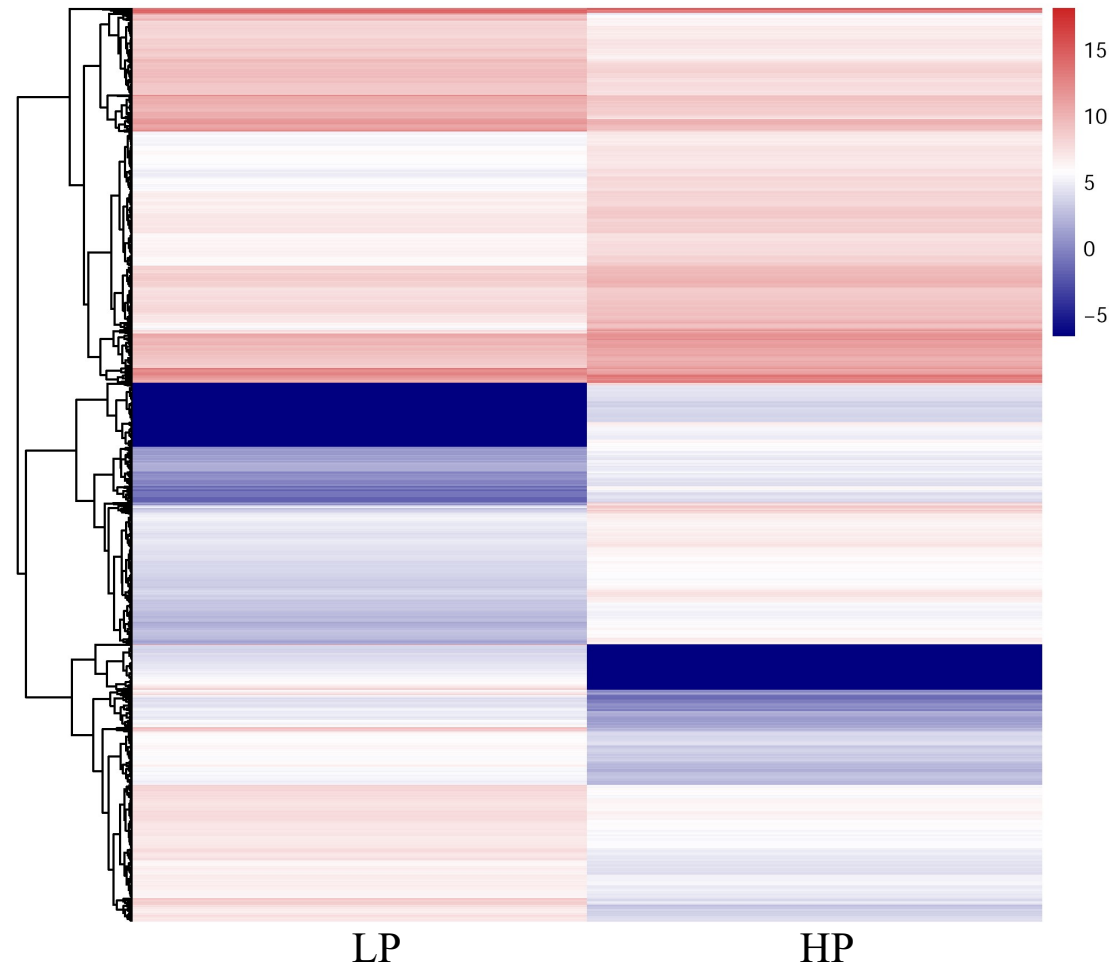Fig. S1

Fig. S1. Clustering analysis of the DEGs under two P conditions. The transcripts of DEGs were normalized as $\log_2(\text{FPKM})$. Expression levels ranged from red to blue indicate high to low expression for genes, respectively. LP and HP represent 0 and 250 µM KH_2PO_4 supply treatments, respectively.