

## Report

	efaecium_canu.contigs	efaecium_spades.contigs
# contigs (>= 0 bp)	9	23
# contigs (>= 1000 bp)	9	13
# contigs (>= 5000 bp)	9	12
# contigs (>= 10000 bp)	8	10
# contigs (>= 25000 bp)	5	8
# contigs (>= 50000 bp)	2	6
Total length (>= 0 bp)	3159448	3167825
Total length (>= 1000 bp)	3159448	3166447
Total length (>= 5000 bp)	3159448	3163189
Total length (>= 10000 bp)	3149661	3147021
Total length (>= 25000 bp)	3099591	3119243
Total length (>= 50000 bp)	3006270	3049727
# contigs	9	13
Largest contig	2775643	1751056
Total length	3159448	3166447
Reference length	3168410	3168410
GC (%)	37.78	37.69
Reference GC (%)	37.70	37.70
N50	2775643	1751056
NG50	2775643	1751056
N75	2775643	847797
NG75	2775643	847797
L50	1	1
LG50	1	1
L75	1	2
LG75	1	2
# misassemblies	7	5
# misassembled contigs	5	3
Misassembled contigs length	3078811	267396
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	1
# unaligned contigs	0 + 0 part	1 + 1 part
Unaligned length	0	7618
Genome fraction (%)	98.309	99.088
Duplication ratio	1.014	1.006
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	10.14	25.13
# indels per 100 kbp	14.51	5.13
Largest alignment	2148961	1751056
Total aligned length	3155449	3141966
NA50	2148961	1751056
NGA50	2148961	1751056
NA75	626682	847797
NGA75	626682	847797
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

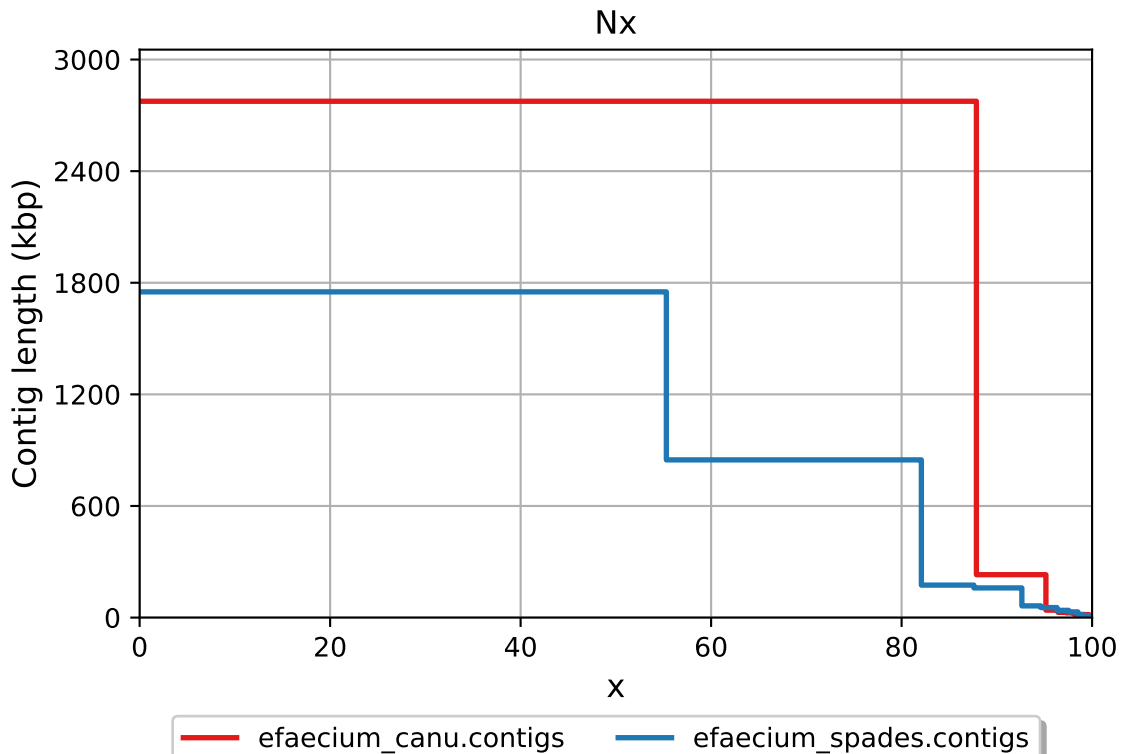
	efaecium_canu.contigs	efaecium_spades.contigs
# misassemblies	7	5
# contig misassemblies	7	5
# c. relocations	5	1
# c. translocations	2	4
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	5	3
Misassembled contigs length	3078811	267396
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	1
# mismatches	316	789
# indels	452	161
# indels (<= 5 bp)	441	146
# indels (> 5 bp)	11	15
Indels length	647	420

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).

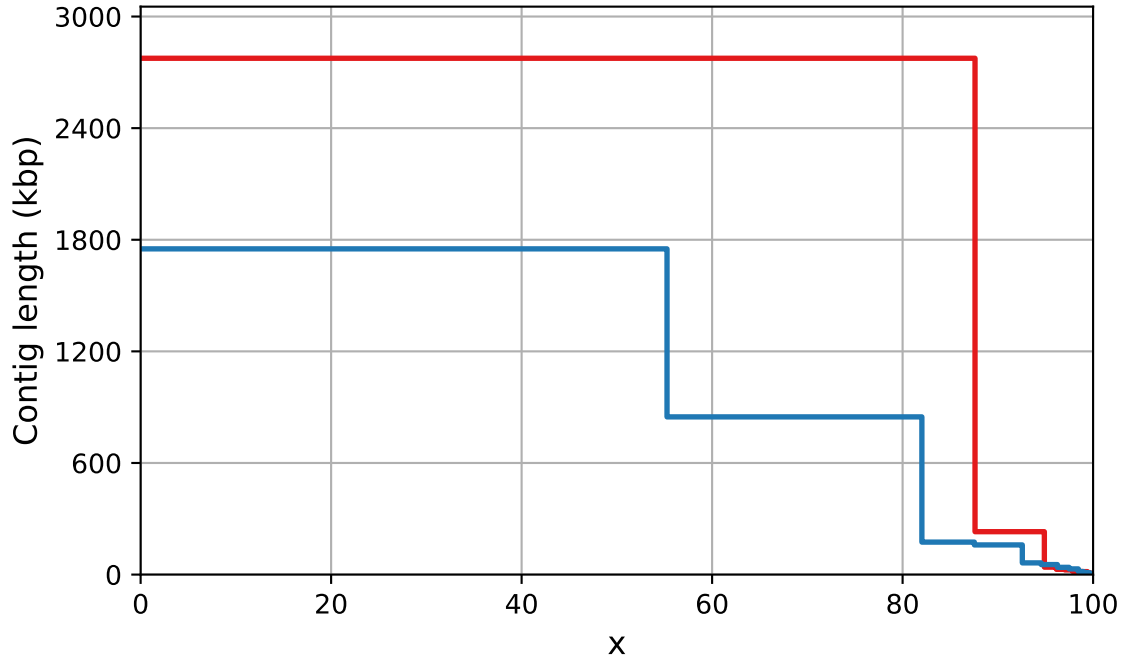
## Unaligned report

	efaecium_canu.contigs	efaecium_spades.contigs
# fully unaligned contigs	0	1
Fully unaligned length	0	3258
# partially unaligned contigs	0	1
Partially unaligned length	0	4360
# 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).



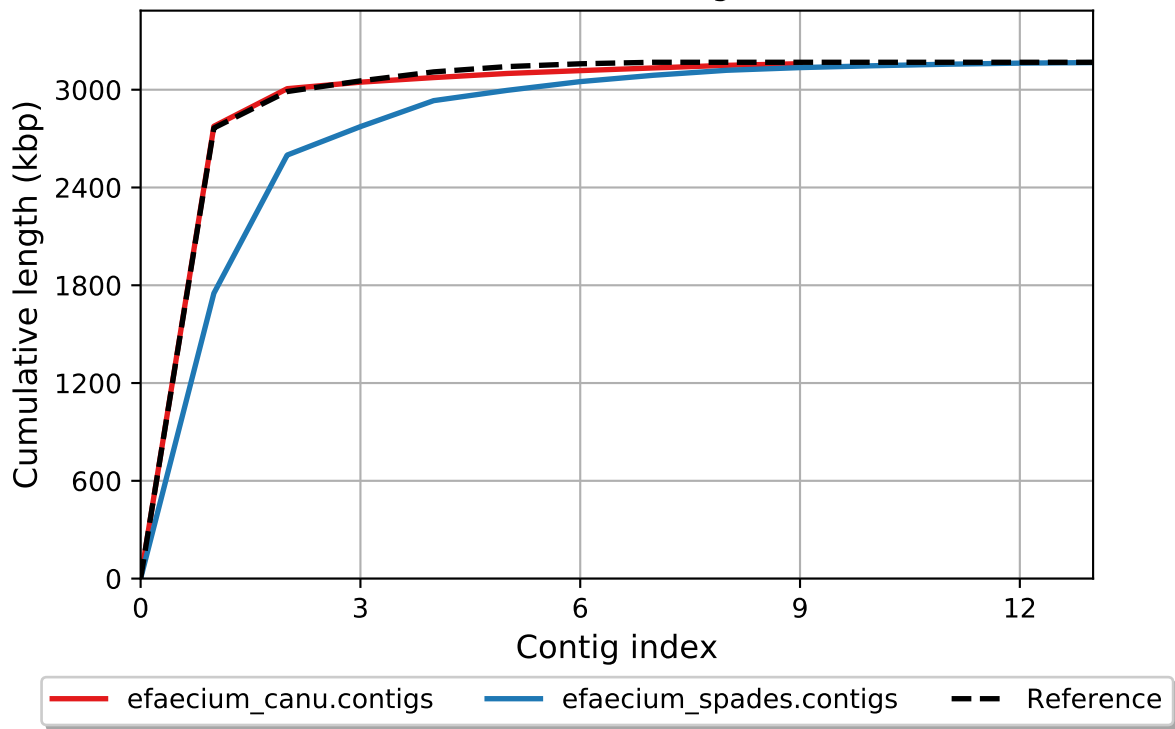
# NGx



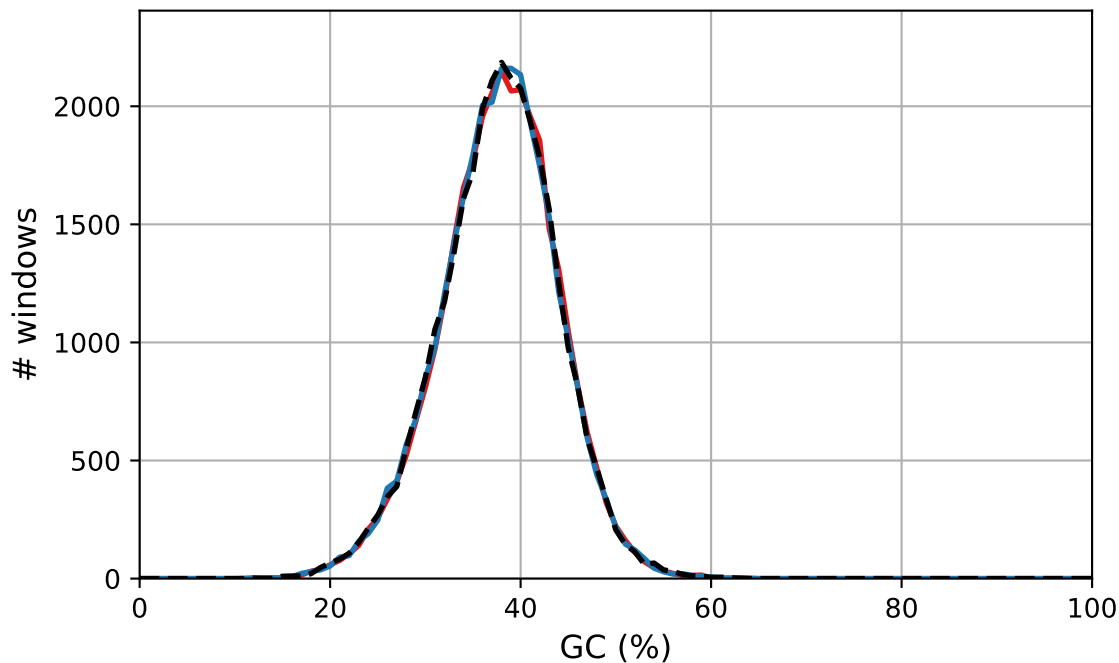
efaecium\_canu.contigs

efaecium\_spades.contigs

Cumulative length

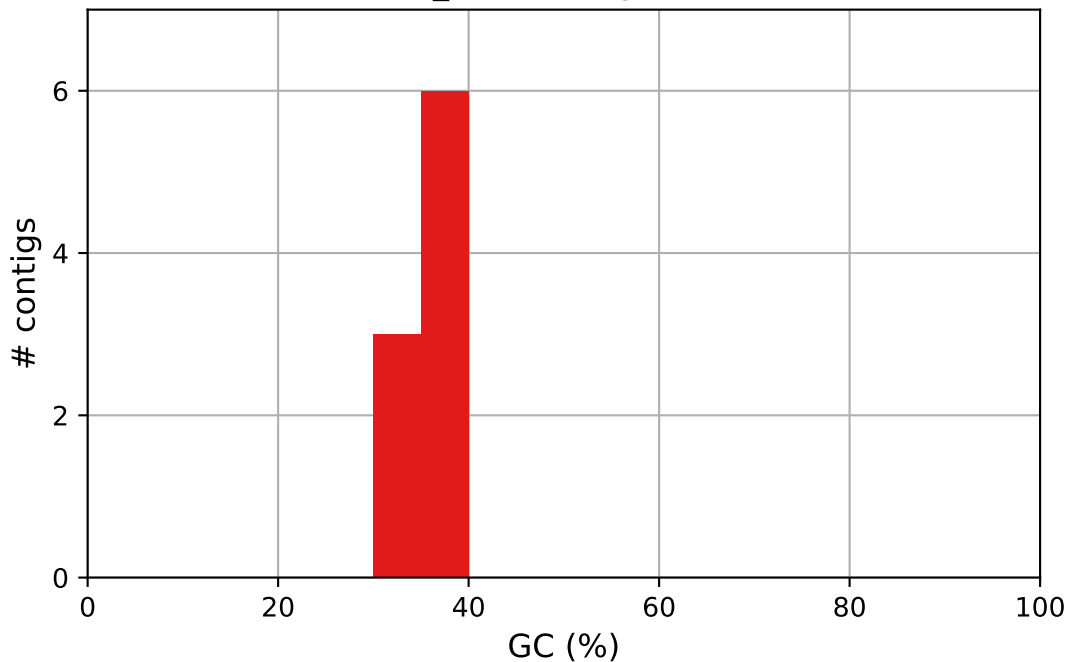


GC content



efaecium\_canu.contigs      efaecium\_spades.contigs      Reference

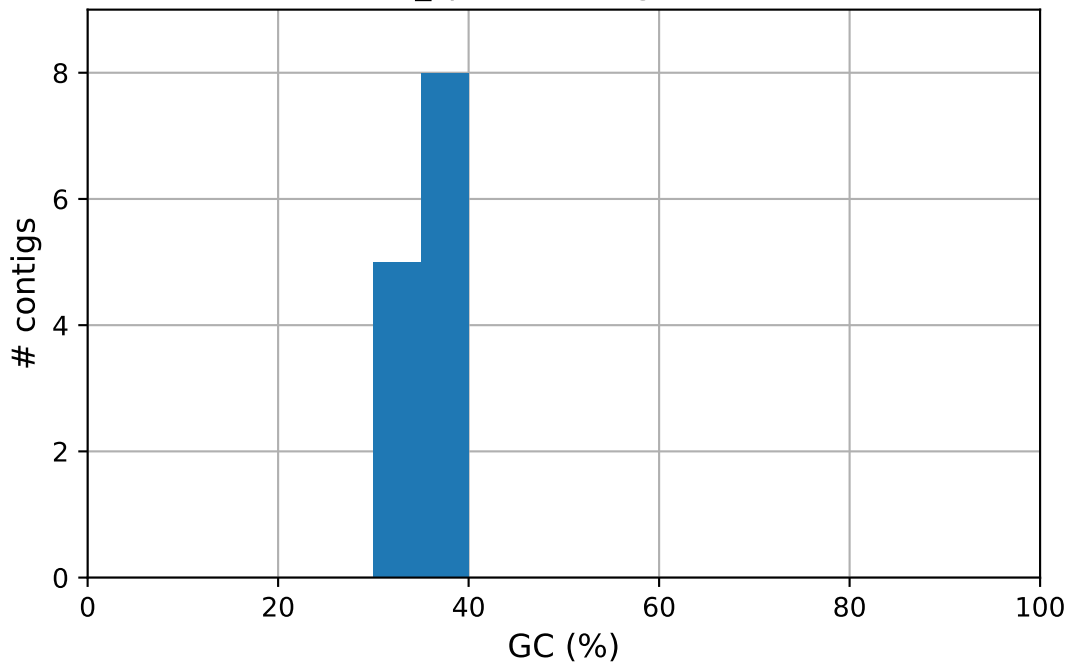
efaecium\_canu.contigs GC content



efaecium\_canu.contigs

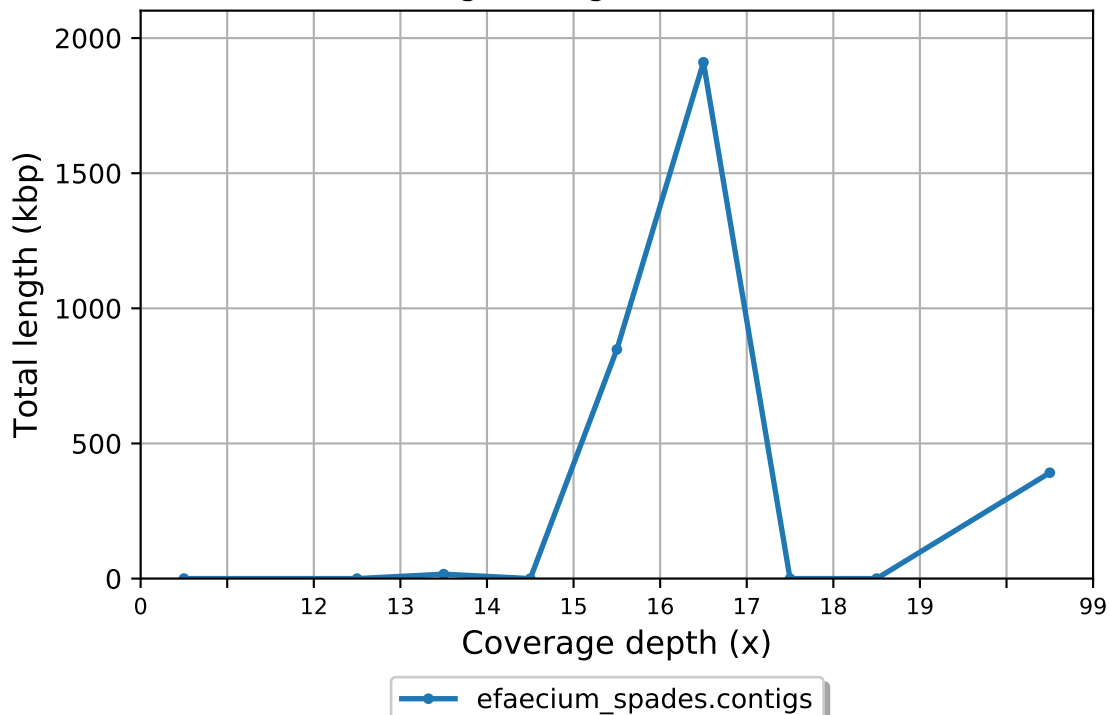


efaecium\_spades.contigs GC content

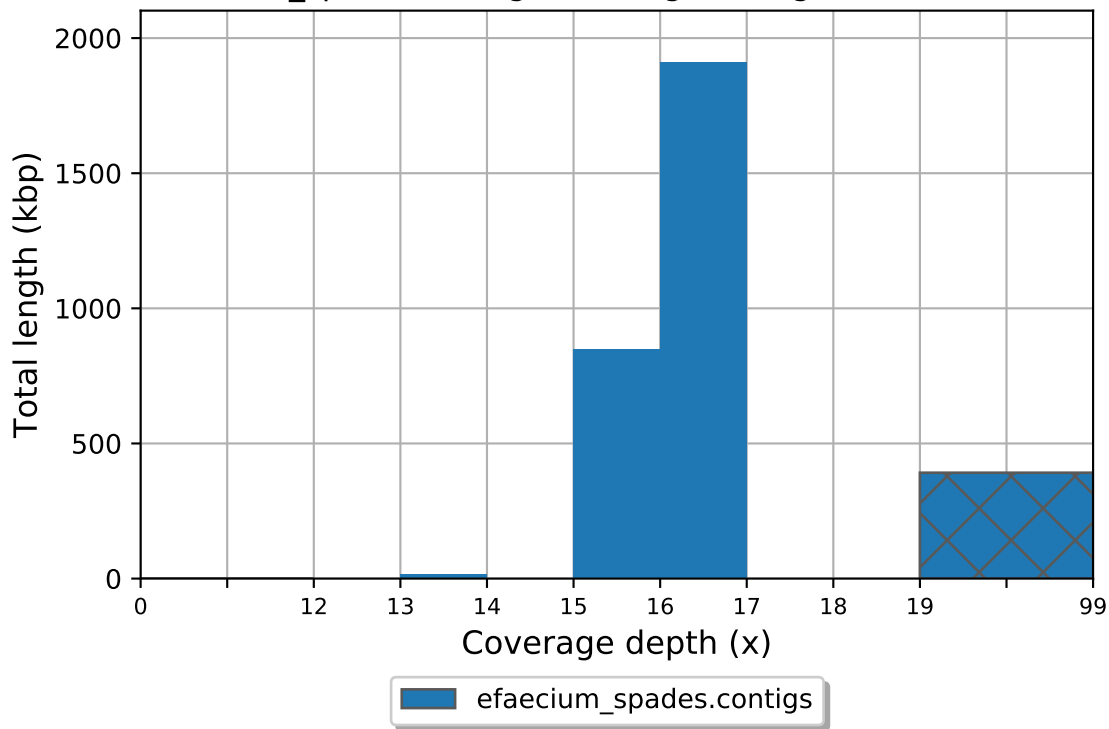


efaecium\_spades.contigs

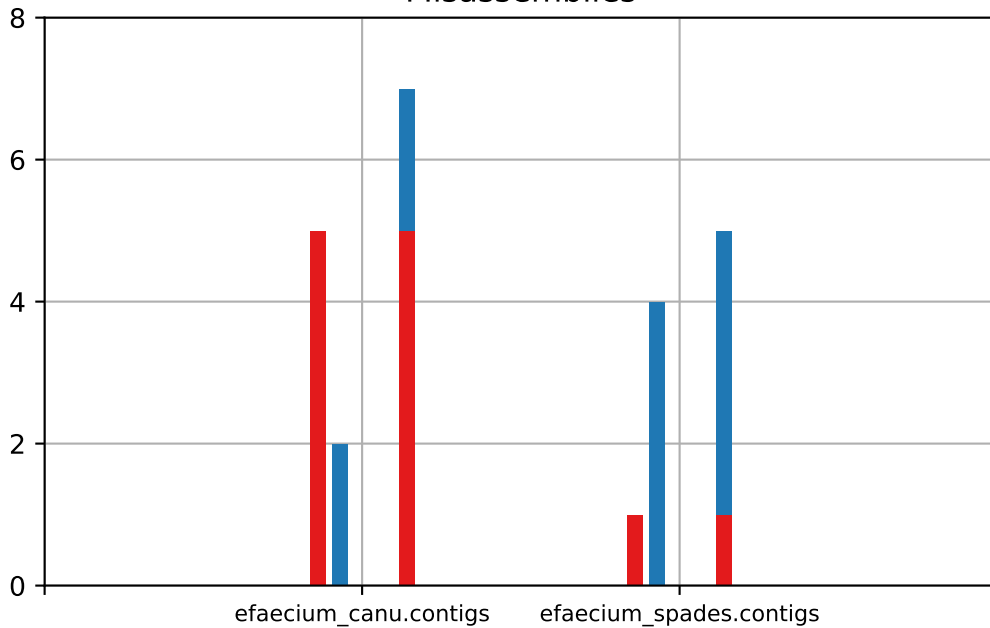
Coverage histogram (bin size: 1x)



efaecium\_spades.contigs coverage histogram (bin size: 1x)



## Misassemblies

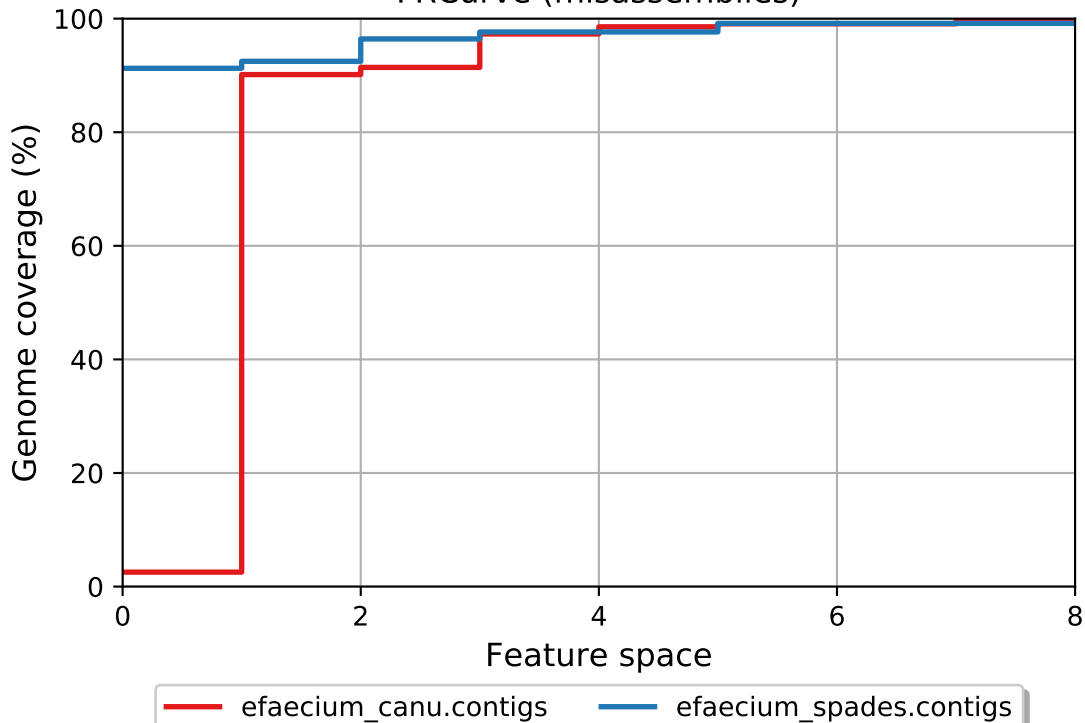


# relocations

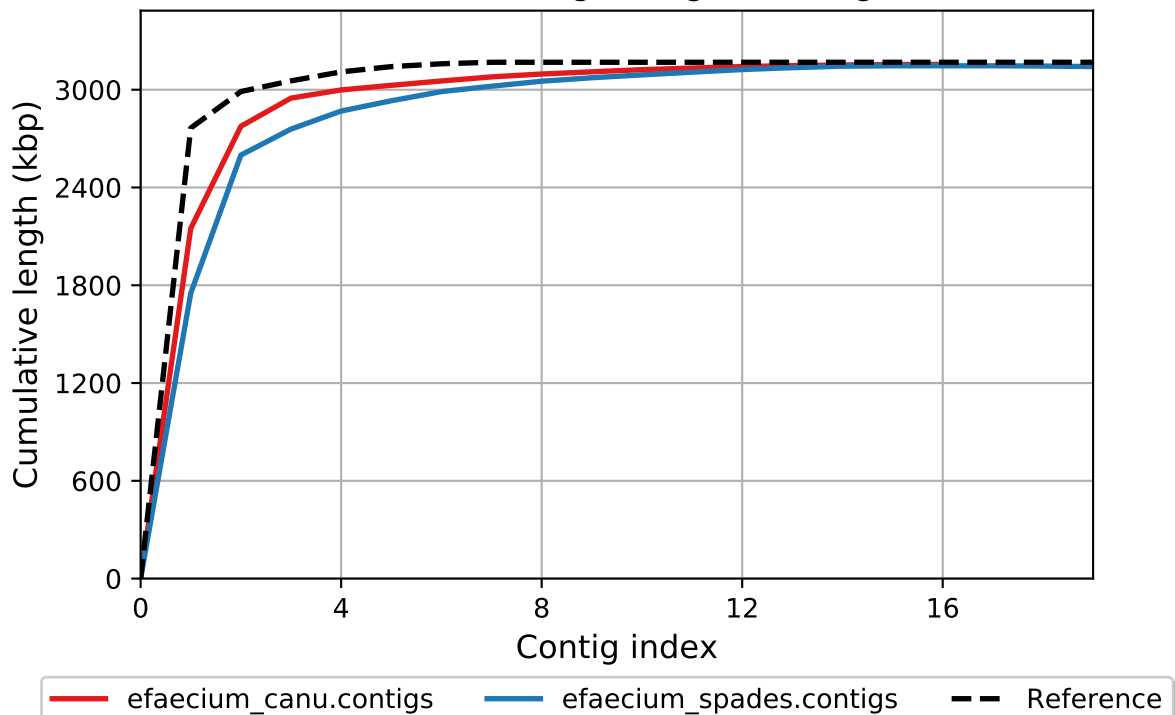


# translocations

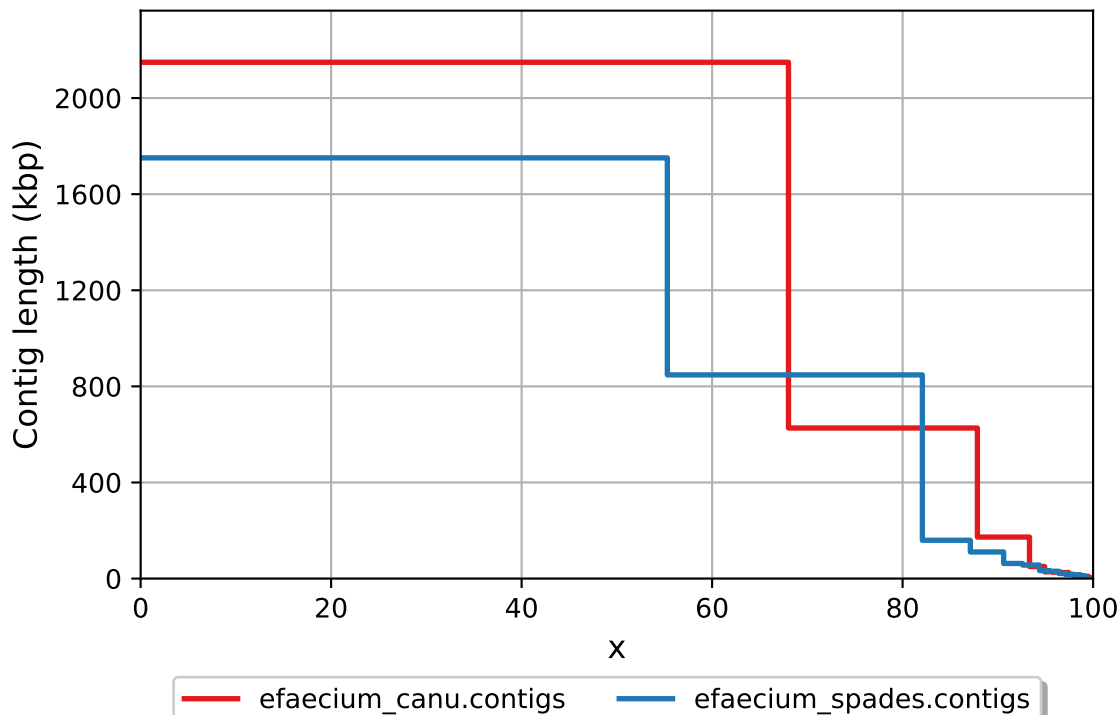
FRCurve (misassemblies)



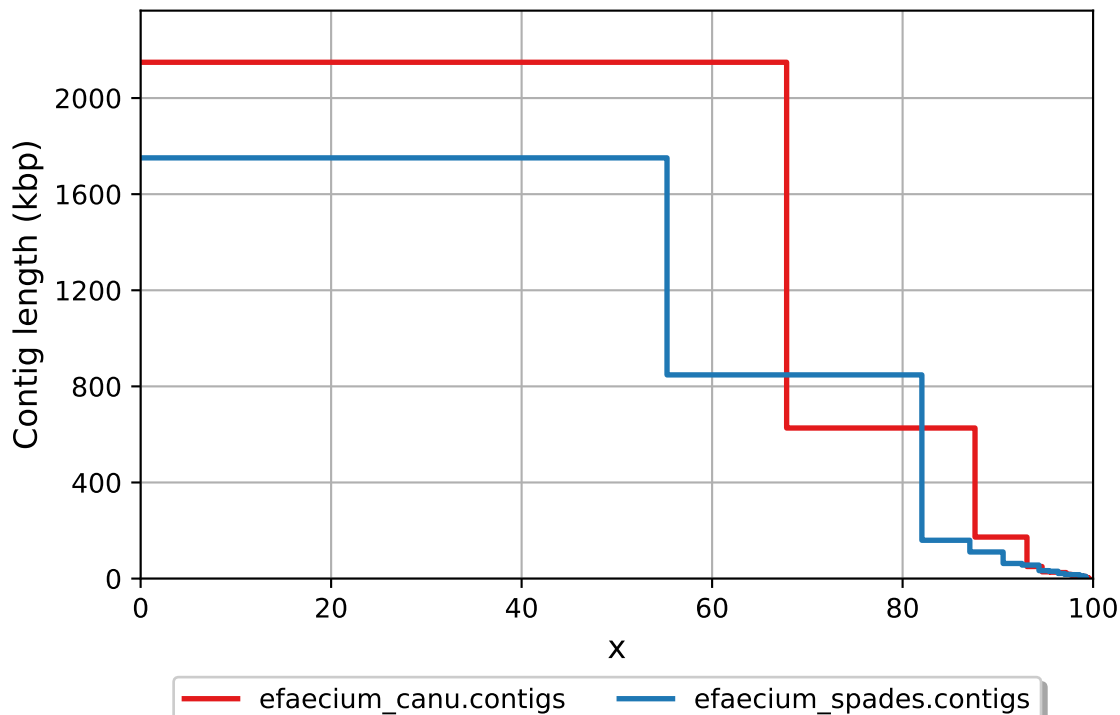
Cumulative length (aligned contigs)



NAx

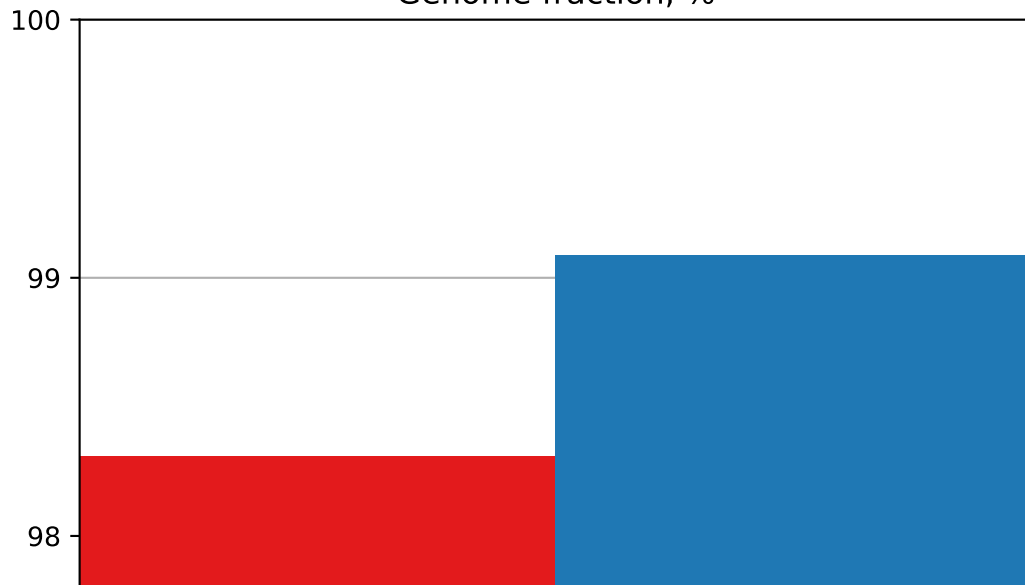


# NGAx





Genome fraction, %



efaecium\_canu.contigs



efaecium\_spades.contigs