Report

	GCF_000166655.1_ASM16665v1_genomic
# contigs (>= 0 bp)	21
# contigs (>= 1000 bp)	21
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	16
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1531091
Total length (>= 1000 bp)	1531091
Total length (>= 5000 bp)	1531091
Total length (>= 10000 bp)	1531091
Total length (>= 25000 bp)	1418966
Total length (>= 50000 bp)	1036456
# contigs	21
Largest contig	922801
Total length	1531091
Reference length	1521208
GC (%)	28.33
Reference GC (%)	28.18
N50	922801
NG50	922801
N90	26981
NG90	26981
auN	569450.0
auNG	573149.7
L50	1
LG50	1
L90	15
LG90	15
# misassemblies	29
# misassembled contigs	11
Misassembled contigs length	1245026
# local misassemblies	24
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 18 part
Unaligned length	191570
Genome fraction (%)	80.587
Duplication ratio	1.090
# N's per 100 kbp	0.26
# mismatches per 100 kbp	992.45
# indels per 100 kbp	62.44
# genomic features	1283 + 49 part
Largest alignment	909883
Total aligned length	1335588
NA50	909883
NGA50	909883
NA90	-
NGA90	-
auNA	545949.6
auNGA	549496.6
LA50	1
LGA50	1
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).
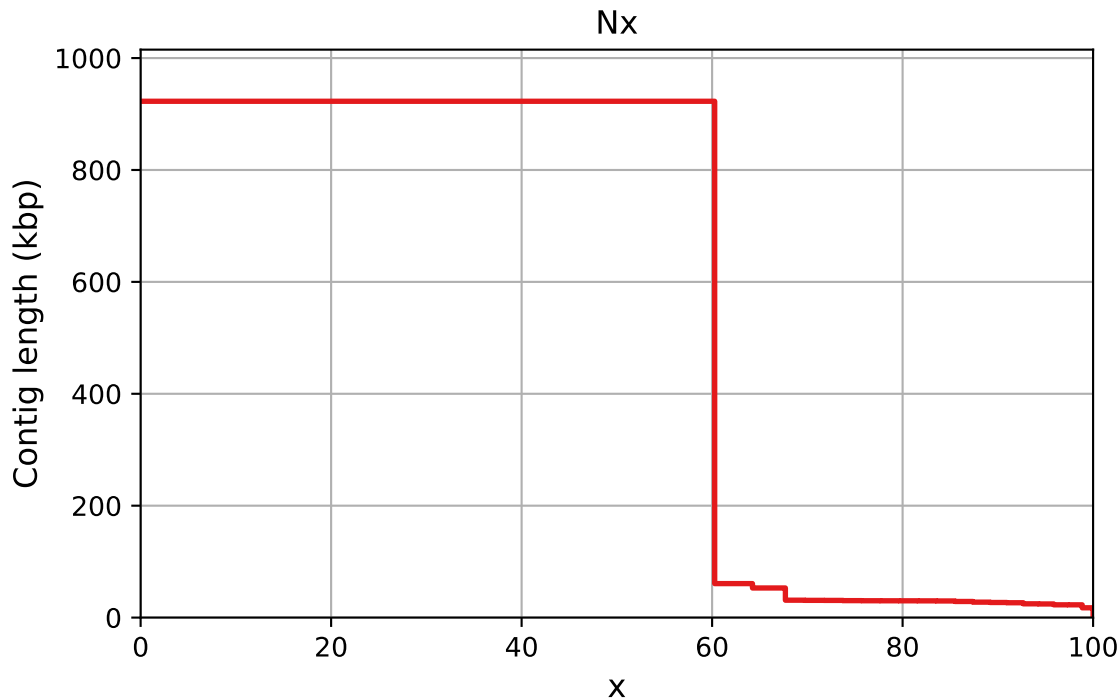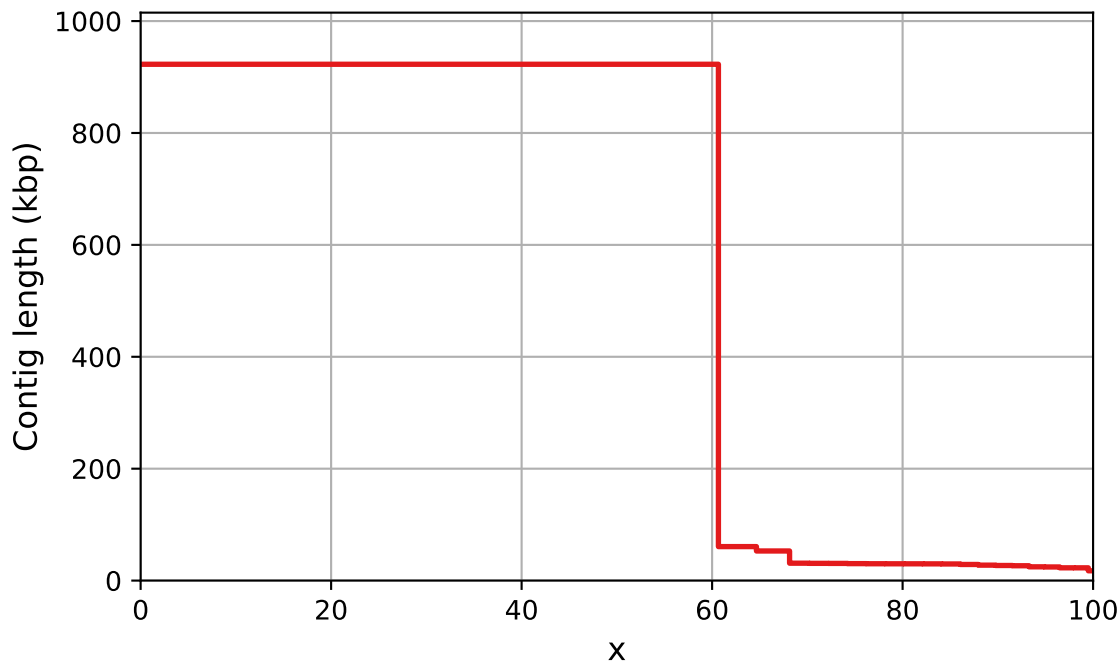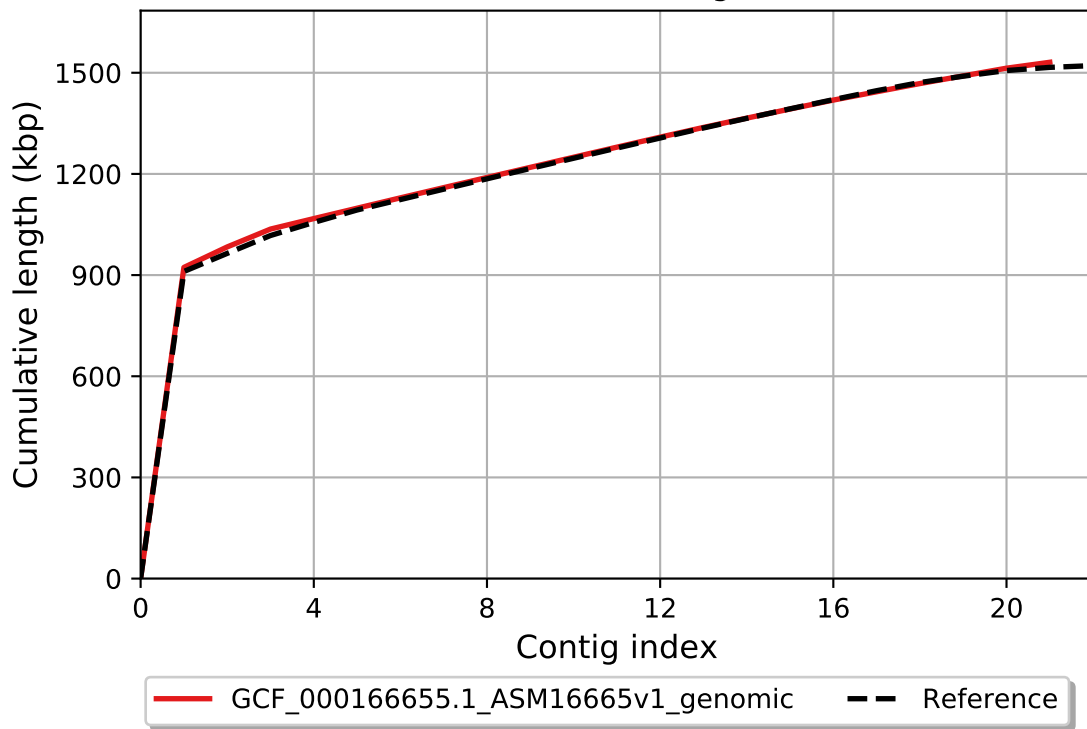
Misassemblies report

	GCF_000166655.1_ASM16665v1_genomic
# misassemblies	29
# contig misassemblies	29
# c. relocations	3
# c. translocations	26
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	11
Misassembled contigs length	1245026
# local misassemblies	24
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	13255
# indels	834
# indels (<= 5 bp)	763
# indels (> 5 bp)	71
Indels length	3779

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

	GCF_000166655.1_ASM16665v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	18
Partially unaligned length	191570
# N's	4

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).
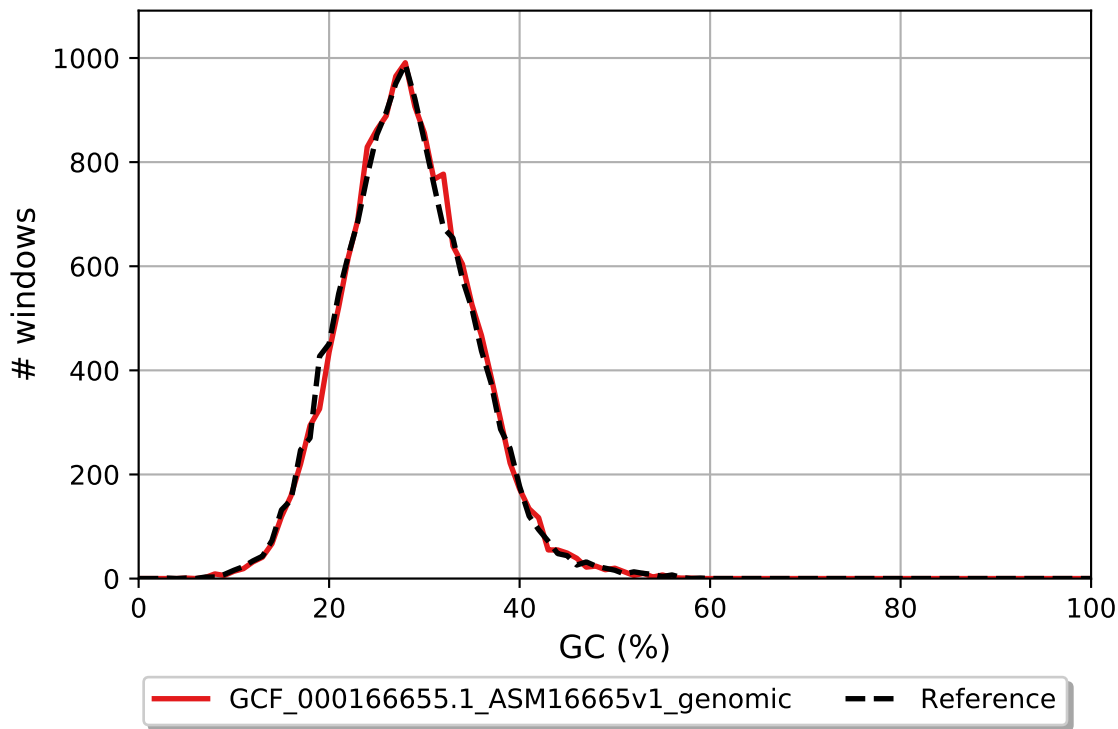
Nx

GCF_000166655.1_ASM16665v1_genomic

NGx

Contig length (kbp) vs x

GCF_000166655.1_ASM16665v1_genomic

Cumulative length

GC content

windows vs GC (%)

GCF_000166655.1_ASM16665v1_genomic — Reference

GCF_000166655.1_ASM16665v1_genomic GC content

Misassemblies

Legend:
- # relocations (red)
- # translocations (blue)

GCF_000166655.1_ASM16665v1_genomic

FRCurve (misassemblies)
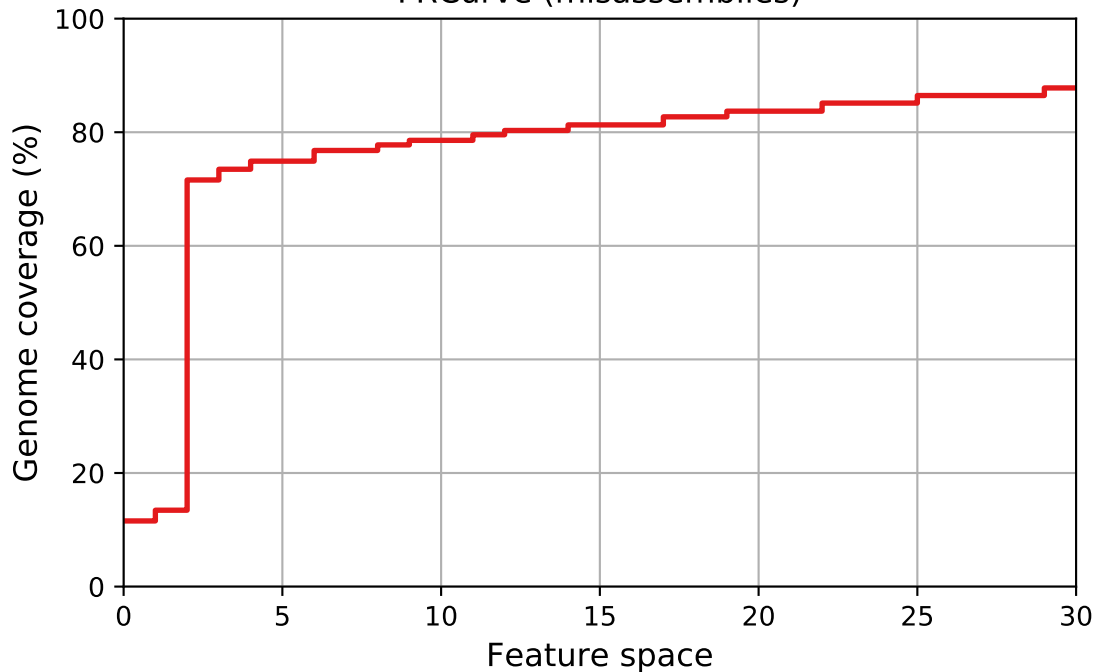
GCF_000166655.1_ASM16665v1_genomic

Cumulative length (aligned contigs)
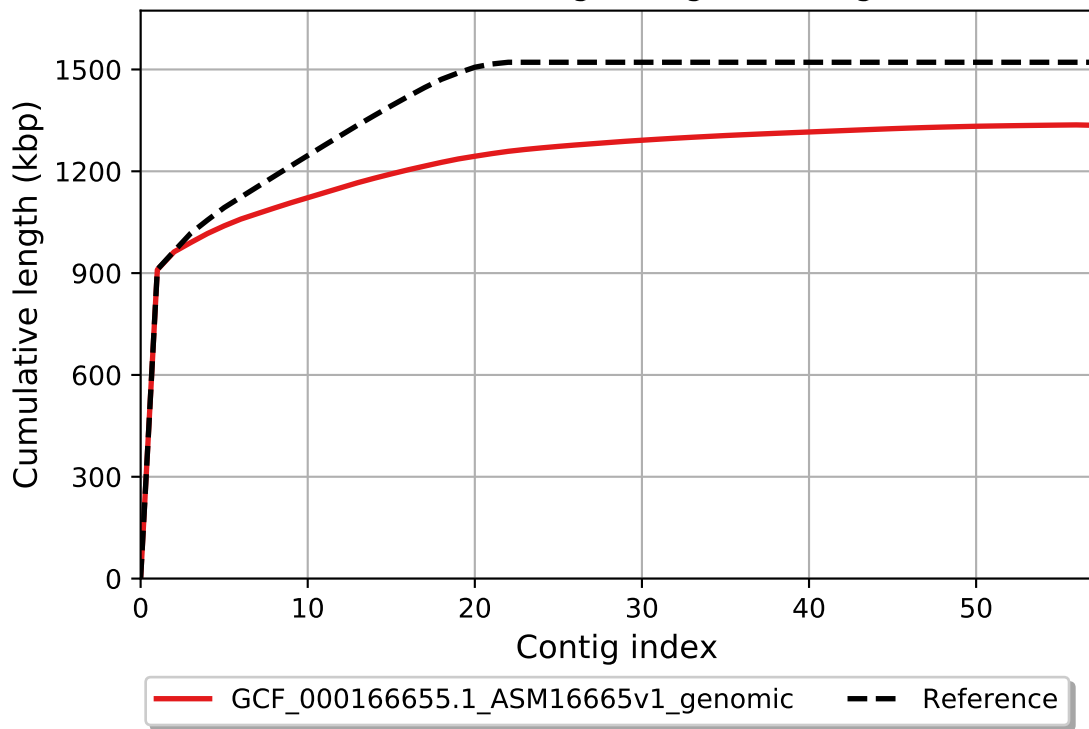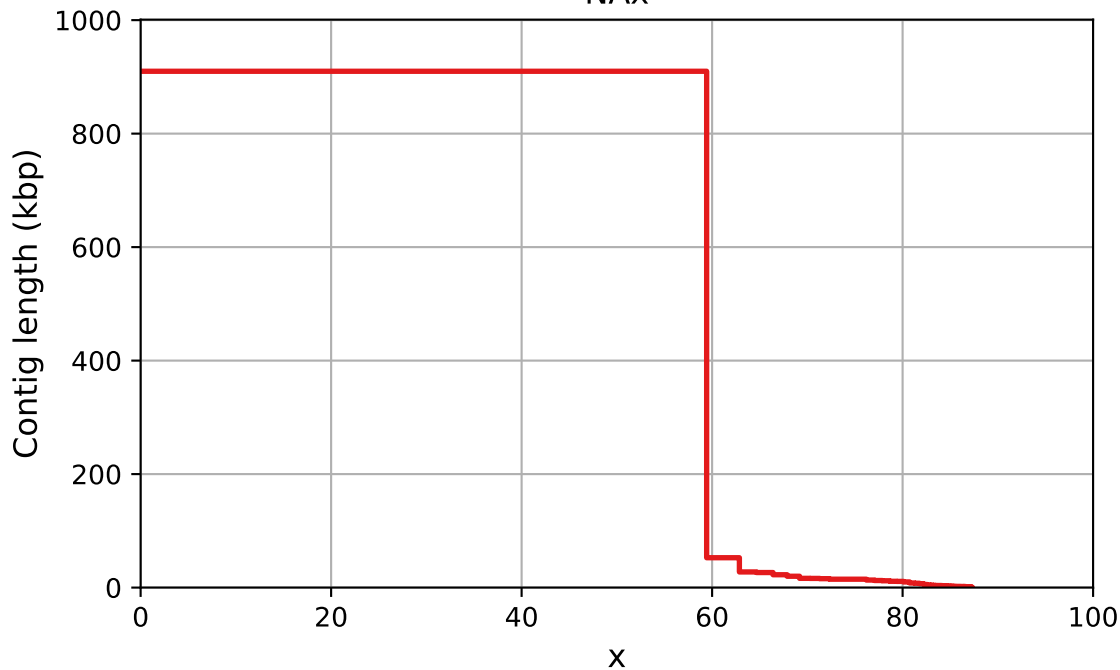
NAx

- GCF_000166655.1_ASM16665v1_genomic
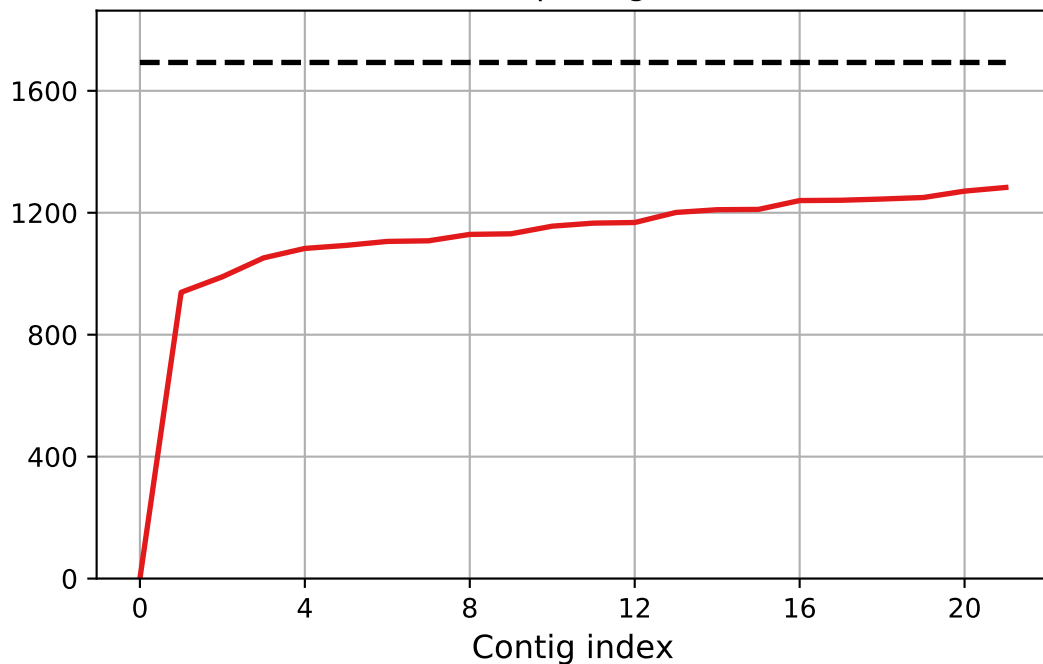
NGAx
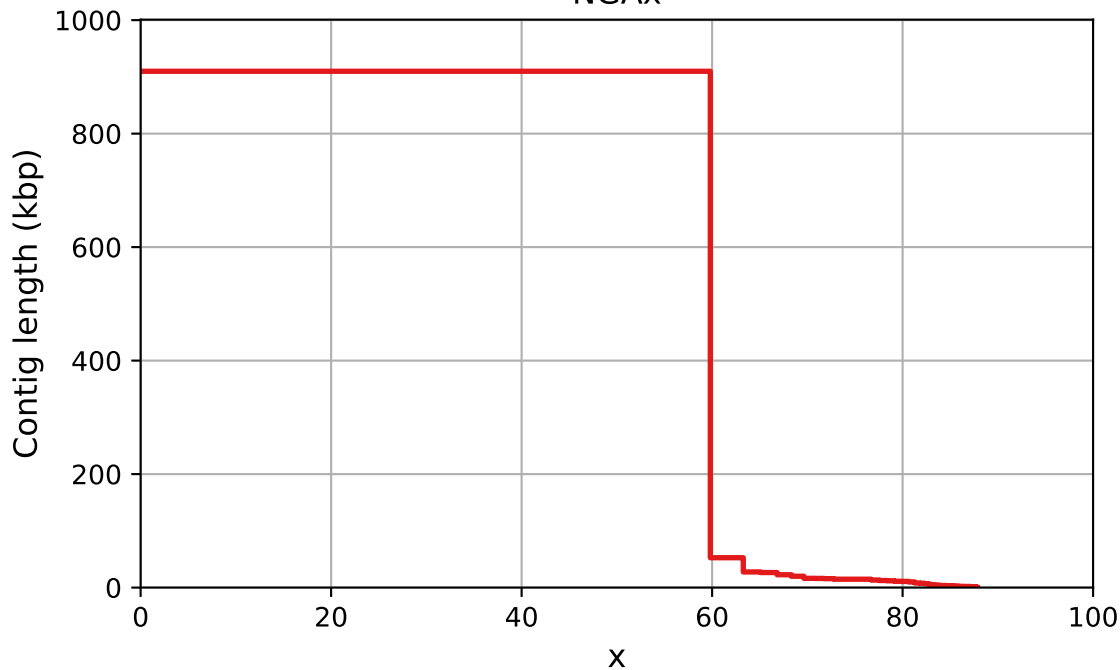
Cumulative # complete genomic features
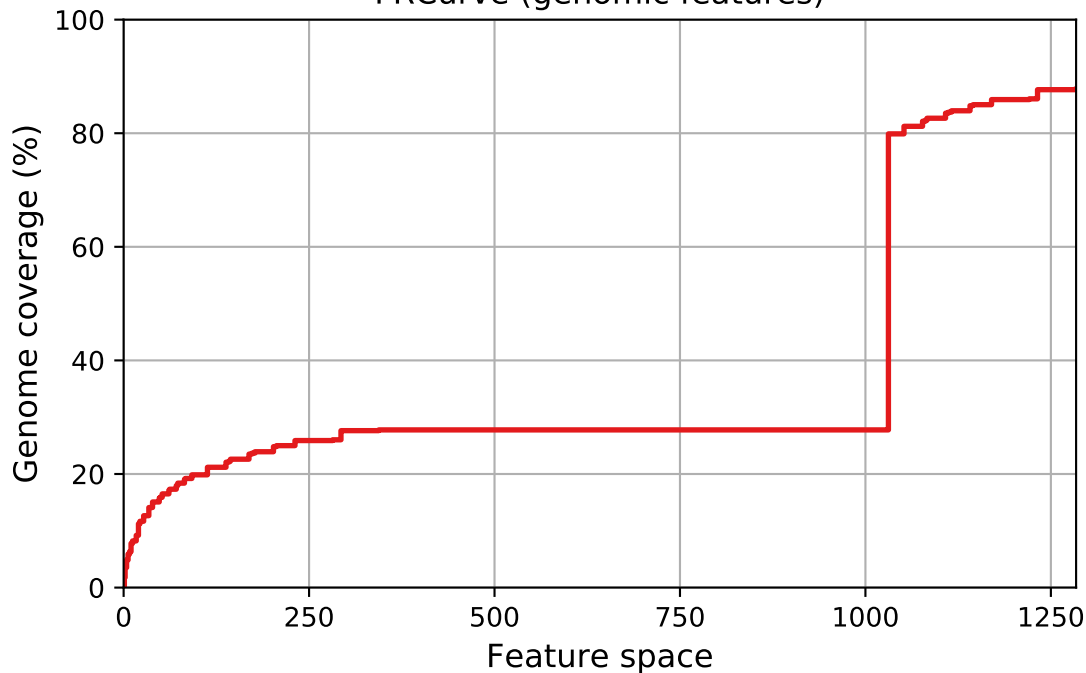
FRCurve (genomic features)

GCF_000166655.1_ASM16665v1_genomic