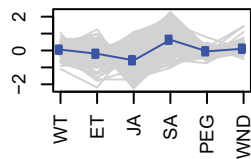


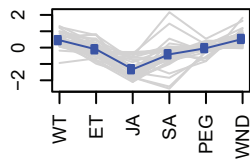
centered log₂(TPM+1)

c1, 138 genes



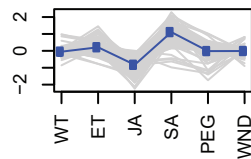
centered log₂(TPM+1)

c2, 37 genes



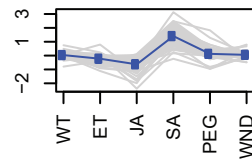
centered log₂(TPM+1)

c3, 128 genes



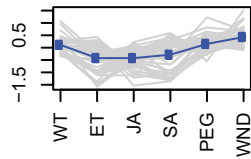
centered log₂(TPM+1)

c4, 58 genes



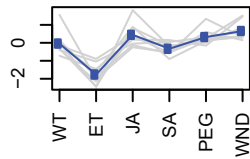
centered log₂(TPM+1)

c5, 46 genes



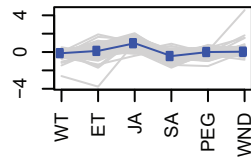
centered log₂(TPM+1)

c6, 9 genes



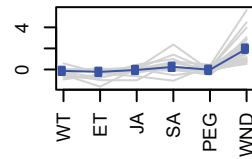
centered log₂(TPM+1)

c7, 213 genes



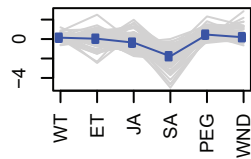
centered log₂(TPM+1)

c8, 24 genes



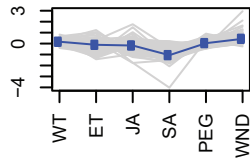
centered log₂(TPM+1)

c9, 156 genes



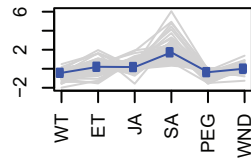
centered log₂(TPM+1)

c10, 64 genes



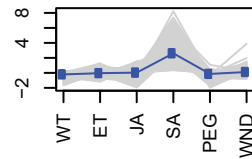
centered log₂(TPM+1)

c11, 181 genes



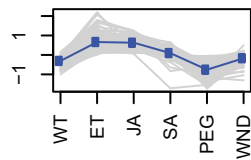
centered log₂(TPM+1)

c12, 478 genes



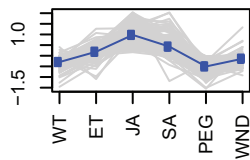
centered log₂(TPM+1)

c13, 115 genes



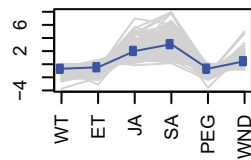
centered log₂(TPM+1)

c14, 159 genes



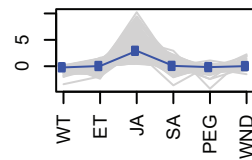
centered log₂(TPM+1)

c15, 165 genes



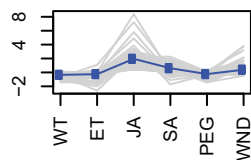
centered log₂(TPM+1)

c16, 379 genes



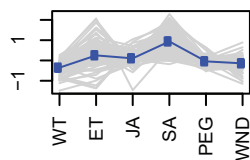
centered log₂(TPM+1)

c17, 96 genes



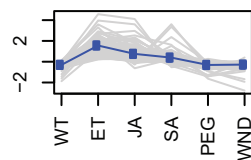
centered log₂(TPM+1)

c18, 104 genes



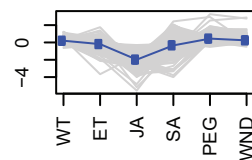
centered log₂(TPM+1)

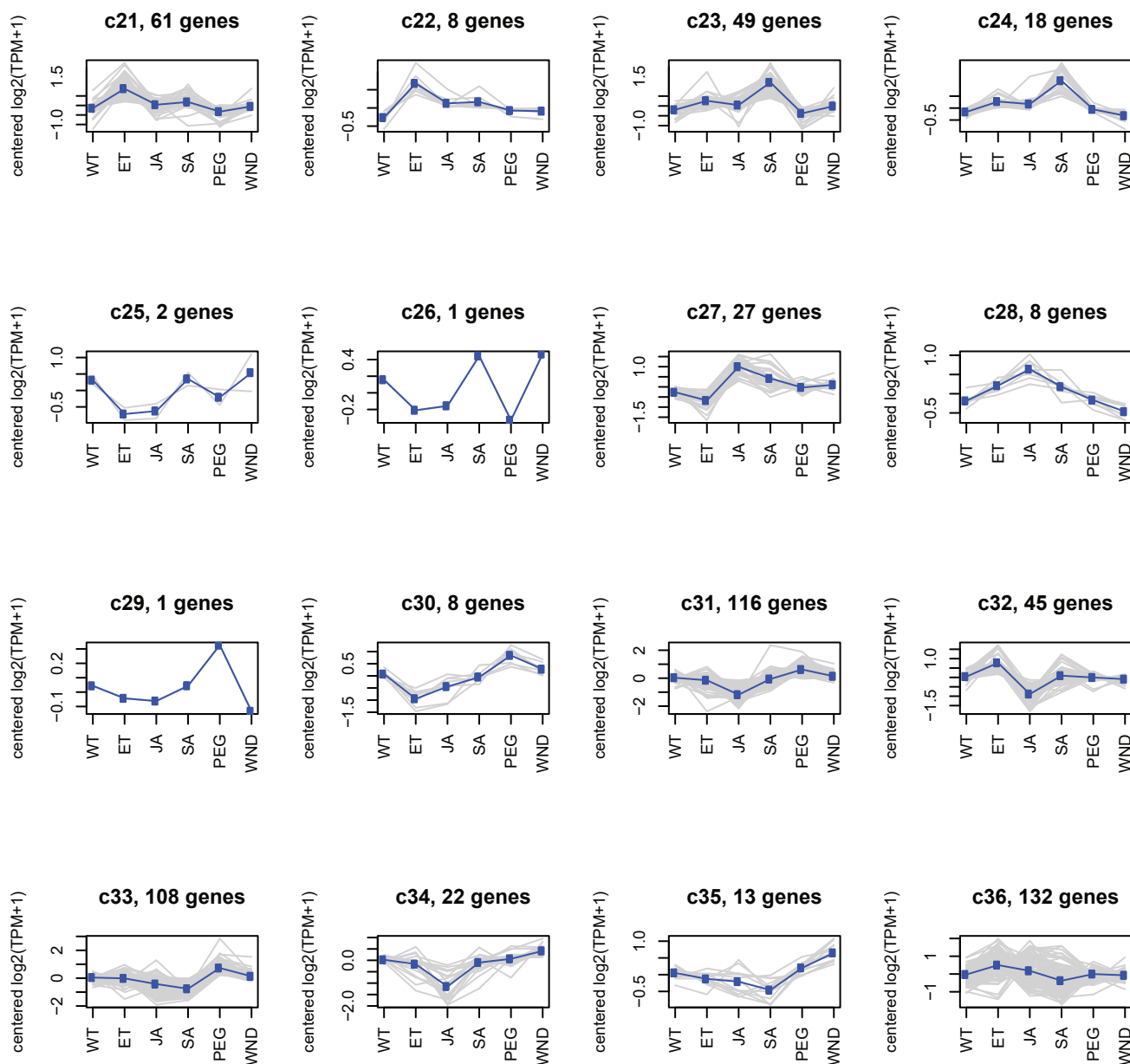
c19, 76 genes



centered log₂(TPM+1)

c20, 303 genes





Supplementary Figure 3. Gene expression profiles of top differentially expressed genes (DEGs).

Top DEGs (FDR < 0.001, FC > 4 in at least one pairwise comparison) were clustered with DEclust into 36 clusters. For each cluster, the mean expression profile is shown as a blue line. TPM = transcripts per million. WT, ET, JA, SA, PEG, and WND, denote water, ethanol, jasmonic acid, salicylic acid, polyethylene glycol, and wounding treatments, respectively.