

# Report

	AJ292.CanuH.p1
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5517289
Total length (>= 1000 bp)	5517289
Total length (>= 5000 bp)	5517289
Total length (>= 10000 bp)	5517289
Total length (>= 25000 bp)	5479035
Total length (>= 50000 bp)	5442825
# contigs	4
Largest contig	5442825
Total length	5517289
Reference length	5445112
GC (%)	57.64
Reference GC (%)	57.62
N50	5442825
NG50	5442825
N75	5442825
NG75	5442825
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 (%)	100.000
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.13
# indels per 100 kbp	1.38
Largest alignment	5442825
Total aligned length	5517289
NA50	5442825
NGA50	5442825
NA75	5442825
NGA75	5442825
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.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	7
# indels	75
# indels ( $\leq 5$ bp)	75
# indels ( $> 5$ bp)	0
Indels length	78

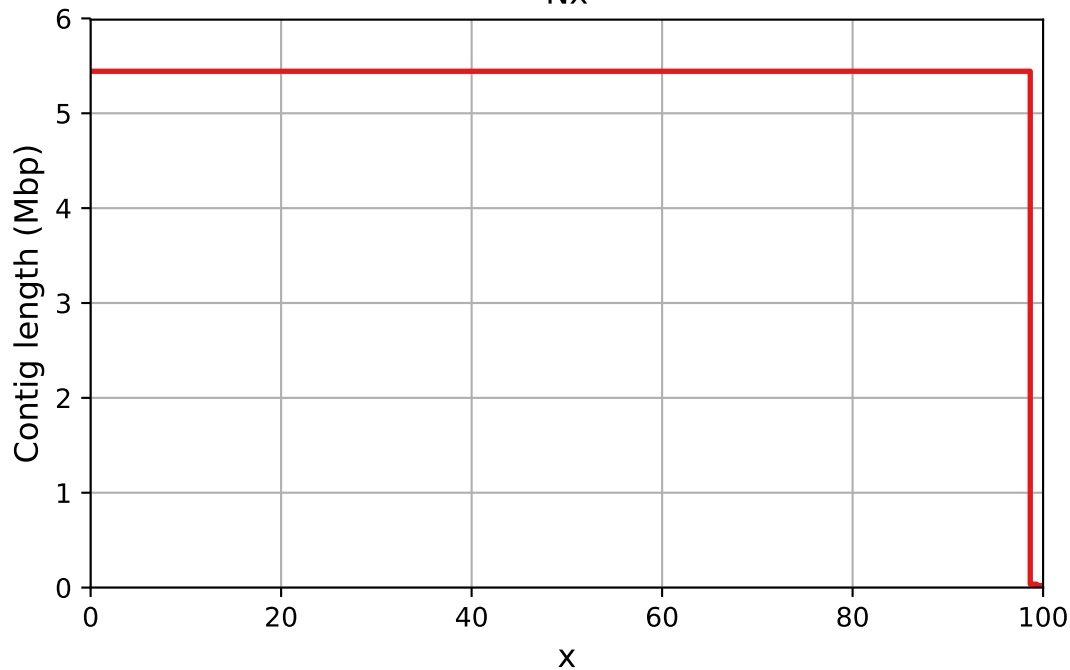
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ292.CanuH.p1
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

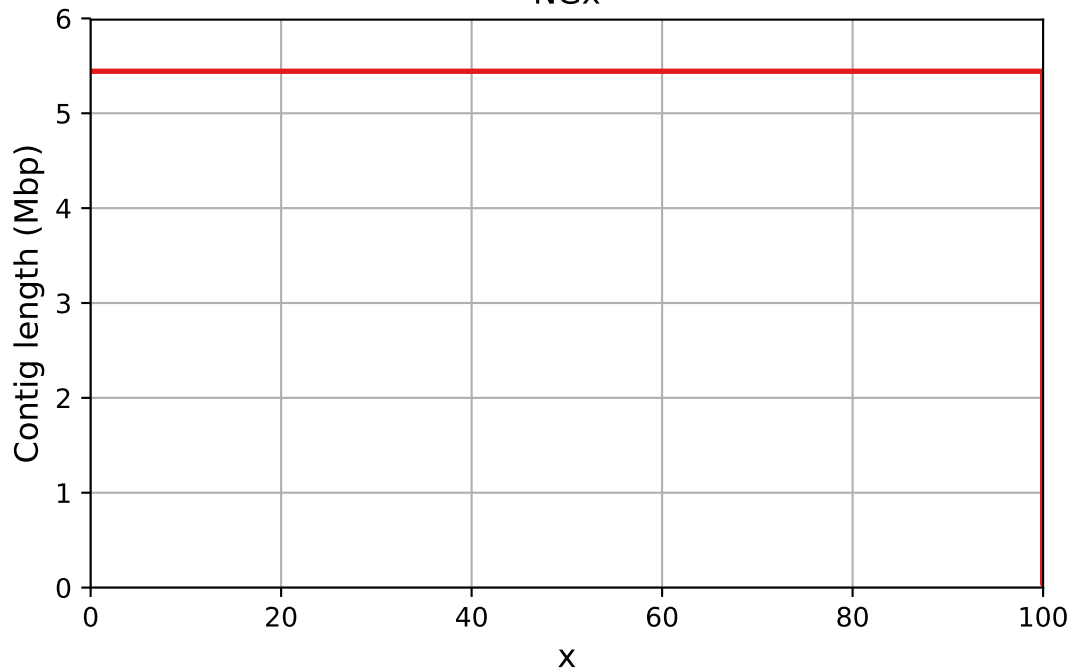
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

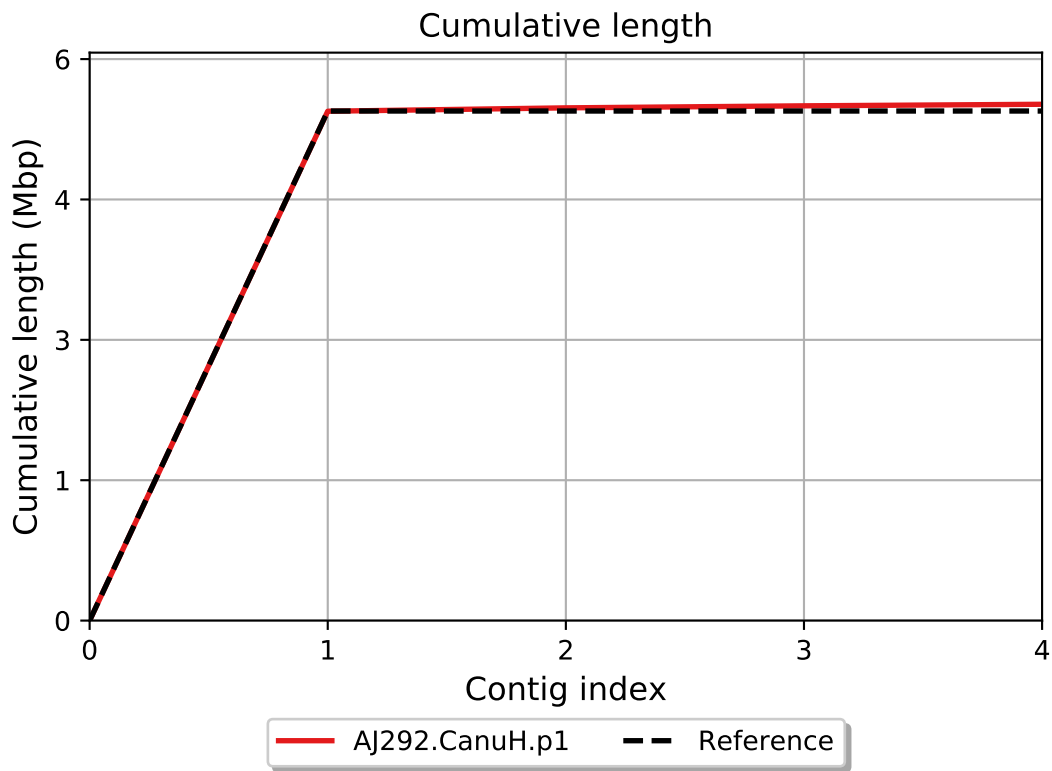


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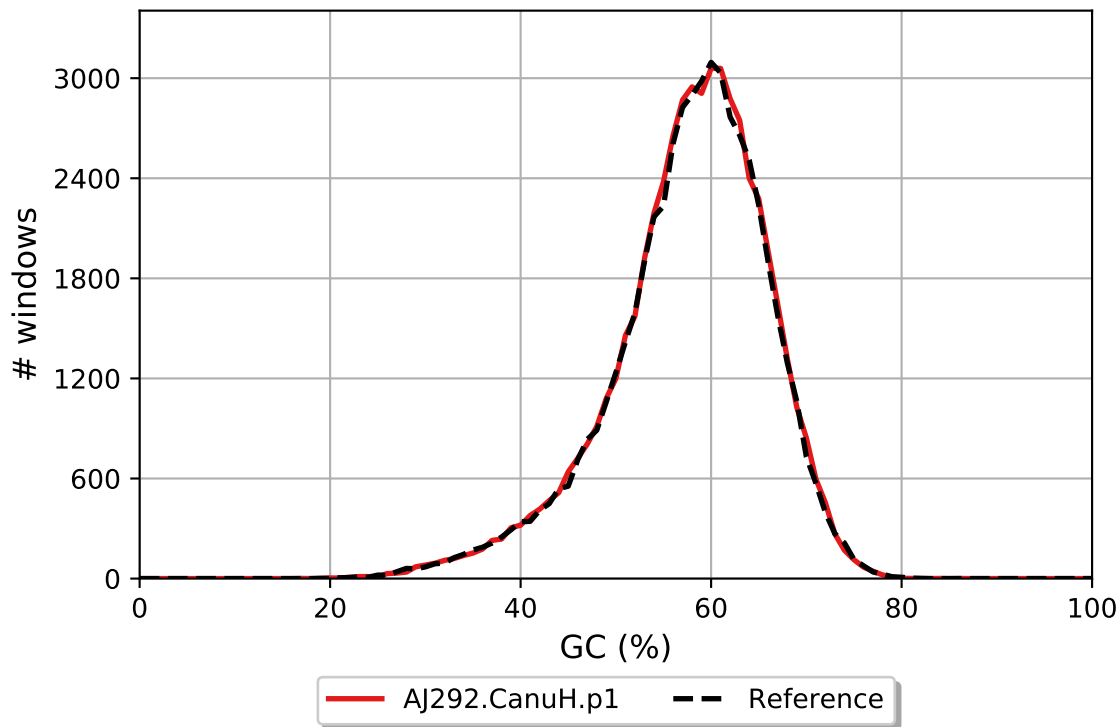
NGx



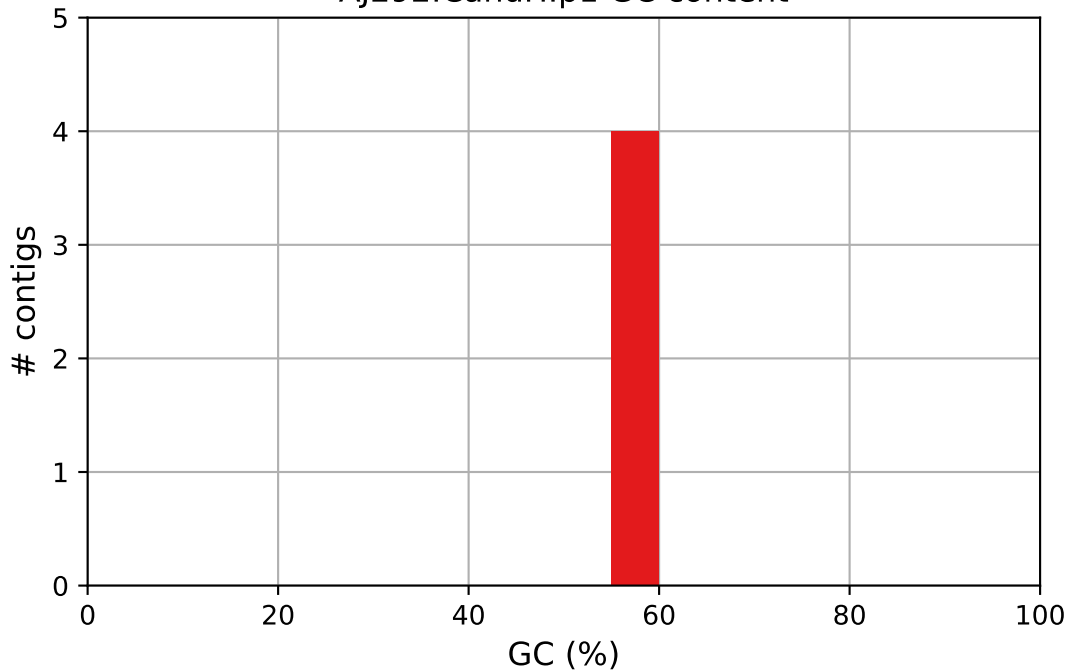
Aj292.CanuH.p1




## GC content



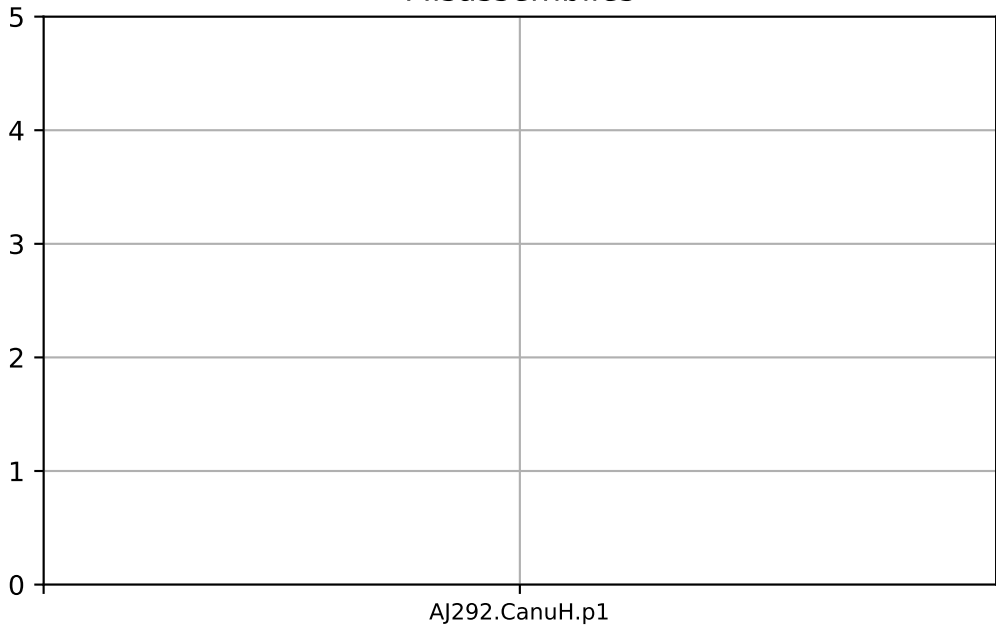
AJ292.CanuH.p1 GC content



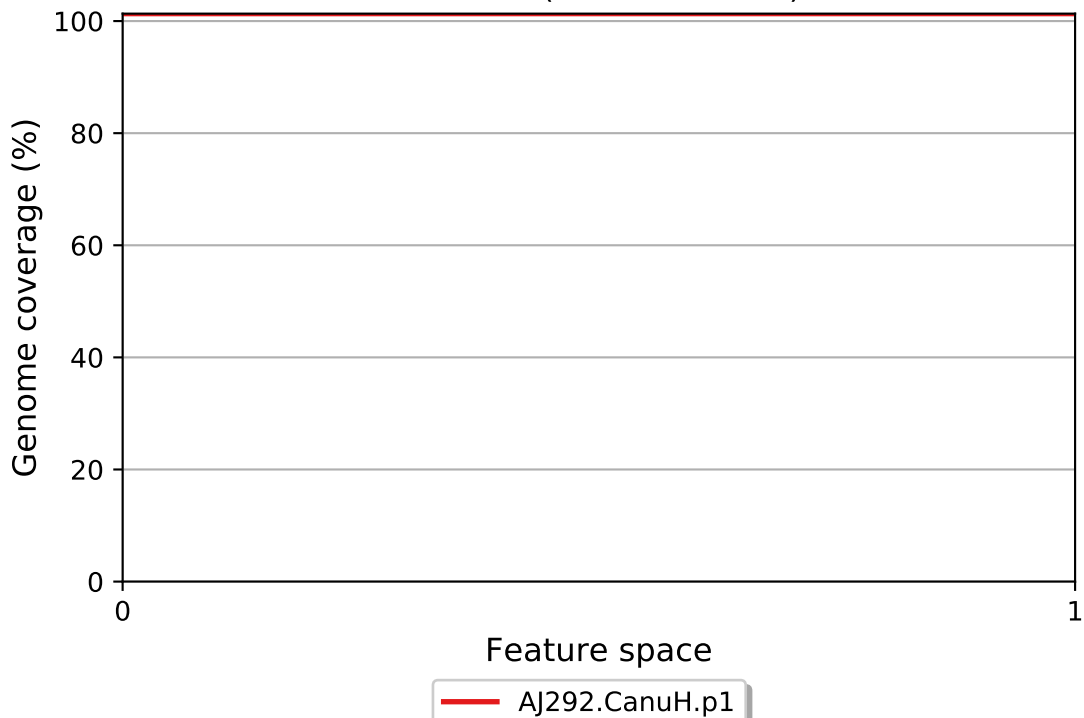
 AJ292.CanuH.p1



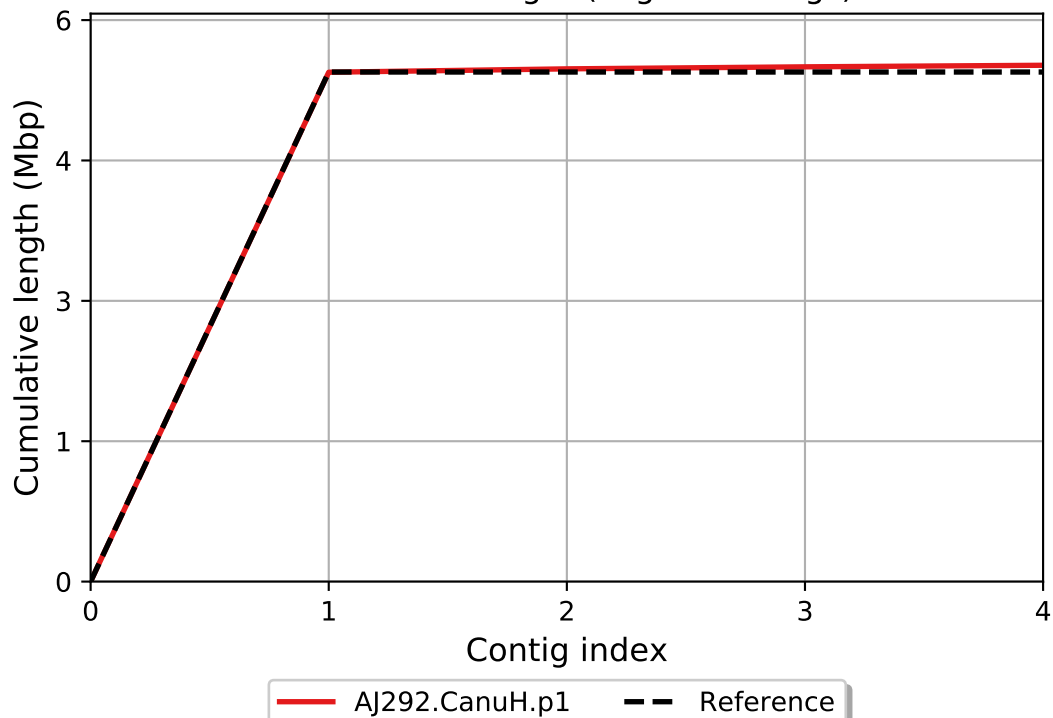
## Misassemblies



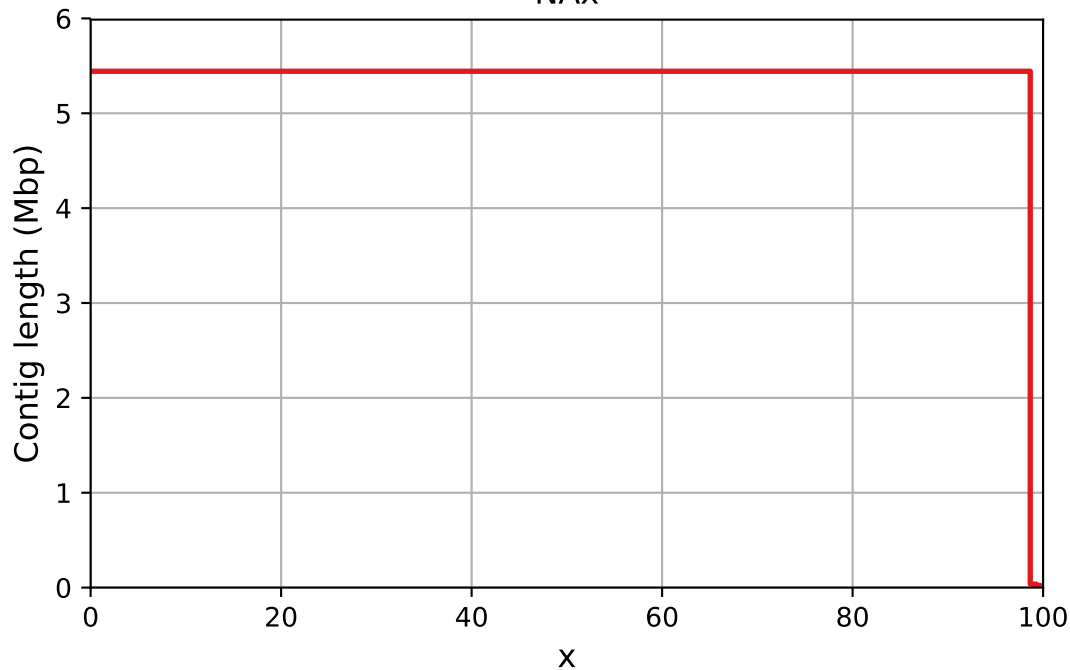
FRCurve (misassemblies)



Cumulative length (aligned contigs)

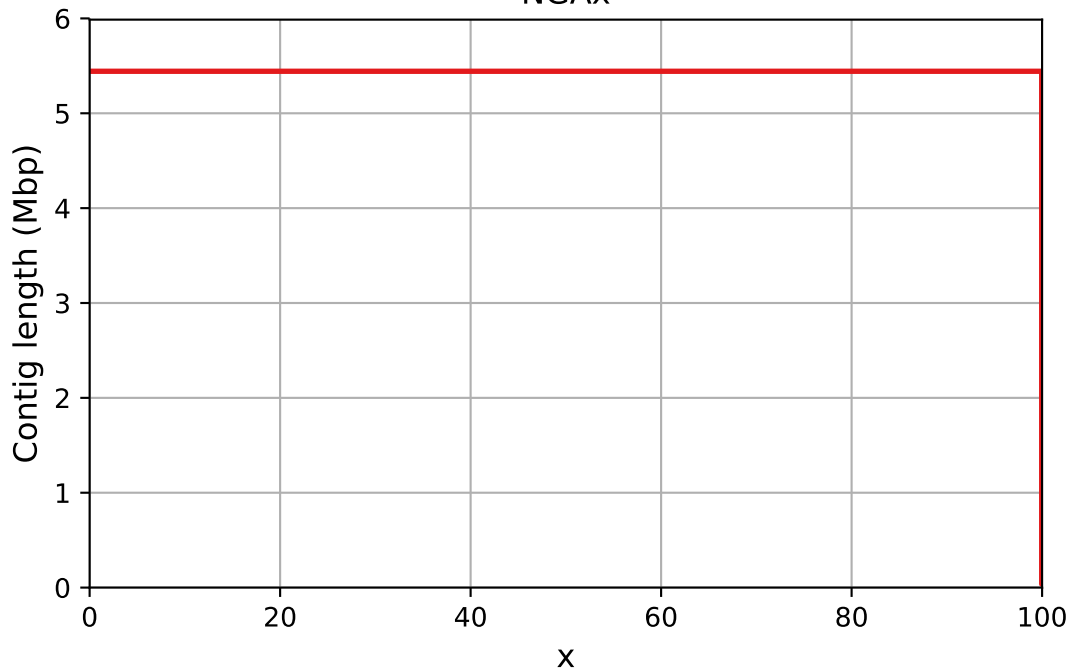


NAx



Aj292.CanuH.p1

NGAx



Aj292.CanuH.p1