

Report

| | contigs |
|-----------------------------|------------|
| # contigs (>= 1000 bp) | 38 |
| # contigs (>= 5000 bp) | 1 |
| # contigs (>= 10000 bp) | 1 |
| # contigs (>= 25000 bp) | 1 |
| # contigs (>= 50000 bp) | 0 |
| Total length (>= 1000 bp) | 97953 |
| Total length (>= 5000 bp) | 42738 |
| Total length (>= 10000 bp) | 42738 |
| Total length (>= 25000 bp) | 42738 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 311 |
| Largest contig | 42738 |
| Total length | 277770 |
| Reference length | 2345508 |
| GC (%) | 37.91 |
| Reference GC (%) | 0.00 |
| N50 | 783 |
| NG50 | - |
| N90 | 545 |
| NG90 | - |
| auN | 7369.8 |
| auNG | 872.8 |
| L50 | 86 |
| LG50 | - |
| L90 | 258 |
| LG90 | - |
| # misassemblies | 19 |
| # misassembled contigs | 16 |
| Misassembled contigs length | 22040 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 1 |
| # unaligned contigs | 0 + 9 part |
| Unaligned length | 52737 |
| Genome fraction (%) | 9.343 |
| Duplication ratio | 1.002 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 1632.81 |
| # indels per 100 kbp | 22.32 |
| Largest alignment | 2122 |
| Total aligned length | 219499 |
| NA50 | 616 |
| NGA50 | - |
| NA90 | - |
| NGA90 | - |
| auNA | 598.7 |
| auNGA | 70.9 |
| LA50 | 168 |
| LGA50 | - |
| LA90 | - |
| LGA90 | - |

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

| | contigs |
|---------------------------------|---------|
| # misassemblies | 19 |
| # contig misassemblies | 19 |
| # c. relocations | 0 |
| # c. translocations | 19 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 16 |
| Misassembled contigs length | 22040 |
| # possibly misassembled contigs | 4 |
| # possible misassemblies | 6 |
| # local misassemblies | 0 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 1 |
| # mismatches | 3584 |
| # indels | 49 |
| # indels (≤ 5 bp) | 43 |
| # indels (> 5 bp) | 6 |
| Indels length | 330 |

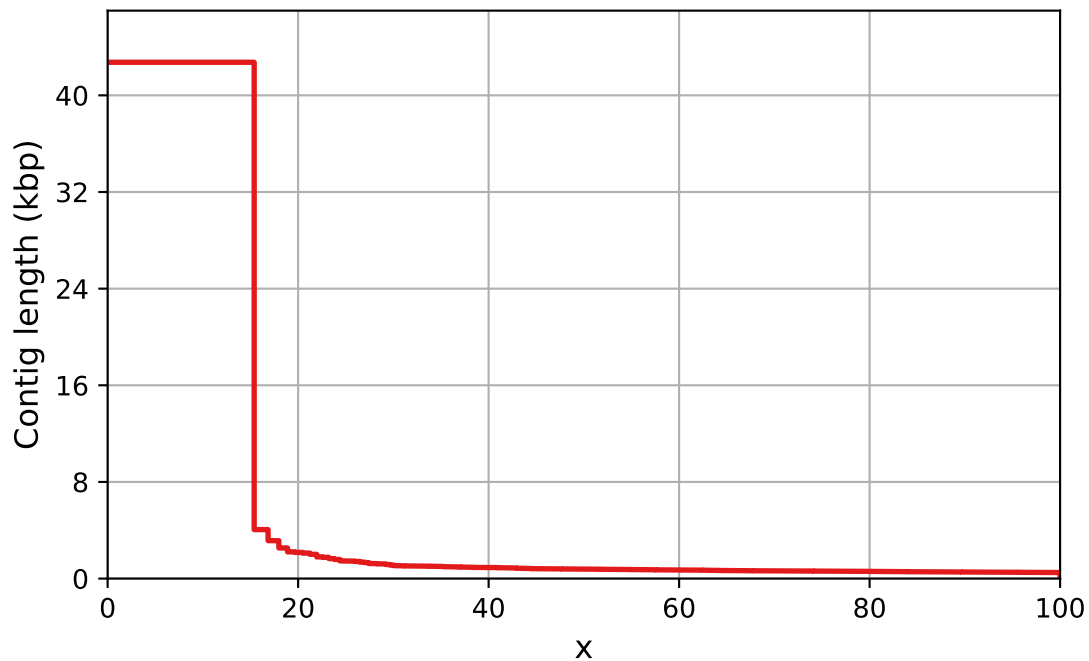
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

| | contigs |
|-------------------------------|---------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 9 |
| Partially unaligned length | 52737 |
| # N's | 0 |

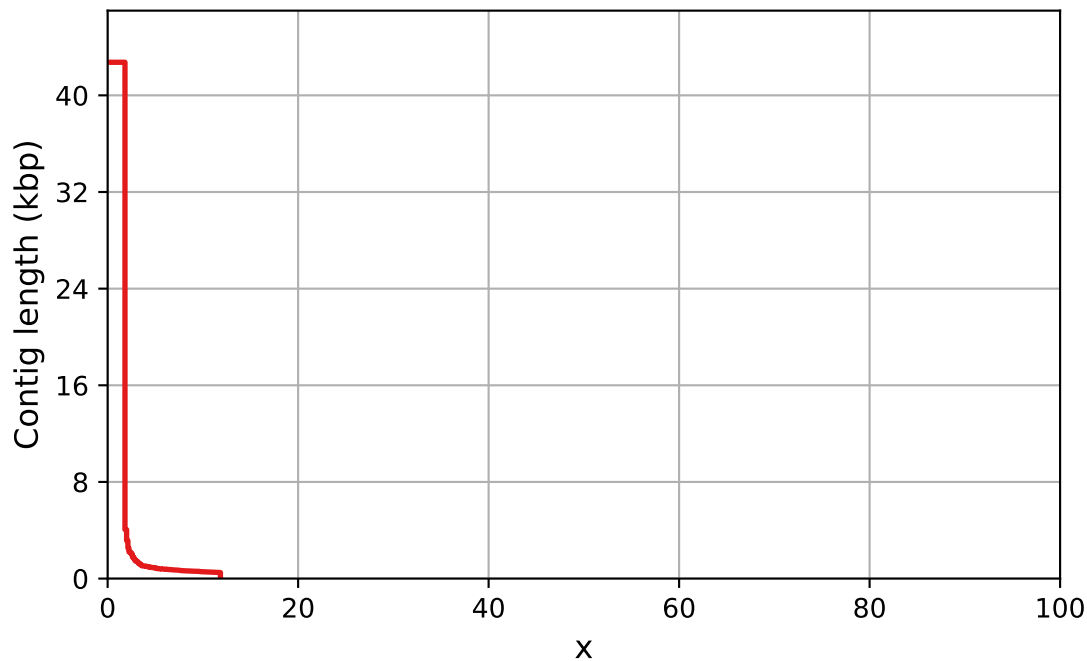
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

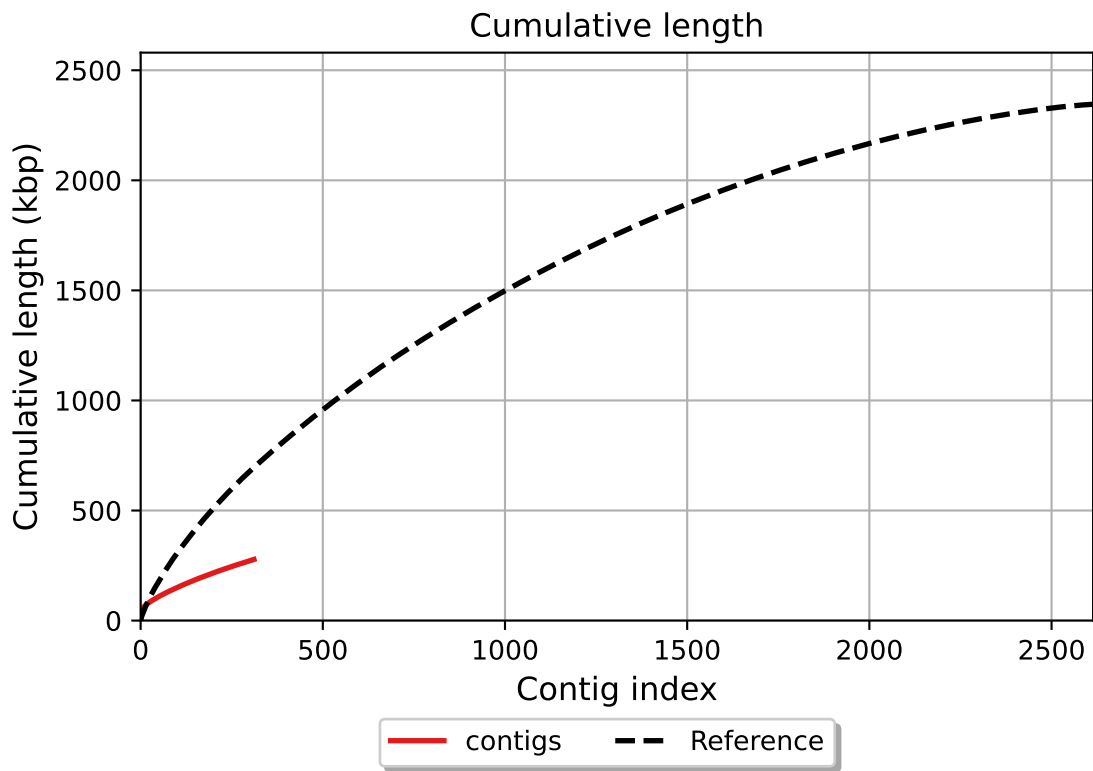


contigs

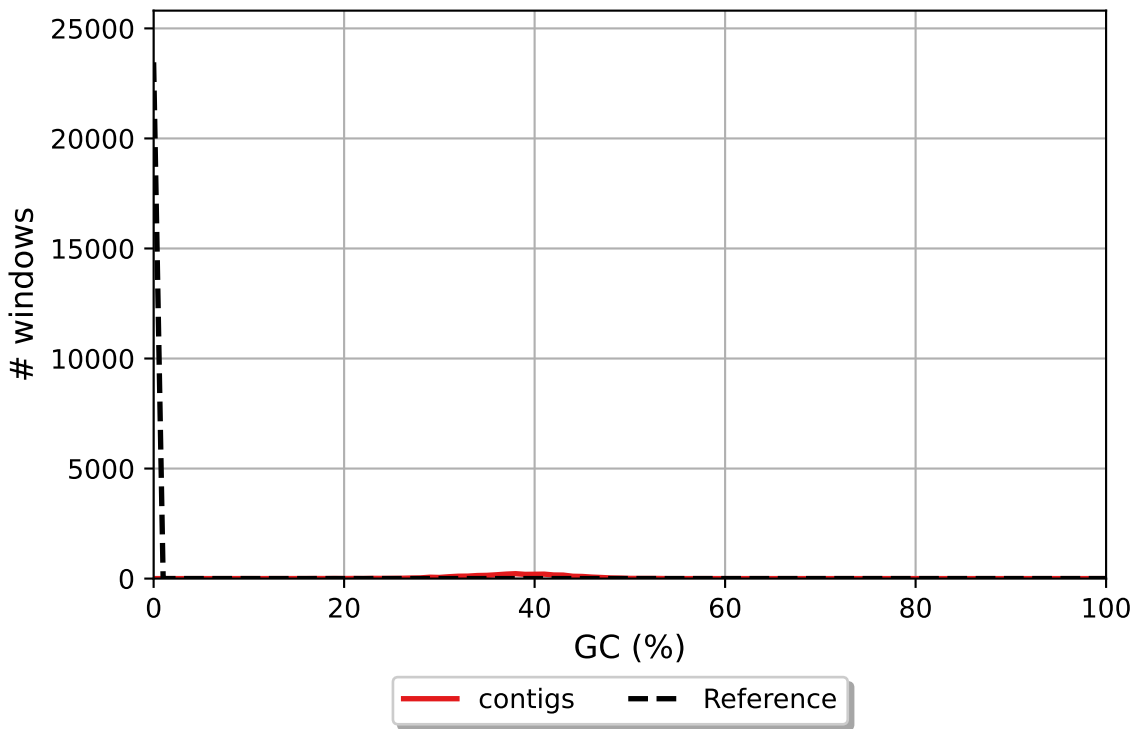
NGx



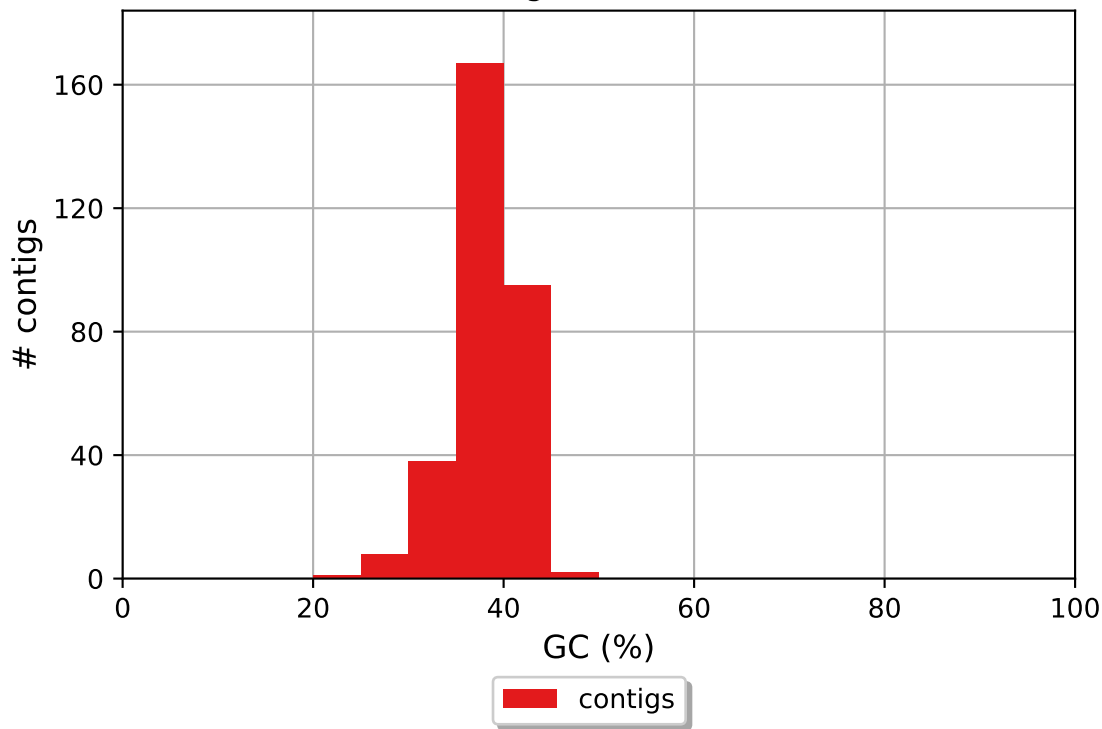
contigs



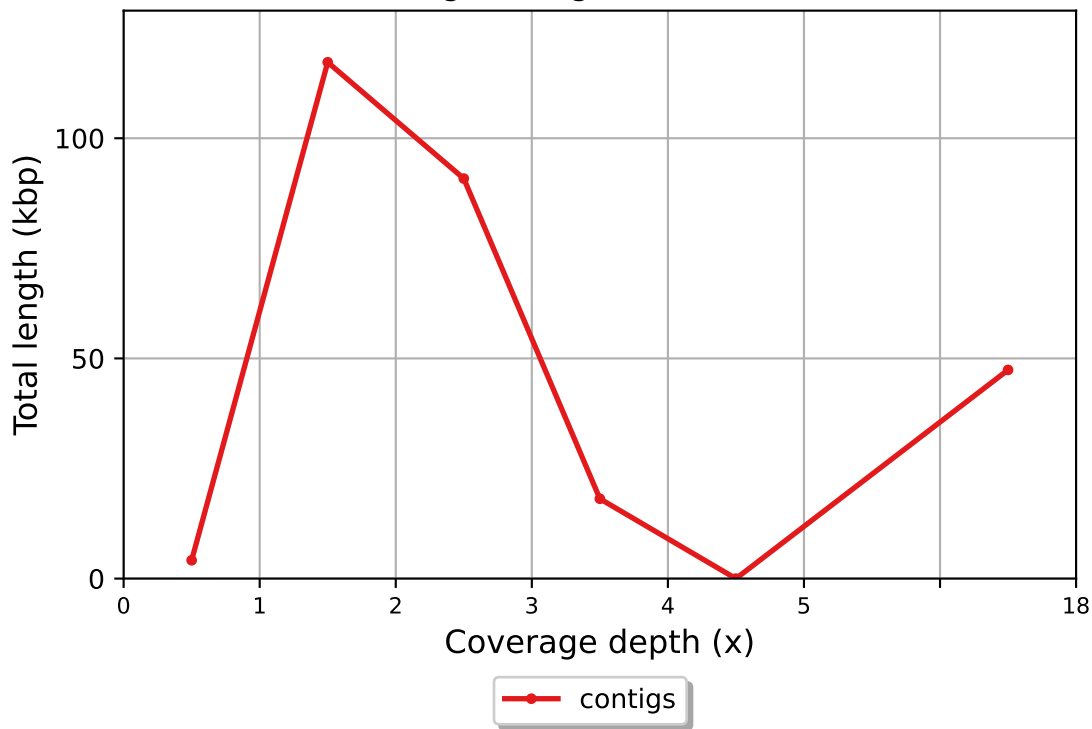
GC content



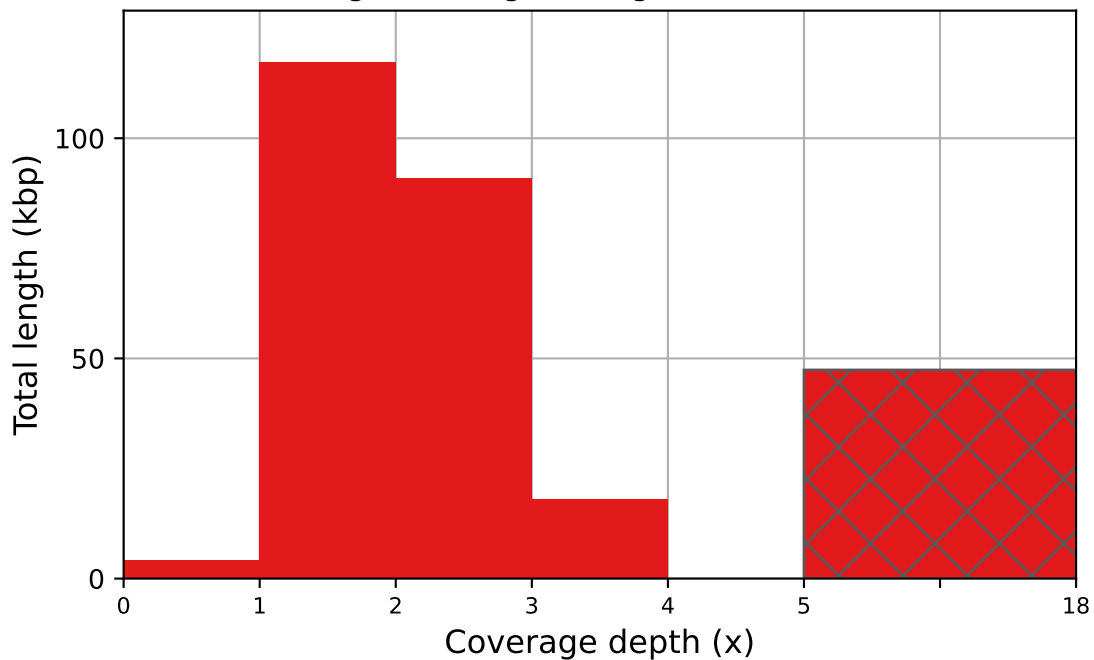
contigs GC content



Coverage histogram (bin size: 1x)

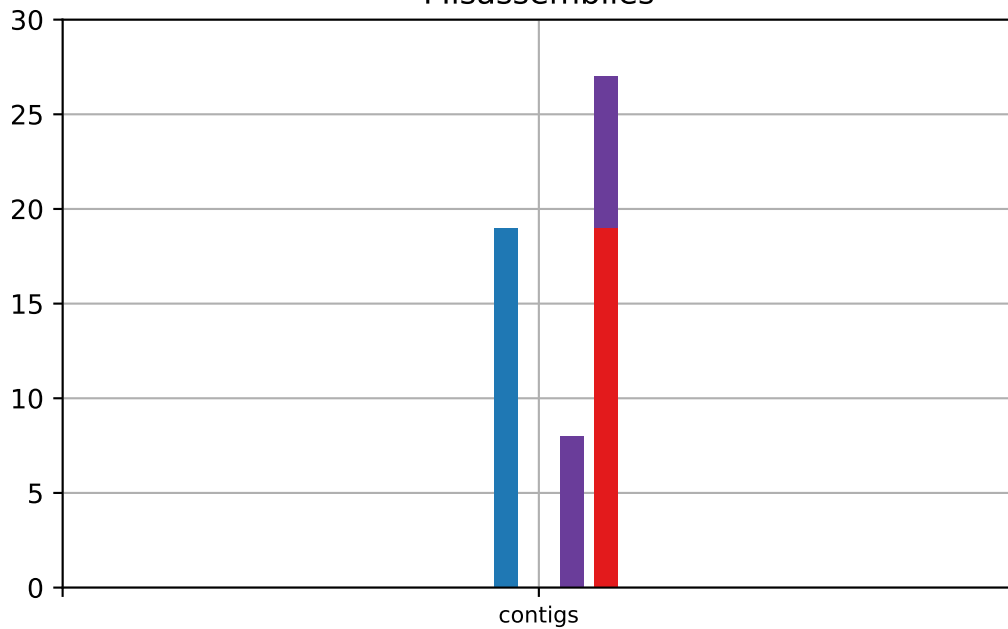


contigs coverage histogram (bin size: 1x)



contigs

Misassemblies

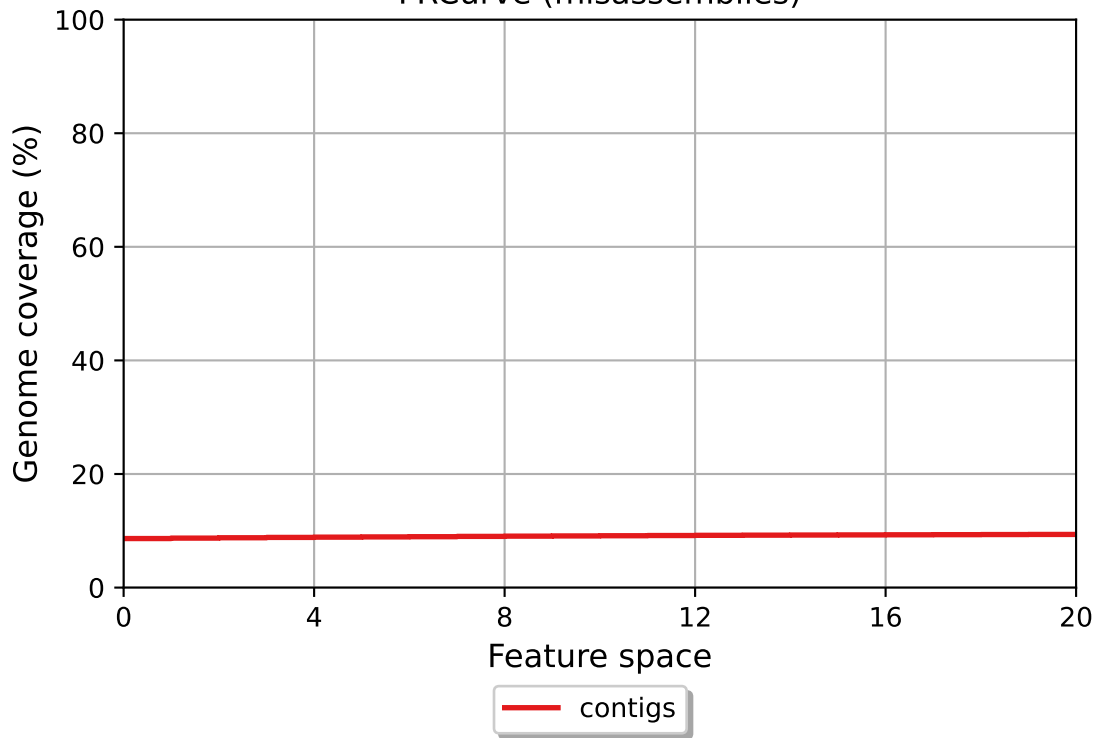


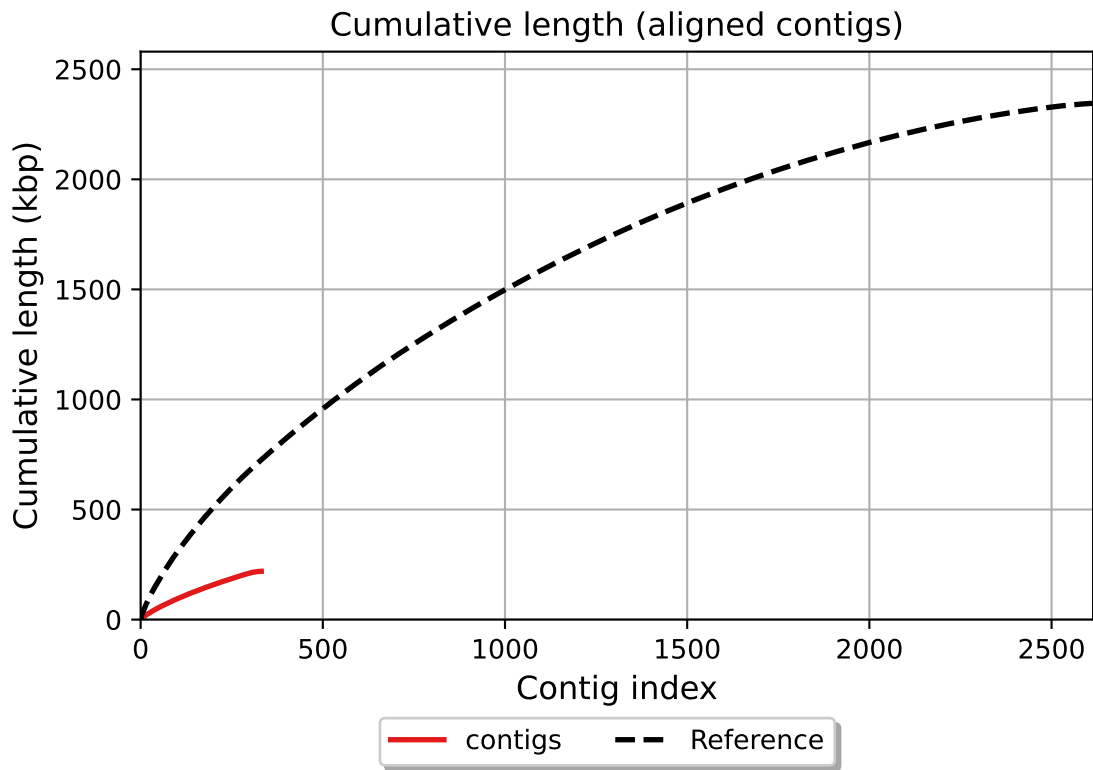
translocations



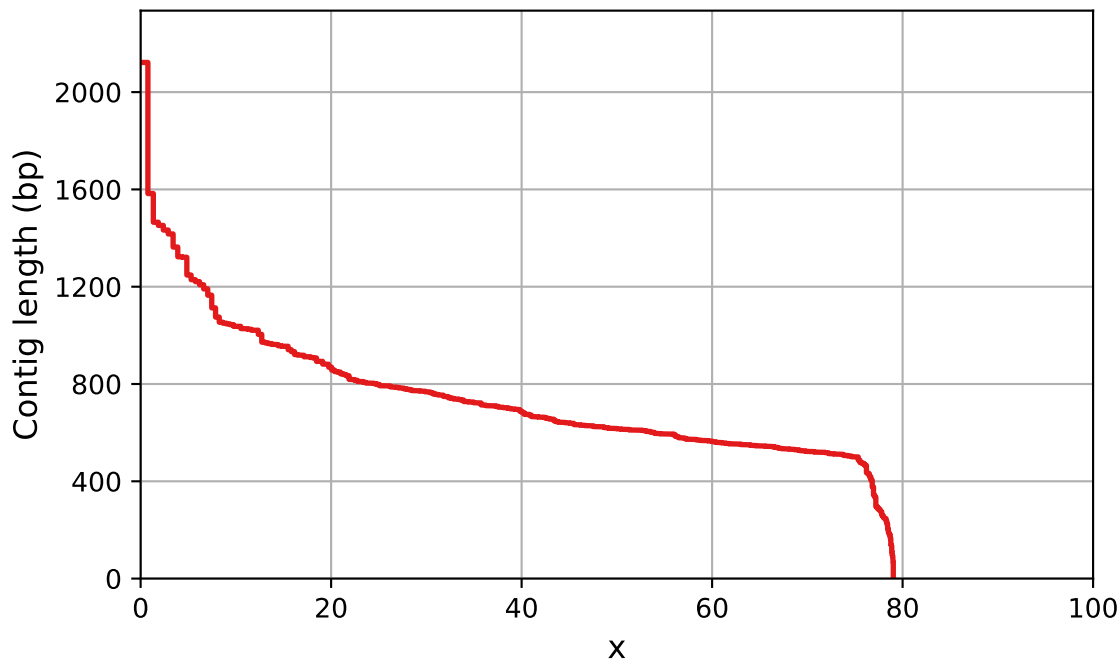
interspecies translocations

FRCurve (misassemblies)





NAx



contigs

NGAx

