

Report

	efaecium_spades.contigs	efaecium_canu.contigs	pilon
# contigs (>= 0 bp)	23	9	9
# contigs (>= 1000 bp)	13	9	9
# contigs (>= 5000 bp)	12	9	9
# contigs (>= 10000 bp)	10	8	8
# contigs (>= 25000 bp)	8	5	5
# contigs (>= 50000 bp)	6	2	2
Total length (>= 0 bp)	3167825	3159448	3159596
Total length (>= 1000 bp)	3166447	3159448	3159596
Total length (>= 5000 bp)	3163189	3159448	3159596
Total length (>= 10000 bp)	3147021	3149661	3149801
Total length (>= 25000 bp)	3119243	3099591	3099716
Total length (>= 50000 bp)	3049727	3006270	3006371
# contigs	13	9	9
Largest contig	1751056	2775643	2775723
Total length	3166447	3159448	3159596
Reference length	3168410	3168410	3168410
GC (%)	37.69	37.78	37.78
Reference GC (%)	37.70	37.70	37.70
N50	1751056	2775643	2775723
NG50	1751056	2775643	2775723
N75	847797	2775643	2775723
NG75	847797	2775643	2775723
L50	1	1	1
LG50	1	1	1
L75	2	1	1
LG75	2	1	1
# misassemblies	5	7	7
# misassembled contigs	3	5	5
Misassembled contigs length	267396	3078811	3078924
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	1	0	0
# unaligned contigs	1 + 1 part	0 + 0 part	0 + 0 part
Unaligned length	7618	0	0
Genome fraction (%)	99.088	98.309	98.309
Duplication ratio	1.006	1.014	1.014
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	25.13	10.14	10.56
# indels per 100 kbp	5.13	14.51	7.99
Largest alignment	1751056	2148961	2149027
Total aligned length	3141966	3155449	3155597
NA50	1751056	2148961	2149027
NGA50	1751056	2148961	2149027
NA75	847797	626682	626696
NGA75	847797	626682	626696
LA50	1	1	1
LGA50	1	1	1
LA75	2	2	2
LGA75	2	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

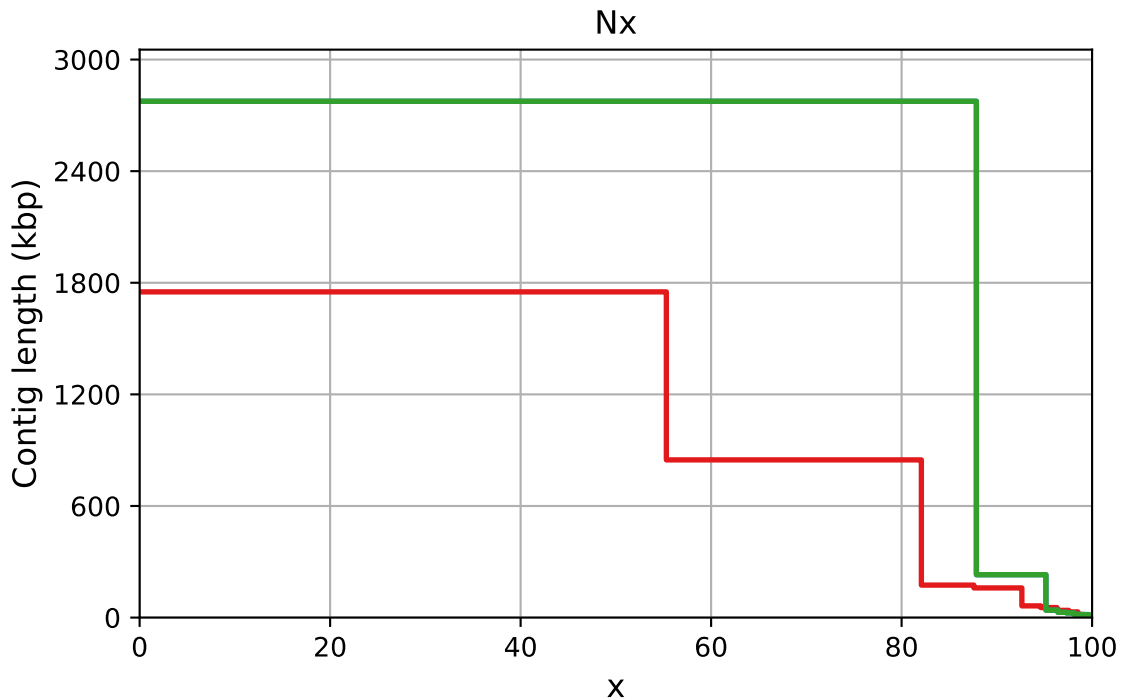
	efaecium_spades.contigs	efaecium_canu.contigs	pilon
# misassemblies	5	7	7
# contig misassemblies	5	7	7
# c. relocations	1	5	5
# c. translocations	4	2	2
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	3	5	5
Misassembled contigs length	267396	3078811	3078924
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	1	0	0
# mismatches	789	316	329
# indels	161	452	249
# indels (<= 5 bp)	146	441	238
# indels (> 5 bp)	15	11	11
Indels length	420	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

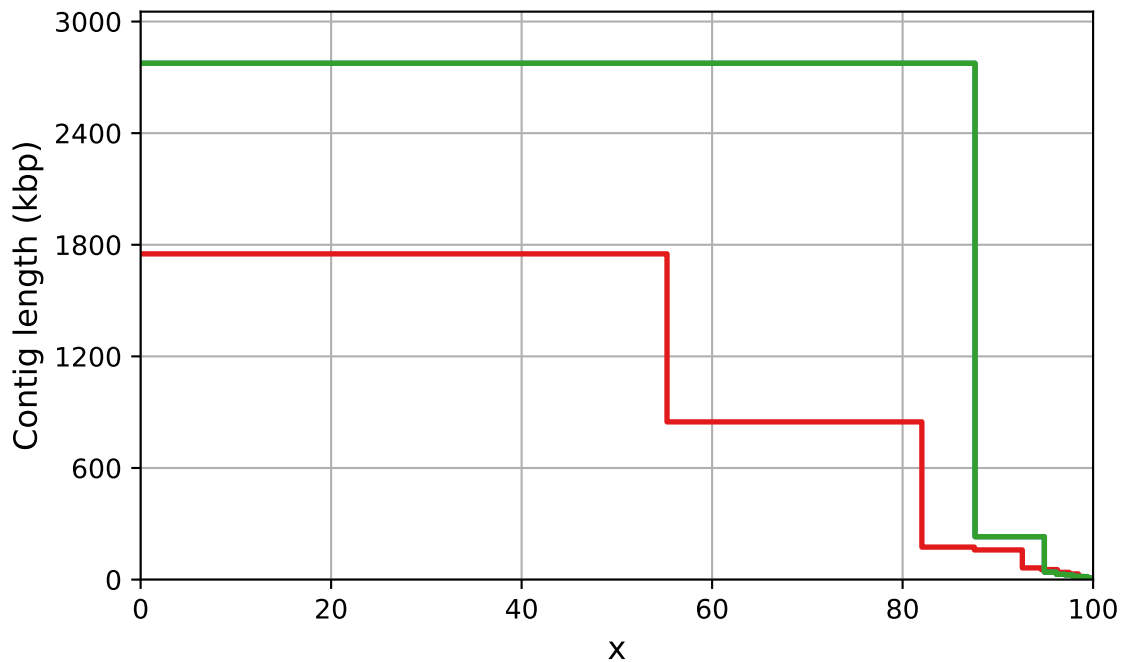
	efaecium_spades.contigs	efaecium_canu.contigs	pilon
# fully unaligned contigs	1	0	0
Fully unaligned length	3258	0	0
# partially unaligned contigs	1	0	0
Partially unaligned length	4360	0	0
# N's	0	0	0

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).



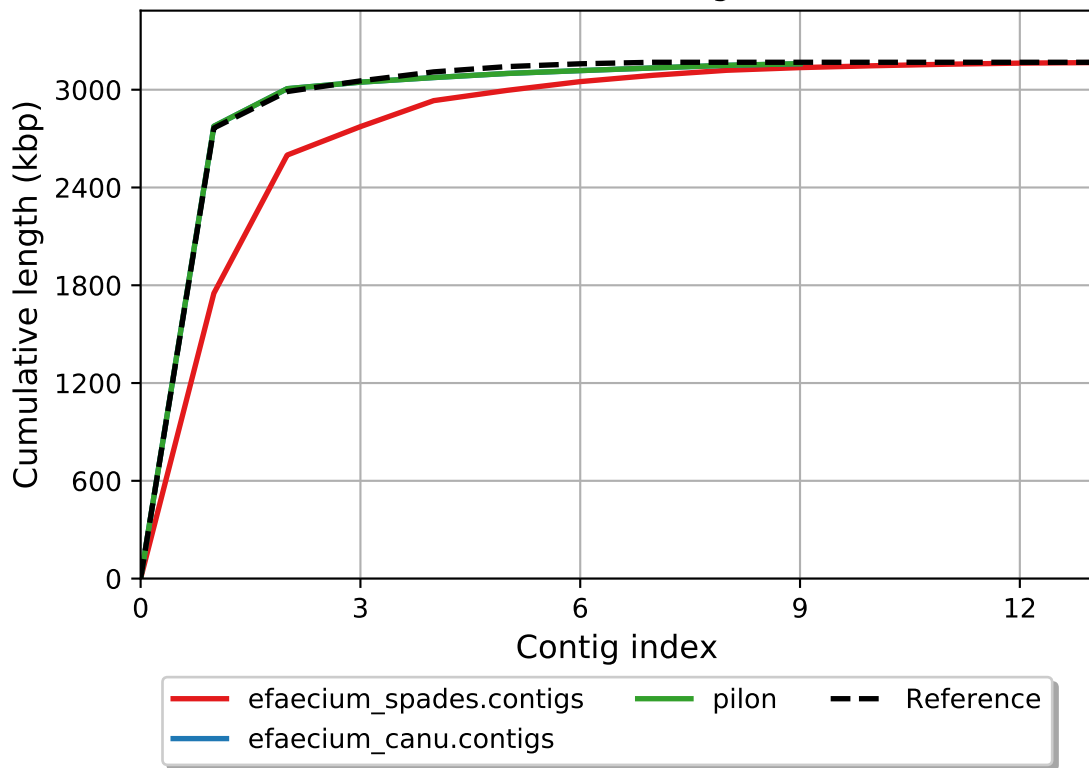
efaecium_spades.contigs efaecium_canu.contigs pilon

NGx

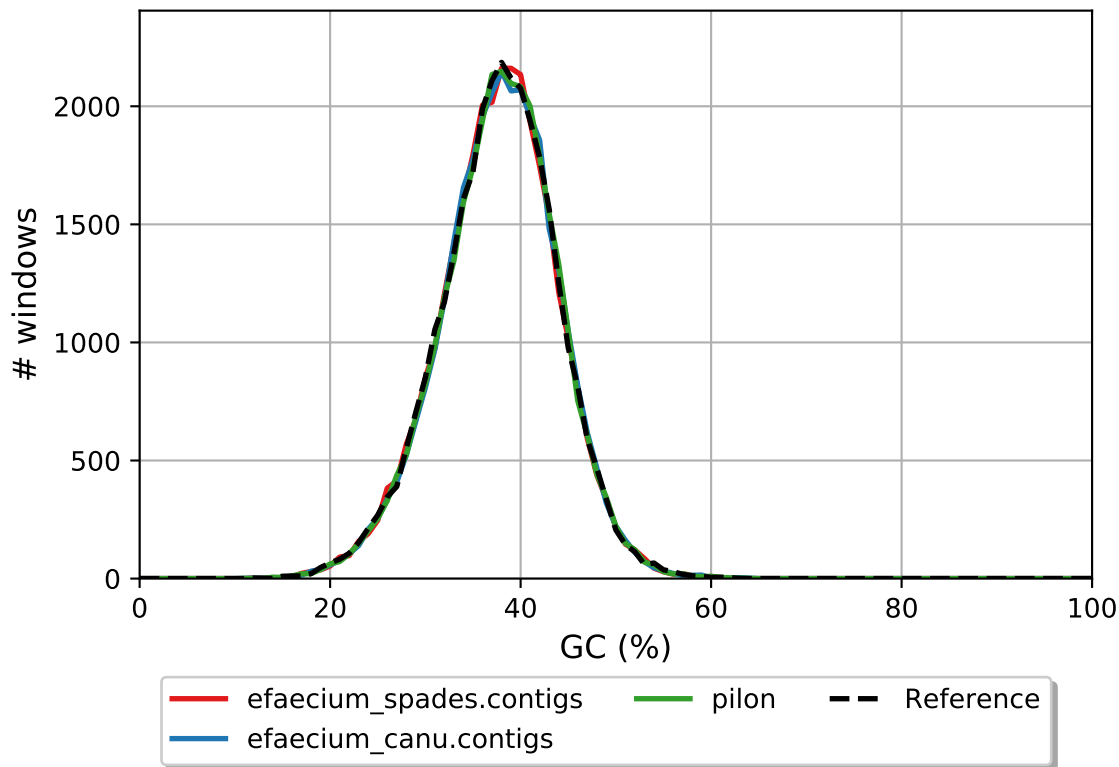


efaecium_spades.contigs efaecium_canu.contigs pilon

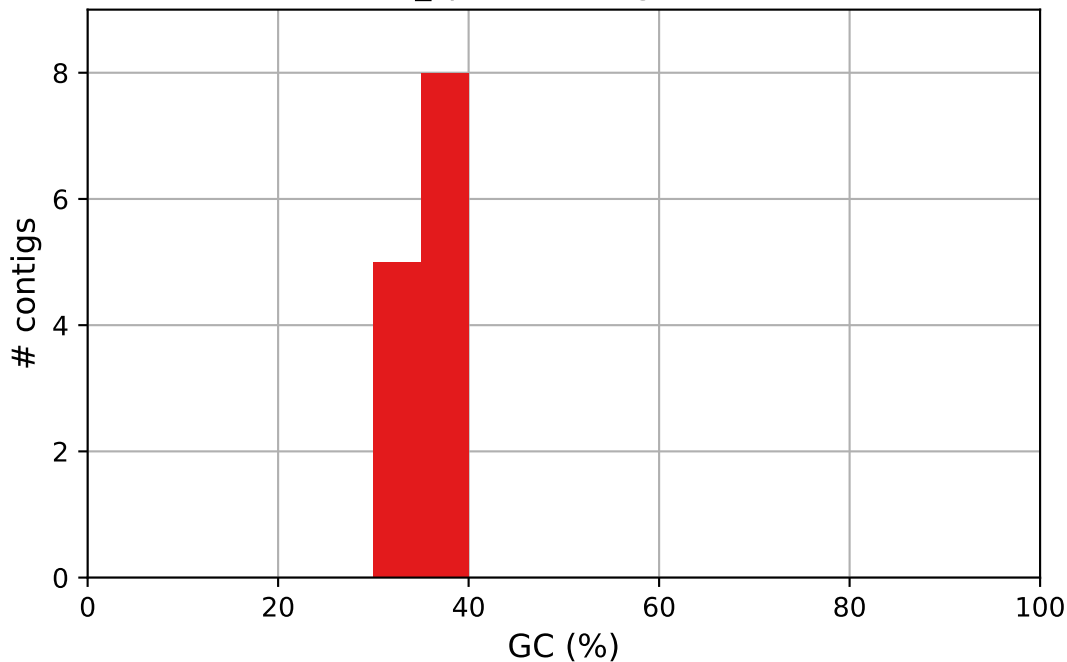
Cumulative length



GC content

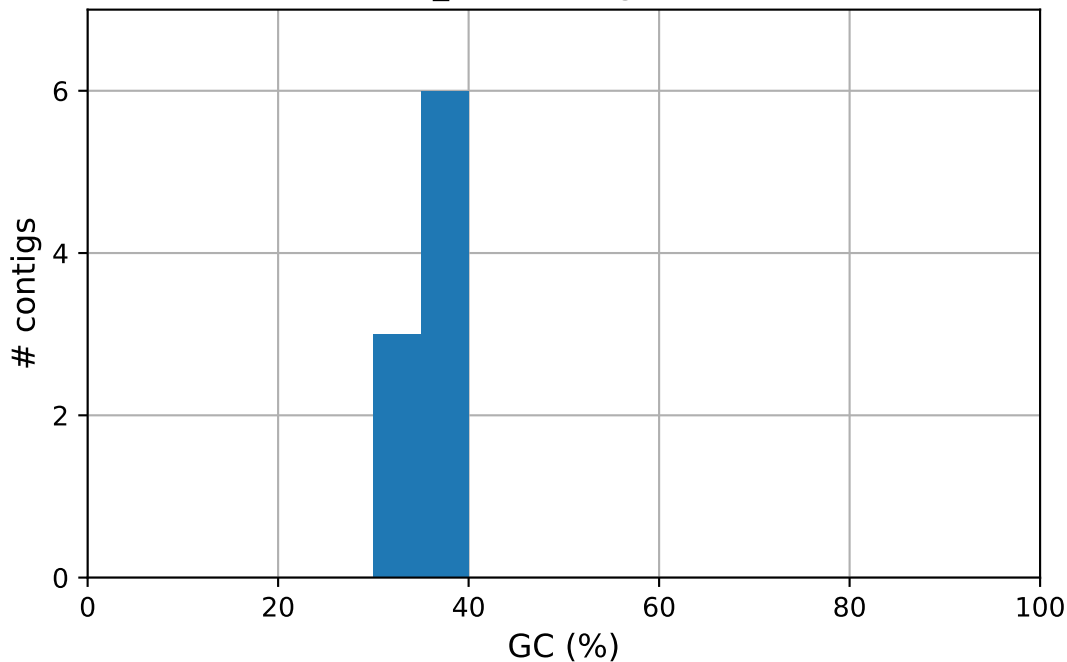


efaecium_spades.contigs GC content



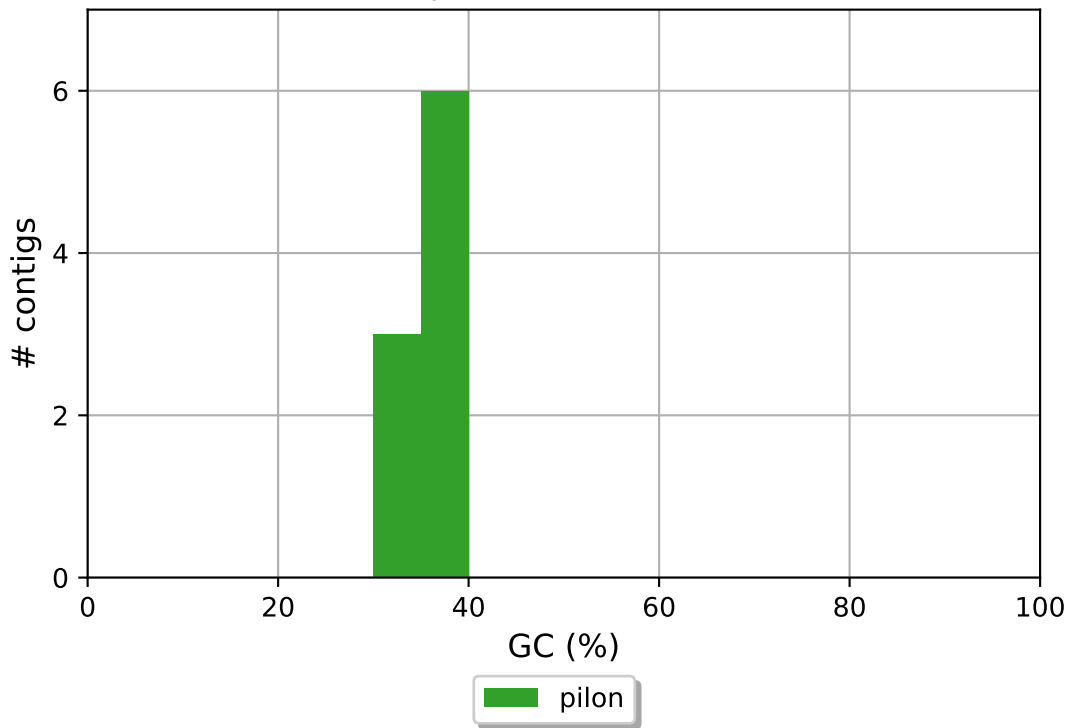
efaecium_spades.contigs

efaecium_canu.contigs GC content

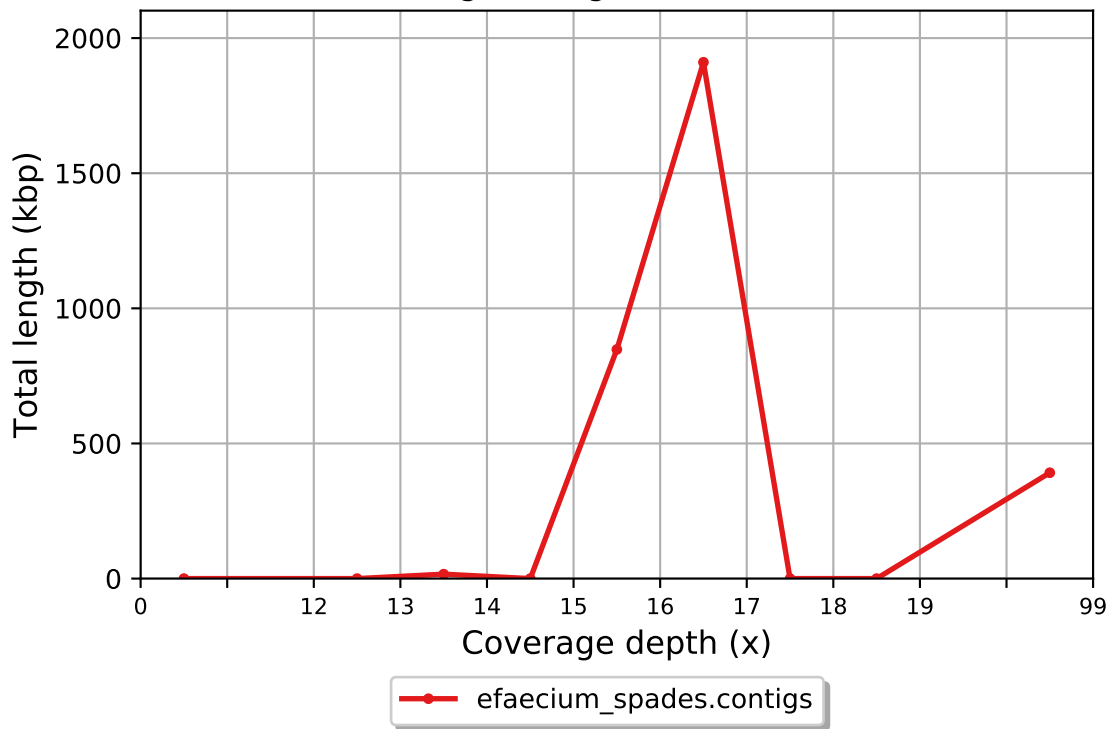


efaecium_canu.contigs

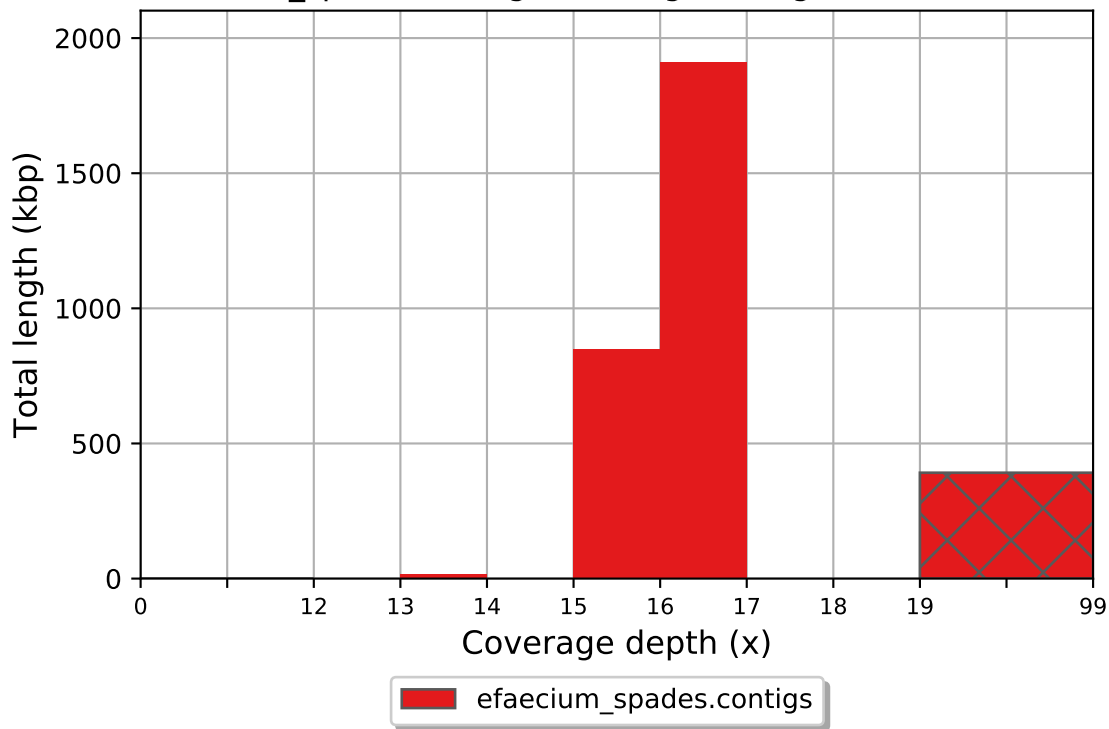
pilon GC content



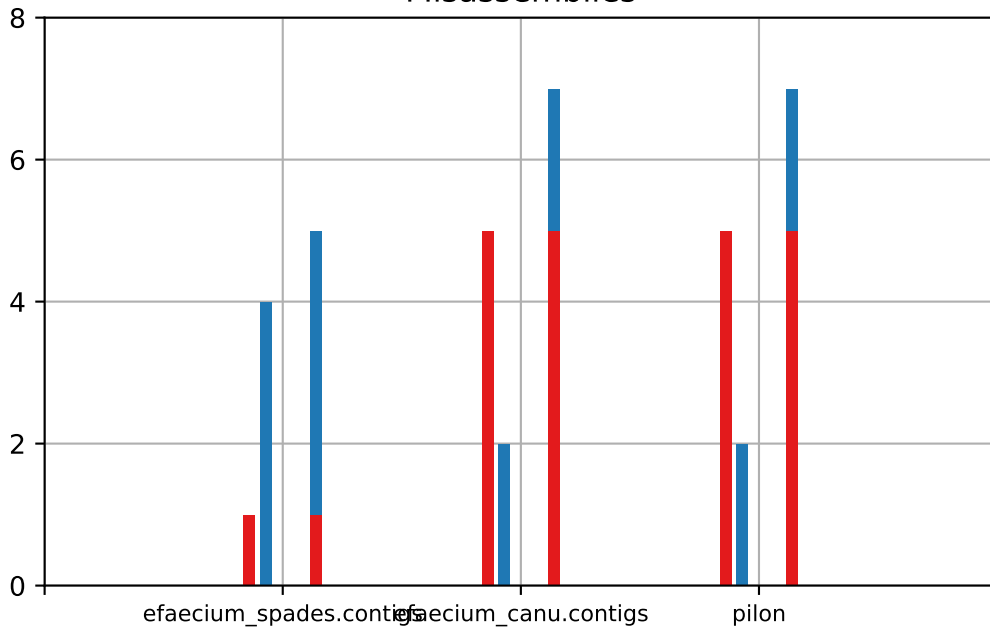
Coverage histogram (bin size: 1x)



efaecium_spades.contigs coverage histogram (bin size: 1x)



Misassemblies

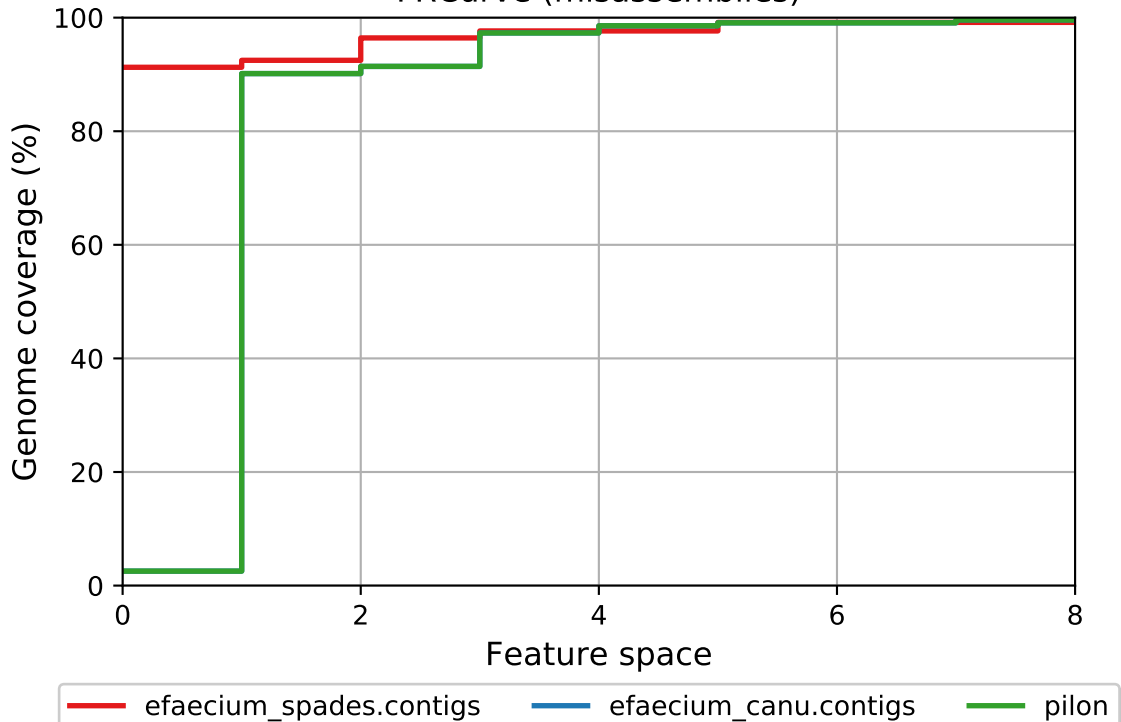


relocations

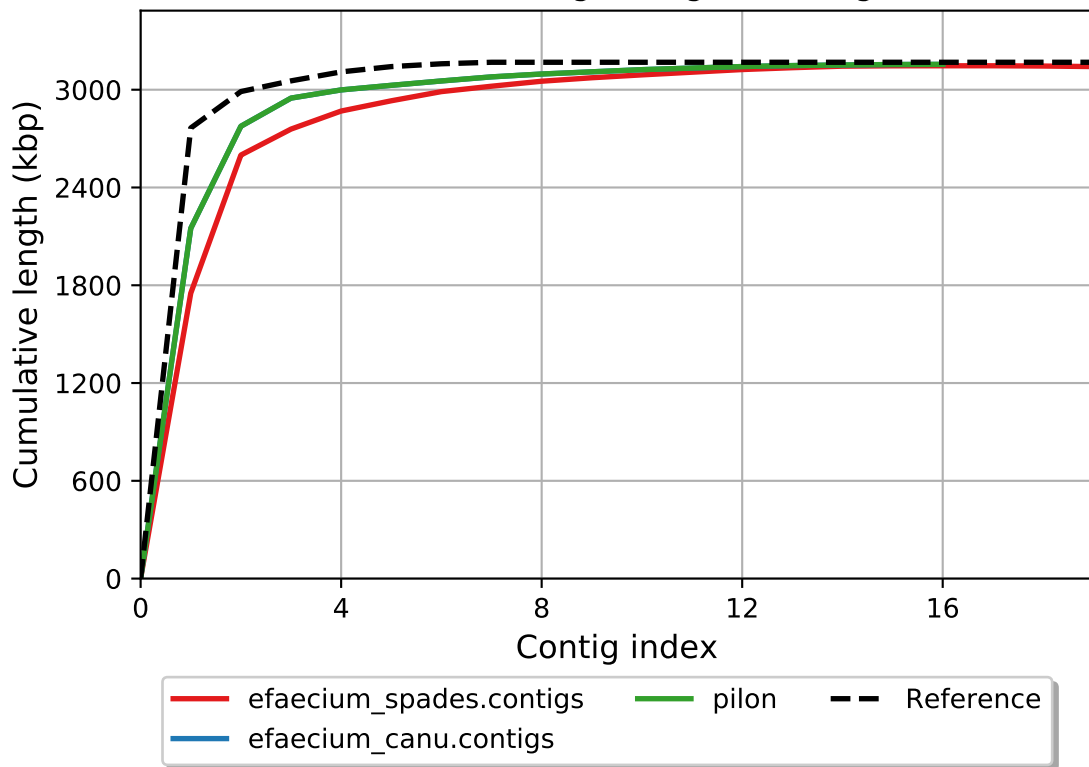


translocations

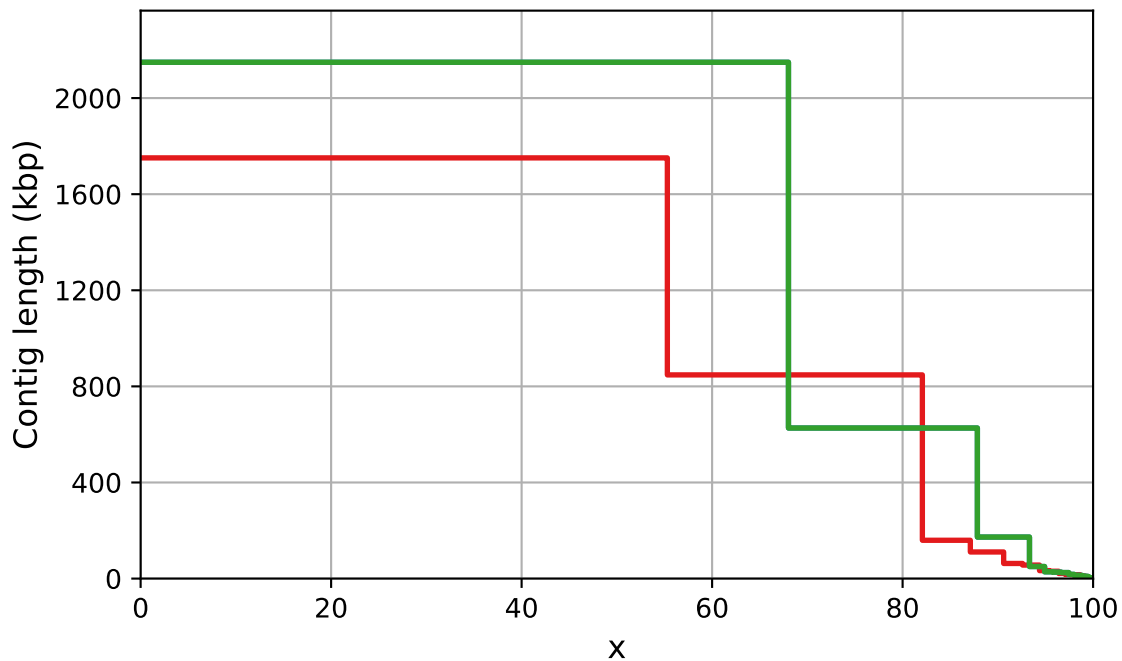
FRCurve (misassemblies)



Cumulative length (aligned contigs)

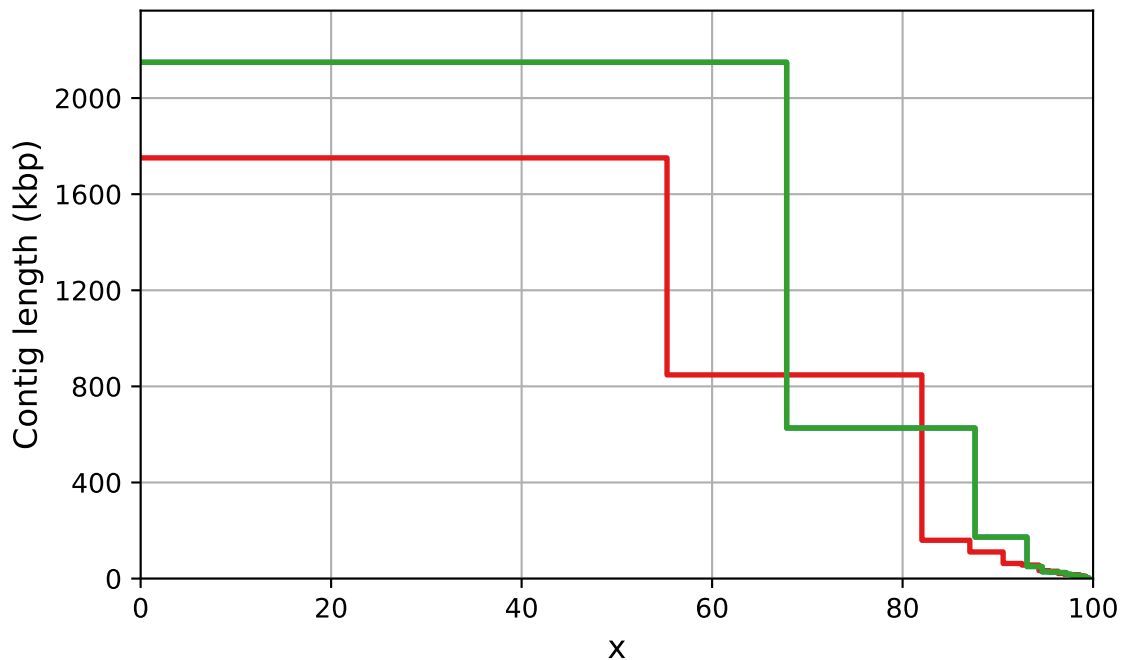


NAx



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NGAx



efaecium_spades.contigs efaecium_canu.contigs pilon

Genome fraction, %

