Report	GCF_000008685.2_ASM868v2_genomic
# contigs (>= 0 bp)	22
# contigs (>= 1000 bp)	22
# contigs (>= 5000 bp)	22
# contigs (>= 10000 bp)	20
# contigs (>= 25000 bp)	17
# contigs (>= 50000 bp)	3
Total length (>= 0 bp)	1521208
Total length (>= 1000 bp)	1521208
Total length (>= 5000 bp)	1521208
Total length (>= 10000 bp)	1506594
Total length (>= 25000 bp)	1446819
Total length (>= 50000 bp)	1017352
# contigs	22
Largest contig	910724
Total length	1521208
Reference length	1521208
GC (%)	28.18
Reference GC (%)	28.18
N50	910724
NG50	910724
N90	28155
NG90	28155
auN	558608.0
auNG	558608.0
L50	1
LG50	1
L90	15
LG90	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.000
# N's per 100 kbp	3.62
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
# genomic features	1693 + 0 part
Largest alignment	910724
Total aligned length	1521208
NA50	910724
NGA50	910724
NA90	28155
NGA90	28155
auNA	558608.0
auNGA	558608.0
LA50	1
LGA50	1
LA90	15
LGA90	15

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).
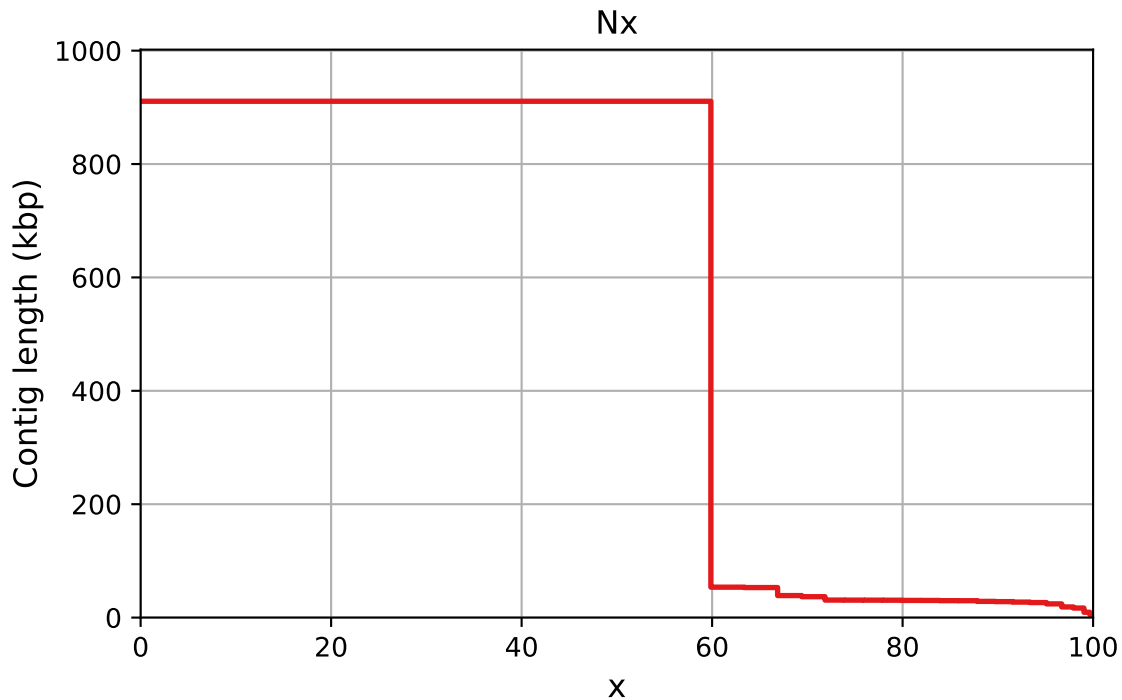
Misassemblies report

	GCF_000008685.2_ASM868v2_genomic
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	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).

Unaligned report

	GCF_000008685.2_ASM868v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	55

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).
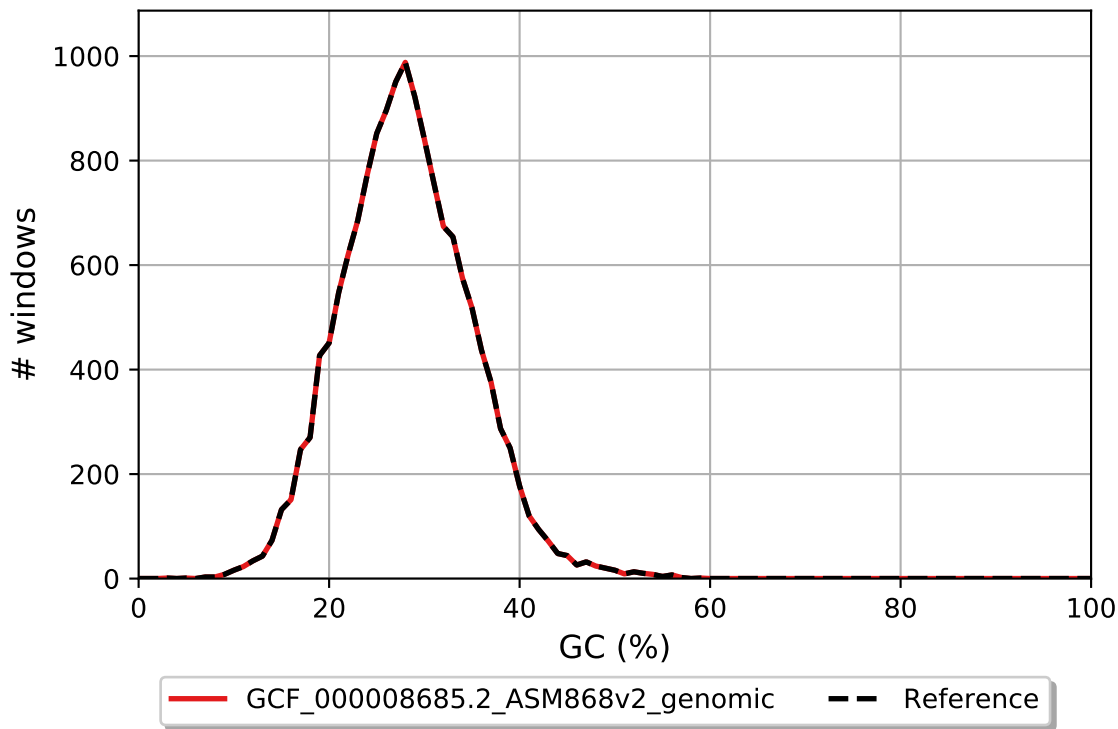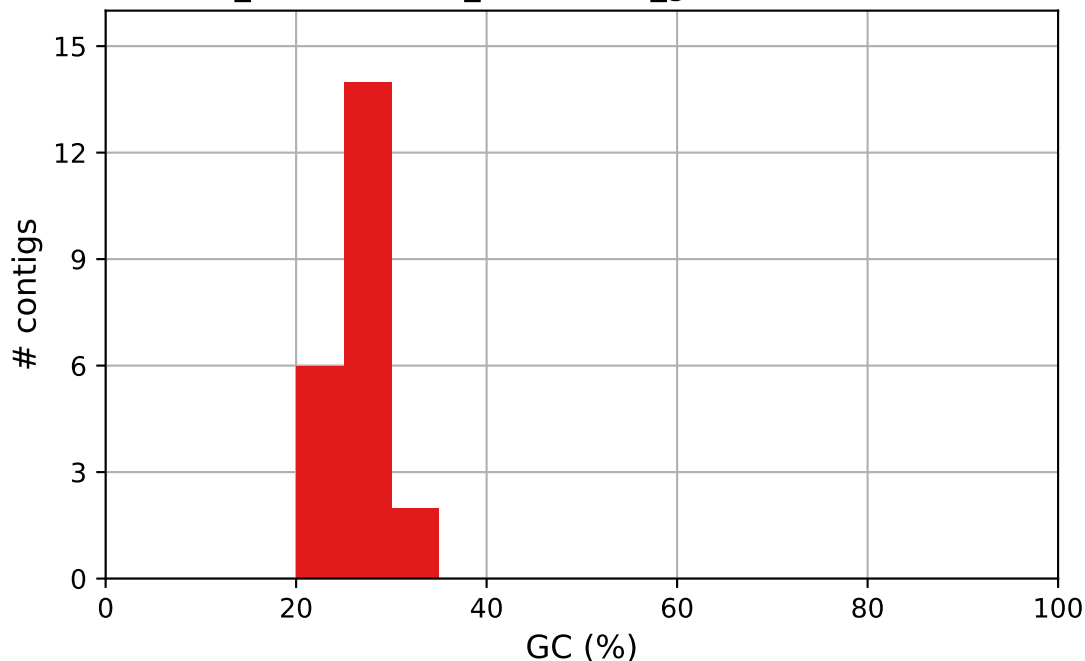
Nx

GCF_000008685.2_ASM868v2_genomic

NGx

GCF_000008685.2_ASM868v2_genomic

Cumulative length

GC content

windows

GC (%)

GCF_000008685.2_ASM868v2_genomic ----- Reference
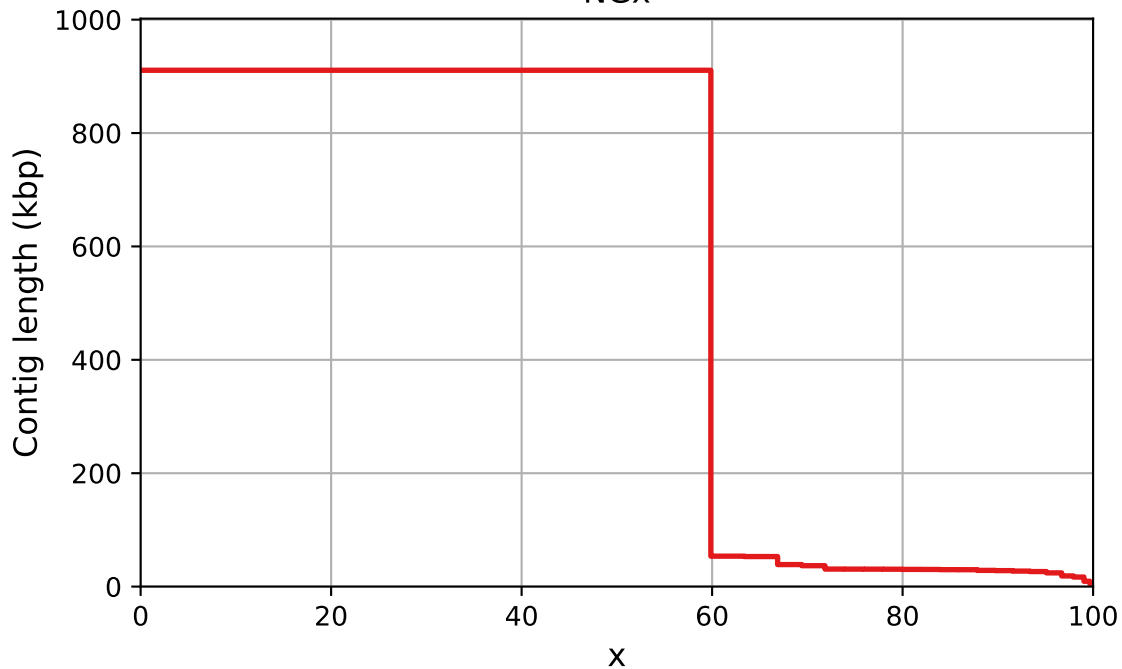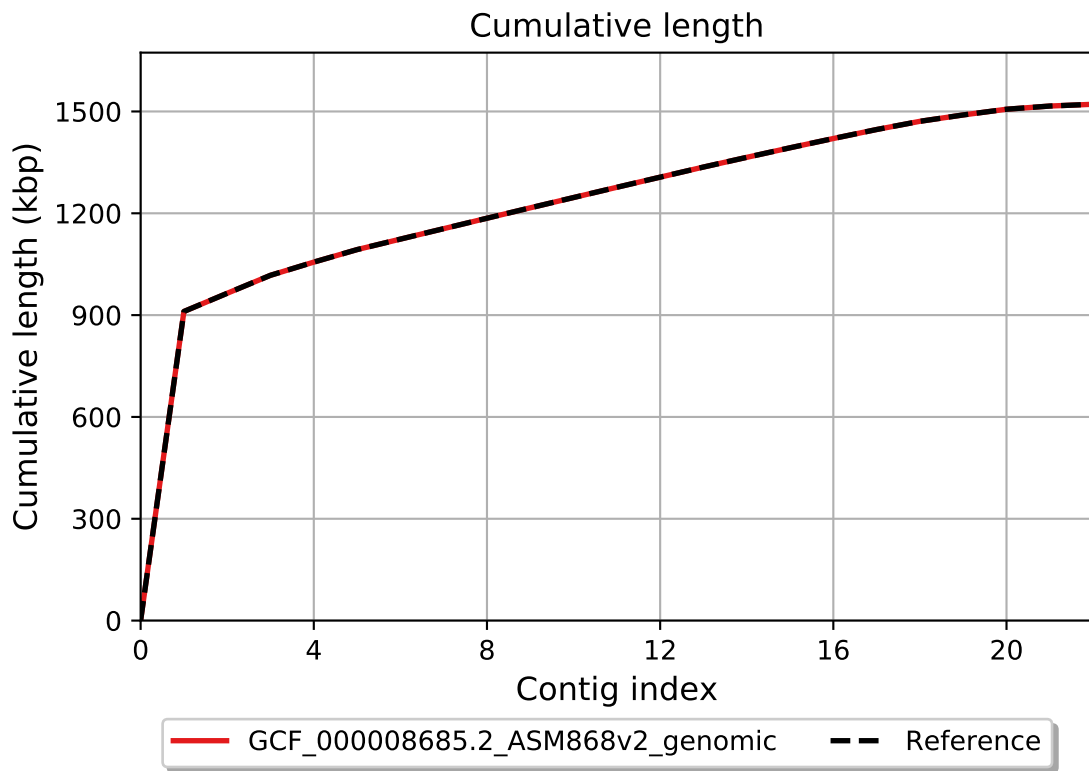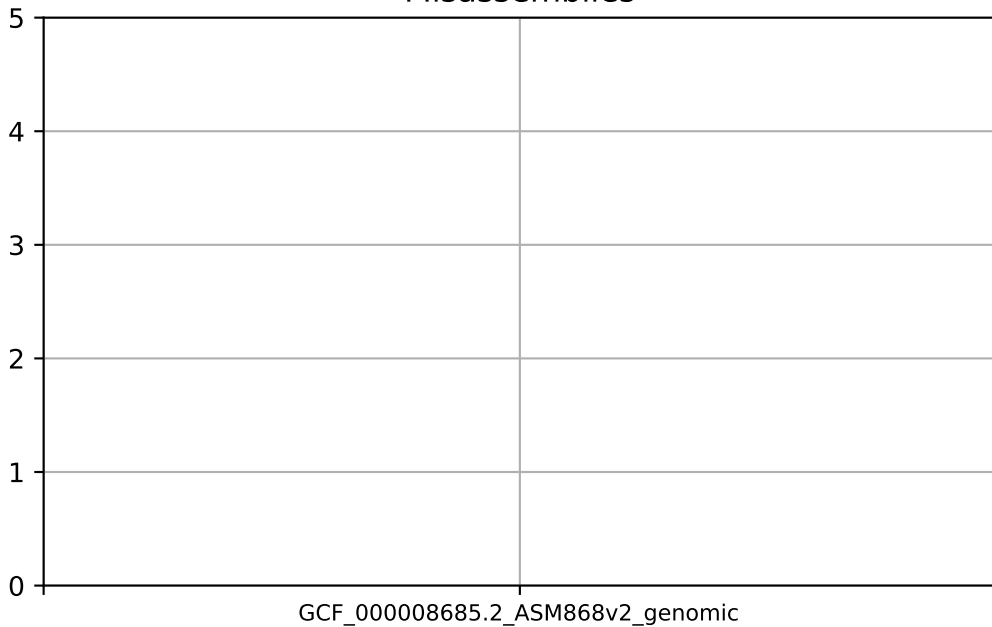
GCF_000008685.2_ASM868v2_genomic GC content

GCF_000008685.2_ASM868v2_genomic

Misassemblies
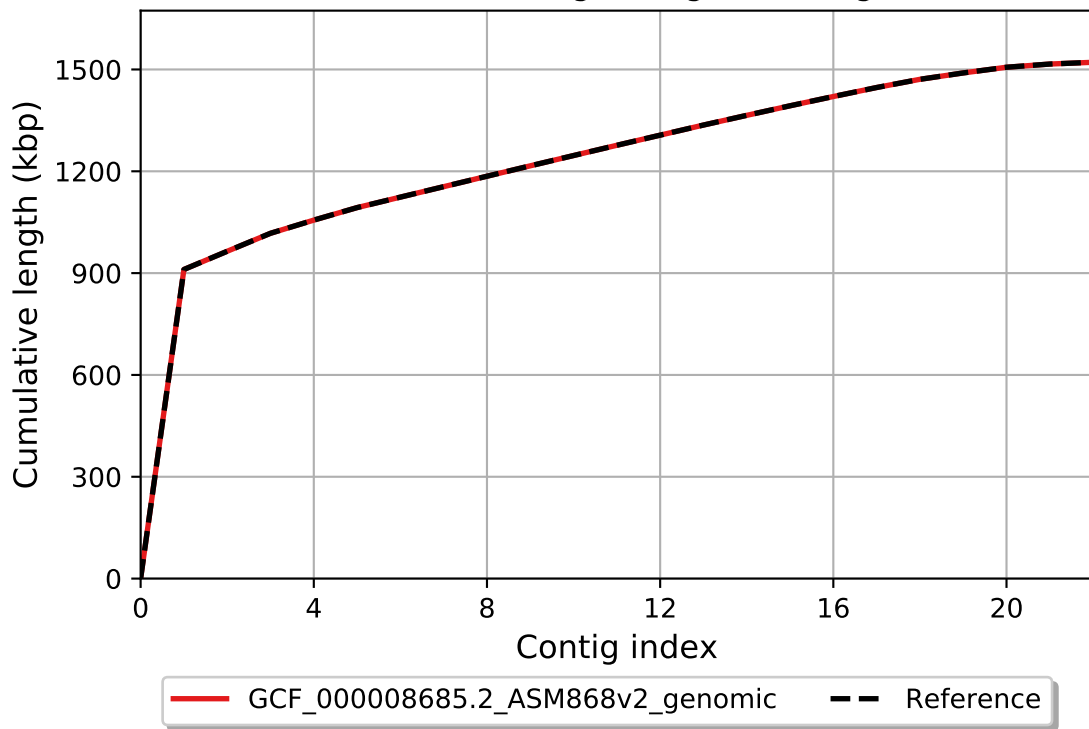
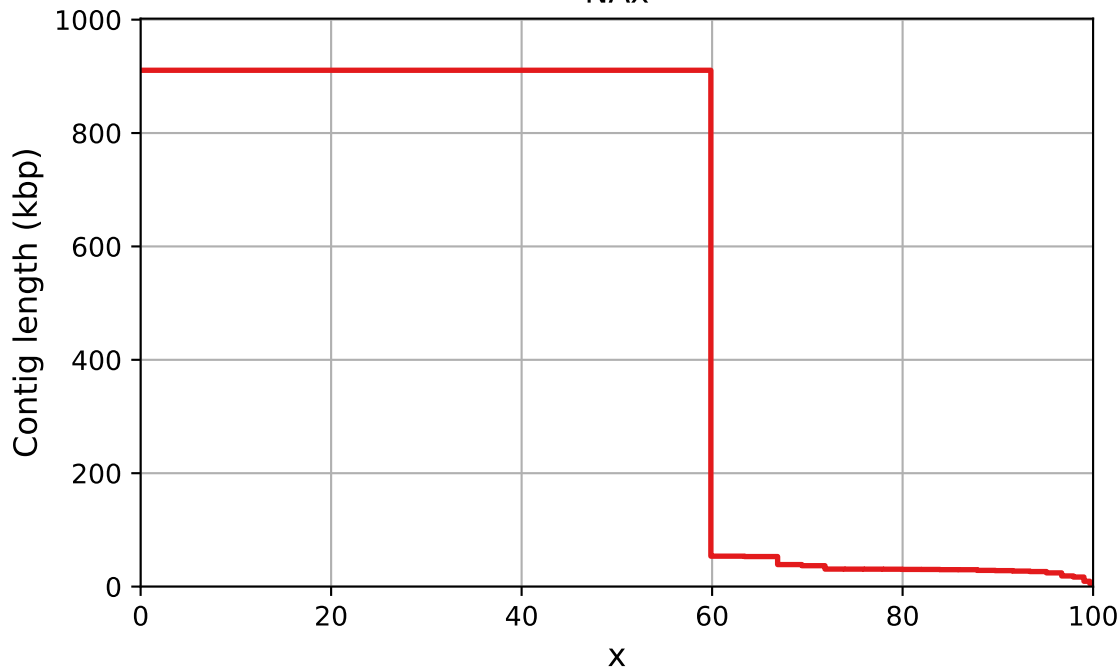GCF_000008685.2_ASM868v2_genomic

FRCurve (misassemblies)

GCF_000008685.2_ASM868v2_genomic

Cumulative length (aligned contigs)

NAx

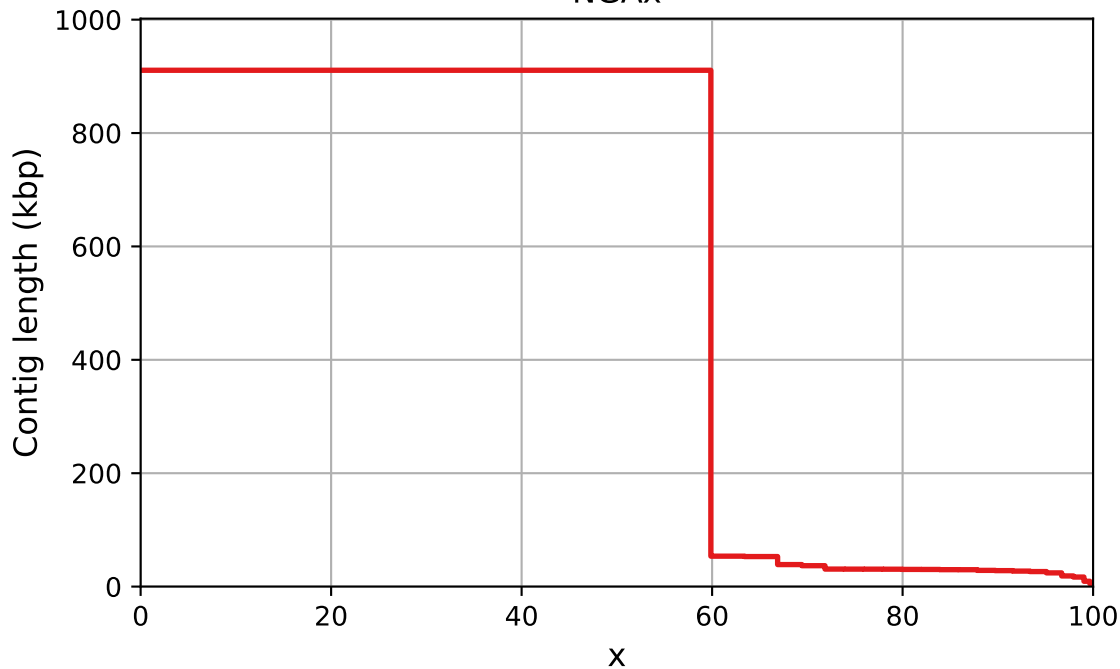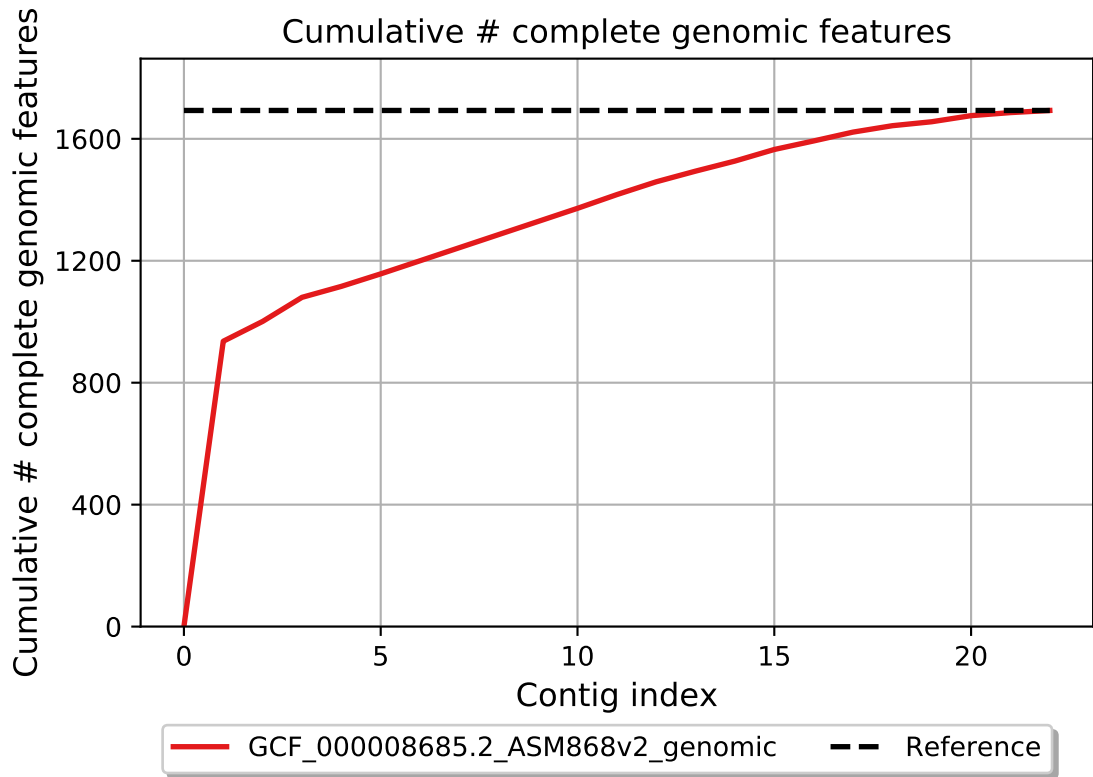GCF_000008685.2_ASM868v2_genomic

NGAx

GCF_000008685.2_ASM868v2_genomic

Cumulative # complete genomic features

FRCurve (genomic features)

GCF_000008685.2_ASM868v2_genomic