

# Report

	efaecium.contigs
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	8
# contigs (>= 25000 bp)	5
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3159448
Total length (>= 1000 bp)	3159448
Total length (>= 5000 bp)	3159448
Total length (>= 10000 bp)	3149661
Total length (>= 25000 bp)	3099591
Total length (>= 50000 bp)	3006270
# contigs	9
Largest contig	2775643
Total length	3159448
Reference length	2919198
GC (%)	37.78
Reference GC (%)	37.88
N50	2775643
NG50	2775643
N75	2775643
NG75	2775643
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	190
# misassembled contigs	1
Misassembled contigs length	2775643
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	3 + 6 part
Unaligned length	561609
Genome fraction (%)	85.111
Duplication ratio	1.046
# N's per 100 kbp	0.00
# mismatches per 100 kbp	390.77
# indels per 100 kbp	18.03
Largest alignment	115727
Total aligned length	2592476
NA50	24552
NGA50	30127
NA75	4951
NGA75	10362
LA50	32
LGA50	27
LA75	88
LGA75	66

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

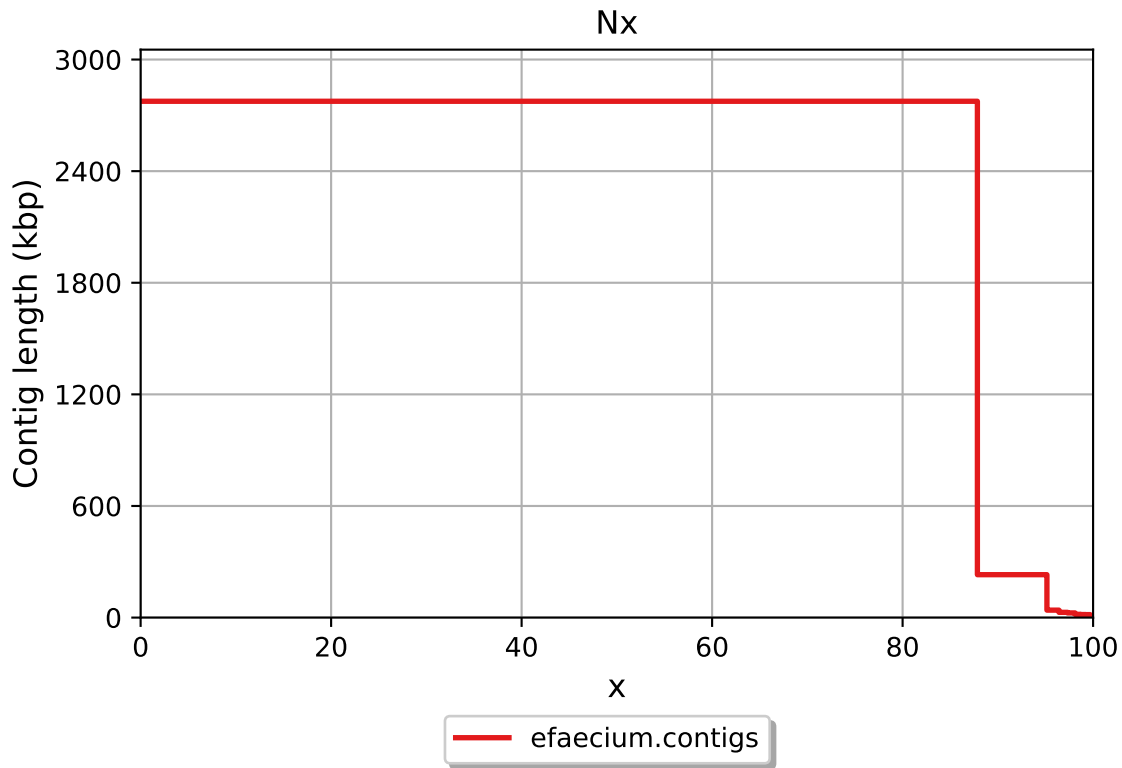
	efaecium.contigs
# misassemblies	190
# contig misassemblies	190
# c. relocations	174
# c. translocations	14
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2775643
# local misassemblies	36
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	9709
# indels	448
# indels (<= 5 bp)	410
# indels (> 5 bp)	38
Indels length	1634

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).

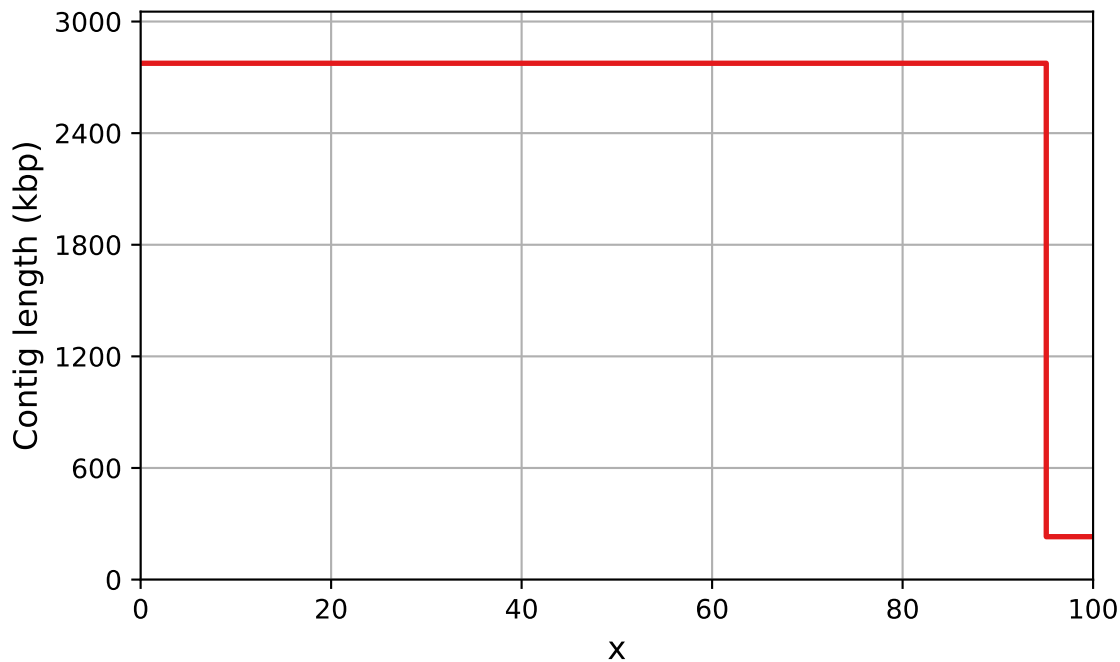
## Unaligned report

	efaecium.contigs
# fully unaligned contigs	3
Fully unaligned length	58690
# partially unaligned contigs	6
Partially unaligned length	502919
# N's	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).

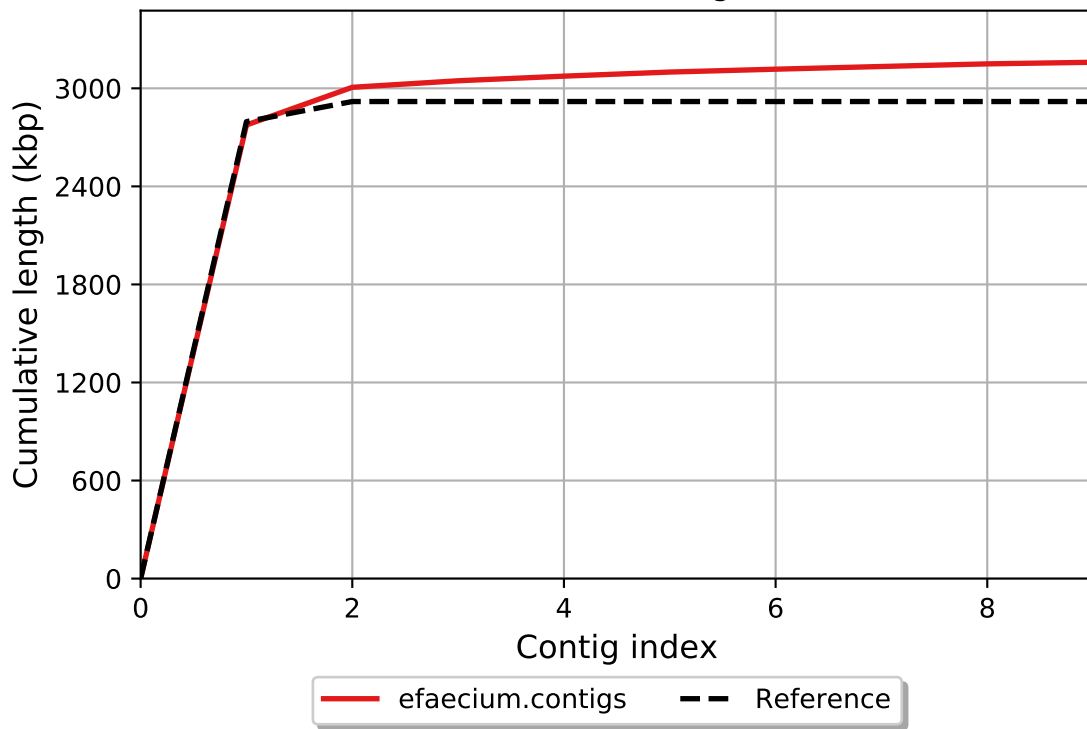


NGx

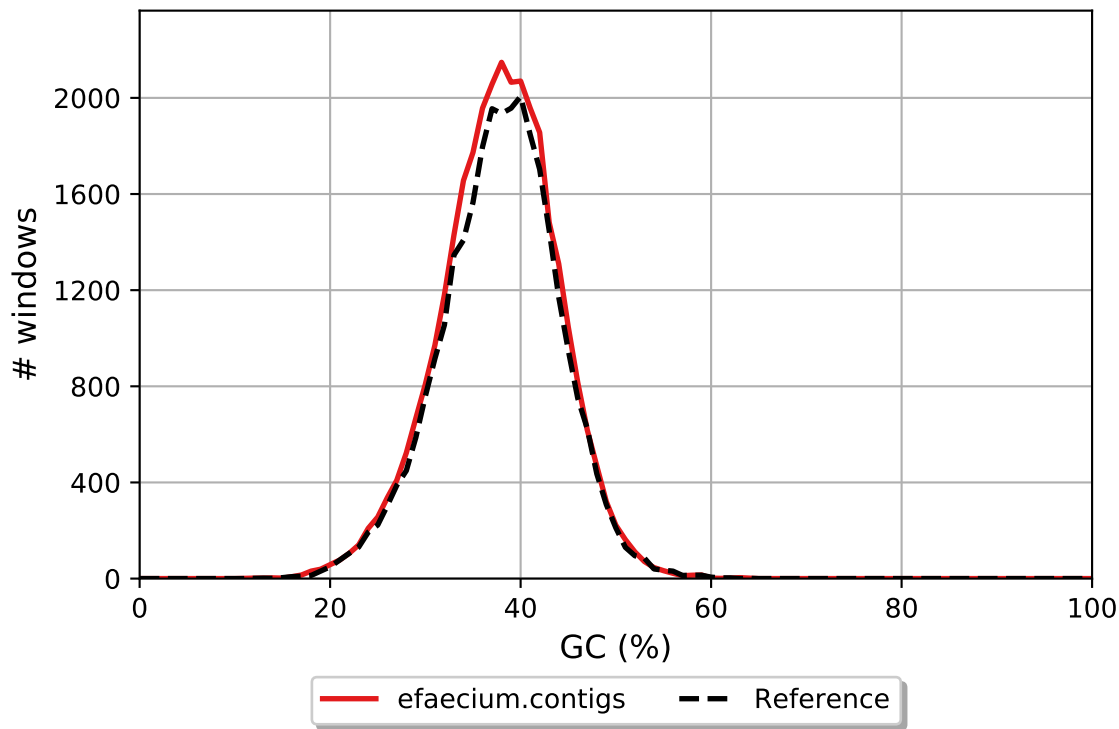


efaecium.contigs

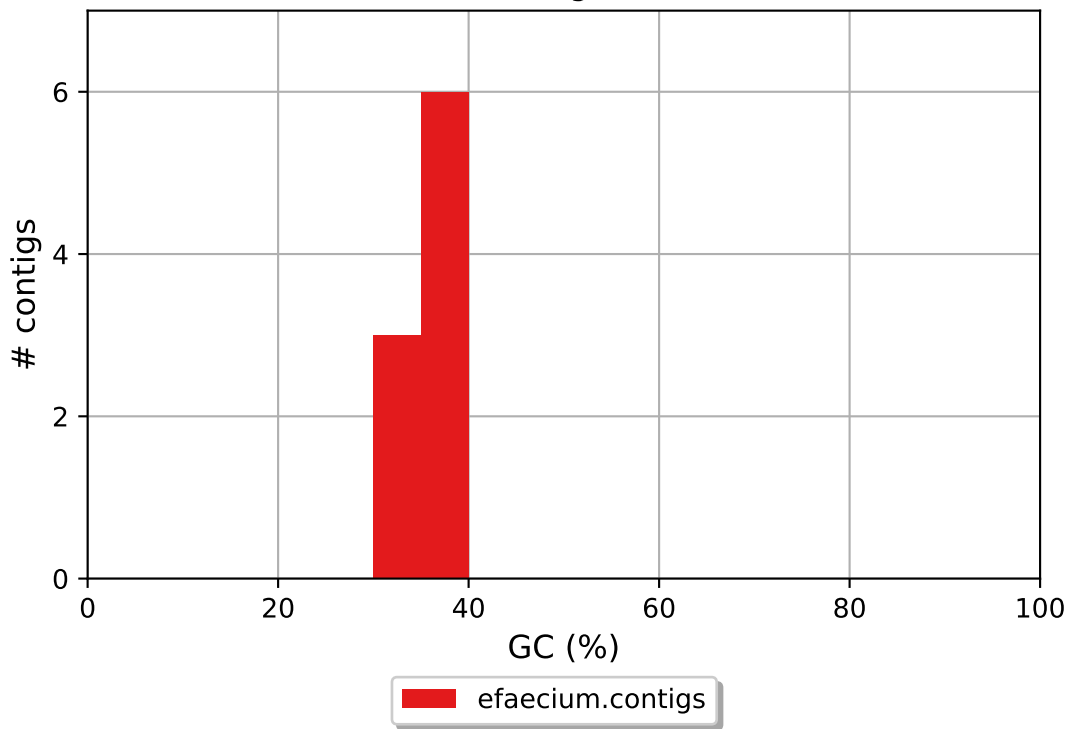
Cumulative length



## GC content

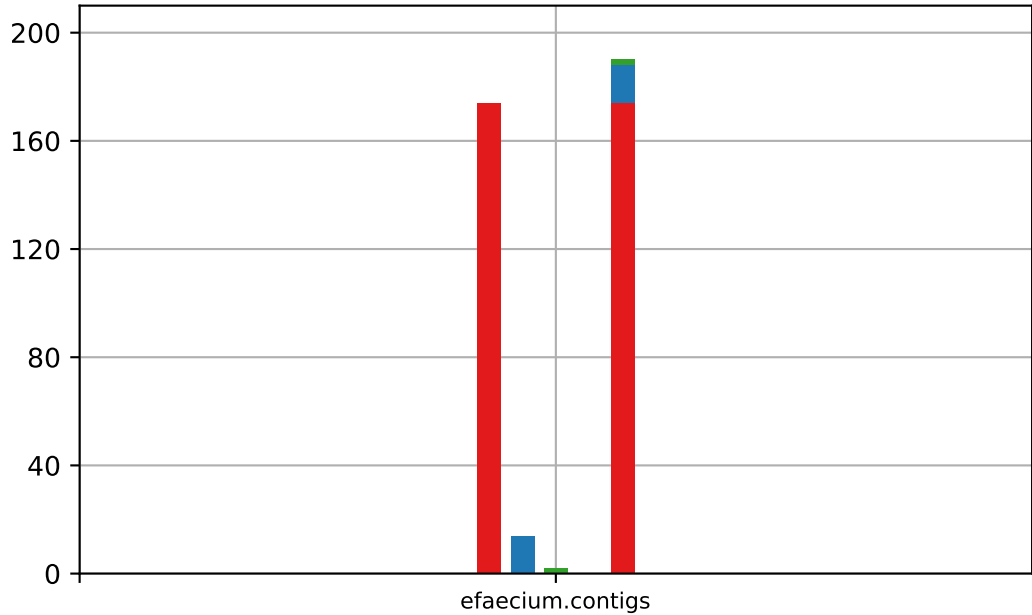


efaecium.contigs GC content





## Misassemblies



# relocations

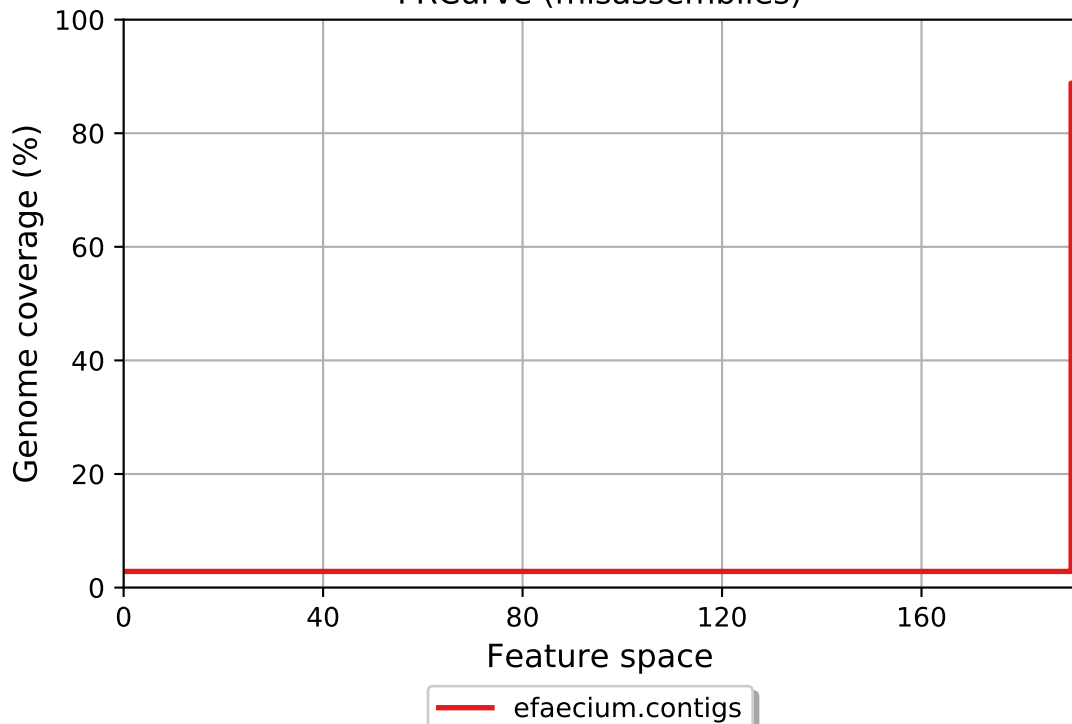


# translocations

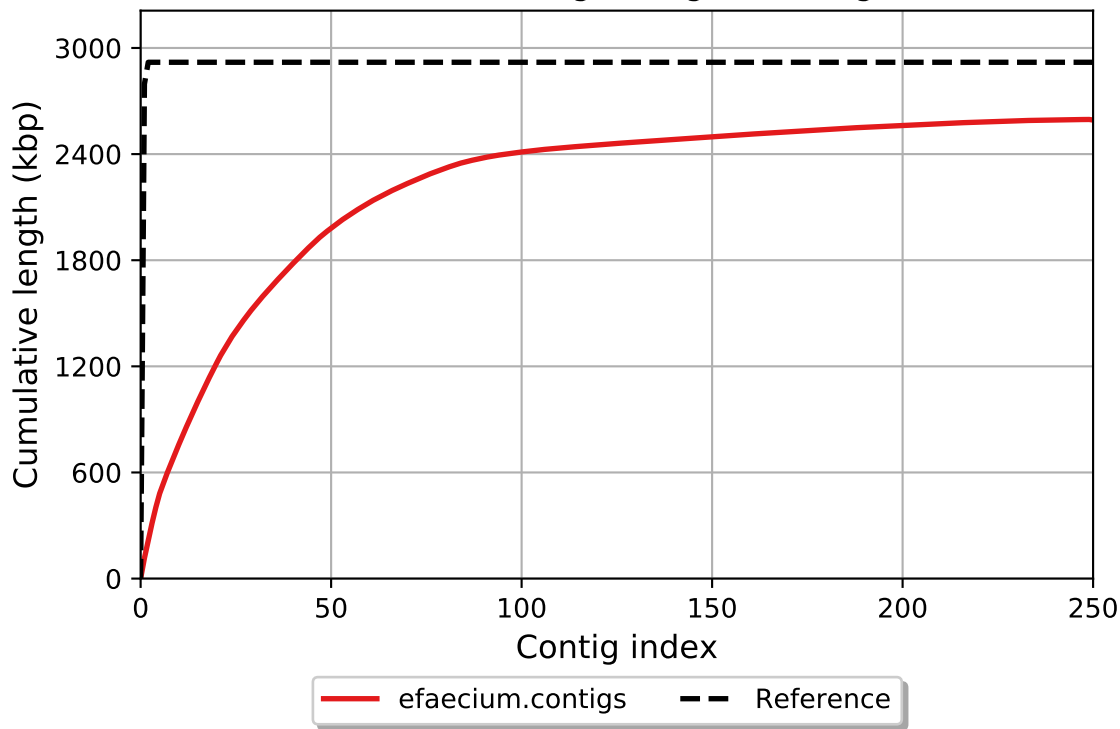


# inversions

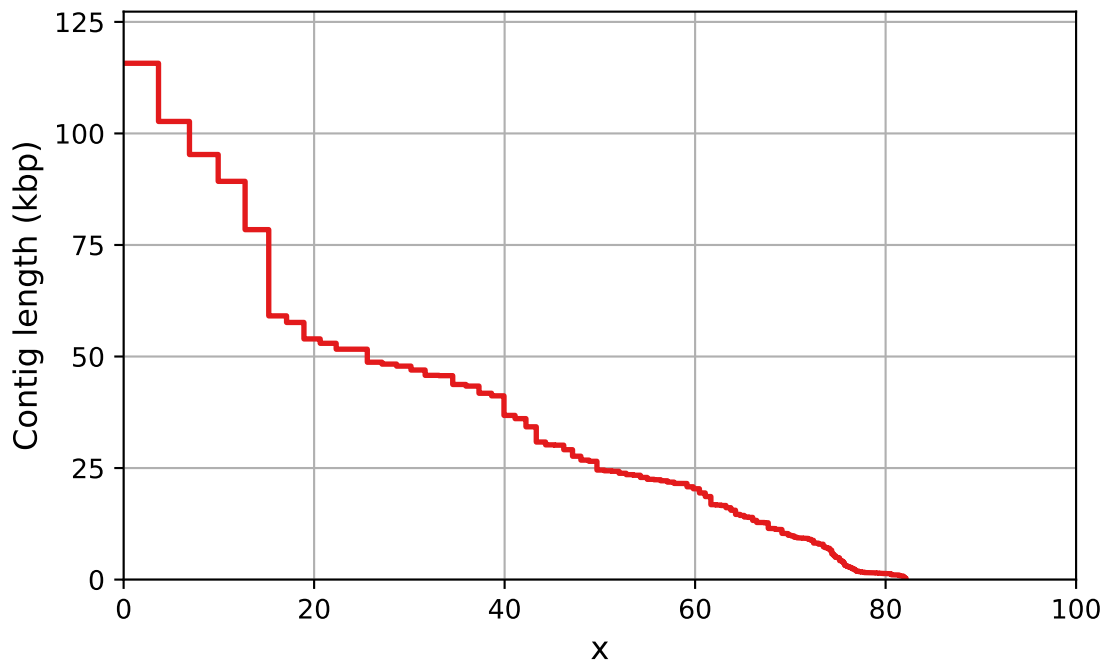
FRCurve (misassemblies)



Cumulative length (aligned contigs)

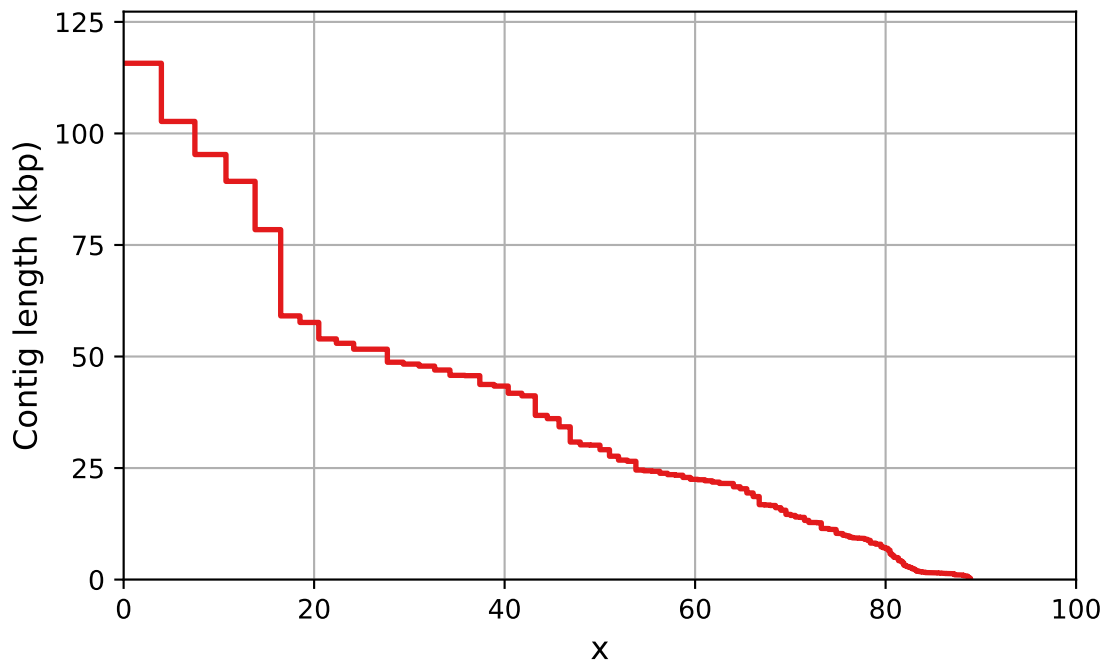


NAx



efaecium.contigs

# NGAx



efaecium.contigs