Report

	GCA_003367295.1_ASM336729v1_genomic
# contigs (>= 0 bp)	16
# contigs (>= 1000 bp)	16
# contigs (>= 5000 bp)	16
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1280240
Total length (>= 1000 bp)	1280240
Total length (>= 5000 bp)	1280240
Total length (>= 10000 bp)	1280240
Total length (>= 25000 bp)	1161007
Total length (>= 50000 bp)	962310
# contigs	16
Largest contig	908512
Total length	1280240
Reference length	1521208
GC (%)	28.24
Reference GC (%)	28.18
N50	908512
NG50	908512
N90	26507
NG90	-
auN	653097.9
auNG	549643.5
L50	1
LG50	1
L90	9
LG90	-
# misassemblies	16
# misassembled contigs	6
Misassembled contigs length	133618
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	0 + 12 part
Unaligned length	123725
Genome fraction (%)	75.032
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	758.69
# indels per 100 kbp	44.05
# genomic features	1183 + 49 part
Largest alignment	904648
Total aligned length	1151059
NA50	904648
NGA50	904648
NA90	-
NGA90	-
auNA	643463.5
auNGA	541535.2
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).
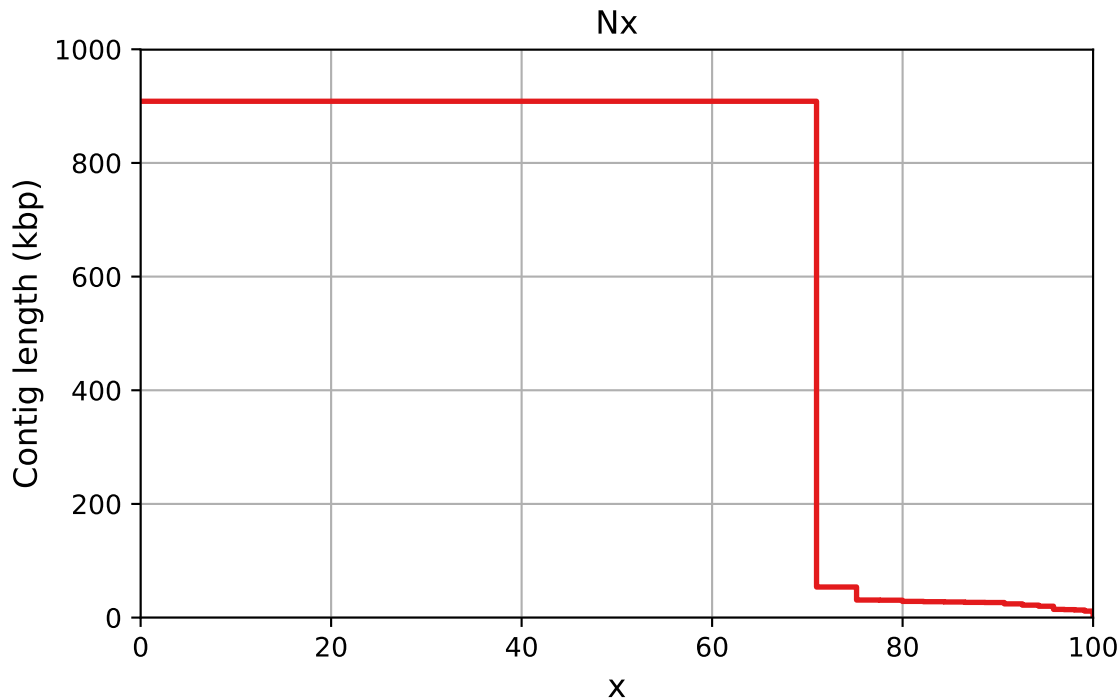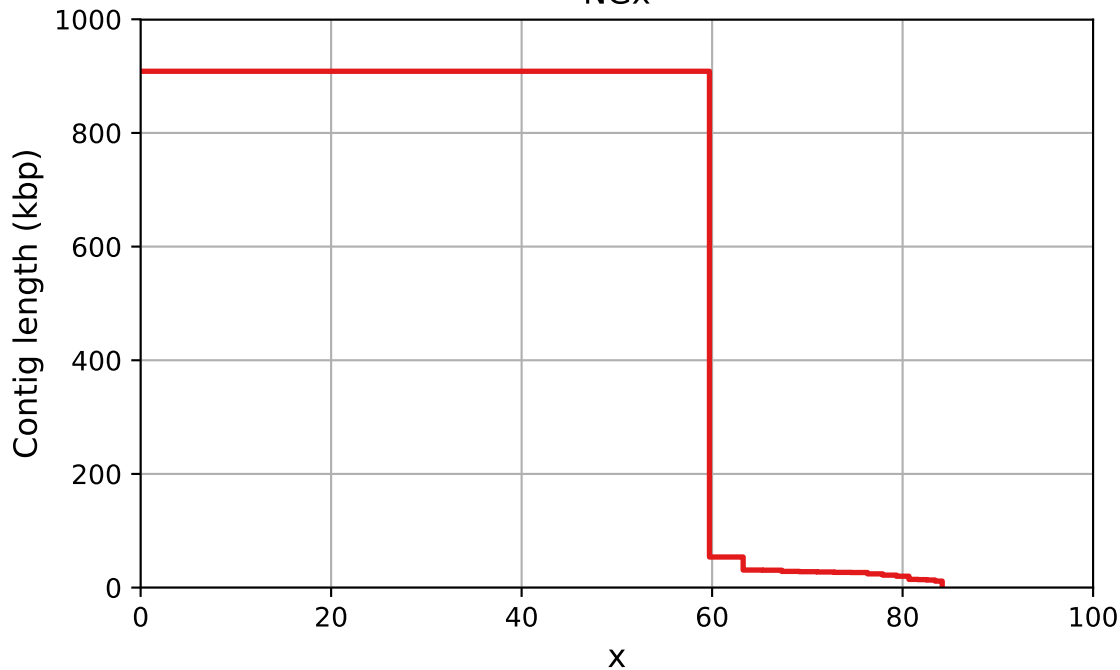
Misassemblies report

	GCA_003367295.1_ASM336729v1_genomic
# misassemblies	16
# contig misassemblies	16
# c. relocations	3
# c. translocations	13
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	6
Misassembled contigs length	133618
# local misassemblies	7
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	8733
# indels	507
# indels (<= 5 bp)	462
# indels (> 5 bp)	45
Indels length	1797

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_003367295.1_ASM336729v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
Partially unaligned length	123725
# 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).
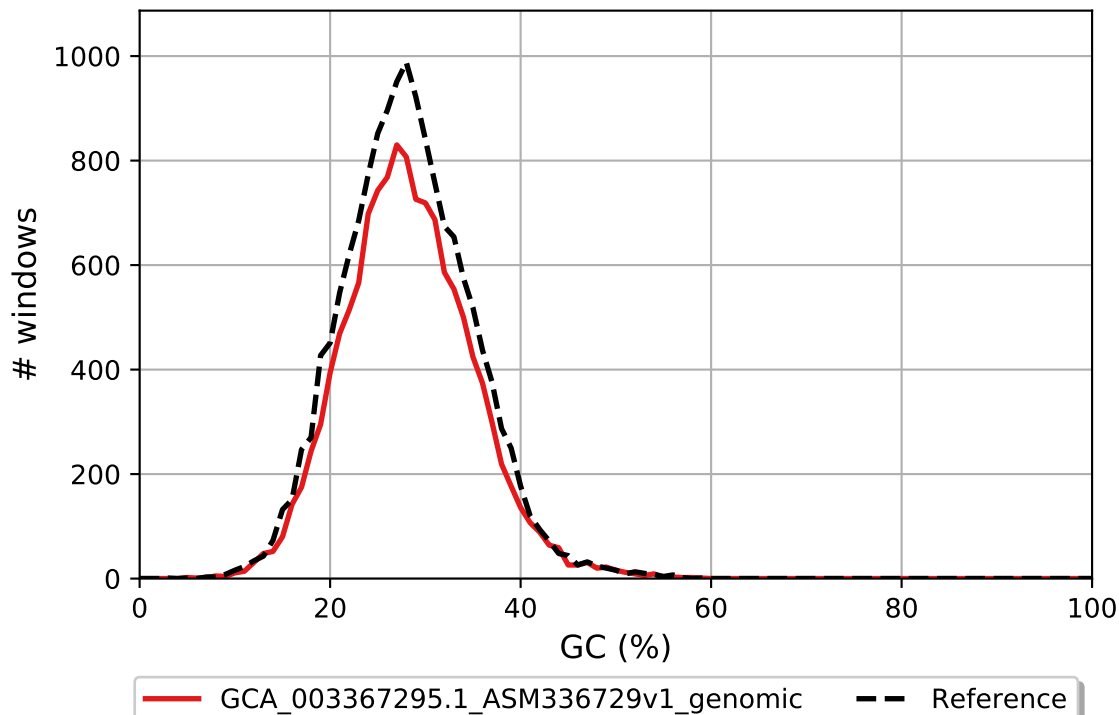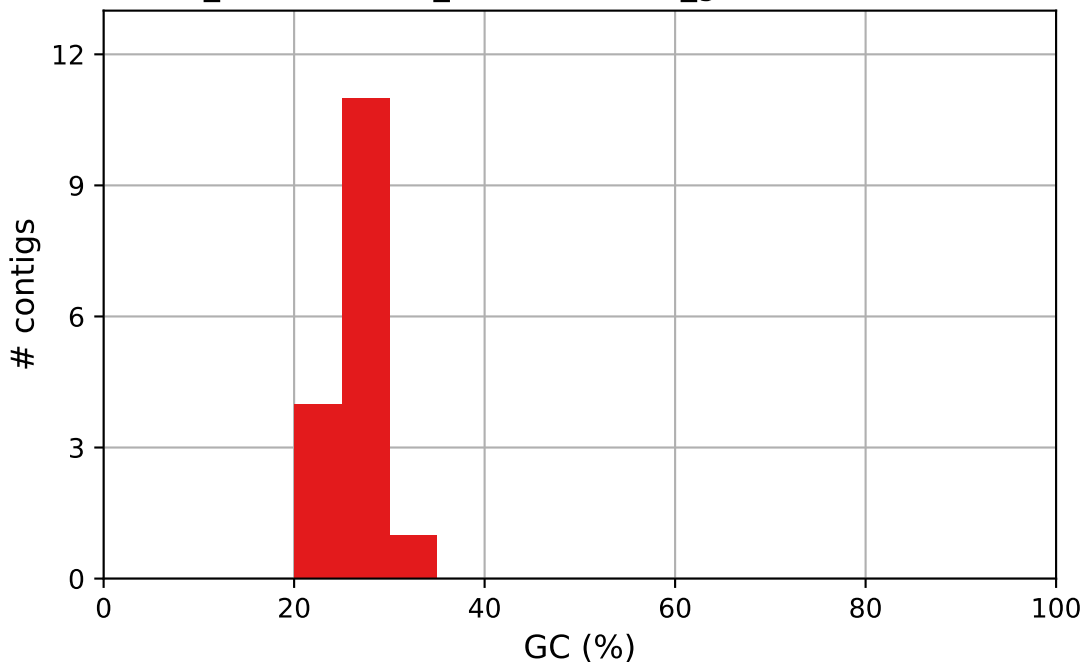
Nx

GCA_003367295.1_ASM336729v1_genomic

NGx

GCA_003367295.1_ASM336729v1_genomic
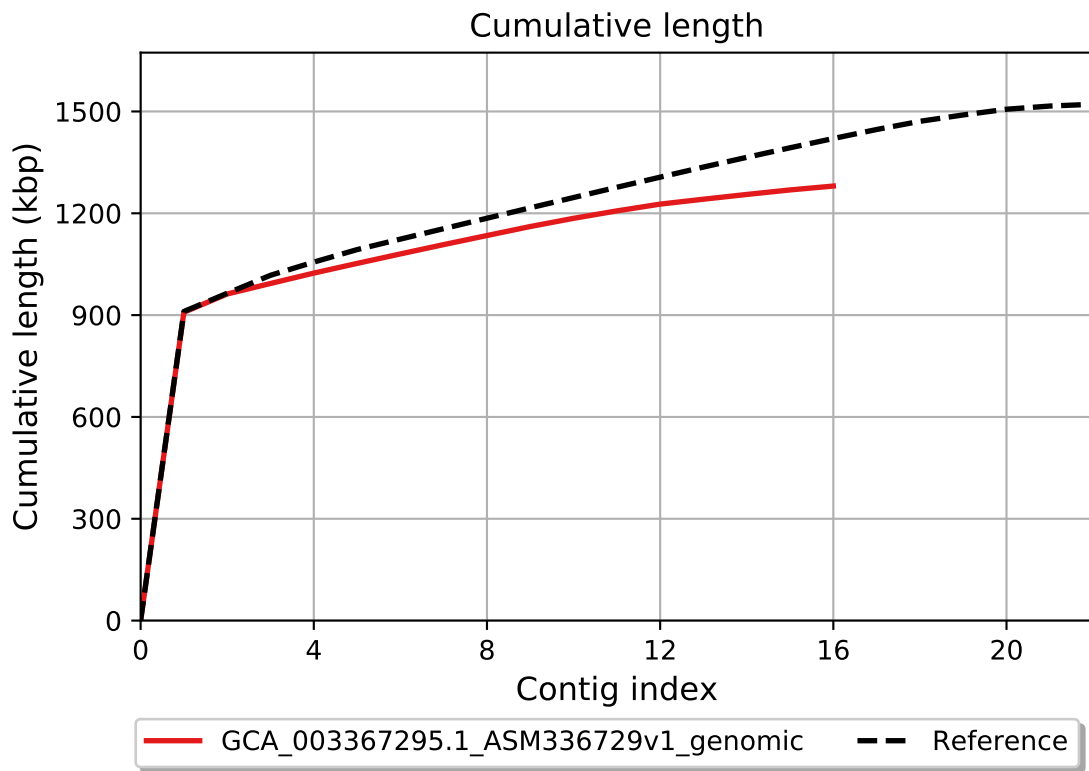
Cumulative length

GC content

GCA_003367295.1_ASM336729v1_genomic GC content

Misassemblies

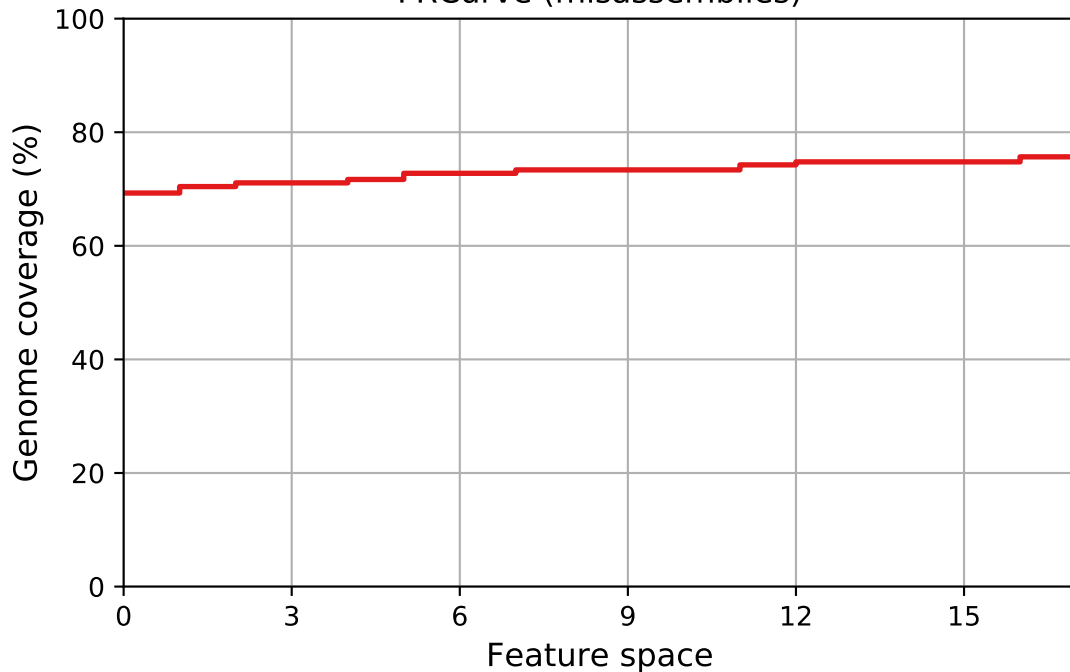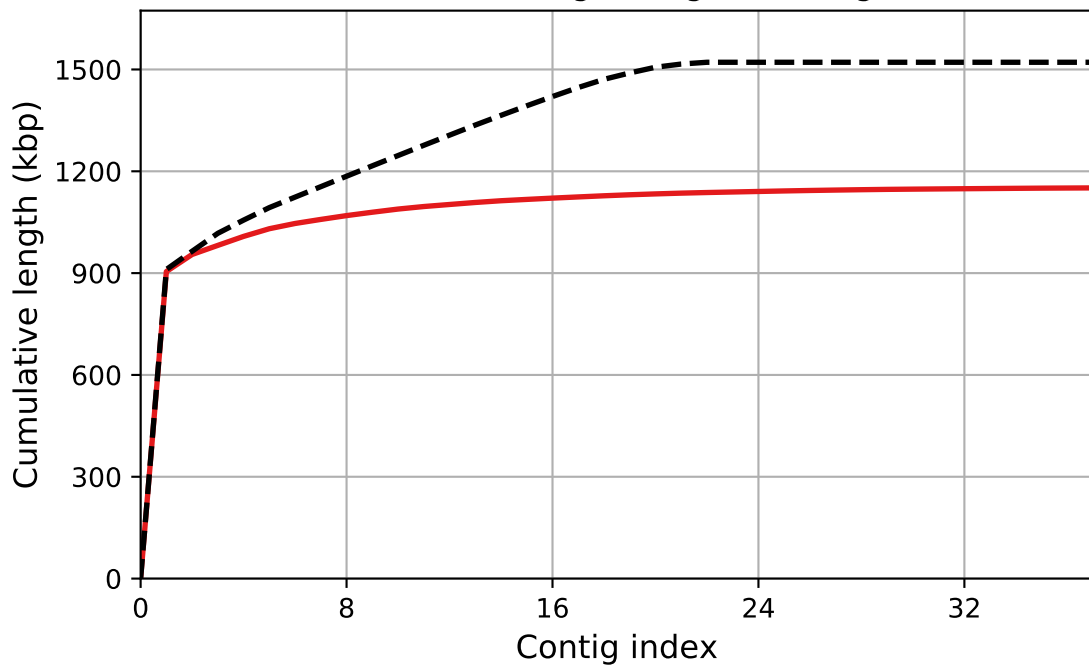GCA_003367295.1_ASM336729v1_genomic

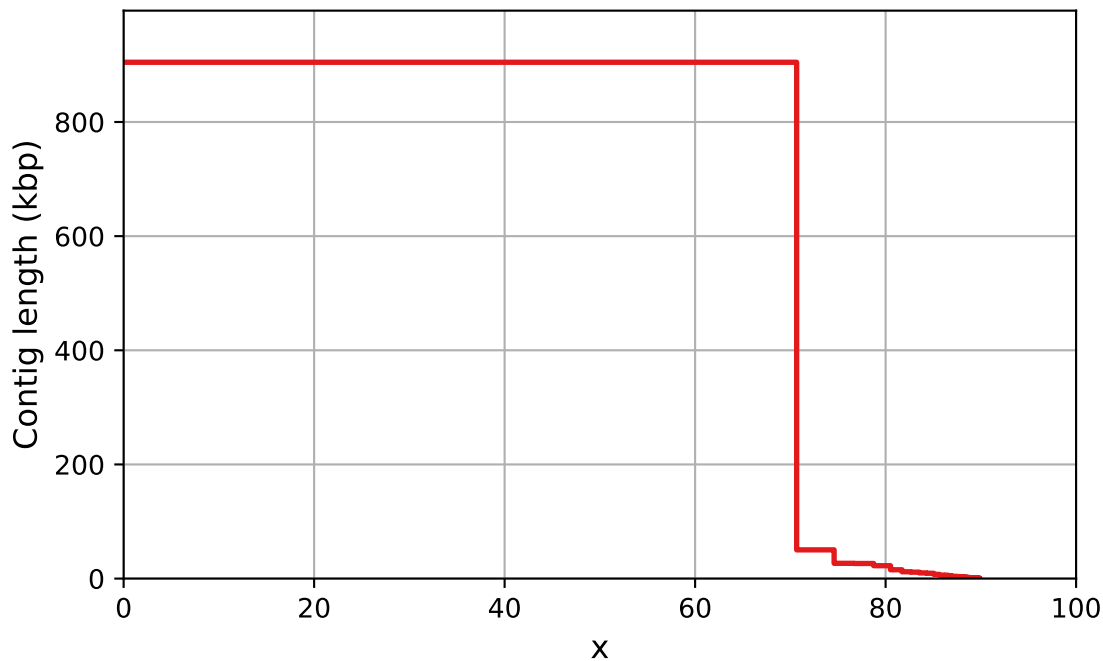■ # relocations   ■ # translocations

FRCurve (misassemblies)

GCA_003367295.1_ASM336729v1_genomic

Cumulative length (aligned contigs)

NAx

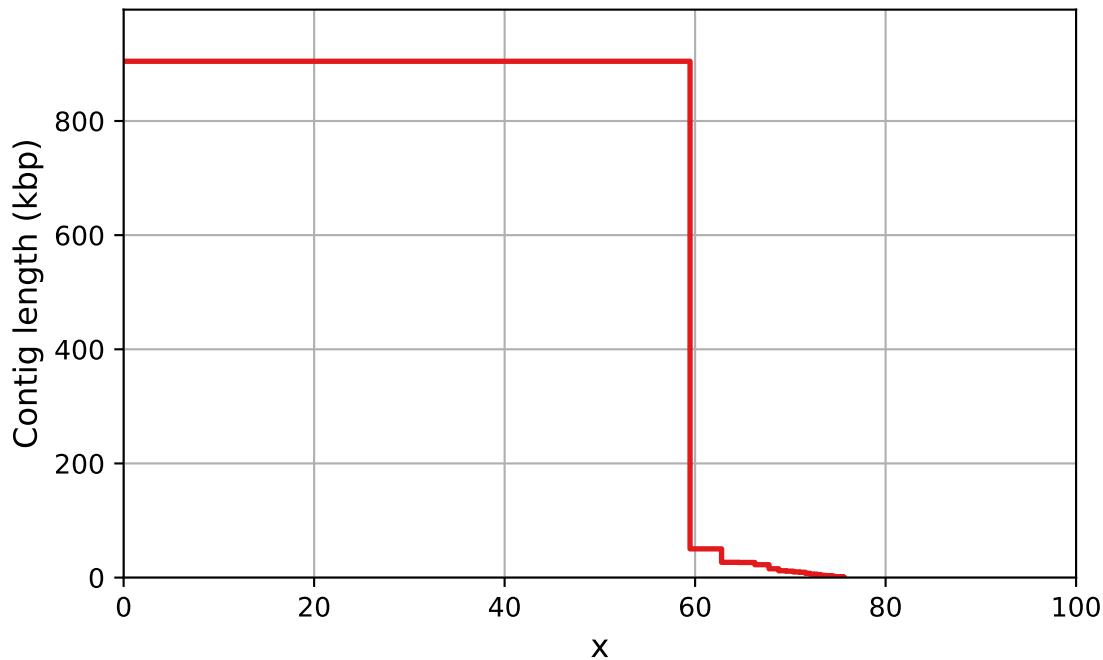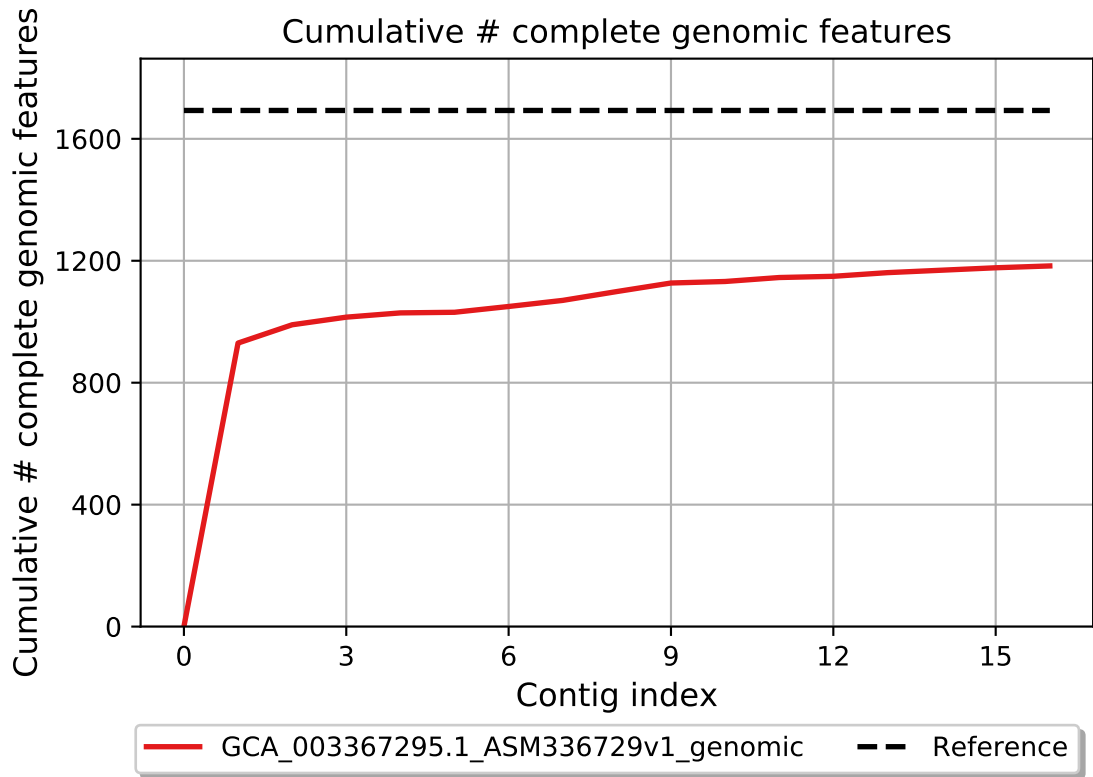Contig length (kbp) vs x

Legend: GCA_003367295.1_ASM336729v1_genomic

NGAx

GCA_003367295.1_ASM336729v1_genomic

Cumulative # complete genomic features

FRCurve (genomic features)

GCA_003367295.1_ASM336729v1_genomic