Report

	GCA_040790745.1_ASM4079074v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	12
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1371468
Total length (>= 1000 bp)	1371468
Total length (>= 5000 bp)	1371468
Total length (>= 10000 bp)	1362746
Total length (>= 25000 bp)	1260568
Total length (>= 50000 bp)	956638
# contigs	18
Largest contig	902797
Total length	1371468
Reference length	1521208
GC (%)	28.18
Reference GC (%)	28.18
N50	902797
NG50	902797
N90	26498
NG90	8722
auN	604810.6
auNG	545276.1
L50	1
LG50	1
L90	12
LG90	18
# misassemblies	18
# misassembled contigs	8
Misassembled contigs length	251347
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	1 + 14 part
Unaligned length	131138
Genome fraction (%)	80.962
Duplication ratio	1.006
# N's per 100 kbp	0.36
# mismatches per 100 kbp	860.85
# indels per 100 kbp	53.89
# genomic features	1284 + 53 part
Largest alignment	902617
Total aligned length	1239475
NA50	902617
NGA50	902617
NA90	912
NGA90	-
auNA	599585.0
auNGA	540564.9
LA50	1
LGA50	1
LA90	39
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).
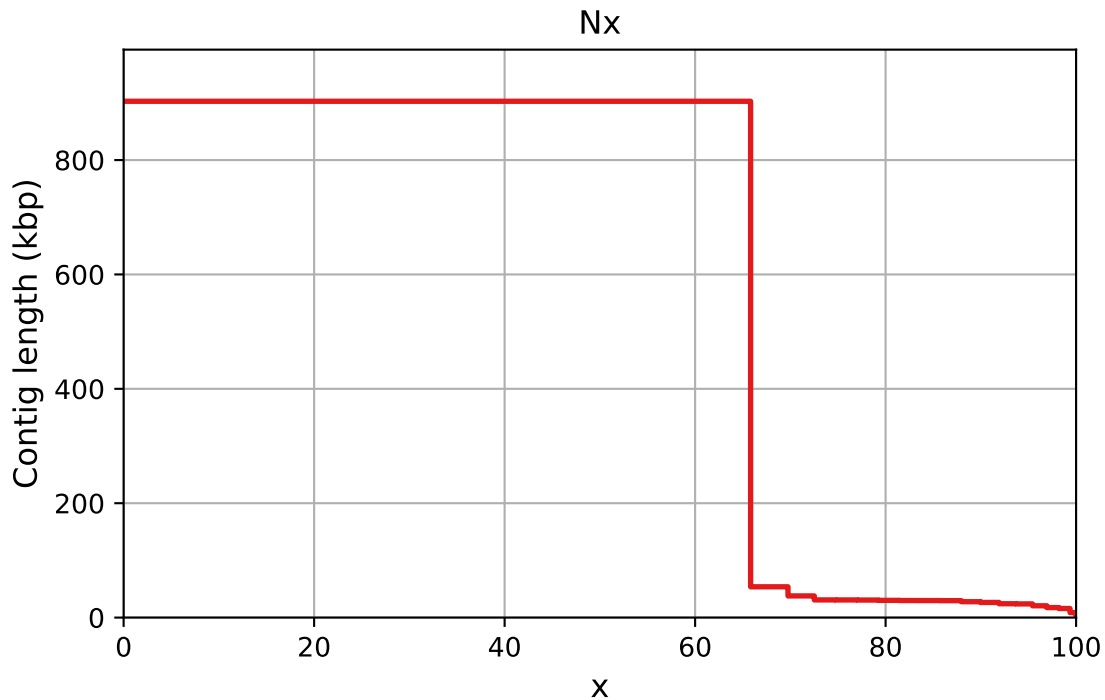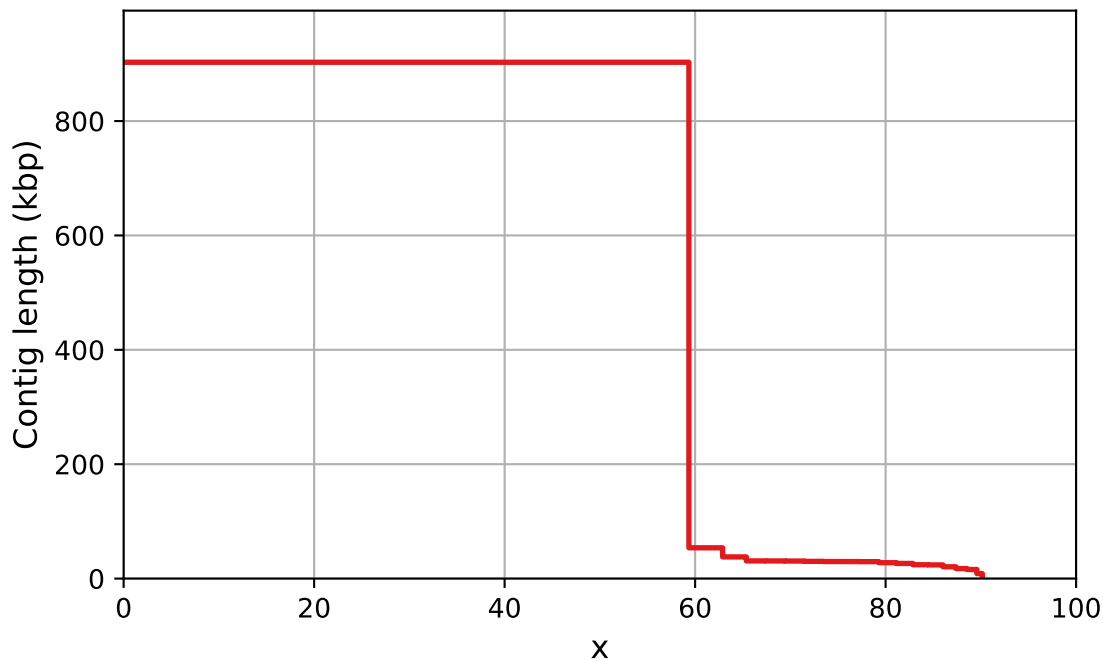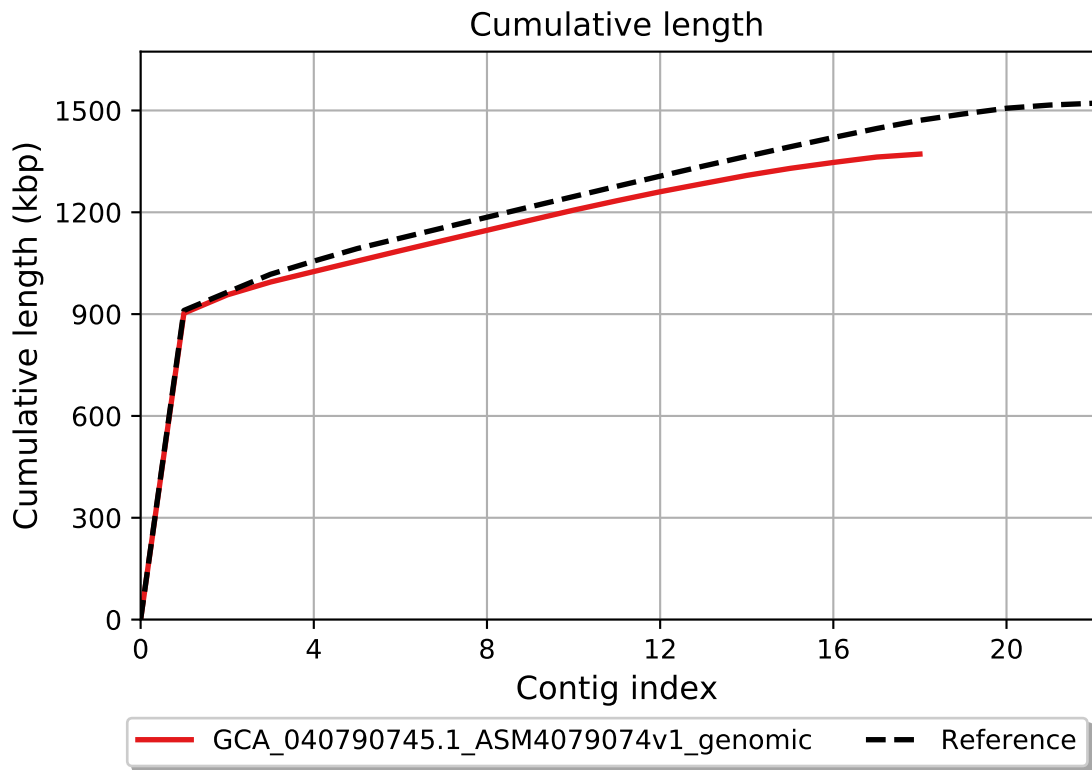
Misassemblies report

	GCA_040790745.1_ASM4079074v1_genomic
# misassemblies	18
# contig misassemblies	18
# c. relocations	4
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	251347
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	10670
# indels	668
# indels (<= 5 bp)	594
# indels (> 5 bp)	74
Indels length	3412

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_040790745.1_ASM4079074v1_genomic
# fully unaligned contigs	1
Fully unaligned length	27767
# partially unaligned contigs	14
Partially unaligned length	103371
# N's	5

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).
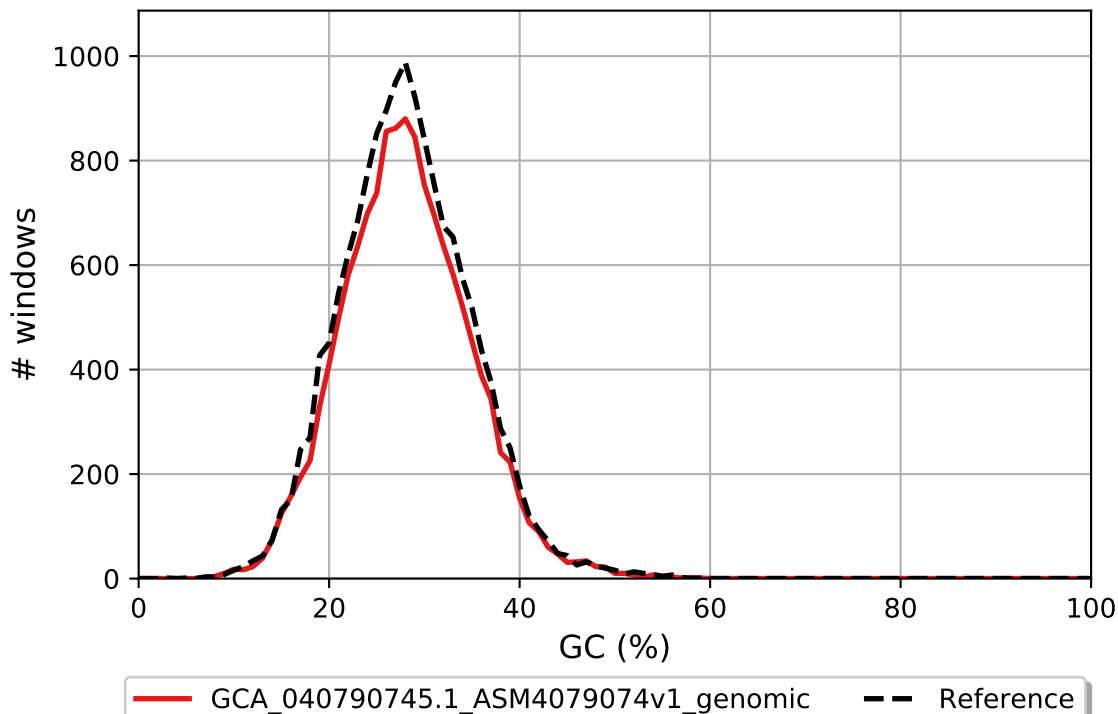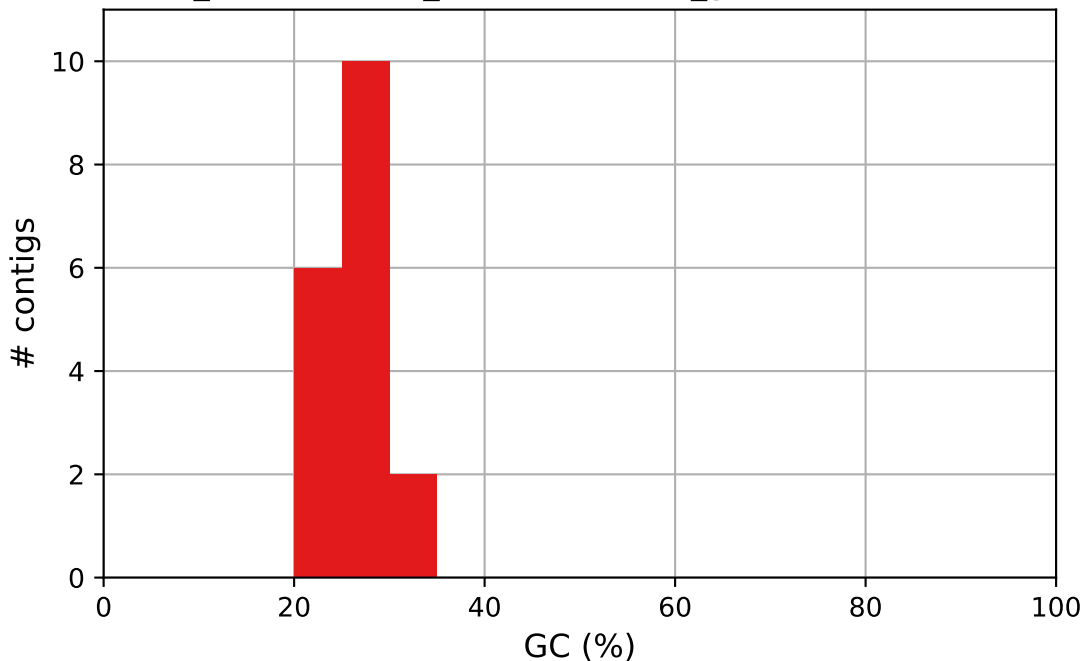
Nx

NGx

GCA_040790745.1_ASM4079074v1_genomic

Cumulative length

GC content

GCA_040790745.1_ASM4079074v1_genomic GC content

Misassemblies

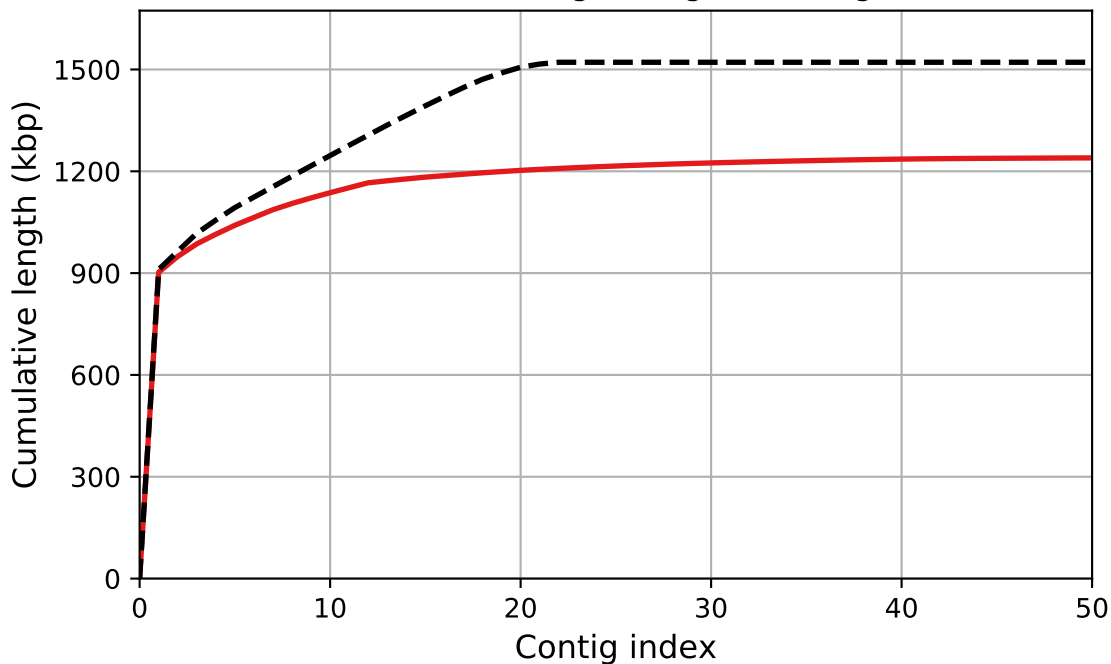GCA_040790745.1_ASM4079074v1_genomic

■ # relocations ■ # translocations

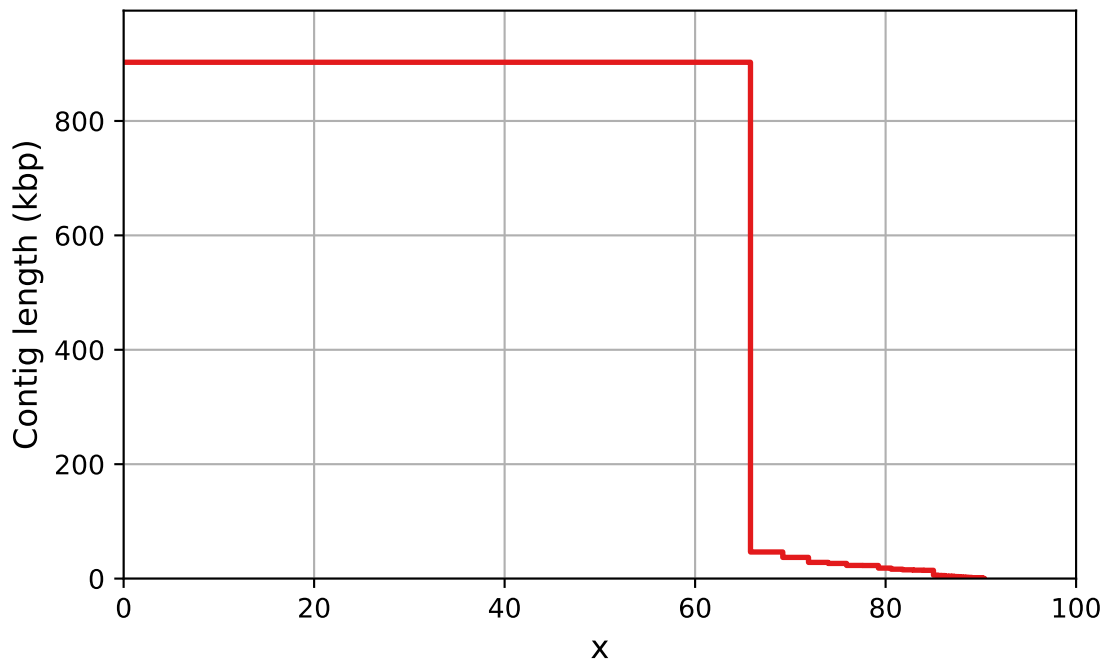FRCurve (misassemblies)
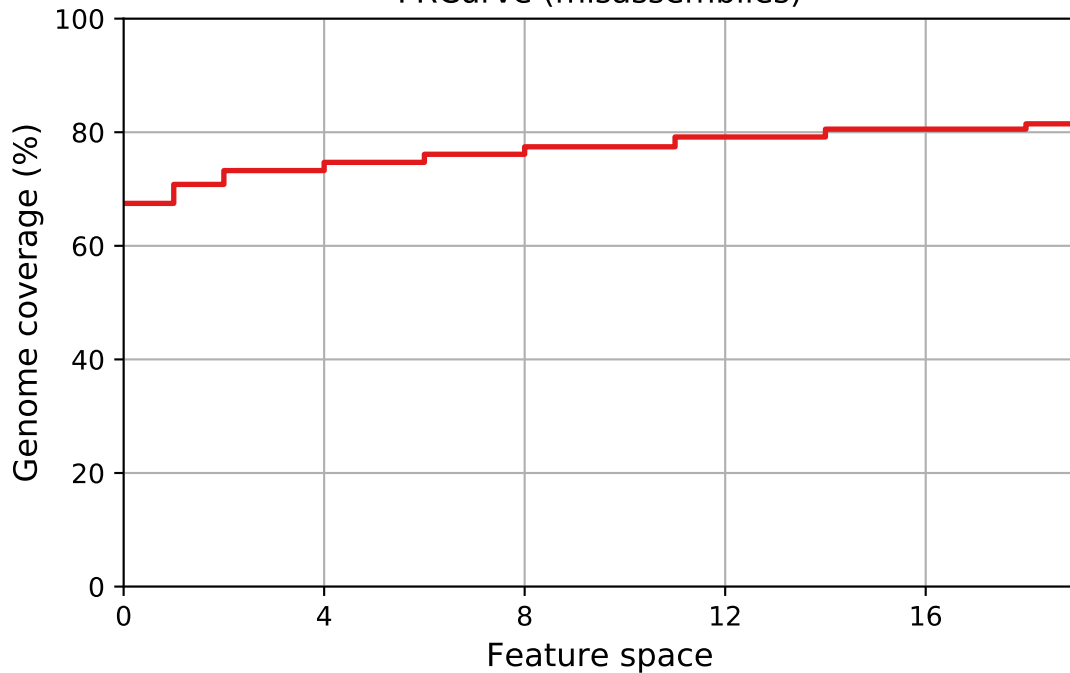
GCA_040790745.1_ASM4079074v1_genomic

Cumulative length (aligned contigs)

NAx
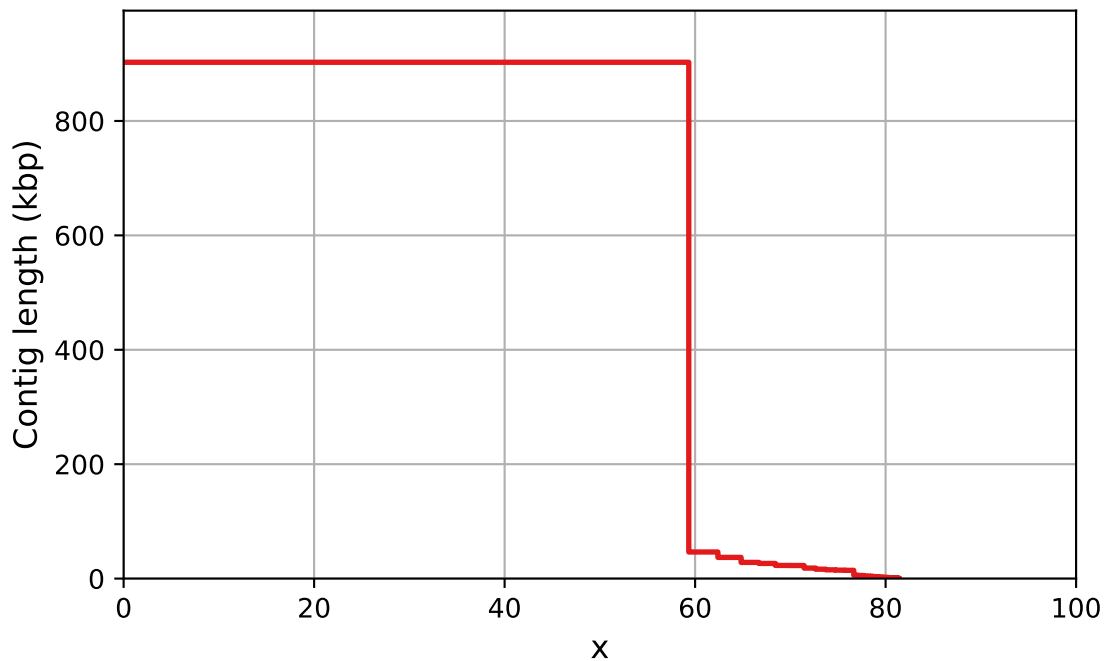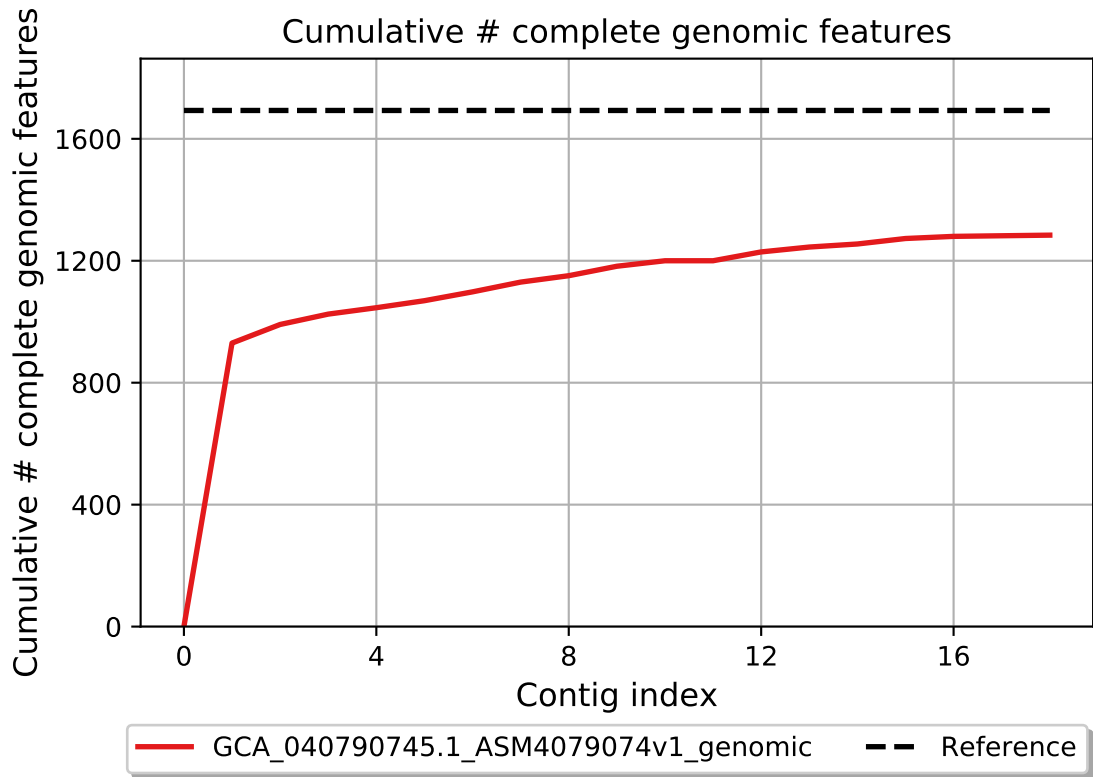
GCA_040790745.1_ASM4079074v1_genomic

NGAx

GCA_040790745.1_ASM4079074v1_genomic

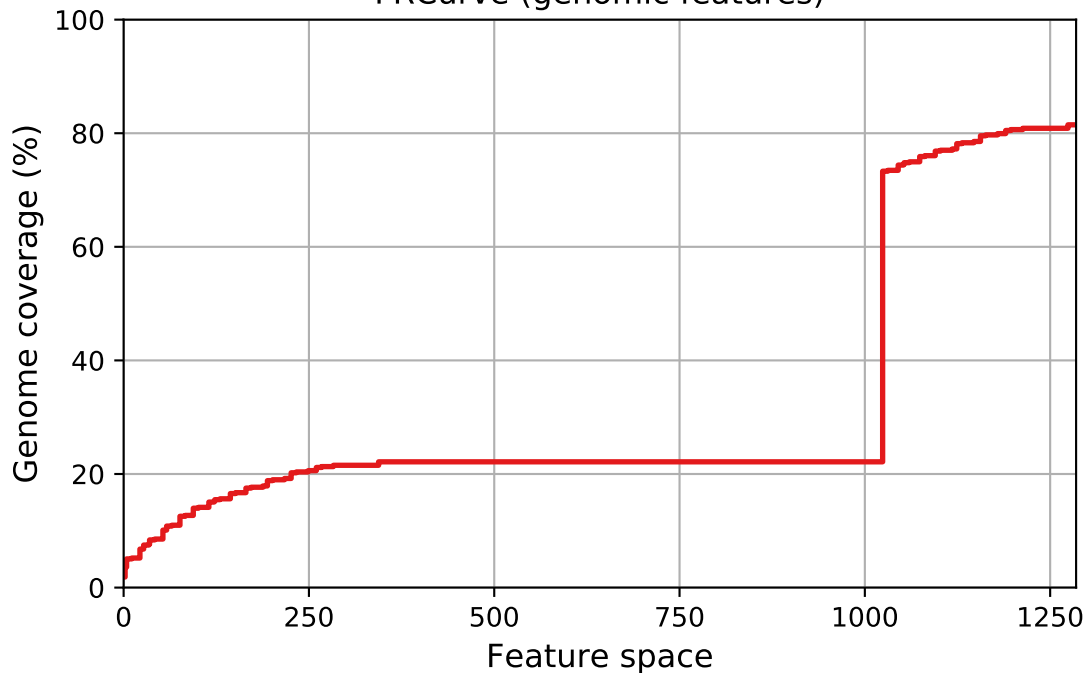Cumulative # complete genomic features

FRCurve (genomic features)

GCA_040790745.1_ASM4079074v1_genomic