Report

	efaecium_canu.contigs	pilon
# contigs (>= 0 bp)	9	9
# contigs (>= 1000 bp)	9	9
# contigs (>= 5000 bp)	9	9
# contigs (>= 10000 bp)	8	8
# contigs (>= 25000 bp)	5	5
# contigs (>= 50000 bp)	2	2
Total length (>= 0 bp)	3159448	3159596
Total length (>= 1000 bp)	3159448	3159596
Total length (>= 5000 bp)	3159448	3159596
Total length (>= 10000 bp)	3149661	3149801
Total length (>= 25000 bp)	3099591	3099716
Total length (>= 50000 bp)	3006270	3006371
# contigs	9	9
Largest contig	2775643	2775723
Total length	3159448	3159596
Reference length	3168410	3168410
GC (%)	37.78	37.78
Reference GC (%)	37.70	37.70
N50	2775643	2775723
NG50	2775643	2775723
N75	2775643	2775723
NG75	2775643	2775723
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	7	7
# misassembled contigs	5	5
Misassembled contigs length	3078811	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	10.14	10.56
# indels per 100 kbp	14.51	7.99
Largest alignment	2148961	2149027
Total aligned length	3155449	3155597
NA50	2148961	2149027
NGA50	2148961	2149027
NA75	626682	626696
NGA75	626682	626696
LA50	1	1
LGA50	1	1
LA75	2	2
LGA75	2	2

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

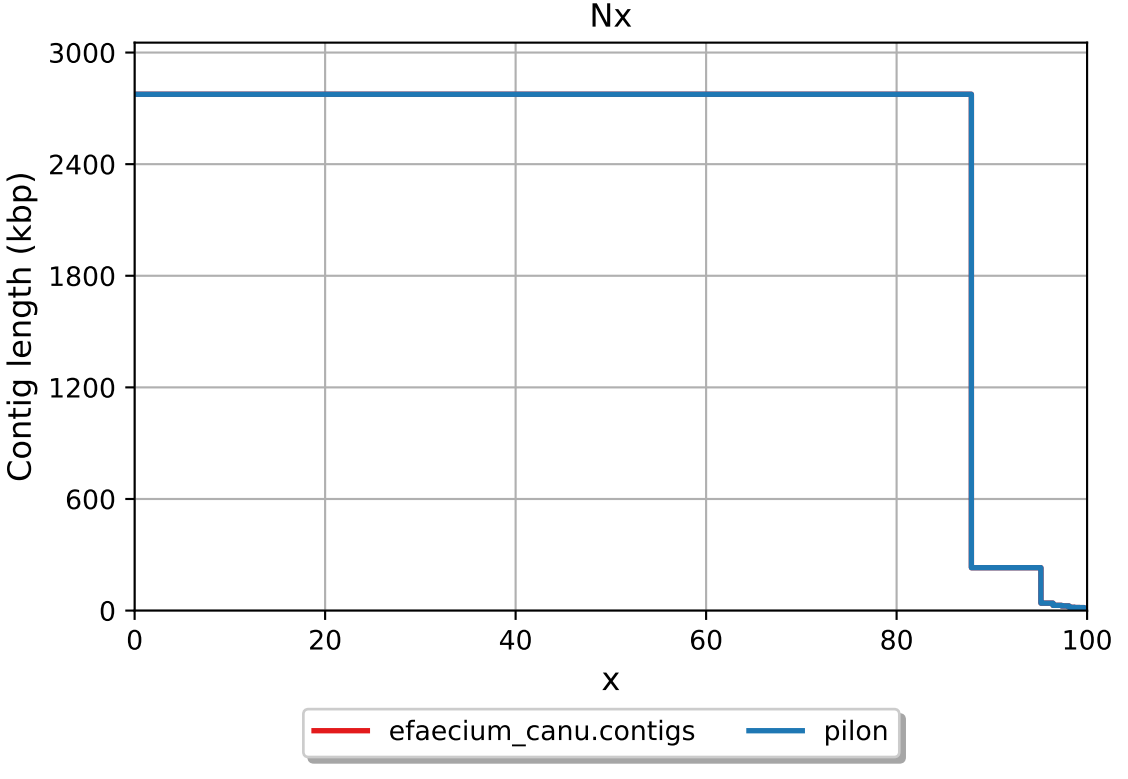
	efaecium_canu.contigs	pilon
# misassemblies	7	7
# contig misassemblies	7	7
# c. relocations	5	5
# c. translocations	2	2
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	5	5
Misassembled contigs length	3078811	3078924
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	316	329
# indels	452	249
# indels (<= 5 bp)	441	238
# indels (> 5 bp)	11	11
Indels length	647	433

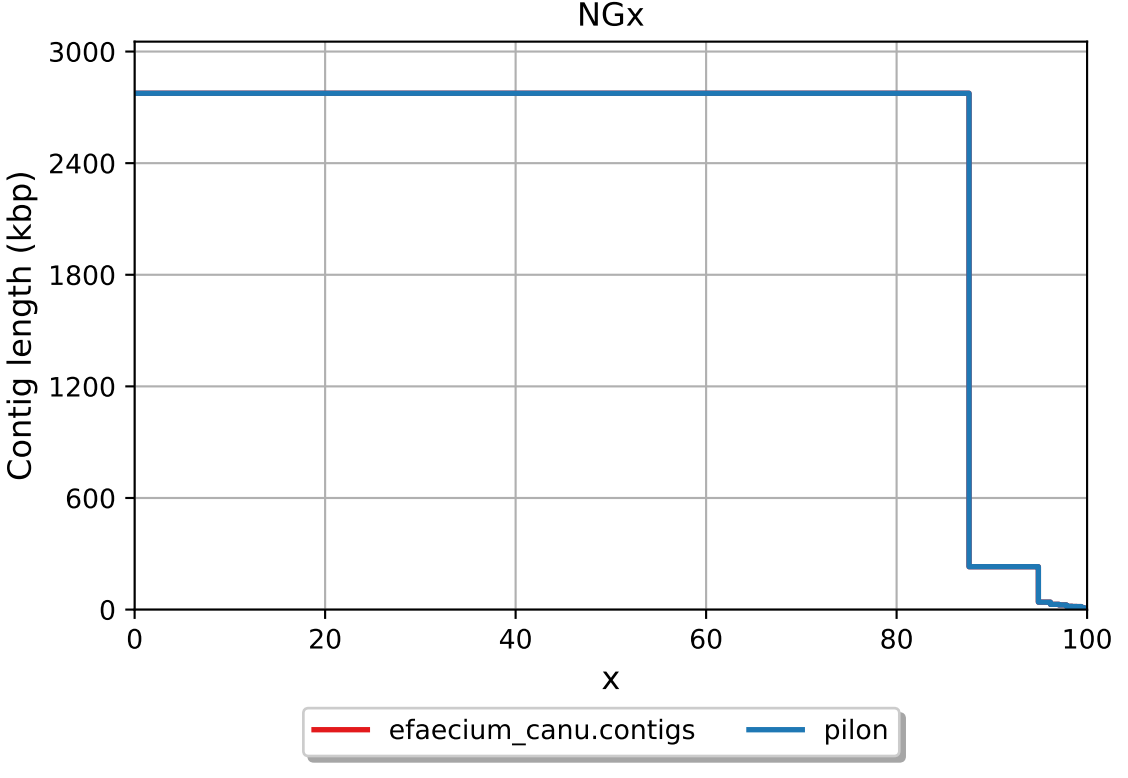
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

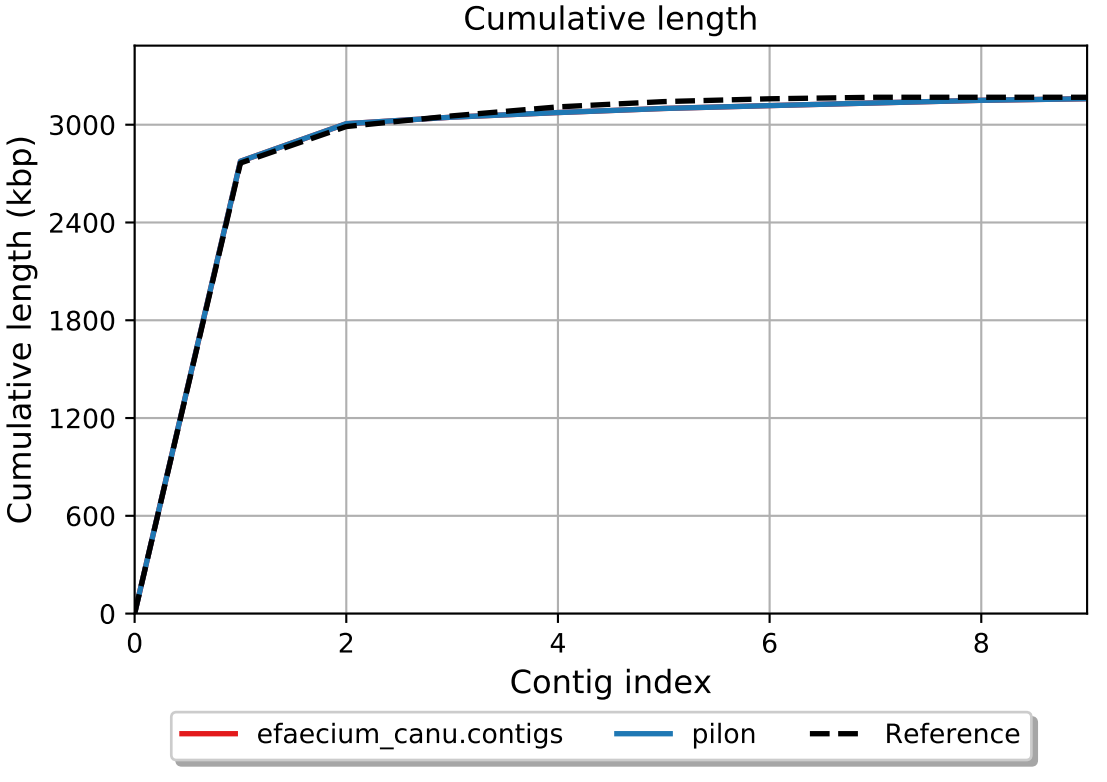
Unaligned report

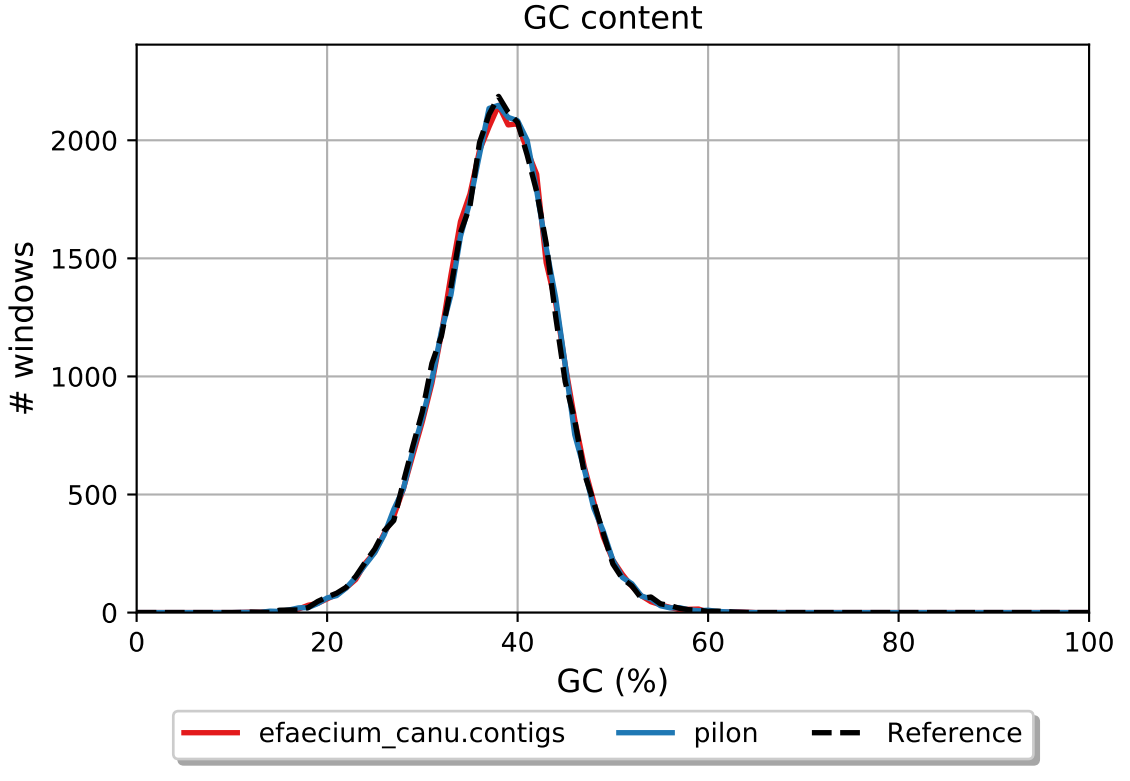
	efaecium_canu.contigs	pilon
# fully unaligned contigs	0	0
Fully unaligned length	0	0
# partially unaligned contigs	0	0
Partially unaligned length	0	0
# N's	0	0

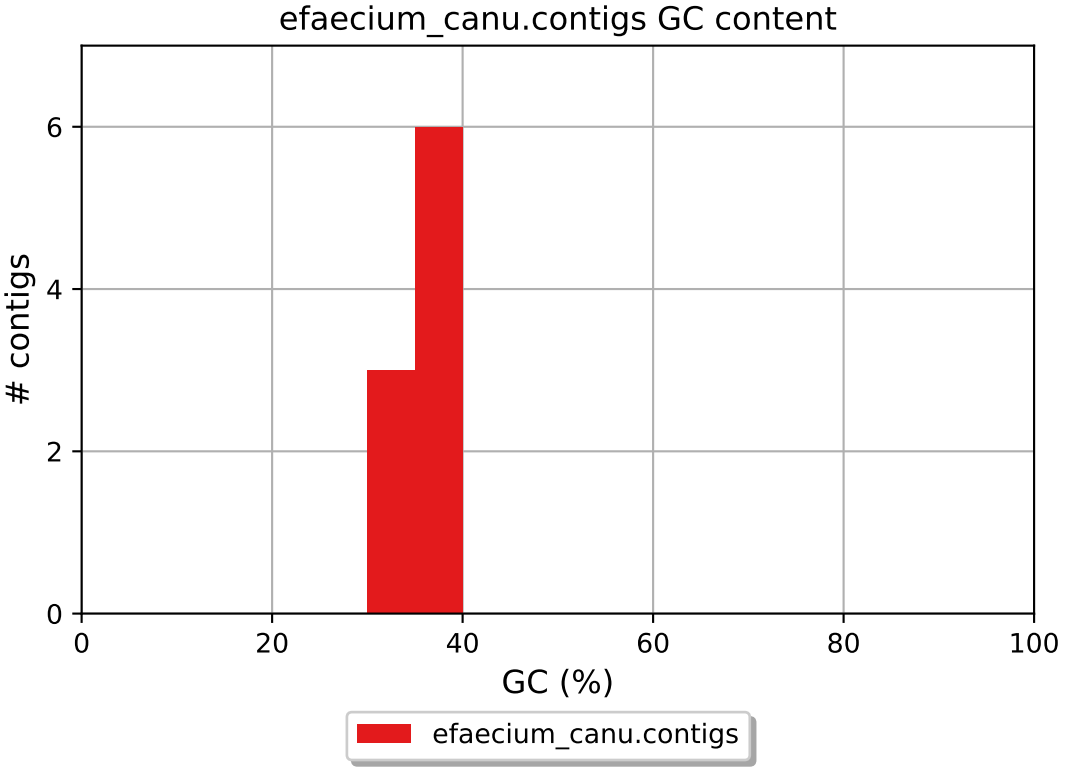
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

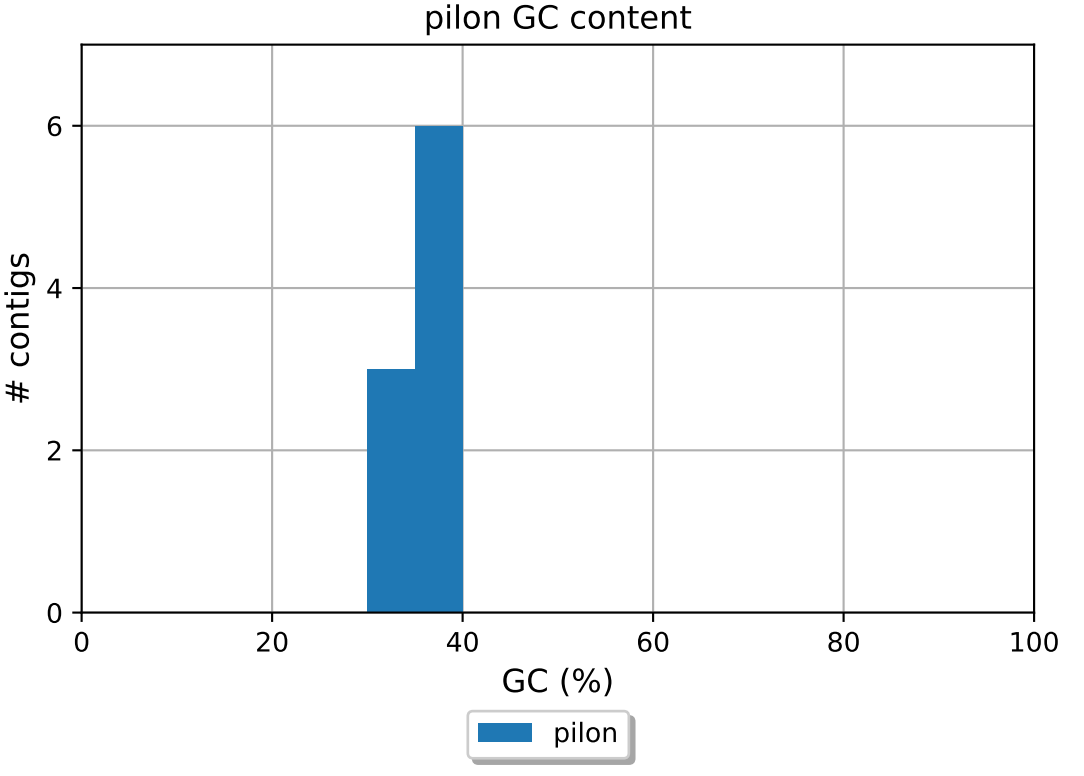

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
efaecium_canu.contigs
pilon

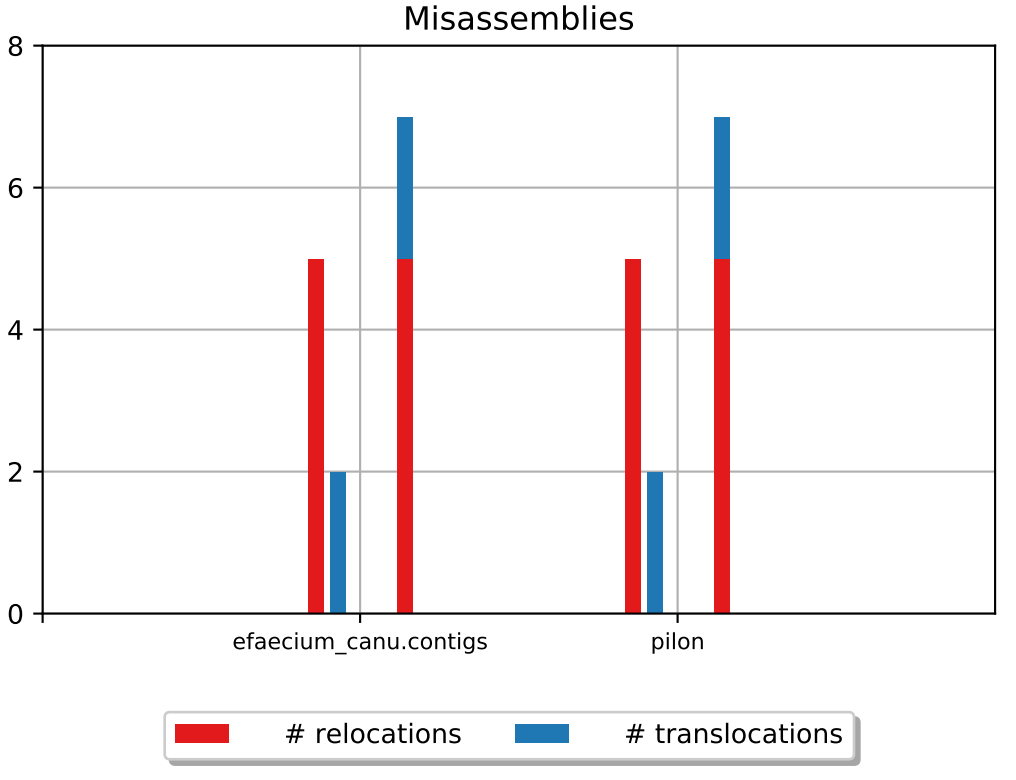

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
efaecium_canu.contigs
pilon

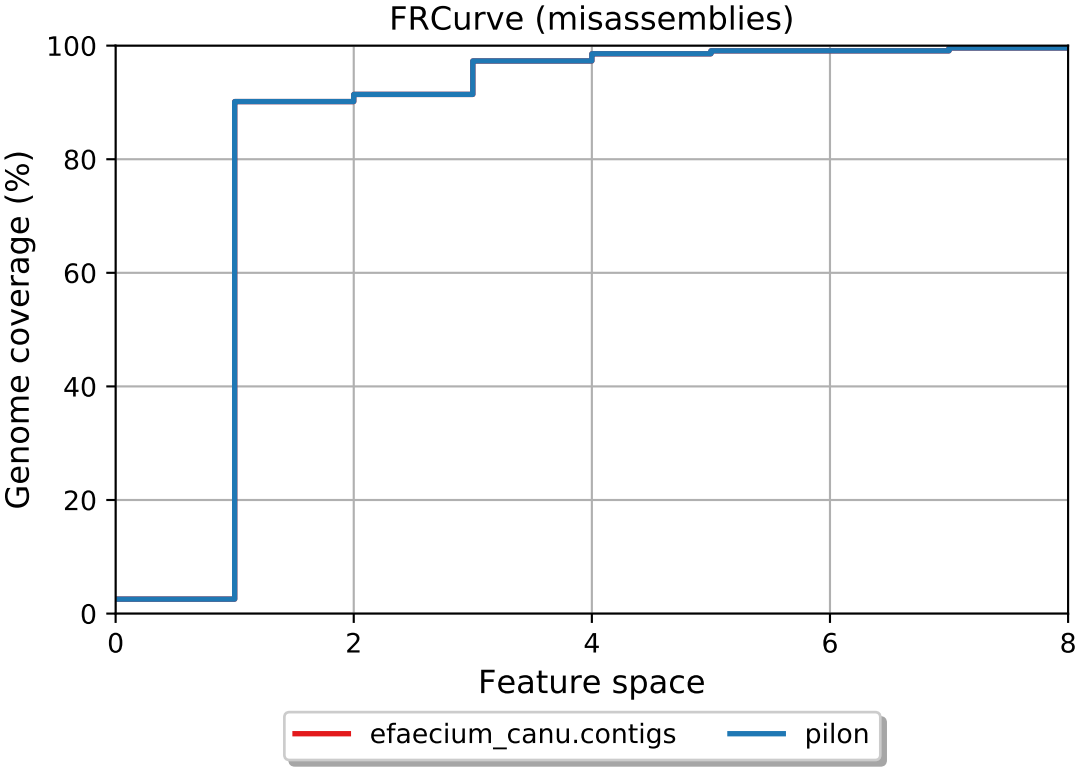

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
Contig index
efaecium_canu.contigs
pilon
Reference

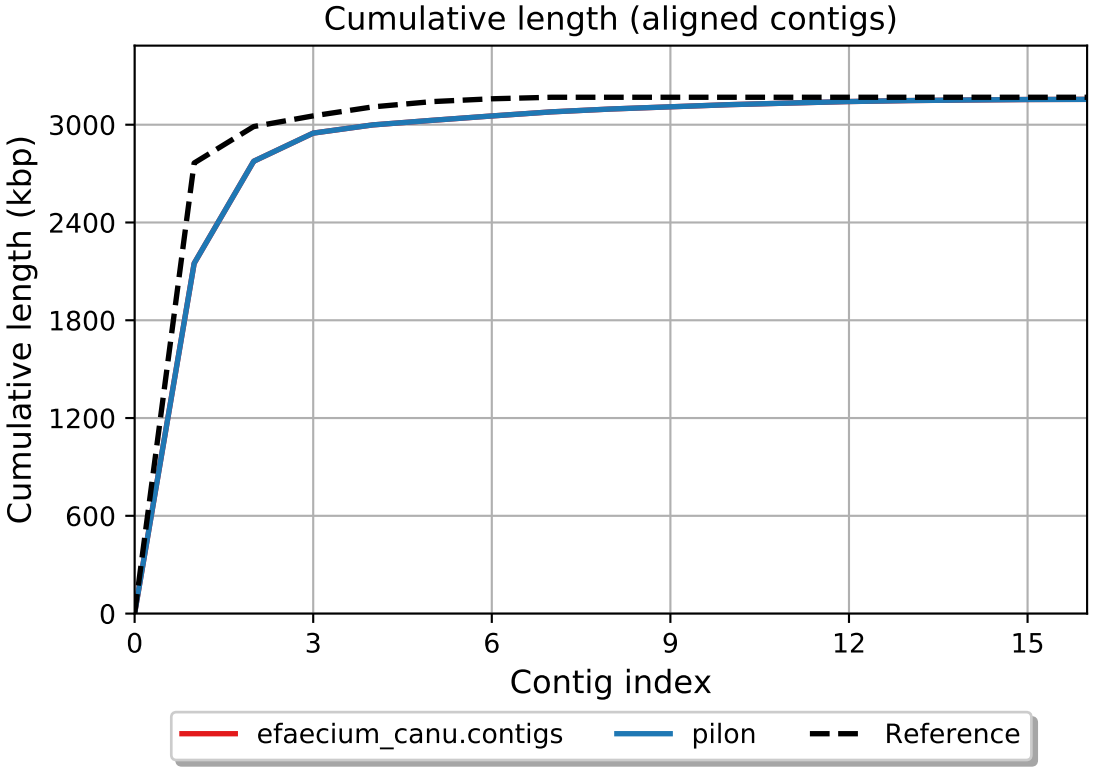

GC content
windows
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
efaecium_canu.contigs
pilon
Reference

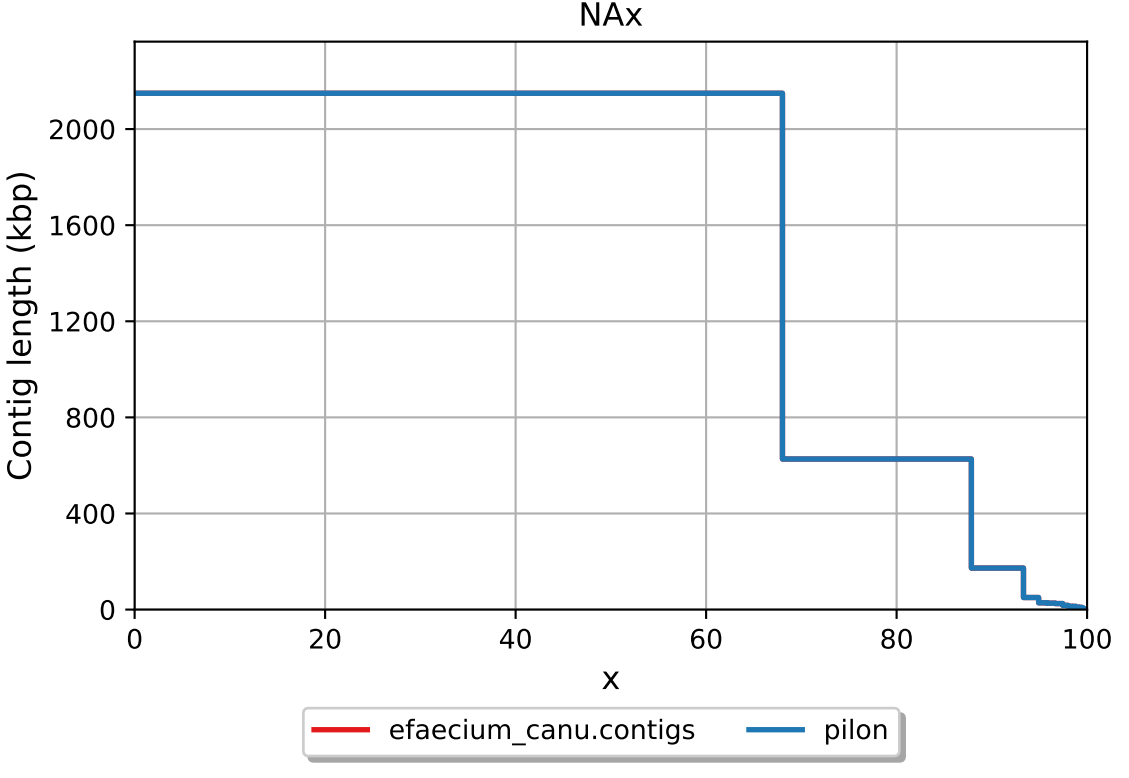

efaecium_canu.contigs GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
efaecium_canu.contigs

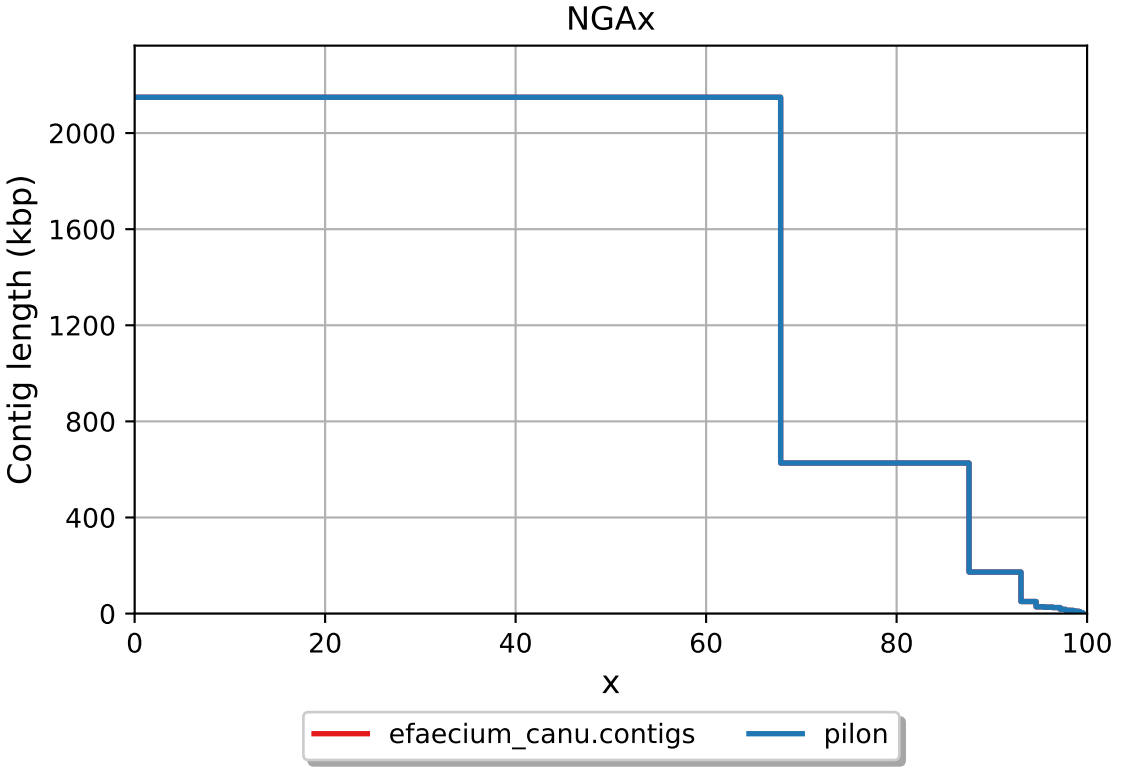

pilon GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
pilon

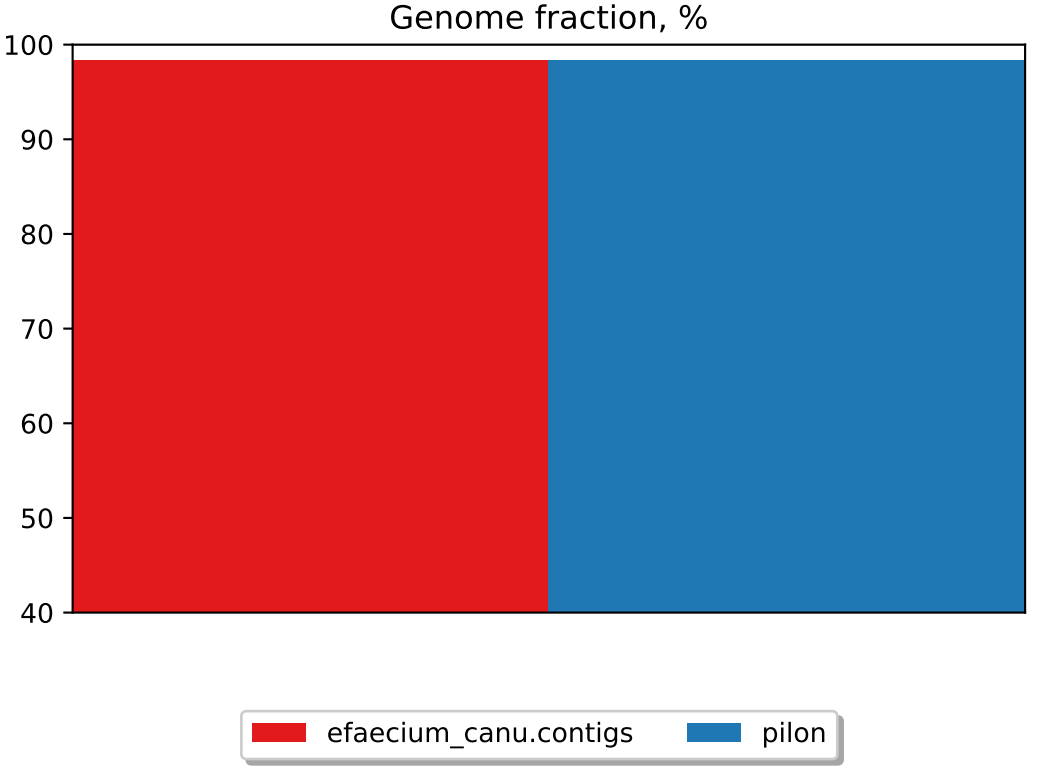

Misassemblies
8
6
4
2
0
efaecium_canu.contigs
pilon
relocations
translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
2
4
6
8
Feature space
efaecium_canu.contigs
pilon


Cumulative length (aligned contigs)
Cumulative length (kbp)
0
600
1200
1800
2400
3000
0
3
6
9
12
15
Contig index
efaecium_canu.contigs
pilon
Reference


NAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
efaecium_canu.contigs
pilon


NGAx
Contig length (kbp)
2000
1600
1200
800
400
0
0
20
40
60
80
100
x
efaecium_canu.contigs
pilon


Genome fraction, %
100
90
80
70
60
50
40
efaecium_canu.contigs
pilon