

Report

	GCF_000172295.2_ASM17229v2_genomic
# contigs (>= 0 bp)	53
# contigs (>= 1000 bp)	51
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	39
# contigs (>= 25000 bp)	24
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	1344204
Total length (>= 1000 bp)	1342458
Total length (>= 5000 bp)	1330101
Total length (>= 10000 bp)	1285483
Total length (>= 25000 bp)	1027057
Total length (>= 50000 bp)	463943
# contigs	53
Largest contig	88934
Total length	1344204
Reference length	1521208
GC (%)	28.32
Reference GC (%)	28.18
N50	35743
NG50	31052
N90	15963
NG90	-
auN	41660.0
auNG	36812.5
L50	13
LG50	15
L90	34
LG90	-
# misassemblies	9
# misassembled contigs	6
Misassembled contigs length	197042
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	2 + 9 part
Unaligned length	133787
Genome fraction (%)	77.523
Duplication ratio	1.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	850.71
# indels per 100 kbp	63.80
# genomic features	1186 + 74 part
Largest alignment	88929
Total aligned length	1210051
NA50	35743
NGA50	25206
NA90	444
NGA90	-
auNA	36637.8
auNGA	32374.7
LA50	13
LGA50	16
LA90	62
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_000172295.2_ASM17229v2_genomic
# misassemblies	9
# contig misassemblies	9
# c. relocations	3
# c. translocations	6
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	197042
# local misassemblies	5
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	10294
# indels	772
# indels (<= 5 bp)	682
# indels (> 5 bp)	90
Indels length	2997

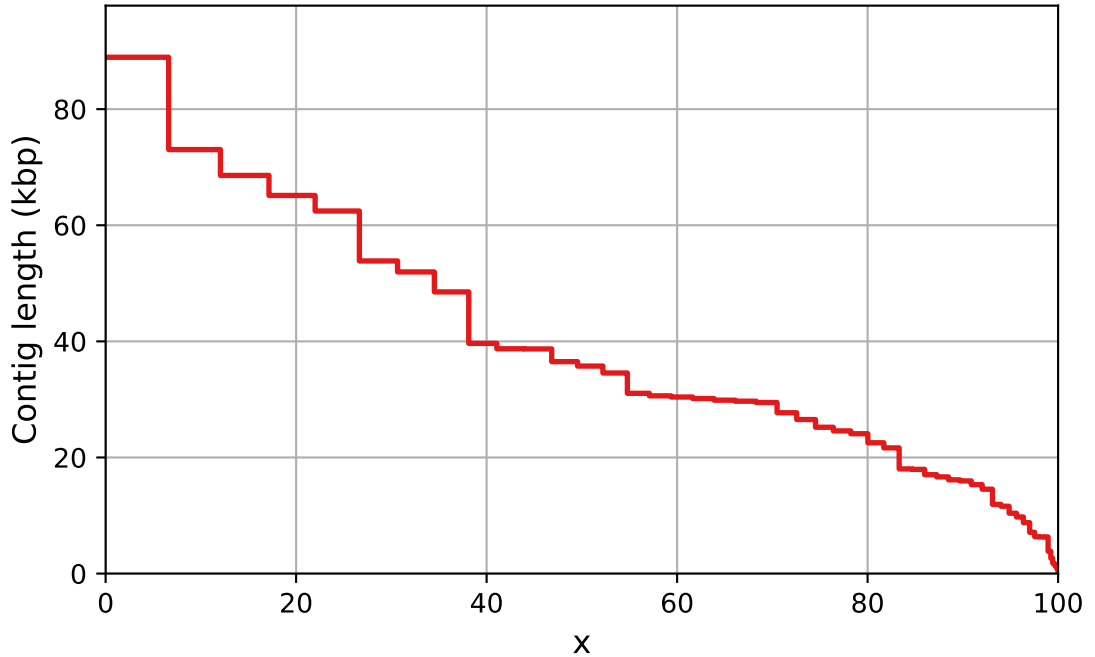
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	GCF_000172295.2_ASM17229v2_genomic
# fully unaligned contigs	2
Fully unaligned length	62255
# partially unaligned contigs	9
Partially unaligned length	71532
# N's	0

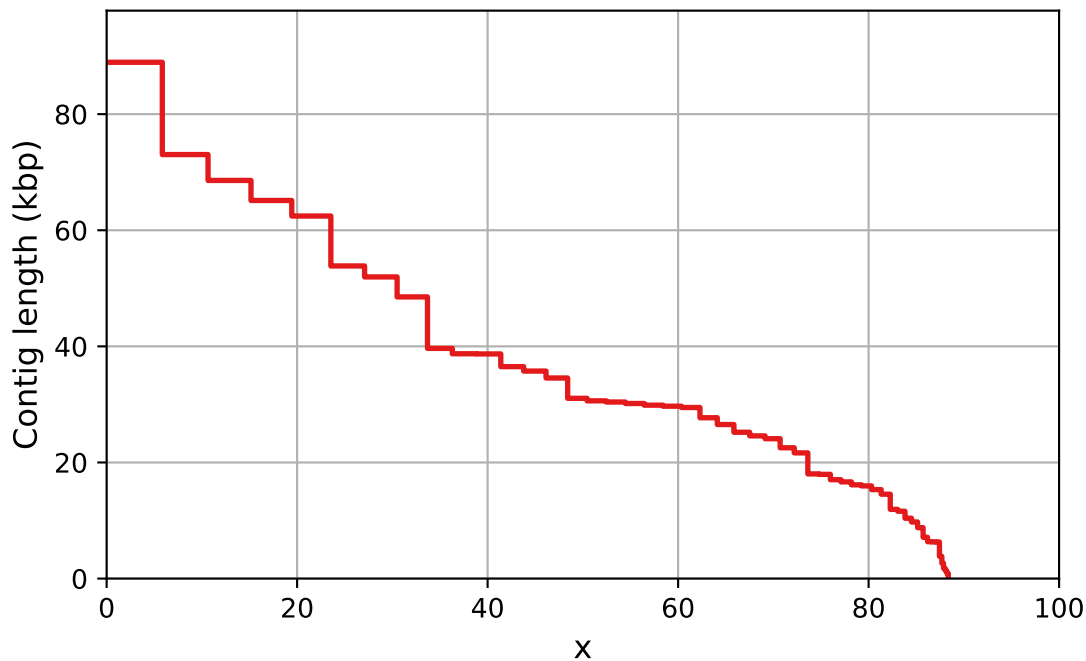
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

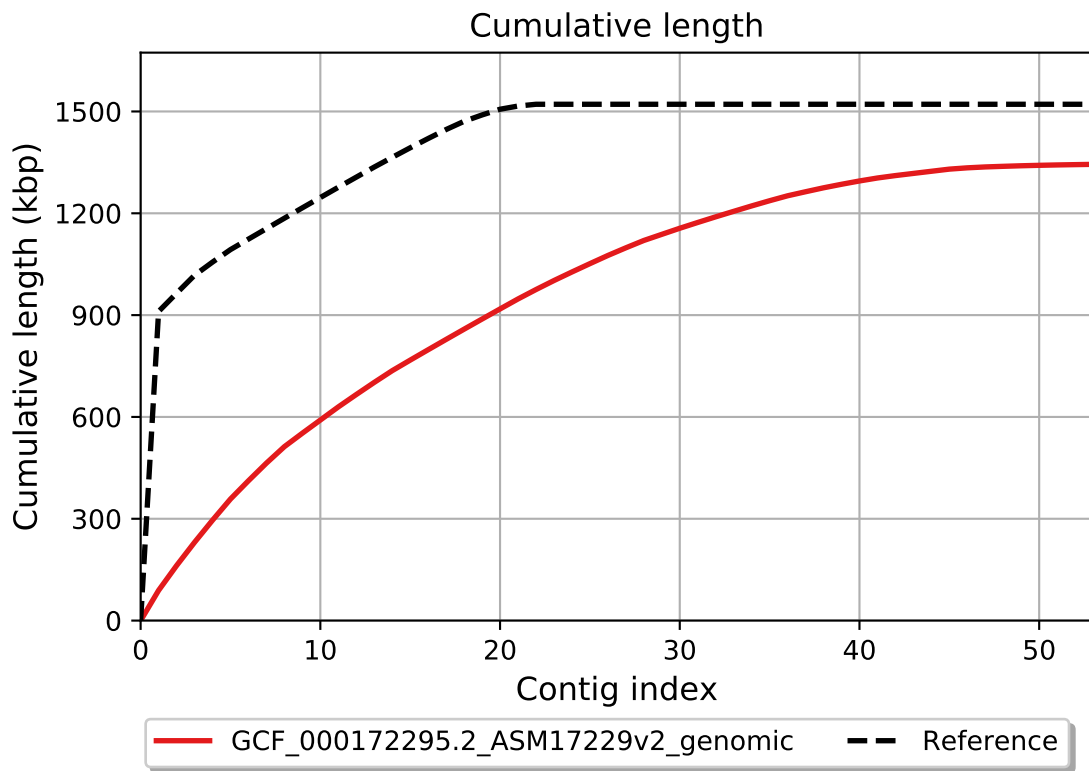


GCF\_000172295.2\_ASM17229v2\_genomic

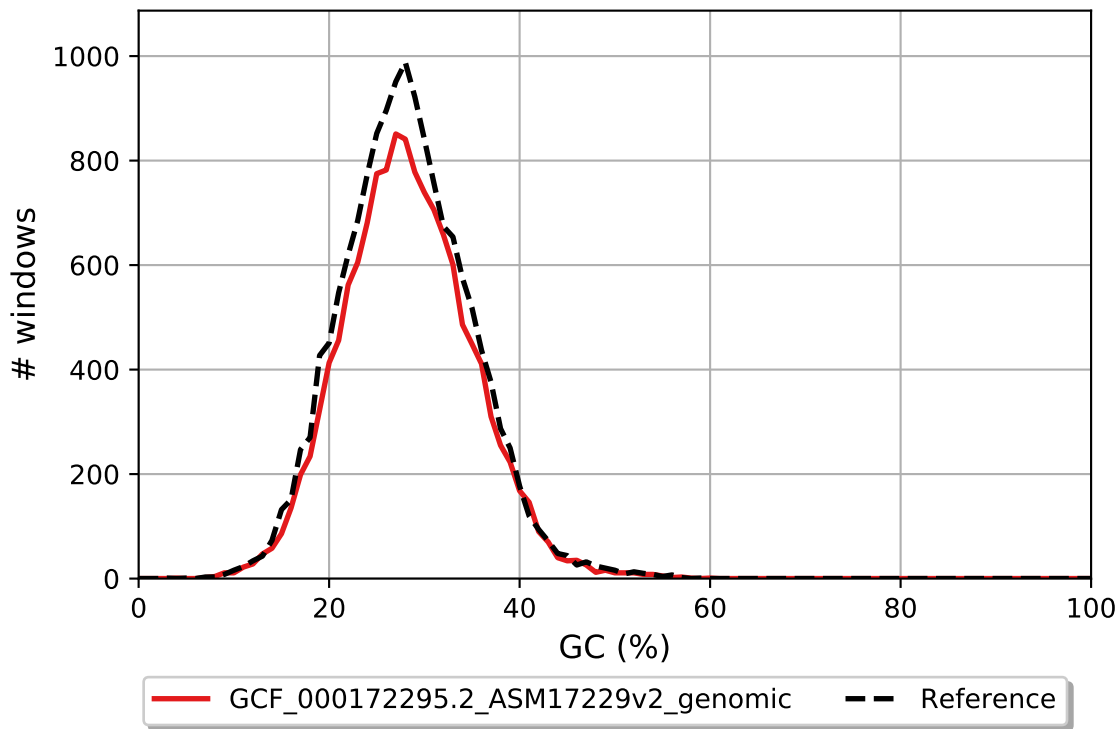
# NGx



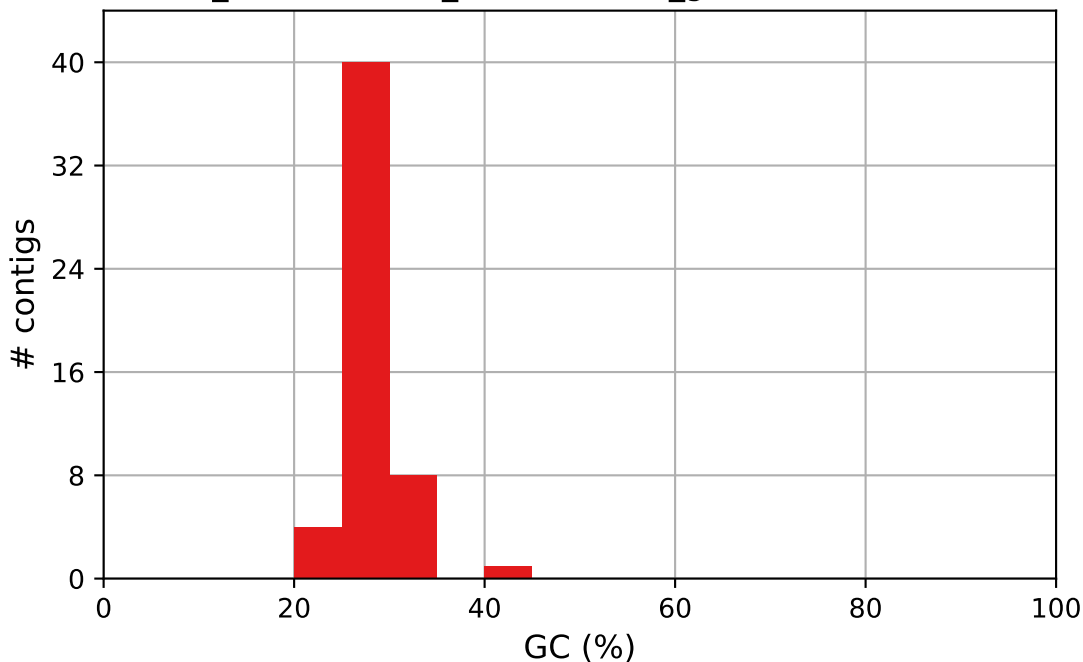
— GCF\_000172295.2\_ASM17229v2\_genomic



## GC content



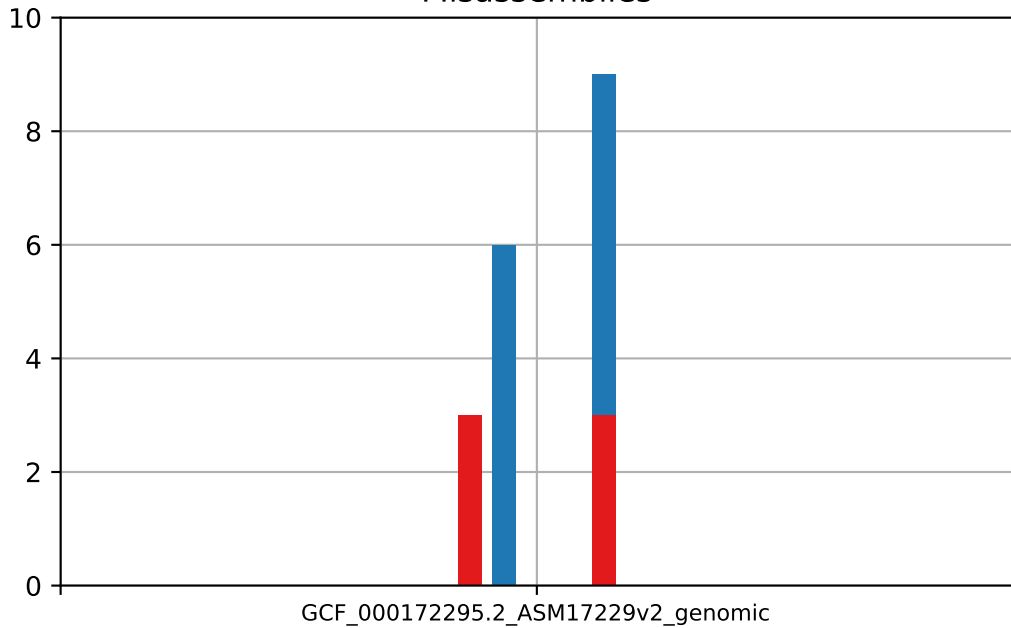
GCF\_000172295.2\_ASM17229v2\_genomic GC content



GCF\_000172295.2\_ASM17229v2\_genomic



## Misassemblies

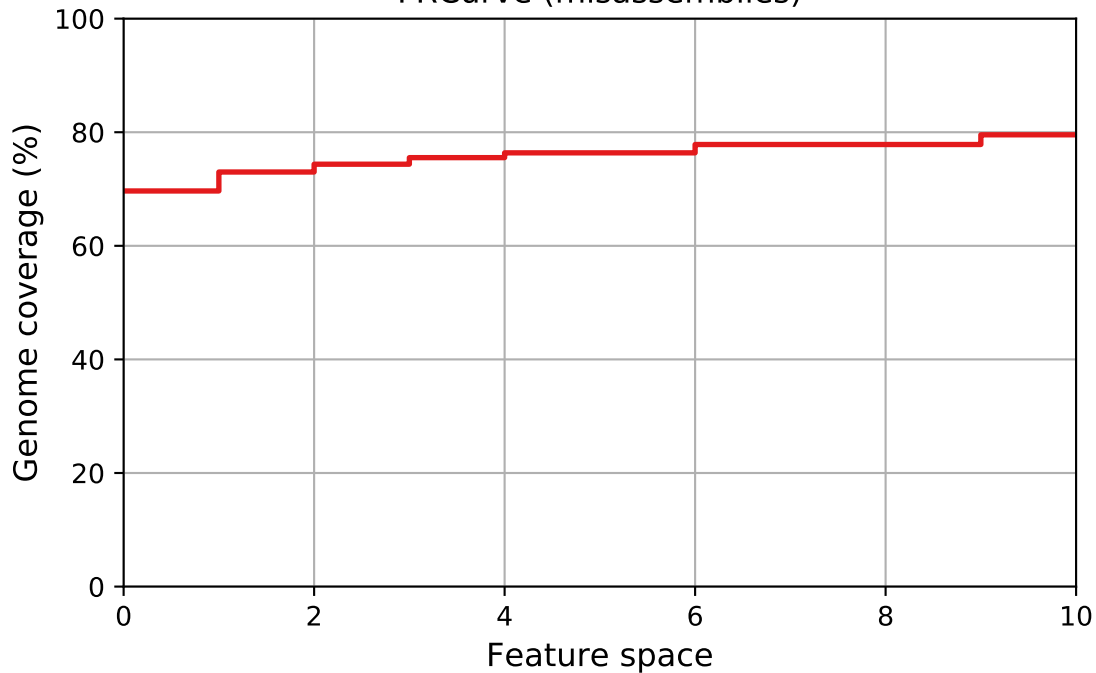


# relocations



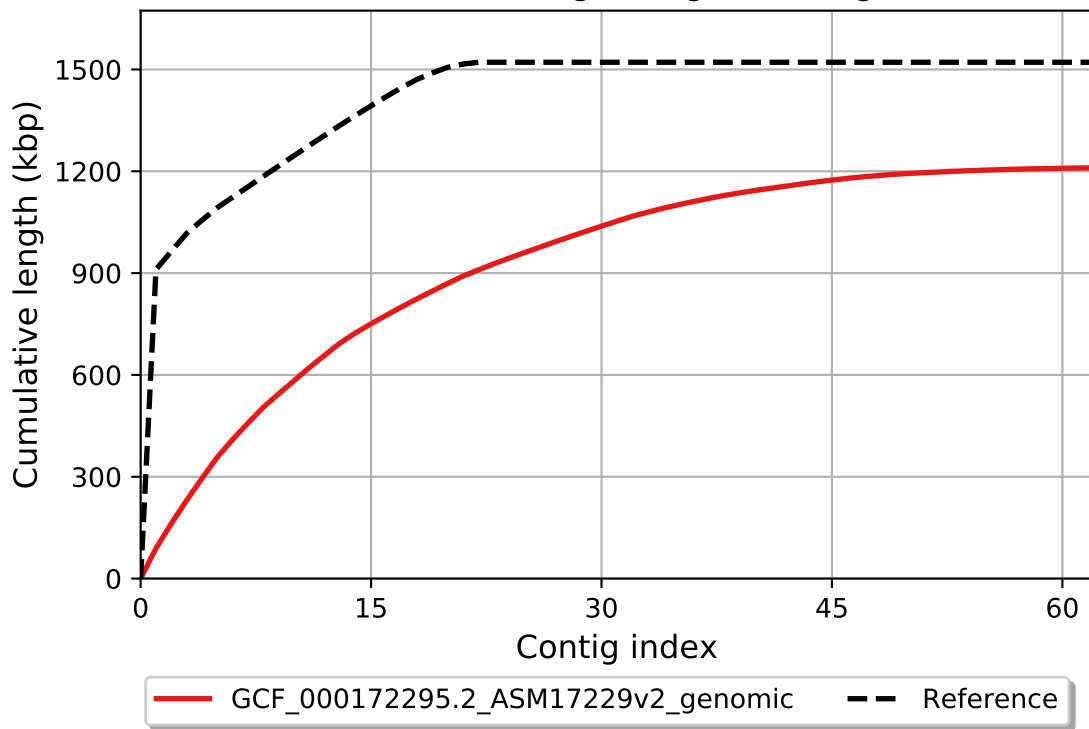
# translocations

FRCurve (misassemblies)

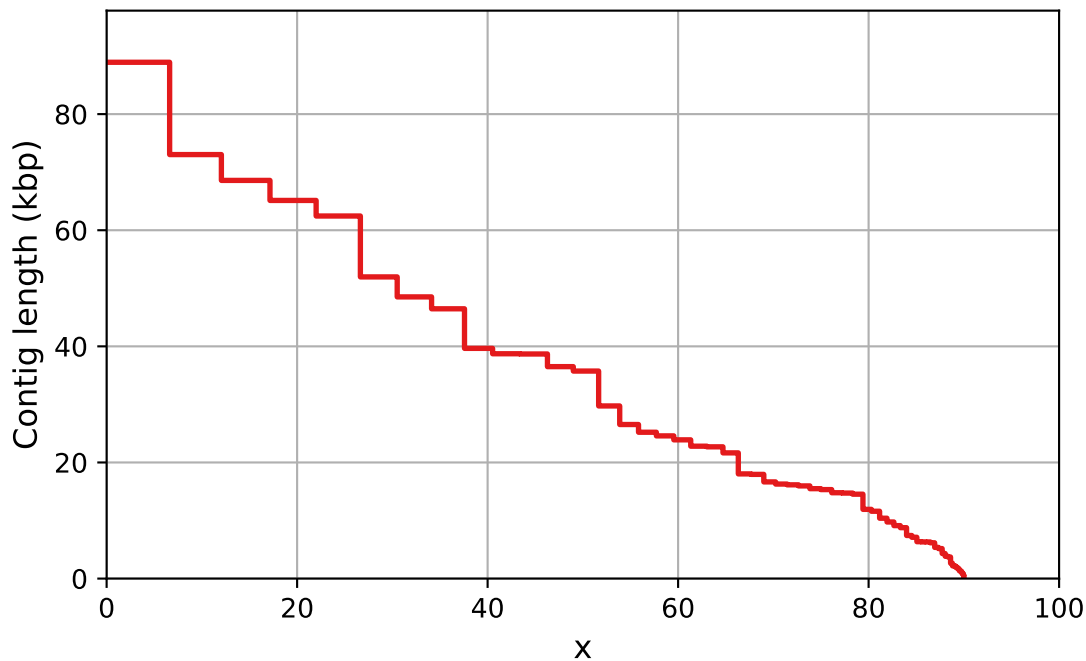


— GCF\_000172295.2\_ASM17229v2\_genomic

Cumulative length (aligned contigs)

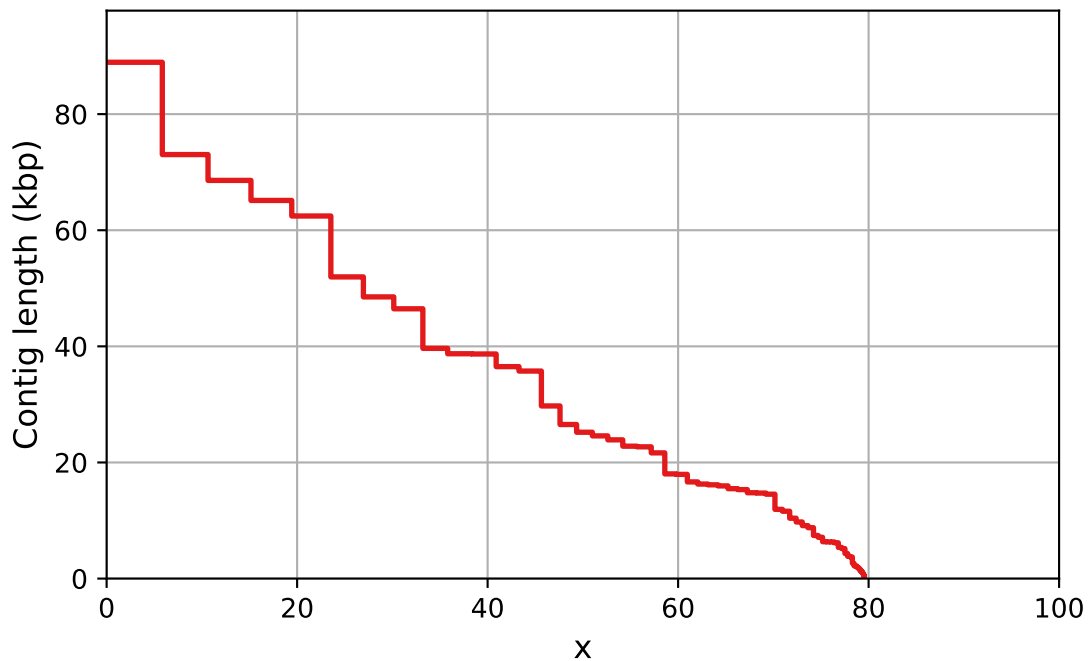


NAx



— GCF\_000172295.2\_ASM17229v2\_genomic

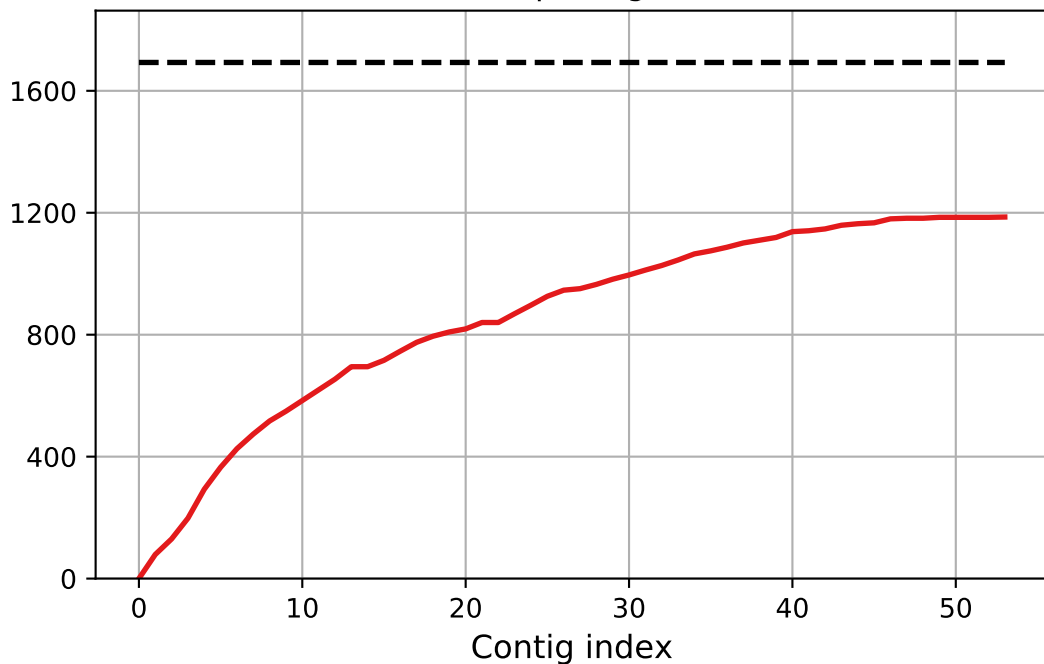
# NGAx



— GCF\_000172295.2\_ASM17229v2\_genomic

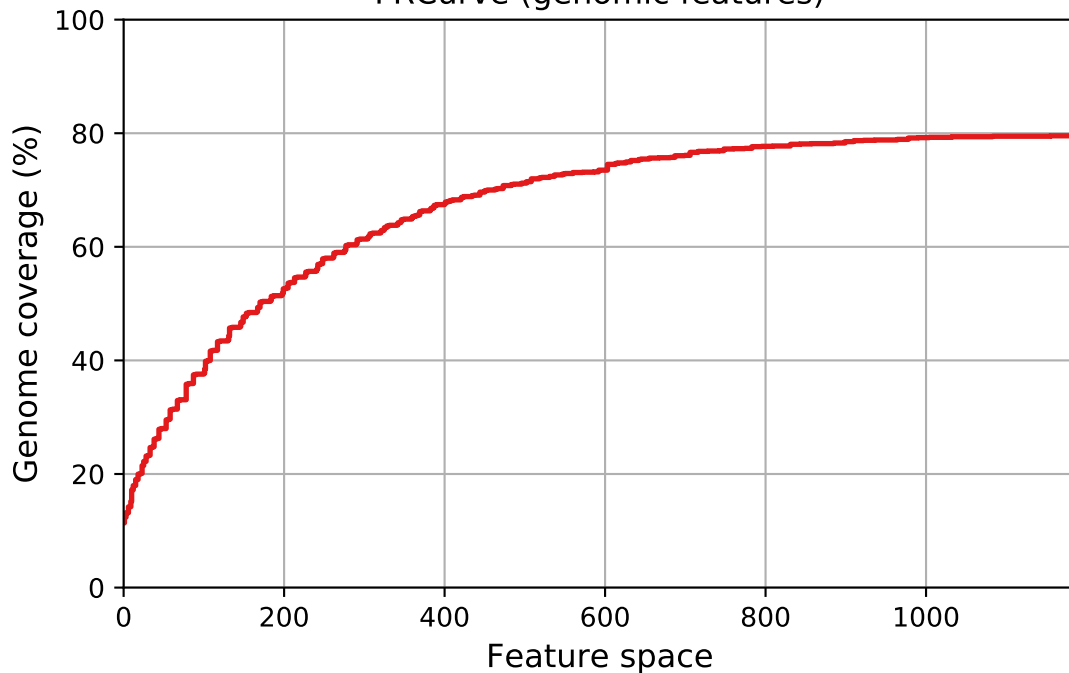
Cumulative # complete genomic features

Cumulative # complete genomic features



GCF\_000172295.2\_ASM17229v2\_genomic      Reference

FRCurve (genomic features)



— GCF\_000172295.2\_ASM17229v2\_genomic