

Report

	Enterococci.contigs
# contigs (≥ 0 bp)	8
# contigs (≥ 1000 bp)	8
# contigs (≥ 5000 bp)	7
# contigs (≥ 10000 bp)	7
# contigs (≥ 25000 bp)	5
# contigs (≥ 50000 bp)	2
Total length (≥ 0 bp)	3143156
Total length (≥ 1000 bp)	3143156
Total length (≥ 5000 bp)	3138760
Total length (≥ 10000 bp)	3138760
Total length (≥ 25000 bp)	3110222
Total length (≥ 50000 bp)	2999932
# contigs	8
Largest contig	2773588
Total length	3143156
Reference length	2765010
GC (%)	37.78
Reference GC (%)	38.11
N50	2773588
NG50	2773588
N75	2773588
NG75	2773588
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2773588
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	5 + 2 part
Unaligned length	325102
Genome fraction (%)	100.000
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.04
# indels per 100 kbp	4.38
Largest alignment	2195332
Total aligned length	2818055
NA50	2195332
NGA50	2195332
NA75	578256
NGA75	2195332
LA50	1
LGA50	1
LA75	2
LGA75	1

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

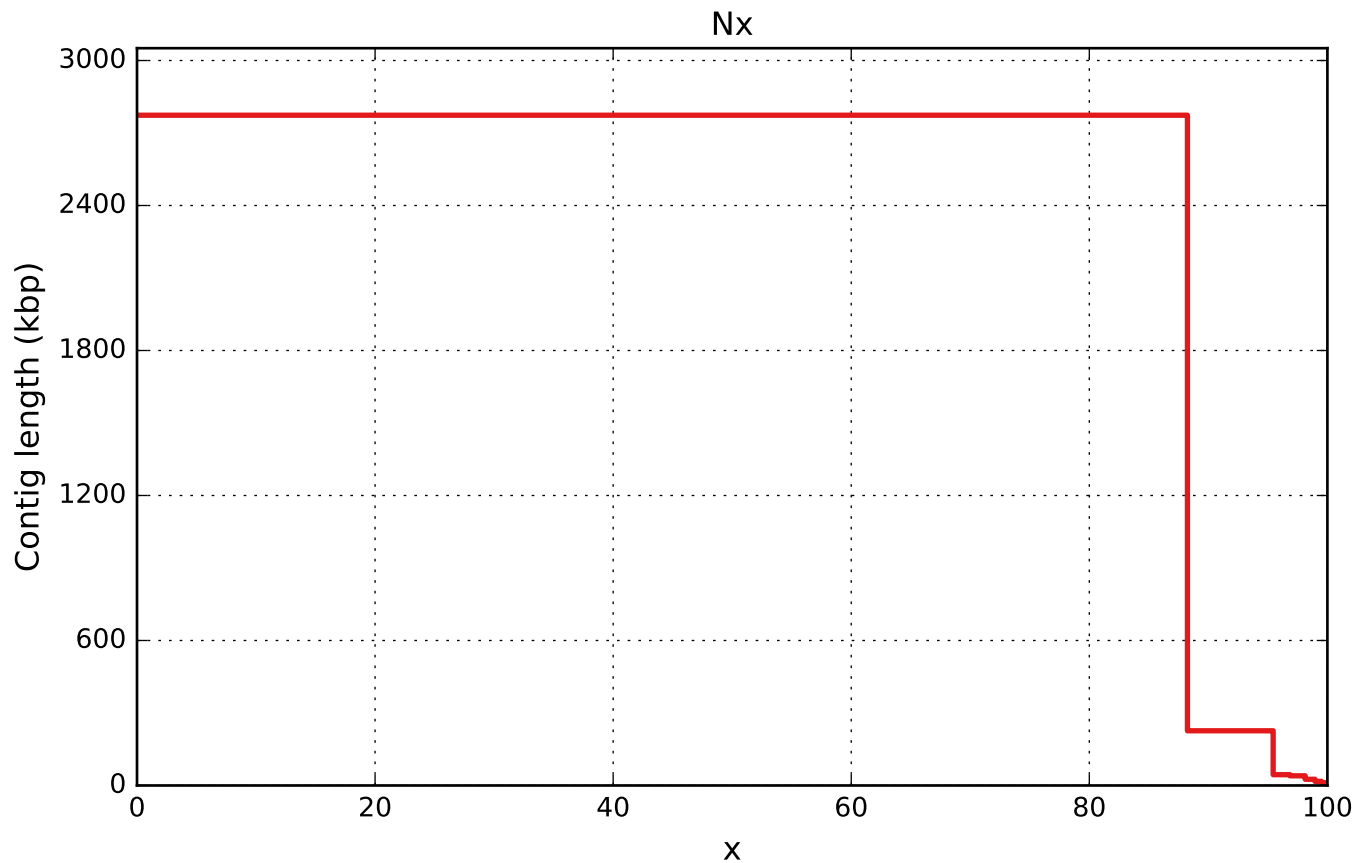
	Enterococci.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2773588
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	1
# indels	121
# indels (<= 5 bp)	121
# indels (> 5 bp)	0
Indels length	123

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).

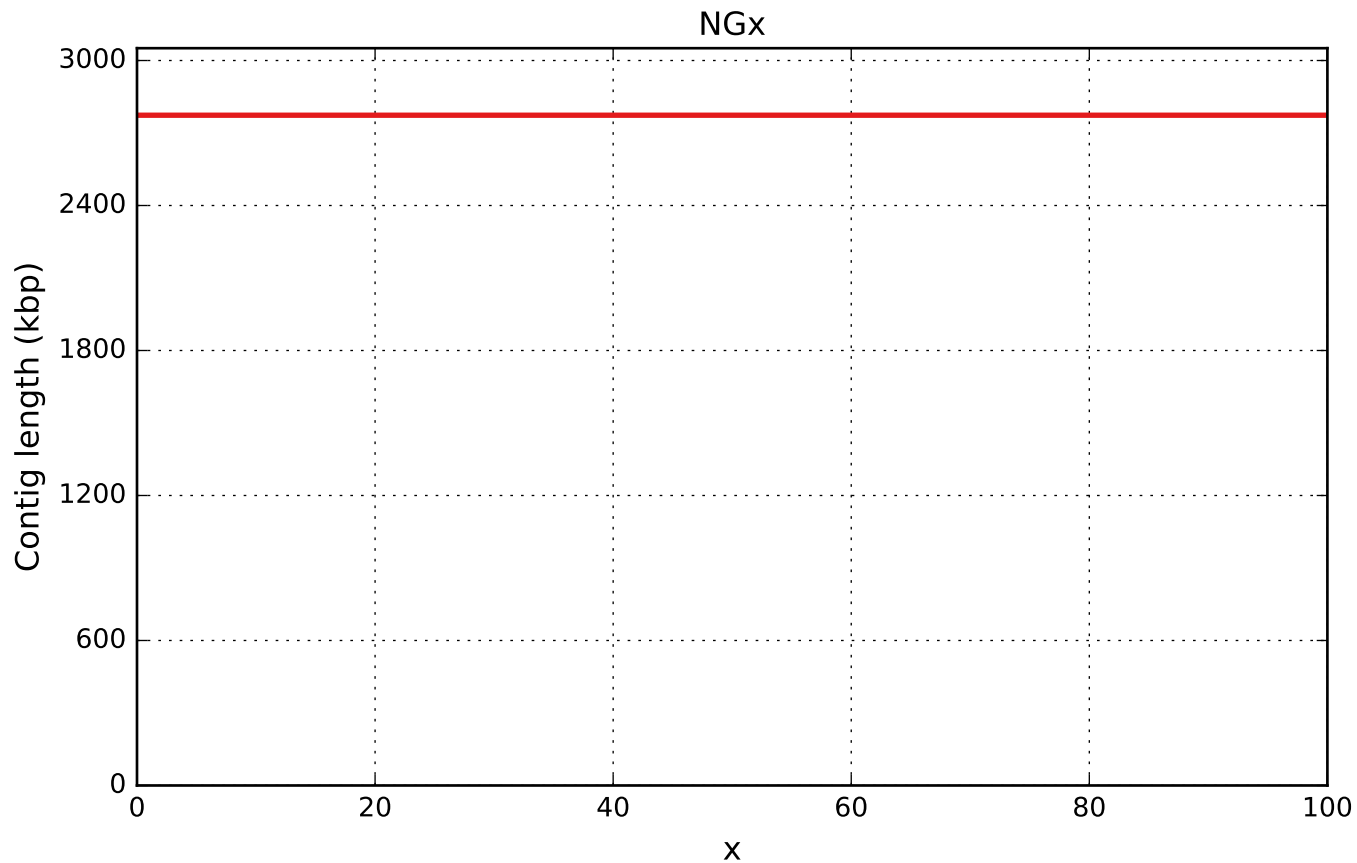
Unaligned report

	Enterococci.contigs
# fully unaligned contigs	5
Fully unaligned length	103207
# partially unaligned contigs	2
Partially unaligned length	221895
# N's	0

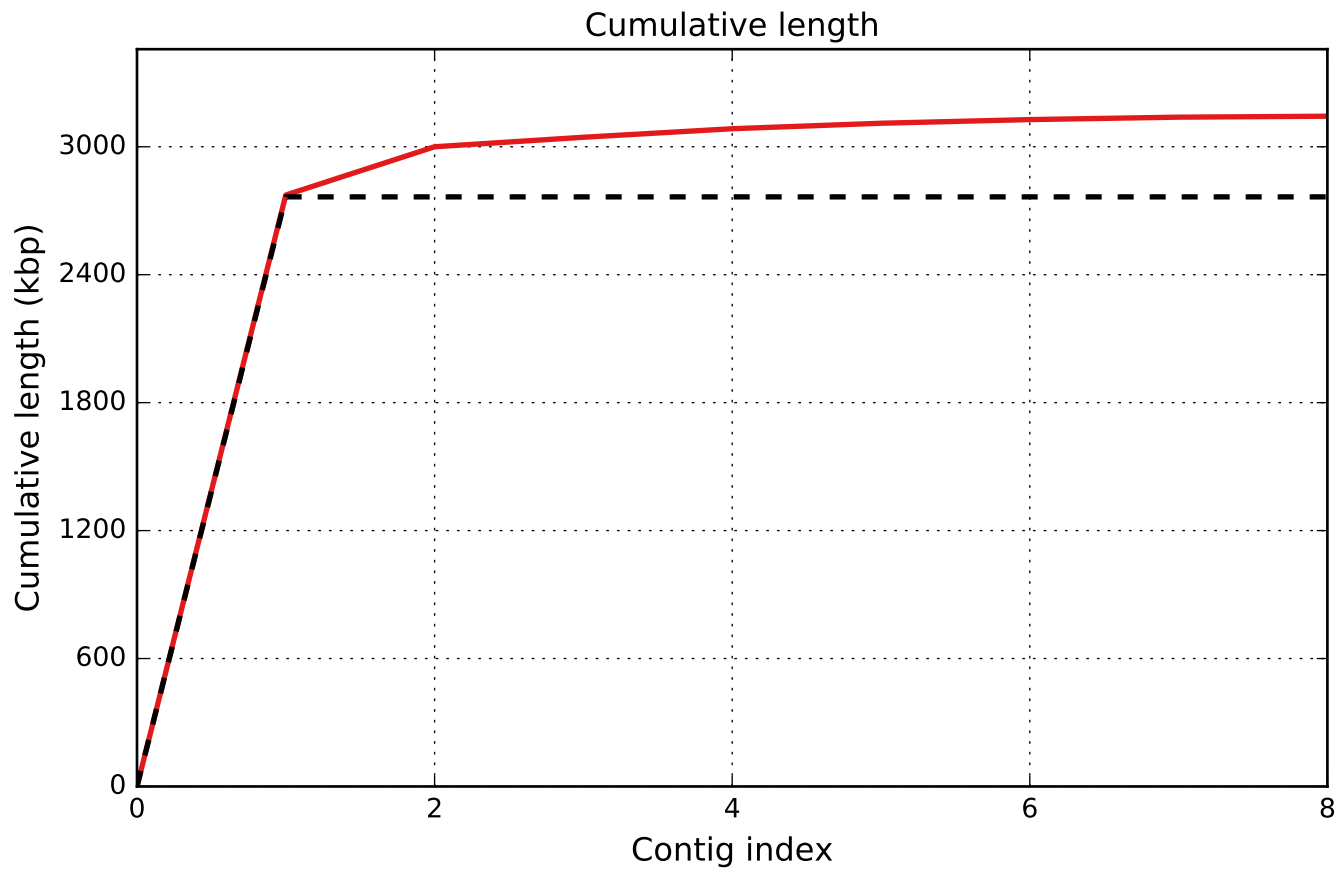
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

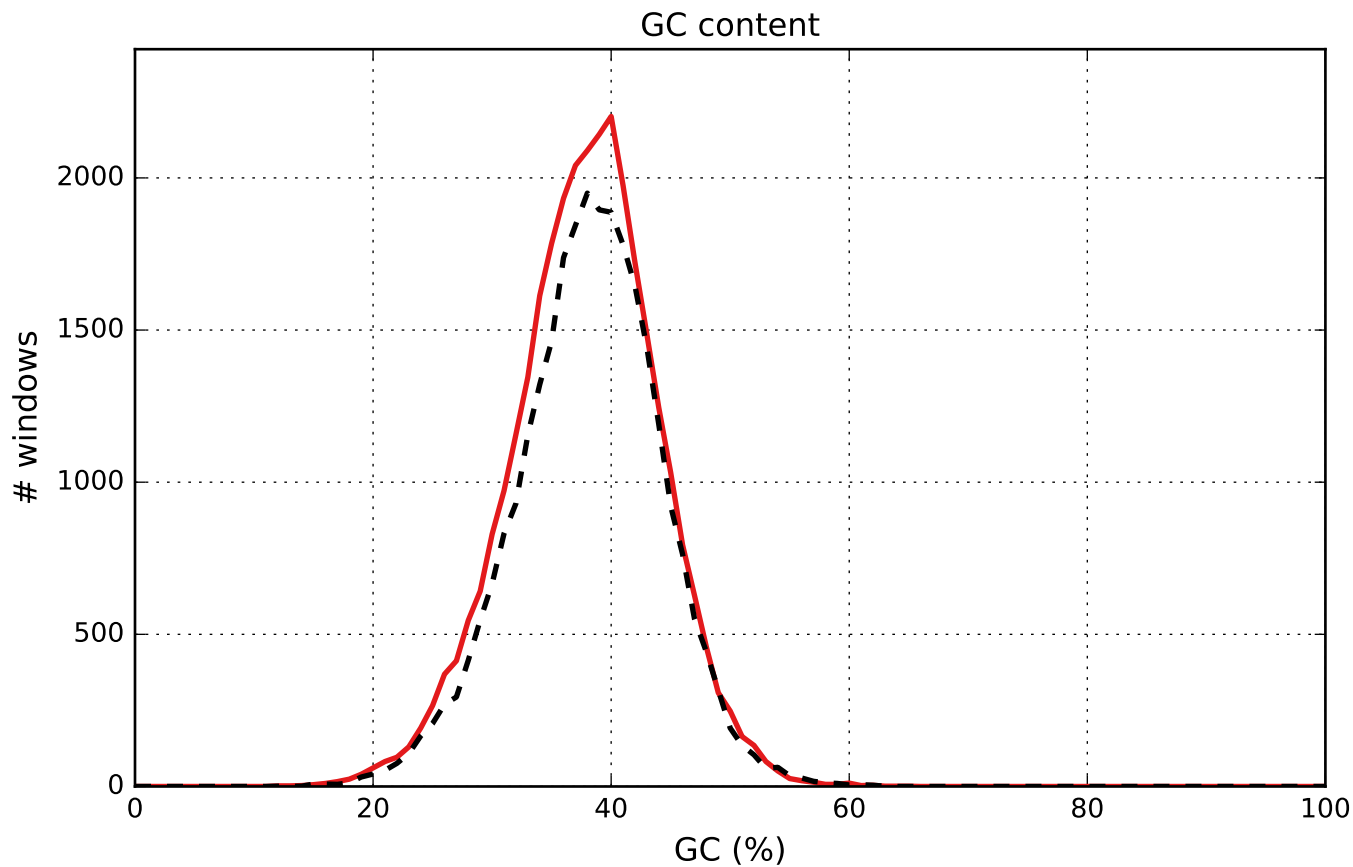


— Enterococci.contigs

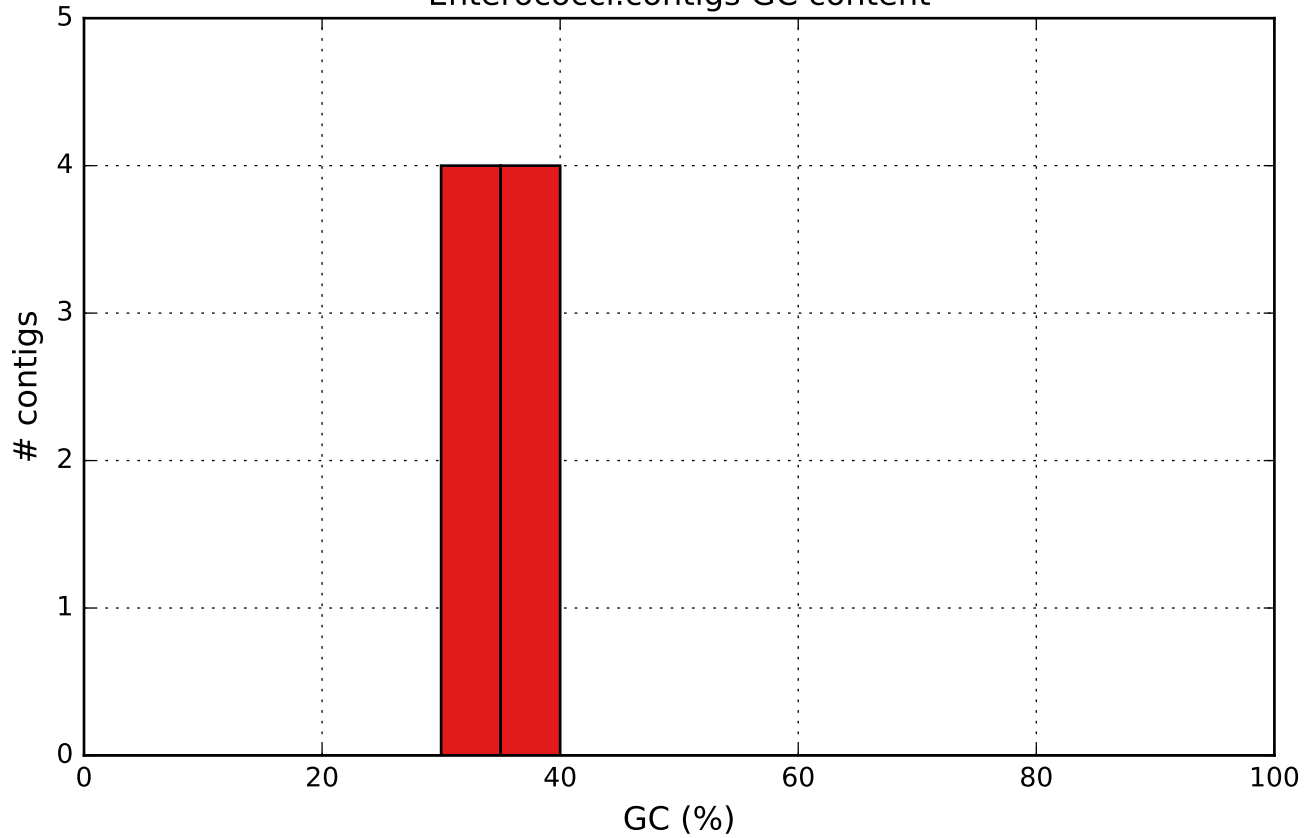


— Enterococci.contigs

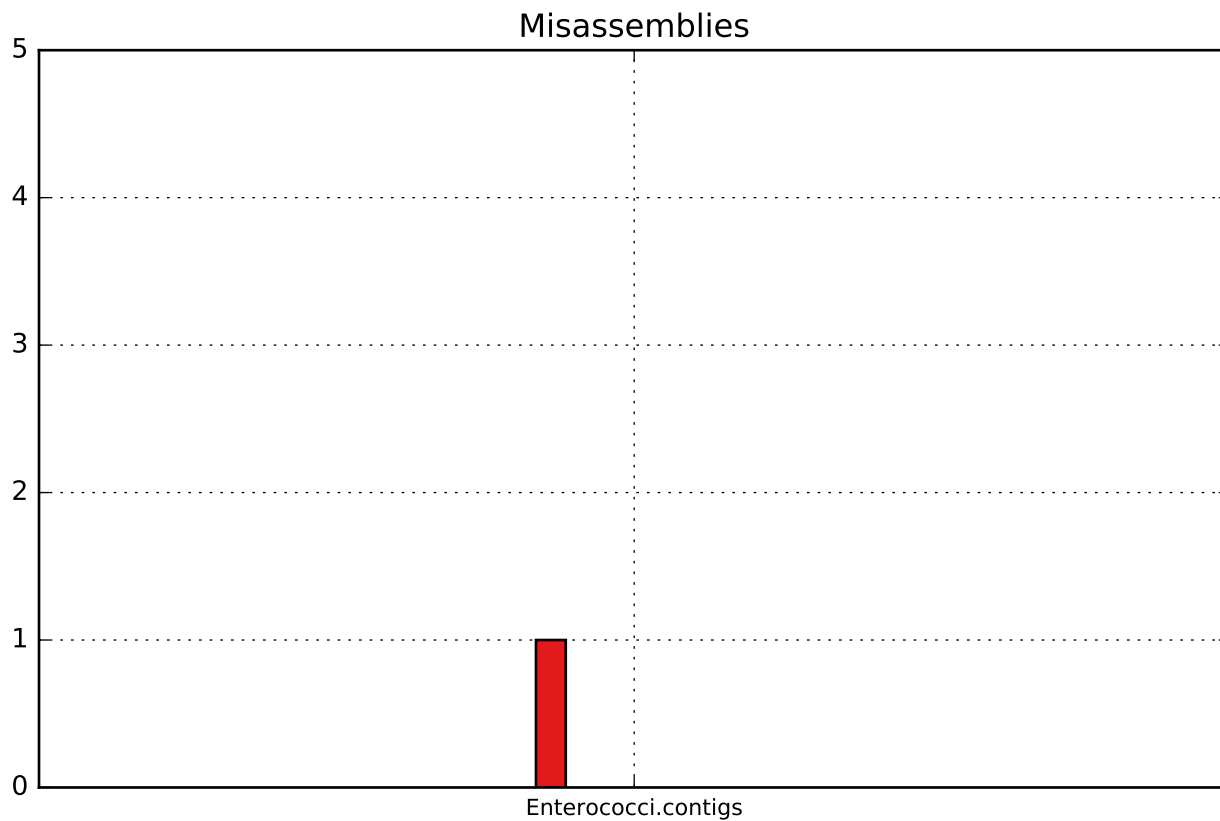




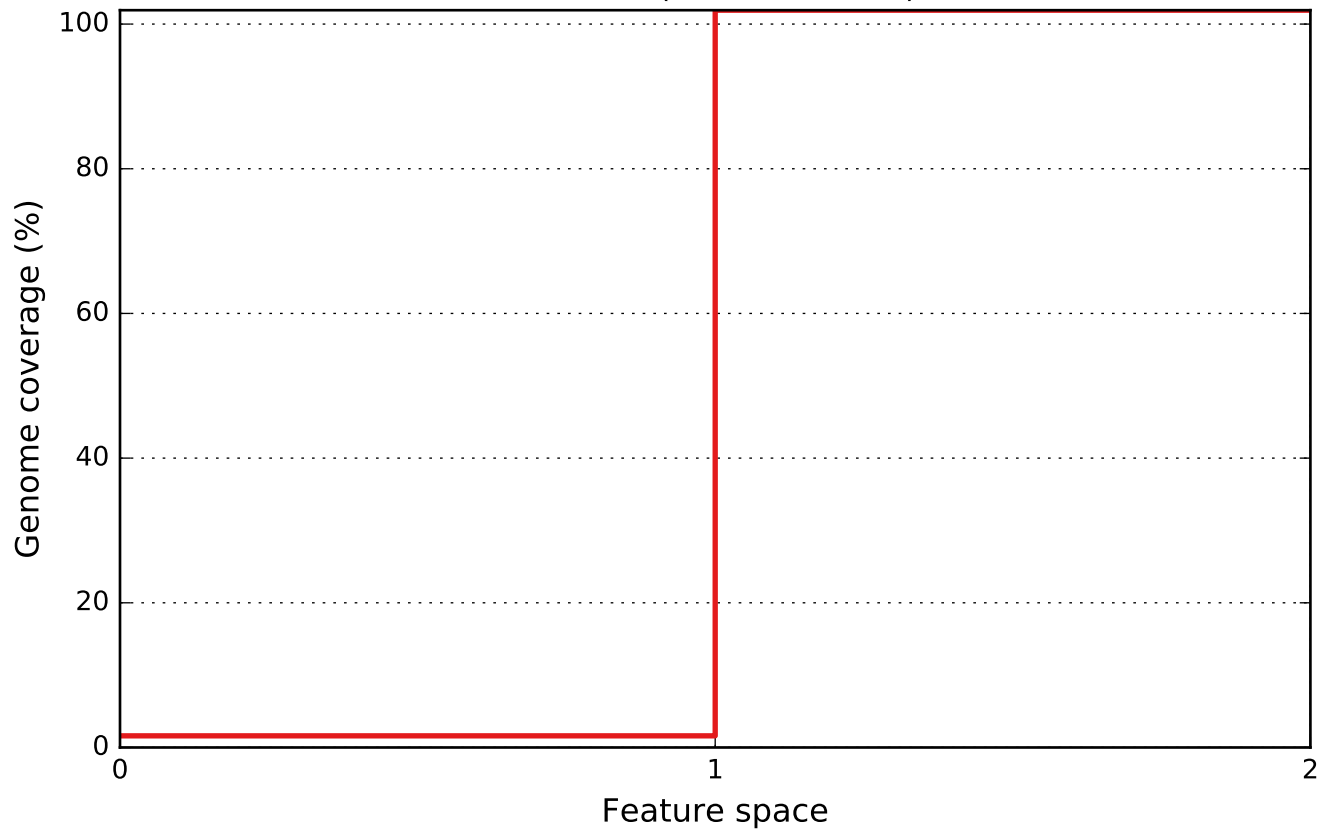
Enterococci.contigs GC content



Enterococci.contigs

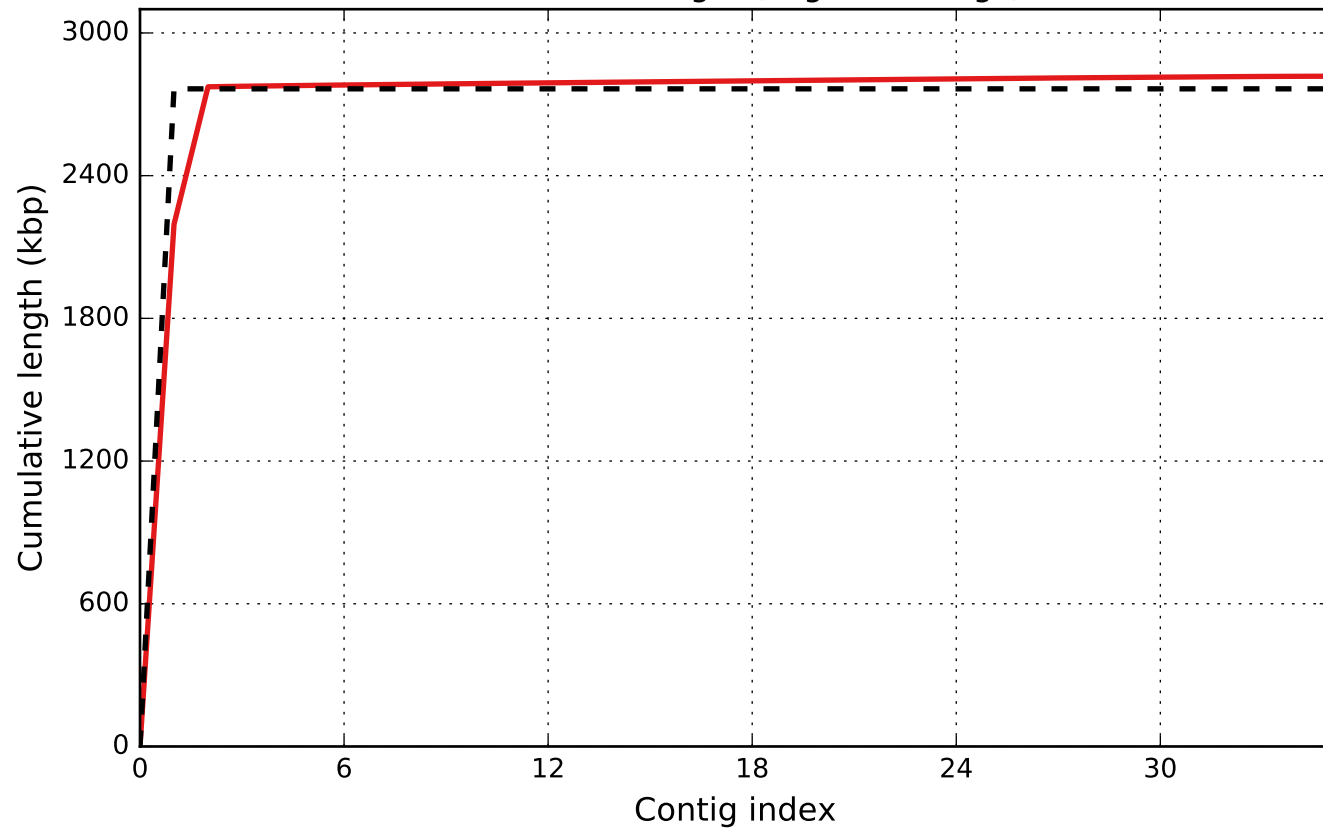


FRCurve (misassemblies)

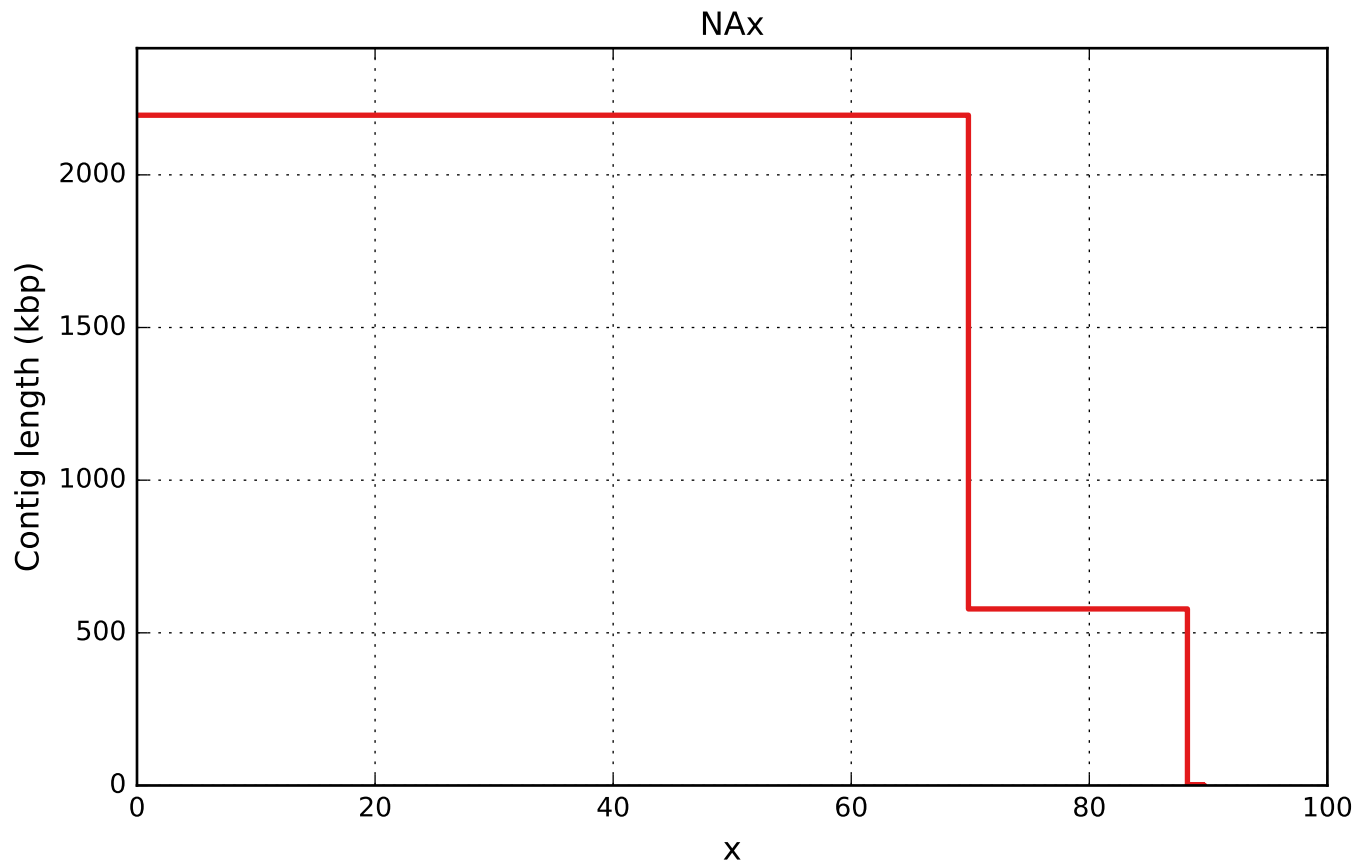


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Cumulative length (aligned contigs)

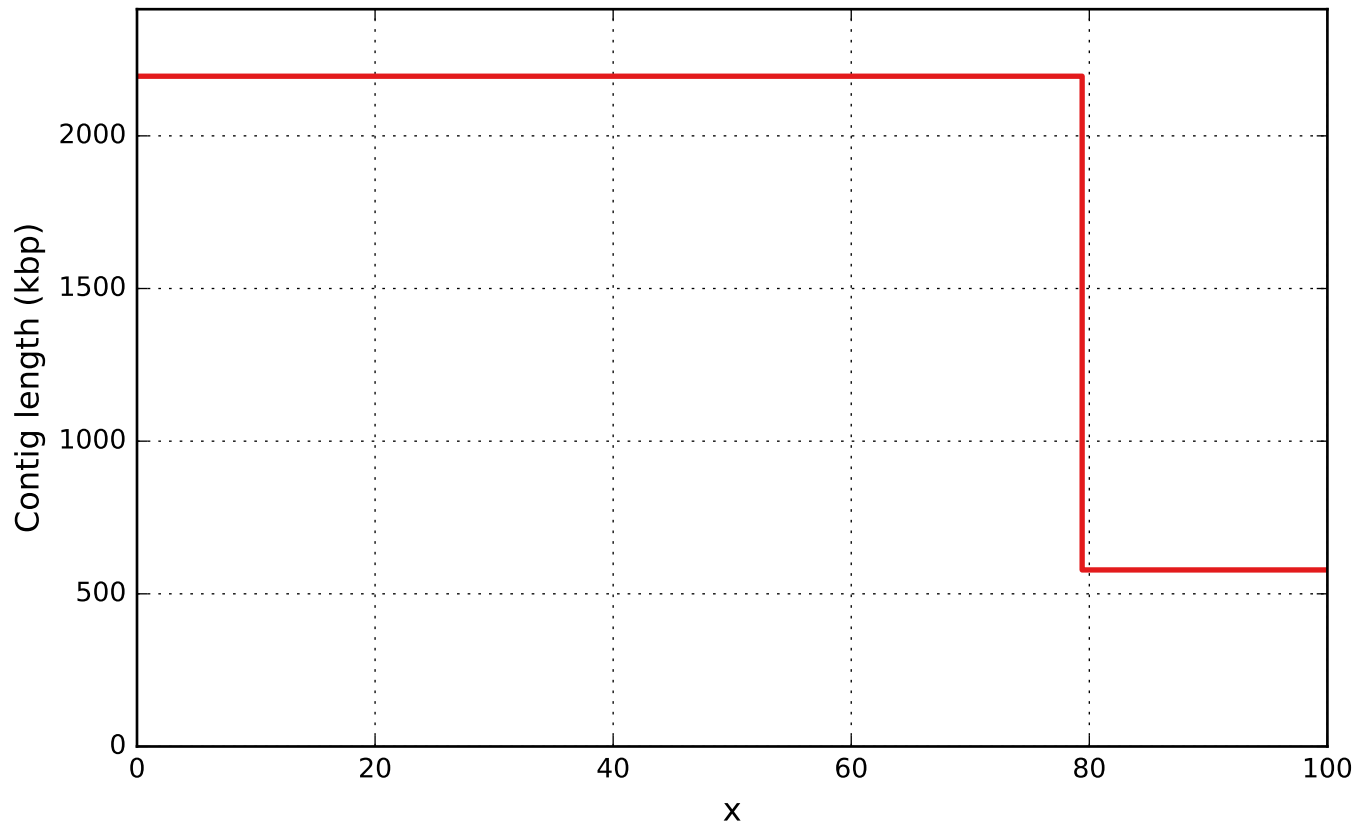


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NGAx



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