Report

	GCF_000181555.2_ASM18155v2_genomic
# contigs (>= 0 bp)	32
# contigs (>= 1000 bp)	28
# contigs (>= 5000 bp)	21
# contigs (>= 10000 bp)	21
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1469834
Total length (>= 1000 bp)	1466865
Total length (>= 5000 bp)	1456916
Total length (>= 10000 bp)	1456916
Total length (>= 25000 bp)	1314751
Total length (>= 50000 bp)	962699
# contigs	31
Largest contig	908814
Total length	1469559
Reference length	1521208
GC (%)	28.13
Reference GC (%)	28.18
N50	908814
NG50	908814
N90	24910
NG90	23638
auN	573107.5
auNG	553649.0
L50	1
LG50	1
L90	15
LG90	17
# misassemblies	18
# misassembled contigs	10
Misassembled contigs length	1172359
# local misassemblies	26
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	0 + 19 part
Unaligned length	209130
Genome fraction (%)	79.320
Duplication ratio	1.044
# N's per 100 kbp	5.65
# mismatches per 100 kbp	881.52
# indels per 100 kbp	57.29
# genomic features	1264 + 39 part
Largest alignment	468260
Total aligned length	1260214
NA50	435160
NGA50	435160
NA90	-
NGA90	-
auNA	282674.8
auNGA	273077.2
LA50	2
LGA50	2
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).
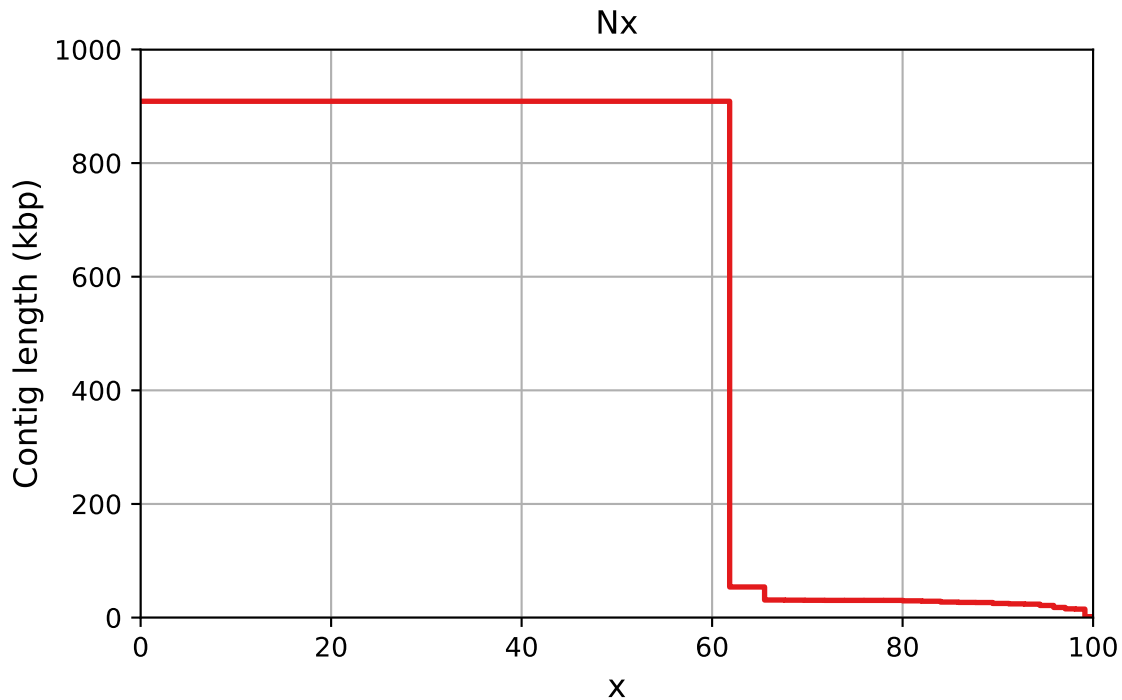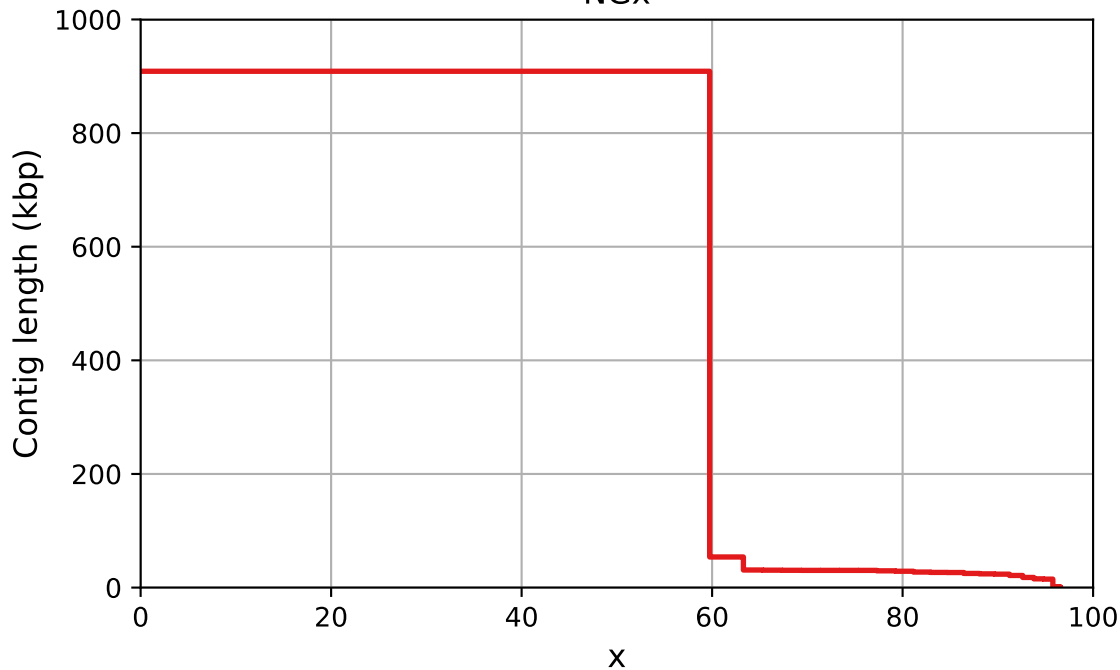
Misassemblies report

	GCF_000181555.2_ASM18155v2_genomic
# misassemblies	18
# contig misassemblies	18
# c. relocations	4
# c. translocations	14
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	1172359
# local misassemblies	26
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	11109
# indels	722
# indels (<= 5 bp)	634
# indels (> 5 bp)	88
Indels length	5434

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_000181555.2_ASM18155v2_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	19
Partially unaligned length	209130
# N's	83

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).
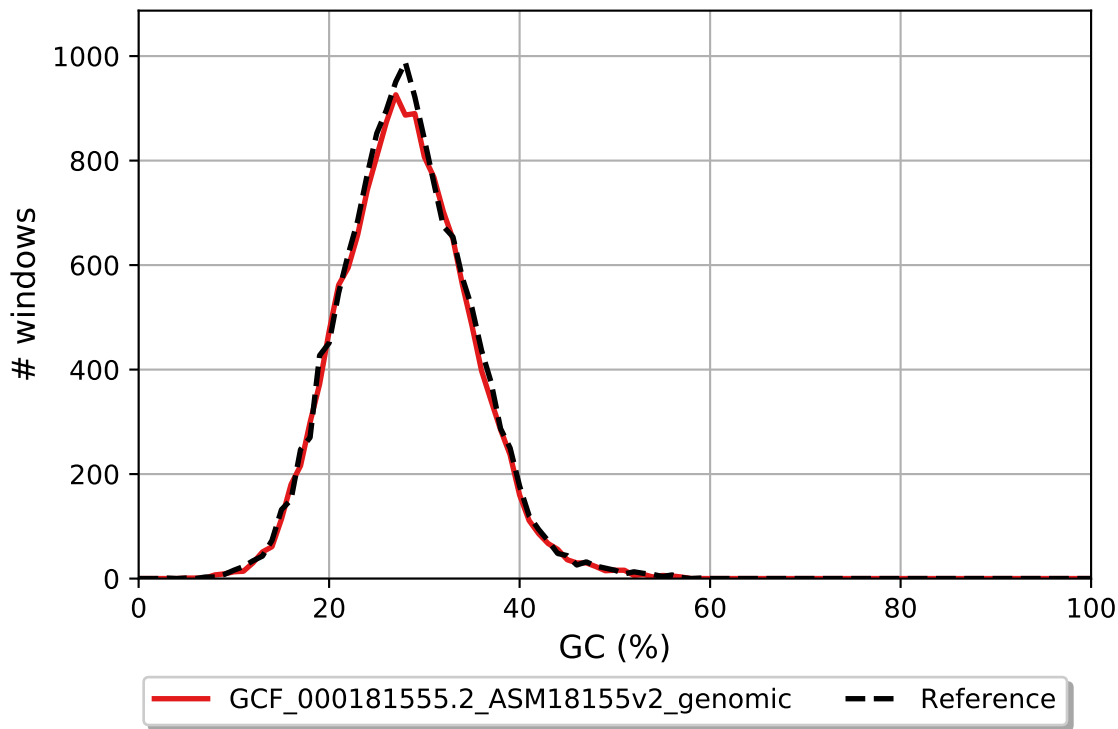
Nx

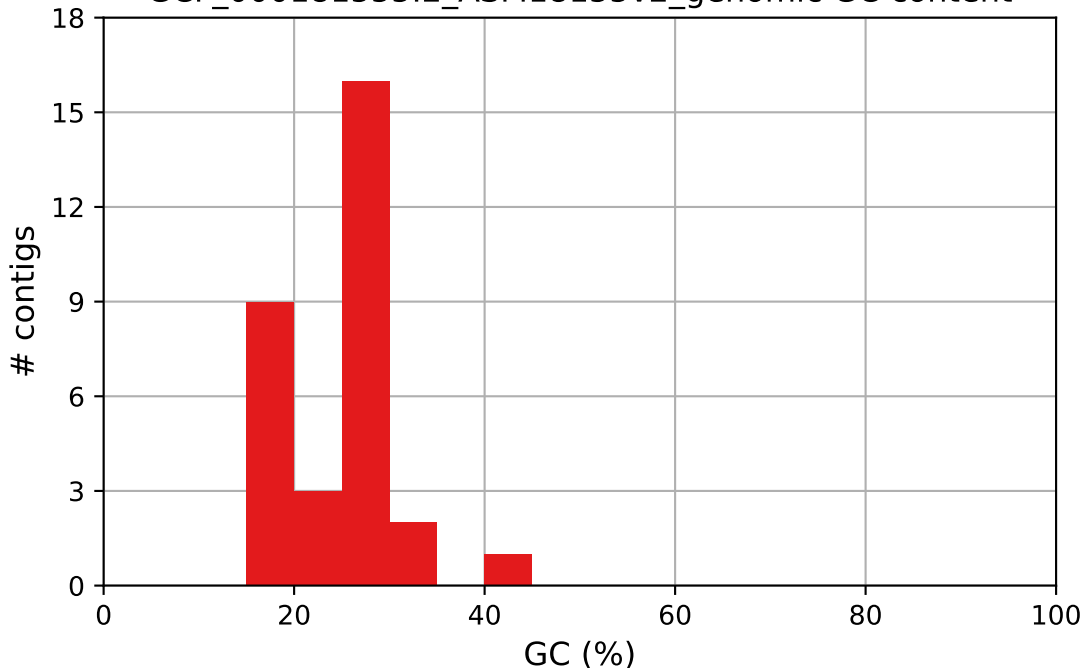GCF_000181555.2_ASM18155v2_genomic

NGx

GCF_000181555.2_ASM18155v2_genomic
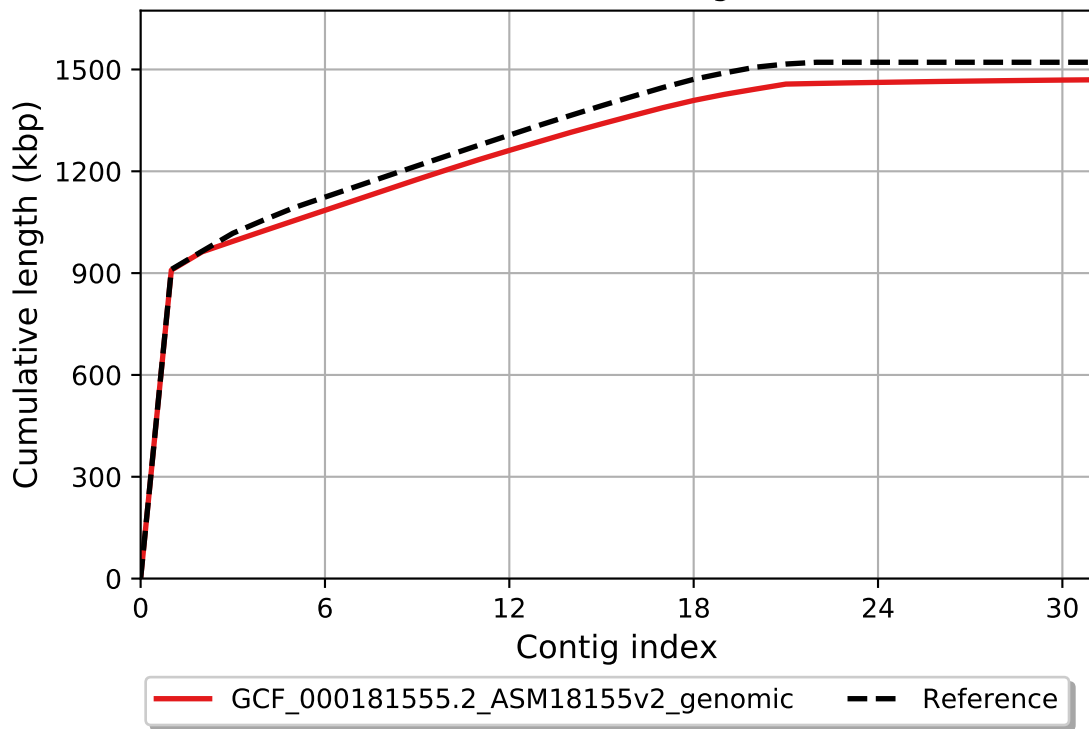
Cumulative length

GC content

GCF_000181555.2_ASM18155v2_genomic GC content
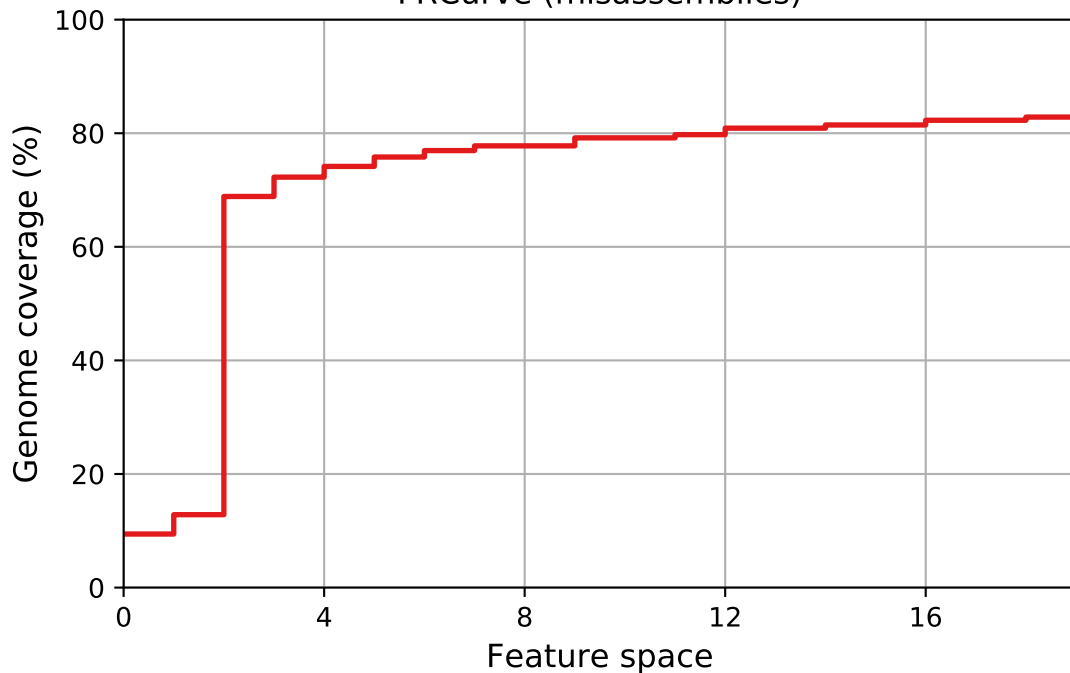
Misassemblies
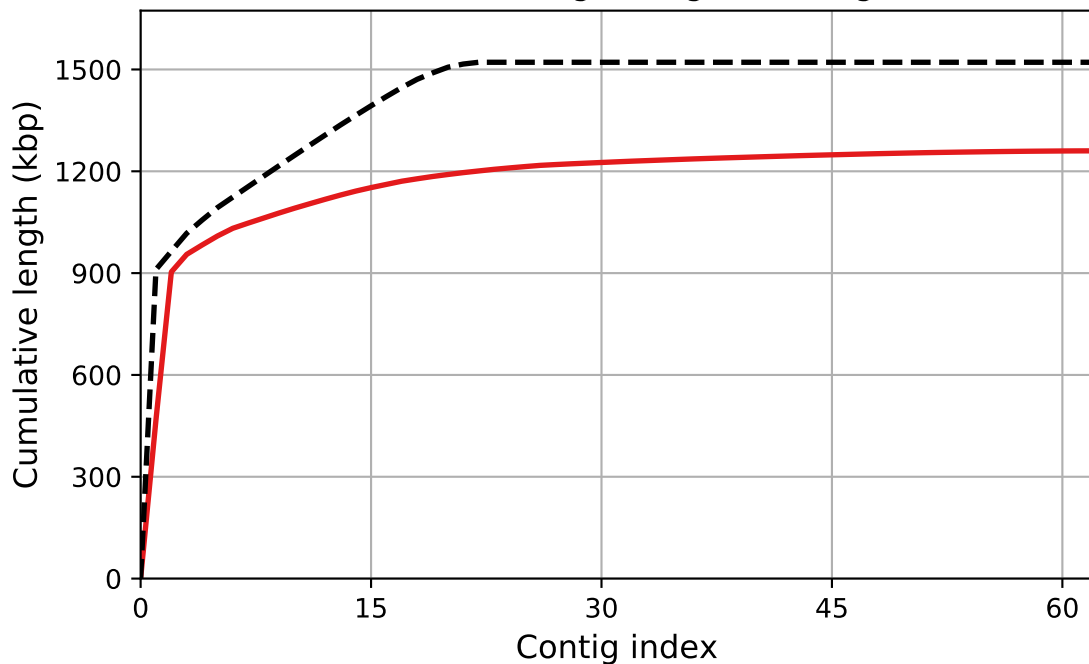
GCF_000181555.2_ASM18155v2_genomic
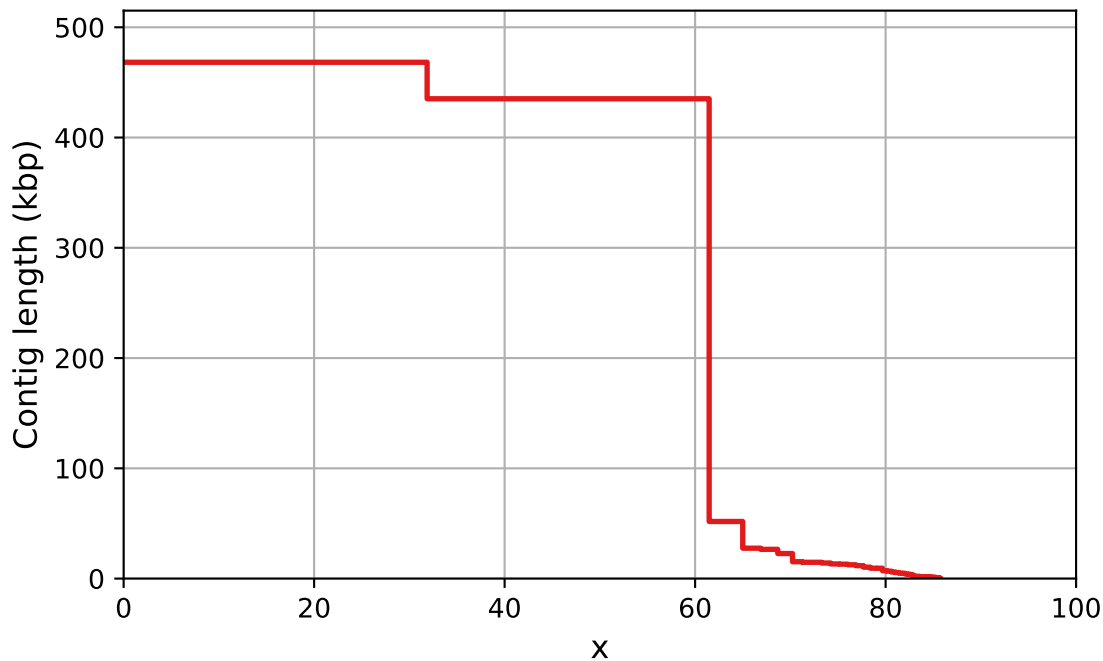
- # relocations
- # translocations

FRCurve (misassemblies)

GCF_000181555.2_ASM18155v2_genomic

Cumulative length (aligned contigs)

NAx

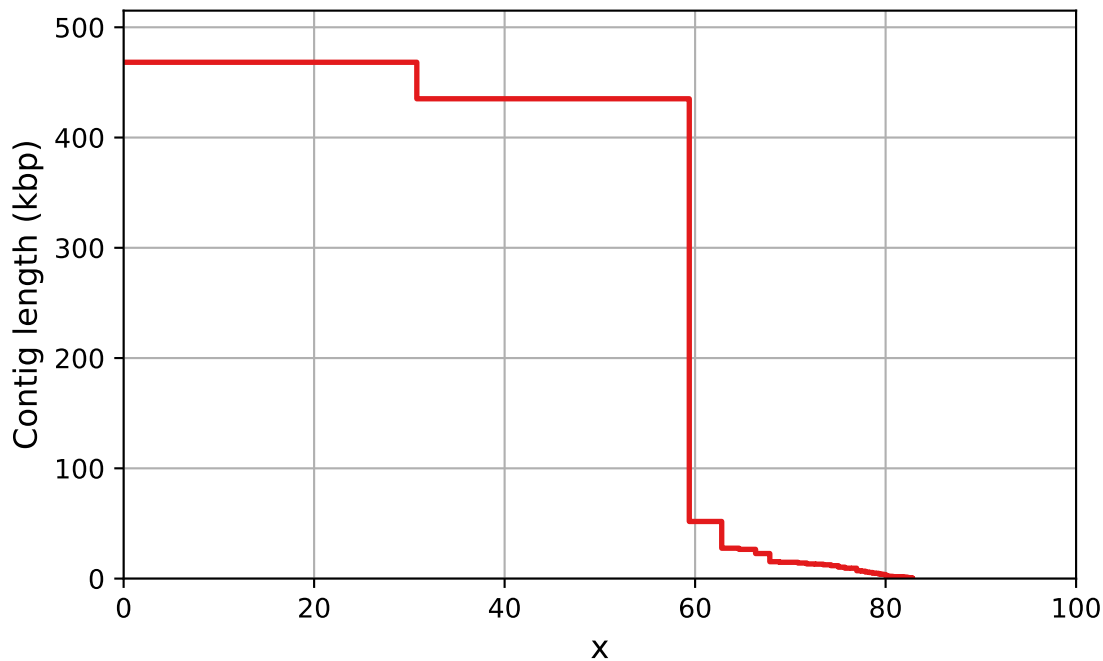GCF_000181555.2_ASM18155v2_genomic

NGAx

GCF_000181555.2_ASM18155v2_genomic

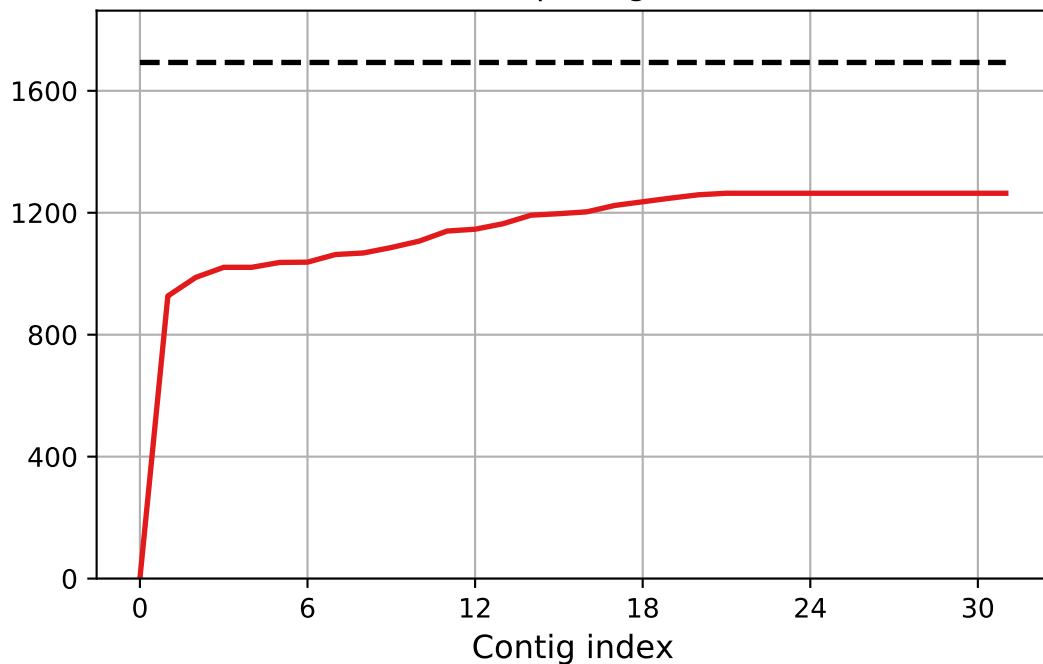Cumulative # complete genomic features

FRCurve (genomic features)

GCF_000181555.2_ASM18155v2_genomic