

Report

	pilon_assembly_improvement
# contigs (>= 0 bp)	688
# contigs (>= 1000 bp)	688
# contigs (>= 5000 bp)	596
# contigs (>= 10000 bp)	456
# contigs (>= 25000 bp)	170
# contigs (>= 50000 bp)	92
Total length (>= 0 bp)	26279748
Total length (>= 1000 bp)	26279748
Total length (>= 5000 bp)	25984908
Total length (>= 10000 bp)	24906596
Total length (>= 25000 bp)	20525590
Total length (>= 50000 bp)	17928984
# contigs	688
Largest contig	788557
Total length	26279748
Reference length	715230256
GC (%)	31.70
Reference GC (%)	32.64
N50	180832
N75	29024
L50	40
L75	140
# misassemblies	266
# misassembled contigs	144
Misassembled contigs length	10323389
# local misassemblies	447
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	29
# unaligned contigs	7 + 166 part
Unaligned length	1051695
Genome fraction (%)	3.070
Duplication ratio	1.154
# N's per 100 kbp	0.00
# mismatches per 100 kbp	590.51
# indels per 100 kbp	196.47
Largest alignment	788557
Total aligned length	25149133
NA50	102674
NGA50	-
NA75	22528
LA50	56
LA75	203

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

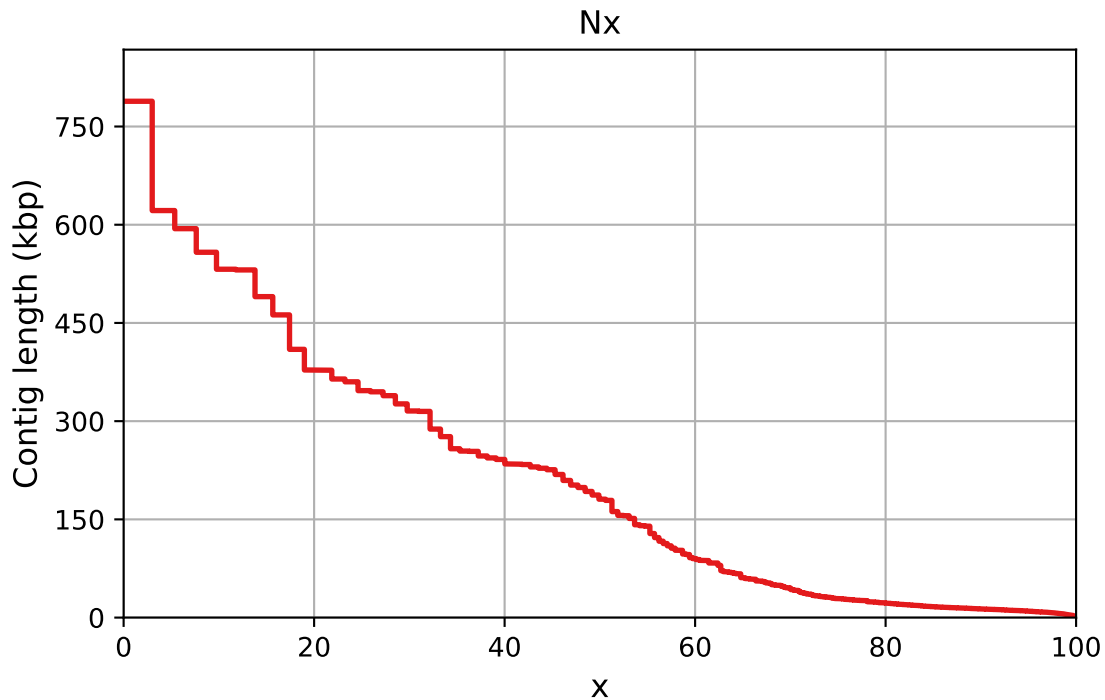
	pilon_assembly_improvement
# misassemblies	266
# contig misassemblies	266
# c. relocations	130
# c. translocations	134
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	144
Misassembled contigs length	10323389
# local misassemblies	447
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	29
# mismatches	129108
# indels	42955
# indels (<= 5 bp)	40203
# indels (> 5 bp)	2752
Indels length	98430

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

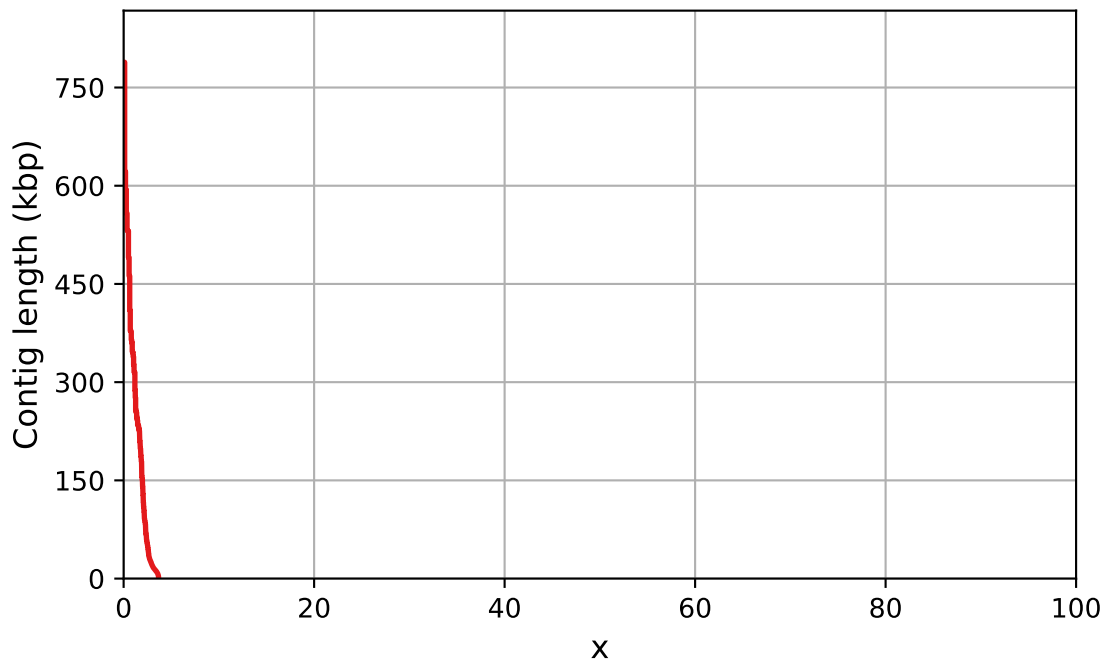
	pilon_assembly_improvement
# fully unaligned contigs	7
Fully unaligned length	44719
# partially unaligned contigs	166
Partially unaligned length	1006976
# N's	0

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).

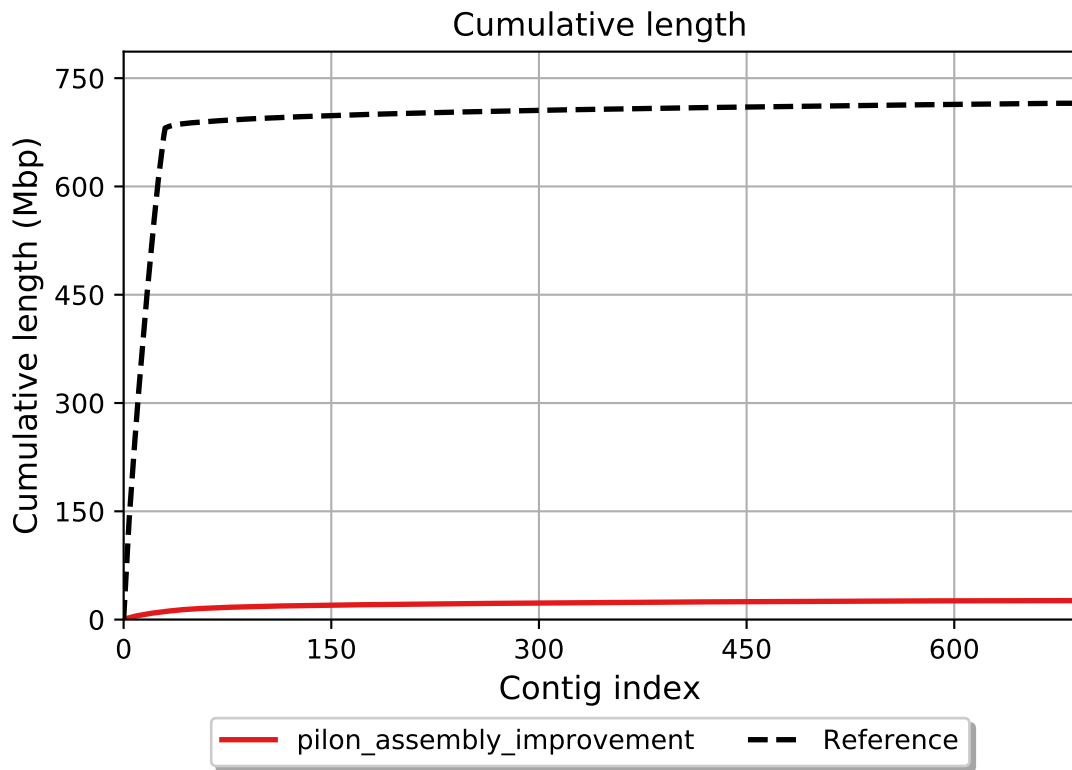


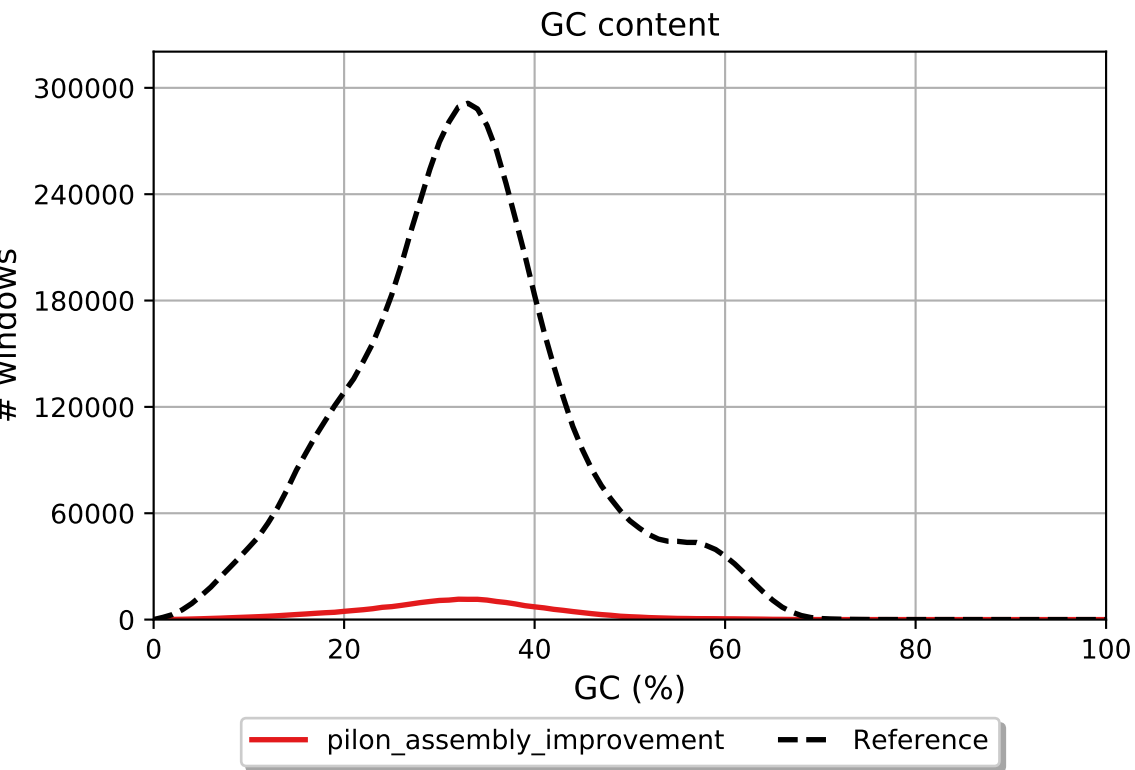
pilon_assembly_improvement

NGx

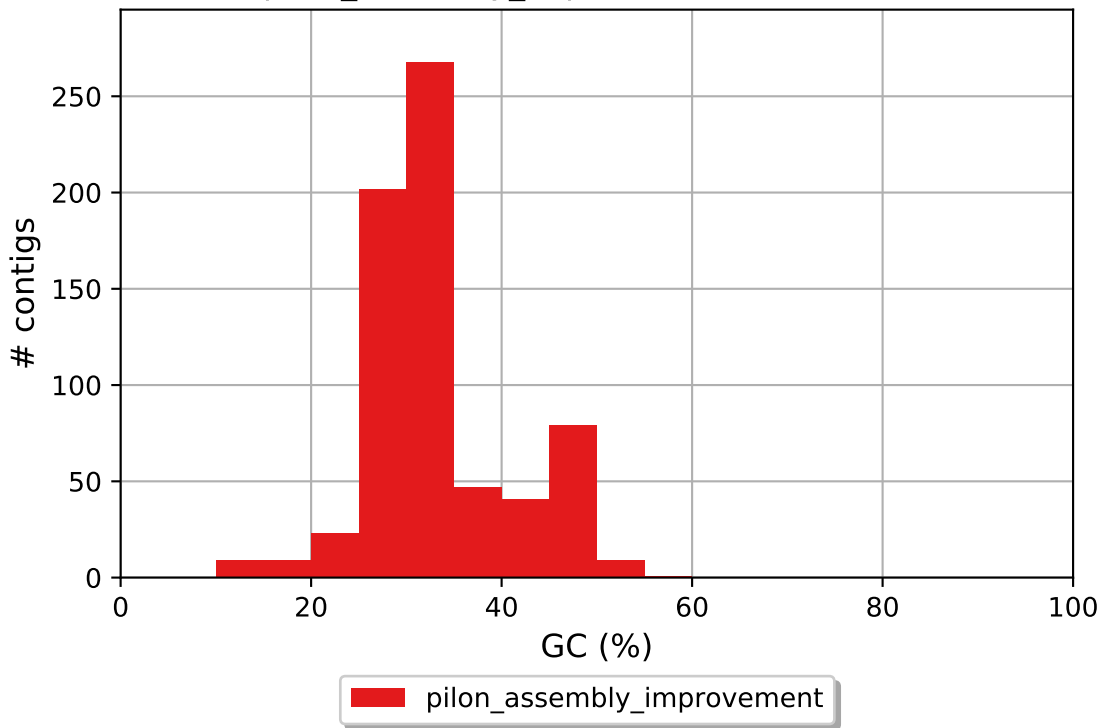


— pilon_assembly_improvement

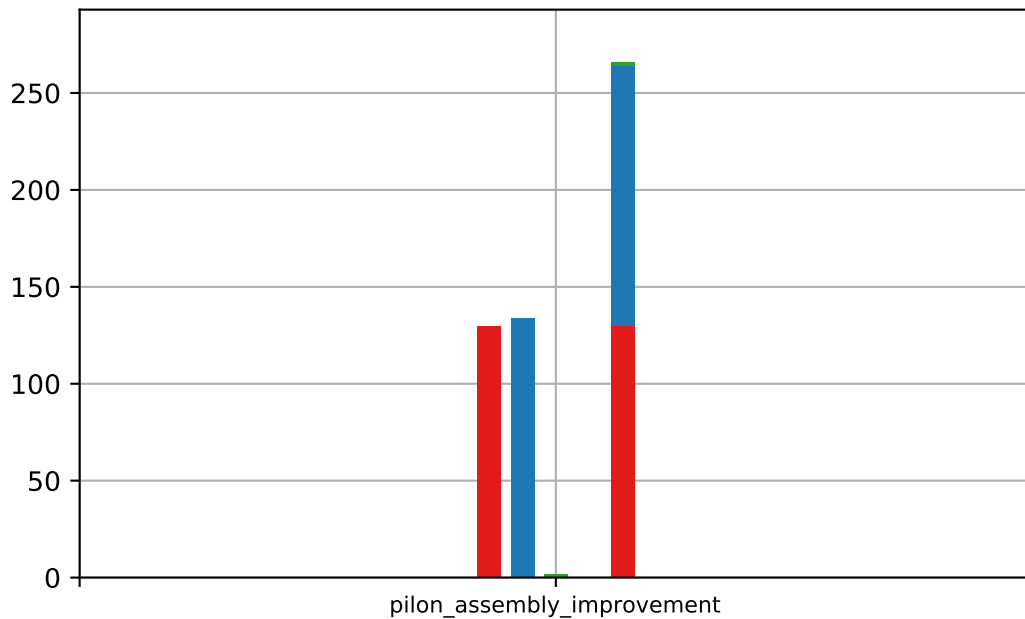




pilon_assembly_improvement GC content



Misassemblies



relocations

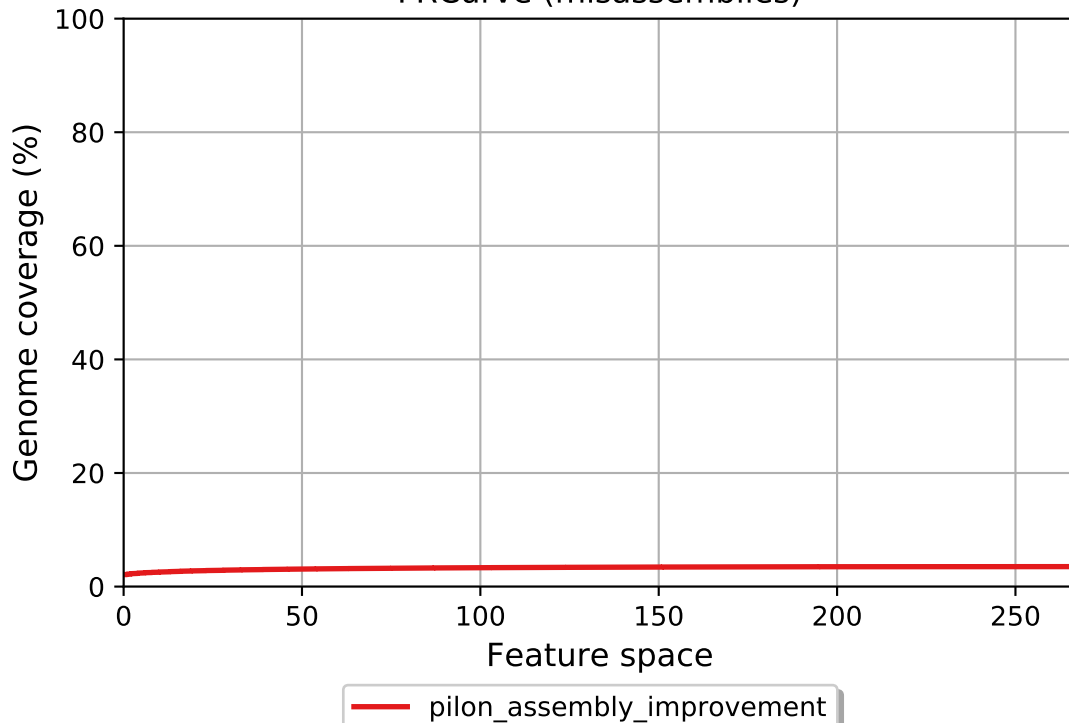


translocations

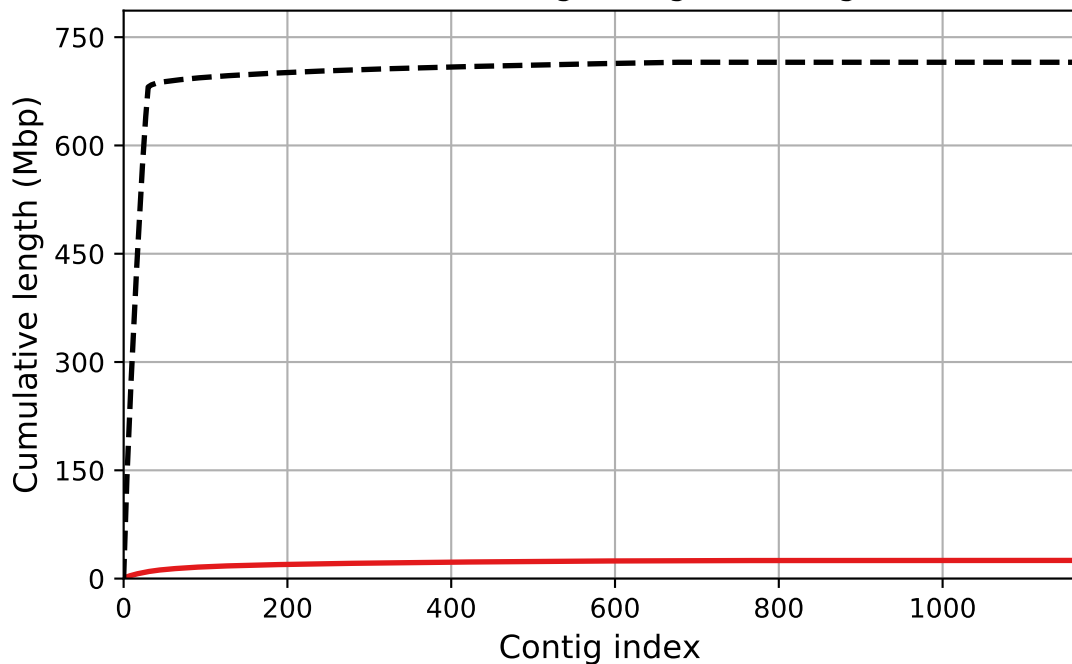


inversions

FRCurve (misassemblies)

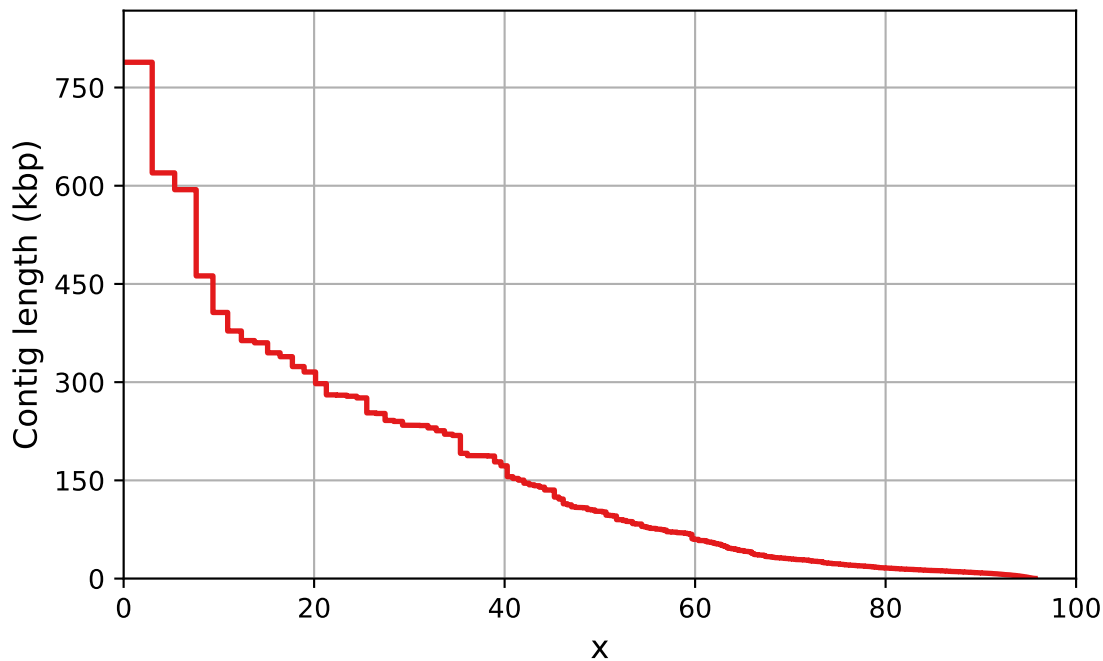


Cumulative length (aligned contigs)



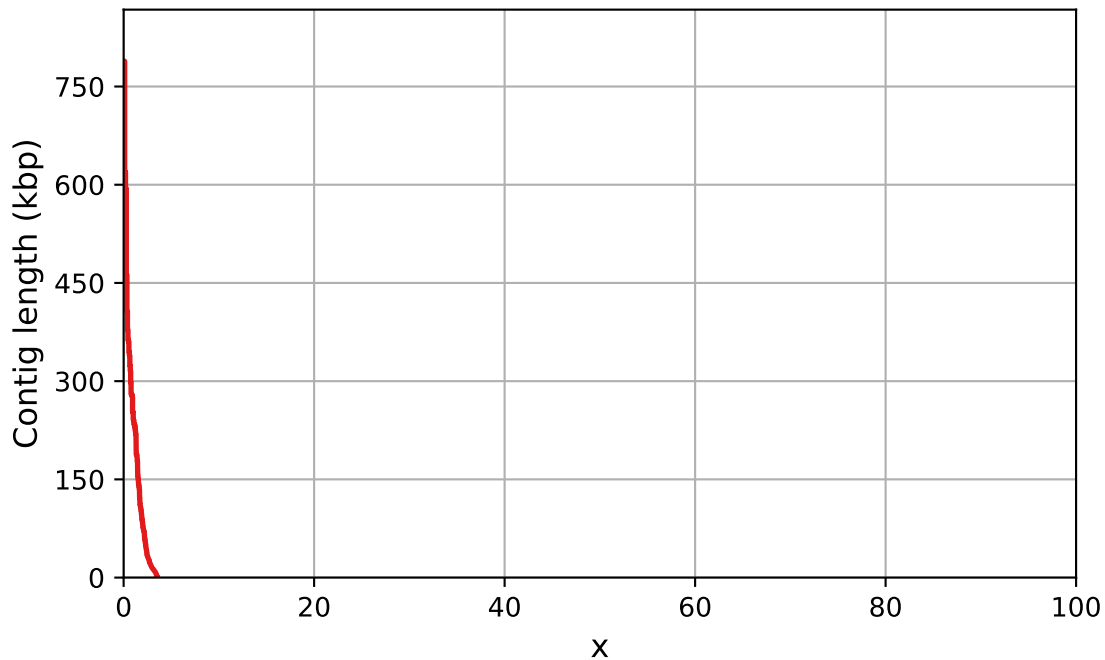
— pilon_assembly_improvement - - Reference

NAx



— pilon_assembly_improvement

NGAx



— pilon_assembly_improvement