

Report

	consensus
# 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)	5104808
Total length (>= 1000 bp)	5104808
Total length (>= 5000 bp)	5104808
Total length (>= 10000 bp)	5104808
Total length (>= 25000 bp)	5104808
Total length (>= 50000 bp)	5104808
# contigs	3
Largest contig	3318770
Total length	5104808
Reference length	5104813
GC (%)	52.19
Reference GC (%)	52.19
N50	3318770
NG50	3318770
N90	1676979
NG90	1676979
auN	2710853.5
auNG	2710850.9
L50	1
LG50	1
L90	2
LG90	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.27
# indels per 100 kbp	0.18
Largest alignment	3318770
Total aligned length	5104808
NA50	3318770
NGA50	3318770
NA90	1676979
NGA90	1676979
auNA	2710853.5
auNGA	2710850.9
LA50	1
LGA50	1
LA90	2
LGA90	2

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

	consensus
# 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	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	14
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	9

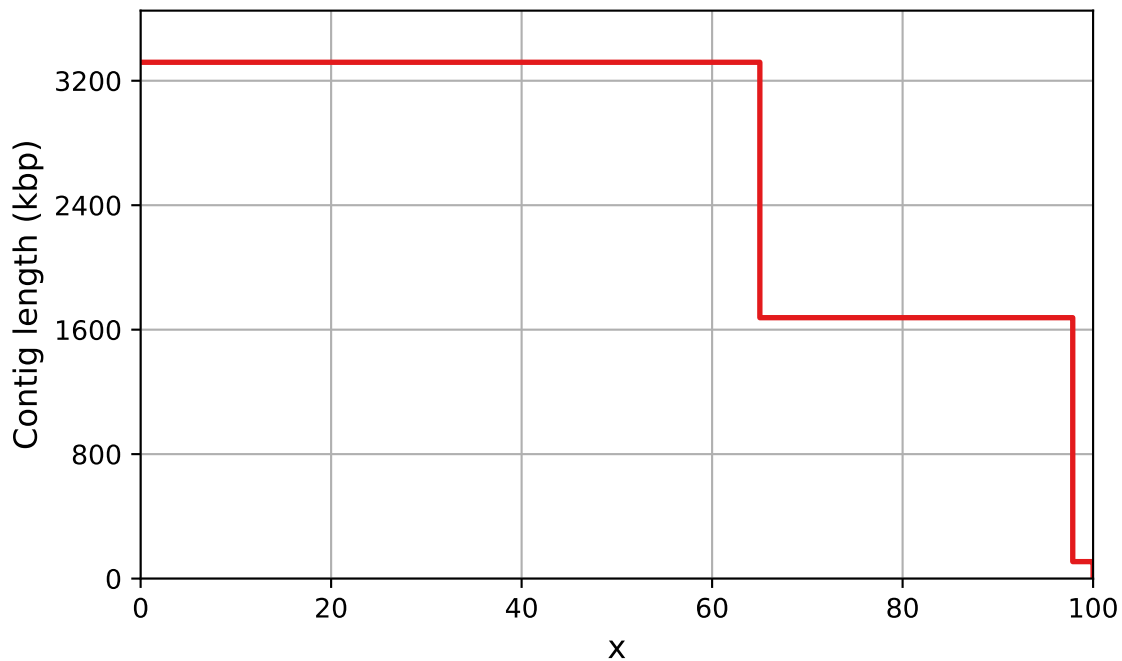
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	consensus
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

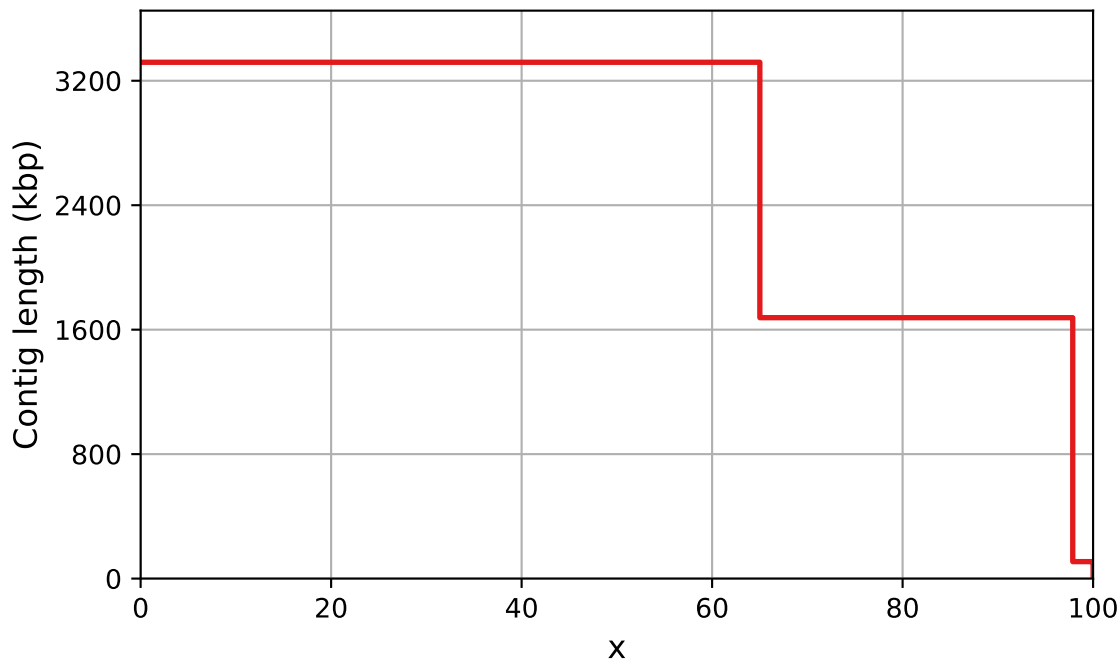
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



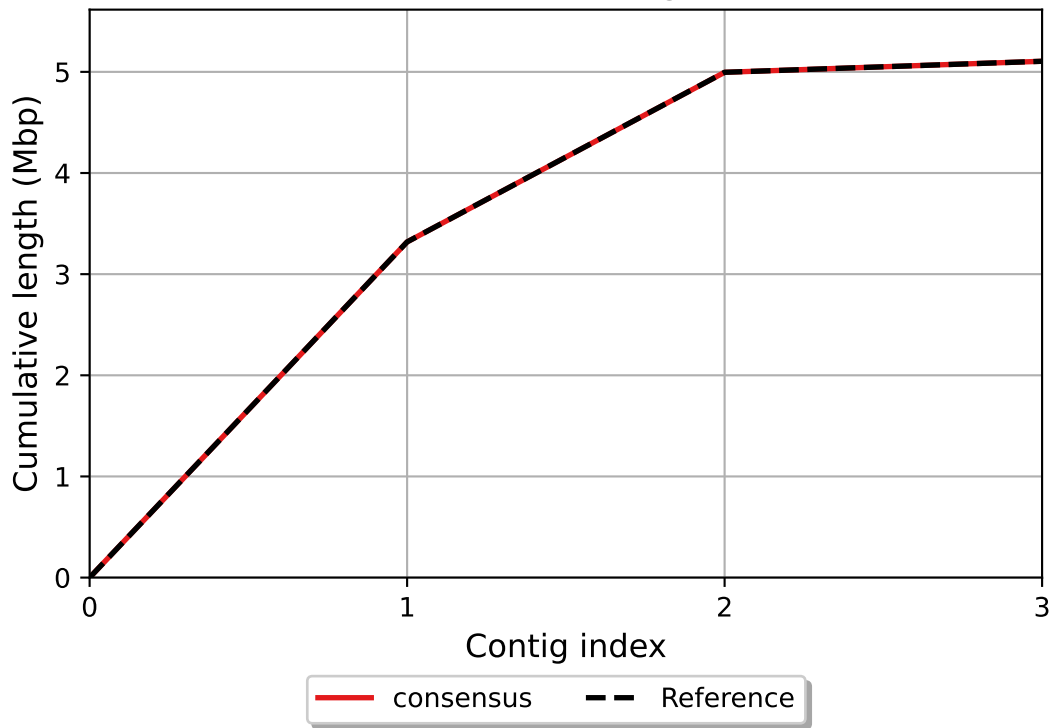
consensus

NGx

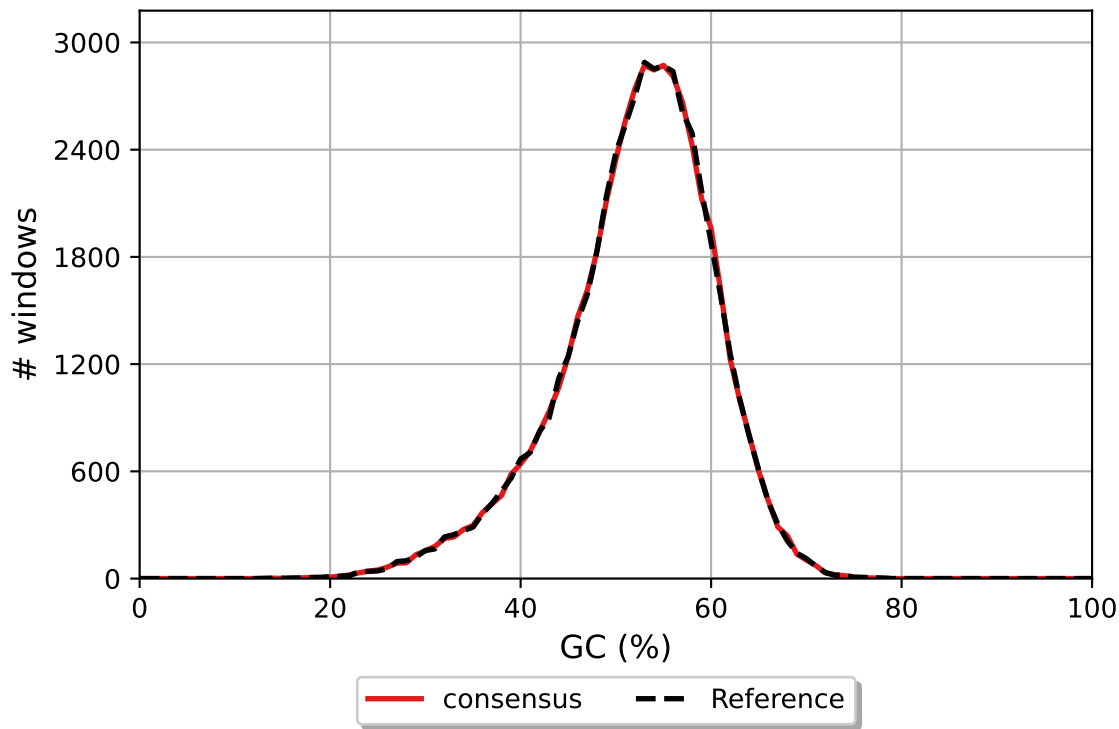


— consensus

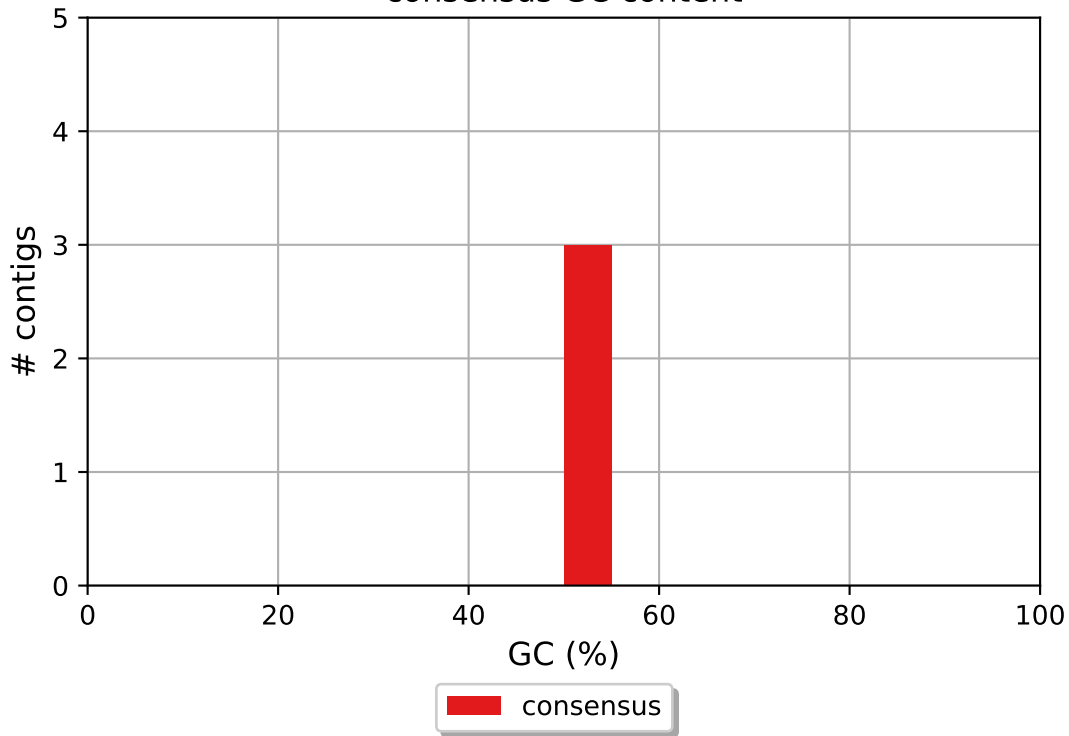
Cumulative length



## GC content



consensus GC content

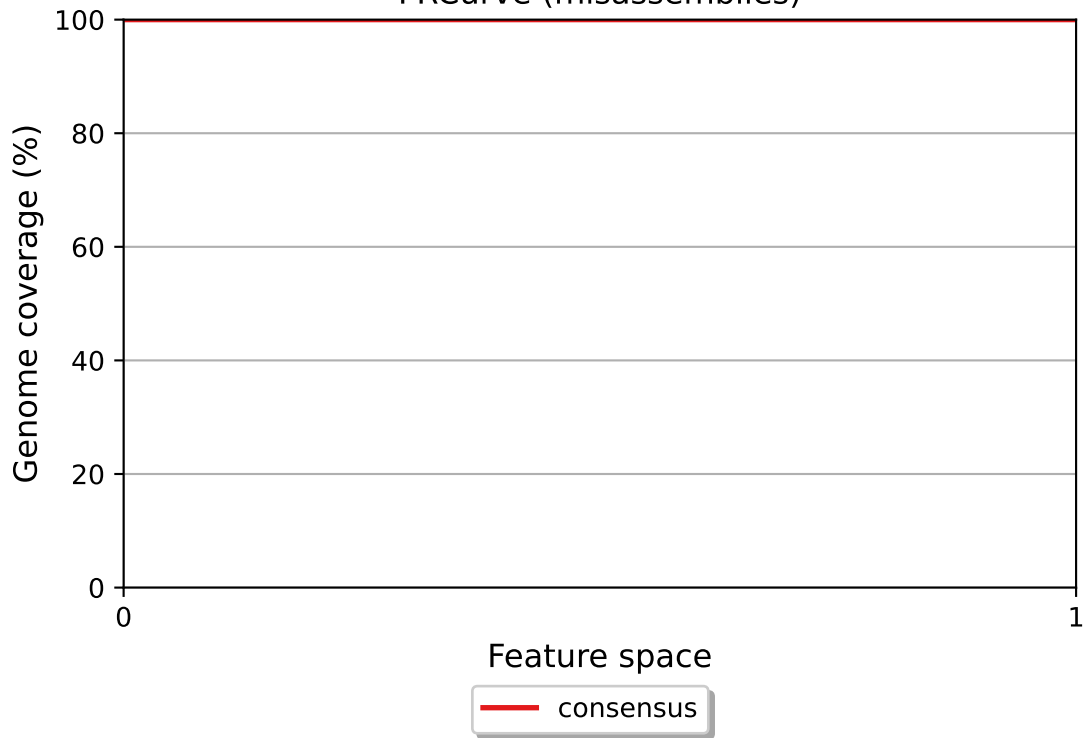




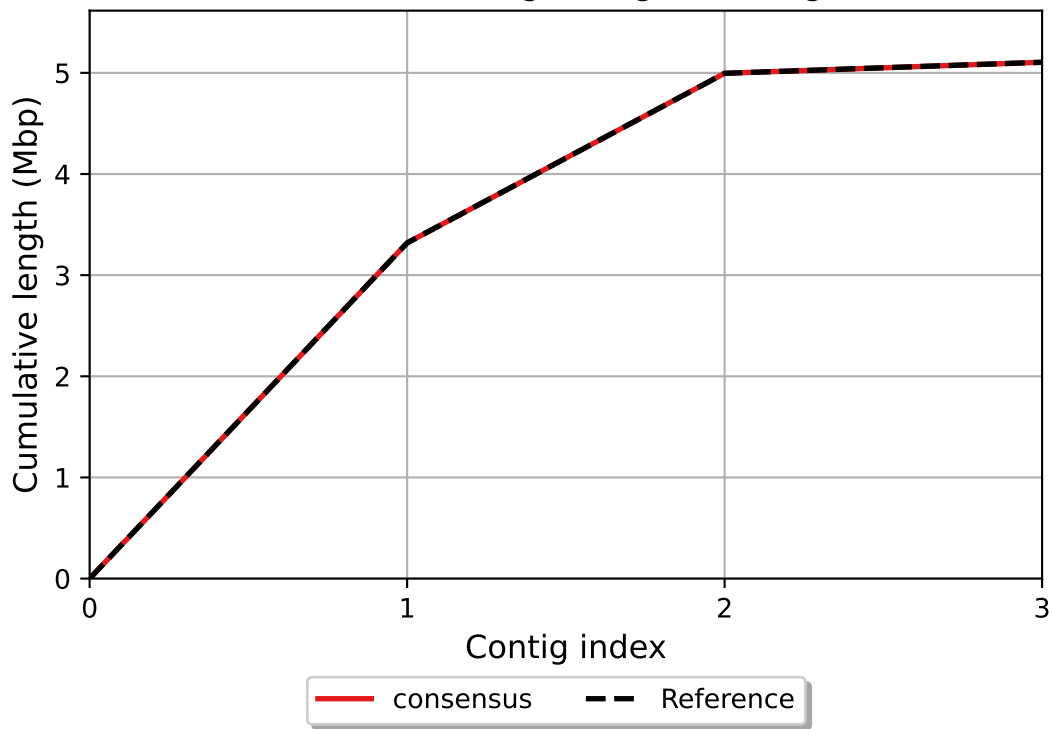
## Misassemblies



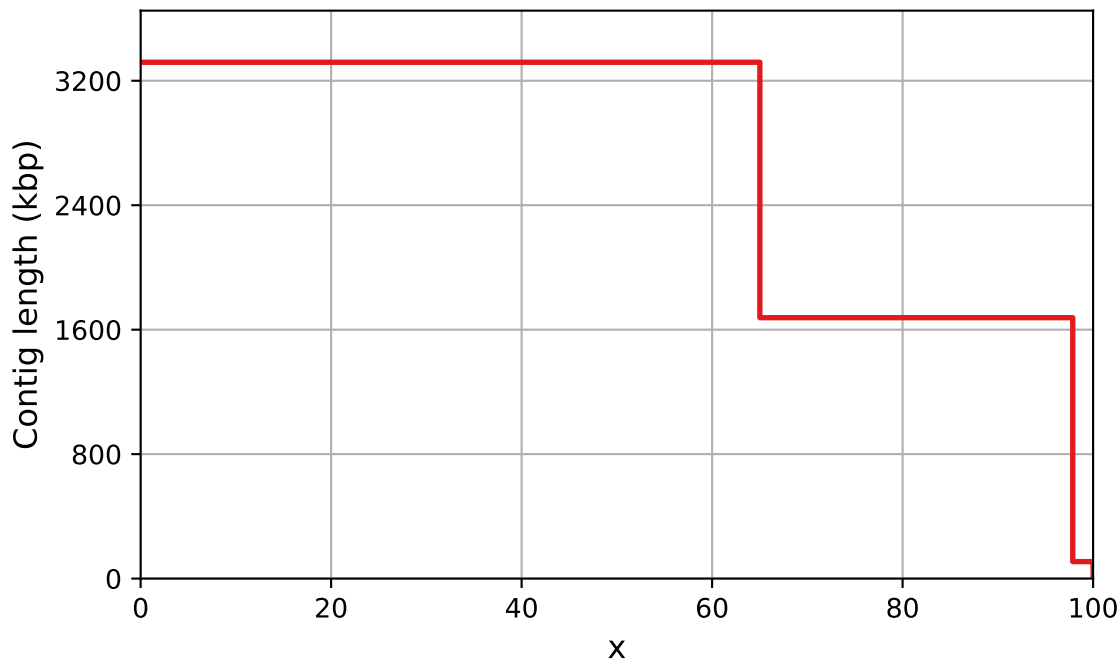
FRCurve (misassemblies)



Cumulative length (aligned contigs)

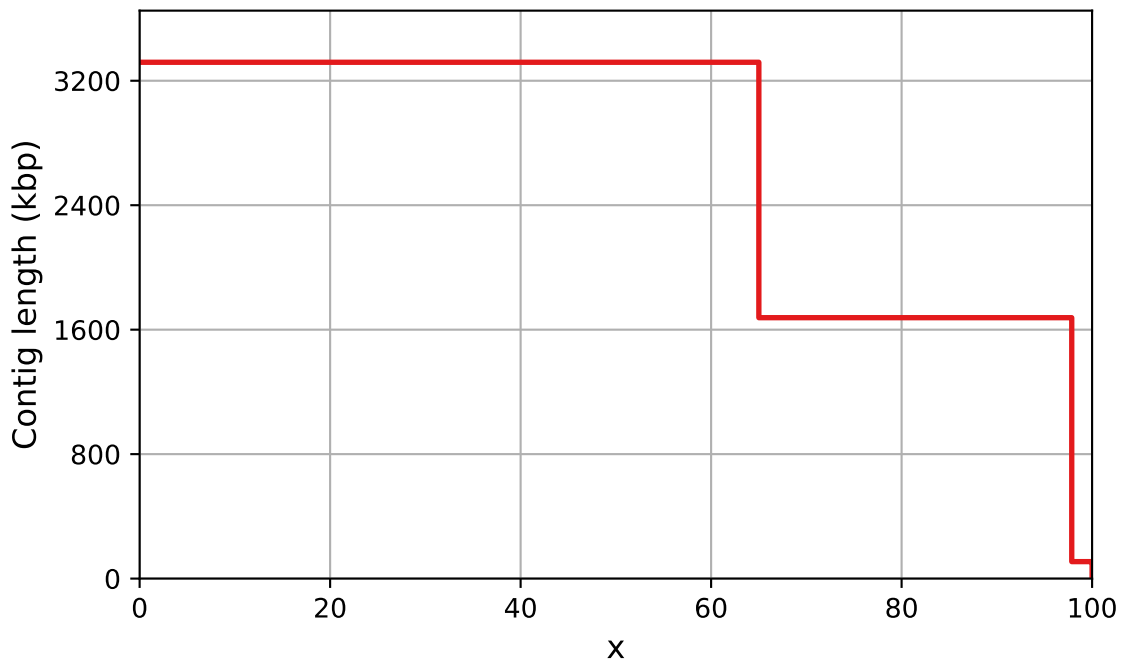


NAx



consensus

# NGAx



— consensus