

# Report

	Final_genome_with_Reference.fa.masked
# contigs (>= 0 bp)	3
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	3
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	19099067
Total length (>= 1000 bp)	19099067
Total length (>= 5000 bp)	19099067
Total length (>= 10000 bp)	19099067
Total length (>= 25000 bp)	19099067
Total length (>= 50000 bp)	19099067
# contigs	3
Largest contig	14886168
Total length	19099067
Reference length	22250686
GC (%)	36.27
Reference GC (%)	36.74
N50	14886168
NG50	14886168
N90	3253290
NG90	-
auN	12204928.3
auNG	10476204.8
L50	1
LG50	1
L90	2
LG90	-
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	194289
Genome fraction (%)	84.979
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	21.50
# indels per 100 kbp	25.60
Largest alignment	14753741
Total aligned length	18904374
NA50	14753741
NGA50	14753741
NA90	3239109
NGA90	-
auNA	11989882.9
auNGA	10291618.7
LA50	1
LGA50	1
LA90	2
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

	Final_genome_with_Reference.fa.masked
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	4
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	4065
# indels	4839
# indels (<= 5 bp)	4779
# indels (> 5 bp)	60
Indels length	6546

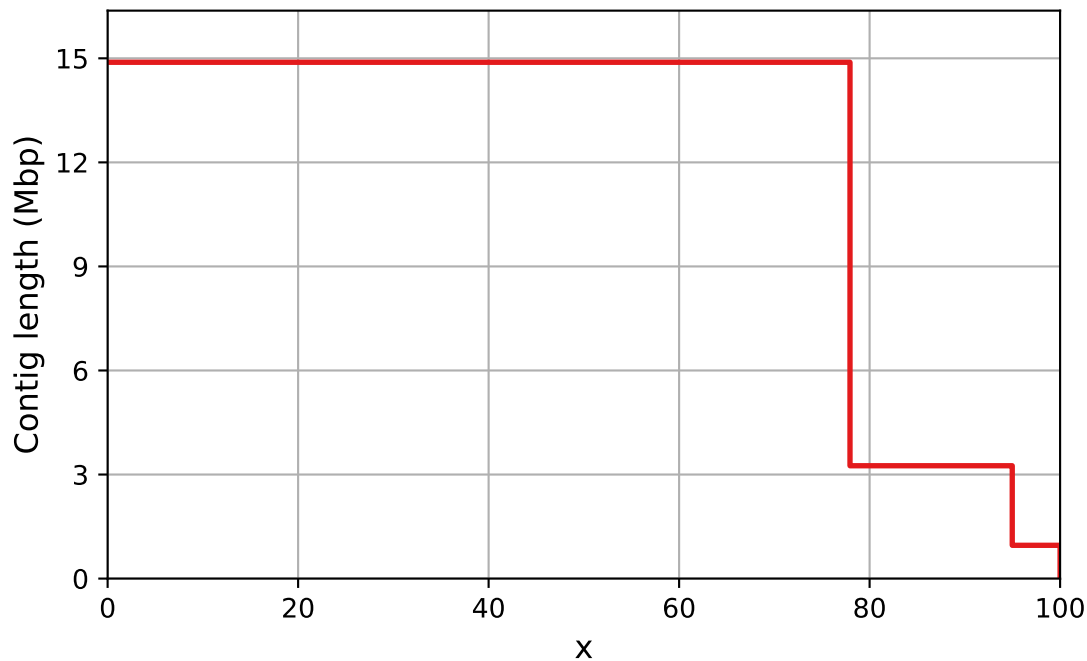
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	Final_genome_with_Reference.fa.masked
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	194289
# N's	0

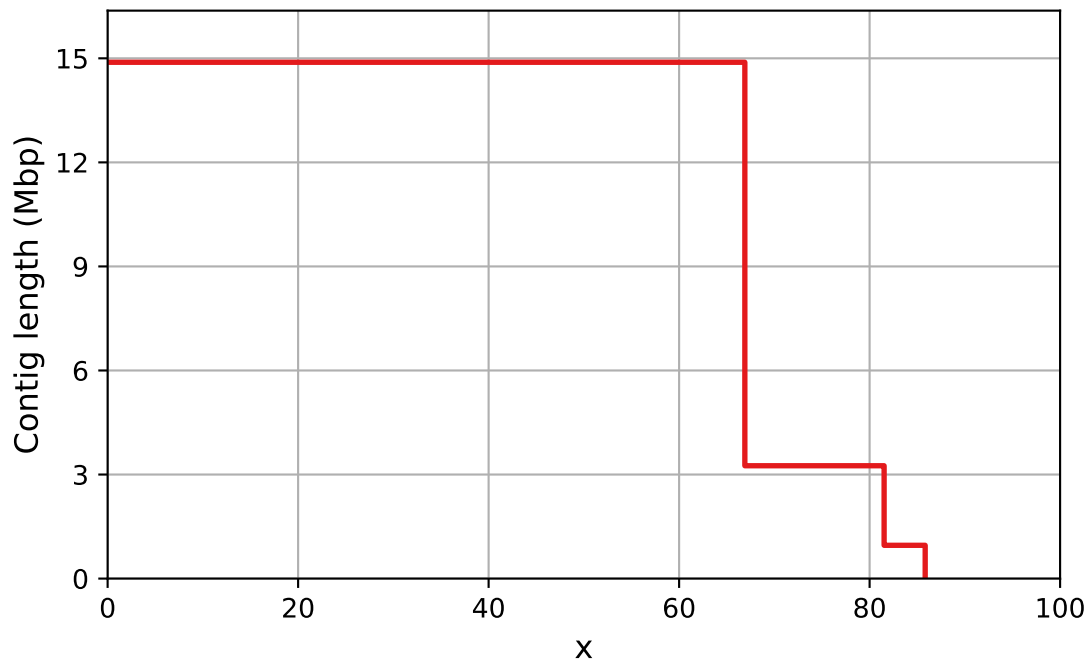
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



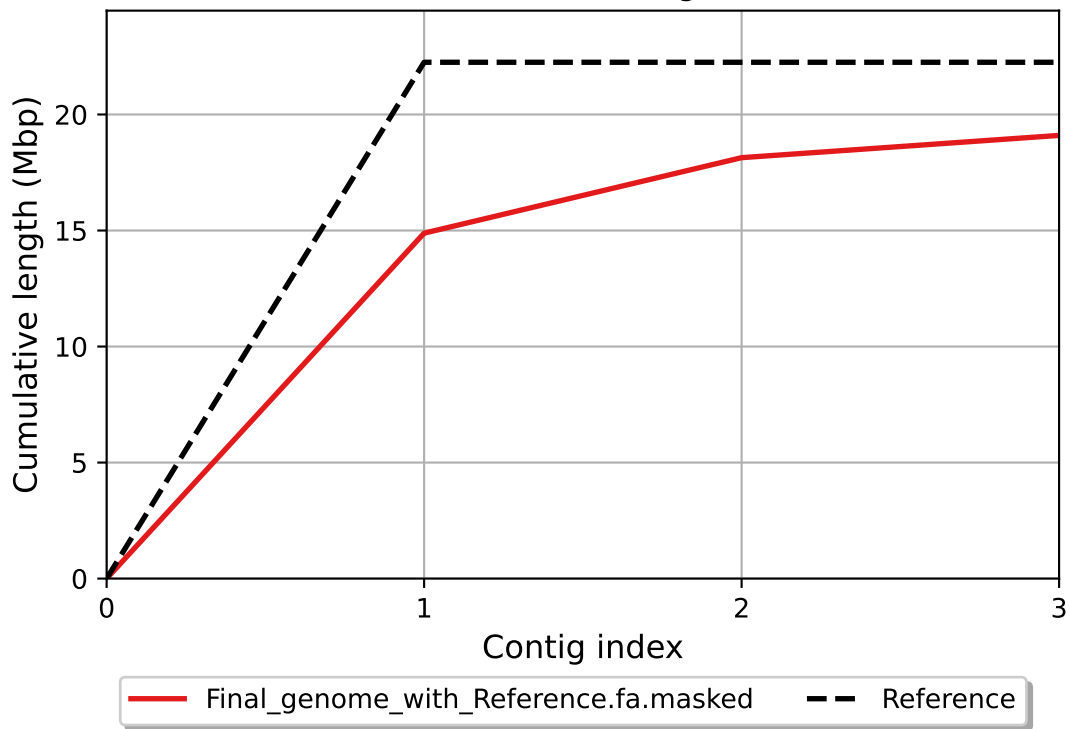
Final\_genome\_with\_Reference.fa.masked

# NGx

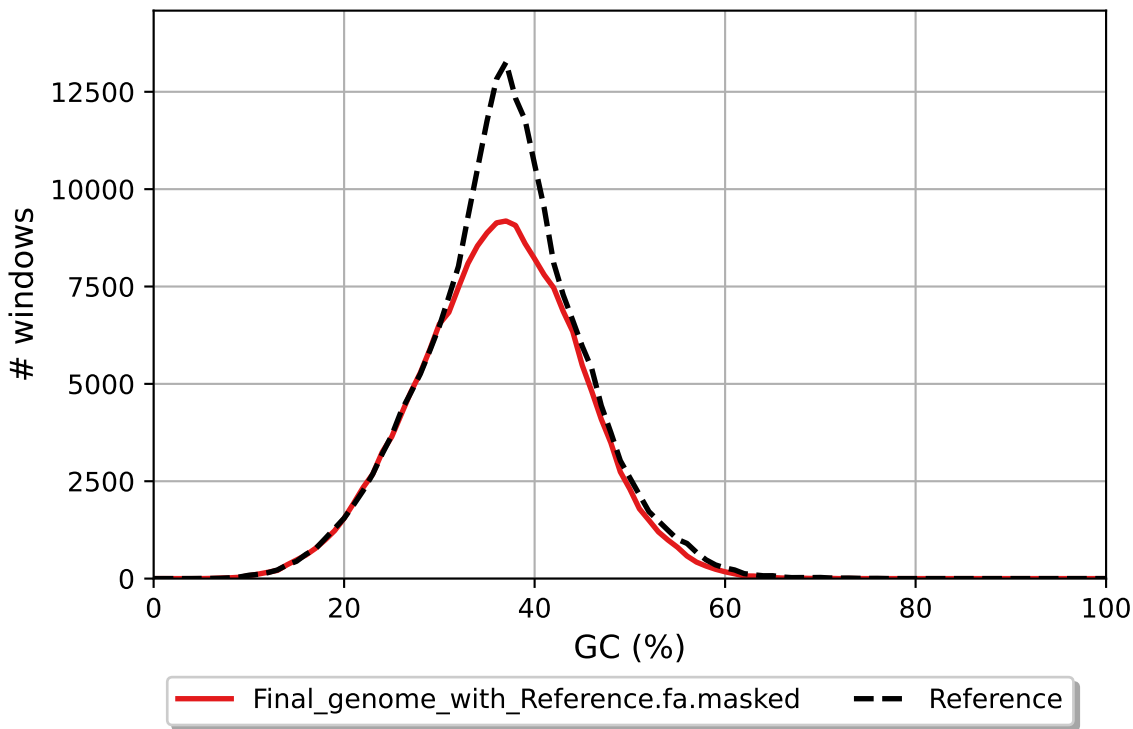


Final\_genome\_with\_Reference.fa.masked

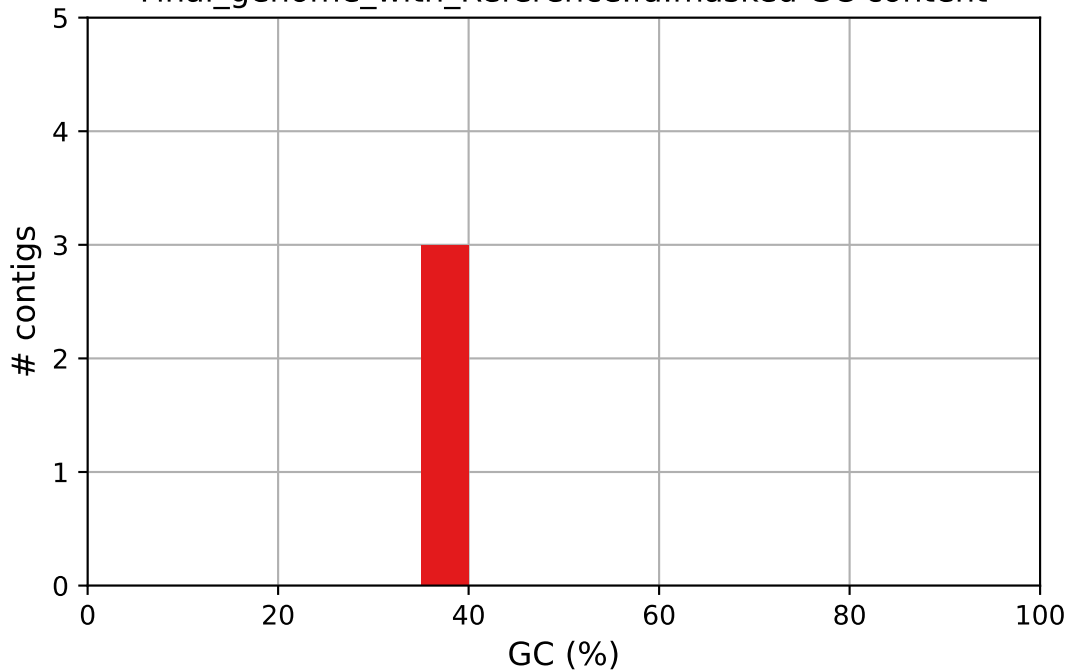
Cumulative length



GC content



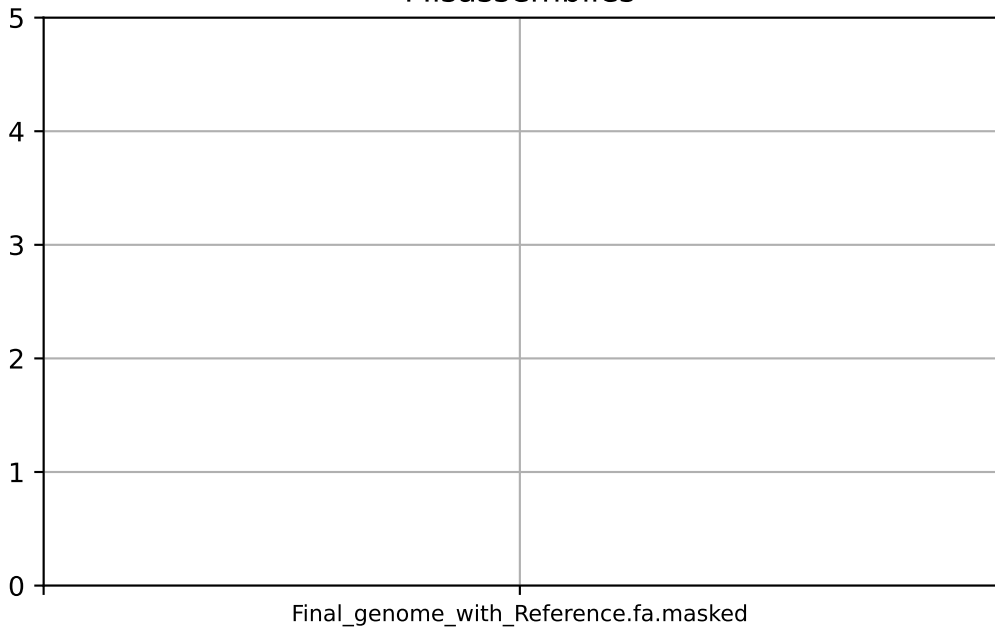
Final\_genome\_with\_Reference.fa.masked GC content



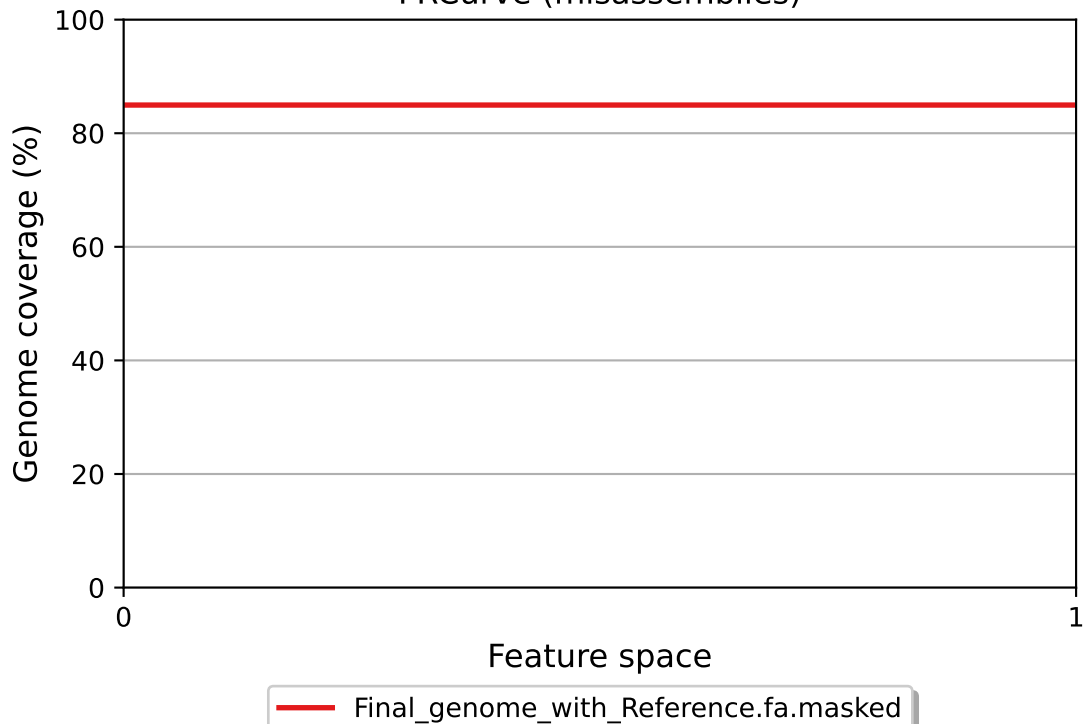
Final\_genome\_with\_Reference.fa.masked



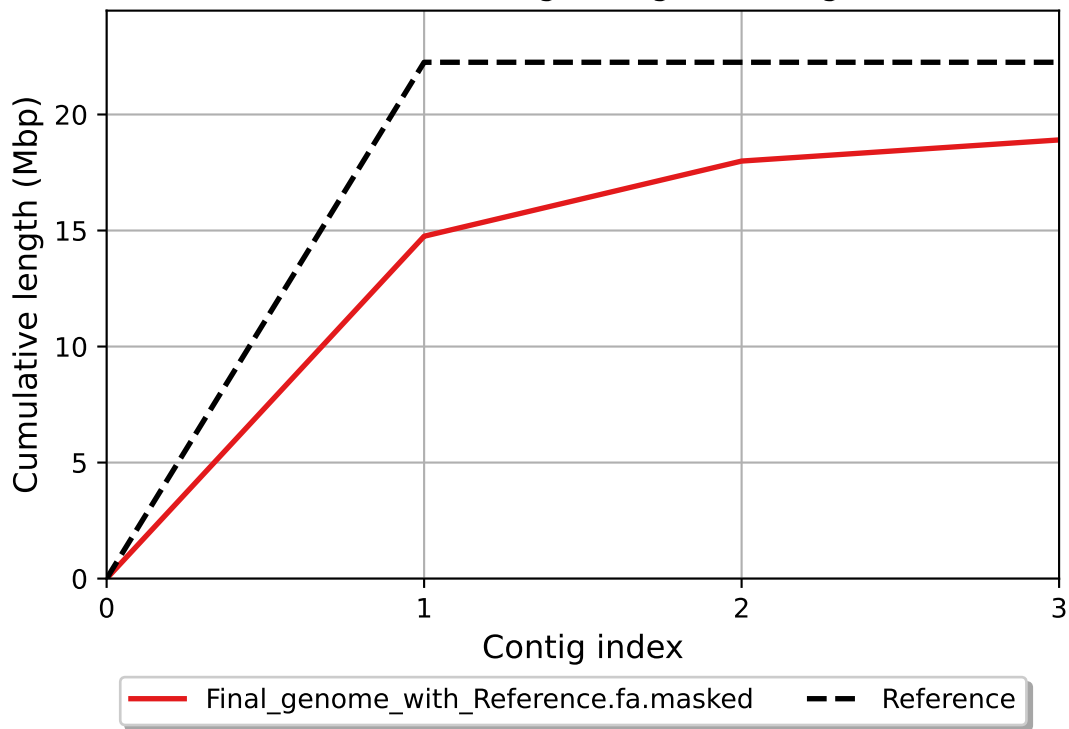
## Misassemblies



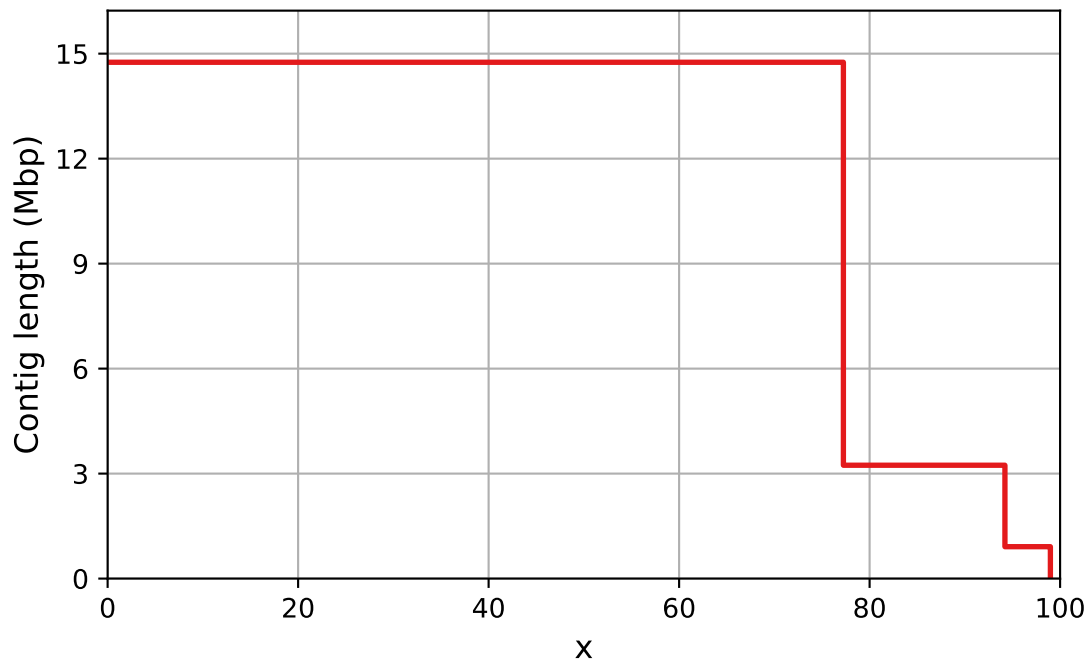
FRCurve (misassemblies)



Cumulative length (aligned contigs)

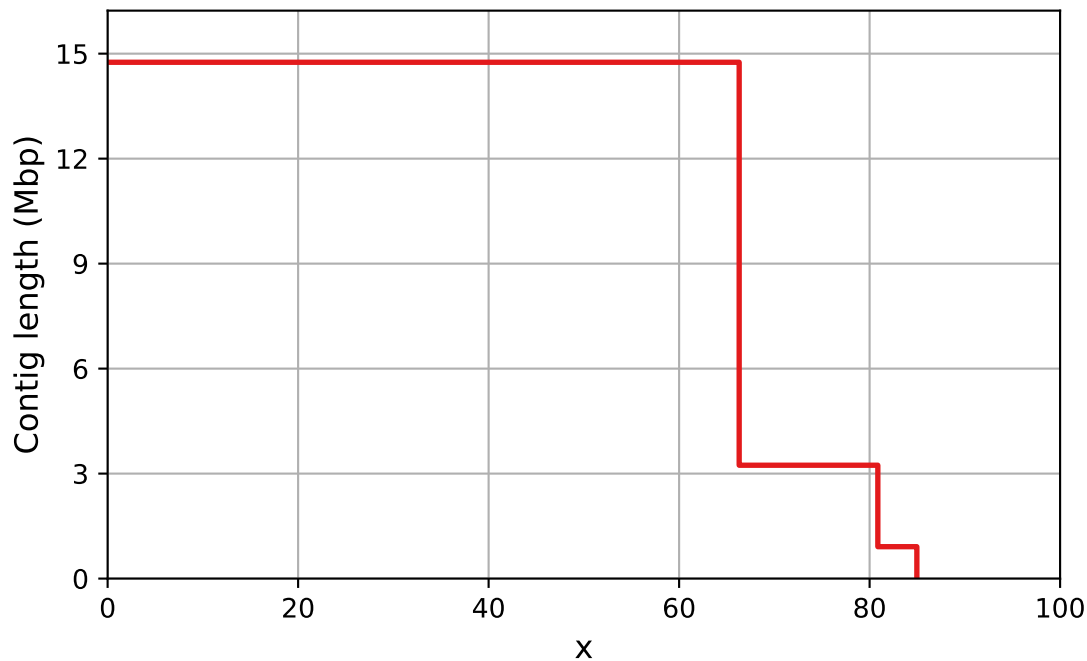


NAx



Final\_genome\_with\_Reference.fa.masked

# NGAx



Final\_genome\_with\_Reference.fa.masked