

## Report

	tig00000033_pilon
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	26287
Total length (>= 1000 bp)	26287
Total length (>= 5000 bp)	26287
Total length (>= 10000 bp)	26287
Total length (>= 25000 bp)	26287
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	26287
Total length	26287
Reference length	65558
GC (%)	32.73
Reference GC (%)	32.05
N50	26287
N75	26287
L50	1
L75	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 (%)	40.099
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.80
# indels per 100 kbp	11.41
Largest alignment	26287
Total aligned length	26287
NA50	26287
NGA50	-
NA75	26287
LA50	1
LA75	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

	tig00000033_pilon
# 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	1
# indels	3
# indels (<= 5 bp)	3
# indels (> 5 bp)	0
Indels length	3

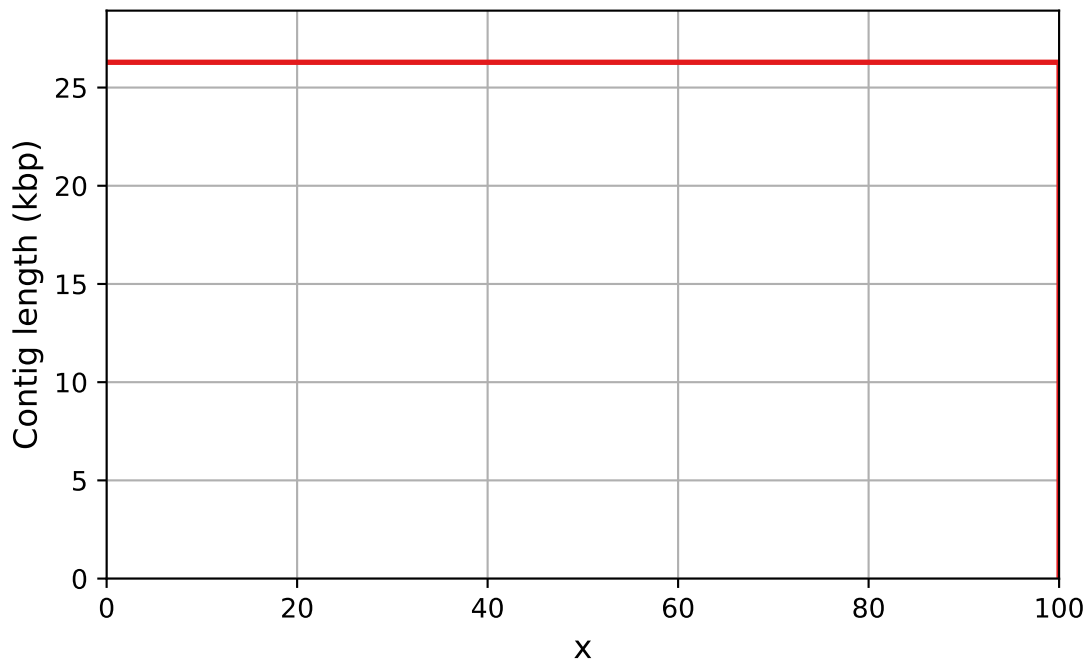
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	tig00000033_pilon
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

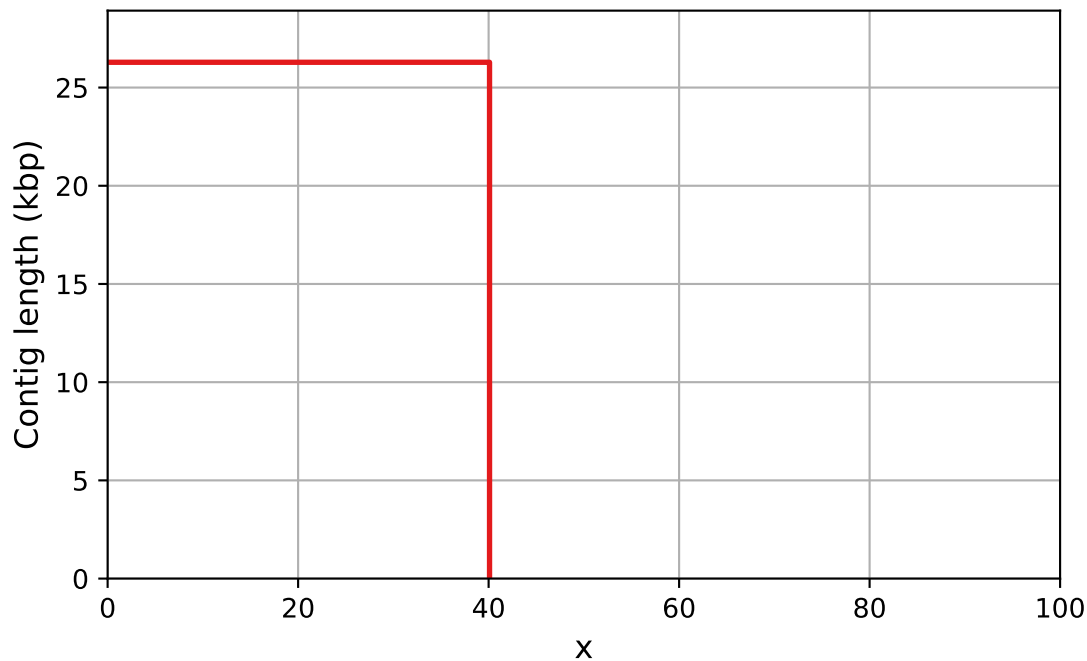
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



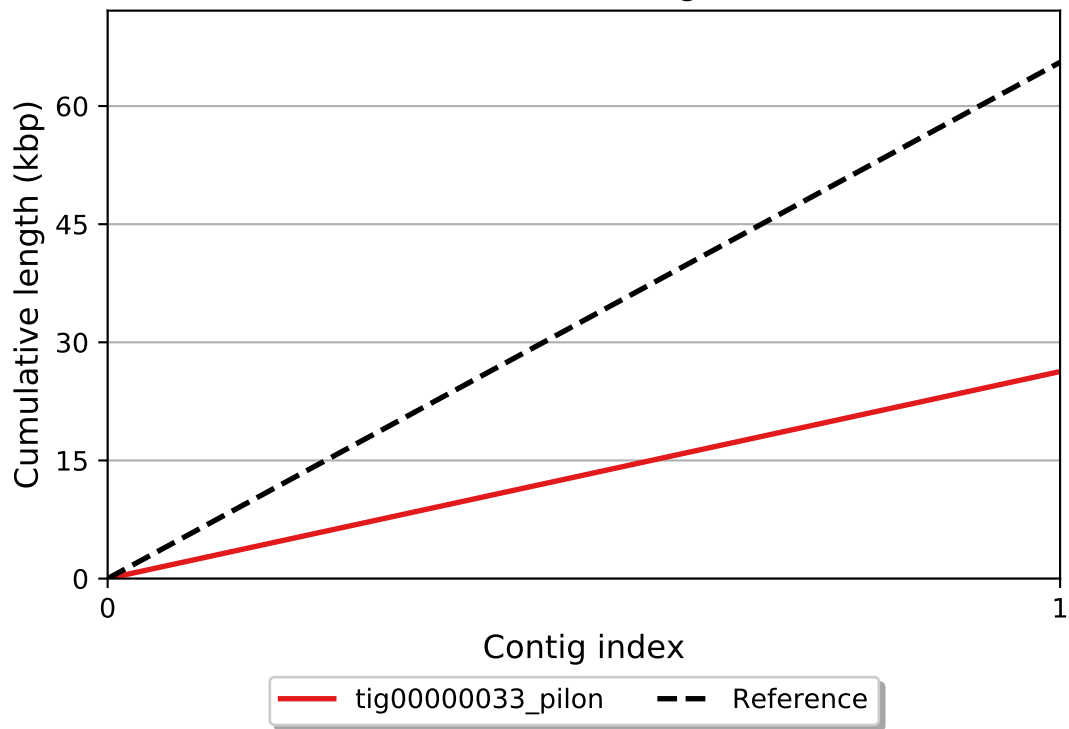
— tig00000033\_pilon

NGx

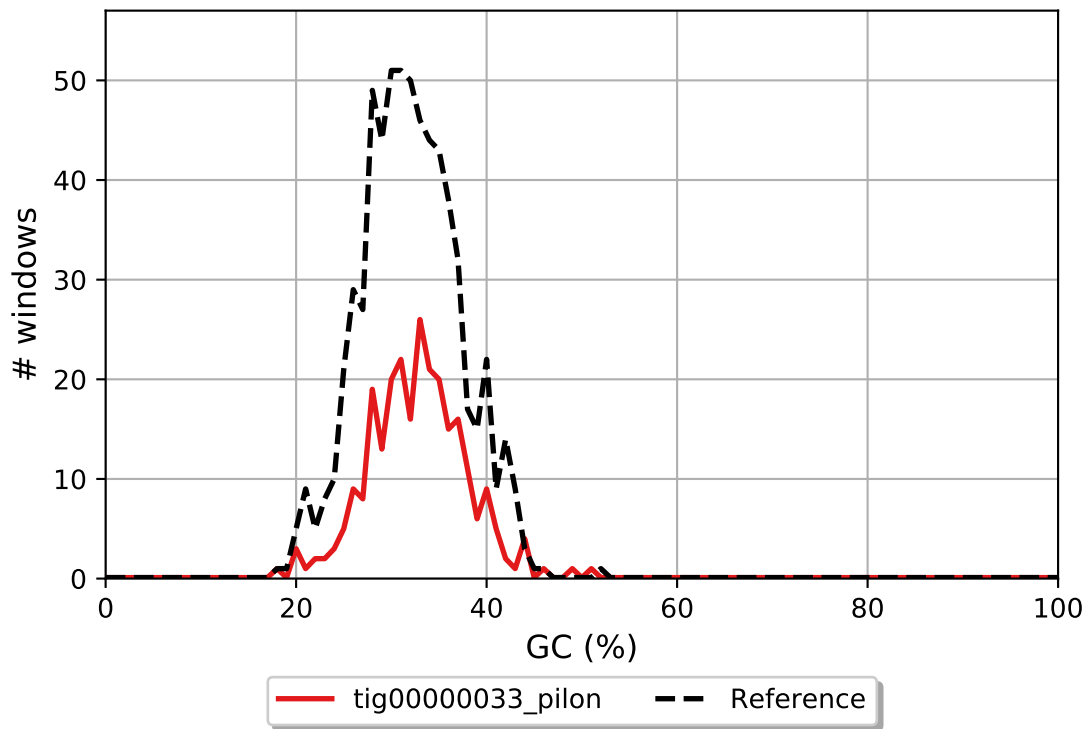


— tig00000033\_pilon

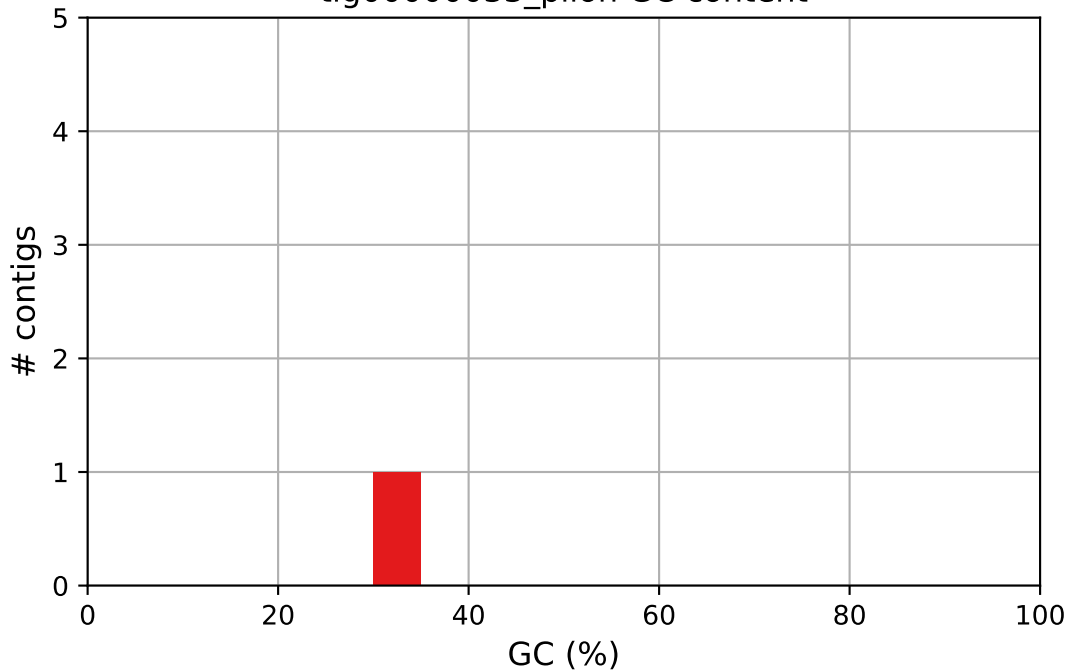
Cumulative length



## GC content



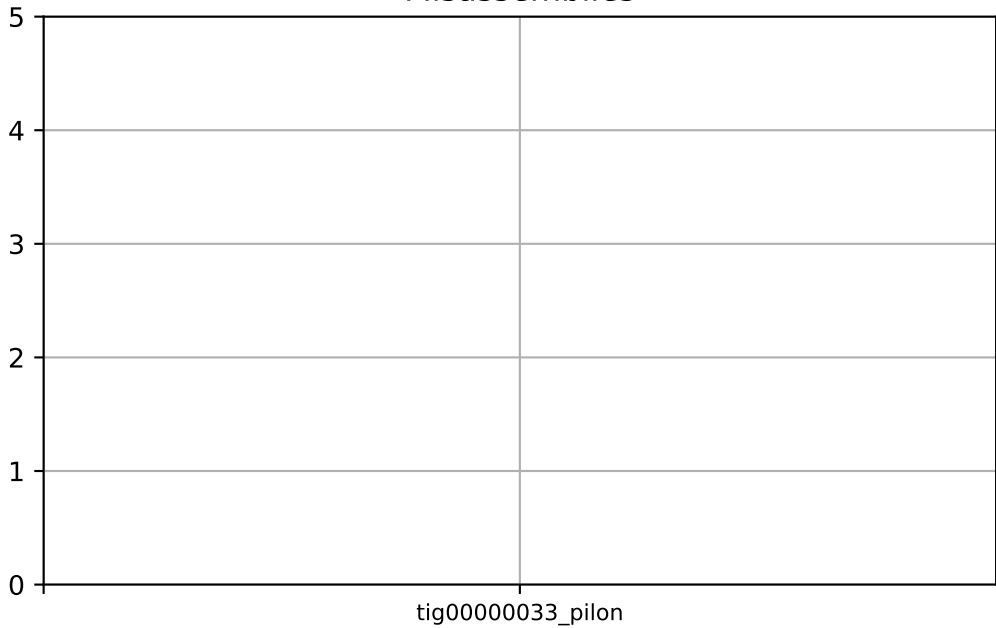
tig00000033\_pilon GC content



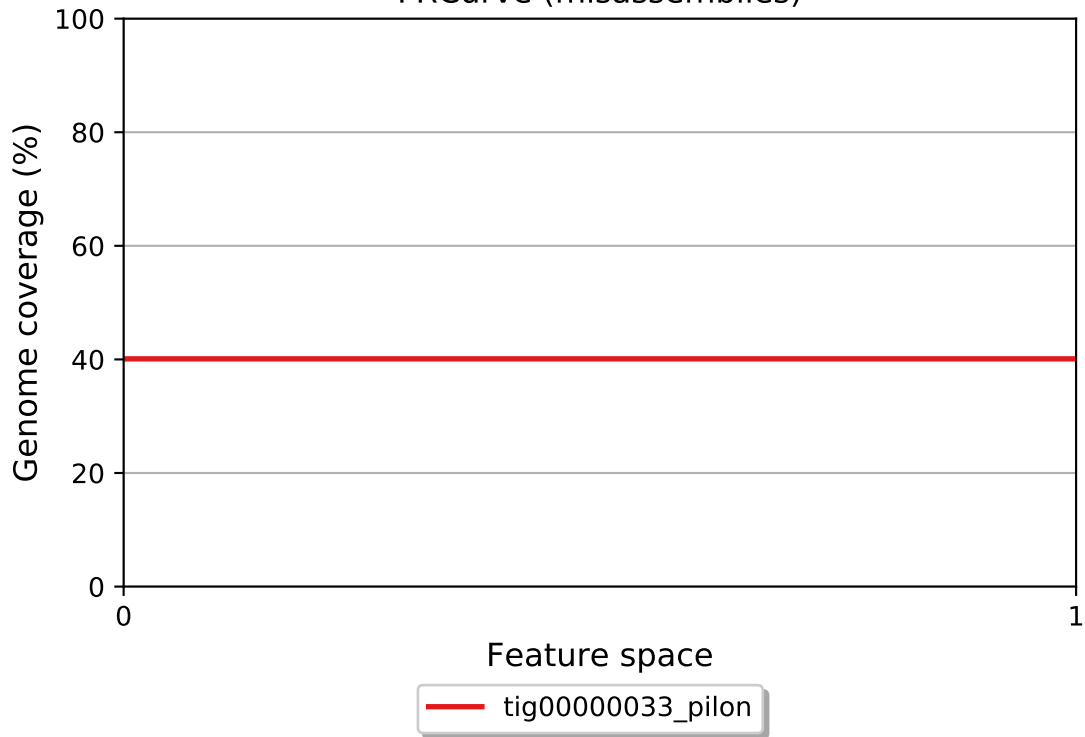
tig00000033\_pilon



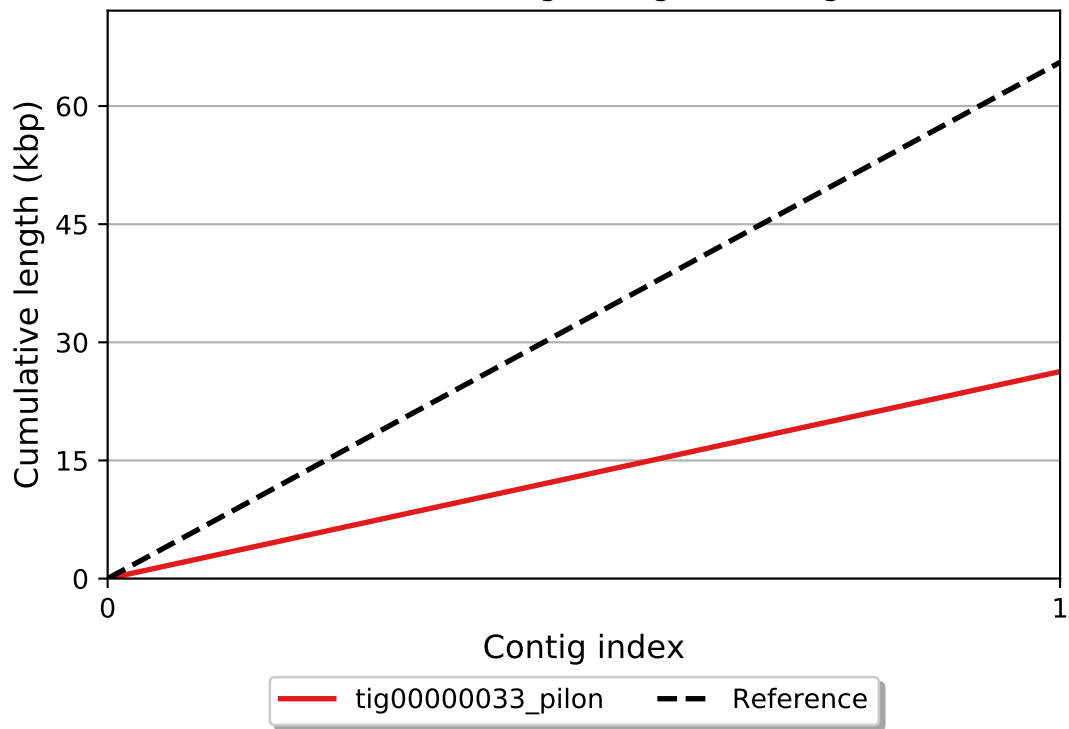
## Misassemblies



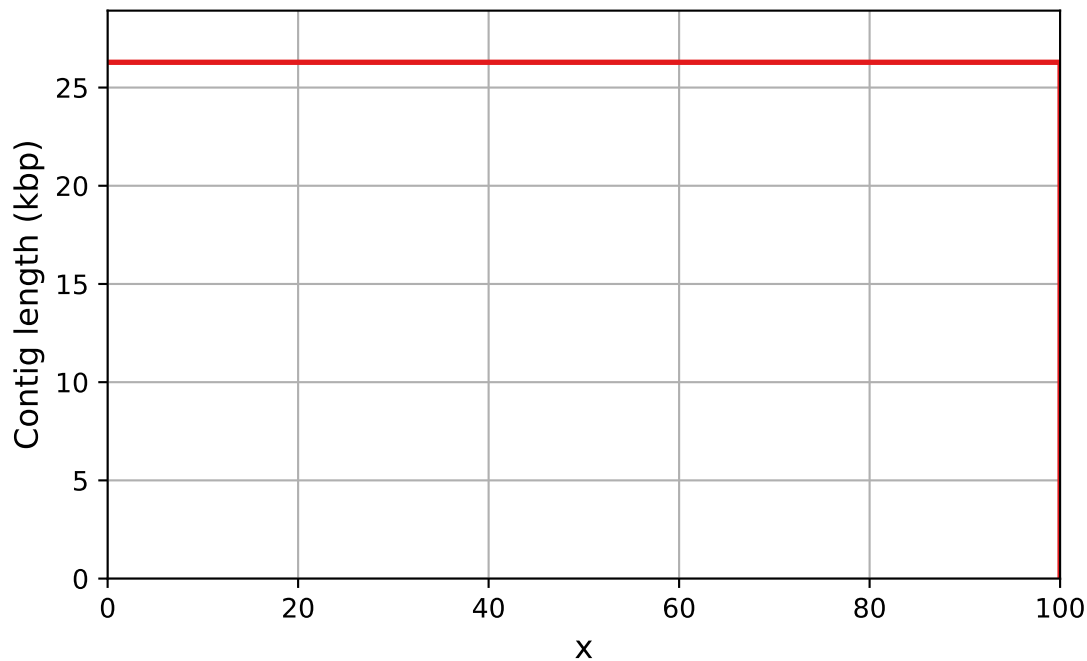
FRCurve (misassemblies)



Cumulative length (aligned contigs)

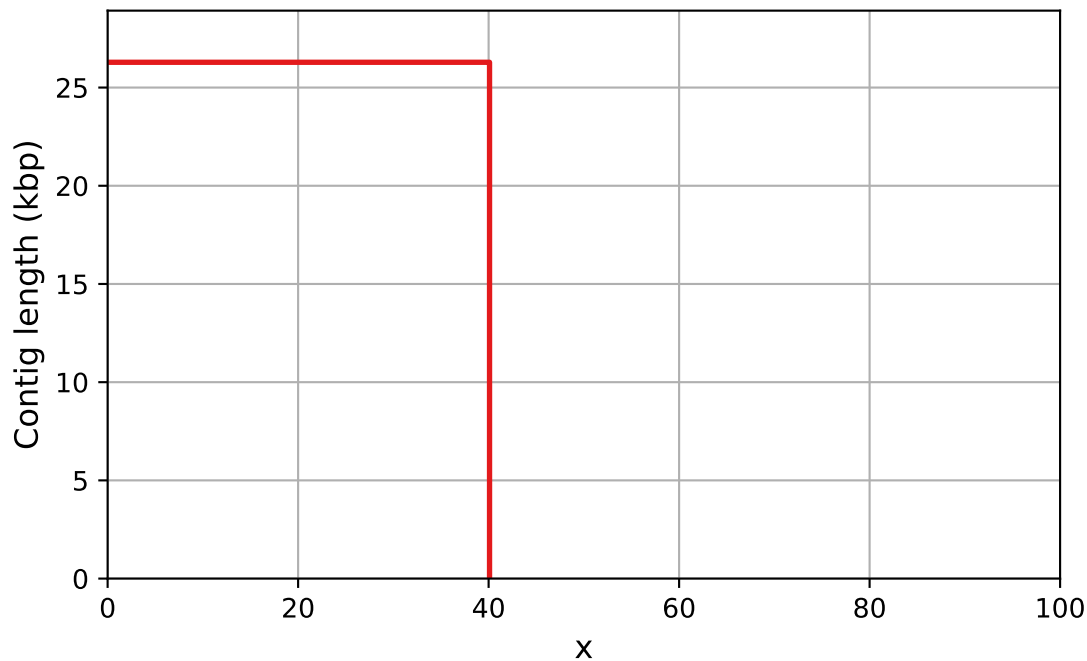


NAx



— tig00000033\_pilon

# NGAx



— tig00000033\_pilon