

Report

	AJ055.MiniL
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	18
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	5602098
Total length (>= 1000 bp)	5602098
Total length (>= 5000 bp)	5602098
Total length (>= 10000 bp)	5602098
Total length (>= 25000 bp)	5602098
Total length (>= 50000 bp)	5553050
# contigs	18
Largest contig	833810
Total length	5602098
Reference length	5504133
GC (%)	57.17
Reference GC (%)	57.38
N50	455694
NG50	455694
N75	243471
NG75	353027
L50	5
LG50	5
L75	9
LG75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	163066
Genome fraction (%)	97.962
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	49.96
# indels per 100 kbp	726.07
Largest alignment	833675
Total aligned length	5435975
NA50	455694
NGA50	455694
NA75	243400
NGA75	351127
LA50	5
LGA50	5
LA75	9
LGA75	8

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

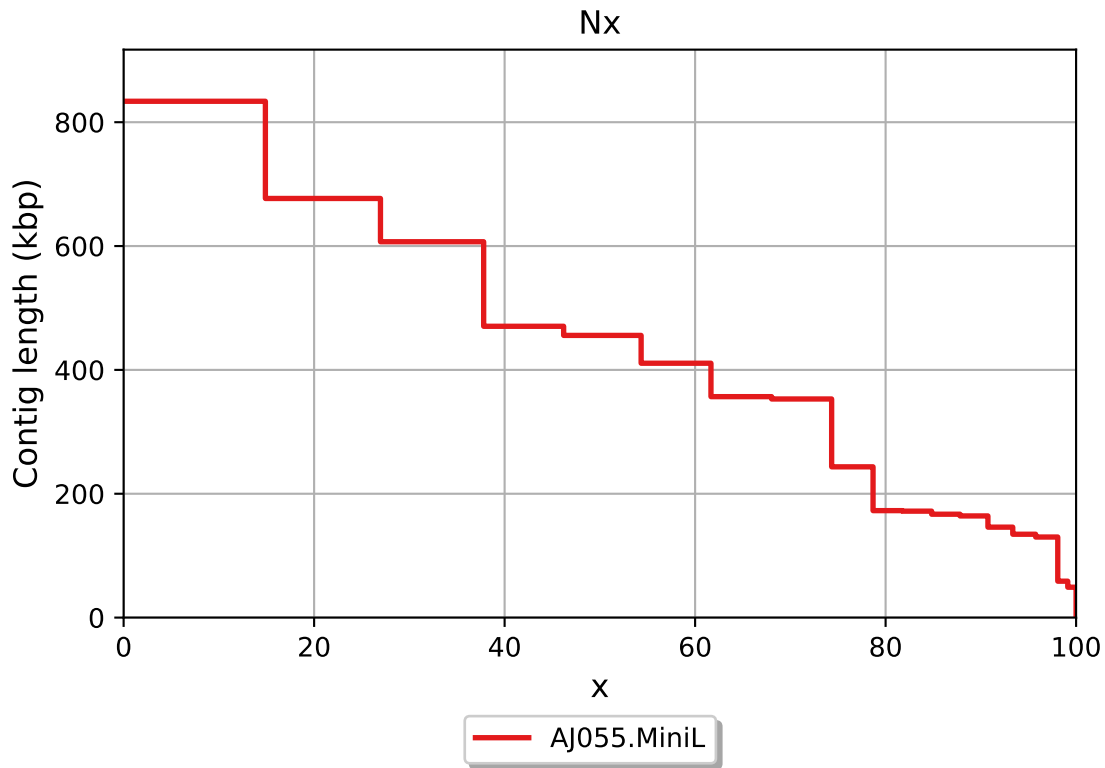
	AJ055.MinilL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# unaligned mis. contigs	0
# mismatches	2694
# indels	39149
# indels (≤ 5 bp)	38951
# indels (> 5 bp)	198
Indels length	51414

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).

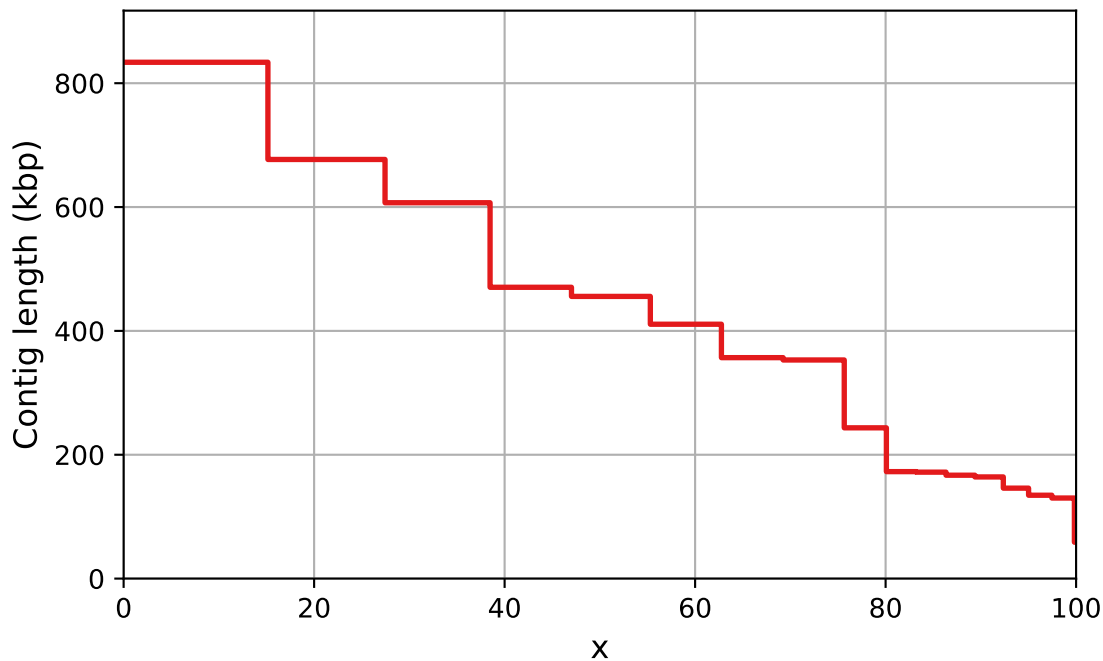
Unaligned report

	AJ055.MiniL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	163066
# 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).

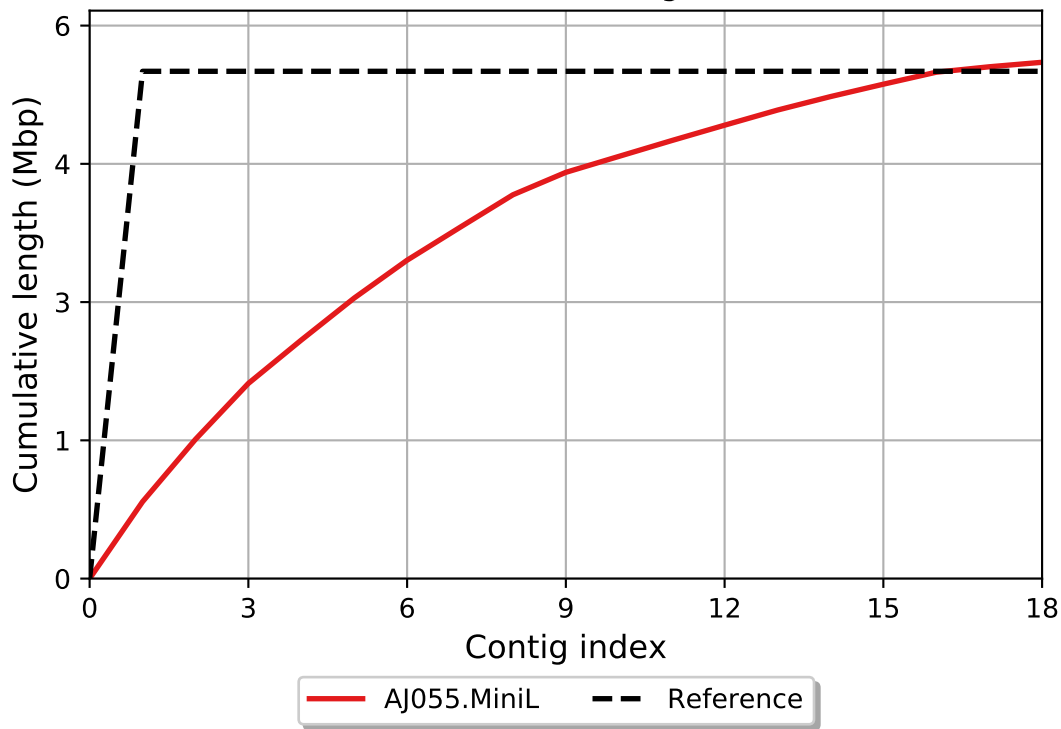


NGx

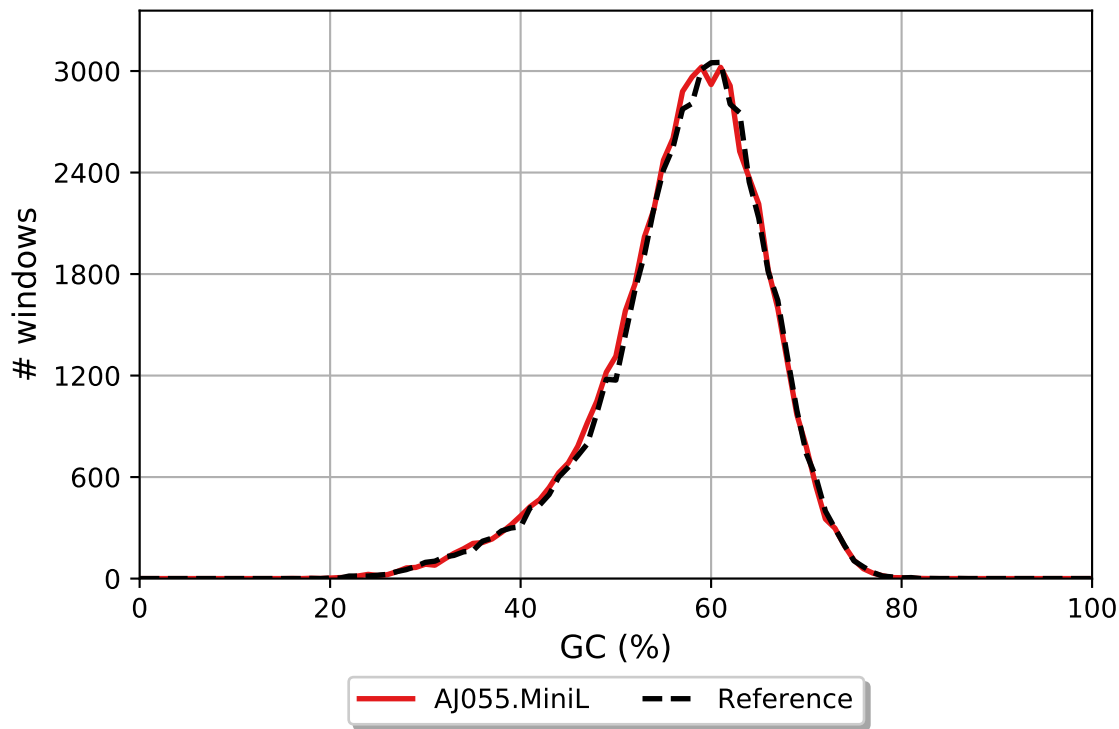


AJ055.MiniL

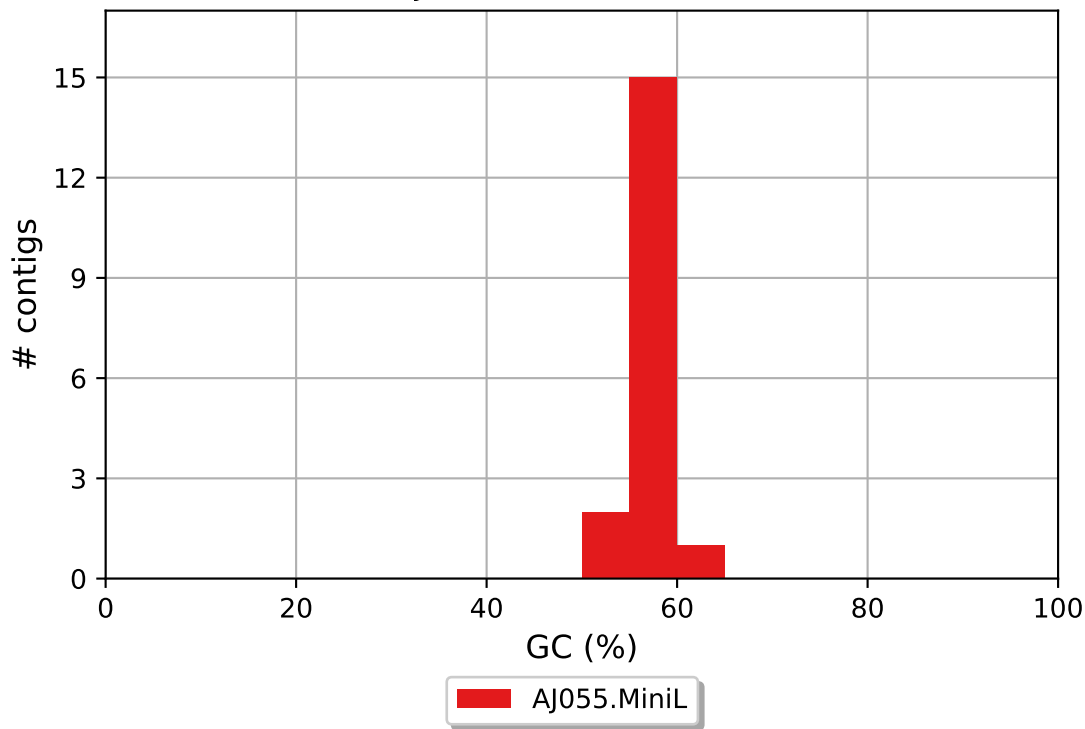
Cumulative length



GC content



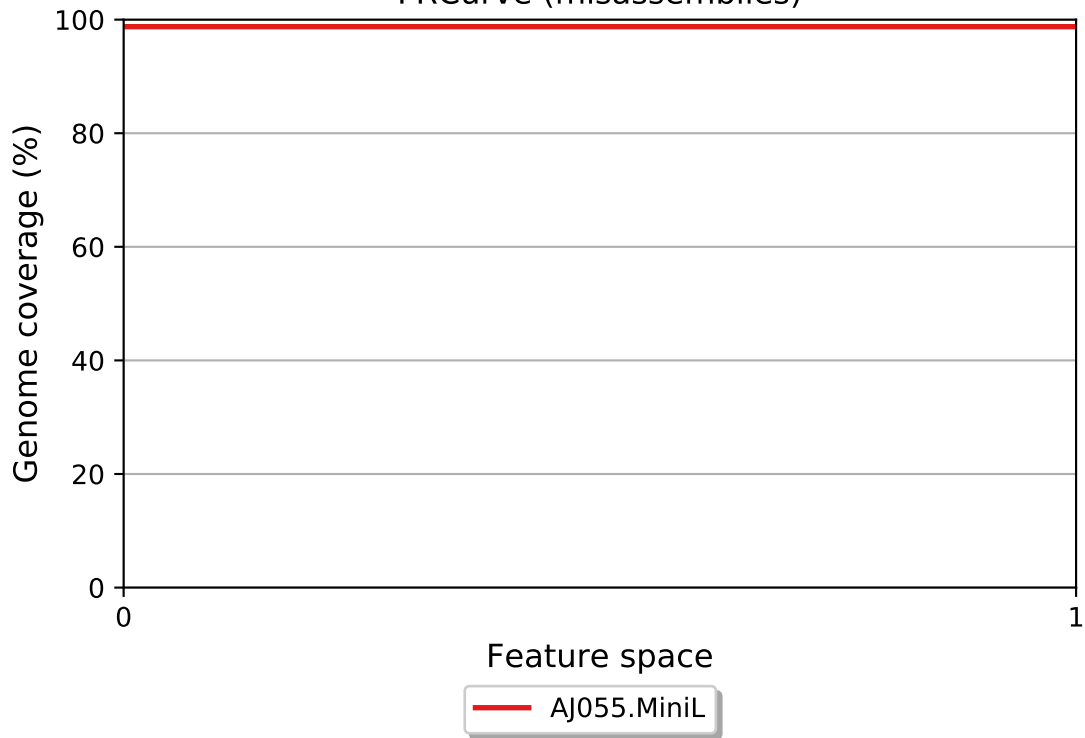
AJ055.MiniL GC content



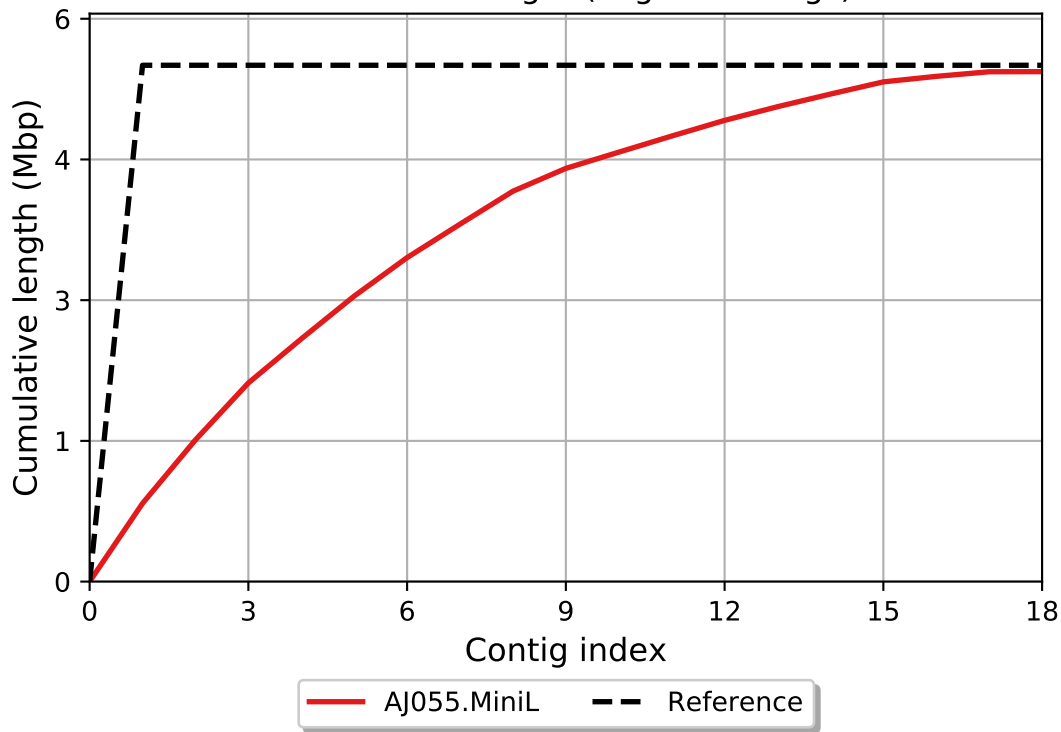
Misassemblies



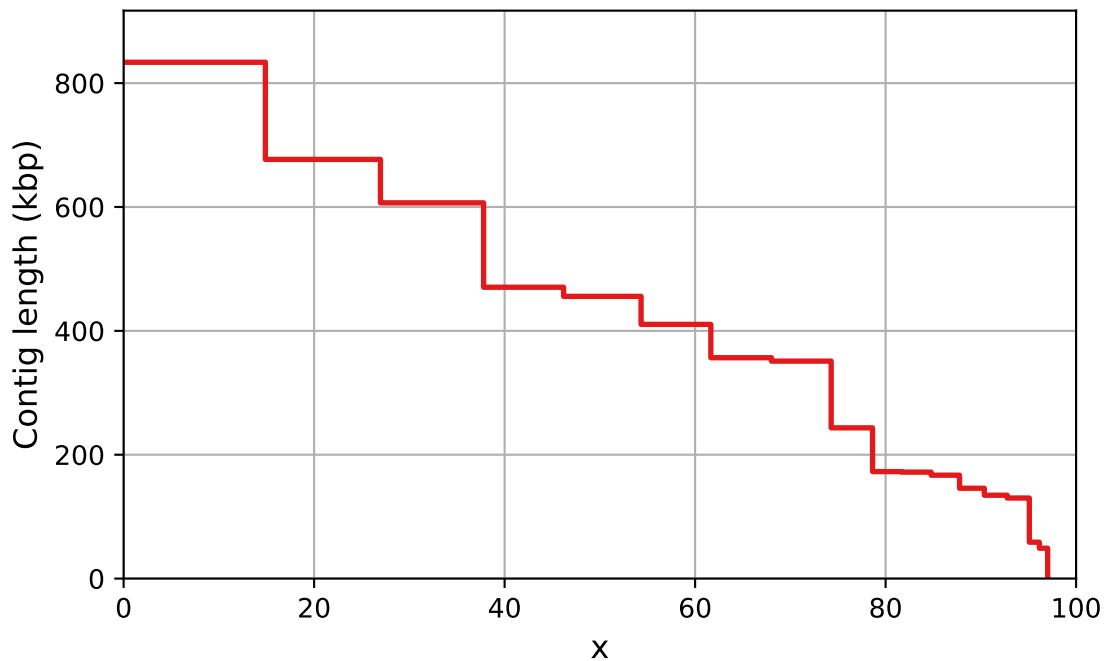
FRCurve (misassemblies)



Cumulative length (aligned contigs)

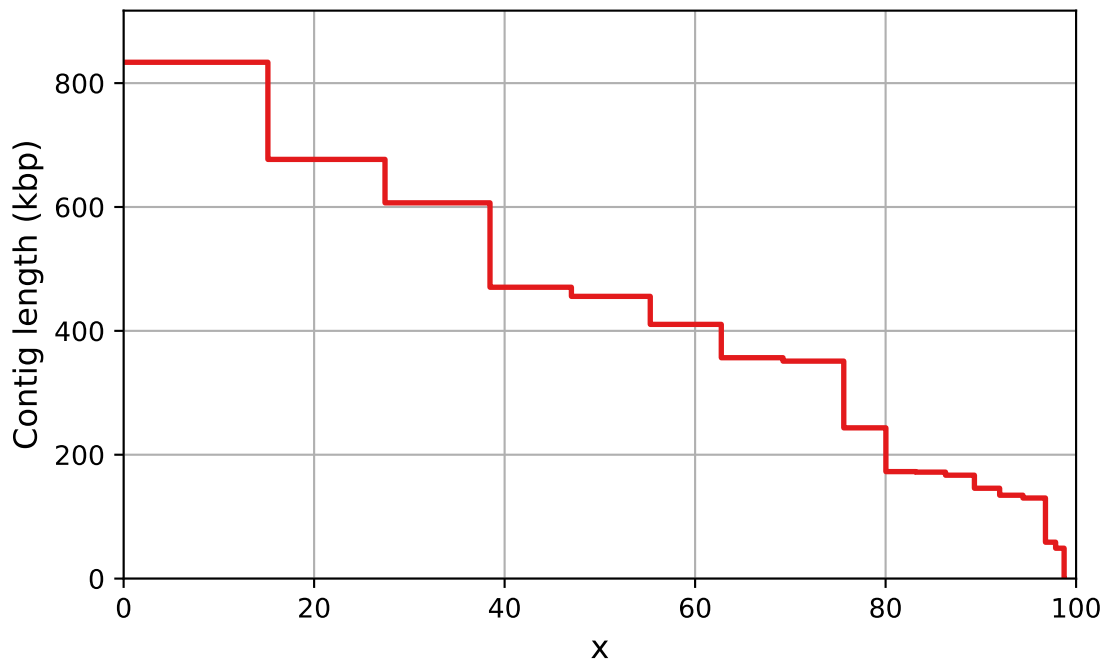


NAx



AJ055.MiniL

NGAx



AJ055.MiniL