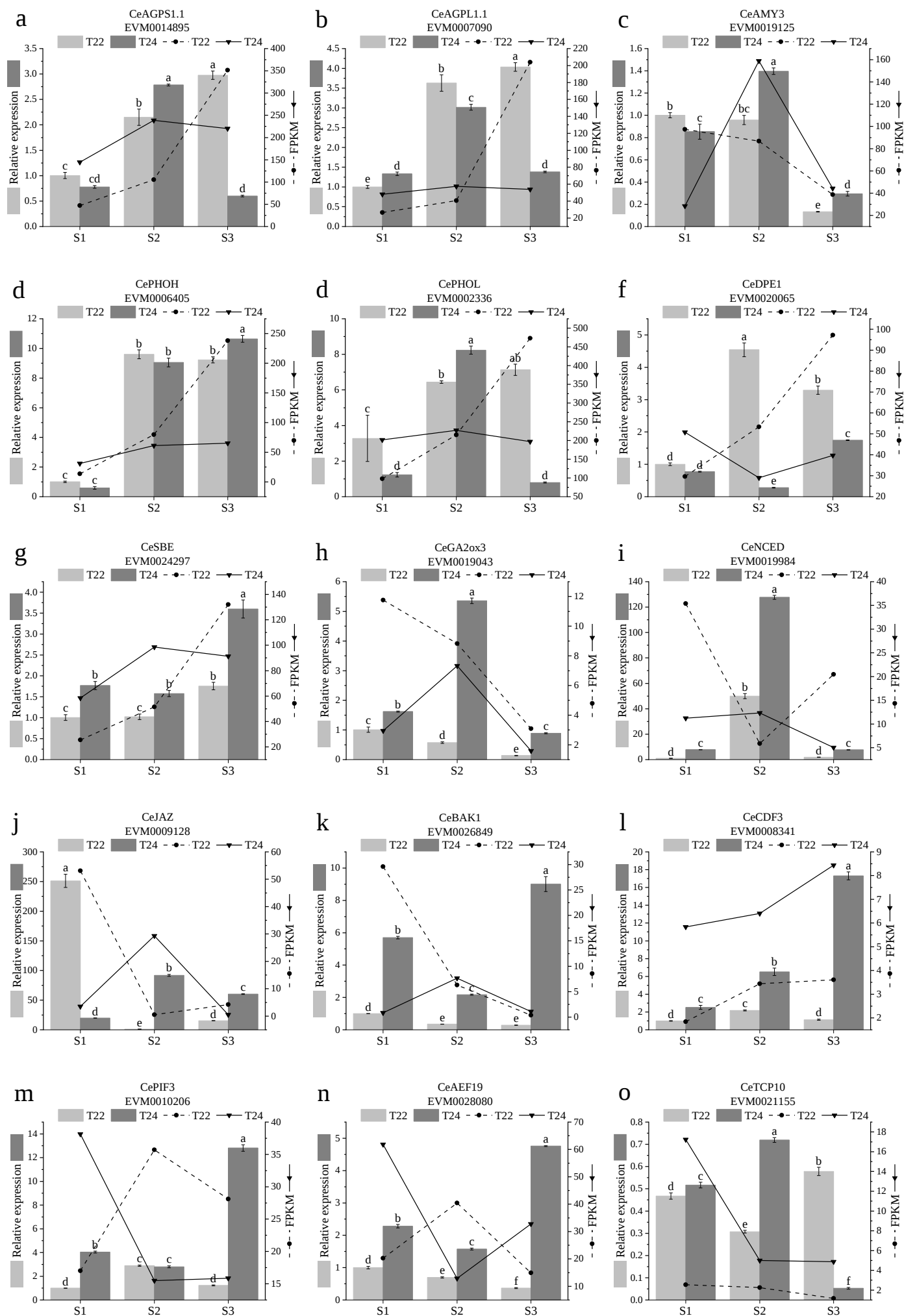




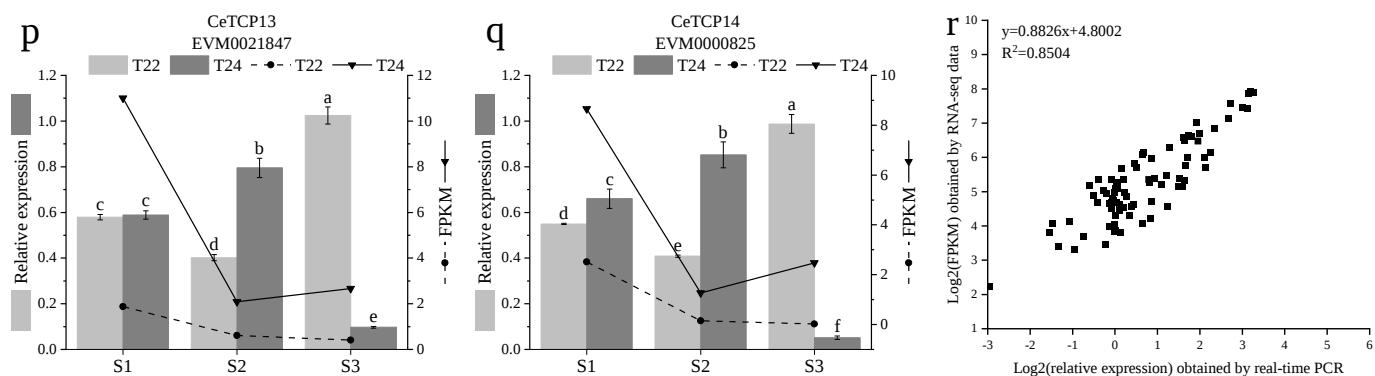


Figure S2 qRT-PCR validation of differential expression. The transcript levels of 17 genes, including 7 genes involved in starch metabolism (a-g), 4 genes belong to plant hormone signal transduction(h-k) and 6 TFs mostly associated with corm expansion (l-q), in T22 (broken line) and T24 (solid line) and the corresponding FPKM of RNA-seq data. Light grey bar represented the RNA-seq data in T22; Dark grey bar represented the RNA-seq data in T24. The left y-axis shows the relative gene expression levels analyzed by qRT-PCR, and the right y-axis shows the RNA-seq data. The error bars represent SE (n=3) and different letters on top indicate the significant difference at 0.05 level. (r) The correlation analysis of the gene expression ratios obtained from RNA-seq and qRT-PCR. The RNA-seq log2 value of the FPKM (y-axis) was plotted against the qRT-PCR log2 value of relative expression (x-axis).