

Report

	NA12878_GRCh38_phased_possorted_bam_filtered.long
# contigs (>= 0 bp)	16439
# contigs (>= 1000 bp)	744
# contigs (>= 5000 bp)	37
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6845786
Total length (>= 1000 bp)	1509135
Total length (>= 5000 bp)	303957
Total length (>= 10000 bp)	108928
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3039
Largest contig	24414
Total length	3039010
Reference length	45867
GC (%)	42.73
Reference GC (%)	39.17
N50	994
NG50	24414
N75	667
NG75	20540
L50	755
LG50	1
L75	1710
LG75	2
# 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	3024 + 2 part
Unaligned length	2997964
Genome fraction (%)	84.006
Duplication ratio	1.065
# N's per 100 kbp	0.00
# mismatches per 100 kbp	41.53
# indels per 100 kbp	10.38
Largest alignment	6125
Total aligned length	38909
NGA50	4669
NGA75	1618
LGA50	5
LGA75	9

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

	NA12878_GRCh38_phased_possorted_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	16
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	5

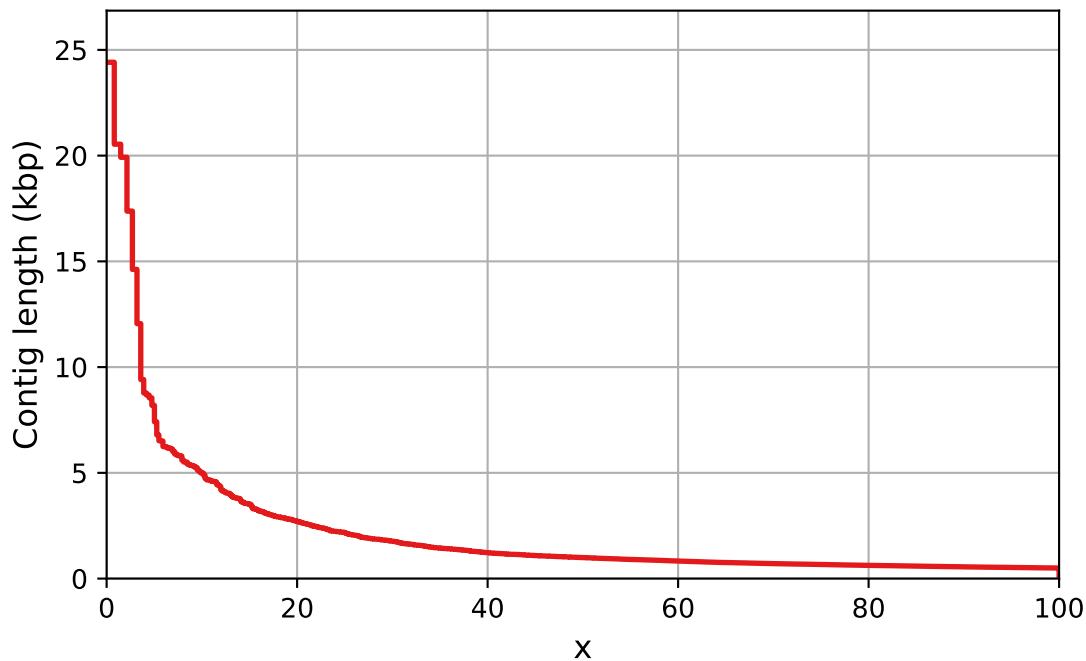
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	NA12878_GRCh38_phased_possorted_bam_filtered.long
# fully unaligned contigs	3024
Fully unaligned length	2987827
# partially unaligned contigs	2
Partially unaligned length	10137
# N's	0

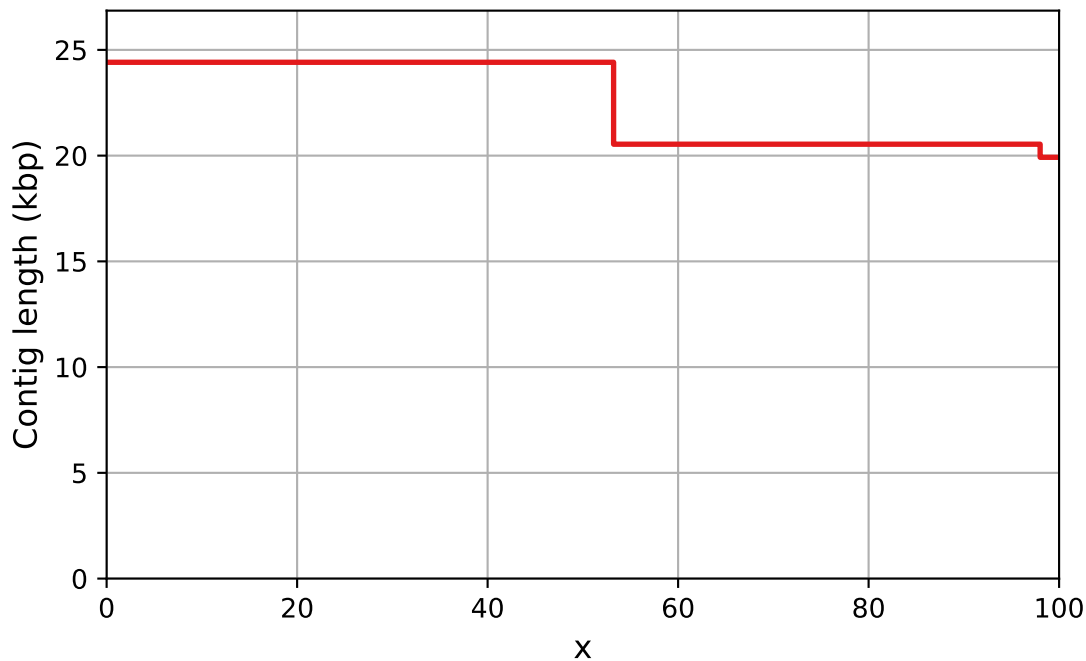
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



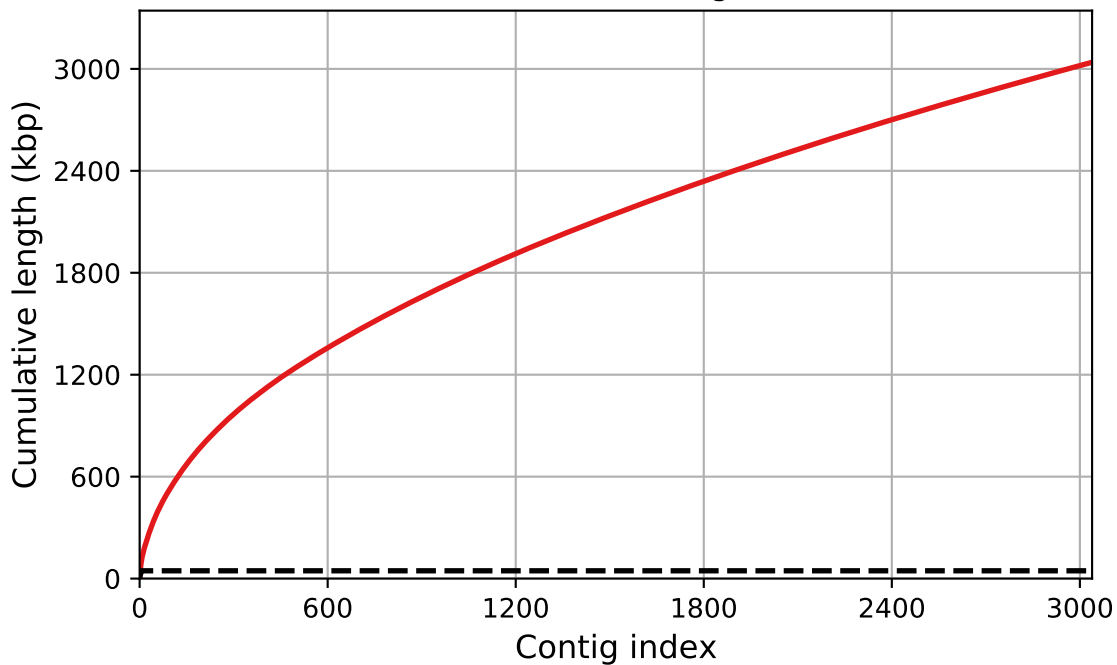
— NA12878_GRCh38_phased_possorted_bam_filtered.long

NGx



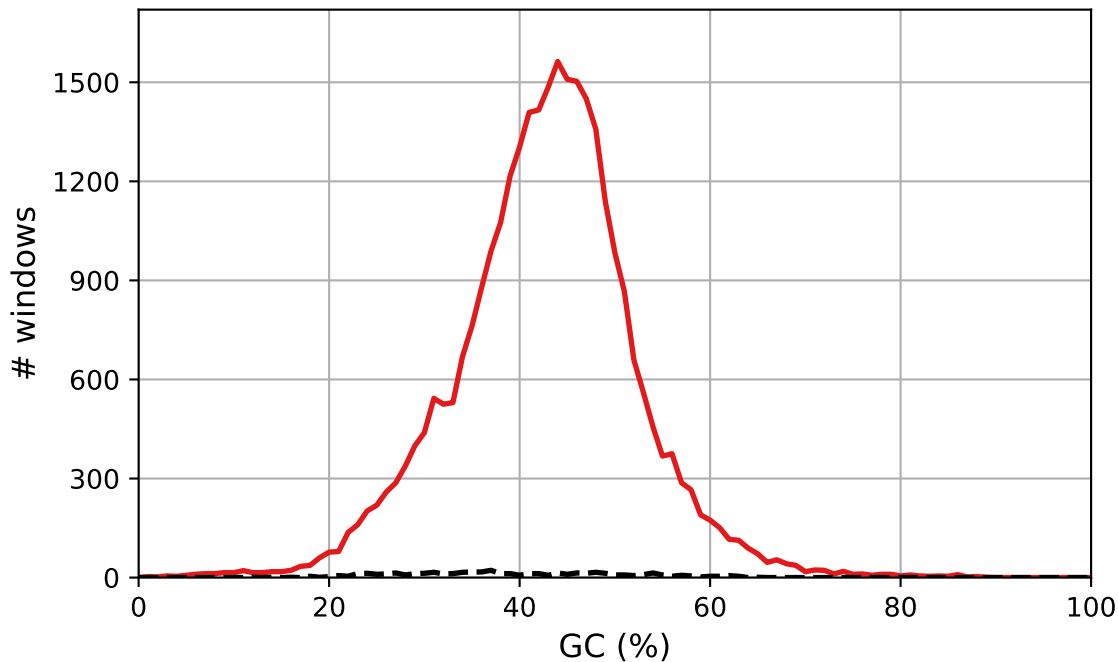
— NA12878_GRCh38_phased_possorted_bam_filtered.long

Cumulative length



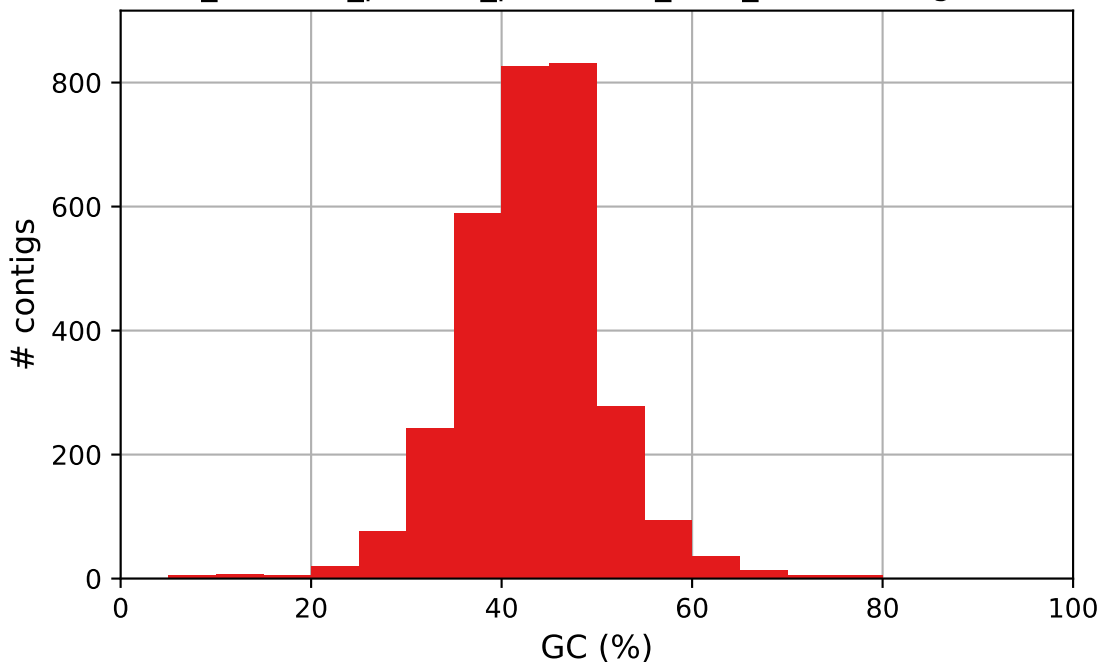
— NA12878_GRCh38_phased_possorted_bam_filtered.long - - Reference

GC content



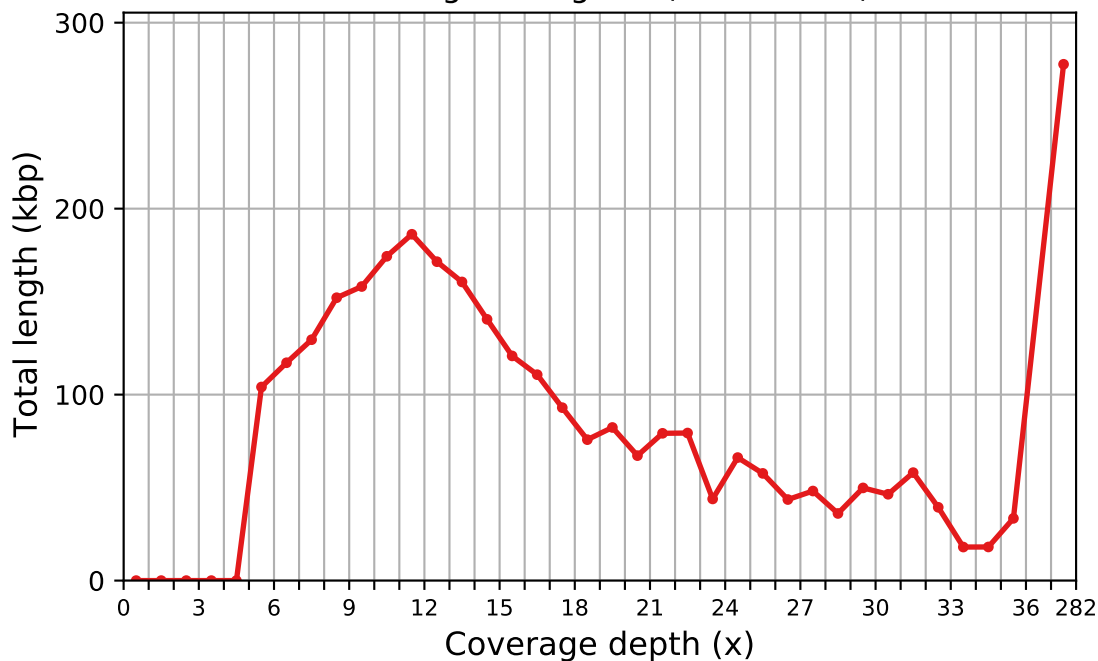
— NA12878_GRCh38_phased_possorted_bam_filtered.long - - Reference

NA12878_GRCh38_phased_possorted_bam_filtered.long GC content



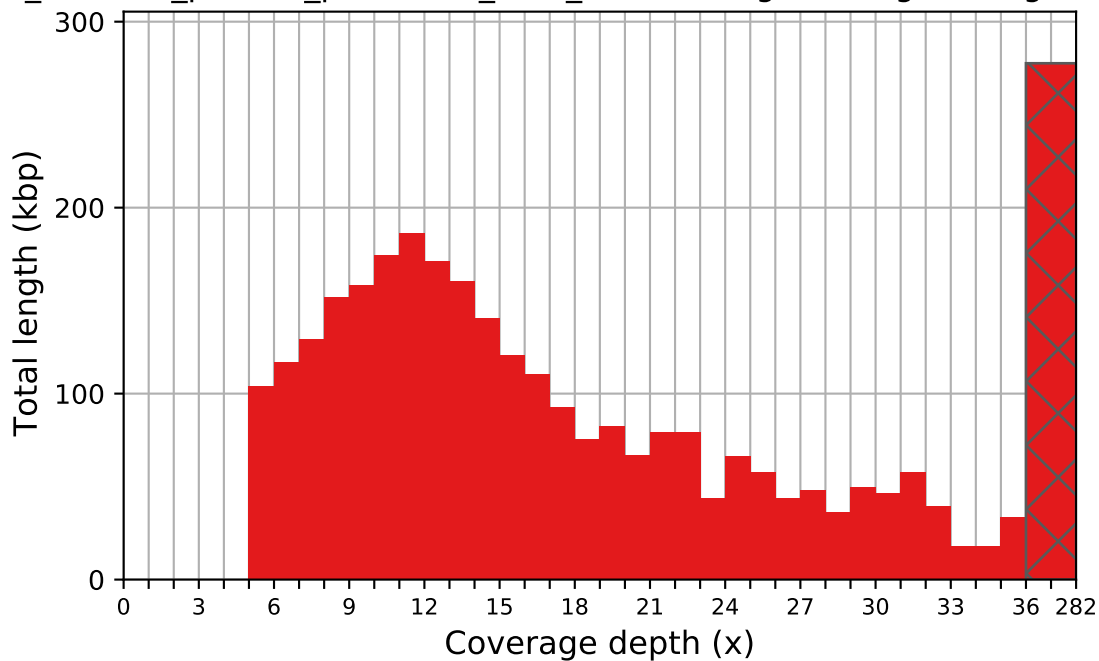
NA12878_GRCh38_phased_possorted_bam_filtered.long

Coverage histogram (bin size: 1x)



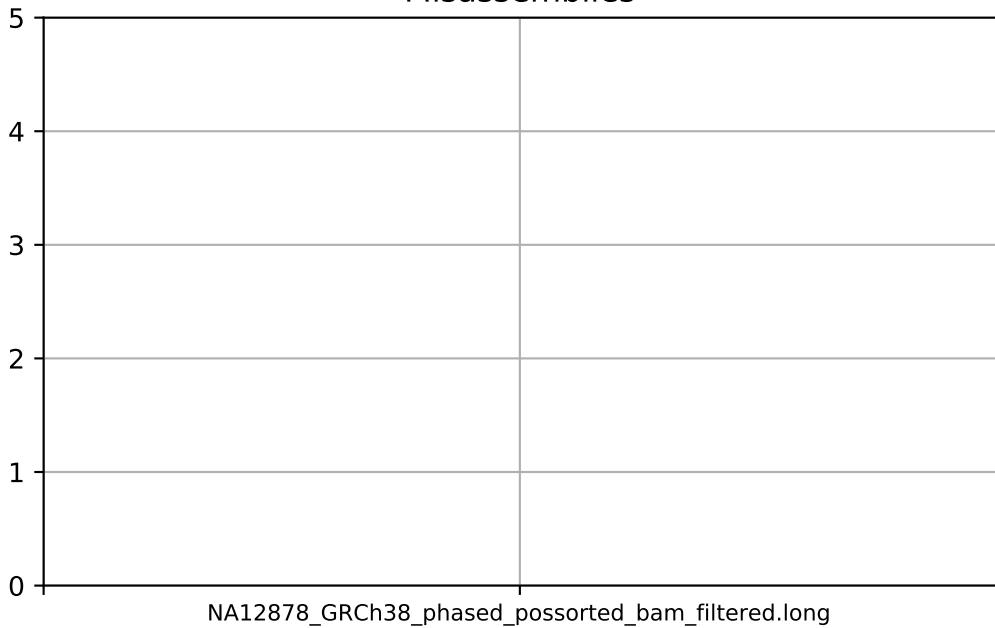
NA12878_GRCh38_phased_possorted_bam_filtered.long

NA12878_GRCh38_phased_possorted_bam_filtered.long coverage histogram (bin s

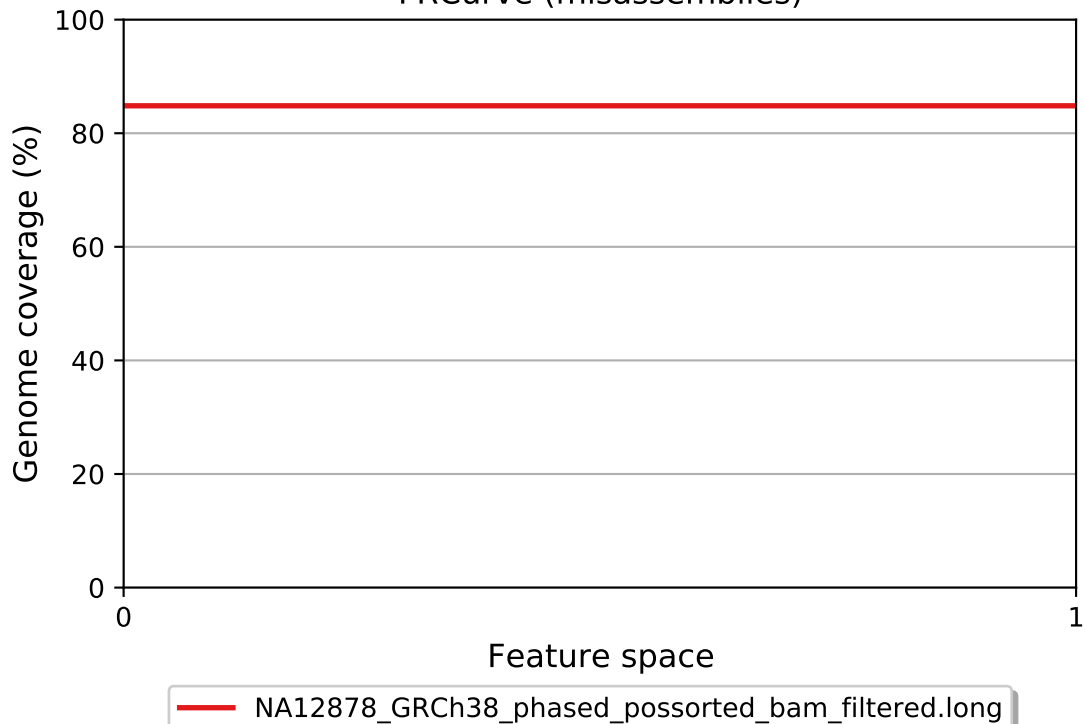


NA12878_GRCh38_phased_possorted_bam_filtered.long

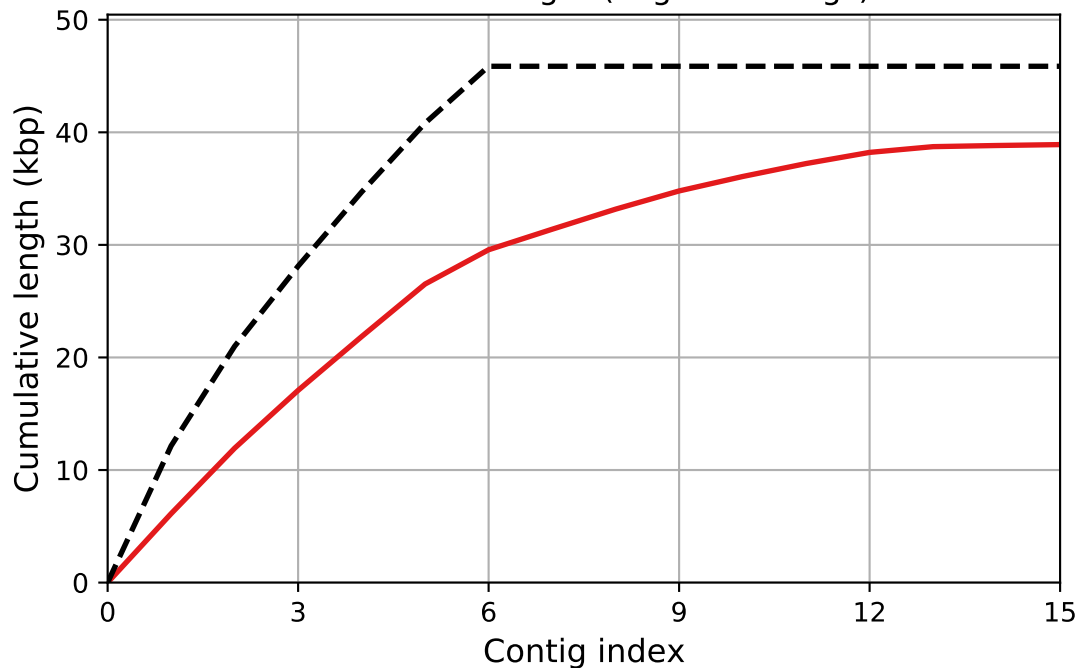
Misassemblies



FRCurve (misassemblies)

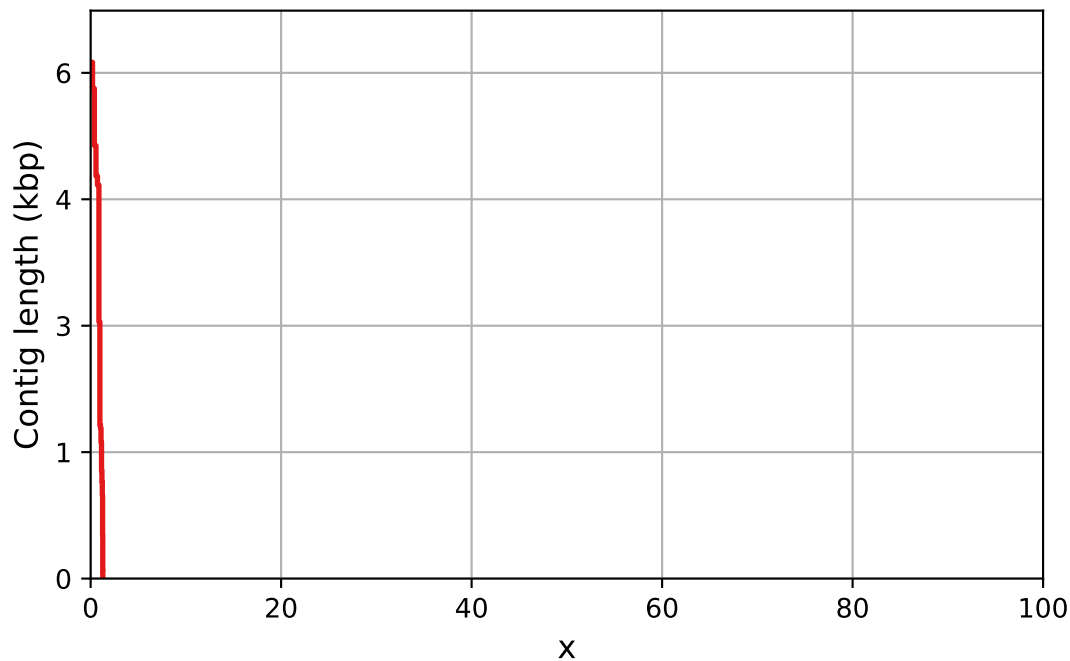


Cumulative length (aligned contigs)



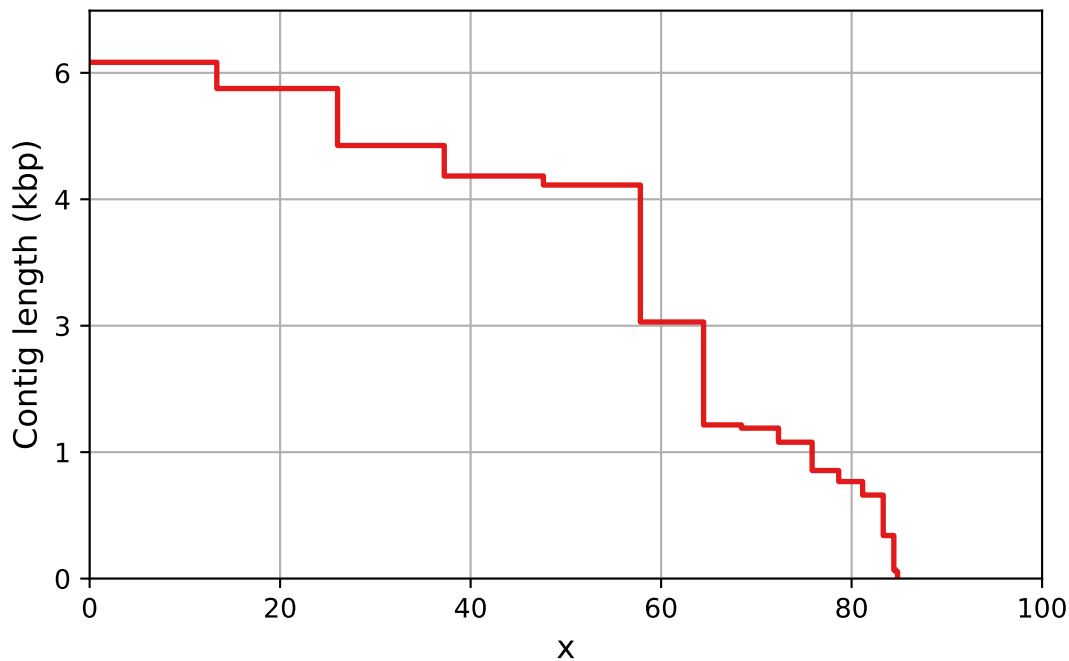
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NAx



— NA12878_GRCh38_phased_possorted_bam_filtered.long

NGAx



— NA12878_GRCh38_phased_possorted_bam_filtered.long