**Supplementary Table S1.** Assembly statistics. The FALCON assembly was generated with PacBio long reads. The Dovetail HiRise pipeline used Hi-C data to improve the FALCON assembly. Statistics are generated by Dovetail Genomics.

|  |  |  |
| --- | --- | --- |
| Assembly | FALCON | Dovetail HiRise |
| Total Length | 135.85 Mb | 135.86 Mb |
| L50/N50 | 10 scaffolds; 4.042 Mb | 3 scaffolds; 21.502 Mb |
| L90/N90 | 38 scaffolds; 0.659 Mb | 6 scaffolds; 17.248 Mb |
| Longest Scaffold | 11,873,675 bp | 25,790,997 bp |
| Number of scaffolds | 298 | 235 |
| Number of scaffolds > 1kb | 298 | 235 |
| Number of gaps | 0 | 64 |
| Percent of genome in gaps  | 0.00% | 0.00% |

**Supplementary Table S2.** Summary statistics of the PacBio data used in the study. Statistics are generated by Dovetail Genomics.

|  |  |
| --- | --- |
| Input data | 1.3 M reads containing 100x coverage |
| Total # Error Corrected Reads | 0.8 M containing 63x coverage (assuming genome size of 131 Mbp) |
| N50 length of Error Corrected Reads | 13.9 kbp |
| Maximum length of Error Corrected Reads | 5.7 kbp |

**Supplementary Table S3.** Additional statistics for the HiRise assembly. Statistics are generated by Dovetail Genomics.

|  |  |
| --- | --- |
| Number of breaks made to input assembly by HiRise | 1 |
| Number of joins made by HiRise | 64 |
| Number of gaps closed after HiRise | 0 |
| Library 1 stats | 418M read pairs; 2x151 bp |