

# Report

	AJ292.MiniL
# 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)	5466090
Total length (>= 1000 bp)	5466090
Total length (>= 5000 bp)	5466090
Total length (>= 10000 bp)	5466090
Total length (>= 25000 bp)	5466090
Total length (>= 50000 bp)	5466090
# contigs	2
Largest contig	3797896
Total length	5466090
Reference length	5445112
GC (%)	57.55
Reference GC (%)	57.62
N50	3797896
NG50	3797896
N75	1668194
NG75	1668194
L50	1
LG50	1
L75	2
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.969
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	26.97
# indels per 100 kbp	481.63
Largest alignment	3797549
Total aligned length	5465701
NA50	3797549
NGA50	3797549
NA75	1668152
NGA75	1668152
LA50	1
LGA50	1
LA75	2
LGA75	2

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

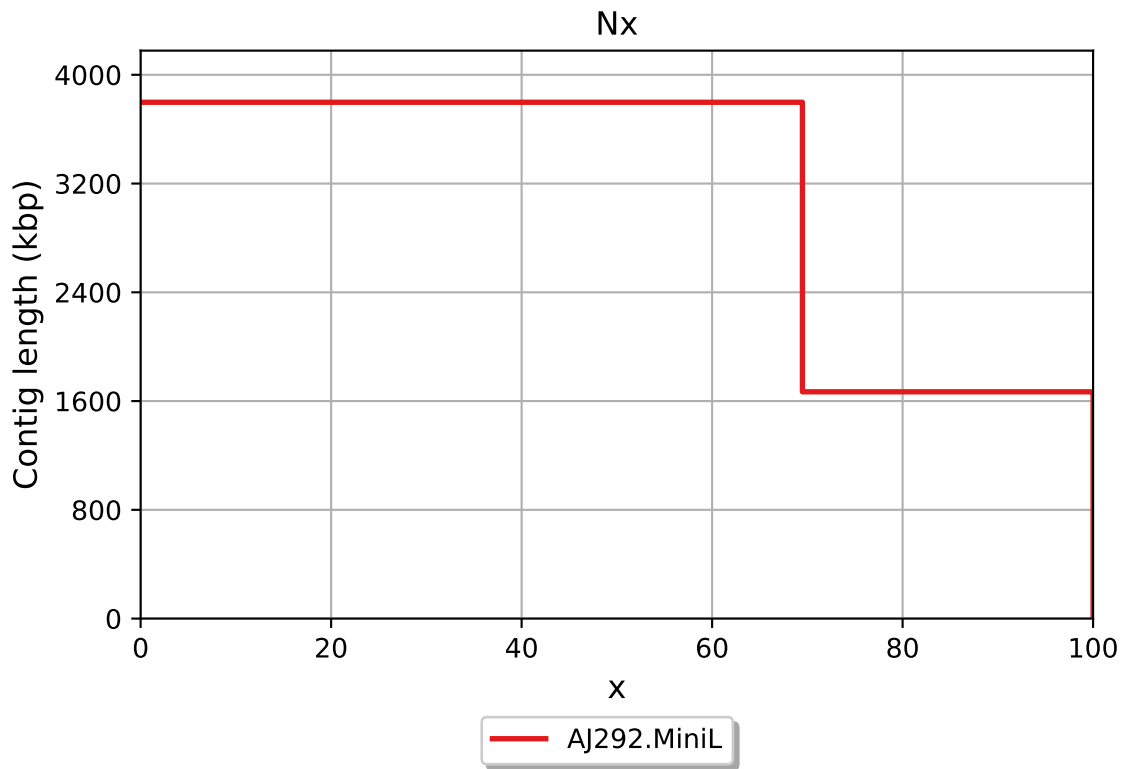
	AJ292.MinilL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned mis. contigs	0
# mismatches	1468
# indels	26217
# indels ( $\leq 5$ bp)	26088
# indels ( $> 5$ bp)	129
Indels length	34991

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).

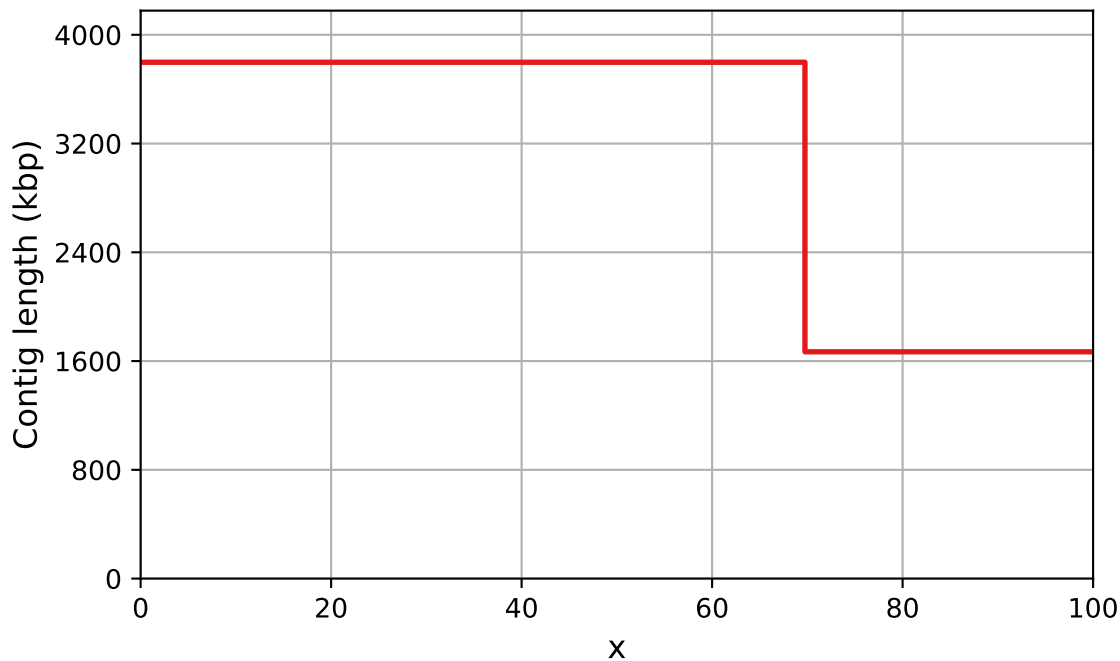
## Unaligned report

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

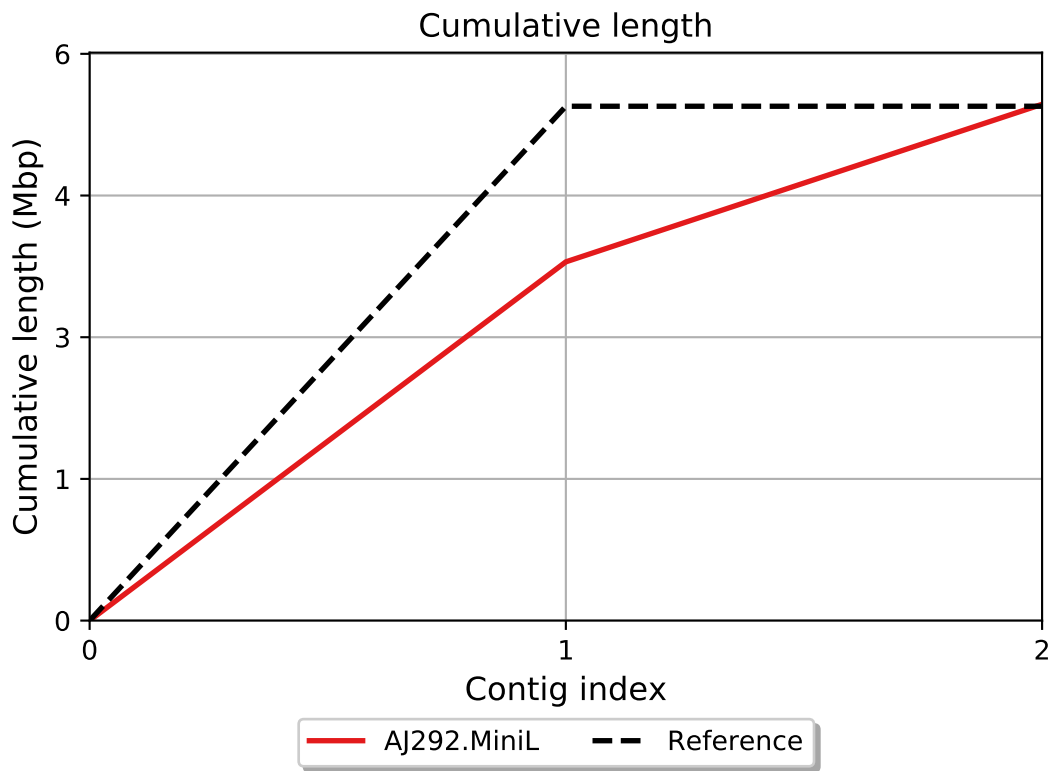
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



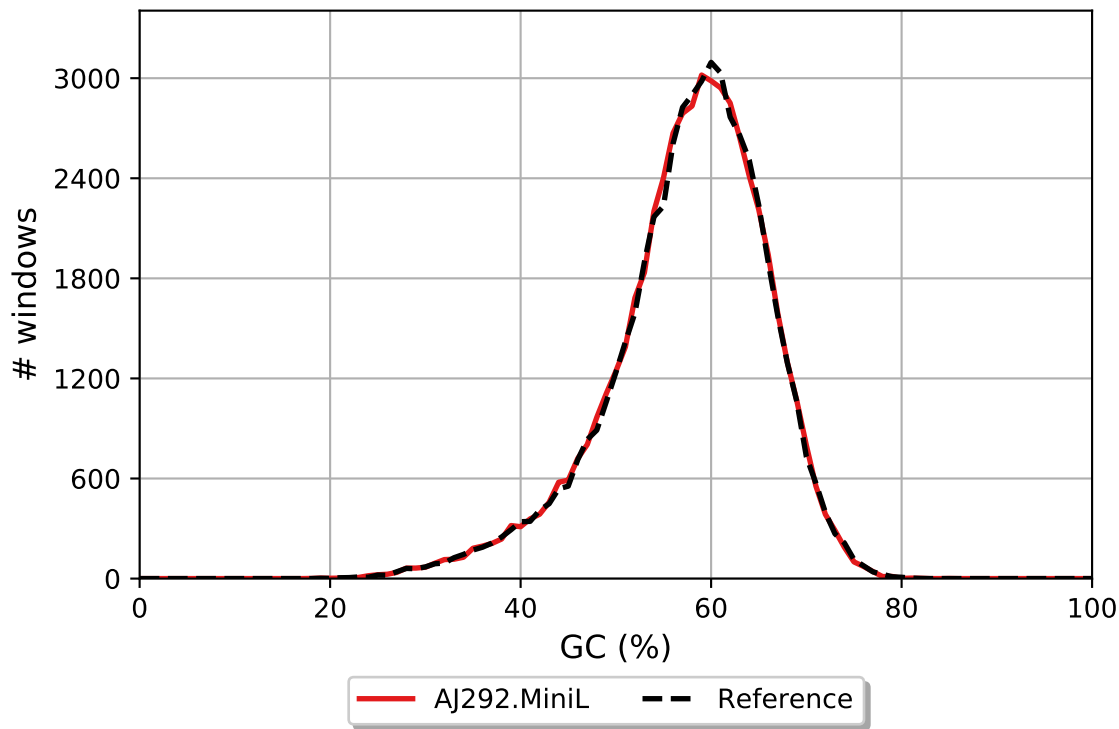
NGx



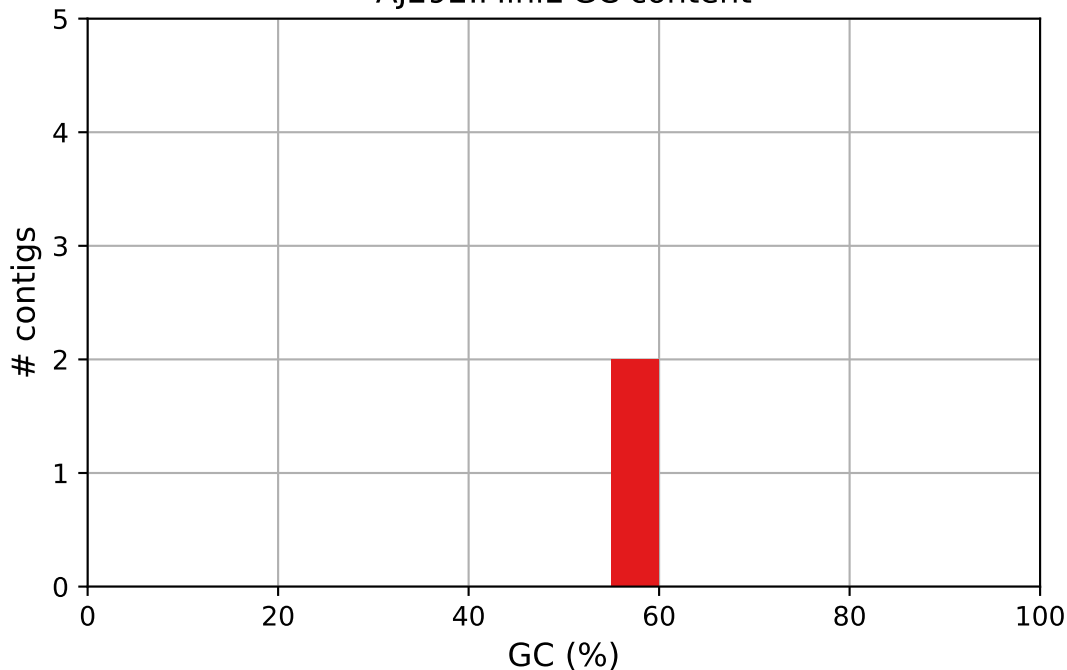
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## GC content



AJ292.MiniL GC content



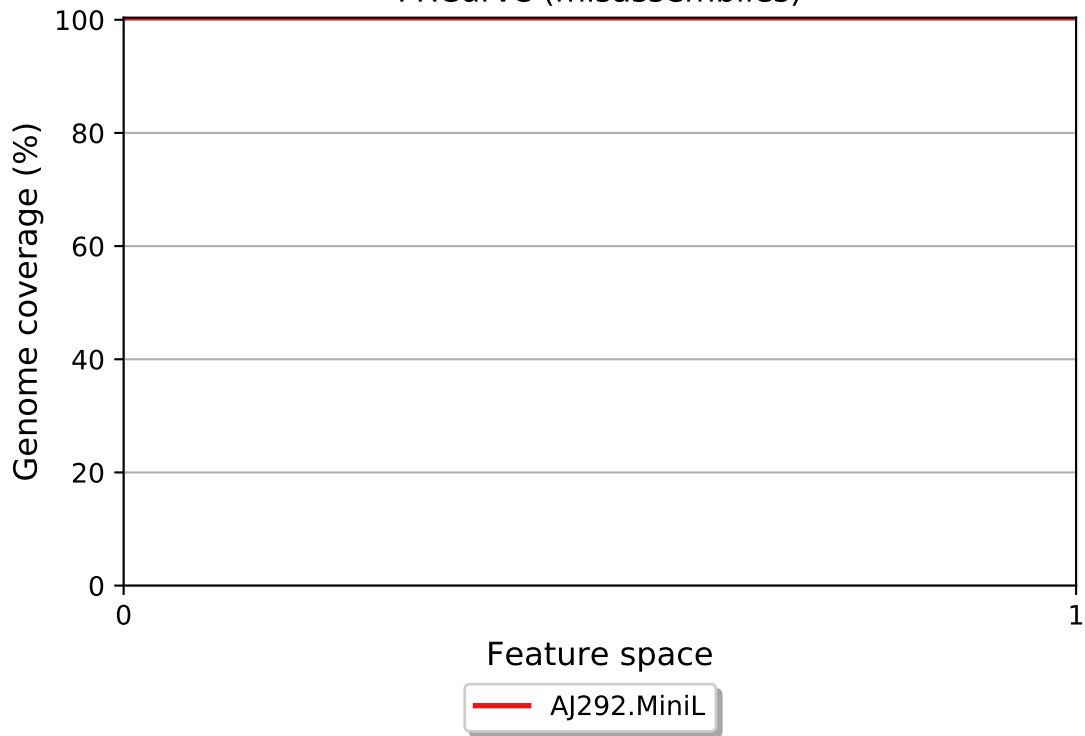
AJ292.MiniL

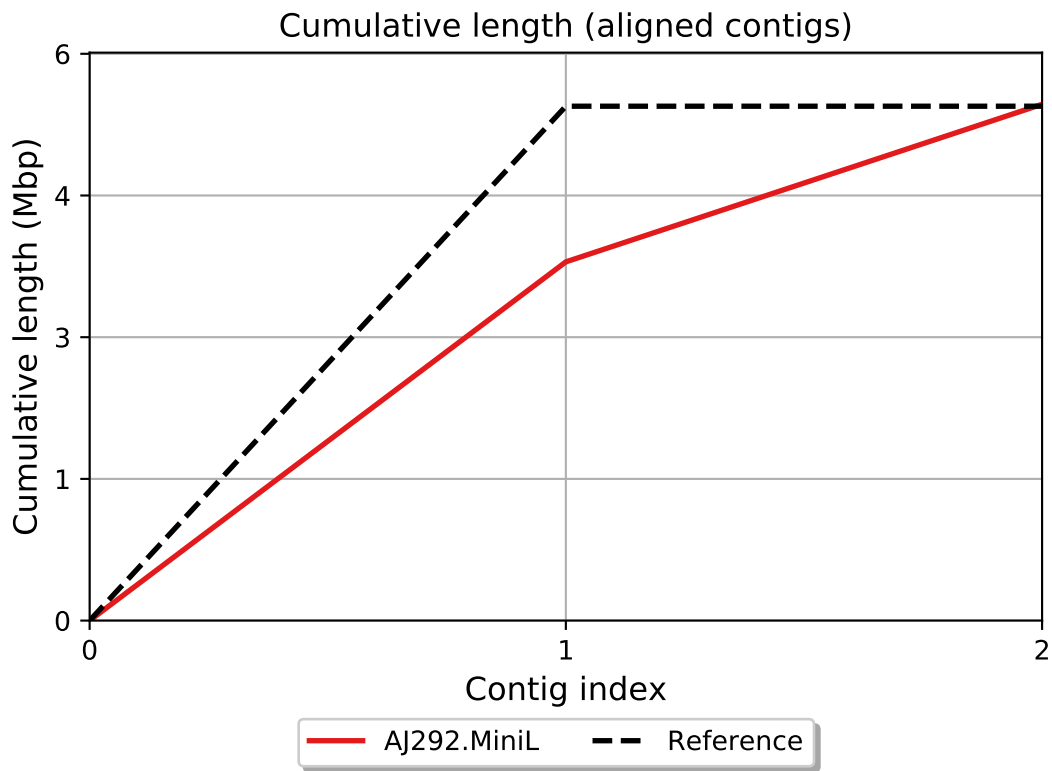


## Misassemblies

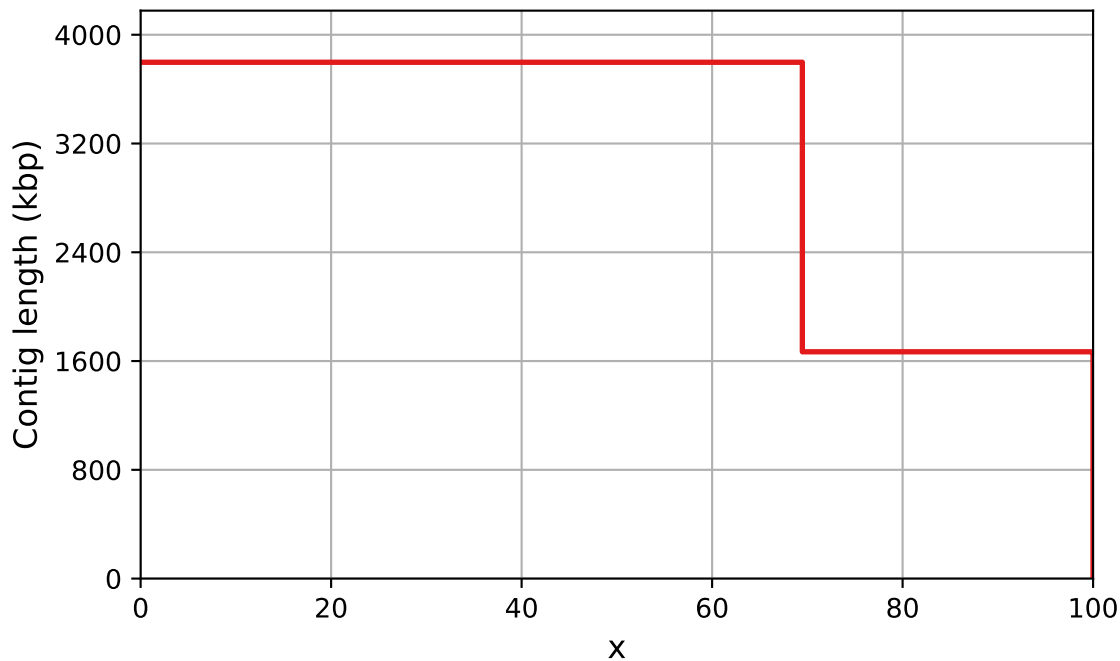


FRCurve (misassemblies)



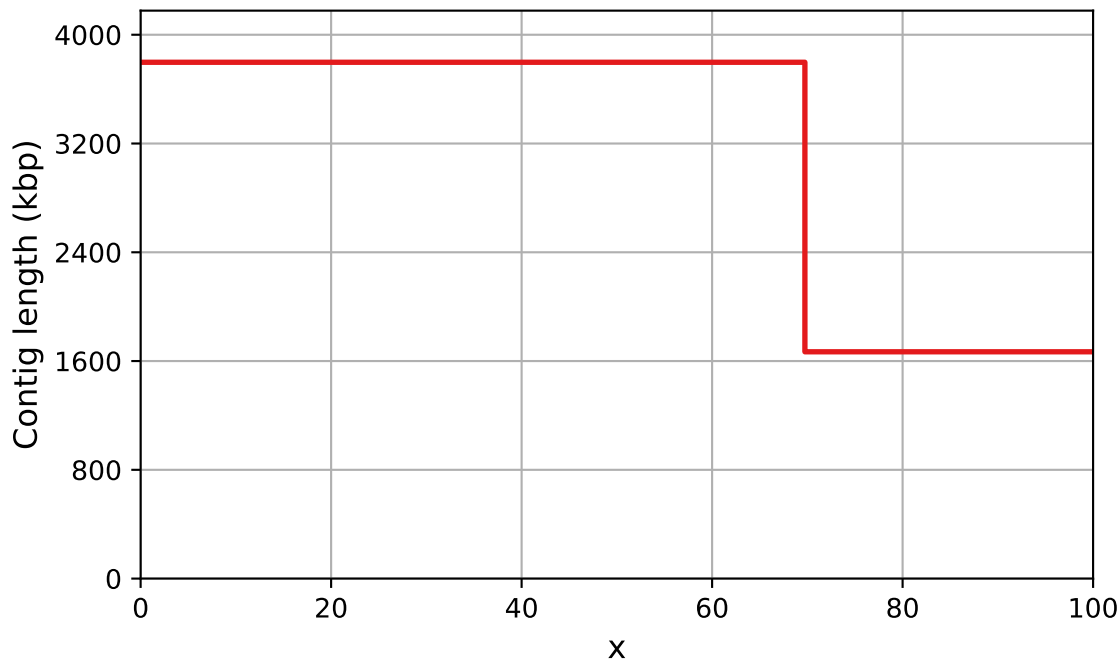


NAx



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NGAx



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