

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	2765010	2765010
GC (%)	37.78	37.78
Reference GC (%)	38.11	38.11
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	3	4
# misassembled contigs	2	2
Misassembled contigs length	2782003	2783322
# local misassemblies	0	0
# unaligned mis. contigs	1	1
# unaligned contigs	4 + 3 part	4 + 3 part
Unaligned length	322065	322051
Genome fraction (%)	100.000	100.000
Duplication ratio	1.020	1.020
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	0.00	0.04
# indels per 100 kbp	0.22	4.38
Largest alignment	2195417	2195330
Total aligned length	2818986	2820305
NA50	2195417	2195330
NGA50	2195417	2195330
NA75	578286	578258
NGA75	2195417	2195330
LA50	1	1
LGA50	1	1
LA75	2	2
LGA75	1	1

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

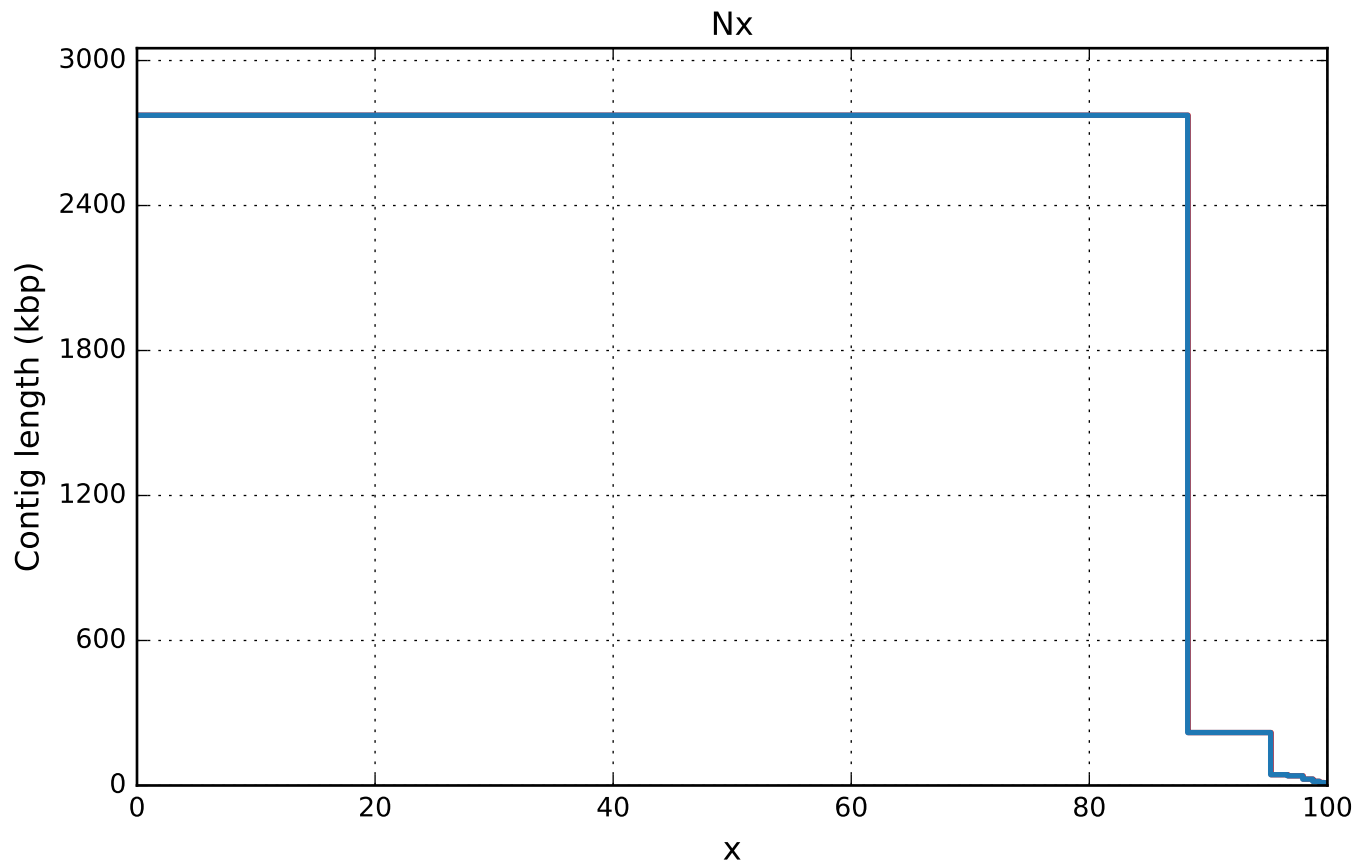
	pilon	efaecium.contigs
# misassemblies	3	4
# relocations	3	4
# translocations	0	0
# inversions	0	0
# misassembled contigs	2	2
Misassembled contigs length	2782003	2783322
# local misassemblies	0	0
# unaligned mis. contigs	1	1
# mismatches	0	1
# indels	6	121
# indels (<= 5 bp)	6	121
# indels (> 5 bp)	0	0
Indels length	6	123

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).

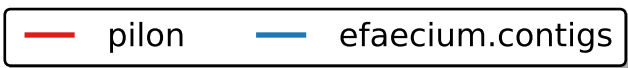
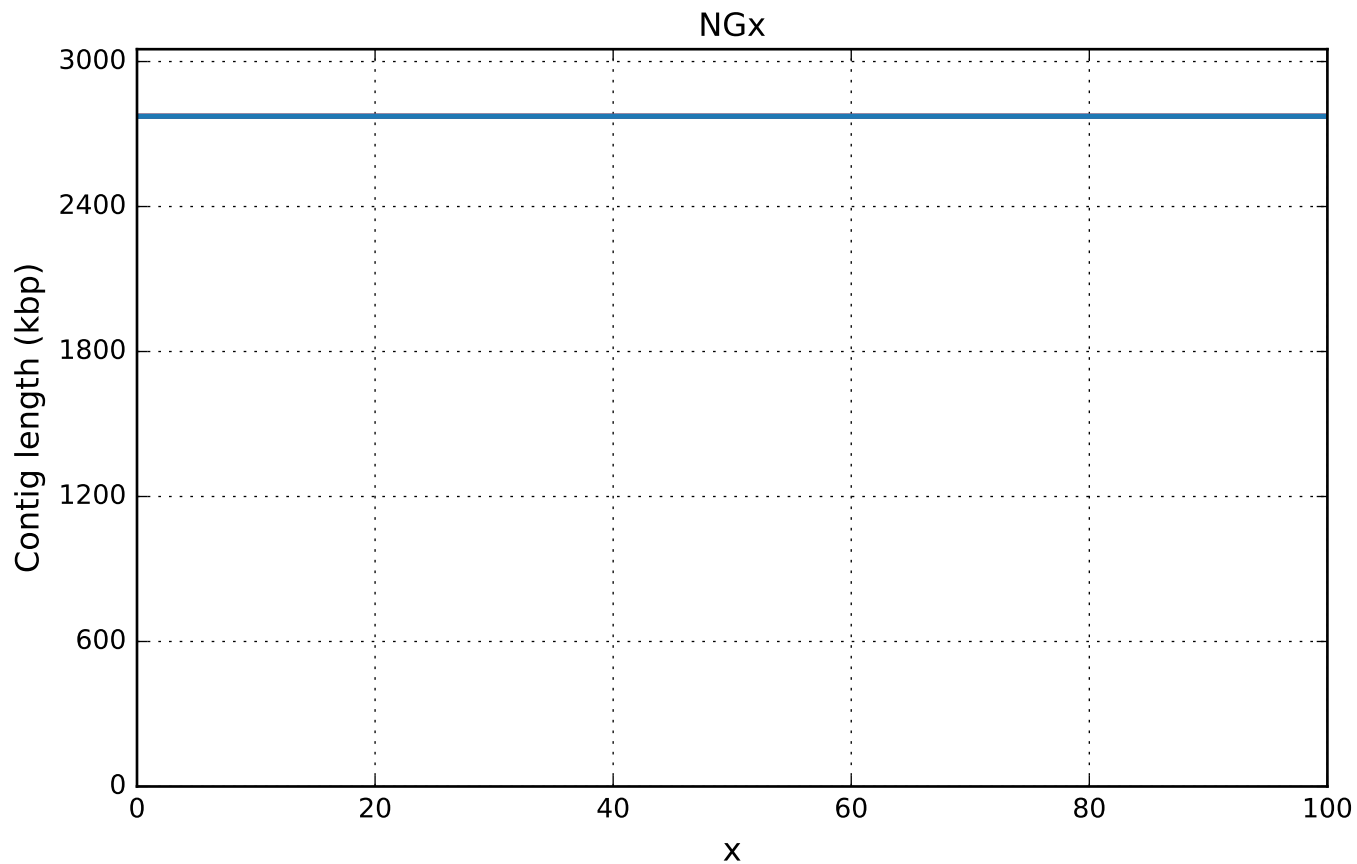
Unaligned report

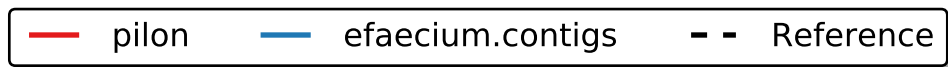
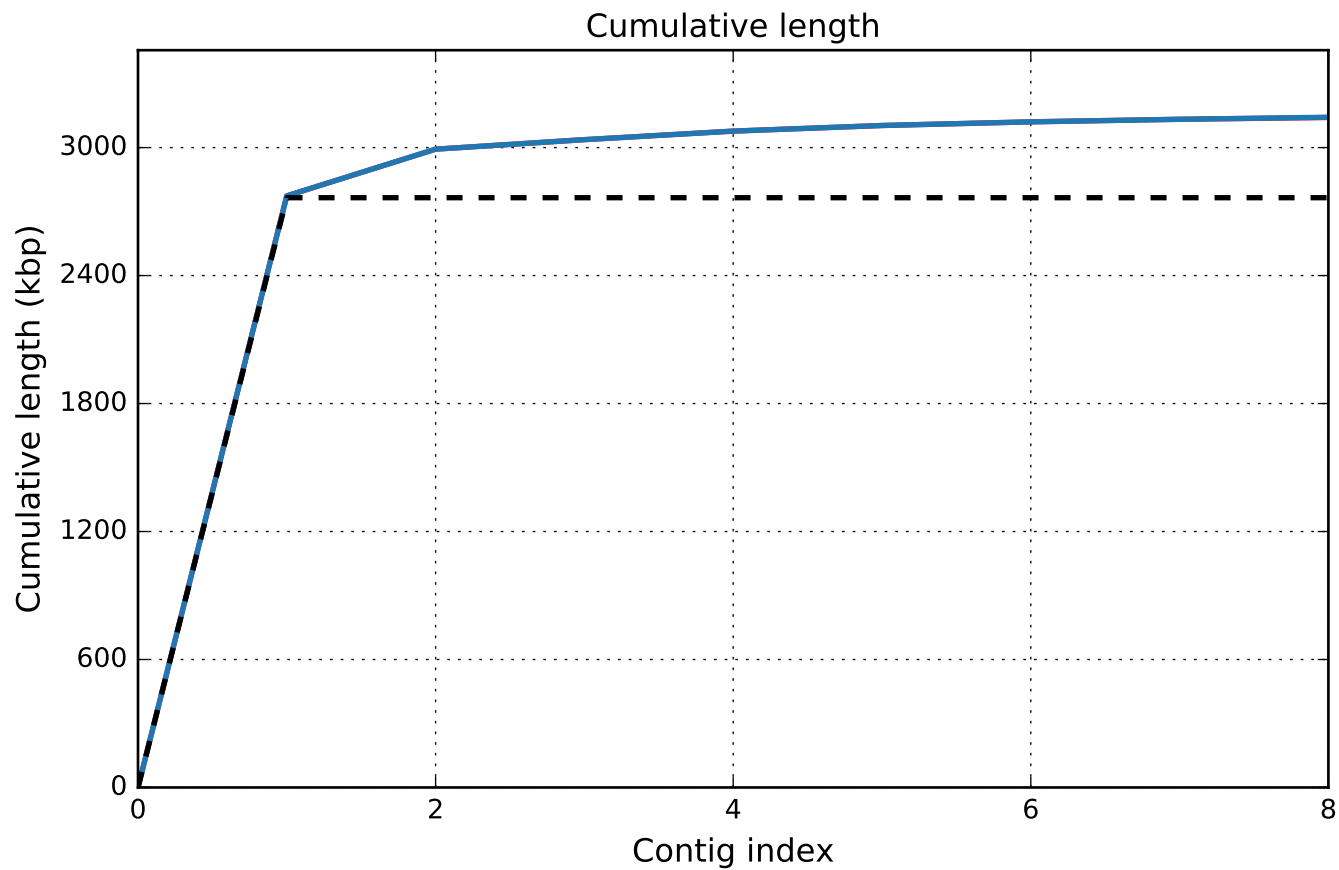
	pilon	efaecium.contigs
# fully unaligned contigs	4	4
Fully unaligned length	100053	100025
# partially unaligned contigs	3	3
Partially unaligned length	222012	222026
# N's	0	0

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).

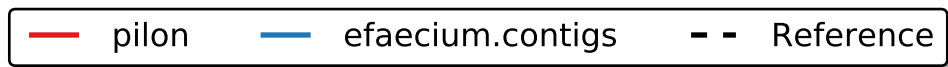
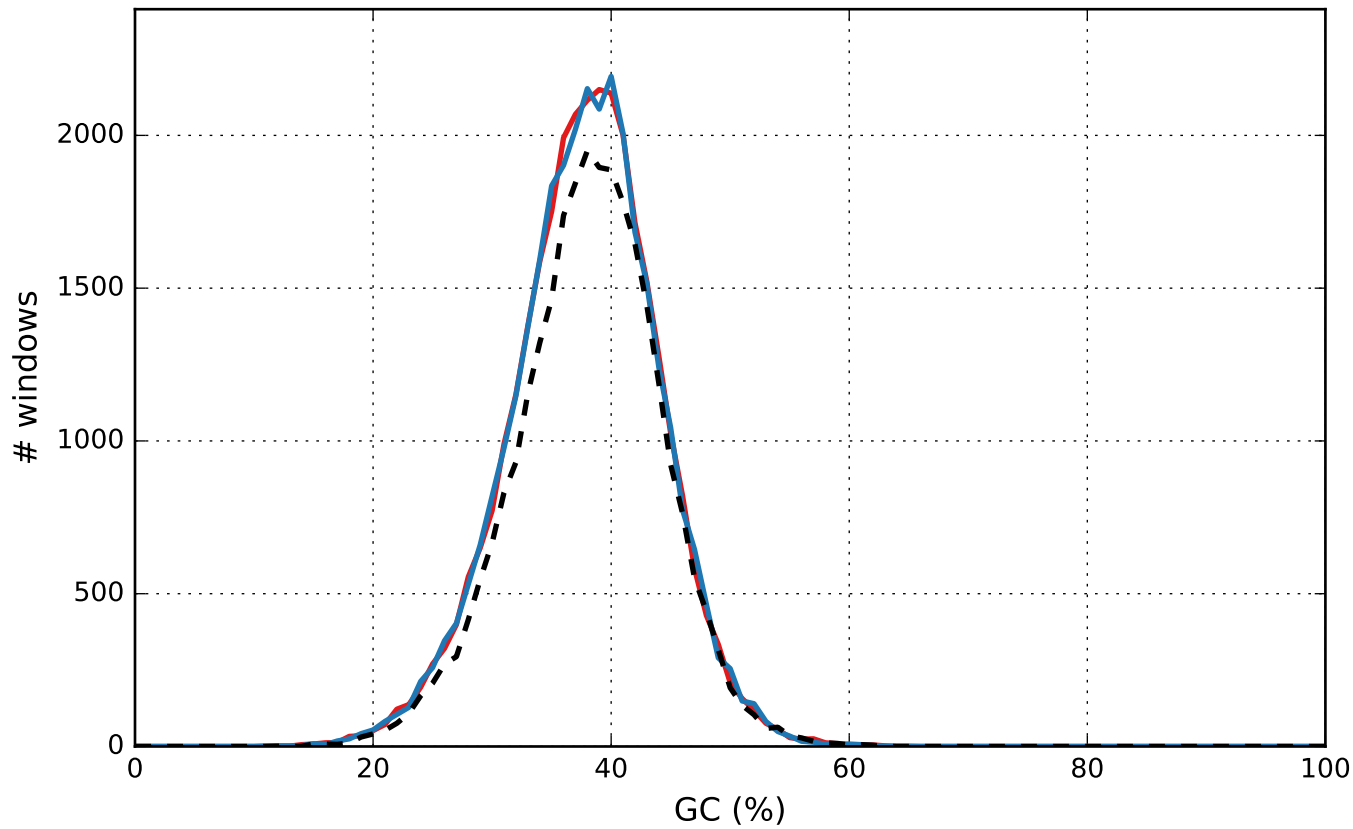


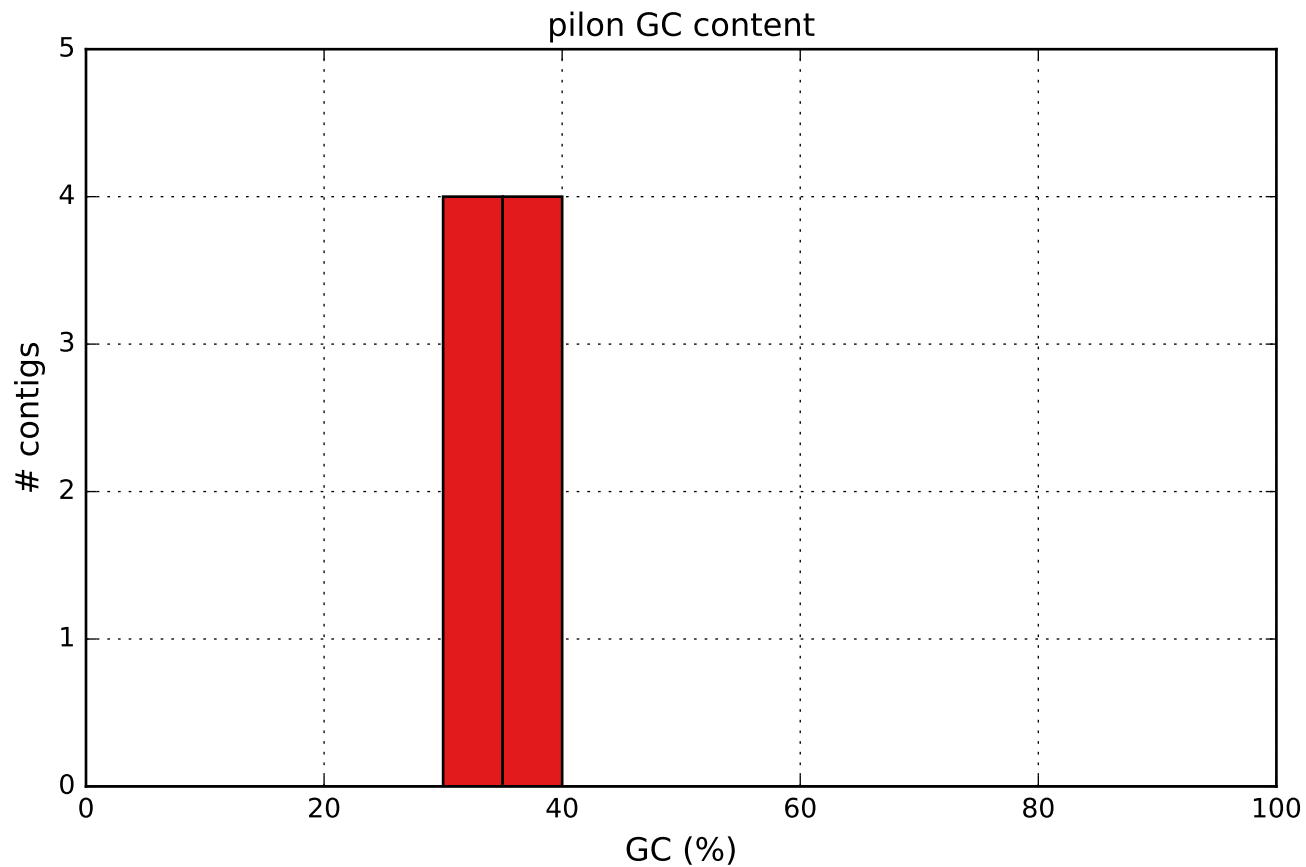
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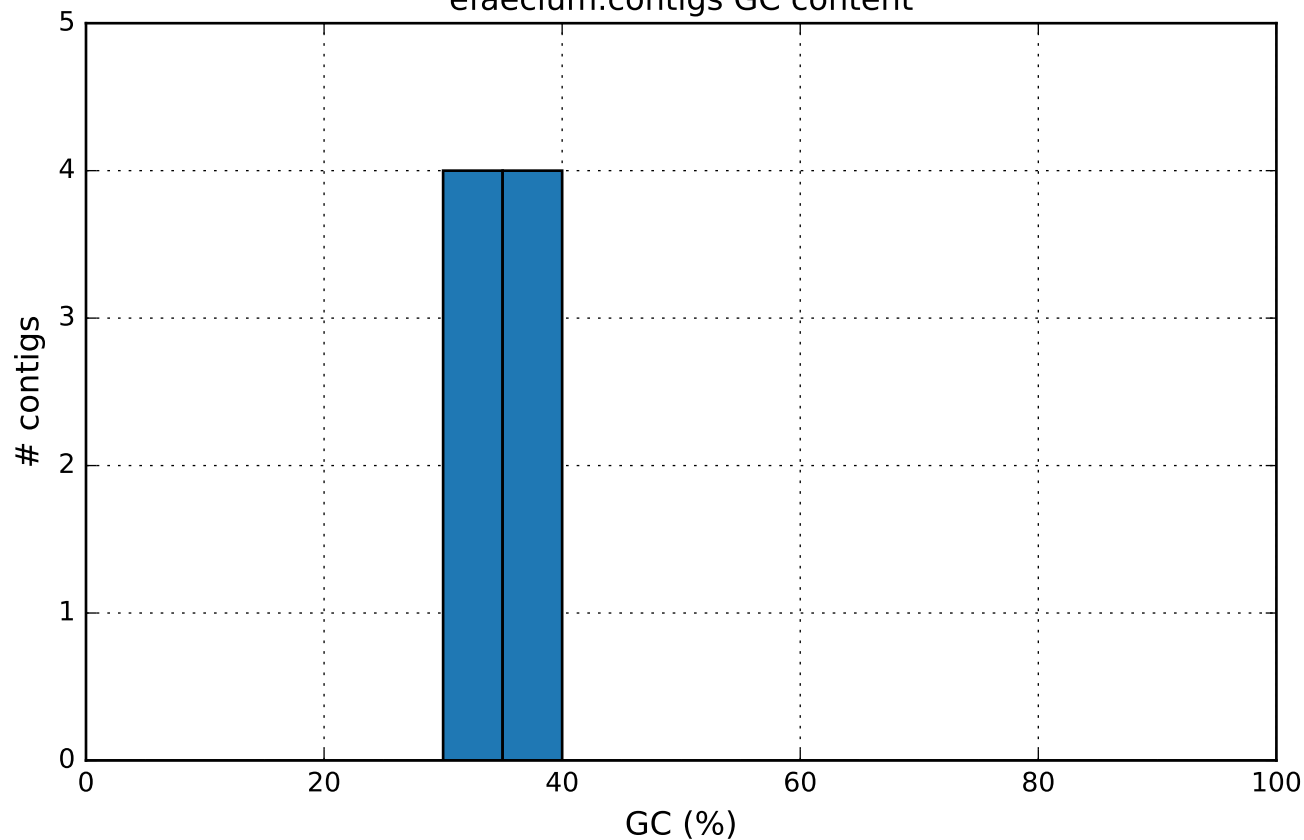


GC content

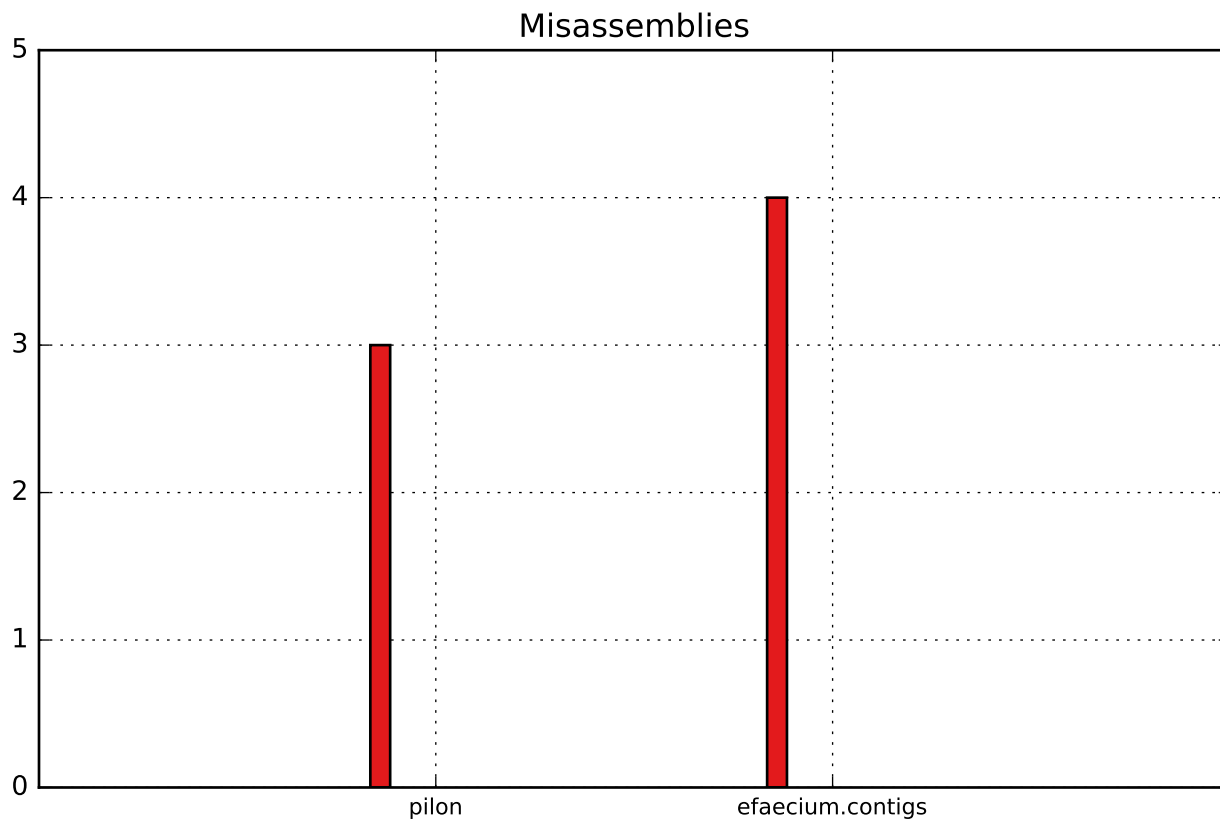




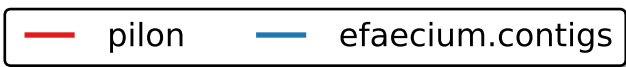
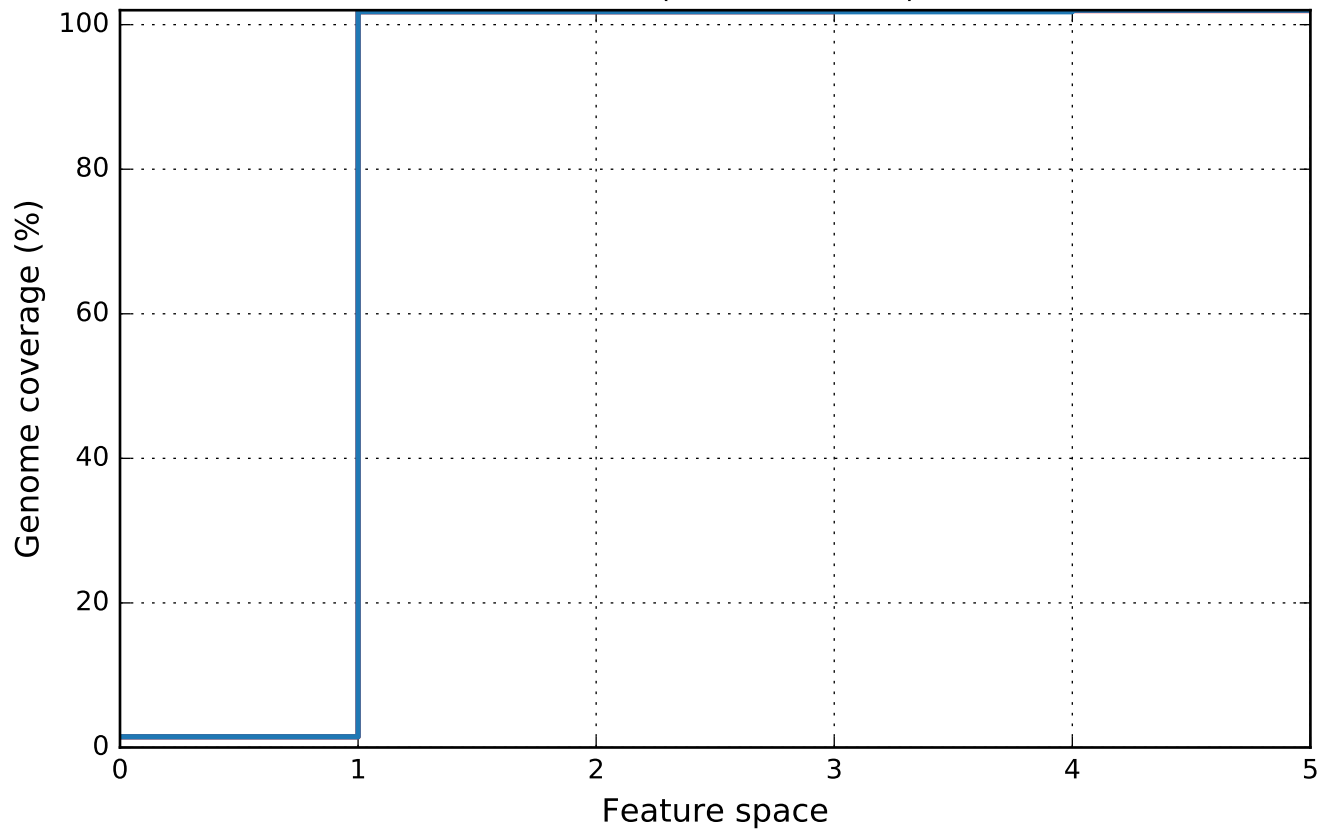
efaecium.contigs GC content



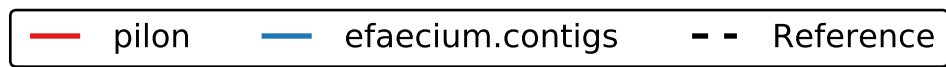
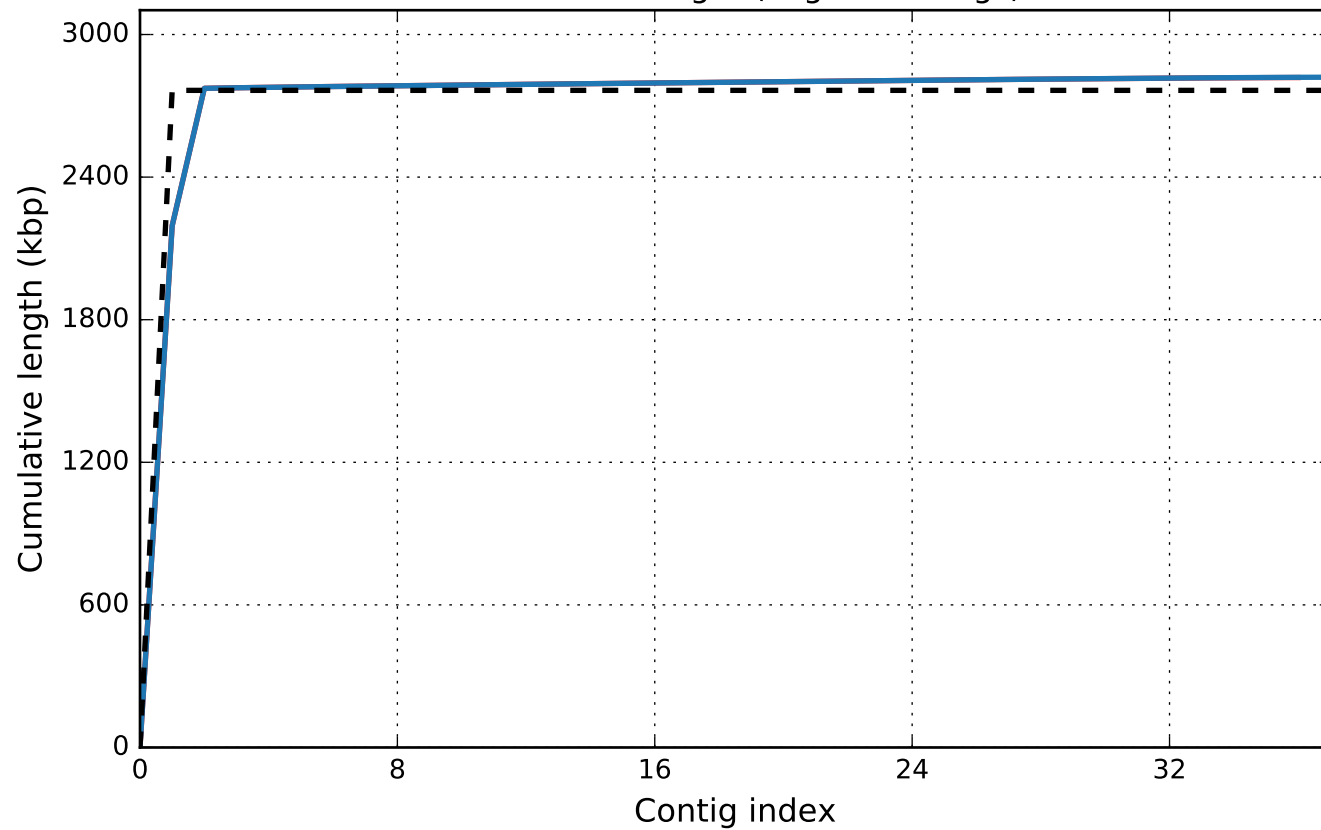
efaecium.contigs

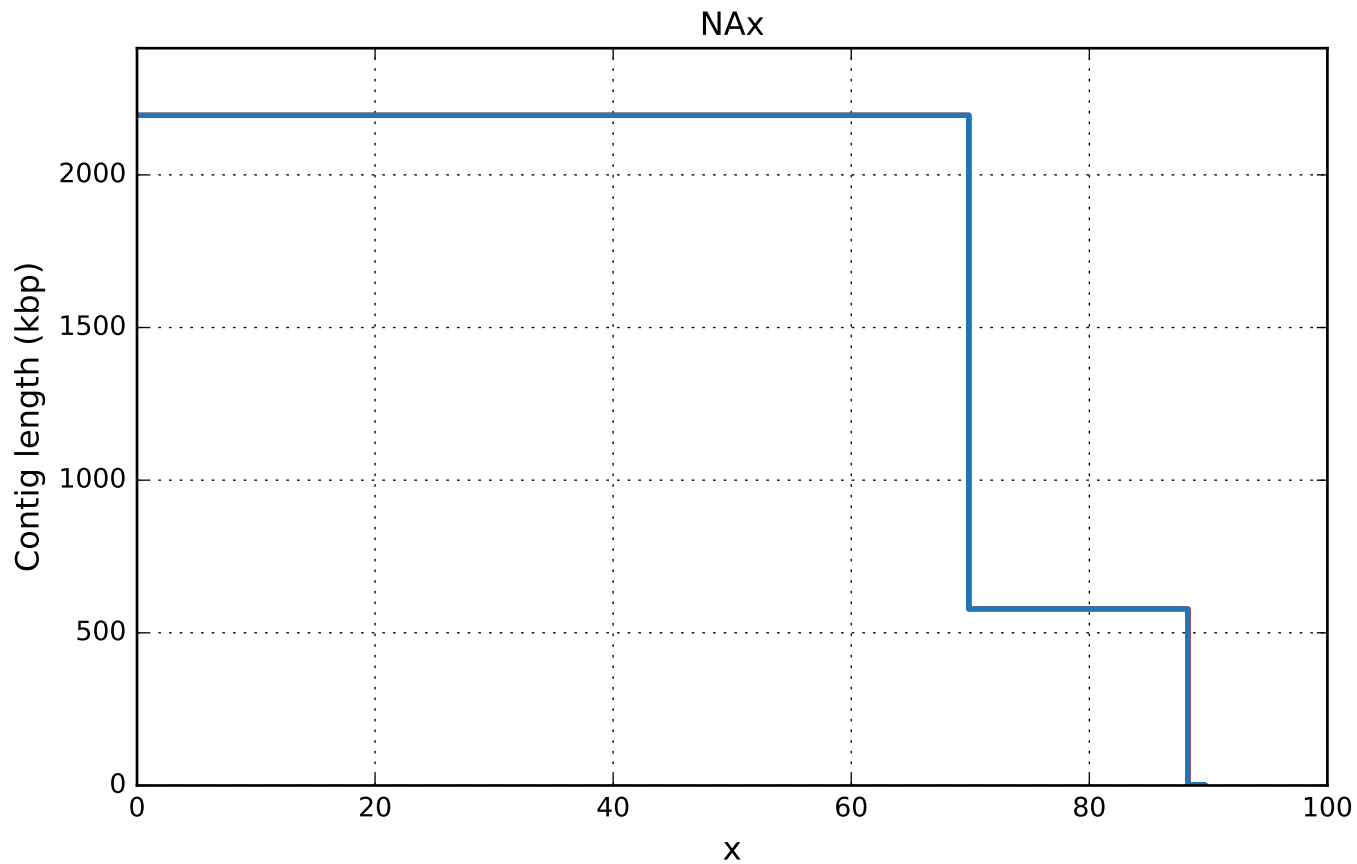


FRCurve (misassemblies)



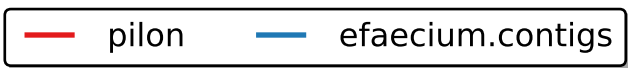
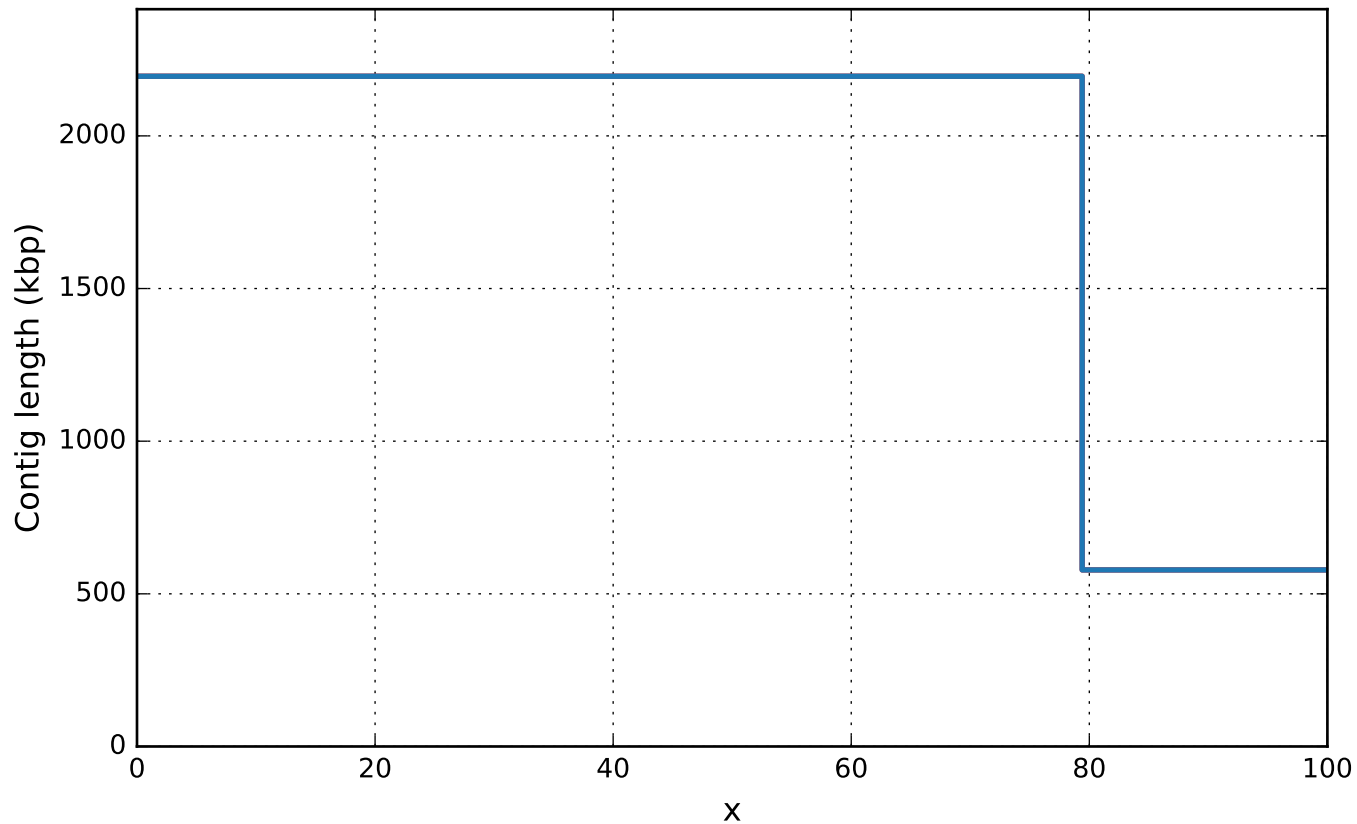
Cumulative length (aligned contigs)

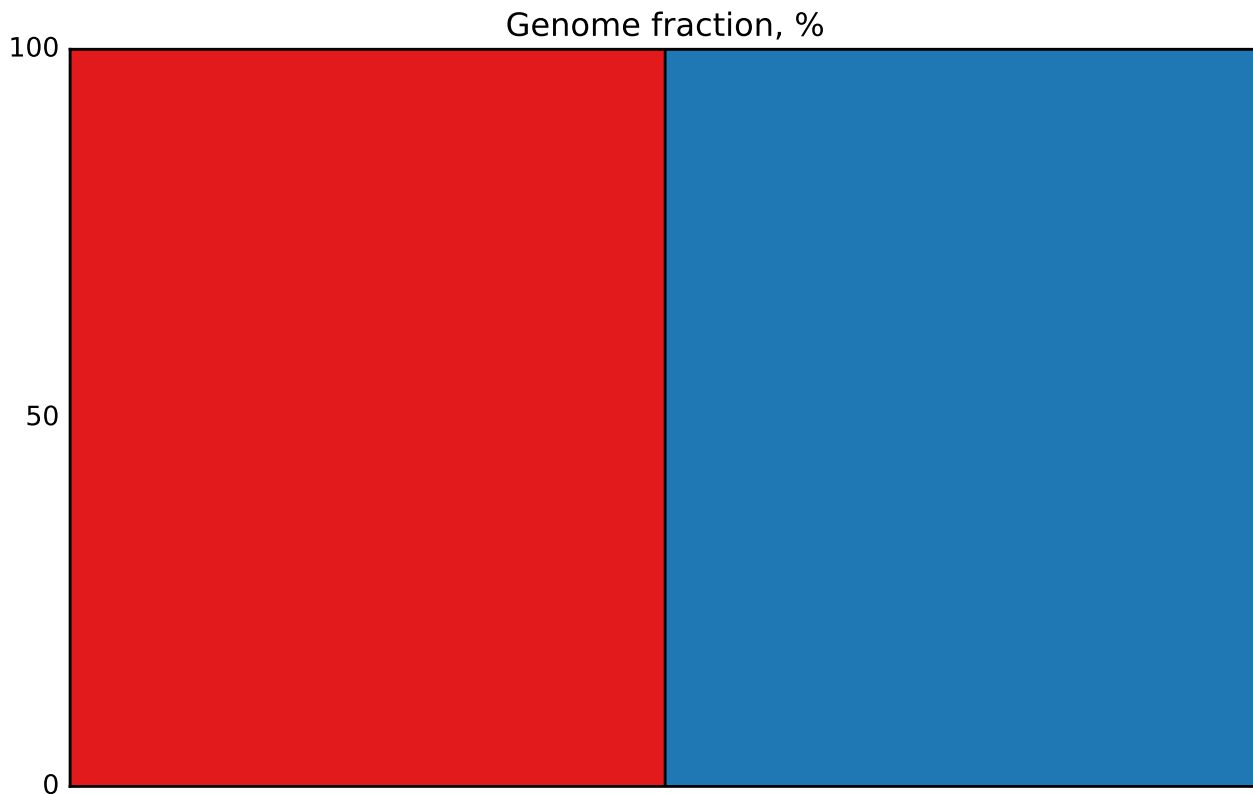




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NGAx





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