Report

	AJ292.SGAL
# contigs (>= 0 bp)	1138
# contigs (>= 1000 bp)	724
# contigs (>= 5000 bp)	359
# contigs (>= 10000 bp)	175
# contigs (>= 25000 bp)	19
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5443260
Total length (>= 1000 bp)	5299562
Total length (>= 5000 bp)	4295094
Total length (>= 10000 bp)	2996106
Total length (>= 25000 bp)	604402
Total length (>= 50000 bp)	53154
# contigs	798
Largest contig	53154
Total length	5353915
Reference length	5445112
GC (%)	57.84
Reference GC (%)	57.62
N50	11507
NG50	11318
N75	6029
NG75	5846
L50	146
LG50	150
L75	309
LG75	320
# 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 (%)	97.563
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.19
# indels per 100 kbp	0.17
Largest alignment	53154
Total aligned length	5353895
NA50	11507
NGA50	11318
NA75	6029
NGA75	5846
LA50	146
LGA50	150
LA75	309
LGA75	320

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

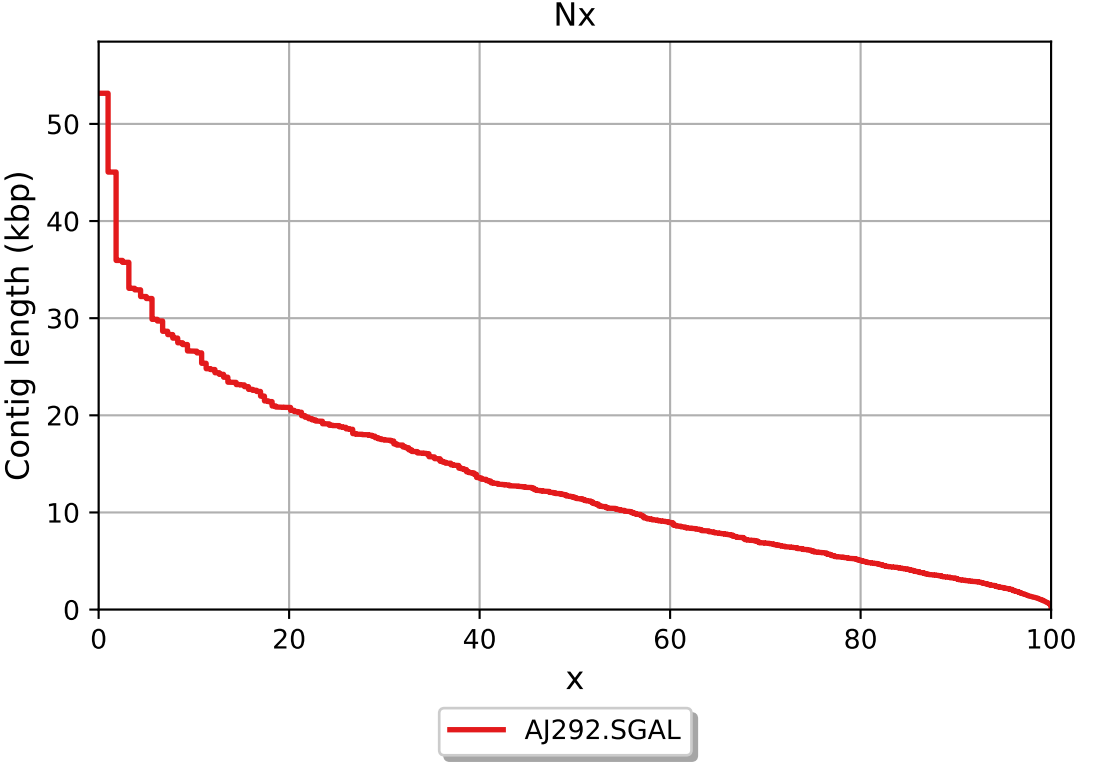
	AJ292.SGAL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	10
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	9

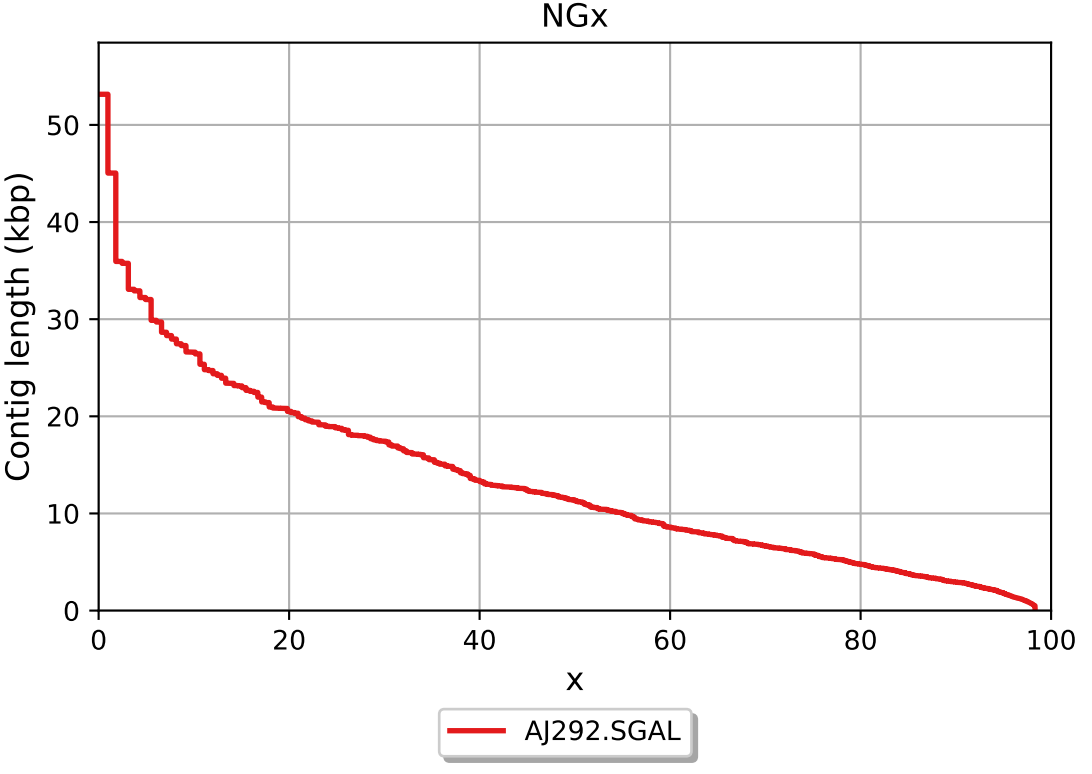
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

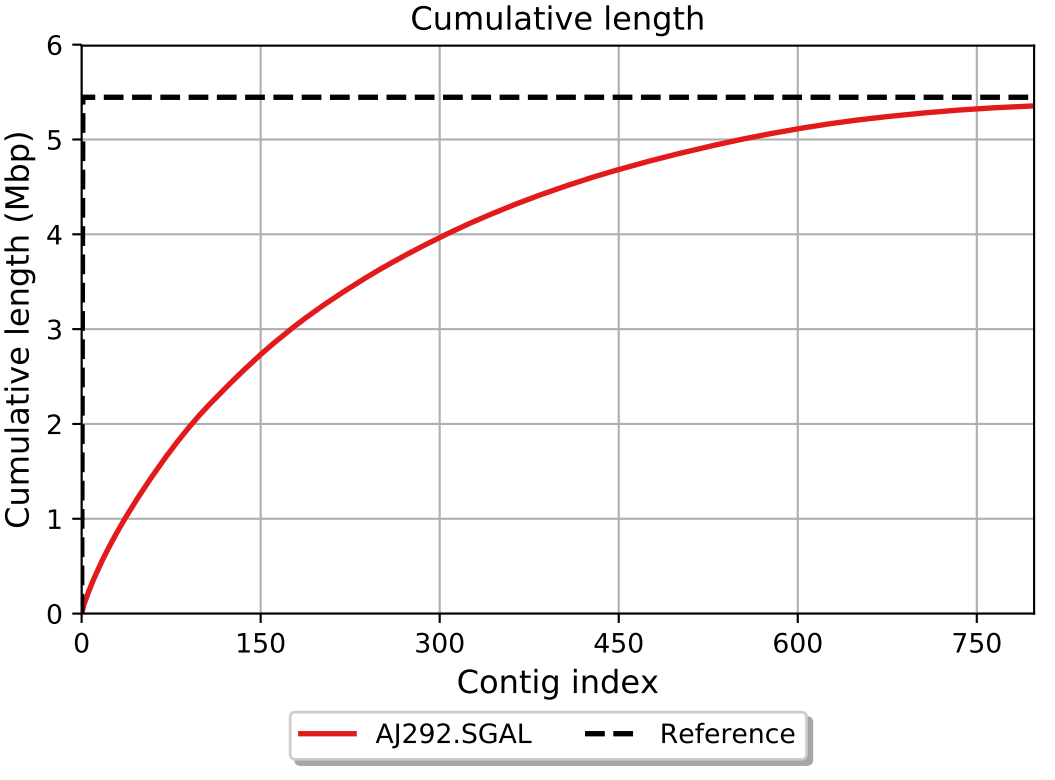
Unaligned report

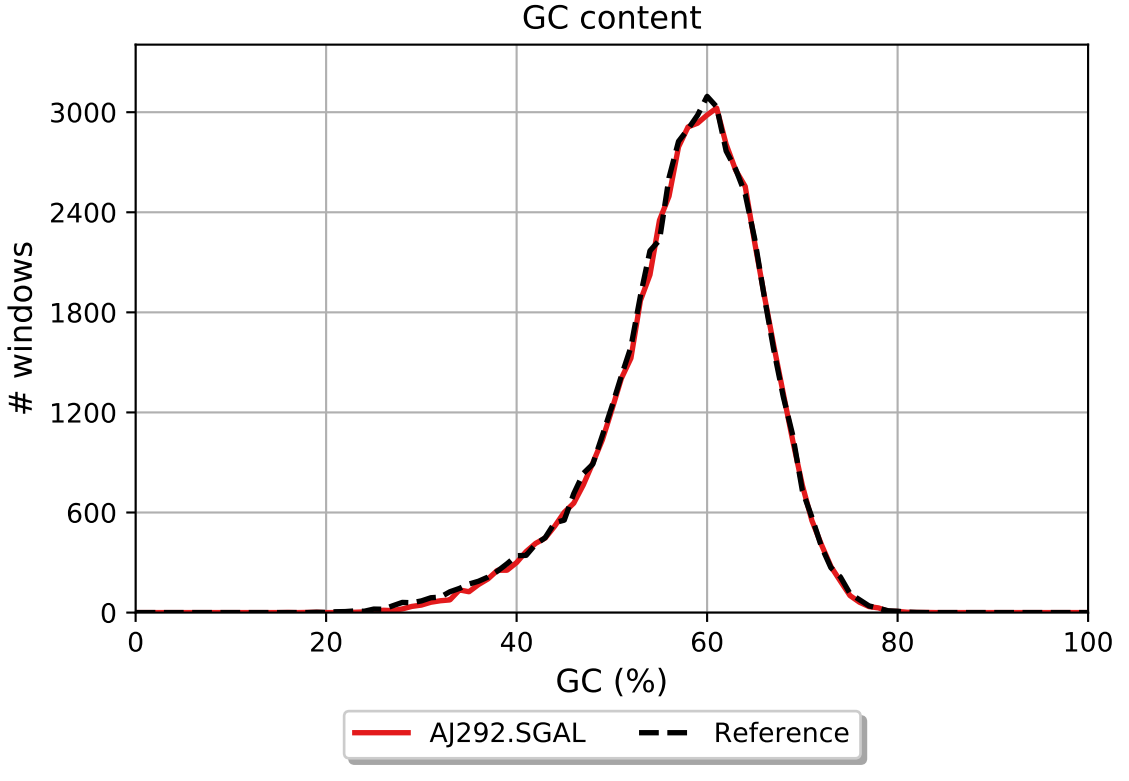
	AJ292.SGAL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

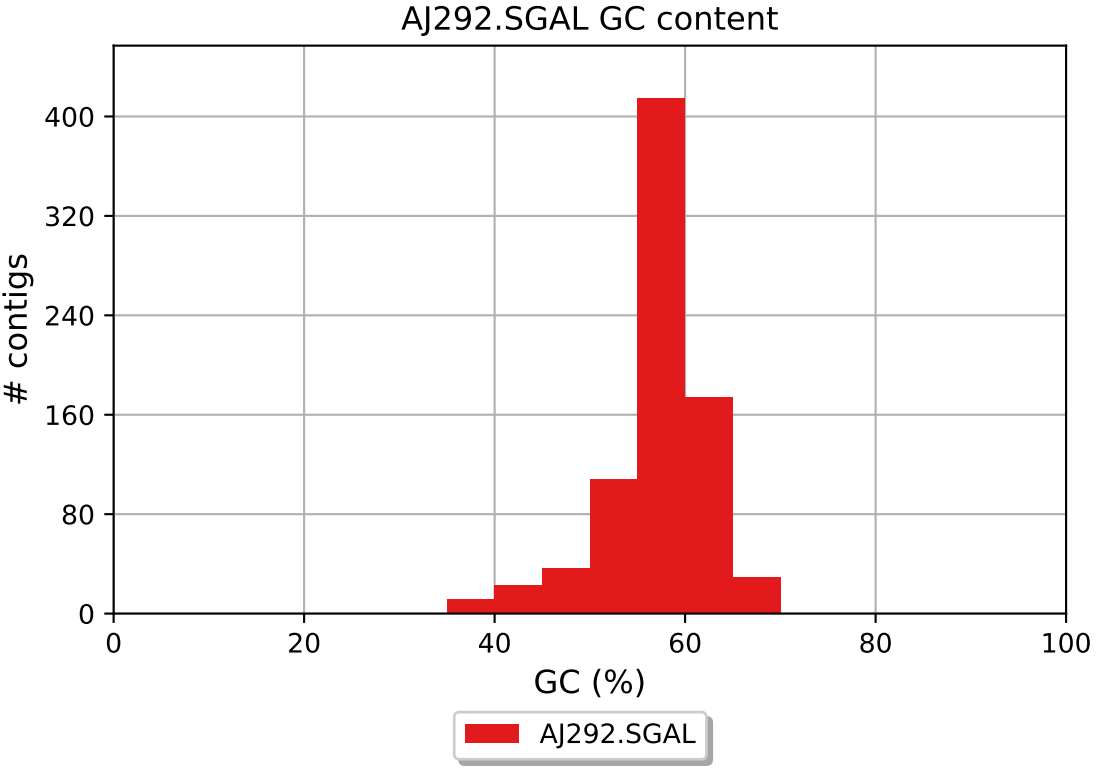
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

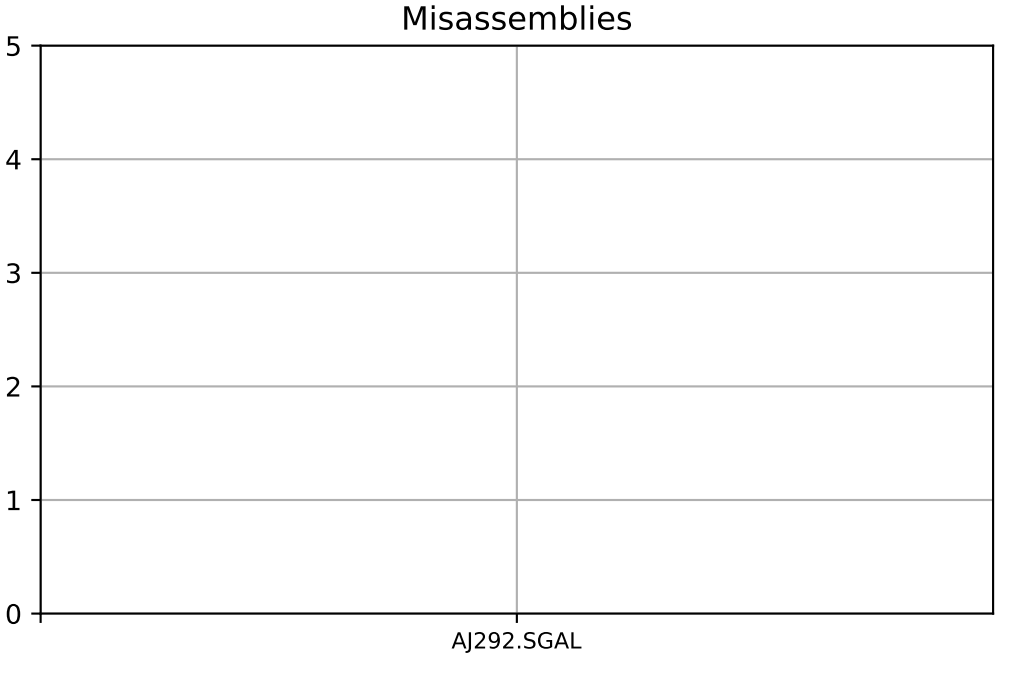

Nx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
AJ292.SGAL

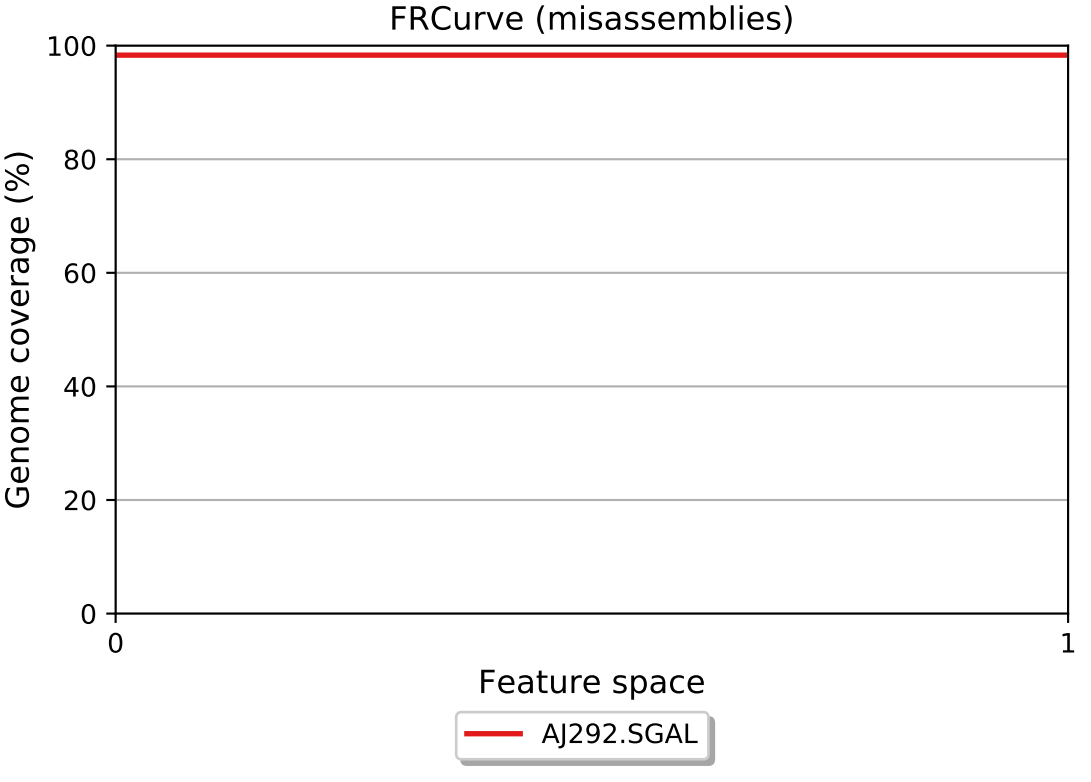

NGx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
AJ292.SGAL

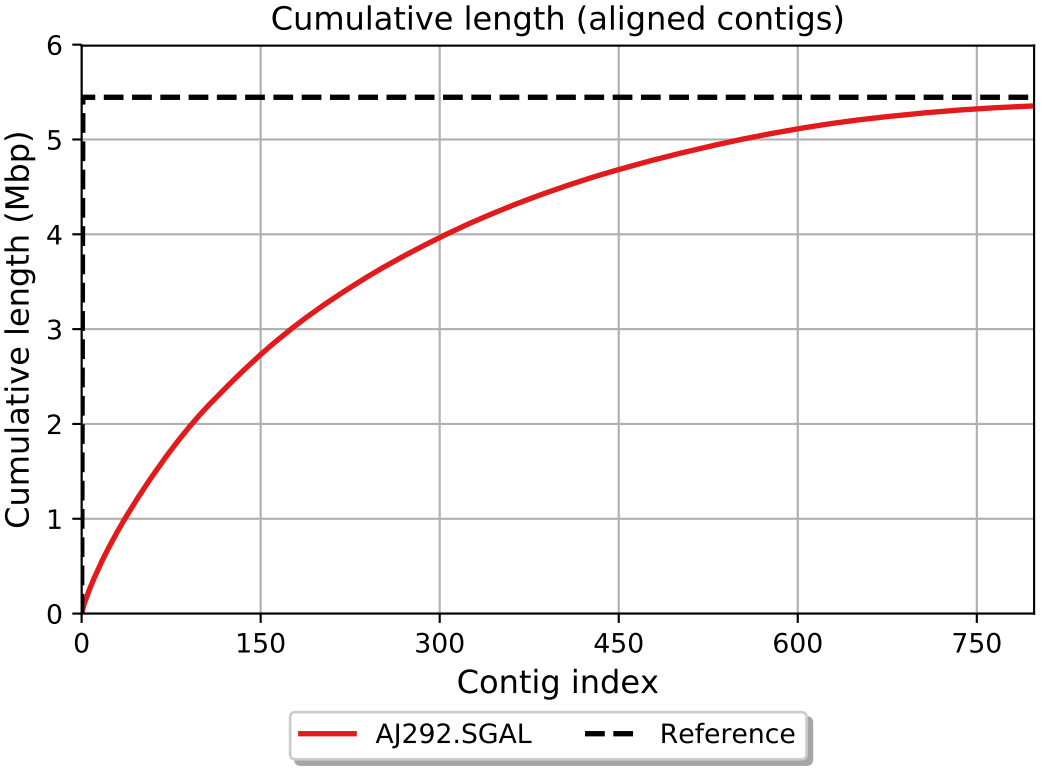

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
150
300
450
600
750
Contig index
AJ292.SGAL
Reference

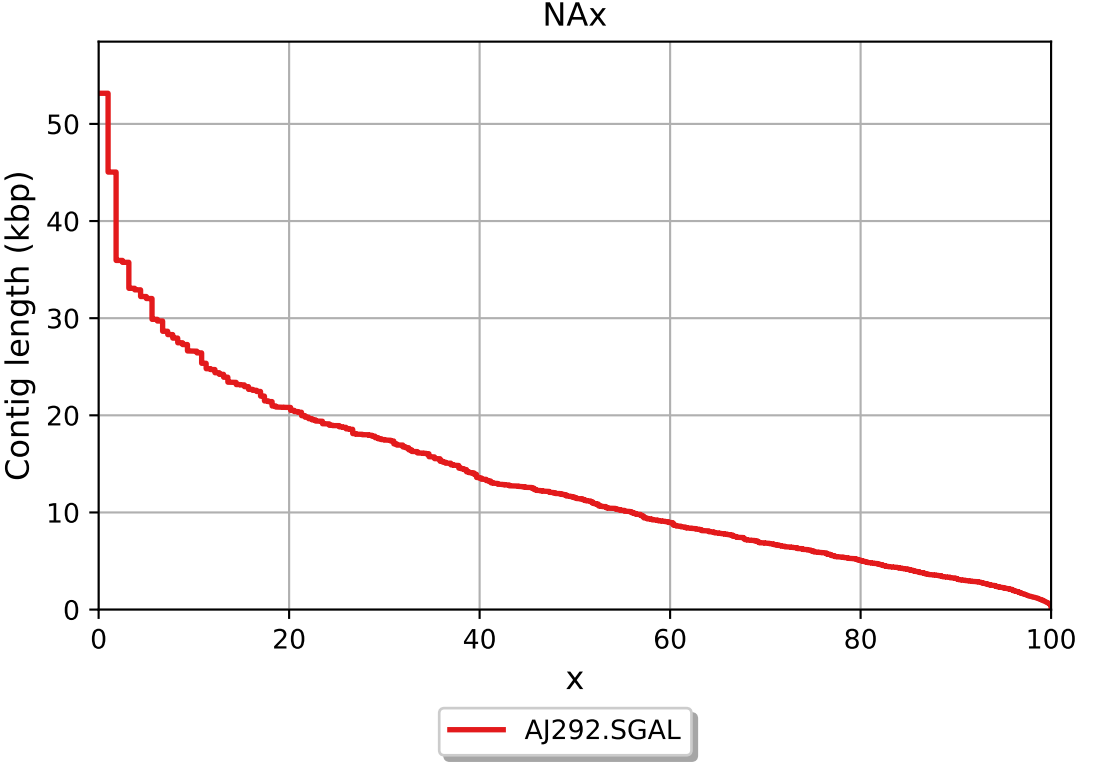

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
AJ292.SGAL
Reference

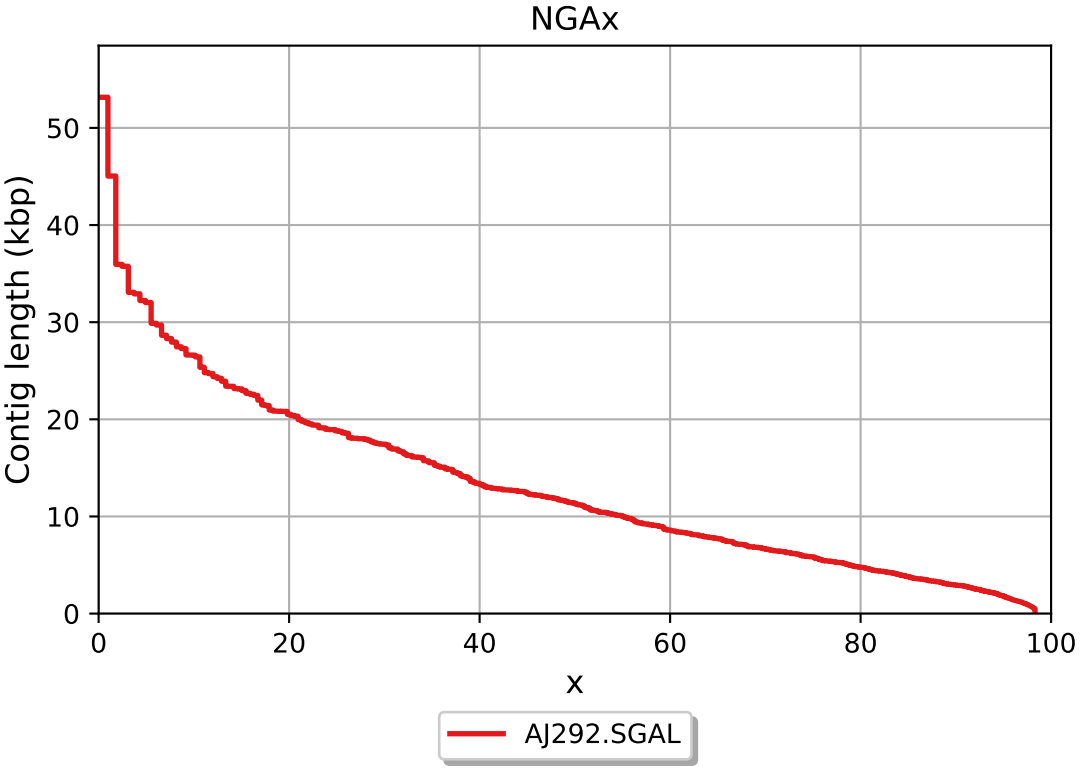

AJ292.SGAL GC content
contigs
0
80
160
240
320
400
0
20
40
60
80
100
GC (%)
AJ292.SGAL


Misassemblies
5
4
3
2
1
0
AJ292.SGAL


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
150
300
450
600
750
Contig index
AJ292.SGAL
Reference


NAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
AJ292.SGAL


NGAx
Contig length (kbp)
0
10
20
30
40
50
0
20
40
60
80
100
x
AJ292.SGAL