

Report

	AJ292.Metasm
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5496807
Total length (>= 1000 bp)	5496807
Total length (>= 5000 bp)	5496807
Total length (>= 10000 bp)	5496807
Total length (>= 25000 bp)	5458553
Total length (>= 50000 bp)	5458553
# contigs	3
Largest contig	5458553
Total length	5496807
Reference length	5445112
GC (%)	57.63
Reference GC (%)	57.62
N50	5458553
NG50	5458553
N75	5458553
NG75	5458553
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	5458553
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.15
# indels per 100 kbp	13.31
Largest alignment	4453337
Total aligned length	5496807
NA50	4453337
NGA50	4453337
NA75	4453337
NGA75	4453337
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

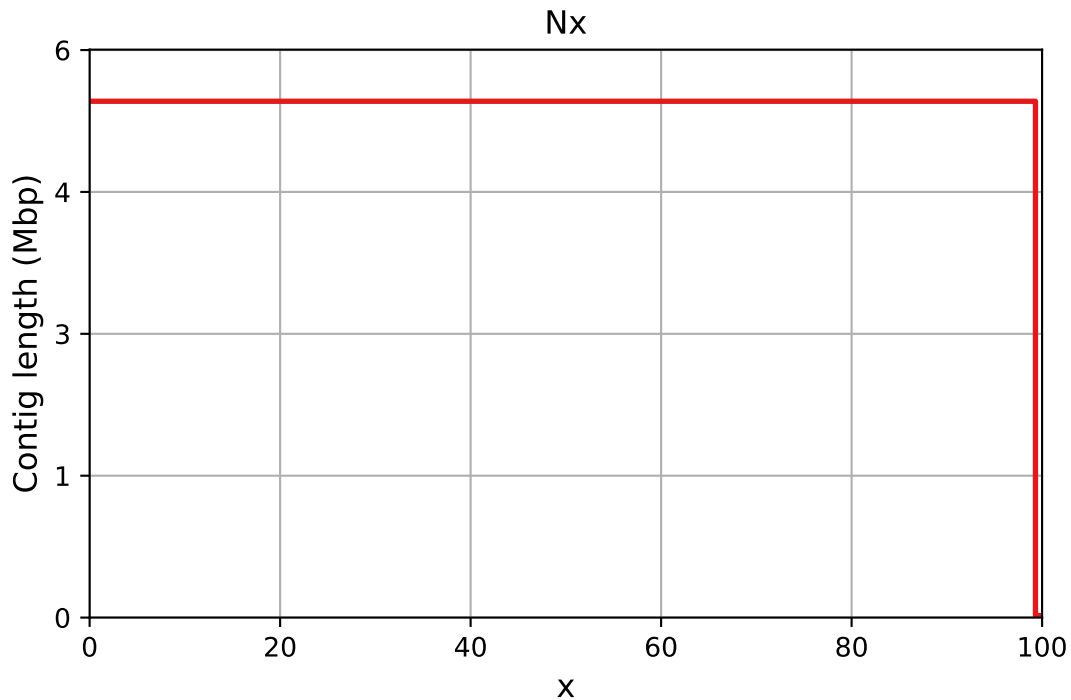
	AJ292.Metasm
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	5458553
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	8
# indels	725
# indels (≤ 5 bp)	725
# indels (> 5 bp)	0
Indels length	727

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

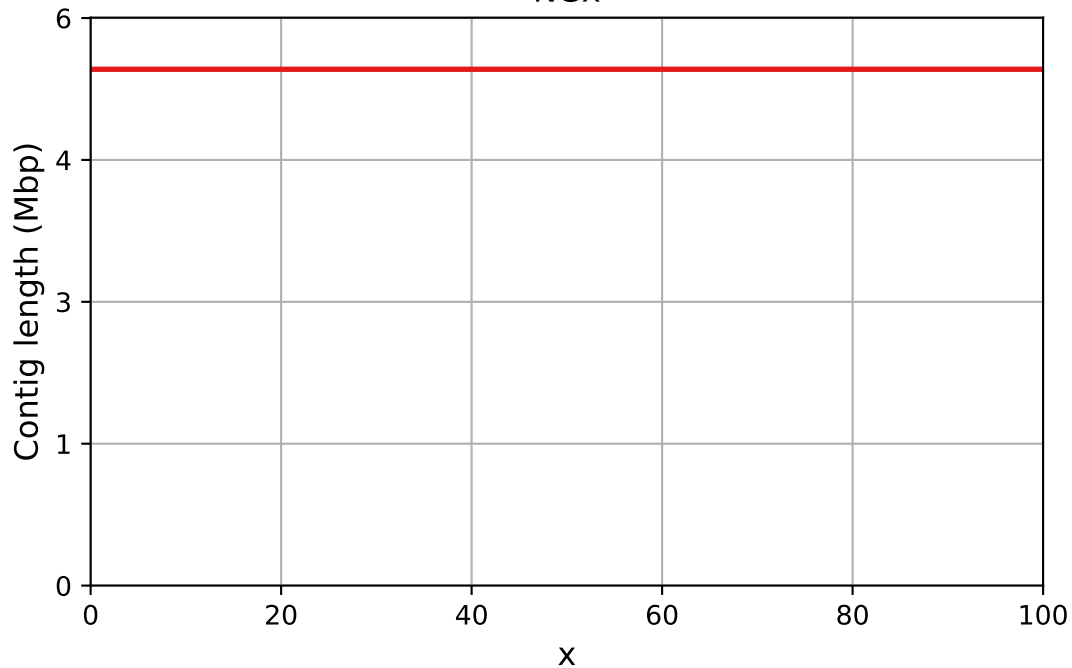
	AJ292.Metasm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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

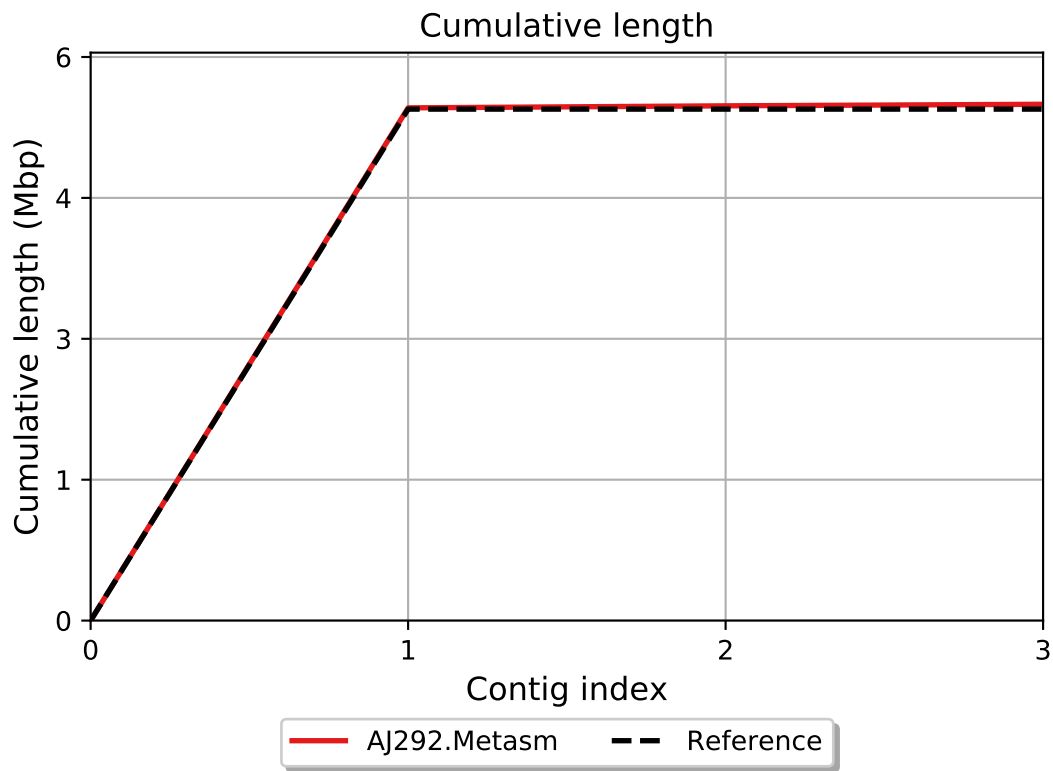


AJ292.Metasm

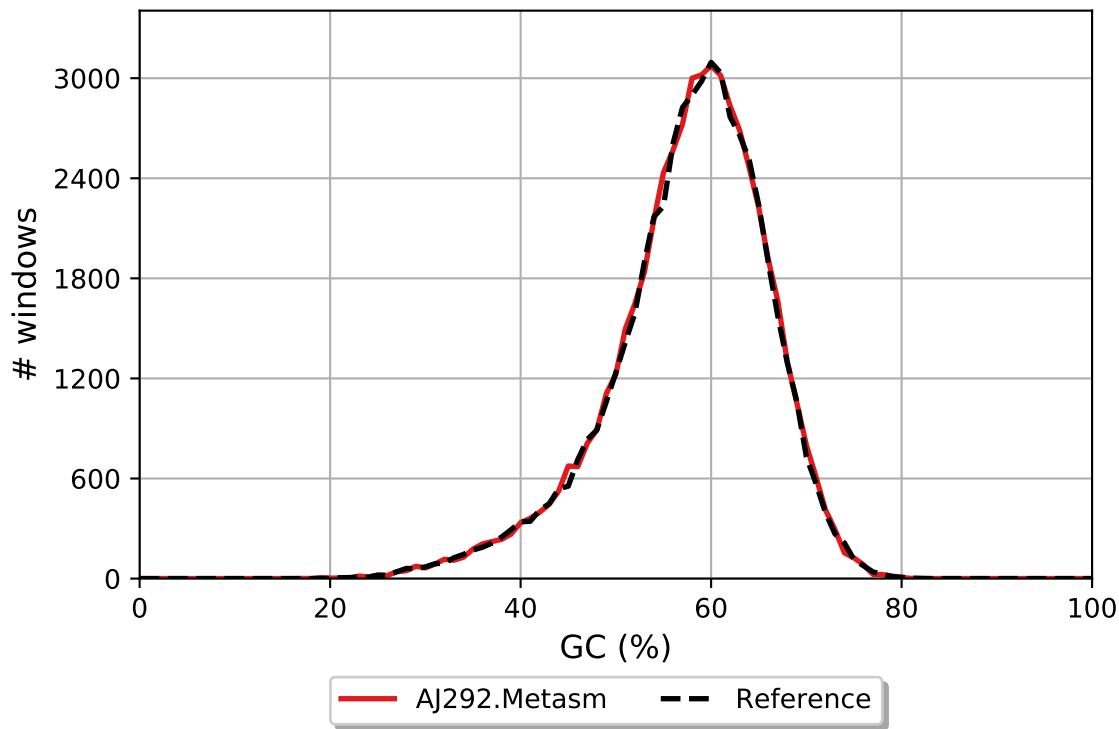
NGx



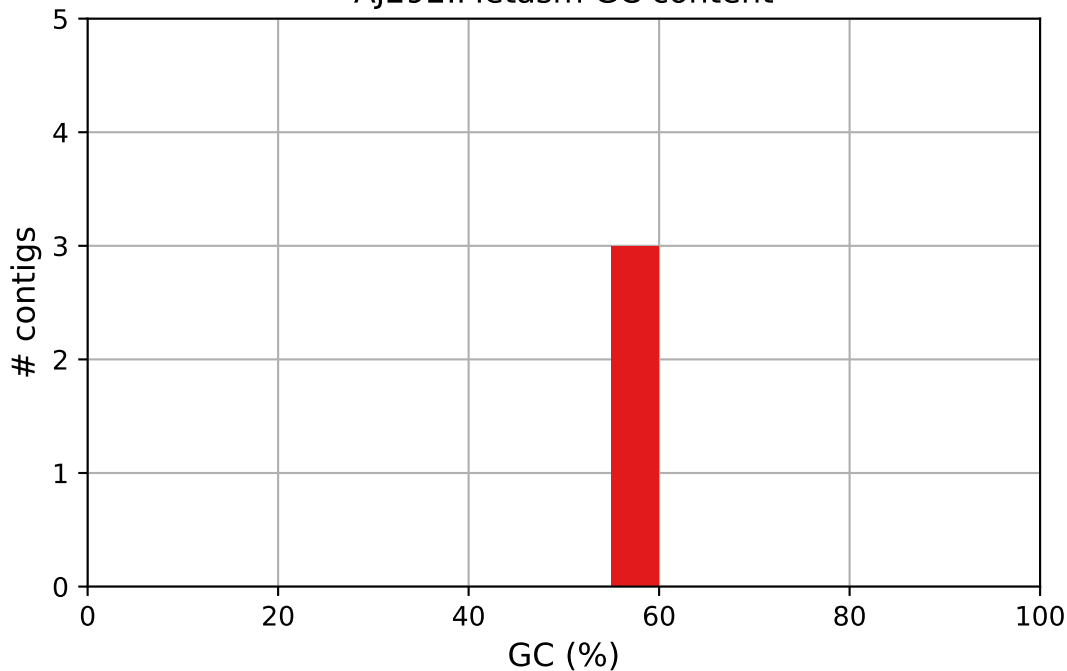
AJ292.Metasm




GC content

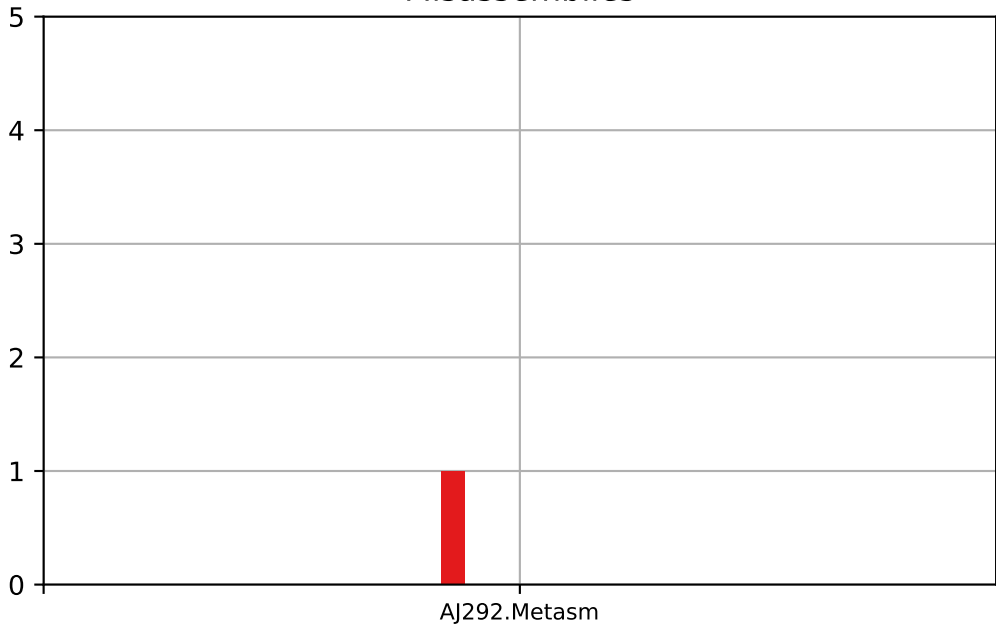


AJ292.Metasm GC content

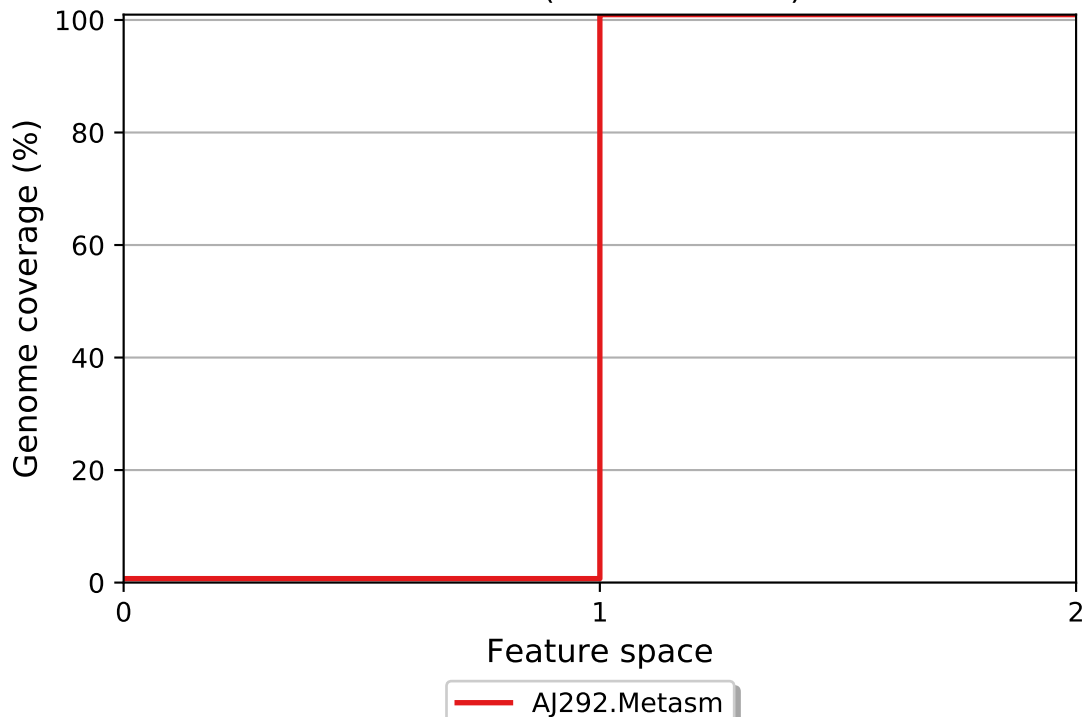


 AJ292.Metasm

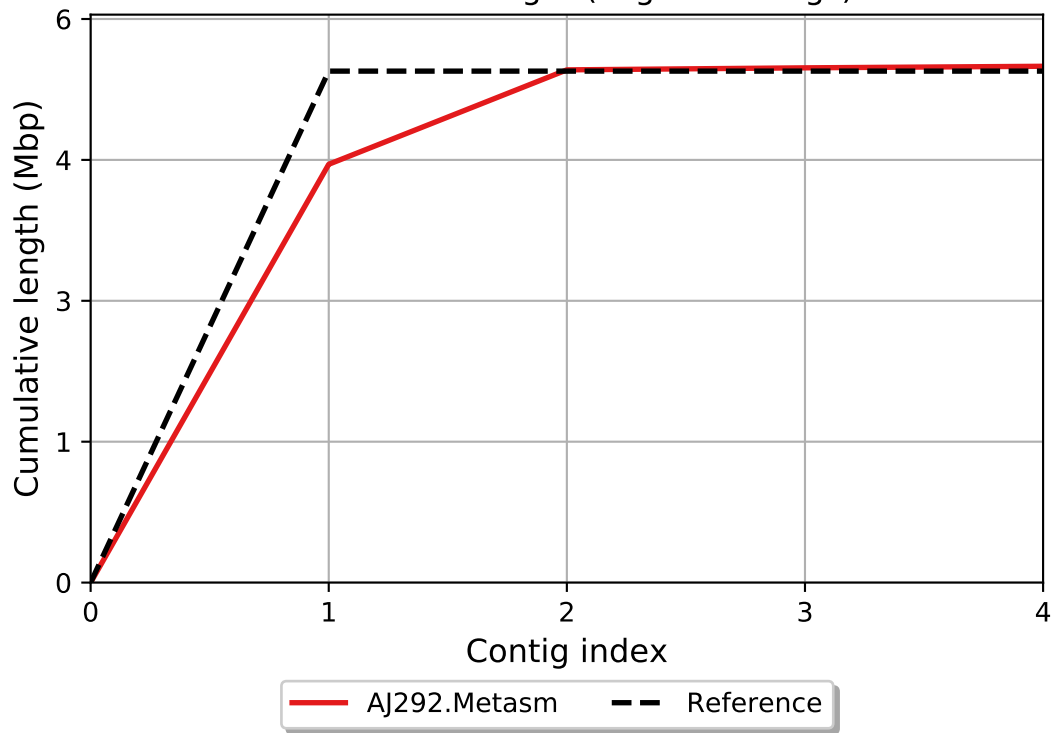
Misassemblies



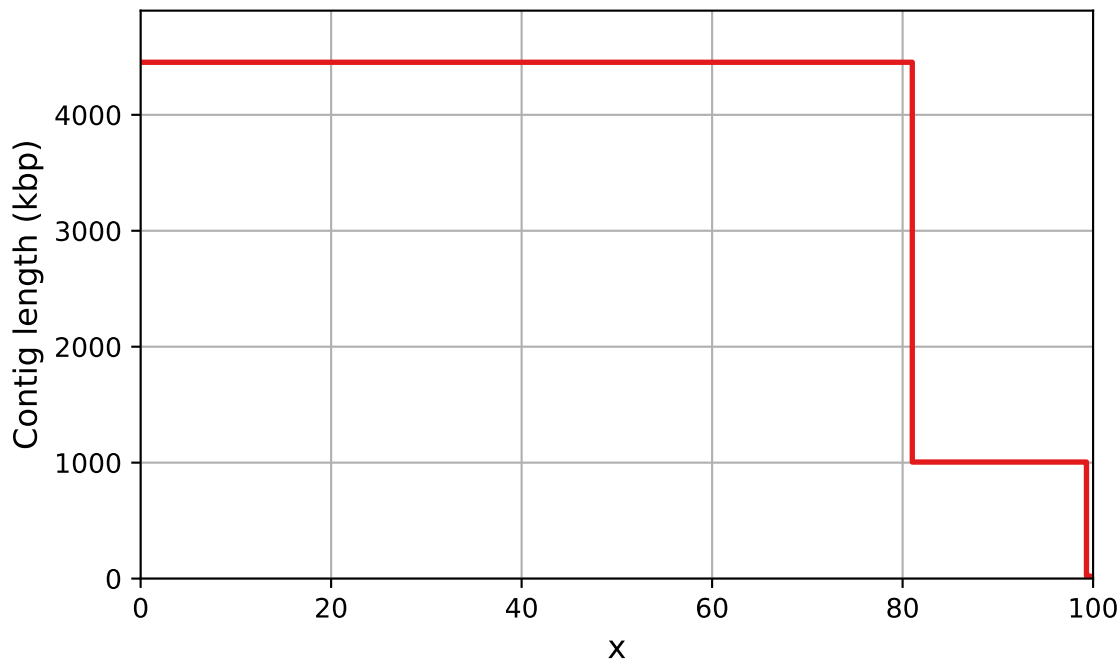
FRCurve (misassemblies)



Cumulative length (aligned contigs)

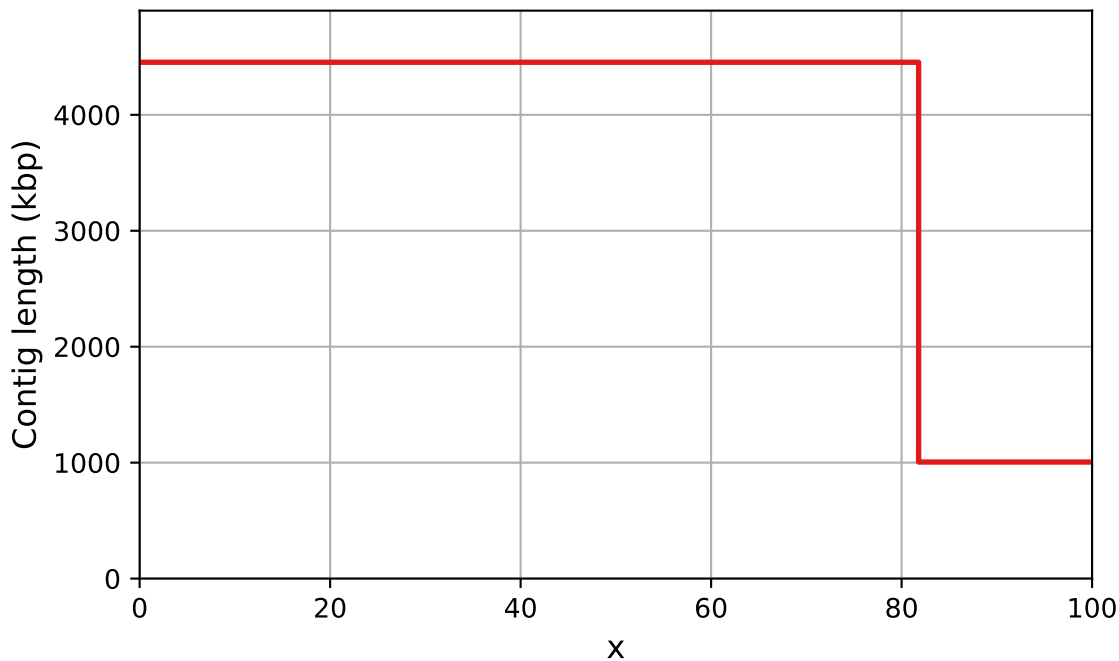


NAx



AJ292.Metasm

NGAx



AJ292.Metasm