Report

	GCA_040790735.1_ASM4079073v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	13
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1391486
Total length (>= 1000 bp)	1391486
Total length (>= 5000 bp)	1391486
Total length (>= 10000 bp)	1391486
Total length (>= 25000 bp)	1288594
Total length (>= 50000 bp)	963376
# contigs	18
Largest contig	909471
Total length	1391486
Reference length	1521208
GC (%)	28.27
Reference GC (%)	28.18
N50	909471
NG50	909471
N90	27192
NG90	18015
auN	605012.4
auNG	553419.5
L50	1
LG50	1
L90	12
LG90	17
# misassemblies	20
# misassembled contigs	11
Misassembled contigs length	1204252
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 16 part
Unaligned length	156722
Genome fraction (%)	78.701
Duplication ratio	1.031
# N's per 100 kbp	0.07
# mismatches per 100 kbp	833.46
# indels per 100 kbp	45.12
# genomic features	1268 + 33 part
Largest alignment	468258
Total aligned length	1234607
NA50	435179
NGA50	435179
NA90	-
NGA90	-
auNA	298641.1
auNGA	273174.2
LA50	2
LGA50	2
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).
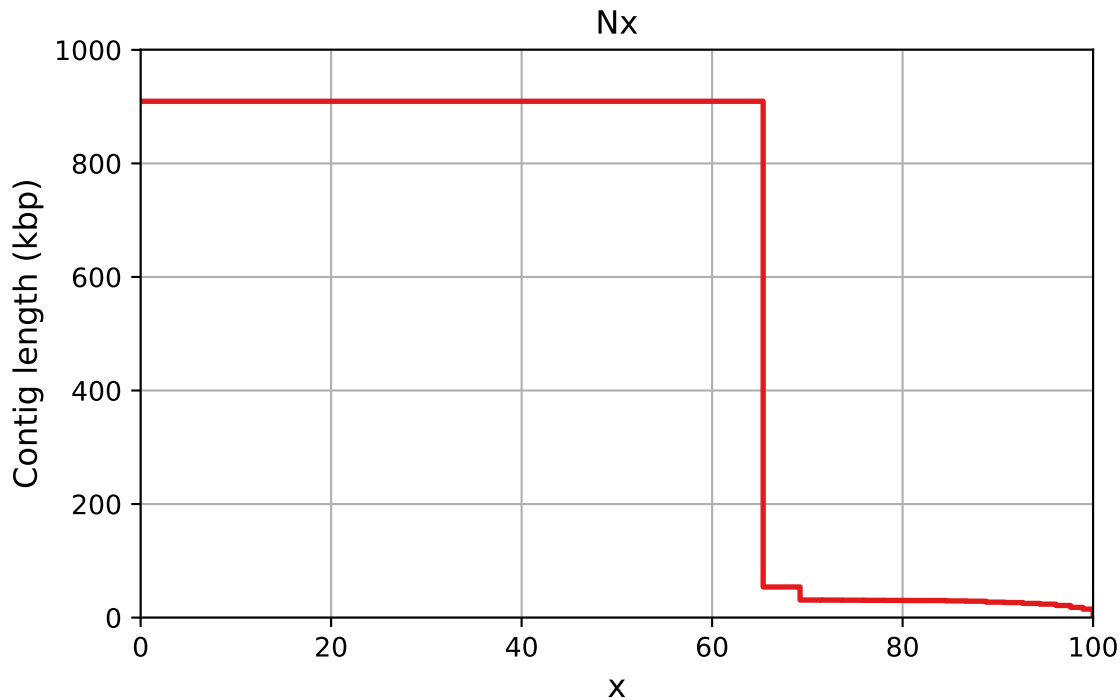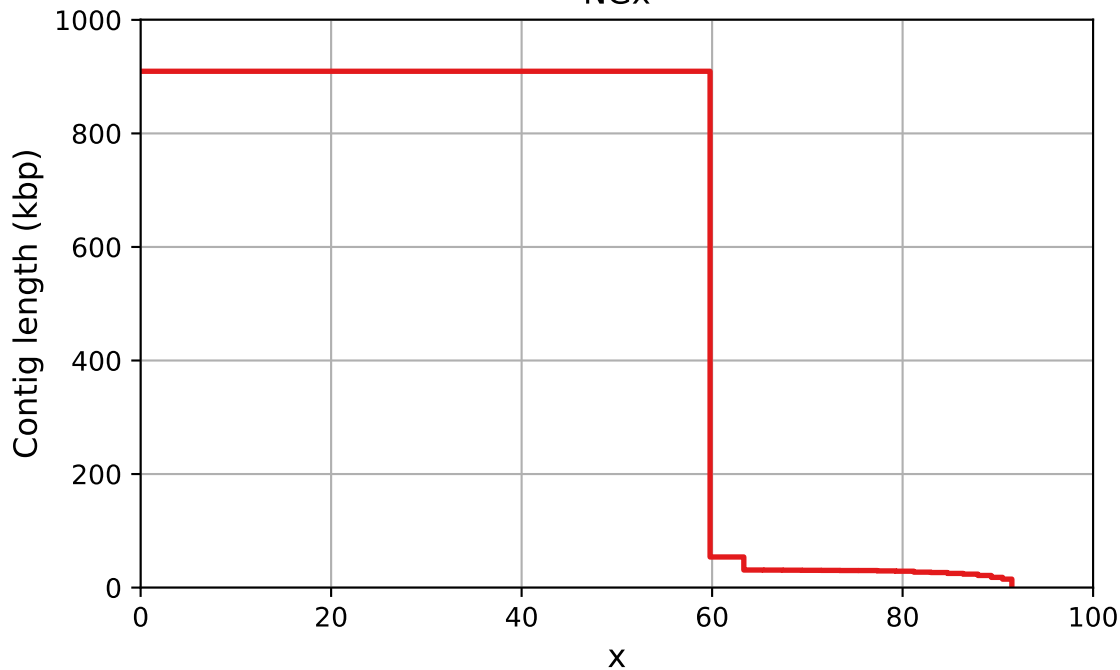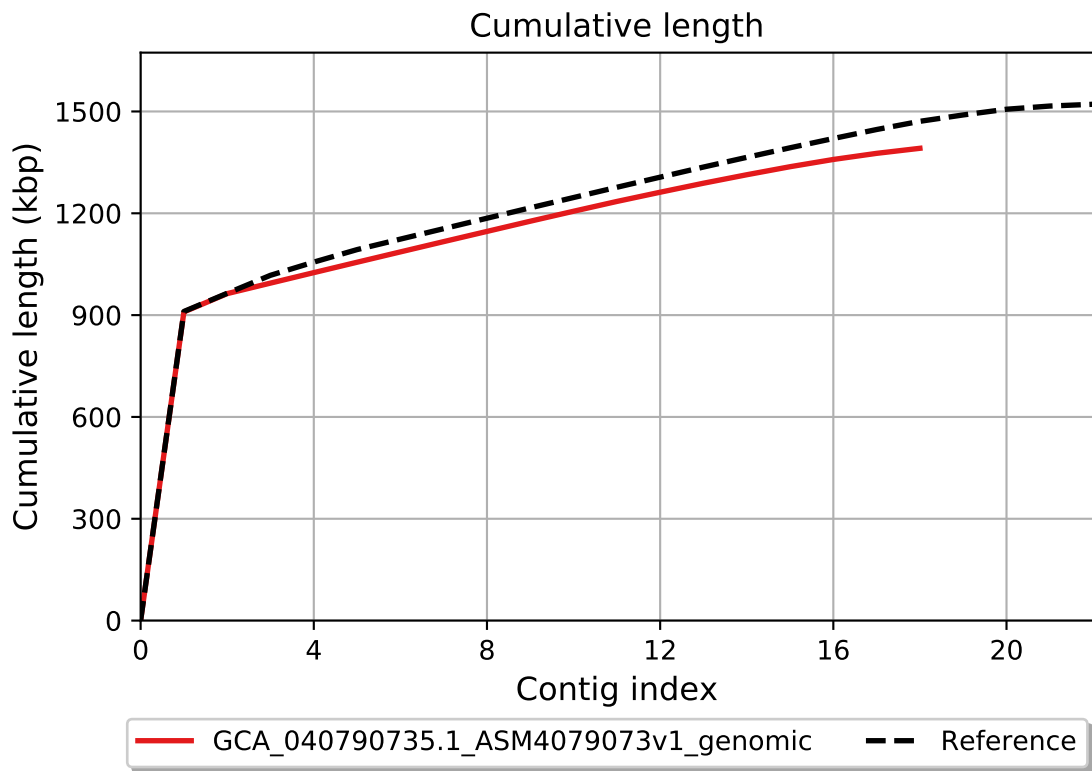
Misassemblies report

	GCA_040790735.1_ASM4079073v1_genomic
# misassemblies	20
# contig misassemblies	20
# c. relocations	6
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	1204252
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	10290
# indels	557
# indels (<= 5 bp)	496
# indels (> 5 bp)	61
Indels length	2581

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

	GCA_040790735.1_ASM4079073v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	16
Partially unaligned length	156722
# 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).
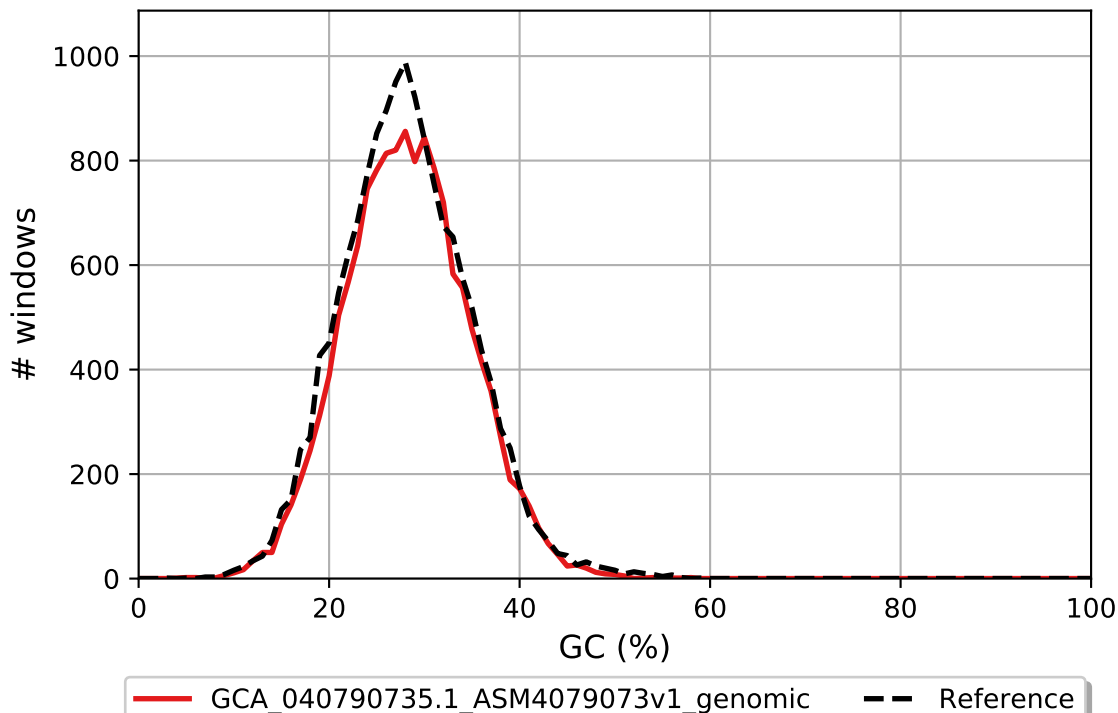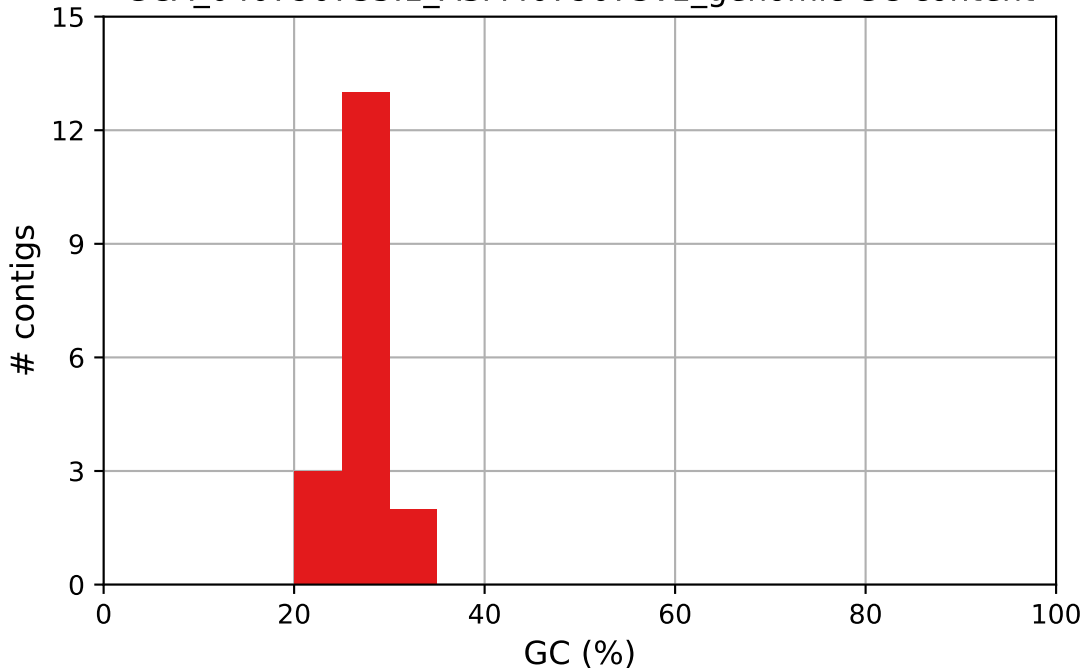
Nx

GCA_040790735.1_ASM4079073v1_genomic

NGx

GCA_040790735.1_ASM4079073v1_genomic

Cumulative length

GC content

GCA_040790735.1_ASM4079073v1_genomic GC content

Misassemblies

GCA_040790735.1_ASM4079073v1_genomic
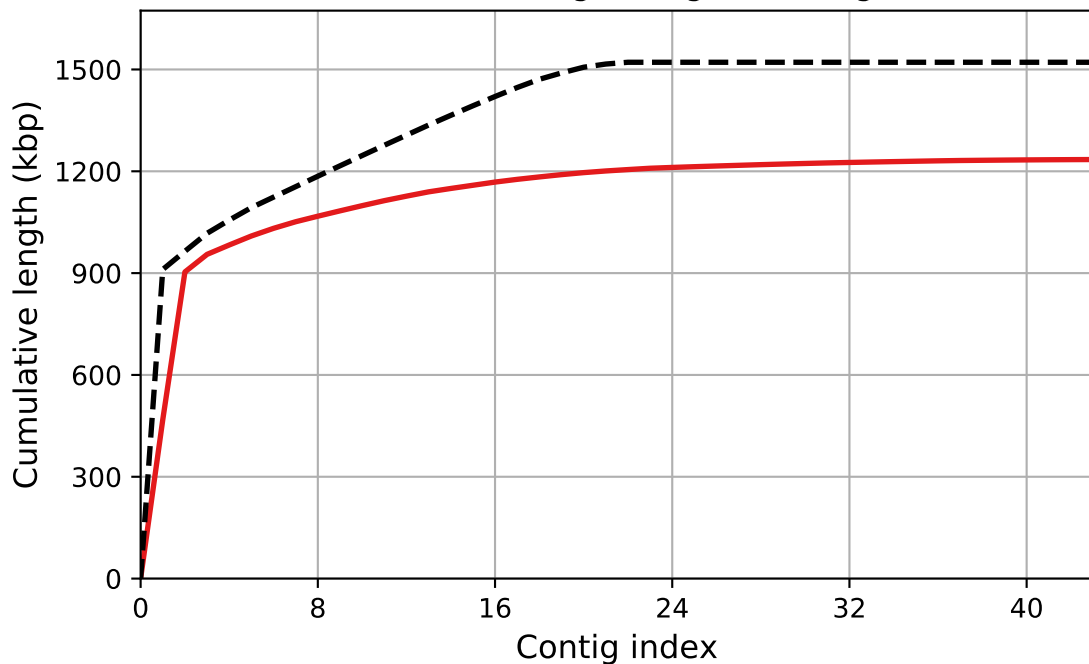
■ # relocations   ■ # translocations

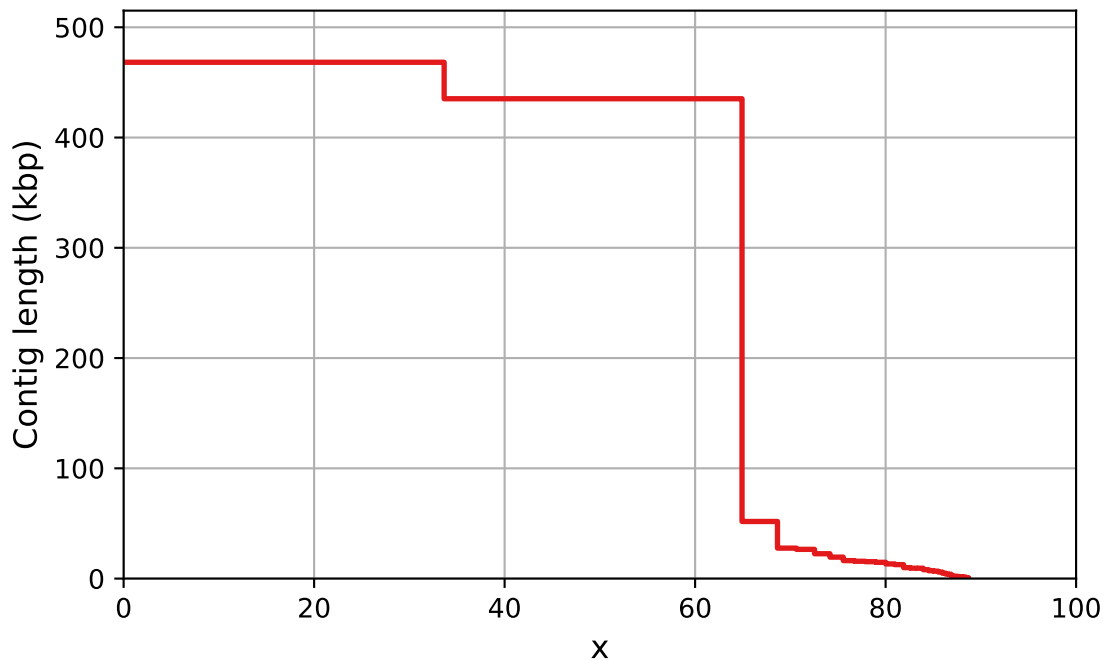FRCurve (misassemblies)
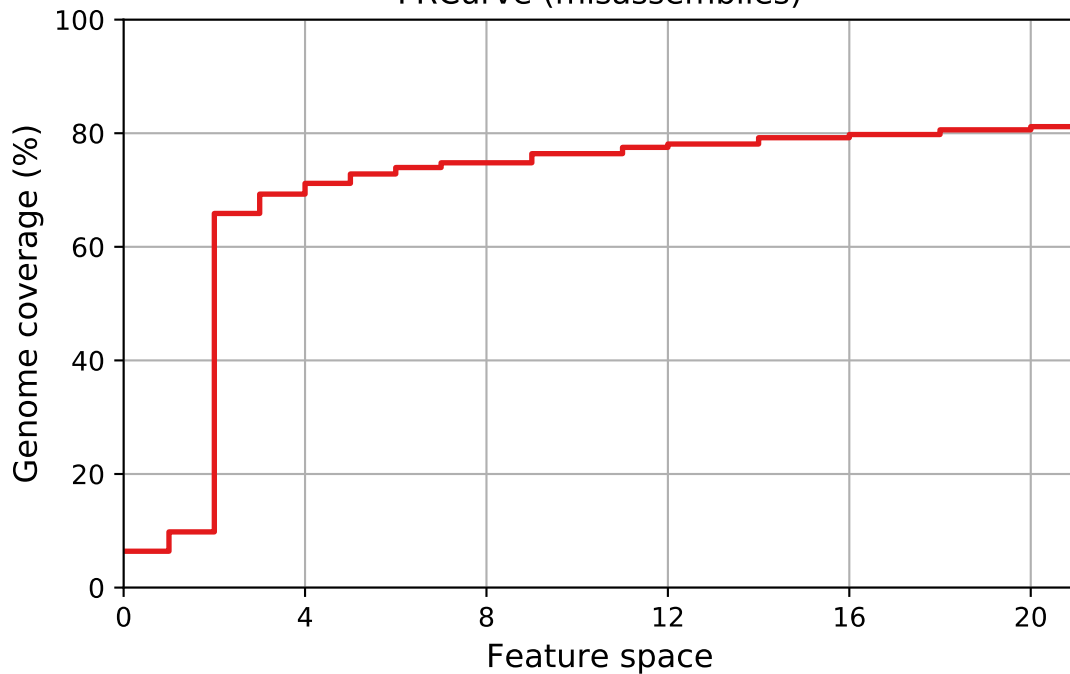
GCA_040790735.1_ASM4079073v1_genomic

Cumulative length (aligned contigs)
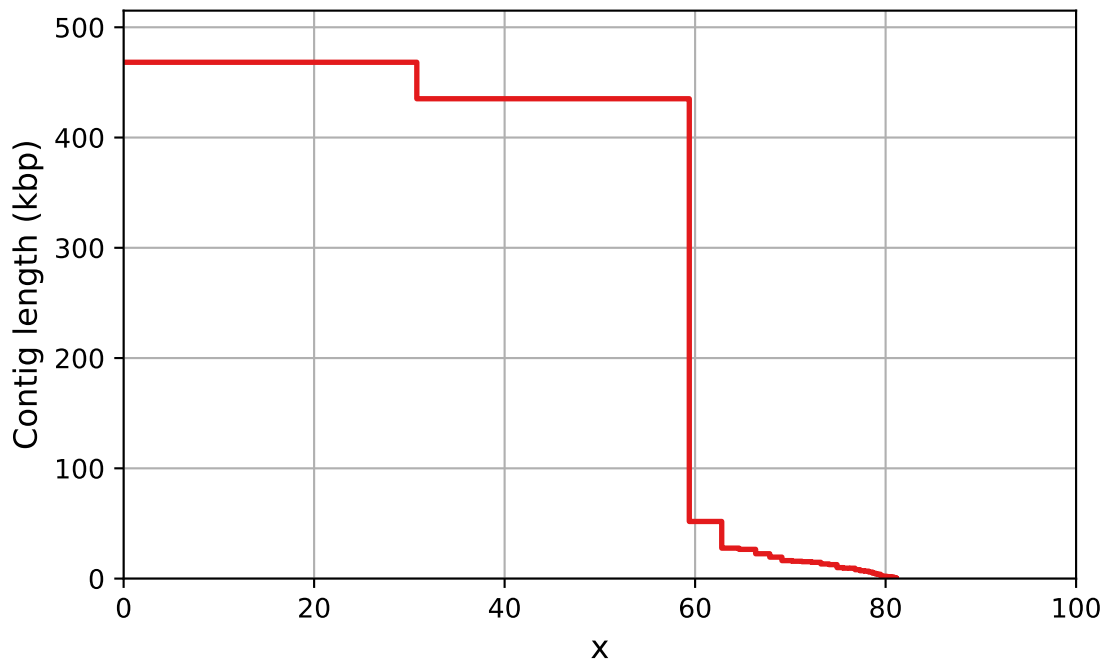
NAx

GCA_040790735.1_ASM4079073v1_genomic
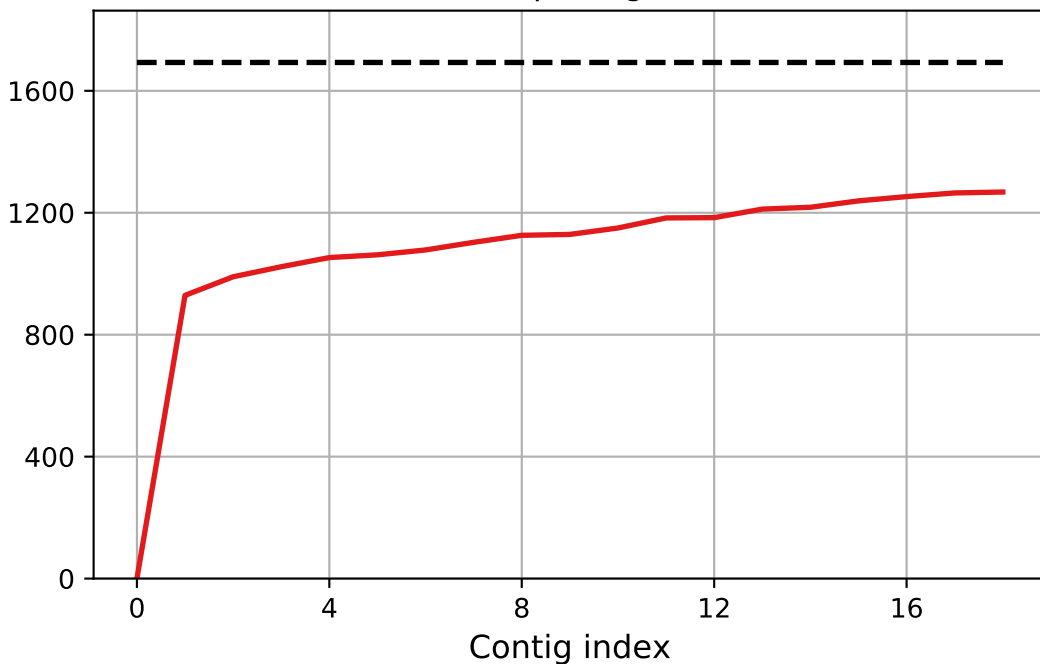
NGAx

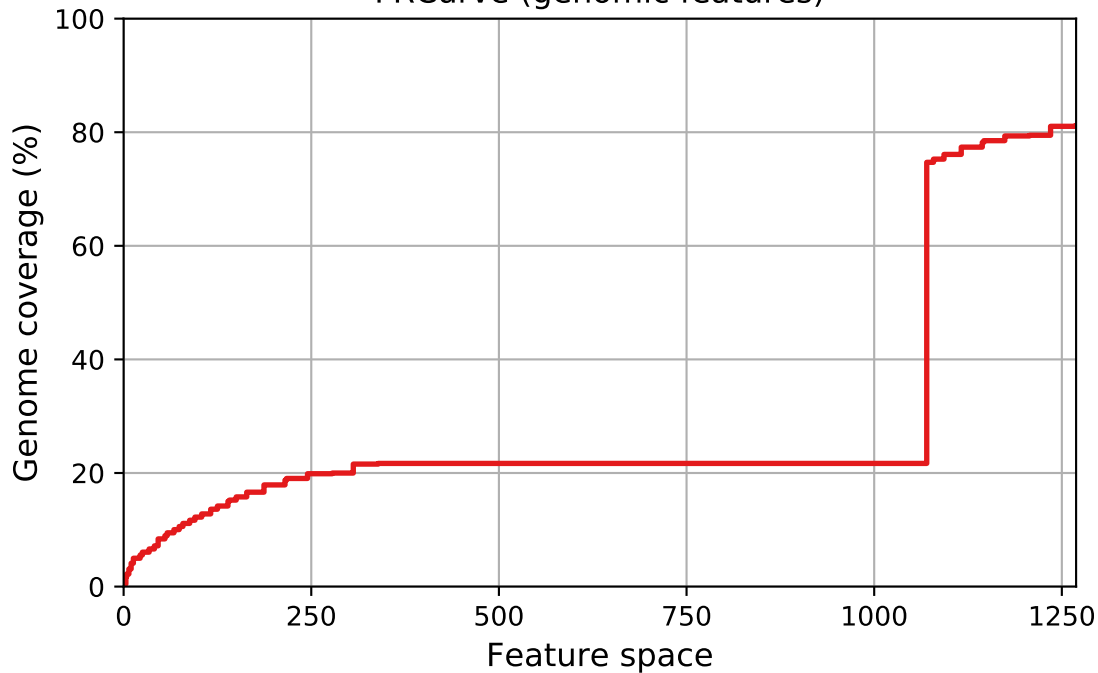GCA_040790735.1_ASM4079073v1_genomic

Cumulative # complete genomic features

FRCurve (genomic features)

GCA_040790735.1_ASM4079073v1_genomic