

Report

| | dataset_3.dat | dataset_4.dat |
|--------------------------------|---------------|---------------|
| # contigs (≥ 0 bp) | 47 | 35 |
| # contigs (≥ 1000 bp) | 11 | 7 |
| Total length (≥ 0 bp) | 187773 | 179095 |
| Total length (≥ 1000 bp) | 173623 | 169301 |
| # contigs | 20 | 12 |
| Largest contig | 55106 | 55421 |
| Total length | 180875 | 173140 |
| Reference length | 124998 | 124998 |
| GC (%) | 45.35 | 45.15 |
| Reference GC (%) | 45.30 | 45.30 |
| N50 | 49658 | 49658 |
| NG50 | 49658 | 49658 |
| N75 | 17535 | 27260 |
| NG75 | 49658 | 49658 |
| L50 | 2 | 2 |
| LG50 | 2 | 2 |
| L75 | 4 | 3 |
| LG75 | 2 | 2 |
| # misassemblies | 0 | 0 |
| # misassembled contigs | 0 | 0 |
| Misassembled contigs length | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # unaligned contigs | 4 + 0 part | 3 + 0 part |
| Unaligned length | 53102 | 51257 |
| Genome fraction (%) | 98.002 | 97.942 |
| Duplication ratio | 1.043 | 1.002 |
| # N's per 100 kbp | 7.74 | 0.00 |
| # mismatches per 100 kbp | 35.92 | 27.77 |
| # indels per 100 kbp | 1.63 | 0.00 |
| Largest alignment | 55106 | 55421 |
| NA50 | 17534 | 16099 |
| NGA50 | 27969 | 27260 |
| NGA75 | 17534 | 16099 |
| LA50 | 3 | 3 |
| LGA50 | 2 | 2 |
| LGA75 | 3 | 3 |

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

| | dataset_3.dat | dataset_4.dat |
|---------------------------------|---------------|---------------|
| # misassemblies | 0 | 0 |
| # relocations | 0 | 0 |
| # translocations | 0 | 0 |
| # inversions | 0 | 0 |
| # interspecies translocations | 0 | 0 |
| # possibly misassembled contigs | 0 | 0 |
| # misassembled contigs | 0 | 0 |
| Misassembled contigs length | 0 | 0 |
| # local misassemblies | 0 | 0 |
| # mismatches | 44 | 34 |
| # indels | 2 | 0 |
| # short indels | 2 | 0 |
| # long indels | 0 | 0 |
| Indels length | 2 | 0 |

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Unaligned report

| | dataset_3.dat | dataset_4.dat |
|-------------------------------|---------------|---------------|
| # fully unaligned contigs | 4 | 3 |
| Fully unaligned length | 53102 | 51257 |
| # partially unaligned contigs | 0 | 0 |
| # with misassembly | 0 | 0 |
| # both parts are significant | 0 | 0 |
| Partially unaligned length | 0 | 0 |
| # N's | 14 | 0 |

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