Report

	AJ218.MiniH.p3
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	5668517
Total length (>= 1000 bp)	5668517
Total length (>= 5000 bp)	5668517
Total length (>= 10000 bp)	5668517
Total length (>= 25000 bp)	5668517
Total length (>= 50000 bp)	5668517
# contigs	2
Largest contig	5466146
Total length	5668517
Reference length	5465981
GC (%)	57.14
Reference GC (%)	57.29
N50	5466146
NG50	5466146
N75	5466146
NG75	5466146
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	190155
Genome fraction (%)	100.000
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.13
# indels per 100 kbp	3.84
Largest alignment	5466142
Total aligned length	5478358
NA50	5466142
NGA50	5466142
NA75	5466142
NGA75	5466142
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

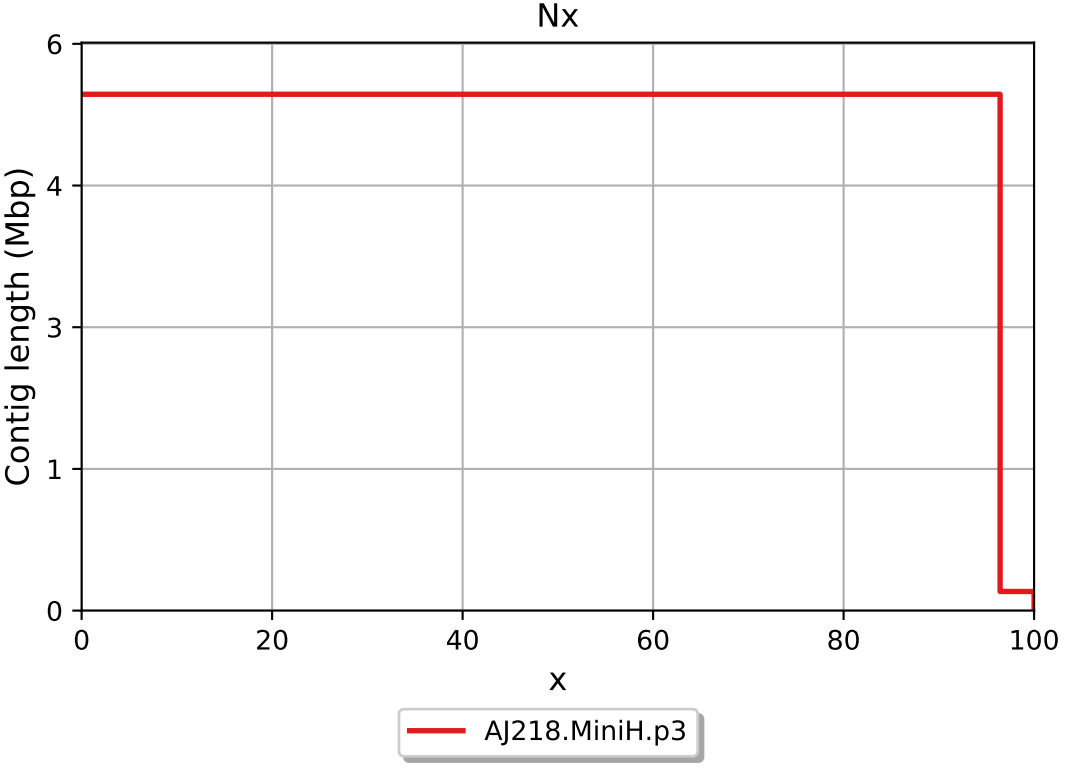
	AJ218.MiniH.p3
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	7
# indels	210
# indels (<= 5 bp)	210
# indels (> 5 bp)	0
Indels length	284

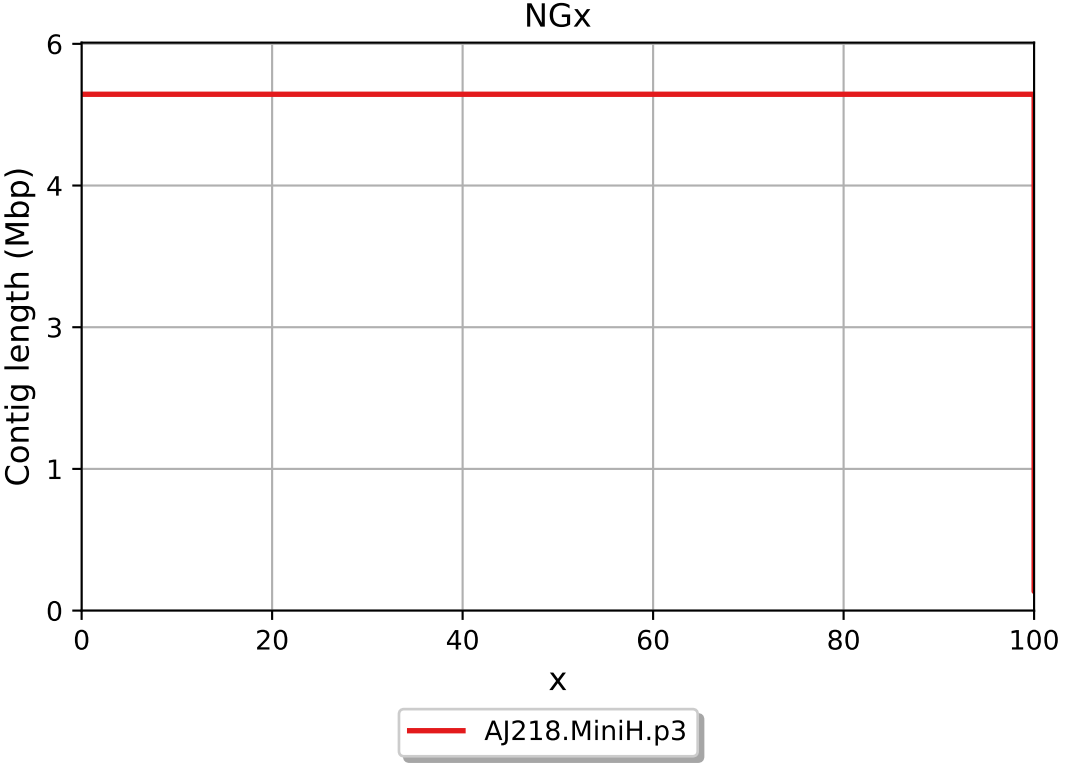
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

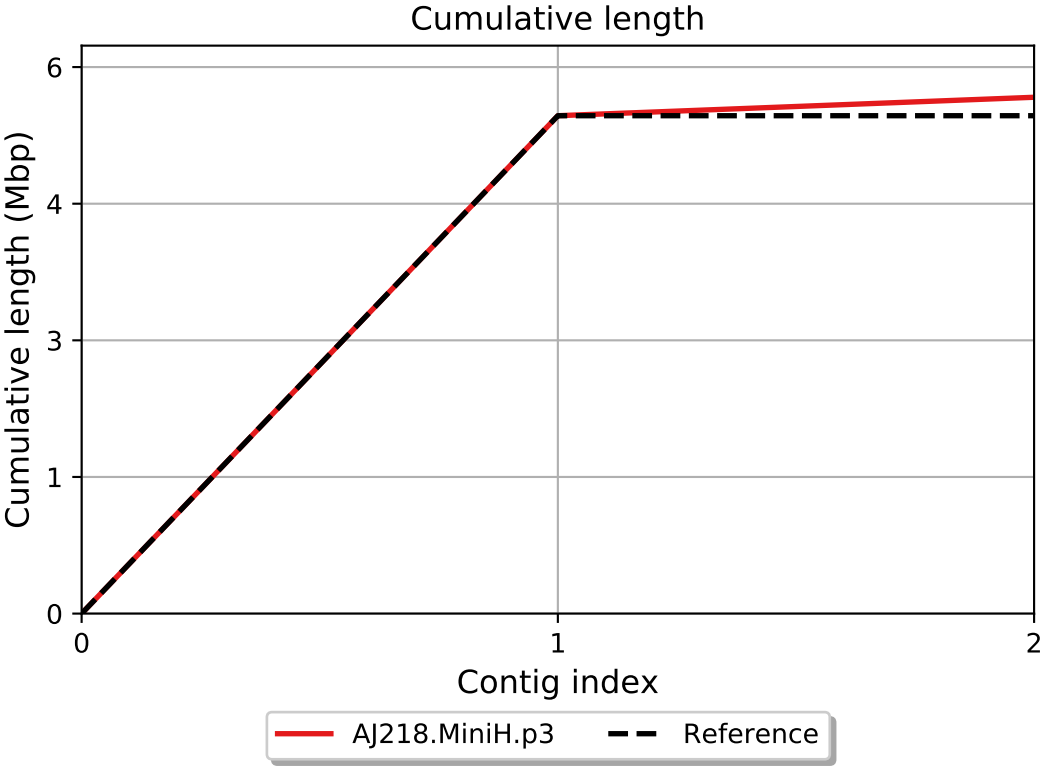
Unaligned report

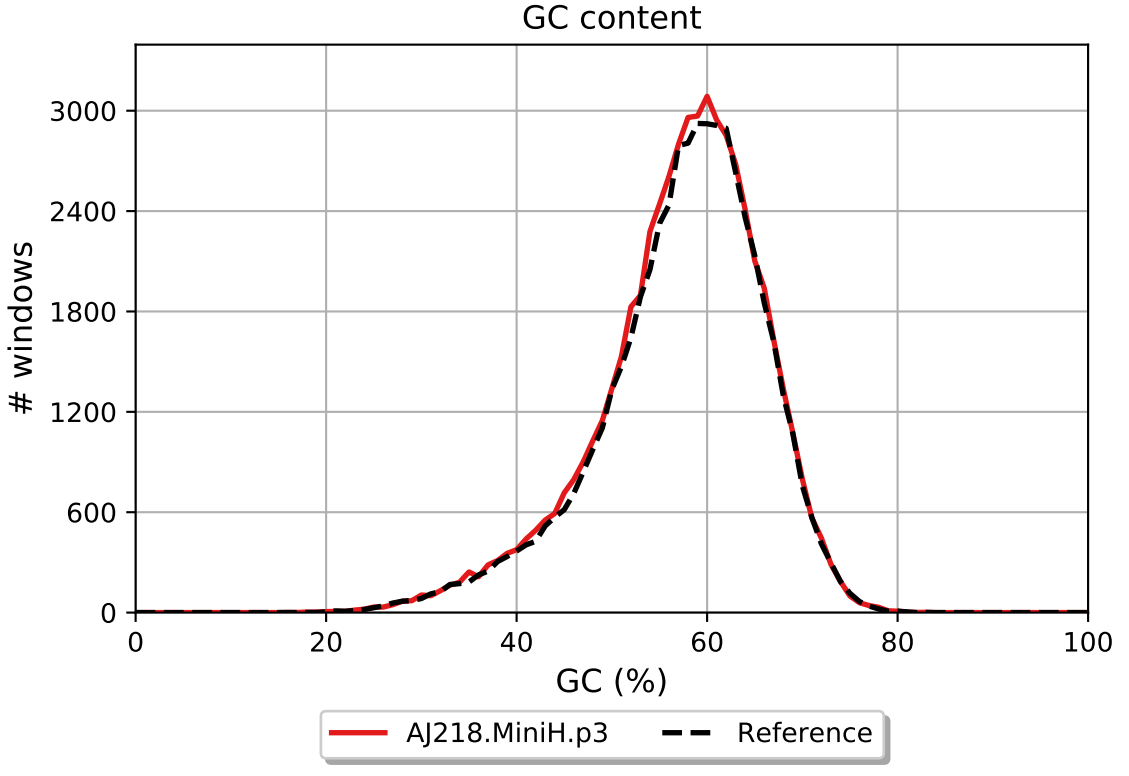
	AJ218.MiniH.p3
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	190155
# N's	0

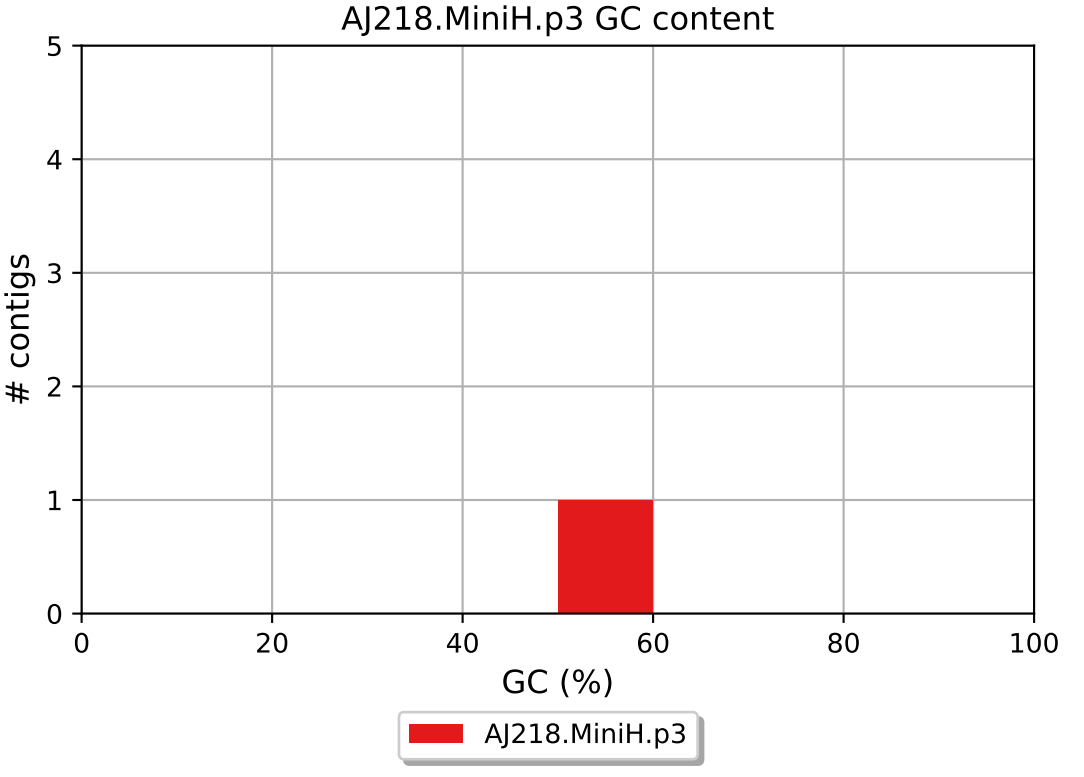
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

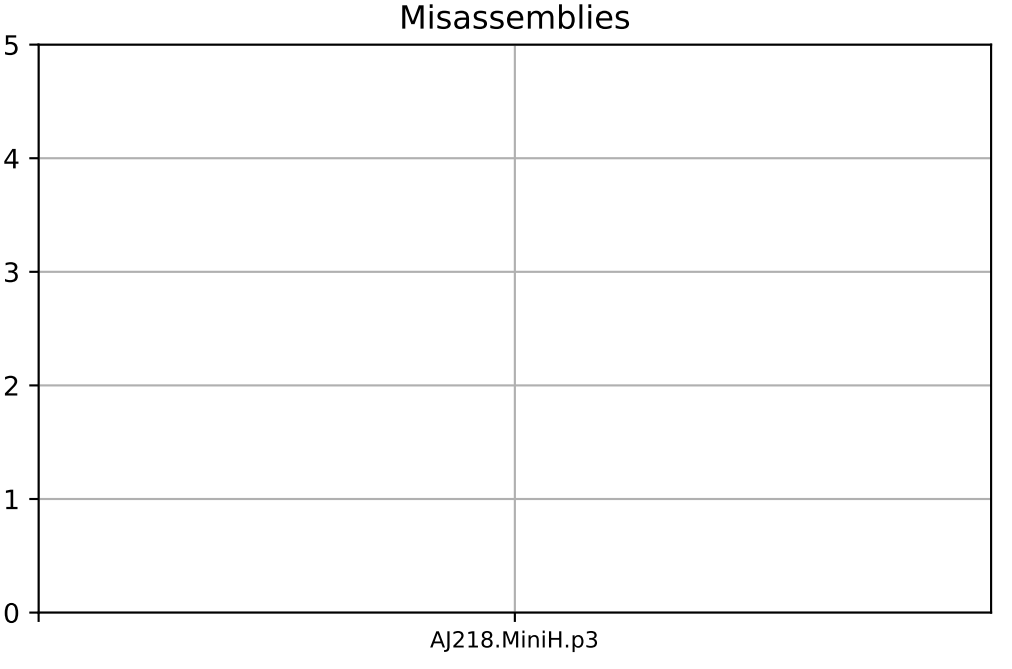

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ218.MiniH.p3

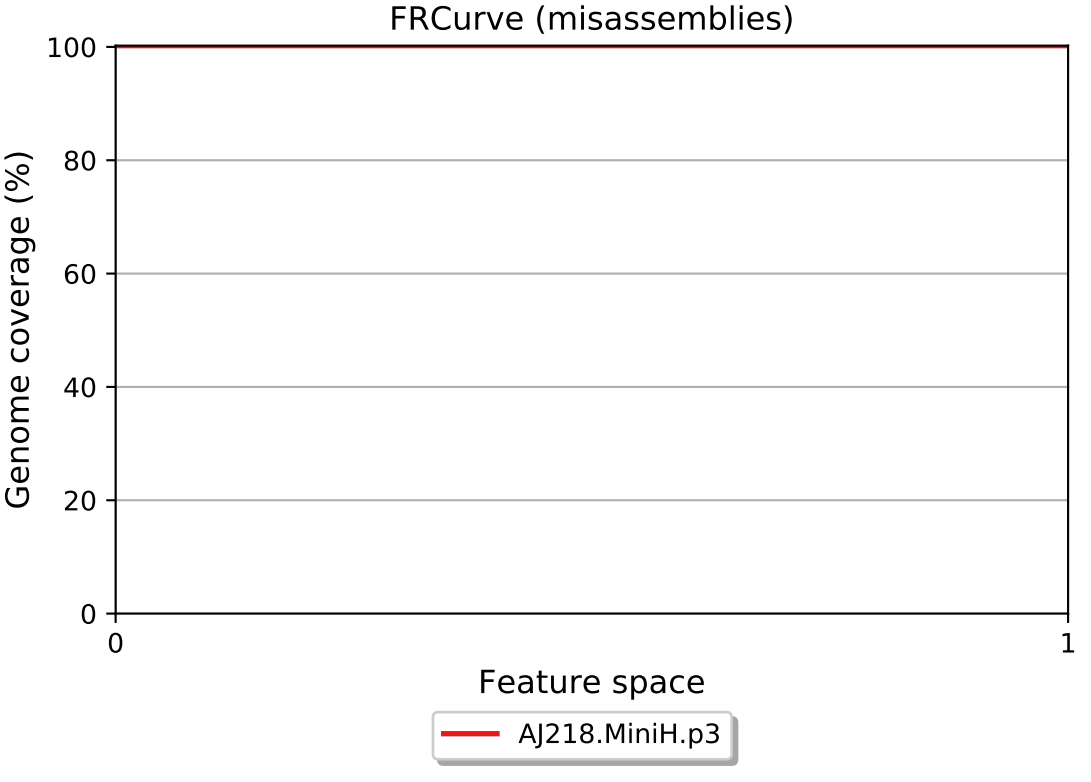

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ218.MiniH.p3

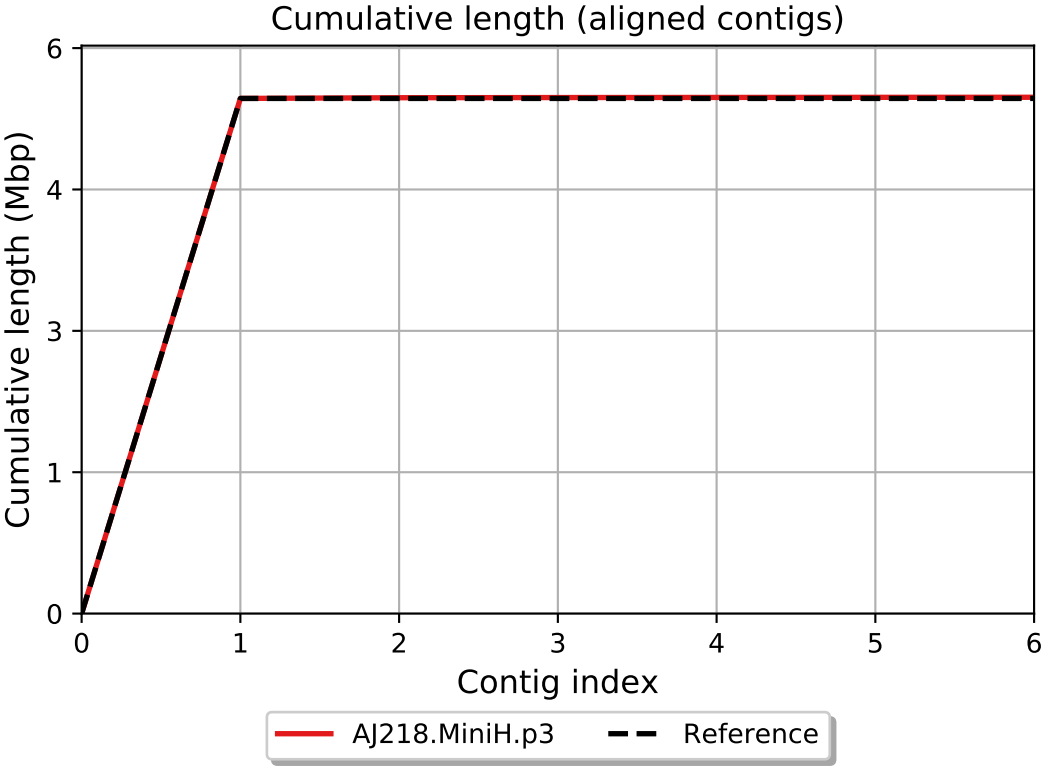

Cumulative length
Cumulative length (Mbp)
6
4
3
1
0
0
1
2
Contig index
AJ218.MiniH.p3
Reference

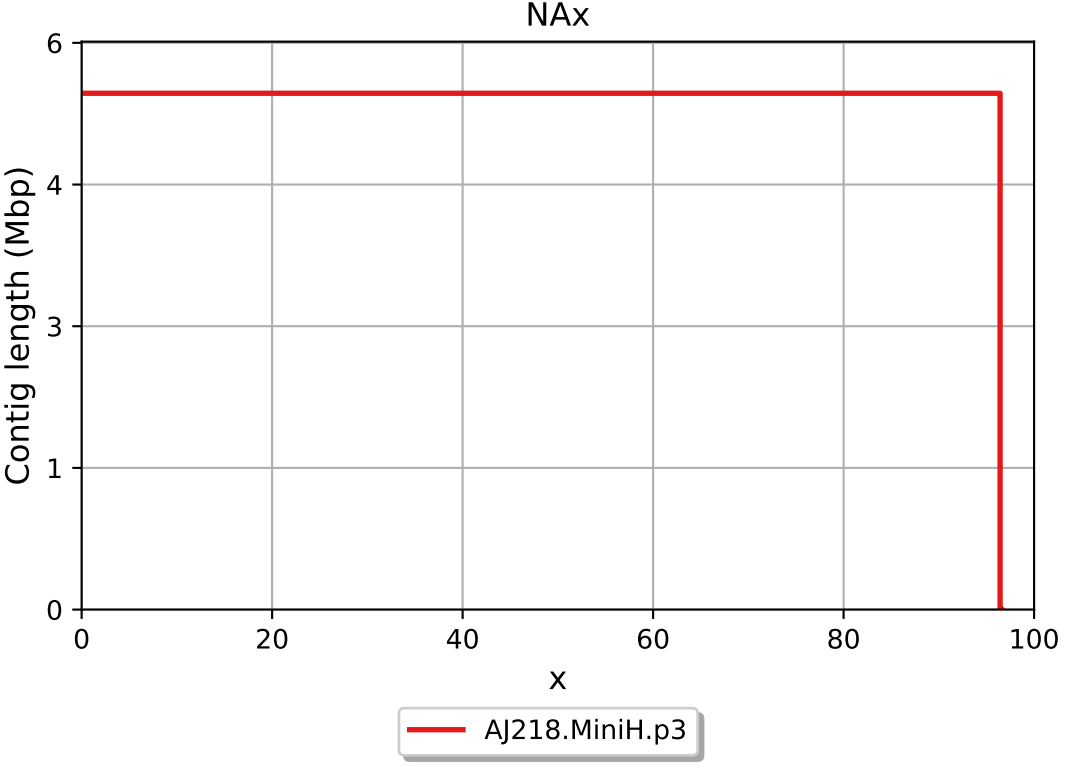

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
AJ218.MiniH.p3
Reference

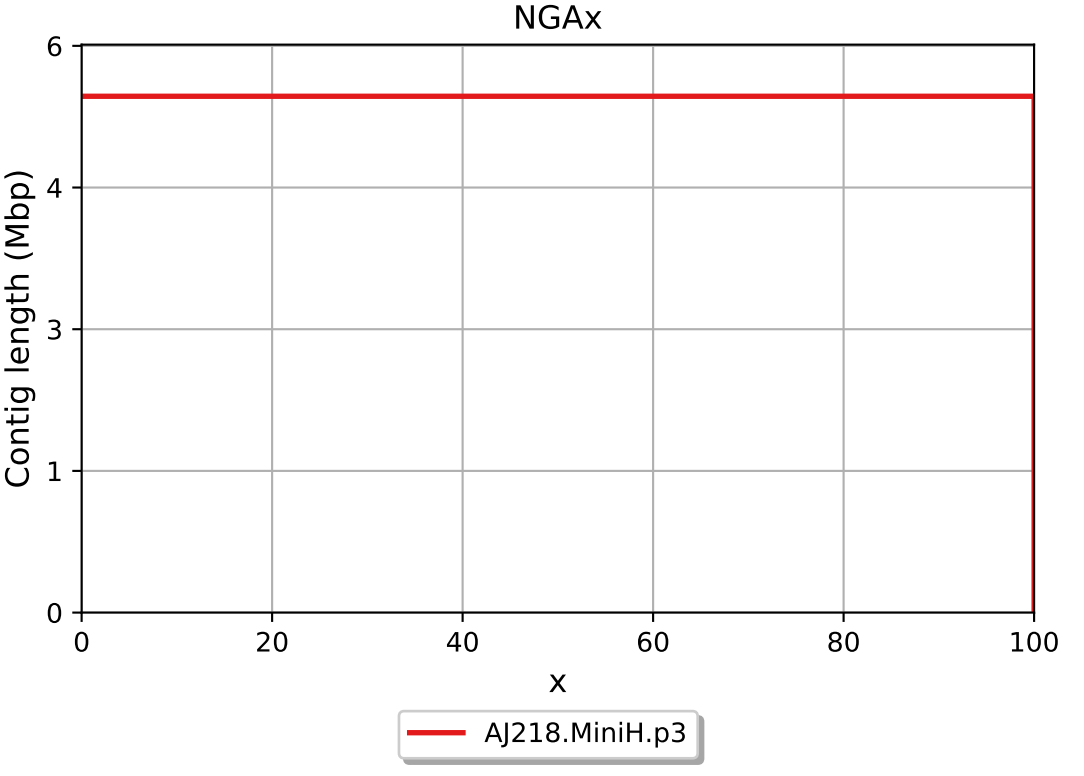

AJ218.MiniH.p3 GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
AJ218.MiniH.p3


Misassemblies
5
4
3
2
1
0
AJ218.MiniH.p3


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
AJ218.MiniH.p3


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
1
2
3
4
5
6
Contig index
AJ218.MiniH.p3
Reference


NAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ218.MiniH.p3


NGAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
AJ218.MiniH.p3