

Report

	pilon
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	6
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3126531
Total length (>= 1000 bp)	3126531
Total length (>= 5000 bp)	3126531
Total length (>= 10000 bp)	3098699
Total length (>= 25000 bp)	3087299
Total length (>= 50000 bp)	2992688
# contigs	9
Largest contig	2773702
Total length	3126531
Reference length	3151876
GC (%)	37.80
Reference GC (%)	37.71
N50	2773702
NG50	2773702
N75	2773702
NG75	2773702
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	28
# misassembled contigs	7
Misassembled contigs length	3090258
# 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 (%)	97.825
Duplication ratio	1.014
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.40
# indels per 100 kbp	3.63
Largest alignment	1084784
Total aligned length	3120924
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

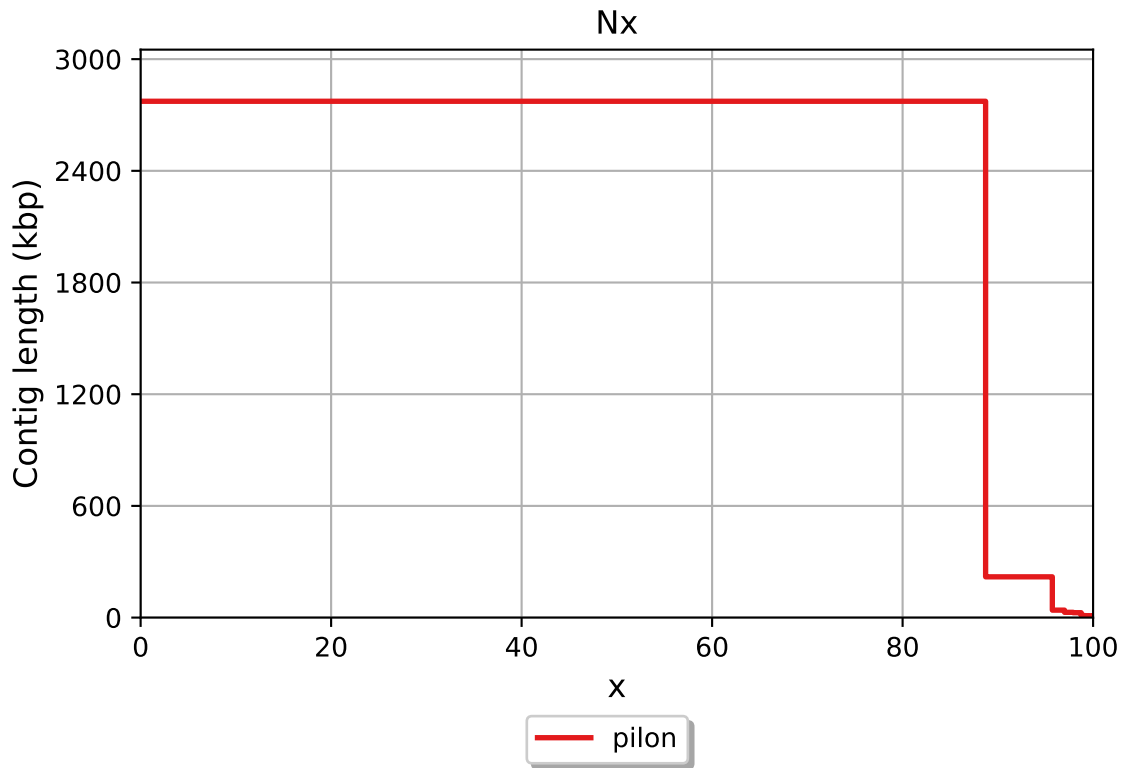
	pilon
# misassemblies	28
# contig misassemblies	28
# c. relocations	4
# c. translocations	24
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	7
Misassembled contigs length	3090258
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	999
# indels	112
# indels (<= 5 bp)	110
# indels (> 5 bp)	2
Indels length	151

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).

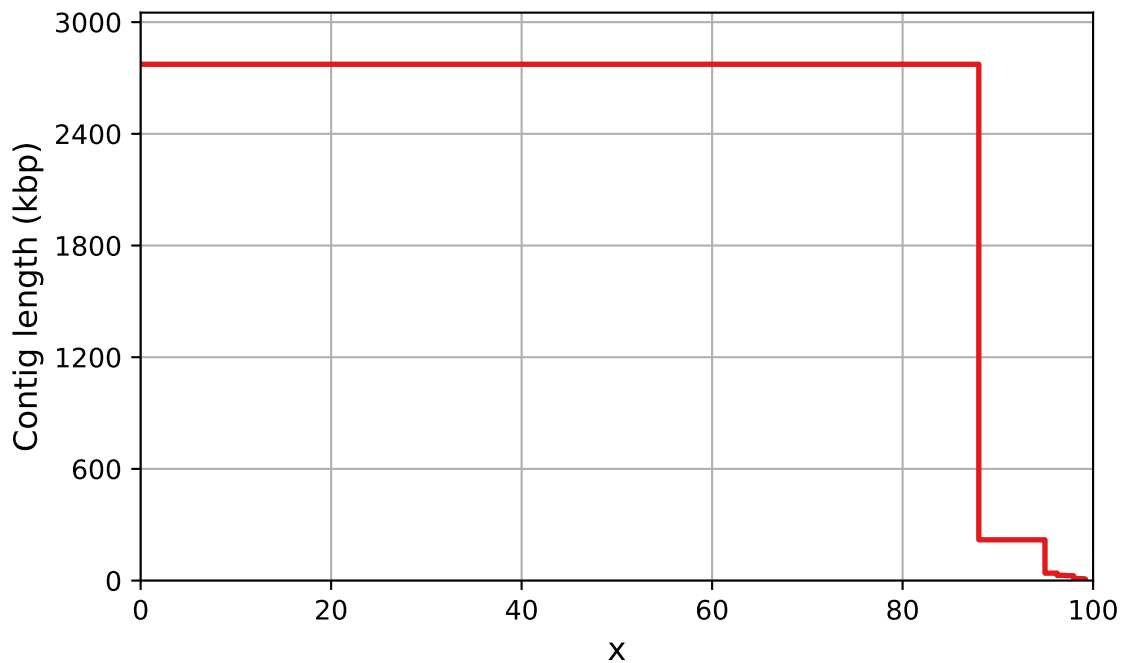
Unaligned report

	pilon
# 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).

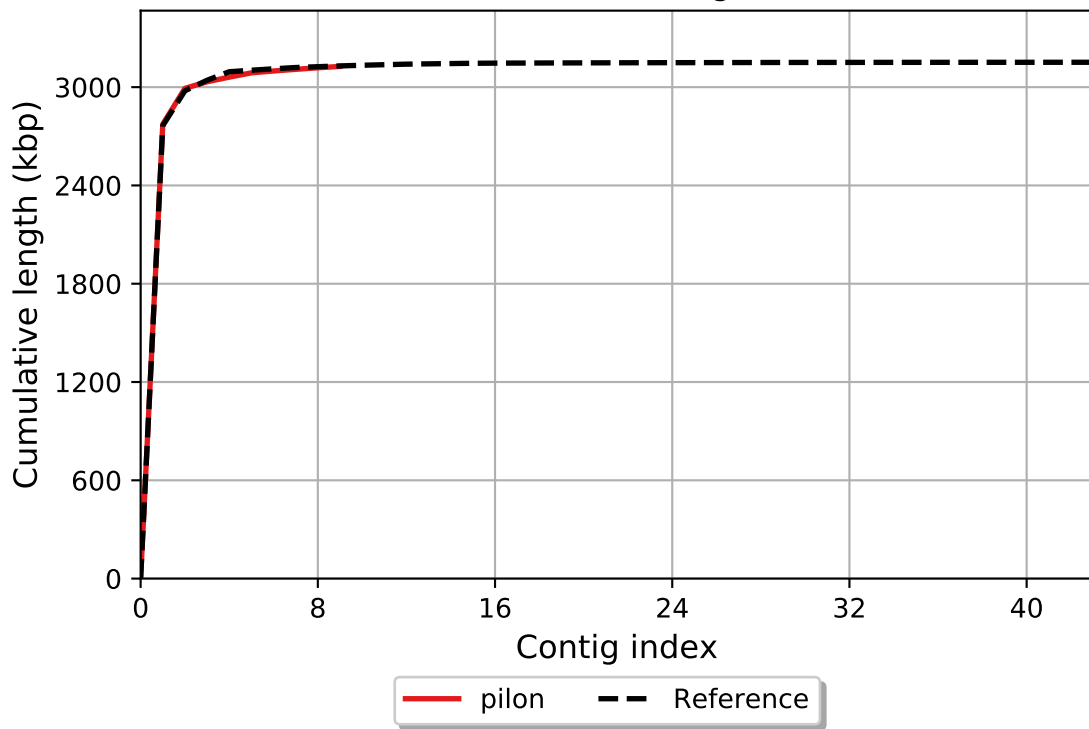


NGx

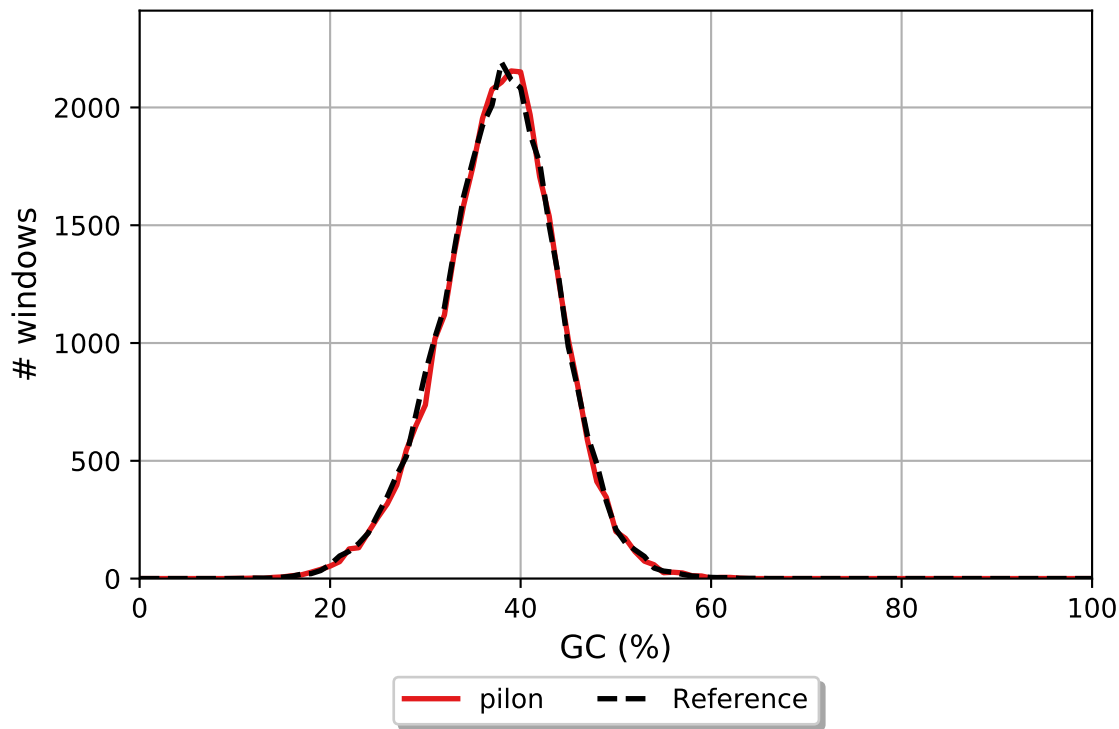


pilon

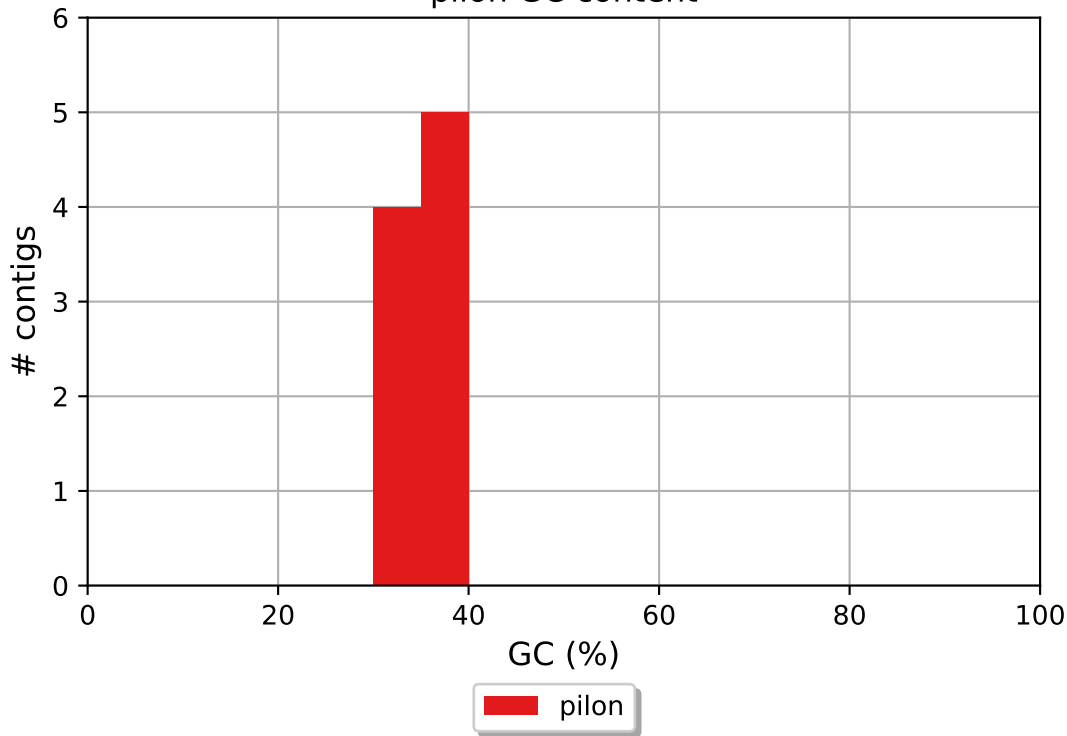
Cumulative length



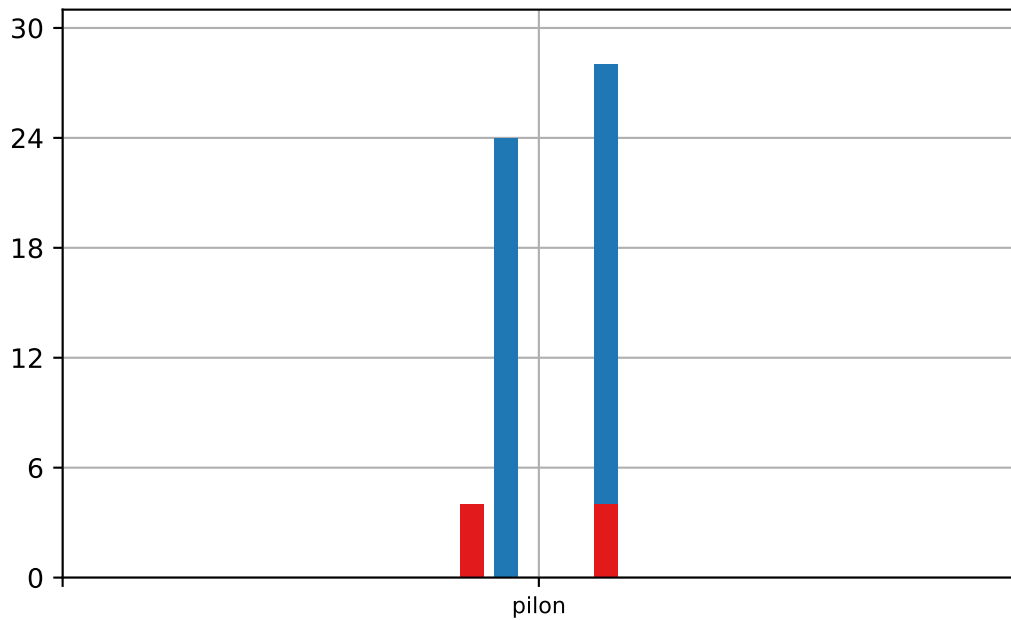
GC content



pilon GC content



Misassemblies

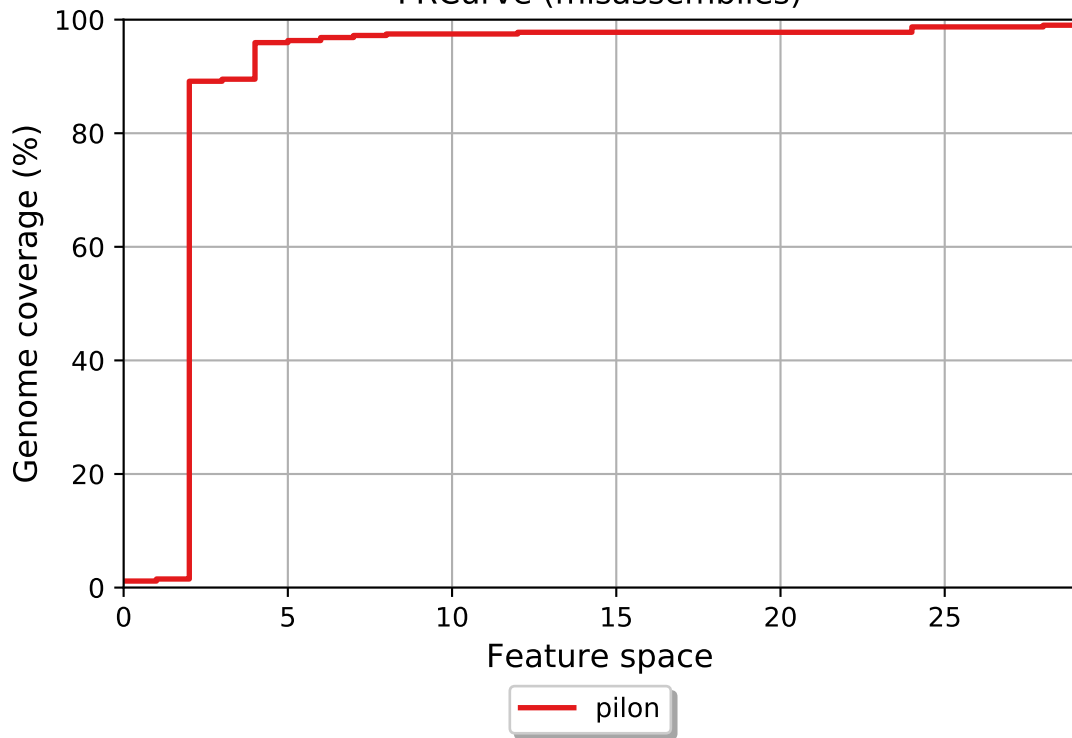


relocations

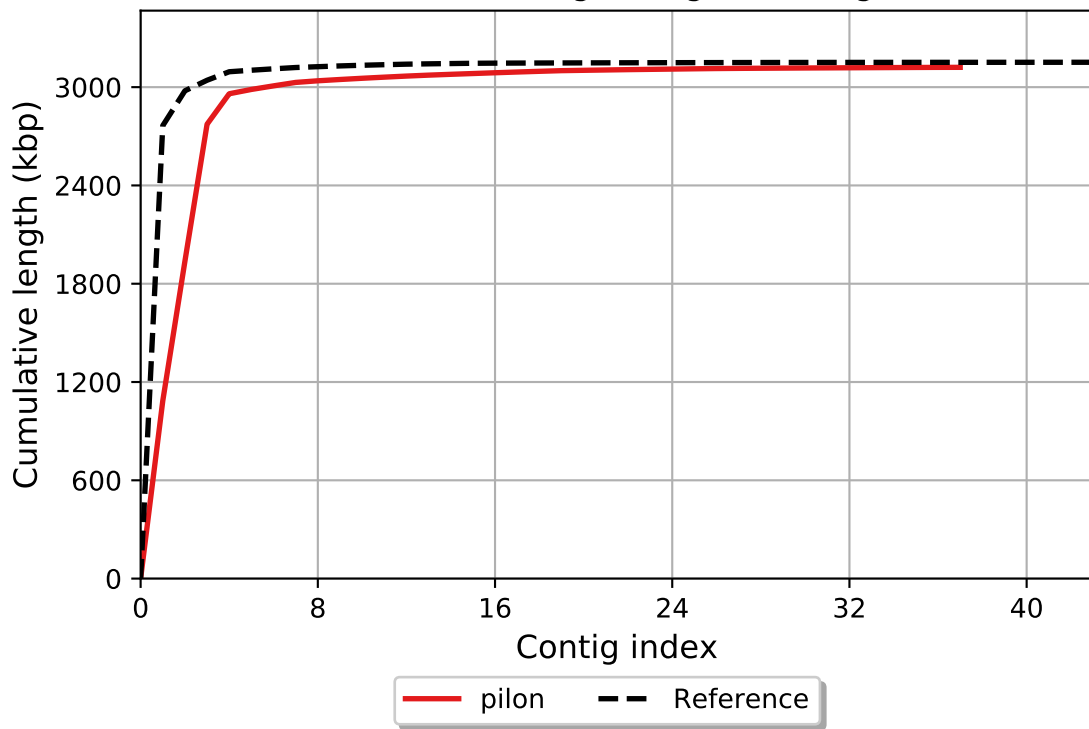


translocations

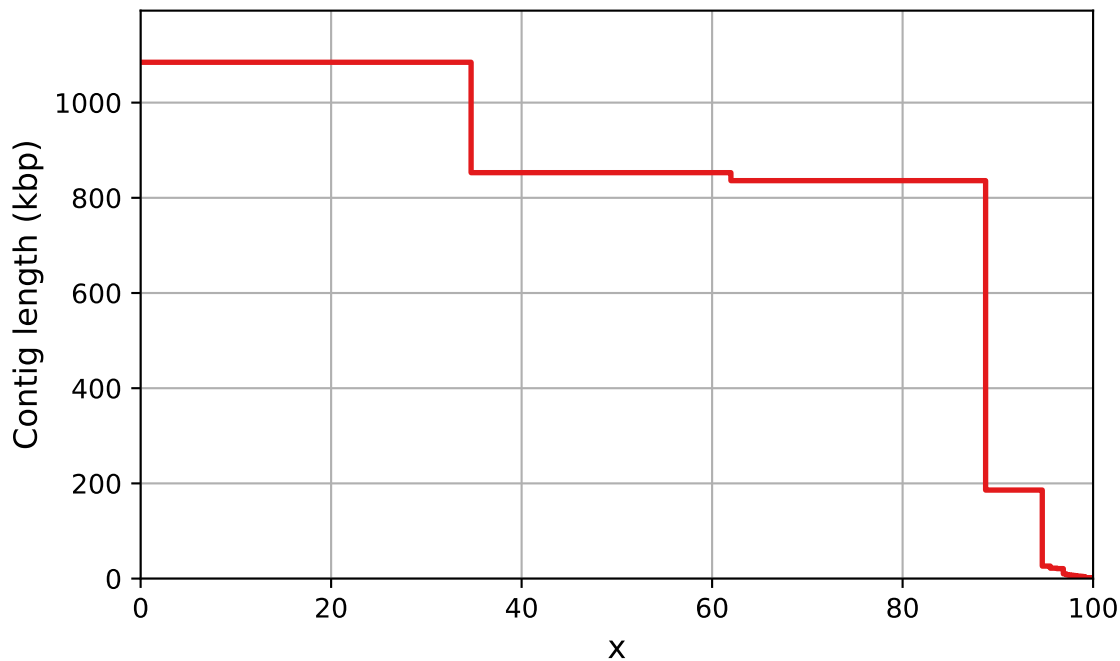
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



pilon

NGAx

