

# Report

	pilon	efaecium.contigs
# contigs (>= 0 bp)	8	8
# contigs (>= 1000 bp)	8	8
# contigs (>= 5000 bp)	8	8
# contigs (>= 10000 bp)	7	7
# contigs (>= 25000 bp)	5	5
# contigs (>= 50000 bp)	2	2
Total length (>= 0 bp)	3141050	3142355
Total length (>= 1000 bp)	3141050	3142355
Total length (>= 5000 bp)	3141050	3142355
Total length (>= 10000 bp)	3132750	3132621
Total length (>= 25000 bp)	3103593	3103475
Total length (>= 50000 bp)	2992680	2992580
# contigs	8	8
Largest contig	2773703	2773588
Total length	3141050	3142355
Reference length	1753437	1753437
GC (%)	37.78	37.78
Reference GC (%)	37.94	37.94
N50	2773703	2773588
NG50	2773703	2773588
N75	2773703	2773588
NG75	2773703	2773588
L50	1	1
LG50	1	1
L75	1	1
LG75	1	1
# misassemblies	31	32
# misassembled contigs	2	2
Misassembled contigs length	2782003	2783322
# local misassemblies	4	4
# unaligned mis. contigs	1	1
# unaligned contigs	4 + 4 part	4 + 4 part
Unaligned length	1265371	1265326
Genome fraction (%)	100.000	100.000
Duplication ratio	1.070	1.070
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.06
# indels per 100 kbp	0.29	4.96
Largest alignment	1183847	1183792
Total aligned length	1875680	1877030
NA50	578286	578258
NGA50	1183847	1183792
NGA75	578286	578258
LA50	2	2
LGA50	1	1
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

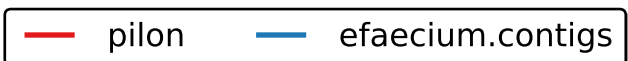
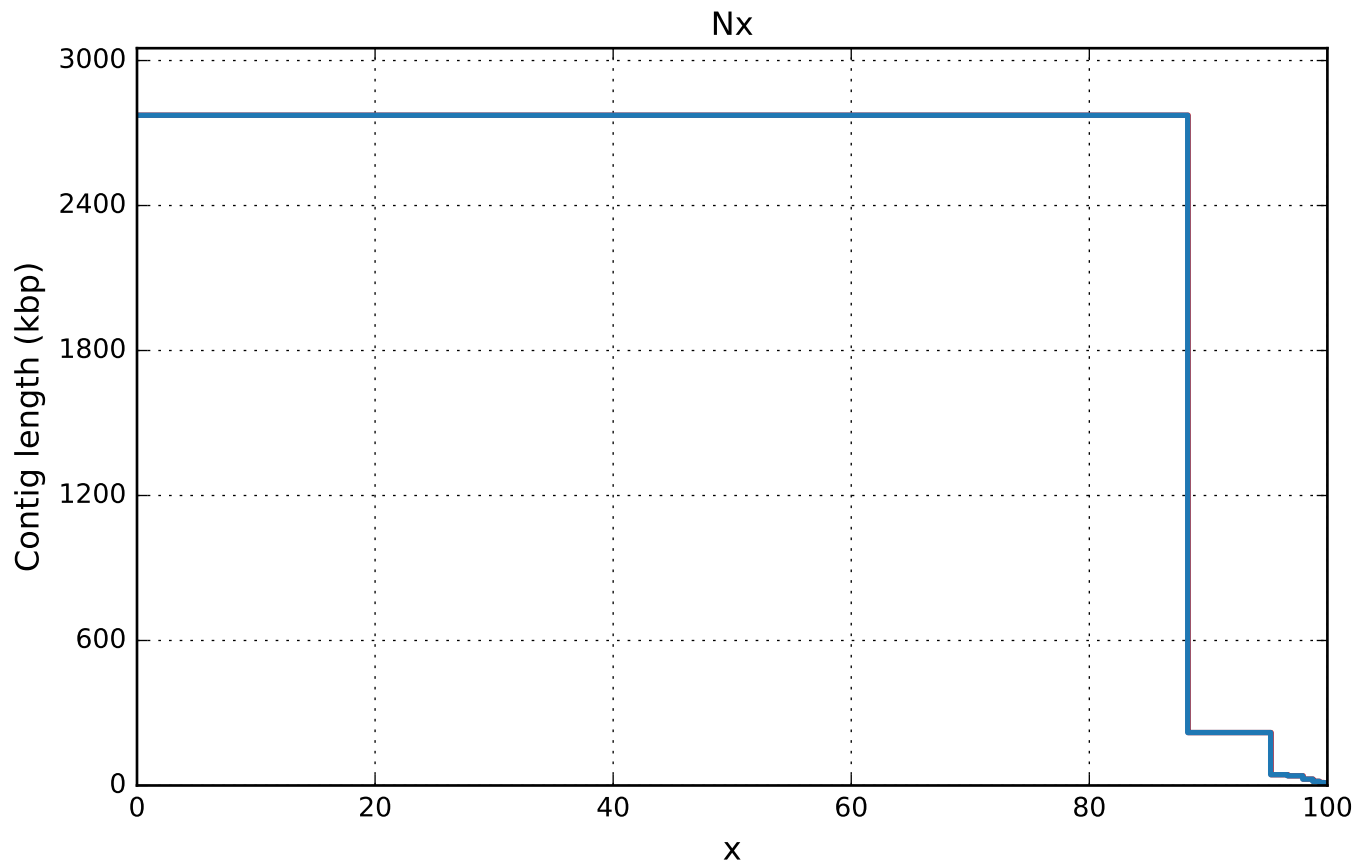
	pilon	efaecium.contigs
# misassemblies	31	32
# relocations	31	32
# translocations	0	0
# inversions	0	0
# misassembled contigs	2	2
Misassembled contigs length	2782003	2783322
# local misassemblies	4	4
# unaligned mis. contigs	1	1
# mismatches	0	1
# indels	5	87
# indels (<= 5 bp)	5	87
# indels (> 5 bp)	0	0
Indels length	5	88

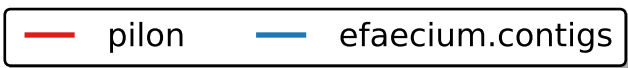
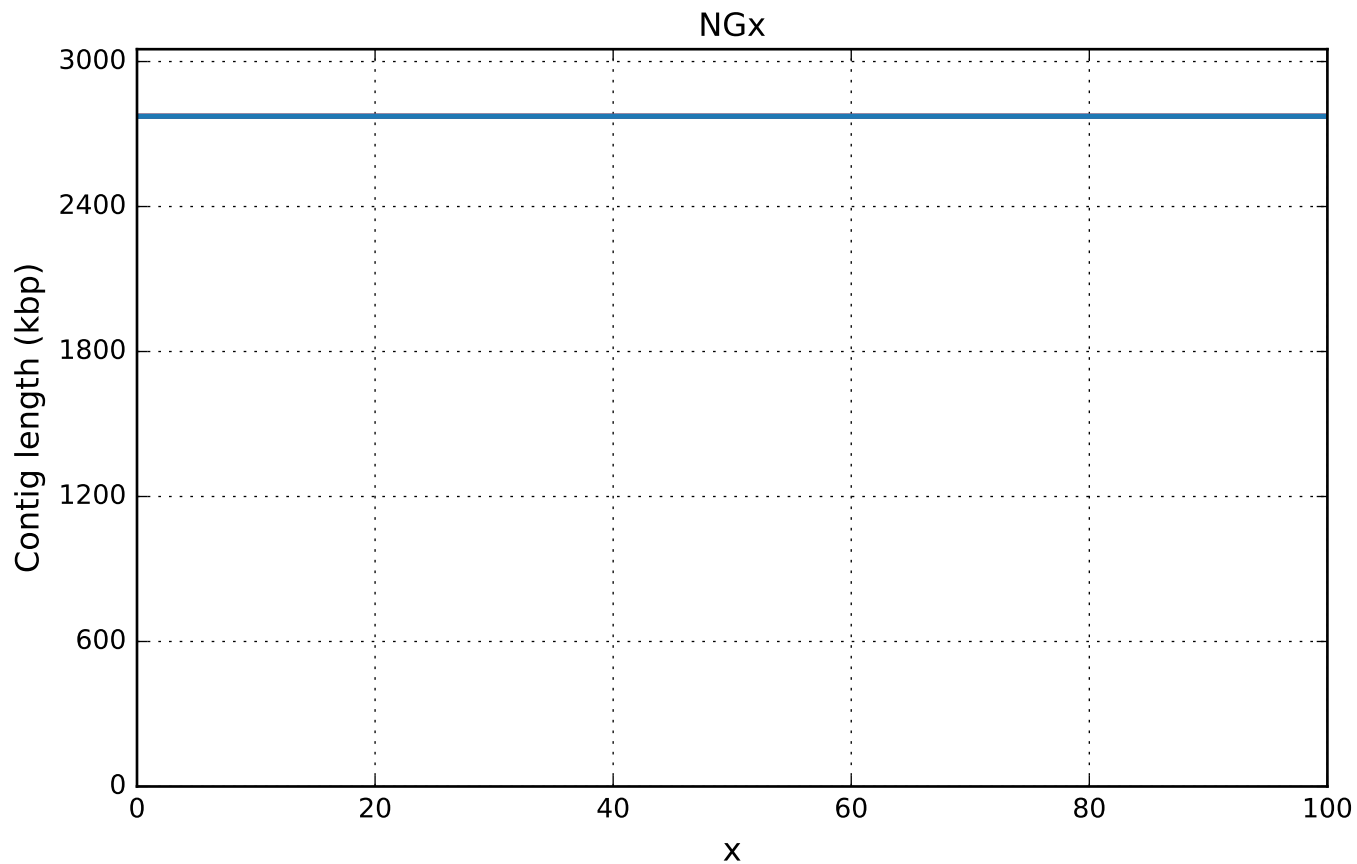
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

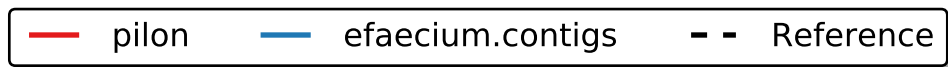
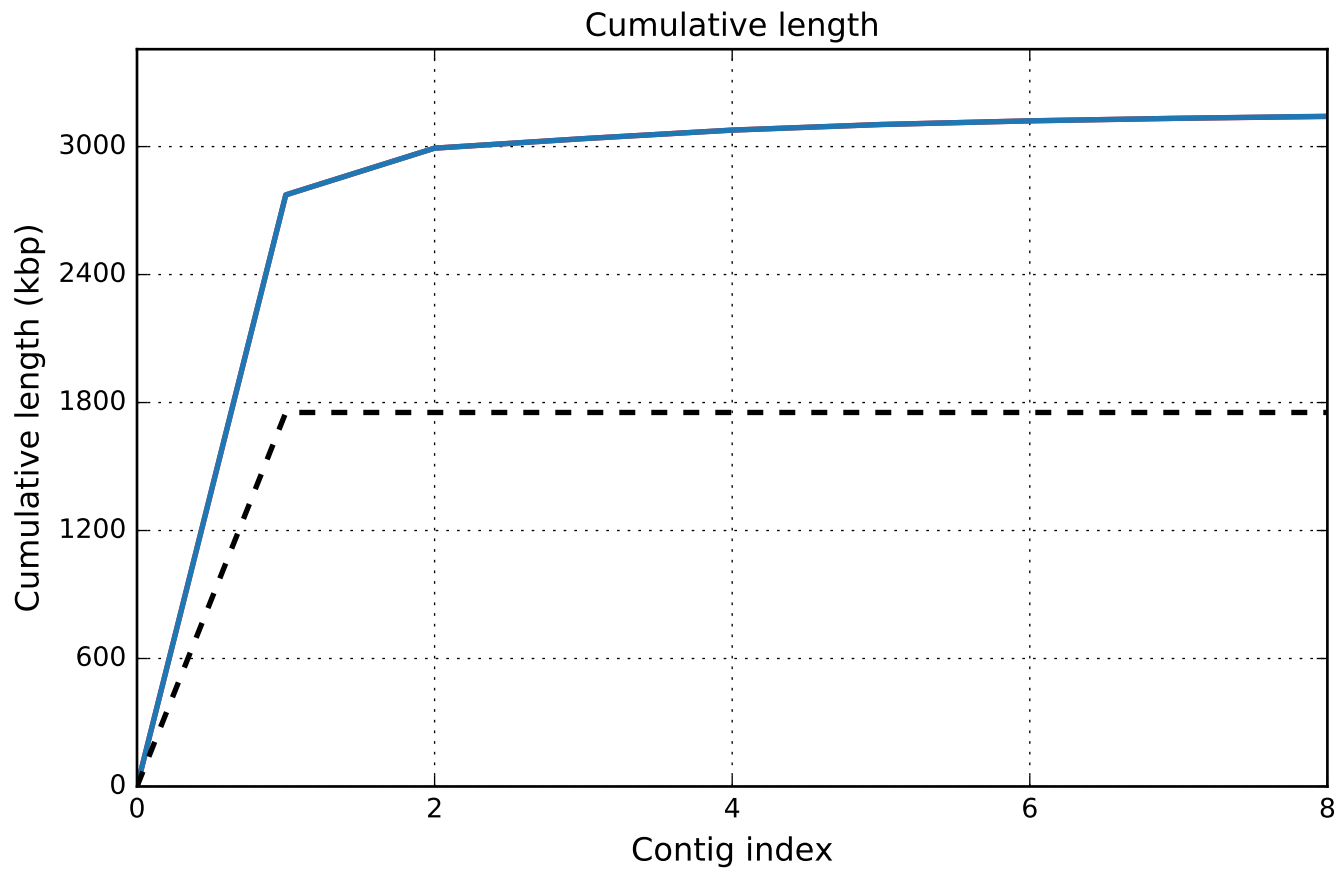
## Unaligned report

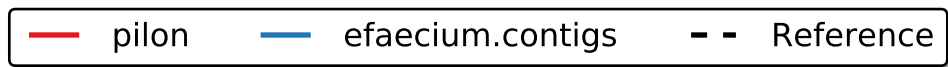
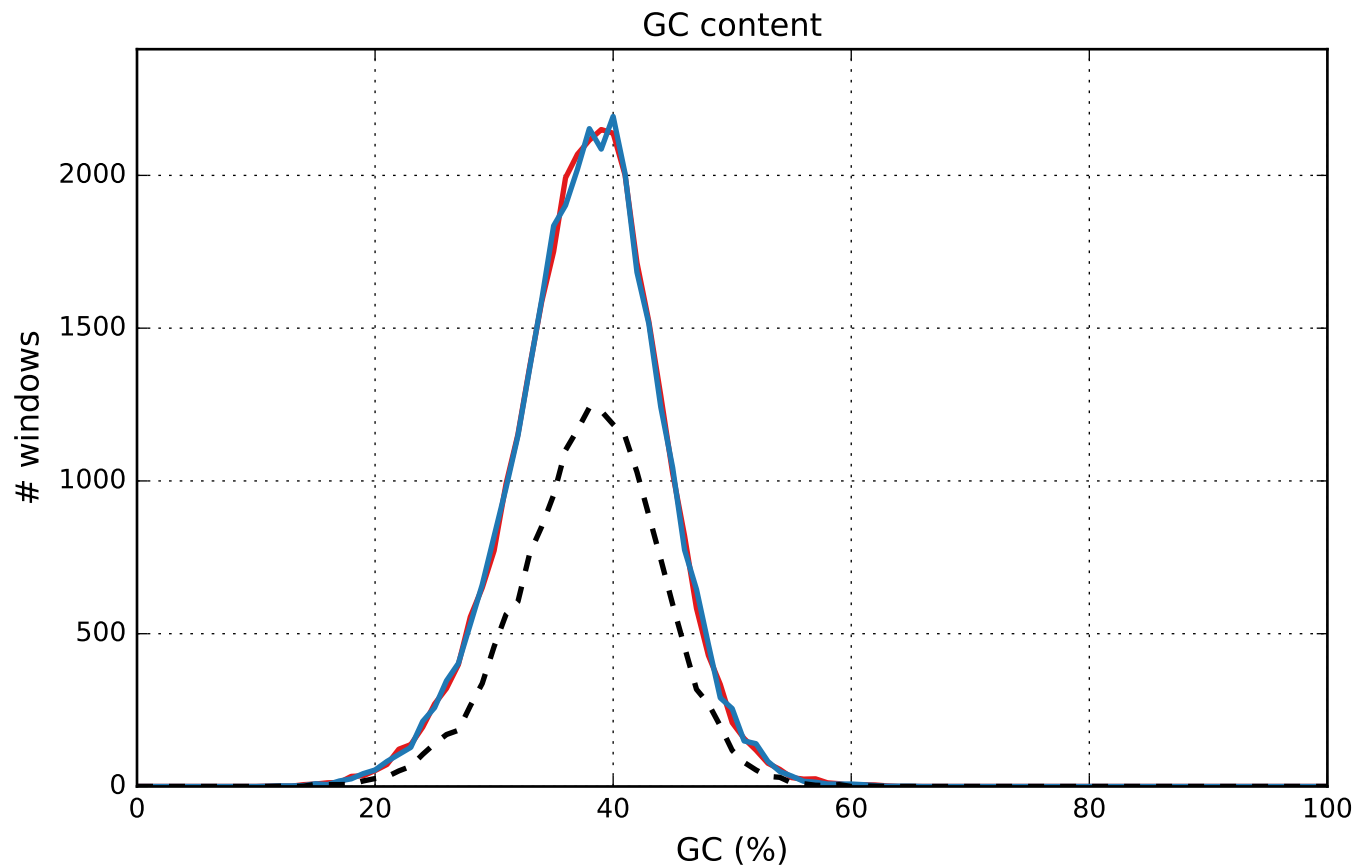
	pilon	efaecium.contigs
# fully unaligned contigs	4	4
Fully unaligned length	100053	100025
# partially unaligned contigs	4	4
Partially unaligned length	1165318	1165301
# N's	0	0

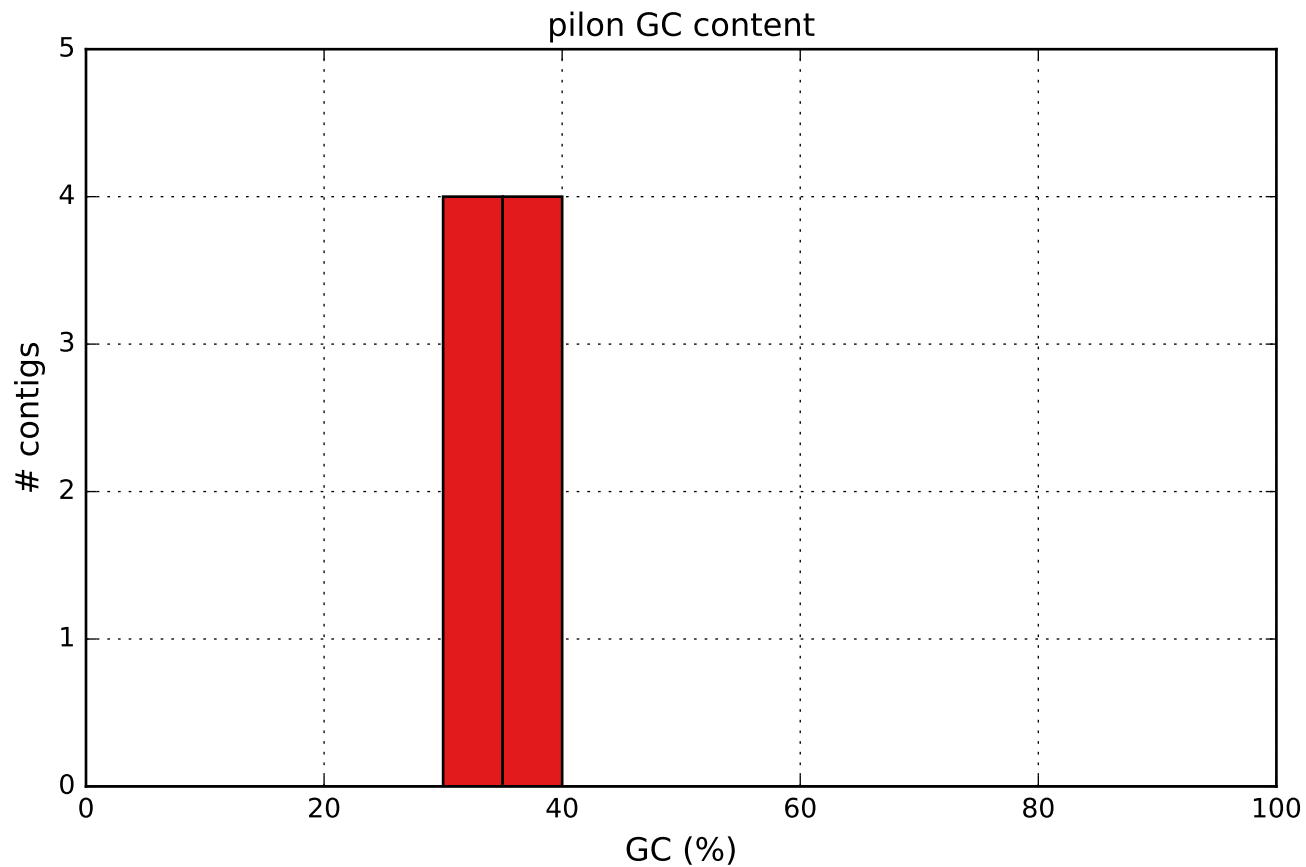
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).





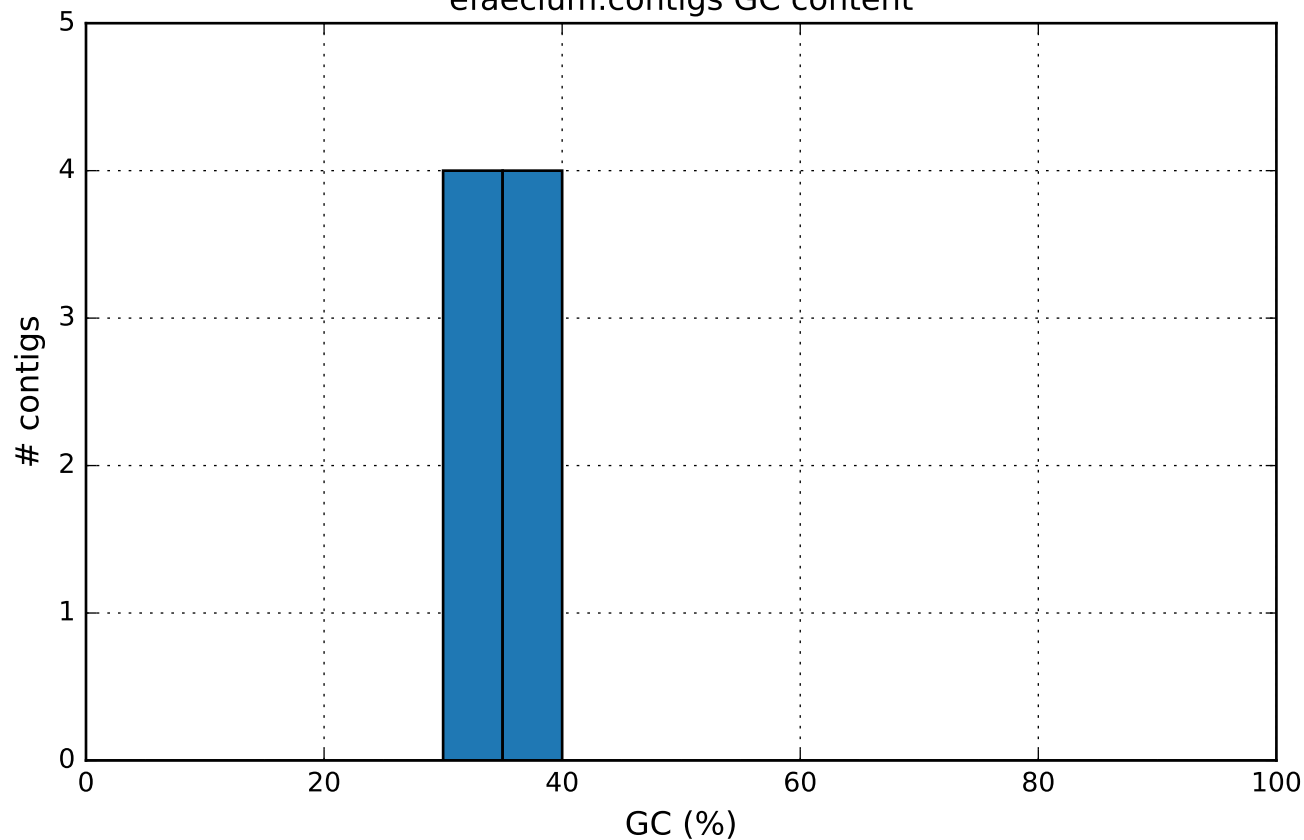






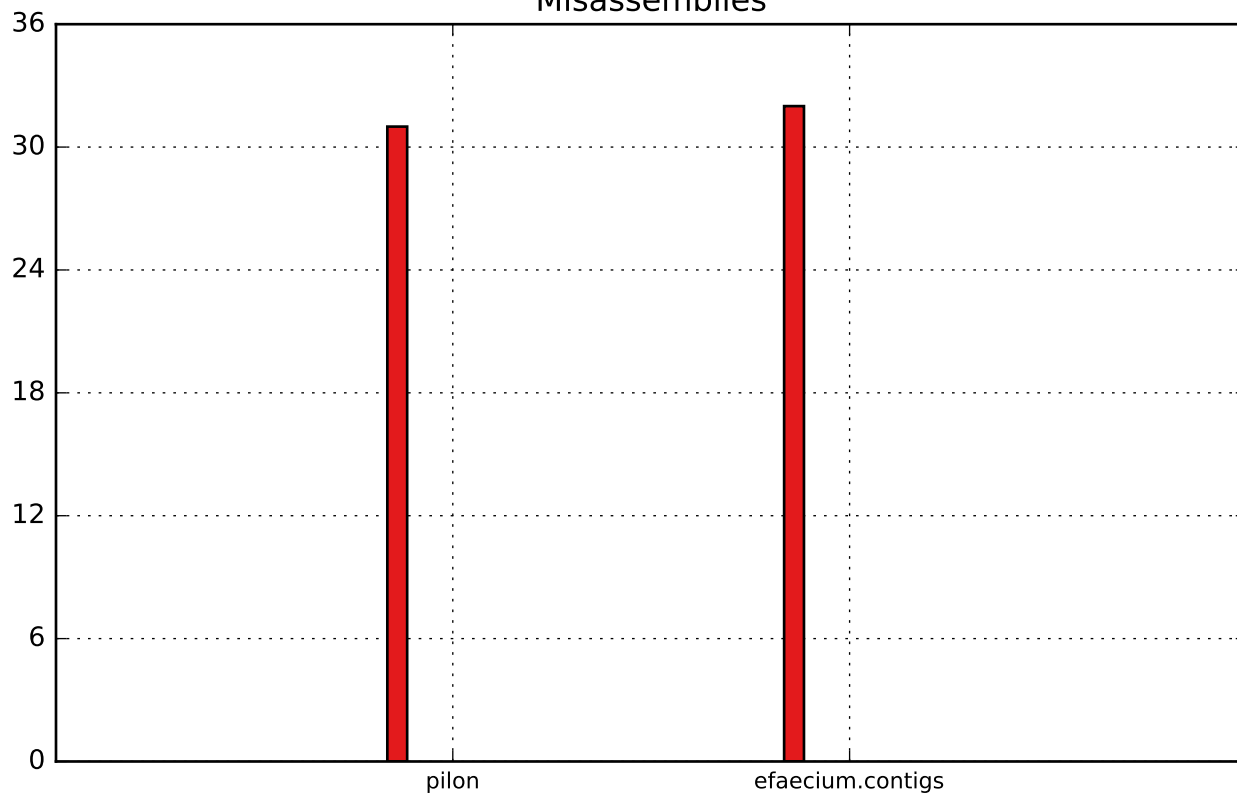


efaecium.contigs GC content



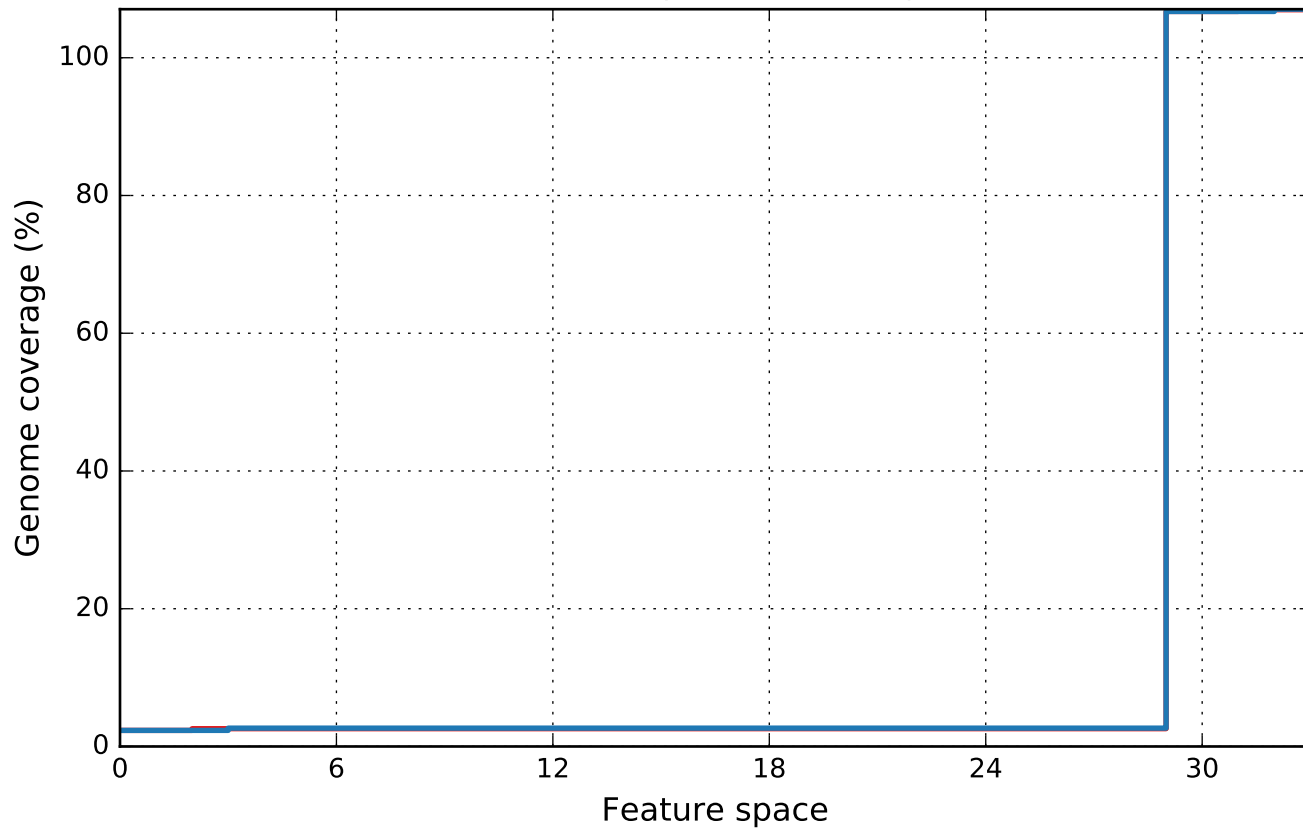
efaecium.contigs

# Misassemblies



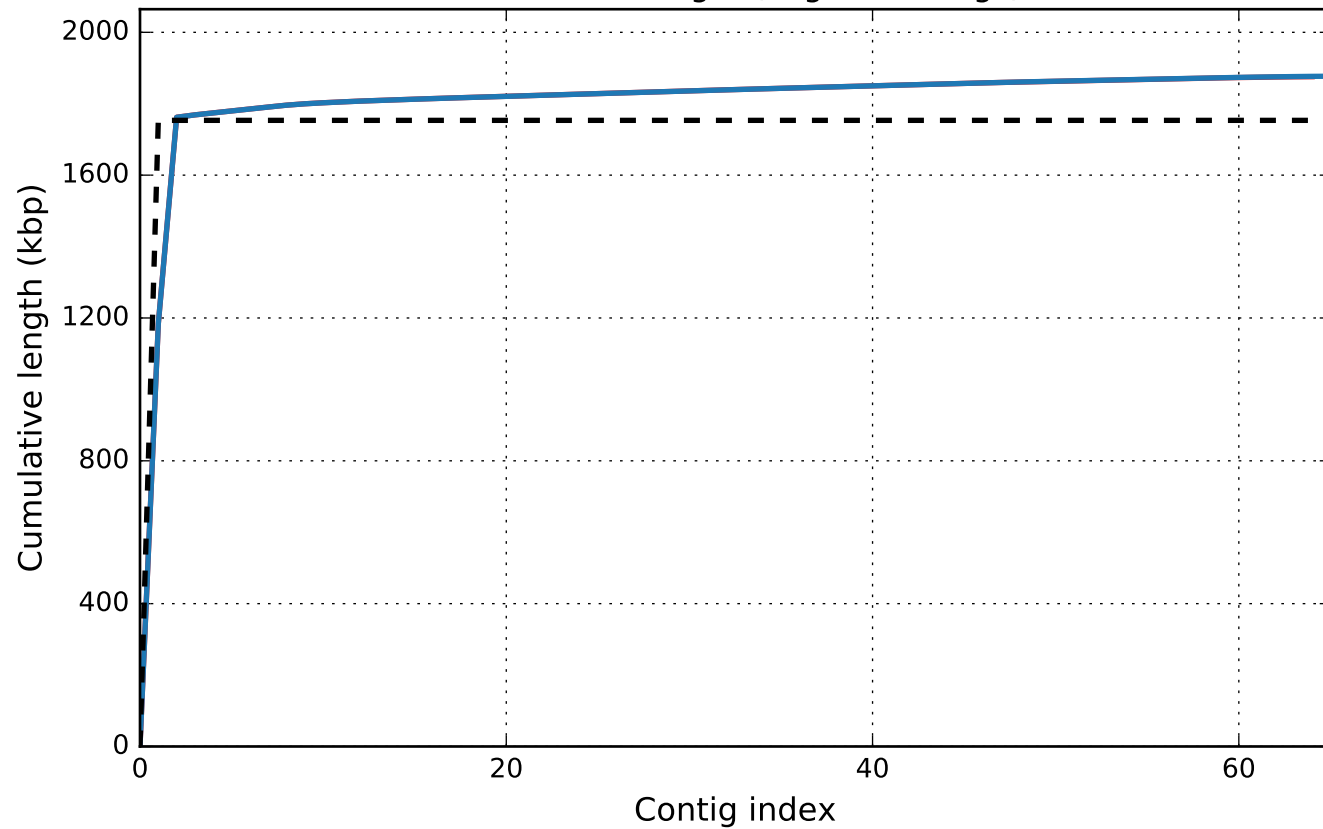
 # relocations

FRCurve (misassemblies)

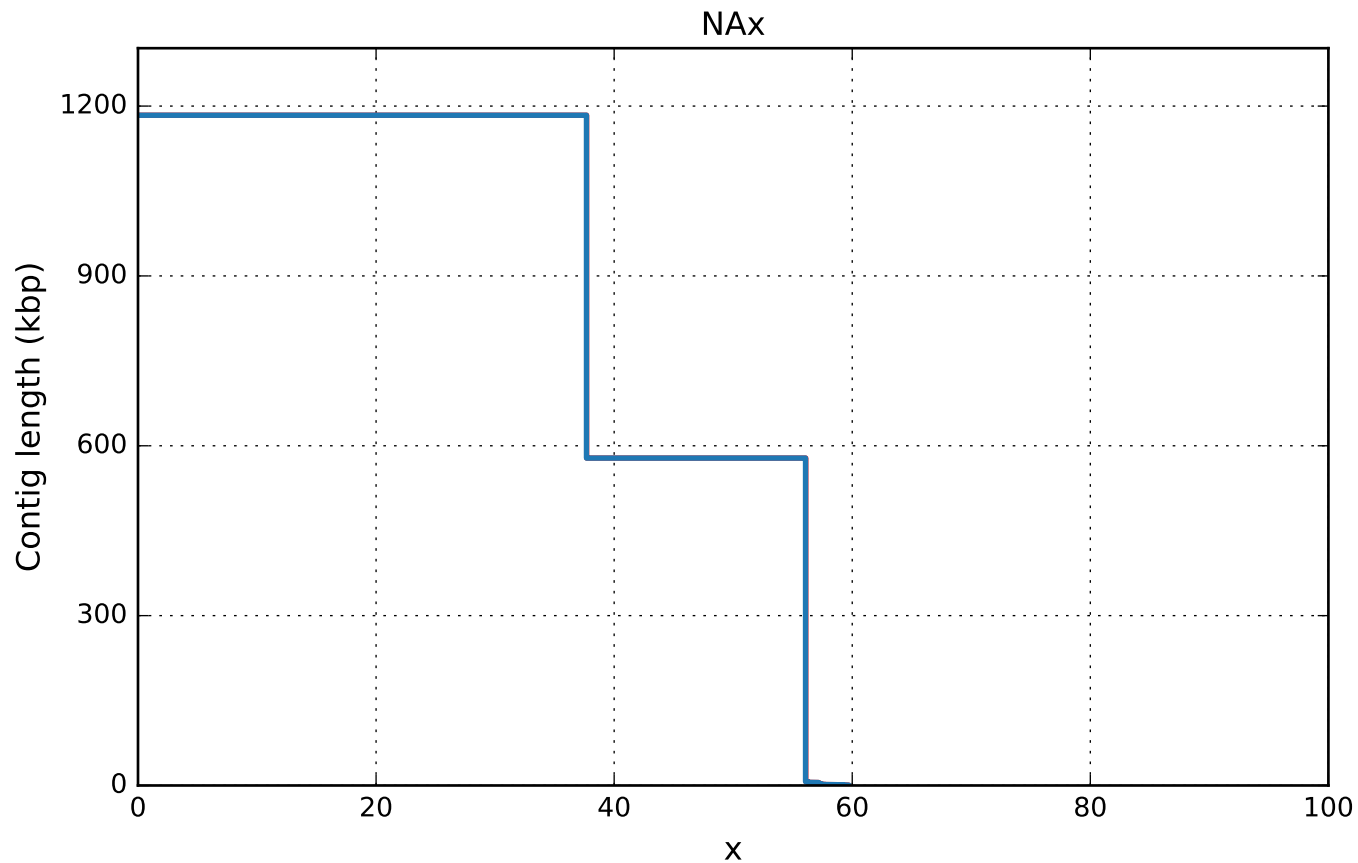


— pilon — efaecium.contigs

Cumulative length (aligned contigs)

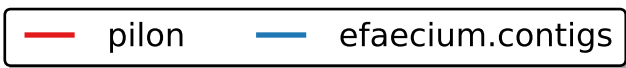
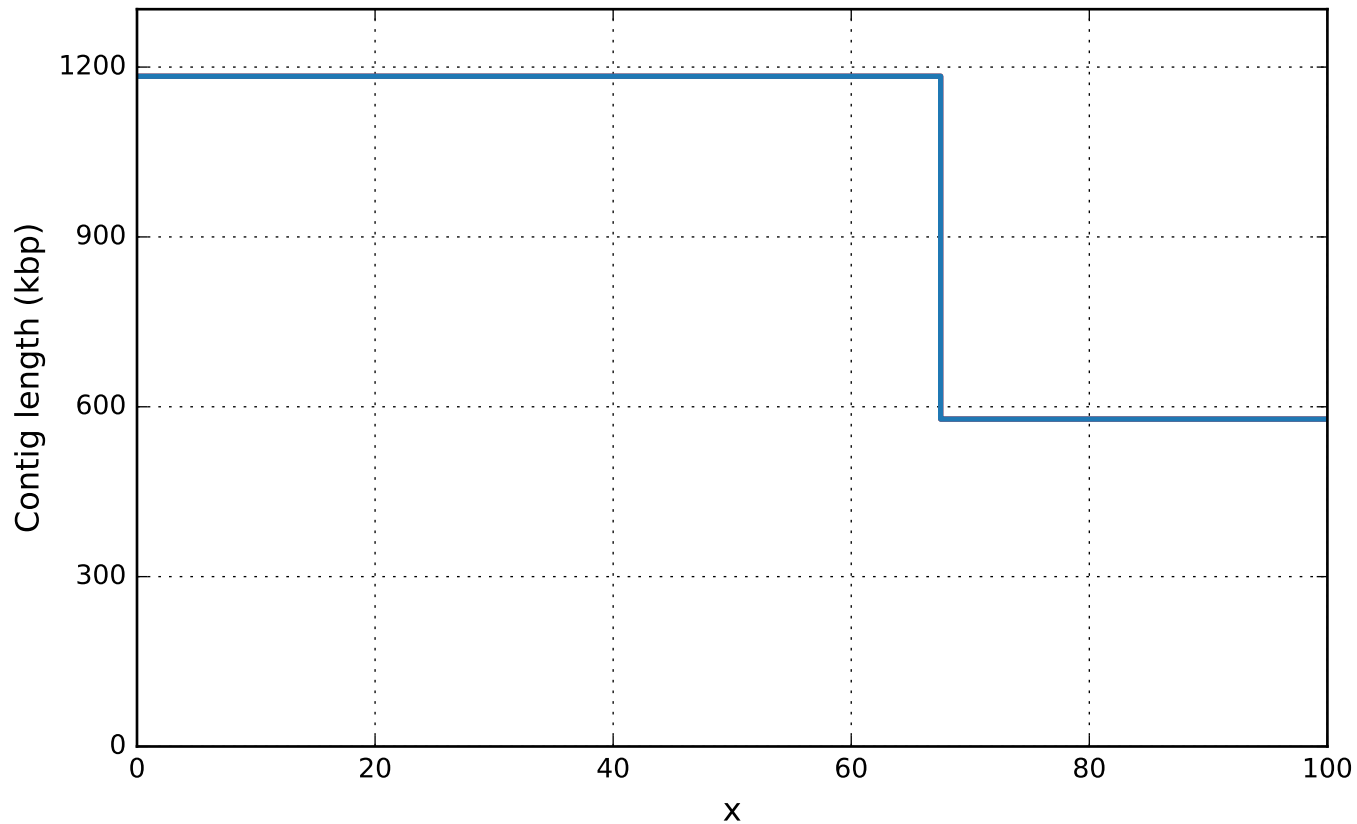


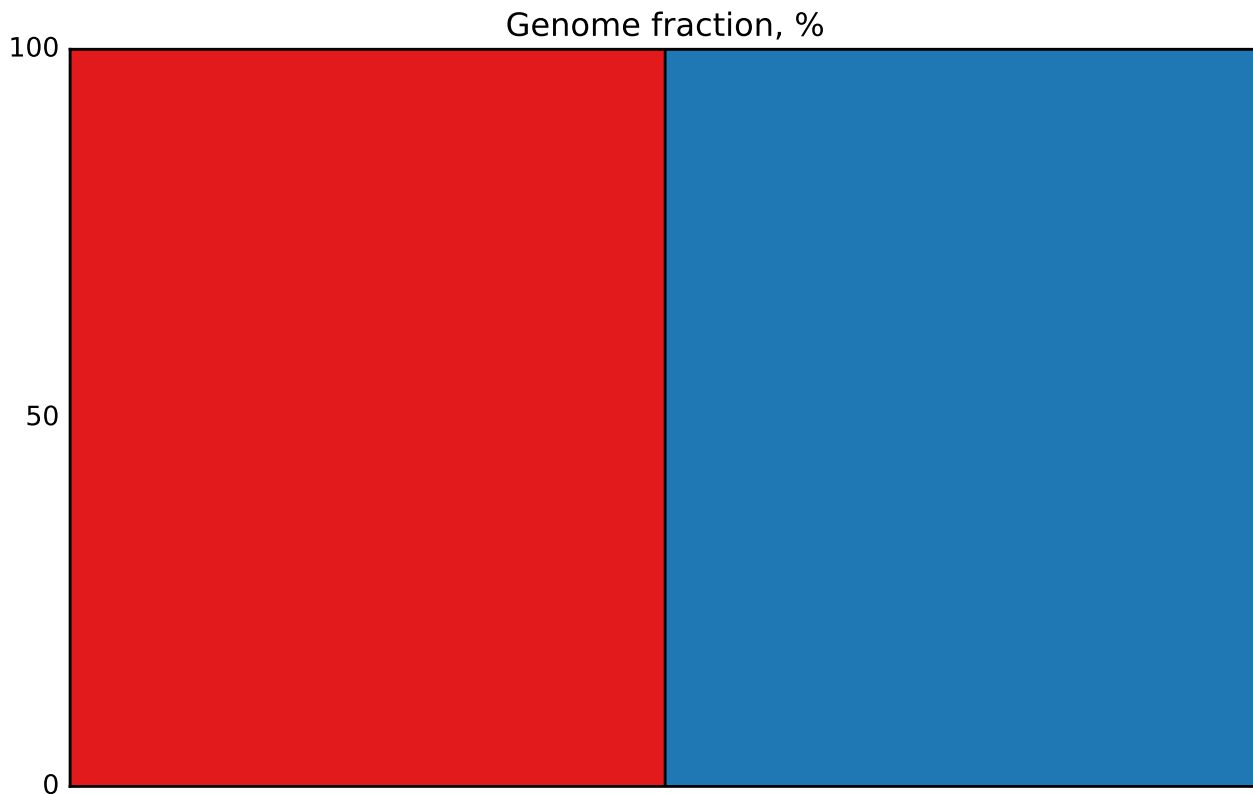
— pilon — efaecium.contigs - - Reference



— pilon — efaecium.contigs

# NGAx





 pilon     efaecium.contigs