

Report

	assembly_consensus
# contigs (>= 0 bp)	64
# contigs (>= 1000 bp)	64
# contigs (>= 5000 bp)	63
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	54
# contigs (>= 50000 bp)	41
Total length (>= 0 bp)	59516388
Total length (>= 1000 bp)	59516388
Total length (>= 5000 bp)	59512718
Total length (>= 10000 bp)	59495934
Total length (>= 25000 bp)	59361442
Total length (>= 50000 bp)	58910564
# contigs	64
Largest contig	13012991
Total length	59516388
Reference length	64444167
GC (%)	43.80
Reference GC (%)	43.80
N50	5342995
NG50	5217347
N75	2207099
NG75	1850264
L50	4
LG50	5
L75	8
LG75	10
# misassemblies	9
# misassembled contigs	5
Misassembled contigs length	13662233
# local misassemblies	2483
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	2
# unaligned mis. contigs	14
# unaligned contigs	11 + 53 part
Unaligned length	10618384
Genome fraction (%)	78.330
Duplication ratio	0.976
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1432.95
# indels per 100 kbp	1652.10
Largest alignment	5845366
Total aligned length	48898906
NA50	3999987
NGA50	3866049
NA75	621717
NGA75	4460
LA50	6
LGA50	7
LA75	15
LGA75	91

All statistics are based on contigs of size >= 3000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

	assembly_consensus
# misassemblies	9
# contig misassemblies	9
# c. relocations	9
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	13662233
# local misassemblies	2483
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	2
# unaligned mis. contigs	14
# mismatches	717726
# indels	827493
# indels (<= 5 bp)	803287
# indels (> 5 bp)	24206
Indels length	1410416

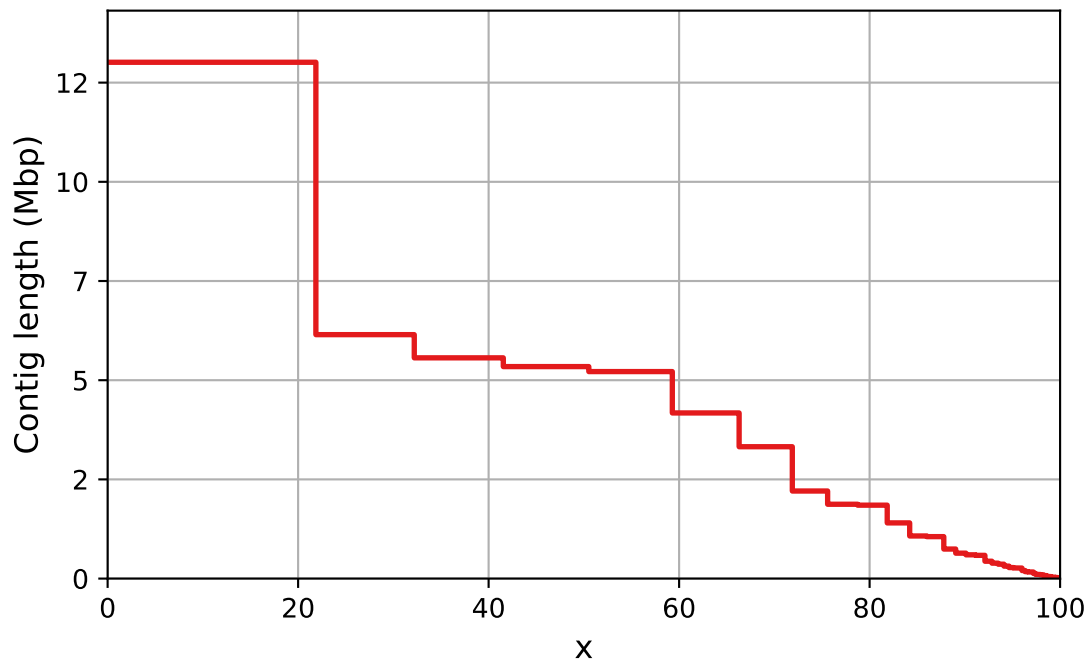
All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	assembly_consensus
# fully unaligned contigs	11
Fully unaligned length	330759
# partially unaligned contigs	53
Partially unaligned length	10287625
# N's	0

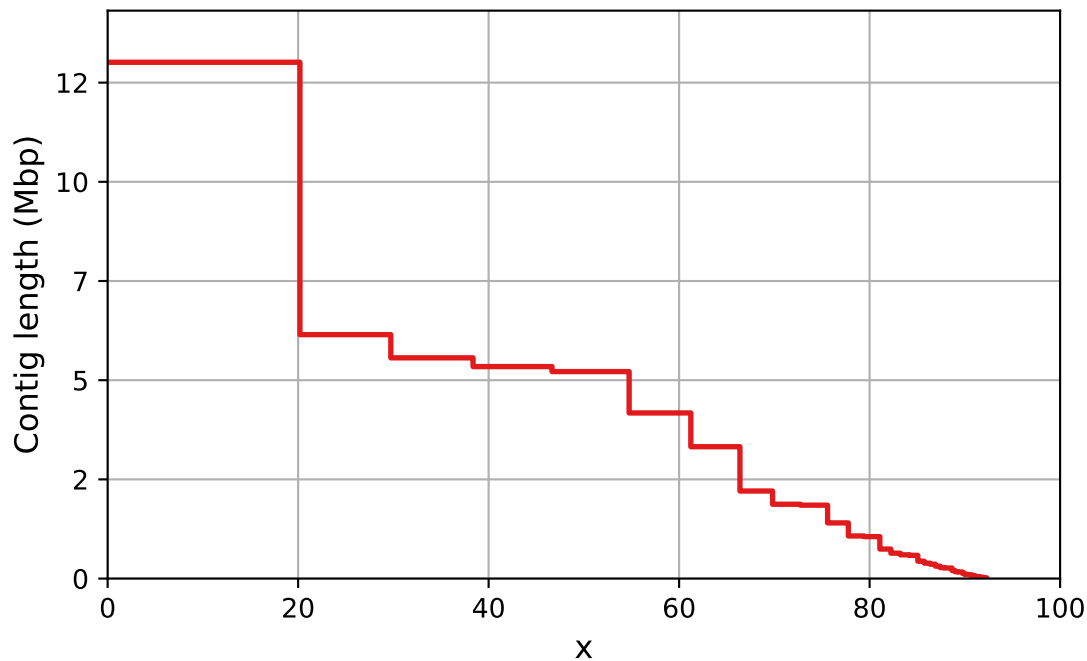
All statistics are based on contigs of size  $\geq 3000$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



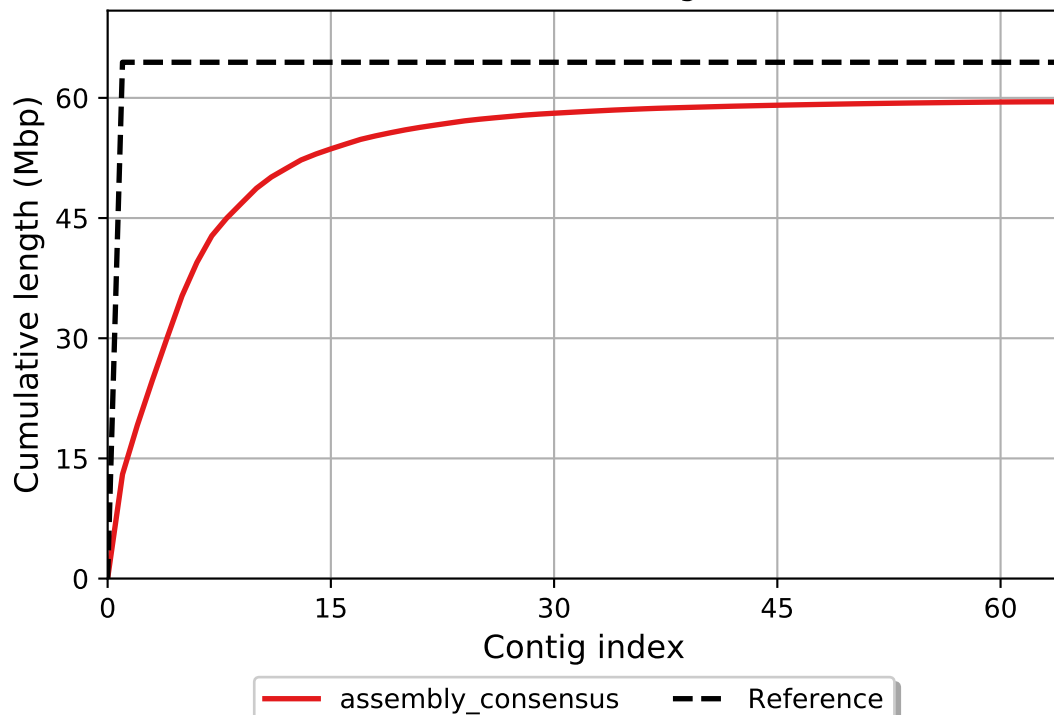
— assembly\_consensus

# NGx

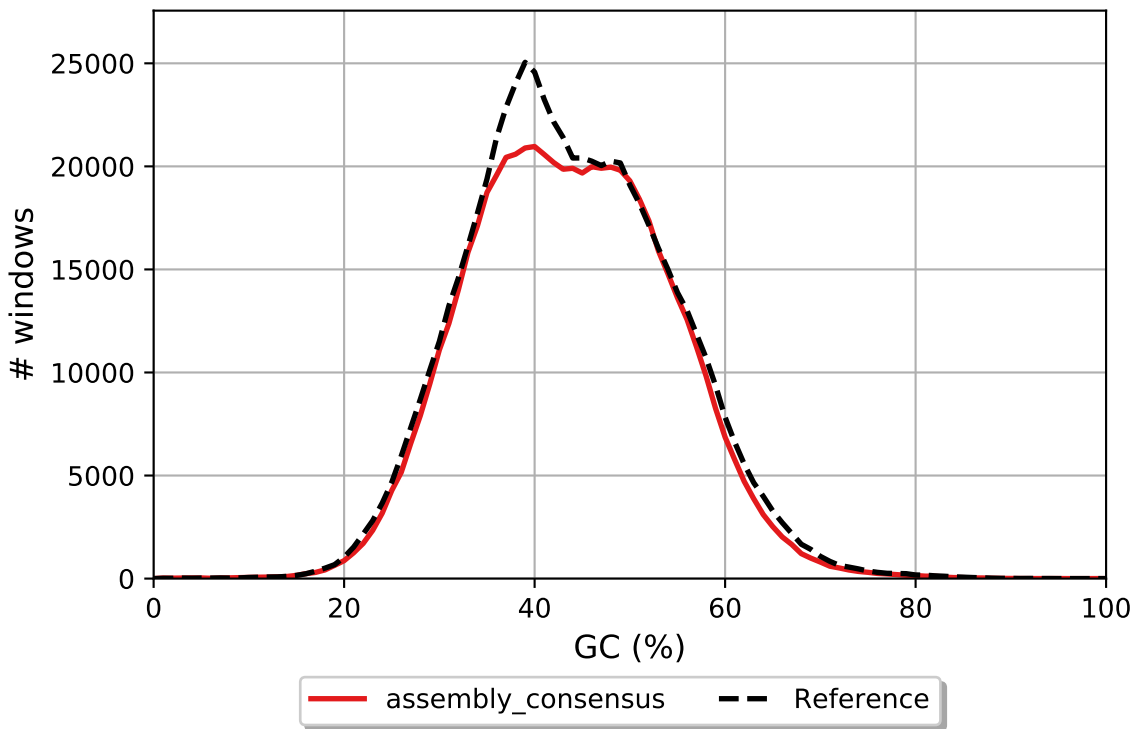


— assembly\_consensus

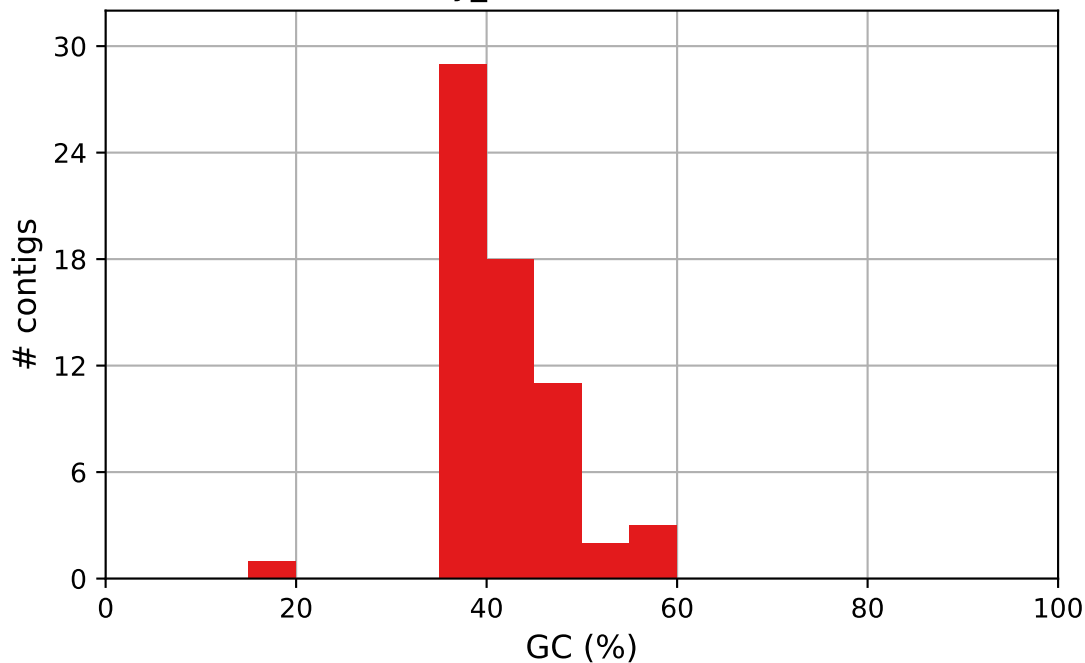
Cumulative length



GC content



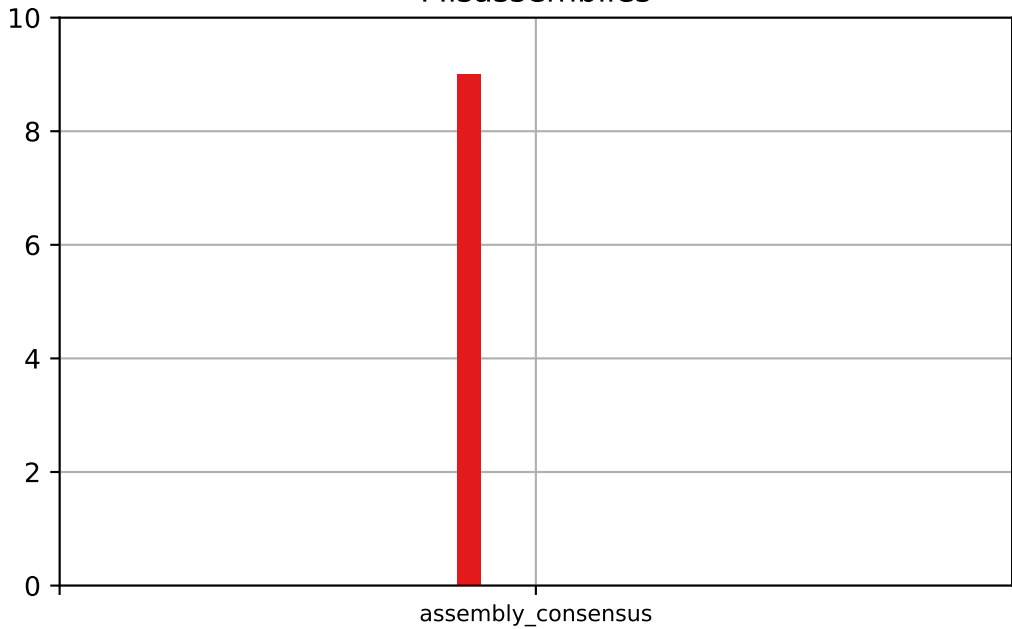
assembly\_consensus GC content



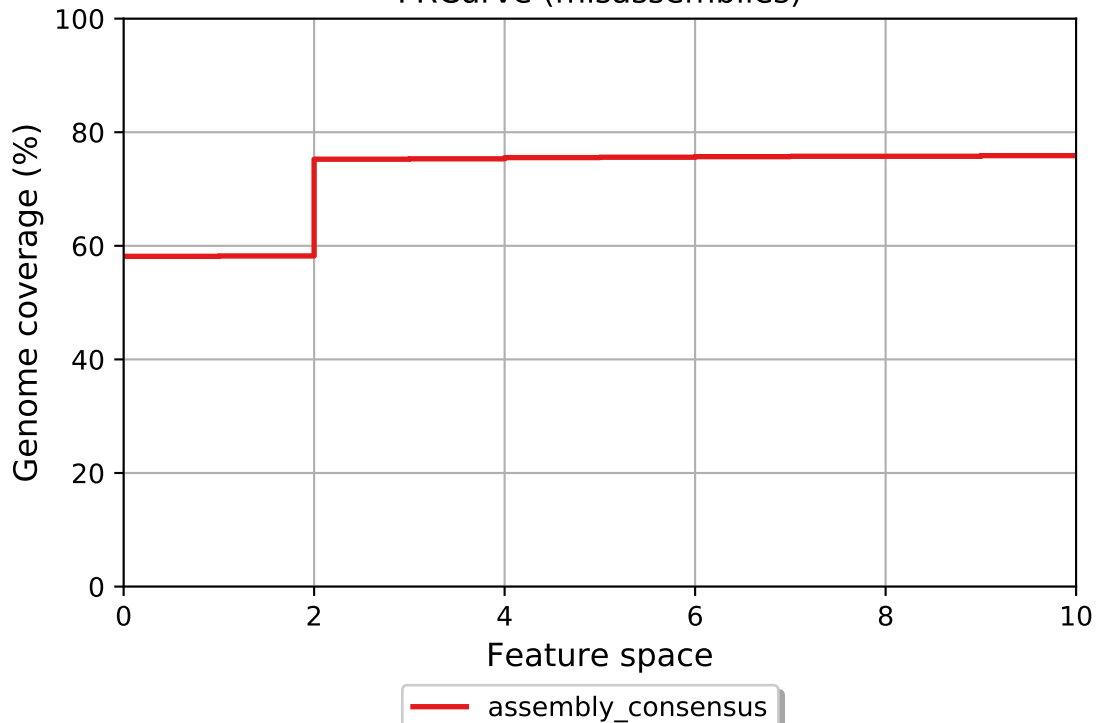
assembly\_consensus



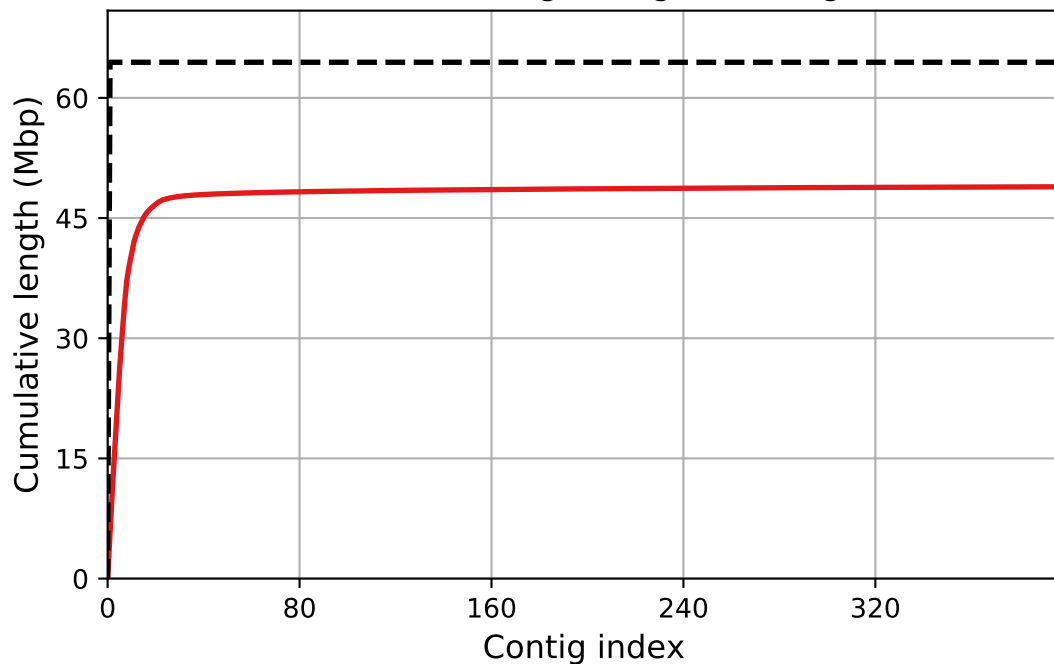
## Misassemblies



FRCurve (misassemblies)

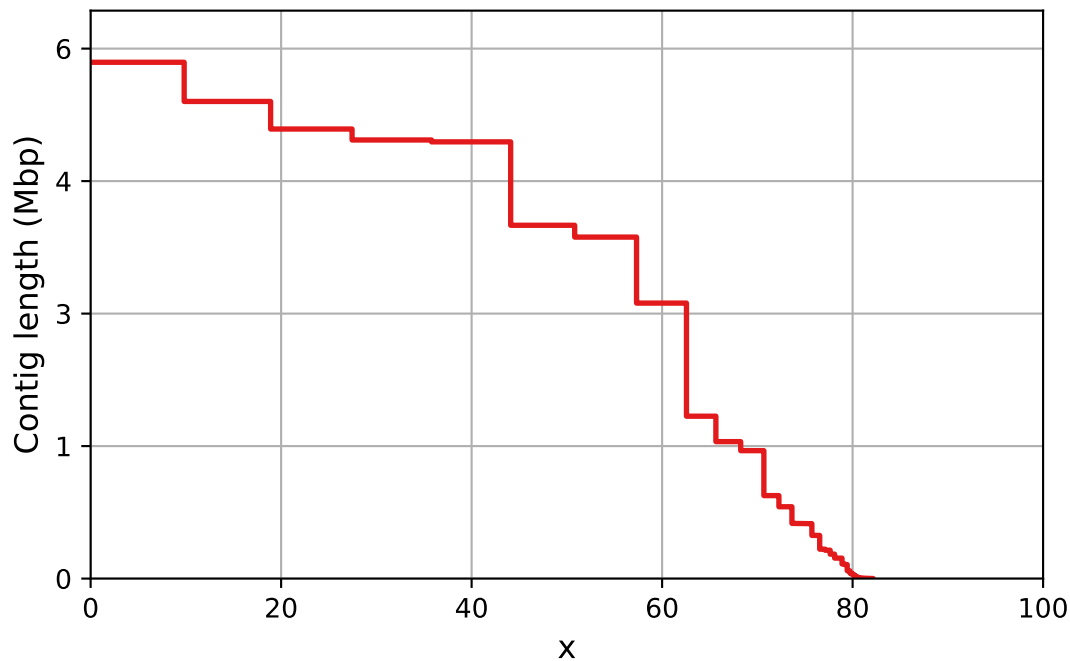


Cumulative length (aligned contigs)



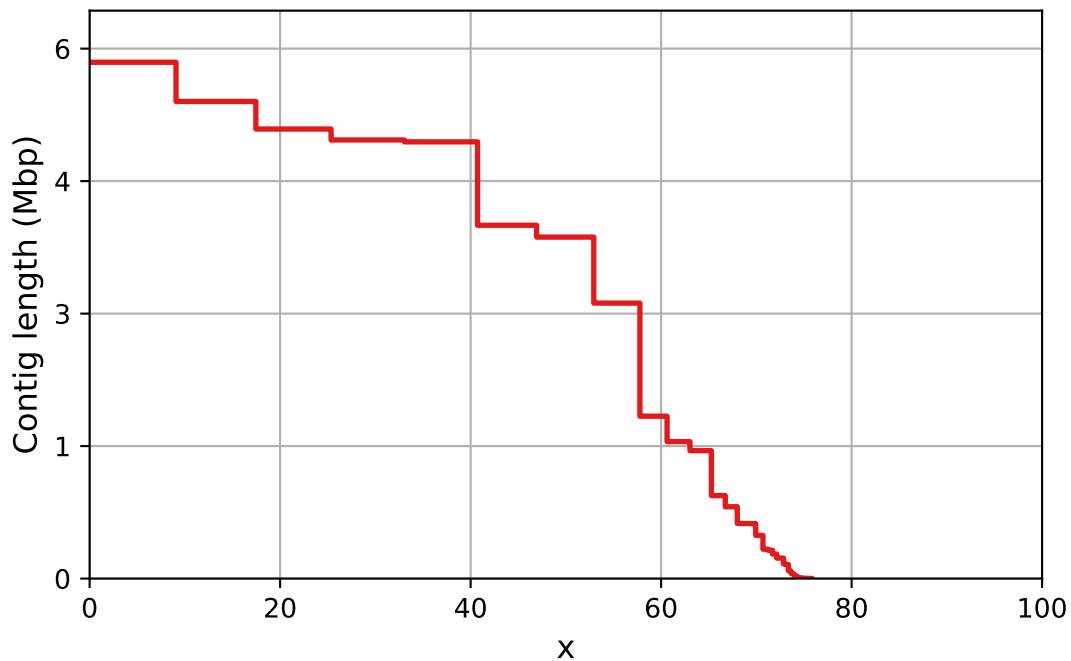
— assembly\_consensus    - - Reference

NAx



— assembly\_consensus

# NGAx



— assembly\_consensus