

## Report

	polished_assembly_66
# 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)	8771744
Total length (>= 1000 bp)	8771744
Total length (>= 5000 bp)	8771744
Total length (>= 10000 bp)	8771744
Total length (>= 25000 bp)	8771744
Total length (>= 50000 bp)	8771744
# contigs	4
Largest contig	6995913
Total length	8771744
Reference length	9619655
GC (%)	72.00
Reference GC (%)	71.93
N50	6995913
NG50	6995913
N75	6995913
NG75	1054385
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 (%)	90.960
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.00
# indels per 100 kbp	3.38
Largest alignment	6995913
Total aligned length	8771733
NA50	6995913
NGA50	6995913
NA75	6995913
NGA75	1054385
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

	polished_assembly_66
# 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	175
# indels	296
# indels (<= 5 bp)	294
# indels (> 5 bp)	2
Indels length	430

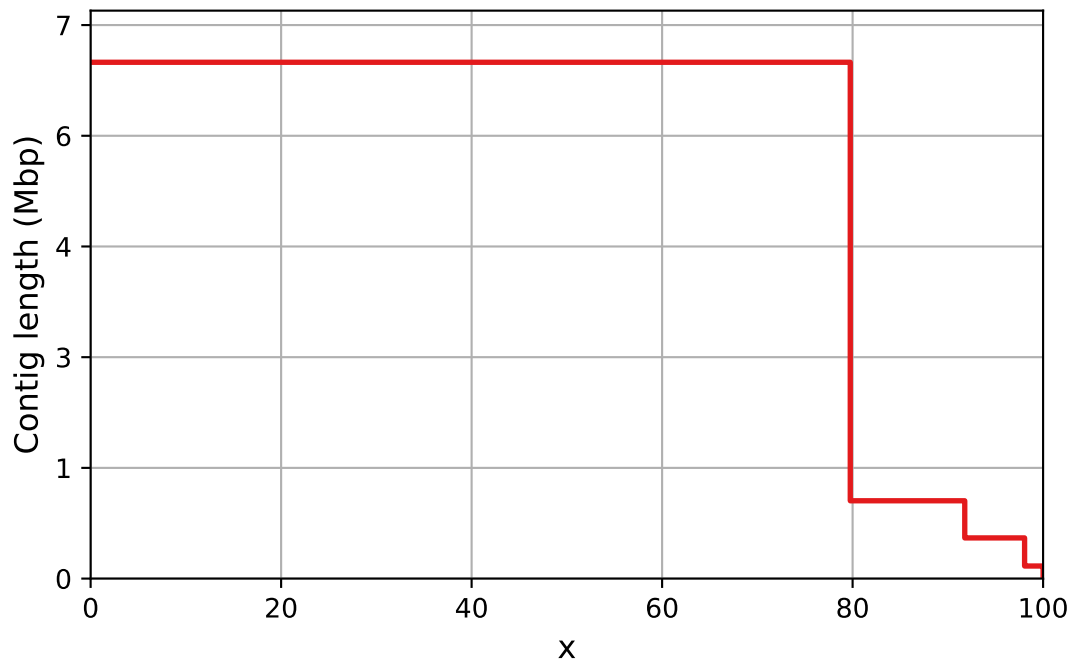
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	polished_assembly_66
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

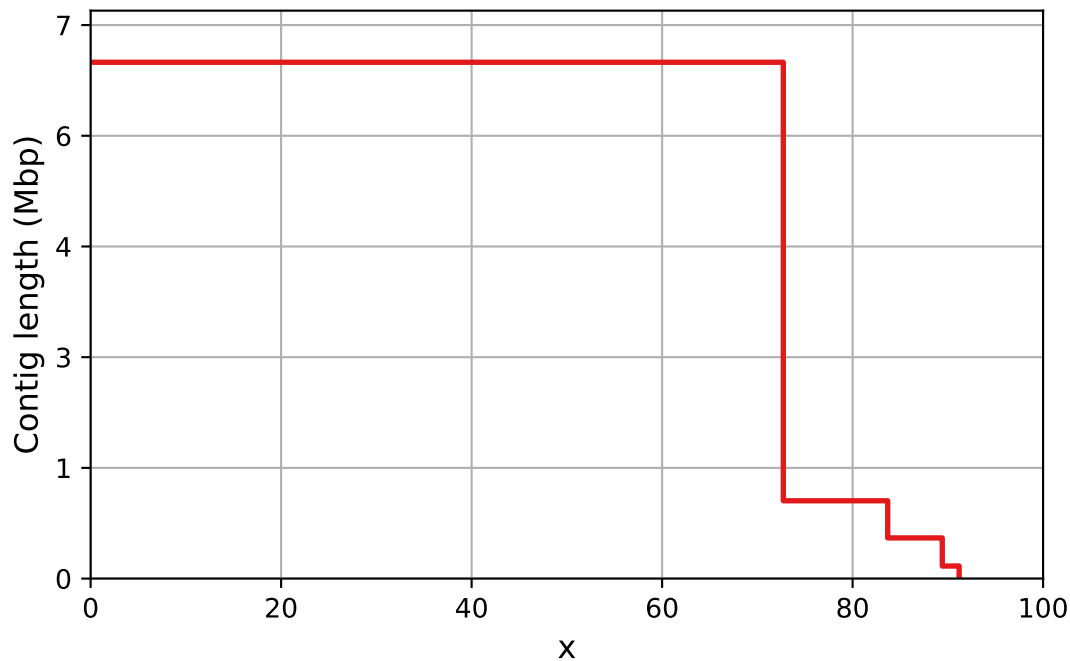
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



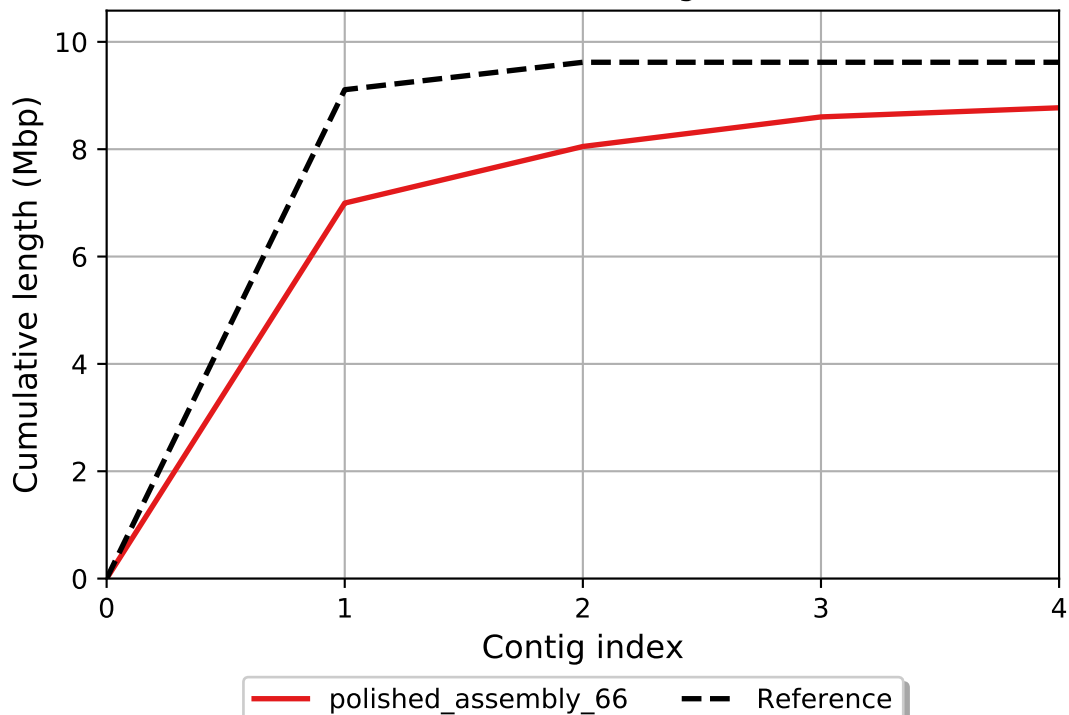
polished\_assembly\_66

# NGx

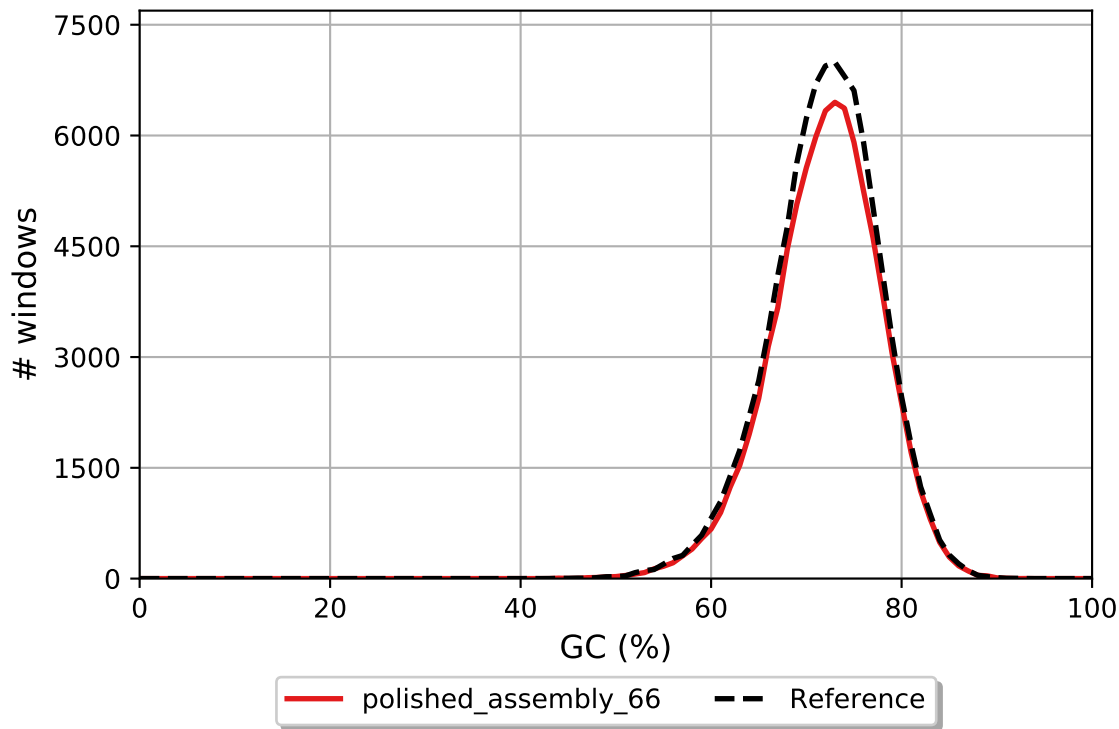


polished\_assembly\_66

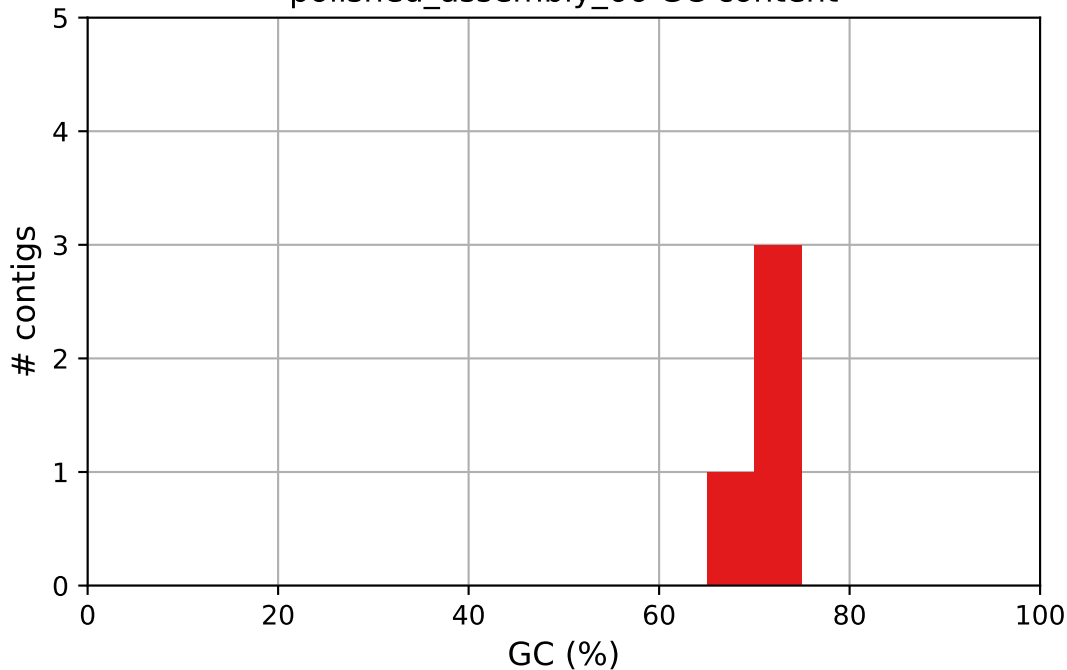
Cumulative length



GC content



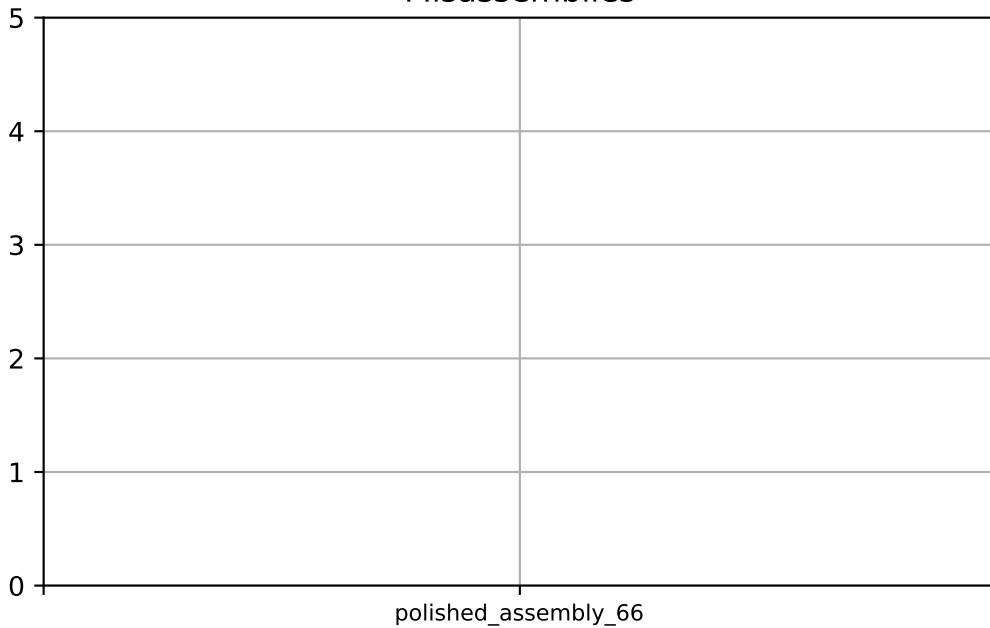
polished\_assembly\_66 GC content



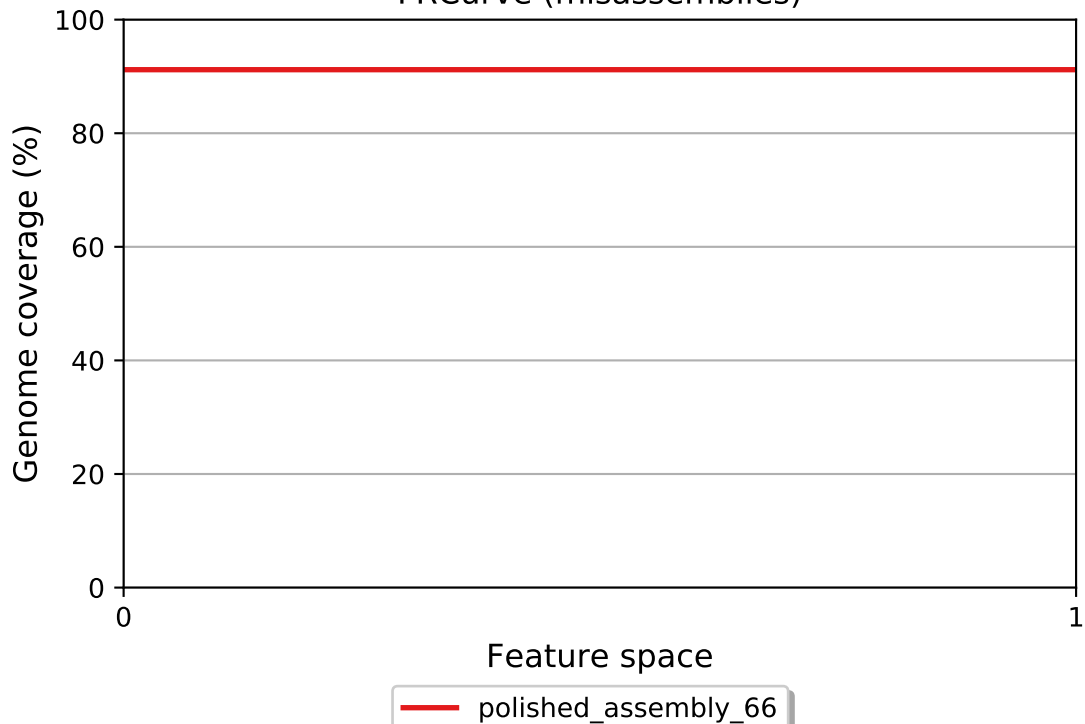
polished\_assembly\_66



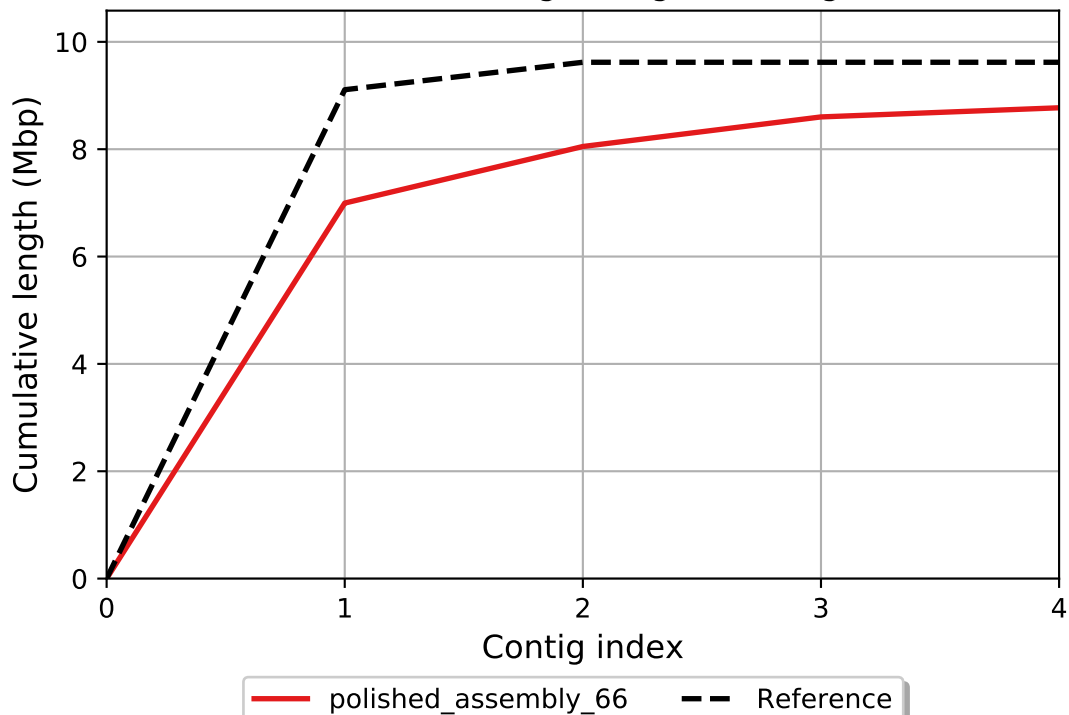
## Misassemblies



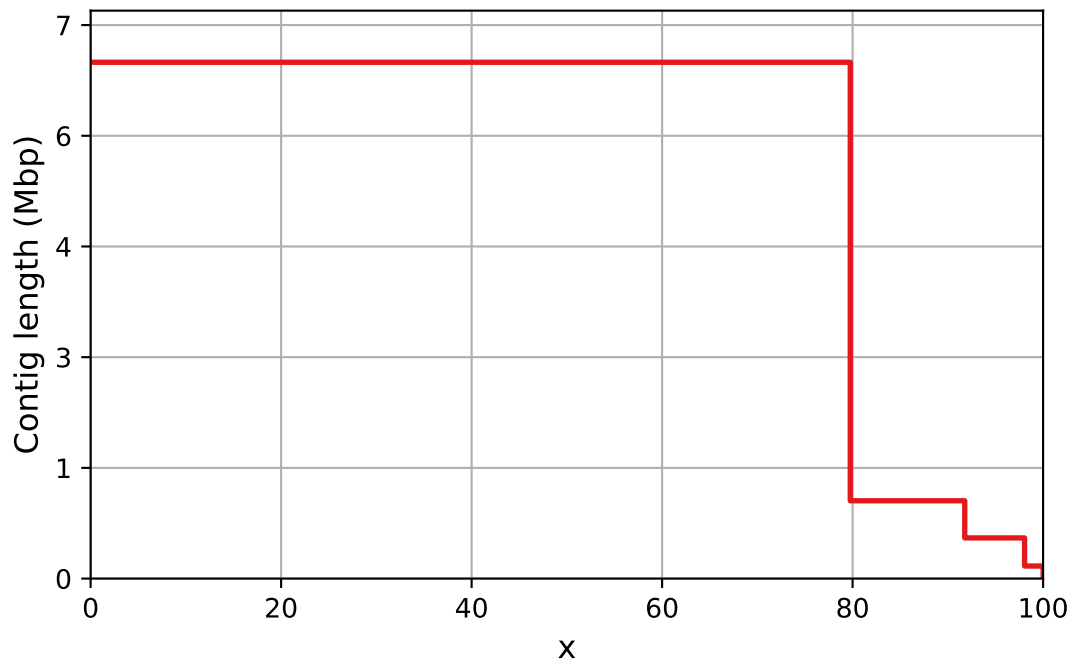
FRCurve (misassemblies)



Cumulative length (aligned contigs)

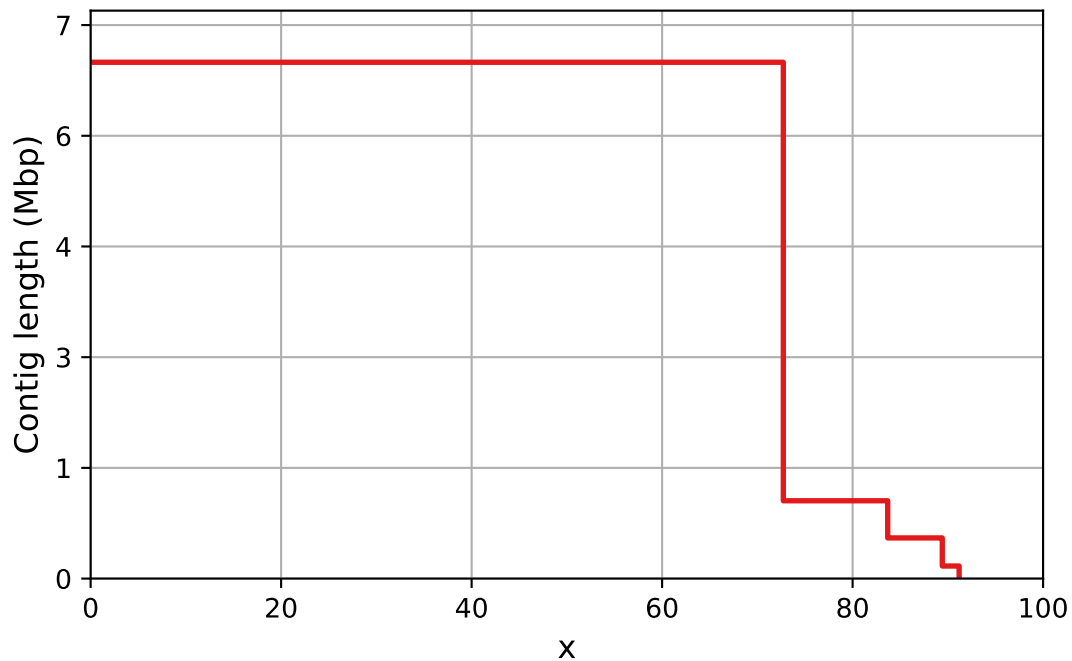


NAx



polished\_assembly\_66

# NGAx



polished\_assembly\_66