

Report

	efaecium.contigs
# contigs (>= 0 bp)	8
# contigs (>= 1000 bp)	8
# contigs (>= 5000 bp)	8
# contigs (>= 10000 bp)	7
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3142355
Total length (>= 1000 bp)	3142355
Total length (>= 5000 bp)	3142355
Total length (>= 10000 bp)	3132621
Total length (>= 25000 bp)	3103475
Total length (>= 50000 bp)	2992580
# contigs	8
Largest contig	2773588
Total length	3142355
Reference length	1753437
GC (%)	37.78
Reference GC (%)	37.94
N50	2773588
NG50	2773588
N75	2773588
NG75	2773588
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	32
# misassembled contigs	2
Misassembled contigs length	2783322
# local misassemblies	4
# unaligned mis. contigs	1
# unaligned contigs	4 + 4 part
Unaligned length	1265326
Genome fraction (%)	100.000
Duplication ratio	1.070
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.06
# indels per 100 kbp	4.96
Largest alignment	1183792
Total aligned length	1877030
NA50	578258
NGA50	1183792
NGA75	578258
LA50	2
LGA50	1
LGA75	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

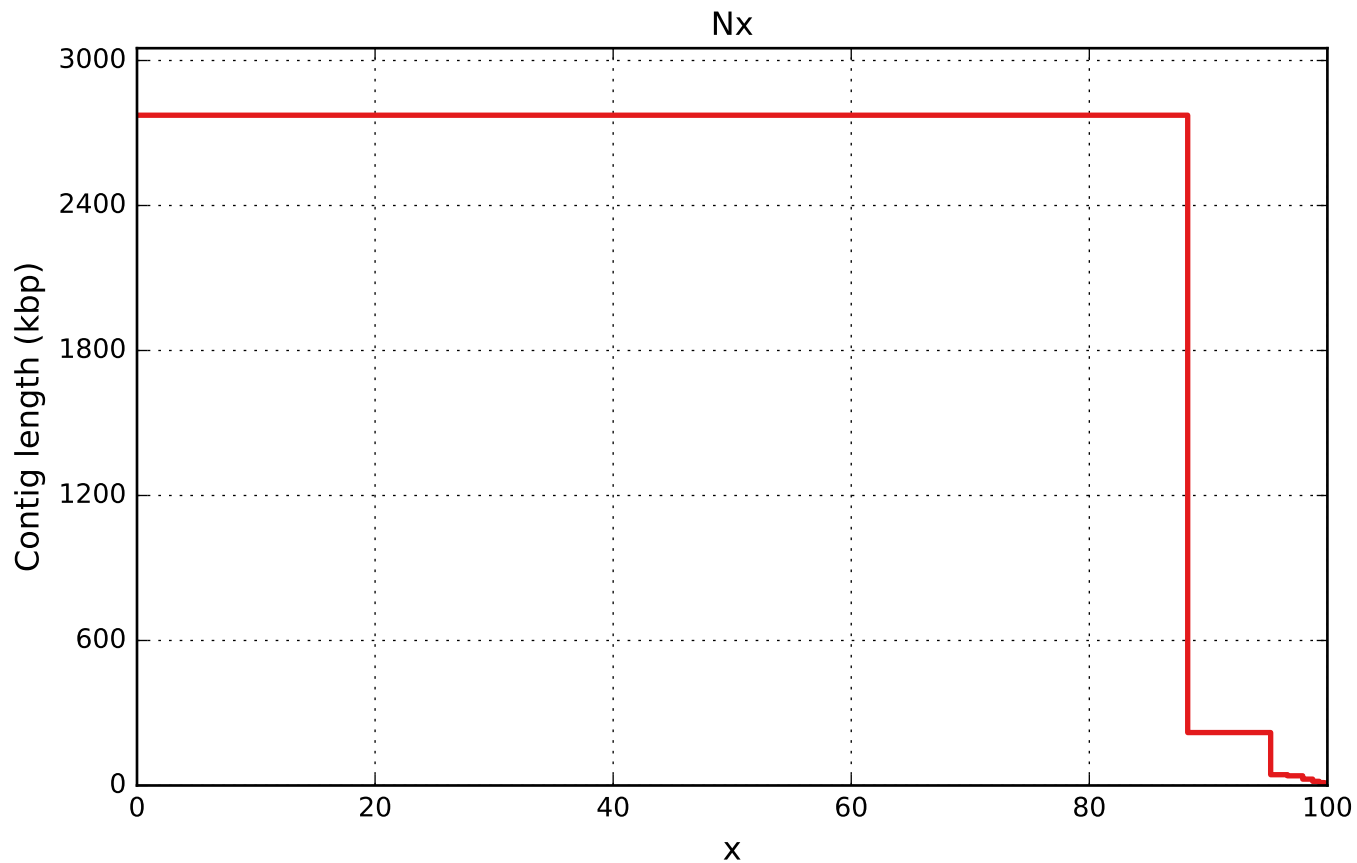
	efaecium.contigs
# misassemblies	32
# relocations	32
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	2783322
# local misassemblies	4
# unaligned mis. contigs	1
# mismatches	1
# indels	87
# indels (<= 5 bp)	87
# indels (> 5 bp)	0
Indels length	88

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).

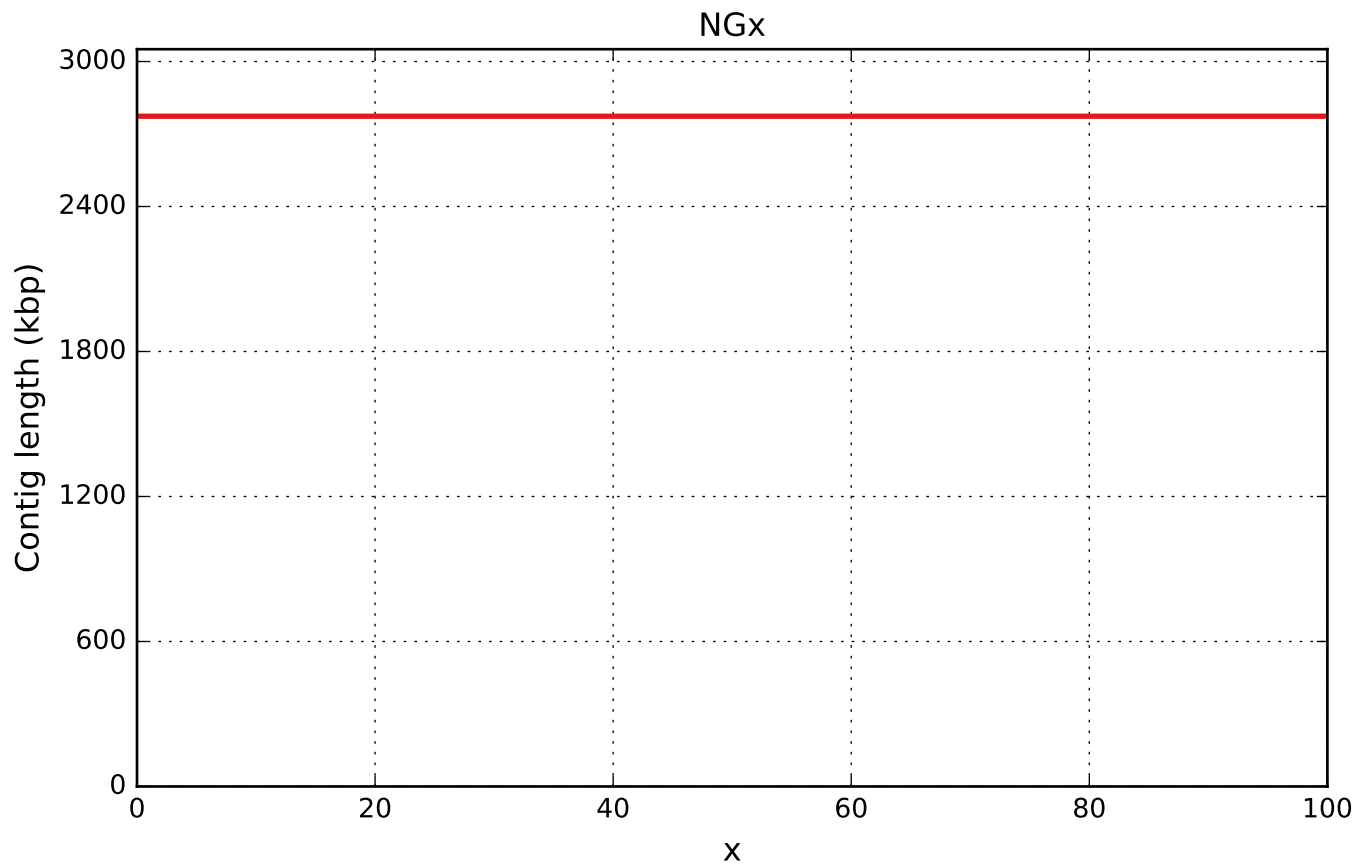
Unaligned report

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

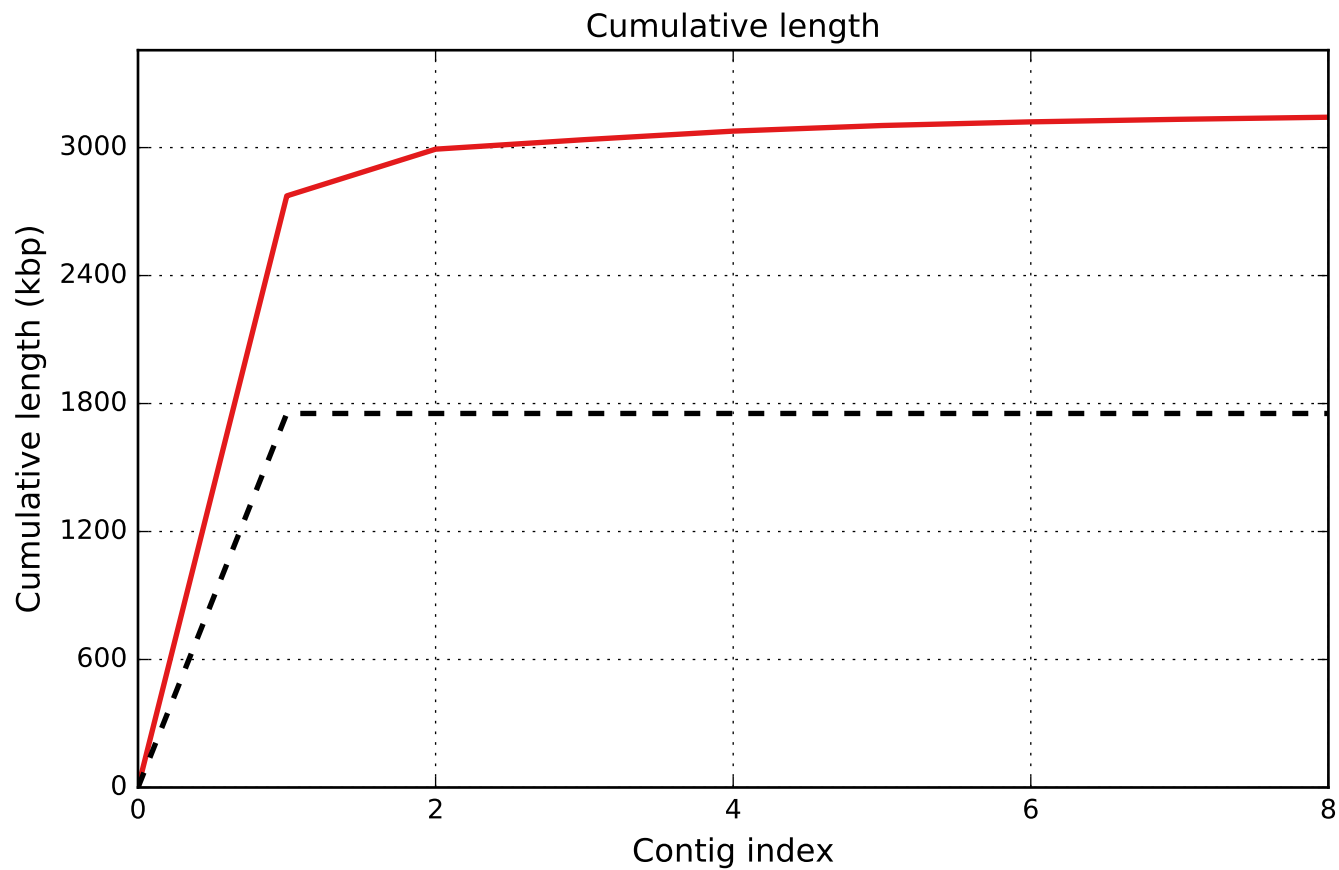
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



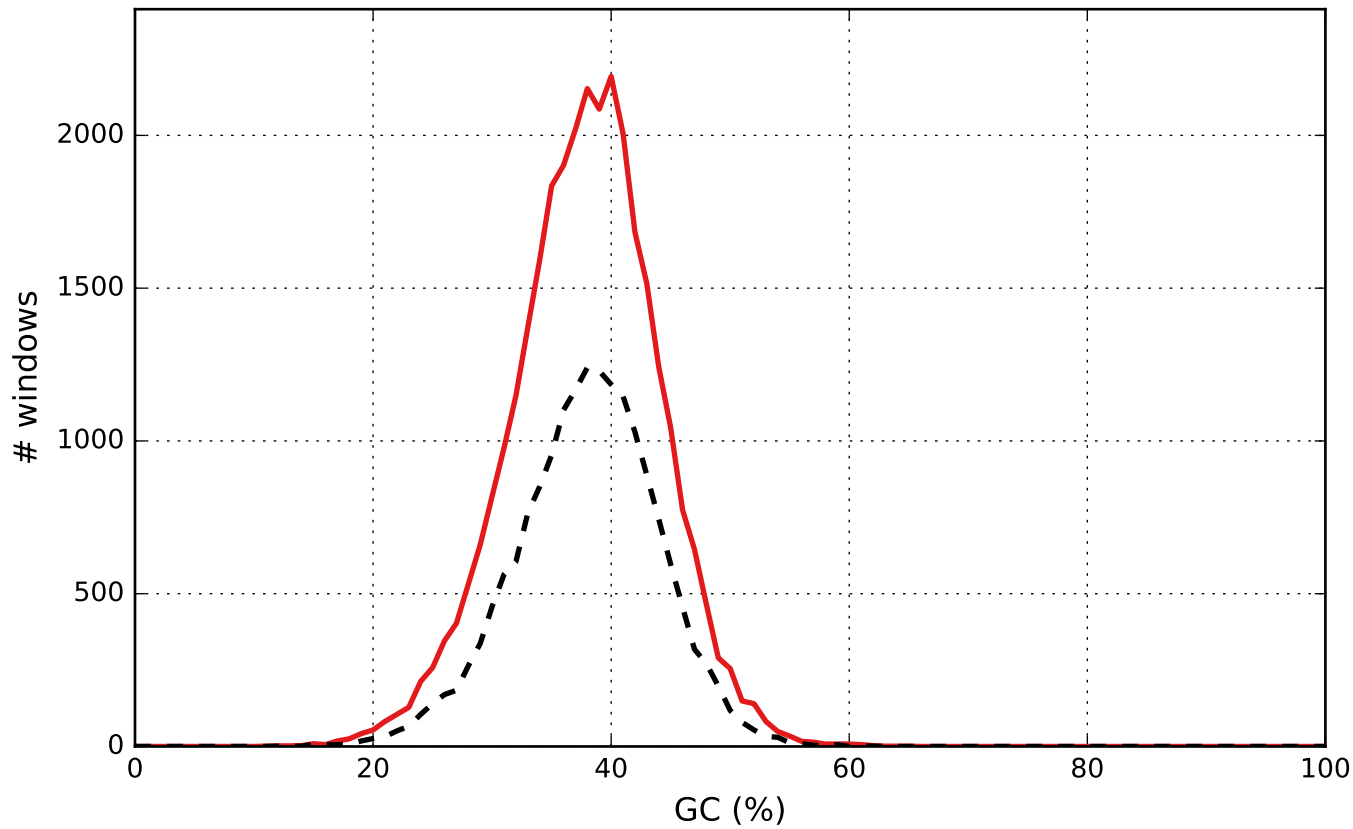
efaecium.contigs

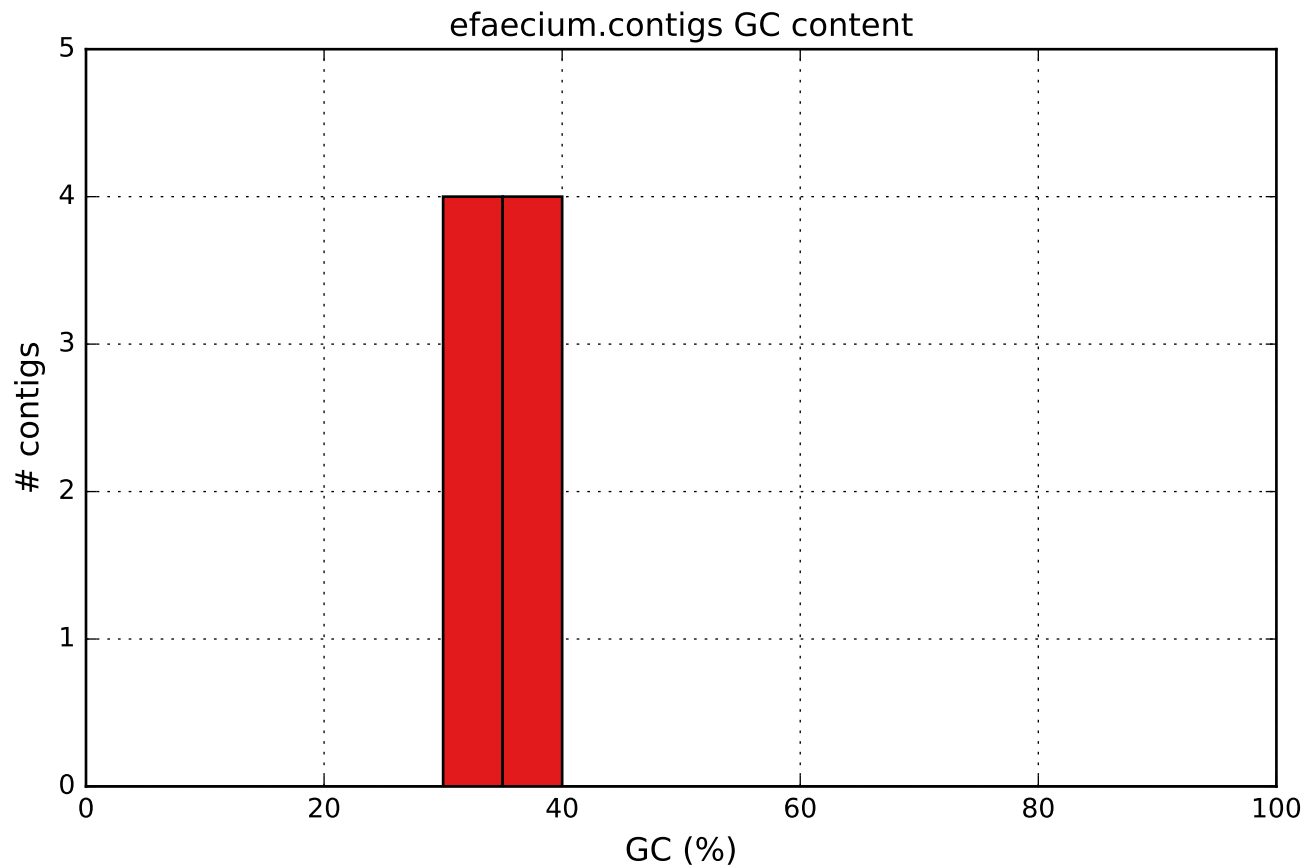


efaecium.contigs

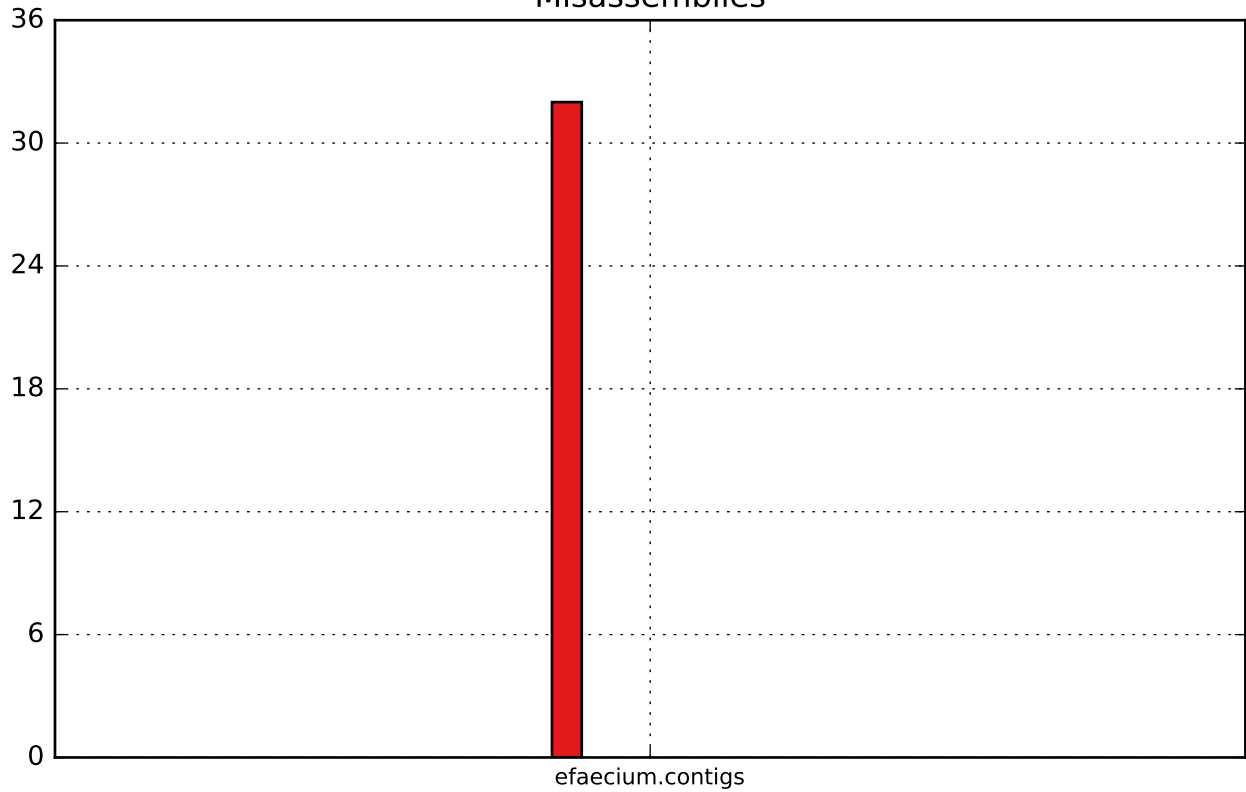


GC content

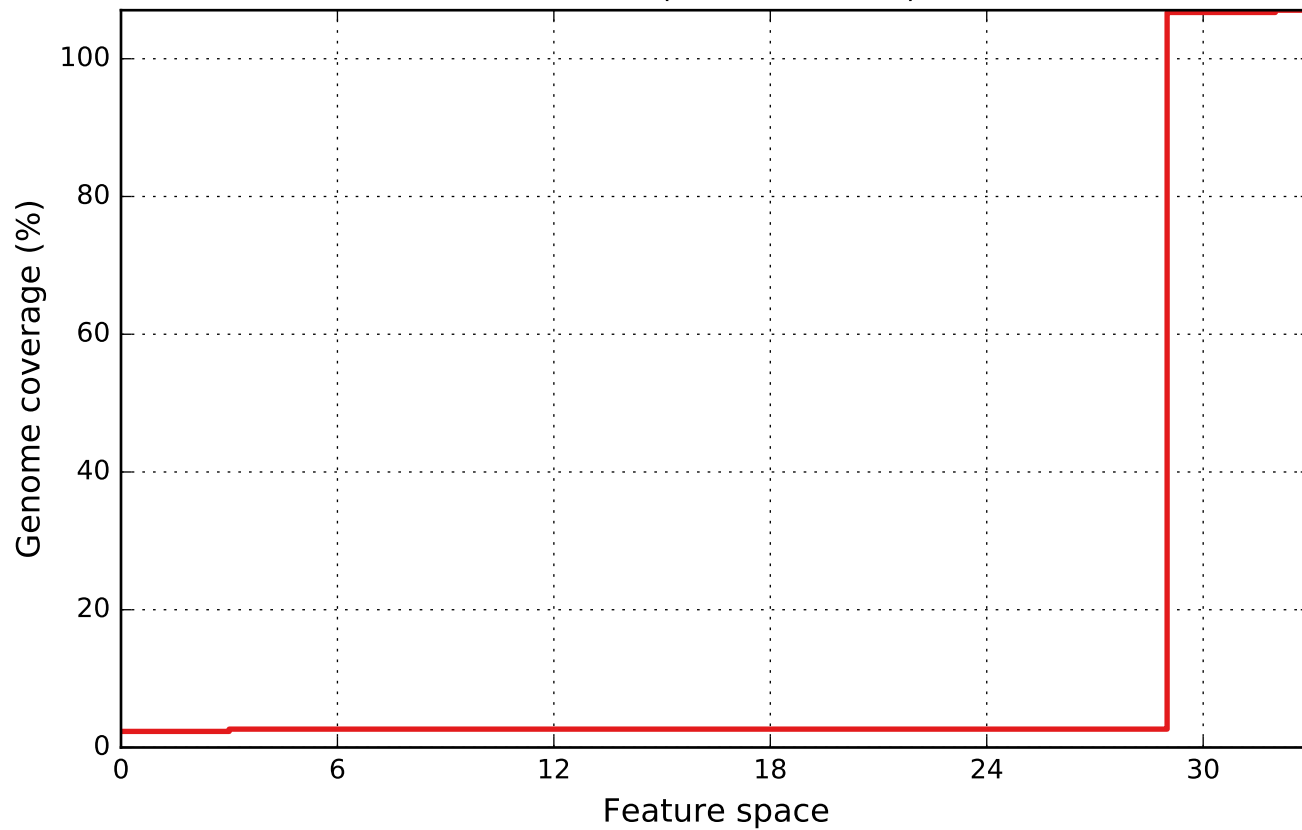




Misassemblies

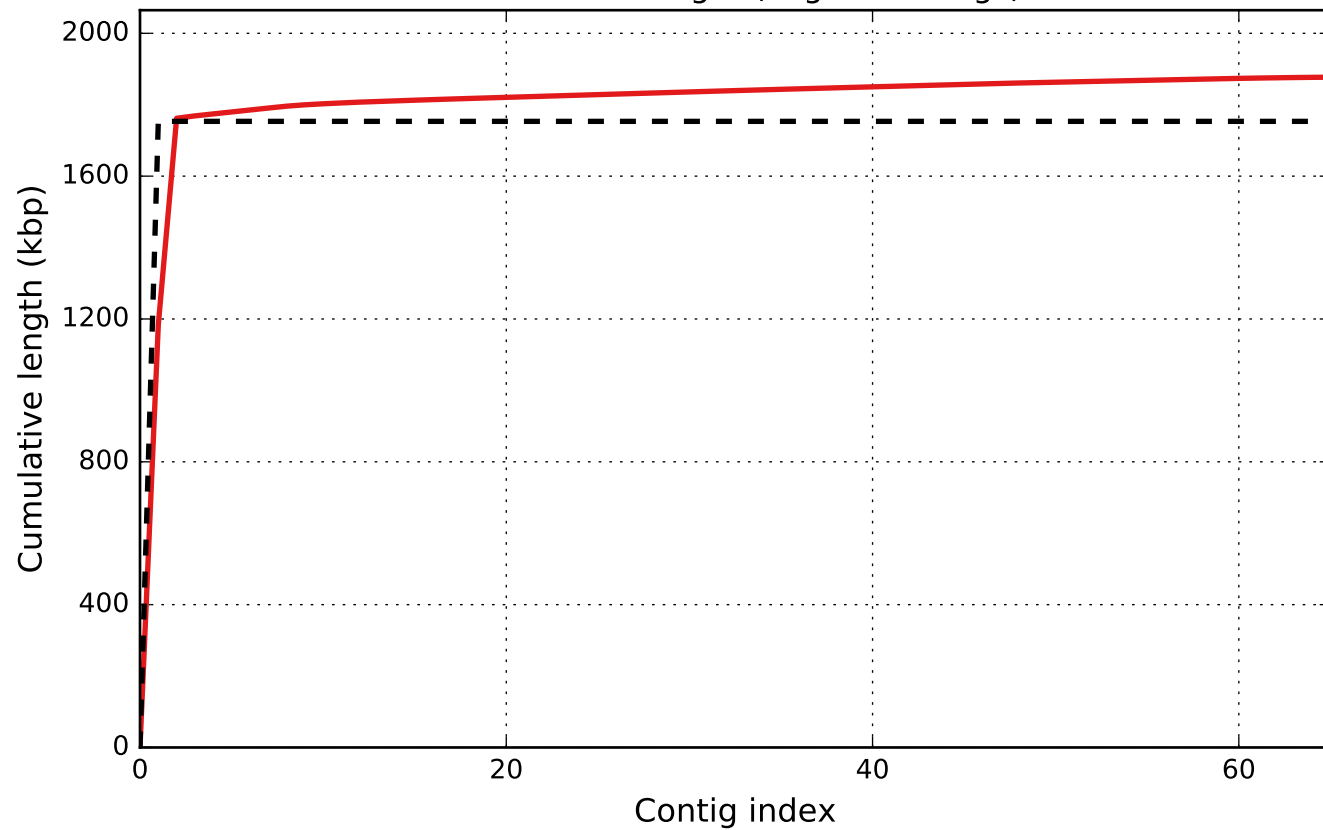


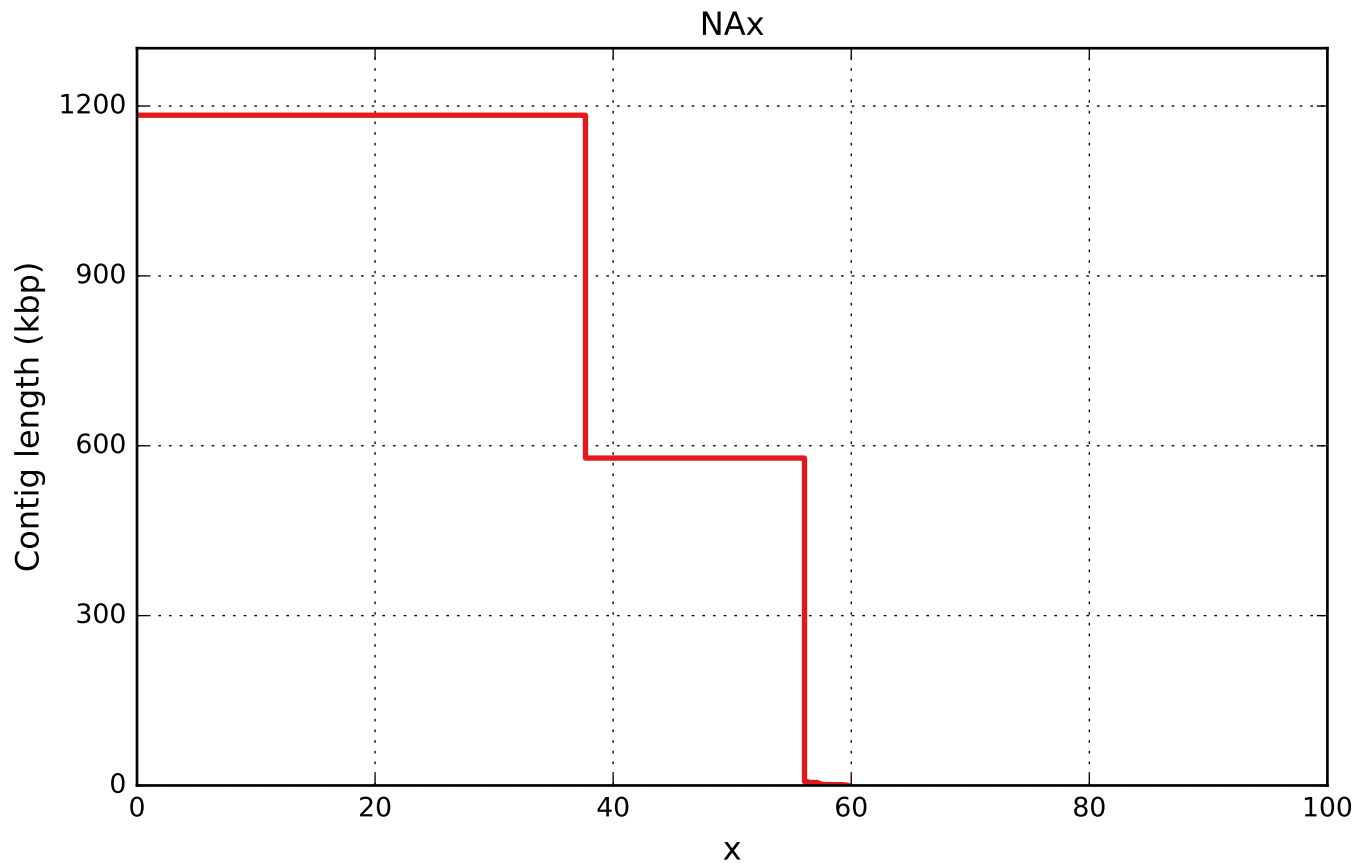
FRCurve (misassemblies)



efaecium.contigs

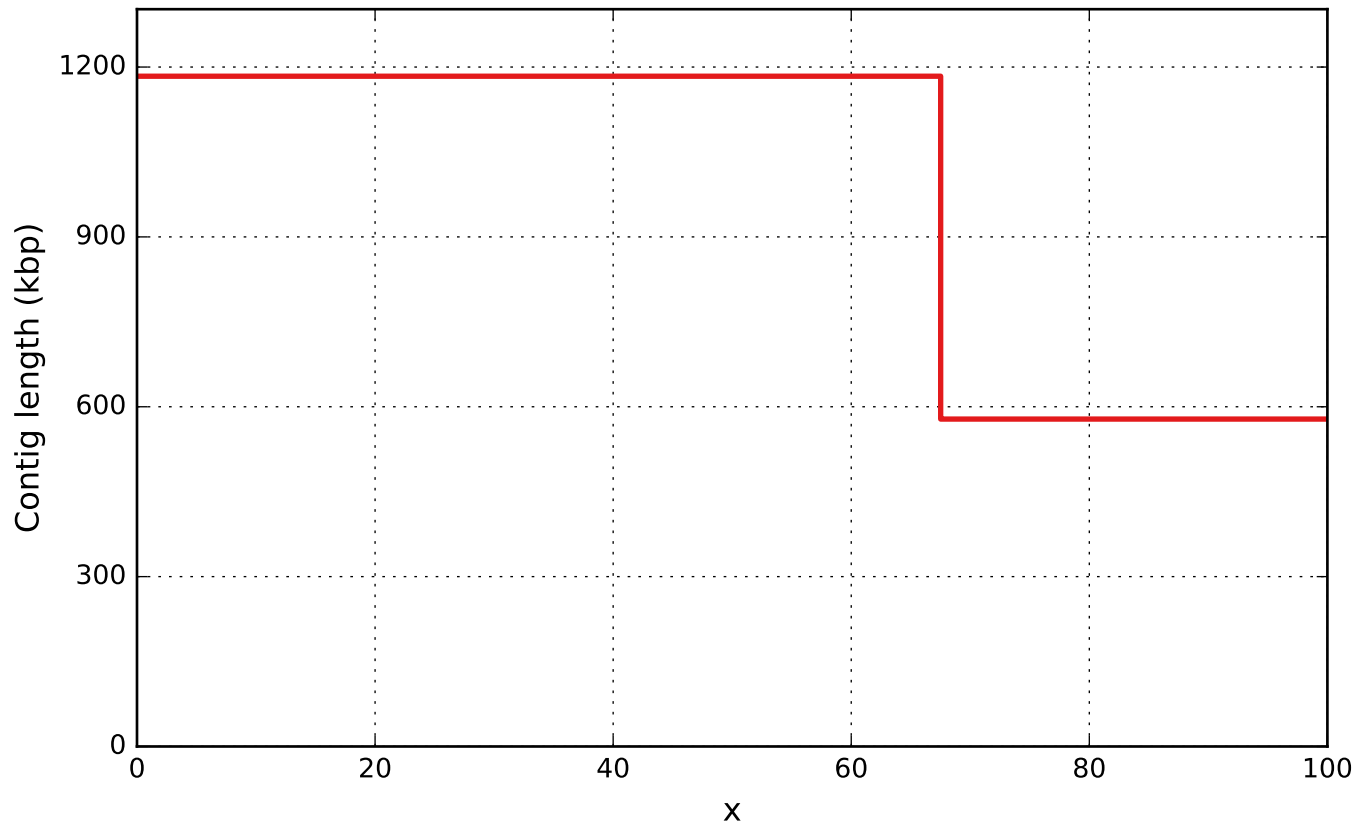
Cumulative length (aligned contigs)





— efaecium.contigs

NGAx



efaecium.contigs