# Report

| | microbe-8_fa | microbe-8_fa_broken |
|---|---|---|
| # contigs (>= 0 bp) | 443 | - |
| # contigs (>= 1000 bp) | 71 | 75 |
| Total length (>= 0 bp) | 5601621 | - |
| Total length (>= 1000 bp) | 5541847 | 5539922 |
| # contigs | 77 | 86 |
| Largest contig | 467390 | 467390 |
| Total length | 5545630 | 5545081 |
| Reference length | 5682322 | 5682322 |
| GC (%) | 57.19 | 57.19 |
| Reference GC (%) | 57.12 | 57.12 |
| N50 | 160025 | 160025 |
| NG50 | 160025 | 160025 |
| N90 | 45645 | 43442 |
| NG90 | 35266 | 31305 |
| auN | 189934.7 | 185308.3 |
| auNG | 185365.7 | 180832.6 |
| L50 | 12 | 12 |
| LG50 | 12 | 12 |
| L90 | 34 | 35 |
| LG90 | 37 | 39 |
| # misassemblies | 77 | 77 |
| # misassembled contigs | 34 | 35 |
| Misassembled contigs length | 4584292 | 4544981 |
| # local misassemblies | 27 | 27 |
| # scaffold gap ext. mis. | 0 | - |
| # scaffold gap loc. mis. | 0 | - |
| # unaligned mis. contigs | 3 | 3 |
| # unaligned contigs | 14 + 45 part | 15 + 46 part |
| Unaligned length | 725787 | 725892 |
| Genome fraction (%) | 84.959 | 85.279 |
| Duplication ratio | 1.007 | 1.008 |
| # N's per 100 kbp | 10.46 | 0.56 |
| # mismatches per 100 kbp | 685.04 | 686.29 |
| # indels per 100 kbp | 20.36 | 19.55 |
| # genomic features | 9652 + 232 part | 9641 + 234 part |
| Complete BUSCO (%) | 97.30 | 97.30 |
| Partial BUSCO (%) | 0.00 | 0.00 |
| # predicted rRNA genes | 2 + 3 part | 2 + 3 part |
| Largest alignment | 313449 | 313449 |
| Total aligned length | 4818722 | 4817954 |
| NA50 | 65208 | 65208 |
| NGA50 | 63744 | 63744 |
| NA90 | - | - |
| NGA90 | - | - |
| auNA | 82880.8 | 82701.5 |
| auNGA | 80887.1 | 80704.1 |
| LA50 | 24 | 24 |
| LGA50 | 25 | 25 |
| 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).
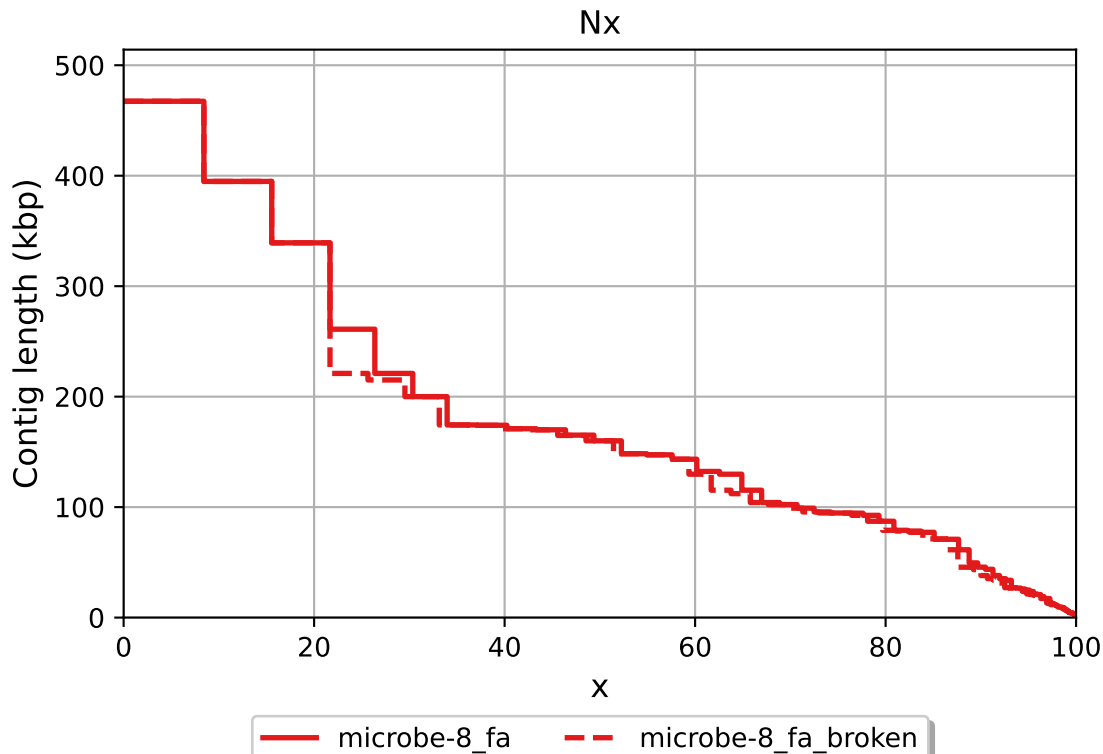
# Misassemblies report
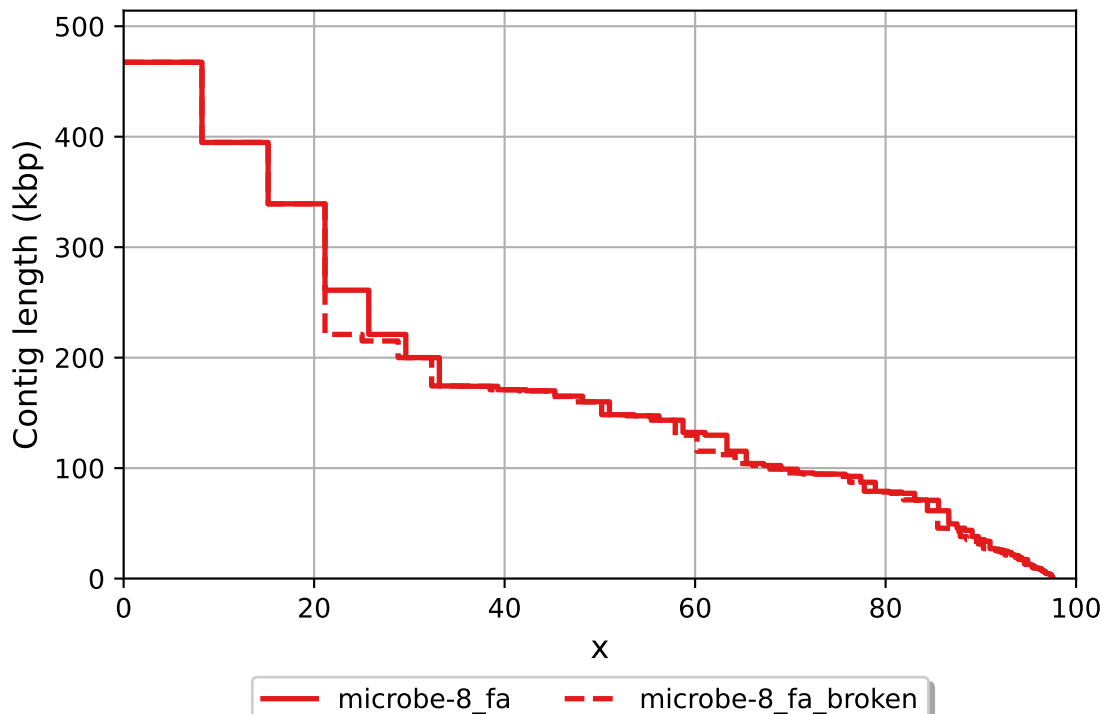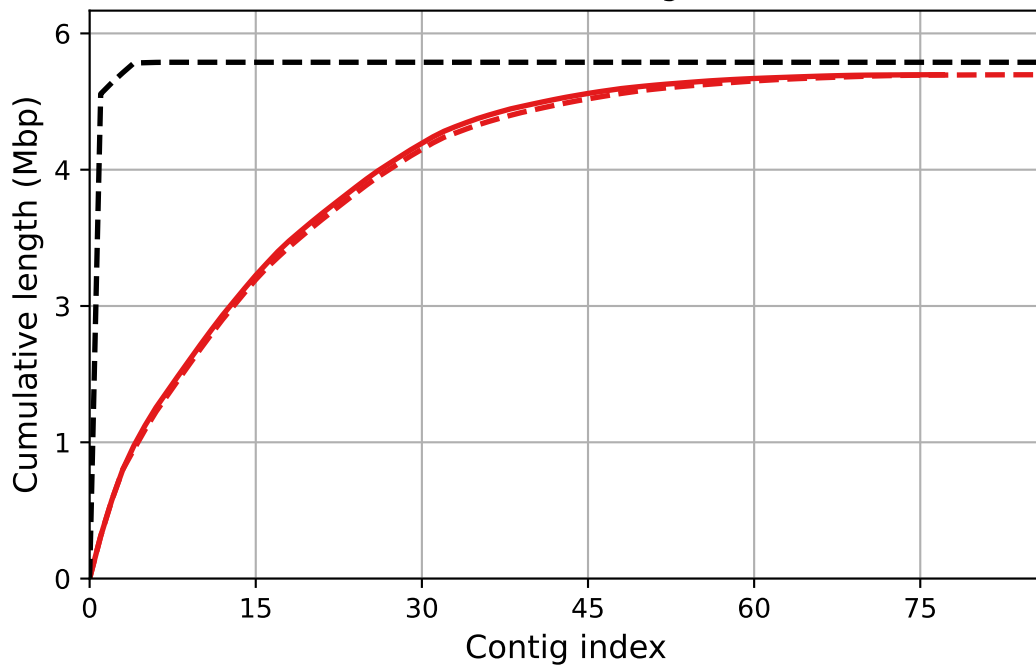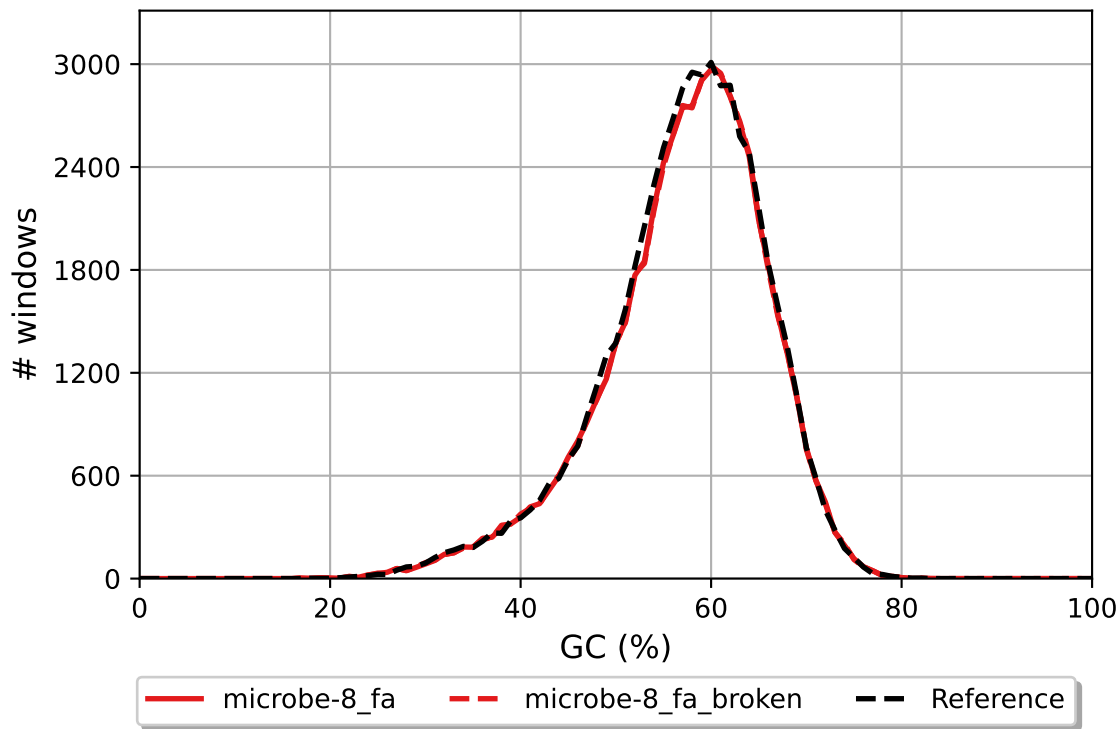
| | microbe-8_fa | microbe-8_fa_broken |
|---|---|---|
| # misassemblies | 77 | 77 |
| # contig misassemblies | 77 | 77 |
| # c. relocations | 73 | 73 |
| # c. translocations | 4 | 4 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 0 | 0 |
| # s. relocations | 0 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 34 | 35 |
| Misassembled contigs length | 4584292 | 4544981 |
| # local misassemblies | 27 | 27 |
| # scaffold gap ext. mis. | 0 | - |
| # scaffold gap loc. mis. | 0 | - |
| # unaligned mis. contigs | 3 | 3 |
| # mismatches | 33010 | 33065 |
| # indels | 981 | 942 |
| # indels (<= 5 bp) | 863 | 837 |
| # indels (> 5 bp) | 118 | 105 |
| Indels length | 9573 | 8906 |

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

| | microbe-8_fa | microbe-8_fa_broken |
|---|---|---|
| # fully unaligned contigs | 14 | 15 |
| Fully unaligned length | 63486 | 63819 |
| # partially unaligned contigs | 45 | 46 |
| Partially unaligned length | 662301 | 662073 |
| # N's | 580 | 31 |

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).
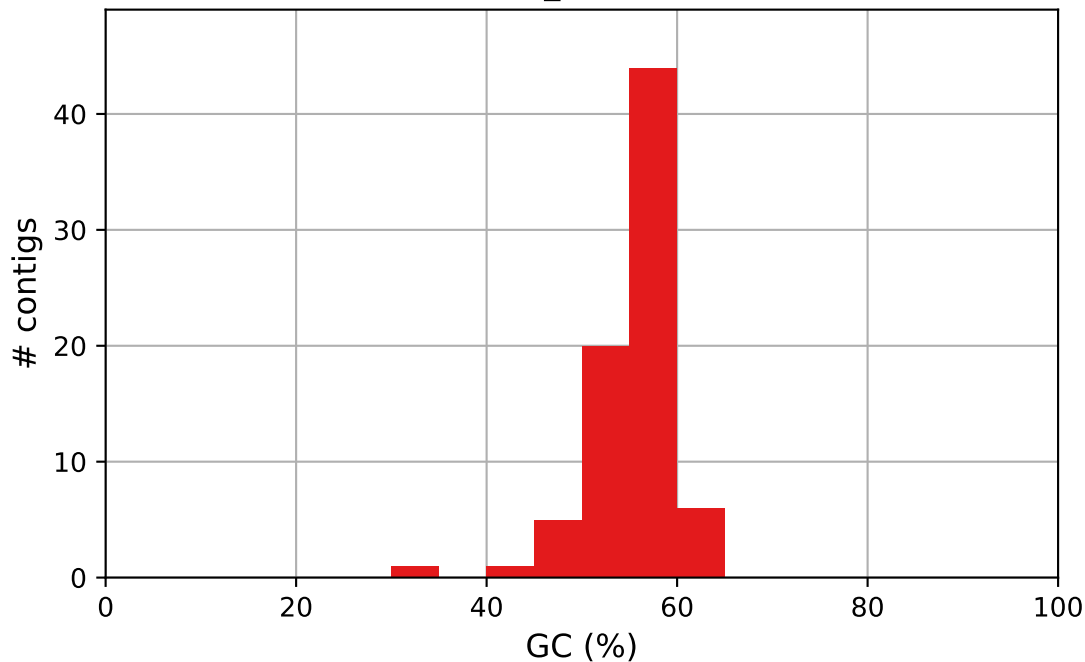
Nx

NGx

Cumulative length

GC content

microbe-8_fa GC content

microbe-8_fa_broken GC content

Misassemblies

FRCurve (misassemblies)
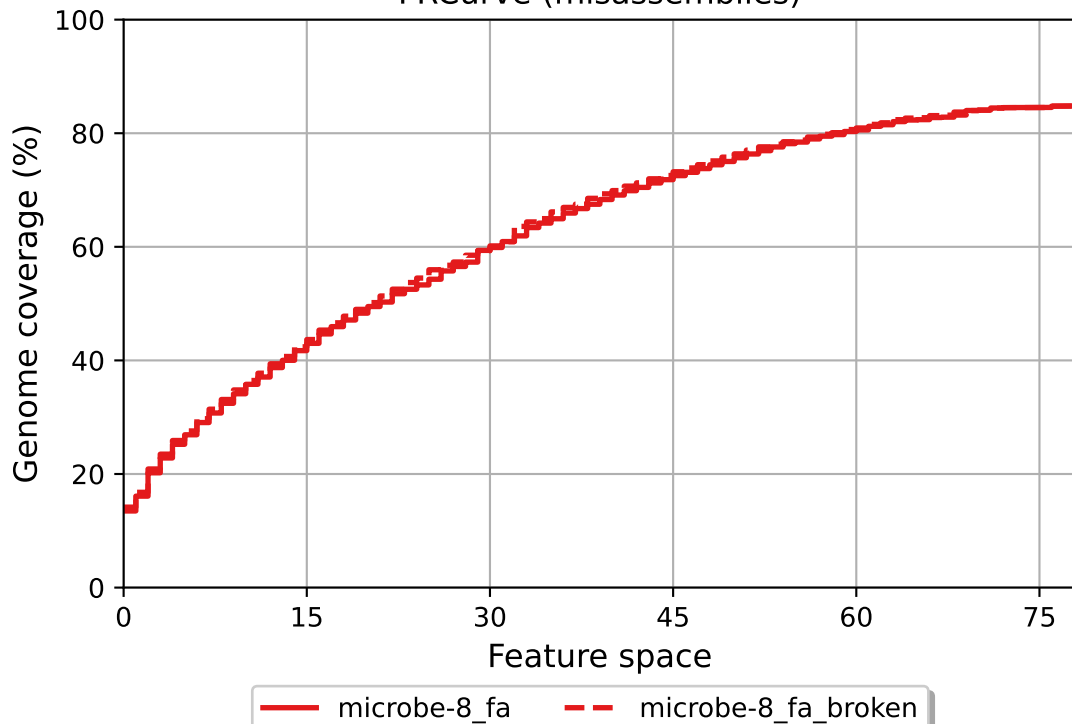
Cumulative length (aligned contigs)

NAx
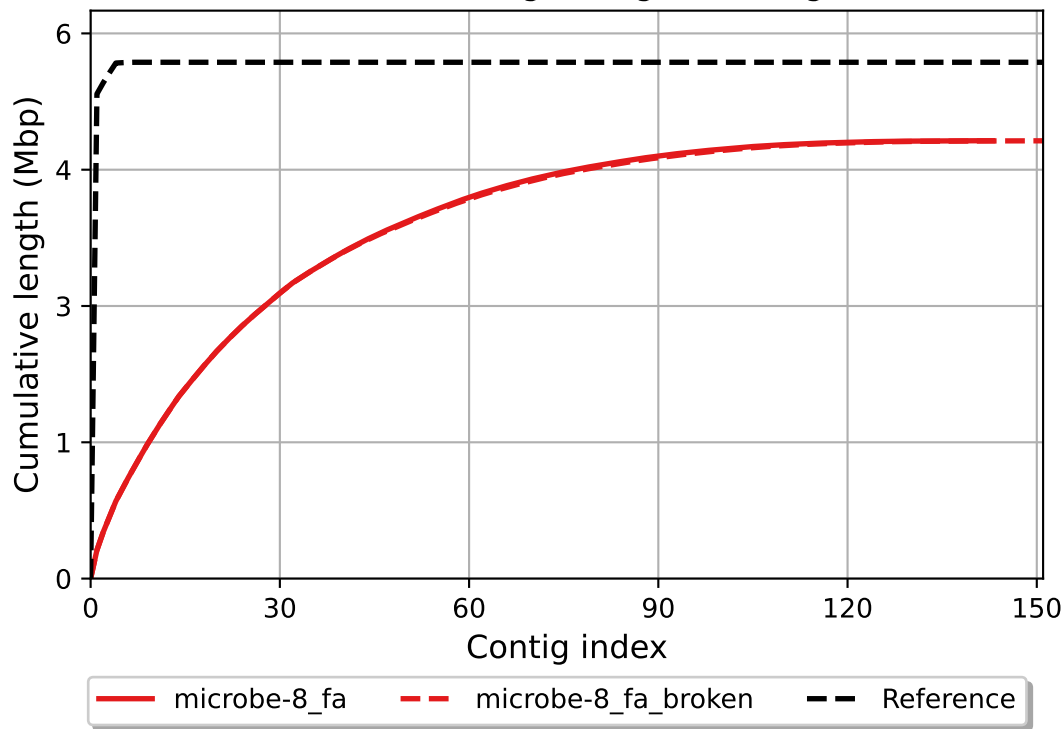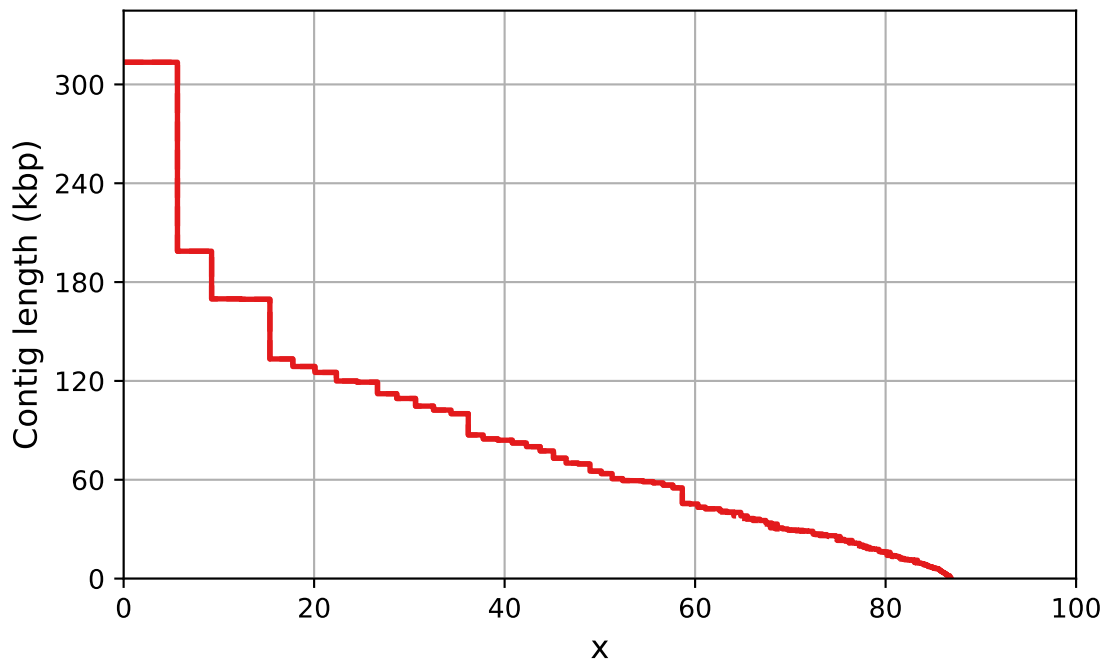
NGAx
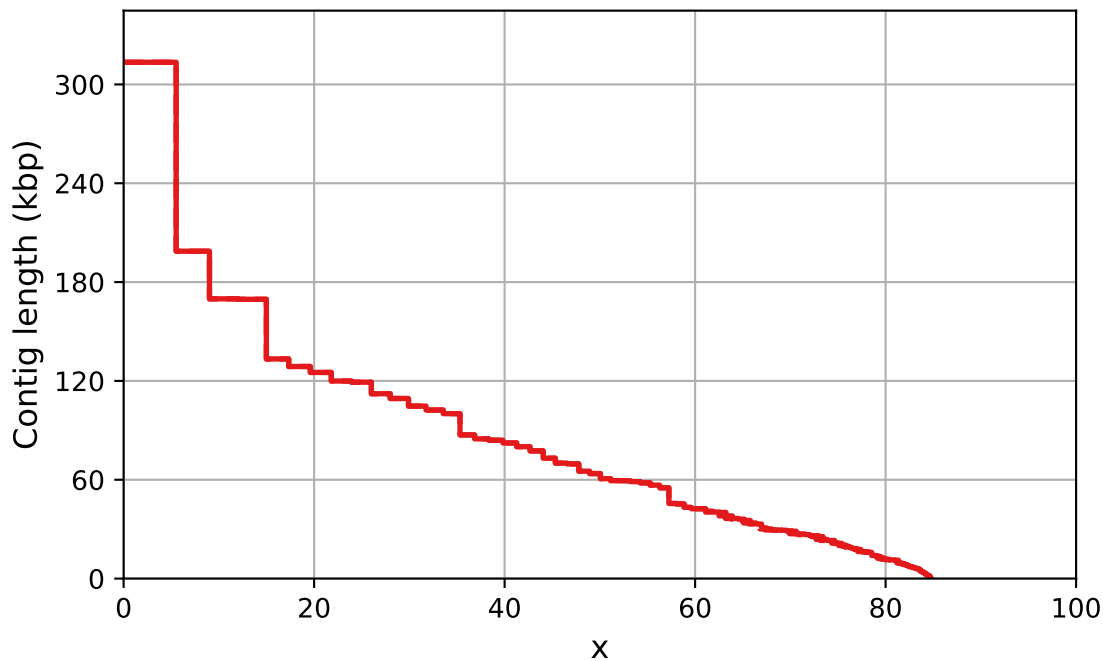
Cumulative # complete genomic features
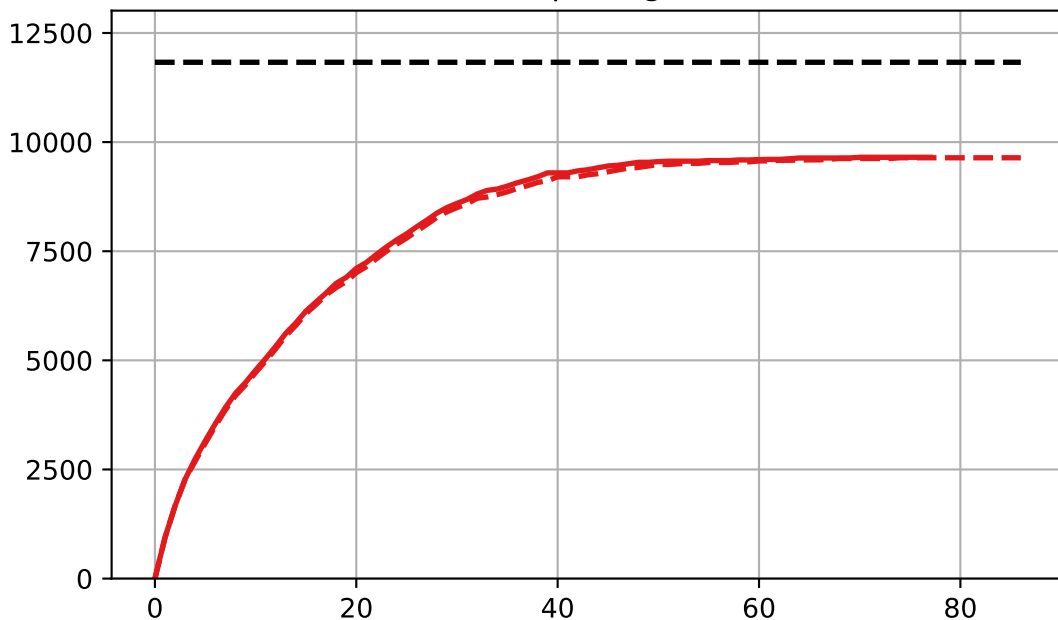
FRCurve (genomic features)
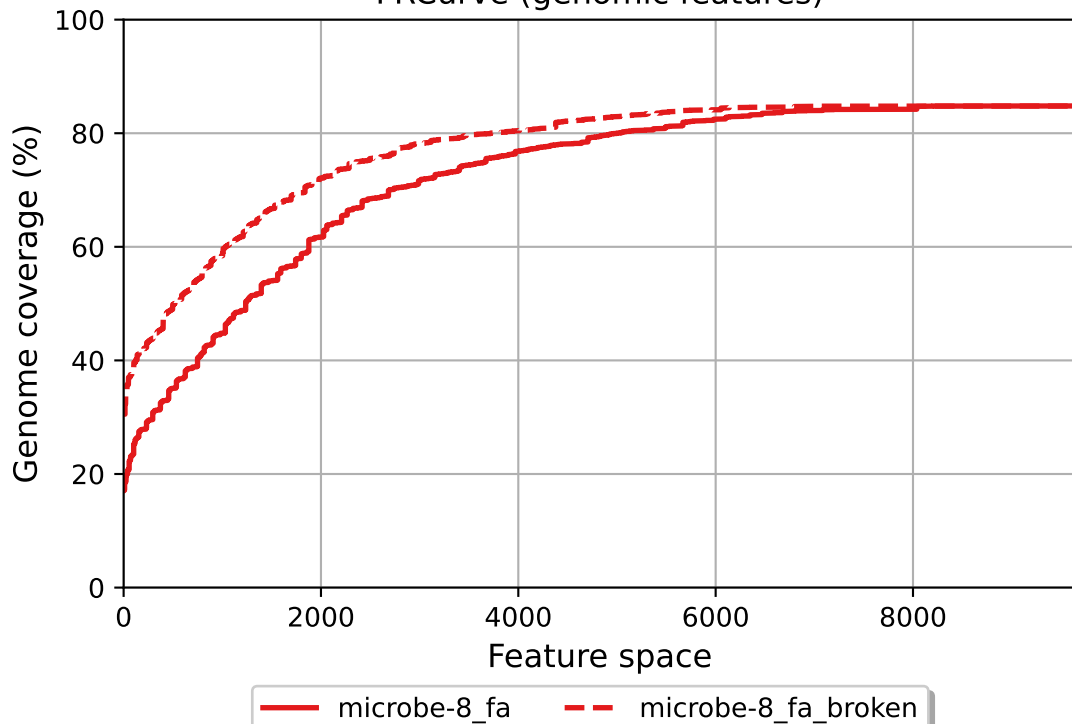
# complete genomic features
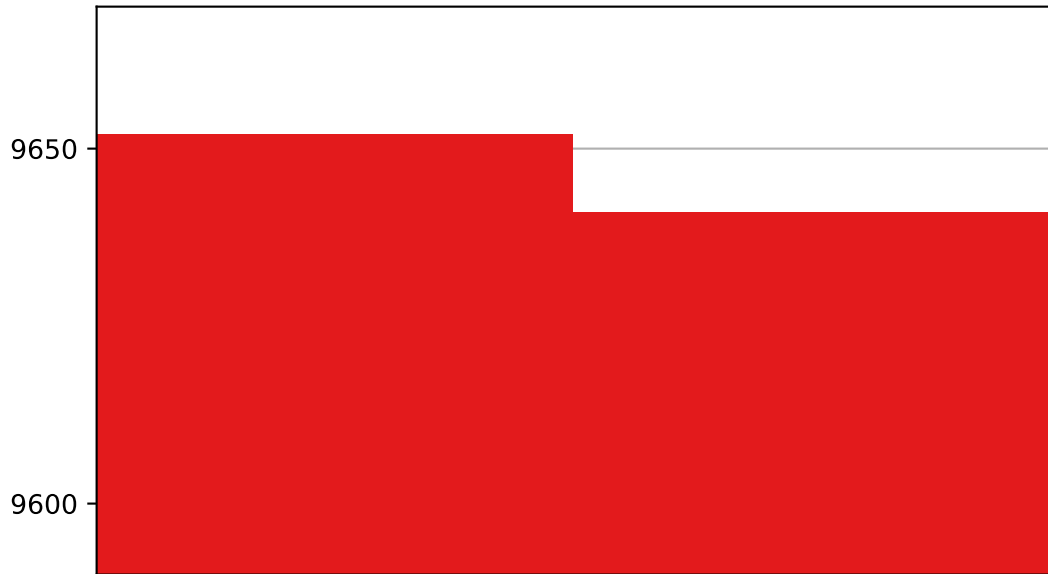
microbe-8_fa  microbe-8_fa_broken

Genome fraction, %