

Report

	Aj292.SpadesLRL
# contigs (>= 0 bp)	27
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	10
# contigs (>= 50000 bp)	10
Total length (>= 0 bp)	5449481
Total length (>= 1000 bp)	5446000
Total length (>= 5000 bp)	5435047
Total length (>= 10000 bp)	5435047
Total length (>= 25000 bp)	5435047
Total length (>= 50000 bp)	5435047
# contigs	15
Largest contig	1731157
Total length	5446618
Reference length	5445112
GC (%)	57.62
Reference GC (%)	57.62
N50	610748
NG50	610748
N75	480226
NG75	480226
L50	3
LG50	3
L75	5
LG75	5
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	2554195
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.884
Duplication ratio	1.001
# N's per 100 kbp	1.84
# mismatches per 100 kbp	4.71
# indels per 100 kbp	1.64
Largest alignment	1152521
Total aligned length	5443429
NA50	578636
NGA50	578636
NA75	480226
NGA75	480226
LA50	4
LGA50	4
LA75	6
LGA75	6

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

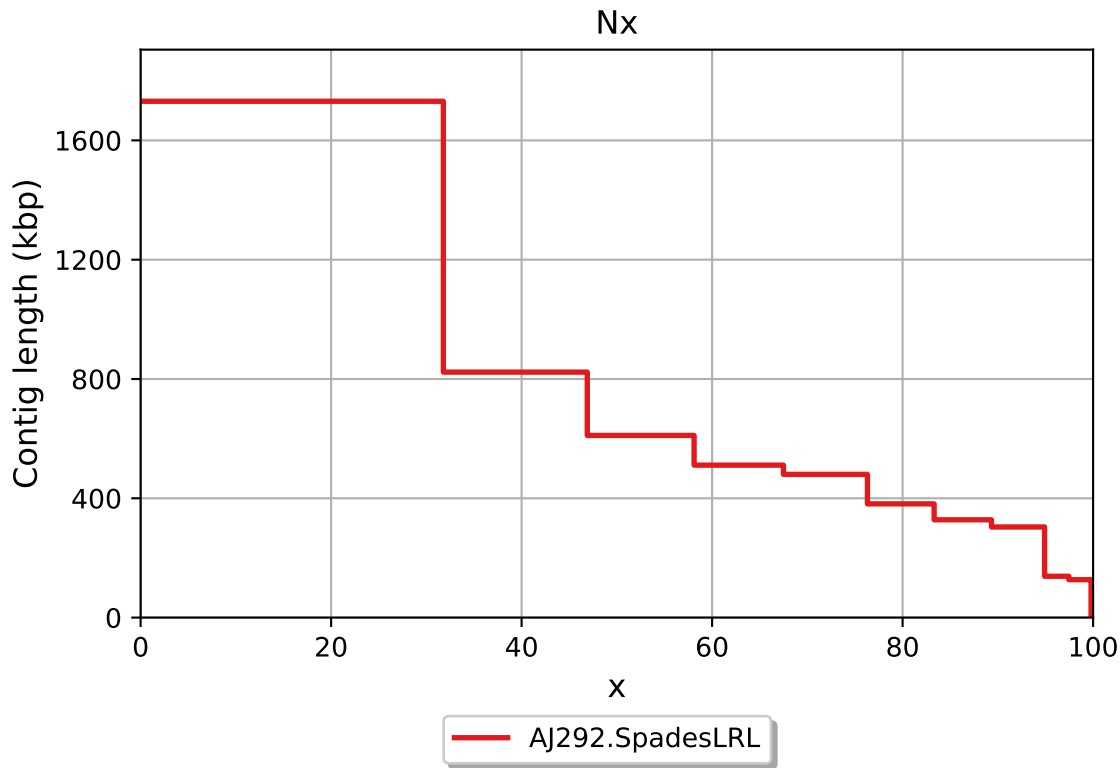
	AJ292.SpadesLRL
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	2554195
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	256
# indels	89
# indels (≤ 5 bp)	89
# indels (> 5 bp)	0
Indels length	99

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).

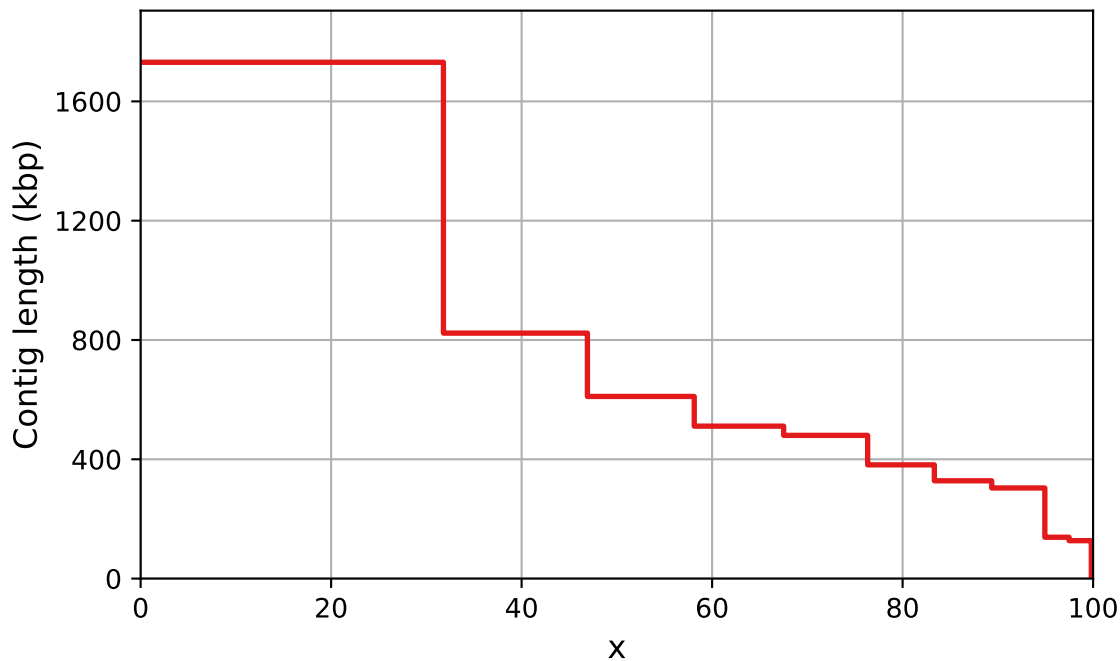
Unaligned report

	AJ292.SpadesLRL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	100

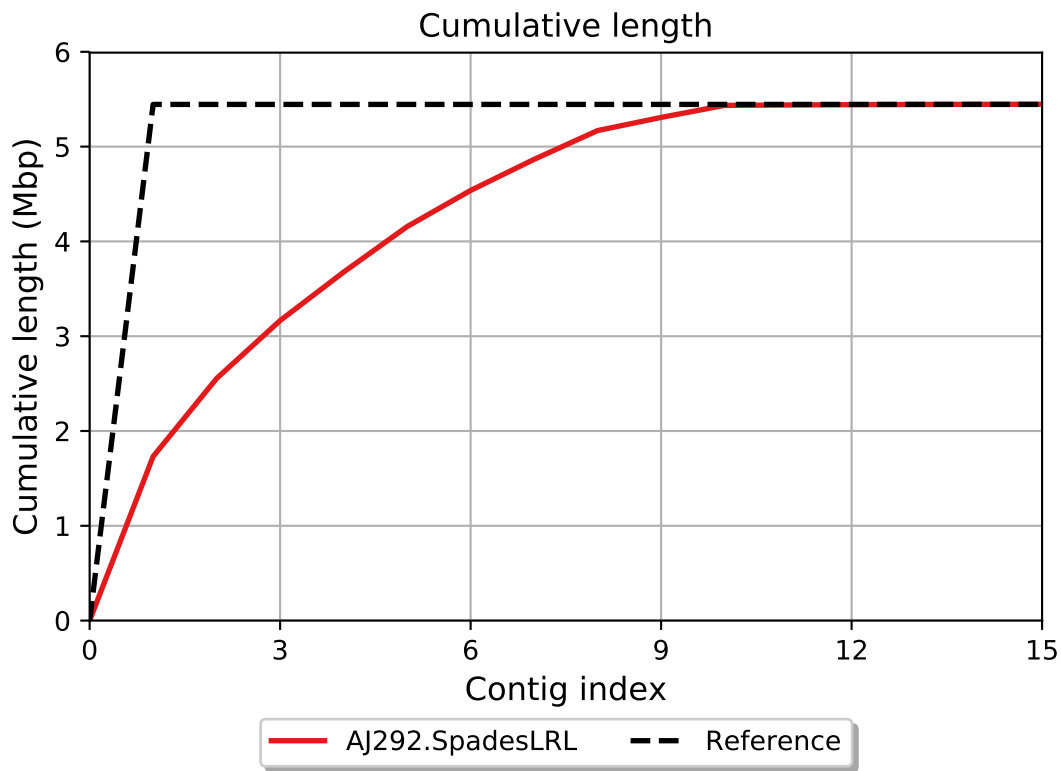
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



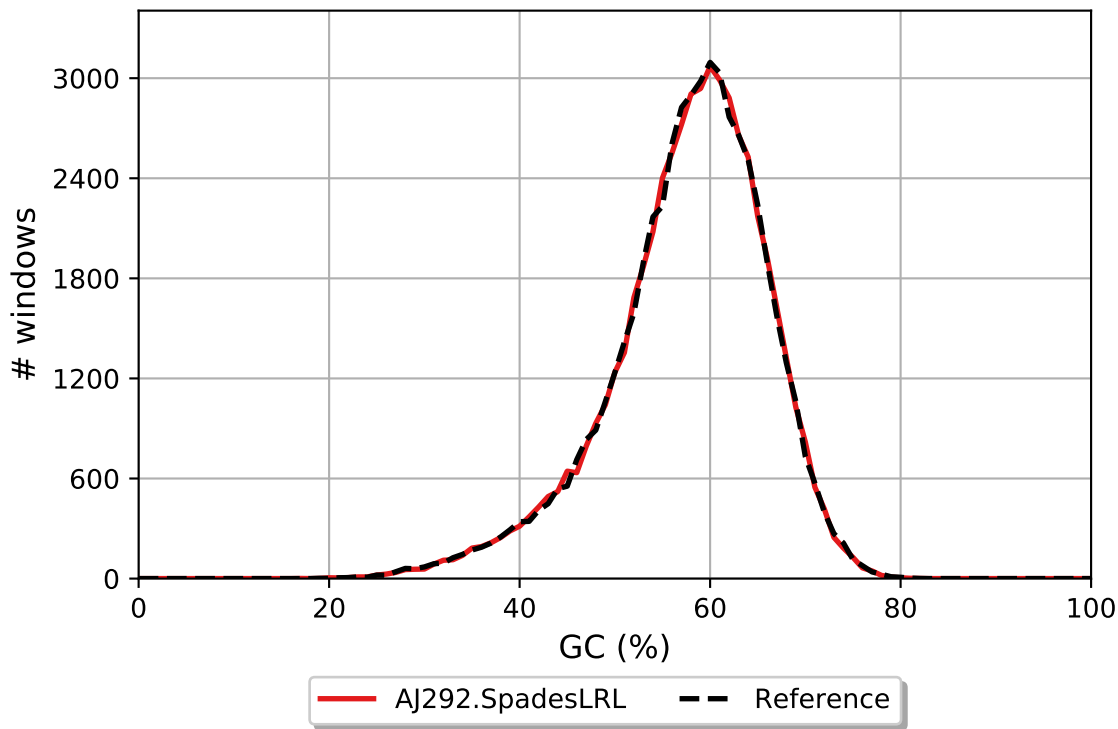
NGx



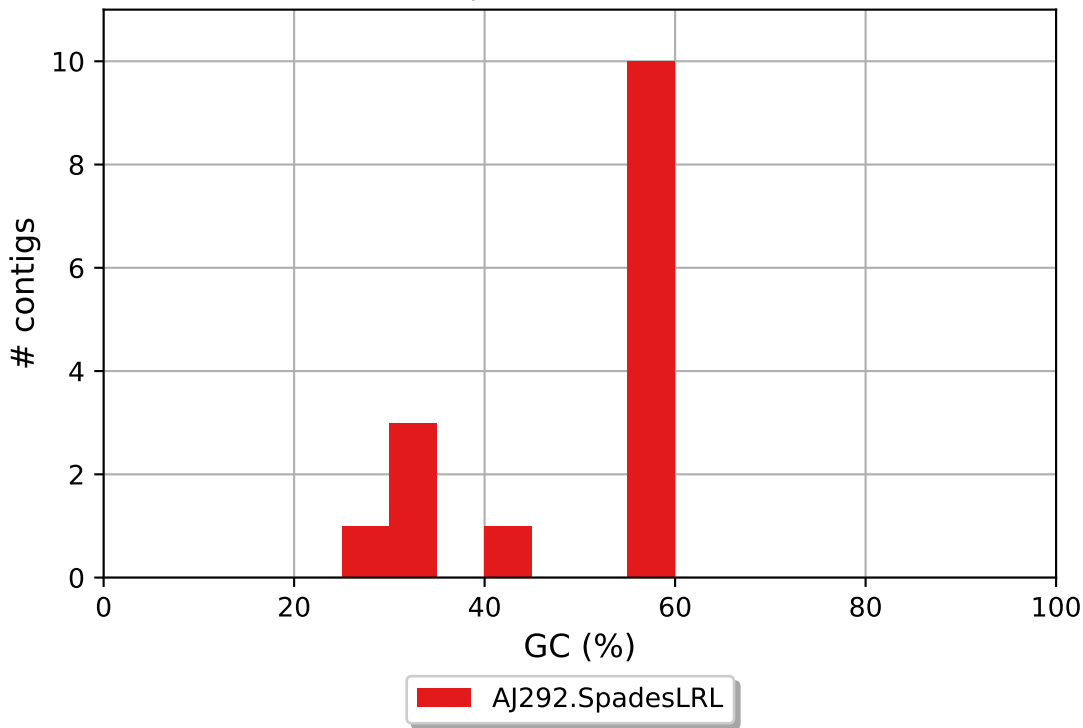
AJ292.SpadesLRL



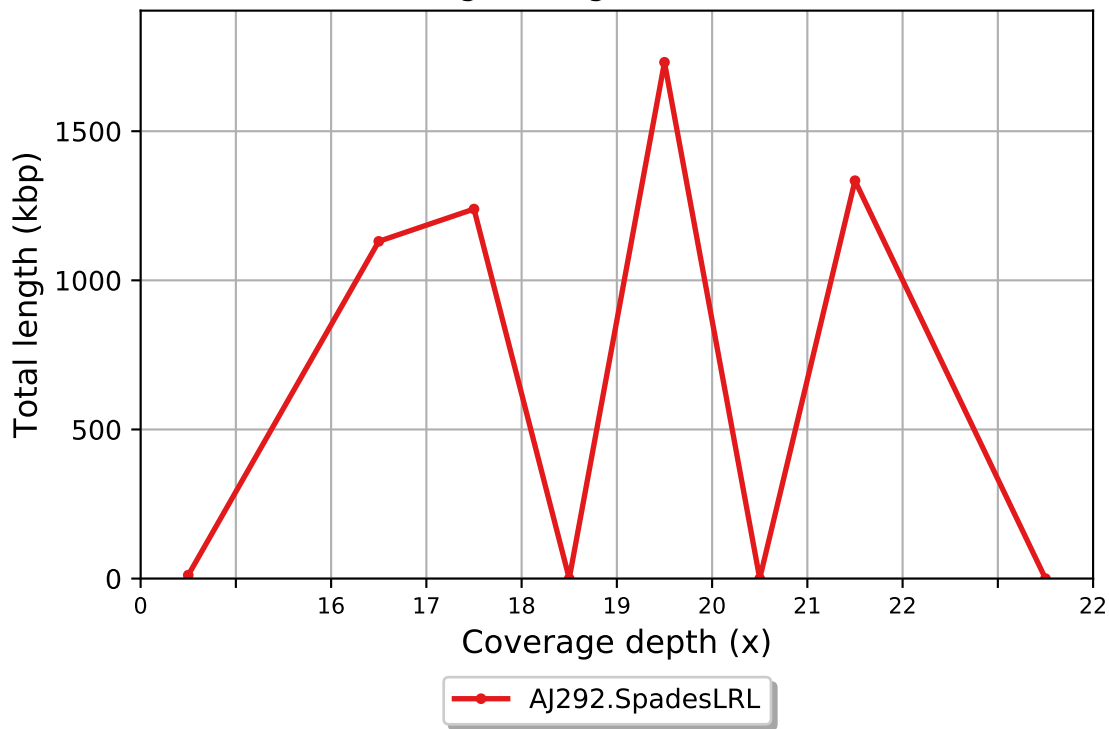
GC content



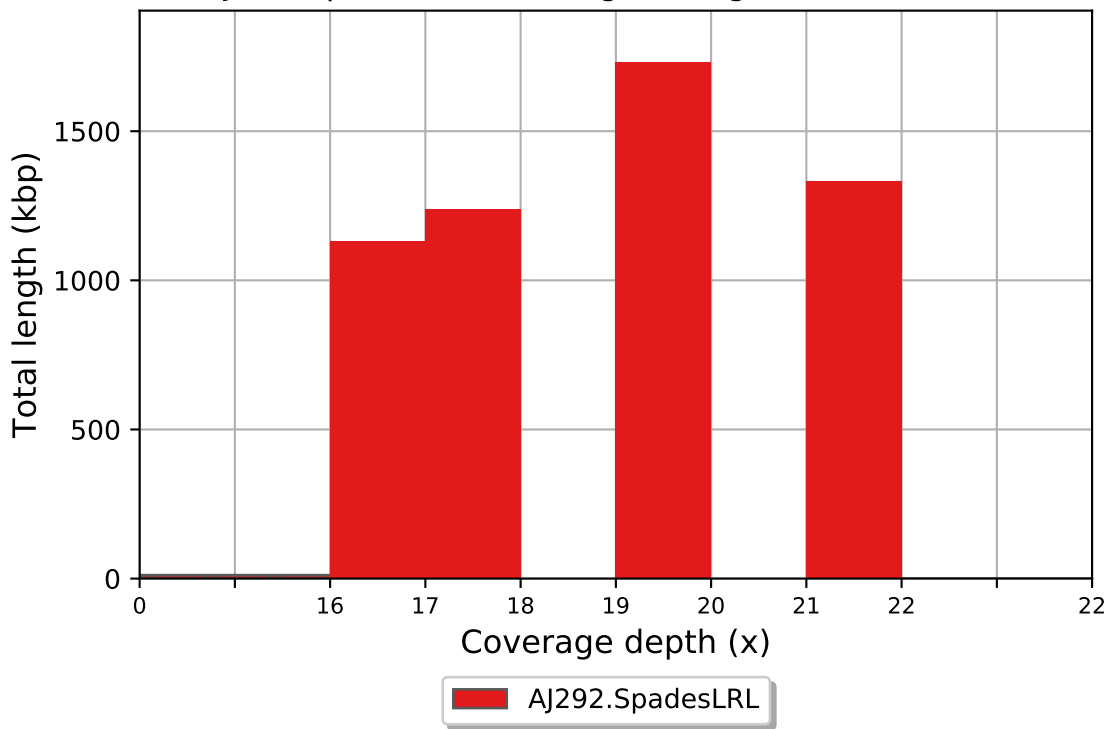
AJ292.SpadesLRL GC content



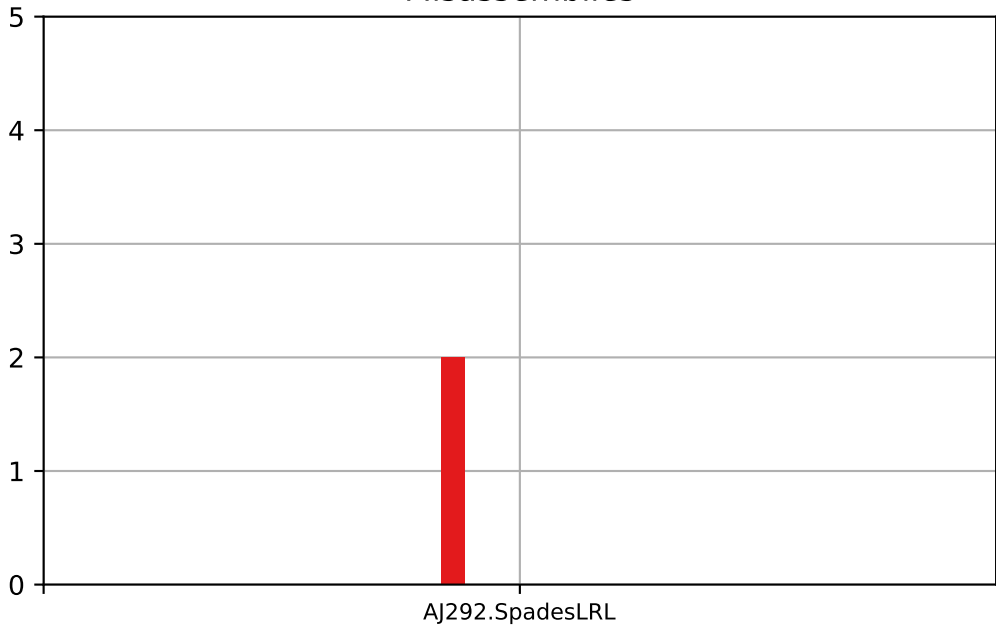
Coverage histogram (bin size: 1x)



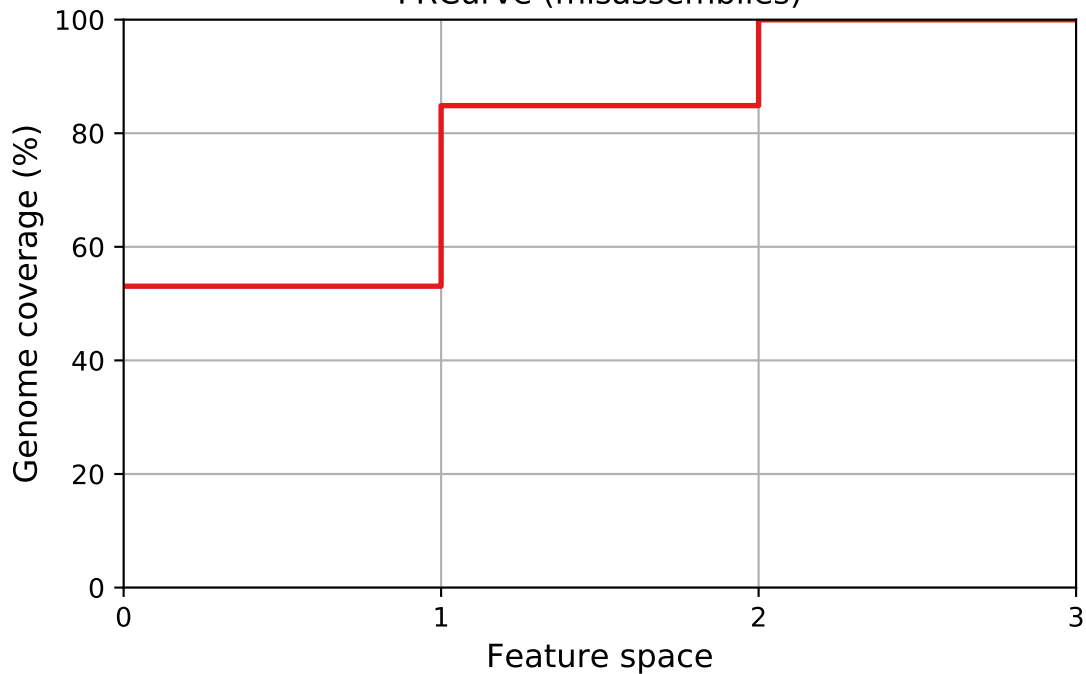
AJ292.SpadesLRL coverage histogram (bin size: 1x)



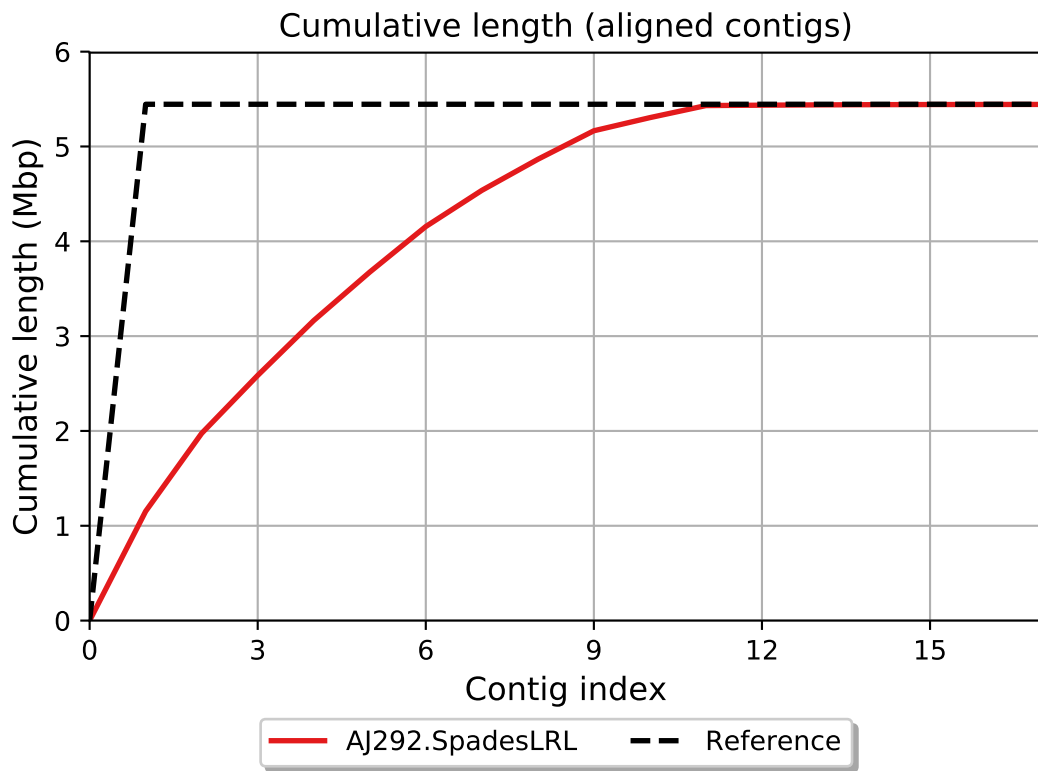
Misassemblies



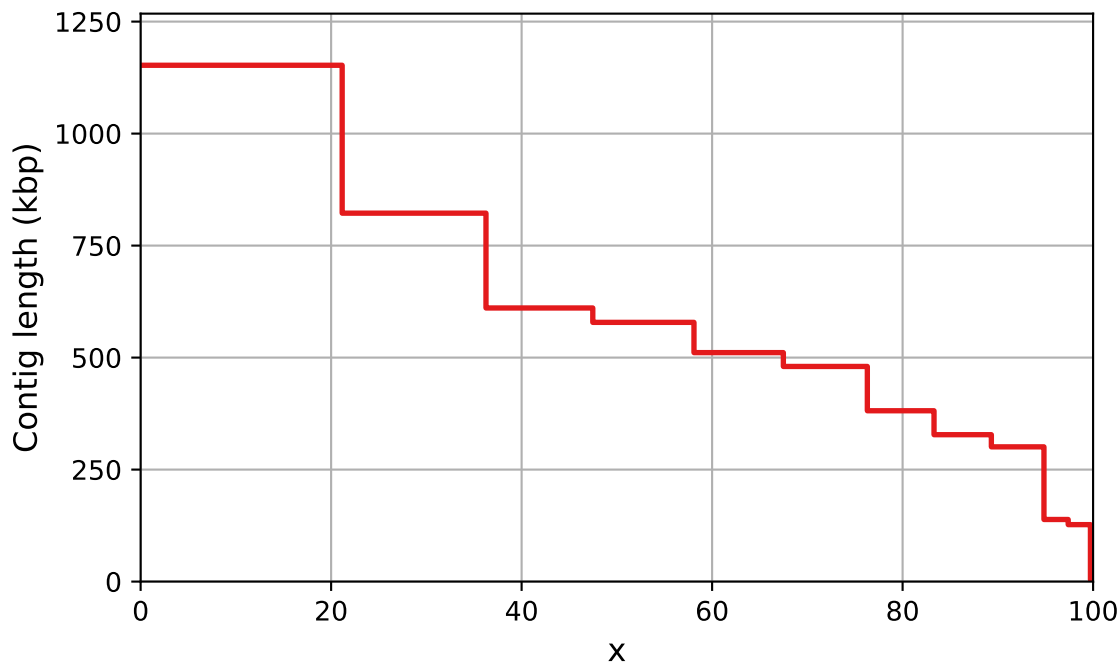
FRCurve (misassemblies)



AJ292.SpadesLRL

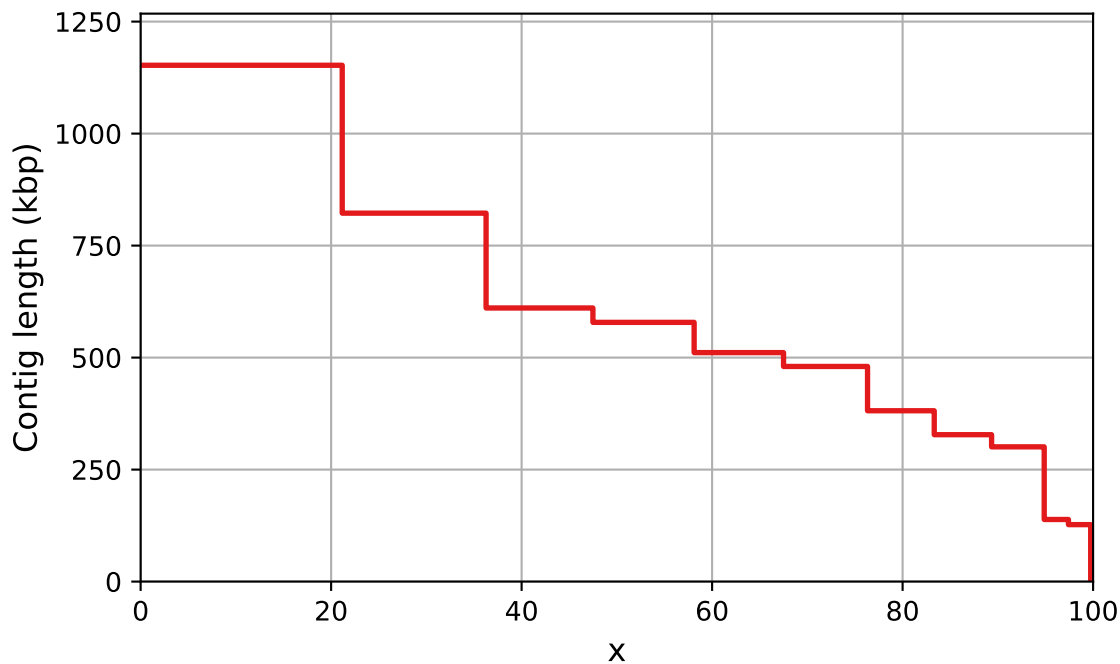


NAx



AJ292.SpadesLRL

NGAx



AJ292.SpadesLRL