

Report

	canu_pacbio.contigs
# contigs (>= 0 bp)	10
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3166158
Total length (>= 1000 bp)	3166158
Total length (>= 5000 bp)	3166158
Total length (>= 10000 bp)	3147084
Total length (>= 25000 bp)	3100980
Total length (>= 50000 bp)	2986958
# contigs	10
Largest contig	2775618
Total length	3166158
Reference length	3052572
GC (%)	37.73
Reference GC (%)	37.87
N50	2775618
NG50	2775618
N75	2775618
NG75	2775618
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	159
# misassembled contigs	6
Misassembled contigs length	3042849
# local misassemblies	19
# unaligned mis. contigs	3
# unaligned contigs	1 + 7 part
Unaligned length	368618
Genome fraction (%)	87.353
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	177.95
# indels per 100 kbp	19.39
Largest alignment	209800
Total aligned length	2797201
NA50	107749
NGA50	109973
NA75	15948
NGA75	22829
LA50	11
LGA50	10
LA75	33
LGA75	28

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

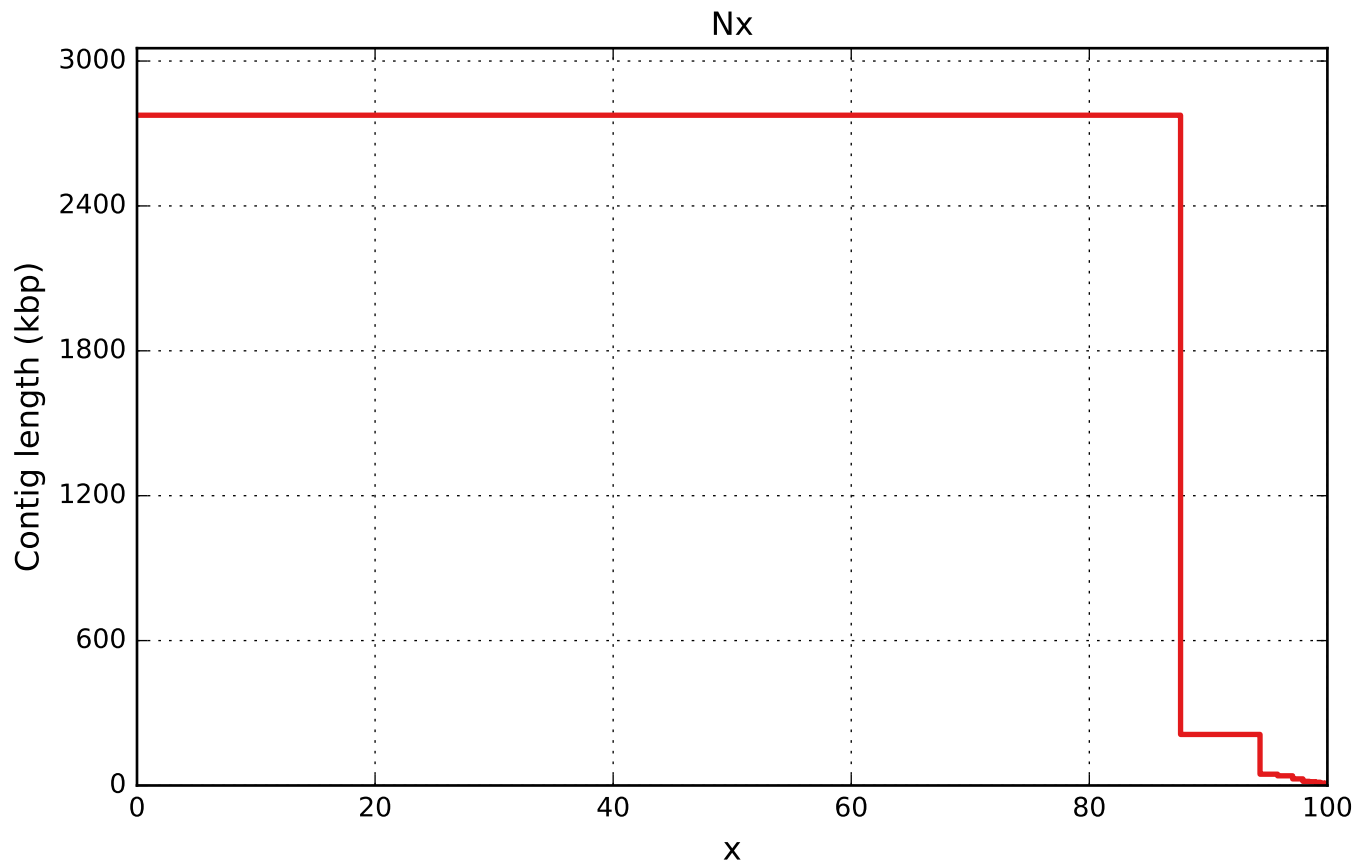
	canu_pacbio.contigs
# misassemblies	159
# relocations	100
# translocations	59
# inversions	0
# misassembled contigs	6
Misassembled contigs length	3042849
# local misassemblies	19
# unaligned mis. contigs	3
# mismatches	4745
# indels	517
# indels (≤ 5 bp)	500
# indels (> 5 bp)	17
Indels length	956

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).

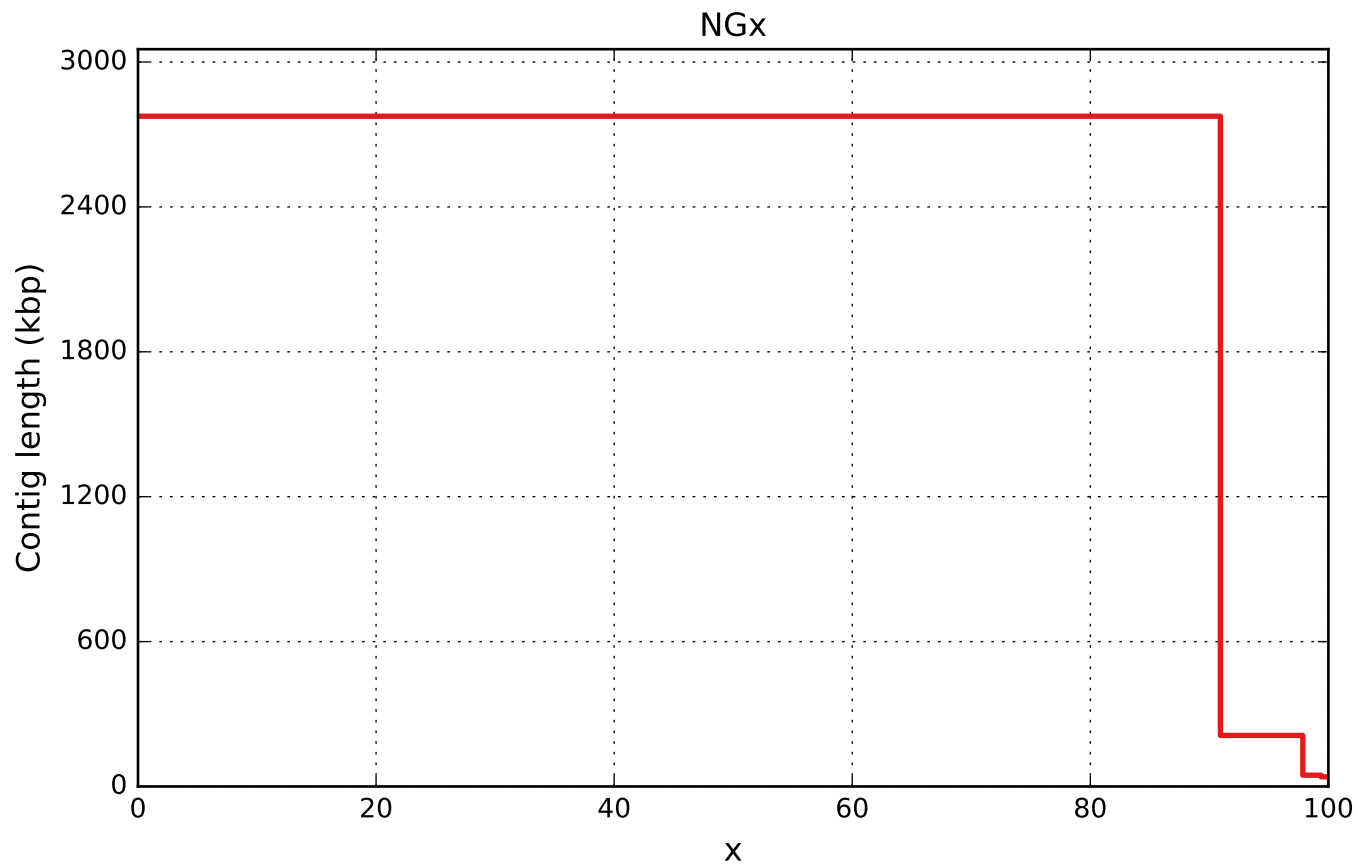
Unaligned report

	canu_pacbio.contigs
# fully unaligned contigs	1
Fully unaligned length	9287
# partially unaligned contigs	7
Partially unaligned length	359331
# N's	0

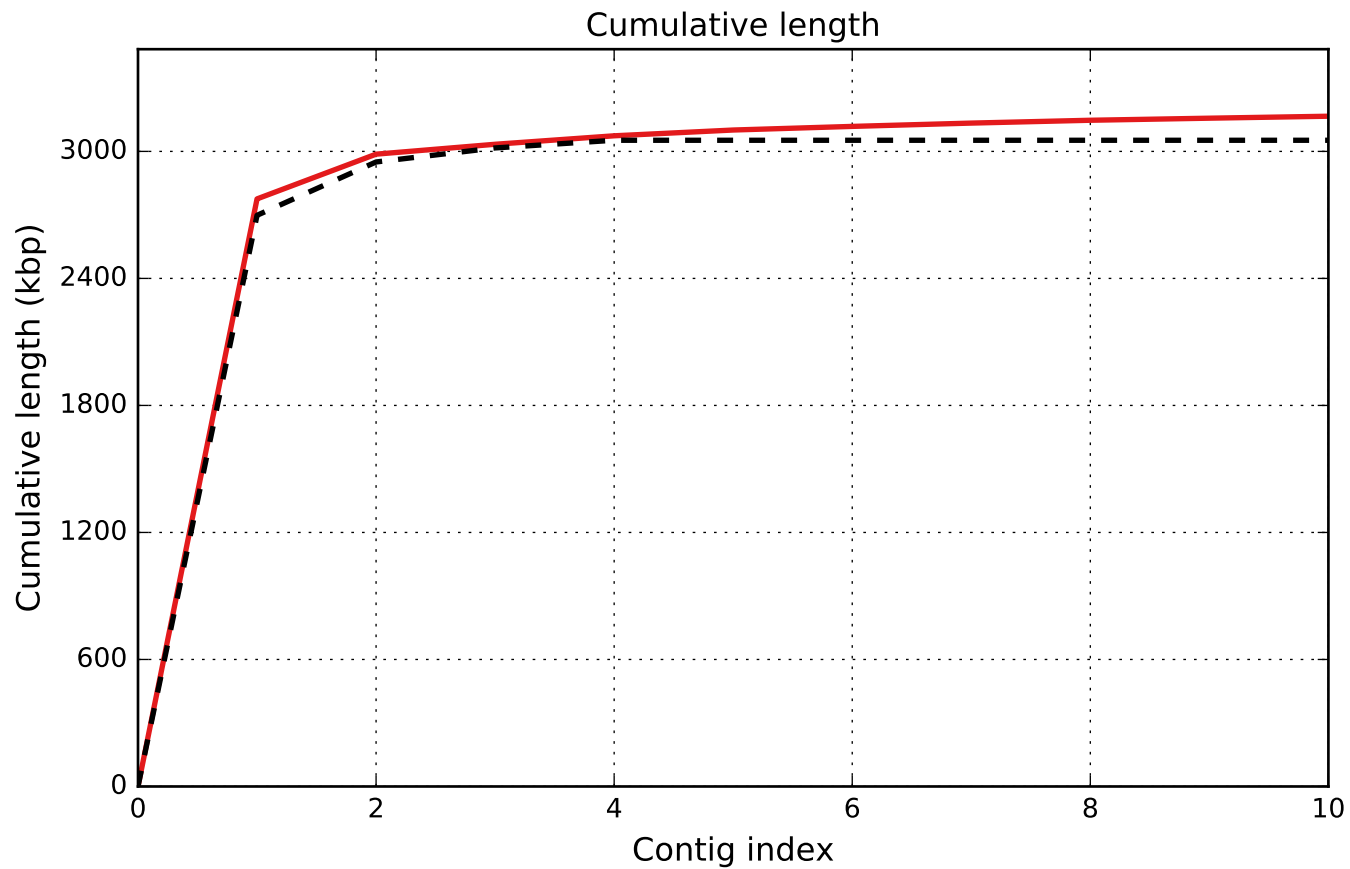
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



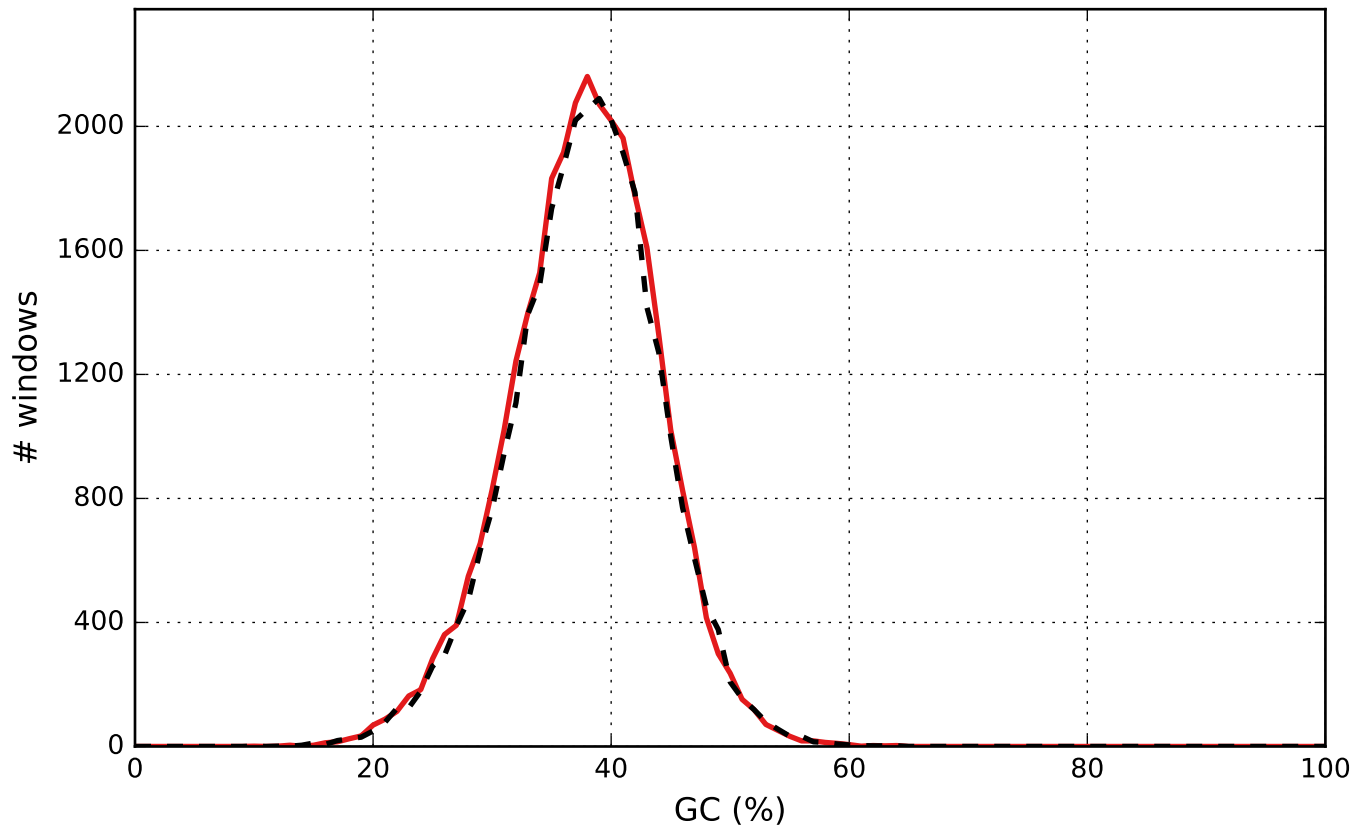
— canu_pacbio.contigs

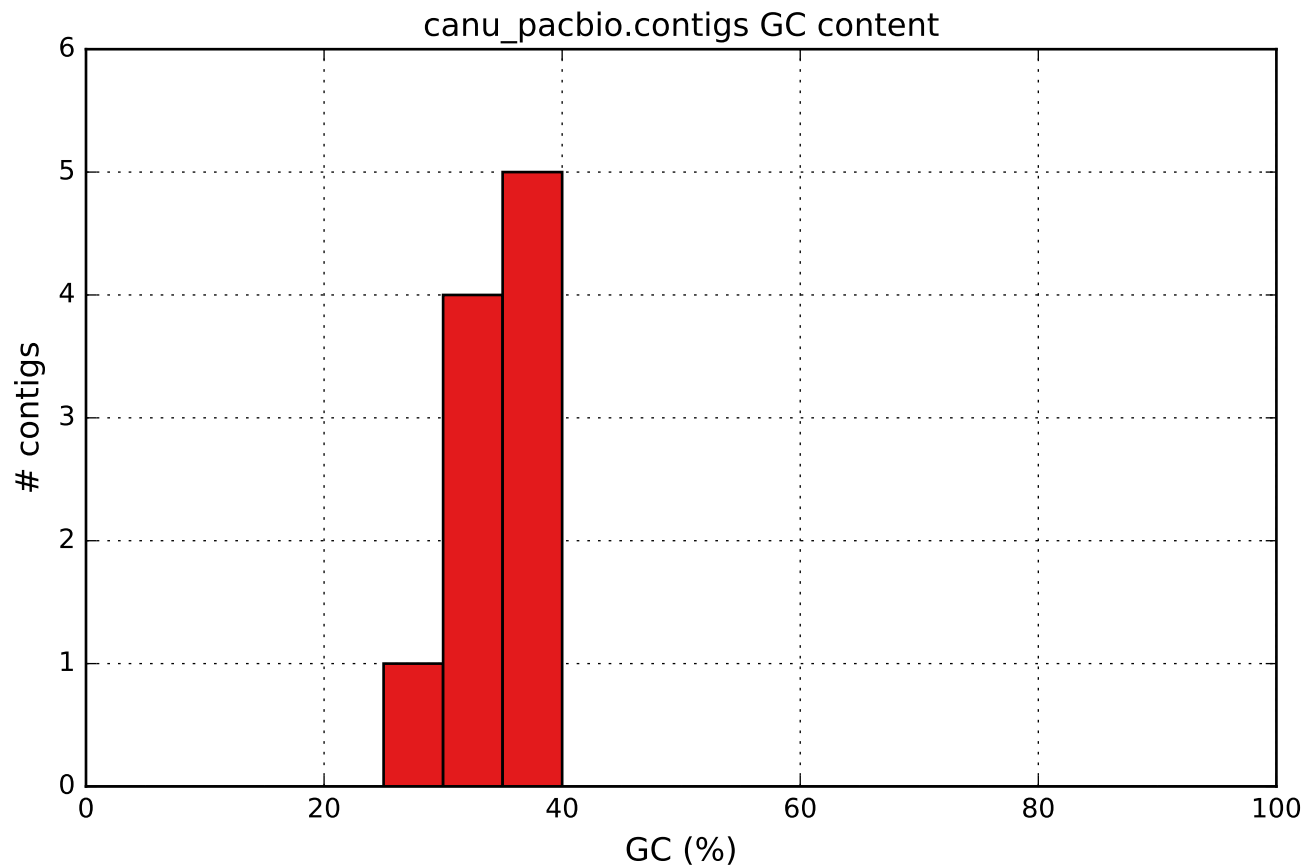


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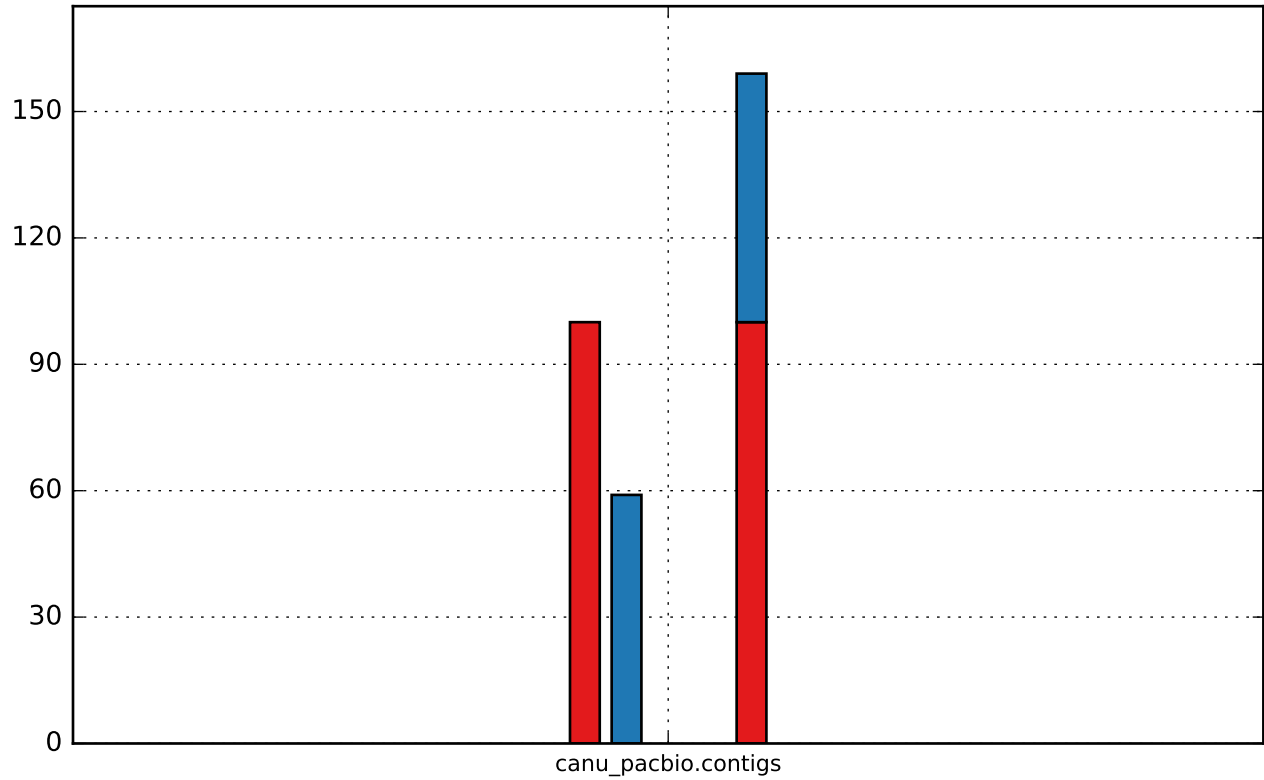
GC content



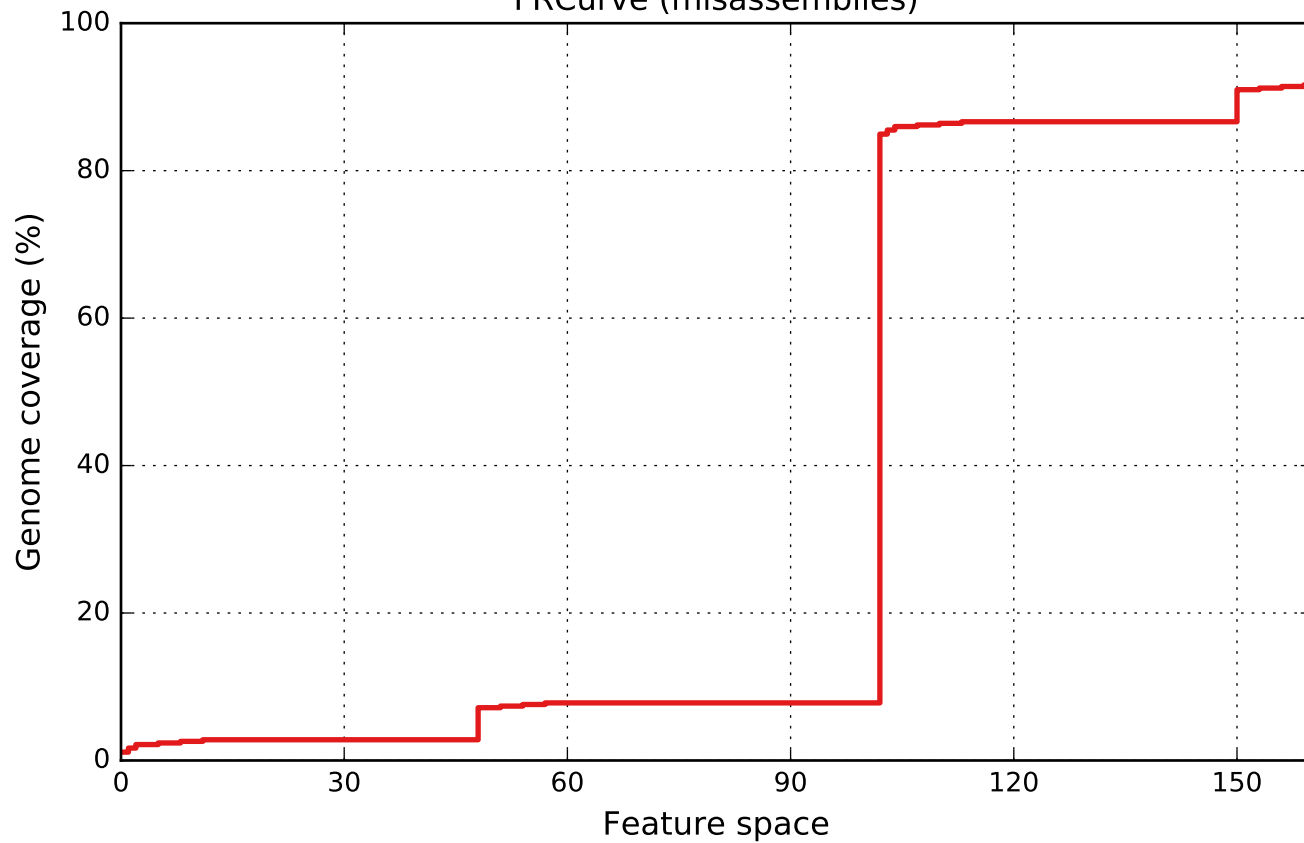


canu_pacbio.contigs

Misassemblies

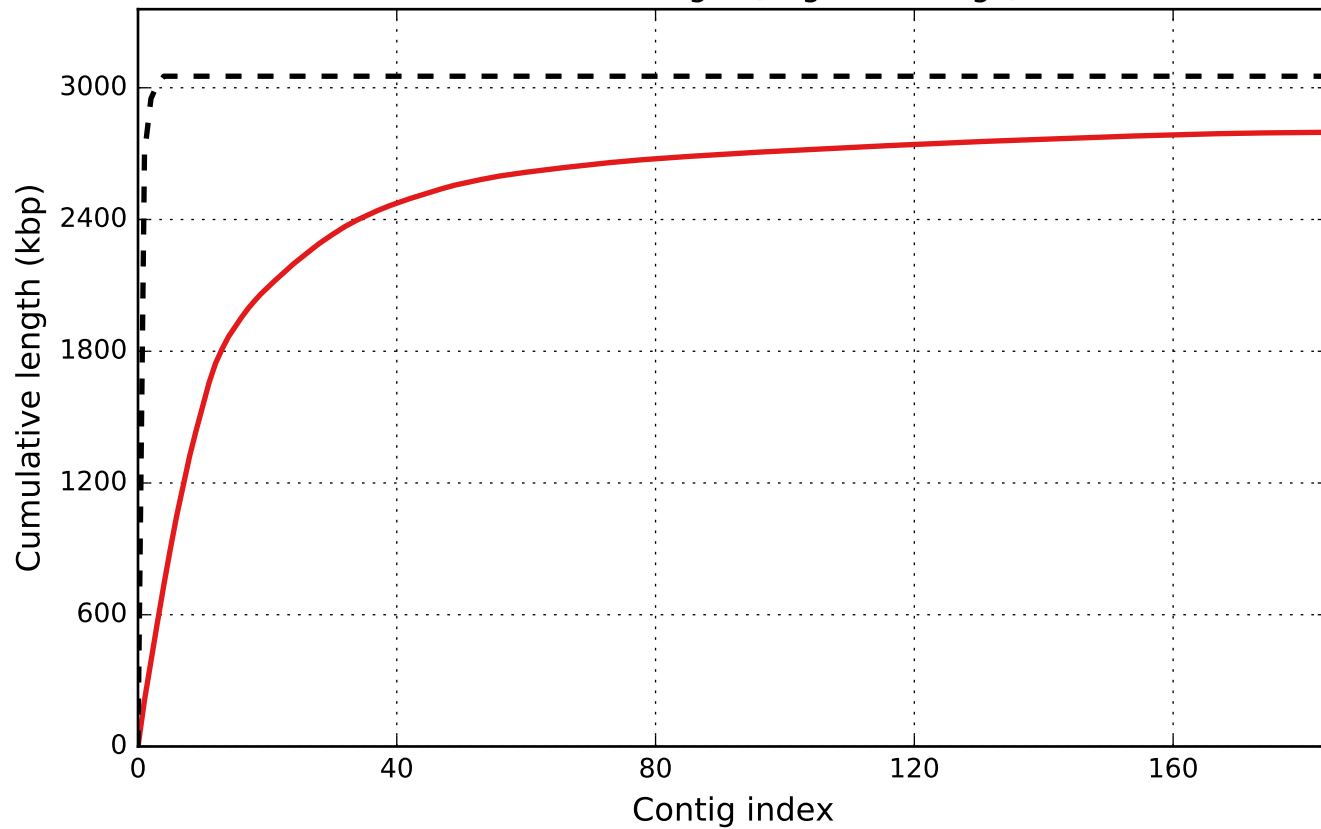


FRCurve (misassemblies)

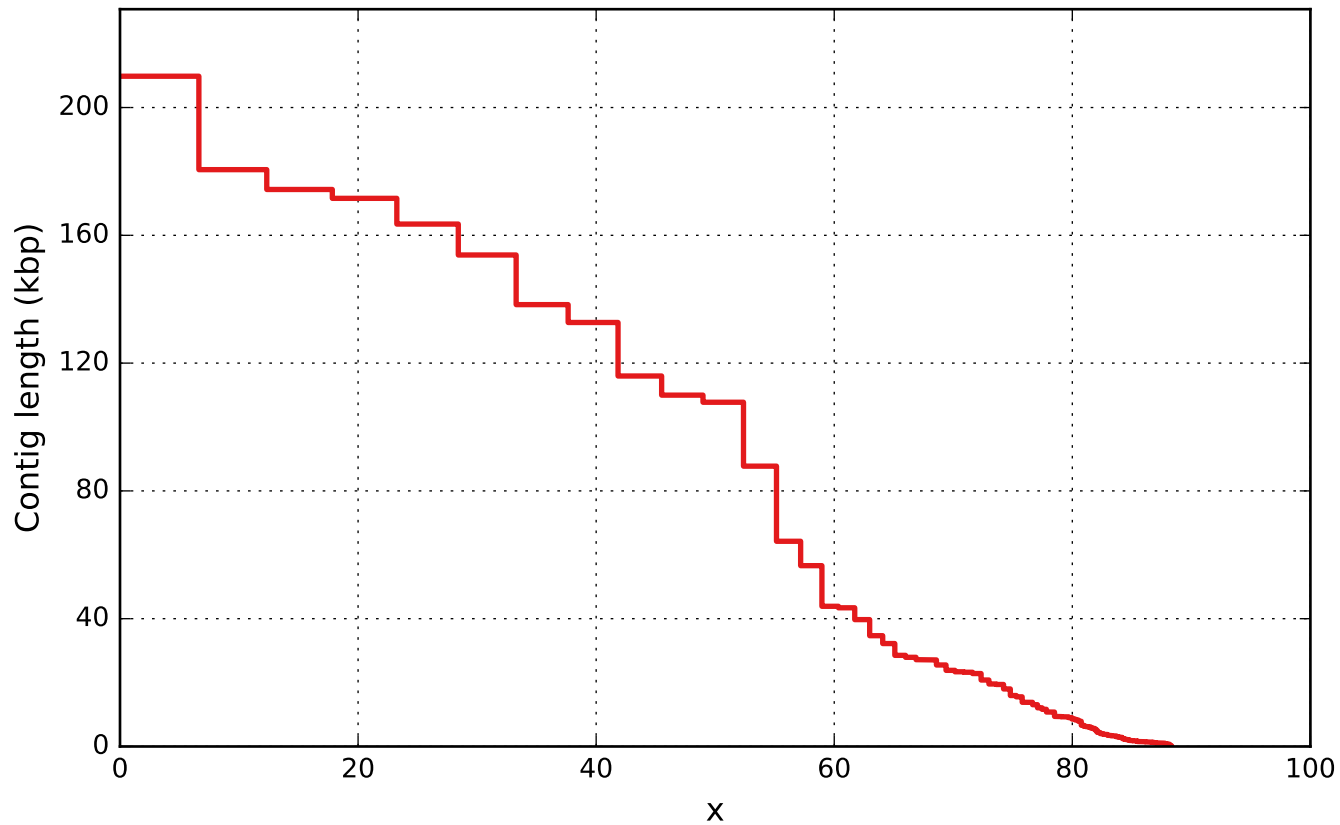


— canu_pacbio.contigs

Cumulative length (aligned contigs)

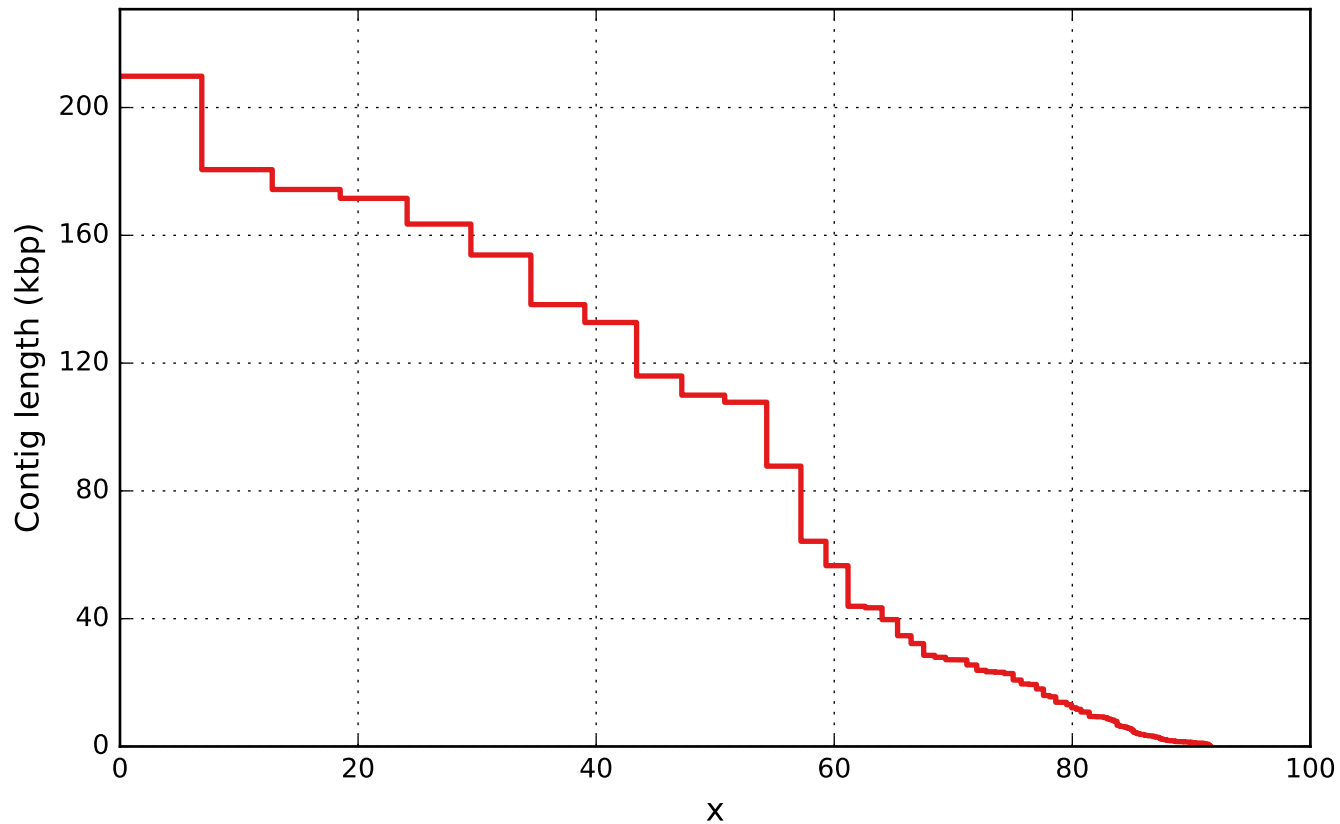


NAx



— canu_pacbio.contigs

NGAx



— canu_pacbio.contigs