

Report

| | final.contigs |
|-----------------------------|------------------|
| # contigs (>= 0 bp) | 228719 |
| # contigs (>= 1000 bp) | 14571 |
| # contigs (>= 5000 bp) | 665 |
| # contigs (>= 10000 bp) | 90 |
| # contigs (>= 25000 bp) | 2 |
| # contigs (>= 50000 bp) | 1 |
| Total length (>= 0 bp) | 118184697 |
| Total length (>= 1000 bp) | 29216887 |
| Total length (>= 5000 bp) | 5101896 |
| Total length (>= 10000 bp) | 1301342 |
| Total length (>= 25000 bp) | 98643 |
| Total length (>= 50000 bp) | 63871 |
| # contigs | 66434 |
| Largest contig | 63871 |
| Total length | 63625827 |
| Reference length | 31445514 |
| N50 | 921 |
| N90 | 549 |
| auN | 1951.2 |
| L50 | 17280 |
| L90 | 54273 |
| # misassemblies | 219 |
| # misassembled contigs | 211 |
| Misassembled contigs length | 256350 |
| # local misassemblies | 52 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 37 |
| # unaligned contigs | 54770 + 453 part |
| Unaligned length | 52958634 |
| Genome fraction (%) | 31.602 |
| Duplication ratio | 1.058 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 4350.54 |
| # indels per 100 kbp | 105.30 |
| Largest alignment | 18493 |
| Total aligned length | 10054350 |
| NA50 | - |
| NA90 | - |
| auNA | 245.5 |
| LA50 | - |
| LA90 | - |

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

| | final.contigs |
|----------------------------------|---------------|
| # misassemblies | 219 |
| # contig misassemblies | 219 |
| # c. relocations | 78 |
| # c. translocations | 26 |
| # c. inversions | 3 |
| # c. interspecies translocations | 112 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # s. interspecies translocations | 0 |
| # misassembled contigs | 211 |
| Misassembled contigs length | 256350 |
| # possibly misassembled contigs | 429 |
| # possible misassemblies | 451 |
| # local misassemblies | 52 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 37 |
| # mismatches | 437419 |
| # indels | 10587 |
| # indels (<= 5 bp) | 10188 |
| # indels (> 5 bp) | 399 |
| Indels length | 25851 |

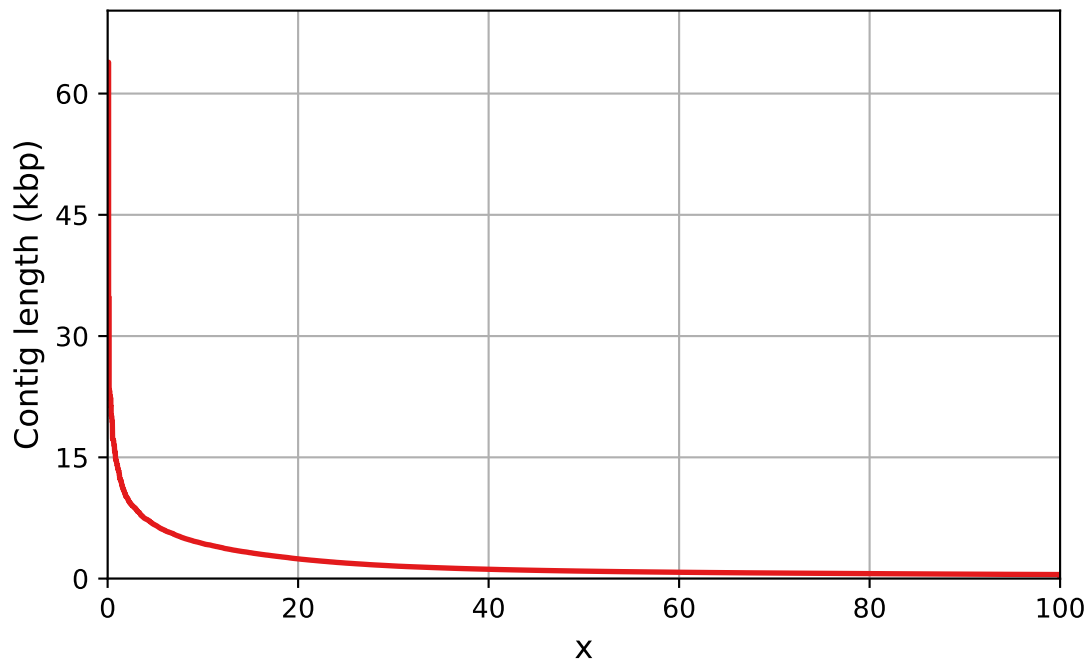
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 54770 |
| Fully unaligned length | 52459967 |
| # partially unaligned contigs | 453 |
| Partially unaligned length | 498667 |
| # N's | 0 |

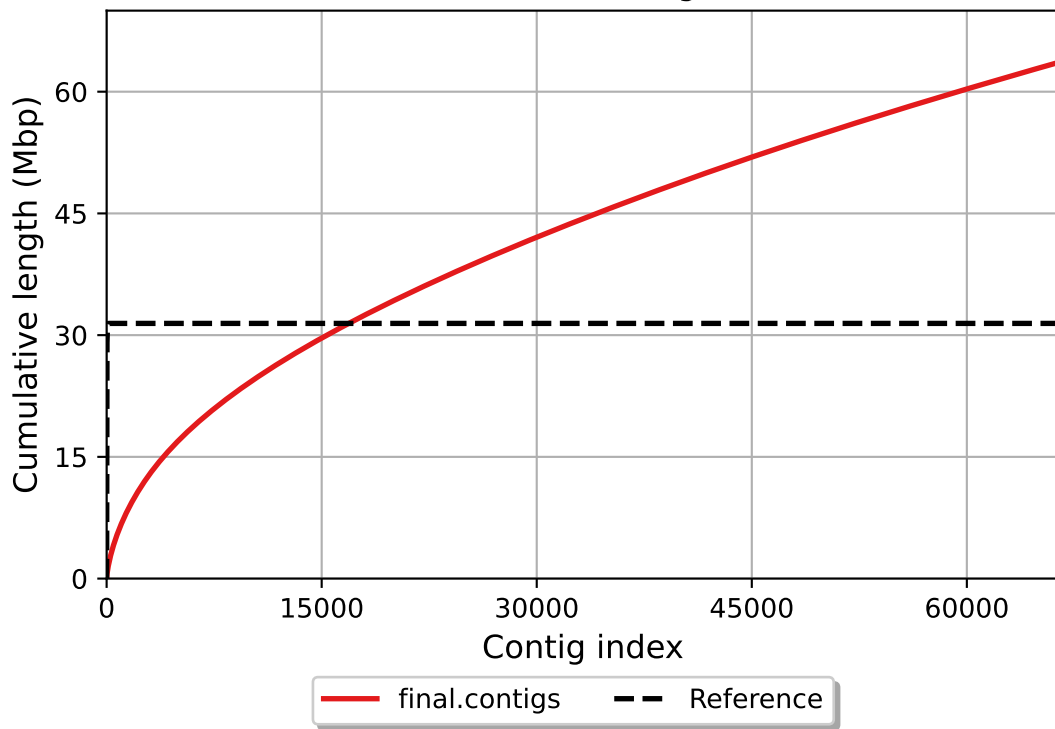
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

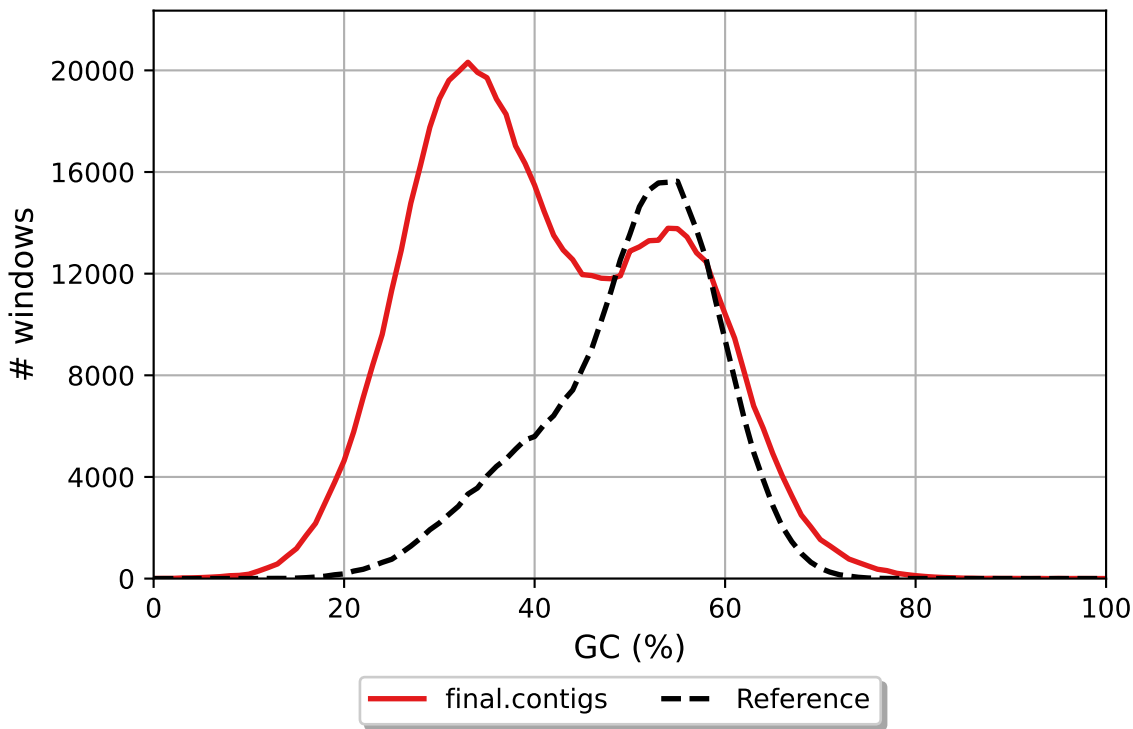


— final.contigs

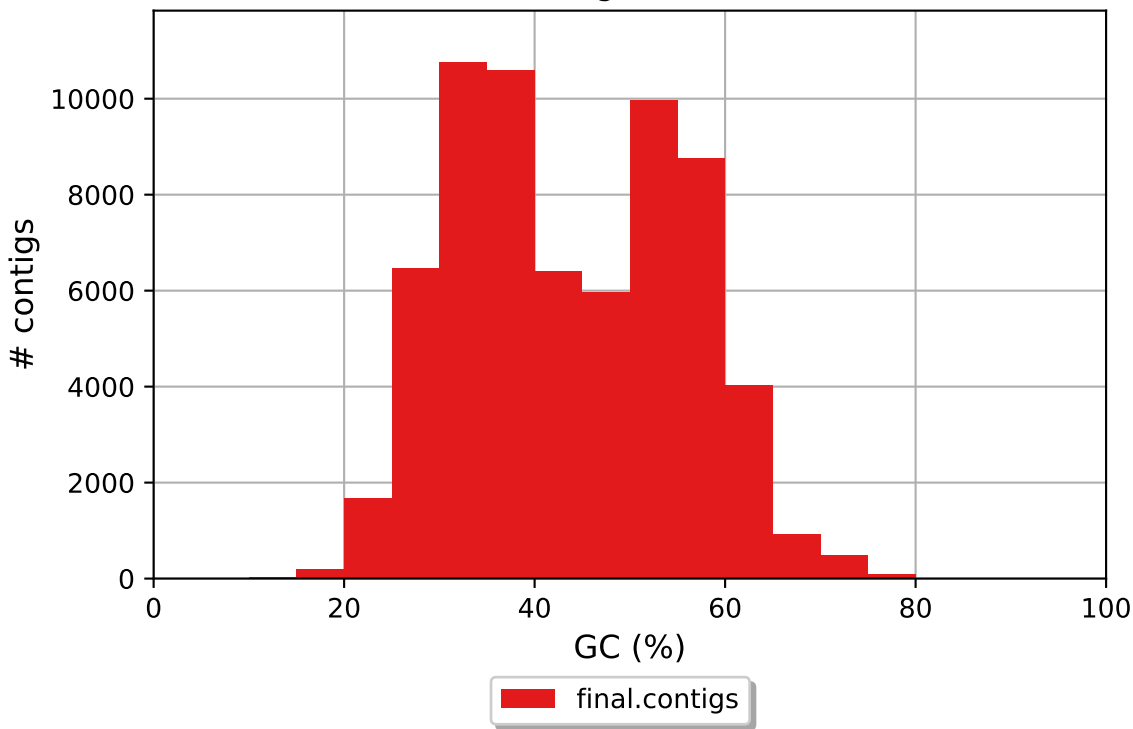
Cumulative length



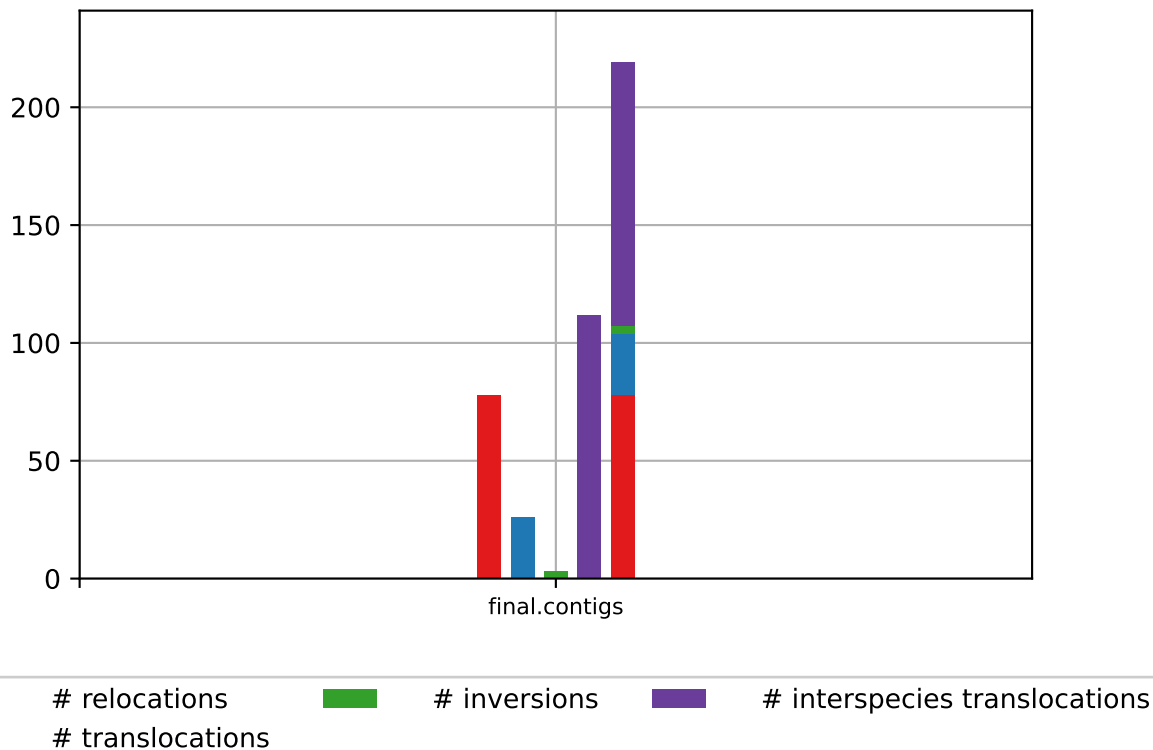
GC content



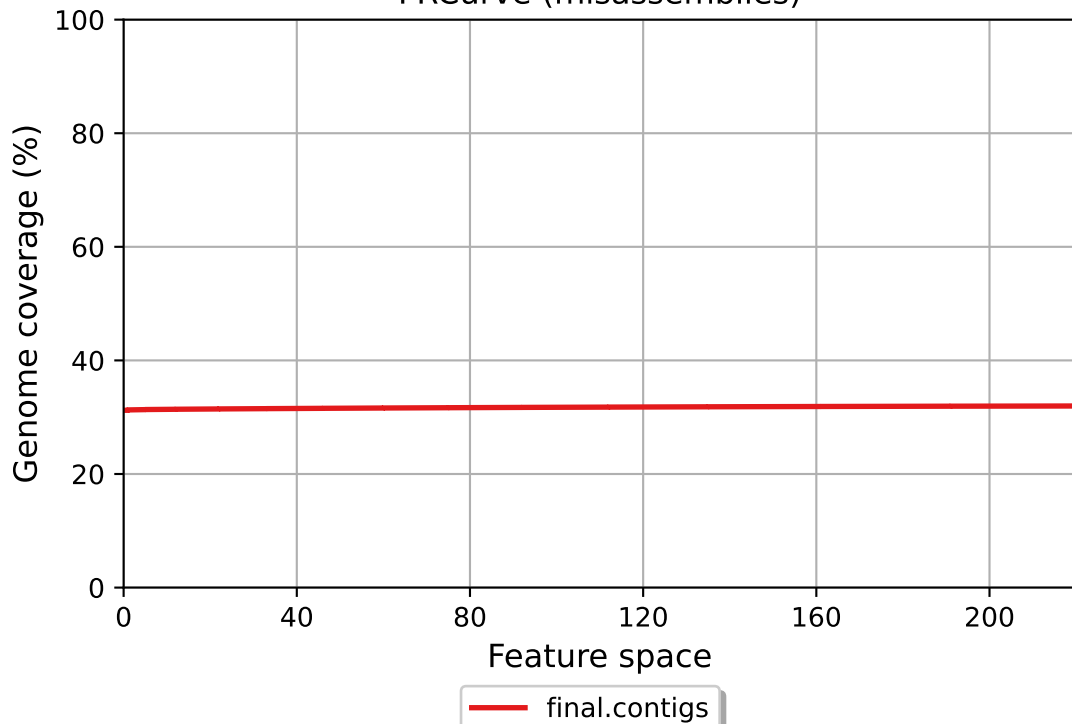
final.contigs GC content



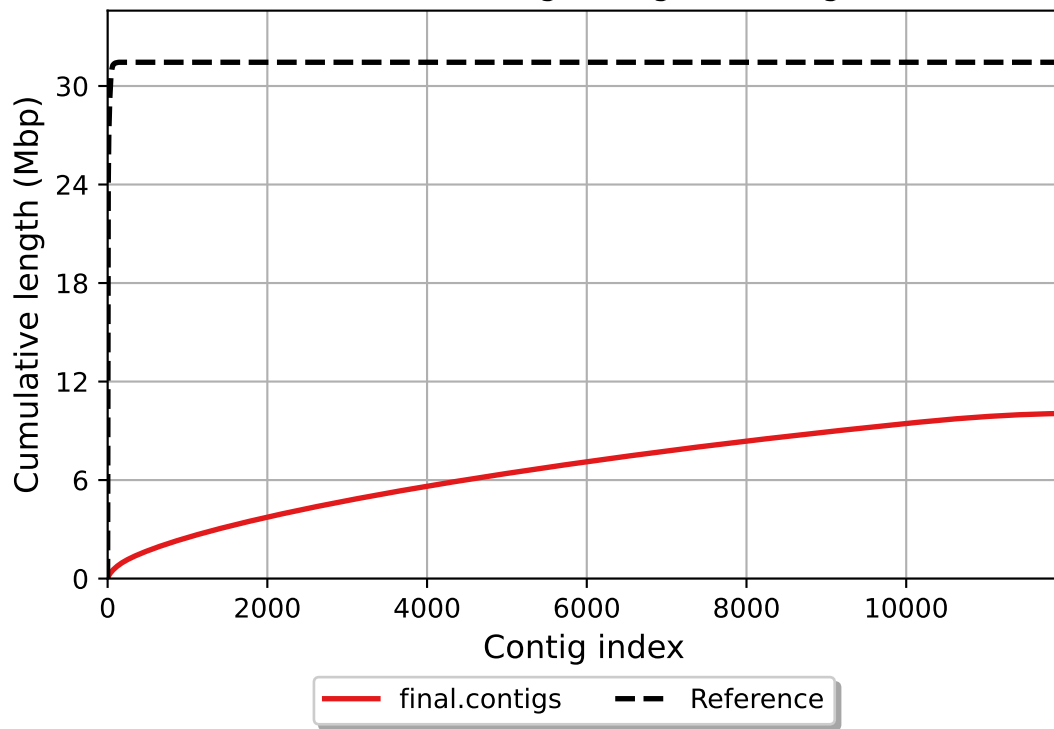
Misassemblies



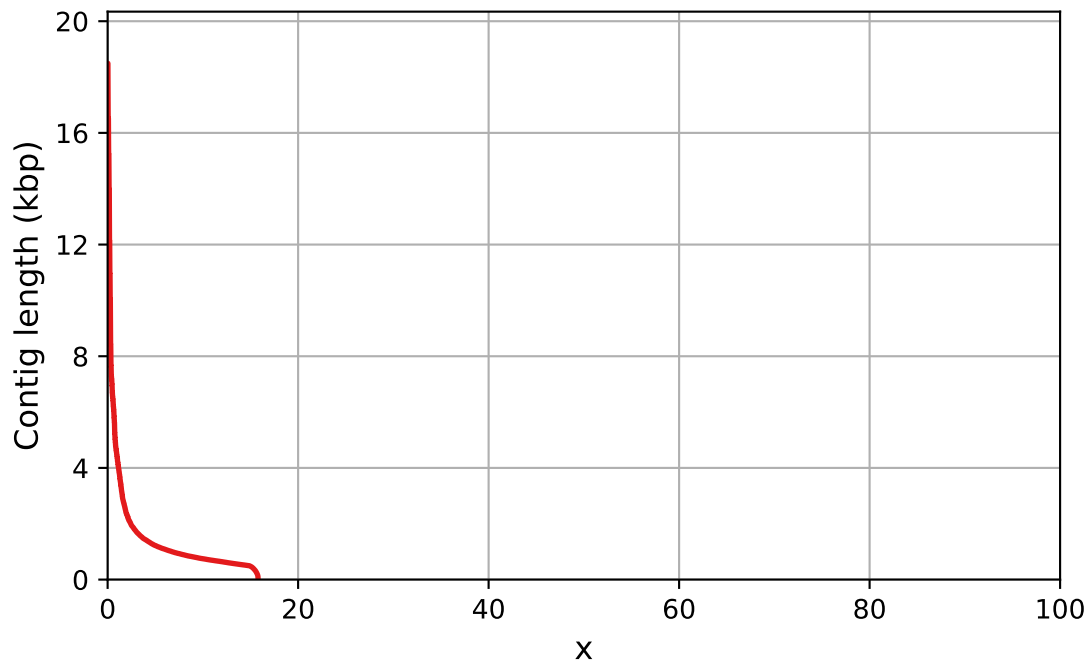
FRCurve (misassemblies)



Cumulative length (aligned contigs)



NAx



— final.contigs