

Report

	sim25M.SpadesLRL
# contigs (>= 0 bp)	992
# contigs (>= 1000 bp)	161
# contigs (>= 5000 bp)	109
# contigs (>= 10000 bp)	97
# contigs (>= 25000 bp)	74
# contigs (>= 50000 bp)	60
Total length (>= 0 bp)	25204006
Total length (>= 1000 bp)	24972951
Total length (>= 5000 bp)	24864278
Total length (>= 10000 bp)	24772308
Total length (>= 25000 bp)	24356264
Total length (>= 50000 bp)	23895615
# contigs	292
Largest contig	2267284
Total length	25060402
Reference length	25000020
GC (%)	43.72
Reference GC (%)	43.69
N50	653521
NG50	653521
N75	429370
NG75	429370
L50	13
LG50	13
L75	25
LG75	25
# misassemblies	87
# misassembled contigs	39
Misassembled contigs length	8316509
# local misassemblies	53
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	1978
Genome fraction (%)	99.468
Duplication ratio	1.008
# N's per 100 kbp	0.08
# mismatches per 100 kbp	52.15
# indels per 100 kbp	3.17
Largest alignment	2267284
Total aligned length	25043025
NA50	524800
NGA50	524800
NA75	276994
NGA75	276994
LA50	15
LGA50	15
LA75	30
LGA75	30

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

	sim25M.SpadesLRL
# misassemblies	87
# relocations	87
# translocations	0
# inversions	0
# misassembled contigs	39
Misassembled contigs length	8316509
# local misassemblies	53
# unaligned mis. contigs	0
# mismatches	12967
# indels	788
# indels (≤ 5 bp)	687
# indels (> 5 bp)	101
Indels length	2704

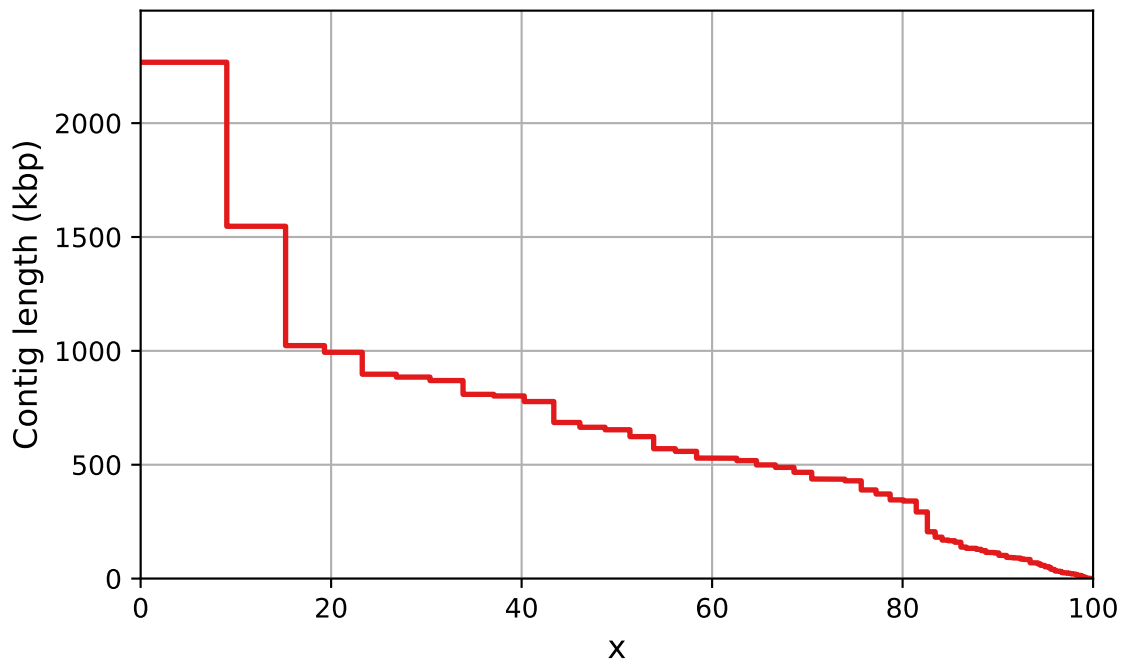
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	sim25M.SpadesLRL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	1978
# N's	20

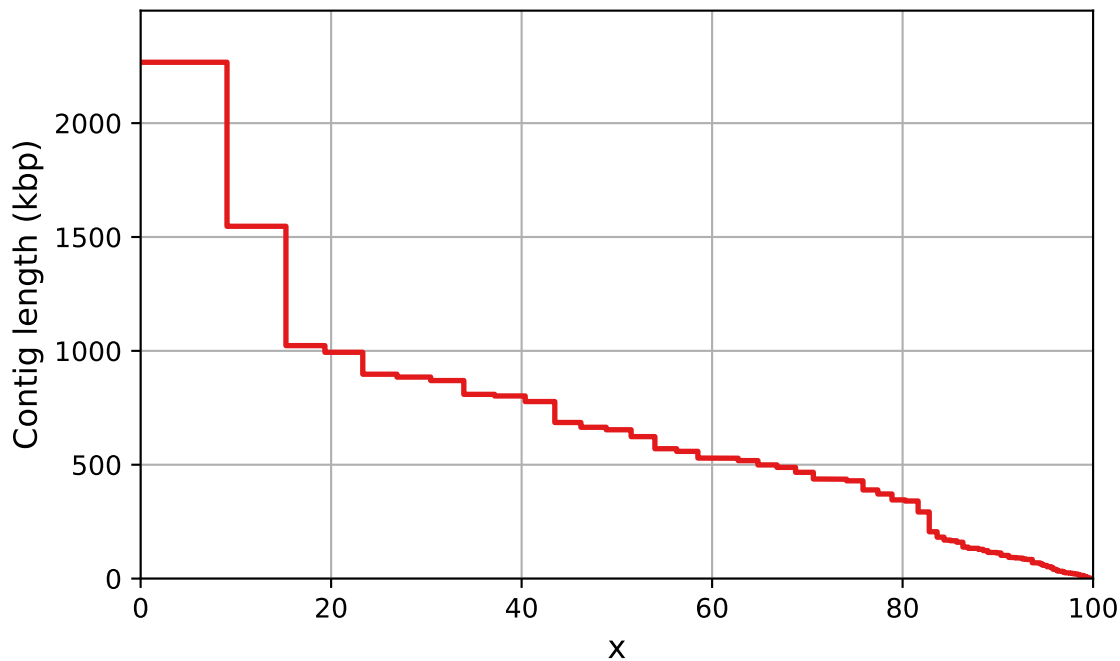
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



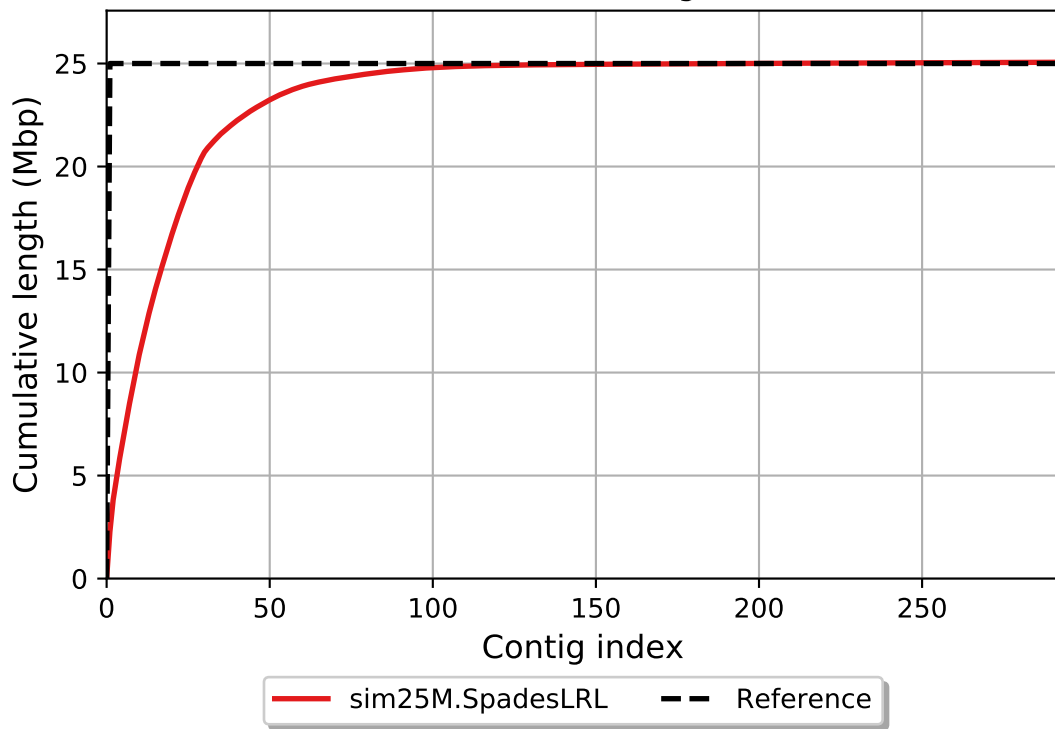
sim25M.SpadesLRL

NGx

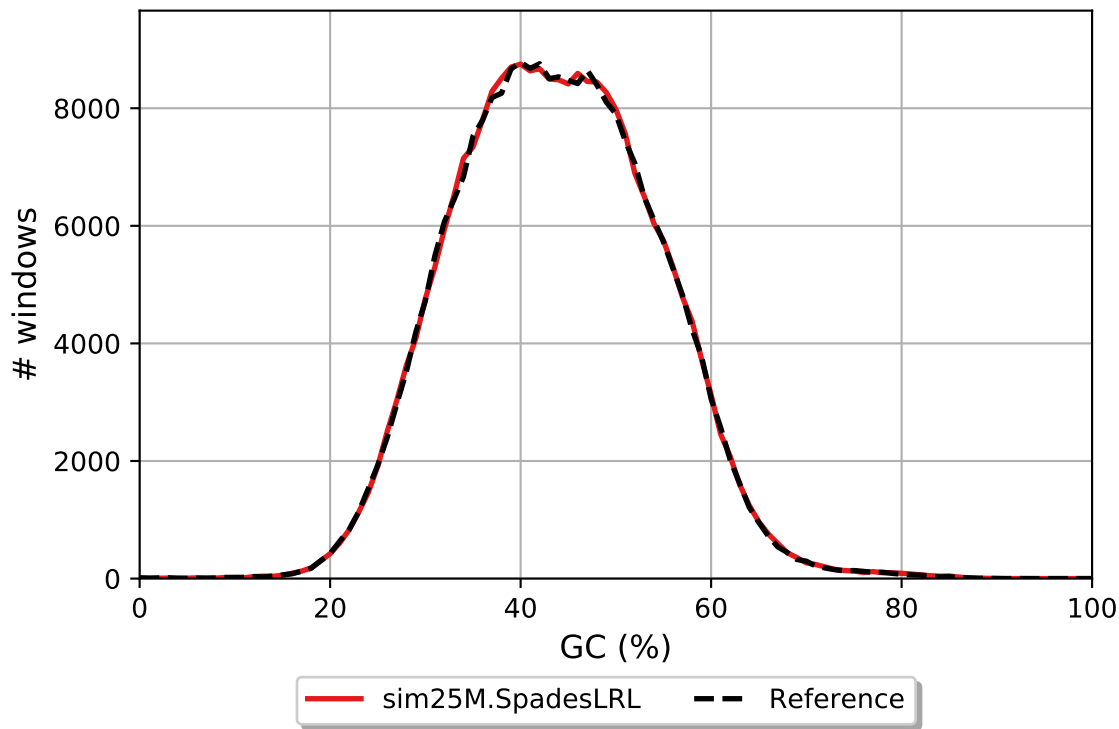


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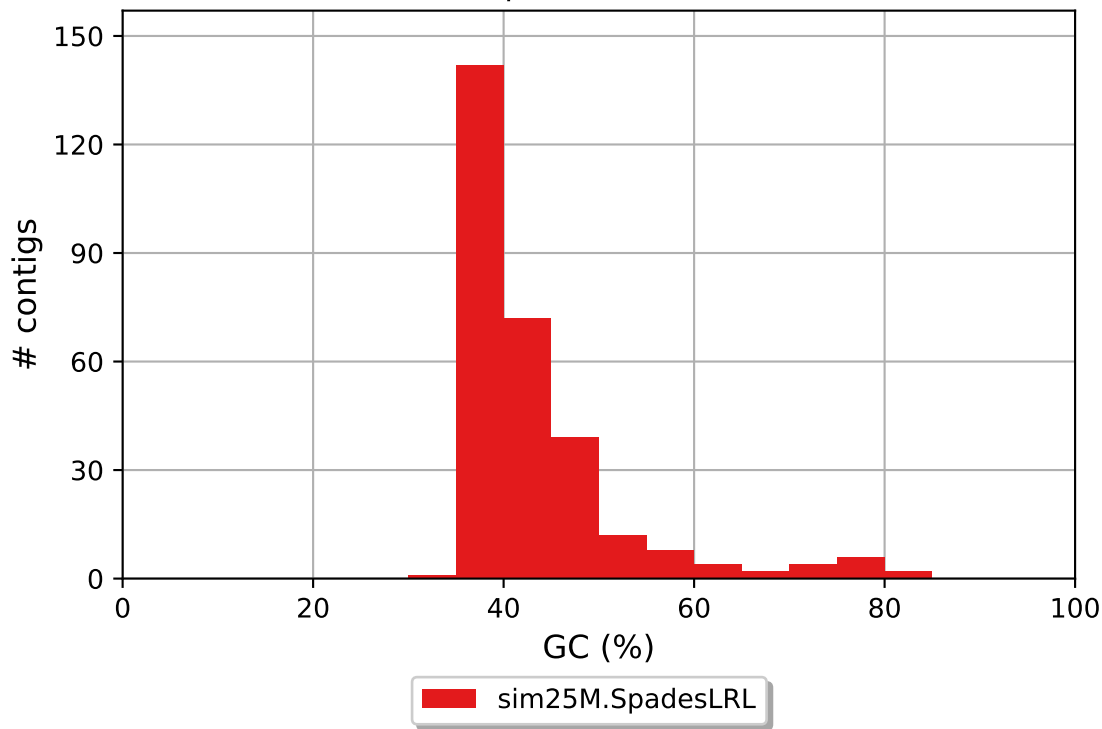
Cumulative length



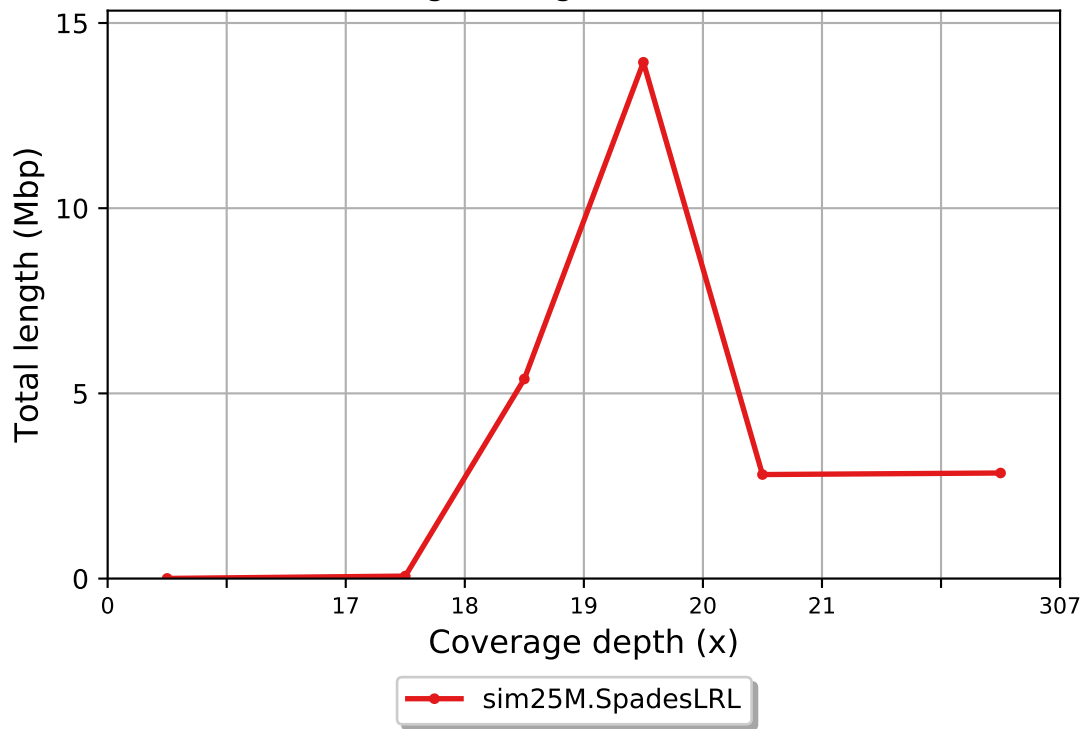
GC content



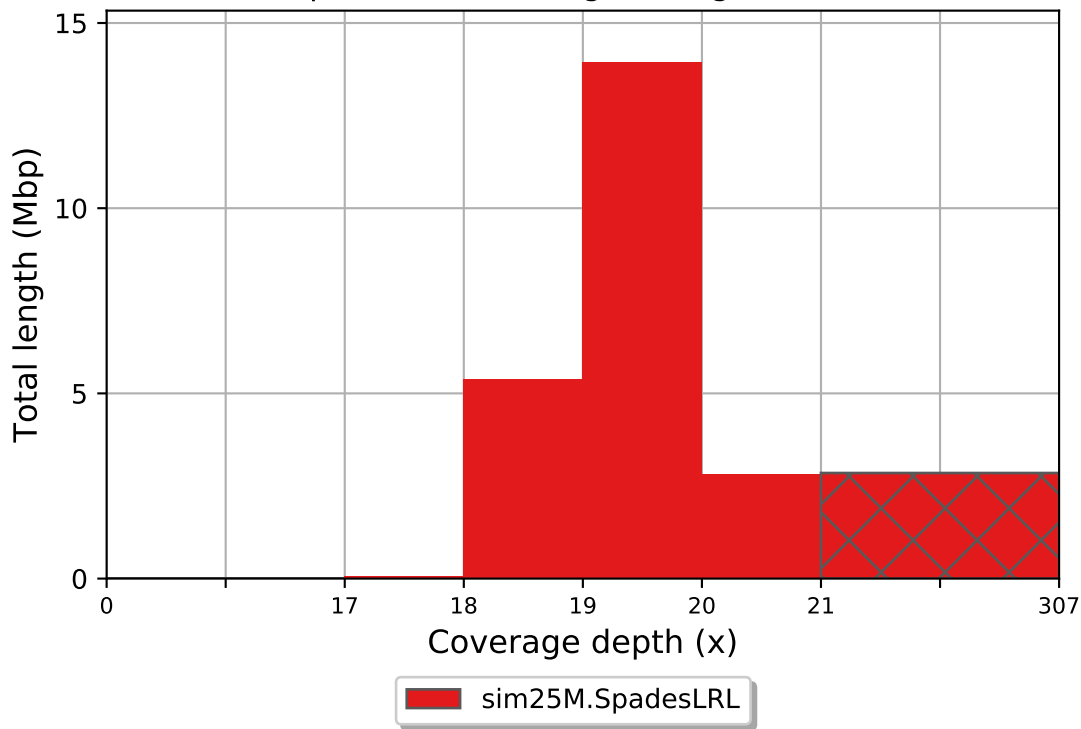
sim25M.SpadesLRL GC content



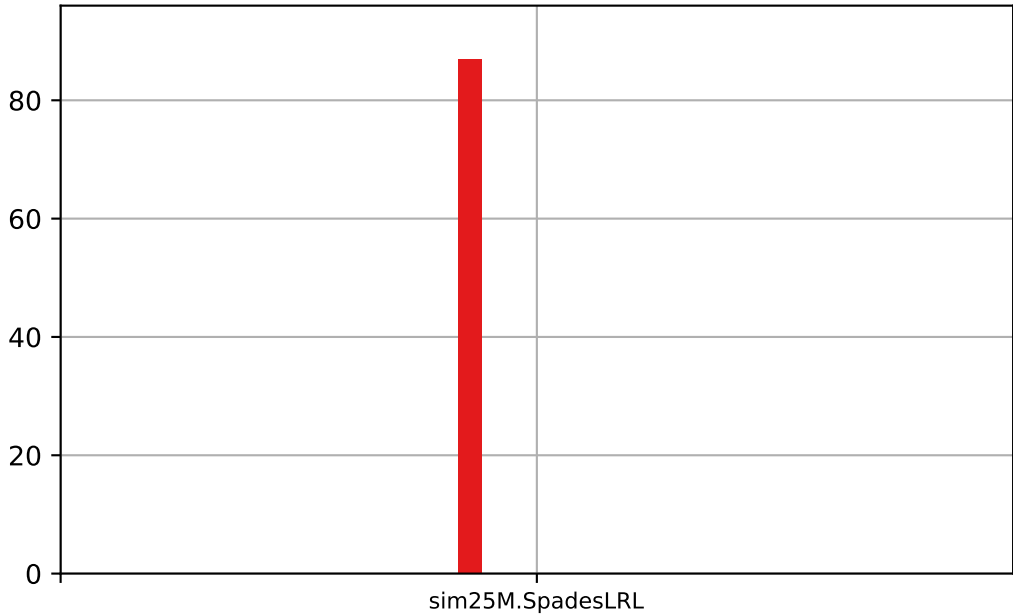
Coverage histogram (bin size: 1x)



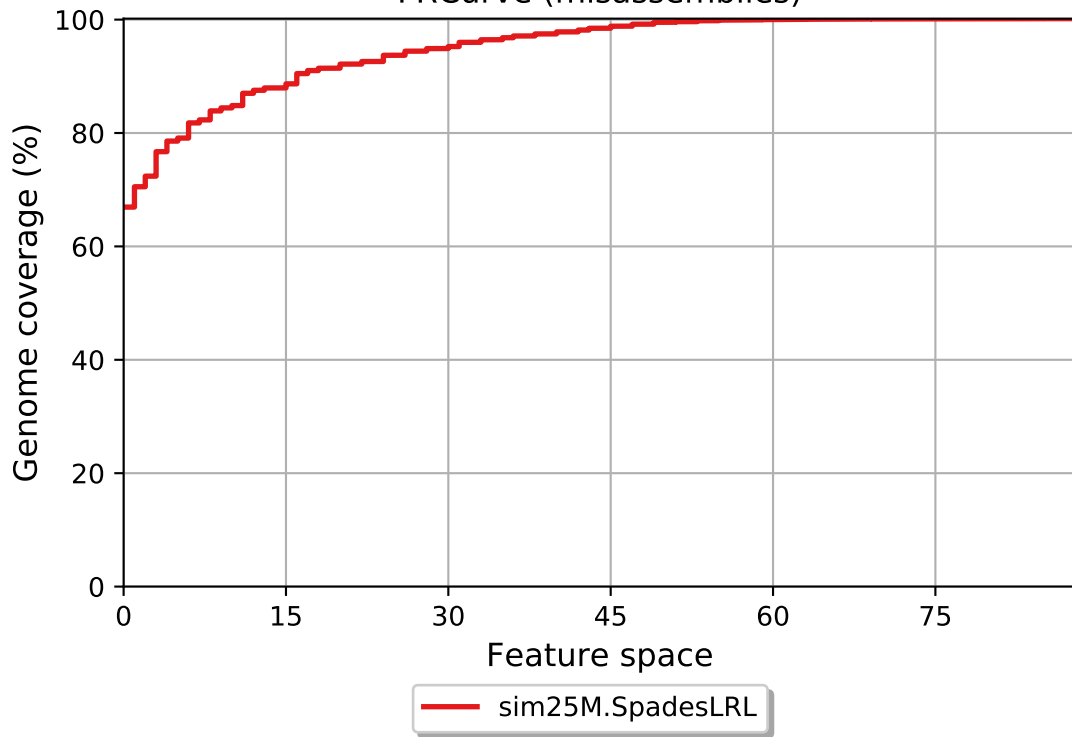
sim25M.SpadesLRL coverage histogram (bin size: 1x)



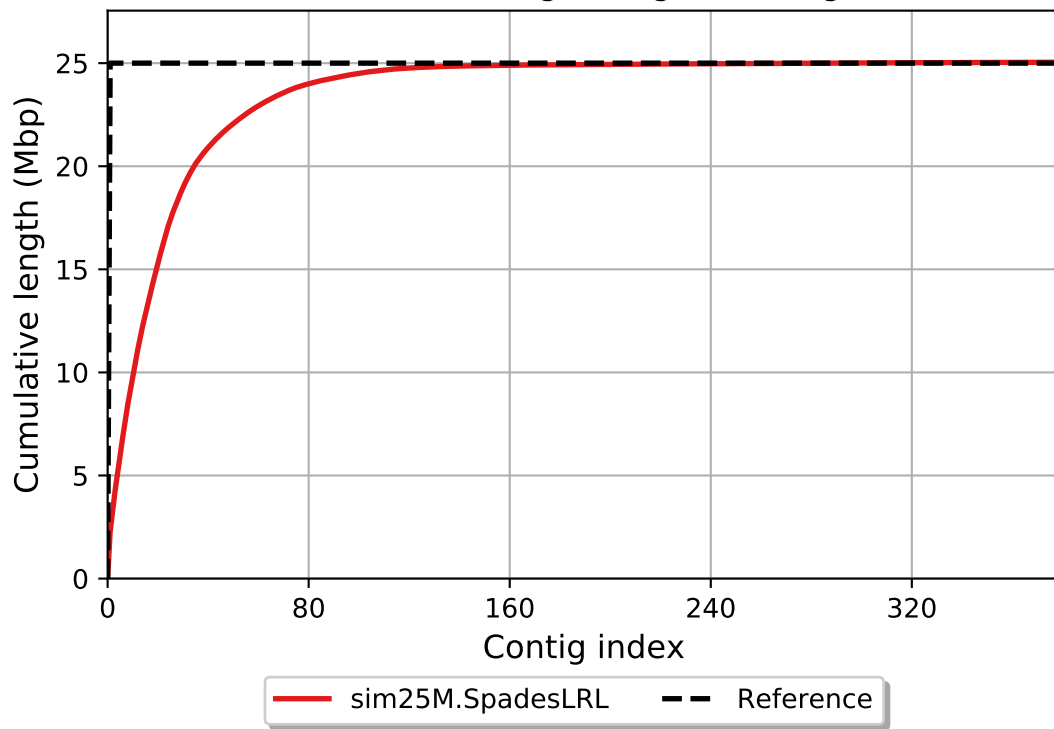
Misassemblies



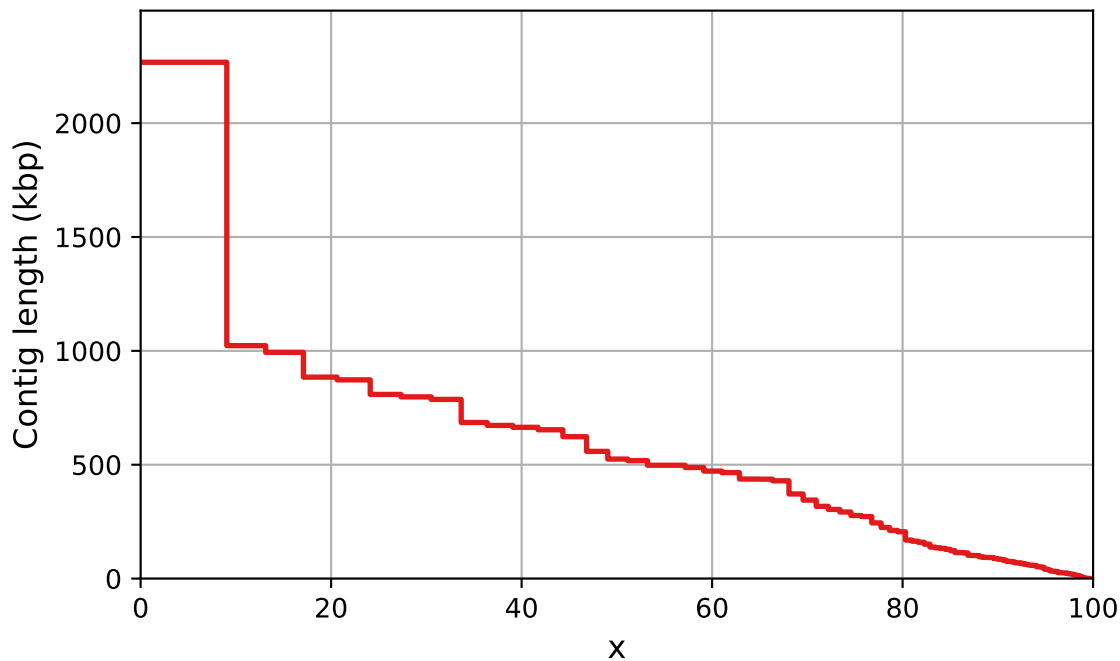
FRCurve (misassemblies)



Cumulative length (aligned contigs)

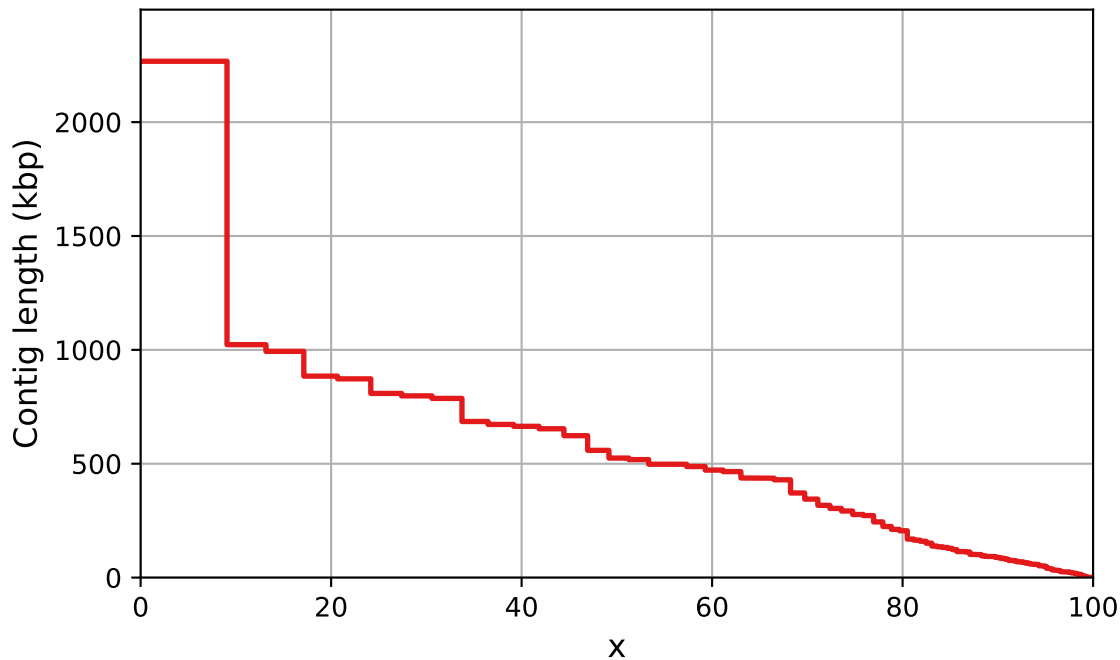


NAx



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NGAx



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