Report

	AJ292.SGAH
# contigs (>= 0 bp)	2148
# contigs (>= 1000 bp)	1174
# contigs (>= 5000 bp)	352
# contigs (>= 10000 bp)	108
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5660136
Total length (>= 1000 bp)	5319179
Total length (>= 5000 bp)	3226072
Total length (>= 10000 bp)	1540333
Total length (>= 25000 bp)	78946
Total length (>= 50000 bp)	0
# contigs	1357
Largest contig	27490
Total length	5453167
Reference length	5445112
GC (%)	57.79
Reference GC (%)	57.62
N50	6126
NG50	6126
N75	3477
NG75	3480
L50	262
LG50	262
L75	562
LG75	560
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.769
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.06
# indels per 100 kbp	0.19
Largest alignment	27490
Total aligned length	5453165
NA50	6126
NGA50	6126
NA75	3477
NGA75	3480
LA50	262
LGA50	262
LA75	562
LGA75	560

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

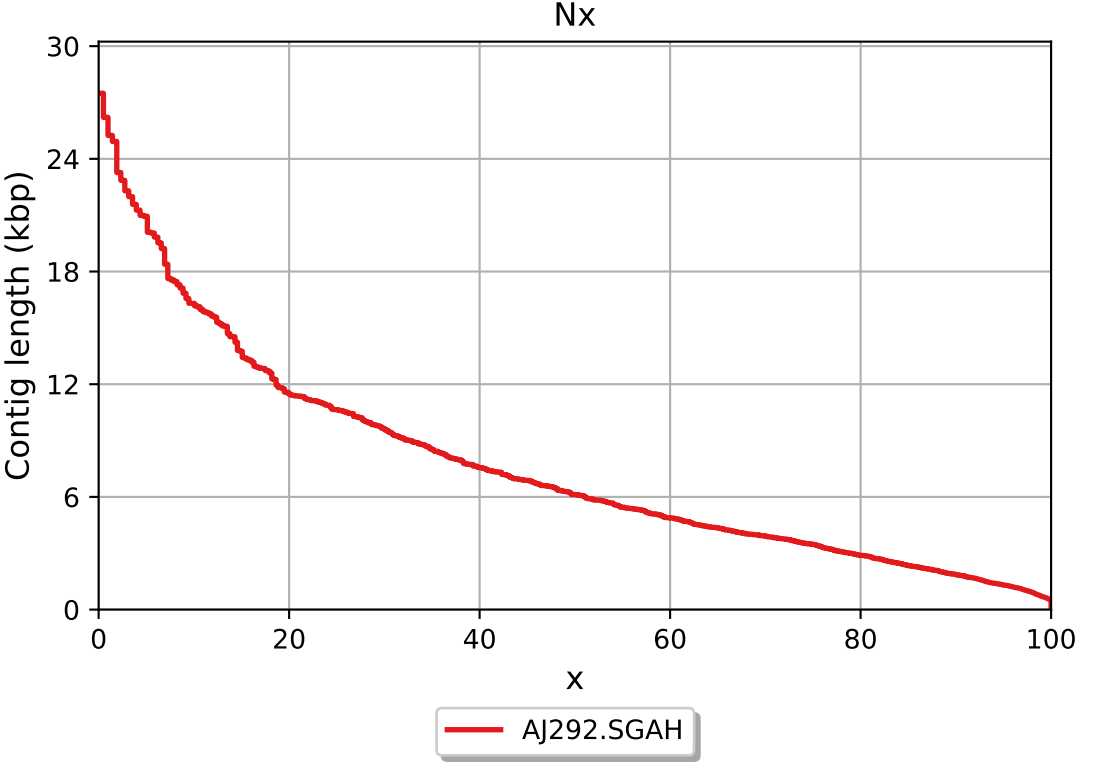
	AJ292.SGAH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	3
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	10

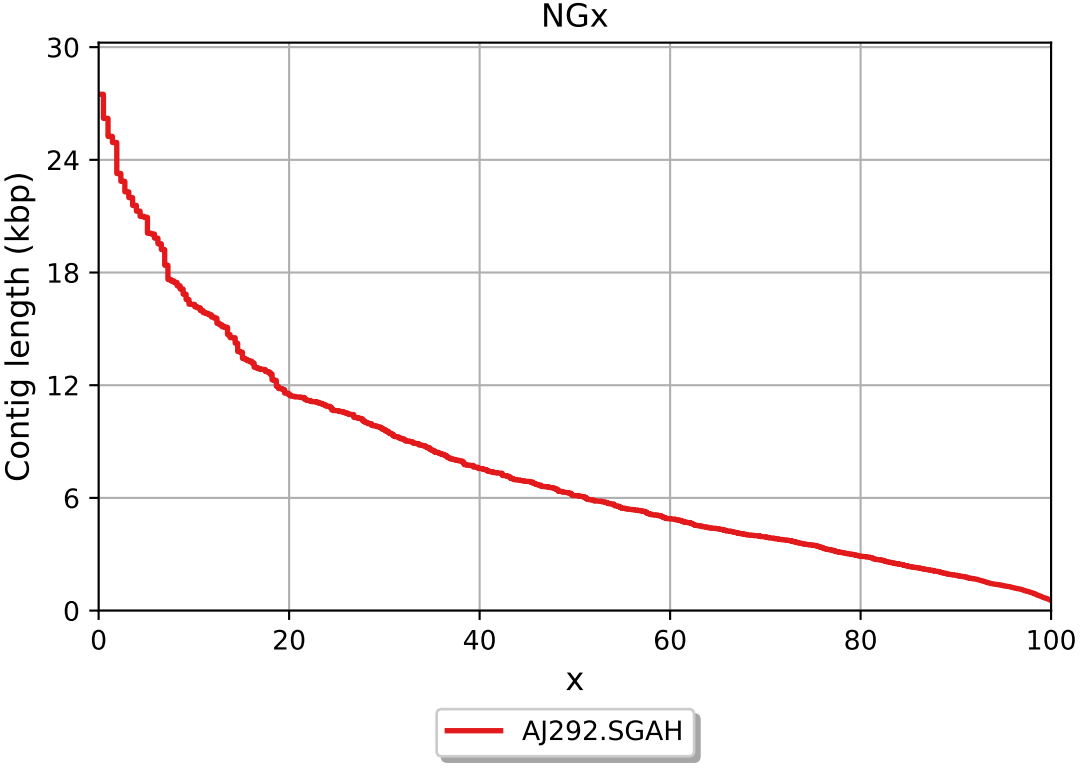
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

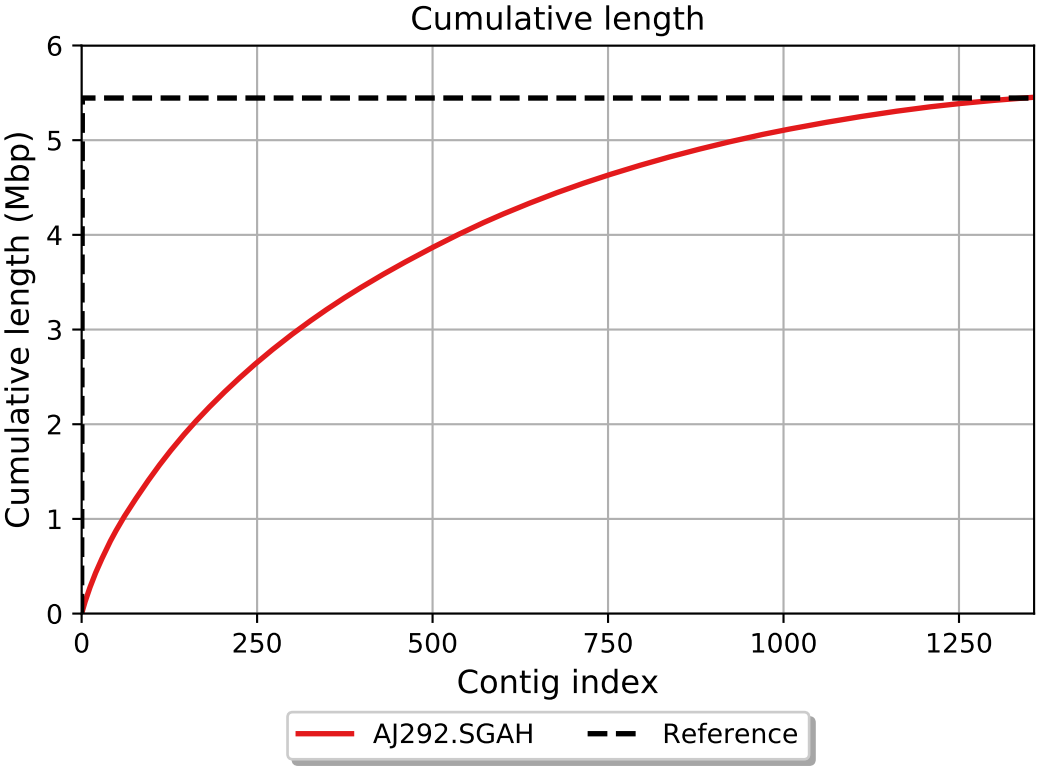
Unaligned report

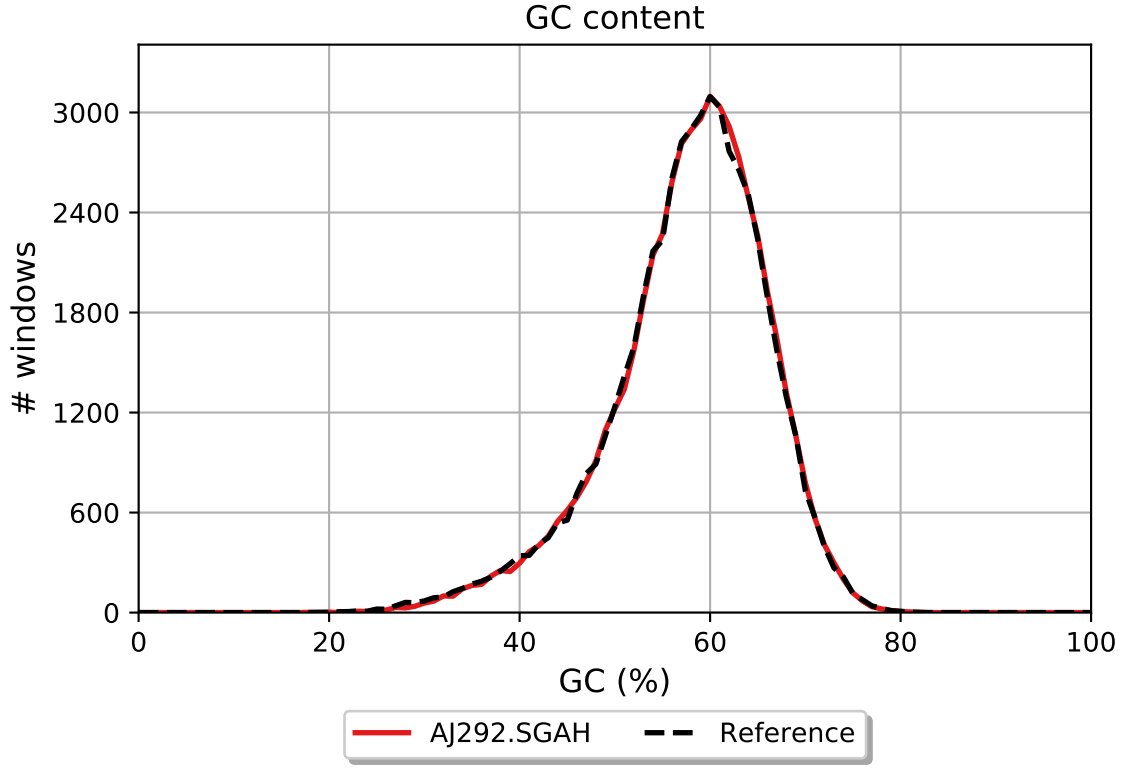
	AJ292.SGAH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

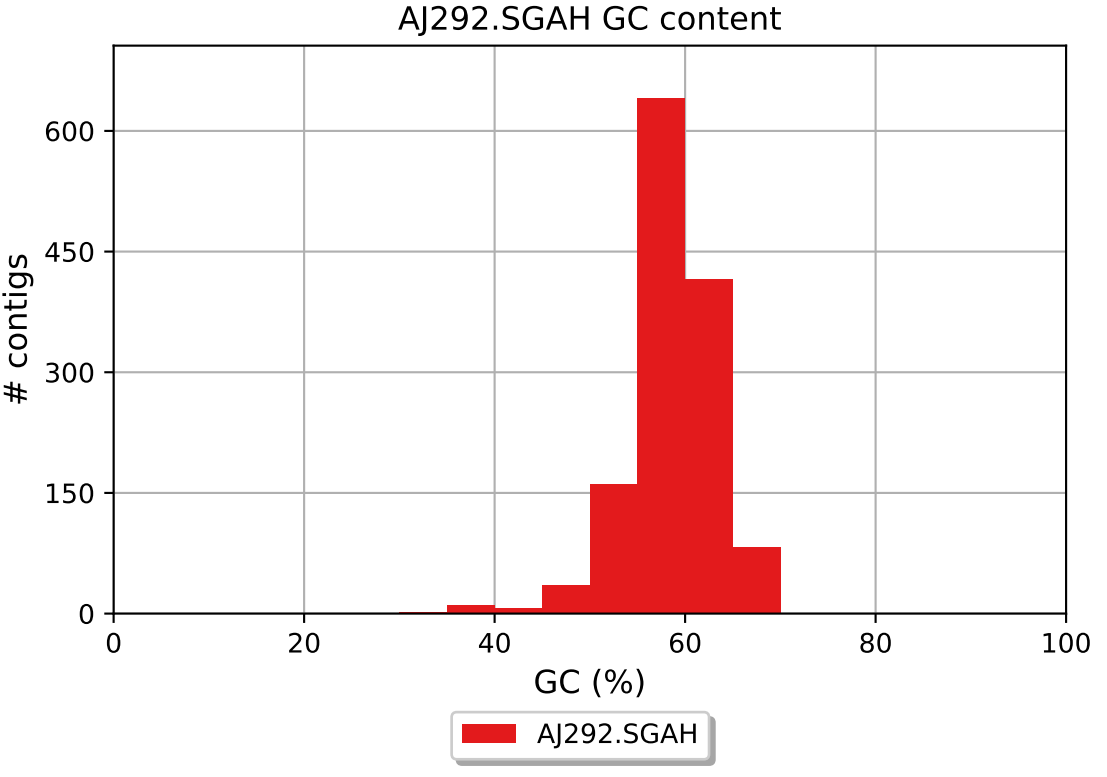
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

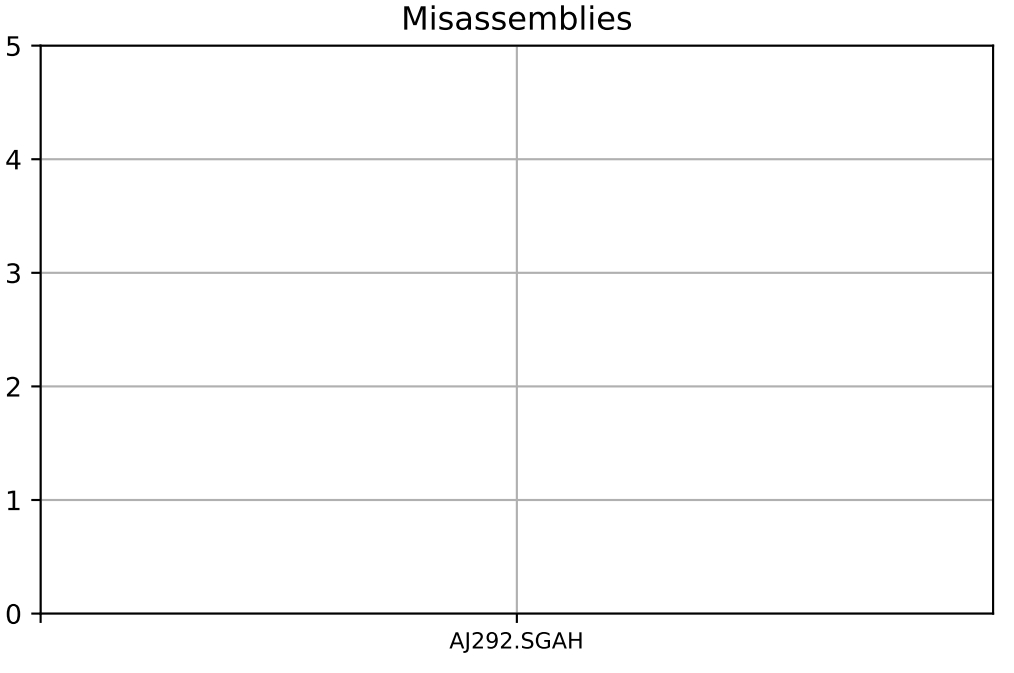

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
AJ292.SGAH

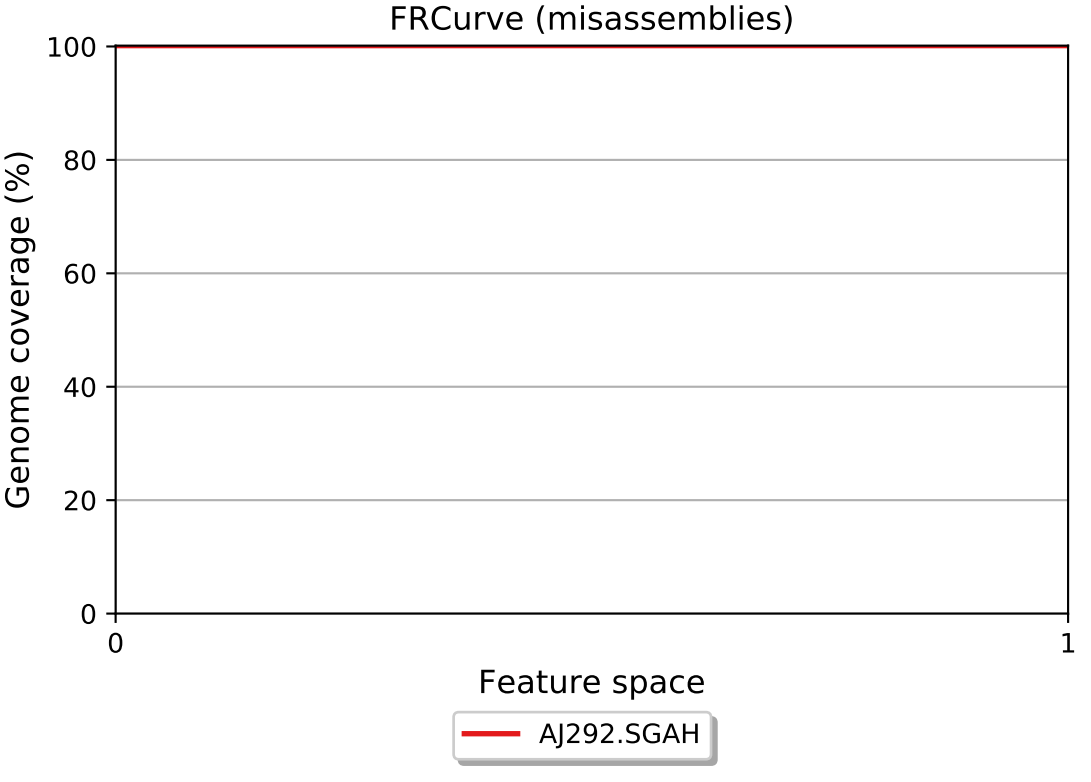

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
AJ292.SGAH

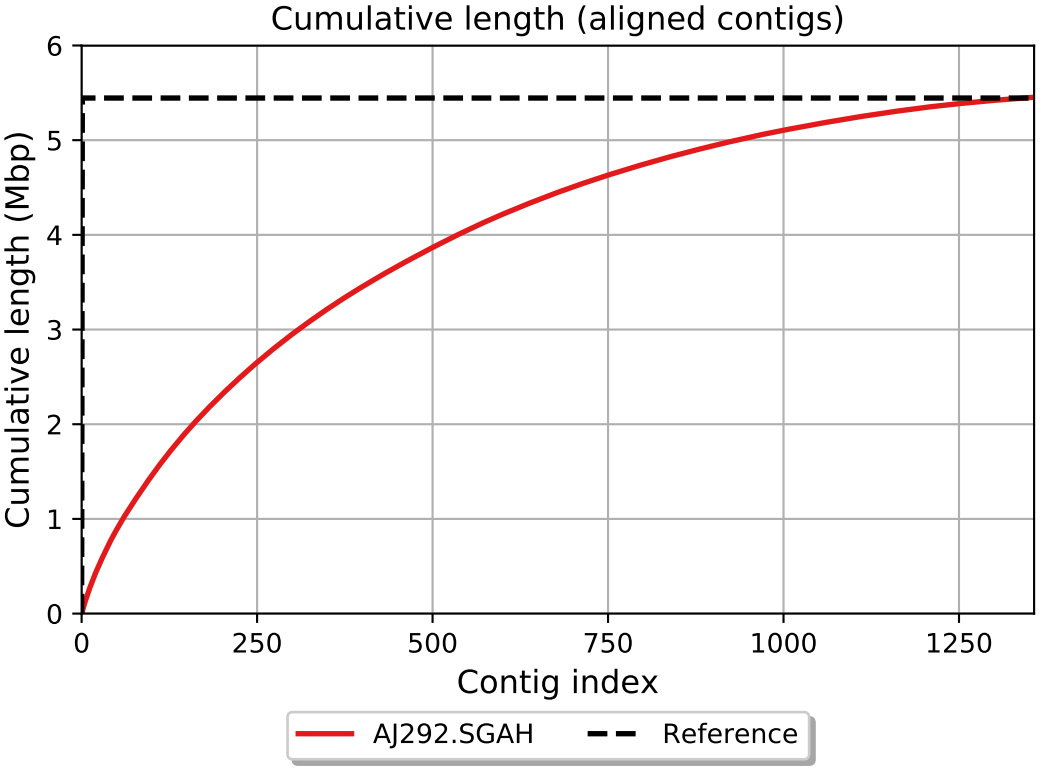

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
250
500
750
1000
1250
Contig index
AJ292.SGAH
Reference

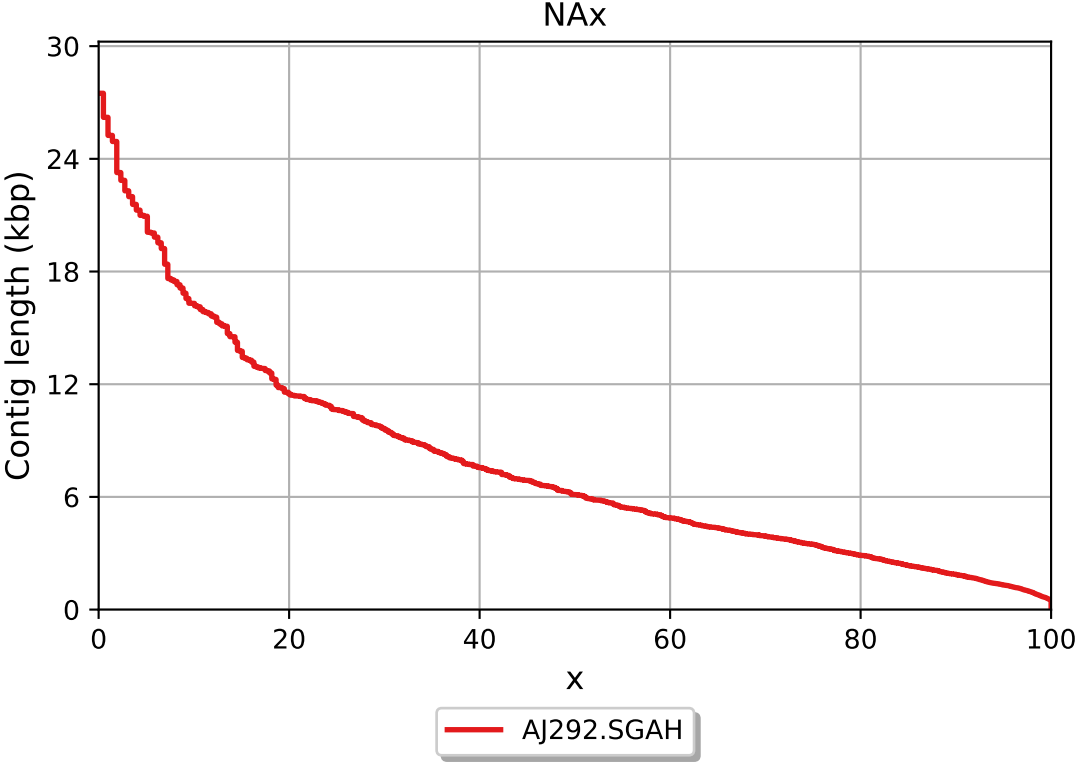

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ292.SGAH
Reference

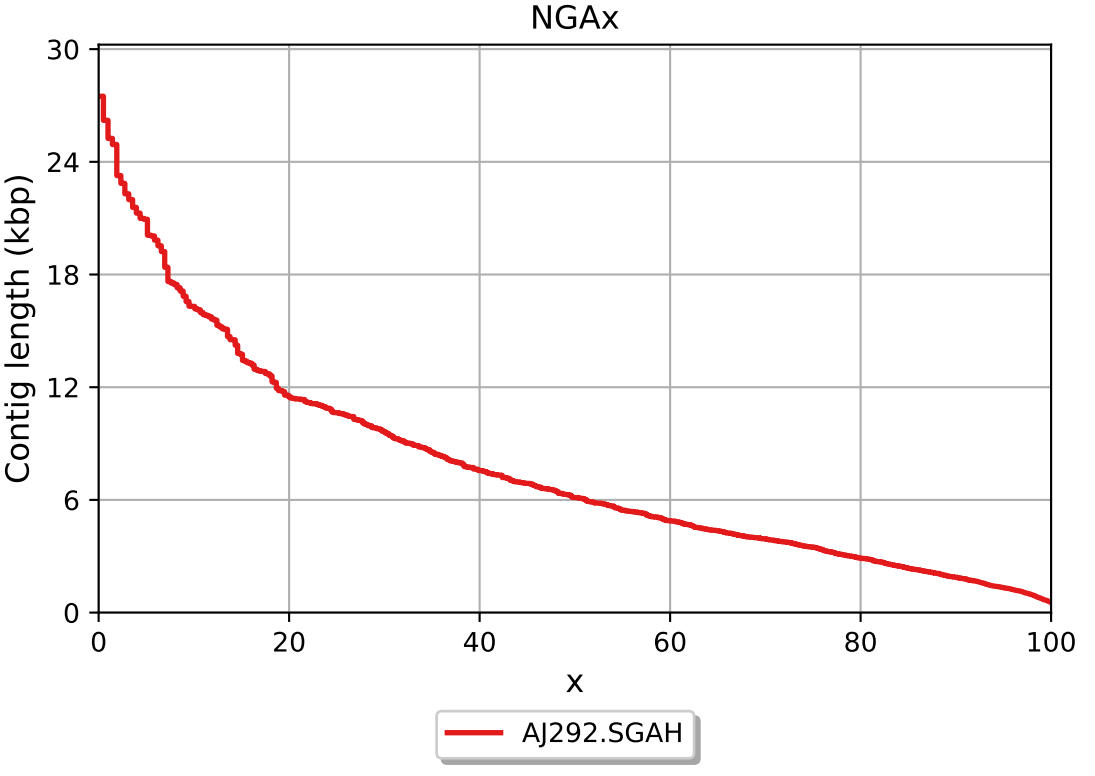

AJ292.SGAH GC content
contigs
0
150
300
450
600
0
20
40
60
80
100
GC (%)
AJ292.SGAH


Misassemblies
5
4
3
2
1
0
AJ292.SGAH


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
250
500
750
1000
1250
Contig index
AJ292.SGAH
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
AJ292.SGAH


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
AJ292.SGAH