Report

	AJ055.CanuL.cr
# contigs (>= 0 bp)	2000
# contigs (>= 1000 bp)	1991
# contigs (>= 5000 bp)	1340
# contigs (>= 10000 bp)	838
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	19363656
Total length (>= 1000 bp)	19355966
Total length (>= 5000 bp)	17505348
Total length (>= 10000 bp)	13827986
Total length (>= 25000 bp)	1518398
Total length (>= 50000 bp)	0
# contigs	1999
Largest contig	38164
Total length	19363414
Reference length	5504133
GC (%)	57.08
Reference GC (%)	57.38
N50	14466
NG50	22250
N75	9164
NG75	20388
L50	493
LG50	106
L75	911
LG75	171
# misassemblies	53
# misassembled contigs	52
Misassembled contigs length	876728
# local misassemblies	37
# unaligned mis. contigs	4
# unaligned contigs	234 + 159 part
Unaligned length	1584519
Genome fraction (%)	94.442
Duplication ratio	3.420
# N's per 100 kbp	0.00
# mismatches per 100 kbp	95.67
# indels per 100 kbp	705.65
Largest alignment	35485
Total aligned length	17695923
NA50	13090
NGA50	21061
NA75	7218
NGA75	19385
LA50	527
LGA50	113
LA75	1016
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

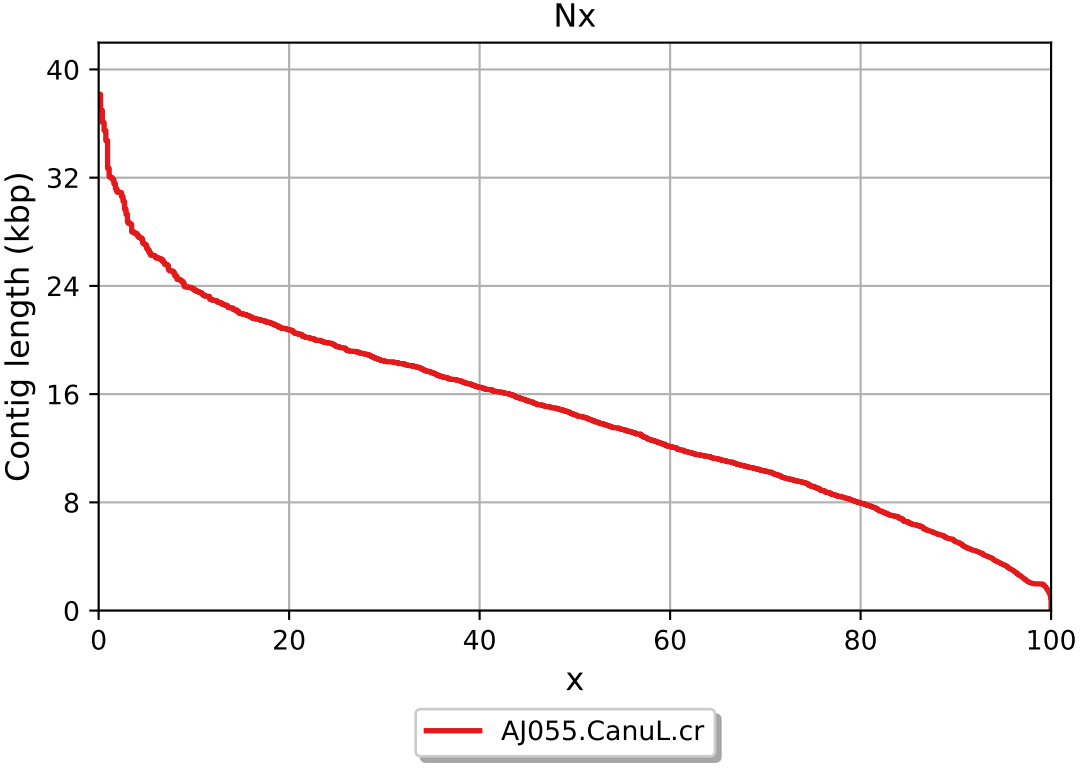
	AJ055.CanuL.cr
# misassemblies	53
# relocations	53
# translocations	0
# inversions	0
# misassembled contigs	52
Misassembled contigs length	876728
# local misassemblies	37
# unaligned mis. contigs	4
# mismatches	4973
# indels	36681
# indels (<= 5 bp)	36426
# indels (> 5 bp)	255
Indels length	46197

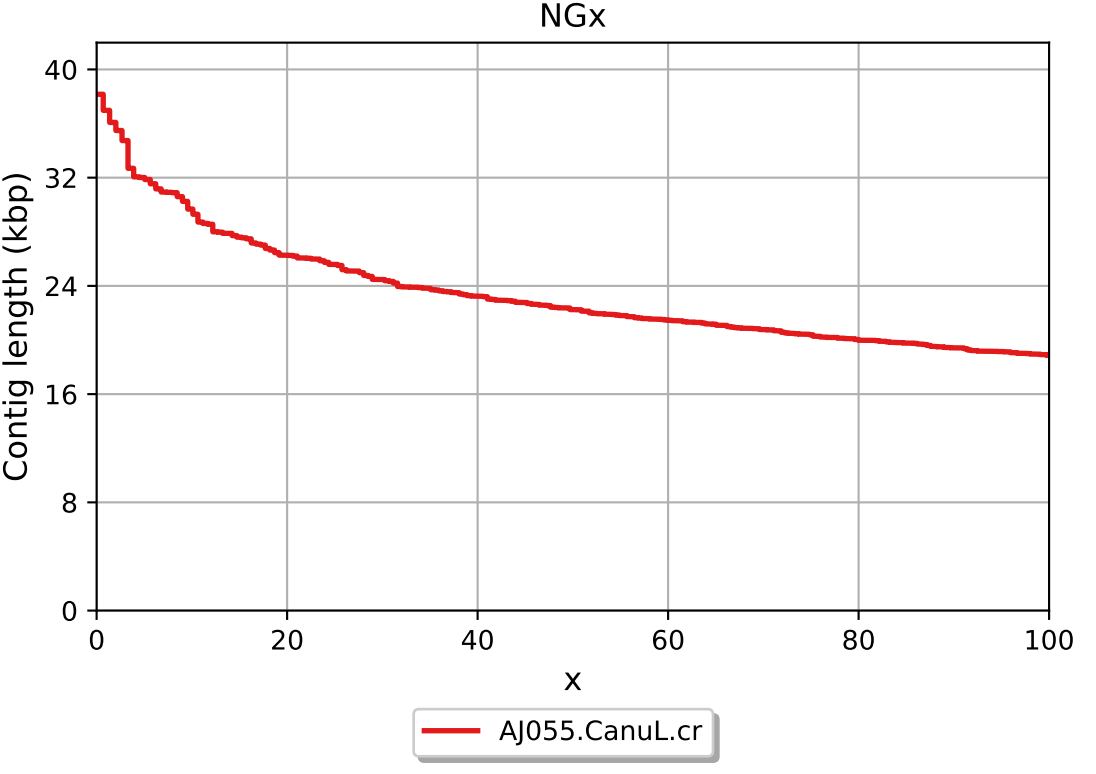
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

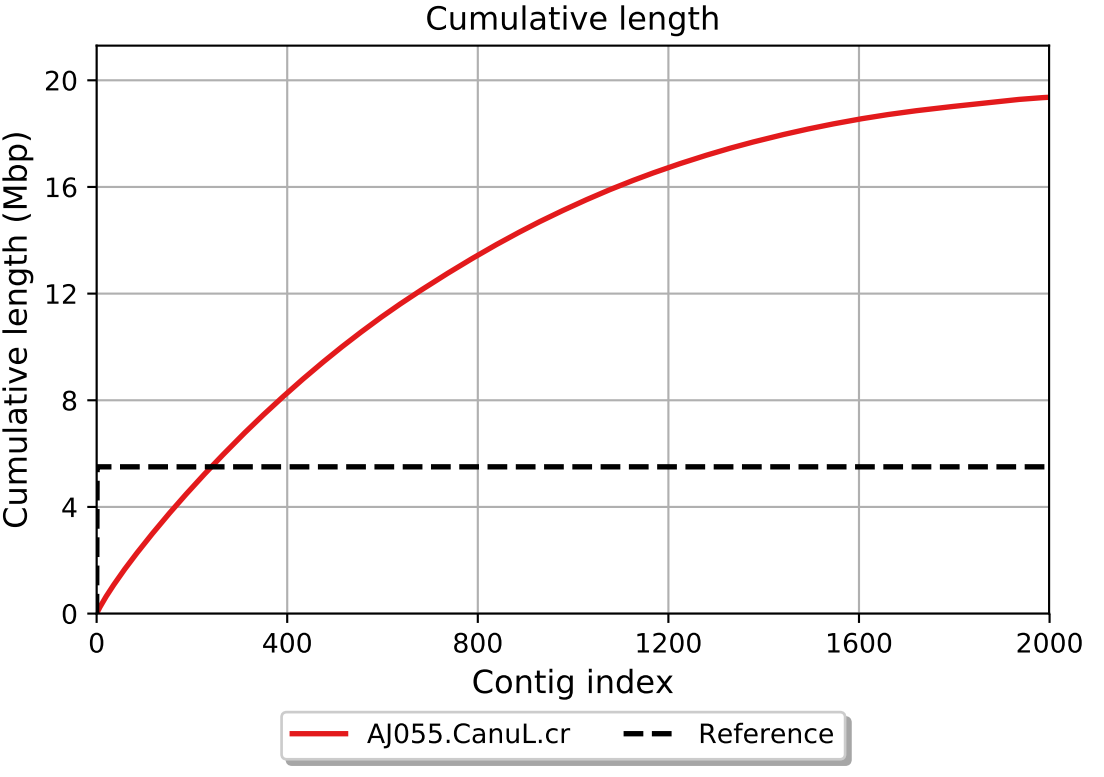
Unaligned report

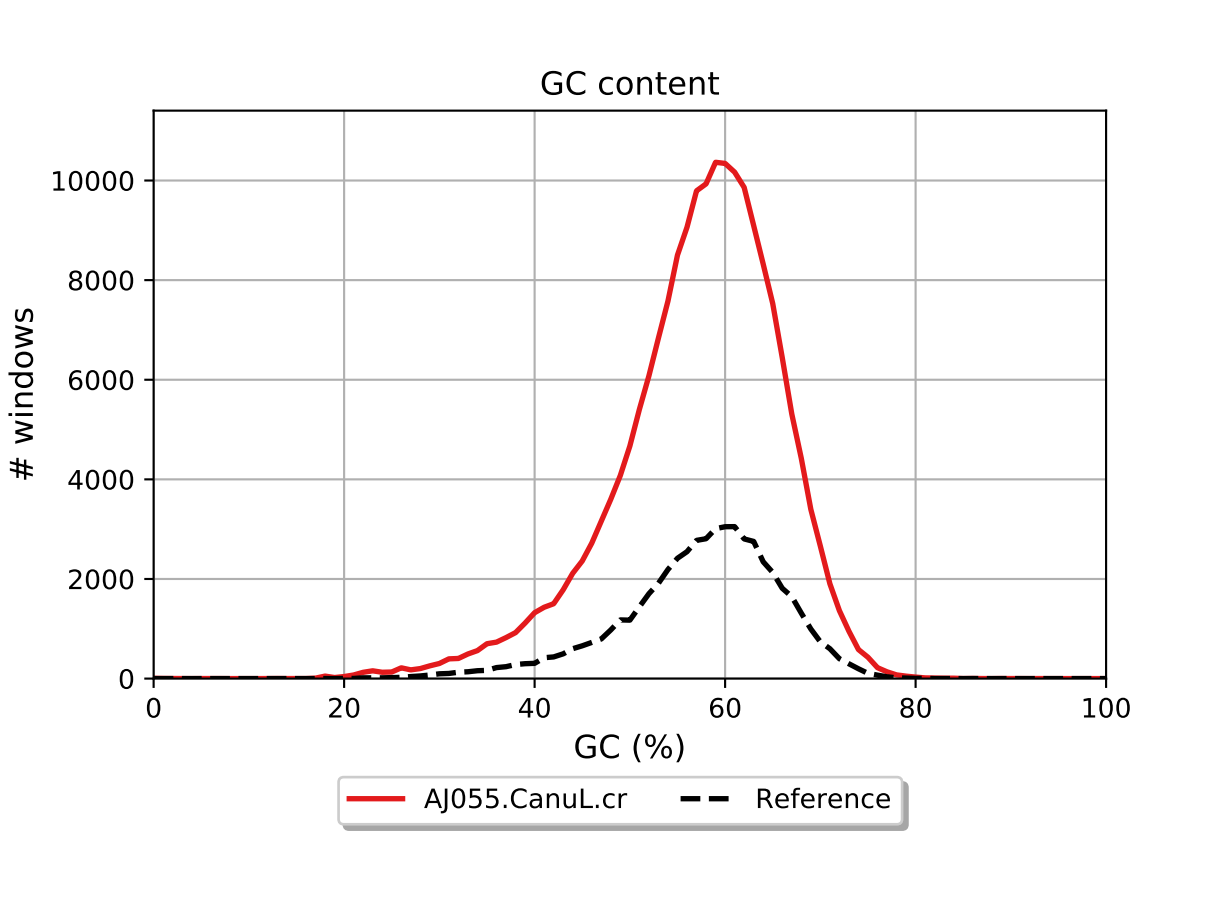
	AJ055.CanuL.cr
# fully unaligned contigs	234
Fully unaligned length	993210
# partially unaligned contigs	159
Partially unaligned length	591309
# N's	0

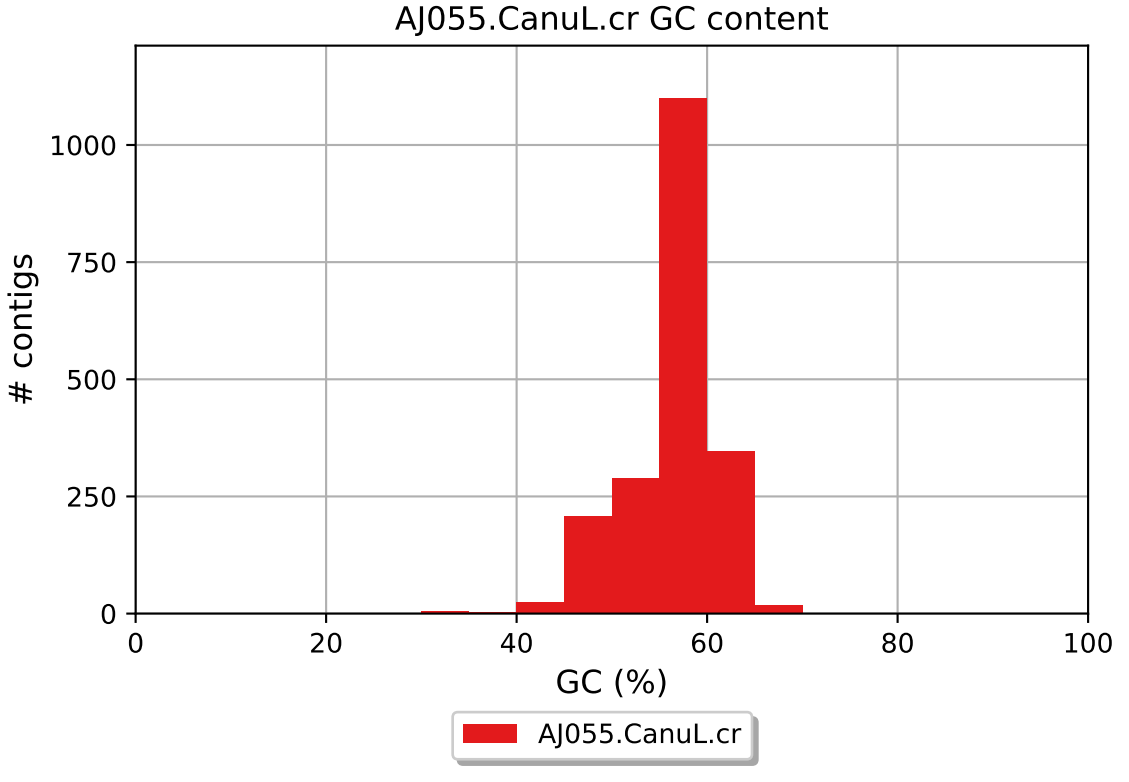
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

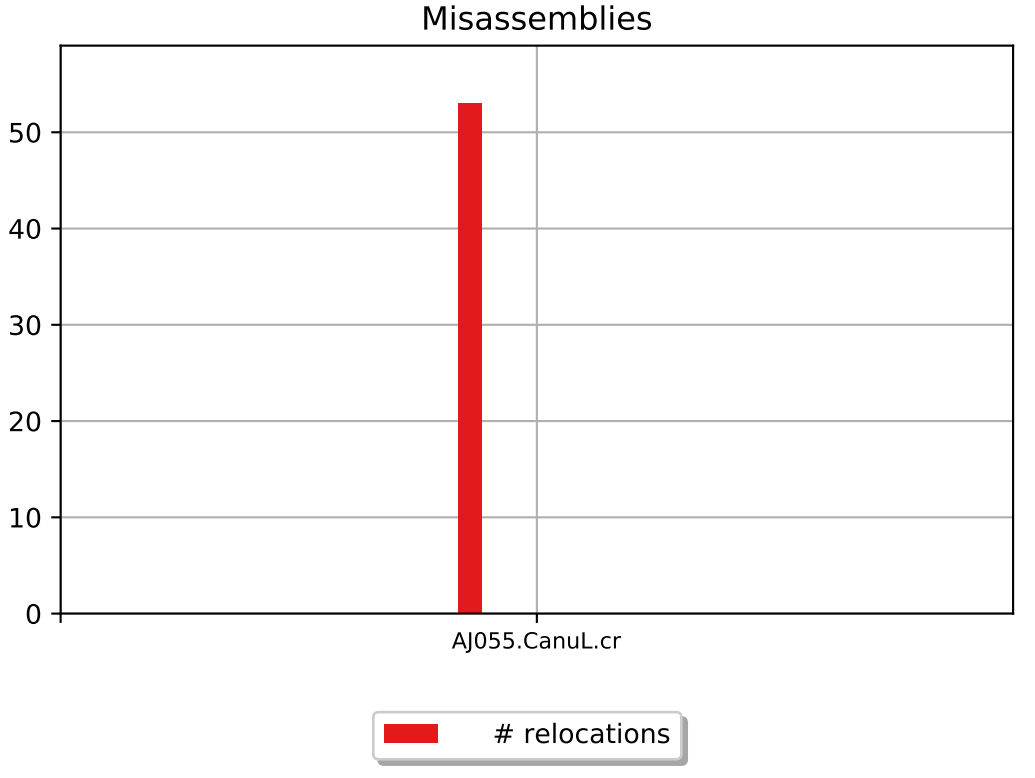

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
AJ055.CanuL.cr

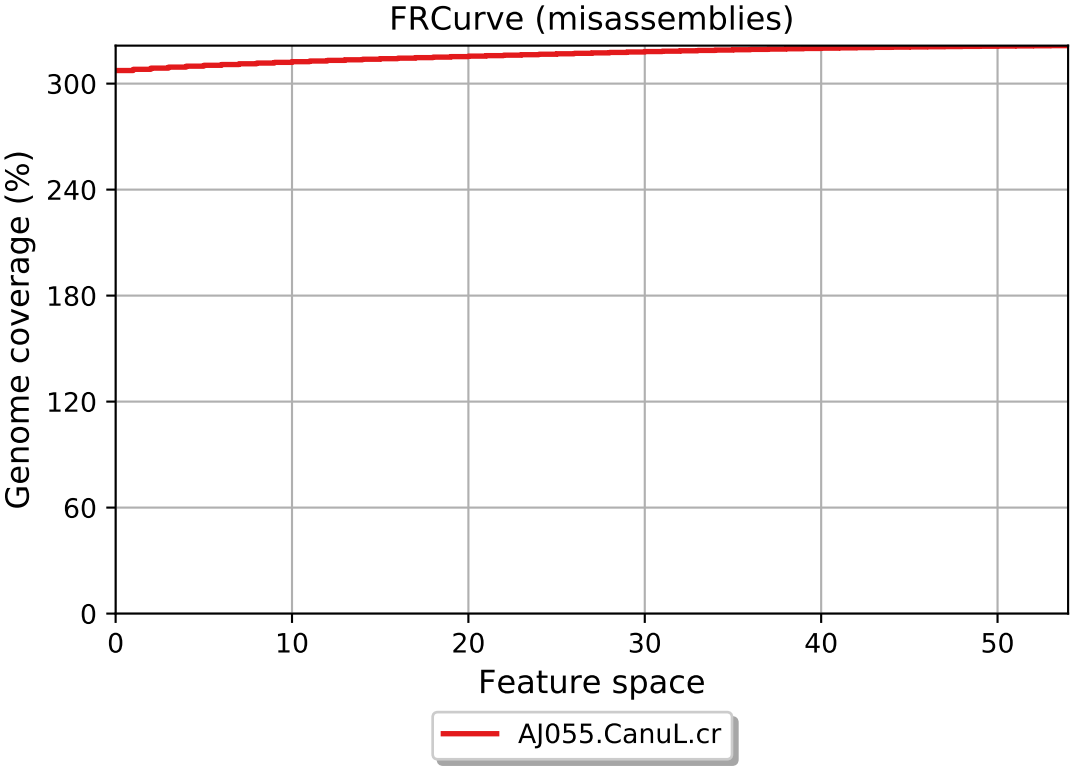

NGx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
AJ055.CanuL.cr

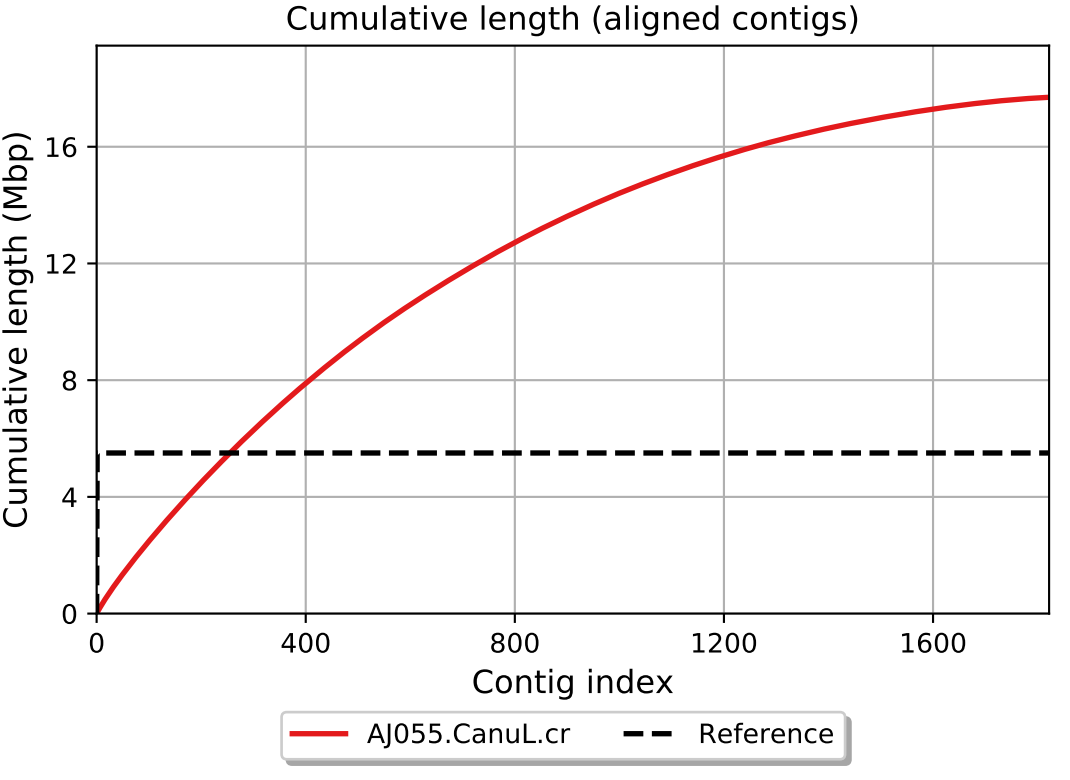

Cumulative length
Cumulative length (Mbp)
20
16
12
8
4
0
0
400
800
1200
1600
2000
Contig index
AJ055.CanuL.cr
Reference

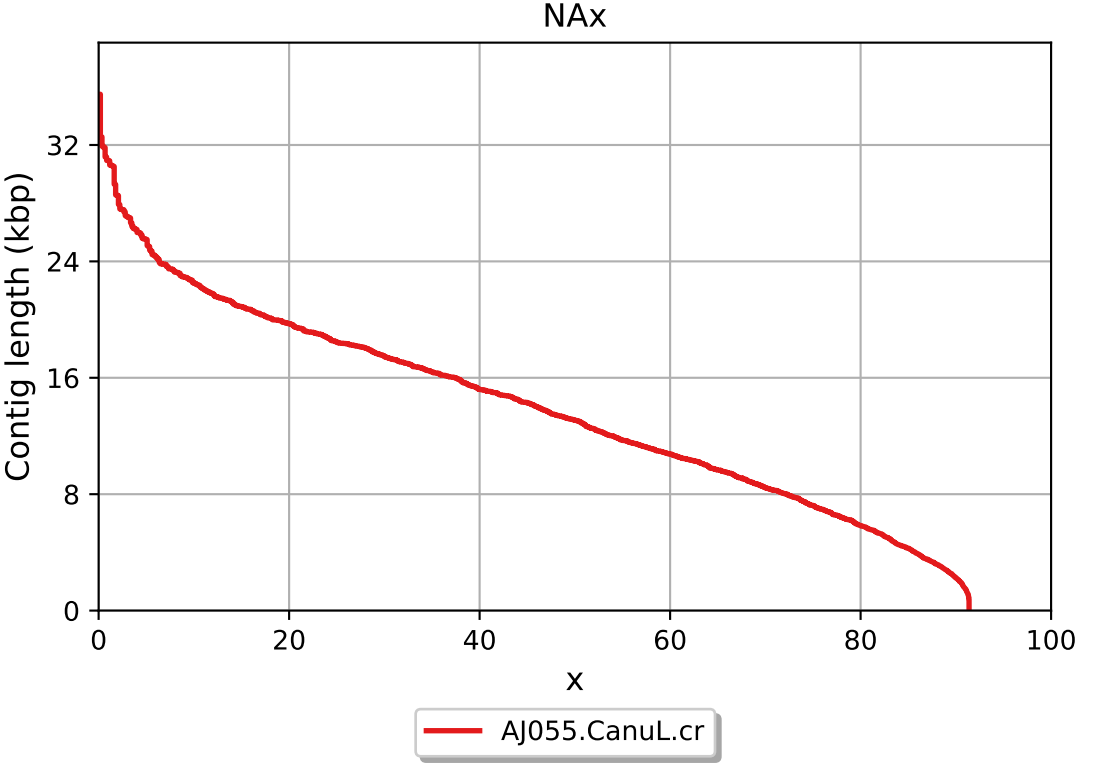

GC content
10000
8000
6000
4000
2000
0
windows
0
20
40
60
80
100
GC (%)
AJ055.CanuL.cr
Reference

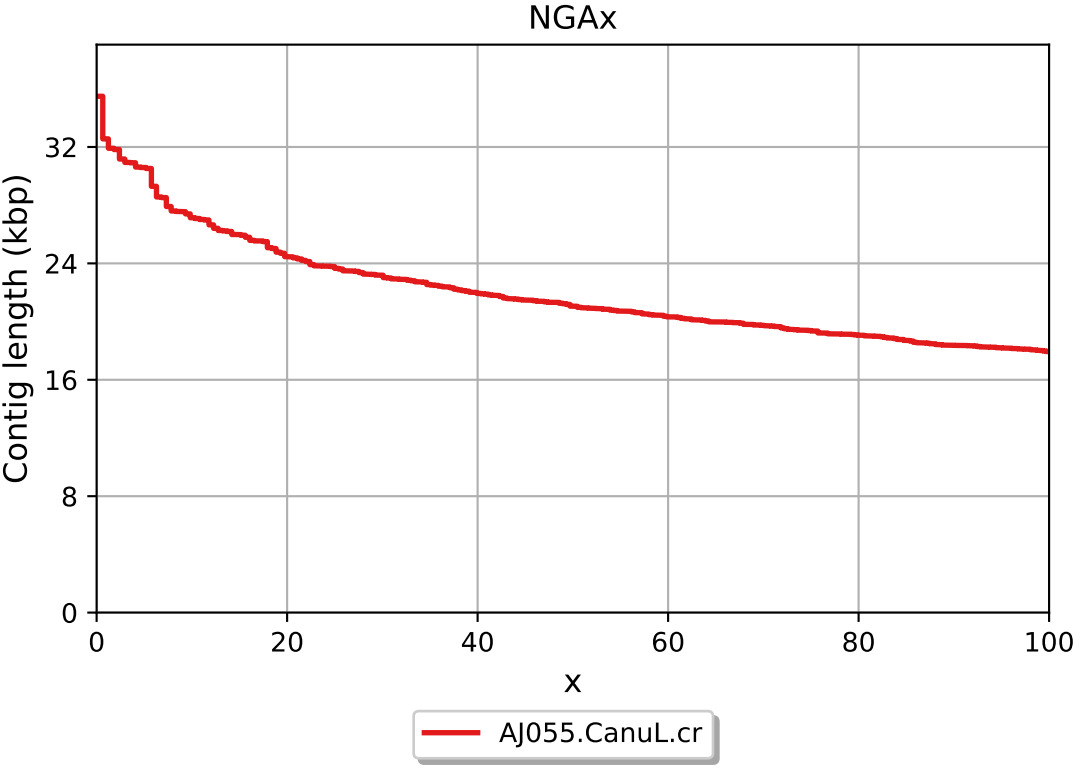

AJ055.CanuL.cr GC content
contigs
1000
750
500
250
0
0
20
40
60
80
100
GC (%)
AJ055.CanuL.cr


Misassemblies
50
40
30
20
10
0
AJ055.CanuL.cr
relocations


FRCurve (misassemblies)
Genome coverage (%)
300
240
180
120
60
0
0
10
20
30
40
50
Feature space
AJ055.CanuL.cr


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
4
8
12
16
0
400
800
1200
1600
Contig index
AJ055.CanuL.cr
Reference


NAx
Contig length (kbp)
0
8
16
24
32
0
20
40
60
80
100
x
AJ055.CanuL.cr


NGAx
Contig length (kbp)
0
8
16
24
32
0
20
40
60
80
100
x
AJ055.CanuL.cr