

## Report

	assembly
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	8766603
Total length (>= 1000 bp)	8766603
Total length (>= 5000 bp)	8766603
Total length (>= 10000 bp)	8766603
Total length (>= 25000 bp)	8766603
Total length (>= 50000 bp)	8766603
# contigs	4
Largest contig	6991805
Total length	8766603
Reference length	9619655
GC (%)	71.99
Reference GC (%)	71.93
N50	6991805
NG50	6991805
N75	6991805
NG75	1053786
L50	1
LG50	1
L75	1
LG75	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 (%)	90.953
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.49
# indels per 100 kbp	60.43
Largest alignment	6991805
Total aligned length	8766592
NA50	6991805
NGA50	6991805
NA75	6991805
NGA75	1053786
LA50	1
LGA50	1
LA75	1
LGA75	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

	assembly
# 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	218
# indels	5287
# indels ( $\leq 5$ bp)	5285
# indels ( $> 5$ bp)	2
Indels length	5561

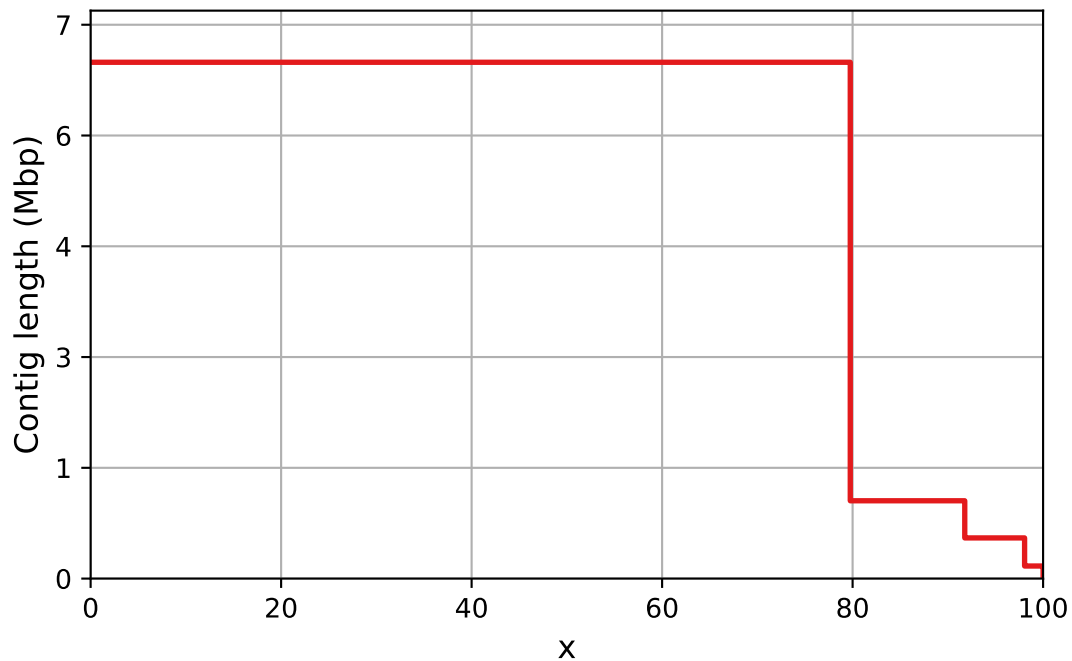
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

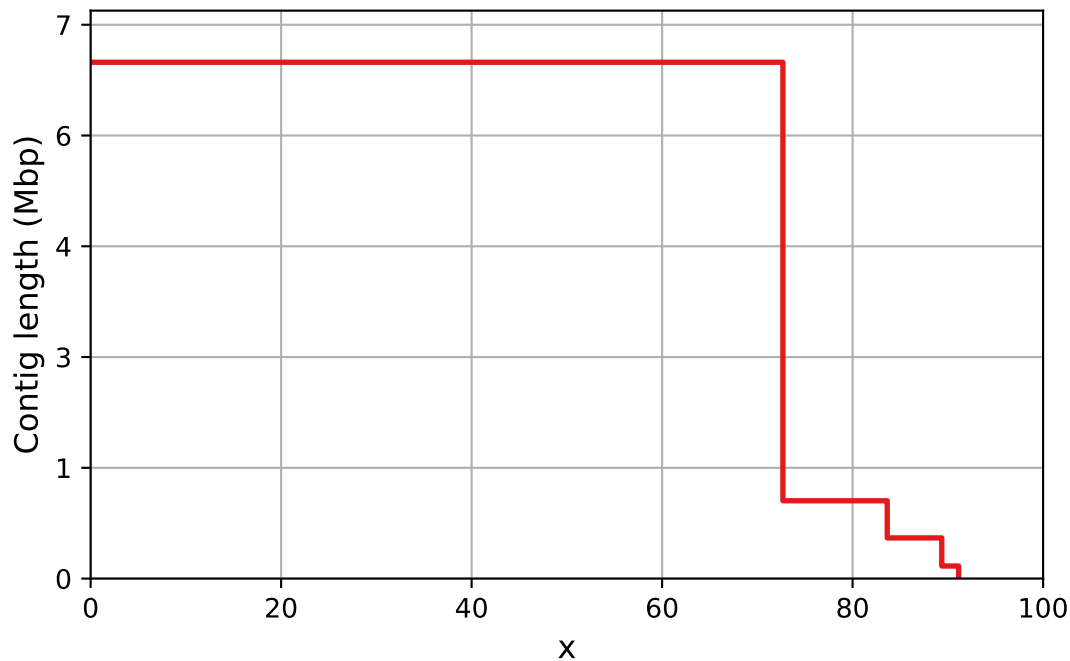
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



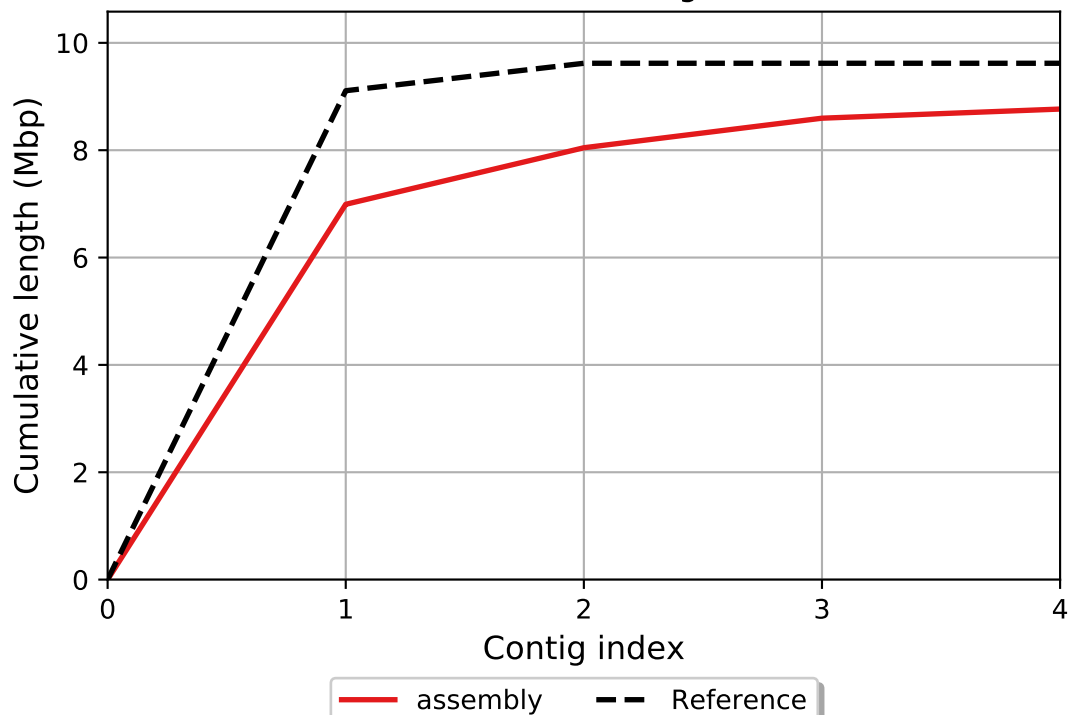
— assembly

# NGx

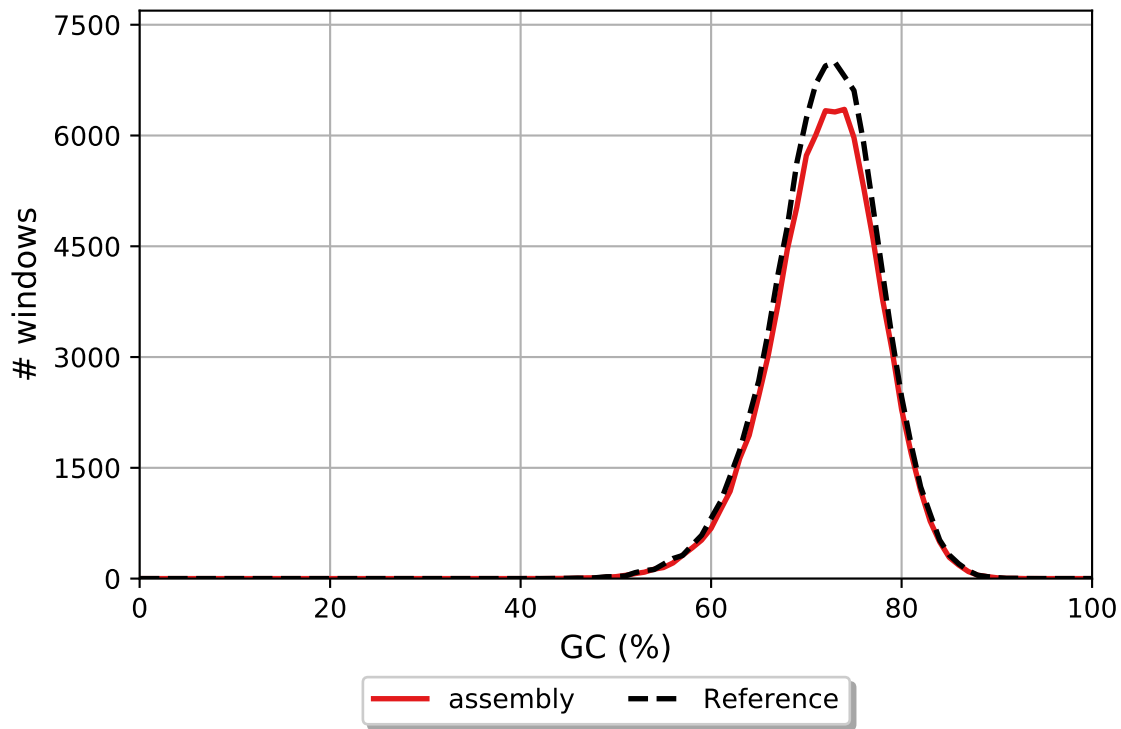


— assembly

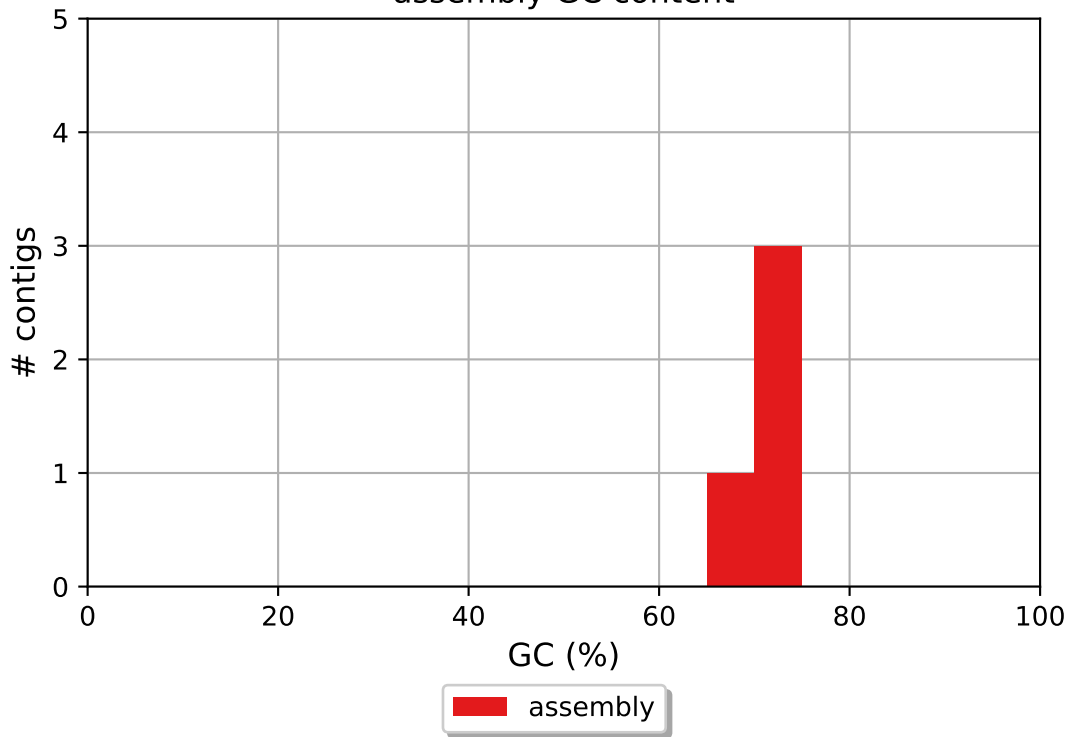
Cumulative length



# GC content

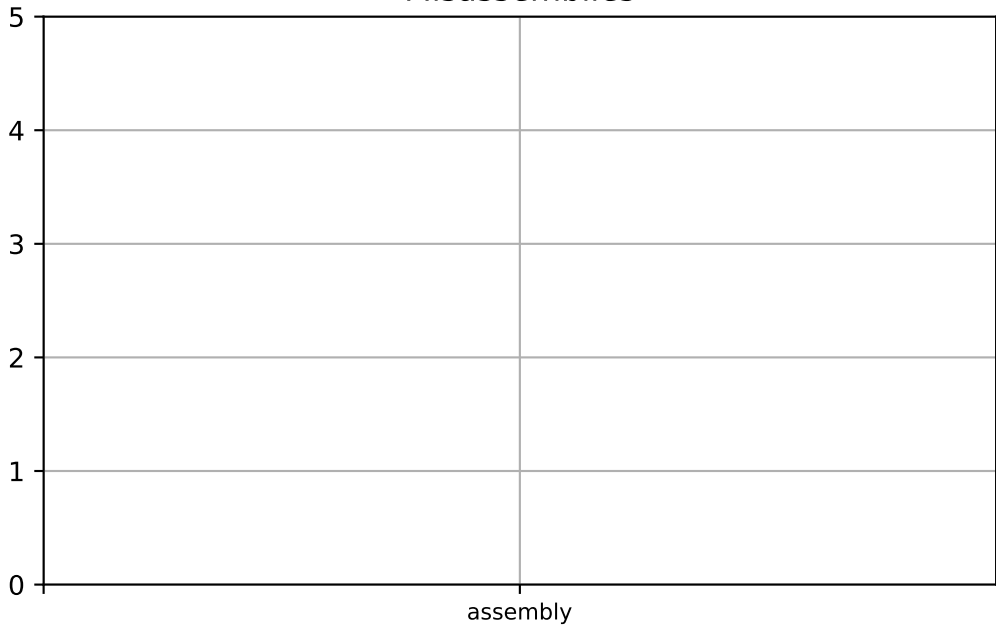


assembly GC content

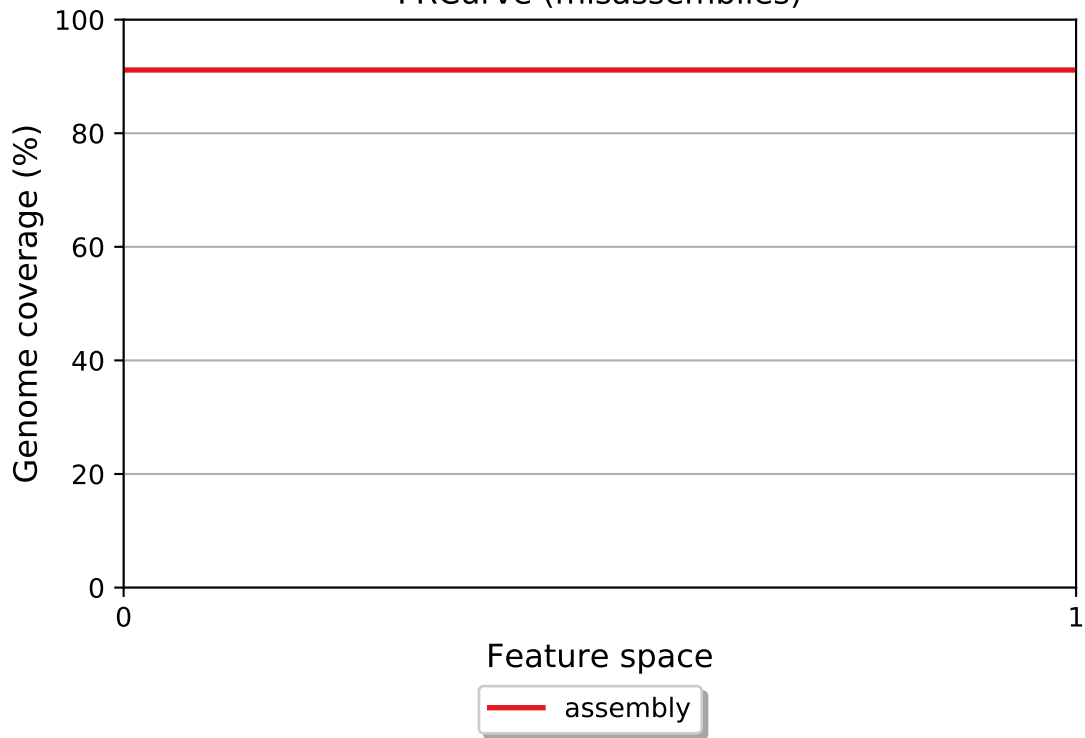




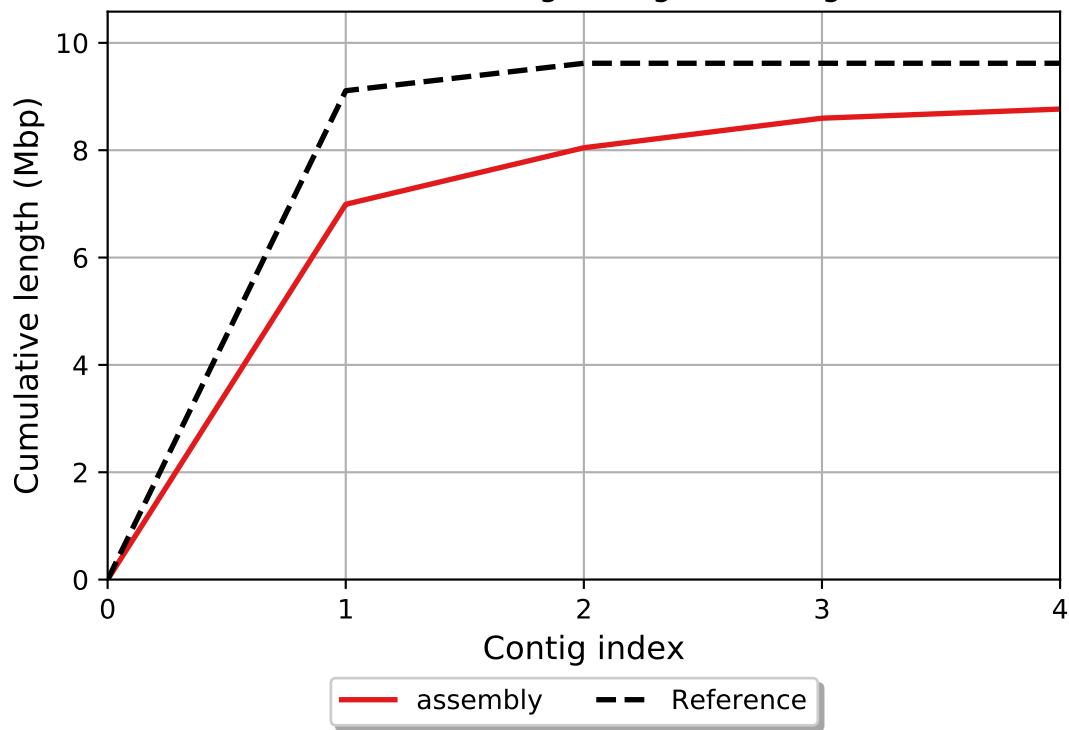
## Misassemblies



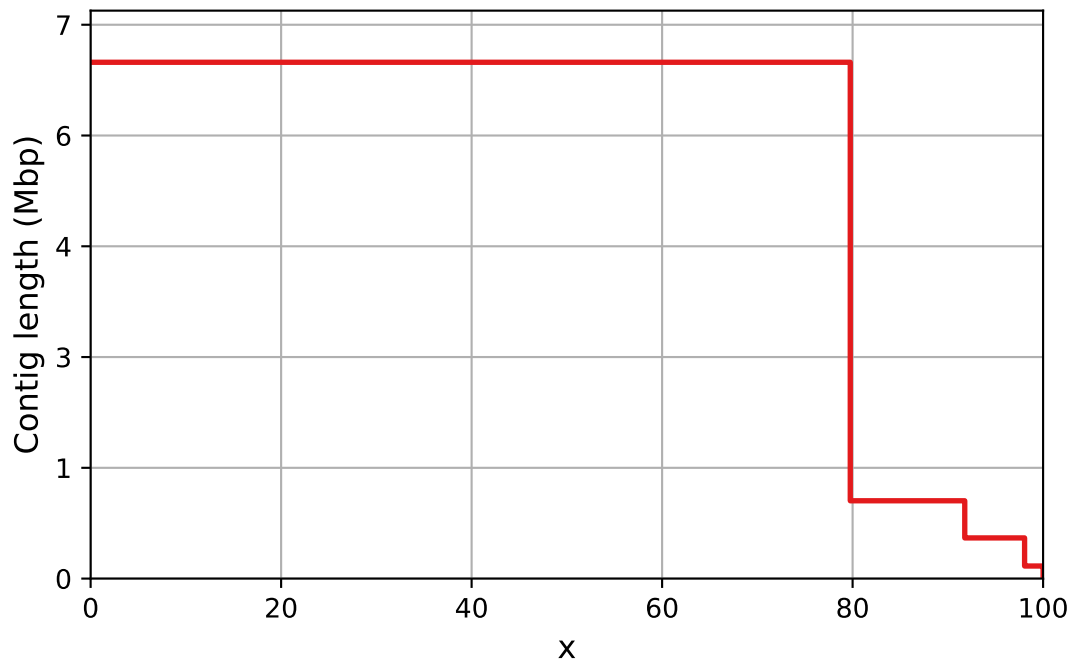
FRCurve (misassemblies)



Cumulative length (aligned contigs)

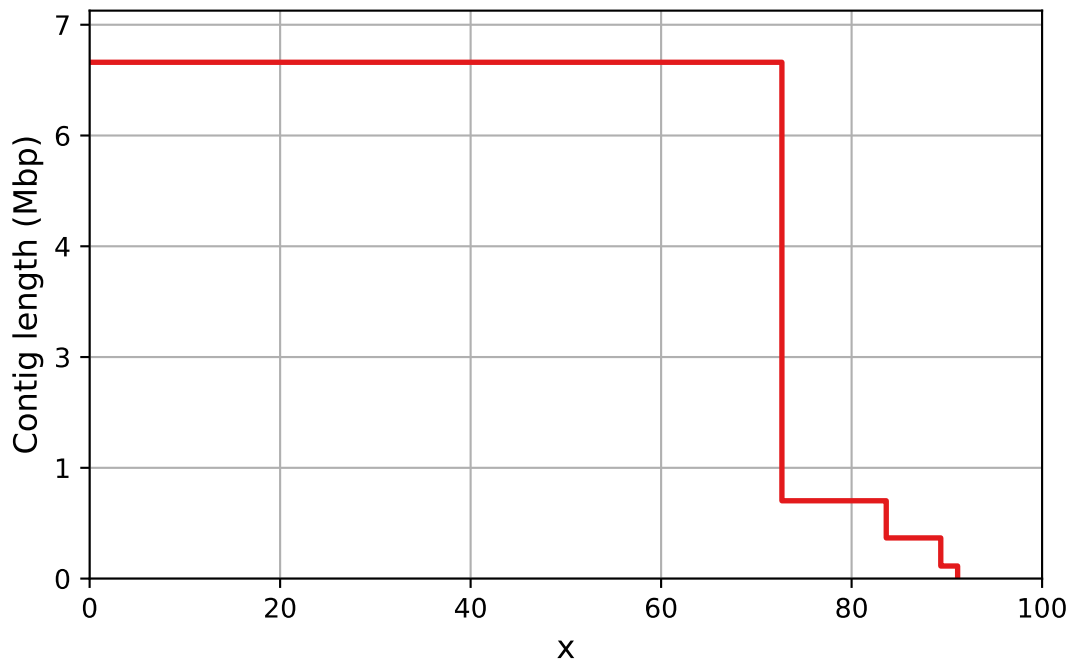


NAx



assembly

# NGAx



— assembly