

Report

	assembly
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	9647671
Total length (>= 1000 bp)	9647671
Total length (>= 5000 bp)	9647671
Total length (>= 10000 bp)	9647671
Total length (>= 25000 bp)	9647671
Total length (>= 50000 bp)	9647671
# contigs	2
Largest contig	9355275
Total length	9647671
Reference length	9660595
GC (%)	71.87
Reference GC (%)	71.88
N50	9355275
NG50	9355275
N75	9355275
NG75	9355275
L50	1
LG50	1
L75	1
LG75	1
# 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 (%)	99.930
Duplication ratio	0.999
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.65
# indels per 100 kbp	62.05
Largest alignment	9355275
Total aligned length	9647664
NA50	9355275
NGA50	9355275
NA75	9355275
NGA75	9355275
LA50	1
LGA50	1
LA75	1
LGA75	1

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	63
# indels	5990
# indels (<= 5 bp)	5988
# indels (> 5 bp)	2
Indels length	6246

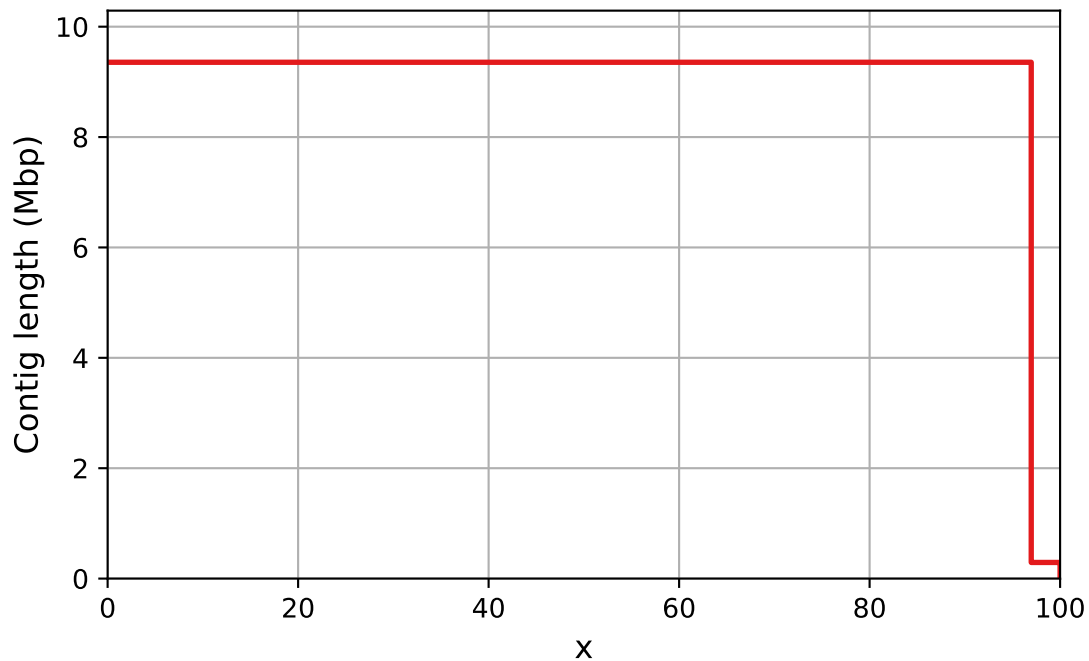
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

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

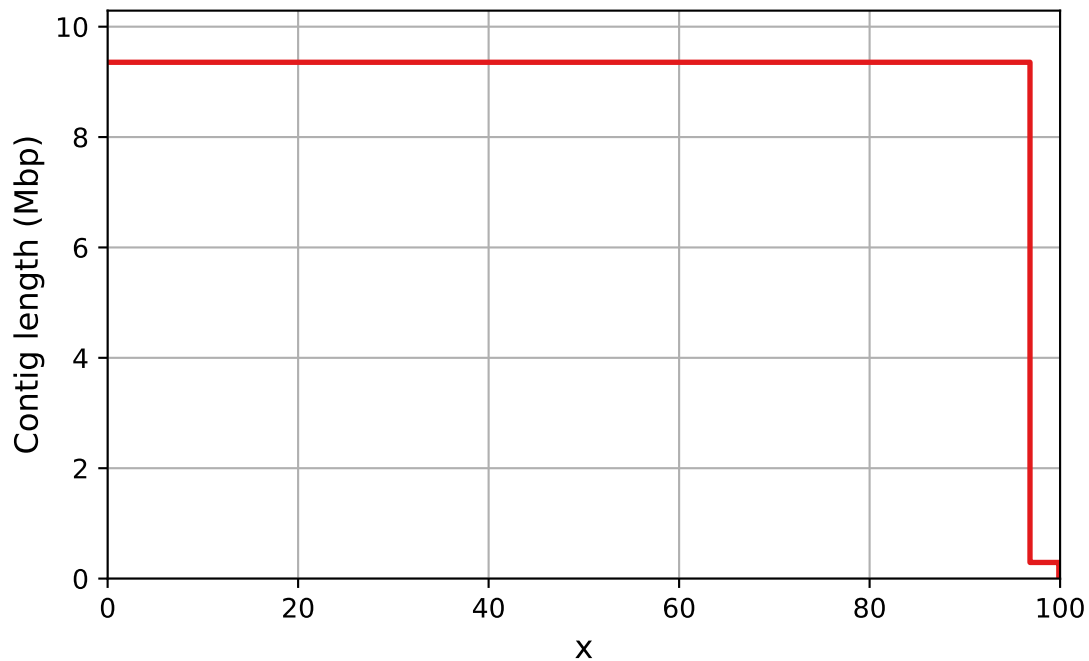
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



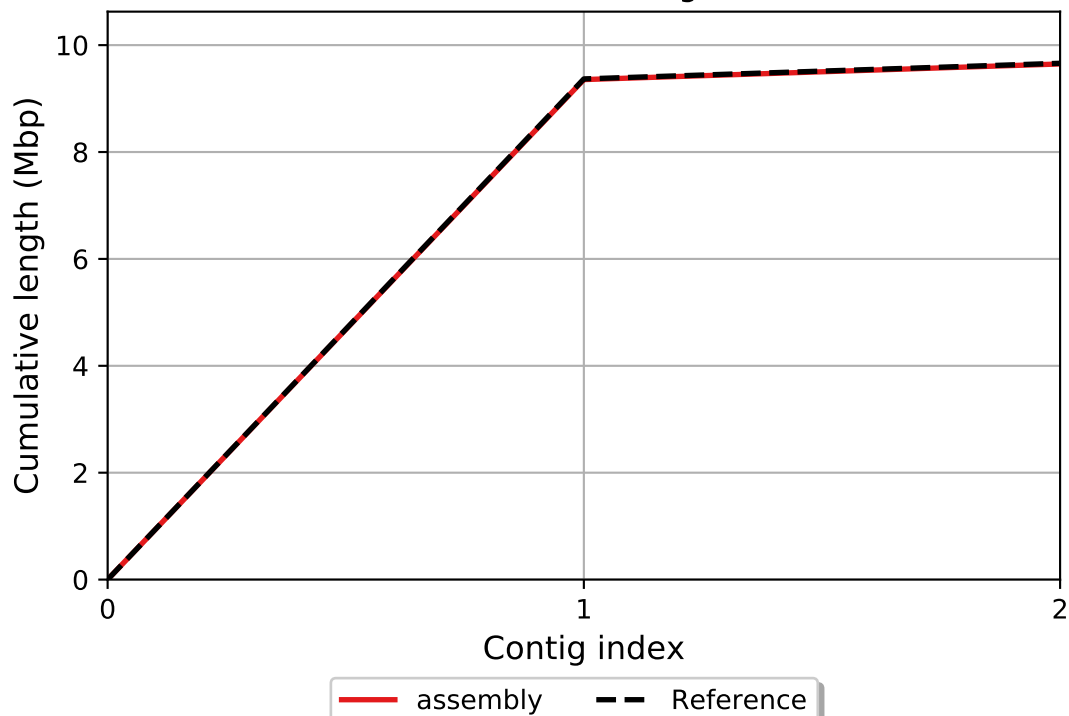
assembly

NGx

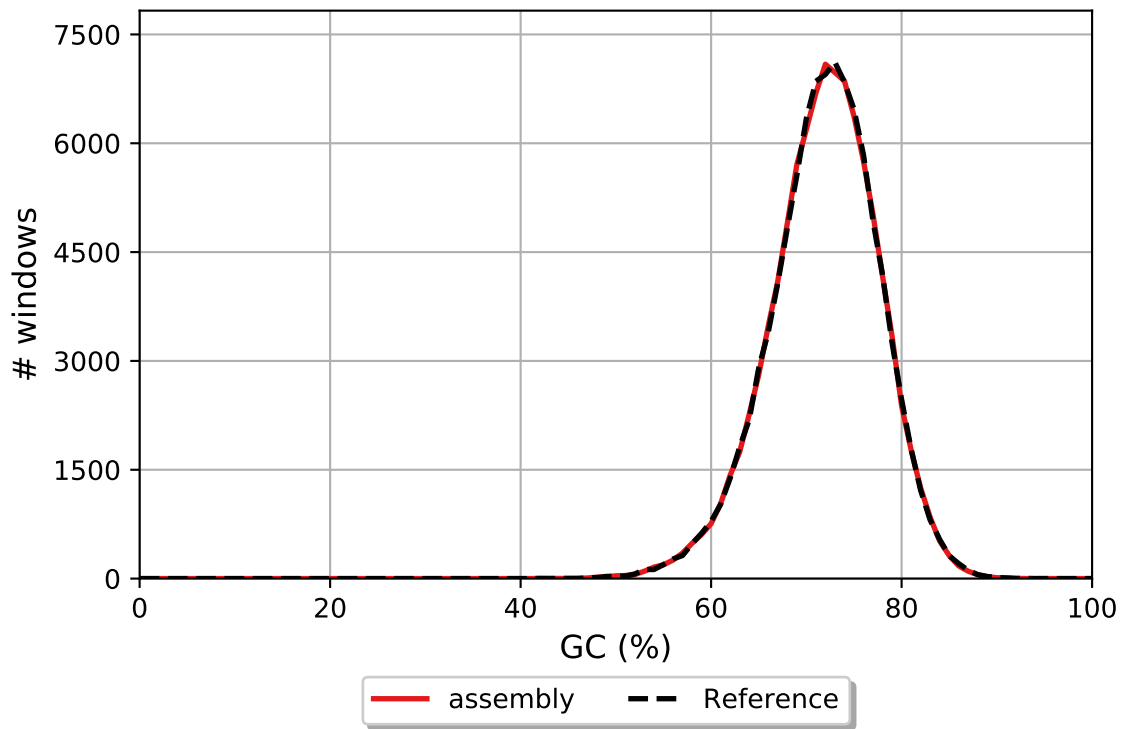


— assembly

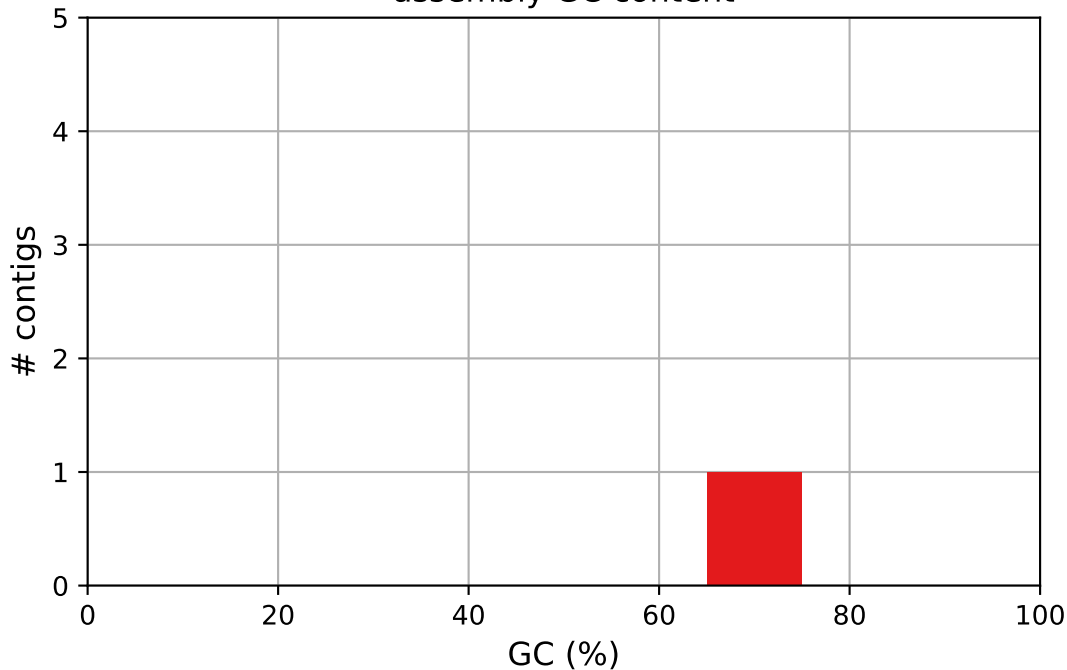
Cumulative length



GC content

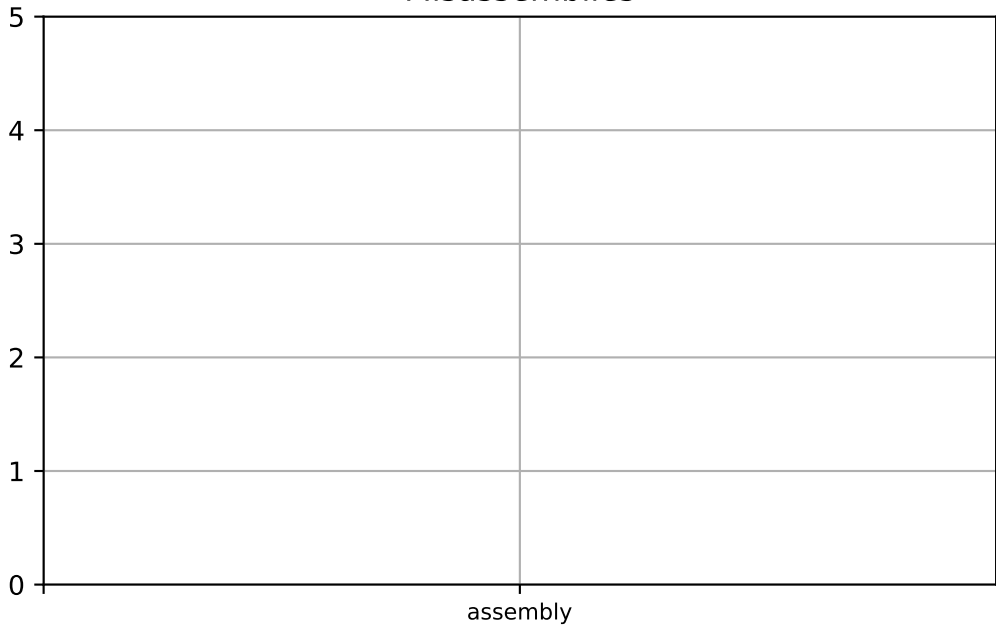


assembly GC content

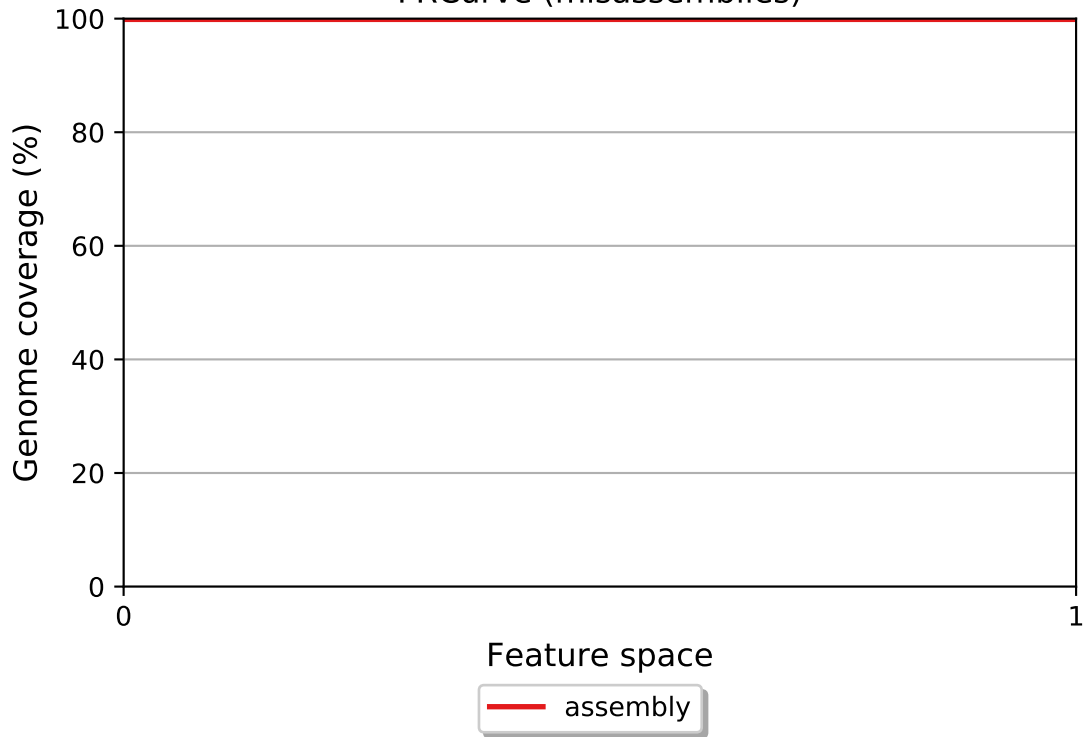


assembly

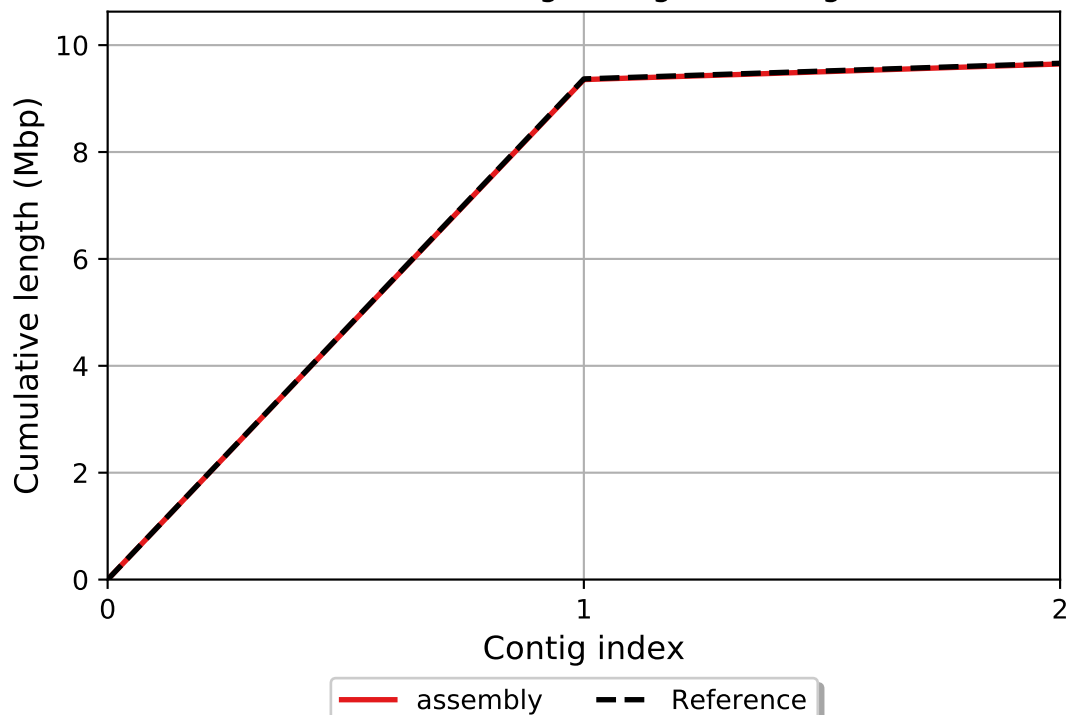
Misassemblies



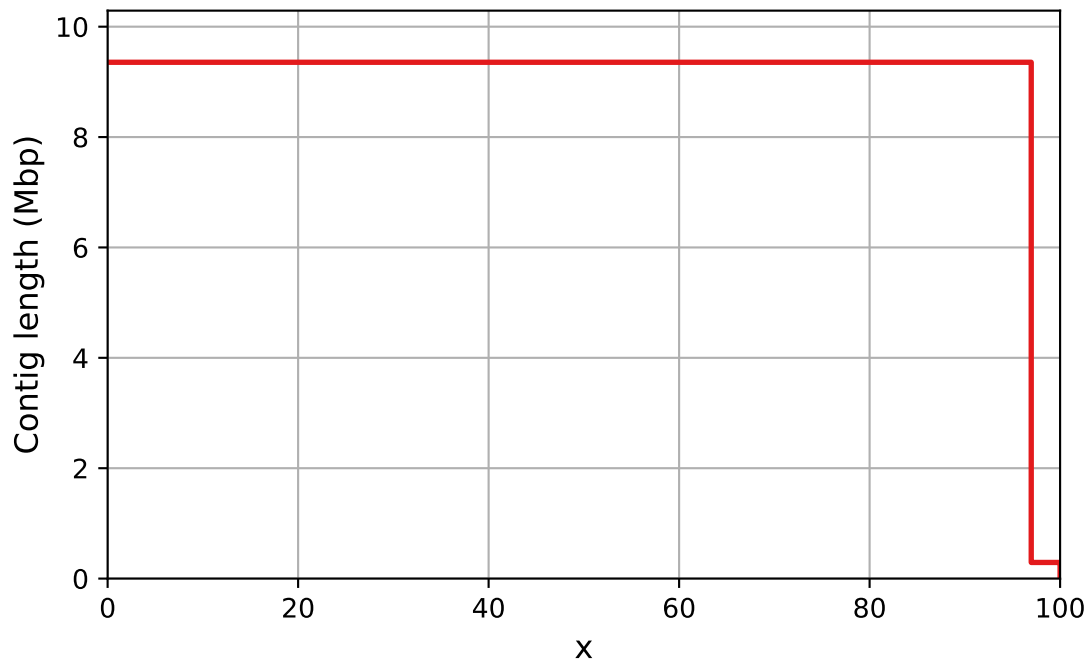
FRCurve (misassemblies)



Cumulative length (aligned contigs)

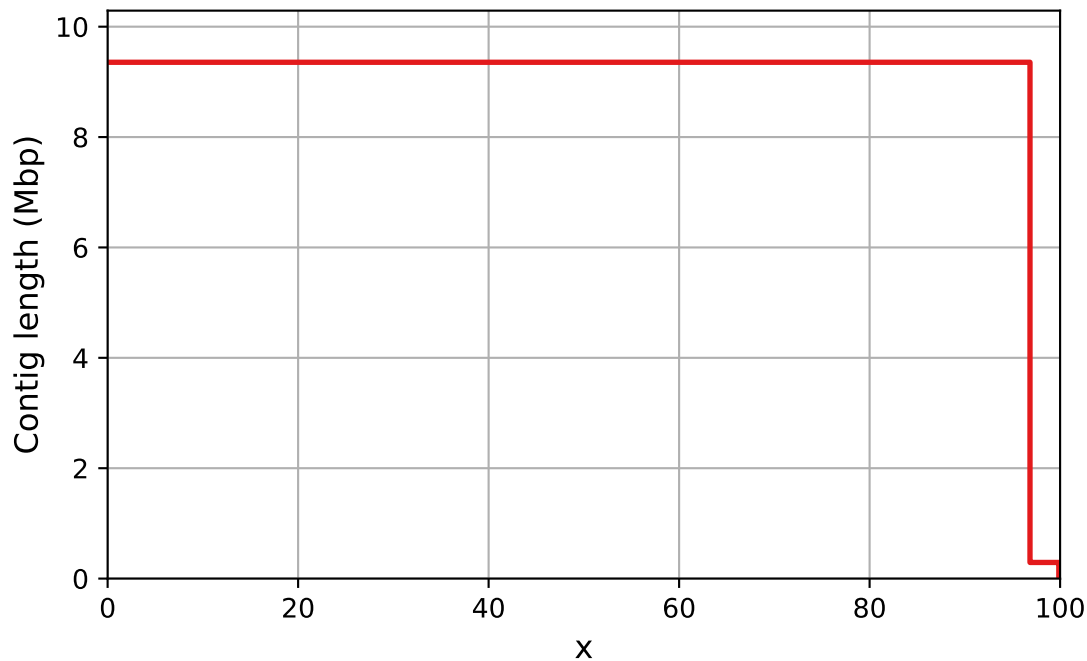


NAx



— assembly

NGAx



— assembly