Report

	AJ292.SpadesH
# contigs (>= 0 bp)	121
# contigs (>= 1000 bp)	45
# contigs (>= 5000 bp)	34
# contigs (>= 10000 bp)	34
# contigs (>= 25000 bp)	32
# contigs (>= 50000 bp)	26
Total length (>= 0 bp)	5419501
Total length (>= 1000 bp)	5399978
Total length (>= 5000 bp)	5370417
Total length (>= 10000 bp)	5370417
Total length (>= 25000 bp)	5330987
Total length (>= 50000 bp)	5114143
# contigs	54
Largest contig	578656
Total length	5406608
Reference length	5445112
GC (%)	57.68
Reference GC (%)	57.62
N50	206004
NG50	206004
N75	165361
NG75	165361
L50	9
LG50	9
L75	16
LG75	16
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	271842
# local misassemblies	16
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	1918
Genome fraction (%)	99.156
Duplication ratio	1.001
# N's per 100 kbp	36.14
# mismatches per 100 kbp	4.13
# indels per 100 kbp	0.74
Largest alignment	578656
Total aligned length	5404580
NA50	202814
NGA50	202814
NA75	134093
NGA75	134093
LA50	9
LGA50	9
LA75	17
LGA75	17

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

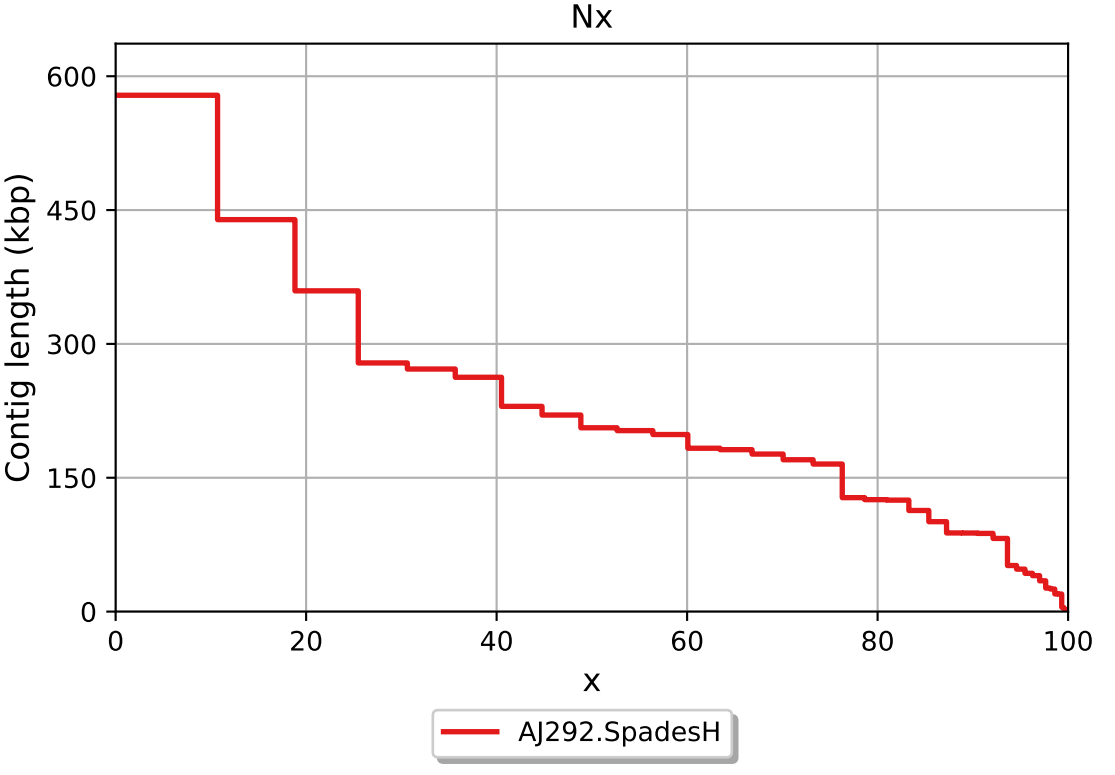
	AJ292.SpadesH
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	271842
# local misassemblies	16
# unaligned mis. contigs	0
# mismatches	223
# indels	40
# indels (<= 5 bp)	33
# indels (> 5 bp)	7
Indels length	343

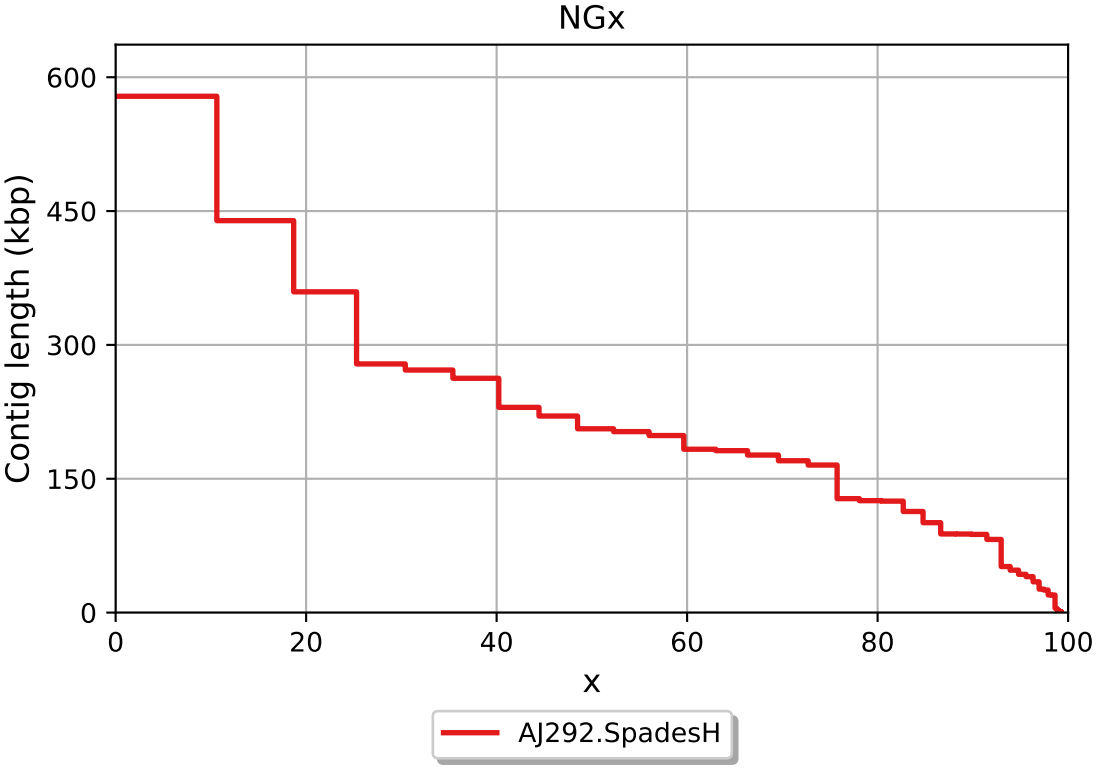
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

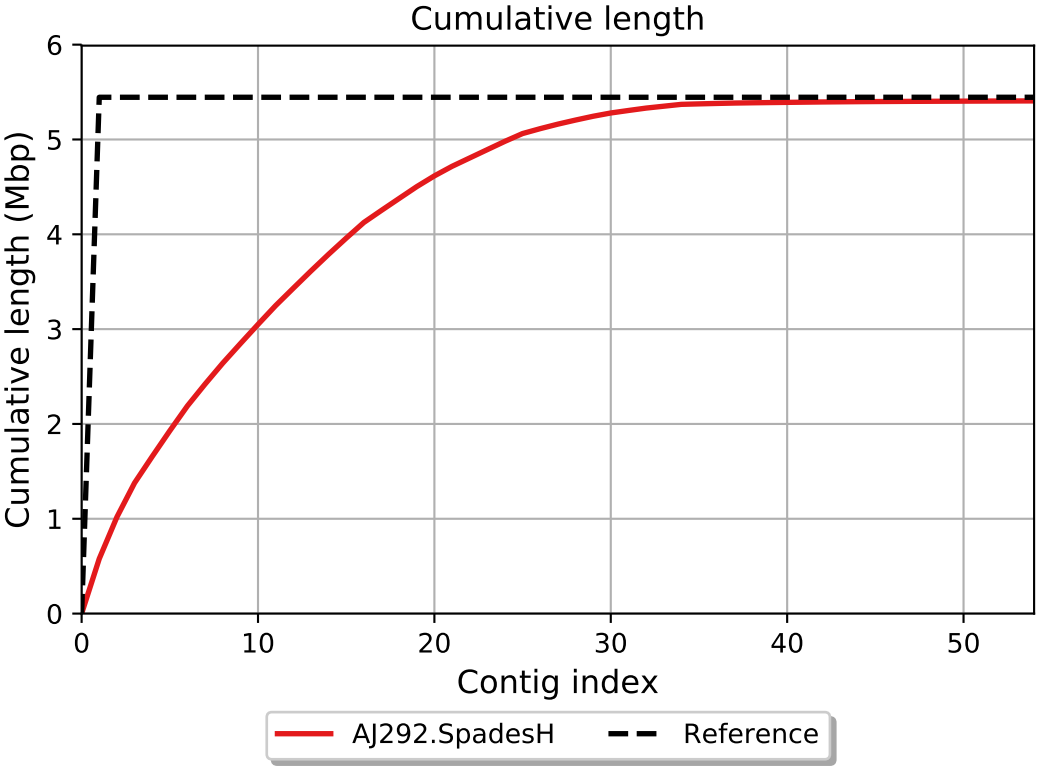
Unaligned report

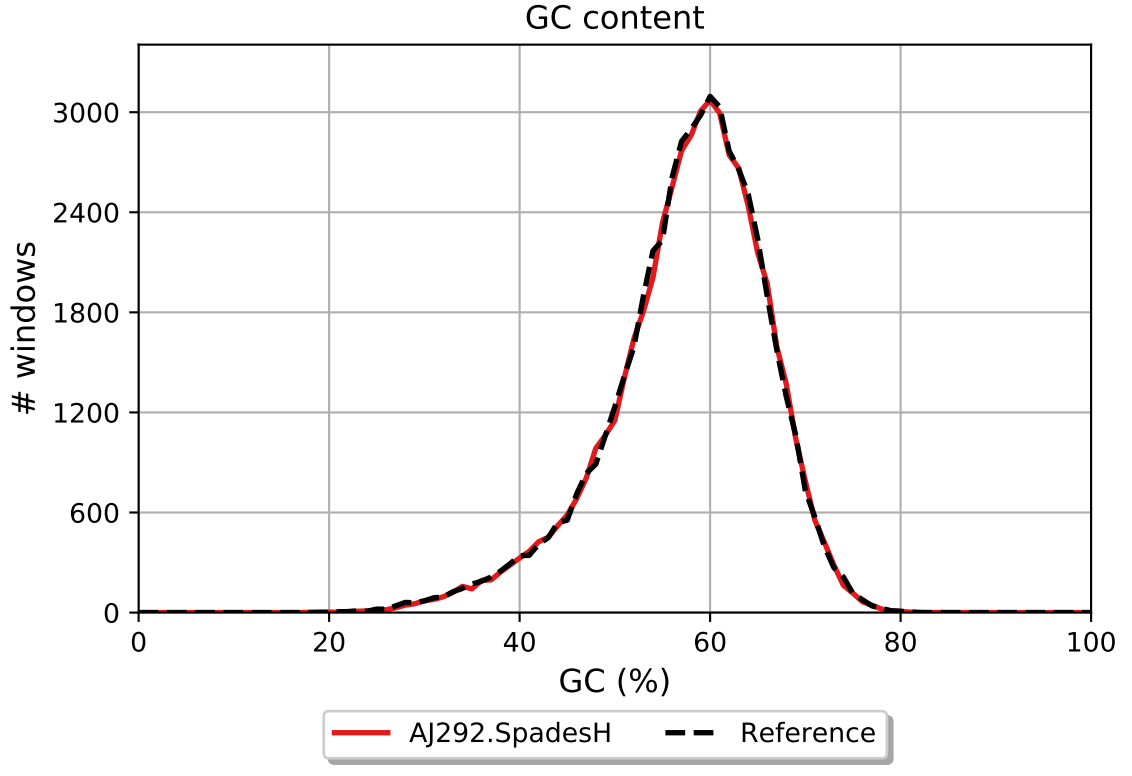
	AJ292.SpadesH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	1918
# N's	1954

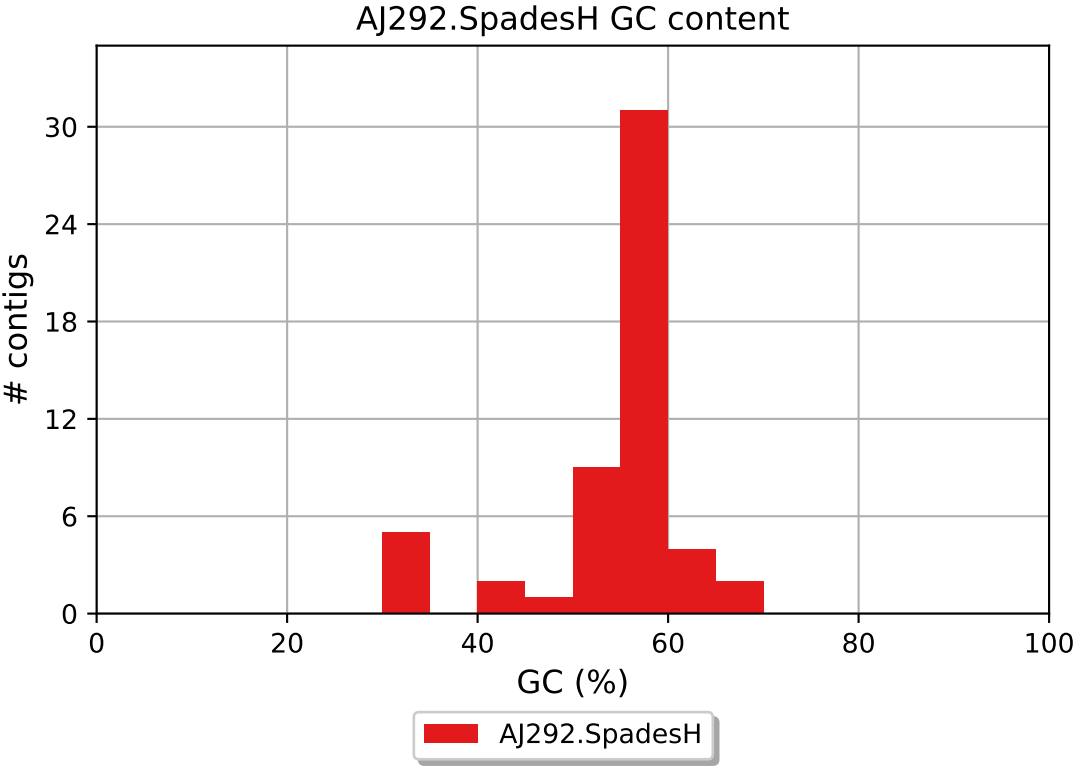
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

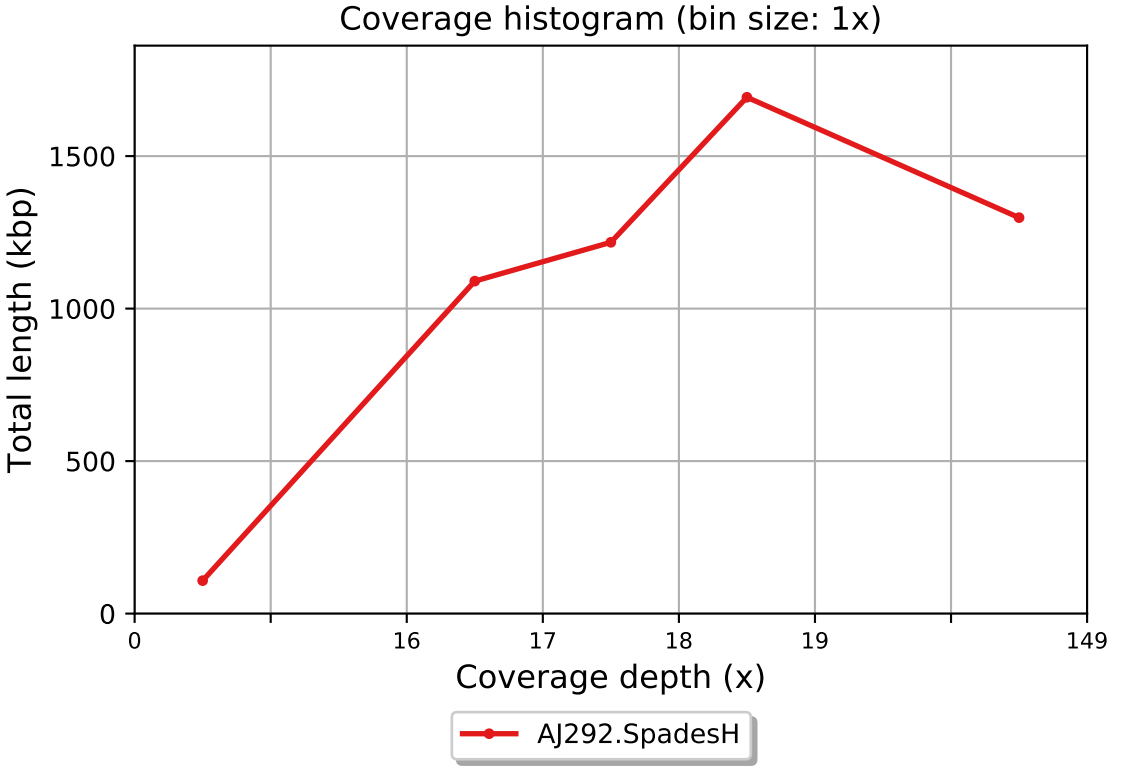

Nx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
AJ292.SpadesH

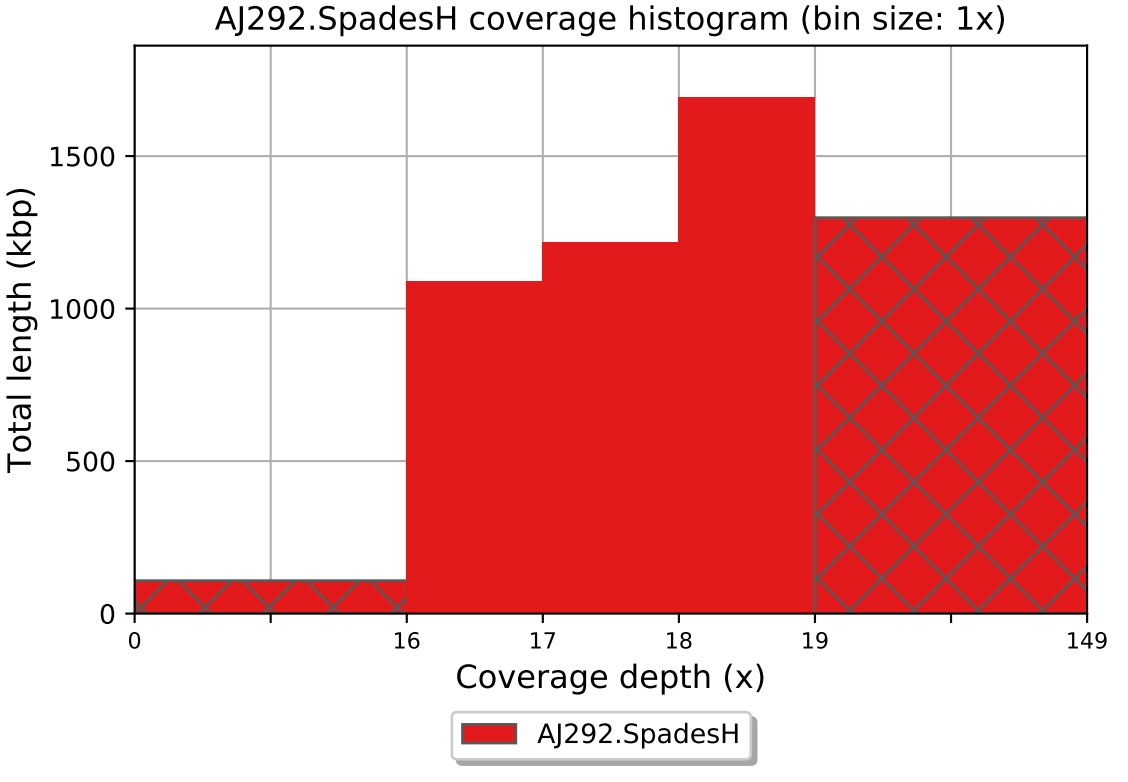

NGx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
AJ292.SpadesH

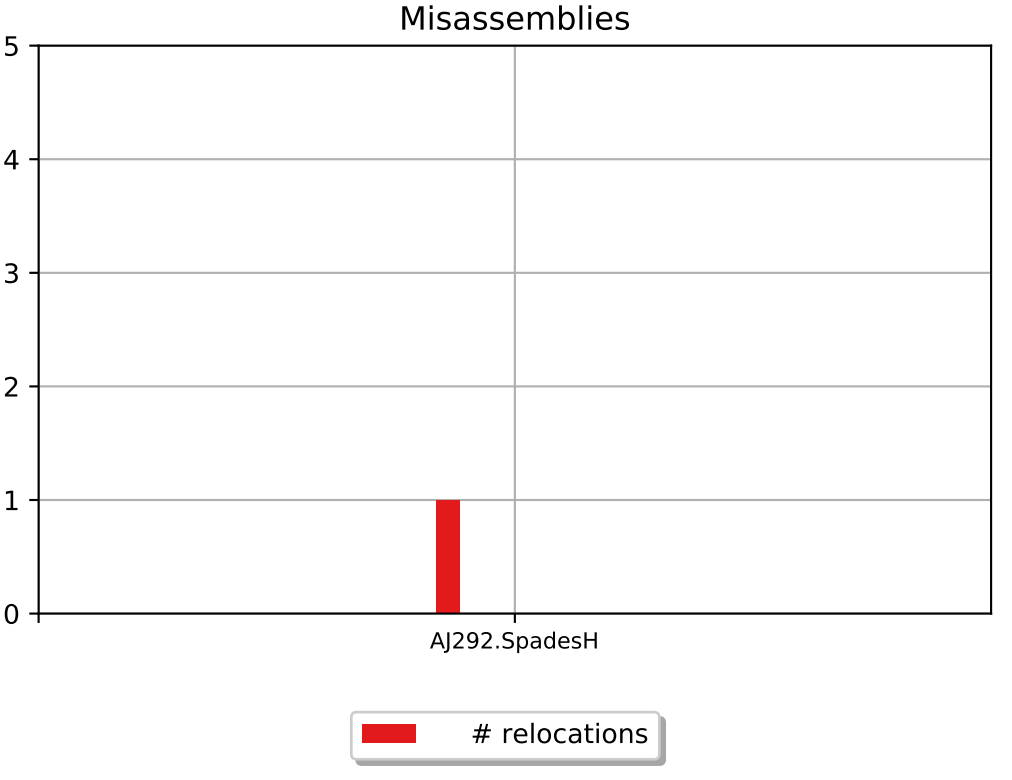

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
10
20
30
40
50
Contig index
AJ292.SpadesH
Reference

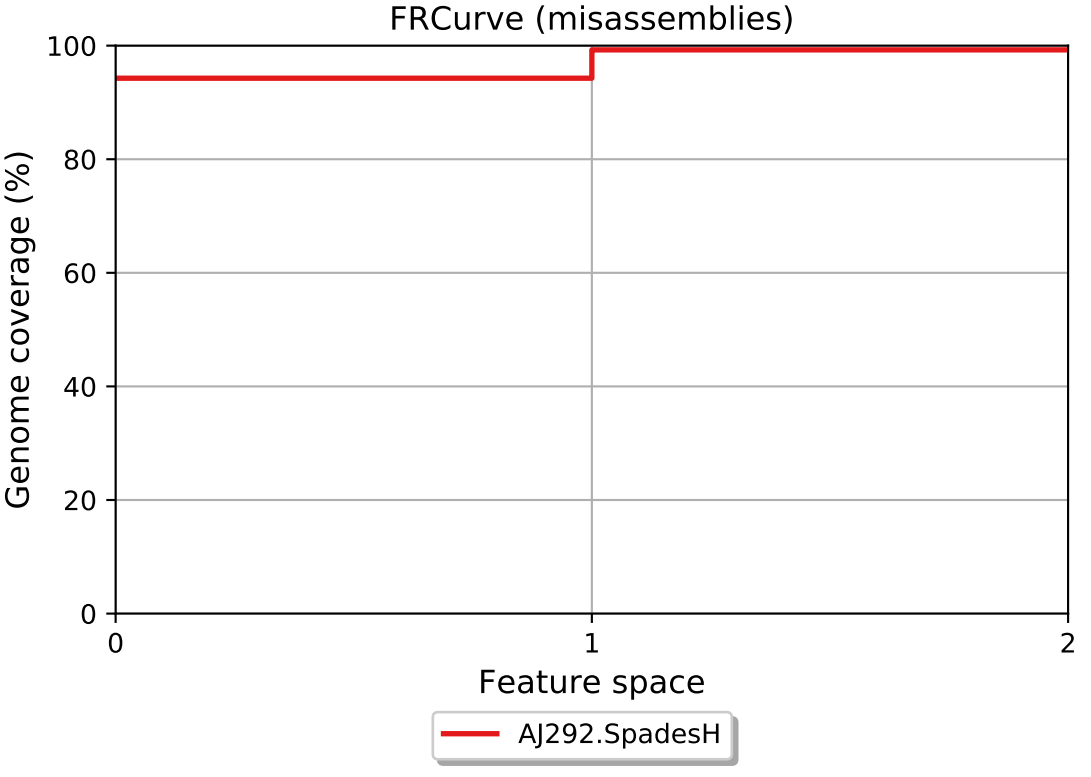

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
AJ292.SpadesH
Reference

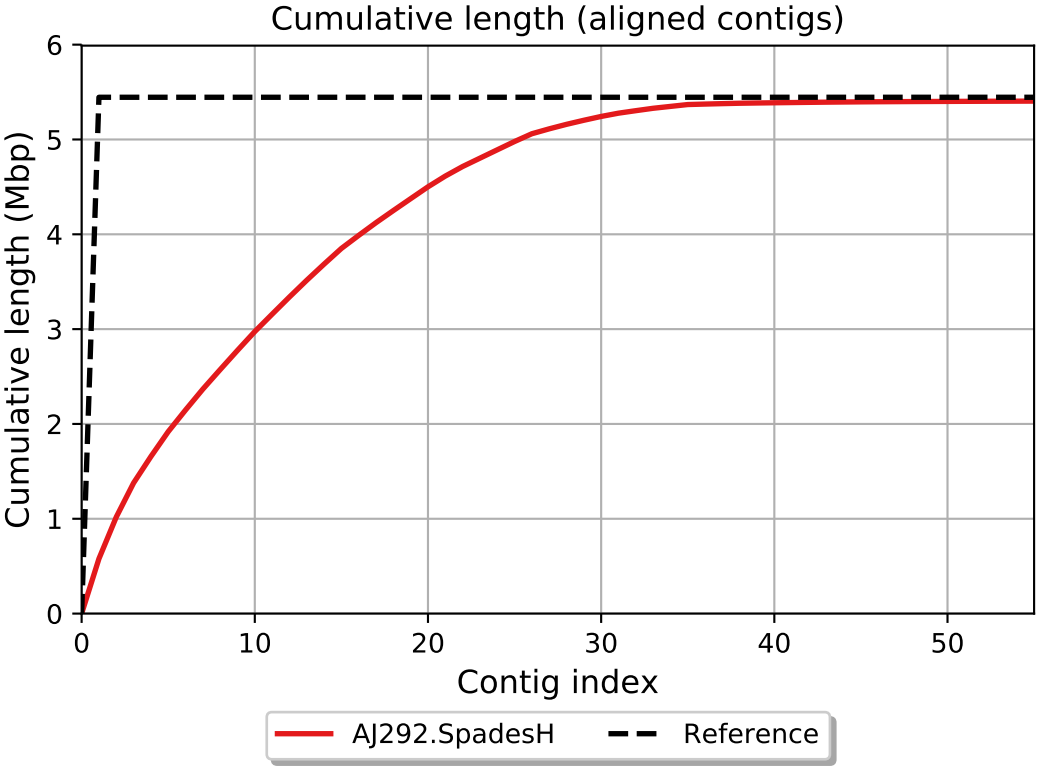

AJ292.SpadesH GC content
contigs
0
6
12
18
24
30
0
20
40
60
80
100
GC (%)
AJ292.SpadesH

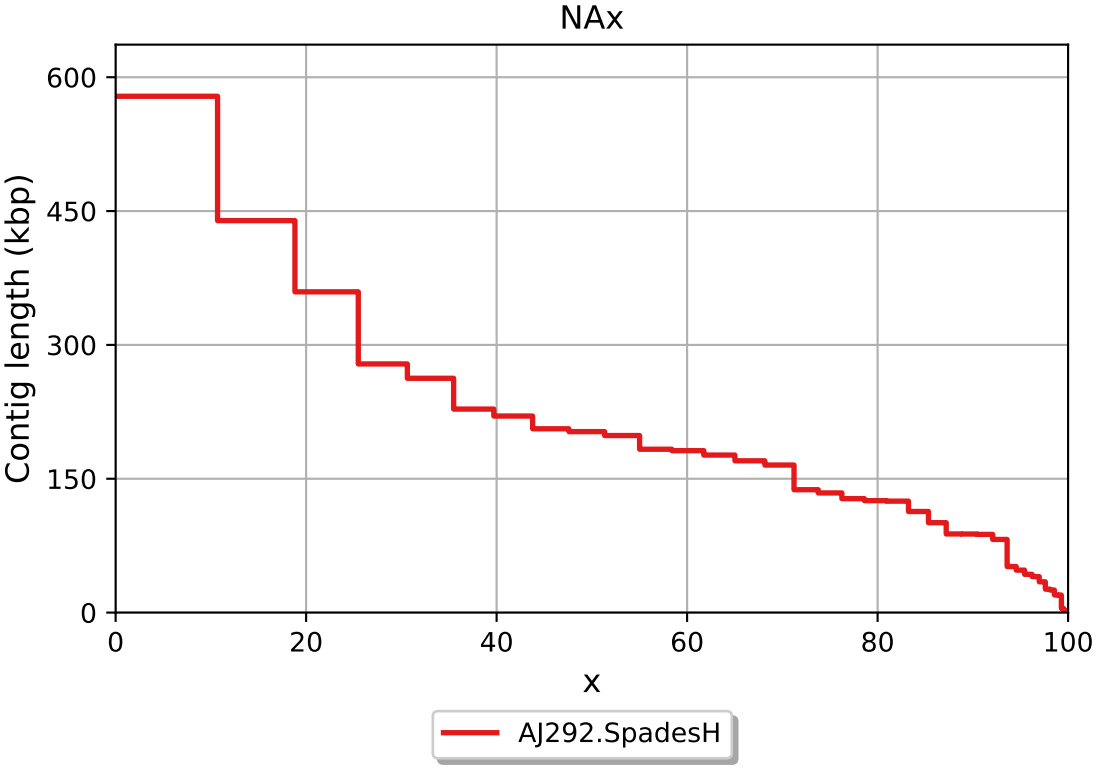

Coverage histogram (bin size: 1x)
Total length (kbp)
1500
1000
500
0
0
16
17
18
19
149
Coverage depth (x)
AJ292.SpadesH

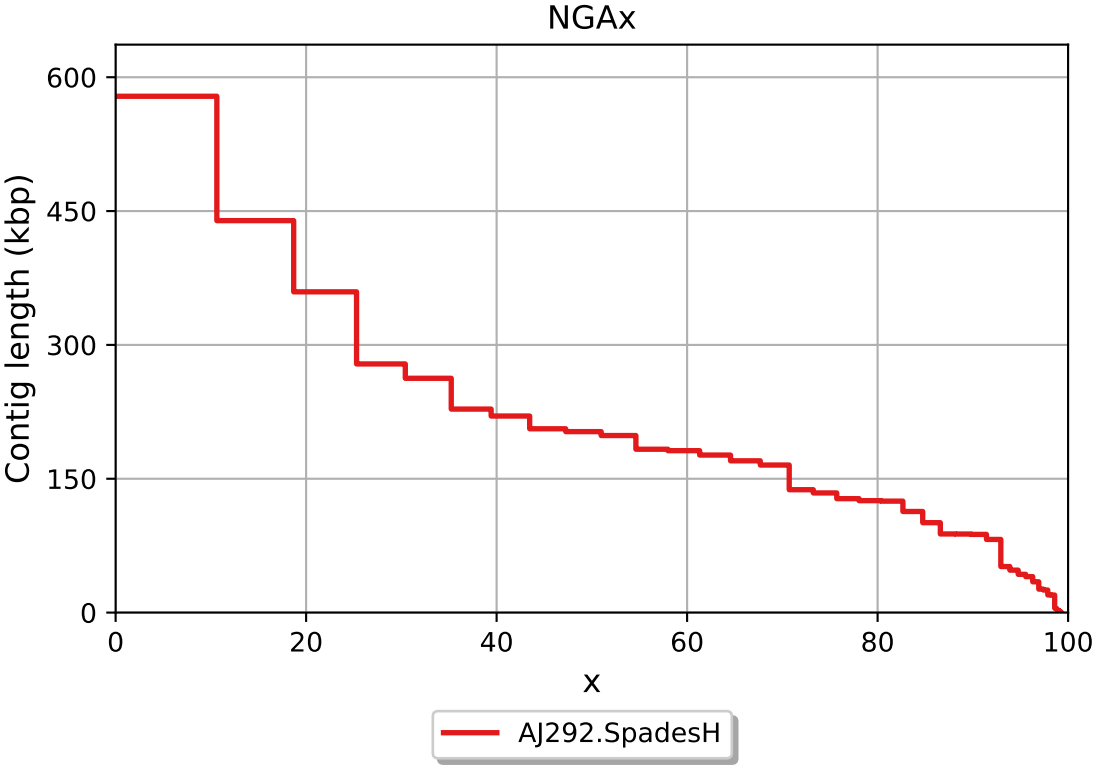

AJ292.SpadesH coverage histogram (bin size: 1x)
Total length (kbp)
0
500
1000
1500
0
16
17
18
19
149
Coverage depth (x)
AJ292.SpadesH


Misassemblies
5
4
3
2
1
0
AJ292.SpadesH
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
AJ292.SpadesH


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
10
20
30
40
50
Contig index
AJ292.SpadesH
Reference


NAx
Contig length (kbp)
600
450
300
150
0
0
20
40
60
80
100
x
AJ292.SpadesH


NGAx
600
450
300
150
0
Contig length (kbp)
0
20
40
60
80
100
x
AJ292.SpadesH