

# Report

GCA_040790715.1_ASM4079071v1_genomic	
# contigs (>= 0 bp)	14
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1289159
Total length (>= 1000 bp)	1289159
Total length (>= 5000 bp)	1289159
Total length (>= 10000 bp)	1289159
Total length (>= 25000 bp)	1222603
Total length (>= 50000 bp)	962616
# contigs	14
Largest contig	908738
Total length	1289159
Reference length	1521208
GC (%)	28.02
Reference GC (%)	28.18
N50	908738
NG50	908738
N90	27454
NG90	-
auN	649834.5
auNG	550707.0
L50	1
LG50	1
L90	9
LG90	-
# misassemblies	20
# misassembled contigs	9
Misassembled contigs length	1163183
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 11 part
Unaligned length	110239
Genome fraction (%)	77.188
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	730.03
# indels per 100 kbp	47.72
# genomic features	1224 + 35 part
Largest alignment	468321
Total aligned length	1177616
NA50	435045
NGA50	435045
NA90	2437
NGA90	-
auNA	321701.9
auNGA	272628.7
LA50	2
LGA50	2
LA90	21
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

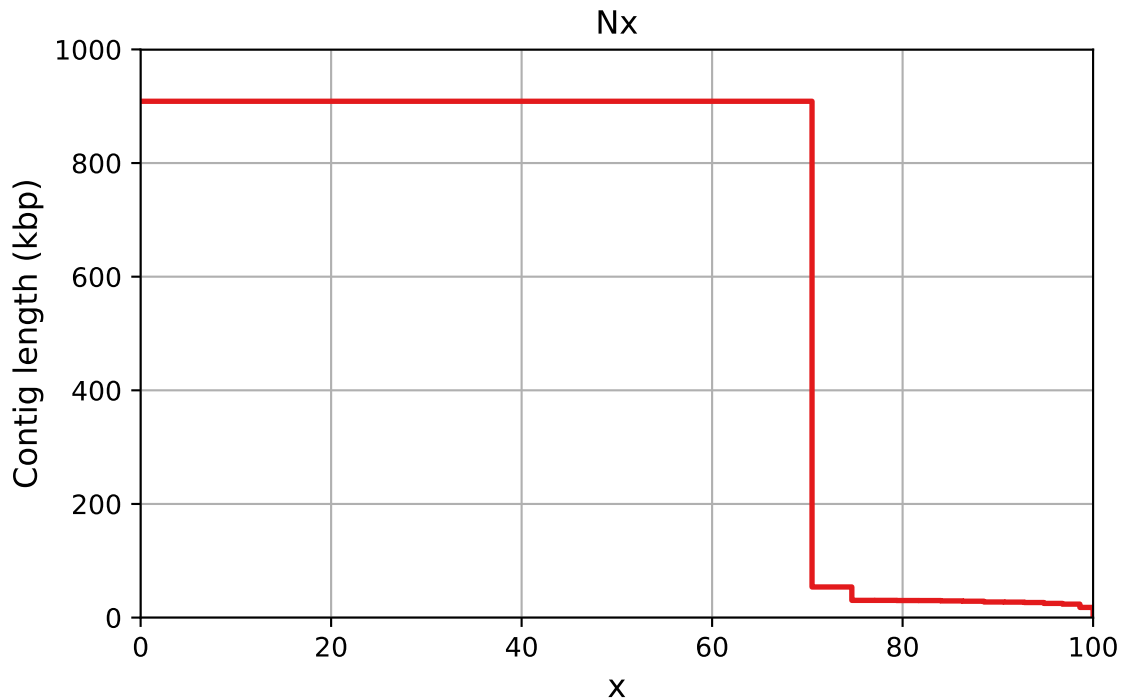
	GCA_040790715.1_ASM4079071v1_genomic
# misassemblies	20
# contig misassemblies	20
# c. relocations	4
# c. translocations	14
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	9
Misassembled contigs length	1163183
# local misassemblies	11
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	8597
# indels	562
# indels (<= 5 bp)	486
# indels (> 5 bp)	76
Indels length	4703

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

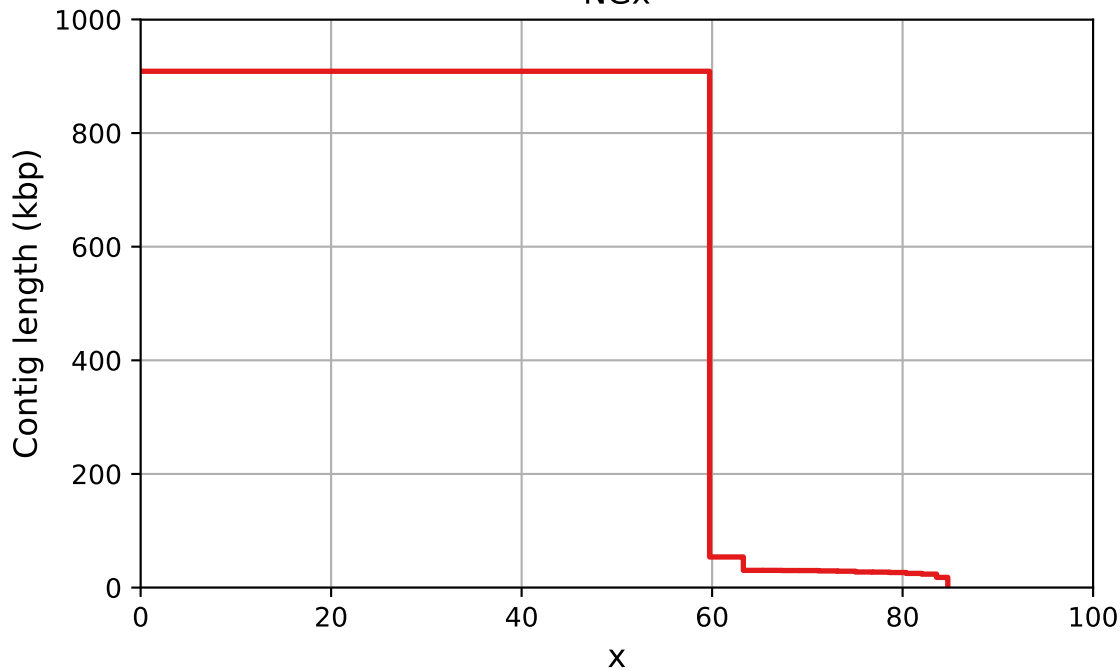
	GCA_040790715.1_ASM4079071v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	11
Partially unaligned length	110239
# N's	0

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).

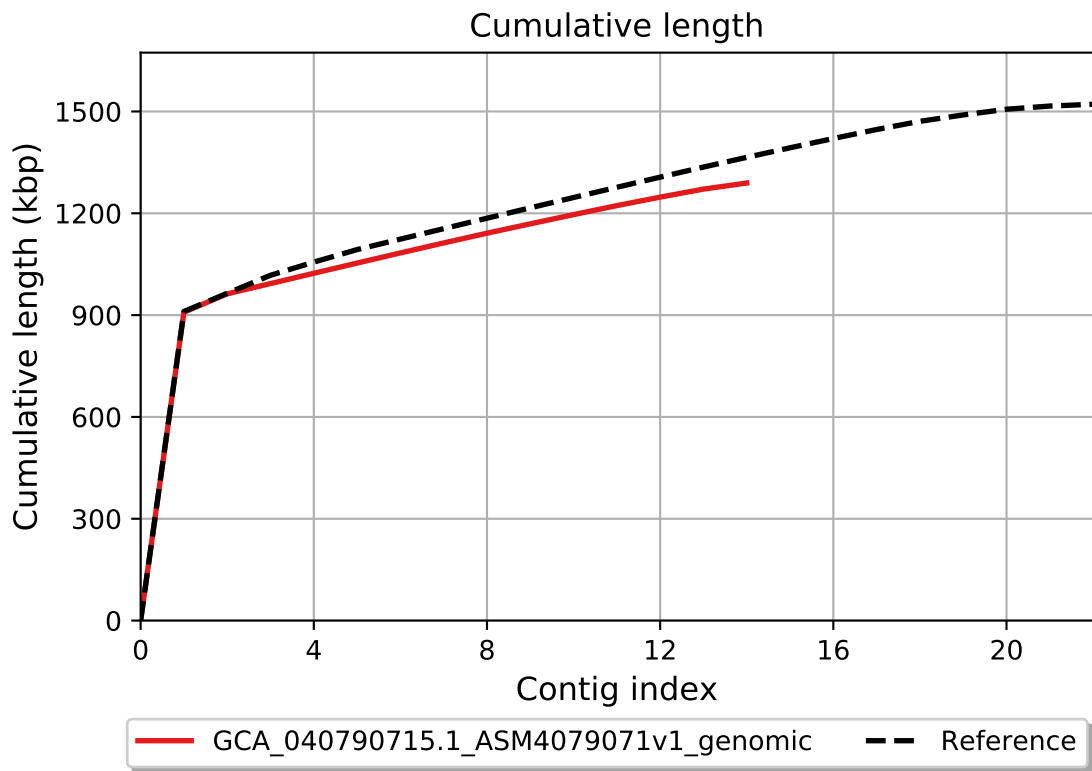


— GCA\_040790715.1\_ASM4079071v1\_genomic

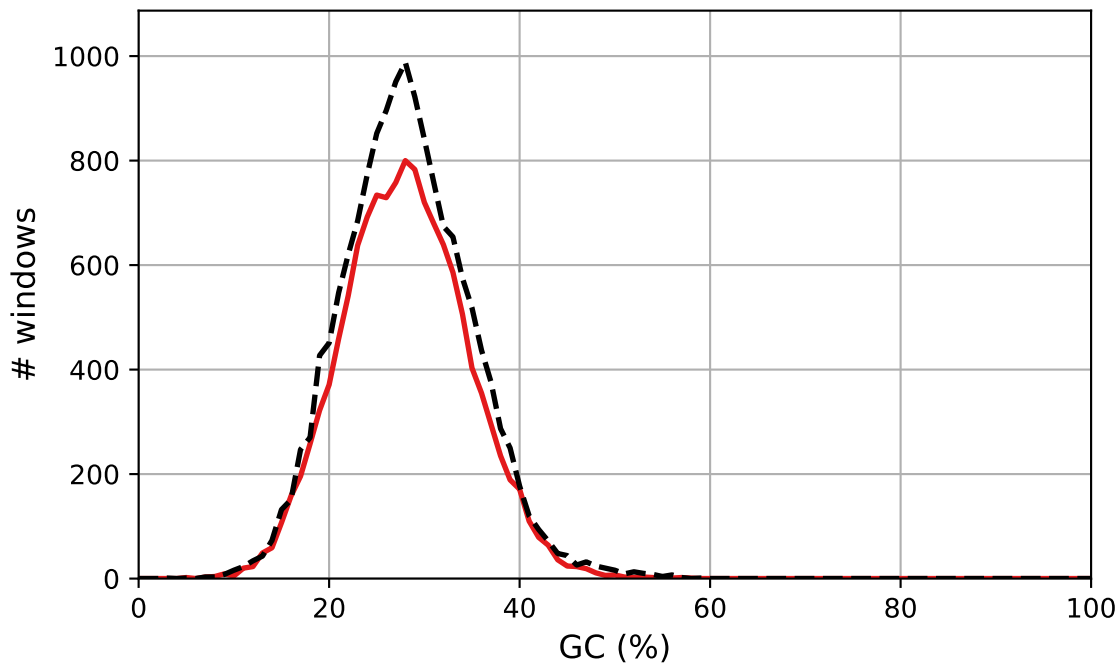
NGx



— GCA\_040790715.1\_ASM4079071v1\_genomic



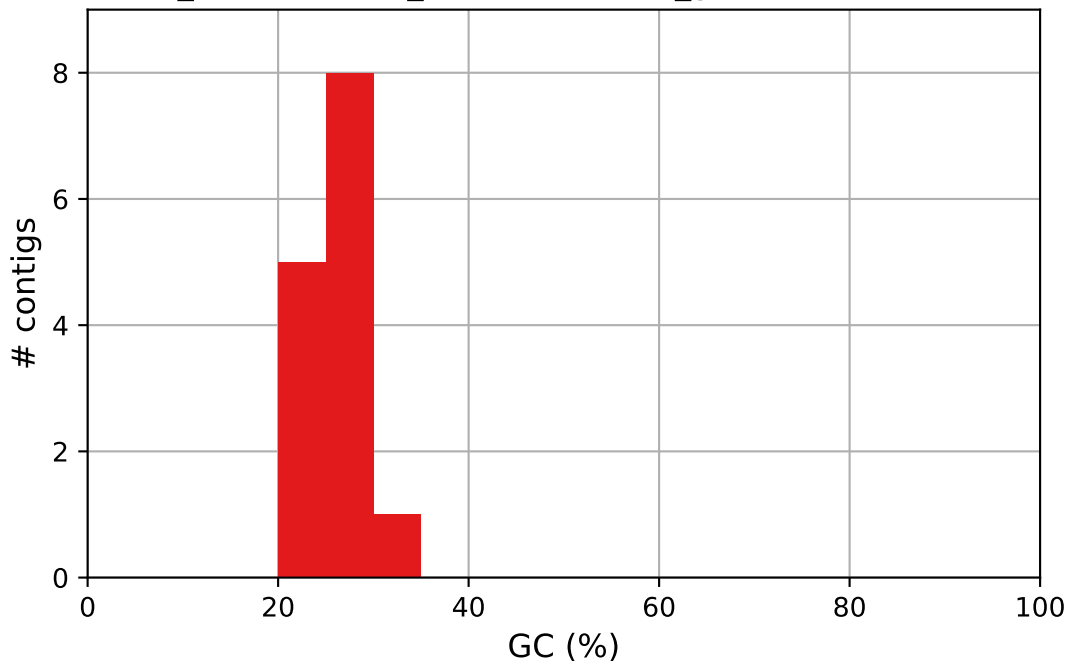
## GC content



GCA\_040790715.1\_ASM4079071v1\_genomic

Reference

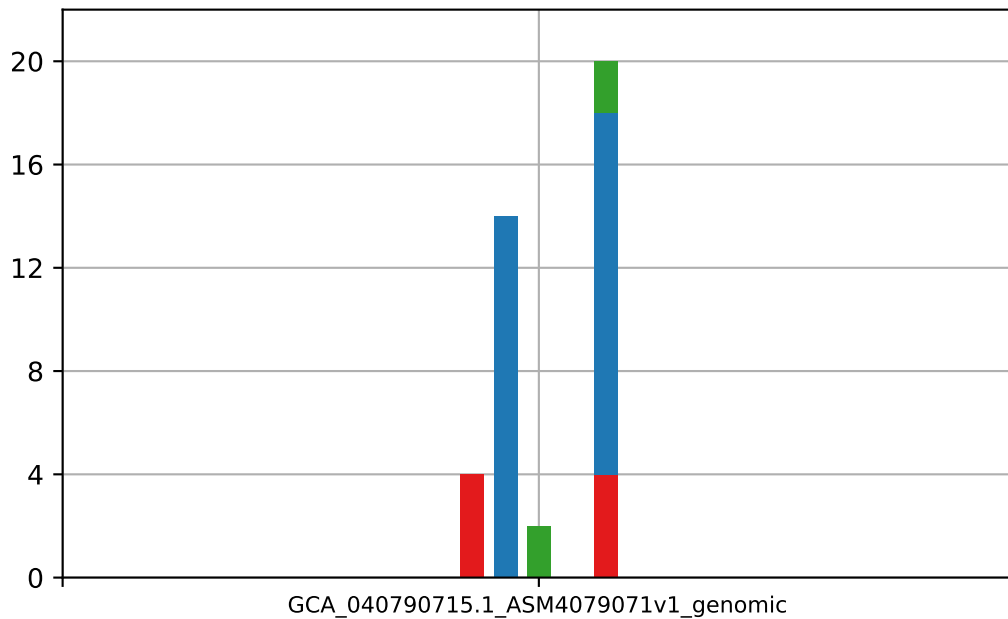
GCA\_040790715.1\_ASM4079071v1\_genomic GC content



GCA\_040790715.1\_ASM4079071v1\_genomic



## Misassemblies



# relocations

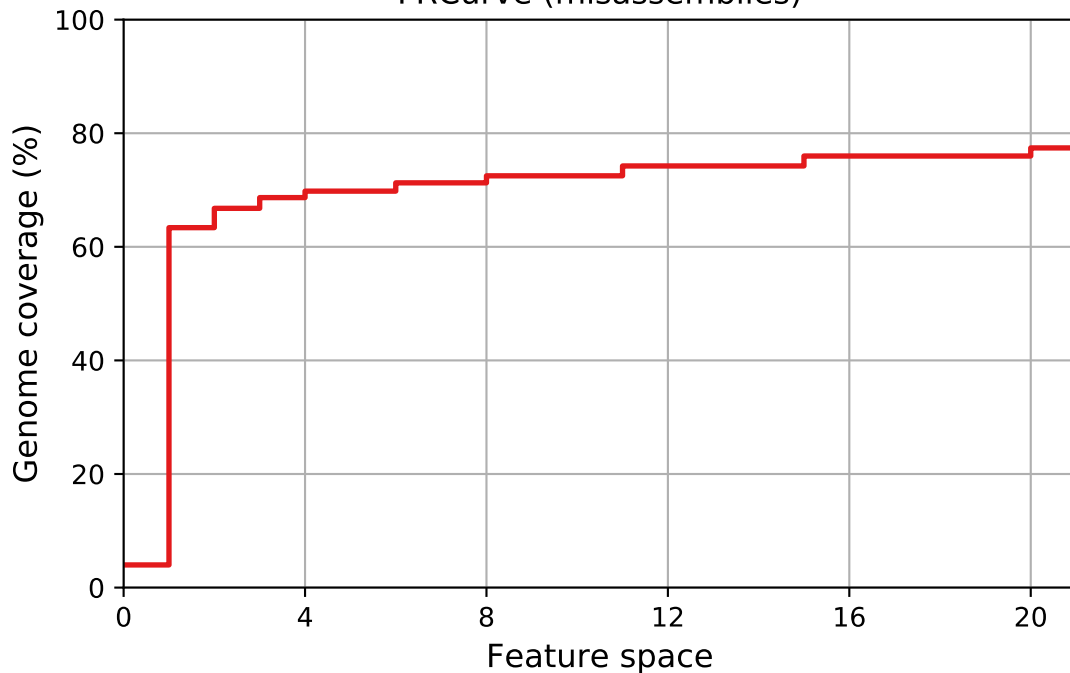


# translocations



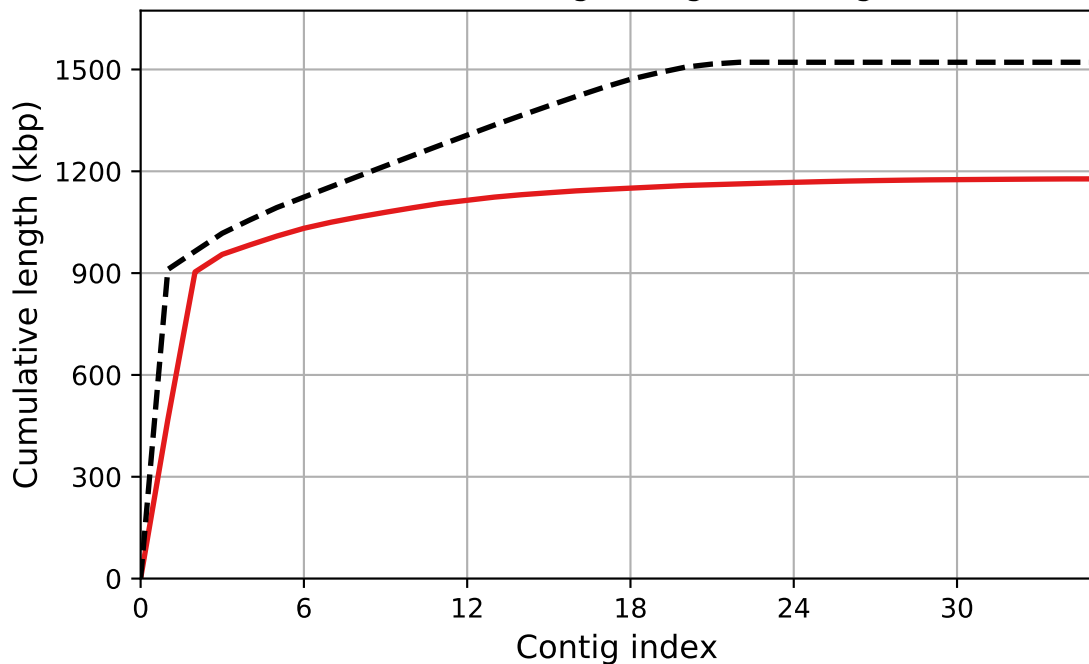
# inversions

FRCurve (misassemblies)



— GCA\_040790715.1\_ASM4079071v1\_genomic

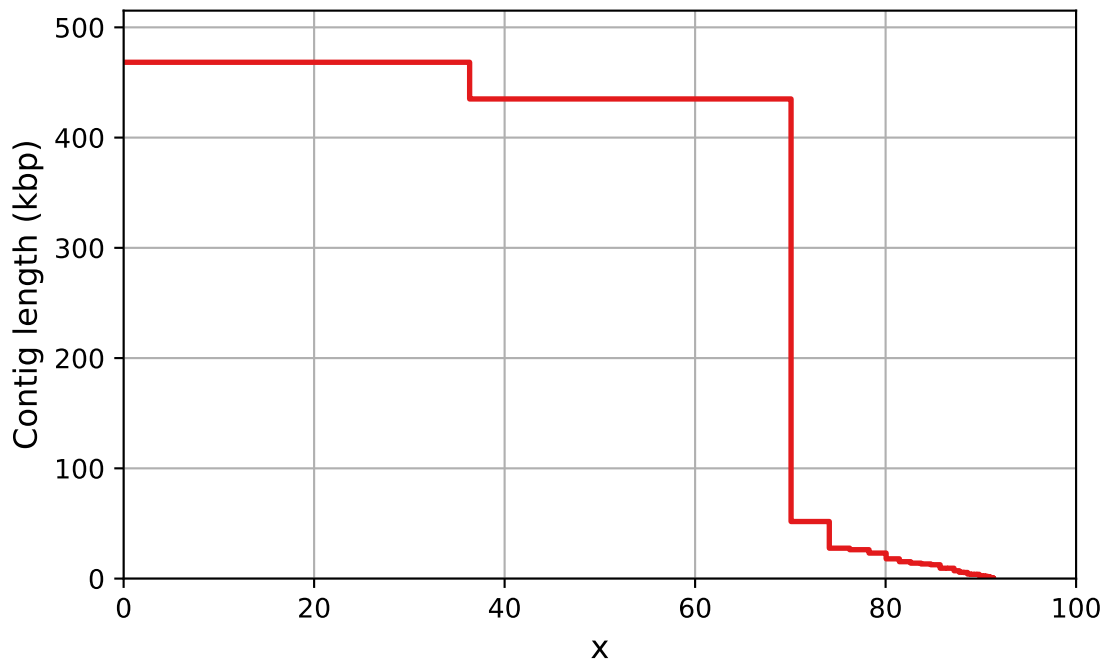
Cumulative length (aligned contigs)



GCA\_040790715.1\_ASM4079071v1\_genomic

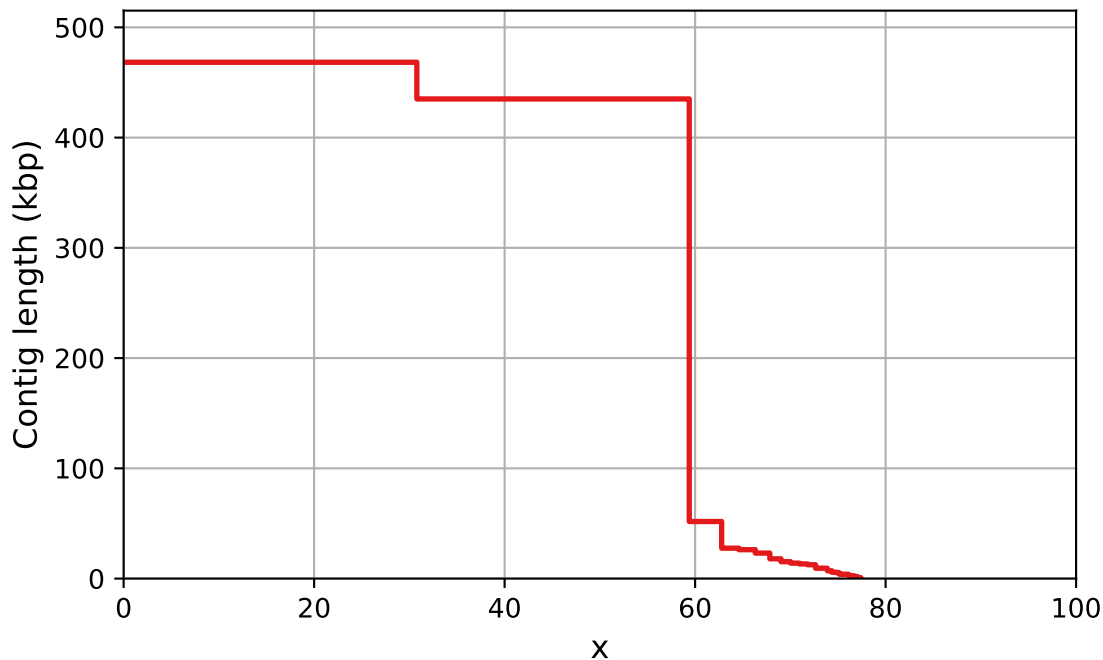
Reference

NAx

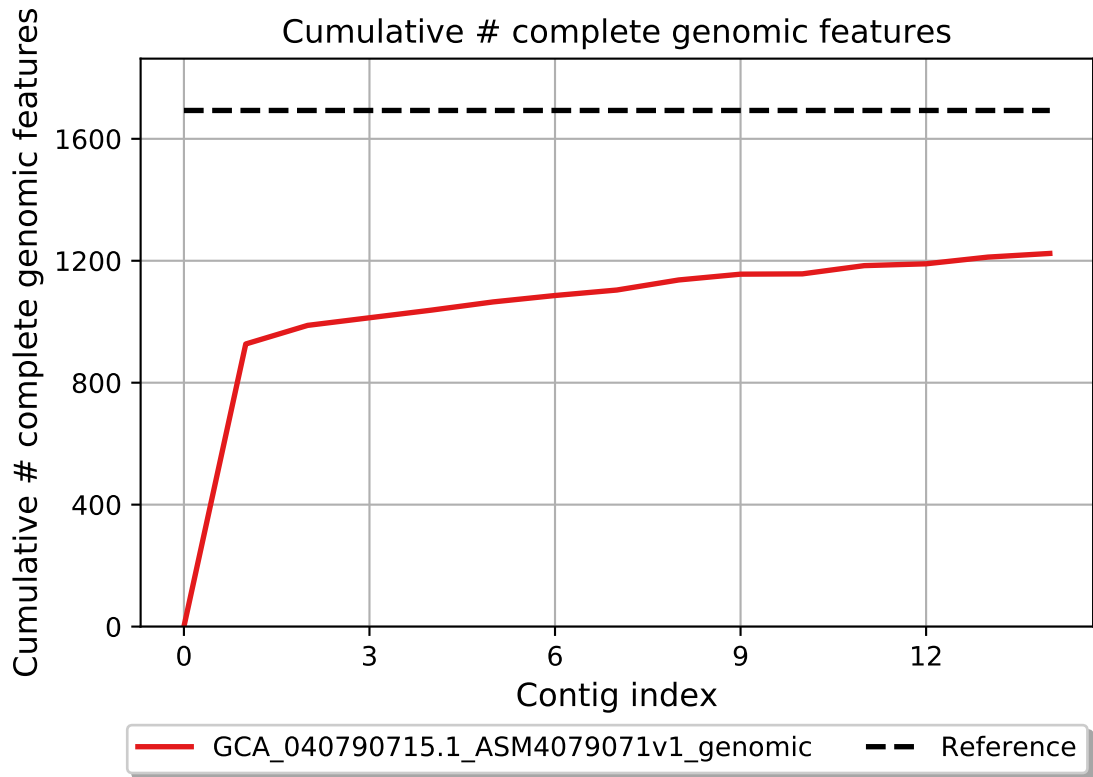


— GCA\_040790715.1\_ASM4079071v1\_genomic

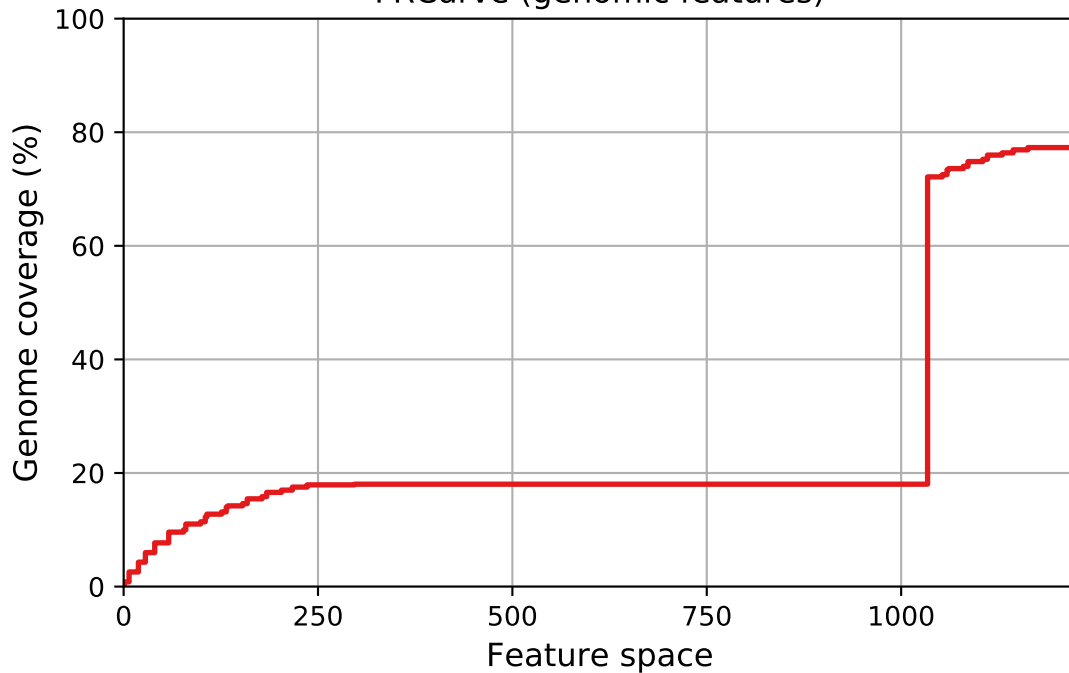
# NGAx



— GCA\_040790715.1\_ASM4079071v1\_genomic



FRCurve (genomic features)



— GCA\_040790715.1\_ASM4079071v1\_genomic