

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	9508
Largest contig	3116
Total length	2783972
Reference length	8771
GC (%)	42.87
Reference GC (%)	48.03
N50	271
NG50	2944
N75	223
NG75	2790
L50	3326
LG50	2
L75	6197
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	9495 + 0 part
Unaligned length	2778454
Genome fraction (%)	40.315
Duplication ratio	1.561
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.28
# indels per 100 kbp	0.00
Largest alignment	526
Total aligned length	3577
NGA50	-

All statistics are based on contigs of size >= 200 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

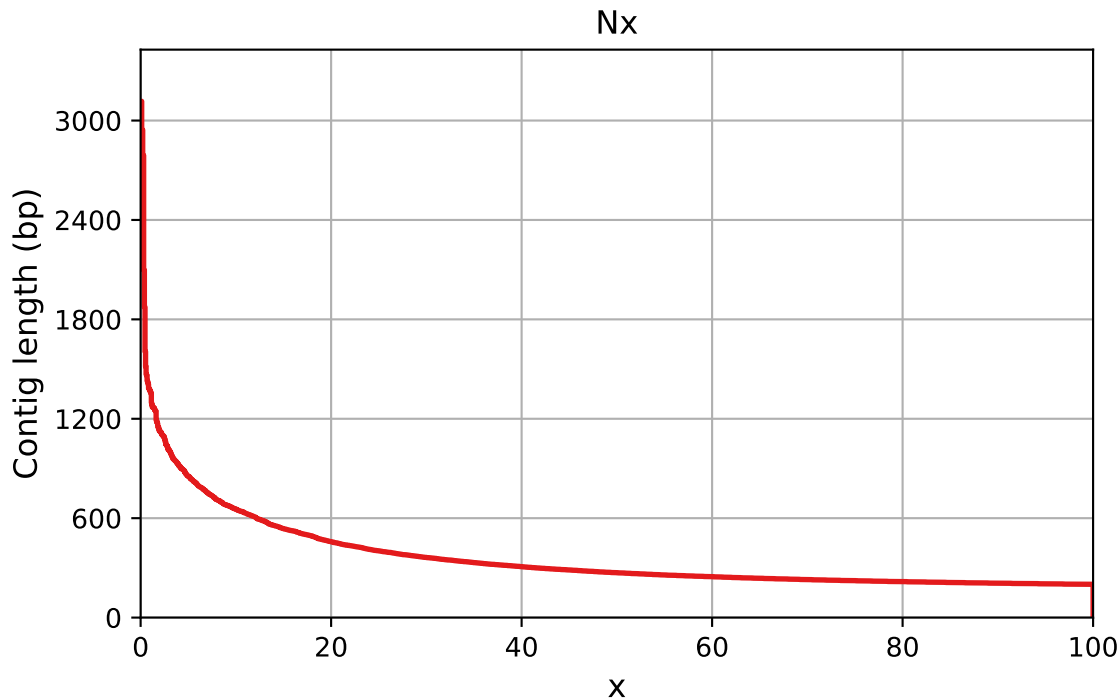
	pos_sorted_bam_filtered.long
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

All statistics are based on contigs of size ≥ 200 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

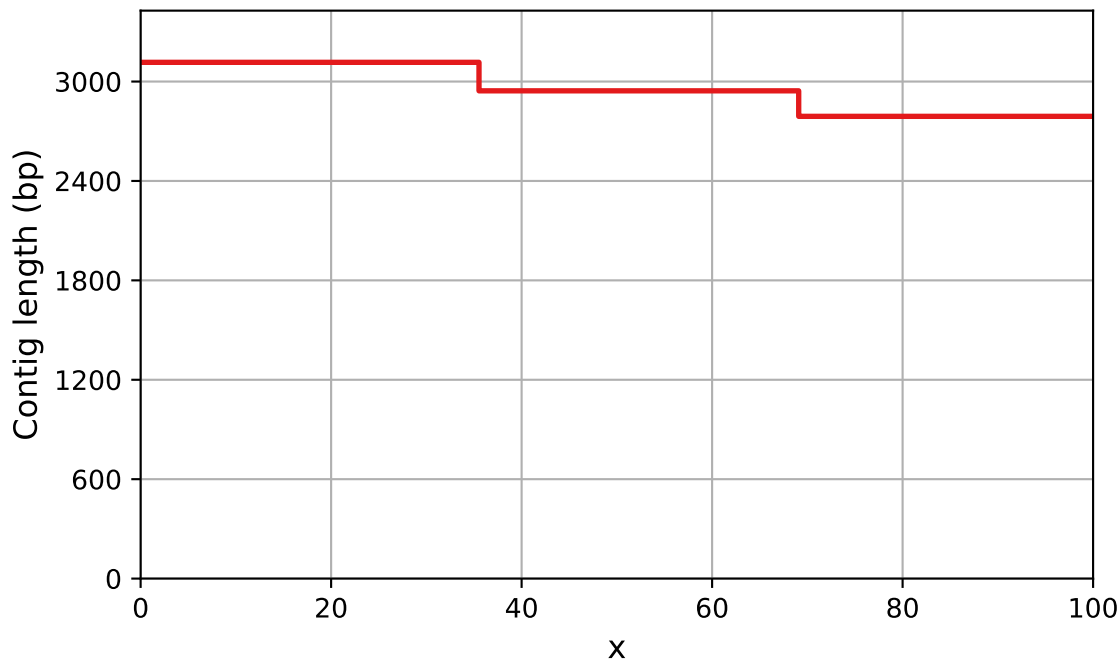
	pos_sorted_bam_filtered.long
# fully unaligned contigs	9495
Fully unaligned length	2778454
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size ≥ 200 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

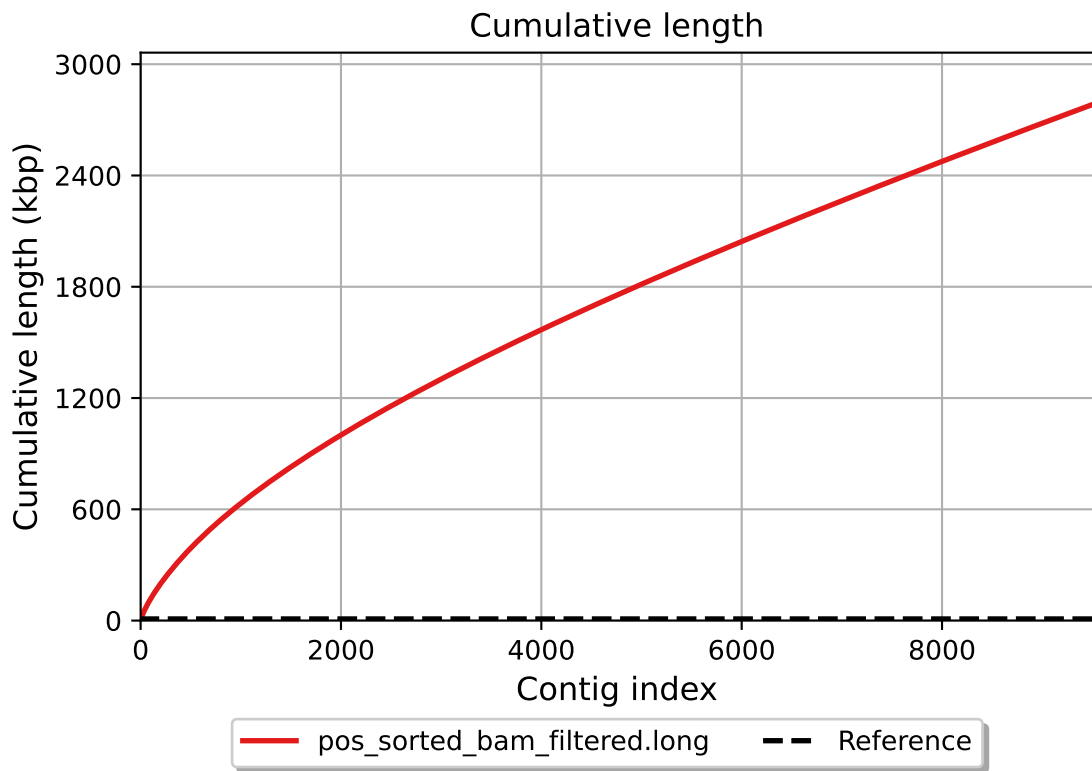


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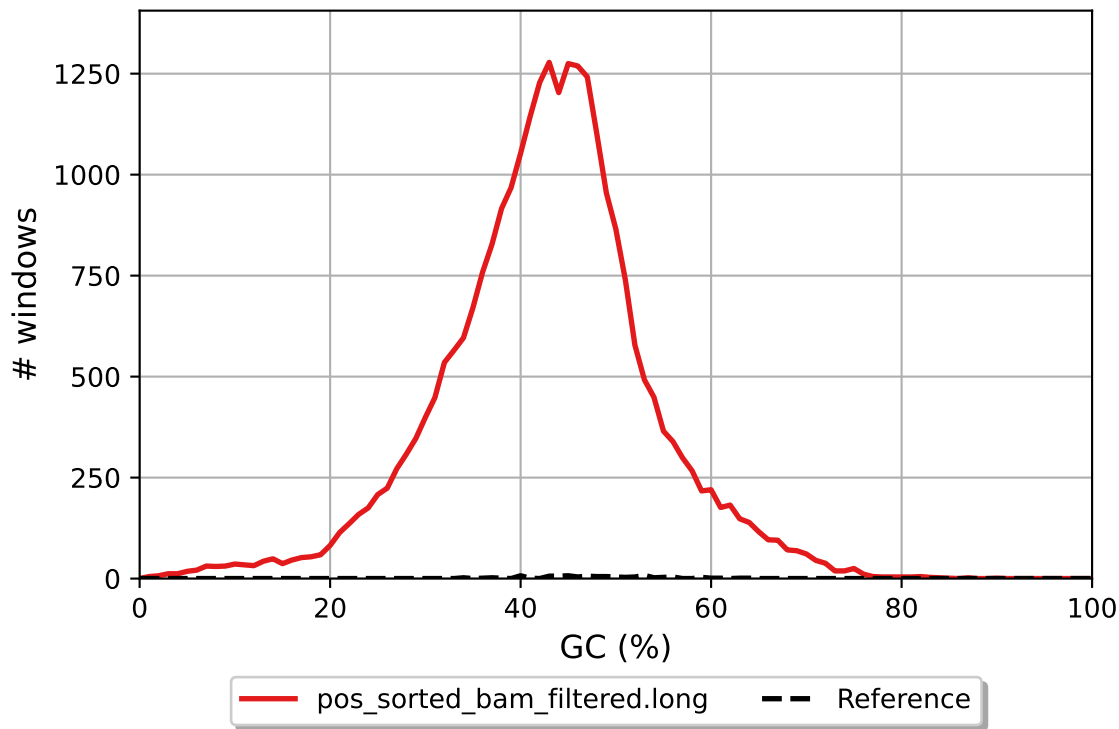
NGx



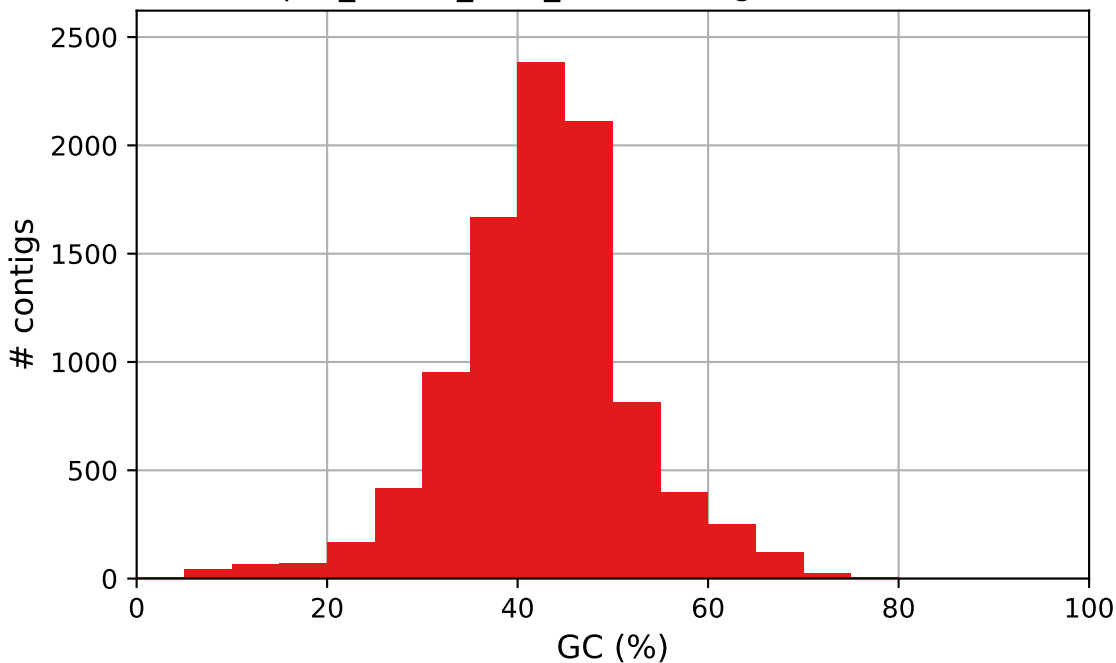
pos_sorted_bam_filtered.long



GC content

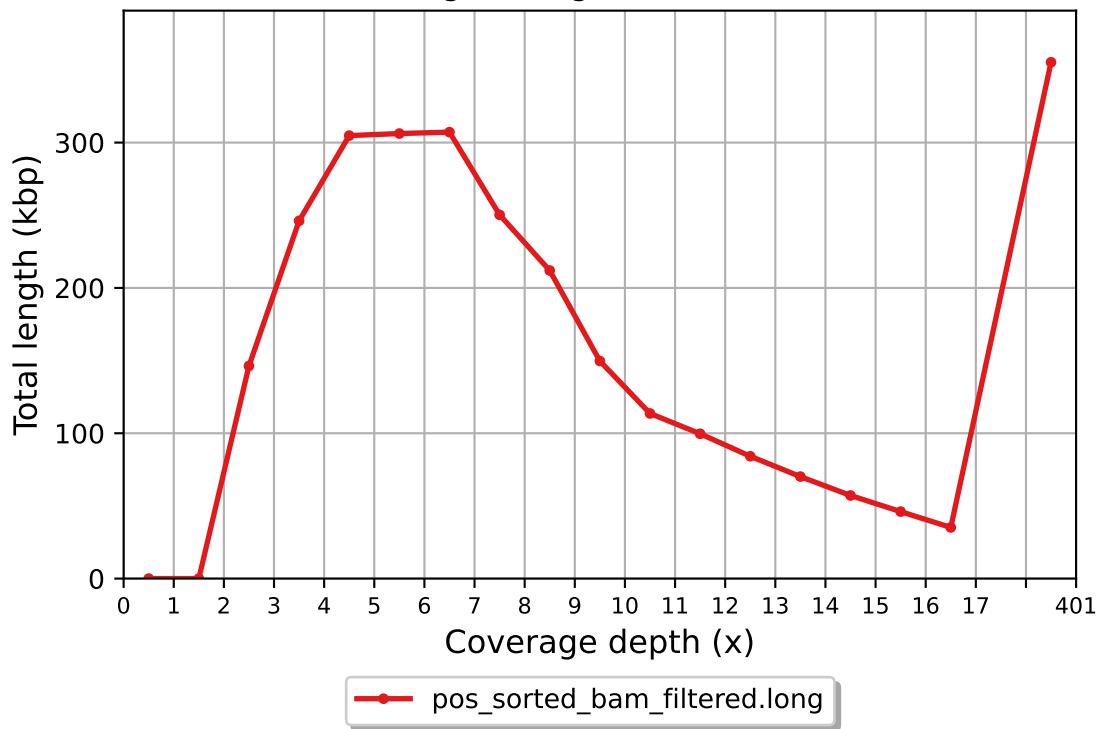


pos_sorted_bam_filtered.long GC content

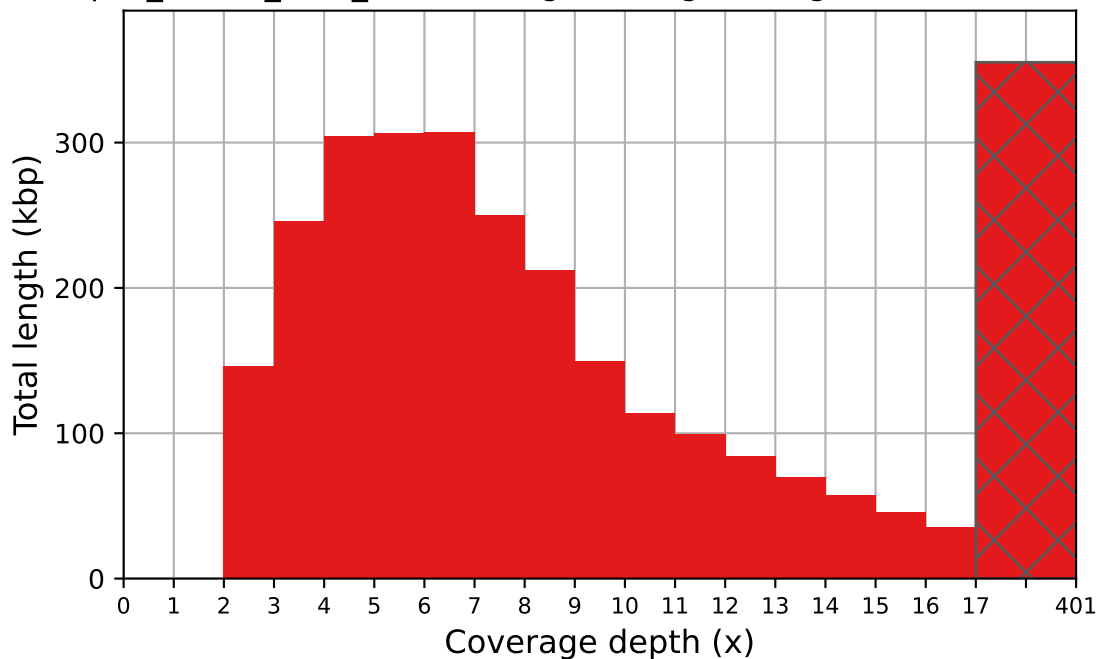


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Coverage histogram (bin size: 1x)

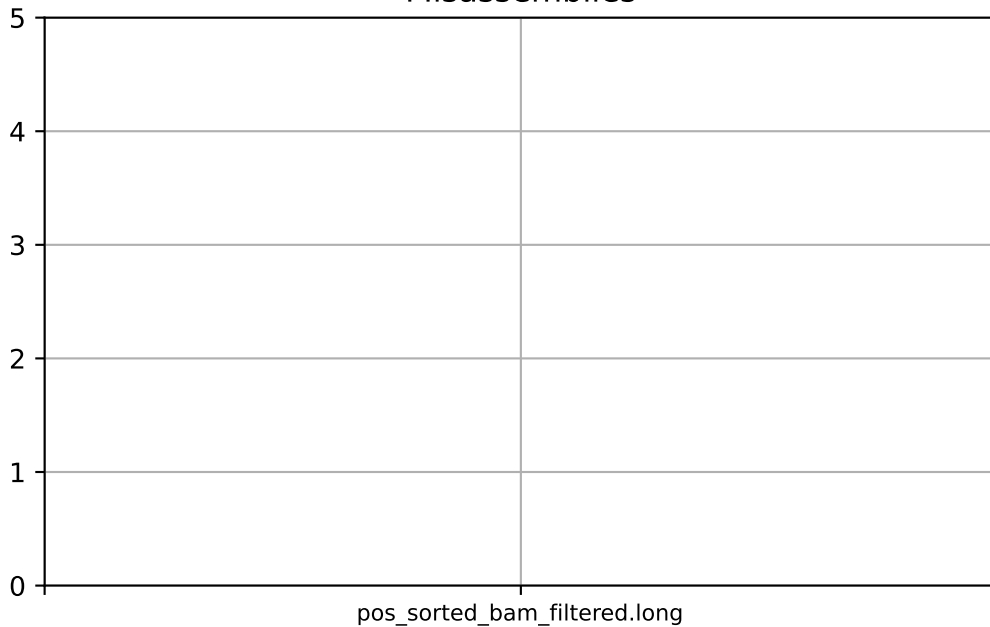


pos_sorted_bam_filtered.long coverage histogram (bin size: 1x)

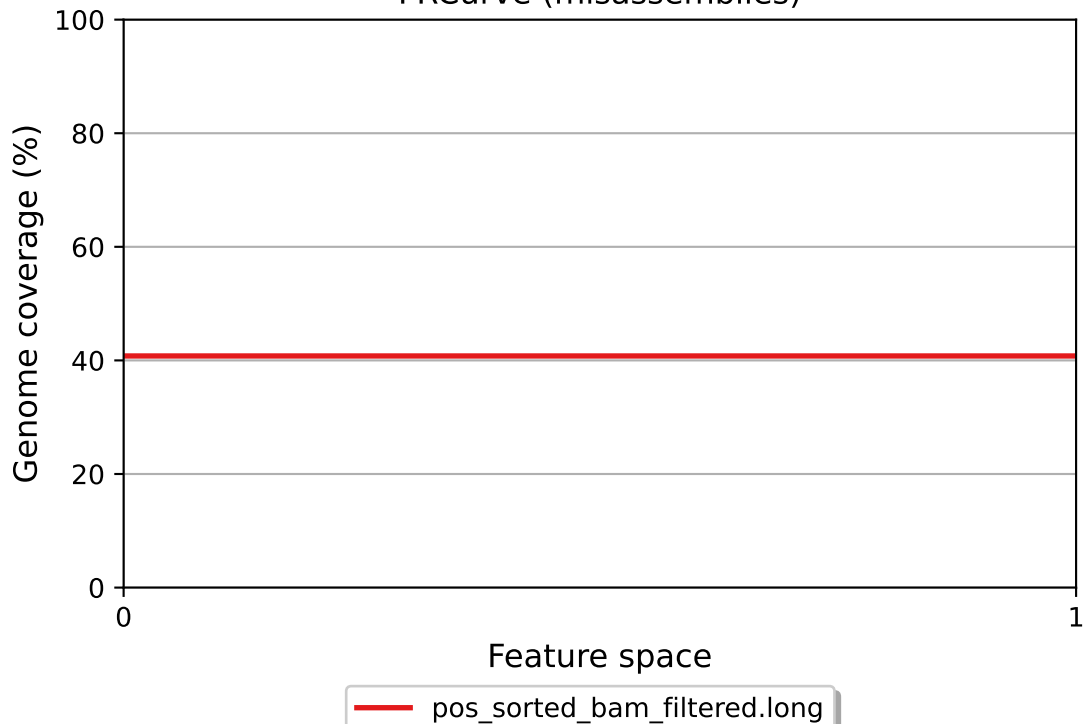


pos_sorted_bam_filtered.long

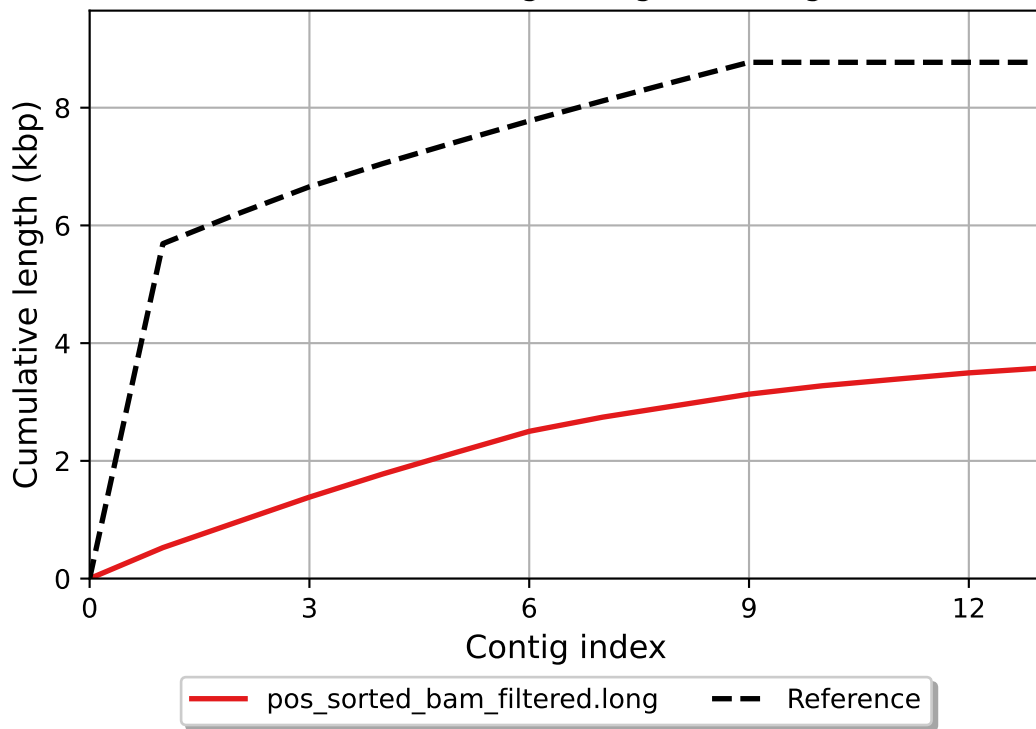
Misassemblies



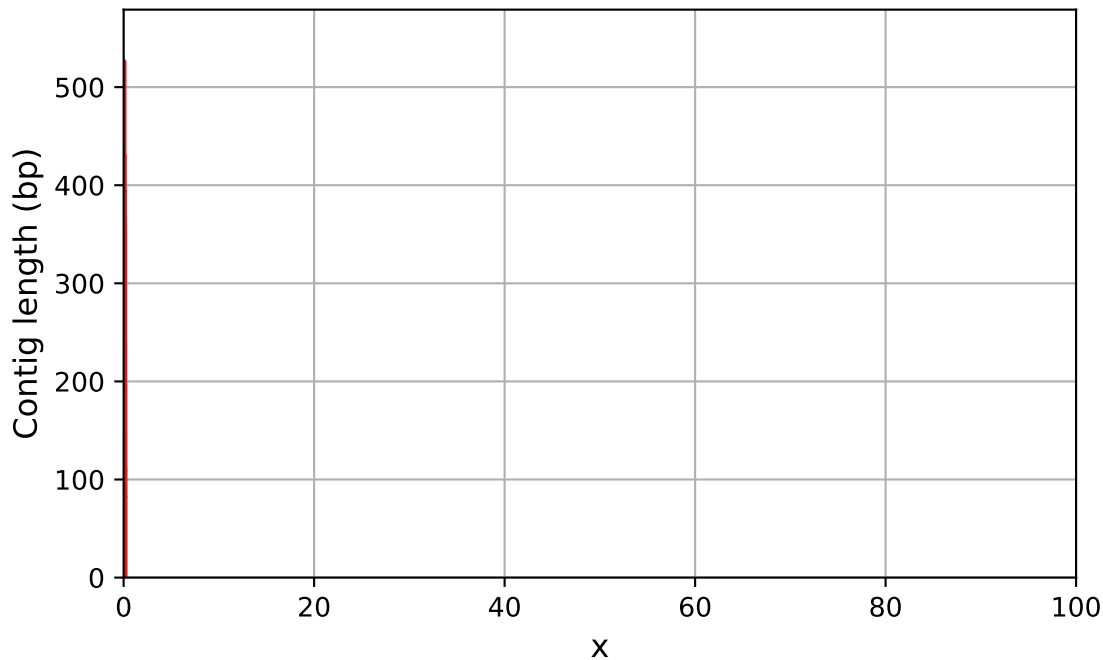
FRCurve (misassemblies)



Cumulative length (aligned contigs)

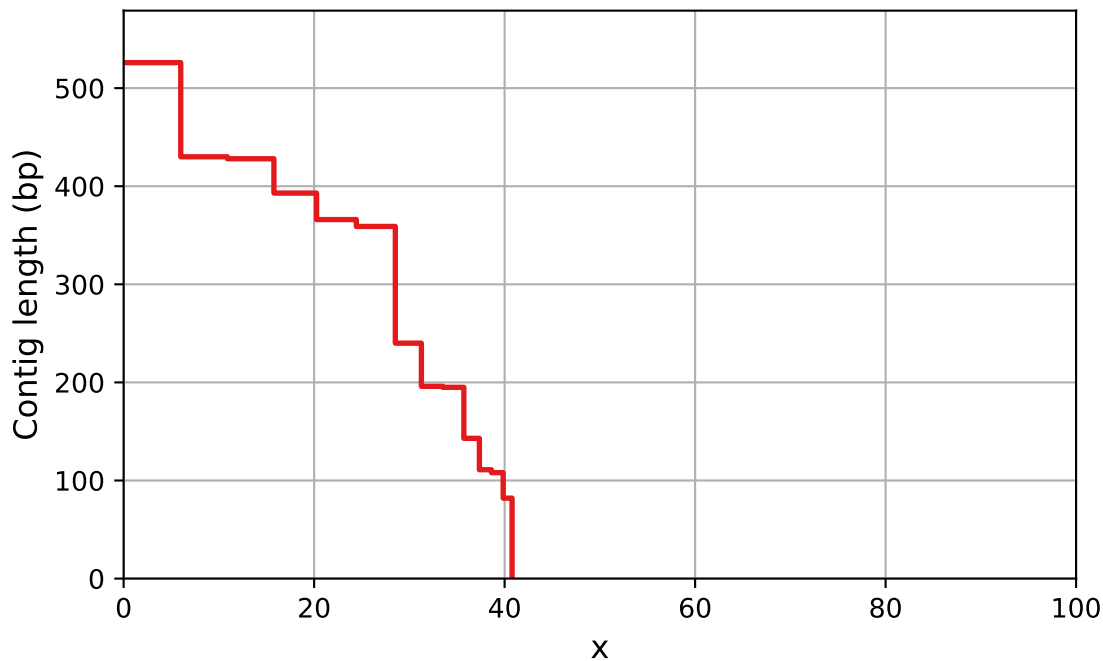


NAx



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NGAx



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