

Report

| | scaffolds |
|---------------------------------|------------|
| # contigs (≥ 1000 bp) | 205 |
| # contigs (≥ 5000 bp) | 58 |
| # contigs (≥ 10000 bp) | 26 |
| # contigs (≥ 25000 bp) | 4 |
| # contigs (≥ 50000 bp) | 0 |
| Total length (≥ 1000 bp) | 1022627 |
| Total length (≥ 5000 bp) | 717912 |
| Total length (≥ 10000 bp) | 490228 |
| Total length (≥ 25000 bp) | 148504 |
| Total length (≥ 50000 bp) | 0 |
| # contigs | 333 |
| Largest contig | 46453 |
| Total length | 1109156 |
| Reference length | 4641652 |
| GC (%) | 50.59 |
| Reference GC (%) | 50.79 |
| N50 | 8143 |
| N75 | 3190 |
| L50 | 34 |
| L75 | 88 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 3 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 23.628 |
| Duplication ratio | 1.011 |
| # N's per 100 kbp | 654.19 |
| # mismatches per 100 kbp | 842.58 |
| # indels per 100 kbp | 2.74 |
| Largest alignment | 43816 |
| NA50 | 8143 |
| NGA50 | - |
| NA75 | 3114 |
| LA50 | 34 |
| LA75 | 90 |

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

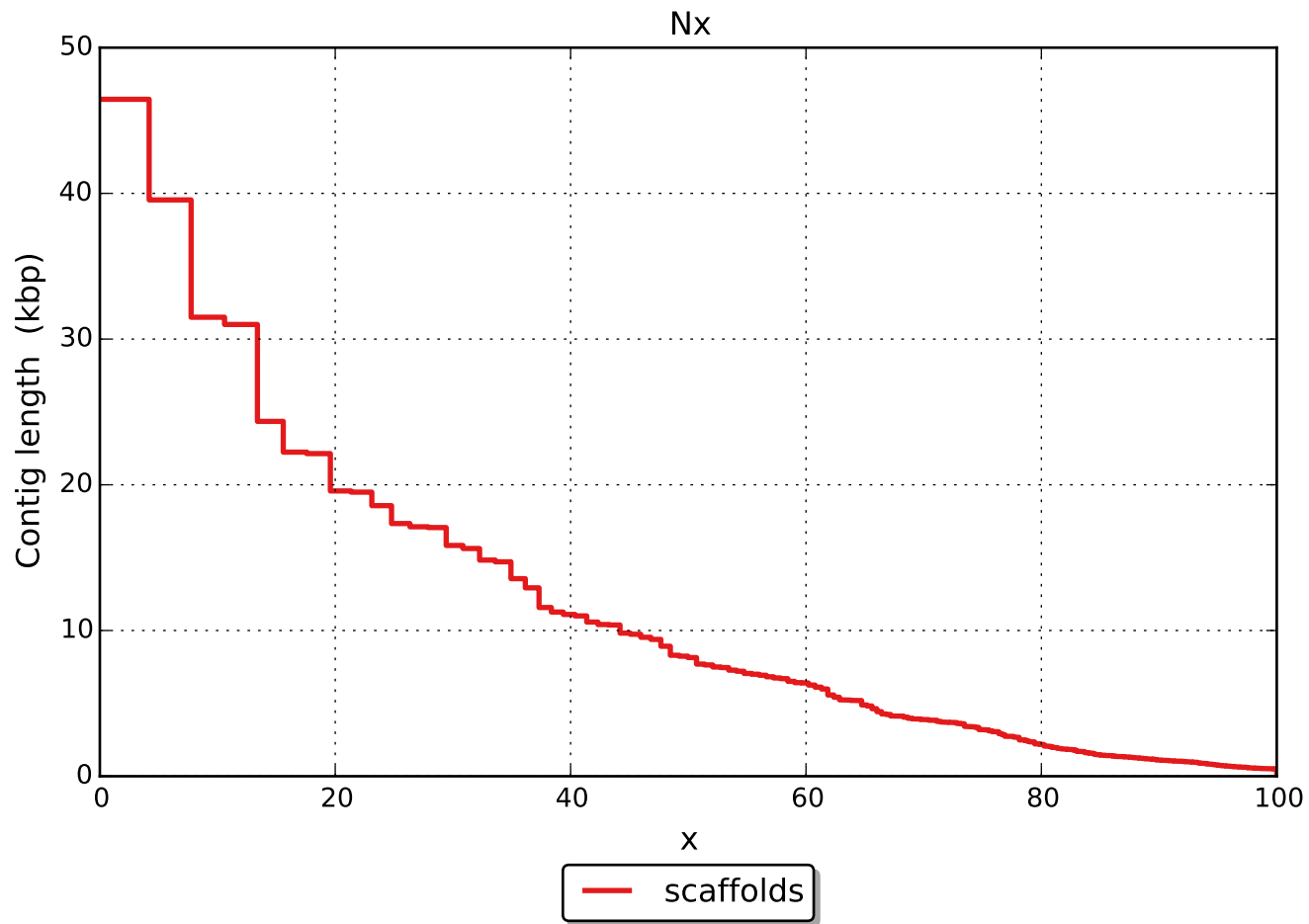
| | scaffolds |
|---------------------------------|-----------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 5 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 3 |
| # mismatches | 9241 |
| # indels | 30 |
| # short indels | 10 |
| # long indels | 20 |
| Indels length | 1110 |

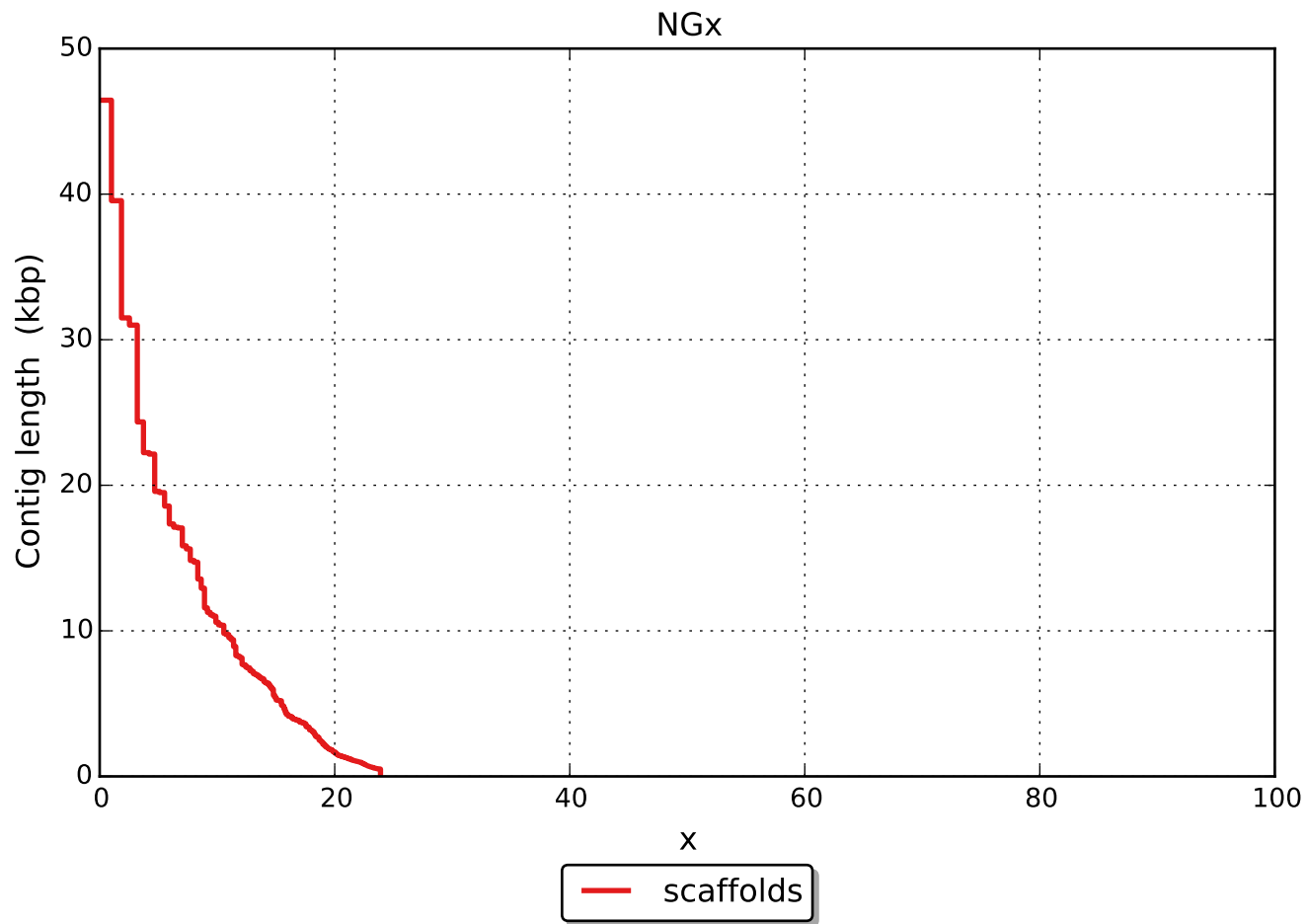
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

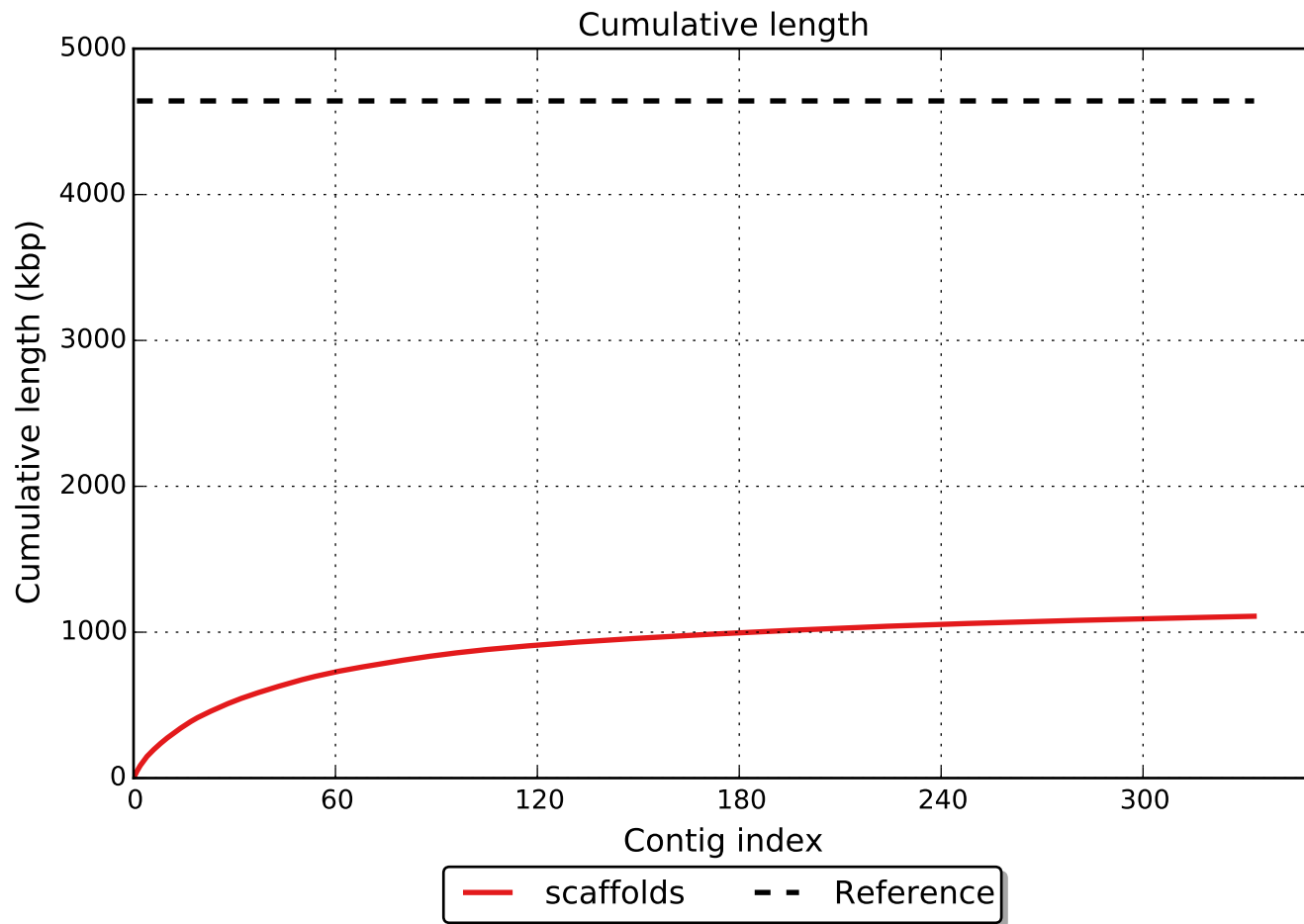
Unaligned report

| | 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 | 7256 |

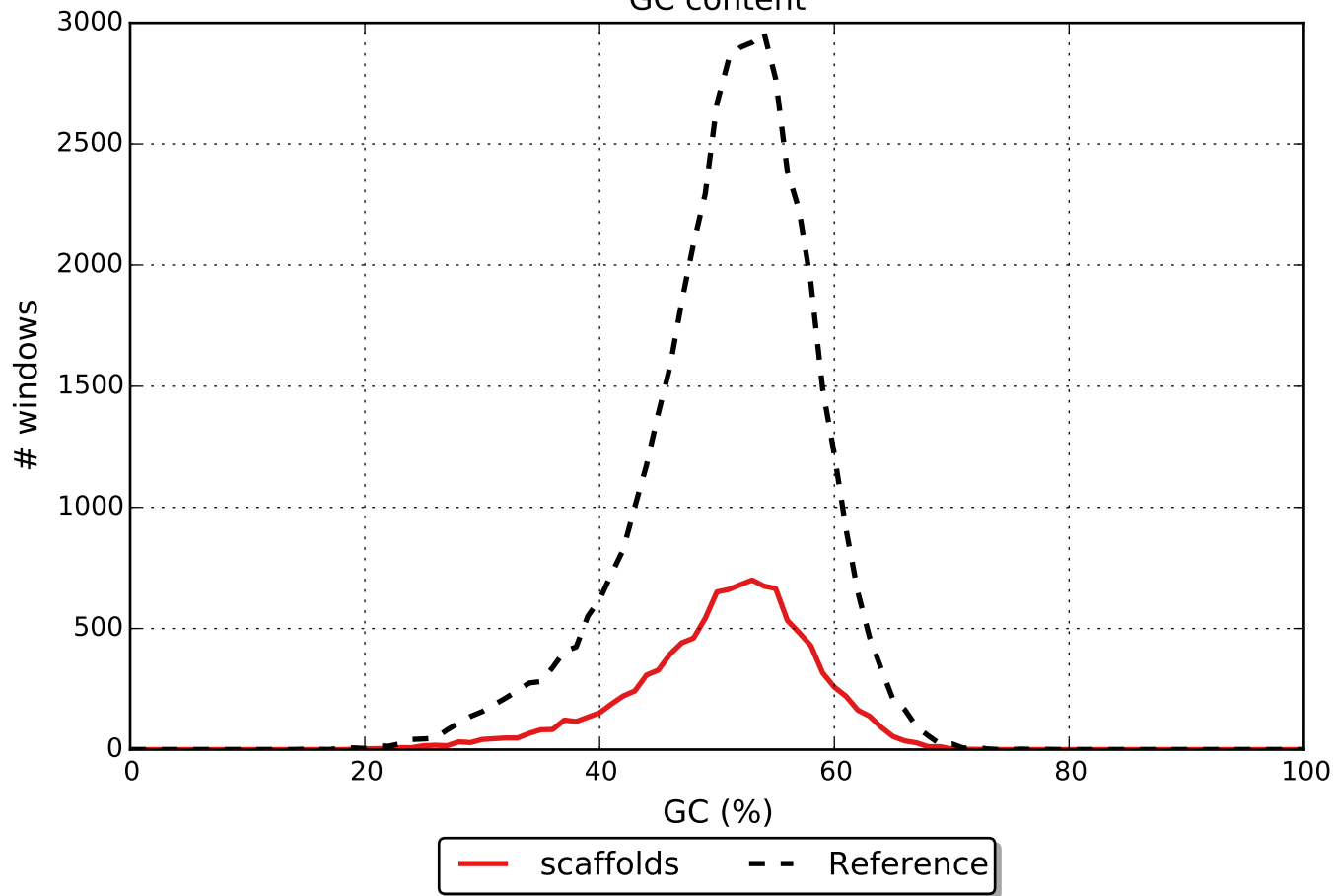
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







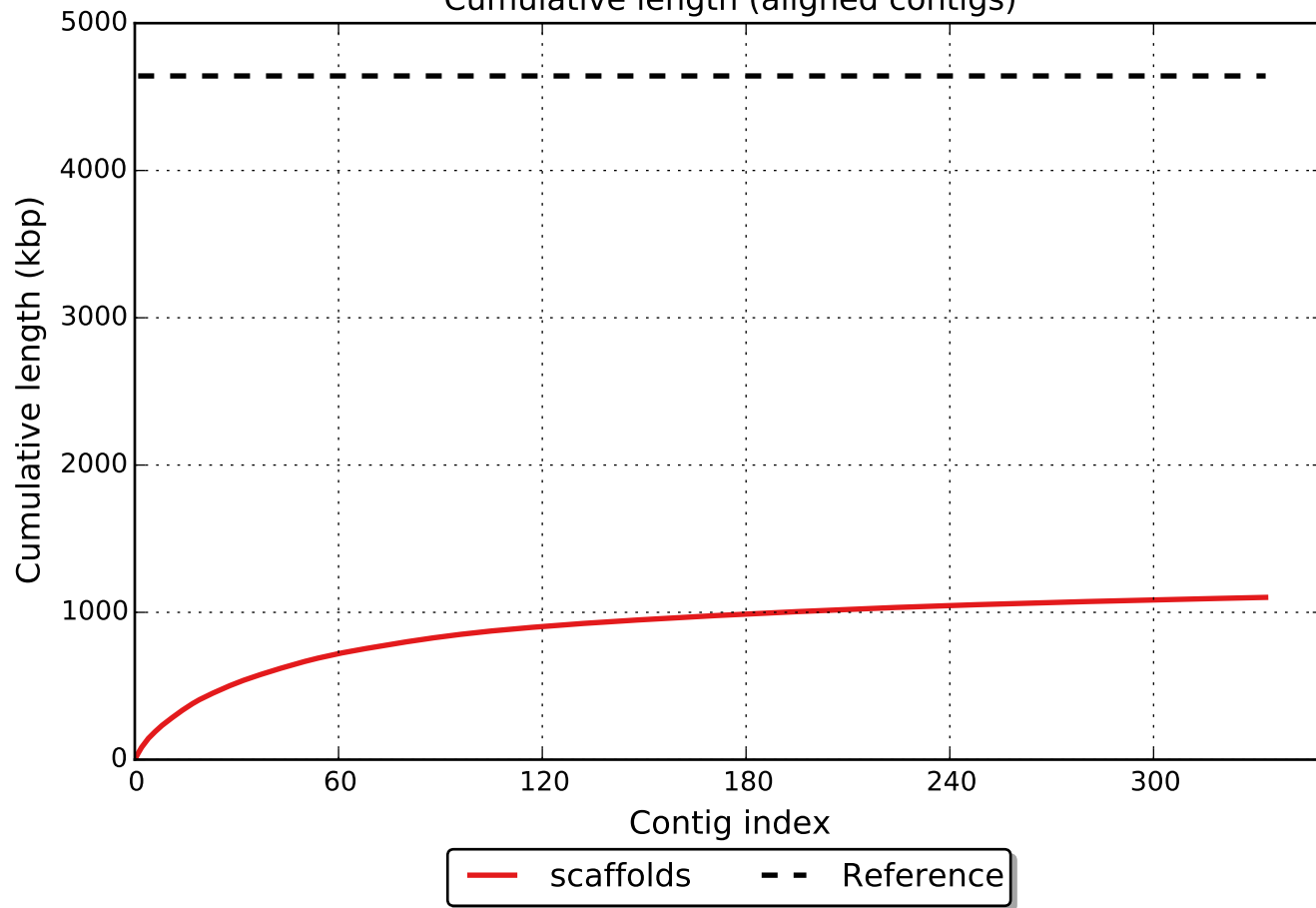
GC content

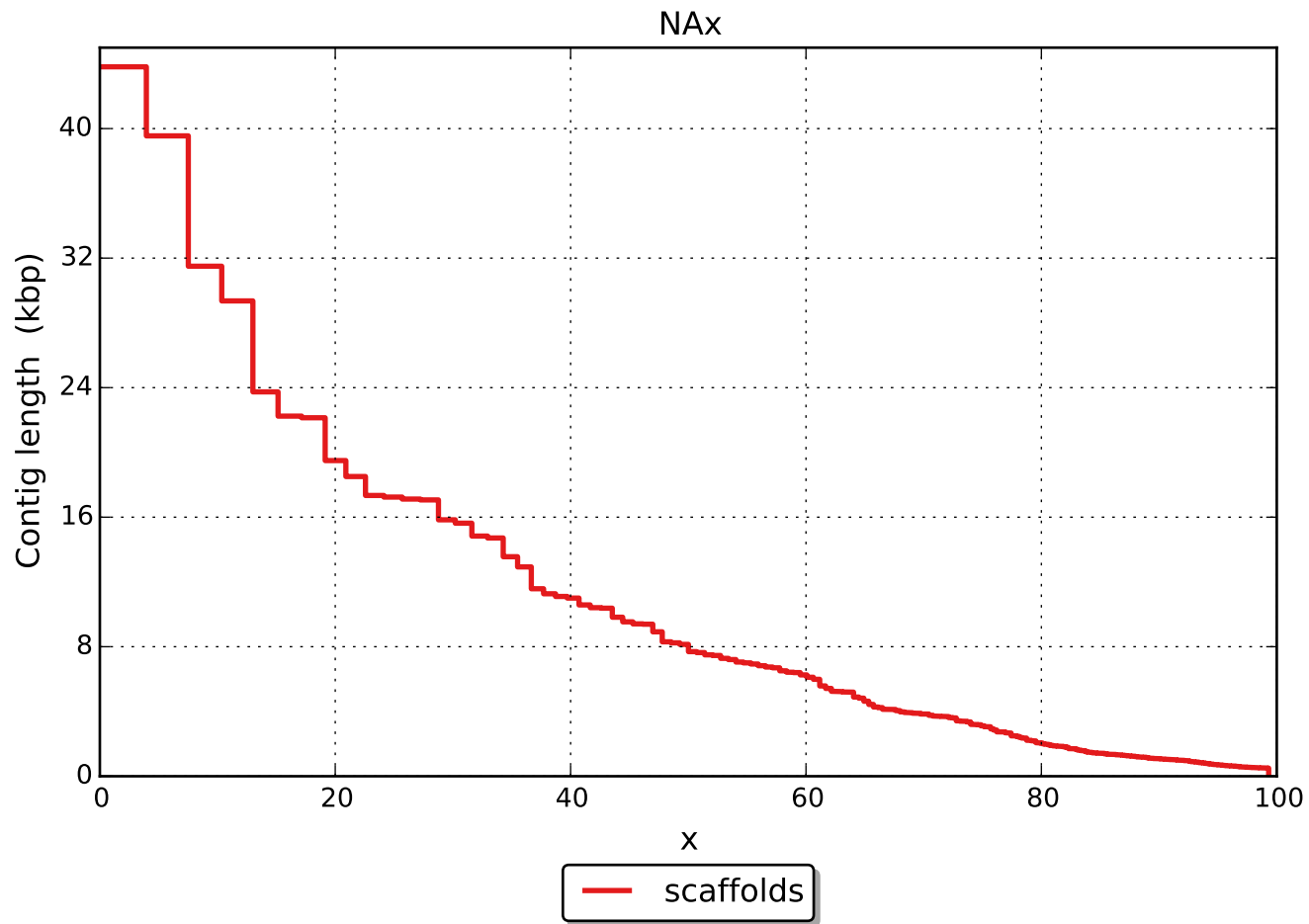


Misassemblies



Cumulative length (aligned contigs)





NGAx

