

## Report

	pilon_not_trimmed	pilon
# contigs ( $\geq 0$ bp)	9	9
# contigs ( $\geq 1000$ bp)	9	9
# contigs ( $\geq 5000$ bp)	9	9
# contigs ( $\geq 10000$ bp)	8	8
# contigs ( $\geq 25000$ bp)	5	5
# contigs ( $\geq 50000$ bp)	2	2
Total length ( $\geq 0$ bp)	3159597	3159596
Total length ( $\geq 1000$ bp)	3159597	3159596
Total length ( $\geq 5000$ bp)	3159597	3159596
Total length ( $\geq 10000$ bp)	3149801	3149801
Total length ( $\geq 25000$ bp)	3099716	3099716
Total length ( $\geq 50000$ bp)	3006371	3006371
# contigs	9	9
Largest contig	2775723	2775723
Total length	3159597	3159596
Reference length	3168410	3168410
GC (%)	37.78	37.78
Reference GC (%)	37.70	37.70
N50	2775723	2775723
NG50	2775723	2775723
N75	2775723	2775723
NG75	2775723	2775723
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	7	7
# misassembled contigs	5	5
Misassembled contigs length	3078924	3078924
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 0 part	0 + 0 part
Unaligned length	0	0
Genome fraction (%)	98.309	98.309
Duplication ratio	1.014	1.014
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	10.59	10.56
# indels per 100 kbp	8.03	7.99
Largest alignment	2149027	2149027
Total aligned length	3155598	3155597
NA50	2149027	2149027
NGA50	2149027	2149027
NA75	626696	626696
NGA75	626696	626696
LA50	1	1
LGA50	1	1
LA75	2	2
LGA75	2	2

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).

## Misassemblies report

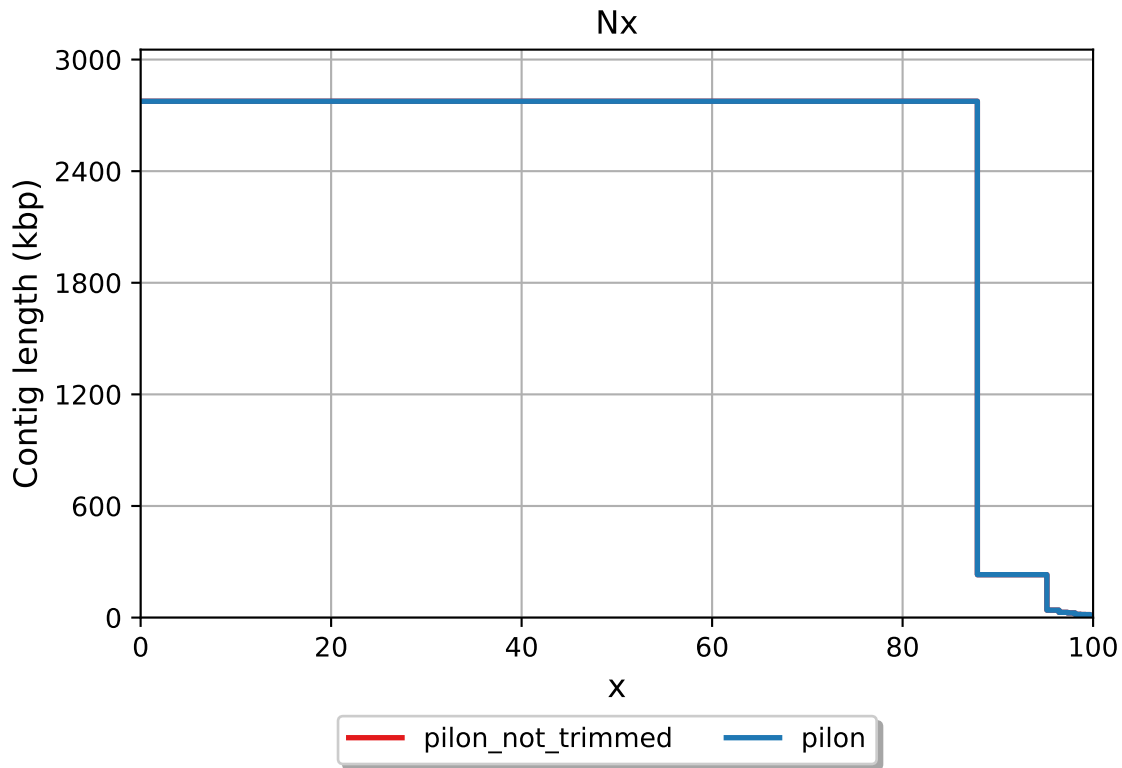
	pilon_not_trimmed	pilon
# misassemblies	7	7
# contig misassemblies	7	7
# c. relocations	5	5
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	5	5
Misassembled contigs length	3078924	3078924
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	330	329
# indels	250	249
# indels (<= 5 bp)	239	238
# indels (> 5 bp)	11	11
Indels length	434	433

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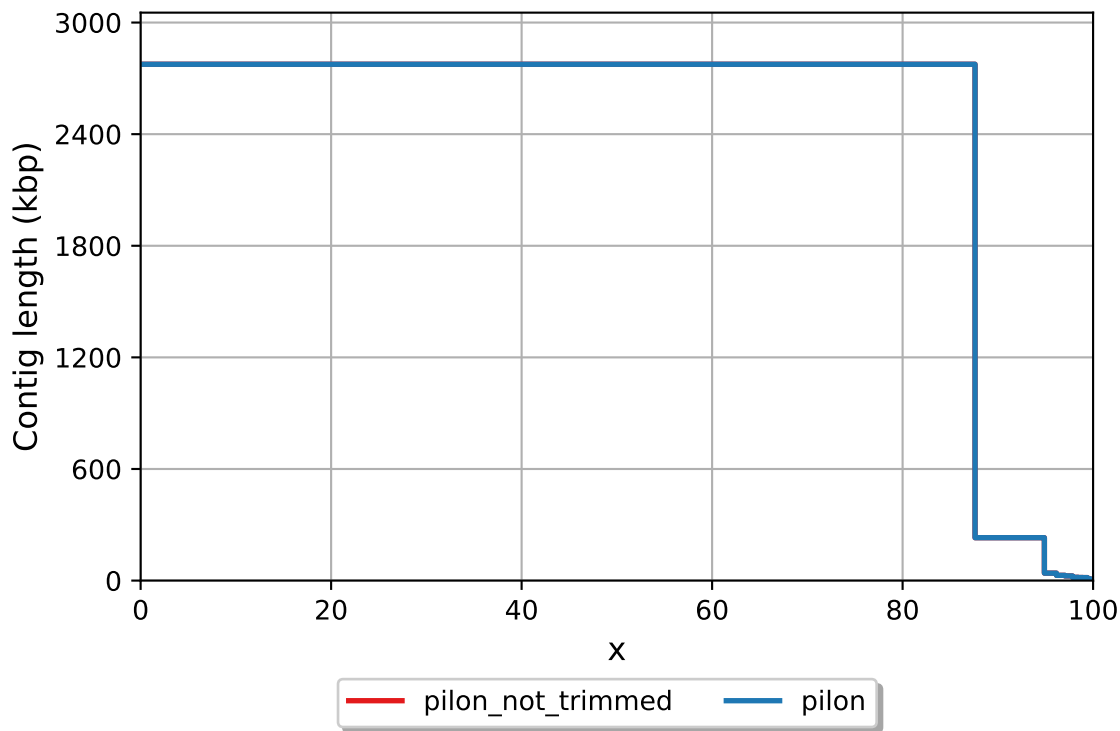
## Unaligned report

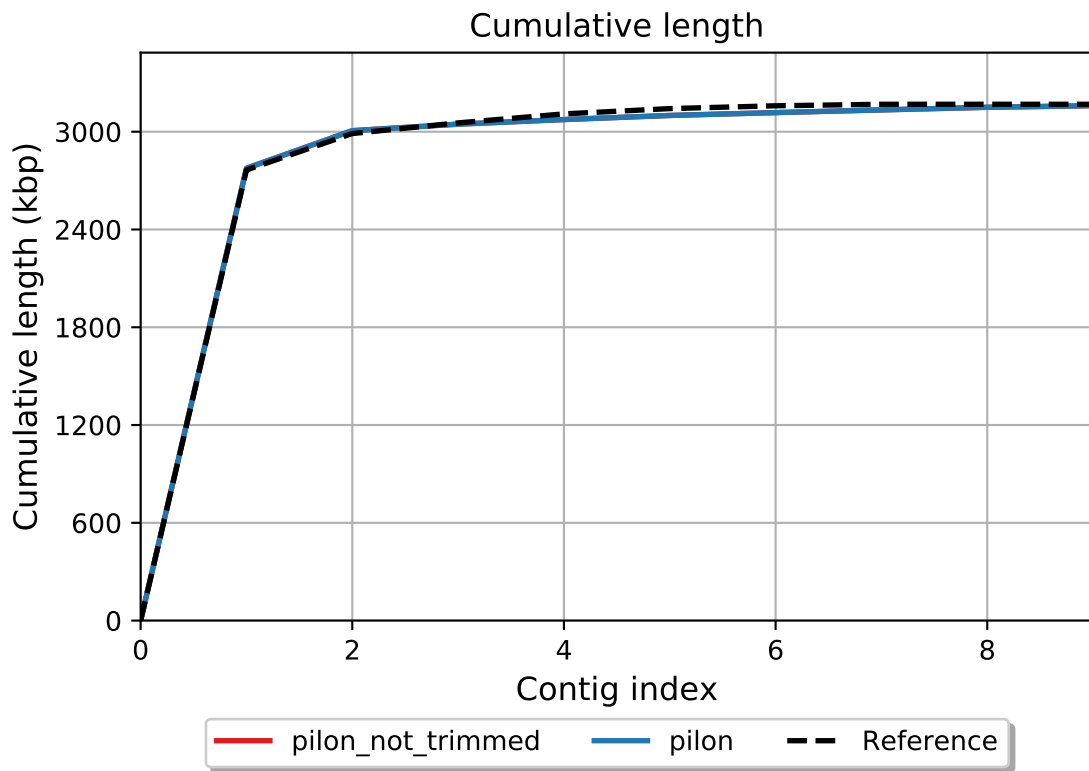
	pilon_not_trimmed	pilon
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

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).

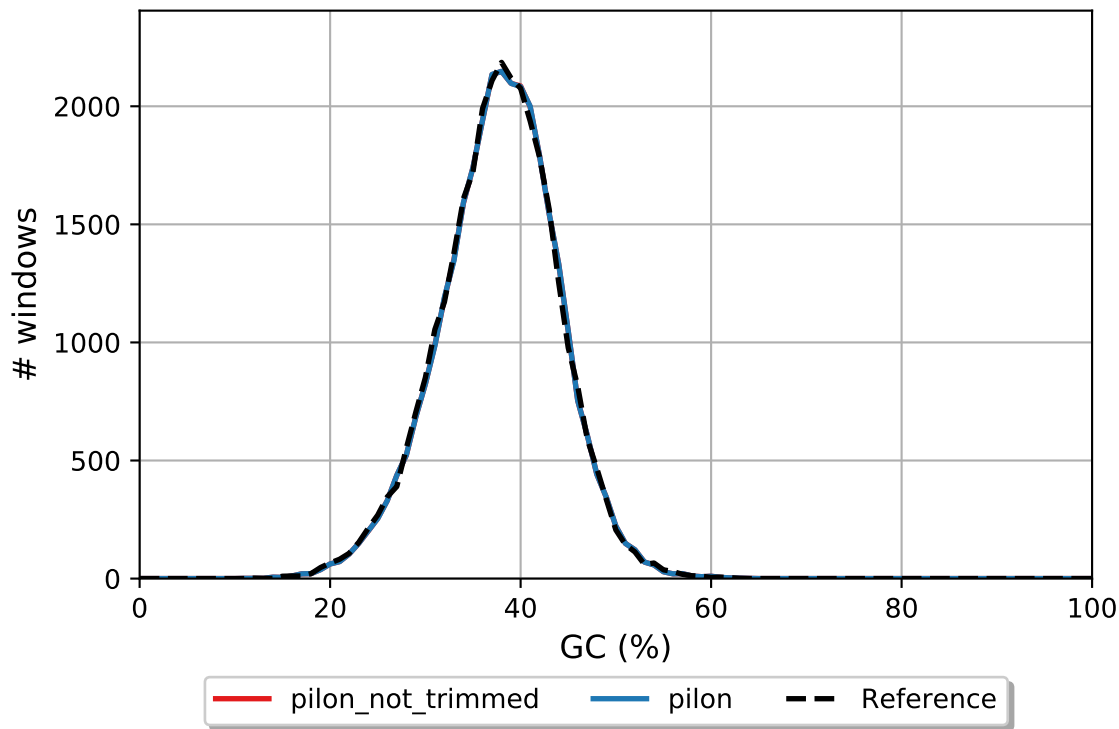


# NGx

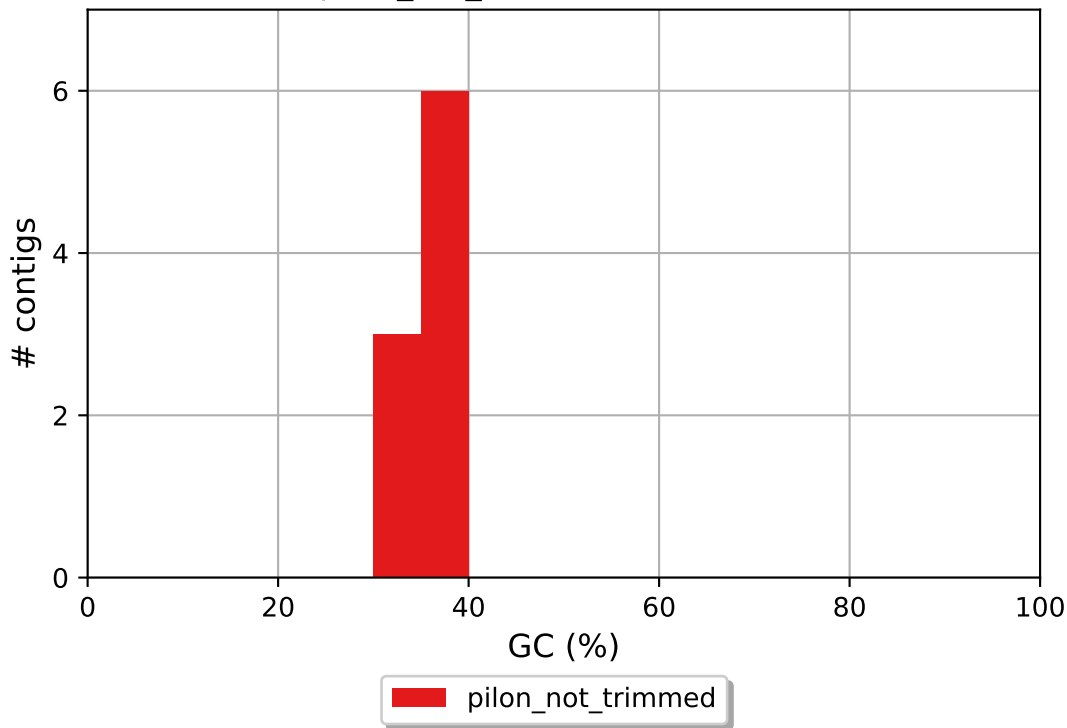




GC content

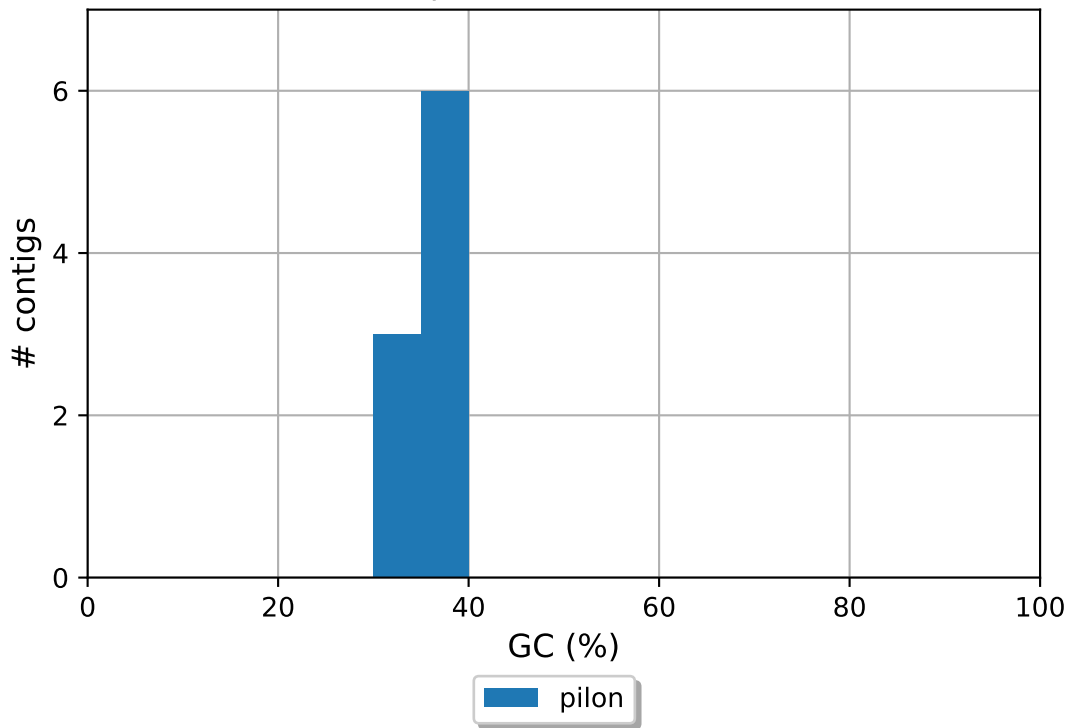


pilon\_not\_trimmed GC content

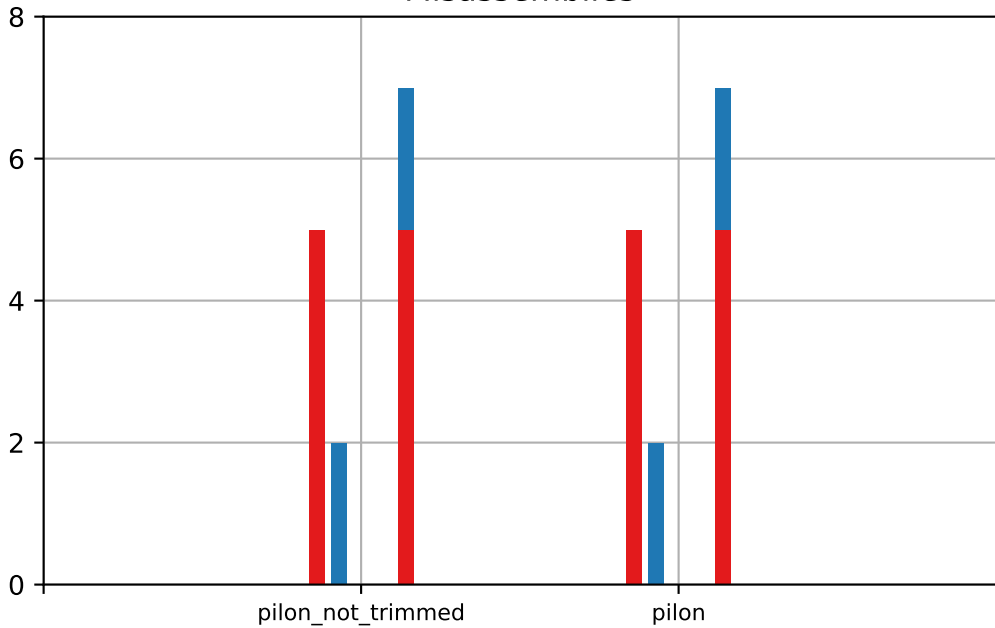




pilon GC content



## Misassemblies

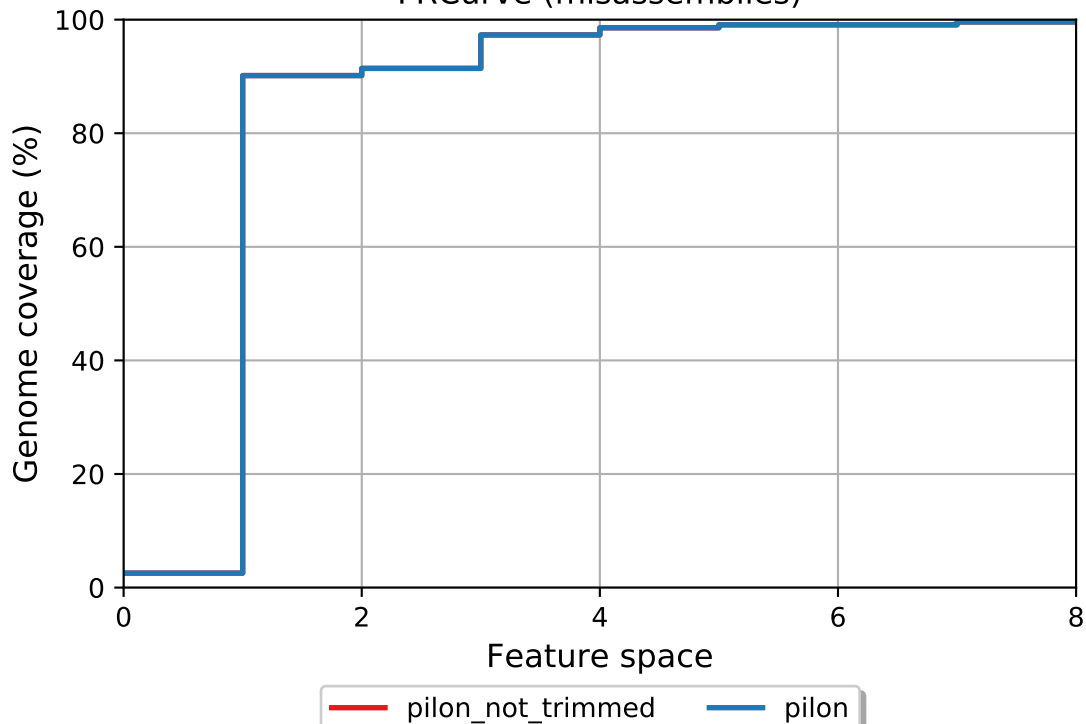


# relocations

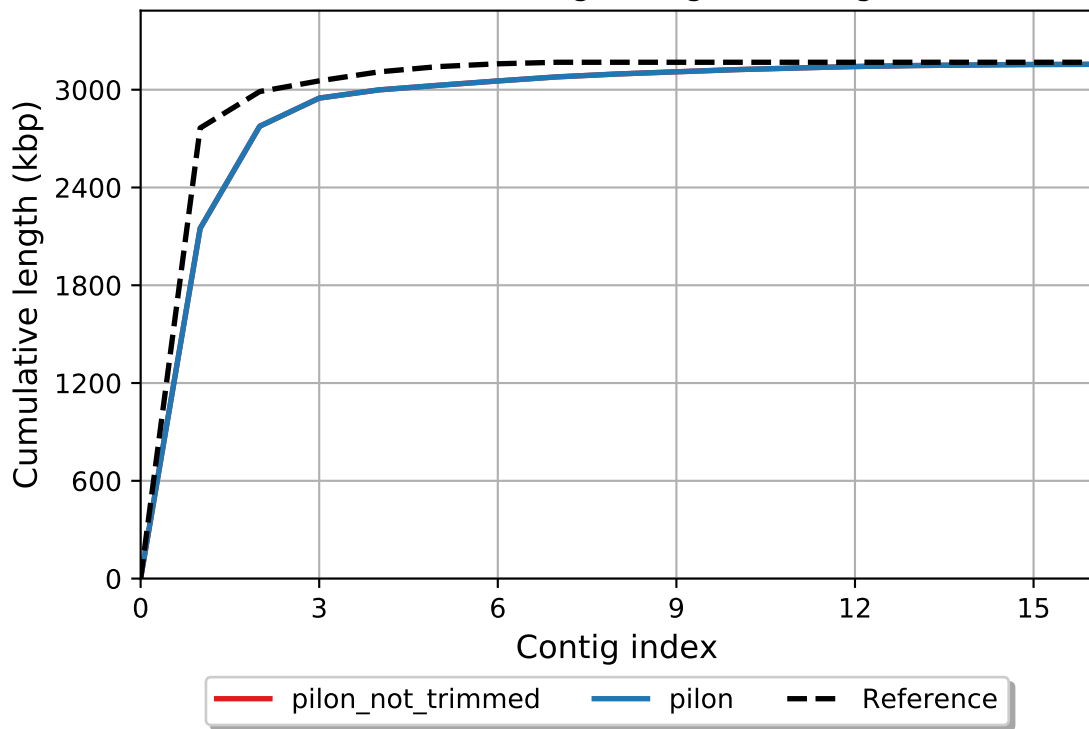


# translocations

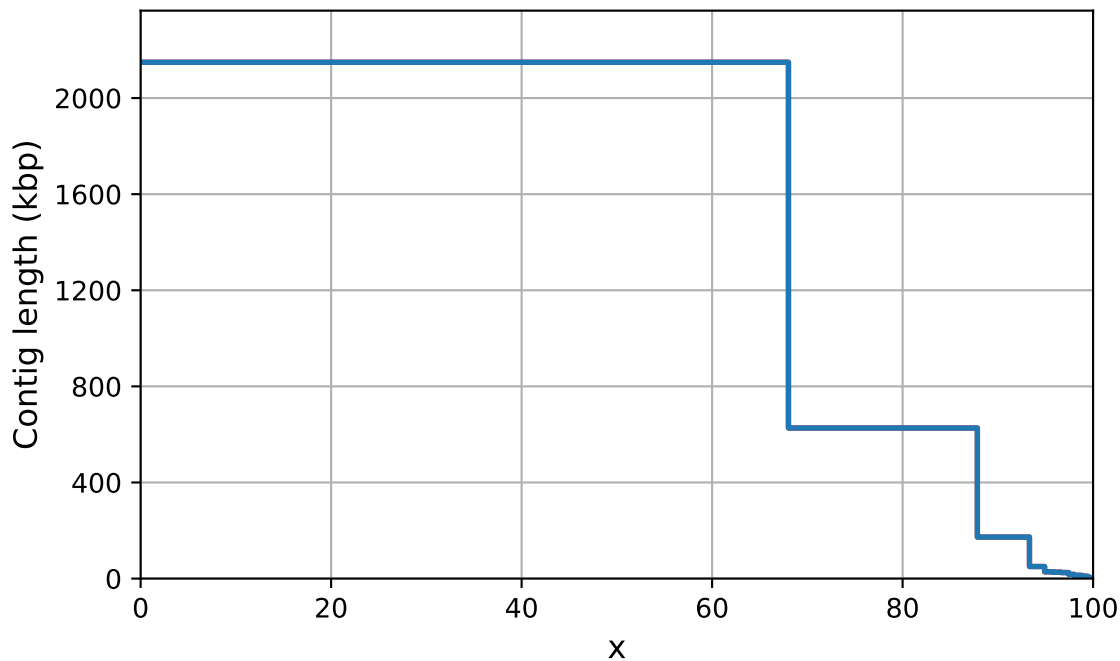
FRCurve (misassemblies)



Cumulative length (aligned contigs)

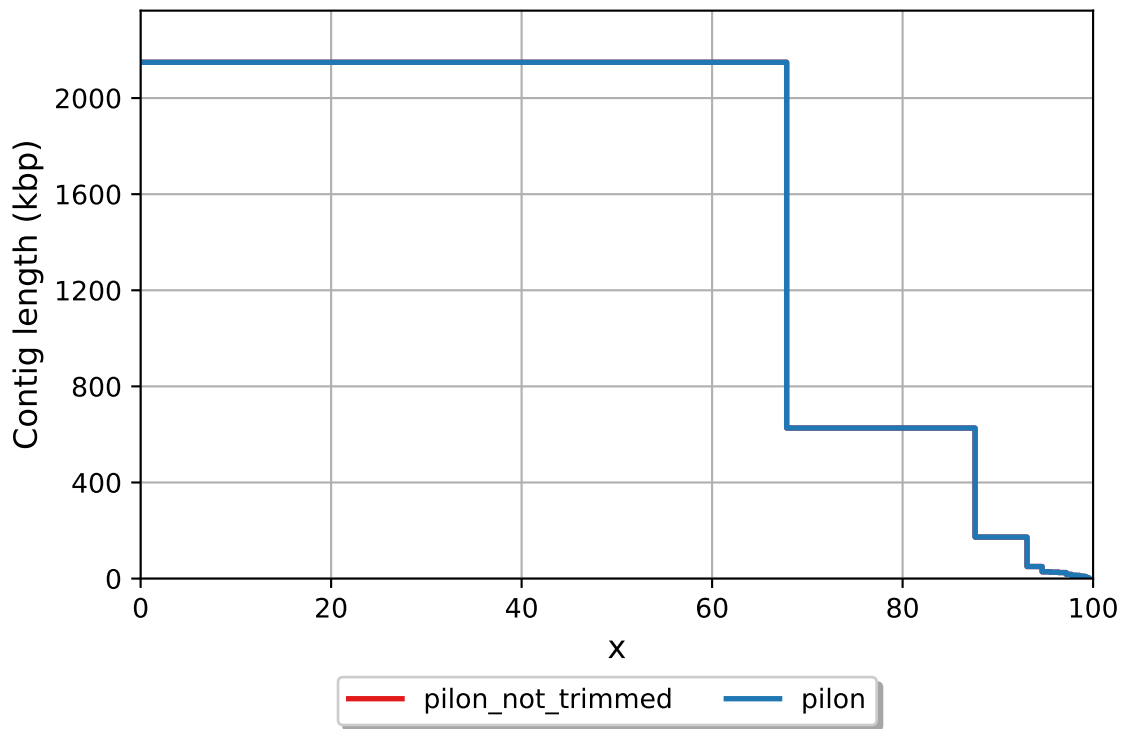


NAx

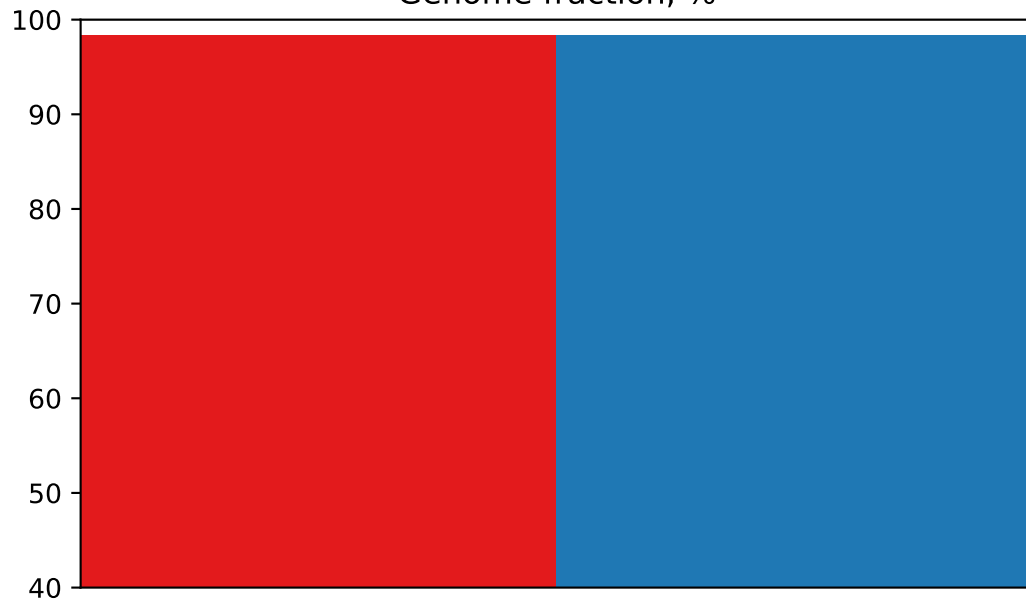


pilon\_not\_trimmed pilon

## NGAx



Genome fraction, %



pilon\_not\_trimmed



pilon