



**Supplemental Figure 1.** Hierarchical clustering of transcriptional changes shows clearly the dynamics of the different time course experiments.

Temporal expression patterns for the *flu* (A), CAT2HP1+HL (B), LOH2+AAL-toxin (C), KO-*Apx1*+HL (D) and MV (E) experiments are presented. After data processing, as described in “Materials and Methods”, a coefficient of variation (CV) was used as a selection criterion for differential gene expression. The CV was calculated as the ratio of the SD and the average expression over the time course. A threshold for positive response was set at  $CV > 0.9$ , resulting in 841, 907, 872, 365 and 644 genes for A, B, C, D and E, respectively. The color of each gene indicates its expression level relative to its mean across all time points. Expression levels higher, equal or lower than the mean level are represented by red, black or green, respectively.