Report

	AJ055.SpadesLRL
# contigs (>= 0 bp)	72
# contigs (>= 1000 bp)	15
# contigs (>= 5000 bp)	12
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	9
Total length (>= 0 bp)	5677347
Total length (>= 1000 bp)	5662727
Total length (>= 5000 bp)	5653948
Total length (>= 10000 bp)	5646162
Total length (>= 25000 bp)	5635515
Total length (>= 50000 bp)	5598181
# contigs	16
Largest contig	1845647
Total length	5663299
Reference length	5504133
GC (%)	57.25
Reference GC (%)	57.38
N50	1571477
NG50	1571477
N75	552169
NG75	552169
L50	2
LG50	2
L75	4
LG75	4
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1845647
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	164688
Genome fraction (%)	99.882
Duplication ratio	1.000
# N's per 100 kbp	1.77
# mismatches per 100 kbp	5.57
# indels per 100 kbp	1.75
Largest alignment	1587076
Total aligned length	5498433
NA50	1571477
NGA50	1571477
NA75	552169
NGA75	552169
LA50	2
LGA50	2
LA75	4
LGA75	4

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

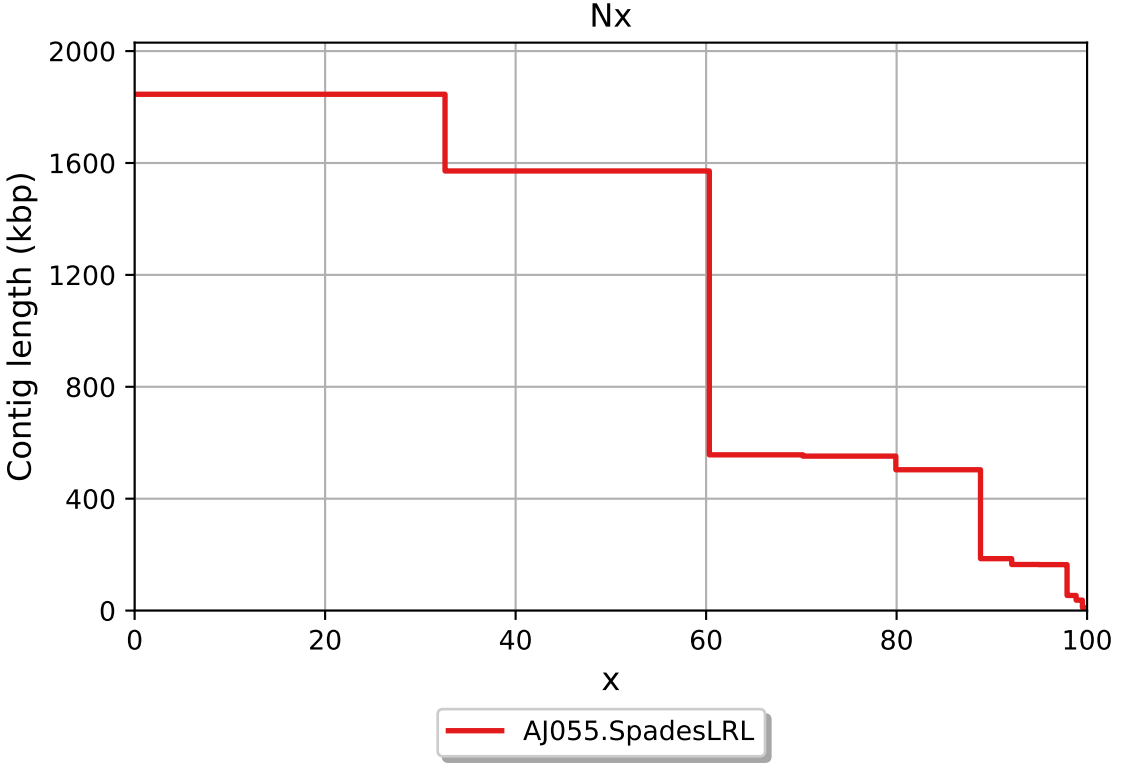
	AJ055.SpadesLRL
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1845647
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	306
# indels	96
# indels (<= 5 bp)	93
# indels (> 5 bp)	3
Indels length	318

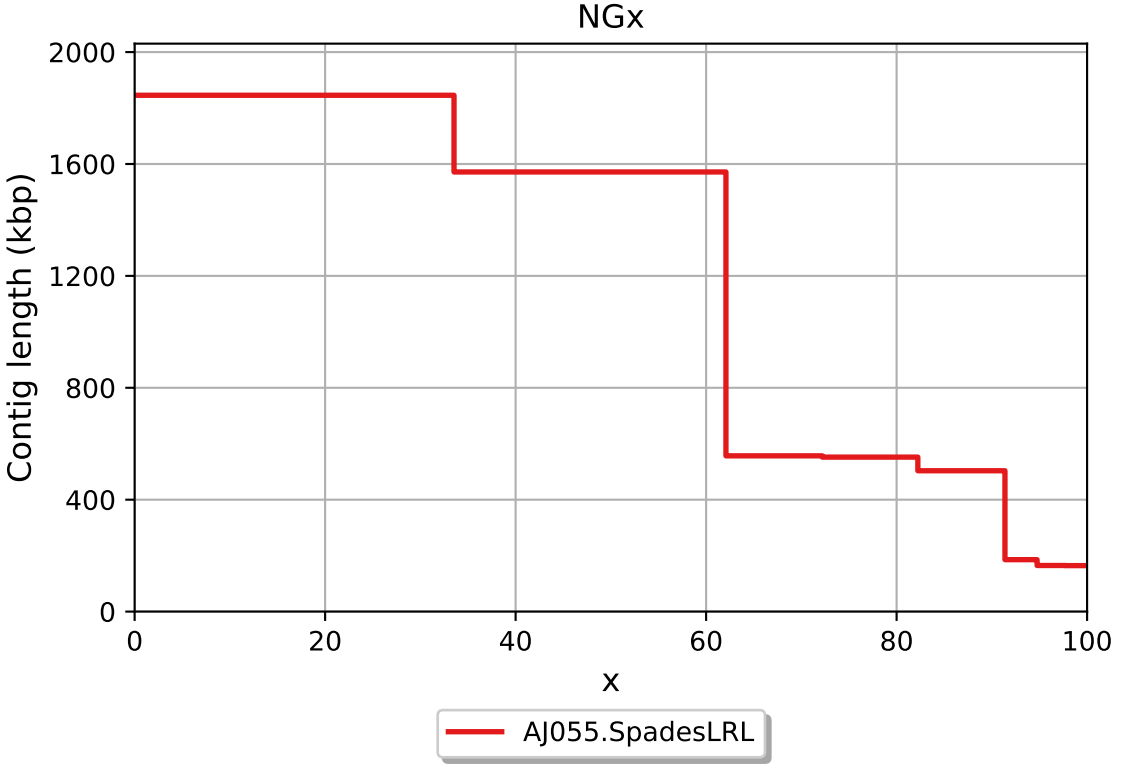
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

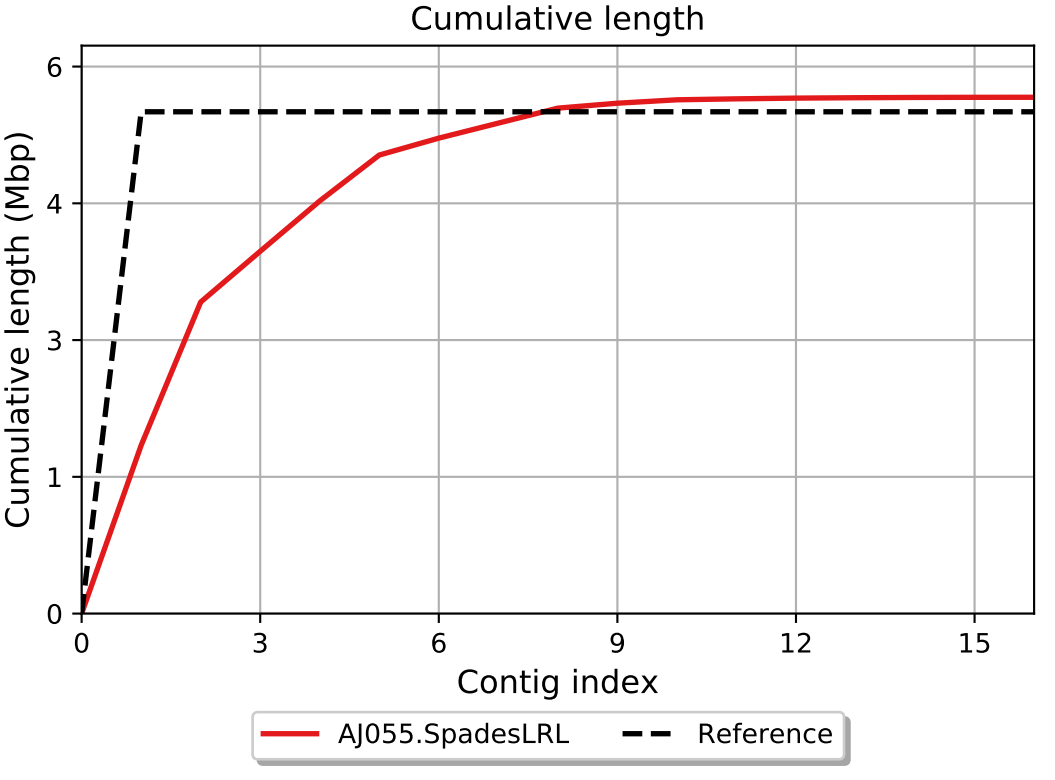
Unaligned report

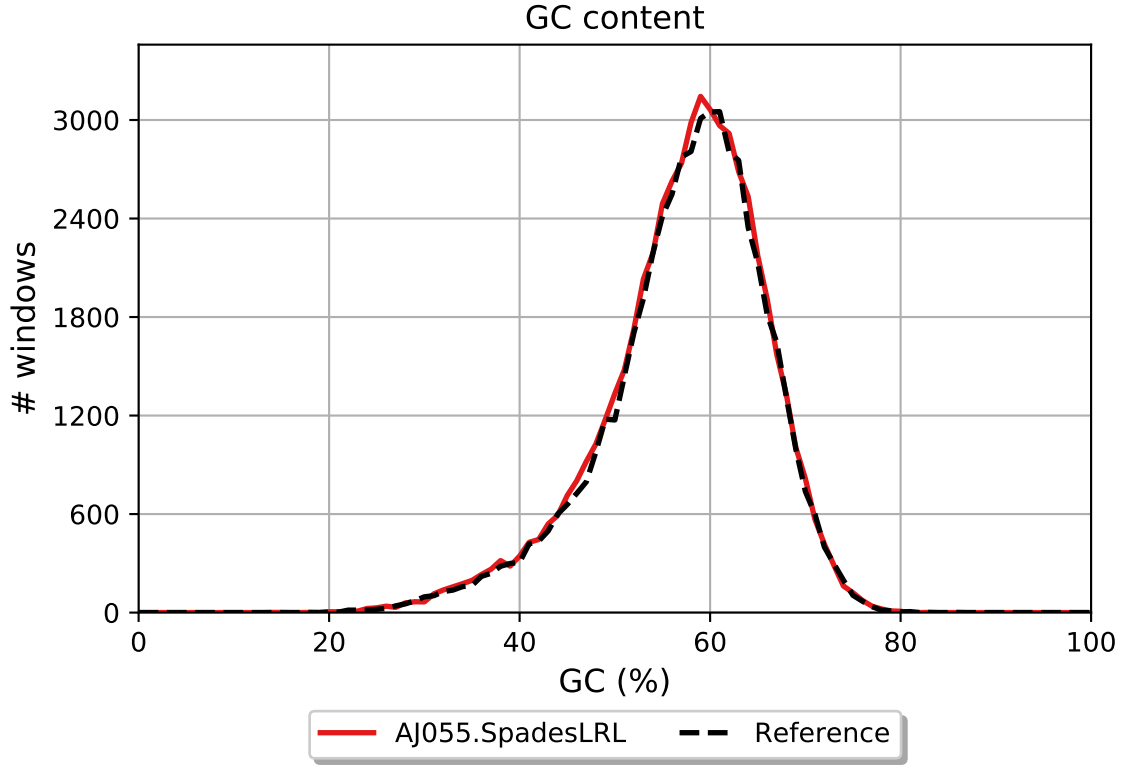
	AJ055.SpadesLRL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	164688
# N's	100

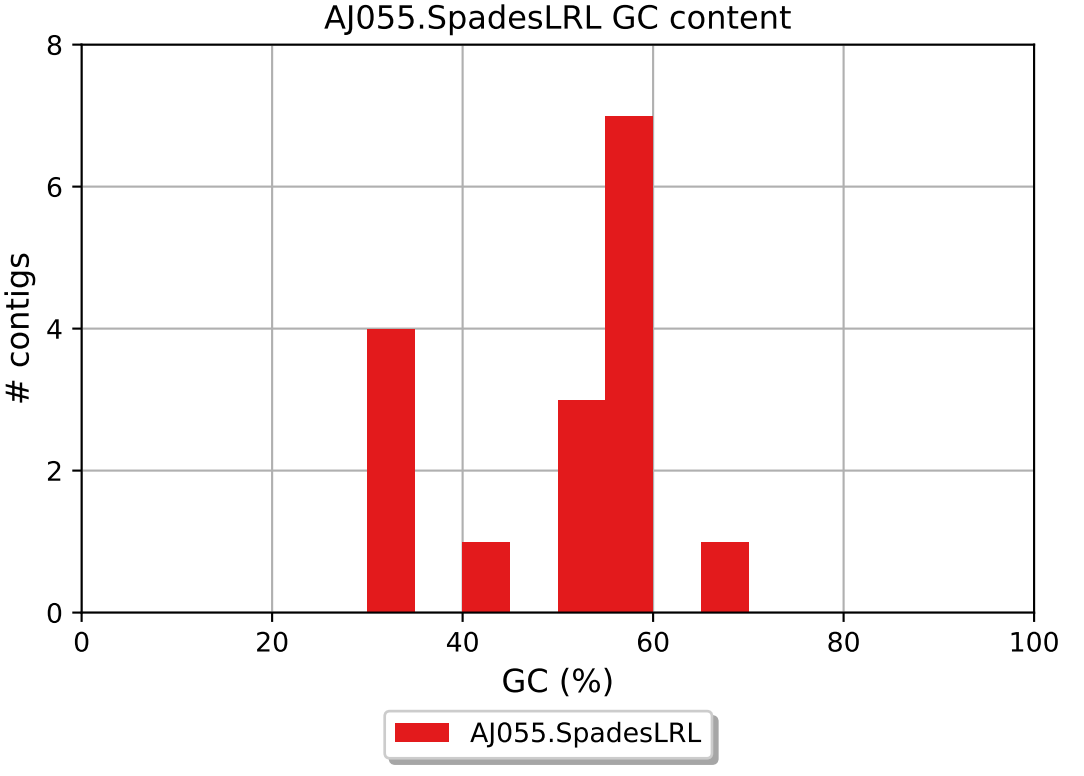
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

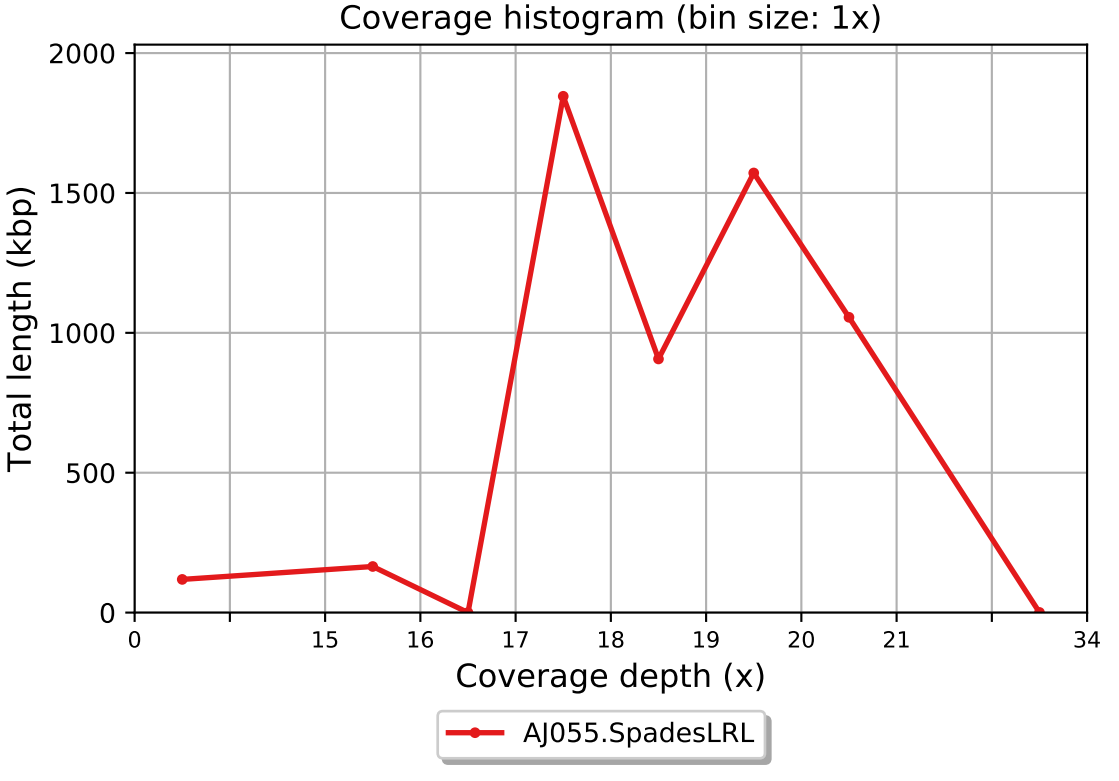

Nx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
AJ055.SpadesLRL

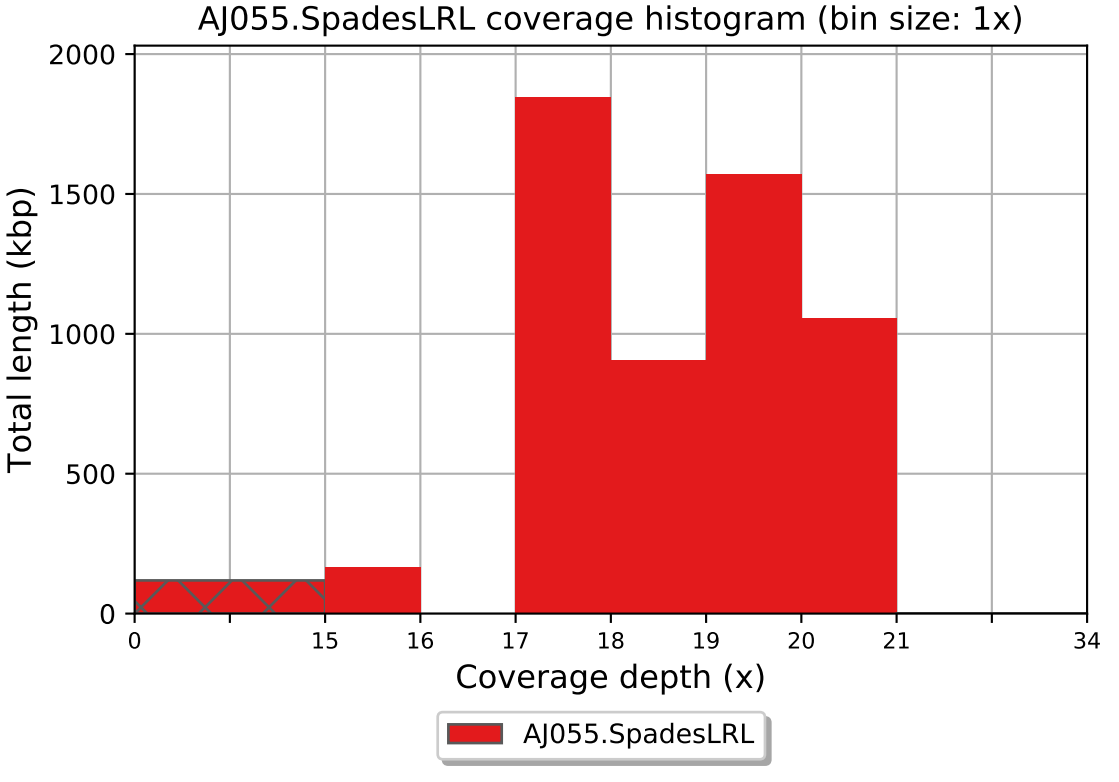

NGx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
AJ055.SpadesLRL

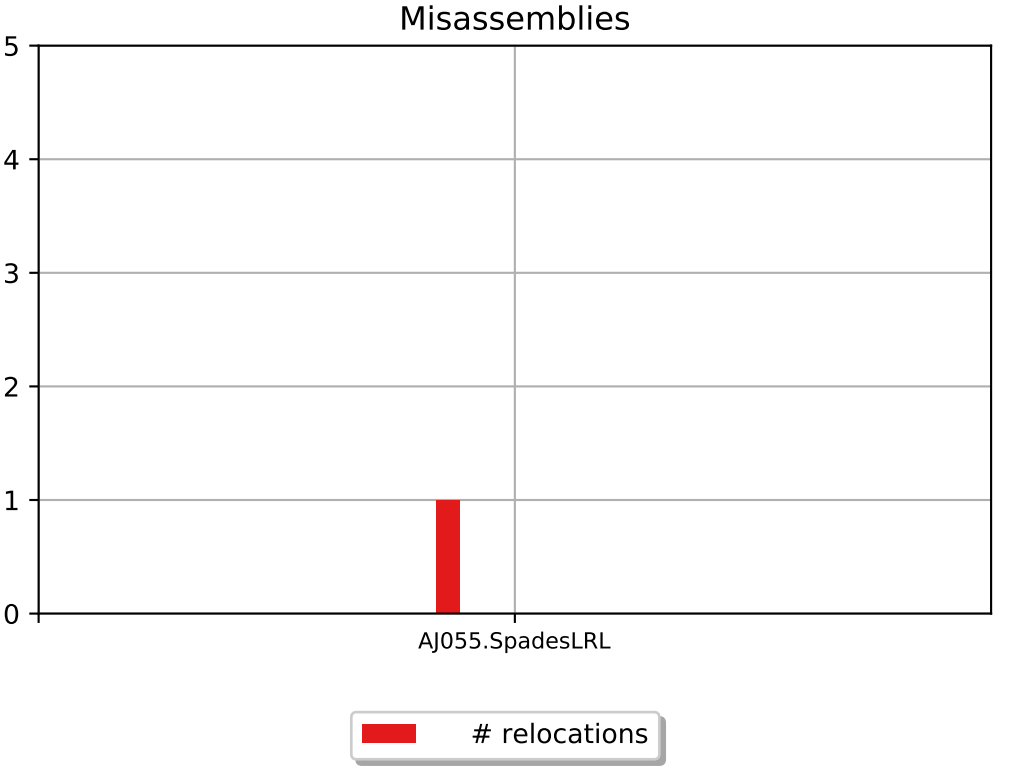

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
3
6
9
12
15
Contig index
AJ055.SpadesLRL
Reference

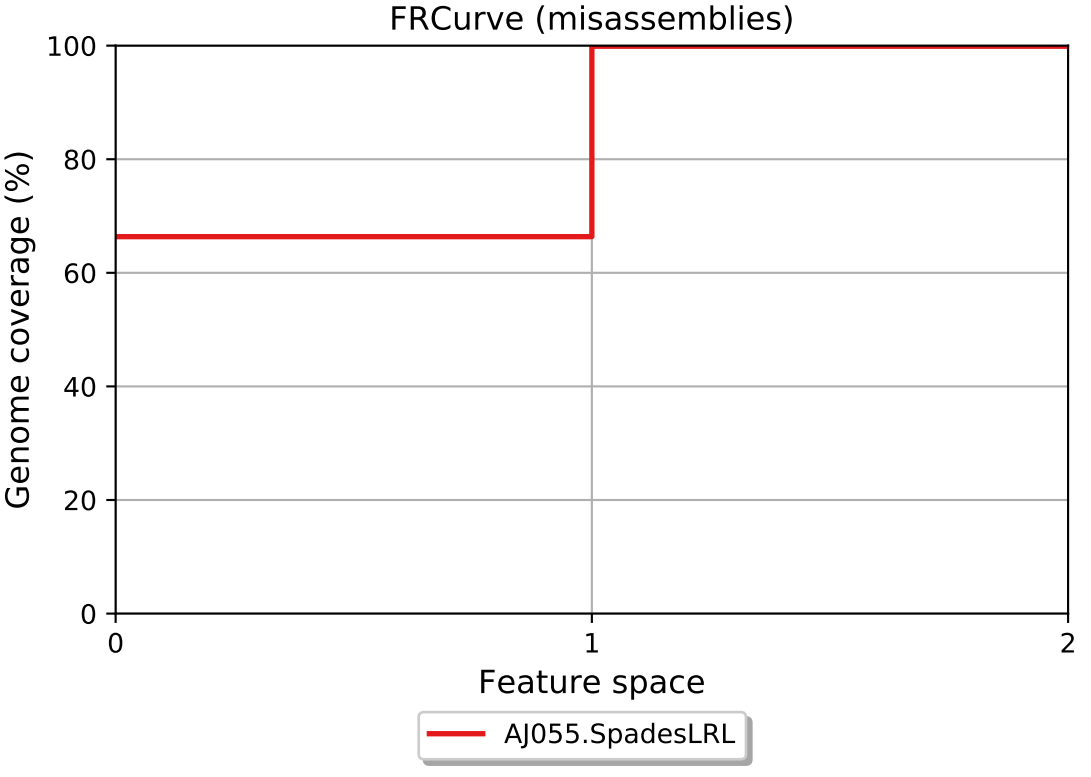

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
AJ055.SpadesLRL
Reference

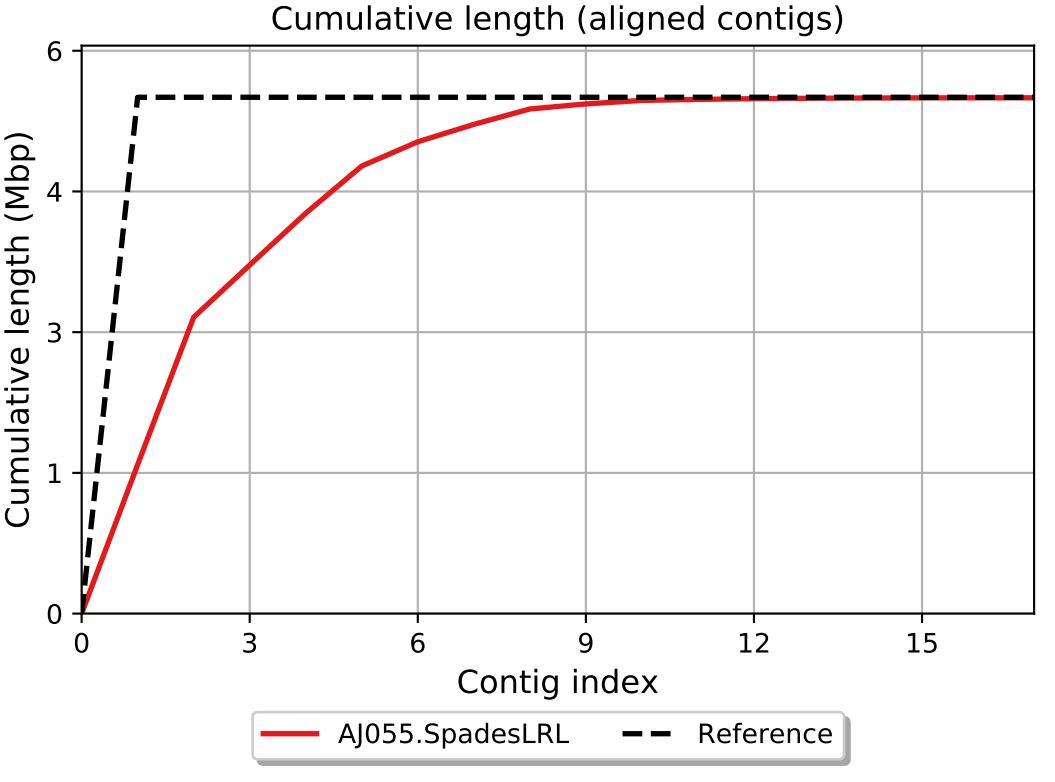

AJ055.SpadesLRL GC content
contigs
GC (%)
0
2
4
6
8
0
20
40
60
80
100
AJ055.SpadesLRL

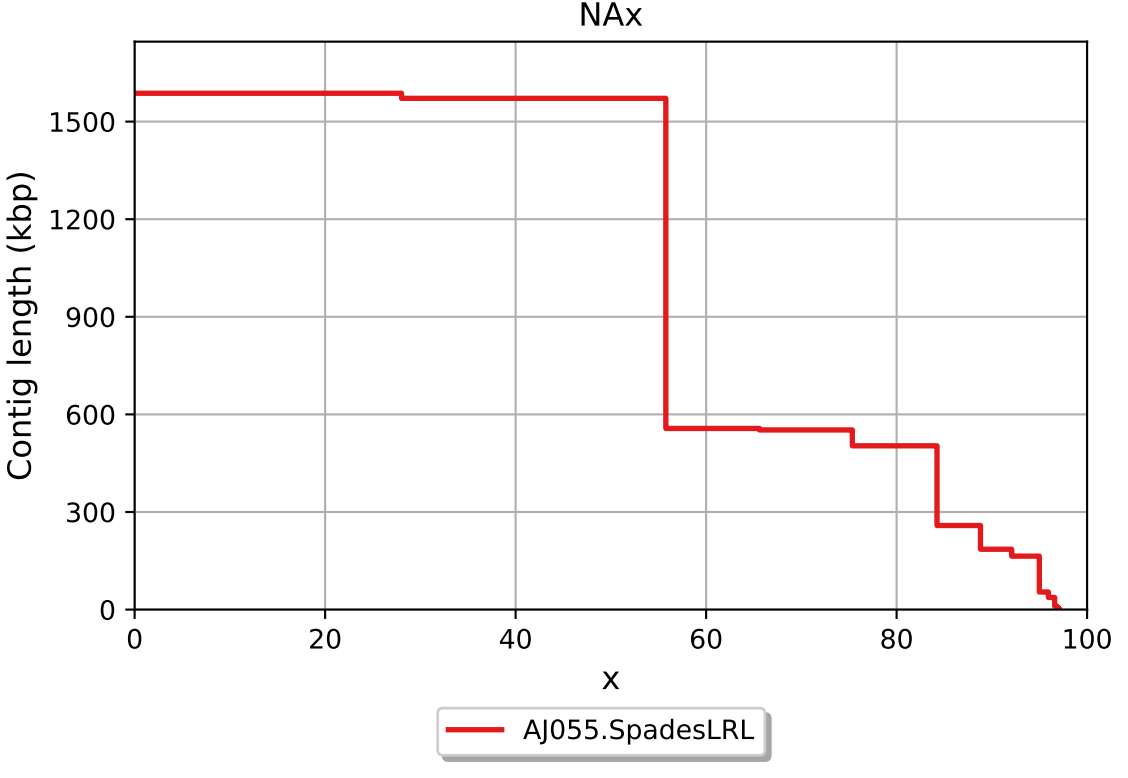

Coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
15
16
17
18
19
20
21
34
Coverage depth (x)
AJ055.SpadesLRL

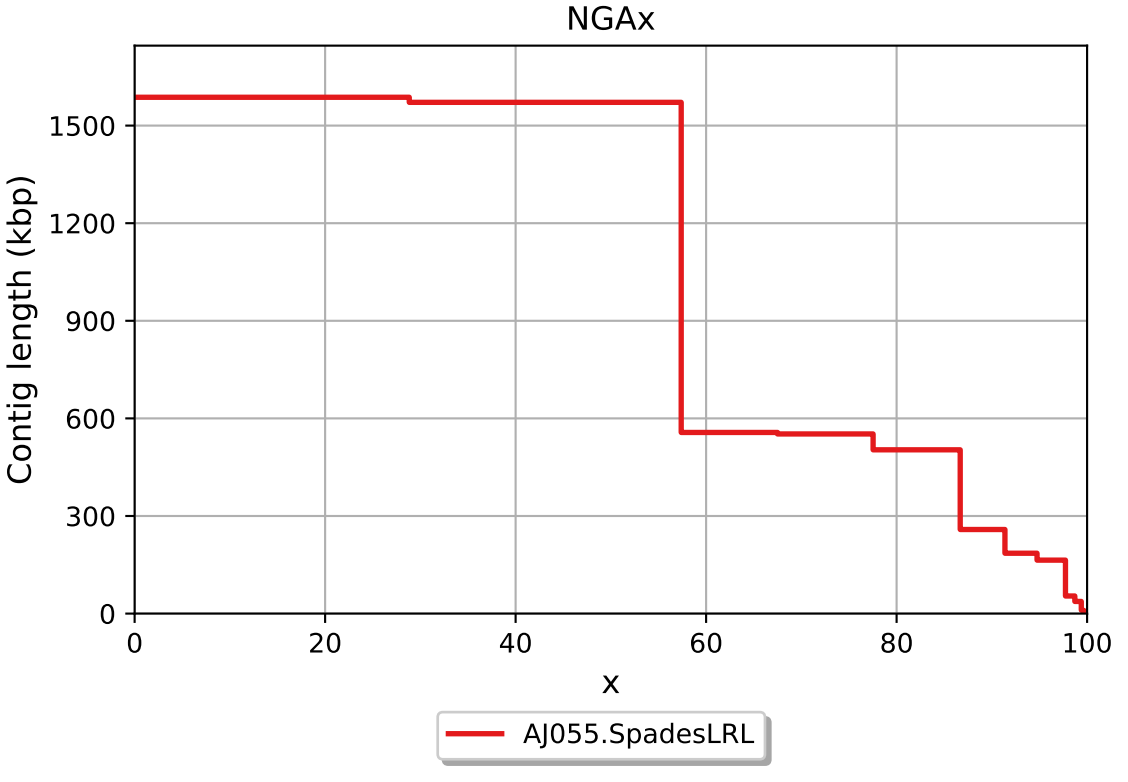

AJ055.SpadesLRL coverage histogram (bin size: 1x)
Total length (kbp)
2000
1500
1000
500
0
0
15
16
17
18
19
20
21
34
Coverage depth (x)
AJ055.SpadesLRL


Misassemblies
5
4
3
2
1
0
AJ055.SpadesLRL
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
AJ055.SpadesLRL


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
3
6
9
12
15
Contig index
AJ055.SpadesLRL
Reference


NAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
AJ055.SpadesLRL


NGAx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
AJ055.SpadesLRL