

# Report

GCF_000172315.2_ASM17231v2_genomic	
# contigs (>= 0 bp)	26
# contigs (>= 1000 bp)	26
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	20
# contigs (>= 50000 bp)	9
Total length (>= 0 bp)	1294354
Total length (>= 1000 bp)	1294354
Total length (>= 5000 bp)	1286504
Total length (>= 10000 bp)	1286504
Total length (>= 25000 bp)	1268323
Total length (>= 50000 bp)	953321
# contigs	26
Largest contig	209169
Total length	1294354
Reference length	1521208
GC (%)	28.35
Reference GC (%)	28.18
N50	83077
NG50	59106
N90	27775
NG90	-
auN	110279.2
auNG	93833.6
L50	5
LG50	6
L90	17
LG90	-
# misassemblies	9
# misassembled contigs	2
Misassembled contigs length	84535
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 10 part
Unaligned length	155281
Genome fraction (%)	74.432
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	697.00
# indels per 100 kbp	38.81
# genomic features	1159 + 48 part
Largest alignment	209169
Total aligned length	1138880
NA50	83077
NGA50	59106
NA90	-
NGA90	-
auNA	103956.8
auNGA	88454.0
LA50	5
LGA50	6
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

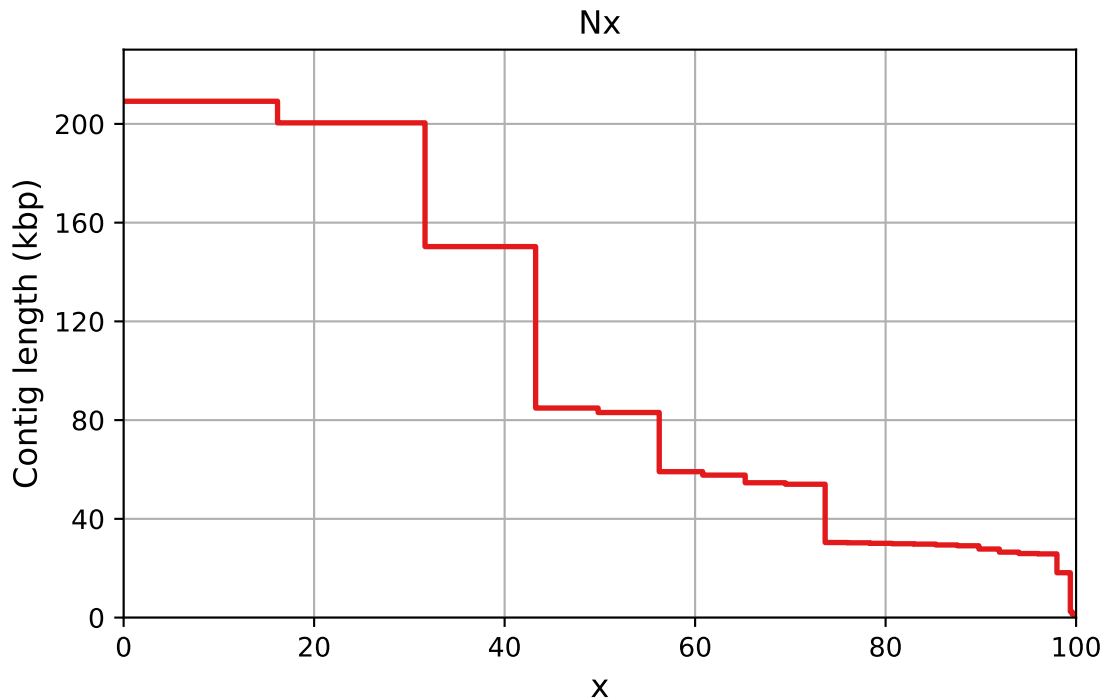
	GCF_000172315.2_ASM17231v2_genomic
# misassemblies	9
# contig misassemblies	9
# c. relocations	1
# c. translocations	8
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	2
Misassembled contigs length	84535
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	2
# mismatches	7938
# indels	442
# indels (<= 5 bp)	413
# indels (> 5 bp)	29
Indels length	1405

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

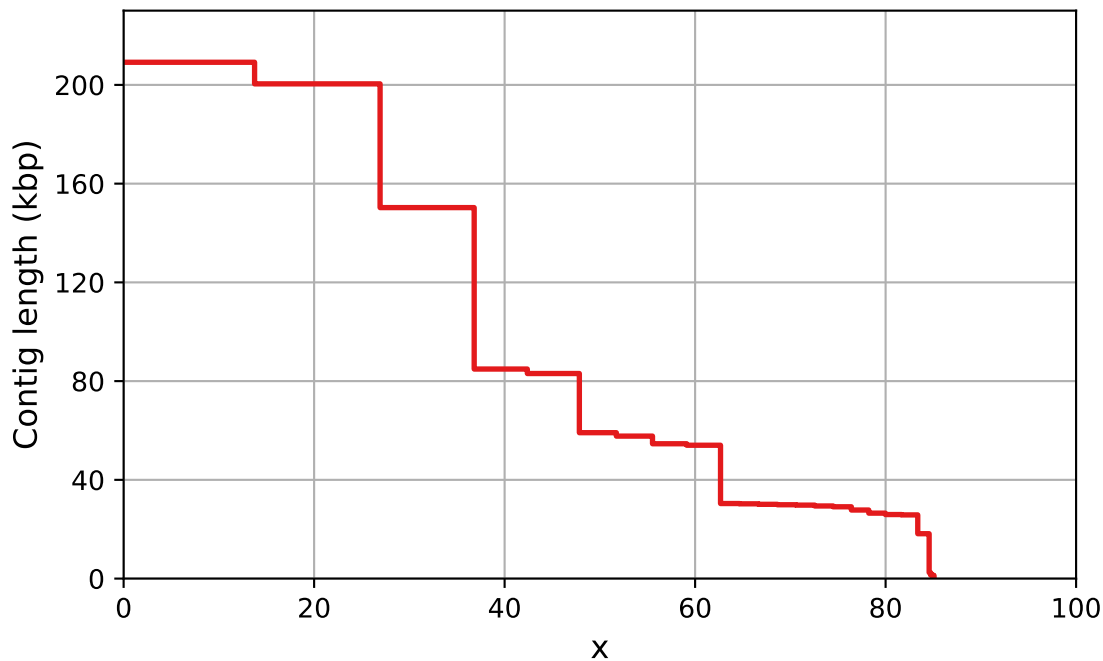
	GCF_000172315.2_ASM17231v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	10
Partially unaligned length	155281
# N's	0

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).



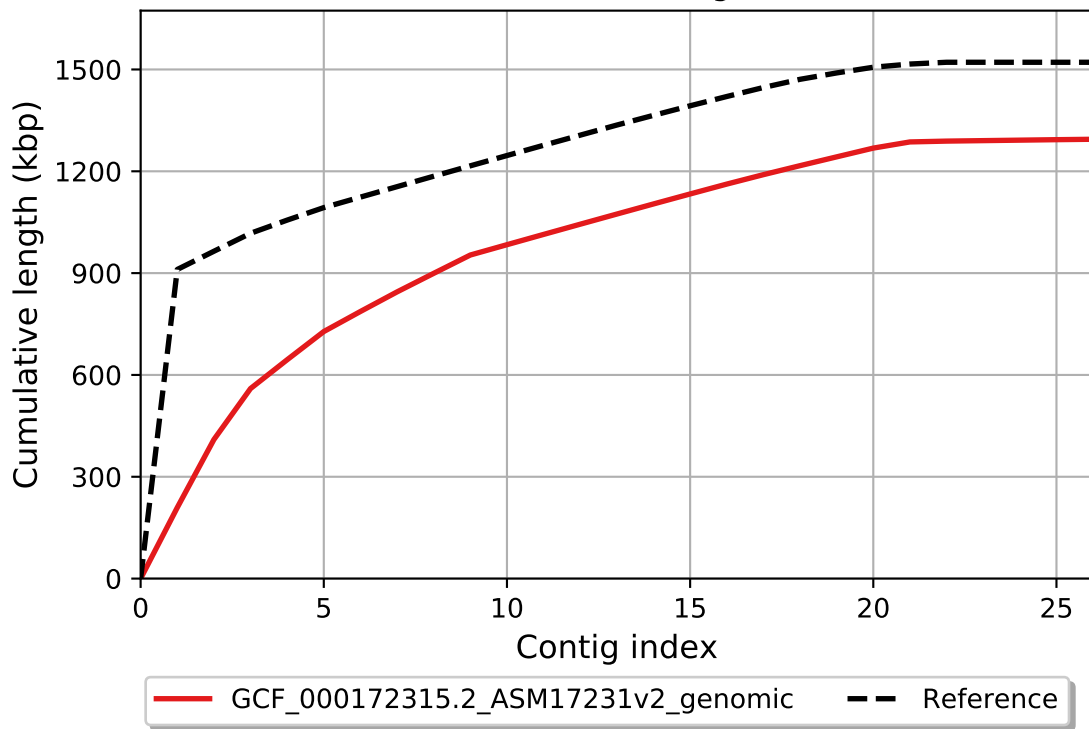
— GCF\_000172315.2\_ASM17231v2\_genomic

NGx

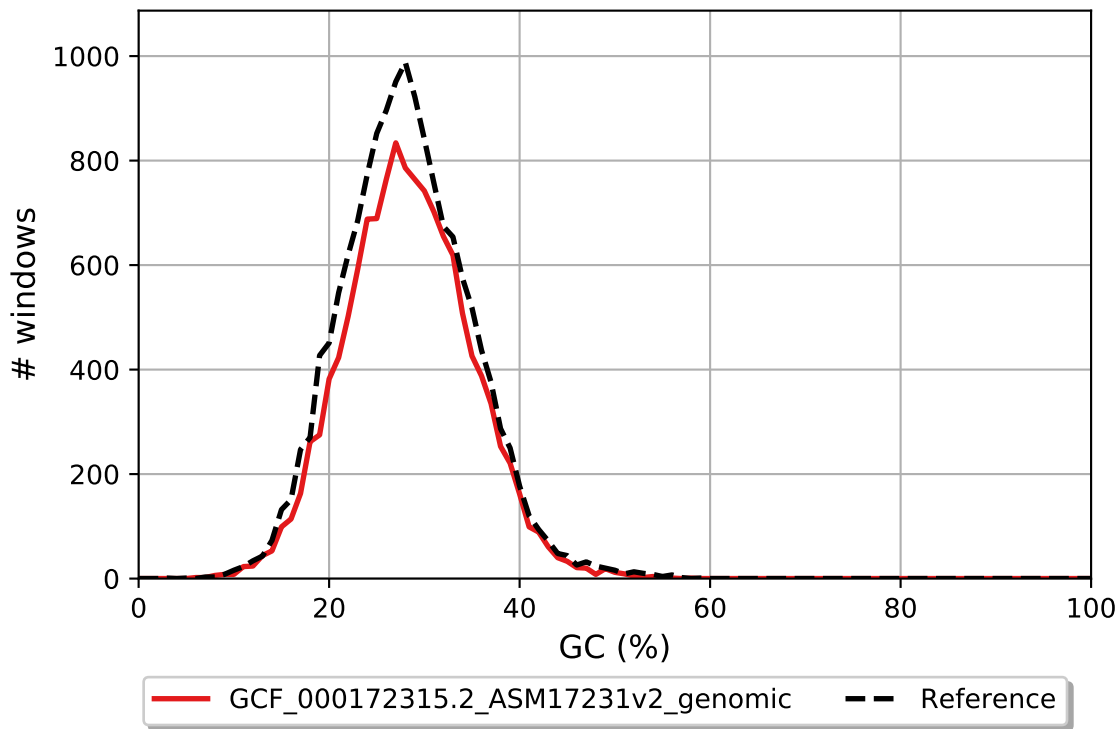


— GCF\_000172315.2\_ASM17231v2\_genomic

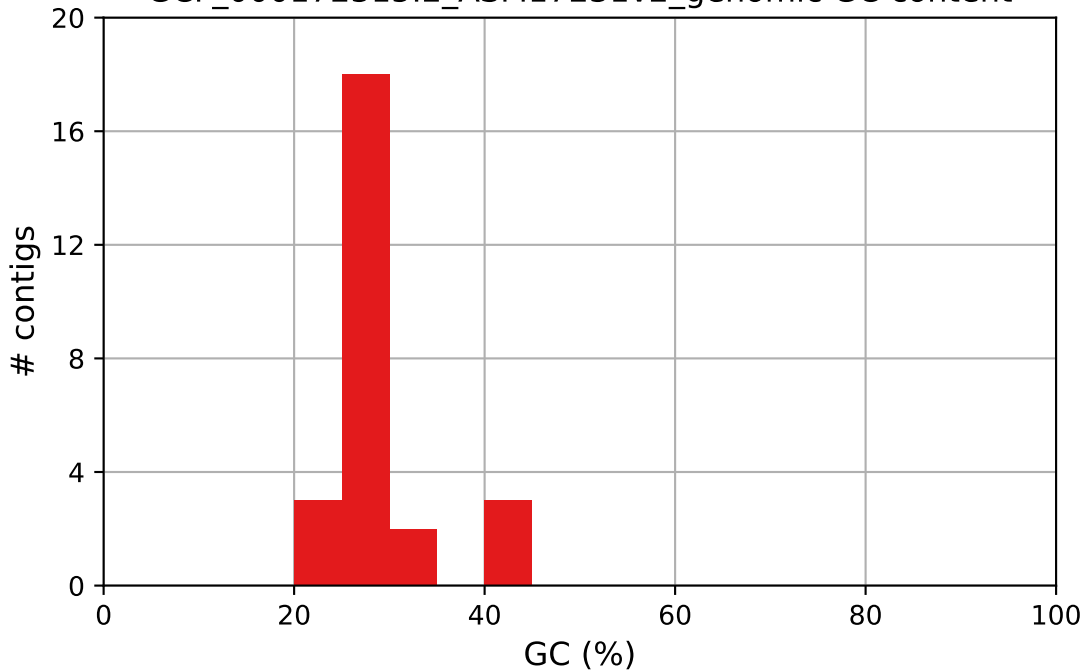
Cumulative length



GC content



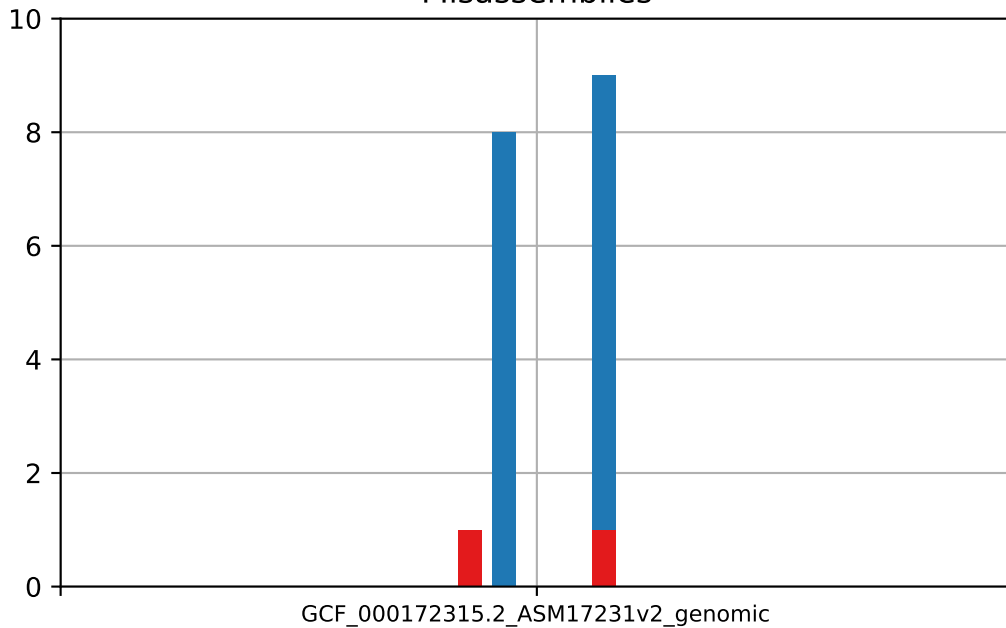
GCF\_000172315.2\_ASM17231v2\_genomic GC content



GCF\_000172315.2\_ASM17231v2\_genomic



## Misassemblies

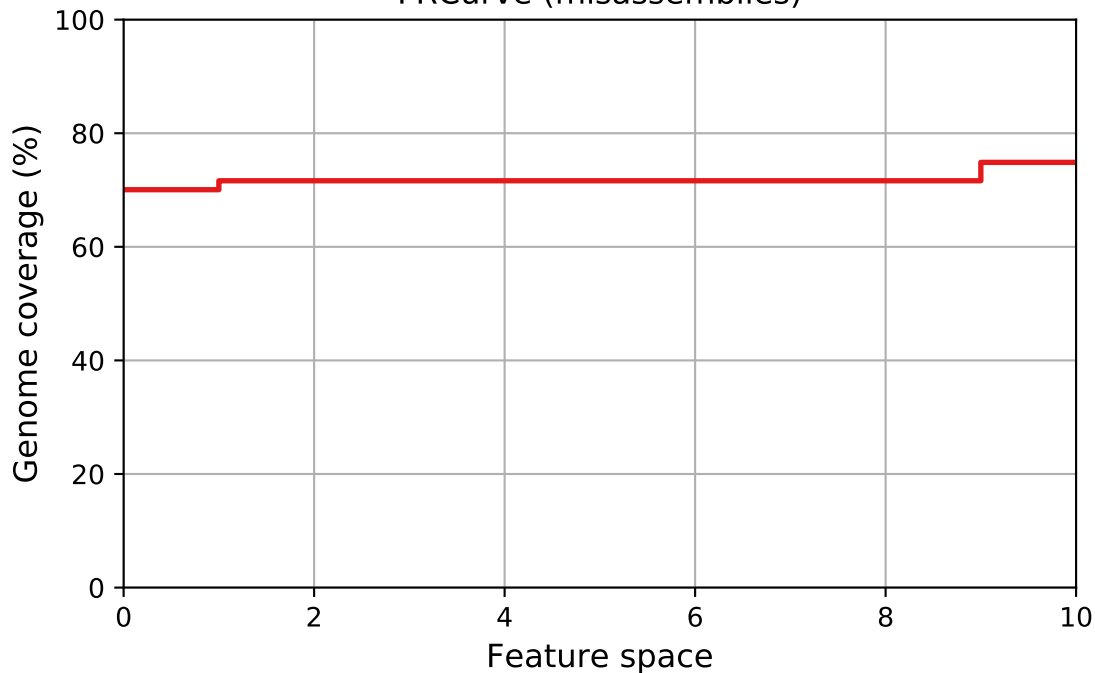


# relocations



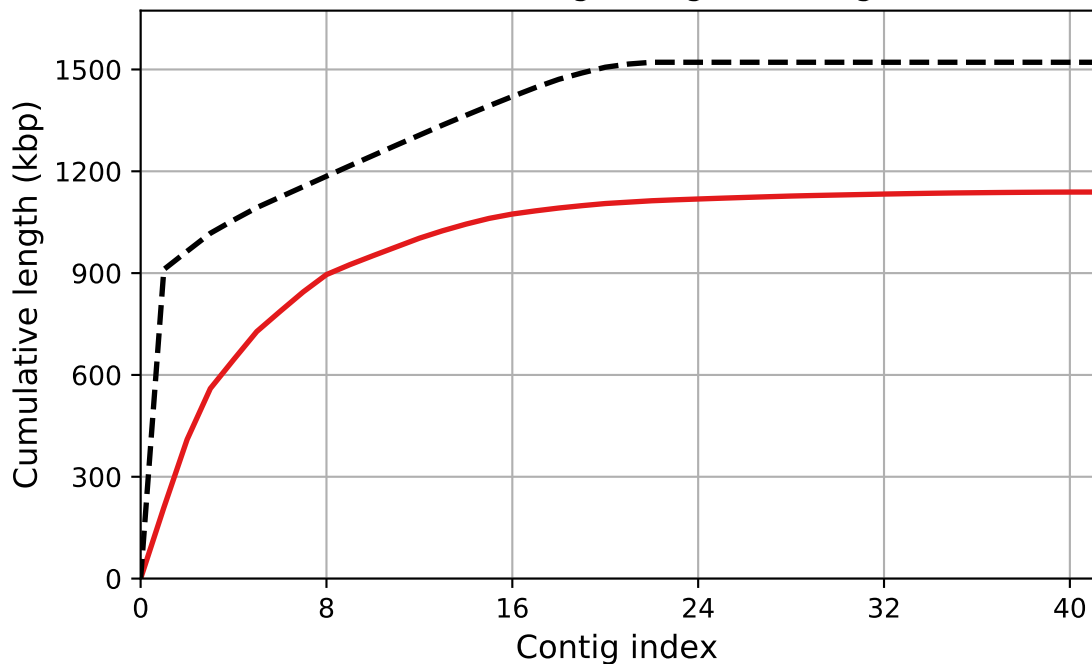
# translocations

FRCurve (misassemblies)



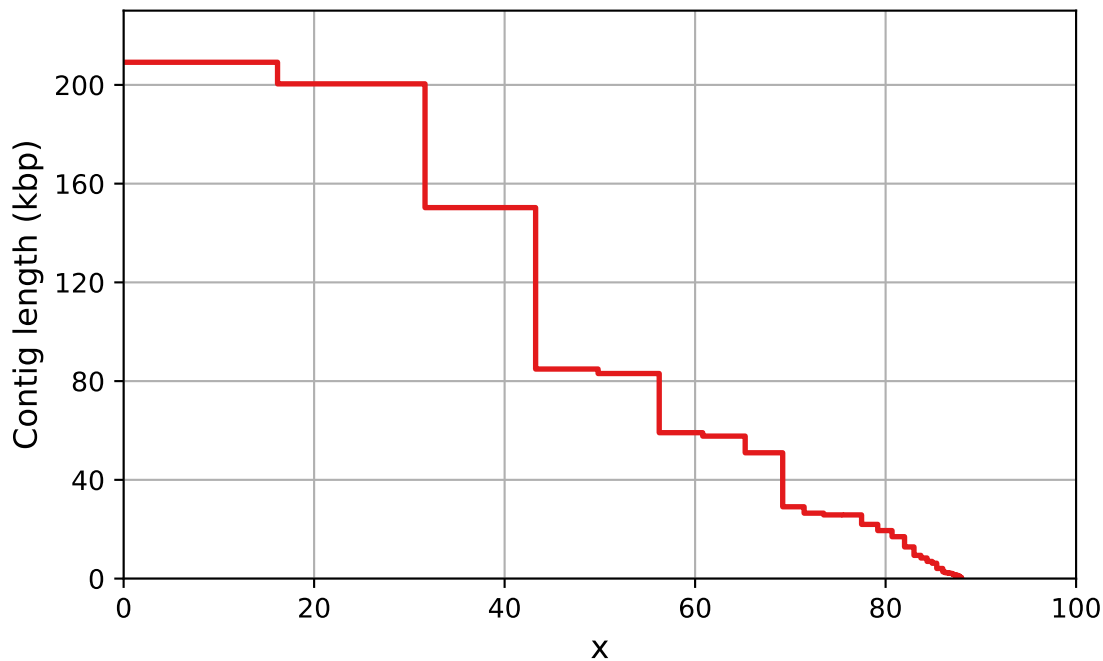
— GCF\_000172315.2\_ASM17231v2\_genomic

Cumulative length (aligned contigs)



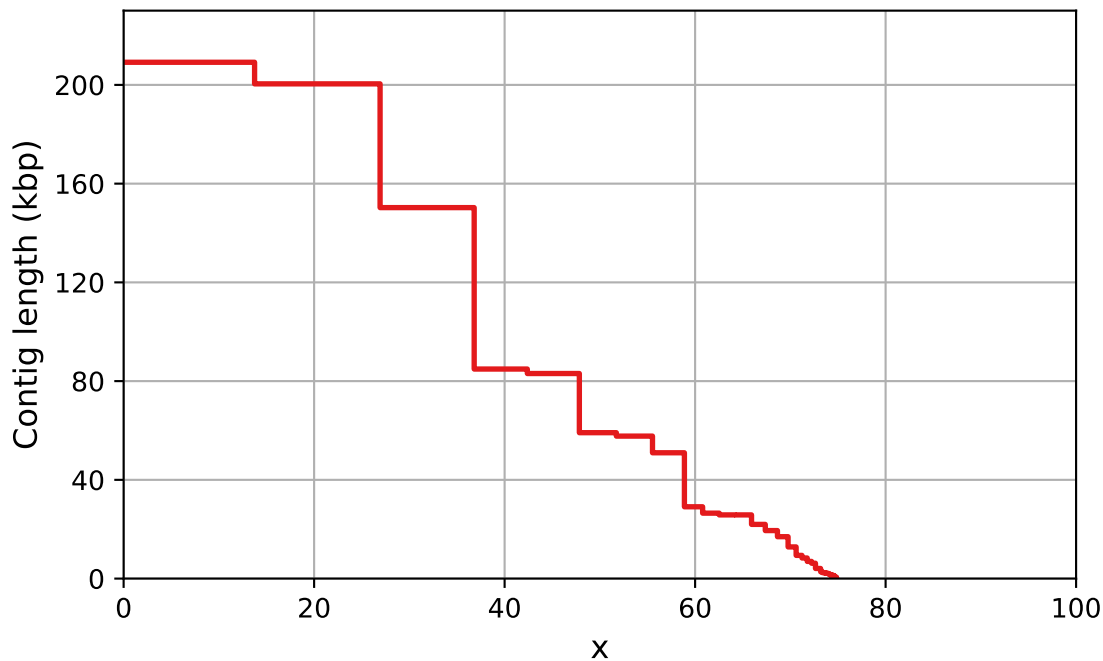
— GCF\_000172315.2\_ASM17231v2\_genomic    - - Reference

NAx



GCF\_000172315.2\_ASM17231v2\_genomic

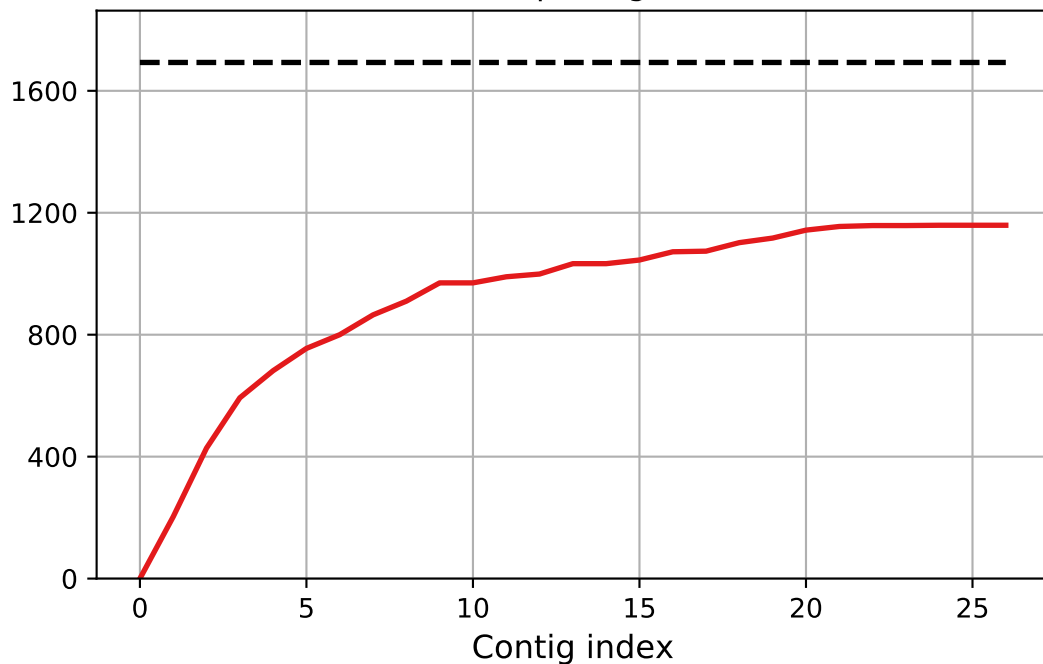
# NGAx



— GCF\_000172315.2\_ASM17231v2\_genomic

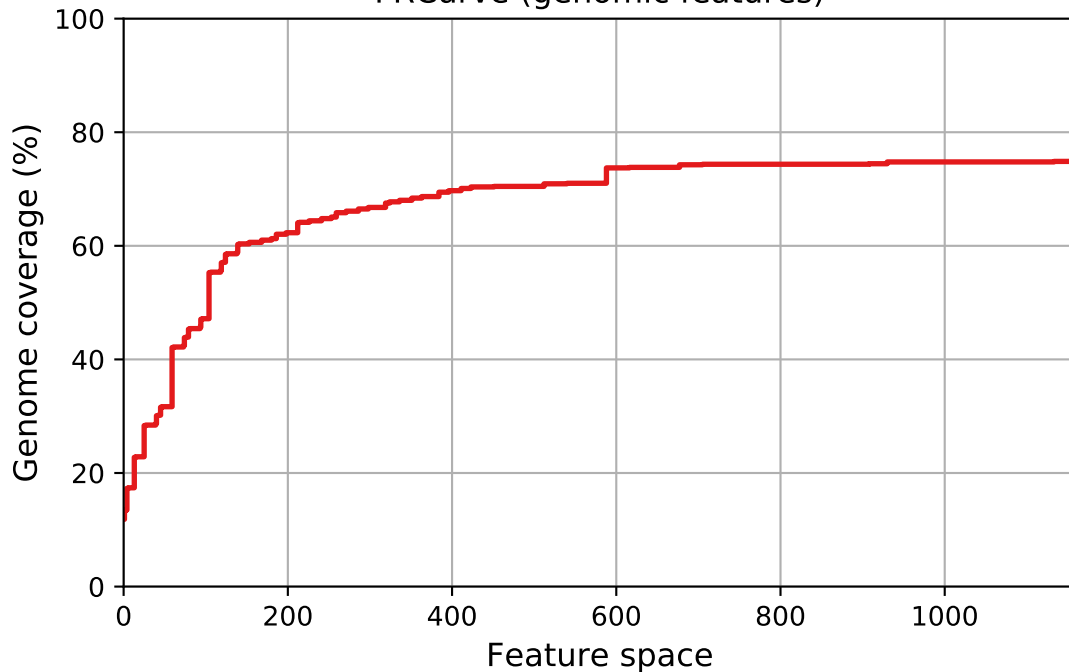
Cumulative # complete genomic features

Cumulative # complete genomic features



— GCF\_000172315.2\_ASM17231v2\_genomic    - - Reference

FRCurve (genomic features)



— GCF\_000172315.2\_ASM17231v2\_genomic