## Report

| # contigs (>= 1000 bp)  # contigs (>= 5000 bp)  # contigs (>= 10000 bp)  # contigs (>= 25000 bp)  # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 5000 bp)  Total length (>= 5000 bp)  Total length (>= 25000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  12  Largest contig  14321  Total length  39604  Reference length  4052370  GC (%)  41.74  Reference GC (%)  N50  10809  N75  2135  L50  2  L75  # misassemblies  # misassembled contigs  Misassembled contigs  Misassembled contigs  # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  2  # unaligned length  36369  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  1000  # mismatches per 100 kbp  Largest alignment  Total aligned length  1420  NGA50   |                        | final.contigs                                    |
|--|------------------------|--|
| # contigs (>= 5000 bp) 2 # contigs (>= 10000 bp) 2 # contigs (>= 25000 bp) 0 # contigs (>= 50000 bp) 0 # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 36986 Total length (>= 5000 bp) 25130 Total length (>= 10000 bp) 25130 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 12 Largest contig 14321 Total length 39604 Reference length 4052370 GC (%) 41.74 Reference GC (%) 59.44 N50 10809 N75 2135 L50 2 L75 4 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 1 + 7 part Unaligned length 36369 Genome fraction (%) 0.029 Duplication ratio 2.714 # N's per 100 kbp 0.00 Largest alignment 371 Total aligned length 371 Total aligned length 1420  | # contigs (>= 1000 hp) |  |
| # contigs (>= 10000 bp)  |                        | ļ  |
| # contigs (>= 25000 bp)  # contigs (>= 50000 bp)  Total length (>= 1000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  Total length (>= 10000 bp)  Total length (>= 25000 bp)  Total length (>= 50000 bp)  Total length (>= 50000 bp)  # contigs  Largest contig  Total length  Reference length  4052370  GC (%)  A1.74  Reference GC (%)  N50  10809  N75  L50  L75  # misassembled contigs  # misassembled contigs  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  Unaligned length  Genome fraction (%)  Duplication ratio  # nises alignment  # indels per 100 kbp  O.00  Largest alignment  Total aligned length  1420   |                        |  |
| # contigs (>= 50000 bp) 0 Total length (>= 1000 bp) 36986 Total length (>= 5000 bp) 25130 Total length (>= 10000 bp) 25130 Total length (>= 25000 bp) 0 Total length (>= 50000 bp) 0 Total length (>= 50000 bp) 0 # contigs 12 Largest contig 14321 Total length 39604 Reference length 4052370 GC (%) 41.74 Reference GC (%) 59.44 N50 10809 N75 2135 L50 2 L75 4 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 Misassembled contigs 0 # scaffold gap ext. mis. 0 # scaffold gap ext. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 1+ 7 part 0 Unaligned length 36369 Genome fraction (%) 0.029 Duplication ratio 2.714 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3775.17 # indels per 100 kbp 0.00 Largest alignment 371 Total aligned length 1420  |                        | ļ  |
| Total length (>= 1000 bp)         36986           Total length (>= 5000 bp)         25130           Total length (>= 10000 bp)         25130           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         14321           Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00 |                        | <del>                                     </del> |
| Total length (>= 5000 bp)         25130           Total length (>= 10000 bp)         25130           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         14321           Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           |                        |  |
| Total length (>= 10000 bp)         25130           Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         14321           Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned contigs         1 + 7 part           Unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371              |                        | ļ  |
| Total length (>= 25000 bp)         0           Total length (>= 50000 bp)         0           # contigs         12           Largest contig         14321           Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned contigs         1 + 7 part           Unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420                     |                        | ļ  |
| Total length (>= 50000 bp)         0           # contigs         12           Largest contig         14321           Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420   |                        | <u> </u>   |
| # contigs 12 Largest contig 14321 Total length 39604 Reference length 4052370 GC (%) 41.74 Reference GC (%) 59.44 N50 10809 N75 2135 L50 2 L75 4 # misassemblies 0 # misassembled contigs 0 Misassembled contigs 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 1 + 7 part Unaligned length 36369 Genome fraction (%) 0.029 Duplication ratio 2.714 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3775.17 # indels per 100 kbp 0.00 Largest alignment 371 Total aligned length 1420  |                        |  |
| Largest contig         14321           Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned contigs         1 + 7 part           Unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| Total length         39604           Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| Reference length         4052370           GC (%)         41.74           Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned contigs         1 + 7 part           Unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| GC (%)       41.74         Reference GC (%)       59.44         N50       10809         N75       2135         L50       2         L75       4         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       2         # unaligned length       36369         Genome fraction (%)       0.029         Duplication ratio       2.714         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3775.17         # indels per 100 kbp       0.00         Largest alignment       371         Total aligned length       1420  |                        |  |
| Reference GC (%)         59.44           N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           Misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned contigs         1 + 7 part           Unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| N50         10809           N75         2135           L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| N75       2135         L50       2         L75       4         # misassemblies       0         Misassembled contigs       0         Misassembled contigs length       0         # local misassemblies       0         # scaffold gap ext. mis.       0         # scaffold gap loc. mis.       0         # unaligned mis. contigs       2         # unaligned contigs       1 + 7 part         Unaligned length       36369         Genome fraction (%)       0.029         Duplication ratio       2.714         # N's per 100 kbp       0.00         # mismatches per 100 kbp       3775.17         # indels per 100 kbp       0.00         Largest alignment       371         Total aligned length       1420   |                        |  |
| L50         2           L75         4           # misassemblies         0           # misassembled contigs         0           Misassembled contigs length         0           # local misassemblies         0           # scaffold gap ext. mis.         0           # scaffold gap loc. mis.         0           # unaligned mis. contigs         2           # unaligned contigs         1 + 7 part           Unaligned length         36369           Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| # misassemblies 0 # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 1 + 7 part Unaligned length 36369 Genome fraction (%) 0.029 Duplication ratio 2.714 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3775.17 # indels per 100 kbp 0.00 Largest alignment 371 Total aligned length 1420  |                        |  |
| # misassemblies 0  # misassembled contigs 0  Misassembled contigs length 0  # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 2  # unaligned contigs 1 + 7 part 1  |                        |  |
| # misassembled contigs 0 Misassembled contigs length 0 # local misassemblies 0 # scaffold gap ext. mis. 0 # scaffold gap loc. mis. 0 # unaligned mis. contigs 2 # unaligned contigs 1 + 7 part Unaligned length 36369 Genome fraction (%) 0.029 Duplication ratio 2.714 # N's per 100 kbp 0.00 # mismatches per 100 kbp 3775.17 # indels per 100 kbp 0.00 Largest alignment 371 Total aligned length 1420  |                        | <u>'</u>   |
| Misassembled contigs length # local misassemblies  # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  1 + 7 part  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  Largest alignment  Total aligned length  0  0  1  1  1  1  1  1  1  1  1  1  1  |                        |  |
| # local misassemblies 0  # scaffold gap ext. mis. 0  # scaffold gap loc. mis. 0  # unaligned mis. contigs 2  # unaligned contigs 1 + 7 part  Unaligned length 36369  Genome fraction (%) 0.029  Duplication ratio 2.714  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3775.17  # indels per 100 kbp 0.00  Largest alignment 371  Total aligned length 1420   |                        |  |
| # scaffold gap ext. mis.  # scaffold gap loc. mis.  # unaligned mis. contigs  # unaligned contigs  1 + 7 part  Unaligned length  Genome fraction (%)  Duplication ratio  # N's per 100 kbp  # mismatches per 100 kbp  Largest alignment  Total aligned length  1420  |                        |  |
| # scaffold gap loc. mis. 0  # unaligned mis. contigs 2  # unaligned contigs 1 + 7 part  Unaligned length 36369  Genome fraction (%) 0.029  Duplication ratio 2.714  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3775.17  # indels per 100 kbp 0.00  Largest alignment 371  Total aligned length 1420  |                        |  |
| # unaligned mis. contigs 2  # unaligned contigs 1 + 7 part  Unaligned length 36369  Genome fraction (%) 0.029  Duplication ratio 2.714  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3775.17  # indels per 100 kbp 0.00  Largest alignment 371  Total aligned length 1420  |                        |  |
| # unaligned contigs  |                        | ļ  |
| Unaligned length 36369  Genome fraction (%) 0.029  Duplication ratio 2.714  # N's per 100 kbp 0.00  # mismatches per 100 kbp 3775.17  # indels per 100 kbp 0.00  Largest alignment 371  Total aligned length 1420  |                        |  |
| Genome fraction (%)         0.029           Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        | <u> </u>   |
| Duplication ratio         2.714           # N's per 100 kbp         0.00           # mismatches per 100 kbp         3775.17           # indels per 100 kbp         0.00           Largest alignment         371           Total aligned length         1420  |                        |  |
| # N's per 100 kbp 0.00  # mismatches per 100 kbp 3775.17  # indels per 100 kbp 0.00  Largest alignment 371  Total aligned length 1420  |                        |  |
| # mismatches per 100 kbp 3775.17 # indels per 100 kbp 0.00 Largest alignment 371 Total aligned length 1420   |                        | ļ  |
| # indels per 100 kbp 0.00 Largest alignment 371 Total aligned length 1420  |                        |  |
| Largest alignment 371 Total aligned length 1420  |                        | 3775.17  |
| Total aligned length 1420  |                        | 0.00   |
|  |                        | 371  |
| NGA50 -  | Total aligned length   | 1420   |
|  | 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 | 3             |
| # possible misassemblies        | 4             |
| # local misassemblies           | 0             |
| # scaffold gap ext. mis.        | 0             |
| # scaffold gap loc. mis.        | 0             |
| # unaligned mis. contigs        | 2             |
| # mismatches                    | 45            |
| # indels                        | 0             |
| # indels (<= 5 bp)              | 0             |
| # indels (> 5 bp)               | 0             |
| Indels length                   | 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).

## Unaligned report

|                               | final.contigs |
|-------------------------------|---------------|
| # fully unaligned contigs     | 1             |
| Fully unaligned length        | 2135          |
| # partially unaligned contigs | 7             |
| Partially unaligned length    | 34234         |
| # 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).



















