Report

	AJ292.MiniH.p1
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	5444912
Total length (>= 1000 bp)	5444912
Total length (>= 5000 bp)	5444912
Total length (>= 10000 bp)	5444912
Total length (>= 25000 bp)	5444912
Total length (>= 50000 bp)	5444912
# contigs	1
Largest contig	5444912
Total length	5444912
Reference length	5445112
GC (%)	57.62
Reference GC (%)	57.62
N50	5444912
NG50	5444912
N75	5444912
NG75	5444912
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.999
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.64
# indels per 100 kbp	29.00
Largest alignment	5444836
Total aligned length	5444836
NA50	5444836
NGA50	5444836
NA75	5444836
NGA75	5444836
LA50	1
LGA50	1
LA75	1
LGA75	1

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

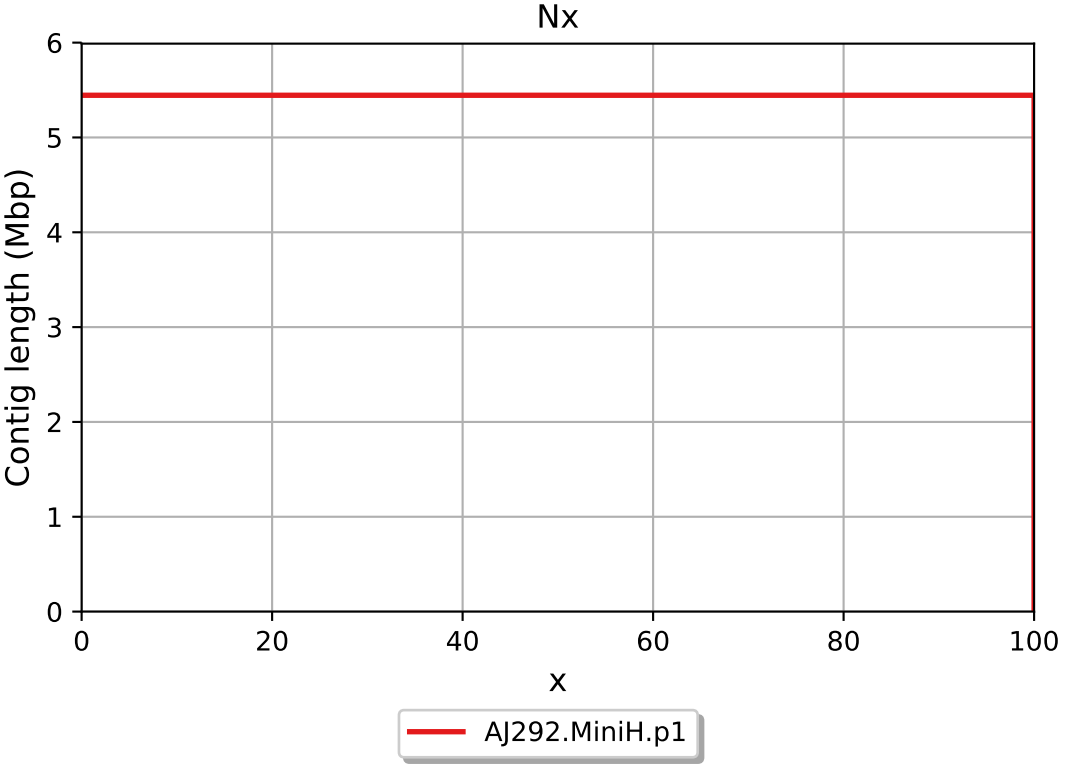
	AJ292.MiniH.p1
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	35
# indels	1579
# indels (<= 5 bp)	1569
# indels (> 5 bp)	10
Indels length	2408

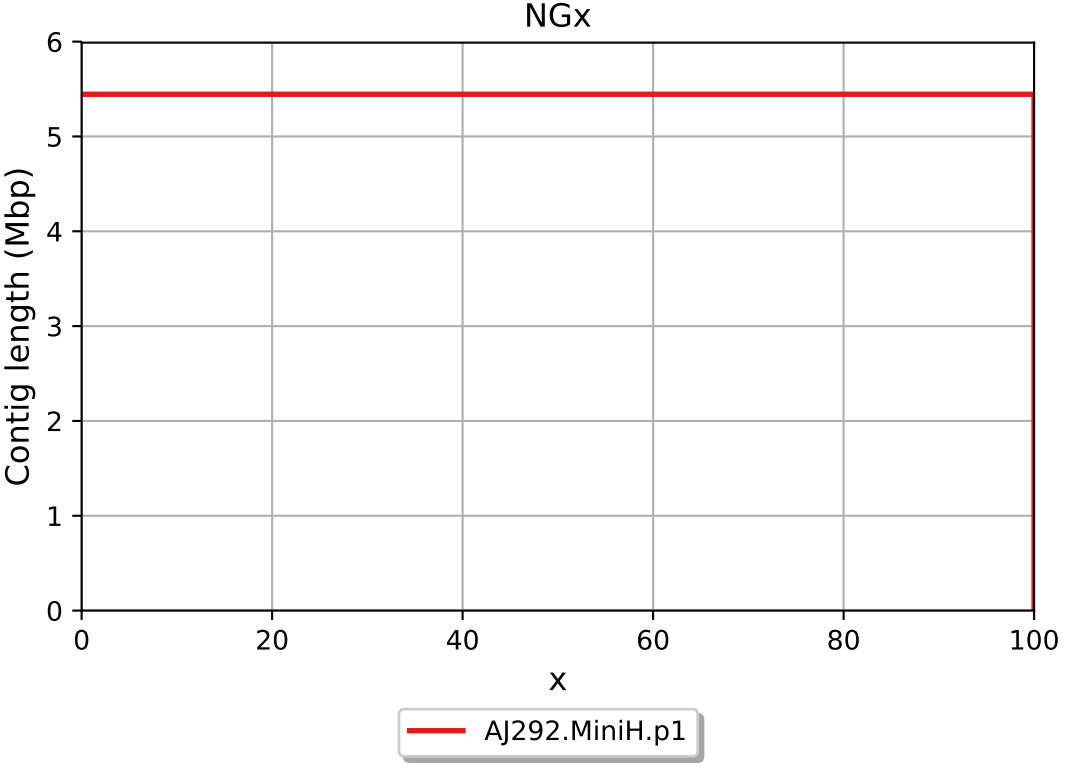
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

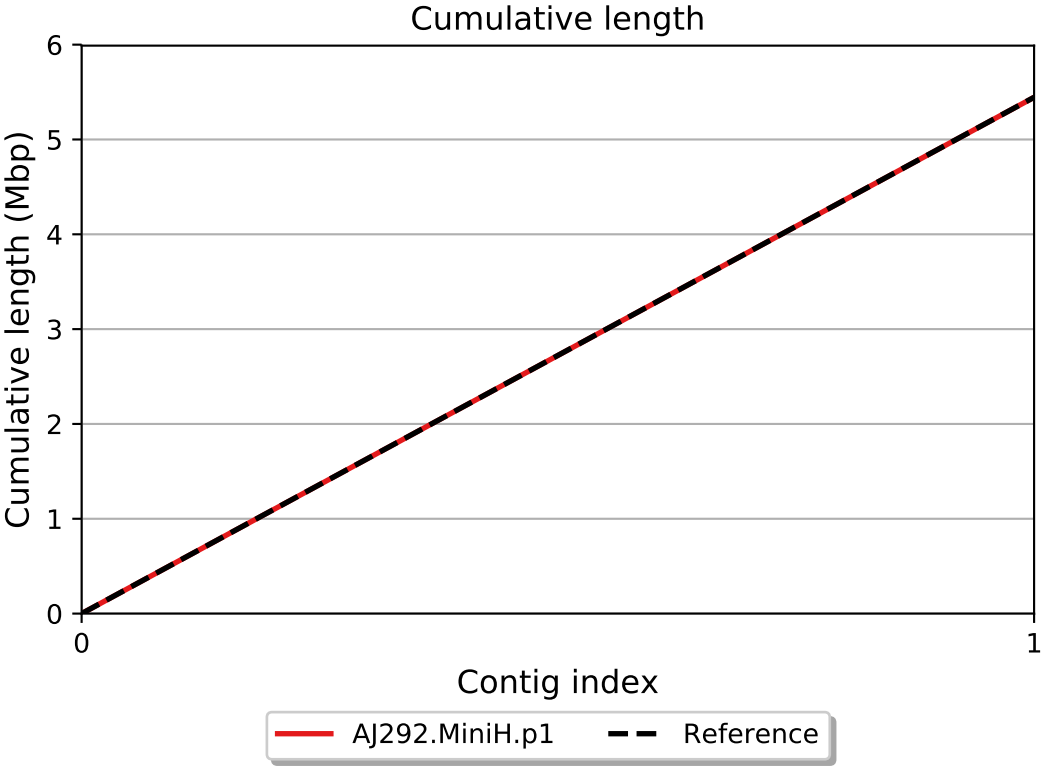
Unaligned report

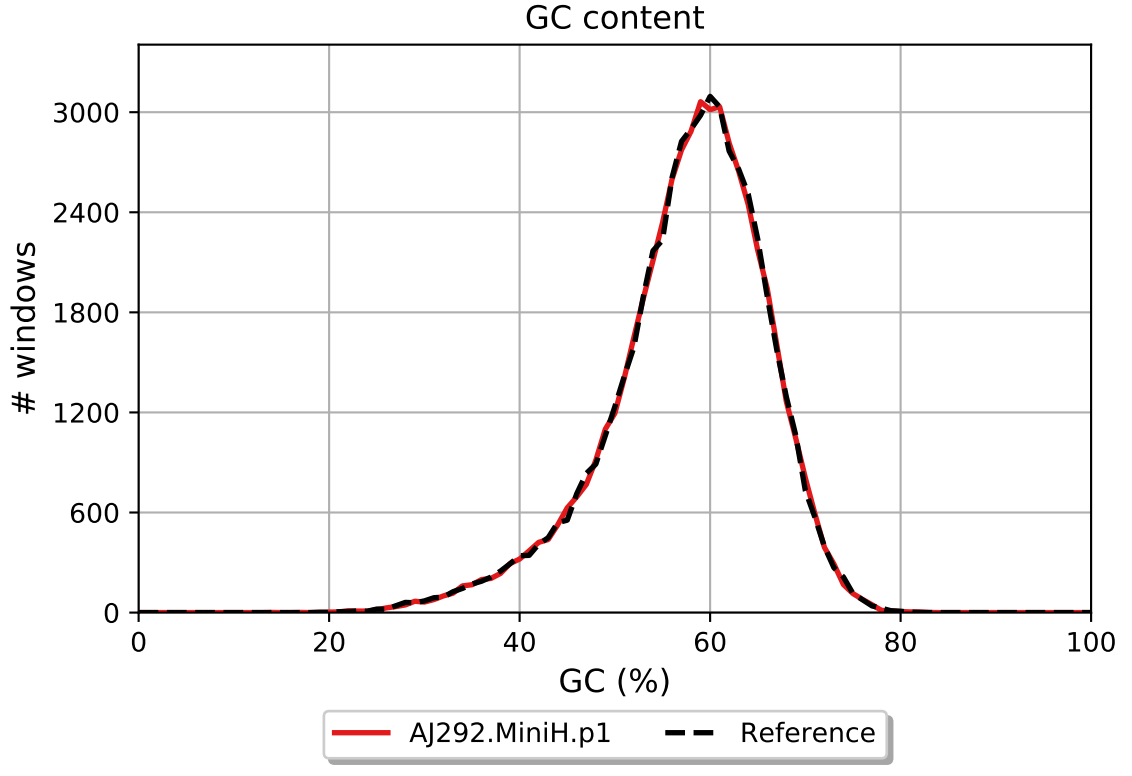
	AJ292.MiniH.p1
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

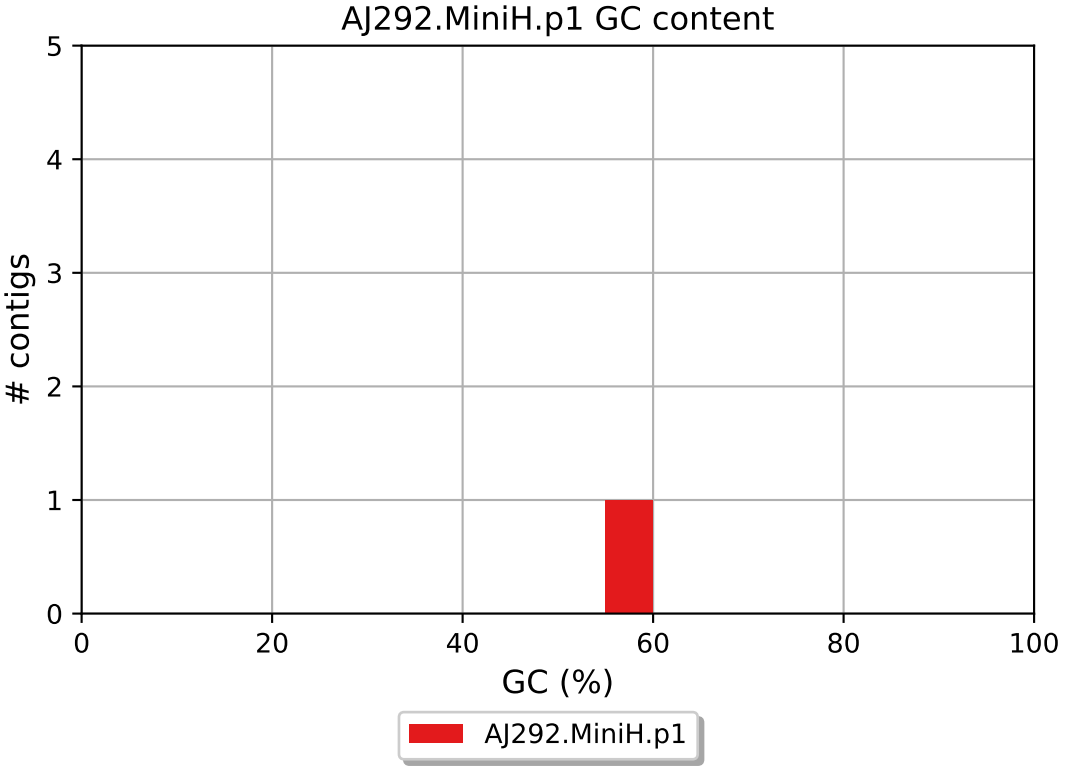
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

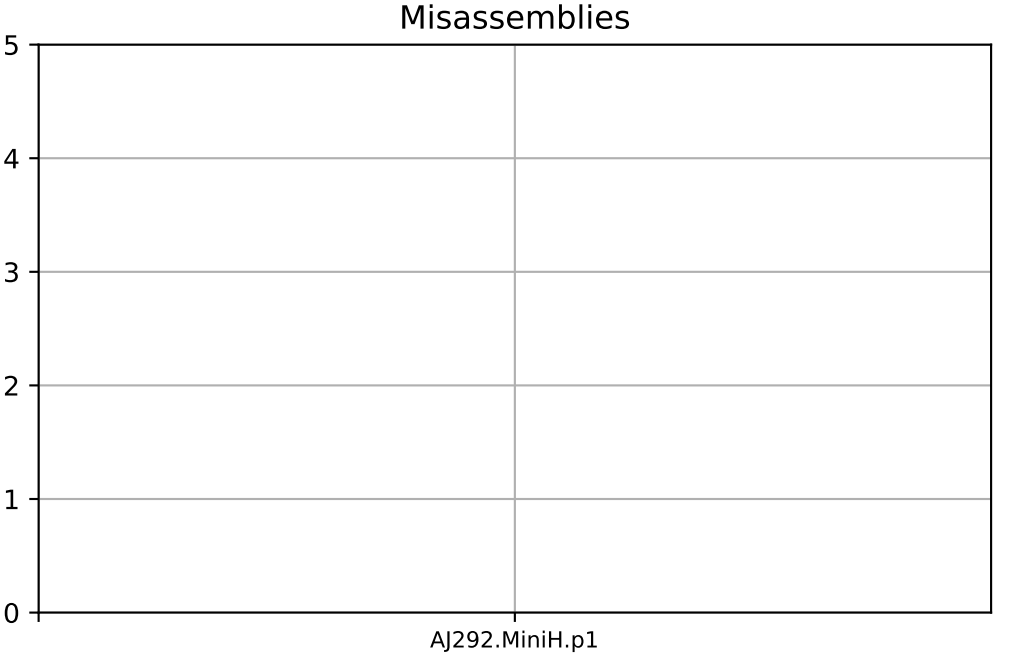

Nx
Contig length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
AJ292.MiniH.p1

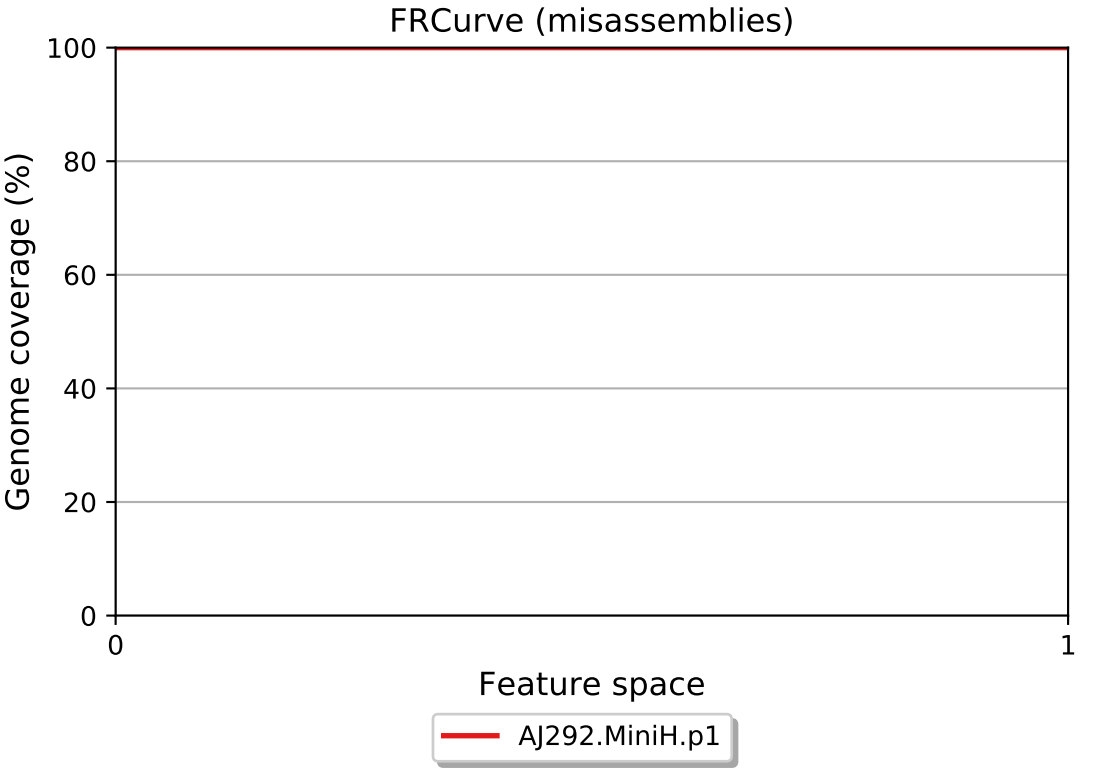

NGx
Contig length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
AJ292.MiniH.p1

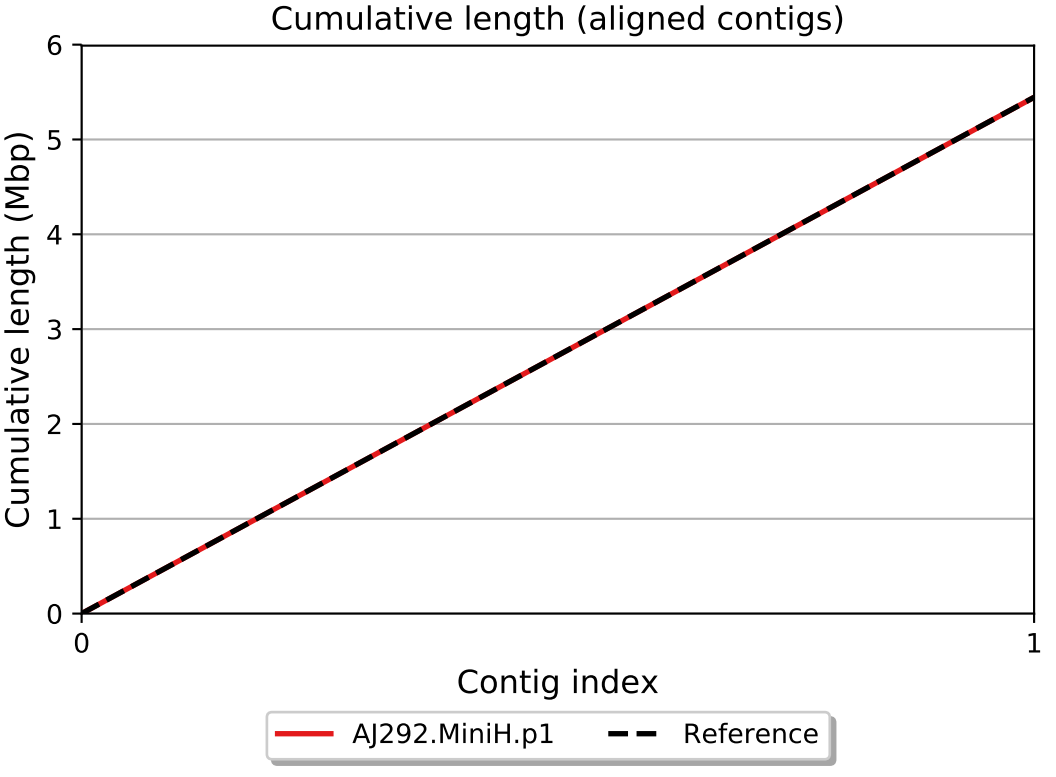

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1
Contig index
AJ292.MiniH.p1
Reference

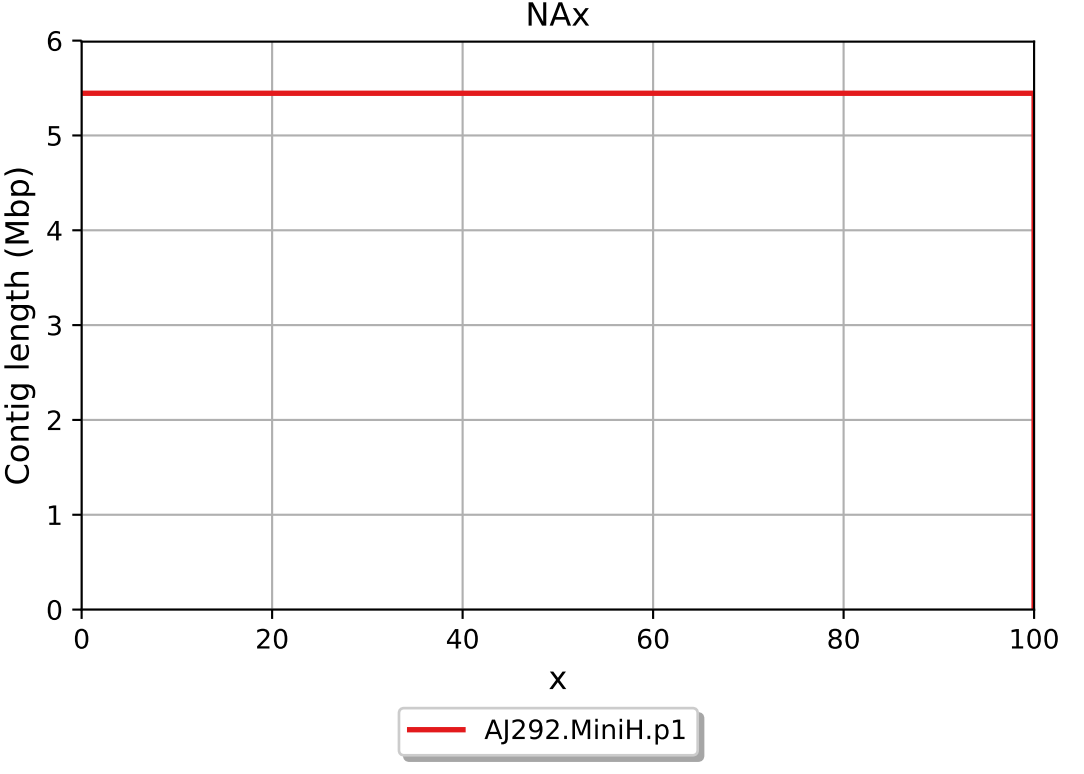

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
AJ292.MiniH.p1
Reference

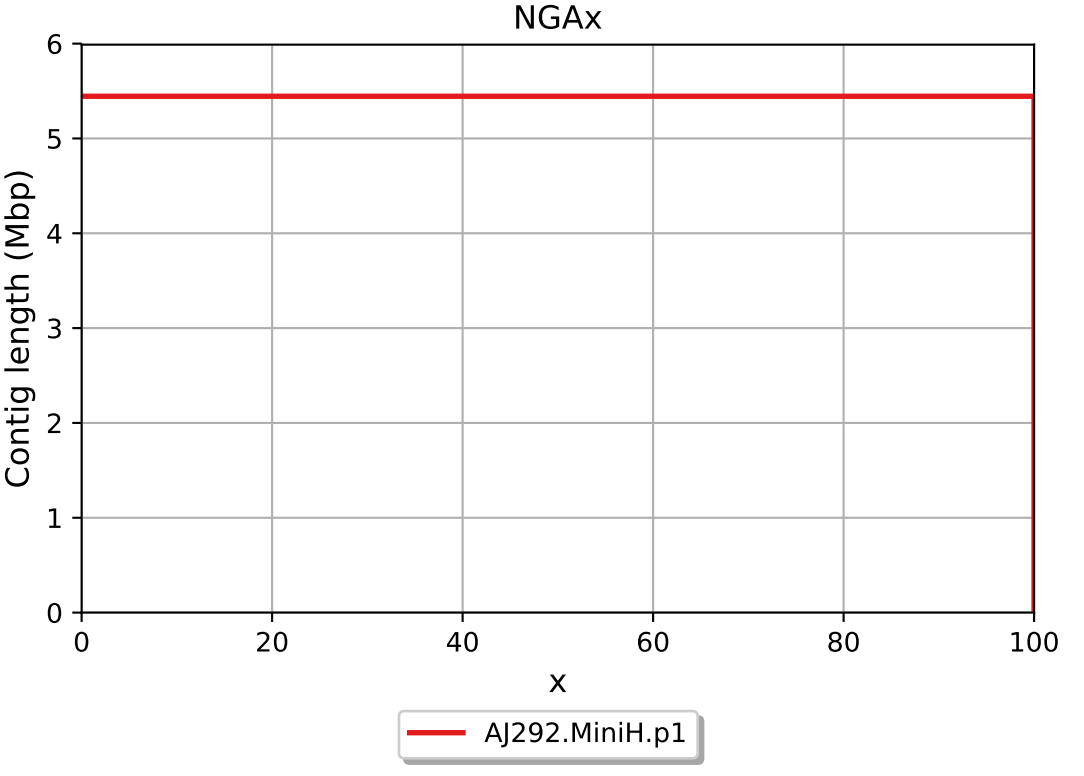

AJ292.MiniH.p1 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
AJ292.MiniH.p1


Misassemblies
5
4
3
2
1
0
AJ292.MiniH.p1


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
AJ292.MiniH.p1


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1
Contig index
AJ292.MiniH.p1
Reference


NAx
Contig length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
AJ292.MiniH.p1


NGAx
Contig length (Mbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
AJ292.MiniH.p1