Report

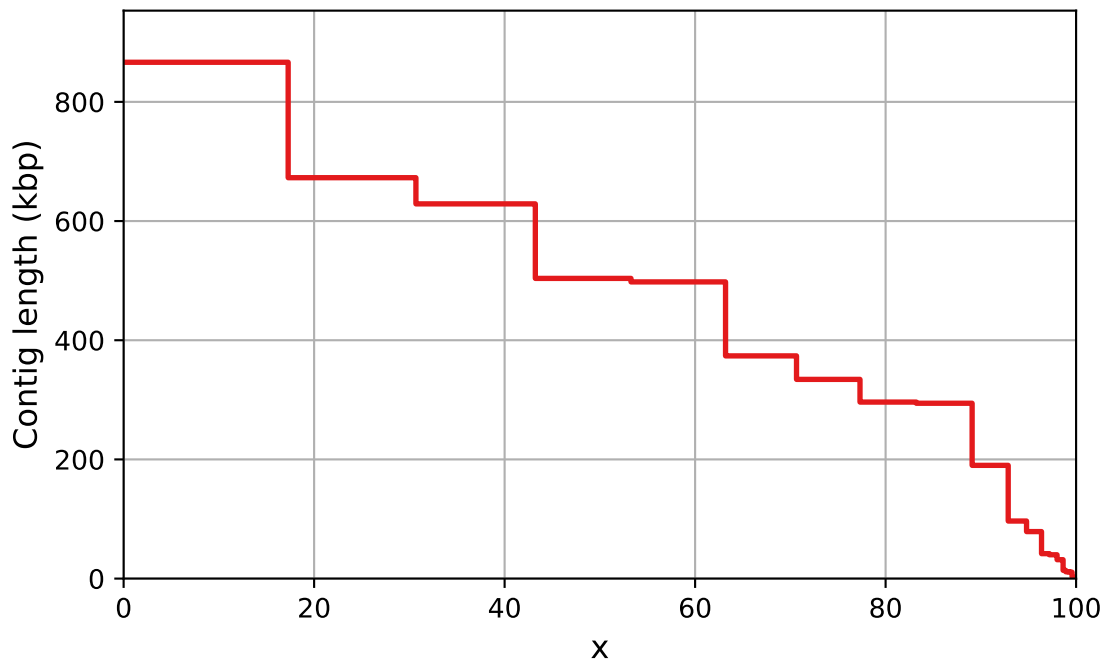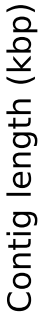|	sim5M.SpadesLRL
# contigs (>= 0 bp)	100
# contigs (>= 1000 bp)	28
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	19
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	12
Total length (>= 0 bp)	5029581
Total length (>= 1000 bp)	5008561
Total length (>= 5000 bp)	4994572
Total length (>= 10000 bp)	4994572
Total length (>= 25000 bp)	4947236
Total length (>= 50000 bp)	4833699
# contigs	38
Largest contig	866471
Total length	5015744
Reference length	5000040
GC (%)	35.85
Reference GC (%)	35.84
N50	503768
NG50	503768
N75	334297
NG75	334297
L50	4
LG50	4
L75	7
LG75	7
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	707703
# local misassemblies	3
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.714
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	47.86
# indels per 100 kbp	1.91
Largest alignment	866471
Total aligned length	5010201
NA50	494811
NGA50	494811
NA75	294247
NGA75	294247
LA50	4
LGA50	4
LA75	8
LGA75	8

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
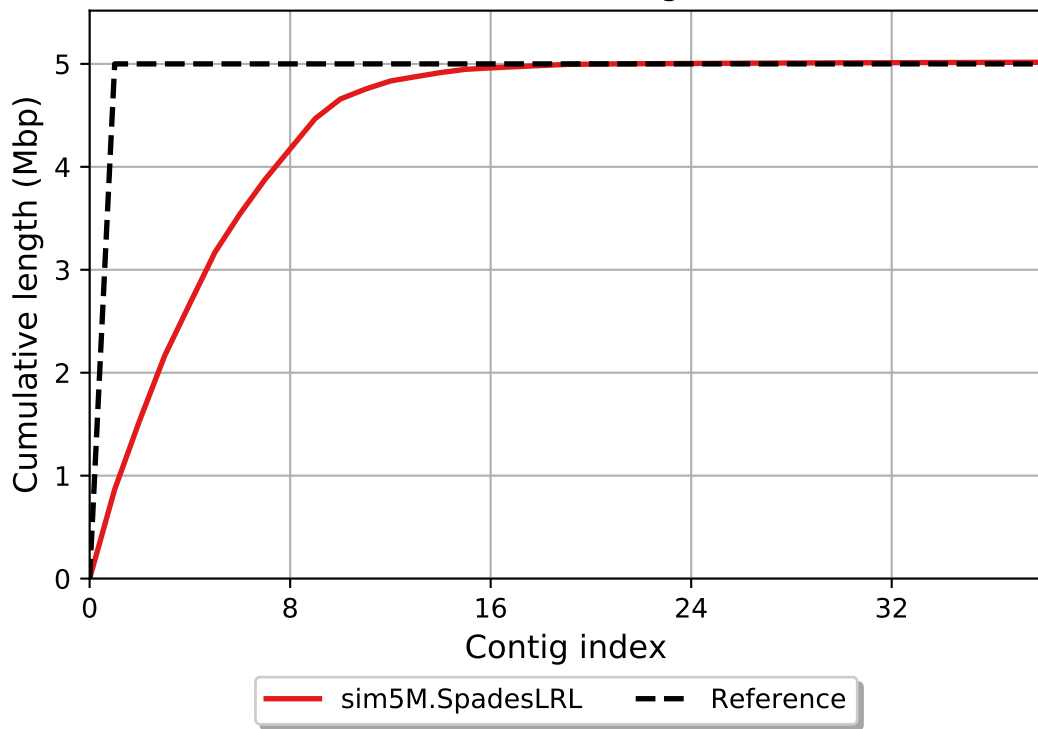
	sim5M.SpadesLRL
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	707703
# local misassemblies	3
# unaligned mis. contigs	0
# mismatches	2386
# indels	95
# indels (<= 5 bp)	89
# indels (> 5 bp)	6
Indels length	238

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

	sim5M.SpadesLRL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).
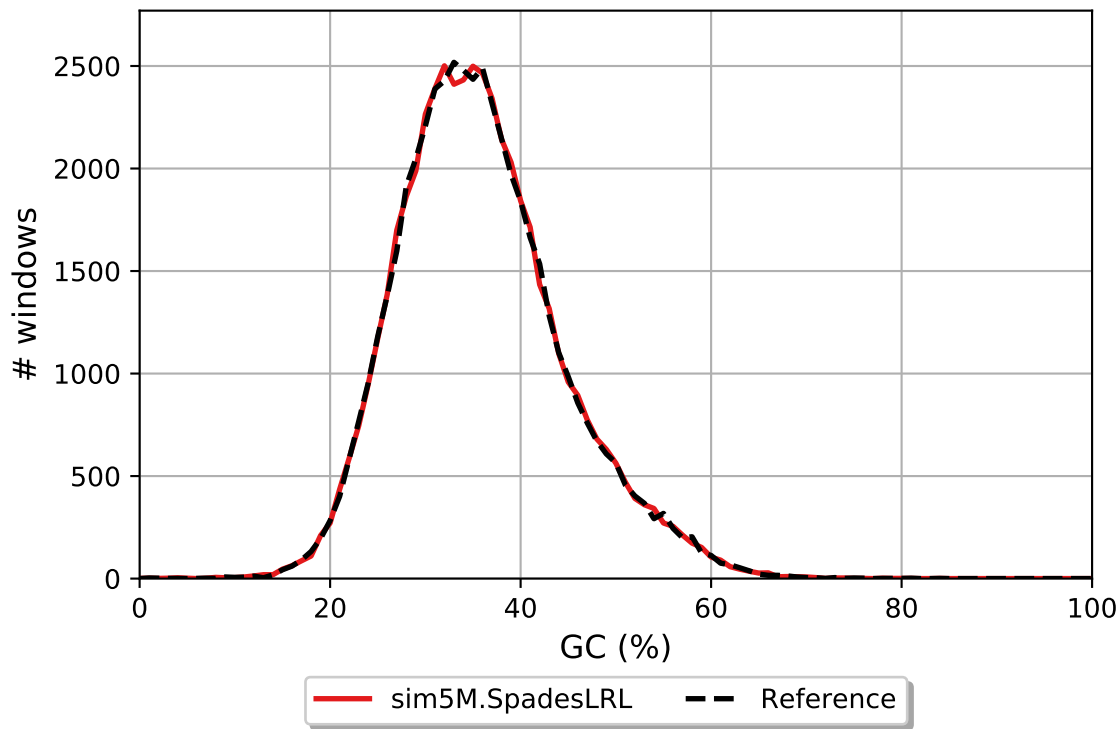
Nx

sim5M.SpadesLRL

NGx

Contig length (kbp) vs x

sim5M.SpadesLRL

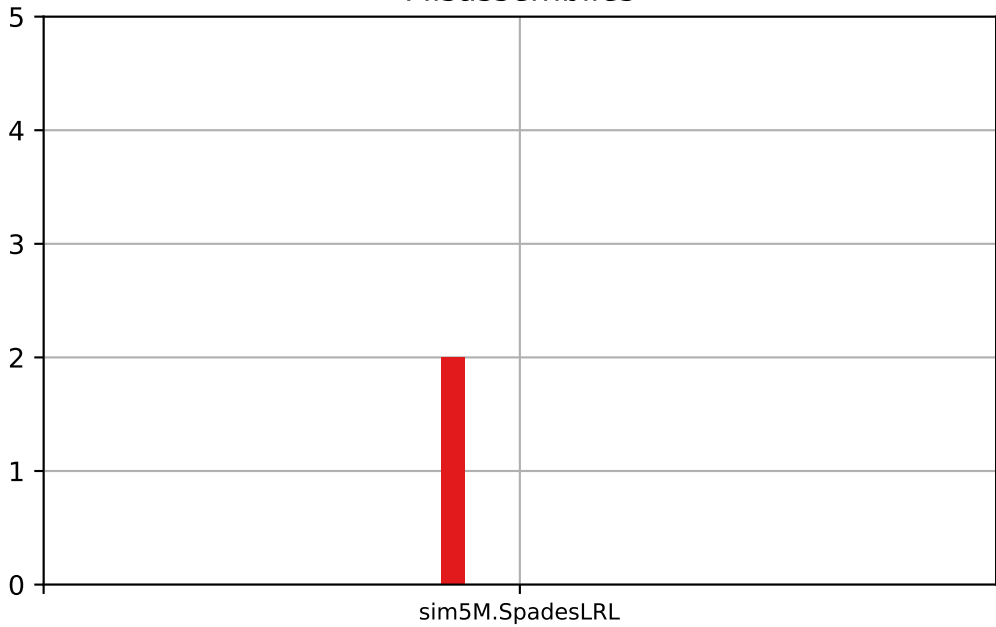Cumulative length

GC content

sim5M.SpadesLRL GC content
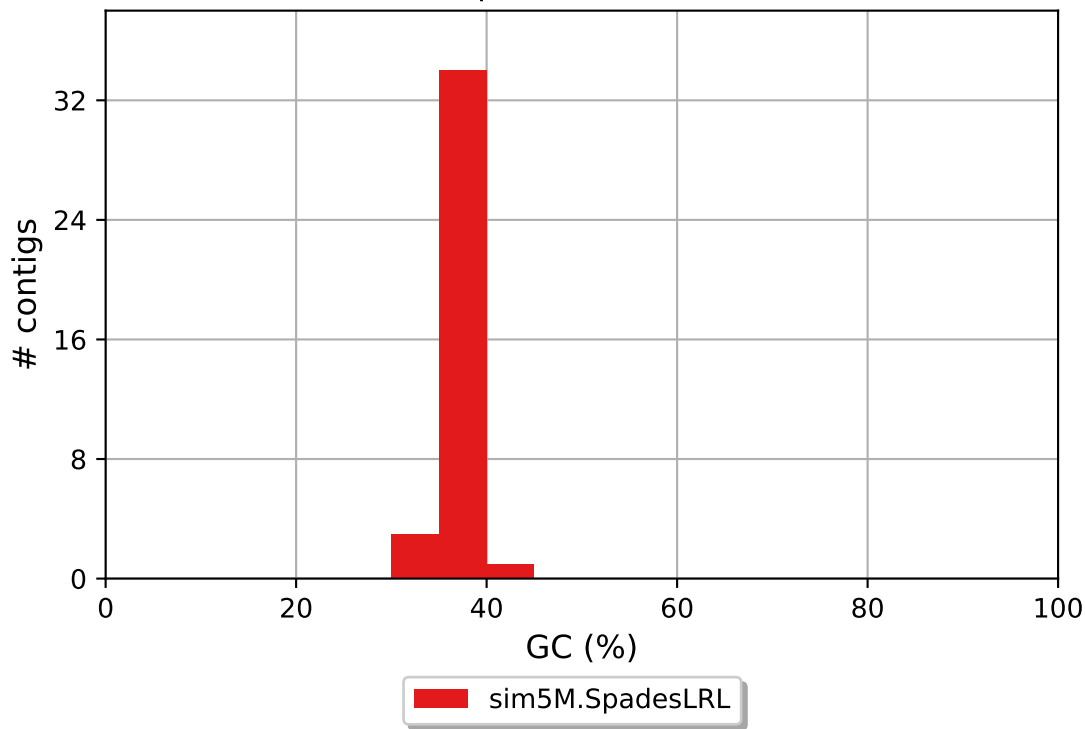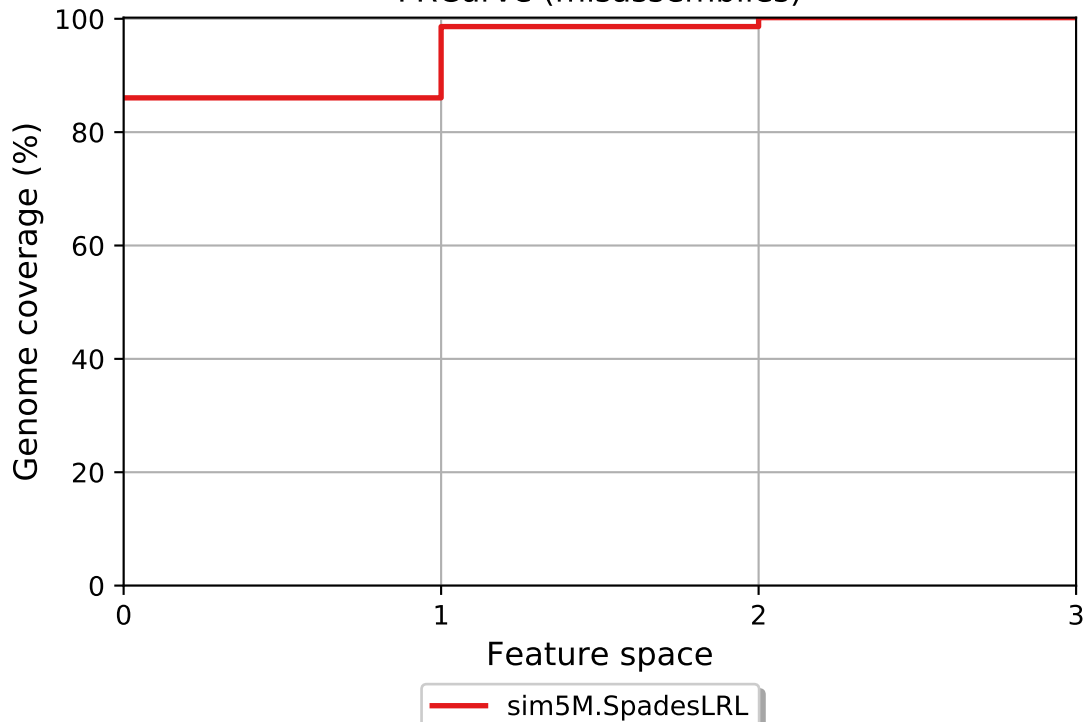
Coverage histogram (bin size: 1x)
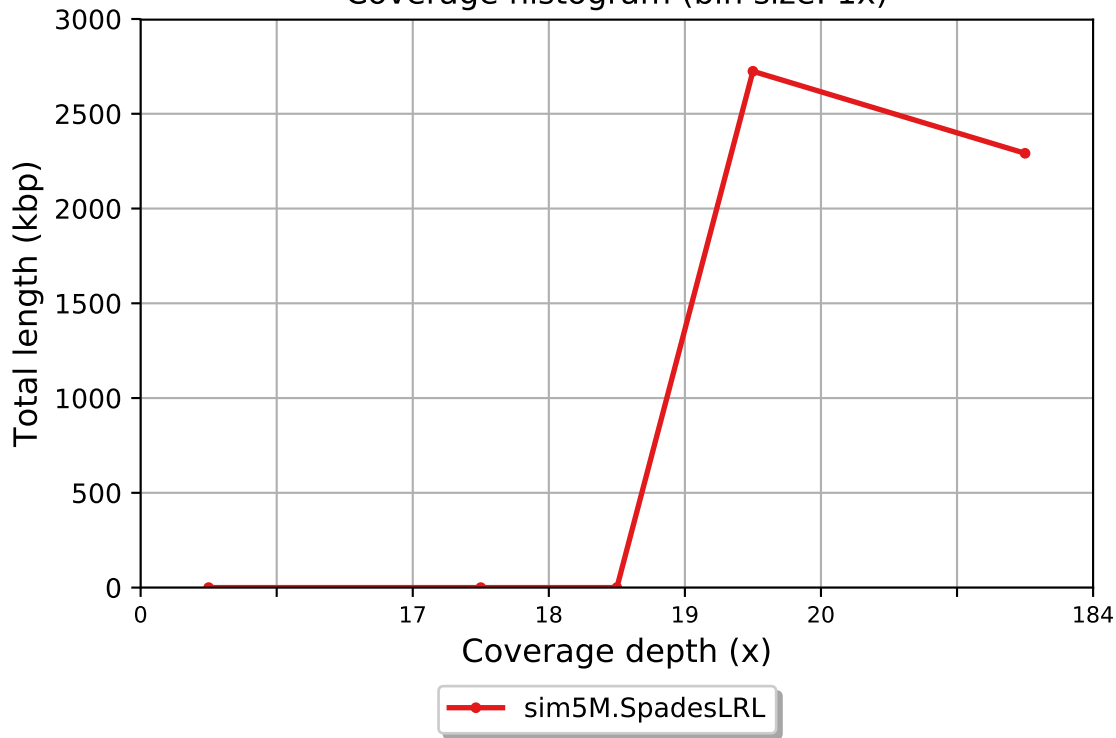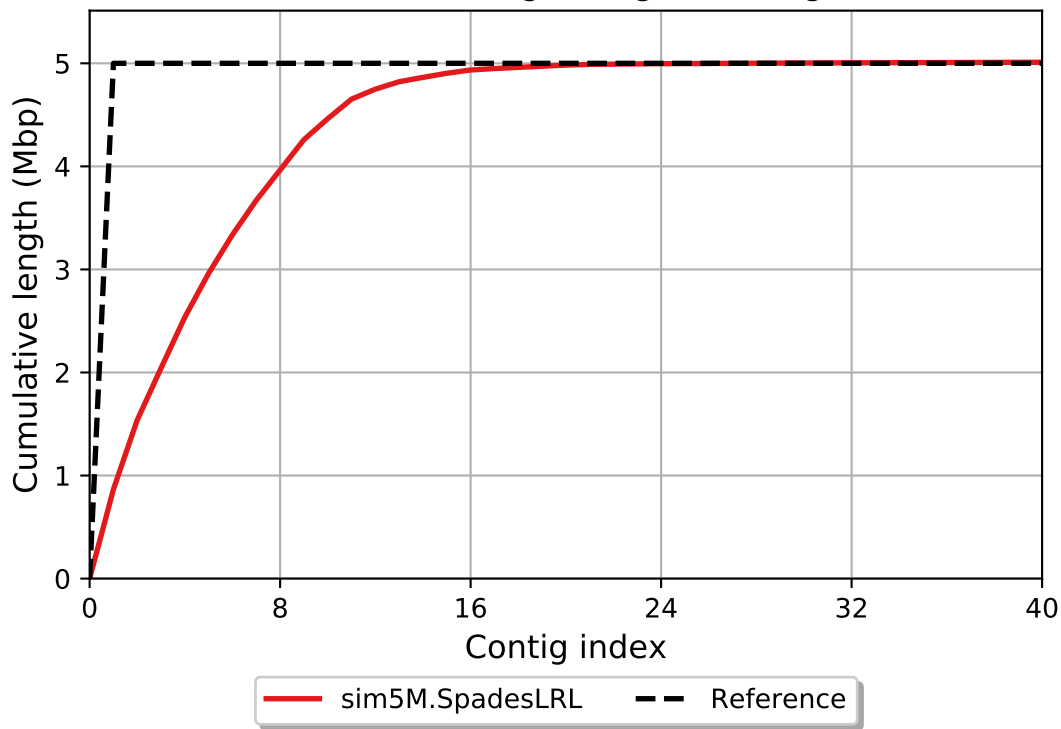
sim5M.SpadesLRL coverage histogram (bin size: 1x)

Misassemblies
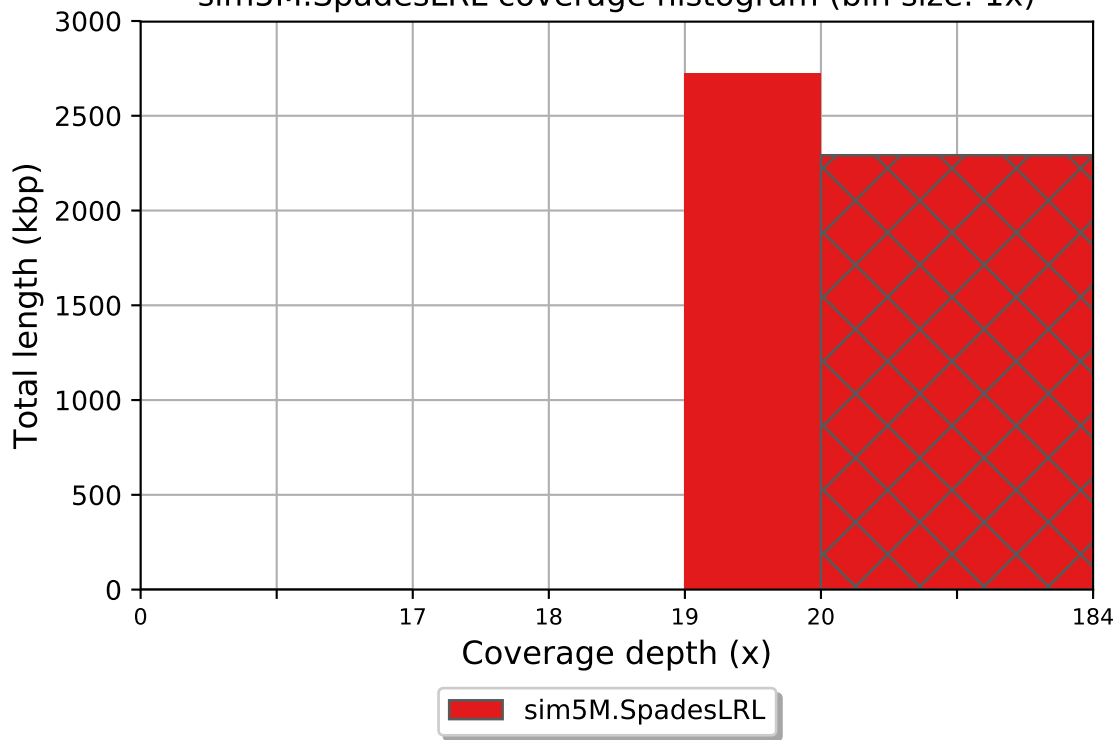
sim5M.SpadesLRL

relocations

FRCurve (misassemblies)

sim5M.SpadesLRL

Cumulative length (aligned contigs)

NAx

NGAx