

# Report

	AJ218.SGAH
# contigs (>= 0 bp)	2286
# contigs (>= 1000 bp)	1111
# contigs (>= 5000 bp)	386
# contigs (>= 10000 bp)	119
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5874435
Total length (>= 1000 bp)	5477962
Total length (>= 5000 bp)	3592263
Total length (>= 10000 bp)	1695658
Total length (>= 25000 bp)	149629
Total length (>= 50000 bp)	0
# contigs	1307
Largest contig	33112
Total length	5619230
Reference length	5465981
GC (%)	57.28
Reference GC (%)	57.29
N50	6970
NG50	7143
N75	3735
NG75	3981
L50	254
LG50	243
L75	531
LG75	501
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	46 + 5 part
Unaligned length	182048
Genome fraction (%)	97.384
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.41
# indels per 100 kbp	0.28
Largest alignment	33112
Total aligned length	5437178
NA50	6581
NGA50	6968
NA75	3400
NGA75	3707
LA50	258
LGA50	246
LA75	551
LGA75	518

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.SGAH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	22
# indels	15
# indels ( $\leq 5$ bp)	15
# indels ( $> 5$ bp)	0
Indels length	15

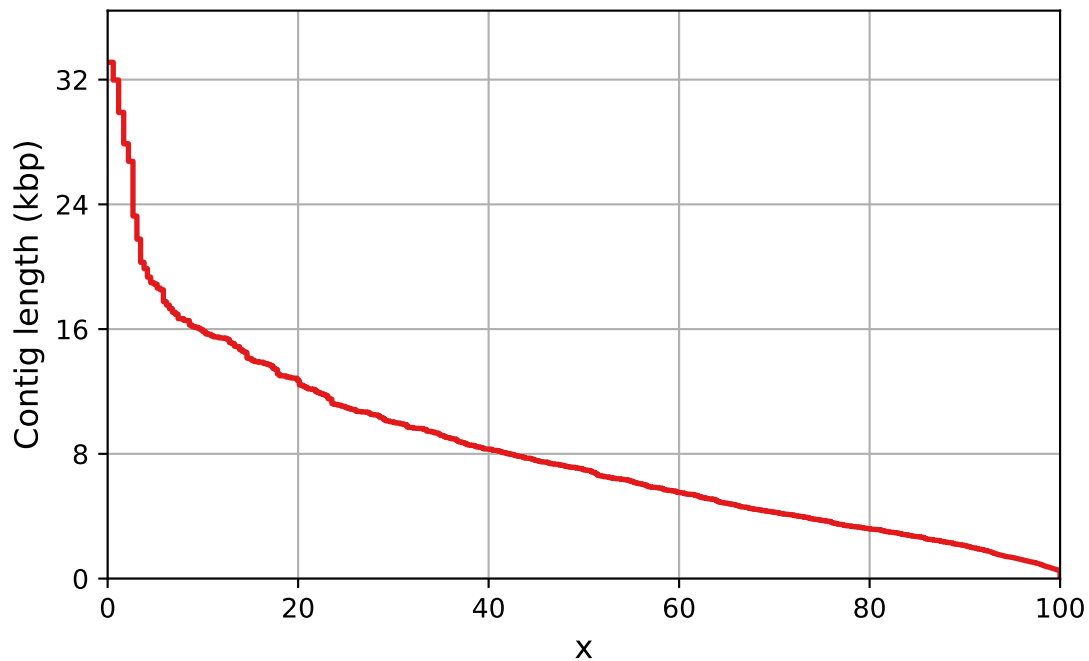
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ218.SGAH
# fully unaligned contigs	46
Fully unaligned length	168755
# partially unaligned contigs	5
Partially unaligned length	13293
# N's	0

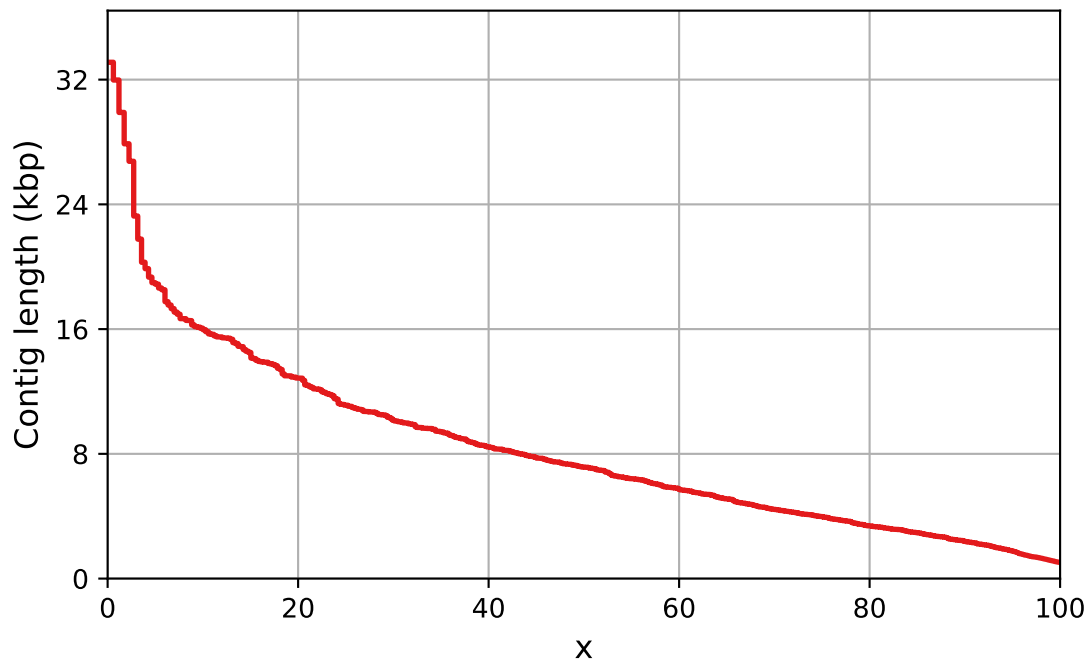
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



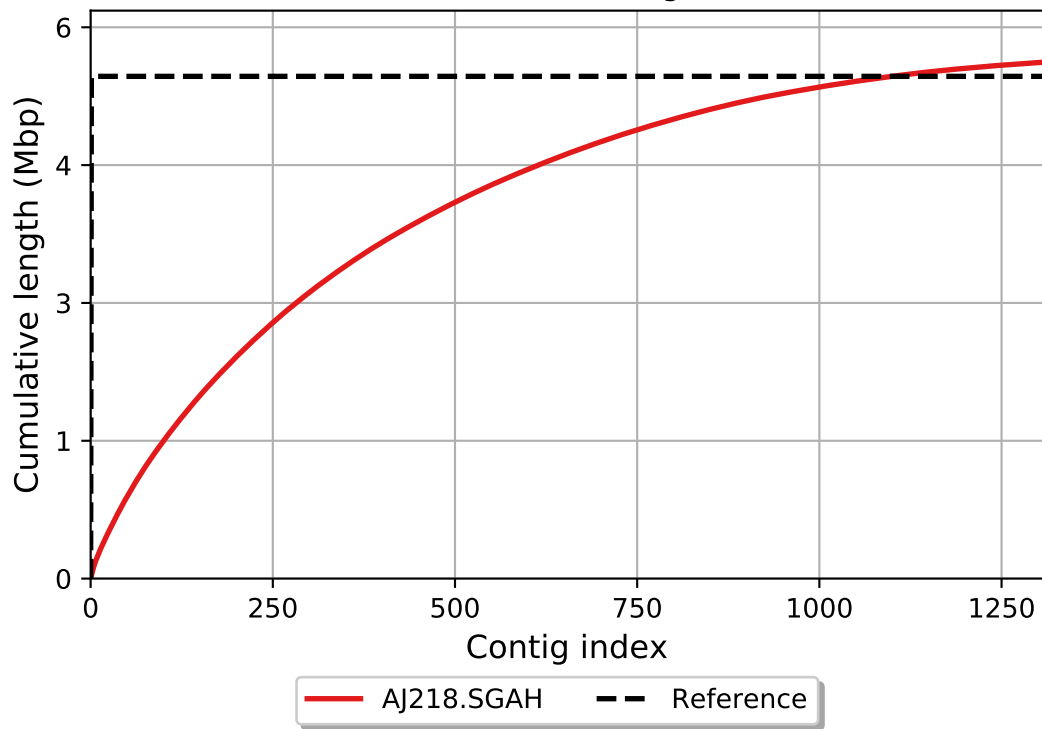
A218.SGAH

NGx

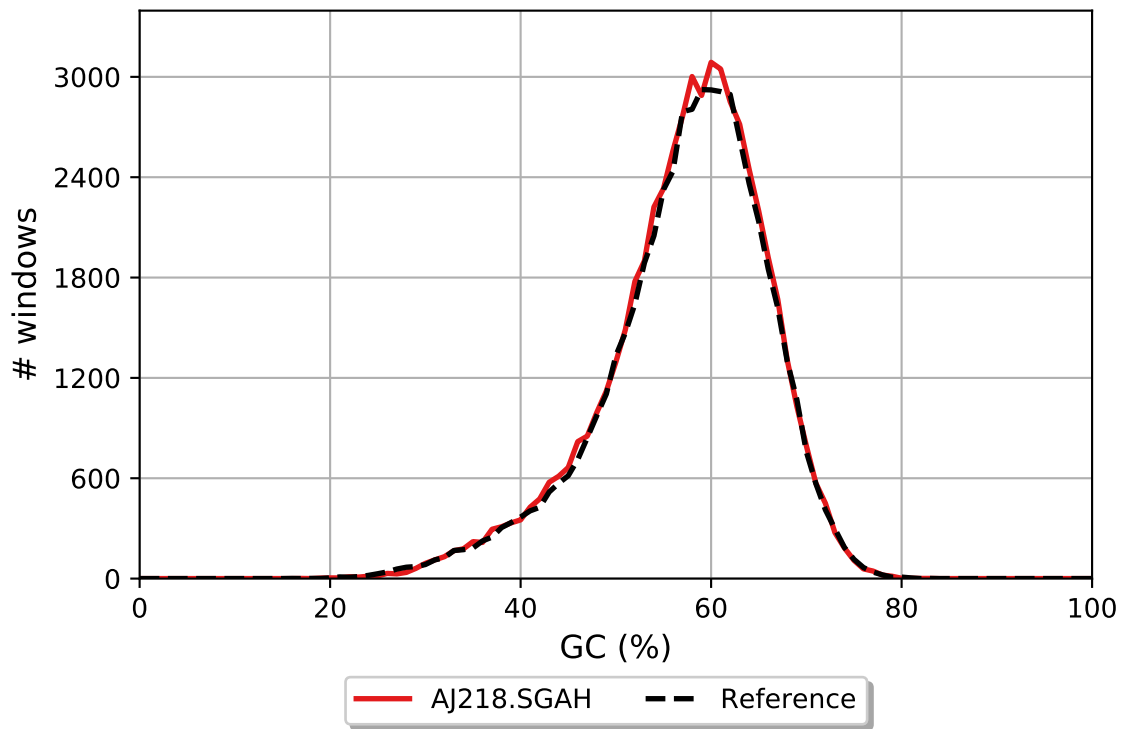


AJ218.SGAH

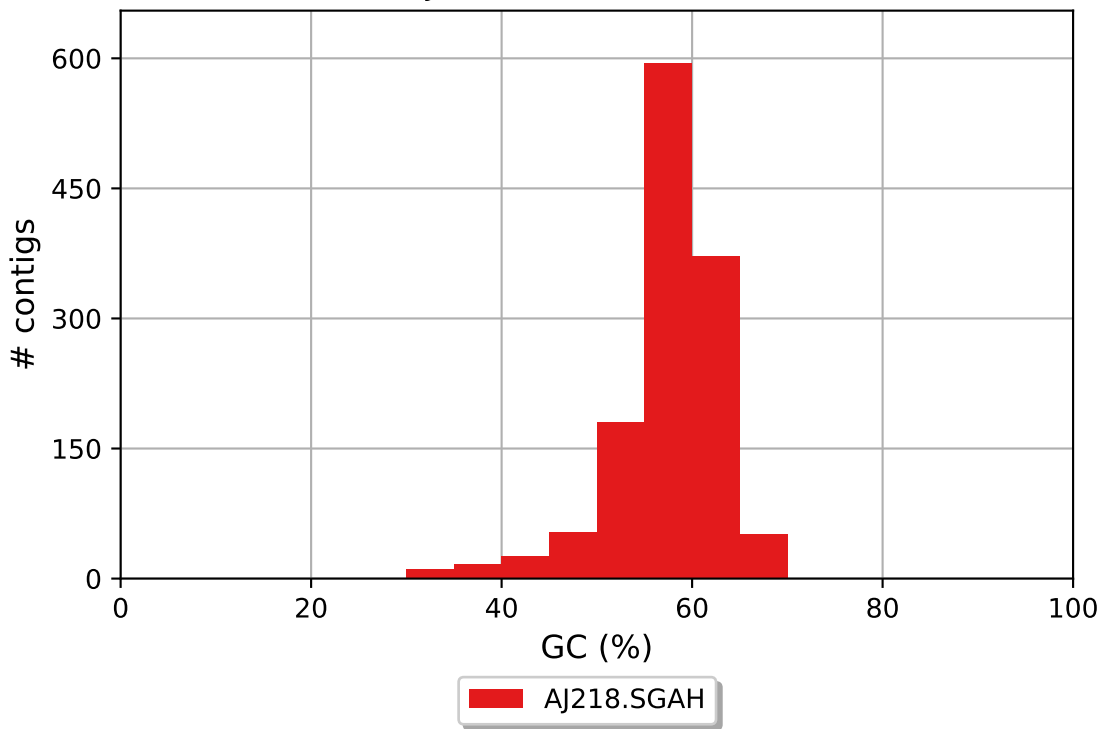
Cumulative length



## GC content



AJ218.SGAH GC content

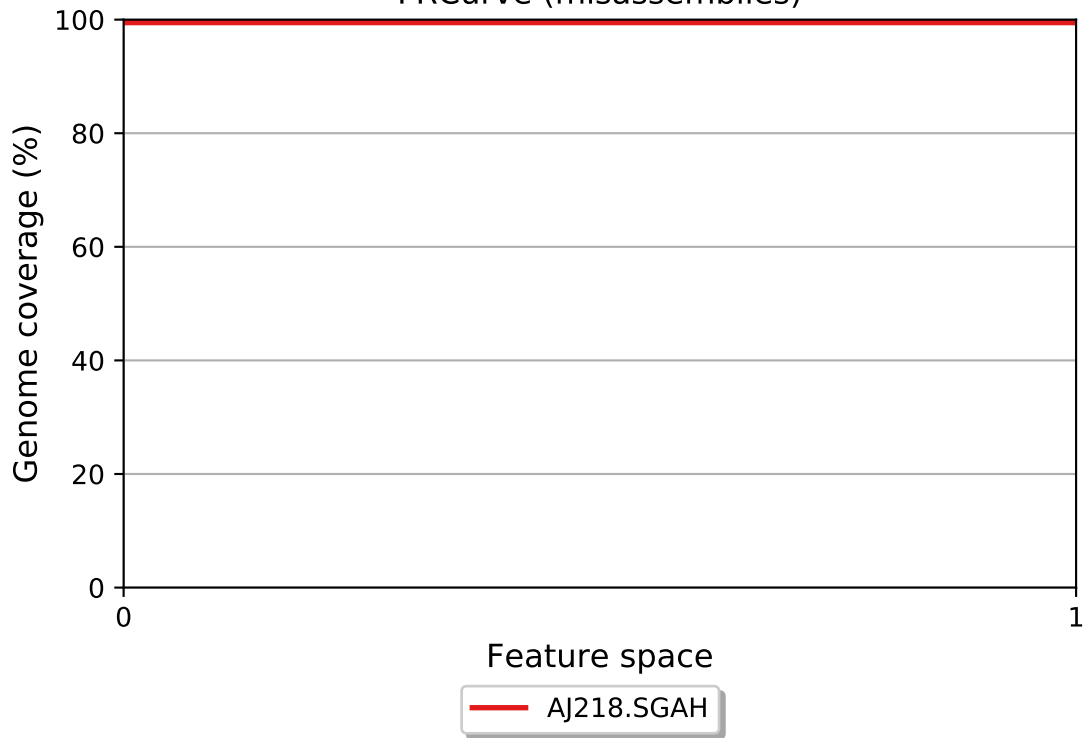




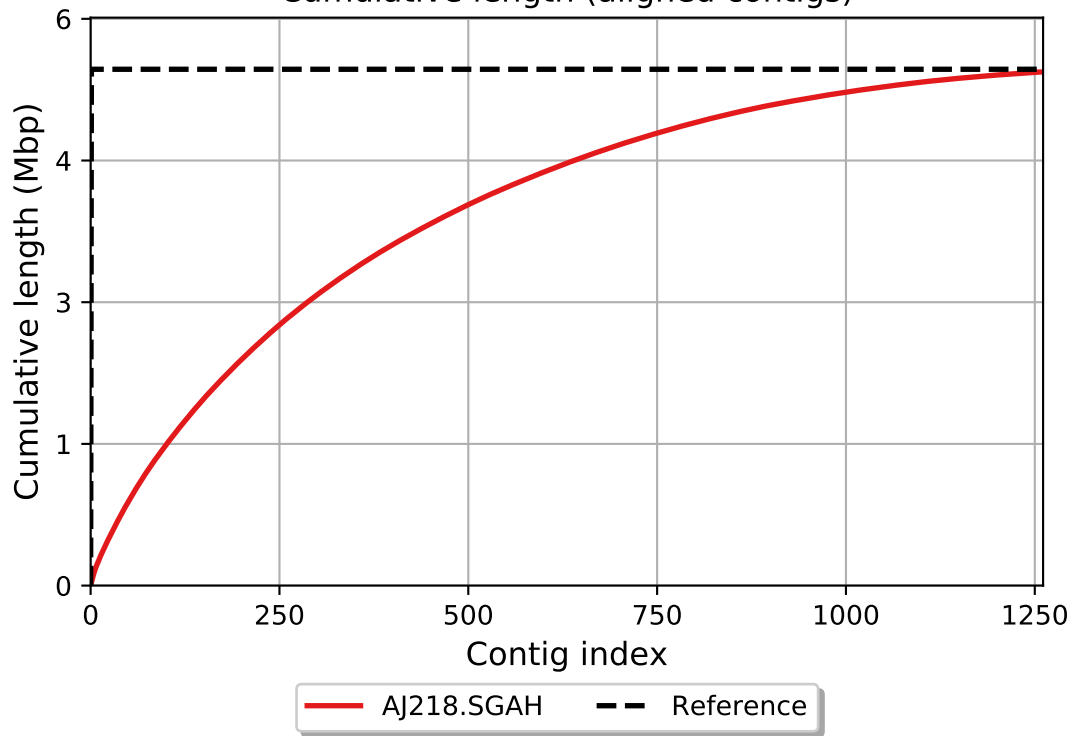
## Misassemblies



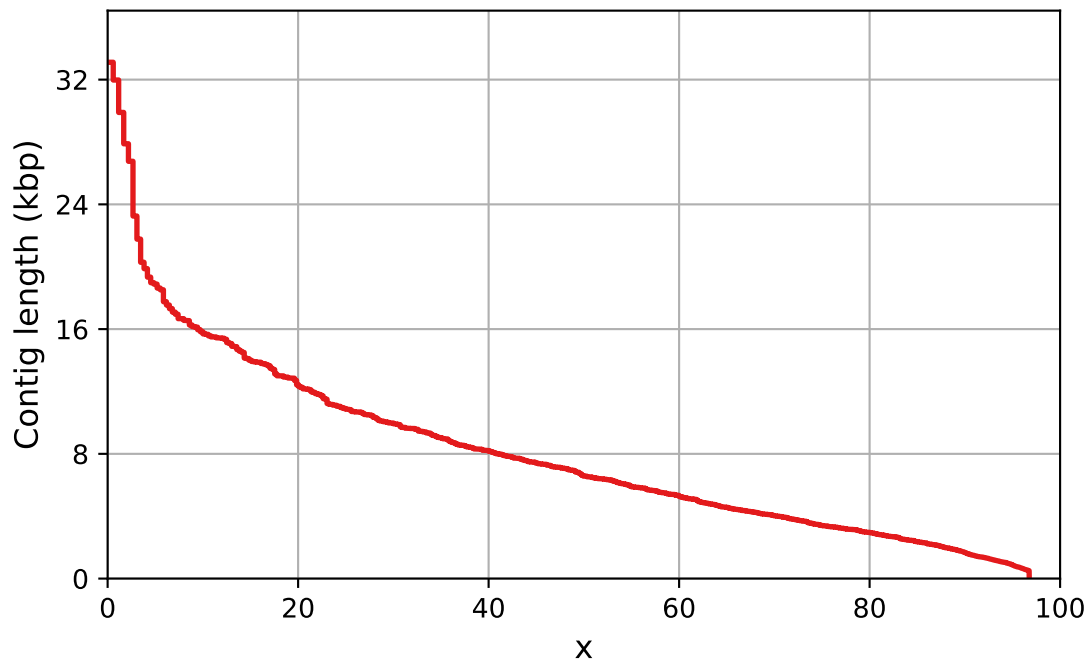
FRCurve (misassemblies)



Cumulative length (aligned contigs)

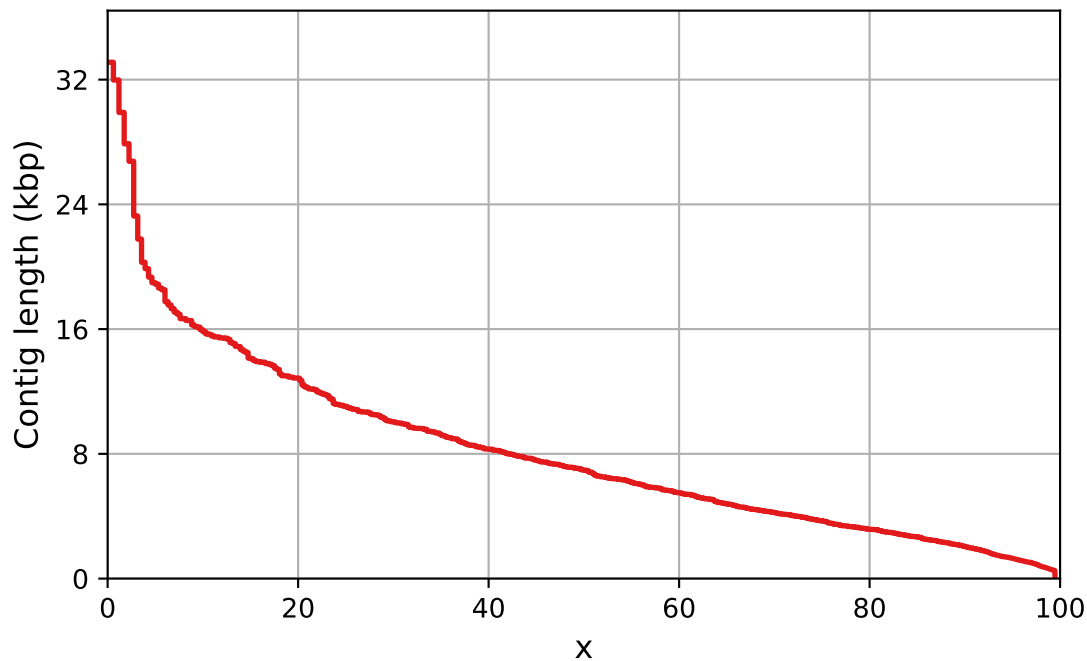


NAx



AJ218.SGAH

# NGAx



AJ218.SGAH