**Table S6 - Significantly enriched GO terms in the DEG sets of the different host plant populations of T. urticae**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| host plant population | GO ID | category | GO-term | up/down\* |
| lima bean | GO:0008233 | MF | peptidase activity | up |
|  |  |  |  |  |
| soybean | GO:0043167 | MF | ion binding | up |
|  | GO:0005615 | CC | extracellular space | down |
|  |  |  |  |  |
| cotton | GO:0008233 | MF | peptidase activity | up |
|  | GO:0005615 | CC | extracellular space | up |
|  |  |  |  |  |
| tomato | GO:0043167 | MF | ion binding | up |
|  | GO:0016301 | MF | kinase activity | up |
|  | GO:0003700 | MF | DNA binding transcription factor activity | up |
|  | GO:0003677 | MF | DNA binding | up |
|  | GO:0008092 | MF | cytoskeleton protein binding | up |
|  | GO:0016887 | MF | ATPase activity | up |
|  | GO:0055085 | BP | transmembrane transport | up |
|  | GO:0007165 | BP | signal transduction | up |
|  | GO:0006464 | BP | cellular protein modification complex | up |
|  | GO:0009058 | BP | biosynthetic process | up |
|  | GO:0005575 | CC | cellular component | up |
|  | GO:0005622 | CC | intracellular component | up |
|  | GO:0032991 | CC | protein-containing complex | up |
|  | GO:0005856 | CC | cytoskeleton | up |
|  | GO:0042254 | BP | ribosome biogenesis | down |
|  |  |  |  |  |
| maize | GO:0016829 | MF | lyase activity | down |
|  | GO:0016746 | MF | transferase activity, transferring acyl groups | down |
|  | GO:0006629 | BP | lipid metabolic process | down |
|  | GO:0005576 | CC | extracellular region | down |

\* GO-terms were either enriched in the up- or downregulated DEGs