Report

	GCA_002442595.2_ASM244259v2_genomic
# contigs (>= 0 bp)	19
# contigs (>= 1000 bp)	19
# contigs (>= 5000 bp)	19
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1409089
Total length (>= 1000 bp)	1409089
Total length (>= 5000 bp)	1409089
Total length (>= 10000 bp)	1400375
Total length (>= 25000 bp)	1318614
Total length (>= 50000 bp)	957413
# contigs	19
Largest contig	903654
Total length	1409089
Reference length	1521208
GC (%)	28.30
Reference GC (%)	28.18
N50	903654
NG50	903654
N90	27643
NG90	18340
auN	590634.8
auNG	547102.7
L50	1
LG50	1
L90	13
LG90	17
# misassemblies	24
# misassembled contigs	12
Misassembled contigs length	374760
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 13 part
Unaligned length	113068
Genome fraction (%)	78.783
Duplication ratio	1.080
# N's per 100 kbp	0.00
# mismatches per 100 kbp	932.37
# indels per 100 kbp	60.88
# genomic features	1250 + 39 part
Largest alignment	903464
Total aligned length	1294341
NA50	903464
NGA50	903464
NA90	2247
NGA90	-
auNA	585142.7
auNGA	542015.4
LA50	1
LGA50	1
LA90	30
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).
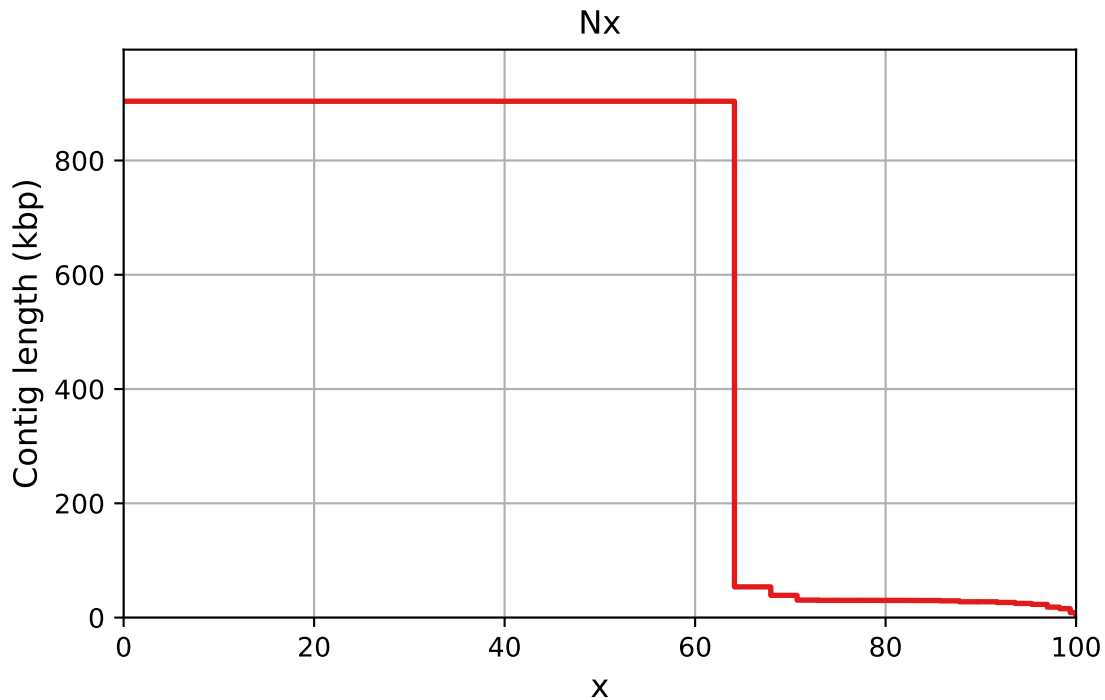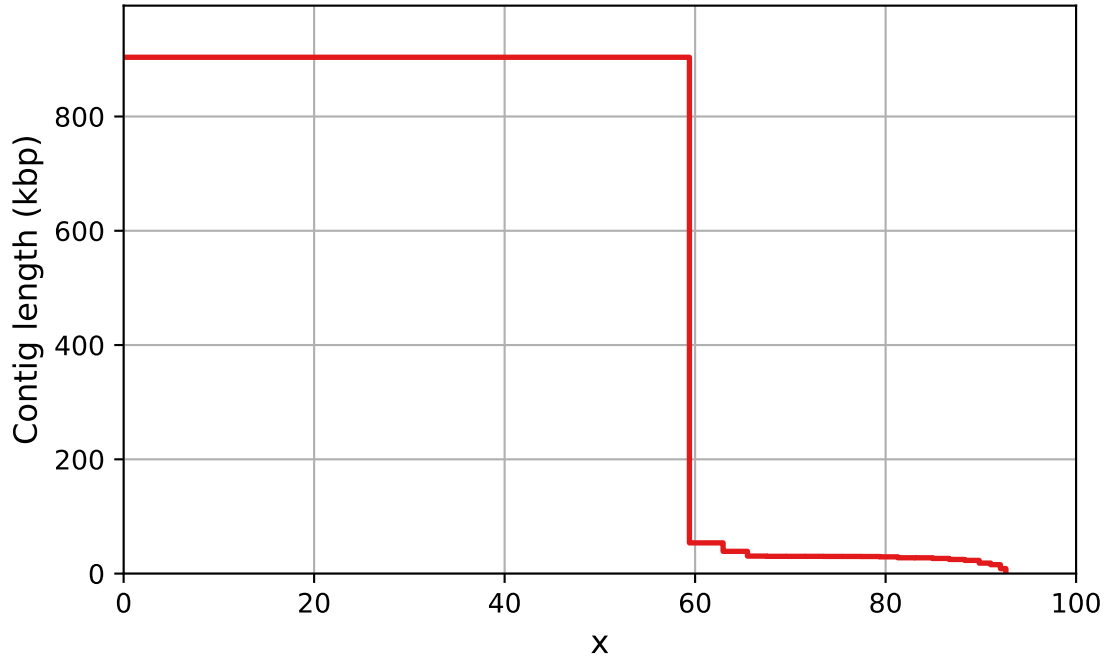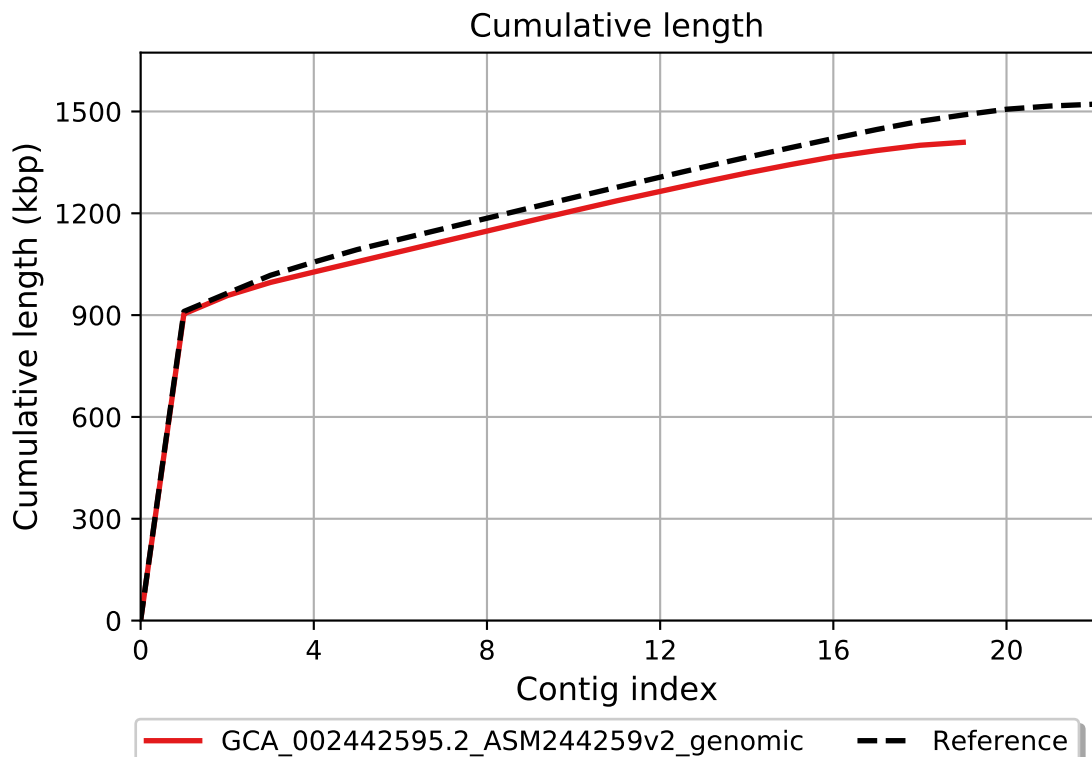
Misassemblies report

	GCA_002442595.2_ASM244259v2_genomic
# misassemblies	24
# contig misassemblies	24
# c. relocations	2
# c. translocations	20
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	12
Misassembled contigs length	374760
# local misassemblies	10
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	12068
# indels	788
# indels (<= 5 bp)	706
# indels (> 5 bp)	82
Indels length	3797

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_002442595.2_ASM244259v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	13
Partially unaligned length	113068
# 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).
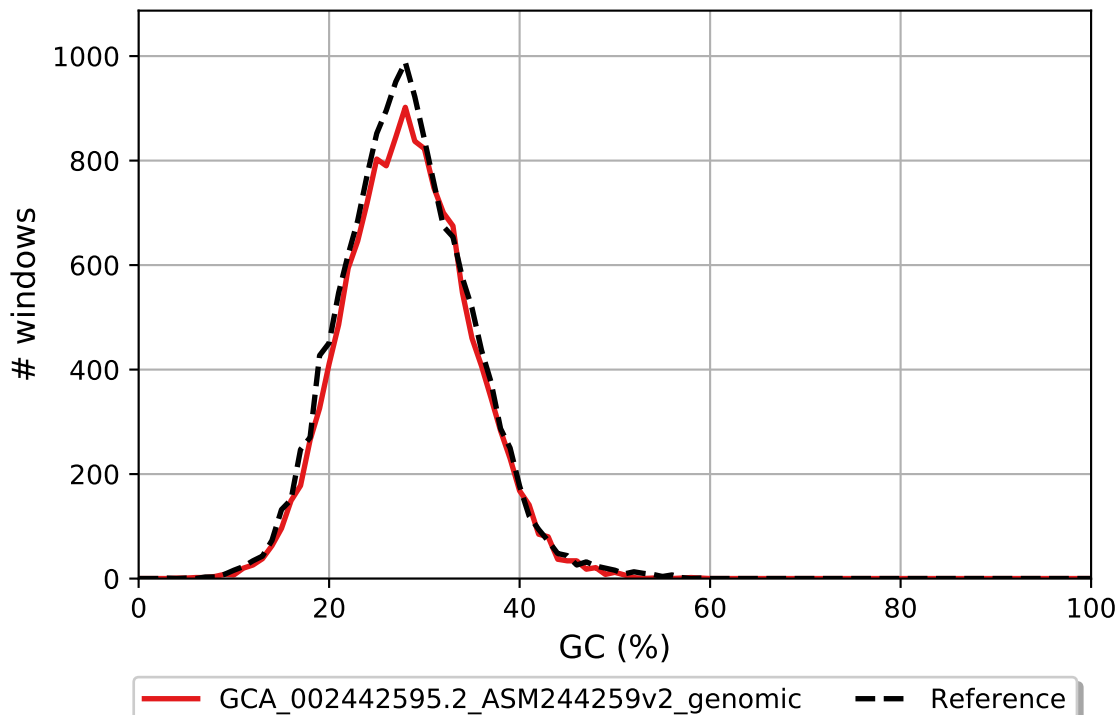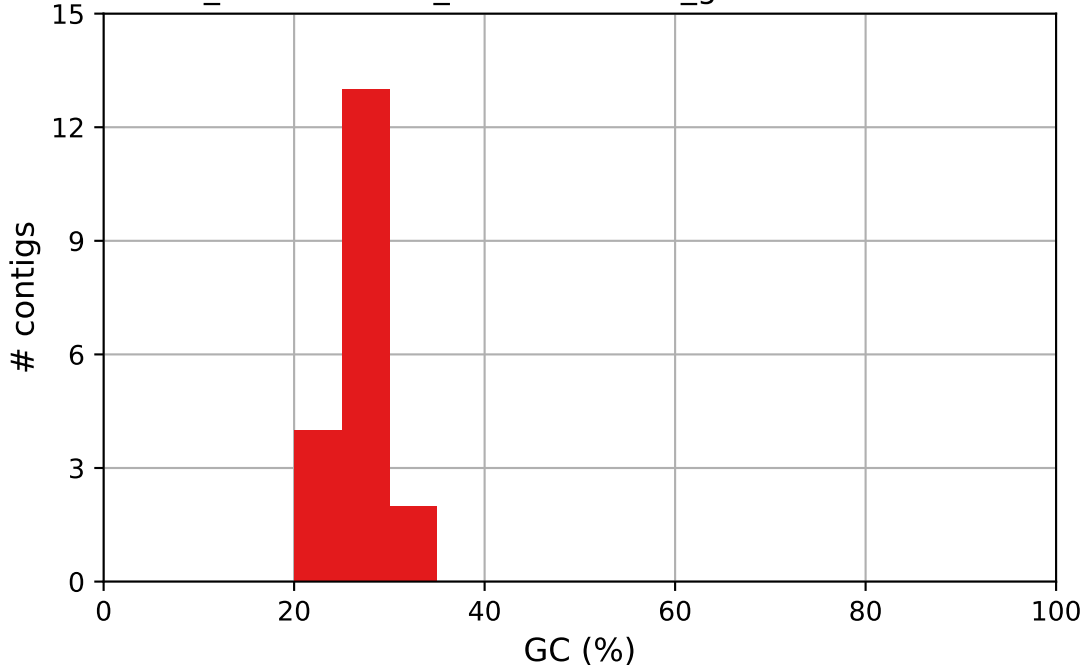
Nx

GCA_002442595.2_ASM244259v2_genomic

NGx

GCA_002442595.2_ASM244259v2_genomic

Cumulative length

GC content

GCA_002442595.2_ASM244259v2_genomic GC content

Misassemblies

GCA_002442595.2_ASM244259v2_genomic
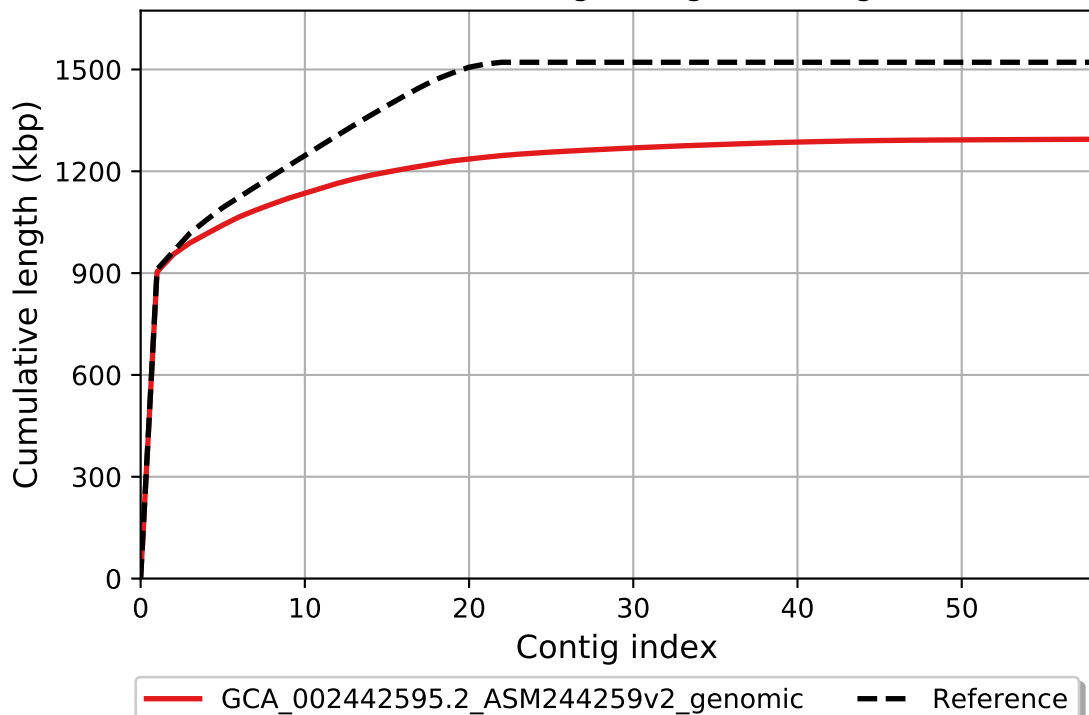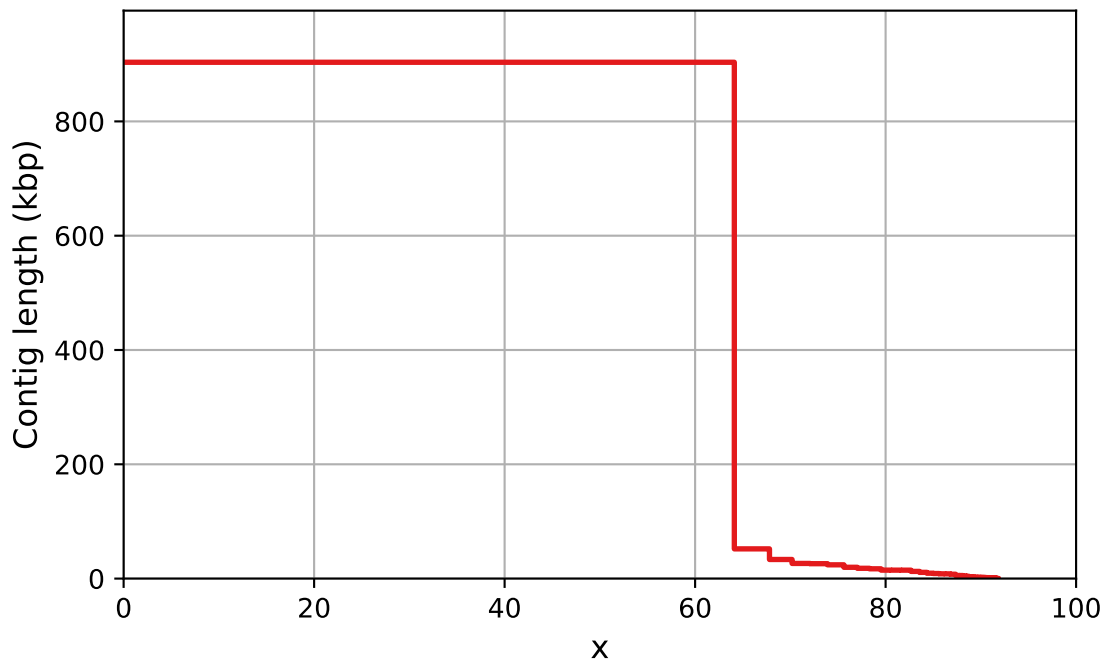
- # relocations
- # translocations
- # inversions

FRCurve (misassemblies)
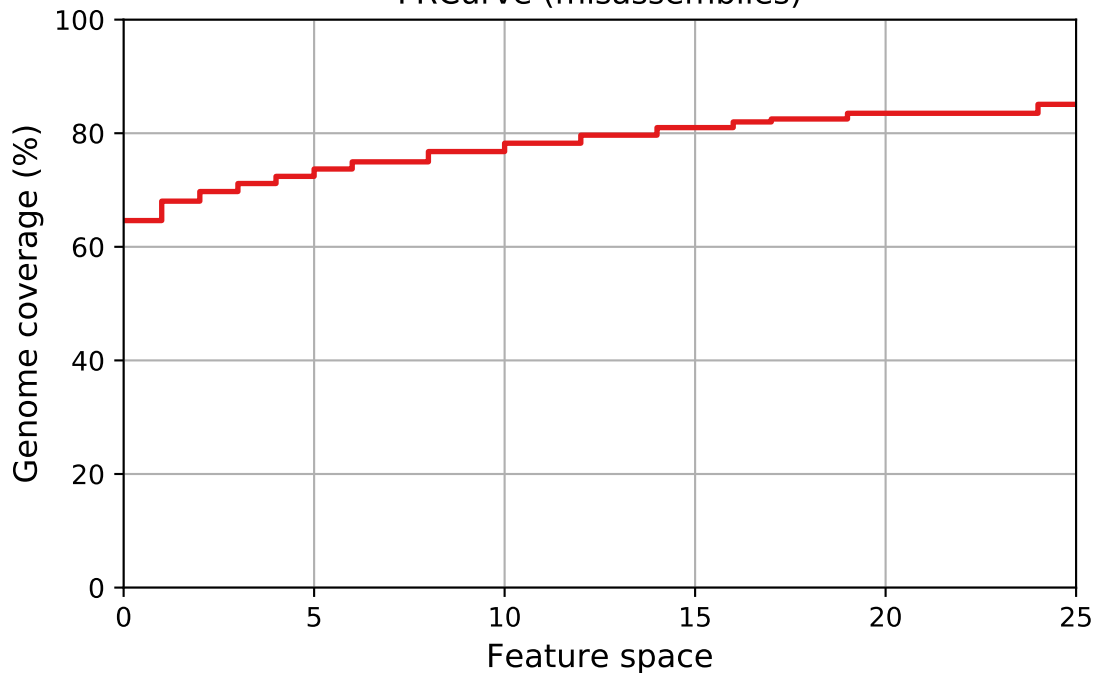
GCA_002442595.2_ASM244259v2_genomic

Cumulative length (aligned contigs)

NAx

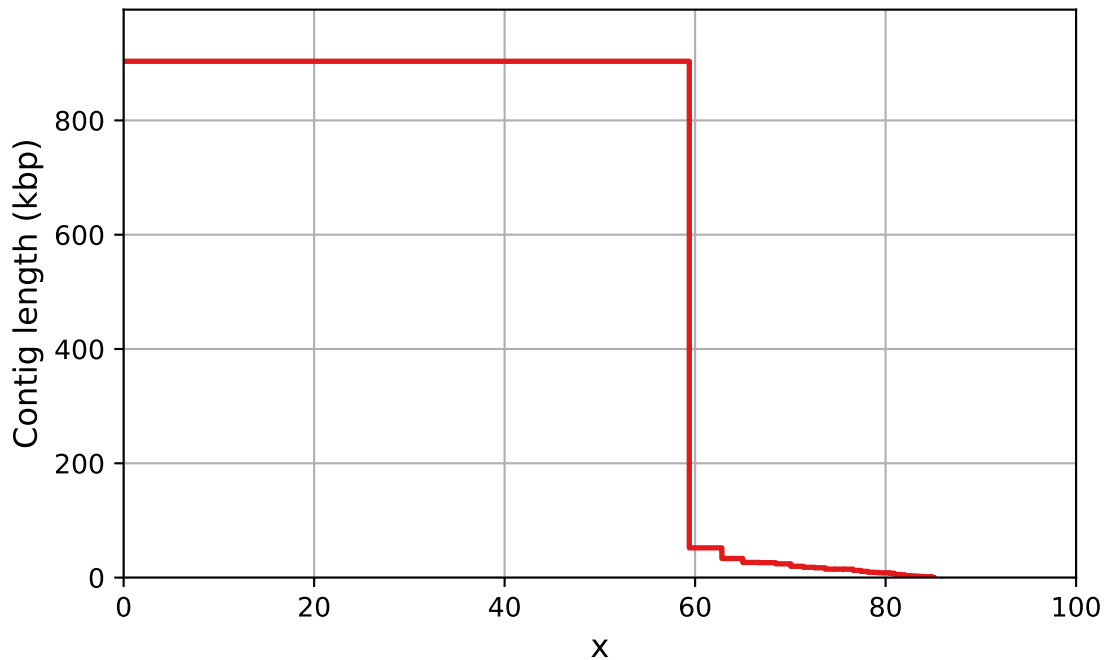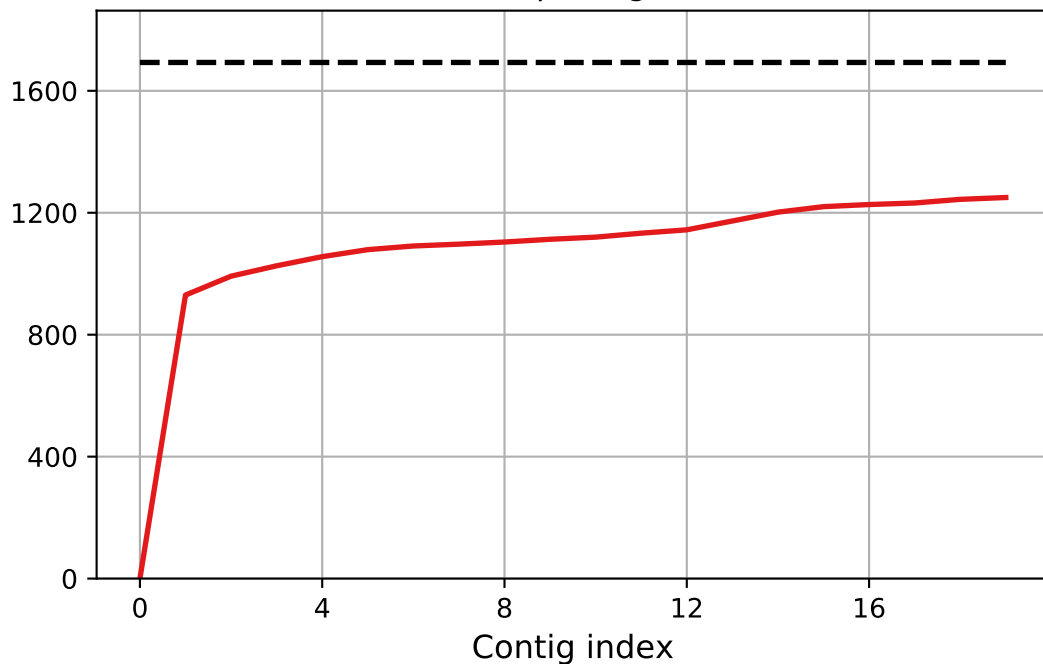GCA_002442595.2_ASM244259v2_genomic

NGAx

Cumulative # complete genomic features
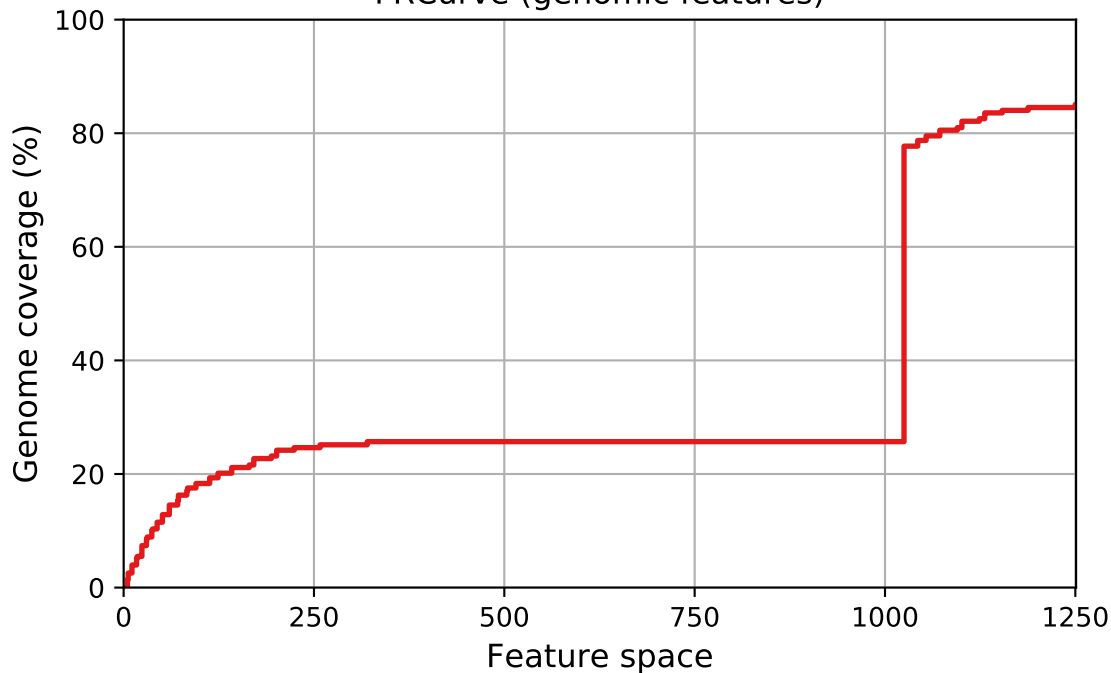
FRCurve (genomic features)

GCA_002442595.2_ASM244259v2_genomic