

**Table S1.** Quality assessment of transcriptome *de novo* assemblies using the Eudicotyledons odb10 dataset in BUSCO v.3.0.

| Lineage        | Assembly                   | Complete |      | Complete, single |      | Complete, duplicated |      | Fragmented |      | Missing |     |
|----------------|----------------------------|----------|------|------------------|------|----------------------|------|------------|------|---------|-----|
|                |                            | Total    | %    | Total            | %    | Total                | %    | Total      | %    | Total   | %   |
| Cam-phorosmeae | <i>B. prostrata</i>        | 1879     | 88.6 | 864              | 40.7 | 1015                 | 47.9 | 121        | 5.7  | 121     | 5.7 |
|                | <i>Sed. sedoides</i>       | 1929     | 90.9 | 1148             | 54.1 | 781                  | 36.8 | 97         | 4.6  | 95      | 4.5 |
|                | <i>T. diffusa</i>          | 1868     | 88.1 | 965              | 45.5 | 903                  | 42.6 | 142        | 6.7  | 111     | 5.2 |
| Salsoleae      | <i>H. scoparia</i>         | 1818     | 85.7 | 1089             | 51.3 | 729                  | 34.4 | 183        | 8.6  | 120     | 5.7 |
|                | <i>Sal. divaricata</i> 184 | 1846     | 87.0 | 599              | 28.2 | 1247                 | 58.8 | 164        | 7.7  | 111     | 5.3 |
|                | <i>Sal. divaricata</i> 198 | 1832     | 86.4 | 606              | 28.6 | 1226                 | 57.8 | 190        | 9.0  | 99      | 4.6 |
|                | <i>Sal. oppositifolia</i>  | 1733     | 81.7 | 480              | 22.6 | 1253                 | 59.1 | 255        | 12.0 | 133     | 6.3 |
|                | <i>Sal. soda</i>           | 1914     | 90.2 | 1273             | 60.0 | 641                  | 30.2 | 126        | 5.9  | 81      | 3.9 |
|                | <i>Sal. webbii</i>         | 1814     | 85.5 | 585              | 27.6 | 1229                 | 57.9 | 149        | 7.0  | 158     | 7.5 |

BUSCOs are categorized into complete, fragmented, and missing. Category 'complete' is subdivided into 'complete and single-copy' and 'complete and duplicated'. The total number of BUSCOs in the Eudicotyledons odb10 dataset was 2121. B., *Bassia*; H., *Hammada*; Sal., *Salsola*; Sed., *Sedobassia*; T., *Threlkeldia*.