

Report

	AJ292.CanuL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1994
# contigs (>= 5000 bp)	1414
# contigs (>= 10000 bp)	956
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	21236144
Total length (>= 1000 bp)	21230546
Total length (>= 5000 bp)	19605092
Total length (>= 10000 bp)	16157882
Total length (>= 25000 bp)	1448446
Total length (>= 50000 bp)	0
# contigs	2000
Largest contig	35596
Total length	21236144
Reference length	5445112
GC (%)	57.33
Reference GC (%)	57.62
N50	15786
NG50	22750
N75	10202
NG75	21230
L50	522
LG50	104
L75	934
LG75	166
# misassemblies	34
# misassembled contigs	33
Misassembled contigs length	540888
# local misassemblies	36
# unaligned mis. contigs	3
# unaligned contigs	143 + 156 part
Unaligned length	794338
Genome fraction (%)	96.564
Duplication ratio	3.888
# N's per 100 kbp	0.00
# mismatches per 100 kbp	58.33
# indels per 100 kbp	389.50
Largest alignment	33842
Total aligned length	20398415
NA50	15129
NGA50	22326
NA75	9427
NGA75	20737
LA50	537
LGA50	107
LA75	973
LGA75	170

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.CanuL.cr
# misassemblies	34
# relocations	32
# translocations	0
# inversions	2
# misassembled contigs	33
Misassembled contigs length	540888
# local misassemblies	36
# unaligned mis. contigs	3
# mismatches	3067
# indels	20480
# indels (≤ 5 bp)	20323
# indels (> 5 bp)	157
Indels length	25706

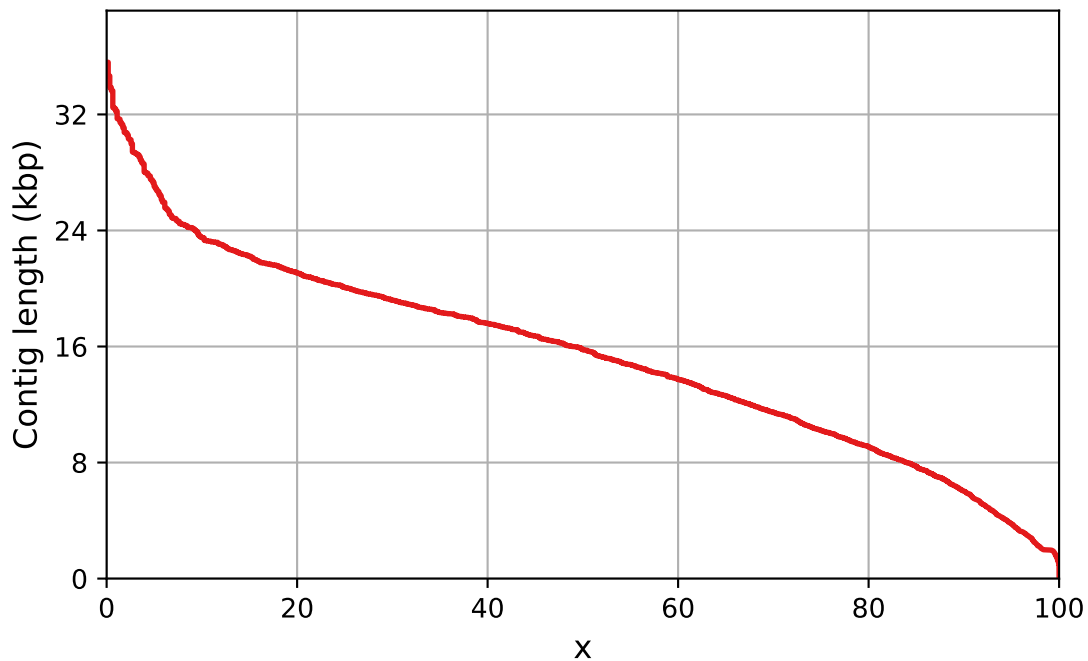
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ292.CanuL.cr
# fully unaligned contigs	143
Fully unaligned length	335836
# partially unaligned contigs	156
Partially unaligned length	458502
# N's	0

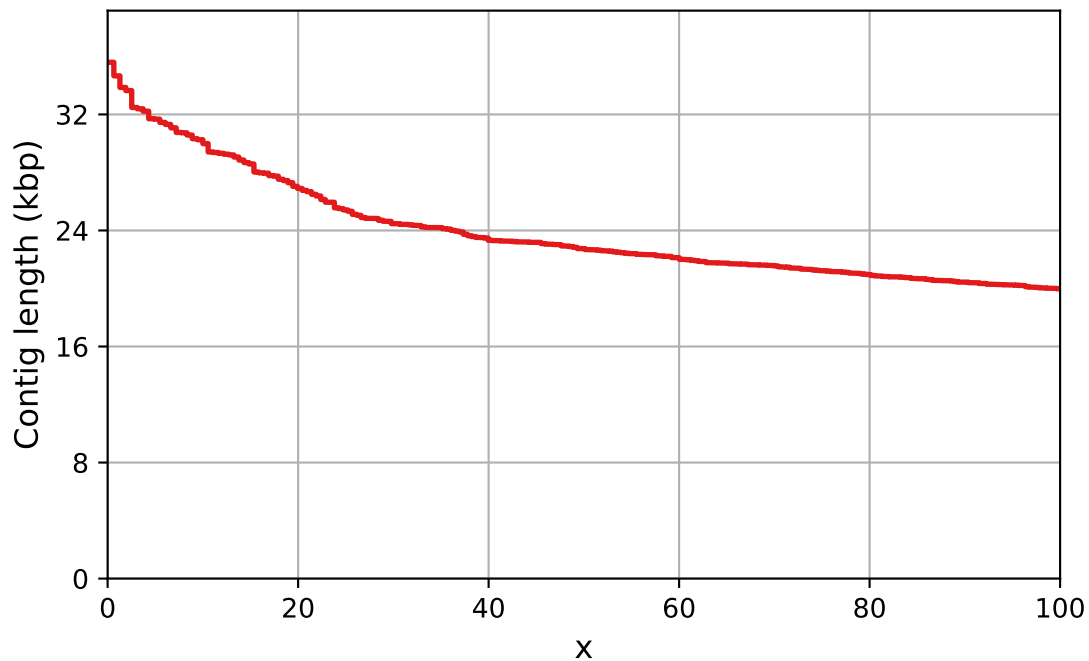
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



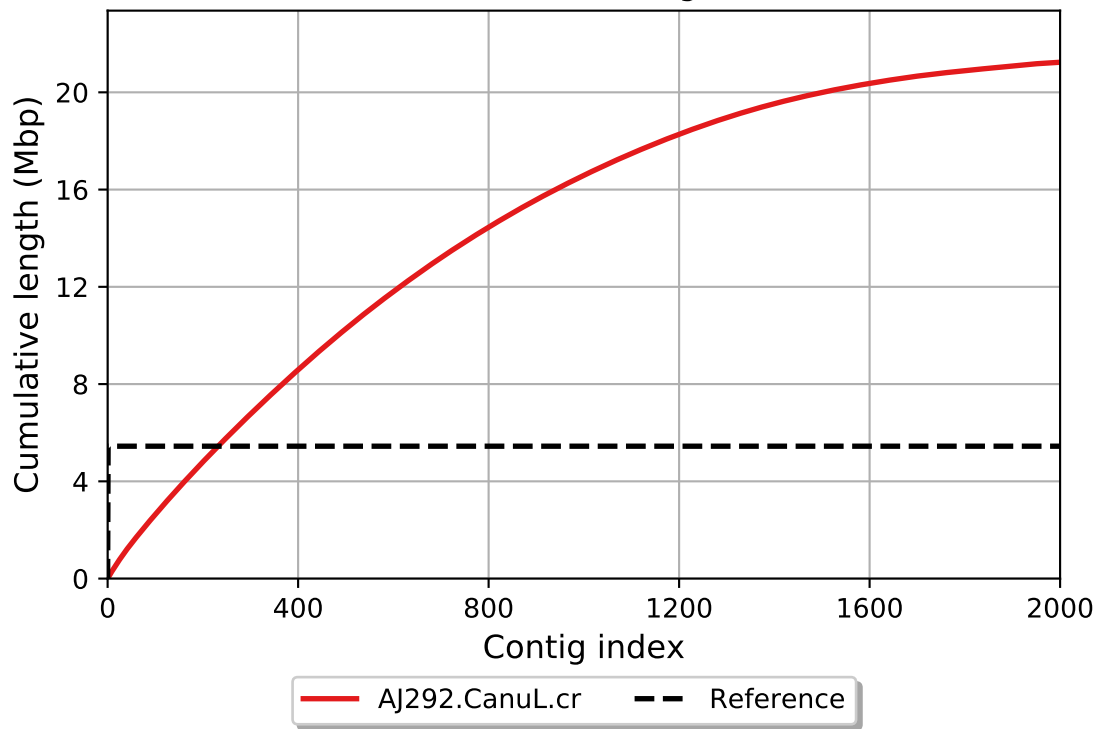
AJ292.CanuL.cr

NGx

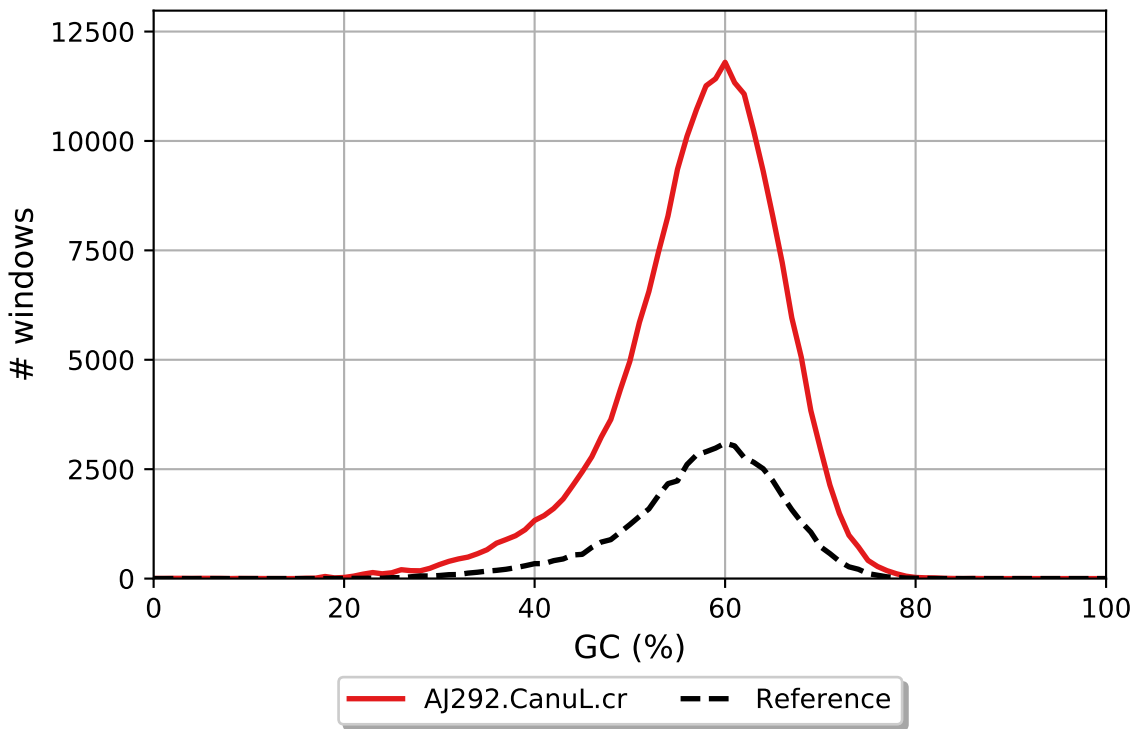


— AJ292.CanuL.cr

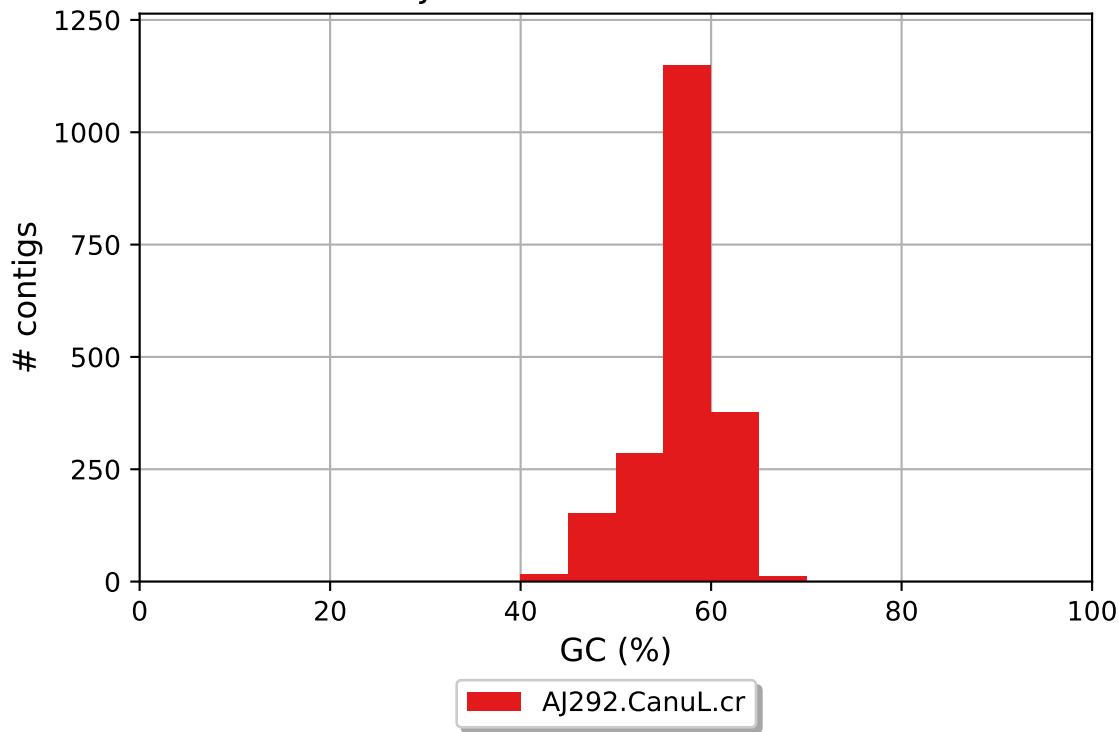
Cumulative length



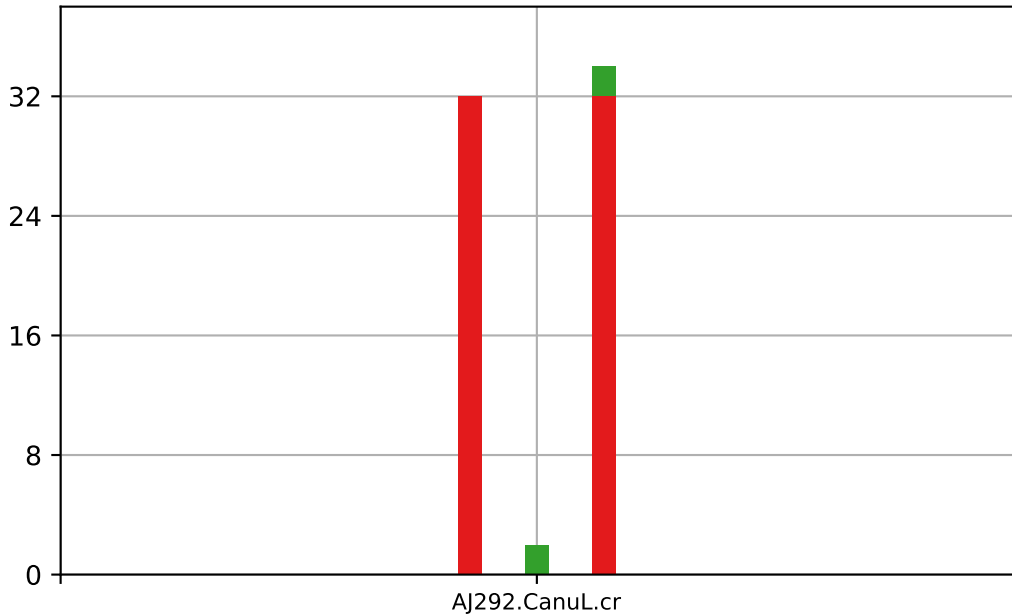
GC content



AJ292.CanuL.cr GC content



Misassemblies

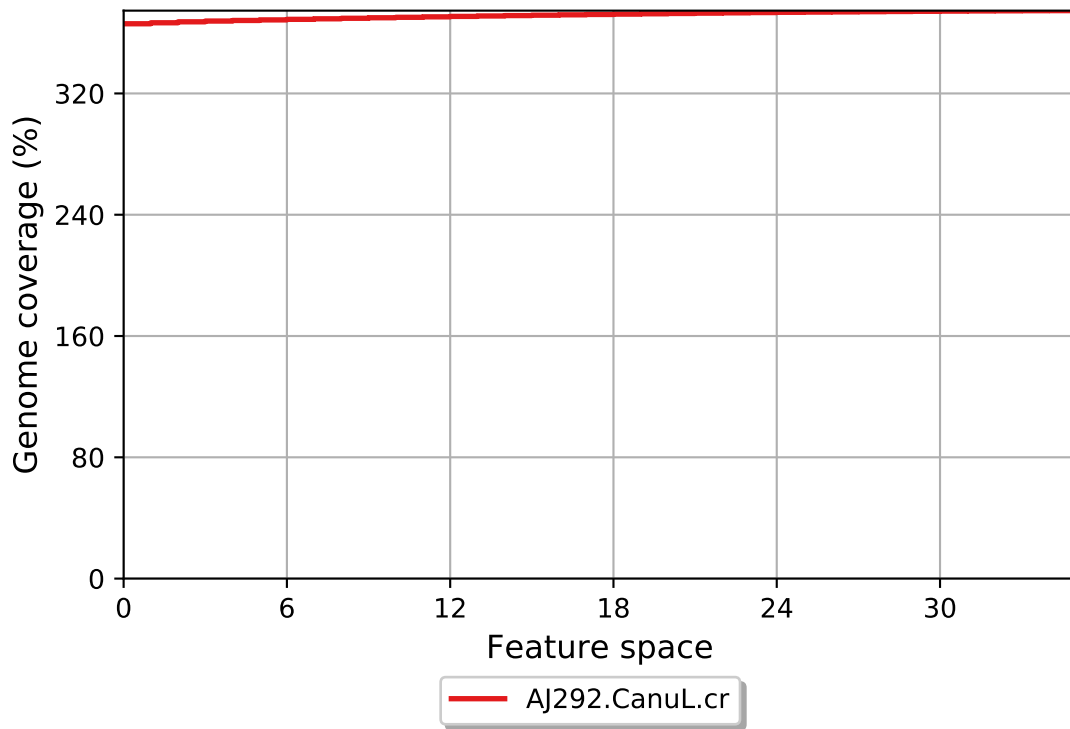


relocations

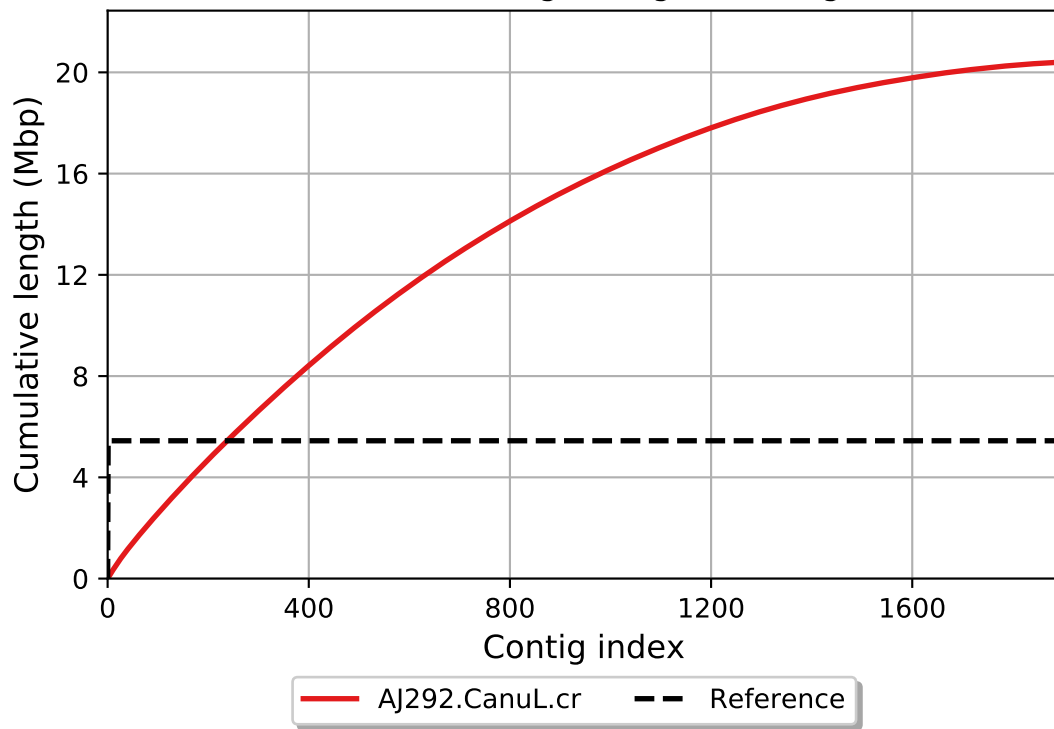


inversions

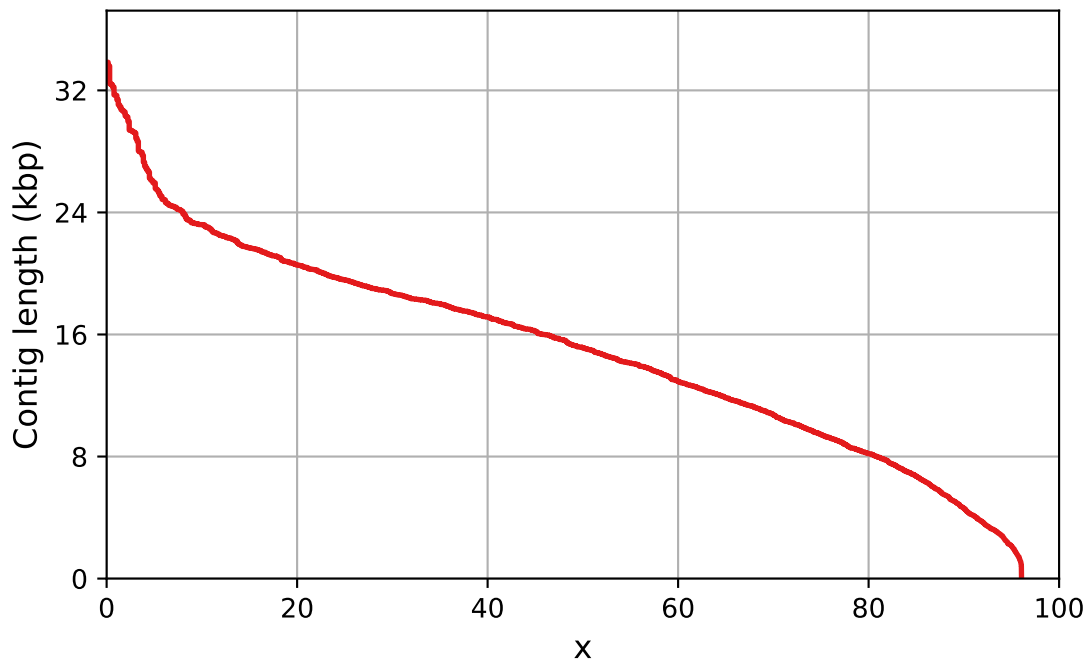
FRCurve (misassemblies)



Cumulative length (aligned contigs)

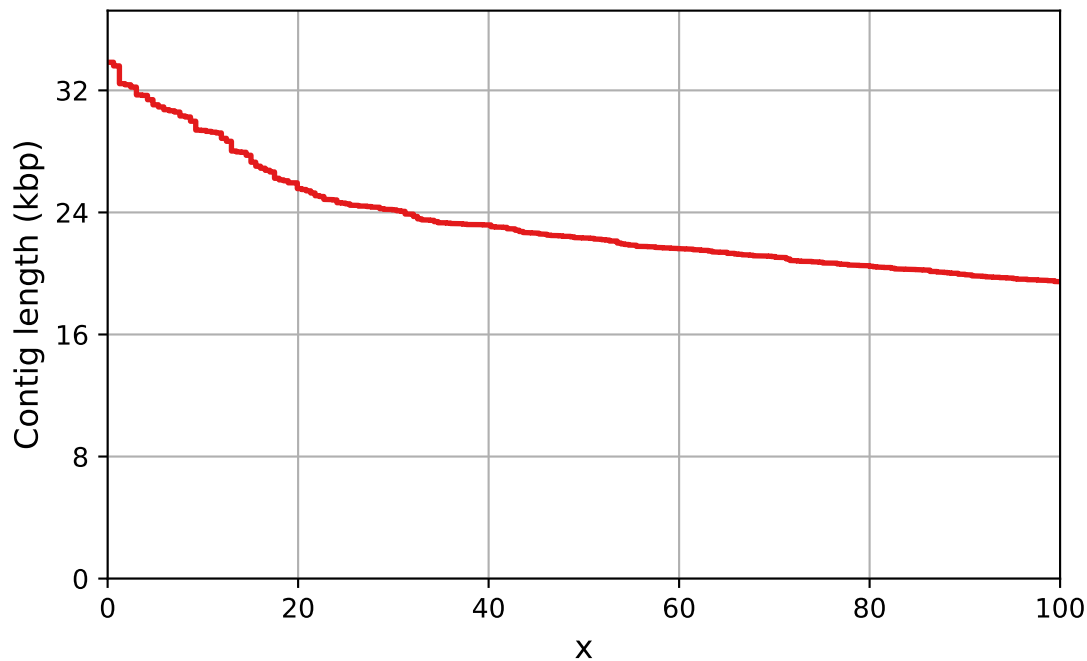


NAx



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NGAx



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