| GO terms | Ref-list (34652) | UP genes | Expect. | Fold enrich. | raw P-value | FDR |
|------------|--|---|--|---|---|---|
| GO:0019941 | 308 | 65 | 37.6 | 1.73 | 1.51E-04 | 2.60E-03 |
| GO:0006511 | 291 | 61 | 35.52 | 1.72 | 2.74E-04 | 3.99E-03 |
| GO:0043162 | 11 | 9 | 1.34 | 6.7 | 1.16E-04 | 2.15E-03 |
| GO:0016192 | 358 | 84 | 43.7 | 1.92 | 4.40E-07 | 1.52E-05 |
| GO:0071985 | 27 | 14 | 3.3 | 4.25 | 6.44E-05 | 1.39E-03 |
| GO:0061919 | 45 | 14 | 5.49 | 2.55 | 4.83E-03 | 3.64E-02 |
| GO:0006914 | 45 | 14 | 5.49 | 2.55 | 4.83E-03 | 3.66E-02 |
| GO:0000422 | 14 | 9 | 1.71 | 5.27 | 4.15E-04 | 5.32E-03 |
| GO:000045 | 23 | 10 | 2.81 | 3.56 | 2.01E-03 | 1.84E-02 |
| - | GO:0019941 GO:0006511 GO:0043162 GO:0016192 GO:0071985 GO:0061919 GO:0006914 GO:0000422 | (34652) GO:0019941 308 GO:0006511 291 GO:0043162 11 GO:0016192 358 GO:0071985 27 GO:0061919 45 GO:0006914 45 GO:000422 14 | (34652) genes GO:0019941 308 65 GO:0006511 291 61 GO:0043162 11 9 GO:0016192 358 84 GO:0071985 27 14 GO:0061919 45 14 GO:006914 45 14 GO:000422 14 9 | (34652) genes GO:0019941 308 65 37.6 GO:0006511 291 61 35.52 GO:0043162 11 9 1.34 GO:0016192 358 84 43.7 GO:0071985 27 14 3.3 GO:006914 45 14 5.49 GO:0006924 14 9 1.71 | (34652) genes enrich. GO:0019941 308 65 37.6 1.73 GO:0006511 291 61 35.52 1.72 GO:0043162 11 9 1.34 6.7 GO:0016192 358 84 43.7 1.92 GO:0071985 27 14 3.3 4.25 GO:006914 45 14 5.49 2.55 GO:0006914 45 14 5.49 2.55 GO:000422 14 9 1.71 5.27 | (34652) genes enrich. P-value GO:0019941 308 65 37.6 1.73 1.51E-04 GO:0006511 291 61 35.52 1.72 2.74E-04 GO:0043162 11 9 1.34 6.7 1.16E-04 GO:0016192 358 84 43.7 1.92 4.40E-07 GO:0071985 27 14 3.3 4.25 6.44E-05 GO:0061919 45 14 5.49 2.55 4.83E-03 GO:0006914 45 14 5.49 2.55 4.83E-03 GO:0000912 14 9 1.71 5.27 4.15E-04 |

Additional file 3: Fig. S3. Functional enrichment of upregulated genes upon TYLCV infection at 21 dpi. Gene ontology (GO) analysis of upregulated genes at 21 dpi (4980 genes with a ratio \geq 1.5-fold, FDR adjusted p-value \leq 0.05, when comparing TYLCV-infected samples versus mock samples) using the PANTHER GO-Slim biological process (statistical overrepresentation test). Only selected statistically significant biological processes are shown (FDR adjusted p-value p \leq 0.05).