Report

	GCA_030445025.1_ASM3044502v1_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)	1008124
Total length (>= 1000 bp)	1008124
Total length (>= 5000 bp)	1008124
Total length (>= 10000 bp)	1008124
Total length (>= 25000 bp)	990842
Total length (>= 50000 bp)	964338
# contigs	4
Largest contig	910663
Total length	1008124
Reference length	1521208
GC (%)	28.40
Reference GC (%)	28.18
N50	910663
NG50	910663
N90	910663
NG90	-
auN	826475.0
auNG	547715.5
L50	1
LG50	1
L90	1
LG90	-
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	17282
# 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 (%)	66.231
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	337.59
# indels per 100 kbp	16.97
# genomic features	1046 + 4 part
Largest alignment	910486
Total aligned length	1007424
NA50	910486
NGA50	910486
NA90	910486
NGA90	-
auNA	826091.5
auNGA	547461.4
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_030445025.1_ASM3044502v1_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	17282
# local misassemblies	2
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	3401
# indels	171
# indels (<= 5 bp)	150
# indels (> 5 bp)	21
Indels length	621

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

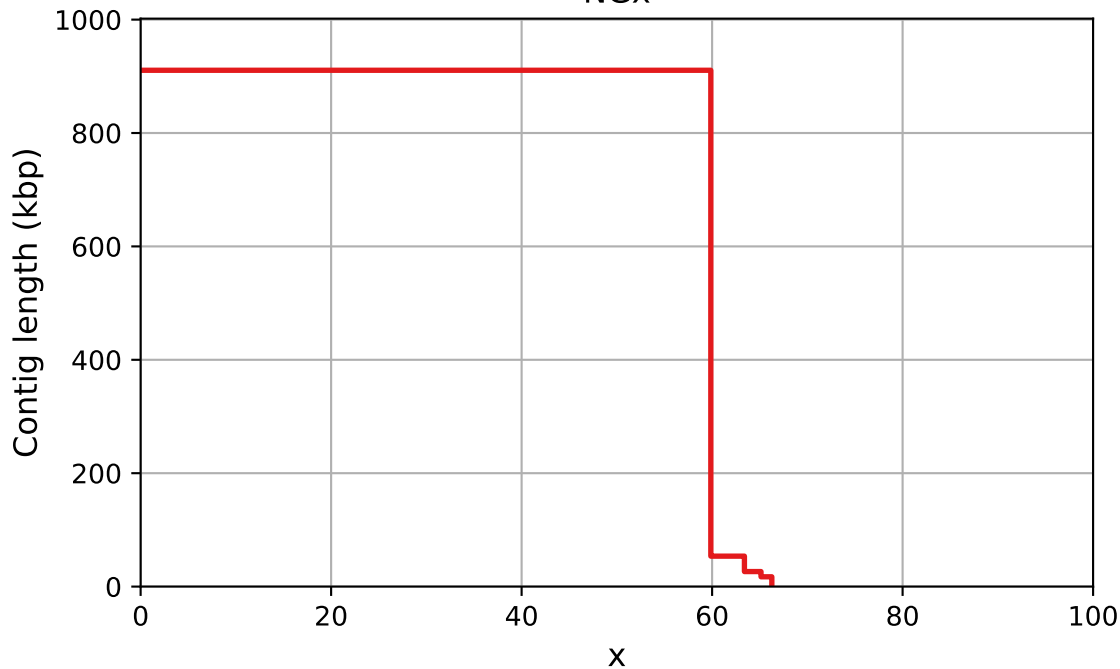|	GCA_030445025.1_ASM3044502v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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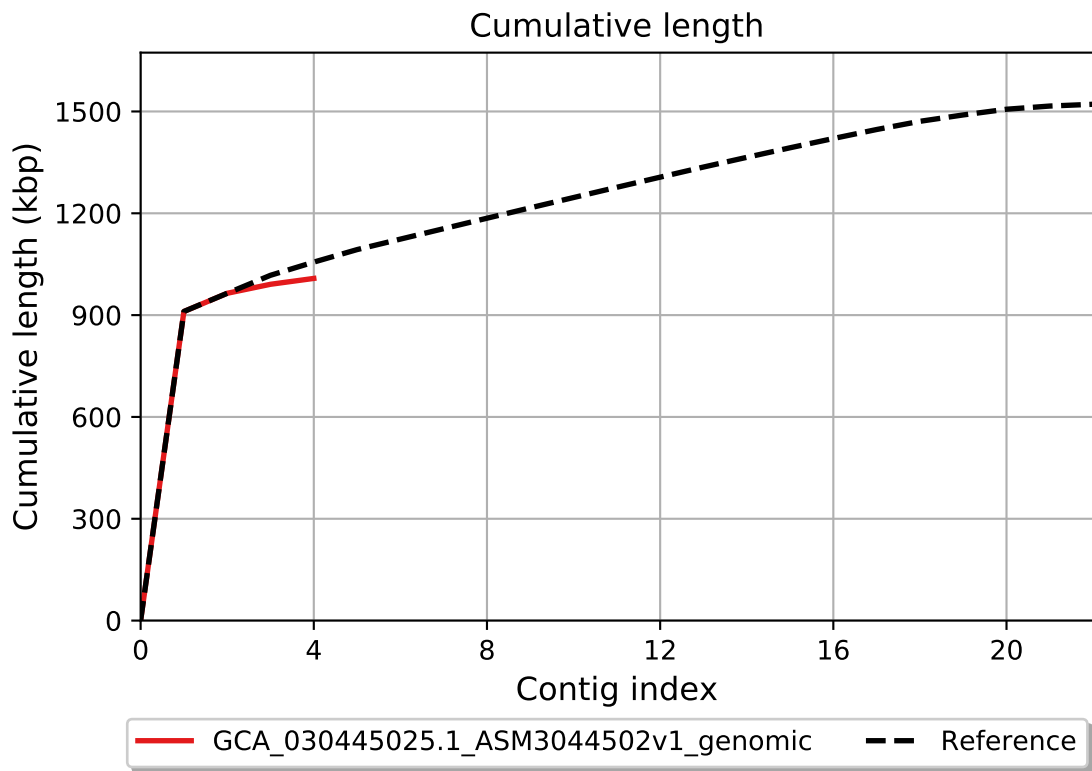(e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Nx
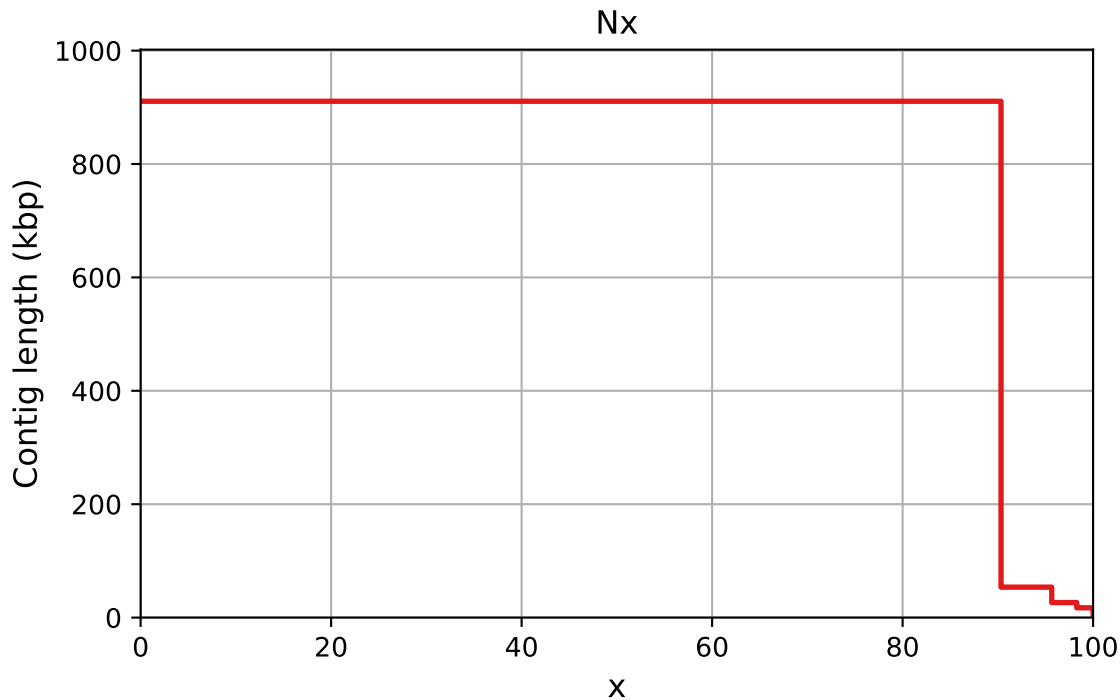
GCA_030445025.1_ASM3044502v1_genomic

NGx

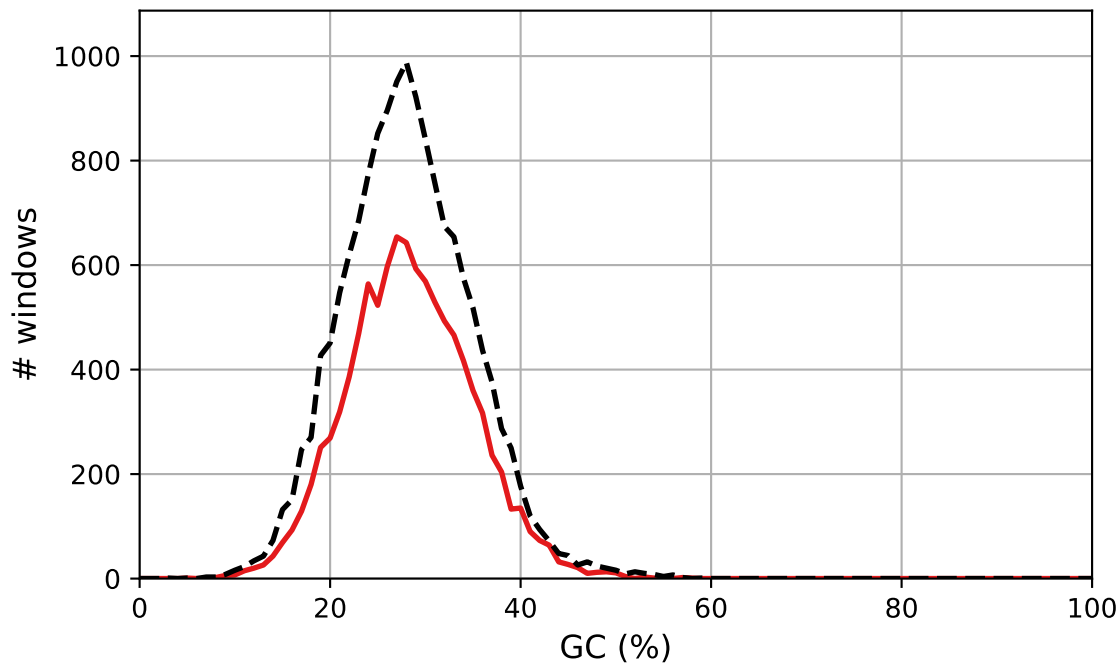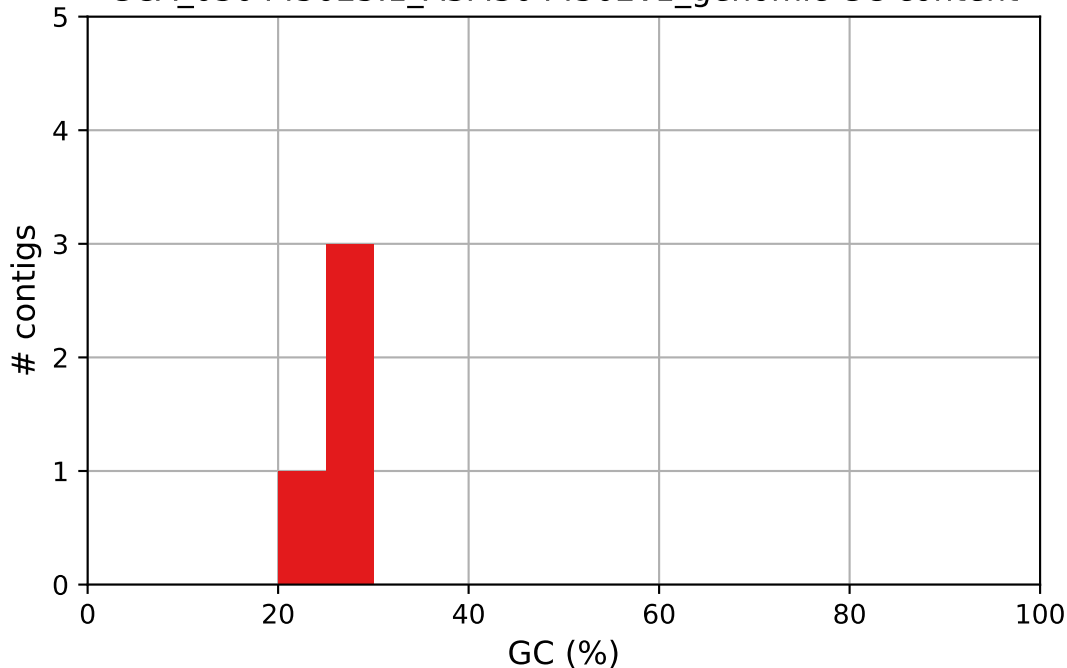GCA_030445025.1_ASM3044502v1_genomic

Cumulative length
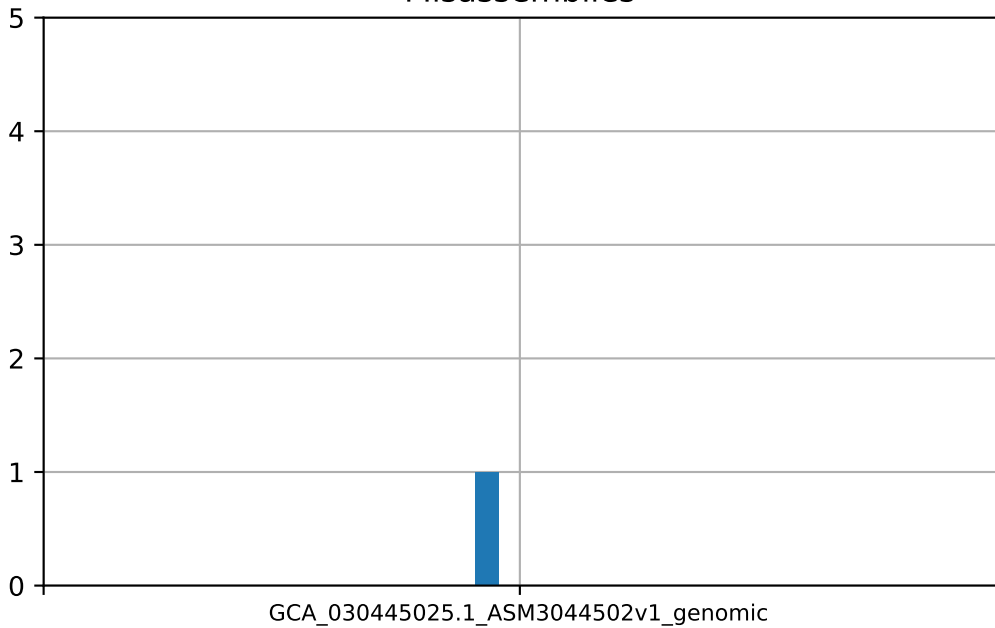
GCA_030445025.1_ASM3044502v1_genomic — — — Reference

GC content

GCA_030445025.1_ASM3044502v1_genomic — Reference

GCA_030445025.1_ASM3044502v1_genomic GC content

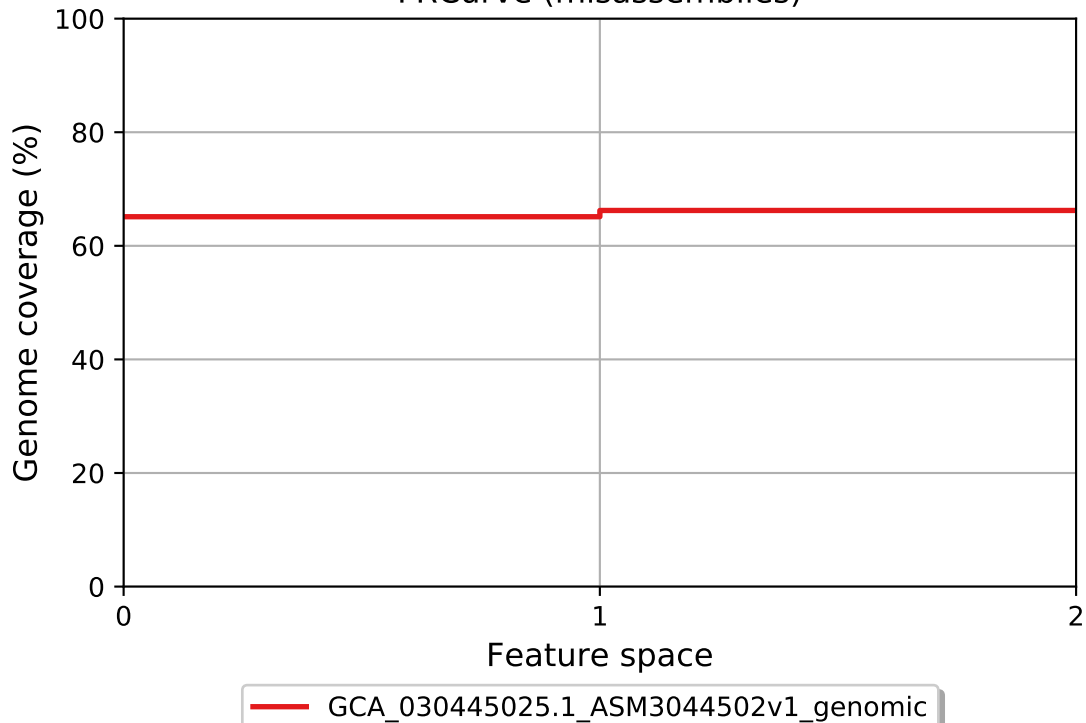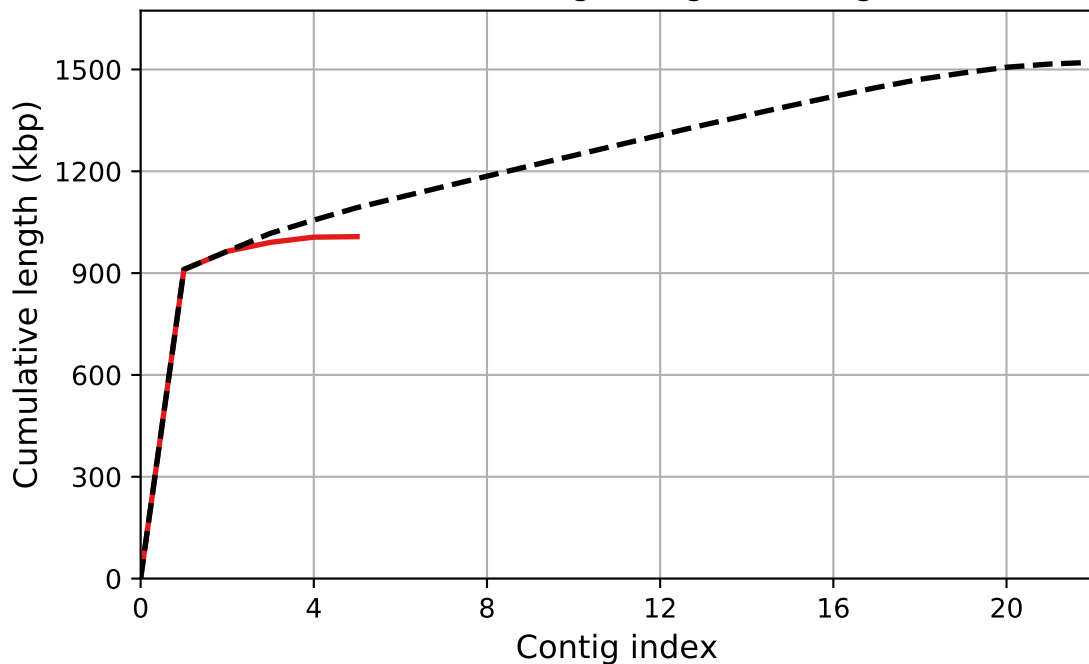Misassemblies

GCA_030445025.1_ASM3044502v1_genomic
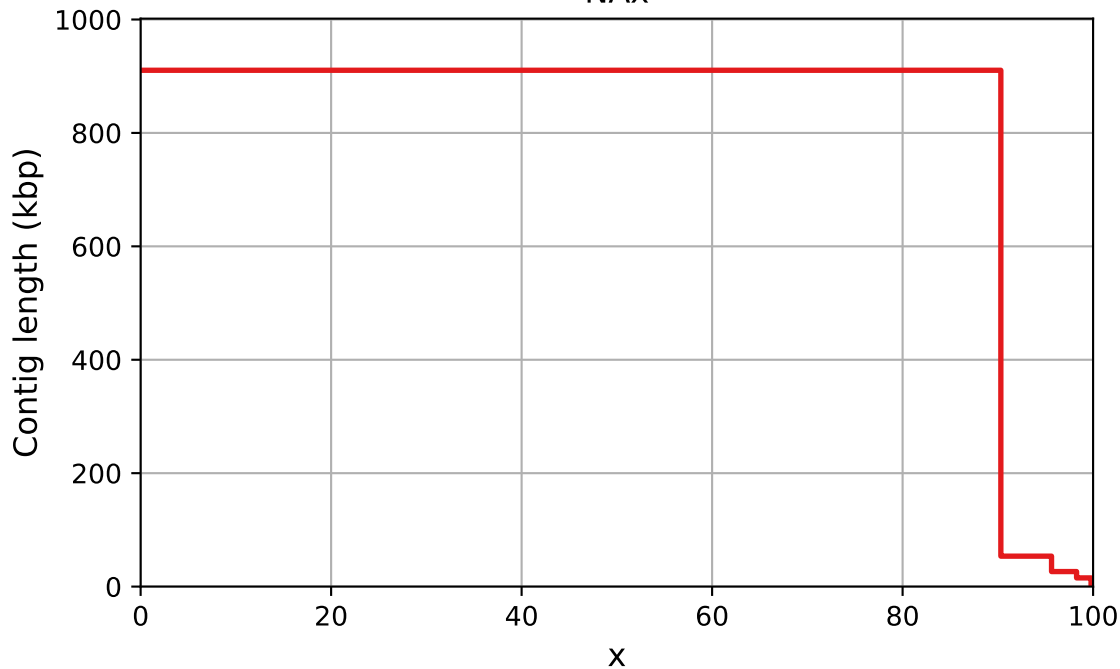
translocations

FRCurve (misassemblies)

GCA_030445025.1_ASM3044502v1_genomic

Cumulative length (aligned contigs)

NAx

Contig length (kbp) vs x

GCA_030445025.1_ASM3044502v1_genomic

NGAx

Cumulative # complete genomic features
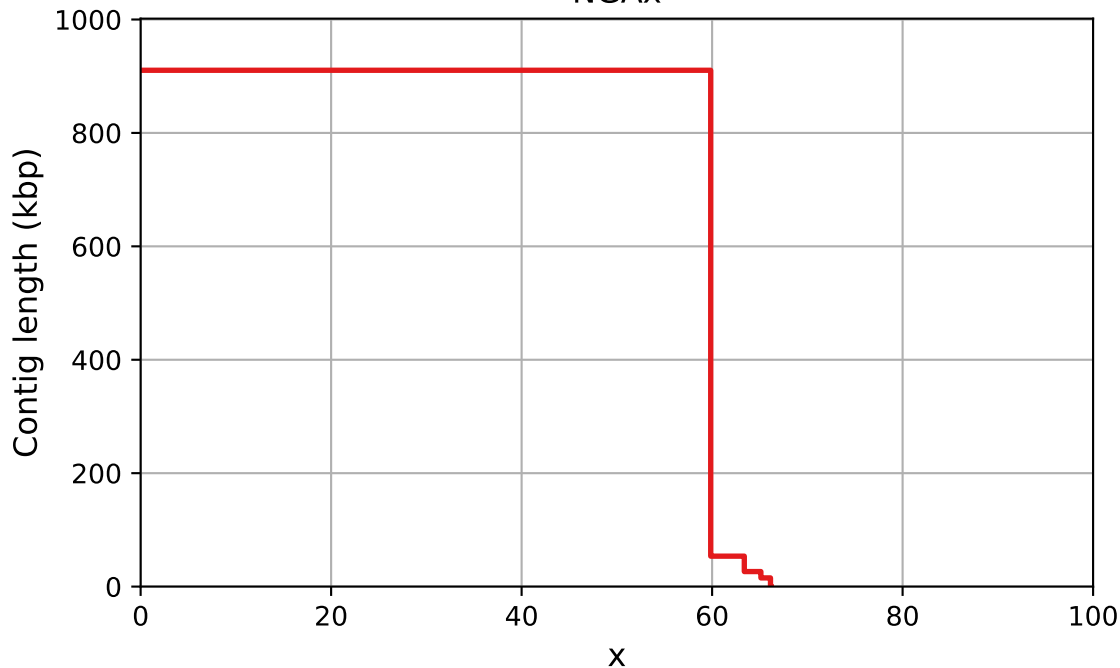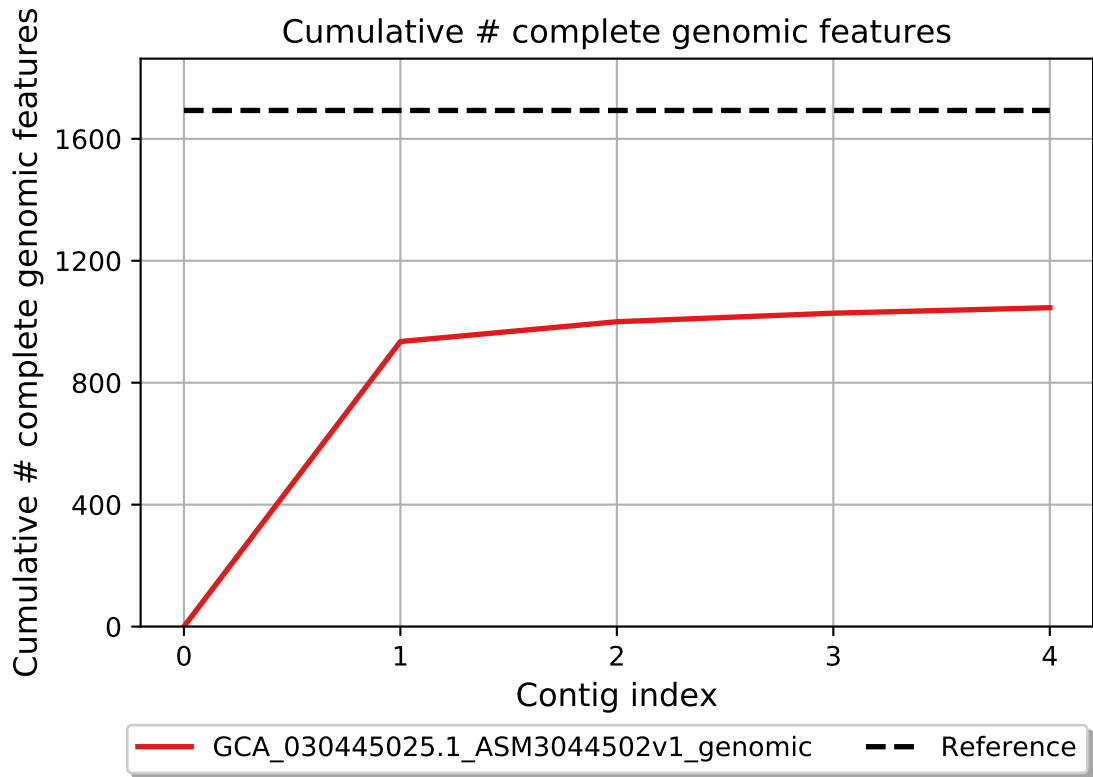
FRCurve (genomic features)

GCA_030445025.1_ASM3044502v1_genomic