

Report

	hifiasm
# contigs (>= 0 bp)	291
# contigs (>= 1000 bp)	291
# contigs (>= 5000 bp)	289
# contigs (>= 10000 bp)	283
# contigs (>= 25000 bp)	257
# contigs (>= 50000 bp)	216
Total length (>= 0 bp)	2632363436
Total length (>= 1000 bp)	2632363436
Total length (>= 5000 bp)	2632354218
Total length (>= 10000 bp)	2632305397
Total length (>= 25000 bp)	2631843951
Total length (>= 50000 bp)	2630379358
# contigs	291
Largest contig	120702424
Total length	2632363436
Reference length	2728222451
GC (%)	41.68
Reference GC (%)	41.67
N50	52637589
NG50	46334307
N75	25290655
NG75	22303466
L50	17
LG50	18
L75	36
LG75	40
# misassemblies	104
# misassembled contigs	28
Misassembled contigs length	659793886
# local misassemblies	180
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	2
# unaligned mis. contigs	0
# unaligned contigs	0 + 20 part
Unaligned length	2757781
Genome fraction (%)	98.774
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.69
# indels per 100 kbp	0.32
Largest alignment	120702424
Total aligned length	2627741661
NA50	46065667
NGA50	45910920
NA75	20707047
NGA75	19731320
LA50	20
LGA50	21
LA75	42
LGA75	45

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

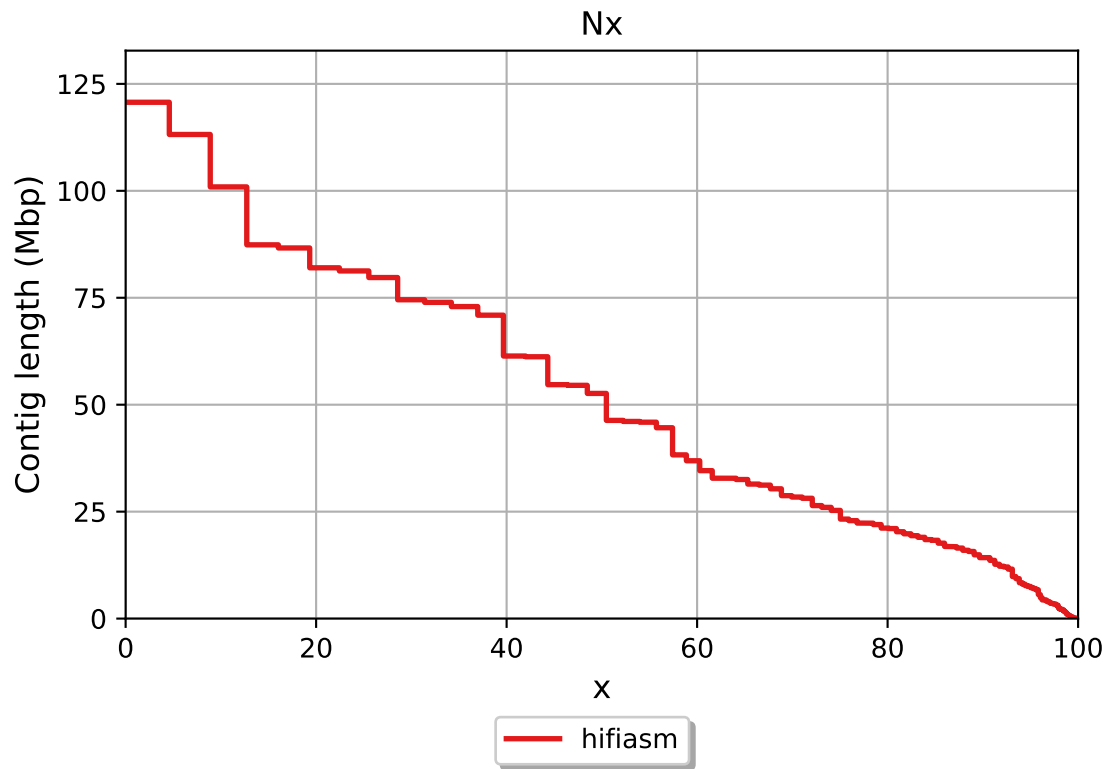
	hifiasm
# misassemblies	104
# contig misassemblies	104
# c. relocations	103
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	28
Misassembled contigs length	659793886
# local misassemblies	180
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	0
# possible TEs	2
# unaligned mis. contigs	0
# mismatches	96870
# indels	8418
# indels (<= 5 bp)	6294
# indels (> 5 bp)	2124
Indels length	979527

All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

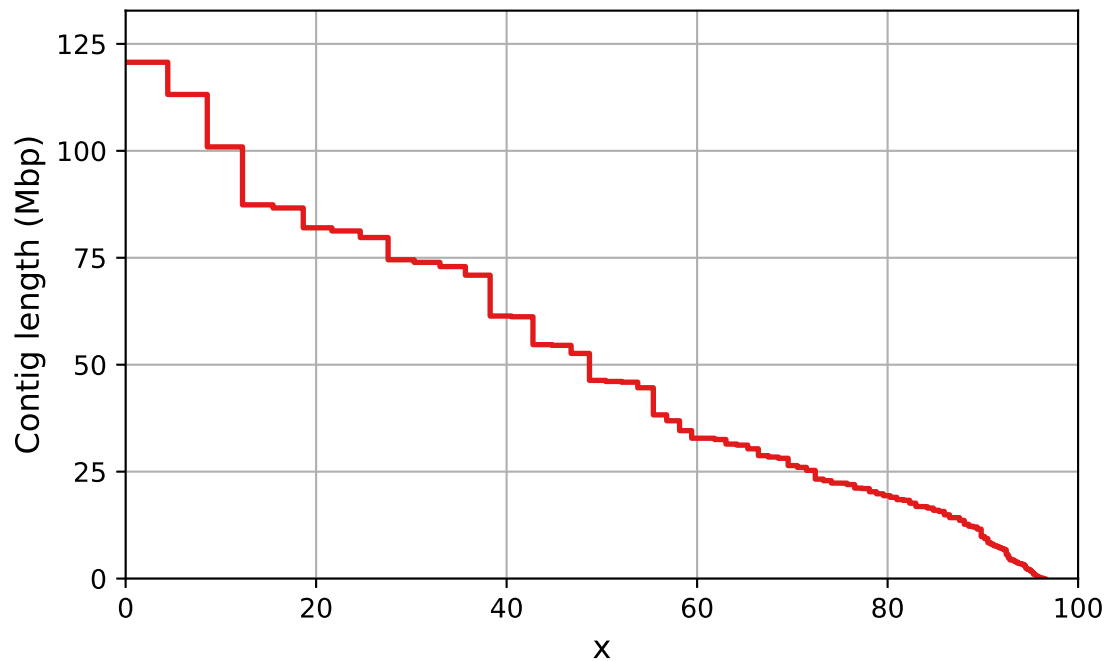
Unaligned report

	hifiasm
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	20
Partially unaligned length	2757781
# N's	0

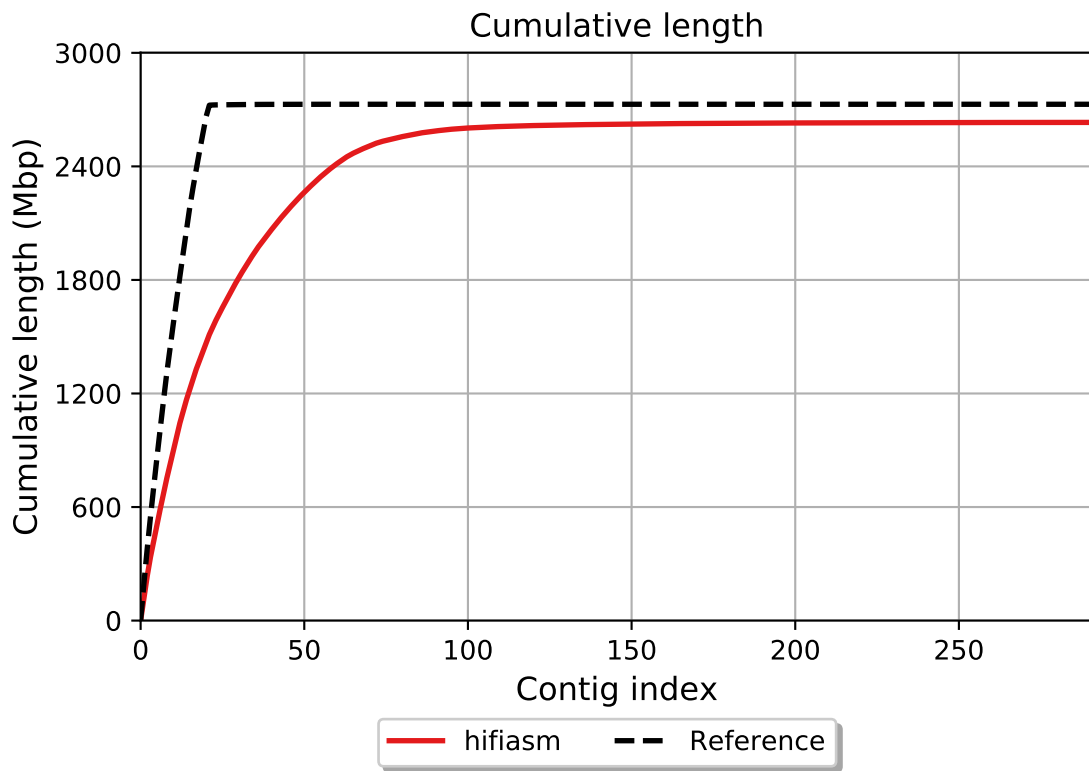
All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



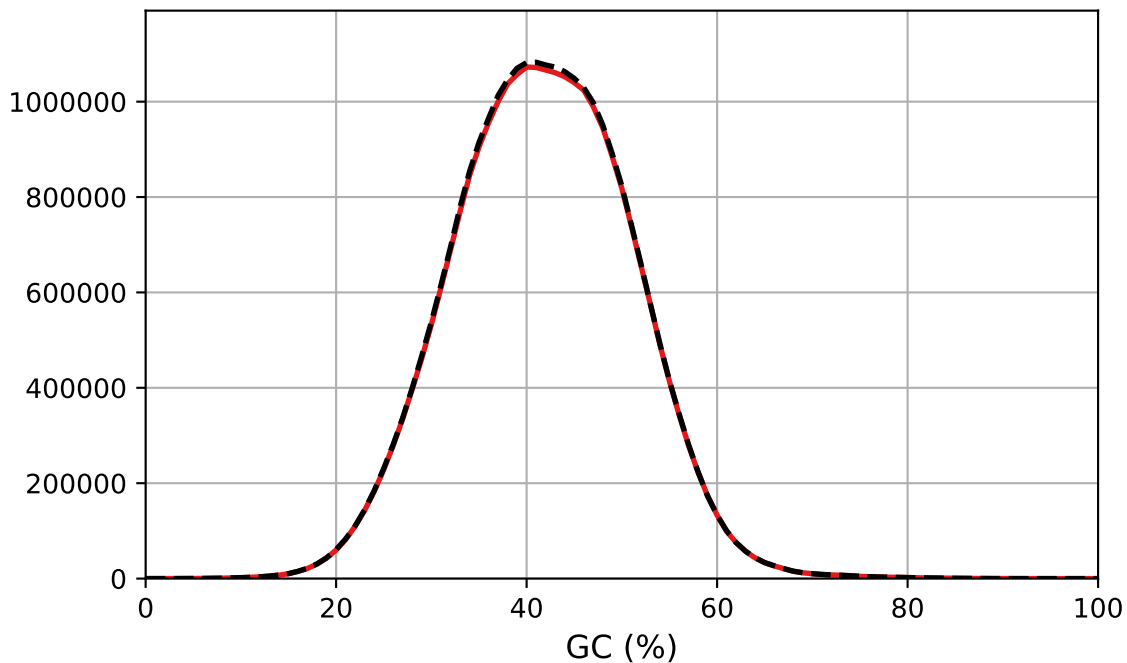
NGx



hifiasm

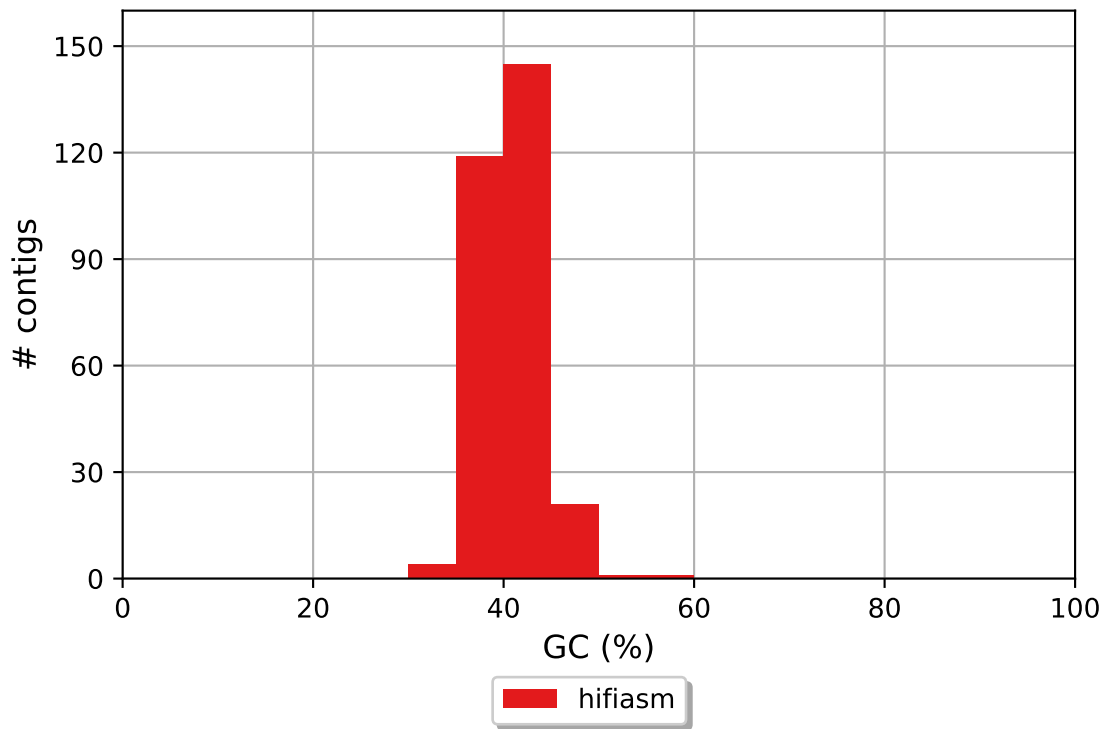


GC content

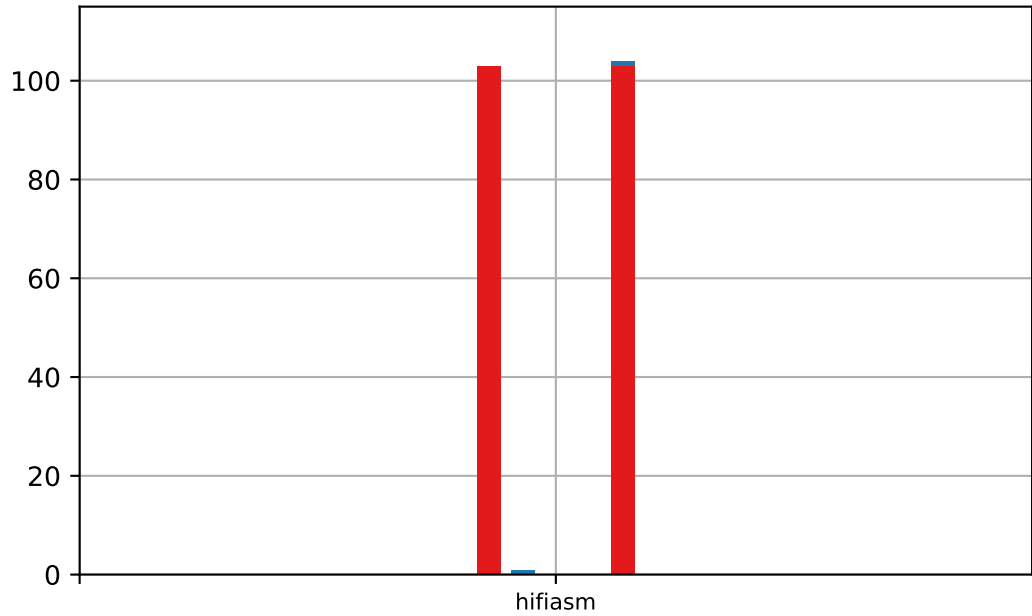


— hifiasm - - Reference

hifiasm GC content



Misassemblies

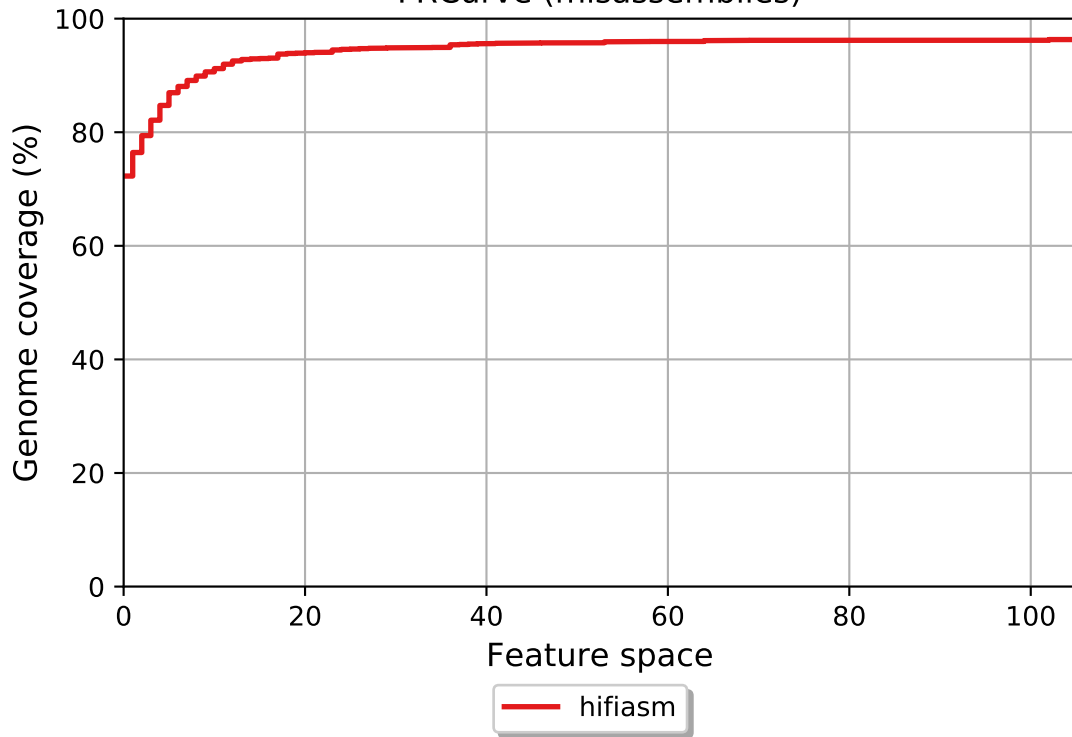


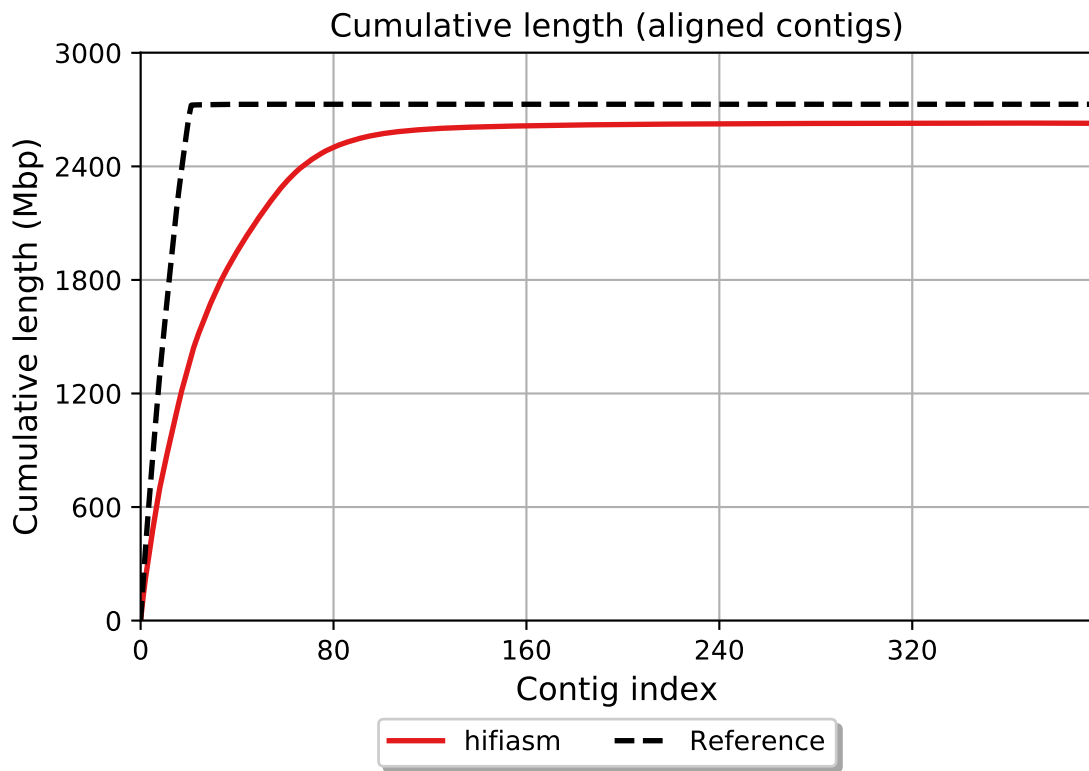
relocations



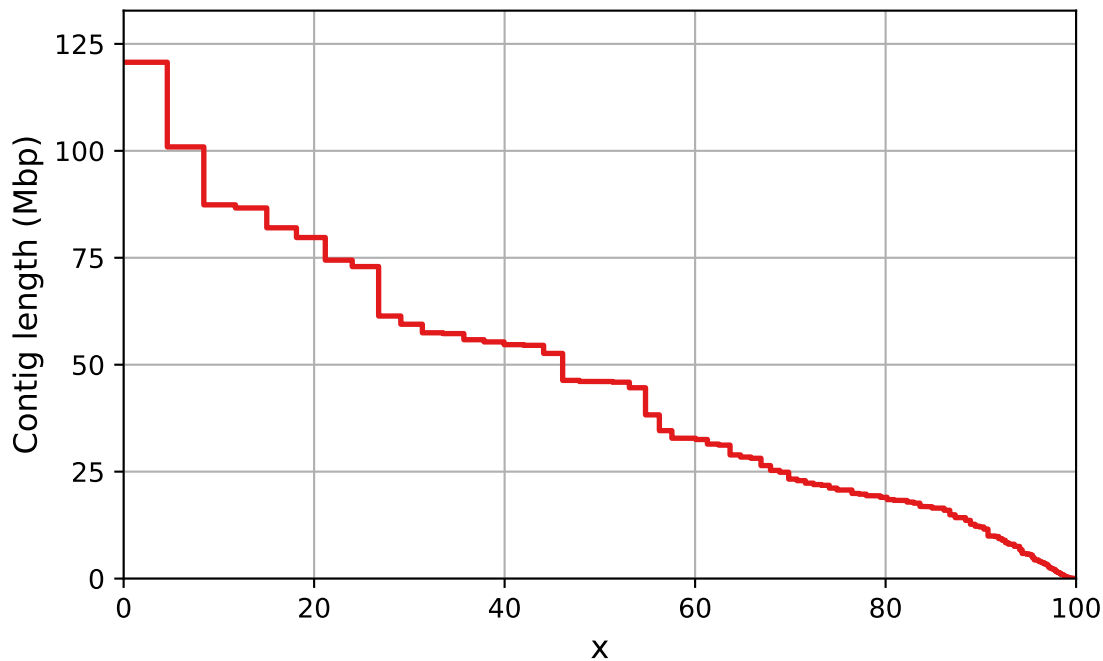
translocations

FRCurve (misassemblies)



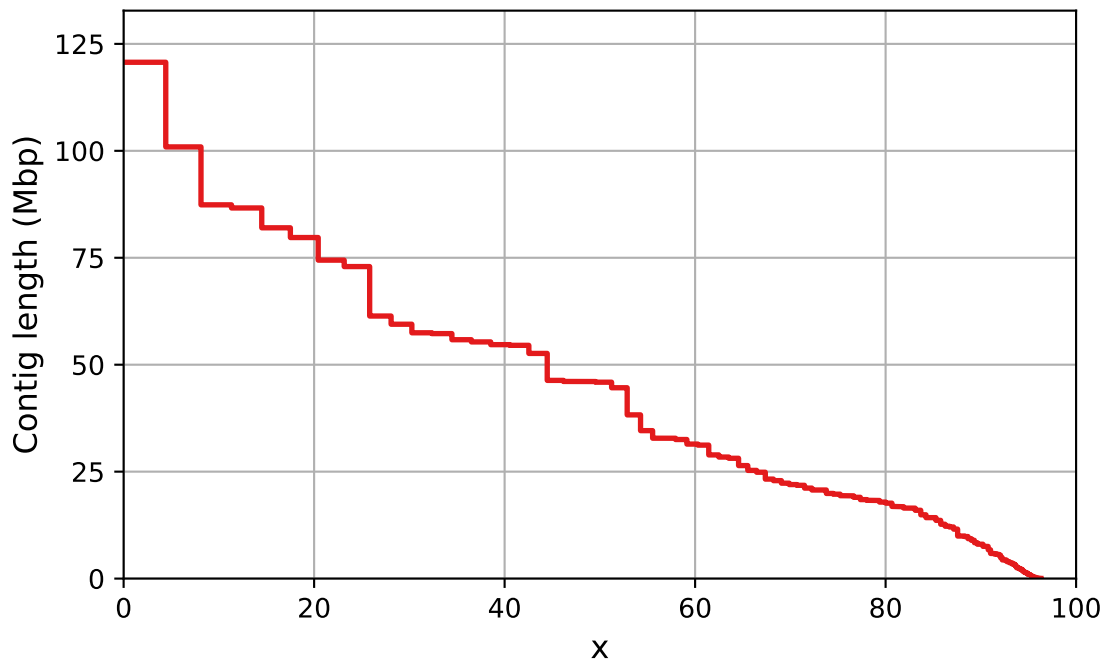


NAx



hifiasm

NGAx



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