Report

	AJ218.SpadesL
# contigs (>= 0 bp)	231
# contigs (>= 1000 bp)	137
# contigs (>= 5000 bp)	96
# contigs (>= 10000 bp)	81
# contigs (>= 25000 bp)	59
# contigs (>= 50000 bp)	35
Total length (>= 0 bp)	5603425
Total length (>= 1000 bp)	5568680
Total length (>= 5000 bp)	5475677
Total length (>= 10000 bp)	5369338
Total length (>= 25000 bp)	4979685
Total length (>= 50000 bp)	4137146
# contigs	161
Largest contig	369879
Total length	5586184
Reference length	5465981
GC (%)	57.21
Reference GC (%)	57.29
N50	102472
NG50	109857
N75	48179
NG75	55877
L50	17
LG50	16
L75	37
LG75	35
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned mis. contigs	0
# unaligned contigs	7 + 6 part
Unaligned length	186737
Genome fraction (%)	98.683
Duplication ratio	1.001
# N's per 100 kbp	3.37
# mismatches per 100 kbp	9.40
# indels per 100 kbp	1.43
Largest alignment	369879
Total aligned length	5398386
NA50	102472
NGA50	109857
NA75	46985
NGA75	48179
LA50	17
LGA50	16
LA75	37
LGA75	35

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

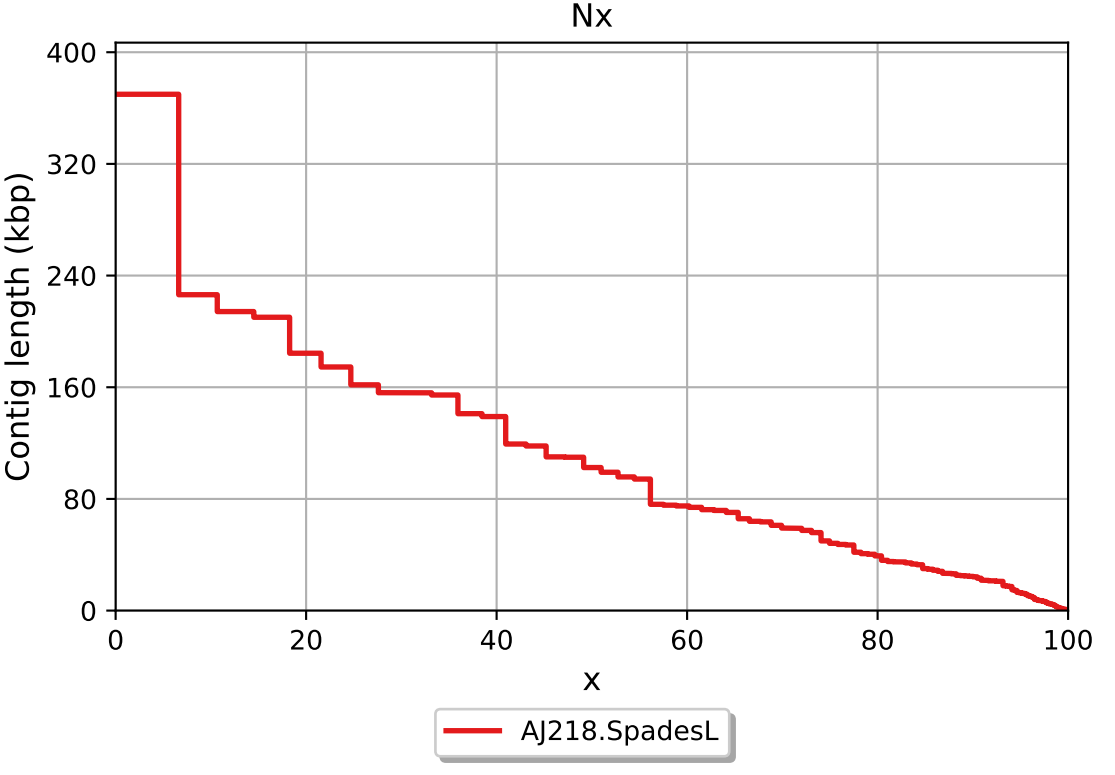
	AJ218.SpadesL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	9
# unaligned mis. contigs	0
# mismatches	507
# indels	77
# indels (<= 5 bp)	65
# indels (> 5 bp)	12
Indels length	239

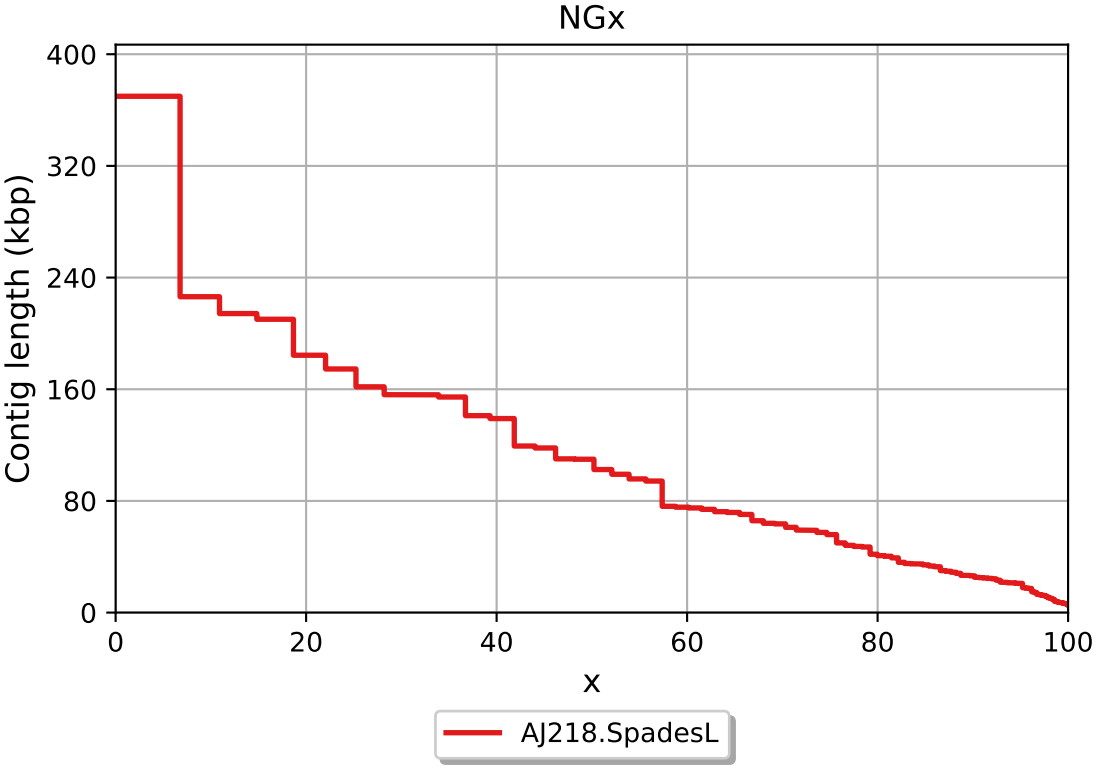
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

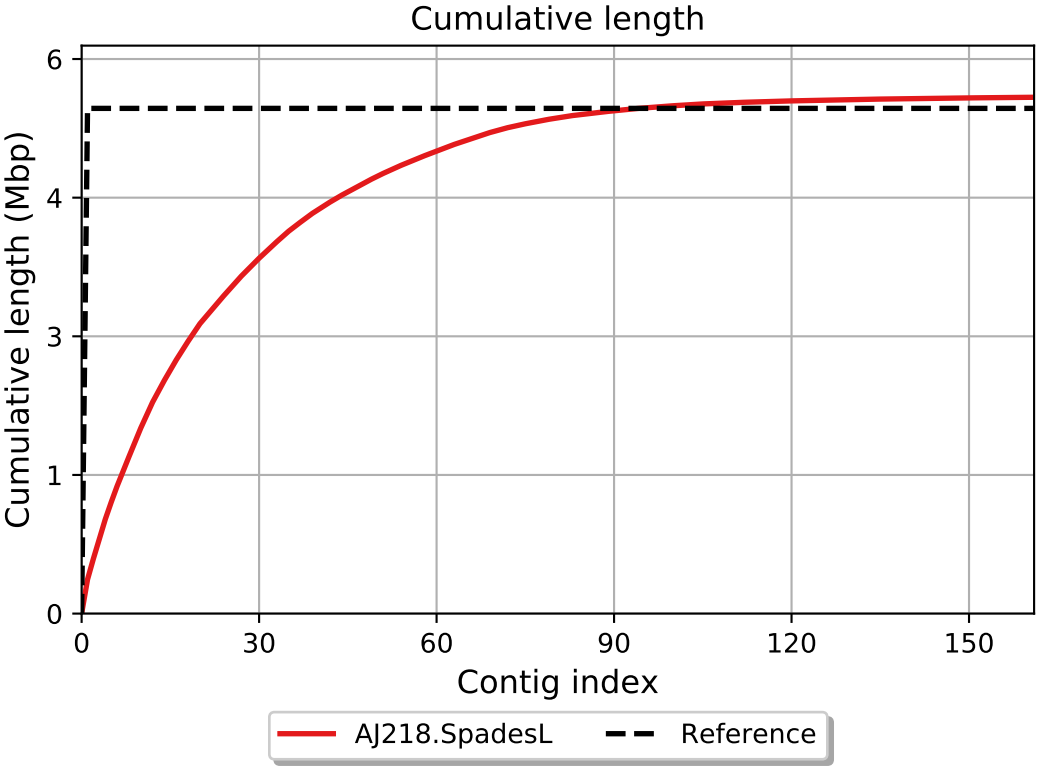
Unaligned report

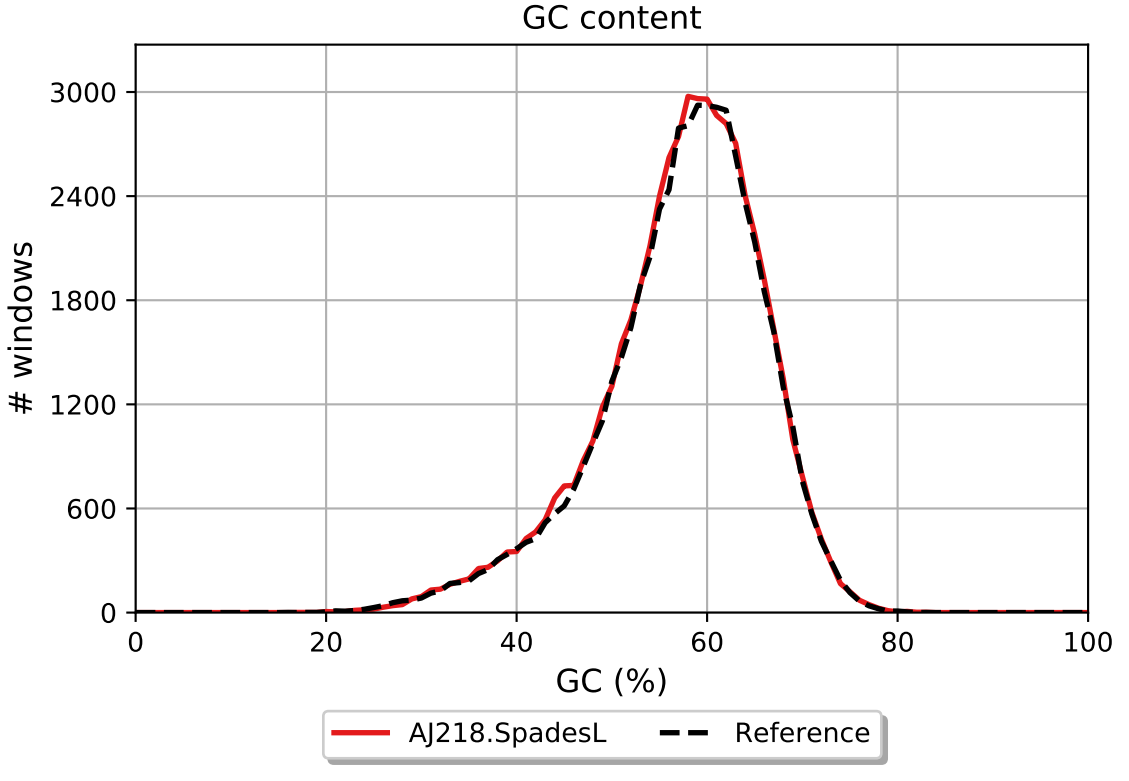
	AJ218.SpadesL
# fully unaligned contigs	7
Fully unaligned length	30102
# partially unaligned contigs	6
Partially unaligned length	156635
# N's	188

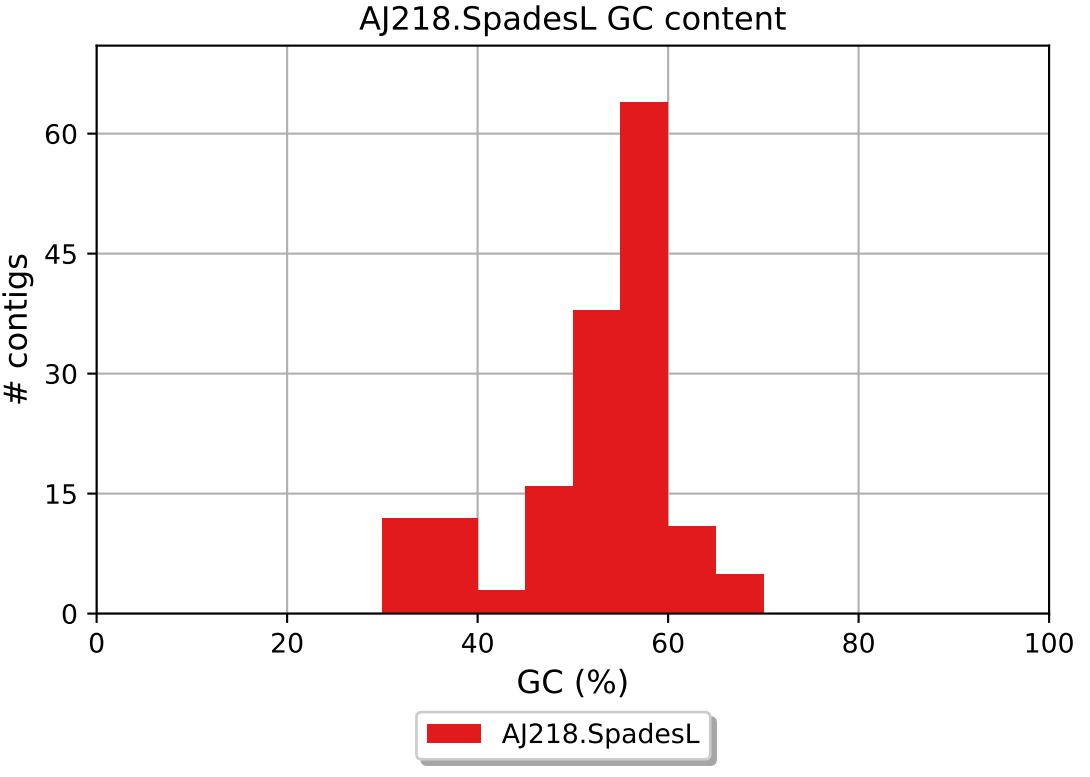
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

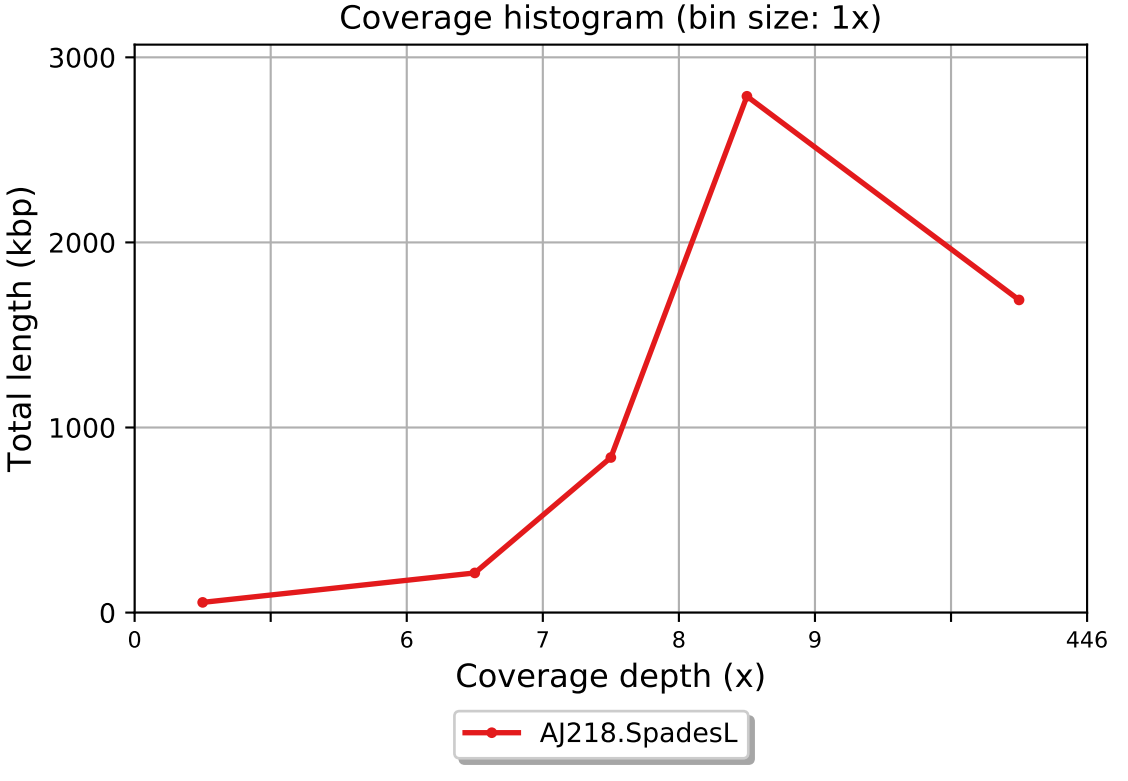

Nx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
AJ218.SpadesL

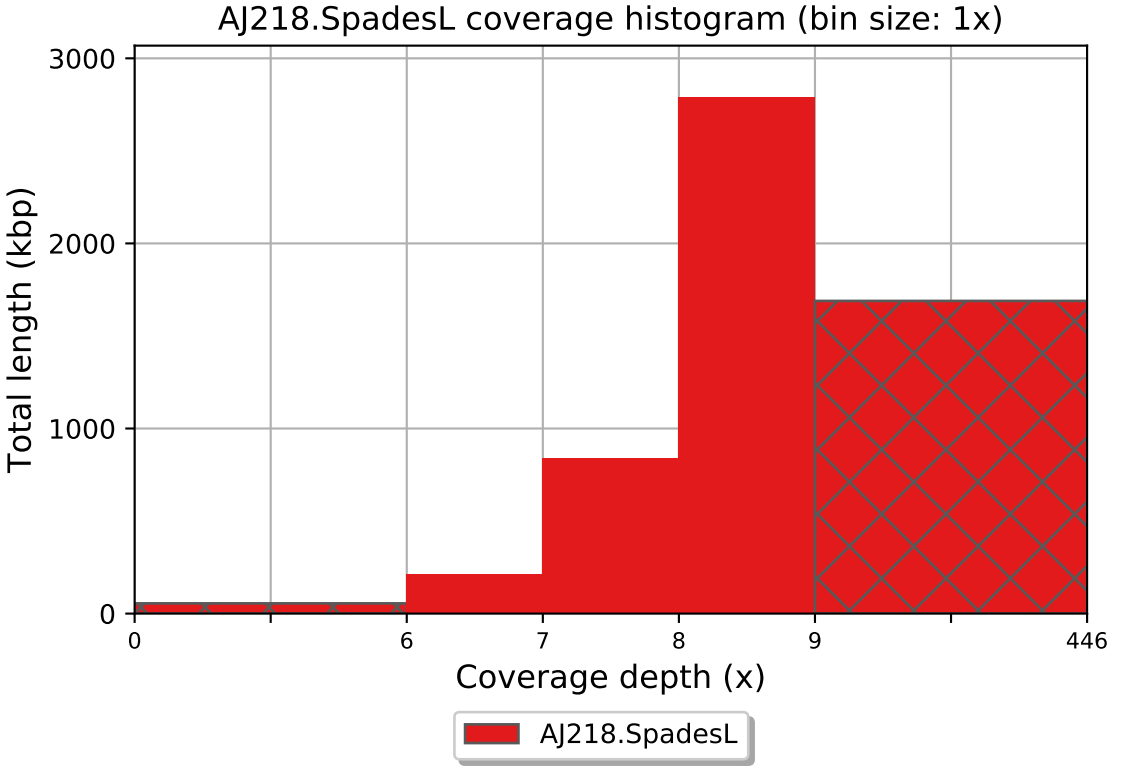

NGx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
AJ218.SpadesL

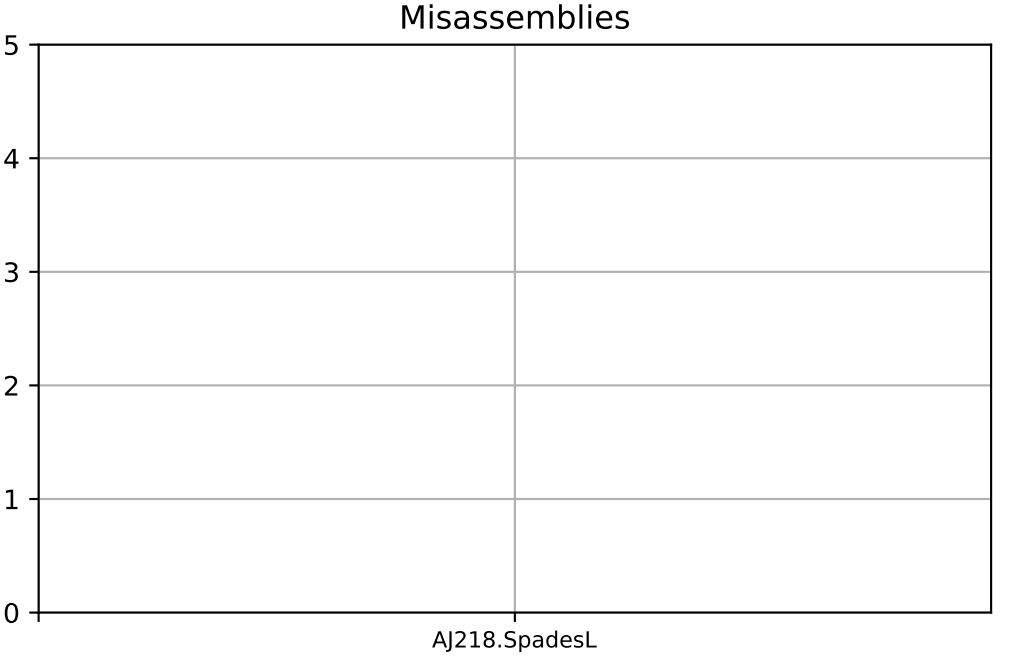

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
30
60
90
120
150
Contig index
AJ218.SpadesL
Reference

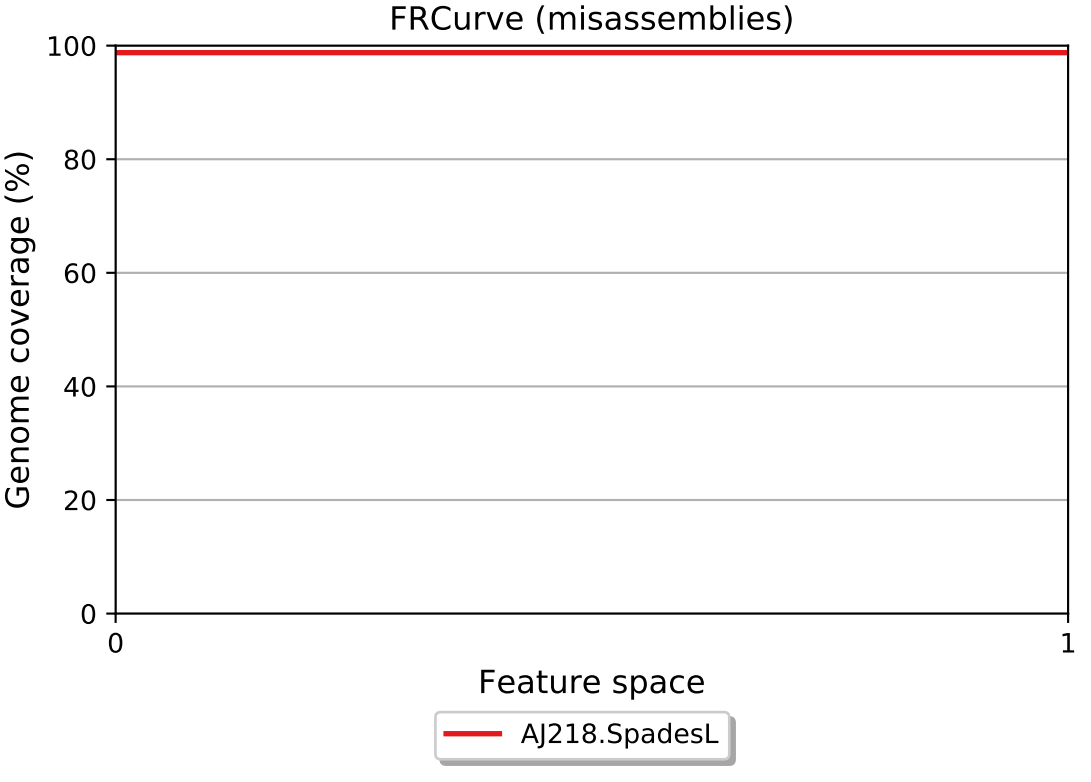

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ218.SpadesL
Reference

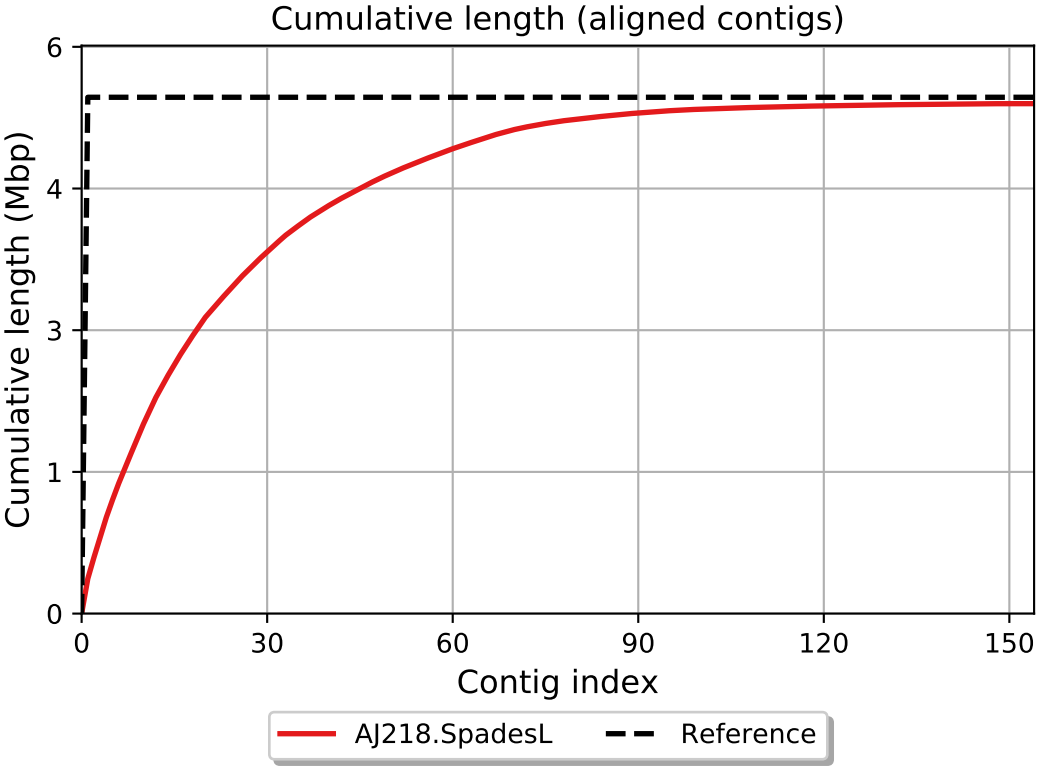

AJ218.SpadesL GC content
contigs
0
15
30
45
60
0
20
40
60
80
100
GC (%)
AJ218.SpadesL

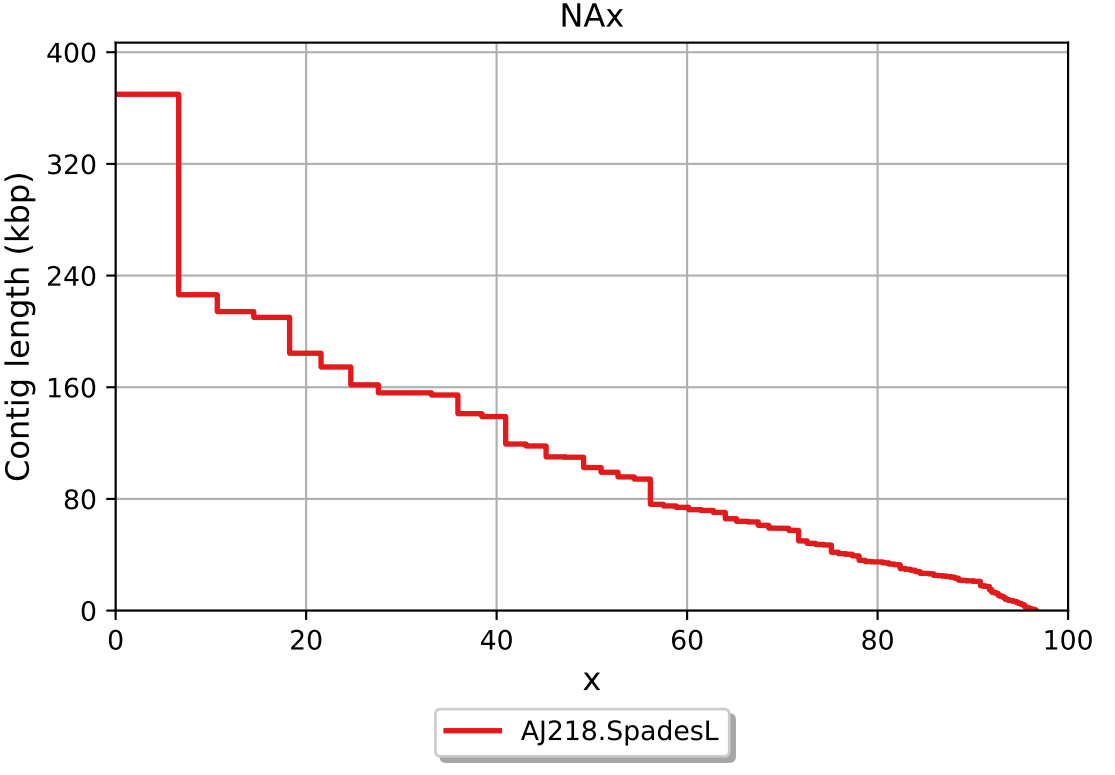

Coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
6
7
8
9
446
Coverage depth (x)
AJ218.SpadesL

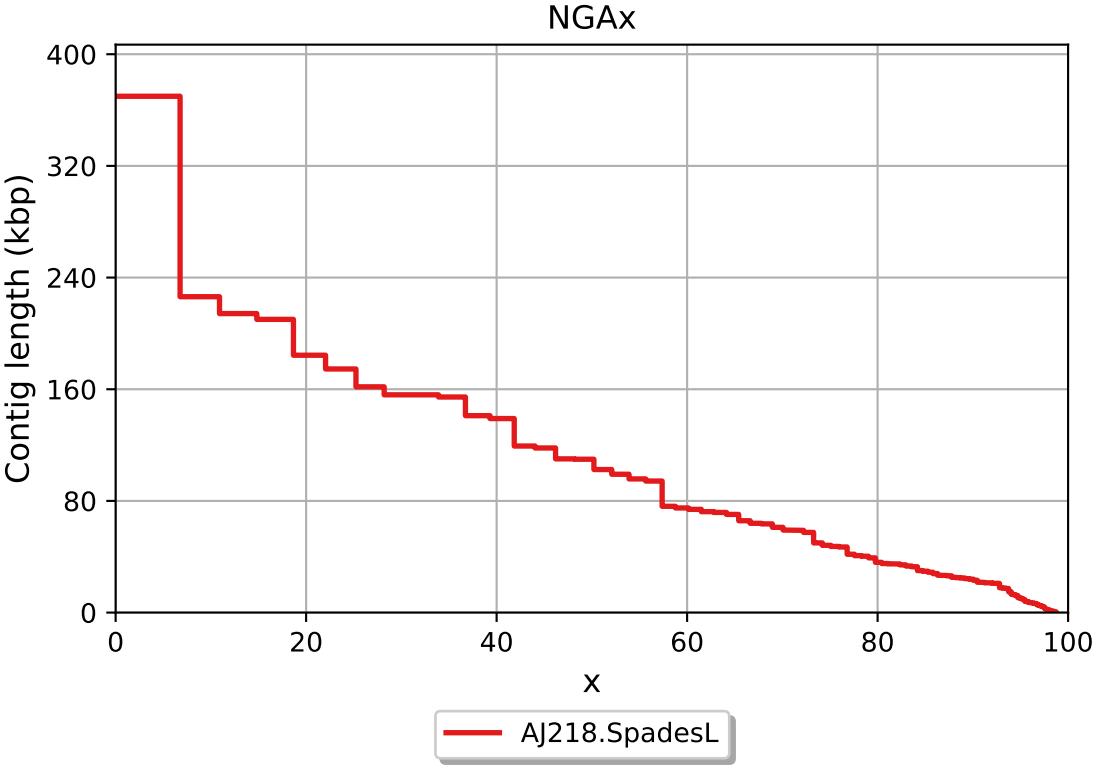

AJ218.SpadesL coverage histogram (bin size: 1x)
Total length (kbp)
3000
2000
1000
0
0
6
7
8
9
446
Coverage depth (x)
AJ218.SpadesL


Misassemblies
5
4
3
2
1
0
AJ218.SpadesL


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
AJ218.SpadesL


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
30
60
90
120
150
Contig index
AJ218.SpadesL
Reference


NAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
AJ218.SpadesL


NGAx
Contig length (kbp)
400
320
240
160
80
0
0
20
40
60
80
100
x
AJ218.SpadesL