

Report

| | SC2248.consensus |
|-----------------------------|------------------|
| # contigs (>= 0 bp) | 1 |
| # contigs (>= 1000 bp) | 1 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 1 |
| # contigs (>= 25000 bp) | 1 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 0 bp) | 29903 |
| Total length (>= 1000 bp) | 29903 |
| Total length (>= 5000 bp) | 29903 |
| Total length (>= 10000 bp) | 29903 |
| Total length (>= 25000 bp) | 29903 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1 |
| Largest contig | 29903 |
| Total length | 29903 |
| Reference length | 29903 |
| GC (%) | 37.99 |
| Reference GC (%) | 37.97 |
| N50 | 29903 |
| NG50 | 29903 |
| N75 | 29903 |
| NG75 | 29903 |
| L50 | 1 |
| LG50 | 1 |
| L75 | 1 |
| LG75 | 1 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 99.679 |
| Duplication ratio | 1.003 |
| # N's per 100 kbp | 324.38 |
| # mismatches per 100 kbp | 53.68 |
| # indels per 100 kbp | 0.00 |
| # genomic features | 21 + 3 part |
| Largest alignment | 29807 |
| Total aligned length | 29807 |
| NA50 | 29807 |
| NGA50 | 29807 |
| NA75 | 29807 |
| NGA75 | 29807 |
| LA50 | 1 |
| LGA50 | 1 |
| LA75 | 1 |
| LGA75 | 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

| | SC2248.consensus |
|-----------------------------|------------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 0 |
| # mismatches | 16 |
| # indels | 0 |
| # indels (<= 5 bp) | 0 |
| # indels (> 5 bp) | 0 |
| Indels length | 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).

Unaligned report

| | SC2248.consensus |
|-------------------------------|------------------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| Partially unaligned length | 0 |
| # N's | 97 |

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



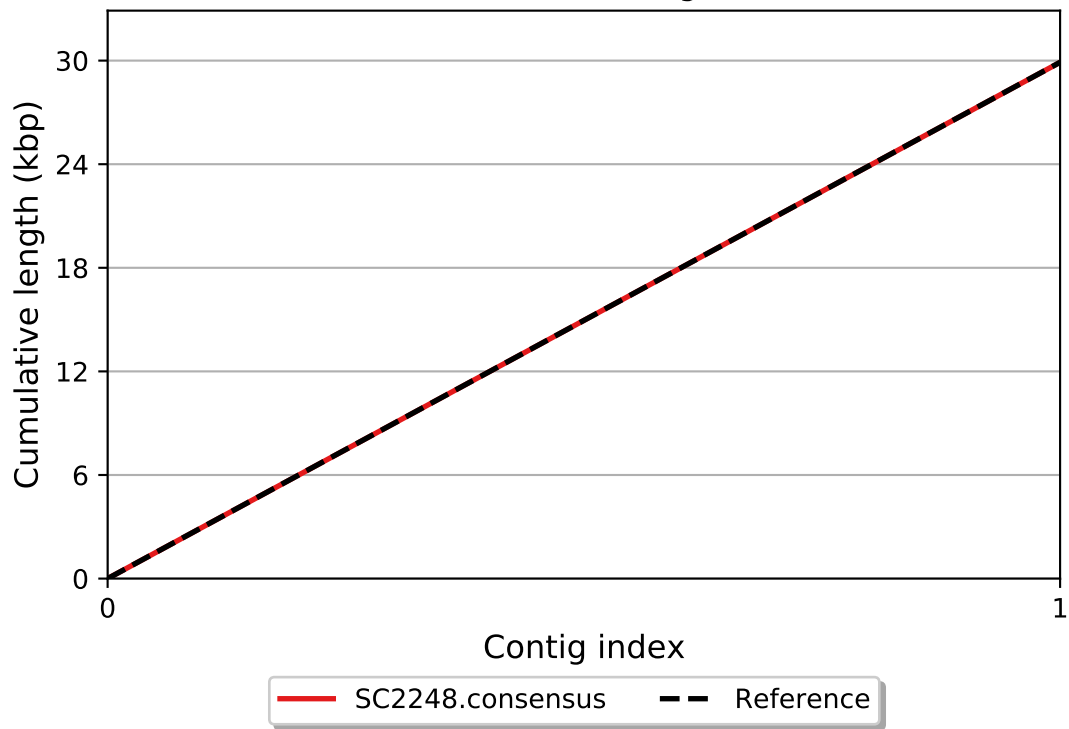
— SC2248.consensus

NGx

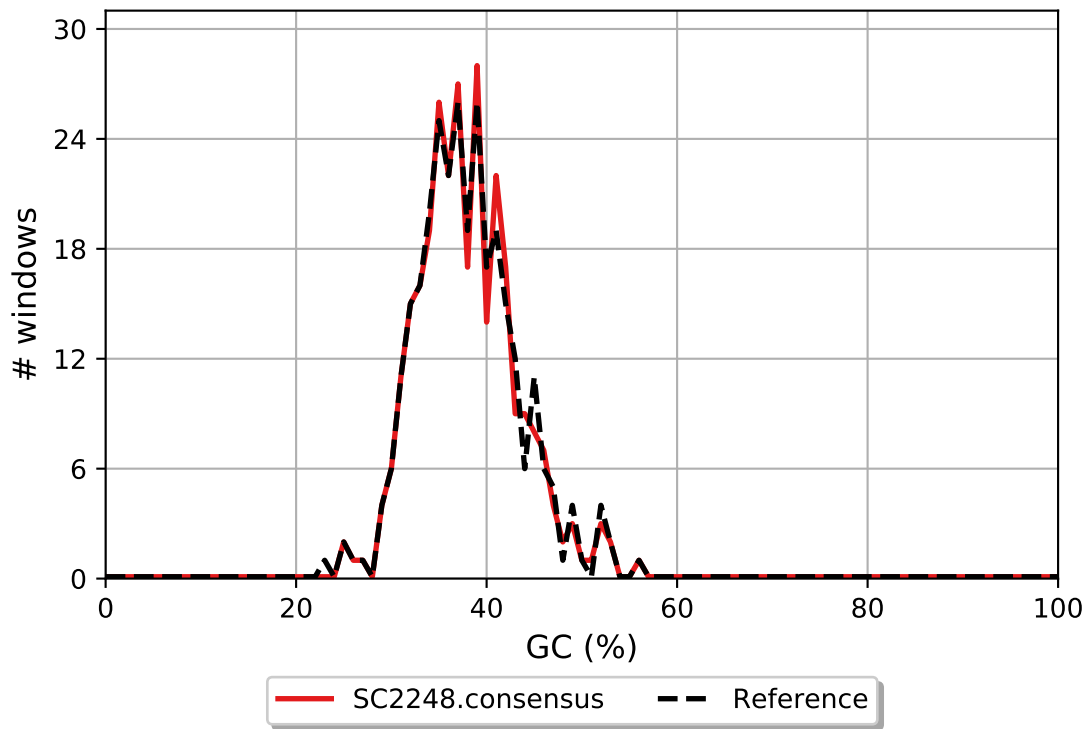


— SC2248.consensus

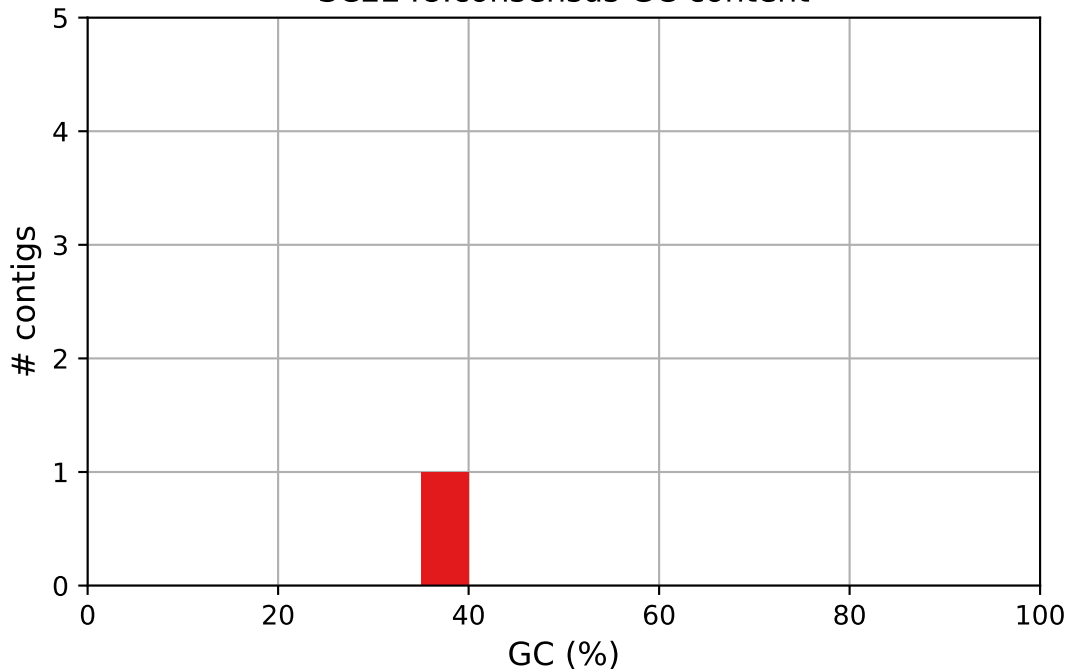
Cumulative length



GC content

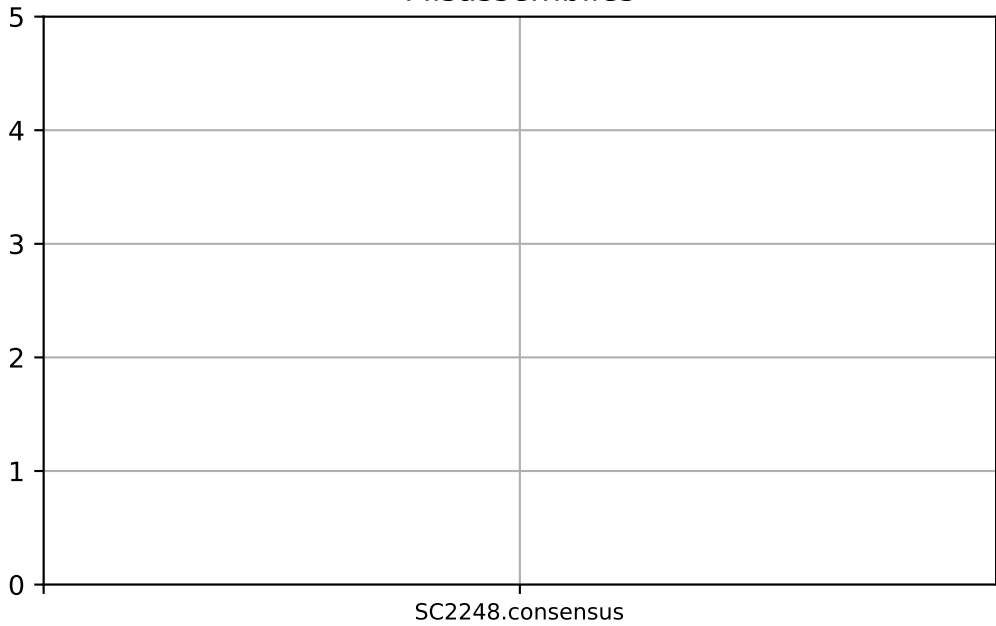


SC2248.consensus GC content

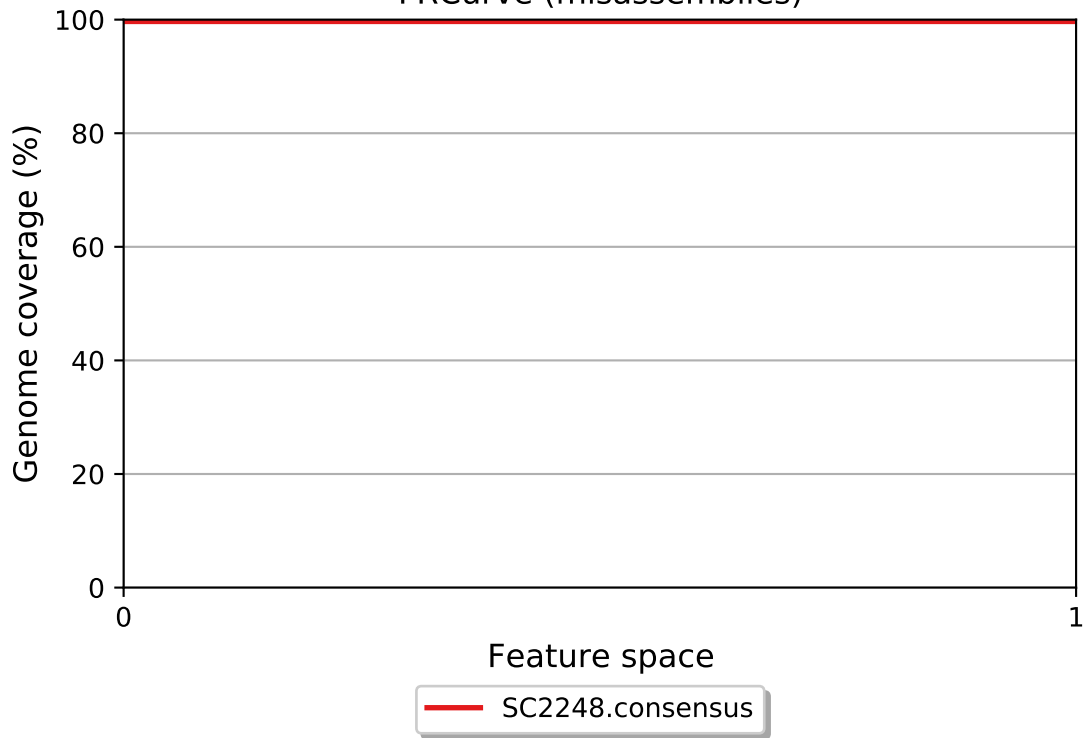


SC2248.consensus

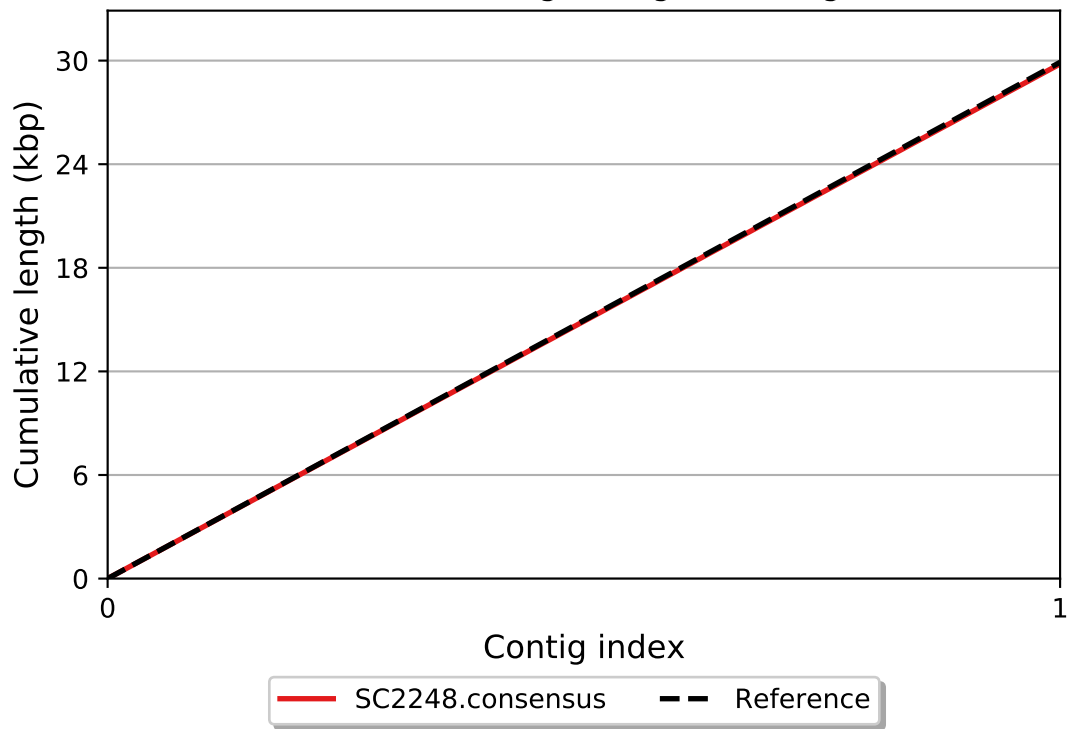
Misassemblies



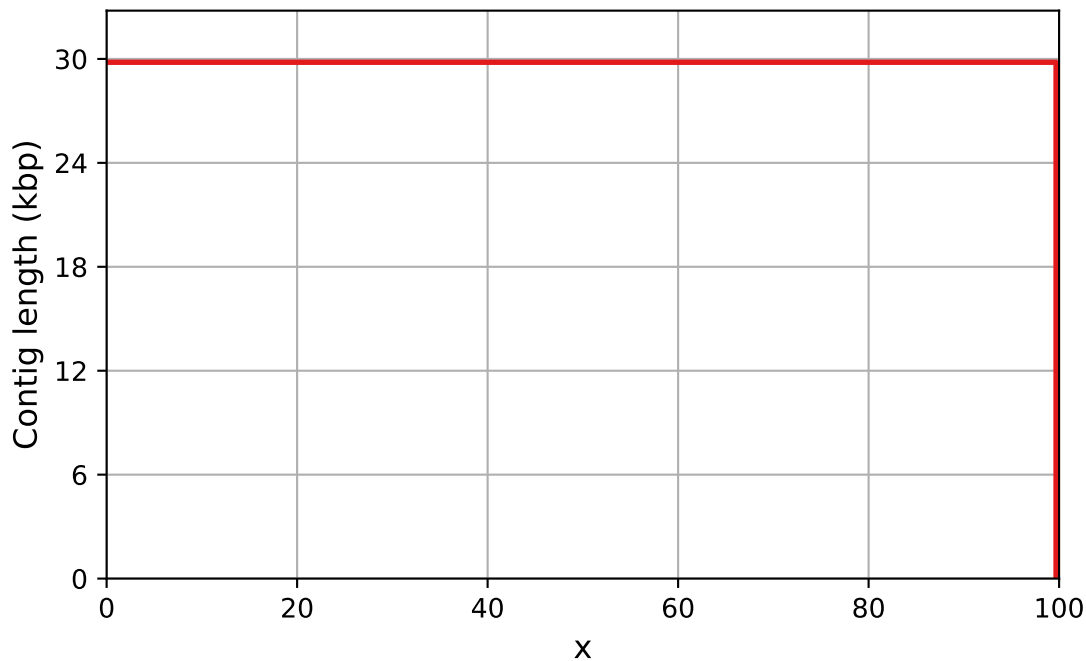
FRCurve (misassemblies)



Cumulative length (aligned contigs)

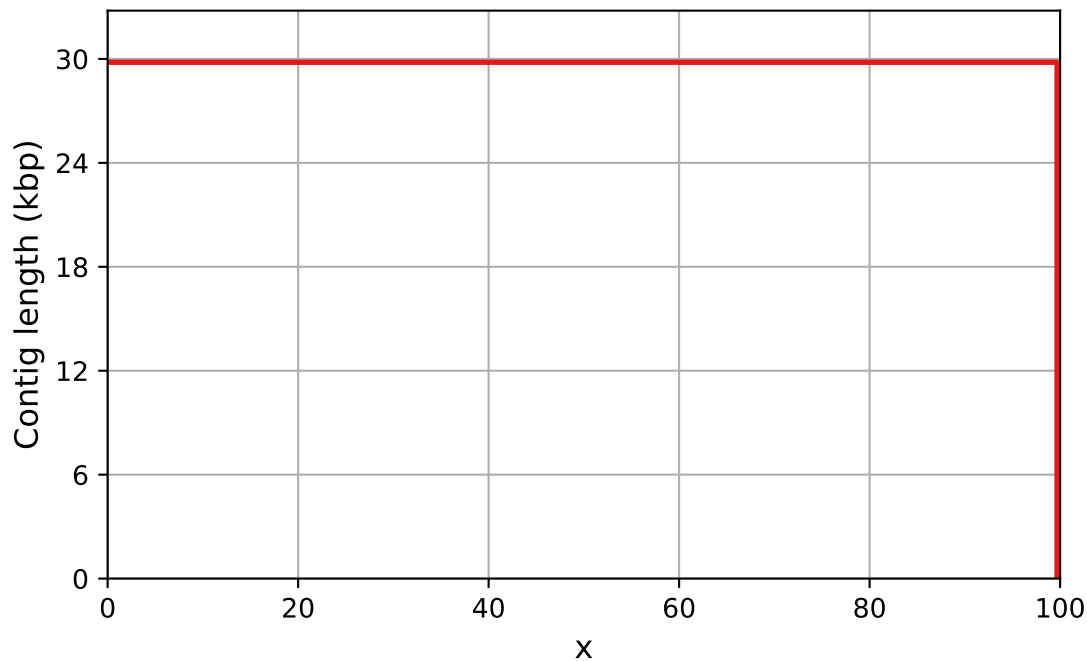


NAx

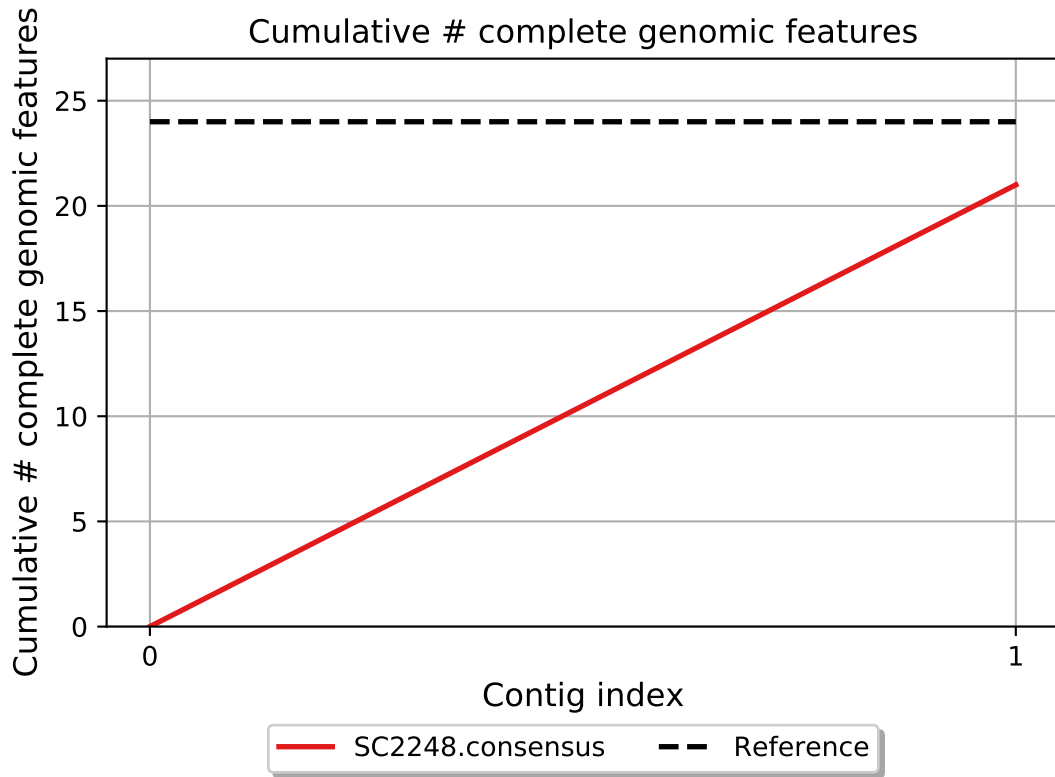


— SC2248.consensus

NGAx



— SC2248.consensus



FRCurve (genomic features)

