

Report

	assembly
# contigs (>= 1000 bp)	219
# contigs (>= 5000 bp)	211
# contigs (>= 10000 bp)	198
# contigs (>= 25000 bp)	134
# contigs (>= 50000 bp)	81
Total length (>= 1000 bp)	33487307
Total length (>= 5000 bp)	33457805
Total length (>= 10000 bp)	33351731
Total length (>= 25000 bp)	32195715
Total length (>= 50000 bp)	30401254
# contigs	221
Largest contig	5242943
Total length	33488547
Reference length	5499334
GC (%)	53.92
Reference GC (%)	55.60
N50	550502
NG50	5242943
N90	55691
NG90	5242943
auN	1267666.1
auNG	7719534.0
L50	15
LG50	1
L90	76
LG90	1
# misassemblies	250
# misassembled contigs	23
Misassembled contigs length	5906094
# local misassemblies	133
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	70
# unaligned contigs	1 + 181 part
Unaligned length	27405472
Genome fraction (%)	84.422
Duplication ratio	1.310
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4168.96
# indels per 100 kbp	533.75
Largest alignment	134742
Total aligned length	6079267
NA50	-
NGA50	30336
NA90	-
NGA90	9870
auNA	6756.2
auNGA	41142.5
LA50	-
LGA50	53
LA90	-
LGA90	174

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	250
# contig misassemblies	250
# c. relocations	250
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	23
Misassembled contigs length	5906094
# possibly misassembled contigs	105
# possible misassemblies	468
# local misassemblies	133
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	70
# mismatches	253442
# indels	32448
# indels (<= 5 bp)	31808
# indels (> 5 bp)	640
Indels length	60817

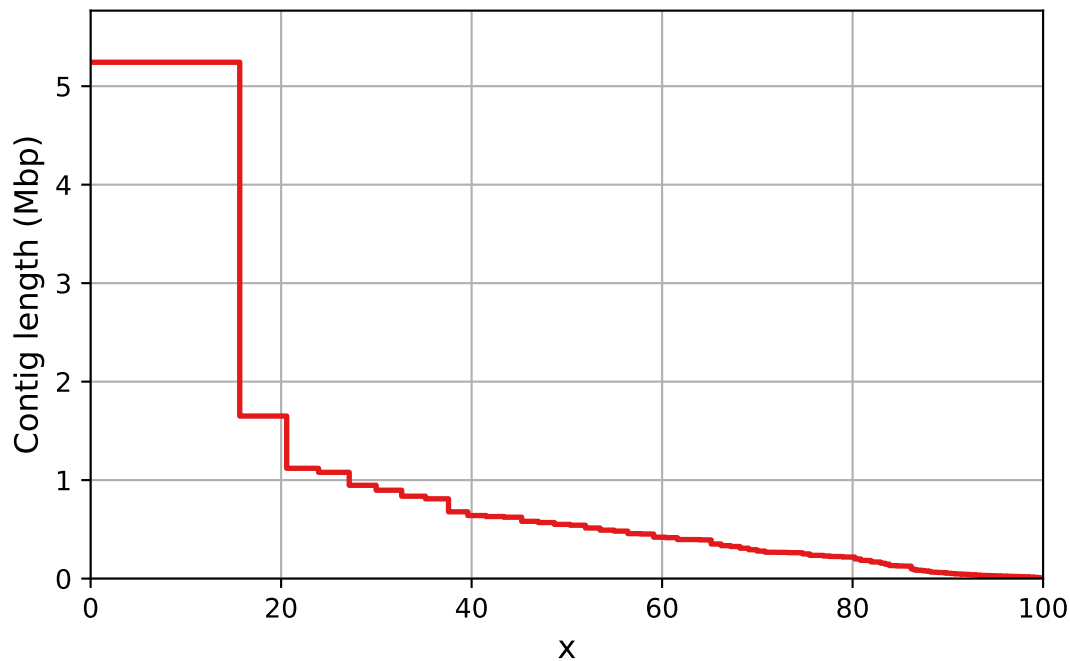
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	assembly
# fully unaligned contigs	1
Fully unaligned length	63661
# partially unaligned contigs	181
Partially unaligned length	27341811
# N's	0

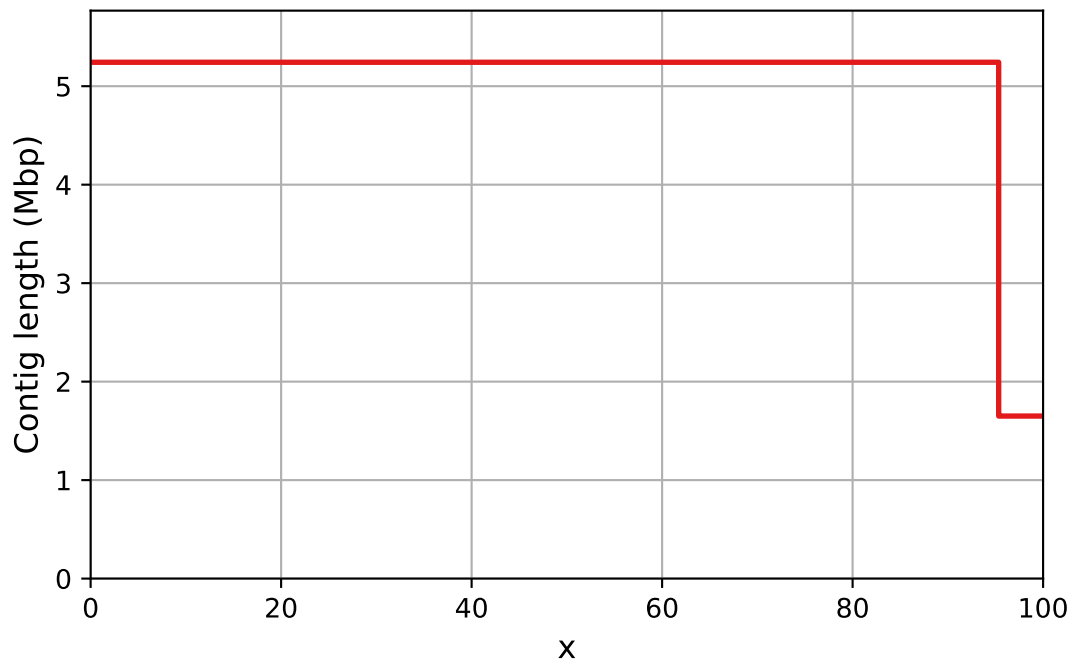
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



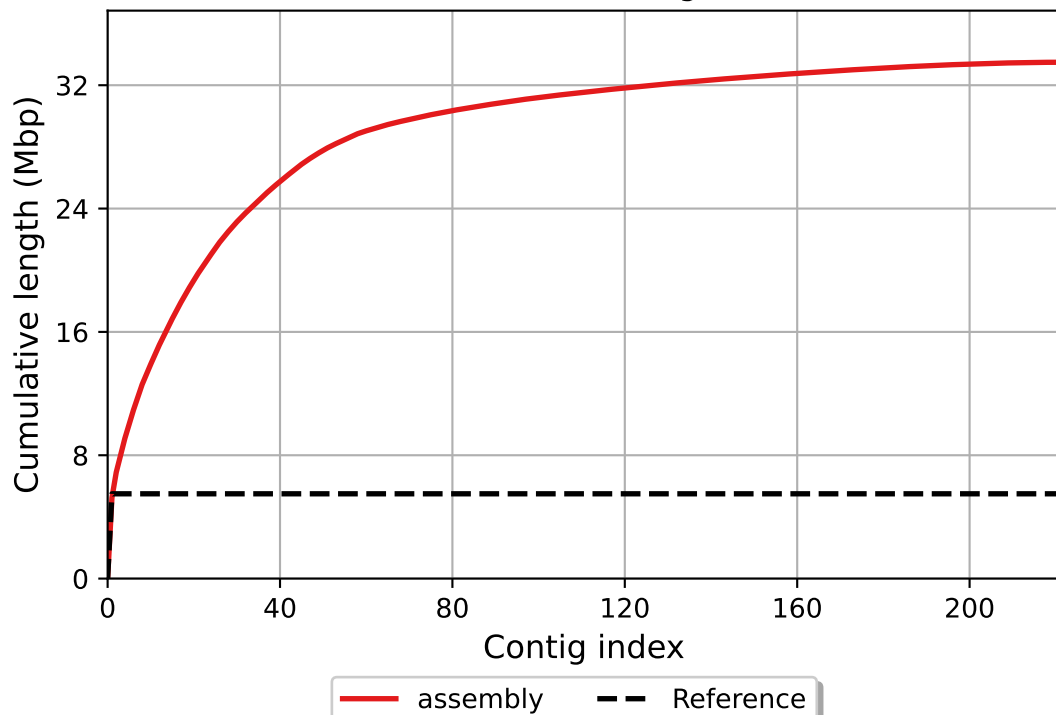
— assembly

NGx

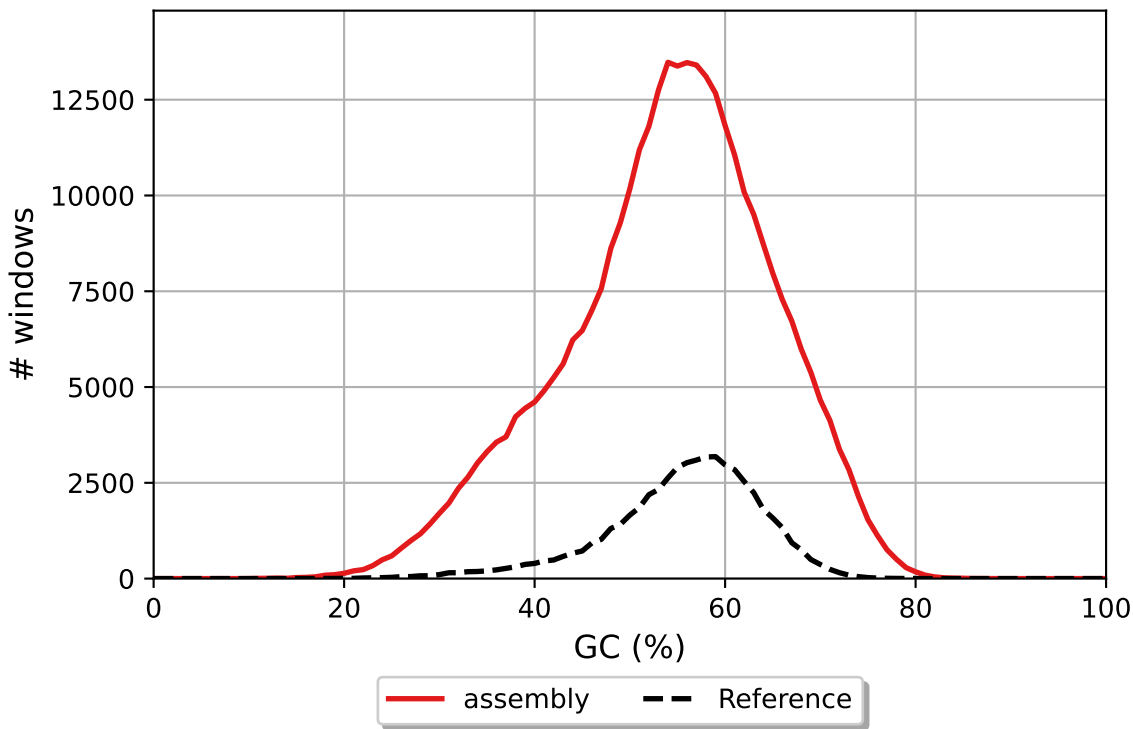


— assembly

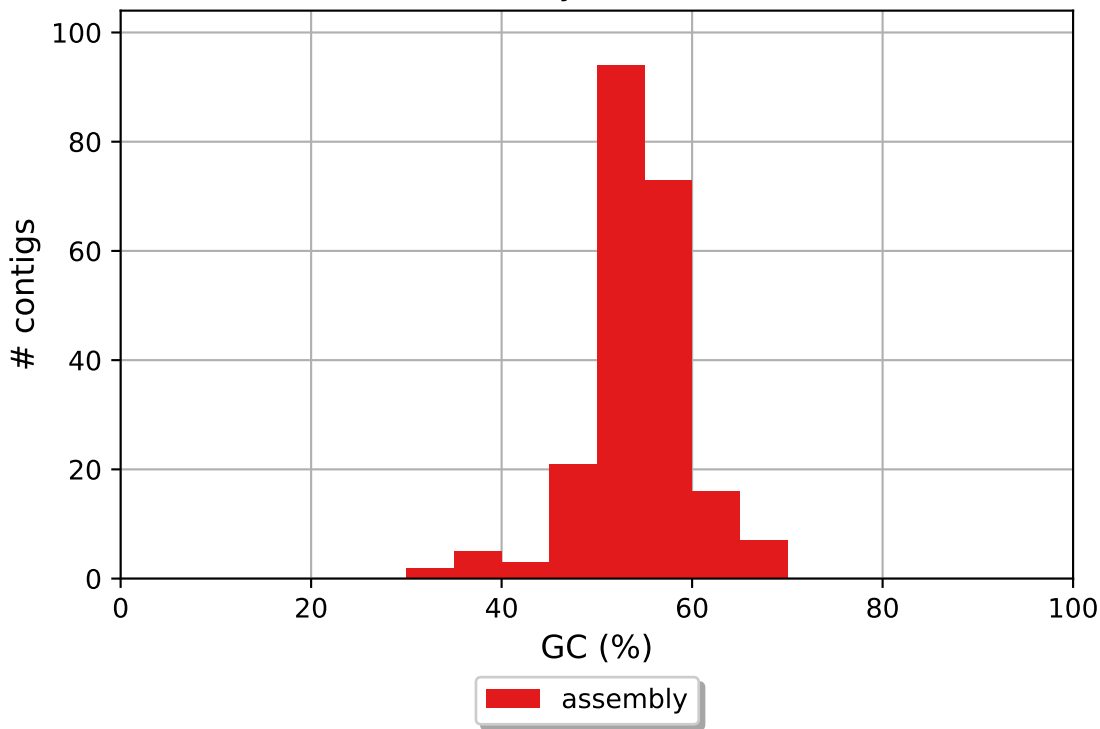
Cumulative length



GC content

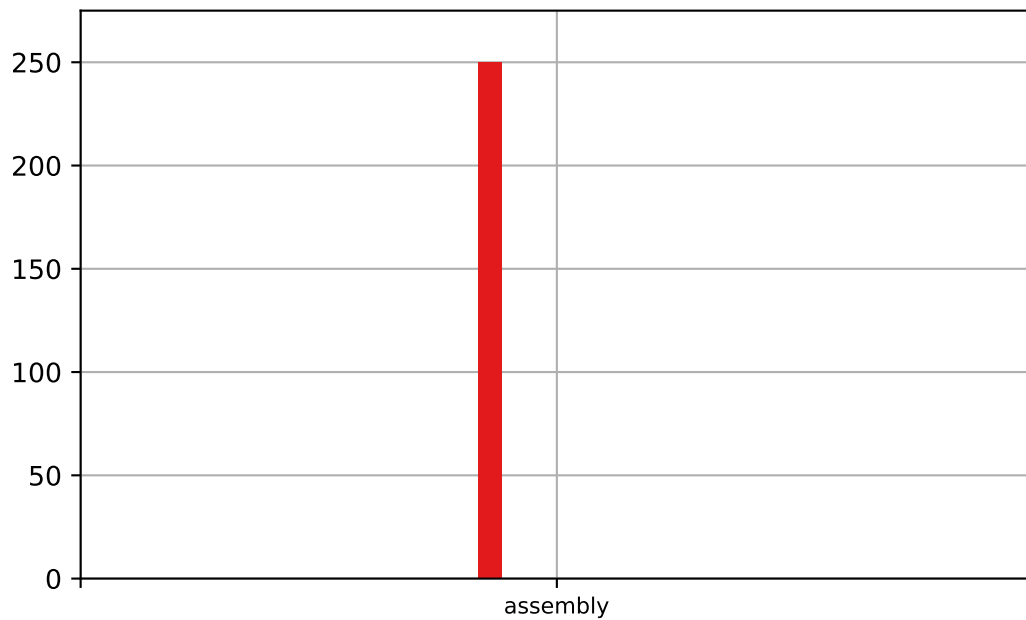


assembly GC content

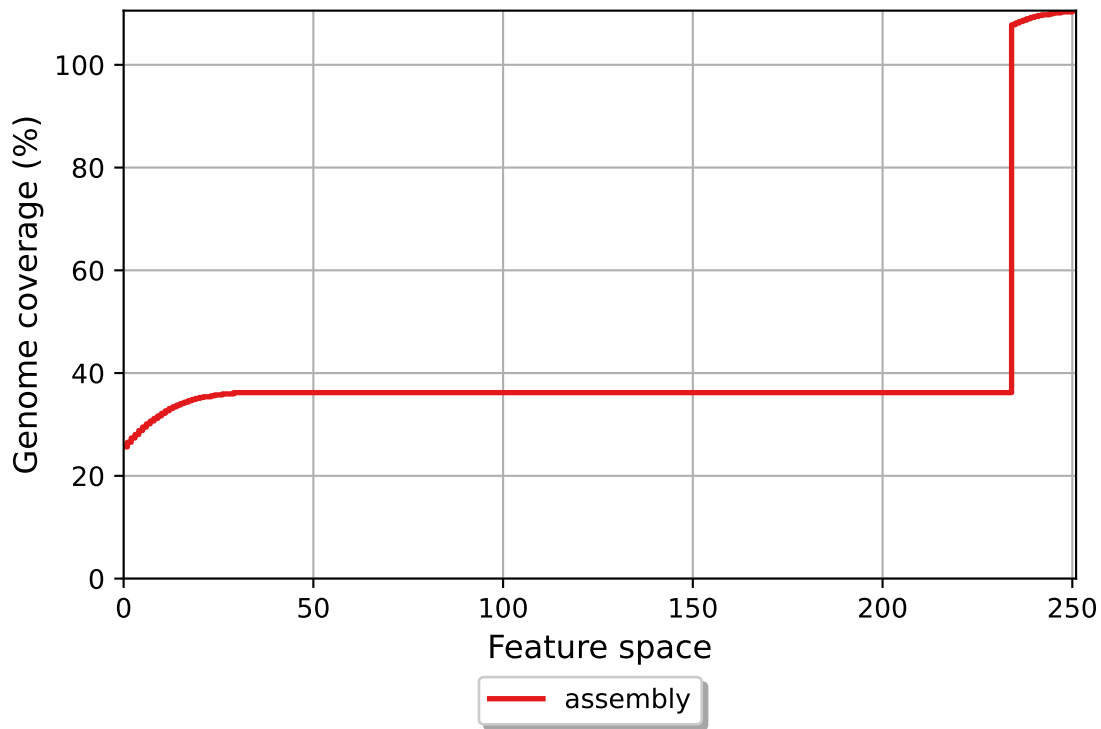




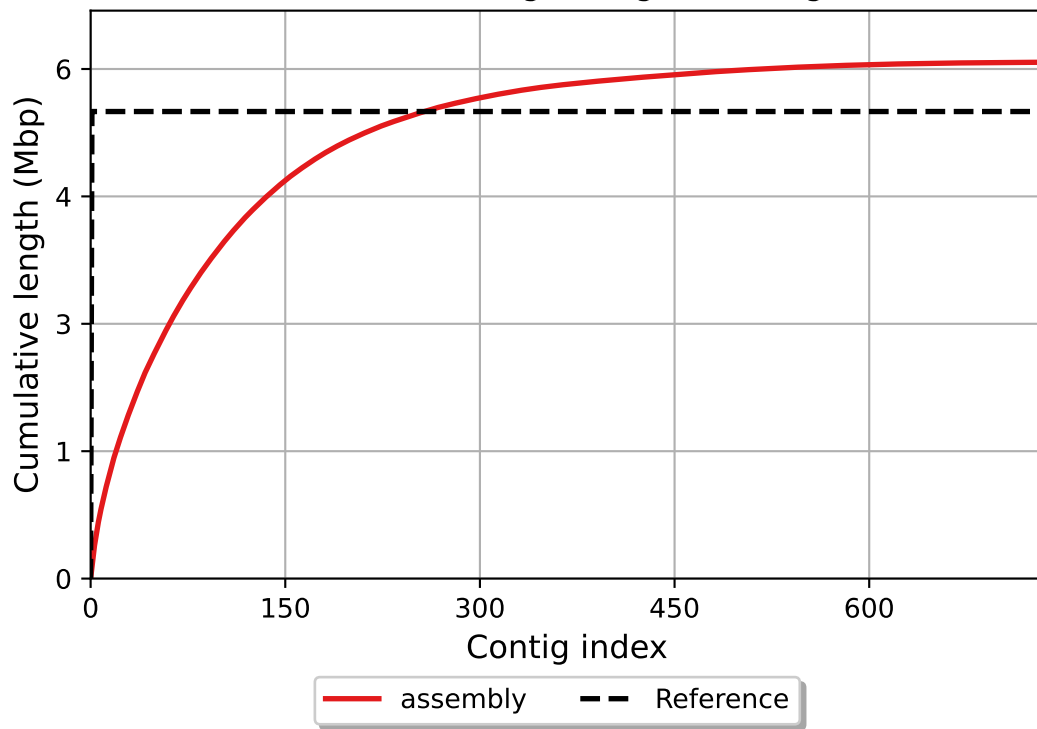
## Misassemblies



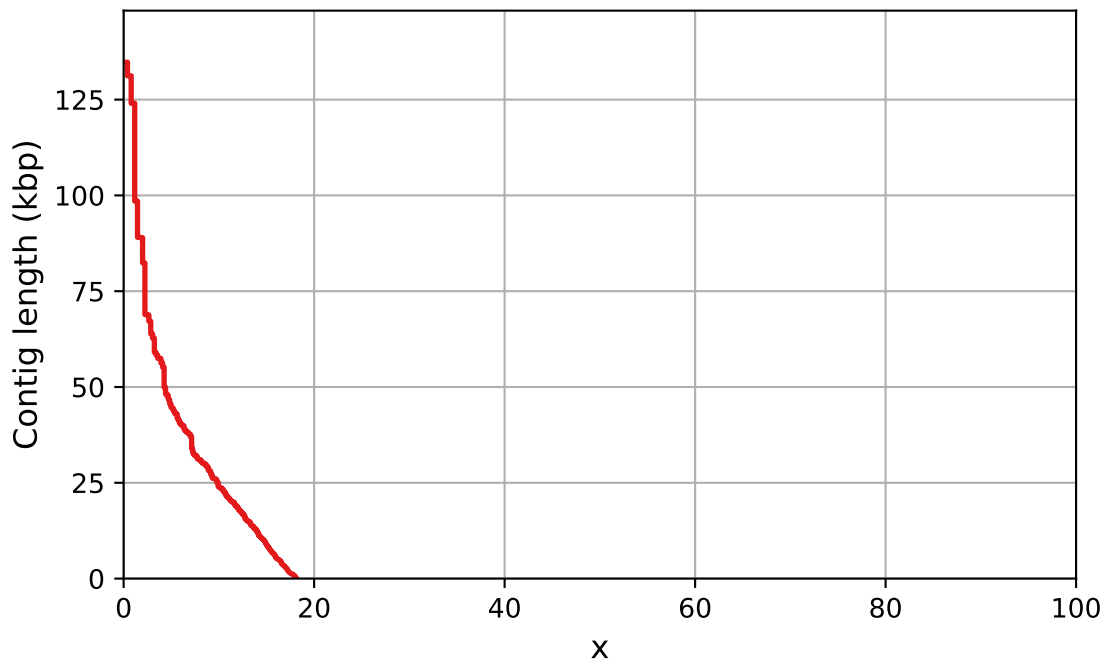
FRCurve (misassemblies)



Cumulative length (aligned contigs)

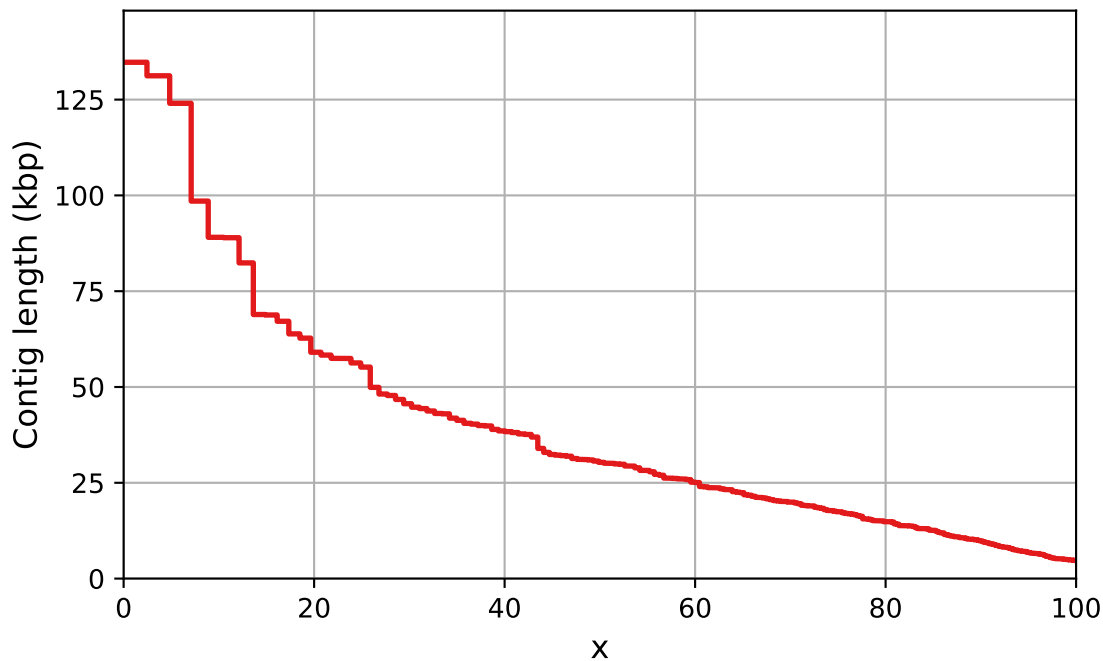


NAx



— assembly

# NGAx



— assembly