

Report

	sim5M.SpadesH
# contigs (>= 0 bp)	323
# contigs (>= 1000 bp)	78
# contigs (>= 5000 bp)	70
# contigs (>= 10000 bp)	65
# contigs (>= 25000 bp)	48
# contigs (>= 50000 bp)	33
Total length (>= 0 bp)	4988546
Total length (>= 1000 bp)	4913906
Total length (>= 5000 bp)	4895174
Total length (>= 10000 bp)	4854603
Total length (>= 25000 bp)	4572675
Total length (>= 50000 bp)	4009820
# contigs	124
Largest contig	281683
Total length	4944427
Reference length	5000040
GC (%)	35.81
Reference GC (%)	35.84
N50	116695
NG50	116695
N75	65903
NG75	63668
L50	14
LG50	14
L75	28
LG75	29
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	228070
# local misassemblies	1
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	969
Genome fraction (%)	98.729
Duplication ratio	1.001
# N's per 100 kbp	19.60
# mismatches per 100 kbp	27.85
# indels per 100 kbp	0.49
Largest alignment	281680
Total aligned length	4943002
NA50	114800
NGA50	114800
NA75	60805
NGA75	59890
LA50	14
LGA50	14
LA75	29
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

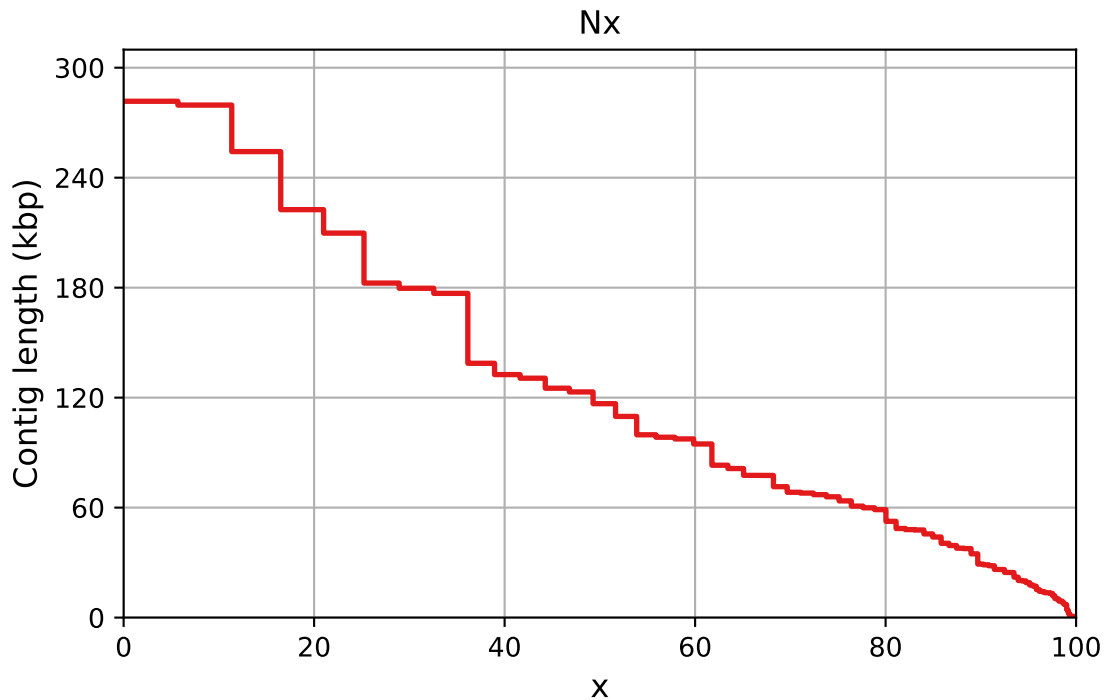
	sim5M.SpadesH
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	228070
# local misassemblies	1
# unaligned mis. contigs	0
# mismatches	1375
# indels	24
# indels (≤ 5 bp)	22
# indels (> 5 bp)	2
Indels length	79

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

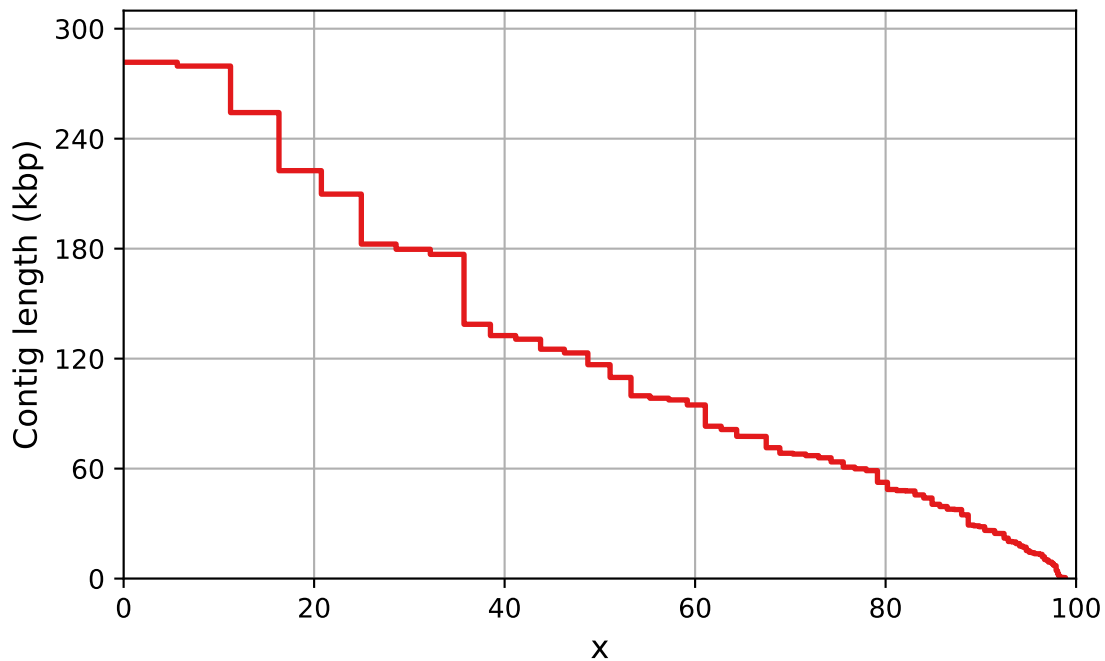
	sim5M.SpadesH
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	969
# N's	969

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).



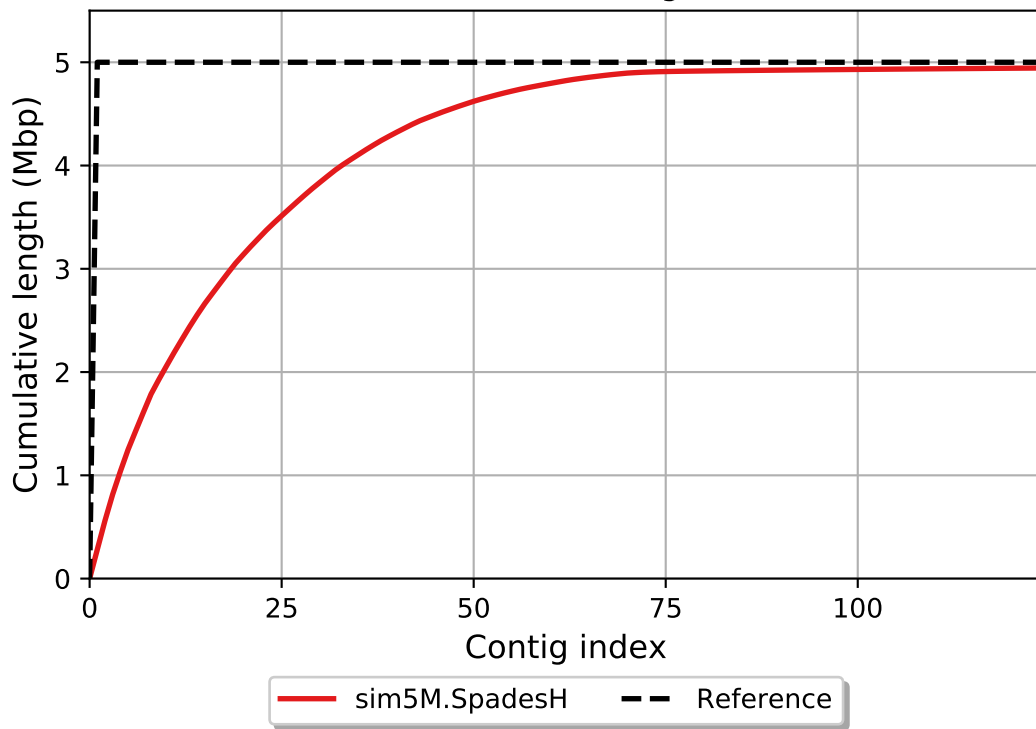
— sim5M.SpadesH

NGx

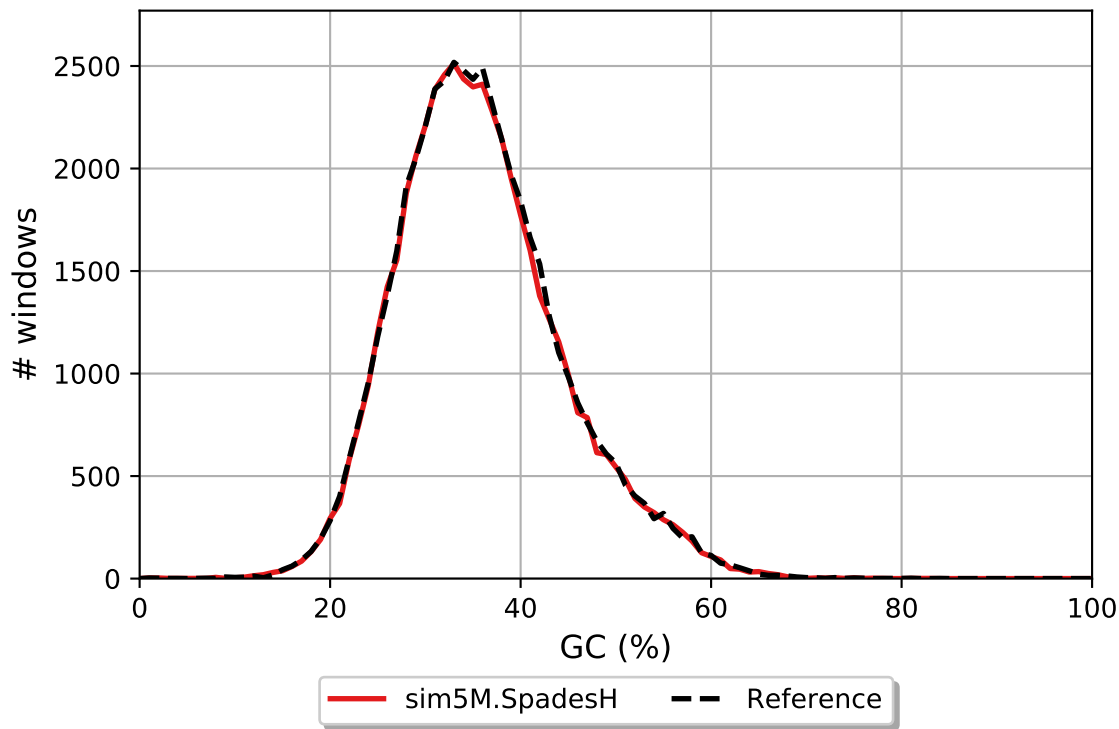


— sim5M.SpadesH

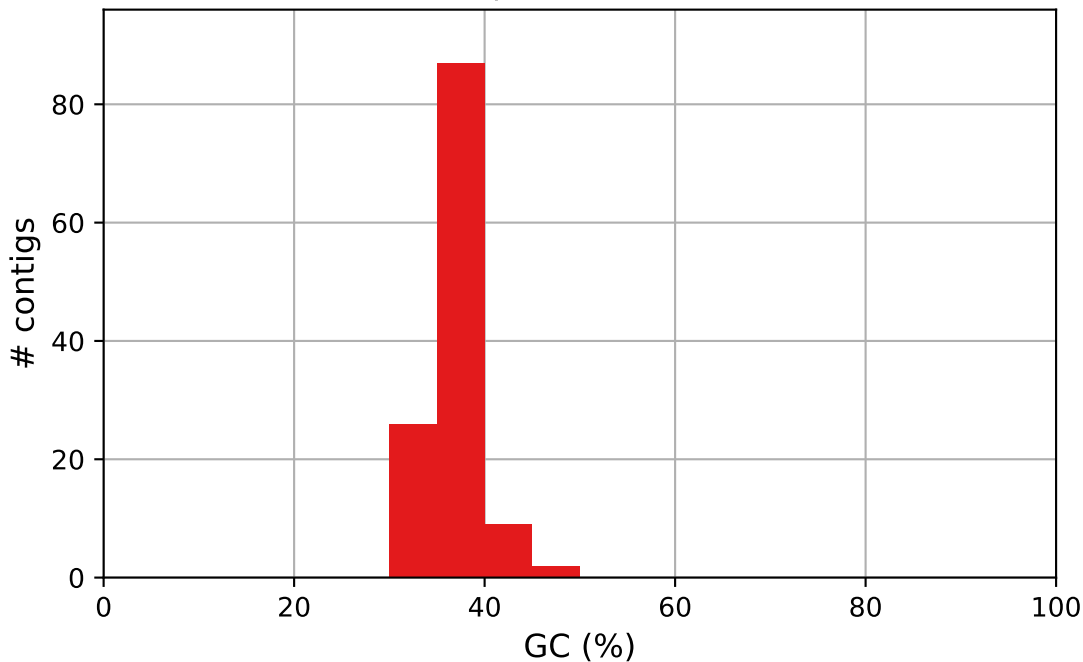
Cumulative length



GC content

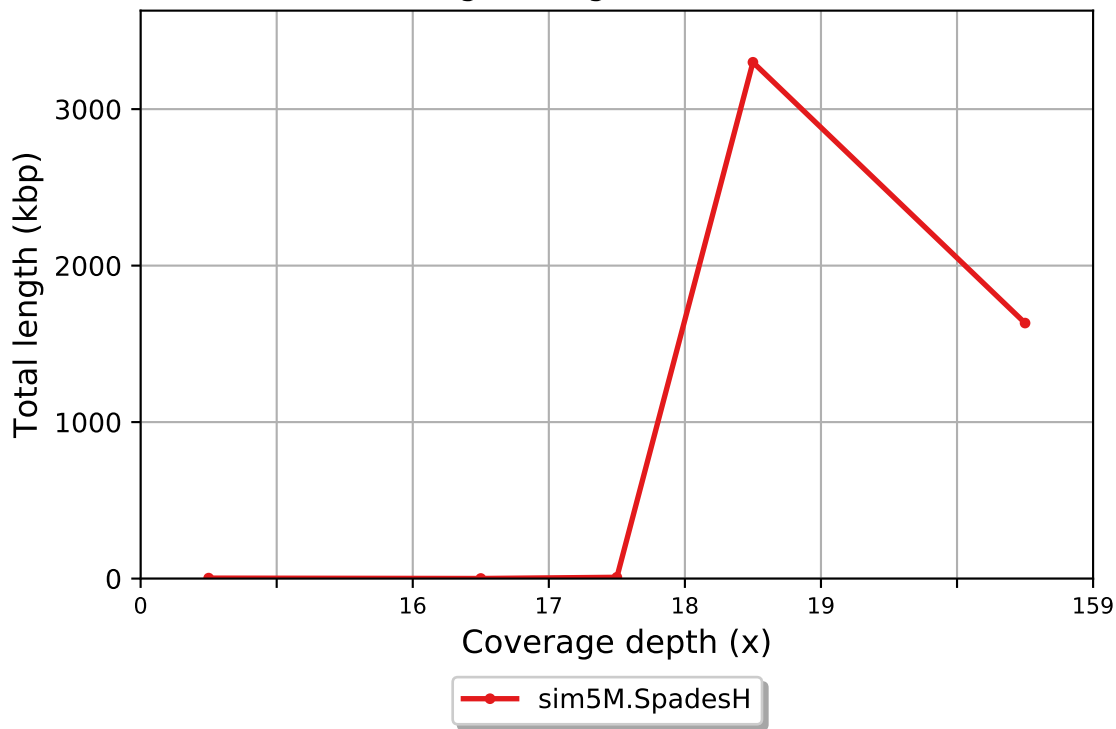


sim5M.SpadesH GC content

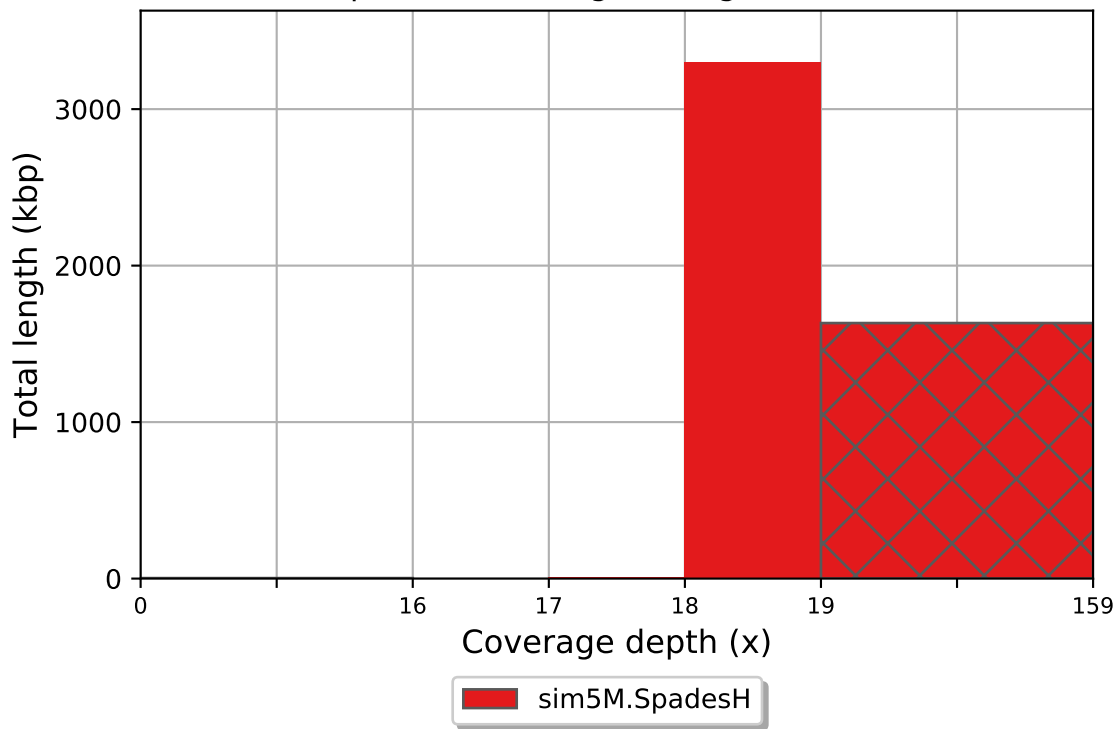


sim5M.SpadesH

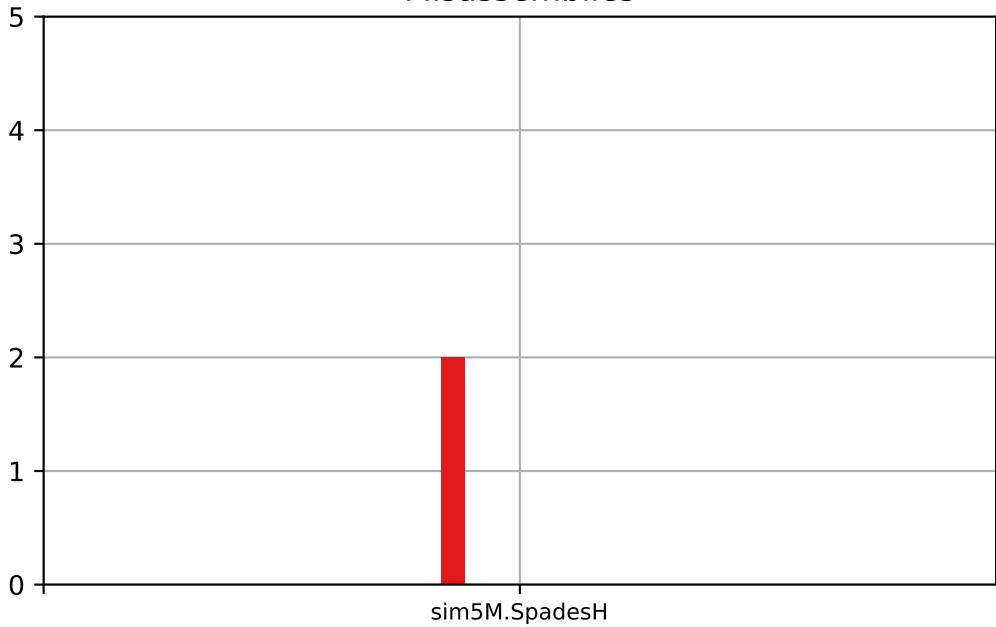
Coverage histogram (bin size: 1x)



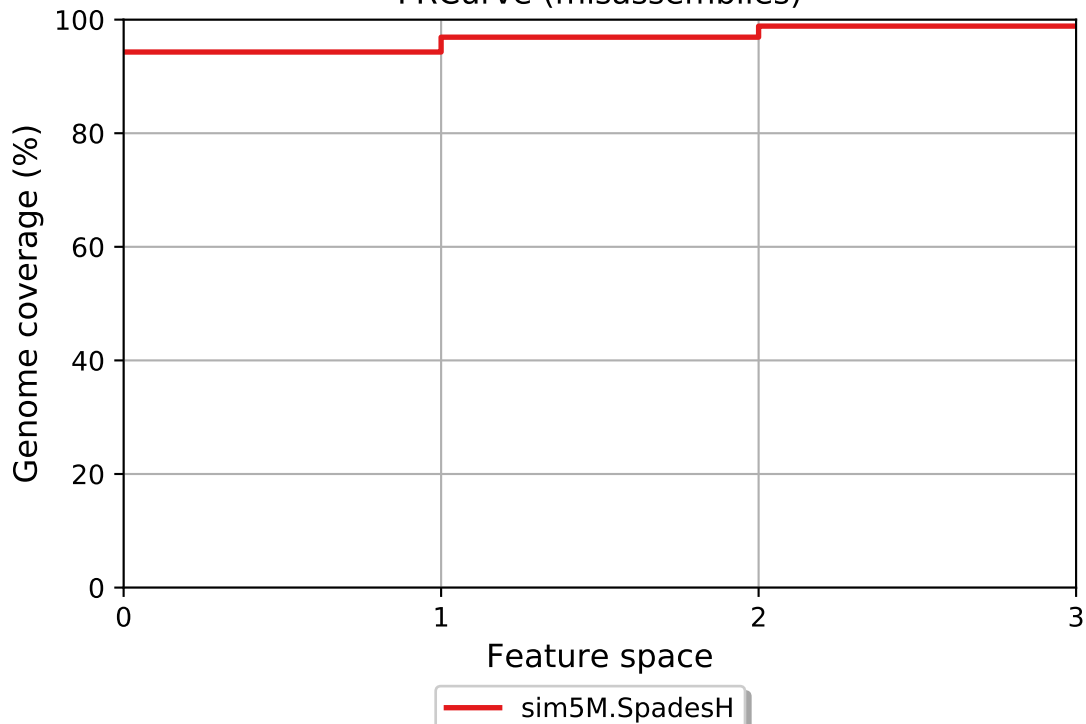
sim5M.SpadesH coverage histogram (bin size: 1x)



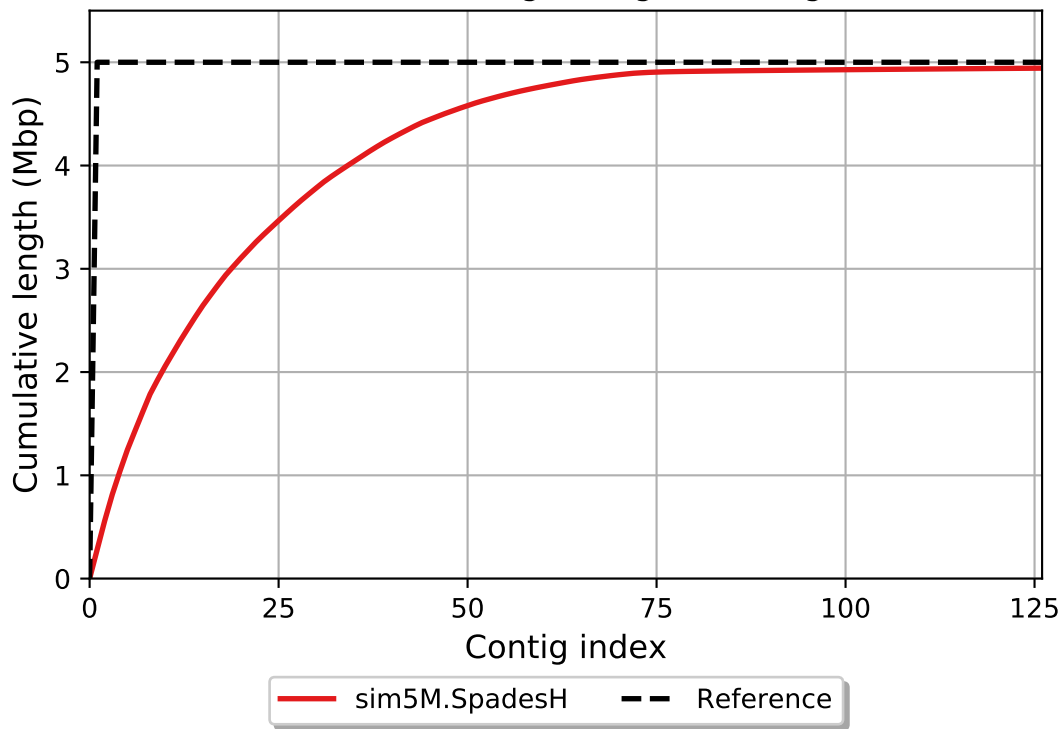
Misassemblies



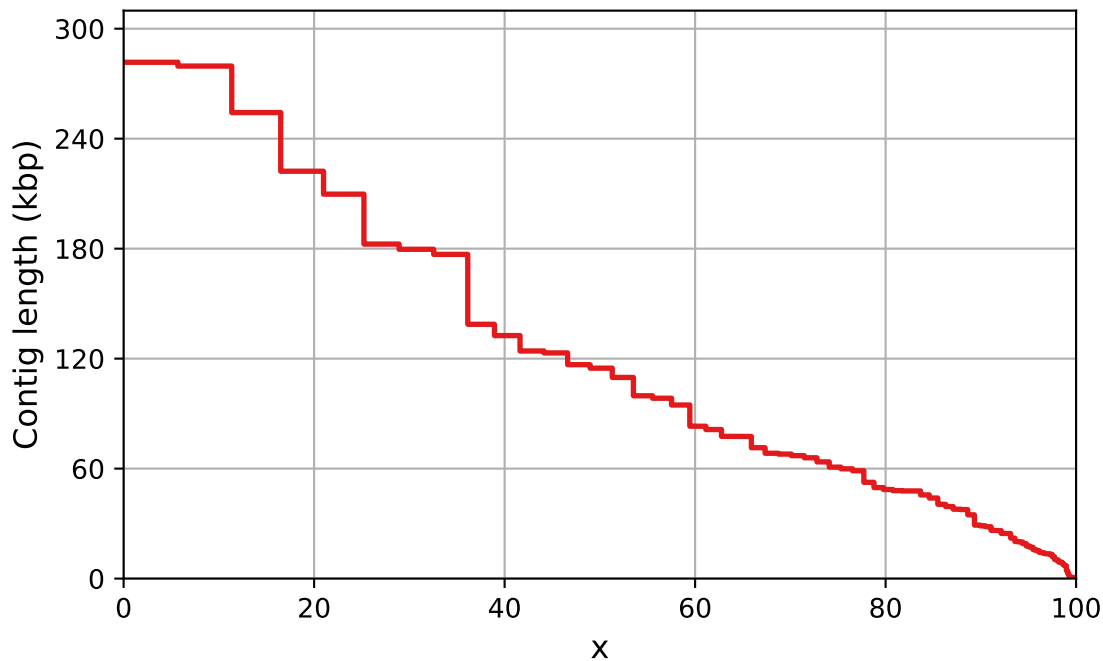
FRCurve (misassemblies)



Cumulative length (aligned contigs)

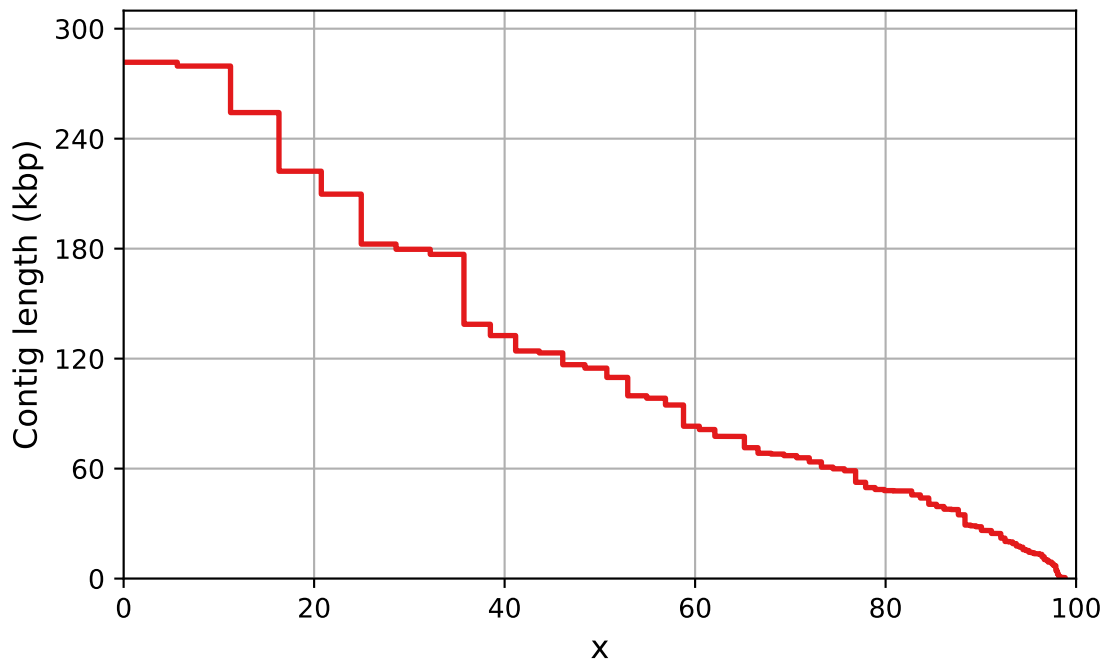


NAx



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NGAx



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