Report

| | anntine. |
|--|------------|
| # contigs (> = 1000 hp) | contigs |
| # contigs (>= 1000 bp) # contigs (>= 5000 bp) | 916 |
| # contigs (>= 5000 bp) # contigs (>= 10000 bp) | 280 65 |
| # contigs (>= 10000 bp) # contigs (>= 25000 bp) | 4 |
| | |
| # contigs (>= 50000 bp) | 4002767 |
| Total length (>= 1000 bp) | 4082767 |
| Total length (>= 5000 bp) | 2425758 |
| Total length (>= 10000 bp) | 920067 |
| Total length (>= 25000 bp) | 125579 |
| Total length (>= 50000 bp) | 0 |
| # contigs | 1077 |
| Largest contig | 36999 |
| Total length | 4194275 |
| Reference length | 4641652 |
| GC (%) | 50.76 |
| Reference GC (%) | 50.79 |
| N50 | 5970 |
| NG50 | 5423 |
| N75 | 3398 |
| NG75 | 2643 |
| L50 | 221 |
| LG50 | 260 |
| L75 | 454 |
| LG75 | 566 |
| # misassemblies | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # unaligned contigs | 0 + 2 part |
| Unaligned length | 437 |
| Genome fraction (%) | 89.448 |
| Duplication ratio | 1.010 |
| # N's per 100 kbp | 0.00 |
| # mismatches per 100 kbp | 997.77 |
| # indels per 100 kbp | 0.82 |
| Largest alignment | 36999 |
| NA50 | 5970 |
| NGA50 | 5423 |
| NA75 | 3398 |
| NGA75 | 2643 |
| LA50 | 221 |
| LGA50 | 260 |
| LA75 | 454 |
| LGA75 | 566 |
| | |

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 |
| # possibly misassembled contigs | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # local misassemblies | 1 |
| # mismatches | 41426 |
| # indels | 34 |
| # short indels | 34 |
| # long indels | 0 |
| Indels length | 41 |

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 | 2 |
| # with misassembly | 0 |
| # both parts are significant | 0 |
| Partially unaligned length | 437 |
| # 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).















