## Report

|                             | contigs    |
|-----------------------------|------------|
| # contigs (>= 0 bp)         | 3591       |
| # contigs (>= 1000 bp)      | 27         |
| # contigs (>= 5000 bp)      | 1          |
| # contigs (>= 10000 bp)     | 0          |
| # contigs (>= 25000 bp)     | 0          |
| # contigs (>= 50000 bp)     | 0          |
| Total length (>= 0 bp)      | 1374626    |
| Total length (>= 1000 bp)   | 43110      |
| Total length (>= 5000 bp)   | 6011       |
| Total length (>= 10000 bp)  | 0          |
| Total length (>= 25000 bp)  | 0          |
| Total length (>= 50000 bp)  | 0          |
| # contigs                   | 567        |
| Largest contig              | 6011       |
| Total length                | 385829     |
| Reference length            | 4641652    |
| GC (%)                      | 50.95      |
| Reference GC (%)            | 50.79      |
| N50                         | 641        |
| N75                         | 555        |
| L50                         | 223        |
| L75                         | 385        |
| # misassemblies             | 16         |
| # misassembled contigs      | 16         |
| Misassembled contigs length | 16579      |
| # local misassemblies       | 2          |
| # unaligned contigs         | 2 + 5 part |
| Unaligned length            | 1888       |
| Genome fraction (%)         | 8.262      |
| Duplication ratio           | 1.001      |
| # N's per 100 kbp           | 0.00       |
| # mismatches per 100 kbp    | 1033.13    |
| # indels per 100 kbp        | 3.39       |
| Largest alignment           | 5731       |
| NA50                        | 632        |
| NGA50                       | -          |
| NA75                        | 551        |
| LA50                        | 228        |
| LA75                        | 392        |
| LA75                        | 392        |

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

|                             | contigs |
|-----------------------------|---------|
| # misassemblies             | 16      |
| # relocations               | 16      |
| # translocations            | 0       |
| # inversions                | 0       |
| # misassembled contigs      | 16      |
| Misassembled contigs length | 16579   |
| # local misassemblies       | 2       |
| # mismatches                | 3962    |
| # indels                    | 13      |
| # short indels              | 13      |
| # long indels               | 0       |
| Indels length               | 17      |

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

|                               | contigs |
|-------------------------------|---------|
| # fully unaligned contigs     | 2       |
| Fully unaligned length        | 1556    |
| # partially unaligned contigs | 5       |
| # with misassembly            | 0       |
| # both parts are significant  | 0       |
| Partially unaligned length    | 332     |
| # 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).















