

Report

	AJ055.MiniCH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1922
# contigs (>= 5000 bp)	1287
# contigs (>= 10000 bp)	809
# contigs (>= 25000 bp)	58
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	18799218
Total length (>= 1000 bp)	18750121
Total length (>= 5000 bp)	16989543
Total length (>= 10000 bp)	13493205
Total length (>= 25000 bp)	1677855
Total length (>= 50000 bp)	0
# contigs	1976
Largest contig	41426
Total length	18790377
Reference length	5504133
GC (%)	56.94
Reference GC (%)	57.38
N50	14600
NG50	22669
N75	9288
NG75	20603
L50	469
LG50	104
L75	872
LG75	168
# misassemblies	97
# misassembled contigs	88
Misassembled contigs length	1337216
# local misassemblies	48
# unaligned mis. contigs	4
# unaligned contigs	471 + 159 part
Unaligned length	4159777
Genome fraction (%)	90.965
Duplication ratio	2.922
# N's per 100 kbp	0.00
# mismatches per 100 kbp	109.27
# indels per 100 kbp	1032.45
Largest alignment	35673
Total aligned length	14606562
NA50	10899
NGA50	20524
NA75	2821
NGA75	18392
LA50	552
LGA50	116
LA75	1301
LGA75	187

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.MiniCH.cr
# misassemblies	97
# relocations	91
# translocations	0
# inversions	6
# misassembled contigs	88
Misassembled contigs length	1337216
# local misassemblies	48
# unaligned mis. contigs	4
# mismatches	5471
# indels	51693
# indels (≤ 5 bp)	51440
# indels (> 5 bp)	253
Indels length	65985

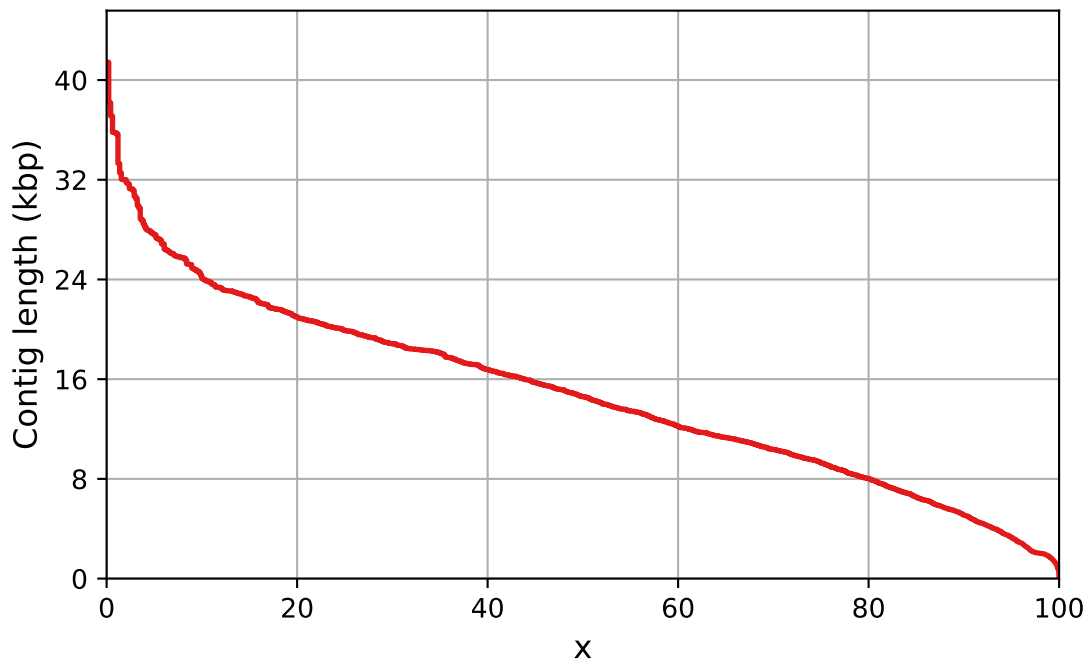
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ055.Minichr
# fully unaligned contigs	471
Fully unaligned length	3565851
# partially unaligned contigs	159
Partially unaligned length	593926
# N's	0

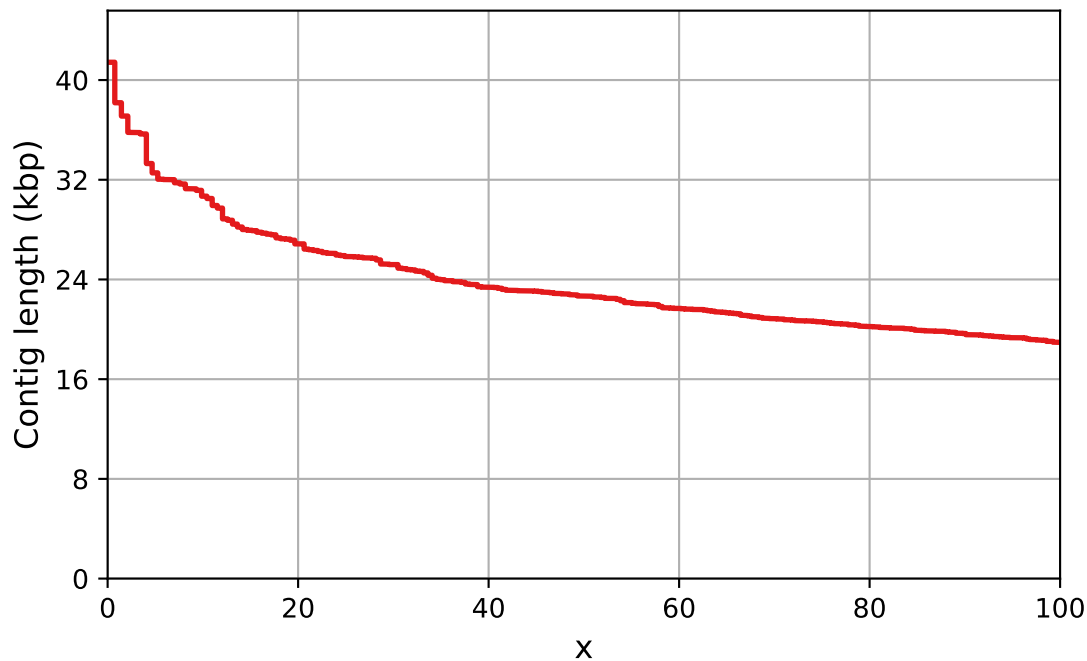
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



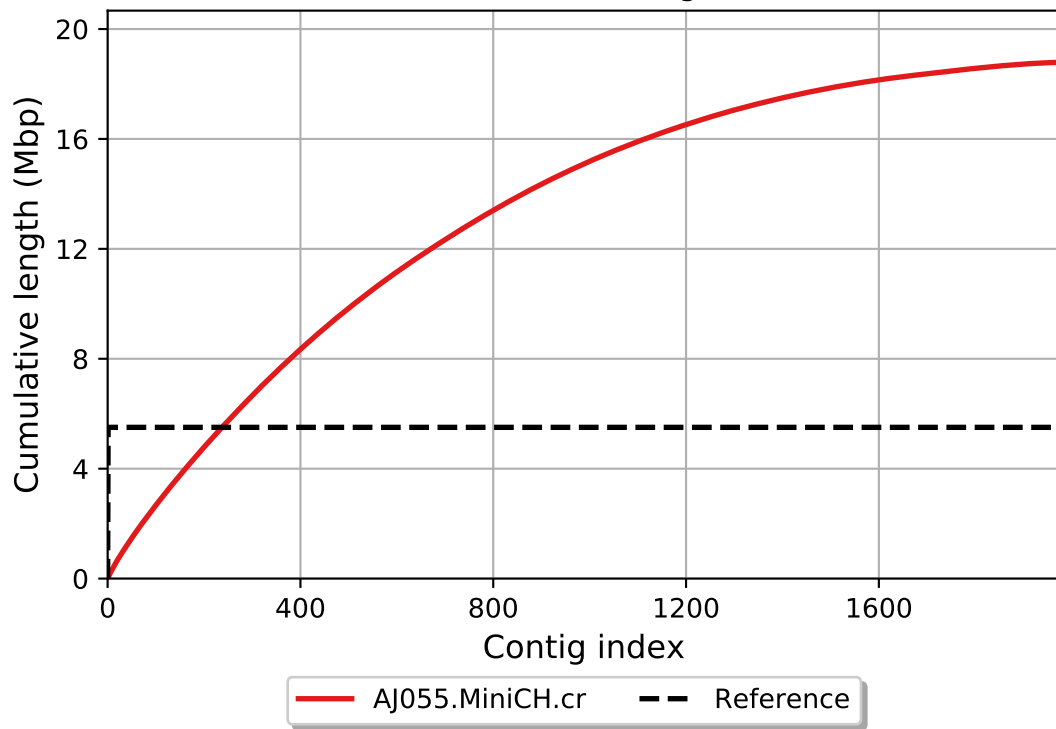
AJ055.MiniCH.cr

NGx

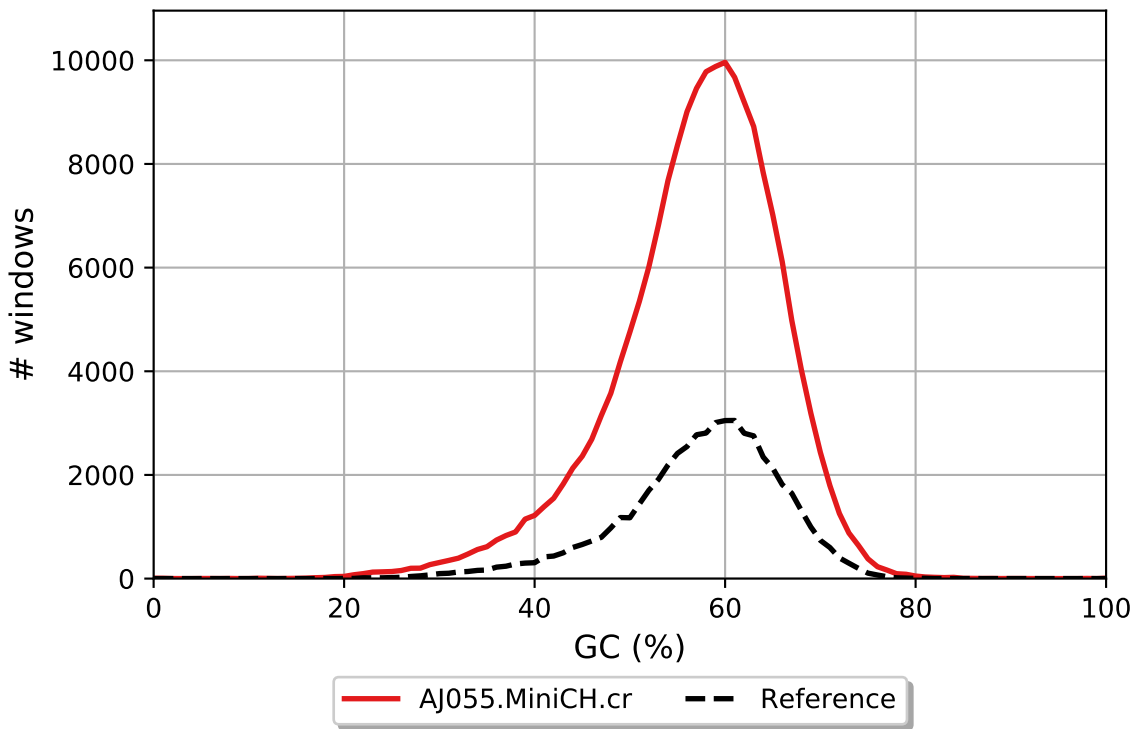


AJ055.MiniCH.cr

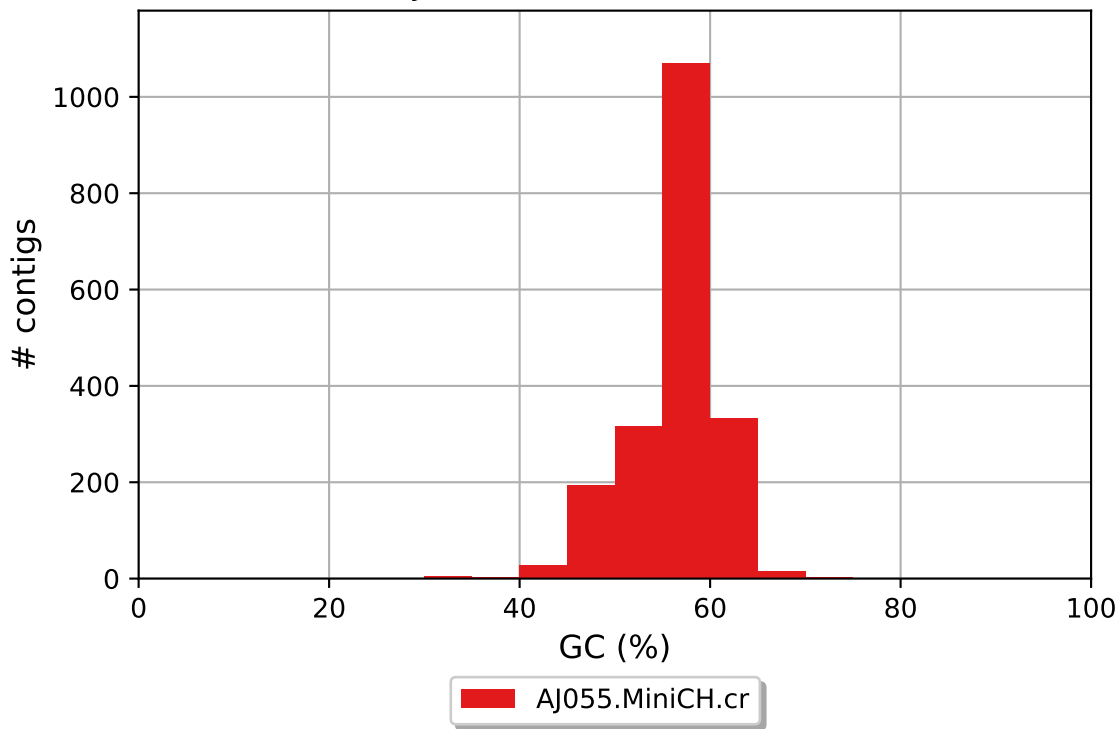
Cumulative length



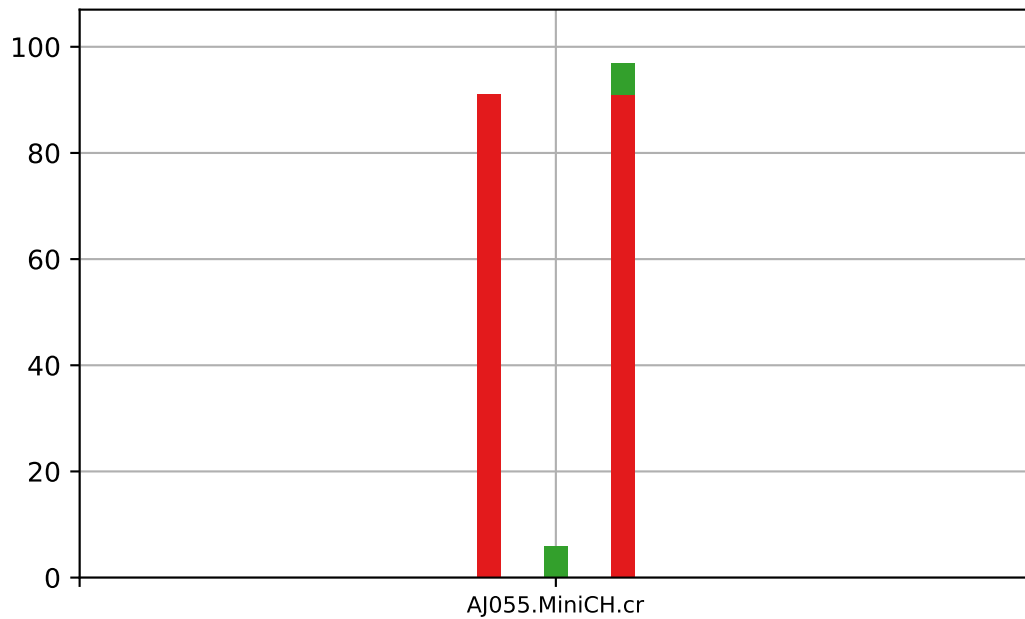
GC content



AJ055.MiniCH.cr GC content



Misassemblies

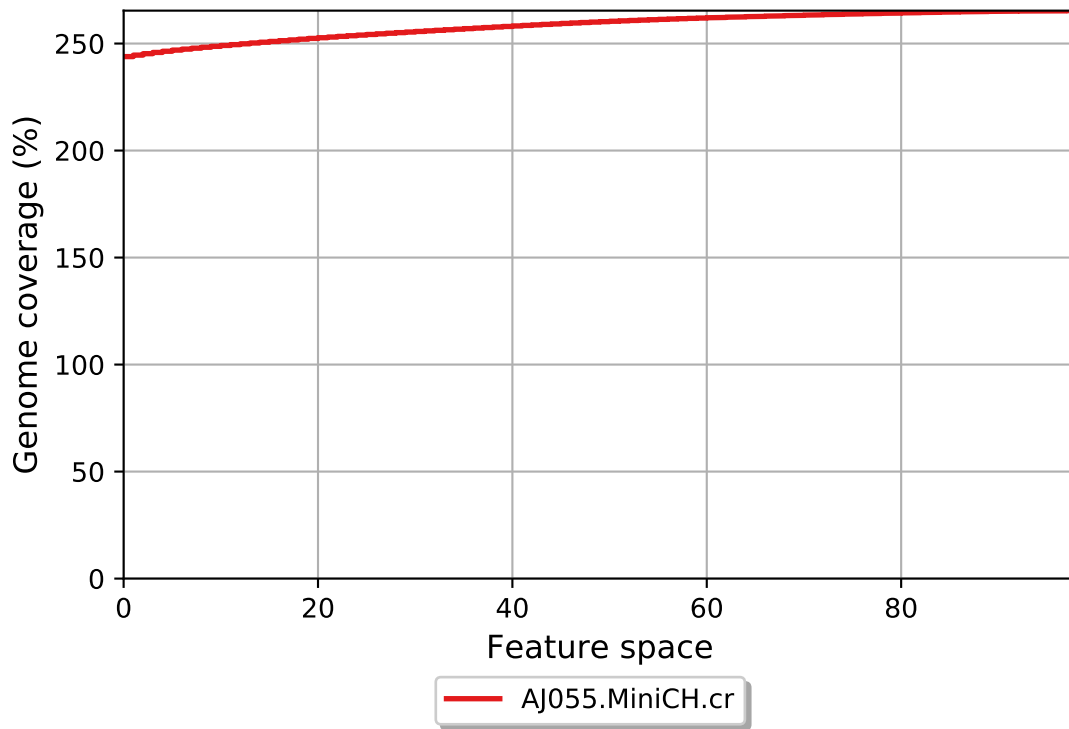


relocations

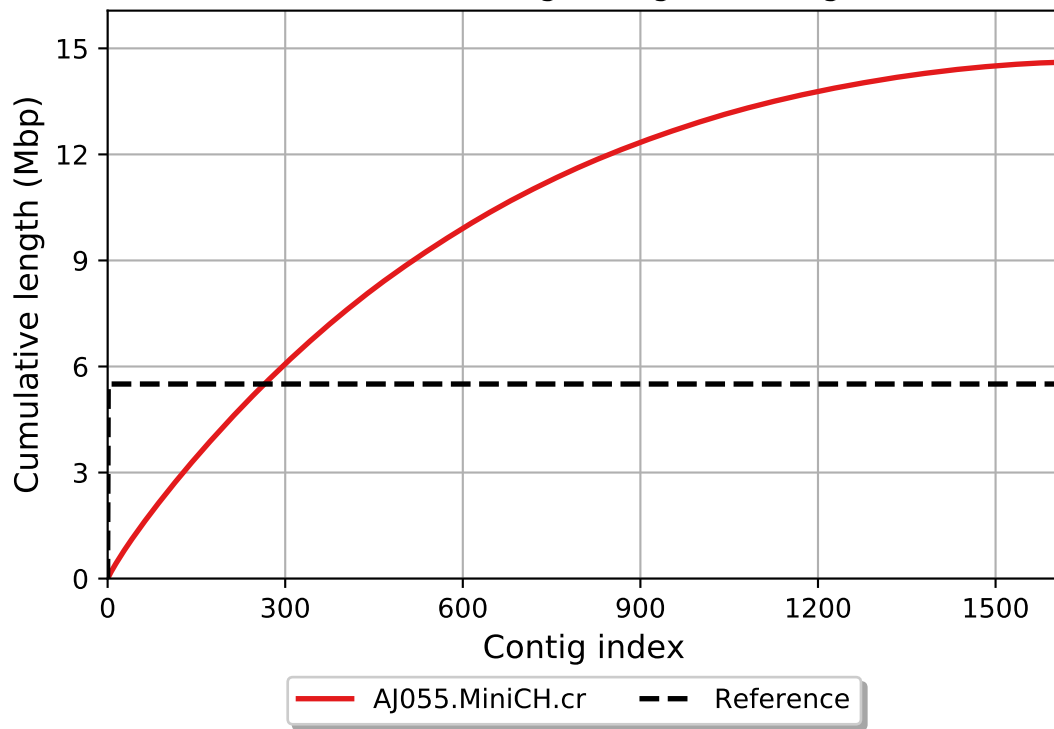


inversions

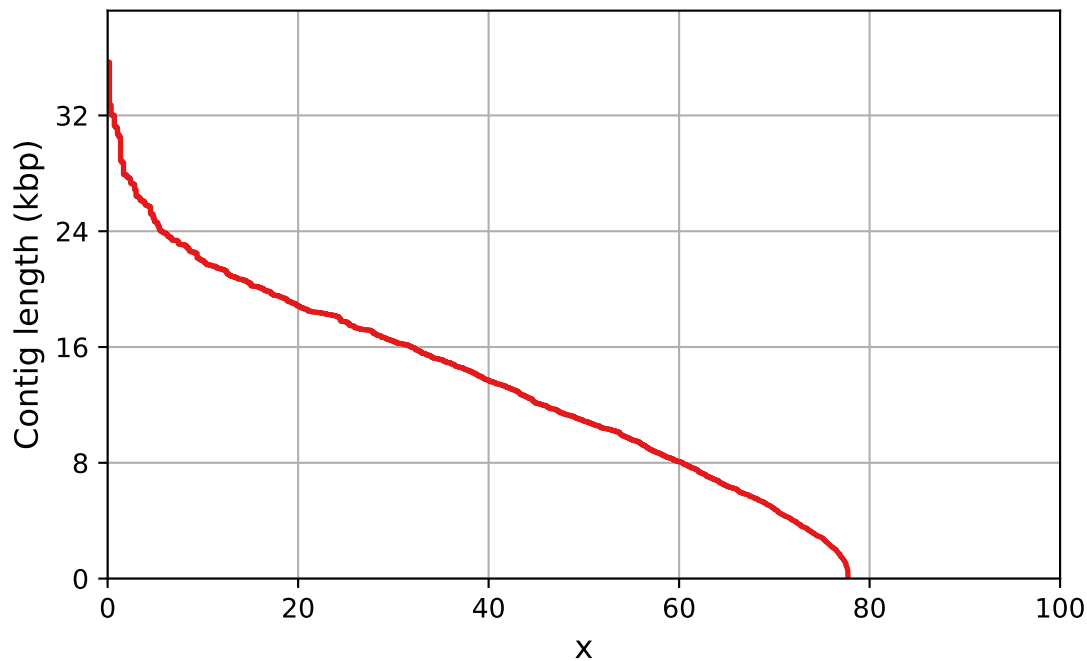
FRCurve (misassemblies)



Cumulative length (aligned contigs)

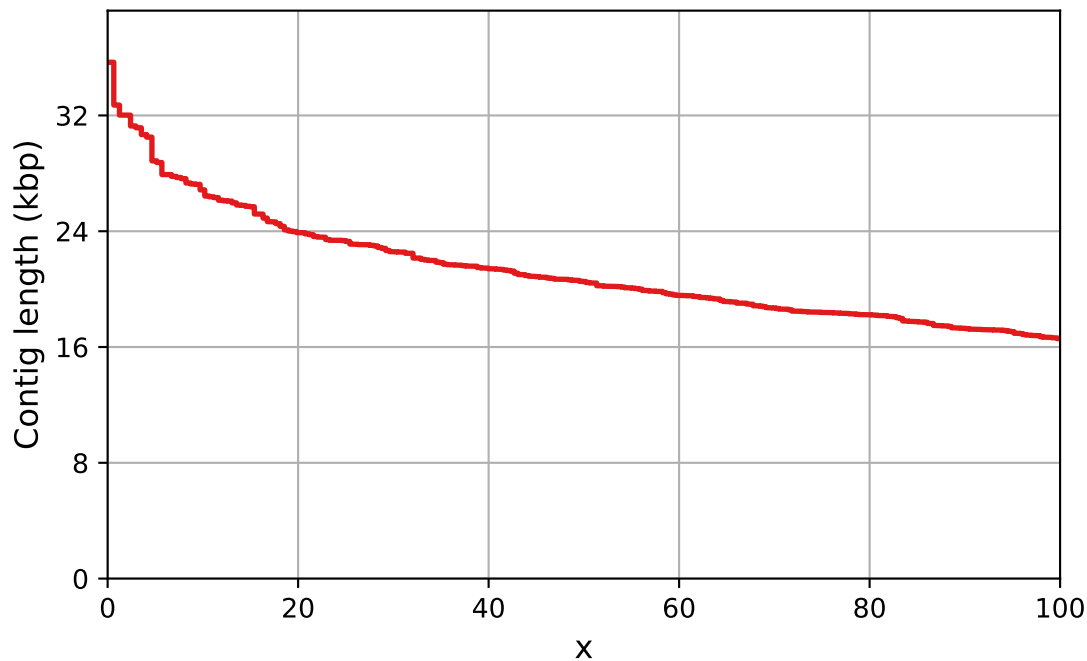


NAx



AJ055.MiniCH.cr

NGAx



AJ055.MiniCH.cr