

| | Report | |
|-----------------------------|-------------|------------------|
| | scaffolds | scaffolds_broken |
| # contigs (>= 0 bp) | 80 | - |
| # contigs (>= 1000 bp) | 48 | 57 |
| # contigs (>= 5000 bp) | 41 | 50 |
| # contigs (>= 10000 bp) | 38 | 47 |
| # contigs (>= 25000 bp) | 34 | 41 |
| # contigs (>= 50000 bp) | 30 | 35 |
| Total length (>= 0 bp) | 6425745 | - |
| Total length (>= 1000 bp) | 6414820 | 6413920 |
| Total length (>= 5000 bp) | 6403294 | 6402394 |
| Total length (>= 10000 bp) | 6385298 | 6384398 |
| Total length (>= 25000 bp) | 6321690 | 6286931 |
| Total length (>= 50000 bp) | 6171899 | 6075814 |
| # contigs | 55 | 64 |
| Largest contig | 668648 | 668648 |
| Total length | 6419571 | 6418671 |
| Reference length | 6264404 | 6264404 |
| GC (%) | 66.39 | 66.39 |
| Reference GC (%) | 66.56 | 66.56 |
| N50 | 303720 | 239845 |
| NG50 | 303720 | 239845 |
| N75 | 160338 | 106343 |
| NG75 | 160338 | 113612 |
| L50 | 7 | 9 |
| LG50 | 7 | 9 |
| L75 | 14 | 19 |
| LG75 | 14 | 18 |
| # misassemblies | 43 | 42 |
| # misassembled contigs | 20 | 20 |
| Misassembled contigs length | 5108685 | 4067034 |
| # local misassemblies | 42 | 42 |
| # scaffold gap ext. mis. | 1 | - |
| # scaffold gap loc. mis. | 6 | - |
| # unaligned mis. contigs | 0 | 0 |
| # unaligned contigs | 1 + 26 part | 1 + 27 part |
| Unaligned length | 403575 | 403122 |
| Genome fraction (%) | 95.939 | 95.937 |
| Duplication ratio | 1.001 | 1.001 |
| # N's per 100 kbp | 14.02 | 0.00 |
| # mismatches per 100 kbp | 493.93 | 493.79 |
| # indels per 100 kbp | 10.48 | 10.45 |
| Largest alignment | 389953 | 389622 |
| Total aligned length | 6014261 | 6014061 |
| NA50 | 125560 | 106343 |
| NGA50 | 137692 | 107066 |
| NA75 | 69741 | 69474 |
| NGA75 | 72080 | 69726 |
| LA50 | 17 | 19 |
| LGA50 | 16 | 18 |
| LA75 | 33 | 38 |
| LGA75 | 32 | 37 |

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

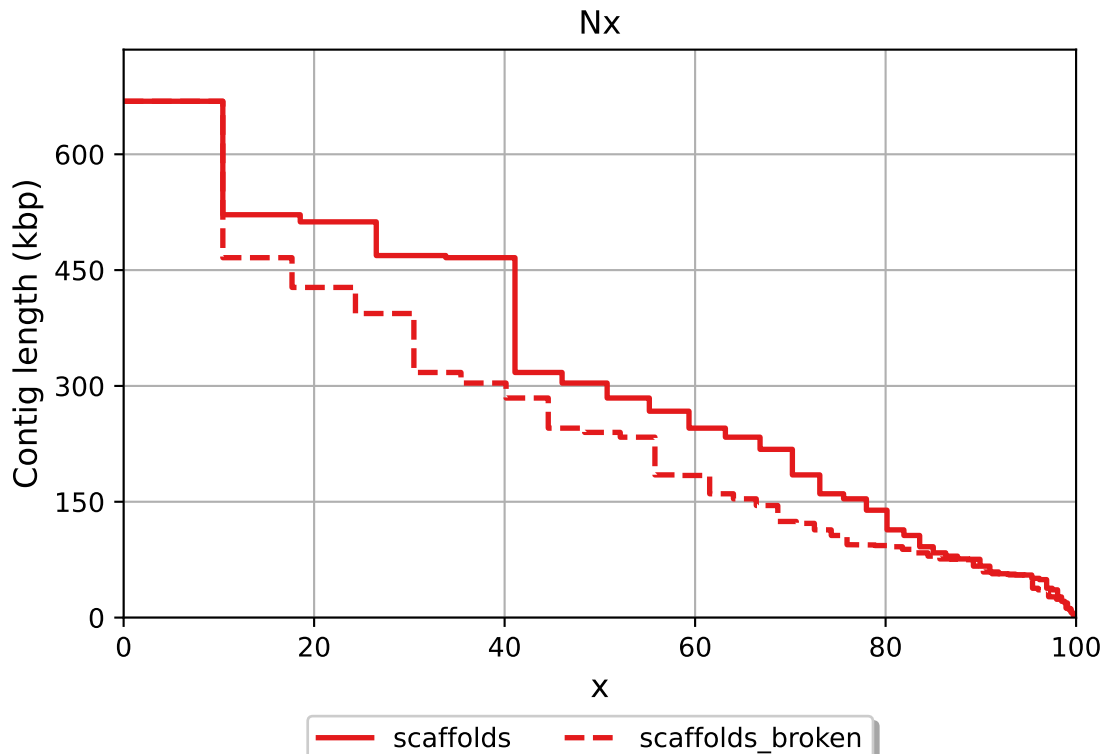
| | scaffolds | scaffolds_broken |
|-----------------------------|-----------|------------------|
| # misassemblies | 43 | 42 |
| # contig misassemblies | 43 | 42 |
| # c. relocations | 43 | 42 |
| # c. translocations | 0 | 0 |
| # c. inversions | 0 | 0 |
| # scaffold misassemblies | 0 | 0 |
| # s. relocations | 0 | 0 |
| # s. translocations | 0 | 0 |
| # s. inversions | 0 | 0 |
| # misassembled contigs | 20 | 20 |
| Misassembled contigs length | 5108685 | 4067034 |
| # local misassemblies | 42 | 42 |
| # scaffold gap ext. mis. | 1 | - |
| # scaffold gap loc. mis. | 6 | - |
| # unaligned mis. contigs | 0 | 0 |
| # mismatches | 29685 | 29676 |
| # indels | 630 | 628 |
| # indels (<= 5 bp) | 540 | 539 |
| # indels (> 5 bp) | 90 | 89 |
| Indels length | 2589 | 2472 |

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).

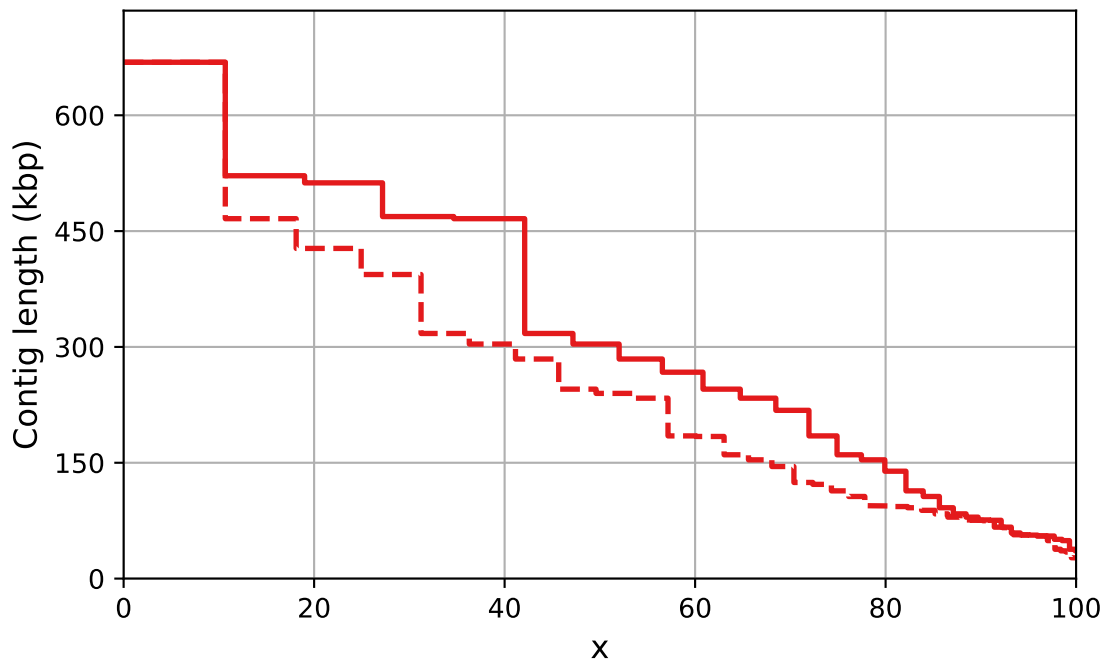
Unaligned report

| | scaffolds | scaffolds_broken |
|-------------------------------|-----------|------------------|
| # fully unaligned contigs | 1 | 1 |
| Fully unaligned length | 37965 | 37965 |
| # partially unaligned contigs | 26 | 27 |
| Partially unaligned length | 365610 | 365157 |
| # N's | 900 | 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).

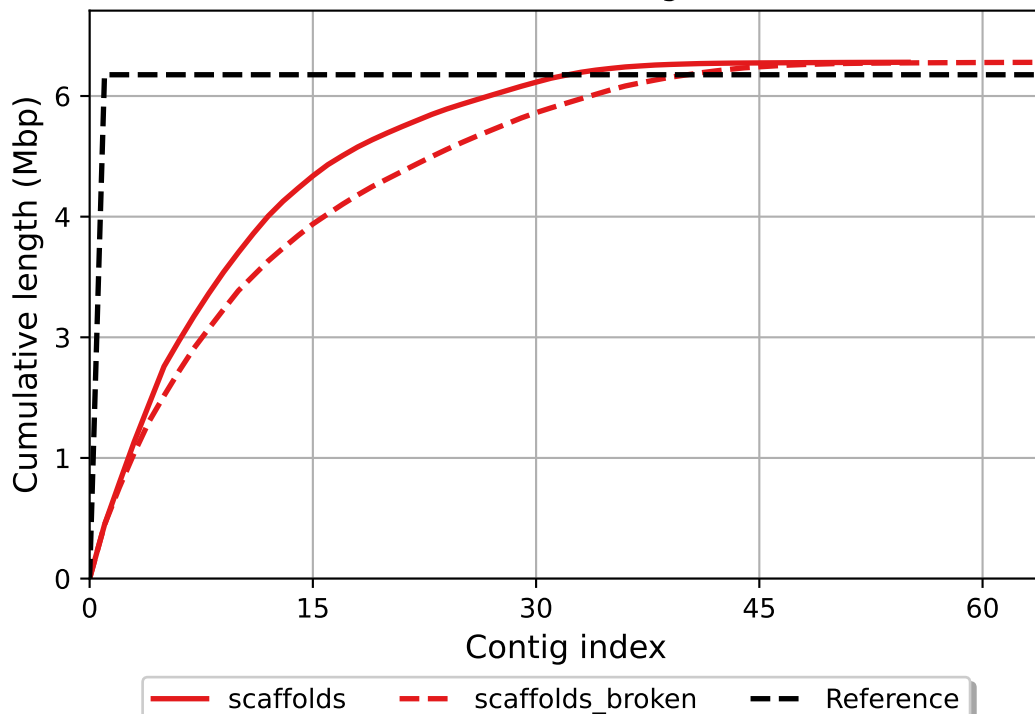


NGx

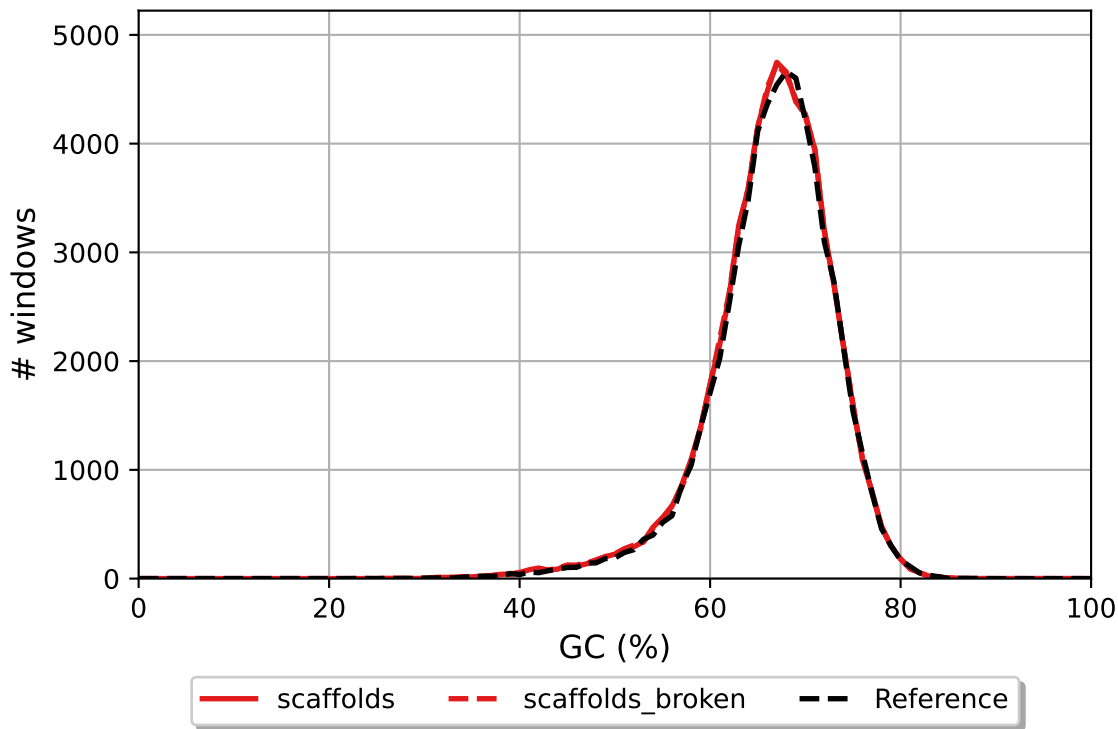


— scaffolds - - - scaffolds_broken

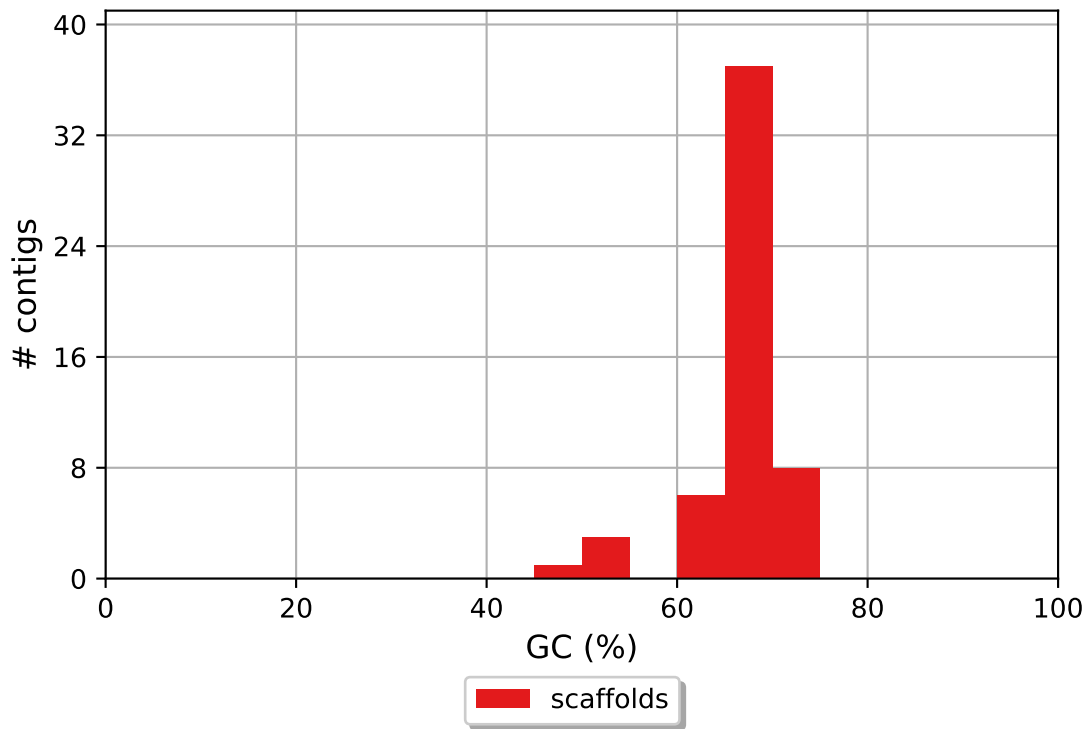
Cumulative length



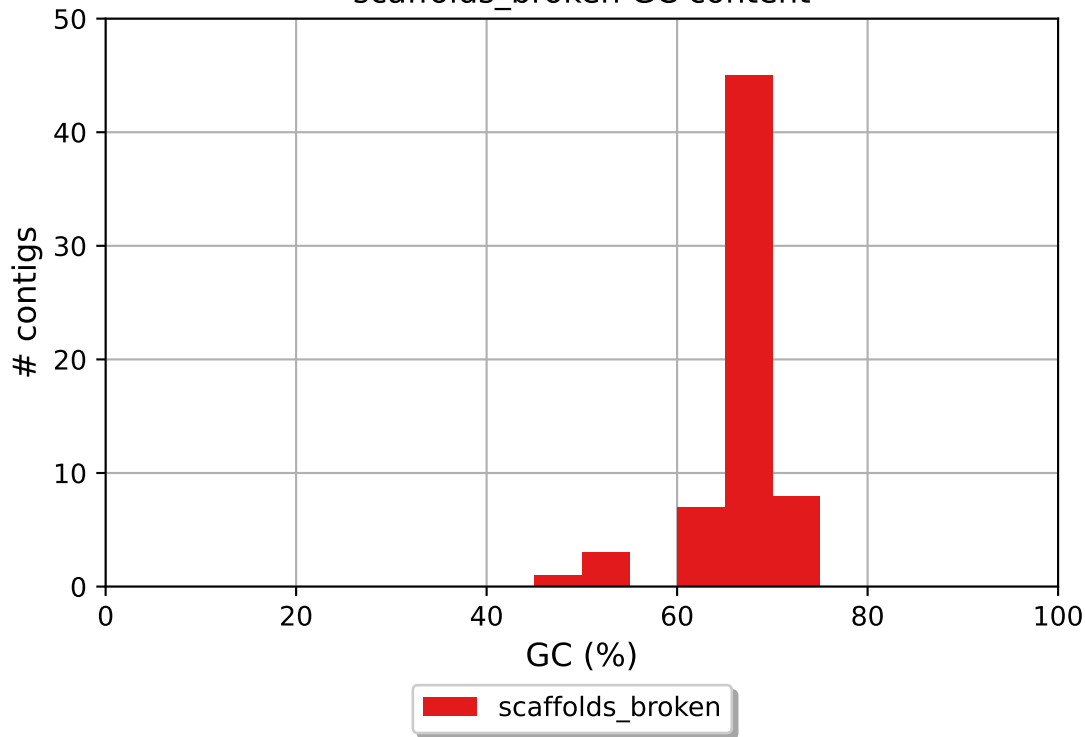
GC content



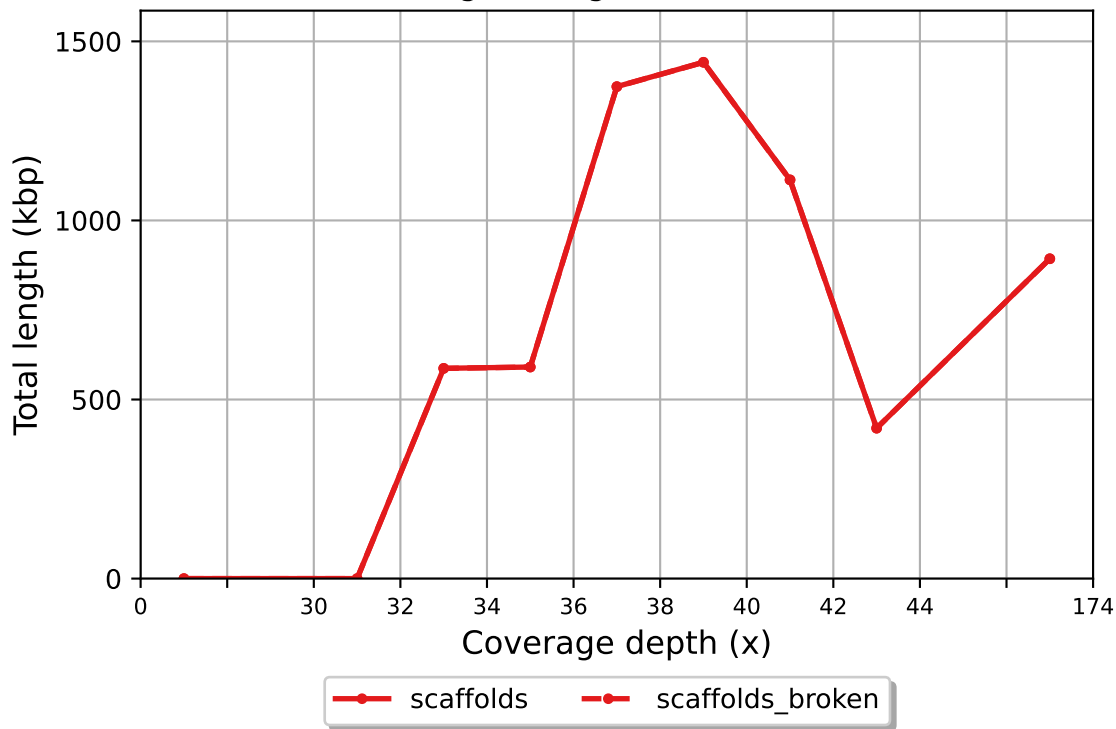
scaffolds GC content



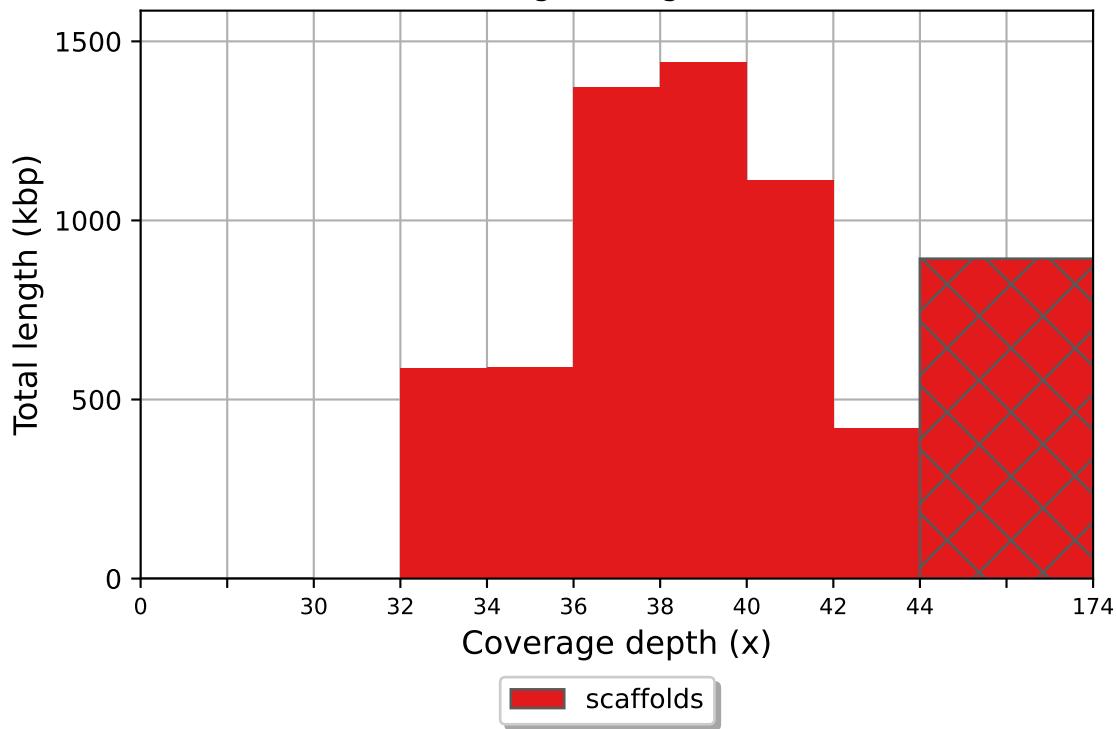
scaffolds_broken GC content



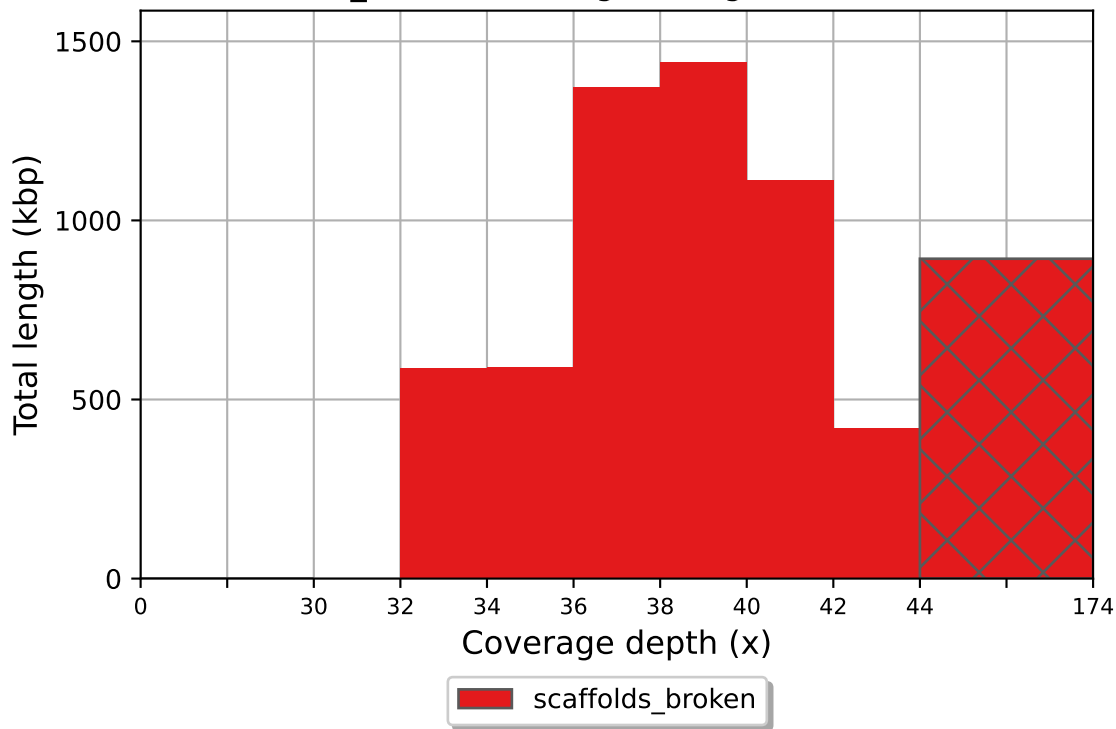
Coverage histogram (bin size: 2x)



scaffolds coverage histogram (bin size: 2x)



scaffolds_broken coverage histogram (bin size: 2x)

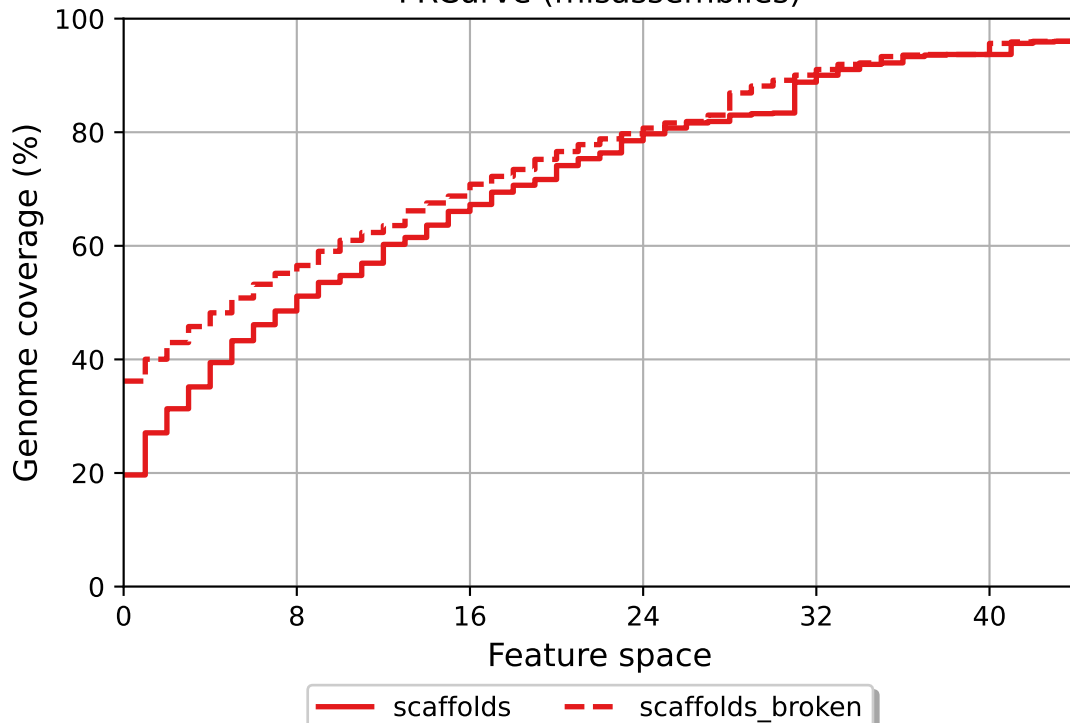


Misassemblies

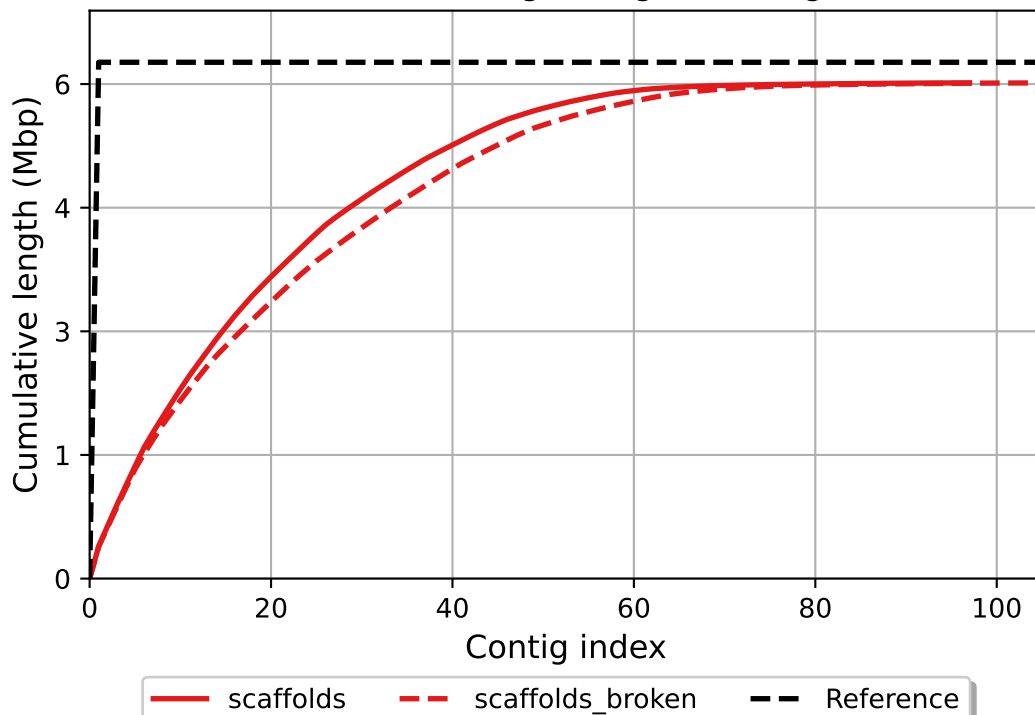


 # relocations

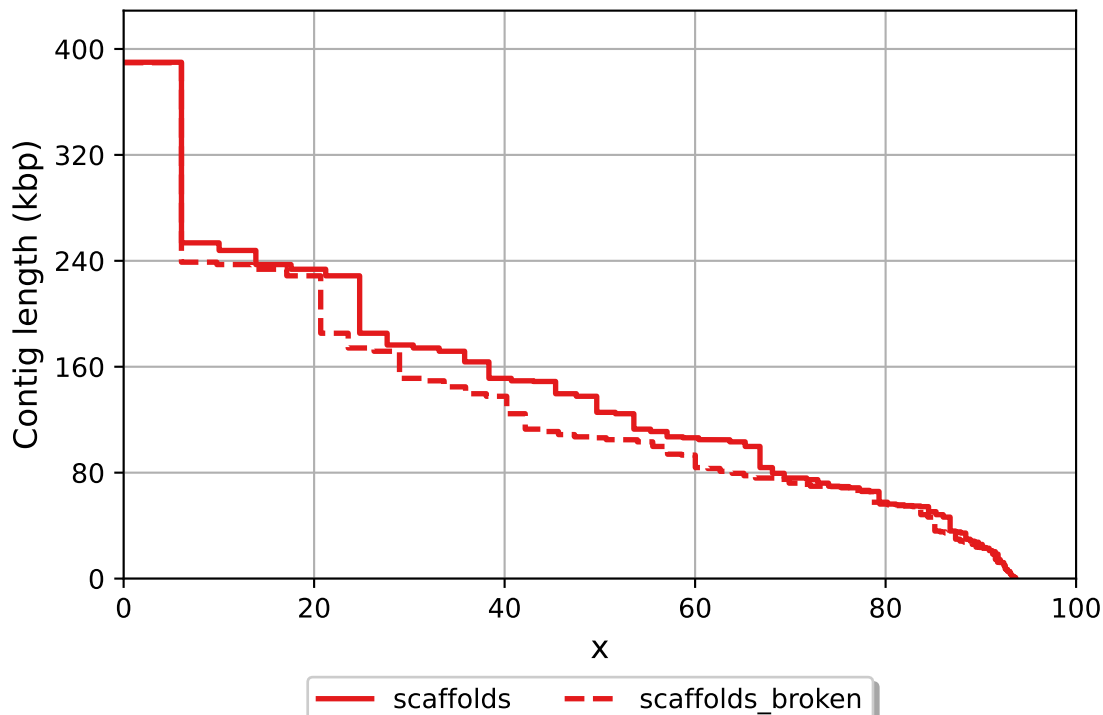
FRCurve (misassemblies)



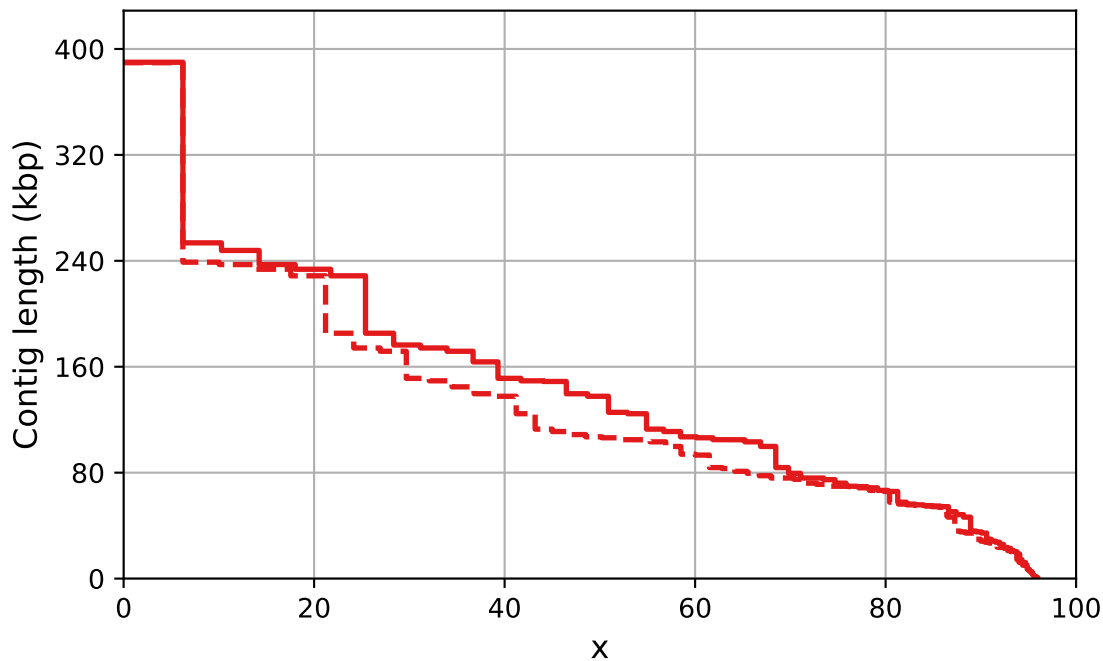
Cumulative length (aligned contigs)



NAx

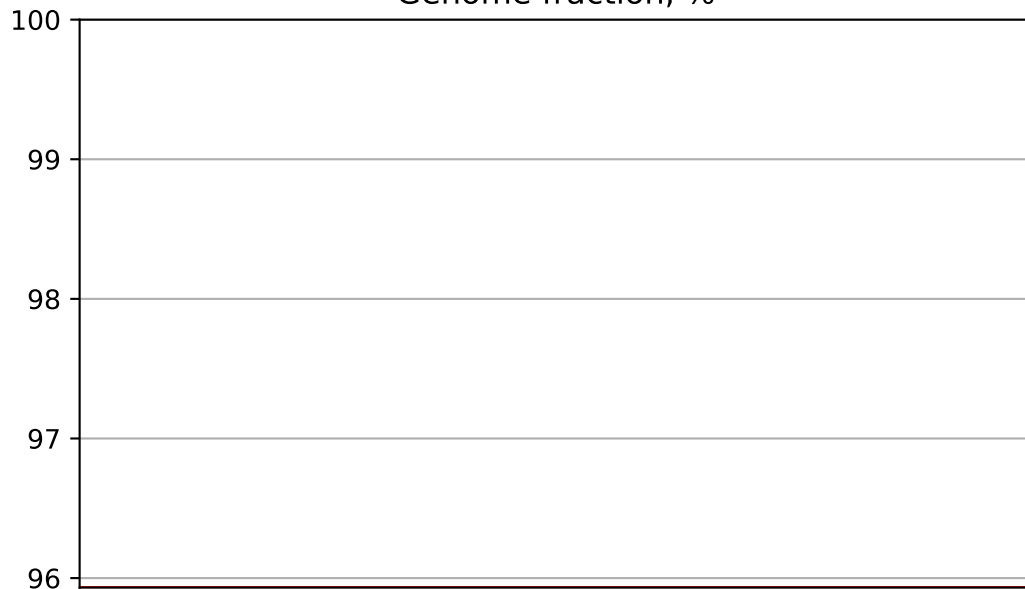


NGAx



— scaffolds - - - scaffolds_broken

Genome fraction, %



scaffolds



scaffolds_broken