Report

	AJ292.MiniCH
# 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)	5464361
Total length (>= 1000 bp)	5464361
Total length (>= 5000 bp)	5464361
Total length (>= 10000 bp)	5464361
Total length (>= 25000 bp)	5464361
Total length (>= 50000 bp)	5464361
# contigs	1
Largest contig	5464361
Total length	5464361
Reference length	5445112
GC (%)	57.60
Reference GC (%)	57.62
N50	5464361
NG50	5464361
N75	5464361
NG75	5464361
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.999
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	9.64
# indels per 100 kbp	247.97
Largest alignment	5463805
Total aligned length	5463805
NA50	5463805
NGA50	5463805
NA75	5463805
NGA75	5463805
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

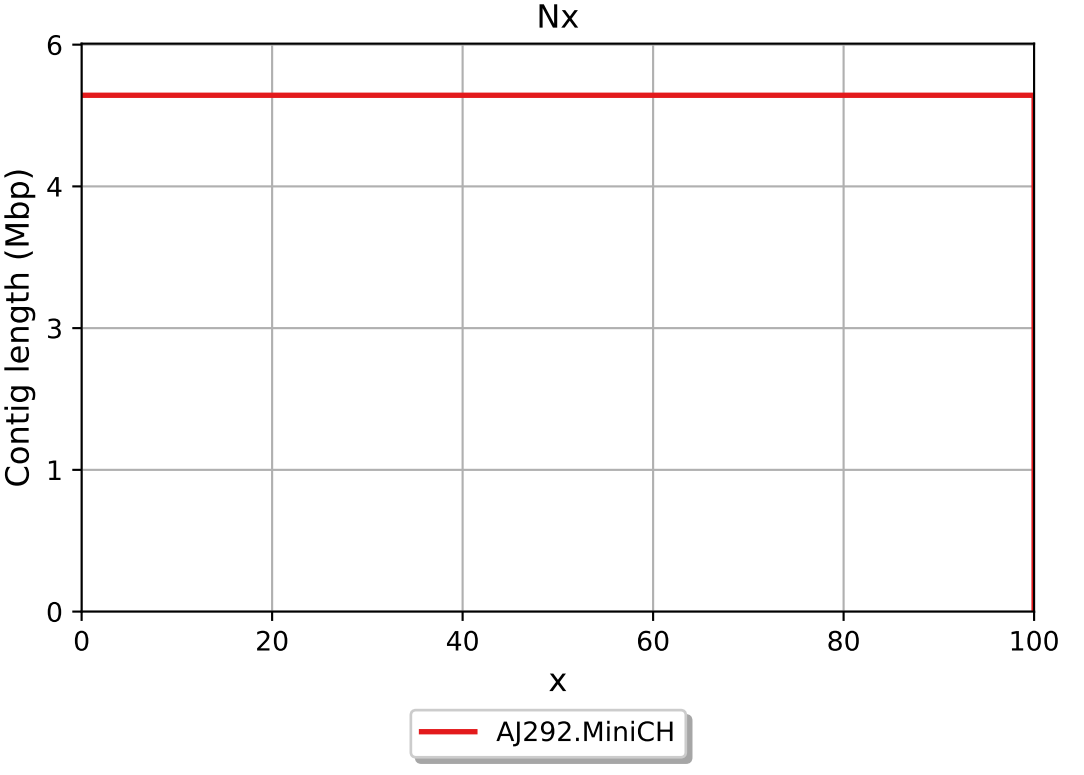
	AJ292.MiniCH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	525
# indels	13502
# indels (<= 5 bp)	13425
# indels (> 5 bp)	77
Indels length	21823

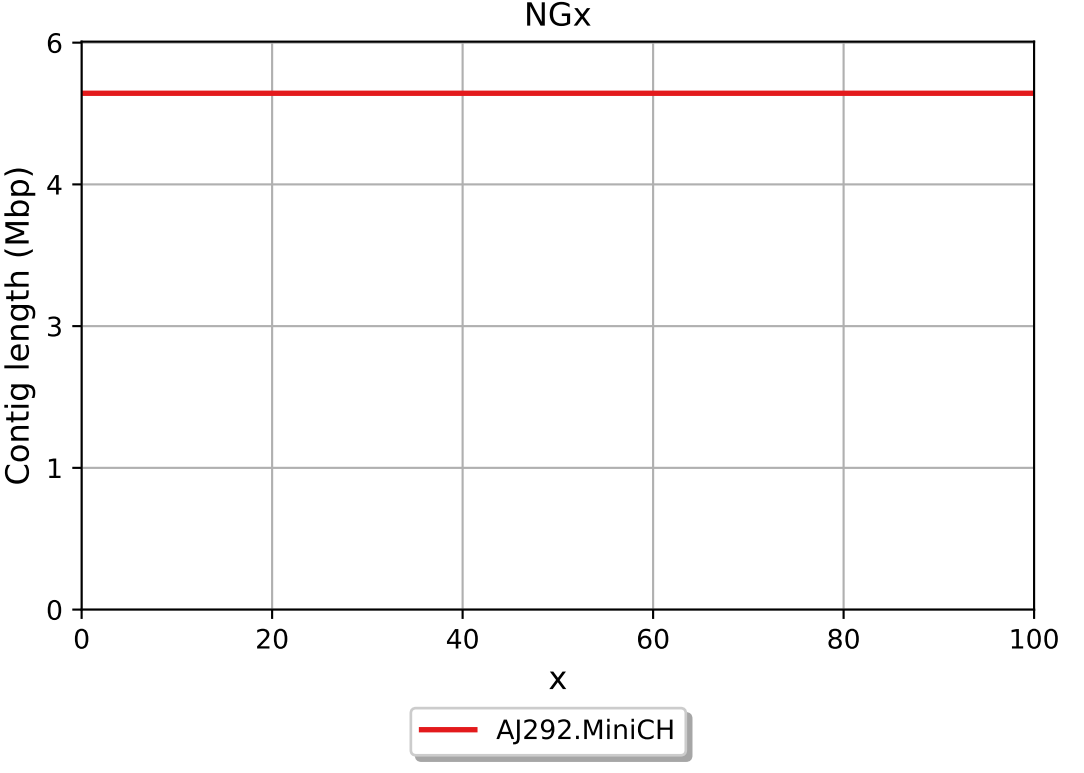
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

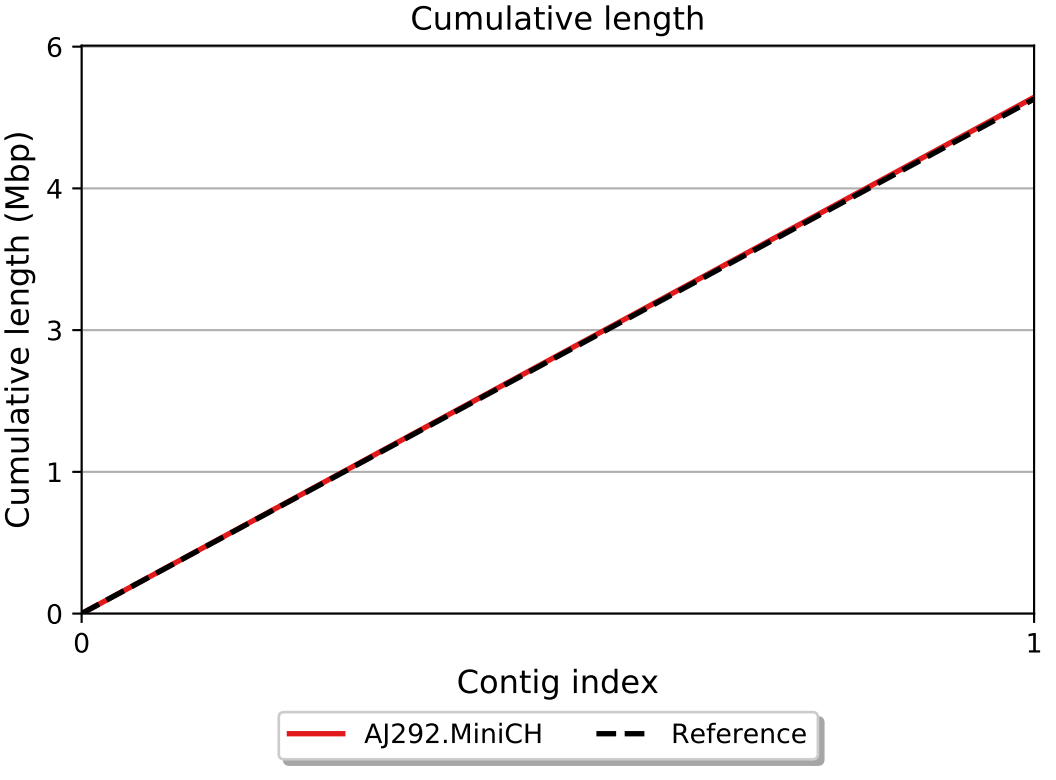
Unaligned report

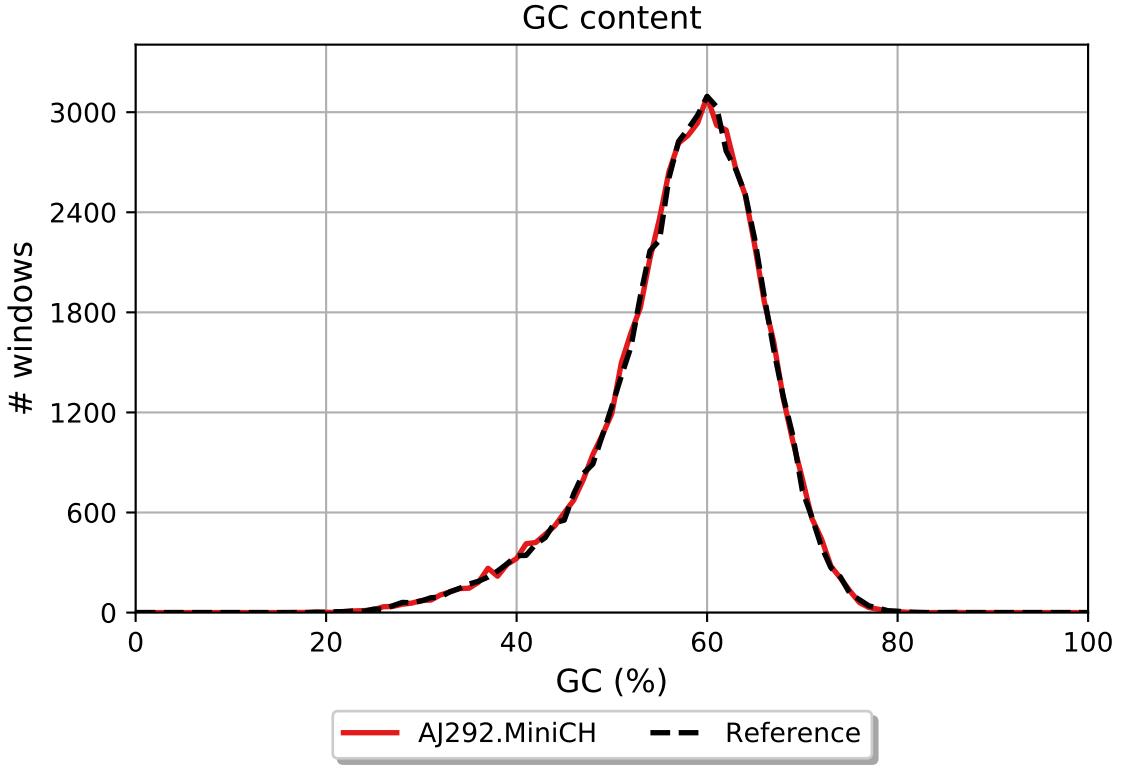
	AJ292.MiniCH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

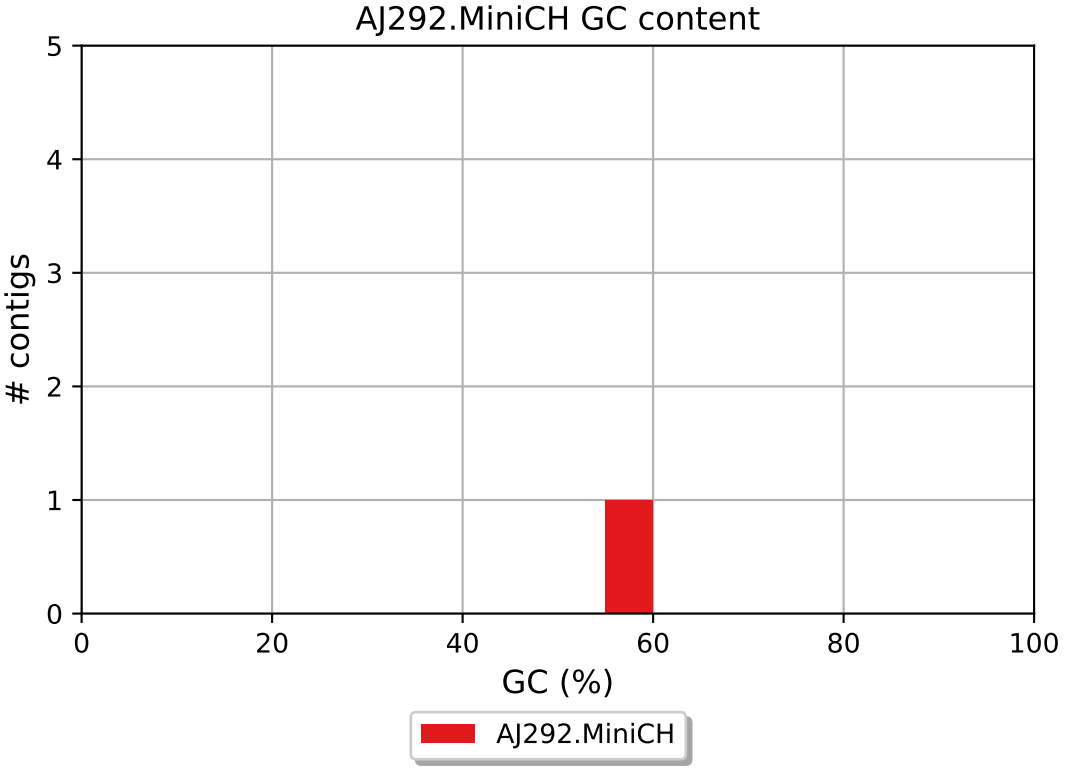
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

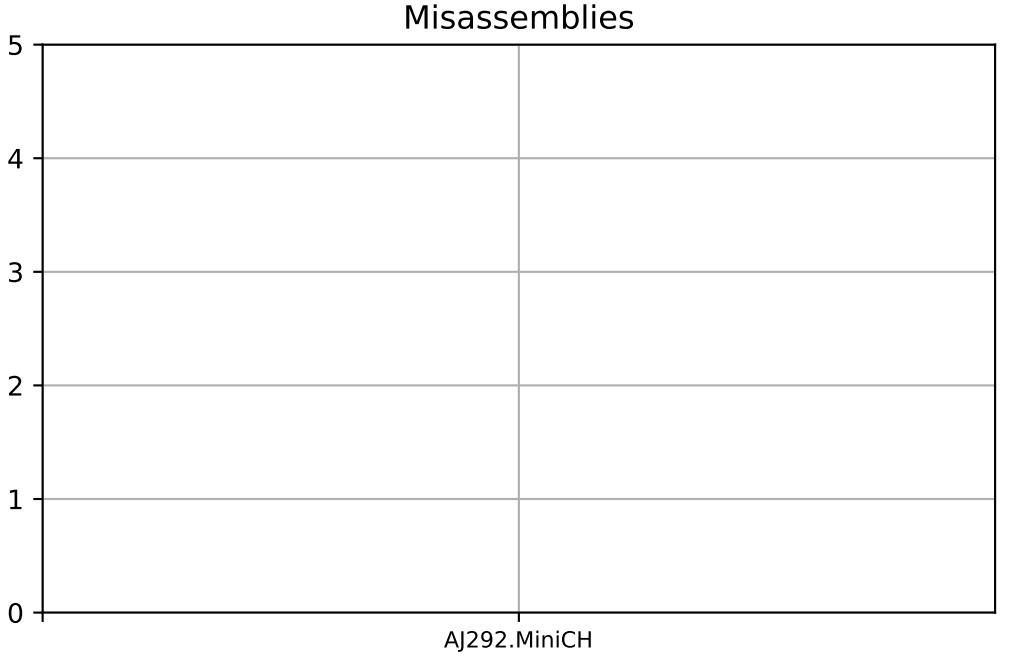

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ292.MiniCH

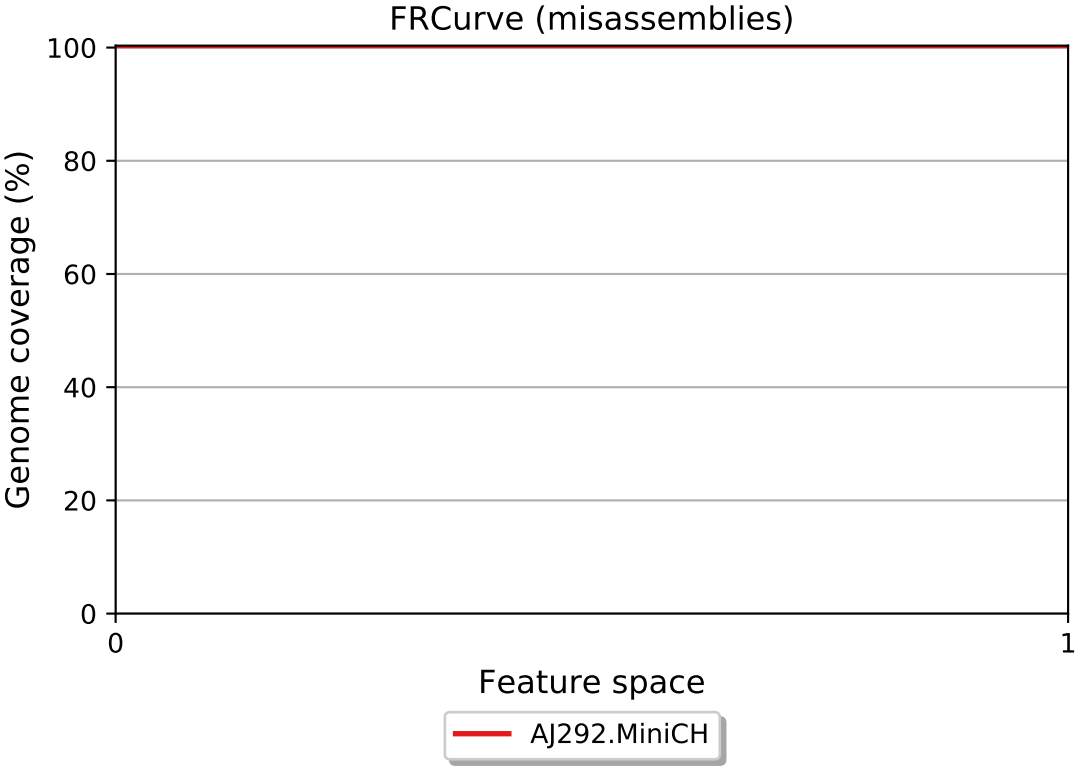

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ292.MiniCH

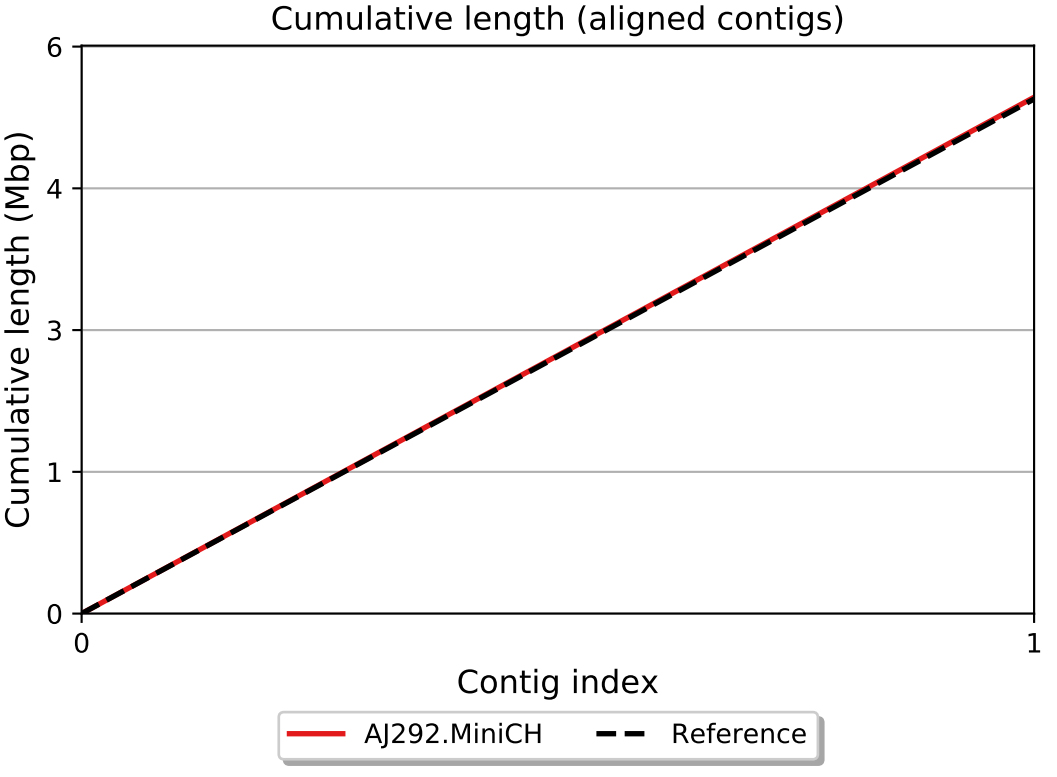

Cumulative length
Cumulative length (Mbp)
6
4
3
1
0
0
1
Contig index
AJ292.MiniCH
Reference

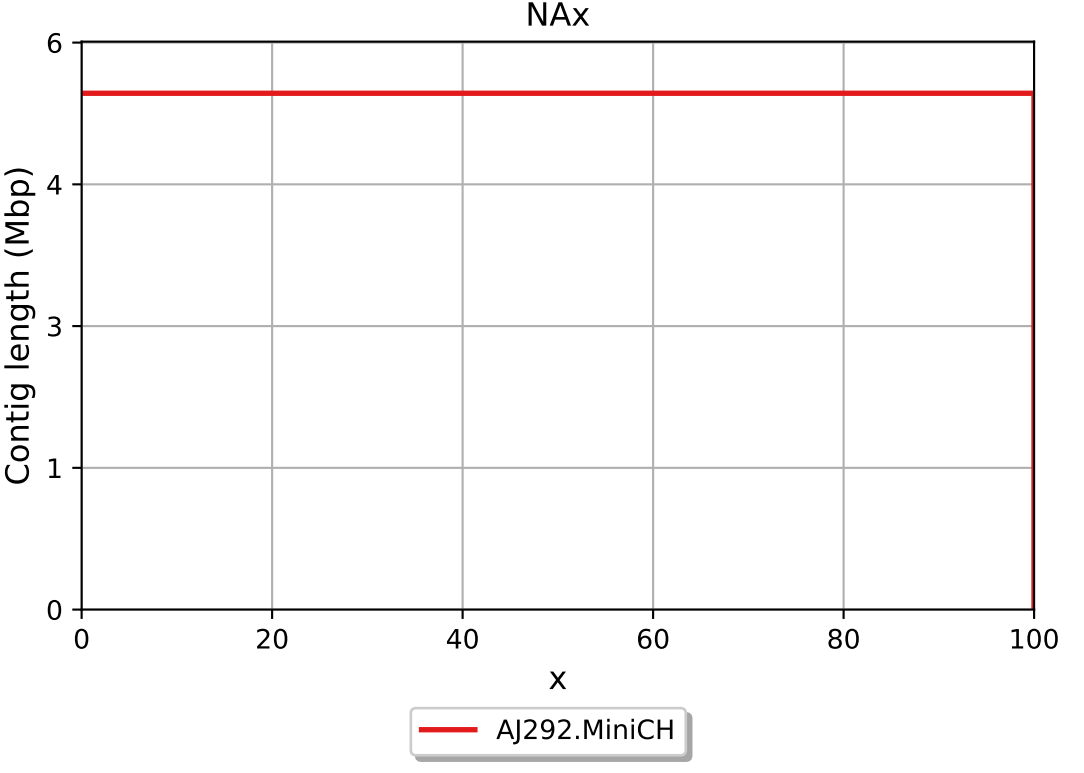

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ292.MiniCH
Reference

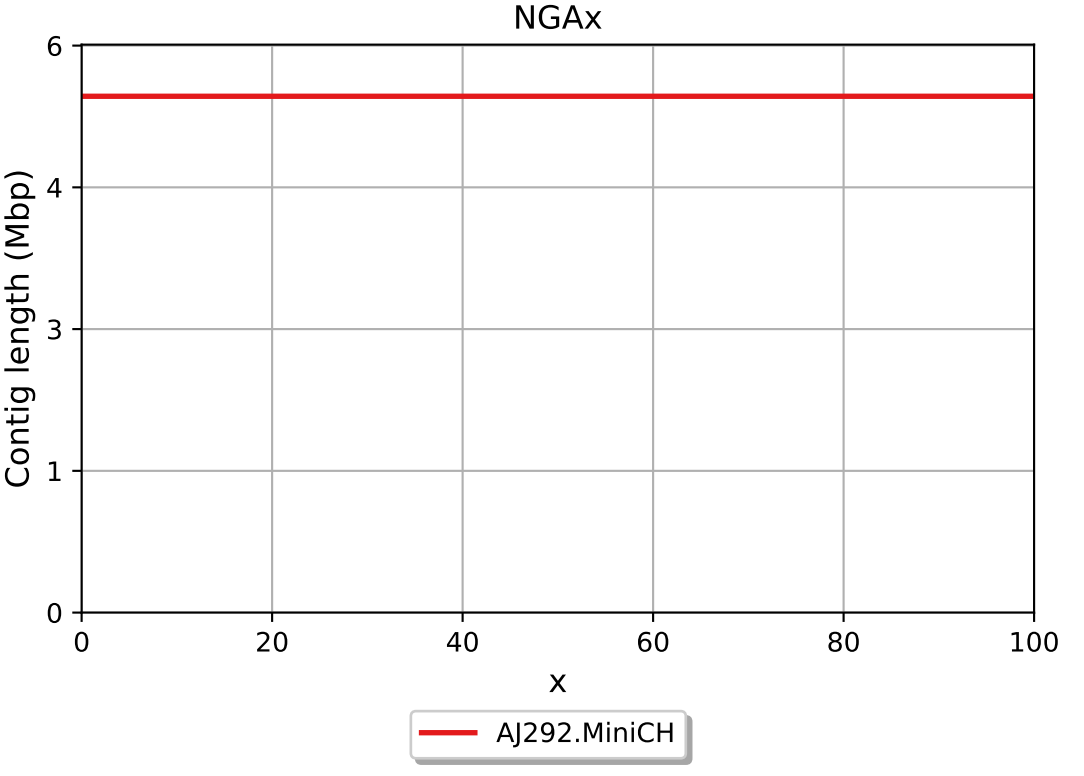

AJ292.MiniCH GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
AJ292.MiniCH


Misassemblies
5
4
3
2
1
0
AJ292.MiniCH


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
6
4
3
1
0
0
1
Contig index
AJ292.MiniCH
Reference


NAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ292.MiniCH


NGAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ292.MiniCH