

## Report

|                                 | scaffolds   |
|---------------------------------|-------------|
| # contigs ( $\geq 0$ bp)        | 408         |
| # contigs ( $\geq 1000$ bp)     | 142         |
| # contigs ( $\geq 5000$ bp)     | 94          |
| # contigs ( $\geq 10000$ bp)    | 90          |
| # contigs ( $\geq 25000$ bp)    | 77          |
| # contigs ( $\geq 50000$ bp)    | 54          |
| Total length ( $\geq 0$ bp)     | 9004717     |
| Total length ( $\geq 1000$ bp)  | 8899397     |
| Total length ( $\geq 5000$ bp)  | 8801812     |
| Total length ( $\geq 10000$ bp) | 8773143     |
| Total length ( $\geq 25000$ bp) | 8562938     |
| Total length ( $\geq 50000$ bp) | 7768873     |
| # contigs                       | 203         |
| Largest contig                  | 475325      |
| Total length                    | 8939282     |
| Reference length                | 9283304     |
| N50                             | 164261      |
| N75                             | 80872       |
| L50                             | 19          |
| L75                             | 39          |
| # misassemblies                 | 229         |
| # misassembled contigs          | 40          |
| Misassembled contigs length     | 4147330     |
| # local misassemblies           | 7           |
| # unaligned contigs             | 32 + 1 part |
| Unaligned length                | 21165       |
| Genome fraction (%)             | 49.495      |
| Duplication ratio               | 1.945       |
| # N's per 100 kbp               | 0.00        |
| # mismatches per 100 kbp        | 1166.57     |
| # indels per 100 kbp            | 1.68        |
| Largest alignment               | 475325      |
| NA50                            | 64354       |
| NA75                            | 23720       |
| LA50                            | 31          |
| LA75                            | 91          |

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

## Misassemblies report

|                                 | scaffolds |
|---------------------------------|-----------|
| # misassemblies                 | 229       |
| # relocations                   | 203       |
| # translocations                | 0         |
| # inversions                    | 22        |
| # interspecies translocations   | 4         |
| # possibly misassembled contigs | 3         |
| # misassembled contigs          | 40        |
| Misassembled contigs length     | 4147330   |
| # local misassemblies           | 7         |
| # mismatches                    | 53601     |
| # indels                        | 77        |
| # short indels                  | 75        |
| # long indels                   | 2         |
| Indels length                   | 100       |

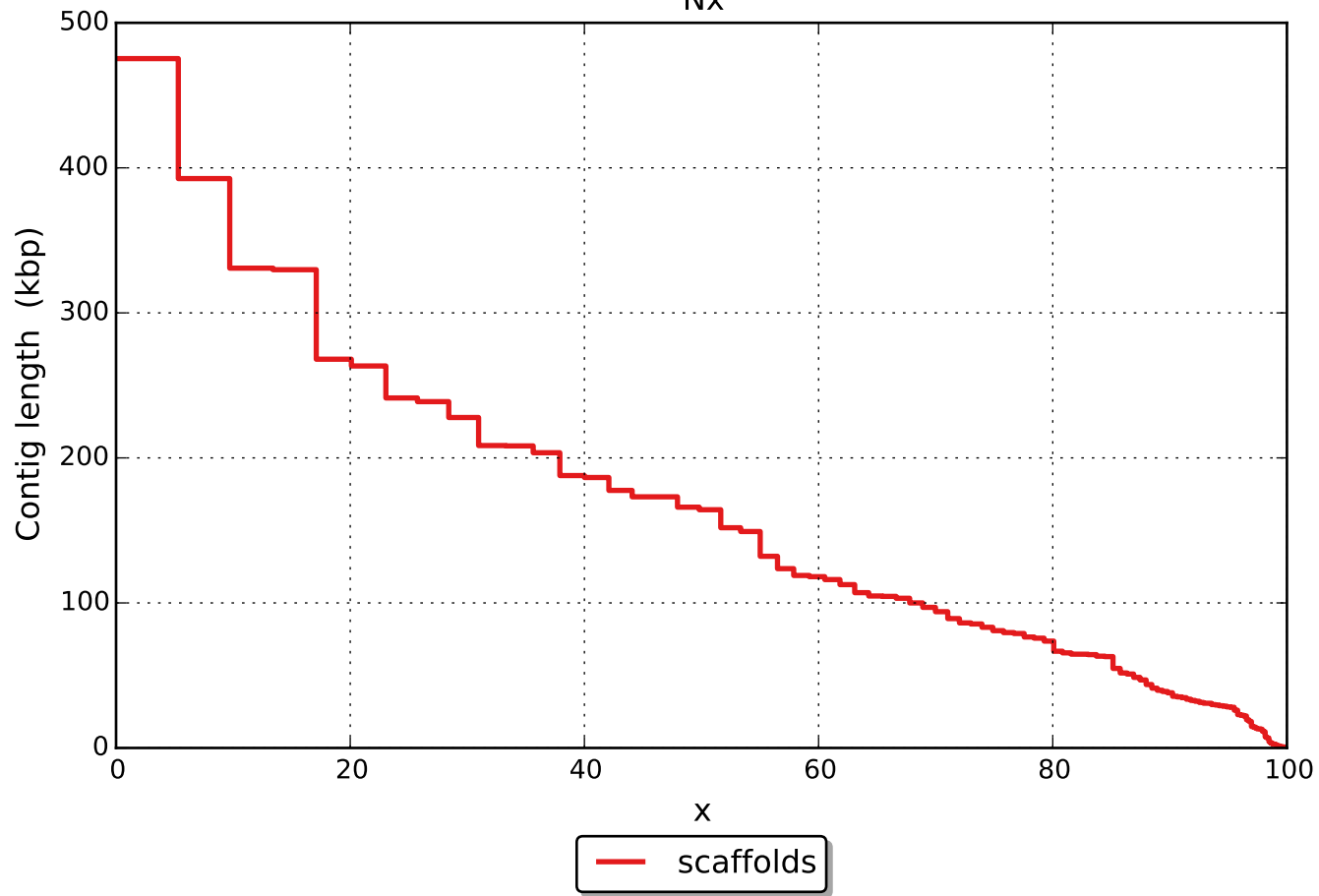
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

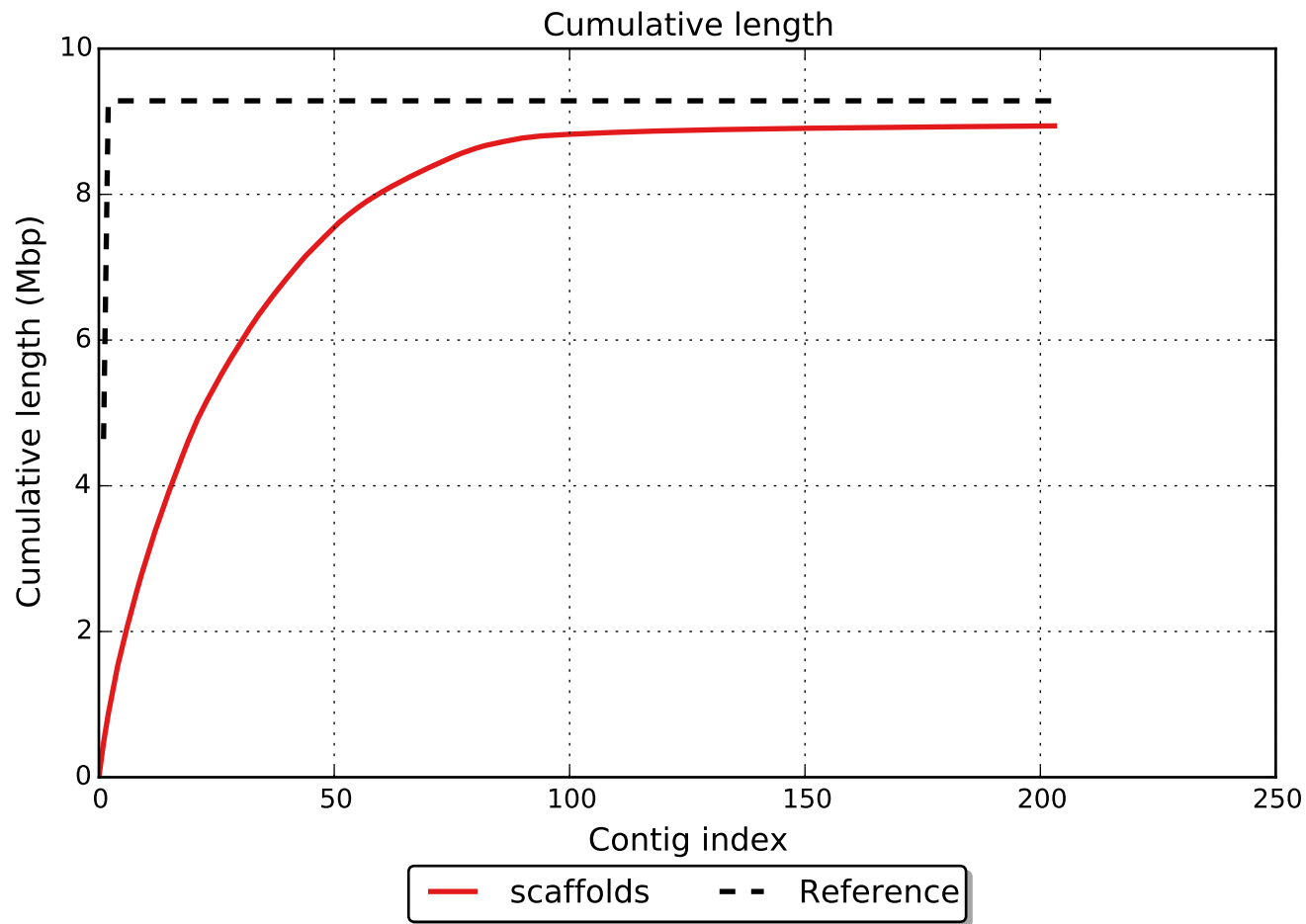
## Unaligned report

|                               | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs     | 32        |
| Fully unaligned length        | 20718     |
| # partially unaligned contigs | 1         |
| # with misassembly            | 0         |
| # both parts are significant  | 0         |
| Partially unaligned length    | 447       |
| # N's                         | 0         |

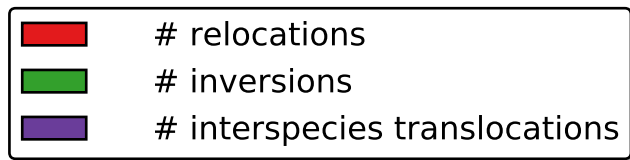
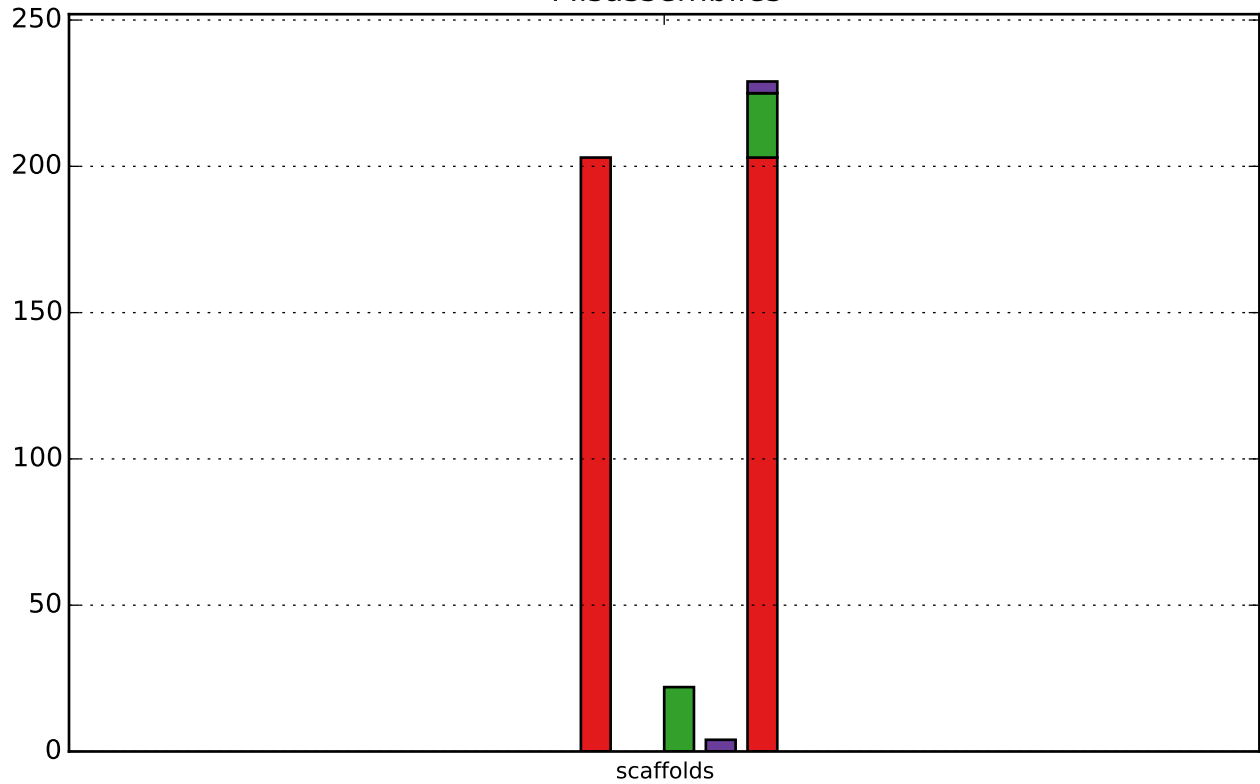
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

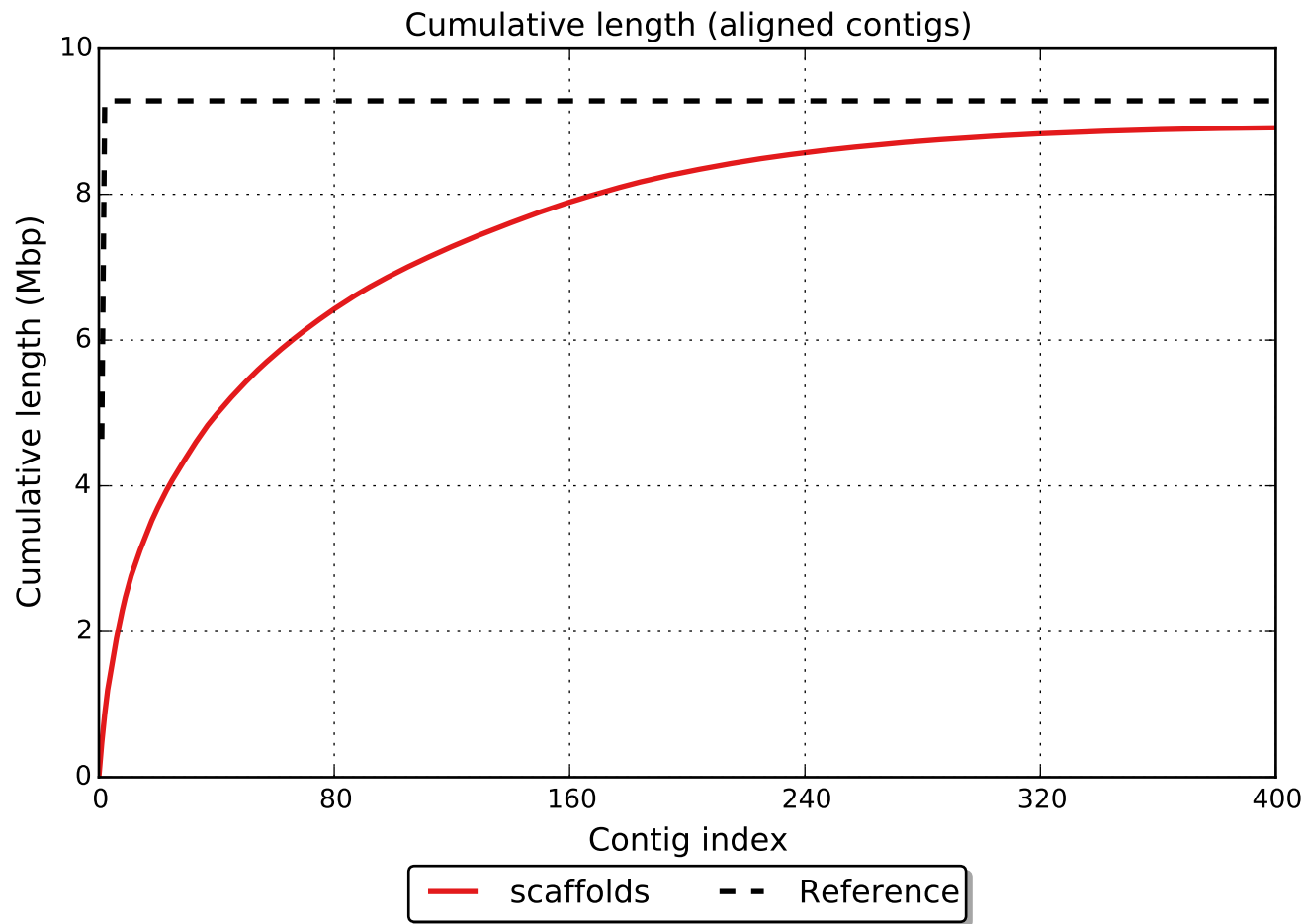
Nx



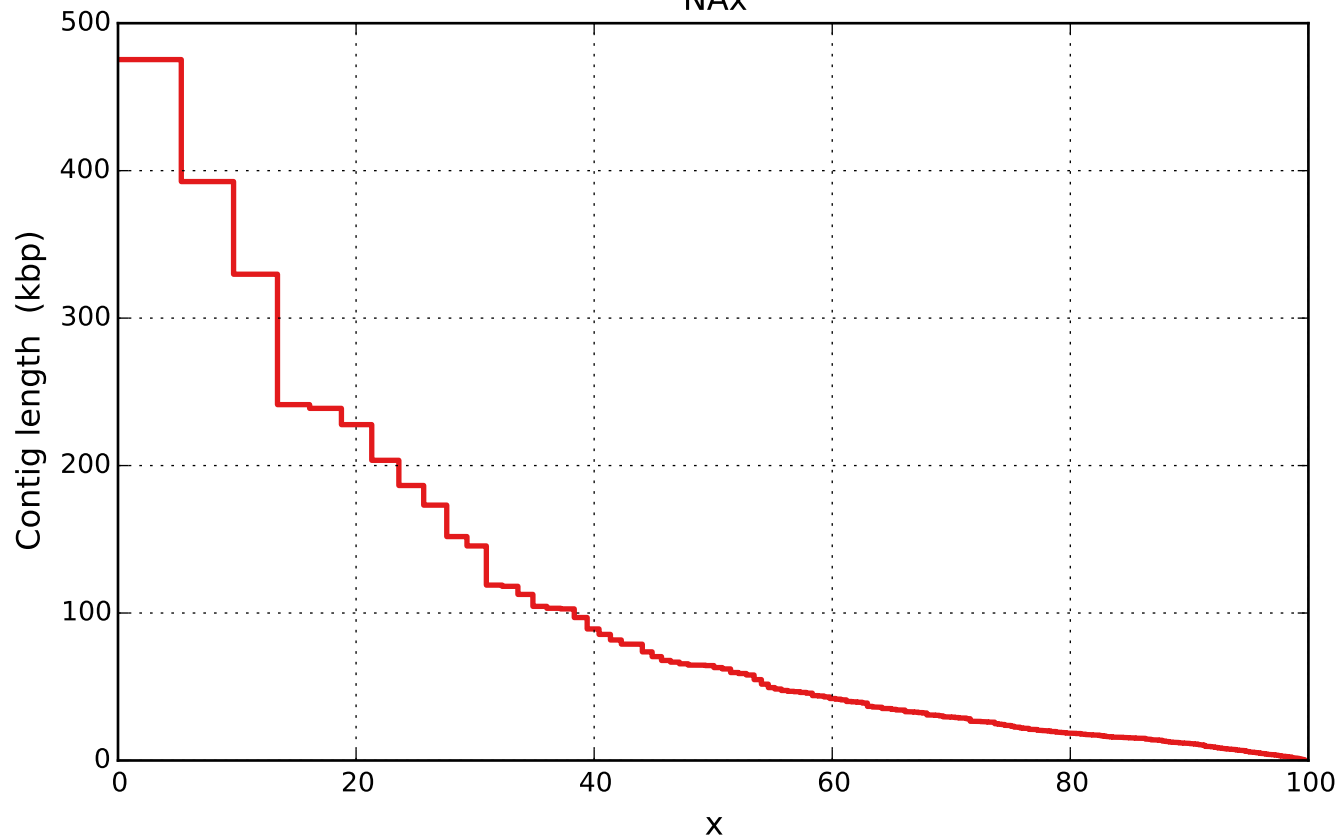


## Misassemblies





NAx



— scaffolds