

Report

	AJ218.SpadesH
# contigs (>= 0 bp)	195
# contigs (>= 1000 bp)	90
# contigs (>= 5000 bp)	65
# contigs (>= 10000 bp)	59
# contigs (>= 25000 bp)	49
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	5614314
Total length (>= 1000 bp)	5583306
Total length (>= 5000 bp)	5529939
Total length (>= 10000 bp)	5488376
Total length (>= 25000 bp)	5321778
Total length (>= 50000 bp)	4700743
# contigs	102
Largest contig	525273
Total length	5591801
Reference length	5465981
GC (%)	57.18
Reference GC (%)	57.29
N50	158473
NG50	158473
N75	68938
NG75	71228
L50	11
LG50	11
L75	24
LG75	23
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned mis. contigs	0
# unaligned contigs	8 + 7 part
Unaligned length	188687
Genome fraction (%)	98.766
Duplication ratio	1.001
# N's per 100 kbp	13.02
# mismatches per 100 kbp	7.87
# indels per 100 kbp	1.15
Largest alignment	524880
Total aligned length	5402362
NA50	158473
NGA50	158473
NA75	68894
NGA75	71228
LA50	11
LGA50	11
LA75	24
LGA75	23

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

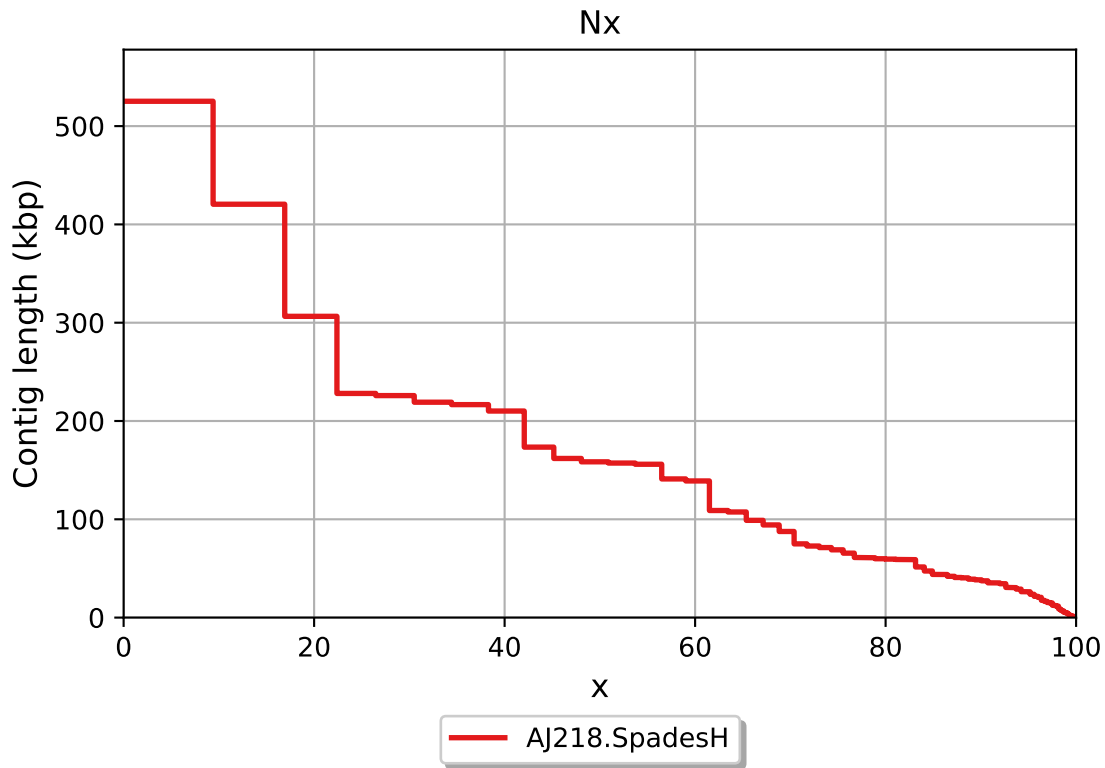
	AJ218.SpadesH
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned mis. contigs	0
# mismatches	425
# indels	62
# indels (≤ 5 bp)	57
# indels (> 5 bp)	5
Indels length	305

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).

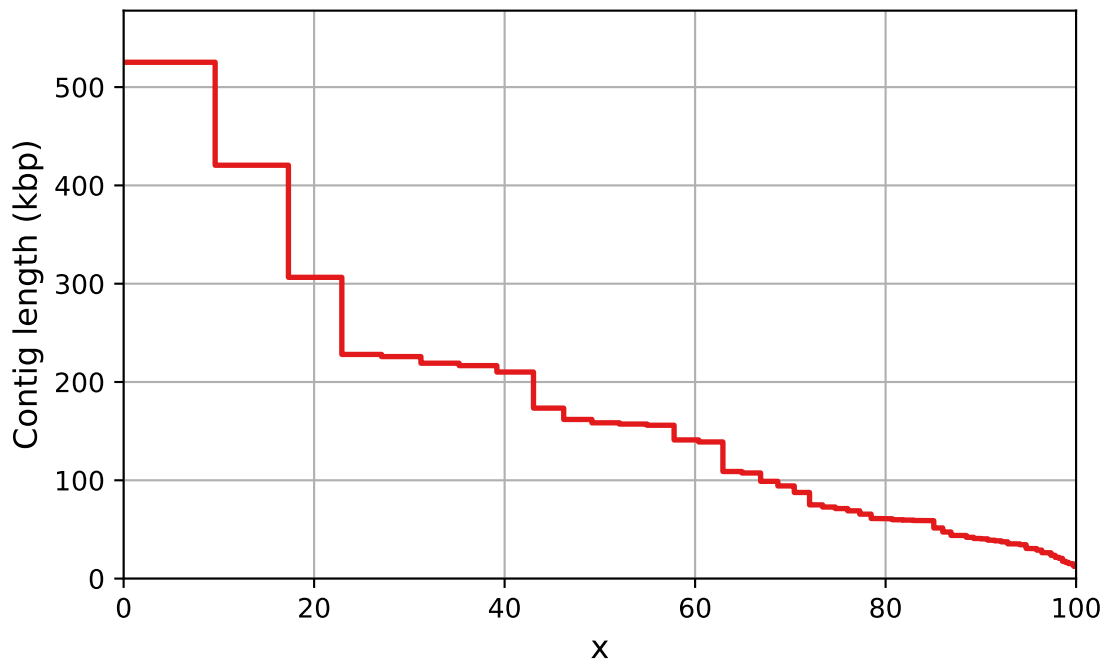
Unaligned report

	AJ218.SpadesH
# fully unaligned contigs	8
Fully unaligned length	44615
# partially unaligned contigs	7
Partially unaligned length	144072
# N's	728

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).

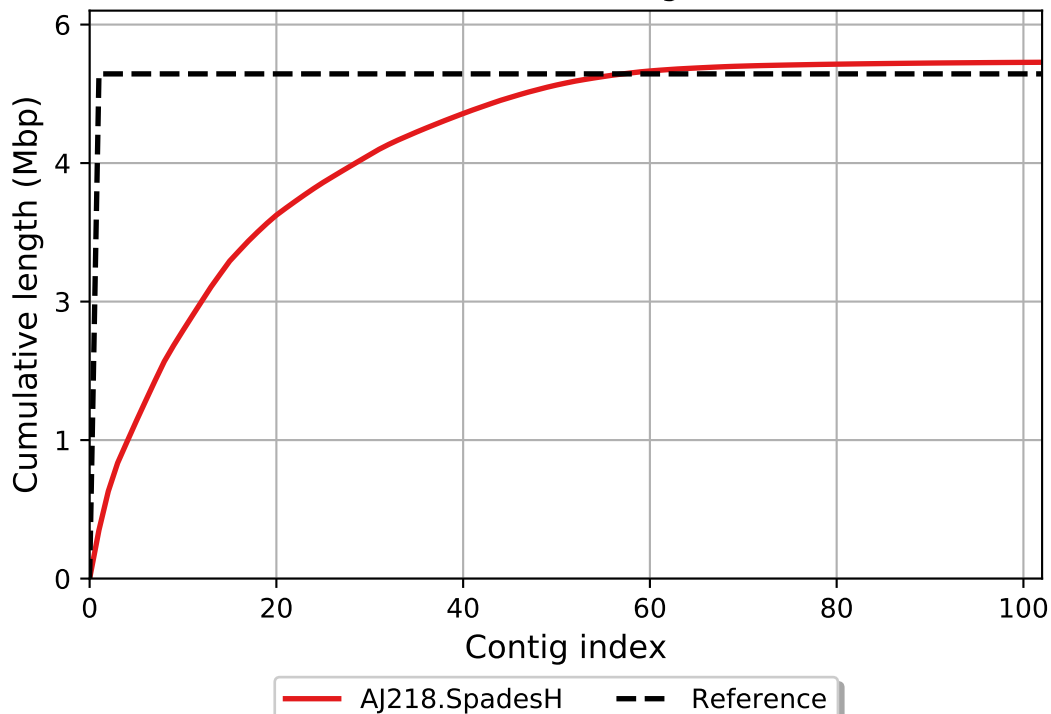


NGx

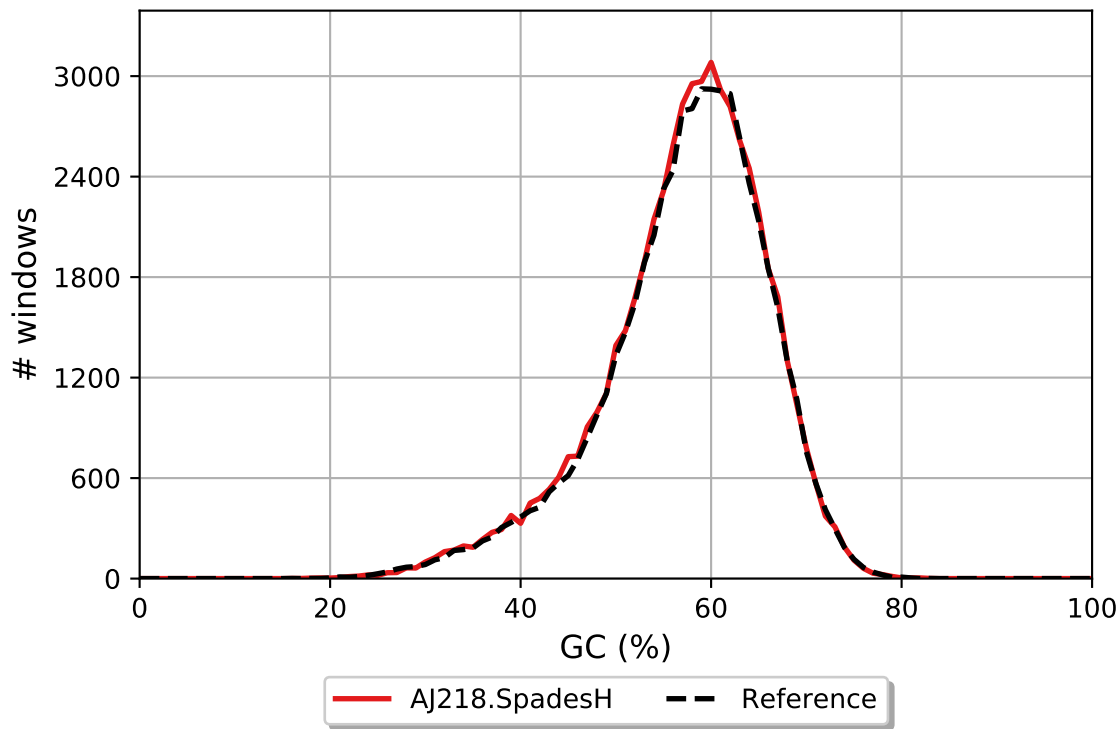


AJ218.SpadesH

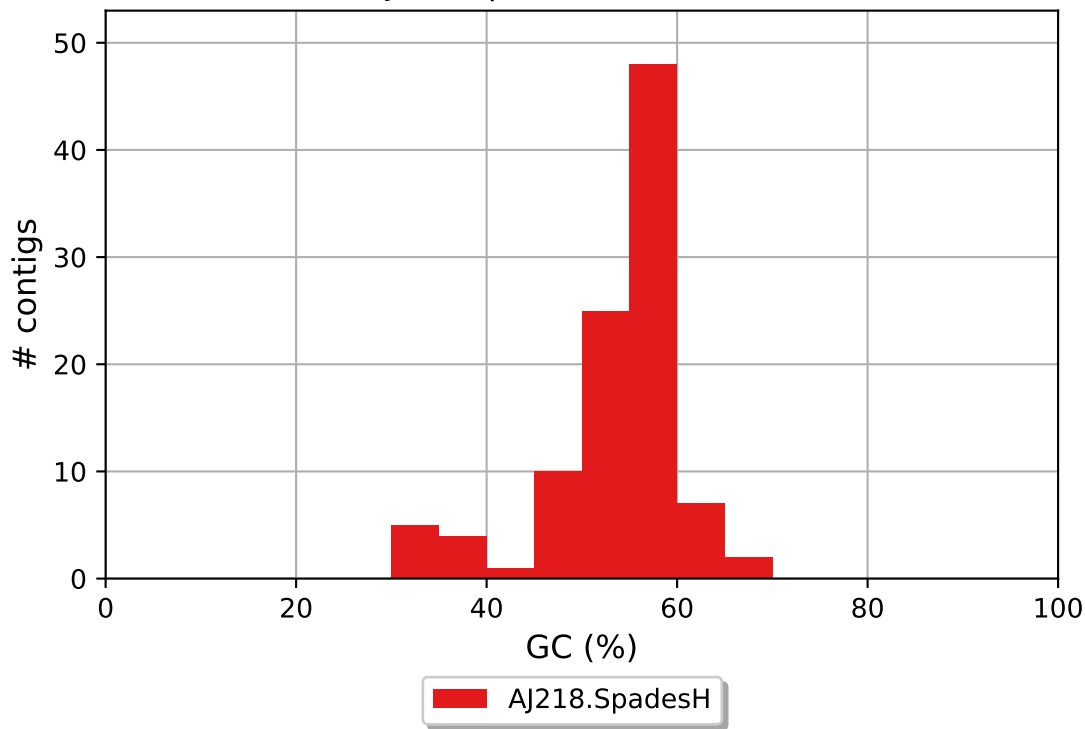
Cumulative length



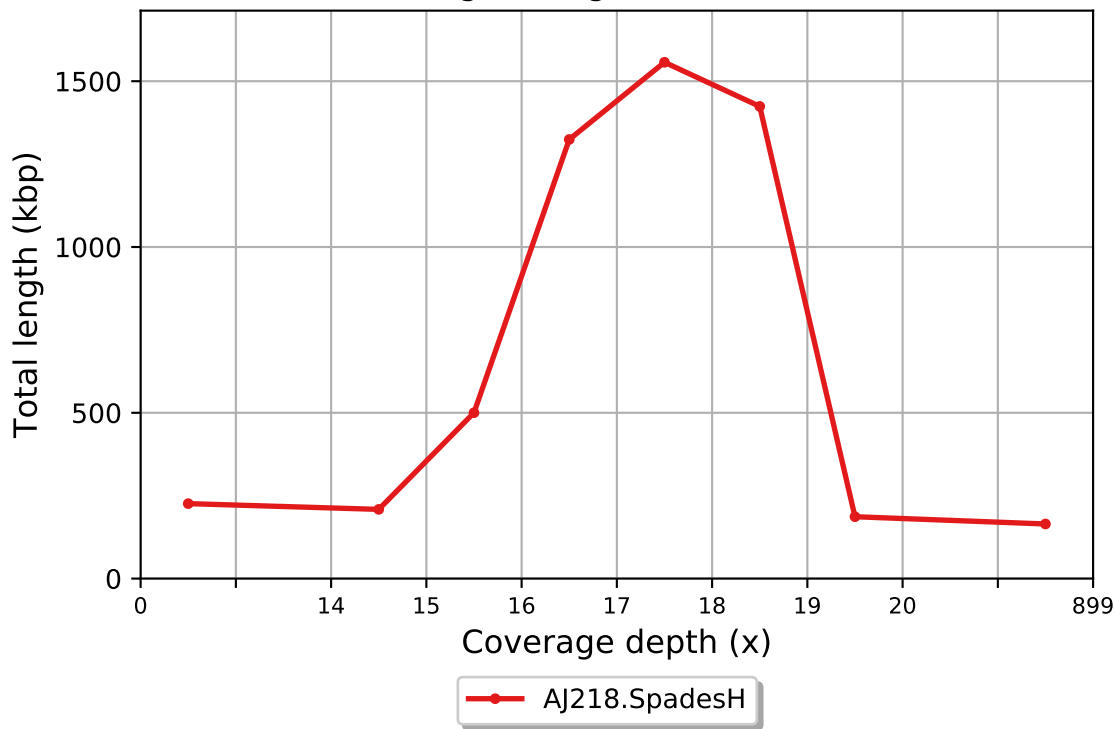
GC content



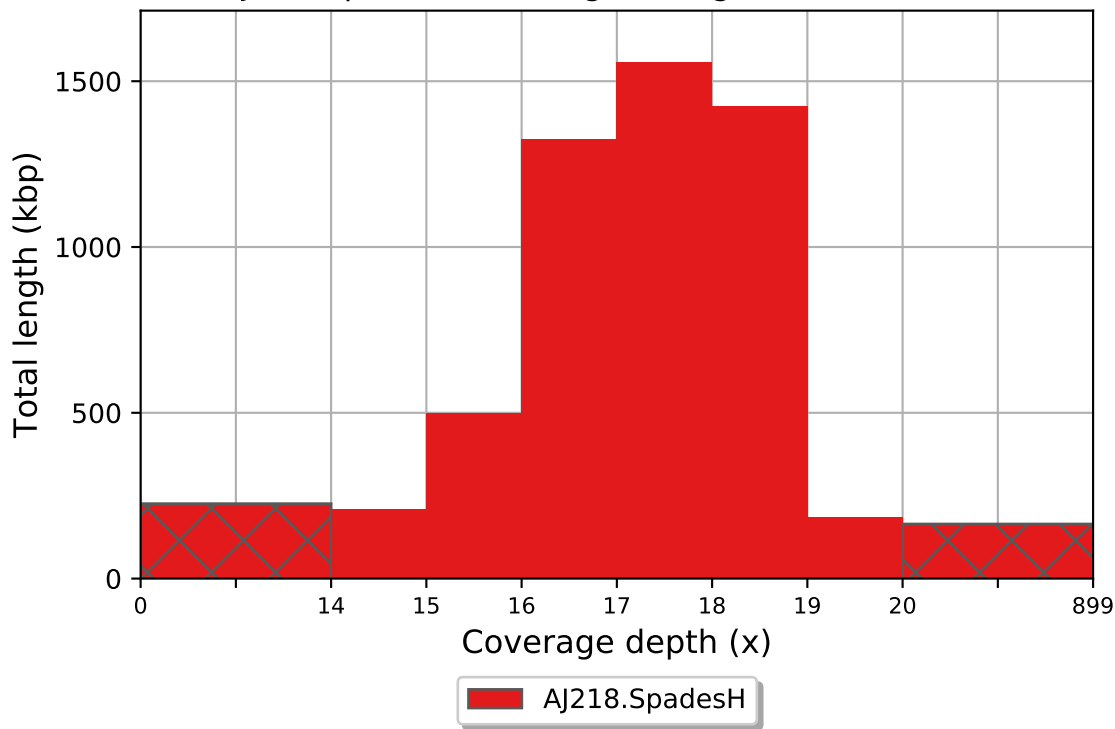
AJ218.SpadesH GC content



Coverage histogram (bin size: 1x)



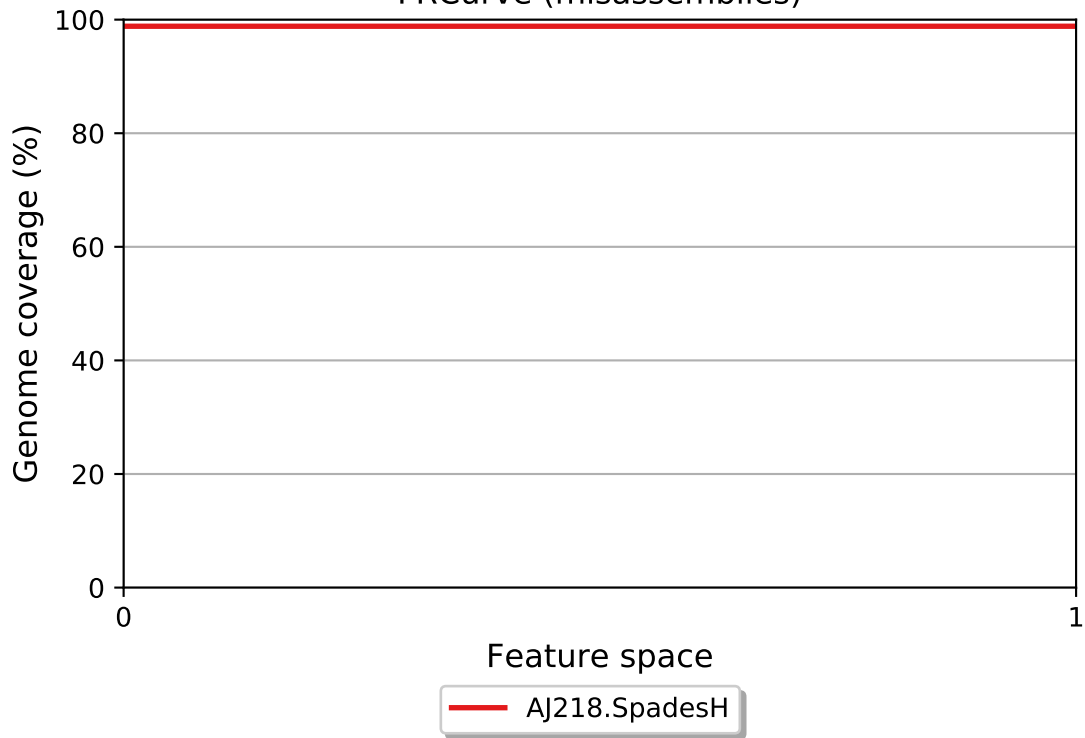
AJ218.SpadesH coverage histogram (bin size: 1x)



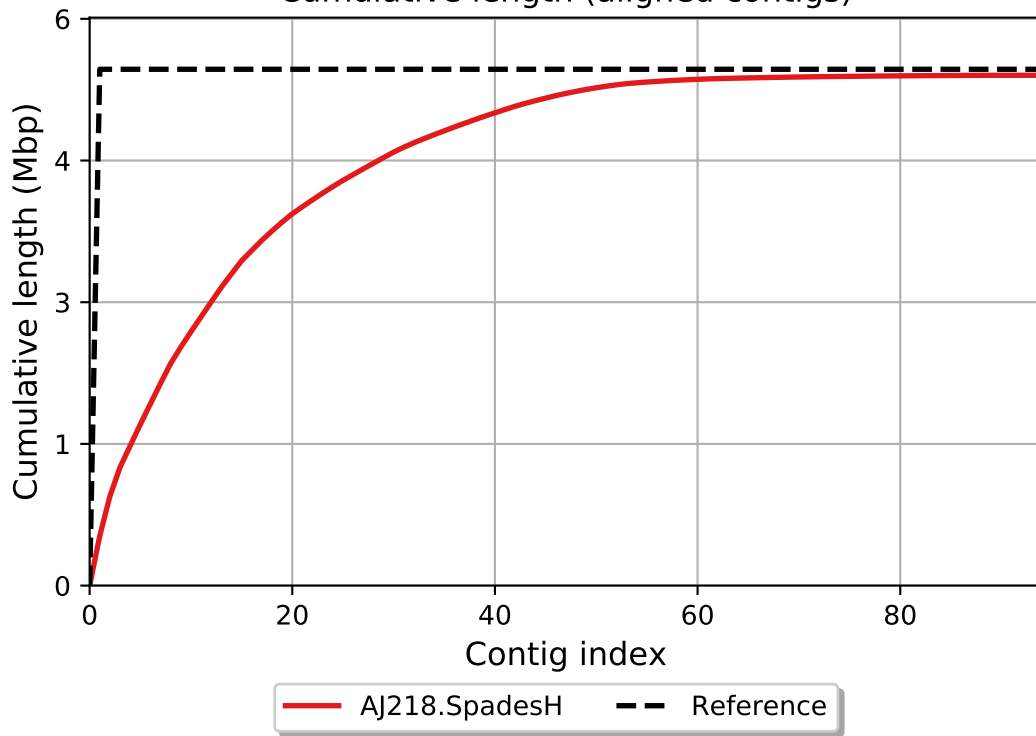
Misassemblies



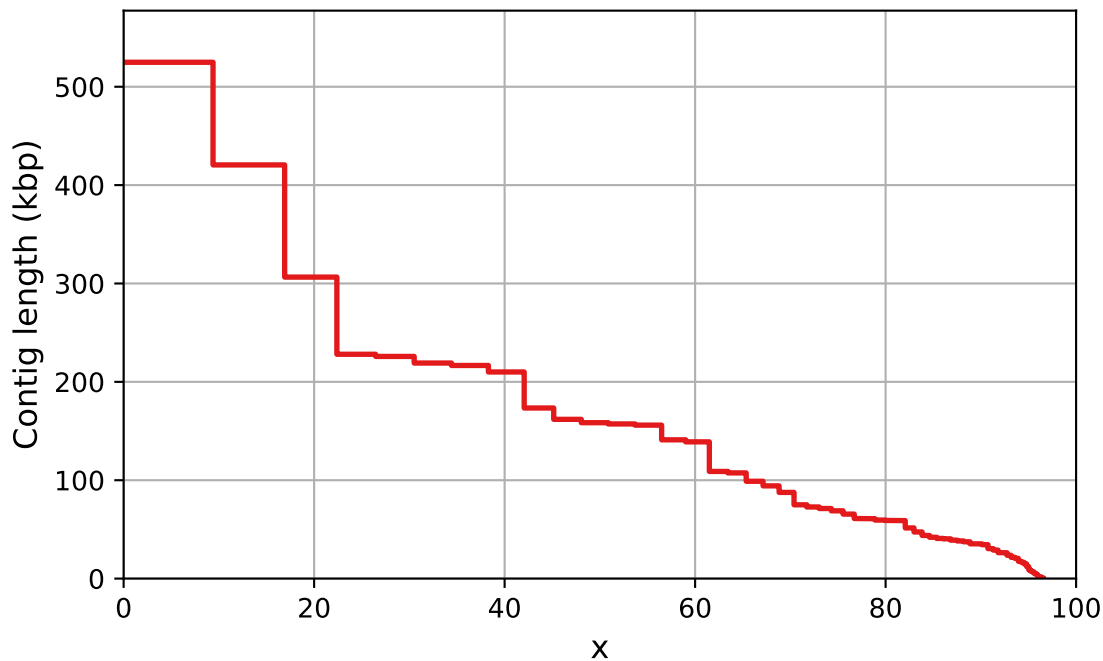
FRCurve (misassemblies)



Cumulative length (aligned contigs)

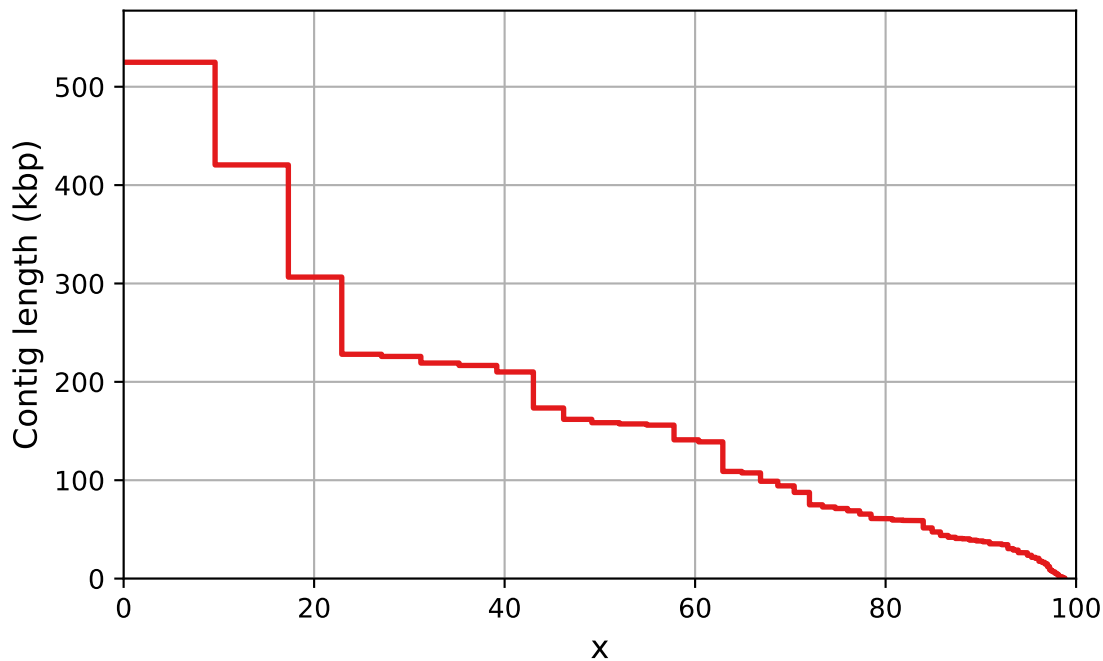


NAx



AJ218.SpadesH

NGAx



AJ218.SpadesH