

Report

	e_faecium.contigs	contigs
# contigs (>= 0 bp)	10	47
# contigs (>= 1000 bp)	10	17
# contigs (>= 5000 bp)	8	15
# contigs (>= 10000 bp)	8	13
# contigs (>= 25000 bp)	4	13
# contigs (>= 50000 bp)	2	11
Total length (>= 0 bp)	3105849	3140988
Total length (>= 1000 bp)	3105849	3134894
Total length (>= 5000 bp)	3097566	3128334
Total length (>= 10000 bp)	3097566	3113685
Total length (>= 25000 bp)	3028058	3113685
Total length (>= 50000 bp)	2957484	3050171
# contigs	10	18
Largest contig	2762464	840748
Total length	3105849	3135413
Reference length	2667210	2667210
GC (%)	37.81	37.66
Reference GC (%)	38.10	38.10
N50	2762464	488217
NG50	2762464	557523
N75	2762464	215377
NG75	2762464	295863
L50	1	3
LG50	1	2
L75	1	5
LG75	1	4
# misassemblies	130	101
# misassembled contigs	3	6
Misassembled contigs length	2792198	2427308
# local misassemblies	45	42
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	5
# unaligned contigs	4 + 6 part	6 + 12 part
Unaligned length	671707	718930
Genome fraction (%)	88.886	88.896
Duplication ratio	1.027	1.019
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	405.52	399.66
# indels per 100 kbp	23.92	16.36
Largest alignment	163404	121158
Total aligned length	2433185	2413643
NA50	32539	31949
NGA50	43337	43042
NA75	2837	1155
NGA75	19555	19417
LA50	22	24
LGA50	16	18
LA75	79	104
LGA75	38	40

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

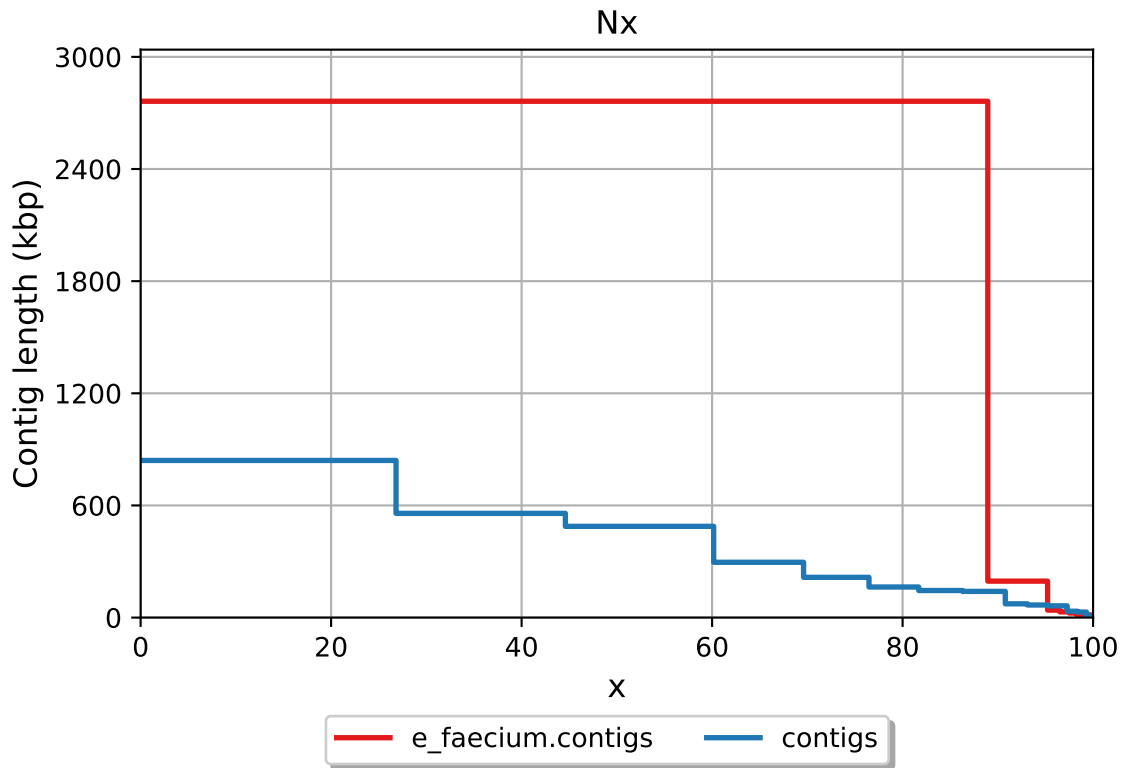
	e_faecium.contigs	contigs
# misassemblies	130	101
# contig misassemblies	130	101
# c. relocations	114	92
# c. translocations	15	8
# c. inversions	1	1
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	3	6
Misassembled contigs length	2792198	2427308
# local misassemblies	45	42
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	5
# mismatches	9614	9476
# indels	567	388
# indels (<= 5 bp)	517	341
# indels (> 5 bp)	50	47
Indels length	2127	1881

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).

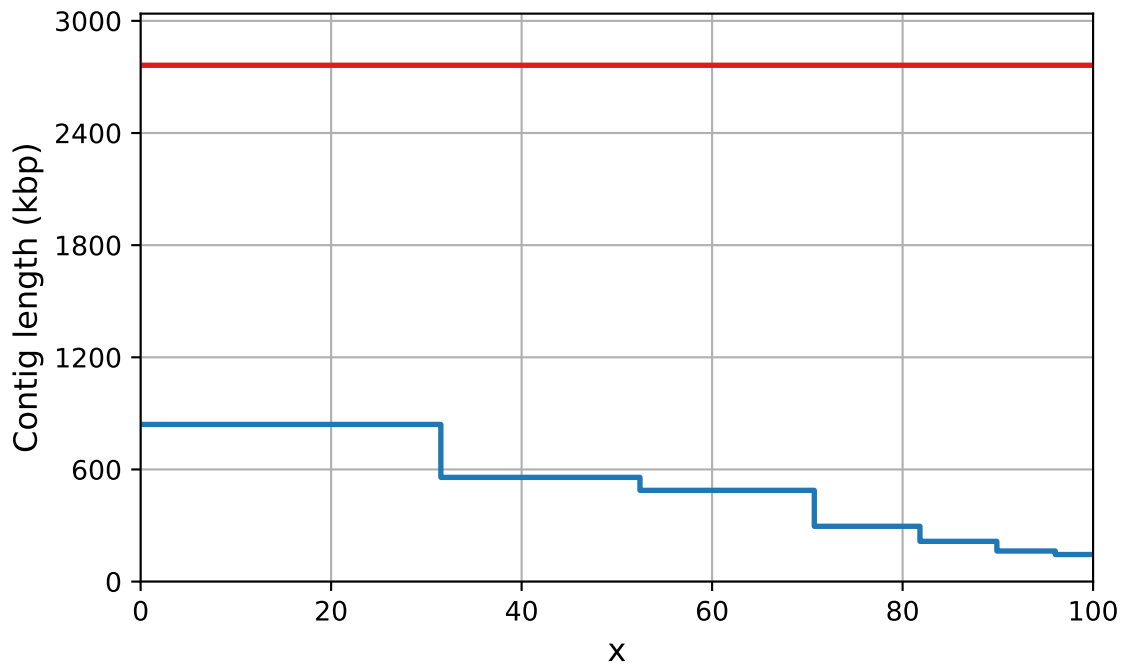
Unaligned report

	e_faecium.contigs	contigs
# fully unaligned contigs	4	6
Fully unaligned length	48057	84625
# partially unaligned contigs	6	12
Partially unaligned length	623650	634305
# N's	0	0

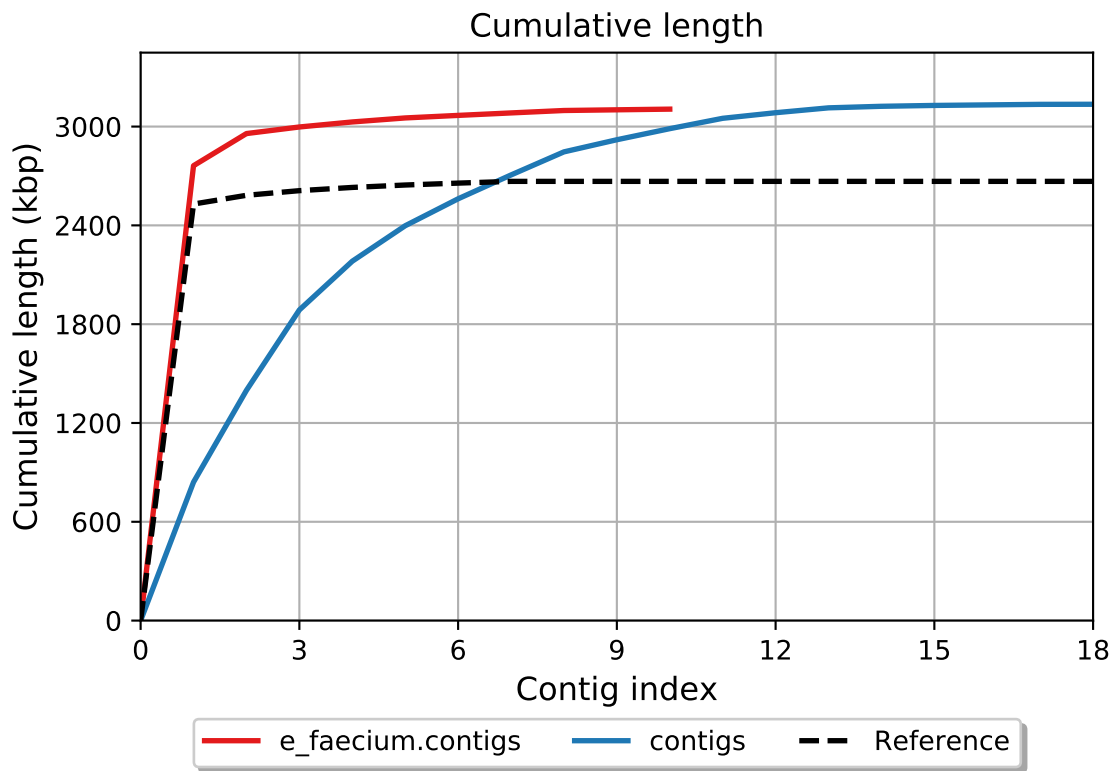
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



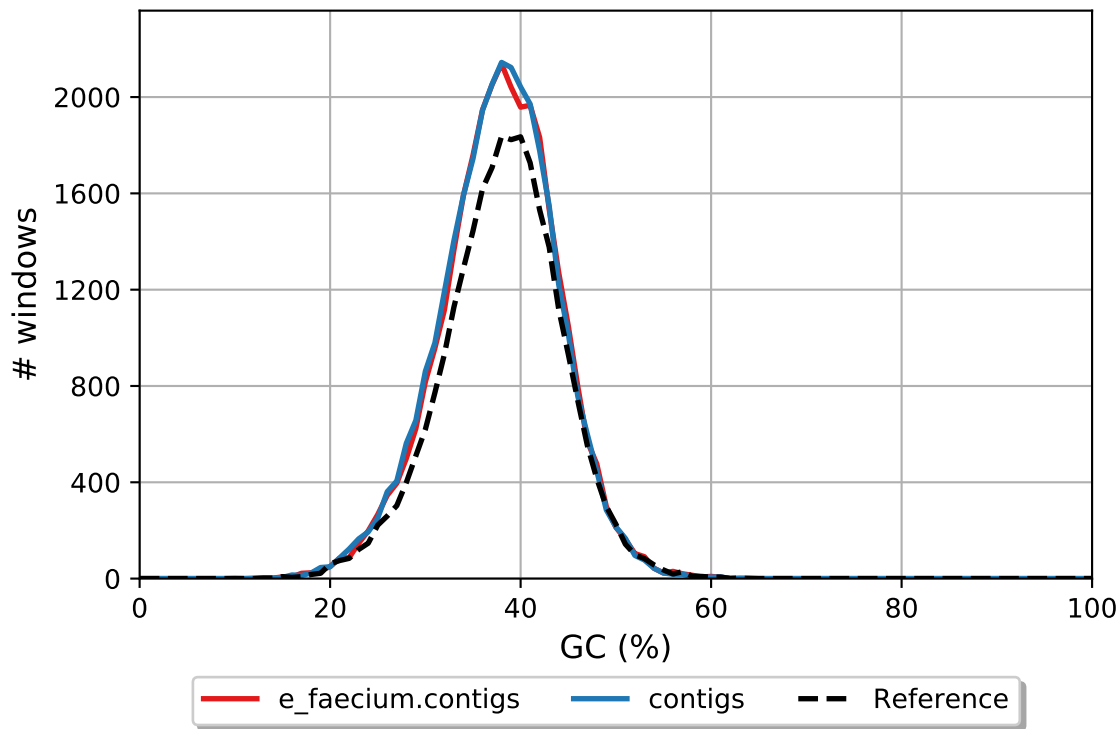
NGx



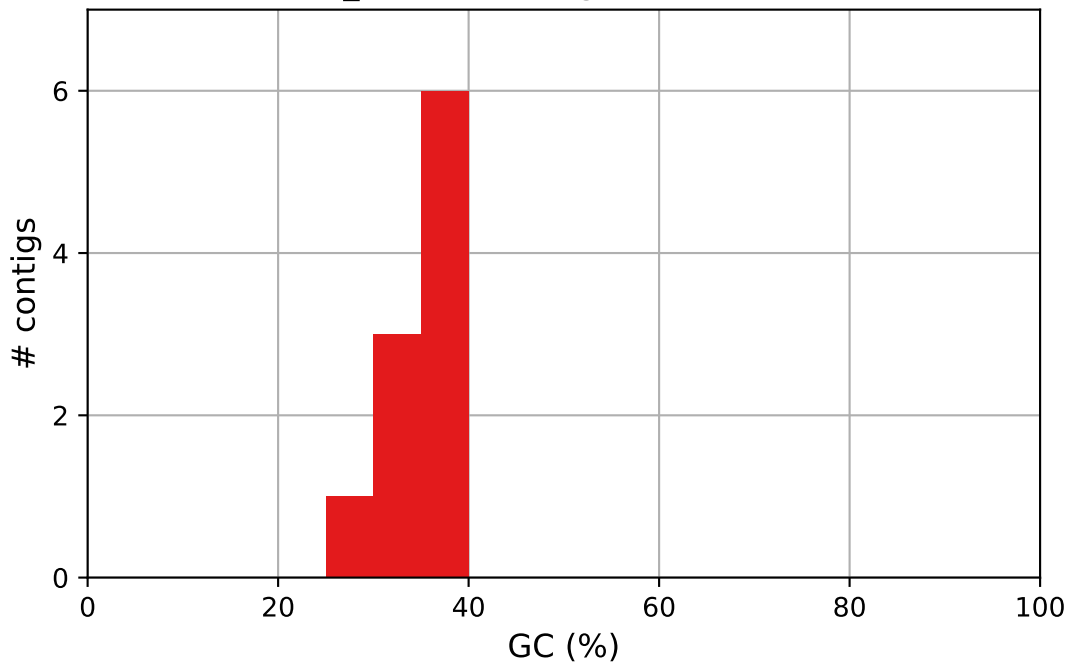
e_faecium.contigs contigs



GC content

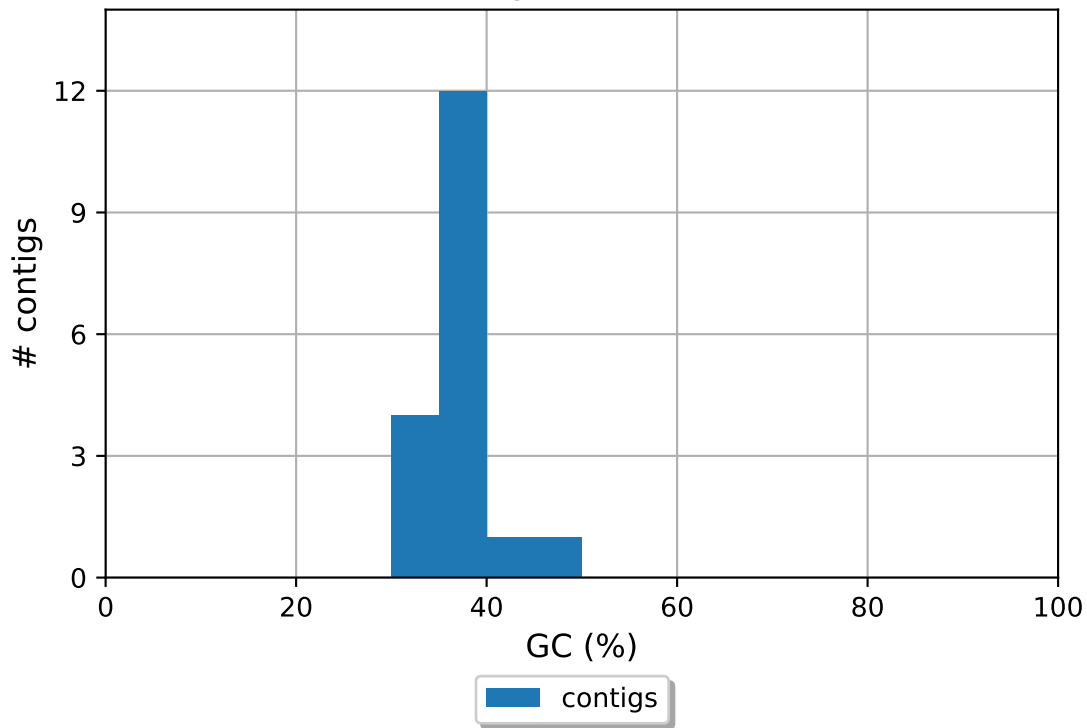


e_faecium.contigs GC content

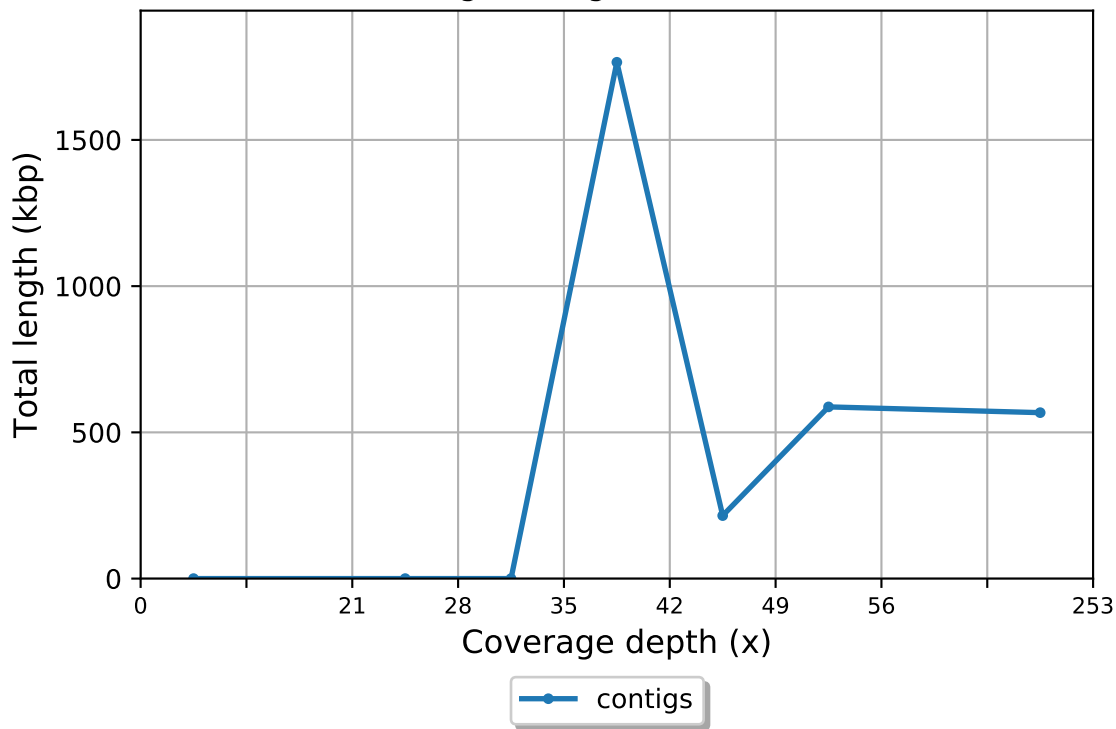


e_faecium.contigs

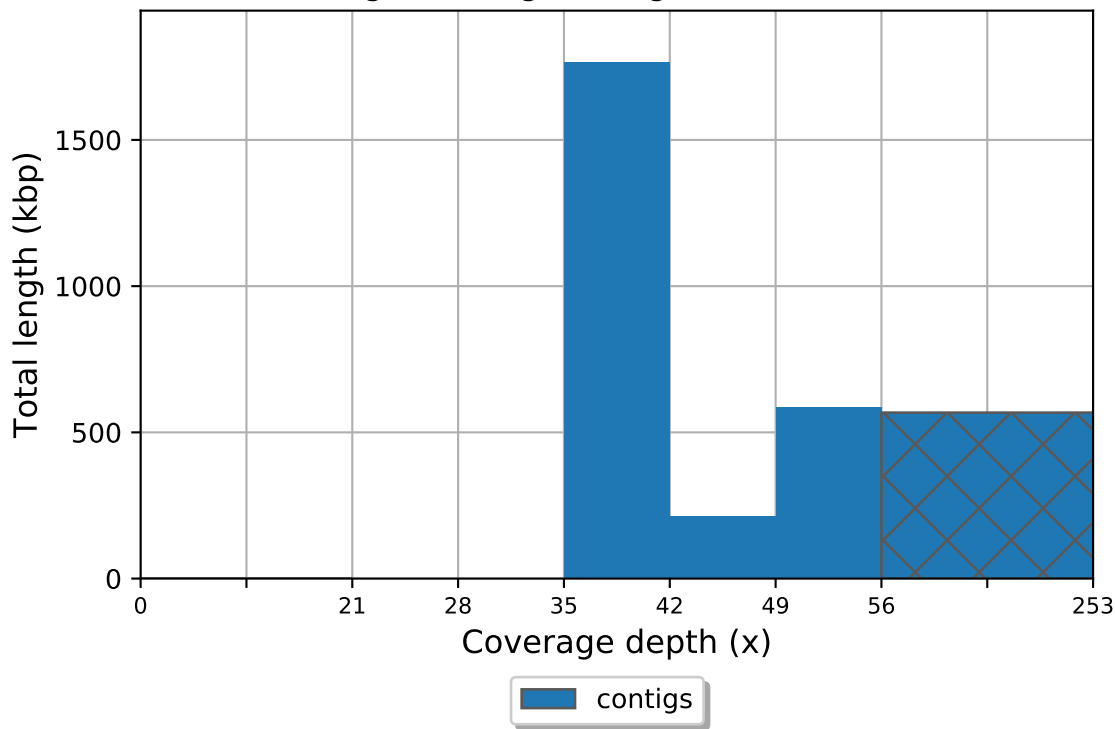
contigs GC content



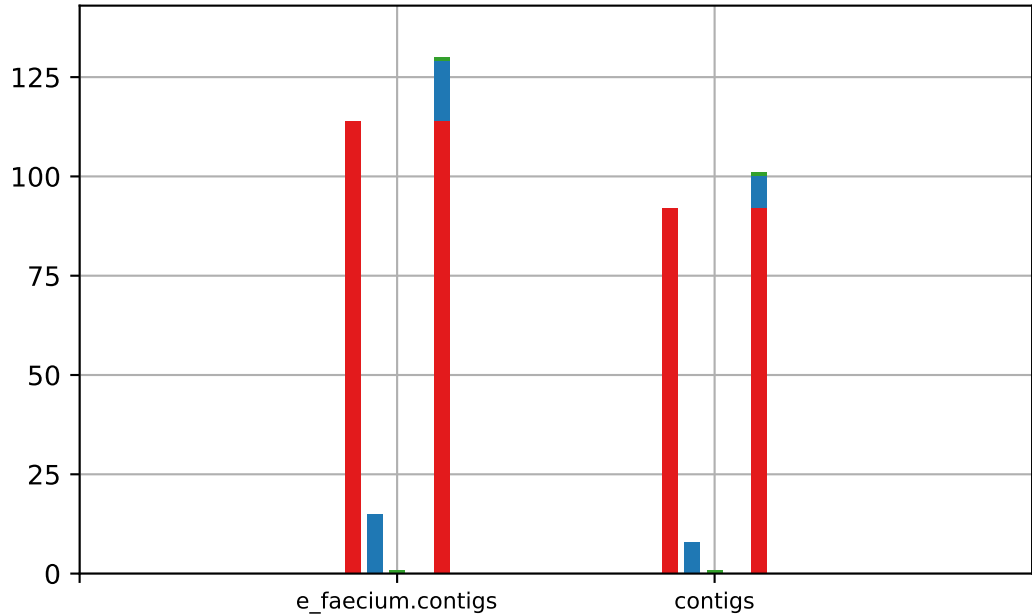
Coverage histogram (bin size: 7x)



contigs coverage histogram (bin size: 7x)



Misassemblies



relocations

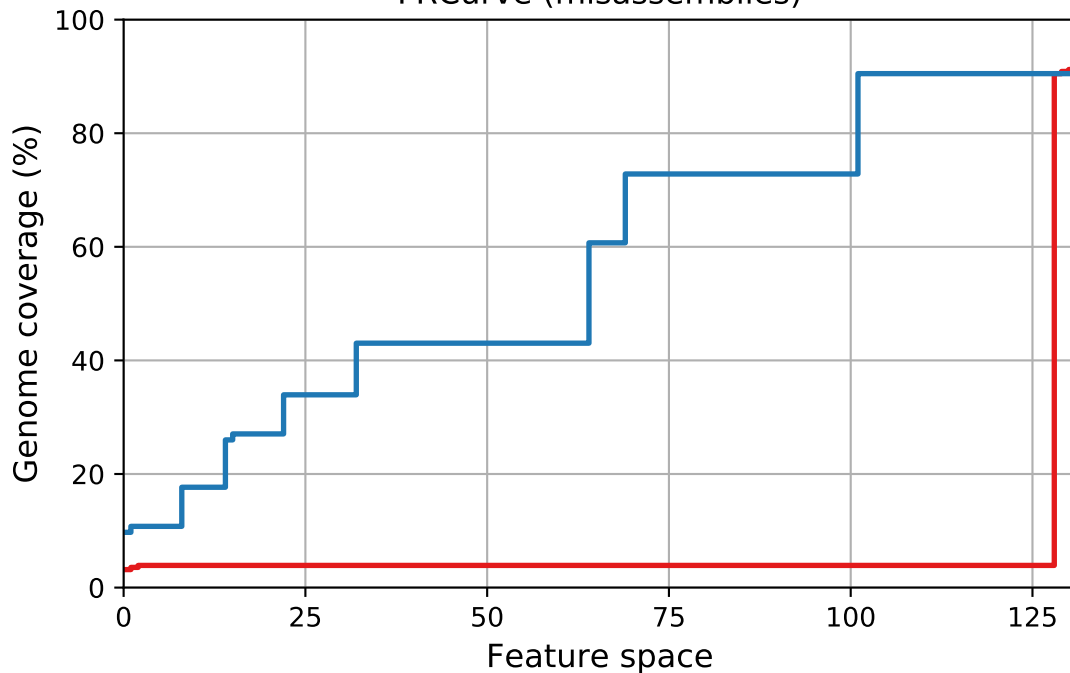


translocations

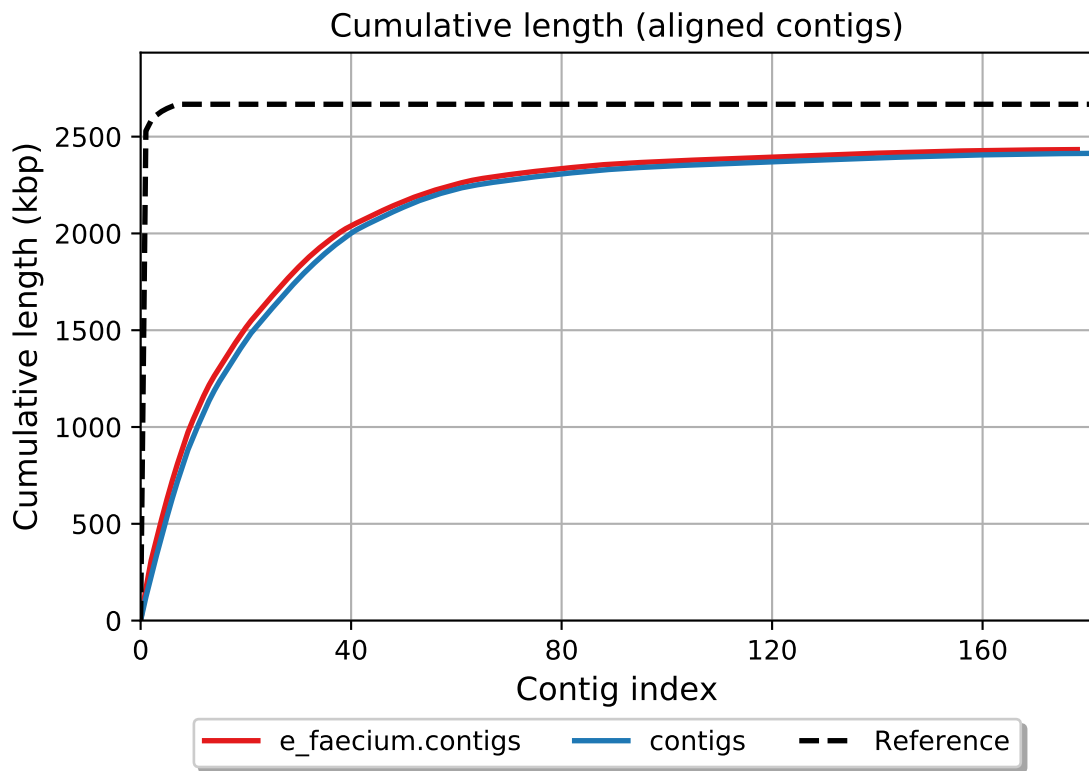


inversions

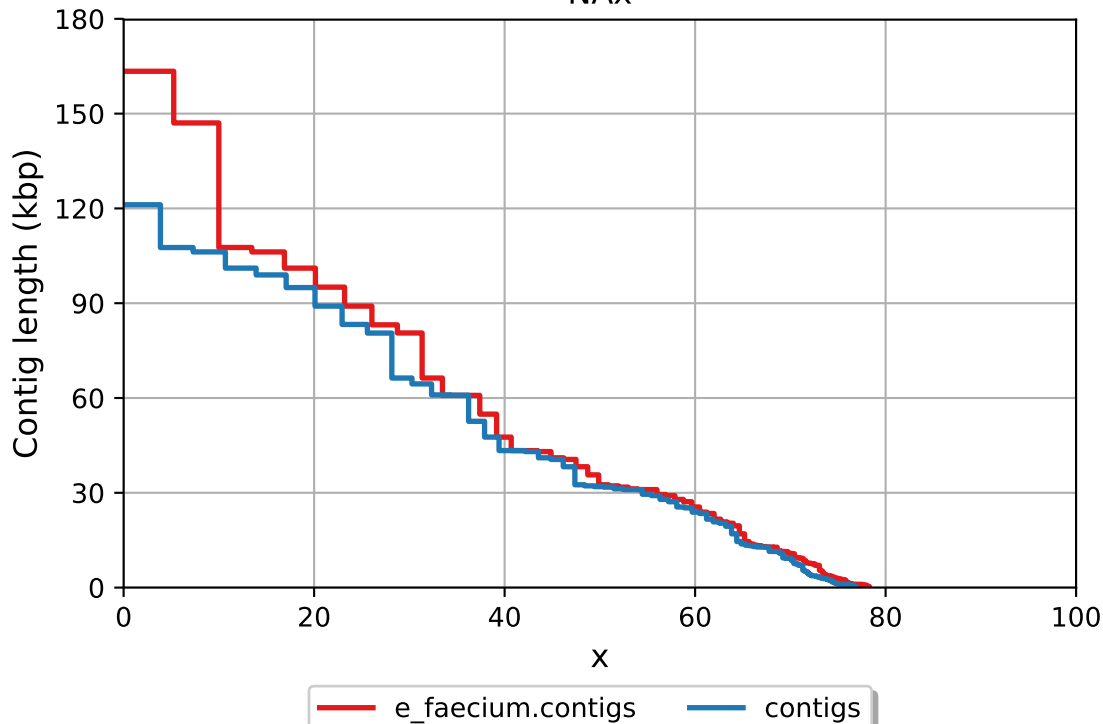
FRCurve (misassemblies)



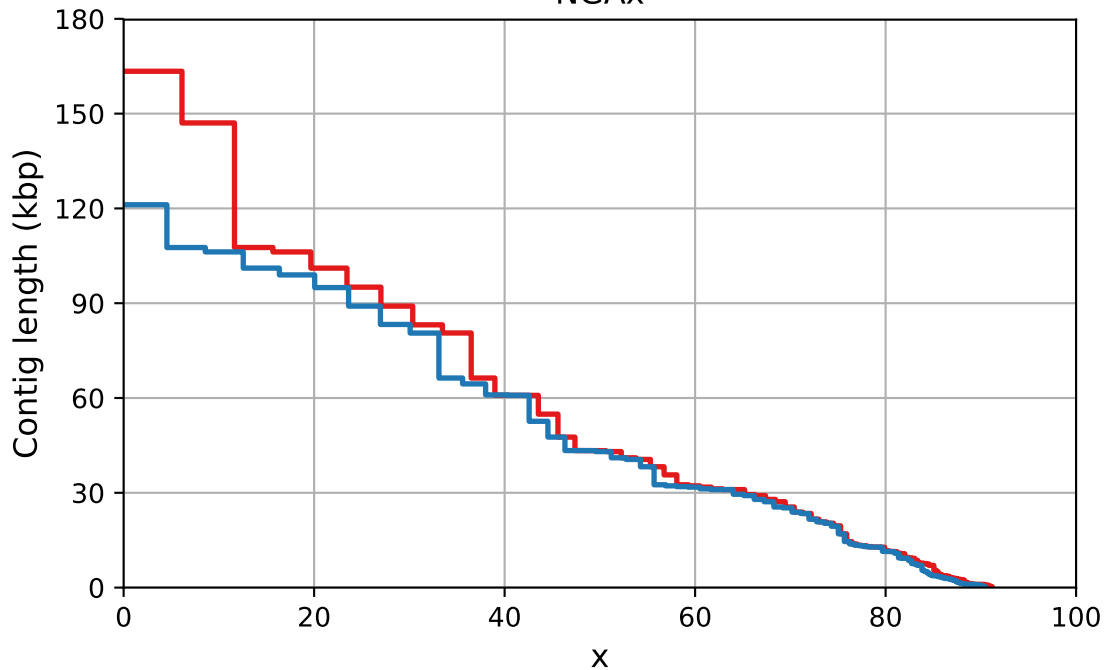
e_faecium.contigs contigs



NAx

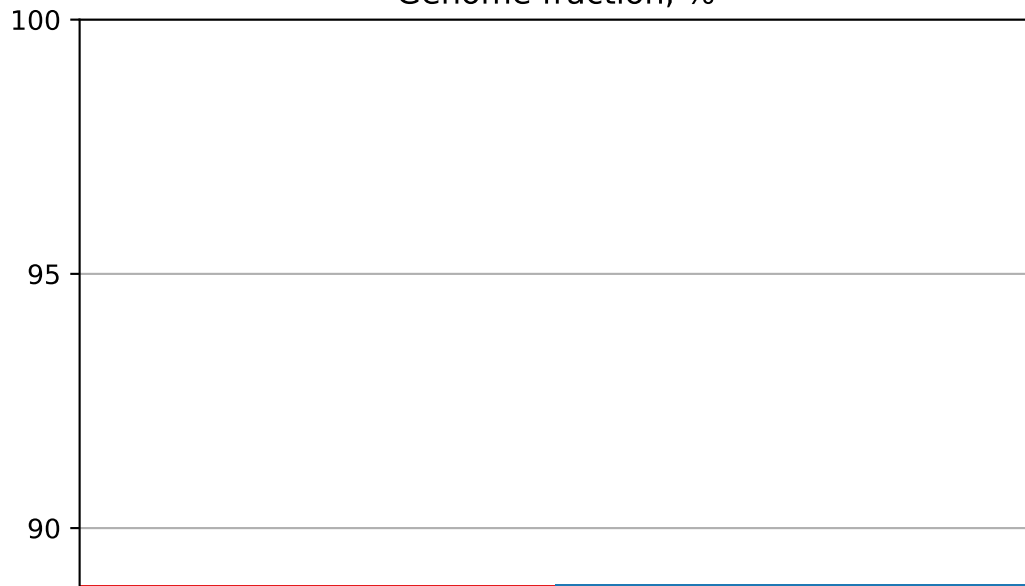


NGAx



e_faecium.contigs contigs

Genome fraction, %



e_faecium.contigs



contigs