

Report

	polished_assembly_72
# 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)	9653782
Total length (>= 1000 bp)	9653782
Total length (>= 5000 bp)	9653782
Total length (>= 10000 bp)	9653782
Total length (>= 25000 bp)	9653782
Total length (>= 50000 bp)	9653782
# contigs	2
Largest contig	9361213
Total length	9653782
Reference length	9660595
GC (%)	71.89
Reference GC (%)	71.88
N50	9361213
NG50	9361213
N75	9361213
NG75	9361213
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	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.24
# indels per 100 kbp	0.66
Largest alignment	9361213
Total aligned length	9653775
NA50	9361213
NGA50	9361213
NA75	9361213
NGA75	9361213
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

	polished_assembly_72
# 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	23
# indels	64
# indels (<= 5 bp)	62
# indels (> 5 bp)	2
Indels length	123

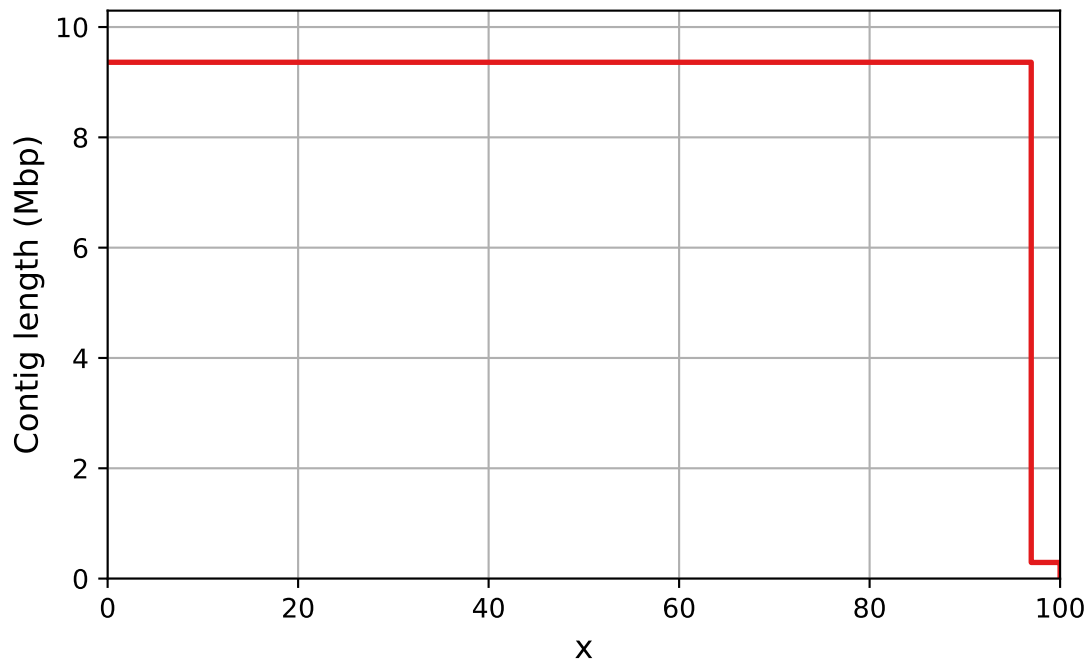
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	polished_assembly_72
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

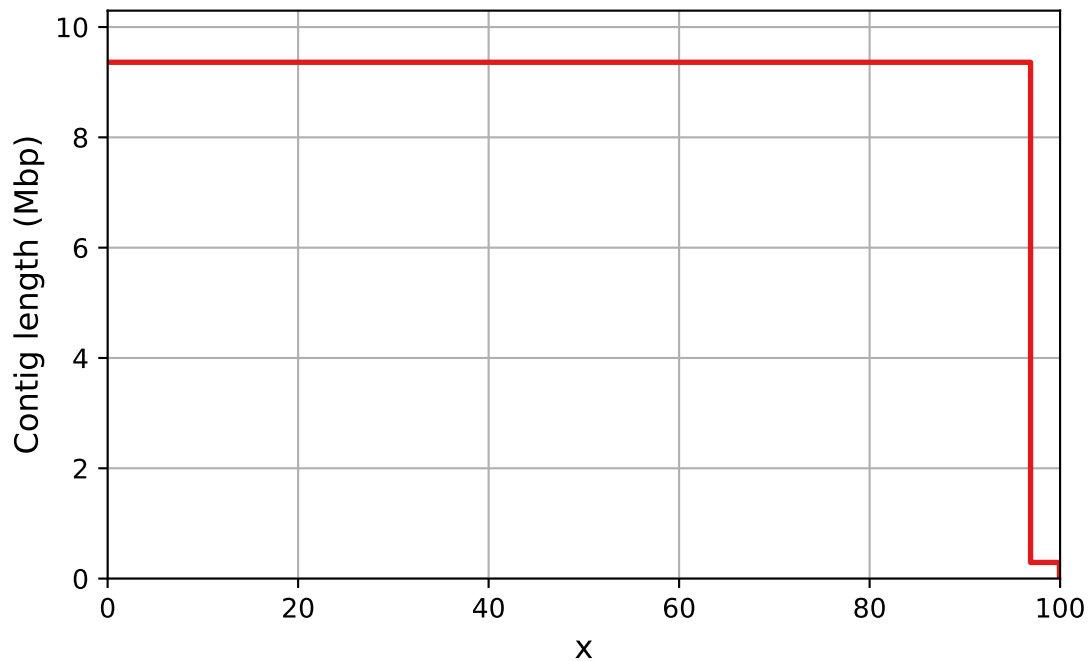
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



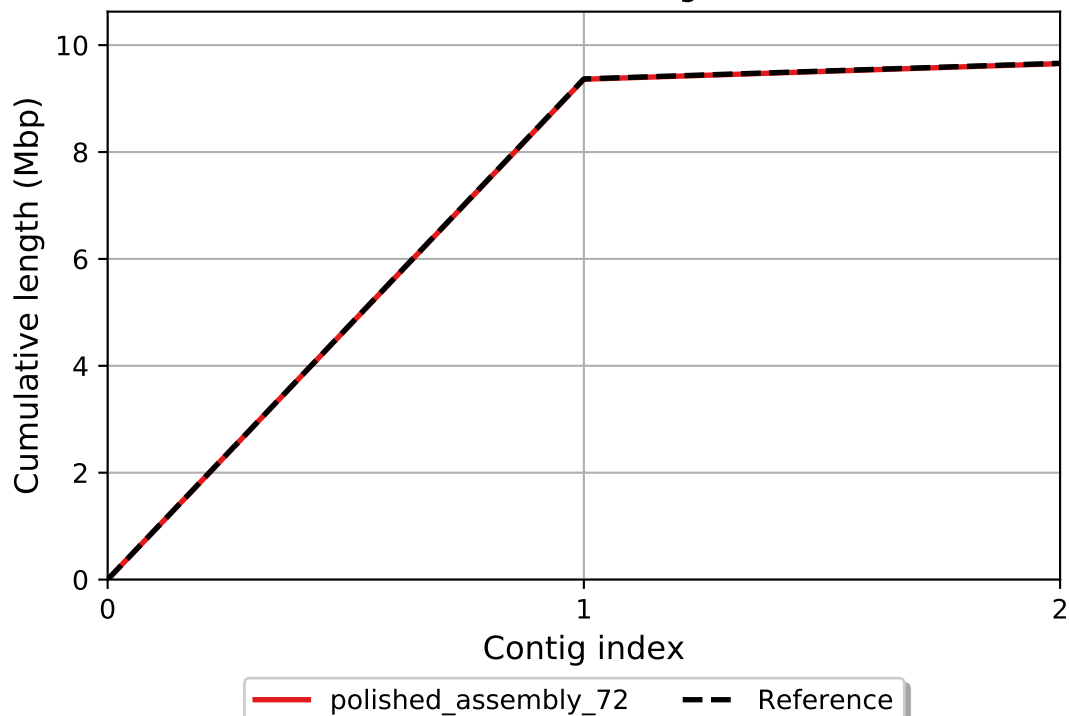
polished_assembly_72

NGx

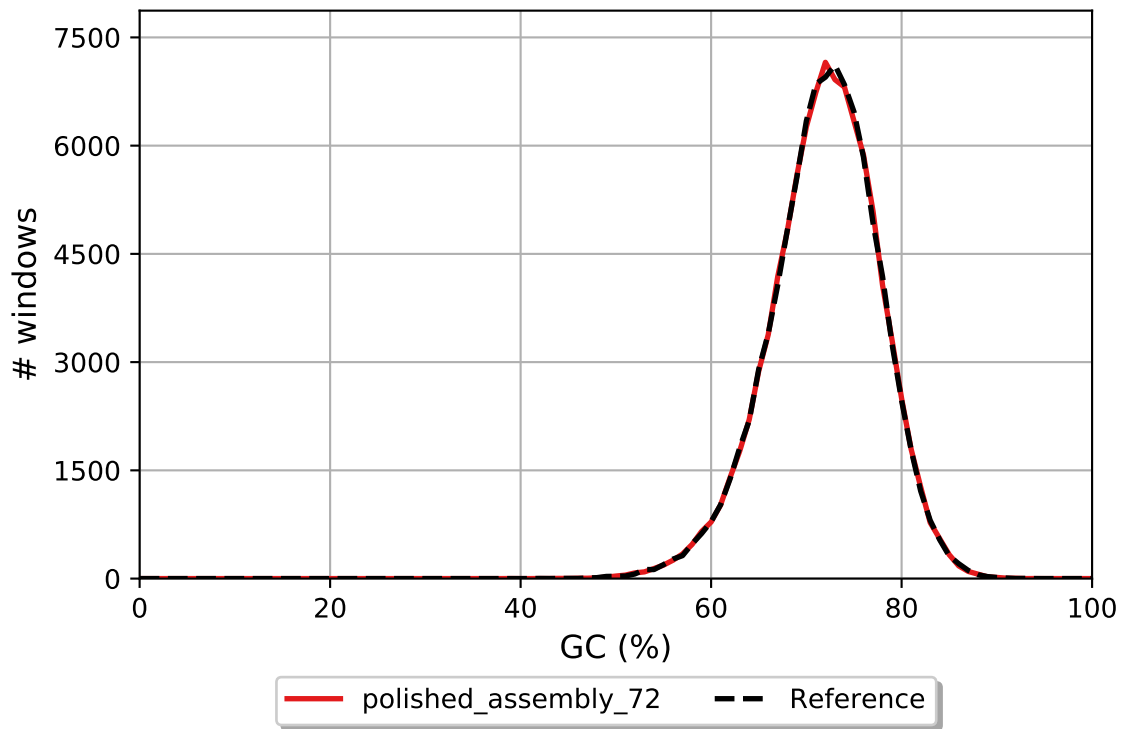


polished_assembly_72

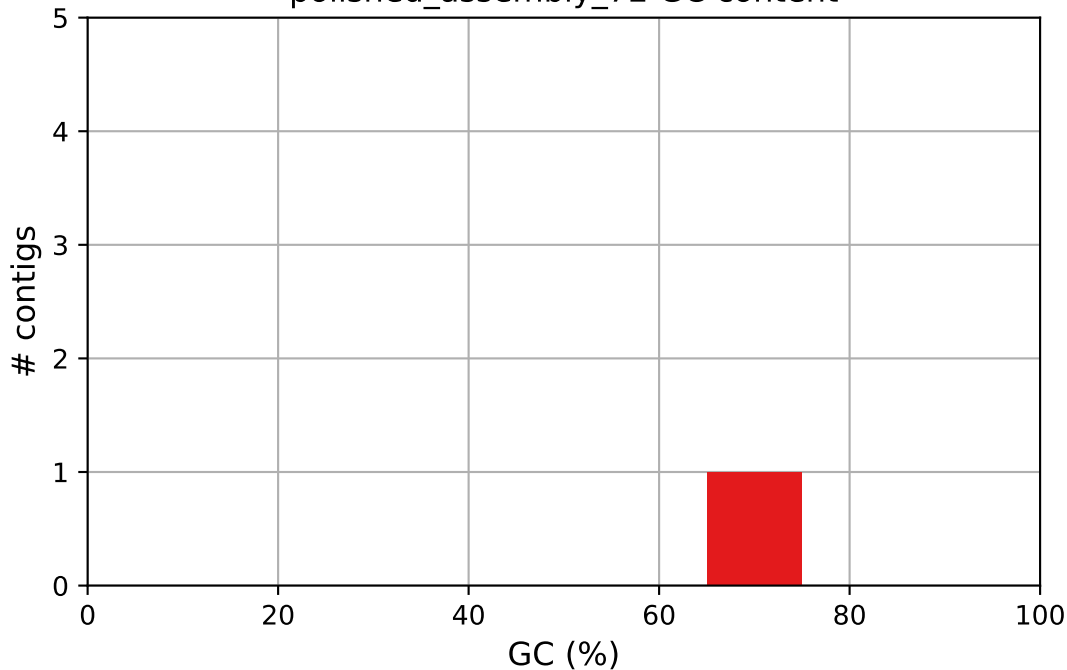
Cumulative length



GC content

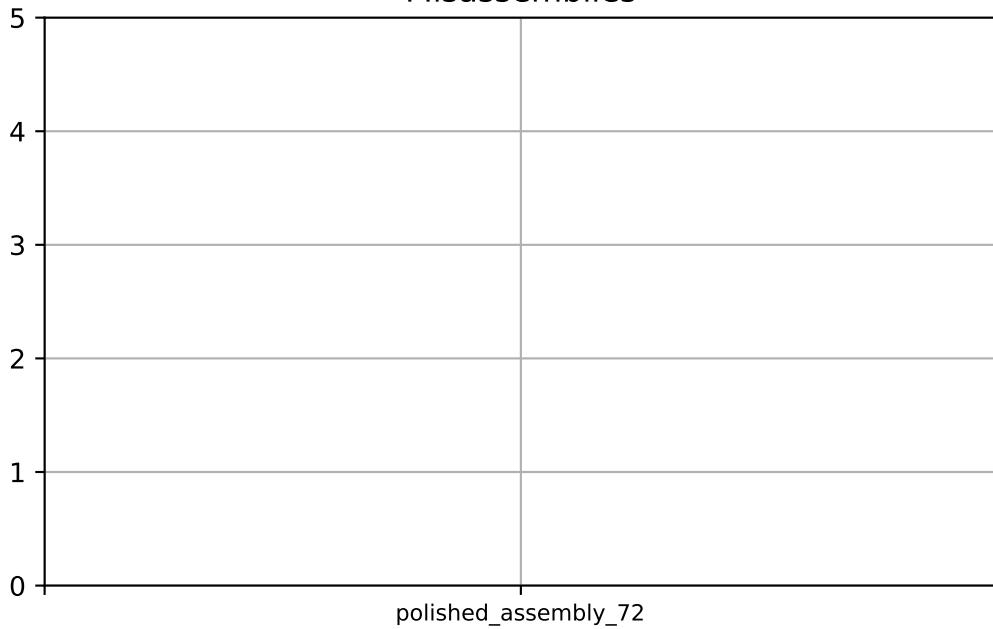


polished_assembly_72 GC content

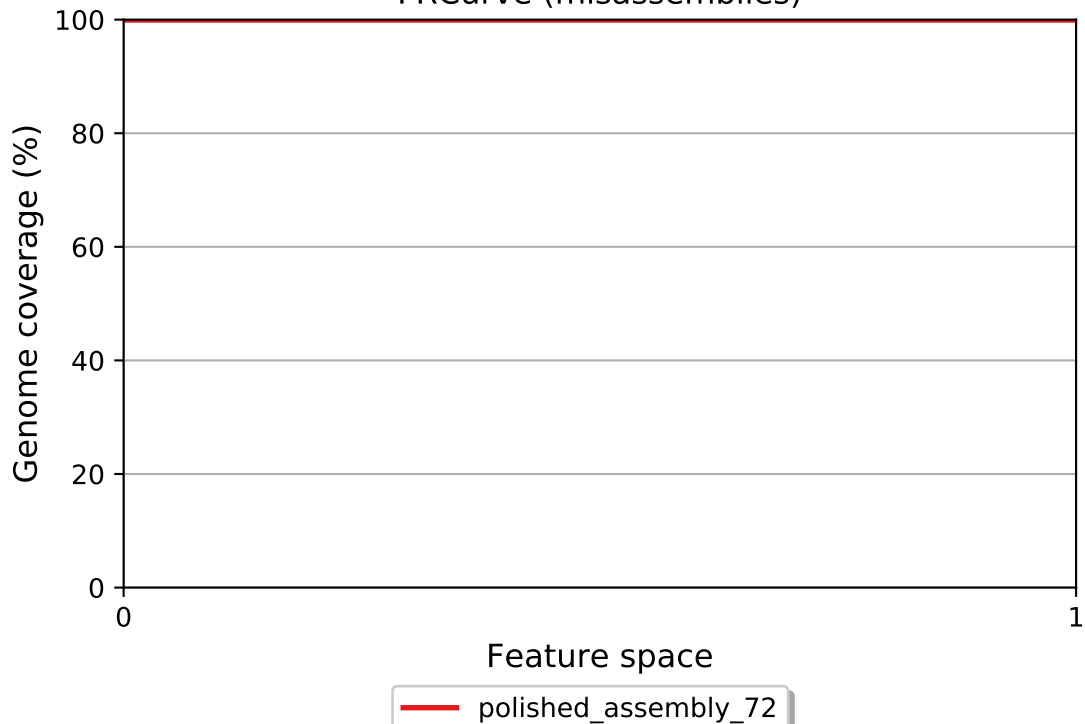


polished_assembly_72

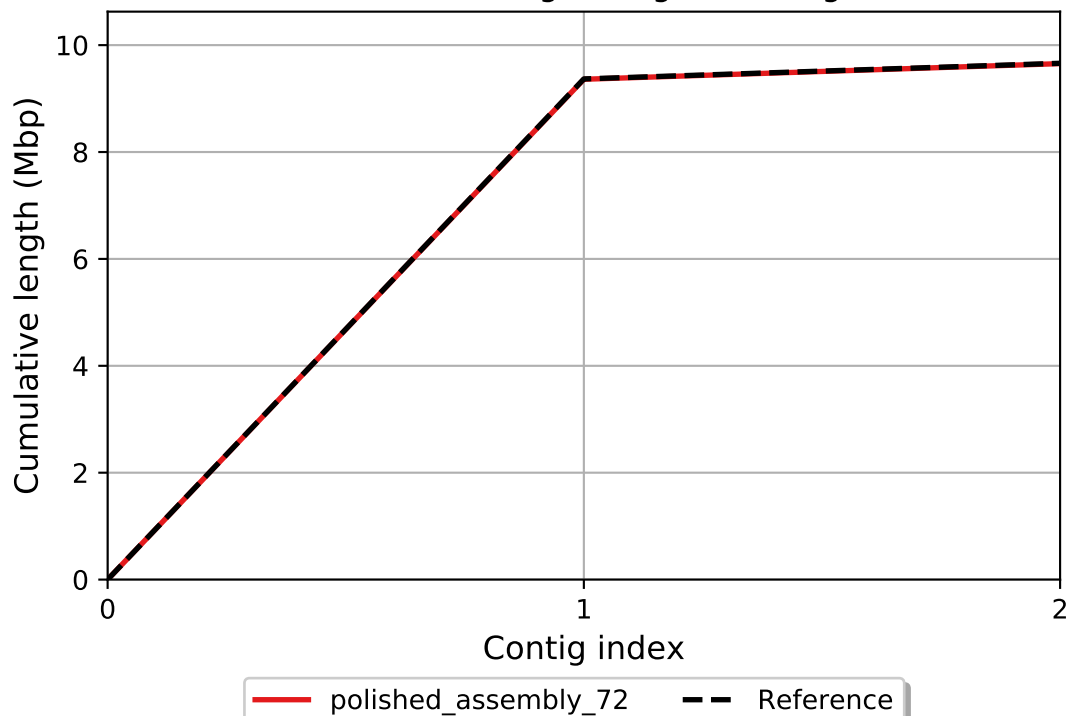
Misassemblies



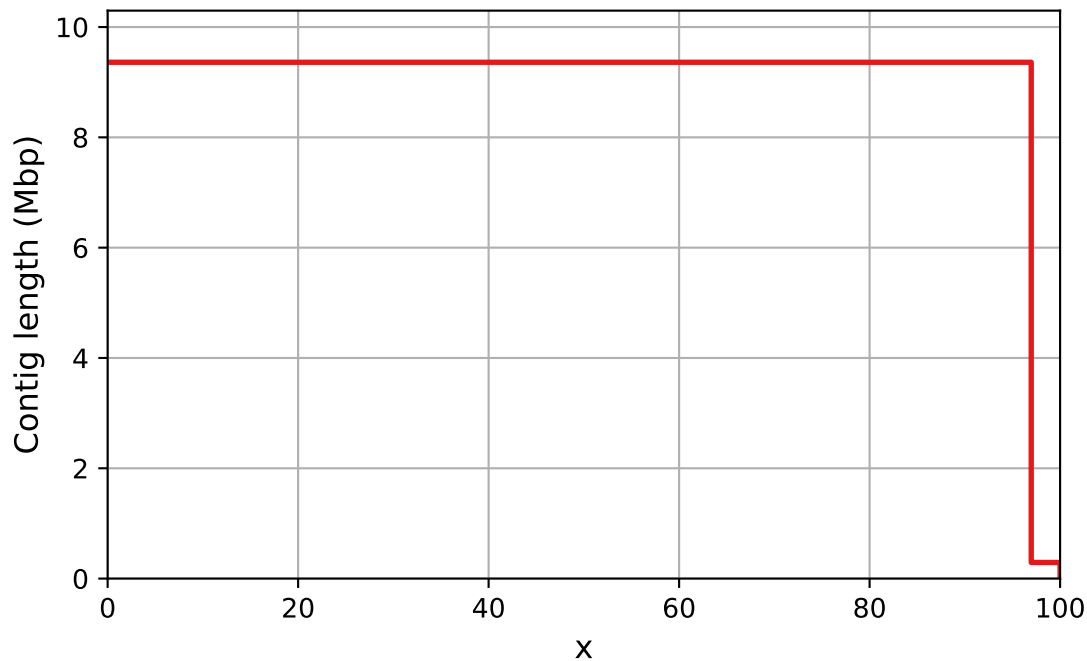
FRCurve (misassemblies)



Cumulative length (aligned contigs)

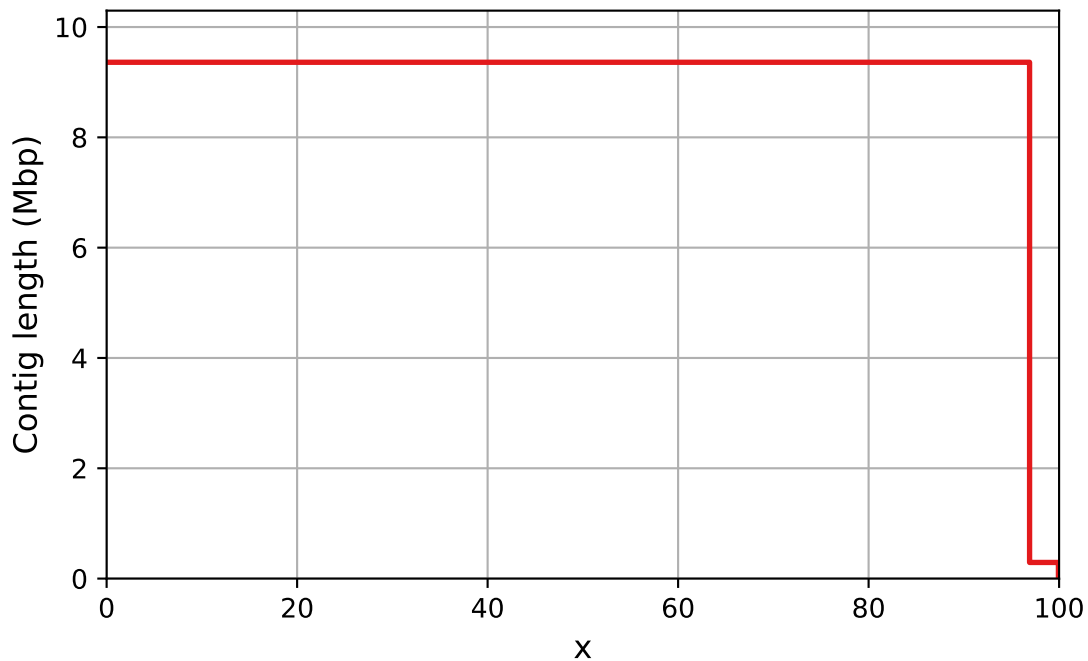


NAx



polished_assembly_72

NGAx



polished_assembly_72