# Report

| | GCF_040790775.1_ASM4079077v1_genomic |
|---|---|
| # contigs (>= 0 bp) | 17 |
| # contigs (>= 1000 bp) | 17 |
| # contigs (>= 5000 bp) | 17 |
| # contigs (>= 10000 bp) | 17 |
| # contigs (>= 25000 bp) | 14 |
| # contigs (>= 50000 bp) | 3 |
| Total length (>= 0 bp) | 1417953 |
| Total length (>= 1000 bp) | 1417953 |
| Total length (>= 5000 bp) | 1417953 |
| Total length (>= 10000 bp) | 1417953 |
| Total length (>= 25000 bp) | 1357768 |
| Total length (>= 50000 bp) | 1014483 |
| # contigs | 17 |
| Largest contig | 907632 |
| Total length | 1417953 |
| Reference length | 1521208 |
| GC (%) | 28.07 |
| Reference GC (%) | 28.18 |
| N50 | 907632 |
| NG50 | 907632 |
| N90 | 28647 |
| NG90 | 24443 |
| auN | 593516.4 |
| auNG | 553230.3 |
| L50 | 1 |
| LG50 | 1 |
| L90 | 12 |
| LG90 | 15 |
| # misassemblies | 4 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 53090 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 2 part |
| Unaligned length | 2903 |
| Genome fraction (%) | 92.908 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1.06 |
| # indels per 100 kbp | 3.96 |
| # genomic features | 1538 + 9 part |
| Largest alignment | 907632 |
| Total aligned length | 1414283 |
| NA50 | 907632 |
| NGA50 | 907632 |
| NA90 | 28599 |
| NGA90 | 20854 |
| auNA | 593283.5 |
| auNGA | 553013.2 |
| LA50 | 1 |
| LGA50 | 1 |
| LA90 | 12 |
| LGA90 | 15 |

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).
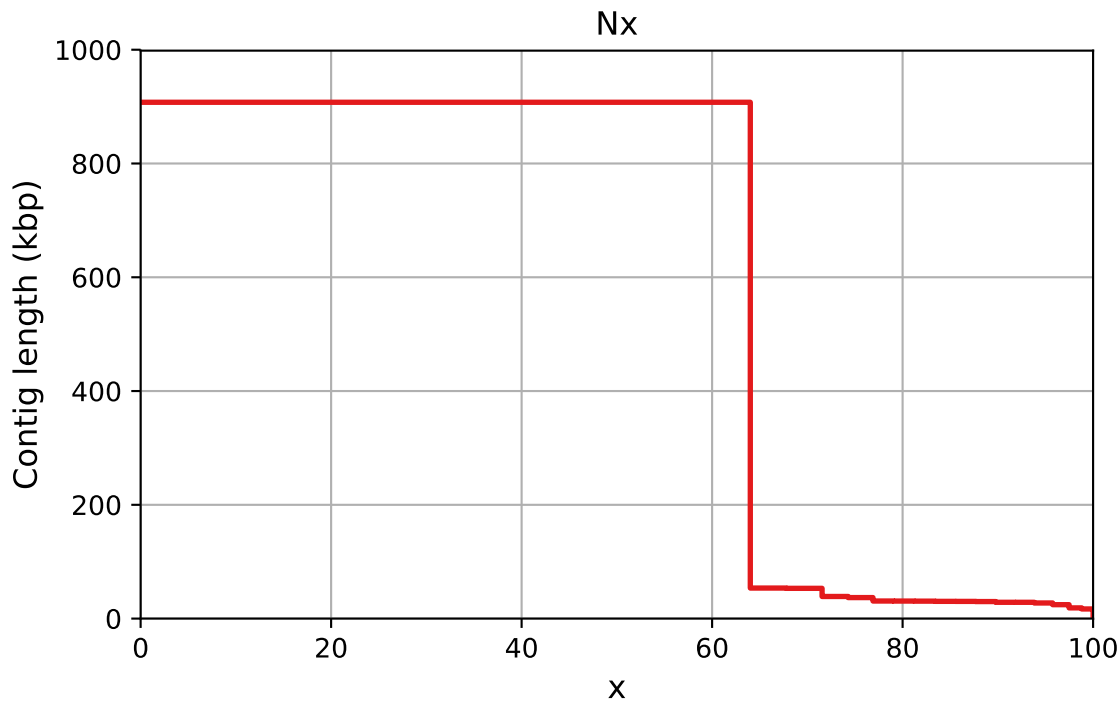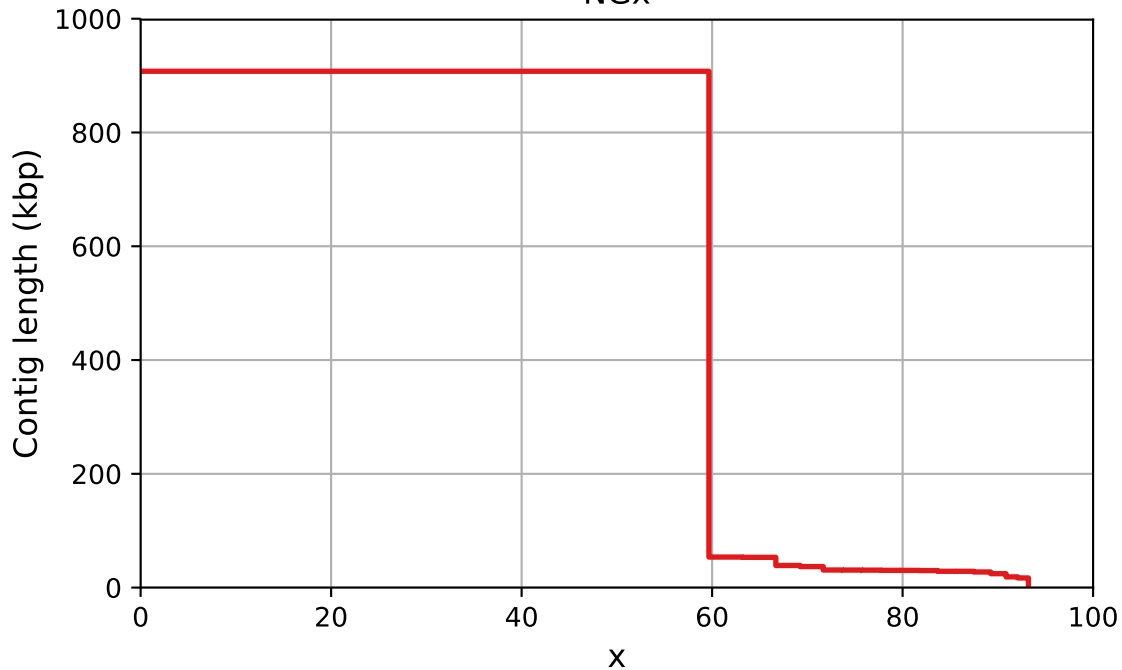
# Misassemblies report

| | GCF_040790775.1_ASM4079077v1_genomic |
|---|---|
| # misassemblies | 4 |
| # contig misassemblies | 4 |
| # c. relocations | 2 |
| # c. translocations | 2 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 2 |
| Misassembled contigs length | 53090 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 15 |
| # indels | 56 |
| # indels (<= 5 bp) | 51 |
| # indels (> 5 bp) | 5 |
| Indels length | 249 |

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_040790775.1_ASM4079077v1_genomic |
|---|---|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 2 |
| Partially unaligned length | 2903 |
| # 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

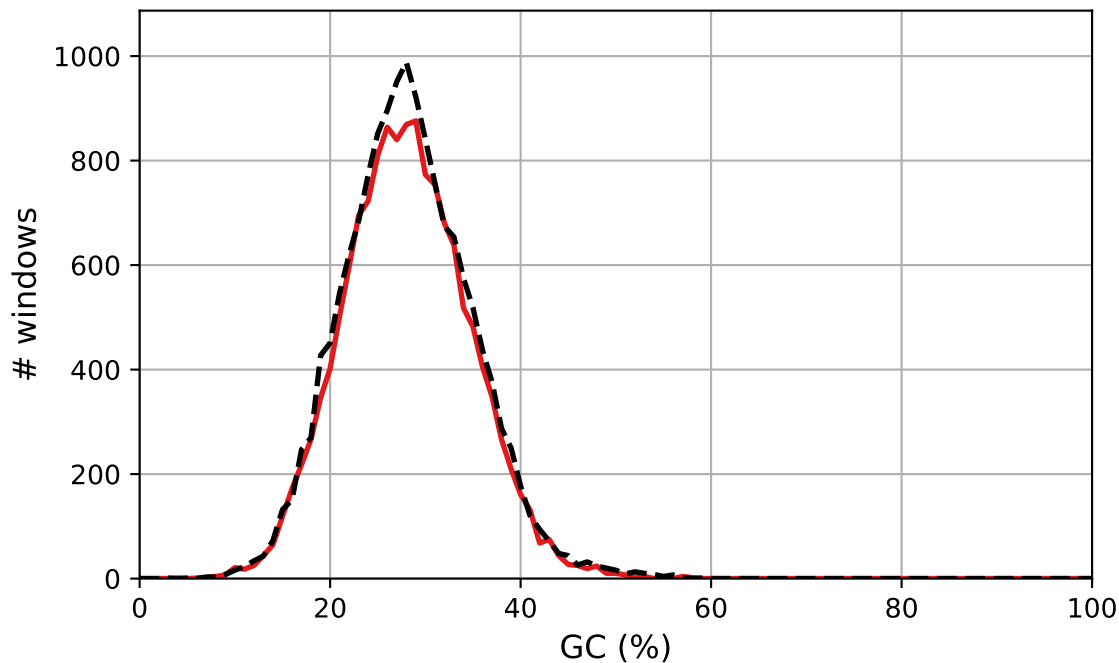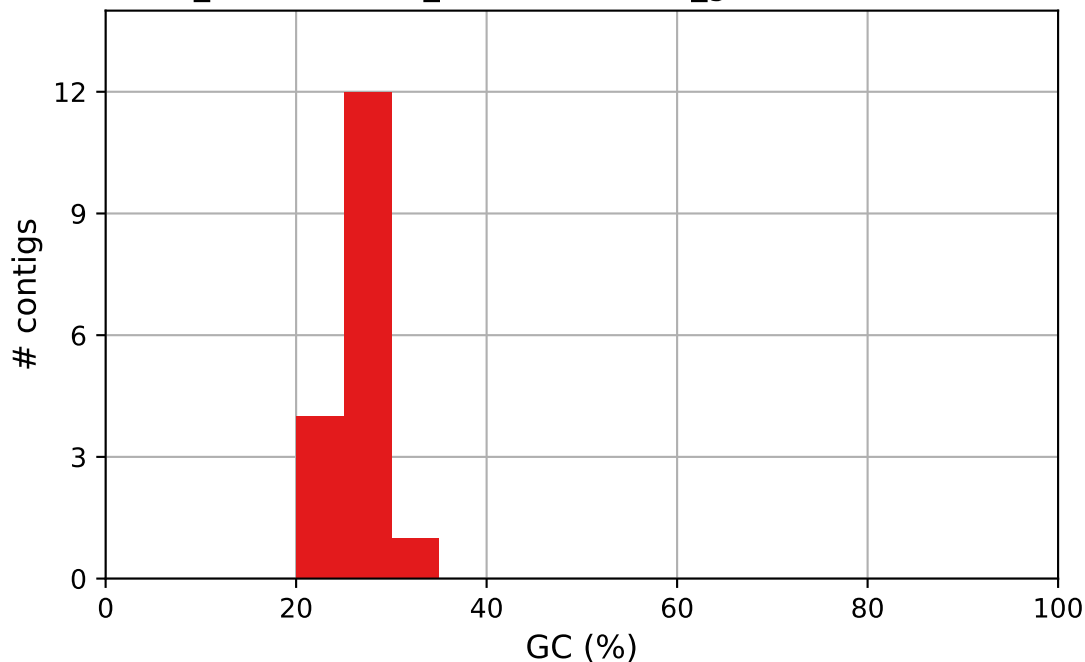GCF_040790775.1_ASM4079077v1_genomic

NGx

GCF_040790775.1_ASM4079077v1_genomic

## Cumulative length

Cumulative length (kbp) vs Contig index

Legend:
- GCF_040790775.1_ASM4079077v1_genomic
- Reference
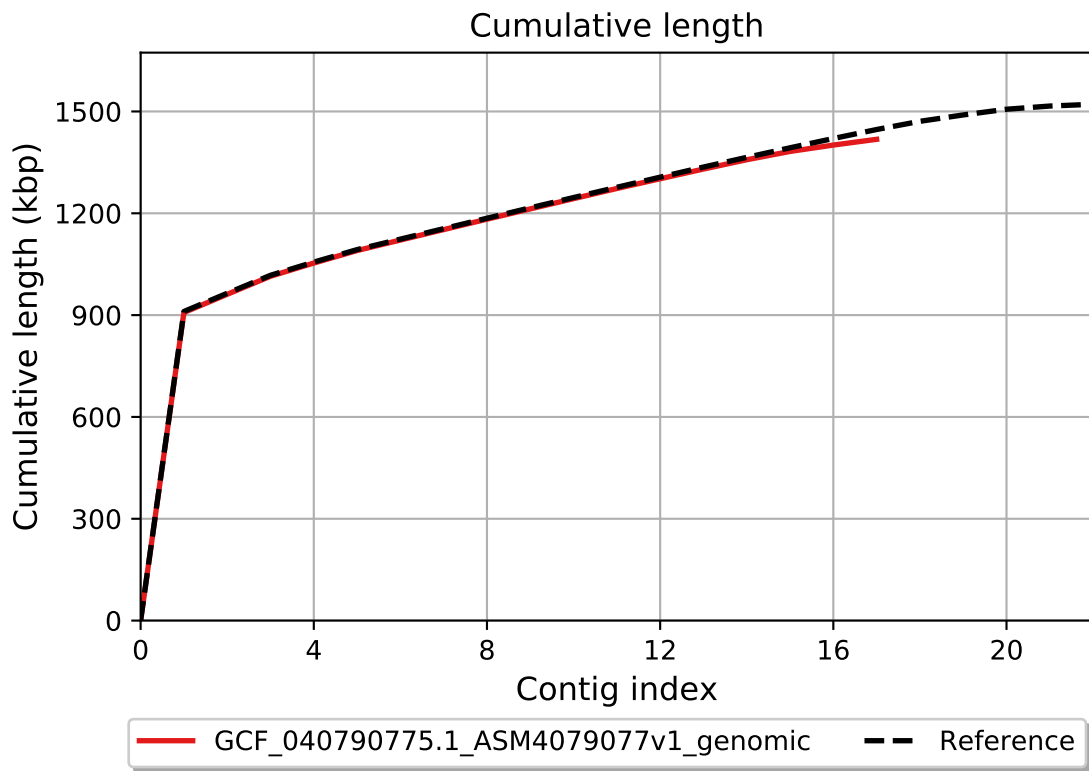
# GC content



GCF_040790775.1_ASM4079077v1_genomic — — Reference

GCF_040790775.1_ASM4079077v1_genomic GC content

Misassemblies

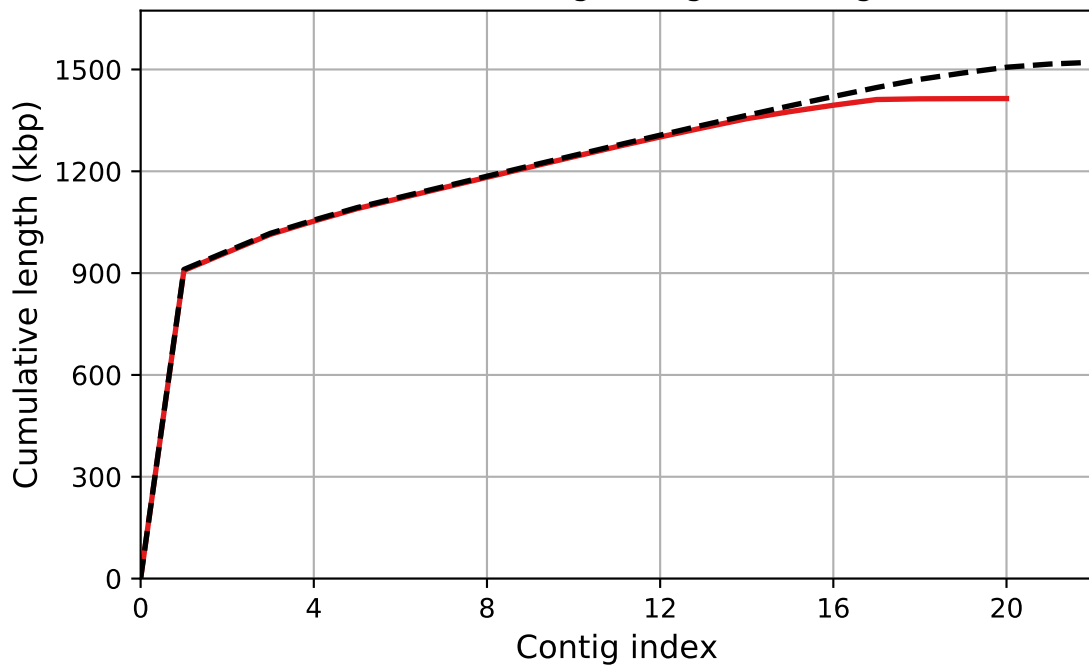GCF_040790775.1_ASM4079077v1_genomic

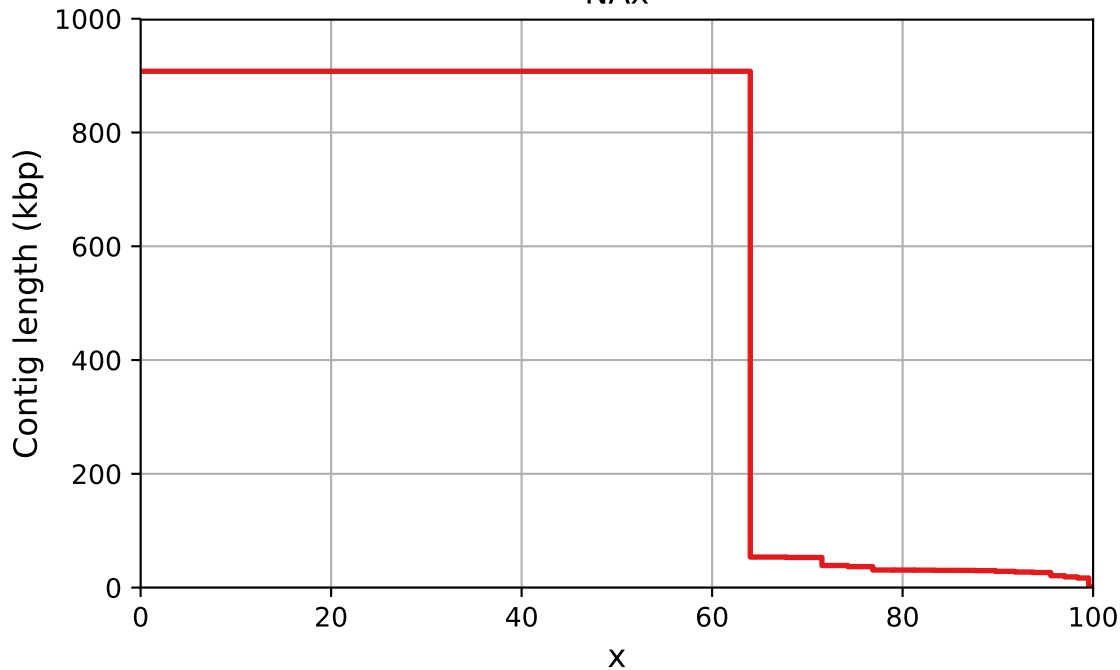█ # relocations   █ # translocations

FRCurve (misassemblies)

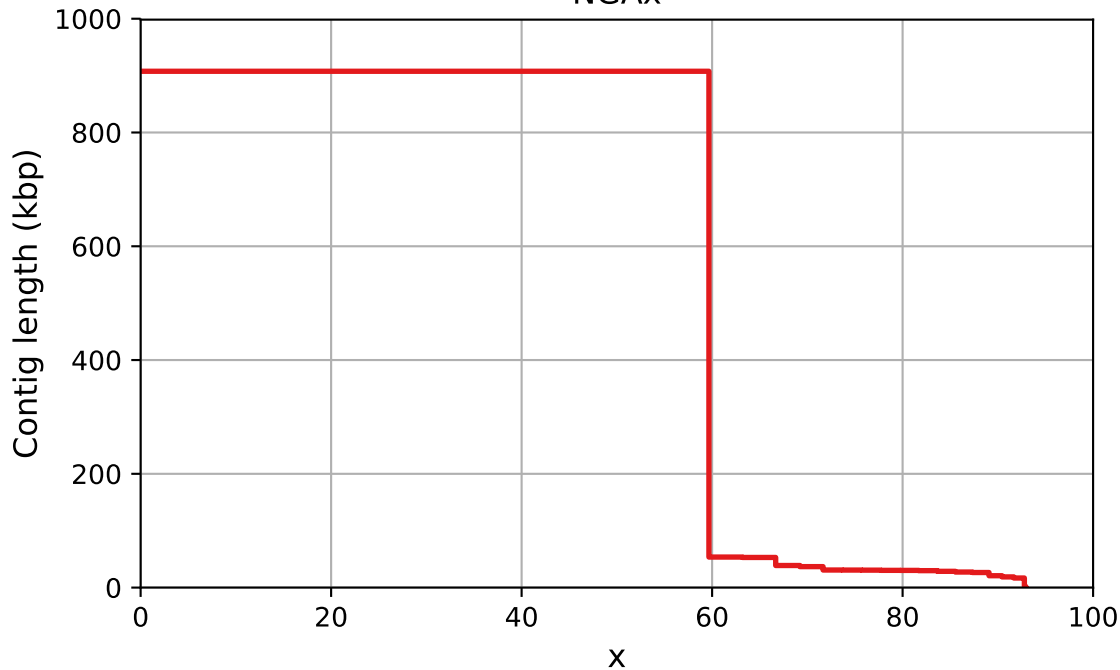GCF_040790775.1_ASM4079077v1_genomic

Cumulative length (aligned contigs)
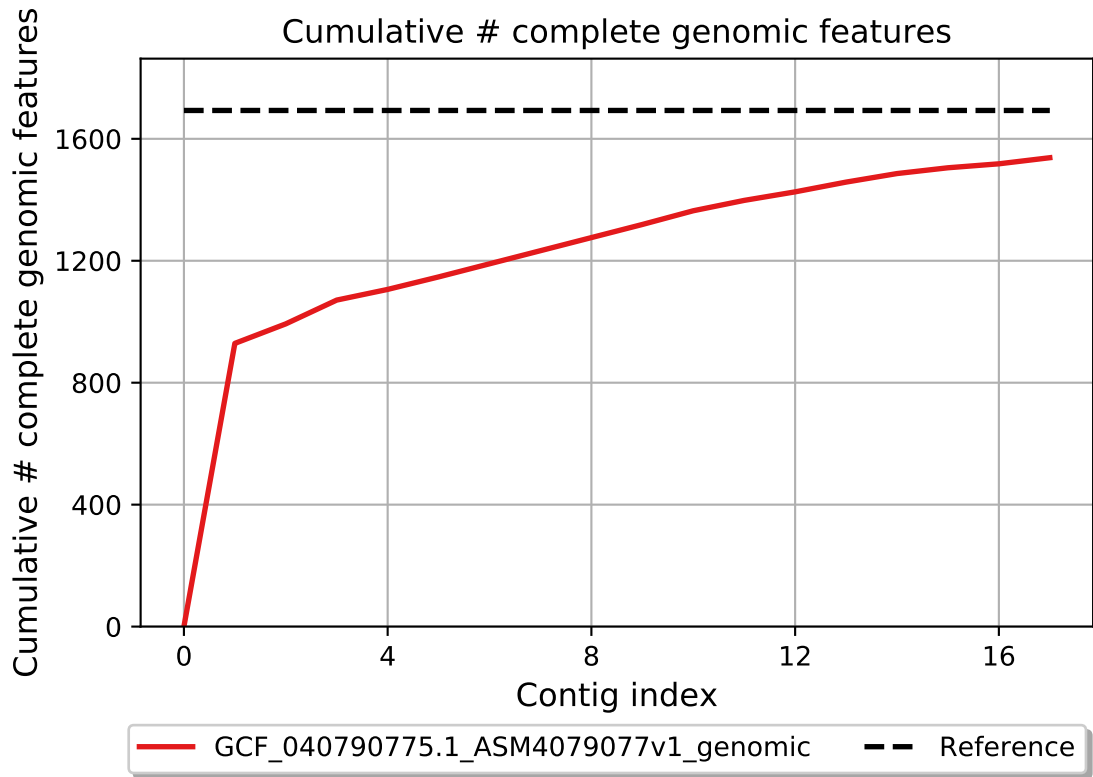
NAx

GCF_040790775.1_ASM4079077v1_genomic

NGAx

GCF_040790775.1_ASM4079077v1_genomic

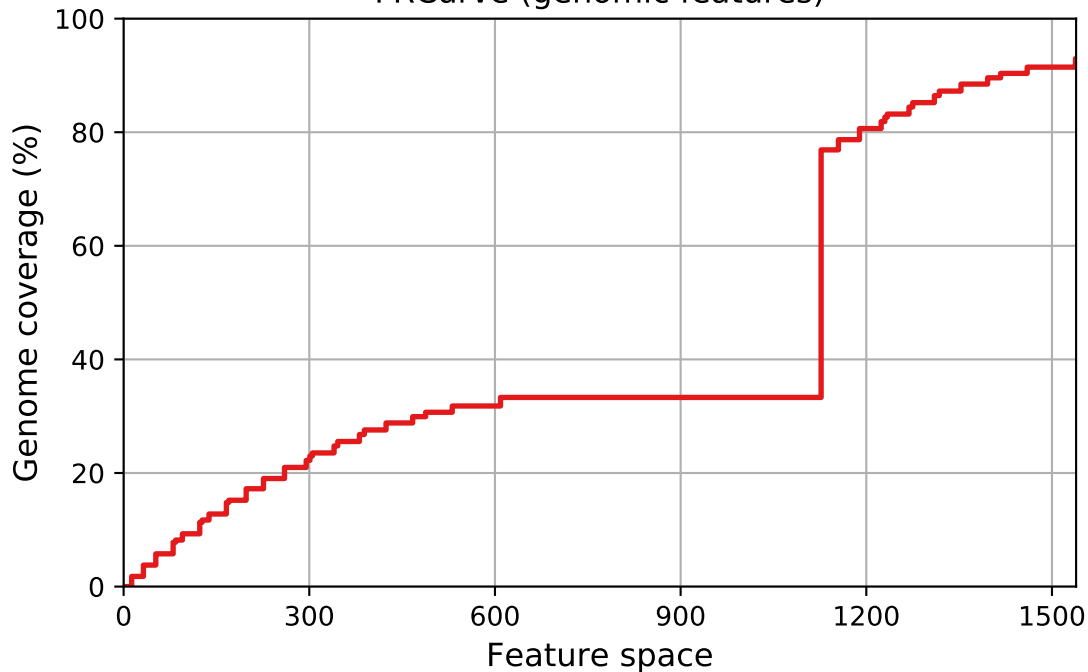Cumulative # complete genomic features

FRCurve (genomic features)

GCF_040790775.1_ASM4079077v1_genomic