

Report

	AJ218.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)	2
Total length (>= 0 bp)	5717621
Total length (>= 1000 bp)	5717621
Total length (>= 5000 bp)	5717621
Total length (>= 10000 bp)	5717621
Total length (>= 25000 bp)	5677396
Total length (>= 50000 bp)	5677396
# contigs	4
Largest contig	5460804
Total length	5717621
Reference length	5465981
GC (%)	57.10
Reference GC (%)	57.29
N50	5460804
NG50	5460804
N75	5460804
NG75	5460804
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	243454
Genome fraction (%)	99.905
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.60
Largest alignment	5460804
Total aligned length	5474167
NA50	5460804
NGA50	5460804
NA75	5460804
NGA75	5460804
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

	AJ218.CanuH.p1
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	0
# indels	33
# indels (≤ 5 bp)	33
# indels (> 5 bp)	0
Indels length	33

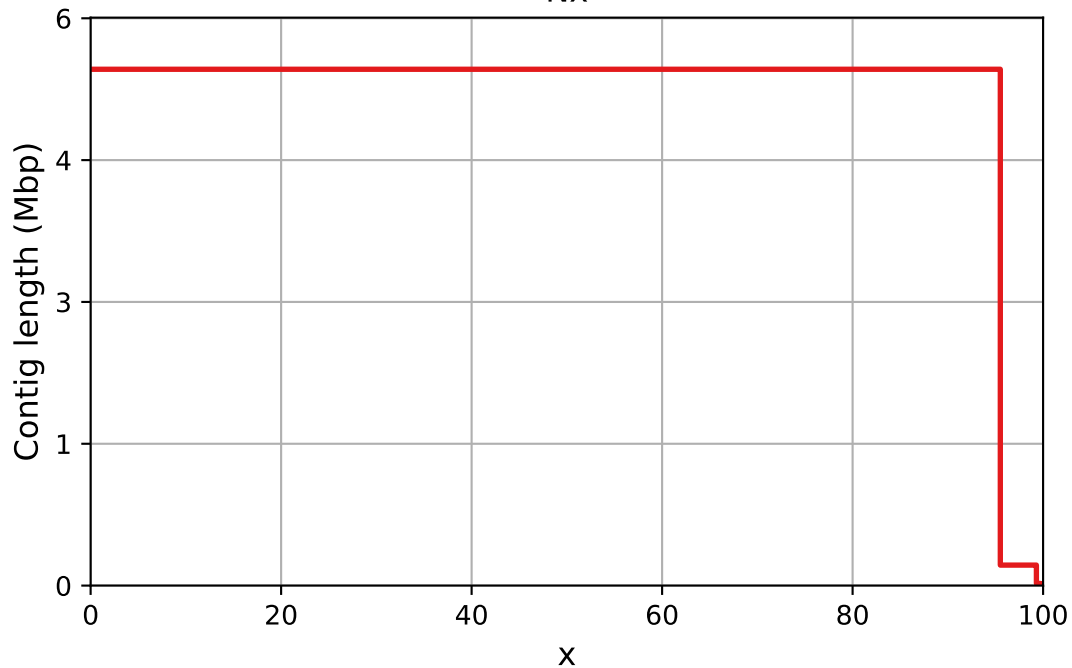
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ218.CanuH.p1
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	243454
# N's	0

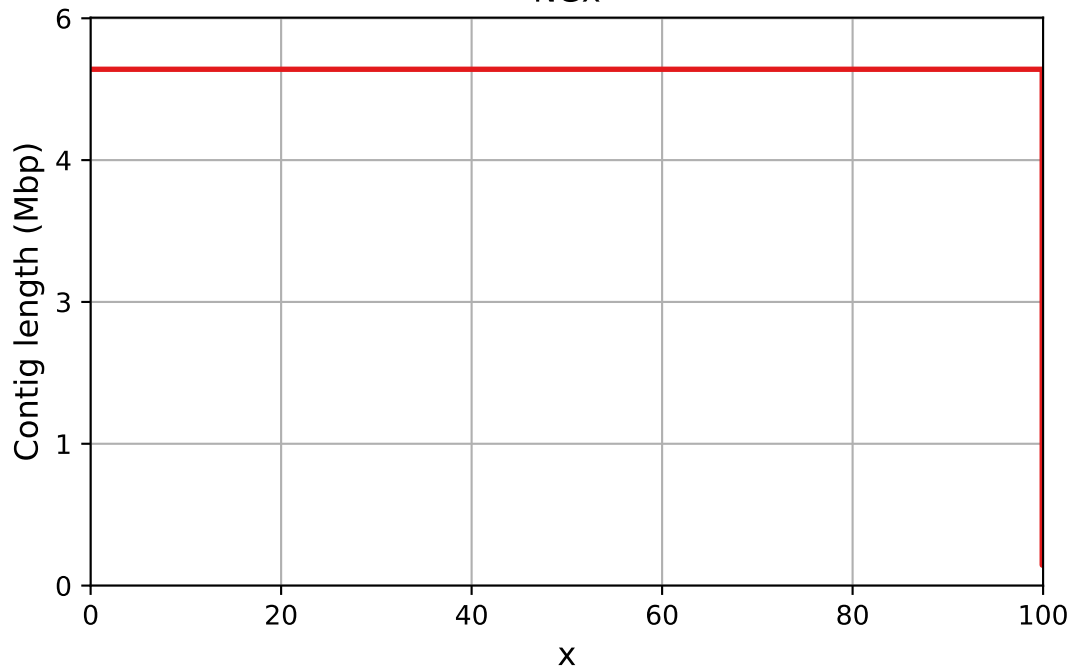
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



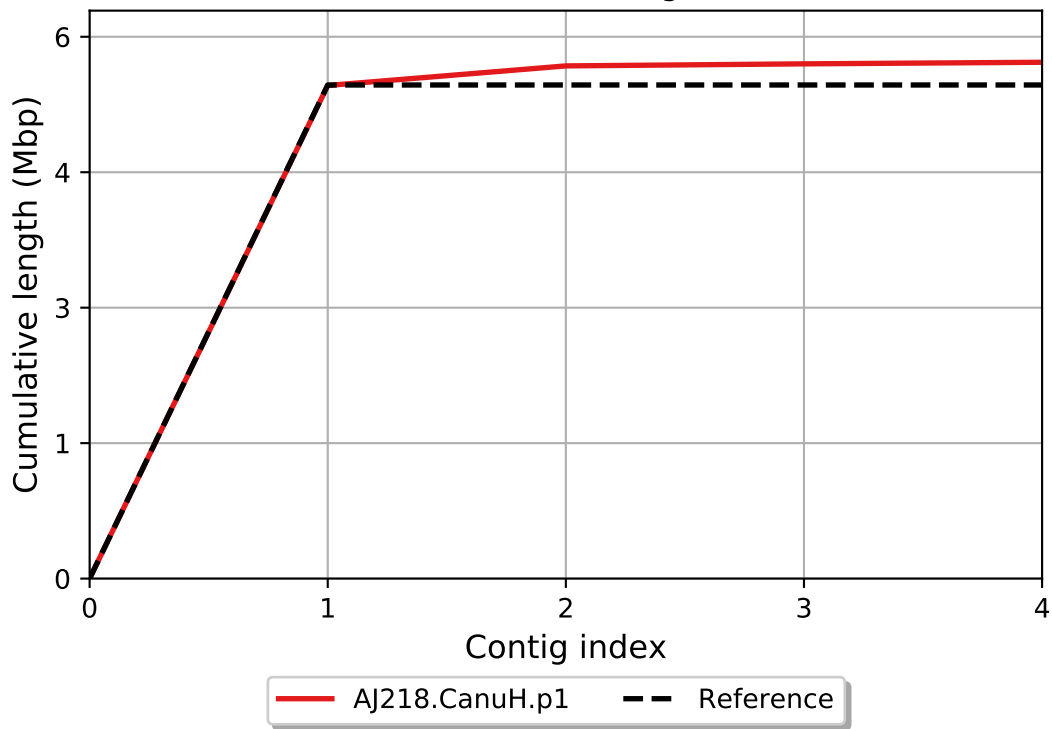
Aj218.CanuH.p1

NGx

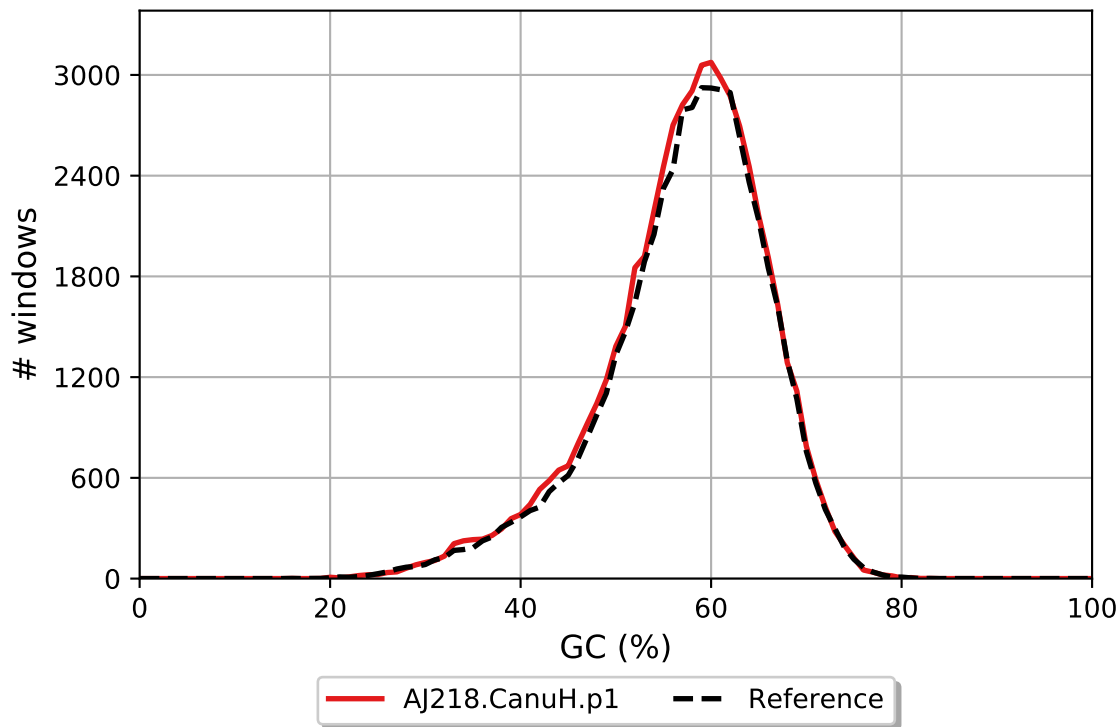


Aj218.CanuH.p1

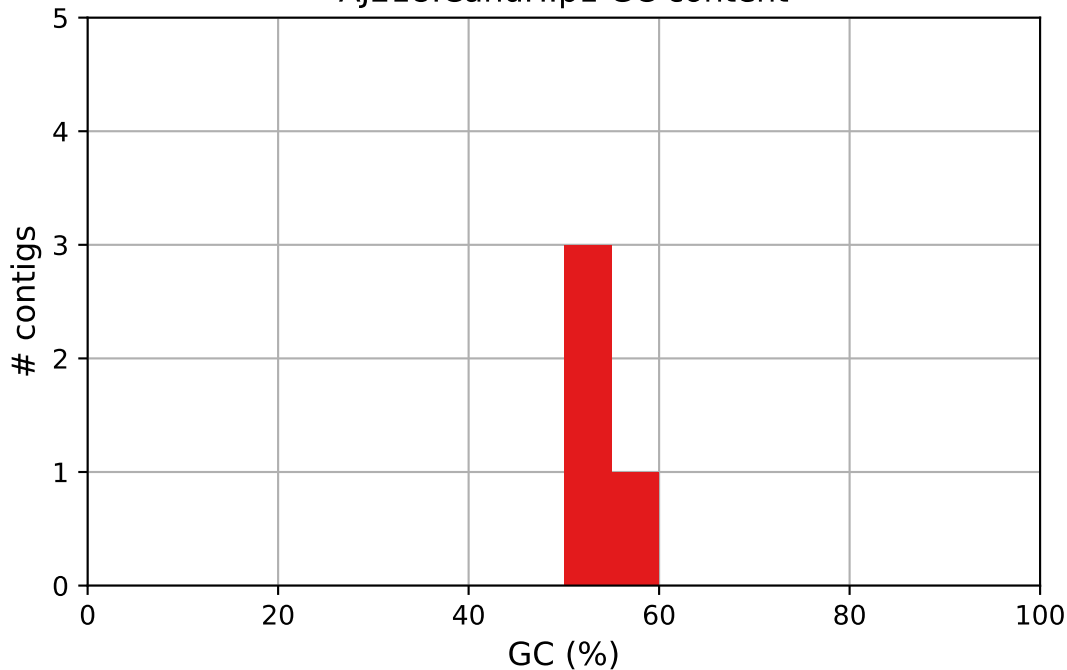
Cumulative length



GC content

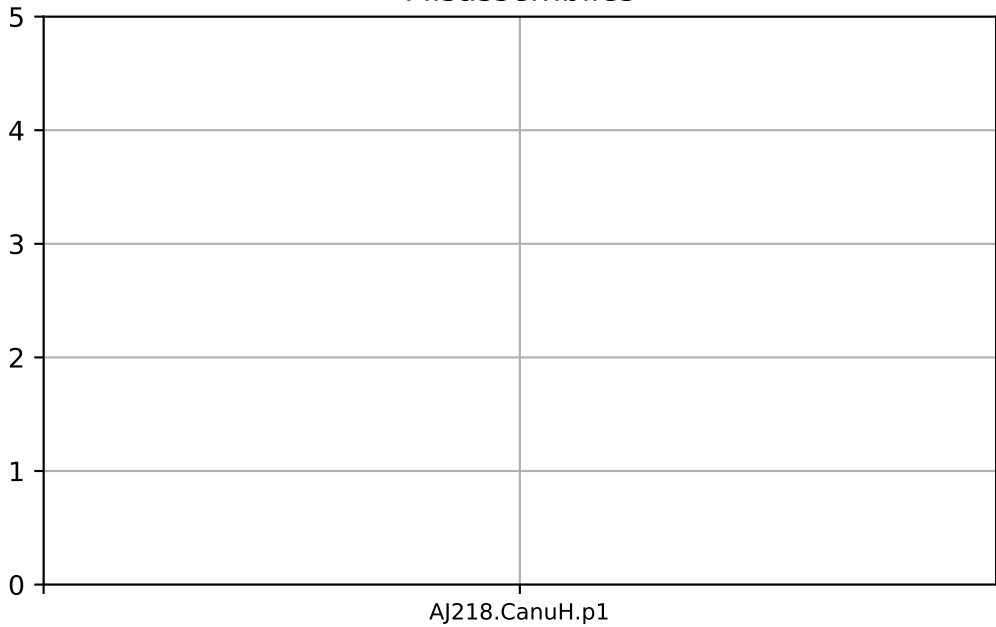


AJ218.CanuH.p1 GC content

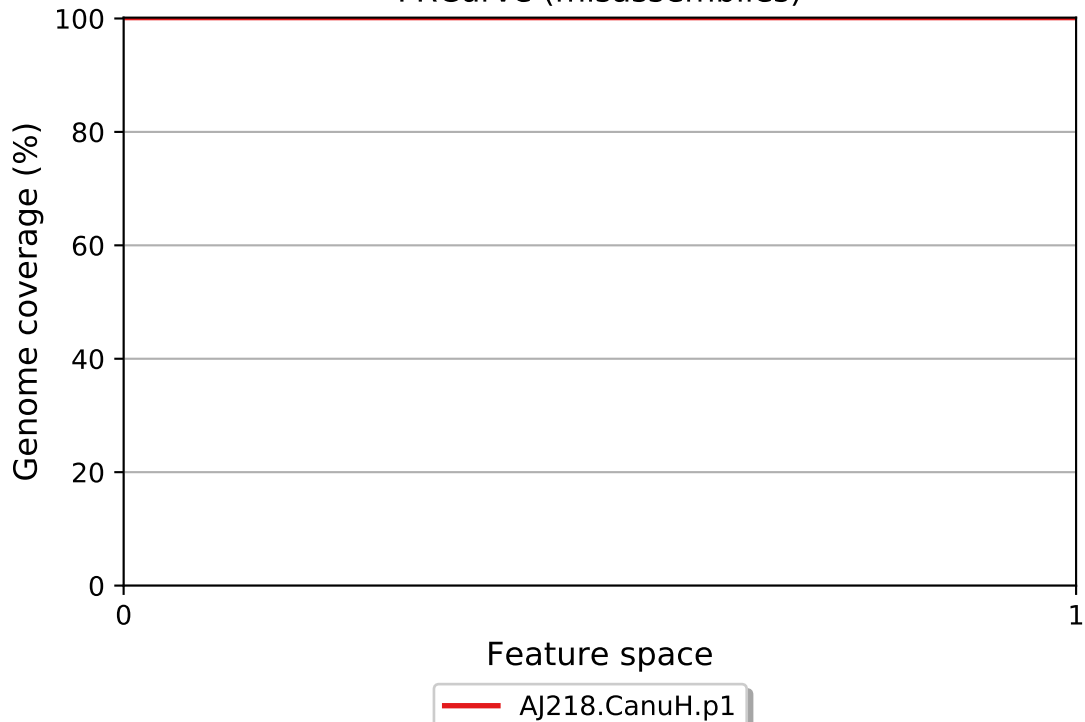


AJ218.CanuH.p1

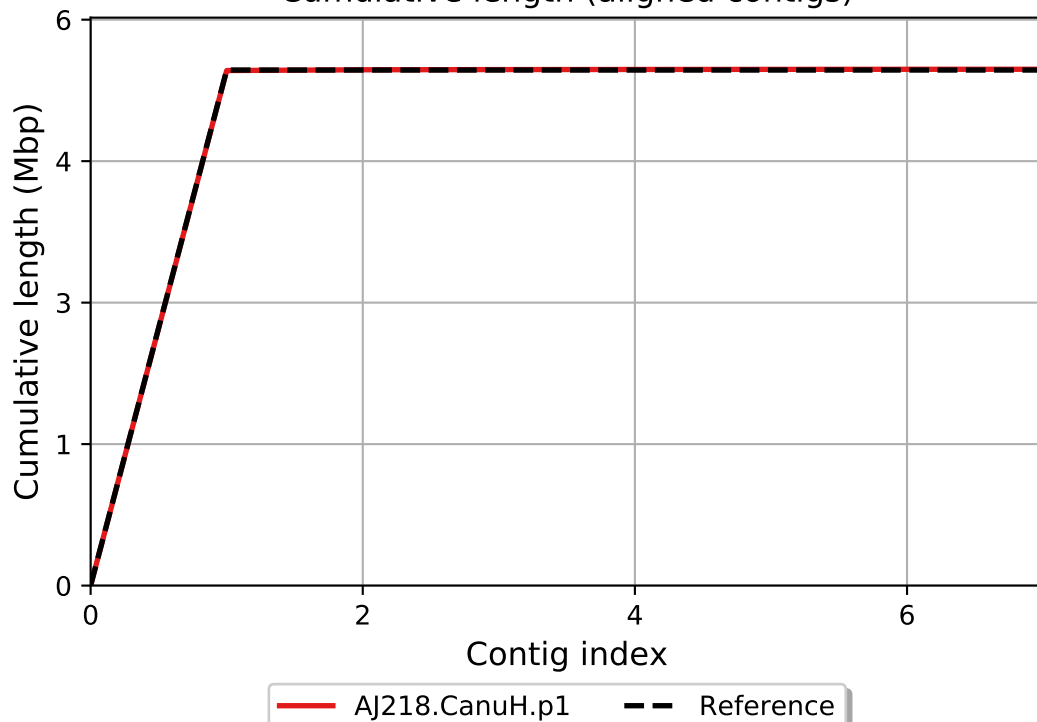
Misassemblies



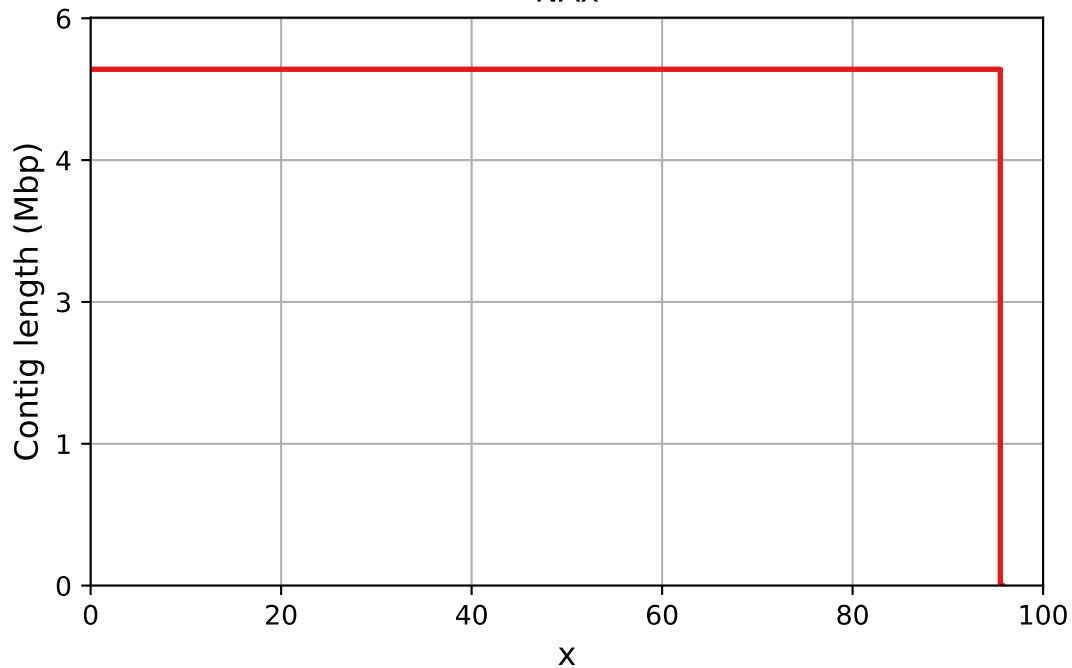
FRCurve (misassemblies)



Cumulative length (aligned contigs)

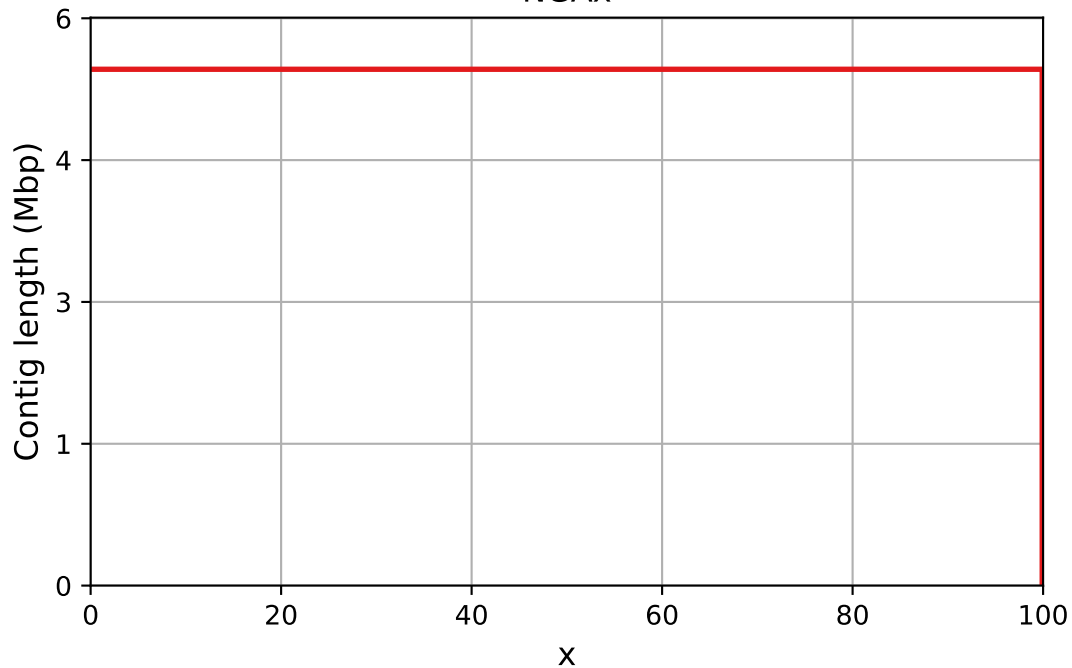


NAx



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NGAx



Aj218.CanuH.p1