

# Report

	AJ292.MiniCL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1938
# contigs (>= 5000 bp)	1317
# contigs (>= 10000 bp)	895
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	20122477
Total length (>= 1000 bp)	20082271
Total length (>= 5000 bp)	18410912
Total length (>= 10000 bp)	15214916
Total length (>= 25000 bp)	1508859
Total length (>= 50000 bp)	0
# contigs	1983
Largest contig	35571
Total length	20116984
Reference length	5445112
GC (%)	57.11
Reference GC (%)	57.62
N50	15758
NG50	22686
N75	10164
NG75	21079
L50	492
LG50	104
L75	883
LG75	166
# misassemblies	66
# misassembled contigs	57
Misassembled contigs length	804975
# local misassemblies	48
# unaligned mis. contigs	11
# unaligned contigs	393 + 177 part
Unaligned length	3213980
Genome fraction (%)	94.240
Duplication ratio	3.294
# N's per 100 kbp	0.00
# mismatches per 100 kbp	86.80
# indels per 100 kbp	848.18
Largest alignment	33973
Total aligned length	16873692
NA50	13365
NGA50	21475
NA75	6022
NGA75	19755
LA50	536
LGA50	109
LA75	1061
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.MiniCL.cr
# misassemblies	66
# relocations	61
# translocations	0
# inversions	5
# misassembled contigs	57
Misassembled contigs length	804975
# local misassemblies	48
# unaligned mis. contigs	11
# mismatches	4454
# indels	43524
# indels ( $\leq 5$ bp)	43339
# indels ( $> 5$ bp)	185
Indels length	54047

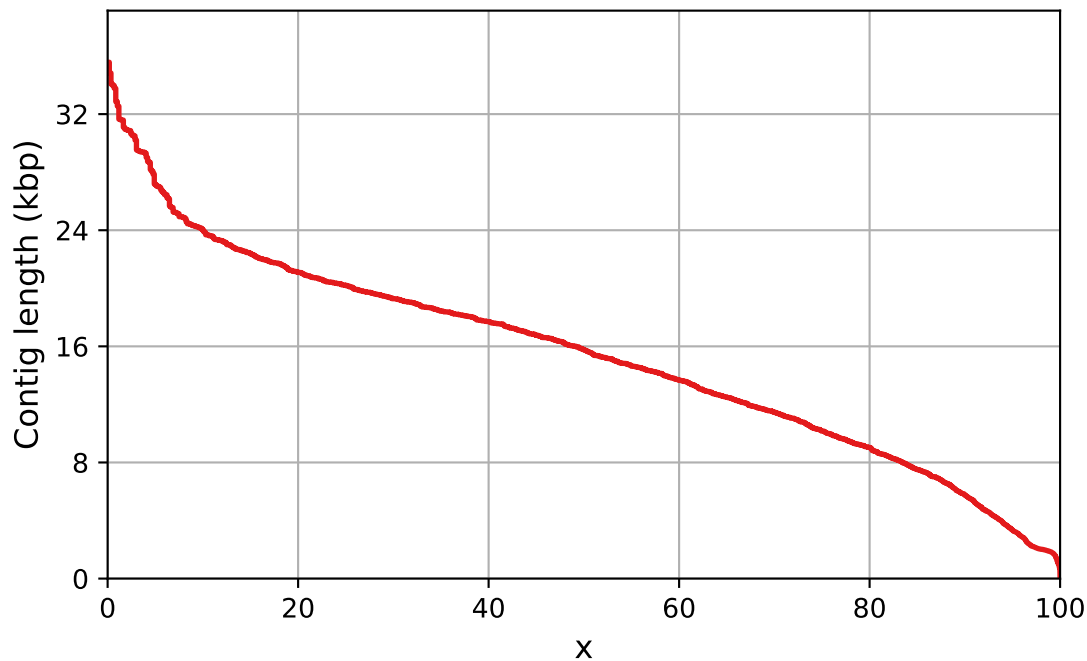
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ292.MinicL.cr
# fully unaligned contigs	393
Fully unaligned length	2571046
# partially unaligned contigs	177
Partially unaligned length	642934
# N's	0

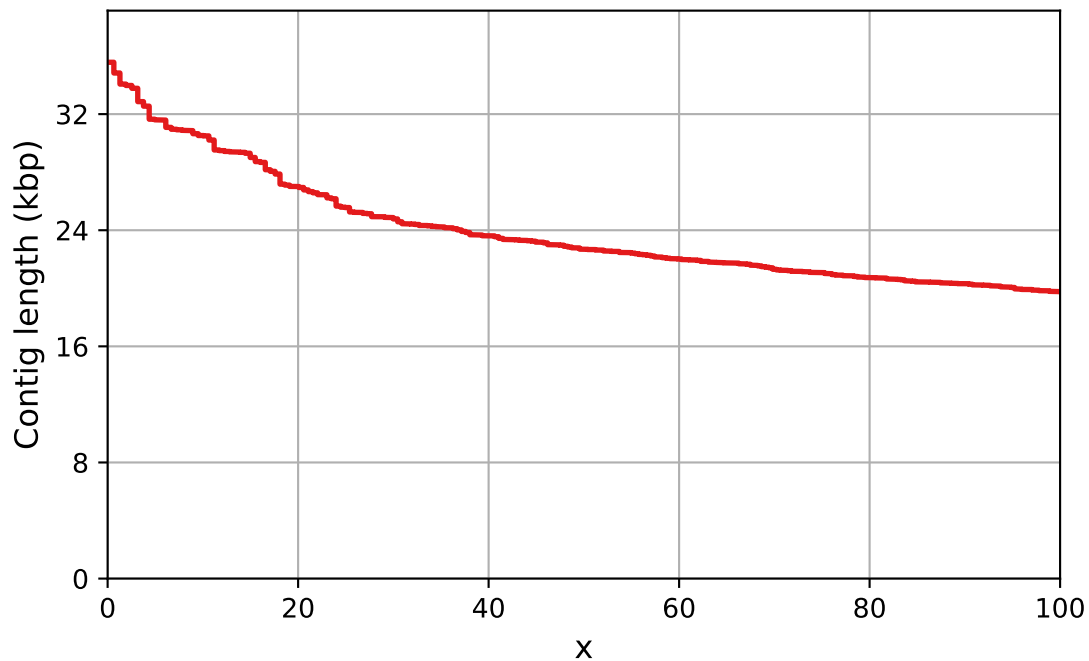
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



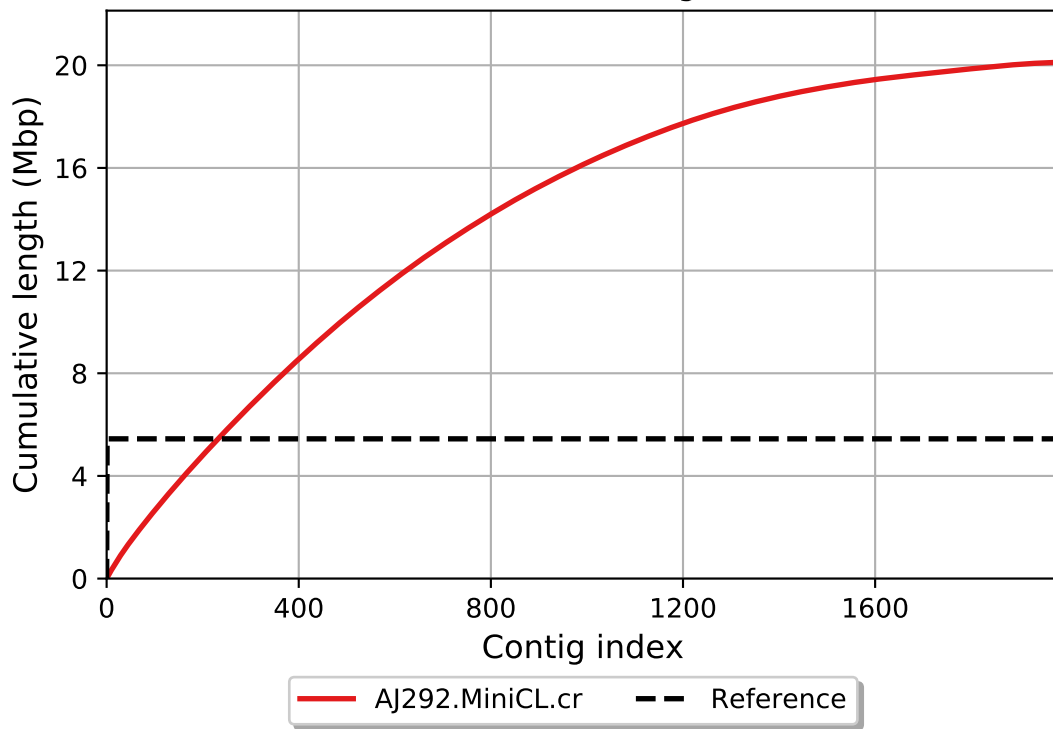
Aj292.MiniCL.cr

NGx

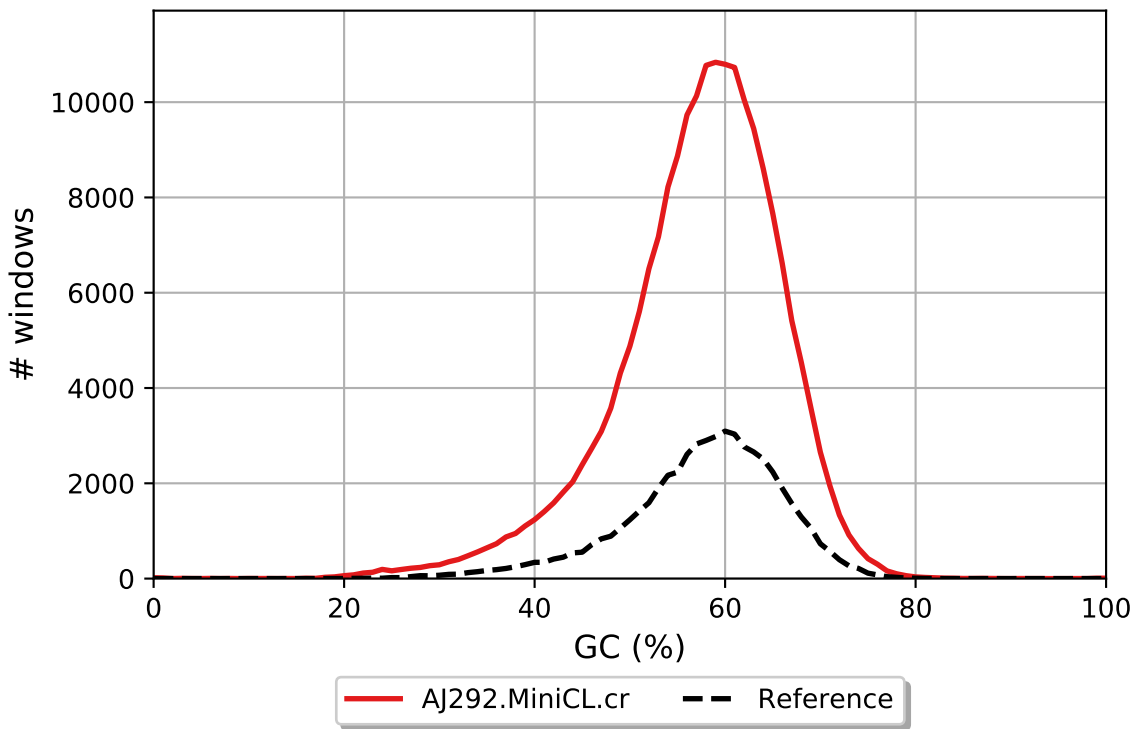


Aj292.MiniCL.cr

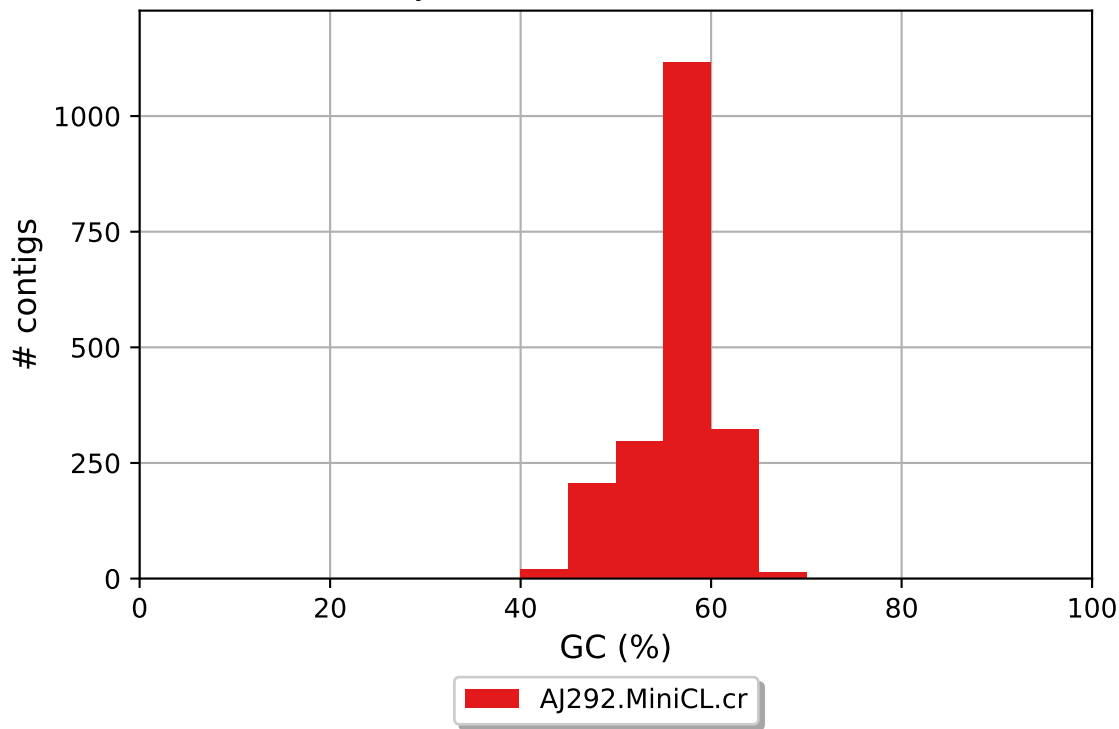
Cumulative length



# GC content

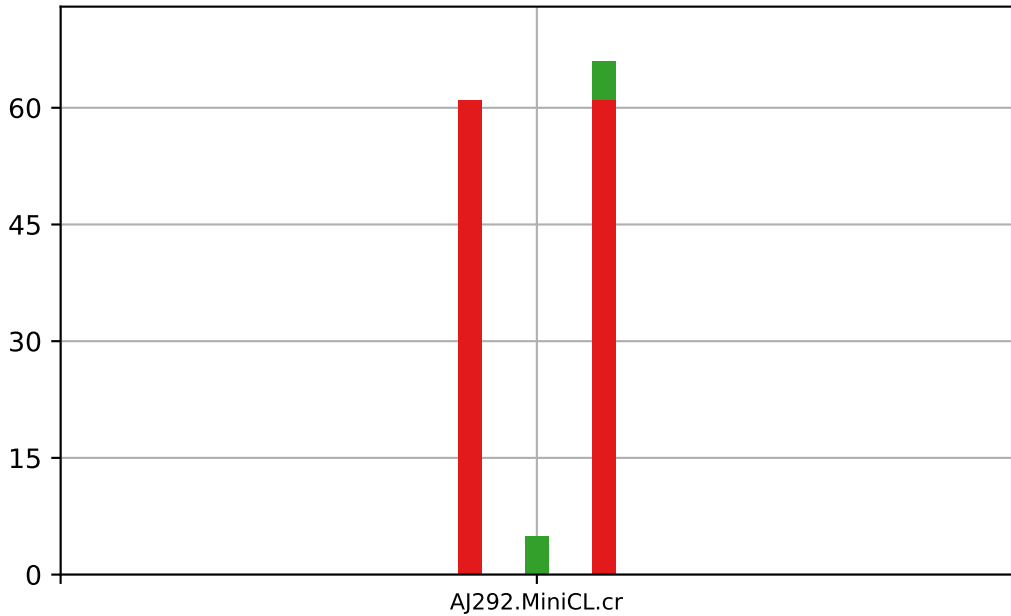


AJ292.MiniCL.cr GC content





## Misassemblies

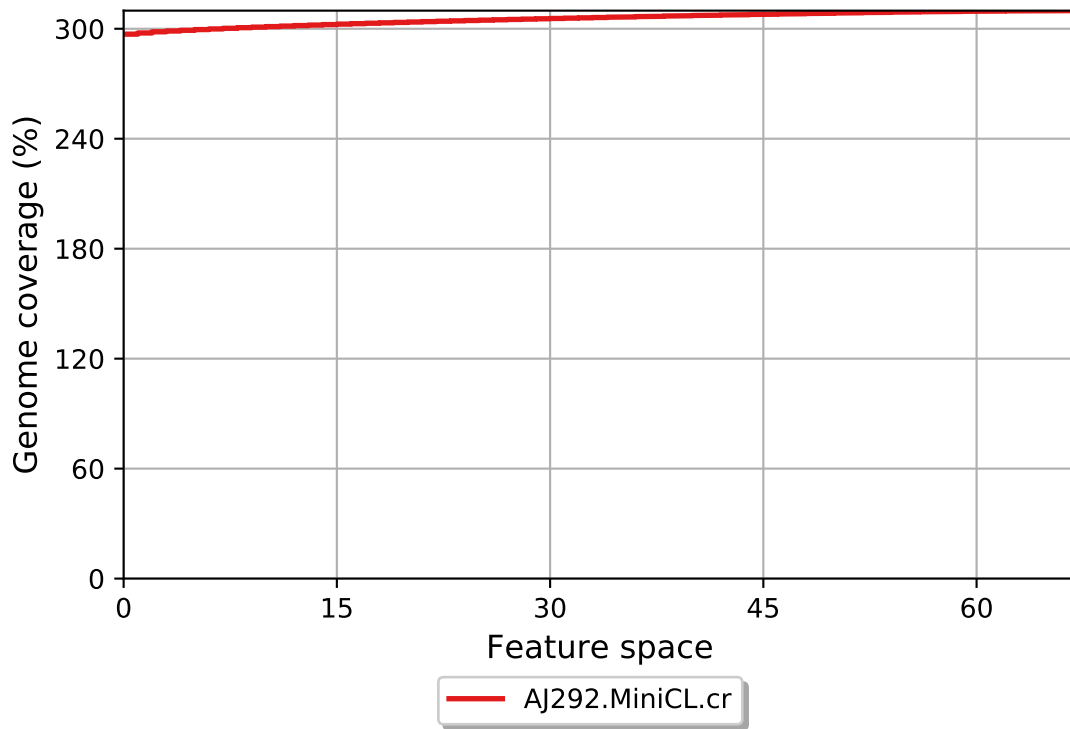


# relocations

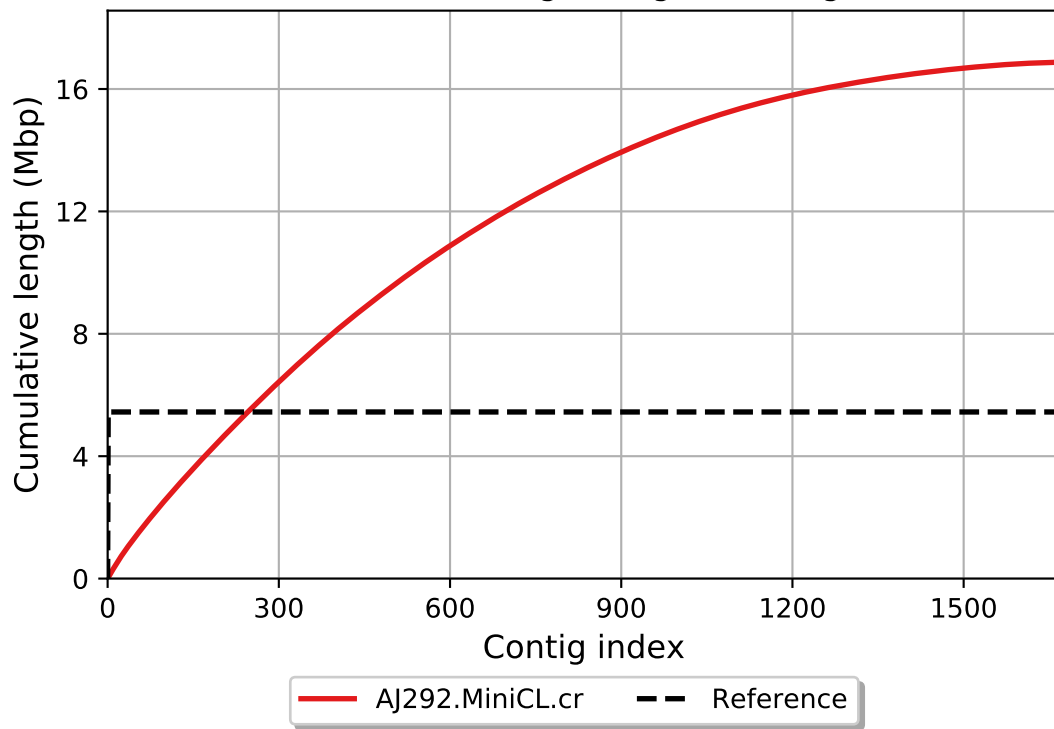


# inversions

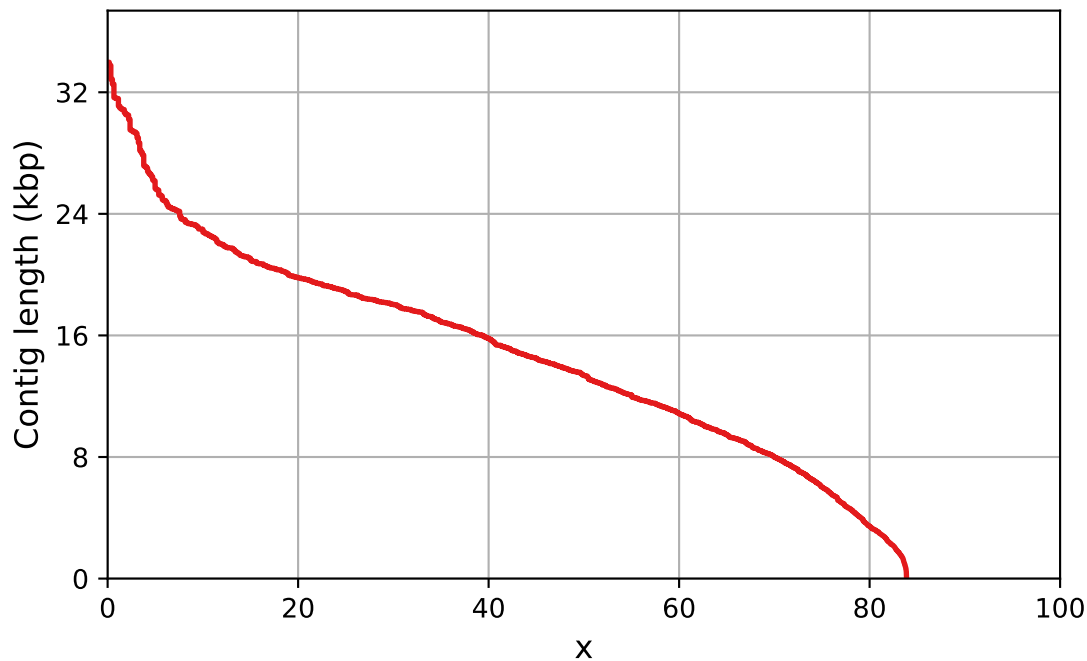
FRCurve (misassemblies)



Cumulative length (aligned contigs)

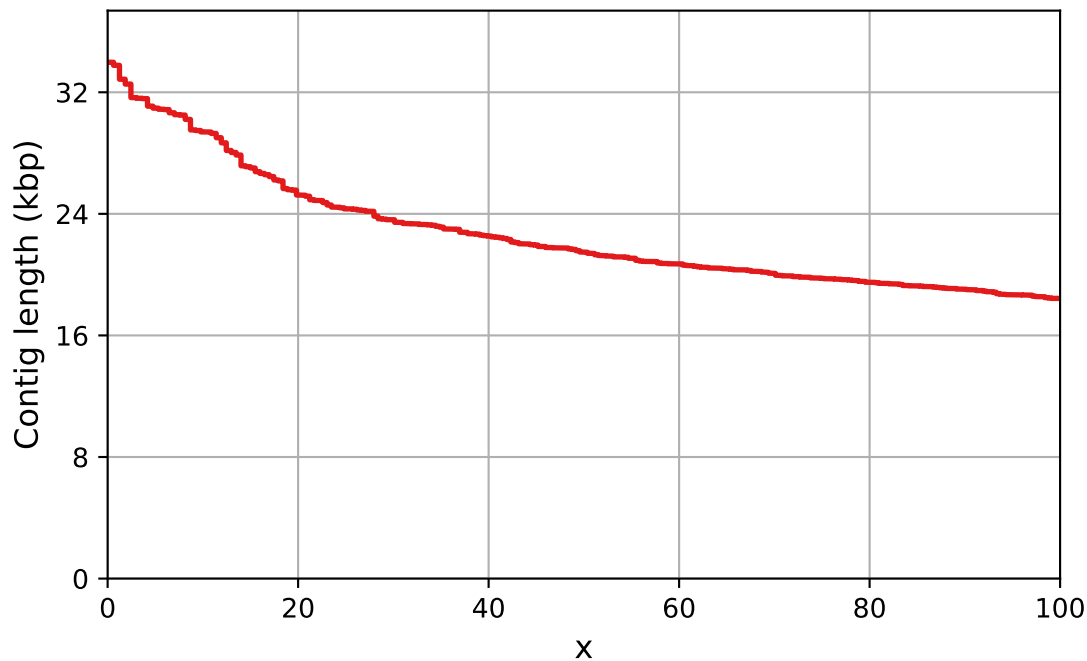


NAx



AJ292.MinicL.cr

# NGAx



— Aj292.MinicL.cr