

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 1000 bp) | 2 |
| # contigs (≥ 5000 bp) | 2 |
| # contigs (≥ 10000 bp) | 2 |
| # contigs (≥ 25000 bp) | 2 |
| # contigs (≥ 50000 bp) | 2 |
| Total length (≥ 1000 bp) | 239239 |
| Total length (≥ 5000 bp) | 239239 |
| Total length (≥ 10000 bp) | 239239 |
| Total length (≥ 25000 bp) | 239239 |
| Total length (≥ 50000 bp) | 239239 |
| # contigs | 3 |
| Largest contig | 132163 |
| Total length | 239986 |
| Reference length | 4641652 |
| GC (%) | 51.37 |
| Reference GC (%) | 50.78 |
| N50 | 132163 |
| N75 | 107076 |
| L50 | 1 |
| L75 | 2 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # unaligned contigs | 0 + 2 part |
| Unaligned length | 231676 |
| Genome fraction (%) | 0.177 |
| Duplication ratio | 1.014 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 4794.44 |
| # indels per 100 kbp | 12.20 |
| Largest alignment | 5170 |
| NGA50 | - |

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

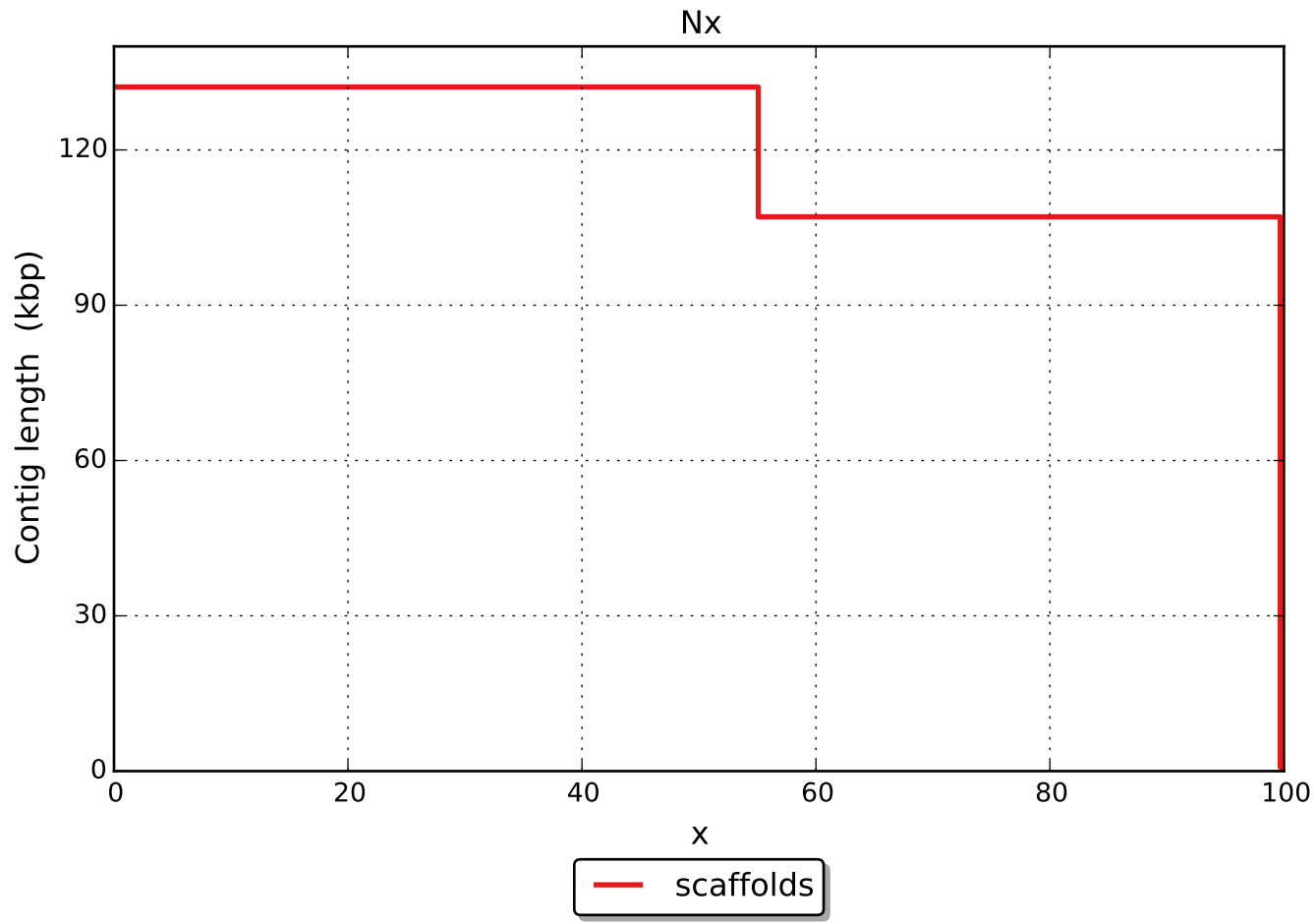
| | scaffolds |
|---------------------------------|-----------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 2 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # mismatches | 393 |
| # indels | 1 |
| # short indels | 1 |
| # long indels | 0 |
| Indels length | 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).

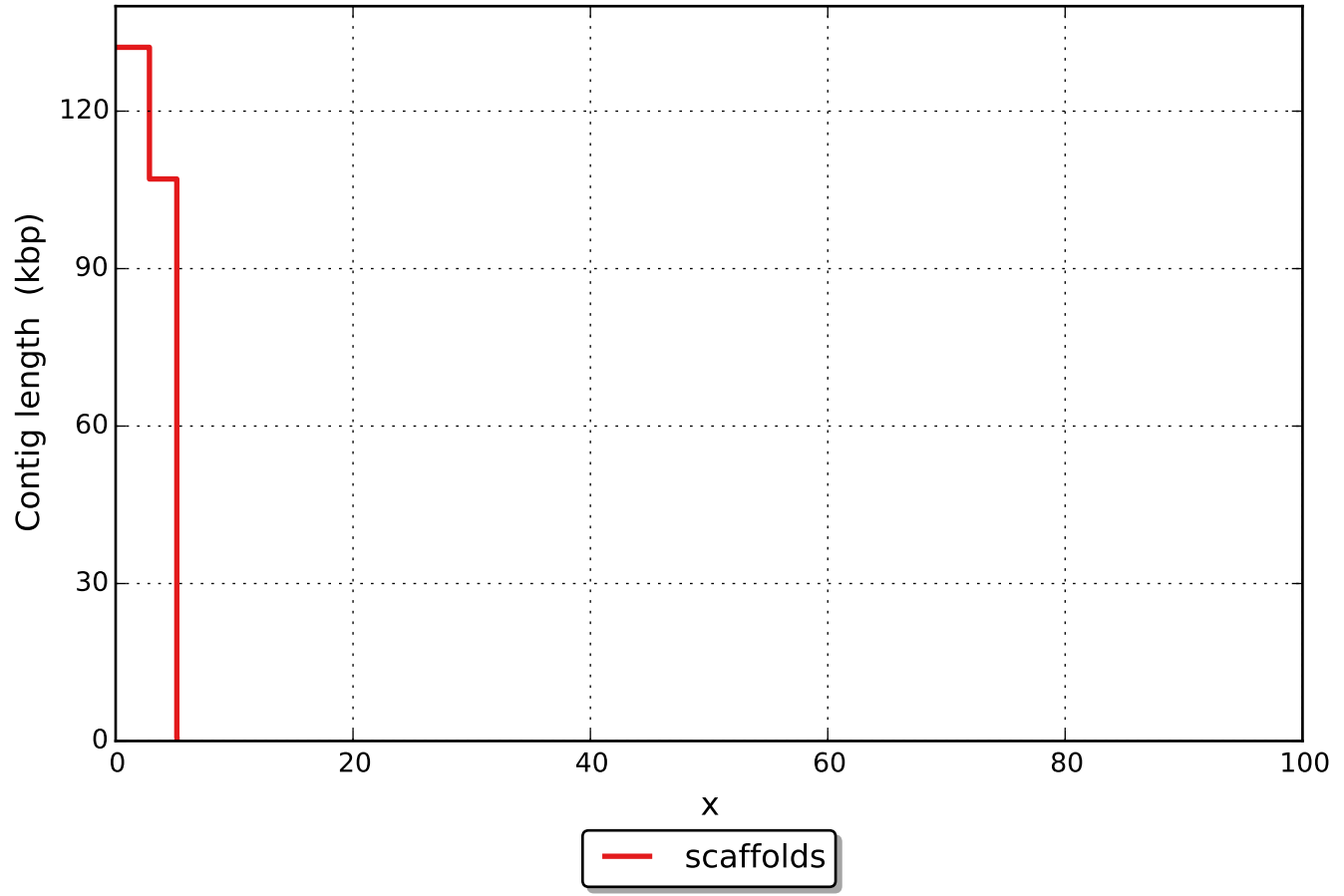
Unaligned report

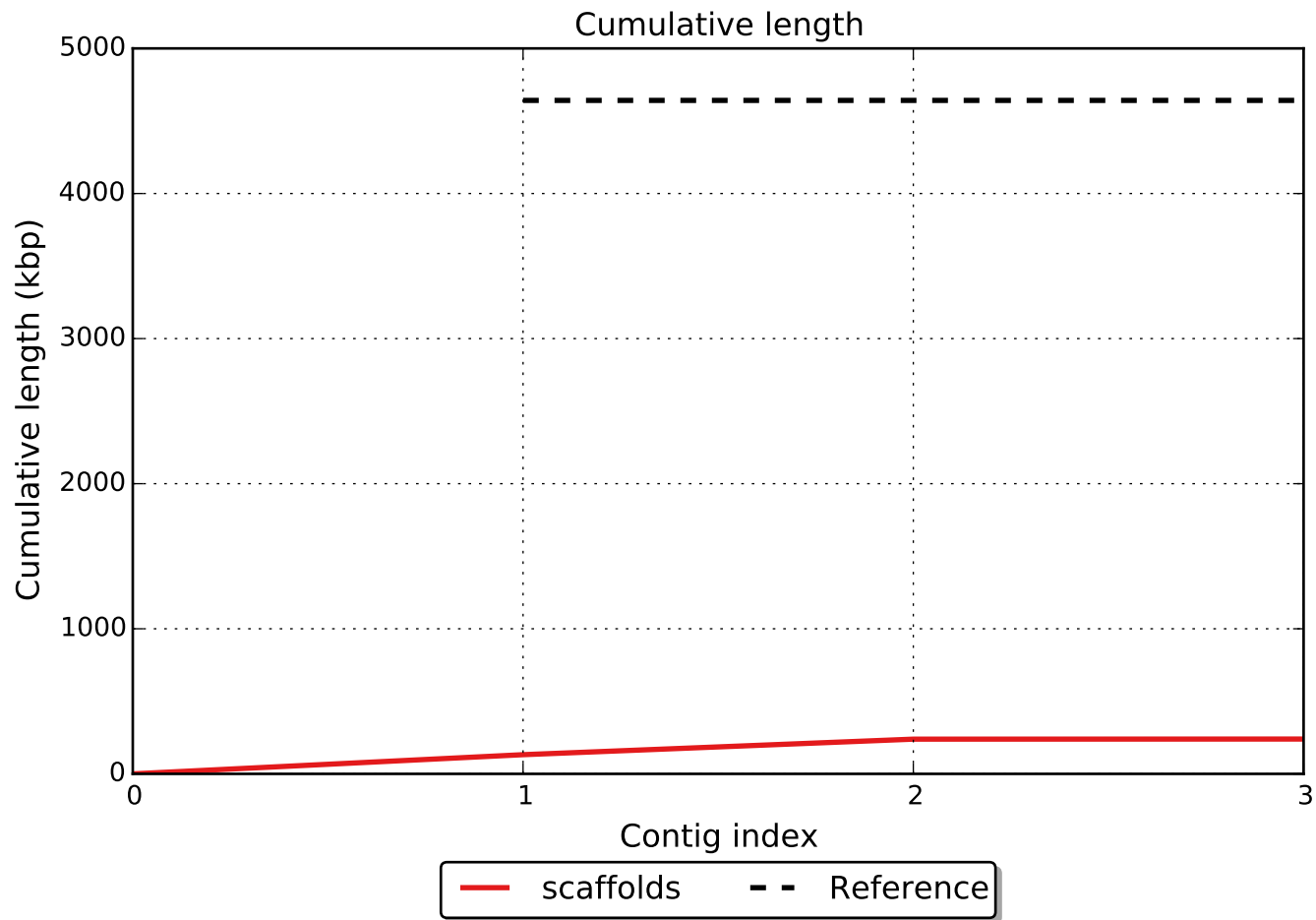
| | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs | 0 |
| Fully unaligned length | 0 |
| # partially unaligned contigs | 2 |
| # with misassembly | 2 |
| # both parts are significant | 2 |
| Partially unaligned length | 231676 |
| # N's | 0 |

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).

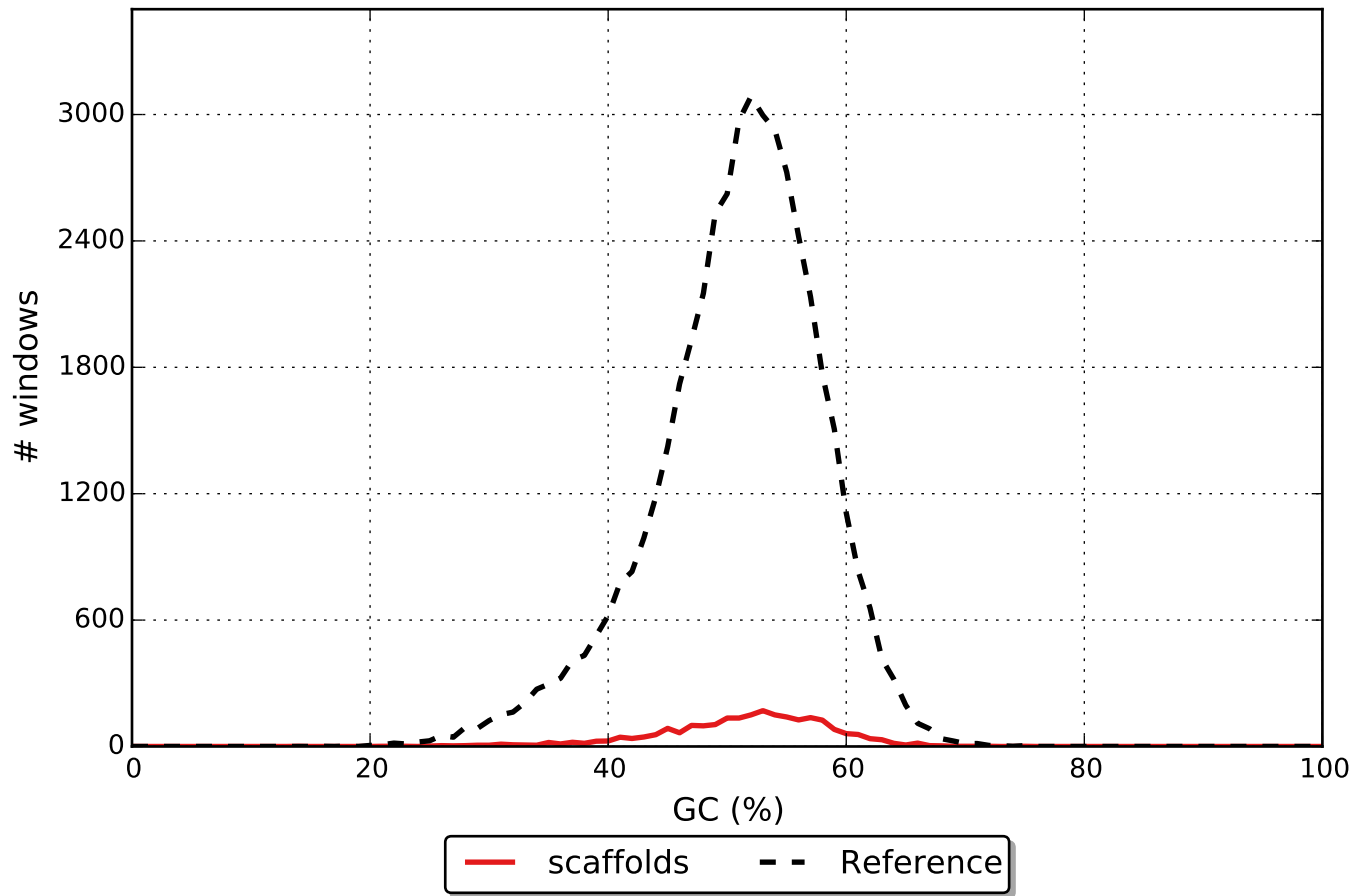


NGx

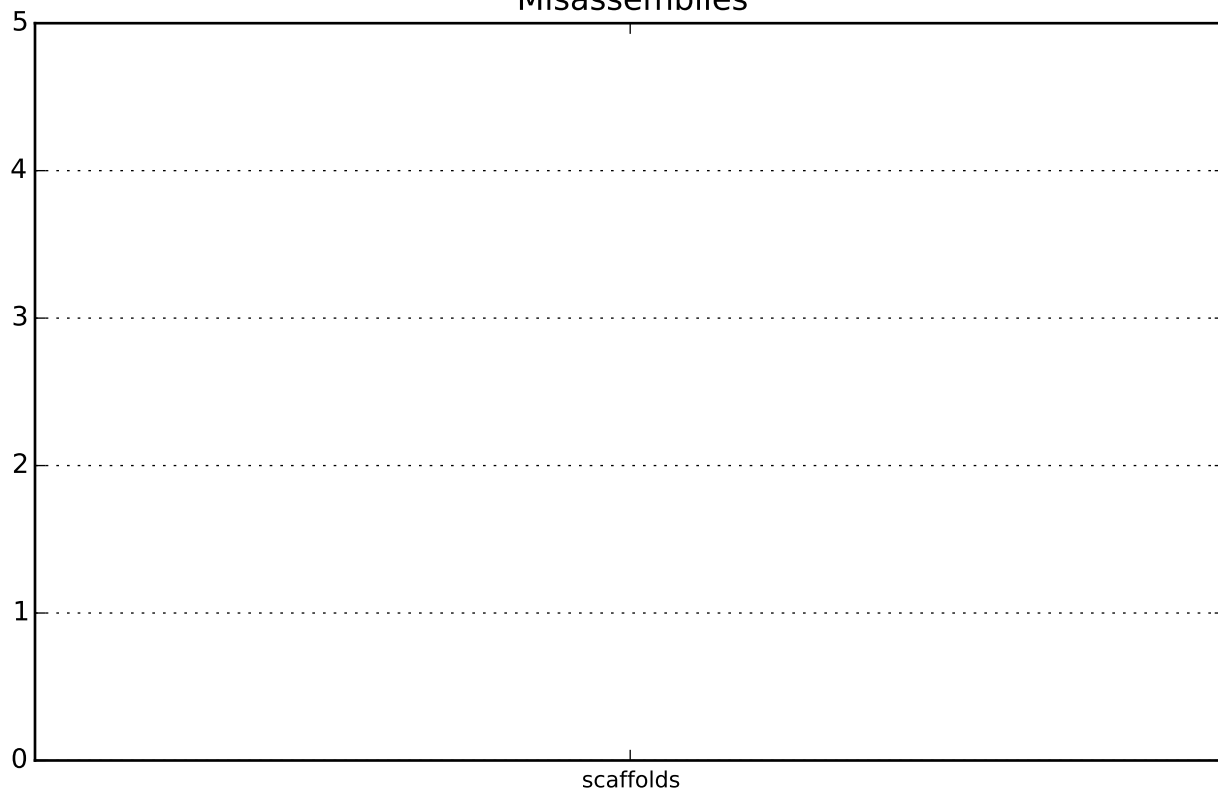




GC content



Misassemblies



Cumulative length (aligned contigs)

