

Report

| | SAMPLE1_PE.scaffolds | SAMPLE2_PE.scaffolds |
|-----------------------------|----------------------|----------------------|
| # contigs (>= 0 bp) | 7 | 27 |
| # contigs (>= 1000 bp) | 3 | 6 |
| # contigs (>= 5000 bp) | 3 | 2 |
| # contigs (>= 10000 bp) | 1 | 1 |
| # contigs (>= 25000 bp) | 0 | 0 |
| # contigs (>= 50000 bp) | 0 | 0 |
| Total length (>= 0 bp) | 36445 | 41598 |
| Total length (>= 1000 bp) | 35151 | 32606 |
| Total length (>= 5000 bp) | 35151 | 16798 |
| Total length (>= 10000 bp) | 20973 | 10441 |
| Total length (>= 25000 bp) | 0 | 0 |
| Total length (>= 50000 bp) | 0 | 0 |
| # contigs | 3 | 9 |
| Largest contig | 20973 | 10441 |
| Total length | 35151 | 34939 |
| Reference length | 29903 | 29903 |
| GC (%) | 39.03 | 39.13 |
| Reference GC (%) | 37.97 | 37.97 |
| N50 | 20973 | 4738 |
| NG50 | 20973 | 6357 |
| N75 | 8704 | 4051 |
| NG75 | 8704 | 4070 |
| L50 | 1 | 3 |
| LG50 | 1 | 2 |
| L75 | 2 | 5 |
| LG75 | 2 | 4 |
| # misassemblies | 0 | 0 |
| # misassembled contigs | 0 | 0 |
| Misassembled contigs length | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 |
| # unaligned contigs | 1 + 0 part | 3 + 0 part |
| Unaligned length | 5474 | 5432 |
| Genome fraction (%) | 98.870 | 98.151 |
| Duplication ratio | 1.004 | 1.005 |
| # N's per 100 kbp | 0.00 | 0.00 |
| # mismatches per 100 kbp | 23.68 | 34.07 |
| # indels per 100 kbp | 0.00 | 3.41 |
| # genomic features | 26 + 6 part | 22 + 8 part |
| Largest alignment | 20951 | 10414 |
| Total aligned length | 29565 | 29404 |
| NA50 | 20951 | 4738 |
| NGA50 | 20951 | 6357 |
| NA75 | 8614 | 2895 |
| NGA75 | 8614 | 4029 |
| LA50 | 1 | 3 |
| LGA50 | 1 | 2 |
| LA75 | 2 | 5 |
| LGA75 | 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

| | SAMPLE1_PE.scaffolds | SAMPLE2_PE.scaffolds |
|-----------------------------|----------------------|----------------------|
| # misassemblies | 0 | 0 |
| # contig misassemblies | 0 | 0 |
| # c. relocations | 0 | 0 |
| # c. translocations | 0 | 0 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 0 | 0 |
| # s. relocations | 0 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 0 | 0 |
| Misassembled contigs length | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # scaffold gap ext. mis. | 0 | 0 |
| # scaffold gap loc. mis. | 0 | 0 |
| # unaligned mis. contigs | 0 | 0 |
| # mismatches | 7 | 10 |
| # indels | 0 | 1 |
| # indels (<= 5 bp) | 0 | 1 |
| # indels (> 5 bp) | 0 | 0 |
| Indels length | 0 | 1 |

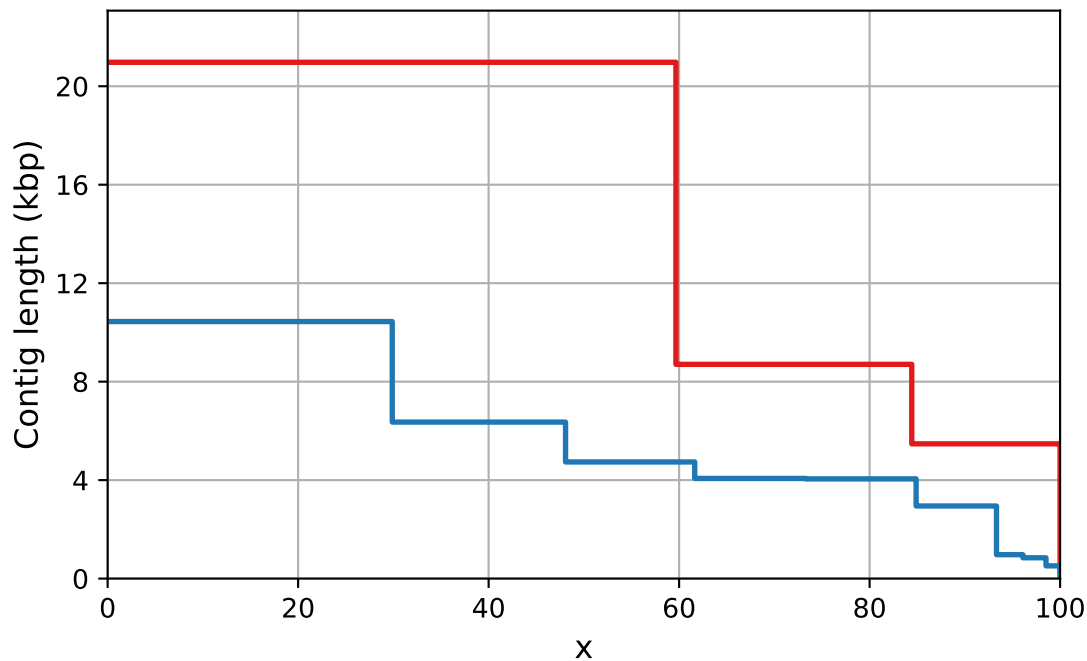
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | SAMPLE1_PE.scaffolds | SAMPLE2_PE.scaffolds |
|-------------------------------|----------------------|----------------------|
| # fully unaligned contigs | 1 | 3 |
| Fully unaligned length | 5474 | 5432 |
| # partially unaligned contigs | 0 | 0 |
| Partially unaligned length | 0 | 0 |
| # N's | 0 | 0 |

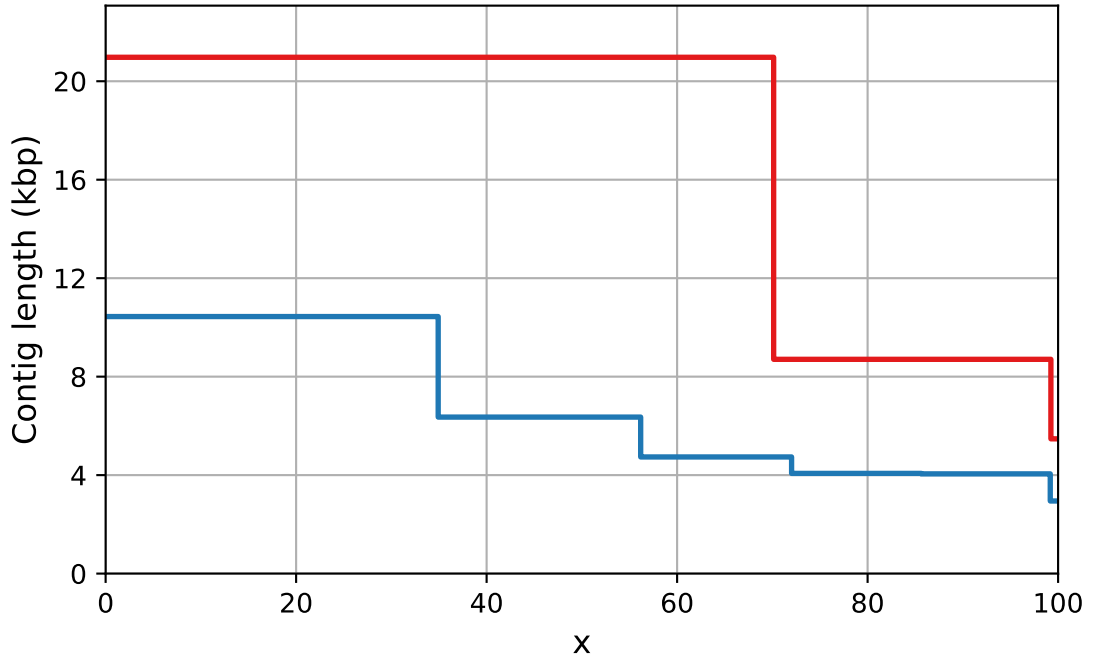
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



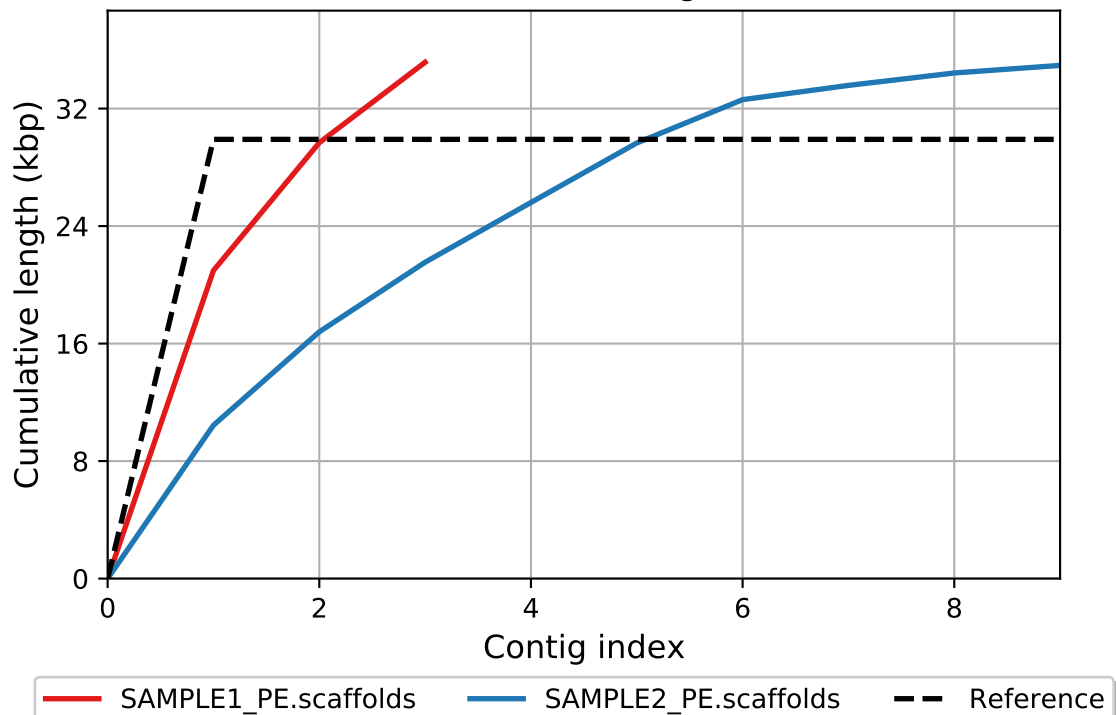
— SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

NGx

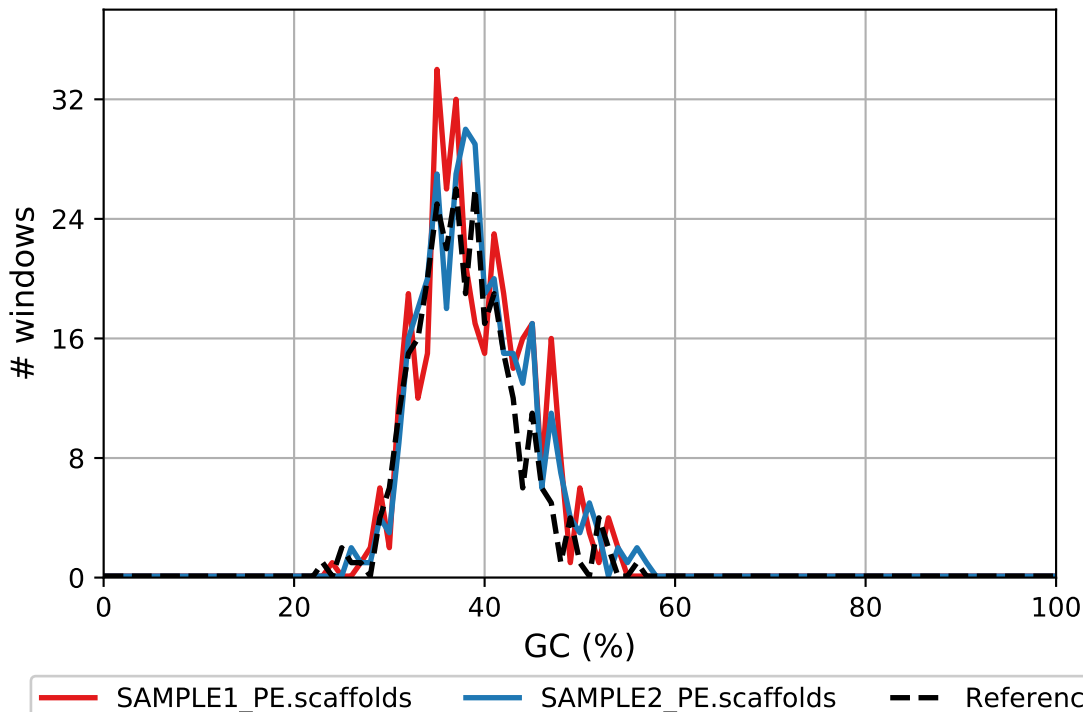


— SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds

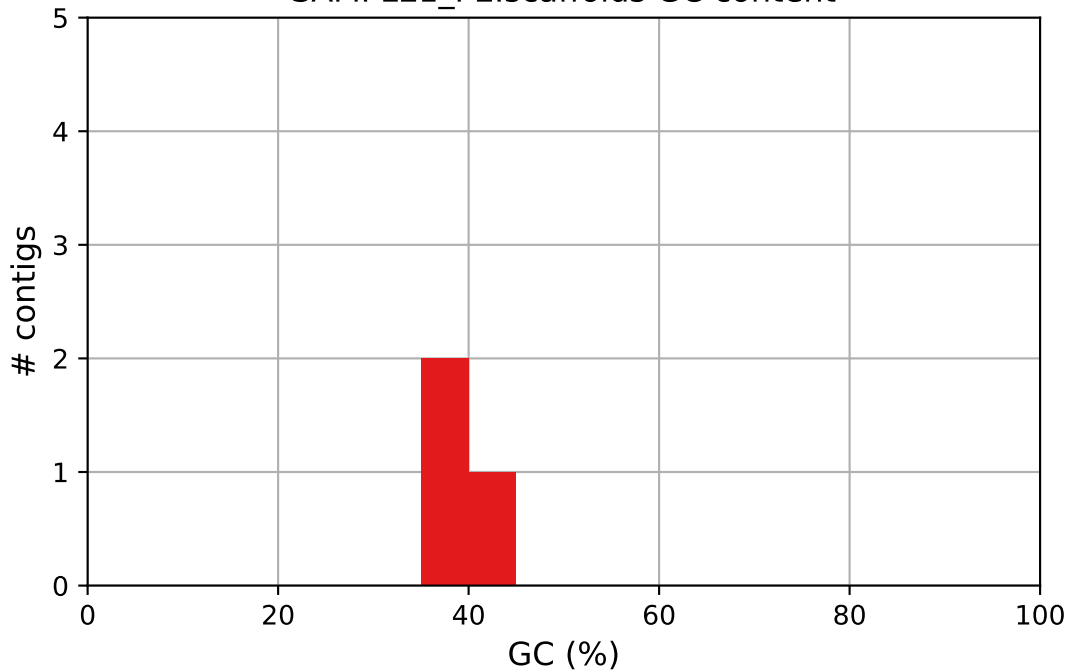
Cumulative length



GC content

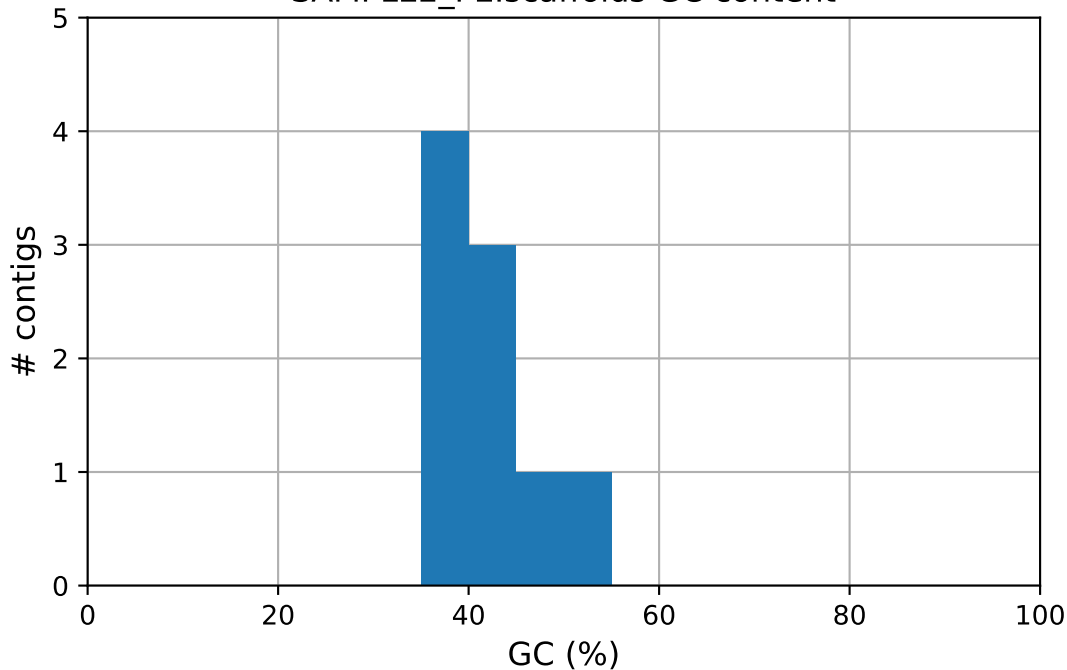


SAMPLE1_PE.scaffolds GC content



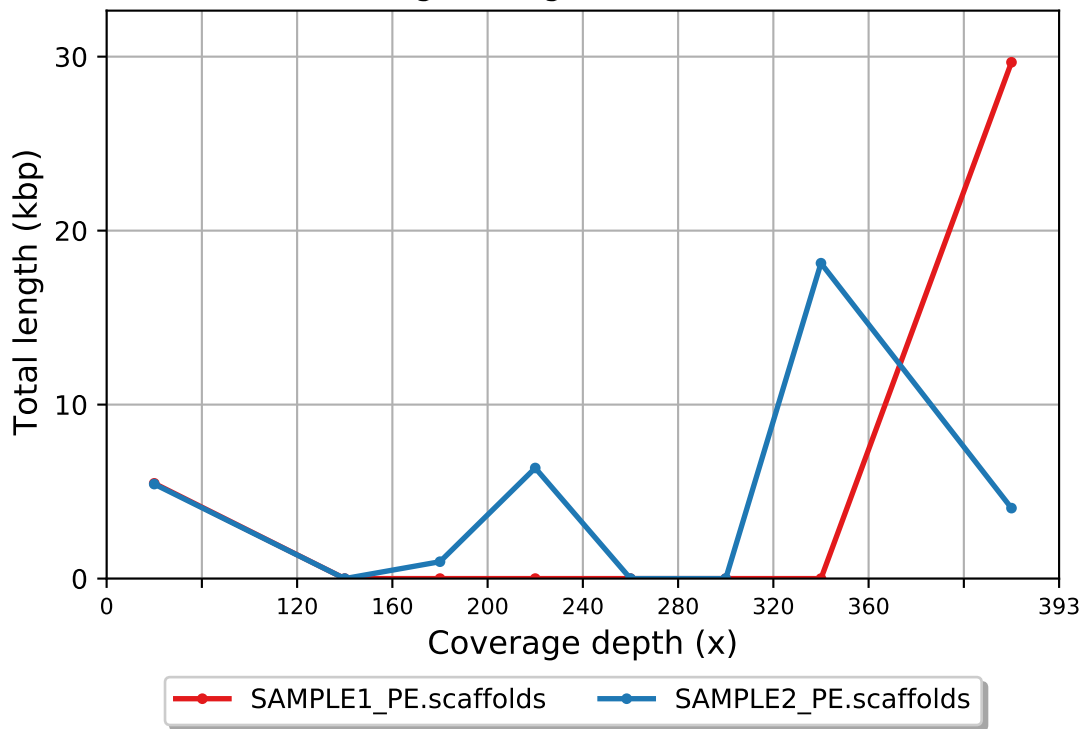
■ SAMPLE1_PE.scaffolds

SAMPLE2_PE.scaffolds GC content

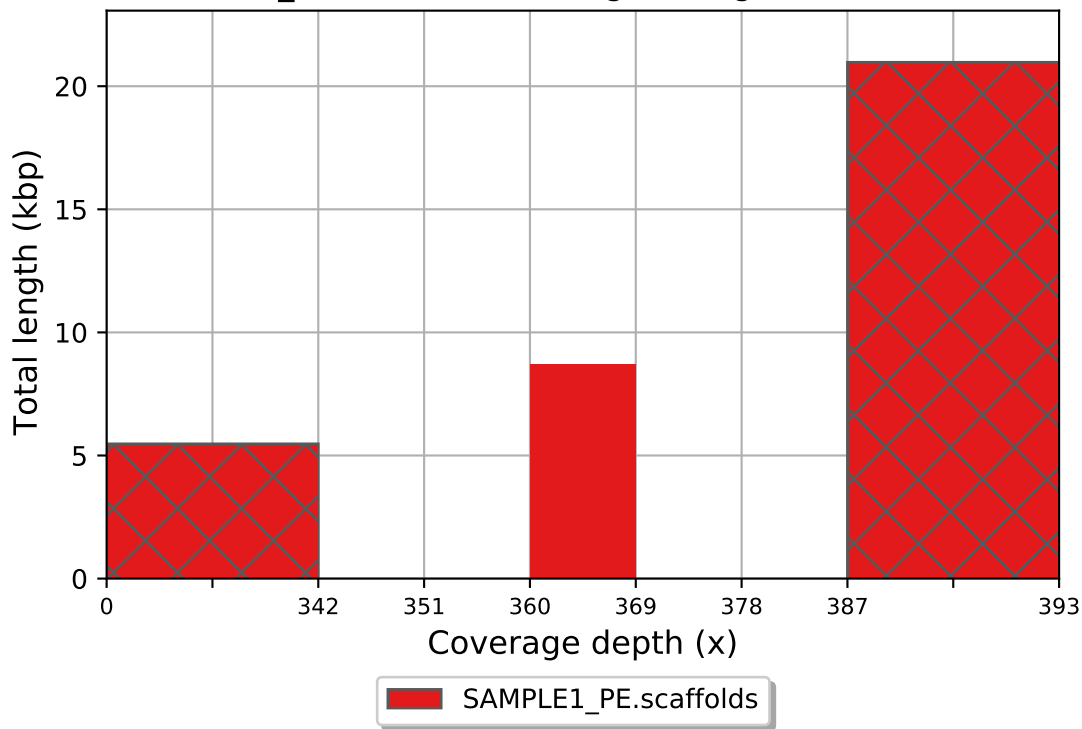


SAMPLE2_PE.scaffolds

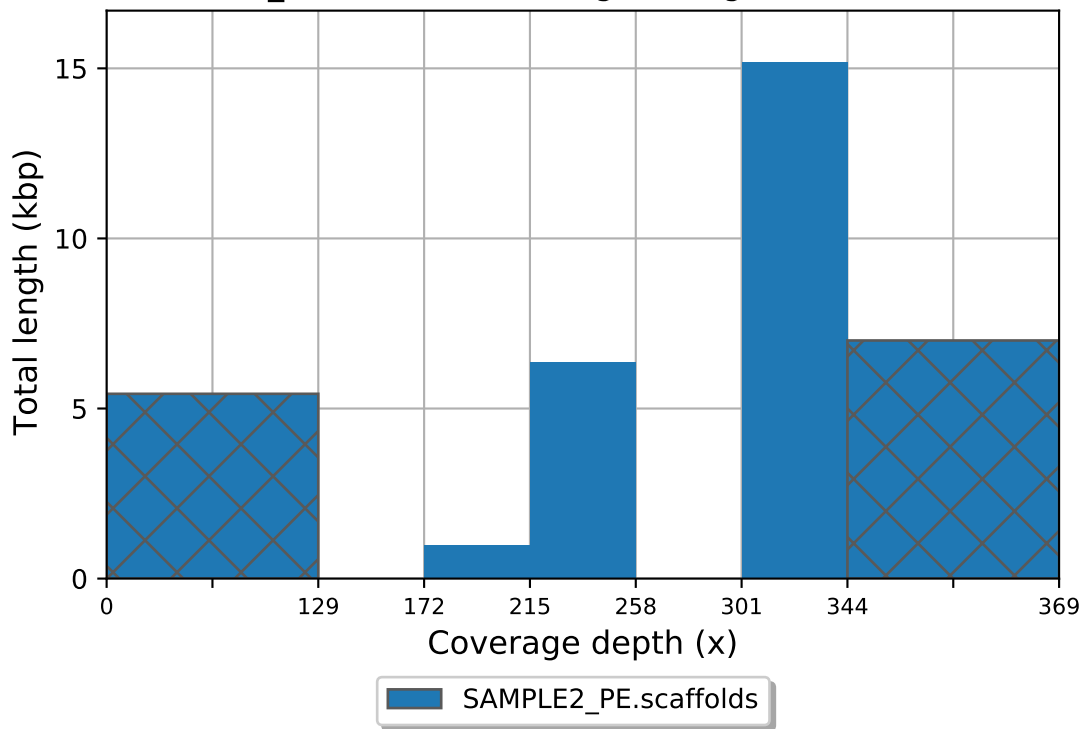
Coverage histogram (bin size: 40x)



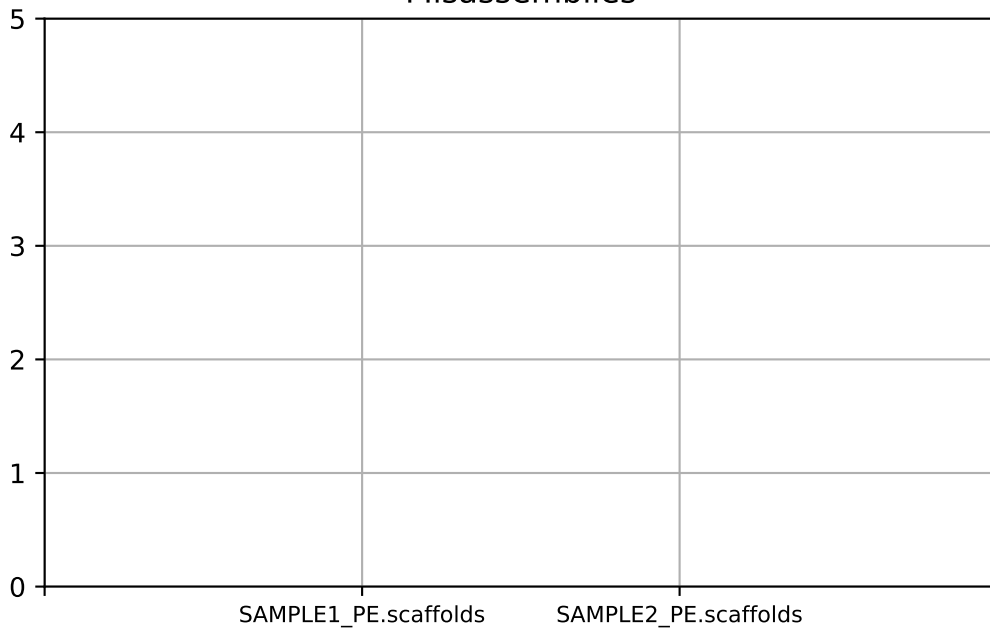
SAMPLE1_PE.scaffolds coverage histogram (bin size: 9x)



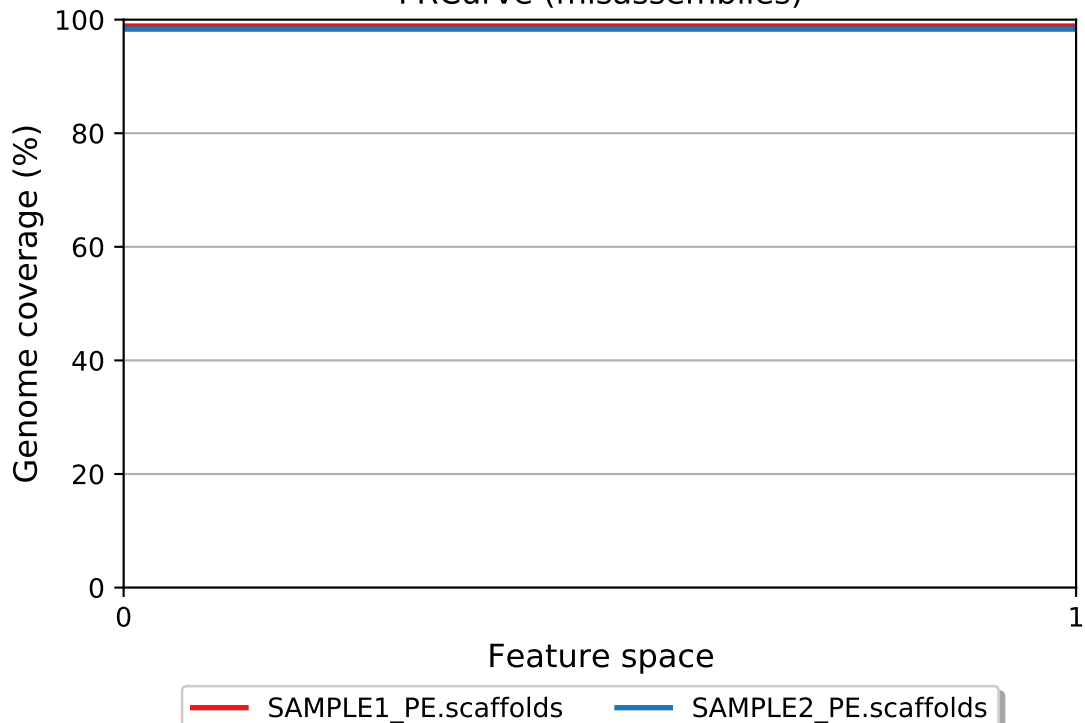
SAMPLE2_PE.scaffolds coverage histogram (bin size: 43x)



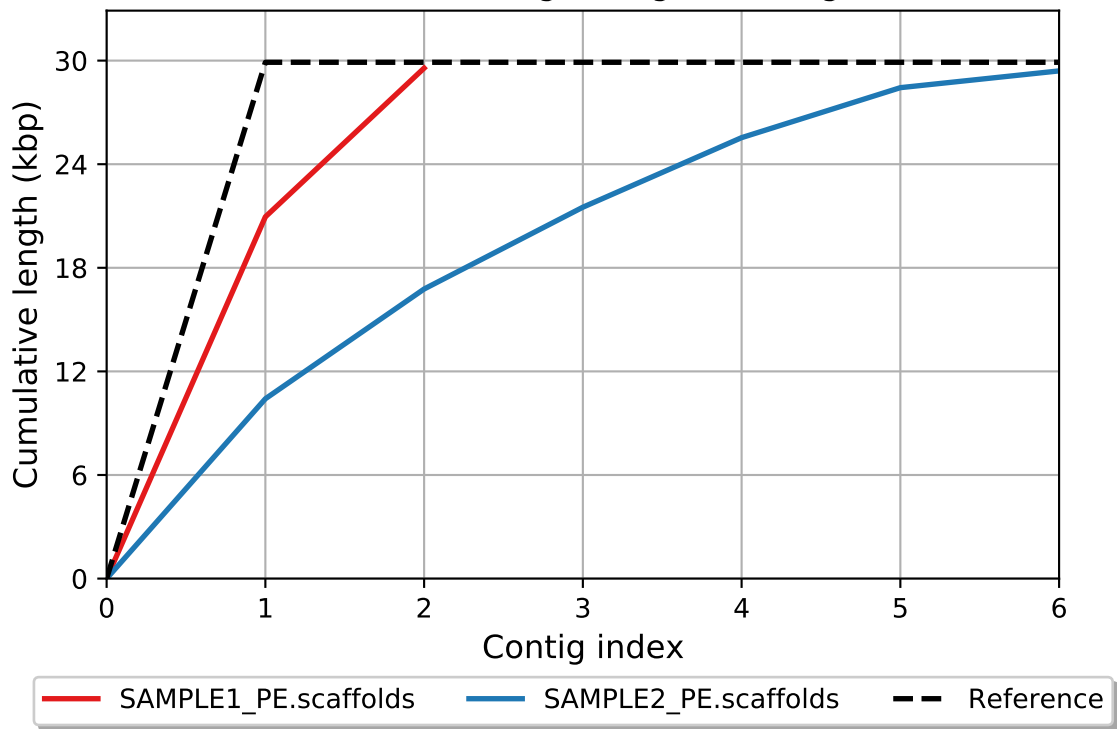
Misassemblies



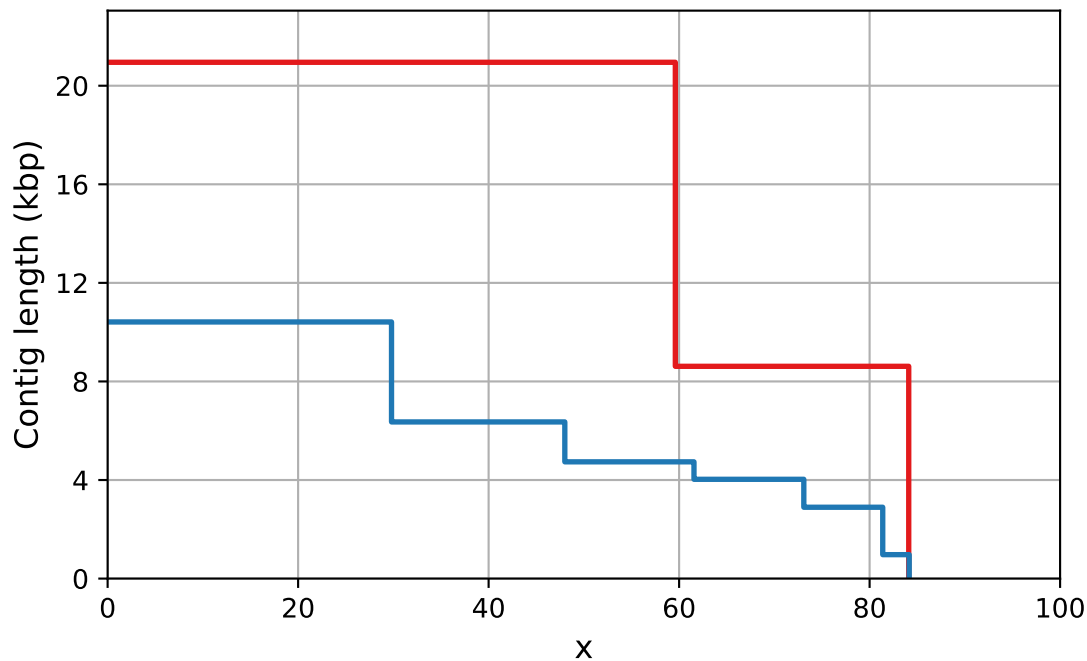
FRCurve (misassemblies)



Cumulative length (aligned contigs)



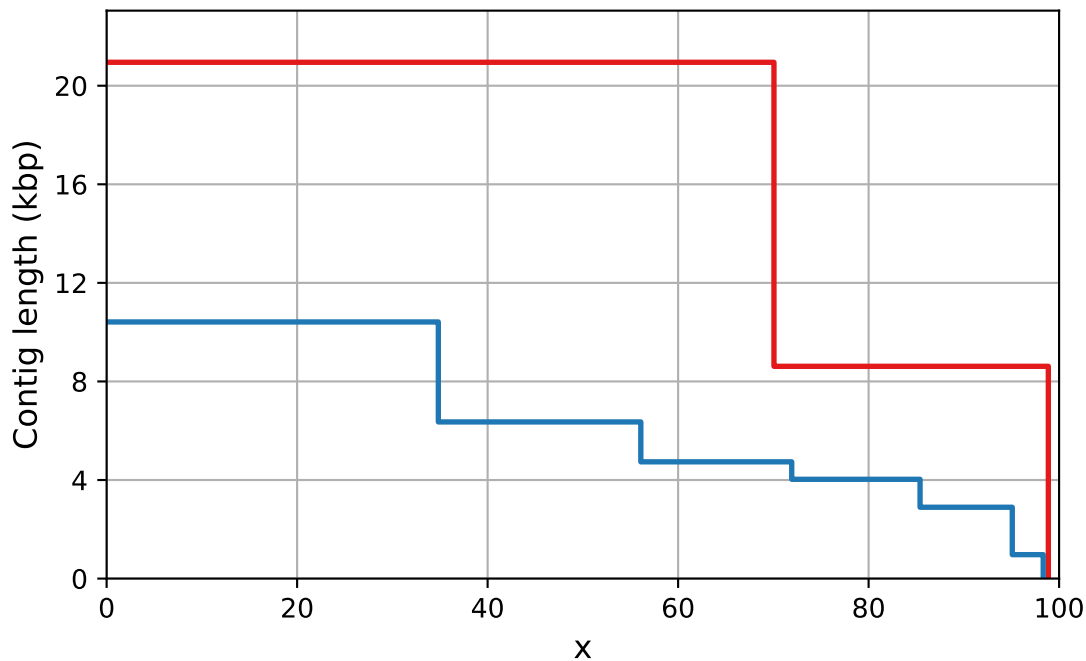
NAx



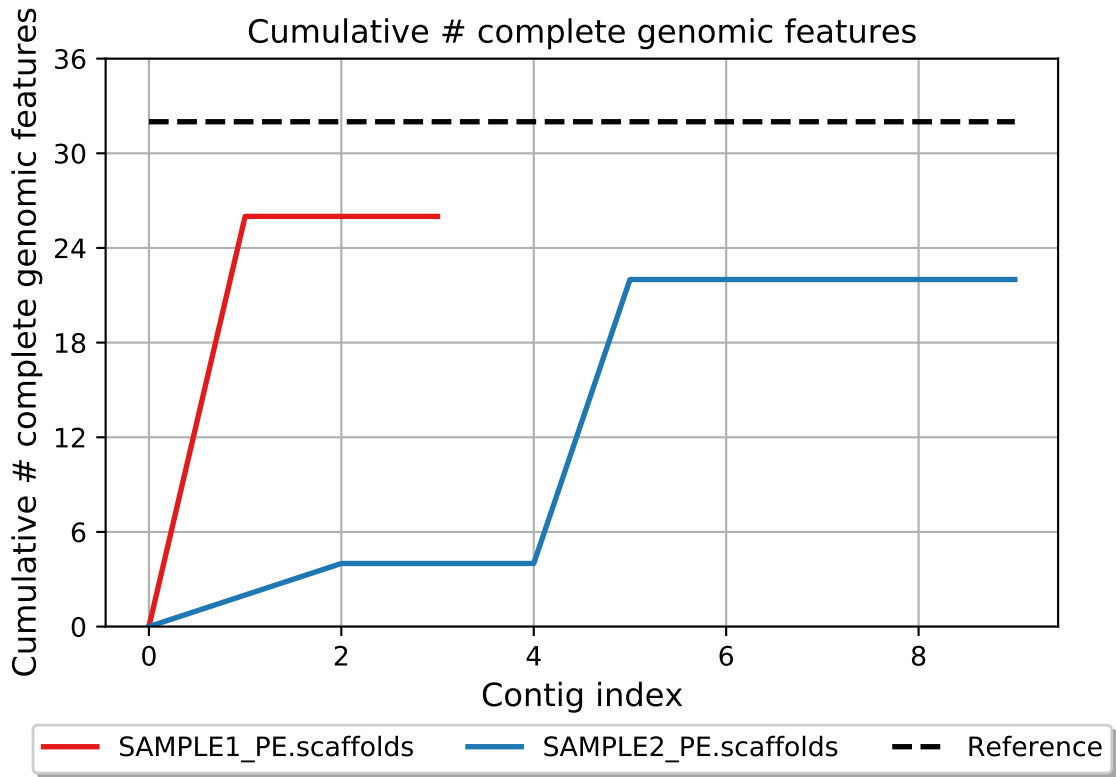
— SAMPLE1_PE.scaffolds

— SAMPLE2_PE.scaffolds

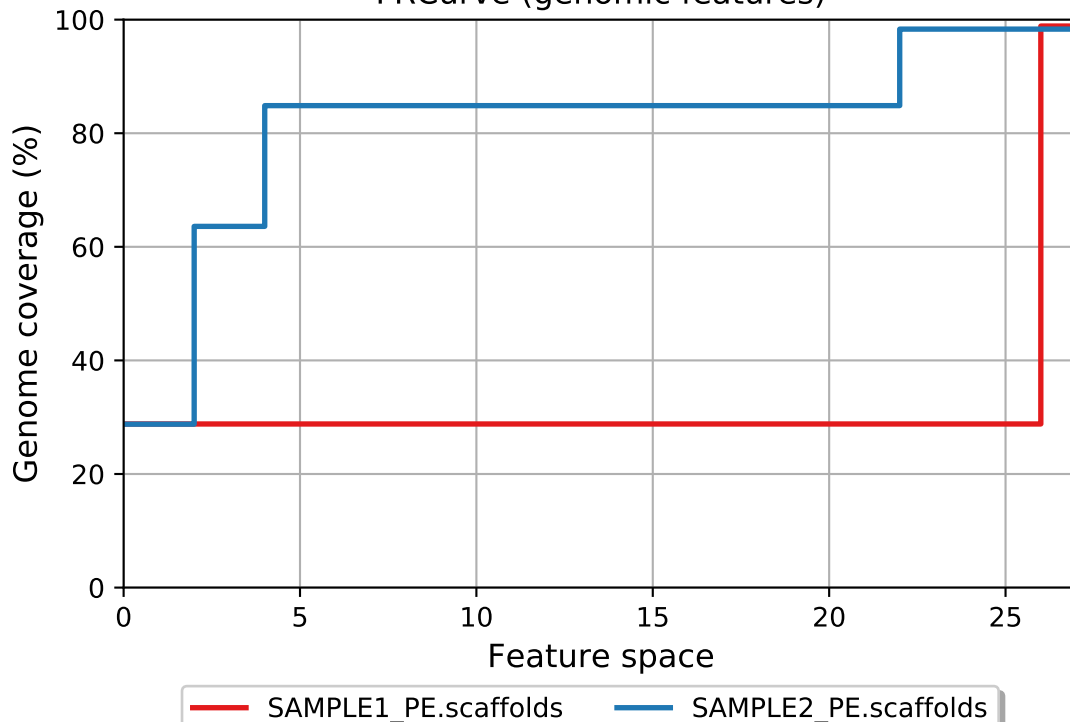
NGAx



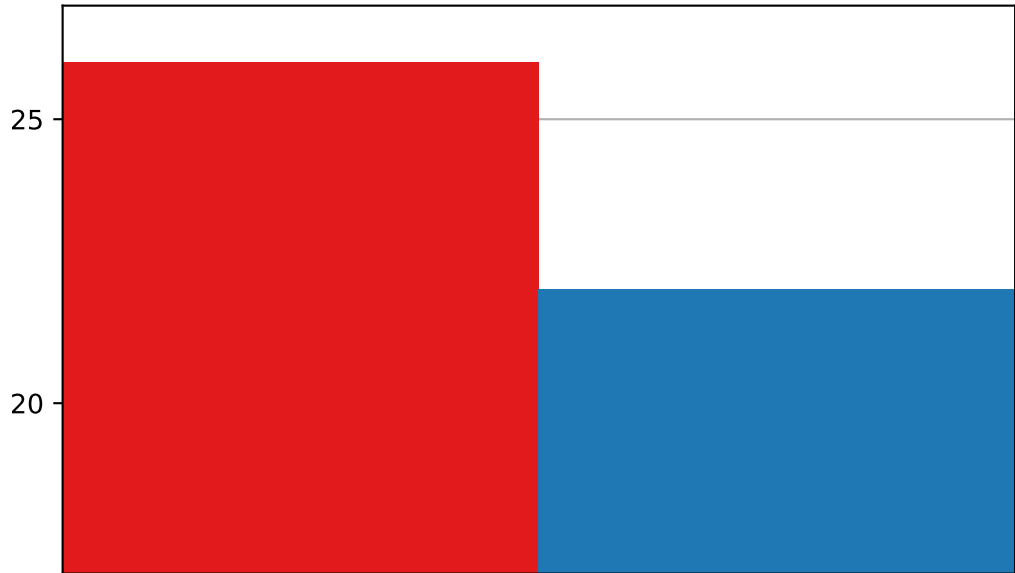
— SAMPLE1_PE.scaffolds — SAMPLE2_PE.scaffolds



FRCurve (genomic features)



complete genomic features

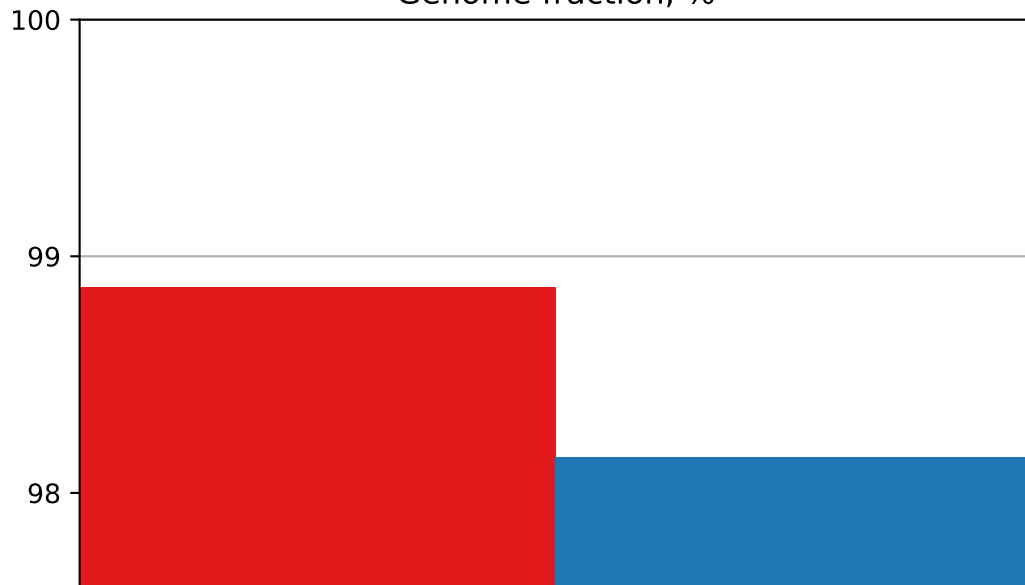


SAMPLE1_PE.scaffolds



SAMPLE2_PE.scaffolds

Genome fraction, %



SAMPLE1_PE.scaffolds



SAMPLE2_PE.scaffolds