

Report

	assembly
# contigs (>= 1000 bp)	284
# contigs (>= 5000 bp)	279
# contigs (>= 10000 bp)	262
# contigs (>= 25000 bp)	224
# contigs (>= 50000 bp)	169
Total length (>= 1000 bp)	62151223
Total length (>= 5000 bp)	62136223
Total length (>= 10000 bp)	62011716
Total length (>= 25000 bp)	61378640
Total length (>= 50000 bp)	59369278
# contigs	284
Largest contig	3416273
Total length	62151223
Reference length	3174691
GC (%)	68.56
Reference GC (%)	68.99
N50	566605
NG50	3416273
N90	117946
NG90	3416273
auN	878205.4
auNG	17192709.3
L50	29
LG50	1
L90	125
LG90	1
# misassemblies	231
# misassembled contigs	21
Misassembled contigs length	3405160
# local misassemblies	52
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	69
# unaligned contigs	0 + 276 part
Unaligned length	58742228
Genome fraction (%)	89.565
Duplication ratio	1.205
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1722.78
# indels per 100 kbp	465.64
Largest alignment	89786
Total aligned length	3407798
NA50	-
NGA50	21022
NA90	-
NGA90	4632
auNA	1312.6
auNGA	25696.2
LA50	-
LGA50	45
LA90	-
LGA90	176

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

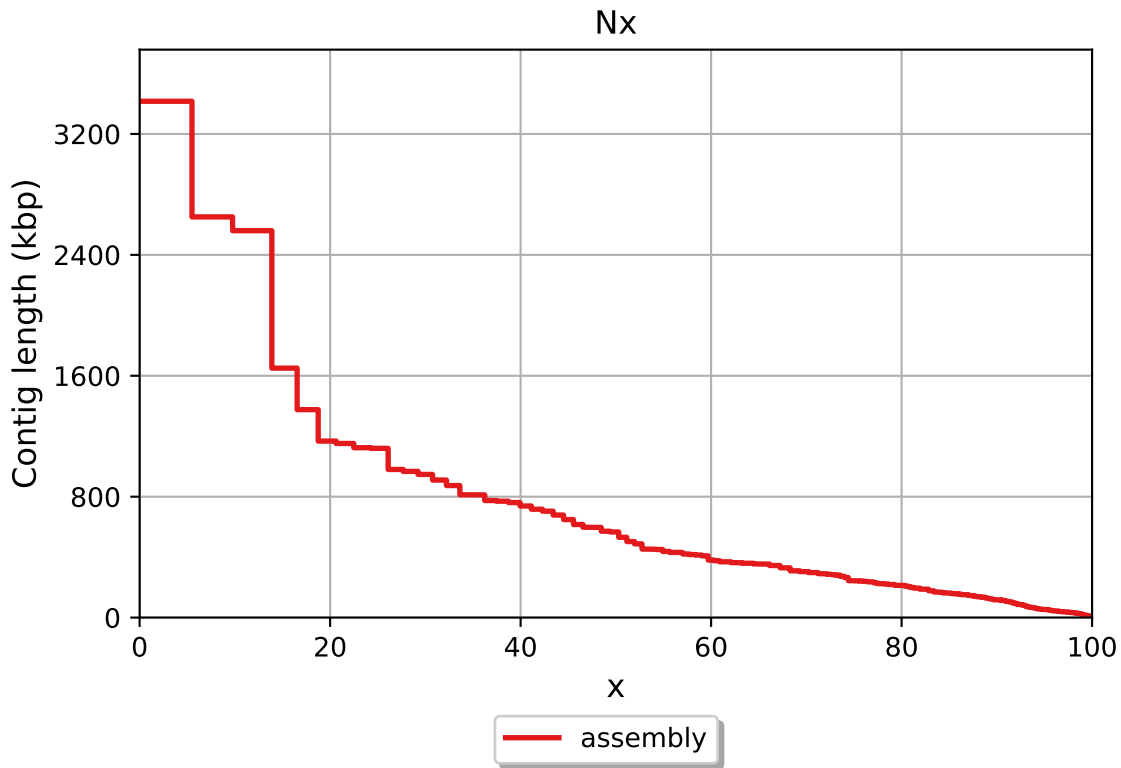
	assembly
# misassemblies	231
# contig misassemblies	231
# c. relocations	230
# c. translocations	0
# c. inversions	1
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	21
Misassembled contigs length	3405160
# possibly misassembled contigs	202
# possible misassemblies	521
# local misassemblies	52
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	69
# mismatches	58709
# indels	15868
# indels (<= 5 bp)	15499
# indels (> 5 bp)	369
Indels length	30612

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).

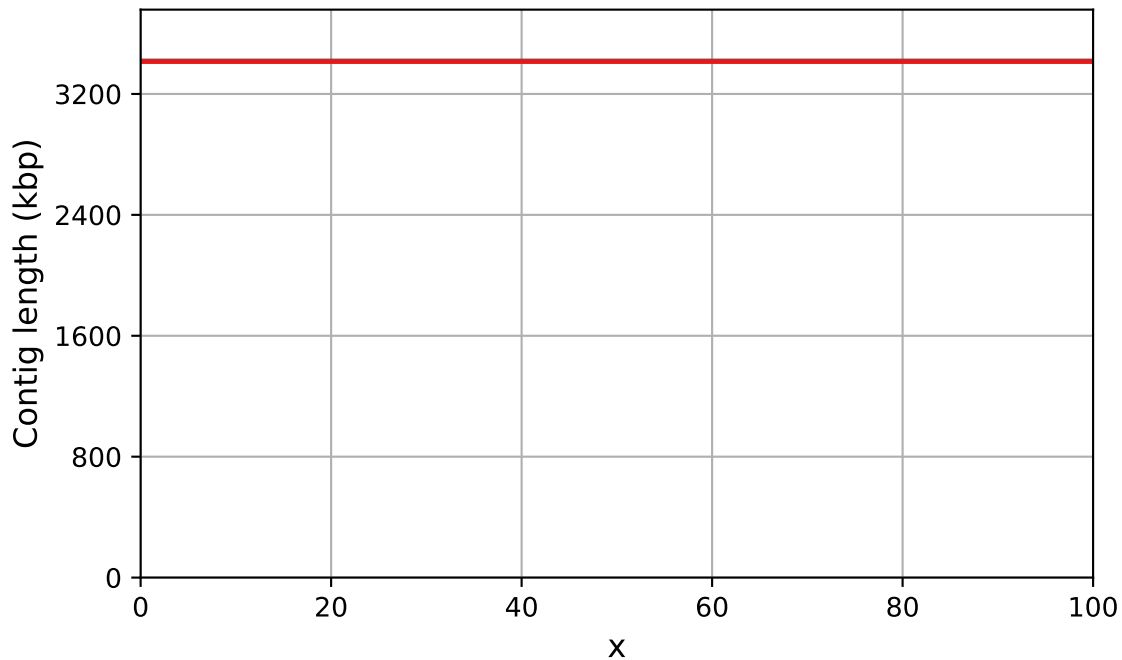
Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	276
Partially unaligned length	58742228
# 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).

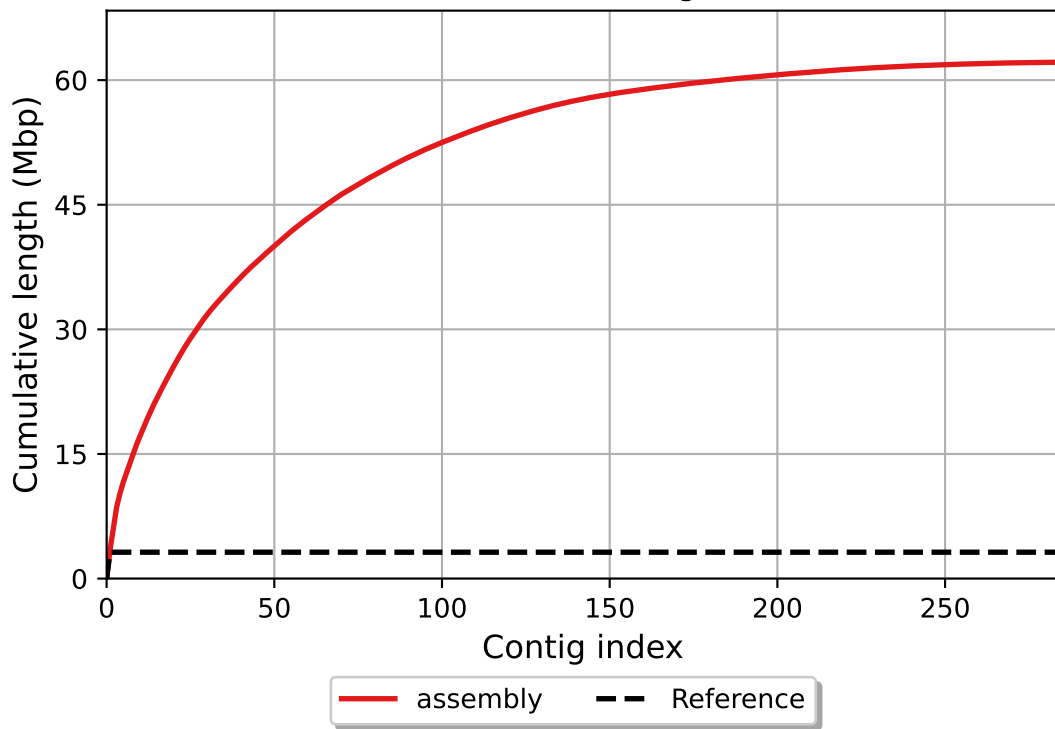


NGx

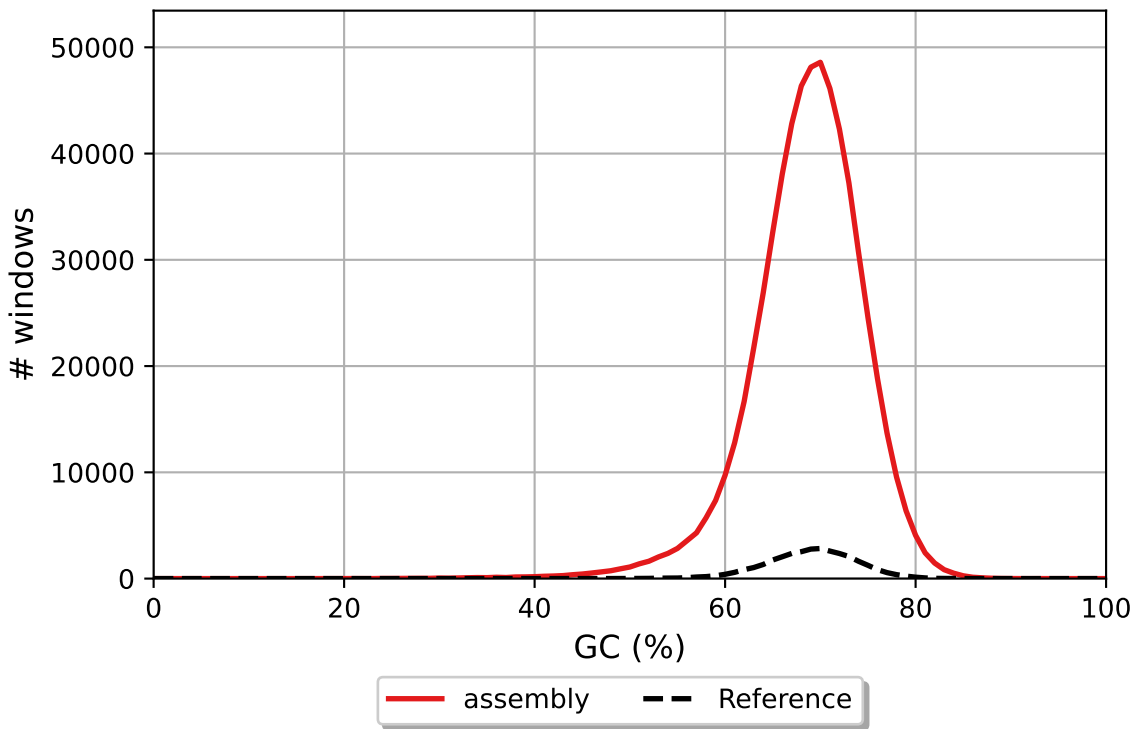


— assembly

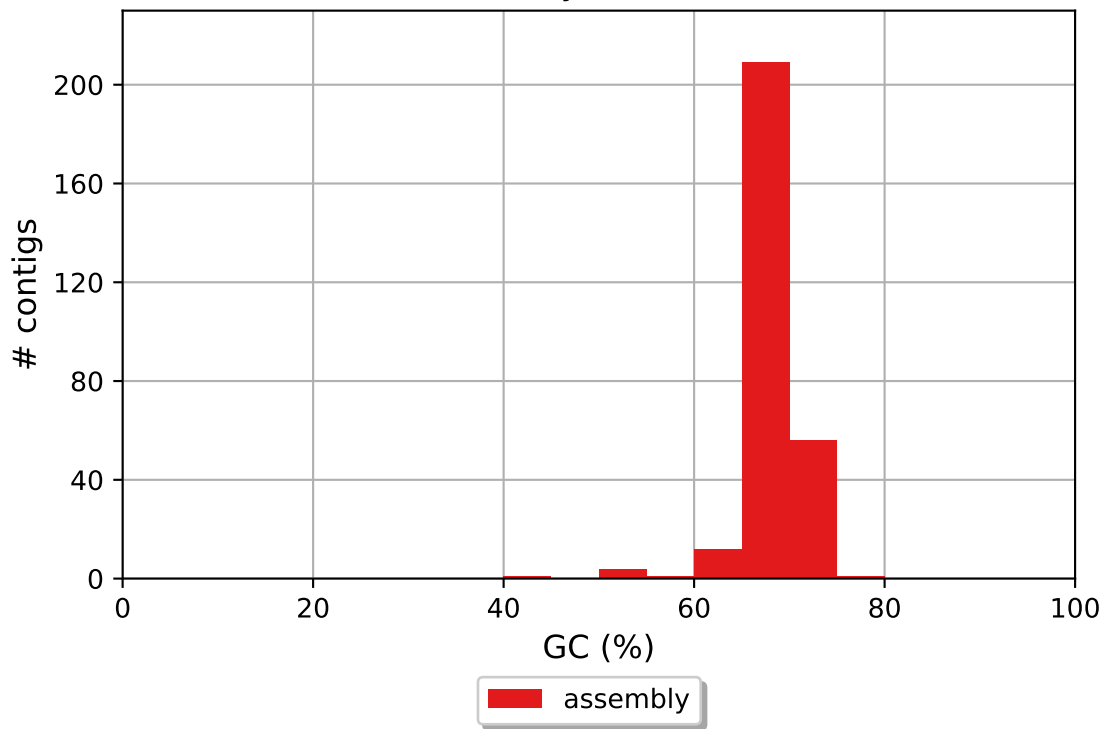
Cumulative length



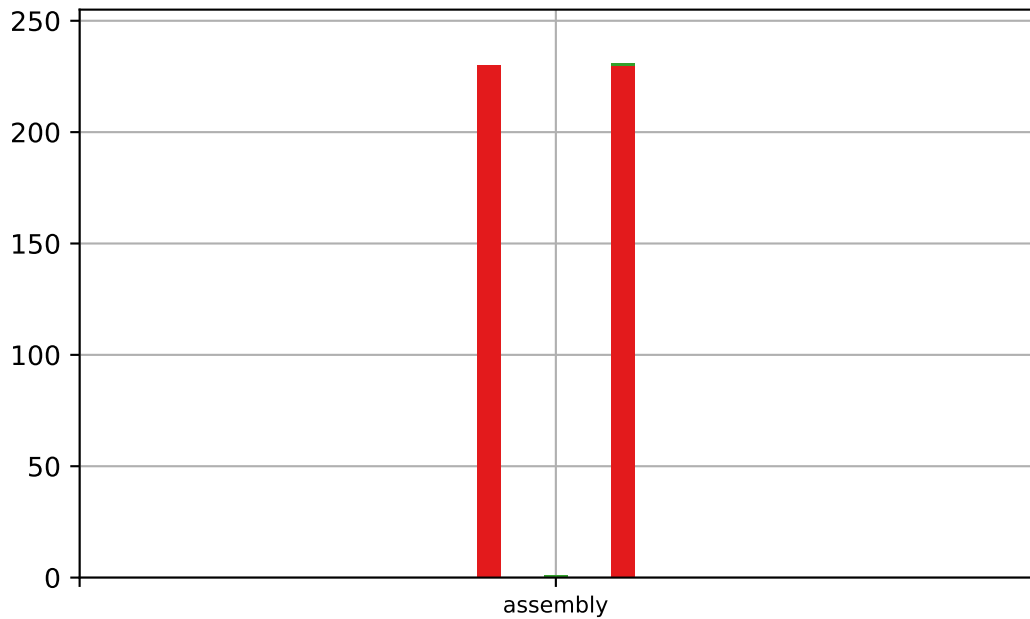
GC content



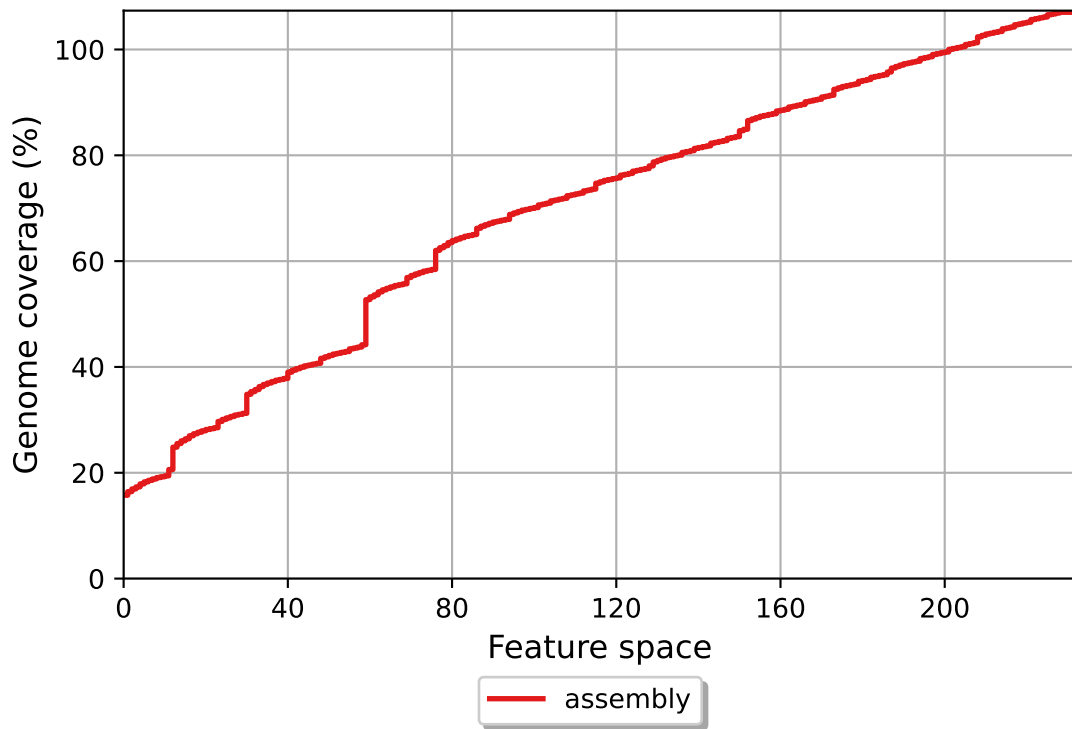
assembly GC content



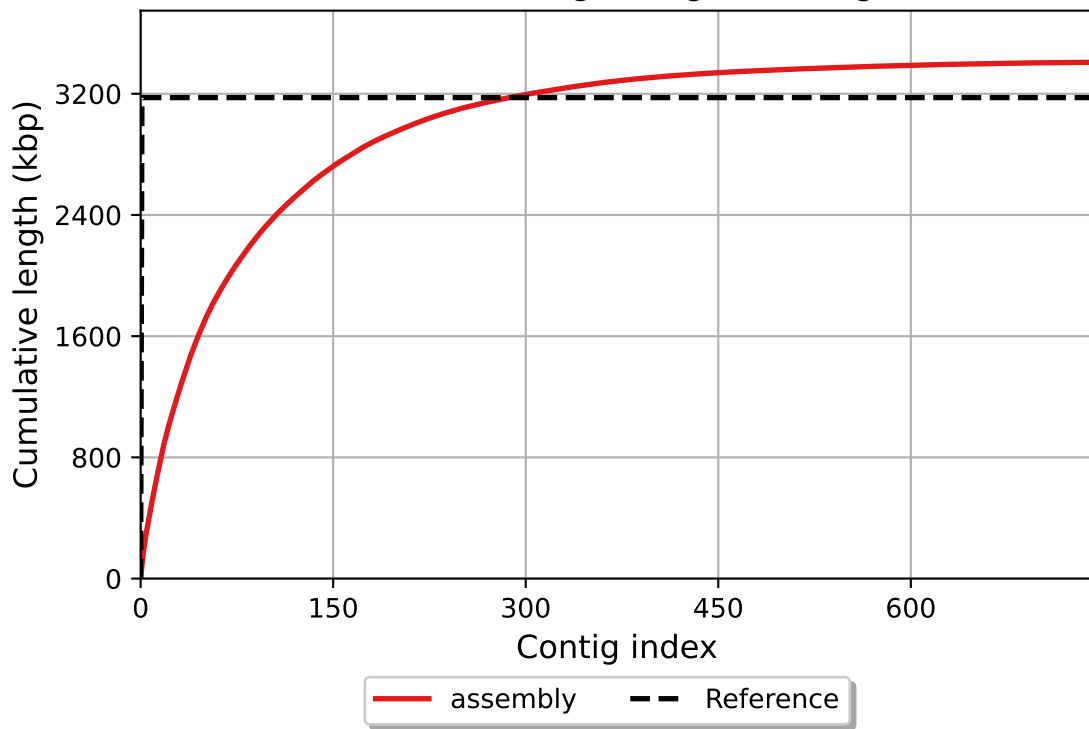
Misassemblies



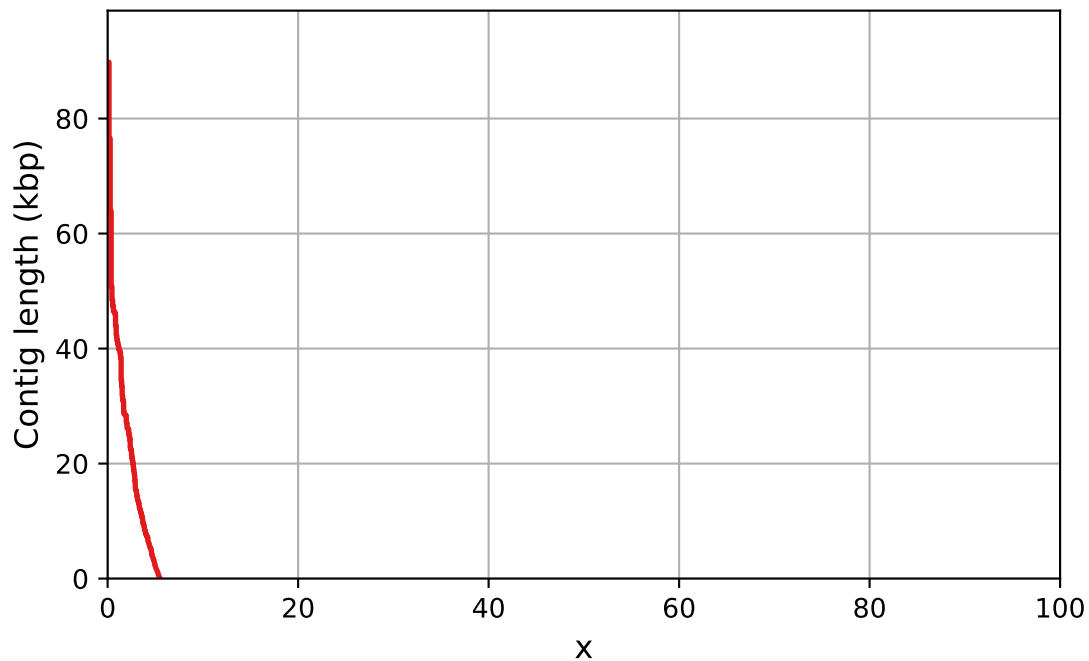
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— assembly

NGAx

