Report

	GCF_024662175.1_ASM2466217v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	18
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1417706
Total length (>= 1000 bp)	1417706
Total length (>= 5000 bp)	1417706
Total length (>= 10000 bp)	1417706
Total length (>= 25000 bp)	1357402
Total length (>= 50000 bp)	974305
# contigs	18
Largest contig	920773
Total length	1417706
Reference length	1521208
GC (%)	28.16
Reference GC (%)	28.18
N50	920773
NG50	920773
N90	28768
NG90	21173
auN	608890.7
auNG	567462.2
L50	1
LG50	1
L90	12
LG90	16
# misassemblies	18
# misassembled contigs	10
Misassembled contigs length	1203046
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 15 part
Unaligned length	177750
Genome fraction (%)	78.659
Duplication ratio	1.036
# N's per 100 kbp	0.00
# mismatches per 100 kbp	844.86
# indels per 100 kbp	51.95
# genomic features	1255 + 46 part
Largest alignment	905132
Total aligned length	1239616
NA50	905132
NGA50	905132
NA90	-
NGA90	-
auNA	582296.2
auNGA	542677.2
LA50	1
LGA50	1
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).
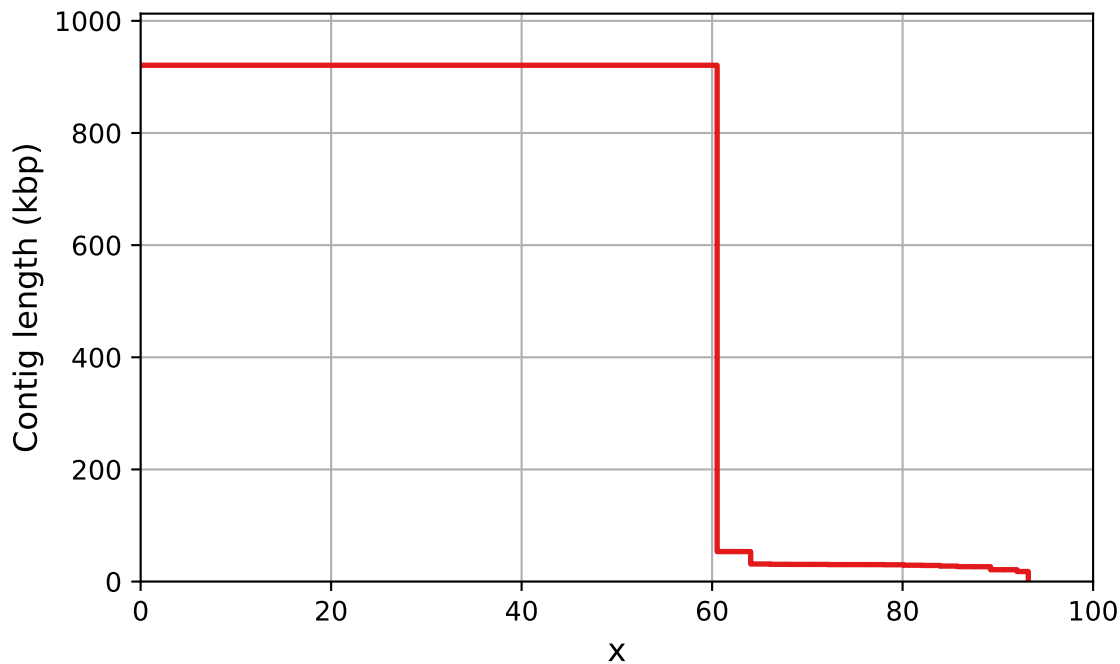
Misassemblies report

	GCF_024662175.1_ASM2466217v1_genomic
# misassemblies	18
# contig misassemblies	18
# c. relocations	5
# c. translocations	13
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	10
Misassembled contigs length	1203046
# local misassemblies	14
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	10473
# indels	644
# indels (<= 5 bp)	577
# indels (> 5 bp)	67
Indels length	4262

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
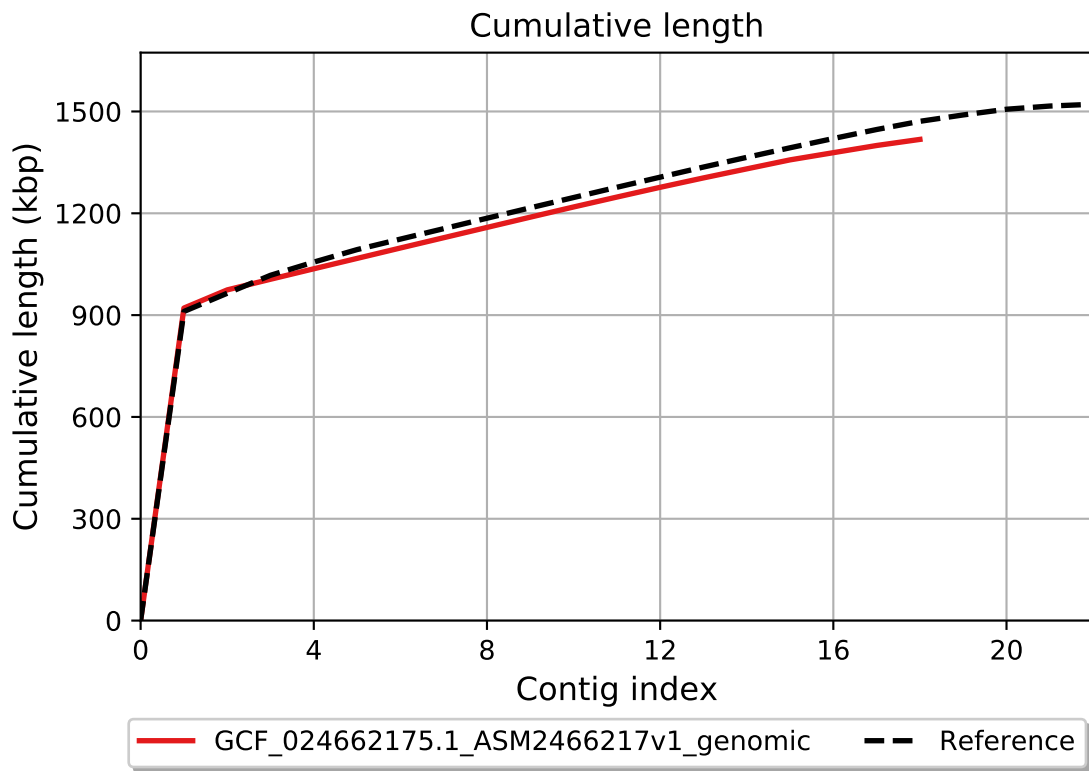
	GCF_024662175.1_ASM2466217v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	15
Partially unaligned length	177750
# N's	0

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).
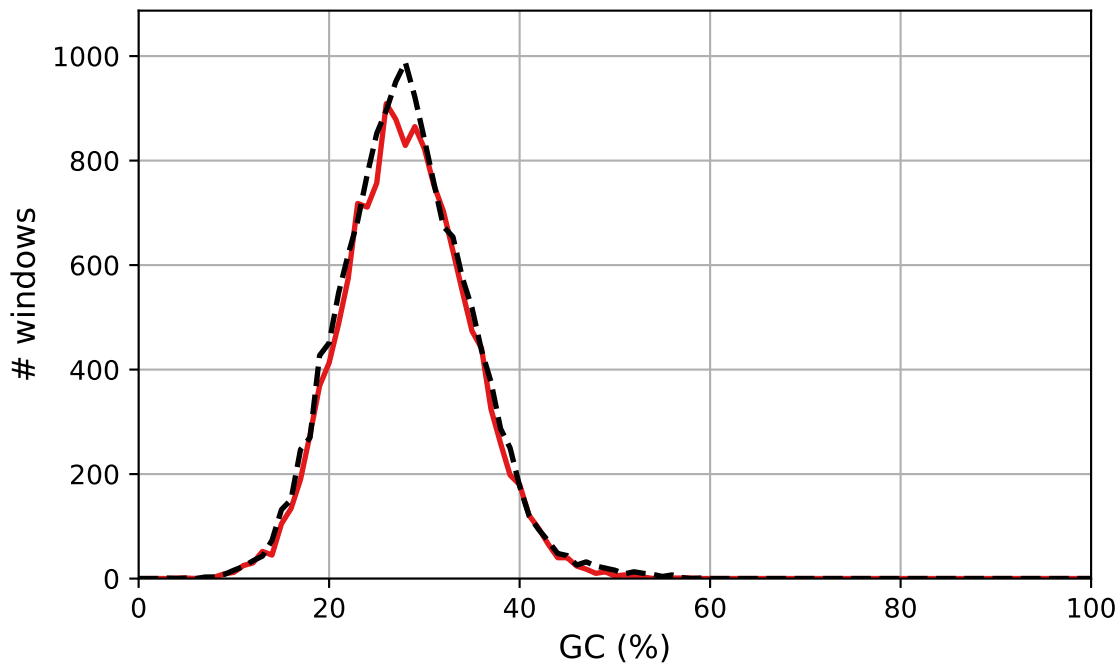
Nx
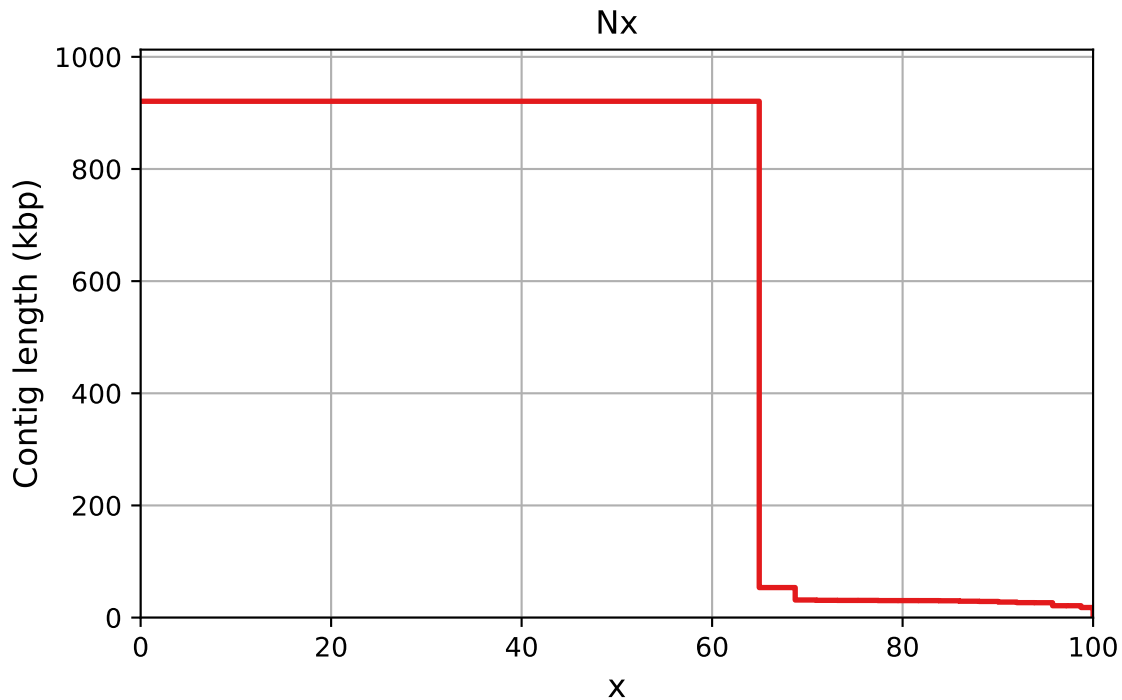
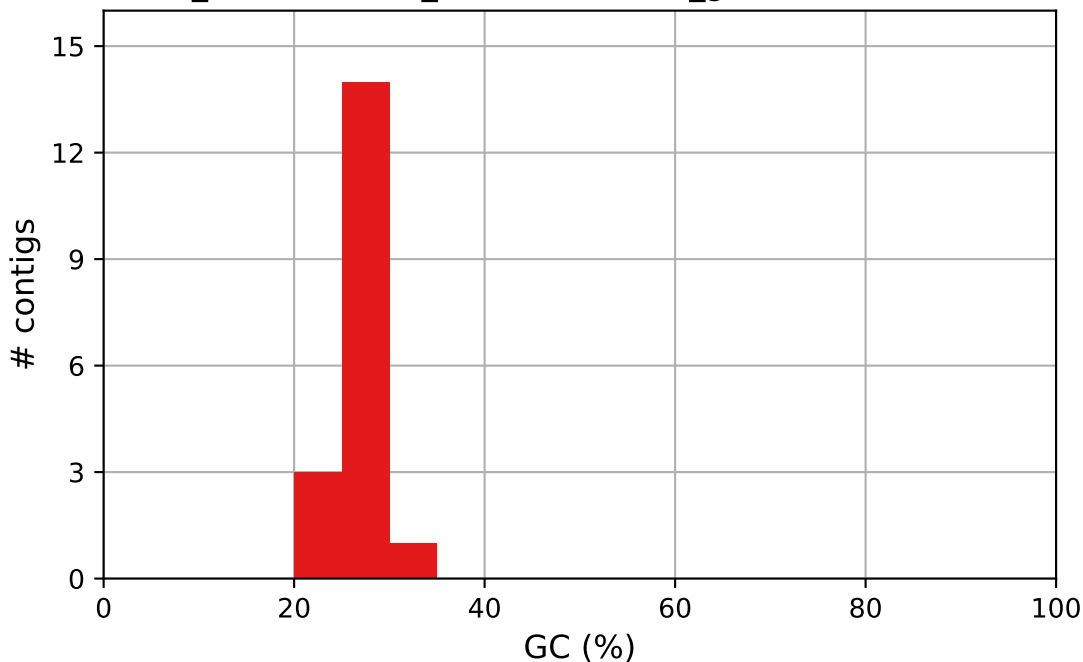GCF_024662175.1_ASM2466217v1_genomic

NGx

GCF_024662175.1_ASM2466217v1_genomic

Cumulative length

—— GCF_024662175.1_ASM2466217v1_genomic	– – Reference

GC content

windows vs GC (%)

Legend: GCF_024662175.1_ASM2466217v1_genomic — Reference

GCF_024662175.1_ASM2466217v1_genomic GC content

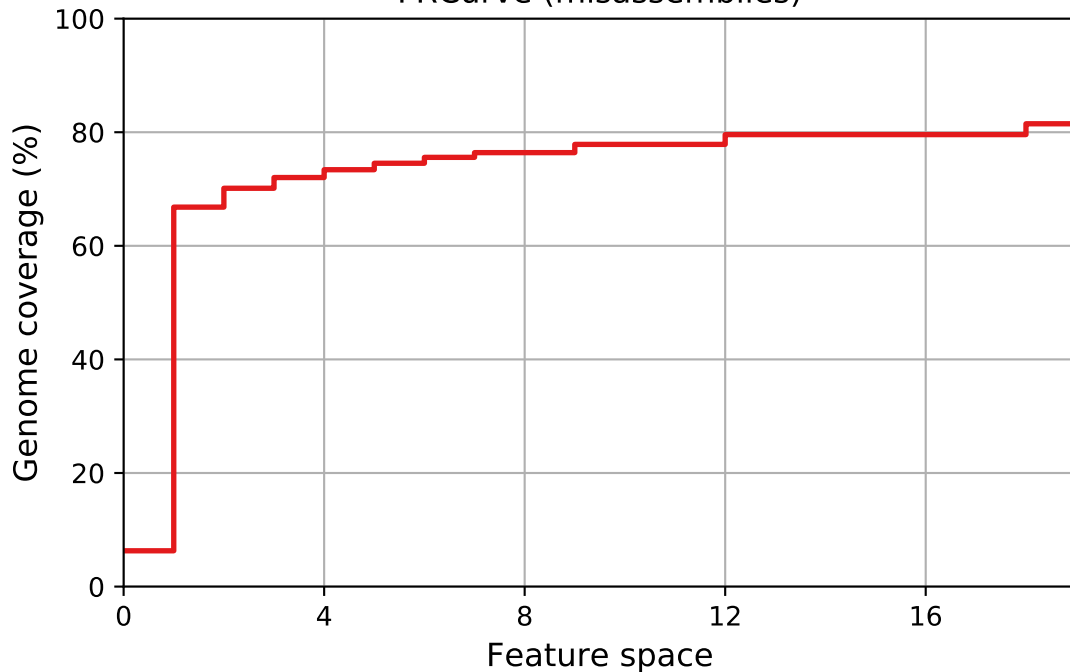Misassemblies
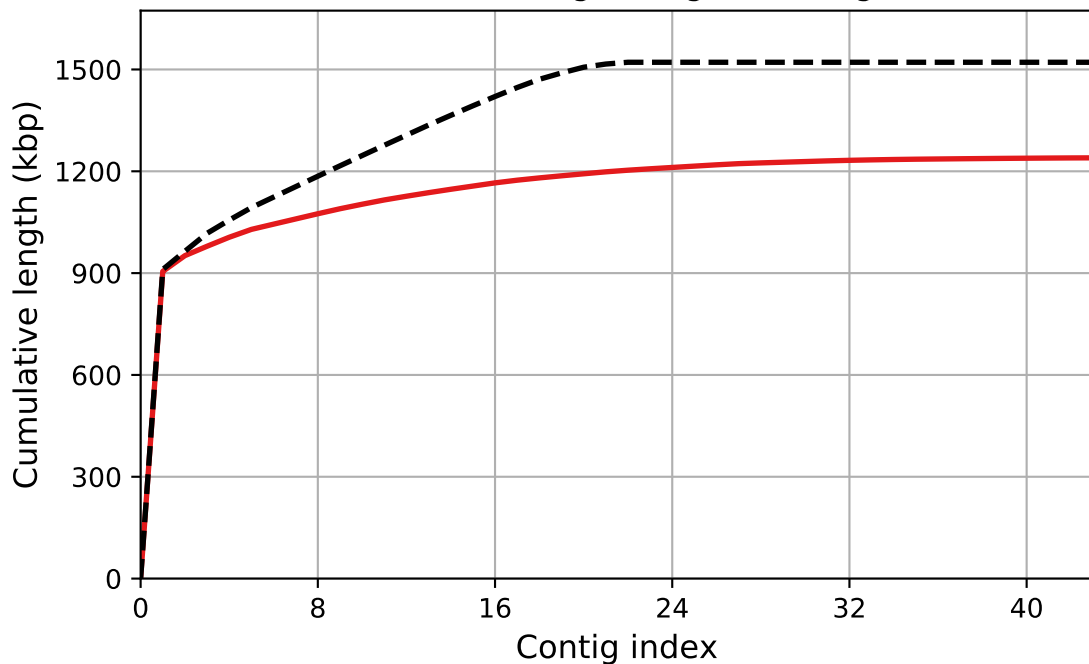
GCF_024662175.1_ASM2466217v1_genomic

■ # relocations   ■ # translocations

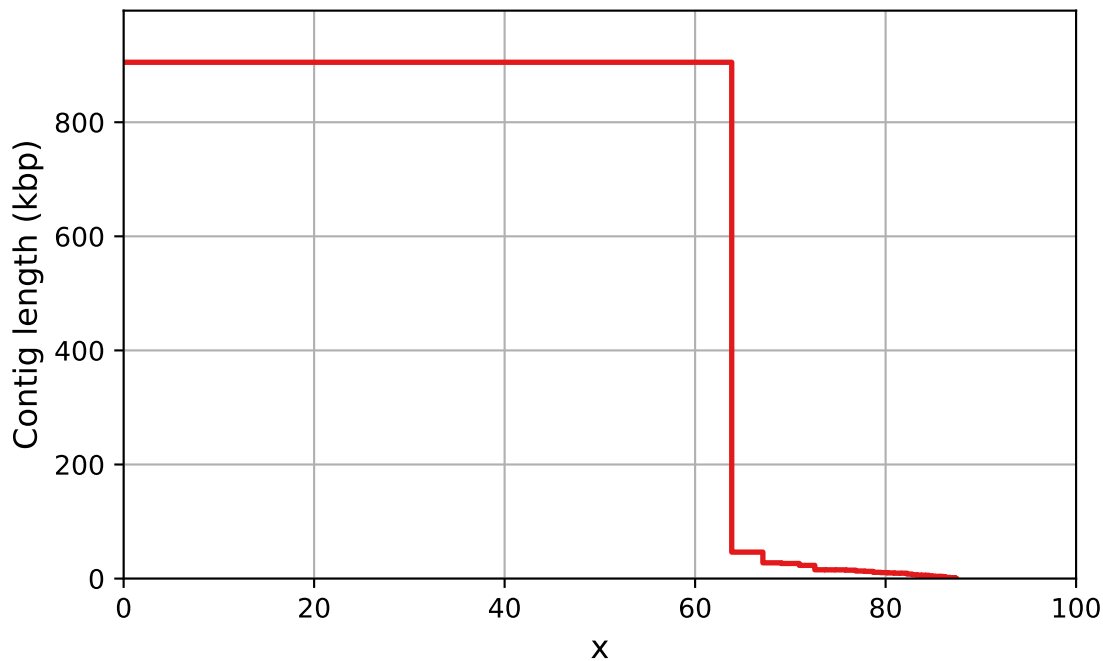FRCurve (misassemblies)

GCF_024662175.1_ASM2466217v1_genomic

Cumulative length (aligned contigs)
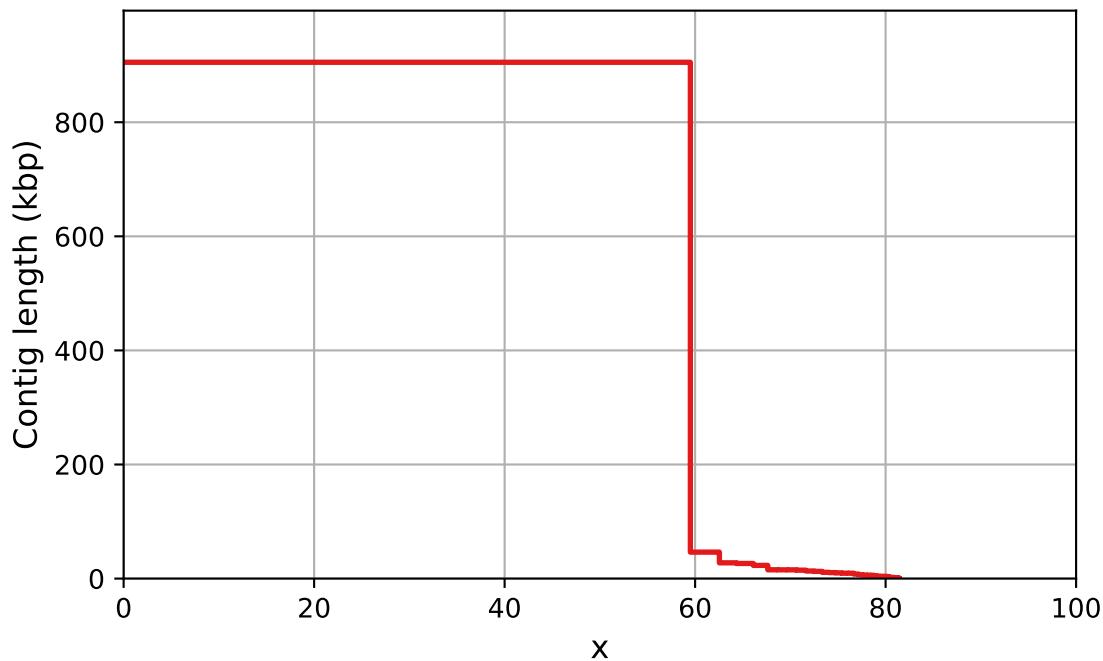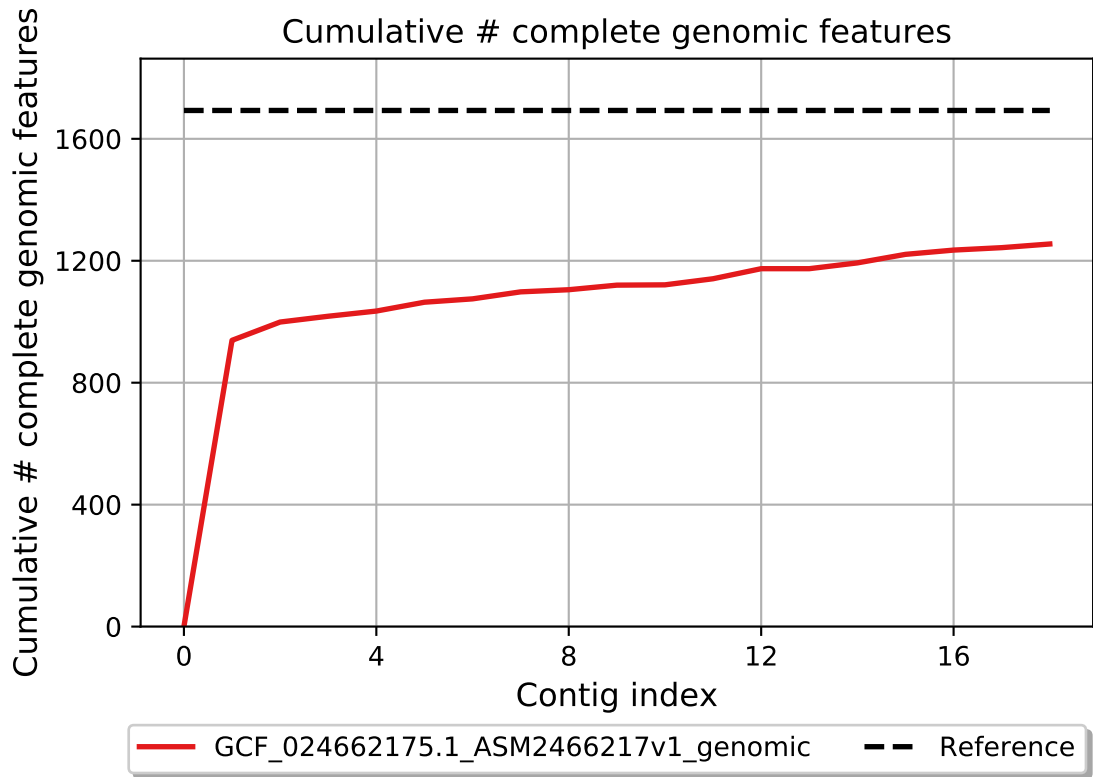
NAx

GCF_024662175.1_ASM2466217v1_genomic

NGAx

GCF_024662175.1_ASM2466217v1_genomic

Cumulative # complete genomic features

FRCurve (genomic features)

GCF_024662175.1_ASM2466217v1_genomic