Report

| | contigs |
|-----------------------------|------------|
| # contigs (>= 0 bp) | 84 |
| # contigs (>= 1000 bp) | 65 |
| # contigs (>= 5000 bp) | 50 |
| # contigs (>= 10000 bp) | 45 |
| # contigs (>= 25000 bp) | 41 |
| # contigs (>= 50000 bp) | 27 |
| Total length (>= 0 bp) | 4569666 |
| Total length (>= 1000 bp) | 4563376 |
| Total length (>= 5000 bp) | 4526701 |
| Total length (>= 10000 bp) | 4486865 |
| Total length (>= 25000 bp) | 4430385 |
| Total length (>= 50000 bp) | 3942835 |
| # contigs | 70 |
| Largest contig | 327064 |
| Total length | 4567183 |
| Reference length | 4641652 |
| GC (%) | 50.74 |
| Reference GC (%) | 50.79 |
| N50 | 175735 |
| NG50 | 175735 |
| N75 | 80764 |
| NG75 | 80764 |
| L50 | 10 |
| LG50 | 10 |
| L75 | 20 |
| LG75 | 20 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # unaligned contigs | 0 + 0 part |
| Unaligned length | 0 |
| Genome fraction (%) | 98.334 |
| Duplication ratio | 1.001 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 6.88 |
| # indels per 100 kbp | 0.37 |
| Largest alignment | 327064 |
| NA50 | 175735 |
| NGA50 | 175735 |
| NA75 | 80764 |
| NGA75 | 80764 |
| LA50 | 10 |
| LGA50 | 10 |
| LA75 | 20 |
| 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

| | contigs |
|-----------------------------|---------|
| # misassemblies | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 2 |
| # mismatches | 314 |
| # indels | 17 |
| # short indels | 17 |
| # long indels | 0 |
| Indels length | 24 |

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

| | 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).















