

## Report

	AJ218.MiniL
# contigs (>= 0 bp)	11
# contigs (>= 1000 bp)	11
# contigs (>= 5000 bp)	11
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	11
Total length (>= 0 bp)	5642861
Total length (>= 1000 bp)	5642861
Total length (>= 5000 bp)	5642861
Total length (>= 10000 bp)	5642861
Total length (>= 25000 bp)	5642861
Total length (>= 50000 bp)	5642861
# contigs	11
Largest contig	1150335
Total length	5642861
Reference length	5465981
GC (%)	57.06
Reference GC (%)	57.29
N50	610819
NG50	610819
N75	496782
NG75	496782
L50	3
LG50	3
L75	6
LG75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned mis. contigs	1
# unaligned contigs	0 + 2 part
Unaligned length	195205
Genome fraction (%)	98.857
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	31.48
# indels per 100 kbp	566.22
Largest alignment	1150331
Total aligned length	5447535
NA50	606793
NGA50	606793
NA75	496779
NGA75	496779
LA50	3
LGA50	3
LA75	6
LGA75	6

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

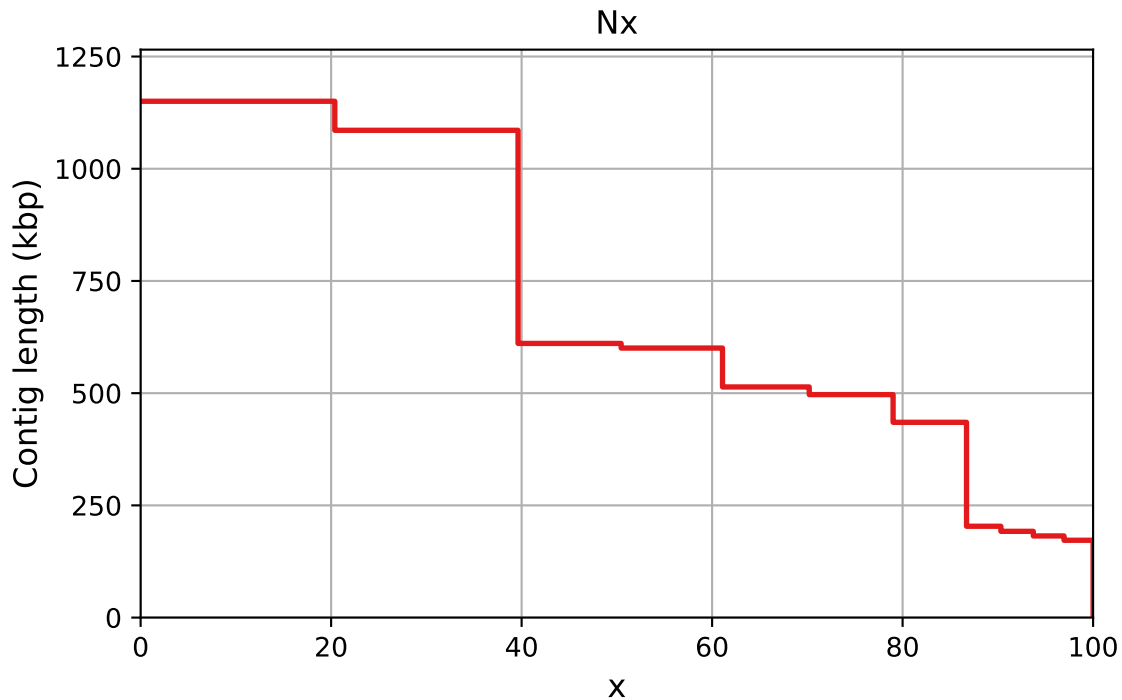
	AJ218.Minil
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned mis. contigs	1
# mismatches	1701
# indels	30596
# indels ( $\leq 5$ bp)	30458
# indels ( $> 5$ bp)	138
Indels length	39799

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

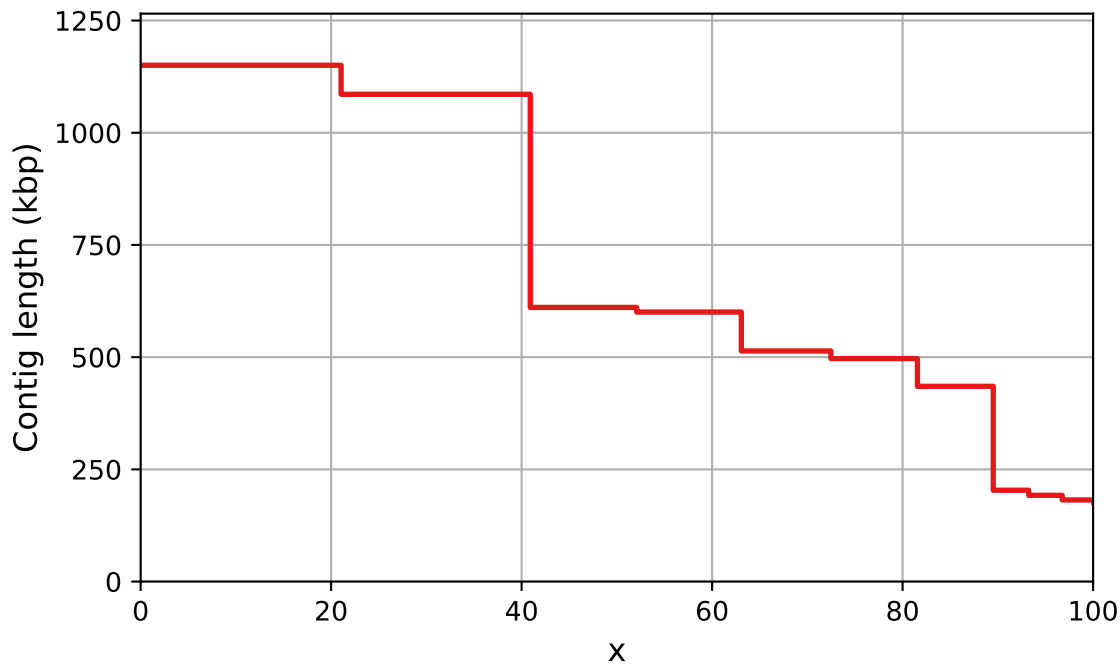
	AJ218.MiniL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	195205
# N's	0

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).



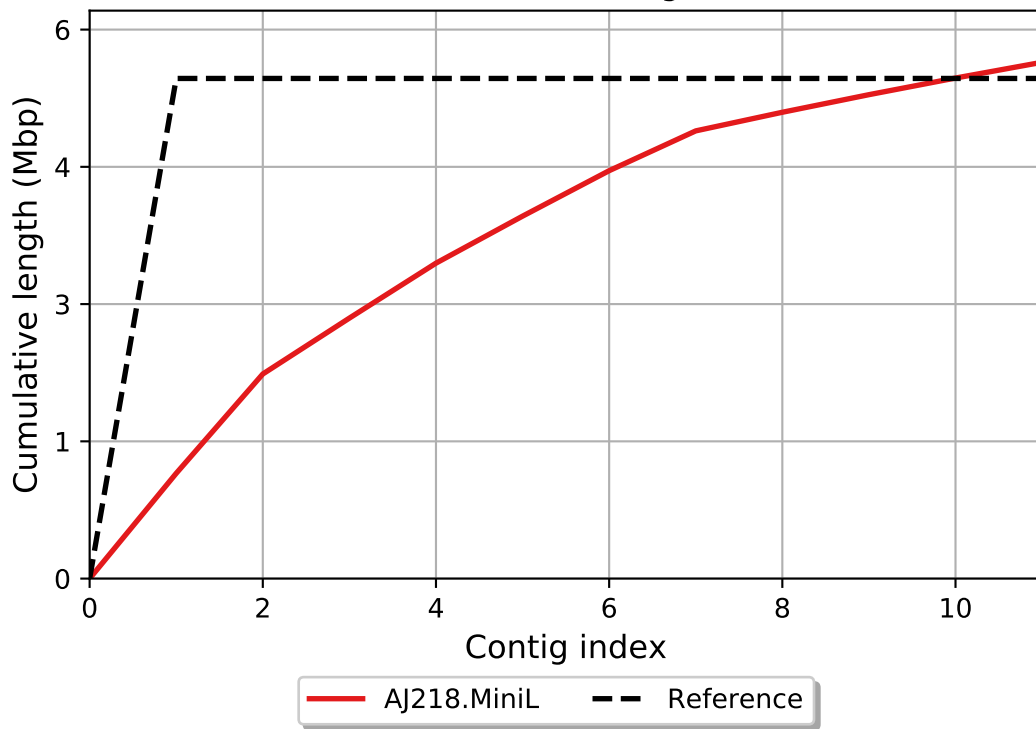
AJ218.MiniL

NGx

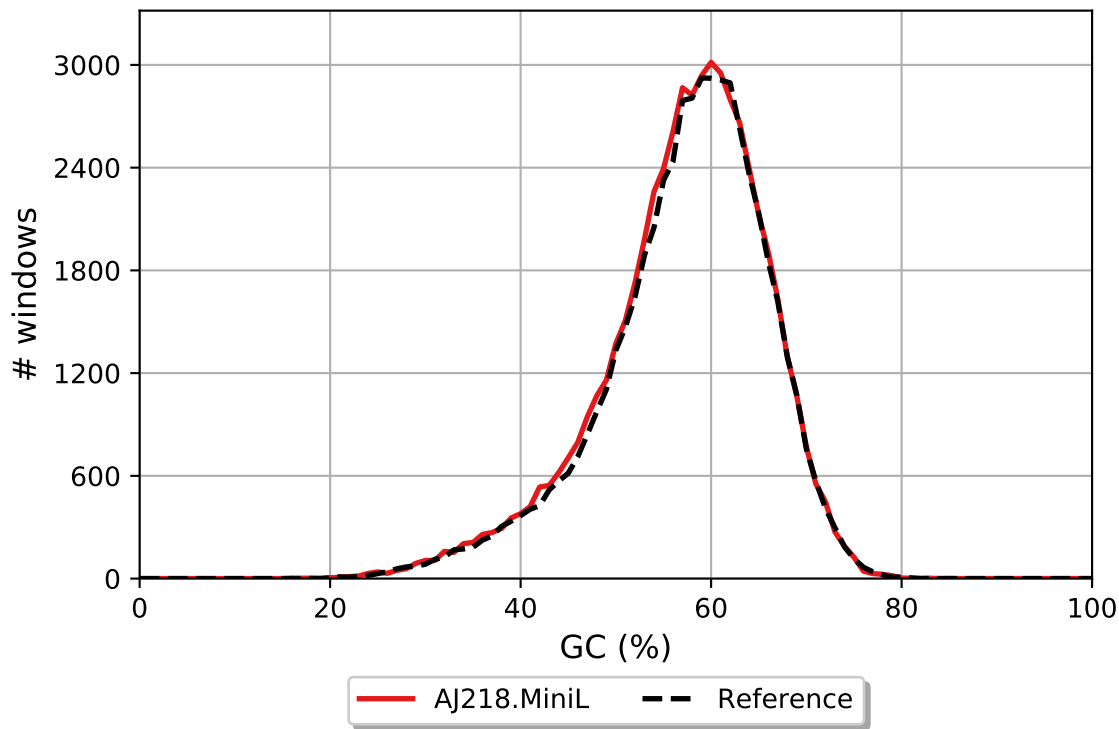


AJ218.MiniL

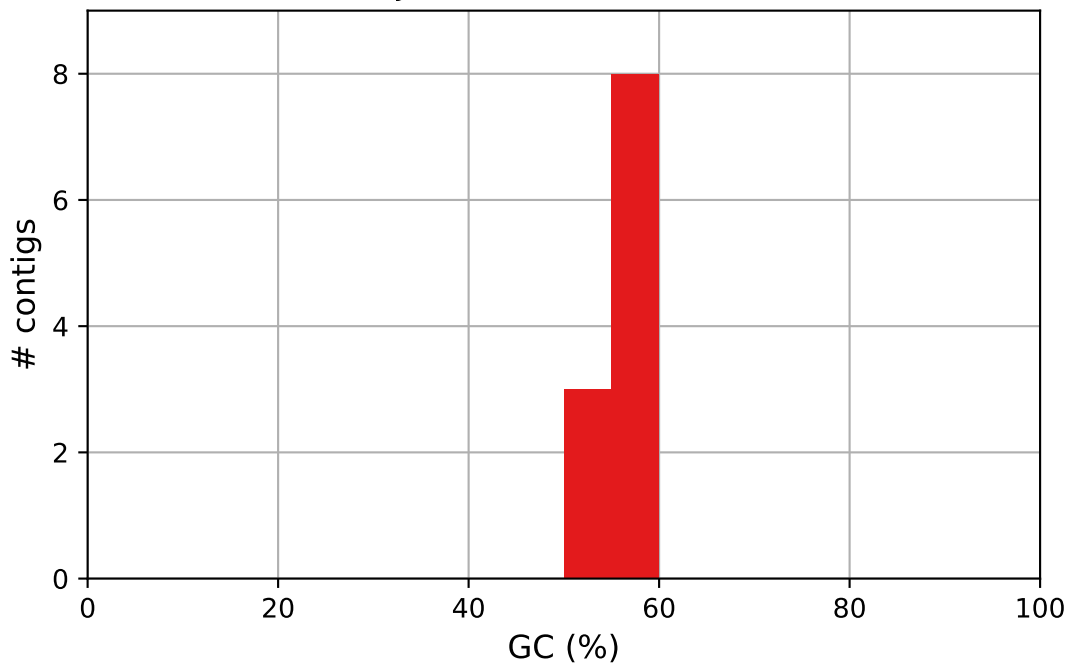
Cumulative length



## GC content



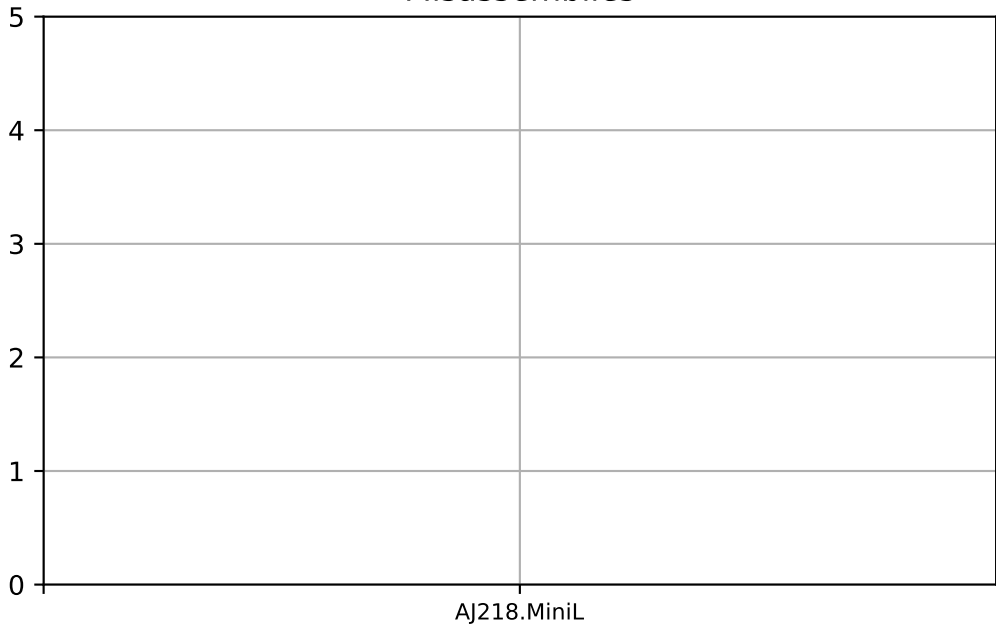
AJ218.Minil GC content



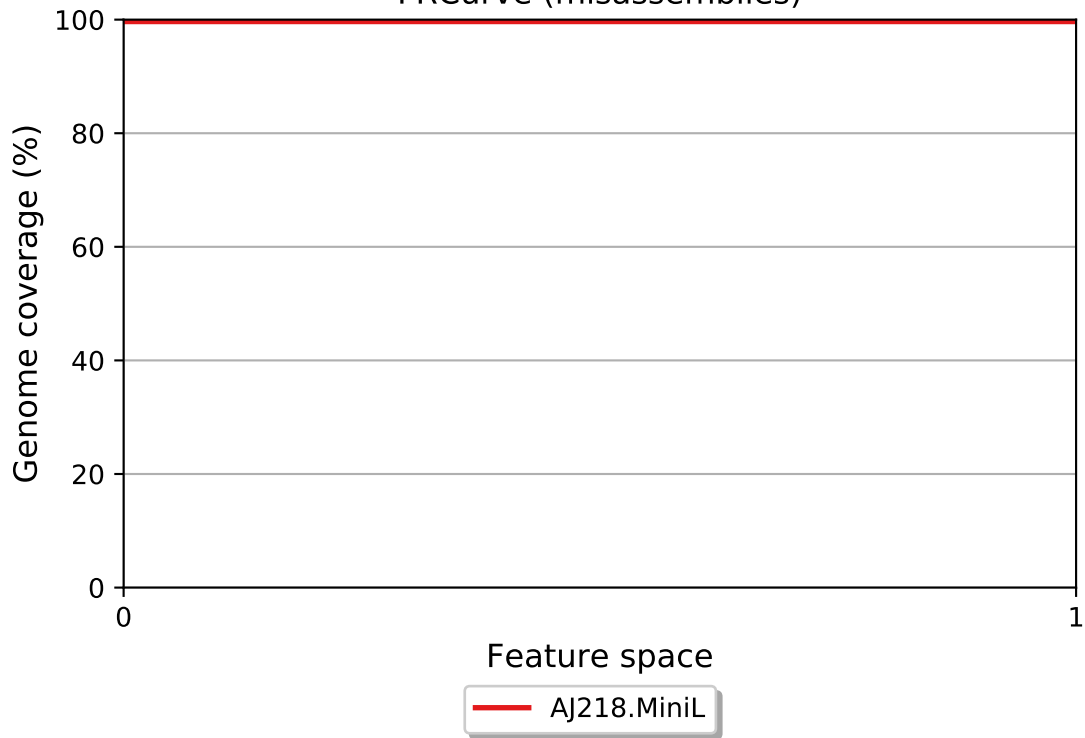
AJ218.Minil

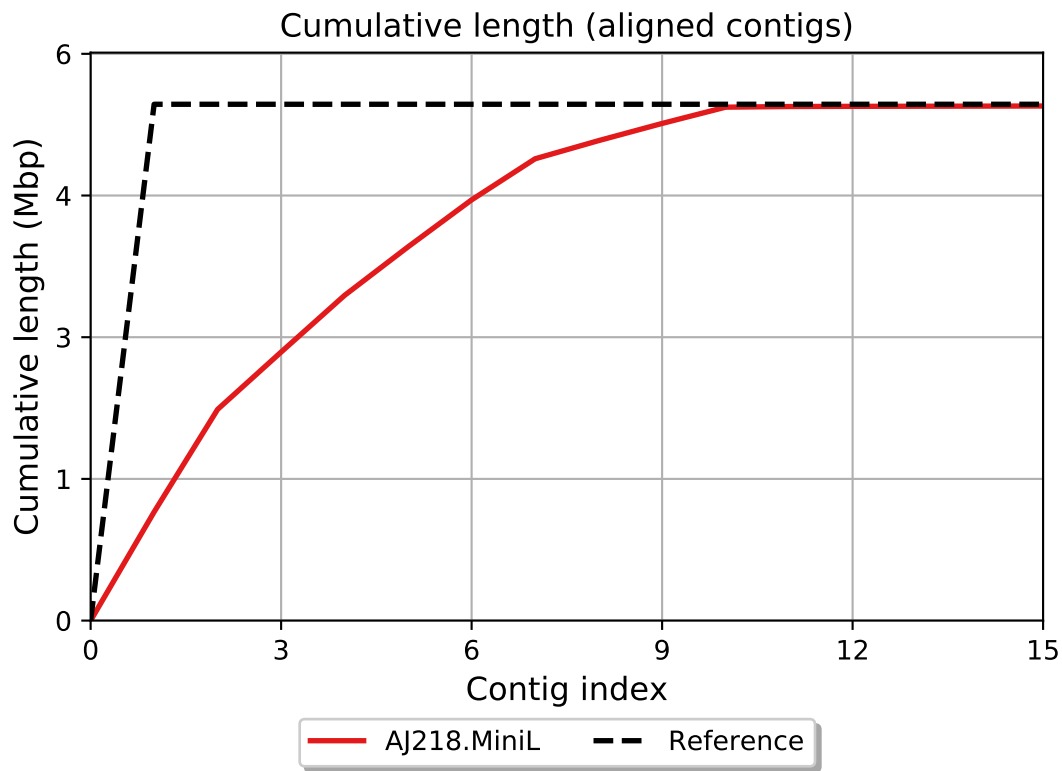


## Misassemblies

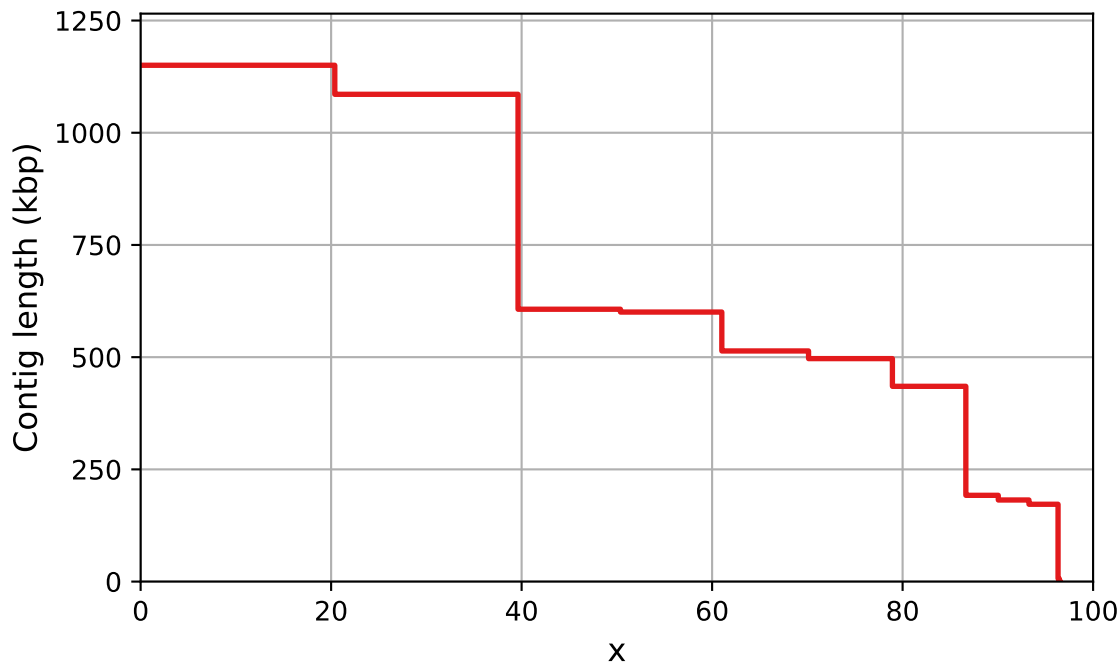


FRCurve (misassemblies)



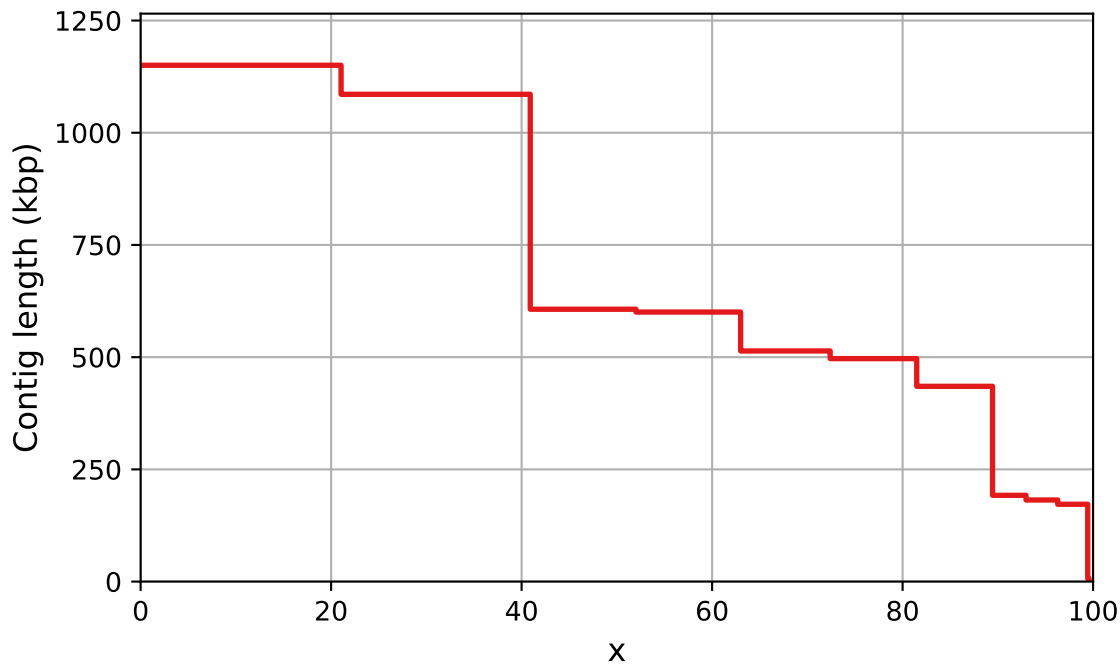


NAx



AJ218.MiniL

# NGAx



AJ218.MiniL