

Report

	assembly
# contigs (>= 1000 bp)	350
# contigs (>= 5000 bp)	347
# contigs (>= 10000 bp)	338
# contigs (>= 25000 bp)	299
# contigs (>= 50000 bp)	229
Total length (>= 1000 bp)	88774211
Total length (>= 5000 bp)	88762926
Total length (>= 10000 bp)	88694858
Total length (>= 25000 bp)	88032080
Total length (>= 50000 bp)	85406283
# contigs	351
Largest contig	5242943
Total length	88774964
Reference length	3802648
GC (%)	62.00
Reference GC (%)	63.27
N50	650452
NG50	5242943
N90	117844
NG90	5242943
auN	1122030.5
auNG	26194436.0
L50	35
LG50	1
L90	160
LG90	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	4838
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	94
# unaligned contigs	2 + 348 part
Unaligned length	87962497
Genome fraction (%)	12.437
Duplication ratio	1.718
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7337.68
# indels per 100 kbp	842.93
Largest alignment	15447
Total aligned length	812287
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	23.8
auNGA	555.0
LA50	-
LGA50	-
LA90	-
LGA90	-

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	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4838
# possibly misassembled contigs	244
# possible misassemblies	471
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	94
# mismatches	59603
# indels	6847
# indels (<= 5 bp)	6678
# indels (> 5 bp)	169
Indels length	12486

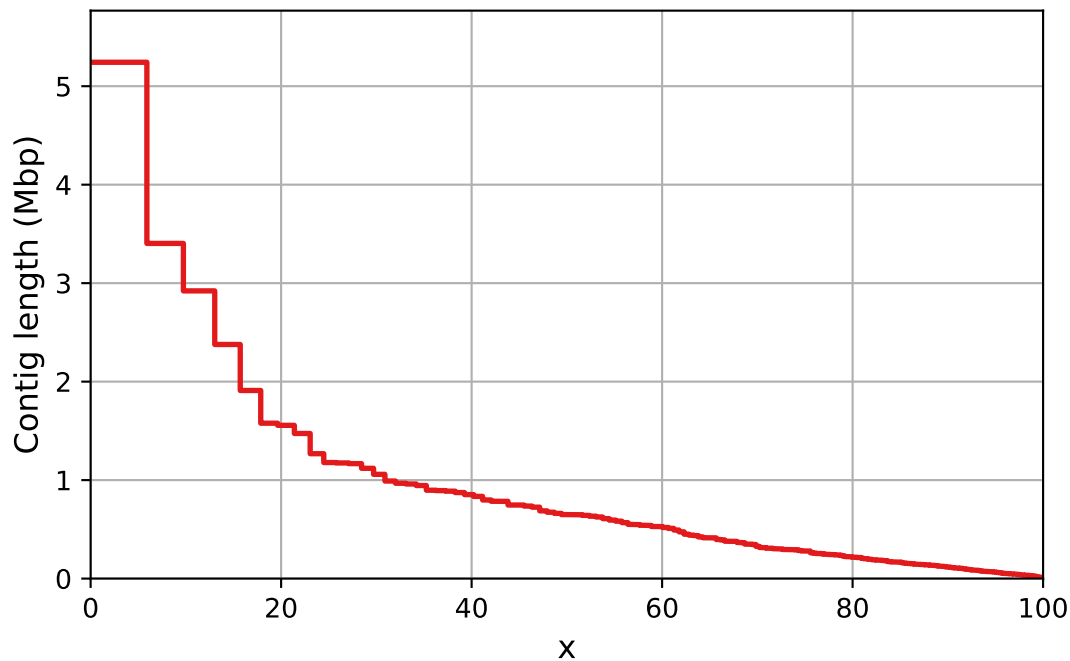
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	assembly
# fully unaligned contigs	2
Fully unaligned length	961086
# partially unaligned contigs	348
Partially unaligned length	87001411
# N's	0

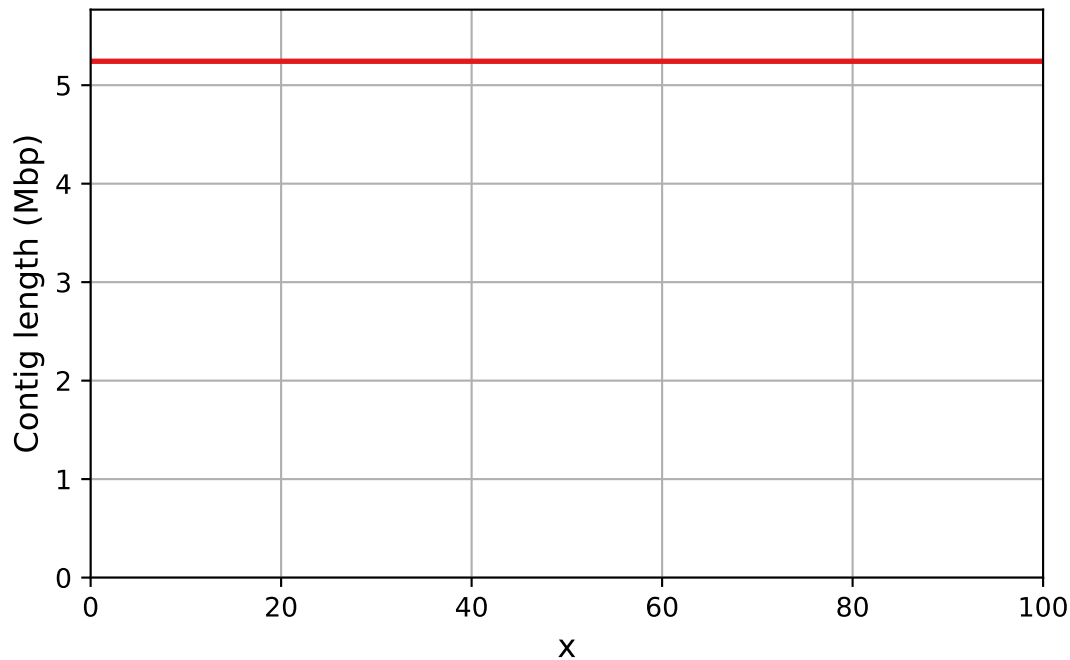
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



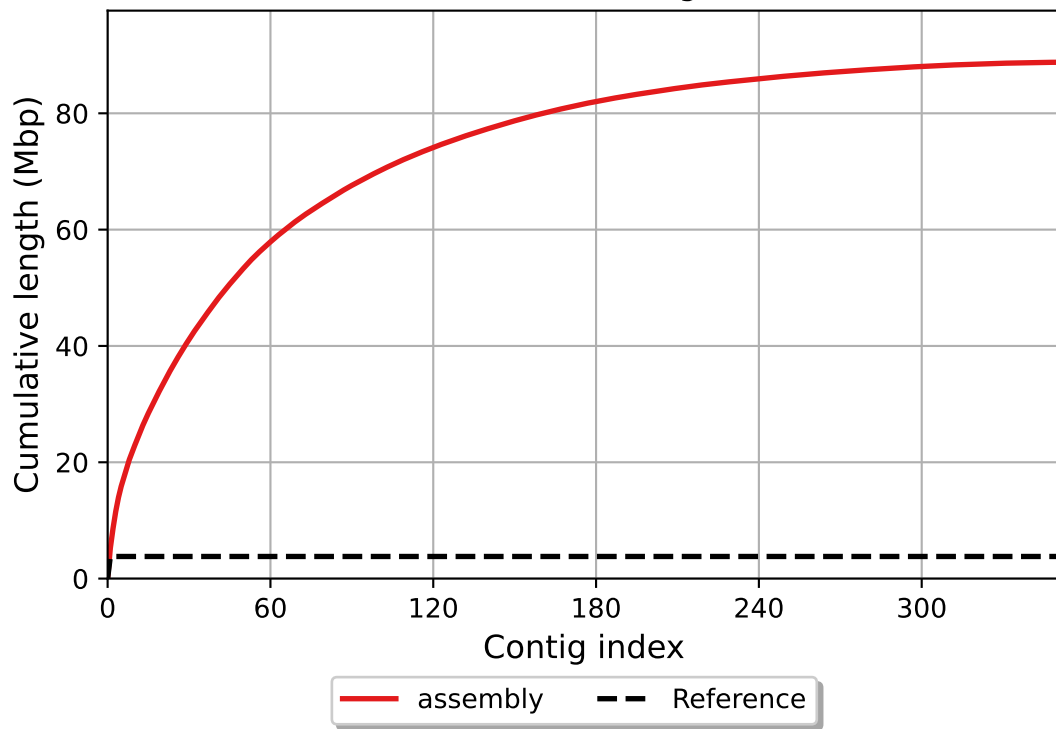
— assembly

NGx

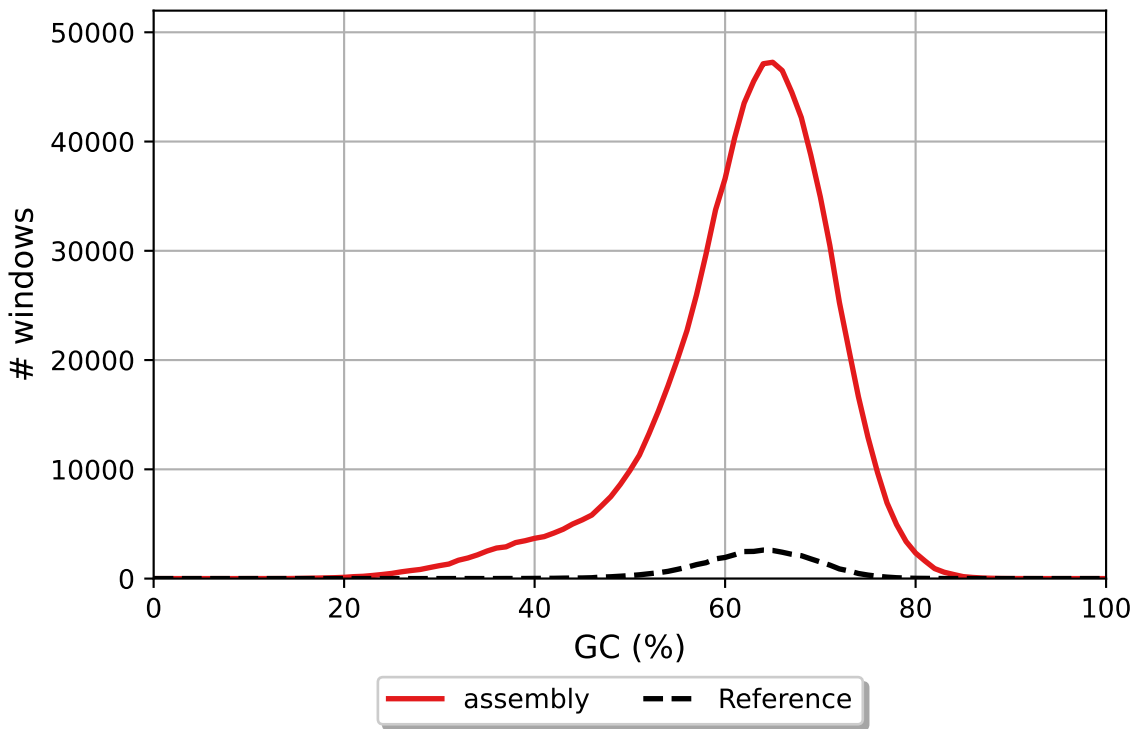


— assembly

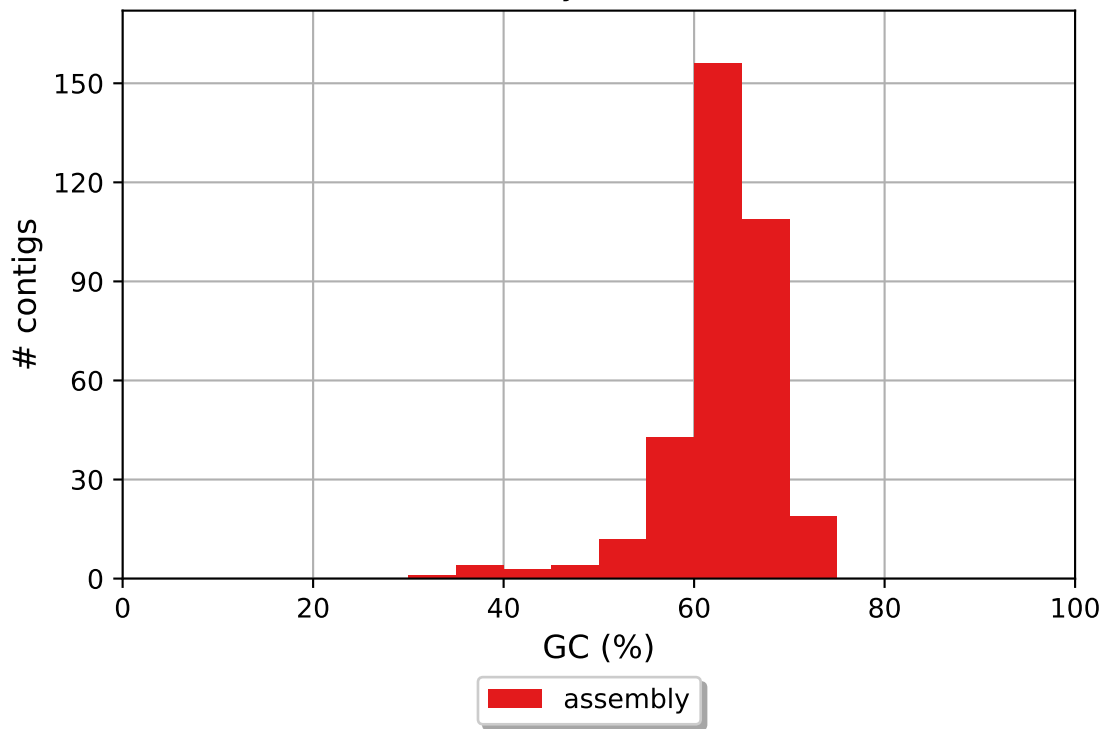
Cumulative length



GC content

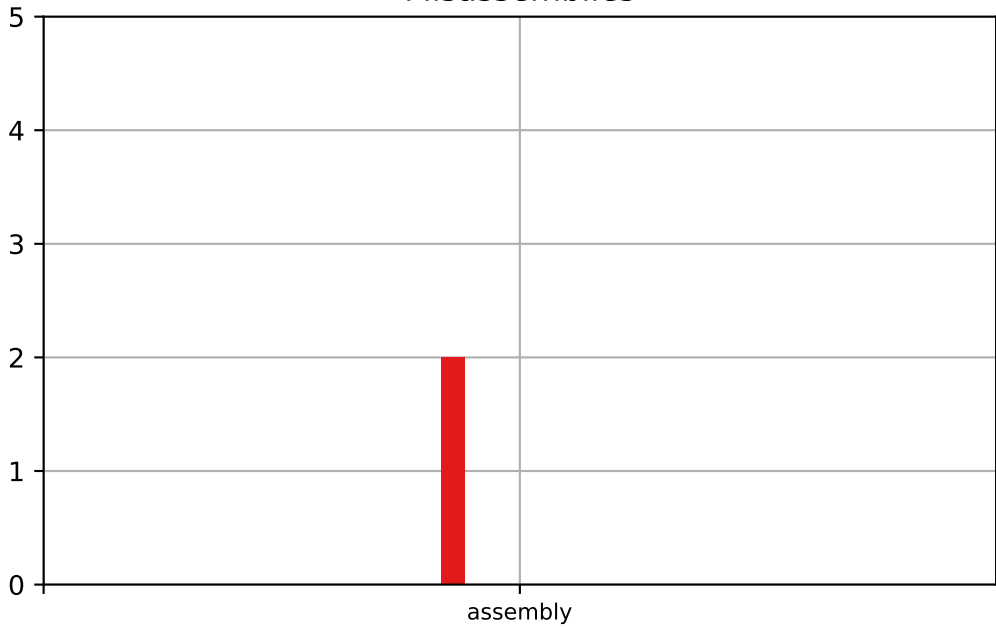


assembly GC content



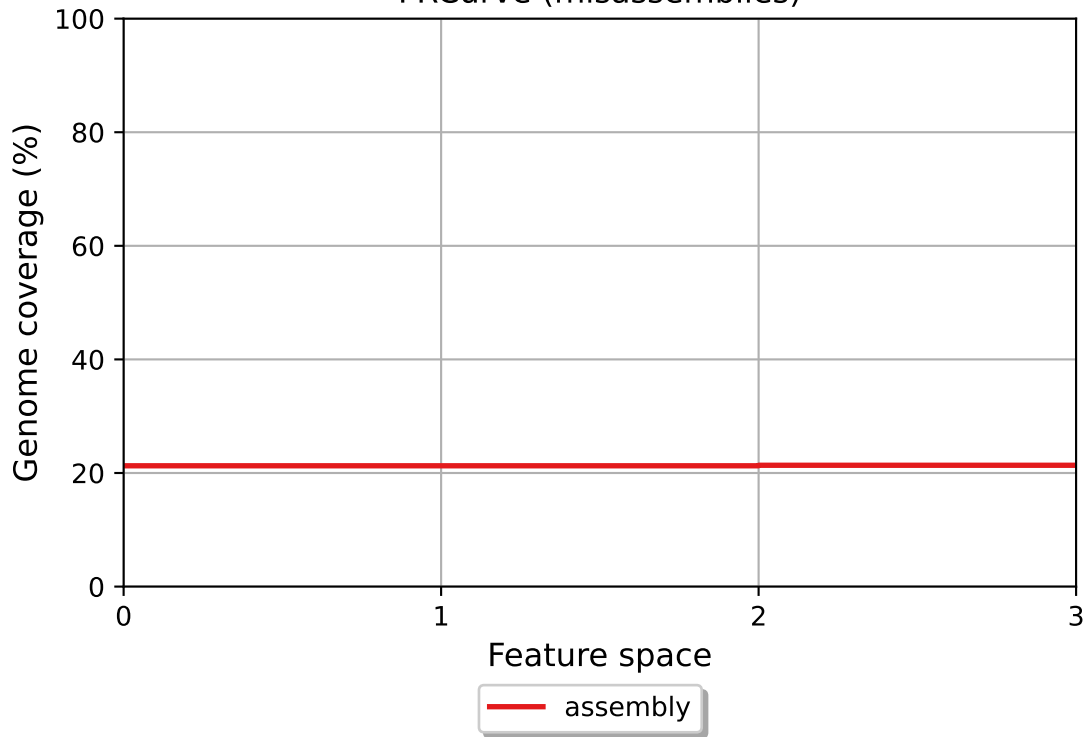


## Misassemblies

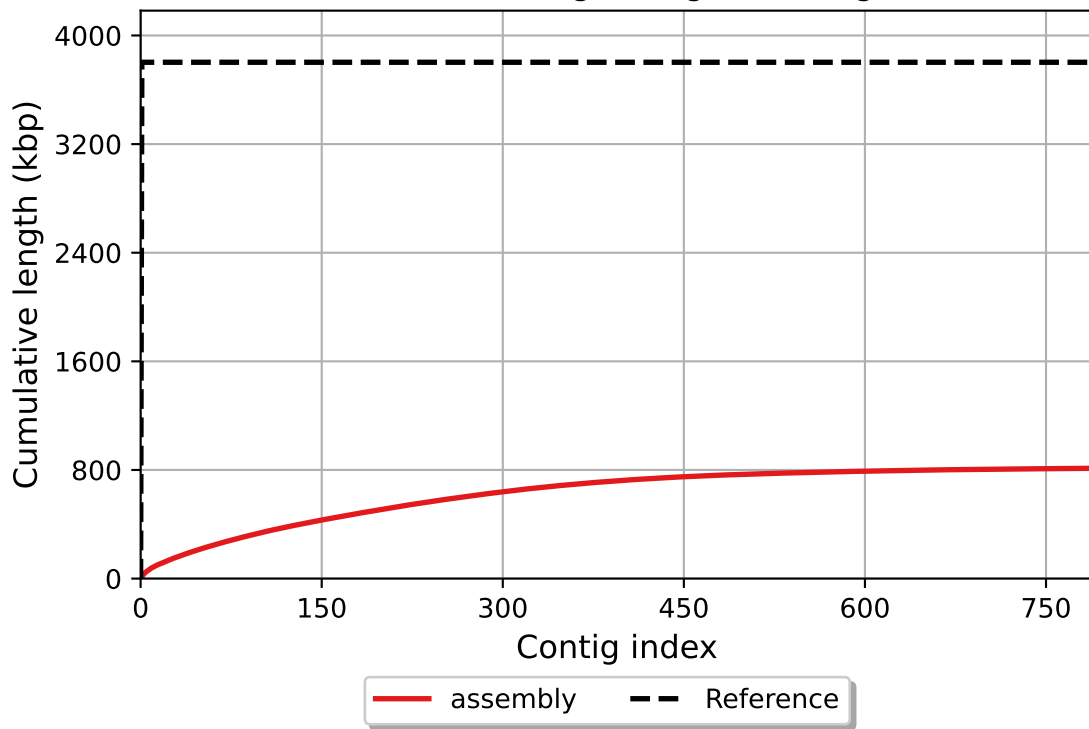


 # relocations

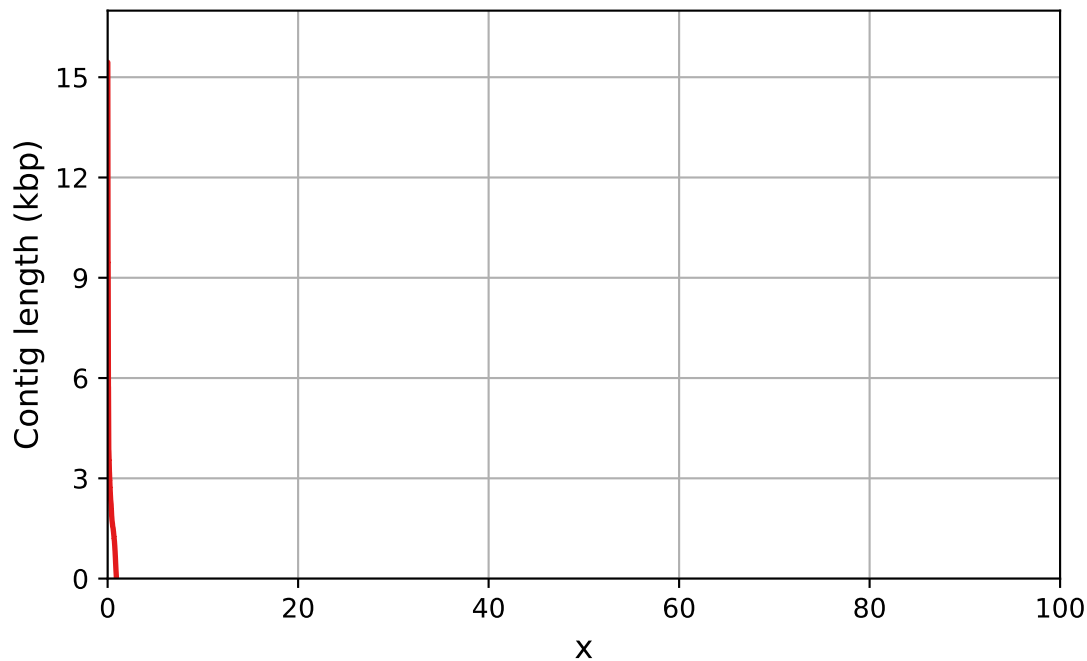
FRCurve (misassemblies)



Cumulative length (aligned contigs)

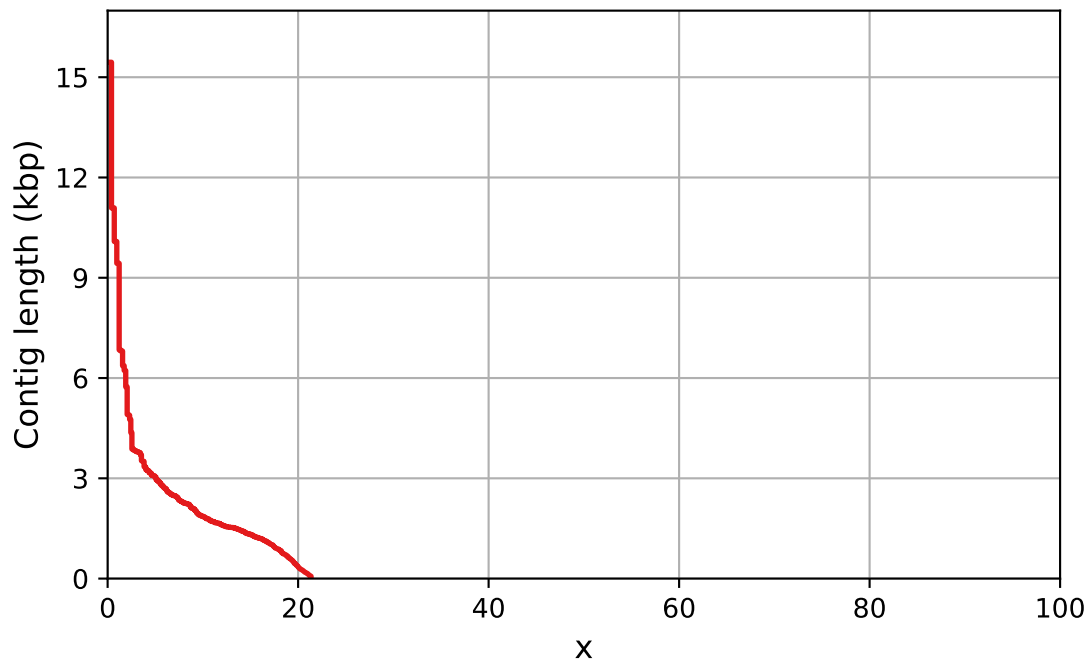


NAx



— assembly

## NGAx



— assembly