

Report

	AJ292.MiniCH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1936
# contigs (>= 5000 bp)	1320
# contigs (>= 10000 bp)	898
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	20140023
Total length (>= 1000 bp)	20098202
Total length (>= 5000 bp)	18436195
Total length (>= 10000 bp)	15238101
Total length (>= 25000 bp)	1499796
Total length (>= 50000 bp)	0
# contigs	1983
Largest contig	35540
Total length	20134498
Reference length	5445112
GC (%)	57.15
Reference GC (%)	57.62
N50	15758
NG50	22673
N75	10195
NG75	21016
L50	493
LG50	104
L75	885
LG75	166
# misassemblies	69
# misassembled contigs	59
Misassembled contigs length	842528
# local misassemblies	49
# unaligned mis. contigs	9
# unaligned contigs	377 + 181 part
Unaligned length	3090839
Genome fraction (%)	94.183
Duplication ratio	3.323
# N's per 100 kbp	0.00
# mismatches per 100 kbp	82.89
# indels per 100 kbp	764.57
Largest alignment	34016
Total aligned length	17013794
NA50	13452
NGA50	21494
NA75	6341
NGA75	19781
LA50	536
LGA50	109
LA75	1053
LGA75	175

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.MiniCH.cr
# misassemblies	69
# relocations	63
# translocations	0
# inversions	6
# misassembled contigs	59
Misassembled contigs length	842528
# local misassemblies	49
# unaligned mis. contigs	9
# mismatches	4251
# indels	39210
# indels (≤ 5 bp)	39060
# indels (> 5 bp)	150
Indels length	49455

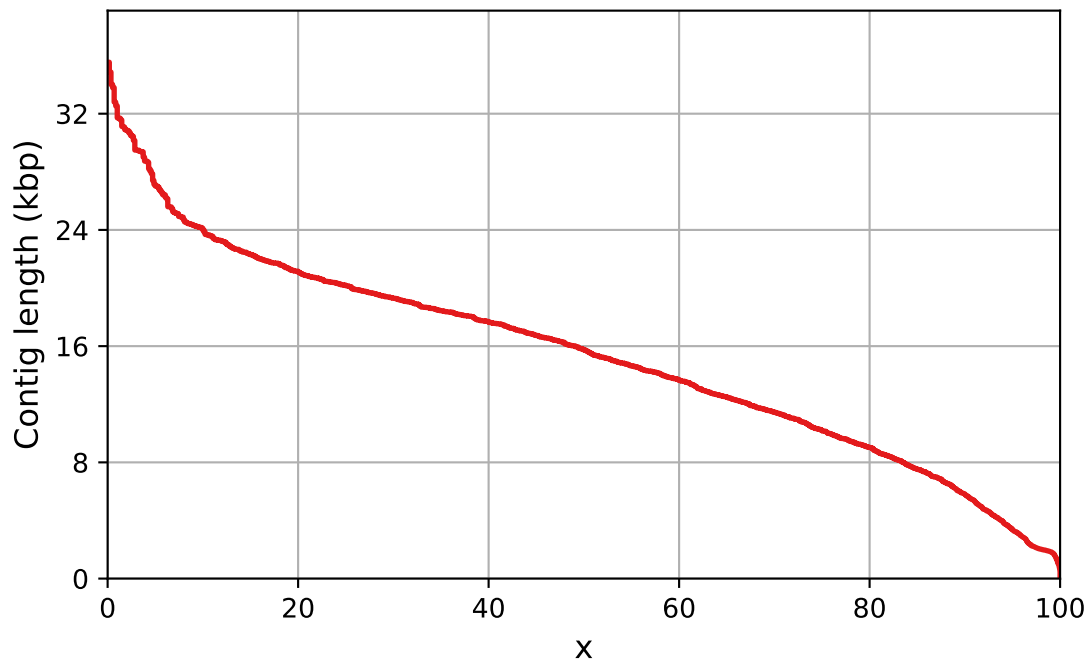
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ292.Minichr
# fully unaligned contigs	377
Fully unaligned length	2418689
# partially unaligned contigs	181
Partially unaligned length	672150
# N's	0

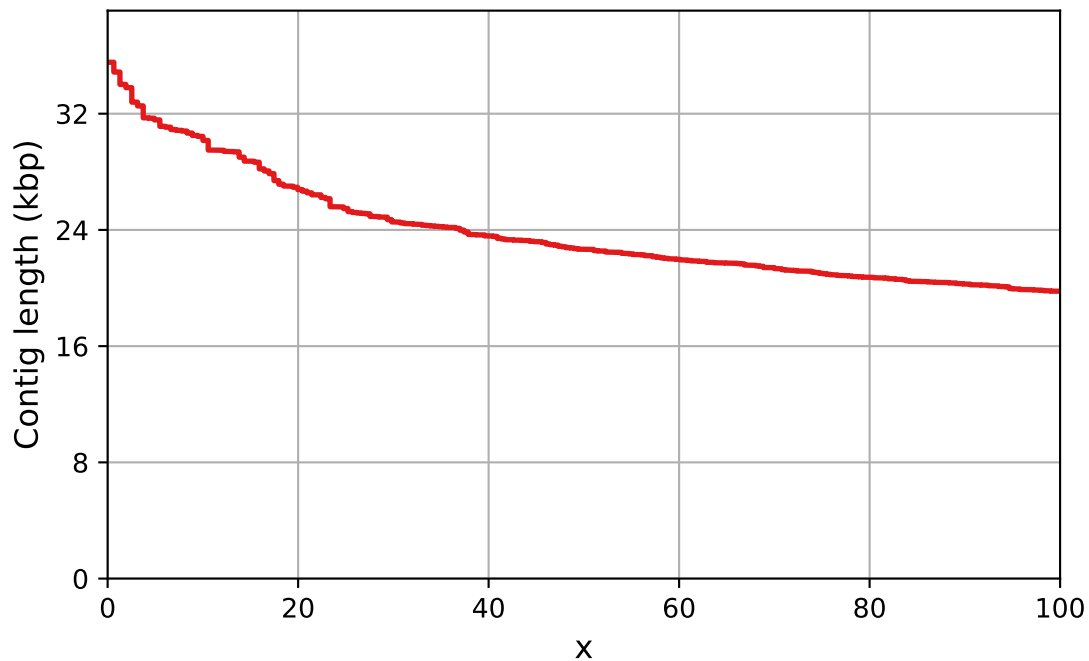
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



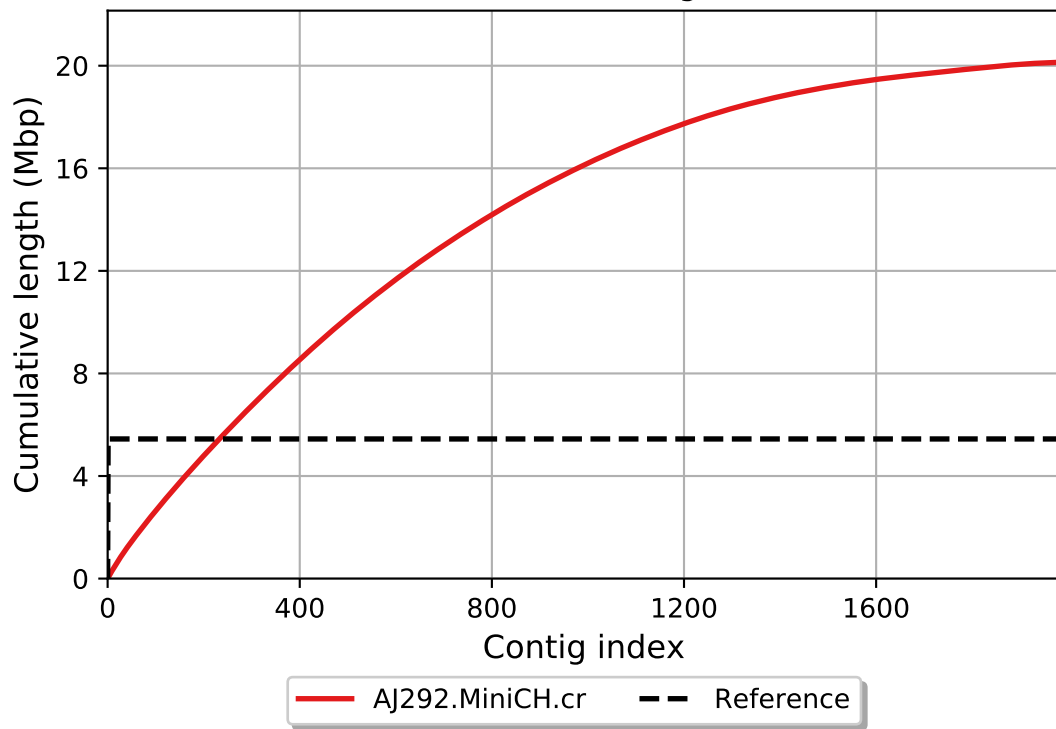
AJ292.MiniCH.cr

NGx

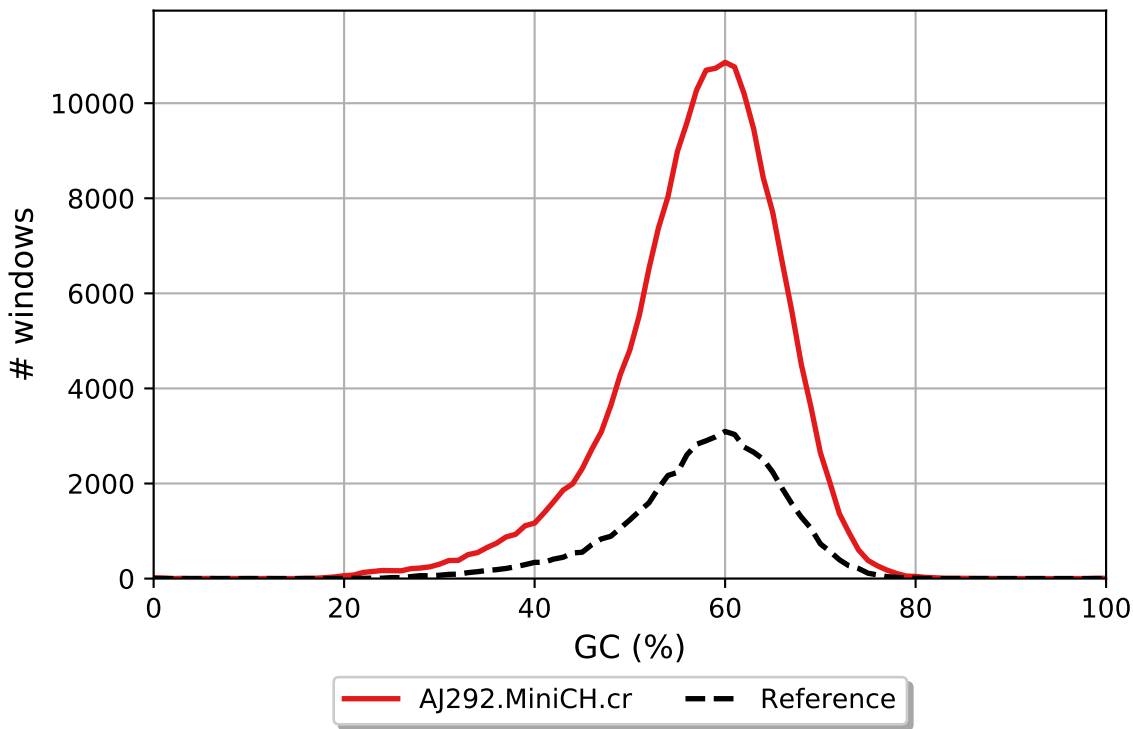


AJ292.MiniCH.cr

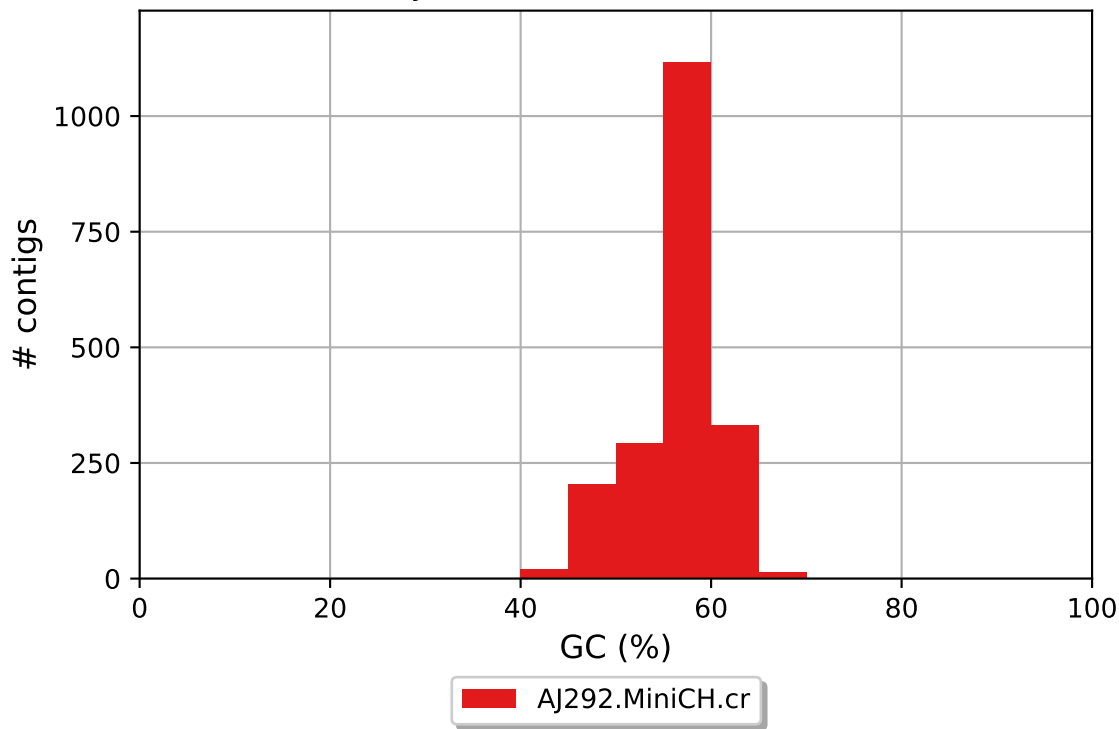
Cumulative length



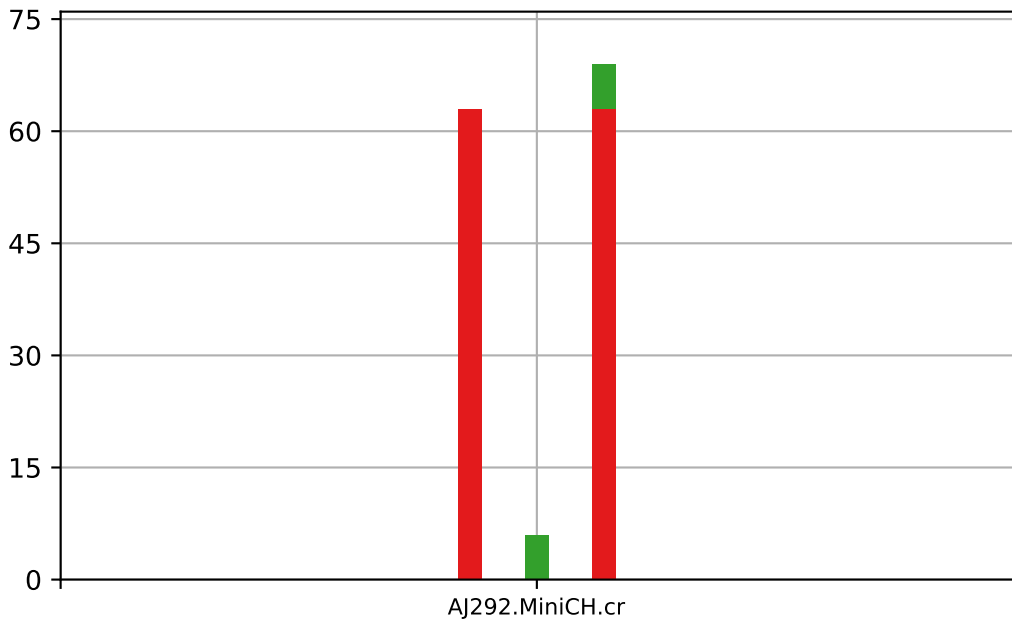
GC content



AJ292.MiniCH.cr GC content



Misassemblies

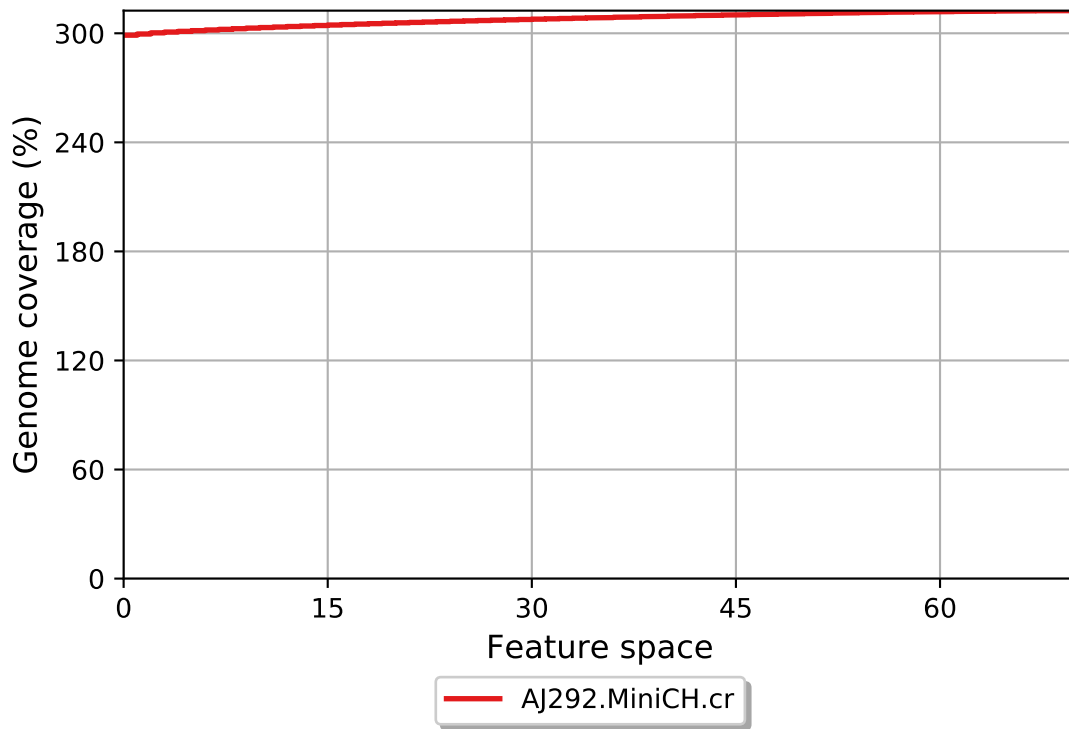


relocations

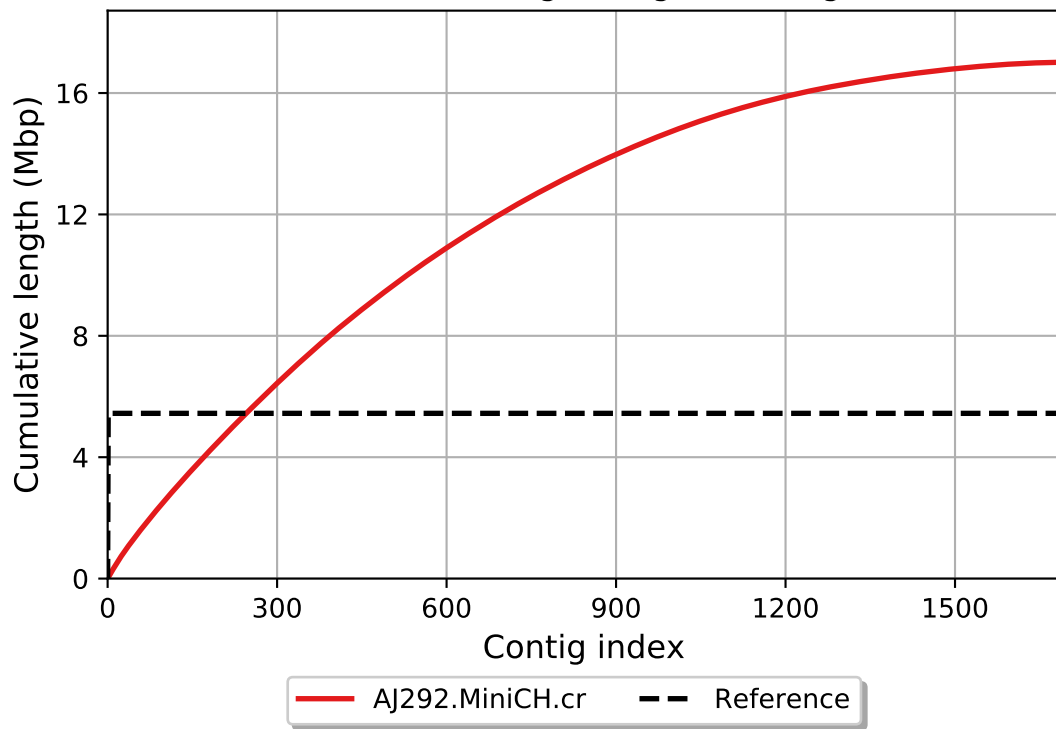


inversions

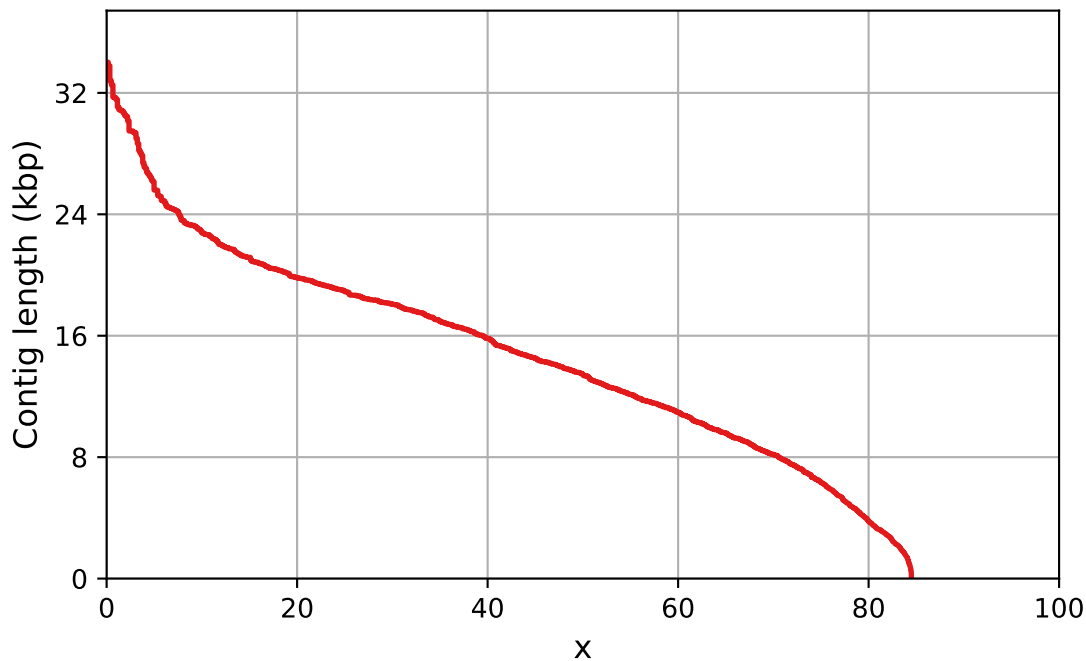
FRCurve (misassemblies)



Cumulative length (aligned contigs)

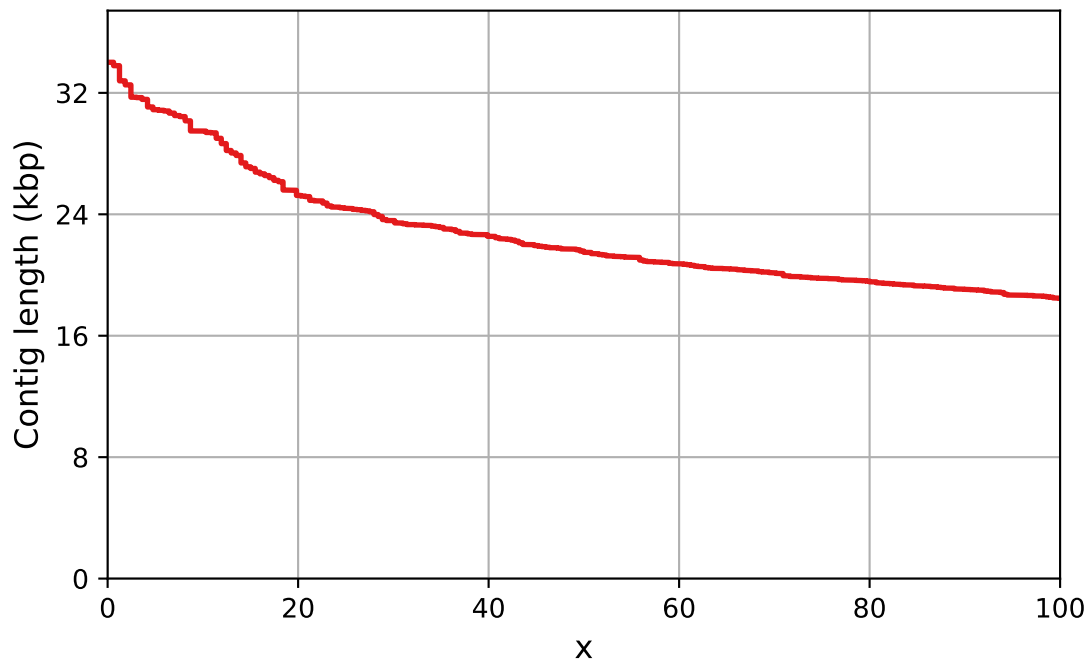


NAx



AJ292.MiniCH.cr

NGAx



AJ292.MiniCH.cr