**Supplemental Table S3.** Summary ofamount on missing data and degenerate bases in the five coding regions with missing data.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Coding regions with missing data** | **Length (bp)** | **Total number of sites** | **Missing sites** | **% Missing** | **Degenerate bases** | **% Ambigous sites** |
| *clpP* | 591 | 21,276 | 4 | 0.0188 | 0 | 0 |
| *matK* | 1,503 | 54,108 | 15 | 0.0277 | 0 | 0 |
| *ndhH* | 1,182 | 42,552 | 9 | 0.0212 | 0 | 0 |
| *rpoB* | 3,183 | 114,588 | 2 | 0.0017 | 0 | 0 |
| *ycf1* | 5,100 | 183,600 | 18 | 0.0098 | 0 | 0 |

**Note**: Length (bp): alignment length, Total number of sites: length of alignment x number of plastomes (36), Missing sites: number of missing sites, % Missing:percentage of missing sites, % Ambiguous sites: percentage of ambiguous sites.