

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 1000 bp) | 202 |
| # contigs (≥ 5000 bp) | 155 |
| # contigs (≥ 10000 bp) | 124 |
| # contigs (≥ 25000 bp) | 59 |
| # contigs (≥ 50000 bp) | 12 |
| Total length (≥ 1000 bp) | 3877089 |
| Total length (≥ 5000 bp) | 3765485 |
| Total length (≥ 10000 bp) | 3531953 |
| Total length (≥ 25000 bp) | 2475094 |
| Total length (≥ 50000 bp) | 823529 |
| # contigs | 222 |
| Largest contig | 132022 |
| Total length | 3890229 |
| Reference length | 4641652 |
| GC (%) | 50.79 |
| Reference GC (%) | 50.79 |
| N50 | 32027 |
| NG50 | 27862 |
| N75 | 17754 |
| NG75 | 10818 |
| L50 | 41 |
| LG50 | 54 |
| L75 | 80 |
| LG75 | 120 |
| # misassemblies | 4 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 152553 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 81.651 |
| Duplication ratio | 1.026 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 915.16 |
| # indels per 100 kbp | 0.37 |
| Largest alignment | 132022 |
| NA50 | 31972 |
| NGA50 | 27492 |
| NA75 | 17458 |
| NGA75 | 10813 |
| LA50 | 42 |
| LGA50 | 55 |
| LA75 | 82 |
| LGA75 | 122 |

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 |
|---------------------------------|-----------|
| # misassemblies | 4 |
| # relocations | 4 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 4 |
| Misassembled contigs length | 152553 |
| # local misassemblies | 2 |
| # mismatches | 34684 |
| # indels | 14 |
| # short indels | 14 |
| # long indels | 0 |
| Indels length | 22 |

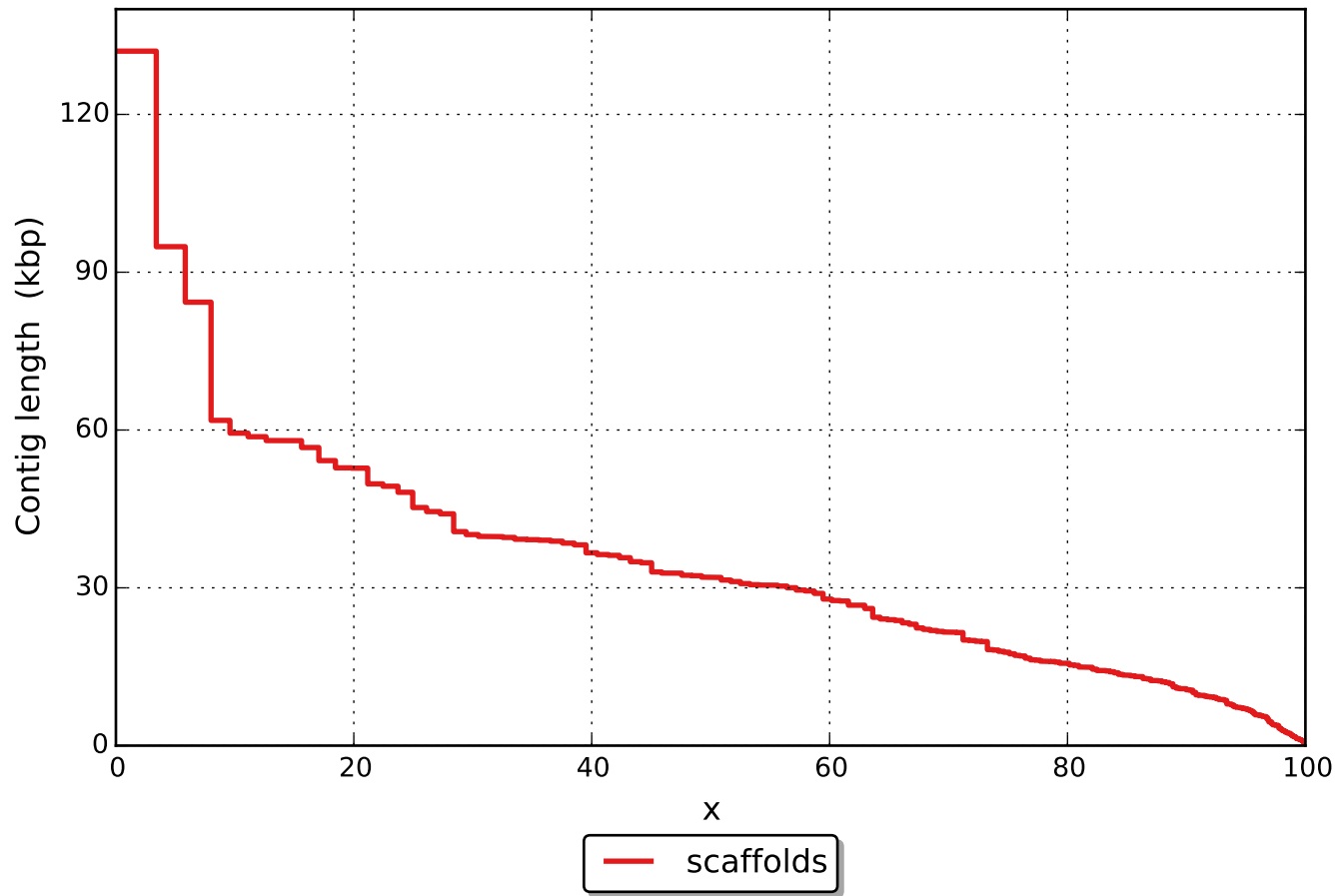
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

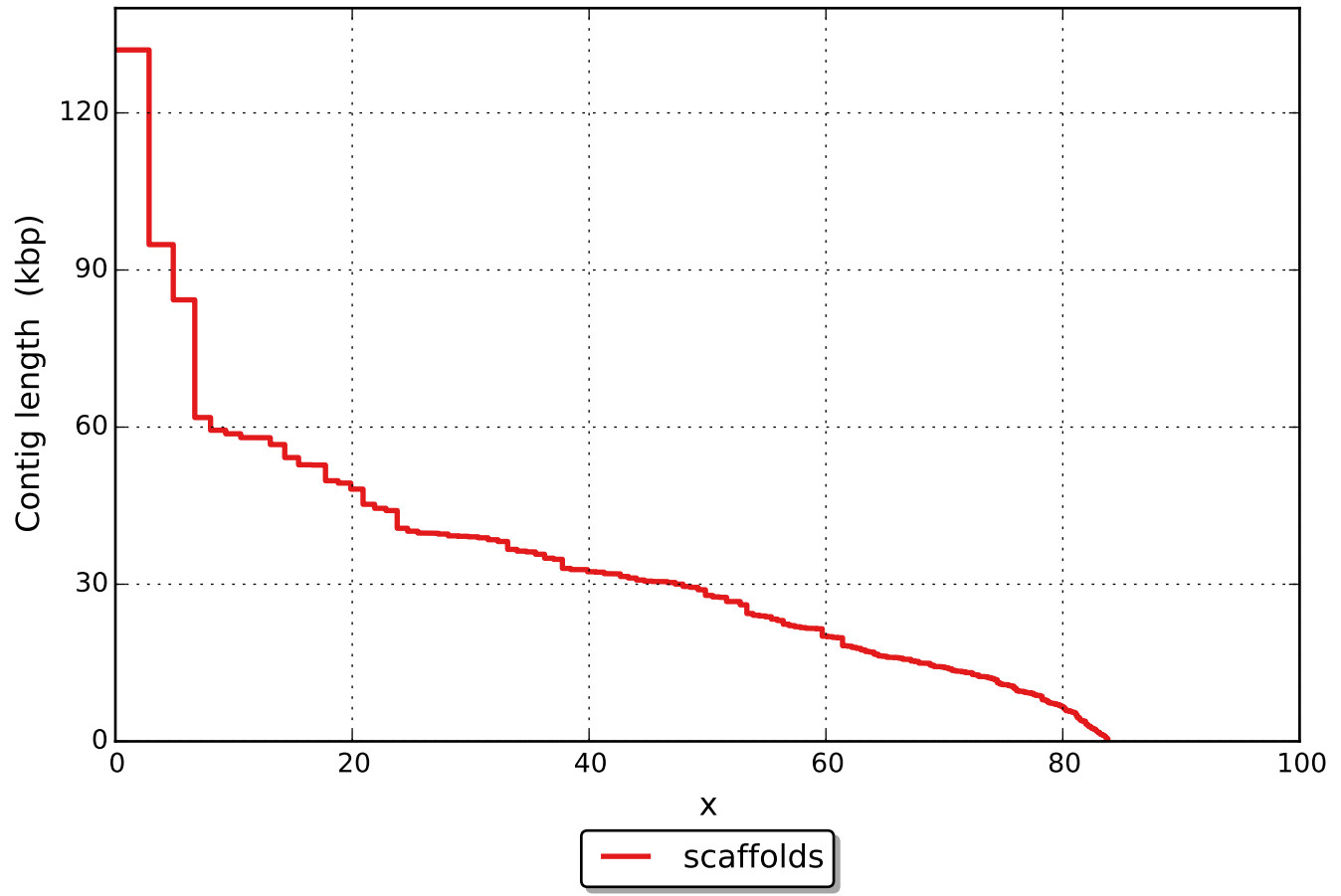
| | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 0 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 0 |
| # N's | 0 |

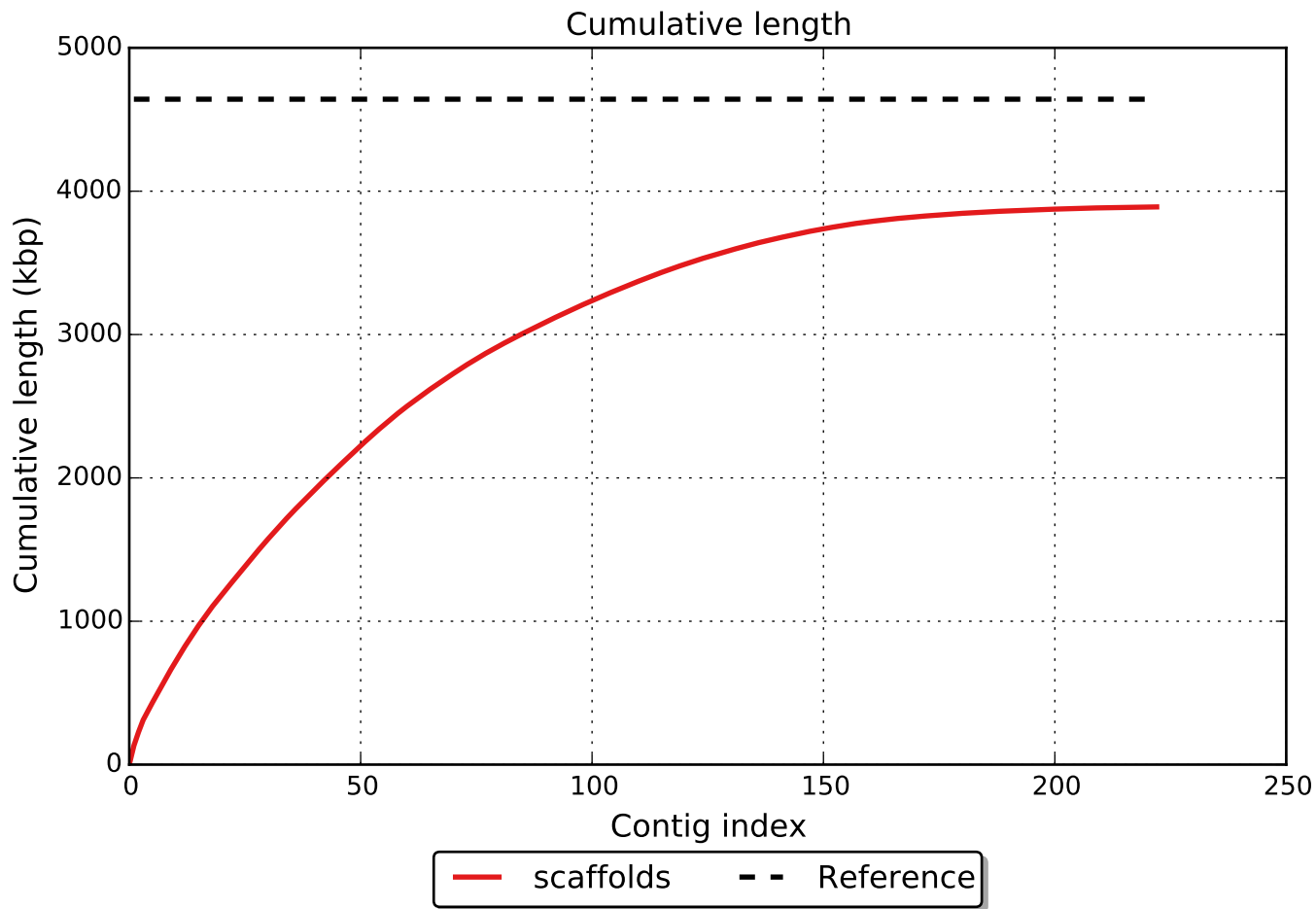
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

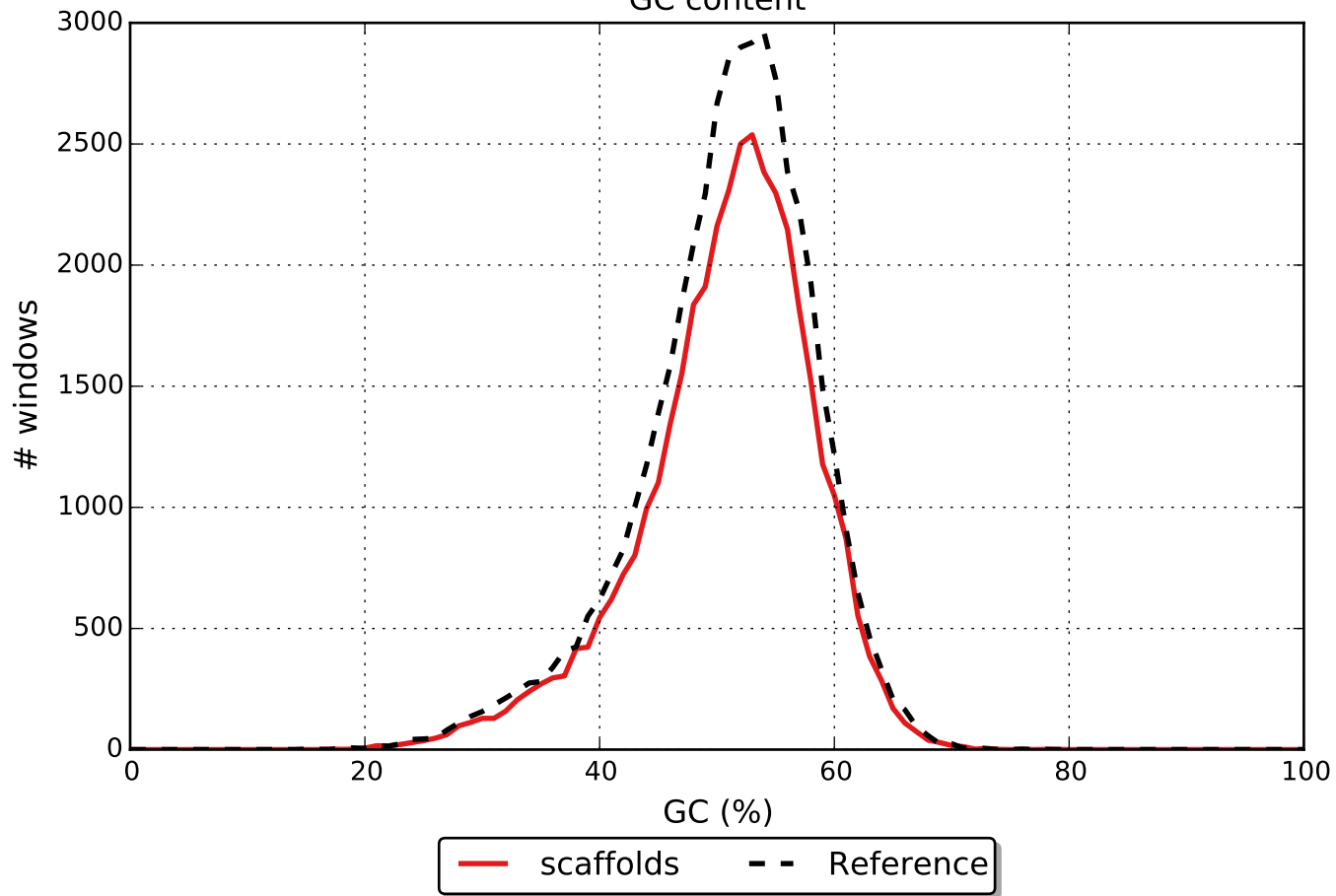


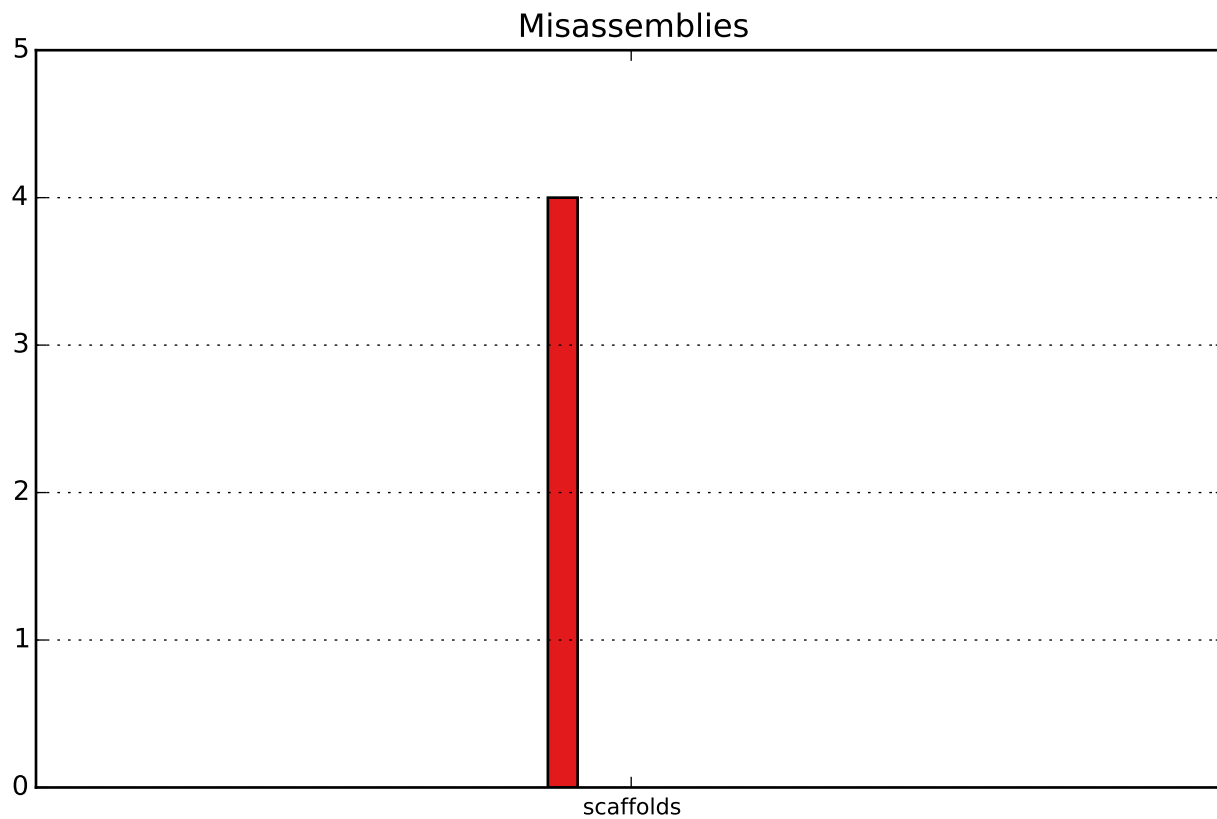
NGx



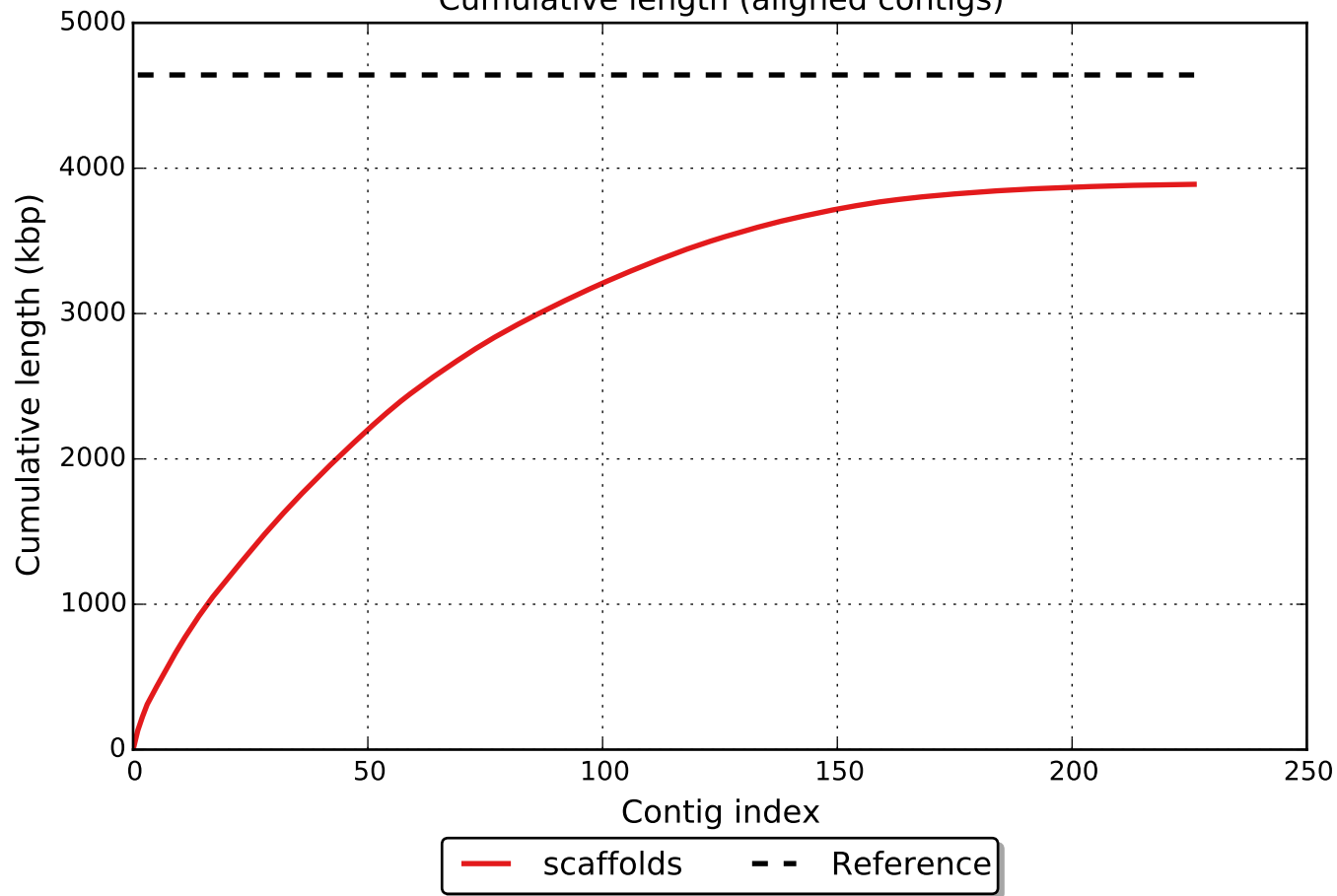


GC content

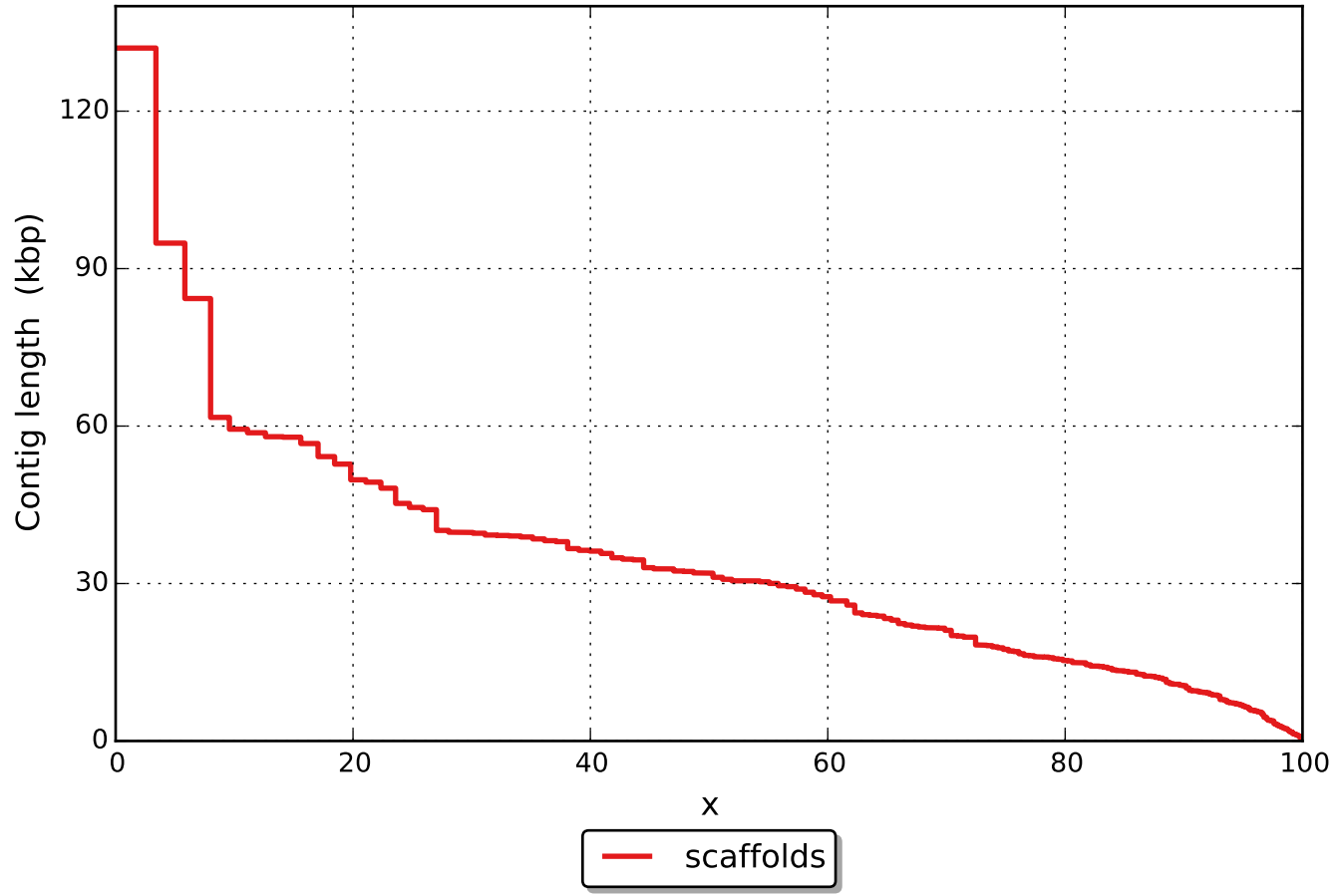




Cumulative length (aligned contigs)



NAx



NGAx

