

Report

	AJ292.SpadesL
# contigs (>= 0 bp)	169
# contigs (>= 1000 bp)	91
# contigs (>= 5000 bp)	72
# contigs (>= 10000 bp)	67
# contigs (>= 25000 bp)	53
# contigs (>= 50000 bp)	33
Total length (>= 0 bp)	5408471
Total length (>= 1000 bp)	5385651
Total length (>= 5000 bp)	5340398
Total length (>= 10000 bp)	5309383
Total length (>= 25000 bp)	5085532
Total length (>= 50000 bp)	4319171
# contigs	104
Largest contig	569275
Total length	5395329
Reference length	5445112
GC (%)	57.70
Reference GC (%)	57.62
N50	127859
NG50	122970
N75	60489
NG75	60489
L50	12
LG50	13
L75	29
LG75	29
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1084
# local misassemblies	11
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.987
Duplication ratio	1.001
# N's per 100 kbp	1.04
# mismatches per 100 kbp	6.22
# indels per 100 kbp	1.02
Largest alignment	569275
Total aligned length	5394955
NA50	127859
NGA50	122970
NA75	60489
NGA75	60489
LA50	12
LGA50	13
LA75	29
LGA75	29

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

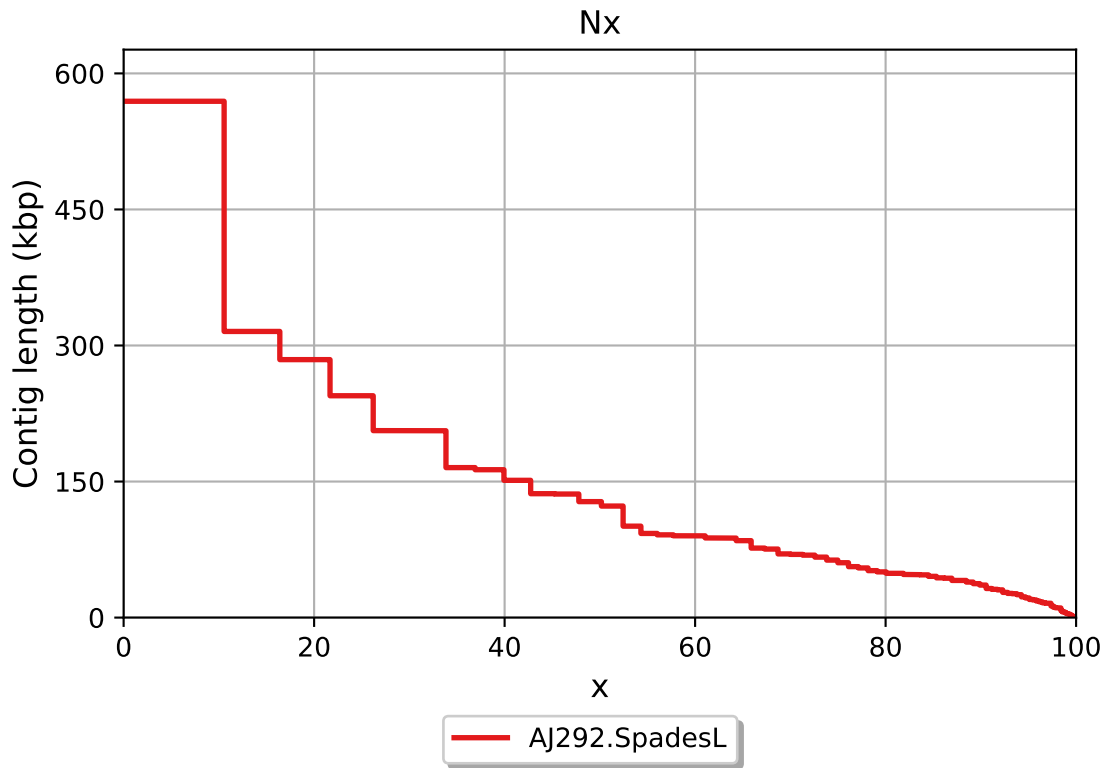
	AJ292.SpadesL
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1084
# local misassemblies	11
# unaligned mis. contigs	0
# mismatches	335
# indels	55
# indels (≤ 5 bp)	45
# indels (> 5 bp)	10
Indels length	220

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).

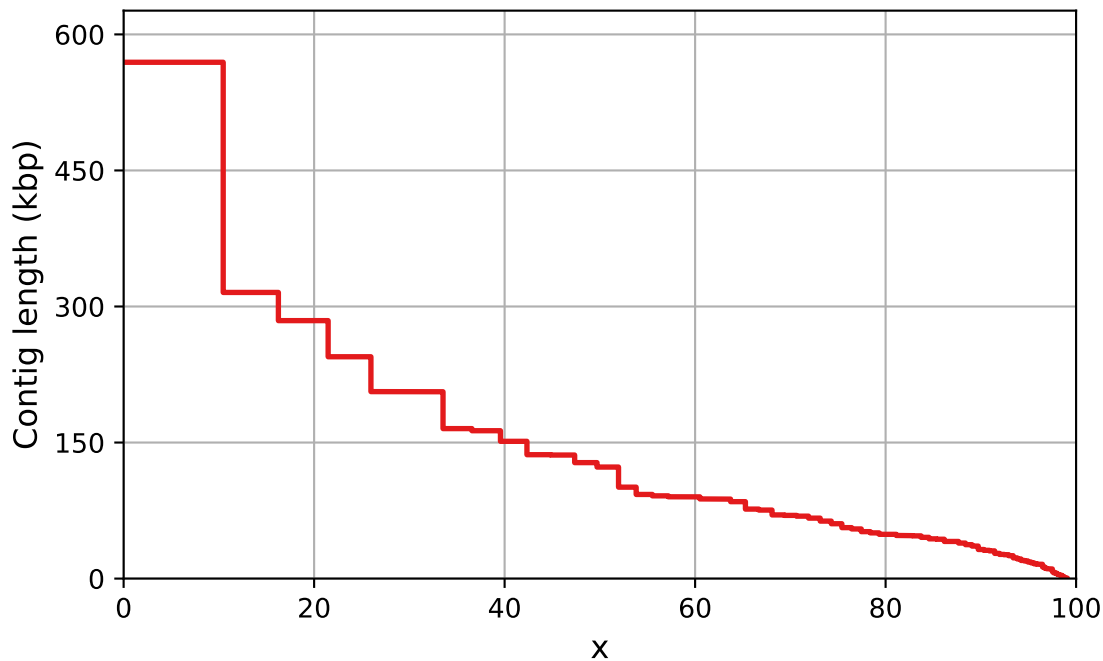
Unaligned report

	AJ292.SpadesL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	56

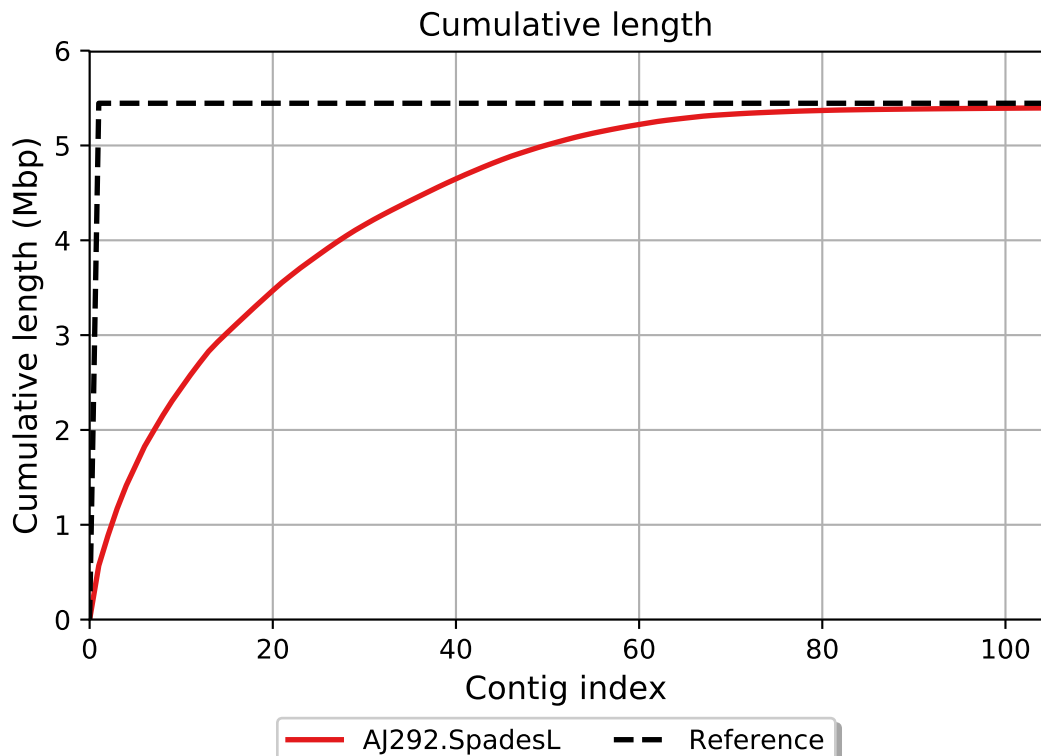
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



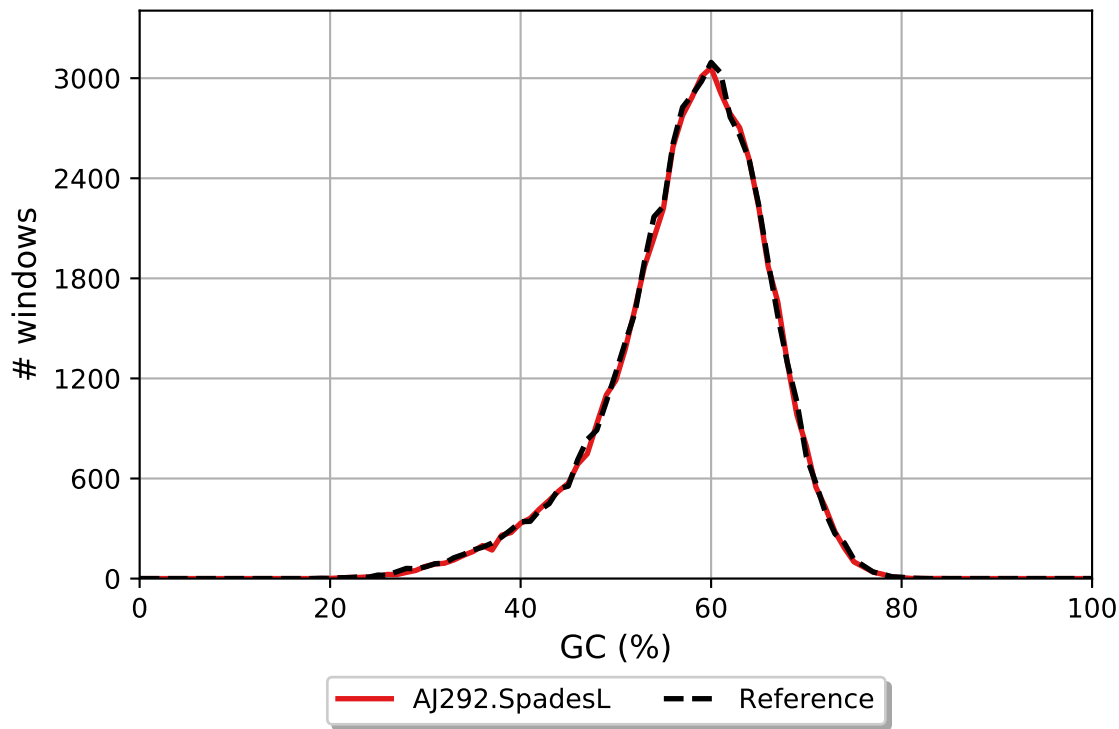
NGx



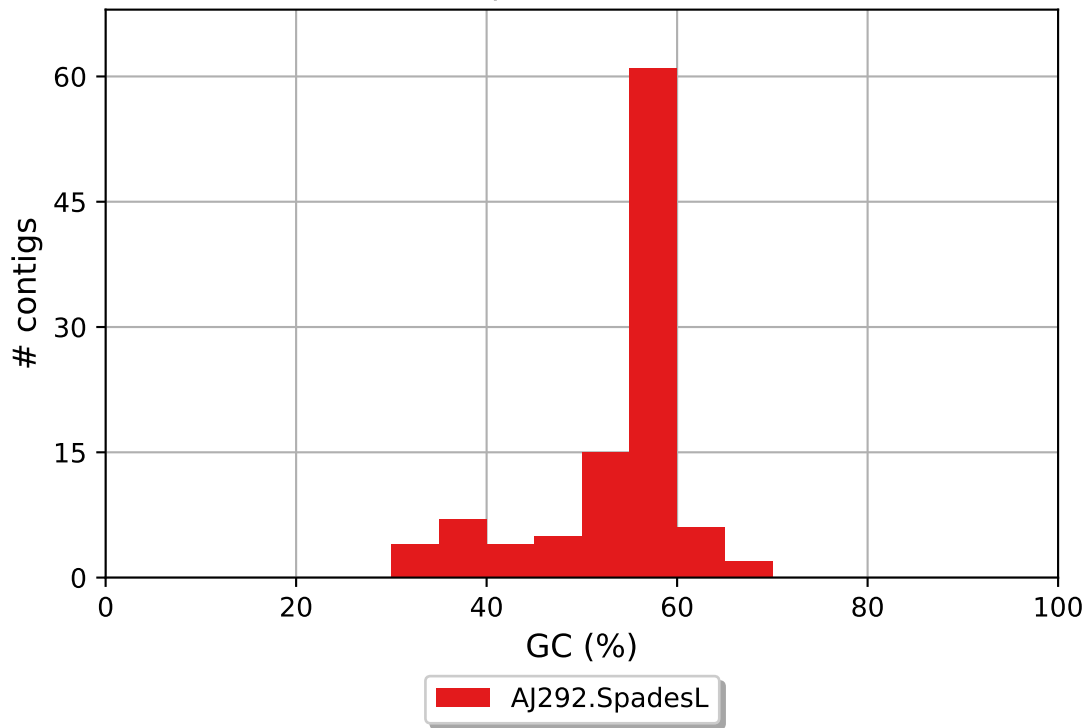
AJ292.SpadesL



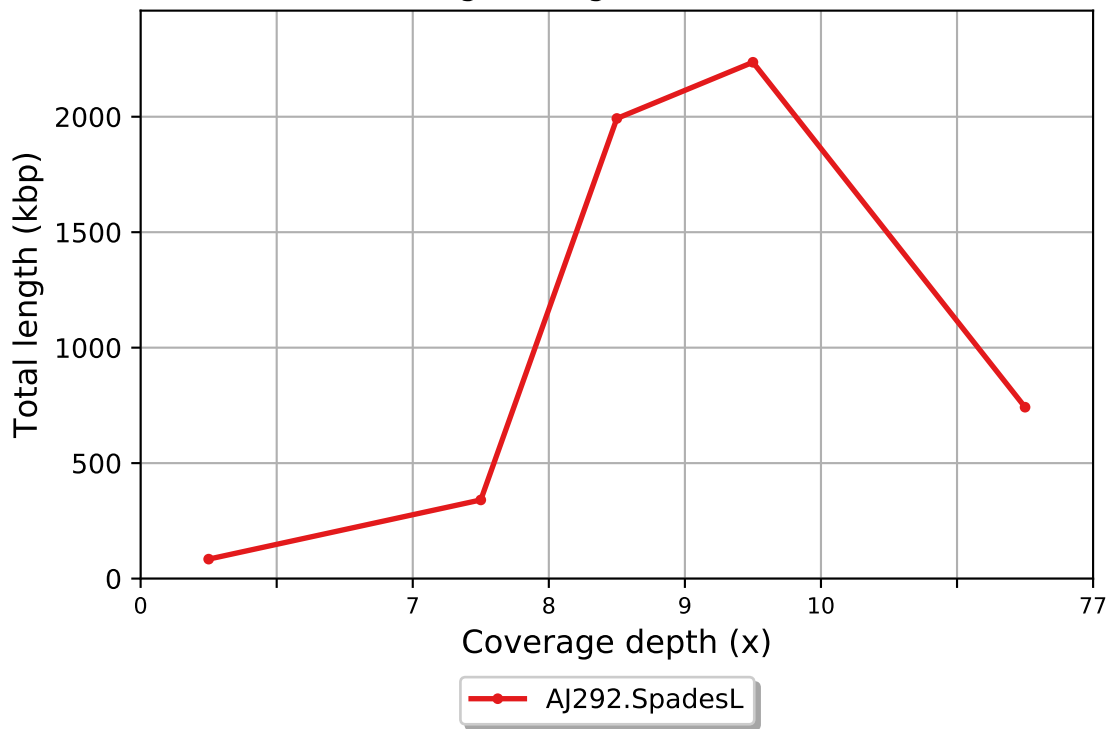
GC content



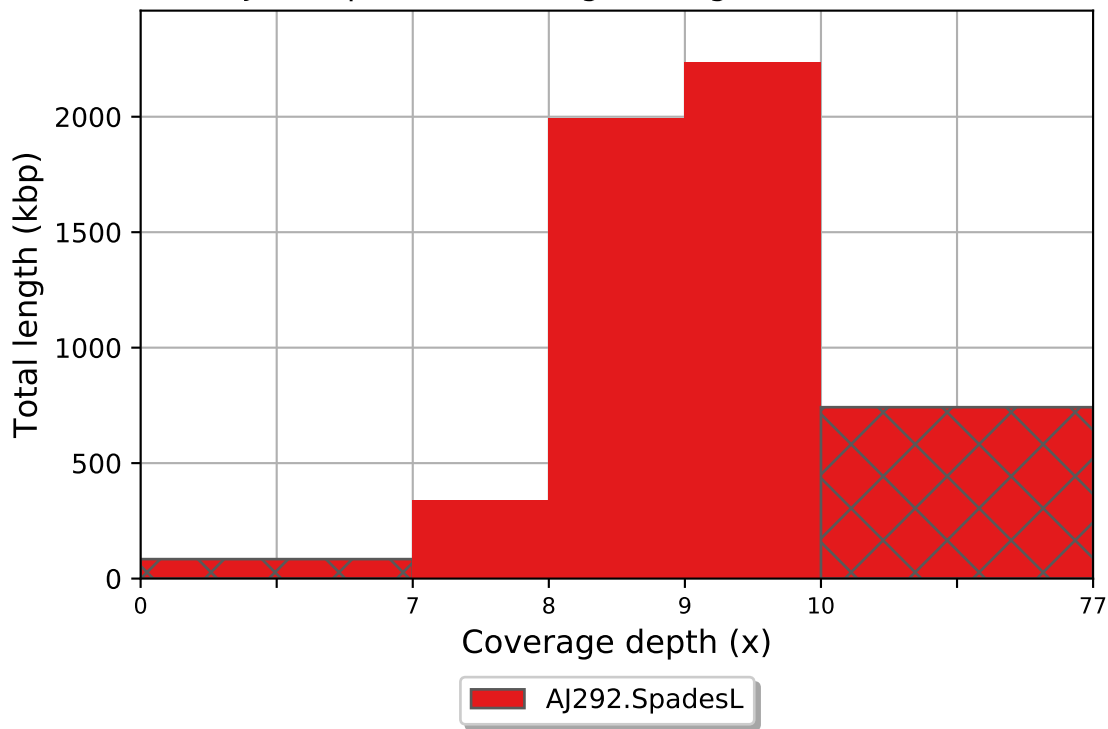
AJ292.SpadesL GC content



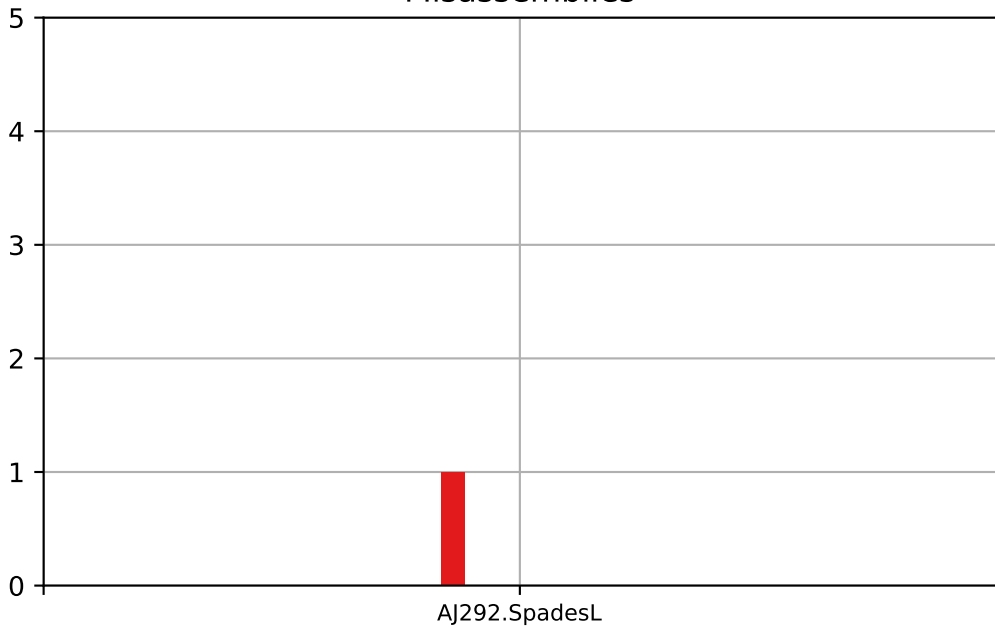
Coverage histogram (bin size: 1x)



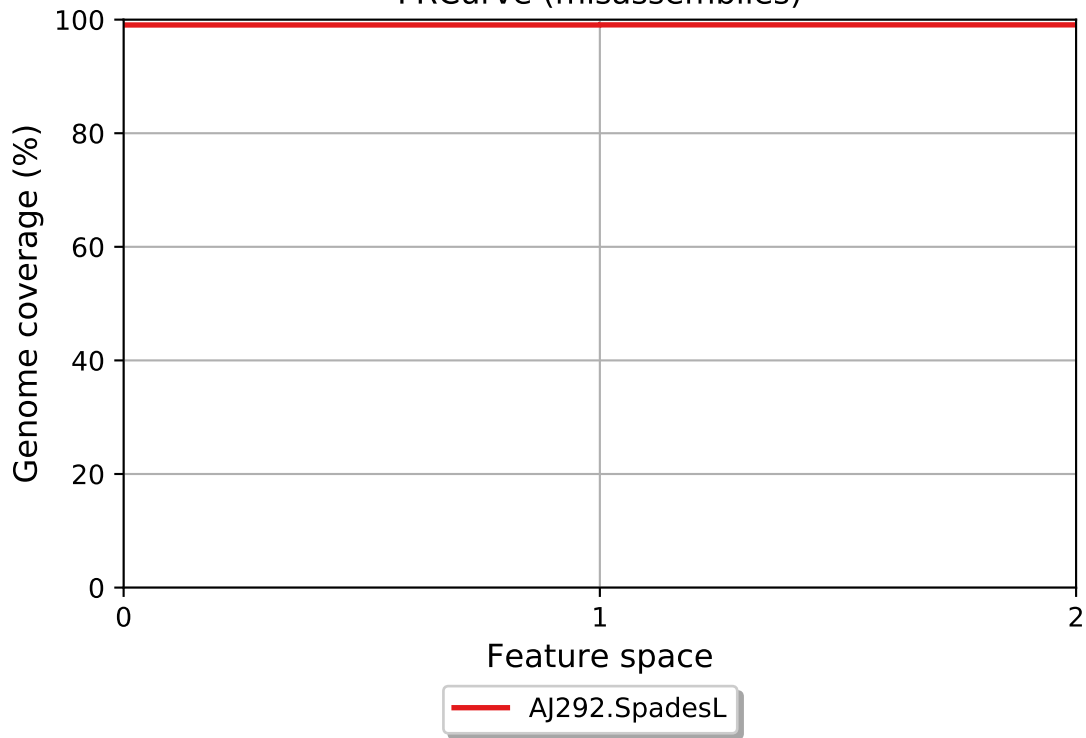
AJ292.SpadesL coverage histogram (bin size: 1x)

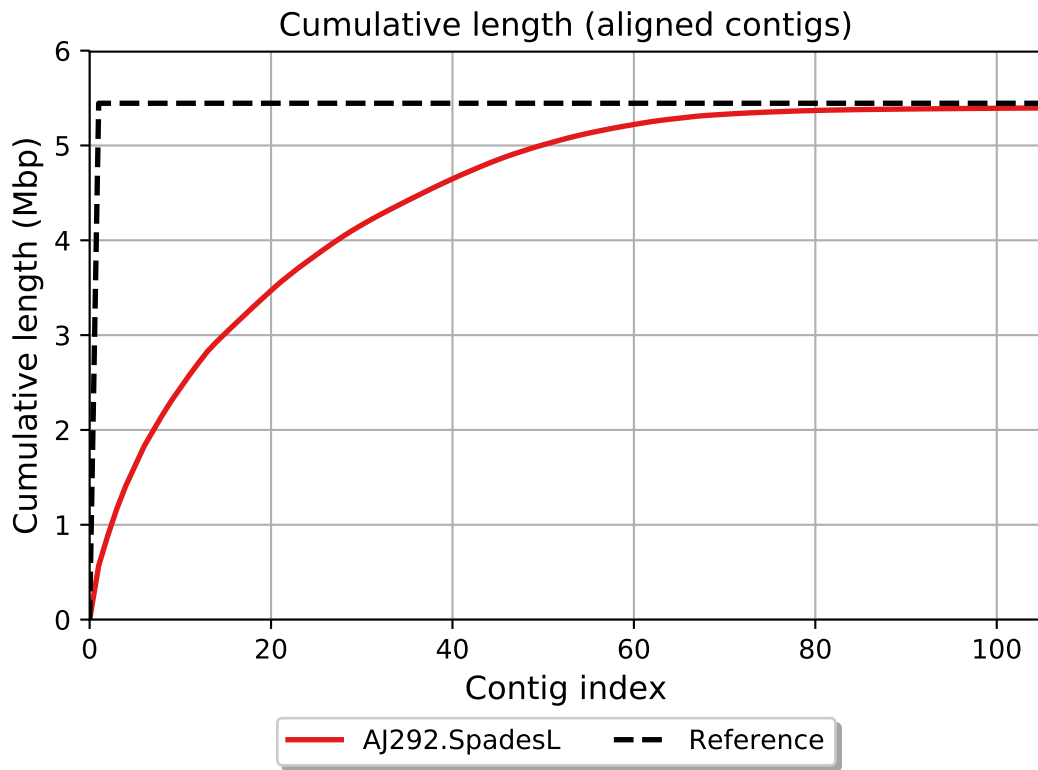


Misassemblies

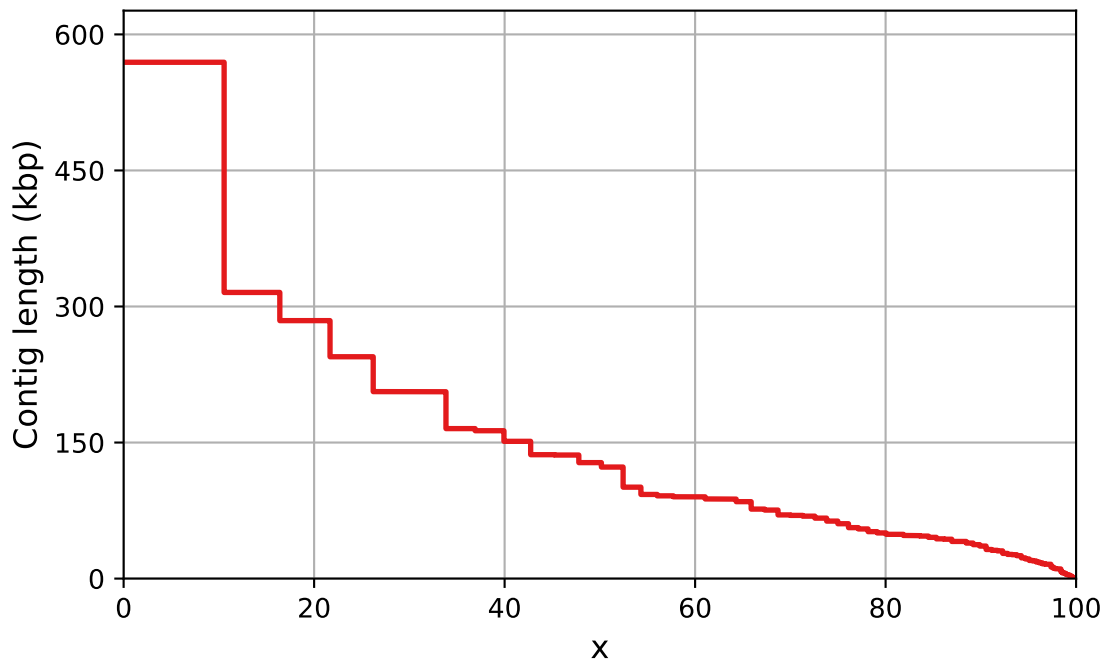


FRCurve (misassemblies)



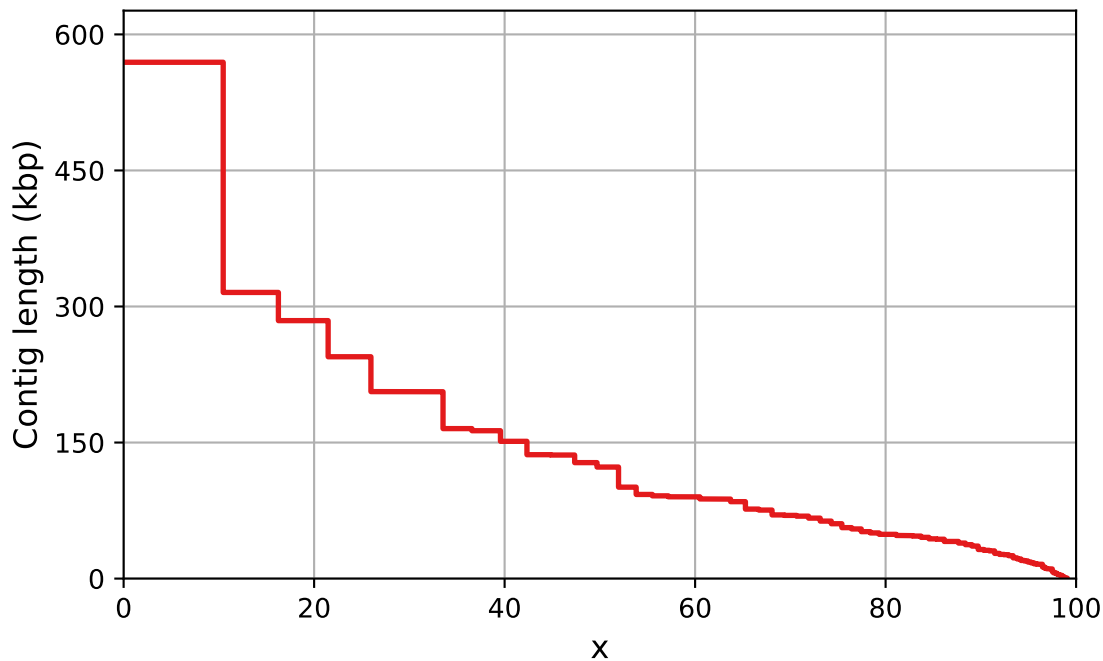


NAx



AJ292.SpadesL

NGAx



AJ292.SpadesL