Report

	GCF_040790755.1_ASM4079075v1_genomic
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1321156
Total length (>= 1000 bp)	1321156
Total length (>= 5000 bp)	1321156
Total length (>= 10000 bp)	1307066
Total length (>= 25000 bp)	1262263
Total length (>= 50000 bp)	957421
# contigs	16
Largest contig	902698
Total length	1321156
Reference length	1521208
GC (%)	28.35
Reference GC (%)	28.18
N50	902698
NG50	902698
N90	29570
NG90	-
auN	626997.0
auNG	544541.5
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	21
# misassembled contigs	10
Misassembled contigs length	293639
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 10 part
Unaligned length	64441
Genome fraction (%)	80.789
Duplication ratio	1.021
# N's per 100 kbp	0.08
# mismatches per 100 kbp	838.73
# indels per 100 kbp	53.63
# genomic features	1287 + 52 part
Largest alignment	902578
Total aligned length	1254867
NA50	902578
NGA50	902578
NA90	8843
NGA90	-
auNA	623028.2
auNGA	541094.6
LA50	1
LGA50	1
LA90	15
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).
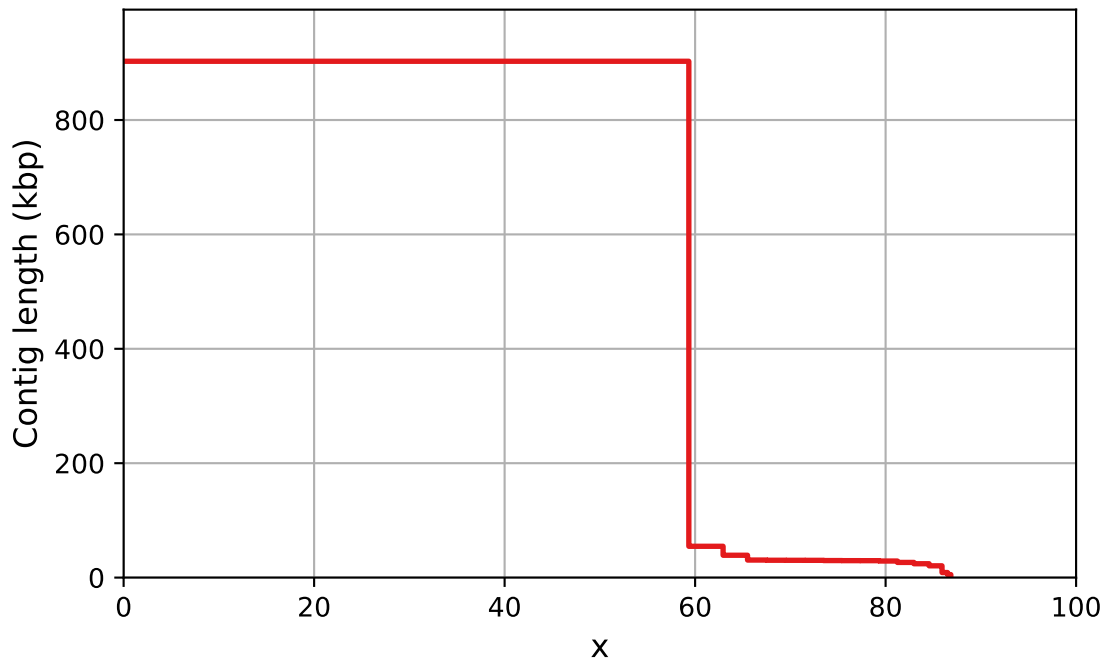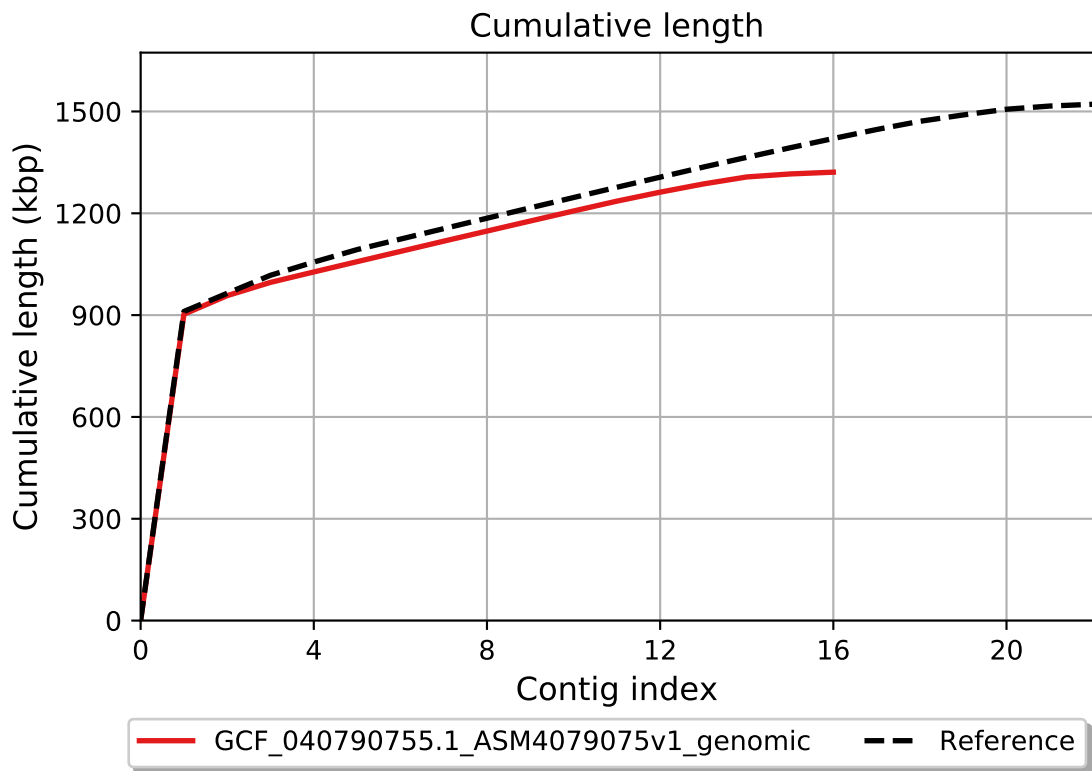
Misassemblies report

	GCF_040790755.1_ASM4079075v1_genomic
# misassemblies	21
# contig misassemblies	21
# c. relocations	4
# c. translocations	17
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	293639
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	10525
# indels	673
# indels (<= 5 bp)	595
# indels (> 5 bp)	78
Indels length	3742

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

	GCF_040790755.1_ASM4079075v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	10
Partially unaligned length	64441
# 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).
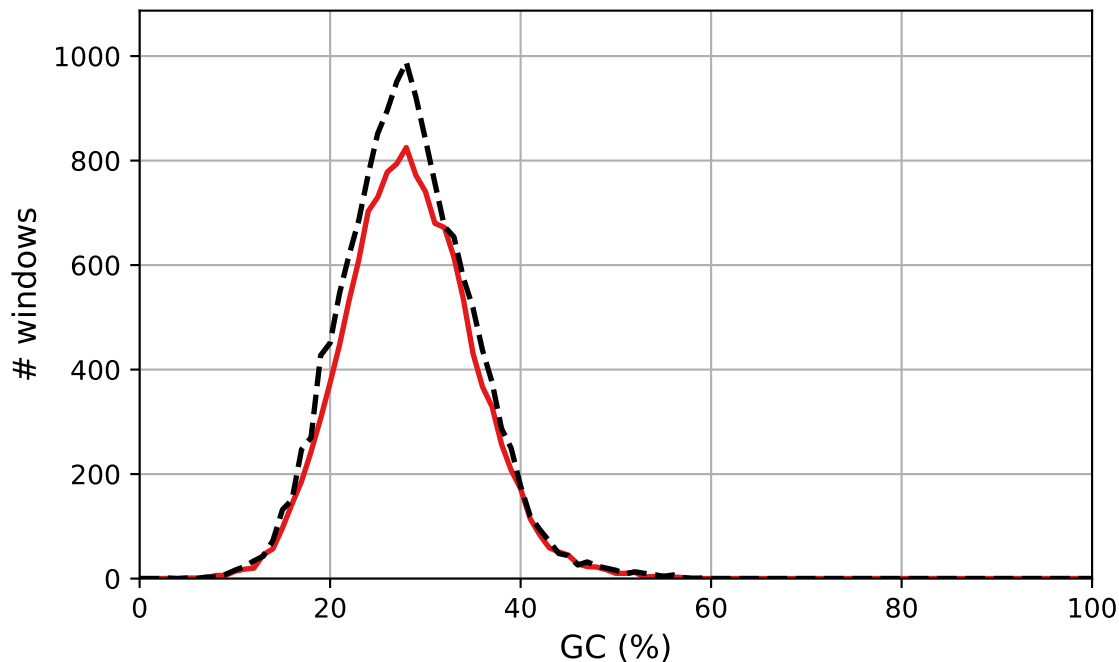
Nx
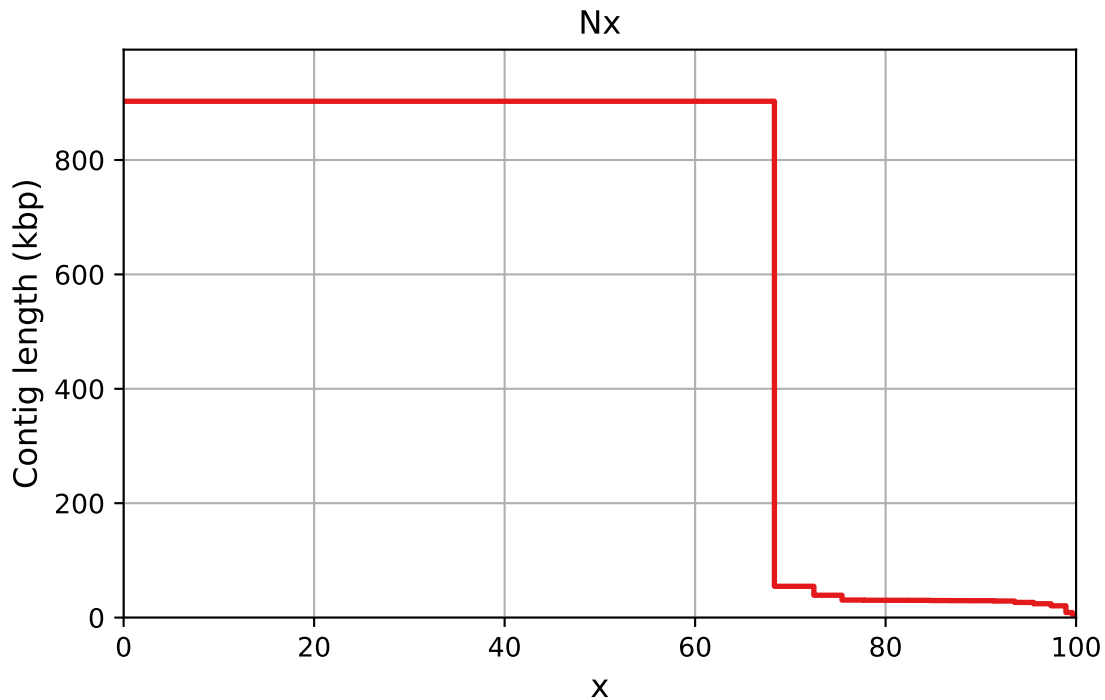
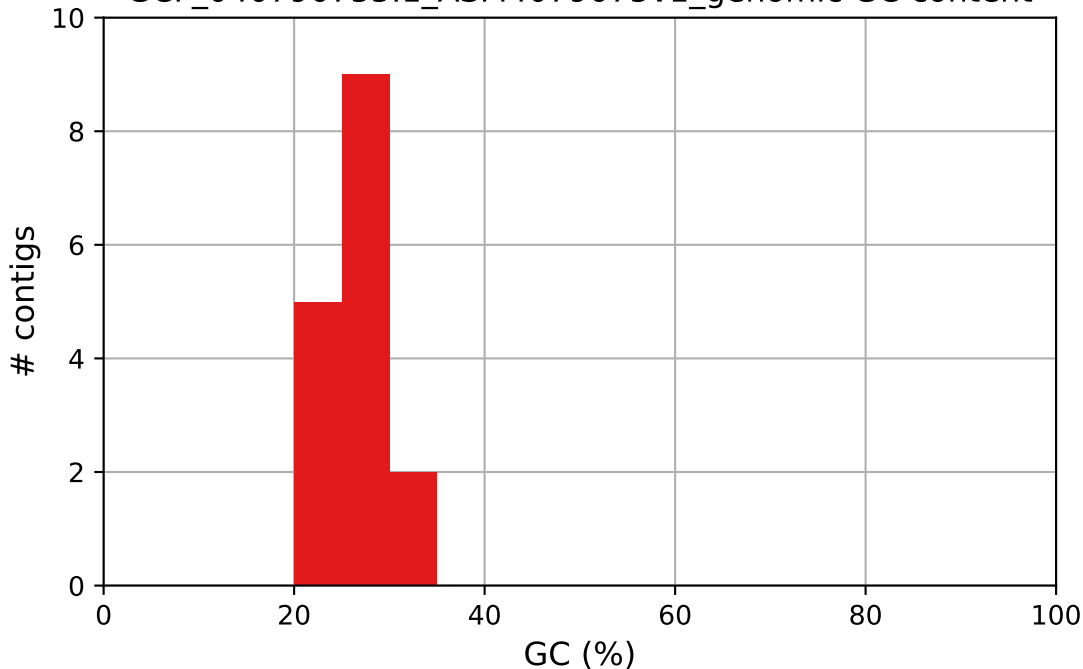GCF_040790755.1_ASM4079075v1_genomic

NGx

GCF_040790755.1_ASM4079075v1_genomic

Cumulative length

GCF_040790755.1_ASM4079075v1_genomic — Reference

GC content

GCF_040790755.1_ASM4079075v1_genomic GC content

Misassemblies
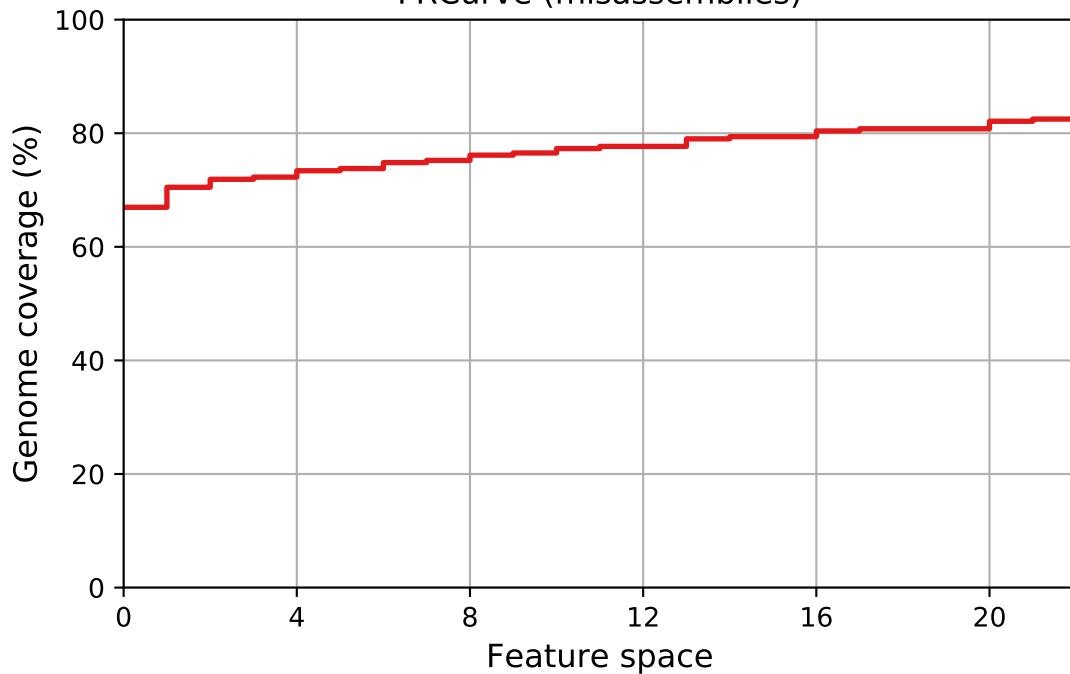
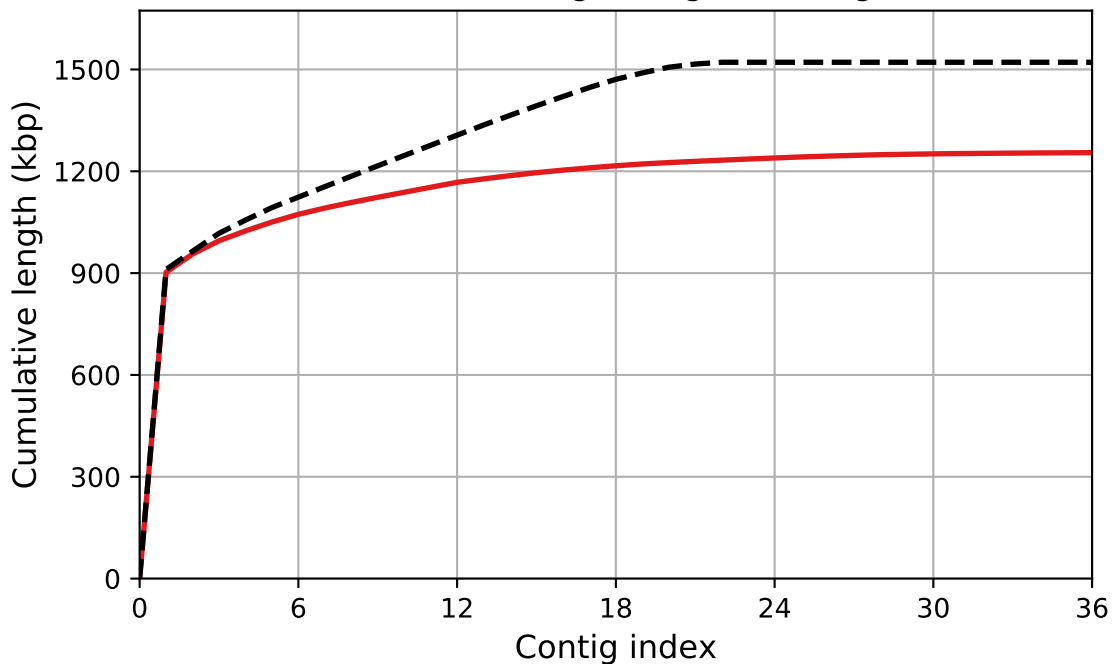GCF_040790755.1_ASM4079075v1_genomic

relocations   # translocations
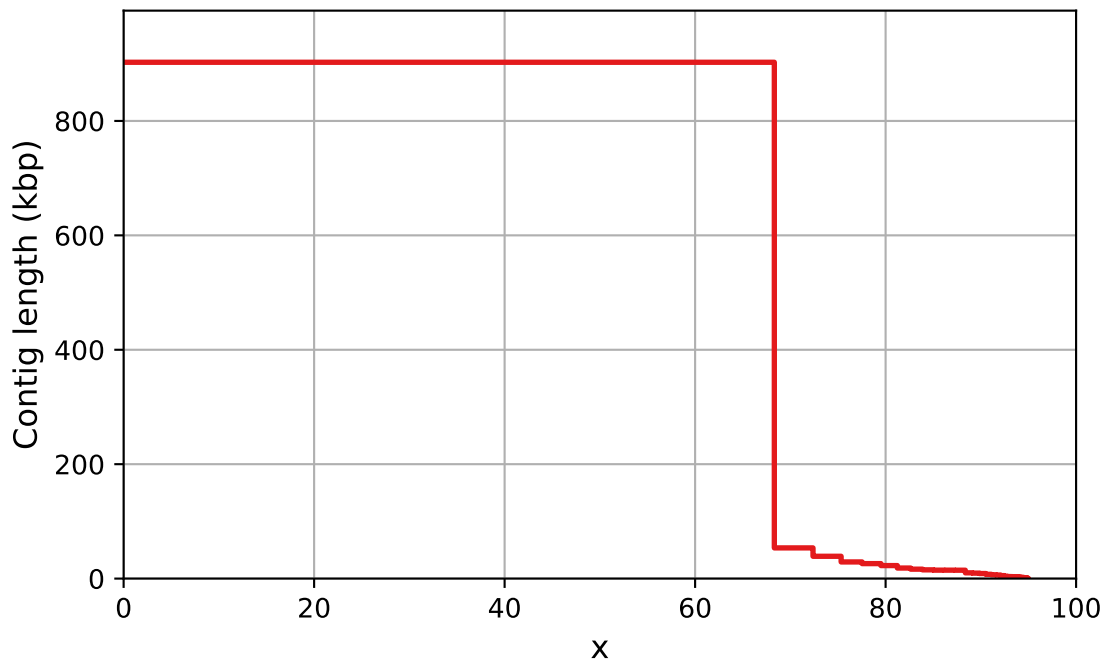
FRCurve (misassemblies)

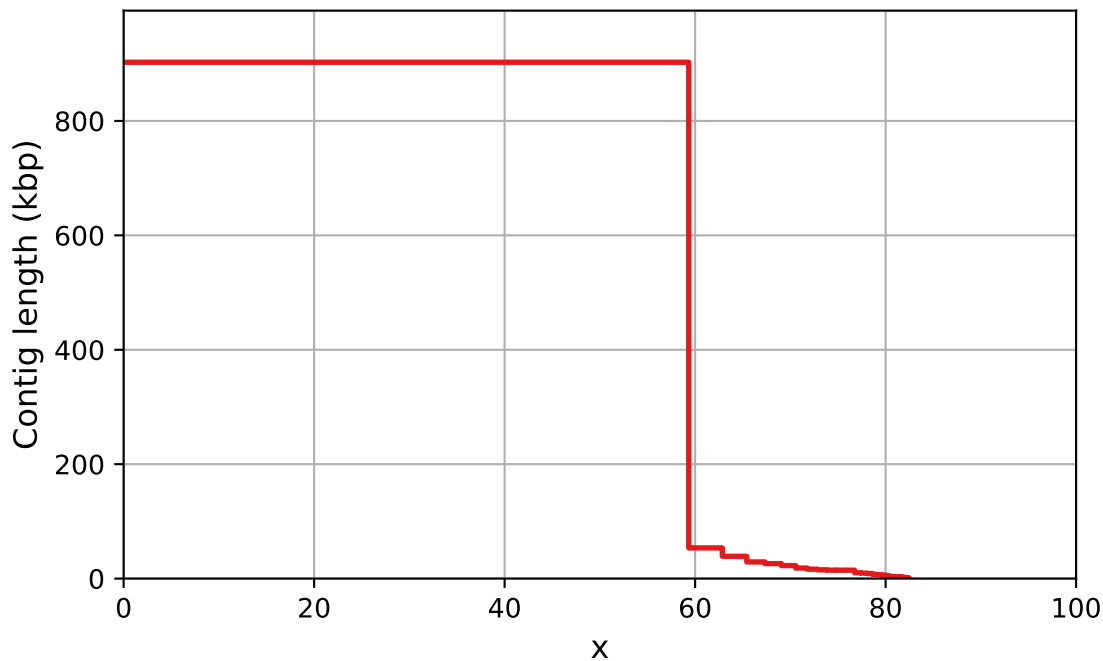GCF_040790755.1_ASM4079075v1_genomic

Cumulative length (aligned contigs)
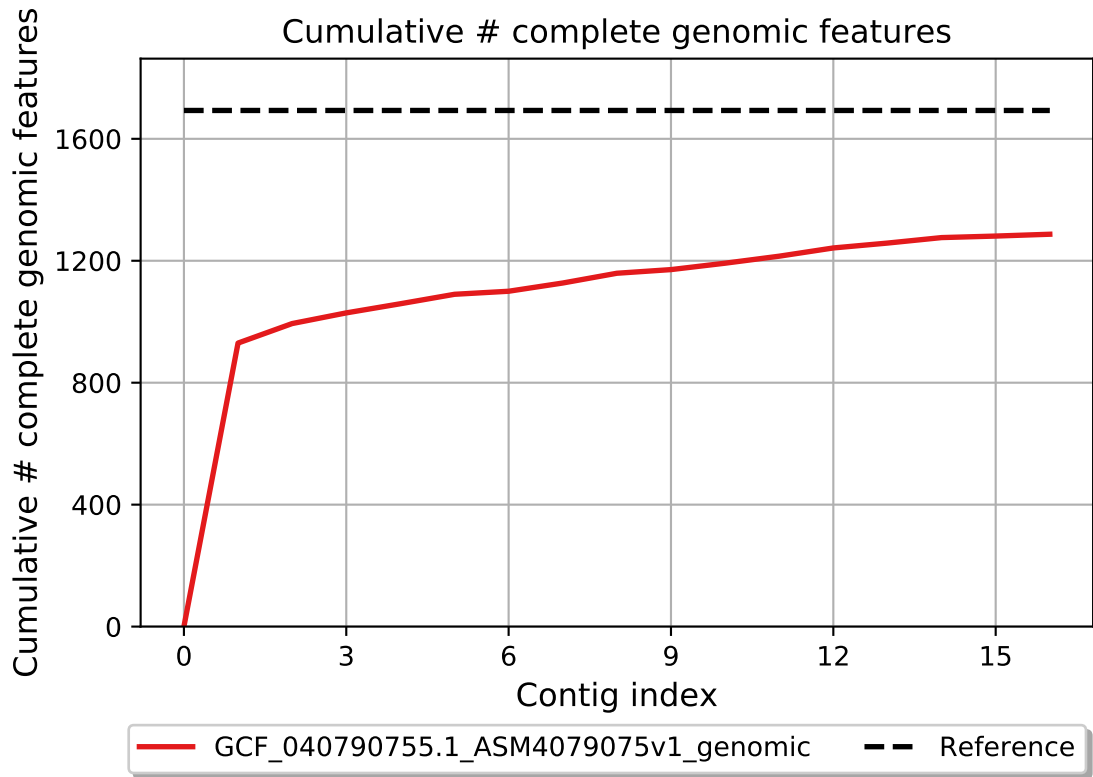
NAx

GCF_040790755.1_ASM4079075v1_genomic

NGAx

GCF_040790755.1_ASM4079075v1_genomic

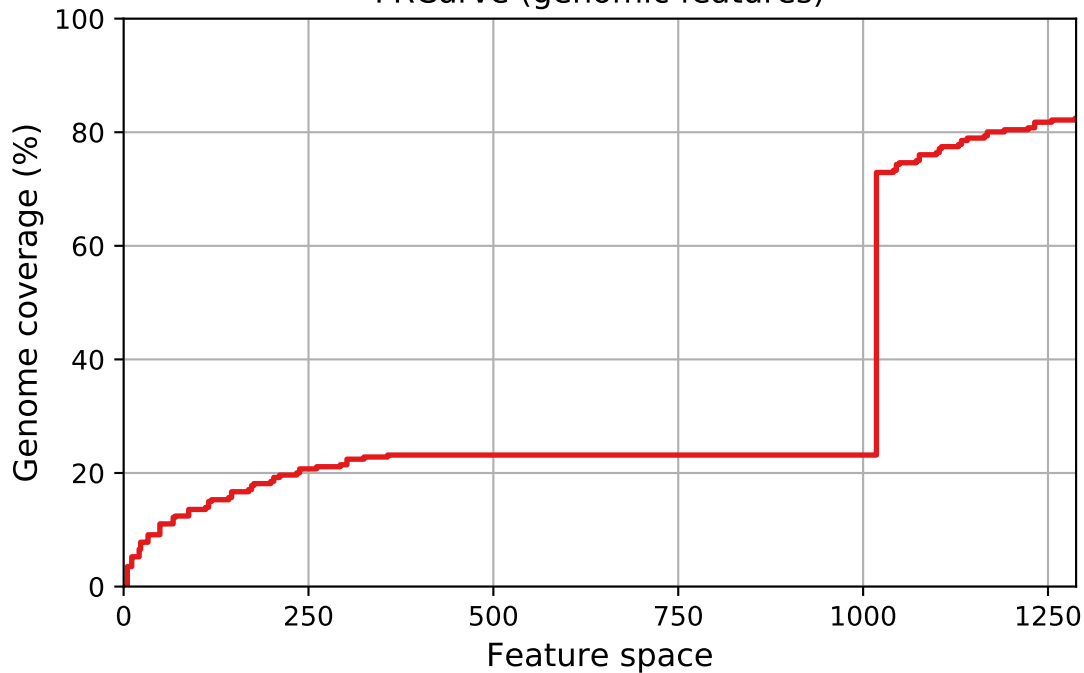Cumulative # complete genomic features

FRCurve (genomic features)

GCF_040790755.1_ASM4079075v1_genomic