

## Report

|                                 | final.contigs |
|---------------------------------|---------------|
| # contigs ( $\geq 1000$ bp)     | 46            |
| # contigs ( $\geq 5000$ bp)     | 2             |
| # contigs ( $\geq 10000$ bp)    | 0             |
| # contigs ( $\geq 25000$ bp)    | 0             |
| # contigs ( $\geq 50000$ bp)    | 0             |
| Total length ( $\geq 1000$ bp)  | 91262         |
| Total length ( $\geq 5000$ bp)  | 17269         |
| Total length ( $\geq 10000$ bp) | 0             |
| Total length ( $\geq 25000$ bp) | 0             |
| Total length ( $\geq 50000$ bp) | 0             |
| # contigs                       | 524           |
| Largest contig                  | 9290          |
| Total length                    | 403236        |
| Reference length                | 2627046       |
| GC (%)                          | 59.77         |
| Reference GC (%)                | 57.63         |
| N50                             | 705           |
| N75                             | 583           |
| L50                             | 181           |
| L75                             | 339           |
| # misassemblies                 | 1             |
| # misassembled contigs          | 1             |
| Misassembled contigs length     | 986           |
| # local misassemblies           | 0             |
| # unaligned mis. contigs        | 1             |
| # unaligned contigs             | 0 + 20 part   |
| Unaligned length                | 47359         |
| Genome fraction (%)             | 13.164        |
| Duplication ratio               | 1.029         |
| # N's per 100 kbp               | 0.00          |
| # mismatches per 100 kbp        | 2870.80       |
| # indels per 100 kbp            | 24.87         |
| Largest alignment               | 4519          |
| Total aligned length            | 349658        |
| NA50                            | 629           |
| NGA50                           | -             |
| NA75                            | 538           |
| LA50                            | 241           |
| LA75                            | 416           |

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

|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 1             |
| # relocations                   | 1             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # interspecies translocations   | 0             |
| # misassembled contigs          | 1             |
| Misassembled contigs length     | 986           |
| # possibly misassembled contigs | 1             |
| # possible misassemblies        | 1             |
| # local misassemblies           | 0             |
| # unaligned mis. contigs        | 1             |
| # mismatches                    | 9928          |
| # indels                        | 86            |
| # indels (<= 5 bp)              | 84            |
| # indels (> 5 bp)               | 2             |
| Indels length                   | 131           |

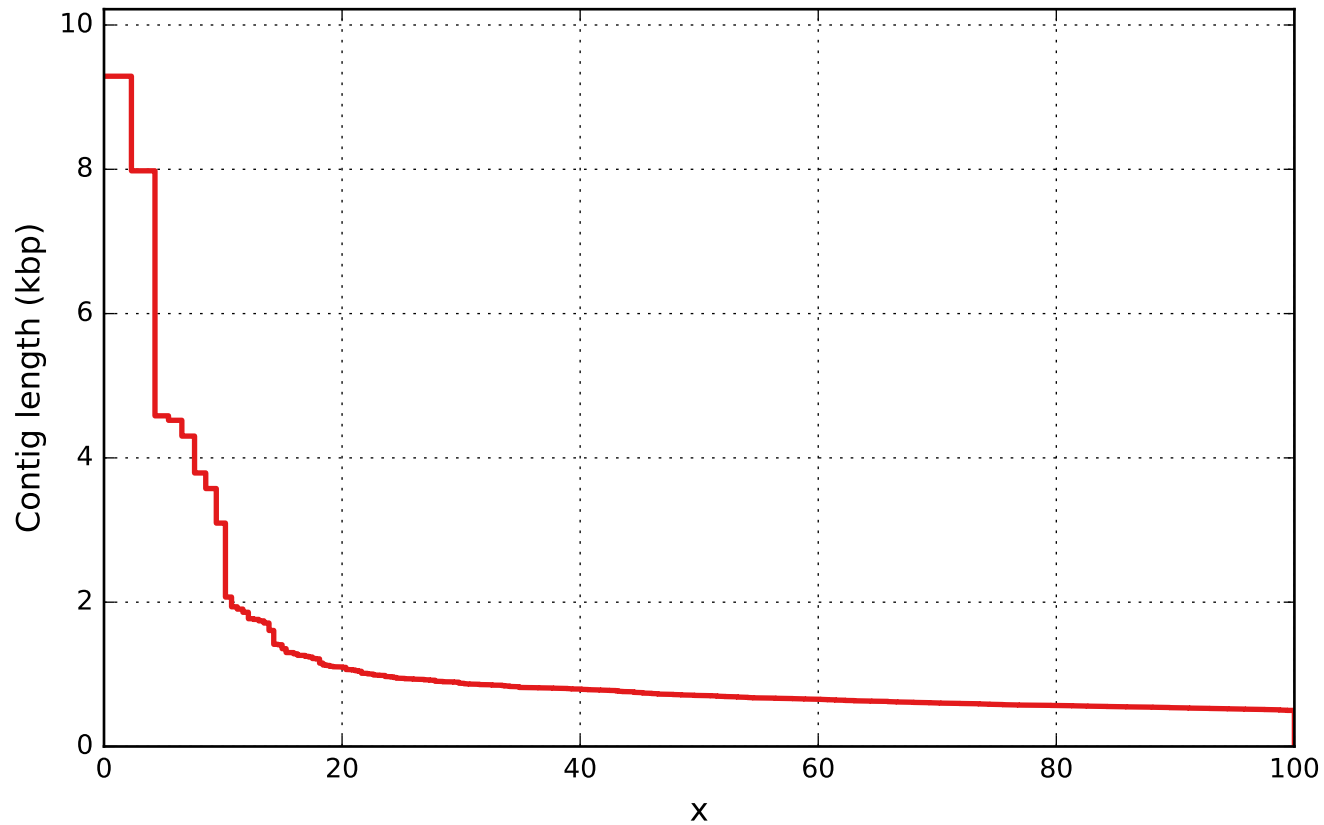
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 20            |
| Partially unaligned length    | 47359         |
| # N's                         | 0             |

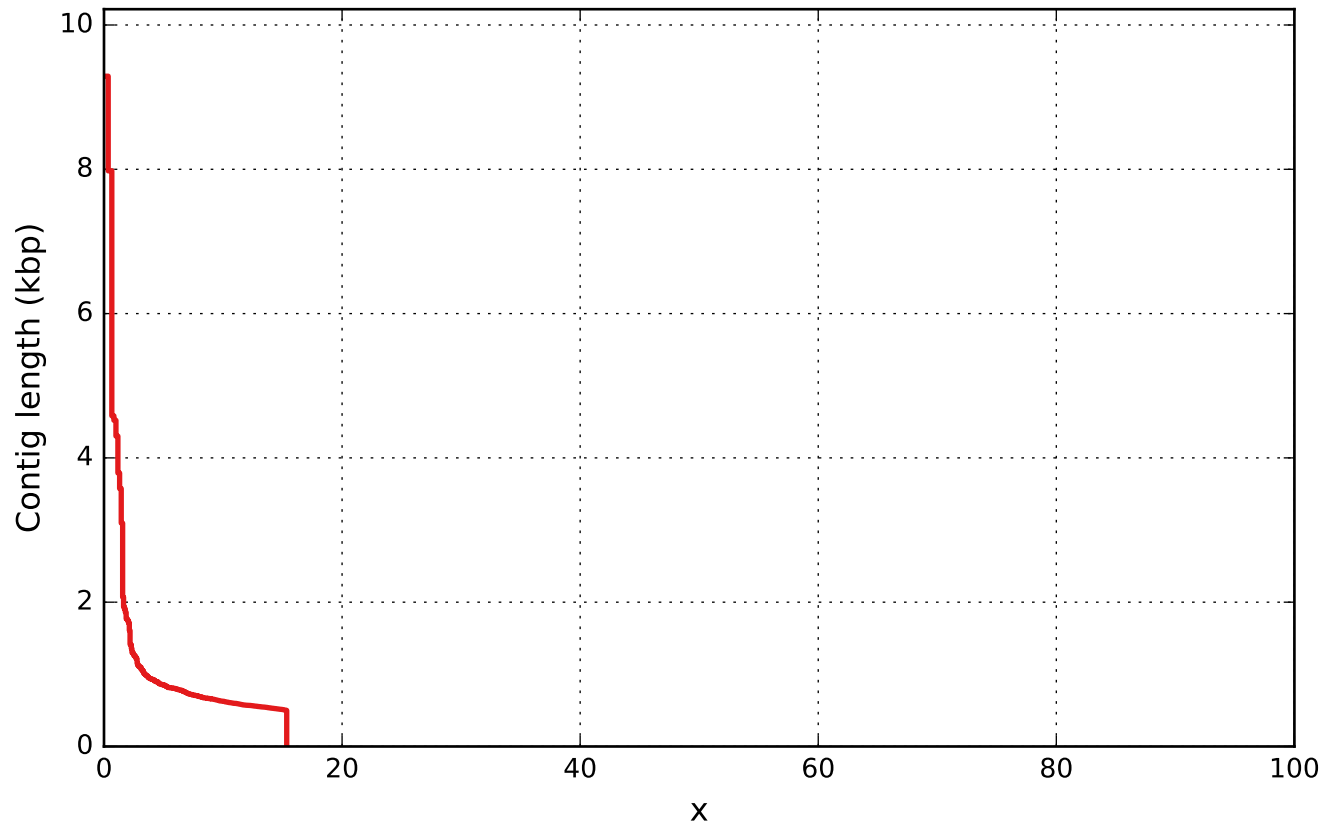
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

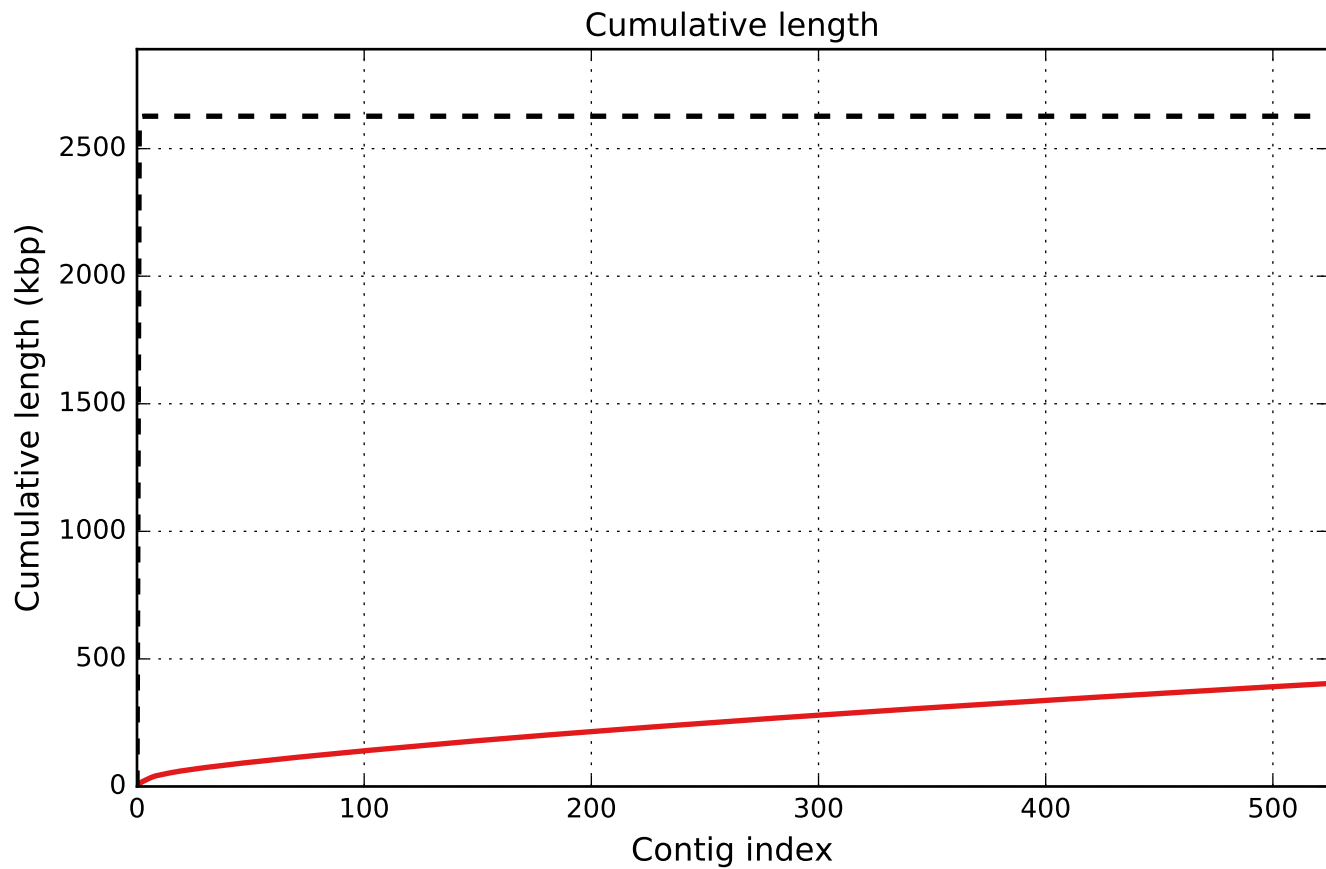


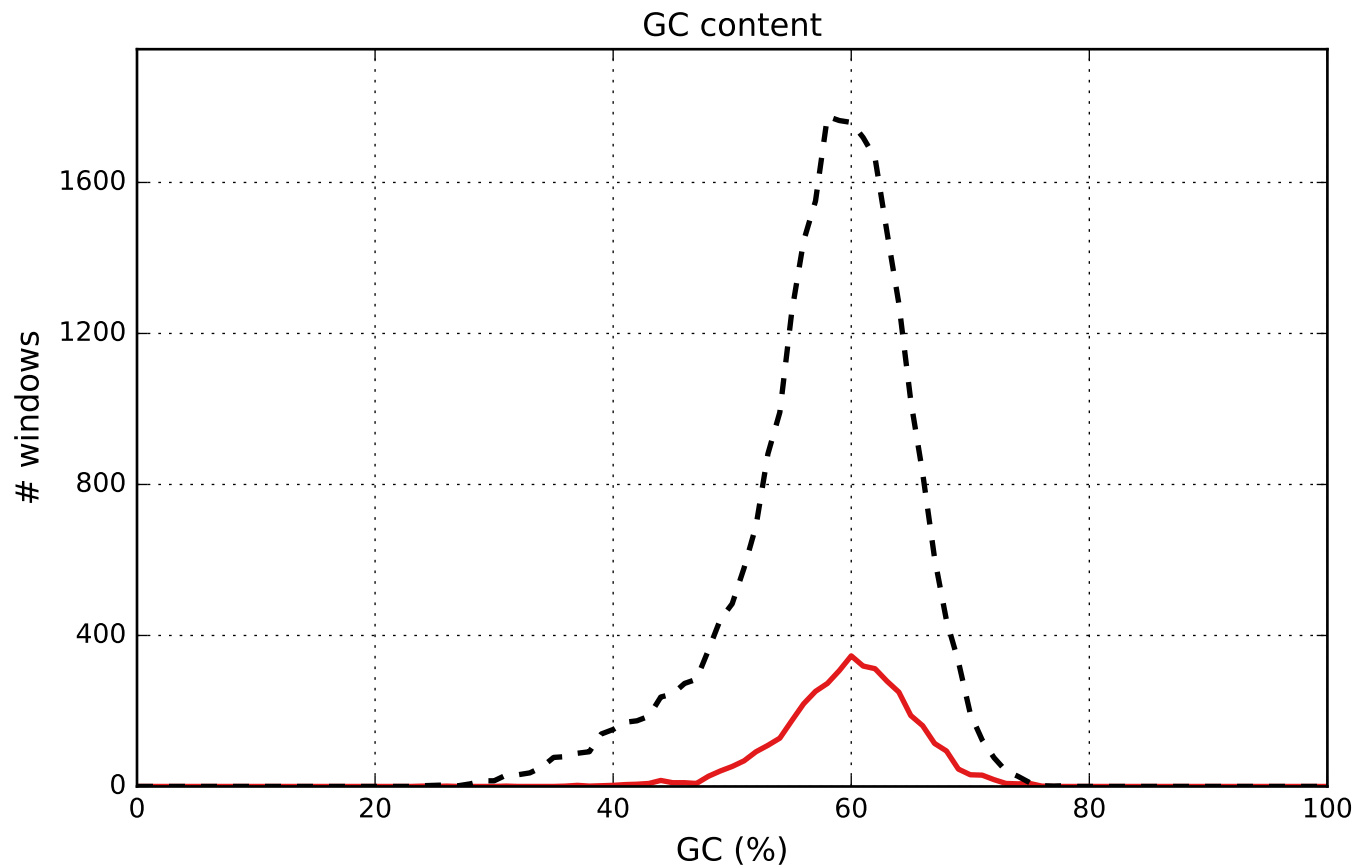
— final.contigs

NGx

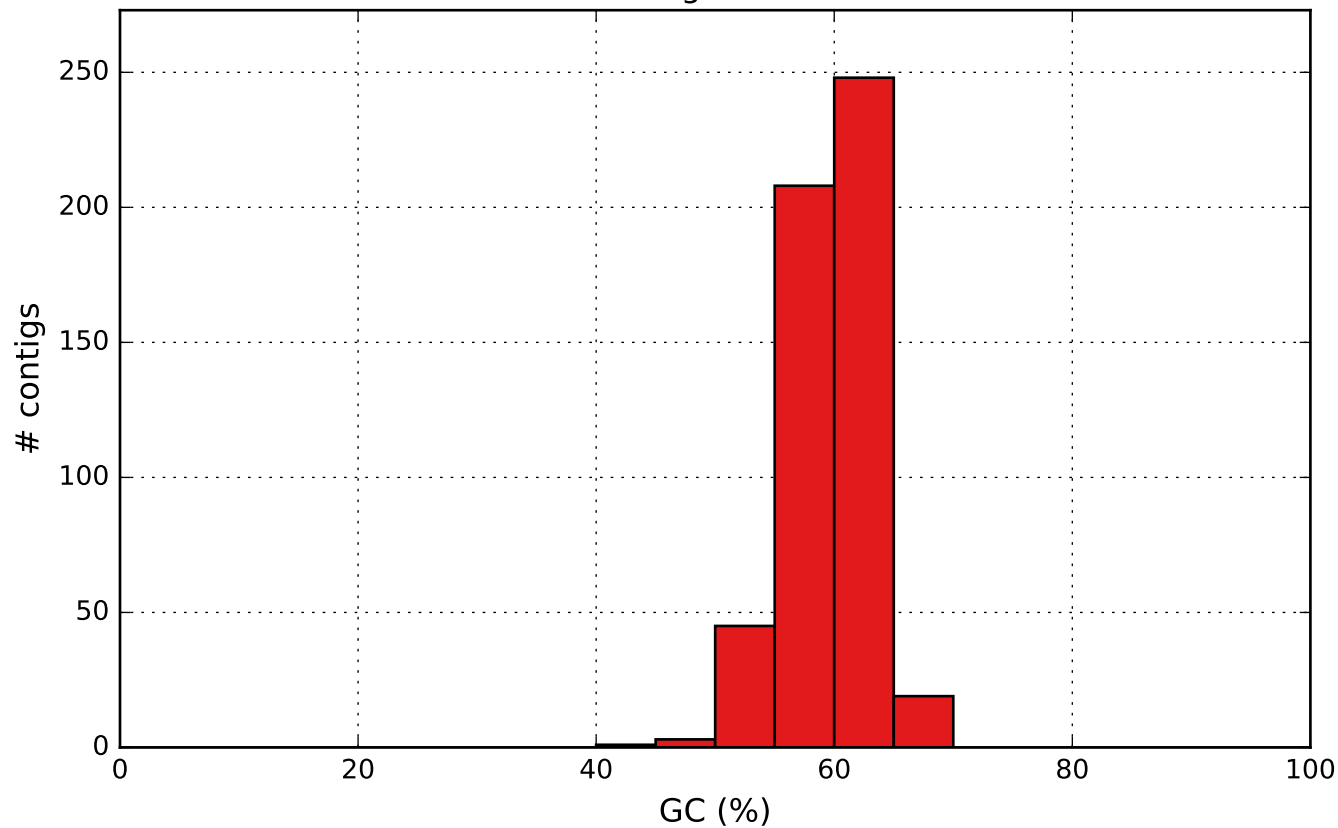


— final.contigs



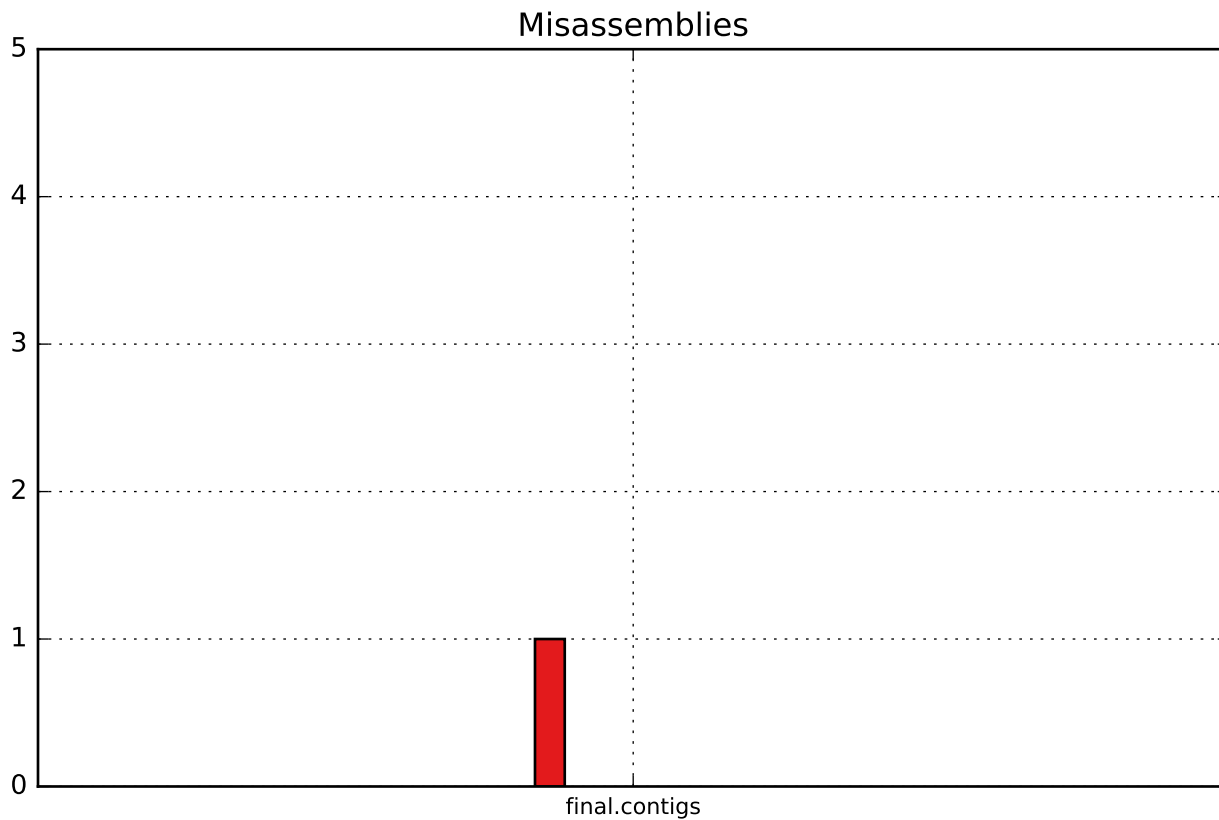


final.contigs GC content

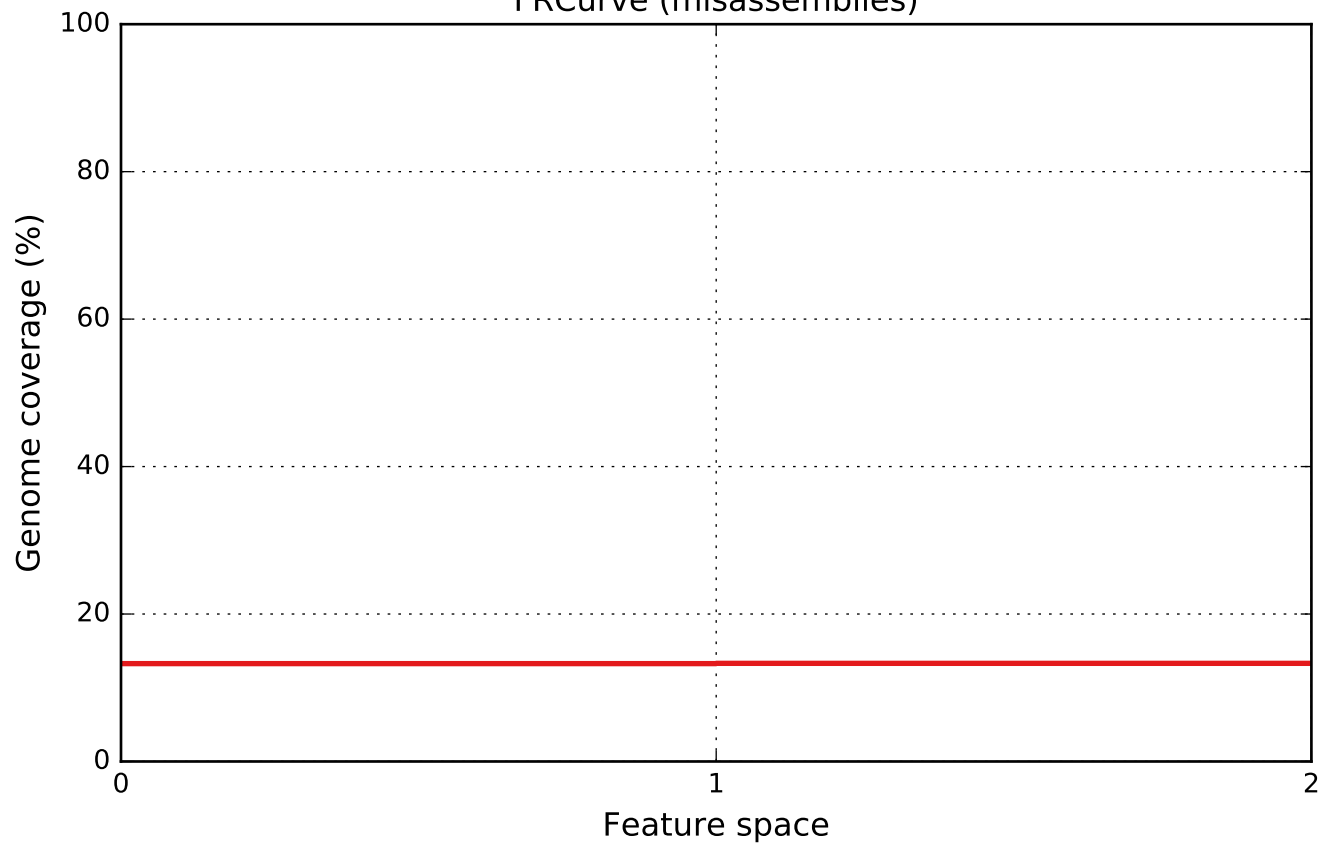


final.contigs



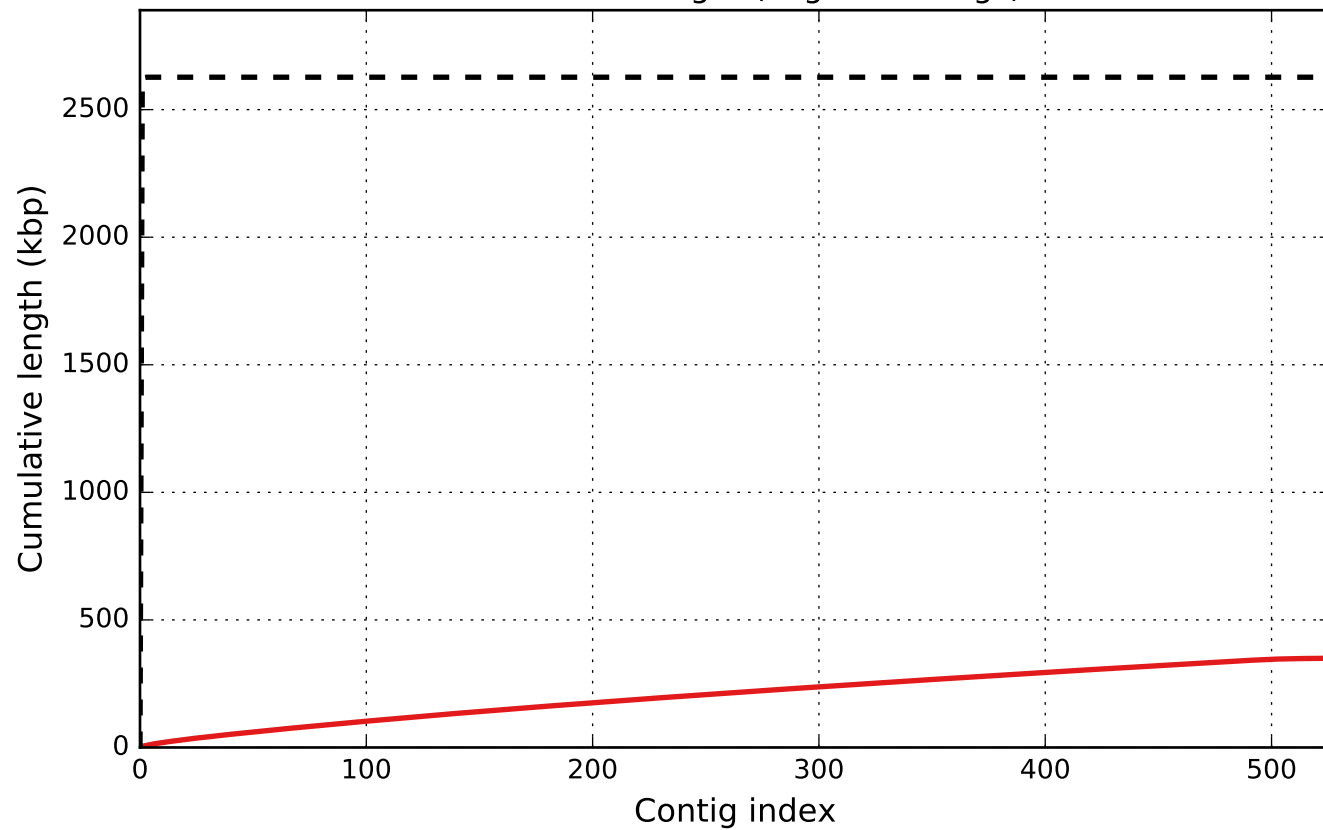


FRCurve (misassemblies)



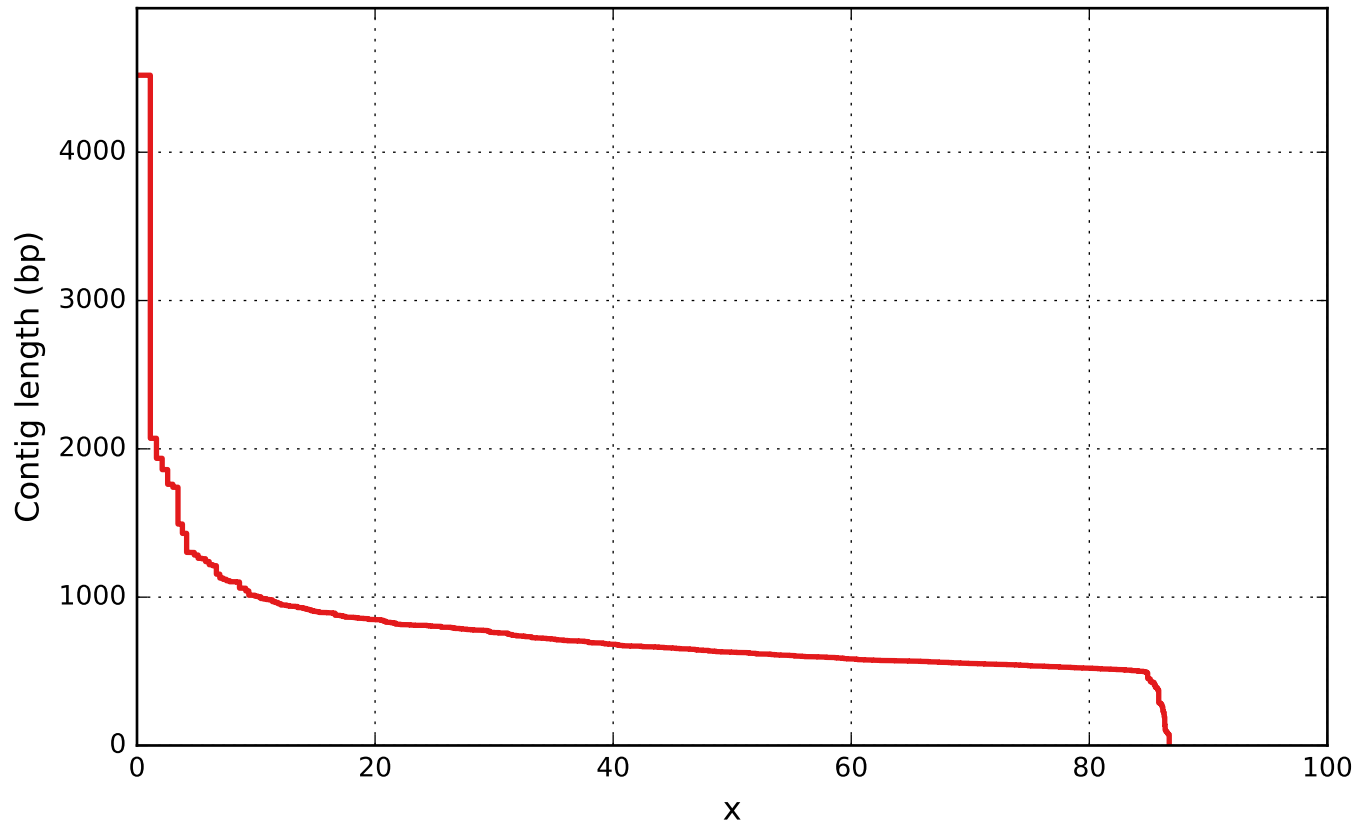
— final.contigs

Cumulative length (aligned contigs)



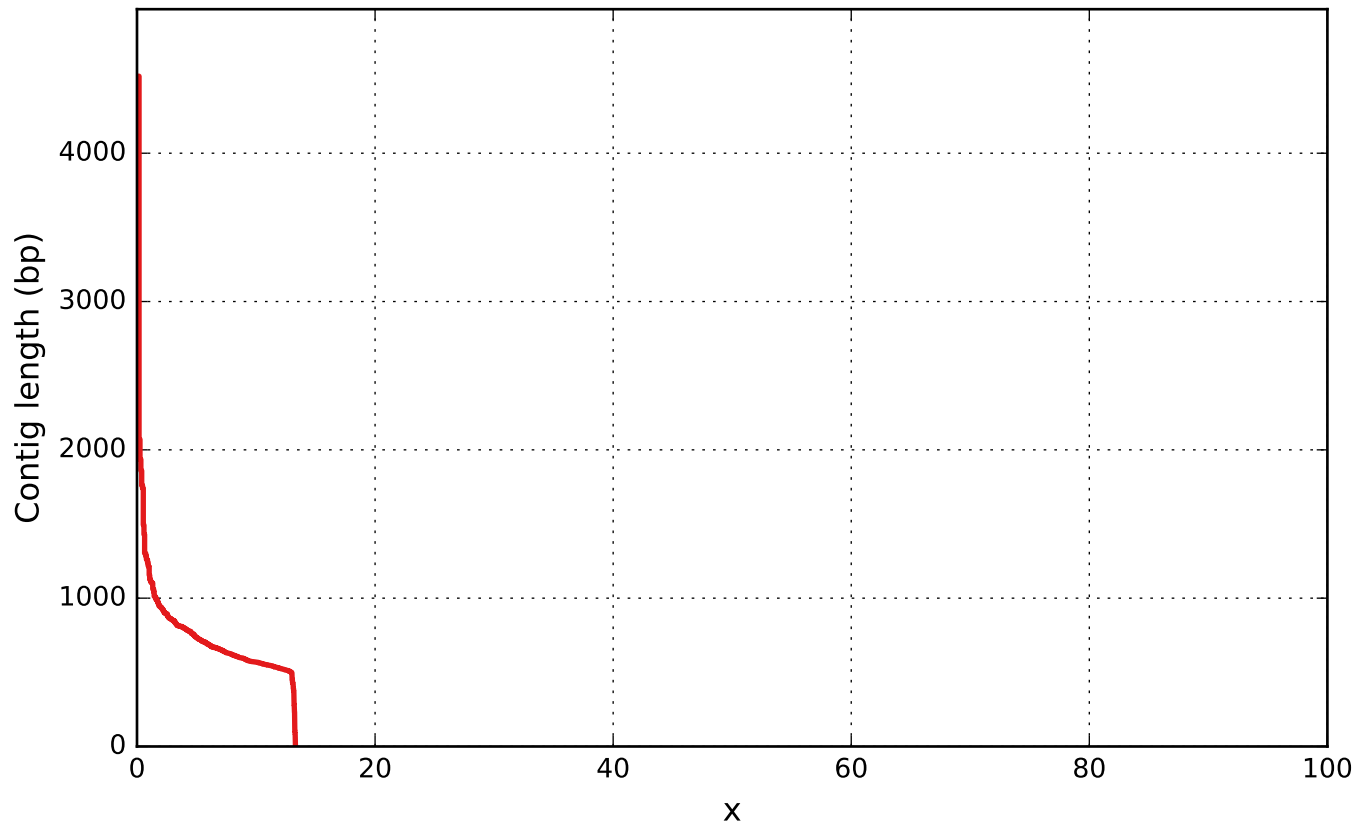
— final.contigs    - - Reference

NAx



— final.contigs

NGAx



— final.contigs