

# Report

|                             | SAMPLE3_SE.AF0.8.consensus | SAMPLE1_PE.AF0.8.consensus | SAMPLE2_PE.AF0.8.consensus |
|-----------------------------|----------------------------|----------------------------|----------------------------|
| # contigs (>= 0 bp)         | 1                          | 1                          | 1                          |
| # contigs (>= 1000 bp)      | 1                          | 1                          | 1                          |
| # contigs (>= 5000 bp)      | 1                          | 1                          | 1                          |
| # contigs (>= 10000 bp)     | 1                          | 1                          | 1                          |
| # contigs (>= 25000 bp)     | 1                          | 1                          | 1                          |
| # contigs (>= 50000 bp)     | 0                          | 0                          | 0                          |
| Total length (>= 0 bp)      | 29782                      | 29782                      | 29649                      |
| Total length (>= 1000 bp)   | 29782                      | 29782                      | 29649                      |
| Total length (>= 5000 bp)   | 29782                      | 29782                      | 29649                      |
| Total length (>= 10000 bp)  | 29782                      | 29782                      | 29649                      |
| Total length (>= 25000 bp)  | 29782                      | 29782                      | 29649                      |
| Total length (>= 50000 bp)  | 0                          | 0                          | 0                          |
| # contigs                   | 1                          | 1                          | 1                          |
| Largest contig              | 29782                      | 29782                      | 29649                      |
| Total length                | 29782                      | 29782                      | 29649                      |
| Reference length            | 29903                      | 29903                      | 29903                      |
| GC (%)                      | 37.72                      | 37.94                      | 38.20                      |
| Reference GC (%)            | 37.97                      | 37.97                      | 37.97                      |
| N50                         | 29782                      | 29782                      | 29649                      |
| NG50                        | 29782                      | 29782                      | 29649                      |
| N75                         | 29782                      | 29782                      | 29649                      |
| NG75                        | 29782                      | 29782                      | 29649                      |
| L50                         | 1                          | 1                          | 1                          |
| LG50                        | 1                          | 1                          | 1                          |
| L75                         | 1                          | 1                          | 1                          |
| LG75                        | 1                          | 1                          | 1                          |
| # misassemblies             | 0                          | 0                          | 0                          |
| # misassembled contigs      | 0                          | 0                          | 0                          |
| Misassembled contigs length | 0                          | 0                          | 0                          |
| # local misassemblies       | 0                          | 0                          | 0                          |
| # scaffold gap ext. mis.    | 0                          | 0                          | 0                          |
| # scaffold gap loc. mis.    | 9                          | 2                          | 10                         |
| # unaligned mis. contigs    | 0                          | 0                          | 0                          |
| # unaligned contigs         | 0 + 0 part                 | 0 + 0 part                 | 0 + 0 part                 |
| Unaligned length            | 0                          | 0                          | 0                          |
| Genome fraction (%)         | 88.199                     | 97.606                     | 85.700                     |
| Duplication ratio           | 1.129                      | 1.020                      | 1.157                      |
| # N's per 100 kbp           | 12853.40                   | 2481.36                    | 14368.11                   |
| # mismatches per 100 kbp    | 0.00                       | 20.56                      | 23.41                      |
| # indels per 100 kbp        | 0.00                       | 0.00                       | 0.00                       |
| # genomic features          | 14 + 12 part               | 23 + 7 part                | 10 + 14 part               |
| Largest alignment           | 26374                      | 29187                      | 25627                      |
| Total aligned length        | 26374                      | 29187                      | 25627                      |
| NA50                        | 26374                      | 29187                      | 25627                      |
| NGA50                       | 26374                      | 29187                      | 25627                      |
| NA75                        | 26374                      | 29187                      | 25627                      |
| NGA75                       | 26374                      | 29187                      | 25627                      |
| LA50                        | 1                          | 1                          | 1                          |
| LGA50                       | 1                          | 1                          | 1                          |
| LA75                        | 1                          | 1                          | 1                          |
| LGA75                       | 1                          | 1                          | 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).

## Misassemblies report

|                             | SAMPLE3_SE.AF0.8.consensus | SAMPLE1_PE.AF0.8.consensus | SAMPLE2_PE.AF0.8.consensus |
|-----------------------------|----------------------------|----------------------------|----------------------------|
| # misassemblies             | 0                          | 0                          | 0                          |
| # contig misassemblies      | 0                          | 0                          | 0                          |
| # c. relocations            | 0                          | 0                          | 0                          |
| # c. translocations         | 0                          | 0                          | 0                          |
| # c. inversions             | 0                          | 0                          | 0                          |
| # scaffold misassemblies    | 0                          | 0                          | 0                          |
| # s. relocations            | 0                          | 0                          | 0                          |
| # s. translocations         | 0                          | 0                          | 0                          |
| # s. inversions             | 0                          | 0                          | 0                          |
| # misassembled contigs      | 0                          | 0                          | 0                          |
| Misassembled contigs length | 0                          | 0                          | 0                          |
| # local misassemblies       | 0                          | 0                          | 0                          |
| # scaffold gap ext. mis.    | 0                          | 0                          | 0                          |
| # scaffold gap loc. mis.    | 9                          | 2                          | 10                         |
| # unaligned mis. contigs    | 0                          | 0                          | 0                          |
| # mismatches                | 0                          | 6                          | 6                          |
| # indels                    | 0                          | 0                          | 0                          |
| # indels (<= 5 bp)          | 0                          | 0                          | 0                          |
| # indels (> 5 bp)           | 0                          | 0                          | 0                          |
| Indels length               | 0                          | 0                          | 0                          |

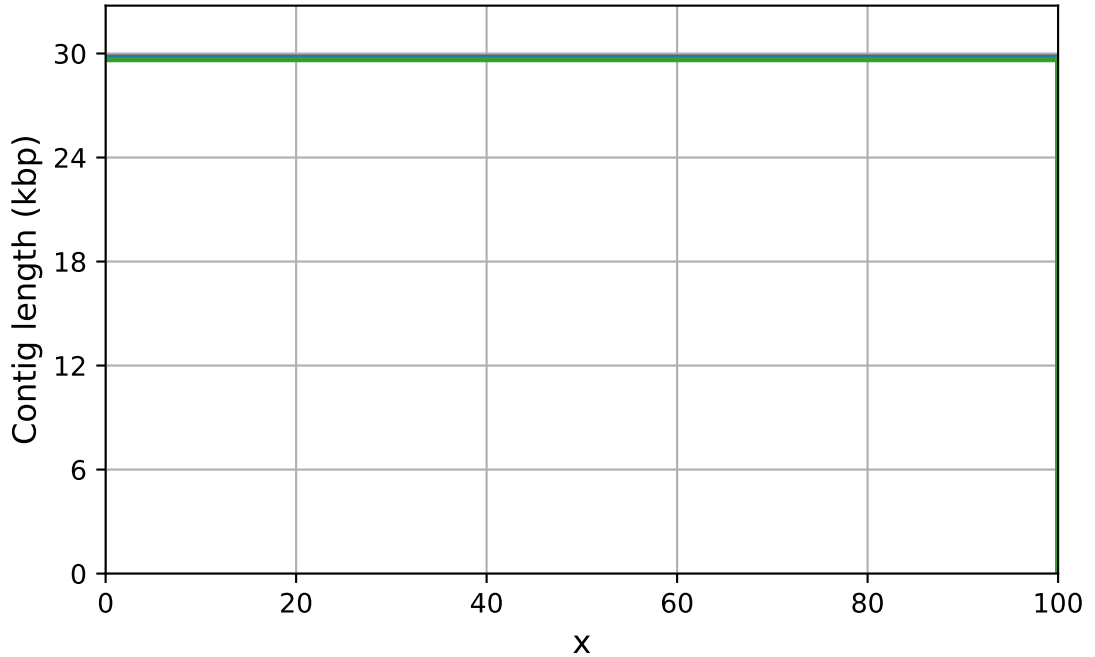
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

|                               | SAMPLE3_SE.AF0.8.consensus | SAMPLE1_PE.AF0.8.consensus | SAMPLE2_PE.AF0.8.consensus |
|-------------------------------|----------------------------|----------------------------|----------------------------|
| # fully unaligned contigs     | 0                          | 0                          | 0                          |
| Fully unaligned length        | 0                          | 0                          | 0                          |
| # partially unaligned contigs | 0                          | 0                          | 0                          |
| Partially unaligned length    | 0                          | 0                          | 0                          |
| # N's                         | 3828                       | 739                        | 4260                       |

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

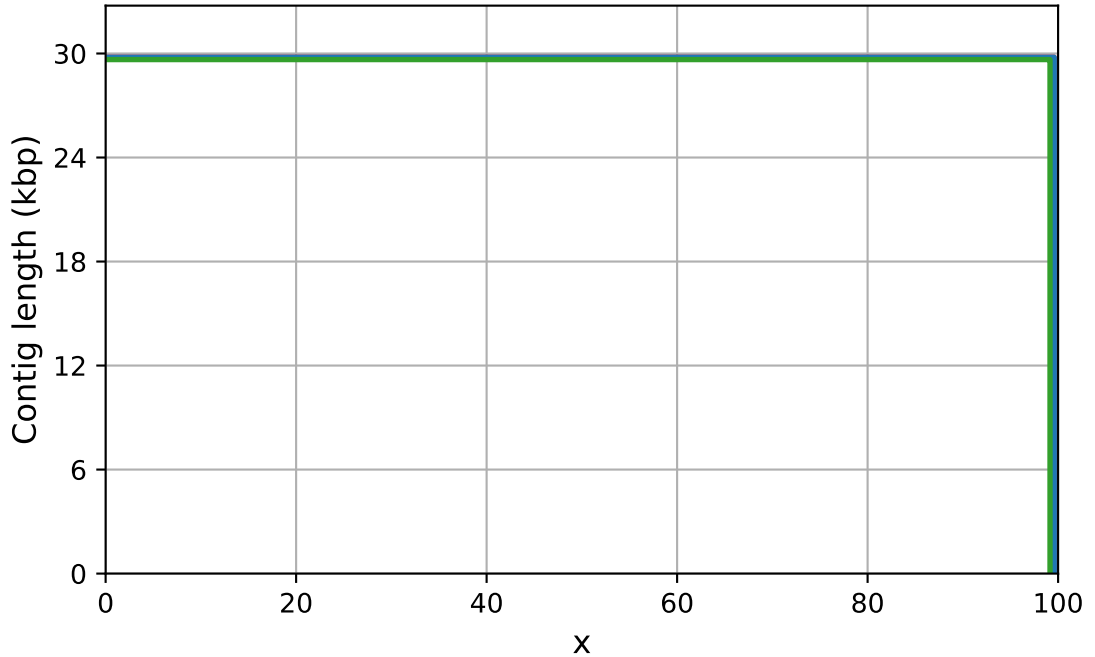


LE3\_SE.AF0.8.consensus

SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus

# NGx

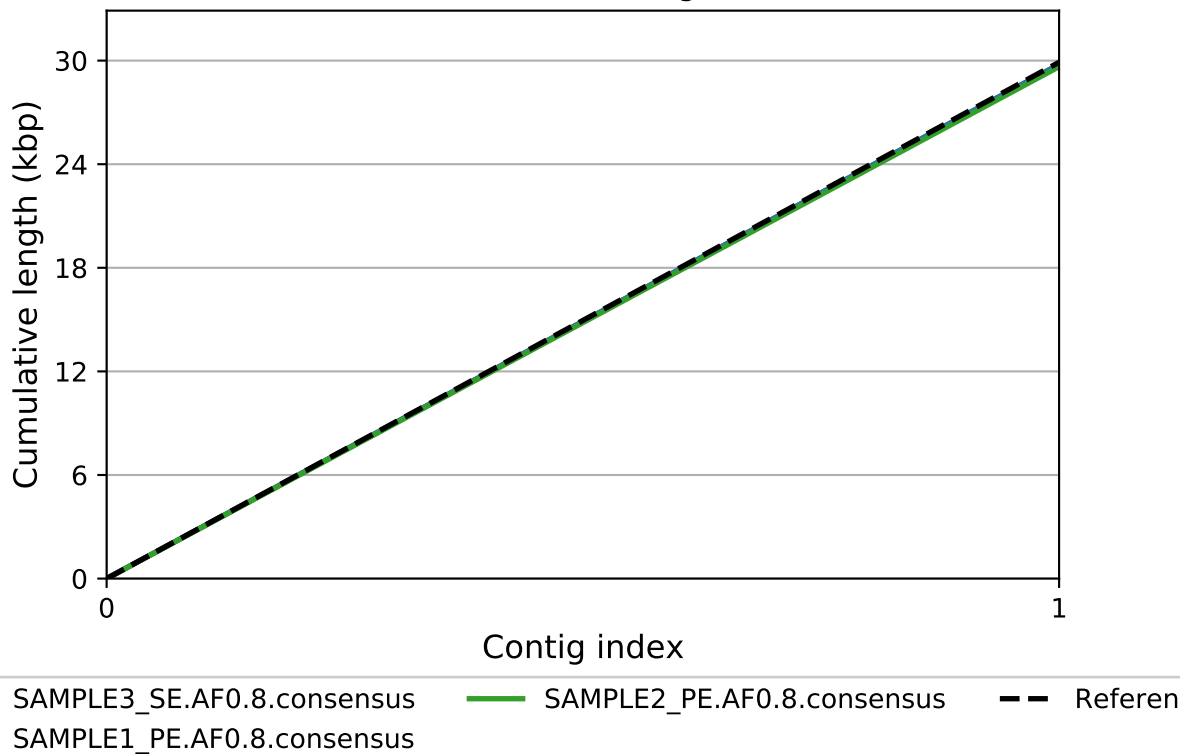


LE3\_SE.AF0.8.consensus

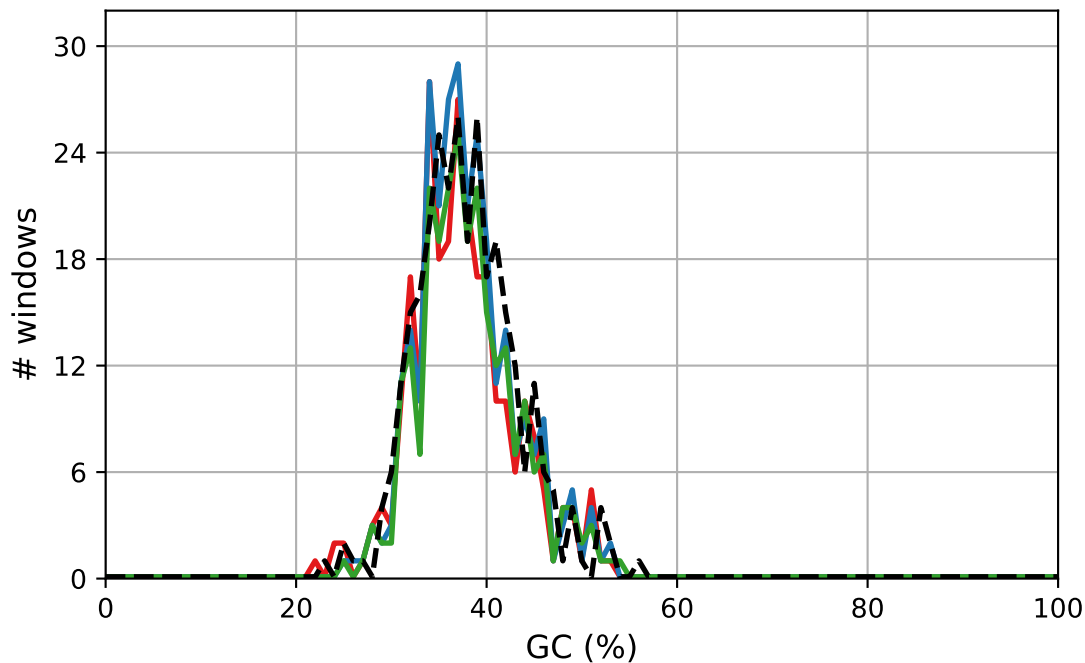
SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus

Cumulative length

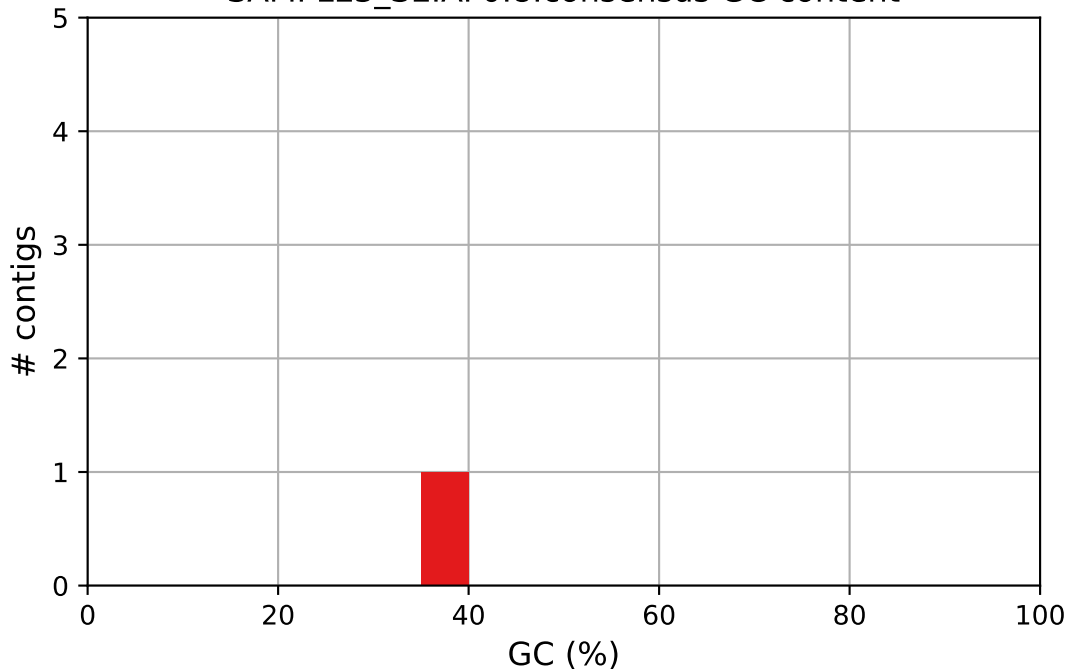


GC content



— SAMPLE3\_SE.AF0.8.consensus    
 — SAMPLE2\_PE.AF0.8.consensus    
 - - Reference  
— SAMPLE1\_PE.AF0.8.consensus

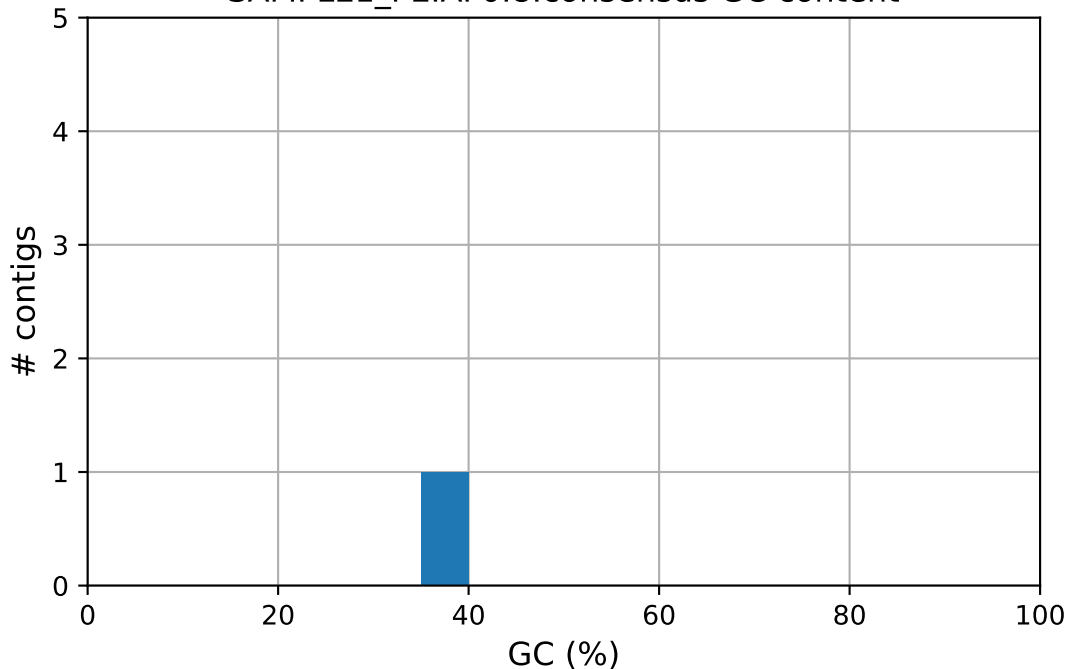
SAMPLE3\_SE.AF0.8.consensus GC content



■ SAMPLE3\_SE.AF0.8.consensus

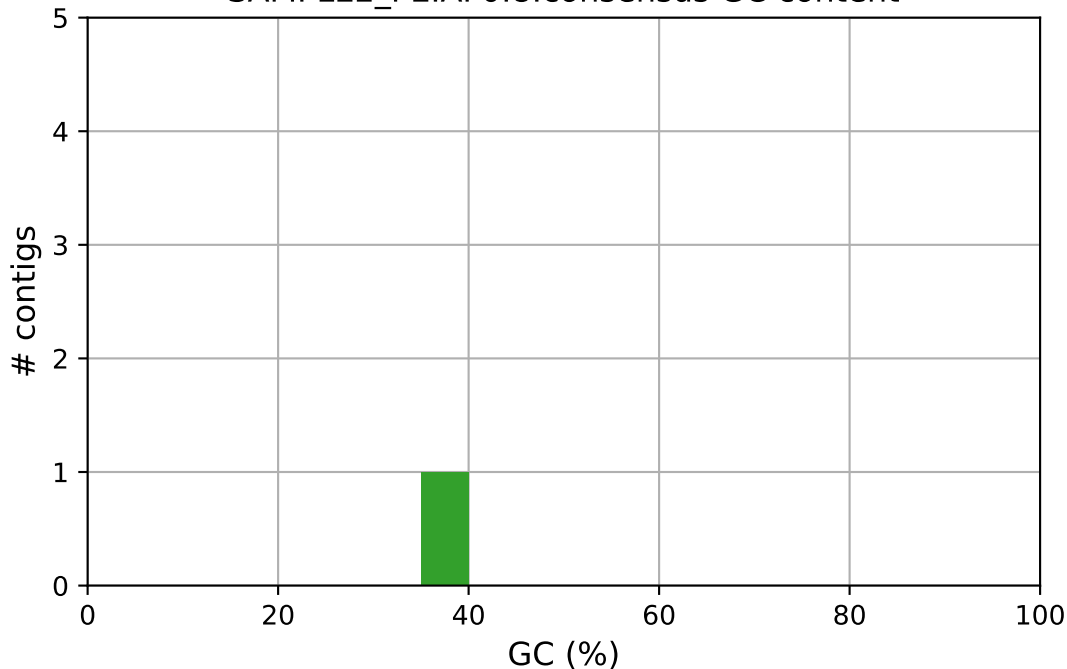


SAMPLE1\_PE.AF0.8.consensus GC content



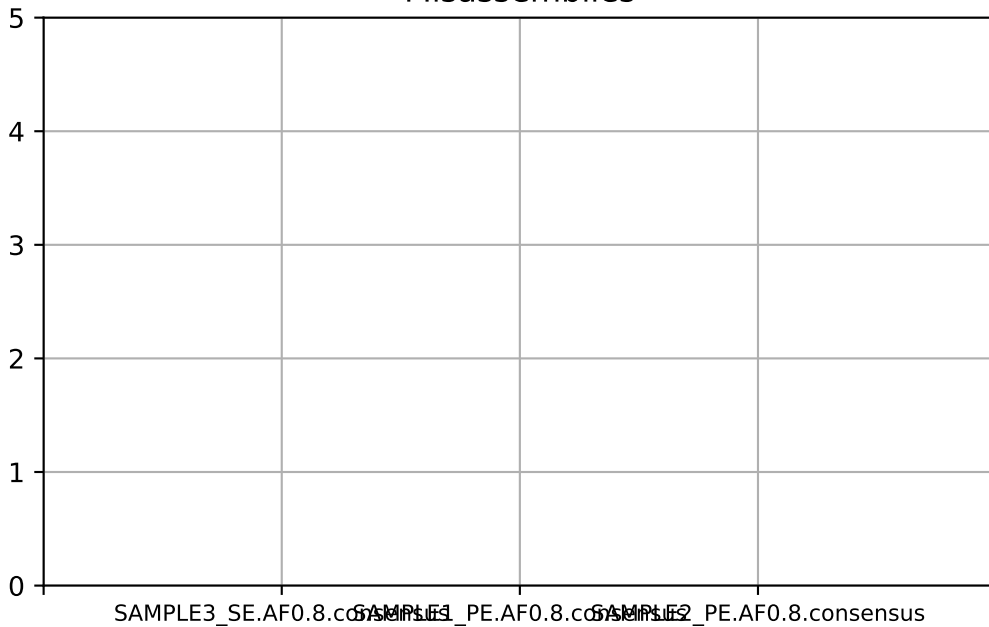
SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus GC content

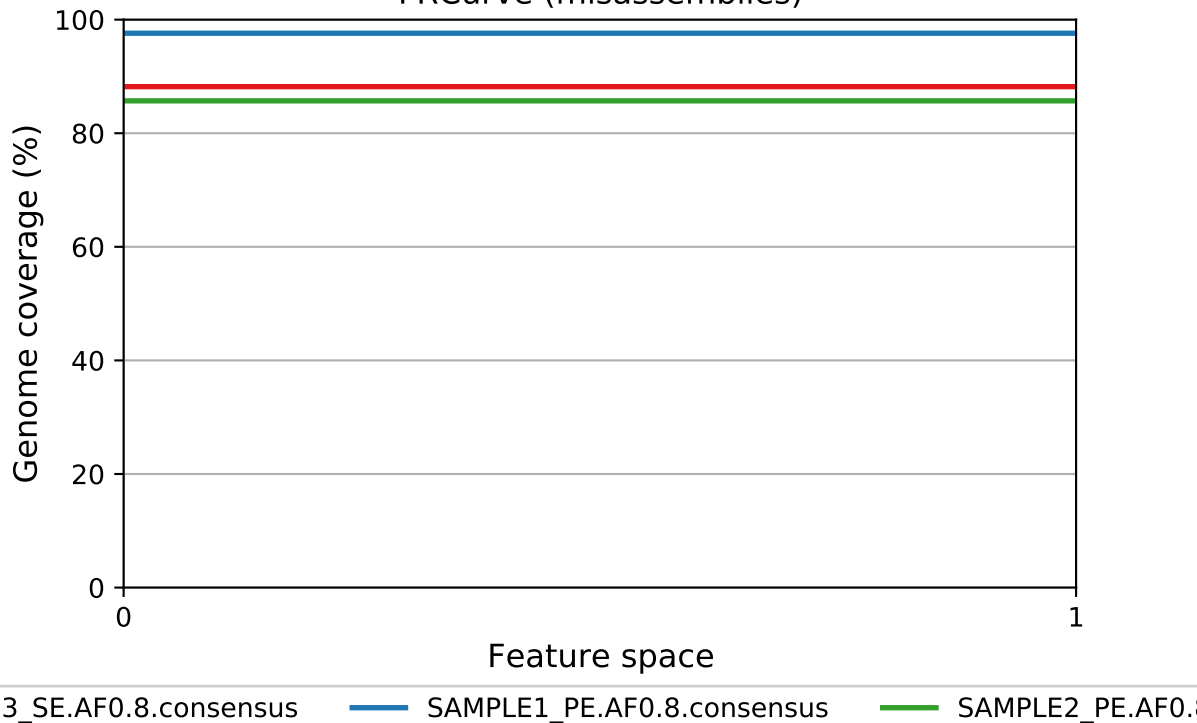


 SAMPLE2\_PE.AF0.8.consensus

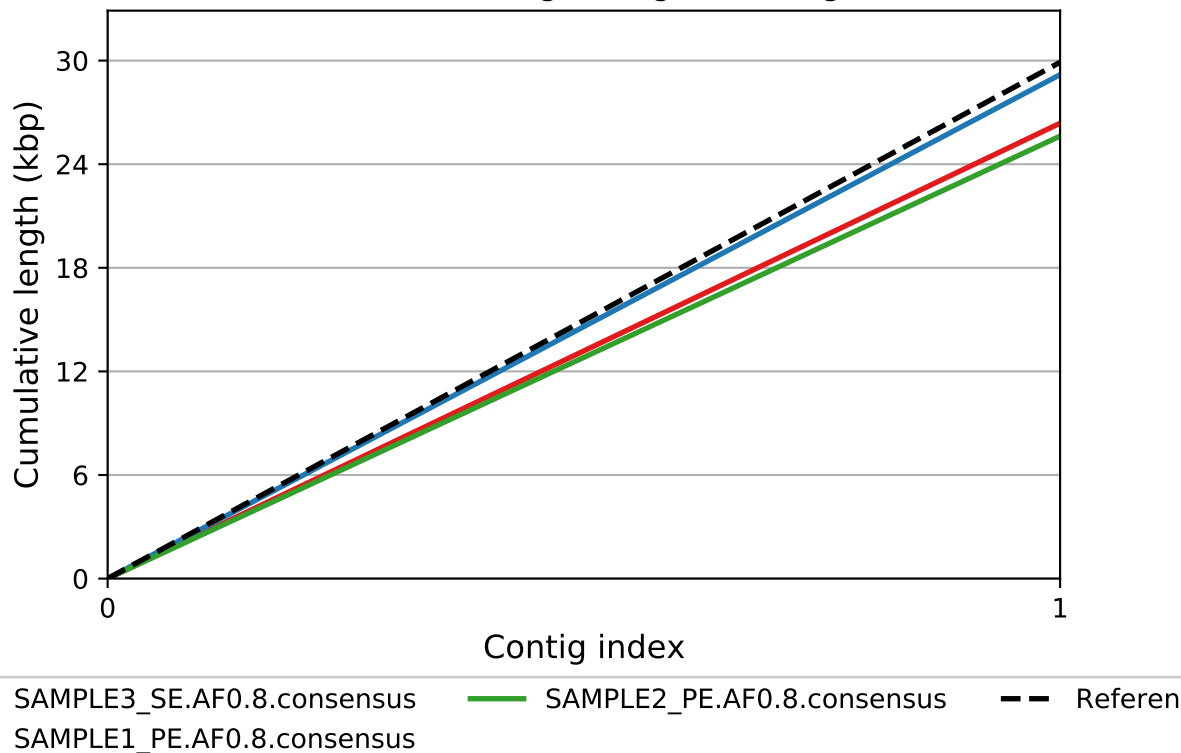
## Misassemblies



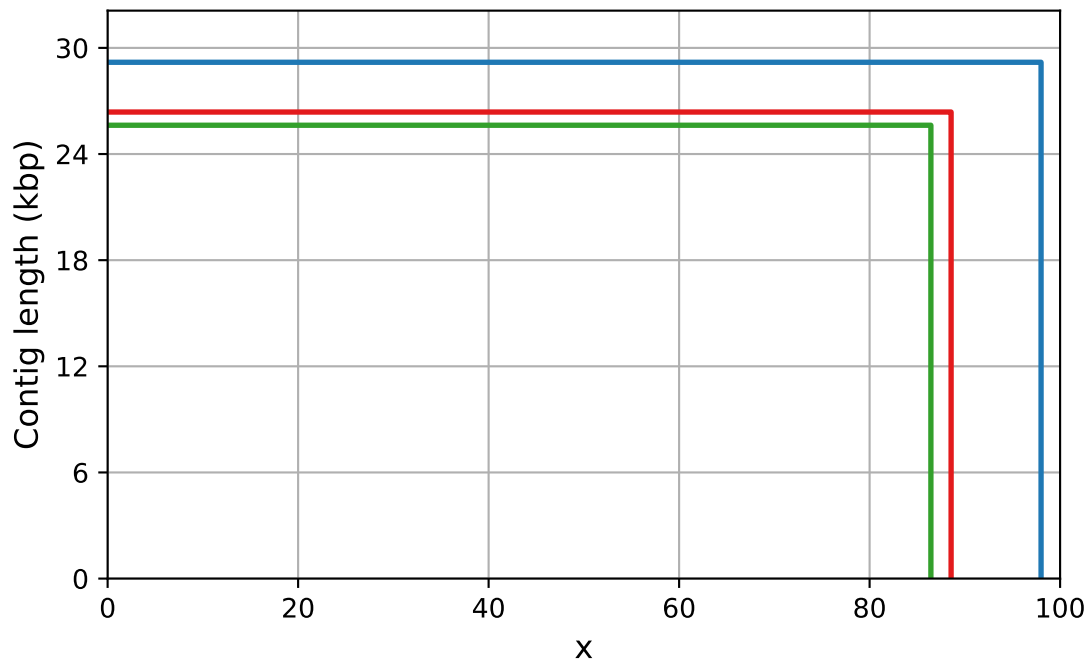
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx

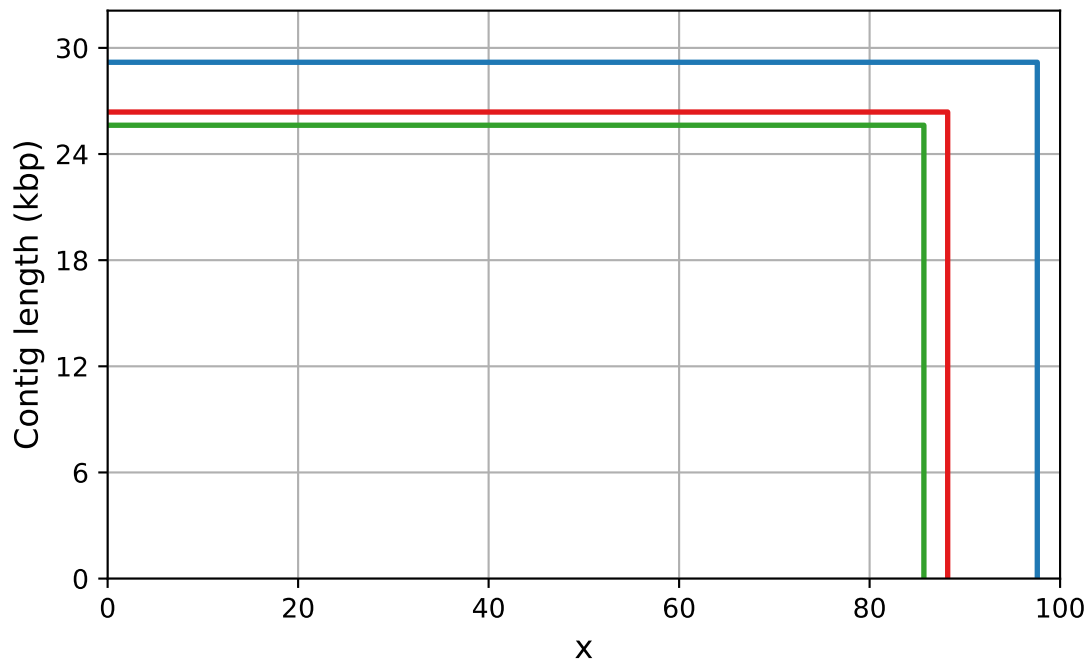


LE3\_SE.AF0.8.consensus

SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus

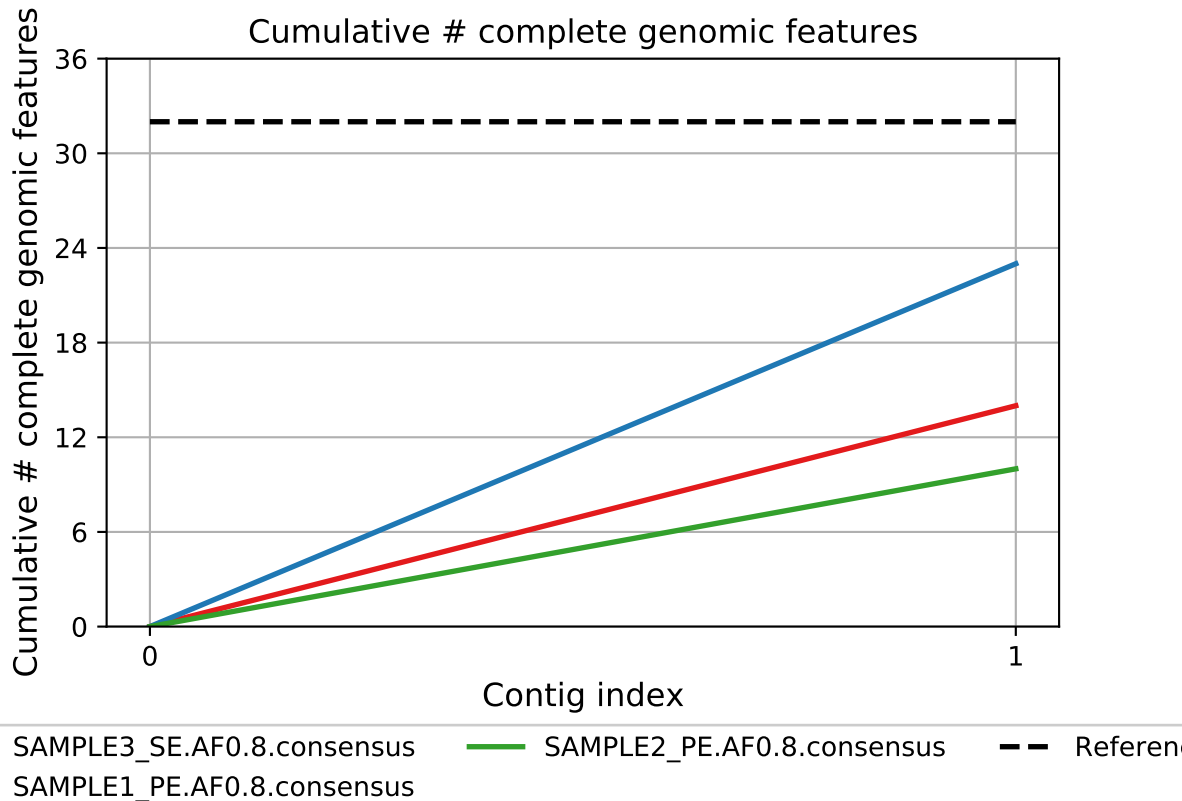
# NGAx



LE3\_SE.AF0.8.consensus

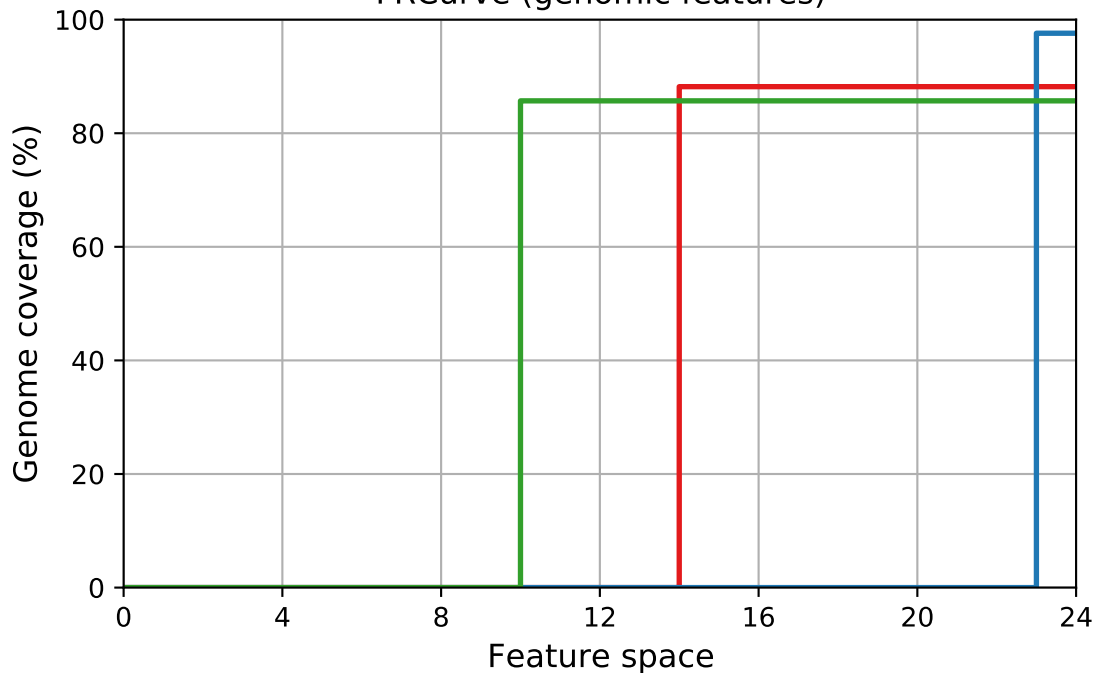
SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus





FRCurve (genomic features)

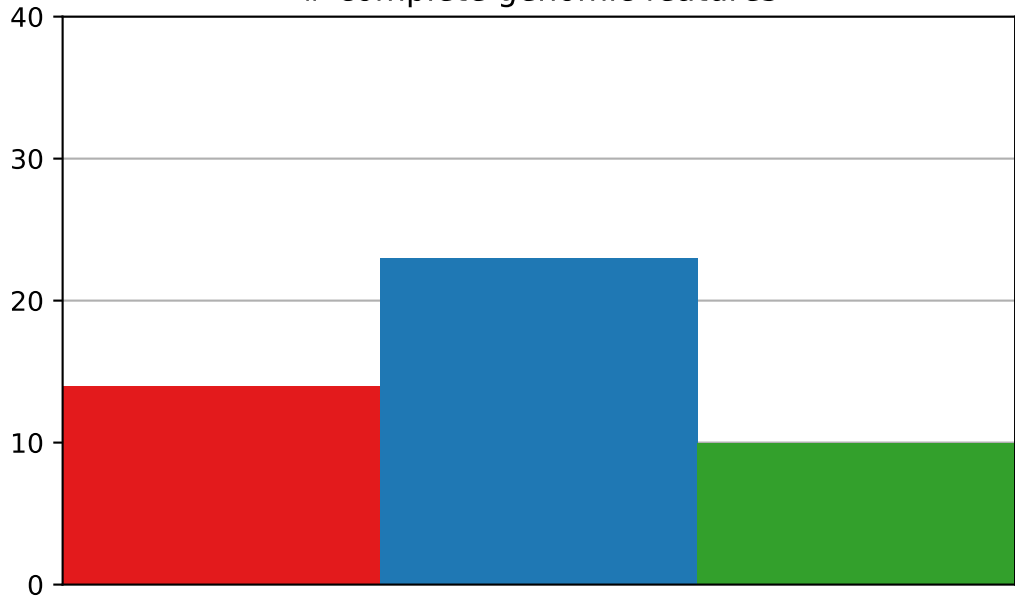


LE3\_SE.AF0.8.consensus

SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus

# complete genomic features

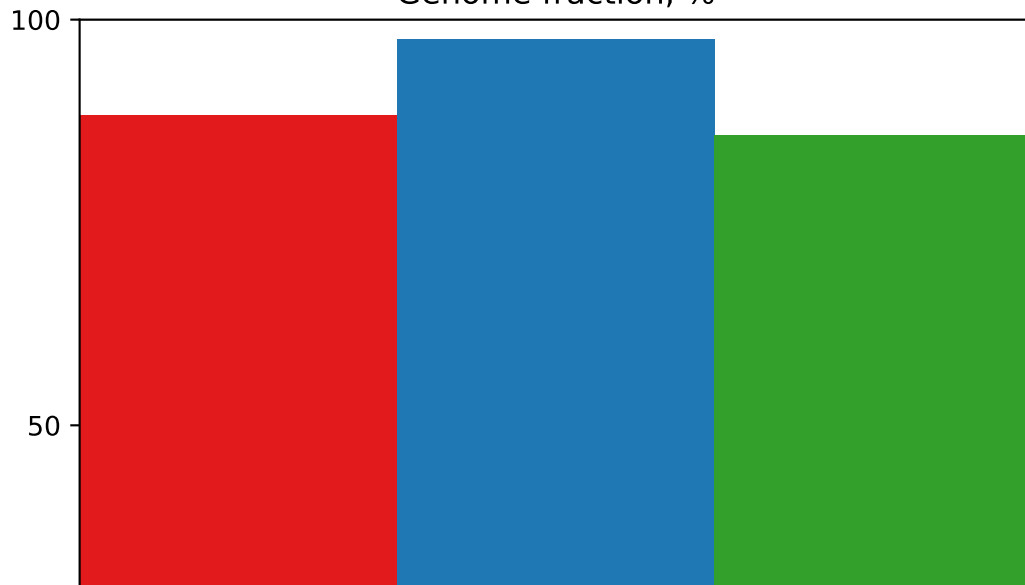


LE3\_SE.AF0.8.consensus

SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus

Genome fraction, %



LE3\_SE.AF0.8.consensus

SAMPLE1\_PE.AF0.8.consensus

SAMPLE2\_PE.AF0.8.consensus