

## Report

	AJ055.SGAH
# contigs (>= 0 bp)	2200
# contigs (>= 1000 bp)	1160
# contigs (>= 5000 bp)	384
# contigs (>= 10000 bp)	99
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5888458
Total length (>= 1000 bp)	5513808
Total length (>= 5000 bp)	3521149
Total length (>= 10000 bp)	1558725
Total length (>= 25000 bp)	322643
Total length (>= 50000 bp)	0
# contigs	1370
Largest contig	37194
Total length	5670252
Reference length	5504133
GC (%)	57.39
Reference GC (%)	57.38
N50	6394
NG50	6594
N75	3500
NG75	3728
L50	262
LG50	249
L75	559
LG75	524
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	24 + 2 part
Unaligned length	162104
Genome fraction (%)	97.757
Duplication ratio	1.024
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.06
# indels per 100 kbp	0.59
Largest alignment	37194
Total aligned length	5508142
NA50	6096
NGA50	6296
NA75	3240
NGA75	3474
LA50	272
LGA50	258
LA75	587
LGA75	550

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.SGAH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	3
# indels	32
# indels ( $\leq 5$ bp)	32
# indels ( $> 5$ bp)	0
Indels length	32

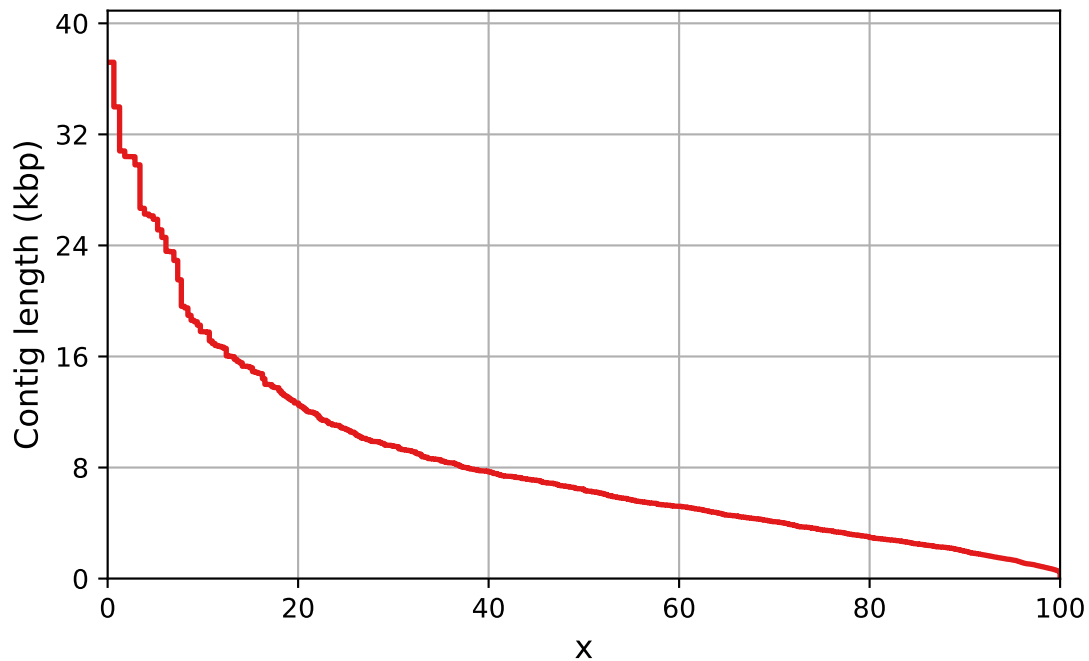
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	AJ055.SGAH
# fully unaligned contigs	24
Fully unaligned length	156137
# partially unaligned contigs	2
Partially unaligned length	5967
# N's	0

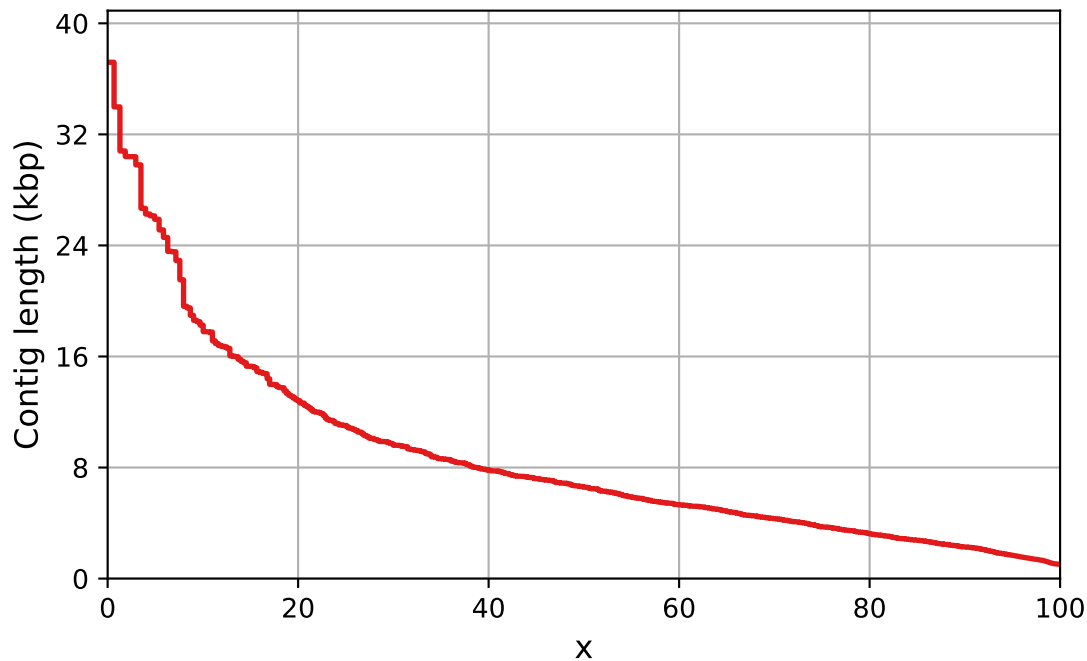
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



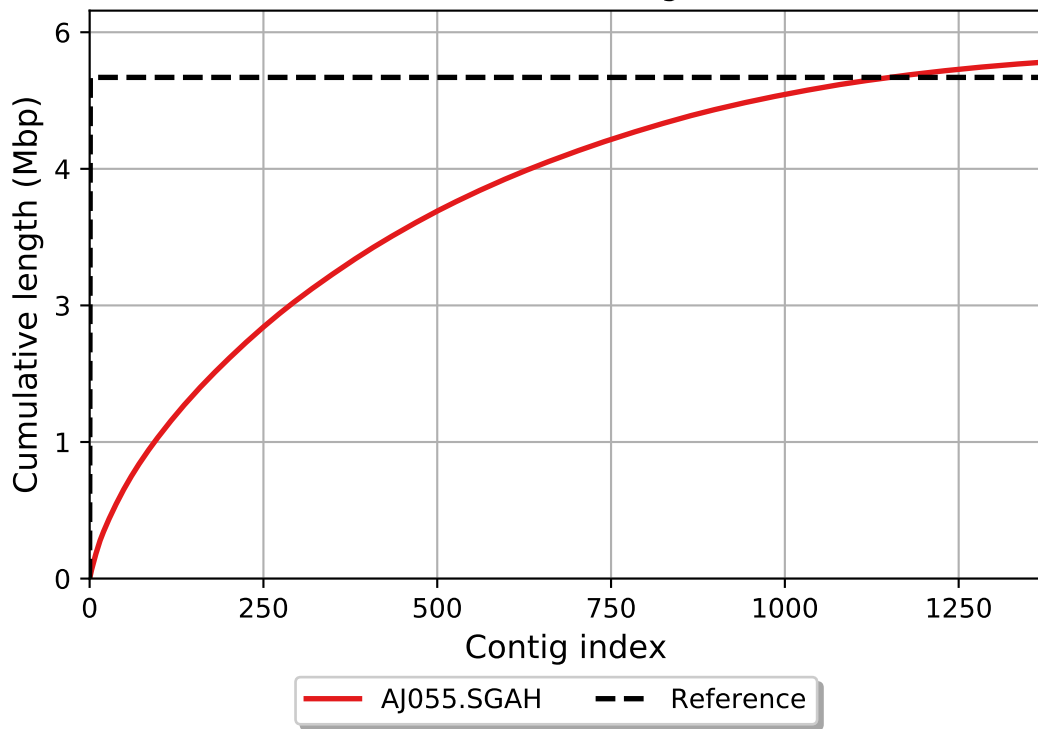
AJO55.SGAH

NGx

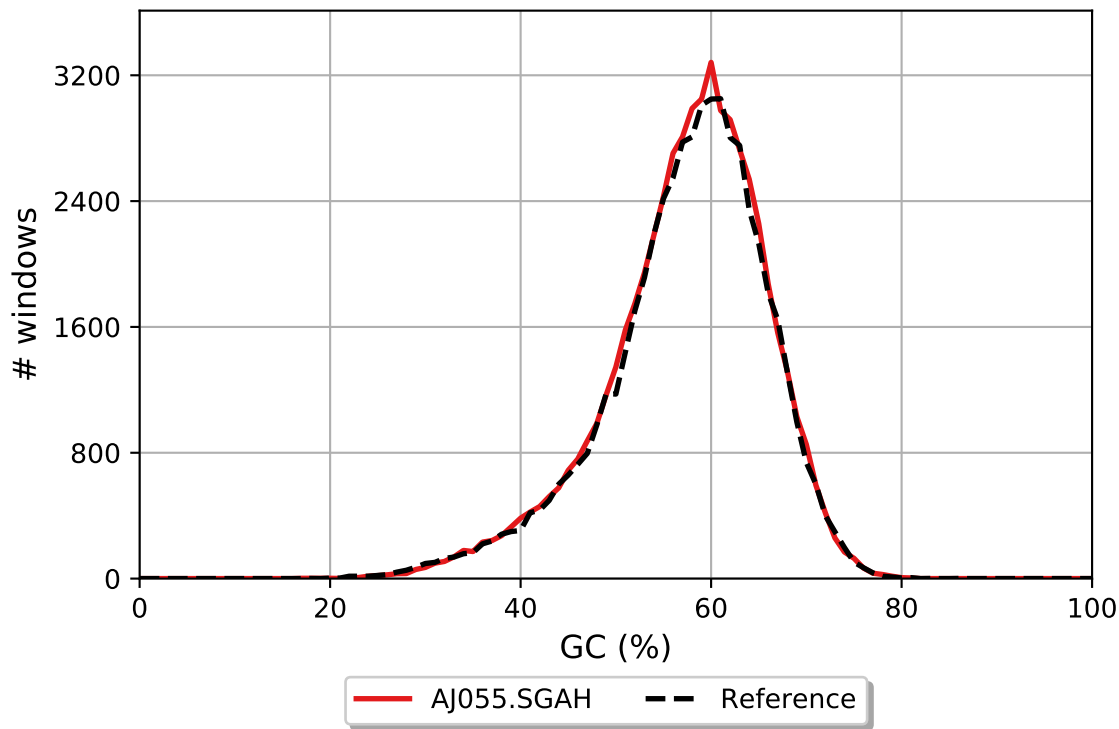


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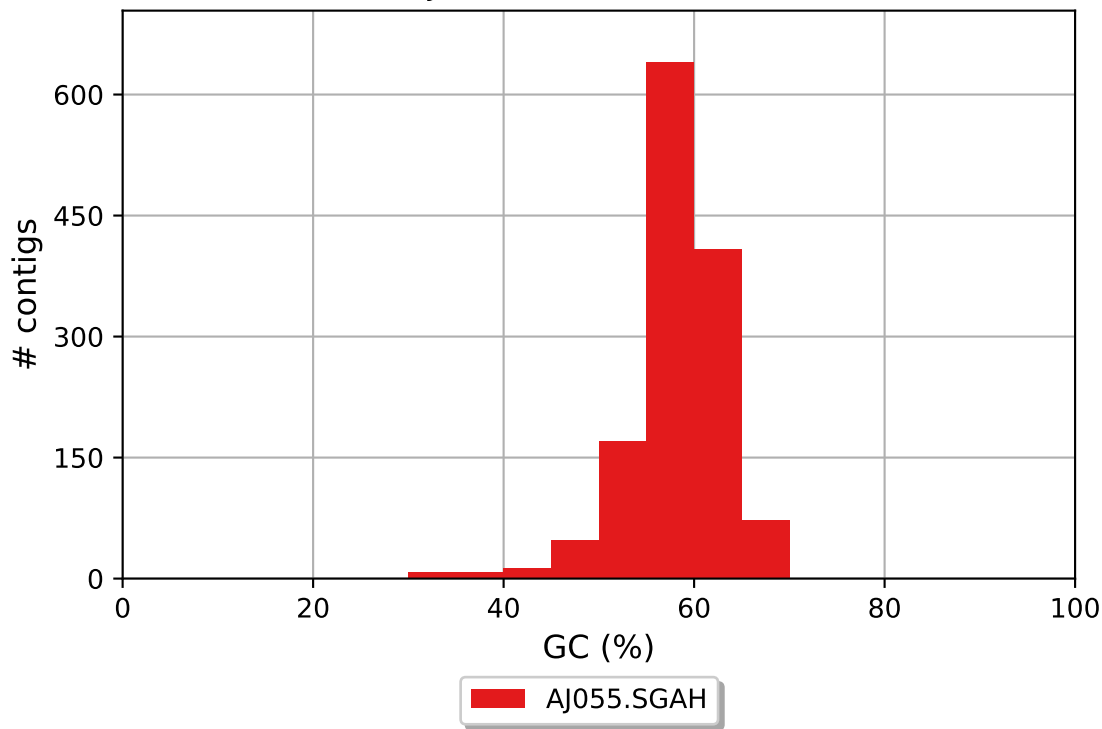
Cumulative length



## GC content



AJ055.SGAH GC content

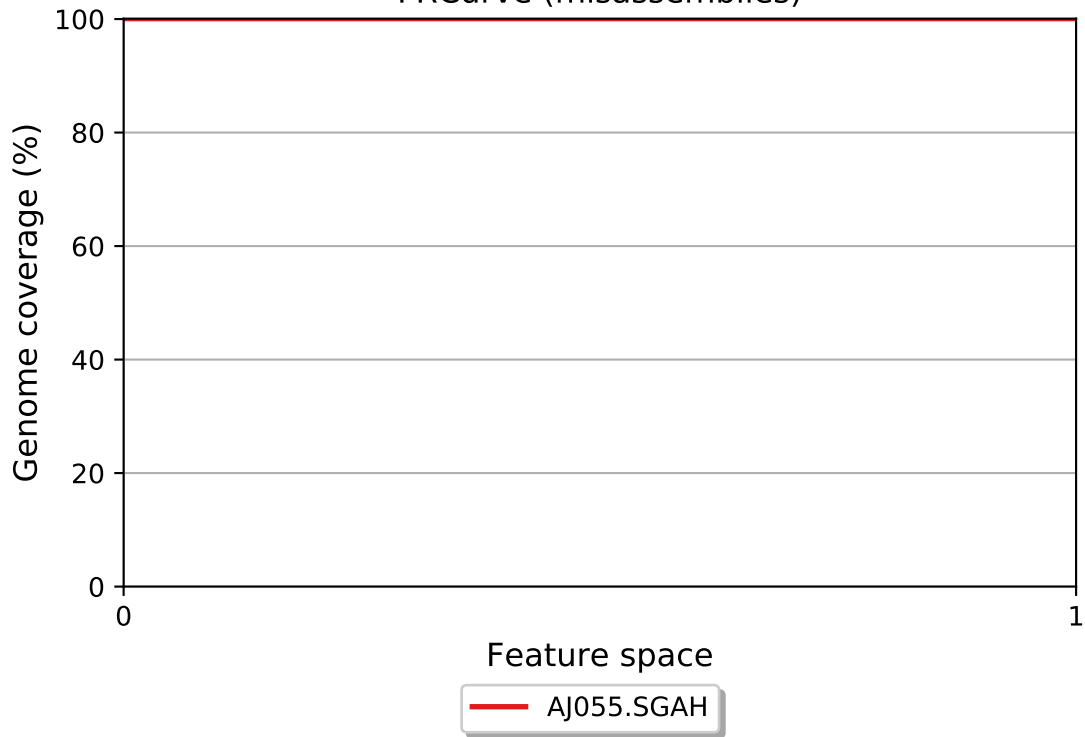




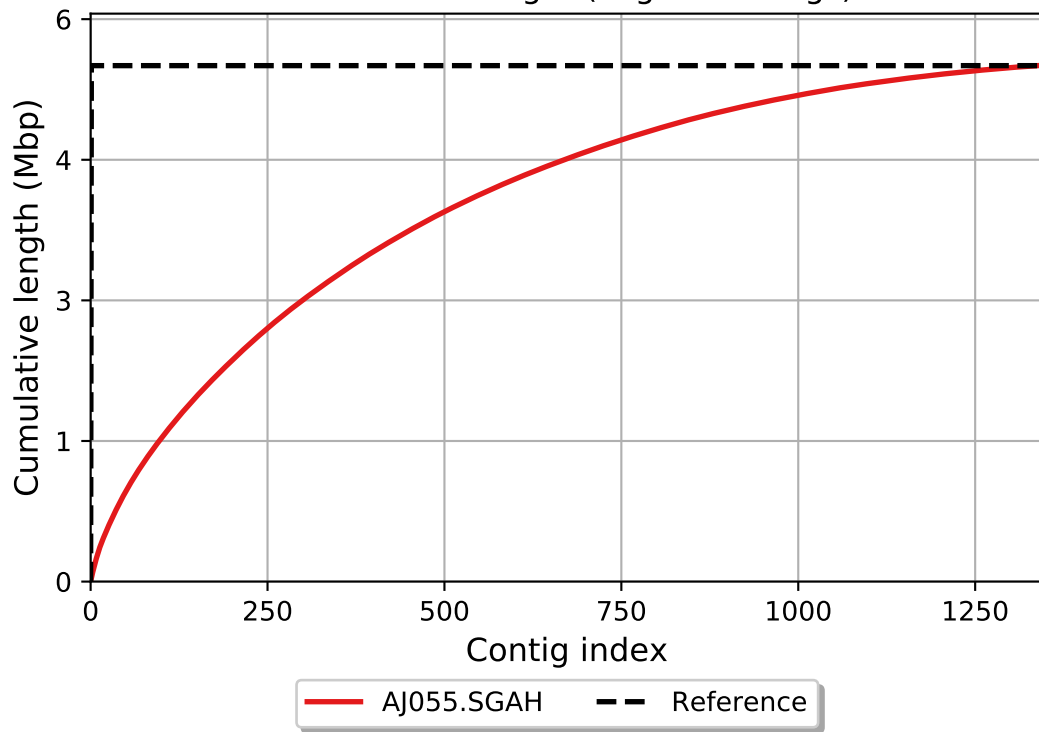
## Misassemblies



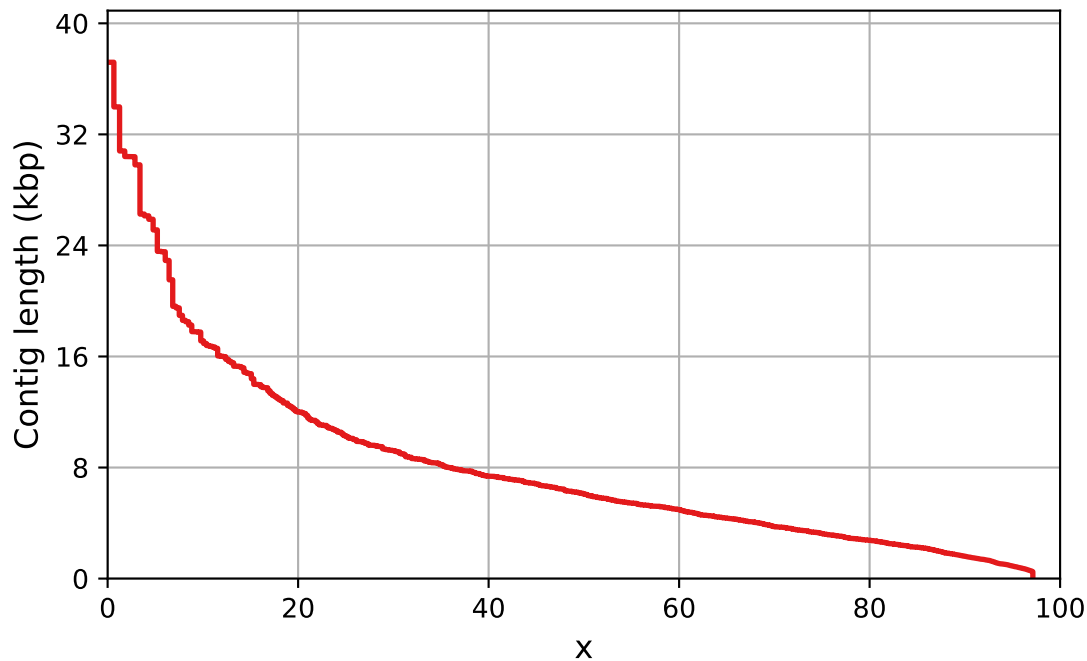
FRCurve (misassemblies)



Cumulative length (aligned contigs)

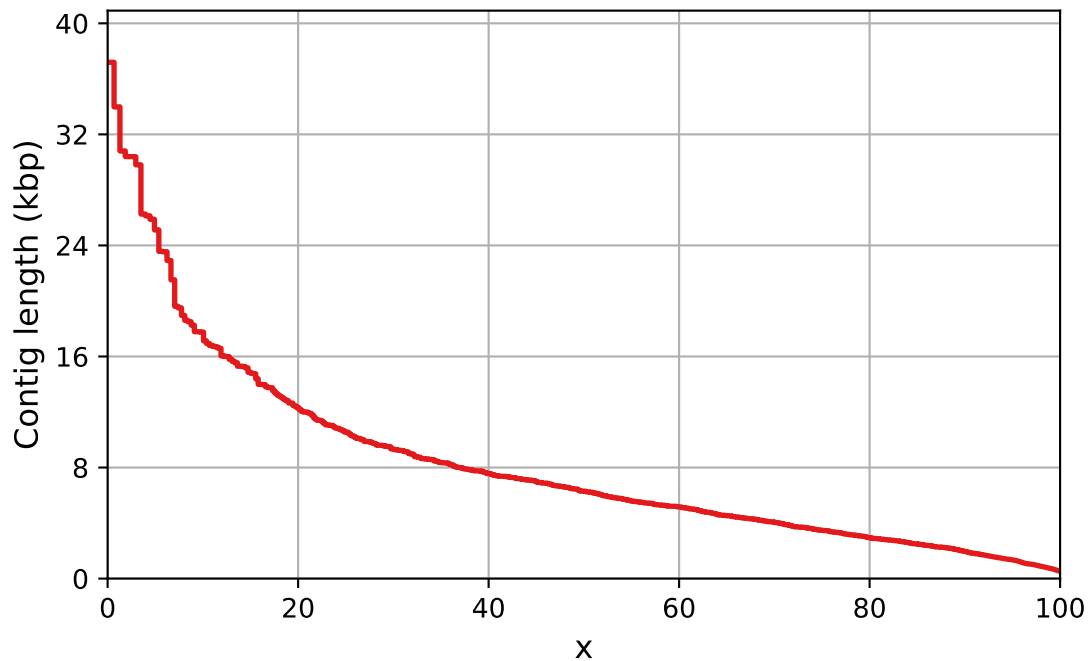


NAx



AJ055.SGAH

# NGAx



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