

## Report

	assembly_test
# contigs (>= 0 bp)	8288
# contigs (>= 1000 bp)	0
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	746382
Total length (>= 1000 bp)	0
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	8288
Largest contig	869
Total length	746382
Reference length	3990777
GC (%)	41.83
Reference GC (%)	36.99
N50	100
N75	56
L50	2149
L75	4685
# misassemblies	16
# misassembled contigs	11
Misassembled contigs length	4671
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	7496 + 0 part
Unaligned length	619943
Genome fraction (%)	2.080
Duplication ratio	1.549
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1745.45
# indels per 100 kbp	143.31
Largest alignment	728
Total aligned length	112205
NGA50	-

All statistics are based on contigs of size >= 50 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

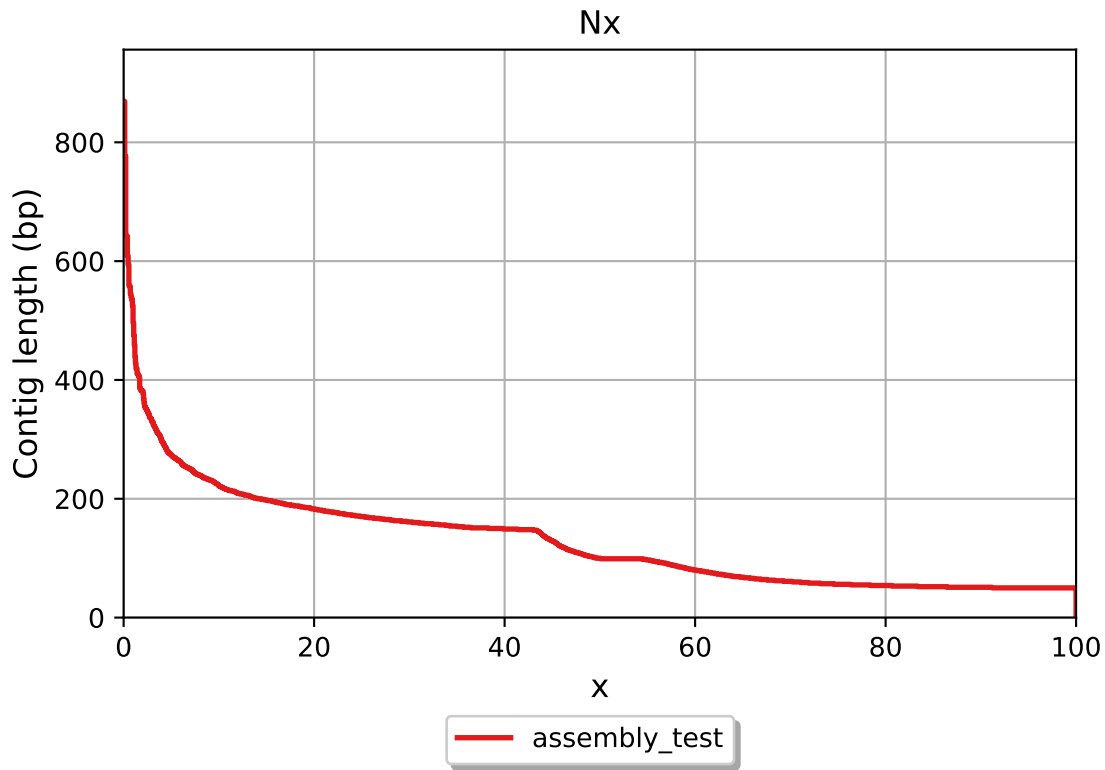
	assembly_test
# misassemblies	16
# contig misassemblies	16
# c. relocations	16
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	4671
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	1425
# indels	117
# indels (<= 5 bp)	117
# indels (> 5 bp)	0
Indels length	163

All statistics are based on contigs of size  $\geq 50$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

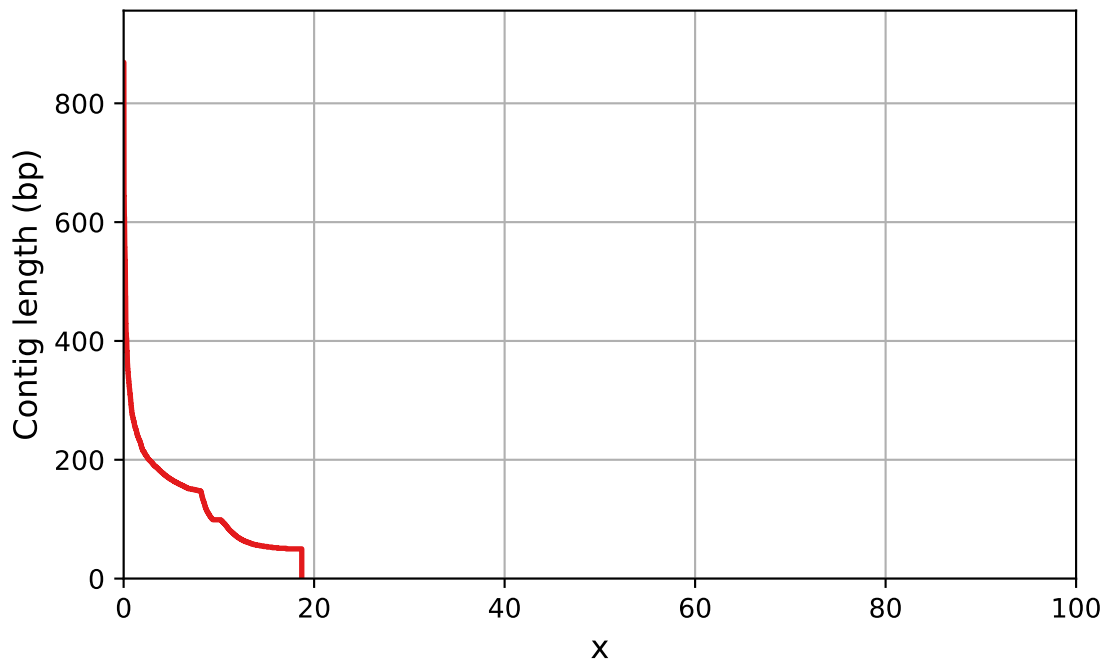
## Unaligned report

	assembly_test
# fully unaligned contigs	7496
Fully unaligned length	619943
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size  $\geq 50$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

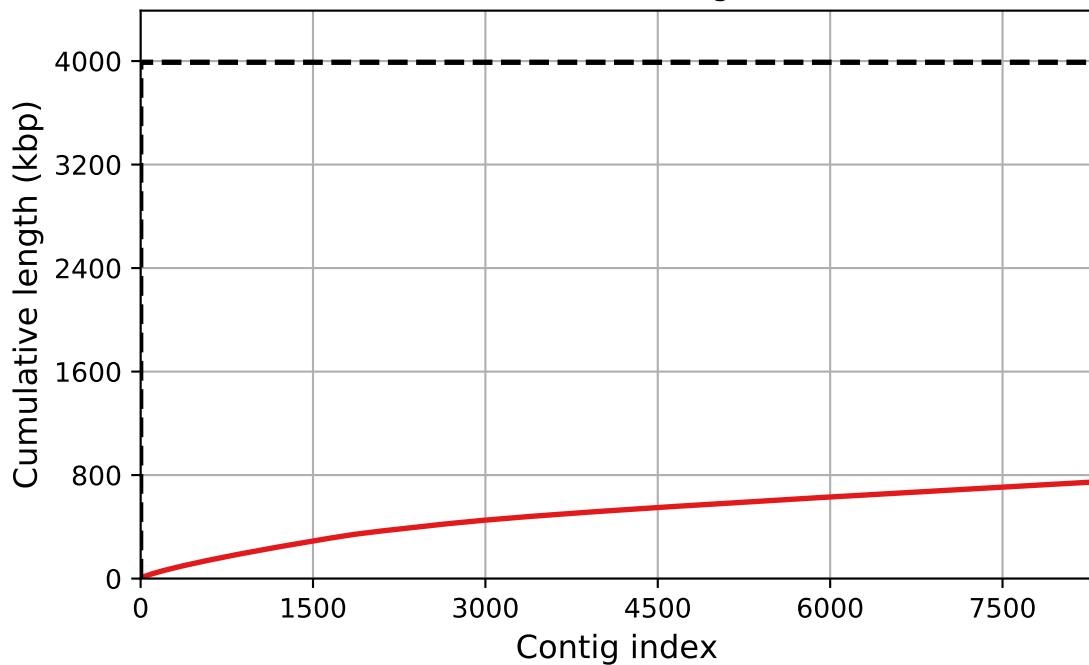


NGx

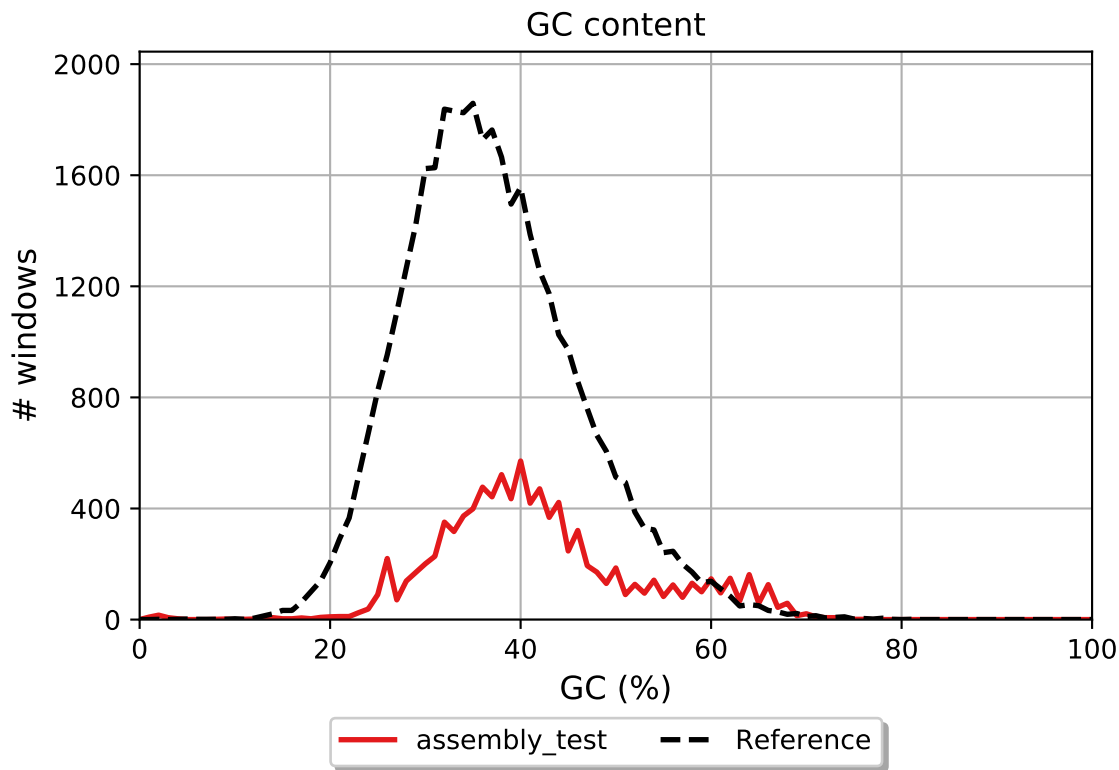


— assembly\_test

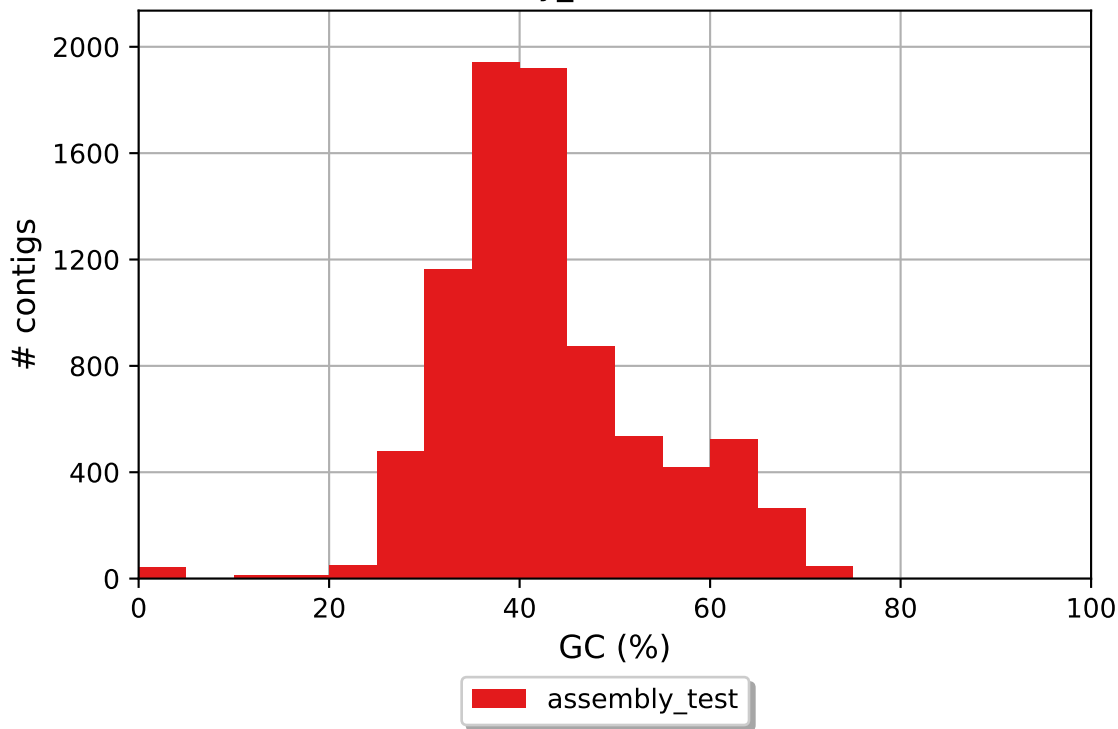
Cumulative length



— assembly\_test    - - Reference

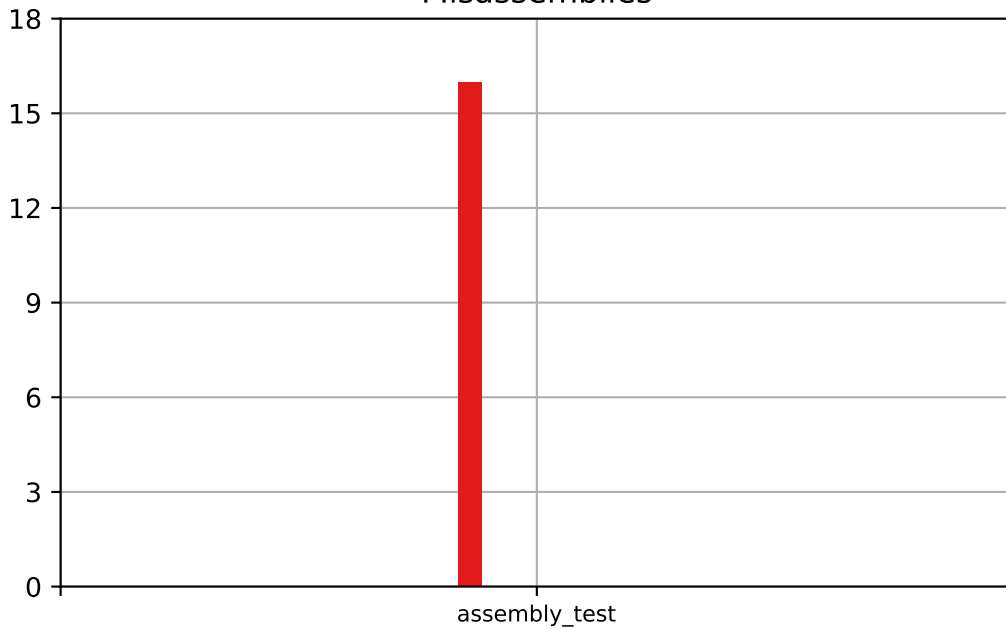


assembly\_test GC content

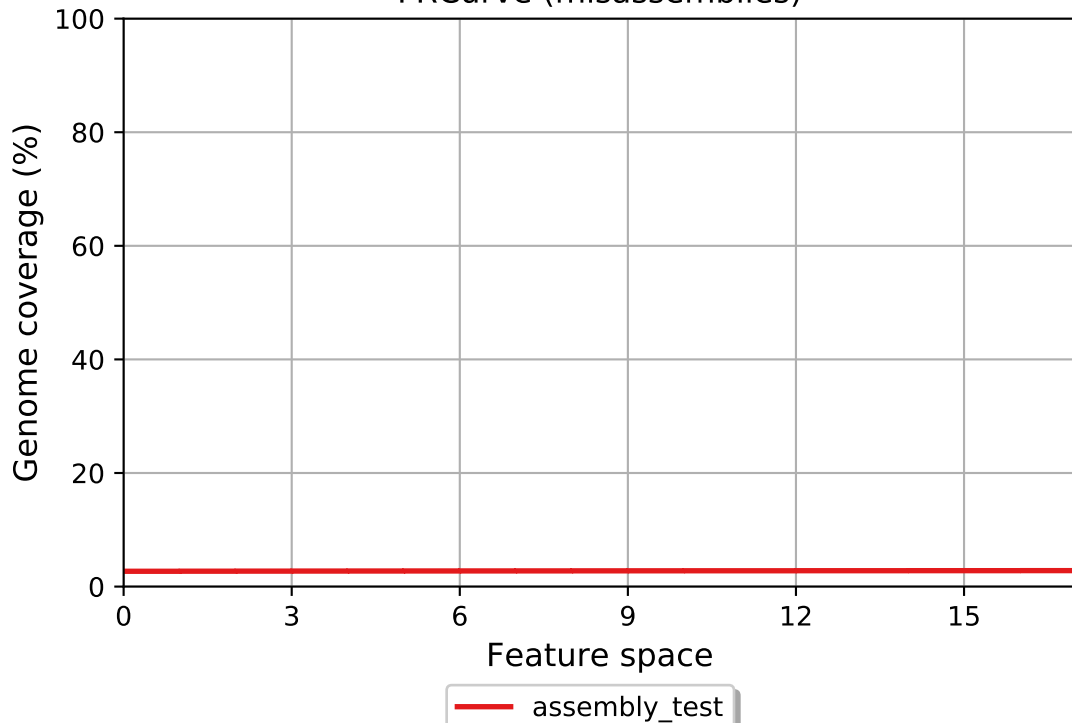




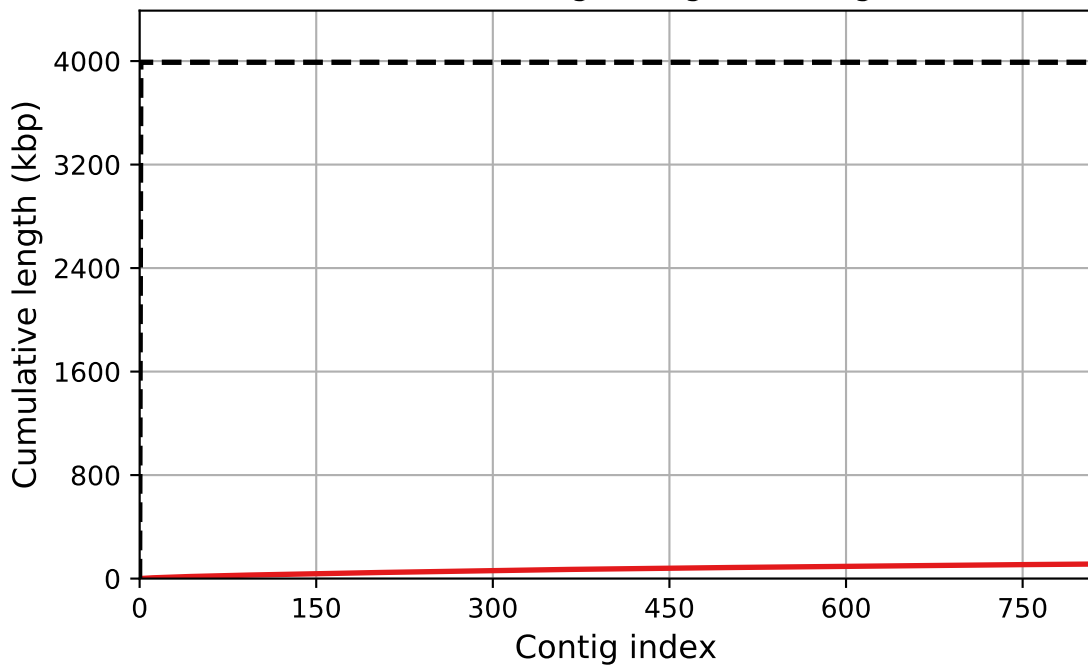
## Misassemblies



FRCurve (misassemblies)

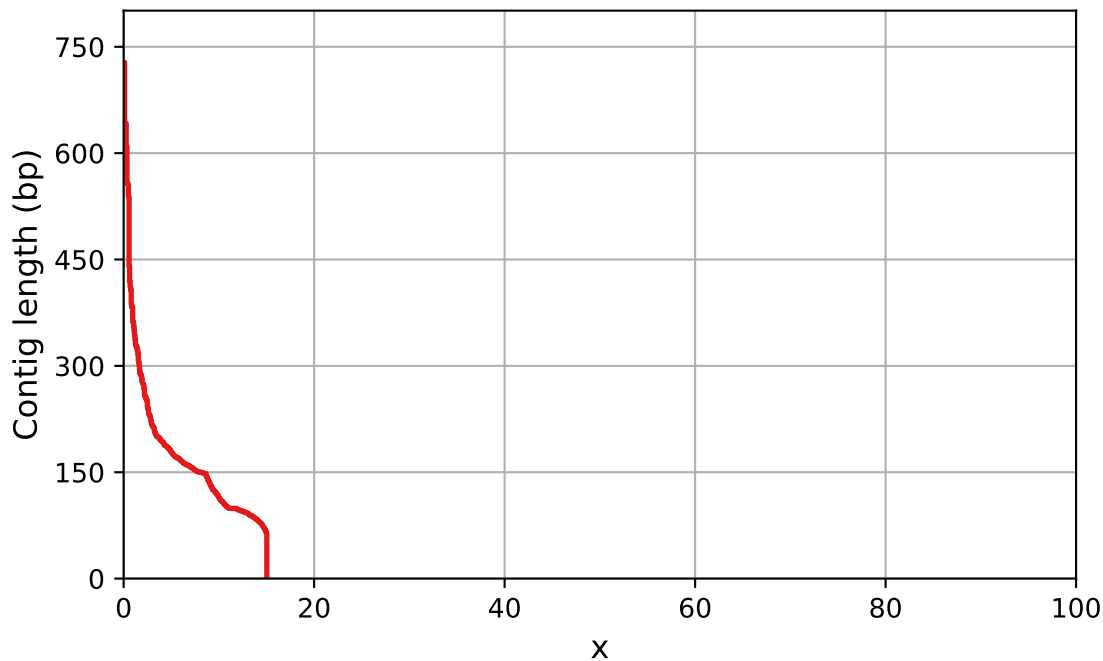


Cumulative length (aligned contigs)



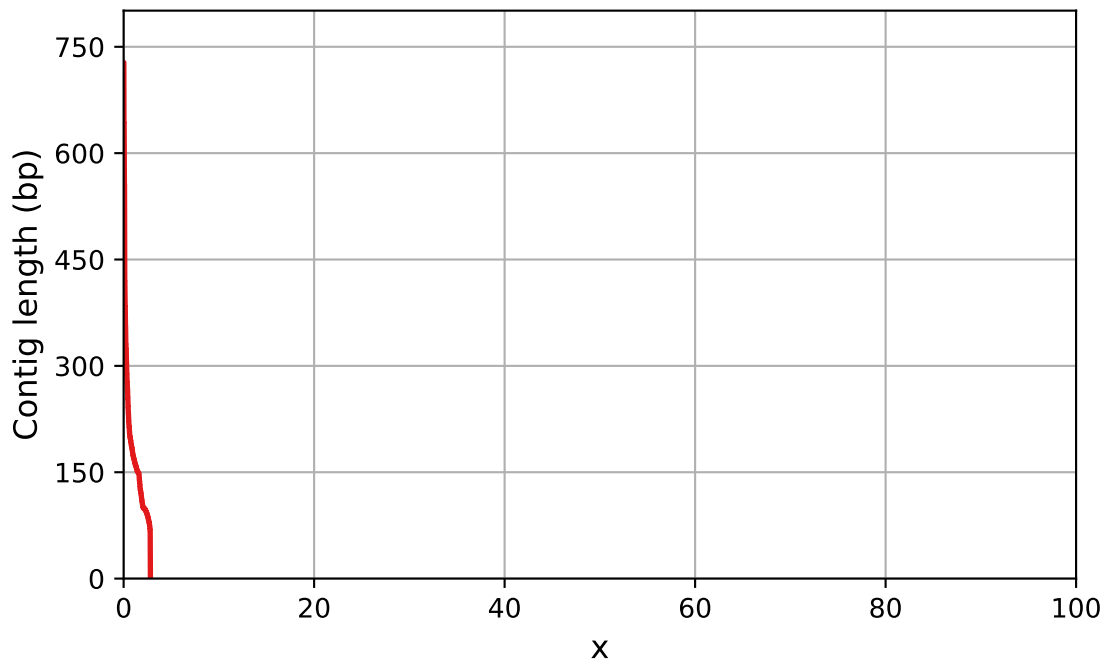
— assembly\_test    - - Reference

NAx



— assembly\_test

# NGAx



— assembly\_test