

## Report

|                                 | contigs    |
|---------------------------------|------------|
| # contigs ( $\geq 0$ bp)        | 124        |
| # contigs ( $\geq 1000$ bp)     | 74         |
| # contigs ( $\geq 5000$ bp)     | 54         |
| # contigs ( $\geq 10000$ bp)    | 50         |
| # contigs ( $\geq 25000$ bp)    | 42         |
| # contigs ( $\geq 50000$ bp)    | 28         |
| Total length ( $\geq 0$ bp)     | 4572739    |
| Total length ( $\geq 1000$ bp)  | 4558730    |
| Total length ( $\geq 5000$ bp)  | 4515193    |
| Total length ( $\geq 10000$ bp) | 4485925    |
| Total length ( $\geq 25000$ bp) | 4367123    |
| Total length ( $\geq 50000$ bp) | 3868961    |
| # contigs                       | 82         |
| Largest contig                  | 327173     |
| Total length                    | 4564352    |
| Reference length                | 4641652    |
| GC (%)                          | 50.75      |
| Reference GC (%)                | 50.79      |
| N50                             | 133059     |
| NG50                            | 133059     |
| N75                             | 87059      |
| NG75                            | 78649      |
| L50                             | 11         |
| LG50                            | 11         |
| L75                             | 21         |
| LG75                            | 22         |
| # misassemblies                 | 0          |
| # misassembled contigs          | 0          |
| Misassembled contigs length     | 0          |
| # local misassemblies           | 1          |
| # unaligned contigs             | 0 + 0 part |
| Unaligned length                | 0          |
| Genome fraction (%)             | 98.306     |
| Duplication ratio               | 1.000      |
| # N's per 100 kbp               | 0.00       |
| # mismatches per 100 kbp        | 0.90       |
| # indels per 100 kbp            | 0.09       |
| Largest alignment               | 327173     |
| NA50                            | 133059     |
| NGA50                           | 133059     |
| NA75                            | 87059      |
| NGA75                           | 78649      |
| LA50                            | 11         |
| LGA50                           | 11         |
| LA75                            | 21         |
| LGA75                           | 22         |

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

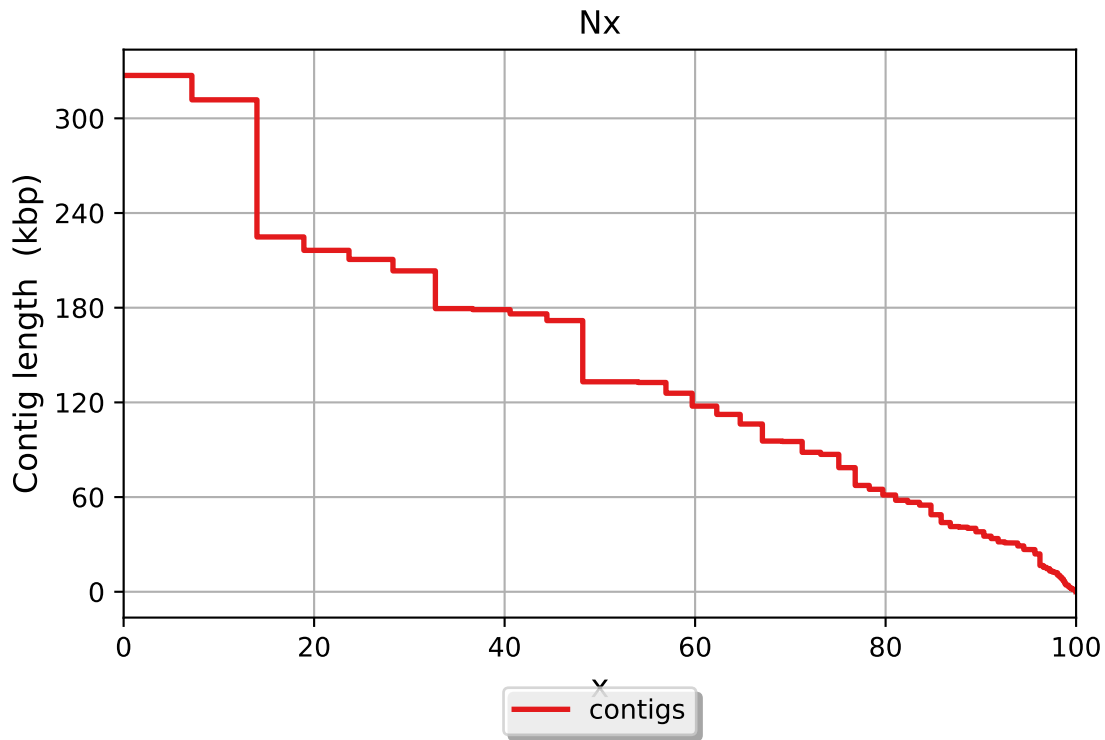
|                             | contigs |
|-----------------------------|---------|
| # misassemblies             | 0       |
| # relocations               | 0       |
| # translocations            | 0       |
| # inversions                | 0       |
| # misassembled contigs      | 0       |
| Misassembled contigs length | 0       |
| # local misassemblies       | 1       |
| # mismatches                | 41      |
| # indels                    | 4       |
| # short indels              | 4       |
| # long indels               | 0       |
| Indels length               | 5       |

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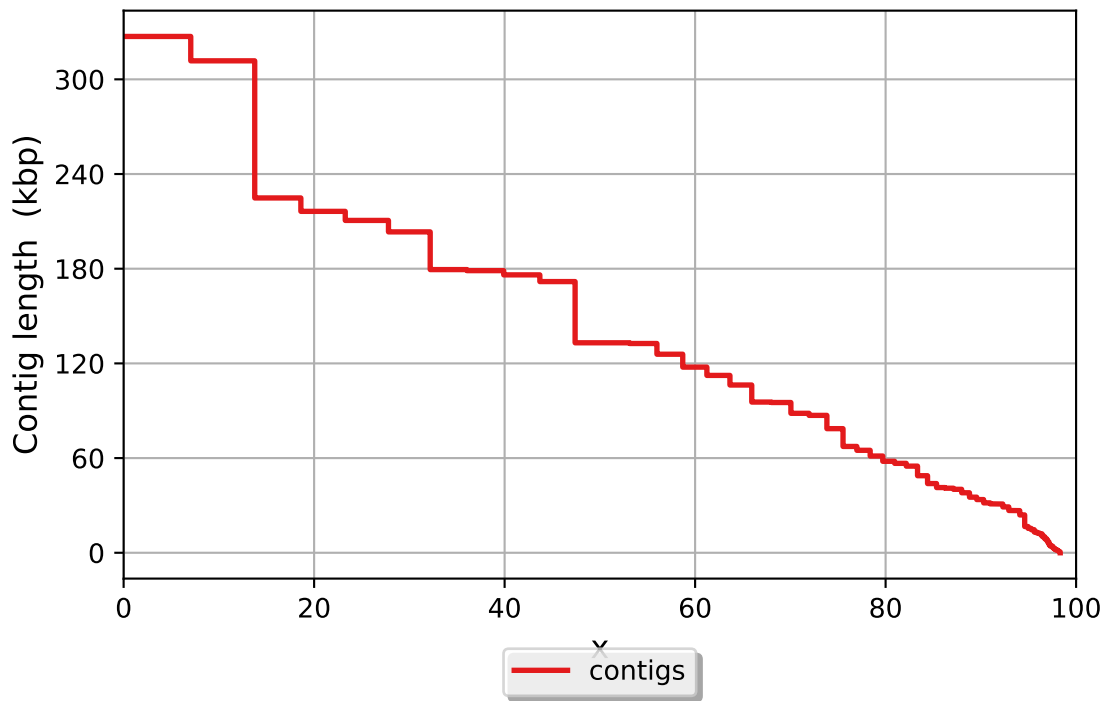
## Unaligned report

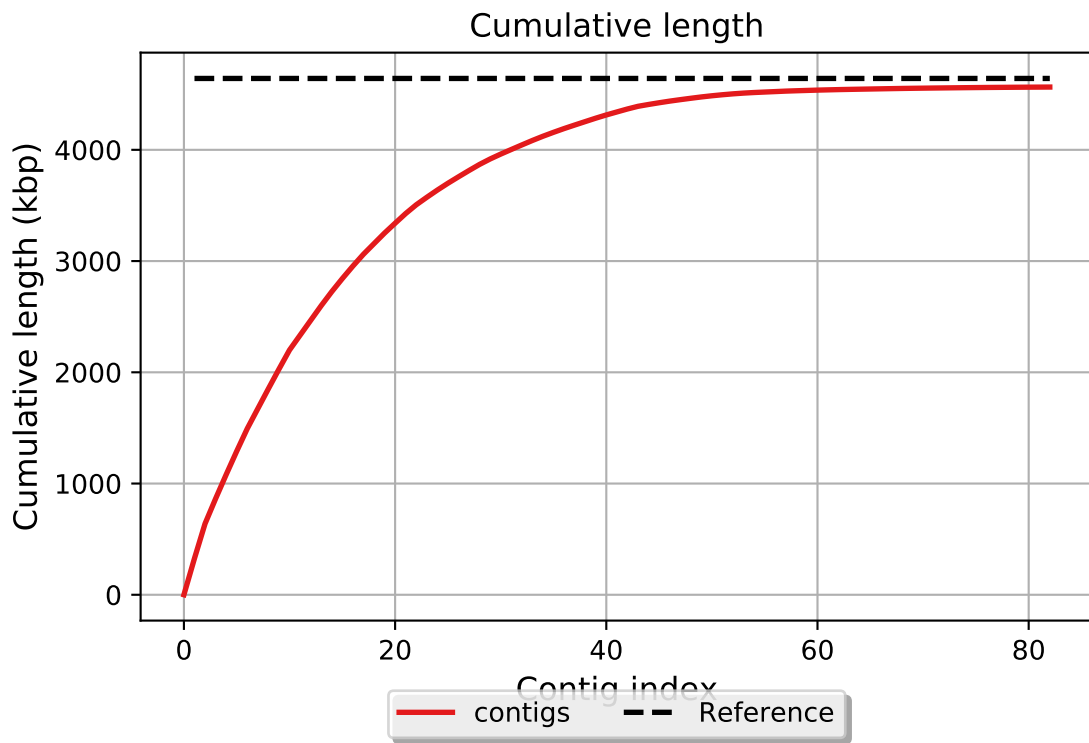
|                               | contigs |
|-------------------------------|---------|
| # fully unaligned contigs     | 0       |
| Fully unaligned length        | 0       |
| # partially unaligned contigs | 0       |
| # with misassembly            | 0       |
| # both parts are significant  | 0 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

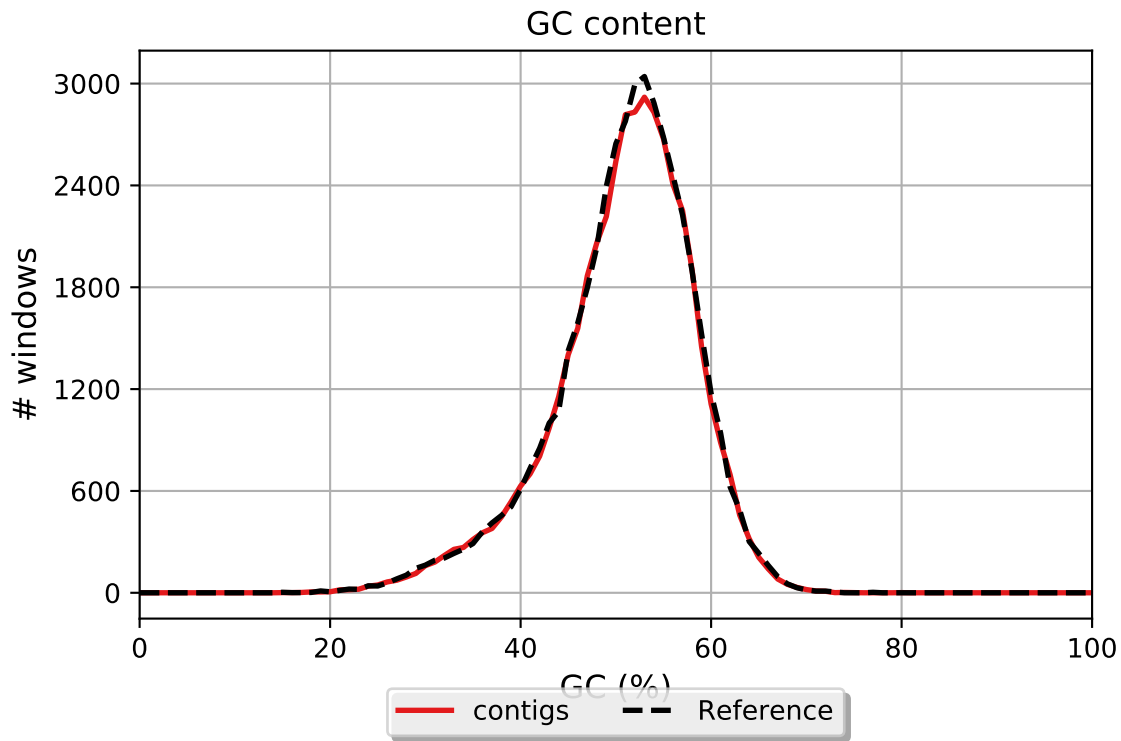
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



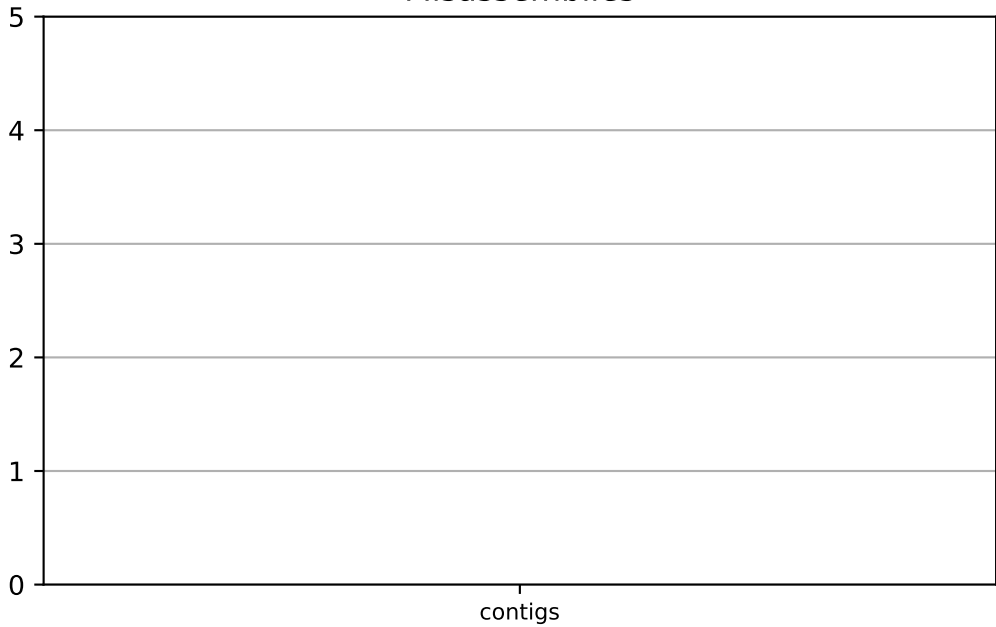
NGx





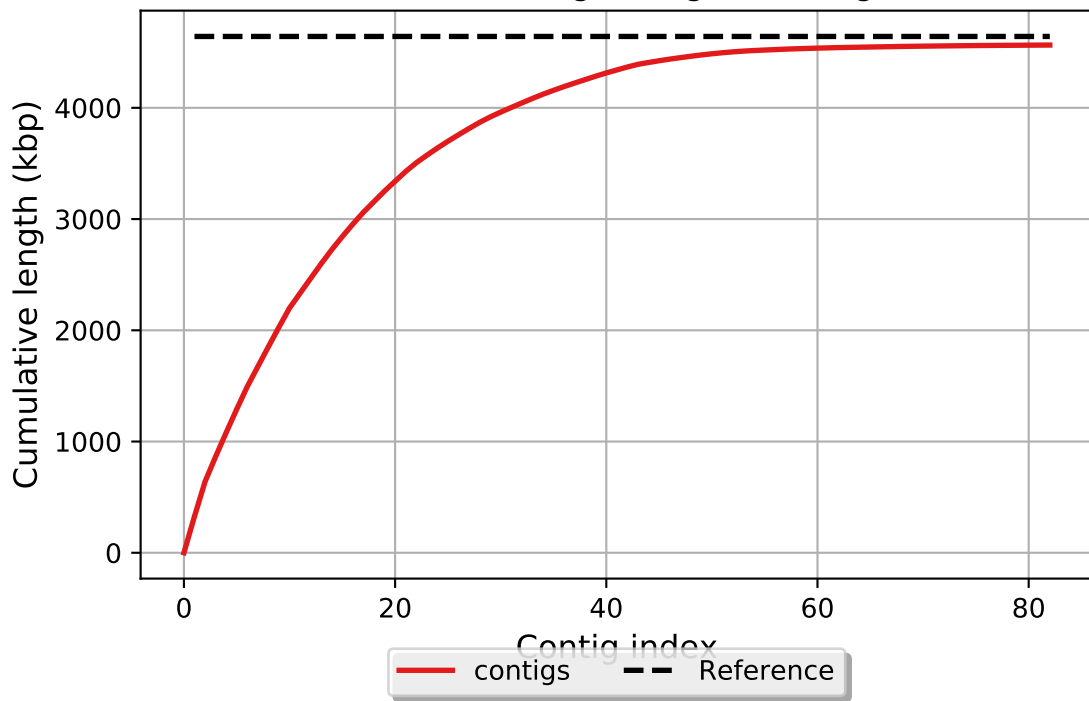


## Misassemblies

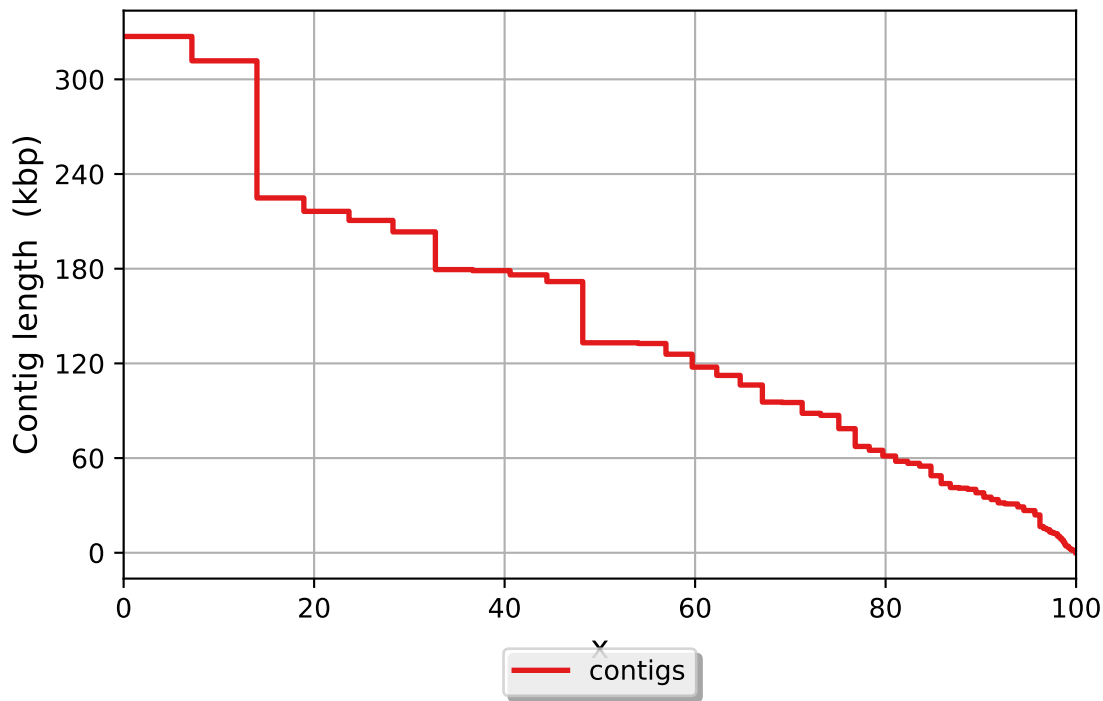




Cumulative length (aligned contigs)



NAx



# NGAx

