

# Report

	AJ218.SGAL
# contigs (>= 0 bp)	1822
# contigs (>= 1000 bp)	1002
# contigs (>= 5000 bp)	392
# contigs (>= 10000 bp)	139
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5709622
Total length (>= 1000 bp)	5411469
Total length (>= 5000 bp)	3820318
Total length (>= 10000 bp)	2025176
Total length (>= 25000 bp)	137719
Total length (>= 50000 bp)	0
# contigs	1172
Largest contig	48400
Total length	5534836
Reference length	5465981
GC (%)	57.41
Reference GC (%)	57.29
N50	7641
NG50	7778
N75	4227
NG75	4365
L50	224
LG50	219
L75	464
LG75	452
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	37 + 5 part
Unaligned length	179045
Genome fraction (%)	96.726
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.76
# indels per 100 kbp	0.21
Largest alignment	48400
Total aligned length	5355772
NA50	7326
NGA50	7452
NA75	3885
NGA75	4011
LA50	228
LGA50	224
LA75	483
LGA75	470

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.SGAL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	40
# indels	11
# indels ( $\leq 5$ bp)	11
# indels ( $> 5$ bp)	0
Indels length	11

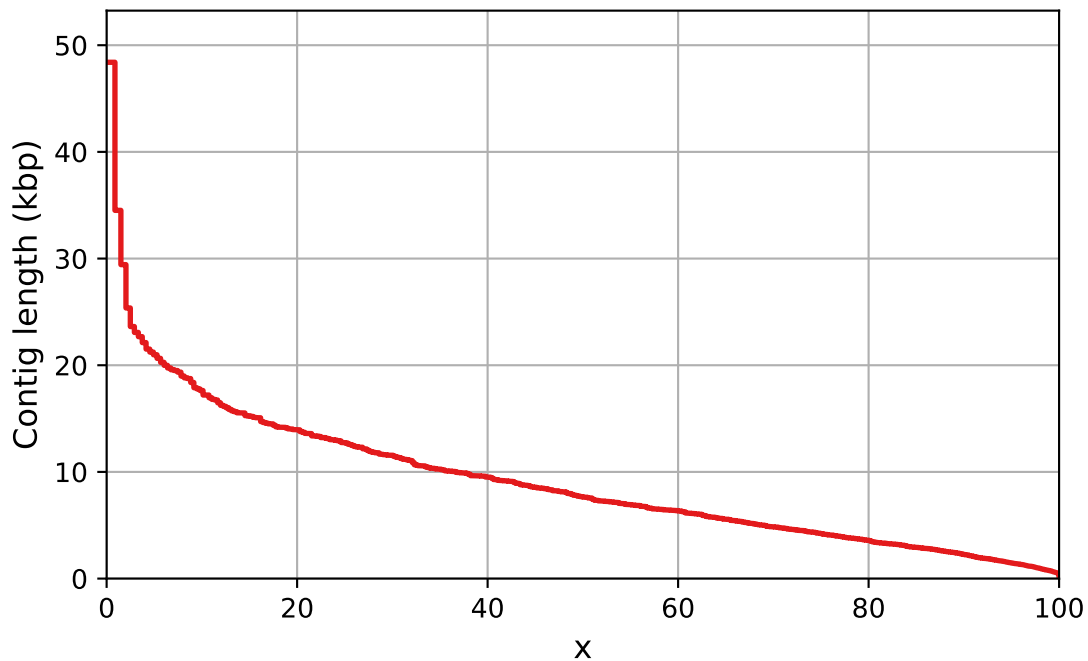
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ218.SGAL
# fully unaligned contigs	37
Fully unaligned length	164529
# partially unaligned contigs	5
Partially unaligned length	14516
# N's	0

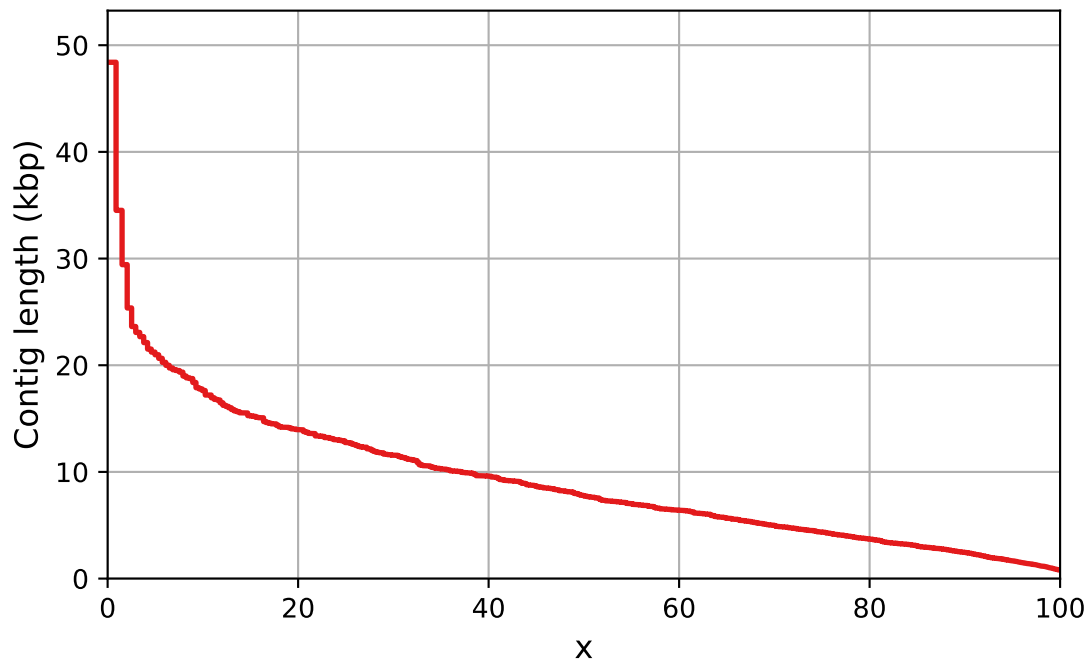
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



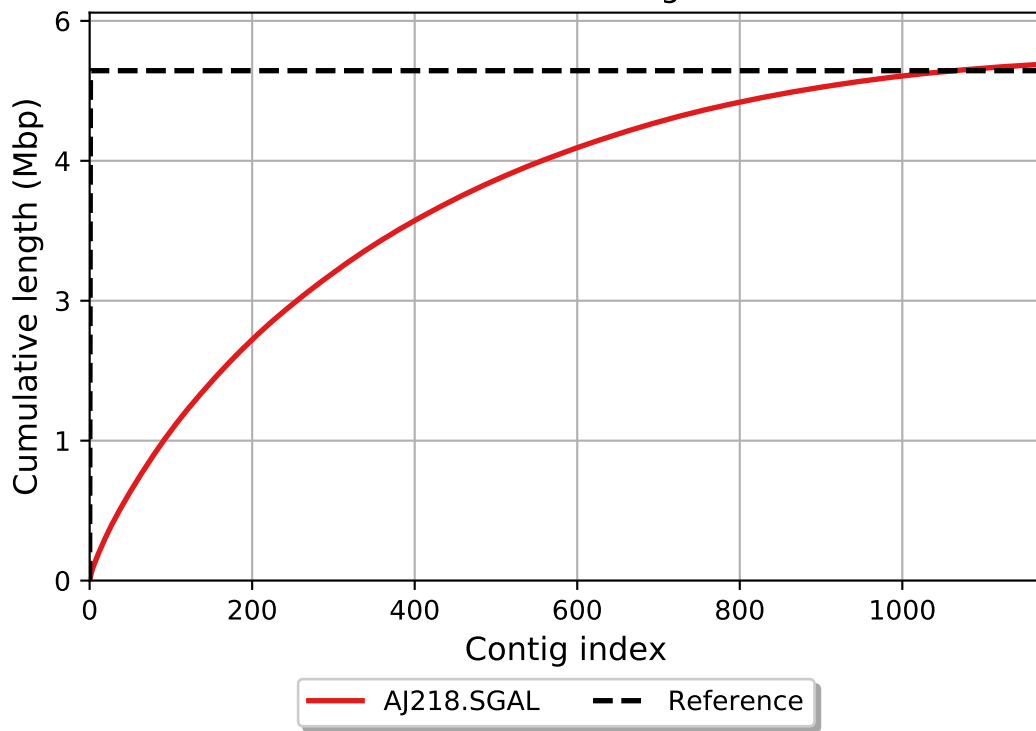
AJ218.SGAL

NGx

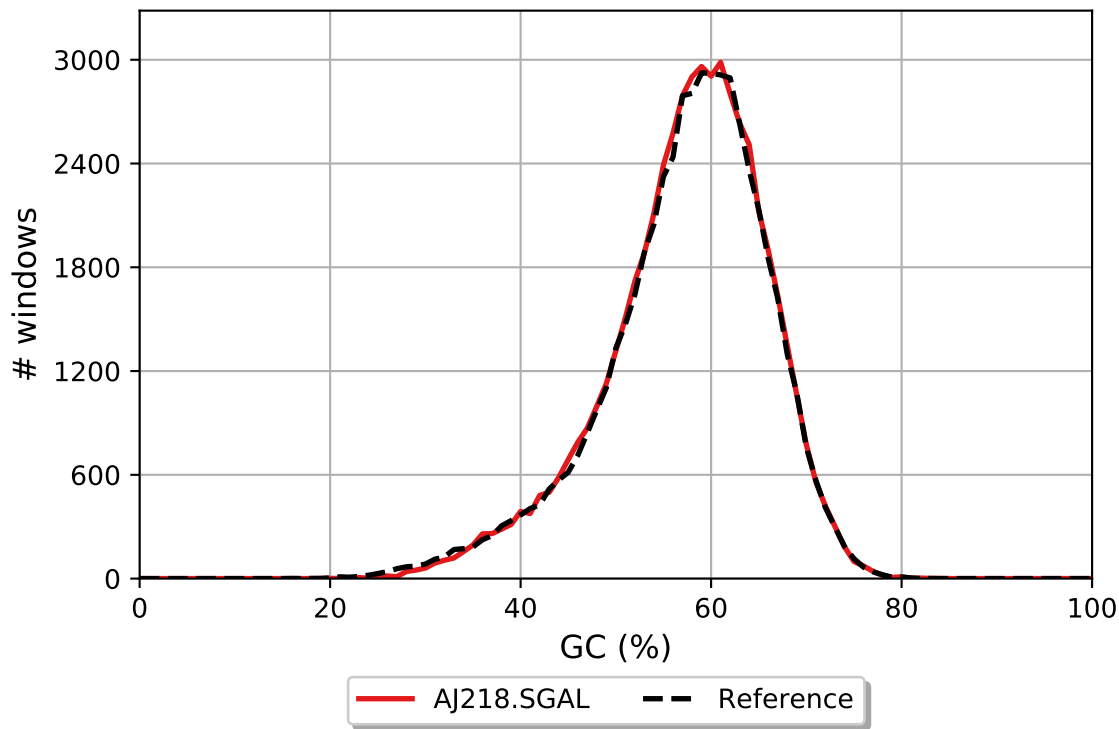


AJ218.SGAL

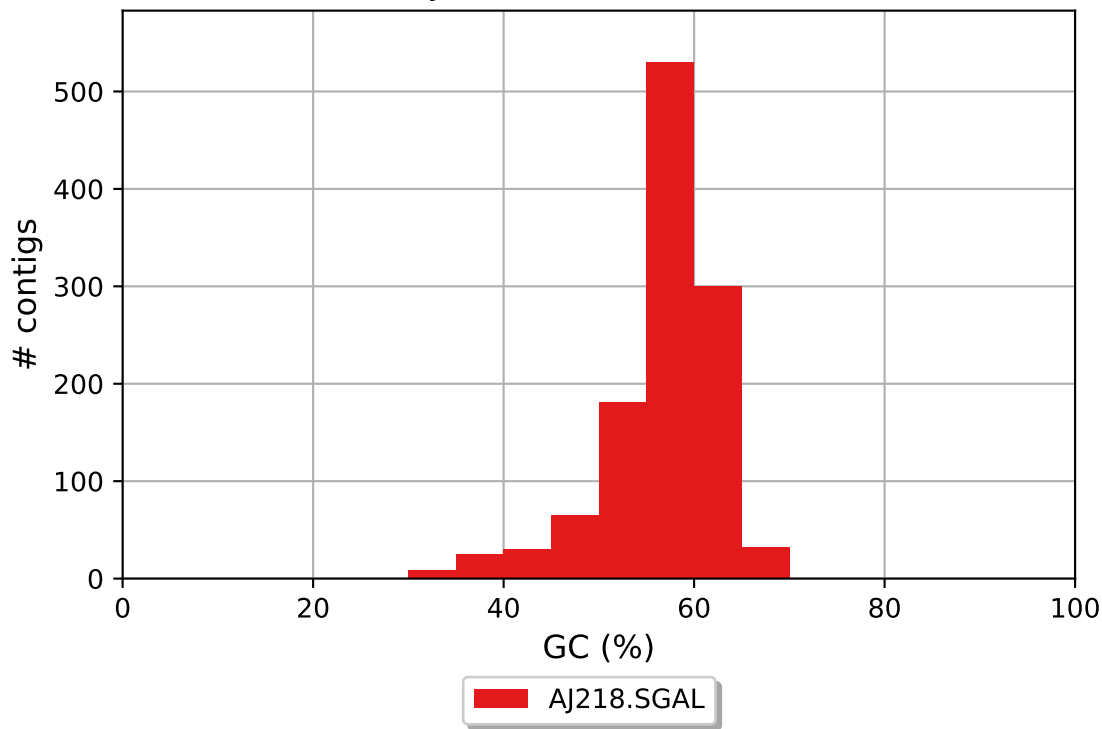
Cumulative length



## GC content



AJ218.SGAL GC content

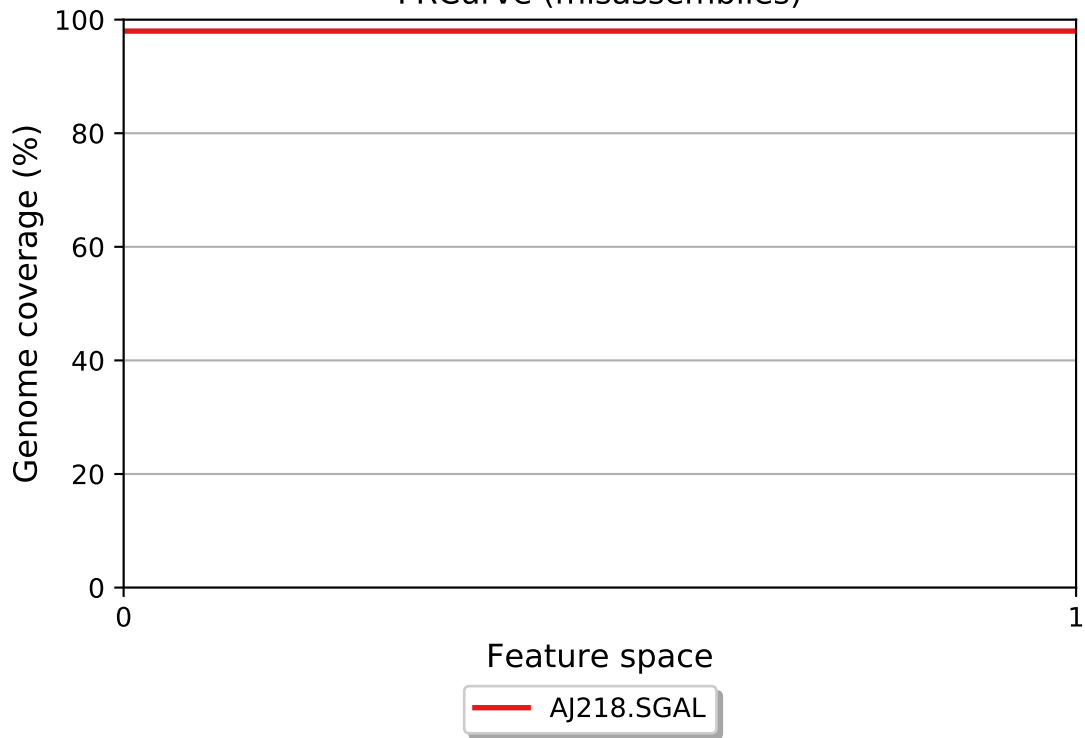


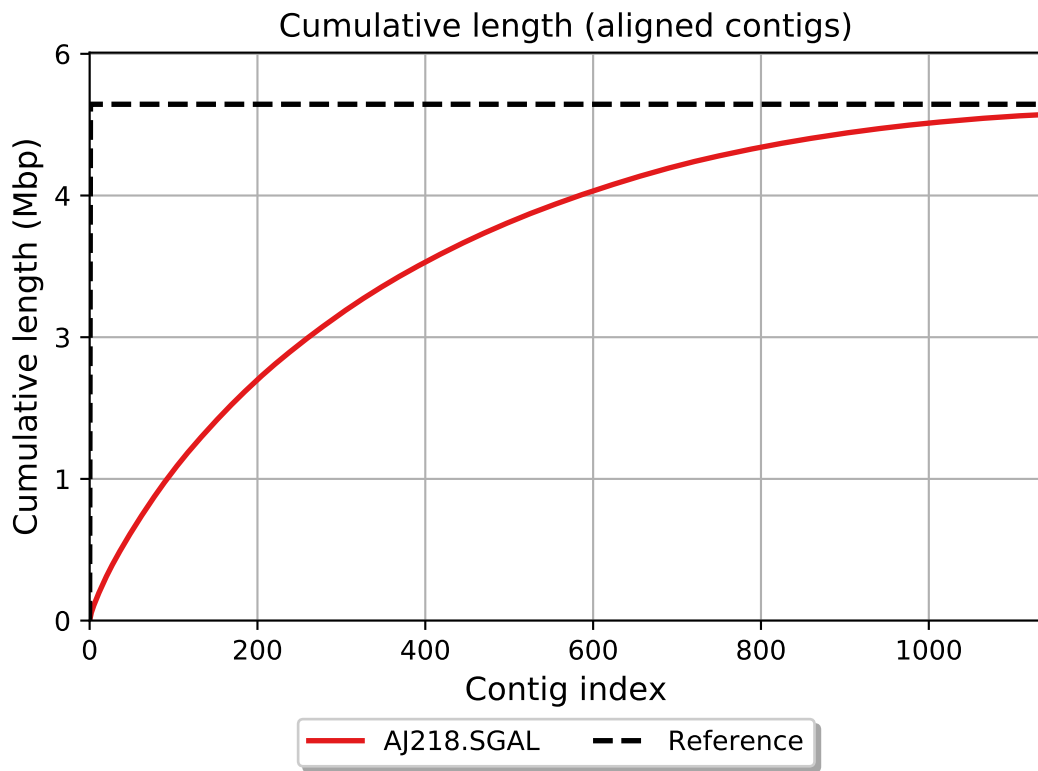


## Misassemblies

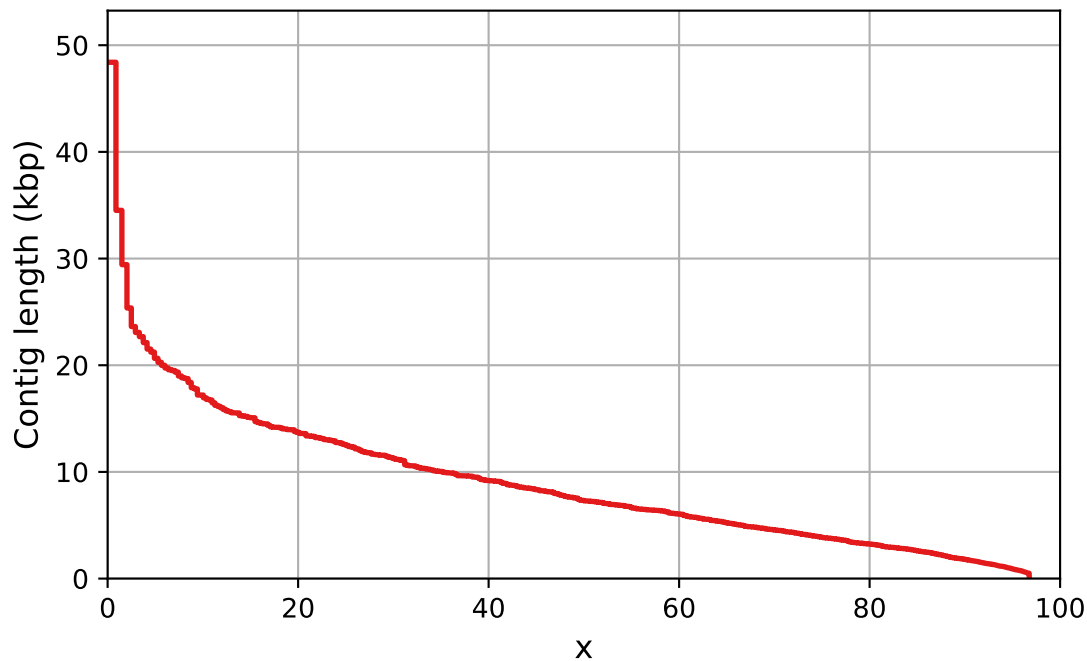


FRCurve (misassemblies)



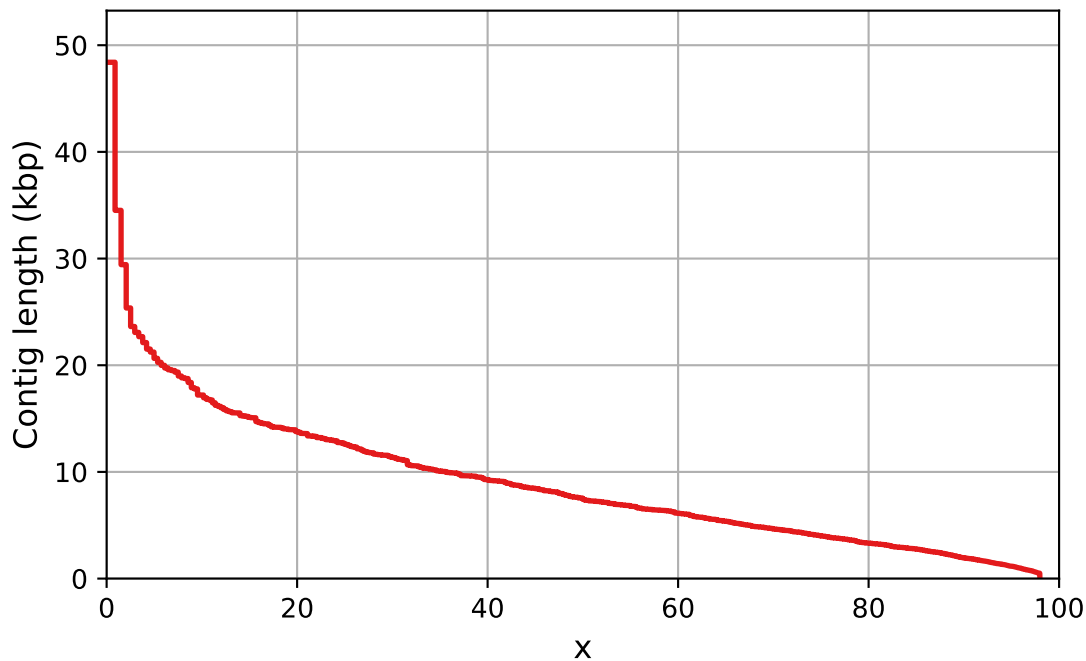


NAx



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# NGAx



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