

# Report

GCF_040790795.1_ASM4079079v1_genomic	
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	11
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1325608
Total length (>= 1000 bp)	1325608
Total length (>= 5000 bp)	1325608
Total length (>= 10000 bp)	1325608
Total length (>= 25000 bp)	1226350
Total length (>= 50000 bp)	970623
# contigs	16
Largest contig	916773
Total length	1325608
Reference length	1521208
GC (%)	28.07
Reference GC (%)	28.18
N50	916773
NG50	916773
N90	26512
NG90	-
auN	643292.9
auNG	560577.0
L50	1
LG50	1
L90	10
LG90	-
# misassemblies	15
# misassembled contigs	8
Misassembled contigs length	1131317
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	0 + 14 part
Unaligned length	159830
Genome fraction (%)	76.097
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	684.36
# indels per 100 kbp	44.78
# genomic features	1201 + 34 part
Largest alignment	467363
Total aligned length	1165617
NA50	434879
NGA50	434879
NA90	-
NGA90	-
auNA	311507.1
auNGA	271452.9
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

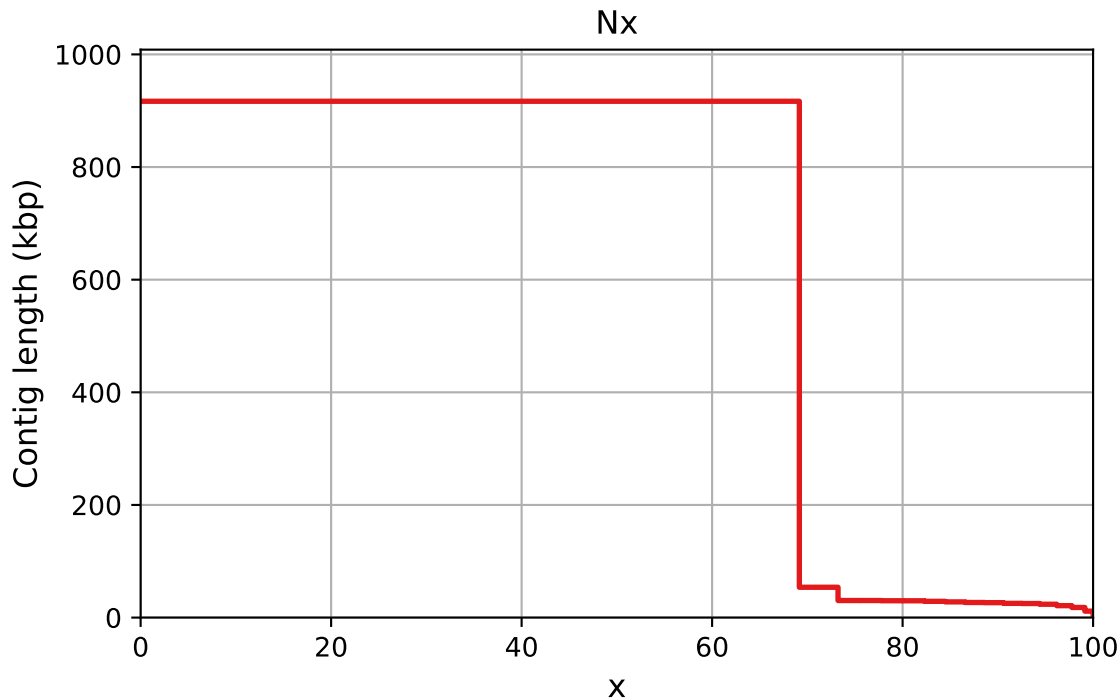
	GCF_040790795.1_ASM4079079v1_genomic
# misassemblies	15
# contig misassemblies	15
# c. relocations	5
# c. translocations	10
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	8
Misassembled contigs length	1131317
# local misassemblies	12
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	7977
# indels	522
# indels (<= 5 bp)	463
# indels (> 5 bp)	59
Indels length	3488

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

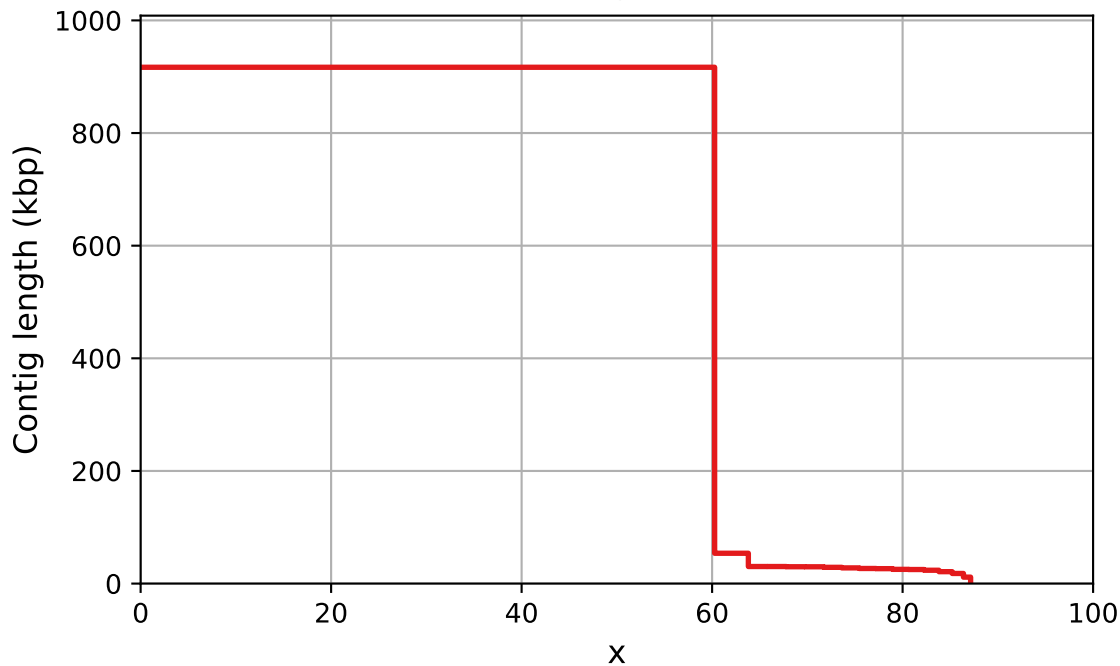
	GCF_040790795.1_ASM4079079v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
Partially unaligned length	159830
# N's	0

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).

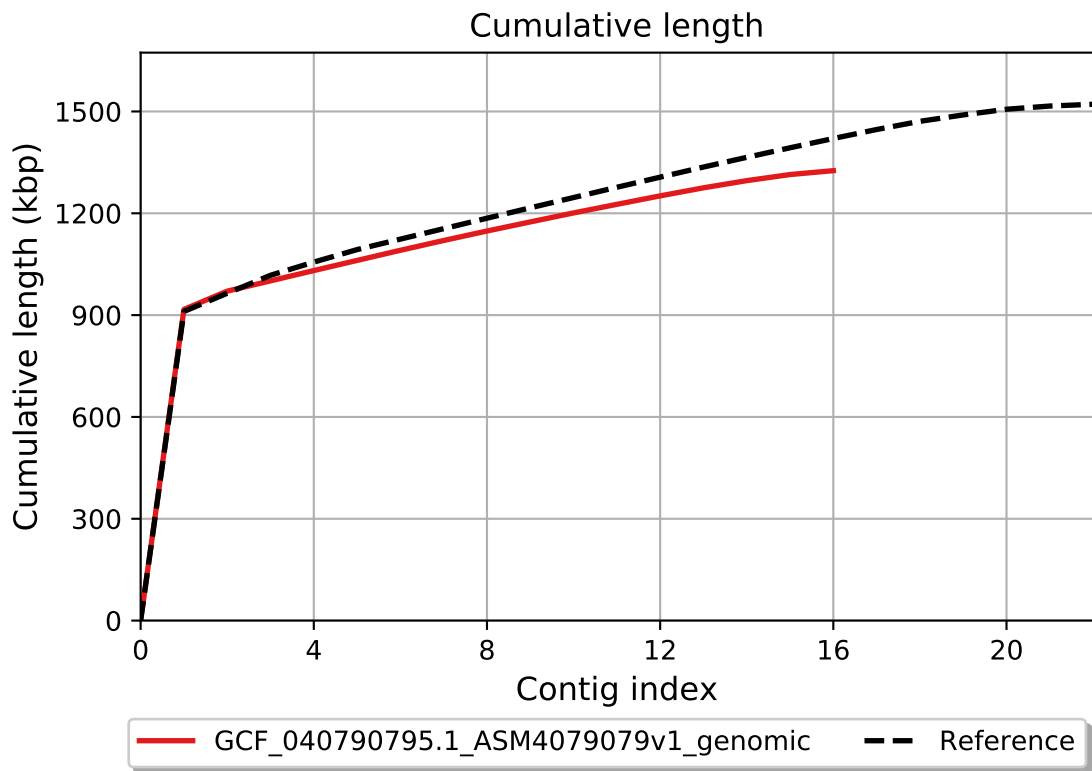


— GCF\_040790795.1\_ASM4079079v1\_genomic

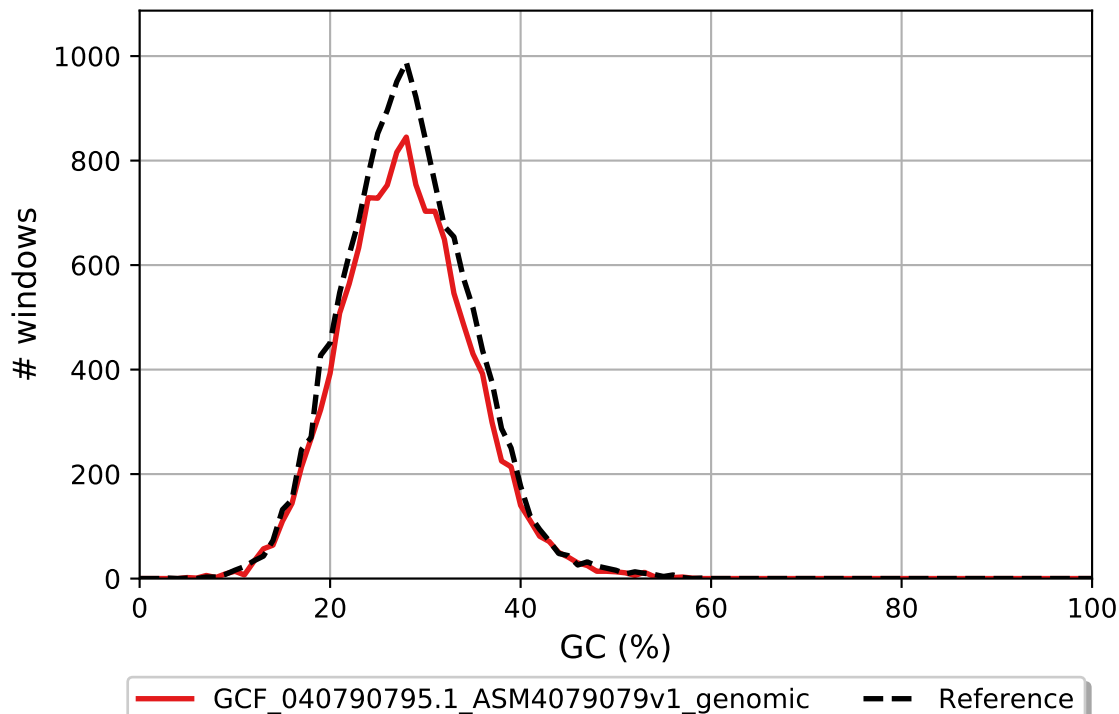
NGx



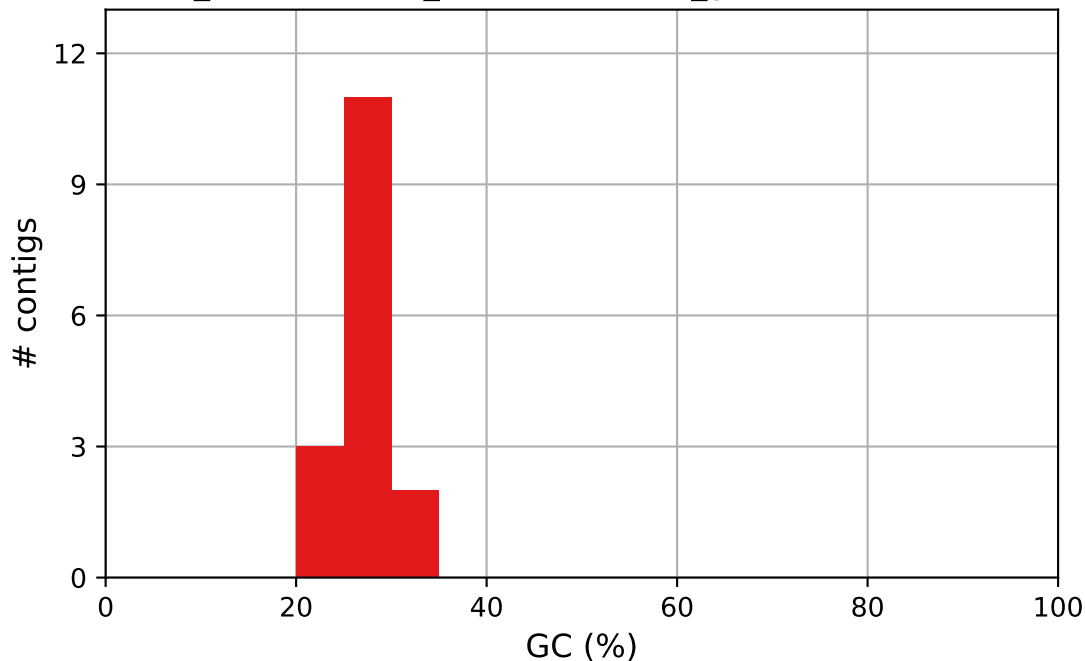
— GCF\_040790795.1\_ASM4079079v1\_genomic



## GC content



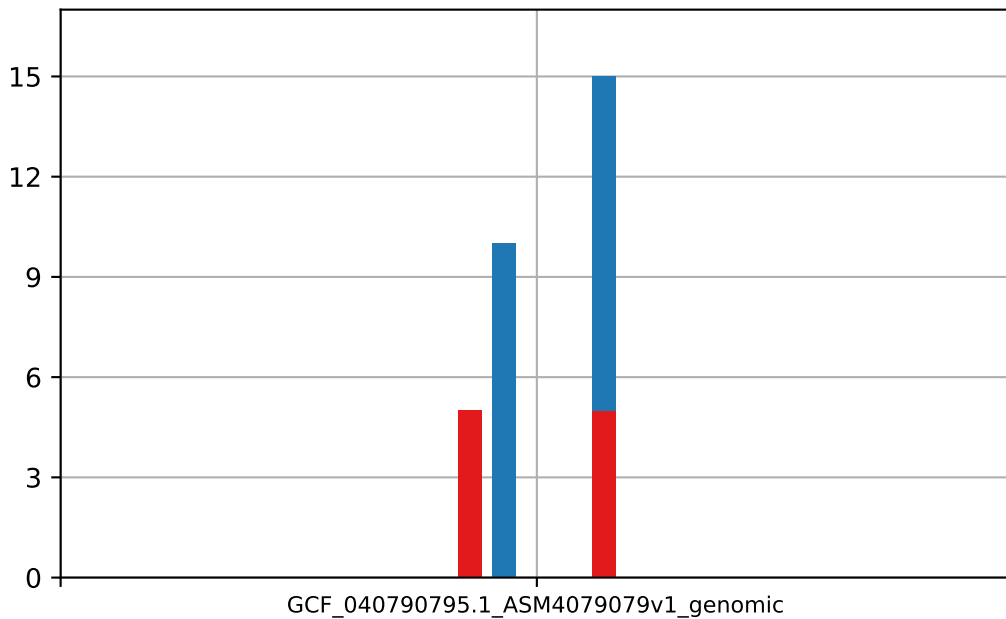
GCF\_040790795.1\_ASM4079079v1\_genomic GC content



■ GCF\_040790795.1\_ASM4079079v1\_genomic



## Misassemblies

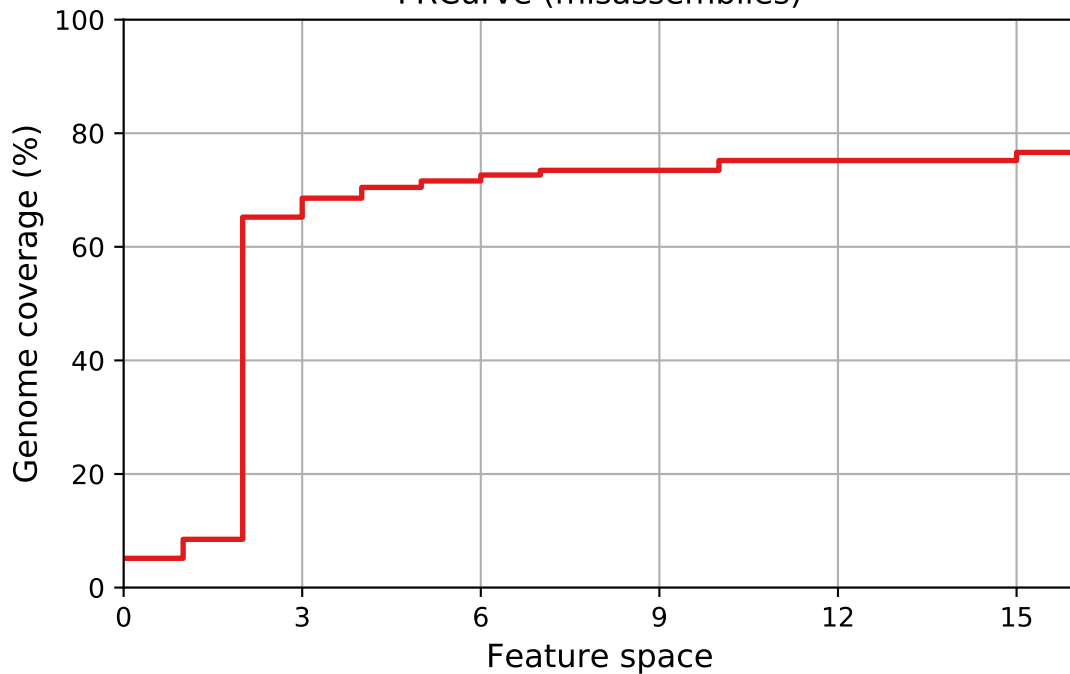


# relocations



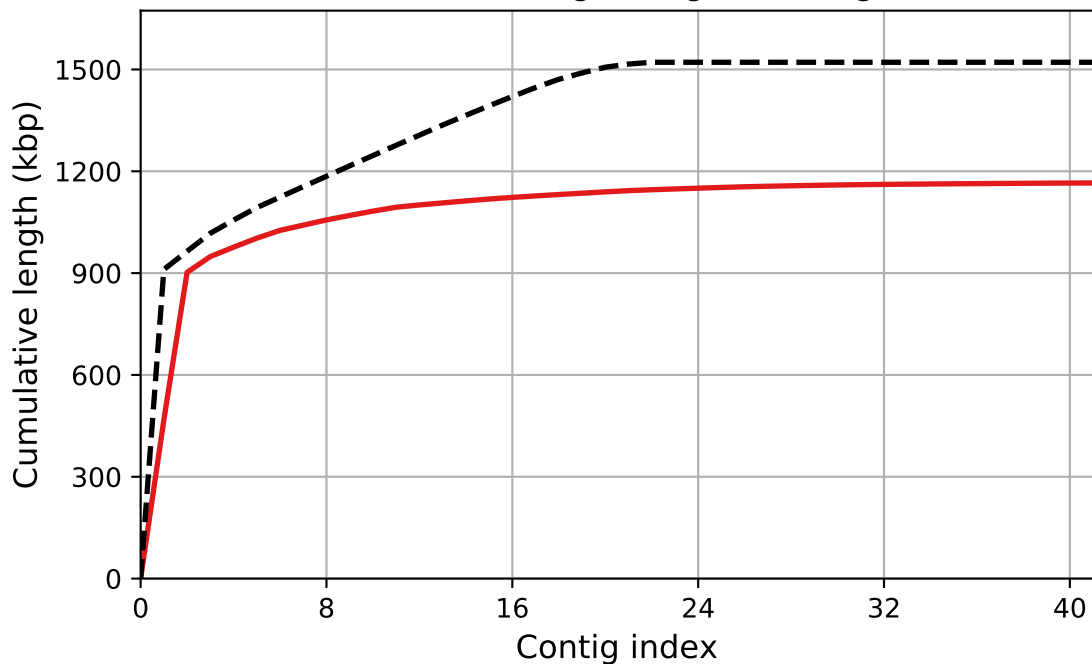
# translocations

FRCurve (misassemblies)



— GCF\_040790795.1\_ASM4079079v1\_genomic

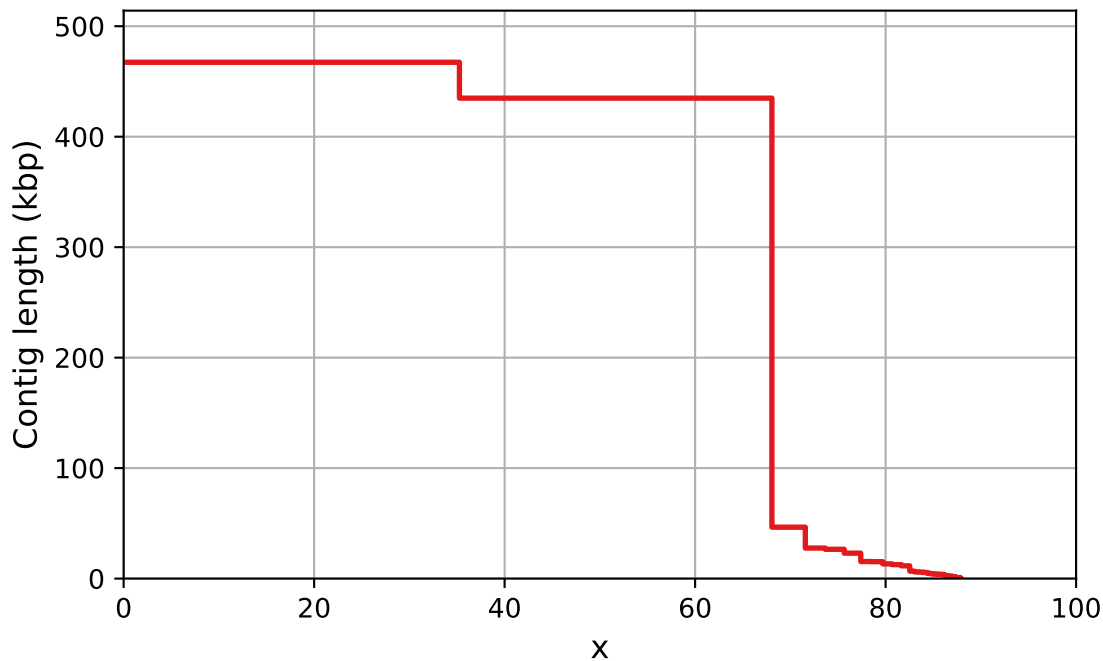
Cumulative length (aligned contigs)



GCF\_040790795.1\_ASM4079079v1\_genomic

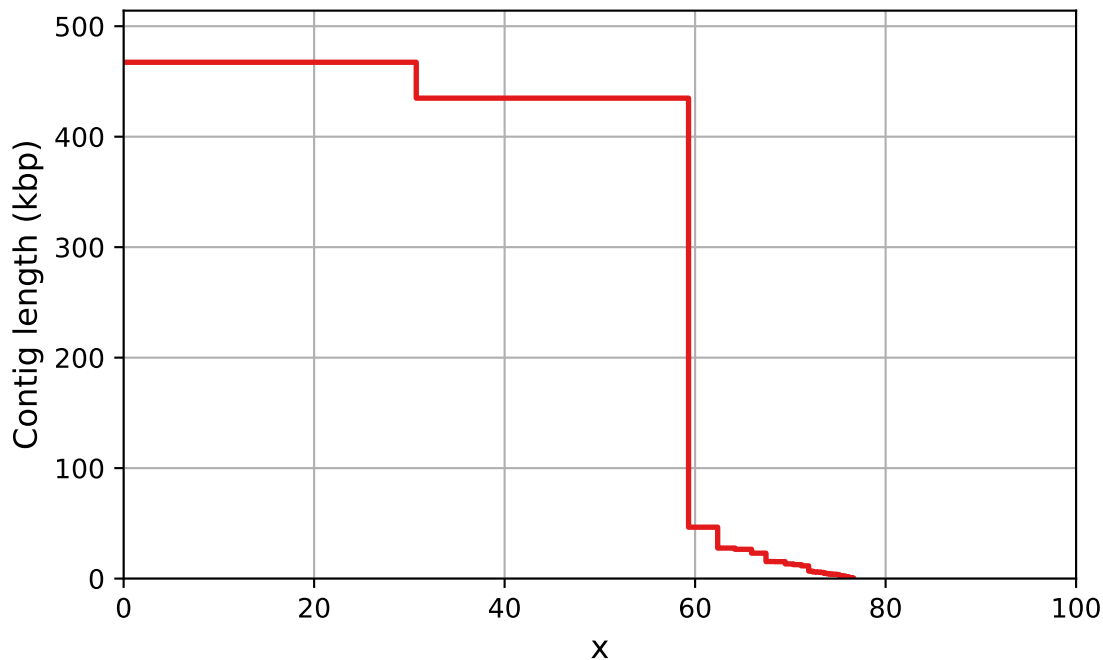
Reference

NAx

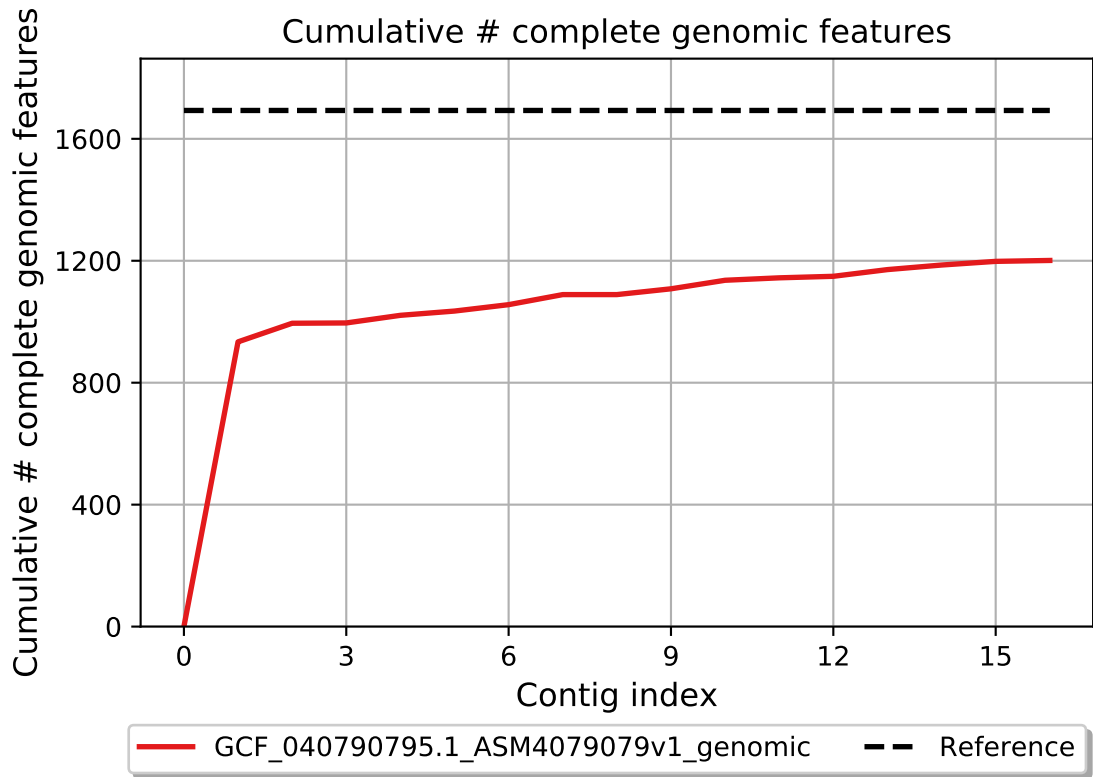


— GCF\_040790795.1\_ASM4079079v1\_genomic

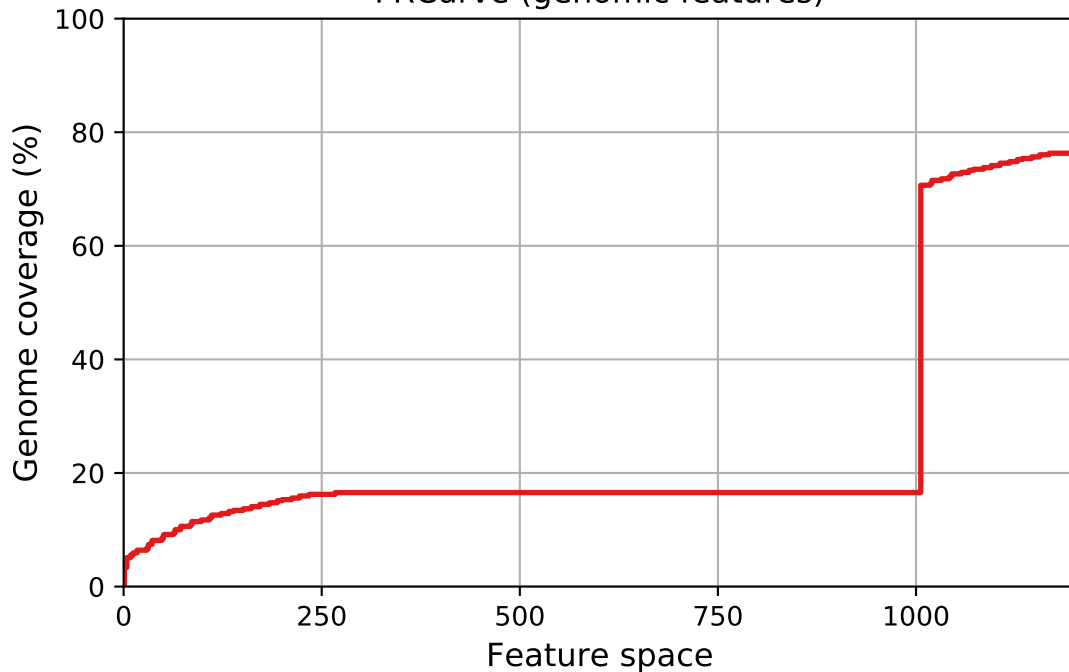
# NGAx



— GCF\_040790795.1\_ASM4079079v1\_genomic



FRCurve (genomic features)



— GCF\_040790795.1\_ASM4079079v1\_genomic