

Report

	AJ218.CanuL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1995
# contigs (>= 5000 bp)	1411
# contigs (>= 10000 bp)	908
# contigs (>= 25000 bp)	41
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	20005440
Total length (>= 1000 bp)	20001010
Total length (>= 5000 bp)	18377612
Total length (>= 10000 bp)	14623306
Total length (>= 25000 bp)	1169240
Total length (>= 50000 bp)	0
# contigs	2000
Largest contig	33830
Total length	20005440
Reference length	5465981
GC (%)	57.09
Reference GC (%)	57.29
N50	14626
NG50	21242
N75	9488
NG75	19498
L50	526
LG50	110
L75	948
LG75	177
# misassemblies	31
# misassembled contigs	30
Misassembled contigs length	394268
# local misassemblies	31
# unaligned mis. contigs	4
# unaligned contigs	127 + 184 part
Unaligned length	1456893
Genome fraction (%)	94.364
Duplication ratio	3.596
# N's per 100 kbp	0.00
# mismatches per 100 kbp	71.06
# indels per 100 kbp	483.99
Largest alignment	33819
Total aligned length	18501989
NA50	13380
NGA50	21096
NA75	7750
NGA75	19190
LA50	544
LGA50	111
LA75	1028
LGA75	179

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.CanuL.cr
# misassemblies	31
# relocations	29
# translocations	0
# inversions	2
# misassembled contigs	30
Misassembled contigs length	394268
# local misassemblies	31
# unaligned mis. contigs	4
# mismatches	3665
# indels	24964
# indels (≤ 5 bp)	24797
# indels (> 5 bp)	167
Indels length	31534

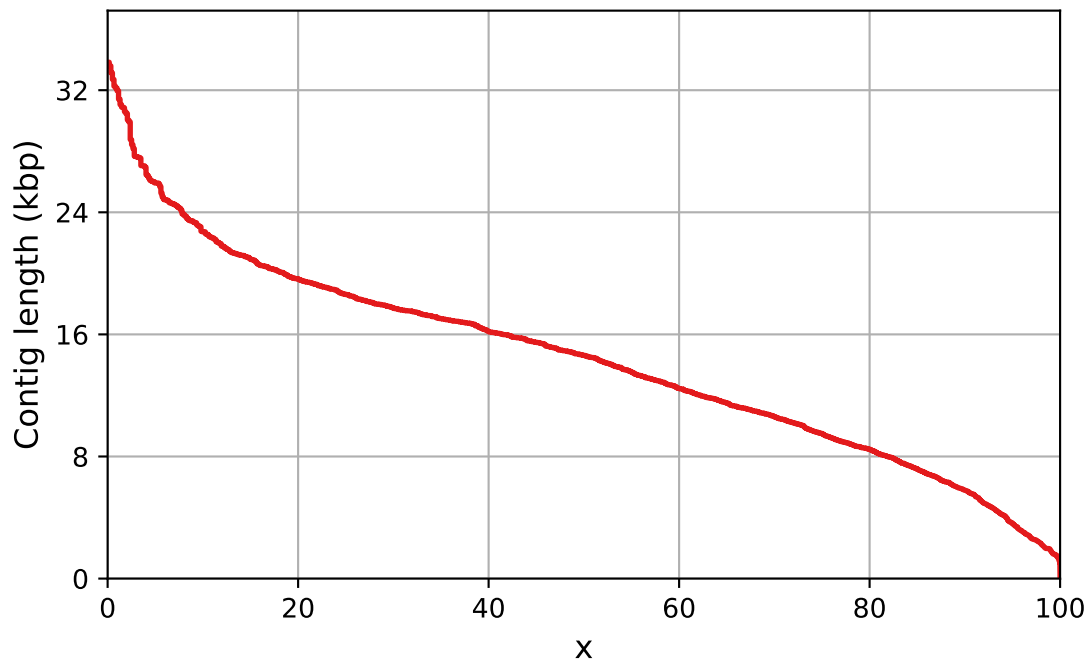
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ218.CanuL.cr
# fully unaligned contigs	127
Fully unaligned length	823980
# partially unaligned contigs	184
Partially unaligned length	632913
# N's	0

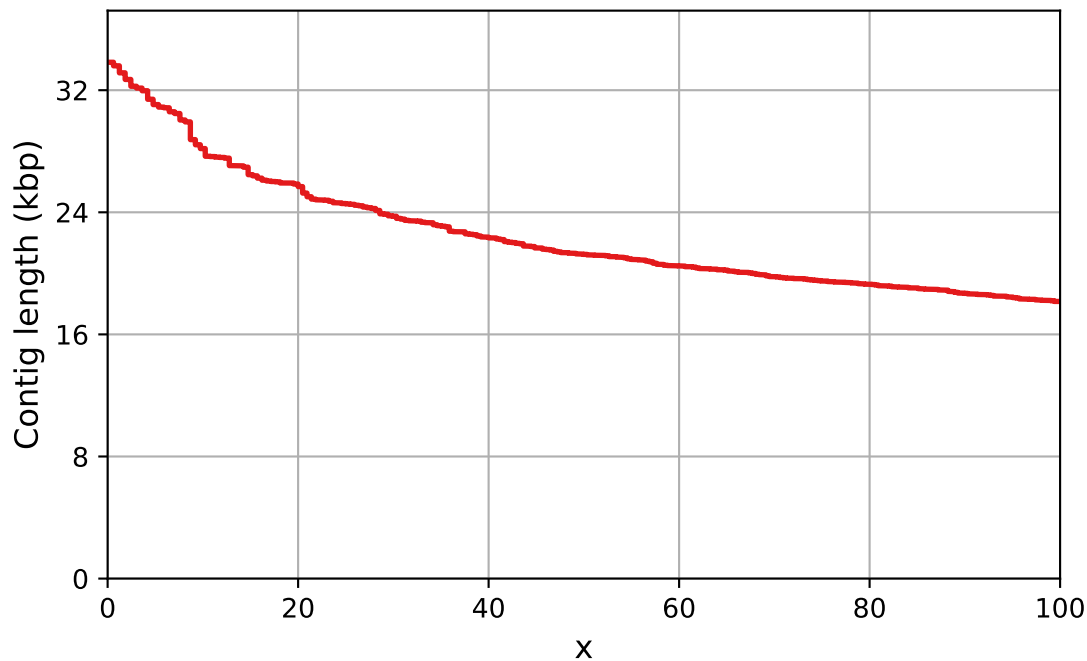
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



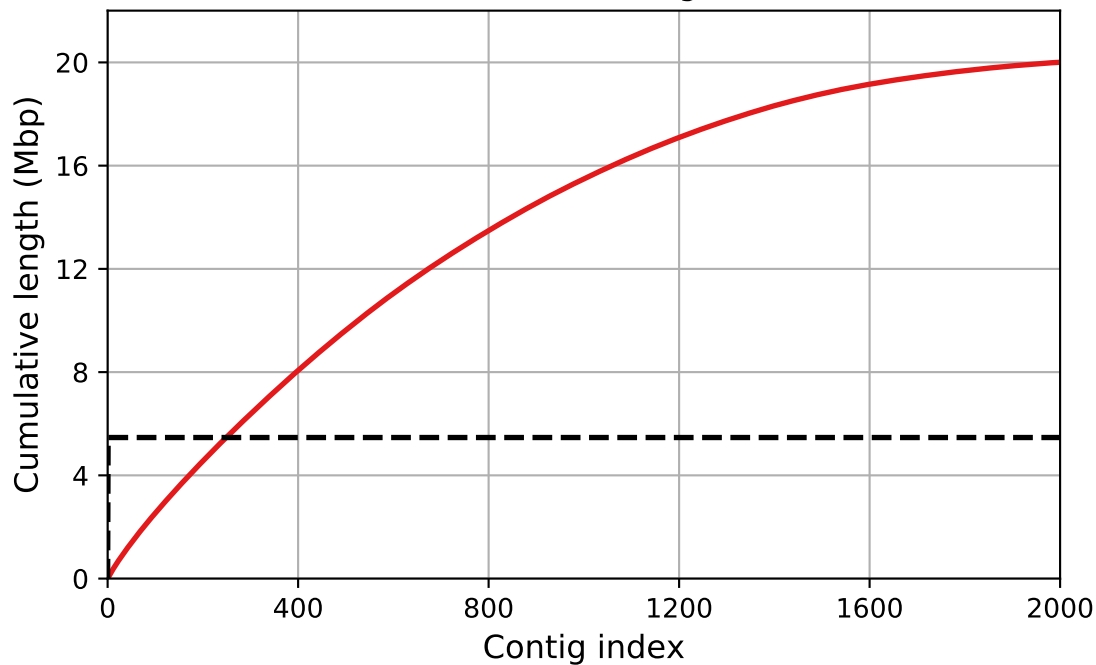
AJ218.CanuL.cr

NGx



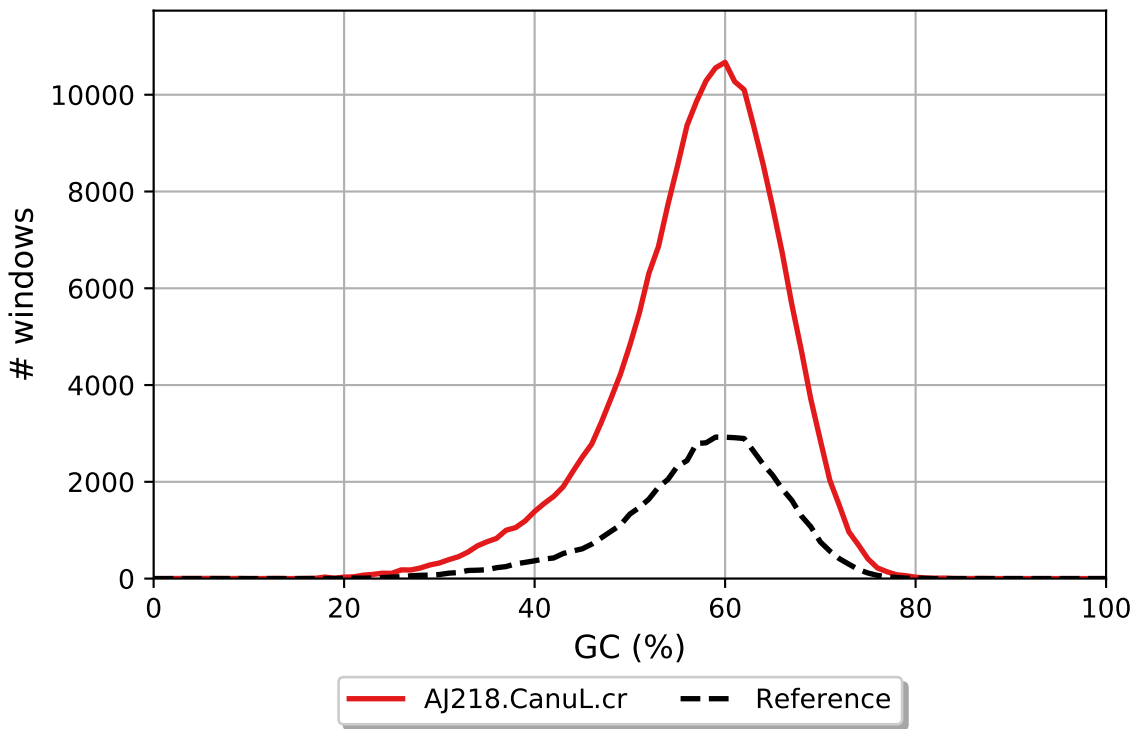
AJ218.CanuL.cr

Cumulative length

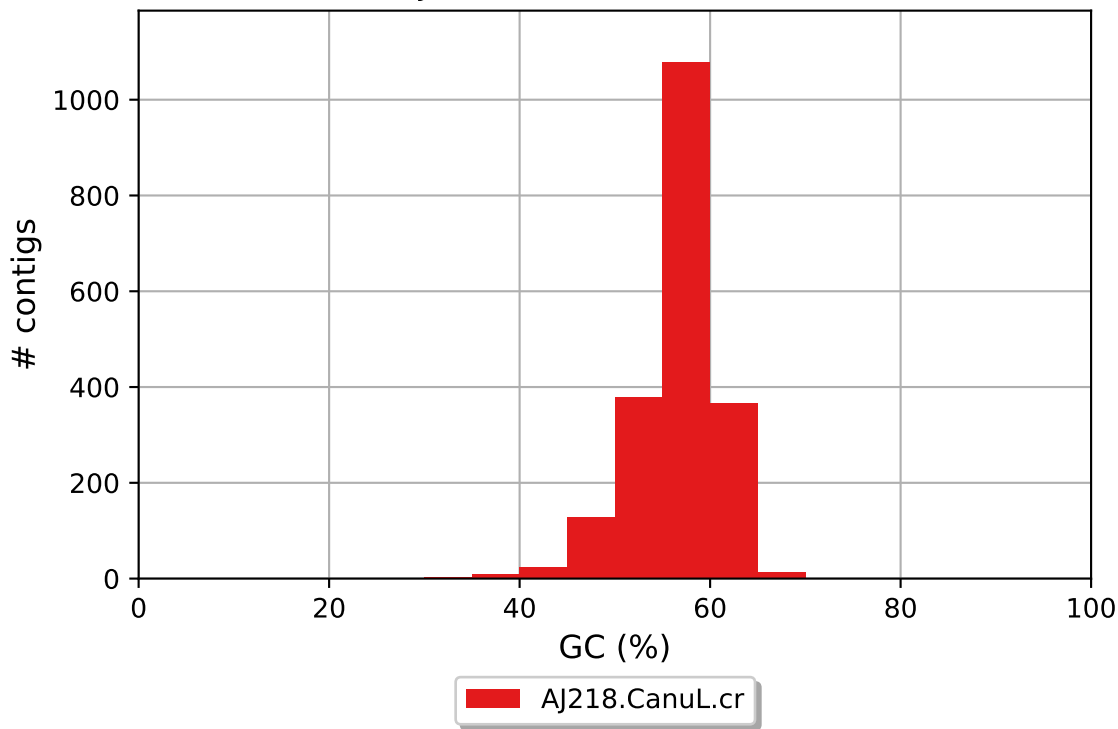


— AJ218.CanuL.cr - - Reference

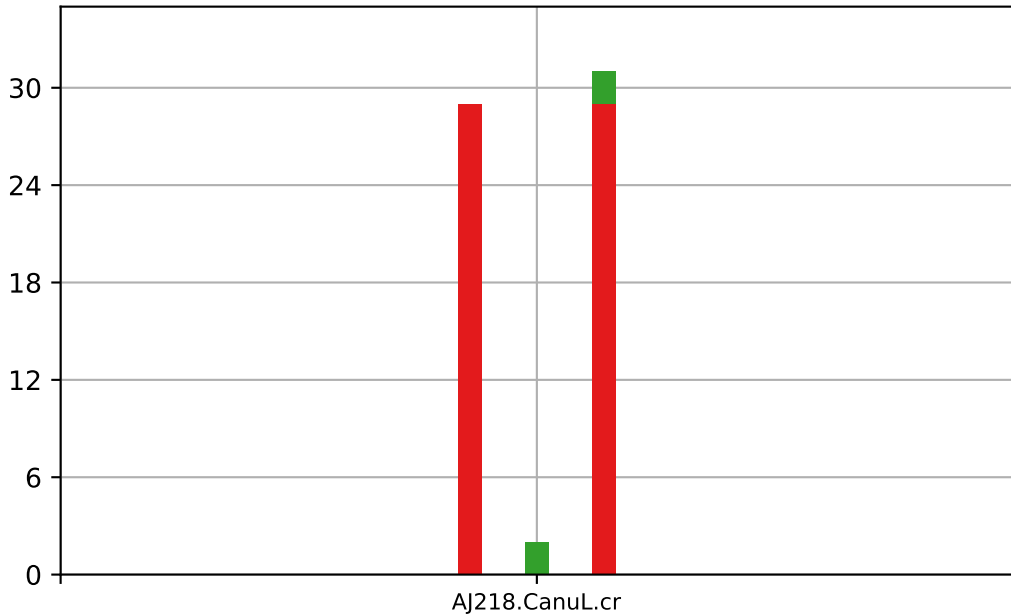
GC content



AJ218.CanuL.cr GC content



Misassemblies

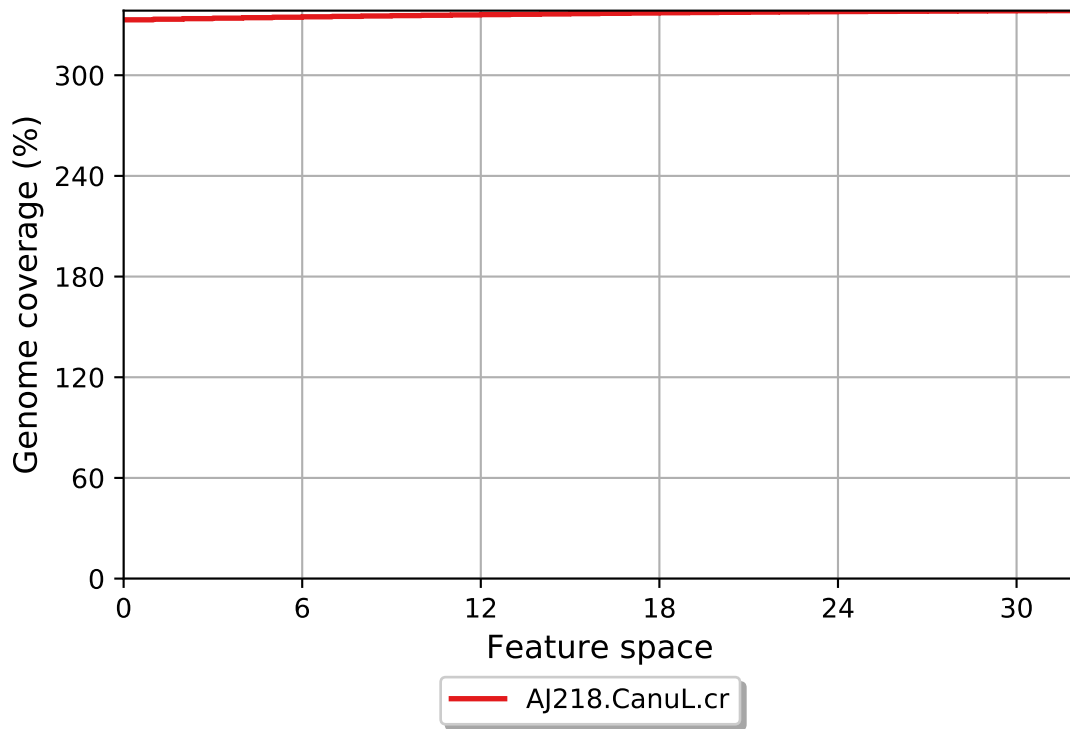


relocations

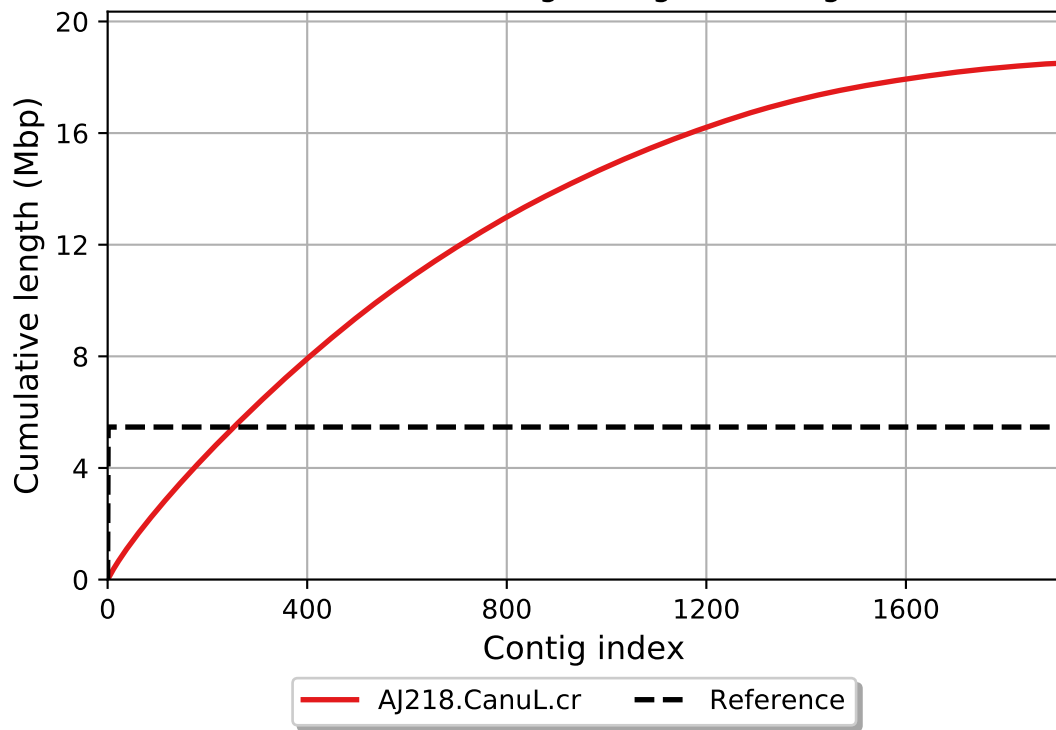


inversions

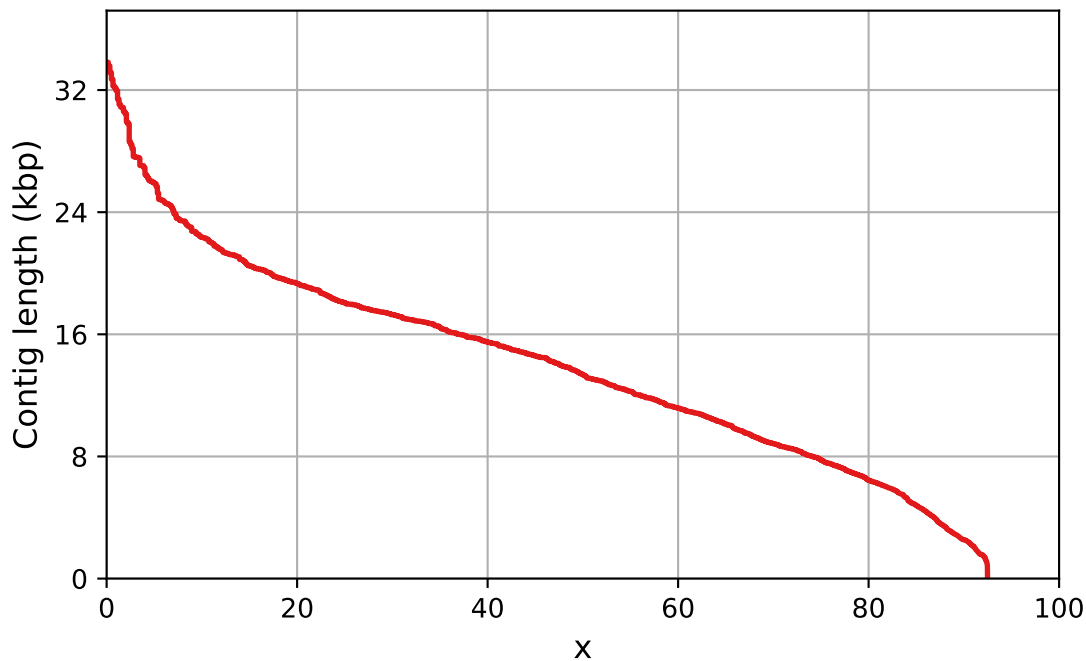
FRCurve (misassemblies)



Cumulative length (aligned contigs)

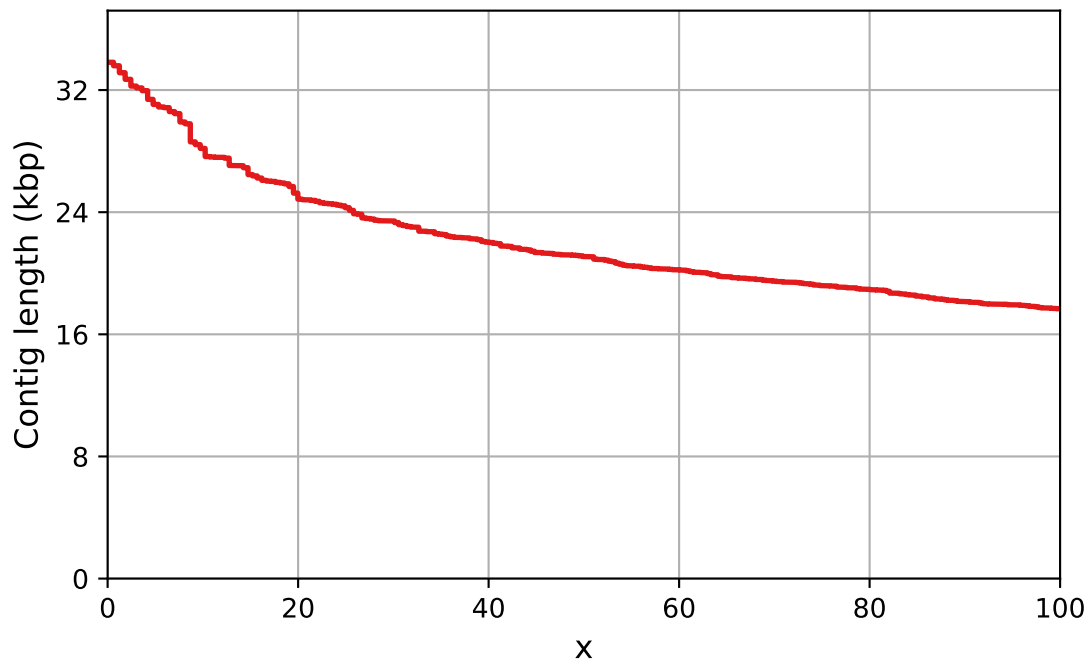


NAx



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NGAx



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