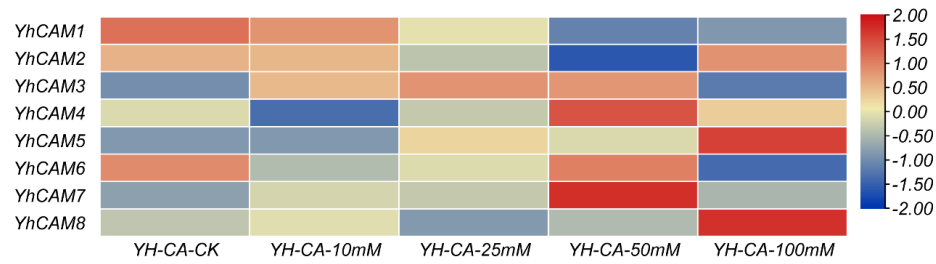
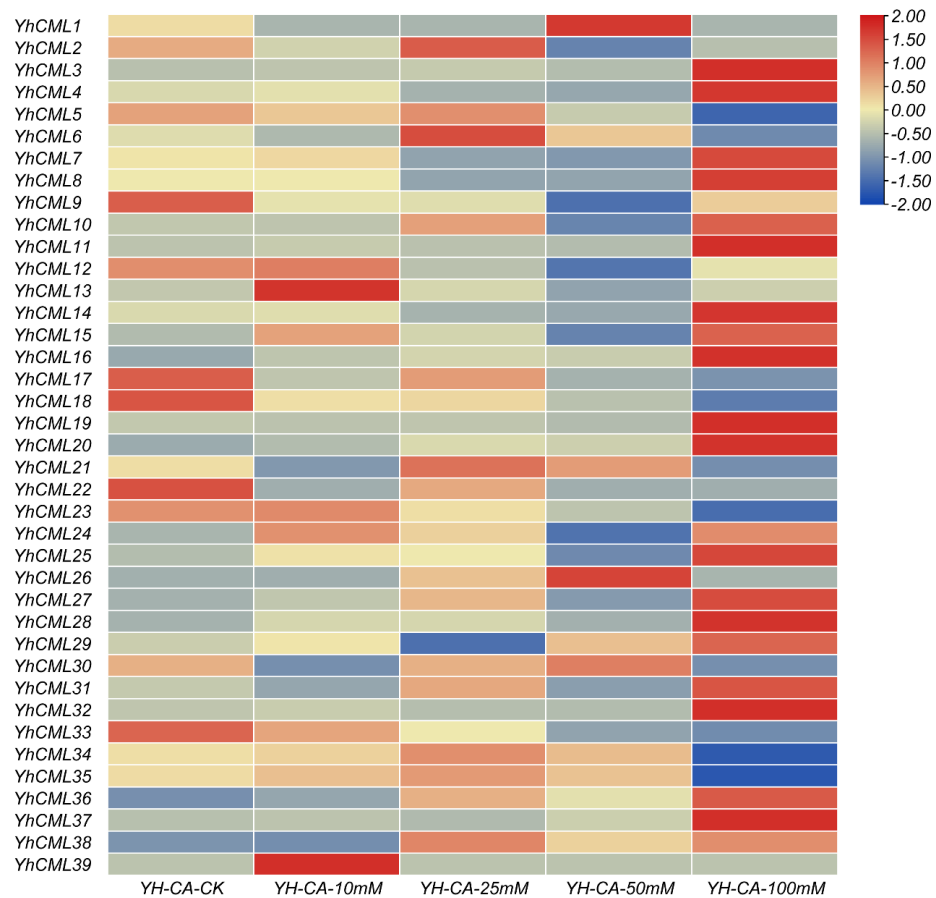


A



B



Supplementary Figure S6: Expression pattern of *YhCAM* genes (A) and *YhCML* genes (B) under CaCl_2 treatment of RNA-seq sequencing. RNA-seq data determined the relative expression levels. The CK (control), YH-Ca-10mM (10mM CaCl_2), YH-Ca-25mM (25mM CaCl_2), YH-Ca-50mM (50mM CaCl_2) and YH-Ca-100mM (100mM CaCl_2) represent different concentrations treatments. The transcript abundance level was normalized and hierarchically clustered using the $\log_2(\text{FPKM} + 1)$ comparison among genes of different treatments. The expression value is presented on the color scale, with red representing high expression and blue representing low expression.