

# Report

	AJ292.MiniH
# 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)	5465679
Total length (>= 1000 bp)	5465679
Total length (>= 5000 bp)	5465679
Total length (>= 10000 bp)	5465679
Total length (>= 25000 bp)	5465679
Total length (>= 50000 bp)	5465679
# contigs	1
Largest contig	5465679
Total length	5465679
Reference length	5445112
GC (%)	57.59
Reference GC (%)	57.62
N50	5465679
NG50	5465679
N75	5465679
NG75	5465679
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	20.05
# indels per 100 kbp	342.92
Largest alignment	5465515
Total aligned length	5465515
NA50	5465515
NGA50	5465515
NA75	5465515
NGA75	5465515
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
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	1092
# indels	18672
# indels ( $\leq 5$ bp)	18548
# indels ( $> 5$ bp)	124
Indels length	28085

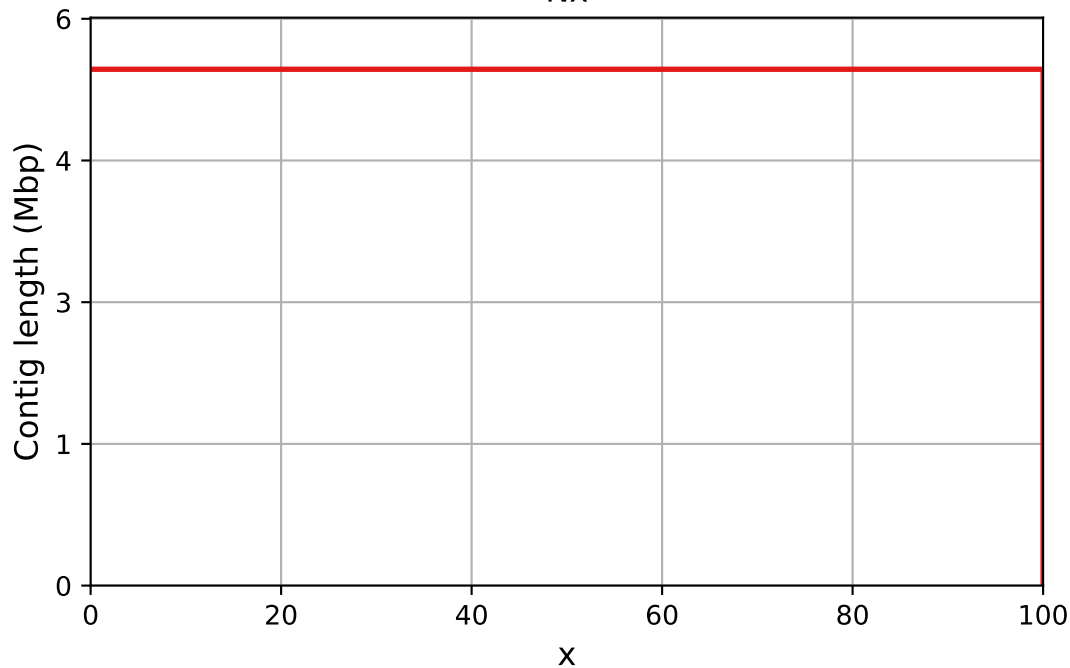
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

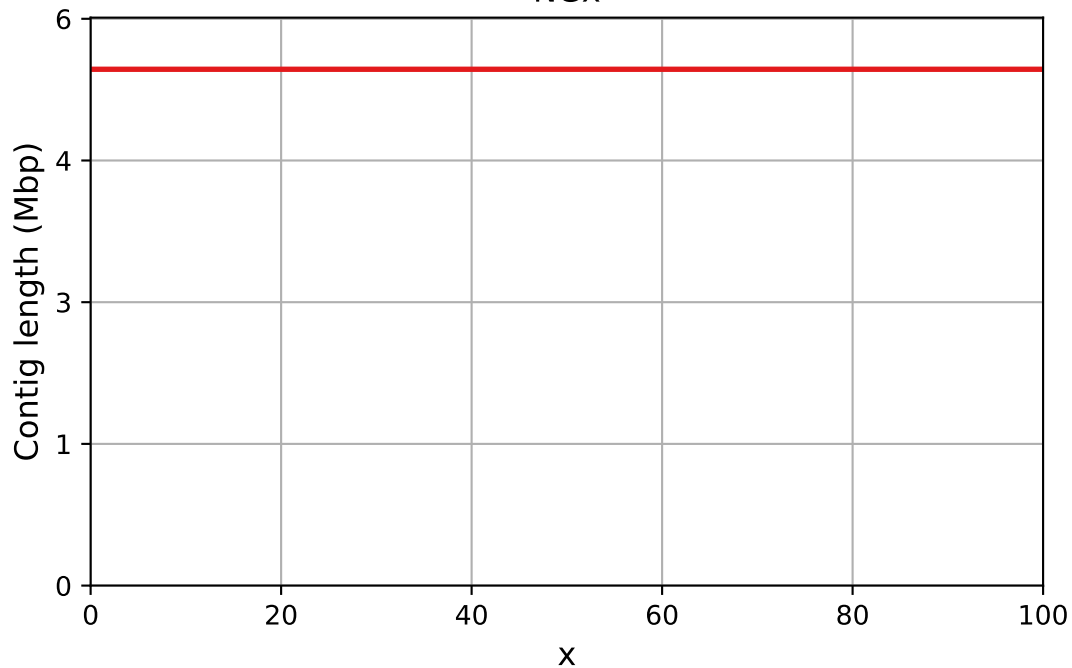
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

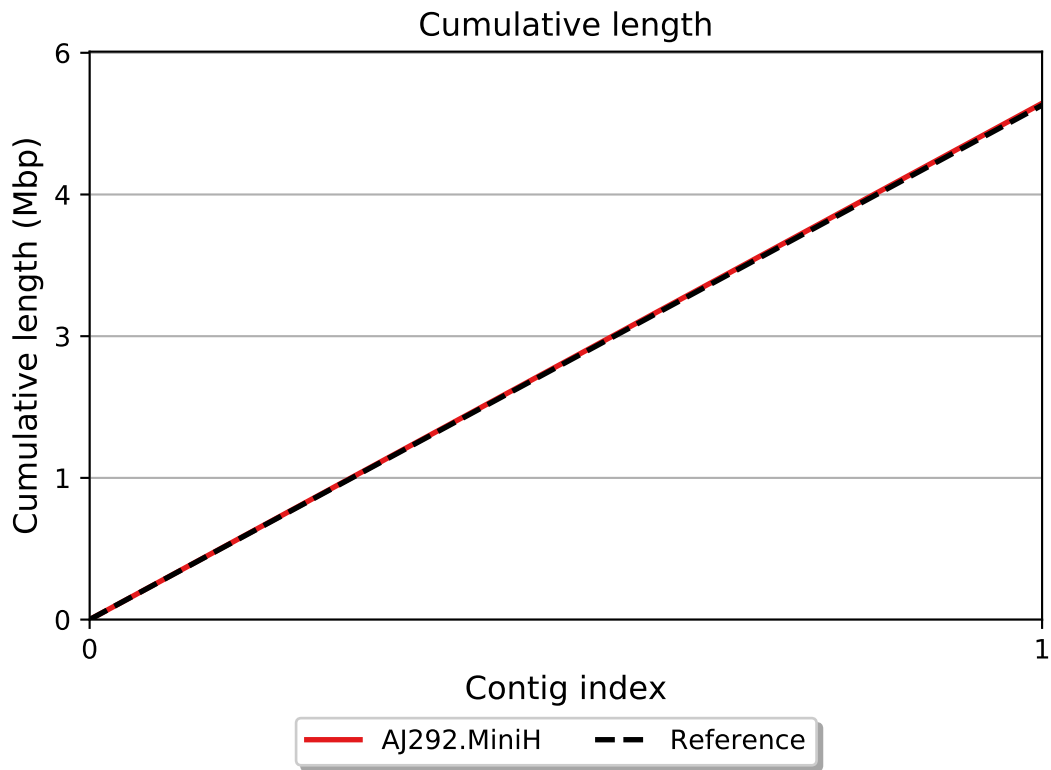


Aj292.MiniH

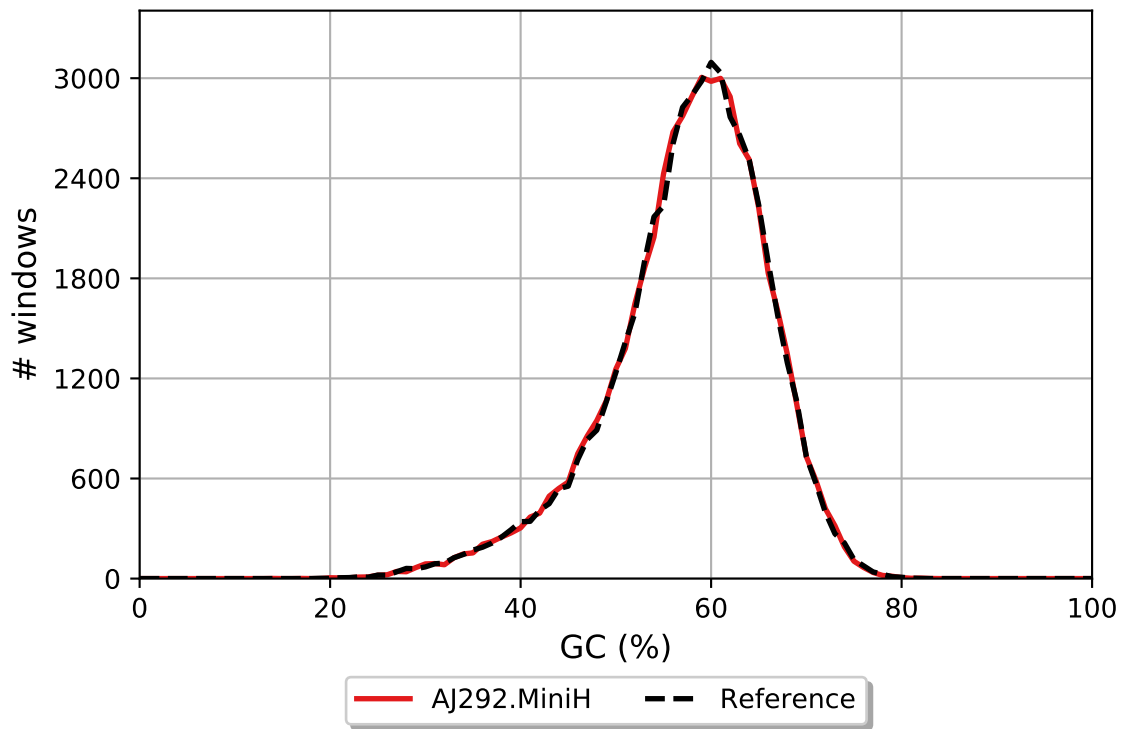
NGx



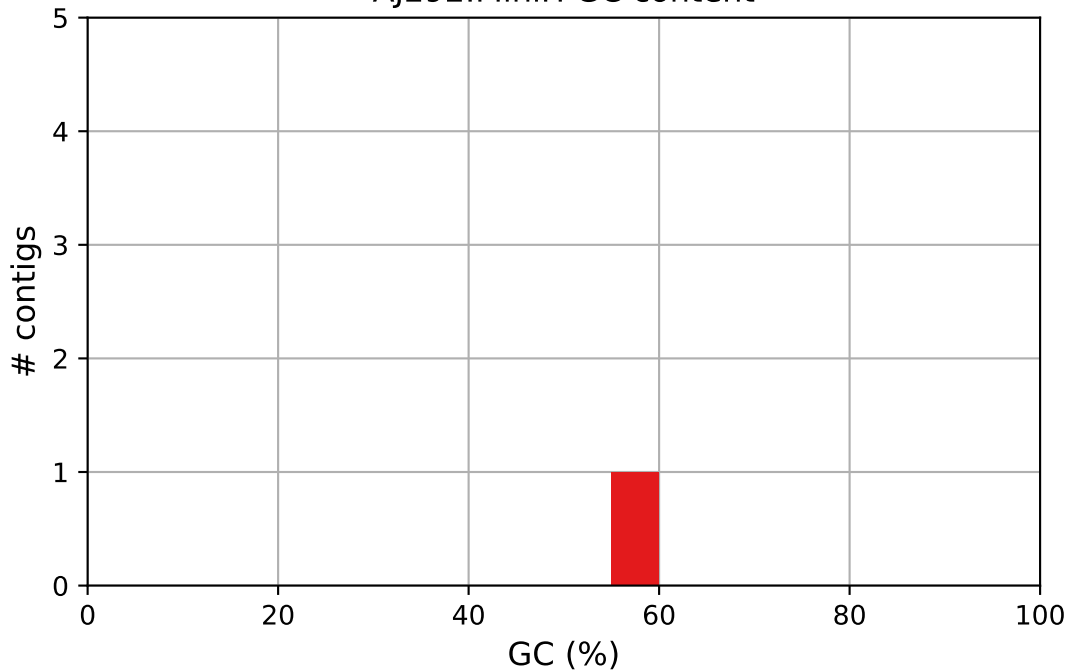
Aj292.MiniH



## GC content



AJ292.MiniH GC content



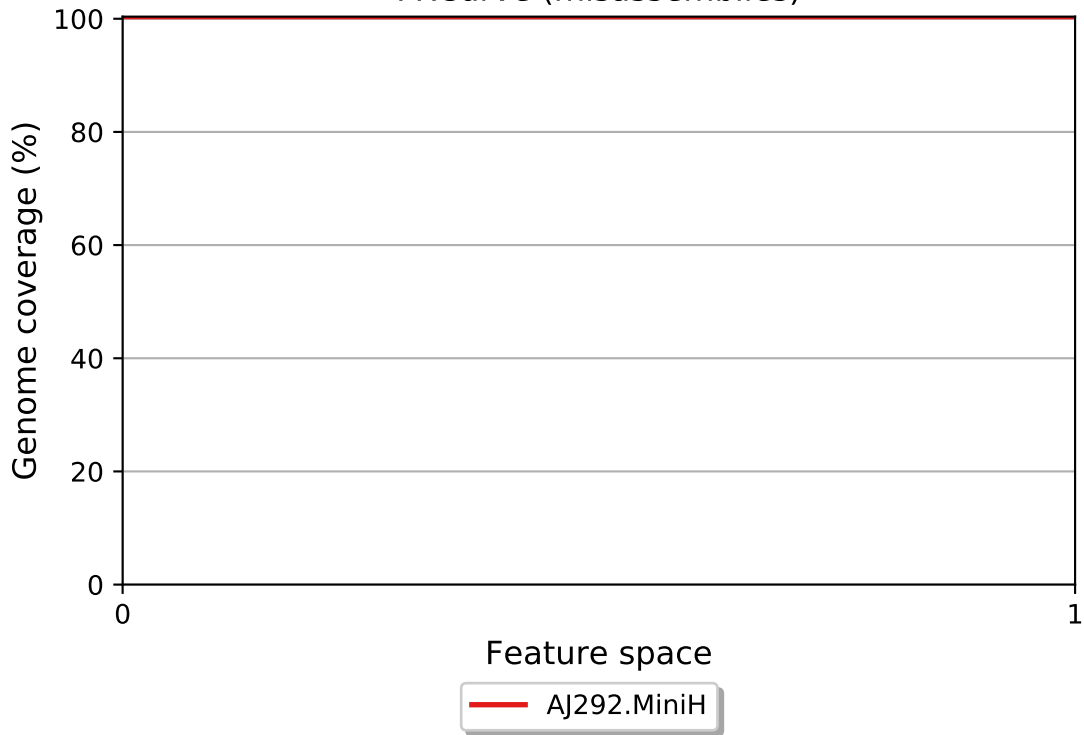
AJ292.MiniH



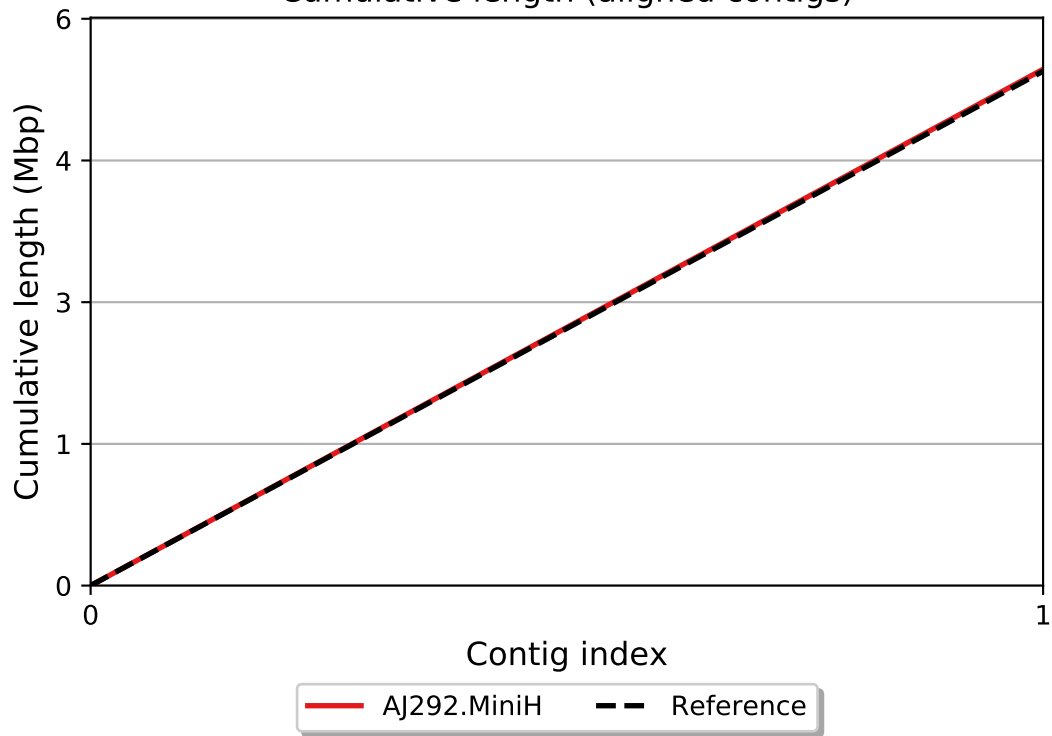
## Misassemblies



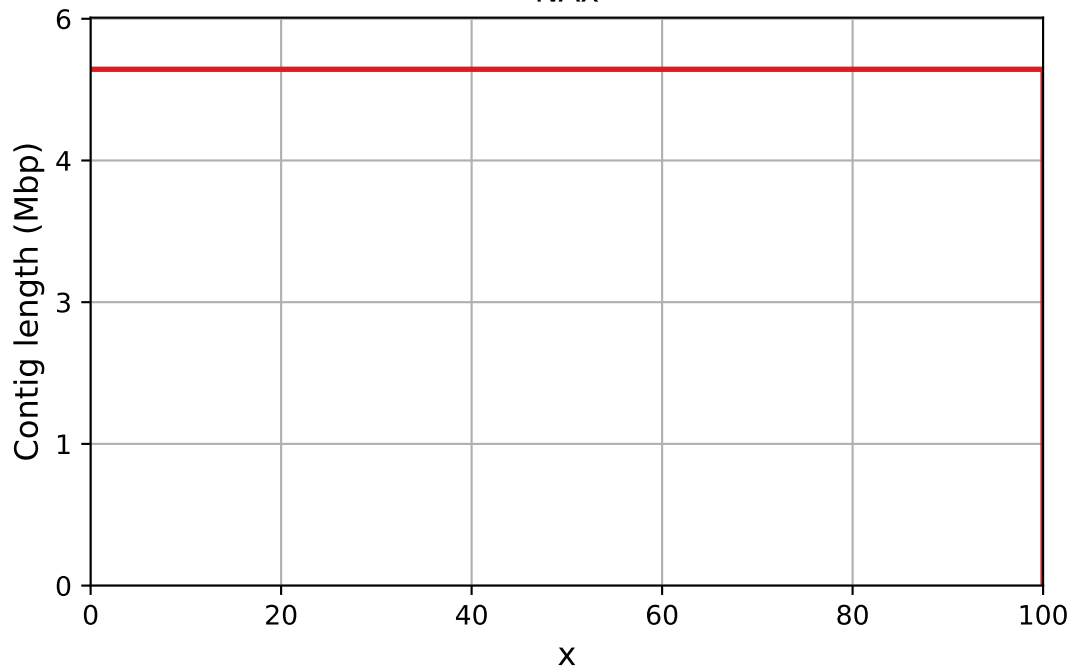
FRCurve (misassemblies)



Cumulative length (aligned contigs)

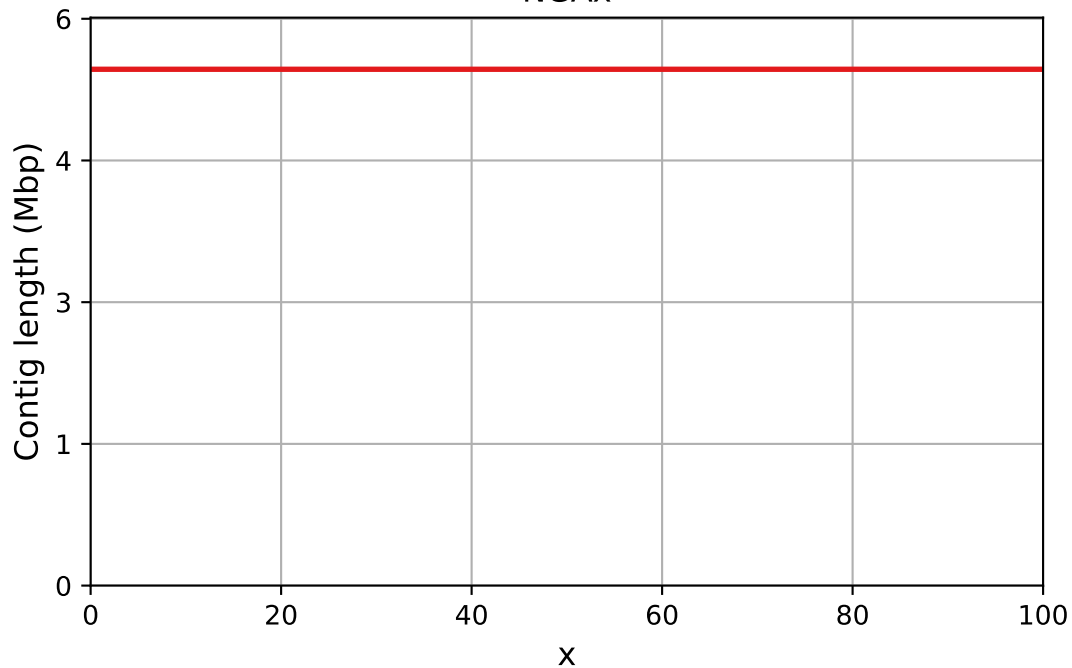


NAx



Aj292.MiniH

NGAx



Aj292.MiniH