Report

	AJ055.Colormap
# contigs (>= 0 bp)	73
# contigs (>= 1000 bp)	73
# contigs (>= 5000 bp)	64
# contigs (>= 10000 bp)	60
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	6030828
Total length (>= 1000 bp)	6030828
Total length (>= 5000 bp)	6006141
Total length (>= 10000 bp)	5974116
Total length (>= 25000 bp)	5601153
Total length (>= 50000 bp)	5327723
# contigs	73
Largest contig	509223
Total length	6030828
Reference length	5504133
GC (%)	57.27
Reference GC (%)	57.38
N50	218907
NG50	305685
N75	104347
NG75	132047
L50	8
LG50	7
L75	18
LG75	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	153473
Genome fraction (%)	97.625
Duplication ratio	1.094
# N's per 100 kbp	0.00
# mismatches per 100 kbp	24.70
# indels per 100 kbp	8.04
Largest alignment	504450
Total aligned length	5871337
NA50	218907
NGA50	305685
NA75	81683
NGA75	130178
LA50	8
LGA50	7
LA75	19
LGA75	15

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

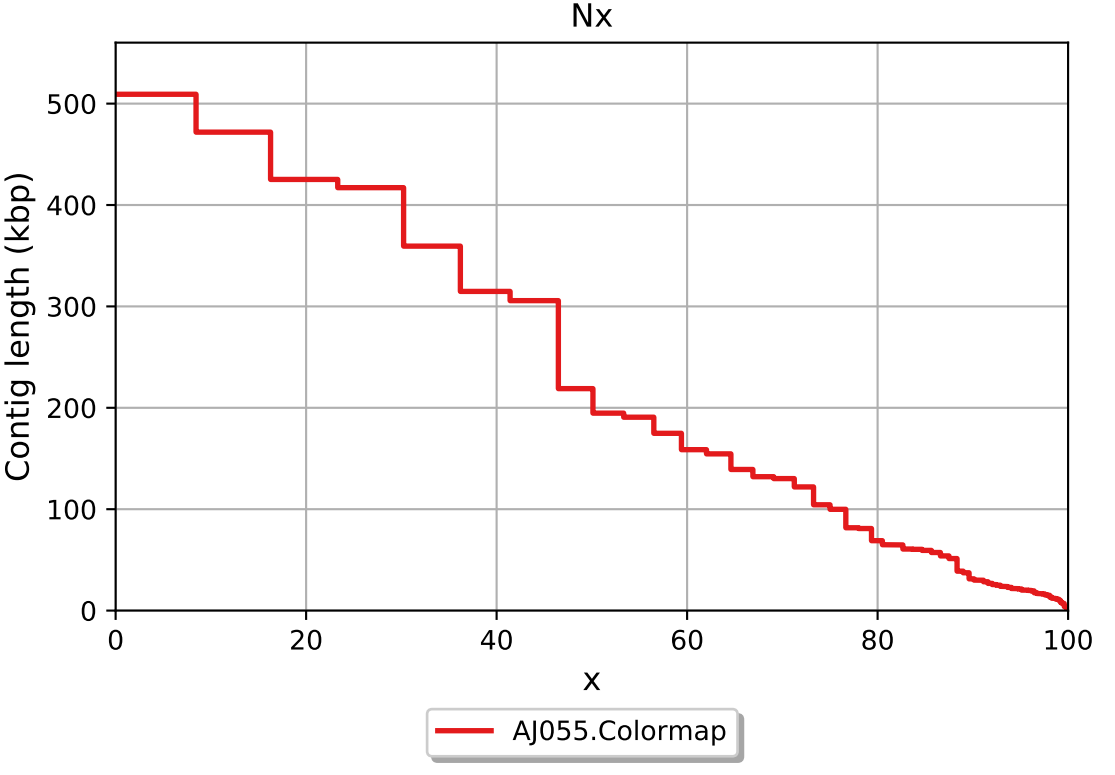
	AJ055.Colormap
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	12
# unaligned mis. contigs	0
# mismatches	1327
# indels	432
# indels (<= 5 bp)	423
# indels (> 5 bp)	9
Indels length	980

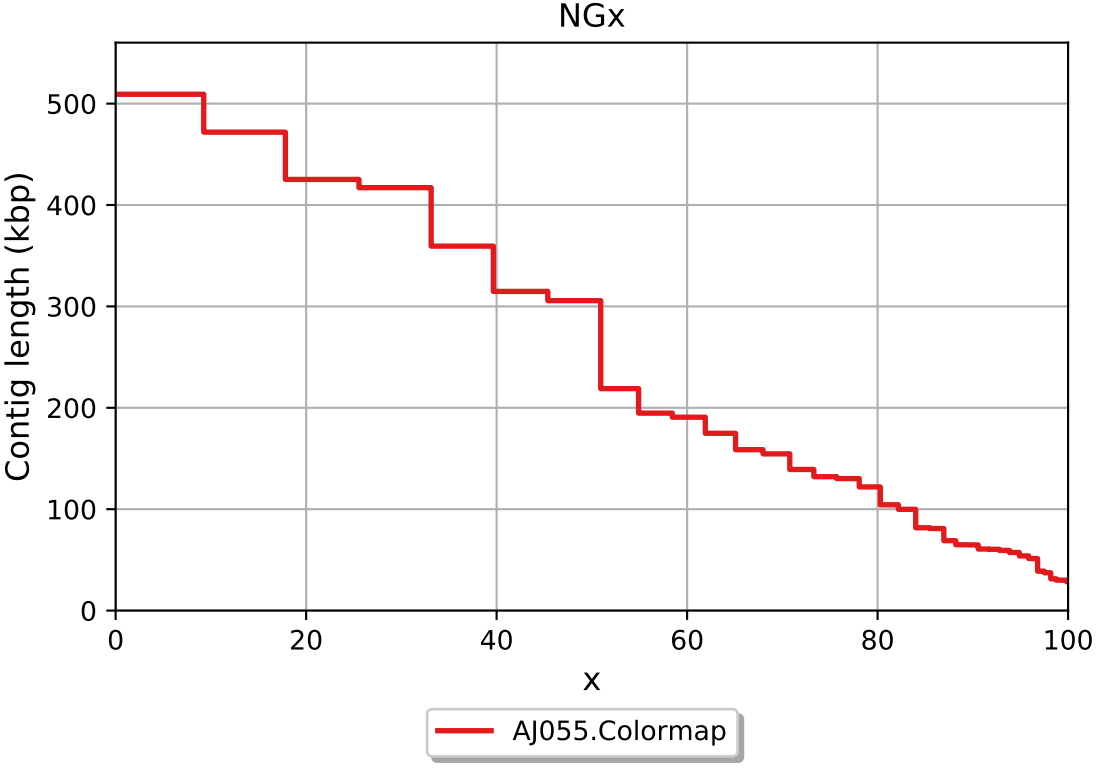
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

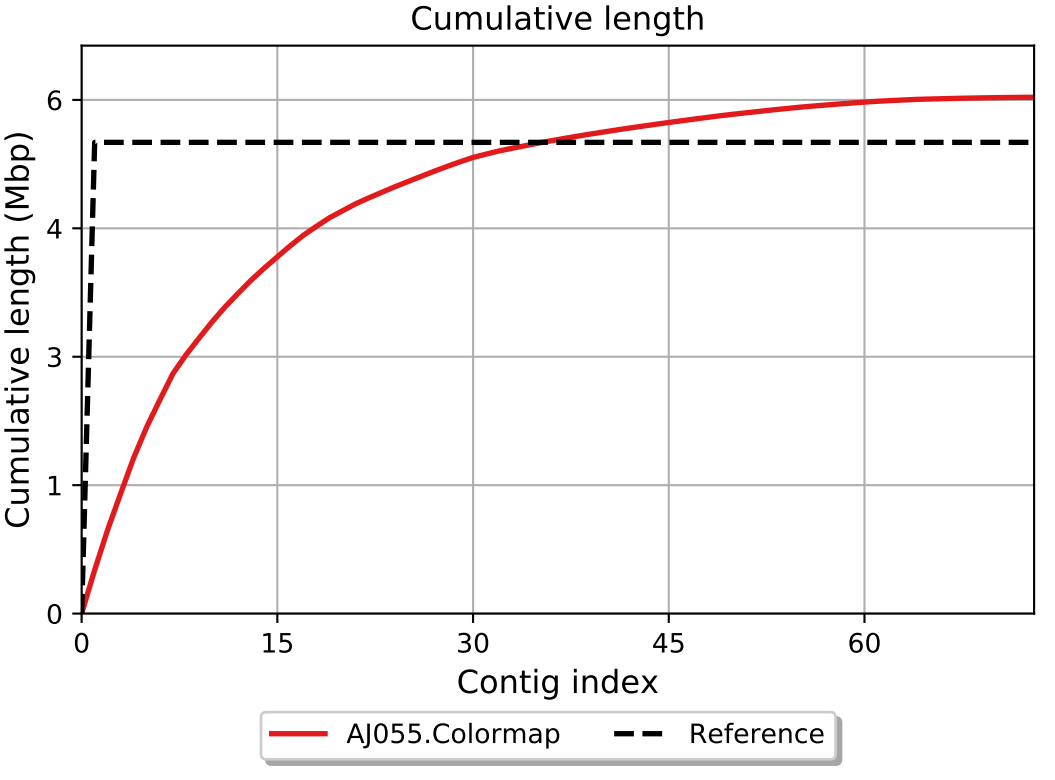
Unaligned report

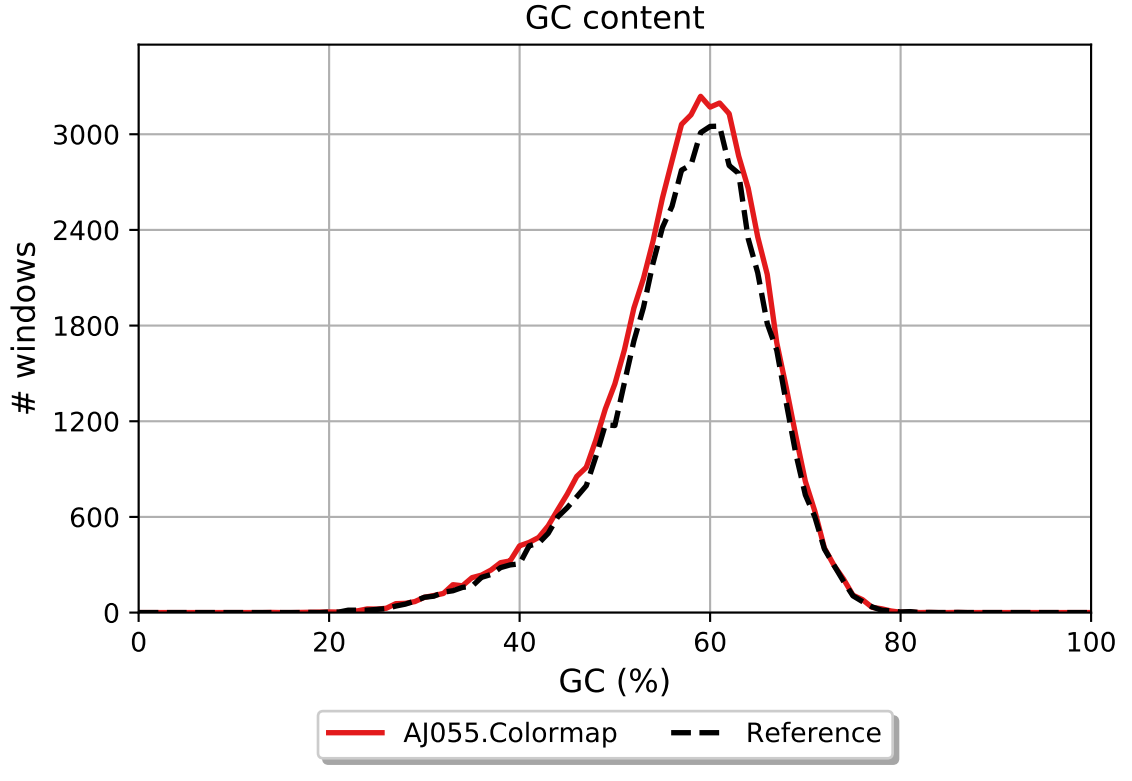
	AJ055.Colormap
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	153473
# N's	0

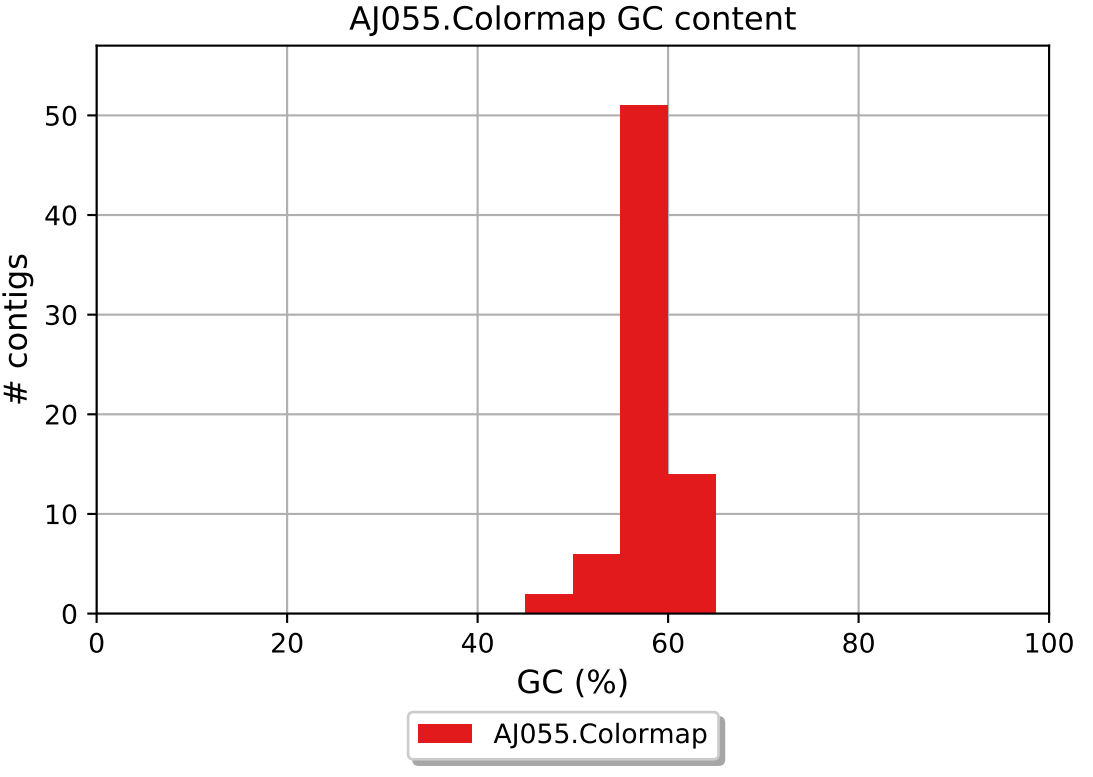
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

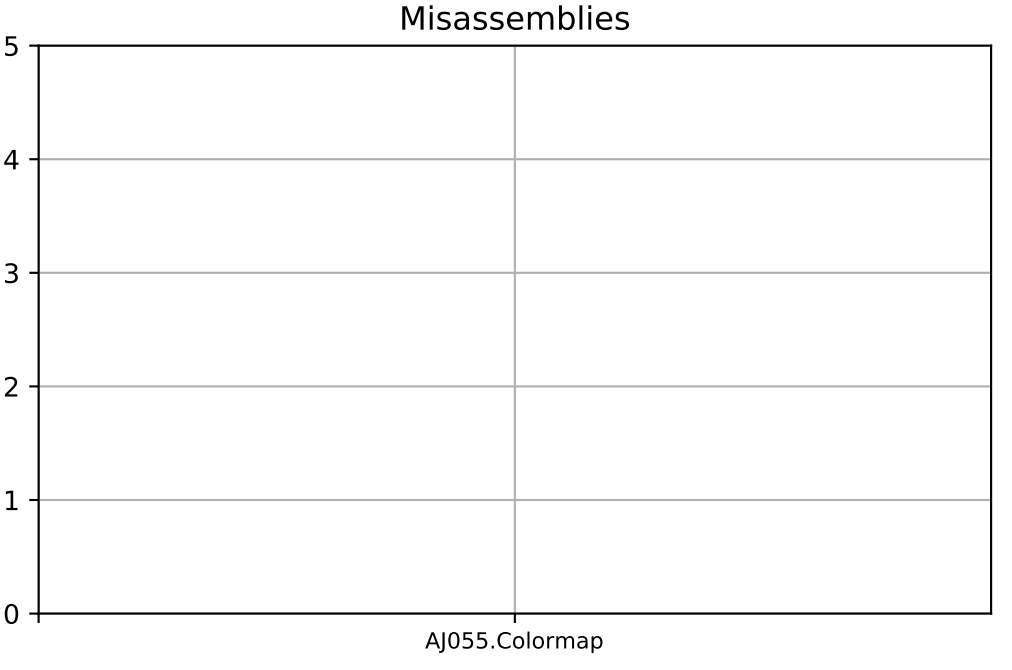

Nx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
AJ055.Colormap

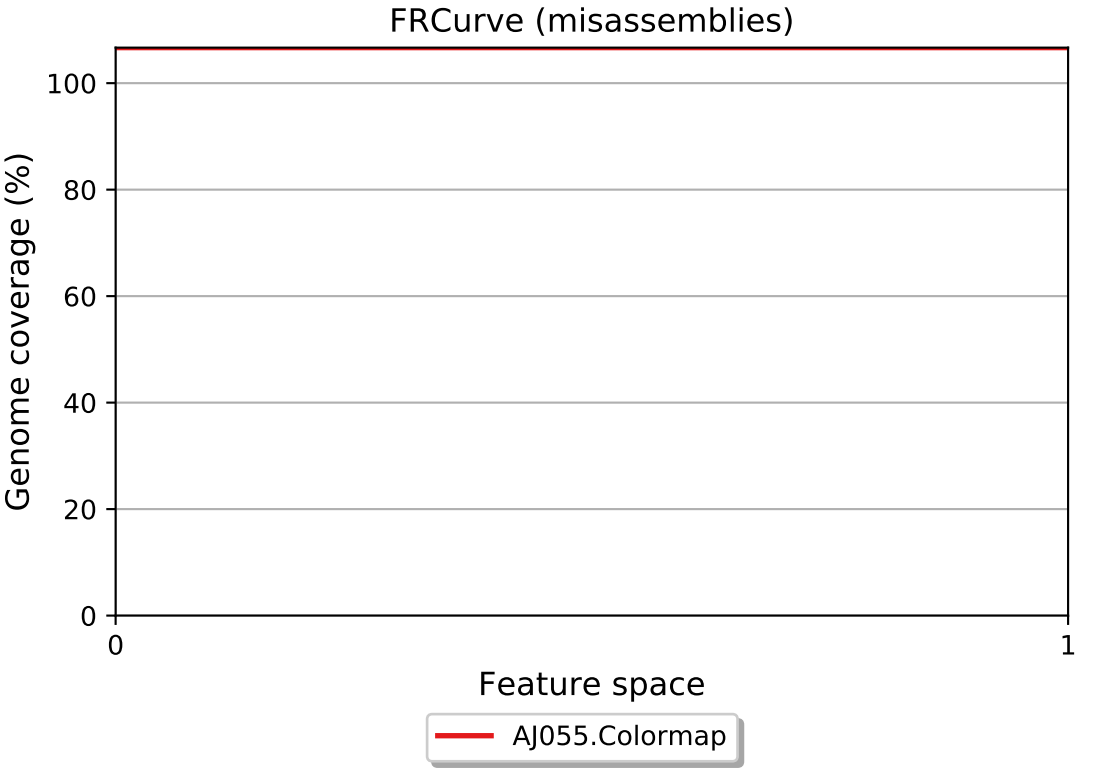

NGx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
AJ055.Colormap

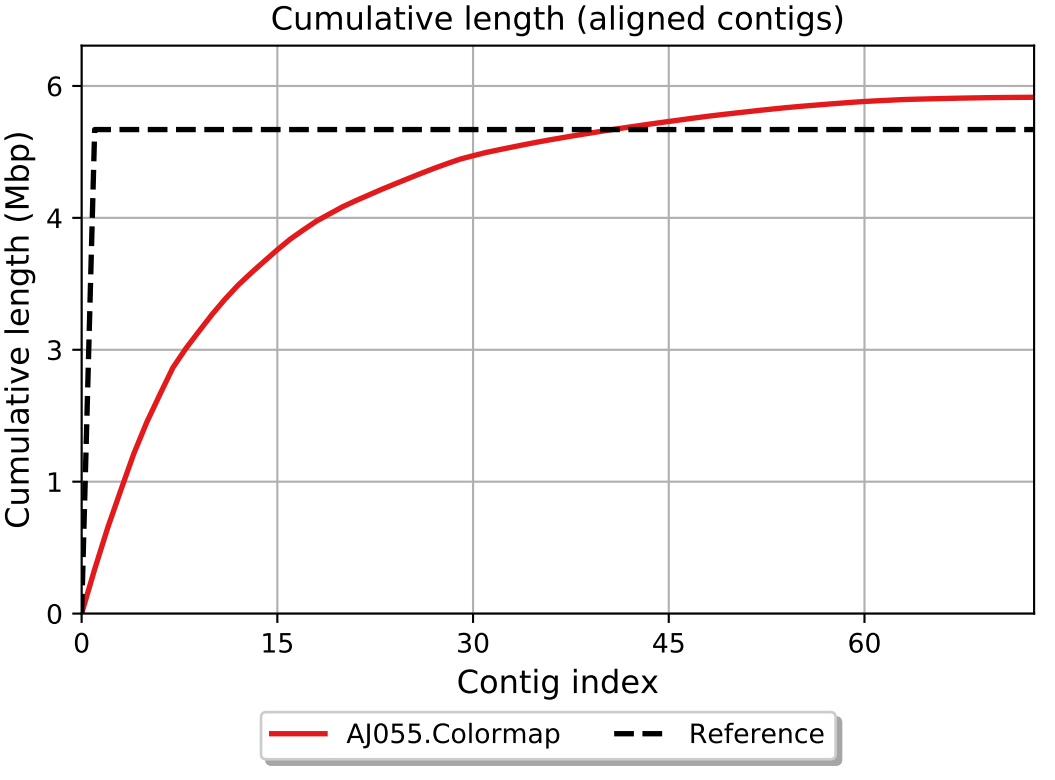

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
15
30
45
60
Contig index
AJ055.Colormap
Reference

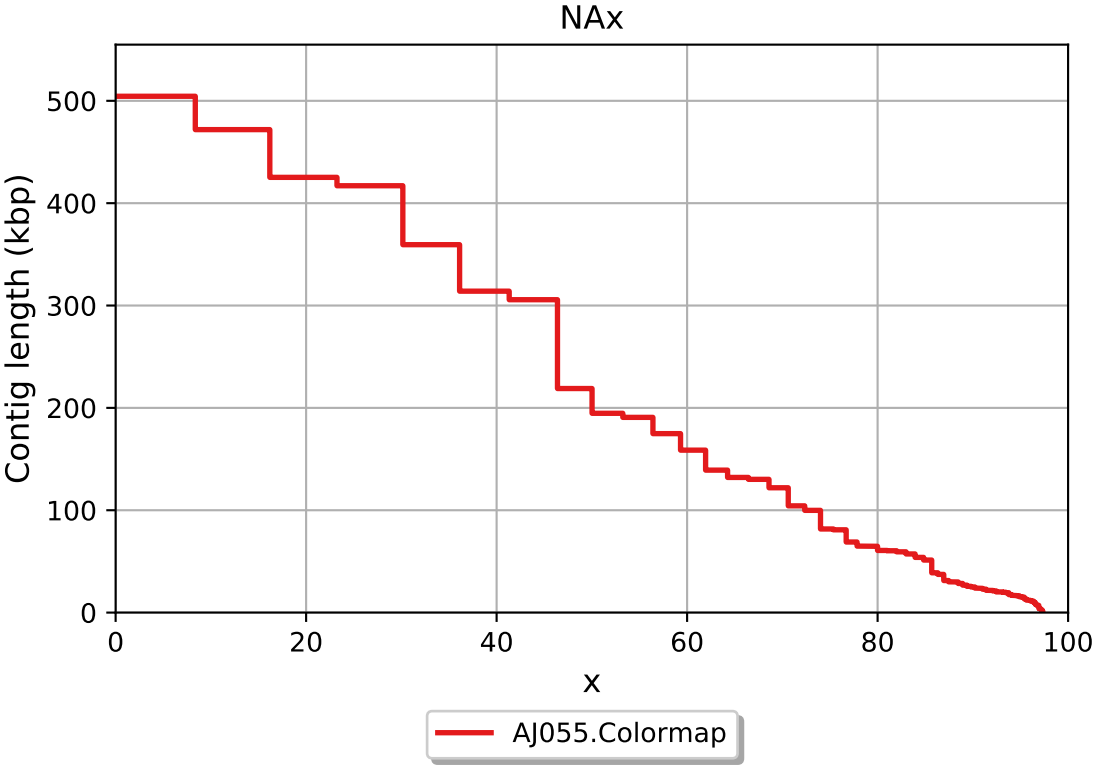

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
AJ055.Colormap
Reference

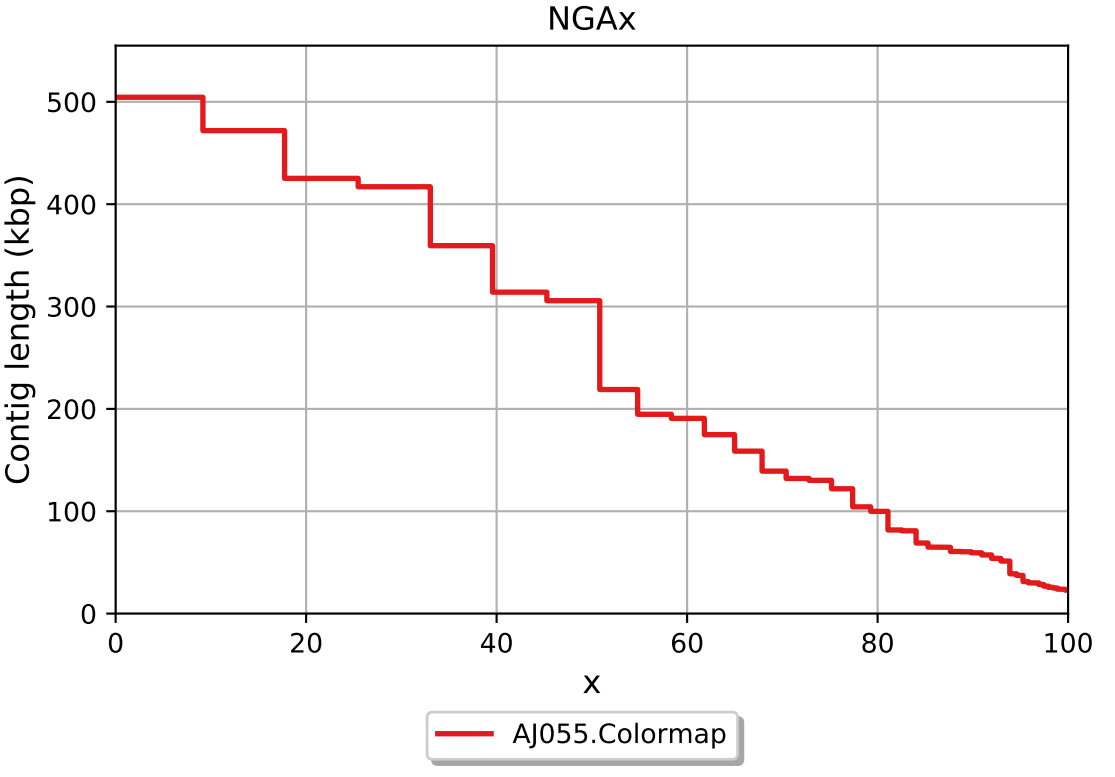

AJ055.Colormap GC content
contigs
0
10
20
30
40
50
0
20
40
60
80
100
GC (%)
AJ055.Colormap


Misassemblies
5
4
3
2
1
0
AJ055.Colormap


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
AJ055.Colormap


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
15
30
45
60
Contig index
AJ055.Colormap
Reference


NAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
AJ055.Colormap


NGAx
Contig length (kbp)
500
400
300
200
100
0
0
20
40
60
80
100
x
AJ055.Colormap