

# Report

	tig00000001_pilon
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2773702
Total length (>= 1000 bp)	2773702
Total length (>= 5000 bp)	2773702
Total length (>= 10000 bp)	2773702
Total length (>= 25000 bp)	2773702
Total length (>= 50000 bp)	2773702
# contigs	1
Largest contig	2773702
Total length	2773702
Reference length	2765031
GC (%)	38.11
Reference GC (%)	38.11
N50	2773702
NG50	2773702
N75	2773702
NG75	2773702
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	2773702
# 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 (%)	99.765
Duplication ratio	1.005
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.39
# indels per 100 kbp	0.98
Largest alignment	1084784
Total aligned length	2773702
NA50	852846
NGA50	852846
NA75	836072
NGA75	836072
LA50	2
LGA50	2
LA75	3
LGA75	3

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

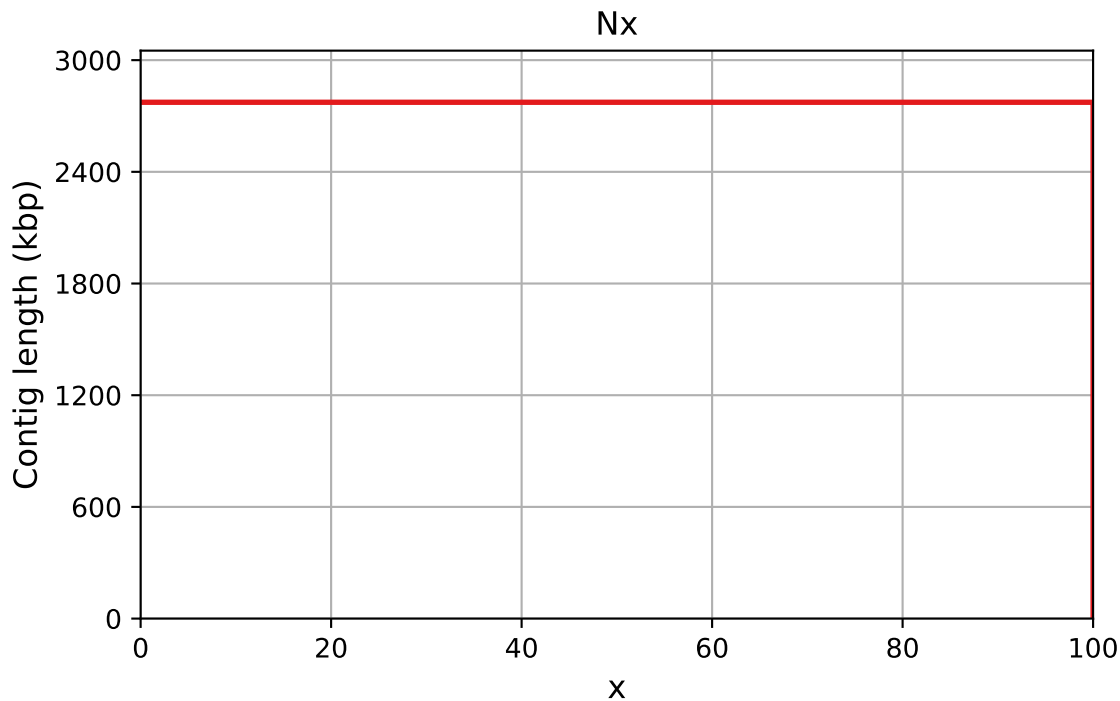
	tig00000001_pilon
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2773702
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	452
# indels	27
# indels (<= 5 bp)	25
# indels (> 5 bp)	2
Indels length	52

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

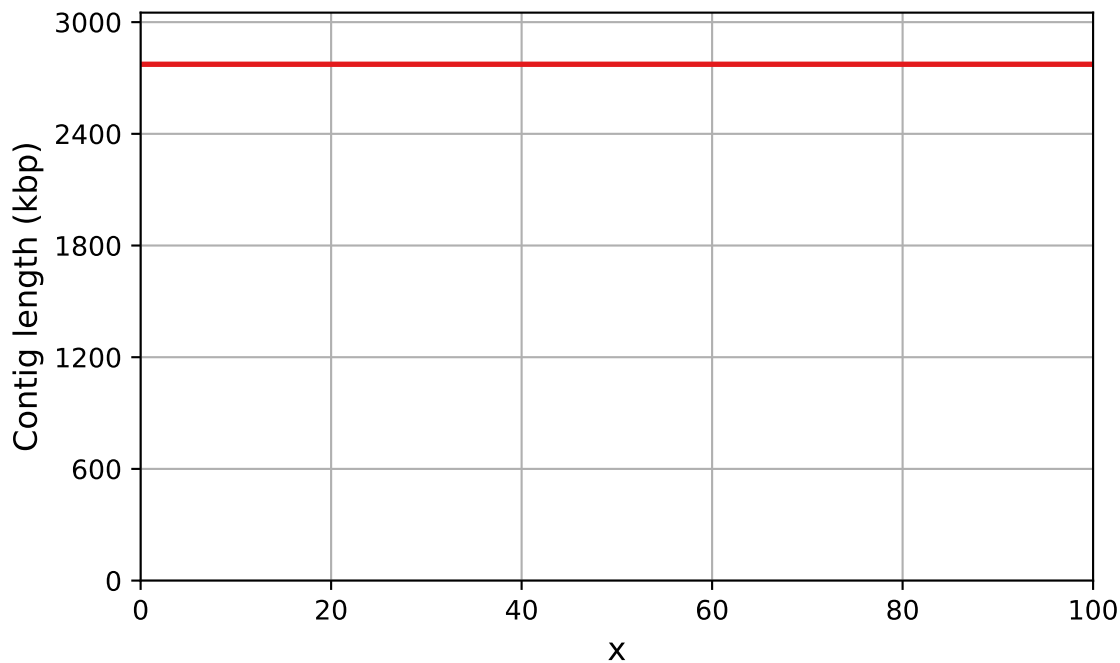
	tig00000001_pilon
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

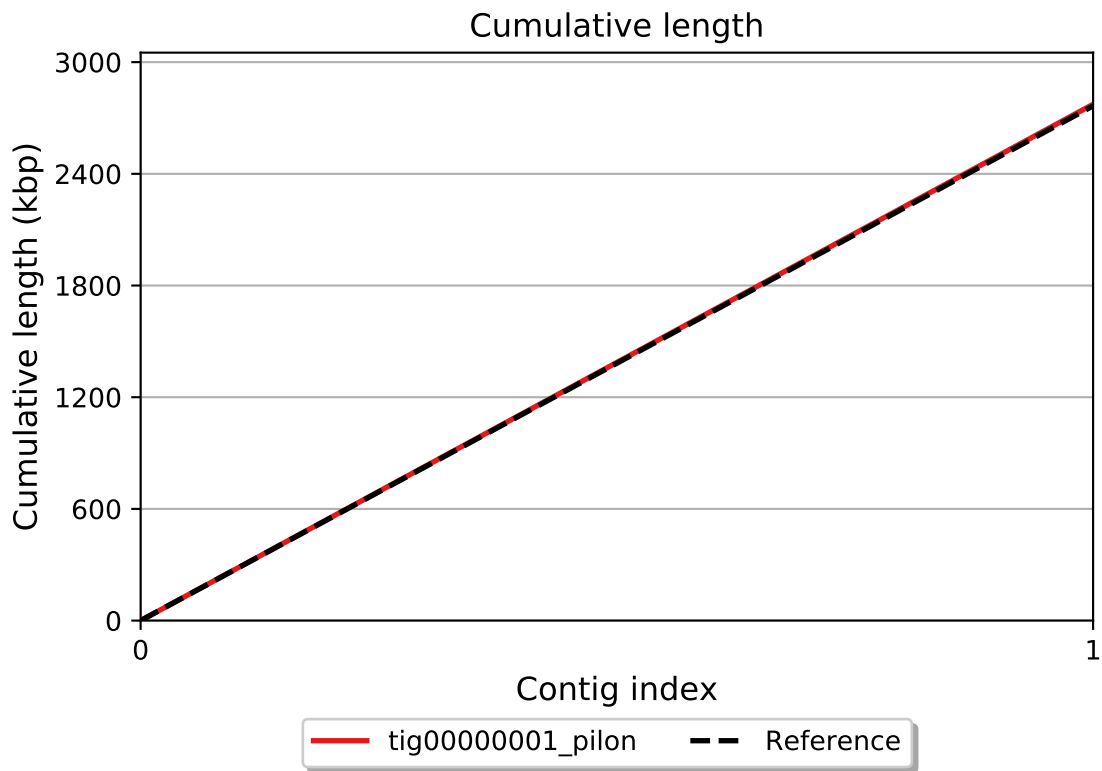


— tig00000001\_pilon

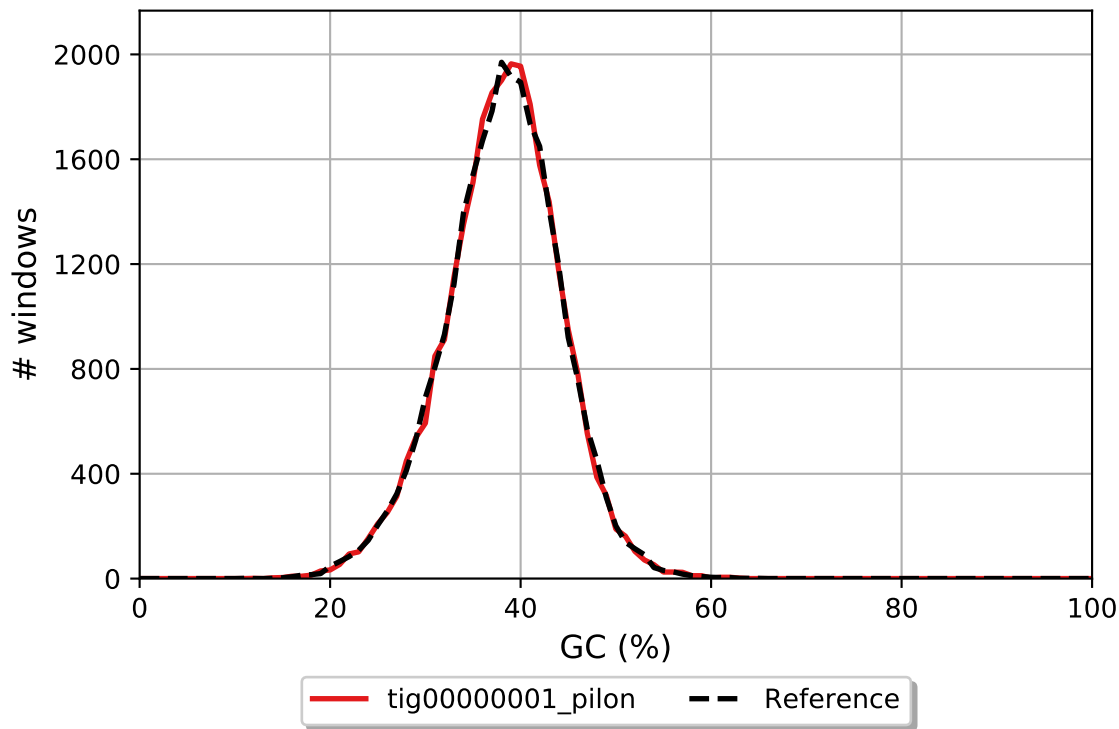
# NGx



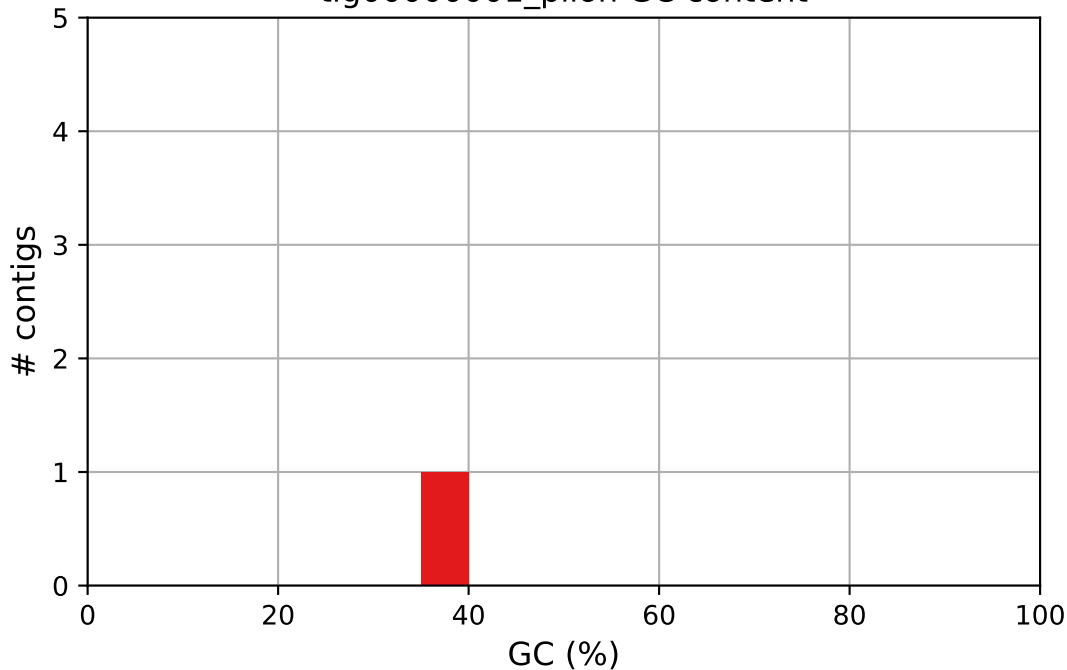
— tig00000001\_pilon



# GC content



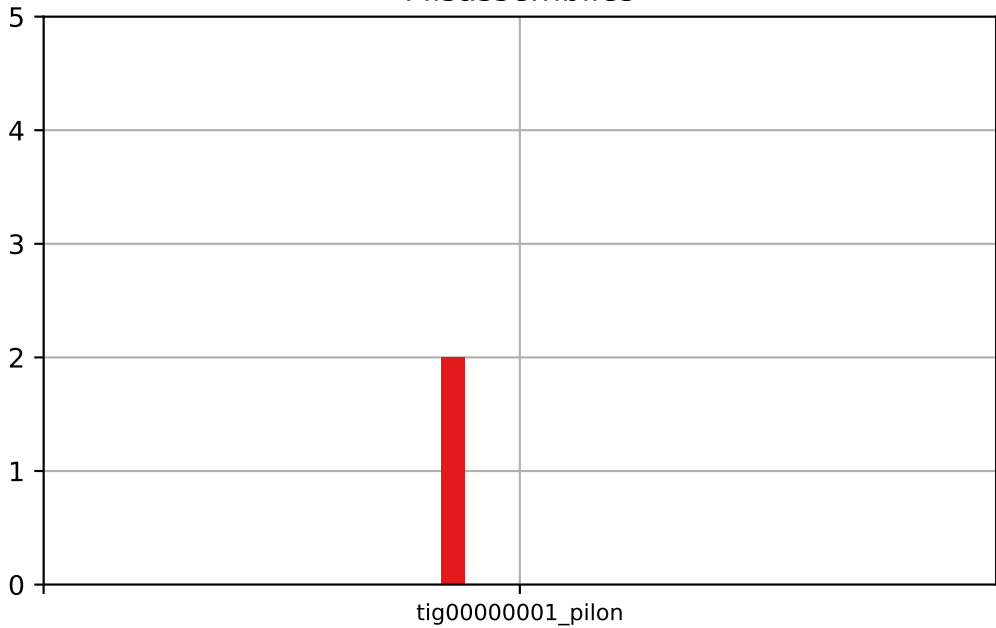
tig00000001\_pilon GC content



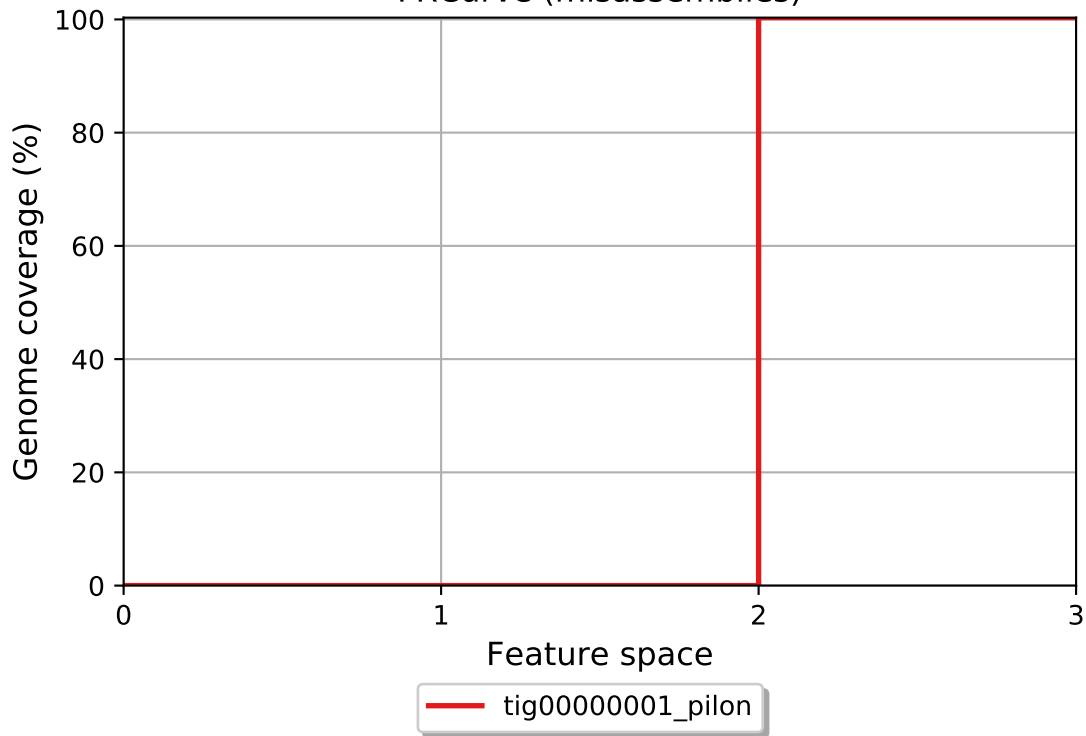
tig00000001\_pilon

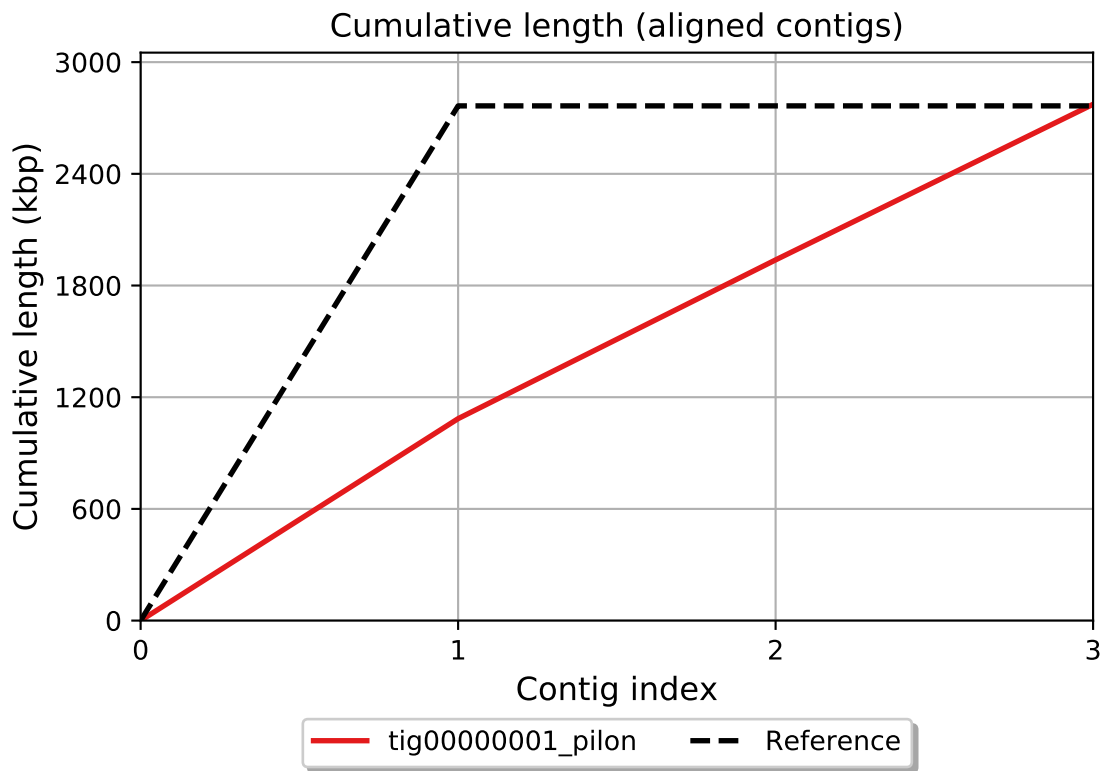


## Misassemblies

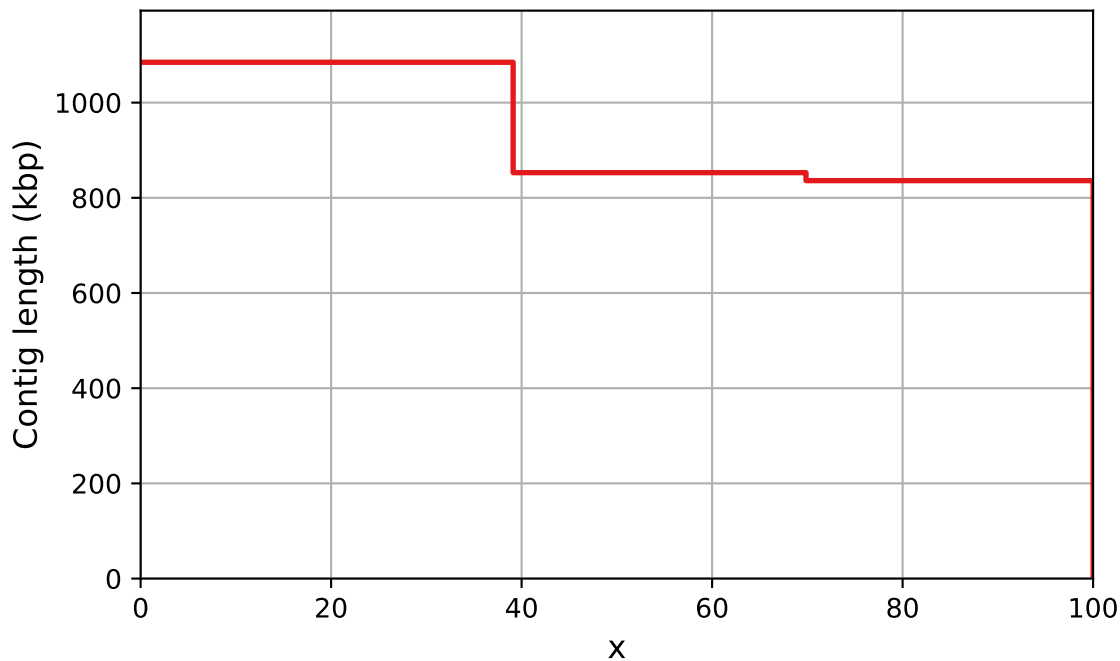


FRCurve (misassemblies)



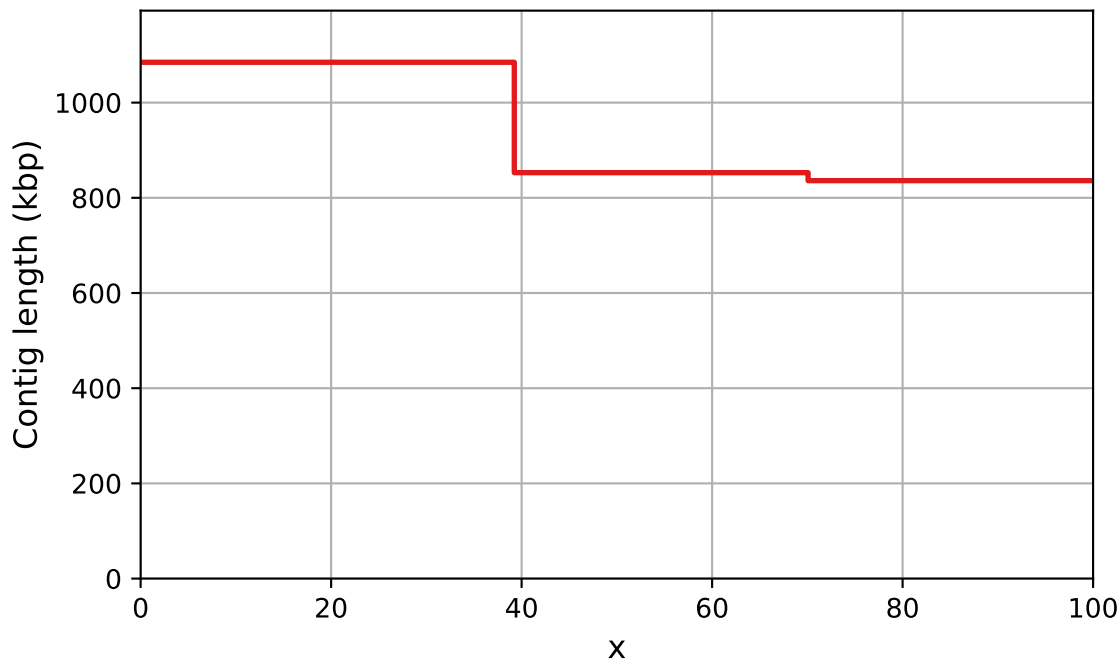


NAx



tig00000001\_pilon

# NGAx



— tig000000001\_pilon