

Table S4. Co-transcribed plastid genes found to be tightly co-expressed as determined by hierarchical clustering analysis of 89 transcriptomes.

| Clusters of homogeneous function | Clusters of heterogeneous function |
|---|---|
| <i>psbD, psbC</i> | <i>rpl14, rpl36, rps11, rpoA</i> |
| <i>atpI, atpH</i> | <i>trnA-ugc, rrn23S</i> |
| <i>atpB, atpE</i> | <i>rps15, ndhH, ndhA</i> |
| <i>ndhK, ndhJ</i> | <i>trnE-uuc, psbM</i> |
| <i>rpoC1, rpoC2</i> | <i>rrn16S, trnI-gau, rrn5S</i> |
| <i>rpl22, rps3</i> | <i>psbB, psbT_c, psbH, petB, petD</i> |
| <i>ndhI, ndhG, ndhE</i> | <i>ndhD, psaC</i> |
| <i>psbF, psbL</i> | <i>psaA, psaB, rps14</i> |
| <i>atpF, atpA</i> | |