

Report

	SRR13577846
# contigs (>= 0 bp)	49
# contigs (>= 1000 bp)	49
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	21
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	12730920
Total length (>= 1000 bp)	12730920
Total length (>= 5000 bp)	12730920
Total length (>= 10000 bp)	12730920
Total length (>= 25000 bp)	12243602
Total length (>= 50000 bp)	12121907
# contigs	49
Largest contig	1506376
Total length	12730920
Reference length	12157105
GC (%)	38.44
Reference GC (%)	38.15
N50	809047
NG50	809047
N75	579659
NG75	609882
L50	6
LG50	6
L75	11
LG75	10
# misassemblies	124
# misassembled contigs	41
Misassembled contigs length	12606913
# local misassemblies	68
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 17 part
Unaligned length	100841
Genome fraction (%)	97.496
Duplication ratio	1.066
# N's per 100 kbp	0.00
# mismatches per 100 kbp	226.72
# indels per 100 kbp	27.17
Largest alignment	843303
Total aligned length	12617941
NA50	273893
NGA50	284119
NA75	137797
NGA75	168184
LA50	13
LGA50	12
LA75	29
LGA75	26

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

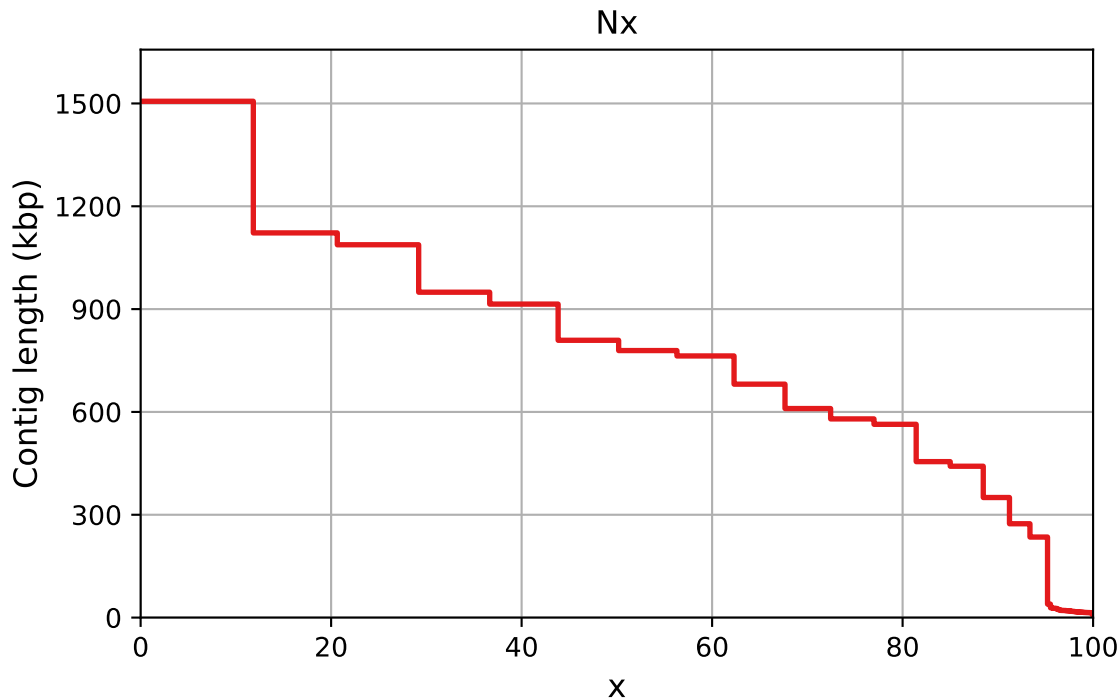
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# misassemblies	124
# contig misassemblies	124
# c. relocations	59
# c. translocations	65
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	41
Misassembled contigs length	12606913
# local misassemblies	68
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	26873
# indels	3220
# indels (<= 5 bp)	2728
# indels (> 5 bp)	492
Indels length	15578

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

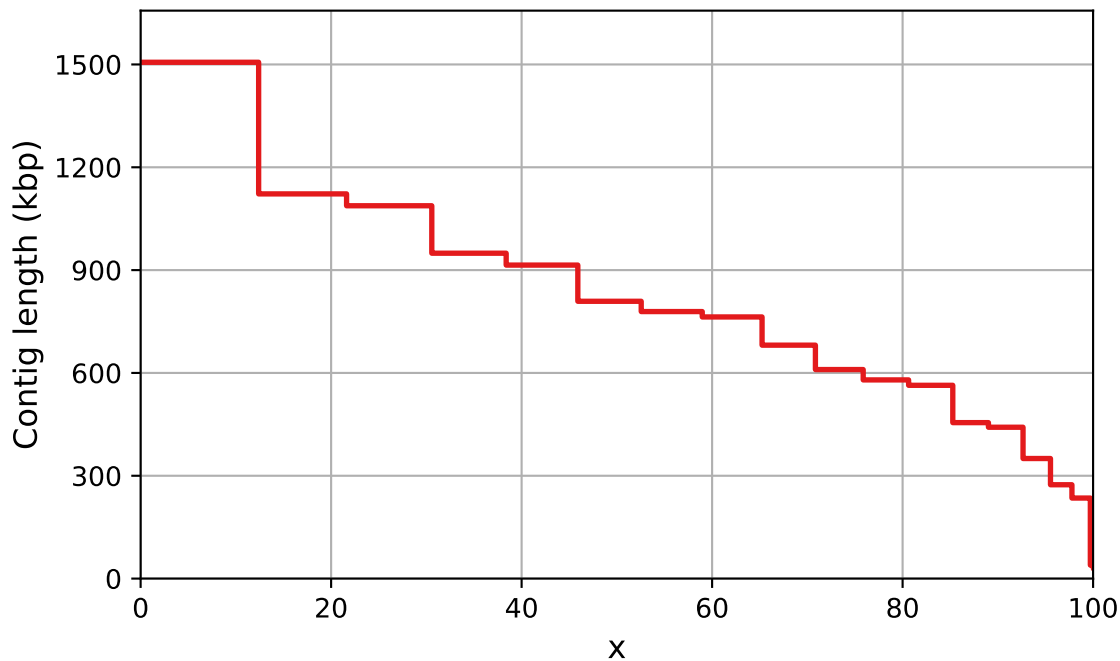
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# fully unaligned contigs	1
Fully unaligned length	16066
# partially unaligned contigs	17
Partially unaligned length	84775
# N's	0

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).



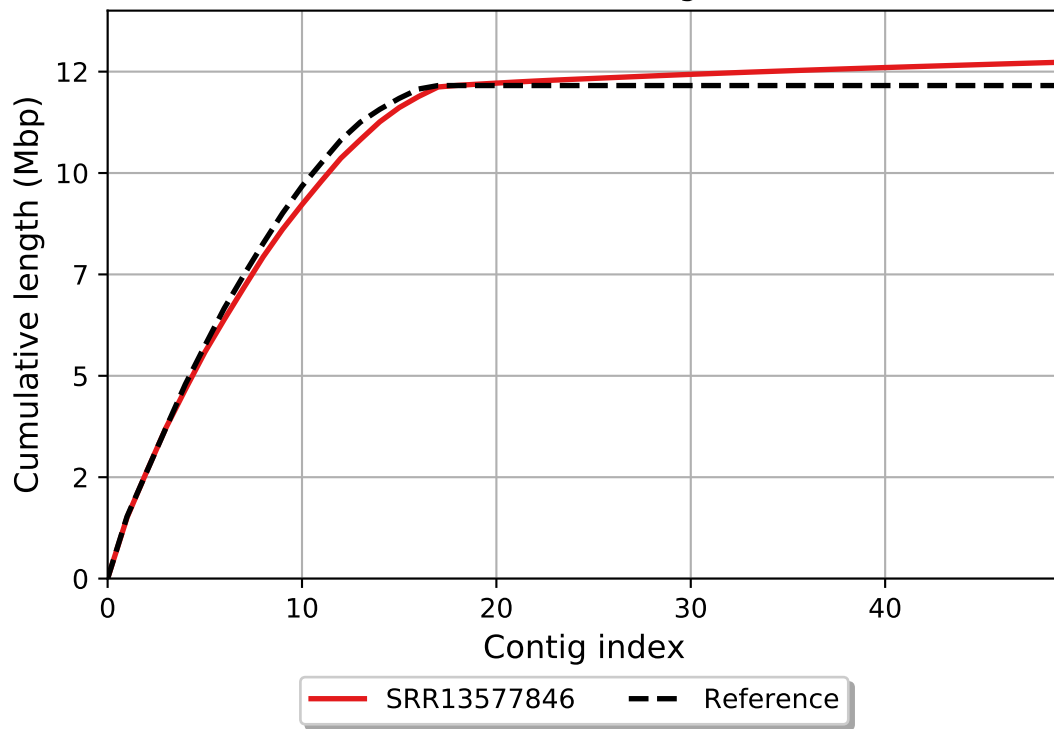
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NGx

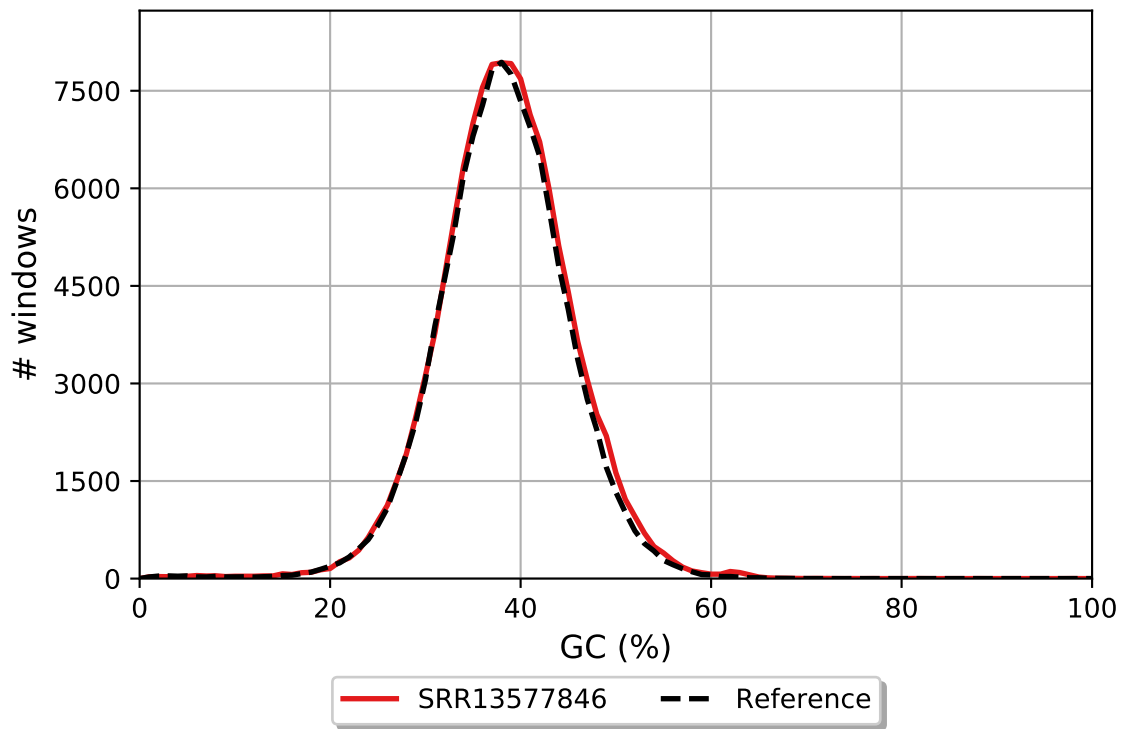


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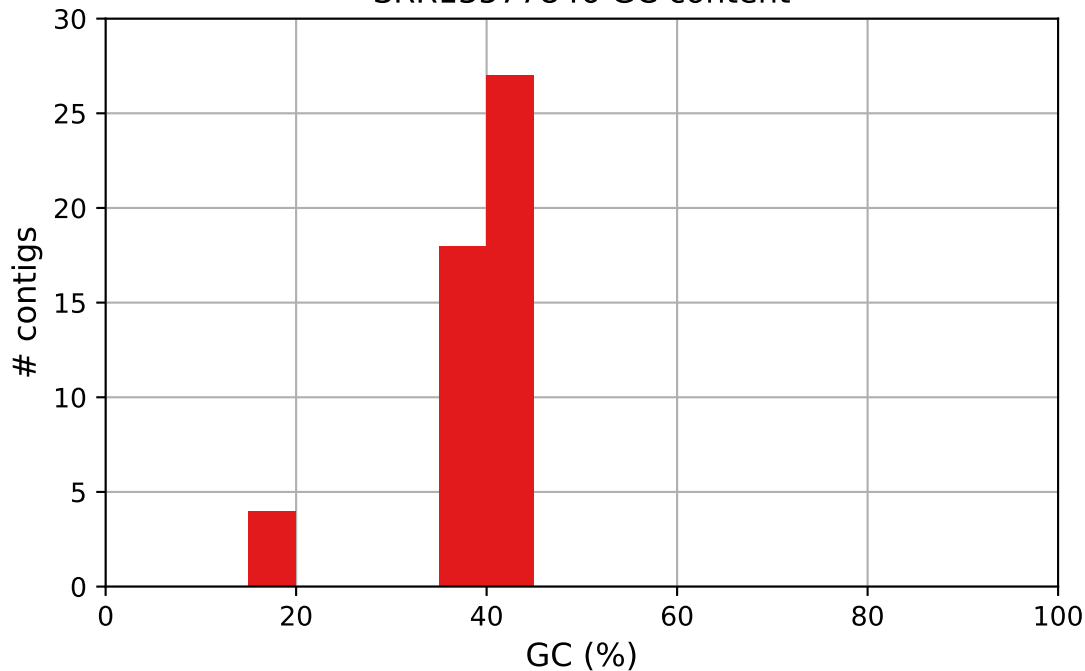
Cumulative length



GC content

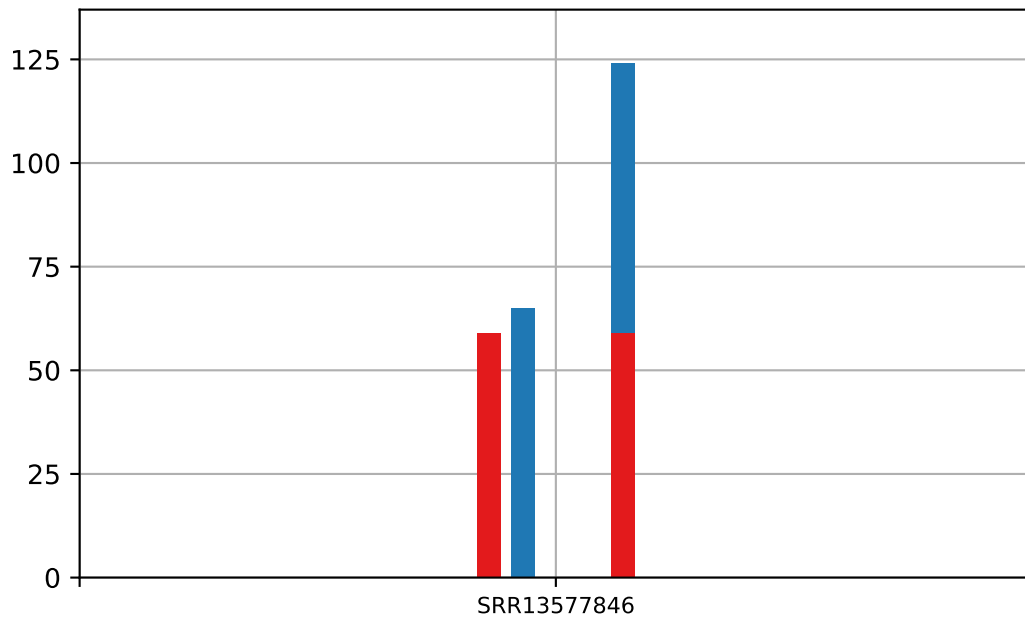


SRR13577846 GC content



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Misassemblies

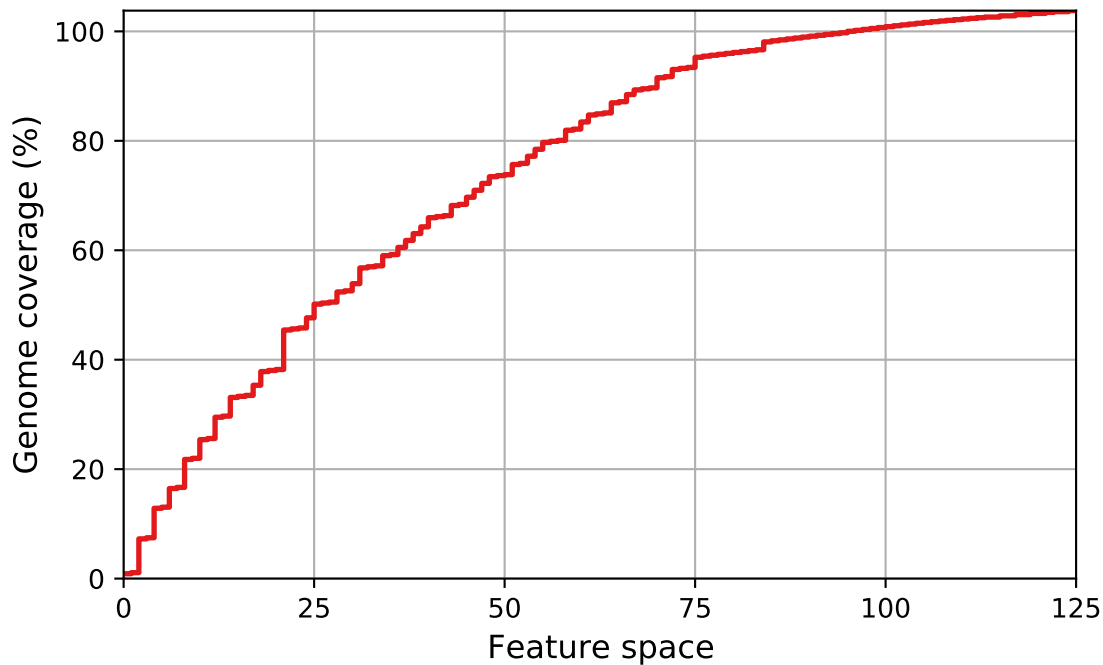


relocations



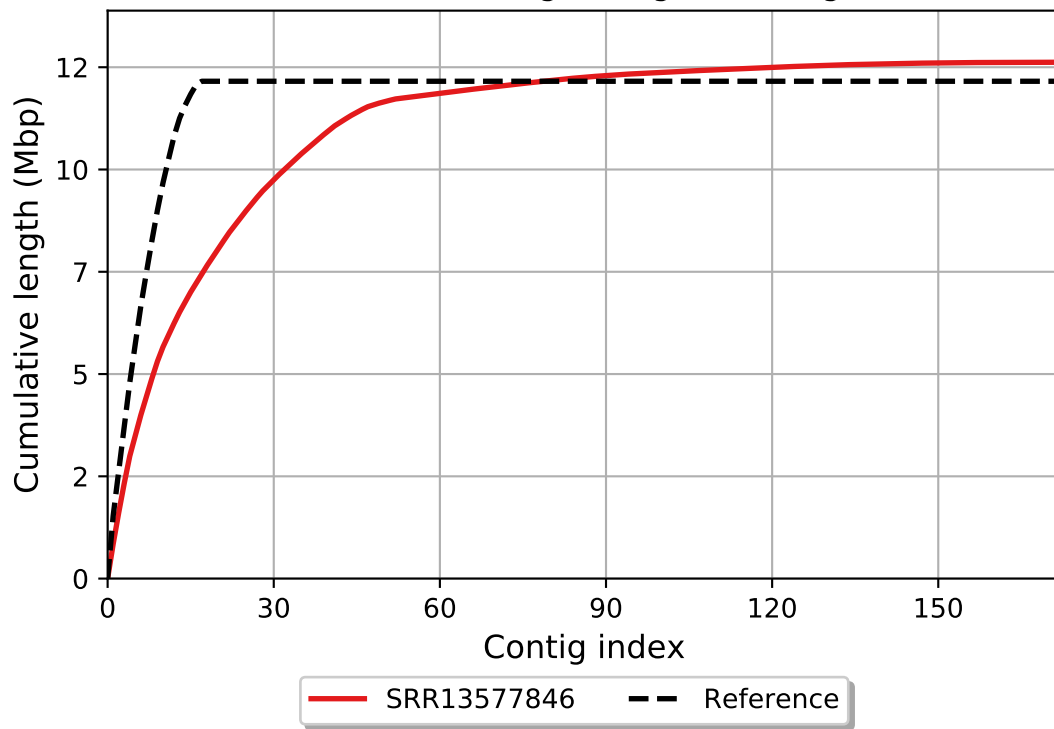
translocations

FRCurve (misassemblies)

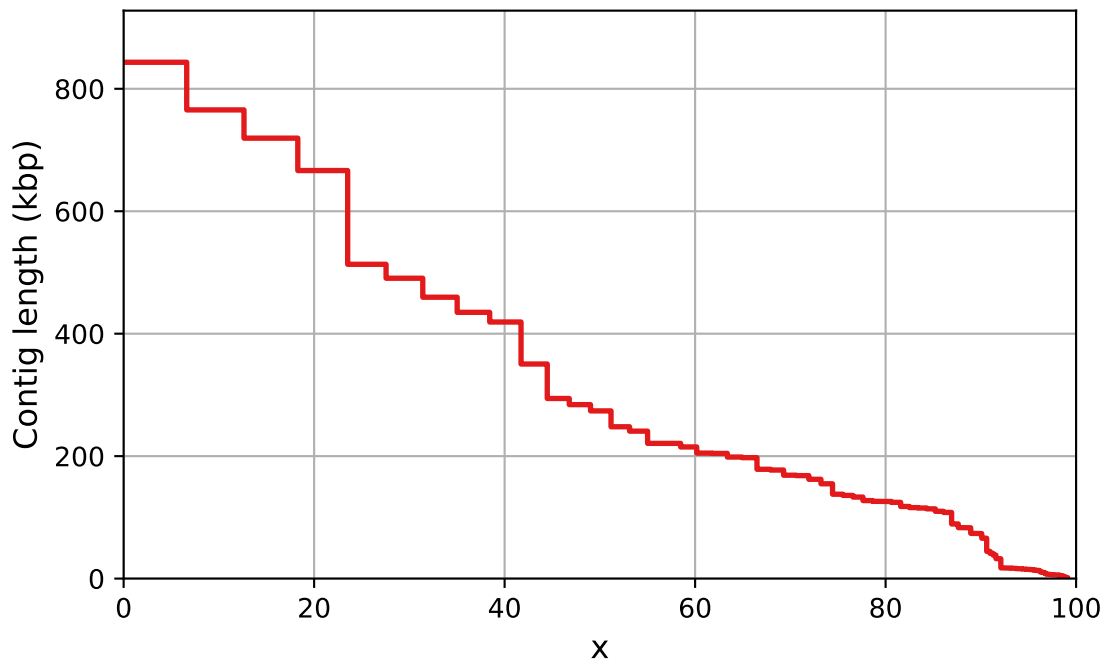


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Cumulative length (aligned contigs)

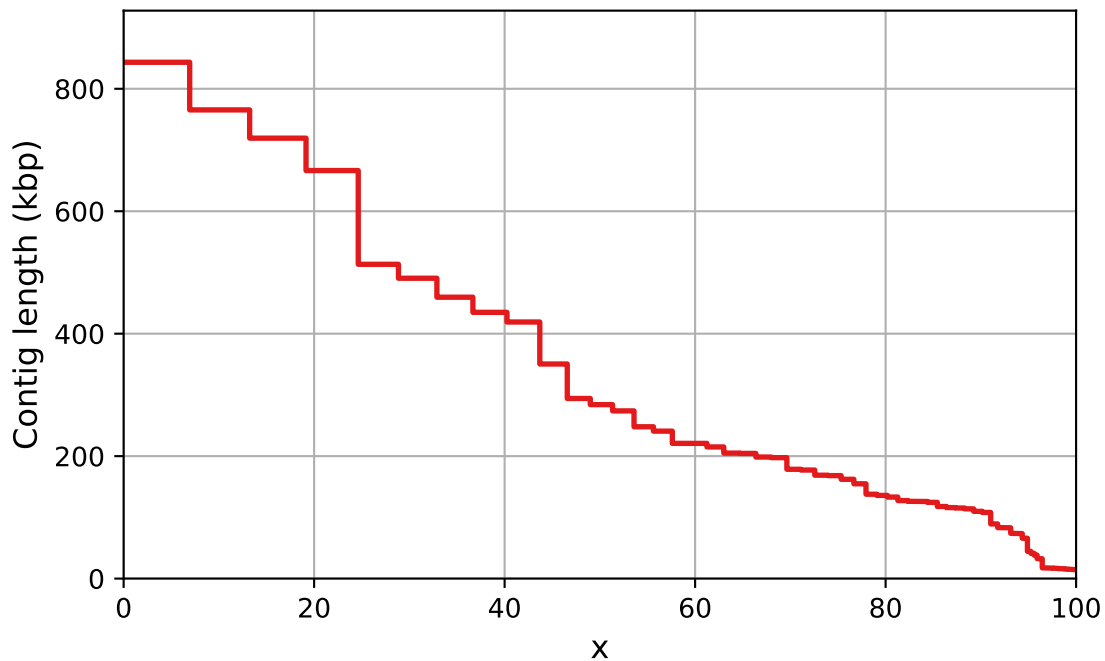


NAx



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NGAx



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