Report

| # contigs (>= 1000 bp) 17 # contigs (>= 5000 bp) 3 # contigs (>= 10000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 49761 Total length (>= 5000 bp) 23066 Total length (>= 10000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 37 Largest contig 8796 Total length 64491 Reference length 3576081 GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 10 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part 1 Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 NGA50 | | final.contigs |
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| GC (%) 55.95 Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Total length | 64491 |
| Reference GC (%) 51.82 N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 Misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Reference length | 3576081 |
| N50 2823 N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | GC (%) | 55.95 |
| N75 1085 L50 6 L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Reference GC (%) | 51.82 |
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| L75 16 # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | N75 | 1085 |
| # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | L50 | 6 |
| # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | L75 | 16 |
| Misassembled contigs length # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # misassemblies | 0 |
| # local misassemblies 1 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # misassembled contigs | 0 |
| # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Misassembled contigs length | 0 |
| # scaffold gap loc. mis. 0 # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # local misassemblies | 1 |
| # unaligned mis. contigs 3 # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # scaffold gap ext. mis. | 0 |
| # unaligned contigs 1 + 24 part Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # scaffold gap loc. mis. | 0 |
| Unaligned length 50973 Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # unaligned mis. contigs | 3 |
| Genome fraction (%) 0.186 Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # unaligned contigs | 1 + 24 part |
| Duplication ratio 2.036 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Unaligned length | 50973 |
| # N's per 100 kbp 0.00 # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Genome fraction (%) | 0.186 |
| # mismatches per 100 kbp 3615.00 # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | Duplication ratio | 2.036 |
| # indels per 100 kbp 135.56 Largest alignment 1743 Total aligned length 8319 | # N's per 100 kbp | 0.00 |
| Largest alignment 1743 Total aligned length 8319 | # mismatches per 100 kbp | 3615.00 |
| Total aligned length 8319 | # indels per 100 kbp | 135.56 |
| , , , , , , , , , , , , , , , , , , , | Largest alignment | 1743 |
| NGA50 - | Total aligned length | 8319 |
| | NGA50 | - |

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

| | final.contigs |
|---------------------------------|---------------|
| # misassemblies | 0 |
| # contig misassemblies | 0 |
| # c. relocations | 0 |
| # c. translocations | 0 |
| # c. inversions | 0 |
| # scaffold misassemblies | 0 |
| # s. relocations | 0 |
| # s. translocations | 0 |
| # s. inversions | 0 |
| # misassembled contigs | 0 |
| Misassembled contigs length | 0 |
| # possibly misassembled contigs | 19 |
| # possible misassemblies | 24 |
| # local misassemblies | 1 |
| # scaffold gap ext. mis. | 0 |
| # scaffold gap loc. mis. | 0 |
| # unaligned mis. contigs | 3 |
| # mismatches | 240 |
| # indels | 9 |
| # indels (<= 5 bp) | 9 |
| # indels (> 5 bp) | 0 |
| Indels length | 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).

Unaligned report

| | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs | 1 |
| Fully unaligned length | 901 |
| # partially unaligned contigs | 24 |
| Partially unaligned length | 50072 |
| # 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).





















