

Report

	pacbio.contigs
# contigs (>= 0 bp)	10
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	9
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3115044
Total length (>= 1000 bp)	3115044
Total length (>= 5000 bp)	3110818
Total length (>= 10000 bp)	3110818
Total length (>= 25000 bp)	3001873
Total length (>= 50000 bp)	2961859
# contigs	10
Largest contig	2762476
Total length	3115044
Reference length	2919198
GC (%)	37.80
Reference GC (%)	37.88
N50	2762476
NG50	2762476
N75	2762476
NG75	2762476
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	189
# misassembled contigs	1
Misassembled contigs length	2762476
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	4 + 6 part
Unaligned length	535902
Genome fraction (%)	84.942
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	390.14
# indels per 100 kbp	20.00
Largest alignment	137654
Total aligned length	2577175
NA50	26511
NGA50	29113
NA75	6591
NGA75	10307
LA50	30
LGA50	27
LA75	83
LGA75	66

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

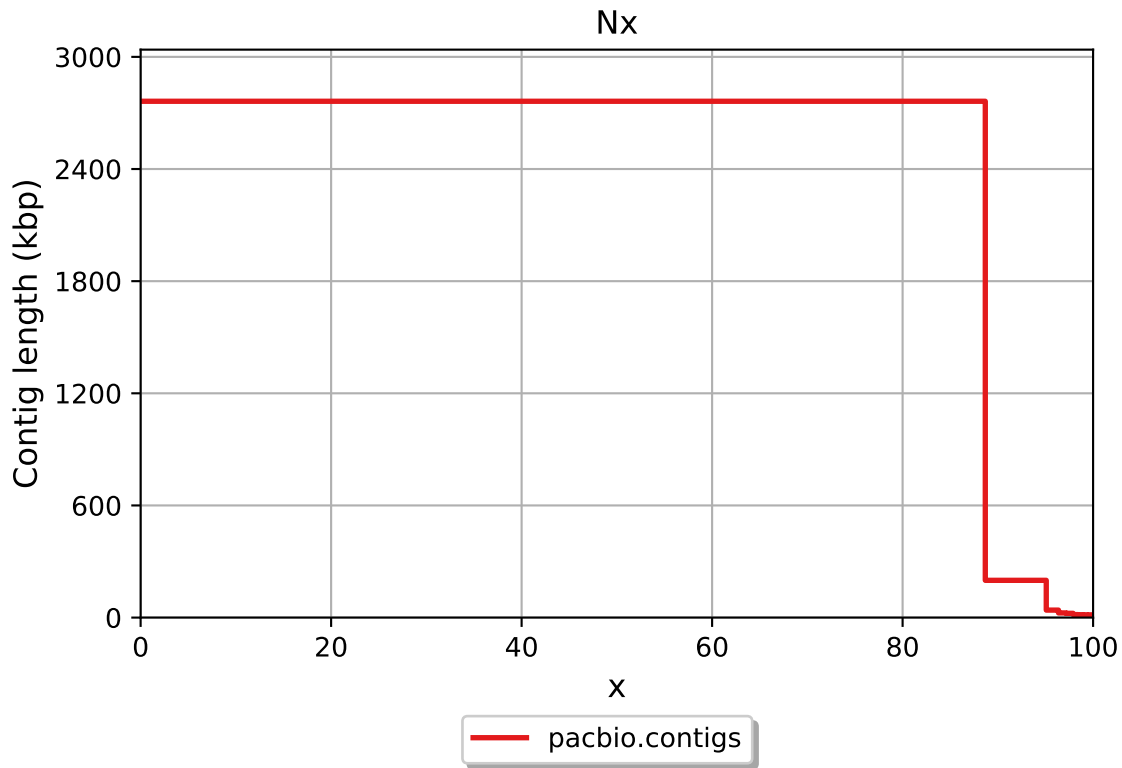
	pacbio.contigs
# misassemblies	189
# contig misassemblies	189
# c. relocations	173
# c. translocations	14
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2762476
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	9674
# indels	496
# indels (<= 5 bp)	460
# indels (> 5 bp)	36
Indels length	1529

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).

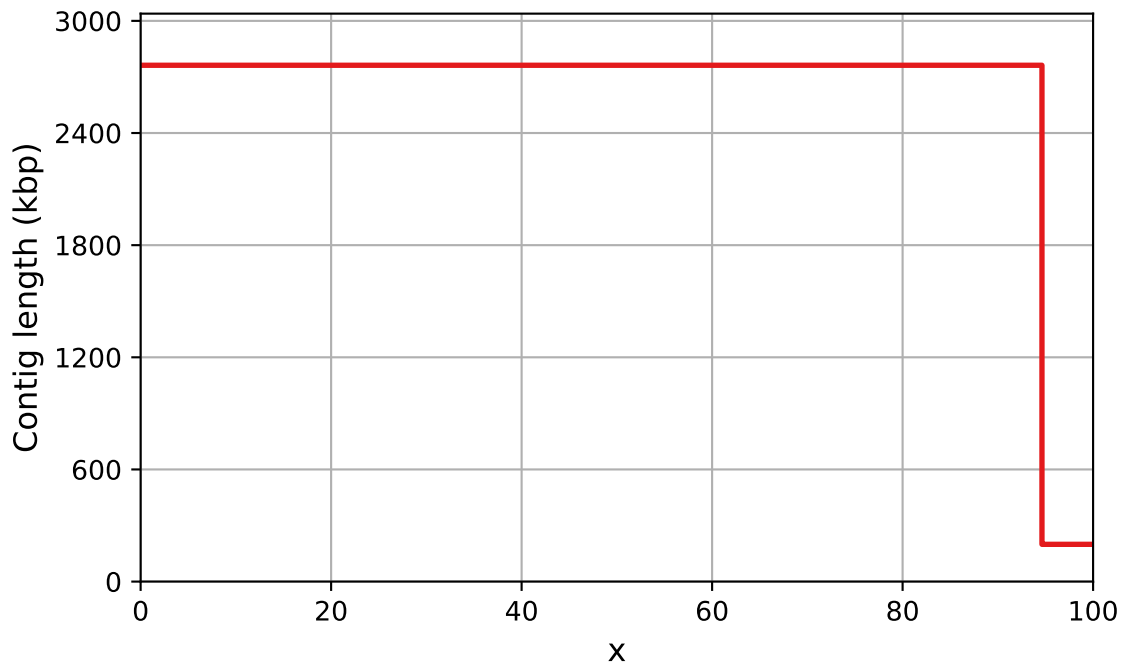
Unaligned report

	pacbio.contigs
# fully unaligned contigs	4
Fully unaligned length	59618
# partially unaligned contigs	6
Partially unaligned length	476284
# 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).

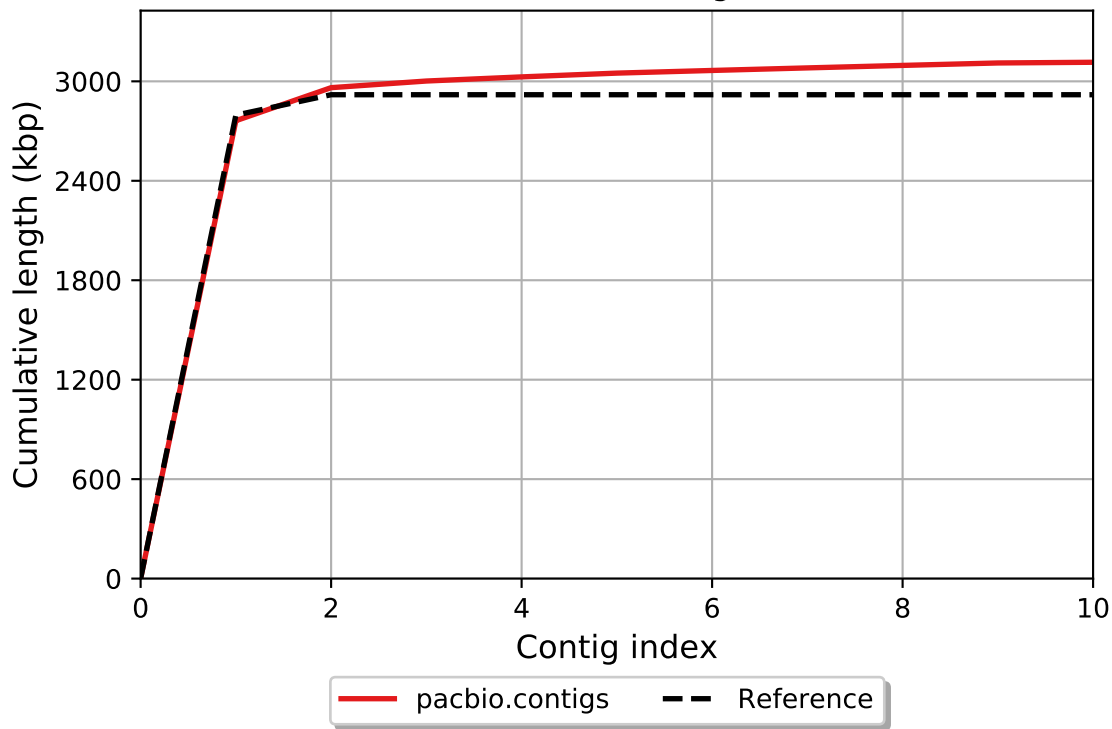


NGx

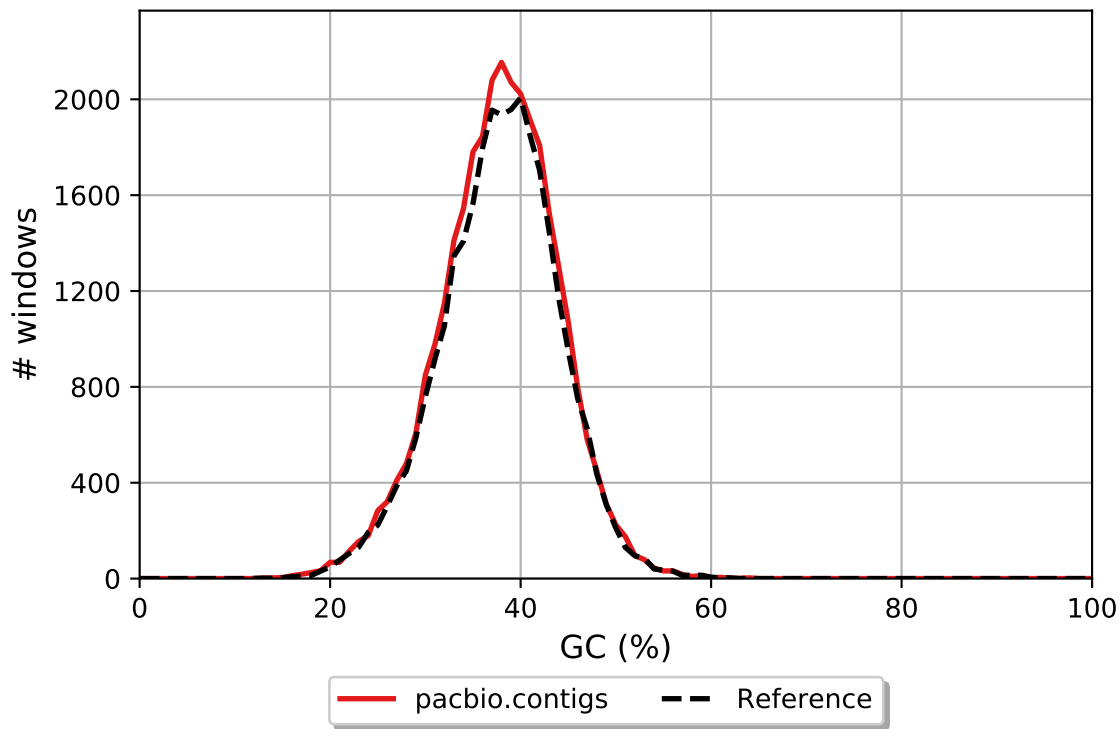


— pacbio.contigs

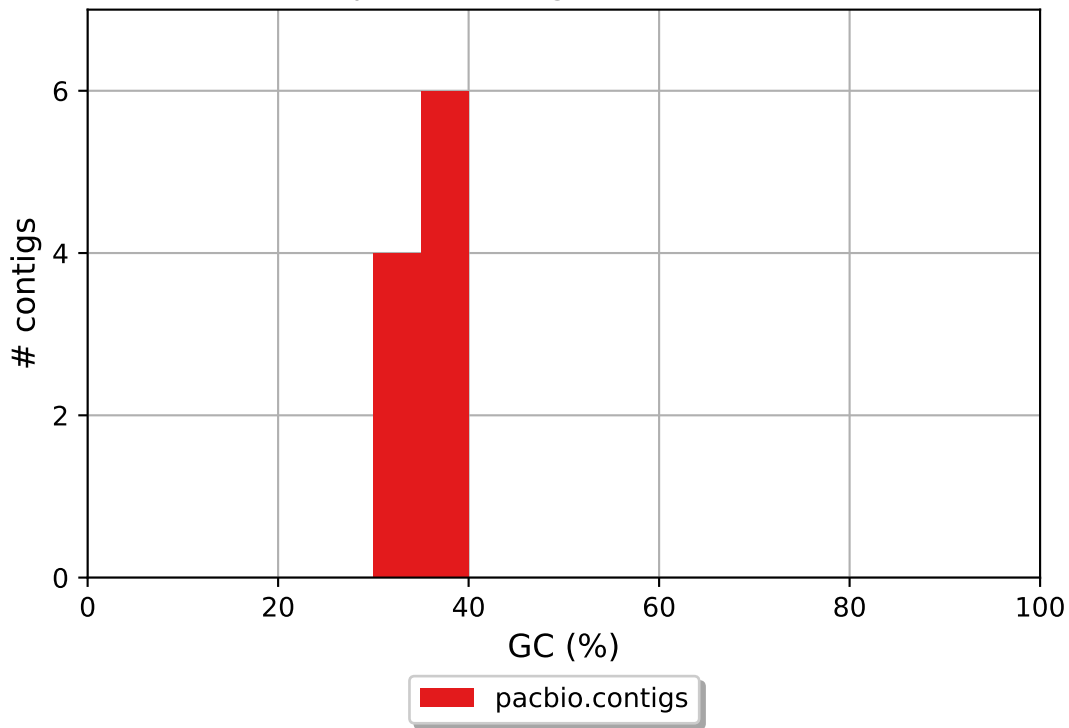
Cumulative length



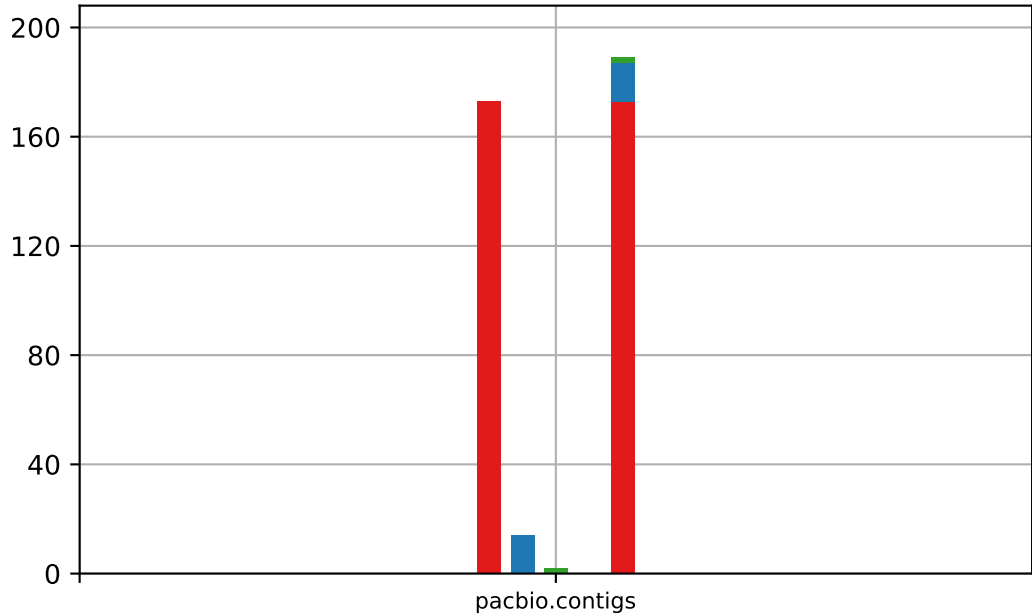
GC content



pacbio.contigs GC content



Misassemblies



relocations

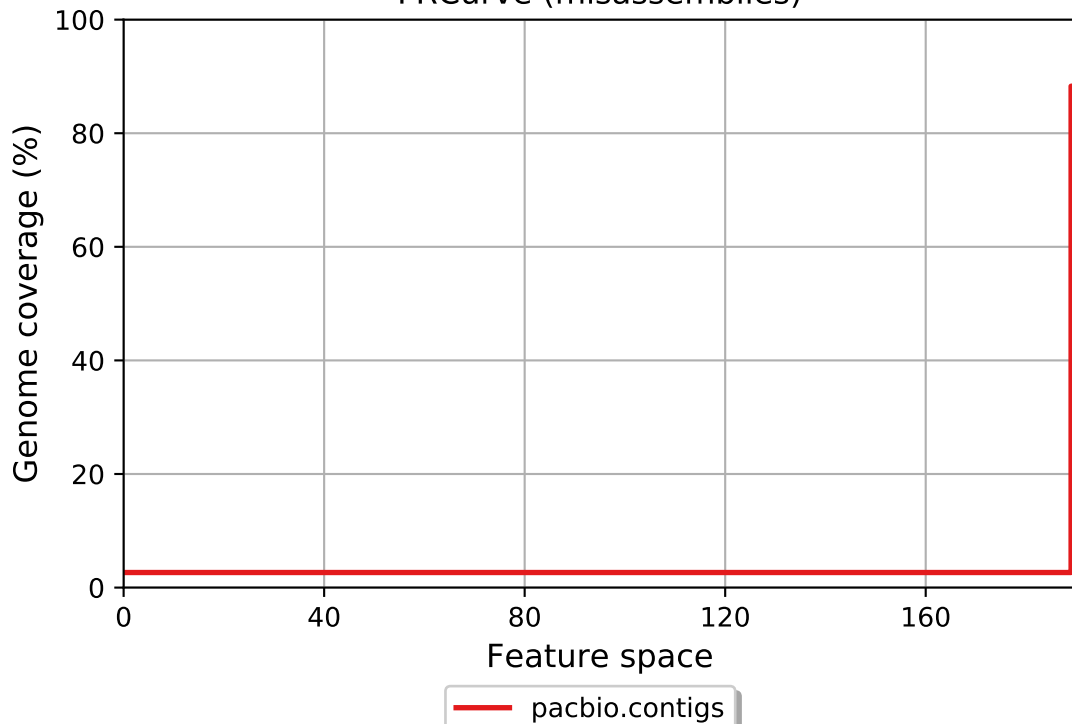


translocations

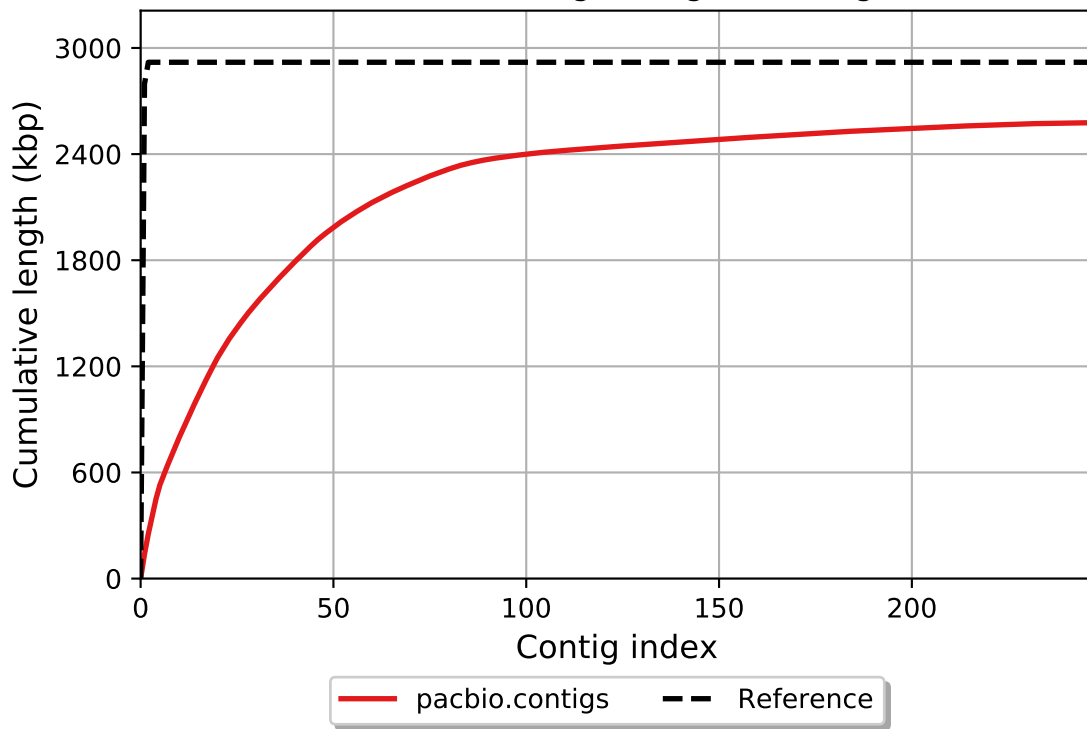


inversions

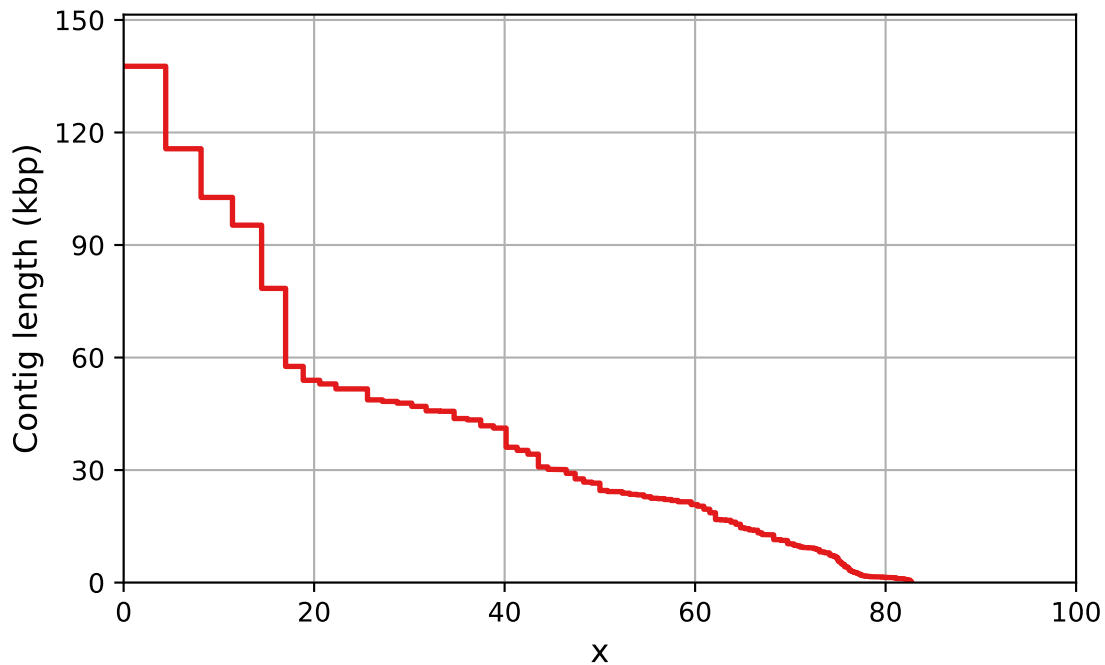
FRCurve (misassemblies)



Cumulative length (aligned contigs)

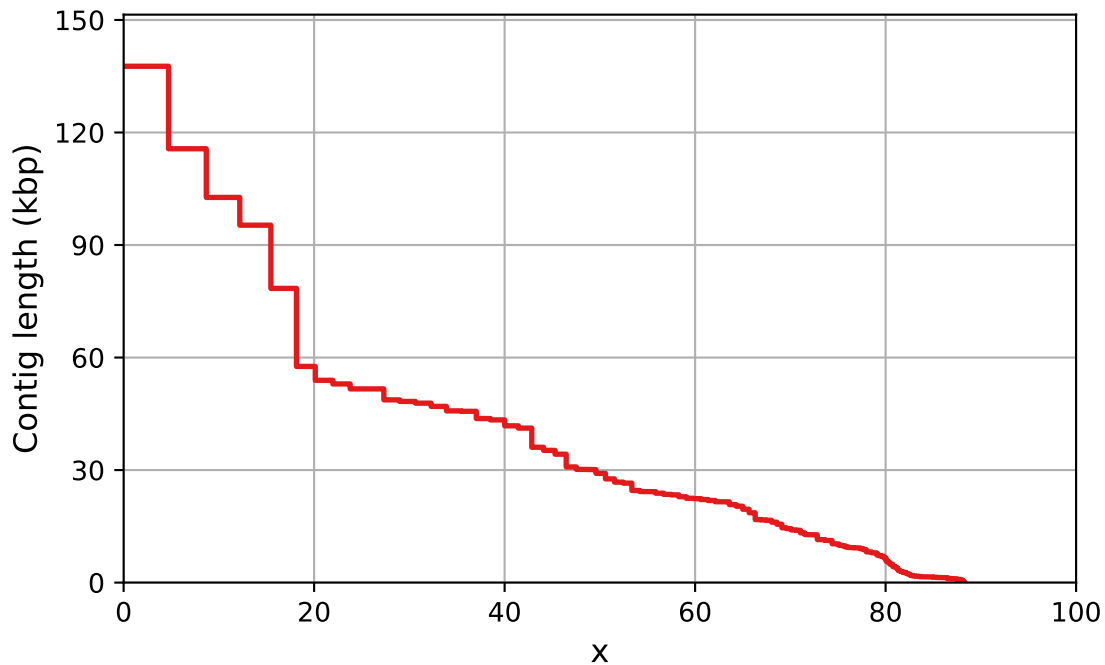


NAx



— pacbio.contigs

NGAx



— pacbio.contigs