

Report

	ecoli.contigs
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	4630756
Total length (>= 1000 bp)	4630756
Total length (>= 5000 bp)	4630756
Total length (>= 10000 bp)	4630756
Total length (>= 25000 bp)	4630756
Total length (>= 50000 bp)	4630756
# contigs	1
Largest contig	4630756
Total length	4630756
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	4630756
NG50	4630756
N75	4630756
NG75	4630756
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	4630756
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.806
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.84
# indels per 100 kbp	81.25
Largest alignment	3963804
Total aligned length	4627919
NA50	3963804
NGA50	3963804
NA75	3963804
NGA75	3963804
LA50	1
LGA50	1
LA75	1
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

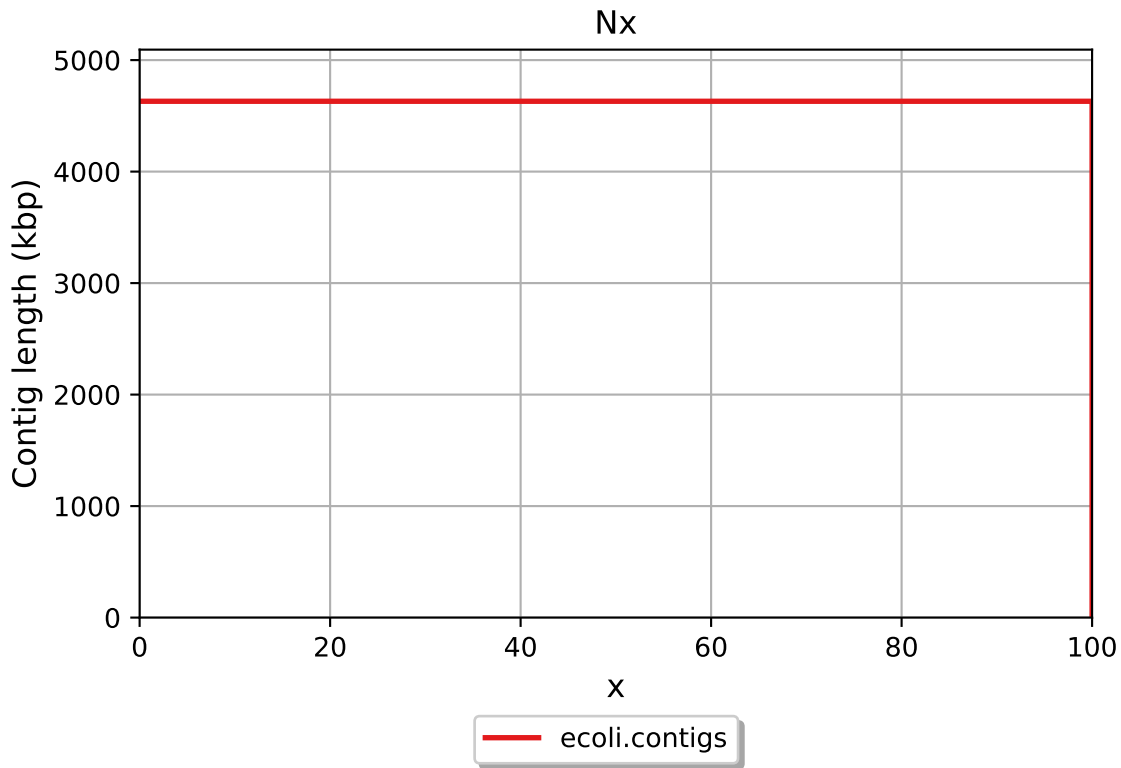
	ecoli.contigs
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4630756
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	39
# indels	3764
# indels (<= 5 bp)	3761
# indels (> 5 bp)	3
Indels length	3848

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).

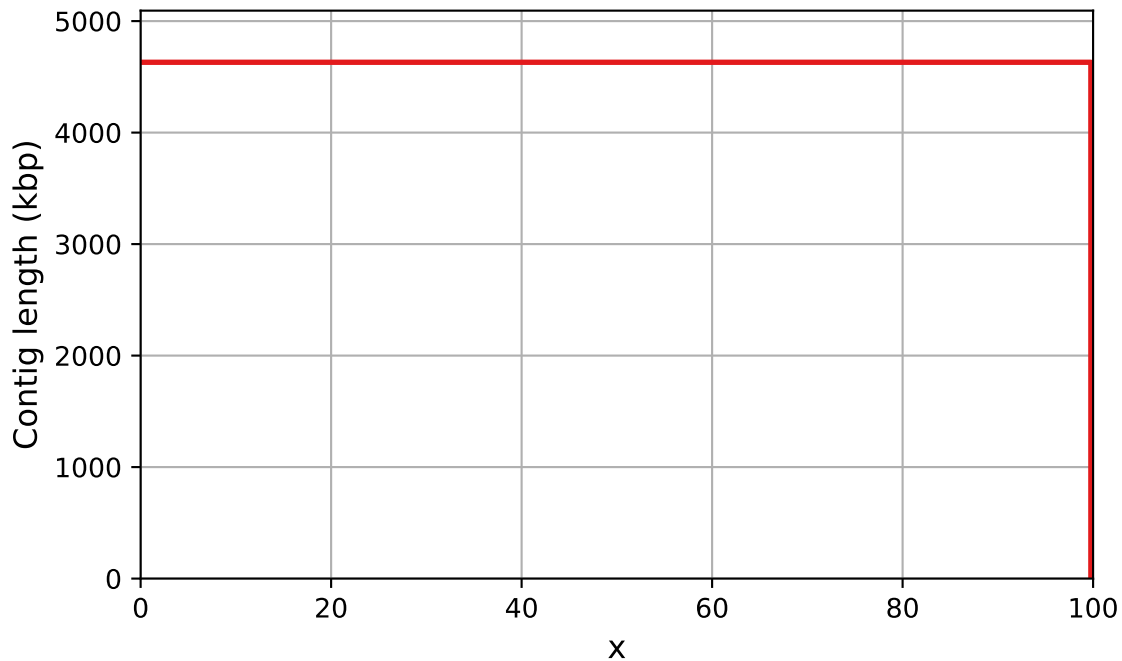
Unaligned report

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

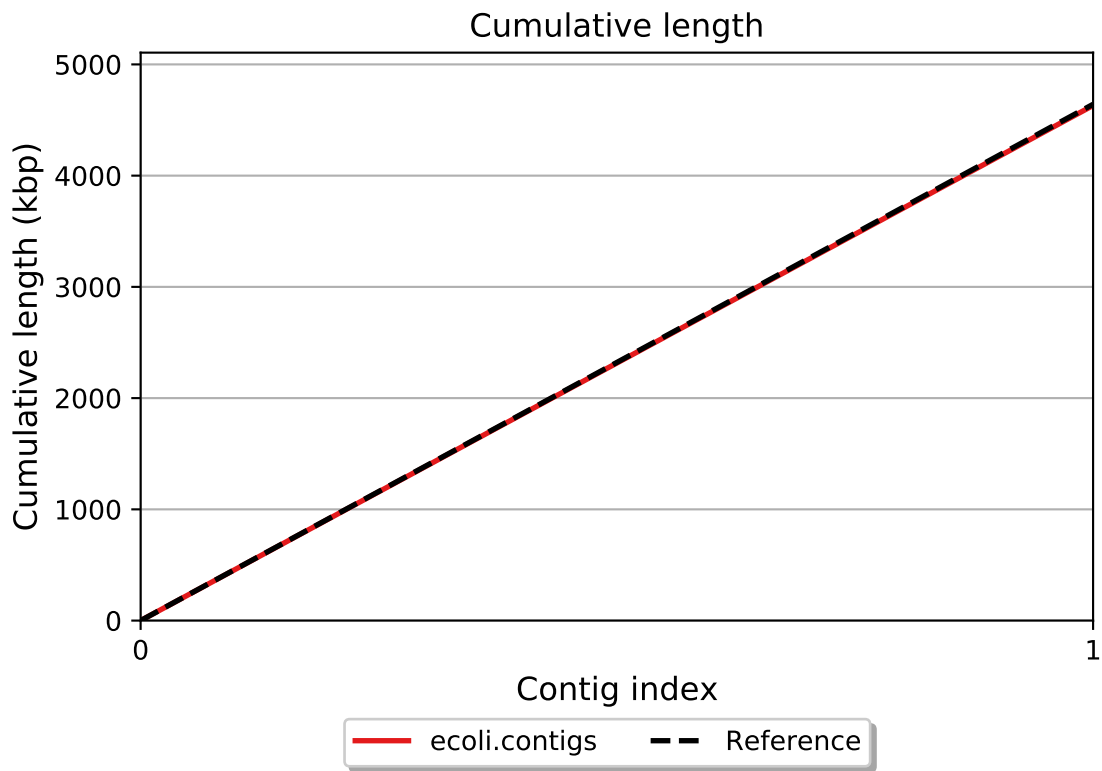
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



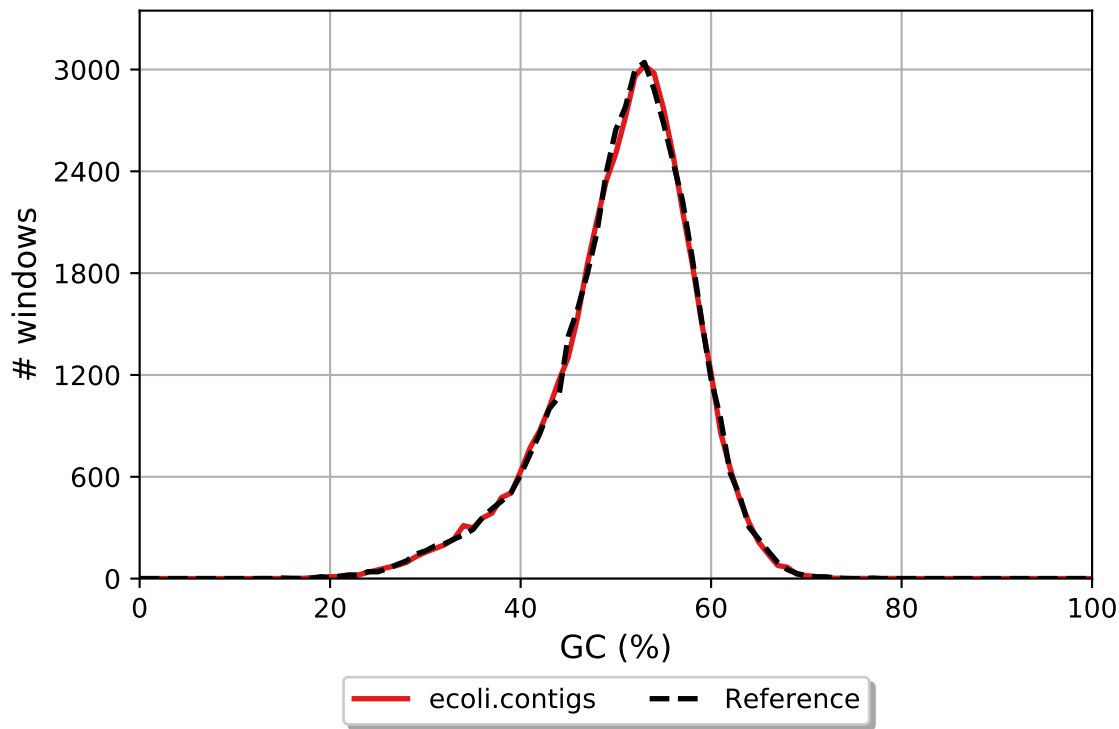
NGx



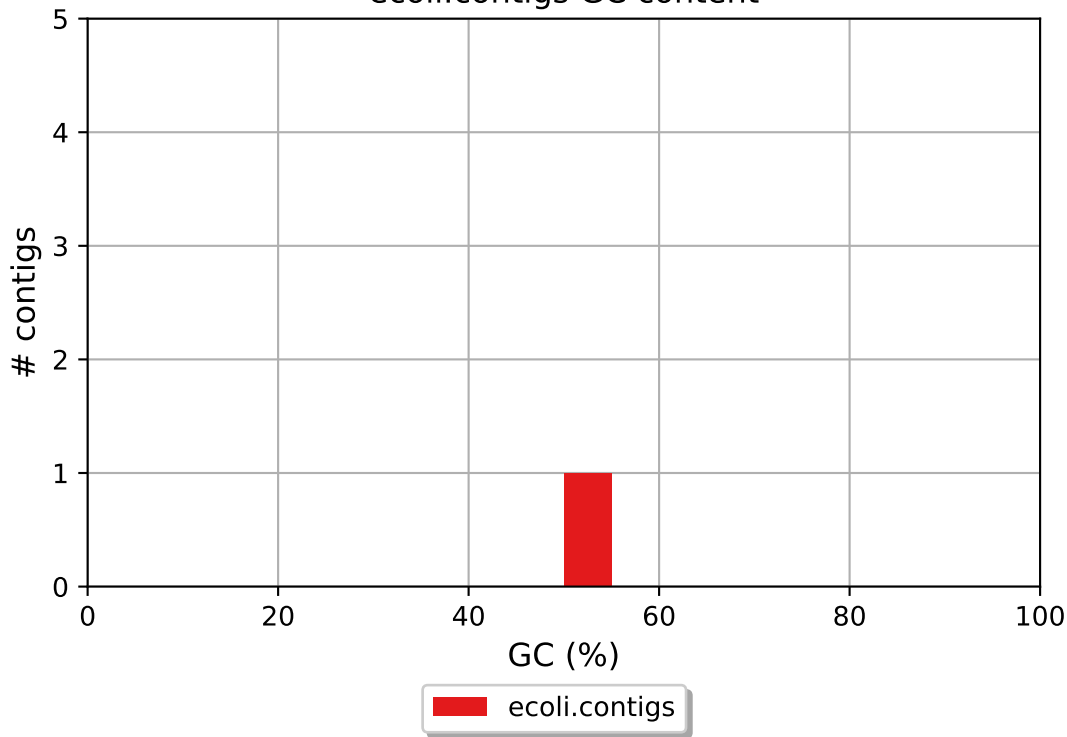
ecoli.contigs



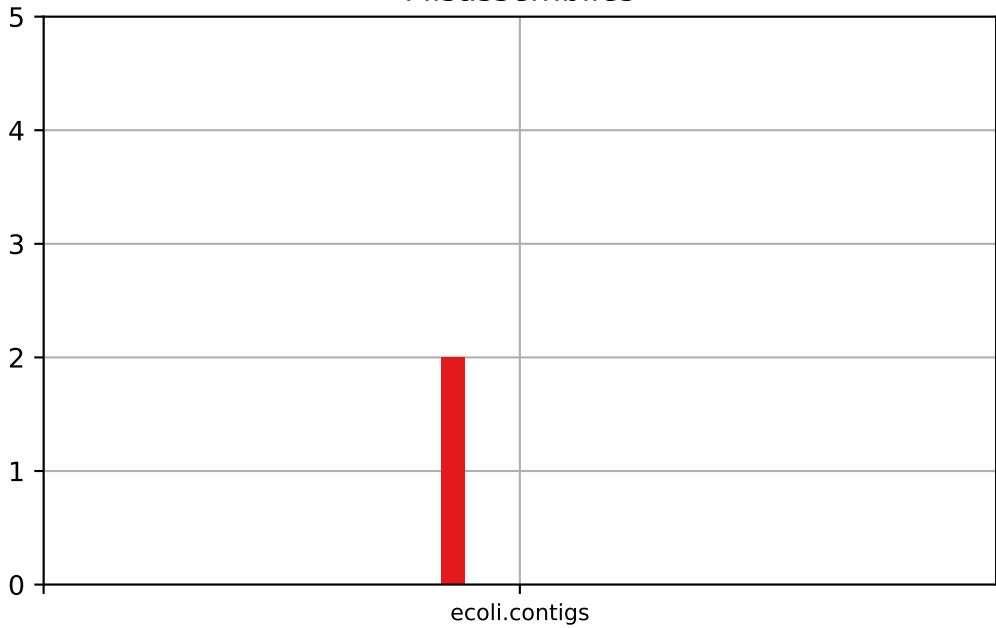
GC content



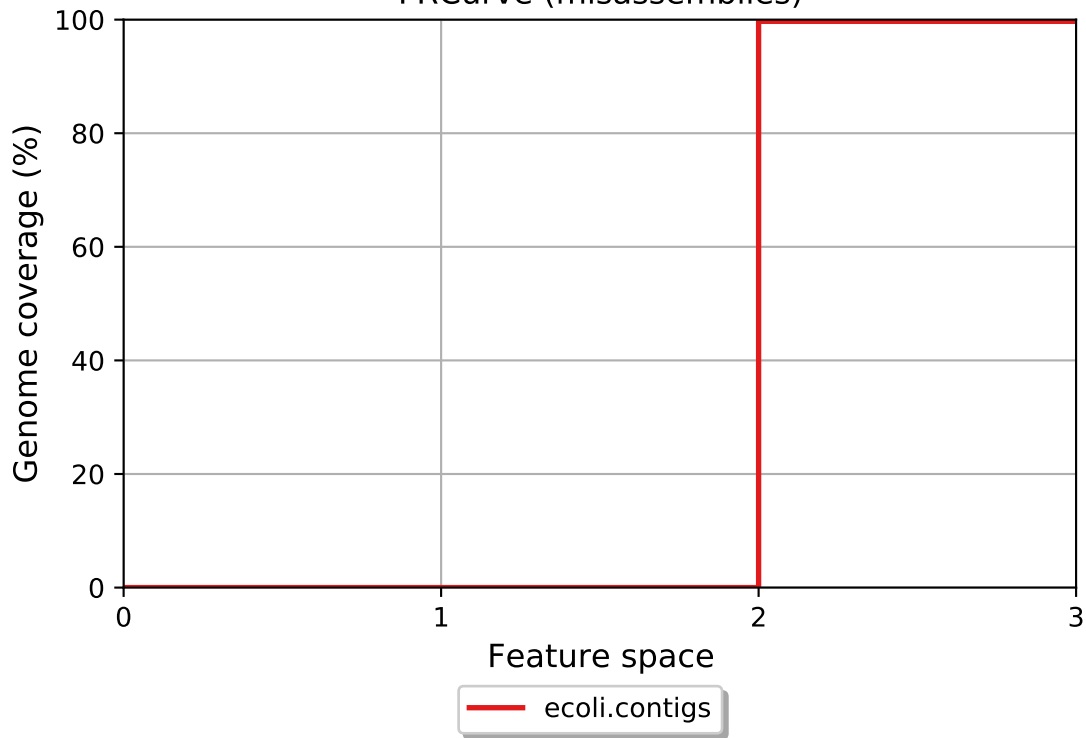
ecoli.contigs GC content



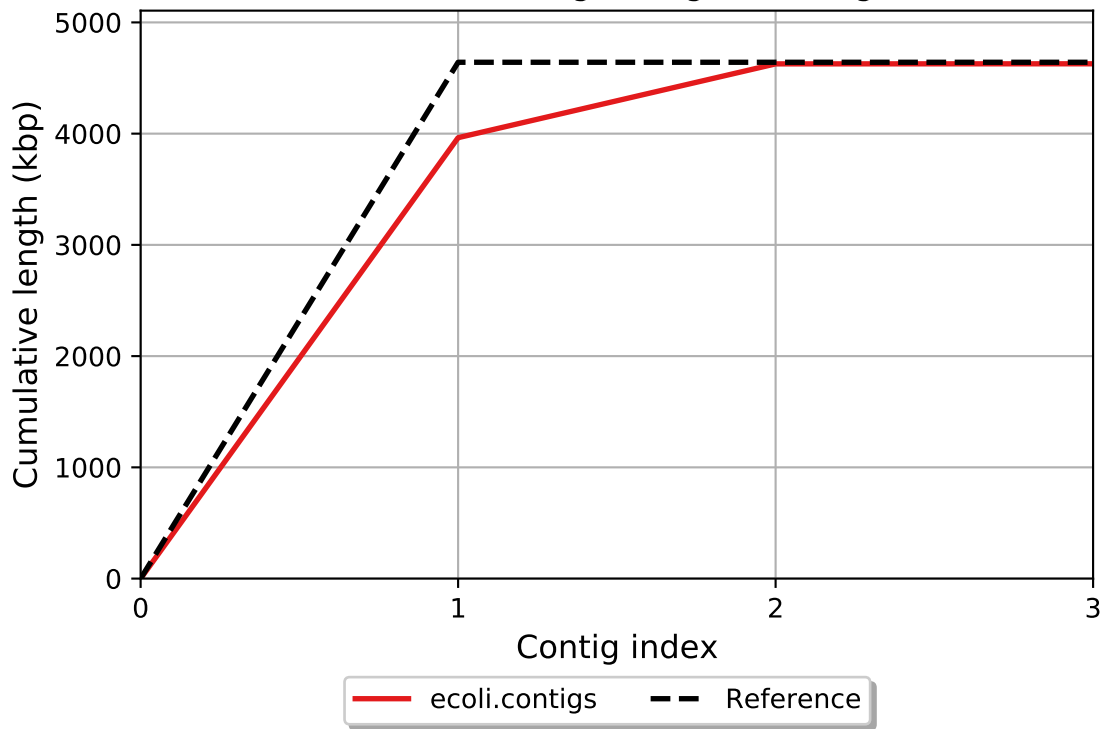
Misassemblies



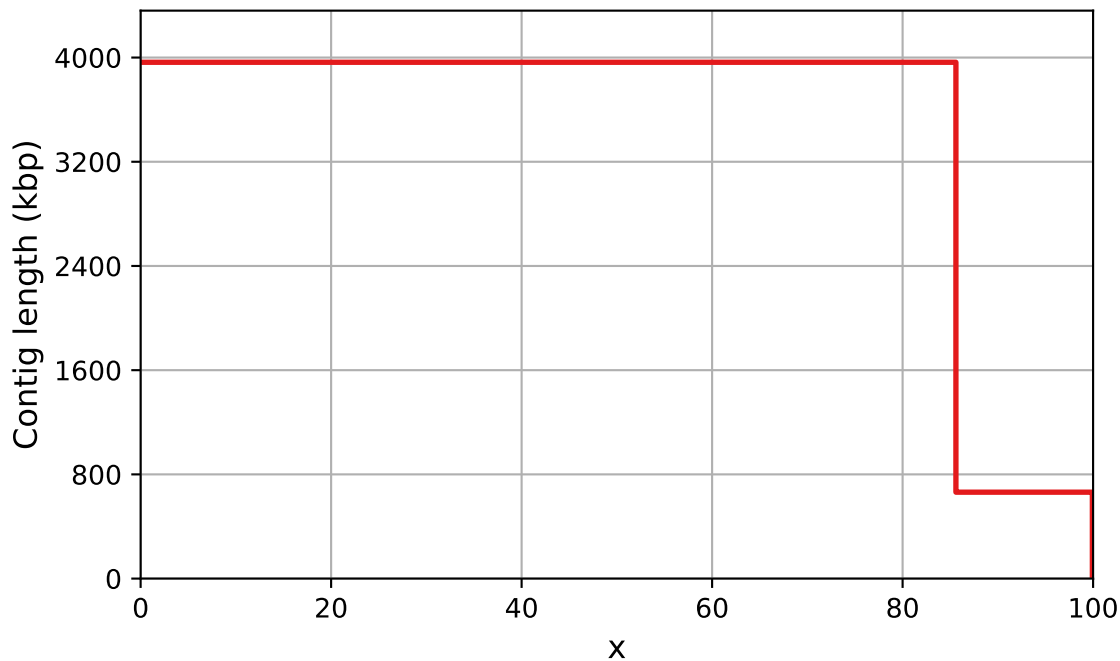
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



ecoli.contigs

NGAx

