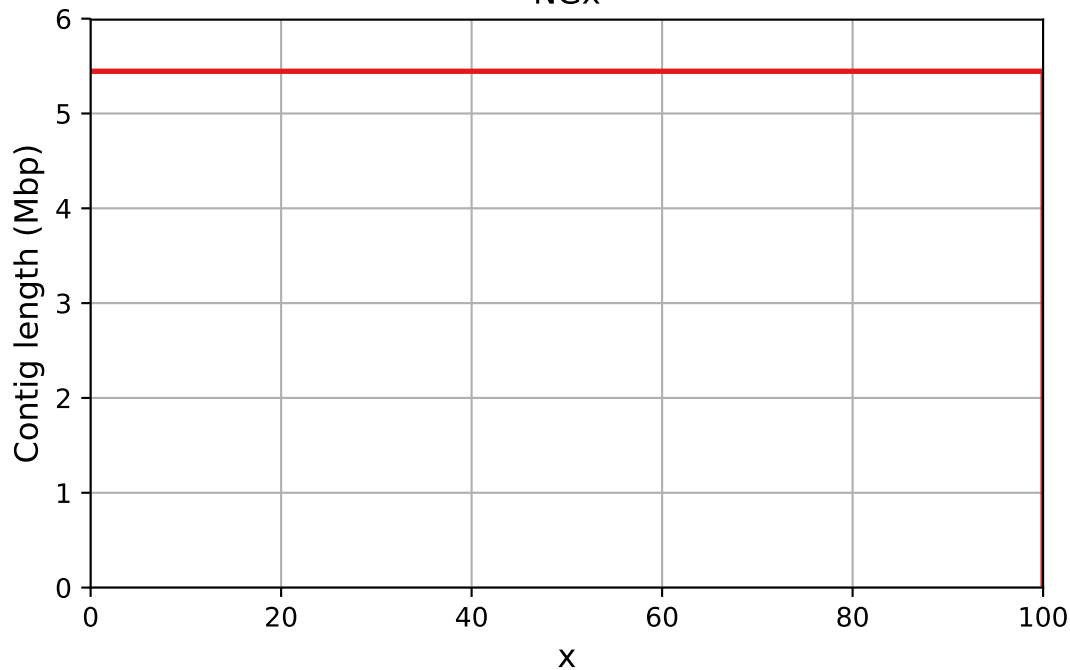
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

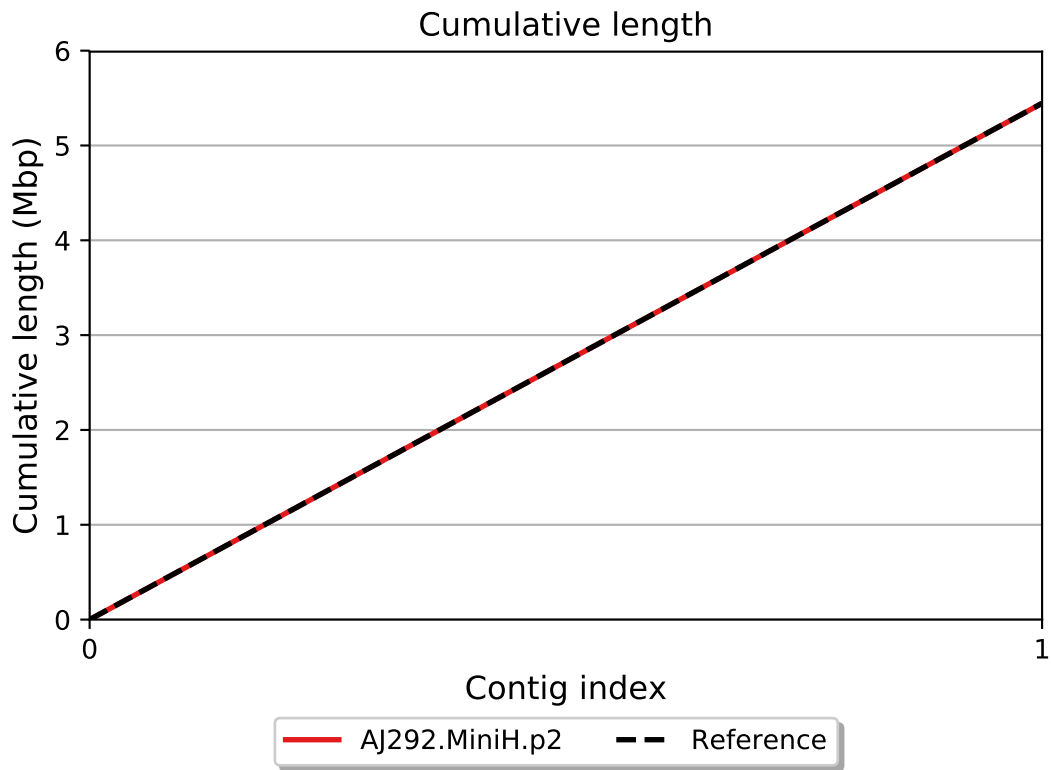


AJ292.MiniH.p2

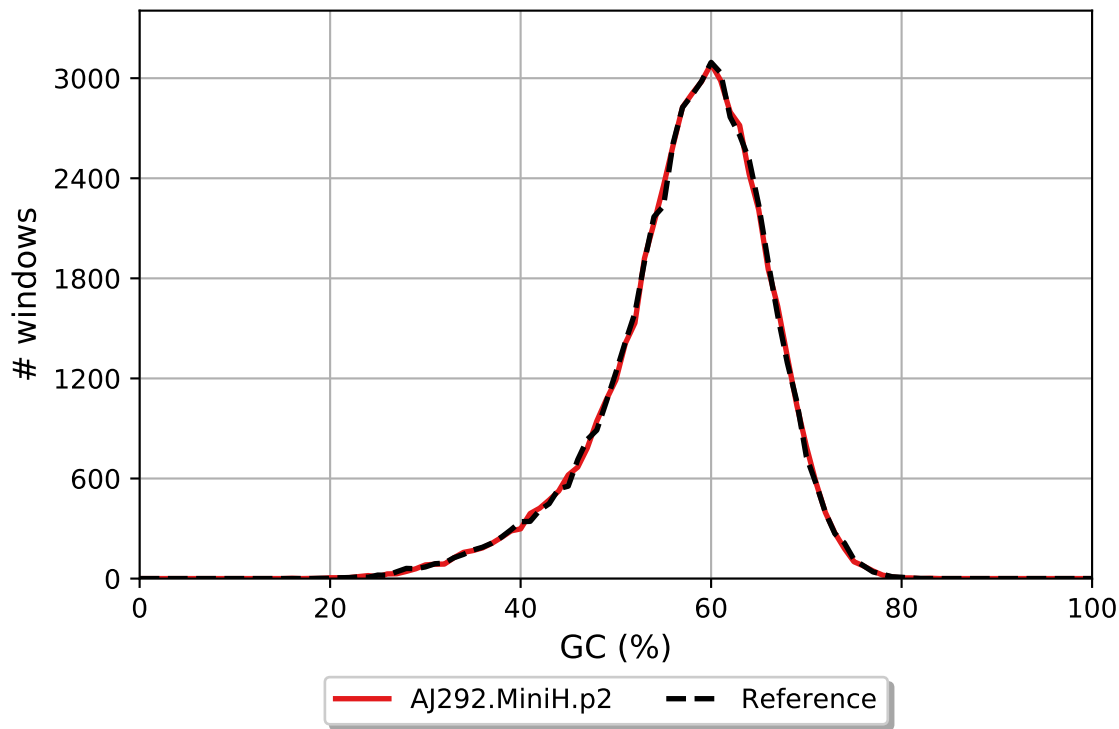
NGx



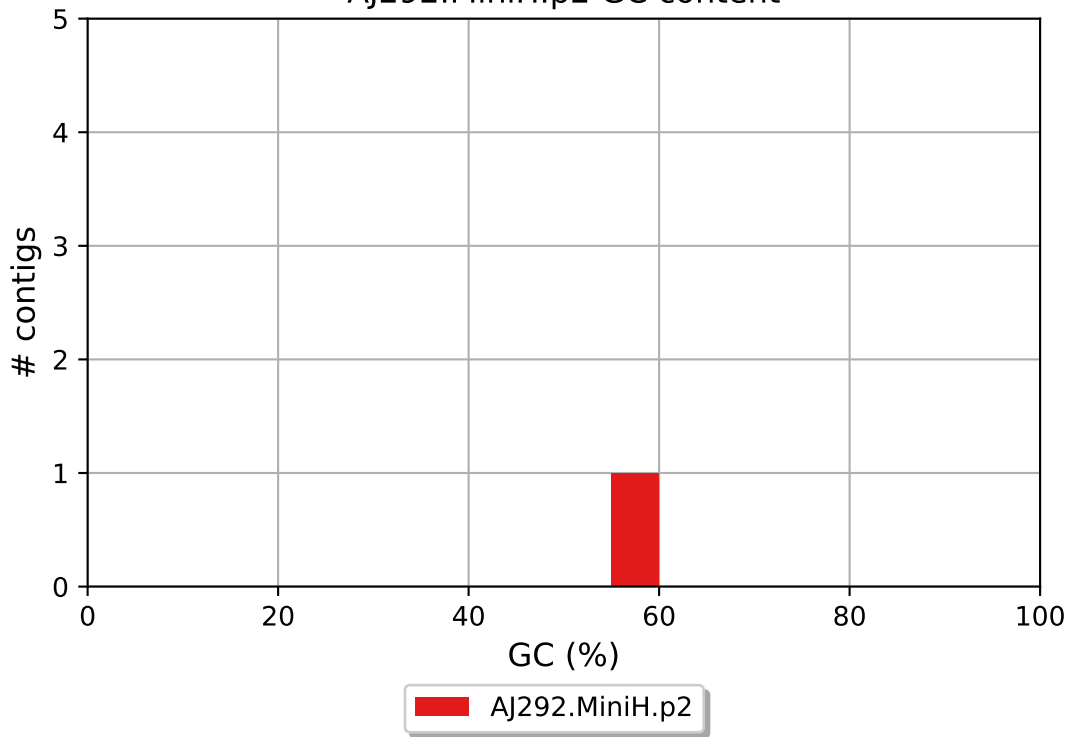
AJ292.MiniH.p2



## GC content

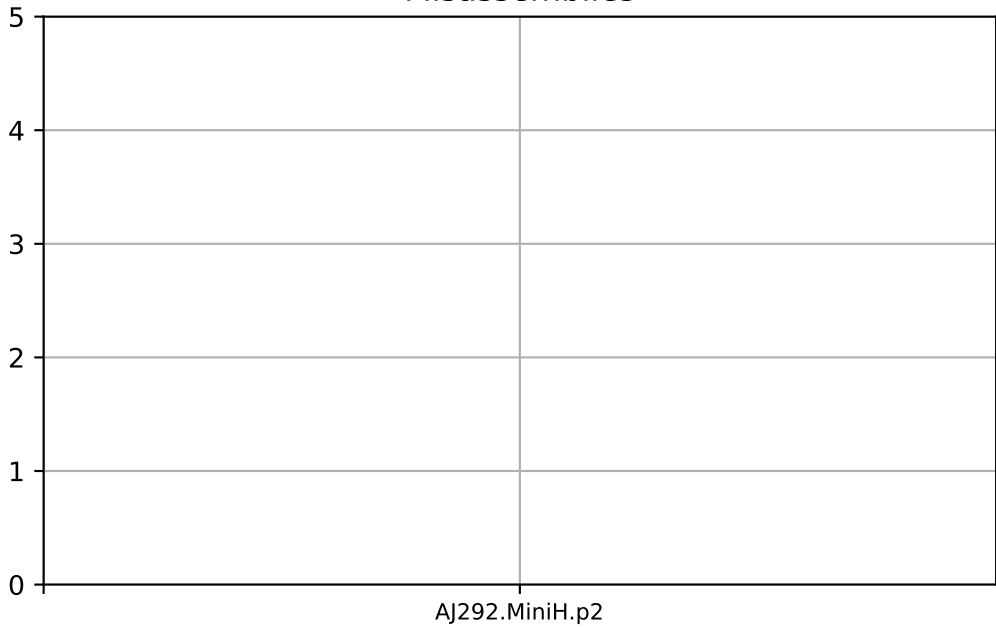


AJ292.MiniH.p2 GC content

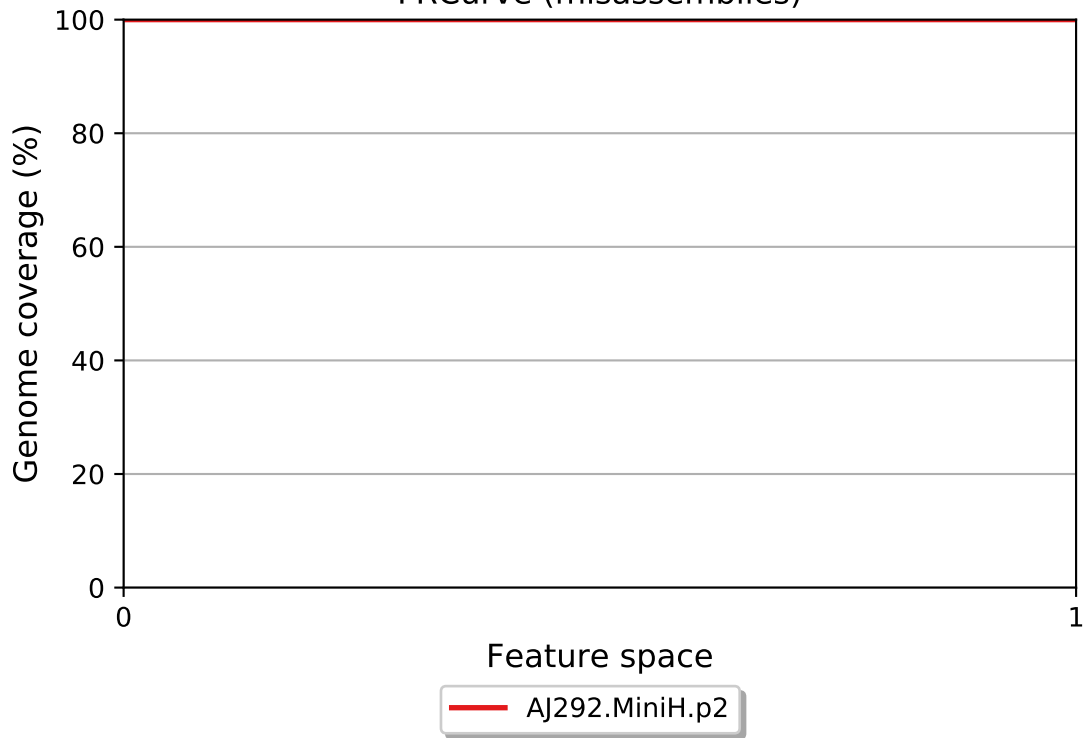




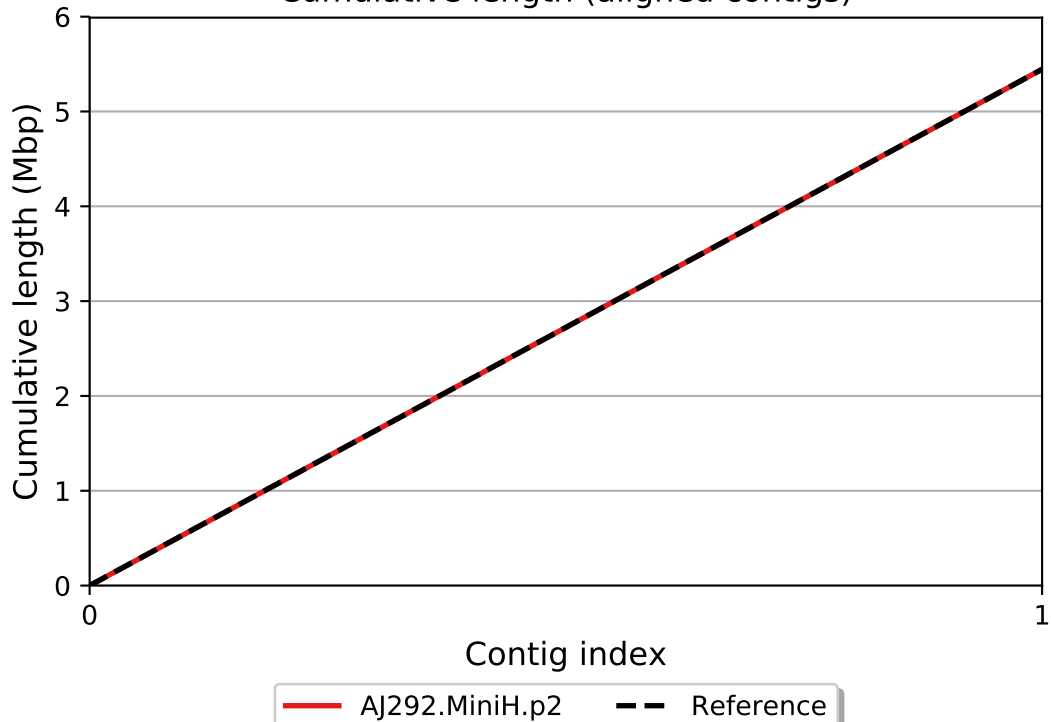
## Misassemblies



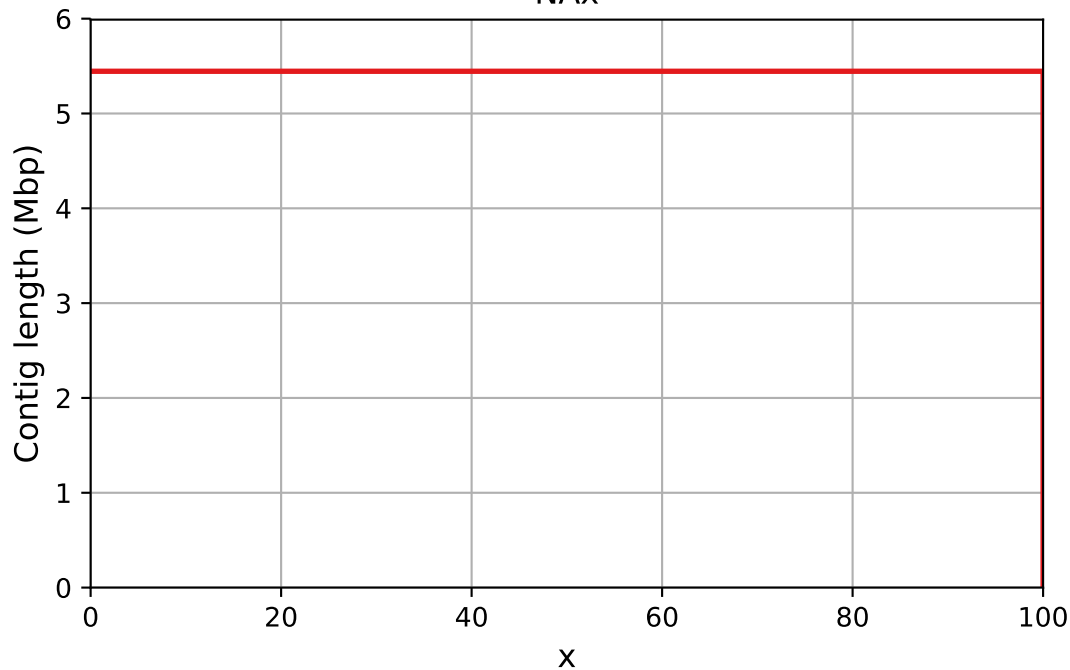
FRCurve (misassemblies)



Cumulative length (aligned contigs)

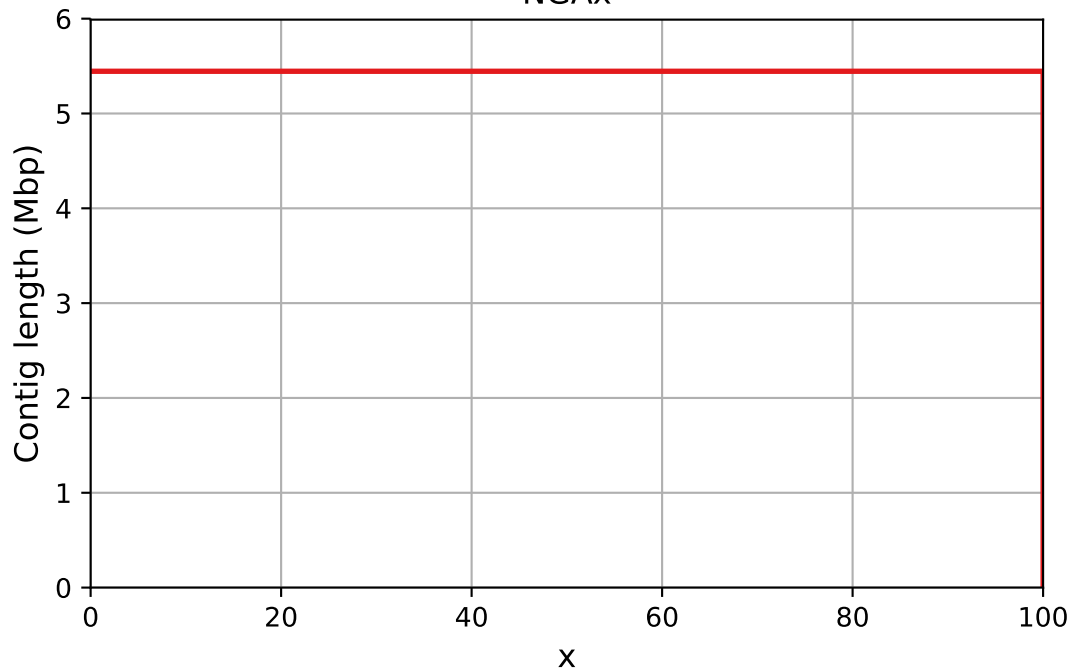


NAx



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NGAx



AJ292.MiniH.p2