	GCA_040790785.1_ASM4079078v1_genomic
# contigs (>= 0 bp)	18
# contigs (>= 1000 bp)	18
# contigs (>= 5000 bp)	18
# contigs (>= 10000 bp)	17
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1383845
Total length (>= 1000 bp)	1383845
Total length (>= 5000 bp)	1383845
Total length (>= 10000 bp)	1375138
Total length (>= 25000 bp)	1310904
Total length (>= 50000 bp)	963746
# contigs	18
Largest contig	910048
Total length	1383845
Reference length	1521208
GC (%)	28.34
Reference GC (%)	28.18
N50	910048
NG50	910048
N90	27456
NG90	18115
auN	608897.0
auNG	553914.4
L50	1
LG50	1
L90	12
LG90	17
# misassemblies	14
# misassembled contigs	5
Misassembled contigs length	134894
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# unaligned contigs	0 + 14 part
Unaligned length	155833
Genome fraction (%)	78.758
Duplication ratio	1.018
# N's per 100 kbp	0.07
# mismatches per 100 kbp	813.36
# indels per 100 kbp	47.49
# genomic features	1269 + 42 part
Largest alignment	904600
Total aligned length	1219136
NA50	904600
NGA50	904600
NA90	-
NGA90	-
auNA	596078.7
auNGA	542253.6
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).
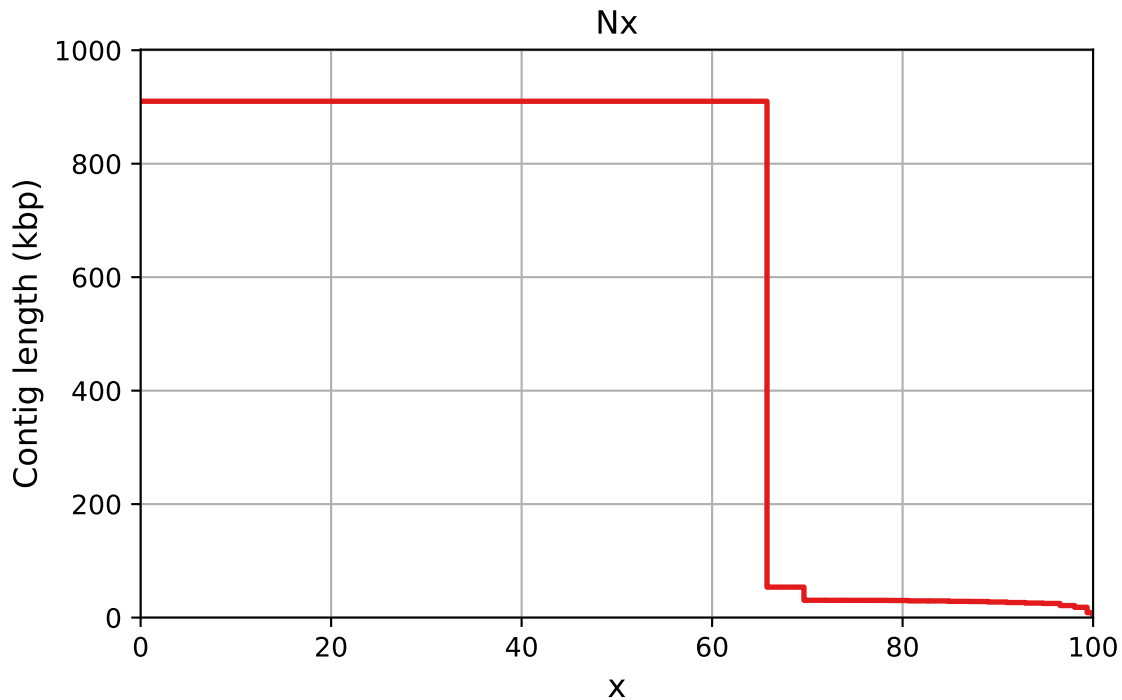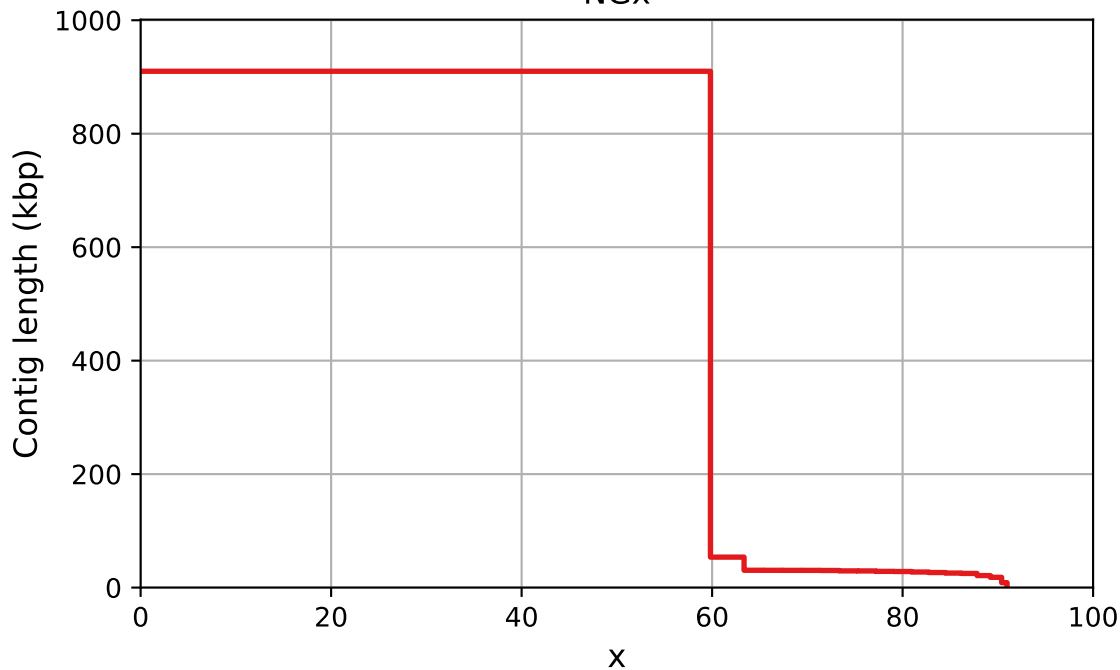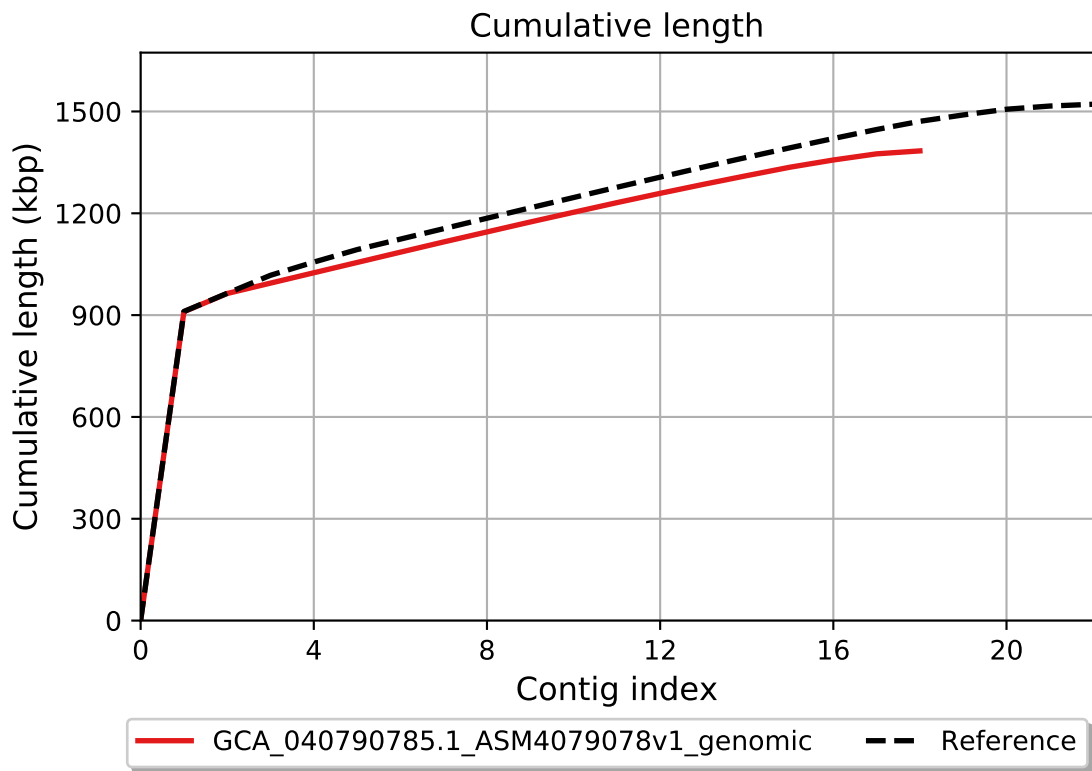
Misassemblies report

	GCA_040790785.1_ASM4079078v1_genomic
# misassemblies	14
# contig misassemblies	14
# c. relocations	2
# c. translocations	12
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	5
Misassembled contigs length	134894
# local misassemblies	6
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	6
# mismatches	9916
# indels	579
# indels (<= 5 bp)	524
# indels (> 5 bp)	55
Indels length	2956

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_040790785.1_ASM4079078v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	14
Partially unaligned length	155833
# N's	1

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).
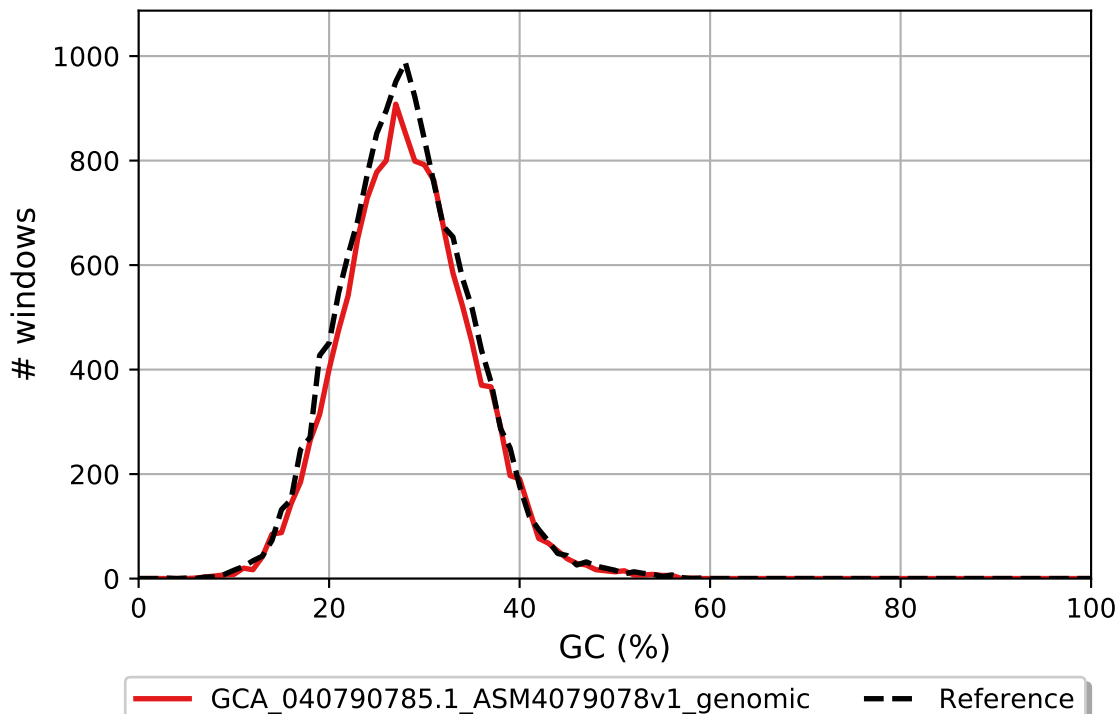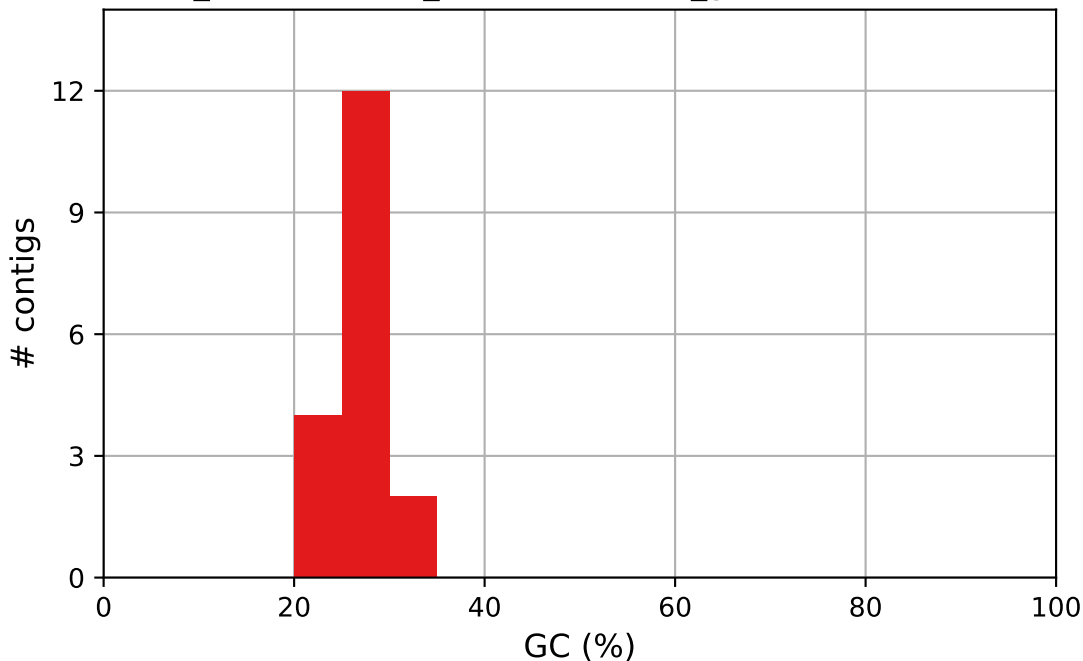
Nx

GCA_040790785.1_ASM4079078v1_genomic

NGx

GCA_040790785.1_ASM4079078v1_genomic

Cumulative length

GC content

GCA_040790785.1_ASM4079078v1_genomic ——— Reference - - -

GCA_040790785.1_ASM4079078v1_genomic GC content

Misassemblies

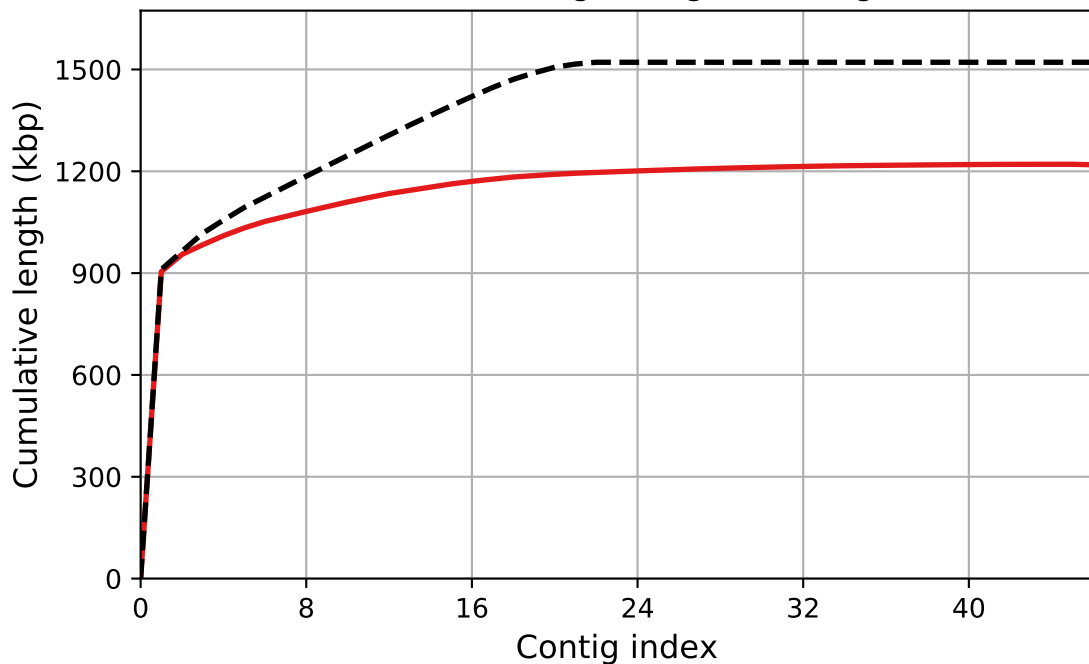GCA_040790785.1_ASM4079078v1_genomic

■ # relocations   ■ # translocations

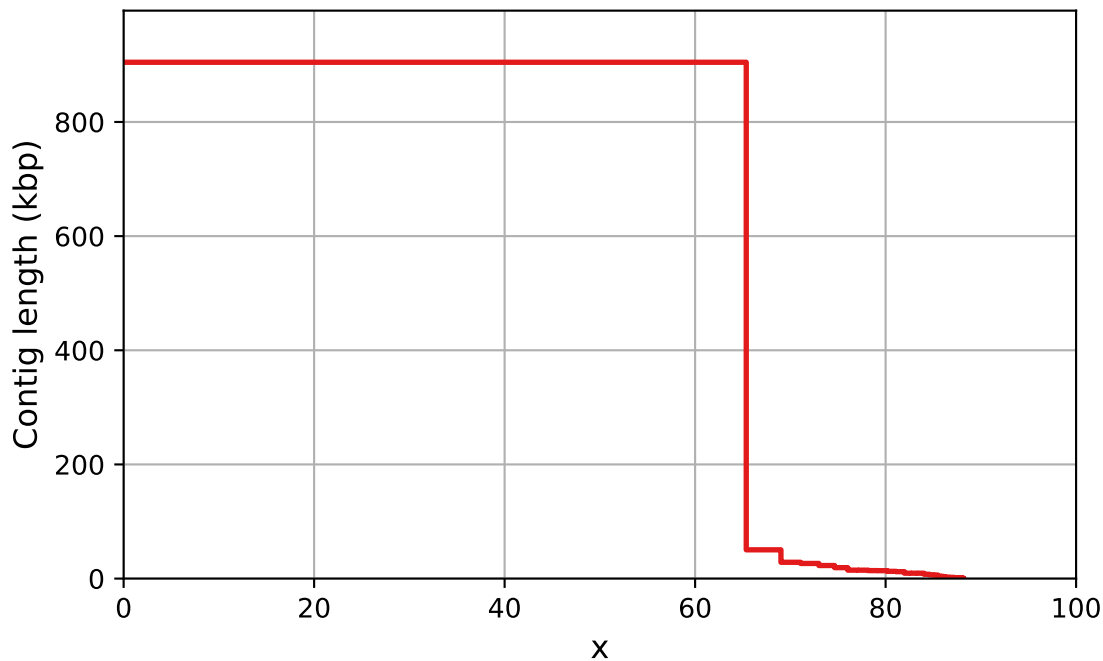FRCurve (misassemblies)
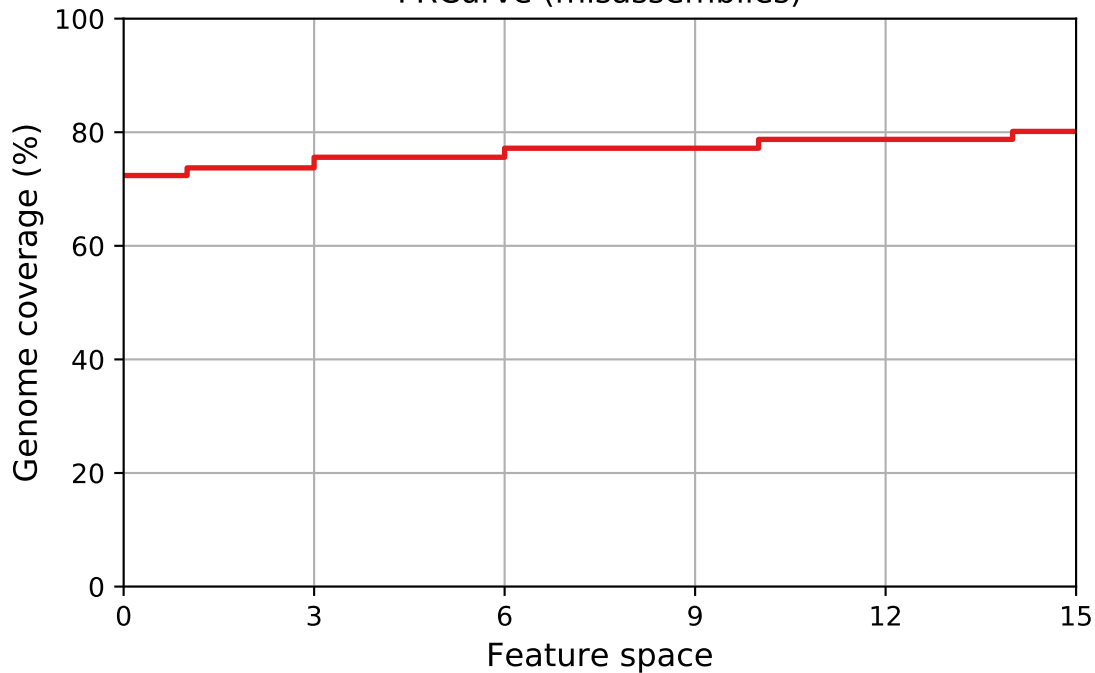
GCA_040790785.1_ASM4079078v1_genomic

Cumulative length (aligned contigs)

NAx

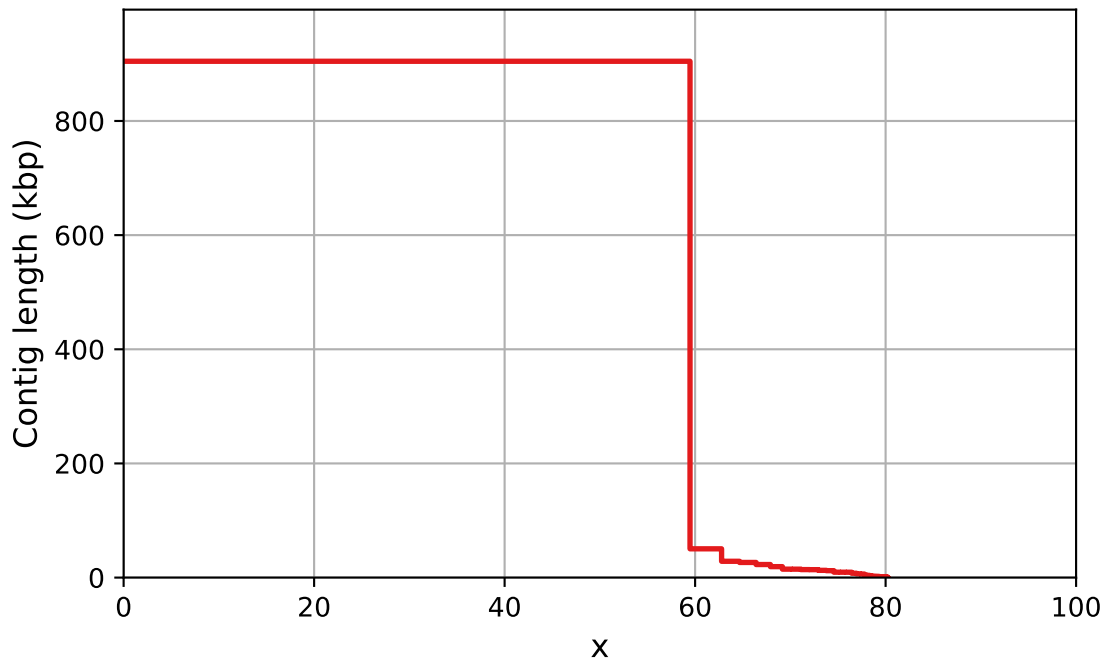GCA_040790785.1_ASM4079078v1_genomic
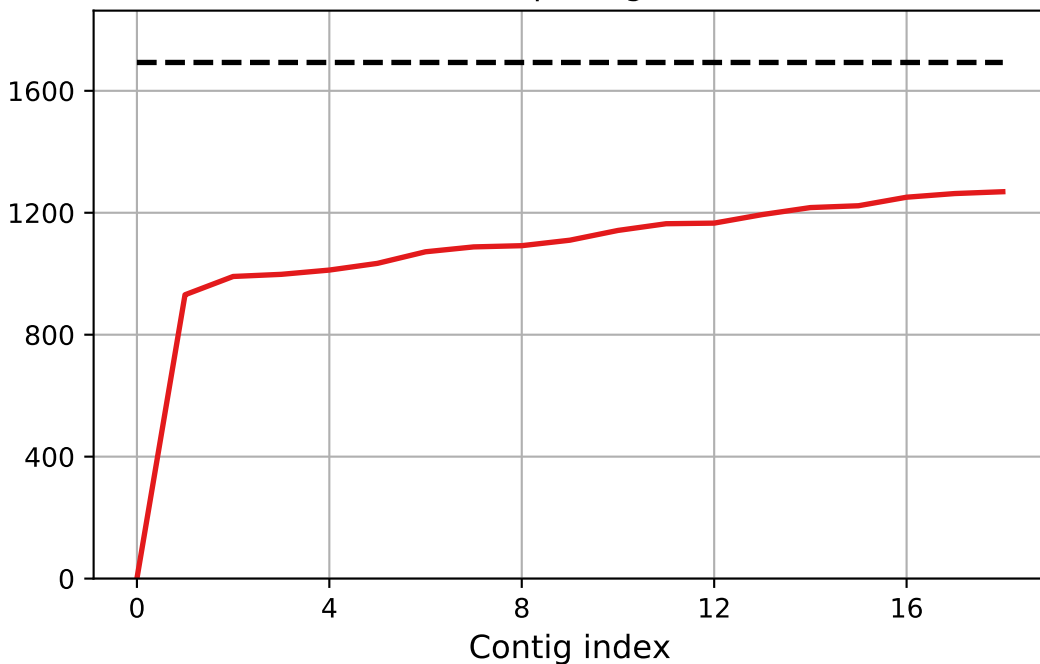
NGAx

GCA_040790785.1_ASM4079078v1_genomic

Cumulative # complete genomic features

FRCurve (genomic features)
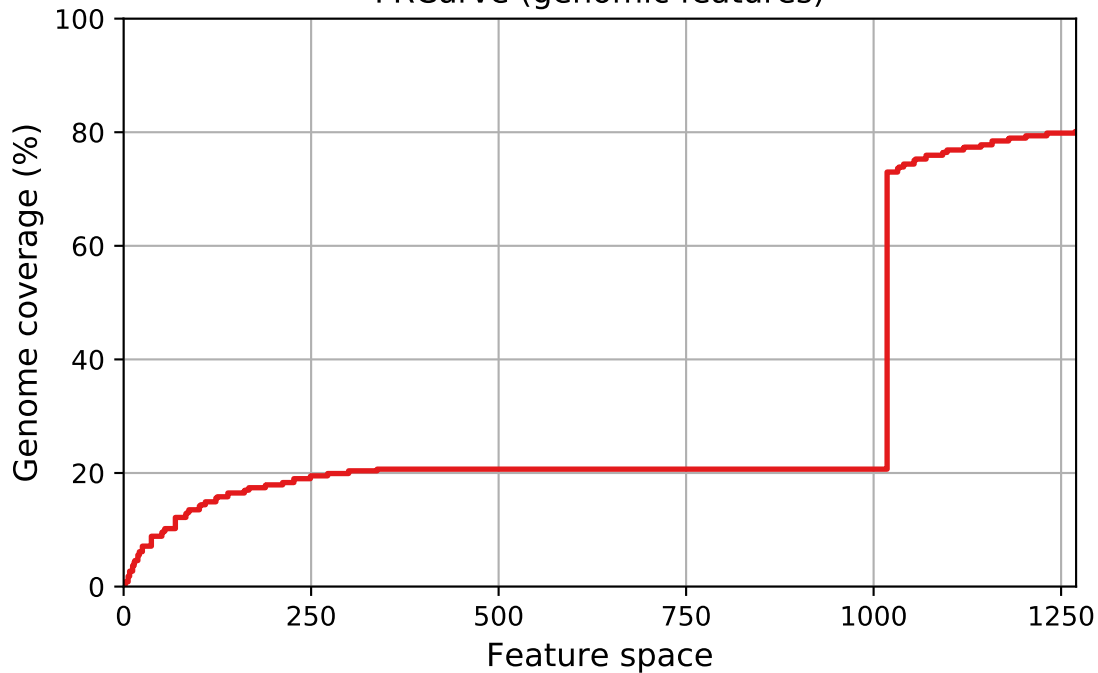
GCA_040790785.1_ASM4079078v1_genomic