**Tables**

Table 1 N50, number of sequences, total length, and percentages of BUSCOs. BUSCOs percentages were calculated using the embryophyte odb9 dataset which contains 1,440 BUSCOS.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Assembly** | **N50 (Mbp)** | **Sequences** | **Total Length (Mbp)** | **Total Unambiguous Length (Mbp)** | **Gene Models** | **Complete BUSCOs** | **Complete single-copy BUSCOs** | **Complete duplicated BUSCOs** | **Fragmented BUSCOs** | **Missing BUSCOs** |
| Darmor-bzh (Reference) | 38.83 | 41 | 850.29 | 738.35 | 101,040 | 97.64 | 13.26 | 84.38 | 0.76 | 1.6 |
| Da-Ae - Final | 48.21 | 3,164 | 1,001.50 | 1,001.41 | 96,442 | 98.2 | 12.6 | 85.6 | 0.7 | 1.1 |
| Darmor-bzh  (19 pseudo molecules) | 38.83 | 19 | 645.4 | 553.41 | 80,927 | 94.7 | 26.6 | 68.1 | 0.6 | 4.7 |
| Da-Ae - Final  (19 pseudo molecules) | 51.43 | 19 | 816.17 | 816.08 | 88,605 | 98.1 | 12.1 | 86.0 | 0.6 | 1.3 |
| Da-Ae Davis Supernova-1.1.5 | 0.14 | 80,371 | 793.05 | 677.83 | NA | 94.38 | 35 | 59.38 | 2.71 | 2.92 |
| Da-Ae Novogene Supernova-1.1.5 | 0.14 | 81,812 | 805.97 | 693.95 | NA | 94.51 | 36.04 | 58.47 | 2.36 | 3.13 |
| Da-Ae Davis Supernova-2 | 1.57 | 35,997 | 918.49 | 811.13 | NA | 97.57 | 19.44 | 78.13 | 0.83 | 1.60 |
| *B. rapa* | 2.03 | 16,823 | 334.23 | 319.72 | NA | 97.71 | 83.68 | 14.03 | 0.69 | 1.60 |
| *B. oleracea* | 2.52 | 19,955 | 571.25 | 534.67 | NA | 97.36 | 83.06 | 14.31 | 1.04 | 1.60 |
| Da-Ae Falcon | 1.79 | 1,852 | 889.44 | 889.44 | NA | 91.74 | 48.13 | 43.61 | 2.78 | 5.49 |
| Da-Ae Falcon Unzip | 1.80 | 1,541 | 878.51 | 878.51 | NA | 92.99 | 47.57 | 45.42 | 2.01 | 5.00 |
| Da-Ae Falcon Unzip Quiver | 1.80 | 1,508 | 880.99 | 880.99 | NA | 98.26 | 17.43 | 80.83 | 0.49 | 1.25 |
| Da-Ae Pilon Falcon Unzip Quiver | 1.80 | 1,508 | 880.87 | 880.87 | NA | 98.26 | 14.79 | 83.47 | 0.56 | 1.18 |
| Da-Ae Dovetail Falcon Unzip Quiver | 35.52 | 709 | 881.08 | 880.99 | NA | 98.26 | 17.99 | 80.28 | 0.55 | 1.19 |
| Da-Ae Canu | 1.59 | 4,008 | 1,004.00 | 1,004.00 | NA | 98.06 | 15.42 | 82.64 | 0.69 | 1.25 |
| Da-Ae Pilon\_Canu | 1.59 | 4,008 | 1,003.52 | 1,003.52 | NA | 98.19 | 13.68 | 84.51 | 0.63 | 1.2 |
| DA-Ae Dovetail\_Pilon\_Canu | 42.79 | 3,190 | 1,003.60 | 1,003.52 | NA | 98.33 | 13.61 | 84.72 | 0.55 | 1.1 |

Table 2 Shared Single Copy BUSCOs

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **BUSCO ID** | **DaAe** | **Darmor-bzh** | **Tapidor** | **B. rapa** | **B. oleracea** | **Description** |
| EOG093600DF | chrA06 | chrA06 | chrC07 | chrA06 | chrC07 | XPG/Rad2 endonuclease |
| EOG093602FO | chrC02 | chrC02 | chrC02 | chrA02 | chrC02 | Pentatricopeptide repeat |
| EOG093602X4 | chrA07 | chrA07 | chrA07 | chrA07 | chrC06 | Uncharacterized protein |
| EOG09360317 | chrC04 | chrA05 | chrC04 | chrA05 | chrC04 | Ribosomal protein S5 domain 2-type fold |
| EOG093603PK | chrA05 | chrA05 | chrA05 | chrA05 | chrC05 | NHL domain-containing protein |
| EOG093604B8 | chrA07 | chrA07 | chrA07 | chrA07 | chrC06 | Golgi transport complex protein-related |
| EOG093604D4 | chrC02 | chrC02 | chrC02 | chrA02 | chrC02 | Elongation factor G, III-V domain |
| EOG0936055R | chrA01 | chrA01 | chrA02 | chrA01 | chrC01 | WW domain-containing protein |
| EOG093605DD | chrC09 | chrA10 | chrC09 | chrA10 | chrC09 | Protein kinase domain |
| EOG093605ZP | chrC08 | chrC08 | chrA01 | chrA08 | chrC08 | Cytochrome P450 |
| EOG093608BO | chrC08 | chrC08 | chrC08 | chrA09 | chrC08 | Putative uncharacterized protein |
| EOG09360B5S | chrA06 | chrA06 | chrA06 | chrA06 | chrC07 | Peptidase C78, ubiquitin fold modifier-specific peptidase 1/ 2 |
| EOG09360CRR | chrC03 | chrA02 | chrA02 | chrA02 | chrC03 | Uncharacterized protein |
| EOG09360DWT | chrC06 | chrC06 | chrC02 | chrA05 | chrC03 | Peptide chain release factor |
| EOG09360ETX | chrA06 | chrA06 | chrA02 | chrA06 | chrC07 | Histone deacetylase superfamily |
| EOG09360EX7 | chrA02 | chrC02 | chrA02 | chrA02 | chrC02 | HAUS augmin-like complex subunit 7-like |
| EOG09360FOF | chrA02 | chrC02 | chrC02 | chrA02 | chrC02 | SRP40, C-terminal |
| EOG09360G99 | chrA02 | chrA02 | chrA02 | chrA02 | chrC02 | Uncharacterized protein |
| EOG09360IS4 | chrC07 | chrC07 | chrC04 | chrA07 | chrC09 | Serine-threonine protein kinase 19 |
| EOG09360MCO | chrA05 | chrC04 | chrA07 | chrA05 | chrC04 | ubiquitin family protein |
| EOG09360N2Y | chrA09 | chrA09 | chrC09 | chrA09 | chrC09 | Oxoglutarate/iron-dependent dioxygenase |
| EOG09360PV7 | chrA10 | chrC05 | chrA10 | chrA10 | chrC05 | Prefoldin |
| EOG09360QHJ | chrC03 | chrC03 | chrC03 | chrA03 | chrC03 | heat shock protein DnaJ, putative, expressed |
| EOG09360ZSS | chrA07 | chrA07 | chrC06 | chrA07 | chrC06 | Uncharacterized protein |

Table 3 Comparison of assembly statistics. Percentages indicate percent change of Da-Ae assembly relative to Darmor-bzh.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **N50** | **Unambiguous Bases** | **Gene Models** | **Complete BUSCOs** |
| Full Assembly | 124% | 136% | 95% | 101% |
| Pseudo Molecules | 132% | 147% | 109% | 104% |