

Report

	e_faecium.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)	3127049
Total length (>= 1000 bp)	3127049
Total length (>= 5000 bp)	3127049
Total length (>= 10000 bp)	3117073
Total length (>= 25000 bp)	3091062
Total length (>= 50000 bp)	2996469
# contigs	8
Largest contig	2773606
Total length	3127049
Reference length	3168410
GC (%)	37.79
Reference GC (%)	37.70
N50	2773606
NG50	2773606
N75	2773606
NG75	2773606
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	7
# misassembled contigs	5
Misassembled contigs length	3062497
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.886
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.00
# indels per 100 kbp	13.38
Largest alignment	2195340
Total aligned length	3127045
NA50	2195340
NGA50	2195340
NA75	578266
NGA75	578266
LA50	1
LGA50	1
LA75	2
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

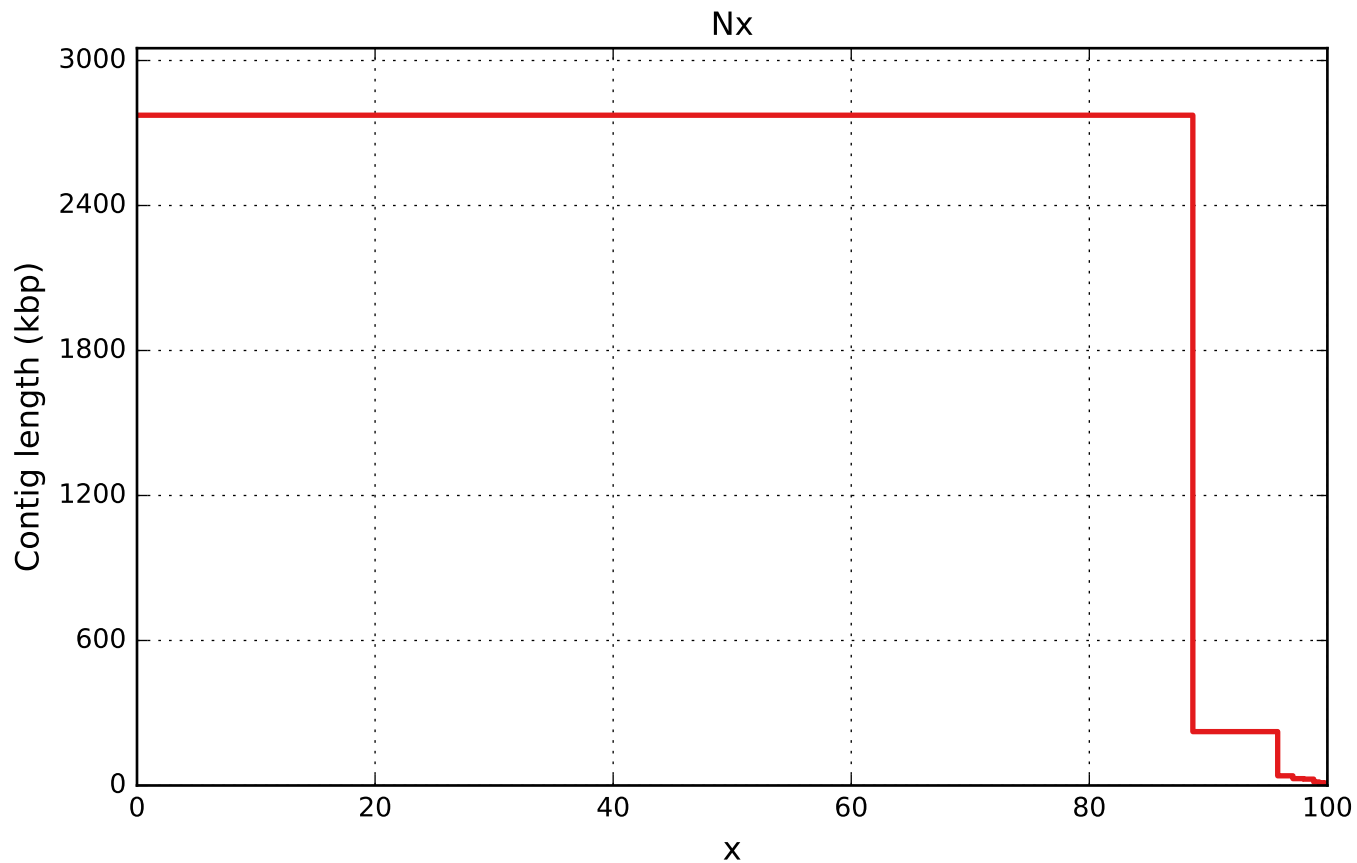
	e_faecium.contigs
# misassemblies	7
# relocations	5
# translocations	2
# inversions	0
# misassembled contigs	5
Misassembled contigs length	3062497
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	62
# indels	415
# indels (<= 5 bp)	406
# indels (> 5 bp)	9
Indels length	563

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

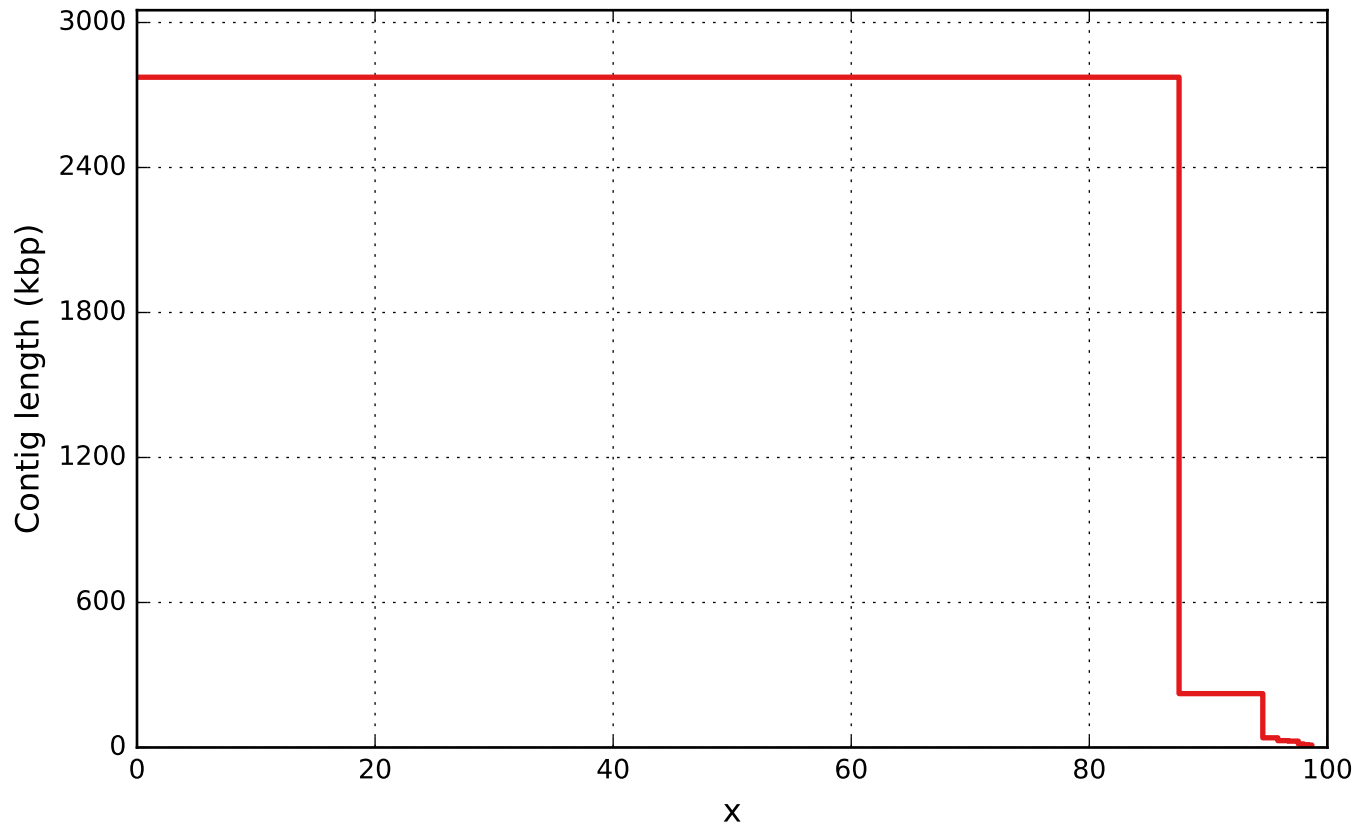
	e_faecium.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

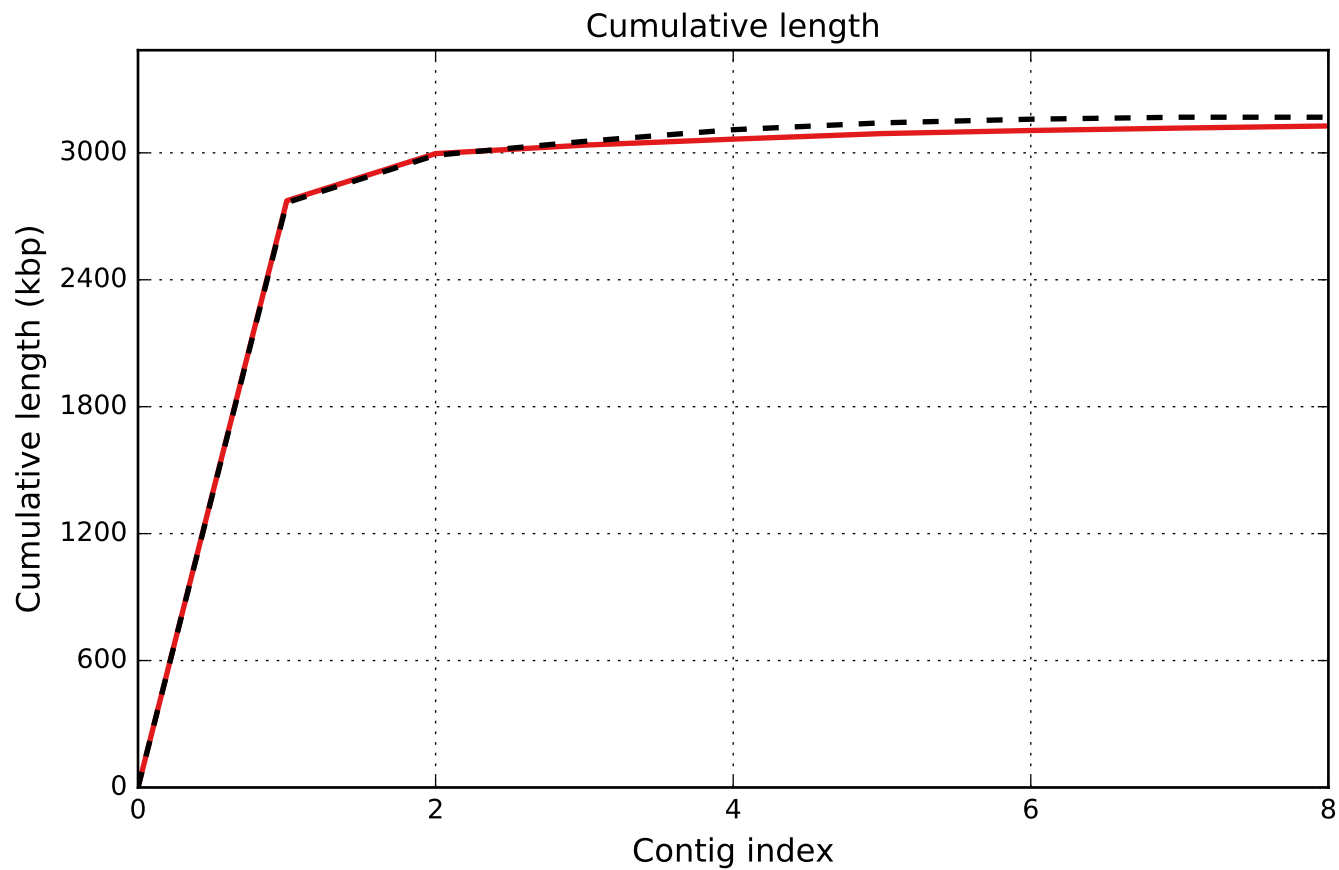


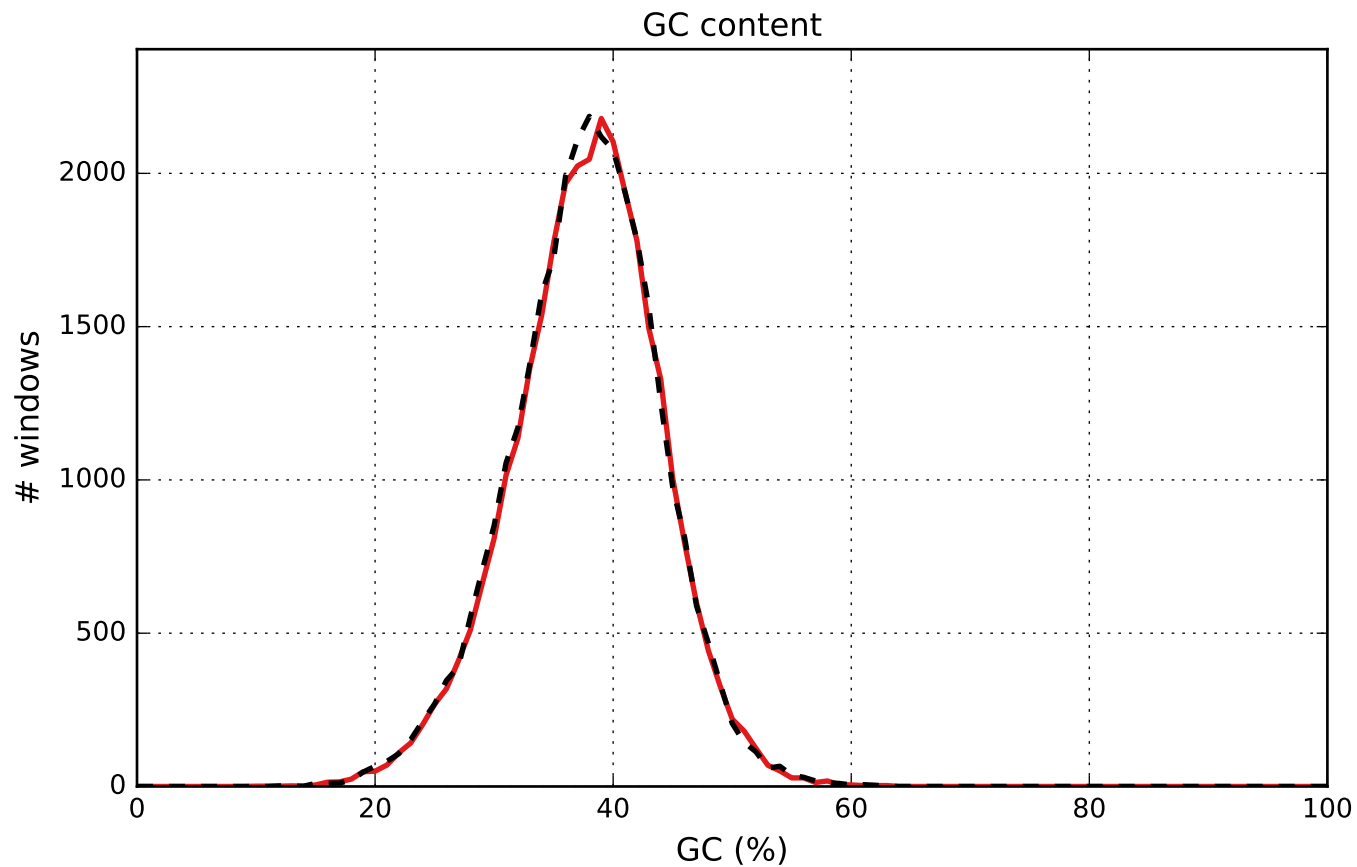
— e_faecium.contigs

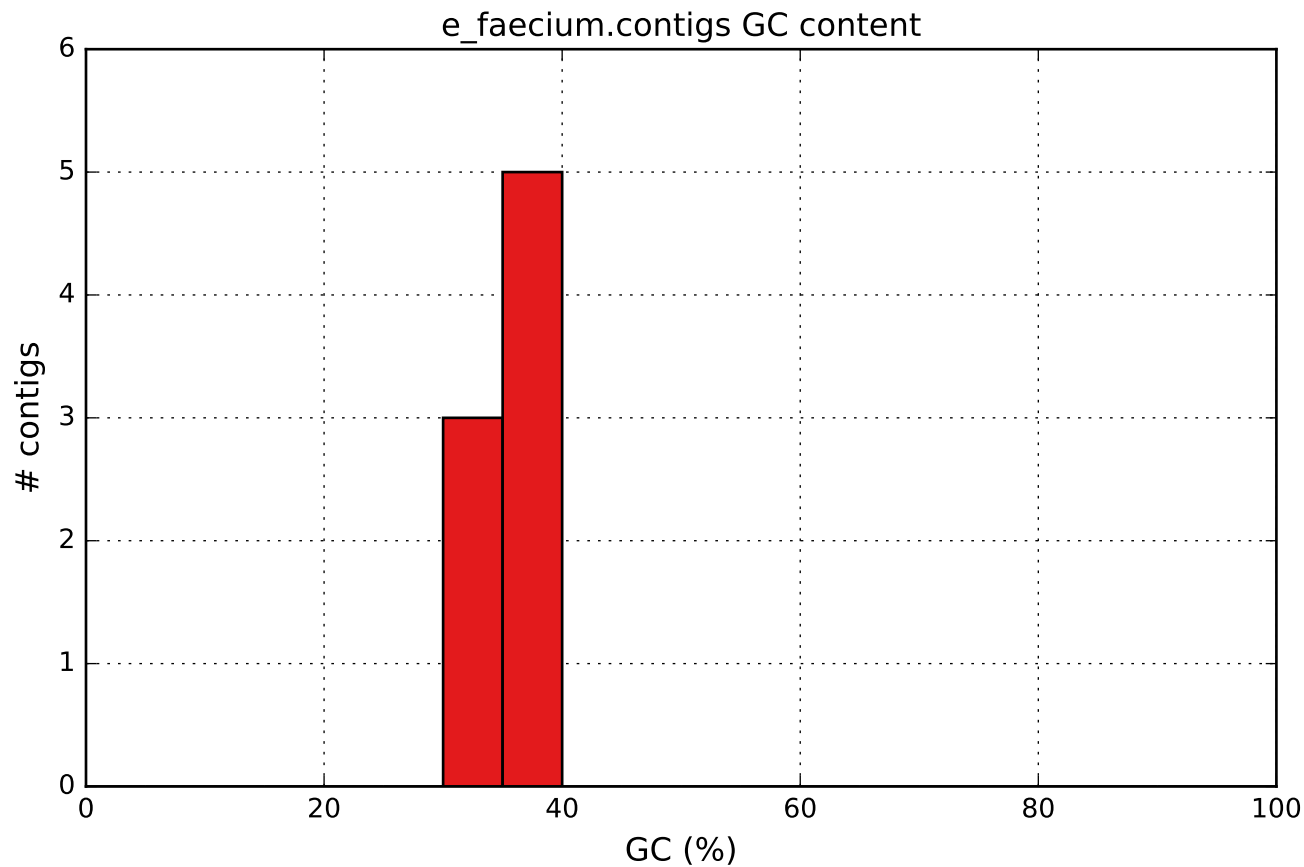
NGx




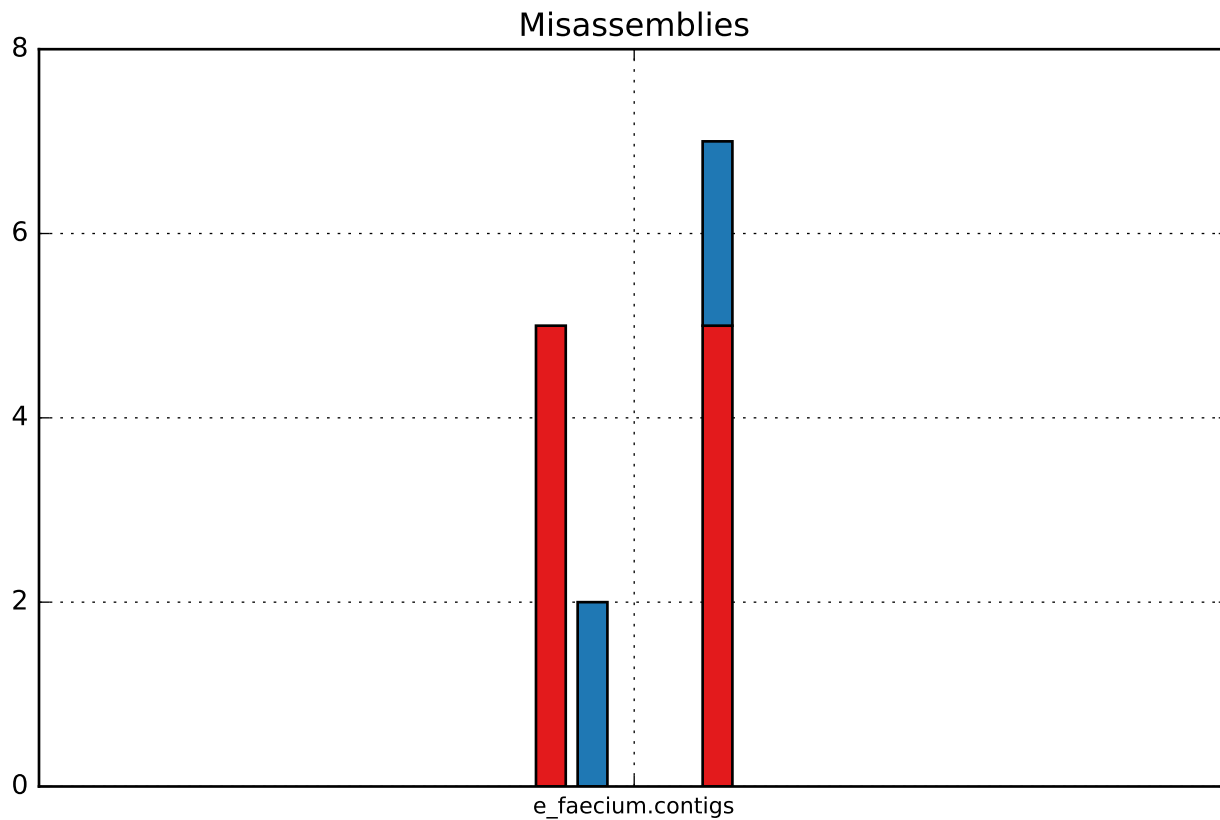
e_faecium.contigs



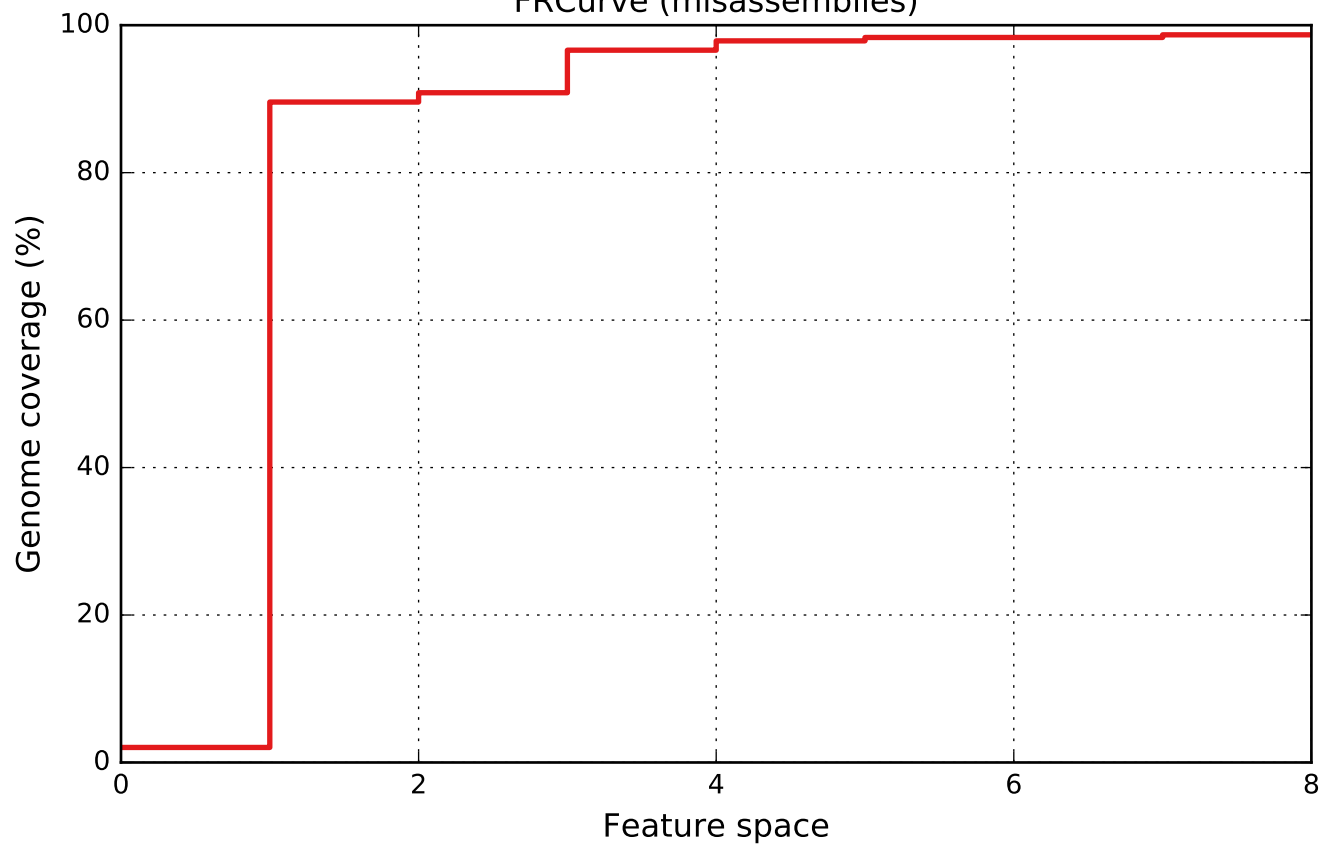




 e_faecium.contigs

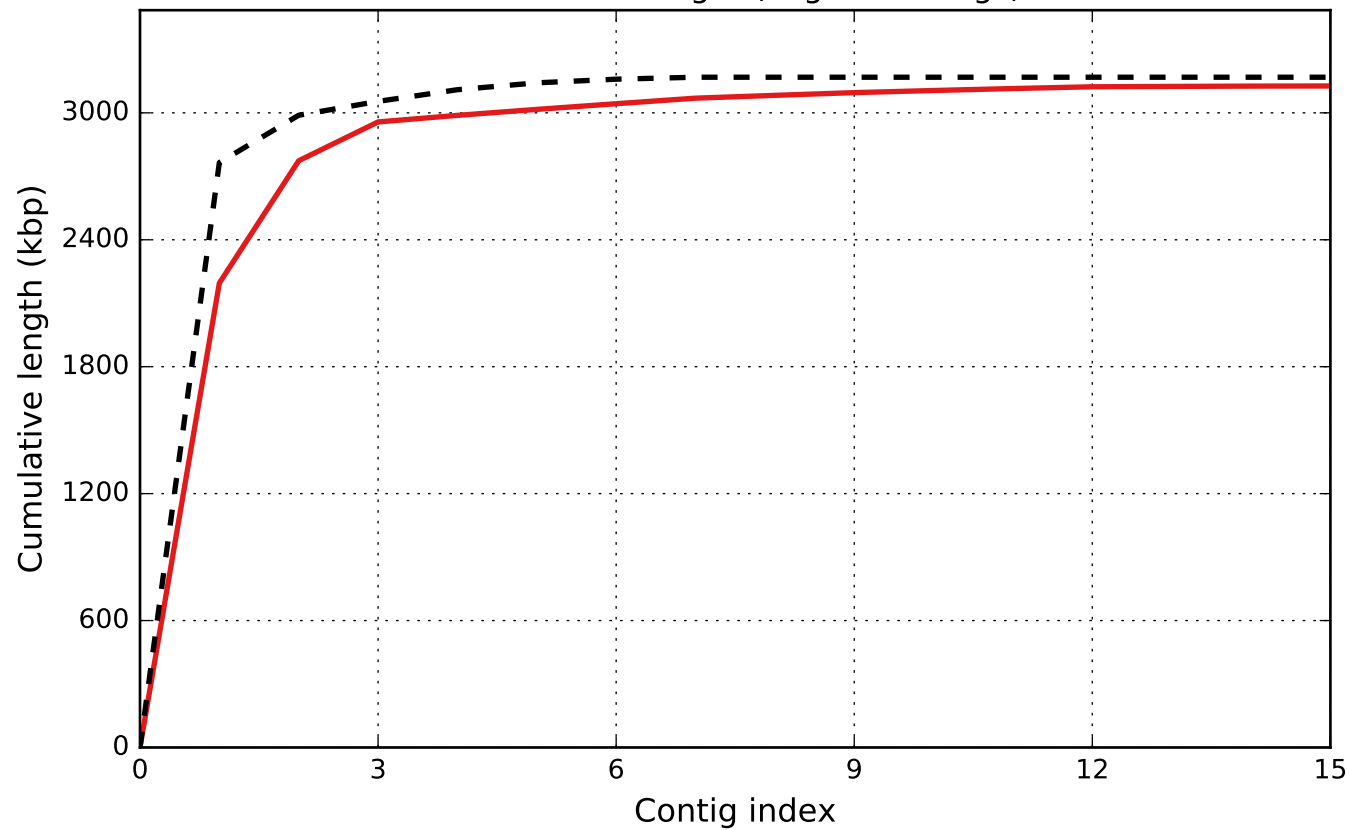


FRCurve (misassemblies)

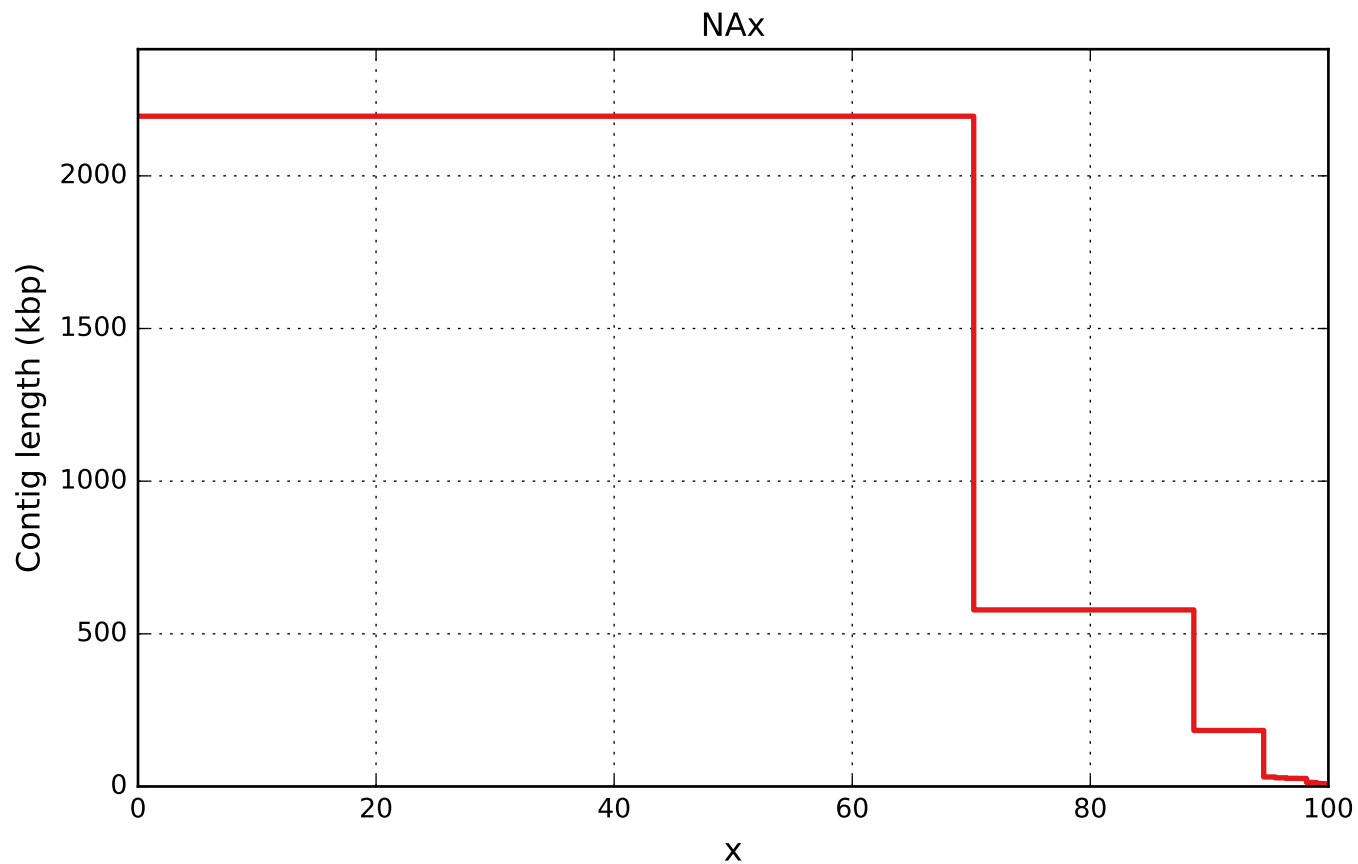


e_faecium.contigs

Cumulative length (aligned contigs)

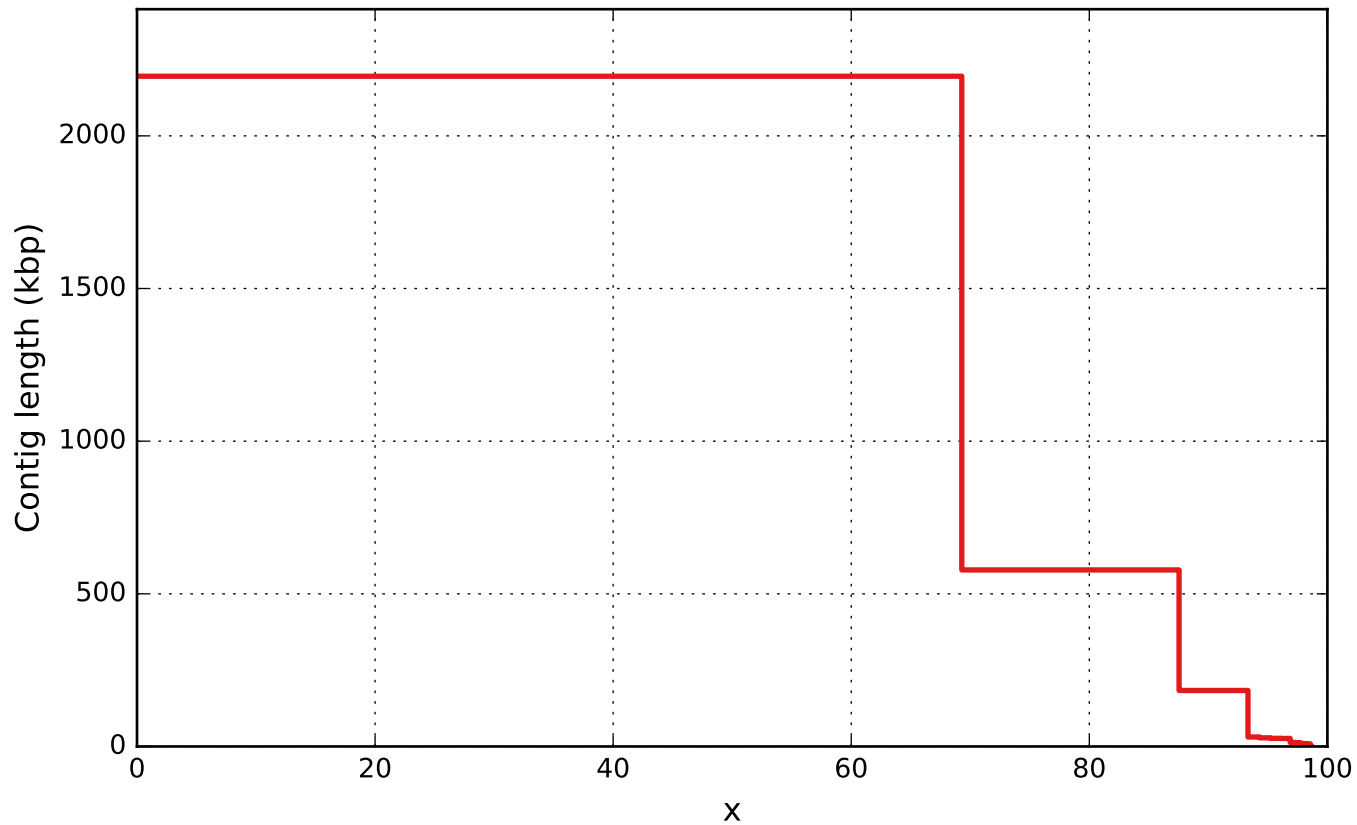


— `e_faecium.contigs` - - Reference



e_faecium.contigs

NGAx



— e_faecium.contigs