

Report

	sim5M.SpadesL
# contigs (>= 0 bp)	425
# contigs (>= 1000 bp)	115
# contigs (>= 5000 bp)	98
# contigs (>= 10000 bp)	89
# contigs (>= 25000 bp)	63
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4997235
Total length (>= 1000 bp)	4910877
Total length (>= 5000 bp)	4868001
Total length (>= 10000 bp)	4797148
Total length (>= 25000 bp)	4360797
Total length (>= 50000 bp)	3282657
# contigs	161
Largest contig	201112
Total length	4942195
Reference length	5000040
GC (%)	35.80
Reference GC (%)	35.84
N50	85214
NG50	81519
N75	38606
NG75	36839
L50	20
LG50	21
L75	42
LG75	43
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	172986
# local misassemblies	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	999
Genome fraction (%)	98.616
Duplication ratio	1.002
# N's per 100 kbp	20.21
# mismatches per 100 kbp	27.70
# indels per 100 kbp	0.53
Largest alignment	201112
Total aligned length	4940625
NA50	81519
NGA50	81519
NA75	36839
NGA75	36169
LA50	21
LGA50	21
LA75	44
LGA75	45

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

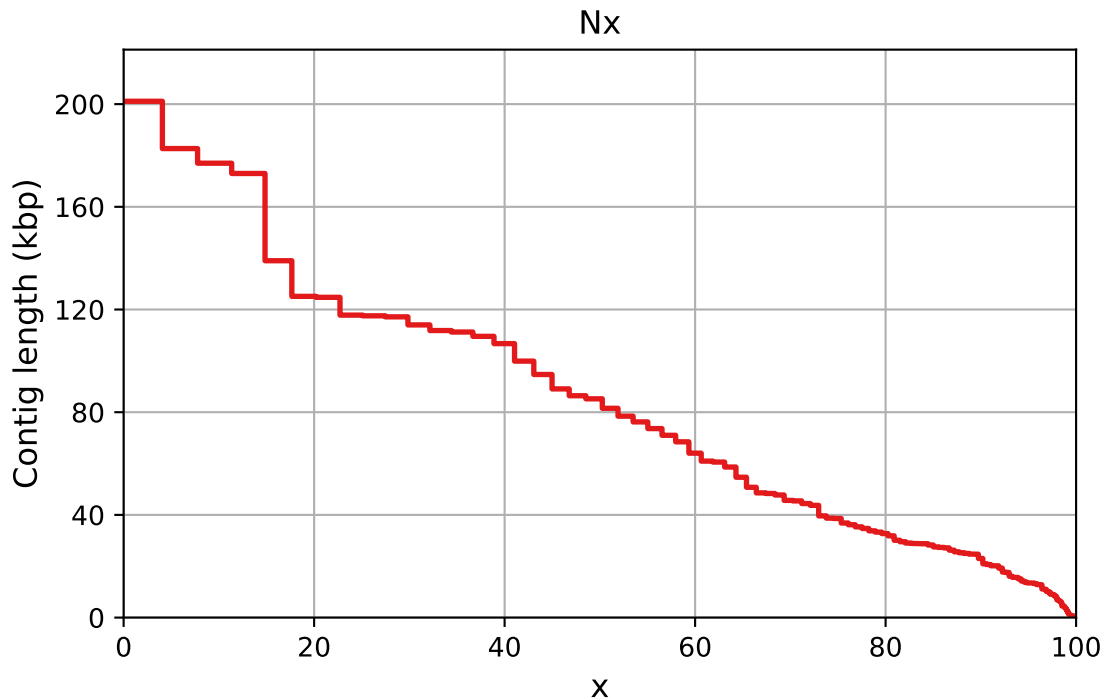
	sim5M.SpadesL
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	172986
# local misassemblies	2
# unaligned mis. contigs	0
# mismatches	1366
# indels	26
# indels (≤ 5 bp)	23
# indels (> 5 bp)	3
Indels length	89

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

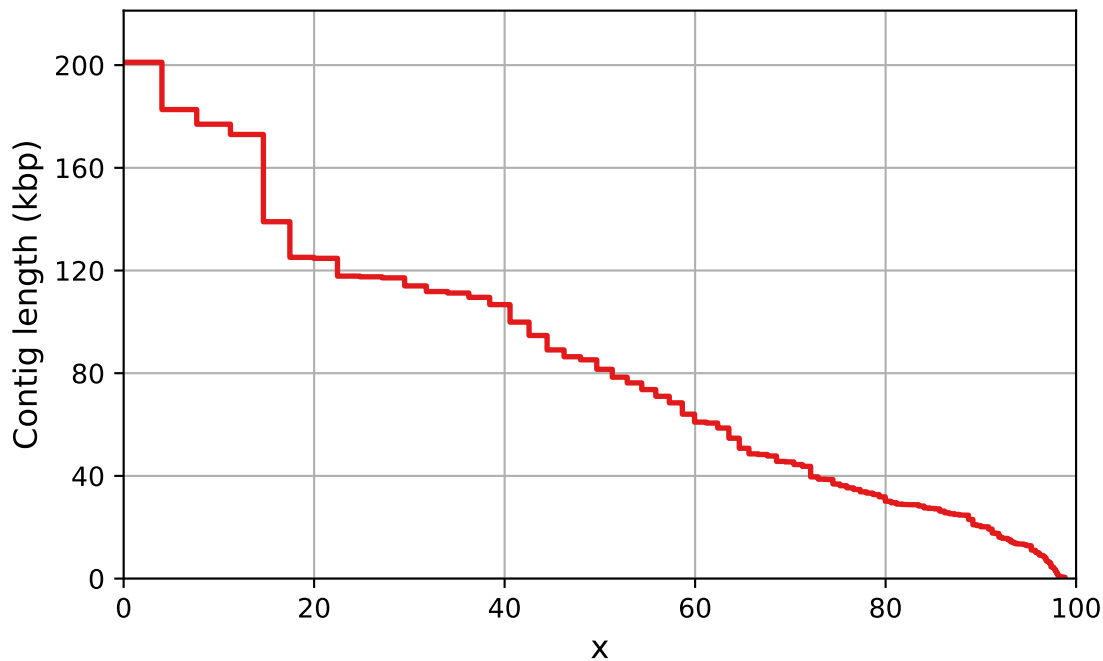
	sim5M.SpadesL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	999
# N's	999

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).



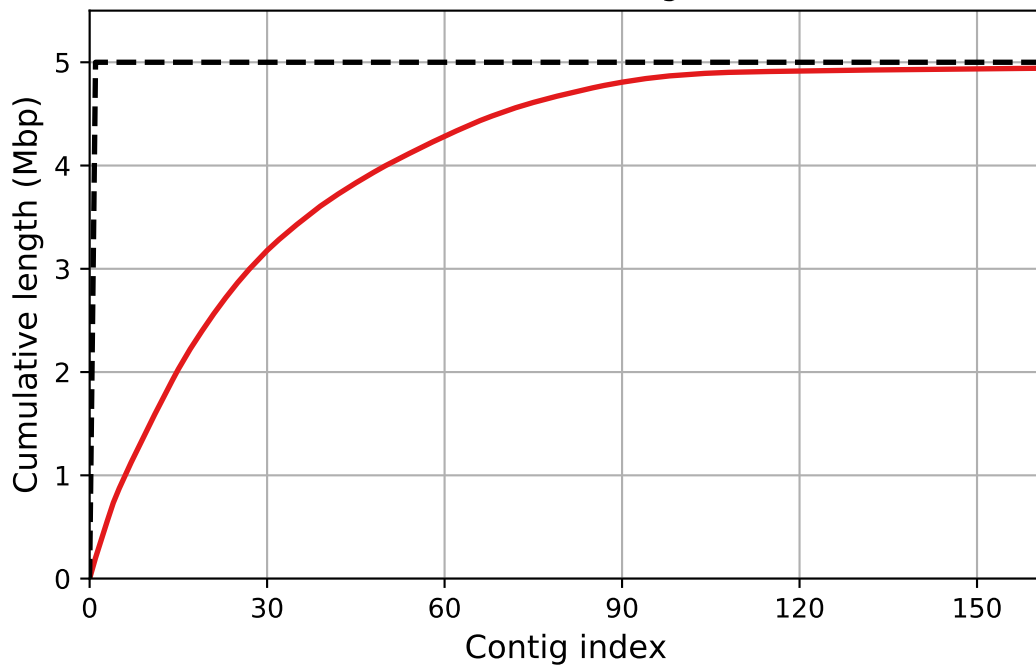
— sim5M.SpadesL

NGx



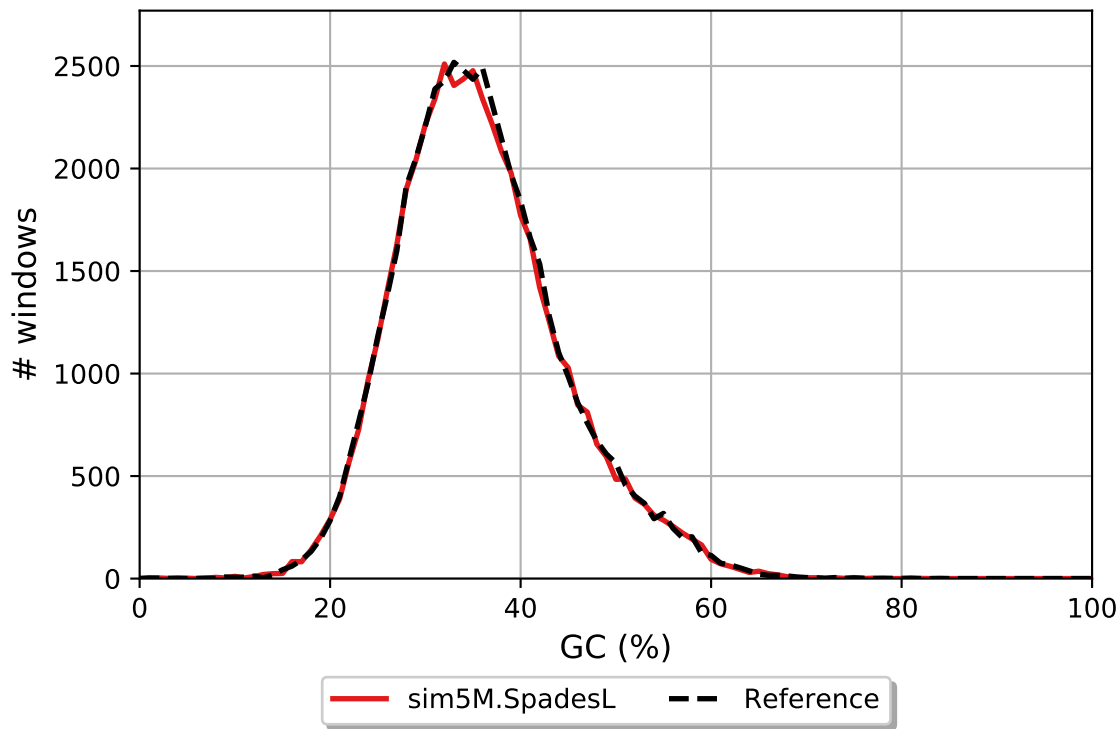
— sim5M.SpadesL

Cumulative length

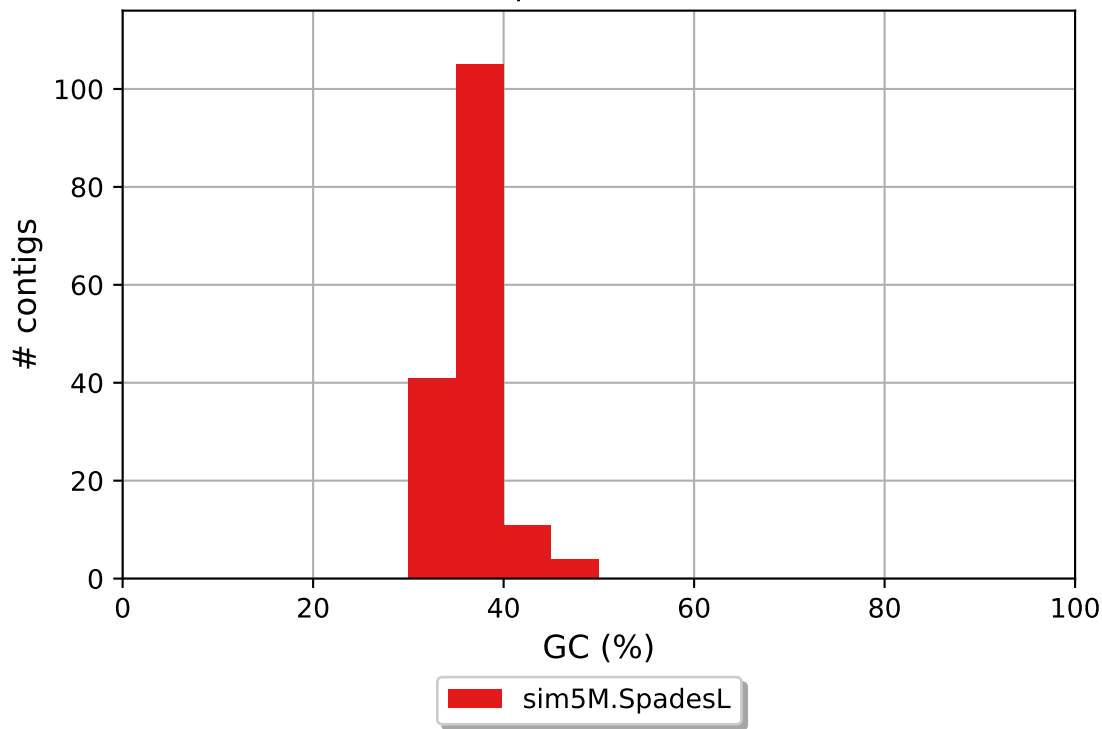


— sim5M.SpadesL - - Reference

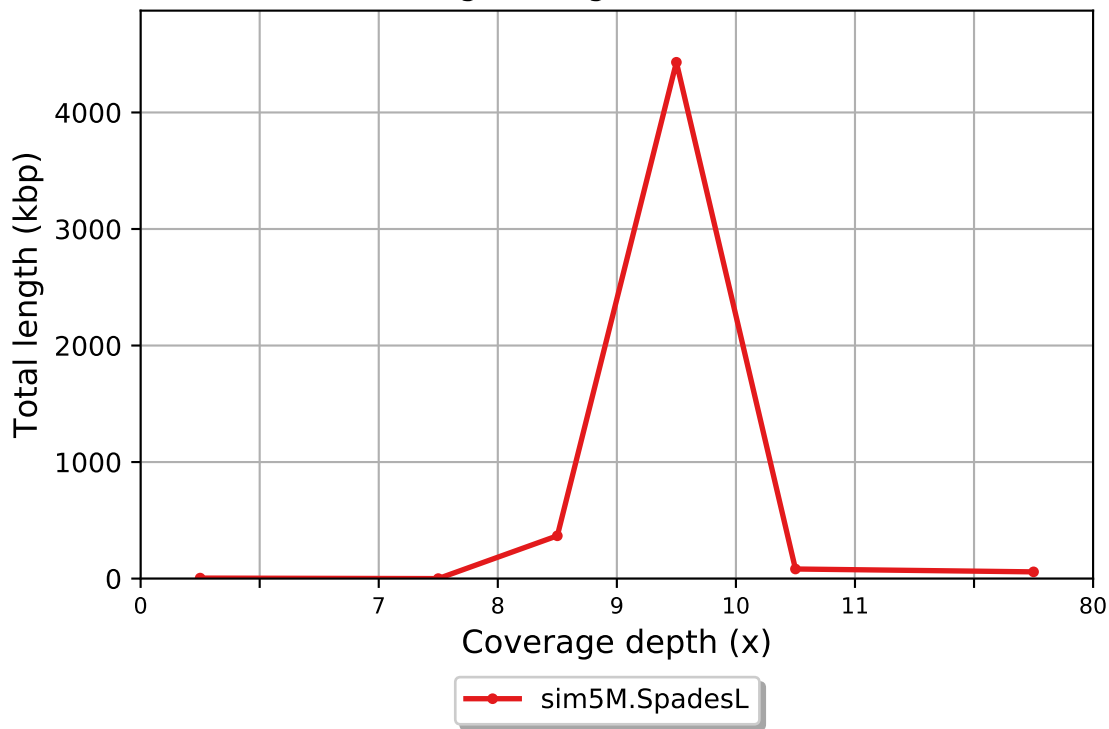
GC content



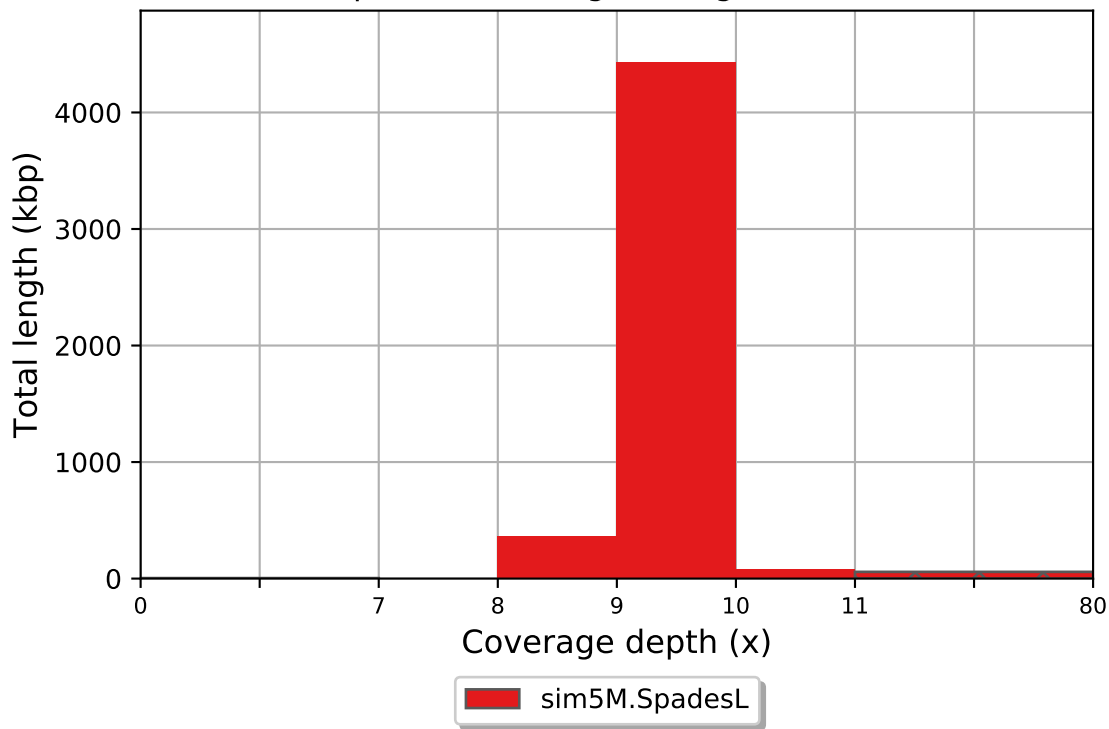
sim5M.SpadesL GC content



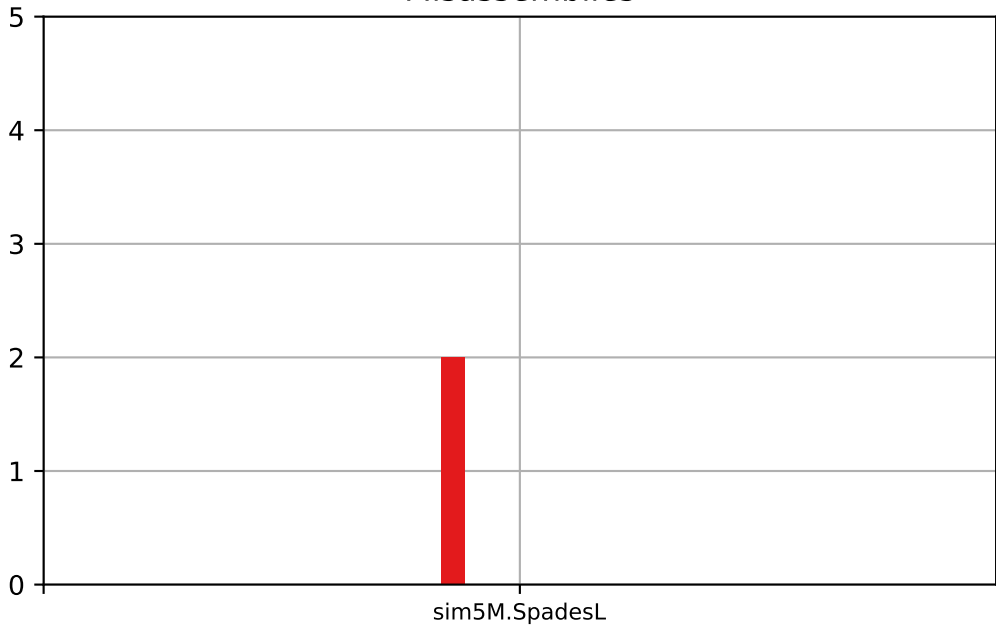
Coverage histogram (bin size: 1x)



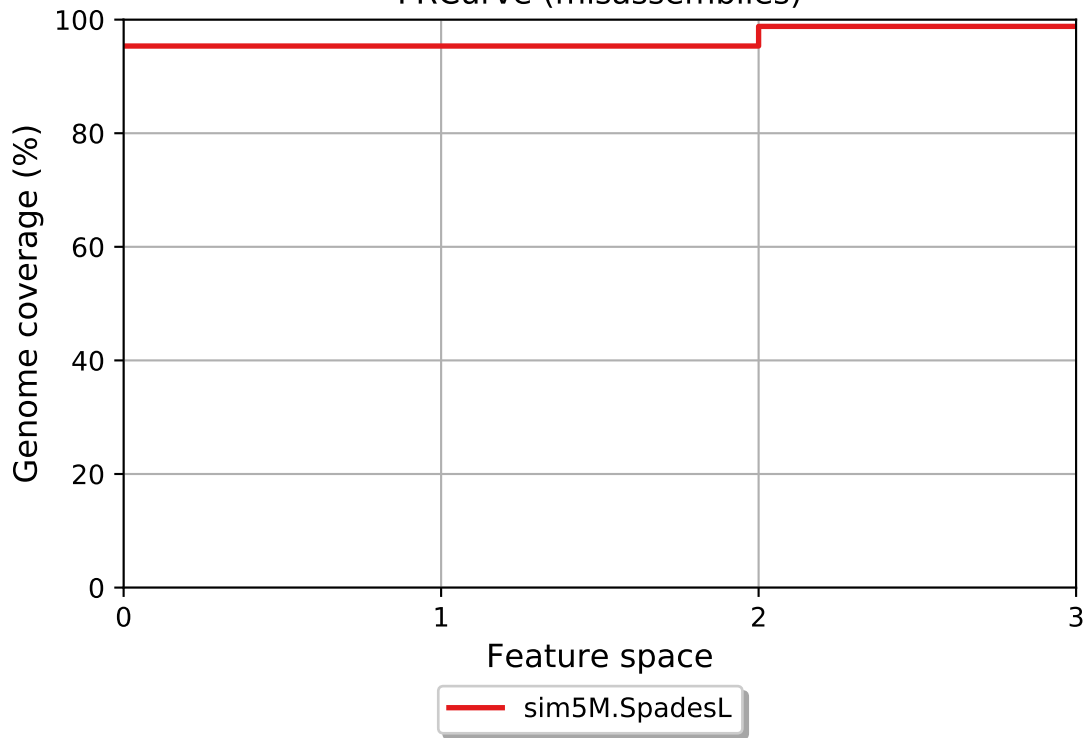
sim5M.SpadesL coverage histogram (bin size: 1x)



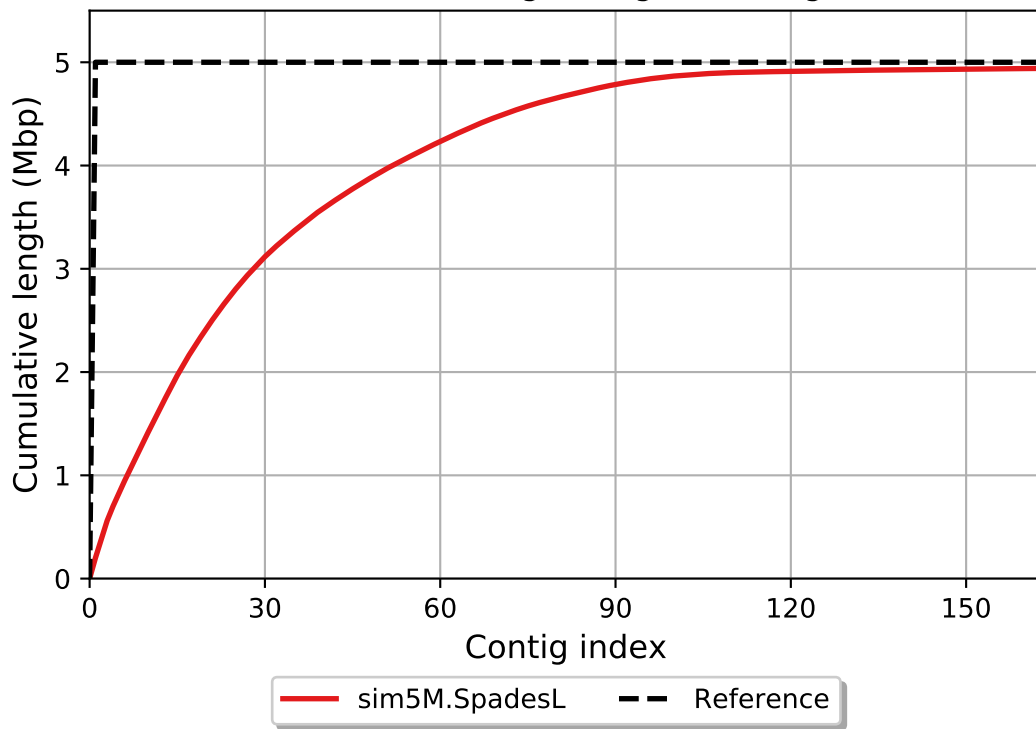
Misassemblies



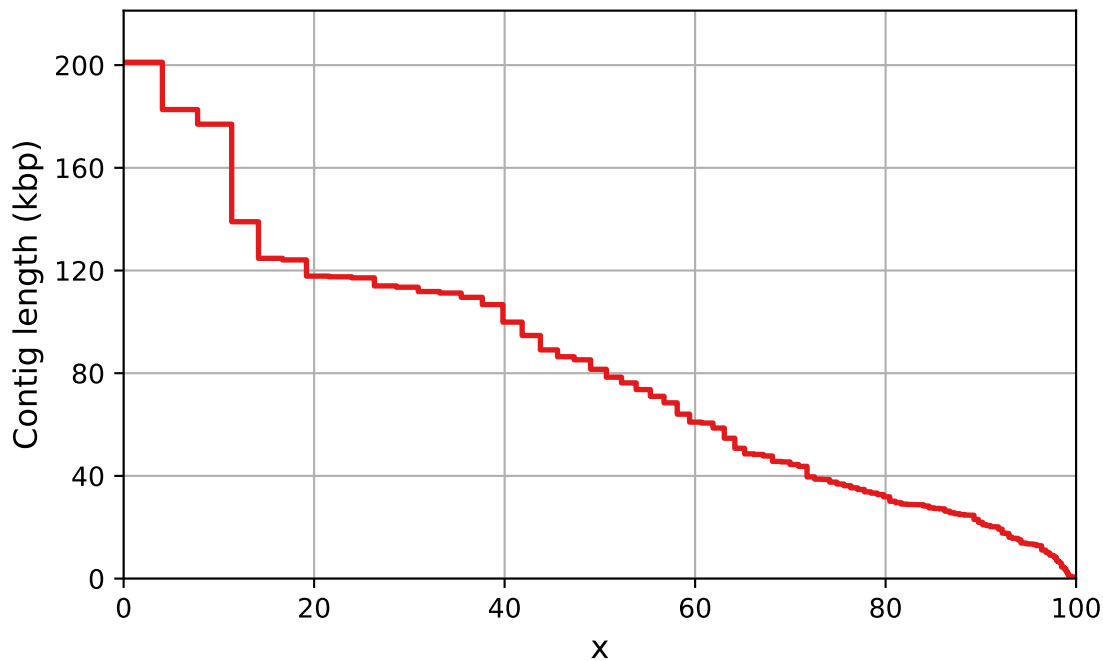
FRCurve (misassemblies)



Cumulative length (aligned contigs)

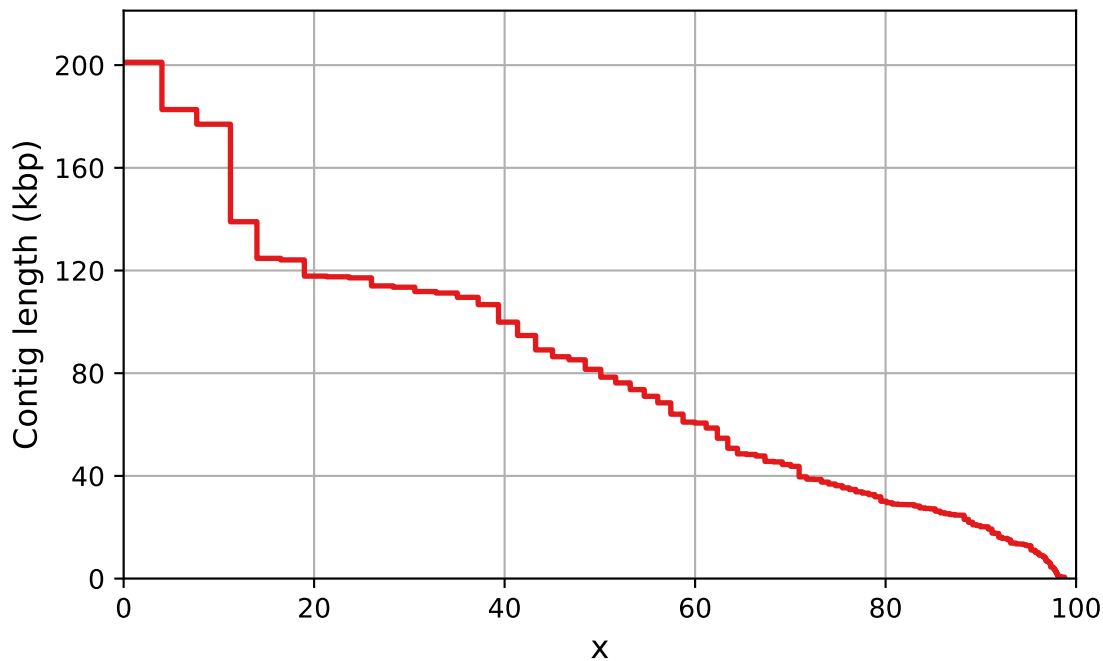


NAx



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NGAx



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