

# Report

	bacteria-1_fa
# contigs (>= 0 bp)	4627
# contigs (>= 1000 bp)	1625
Total length (>= 0 bp)	4692372
Total length (>= 1000 bp)	3285119
# contigs	2783
Largest contig	17550
Total length	4113097
Reference length	4411608
GC (%)	73.29
Reference GC (%)	74.43
N50	1828
NG50	1718
N90	733
NG90	586
auN	2290.7
auNG	2135.7
L50	711
LG50	795
L90	2112
LG90	2520
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	2731 + 27 part
Unaligned length	4072495
Genome fraction (%)	0.920
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3717.86
# indels per 100 kbp	285.06
# genomic features	57 + 29 part
Complete BUSCO (%)	62.16
Partial BUSCO (%)	7.43
# predicted rRNA genes	1 + 1 part
Largest alignment	4409
Total aligned length	32976
NA50	-
NGA50	-
NA90	-
NGA90	-
auNA	17.0
auNGA	15.8
LA50	-
LGA50	-
LA90	-
LGA90	-

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

	bacteria-1_fa
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	1226
# indels	94
# indels (<= 5 bp)	89
# indels (> 5 bp)	5
Indels length	207

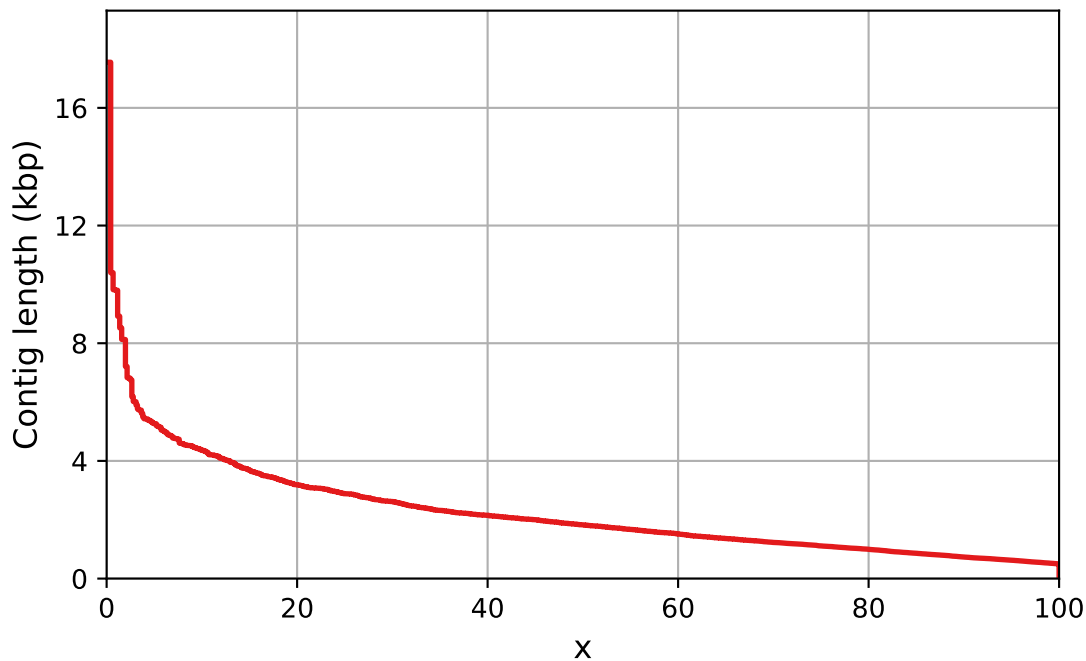
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	bacteria-1_fa
# fully unaligned contigs	2731
Fully unaligned length	4019698
# partially unaligned contigs	27
Partially unaligned length	52797
# N's	0

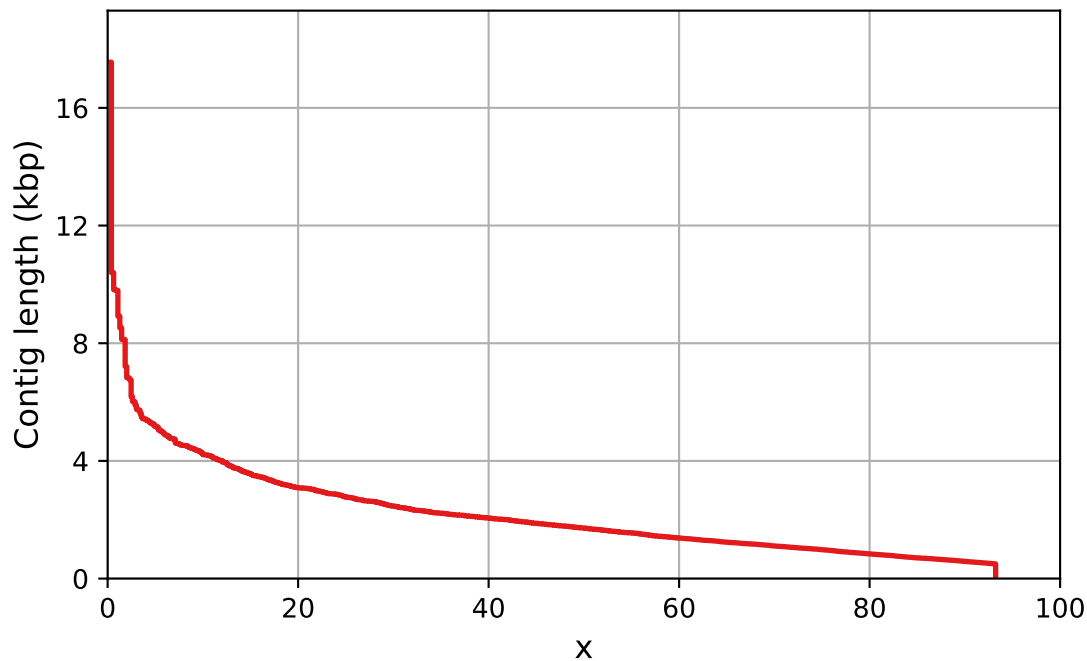
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx



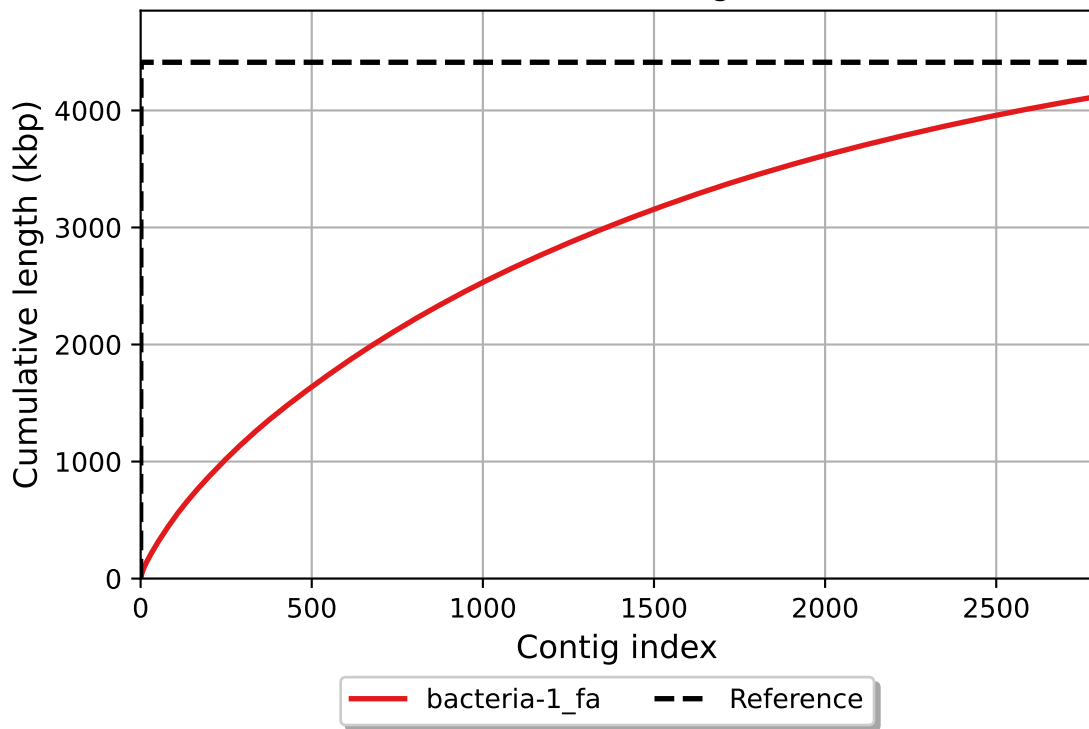
— bacteria-1\_fa

NGx

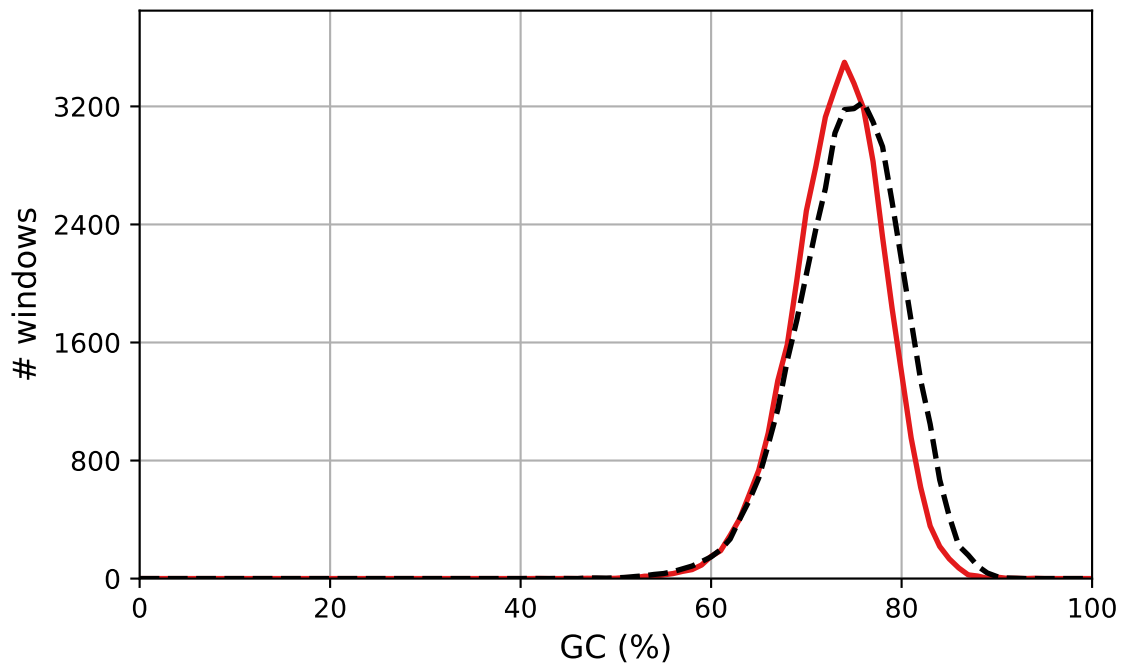


— bacteria-1\_fa

Cumulative length

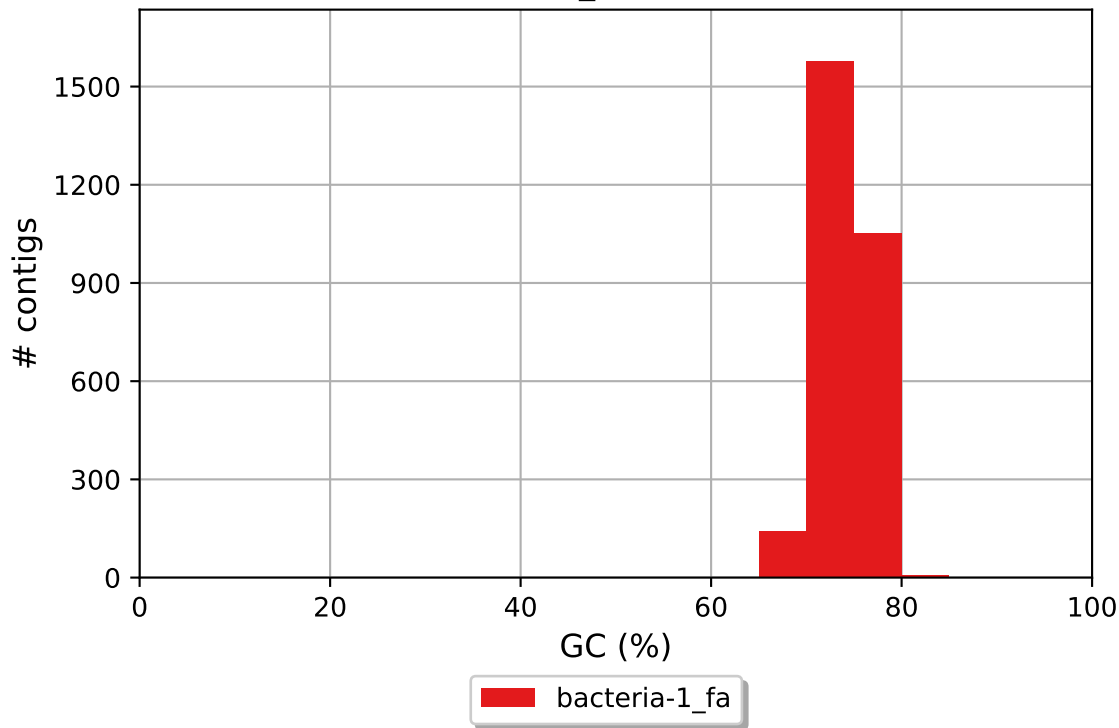


# GC content



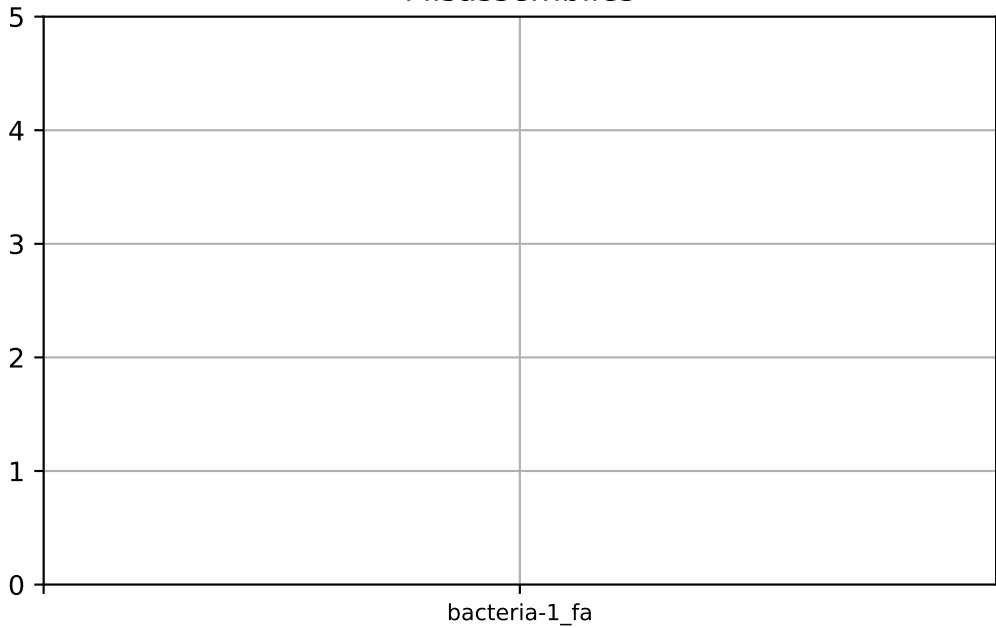
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bacteria-1\_fa GC content

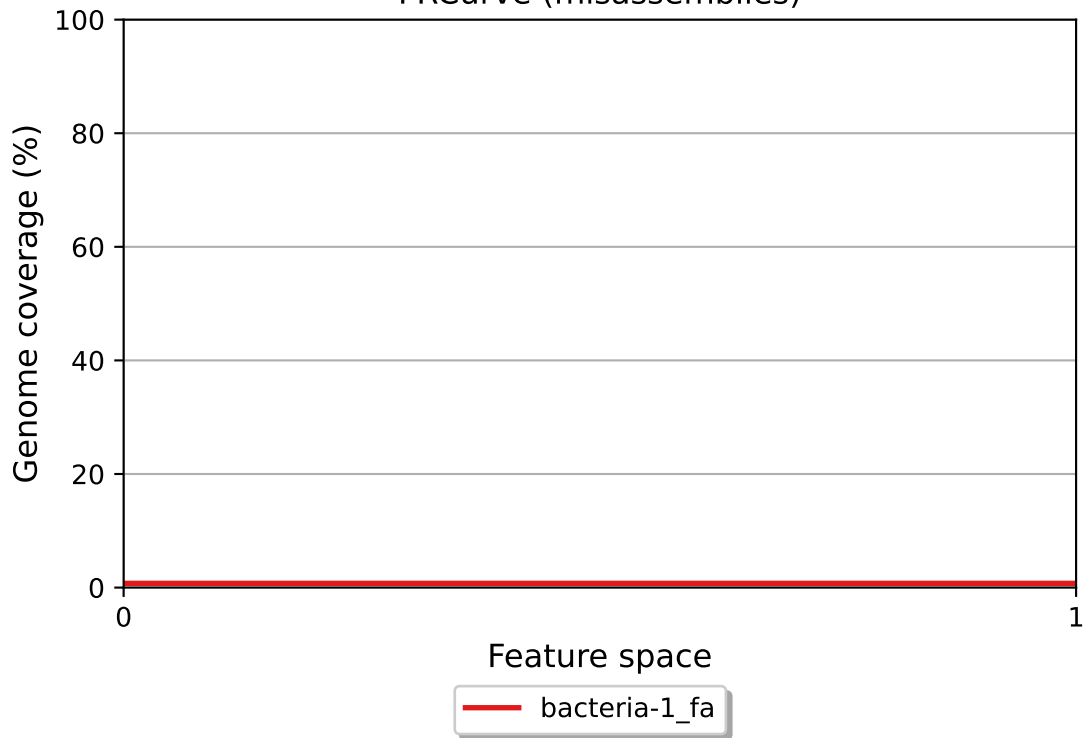




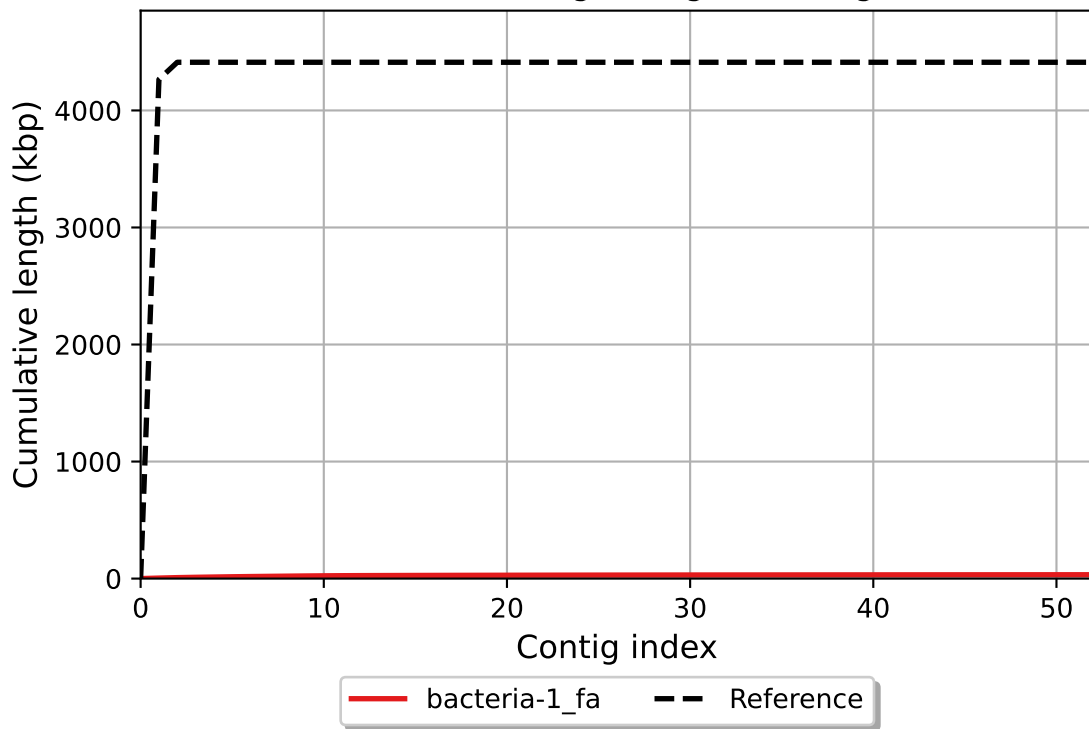
## Misassemblies



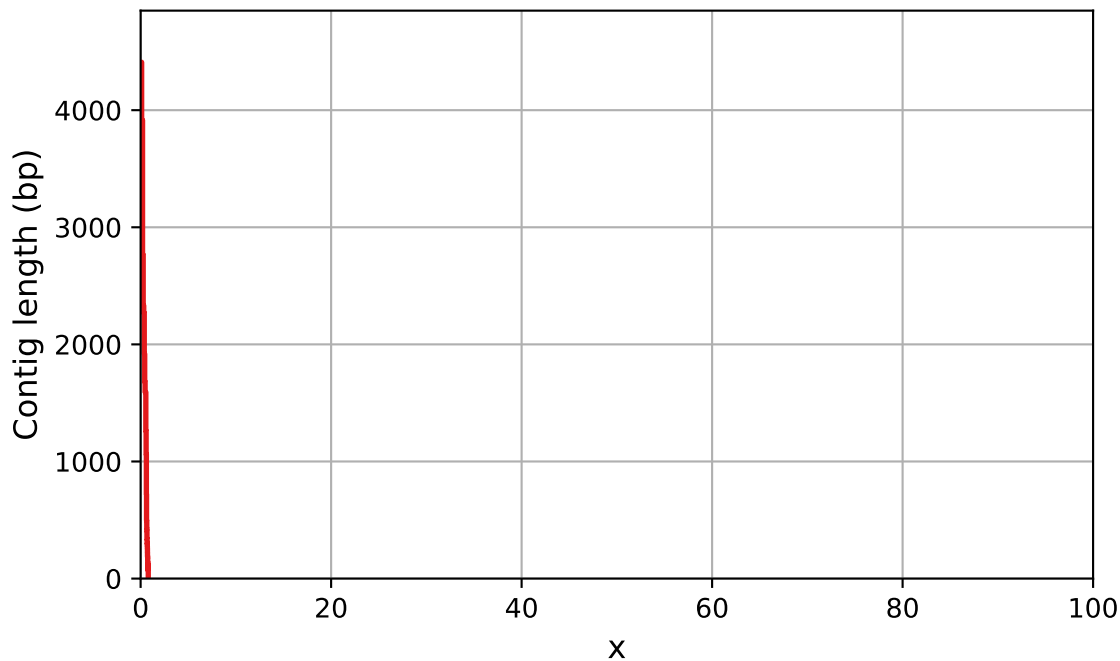
FRCurve (misassemblies)



Cumulative length (aligned contigs)

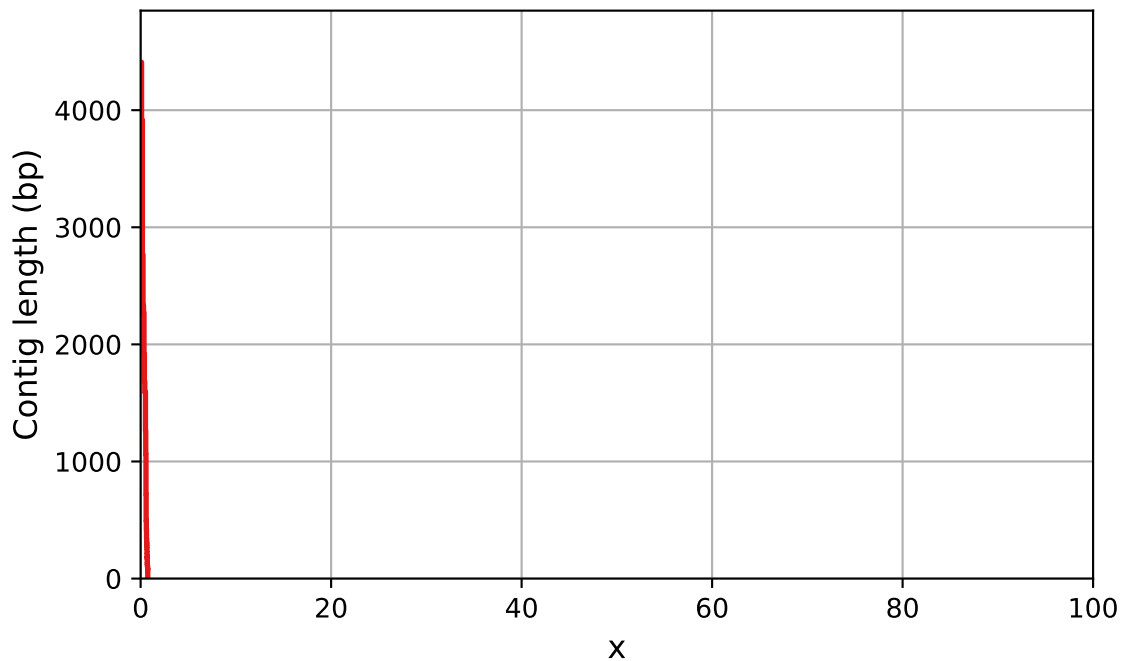


NAx

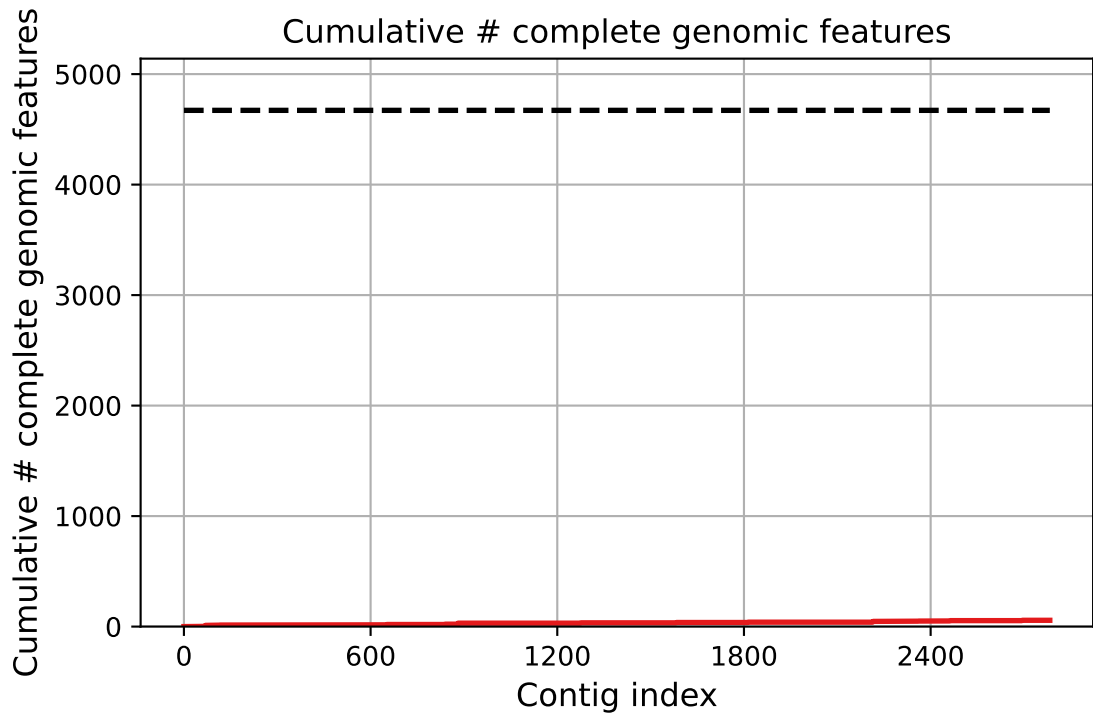


bacteria-1\_fa

# NGAx



— bacteria-1\_fa



FRCurve (genomic features)

