

Supplementary figure 1. Clustered display of genes responding to OPDA, JA, and MeJA treatment.

Data from chemical treatments (OPDA, JA, and MeJA) were analyzed by hierarchical clustering. Result of hierarchical clustering is represented as heat map of gene expression profiles, where red indicates induced and blue indicates repressed. Hierarchical clusters of selected genes are shown. In Cluster 1, genes preferentially responding to OPDA but not to JA and MeJA are shown. Cluster 2 is comprised of genes repressed by OPDA but not JA and MeJA (supplementary file 2). Cluster 1 contains most of ORGs presented in Table 1. On the other hand, Cluster 2 contains most of down-regulated ORGs in Table 2.

Calculation was performed as follows. We first selected 1078 genes for clustering, which include all 172 ORGs and 449 JRGs according to a following criterion;

$$MxAbNRE_g \equiv \max_{tr,t} |NRE_{tr,t,g}| > \log_{10}(3)$$

Then $NRE_{tr,r,t,g}$, the value before unification of duplicate data (see Materials and Methods), was normalized by the $MxAbNRE_g$ and the normalized value was used for clustering.

$$MxAbNNRE_{tr,r,t,g} = \frac{NRE_{tr,r,t,g}}{MxAbNRE_g}$$

The normalized value, $MxAbNNRE_{tr,r,t,g}$, of 1078 genes were hierarchically clustered with their Euclidean distances using ward method in statistical language R.

Almost identical result was obtained when we calculated from $NRE_{tr,t,g}$, the NRE value after unification of duplicate data (data not shown).