

# Report

	AJ218.MiniH.p2
# 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)	5668555
Total length (>= 1000 bp)	5668555
Total length (>= 5000 bp)	5668555
Total length (>= 10000 bp)	5668555
Total length (>= 25000 bp)	5668555
Total length (>= 50000 bp)	5668555
# contigs	2
Largest contig	5466185
Total length	5668555
Reference length	5465981
GC (%)	57.14
Reference GC (%)	57.29
N50	5466185
NG50	5466185
N75	5466185
NG75	5466185
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	4.68
Largest alignment	5466181
Total aligned length	5478396
NA50	5466181
NGA50	5466181
NA75	5466181
NGA75	5466181
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.p2
# 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	256
# indels ( $\leq 5$ bp)	256
# indels ( $> 5$ bp)	0
Indels length	349

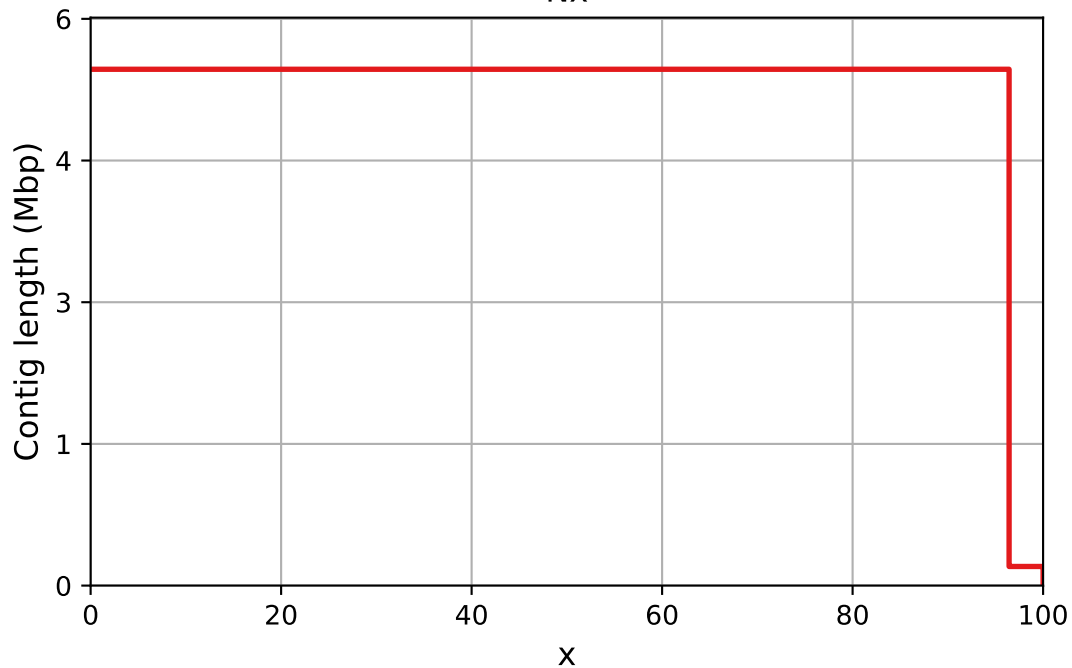
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ218.MiniH.p2
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	190155
# N's	0

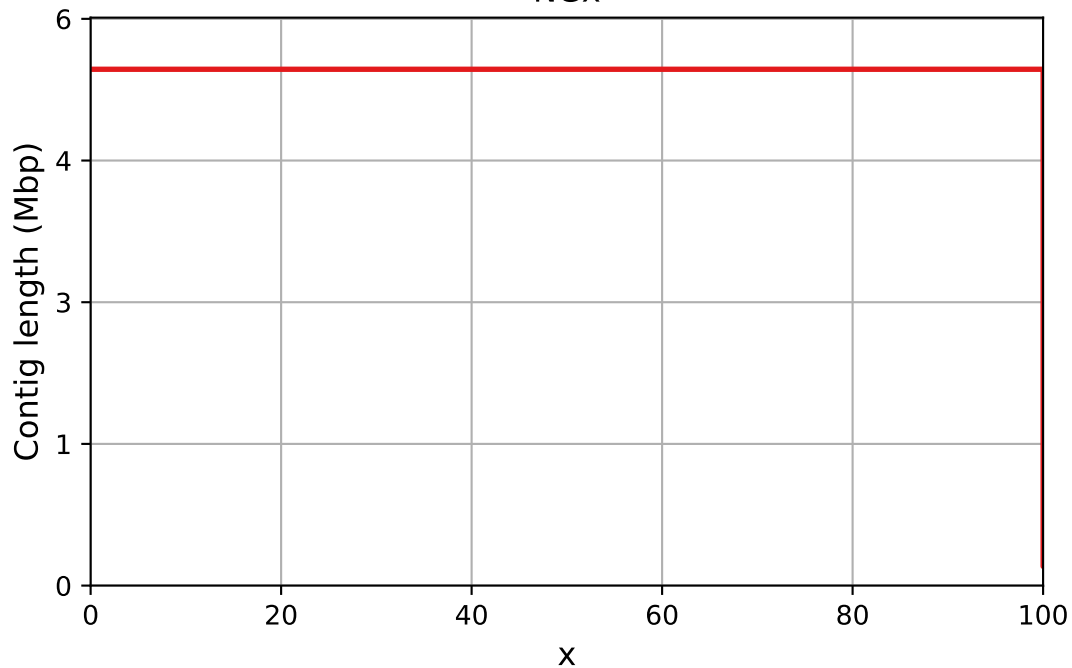
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

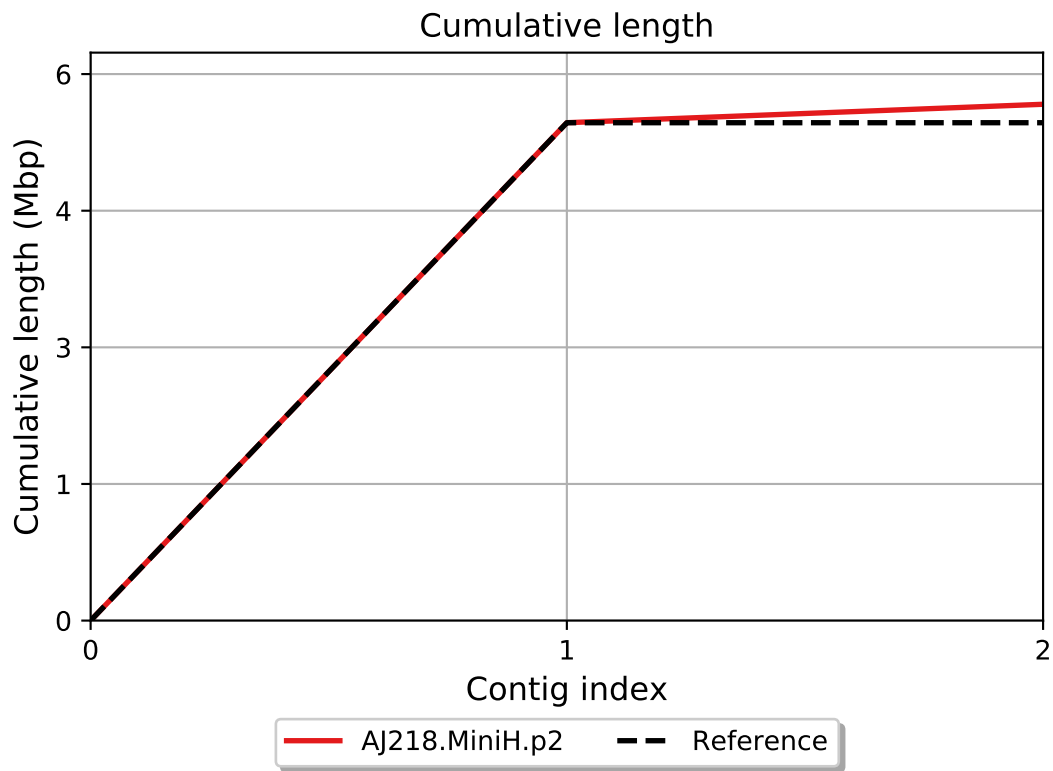


AJ218.MiniH.p2

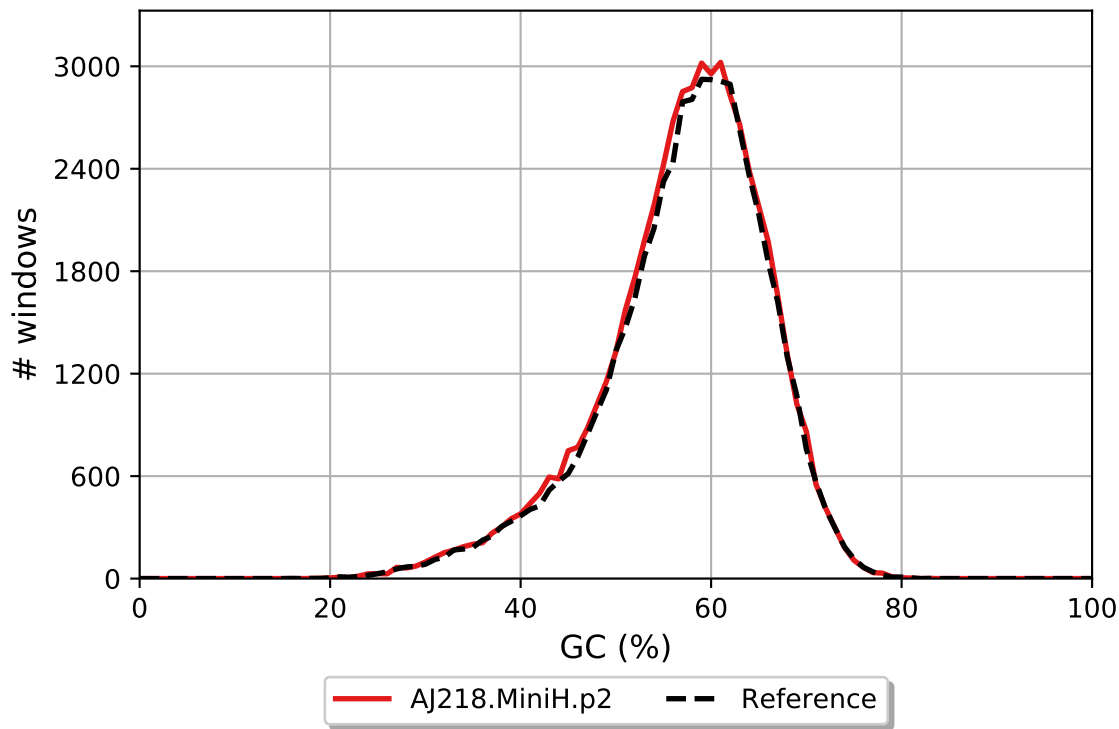
NGx



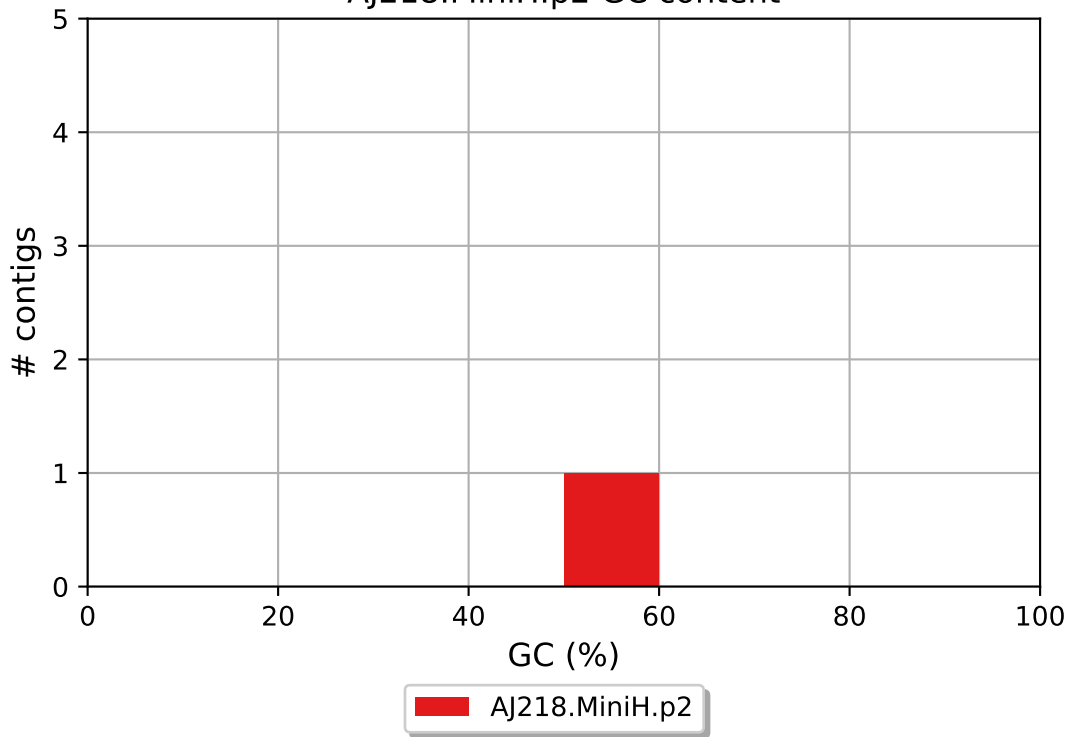
AJ218.MiniH.p2



## GC content



AJ218.MiniH.p2 GC content

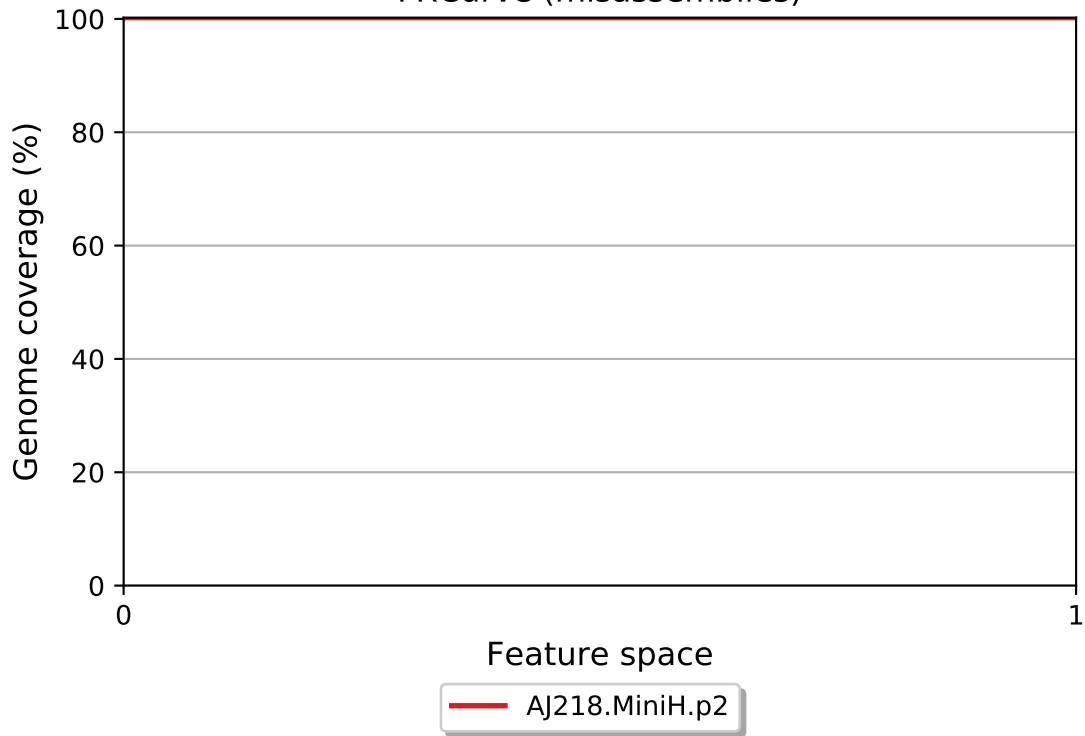




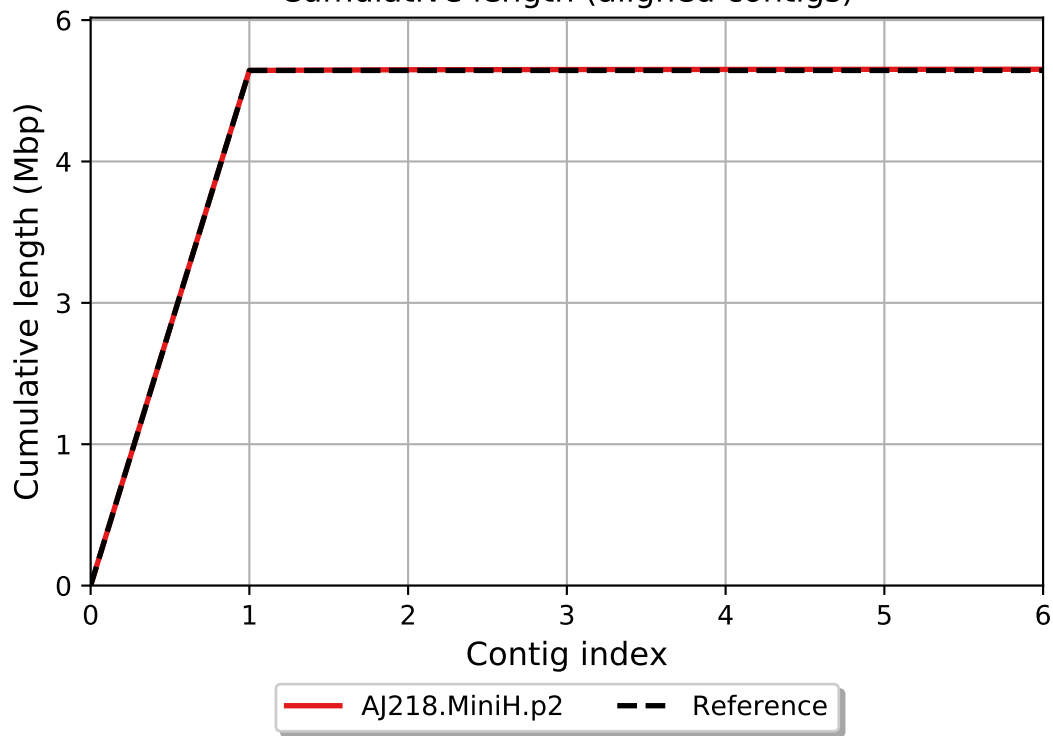
## Misassemblies



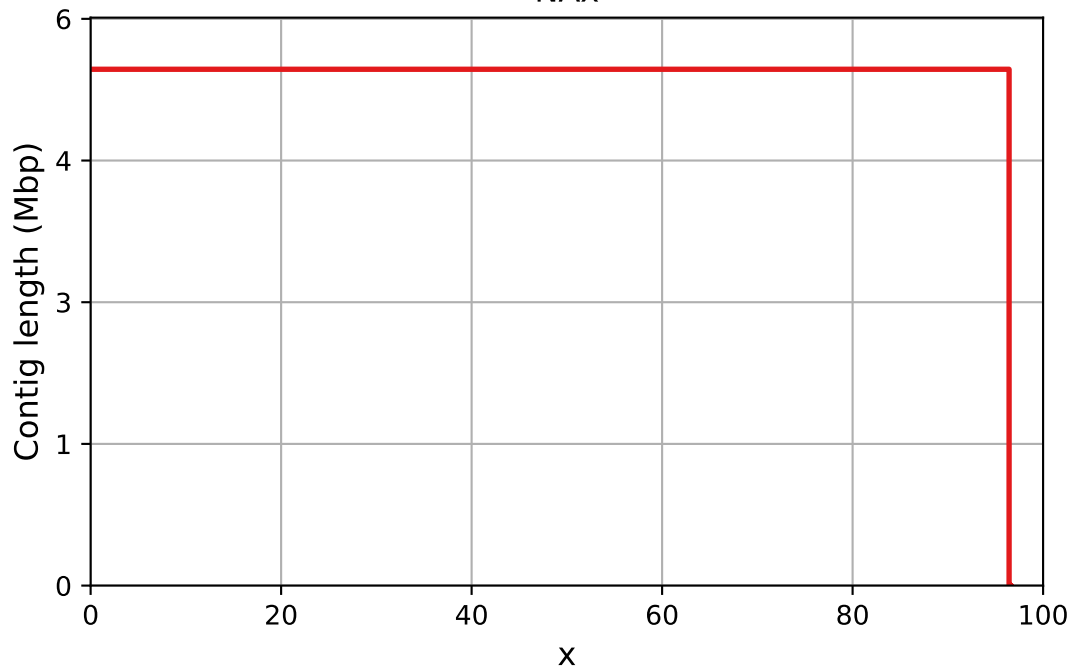
FRCurve (misassemblies)



Cumulative length (aligned contigs)

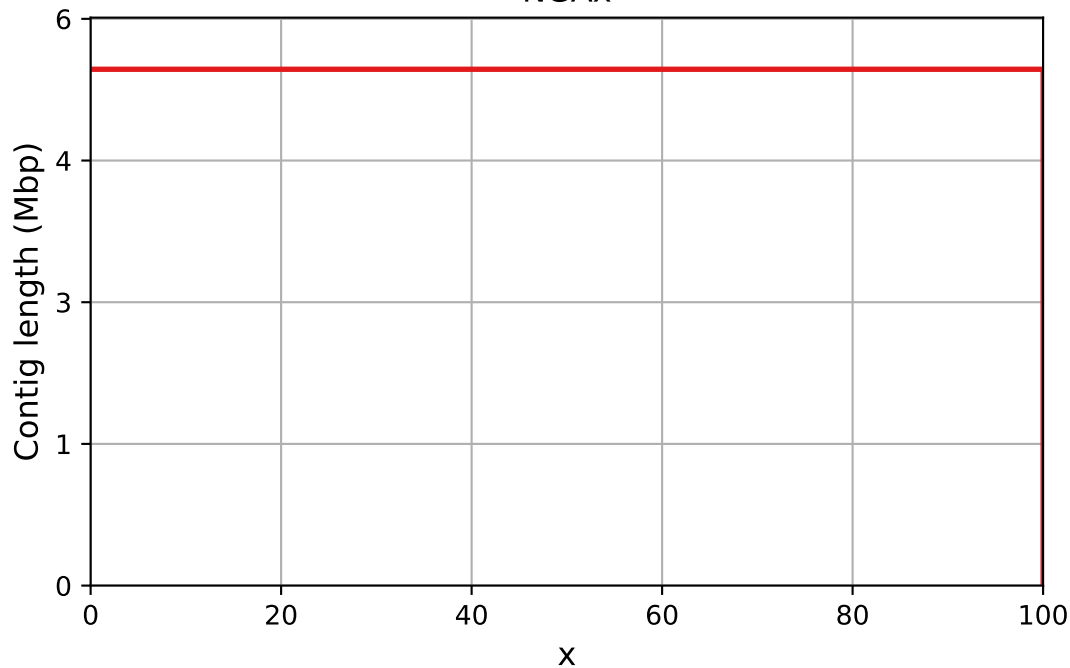


NAx



AJ218.MiniH.p2

NGAx



AJ218.MiniH.p2