

Report

	AJ055.SpadesH
# contigs (>= 0 bp)	172
# contigs (>= 1000 bp)	59
# contigs (>= 5000 bp)	39
# contigs (>= 10000 bp)	36
# contigs (>= 25000 bp)	35
# contigs (>= 50000 bp)	28
Total length (>= 0 bp)	5645760
Total length (>= 1000 bp)	5617763
Total length (>= 5000 bp)	5572923
Total length (>= 10000 bp)	5554887
Total length (>= 25000 bp)	5530953
Total length (>= 50000 bp)	5279658
# contigs	64
Largest contig	585792
Total length	5621063
Reference length	5504133
GC (%)	57.28
Reference GC (%)	57.38
N50	226024
NG50	226024
N75	163120
NG75	163120
L50	9
LG50	9
L75	16
LG75	16
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# unaligned mis. contigs	0
# unaligned contigs	6 + 3 part
Unaligned length	162573
Genome fraction (%)	99.131
Duplication ratio	1.000
# N's per 100 kbp	17.33
# mismatches per 100 kbp	5.22
# indels per 100 kbp	1.45
Largest alignment	585792
Total aligned length	5458002
NA50	226024
NGA50	226024
NA75	163120
NGA75	163120
LA50	9
LGA50	9
LA75	16
LGA75	16

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

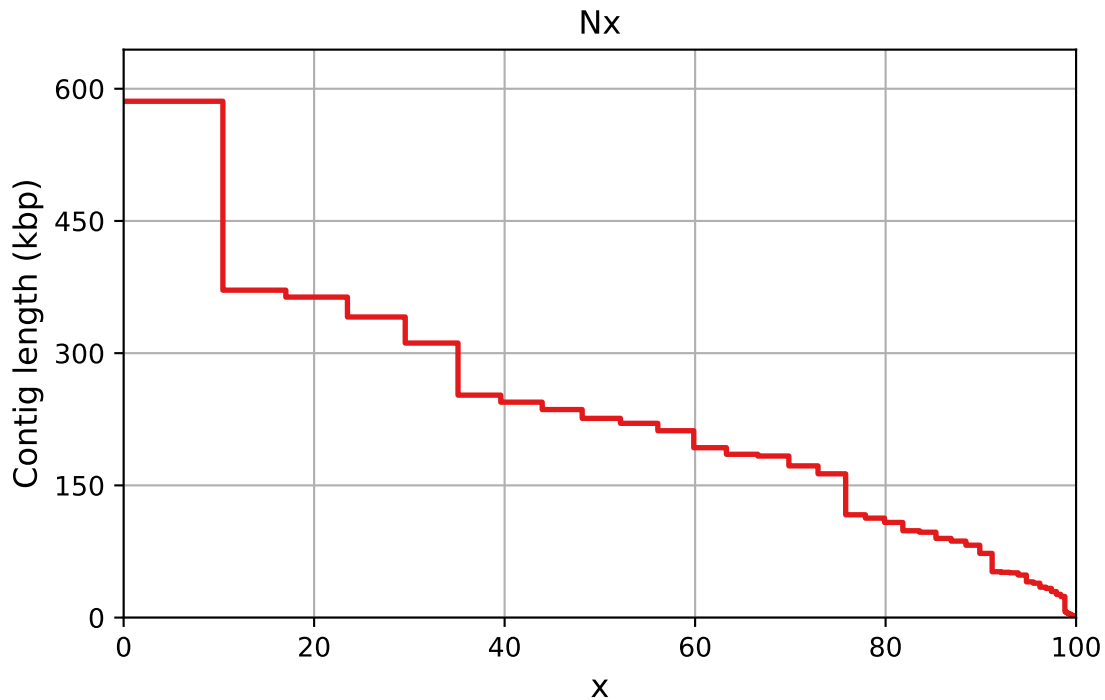
	AJ055.SpadesH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	11
# unaligned mis. contigs	0
# mismatches	285
# indels	79
# indels (≤ 5 bp)	71
# indels (> 5 bp)	8
Indels length	446

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).

Unaligned report

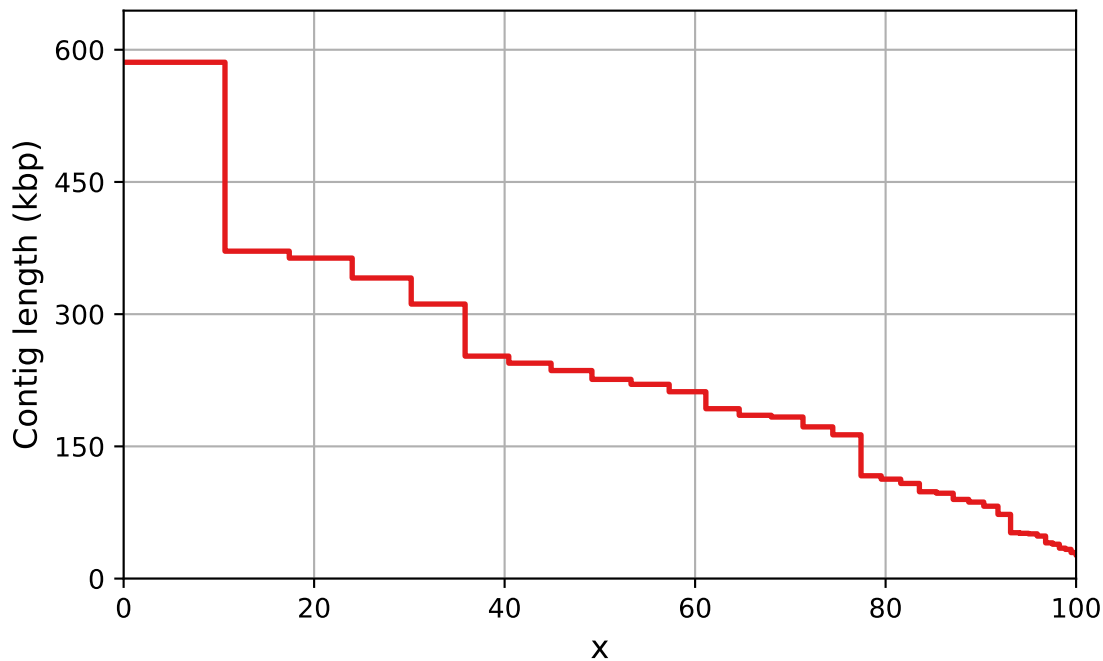
	AJ055.SpadesH
# fully unaligned contigs	6
Fully unaligned length	87094
# partially unaligned contigs	3
Partially unaligned length	75479
# N's	974

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).



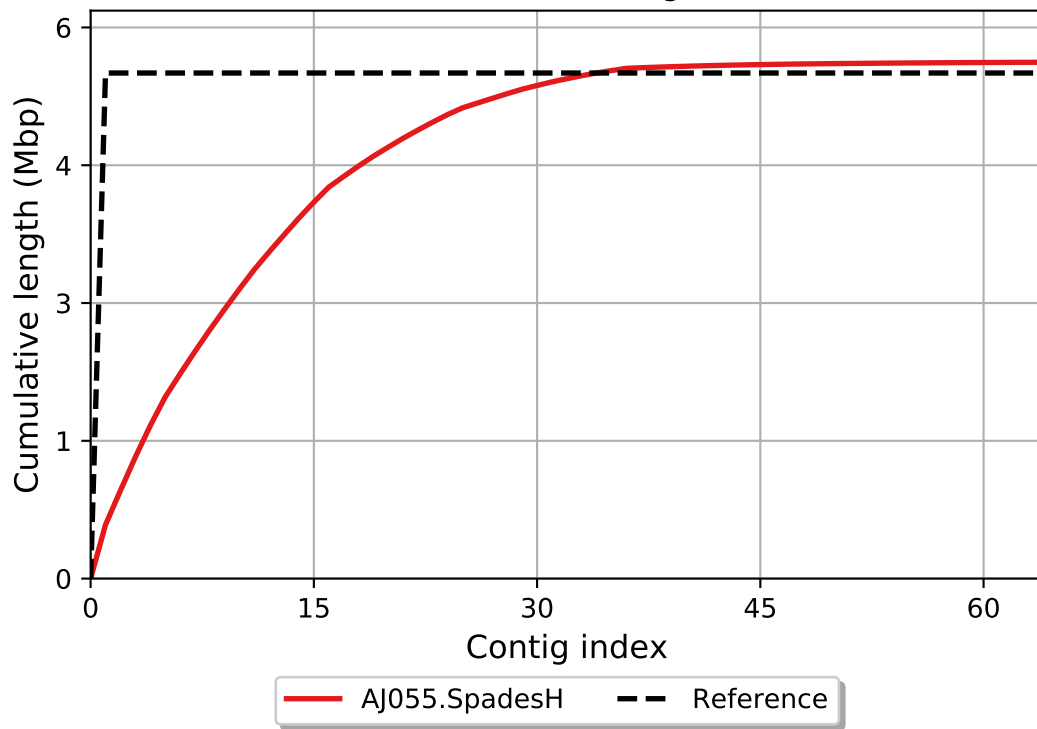
AJ055.SpadesH

NGx

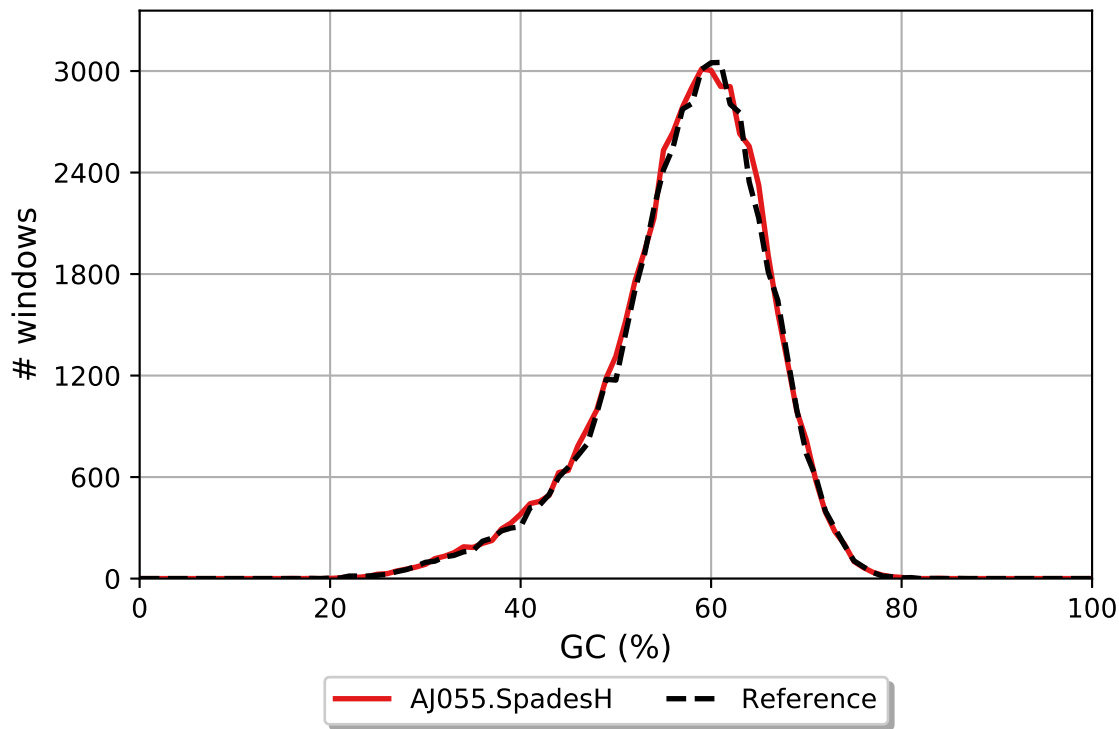


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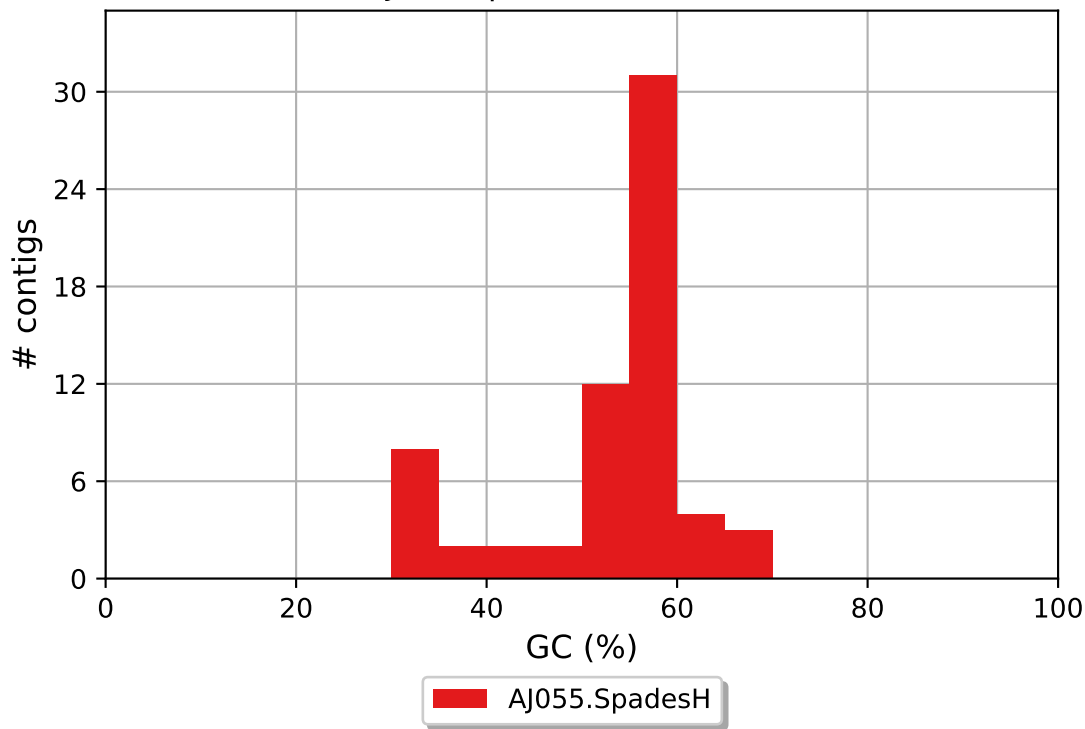
Cumulative length



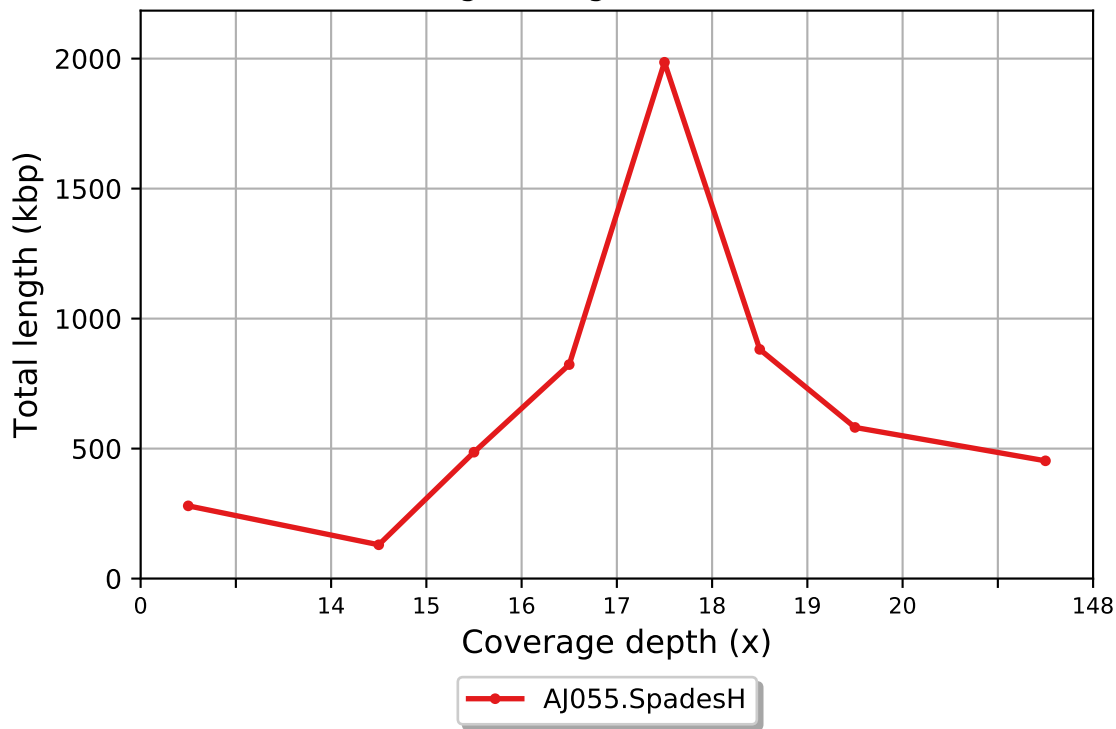
GC content



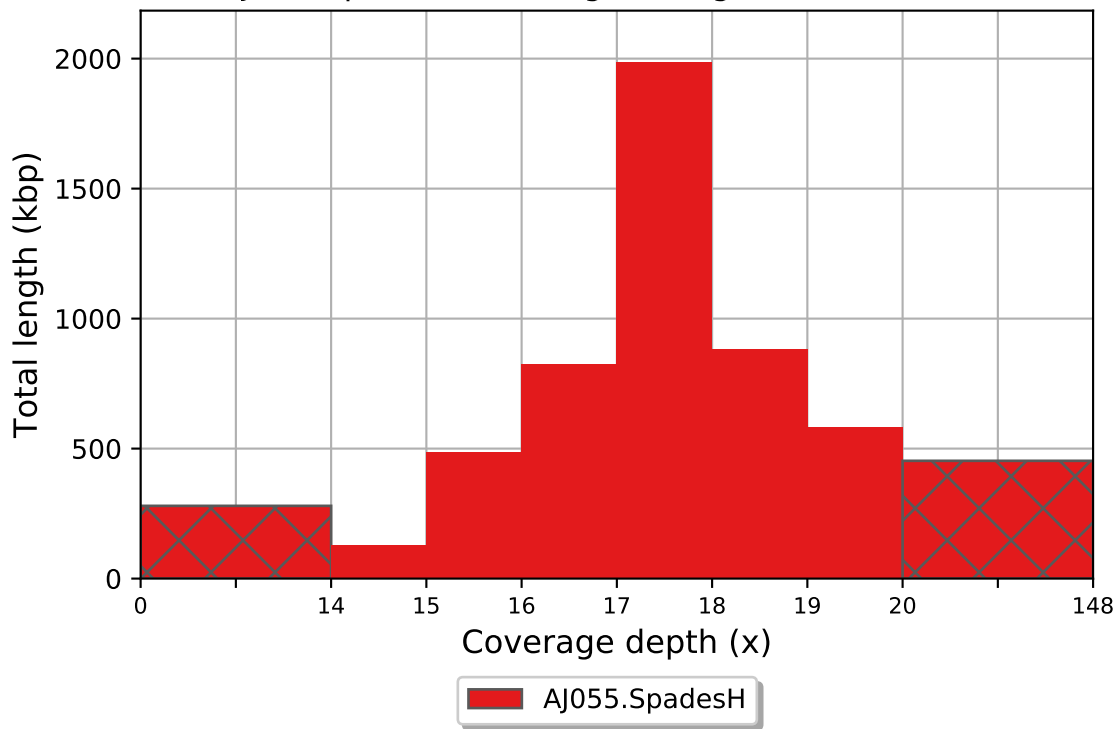
AJ055.SpadesH GC content



Coverage histogram (bin size: 1x)



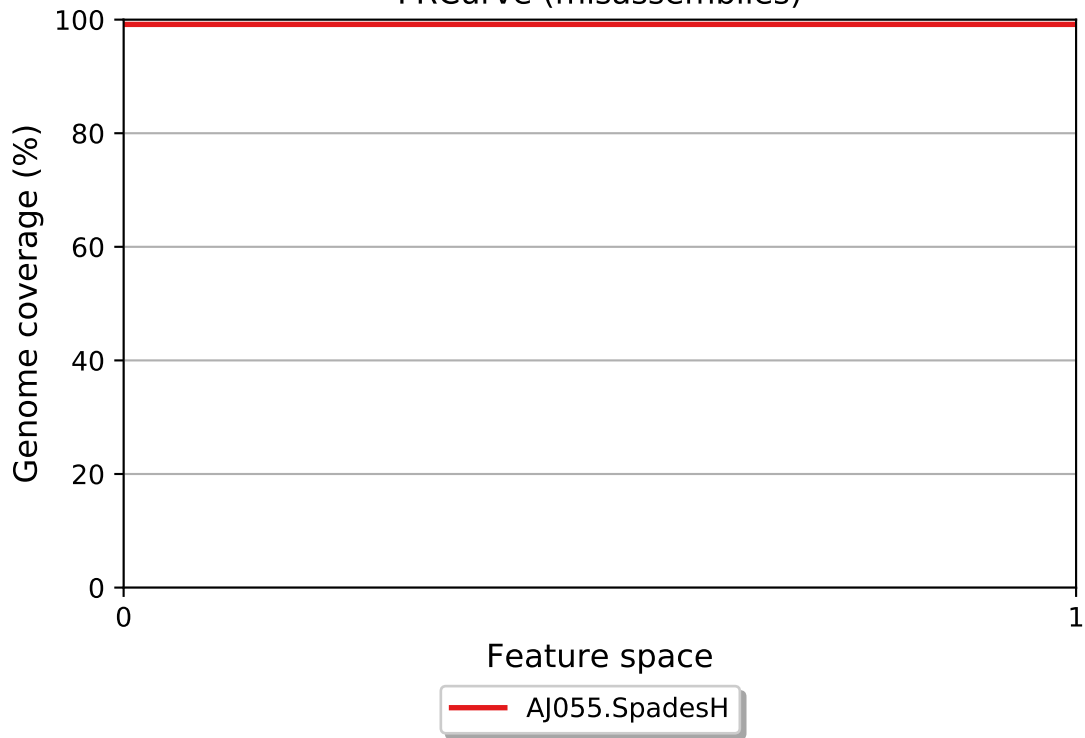
AJ055.SpadesH coverage histogram (bin size: 1x)



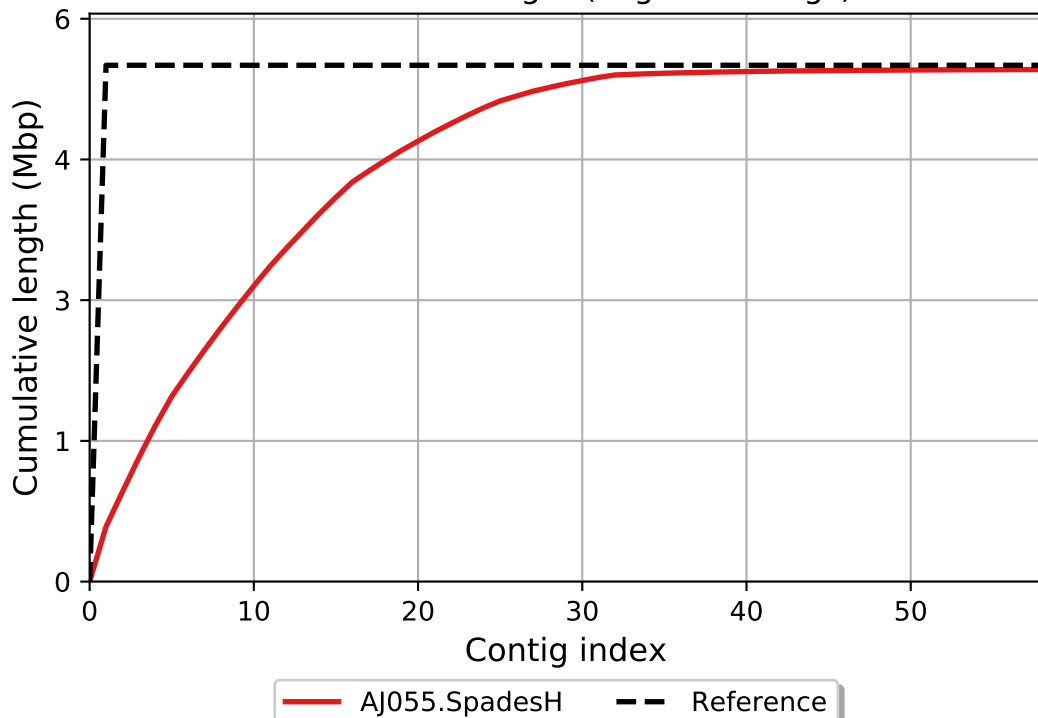
Misassemblies



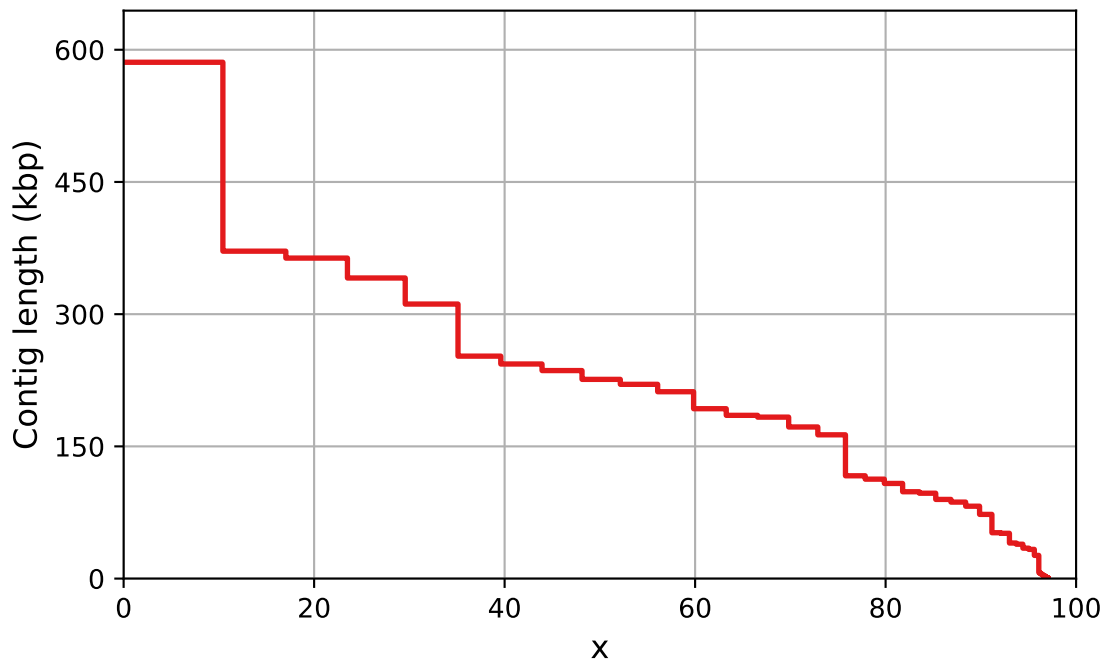
FRCurve (misassemblies)



Cumulative length (aligned contigs)

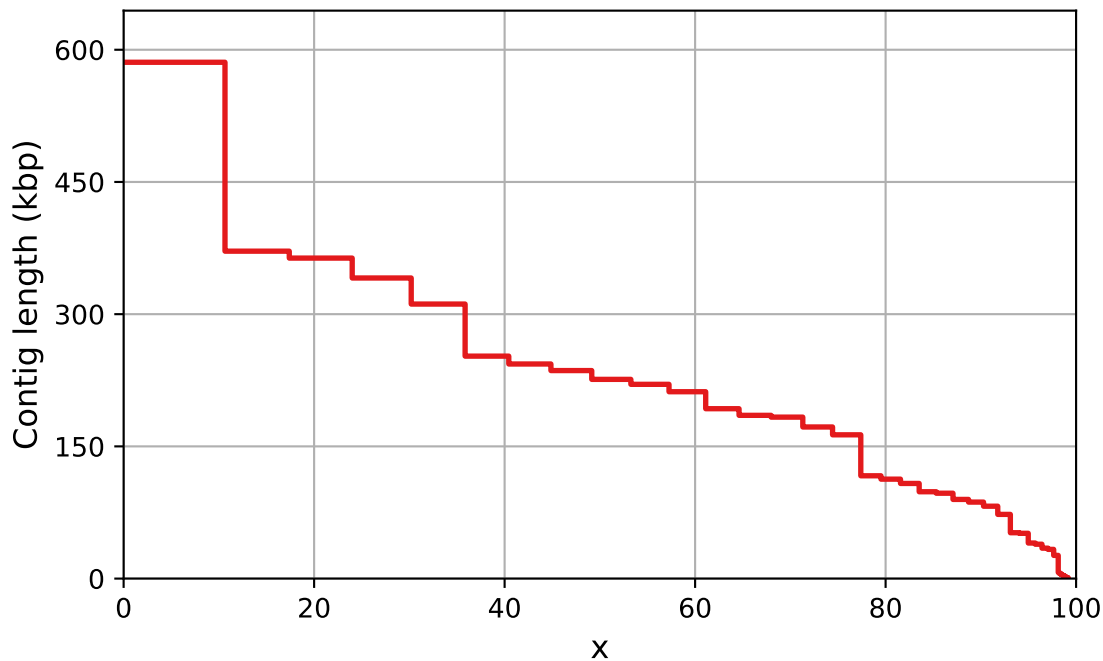


NAx



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NGAx



AJ055.SpadesH