Report

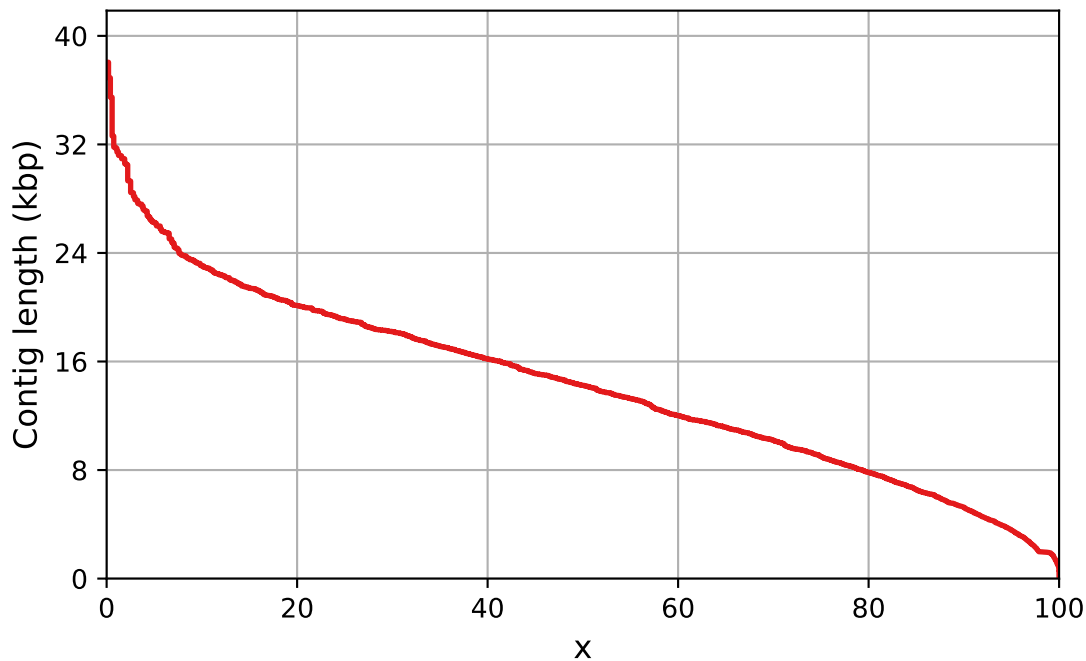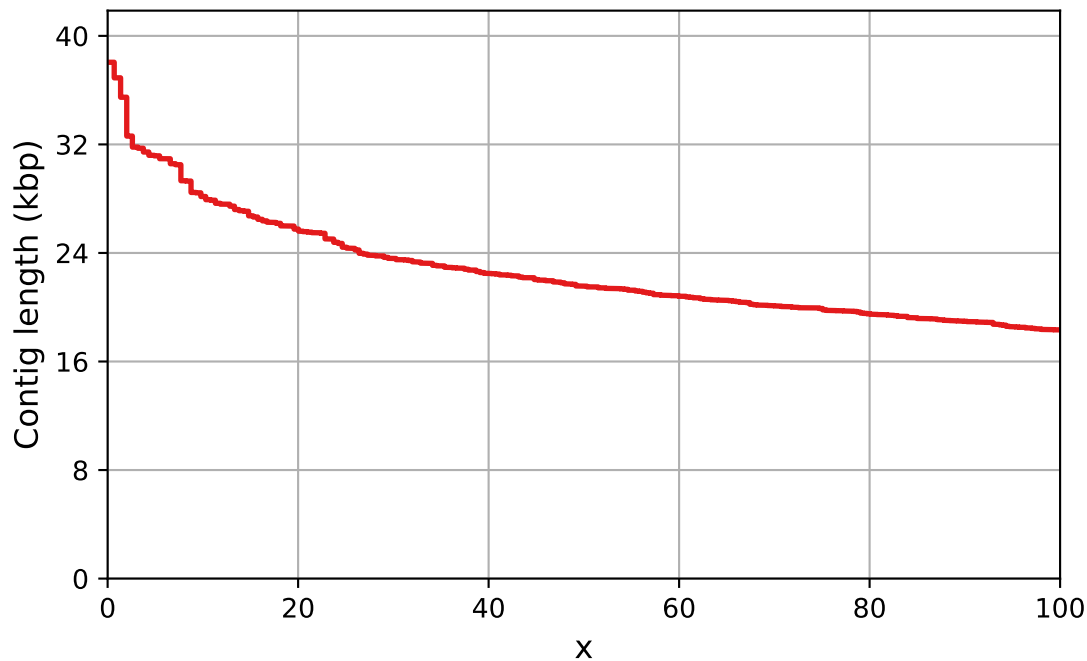|	AJ055.CanuH.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1960
# contigs (>= 5000 bp)	1349
# contigs (>= 10000 bp)	833
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	19127352
Total length (>= 1000 bp)	19099404
Total length (>= 5000 bp)	17334600
Total length (>= 10000 bp)	13559800
Total length (>= 25000 bp)	1306368
Total length (>= 50000 bp)	0
# contigs	1991
Largest contig	38054
Total length	19124602
Reference length	5504133
GC (%)	57.21
Reference GC (%)	57.38
N50	14238
NG50	21550
N75	8996
NG75	19906
L50	499
LG50	110
L75	916
LG75	176
# misassemblies	32
# misassembled contigs	32
Misassembled contigs length	512034
# local misassemblies	31
# unaligned mis. contigs	0
# unaligned contigs	203 + 38 part
Unaligned length	889890
Genome fraction (%)	94.786
Duplication ratio	3.495
# N's per 100 kbp	0.00
# mismatches per 100 kbp	49.78
# indels per 100 kbp	371.26
Largest alignment	35472
Total aligned length	18208888
NA50	13694
NGA50	21249
NA75	8201
NGA75	19452
LA50	512
LGA50	113
LA75	958
LGA75	181

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

	AJ055.CanuH.cr
# misassemblies	32
# relocations	32
# translocations	0
# inversions	0
# misassembled contigs	32
Misassembled contigs length	512034
# local misassemblies	31
# unaligned mis. contigs	0
# mismatches	2597
# indels	19369
# indels (<= 5 bp)	19151
# indels (> 5 bp)	218
Indels length	25720

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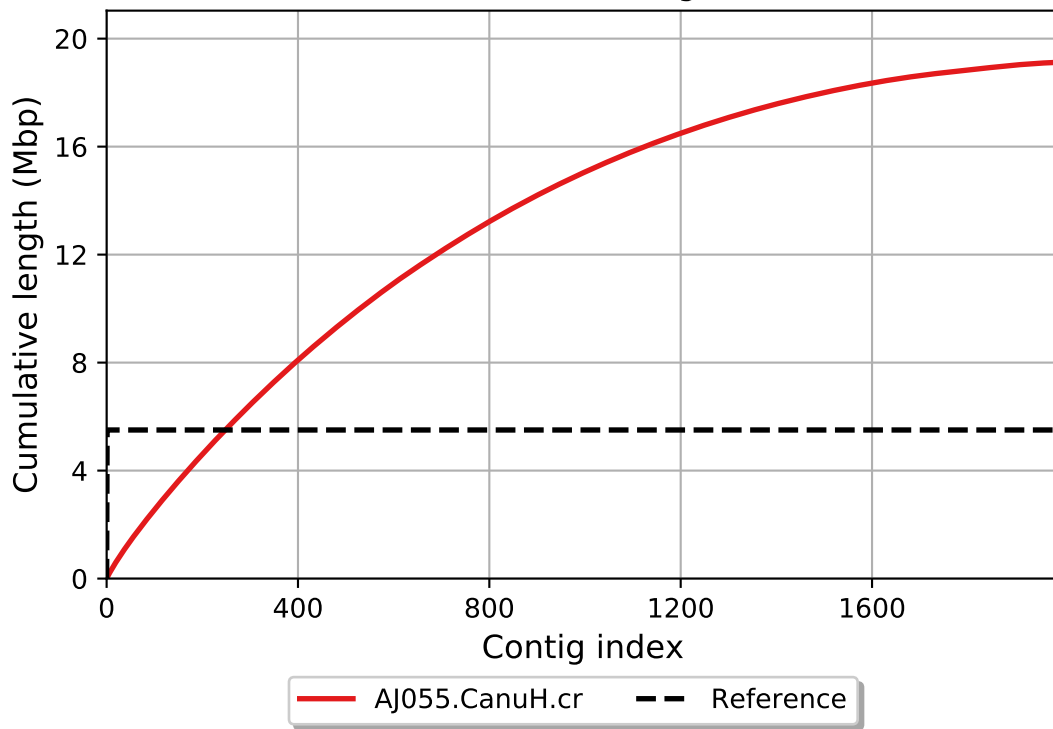(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Unaligned report

	AJ055.CanuH.cr
# fully unaligned contigs	203
Fully unaligned length	799242
# partially unaligned contigs	38
Partially unaligned length	90648
# 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).
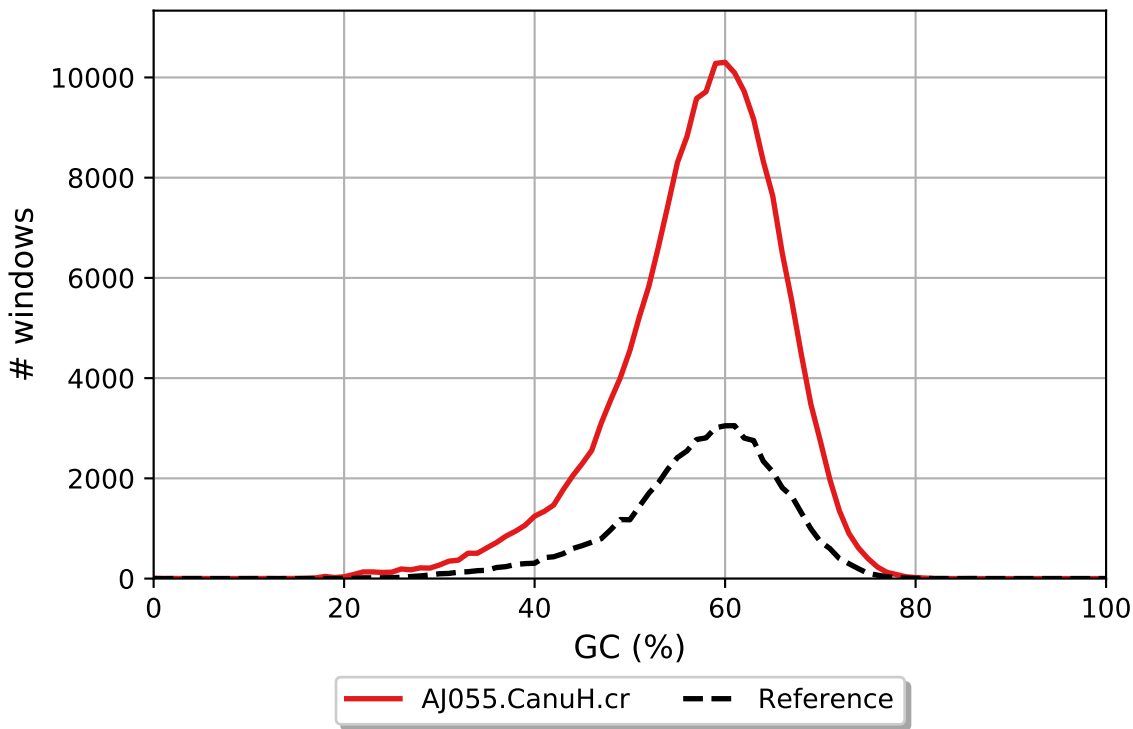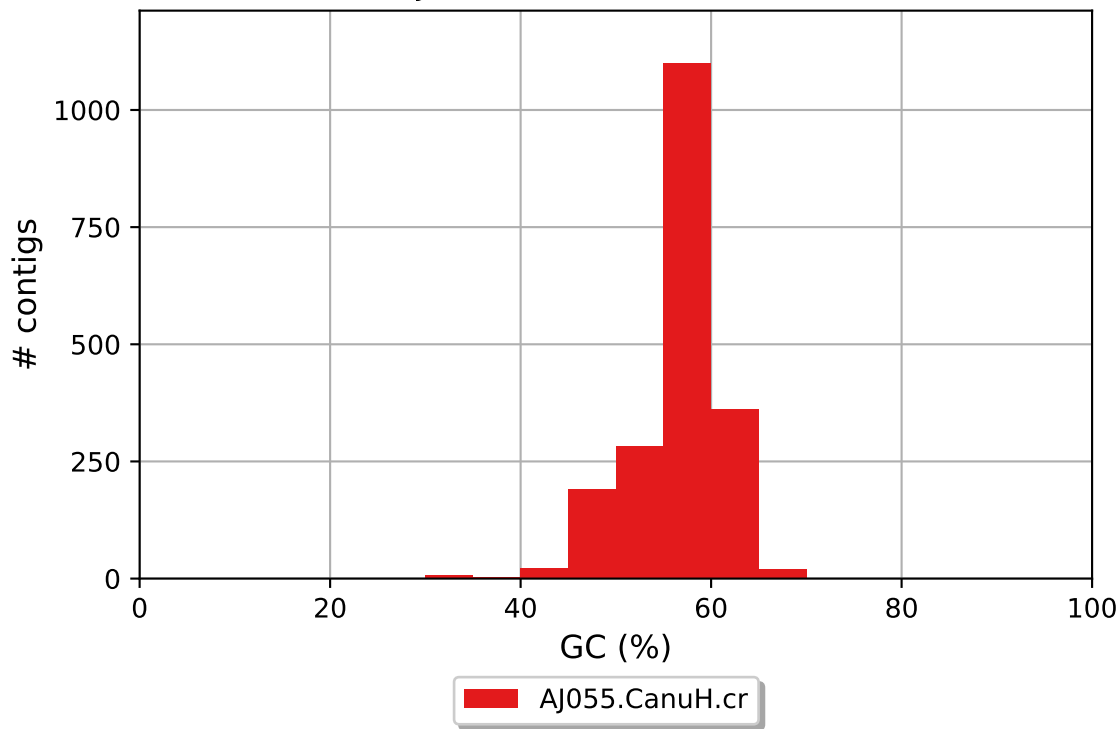
Nx

NGx

AJ055.CanuH.cr

Cumulative length

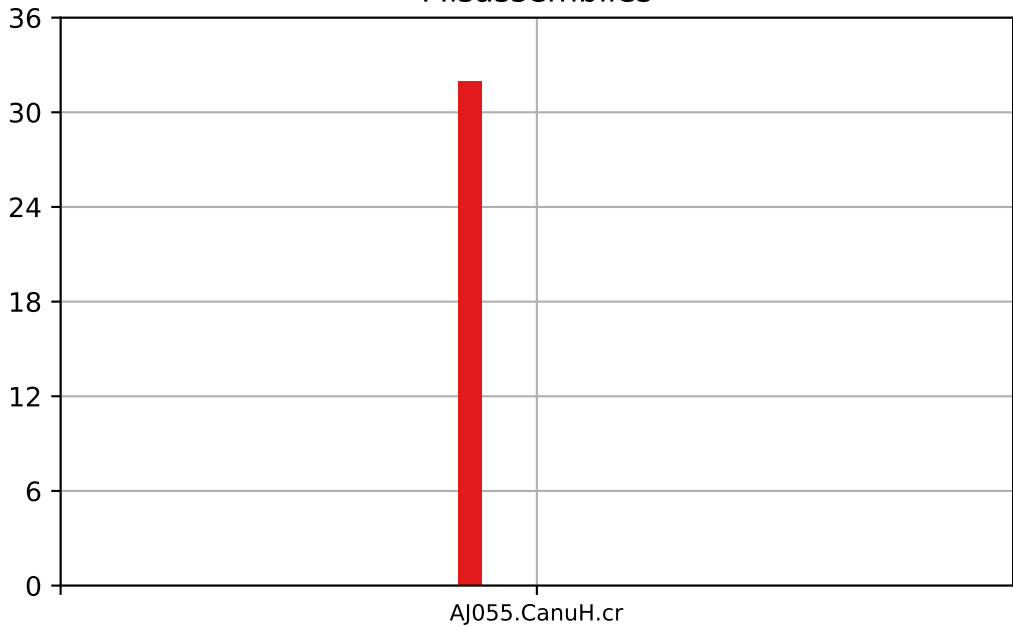Legend: AJ055.CanuH.cr (red solid line), Reference (black dashed line)

X-axis: Contig index
Y-axis: Cumulative length (Mbp)

GC content

windows vs GC (%)

Legend: AJ055.CanuH.cr (red solid line), Reference (black dashed line)
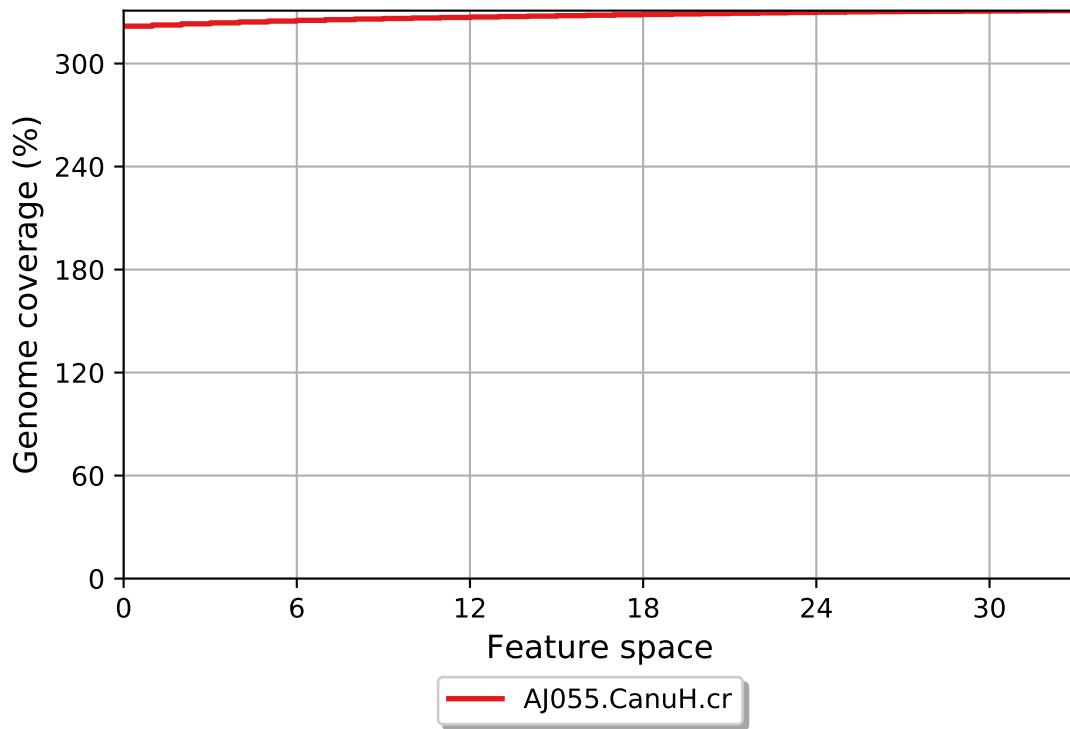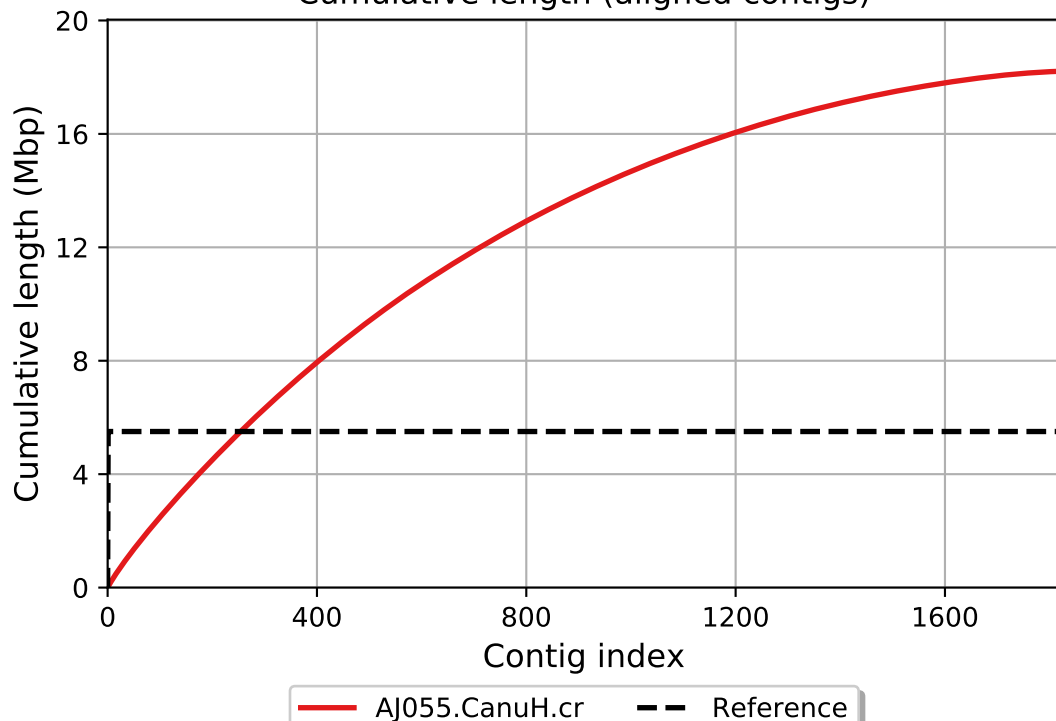
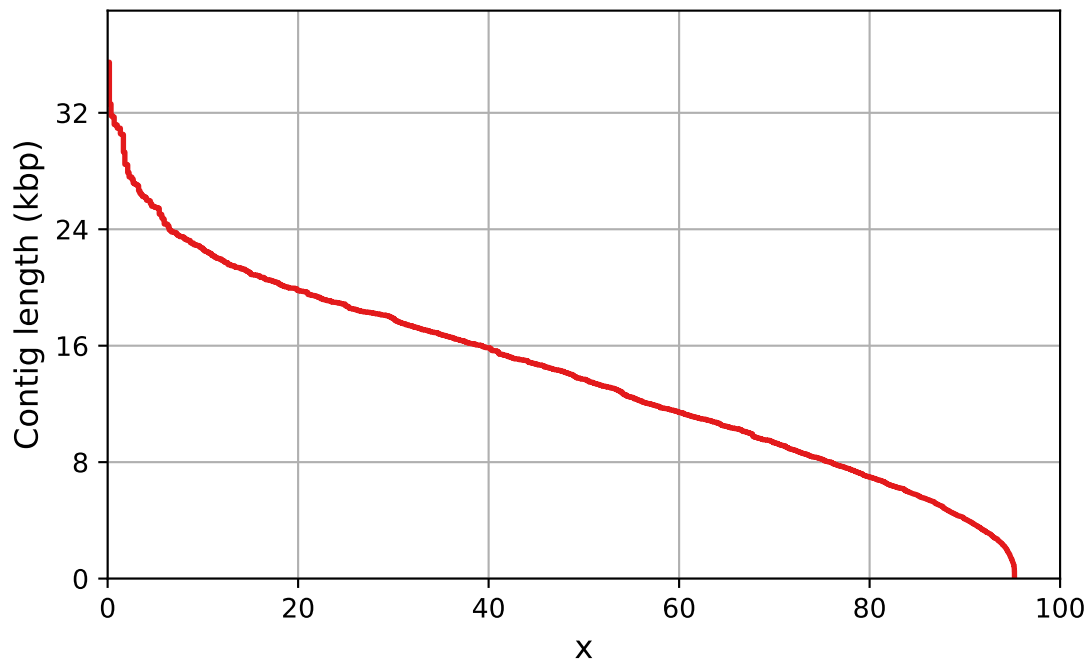AJ055.CanuH.cr GC content

Misassemblies

AJ055.CanuH.cr

relocations

FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

AJ055.CanuH.cr

NGAx