

Report

	canu
# contigs (>= 0 bp)	220
# contigs (>= 1000 bp)	220
# contigs (>= 5000 bp)	217
# contigs (>= 10000 bp)	208
# contigs (>= 25000 bp)	112
# contigs (>= 50000 bp)	65
Total length (>= 0 bp)	122008493
Total length (>= 1000 bp)	122008493
Total length (>= 5000 bp)	121997856
Total length (>= 10000 bp)	121924816
Total length (>= 25000 bp)	120297064
Total length (>= 50000 bp)	118689182
# contigs	219
Largest contig	14950415
Total length	122006507
Reference length	119667750
GC (%)	36.20
Reference GC (%)	36.06
N50	10092069
NG50	10092069
N90	543641
NG90	798456
auN	8244705.2
auNG	8405837.7
L50	5
LG50	5
L90	25
LG90	22
# total reads	1128688
# left	0
# right	0
Mapped (%)	135.05
Reference mapped (%)	144.91
Properly paired (%)	0.0
Reference properly paired (%)	0.0
Avg. coverage depth	73
Reference avg. coverage depth	67
Coverage >= 1x (%)	99.88
Reference coverage >= 1x (%)	98.54
# misassemblies	625
# misassembled contigs	104
Misassembled contigs length	117393025
# local misassemblies	3293
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	56
# unaligned mis. contigs	41
# unaligned contigs	16 + 153 part
Unaligned length	12498375
Genome fraction (%)	89.244
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	731.97
# indels per 100 kbp	156.88
# genomic features	0 + 0 part
Largest alignment	6946206
Total aligned length	109458890
NA50	567344
NGA50	641675
NA90	-
NGA90	8340
auNA	1579465.1
auNGA	1610333.8
LA50	34
LGA50	32
LA90	-
LGA90	557

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Reads report

	canu
# total reads	1128688
# left	0
# right	0
# mapped	1524317
Mapped (%)	135.05
# properly paired	0
Properly paired (%)	0.0
# singletons	0
Singletons (%)	0.0
# misjoint mates	0
Misjoint mates (%)	0.0
Avg. coverage depth	73
Coverage >= 1x (%)	99.88
Coverage >= 5x (%)	99.8
Coverage >= 10x (%)	99.75
# reference mapped	1635611
Reference mapped (%)	144.91
# reference properly paired	0
Reference properly paired (%)	0.0
# reference singletons	0
Reference singletons (%)	0.0
# reference misjoint mates	0
Reference misjoint mates (%)	0.0
Reference avg. coverage depth	67
Reference coverage >= 1x (%)	98.54
Reference coverage >= 5x (%)	96.96
Reference coverage >= 10x (%)	96.18

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

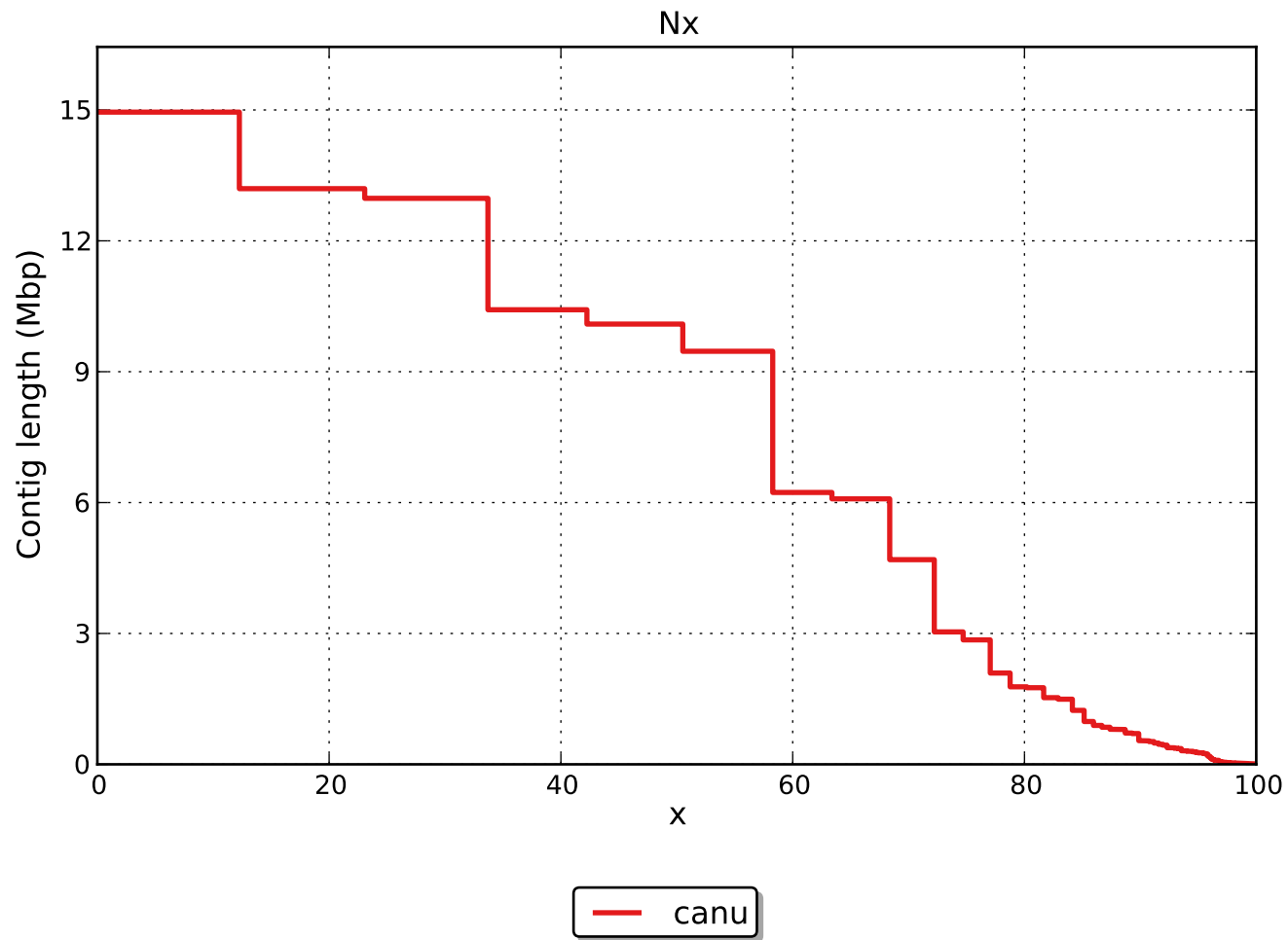
	canu
# misassemblies	625
# contig misassemblies	625
# c. relocations	461
# c. translocations	152
# c. inversions	12
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	104
Misassembled contigs length	117393025
# local misassemblies	3293
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	56
# unaligned mis. contigs	41
# mismatches	801205
# indels	171722
# indels (<= 5 bp)	142090
# indels (> 5 bp)	29632
Indels length	1786054

All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

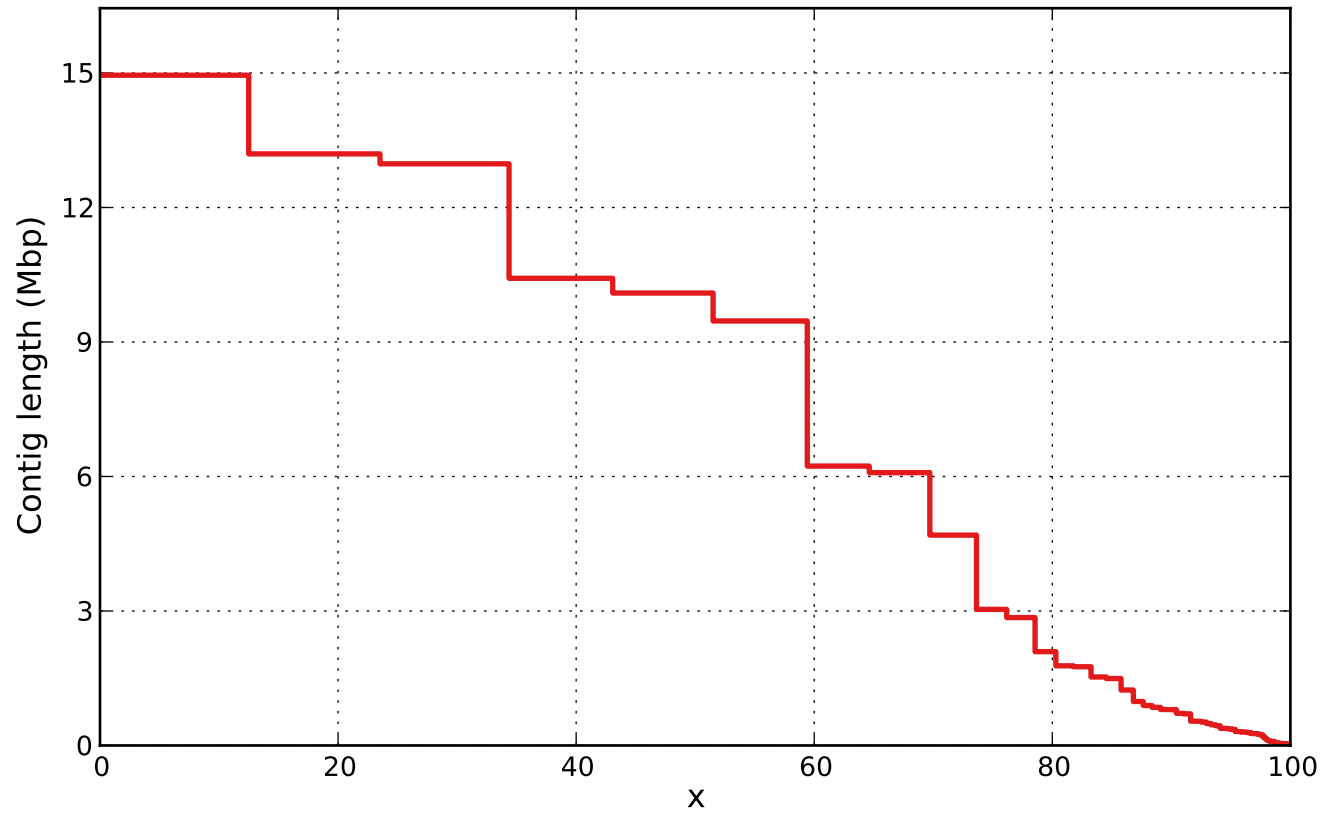
## Unaligned report

	canu
# fully unaligned contigs	16
Fully unaligned length	197356
# partially unaligned contigs	153
Partially unaligned length	12301019
# N's	0

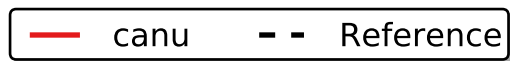
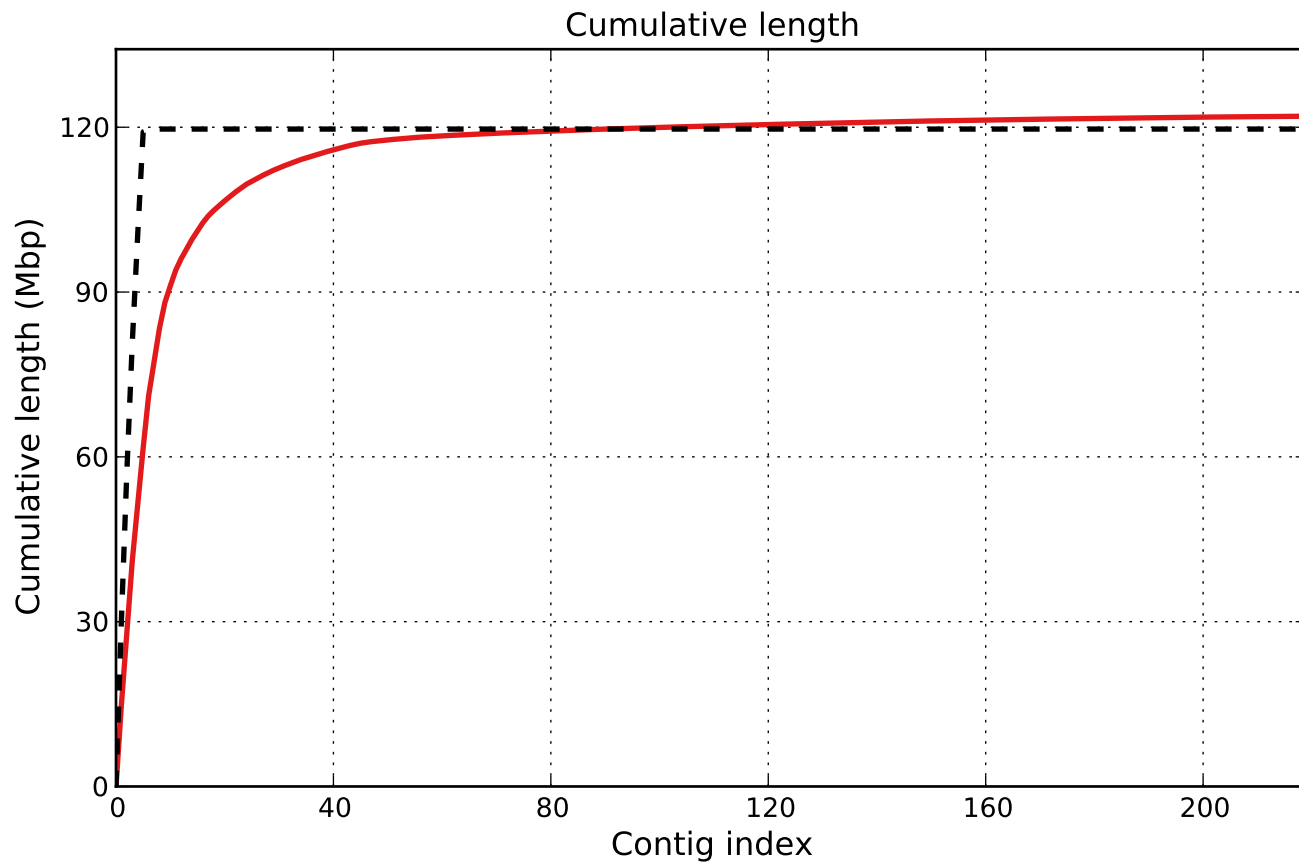
All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

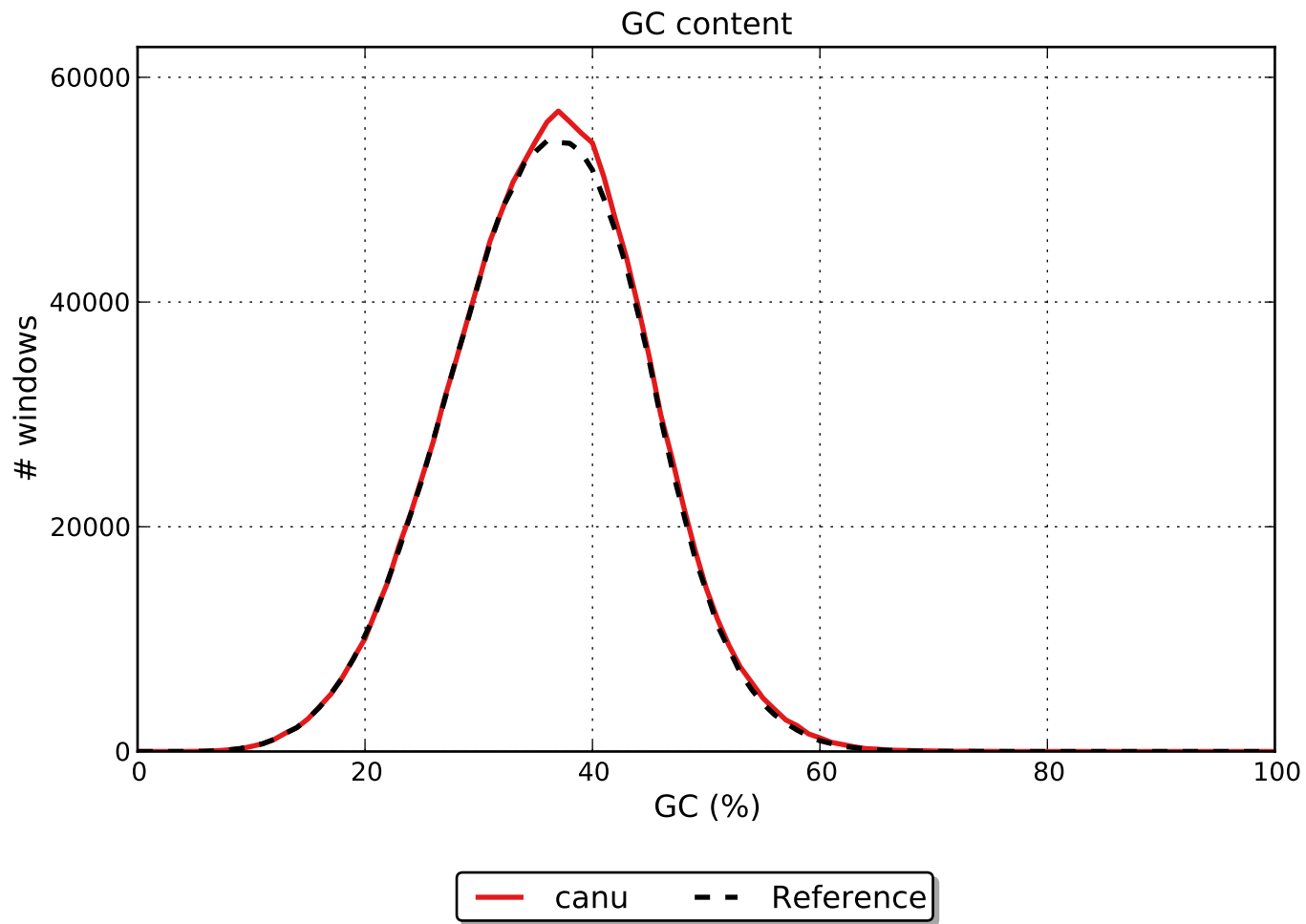


NGx



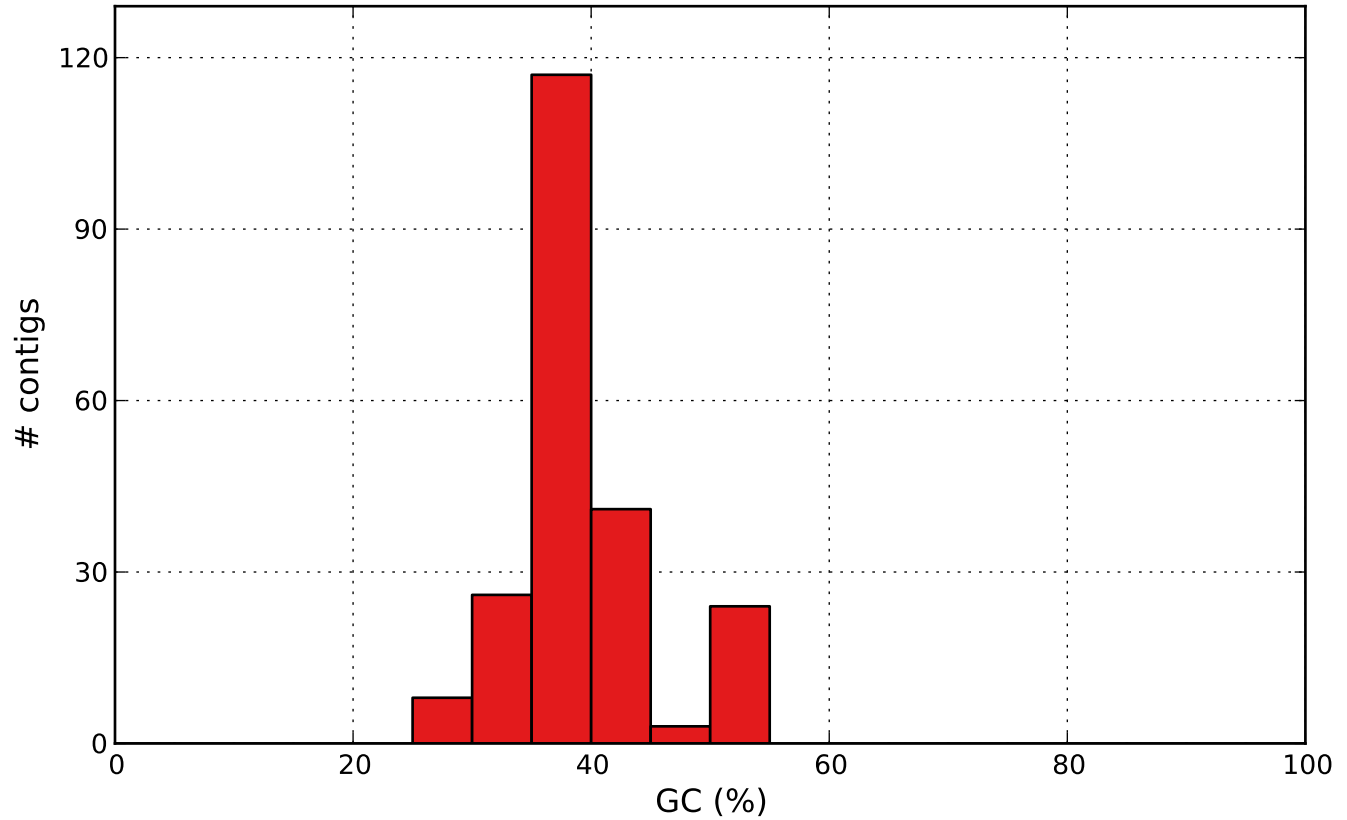
— canu





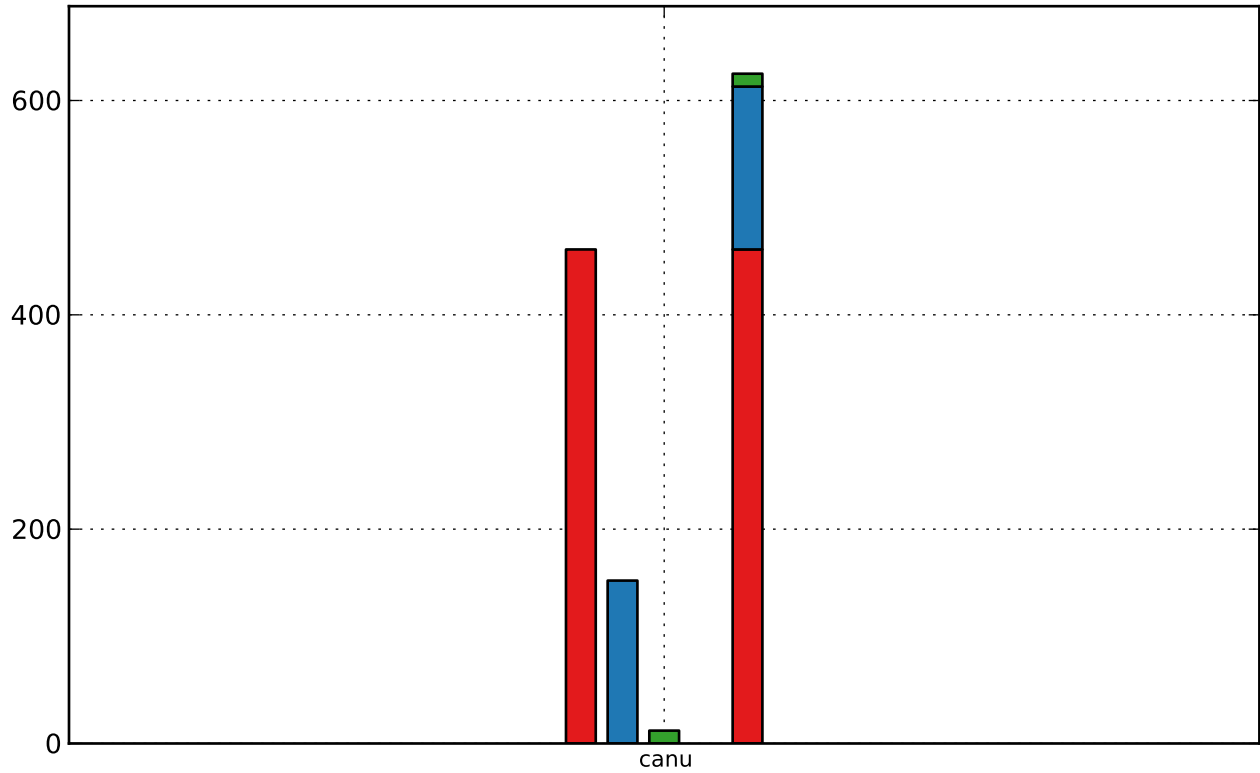


canu GC content



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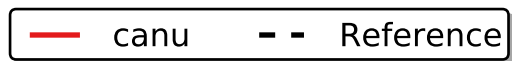
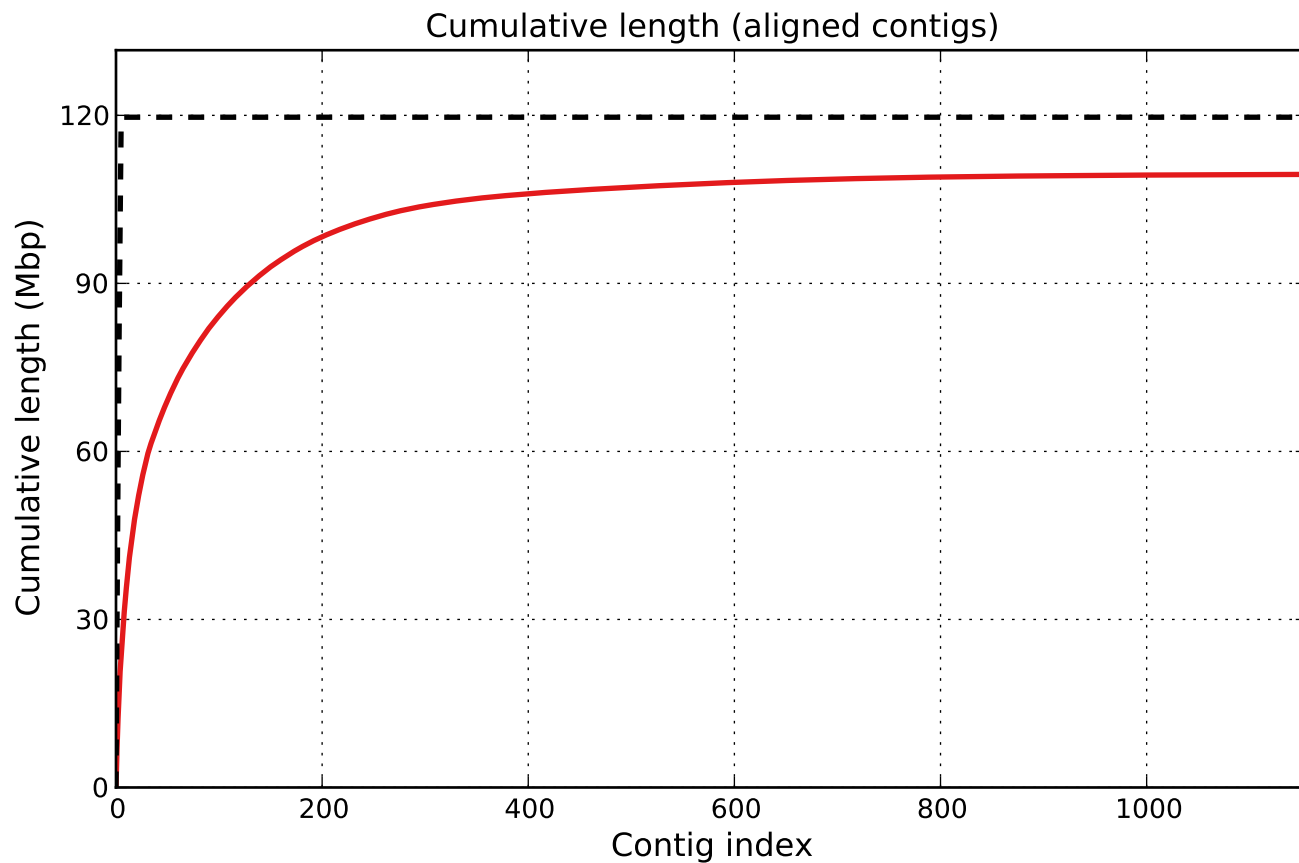
# Misassemblies



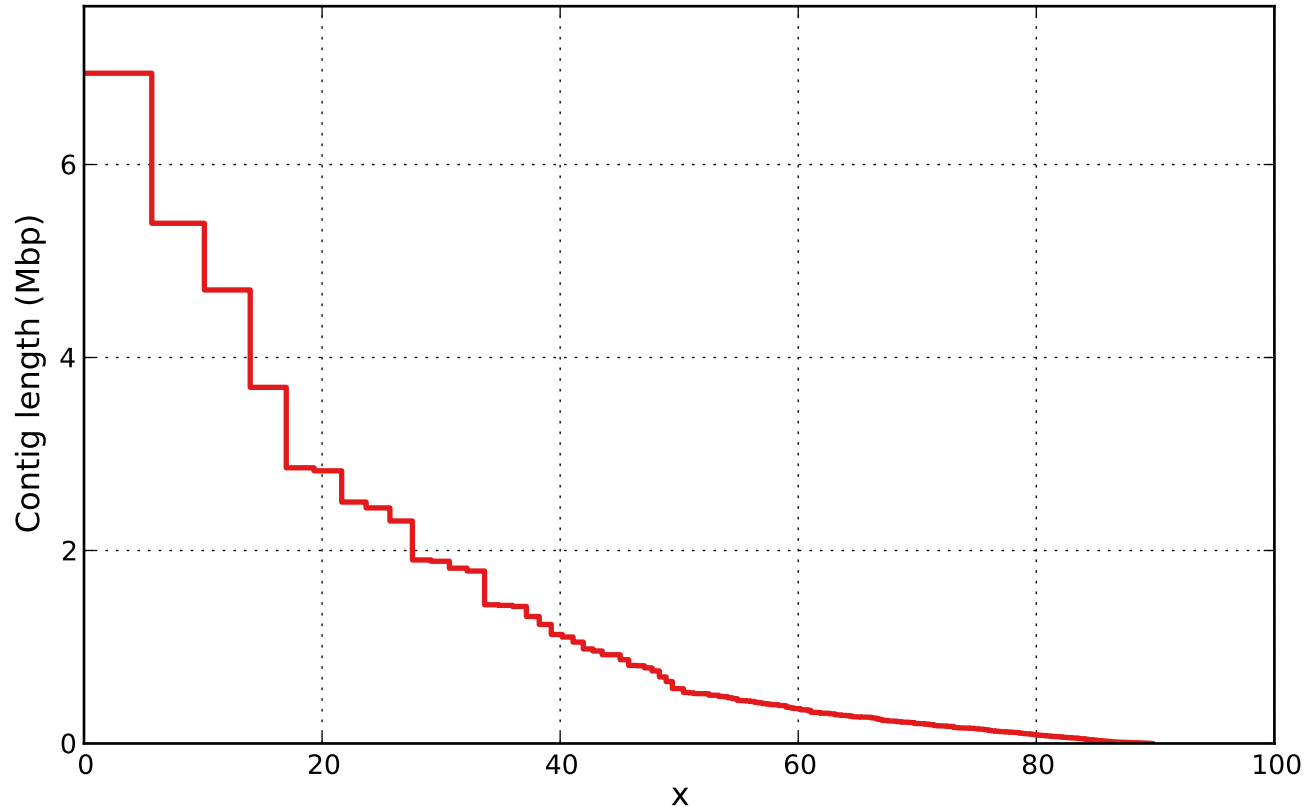
FRCurve (misassemblies)



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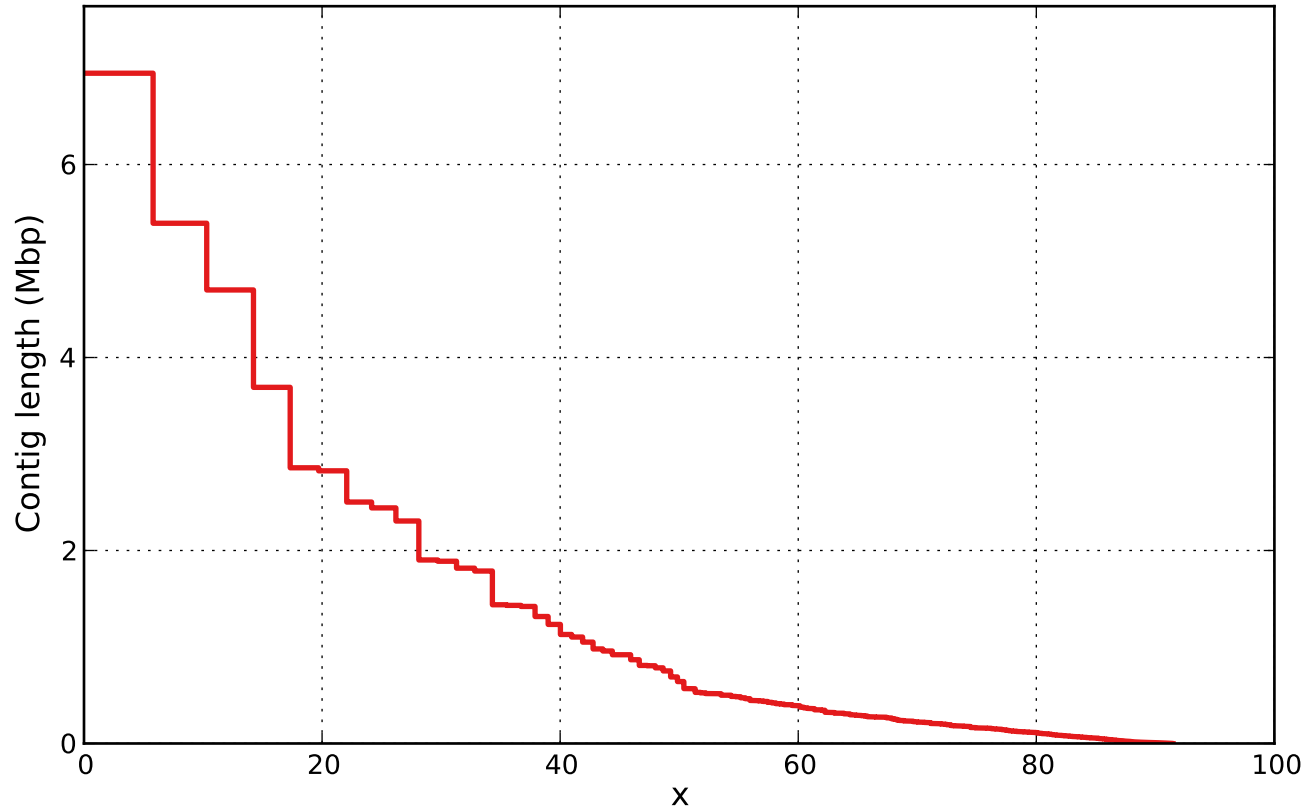


NAx

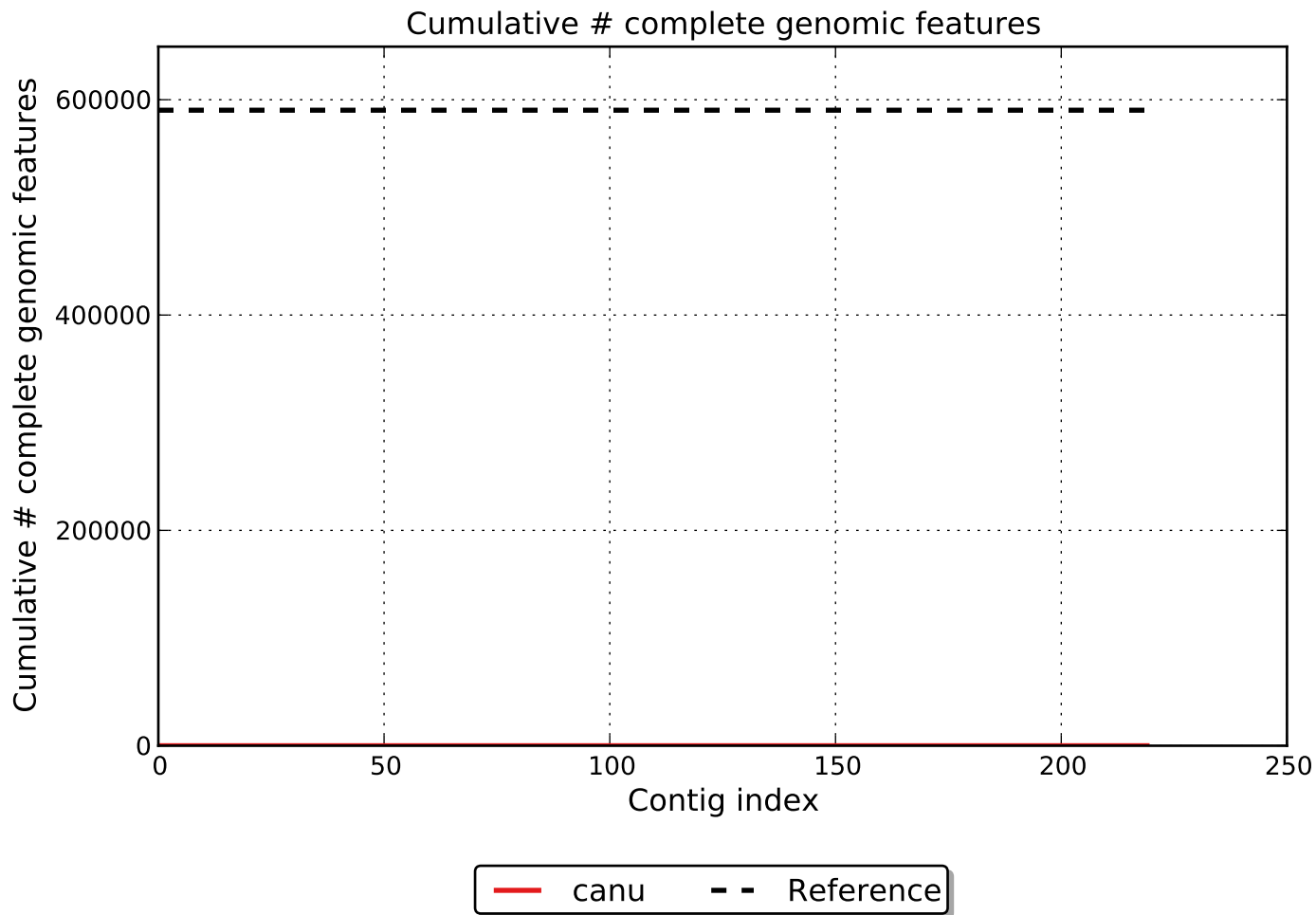


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NGAx



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FRCurve (genomic features)

