

Report

	AJ218.MiniCH
# 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)	5688657
Total length (>= 1000 bp)	5688657
Total length (>= 5000 bp)	5688657
Total length (>= 10000 bp)	5688657
Total length (>= 25000 bp)	5688657
Total length (>= 50000 bp)	5688657
# contigs	2
Largest contig	5485519
Total length	5688657
Reference length	5465981
GC (%)	57.12
Reference GC (%)	57.29
N50	5485519
NG50	5485519
N75	5485519
NG75	5485519
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	5485519
# local misassemblies	4
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	192099
Genome fraction (%)	99.977
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.44
# indels per 100 kbp	248.34
Largest alignment	5049176
Total aligned length	5496411
NA50	5049176
NGA50	5049176
NA75	5049176
NGA75	5049176
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.MiniCH
# misassemblies	2
# relocations	0
# translocations	0
# inversions	2
# misassembled contigs	1
Misassembled contigs length	5485519
# local misassemblies	4
# unaligned mis. contigs	1
# mismatches	516
# indels	13571
# indels (≤ 5 bp)	13502
# indels (> 5 bp)	69
Indels length	21441

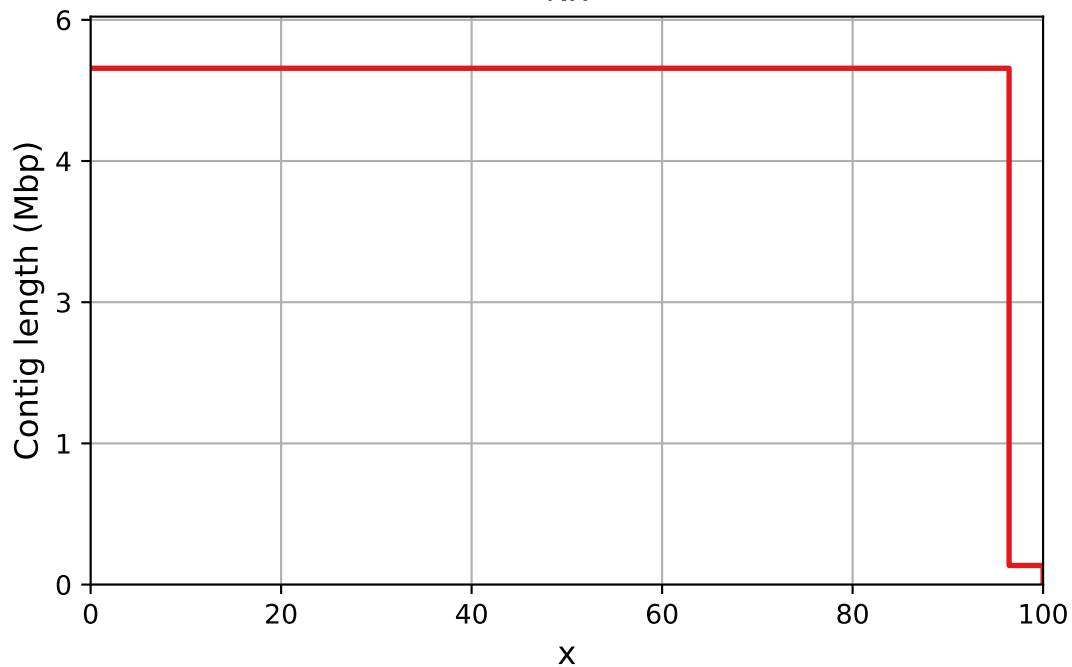
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ218.Minich
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	192099
# N's	0

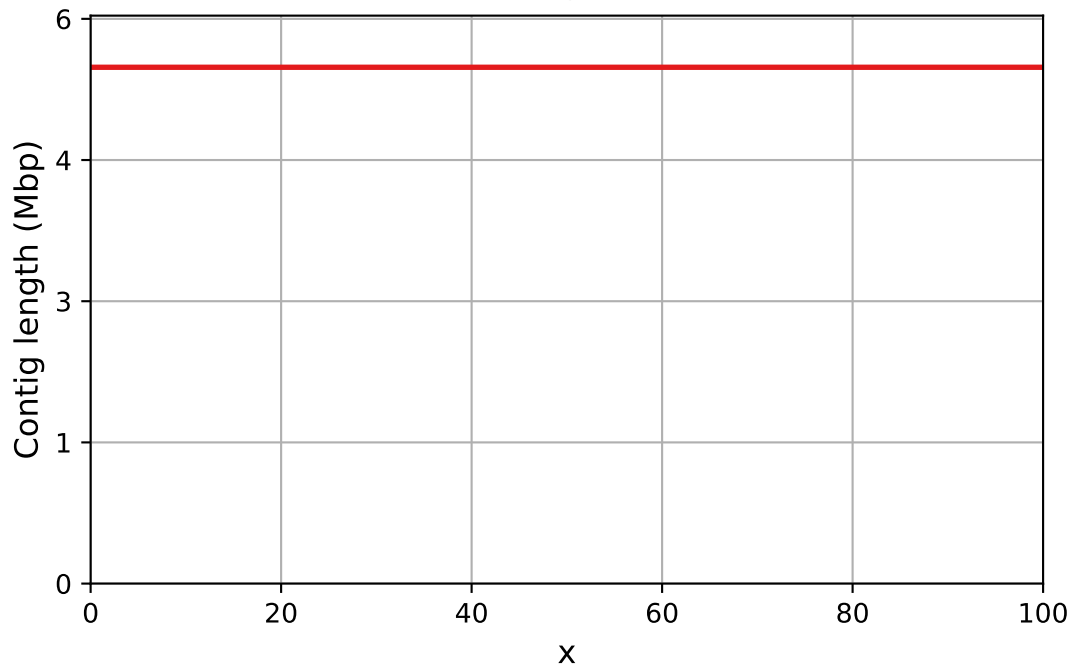
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

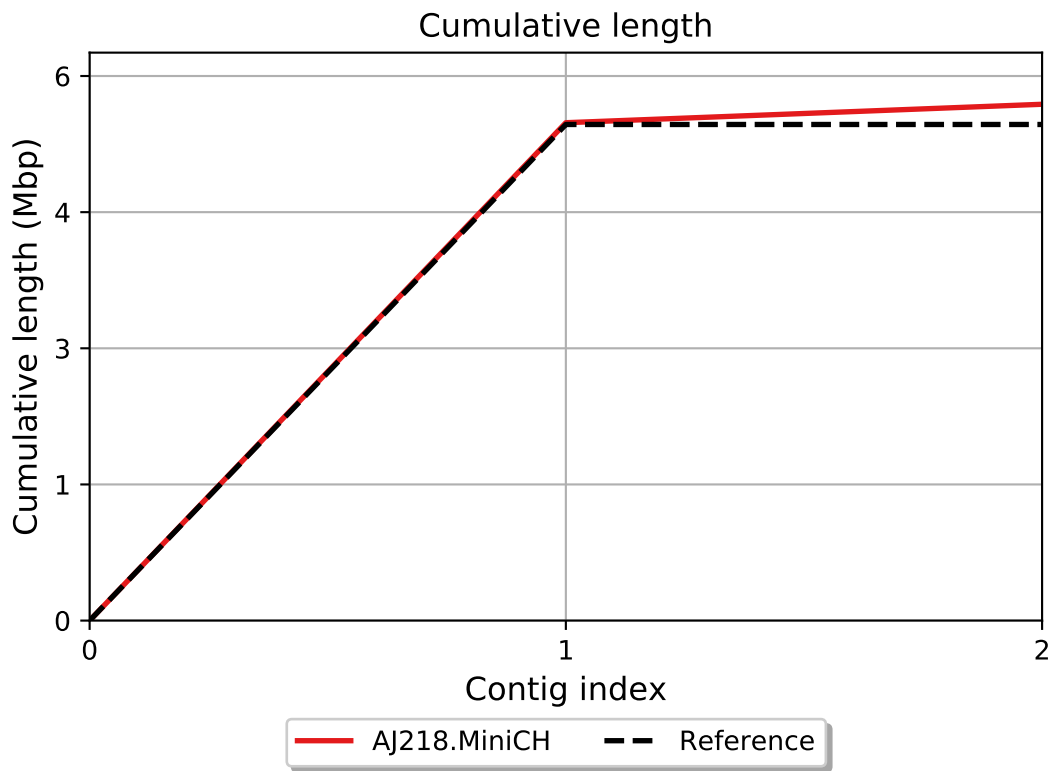


Aj218.MiniCH

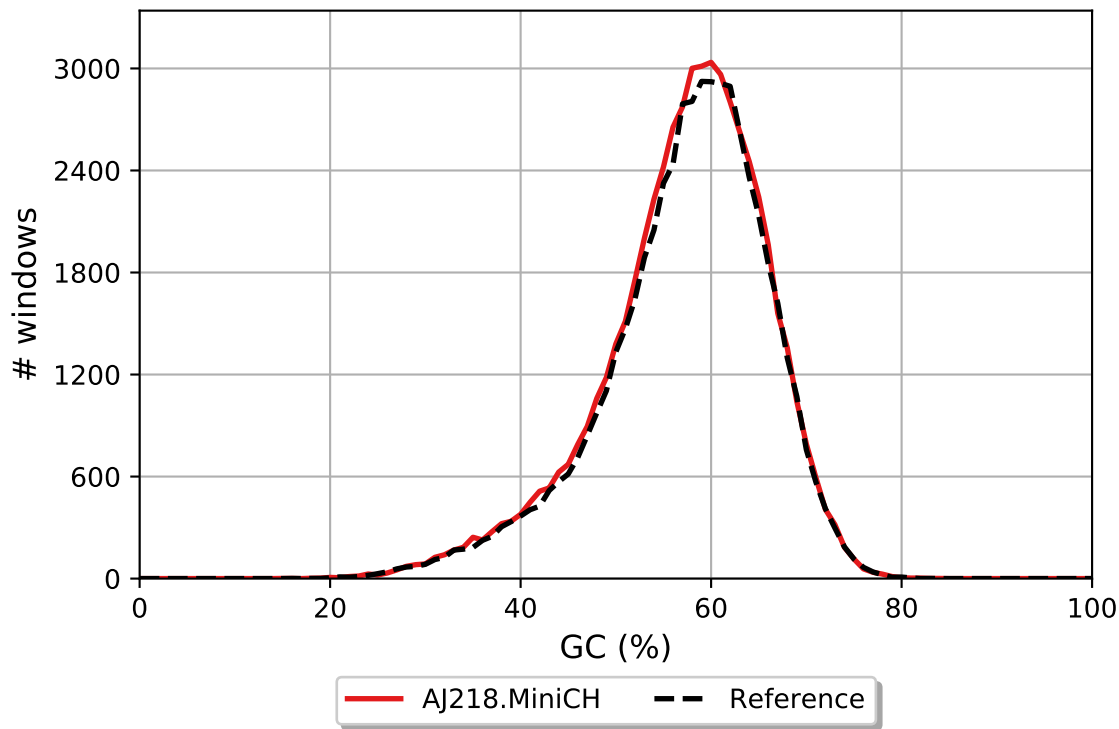
NGx



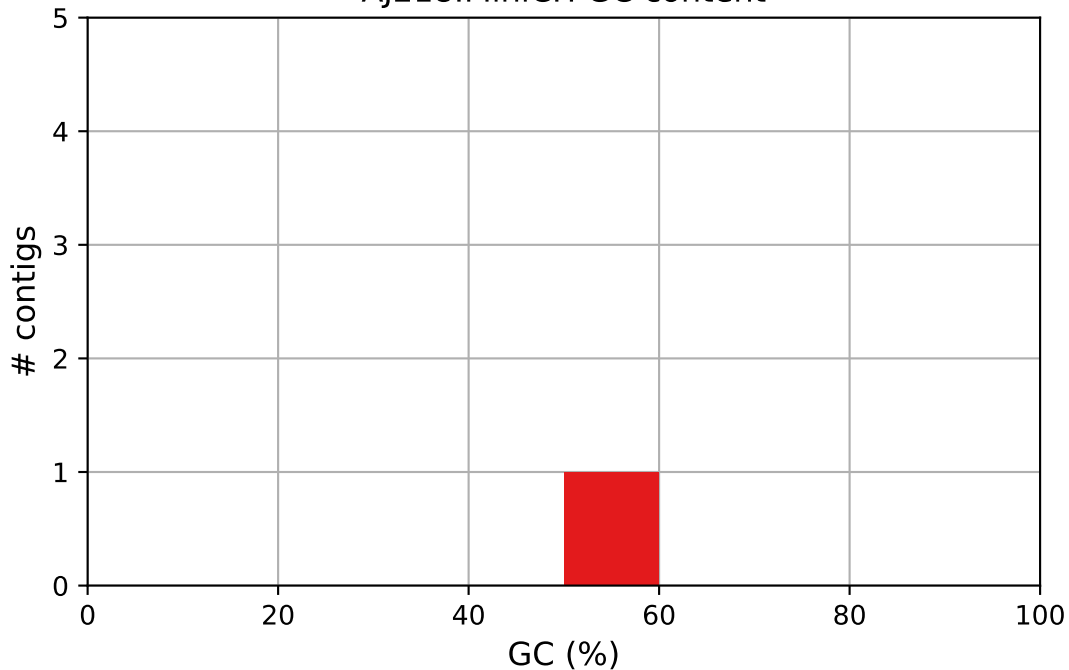
Aj218.MiniCH



GC content

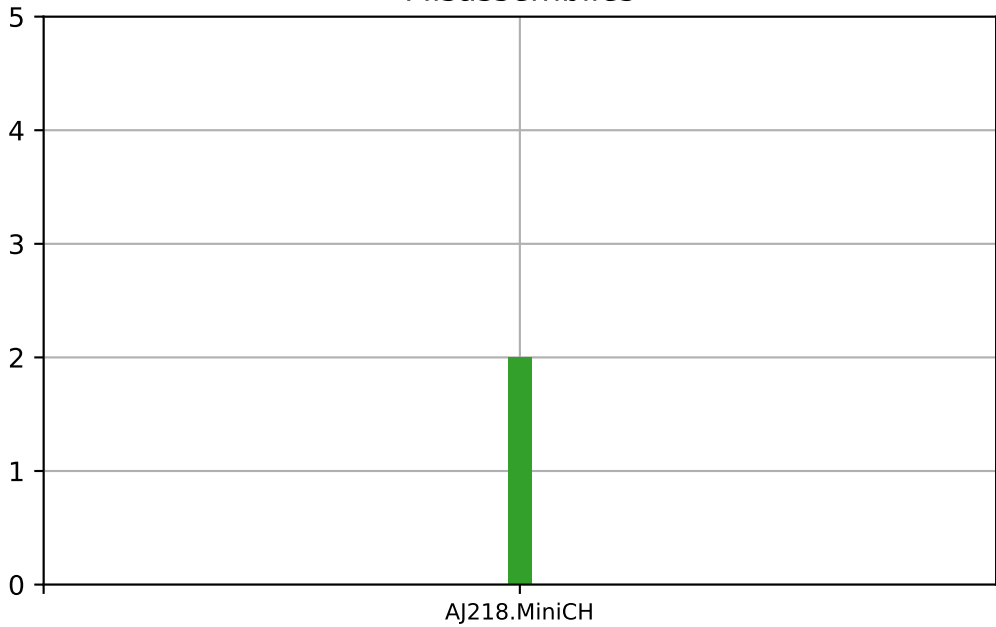


AJ218.MiniCH GC content



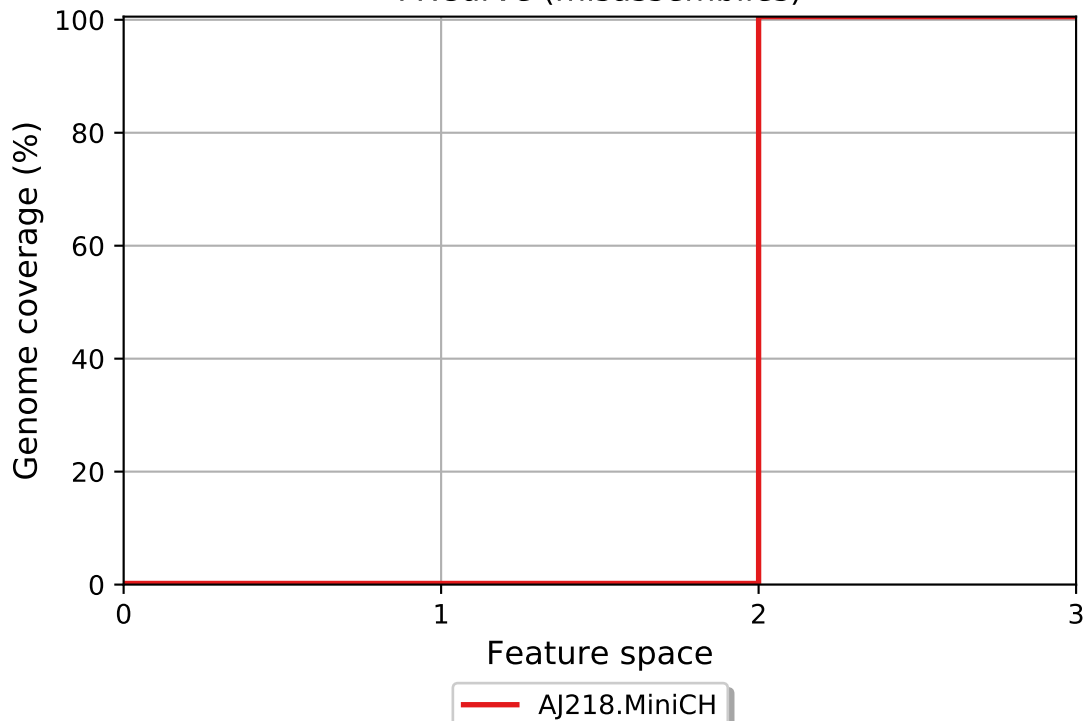
AJ218.MiniCH

Misassemblies

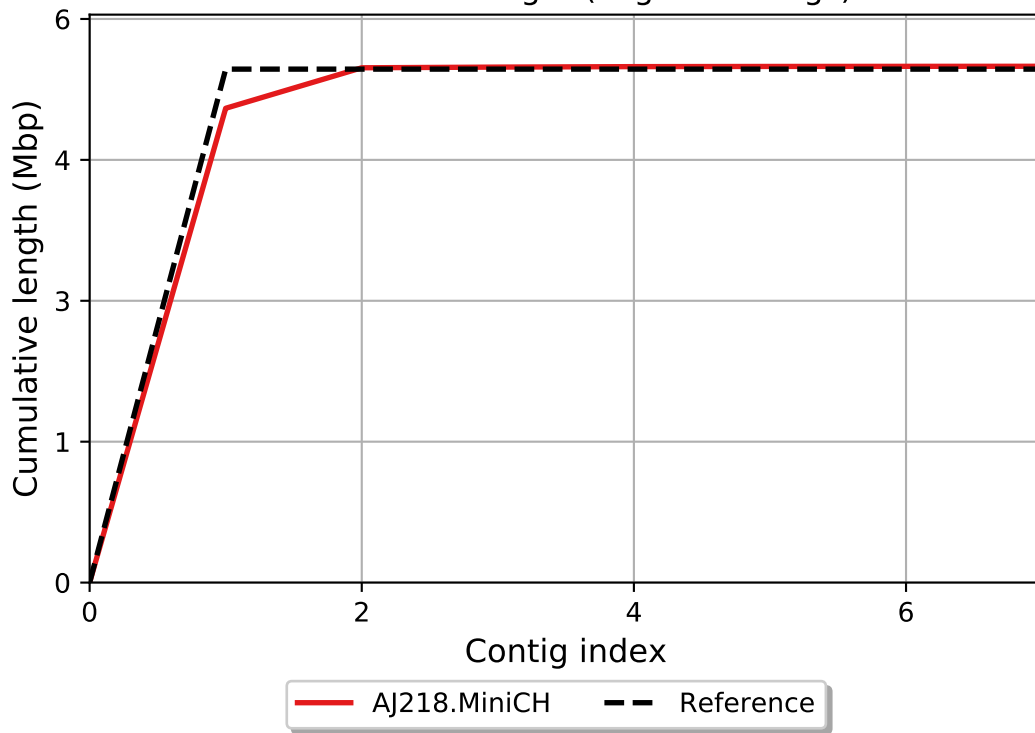


inversions

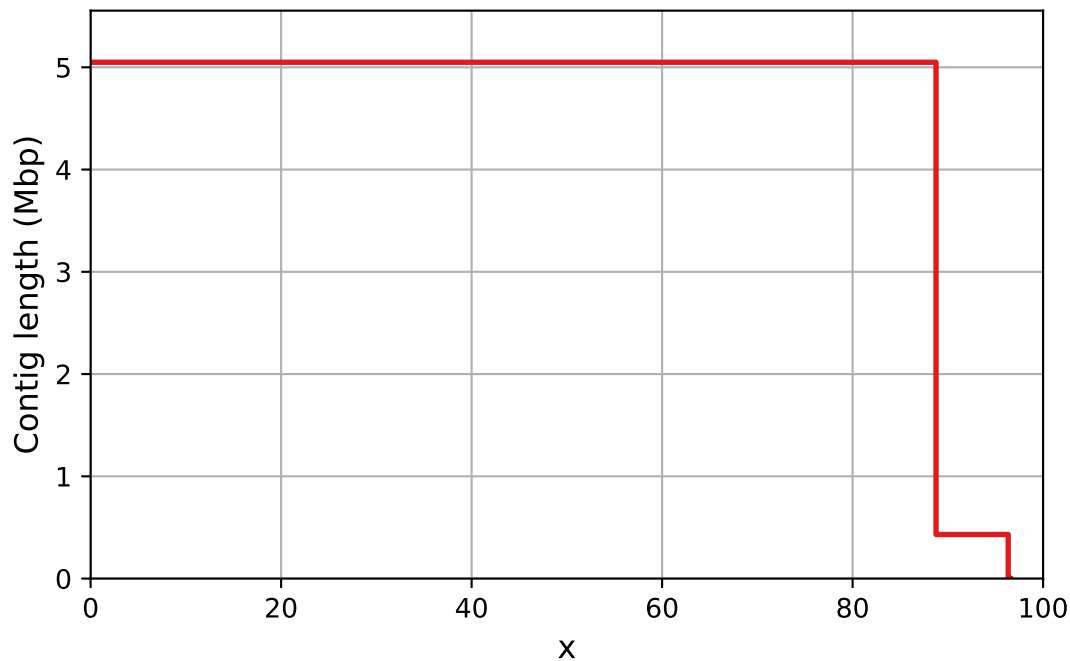
FRCurve (misassemblies)



Cumulative length (aligned contigs)

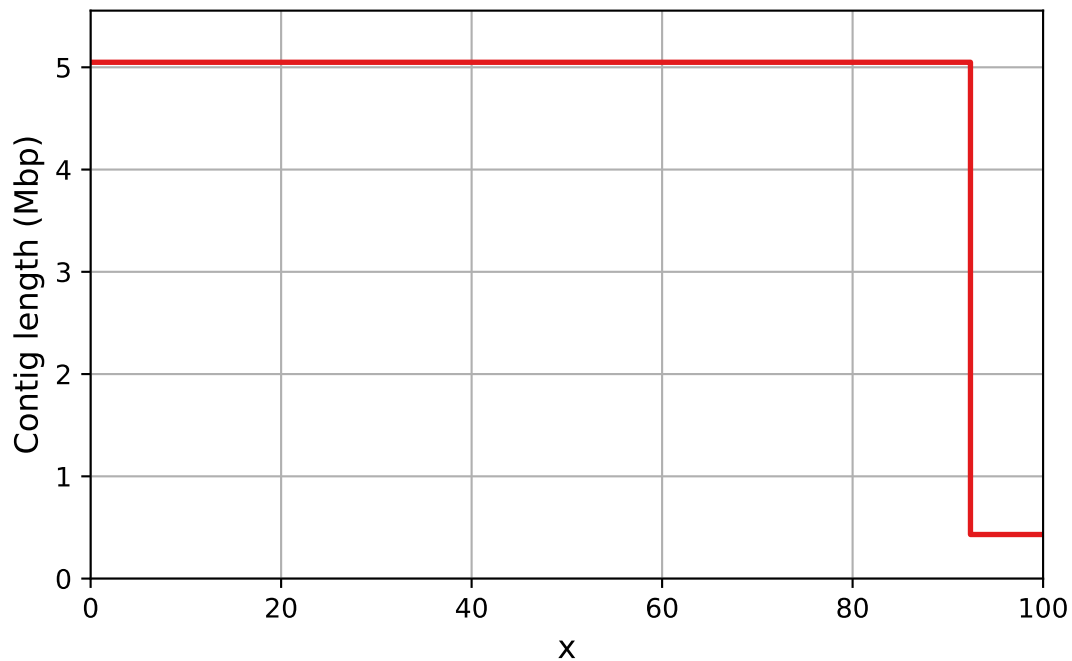


NAx



Aj218.MiniCH

NGAx



Aj218.MiniCH