

Report

	AJ218.MiniH
# 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)	5691650
Total length (>= 1000 bp)	5691650
Total length (>= 5000 bp)	5691650
Total length (>= 10000 bp)	5691650
Total length (>= 25000 bp)	5691650
Total length (>= 50000 bp)	5691650
# contigs	2
Largest contig	5488527
Total length	5691650
Reference length	5465981
GC (%)	57.11
Reference GC (%)	57.29
N50	5488527
NG50	5488527
N75	5488527
NG75	5488527
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# unaligned mis. contigs	1
# unaligned contigs	0 + 1 part
Unaligned length	190855
Genome fraction (%)	99.978
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.72
# indels per 100 kbp	343.89
Largest alignment	5488283
Total aligned length	5500551
NA50	5488283
NGA50	5488283
NA75	5488283
NGA75	5488283
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
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	7
# unaligned mis. contigs	1
# mismatches	859
# indels	18793
# indels (≤ 5 bp)	18685
# indels (> 5 bp)	108
Indels length	27715

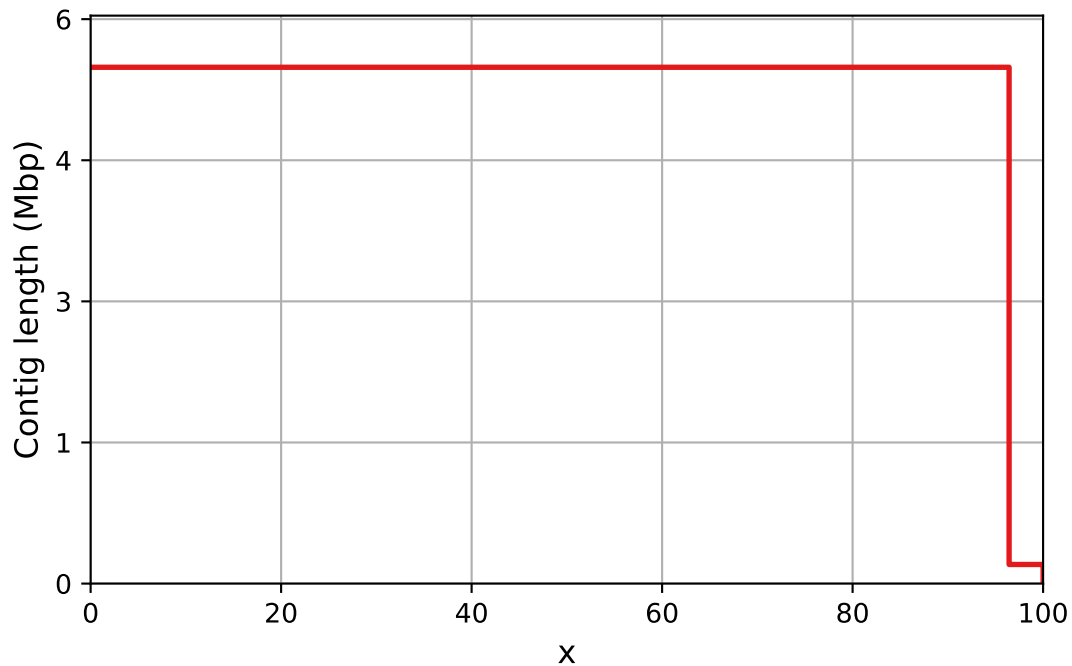
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	AJ218.MiniH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	190855
# N's	0

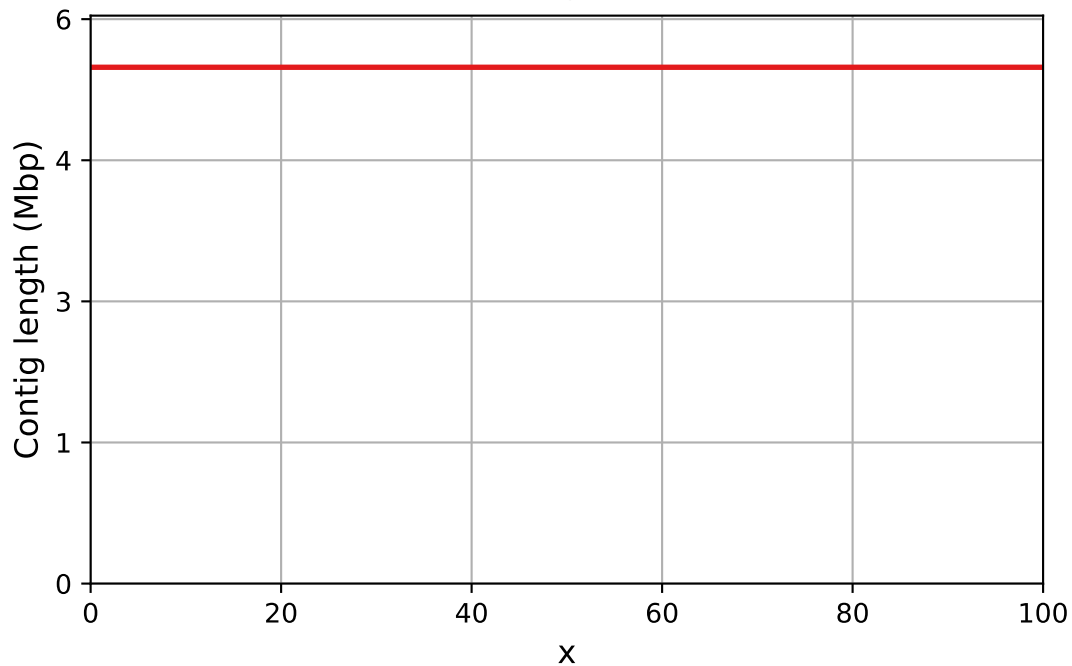
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



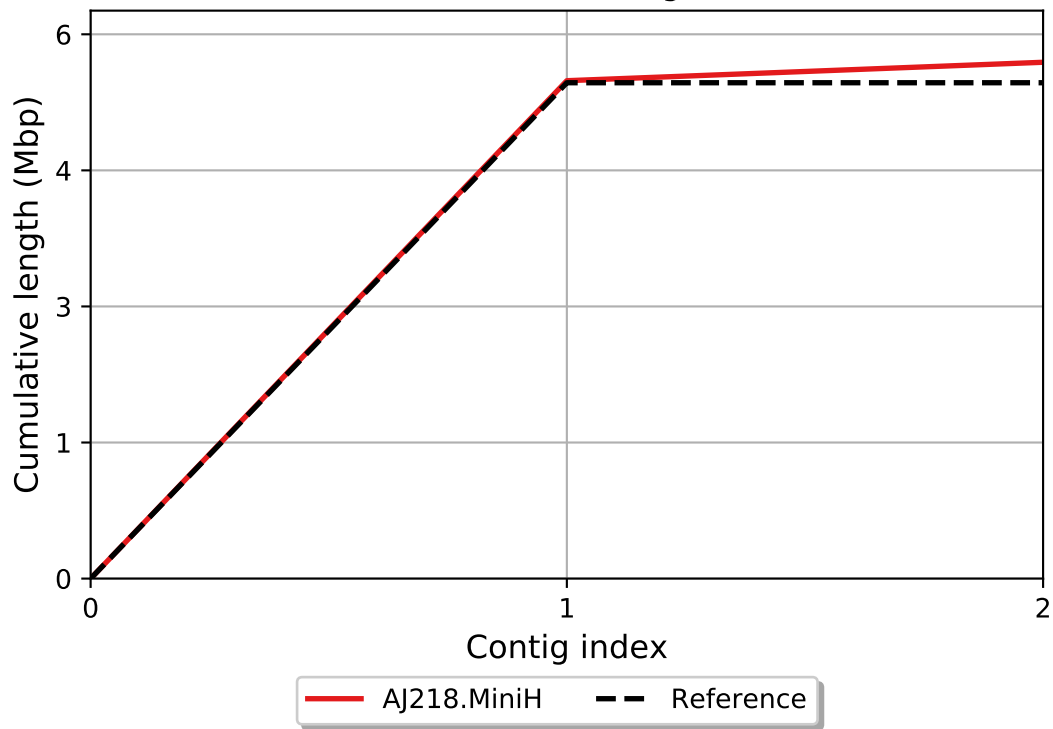
Aj218.MiniH

NGx

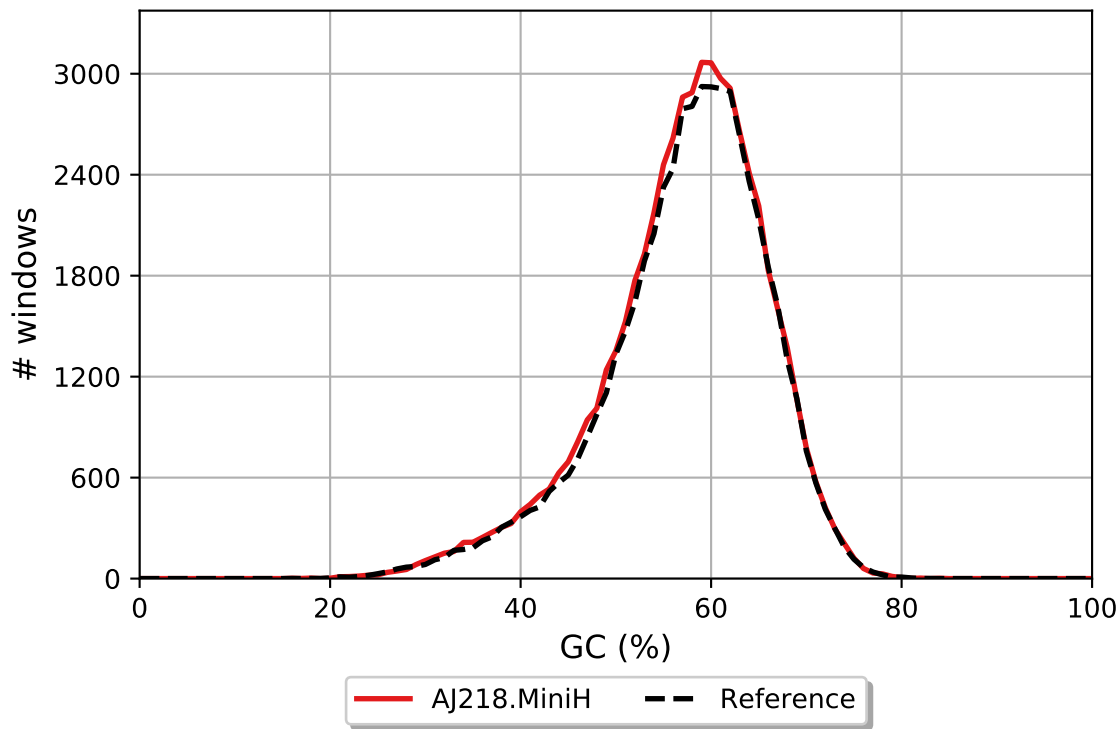


Aj218.MiniH

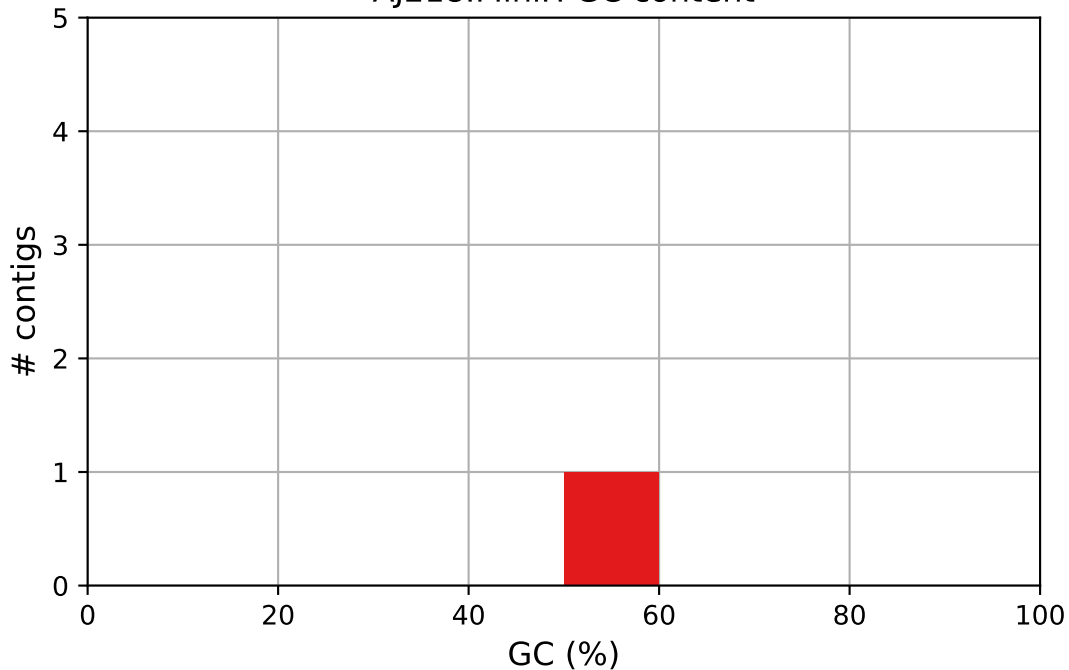
Cumulative length



GC content



AJ218.MiniH GC content

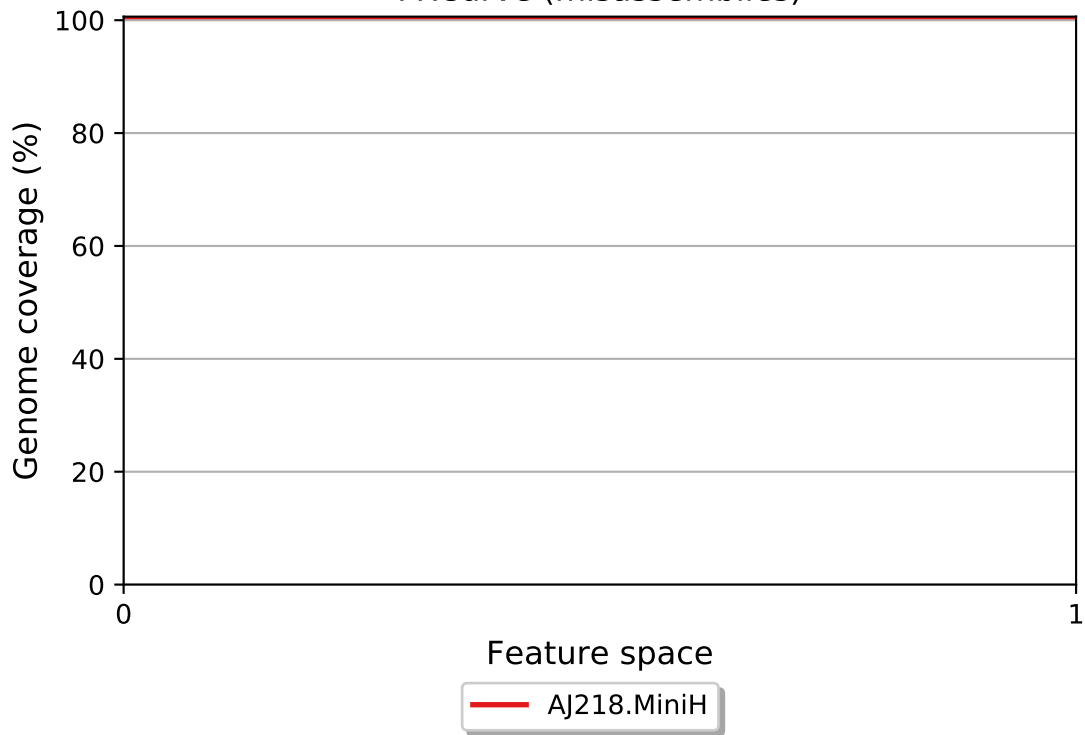


AJ218.MiniH

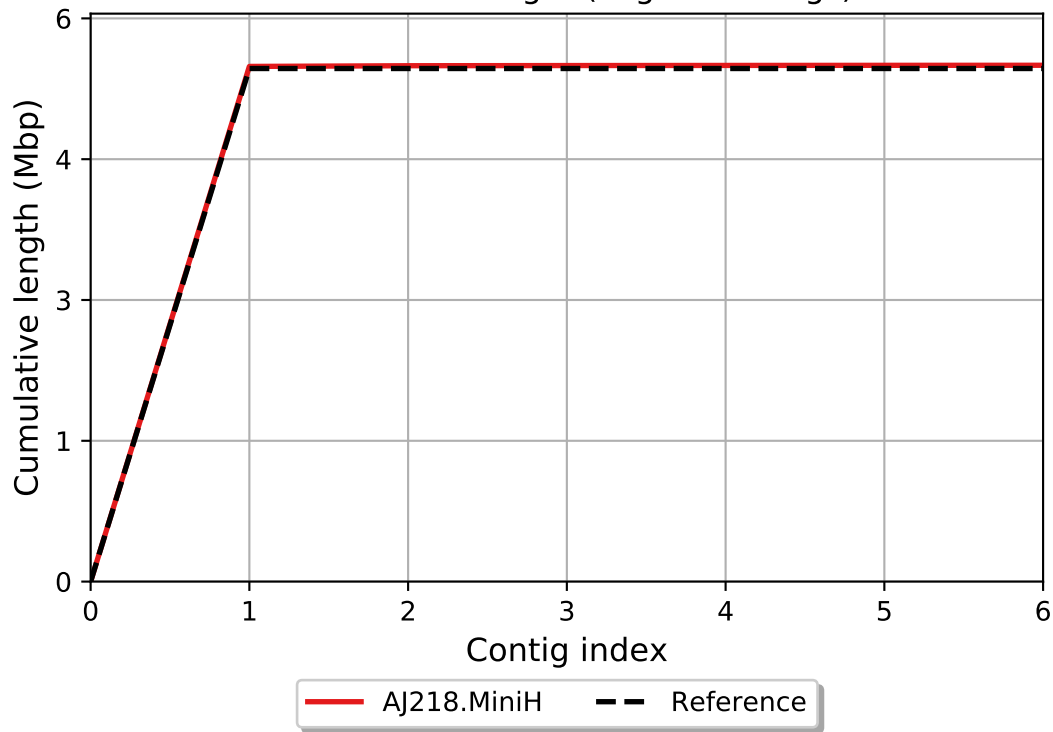
Misassemblies



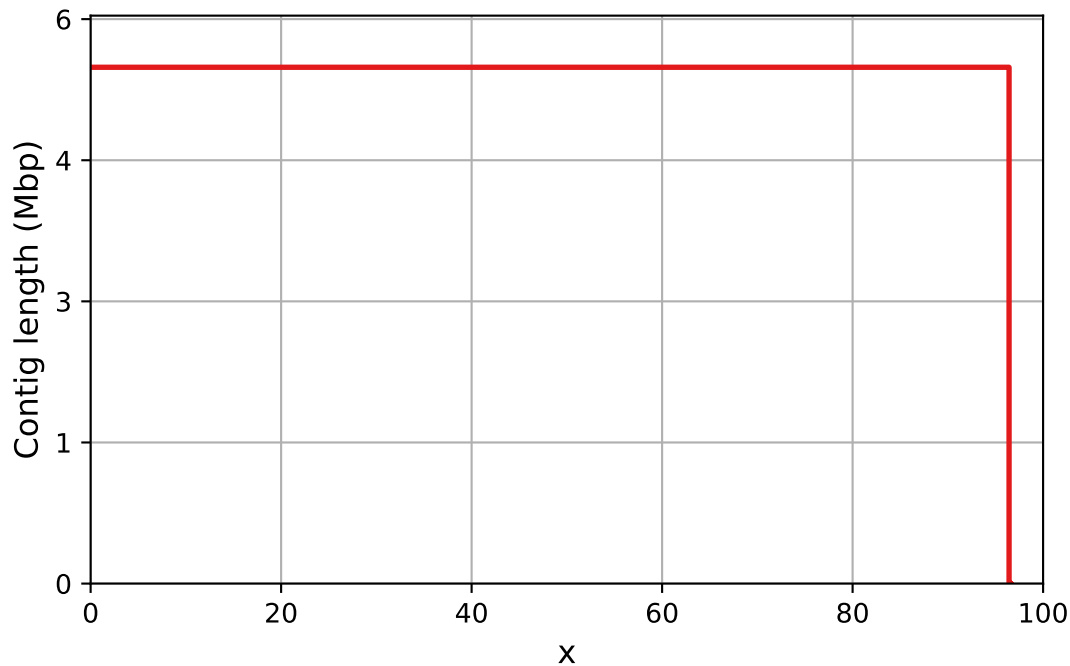
FRCurve (misassemblies)



Cumulative length (aligned contigs)

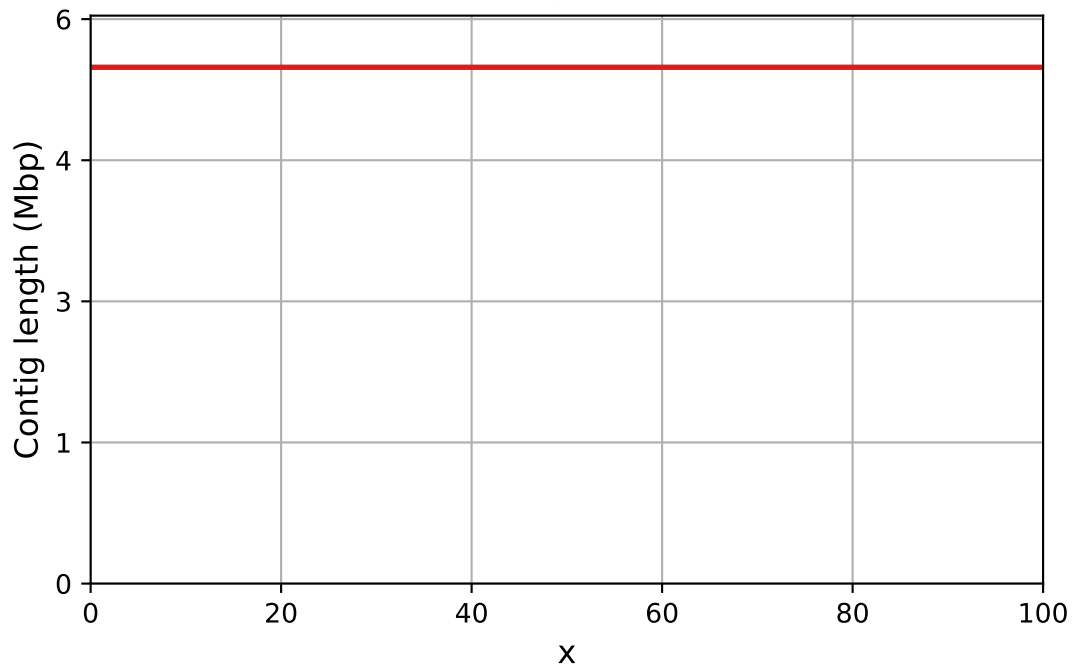


NAx



Aj218.MiniH

NGAx



Aj218.MiniH