

Report

	AJ218.MiniCH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1933
# contigs (>= 5000 bp)	1367
# contigs (>= 10000 bp)	879
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	19466070
Total length (>= 1000 bp)	19424095
Total length (>= 5000 bp)	17910869
Total length (>= 10000 bp)	14278715
Total length (>= 25000 bp)	1392658
Total length (>= 50000 bp)	0
# contigs	1980
Largest contig	34452
Total length	19458977
Reference length	5465981
GC (%)	56.86
Reference GC (%)	57.29
N50	14741
NG50	21691
N75	9452
NG75	19625
L50	504
LG50	108
L75	912
LG75	174
# misassemblies	50
# misassembled contigs	48
Misassembled contigs length	558811
# local misassemblies	56
# unaligned mis. contigs	11
# unaligned contigs	393 + 214 part
Unaligned length	4438800
Genome fraction (%)	90.292
Duplication ratio	3.043
# N's per 100 kbp	0.00
# mismatches per 100 kbp	108.22
# indels per 100 kbp	907.60
Largest alignment	34005
Total aligned length	14987375
NA50	10926
NGA50	19958
NA75	2297
NGA75	18084
LA50	580
LGA50	116
LA75	1363
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

	AJ218.MiniCH.cr
# misassemblies	50
# relocations	46
# translocations	0
# inversions	4
# misassembled contigs	48
Misassembled contigs length	558811
# local misassemblies	56
# unaligned mis. contigs	11
# mismatches	5341
# indels	44793
# indels (≤ 5 bp)	44622
# indels (> 5 bp)	171
Indels length	56184

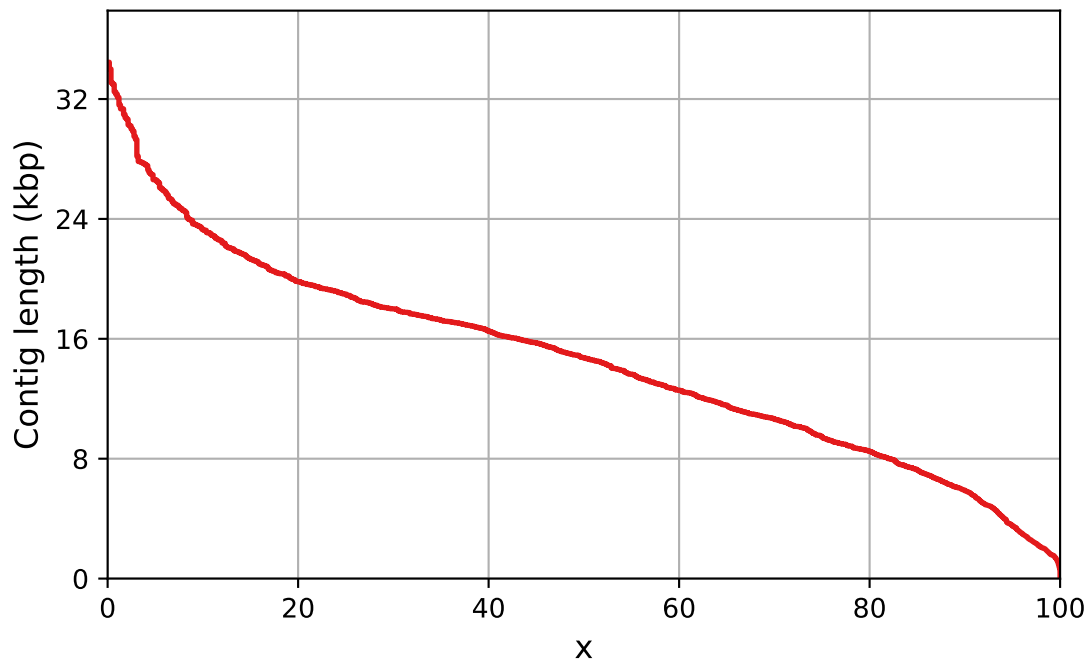
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ218.MiniCH.cr
# fully unaligned contigs	393
Fully unaligned length	3526449
# partially unaligned contigs	214
Partially unaligned length	912351
# N's	0

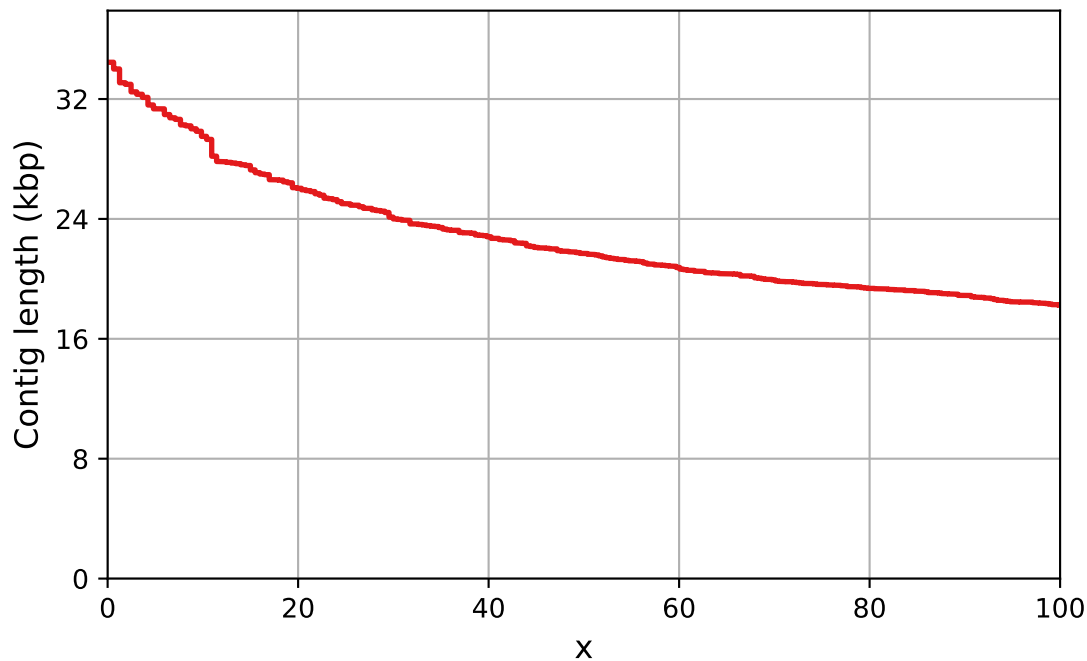
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



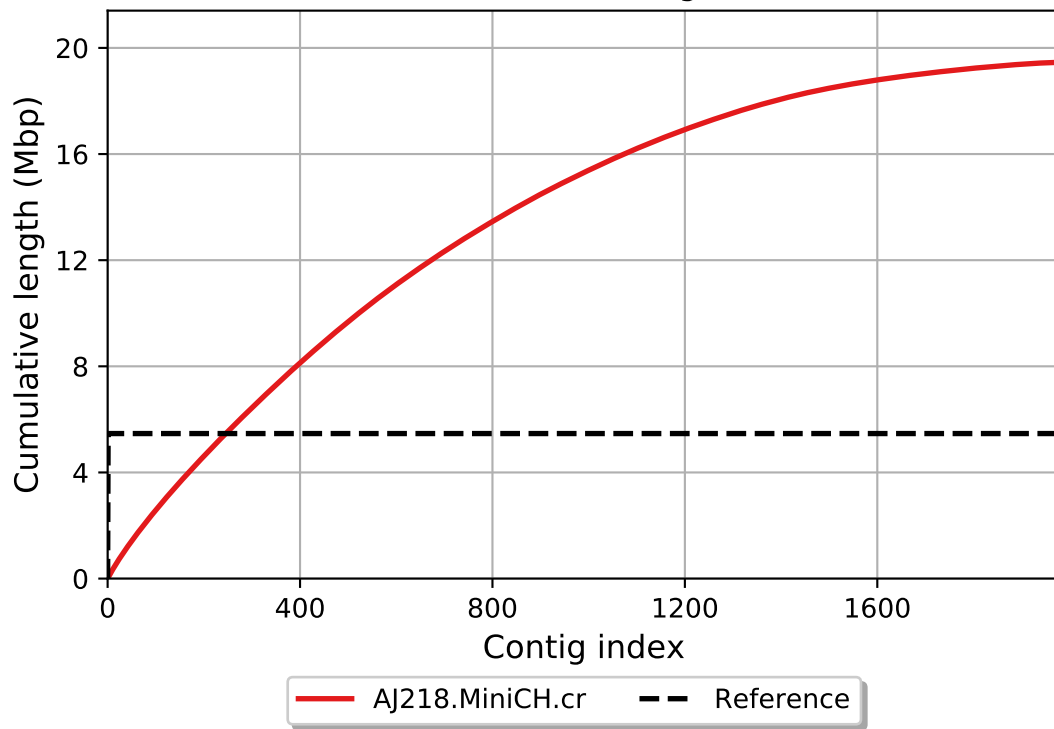
Aj218.MiniCH.cr

NGx

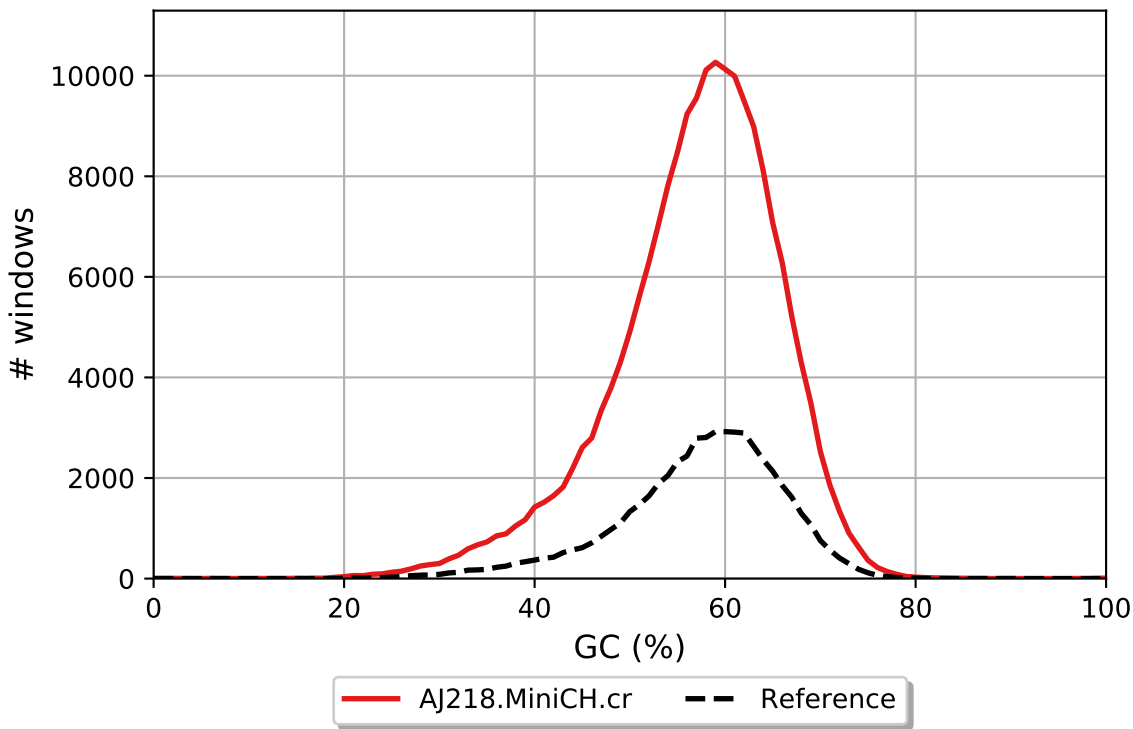


AJ218.MiniCH.cr

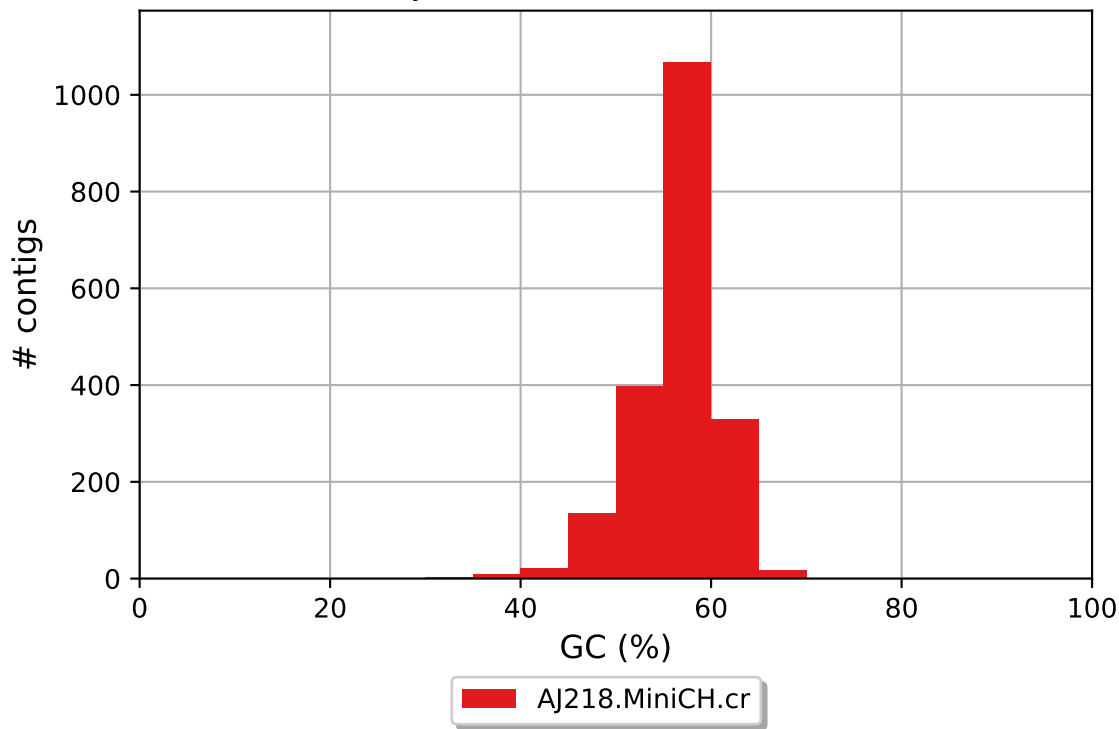
Cumulative length



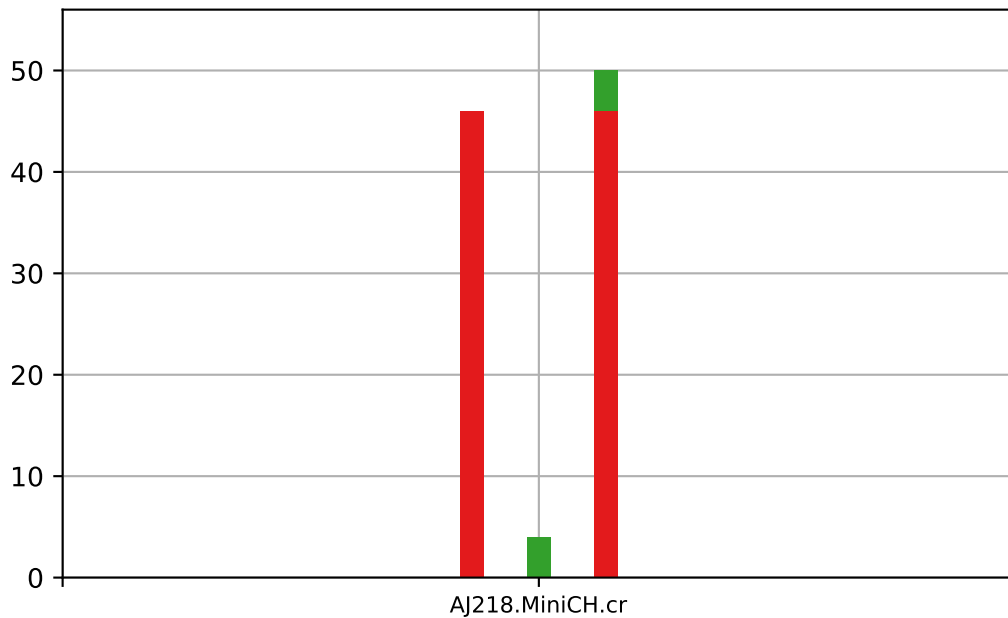
GC content



AJ218.MiniCH.cr GC content



Misassemblies

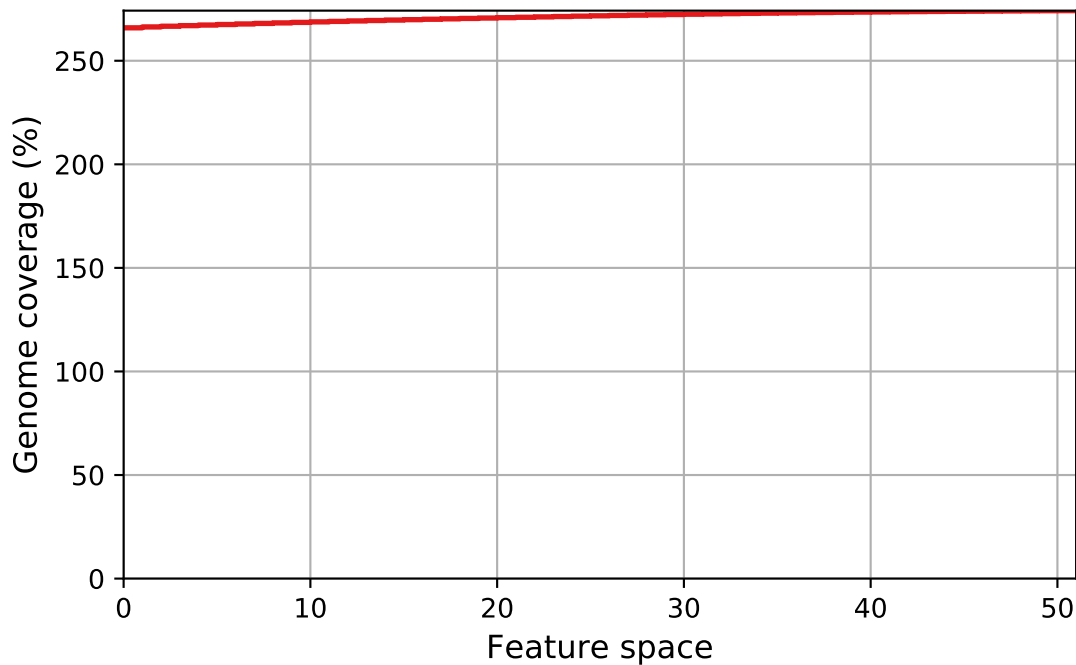


relocations



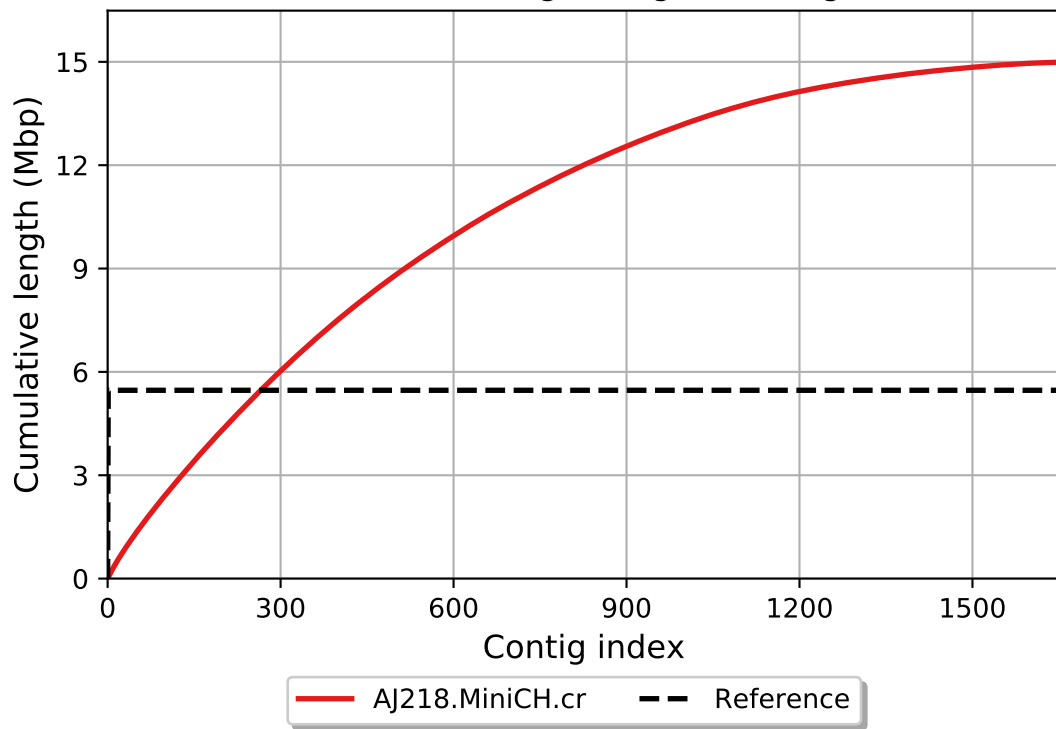
inversions

FRCurve (misassemblies)

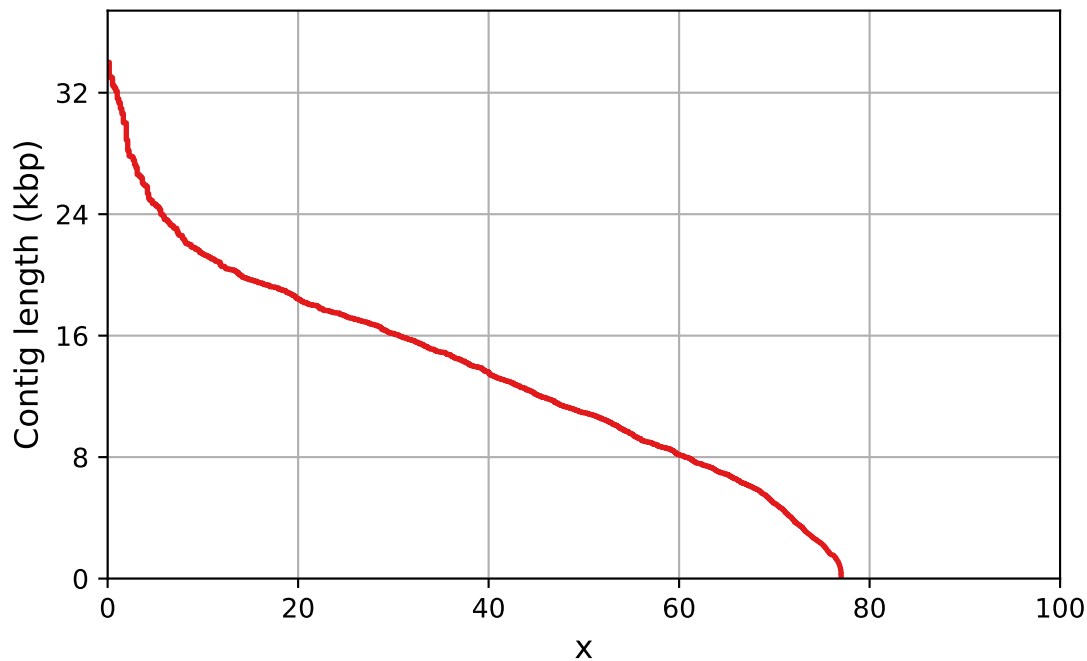


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Cumulative length (aligned contigs)

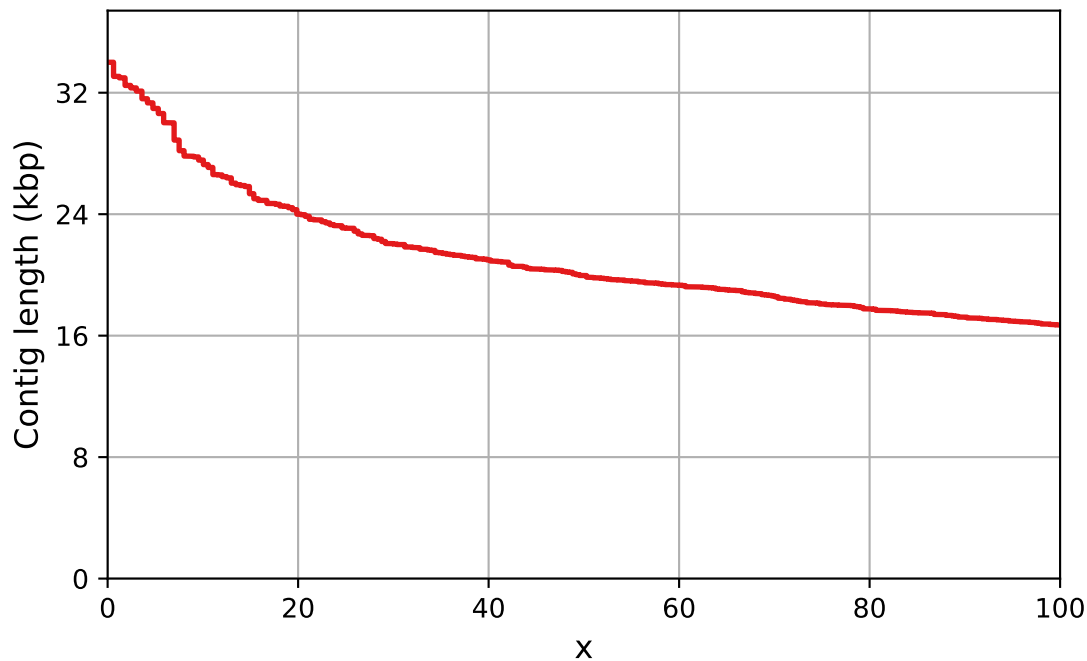


NAx



AJ218.MiniCH.cr

NGAx



AJ218.MiniCH.cr