## Report

| # contigs (>= 1000 bp)   |                             | scaffolds  |
|--|-----------------------------|------------|
| # contigs (>= 5000 bp) 157 # contigs (>= 10000 bp) 114 # contigs (>= 25000 bp) 56 # contigs (>= 50000 bp) 26 Total length (>= 10000 bp) 4679558 Total length (>= 10000 bp) 4507648 Total length (>= 10000 bp) 4186860 Total length (>= 25000 bp) 3234821 Total length (>= 50000 bp) 2177151 # contigs 260 Largest contig 186891 Total length 4699304 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.79 N50 44872 N75 20059 NG75 20519 L50 30 LG50 30 L75 69 LG75 67 # misassemblies 1 # misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 31 LA50 31 LA50 30 LA75 70  | # contias (>= 1000 bp)      |            |
| # contigs (>= 10000 bp)  |                             |            |
| # contigs (>= 25000 bp)  |                             |            |
| # contigs (>= 50000 bp) 26  Total length (>= 1000 bp) 4679558  Total length (>= 5000 bp) 4507648  Total length (>= 10000 bp) 4186860  Total length (>= 25000 bp) 3234821  Total length (>= 50000 bp) 2177151  # contigs 260  Largest contig 186891  Total length 4699304  Reference length 4641652  GC (%) 50.73  Reference GC (%) 50.79  N50 44872  N75 20059  NG75 20519  L50 30  L75 69  LG75 67  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 10  Hocal misassemblies 2  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 88.081  Duplication ratio 1.149  # N's per 100 kbp 0.00  # mismatches per 100 kbp 124.94  # indels per 100 kbp 0.71  Largest alignment 186891  NA50 44646  NGA50 44872  NA75 19199  NGA75 20406  LA50 30  LA75 70  |                             | 56         |
| Total length (>= 1000 bp) 4679558  Total length (>= 5000 bp) 4507648  Total length (>= 10000 bp) 4186860  Total length (>= 25000 bp) 3234821  Total length (>= 50000 bp) 2177151  # contigs 260  Largest contig 186891  Total length 4699304  Reference length 4641652  GC (%) 50.73  Reference GC (%) 50.79  N50 44872  N75 20059  NG75 20519  L50 30  L75 69  LG75 67  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 1  Misassembled contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 88.081  Duplication ratio 1.149  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1124.94  # indels per 100 kbp 0.71  Largest alignment 186891  NA50 44672  NA75 19199  NGA75 20406  LA50 31  LGA50 30  LA75 70   |                             | 26         |
| Total length (>= 5000 bp)  |                             | 4679558    |
| Total length (>= 25000 bp) 3234821  Total length (>= 50000 bp) 2177151  # contigs 260  Largest contig 186891  Total length 4699304  Reference length 4641652  GC (%) 50.73  Reference GC (%) 50.79  N50 44872  N75 20059  NG75 20519  L50 30  L75 69  LG75 67  # misassemblies 1  # misassembled contigs 1  Misassembled contigs 1  Misassembled contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 88.081  Duplication ratio 1.149  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1124.94  # indels per 100 kbp 0.71  Largest alignment 186891  NA50 44646  NGA50 44872  NA75 19199  NGA75 20406  LA50 31  LGA50 30  LA75 70  | Total length (>= 5000 bp)   | 4507648    |
| Total length (>= 50000 bp)         2177151           # contigs         260           Largest contig         186891           Total length         4699304           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         44872           NG50         44872           N75         20559           NG75         20519           L50         30           L75         69           LG75         67           # misassemblies         1           # local misassembled contigs         1           Misassembled contigs length         66116           # local misassemblies         2           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         88.081           Duplication ratio         1.149           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.71           Largest alignment         186891           NA50         44646           NGA50         44872           NA75         19199           N | Total length (>= 10000 bp)  | 4186860    |
| # contigs 260 Largest contig 186891 Total length 4699304 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.79 N50 44872 NG50 44872 N75 20059 NG75 20519 L50 30 LG50 30 L75 69 LG75 67 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70  | Total length (>= 25000 bp)  | 3234821    |
| # contigs 260 Largest contig 186891 Total length 4699304 Reference length 4641652 GC (%) 50.73 Reference GC (%) 50.79 N50 44872 NG50 44872 N75 20059 NG75 20519 L50 30 LG50 30 L75 69 LG75 67 # misassemblies 1 # misassembled contigs 1 Misassembled contigs 1 Misassembled contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70  | Total length (>= 50000 bp)  | 2177151    |
| Total length         4699304           Reference length         4641652           GC (%)         50.73           Reference GC (%)         50.79           N50         44872           NG50         44872           N75         20059           NG75         20519           L50         30           L75         69           LG75         67           # misassemblies         1           # local misassemblies         2           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         88.081           Duplication ratio         1.149           # N's per 100 kbp         0.00           # mismatches per 100 kbp         0.71           Largest alignment         186891           NA50         44646           NGA50         44872           NA75         19199           NGA75         20406           LA50         31           LGA50         30           LA75         70  |                             | 260        |
| Reference length       4641652         GC (%)       50.73         Reference GC (%)       50.79         N50       44872         NG50       44872         N75       20059         NG75       20519         L50       30         LG50       30         L75       69         LG75       67         # misassemblies       1         # local misassembled contigs       1         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | Largest contig              | 186891     |
| GC (%)       50.73         Reference GC (%)       50.79         N50       44872         NG50       44872         N75       20059         NG75       20519         L50       30         L75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | Total length                | 4699304    |
| Reference GC (%)       50.79         N50       44872         NG50       44872         N75       20059         NG75       20519         L50       30         L75       69         LG75       67         # misassemblies       1         # local misassembled contigs       1         # local misassembles       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   | Reference length            | 4641652    |
| N50       44872         NG50       44872         N75       20059         NG75       20519         L50       30         LG50       30         LG75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | GC (%)                      | 50.73      |
| NG50       44872         N75       20059         NG75       20519         L50       30         LG50       30         L75       69         LG75       67         # misassemblies       1         Misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | Reference GC (%)            | 50.79      |
| N75       20059         NG75       20519         L50       30         L75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   | N50                         | 44872      |
| NG75       20519         L50       30         LG50       30         L75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   | NG50                        | 44872      |
| L50       30         LG50       30         L75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | N75                         | 20059      |
| LG50       30         L75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   | NG75                        | 20519      |
| L75       69         LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   | L50                         | 30         |
| LG75       67         # misassemblies       1         # misassembled contigs       1         Misassembled contigs length       66116         # local misassemblies       2         # unaligned contigs       0 + 0 part         Unaligned length       0         Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | LG50                        | 30         |
| # misassemblies 1 # misassembled contigs 1 Misassembled contigs length 66116 # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70  | L75                         | 69         |
| # misassembled contigs 1  Misassembled contigs length 66116  # local misassemblies 2  # unaligned contigs 0 + 0 part  Unaligned length 0  Genome fraction (%) 88.081  Duplication ratio 1.149  # N's per 100 kbp 0.00  # mismatches per 100 kbp 1124.94  # indels per 100 kbp 0.71  Largest alignment 186891  NA50 44646  NGA50 44872  NA75 19199  NGA75 20406  LA50 31  LGA50 30  LA75 70   | LG75                        | 67         |
| Misassembled contigs length         66116           # local misassemblies         2           # unaligned contigs         0 + 0 part           Unaligned length         0           Genome fraction (%)         88.081           Duplication ratio         1.149           # N's per 100 kbp         0.00           # mismatches per 100 kbp         1124.94           # indels per 100 kbp         0.71           Largest alignment         186891           NA50         44646           NGA50         44872           NA75         19199           NGA75         20406           LA50         31           LGA50         30           LA75         70   | # misassemblies             | 1          |
| # local misassemblies 2 # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70   | # misassembled contigs      | 1          |
| # unaligned contigs 0 + 0 part Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70   | Misassembled contigs length | 66116      |
| Unaligned length 0 Genome fraction (%) 88.081 Duplication ratio 1.149 # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70  | # local misassemblies       | 2          |
| Genome fraction (%)       88.081         Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   |                             | 0 + 0 part |
| Duplication ratio       1.149         # N's per 100 kbp       0.00         # mismatches per 100 kbp       1124.94         # indels per 100 kbp       0.71         Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | Unaligned length            | 0          |
| # N's per 100 kbp 0.00 # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70  |                             | 88.081     |
| # mismatches per 100 kbp 1124.94 # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70   |                             |            |
| # indels per 100 kbp 0.71 Largest alignment 186891 NA50 44646 NGA50 44872 NA75 19199 NGA75 20406 LA50 31 LGA50 30 LA75 70  |                             | 0.00       |
| Largest alignment       186891         NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70  | # mismatches per 100 kbp    | 1124.94    |
| NA50       44646         NGA50       44872         NA75       19199         NGA75       20406         LA50       31         LGA50       30         LA75       70   | # indels per 100 kbp        |            |
| NGA50     44872       NA75     19199       NGA75     20406       LA50     31       LGA50     30       LA75     70  | Largest alignment           | 186891     |
| NA75     19199       NGA75     20406       LA50     31       LGA50     30       LA75     70  |                             | 44646      |
| NGA75     20406       LA50     31       LGA50     30       LA75     70   |                             |            |
| LA50     31       LGA50     30       LA75     70   |                             |            |
| LGA50 30<br>LA75 70  |                             |            |
| LA75 70  |                             |            |
|  |                             |            |
| LGA75 68   |                             |            |
|  | LGA75                       | 68         |

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                 | 1         |
| # relocations                   | 1         |
| # translocations                | 0         |
| # inversions                    | 0         |
| # possibly misassembled contigs | 0         |
| # misassembled contigs          | 1         |
| Misassembled contigs length     | 66116     |
| # local misassemblies           | 2         |
| # mismatches                    | 45992     |
| # indels                        | 29        |
| # short indels                  | 29        |
| # long indels                   | 0         |
| Indels length                   | 35        |

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















