

Report

	AJ292.CanuH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1967
# contigs (>= 5000 bp)	1499
# contigs (>= 10000 bp)	1012
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	21970960
Total length (>= 1000 bp)	21947330
Total length (>= 5000 bp)	20603850
Total length (>= 10000 bp)	16941458
Total length (>= 25000 bp)	1380928
Total length (>= 50000 bp)	0
# contigs	1996
Largest contig	34672
Total length	21969846
Reference length	5445112
GC (%)	57.43
Reference GC (%)	57.62
N50	15750
NG50	22572
N75	10514
NG75	21040
L50	545
LG50	105
L75	967
LG75	168
# misassemblies	11
# misassembled contigs	11
Misassembled contigs length	222190
# local misassemblies	29
# unaligned mis. contigs	0
# unaligned contigs	118 + 41 part
Unaligned length	298319
Genome fraction (%)	97.050
Duplication ratio	4.101
# N's per 100 kbp	0.00
# mismatches per 100 kbp	29.73
# indels per 100 kbp	205.26
Largest alignment	33826
Total aligned length	21649361
NA50	15576
NGA50	22440
NA75	10289
NGA75	20846
LA50	550
LGA50	106
LA75	979
LGA75	169

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.CanuH.cr
# misassemblies	11
# relocations	11
# translocations	0
# inversions	0
# misassembled contigs	11
Misassembled contigs length	222190
# local misassemblies	29
# unaligned mis. contigs	0
# mismatches	1571
# indels	10847
# indels (≤ 5 bp)	10720
# indels (> 5 bp)	127
Indels length	14286

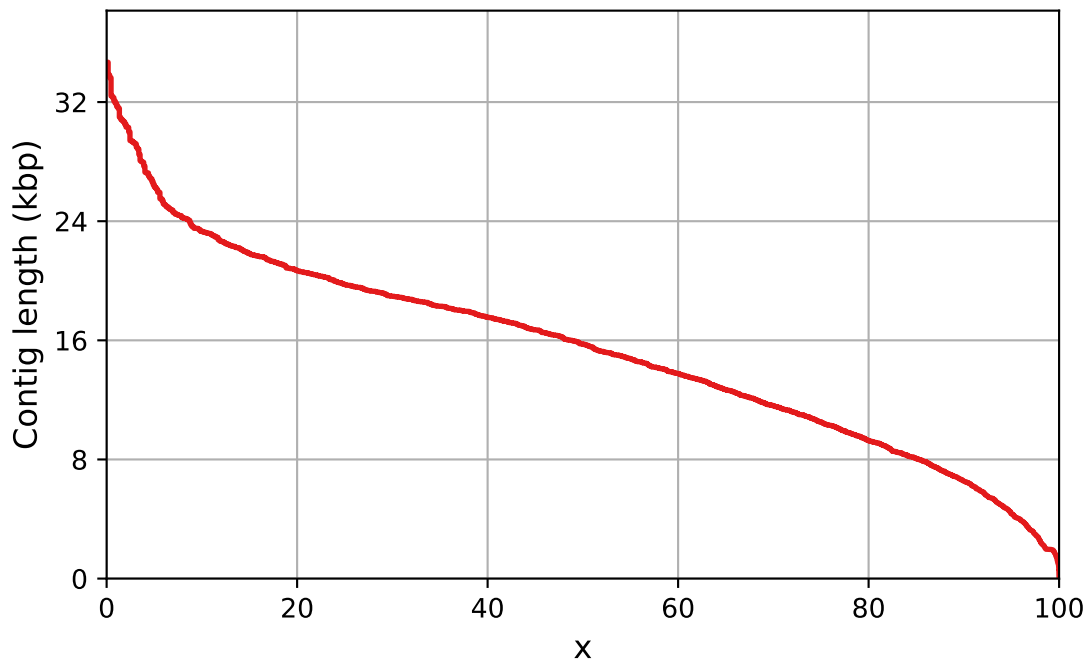
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ292.CanuH.cr
# fully unaligned contigs	118
Fully unaligned length	226968
# partially unaligned contigs	41
Partially unaligned length	71351
# N's	0

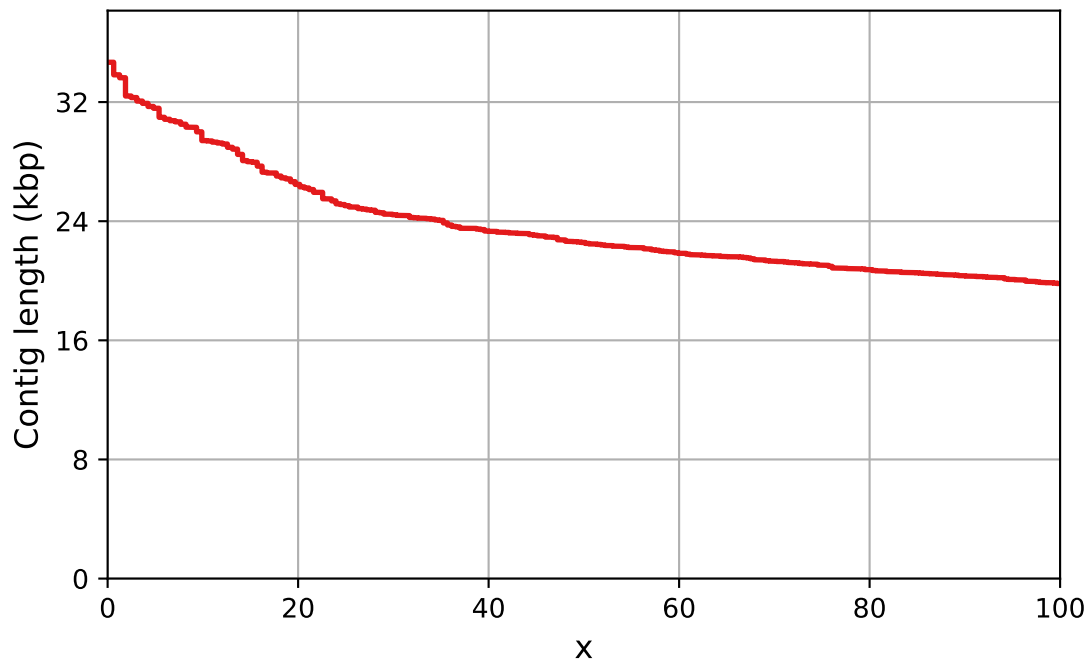
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



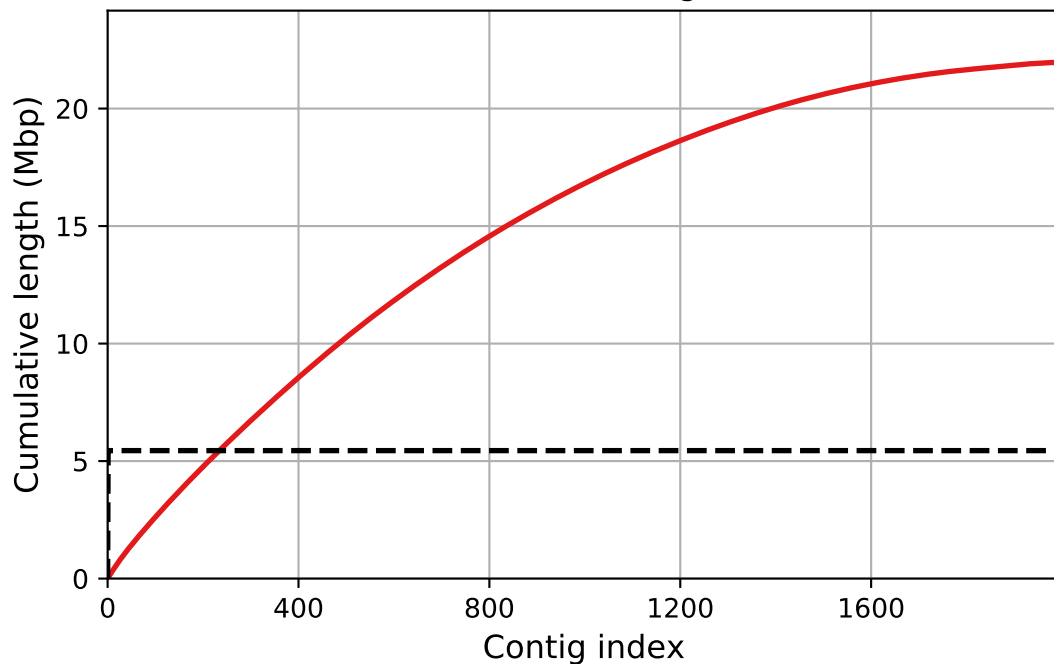
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NGx



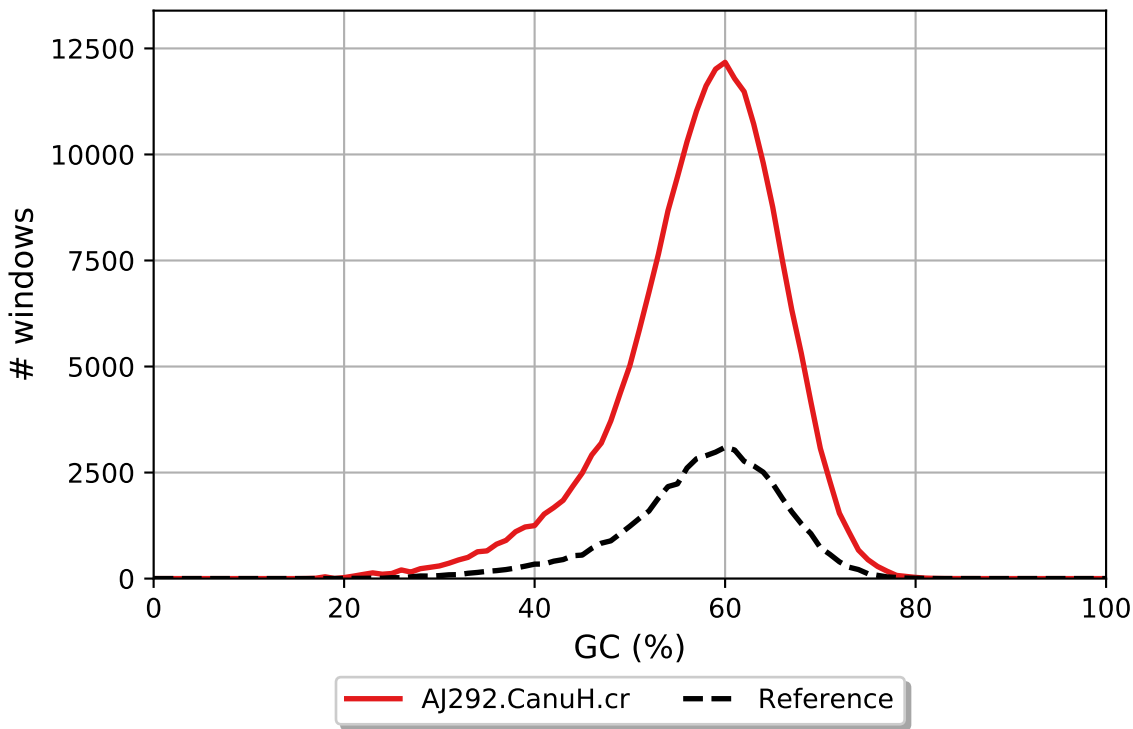
Aj292.CanuH.cr

Cumulative length

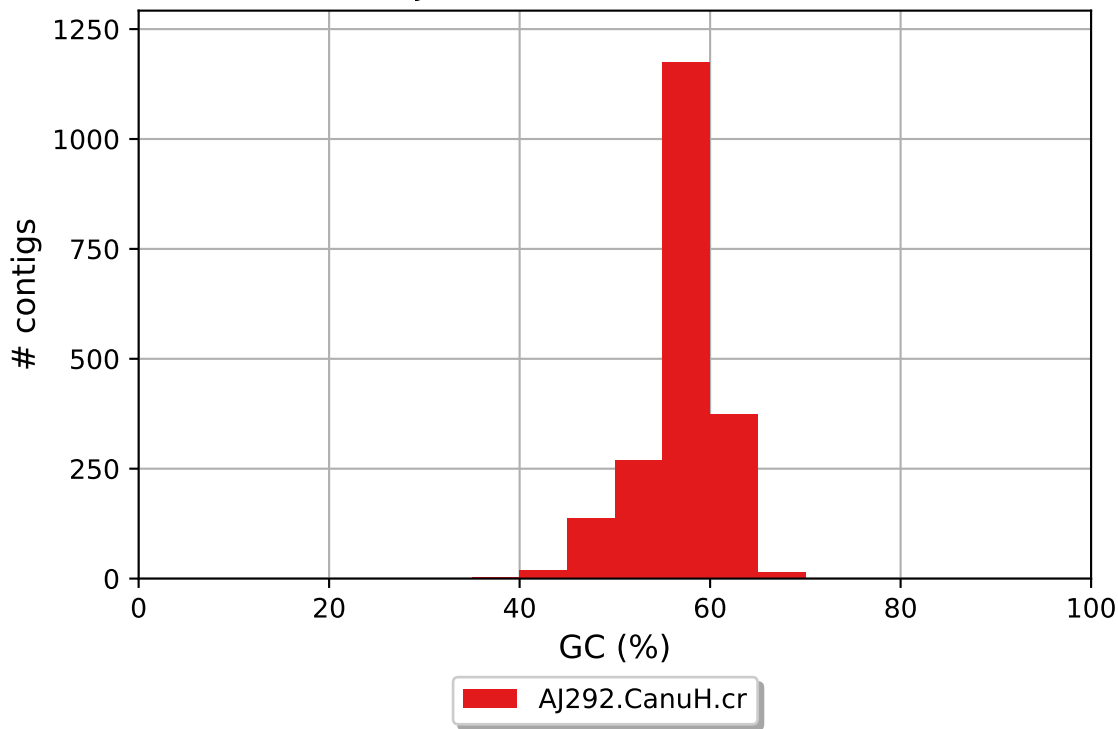


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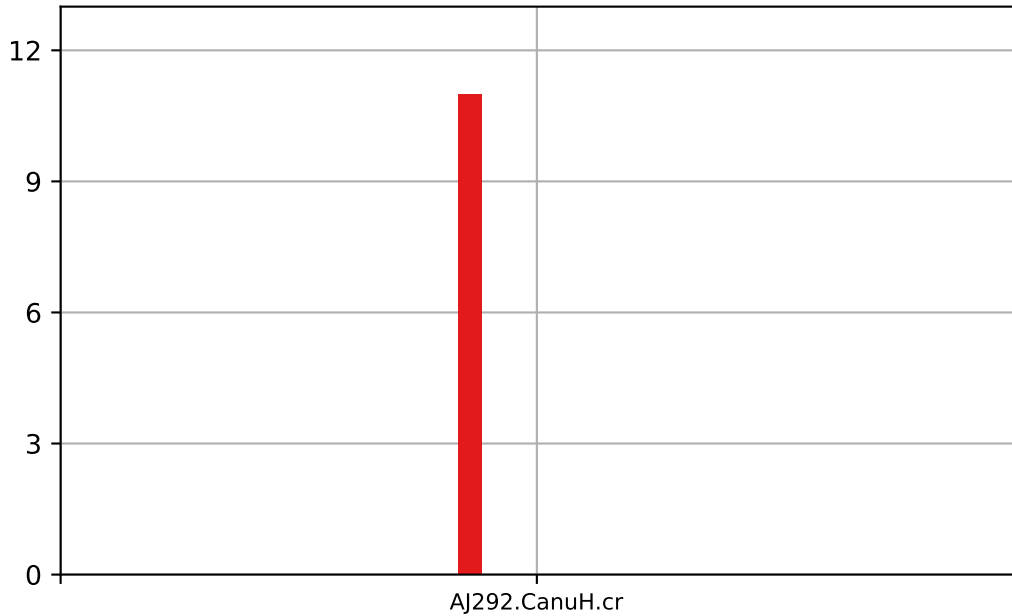
GC content



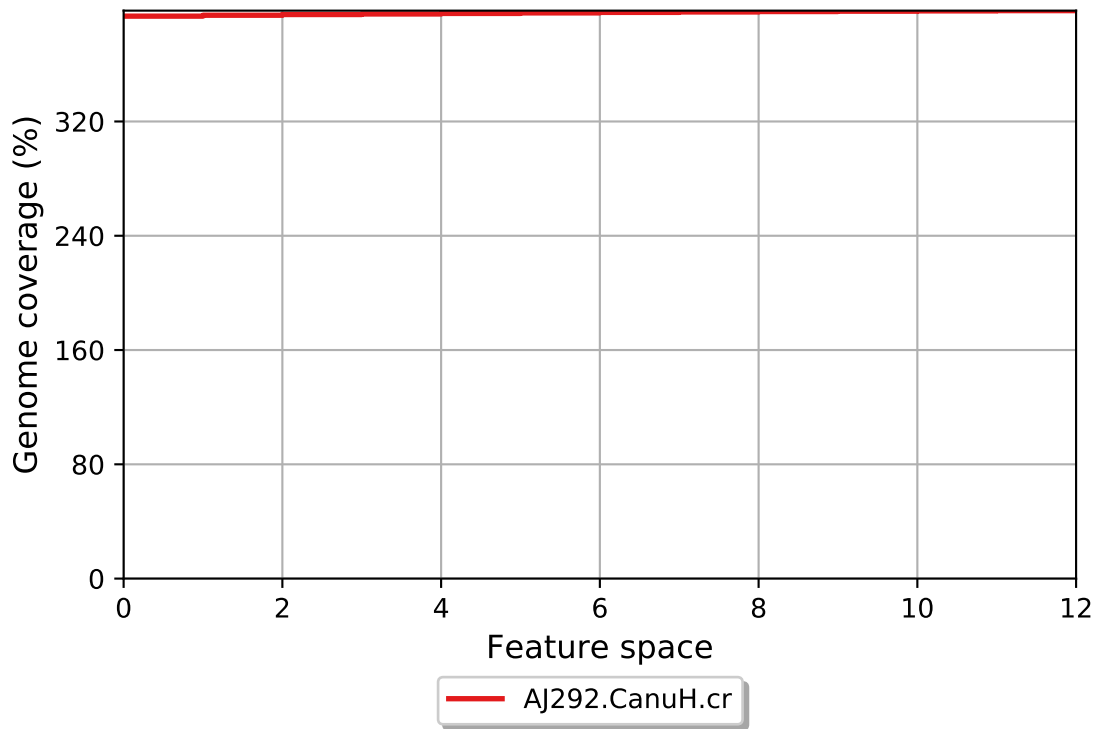
AJ292.CanuH.cr GC content



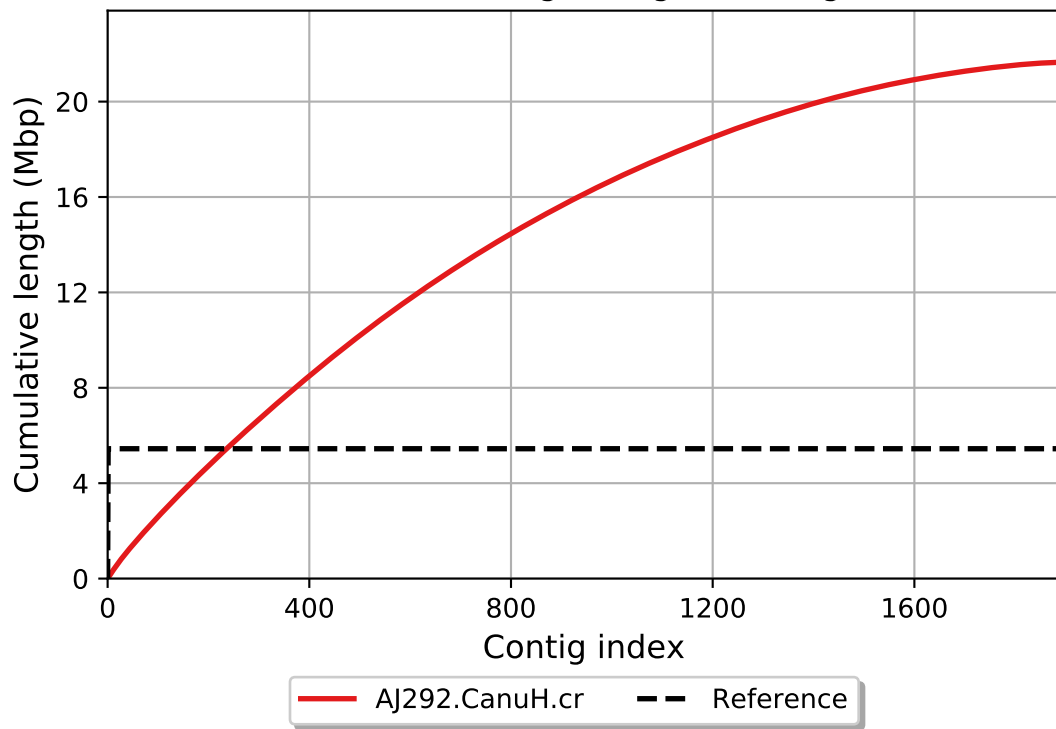
Misassemblies



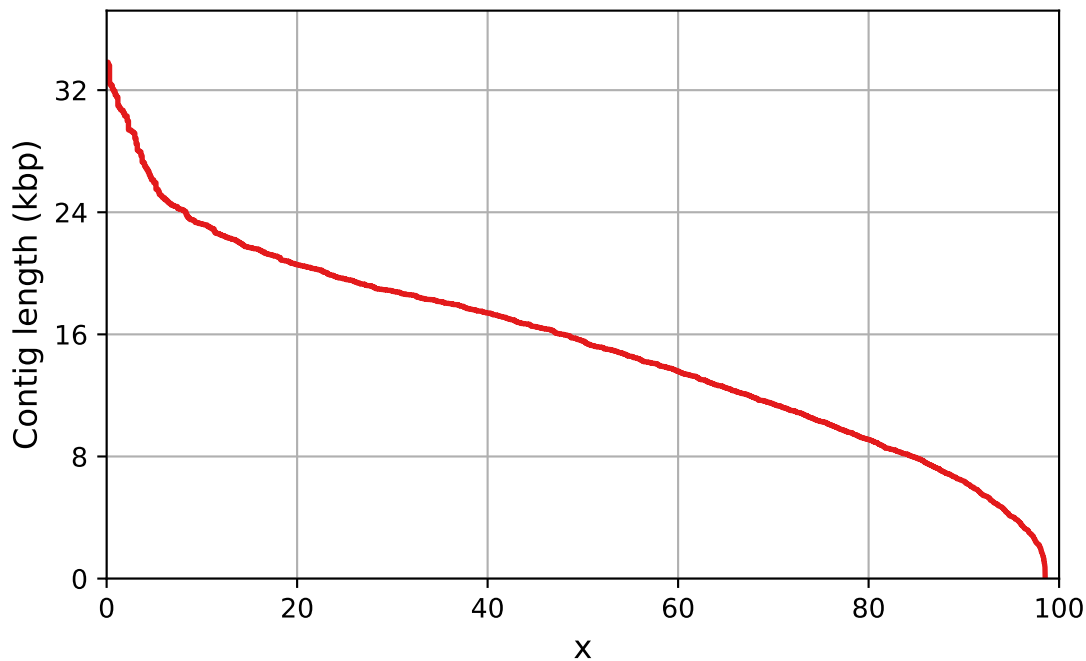
FRCurve (misassemblies)



Cumulative length (aligned contigs)

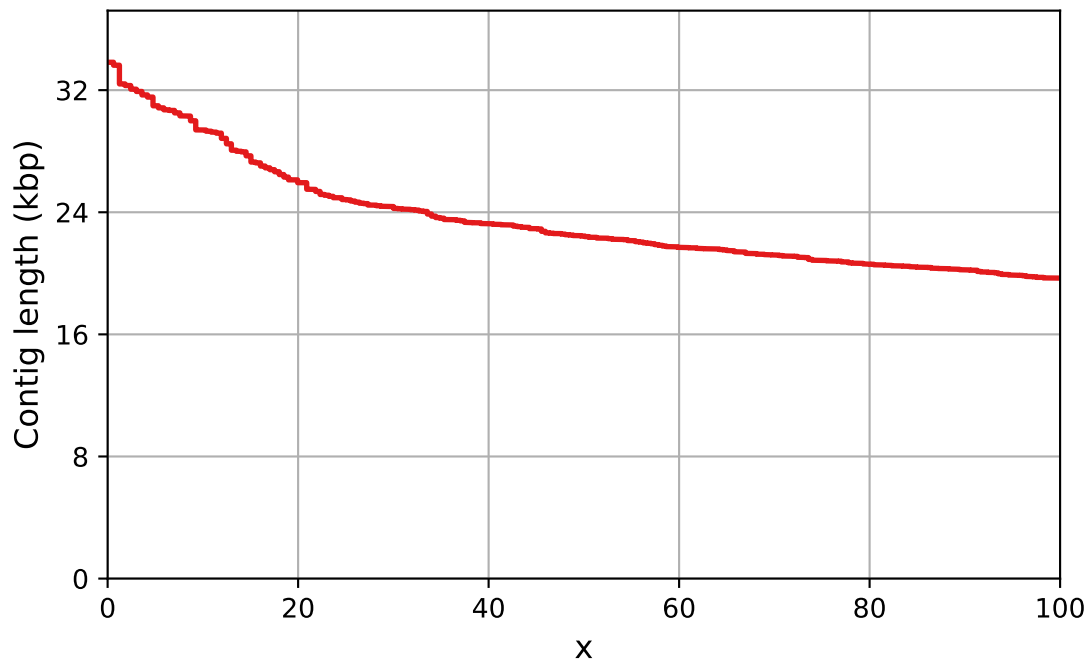


NAx



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NGAx



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