

Report

| | SAMPLE3_SE.scaffolds | SAMPLE1_PE.scaffolds | SAMPLE2_PE.scaffolds |
|-----------------------------|----------------------|----------------------|----------------------|
| # contigs (>= 0 bp) | 2 | 2 | 5 |
| # contigs (>= 1000 bp) | 2 | 2 | 5 |
| # contigs (>= 5000 bp) | 1 | 2 | 2 |
| # contigs (>= 10000 bp) | 1 | 1 | 1 |
| # contigs (>= 25000 bp) | 1 | 0 | 0 |
| # contigs (>= 50000 bp) | 0 | 0 | 0 |
| Total length (>= 0 bp) | 29426 | 29427 | 25591 |
| Total length (>= 1000 bp) | 29426 | 29427 | 25591 |
| Total length (>= 5000 bp) | 25442 | 29427 | 16515 |
| Total length (>= 10000 bp) | 25442 | 20847 | 10284 |
| Total length (>= 25000 bp) | 25442 | 0 | 0 |
| Total length (>= 50000 bp) | 0 | 0 | 0 |
| # contigs | 2 | 2 | 5 |
| Largest contig | 25442 | 20847 | 10284 |
| Total length | 29426 | 29427 | 25591 |
| Reference length | 29903 | 29903 | 29903 |
| GC (%) | 38.00 | 38.00 | 38.45 |
| Reference GC (%) | 37.97 | 37.97 | 37.97 |
| N50 | 25442 | 20847 | 6231 |
| NG50 | 25442 | 20847 | 6231 |
| N75 | 25442 | 8580 | 3761 |
| NG75 | 25442 | 8580 | 3753 |
| L50 | 1 | 1 | 2 |
| LG50 | 1 | 1 | 2 |
| L75 | 1 | 2 | 3 |
| LG75 | 1 | 2 | 4 |
| # misassemblies | 0 | 0 | 0 |
| # misassembled contigs | 0 | 0 | 0 |
| Misassembled contigs length | 0 | 0 | 0 |
| # local misassemblies | 1 | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 | 0 |
| # unaligned contigs | 0 + 0 part | 0 + 0 part | 0 + 0 part |
| Unaligned length | 0 | 0 | 0 |
| Genome fraction (%) | 98.405 | 98.408 | 85.399 |
| Duplication ratio | 1.000 | 1.000 | 1.002 |
| # N's per 100 kbp | 0.00 | 0.00 | 0.00 |
| # mismatches per 100 kbp | 13.59 | 20.39 | 35.24 |
| # indels per 100 kbp | 0.00 | 0.00 | 3.92 |
| # genomic features | 26 + 6 part | 26 + 6 part | 20 + 10 part |
| Largest alignment | 25442 | 20847 | 10284 |
| Total aligned length | 29426 | 29427 | 25536 |
| NA50 | 25442 | 20847 | 6231 |
| NGA50 | 25442 | 20847 | 6231 |
| NA75 | 25442 | 8580 | 3760 |
| NGA75 | 25442 | 8580 | 3699 |
| LA50 | 1 | 1 | 2 |
| LGA50 | 1 | 1 | 2 |
| LA75 | 1 | 2 | 3 |
| LGA75 | 1 | 2 | 4 |

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.scaffolds | SAMPLE1_PE.scaffolds | SAMPLE2_PE.scaffolds |
|-----------------------------|----------------------|----------------------|----------------------|
| # 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 | 1 | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 | 0 |
| # mismatches | 4 | 6 | 9 |
| # indels | 0 | 0 | 1 |
| # indels (<= 5 bp) | 0 | 0 | 1 |
| # indels (> 5 bp) | 0 | 0 | 0 |
| Indels length | 0 | 0 | 1 |

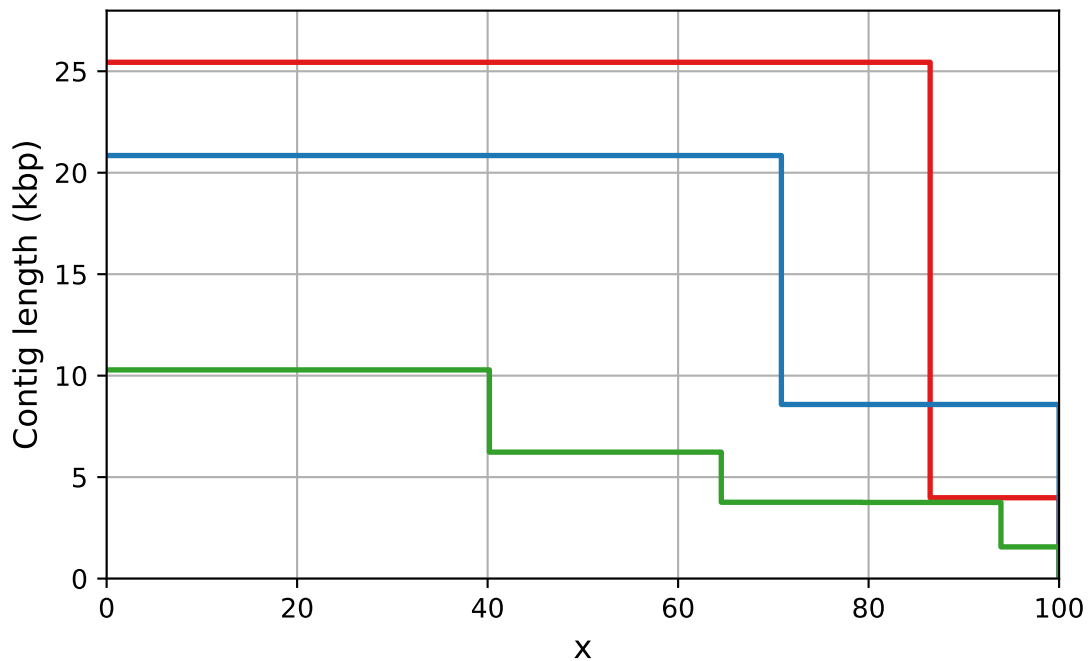
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | SAMPLE3_SE.scaffolds | SAMPLE1_PE.scaffolds | SAMPLE2_PE.scaffolds |
|-------------------------------|----------------------|----------------------|----------------------|
| # 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 | 0 | 0 | 0 |

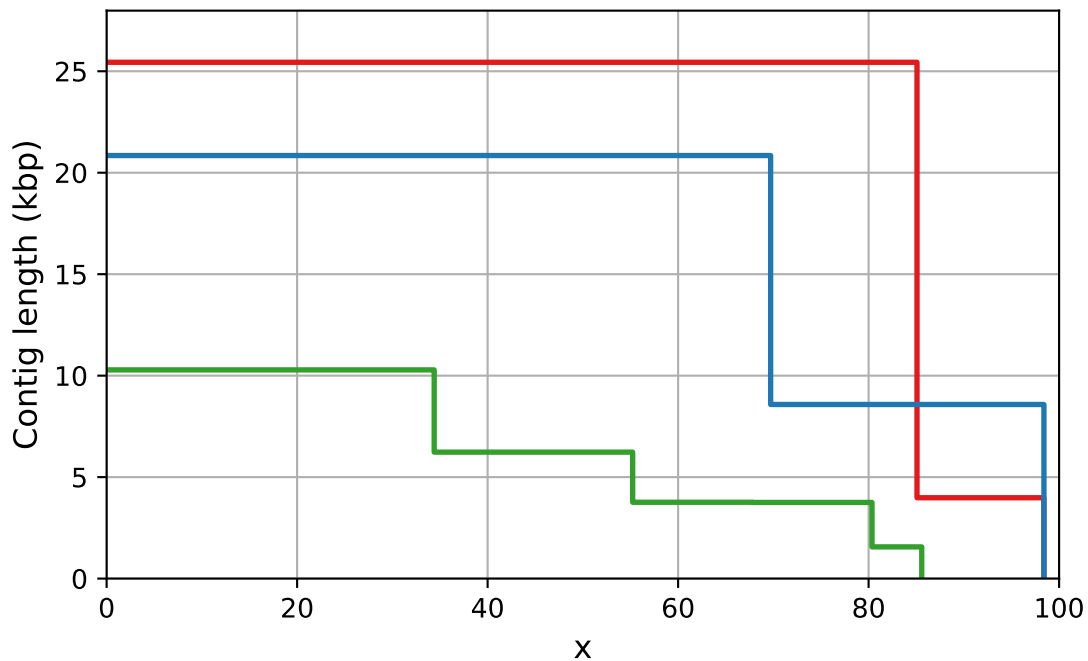
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



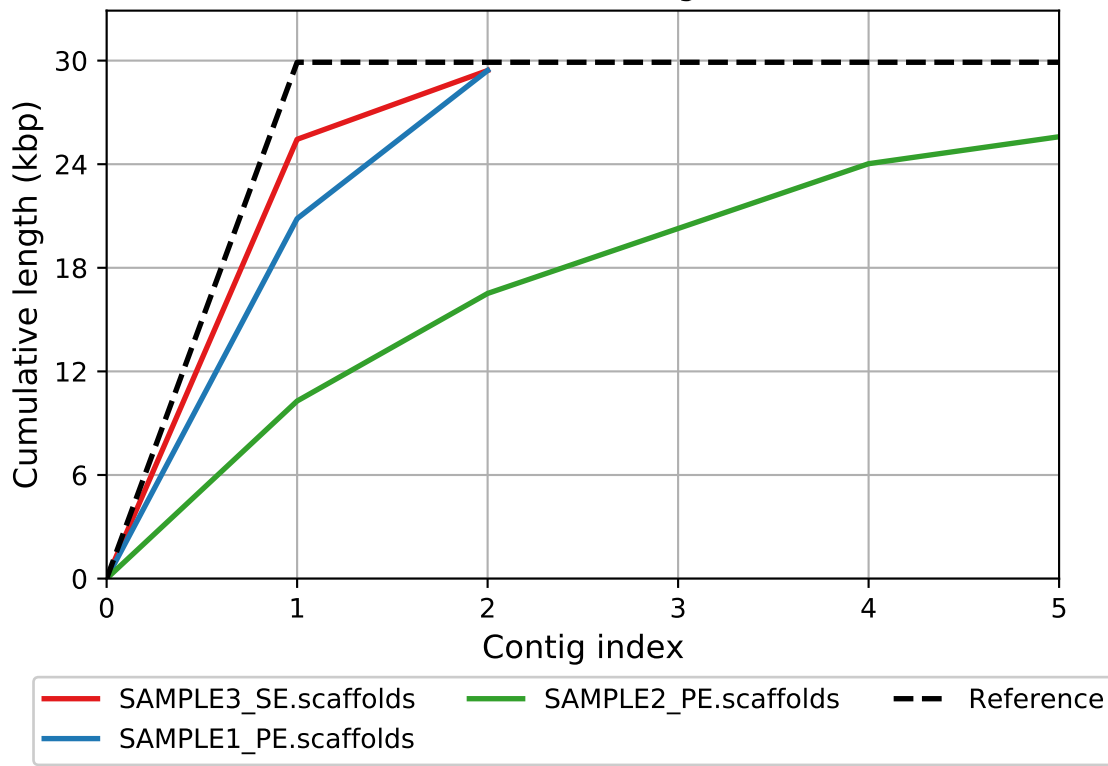
— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

NGx

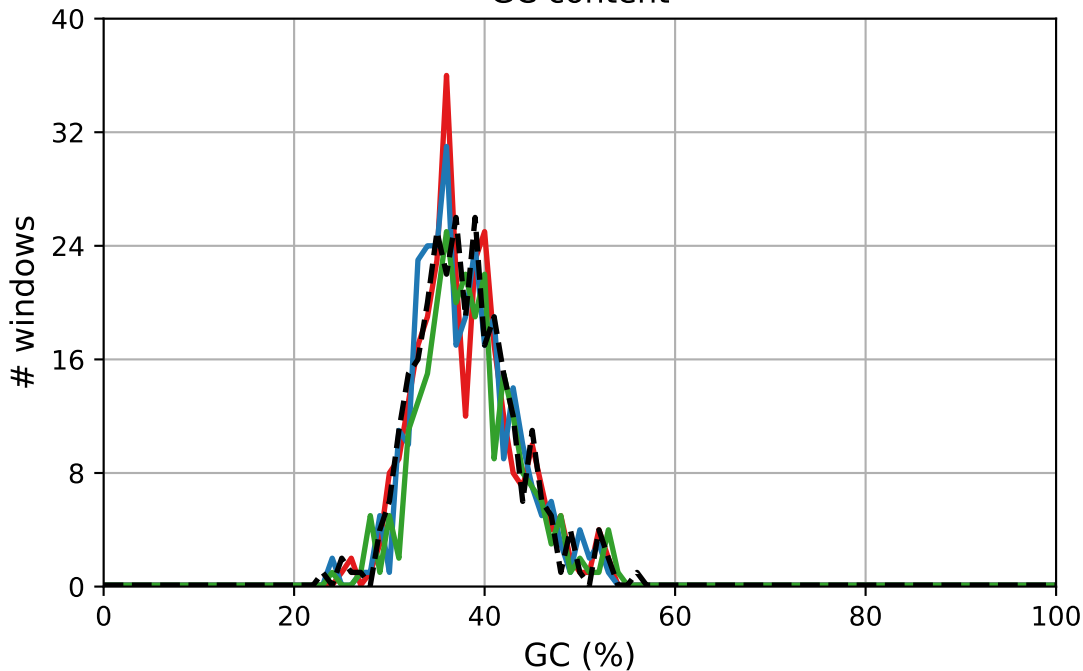


— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

Cumulative length

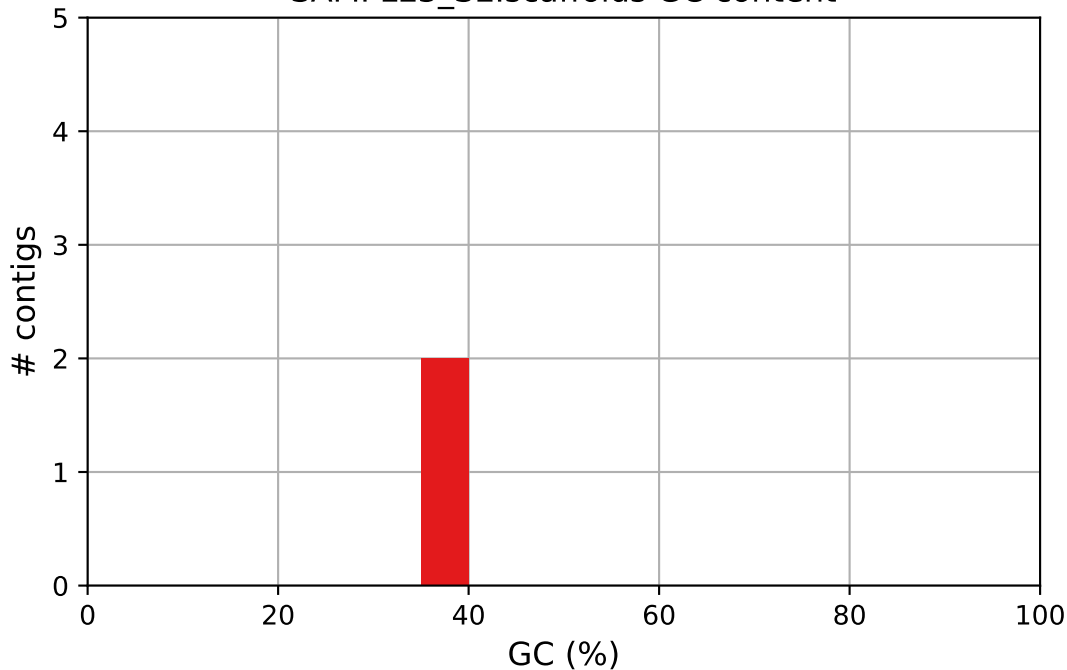


GC content



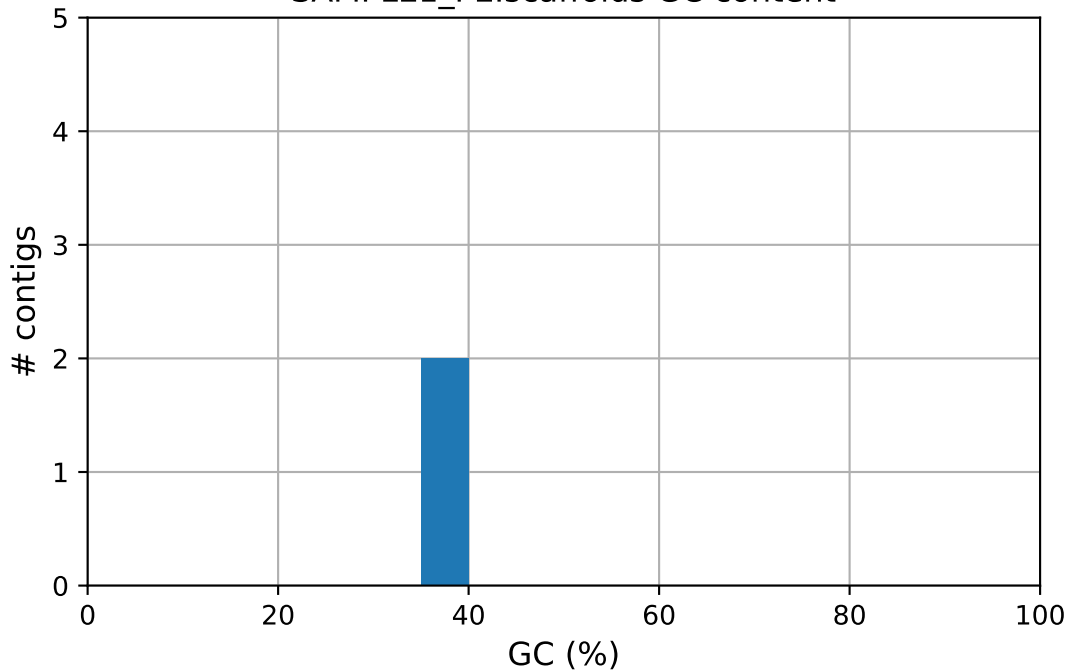
SAMPLE3_SE.scaffolds SAMPLE2_PE.scaffolds -- Reference
SAMPLE1_PE.scaffolds

SAMPLE3_SE.scaffolds GC content



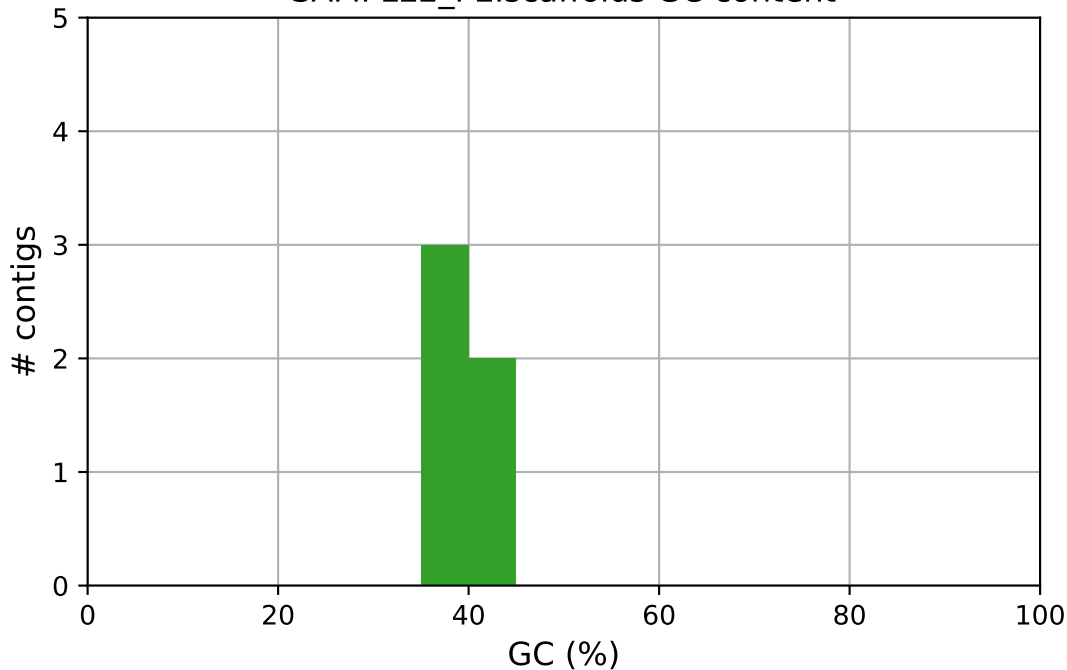
■ SAMPLE3_SE.scaffolds

SAMPLE1_PE.scaffolds GC content



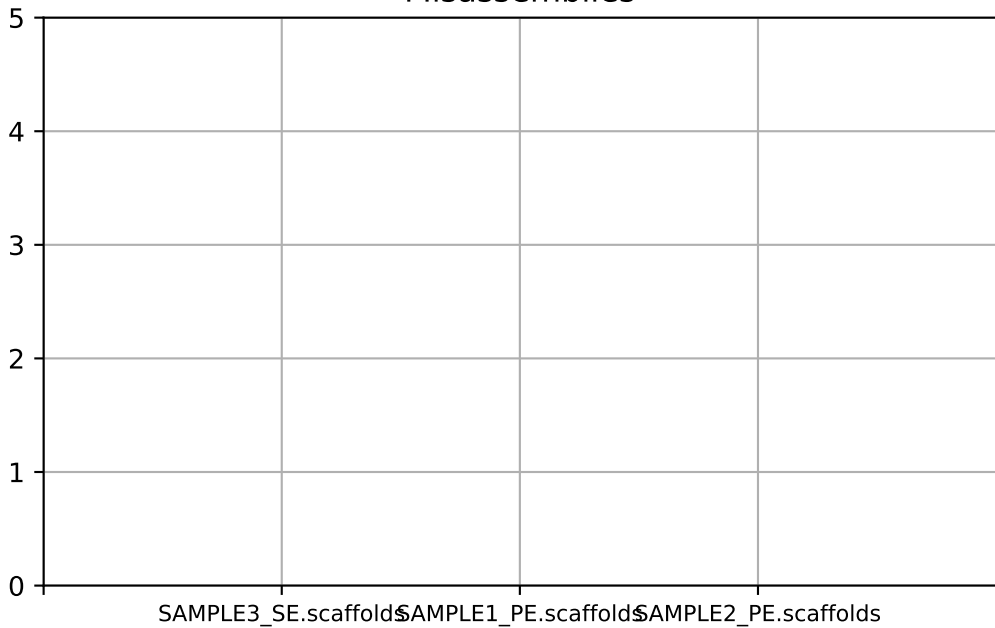
SAMPLE1_PE.scaffolds

SAMPLE2_PE.scaffolds GC content

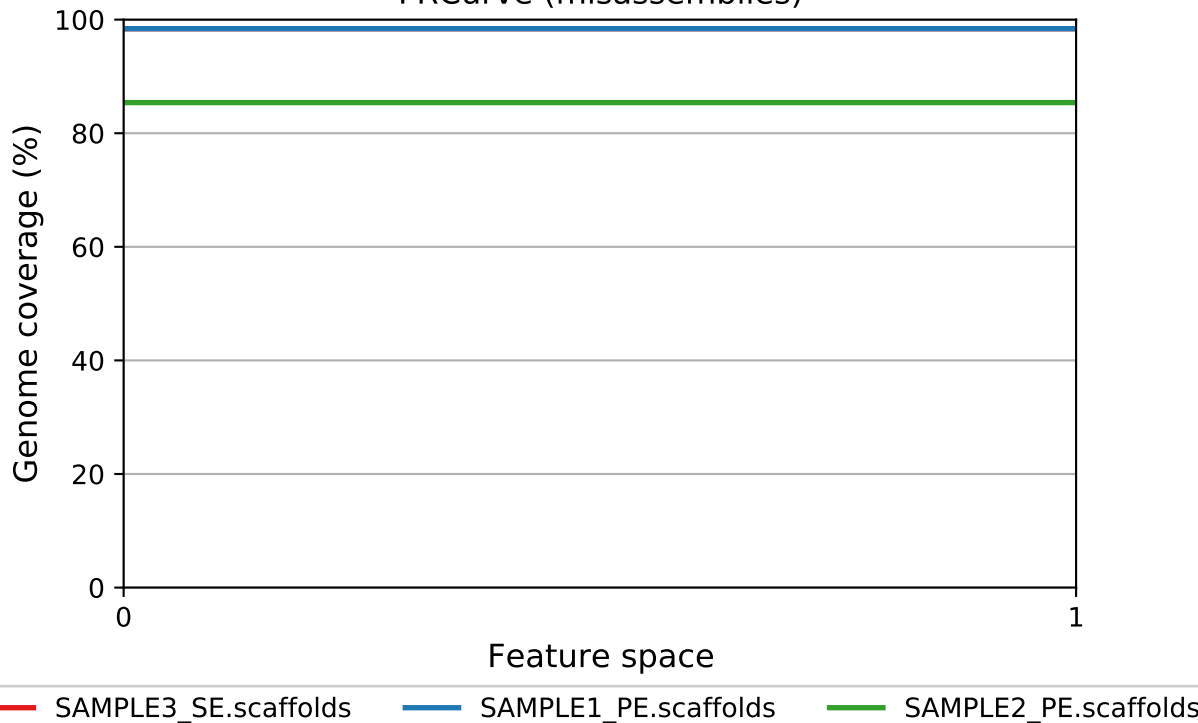


SAMPLE2_PE.scaffolds

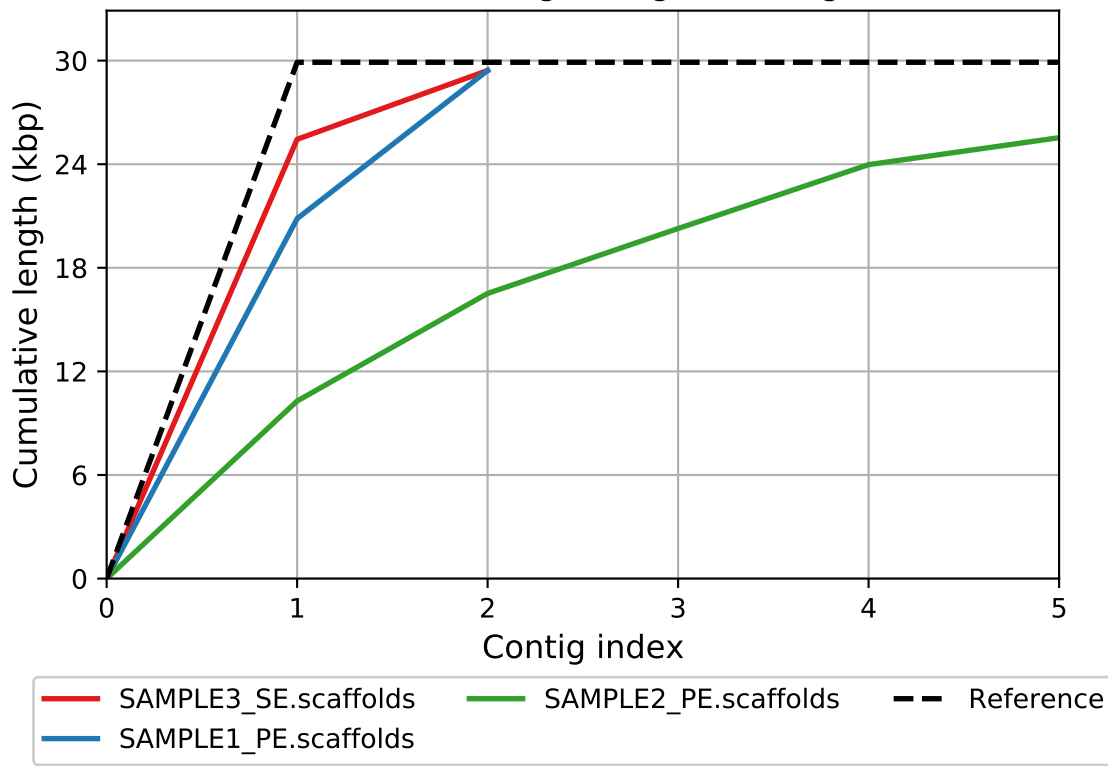
Misassemblies



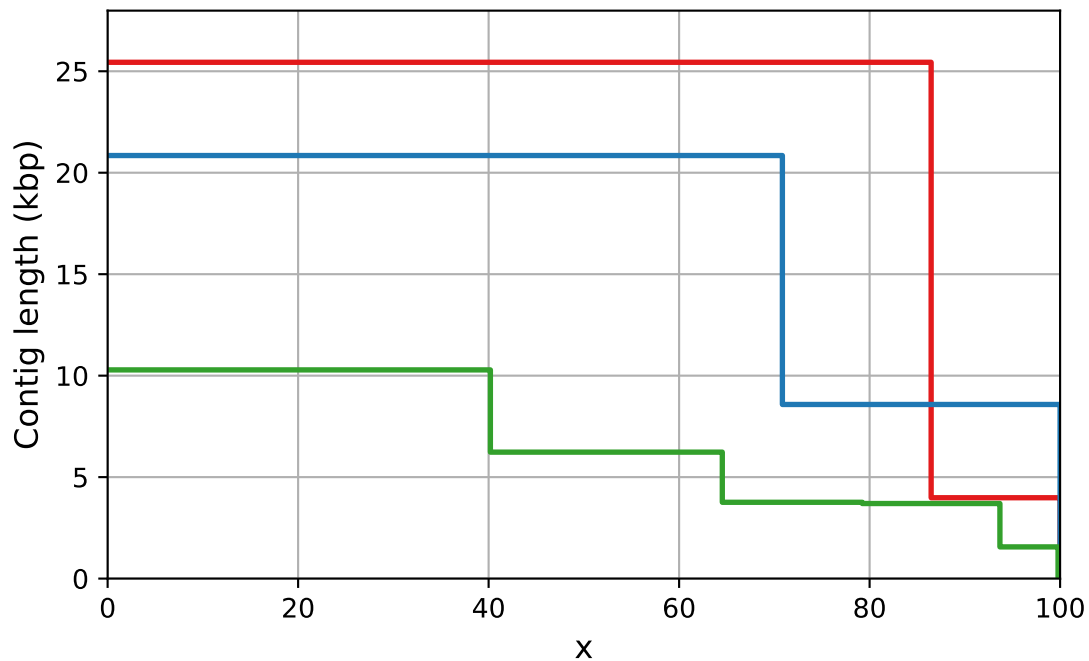
FRCurve (misassemblies)



Cumulative length (aligned contigs)

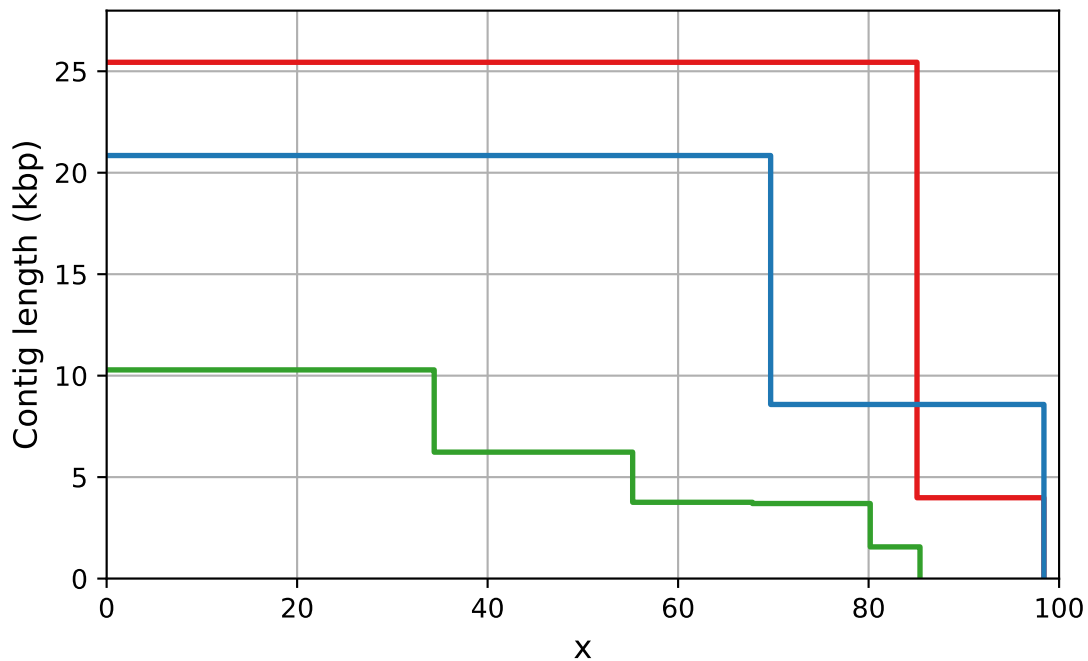


NAx

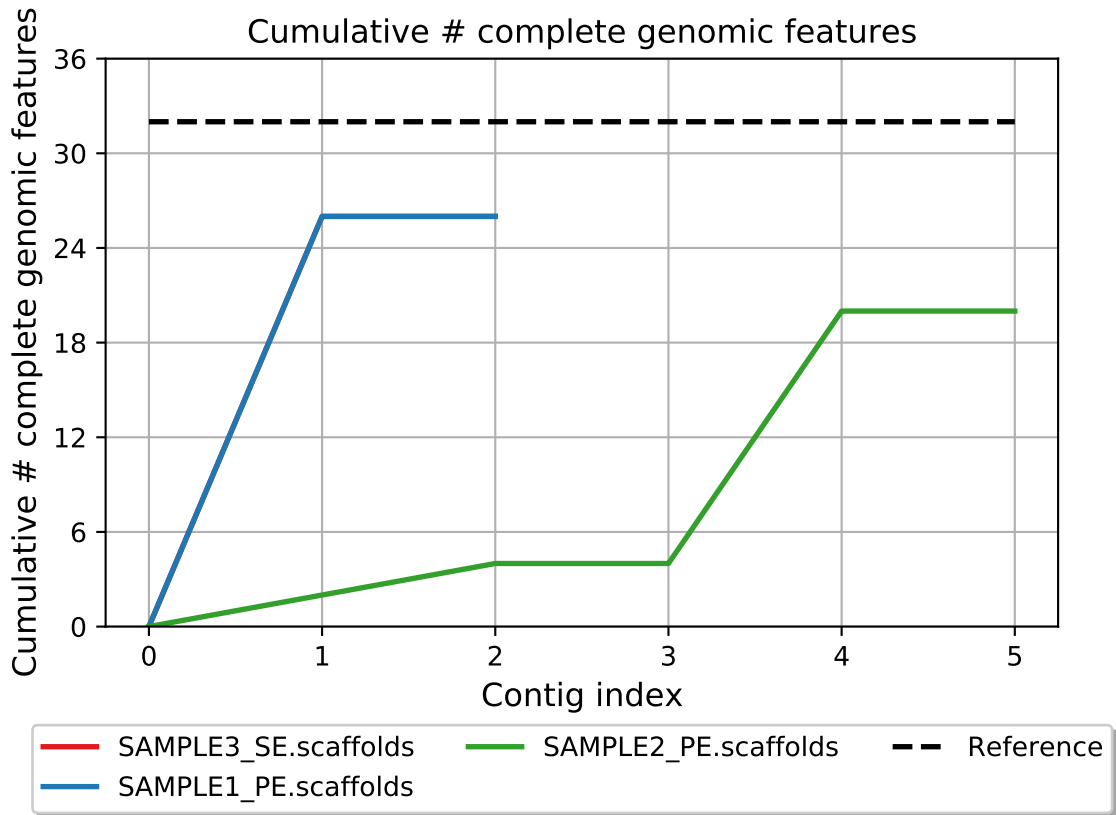


— SAMPLE3_SE.scaffolds — SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

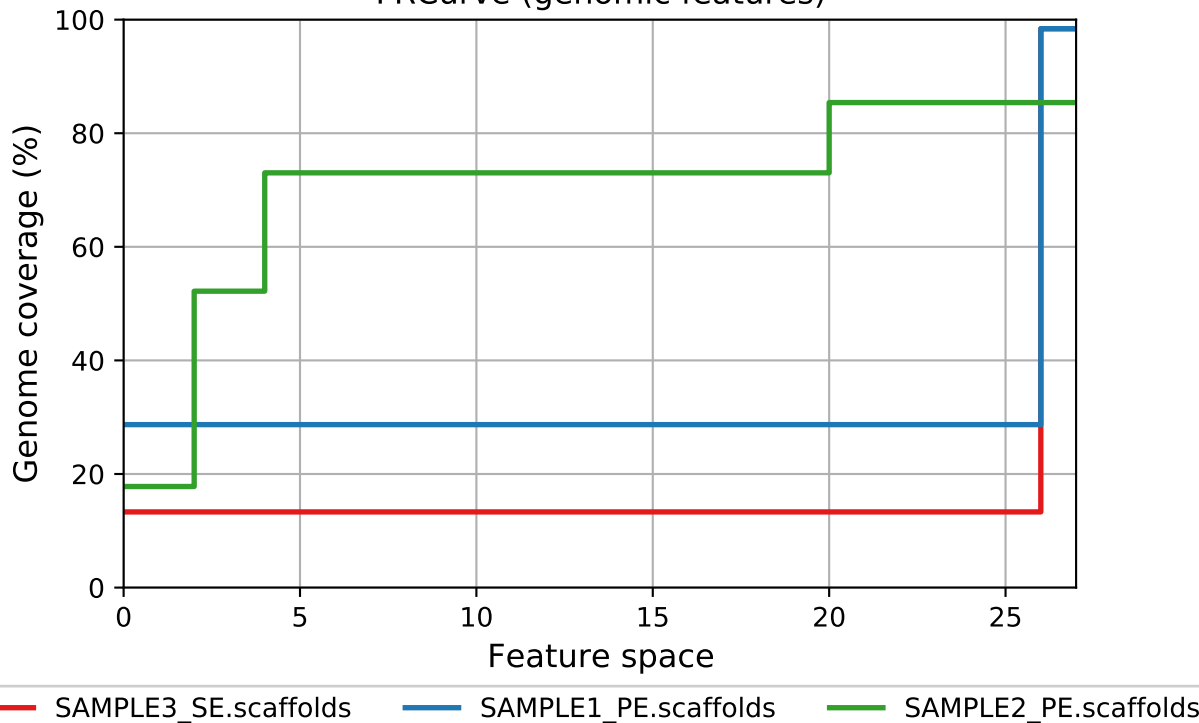
NGAx



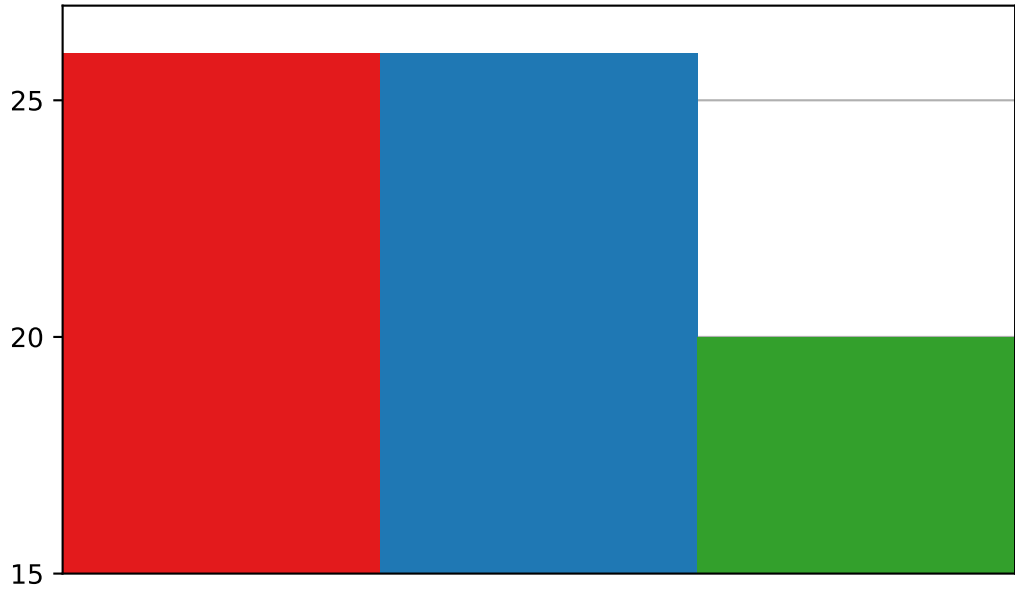
SAMPLE3_SE.scaffolds SAMPLE1_PE.scaffolds SAMPLE2_PE.scaffolds



FRCurve (genomic features)



complete genomic features






■ SAMPLE3_SE.scaffolds ■ SAMPLE1_PE.scaffolds ■ SAMPLE2_PE.scaffolds

Genome fraction, %

100

50

 SAMPLE3_SE.scaffolds  SAMPLE1_PE.scaffolds  SAMPLE2_PE.scaffolds

