

Report

	Aj218.SpadesLRL
# contigs (>= 0 bp)	59
# contigs (>= 1000 bp)	20
# contigs (>= 5000 bp)	13
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	11
Total length (>= 0 bp)	5679337
Total length (>= 1000 bp)	5669505
Total length (>= 5000 bp)	5652101
Total length (>= 10000 bp)	5643088
Total length (>= 25000 bp)	5630523
Total length (>= 50000 bp)	5630523
# contigs	20
Largest contig	1512445
Total length	5669505
Reference length	5465981
GC (%)	57.14
Reference GC (%)	57.29
N50	946530
NG50	946530
N75	329188
NG75	454623
L50	3
LG50	3
L75	5
LG75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	1 + 1 part
Unaligned length	191935
Genome fraction (%)	99.887
Duplication ratio	1.003
# N's per 100 kbp	3.53
# mismatches per 100 kbp	9.10
# indels per 100 kbp	2.18
Largest alignment	1511928
Total aligned length	5474706
NA50	946530
NGA50	946530
NA75	329188
NGA75	454623
LA50	3
LGA50	3
LA75	5
LGA75	4

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

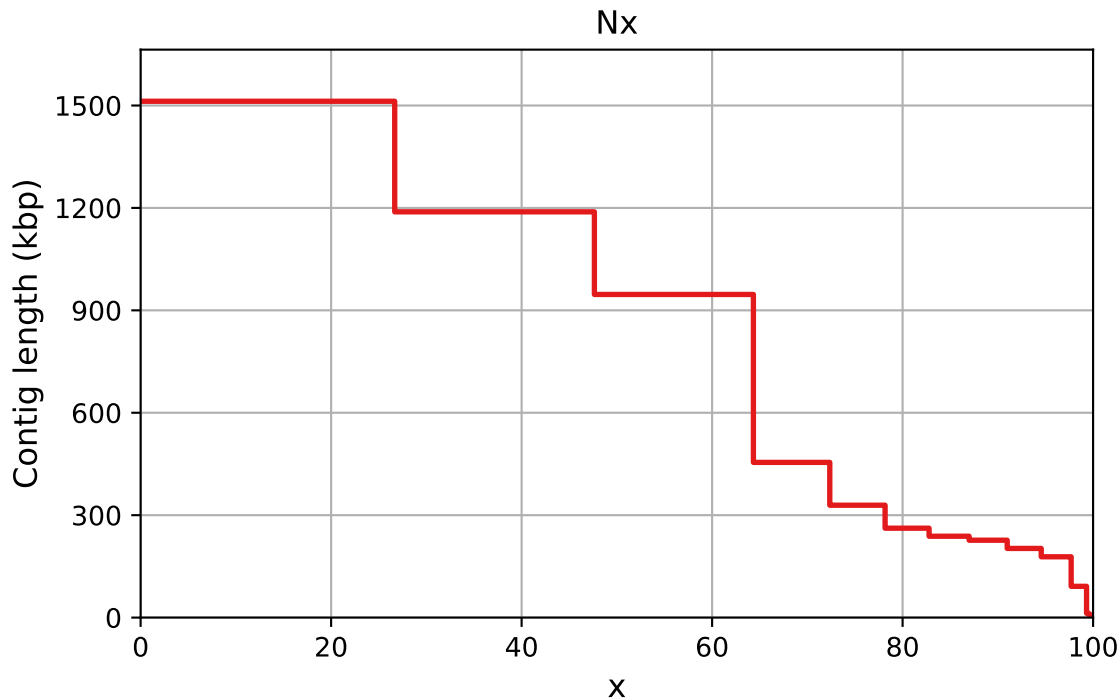
	AJ218.SpadesLRL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	497
# indels	119
# indels (≤ 5 bp)	116
# indels (> 5 bp)	3
Indels length	221

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

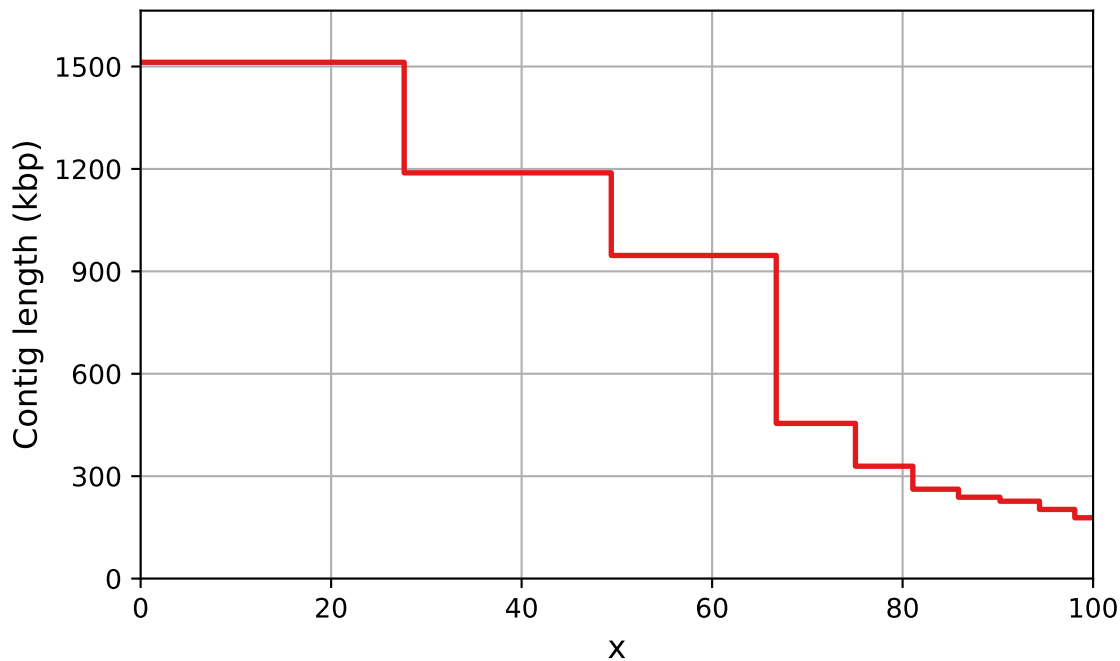
	AJ218.SpadesLRL
# fully unaligned contigs	1
Fully unaligned length	1583
# partially unaligned contigs	1
Partially unaligned length	190352
# N's	200

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).



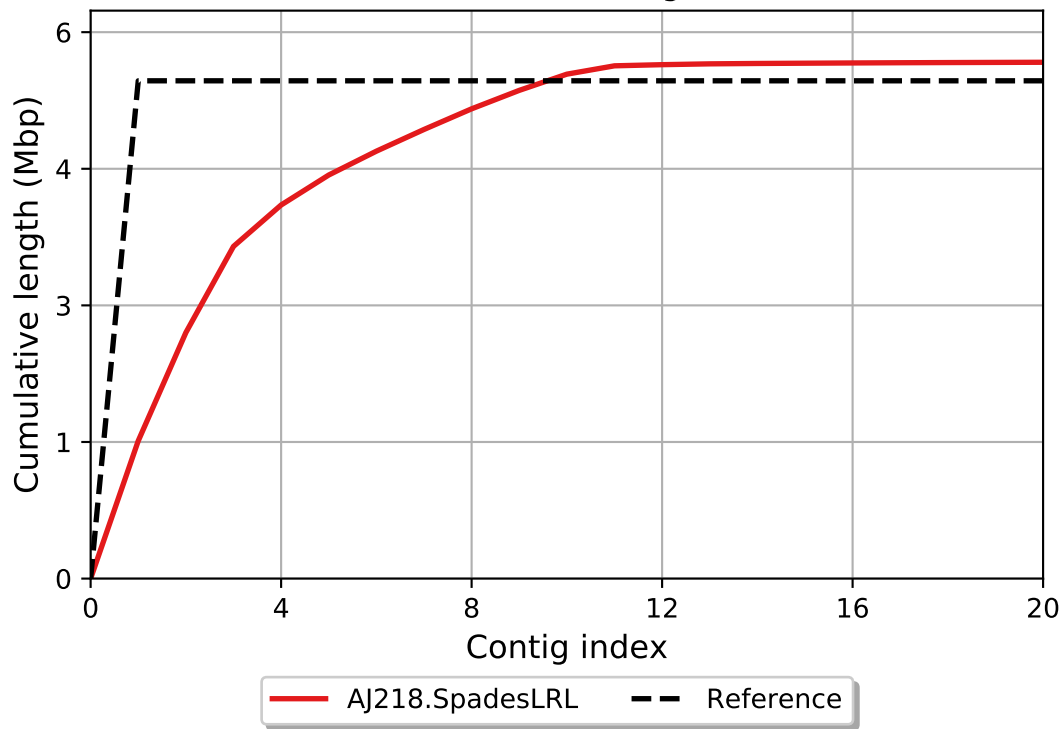
AJ218.SpadesLRL

NGx

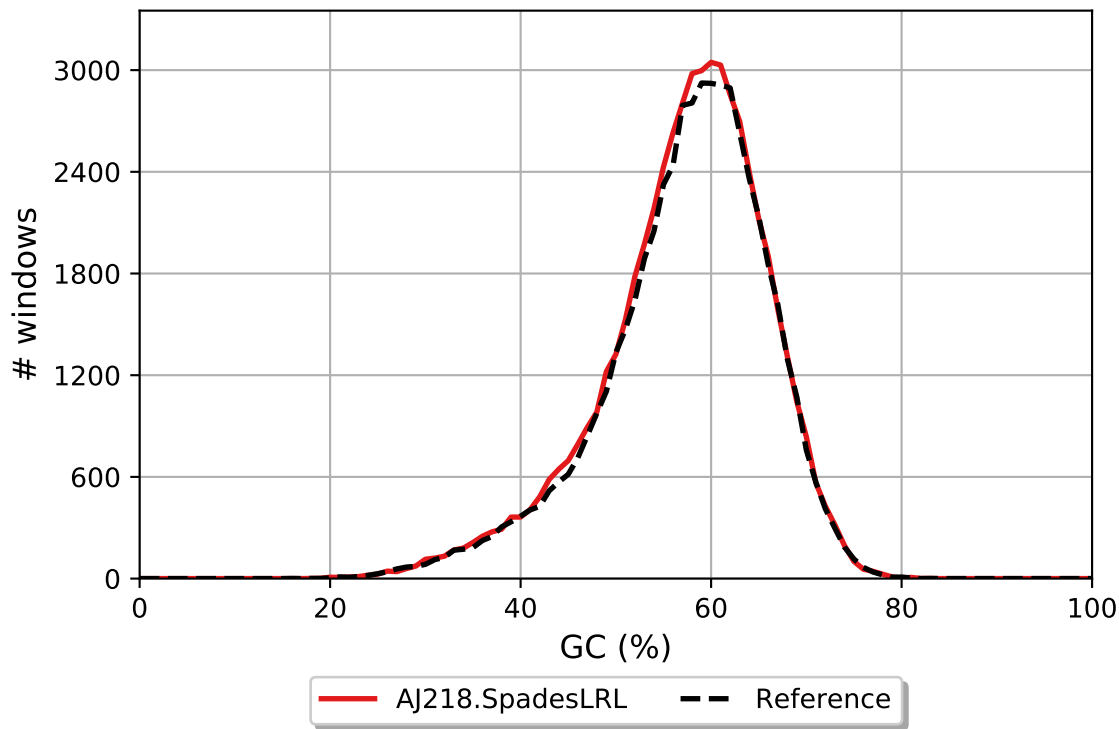


AJ218.SpadesLRL

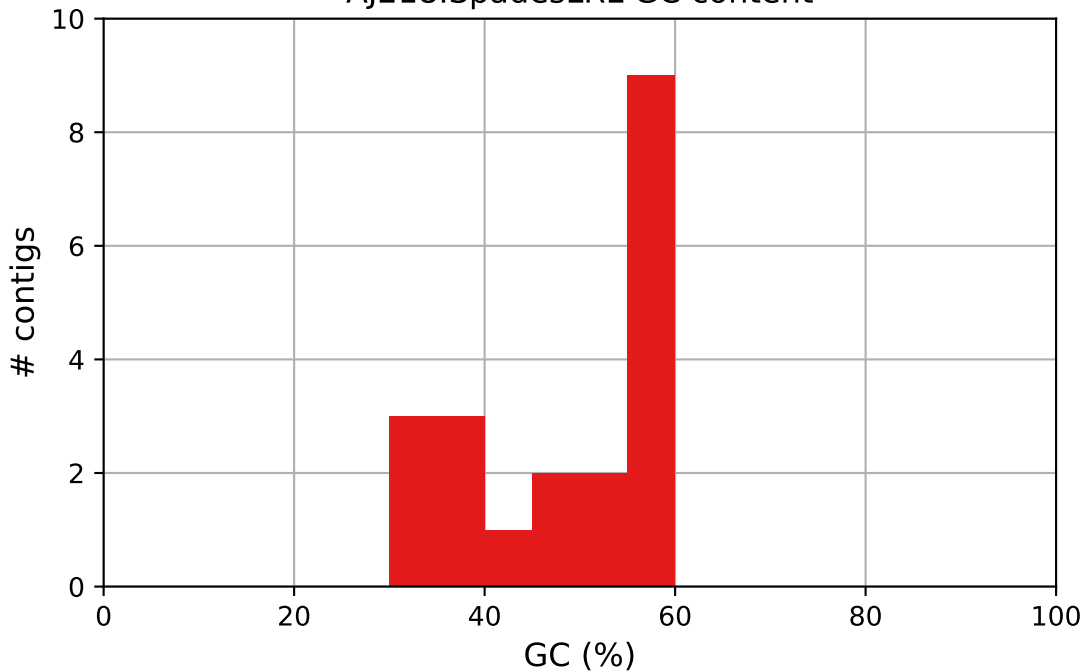
Cumulative length



GC content

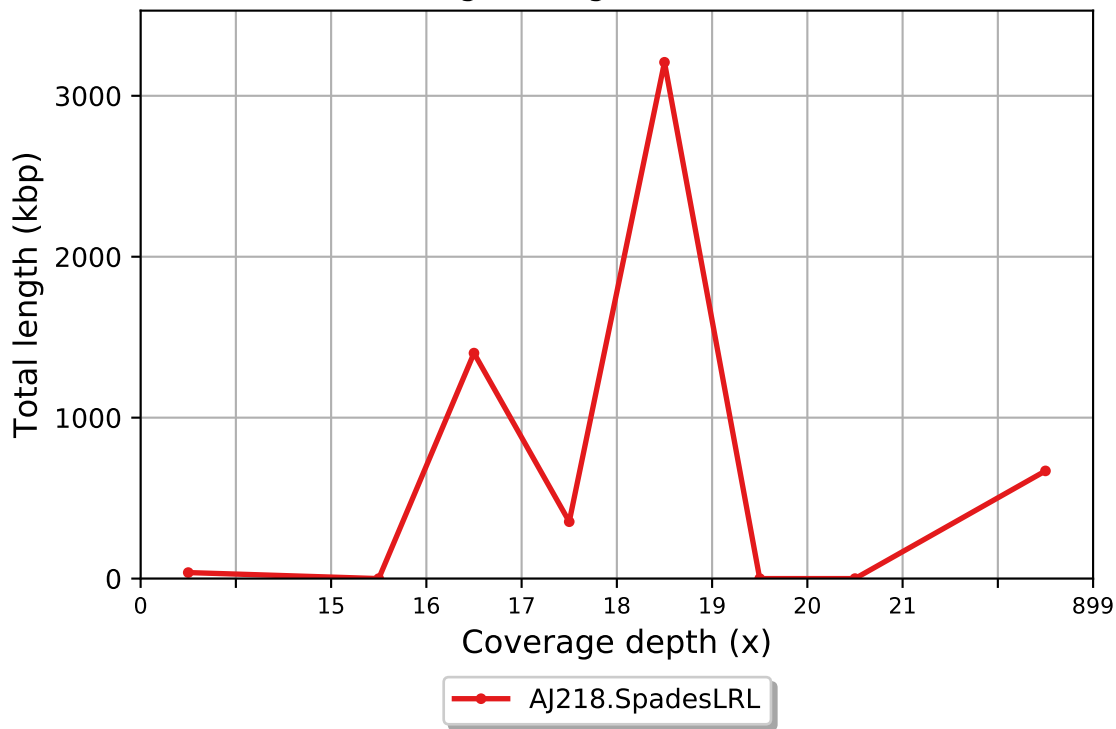


AJ218.SpadesLRL GC content

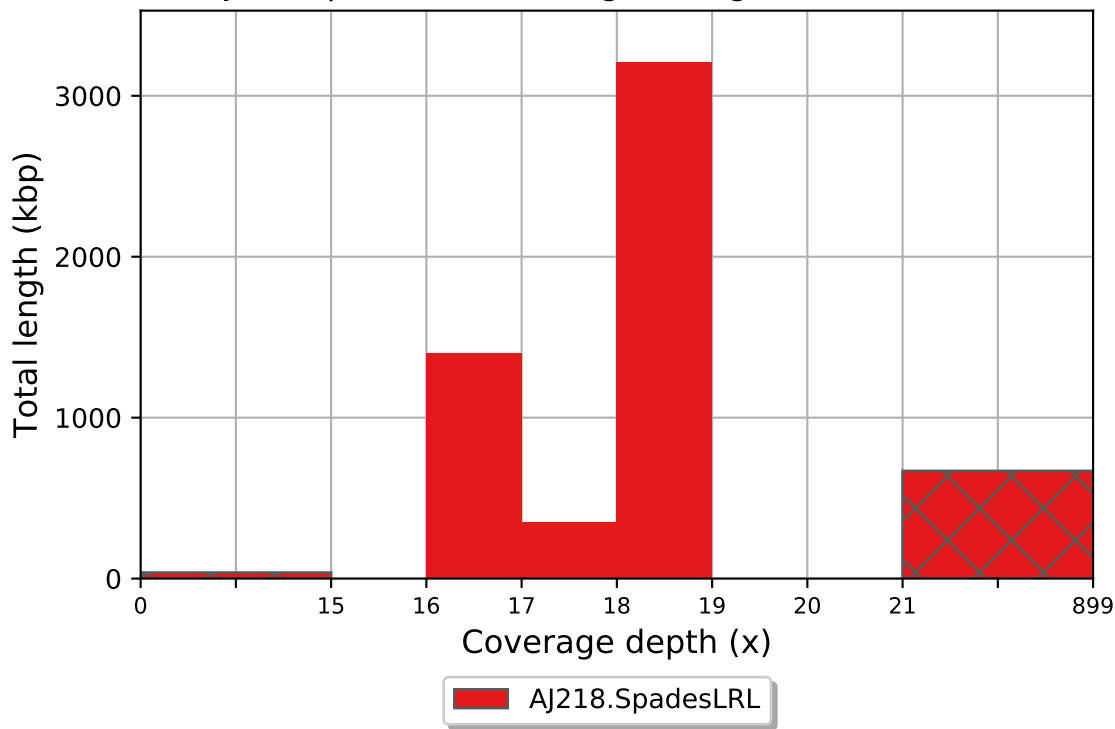


AJ218.SpadesLRL

Coverage histogram (bin size: 1x)



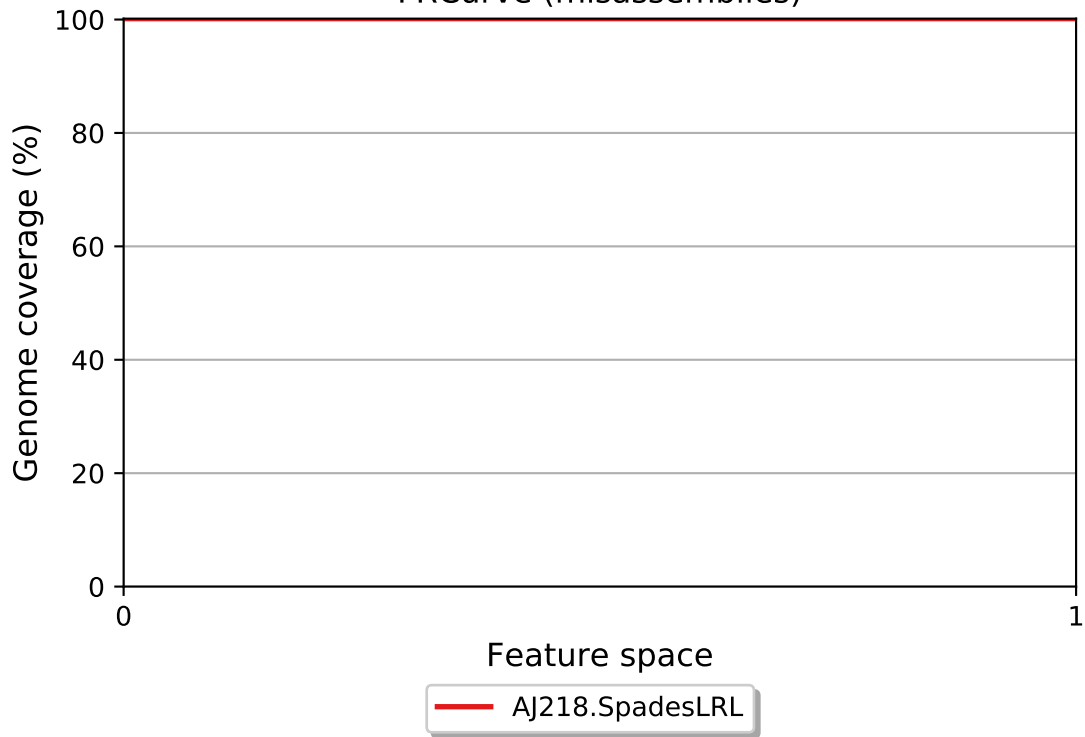
AJ218.SpadesLRL coverage histogram (bin size: 1x)



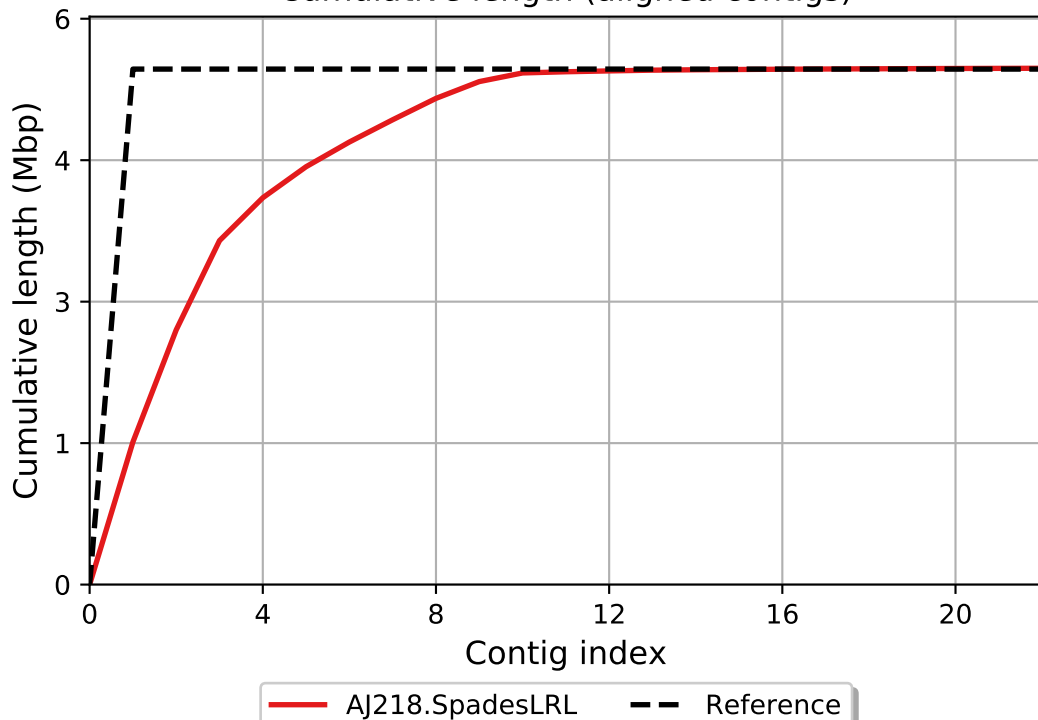
Misassemblies



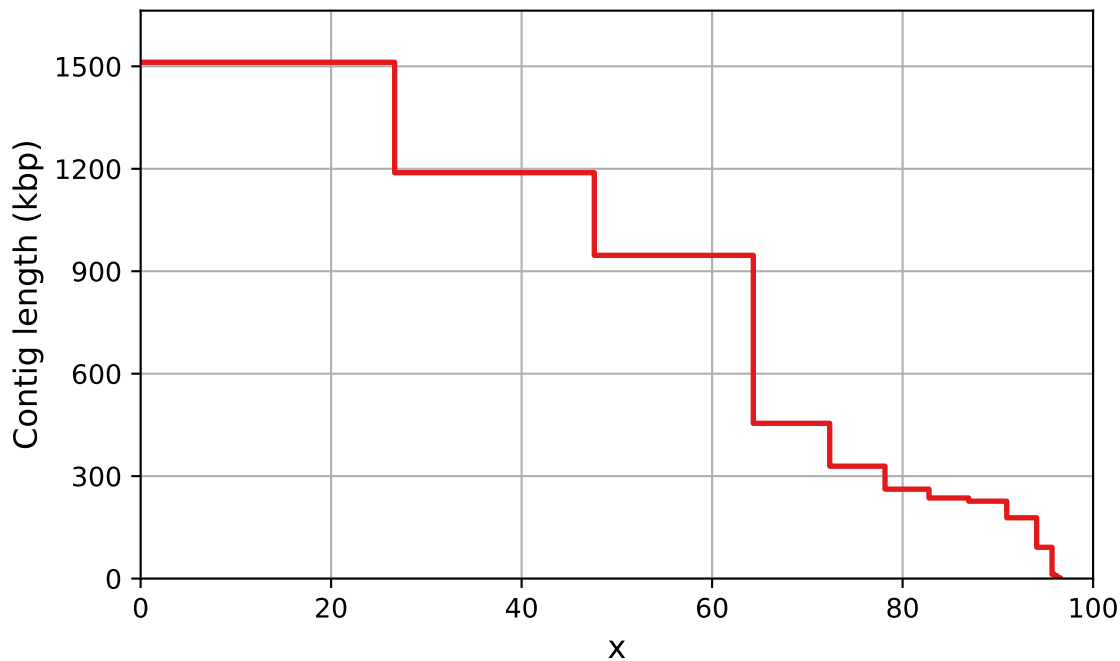
FRCurve (misassemblies)



Cumulative length (aligned contigs)

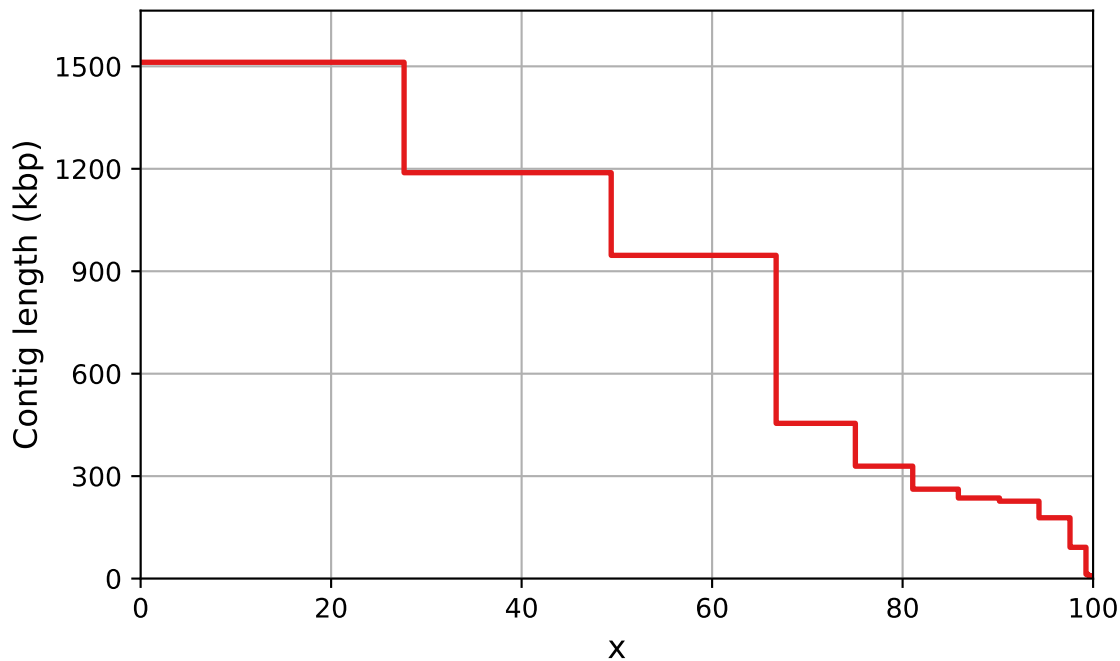


NAx



AJ218.SpadesLRL

NGAx



AJ218.SpadesLRL