

## Report

	AJ218.Metasm
# 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)	9472500
Total length (>= 1000 bp)	9472500
Total length (>= 5000 bp)	9472500
Total length (>= 10000 bp)	9472500
Total length (>= 25000 bp)	9432275
Total length (>= 50000 bp)	9432275
# contigs	4
Largest contig	9215694
Total length	9472500
Reference length	5465981
GC (%)	57.22
Reference GC (%)	57.29
N50	9215694
NG50	9215694
N75	9215694
NG75	9215694
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	9215694
# local misassemblies	1
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	243443
Genome fraction (%)	99.905
Duplication ratio	1.690
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.18
# indels per 100 kbp	12.32
Largest alignment	5244427
Total aligned length	9228948
NA50	5244427
NGA50	5244427
NA75	3299401
NGA75	5244427
LA50	1
LGA50	1
LA75	2
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.Metasm
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	9215694
# local misassemblies	1
# unaligned mis. contigs	1
# mismatches	10
# indels	673
# indels ( $\leq 5$ bp)	672
# indels ( $> 5$ bp)	1
Indels length	688

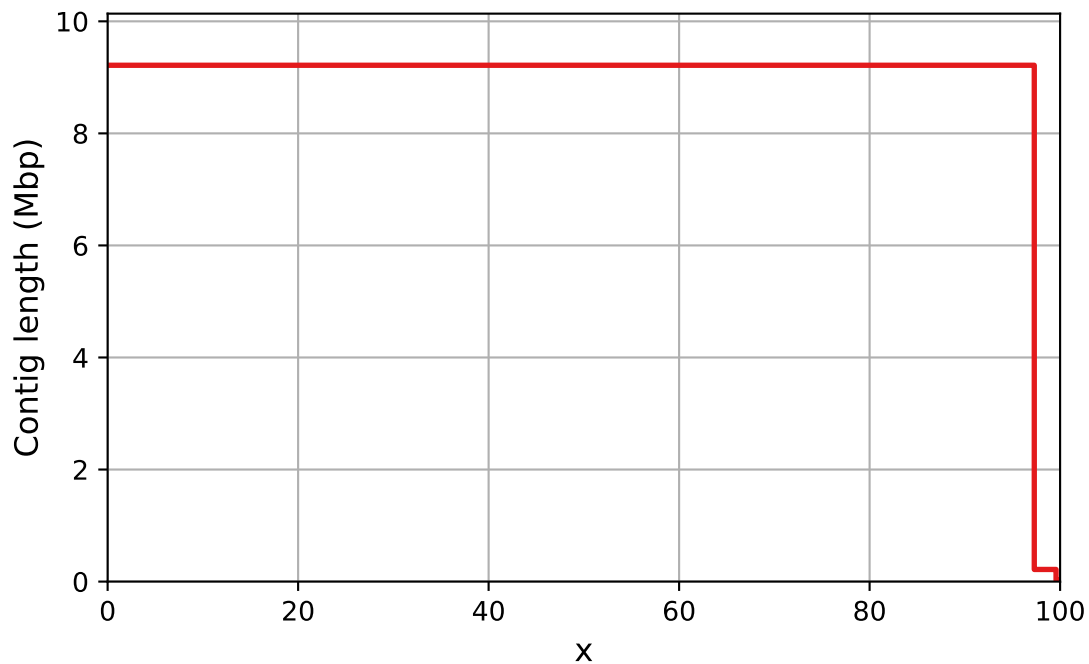
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ218.Metasm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	243443
# N's	0

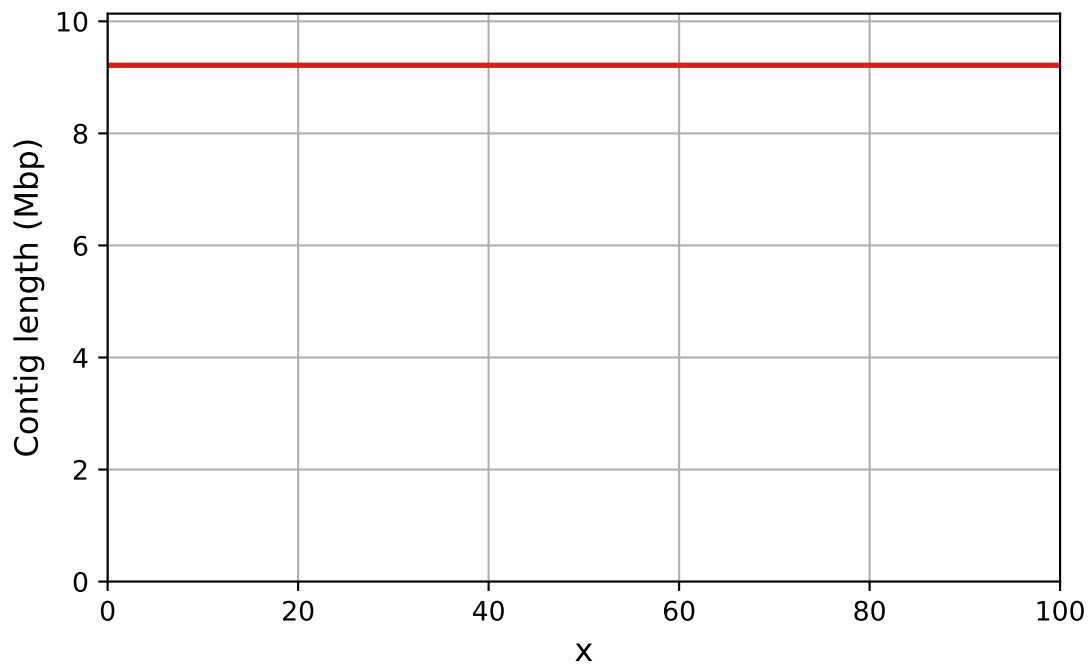
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



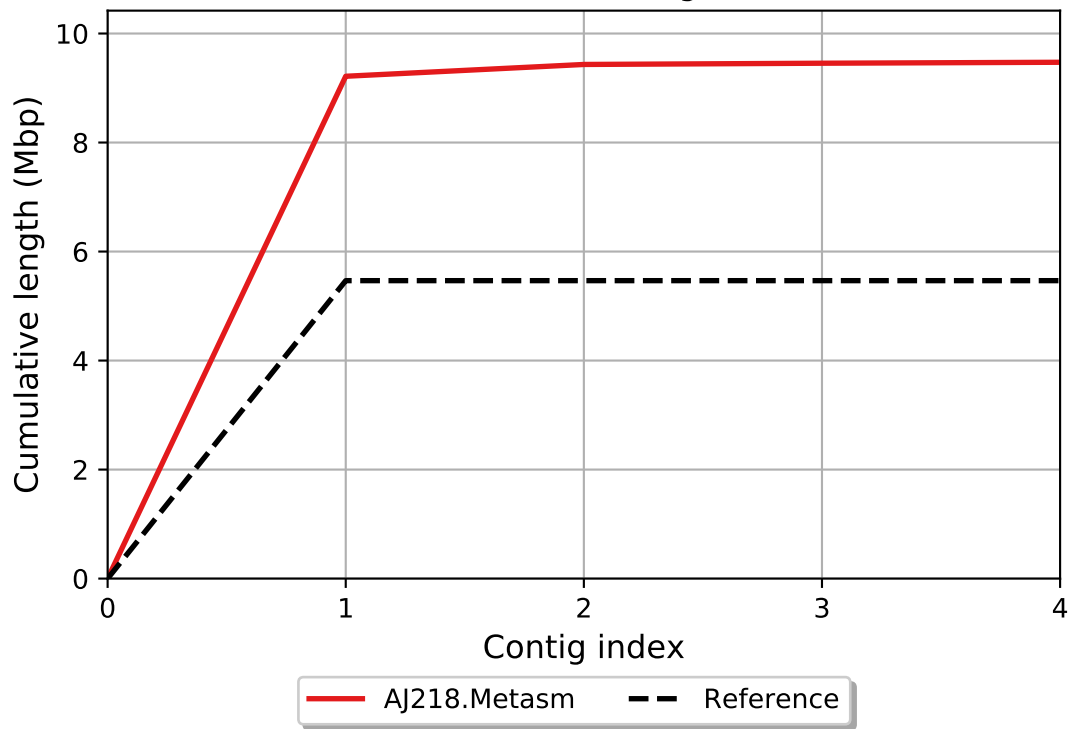
Aj218.Metasm

NGx

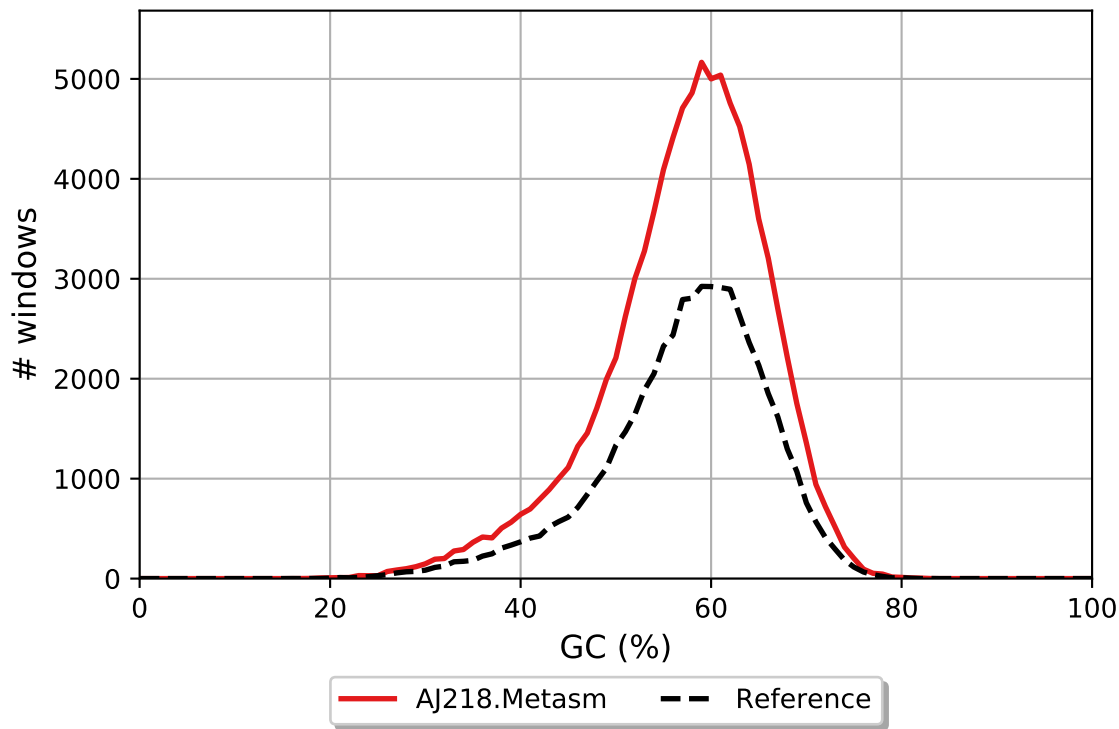


AJ218.Metasm

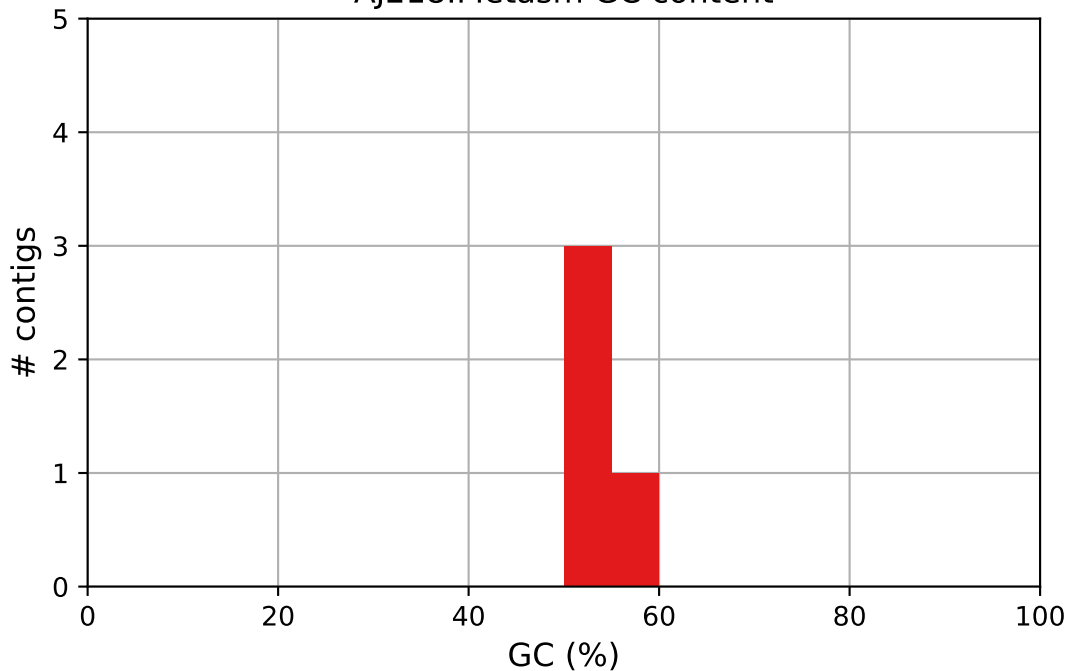
Cumulative length




## GC content



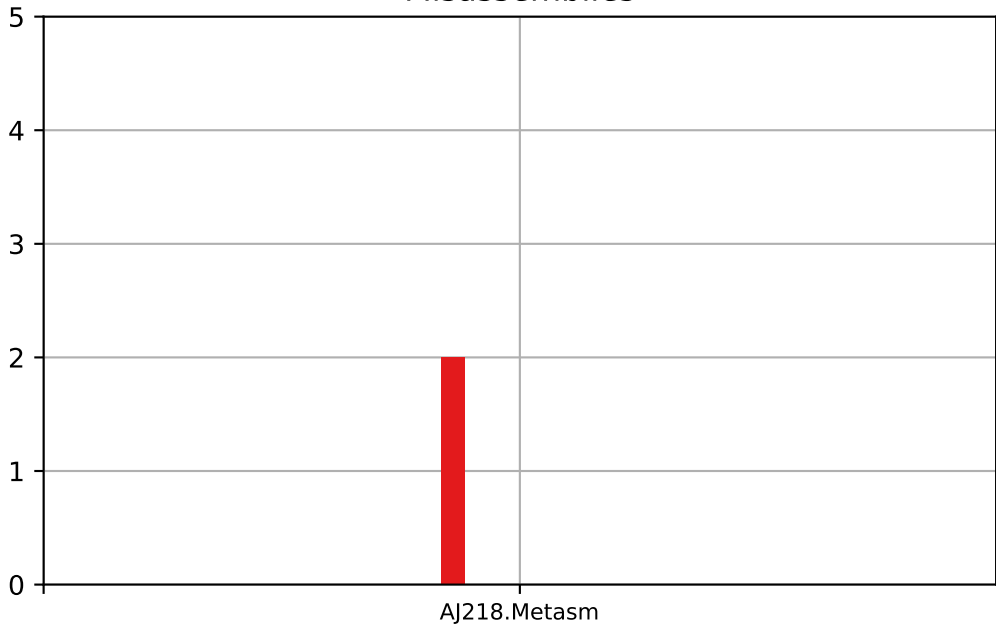
# AJ218.Metasm GC content



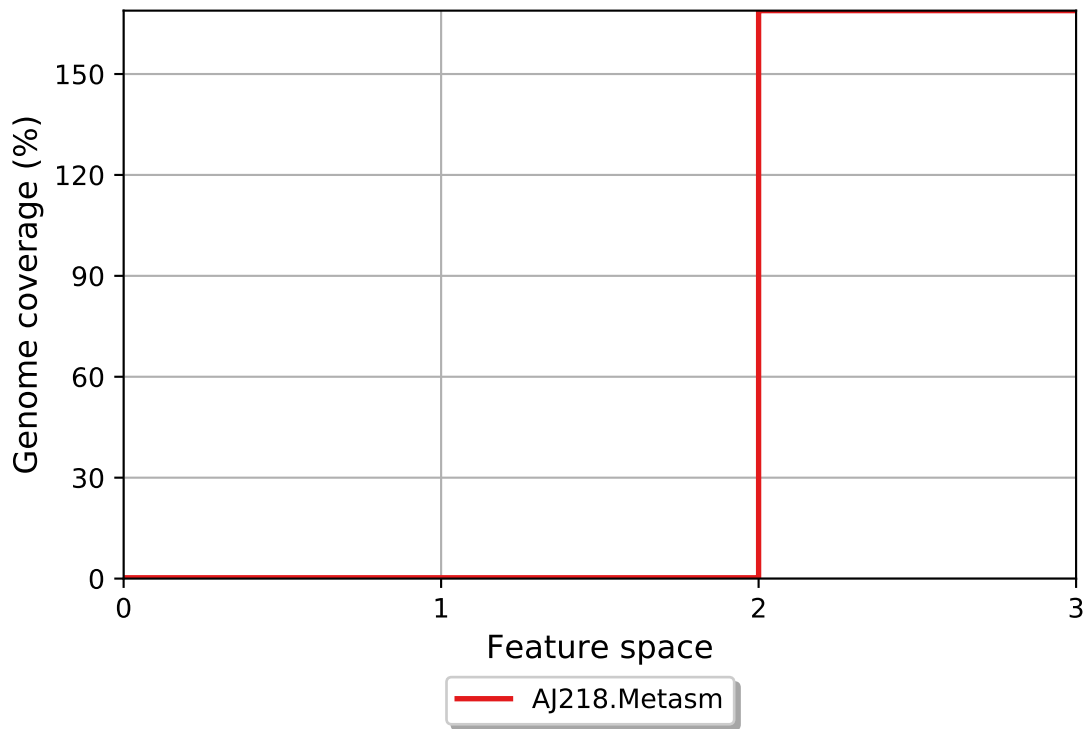
 AJ218.Metasm



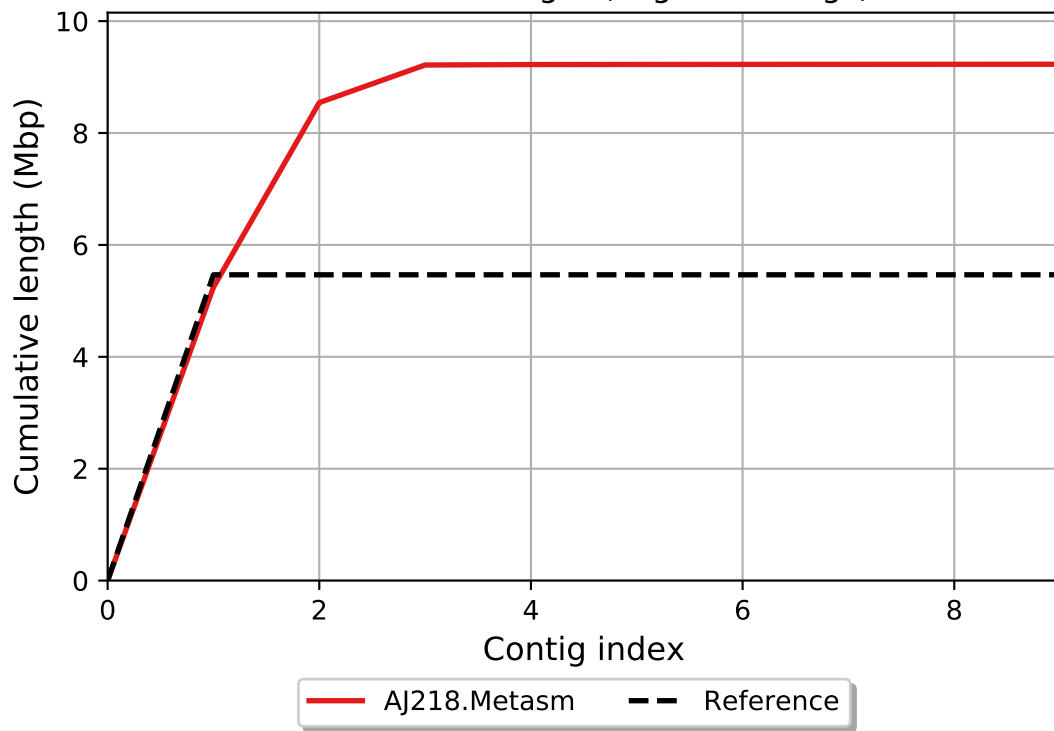
## Misassemblies



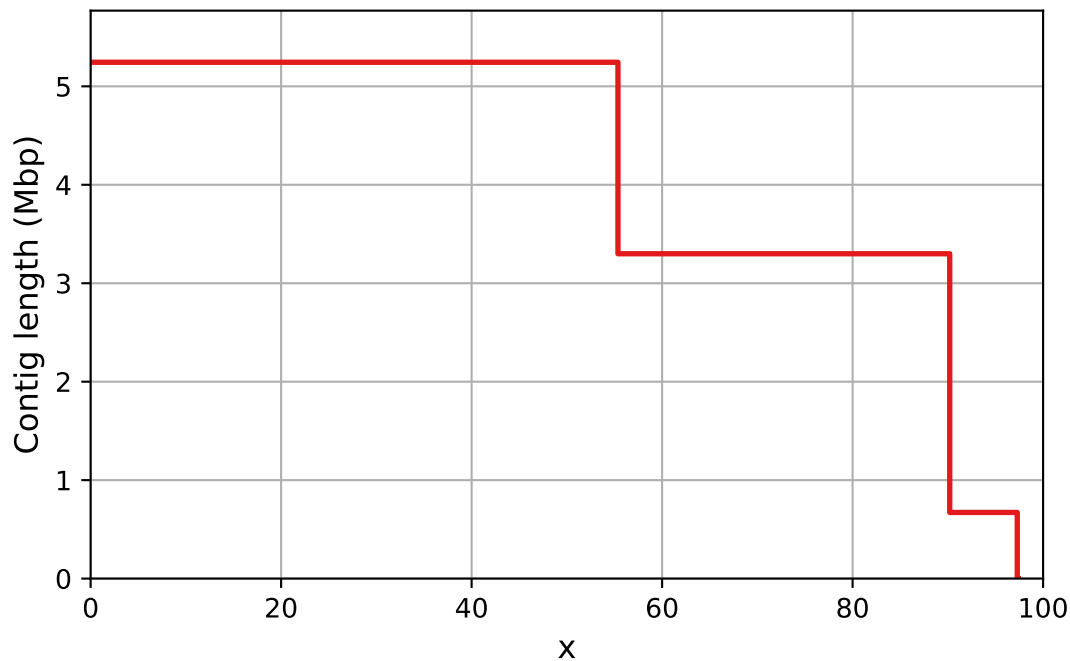
FRCurve (misassemblies)



Cumulative length (aligned contigs)

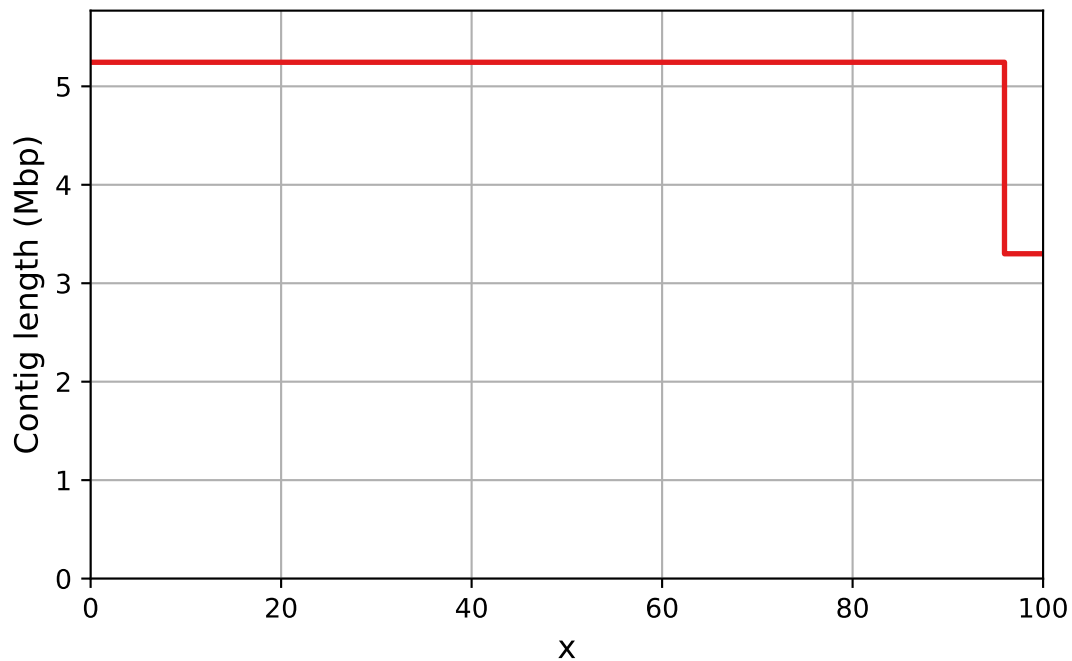


NAx



AJ218.Metasm

NGAx



AJ218.Metasm