**Tables and Figures**

|  |  |
| --- | --- |
| **Enrichment term** | **P-value** |
| GO:0009723~response to ethylene stimulus | 6.78E-14 |
| GO:0009737~response to abscisic acid stimulus | 1.95E-09 |
| GO:0009651~response to salt stress | 6.10E-07 |
| GO:0009414~response to water deprivation | 5.38E-06 |
| GO:0009718~anthocyanin biosynthetic process | 1.26E-04 |
| GO:0009409~response to cold | 0.006 |
| GO:0009408~response to heat | 0.058 |

**Table 1. Examples of enriched plant drought response-related processes identified using MolSig.** Gene groups identified by MolSig were subject to functional ORA. Terms with a P-value of ≤ 0.05 were considered to be enriched in each respective gene group.

**Figure 1. Number of common and non-common functional enriched terms identified by MolSig using either a single gene expression co-correlation graph (GE) or combined GE and GO\_biological process semantic similarity graph (SS).** Gene groups identified by MolSig were subject to functional ORA. Terms with a P-value of ≤ 0.05 were considered to be enriched in each respective gene group.

**B**

**A**

**Figure 2. Comparison of the** **number of common and non-common functional enriched terms identified either by MolSig (GE + SS) or by two clustering algorithms, K-Means (A) and Affinity Propagation (B).** For all algorithms, k was set at 15. Gene groups/clusters identified by the different algorithms were subject to functional ORA. Terms with a P-value of ≤ 0.05 were considered to be enriched in each respective gene group. KM, K-means; AP, Affinity Propagation.