Report

	E_faecium_improved
# 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	580862
Genome fraction (%)	84.999
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	392.78
# indels per 100 kbp	24.62
Largest alignment	137651
Total aligned length	2596659
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

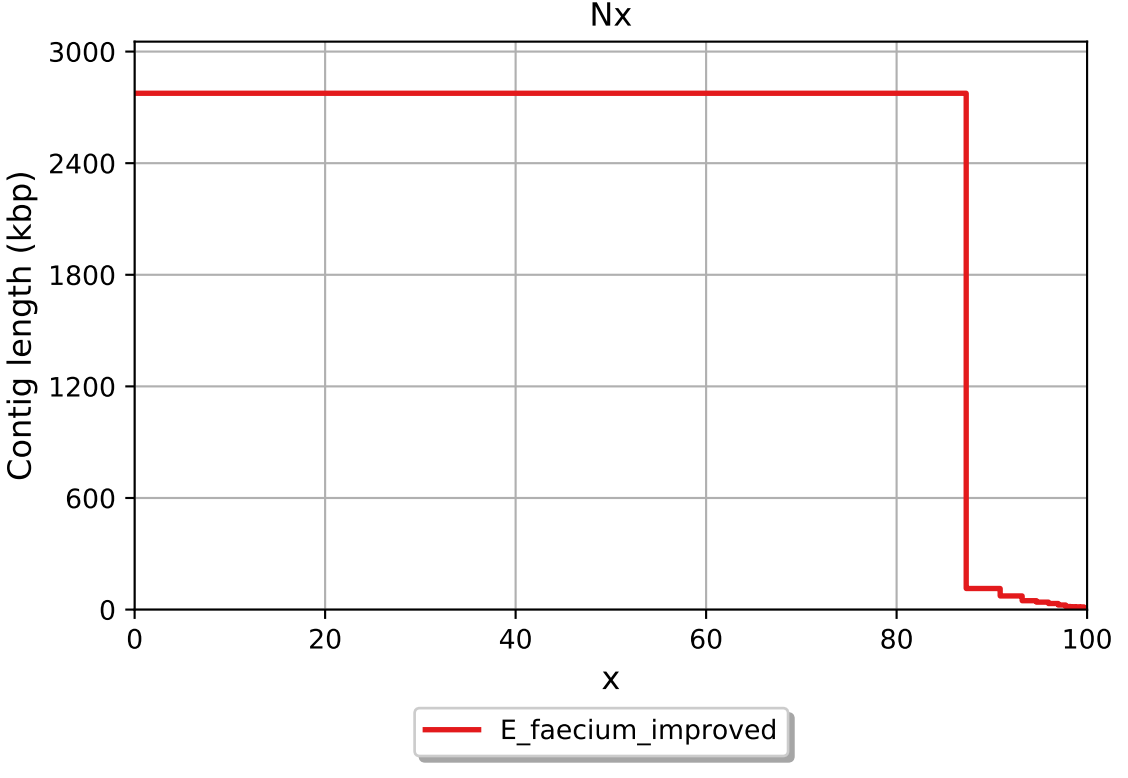
	E_faecium_improved
# misassemblies	190
# contig misassemblies	190
# c. relocations	175
# c. translocations	12
# c. inversions	3
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2775856
# local misassemblies	37
# 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

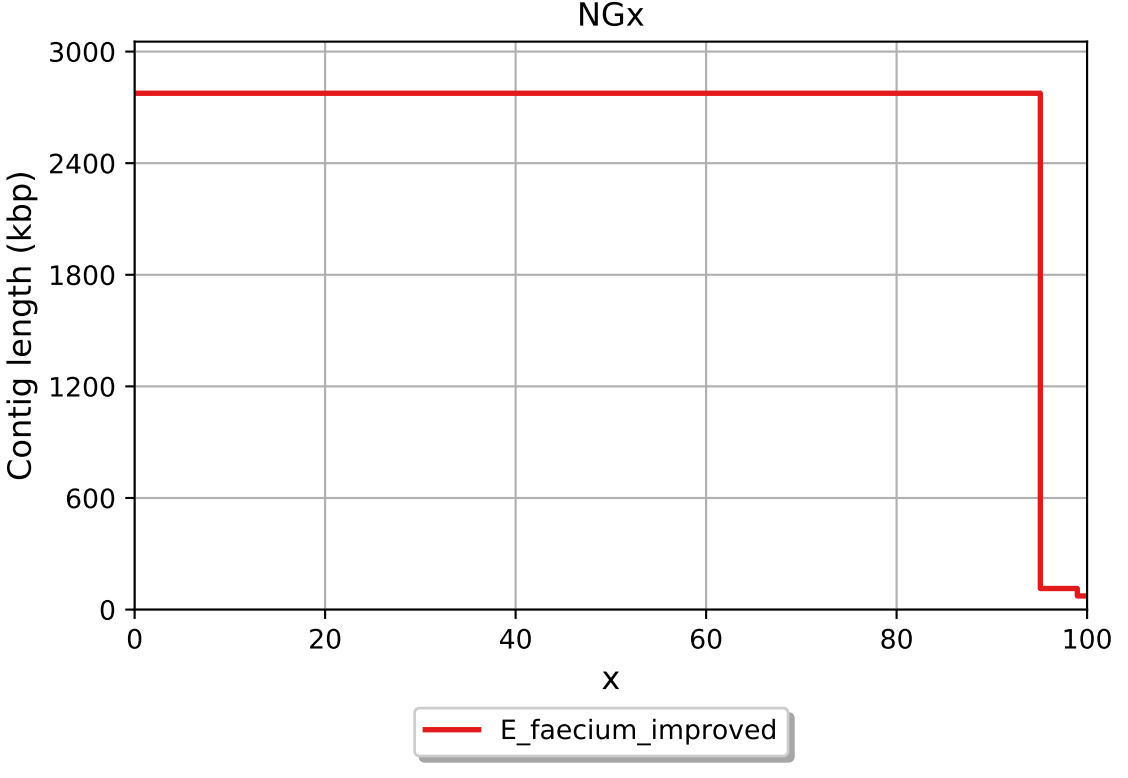
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

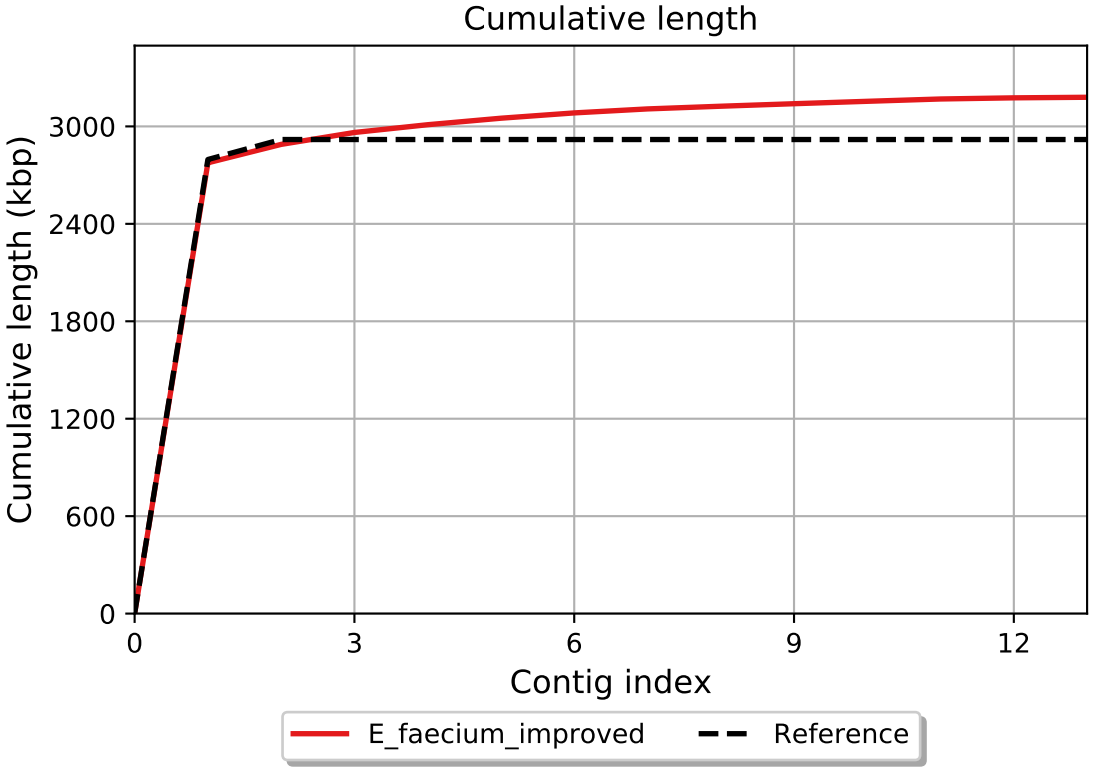
Unaligned report

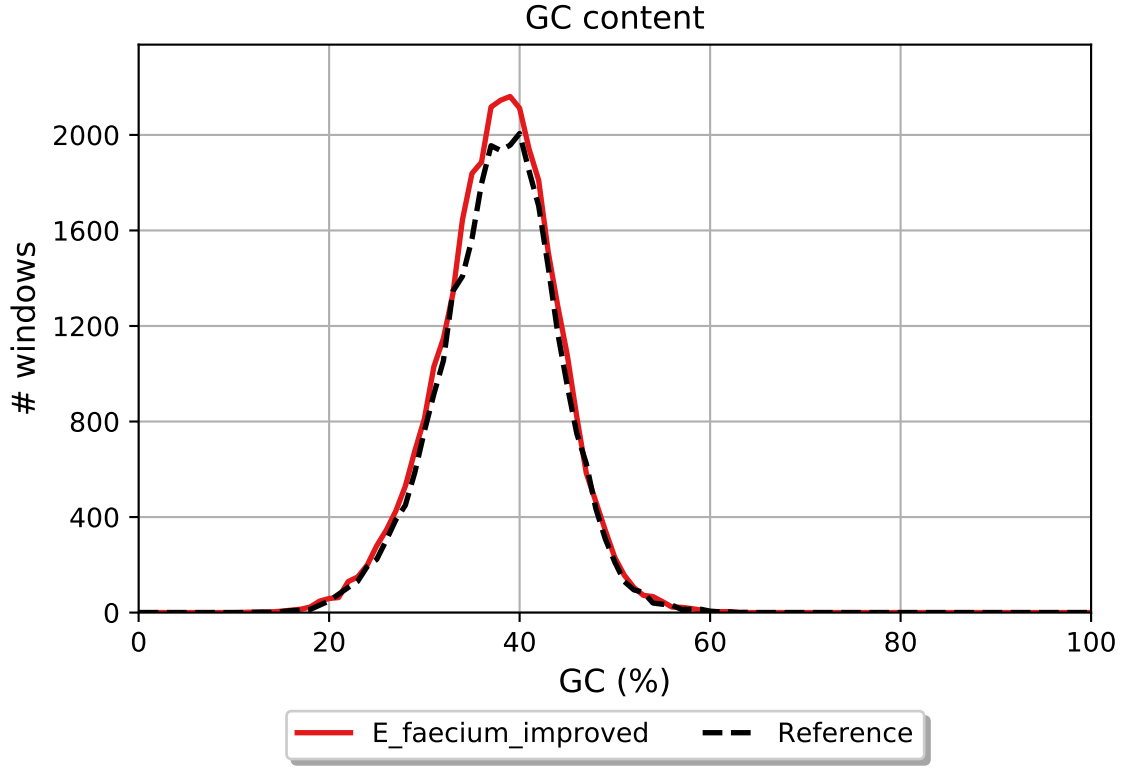
	E_faecium_improved
# fully unaligned contigs	5
Fully unaligned length	65424
# partially unaligned contigs	8
Partially unaligned length	515438
# N's	0

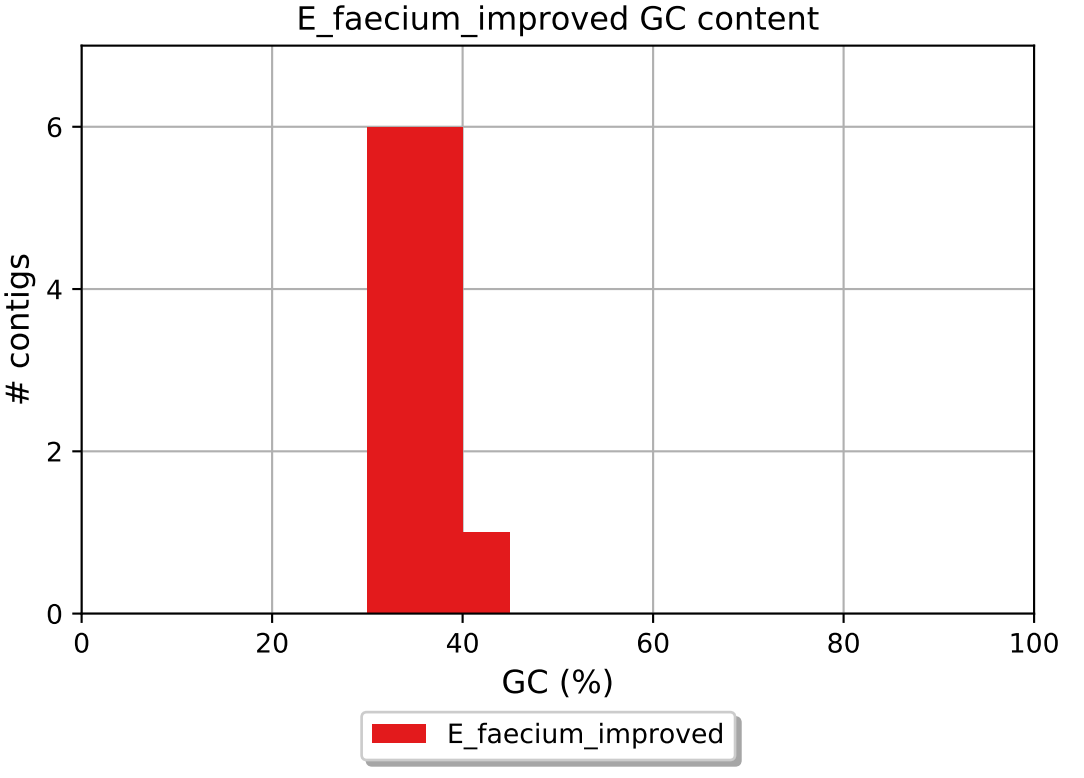
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

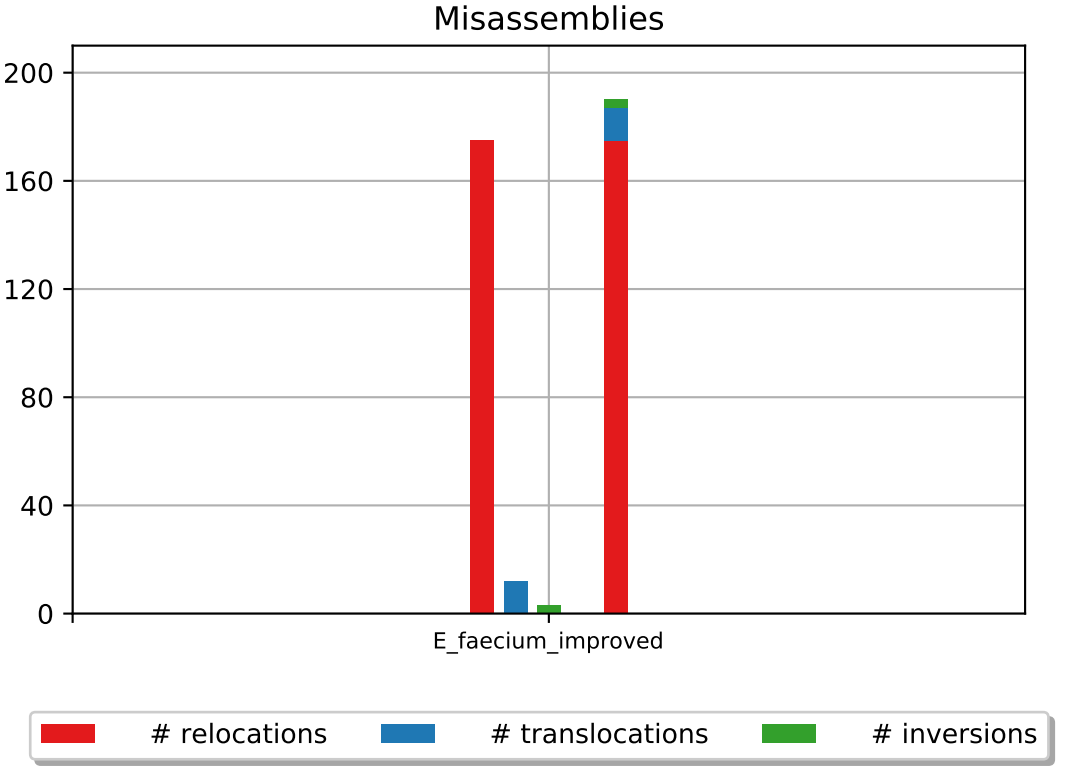

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
E_faecium_improved

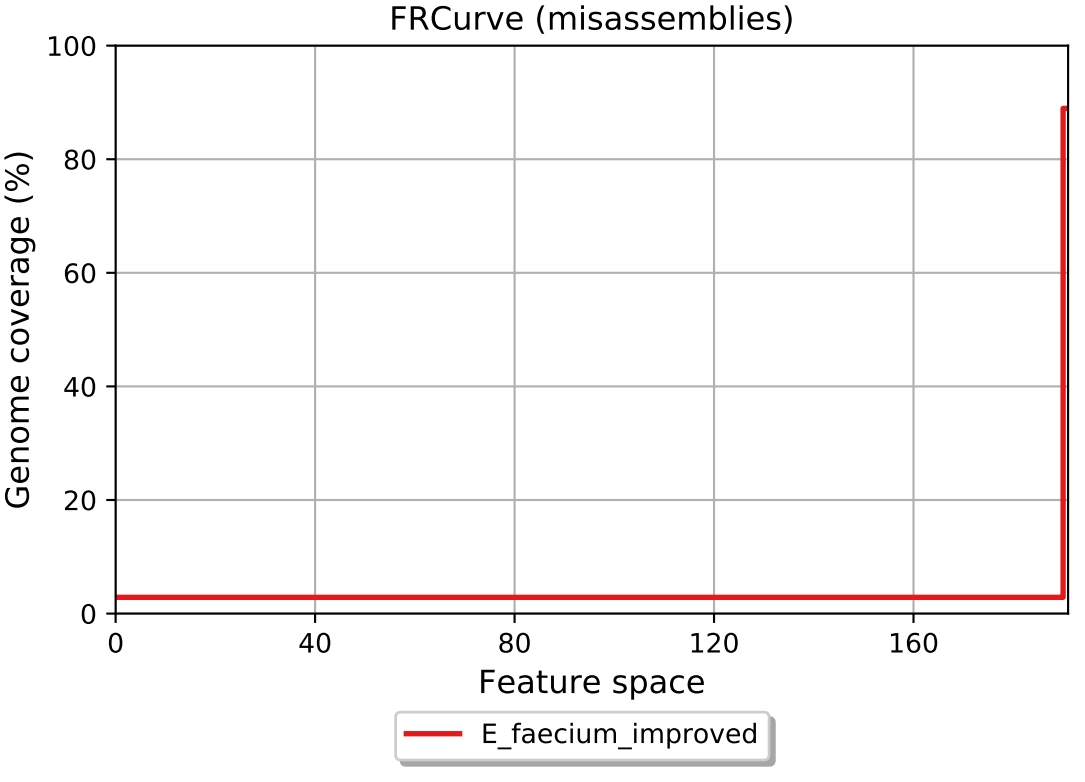

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
E_faecium_improved

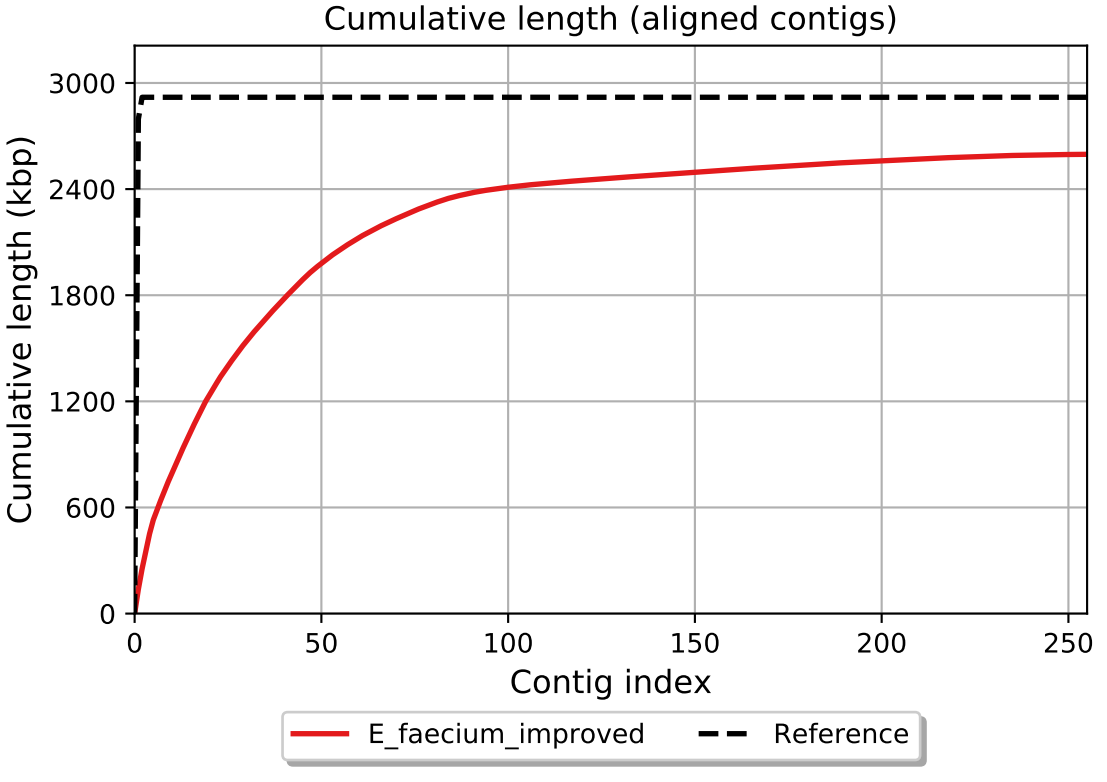

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
3
6
9
12
Contig index
E_faecium_improved
Reference

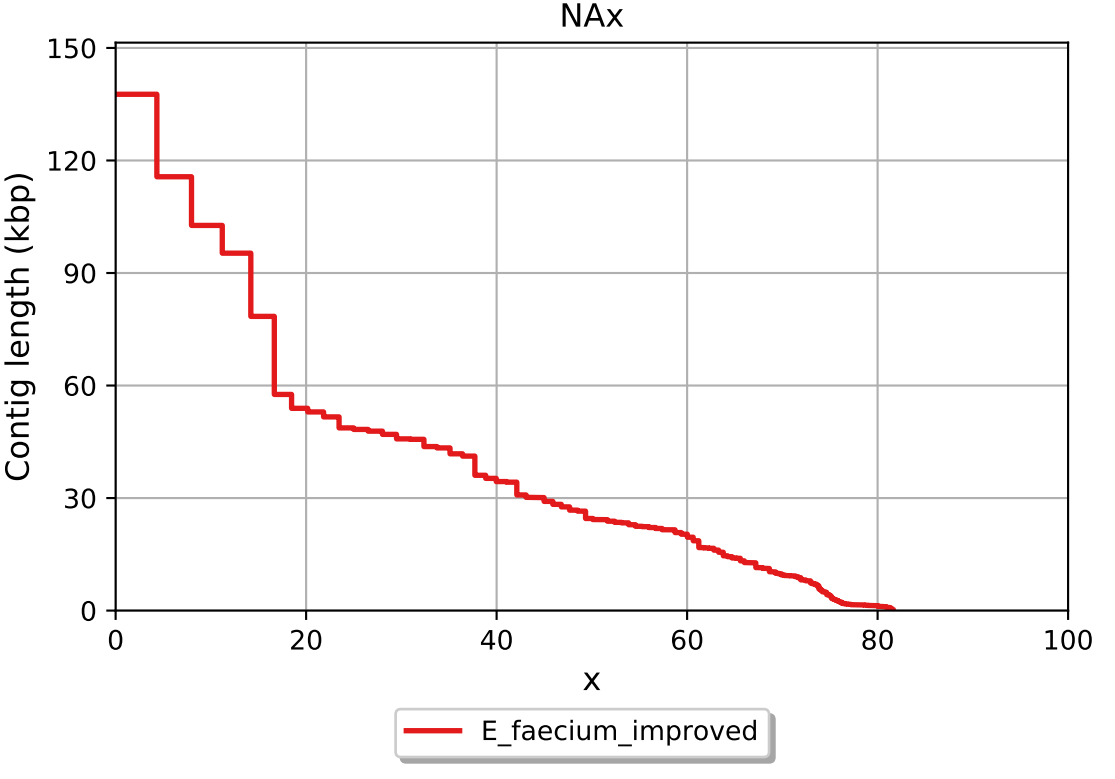

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
E_faecium_improved
Reference

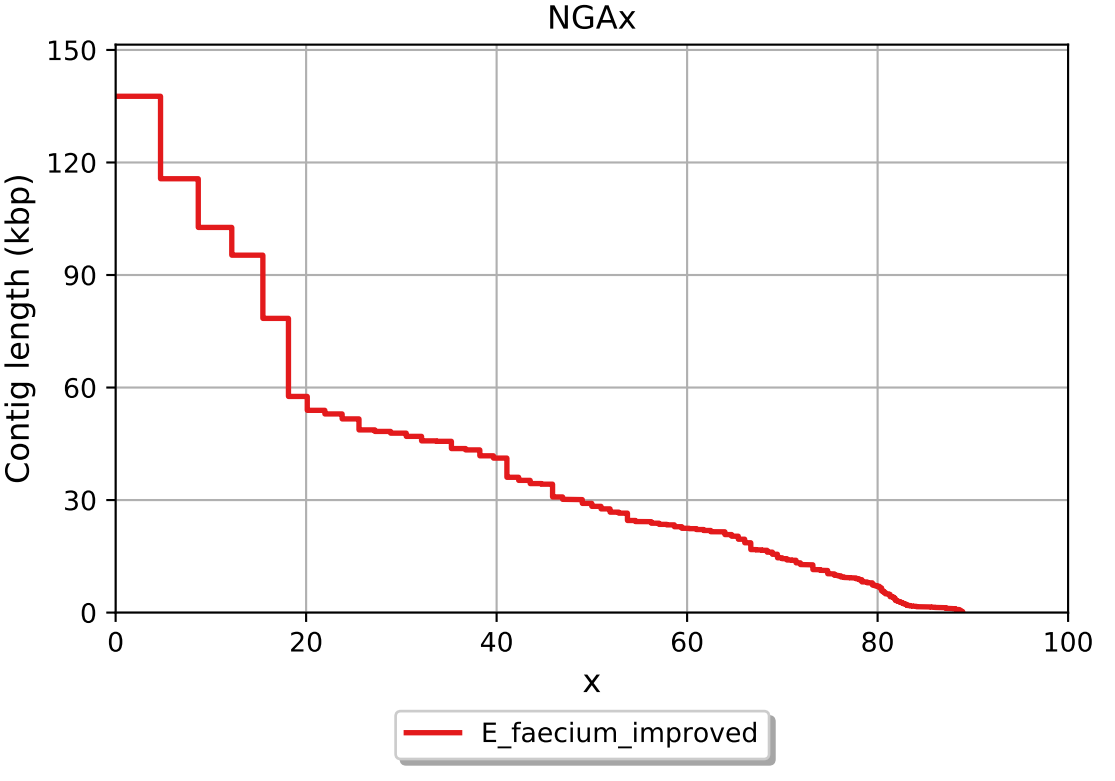

E_faecium_improved GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
E_faecium_improved


Misassemblies
200
160
120
80
40
0
E_faecium_improved
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
40
80
120
160
Feature space
E_faecium_improved


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
50
100
150
200
250
Contig index
E_faecium_improved
Reference


NAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
E_faecium_improved


NGAx
Contig length (kbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
E_faecium_improved