## Report

|                             | scaffolds  |
|-----------------------------|------------|
| # contigs (>= 1000 bp)      | 53         |
| # contigs (>= 5000 bp)      | 48         |
| # contigs (>= 10000 bp)     | 45         |
| # contigs (>= 25000 bp)     | 40         |
| # contigs (>= 50000 bp)     | 27         |
| Total length (>= 1000 bp)   | 5119888    |
| Total length (>= 5000 bp)   | 5108486    |
| Total length (>= 10000 bp)  | 5085853    |
| Total length (>= 25000 bp)  | 5011374    |
| Total length (>= 50000 bp)  | 4569212    |
| # contigs                   | 62         |
| Largest contig              | 768359     |
| Total length                | 5126269    |
| Reference length            | 4641652    |
| GC (%)                      | 50.65      |
| Reference GC (%)            | 50.79      |
| N50                         | 176518     |
| NG50                        | 197282     |
| N75                         | 98460      |
| NG75                        | 122555     |
| L50                         | 9          |
| LG50                        | 8          |
| L75                         | 18         |
| LG75                        | 15         |
| # misassemblies             | 1          |
| # misassembled contigs      | 1          |
| Misassembled contigs length | 36059      |
| # local misassemblies       | 2          |
| # unaligned contigs         | 0 + 1 part |
| Unaligned length            | 585677     |
| Genome fraction (%)         | 97.557     |
| Duplication ratio           | 1.003      |
| # N's per 100 kbp           | 0.33       |
| # mismatches per 100 kbp    | 197.76     |
| # indels per 100 kbp        | 0.57       |
| Largest alignment           | 333124     |
| NA50                        | 153712     |
| NGA50                       | 164567     |
| NA75                        | 67394      |
| NGA75                       | 88487      |
| LA50                        | 12         |
| LGA50                       | 11         |
| LA75                        | 25         |
| LGA75                       | 20         |
|                             |            |

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

|                                 | scaffolds |
|---------------------------------|-----------|
| # misassemblies                 | 1         |
| # relocations                   | 1         |
| # translocations                | 0         |
| # inversions                    | 0         |
| # possibly misassembled contigs | 1         |
| # misassembled contigs          | 1         |
| Misassembled contigs length     | 36059     |
| # local misassemblies           | 2         |
| # mismatches                    | 8955      |
| # indels                        | 26        |
| # short indels                  | 26        |
| # long indels                   | 0         |
| Indels length                   | 30        |

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

|                               | scaffolds |
|-------------------------------|-----------|
| # fully unaligned contigs     | 0         |
| Fully unaligned length        | 0         |
| # partially unaligned contigs | 1         |
| # with misassembly            | 1         |
| # both parts are significant  | 1         |
| Partially unaligned length    | 585677    |
| # N's                         | 17        |

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).















