Report

	AJ055.SpadesL
# contigs (>= 0 bp)	176
# contigs (>= 1000 bp)	89
# contigs (>= 5000 bp)	69
# contigs (>= 10000 bp)	59
# contigs (>= 25000 bp)	46
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	5629473
Total length (>= 1000 bp)	5601380
Total length (>= 5000 bp)	5555202
Total length (>= 10000 bp)	5488537
Total length (>= 25000 bp)	5285297
Total length (>= 50000 bp)	4686049
# contigs	103
Largest contig	342678
Total length	5611391
Reference length	5504133
GC (%)	57.32
Reference GC (%)	57.38
N50	164005
NG50	164005
N75	86650
NG75	89646
L50	12
LG50	12
L75	24
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	17
# unaligned mis. contigs	0
# unaligned contigs	10 + 3 part
Unaligned length	162695
Genome fraction (%)	98.932
Duplication ratio	1.001
# N's per 100 kbp	25.66
# mismatches per 100 kbp	7.09
# indels per 100 kbp	1.40
Largest alignment	342668
Total aligned length	5447750
NA50	164005
NGA50	164005
NA75	86634
NGA75	89646
LA50	12
LGA50	12
LA75	24
LGA75	23

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

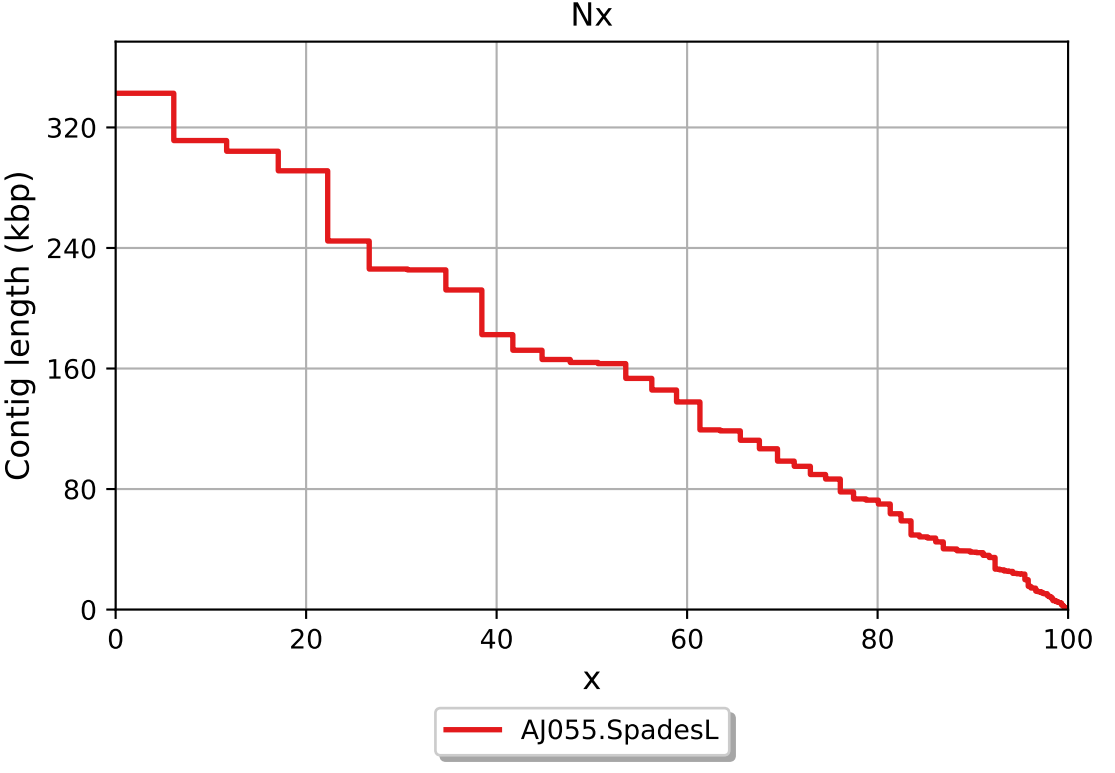
	AJ055.SpadesL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	17
# unaligned mis. contigs	0
# mismatches	386
# indels	76
# indels (<= 5 bp)	70
# indels (> 5 bp)	6
Indels length	338

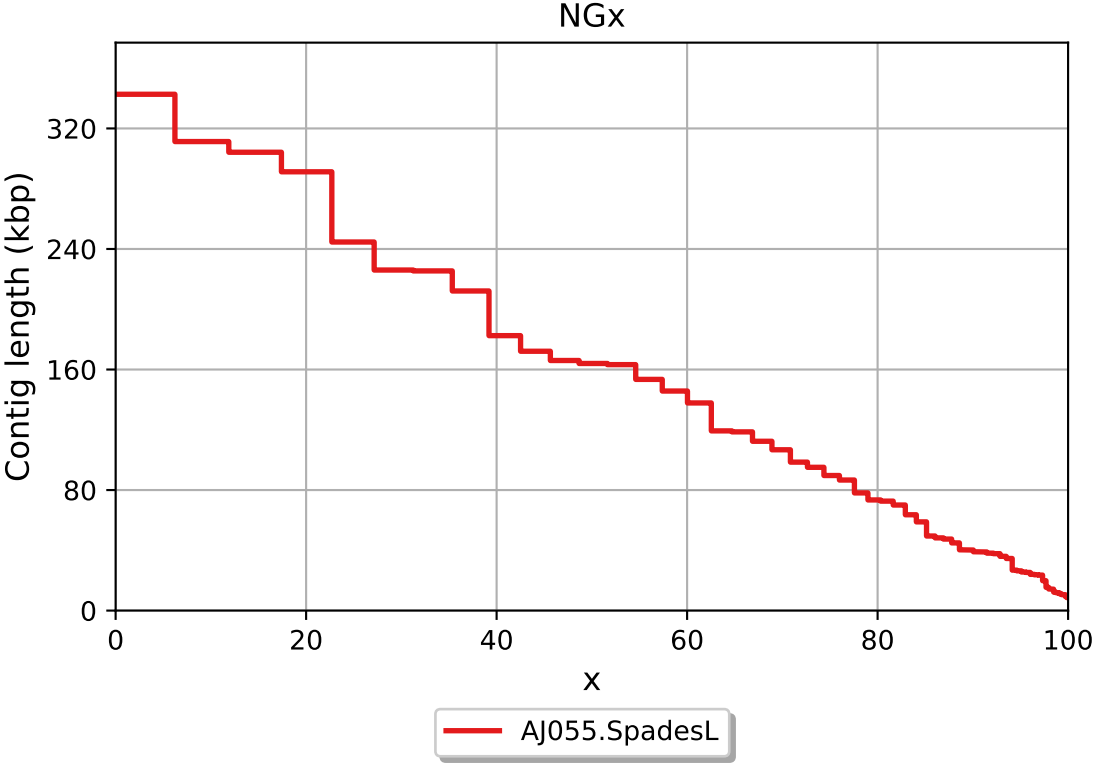
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

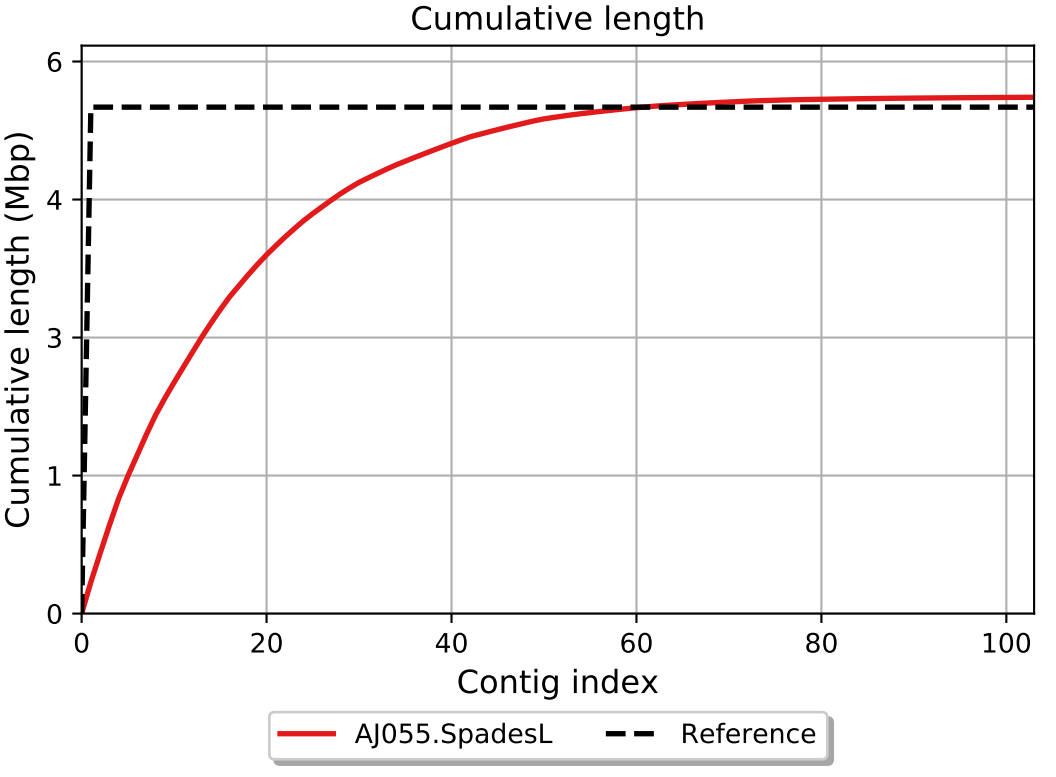
Unaligned report

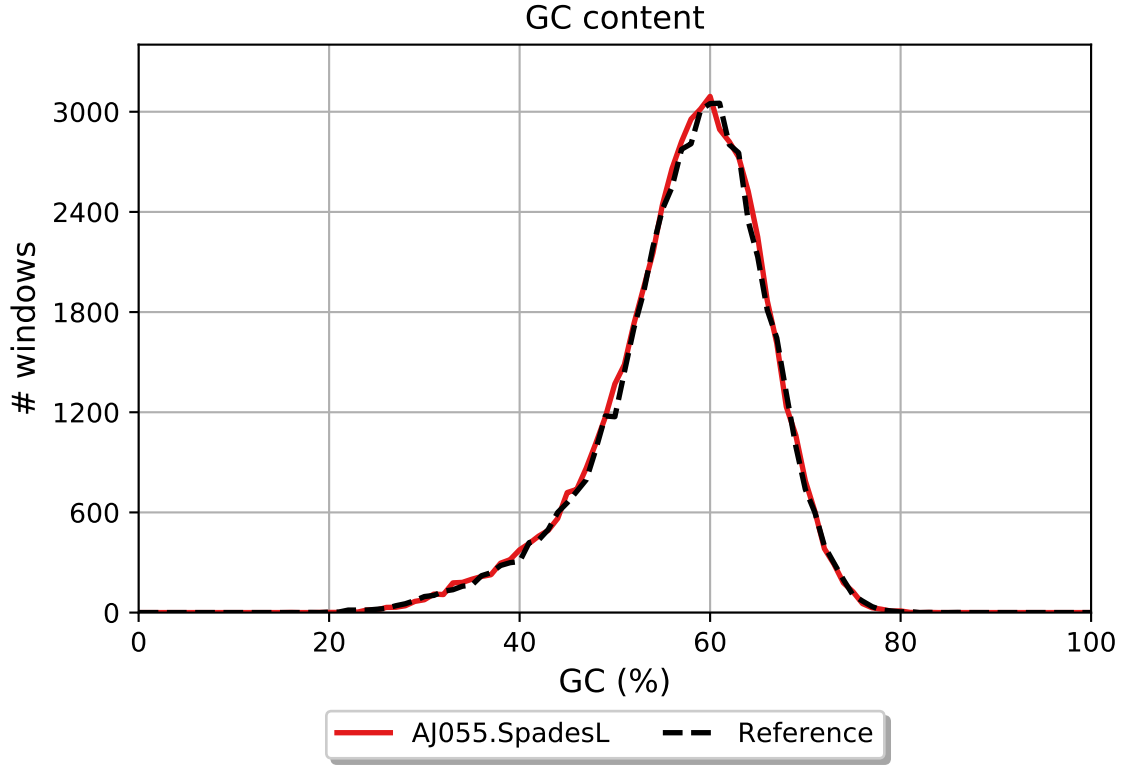
	AJ055.SpadesL
# fully unaligned contigs	10
Fully unaligned length	132575
# partially unaligned contigs	3
Partially unaligned length	30120
# N's	1440

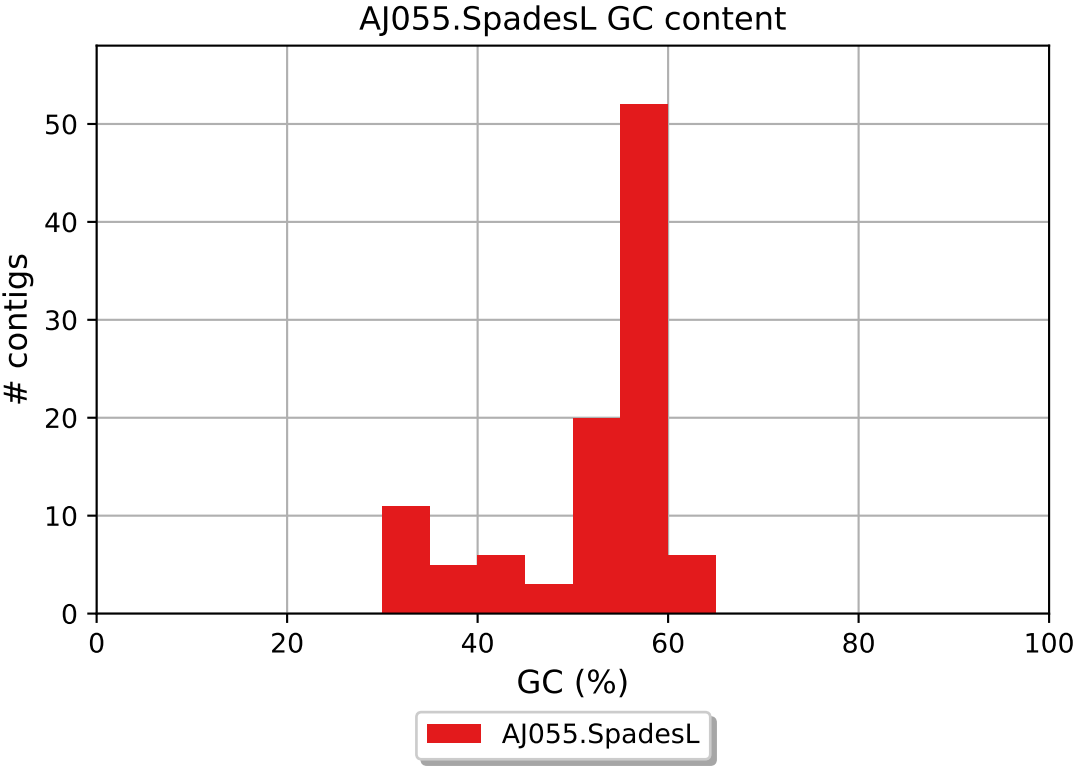
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

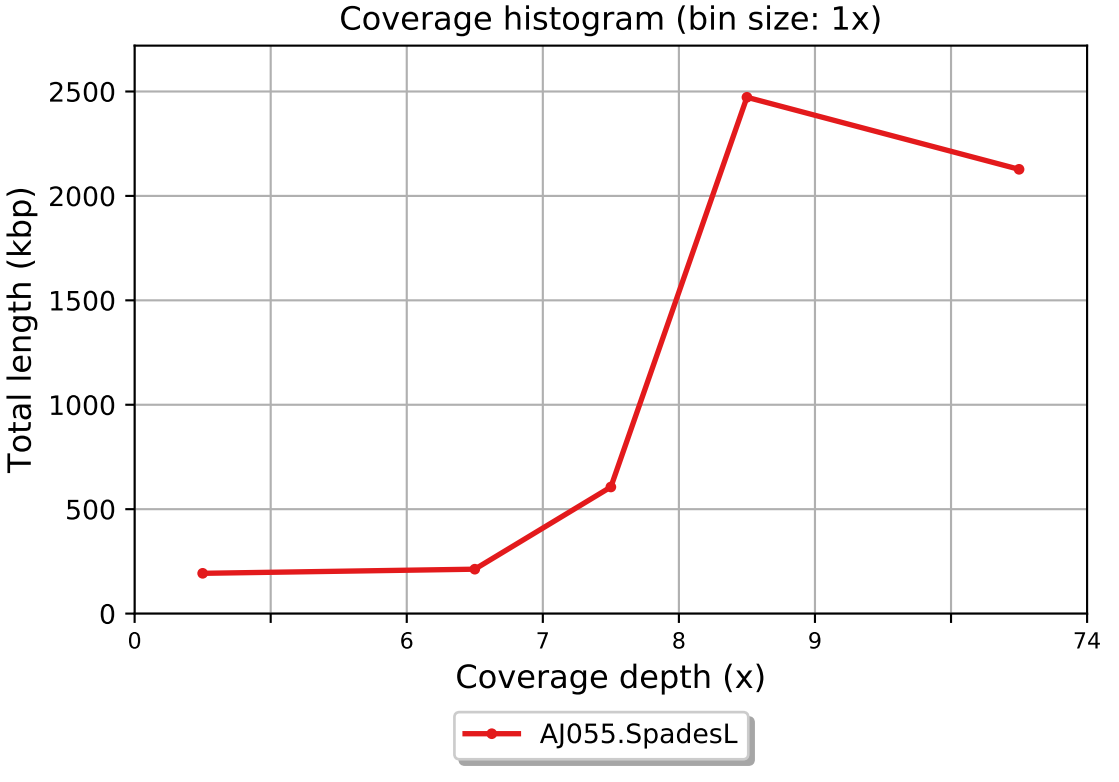

Nx
Contig length (kbp)
320
240
160
80
0
0
20
40
60
80
100
x
AJ055.SpadesL

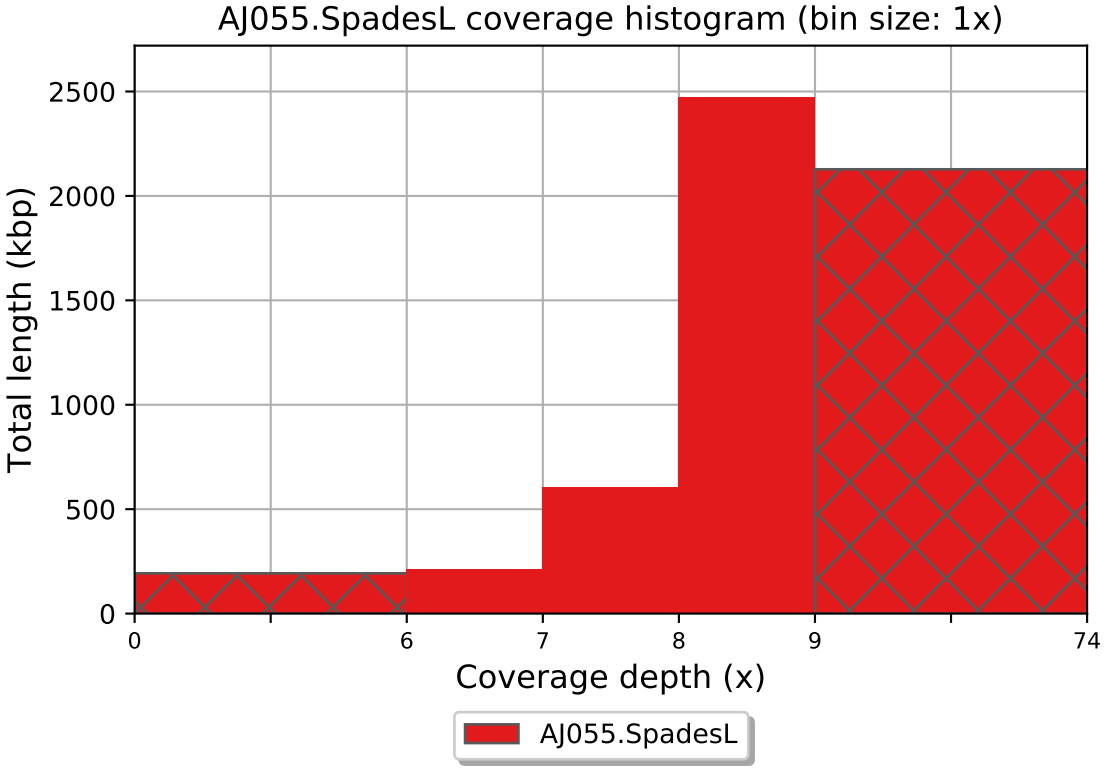

NGx
Contig length (kbp)
320
240
160
80
0
0
20
40
60
80
100
x
AJ055.SpadesL

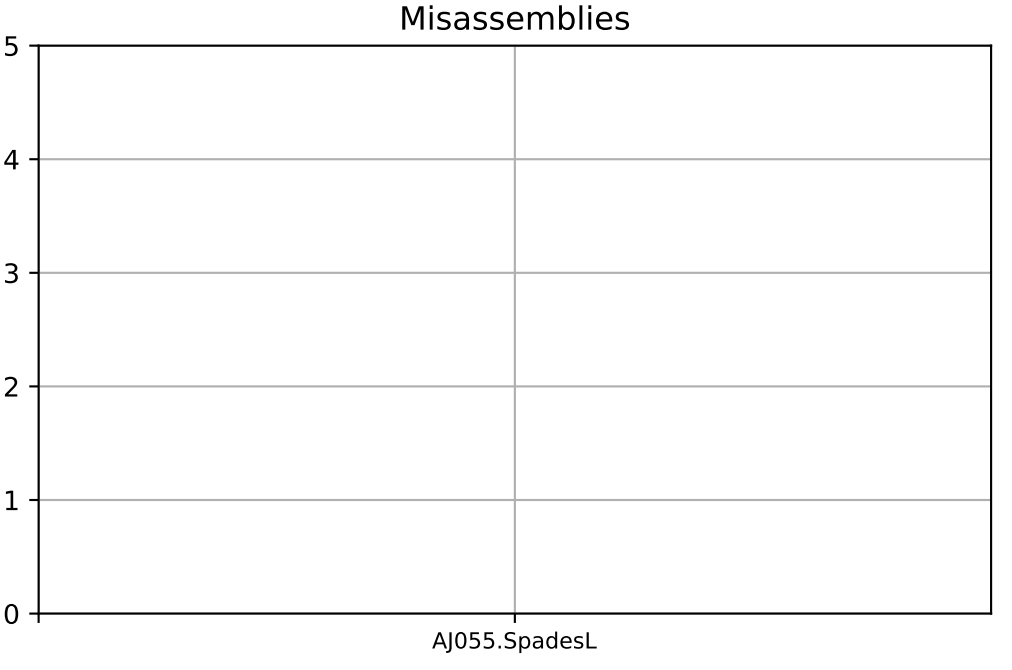

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
Contig index
AJ055.SpadesL
Reference

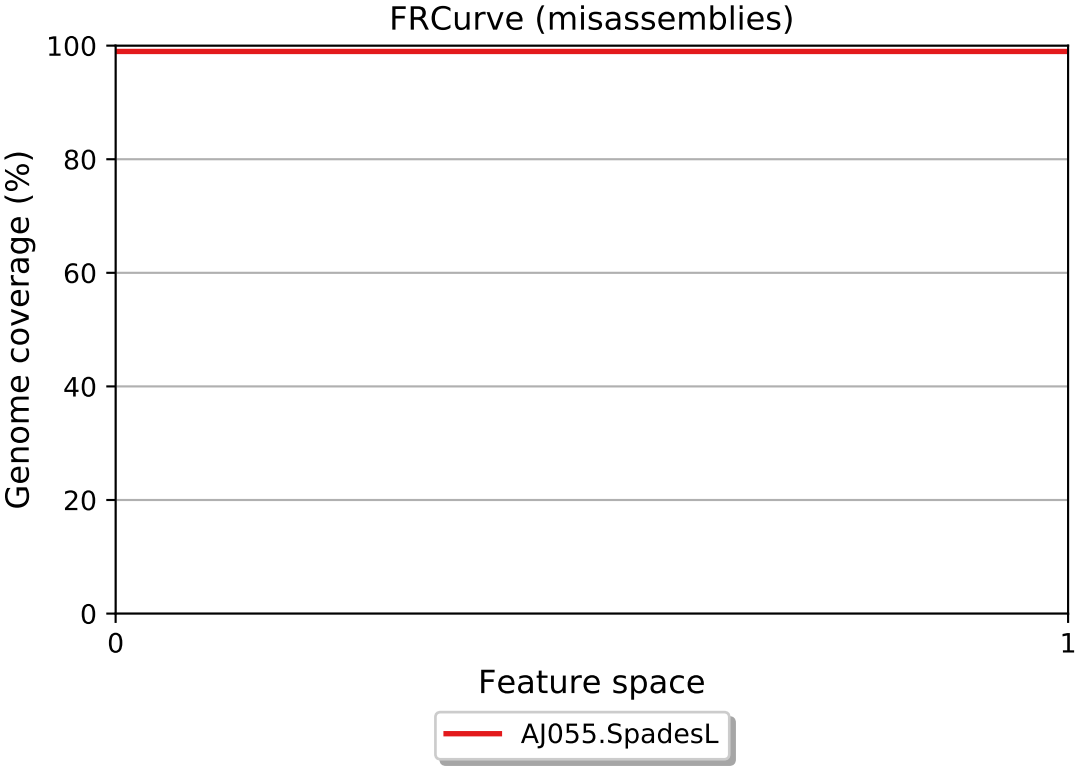

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ055.SpadesL
Reference

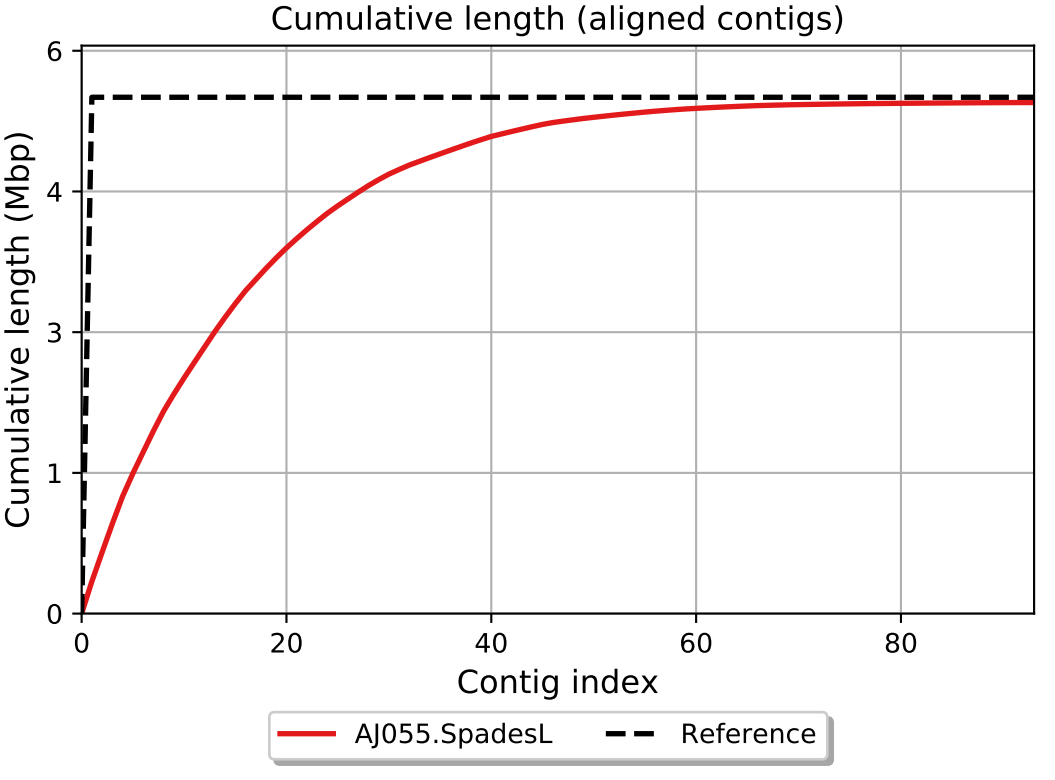

AJ055.SpadesL GC content
contigs
0
10
20
30
40
50
0
20
40
60
80
100
GC (%)
AJ055.SpadesL

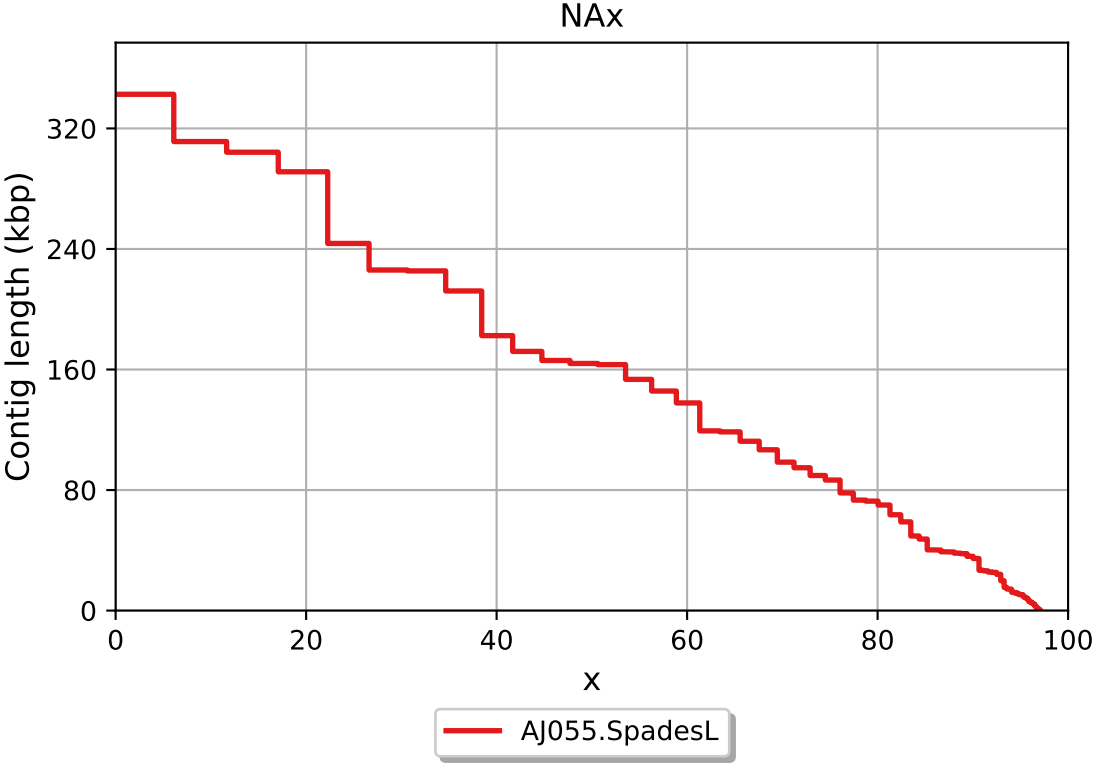

Coverage histogram (bin size: 1x)
Total length (kbp)
2500
2000
1500
1000
500
0
0
6
7
8
9
74
Coverage depth (x)
AJ055.SpadesL

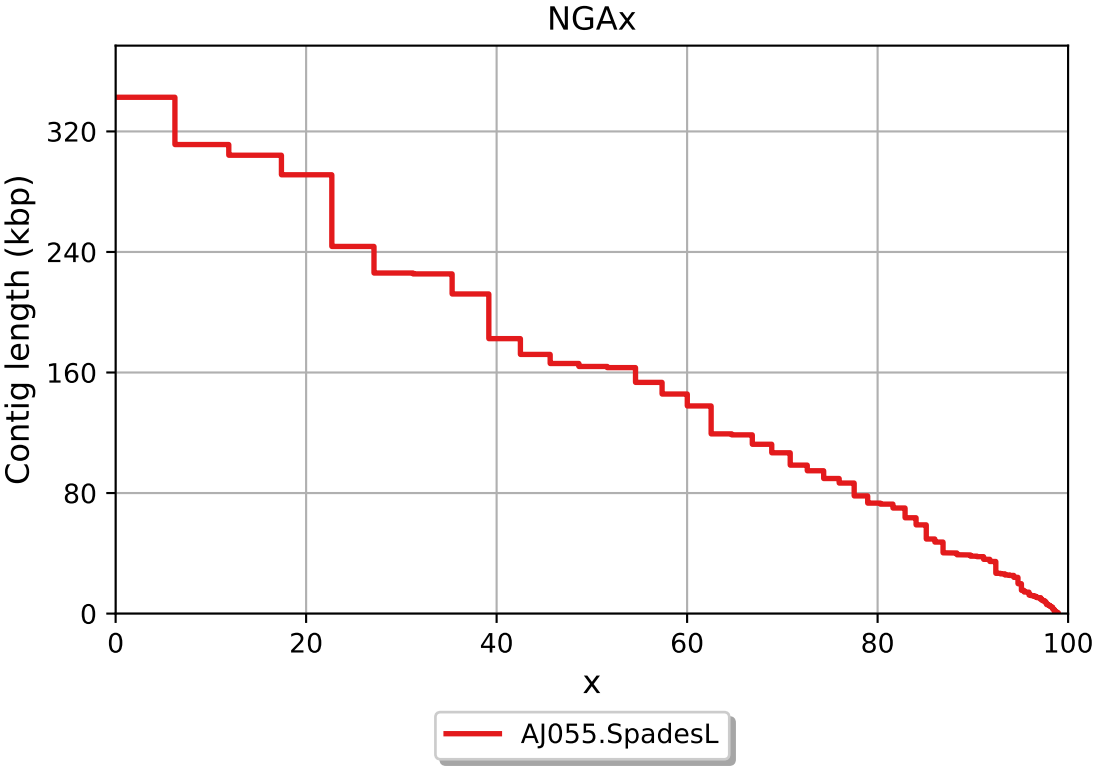

AJ055.SpadesL coverage histogram (bin size: 1x)
Total length (kbp)
2500
2000
1500
1000
500
0
0
6
7
8
9
74
Coverage depth (x)
AJ055.SpadesL


Misassemblies
5
4
3
2
1
0
AJ055.SpadesL


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
20
40
60
80
Contig index
AJ055.SpadesL
Reference


NAx
Contig length (kbp)
320
240
160
80
0
0
20
40
60
80
100
x
AJ055.SpadesL


NGAx
Contig length (kbp)
320
240
160
80
0
0
20
40
60
80
100
x
AJ055.SpadesL