

## Report

|                             | final.contigs |
|-----------------------------|---------------|
| # contigs (>= 1000 bp)      | 4             |
| # contigs (>= 5000 bp)      | 2             |
| # contigs (>= 10000 bp)     | 2             |
| # contigs (>= 25000 bp)     | 0             |
| # contigs (>= 50000 bp)     | 0             |
| Total length (>= 1000 bp)   | 32212         |
| Total length (>= 5000 bp)   | 29461         |
| Total length (>= 10000 bp)  | 29461         |
| Total length (>= 25000 bp)  | 0             |
| Total length (>= 50000 bp)  | 0             |
| # contigs                   | 10            |
| Largest contig              | 16895         |
| Total length                | 36895         |
| Reference length            | 3633537       |
| GC (%)                      | 33.27         |
| Reference GC (%)            | 32.71         |
| N50                         | 12566         |
| N75                         | 12566         |
| L50                         | 2             |
| L75                         | 2             |
| # misassemblies             | 0             |
| # misassembled contigs      | 0             |
| Misassembled contigs length | 0             |
| # local misassemblies       | 0             |
| # unaligned mis. contigs    | 0             |
| # unaligned contigs         | 0 + 7 part    |
| Unaligned length            | 33929         |
| Genome fraction (%)         | 0.043         |
| Duplication ratio           | 1.903         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 3014.75       |
| # indels per 100 kbp        | 128.29        |
| Largest alignment           | 654           |
| Total aligned length        | 1881          |
| 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

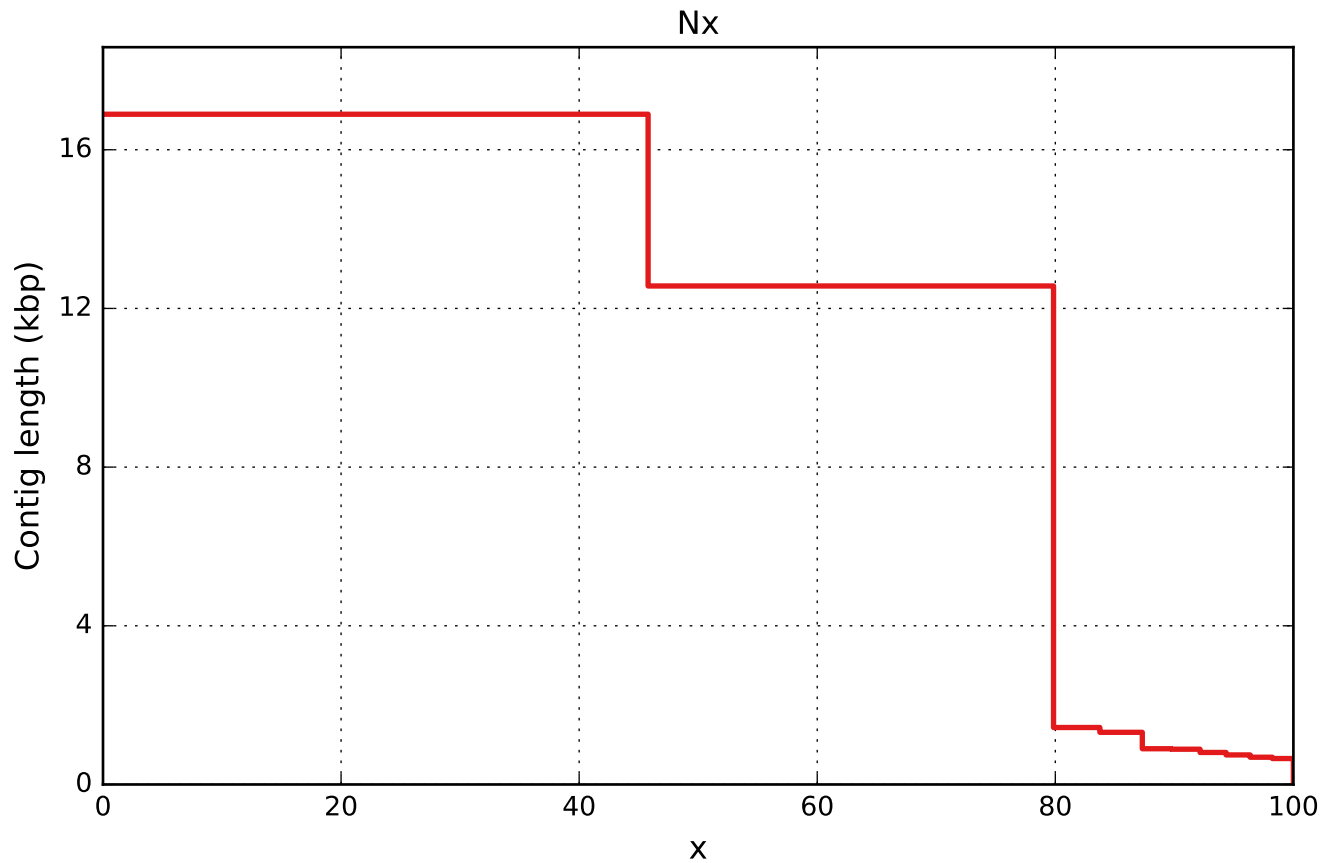
|                                 | final.contigs |
|---------------------------------|---------------|
| # misassemblies                 | 0             |
| # relocations                   | 0             |
| # translocations                | 0             |
| # inversions                    | 0             |
| # interspecies translocations   | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # possibly misassembled contigs | 0             |
| # possible misassemblies        | 0             |
| # local misassemblies           | 0             |
| # unaligned mis. contigs        | 0             |
| # mismatches                    | 47            |
| # indels                        | 2             |
| # indels ( $\leq 5$ bp)         | 2             |
| # indels ( $> 5$ bp)            | 0             |
| Indels length                   | 2             |

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

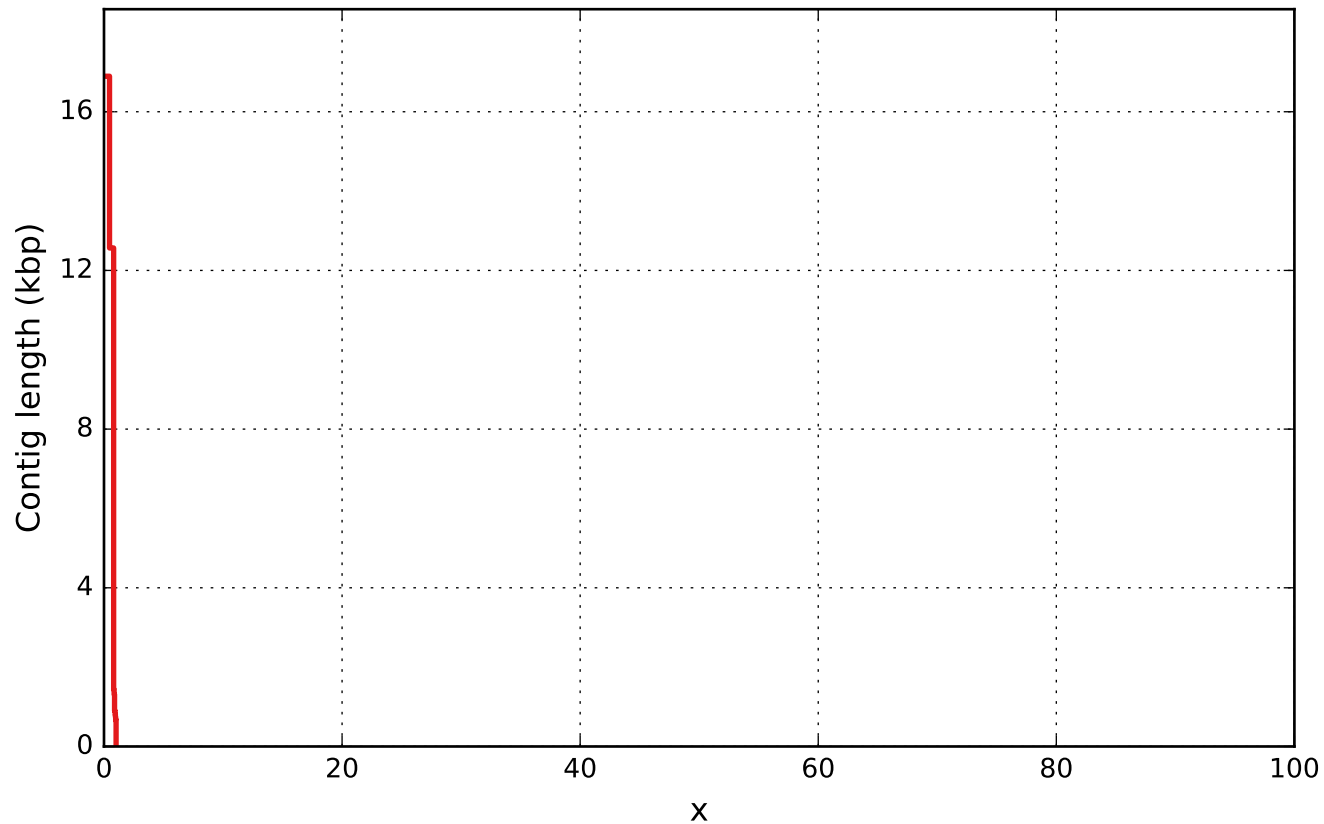
|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 0             |
| Fully unaligned length        | 0             |
| # partially unaligned contigs | 7             |
| Partially unaligned length    | 33929         |
| # 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).

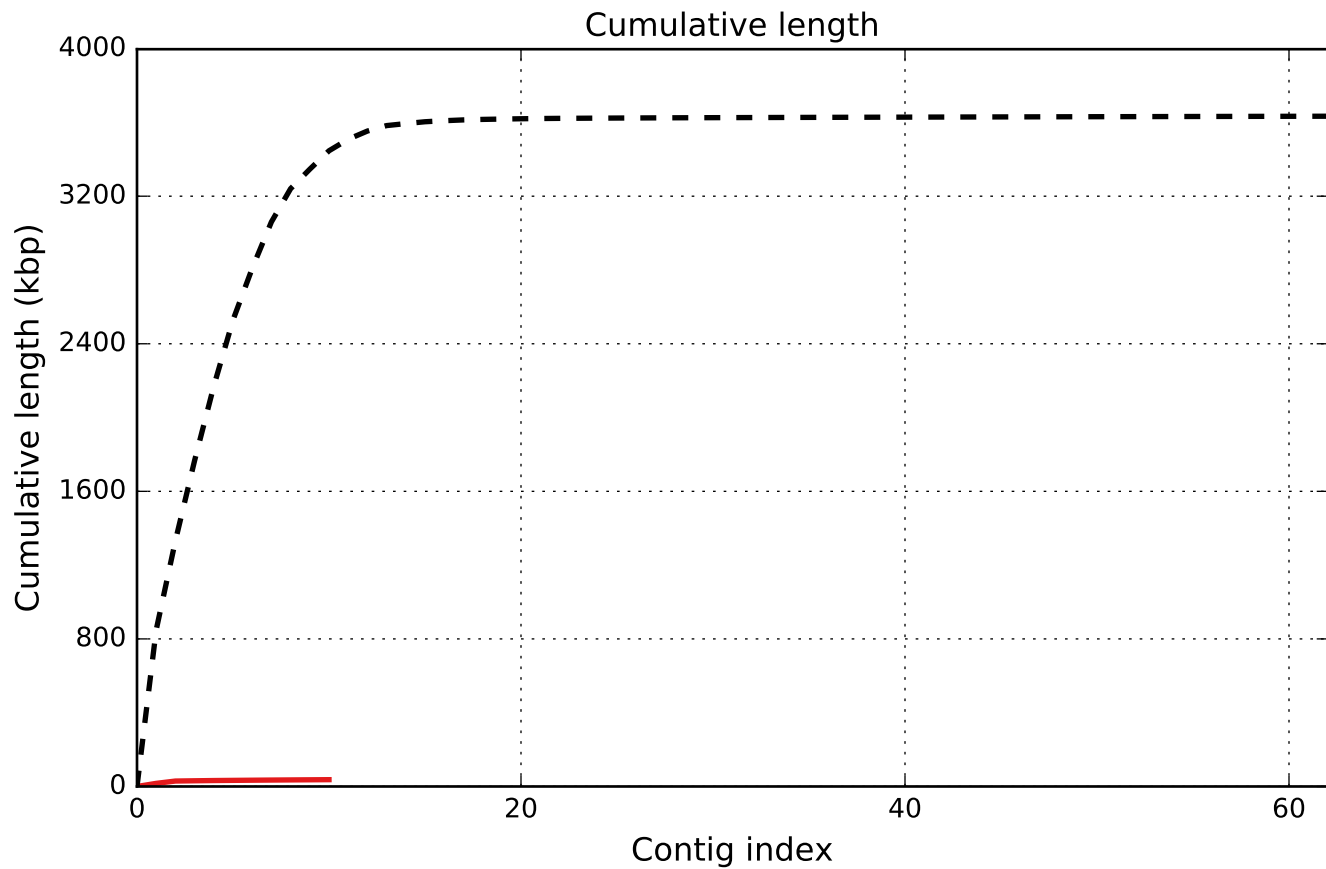


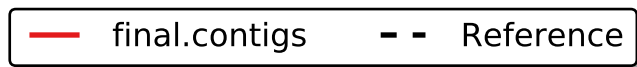
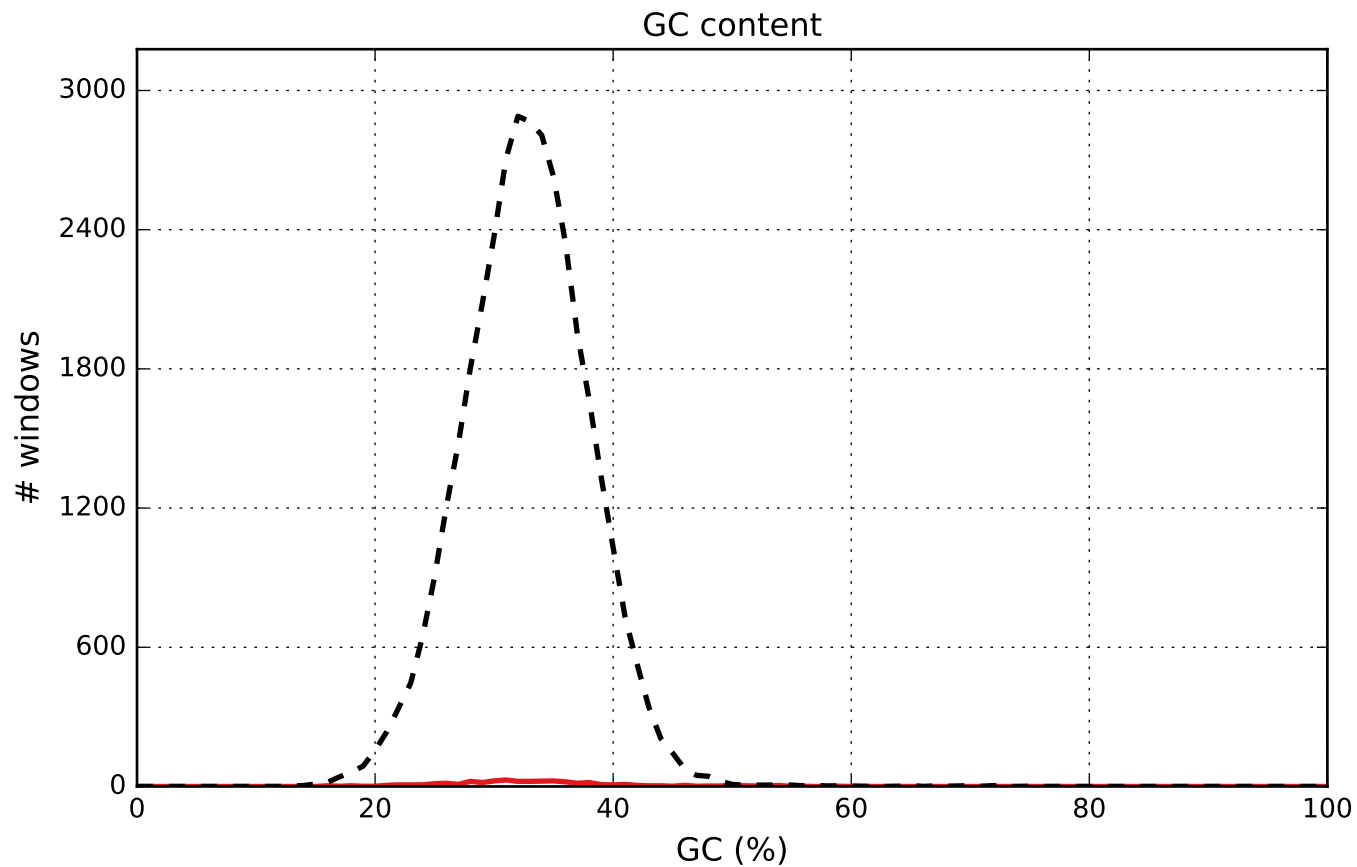
— final.contigs

NGx

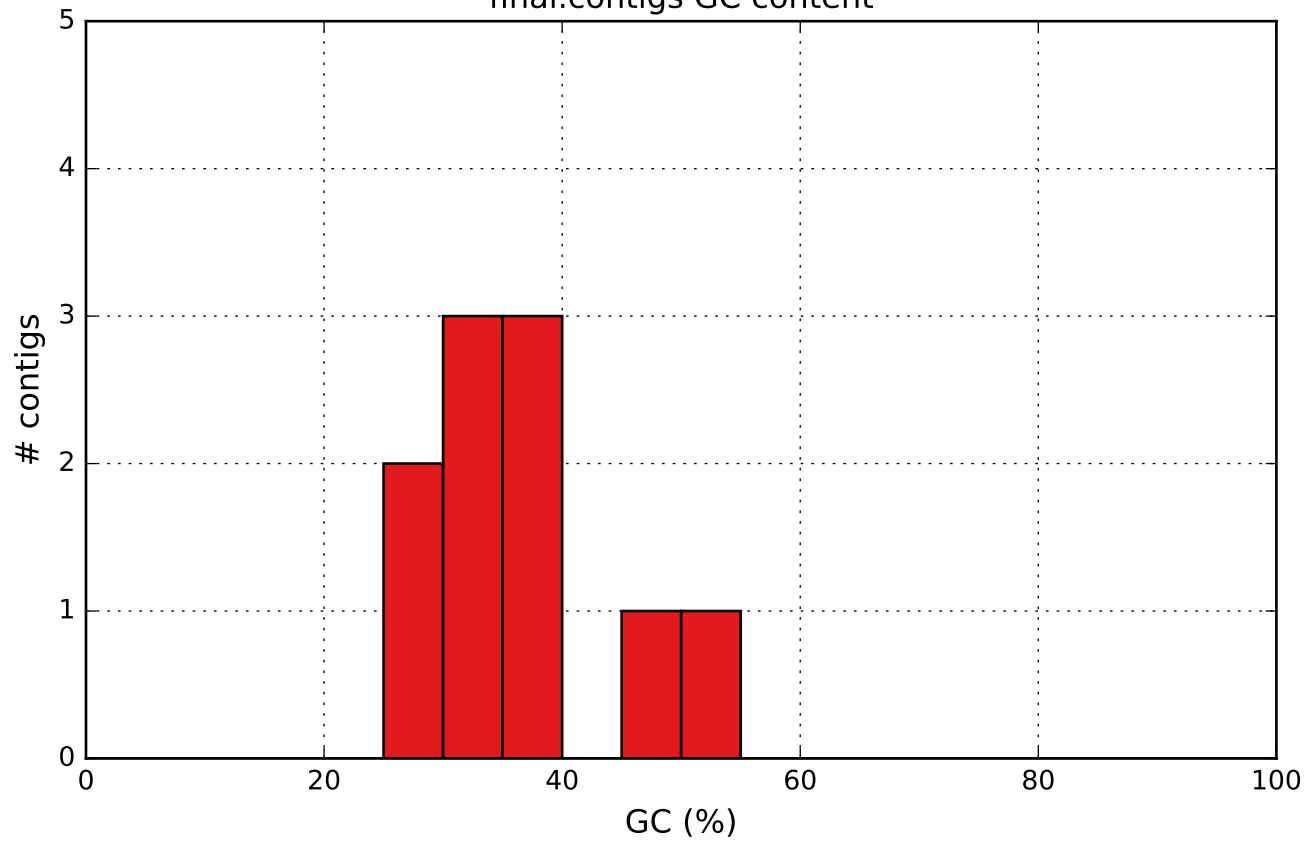


— final.contigs





final.contigs GC content

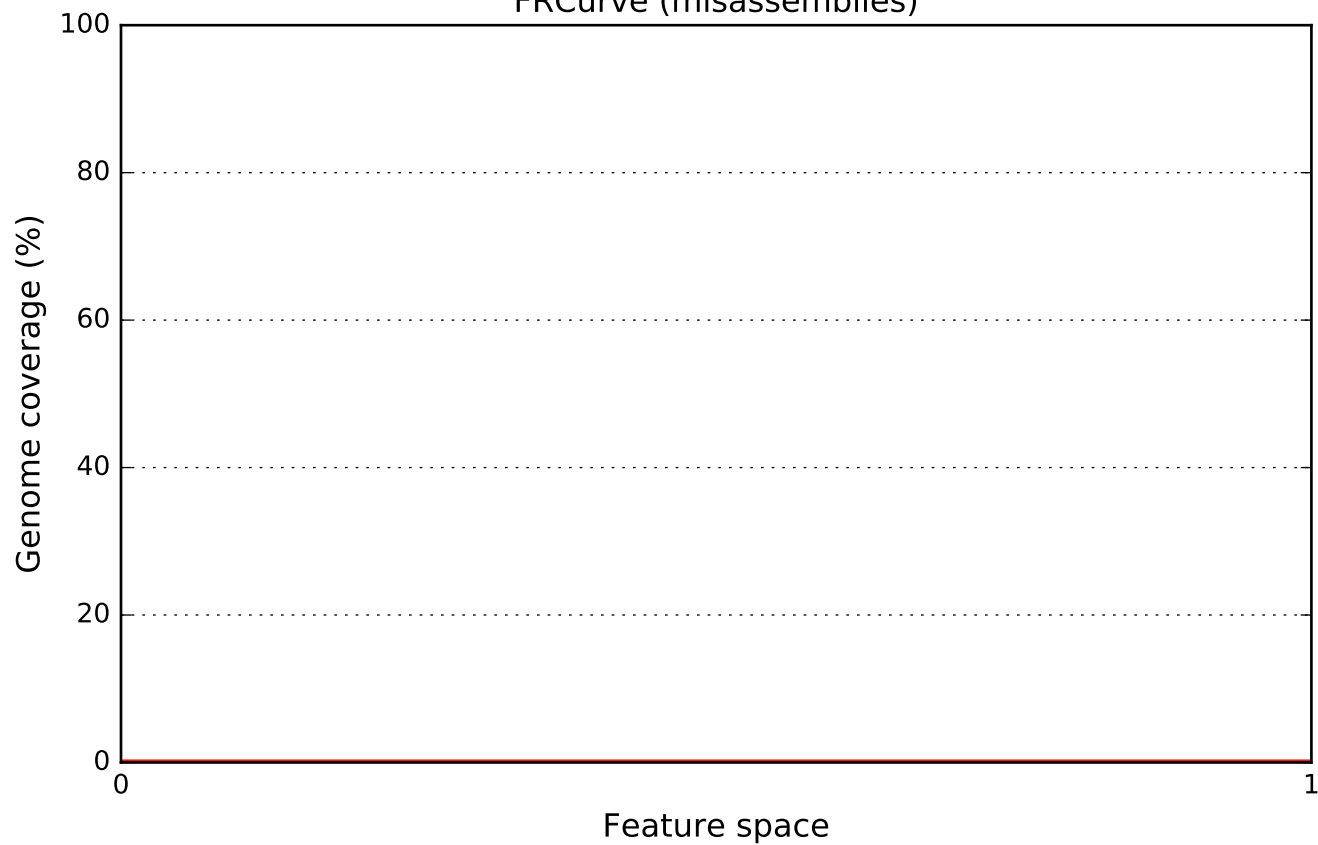


final.contigs



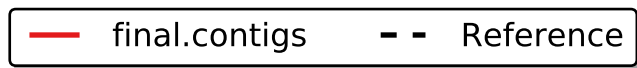
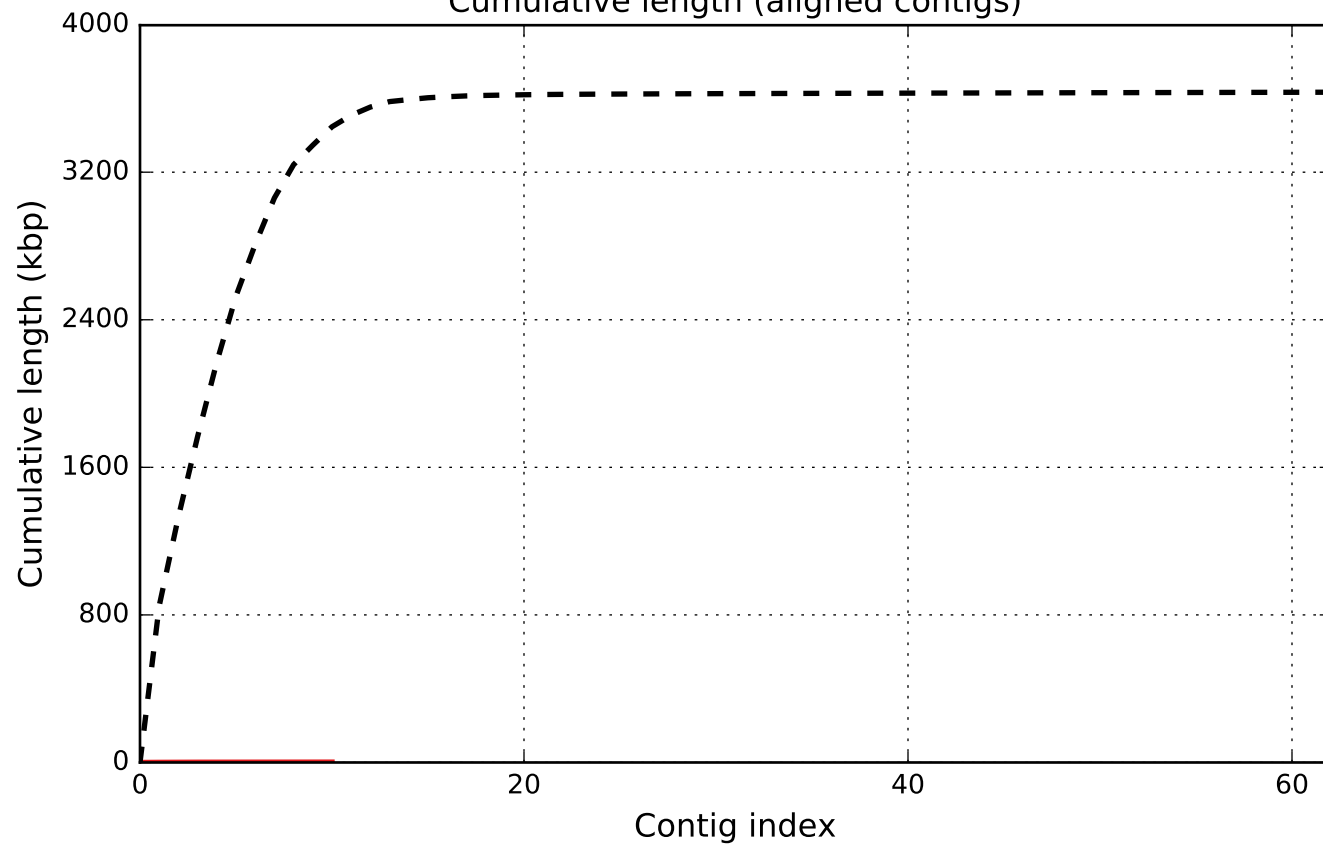


FRCurve (misassemblies)

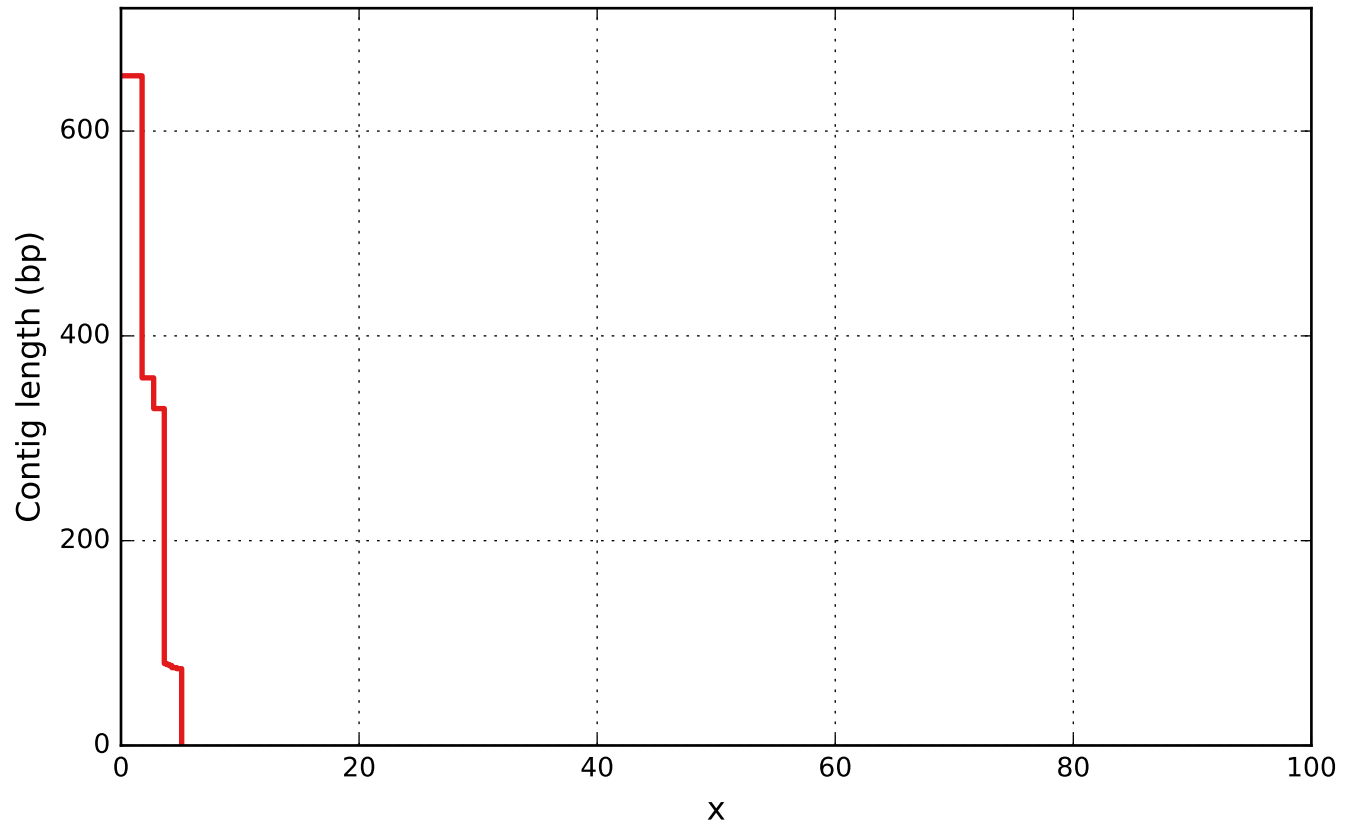


— final.contigs

Cumulative length (aligned contigs)

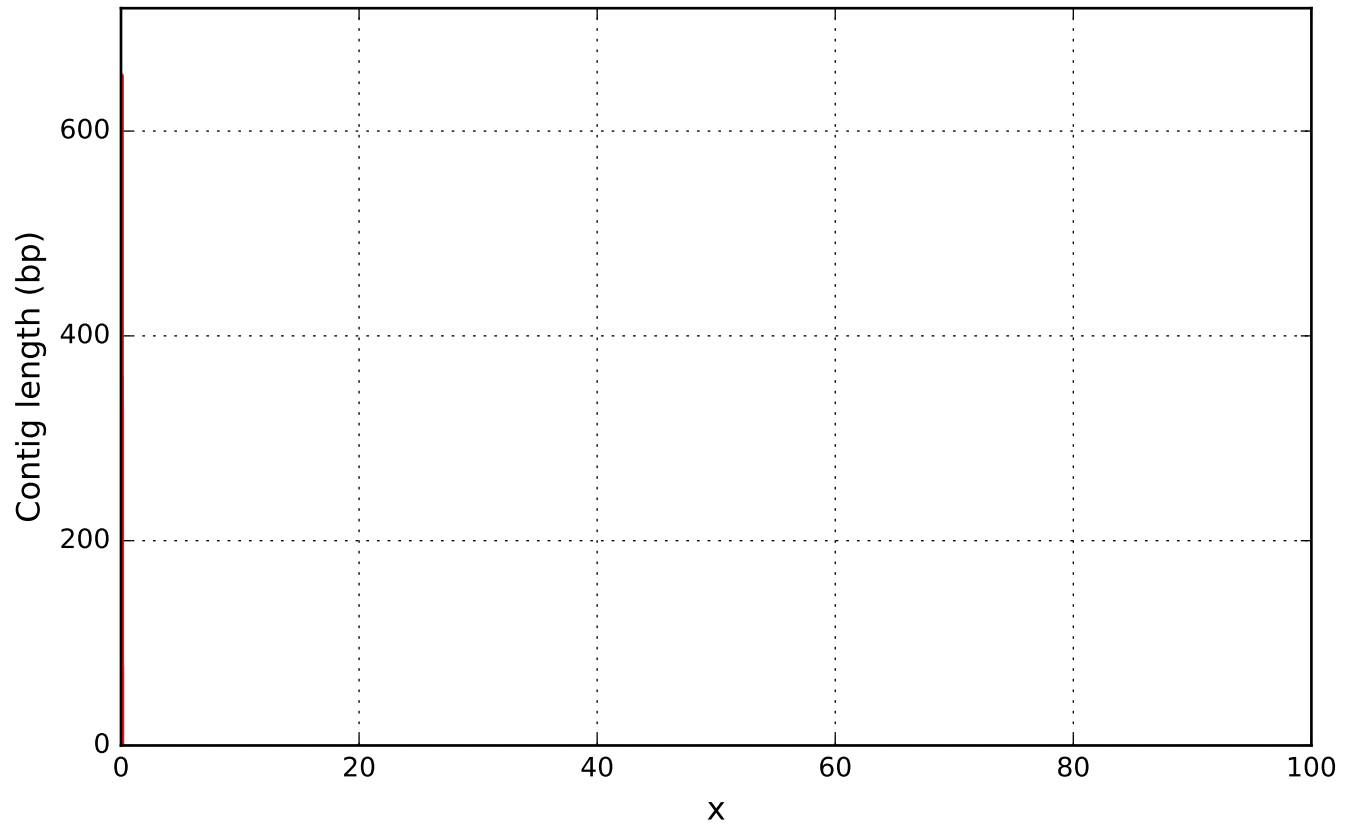


NAx



— final.contigs

NGAx



— final.contigs