	GCA_040790805.1_ASM4079080v1_genomic
# contigs (>= 0 bp)	12
# contigs (>= 1000 bp)	12
# contigs (>= 5000 bp)	12
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	1216633
Total length (>= 1000 bp)	1216633
Total length (>= 5000 bp)	1216633
Total length (>= 10000 bp)	1216633
Total length (>= 25000 bp)	1174743
Total length (>= 50000 bp)	961550
# contigs	12
Largest contig	907880
Total length	1216633
Reference length	1521208
GC (%)	28.44
Reference GC (%)	28.18
N50	907880
NG50	907880
N90	29924
NG90	-
auN	685727.8
auNG	548431.9
L50	1
LG50	1
L90	7
LG90	-
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	968626
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	2737
Genome fraction (%)	79.660
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	51.83
# indels per 100 kbp	13.27
# genomic features	1297 + 12 part
Largest alignment	867188
Total aligned length	1213469
NA50	867188
NGA50	867188
NA90	26603
NGA90	-
auNA	627176.4
auNGA	501603.6
LA50	1
LGA50	1
LA90	8
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).
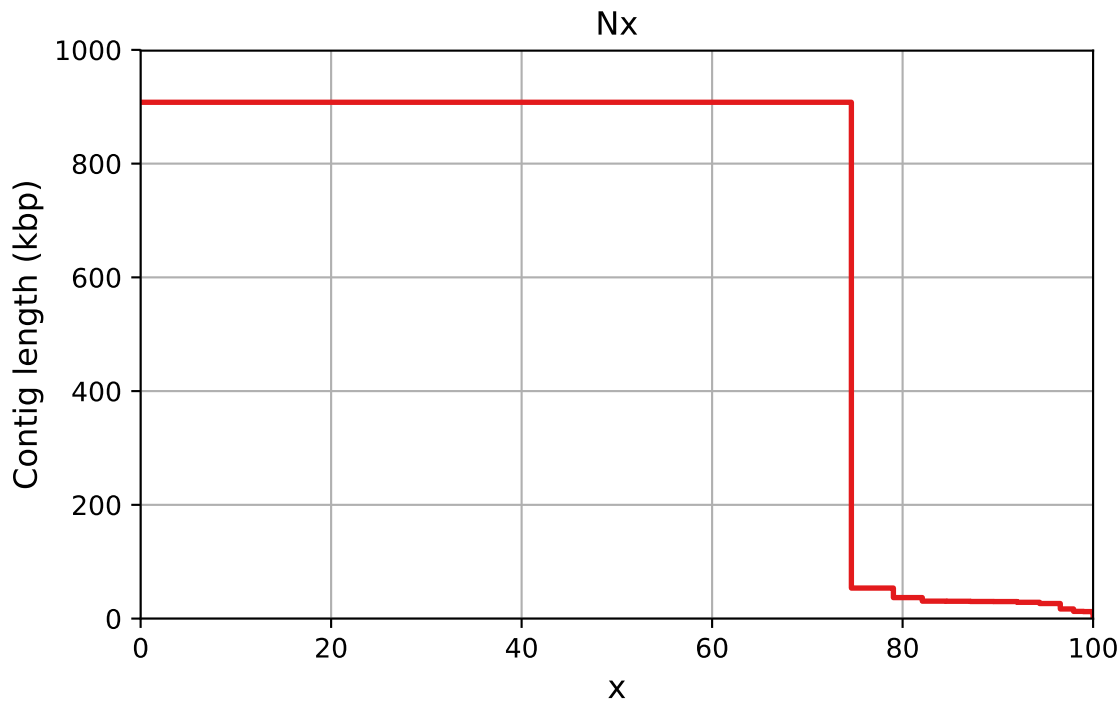
Misassemblies report
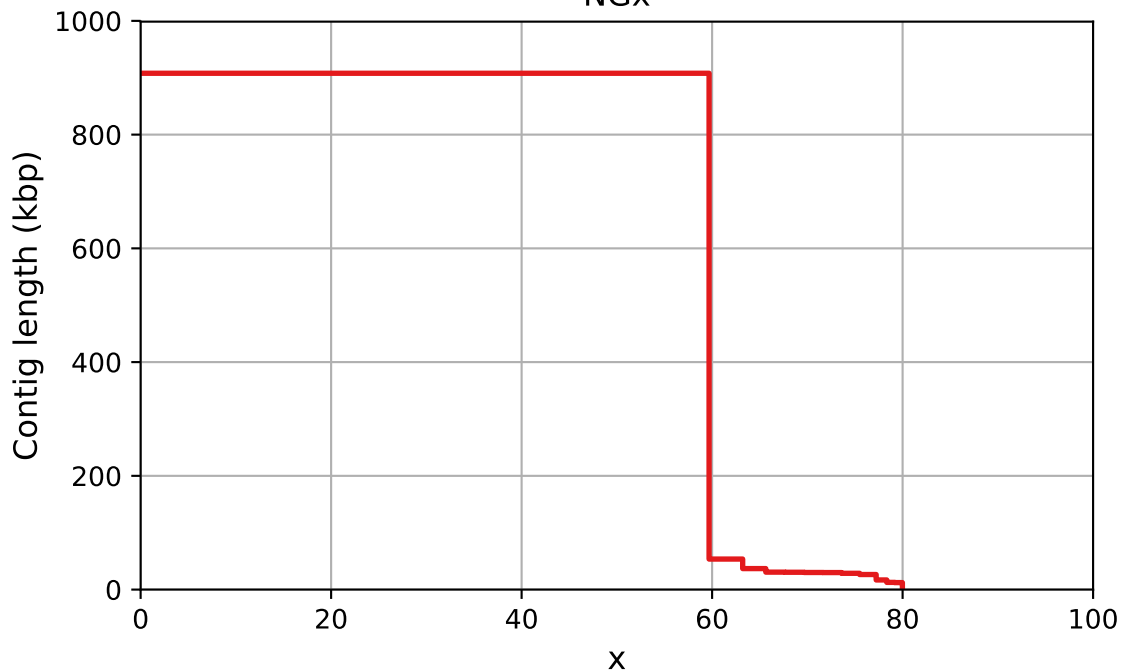
	GCA_040790805.1_ASM4079080v1_genomic
# misassemblies	4
# contig misassemblies	4
# c. relocations	4
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	968626
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	629
# indels	161
# indels (<= 5 bp)	134
# indels (> 5 bp)	27
Indels length	1744

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_040790805.1_ASM4079080v1_genomic
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2737
# 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).

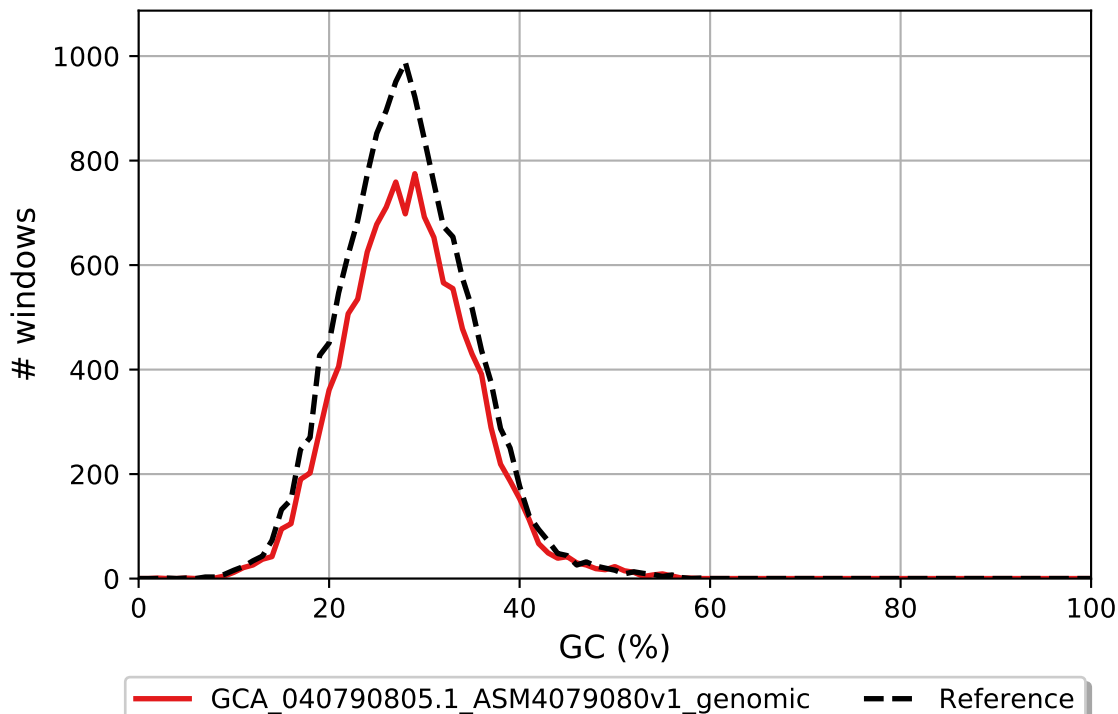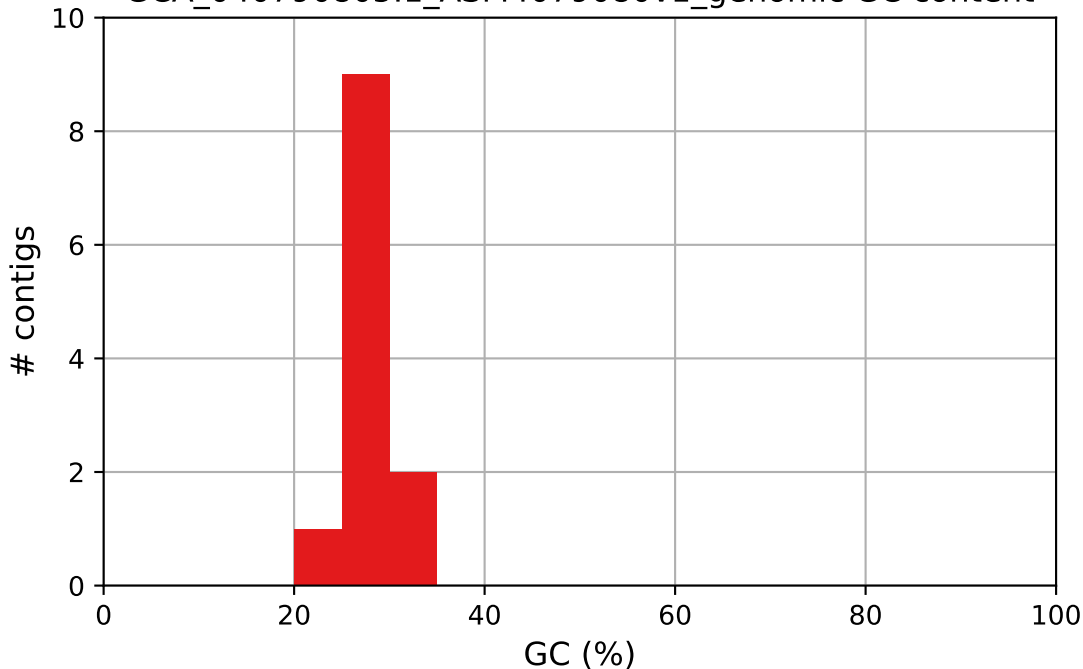Nx

GCA_040790805.1_ASM4079080v1_genomic

NGx

GCA_040790805.1_ASM4079080v1_genomic

Cumulative length

Legend: GCA_040790805.1_ASM4079080v1_genomic — Reference

GC content

GC (%)

windows

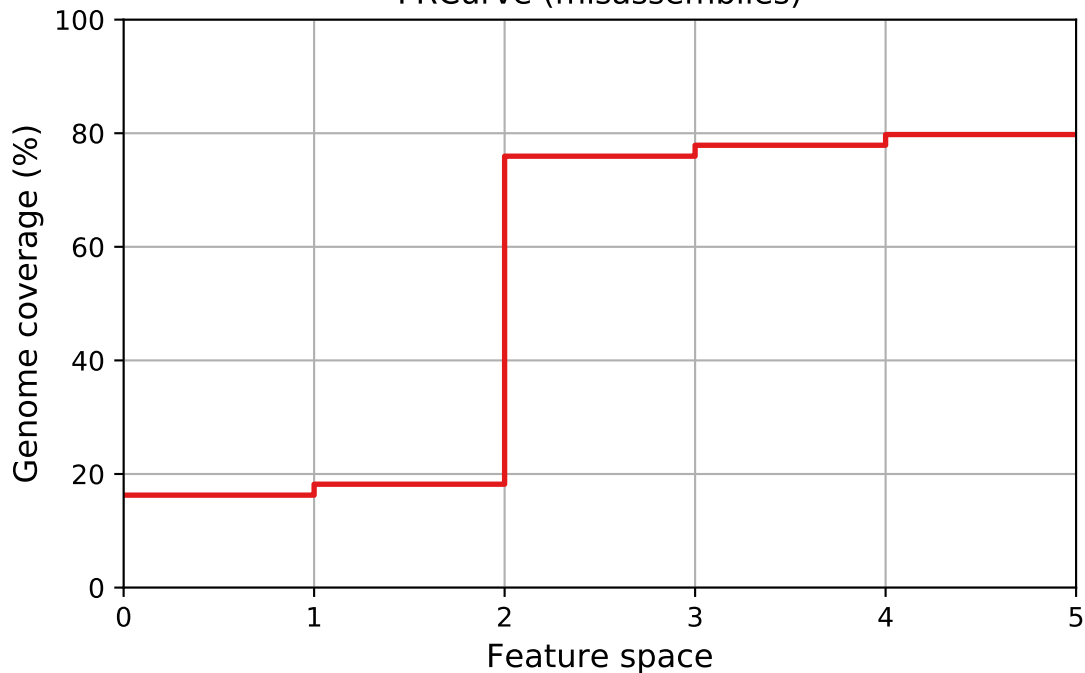- GCA_040790805.1_ASM4079080v1_genomic
- Reference
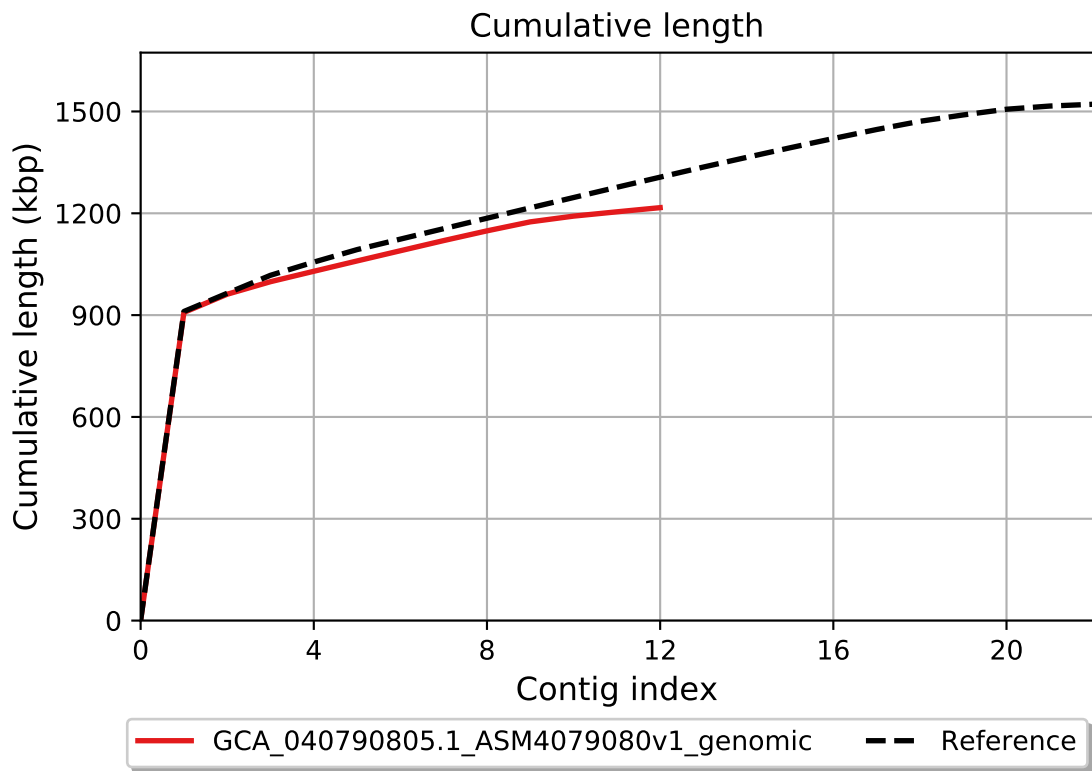
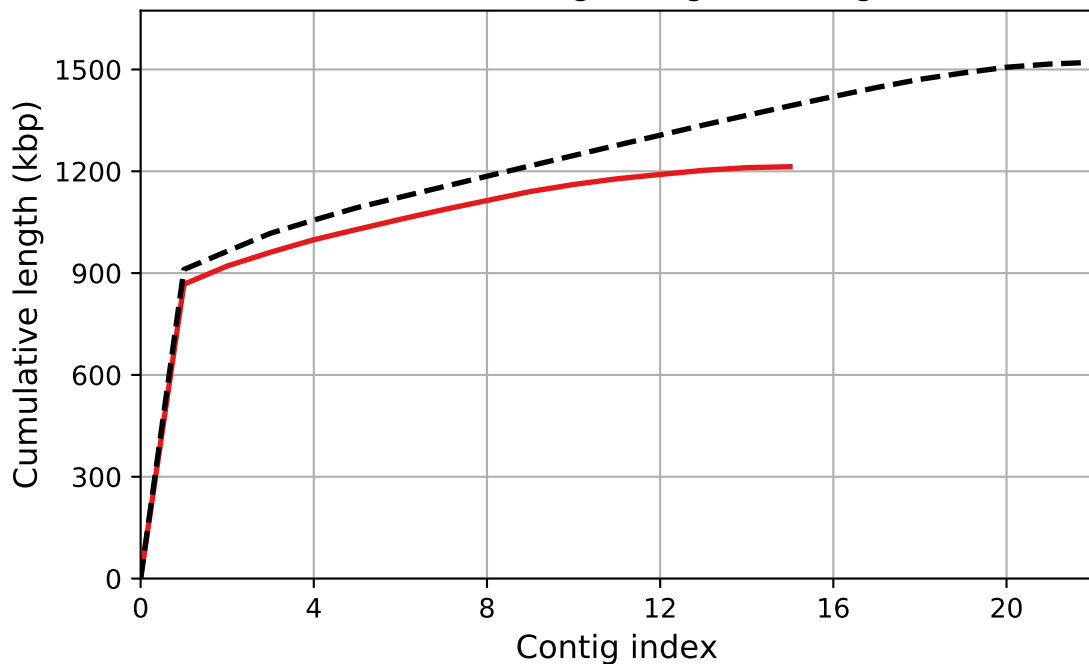GCA_040790805.1_ASM4079080v1_genomic GC content

Misassemblies

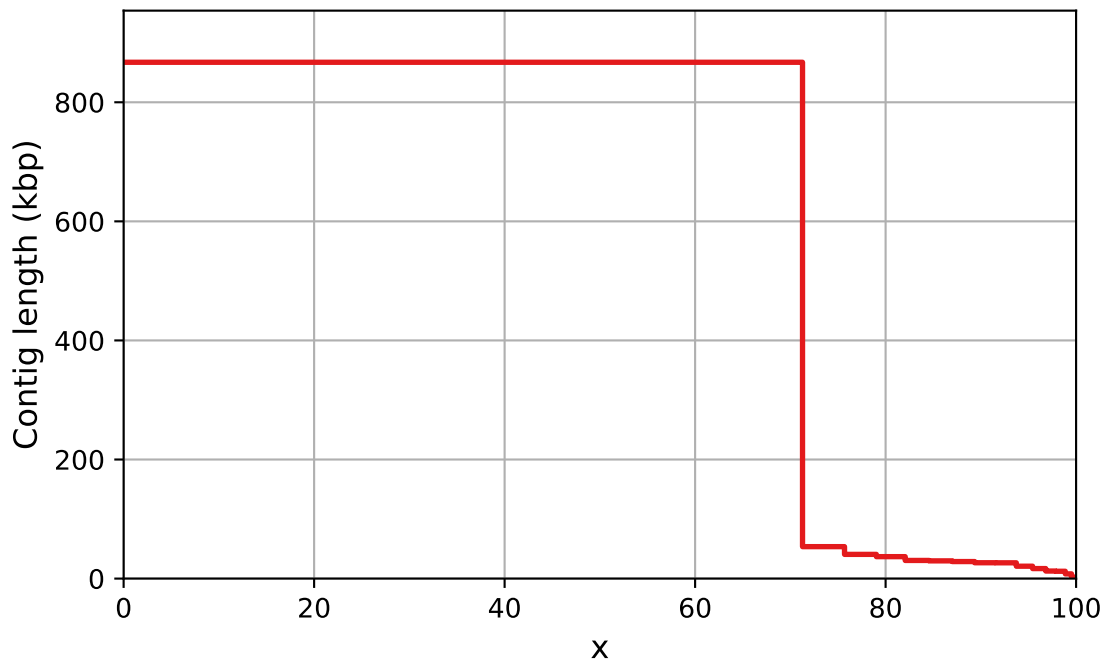FRCurve (misassemblies)

GCA_040790805.1_ASM4079080v1_genomic

Cumulative length (aligned contigs)
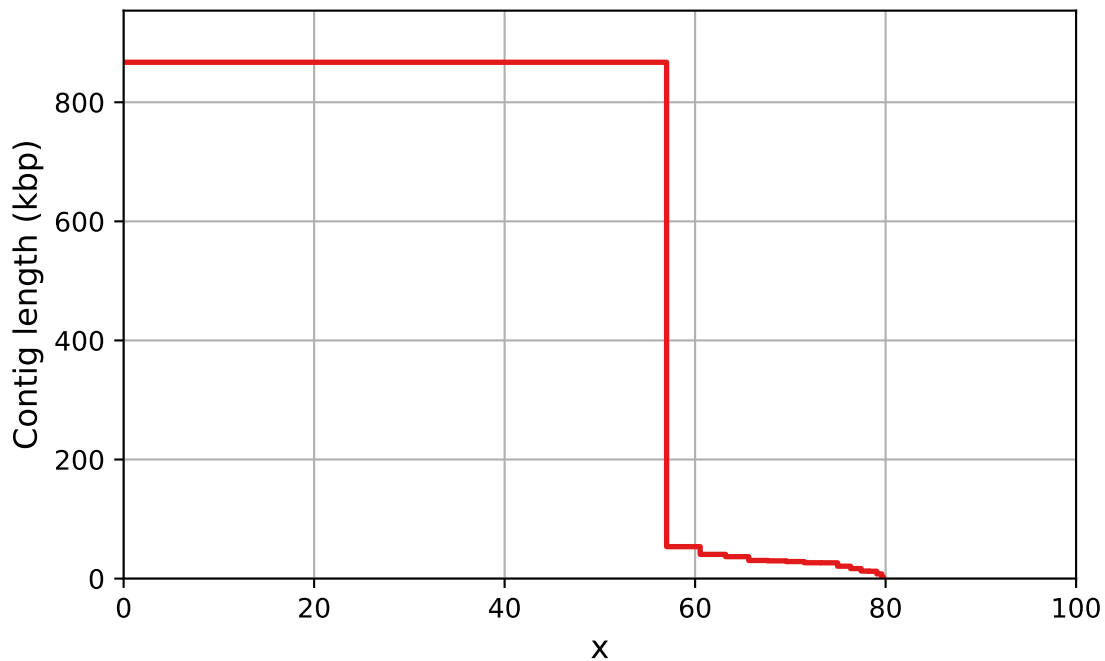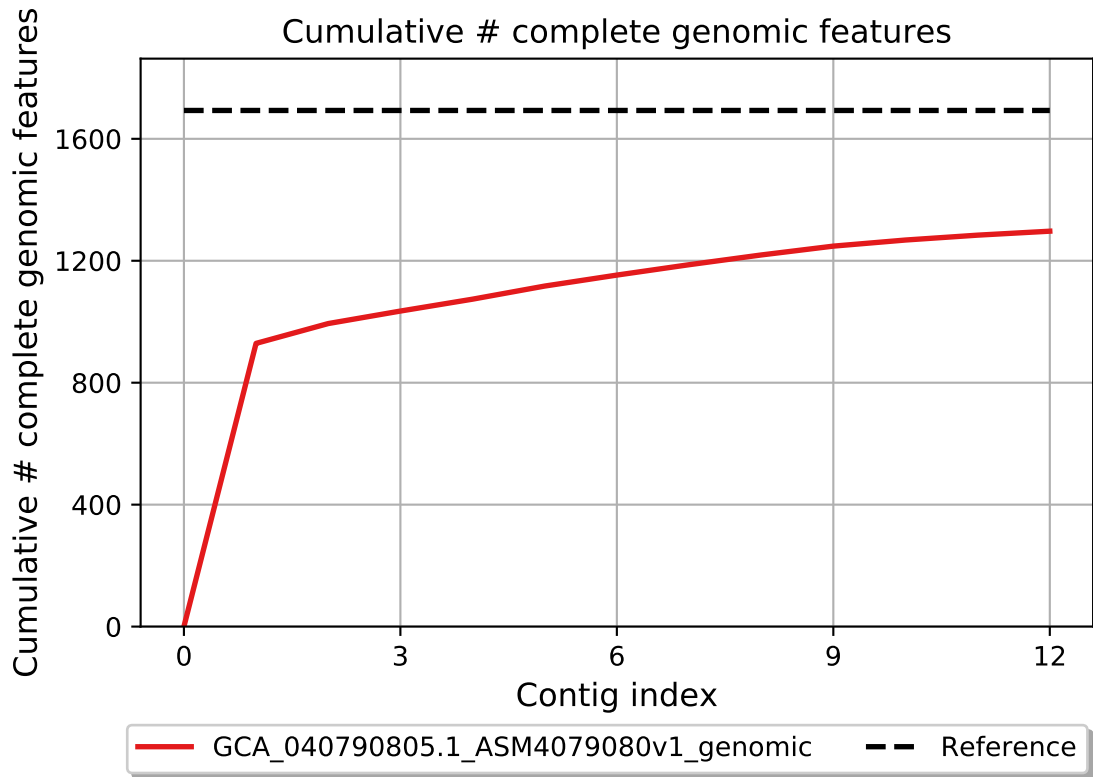
NAx

GCA_040790805.1_ASM4079080v1_genomic

NGAx

GCA_040790805.1_ASM4079080v1_genomic

Cumulative # complete genomic features
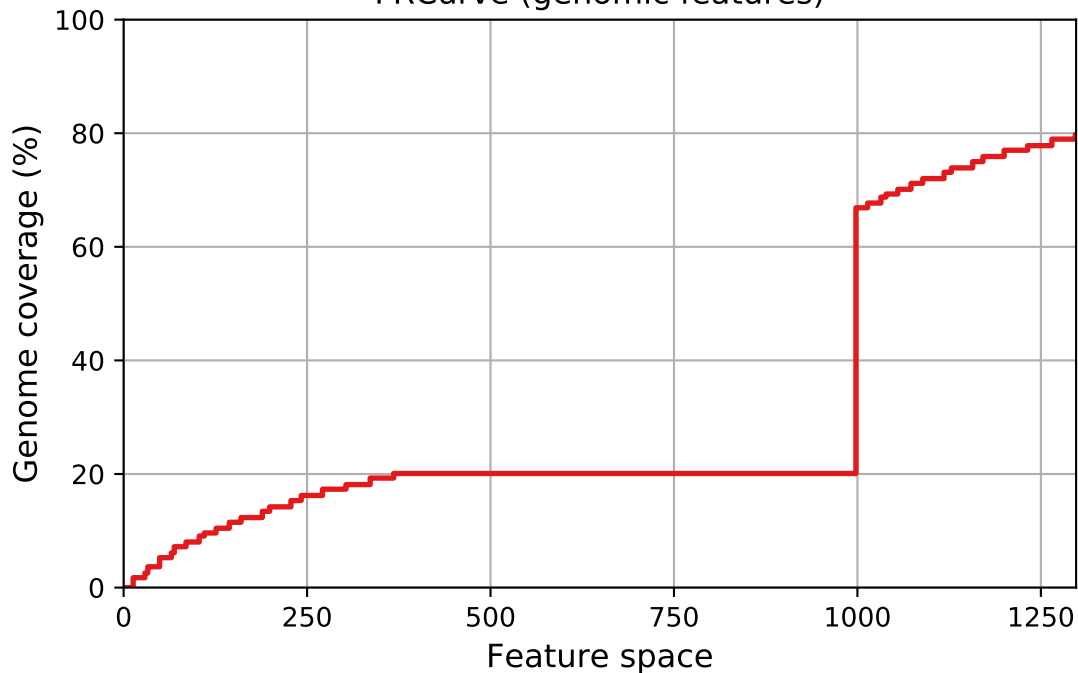
FRCurve (genomic features)

GCA_040790805.1_ASM4079080v1_genomic