

# Report

	AJ055.Colormap.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1897
# contigs (>= 5000 bp)	1254
# contigs (>= 10000 bp)	777
# contigs (>= 25000 bp)	57
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	18492145
Total length (>= 1000 bp)	18431004
Total length (>= 5000 bp)	16645780
Total length (>= 10000 bp)	13118539
Total length (>= 25000 bp)	1655083
Total length (>= 50000 bp)	0
# contigs	1964
Largest contig	41426
Total length	18481489
Reference length	5504133
GC (%)	57.06
Reference GC (%)	57.38
N50	14711
NG50	22573
N75	9183
NG75	20663
L50	460
LG50	104
L75	855
LG75	168
# misassemblies	119
# misassembled contigs	102
Misassembled contigs length	1344865
# local misassemblies	680
# unaligned mis. contigs	36
# unaligned contigs	272 + 304 part
Unaligned length	2760429
Genome fraction (%)	92.462
Duplication ratio	3.089
# N's per 100 kbp	0.00
# mismatches per 100 kbp	90.27
# indels per 100 kbp	98.90
Largest alignment	35746
Total aligned length	15647996
NA50	11467
NGA50	20488
NA75	4954
NGA75	18477
LA50	533
LGA50	115
LA75	1114
LGA75	186

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

	AJ055.Colormap.cr
# misassemblies	119
# relocations	103
# translocations	0
# inversions	16
# misassembled contigs	102
Misassembled contigs length	1344865
# local misassemblies	680
# unaligned mis. contigs	36
# mismatches	4594
# indels	5033
# indels ( $\leq 5$ bp)	4801
# indels ( $> 5$ bp)	232
Indels length	16462

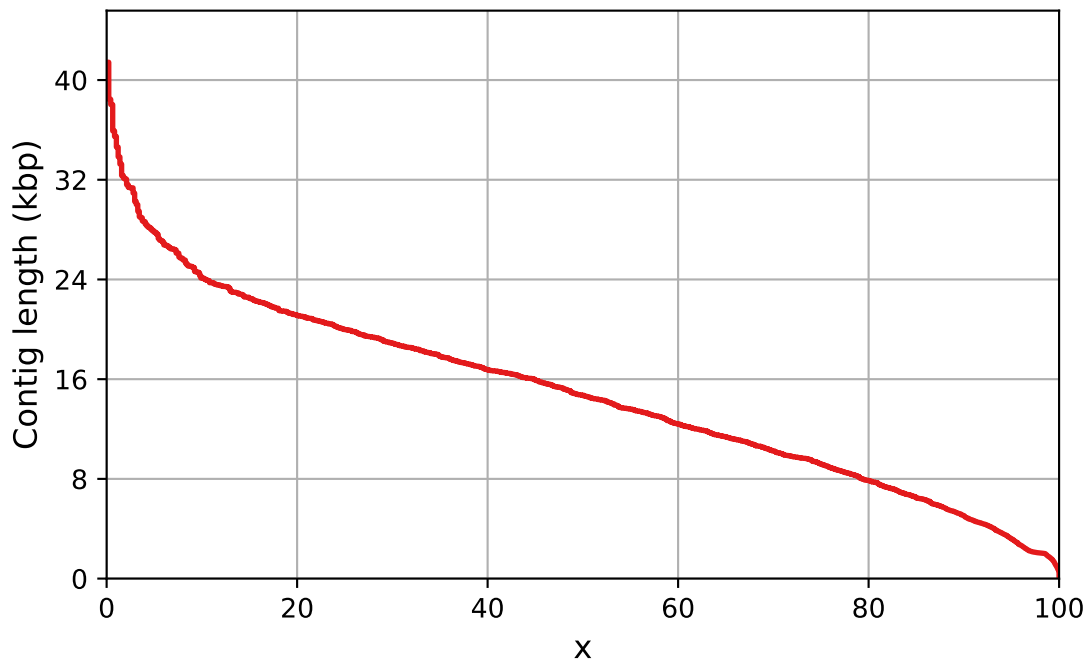
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ055.Colormap.cr
# fully unaligned contigs	272
Fully unaligned length	1465153
# partially unaligned contigs	304
Partially unaligned length	1295276
# N's	0

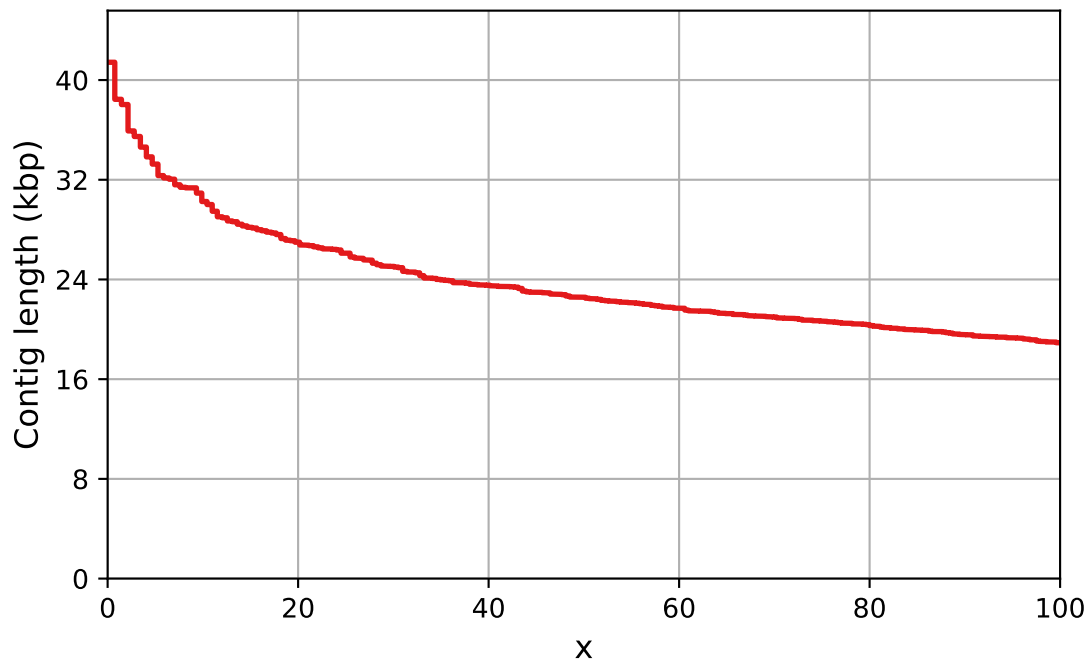
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



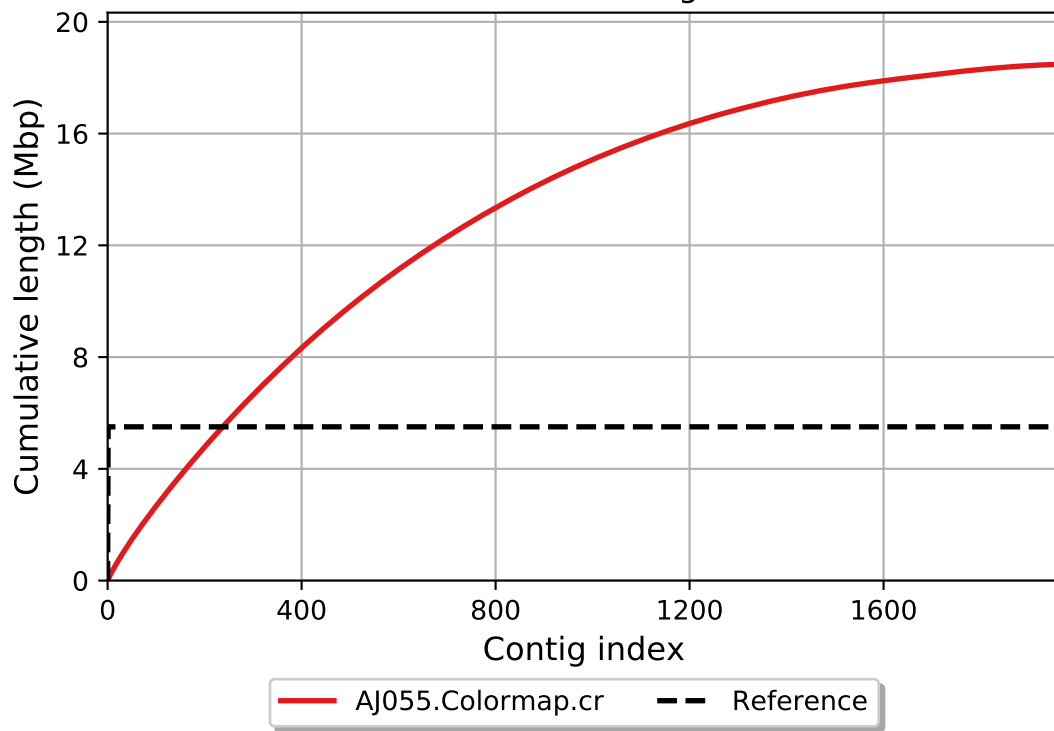
Aj055.Colormap.cr

NGx

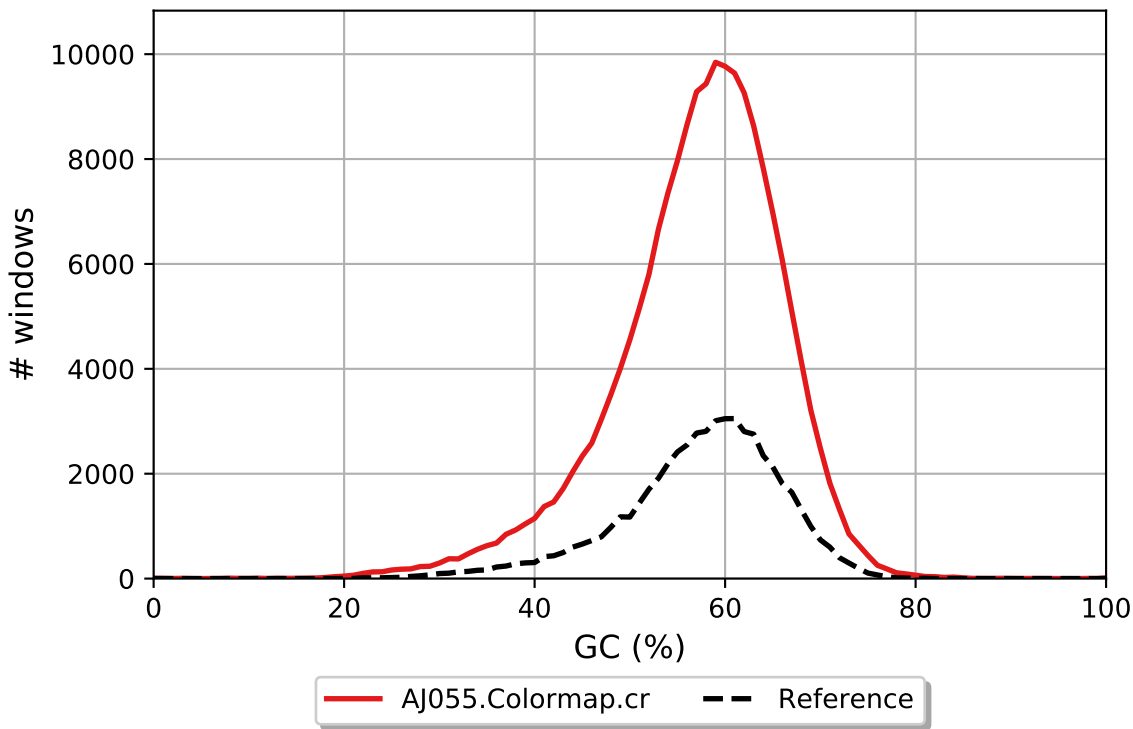


AJ055.Colormap.cr

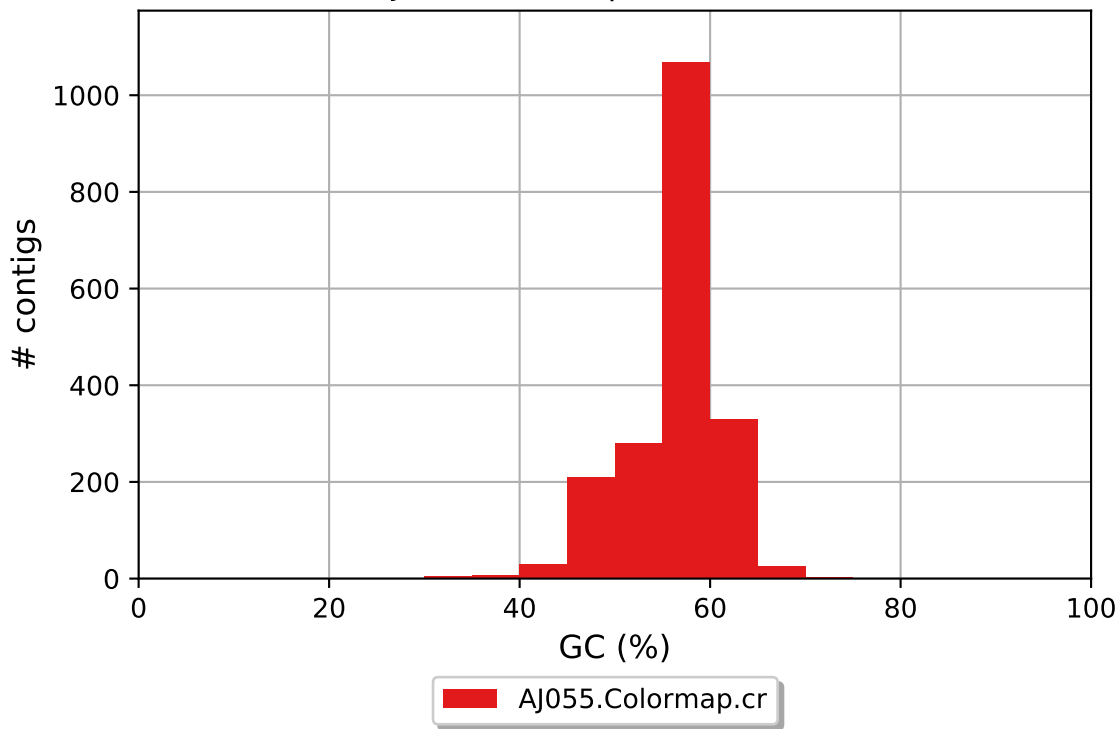
Cumulative length



# GC content

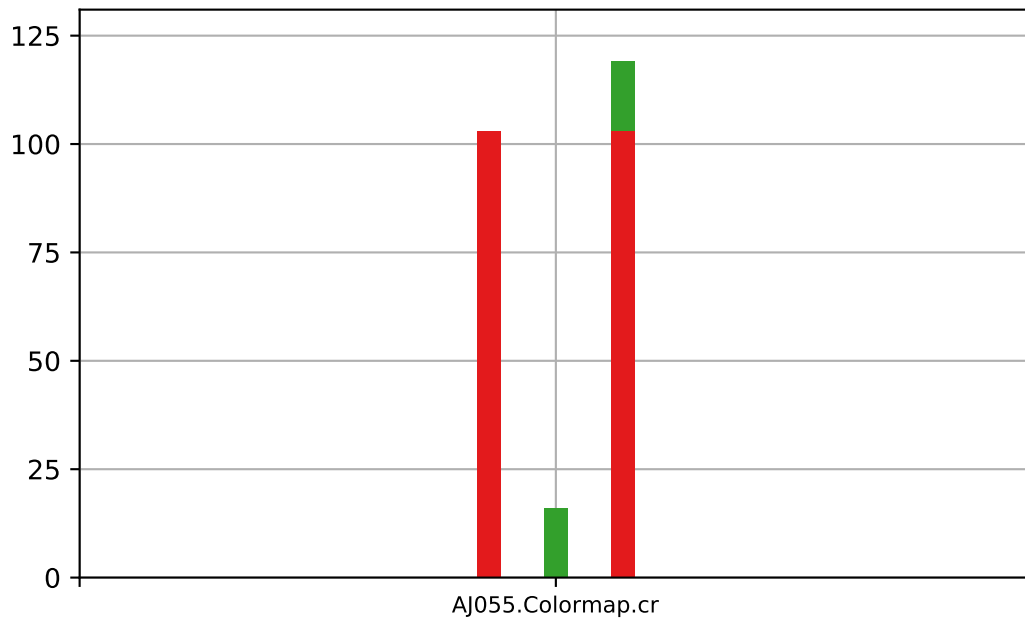


AJ055.Colormap.cr GC content





## Misassemblies

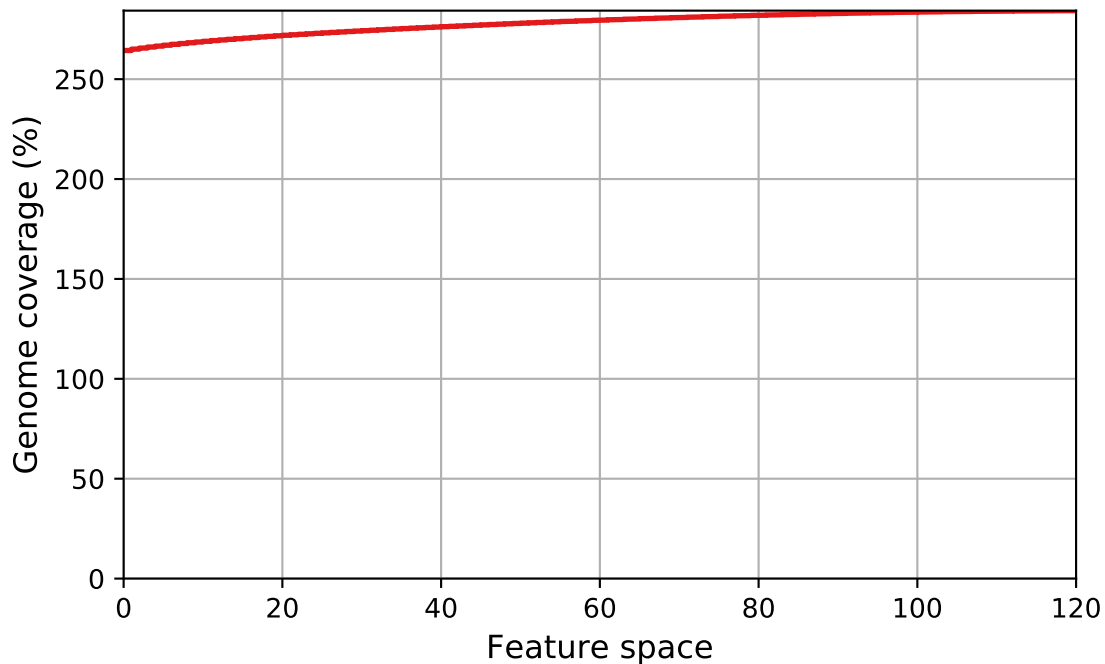


# relocations



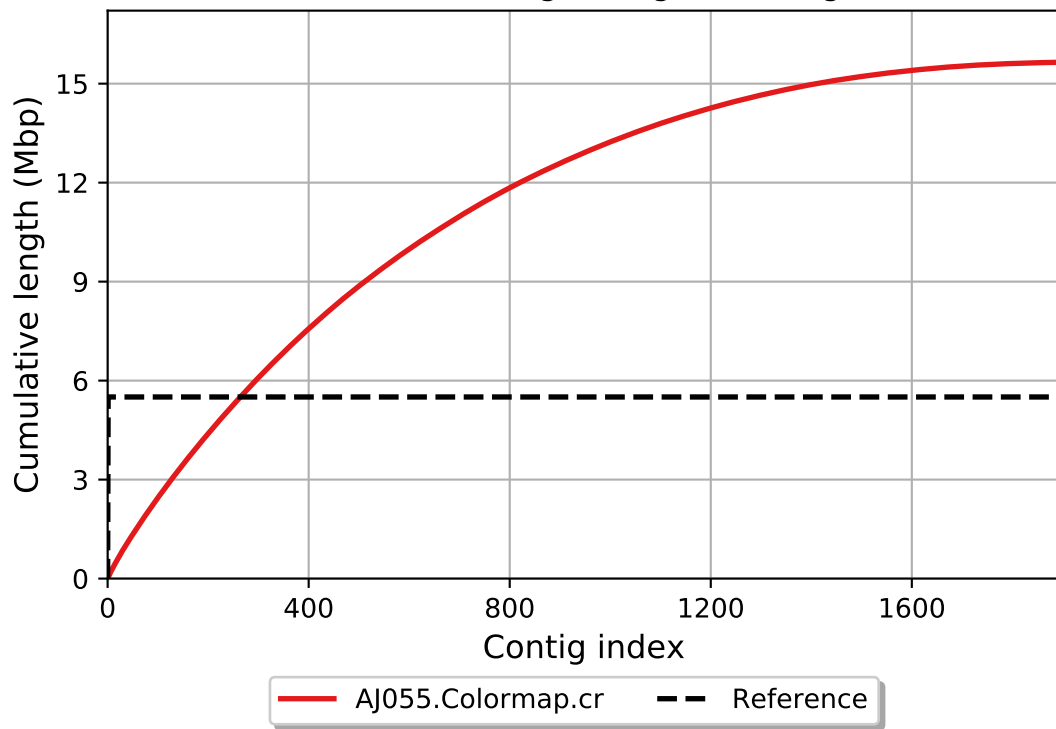
# inversions

FRCurve (misassemblies)

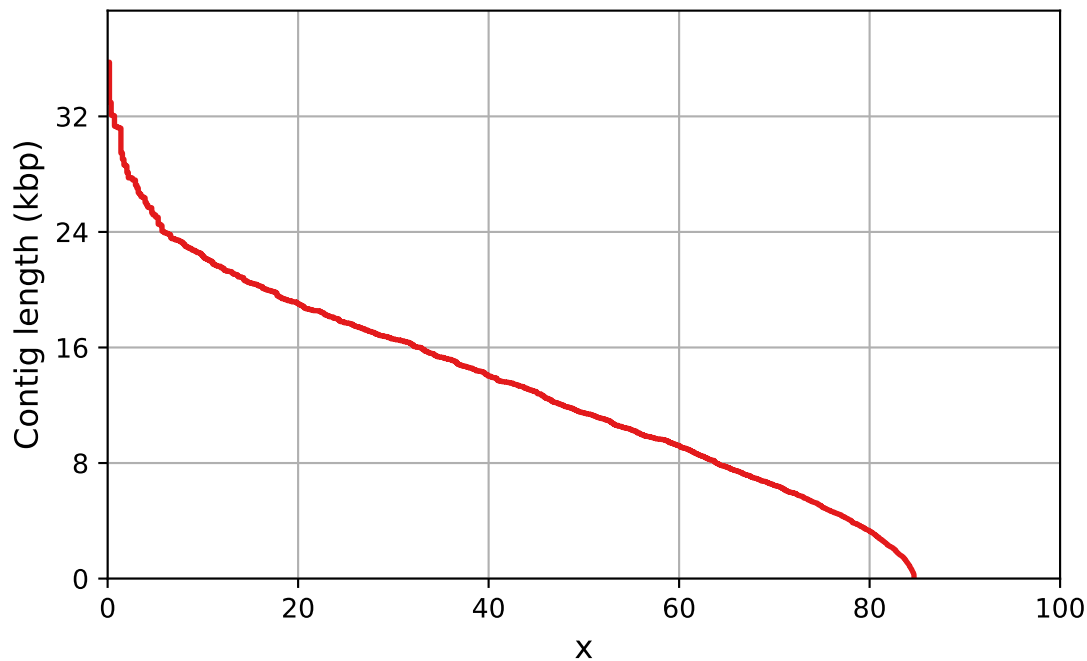


Aj055.Colormap.cr

Cumulative length (aligned contigs)

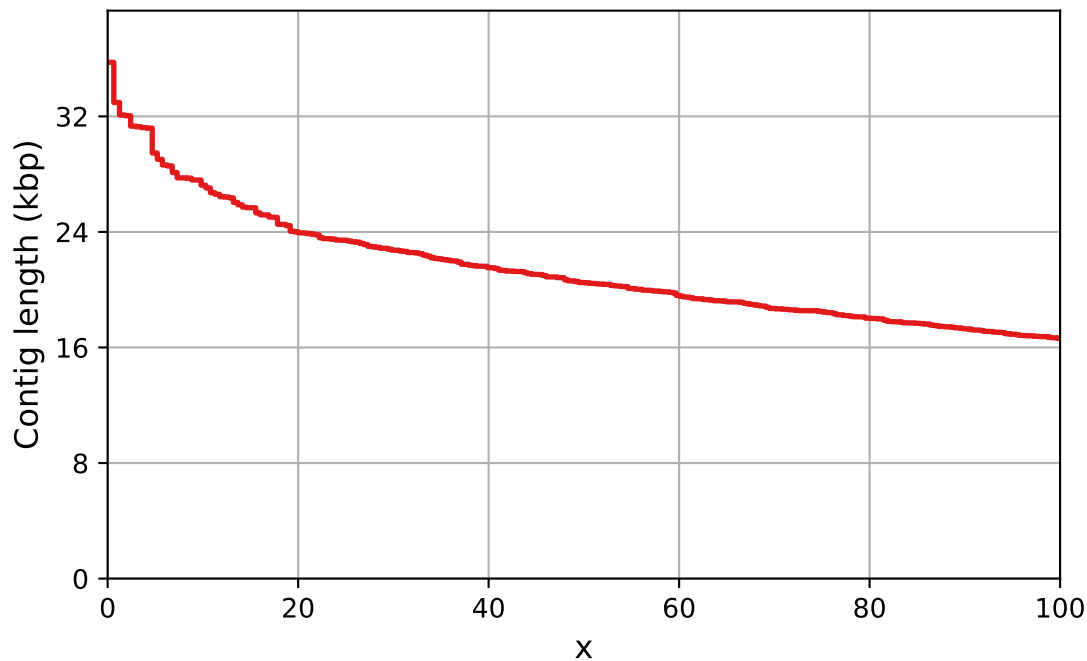


NAx



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## NGAx



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