

Report

	pos_sorted_bam_filtered.long
# contigs (≥ 0 bp)	9508
# contigs (≥ 1000 bp)	67
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	2783972
Total length (≥ 1000 bp)	86587
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	682
Largest contig	3116
Total length	486508
Reference length	8771
GC (%)	43.71
Reference GC (%)	48.03
N50	684
NG50	2944
N75	579
NG75	2790
L50	262
LG50	2
L75	455
LG75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	677 + 0 part
Unaligned length	483616
Genome fraction (%)	24.433
Duplication ratio	1.350
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	526
Total aligned length	2143
NGA50	-

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

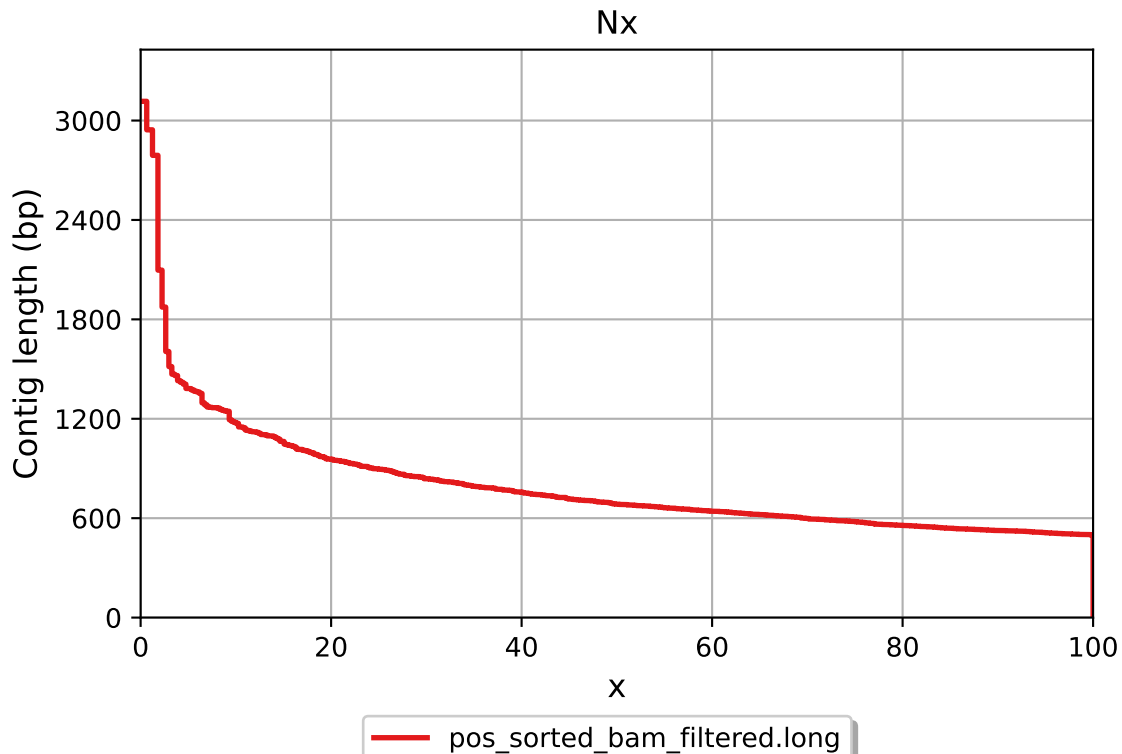
	pos_sorted_bam_filtered.long
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

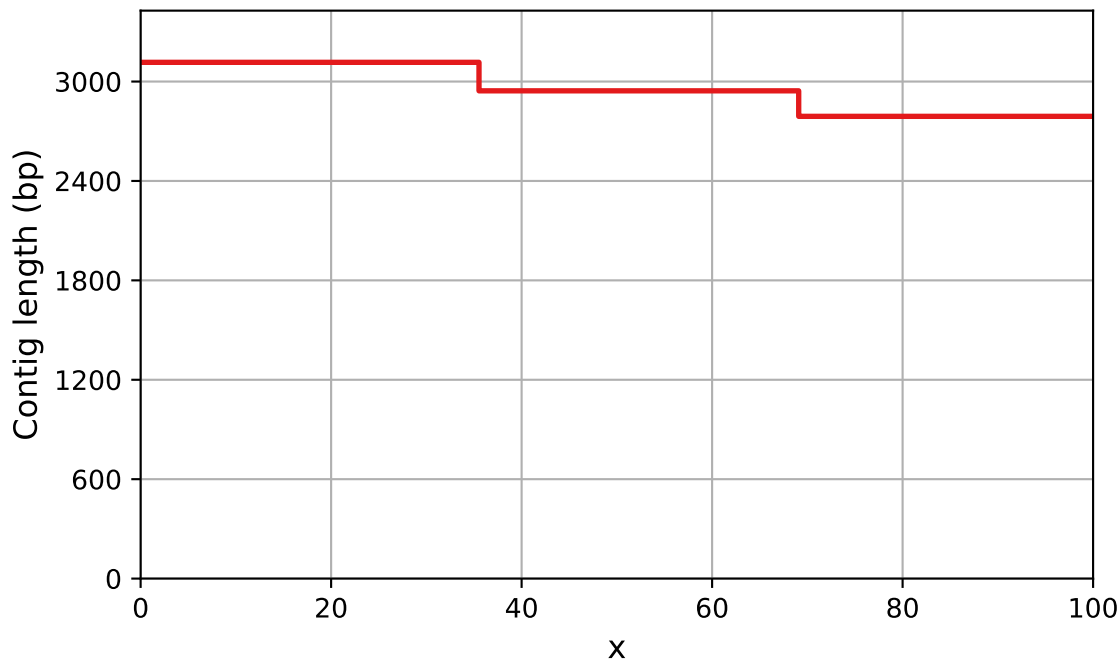
Unaligned report

	pos_sorted_bam_filtered.long
# fully unaligned contigs	677
Fully unaligned length	483616
# partially unaligned contigs	0
Partially unaligned length	0
# 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).

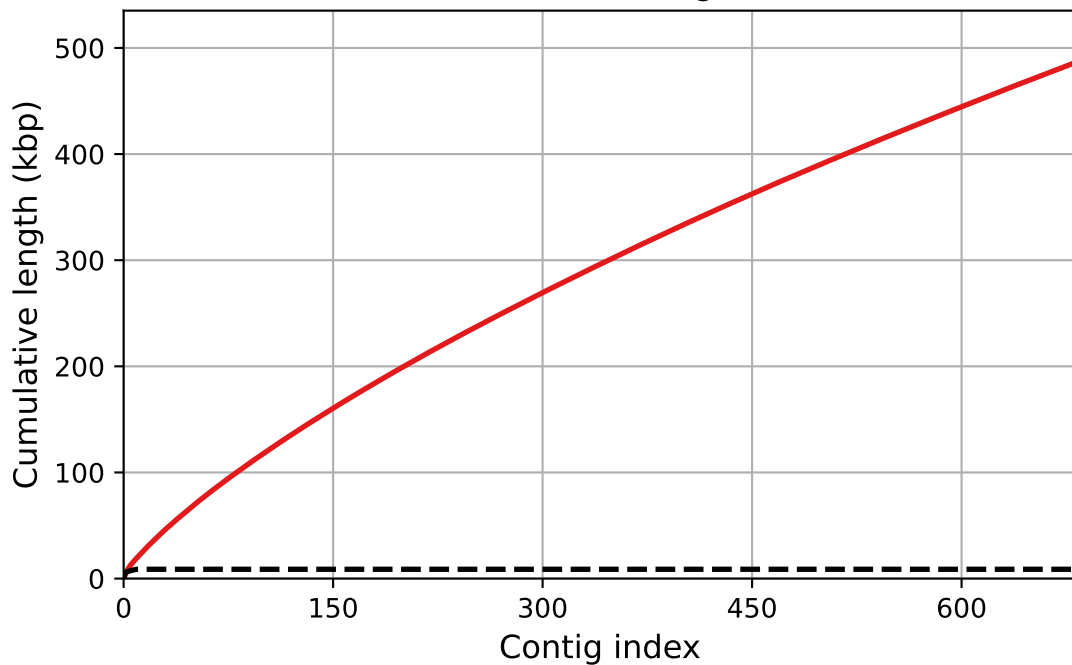


NGx



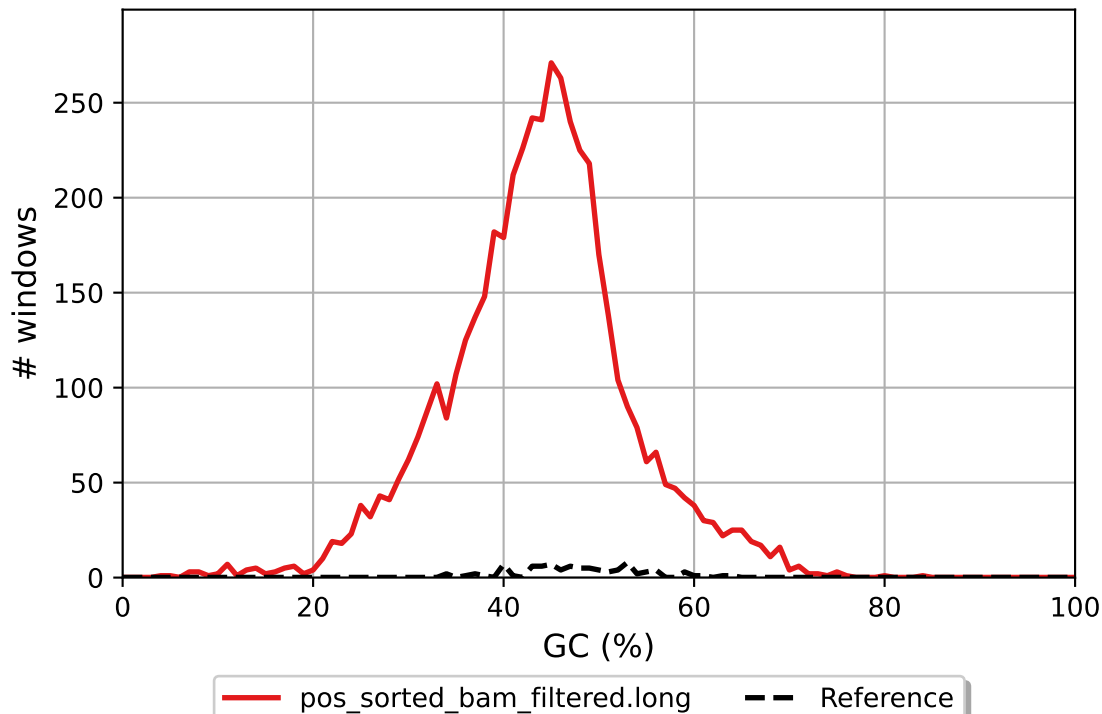
pos_sorted_bam_filtered.long

Cumulative length

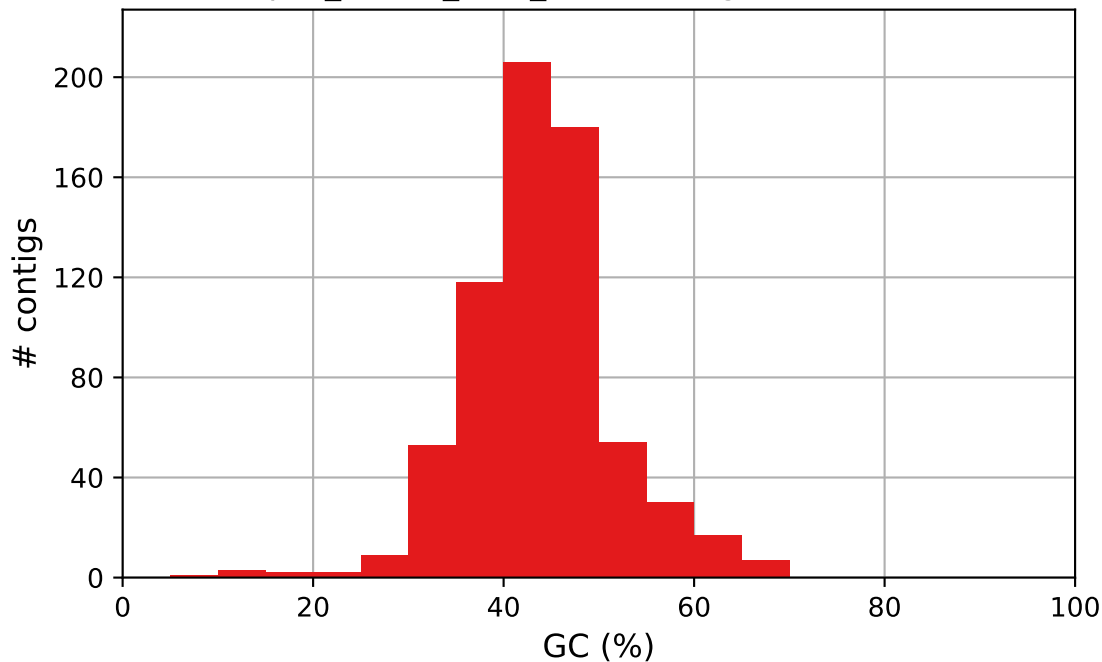


pos_sorted_bam_filtered.long Reference

GC content

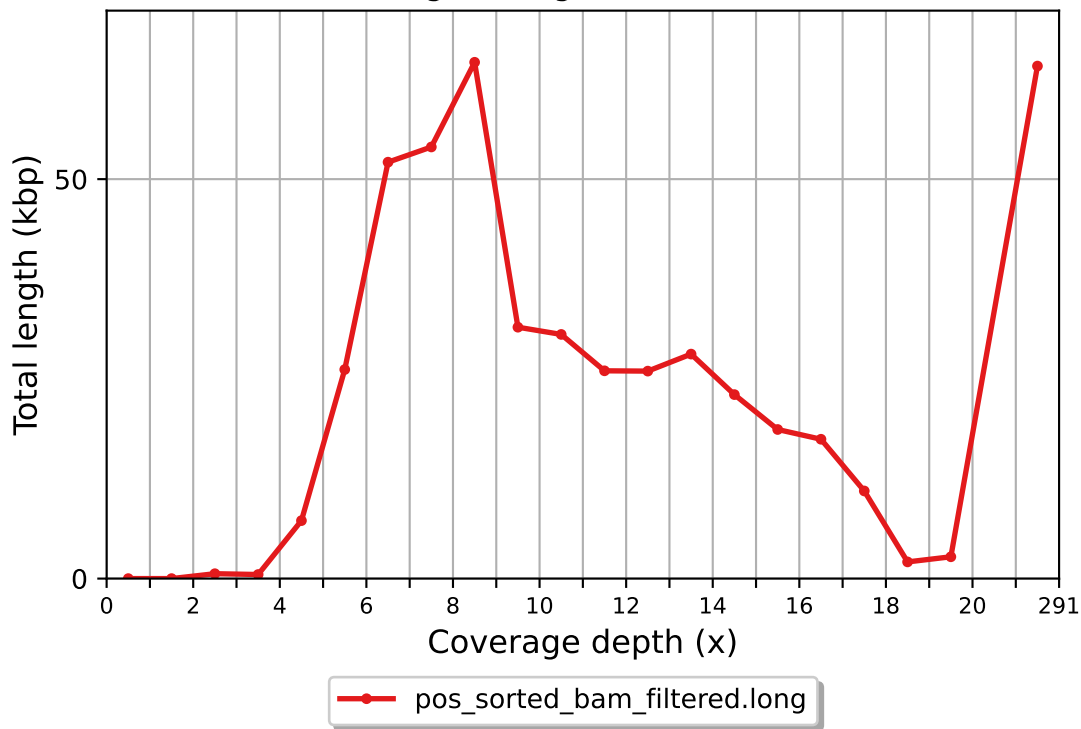


pos_sorted_bam_filtered.long GC content

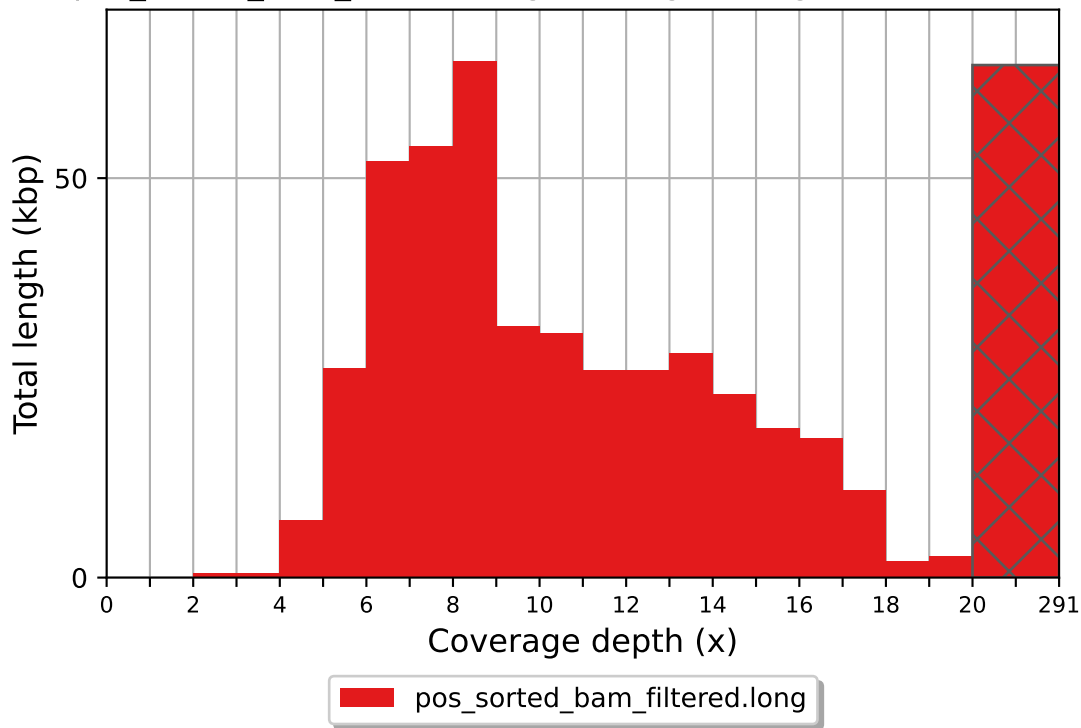


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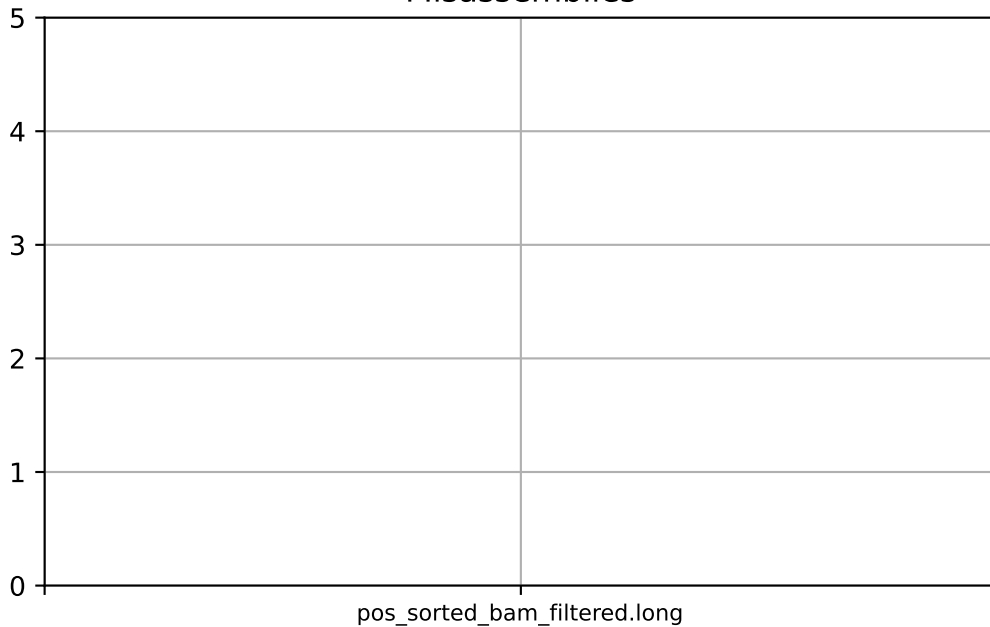
Coverage histogram (bin size: 1x)



pos_sorted_bam_filtered.long coverage histogram (bin size: 1x)



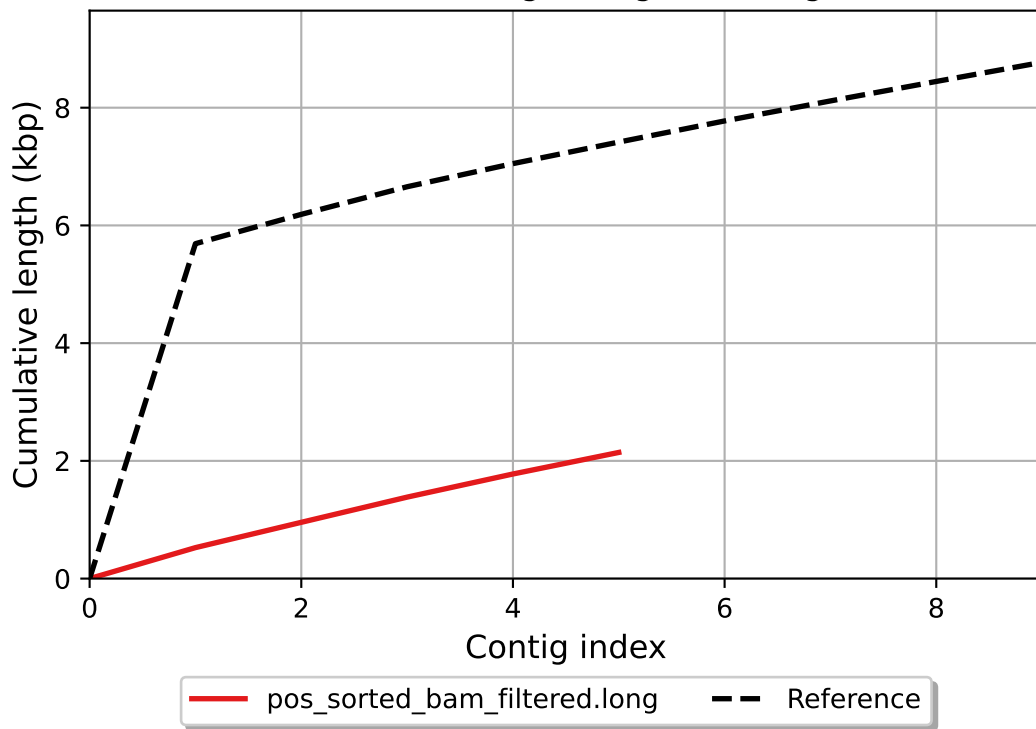
Misassemblies



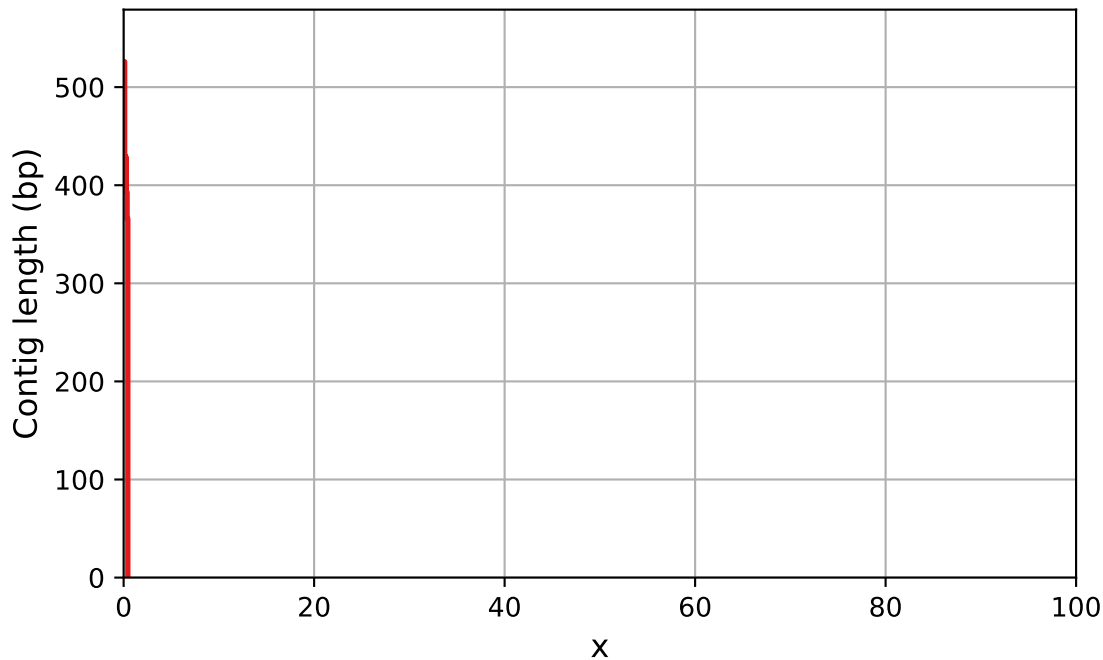
FRCurve (misassemblies)



Cumulative length (aligned contigs)

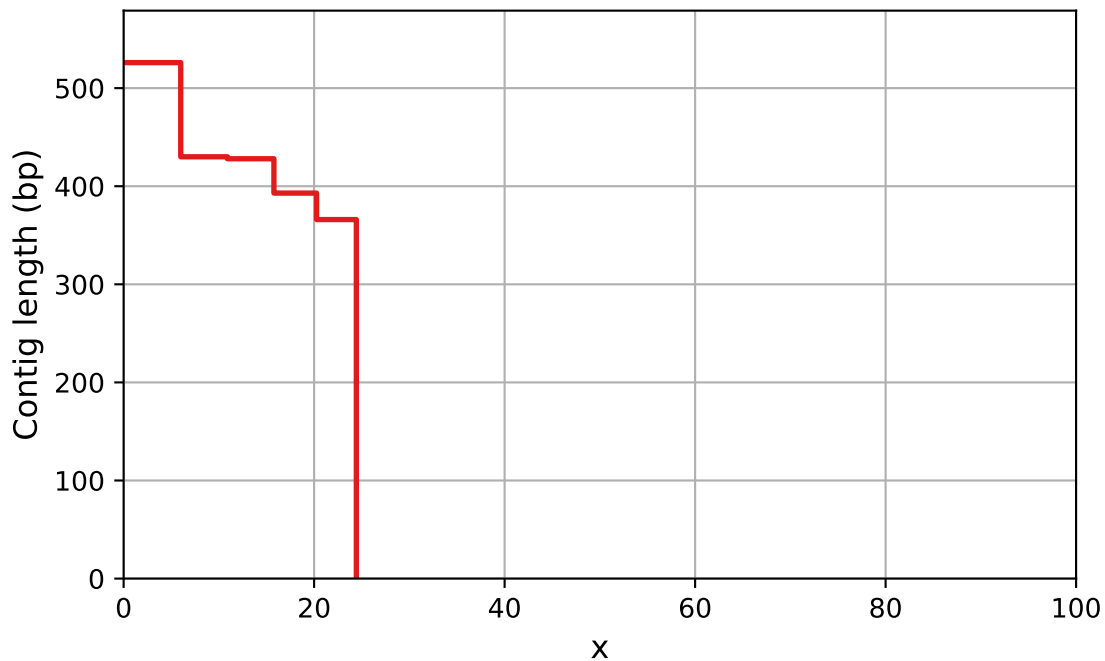


NAx



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NGAx



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