

# Report

	AJ055.SGAL
# contigs (>= 0 bp)	1691
# contigs (>= 1000 bp)	1081
# contigs (>= 5000 bp)	393
# contigs (>= 10000 bp)	120
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5713717
Total length (>= 1000 bp)	5479203
Total length (>= 5000 bp)	3690774
Total length (>= 10000 bp)	1752888
Total length (>= 25000 bp)	86477
Total length (>= 50000 bp)	0
# contigs	1228
Largest contig	33813
Total length	5585990
Reference length	5504133
GC (%)	57.50
Reference GC (%)	57.38
N50	7111
NG50	7167
N75	3969
NG75	4097
L50	243
LG50	237
L75	505
LG75	490
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	44 + 1 part
Unaligned length	158256
Genome fraction (%)	97.119
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.24
# indels per 100 kbp	0.47
Largest alignment	33813
Total aligned length	5427729
NA50	6988
NGA50	7092
NA75	3760
NGA75	3879
LA50	247
LGA50	241
LA75	519
LGA75	503

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

	AJ055.SGAL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	13
# indels	25
# indels ( $\leq 5$ bp)	25
# indels ( $> 5$ bp)	0
Indels length	25

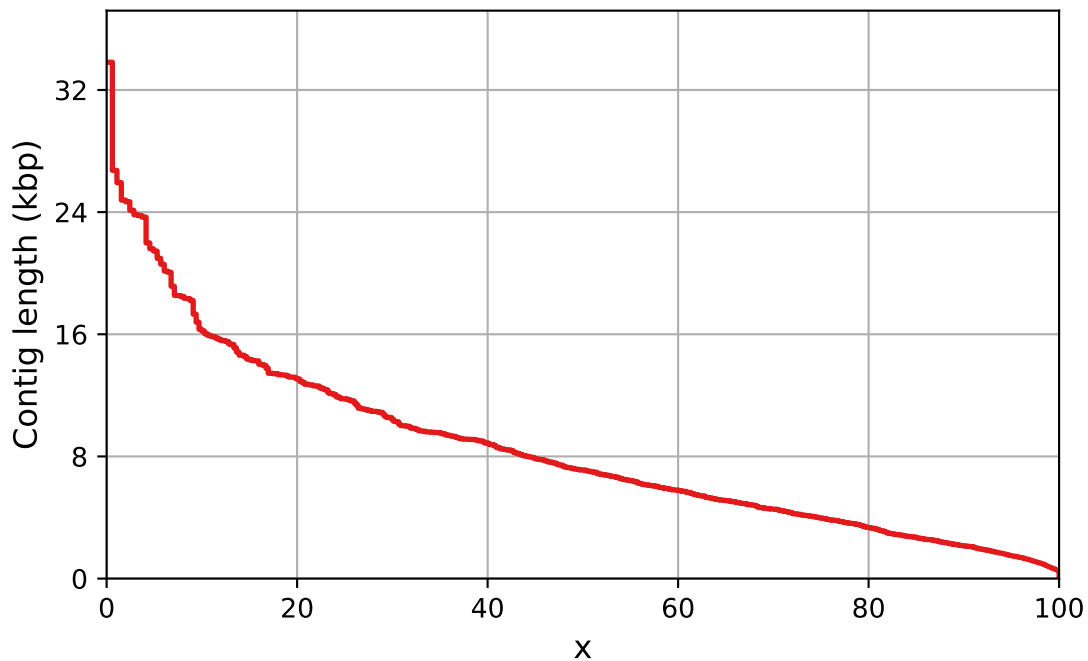
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ055.SGAL
# fully unaligned contigs	44
Fully unaligned length	157459
# partially unaligned contigs	1
Partially unaligned length	797
# N's	0

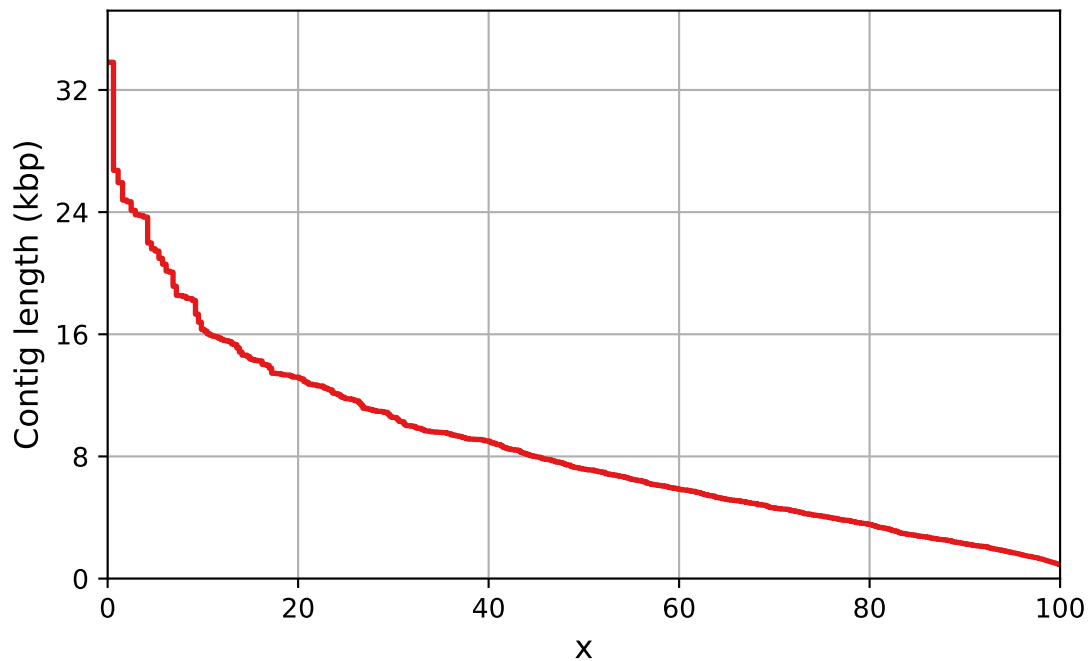
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



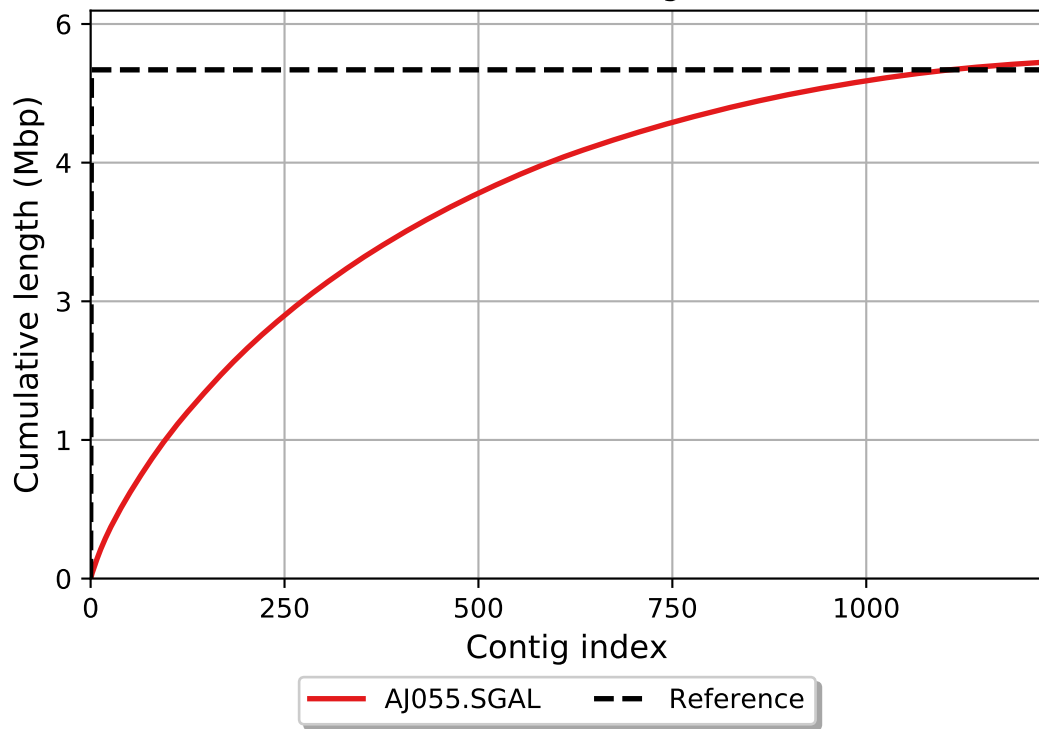
AJ055.SGAL

NGx

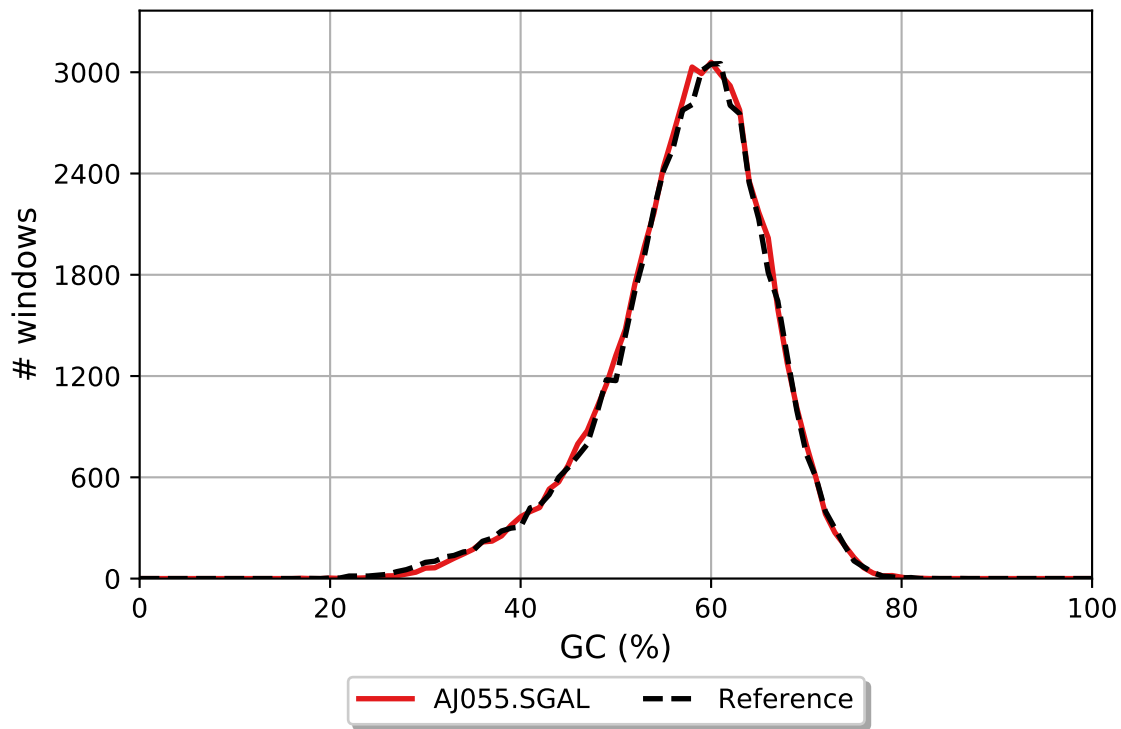


AJ055.SGAL

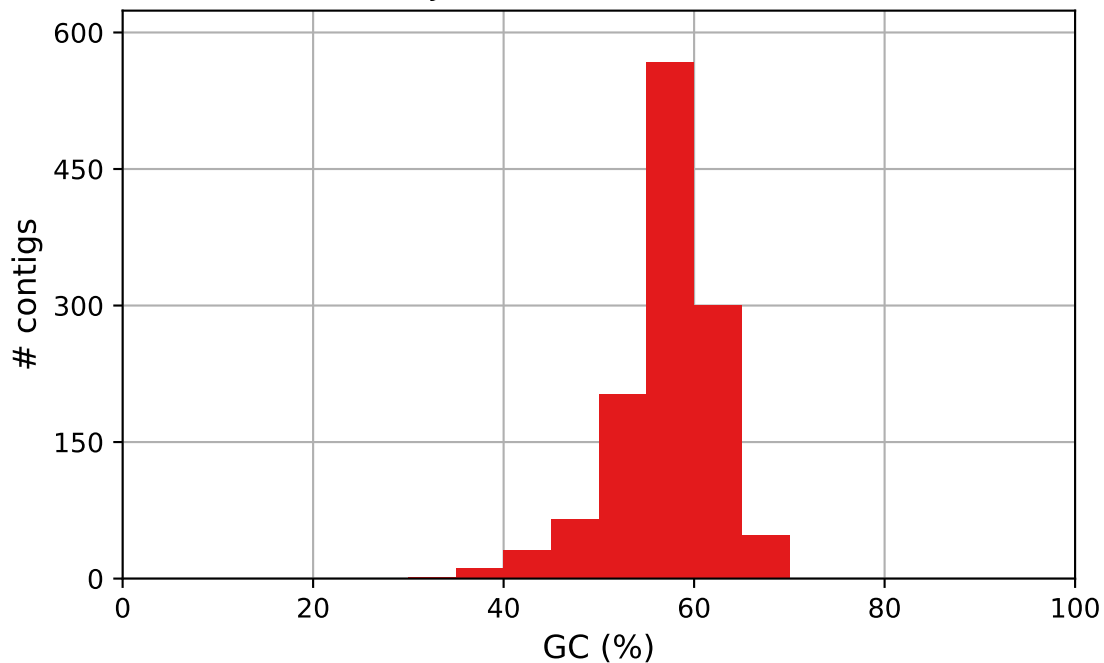
Cumulative length



## GC content



AJ055.SGAL GC content



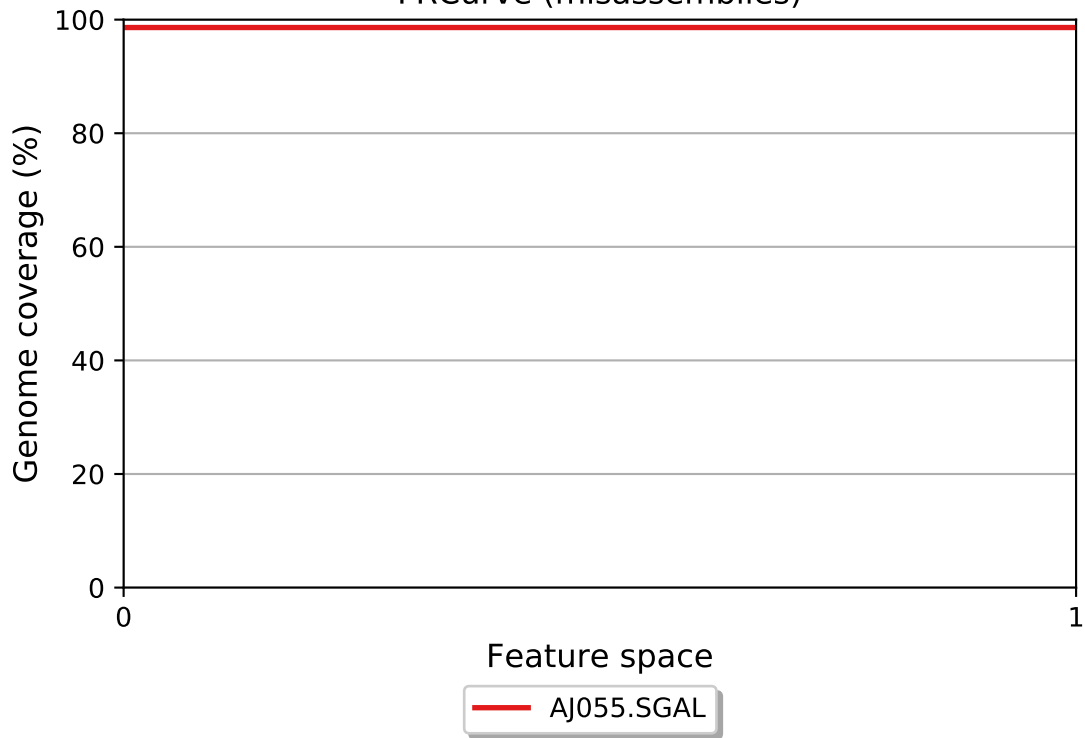
AJ055.SGAL



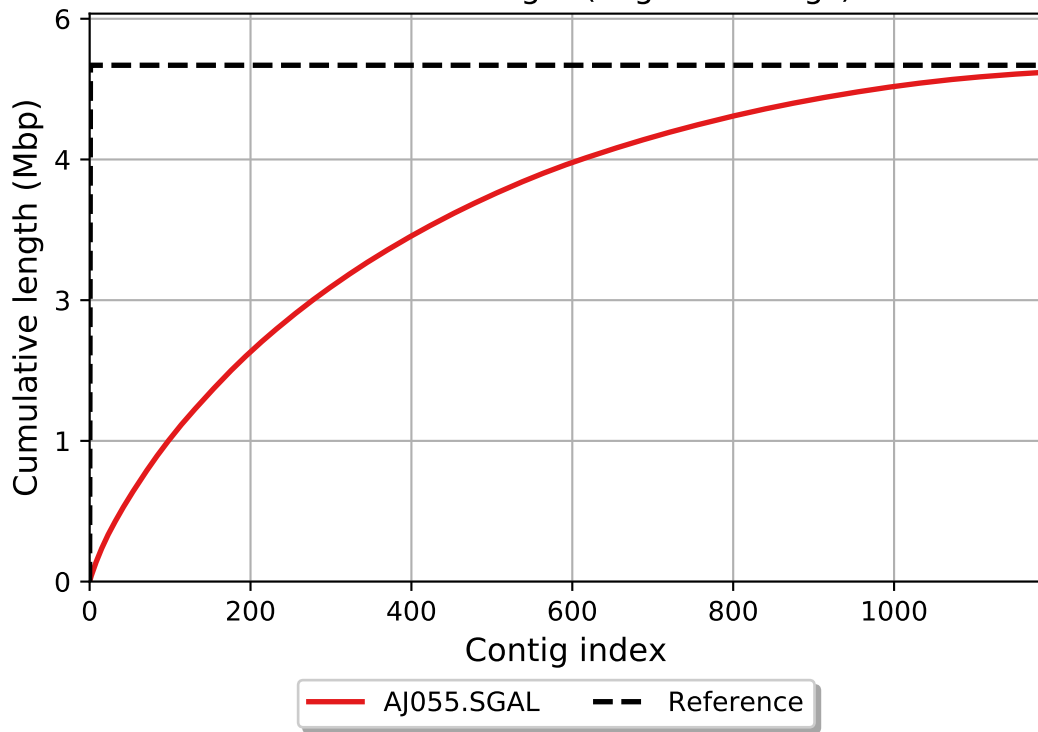
## Misassemblies



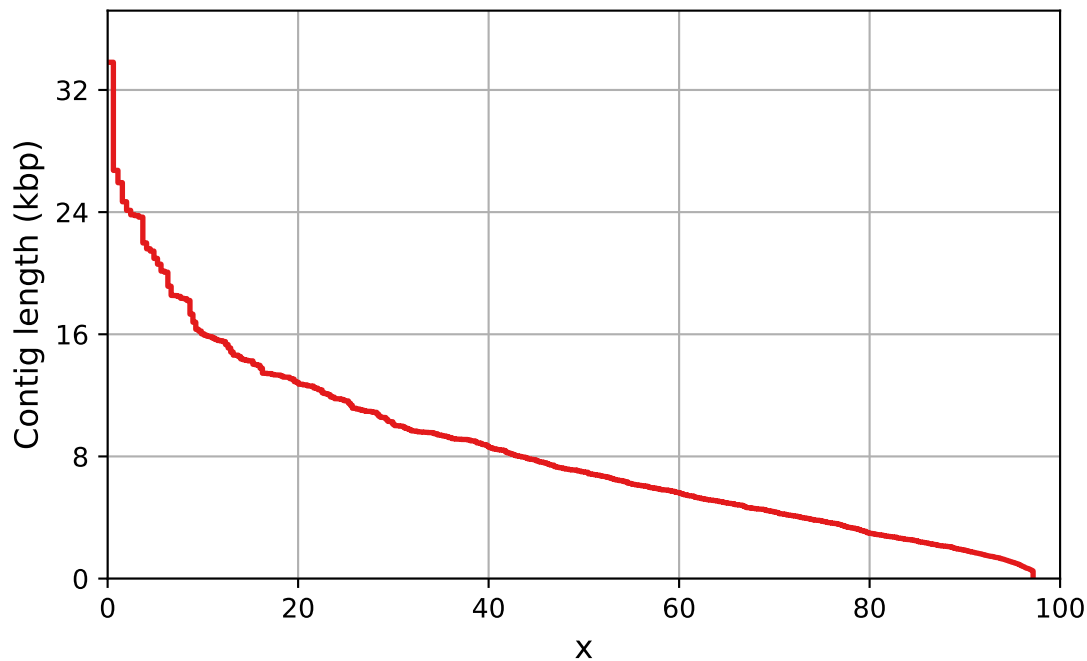
FRCurve (misassemblies)



Cumulative length (aligned contigs)

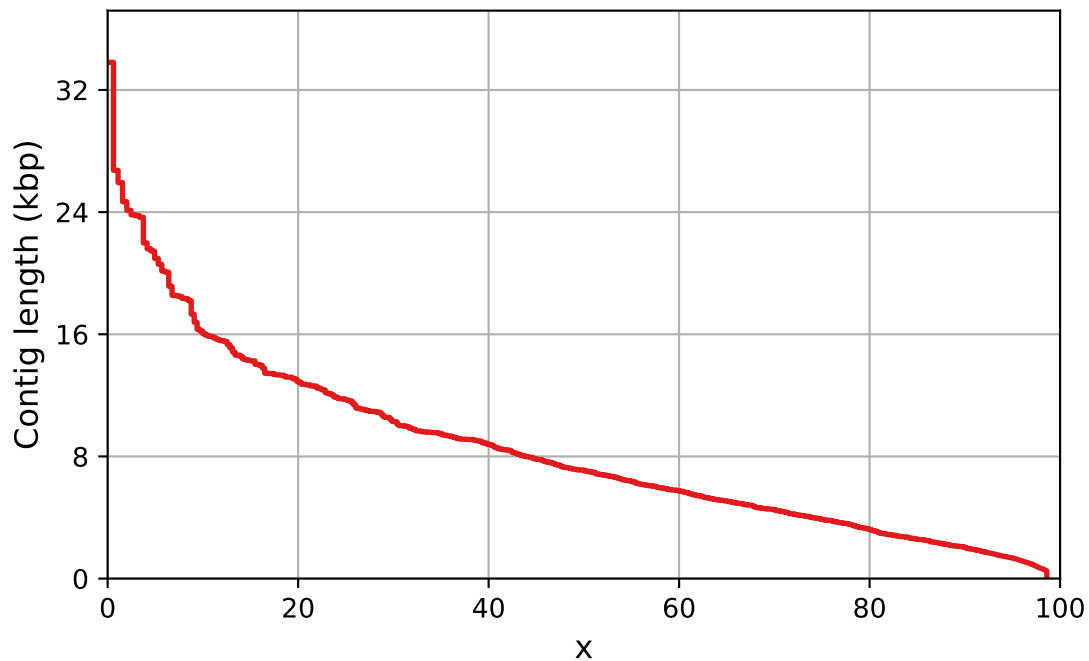


NAx



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# NGAx



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