

Table S2. Summary of rice (spp. *Japonica*) GO category enrichment under photocycles (LDHH).

| GO-ID | GO category | P-value | Correlation P-value | Cluster frequency | Overall frequency |
|-------|---|----------|---------------------|-------------------|-------------------|
| 166 | nucleotide binding | 1.17E-29 | 1.12E-27 | 709/3352 21.1% | 4284/29753 14.3% |
| 6519 | amino acid and derivative metabolic process | 4.20E-26 | 2.02E-24 | 140/3352 4.1% | 490/29753 1.6% |
| 5737 | cytoplasm | 3.87E-25 | 1.24E-23 | 501/3352 14.9% | 2881/29753 9.6% |
| 5623 | cell | 6.37E-22 | 1.53E-20 | 1446/3352 43.1% | 10591/29753 35.5% |
| 5575 | cellular component | 1.61E-18 | 3.08E-17 | 1472/3352 43.9% | 11008/29753 36.9% |
| 5478 | transporter activity | 6.76E-15 | 1.08E-13 | 279/3352 8.3% | 1581/29753 5.3% |
| 6810 | transport | 2.51E-14 | 3.44E-13 | 403/3352 12.0% | 2510/29753 8.4% |
| 5622 | intracellular | 6.85E-12 | 8.21E-11 | 1000/3352 29.8% | 7431/29753 24.9% |
| 16301 | kinase activity | 2.82E-11 | 3.01E-10 | 327/3352 9.7% | 2055/29753 6.9% |
| 16020 | membrane | 2.25E-10 | 2.16E-09 | 580/3352 17.3% | 4076/29753 13.6% |
| 19725 | cellular homeostasis | 1.32E-09 | 1.15E-08 | 45/3352 1.3% | 155/29753 0.5% |
| 6464 | protein modification process | 1.76E-09 | 1.41E-08 | 315/3352 9.3% | 2038/29753 6.8% |
| 19748 | secondary metabolic process | 4.57E-07 | 3.37E-06 | 38/3352 1.1% | 145/29753 0.4% |
| 9056 | catabolic process | 2.02E-06 | 1.38E-05 | 122/3352 3.6% | 716/29753 2.4% |
| 6416 | translation | 2.48E-06 | 1.54E-05 | 151/3352 4.5% | 931/29753 3.1% |
| 5975 | carbohydrate metabolic process | 2.57E-06 | 1.54E-05 | 152/3352 4.5% | 939/29753 3.1% |
| 5739 | mitochondrion | 8.24E-06 | 4.65E-05 | 72/3352 2.1% | 382/29753 1.2% |
| 8150 | biological process | 9.20E-05 | 4.90E-04 | 2566/3352 76.5% | 21984/29753 73.8% |
| 9536 | plastid | 2.63E-04 | 1.33E-03 | 93/3352 2.7% | 578/29753 1.9% |
| 5730 | nucleolus | 3.82E-04 | 1.84E-03 | 7/3352 0.2% | 14/29753 0.0% |
| 8135 | translation factor activity | 9.44E-04 | 4.31E-03 | 31/3352 0.9% | 154/29753 0.5% |
| 45182 | translation regulator activity | 1.05E-03 | 4.60E-03 | 31/3352 0.9% | 155/29753 0.5% |
| 6629 | lipid metabolic process | 1.27E-03 | 5.30E-03 | 105/3352 3.1% | 698/29753 2.3% |
| 19818 | peroxisome | 3.59E-03 | 1.43E-02 | 8/3352 0.2% | 24/29753 0.0% |
| 5783 | endoplasmic reticulum | 5.58E-03 | 2.14E-02 | 32/3352 0.9% | 179/29753 0.6% |
| 15979 | photosynthesis | 6.78E-03 | 2.50E-02 | 37/3352 1.1% | 217/29753 0.7% |
| 5840 | ribosome | 1.25E-02 | 4.45E-02 | 106/3352 3.1% | 761/29753 2.5% |