

Report

	AJ055.MiniCL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1927
# contigs (>= 5000 bp)	1288
# contigs (>= 10000 bp)	807
# contigs (>= 25000 bp)	57
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	18799352
Total length (>= 1000 bp)	18753244
Total length (>= 5000 bp)	16985763
Total length (>= 10000 bp)	13464054
Total length (>= 25000 bp)	1645942
Total length (>= 50000 bp)	0
# contigs	1978
Largest contig	41426
Total length	18791114
Reference length	5504133
GC (%)	56.91
Reference GC (%)	57.38
N50	14601
NG50	22655
N75	9274
NG75	20585
L50	470
LG50	105
L75	873
LG75	168
# misassemblies	99
# misassembled contigs	89
Misassembled contigs length	1352097
# local misassemblies	47
# unaligned mis. contigs	6
# unaligned contigs	478 + 174 part
Unaligned length	4186004
Genome fraction (%)	90.562
Duplication ratio	2.930
# N's per 100 kbp	0.00
# mismatches per 100 kbp	134.01
# indels per 100 kbp	1254.47
Largest alignment	35671
Total aligned length	14579694
NA50	10889
NGA50	20417
NA75	2744
NGA75	18393
LA50	553
LGA50	116
LA75	1309
LGA75	188

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.MiniCL.cr
# misassemblies	99
# relocations	92
# translocations	0
# inversions	7
# misassembled contigs	89
Misassembled contigs length	1352097
# local misassemblies	47
# unaligned mis. contigs	6
# mismatches	6680
# indels	62531
# indels (≤ 5 bp)	62286
# indels (> 5 bp)	245
Indels length	77538

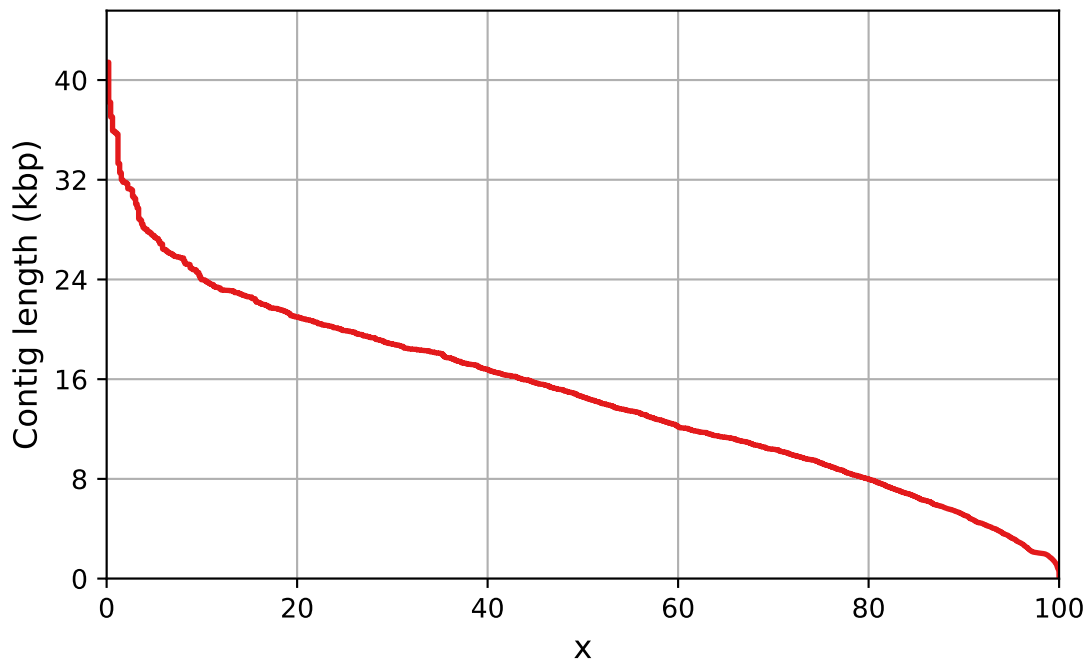
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ055.MinicL.cr
# fully unaligned contigs	478
Fully unaligned length	3552594
# partially unaligned contigs	174
Partially unaligned length	633410
# N's	0

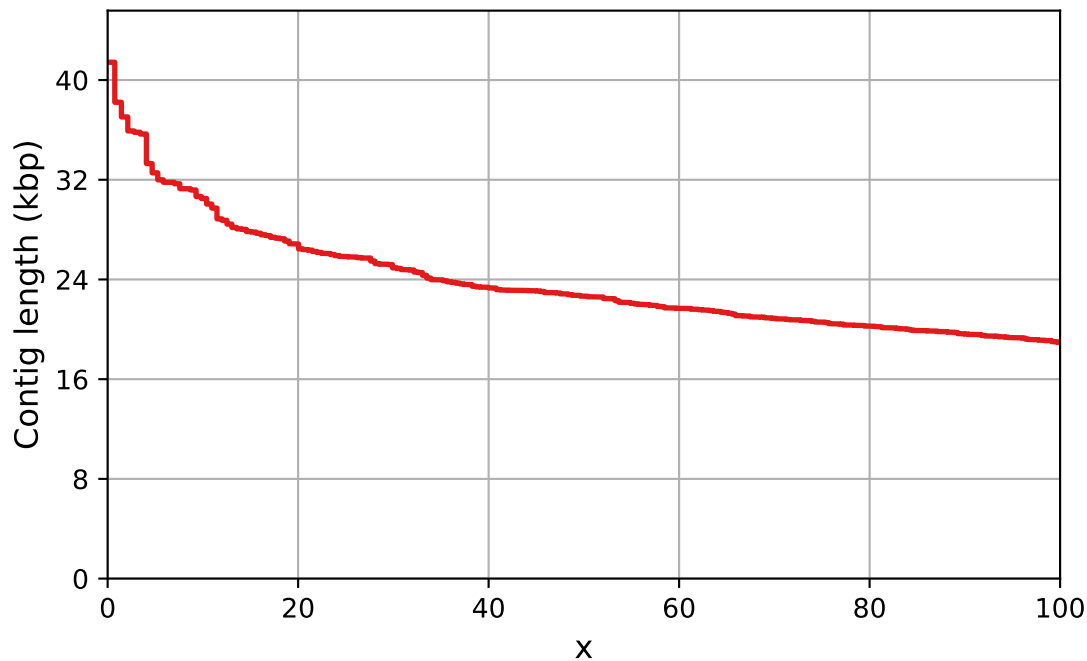
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



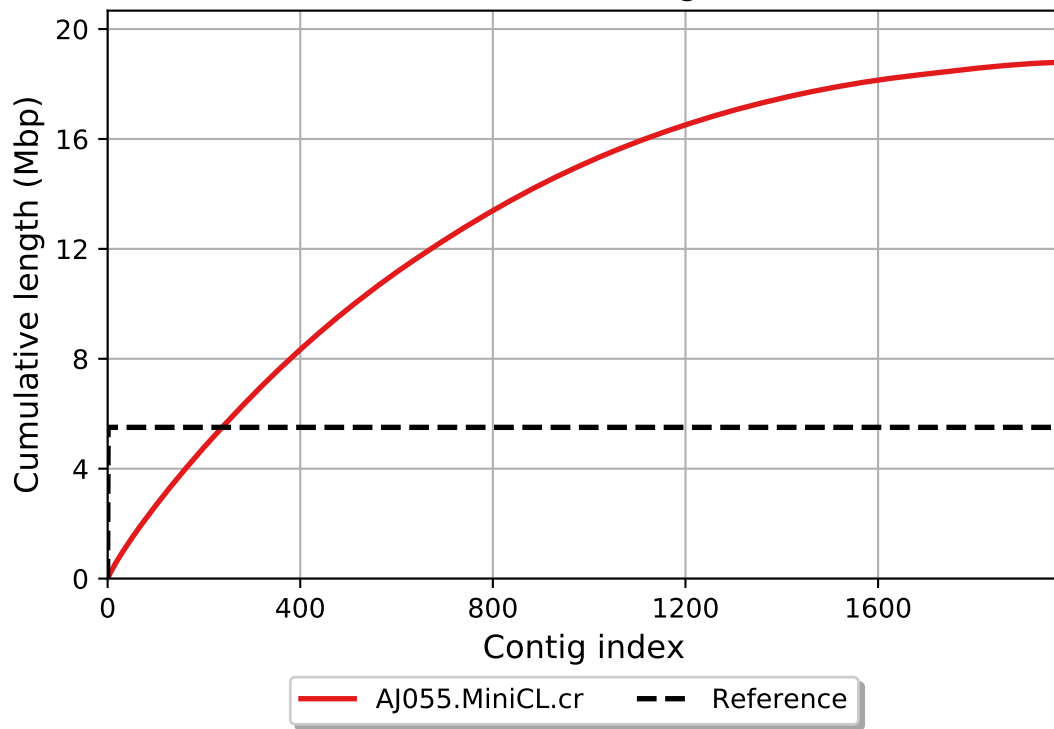
Aj055.MiniCL.cr

NGx

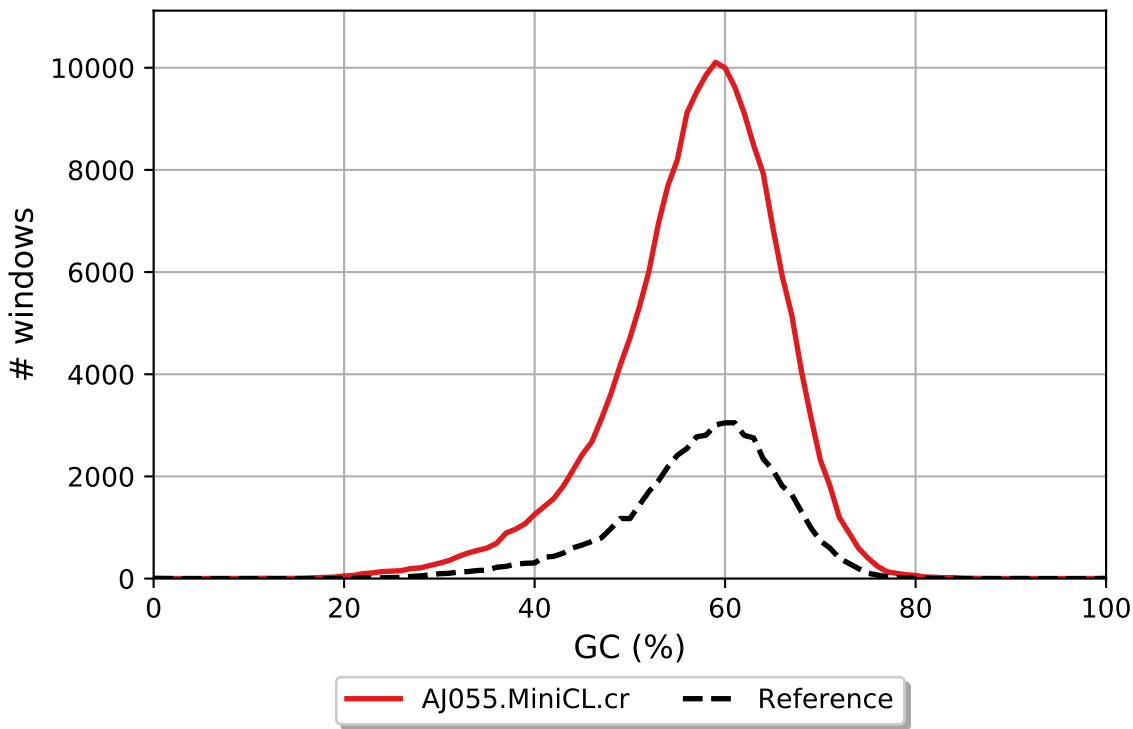


Aj055.MiniCL.cr

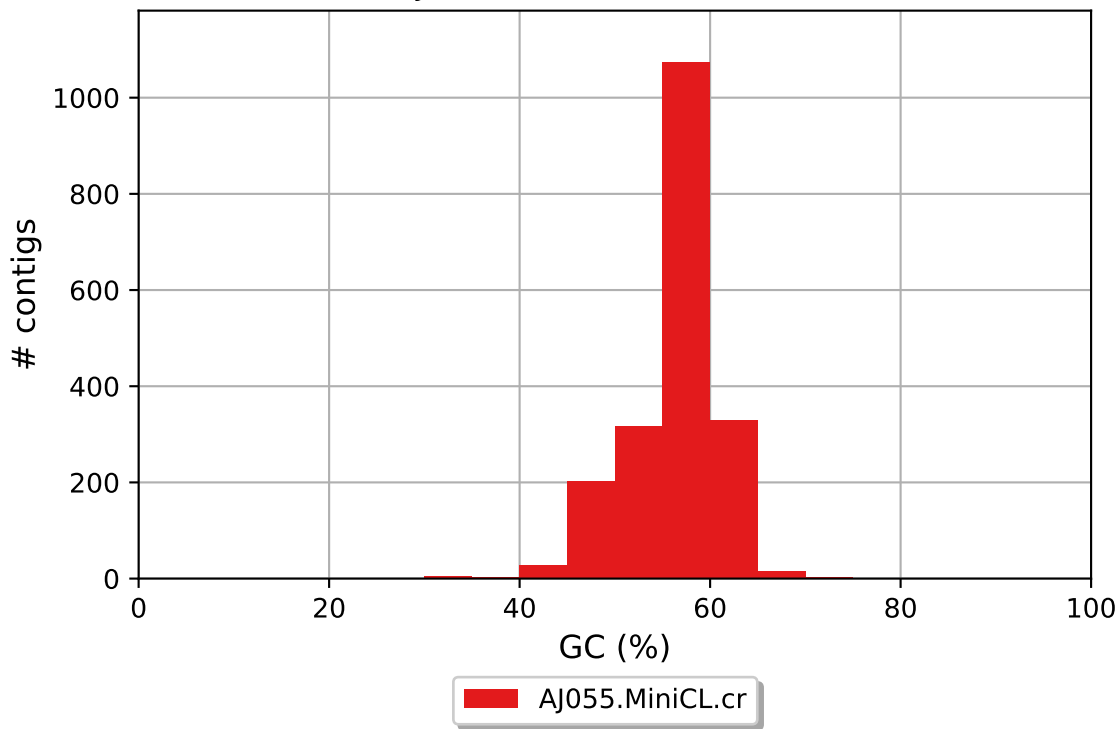
Cumulative length



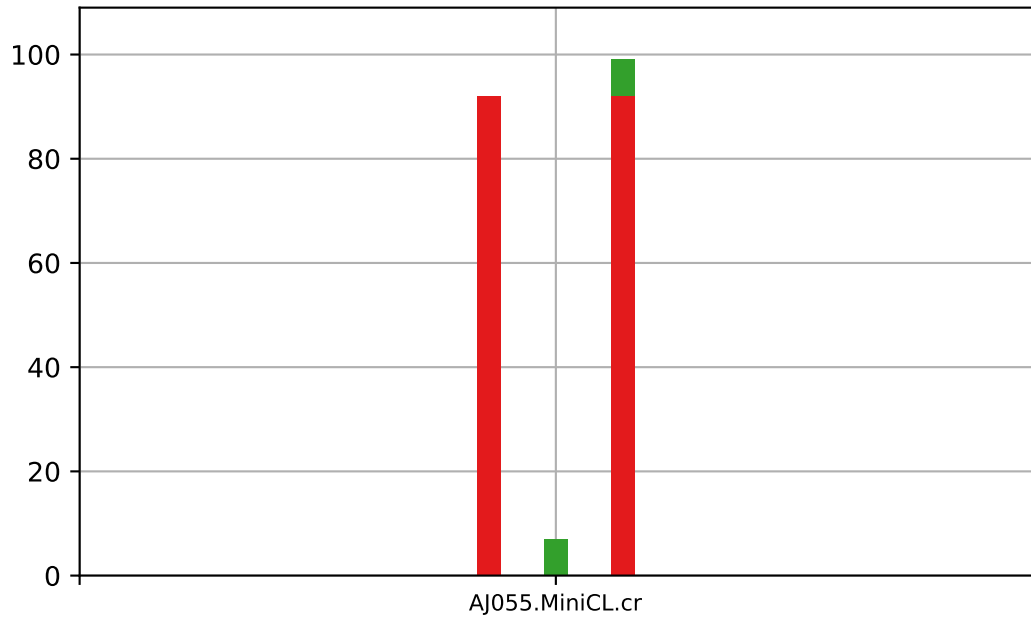
GC content



AJ055.MinicL.cr GC content



Misassemblies

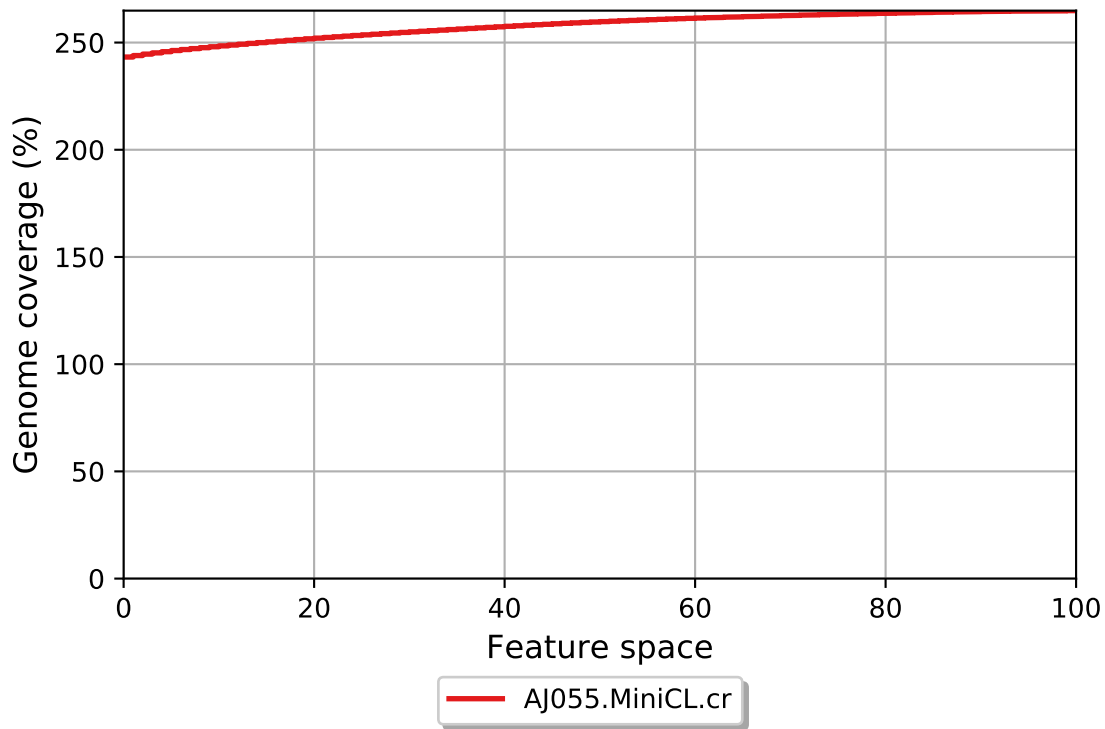


relocations

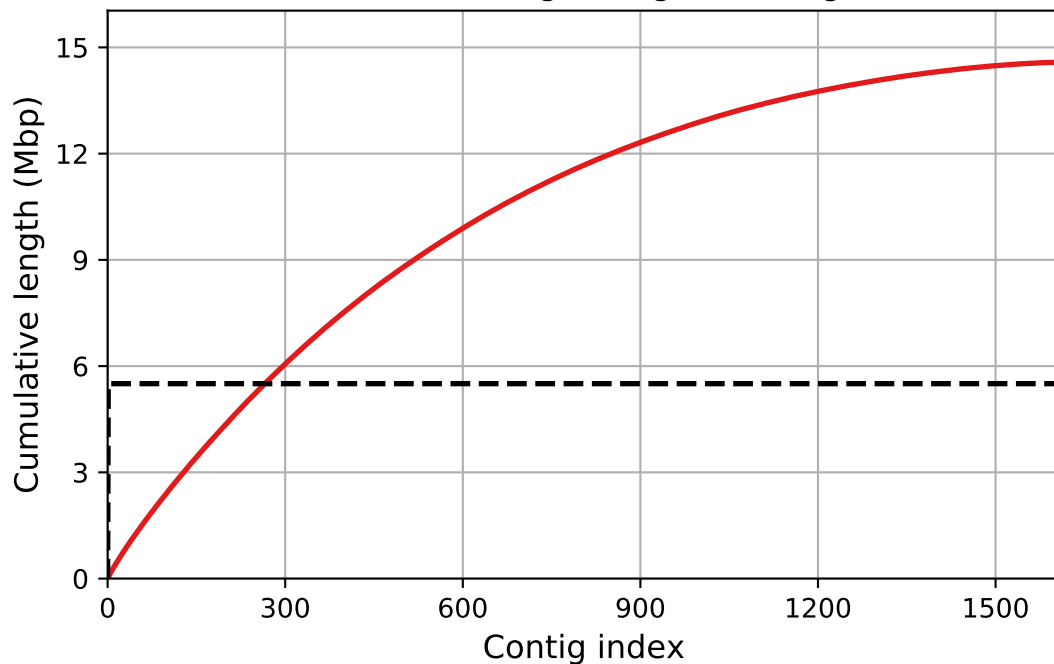


inversions

FRCurve (misassemblies)

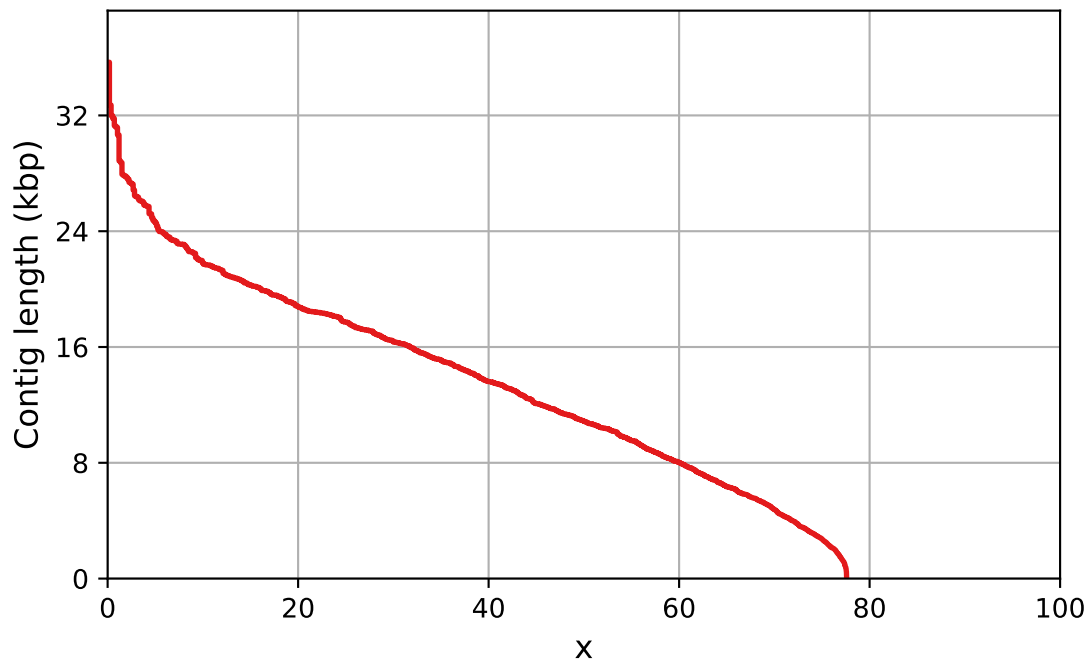


Cumulative length (aligned contigs)



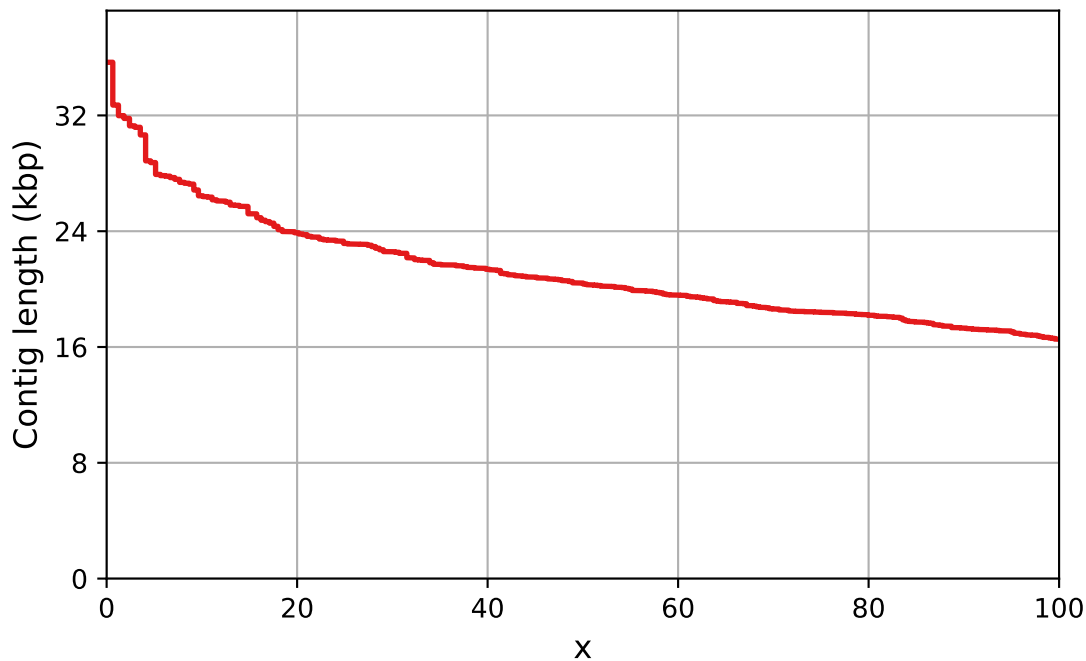
— AJ055.MiniCL.cr - - Reference

NAx



Aj055.MiniCL.cr

NGAx



— Aj055.MinicL.cr