

Report

	faecium.contigs
# contigs (>= 0 bp)	13
# contigs (>= 1000 bp)	13
# contigs (>= 5000 bp)	12
# contigs (>= 10000 bp)	11
# contigs (>= 25000 bp)	6
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	3179422
Total length (>= 1000 bp)	3179422
Total length (>= 5000 bp)	3175915
Total length (>= 10000 bp)	3168876
Total length (>= 25000 bp)	3083119
Total length (>= 50000 bp)	2962638
# contigs	13
Largest contig	2775856
Total length	3179422
Reference length	2919198
GC (%)	37.78
Reference GC (%)	37.88
N50	2775856
NG50	2775856
N75	2775856
NG75	2775856
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	190
# misassembled contigs	1
Misassembled contigs length	2775856
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	5 + 8 part
Unaligned length	580864
Genome fraction (%)	84.982
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	392.86
# indels per 100 kbp	24.63
Largest alignment	137651
Total aligned length	2596655
NA50	24553
NGA50	28323
NA75	4043
NGA75	10360
LA50	32
LGA50	28
LA75	92
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

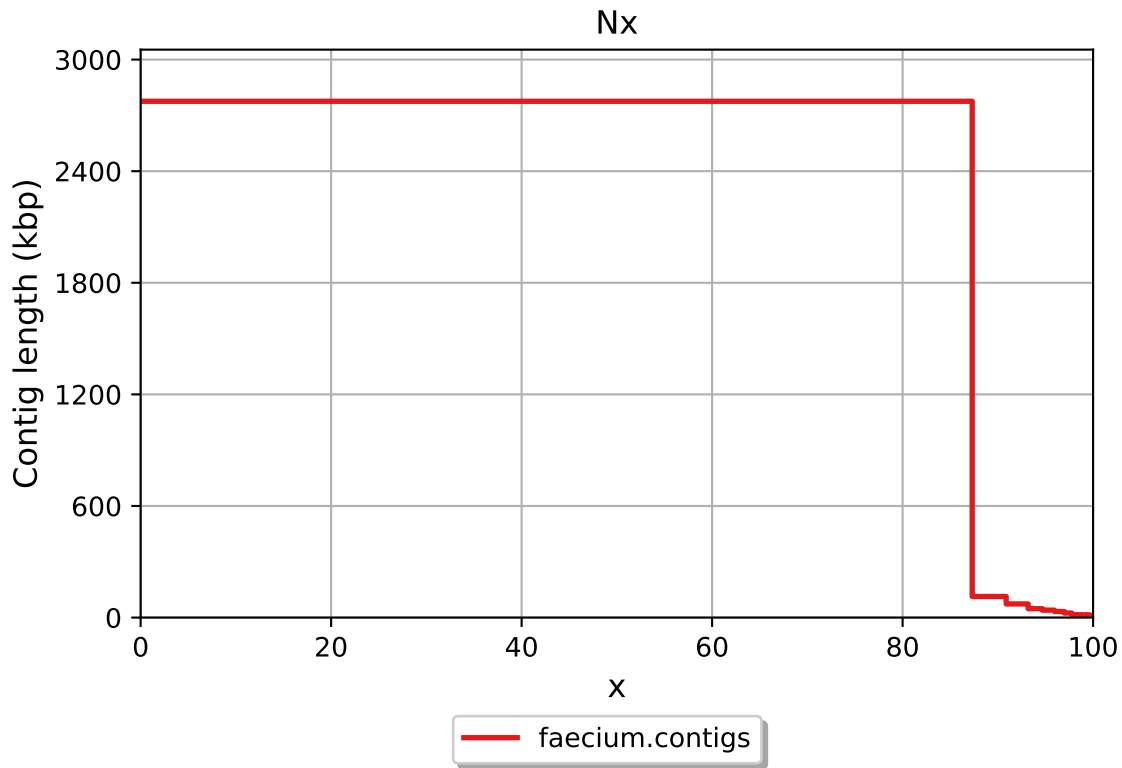
	faecium.contigs
# misassemblies	190
# contig misassemblies	190
# c. relocations	176
# c. translocations	12
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2775856
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	9746
# indels	611
# indels (<= 5 bp)	575
# indels (> 5 bp)	36
Indels length	1672

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).

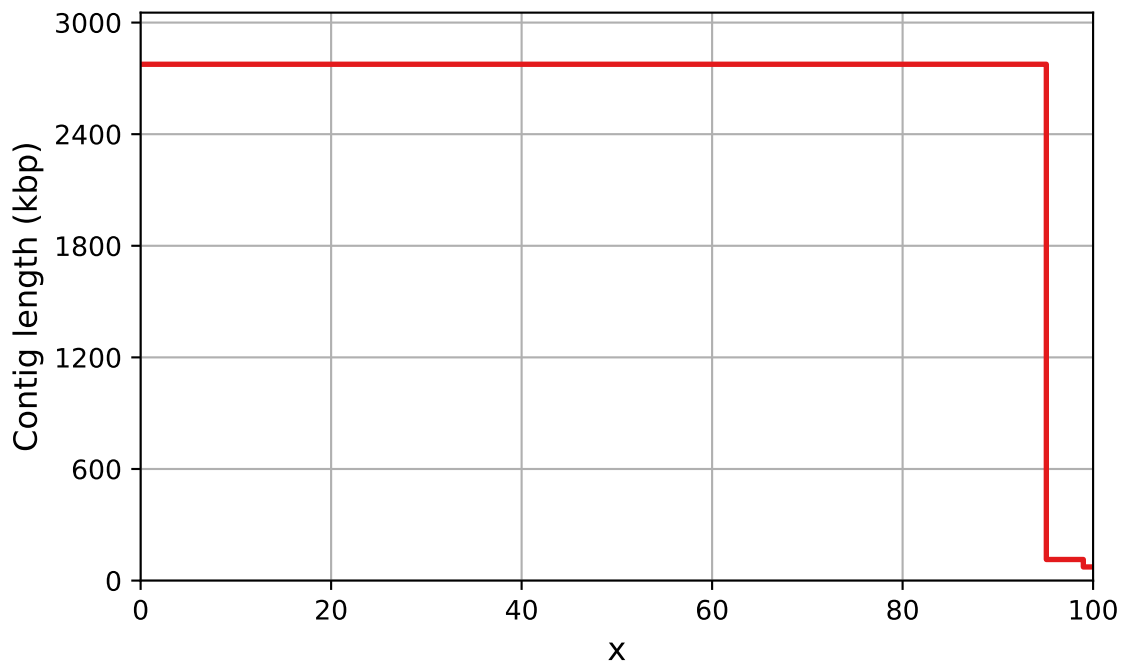
Unaligned report

	faecium.contigs
# fully unaligned contigs	5
Fully unaligned length	65424
# partially unaligned contigs	8
Partially unaligned length	515440
# N's	0

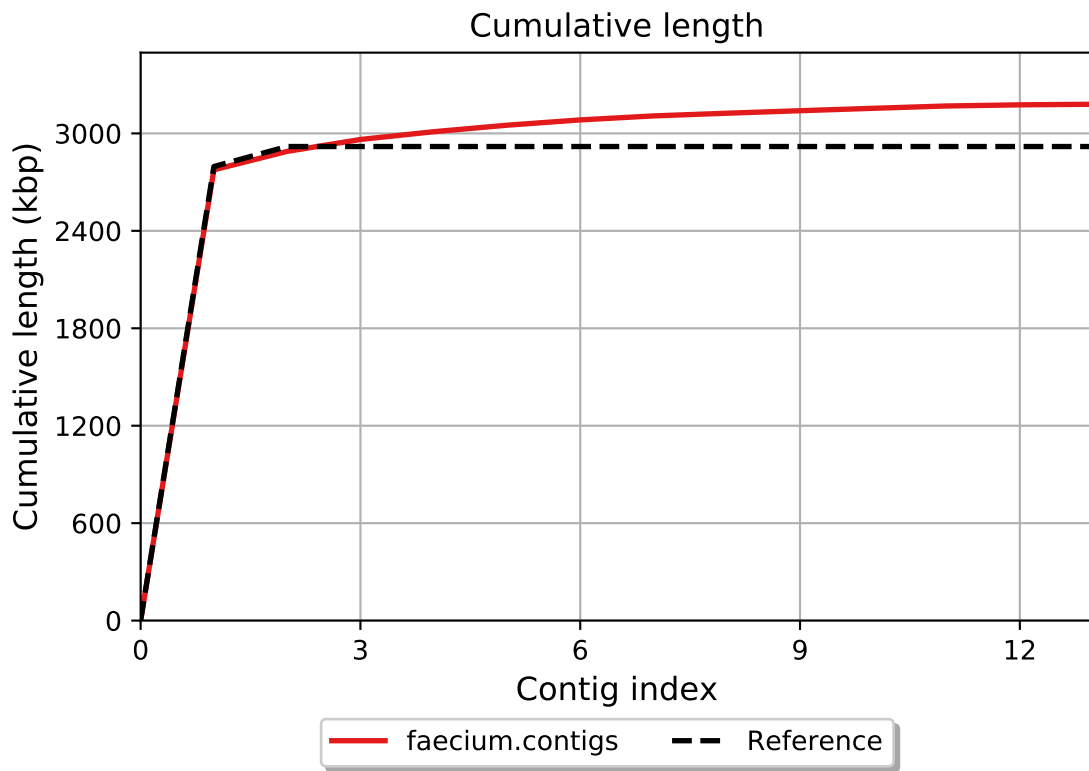
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



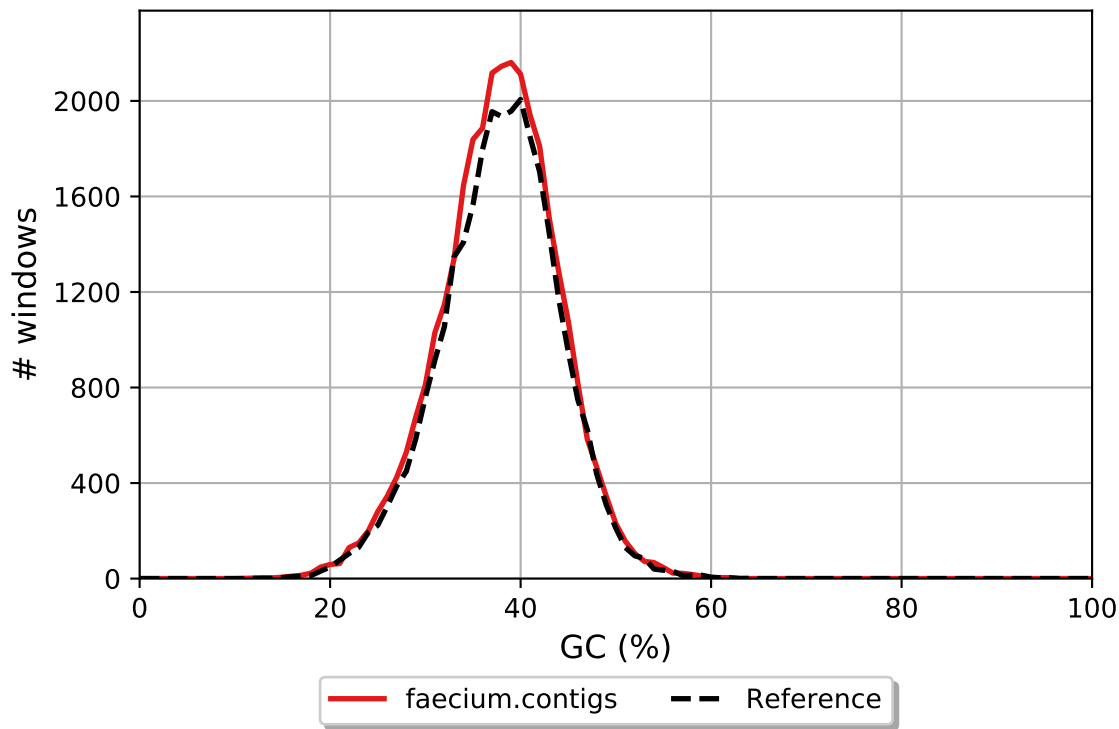
NGx



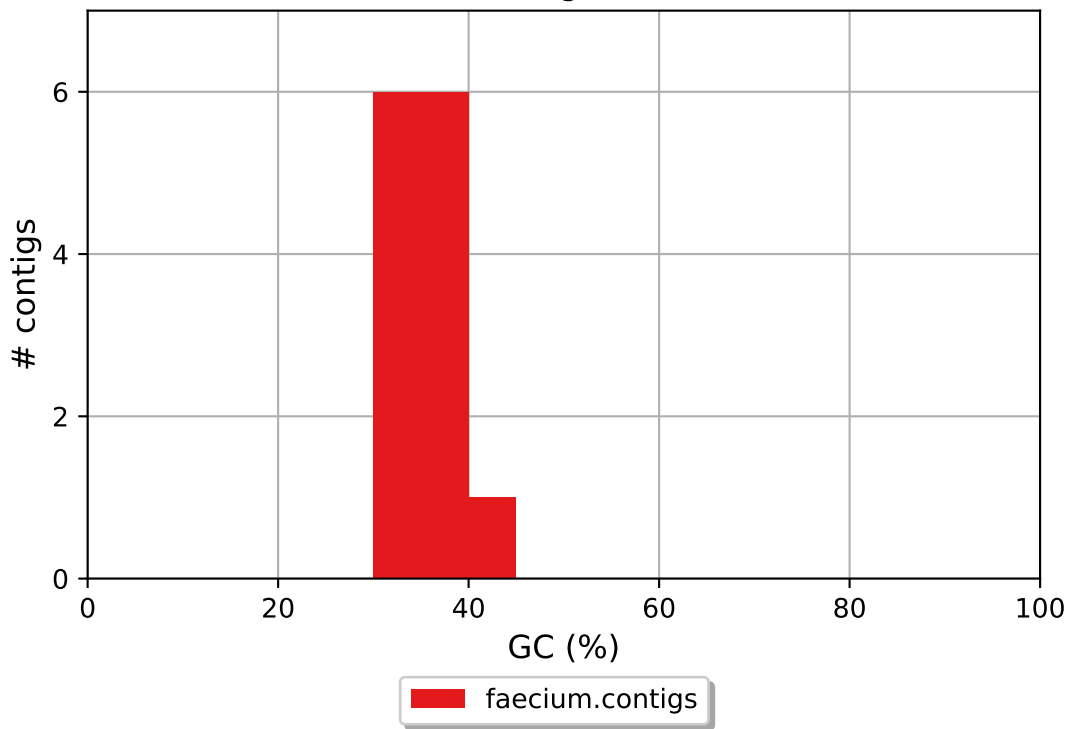
— faecium.contigs



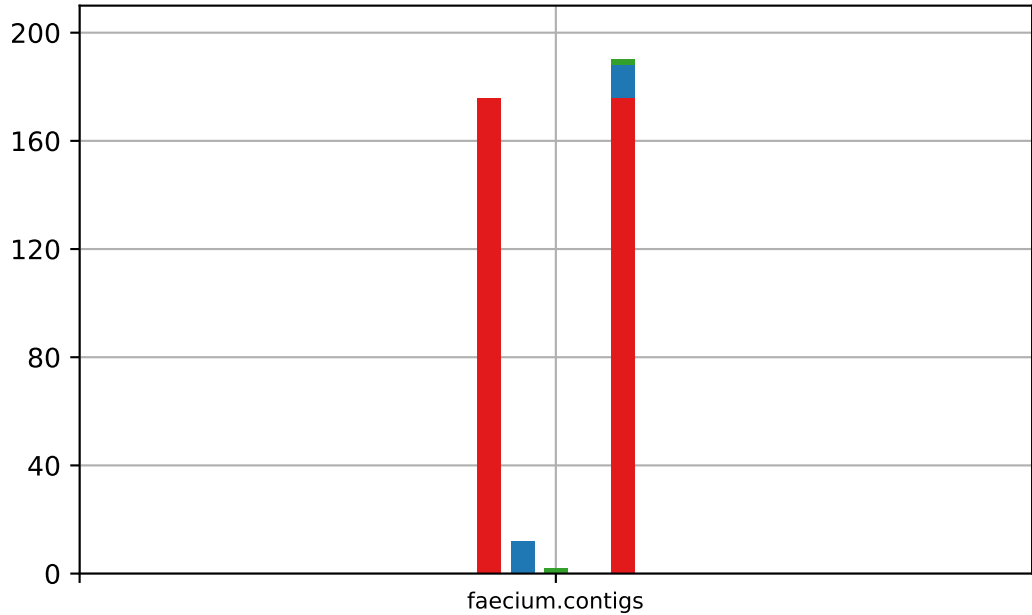
GC content



faecium.contigs GC content



Misassemblies



relocations

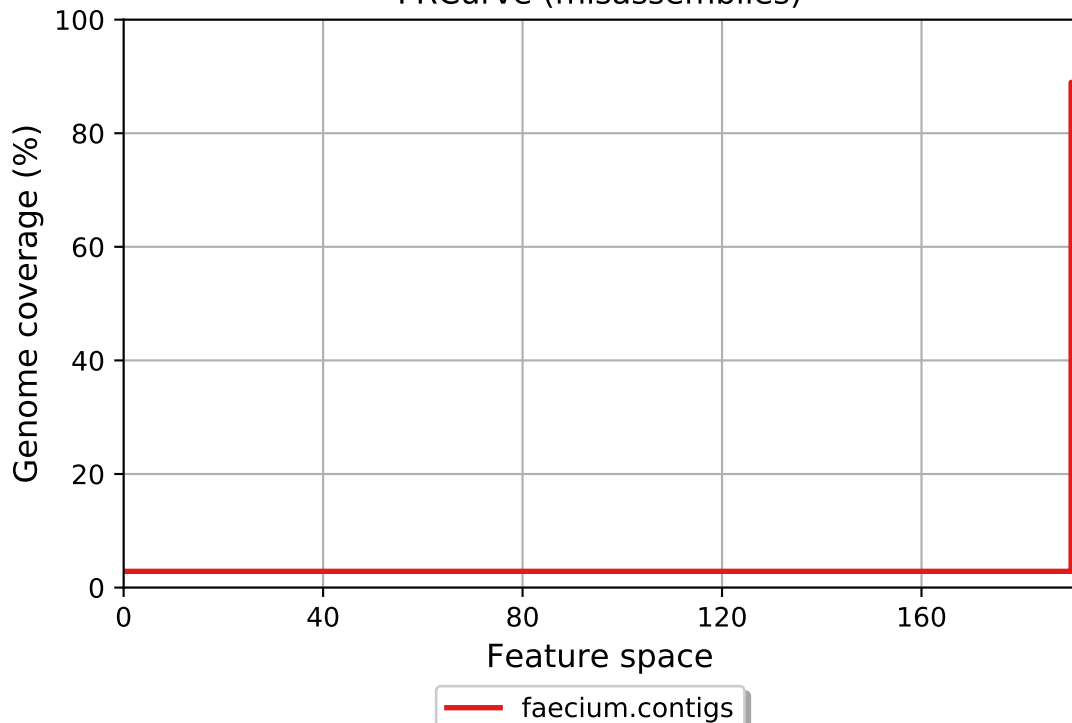


translocations

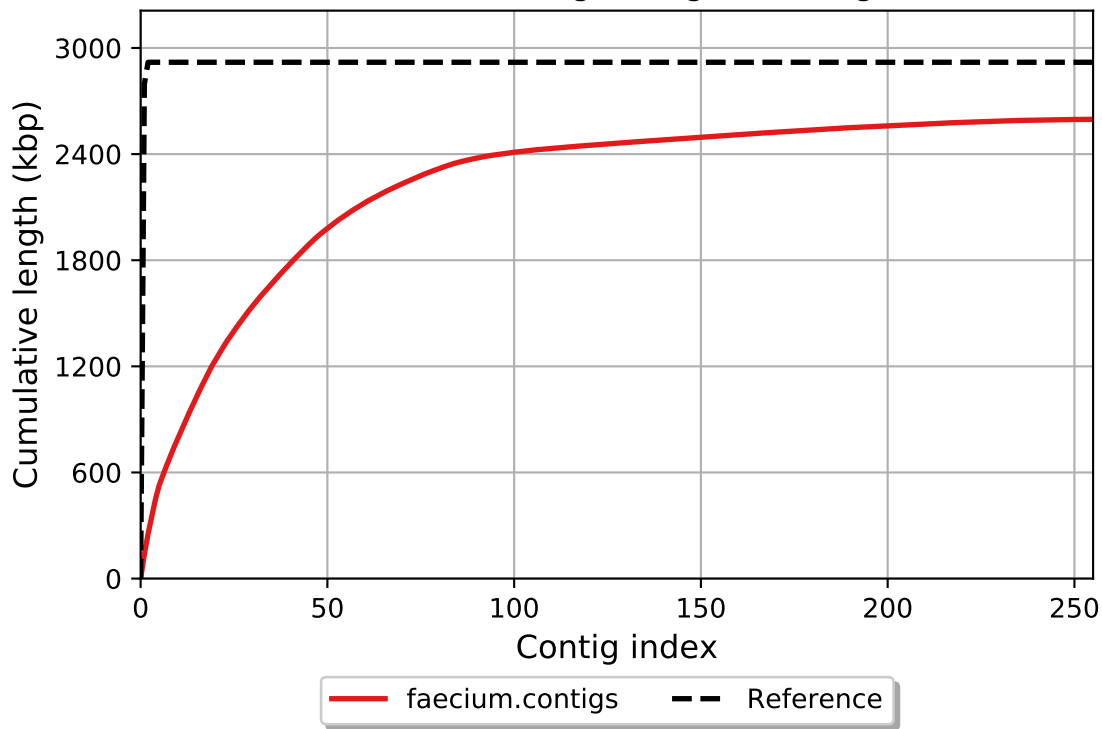


inversions

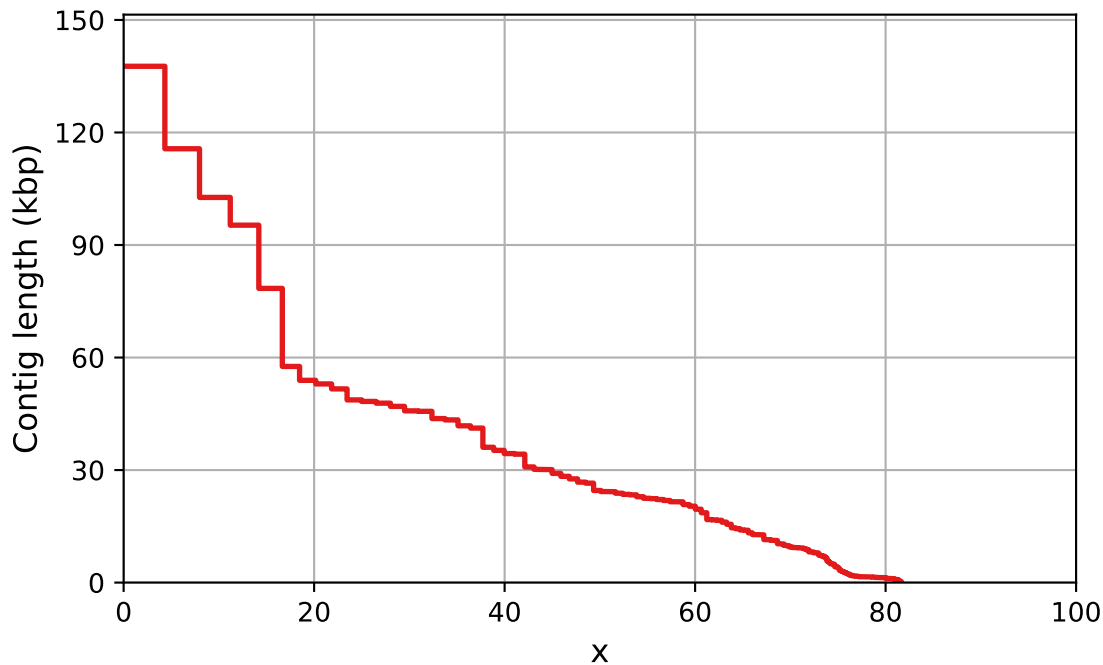
FRCurve (misassemblies)



Cumulative length (aligned contigs)

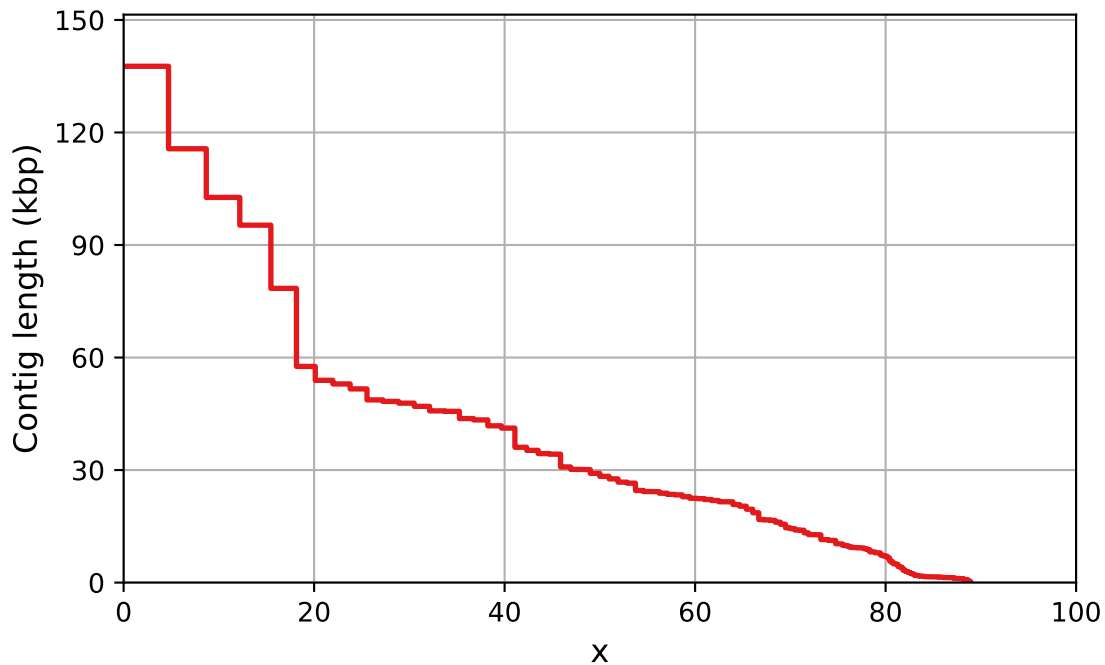


NAx



faecium.contigs

NGAx



faecium.contigs