Report

	GCA_030445005.1_ASM3044500v1_genomic
# contigs (>= 0 bp)	4
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	4
# contigs (>= 10000 bp)	4
# contigs (>= 25000 bp)	3
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1007828
Total length (>= 1000 bp)	1007828
Total length (>= 5000 bp)	1007828
Total length (>= 10000 bp)	1007828
Total length (>= 25000 bp)	990606
Total length (>= 50000 bp)	964152
# contigs	4
Largest contig	910422
Total length	1007828
Reference length	1521208
GC (%)	28.41
Reference GC (%)	28.18
N50	910422
NG50	910422
N90	910422
NG90	-
auN	826283.4
auNG	547427.8
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	17222
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	66.236
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	331.98
# indels per 100 kbp	17.17
# genomic features	1047 + 3 part
Largest alignment	910422
Total aligned length	1007304
NA50	910422
NGA50	910422
NA90	910422
NGA90	-
auNA	826219.8
auNGA	547385.6
LA50	1
LGA50	1
LA90	1
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).
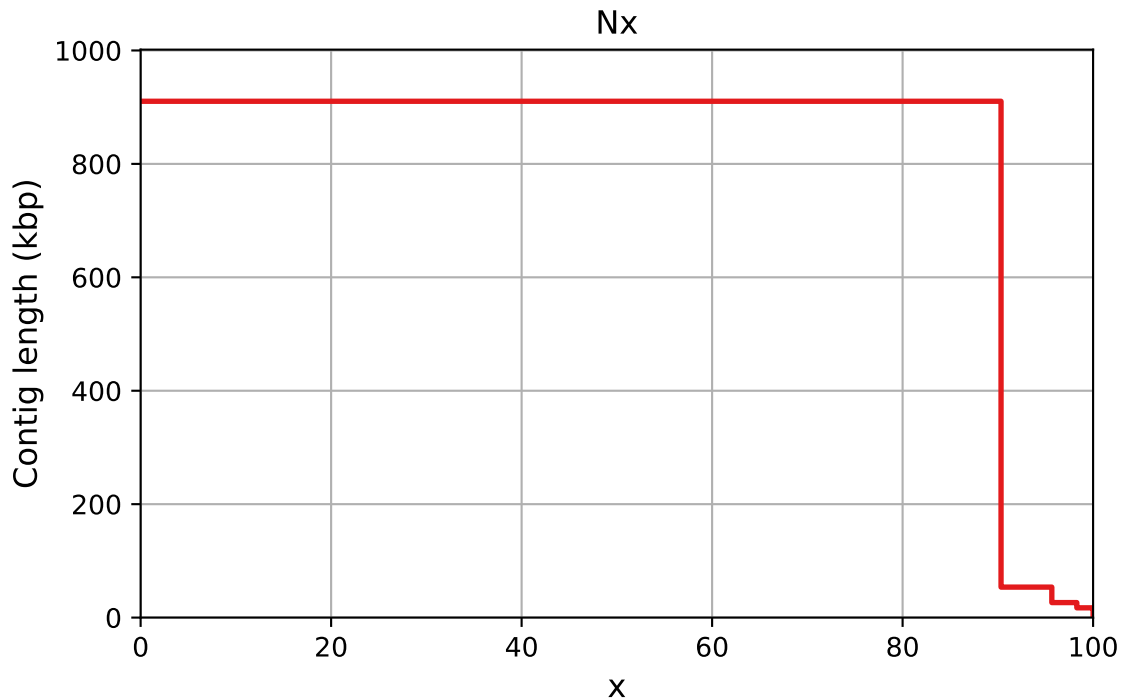
Misassemblies report

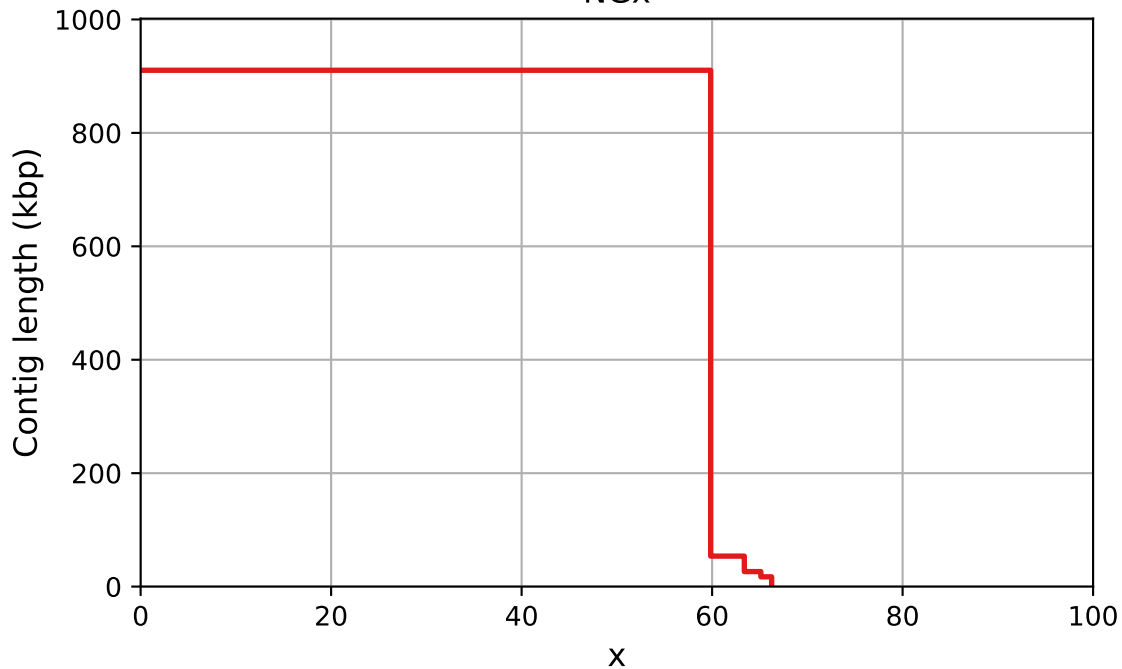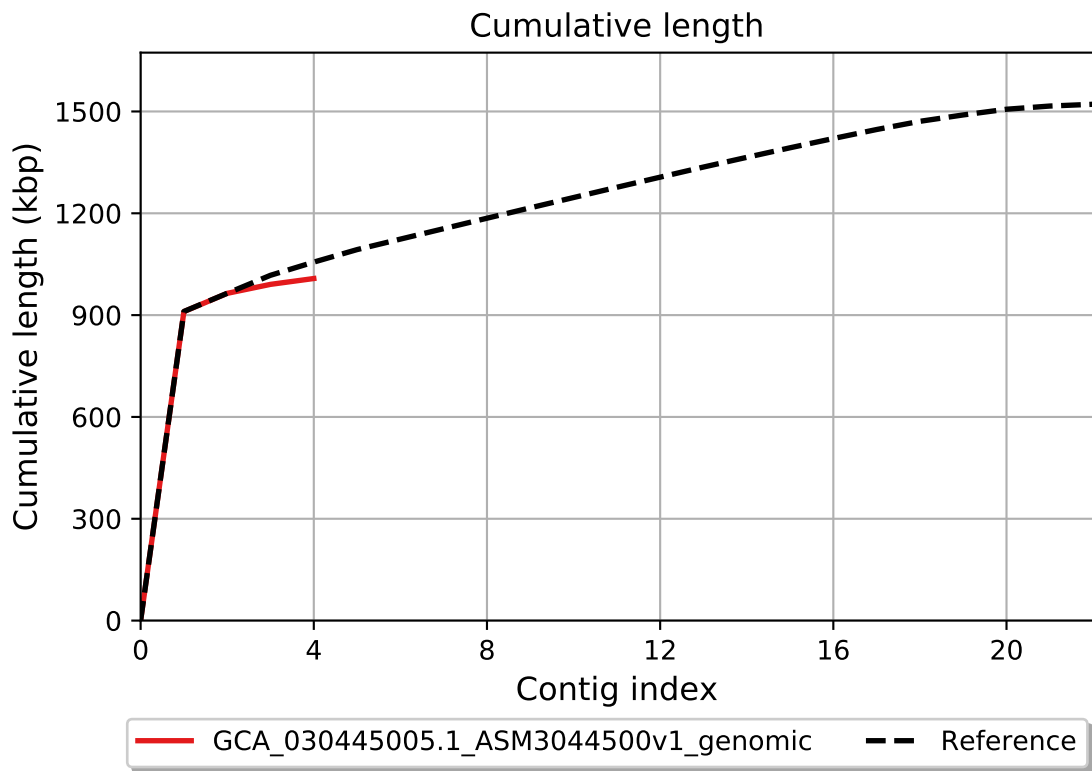|	GCA_030445005.1_ASM3044500v1_genomic
# misassemblies	1
# contig misassemblies	1
# c. relocations	0
# c. translocations	1
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	17222
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3344
# indels	173
# indels (<= 5 bp)	144
# indels (> 5 bp)	29
Indels length	1027

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

	GCA_030445005.1_ASM3044500v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).
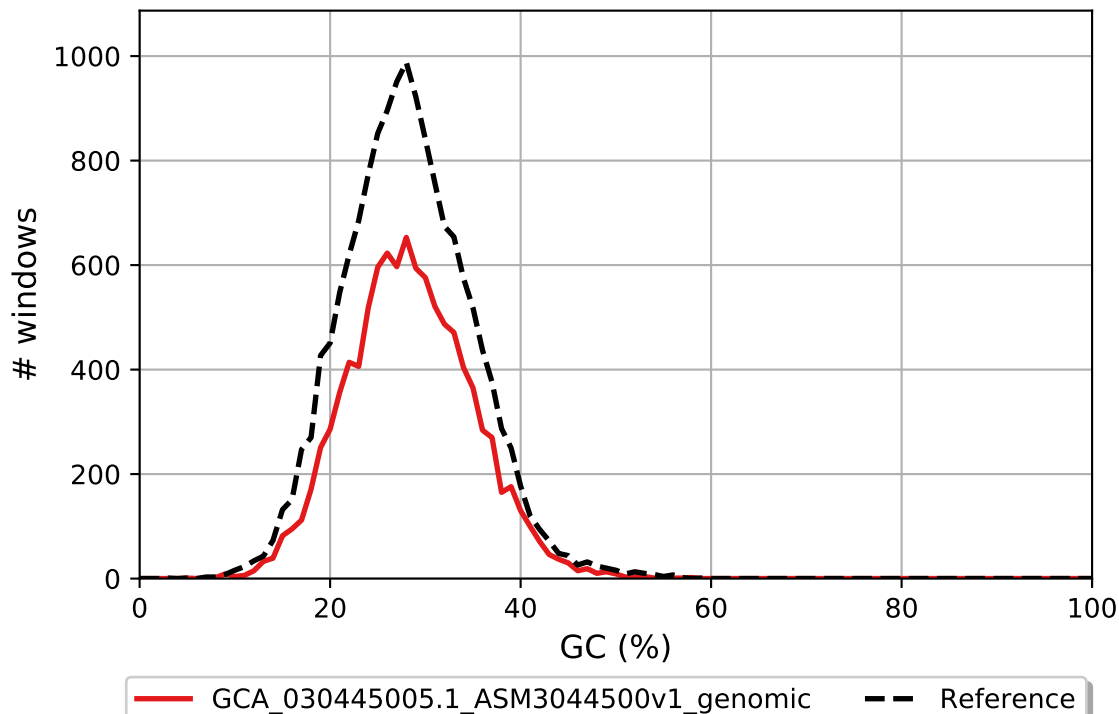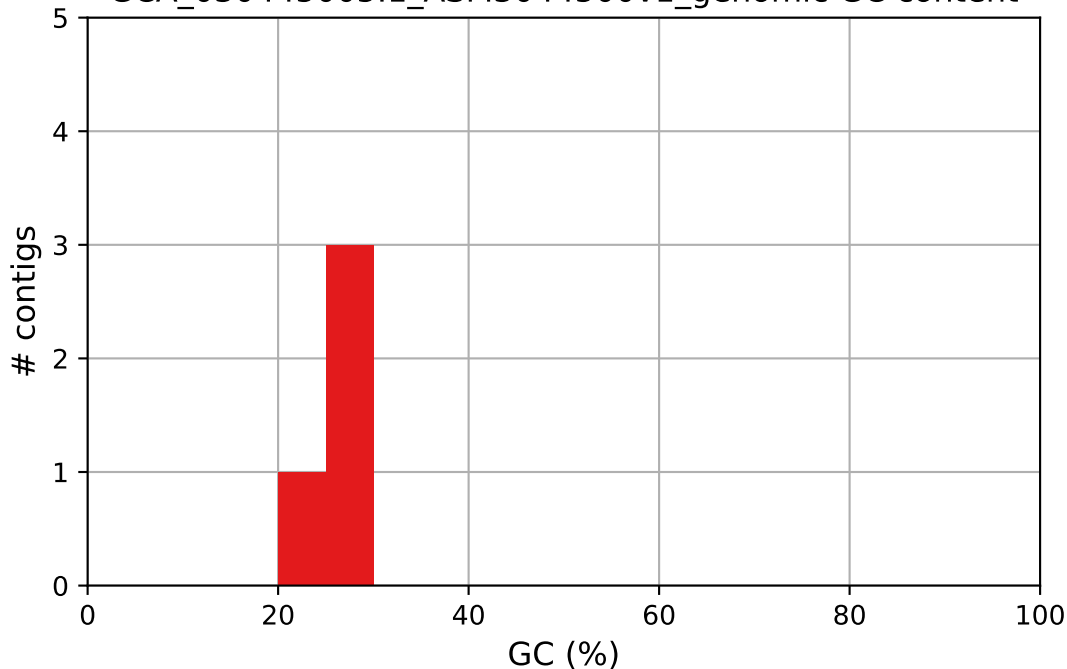
Nx

GCA_030445005.1_ASM3044500v1_genomic

NGx

GCA_030445005.1_ASM3044500v1_genomic

Cumulative length

GC content

GCA_030445005.1_ASM3044500v1_genomic GC content
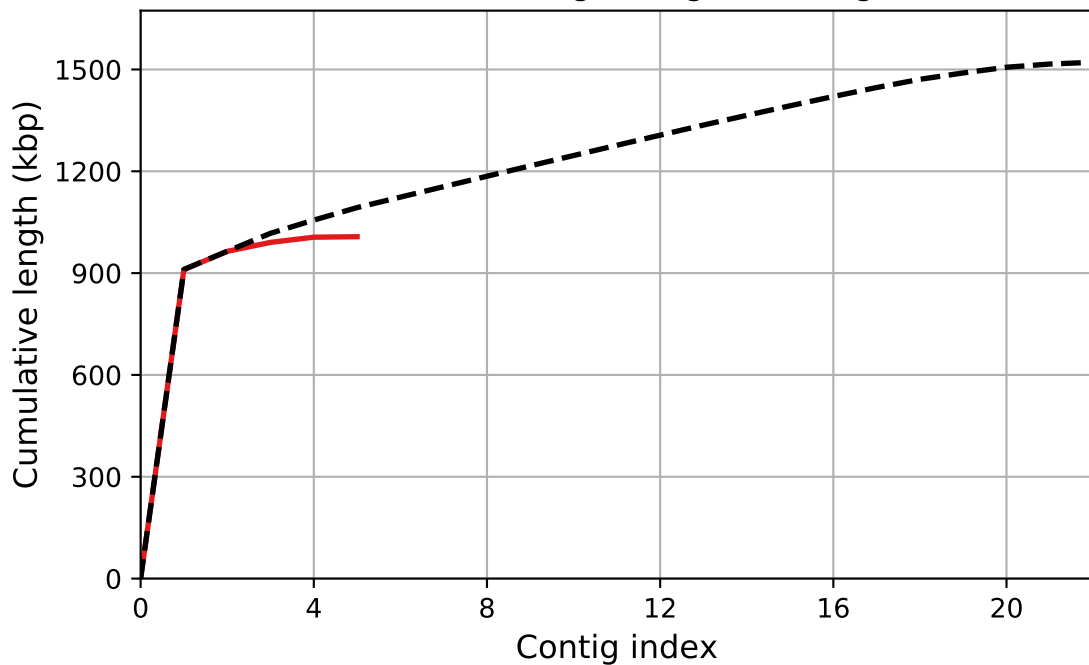
Misassemblies

GCA_030445005.1_ASM3044500v1_genomic

translocations
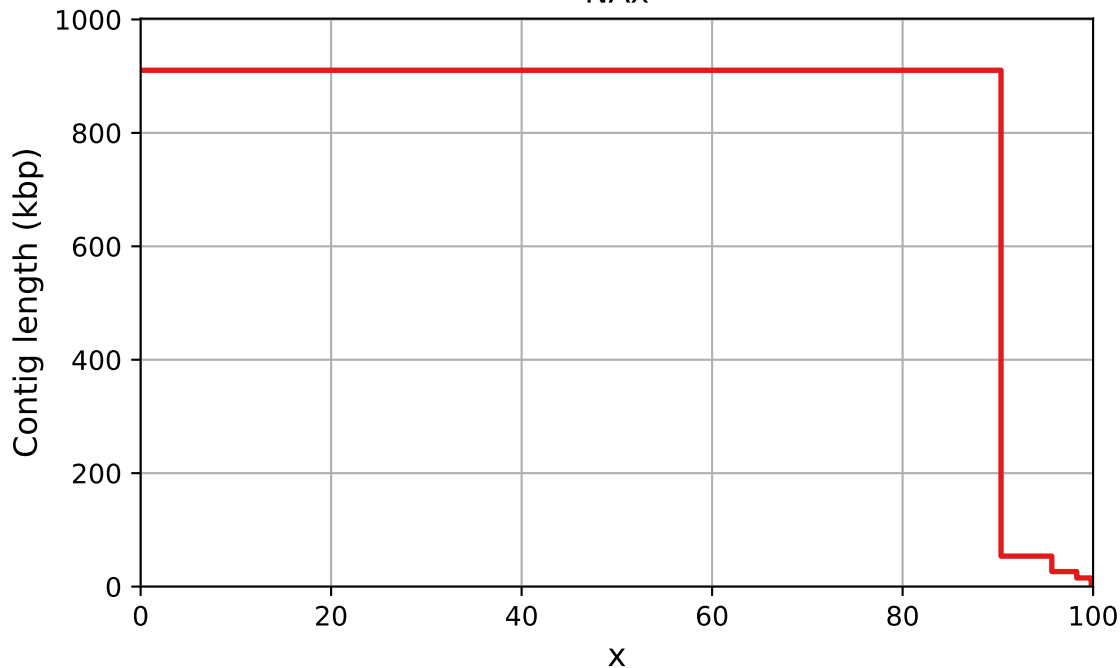
FRCurve (misassemblies)
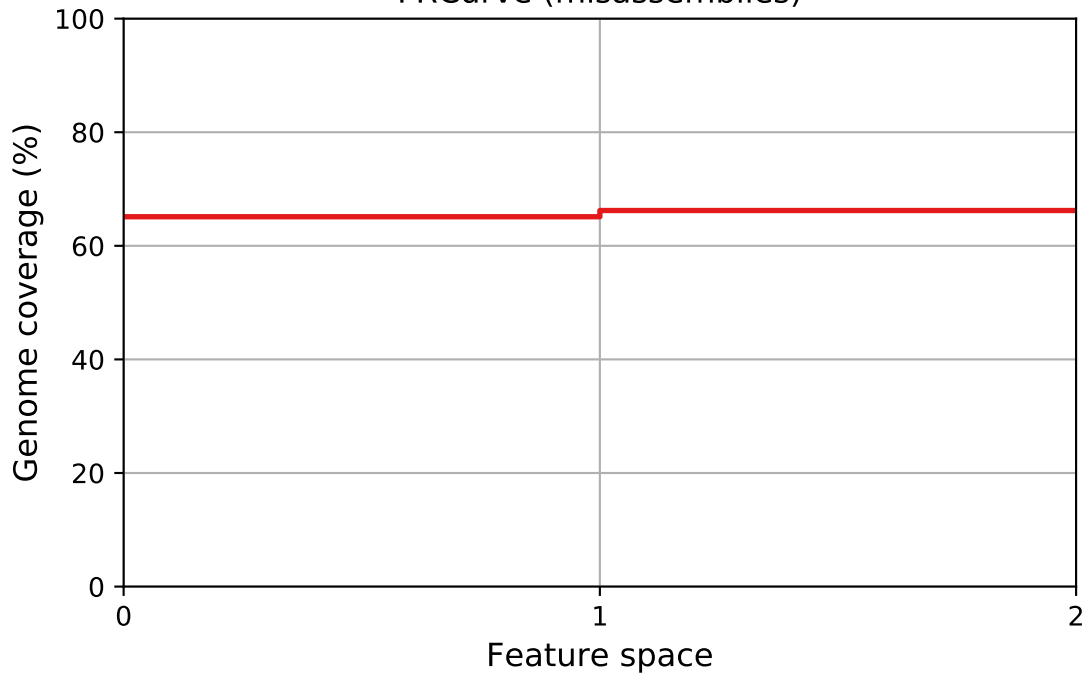
GCA_030445005.1_ASM3044500v1_genomic

Cumulative length (aligned contigs)
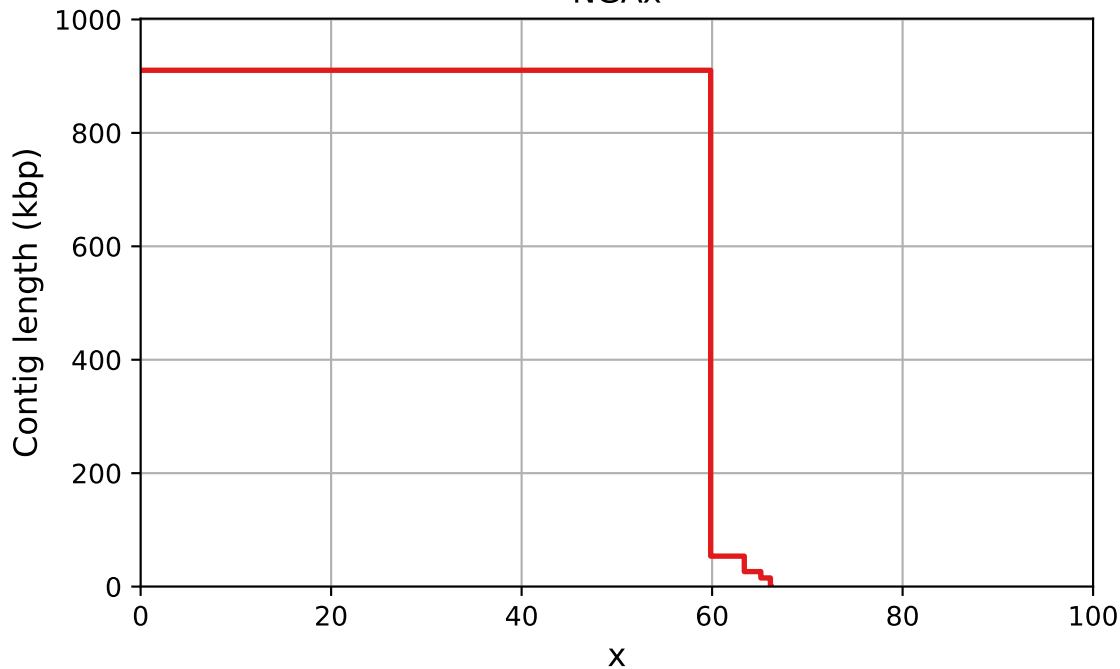
NAx

GCA_030445005.1_ASM3044500v1_genomic

NGAx

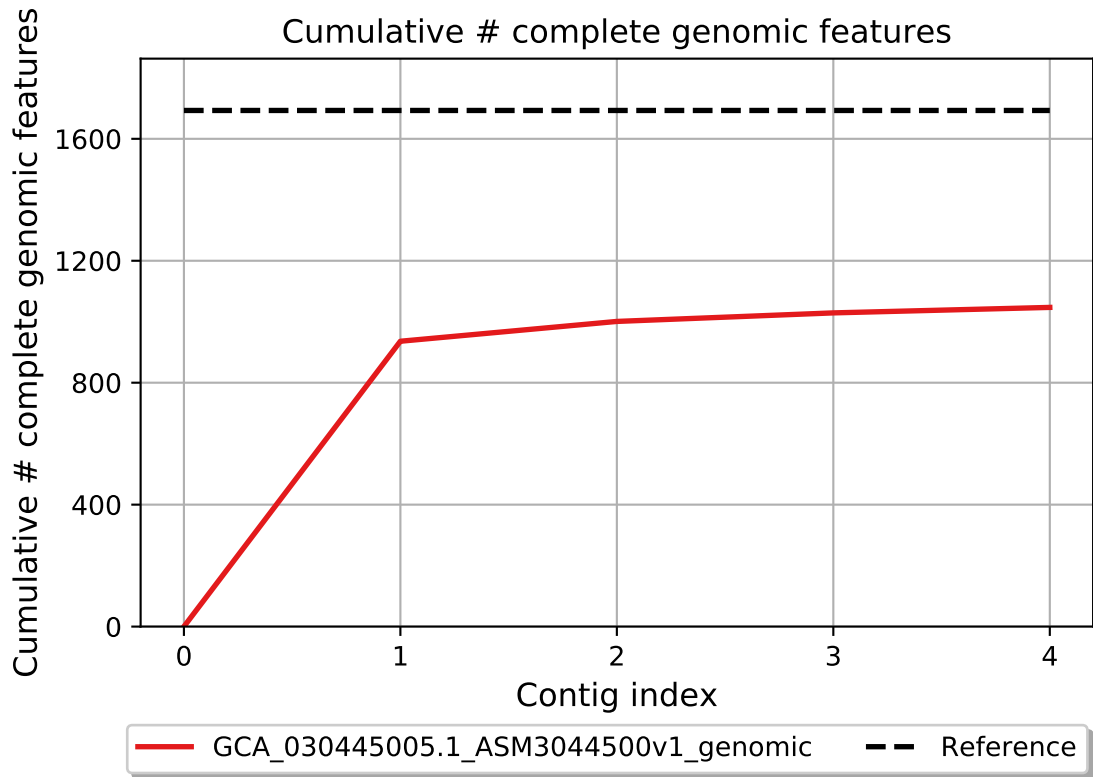GCA_030445005.1_ASM3044500v1_genomic

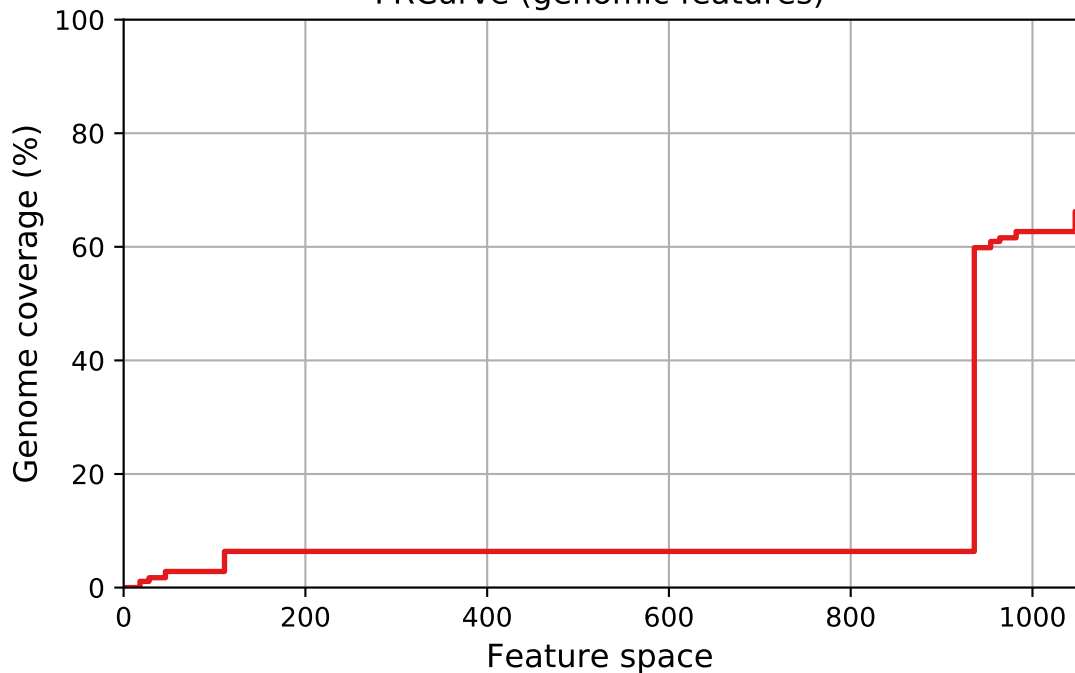Cumulative # complete genomic features

FRCurve (genomic features)

GCA_030445005.1_ASM3044500v1_genomic