## Report

|                             | <i>E</i> :    |
|-----------------------------|---------------|
| " 10001                     | final.contigs |
| # contigs (>= 1000 bp)      | 559           |
| # contigs (>= 5000 bp)      | 335           |
| # contigs (>= 10000 bp)     | 169           |
| # contigs (>= 25000 bp)     | 27            |
| # contigs (>= 50000 bp)     | 2             |
| Total length (>= 1000 bp)   | 4798994       |
| Total length (>= 5000 bp)   | 4225571       |
| Total length (>= 10000 bp)  | 3048952       |
| Total length (>= 25000 bp)  | 913090        |
| Total length (>= 50000 bp)  | 101589        |
| # contigs                   | 603           |
| Largest contig              | 51551         |
| Total length                | 4830724       |
| Reference length            | 4857432       |
| GC (%)                      | 52.20         |
| Reference GC (%)            | 52.22         |
| N50                         | 12532         |
| NG50                        | 12371         |
| N75                         | 7296          |
| NG75                        | 7260          |
| L50                         | 112           |
| LG50                        | 113           |
| L75                         | 238           |
| LG75                        | 241           |
| # misassemblies             | 0             |
| # misassembled contigs      | 0             |
| Misassembled contigs length | 0             |
| # local misassemblies       | 0             |
| # unaligned contigs         | 0 + 0 part    |
| Unaligned length            | 0             |
| Genome fraction (%)         | 98.538        |
| Duplication ratio           | 1.009         |
| # N's per 100 kbp           | 0.00          |
| # mismatches per 100 kbp    | 1.15          |
| # indels per 100 kbp        | 0.00          |
| Largest alignment           | 51551         |
|                             |               |
| NA50                        | 12532         |
| NGA50                       | 12371         |
| NA75                        | 7296          |
| NGA75                       | 7260          |
| LA50                        | 112           |
| LGA50                       | 113           |
| LA75                        | 238           |
| LGA75                       | 241           |

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             |
| # possibly misassembled contigs | 0             |
| # misassembled contigs          | 0             |
| Misassembled contigs length     | 0             |
| # local misassemblies           | 0             |
| # mismatches                    | 55            |
| # indels                        | 0             |
| # short indels                  | 0             |
| # long indels                   | 0             |
| Indels length                   | 0             |

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

|                               | final.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 >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).















