

Report

	SRR15131330-contigs_abyss_fa
# contigs (≥ 0 bp)	1380
# contigs (≥ 1000 bp)	180
Total length (≥ 0 bp)	1945052
Total length (≥ 1000 bp)	1782714
# contigs	199
Largest contig	55986
Total length	1796916
Reference length	2191149
GC (%)	36.67
Reference GC (%)	37.07
N50	17190
NG50	12442
N90	4545
NG90	-
auN	20695.2
auNG	16971.7
L50	31
LG50	45
L90	115
LG90	-
# misassemblies	84
# misassembled contigs	58
Misassembled contigs length	941553
# local misassemblies	19
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	15 + 47 part
Unaligned length	150800
Genome fraction (%)	76.388
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	385.09
# indels per 100 kbp	39.83
Largest alignment	46855
Total aligned length	1637026
NA50	10446
NGA50	7249
NA90	896
NGA90	-
auNA	14307.6
auNGA	11733.4
LA50	46
LGA50	70
LA90	227
LGA90	-

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

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# misassemblies	84
# contig misassemblies	84
# c. relocations	83
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	58
Misassembled contigs length	941553
# local misassemblies	19
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	6304
# indels	652
# indels (<= 5 bp)	489
# indels (> 5 bp)	163
Indels length	4904

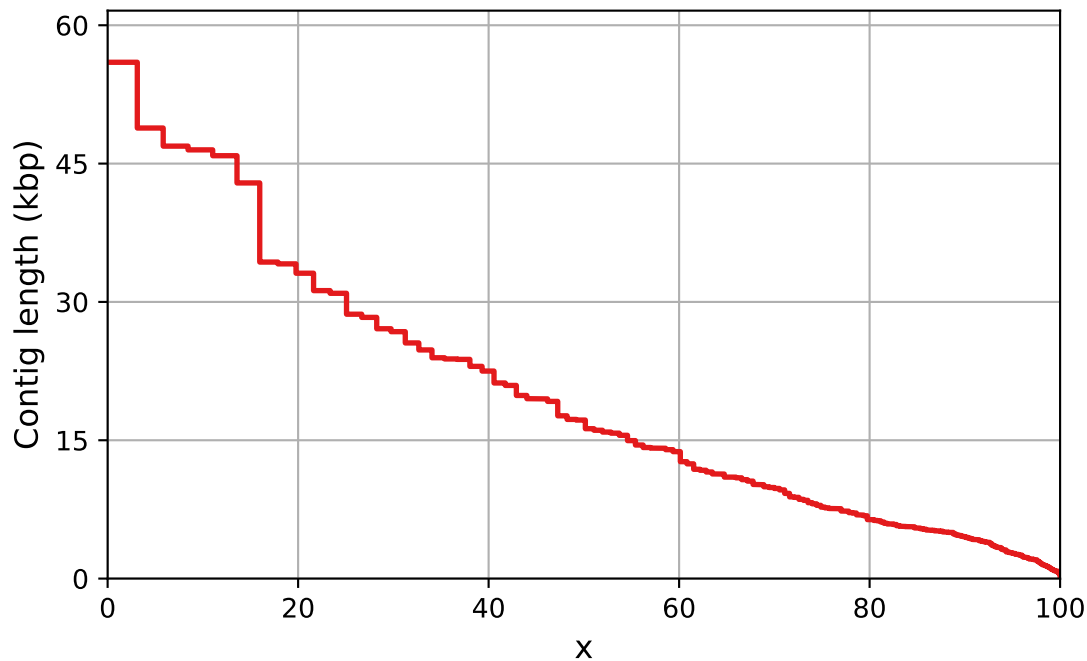
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	SRR15131330-contigs_abyss_fa
# fully unaligned contigs	15
Fully unaligned length	34772
# partially unaligned contigs	47
Partially unaligned length	116028
# N's	0

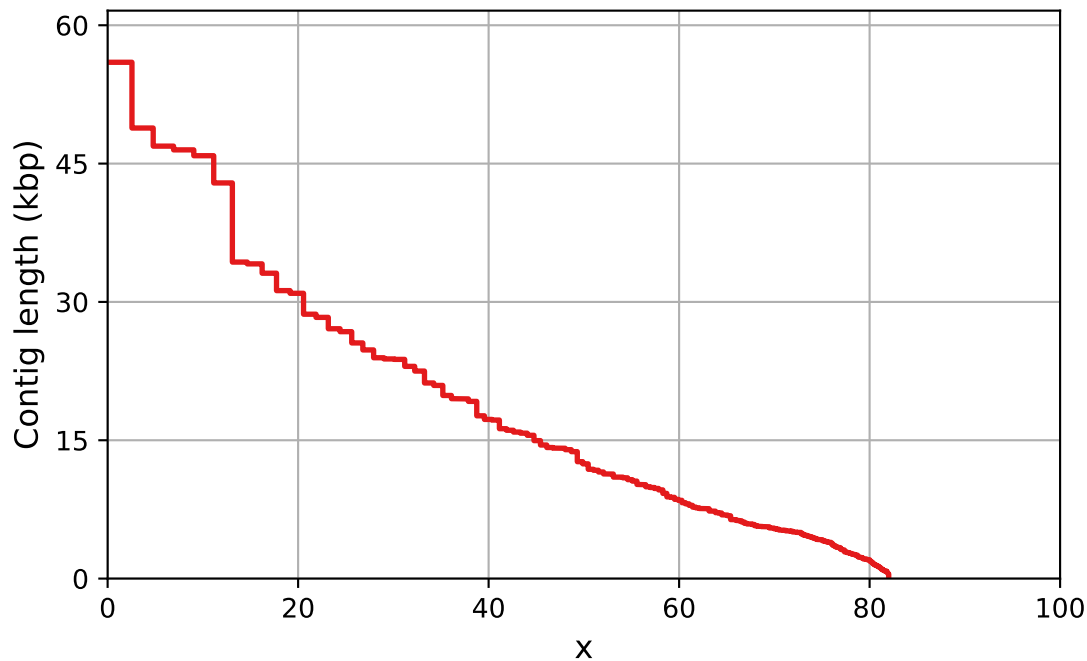
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

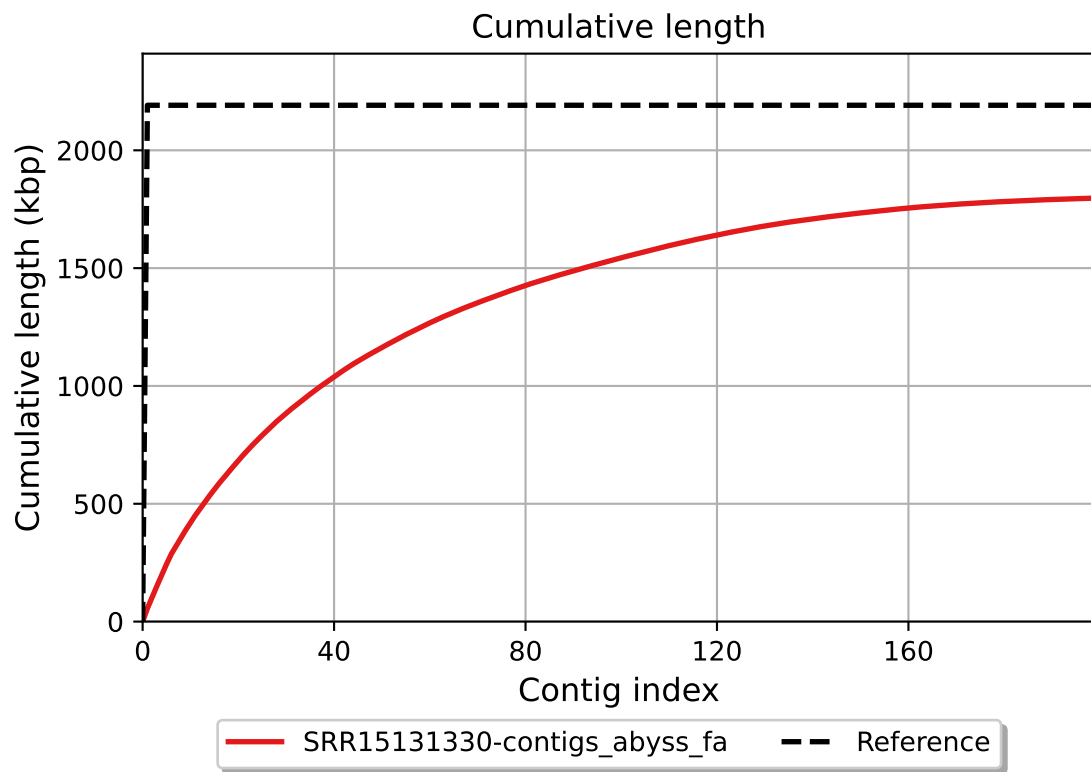


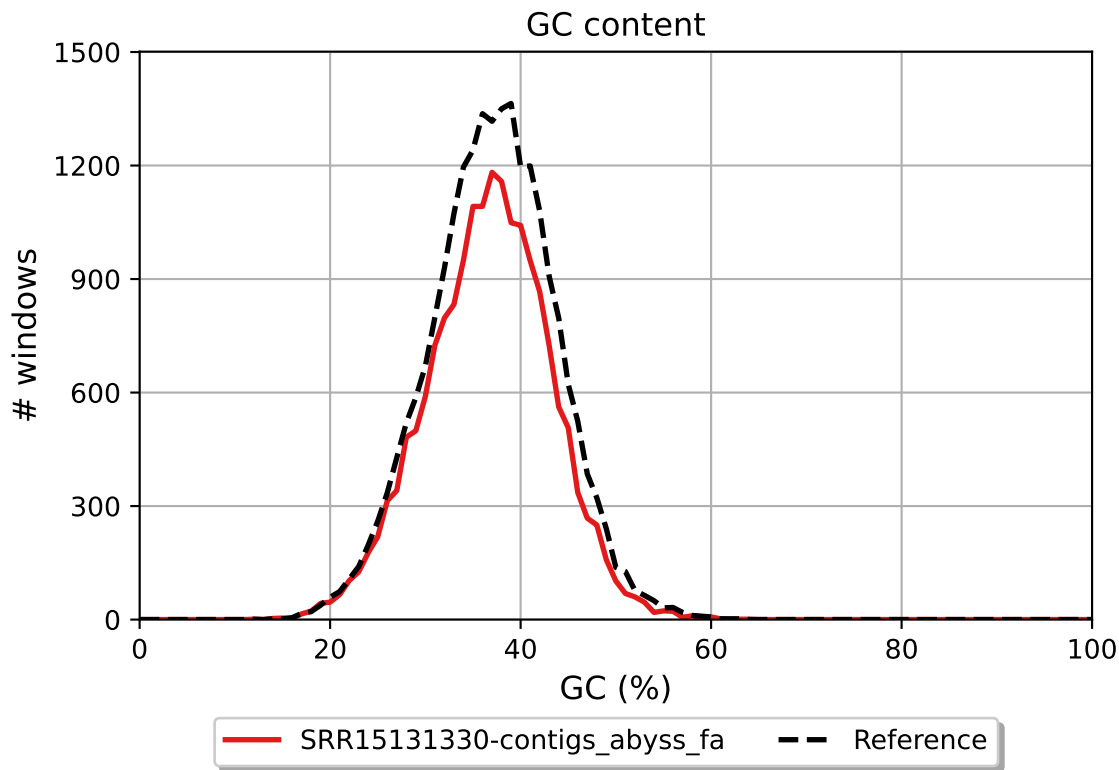
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NGx

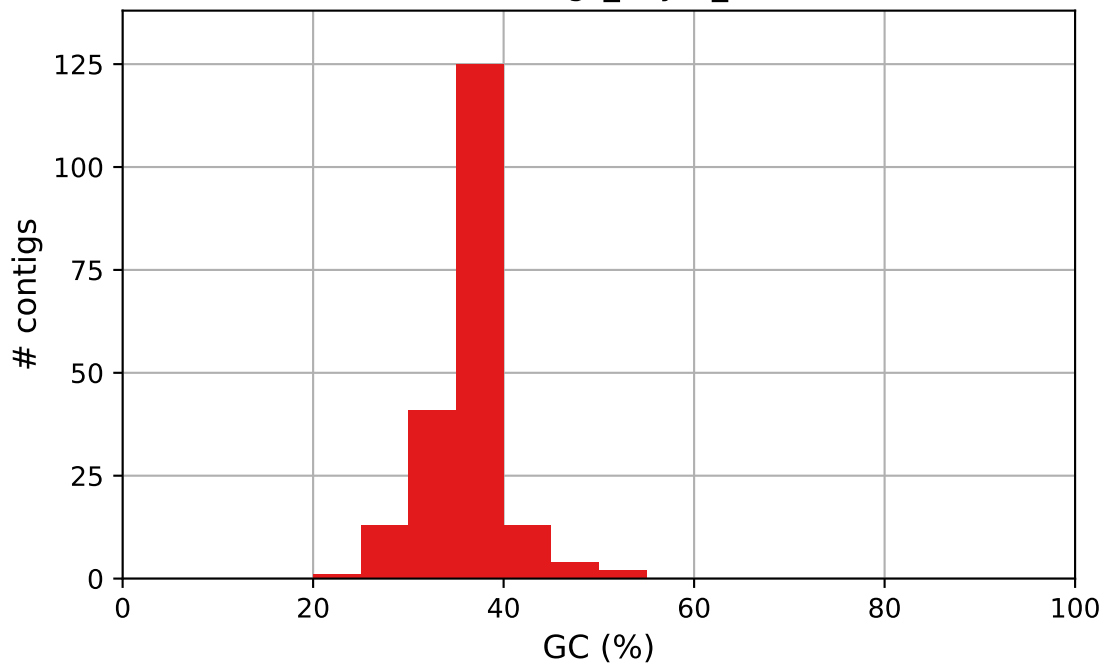


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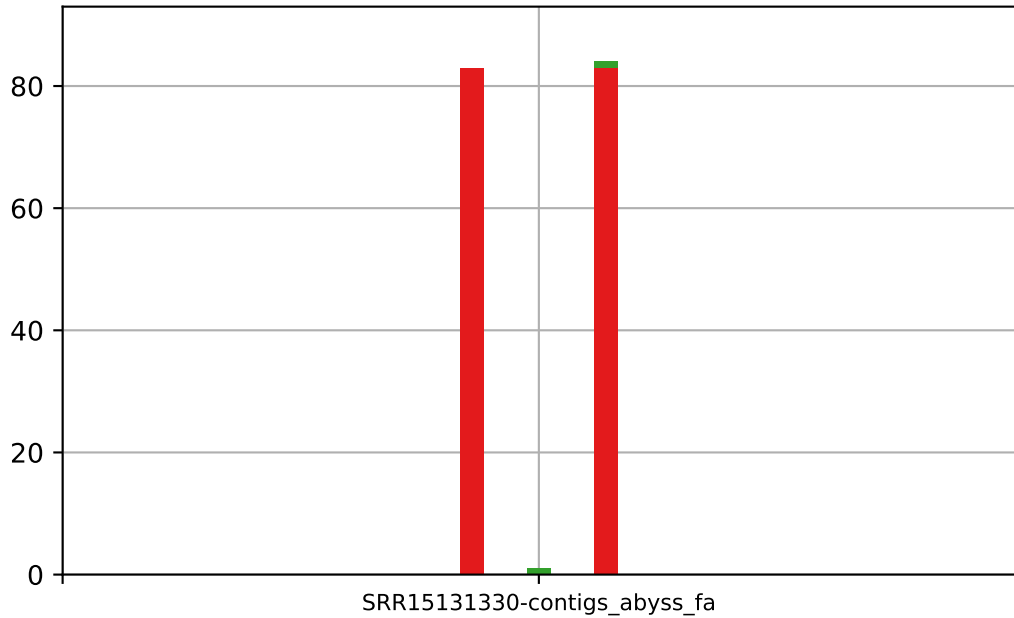


SRR15131330-contigs_abyss_fa GC content

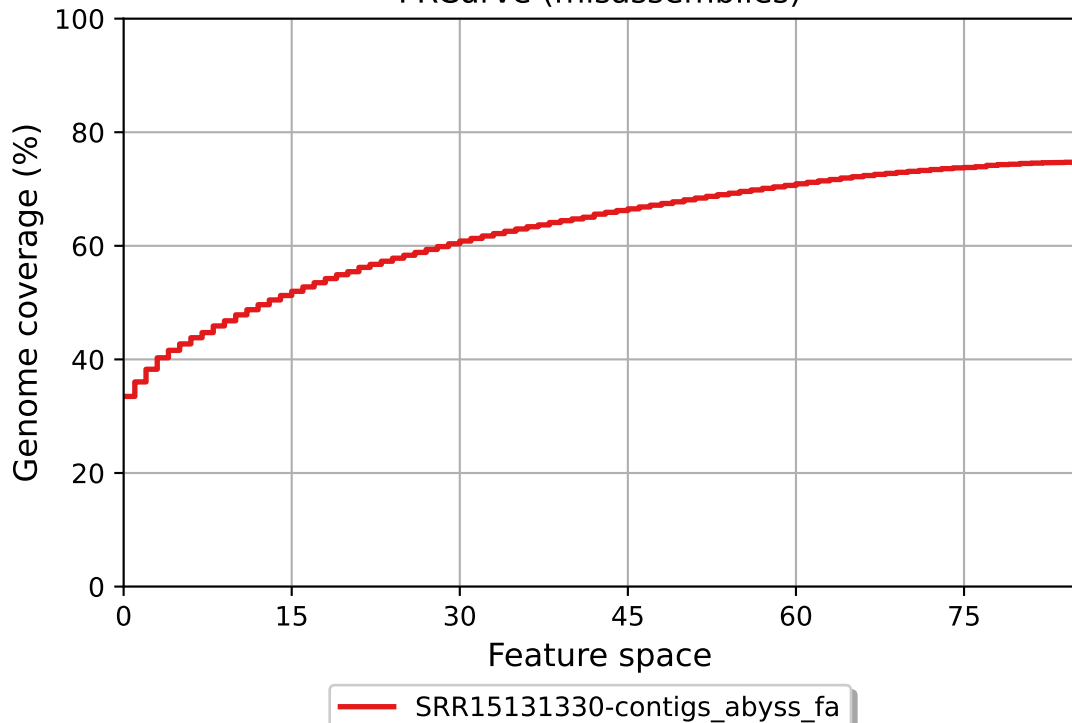


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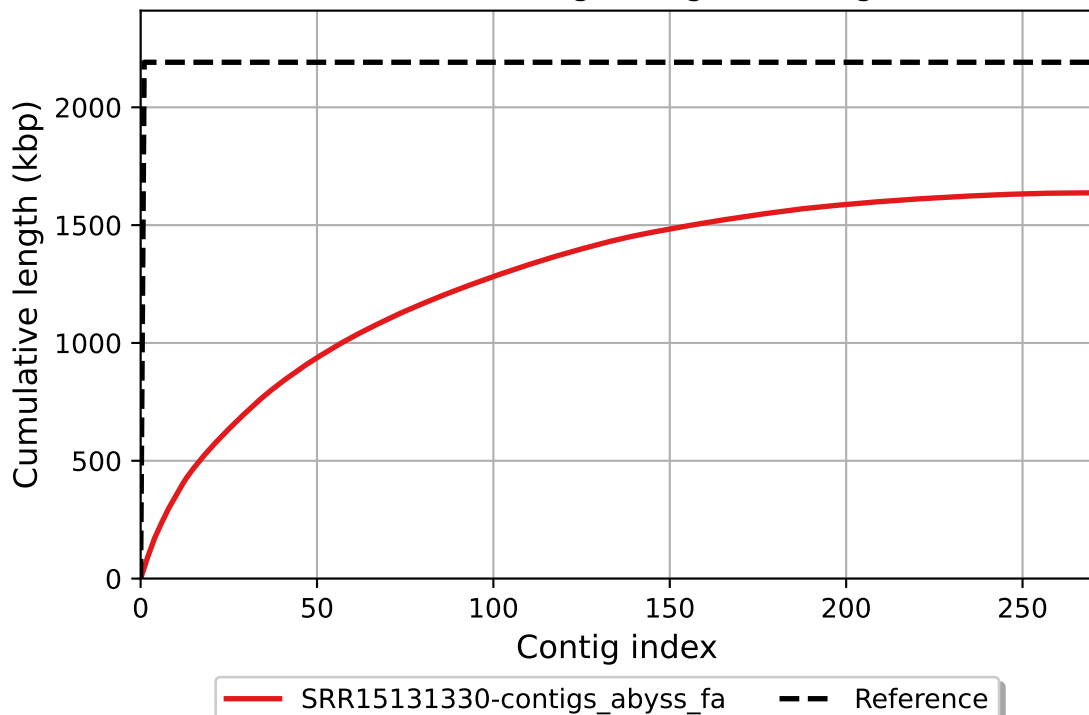
Misassemblies



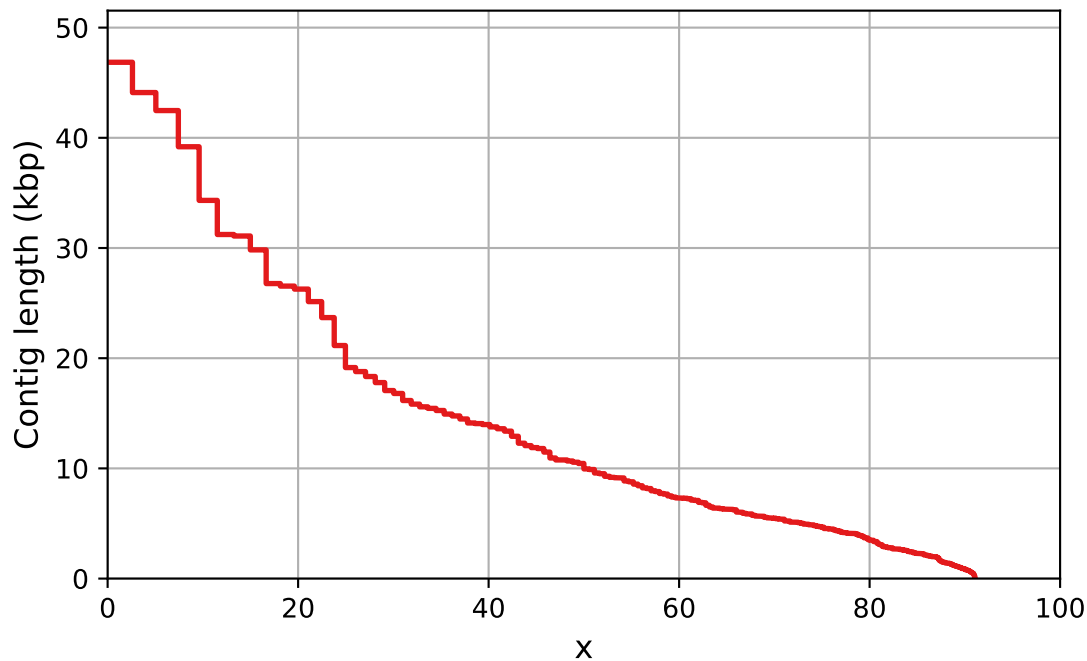
FRCurve (misassemblies)



Cumulative length (aligned contigs)

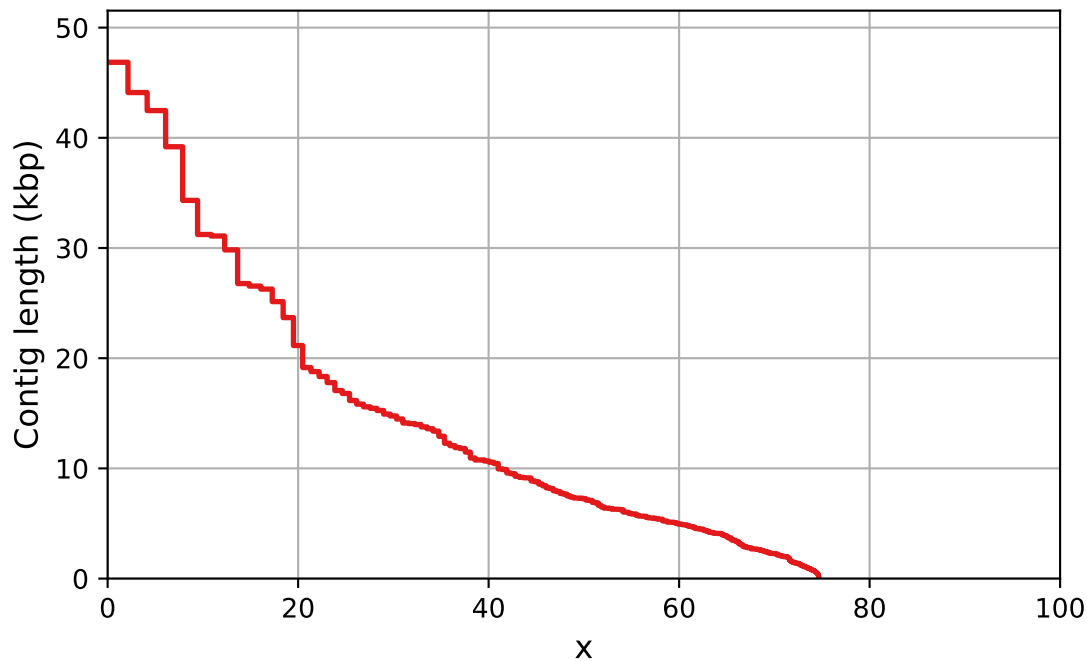


NAx



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NGAx



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