Report

| | scaffolds |
|-----------------------------|-------------|
| # contigs (>= 1000 bp) | 57 |
| # contigs (>= 5000 bp) | 50 |
| # contigs (>= 10000 bp) | 50 |
| # contigs (>= 25000 bp) | 47 |
| # contigs (>= 50000 bp) | 43 |
| Total length (>= 1000 bp) | 8055135 |
| Total length (>= 5000 bp) | 8047447 |
| Total length (>= 10000 bp) | 8047447 |
| Total length (>= 25000 bp) | 8001492 |
| Total length (>= 50000 bp) | 7873706 |
| # contigs | 62 |
| Largest contig | 529642 |
| Total length | 8058538 |
| Reference length | 4641652 |
| GC (%) | 50.76 |
| Reference GC (%) | 50.79 |
| N50 | 264862 |
| NG50 | 324227 |
| N75 | 157835 |
| NG75 | 288223 |
| L50 | 12 |
| LG50 | 6 |
| L75 | 22 |
| LG75 | 10 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # unaligned contigs | 0 + 27 part |
| Unaligned length | 3033062 |
| Genome fraction (%) | 99.195 |
| Duplication ratio | 1.091 |
| # N's per 100 kbp | 0.37 |
| # mismatches per 100 kbp | 449.26 |
| # indels per 100 kbp | 0.98 |
| Largest alignment | 529642 |
| NA50 | 111062 |
| NGA50 | 291704 |
| NGA75 | 240233 |
| LA50 | 14 |
| LGA50 | 6 |
| LGA75 | 10 |
| | |

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 | 0 |
| # relocations | 0 |
| # translocations | 0 |
| # inversions | 0 |
| # possibly misassembled contigs | 26 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 0 |
| # mismatches | 20685 |
| # indels | 45 |
| # short indels | 45 |
| # long indels | 0 |
| Indels length | 48 |

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 | 27 |
| # with misassembly | 20 |
| # both parts are significant | 26 |
| Partially unaligned length | 3033062 |
| # N's | 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).















