**Supplemental Table 2.** Gene ontology enrichment analysis of 62 genes not placed on 7 major assembly pseudomolecules shows enrichment for ribosome and peptide assembly.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| GO.ID | Term | Annotated | Significant | Expected | classic |
| GO:0006412 | translation | 918 | 6 | 0.4 | 4.20E-07 |
| GO:0043043 | peptide biosynthetic process | 927 | 6 | 0.41 | 4.40E-07 |
| GO:0043604 | amide biosynthetic process | 990 | 6 | 0.44 | 6.50E-07 |
| GO:0006518 | peptide metabolic process | 1039 | 6 | 0.46 | 8.70E-07 |
| GO:0043603 | cellular amide metabolic process | 1155 | 6 | 0.51 | 1.60E-06 |
| GO:1901566 | organonitrogen compound biosynthetic process | 1737 | 6 | 0.76 | 1.80E-05 |
| GO:0000028 | ribosomal small subunit assembly | 26 | 2 | 0.01 | 5.50E-05 |
| GO:0019684 | photosynthesis, light reaction | 68 | 2 | 0.03 | 0.00038 |
| GO:0042274 | ribosomal small subunit biogenesis | 83 | 2 | 0.04 | 0.00057 |
| GO:0042255 | ribosome assembly | 98 | 2 | 0.04 | 0.00079 |
| GO:0006091 | generation of precursor metabolites and energy | 475 | 3 | 0.21 | 0.0009 |
| GO:0044271 | cellular nitrogen compound biosynthetic process | 3769 | 6 | 1.66 | 0.00149 |
| GO:0015979 | photosynthesis | 142 | 2 | 0.06 | 0.00164 |
| GO:0034645 | cellular macromolecule biosynthetic process | 3855 | 6 | 1.69 | 0.00169 |
| GO:0009059 | macromolecule biosynthetic process | 3912 | 6 | 1.72 | 0.00183 |
| GO:0010467 | gene expression | 3947 | 6 | 1.73 | 0.00193 |
| GO:0022618 | ribonucleoprotein complex assembly | 179 | 2 | 0.08 | 0.00259 |
| GO:0071826 | ribonucleoprotein complex subunit organization | 186 | 2 | 0.08 | 0.00279 |
| GO:0070925 | organelle assembly | 191 | 2 | 0.08 | 0.00294 |
| GO:0044267 | cellular protein metabolic process | 4607 | 6 | 2.03 | 0.00452 |
| GO:0044249 | cellular biosynthetic process | 5003 | 6 | 2.2 | 0.00706 |
| GO:1901576 | organic substance biosynthetic process | 5137 | 6 | 2.26 | 0.00814 |
| GO:0009058 | biosynthetic process | 5237 | 6 | 2.3 | 0.00903 |
| GO:0019538 | protein metabolic process | 5464 | 6 | 2.4 | 0.01132 |
| GO:0042773 | ATP synthesis coupled electron transport | 29 | 1 | 0.01 | 0.01268 |
| GO:0042254 | ribosome biogenesis | 428 | 2 | 0.19 | 0.01406 |
| GO:0000462 | maturation of SSU-rRNA from tricistronic rRNA transcript | 37 | 1 | 0.02 | 0.01615 |
| GO:0006119 | oxidative phosphorylation | 38 | 1 | 0.02 | 0.01658 |
| GO:0022904 | respiratory electron transport chain | 38 | 1 | 0.02 | 0.01658 |
| GO:0034622 | cellular protein-containing complex assembly | 507 | 2 | 0.22 | 0.0194 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 518 | 2 | 0.23 | 0.0202 |
| GO:0034641 | cellular nitrogen compound metabolic process | 6207 | 6 | 2.73 | 0.02212 |
| GO:0030490 | maturation of SSU-rRNA | 55 | 1 | 0.02 | 0.02393 |
| GO:0065003 | protein-containing complex assembly | 567 | 2 | 0.25 | 0.02395 |
| GO:1901564 | organonitrogen compound metabolic process | 6479 | 6 | 2.85 | 0.0276 |
| GO:0044237 | cellular metabolic process | 11789 | 8 | 5.18 | 0.03097 |
| GO:0043933 | protein-containing complex subunit organization | 664 | 2 | 0.29 | 0.03215 |
| GO:0045333 | cellular respiration | 86 | 1 | 0.04 | 0.03719 |
| GO:0022607 | cellular component assembly | 793 | 2 | 0.35 | 0.04458 |
| GO:0015980 | energy derivation by oxidation of organic compounds | 109 | 1 | 0.05 | 0.04693 |

Note:6 of 10 processes most overrepresented among 62 genes relate to ribosome or peptide assembly (and 6 of 30 remaining significantly overrepresented biological process gene ontologies); classic topGO algorithm using a Fischer exact test of statistical significance.