Report

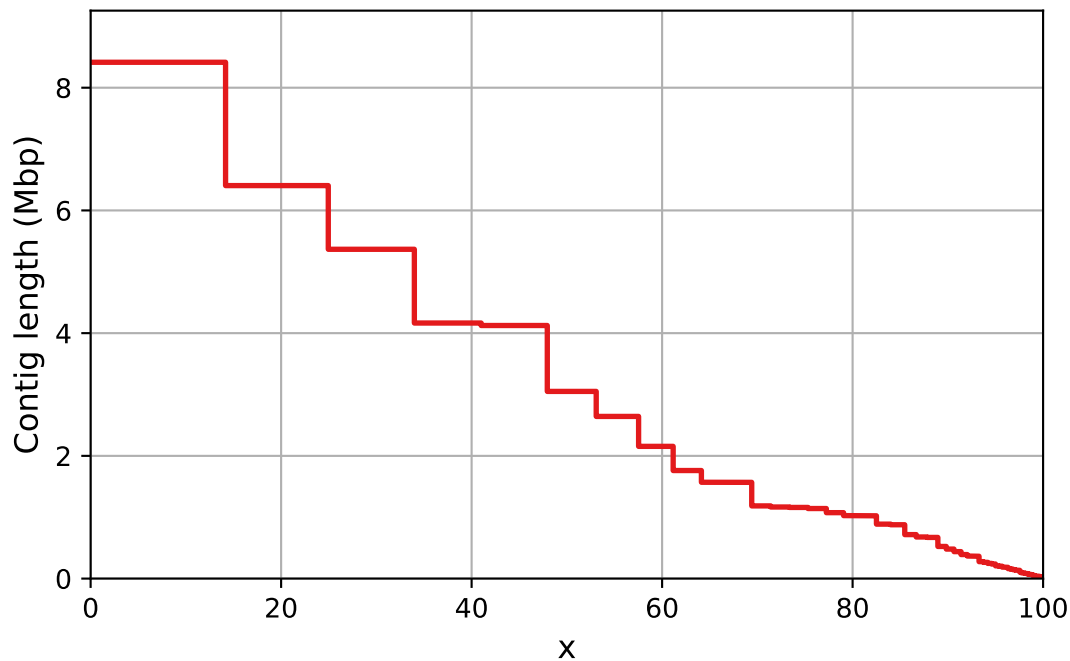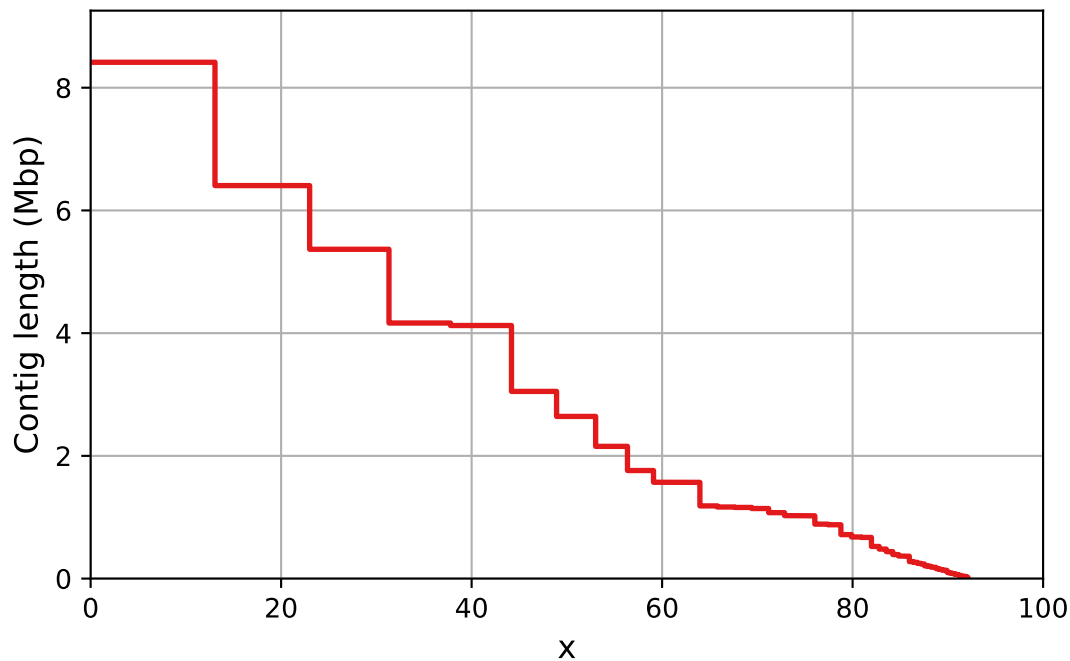|	canu.chr20.scrappie
# contigs (>= 0 bp)	74
# contigs (>= 1000 bp)	74
# contigs (>= 5000 bp)	73
# contigs (>= 10000 bp)	71
# contigs (>= 25000 bp)	67
# contigs (>= 50000 bp)	54
Total length (>= 0 bp)	59392510
Total length (>= 1000 bp)	59392510
Total length (>= 5000 bp)	59390967
Total length (>= 10000 bp)	59378577
Total length (>= 25000 bp)	59324213
Total length (>= 50000 bp)	58848273
# contigs	73
Largest contig	8414576
Total length	59390967
Reference length	64444167
GC (%)	43.46
Reference GC (%)	43.80
N50	3050487
NG50	2642832
N75	1159515
NG75	1023187
L50	6
LG50	7
L75	14
LG75	18
# misassemblies	12
# misassembled contigs	8
Misassembled contigs length	8654259
# local misassemblies	1181
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	12
# unaligned contigs	6 + 67 part
Unaligned length	4037954
Genome fraction (%)	87.709
Duplication ratio	0.987
# N's per 100 kbp	0.00
# mismatches per 100 kbp	587.66
# indels per 100 kbp	1314.70
Largest alignment	8093490
Total aligned length	55350237
NA50	2529146
NGA50	1622860
NA75	985177
NGA75	653187
LA50	6
LGA50	8
LA75	18
LGA75	22

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.chr20.scrappie
# misassemblies	12
# contig misassemblies	12
# c. relocations	12
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	8654259
# local misassemblies	1181
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	12
# mismatches	329592
# indels	737352
# indels (<= 5 bp)	720455
# indels (> 5 bp)	16897
Indels length	1266999

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).
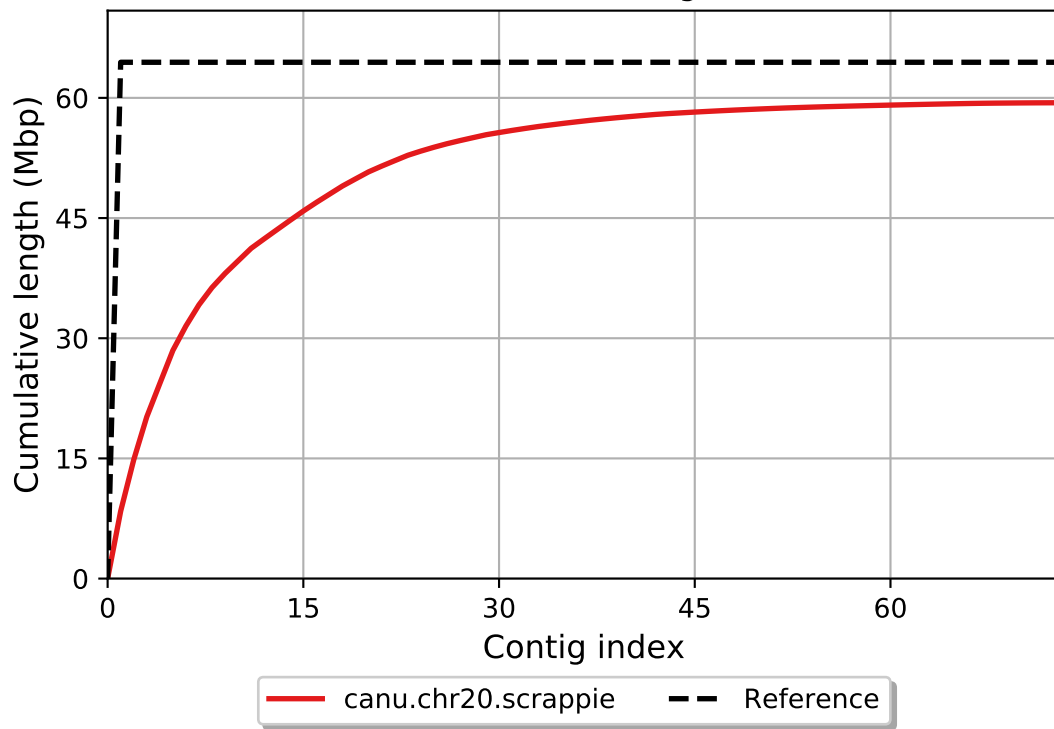
Unaligned report

	canu.chr20.scrappie
# fully unaligned contigs	6
Fully unaligned length	136554
# partially unaligned contigs	67
Partially unaligned length	3901400
# N's	0

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).
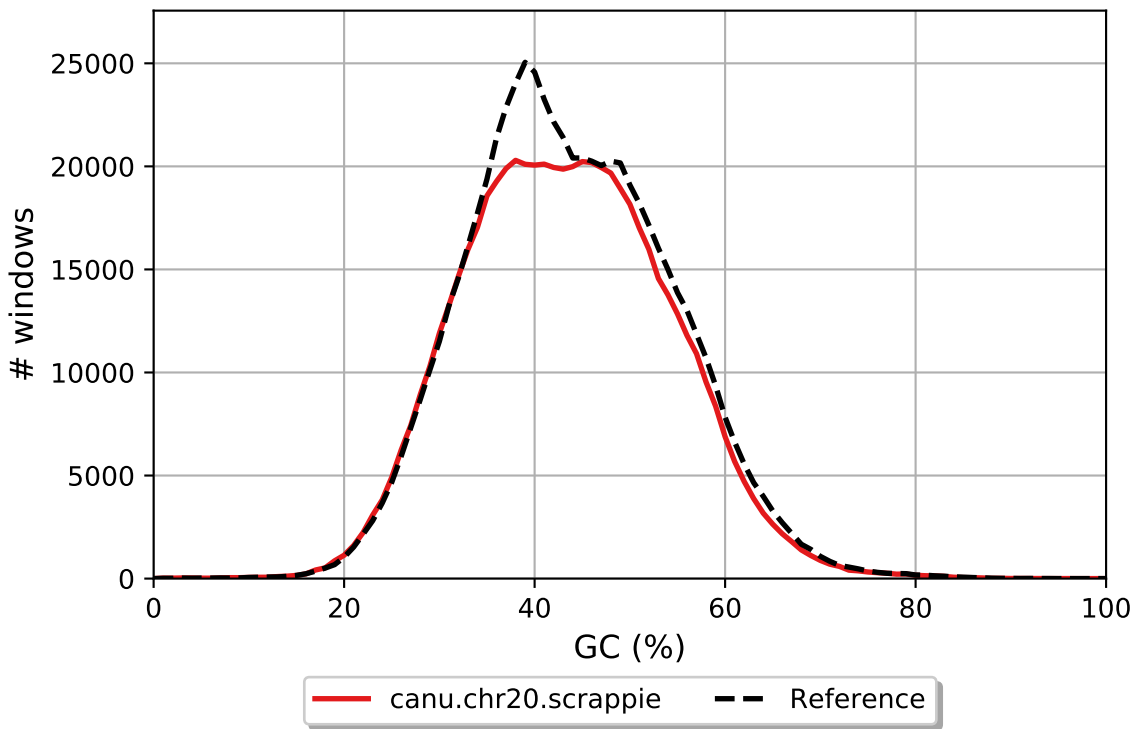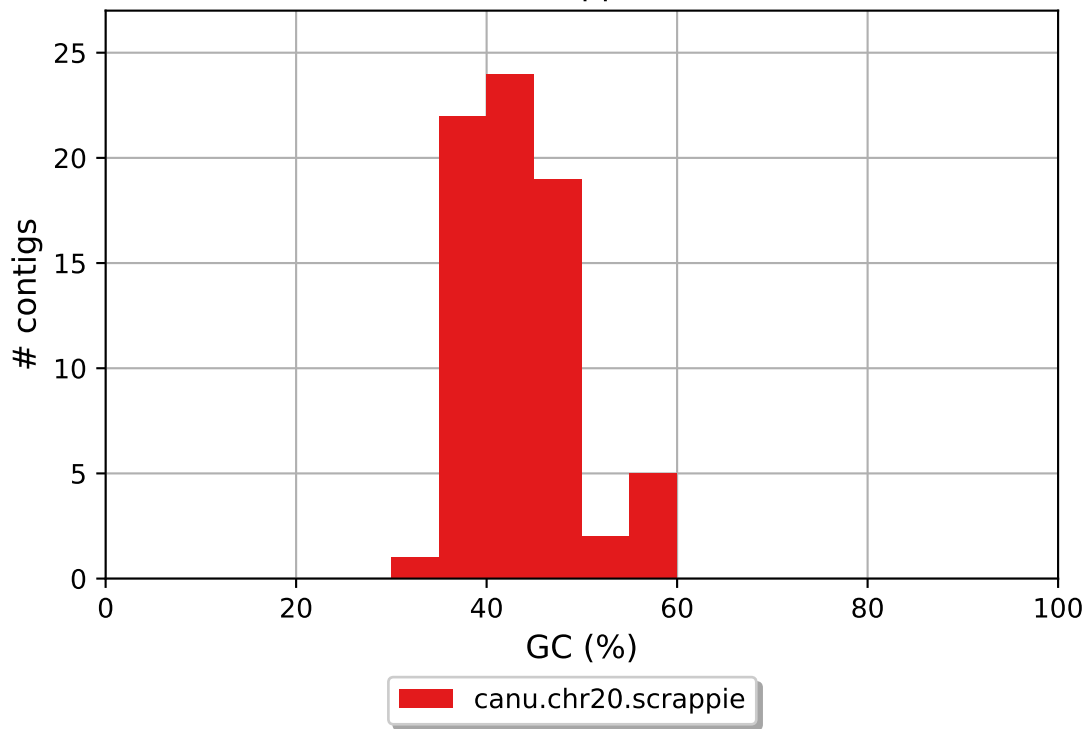
Nx

canu.chr20.scrappie

NGx

Cumulative length

Cumulative length (Mbp) vs Contig index

Legend: canu.chr20.scrappie (red solid line), Reference (black dashed line)

GC content

windows vs GC (%)
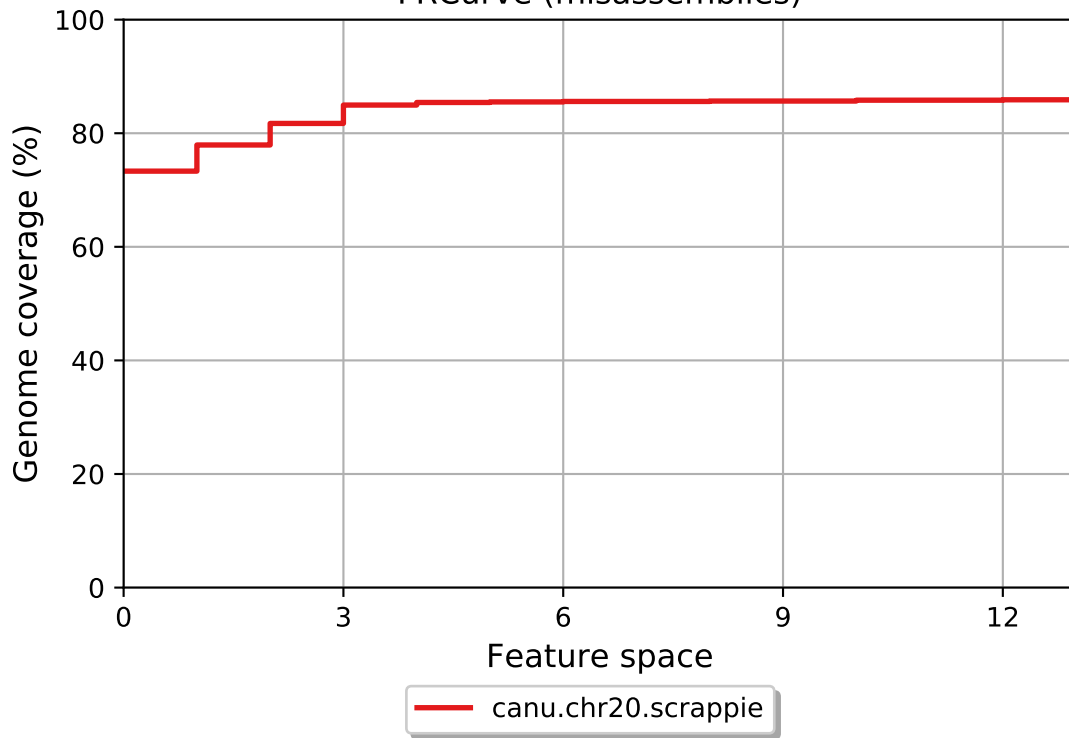
- canu.chr20.scrappie
- Reference

canu.chr20.scrappie GC content
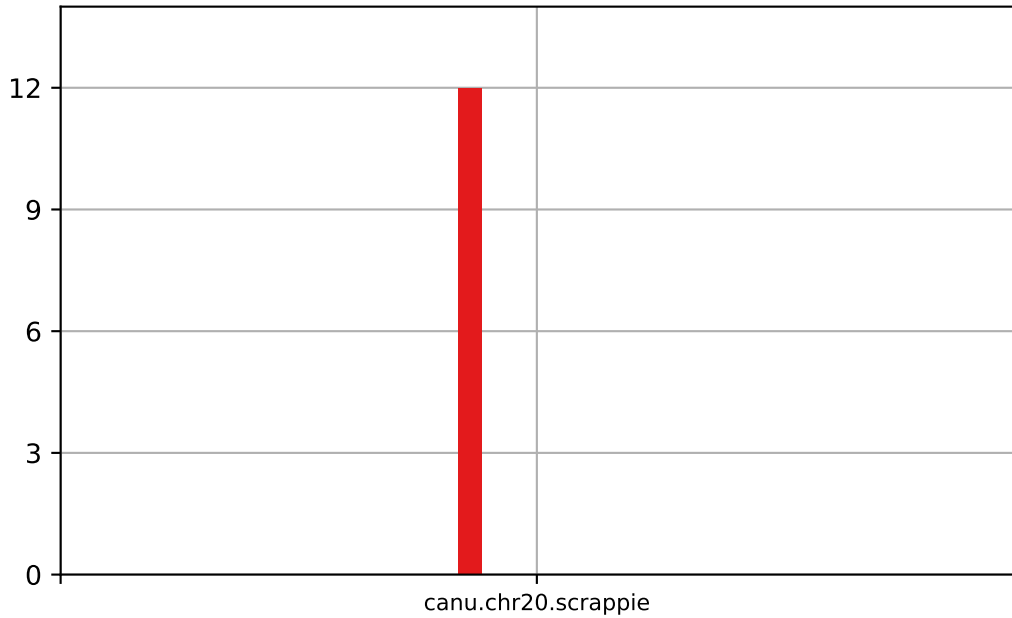
Misassemblies

FRCurve (misassemblies)
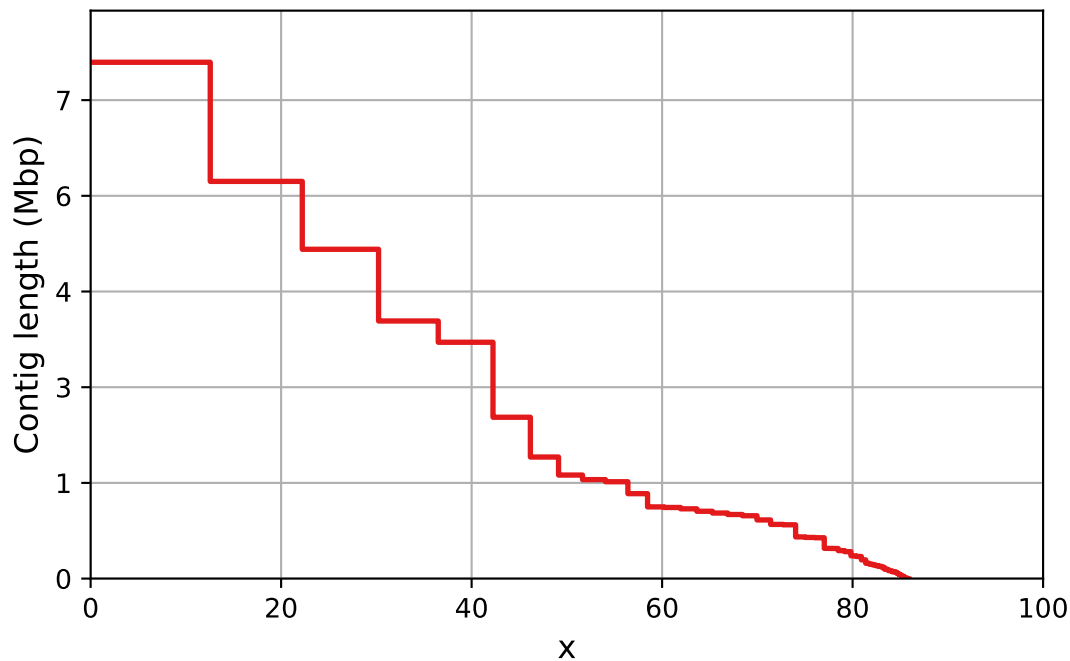
Cumulative length (aligned contigs)

NAx

NGAx