

Report

	campylobacter-8_fa
# contigs (>= 0 bp)	275
# contigs (>= 1000 bp)	118
Total length (>= 0 bp)	1702363
Total length (>= 1000 bp)	1665083
# contigs	131
Largest contig	63938
Total length	1673907
Reference length	1641481
GC (%)	30.46
Reference GC (%)	30.55
N50	24641
NG50	25103
N90	6596
NG90	7091
auN	25373.3
auNG	25874.5
L50	25
LG50	24
L90	74
LG90	69
# misassemblies	14
# misassembled contigs	12
Misassembled contigs length	390382
# local misassemblies	21
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	12 + 24 part
Unaligned length	144564
Genome fraction (%)	93.429
Duplication ratio	1.004
# N's per 100 kbp	0.06
# mismatches per 100 kbp	1187.86
# indels per 100 kbp	51.35
# genomic features	7691 + 316 part
Complete BUSCO (%)	80.41
Partial BUSCO (%)	3.38
# predicted rRNA genes	1 + 0 part
Largest alignment	52982
Total aligned length	1526698
NA50	20175
NGA50	20175
NA90	1666
NGA90	3208
auNA	20610.8
auNGA	21017.9
LA50	28
LGA50	28
LA90	112
LGA90	99

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

	campylobacter-8_fa
# misassemblies	14
# contig misassemblies	14
# c. relocations	14
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	390382
# local misassemblies	21
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	18135
# indels	784
# indels (<= 5 bp)	723
# indels (> 5 bp)	61
Indels length	2570

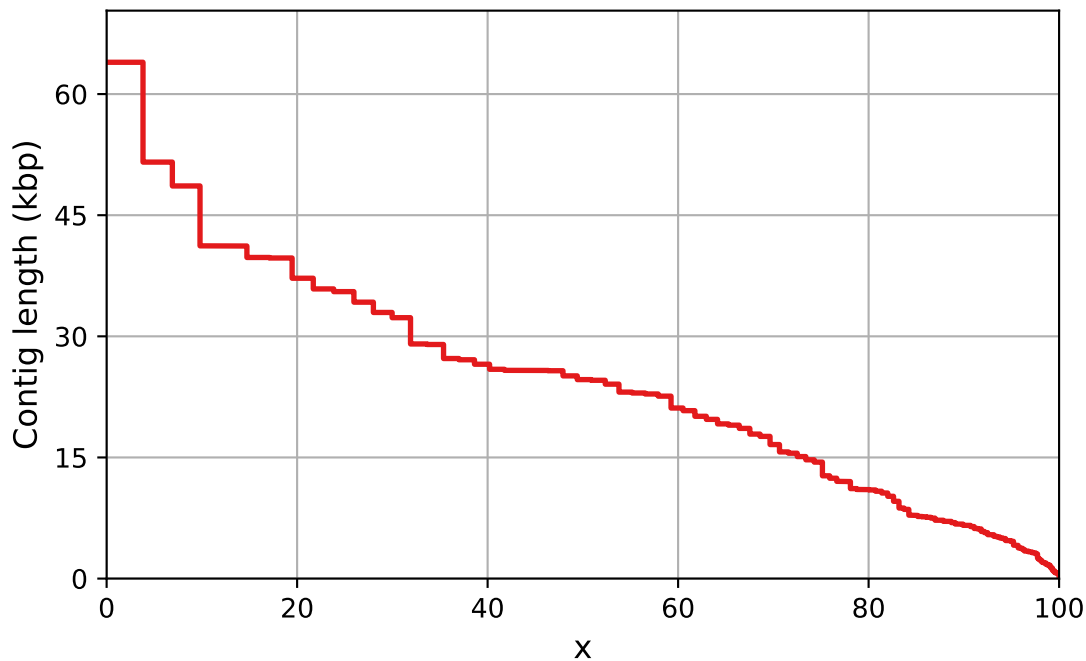
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	campylobacter-8_fa
# fully unaligned contigs	12
Fully unaligned length	66562
# partially unaligned contigs	24
Partially unaligned length	78002
# N's	1

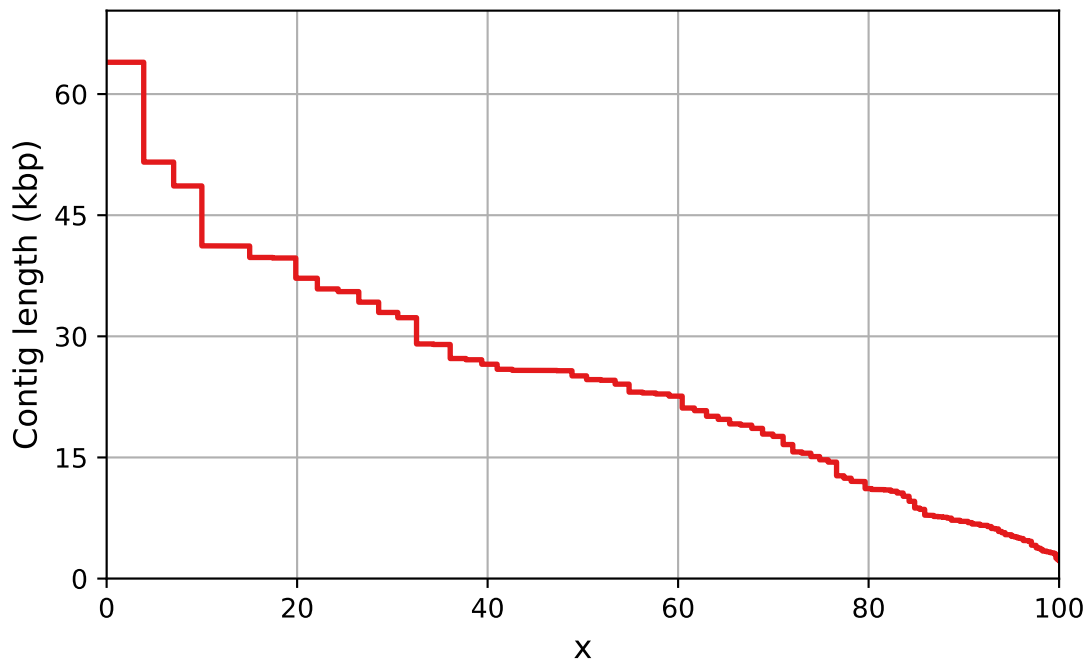
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

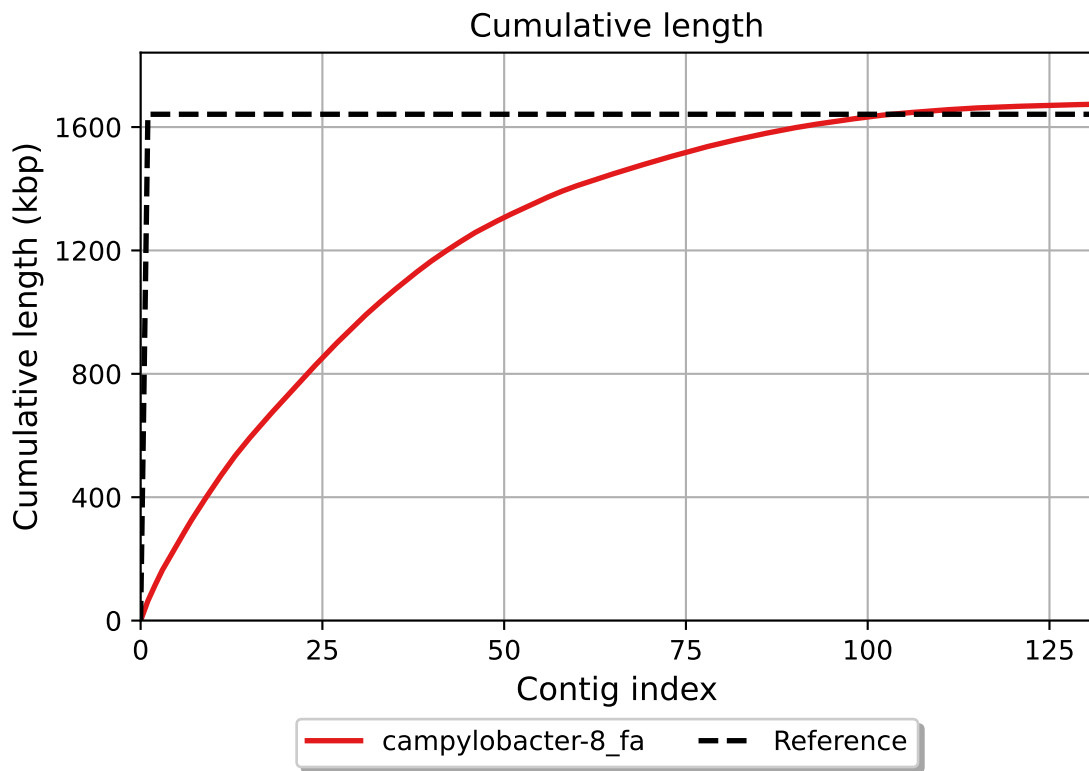


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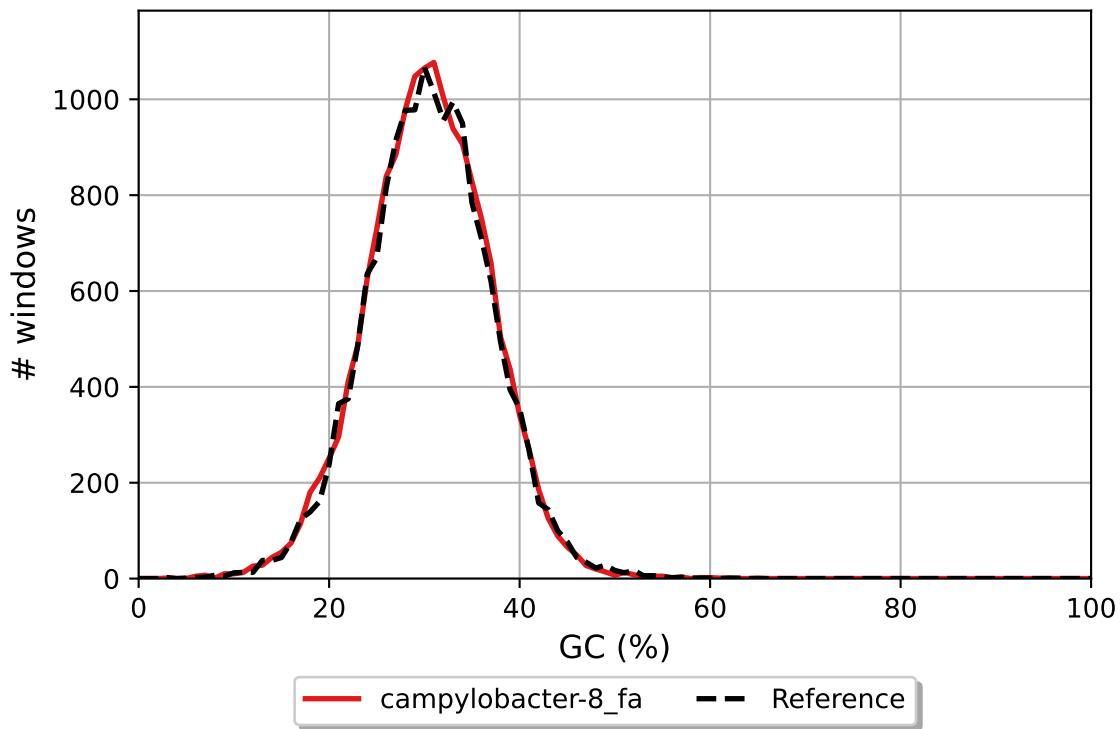
NGx



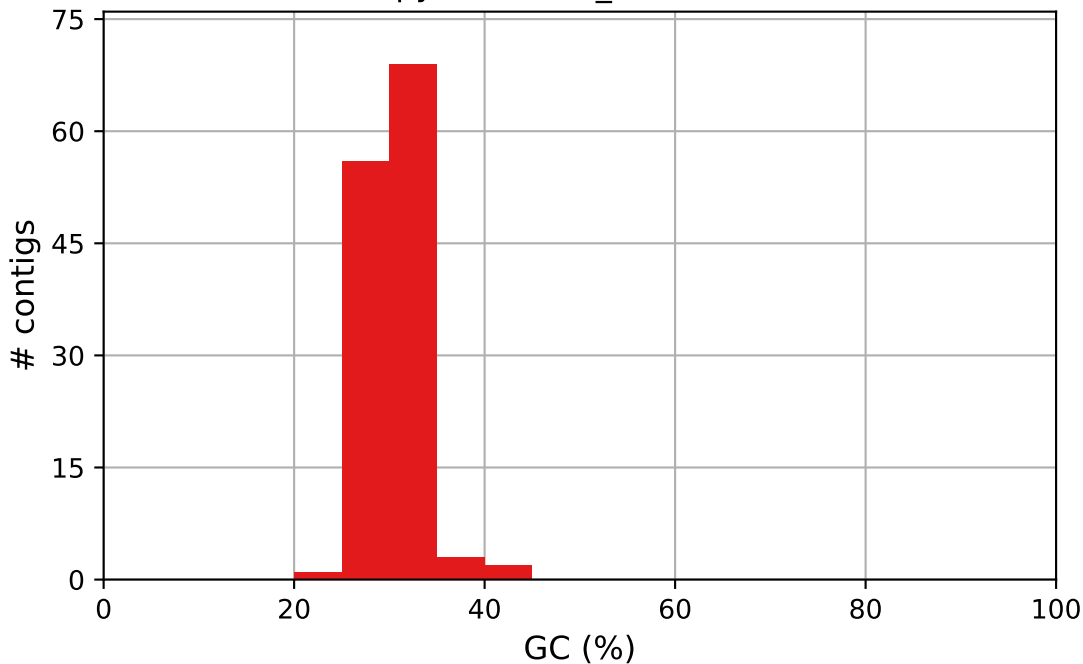
— campylobacter-8_fa



GC content

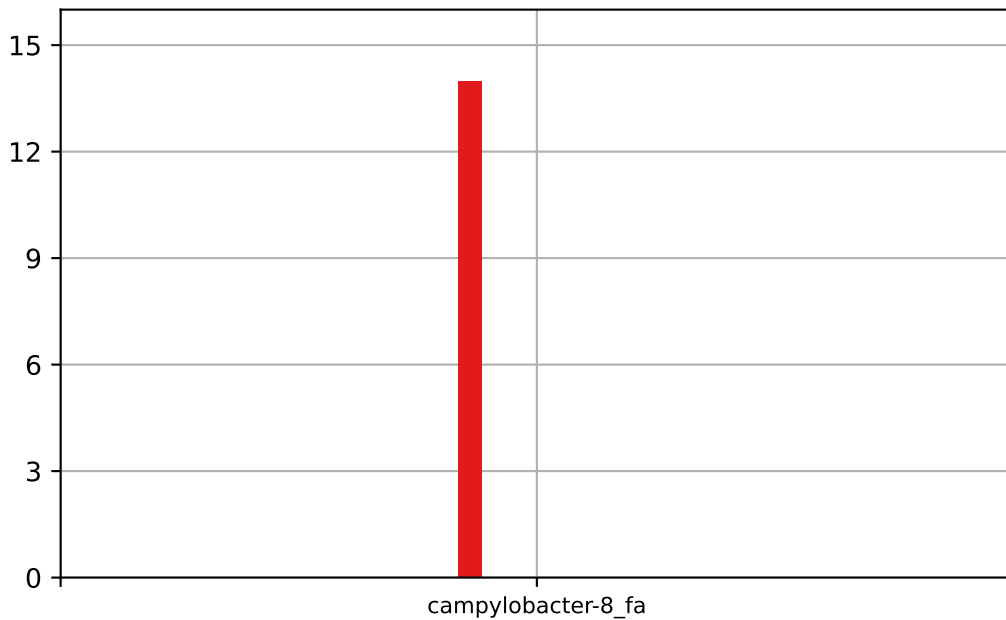


campylobacter-8_fa GC content

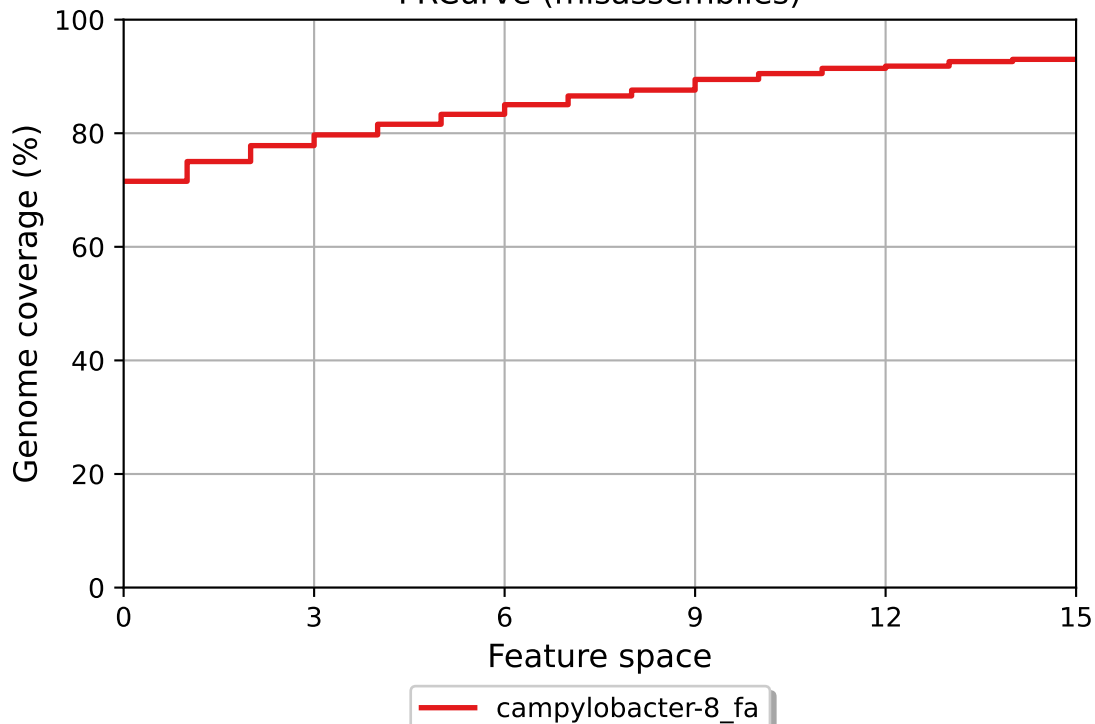


campylobacter-8_fa

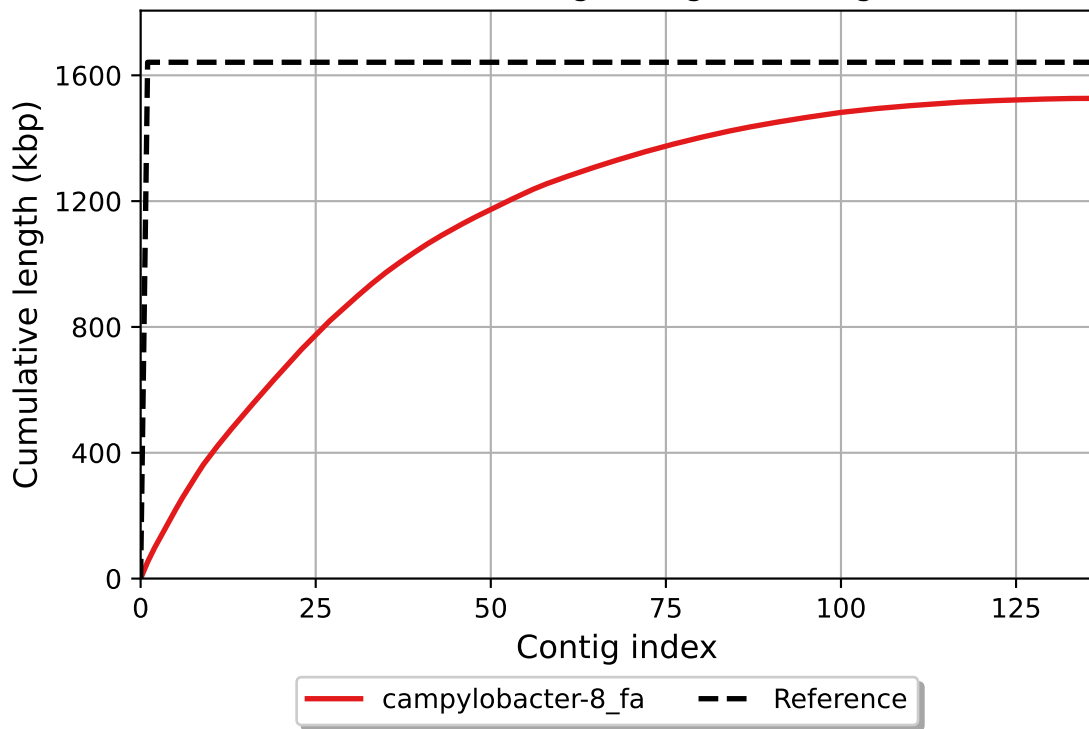
Misassemblies



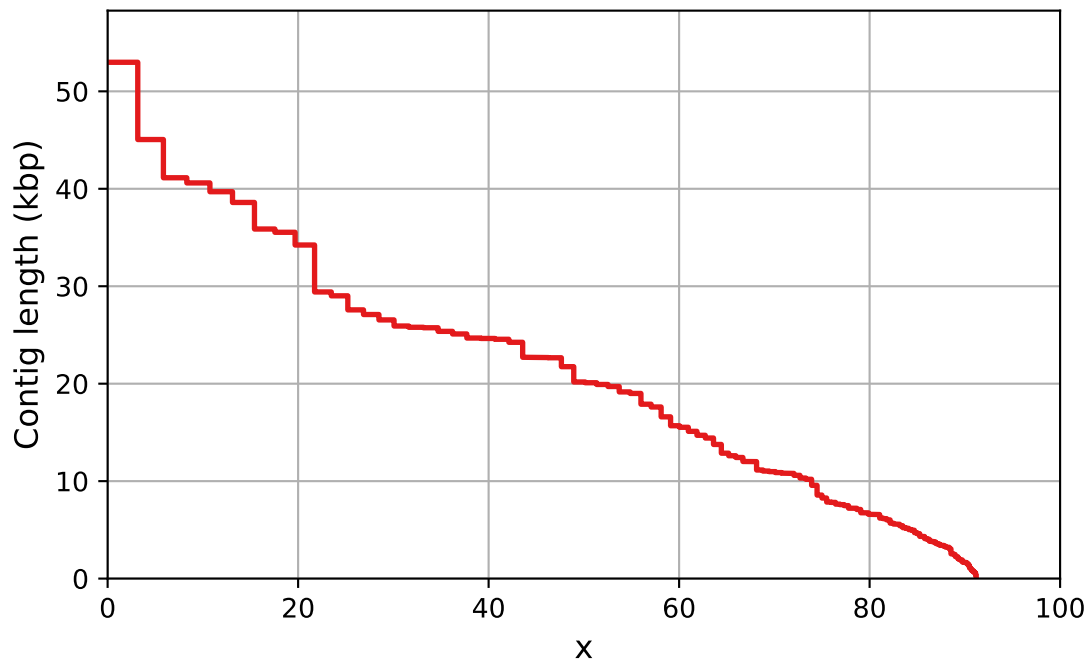
FRCurve (misassemblies)



Cumulative length (aligned contigs)

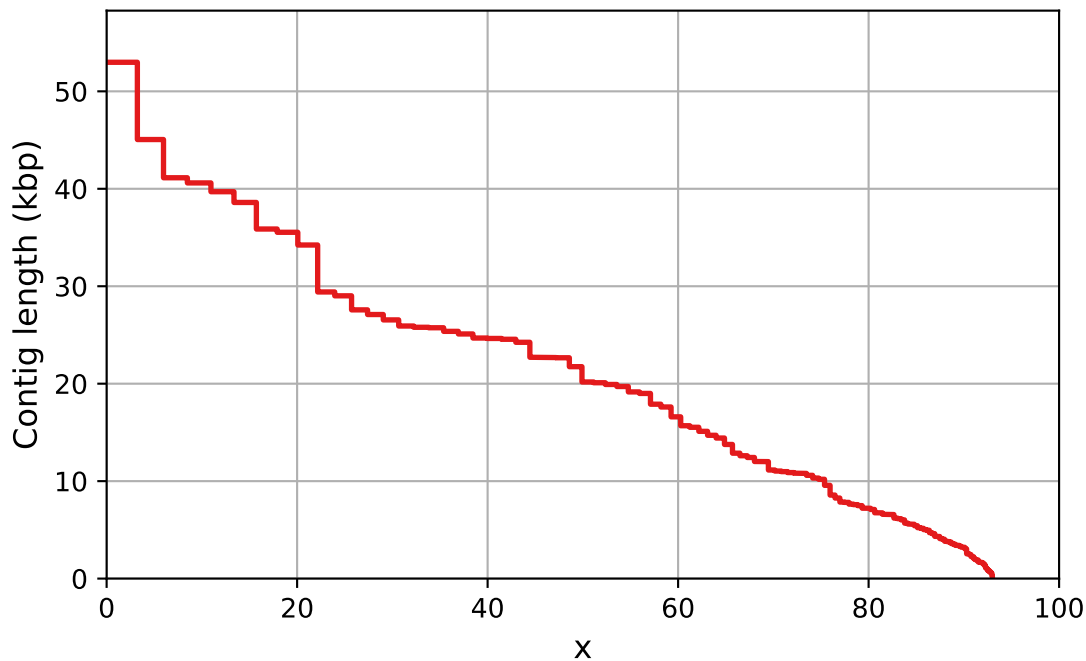


NAx

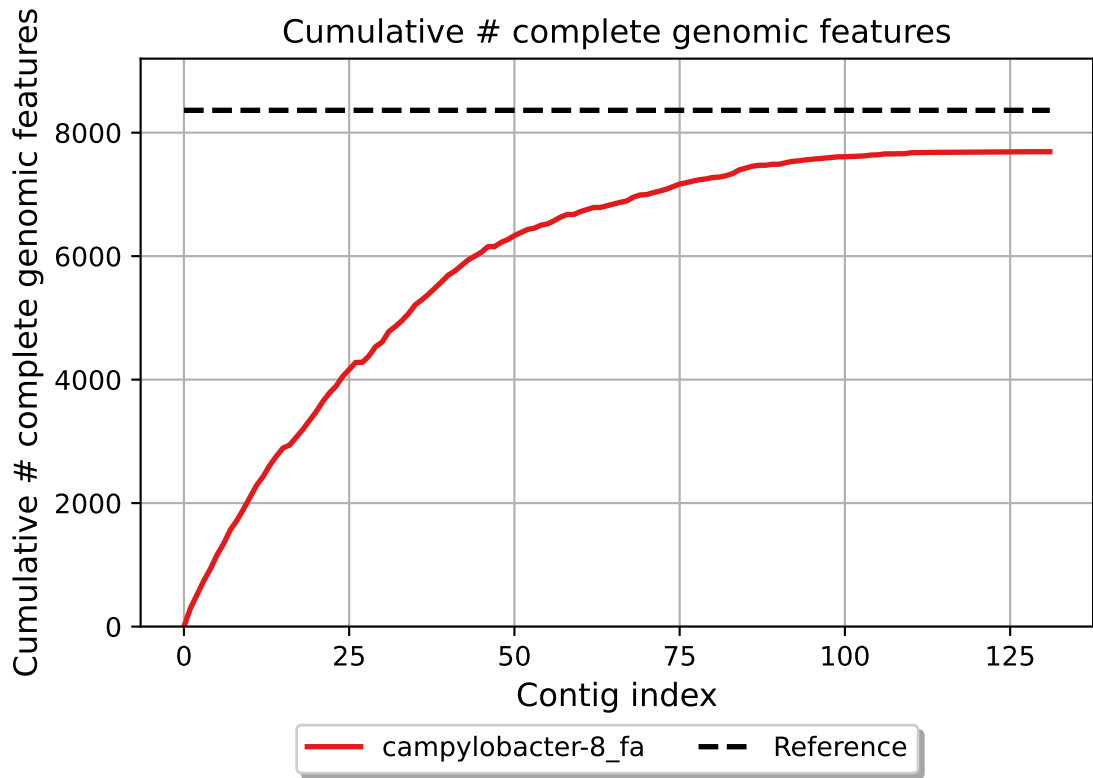


— campylobacter-8_fa

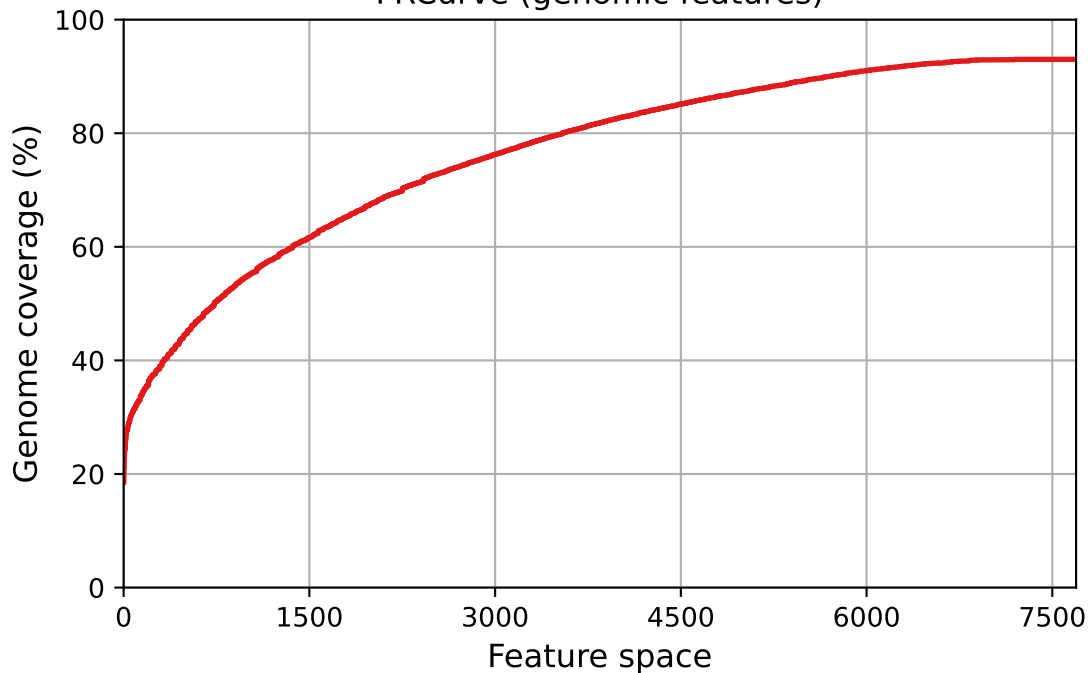
NGAx



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FRCurve (genomic features)



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