Report

	pilon
# contigs (>= 0 bp)	12
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	10
# contigs (>= 10000 bp)	10
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	4
Total length (>= 0 bp)	3192025
Total length (>= 1000 bp)	3192025
Total length (>= 5000 bp)	3185623
Total length (>= 10000 bp)	3185623
Total length (>= 25000 bp)	3141701
Total length (>= 50000 bp)	3043841
# contigs	12
Largest contig	1414516
Total length	3192025
Reference length	2919198
GC (%)	37.71
Reference GC (%)	37.88
N50	1362697
NG50	1362697
N75	1362697
NG75	1362697
L50	2
LG50	2
L75	2
LG75	2
# misassemblies	190
# misassembled contigs	2
Misassembled contigs length	2777213
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# unaligned contigs	3 + 9 part
Unaligned length	592746
Genome fraction (%)	84.985
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	398.49
# indels per 100 kbp	15.08
Largest alignment	137660
Total aligned length	2593861
NA50	24276
NGA50	29114
NA75	2923
NGA75	10307
LA50	32
LGA50	27
LA75	97
LGA75	66

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

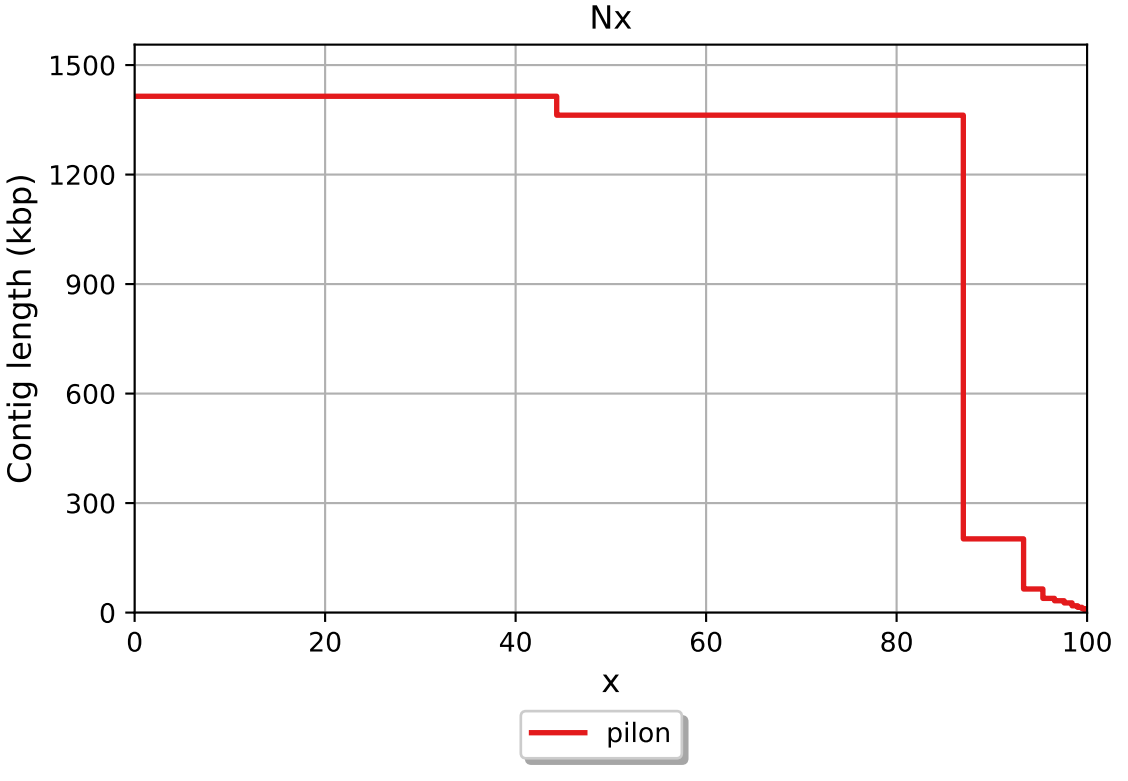
	pilon
# misassemblies	190
# contig misassemblies	190
# c. relocations	174
# c. translocations	14
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	2777213
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	7
# mismatches	9886
# indels	374
# indels (<= 5 bp)	337
# indels (> 5 bp)	37
Indels length	1464

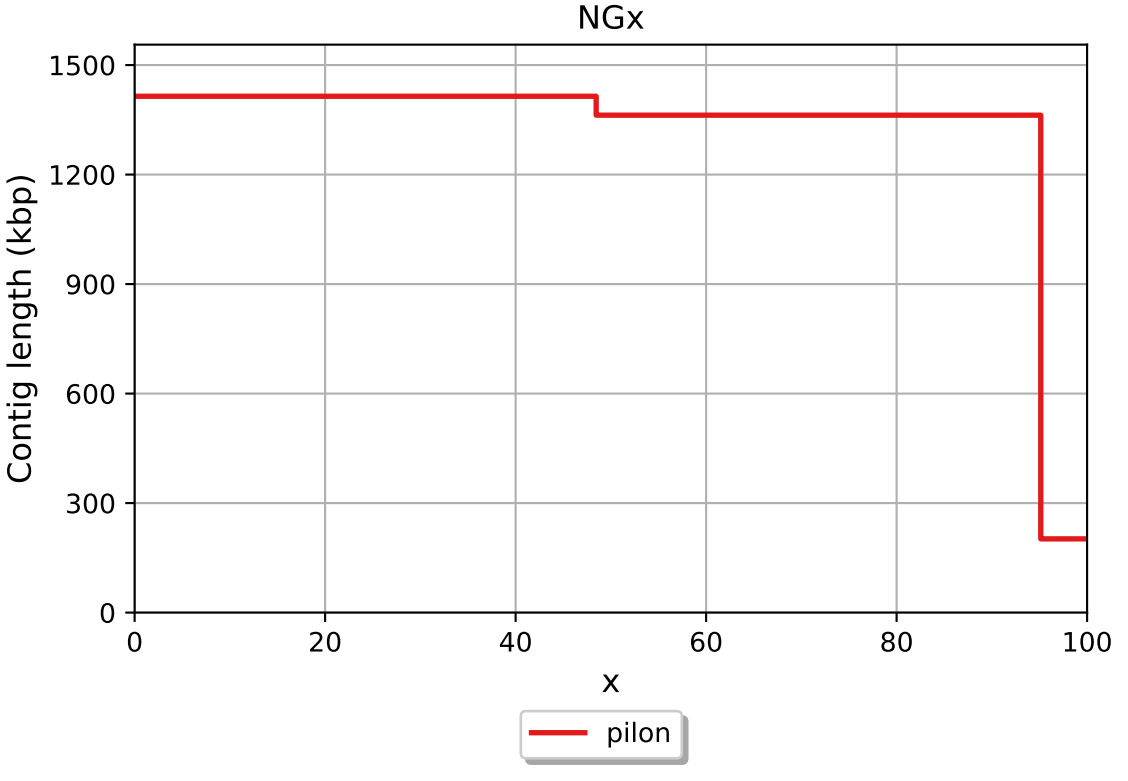
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

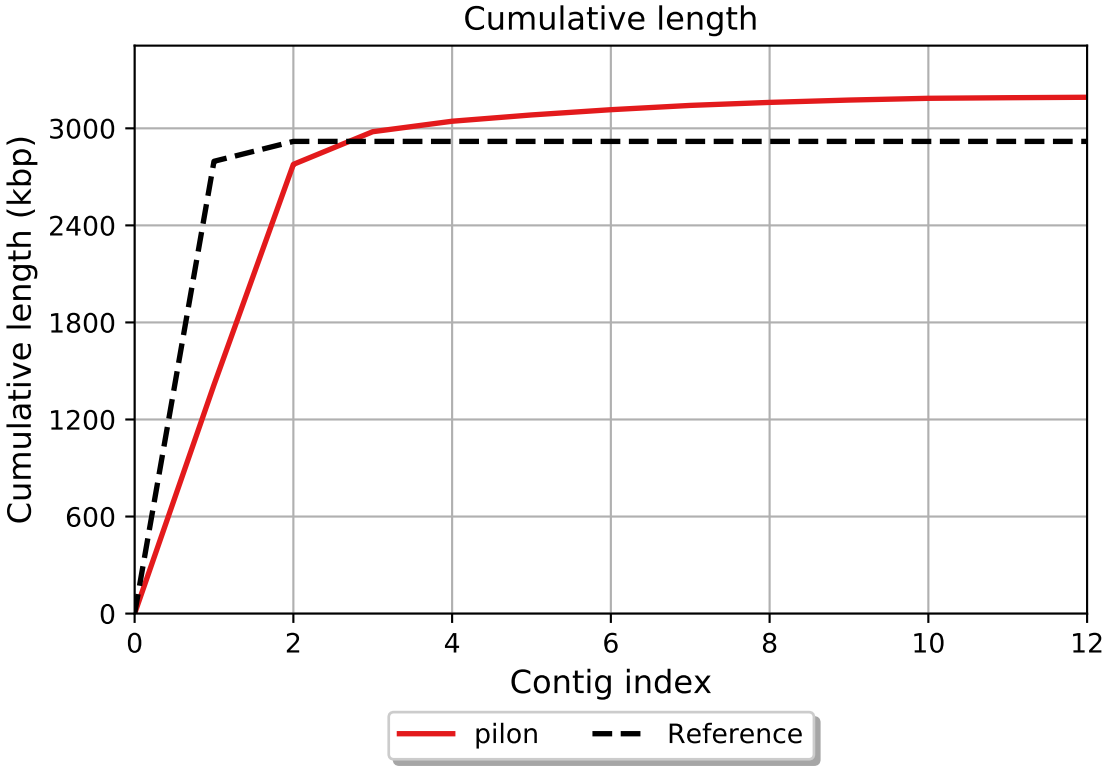
Unaligned report

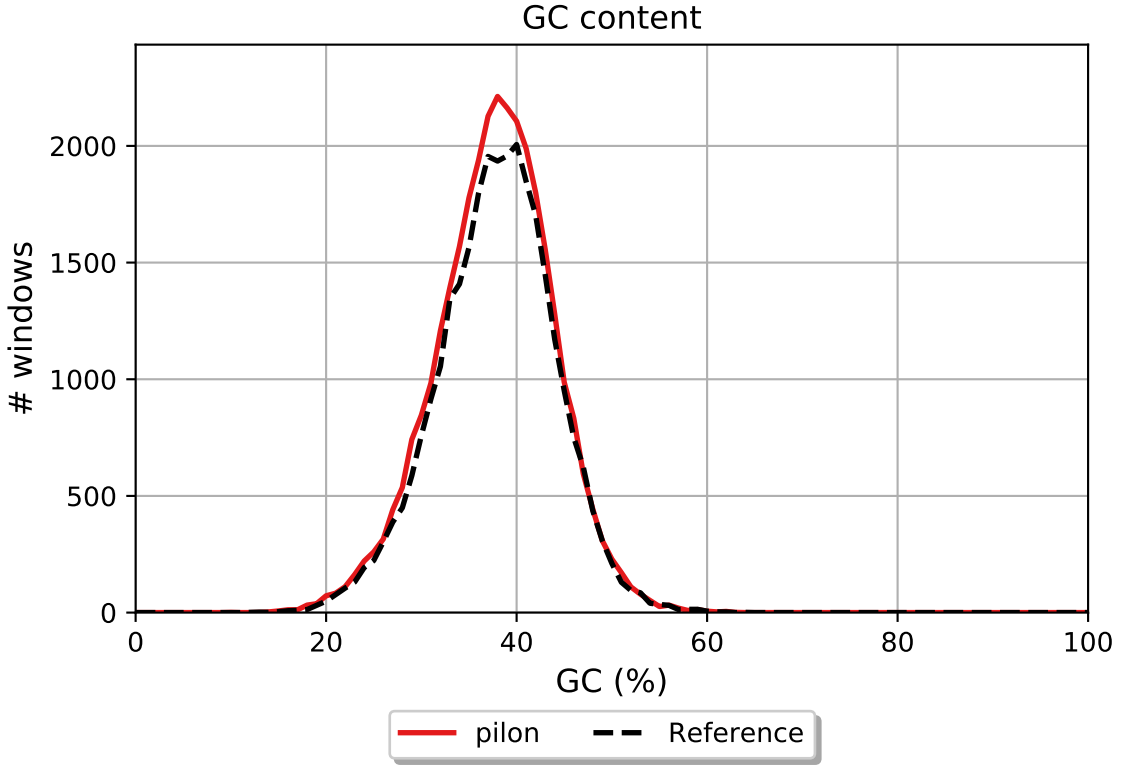
	pilon
# fully unaligned contigs	3
Fully unaligned length	25038
# partially unaligned contigs	9
Partially unaligned length	567708
# N's	0

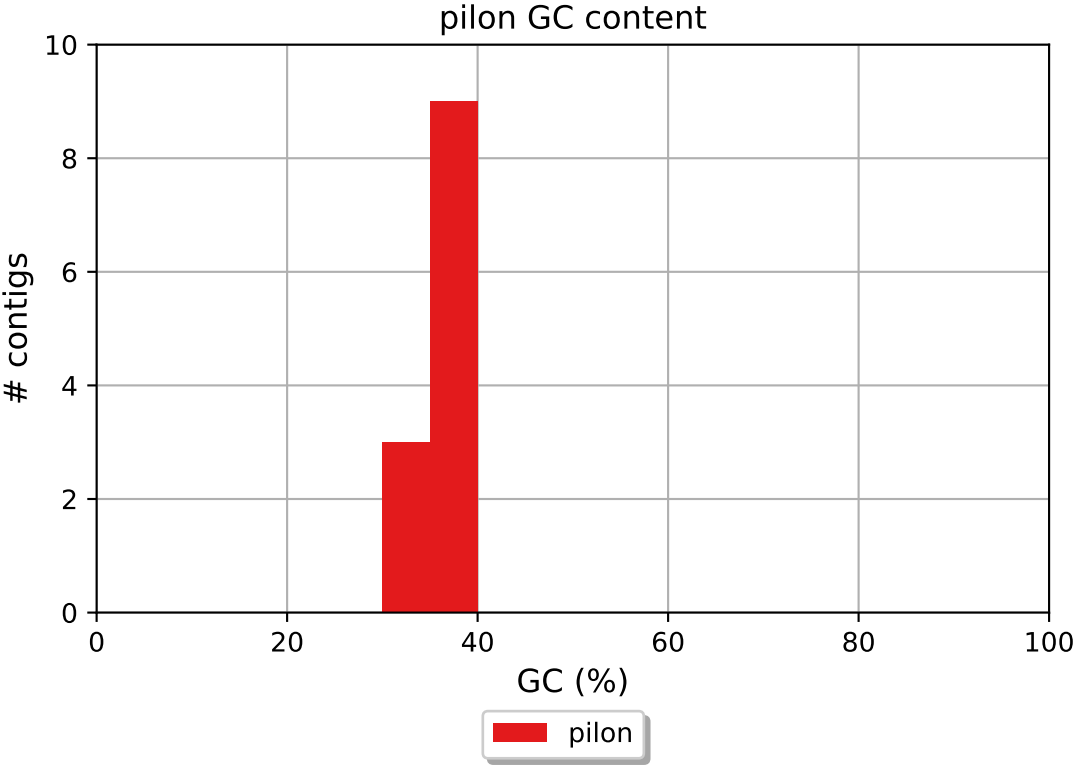
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

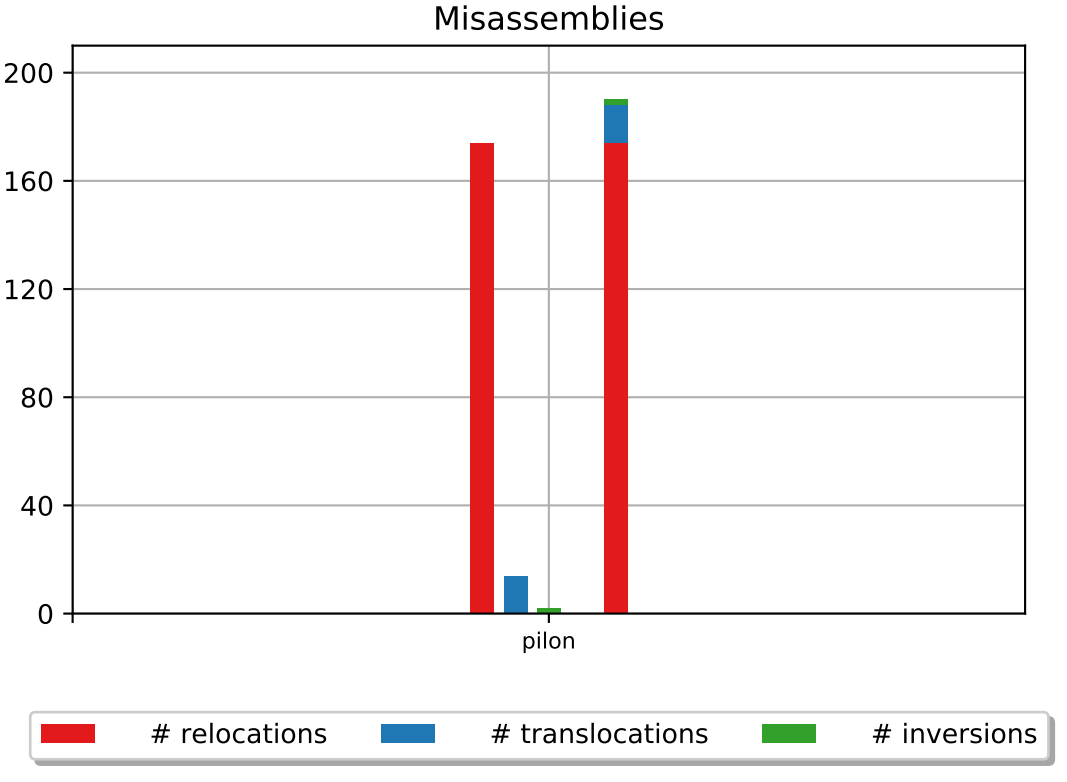

Nx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
pilon

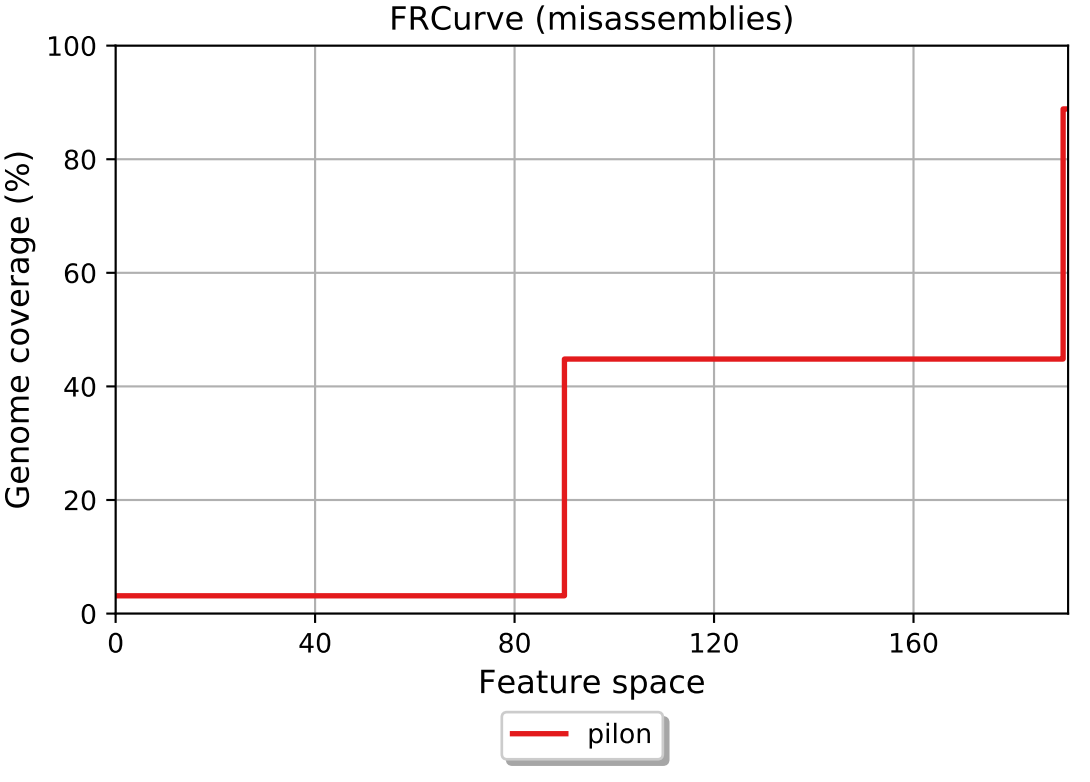

NGx
Contig length (kbp)
1500
1200
900
600
300
0
0
20
40
60
80
100
x
pilon

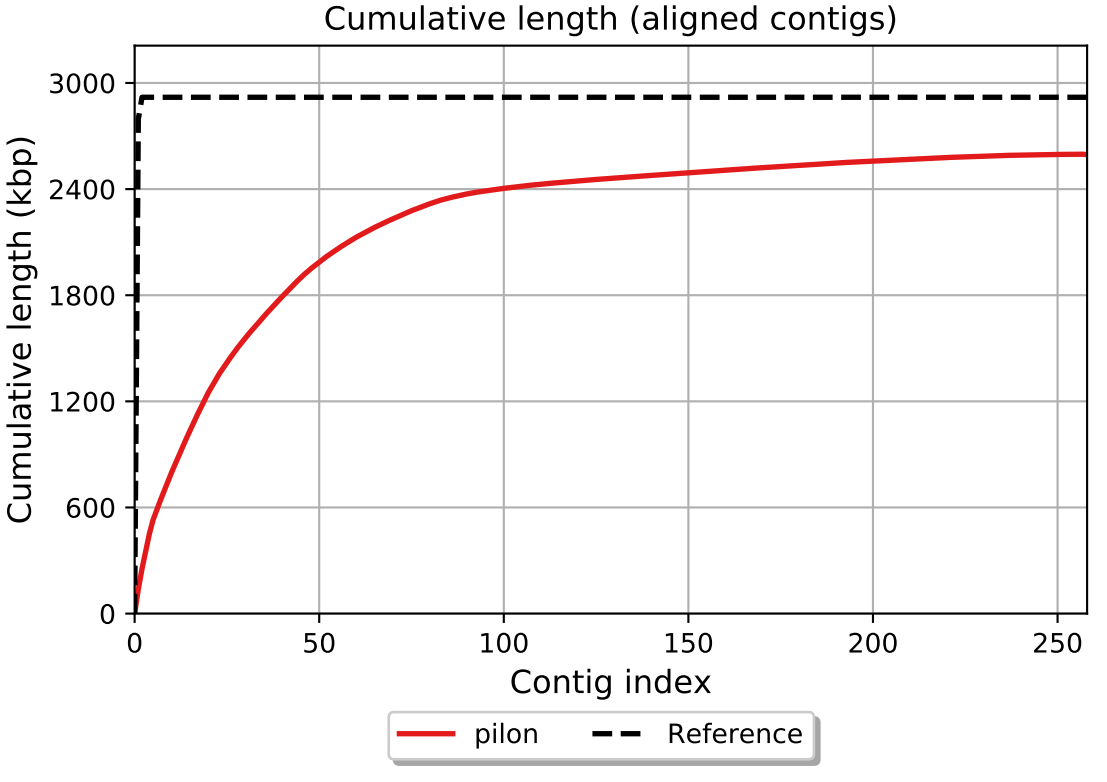

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
10
12
Contig index
pilon
Reference

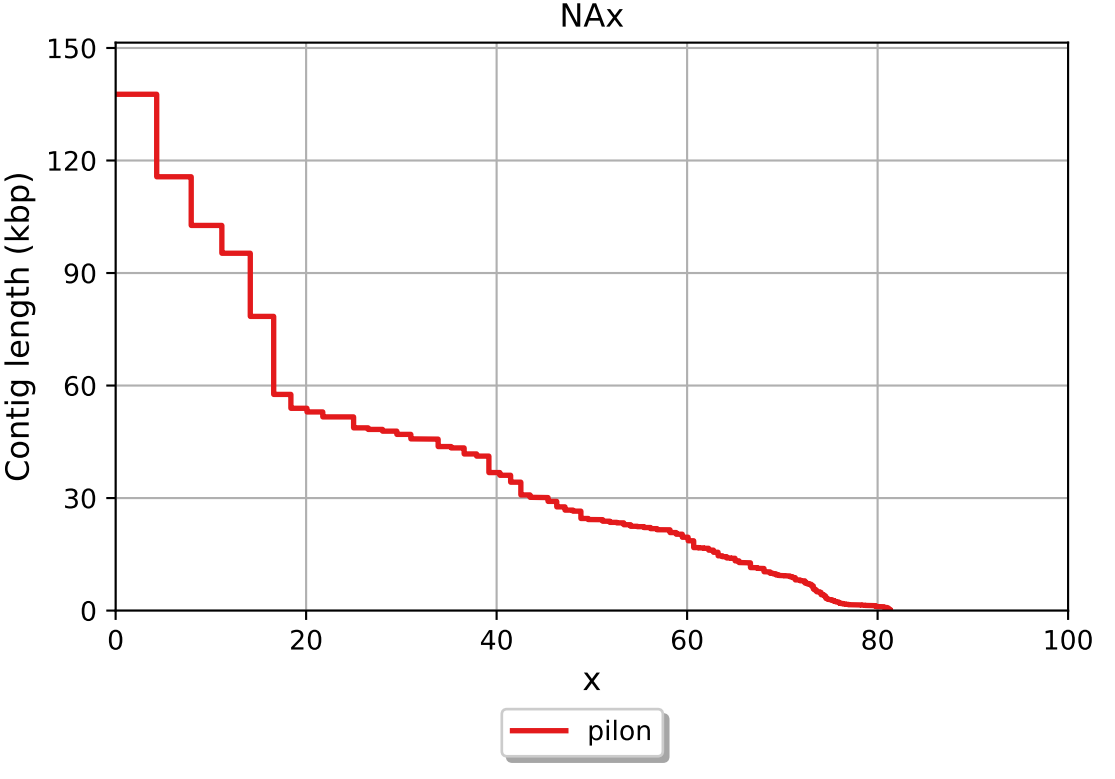

GC content
windows
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
pilon
Reference

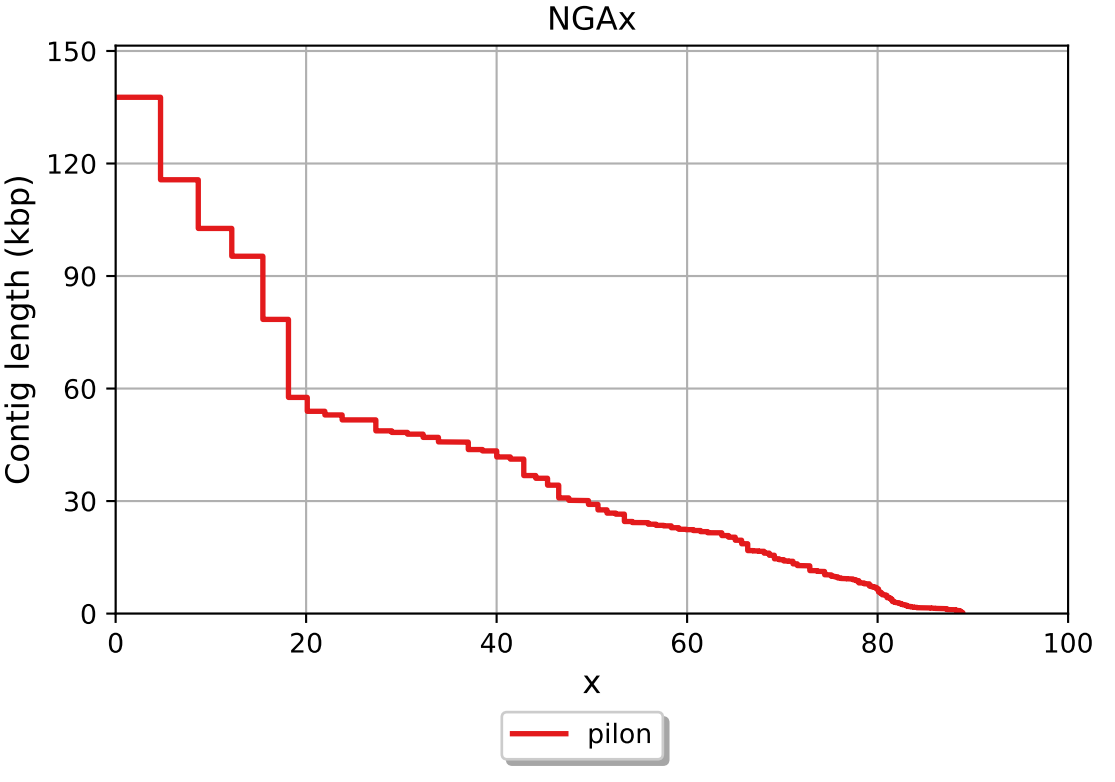

pilon GC content
contigs
GC (%)
0
2
4
6
8
10
0
20
40
60
80
100
pilon


Misassemblies
200
160
120
80
40
0
pilon
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
40
80
120
160
Feature space
pilon


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
50
100
150
200
250
Contig index
pilon
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
pilon


NGAx
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
pilon