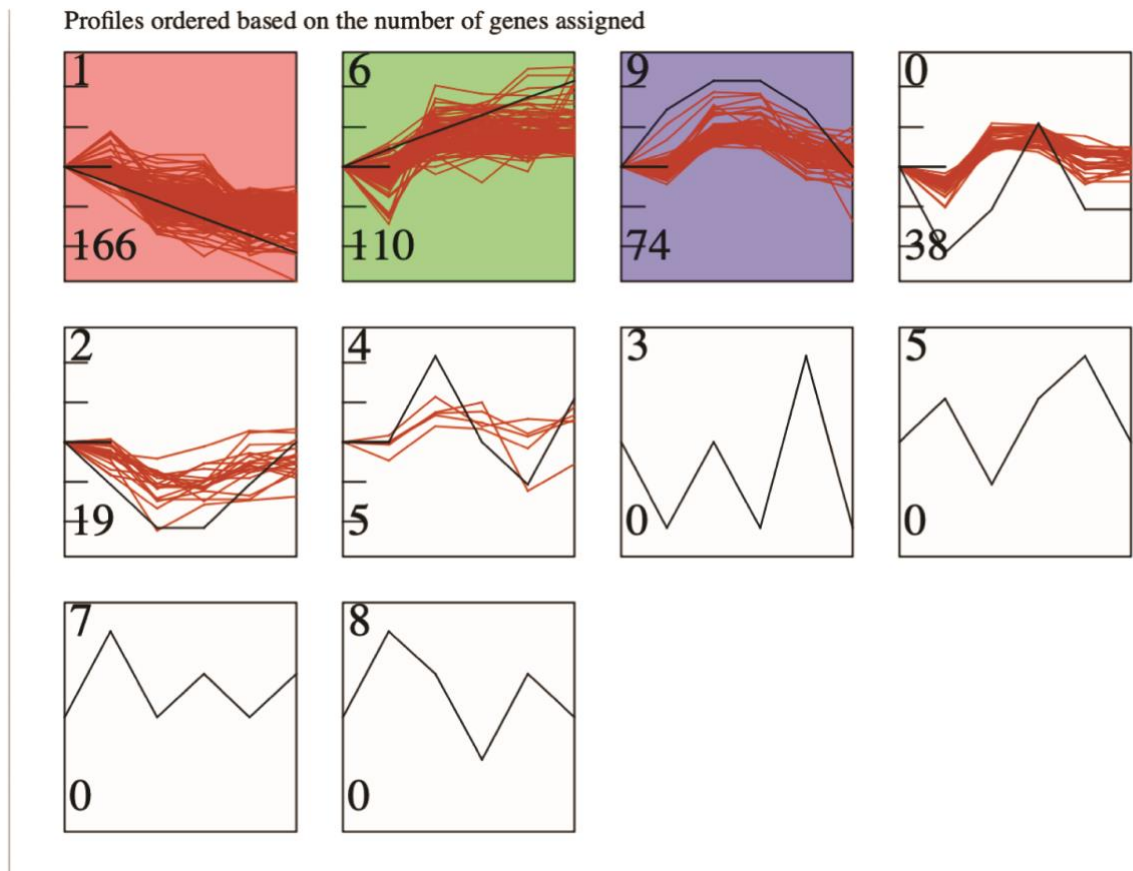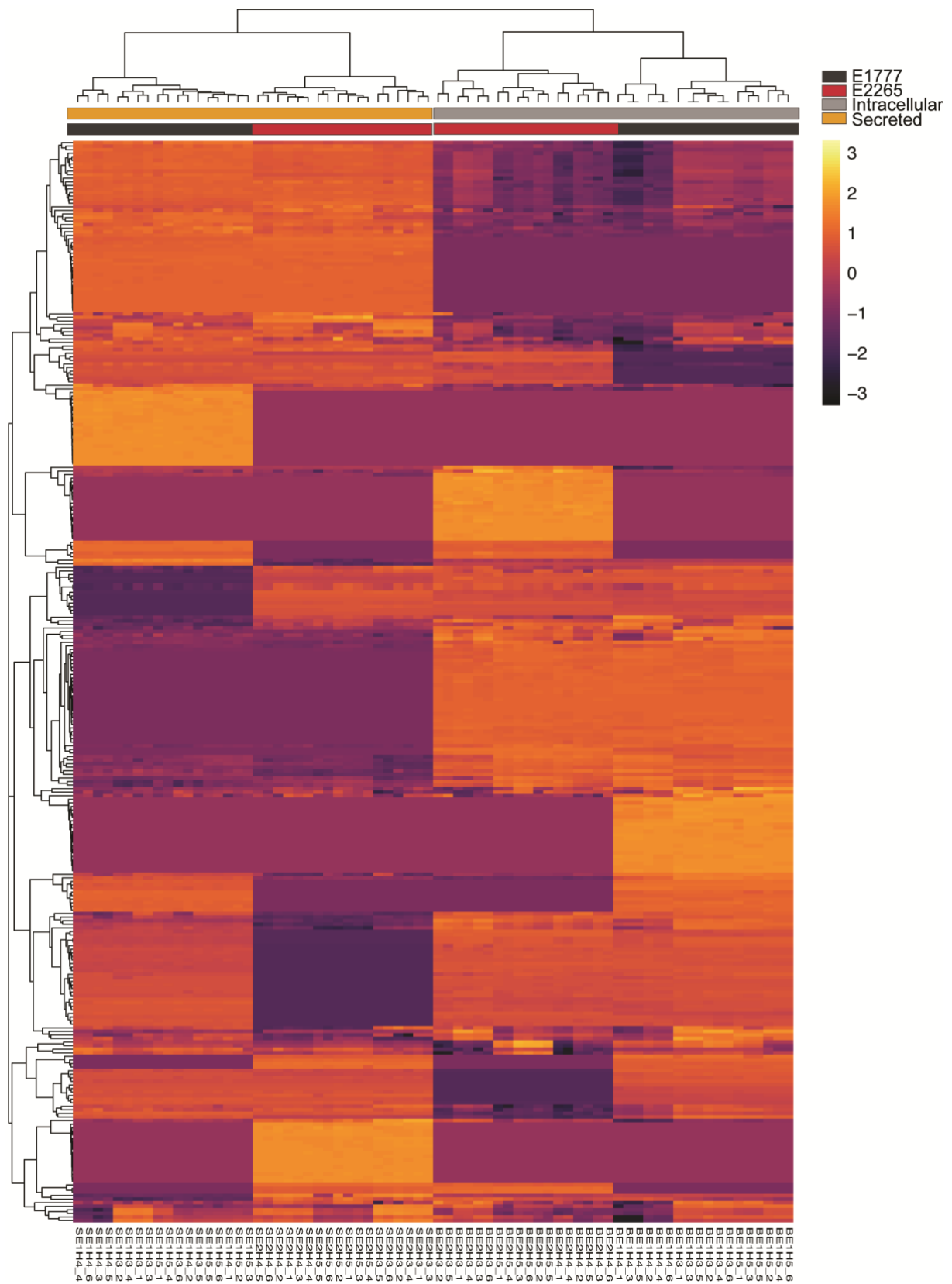# Supplemental Material
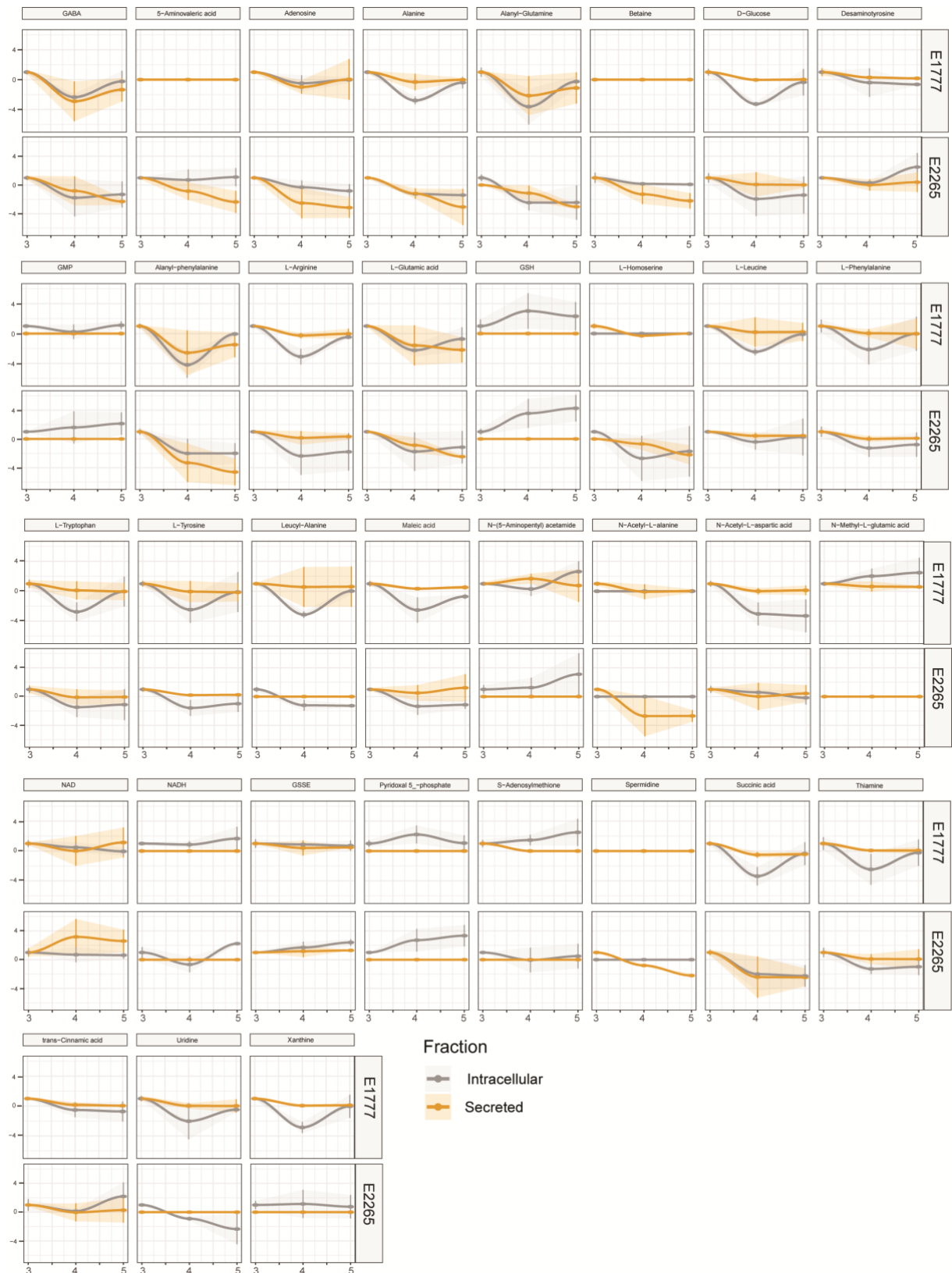
Supplemental Figures

S Figure 1. Identified gene expression patterns by STEM. The profile number on the top left corner of each profile box was assigned by STEM and the number on the bottom left represents the number of genes included in the cluster. Clusters with a p-value > 0.05 were colored.

S Figure 2. Heatmap representation of the abundance of 288 intracellular and secreted metabolites detected in E2265 and E1777.

S Figure 3. Data of the concentration of all significant metabolites are represented in the serial charts. The metabolite concentration is adjusted to 3 h, and the data is presented in fold-change±SD.