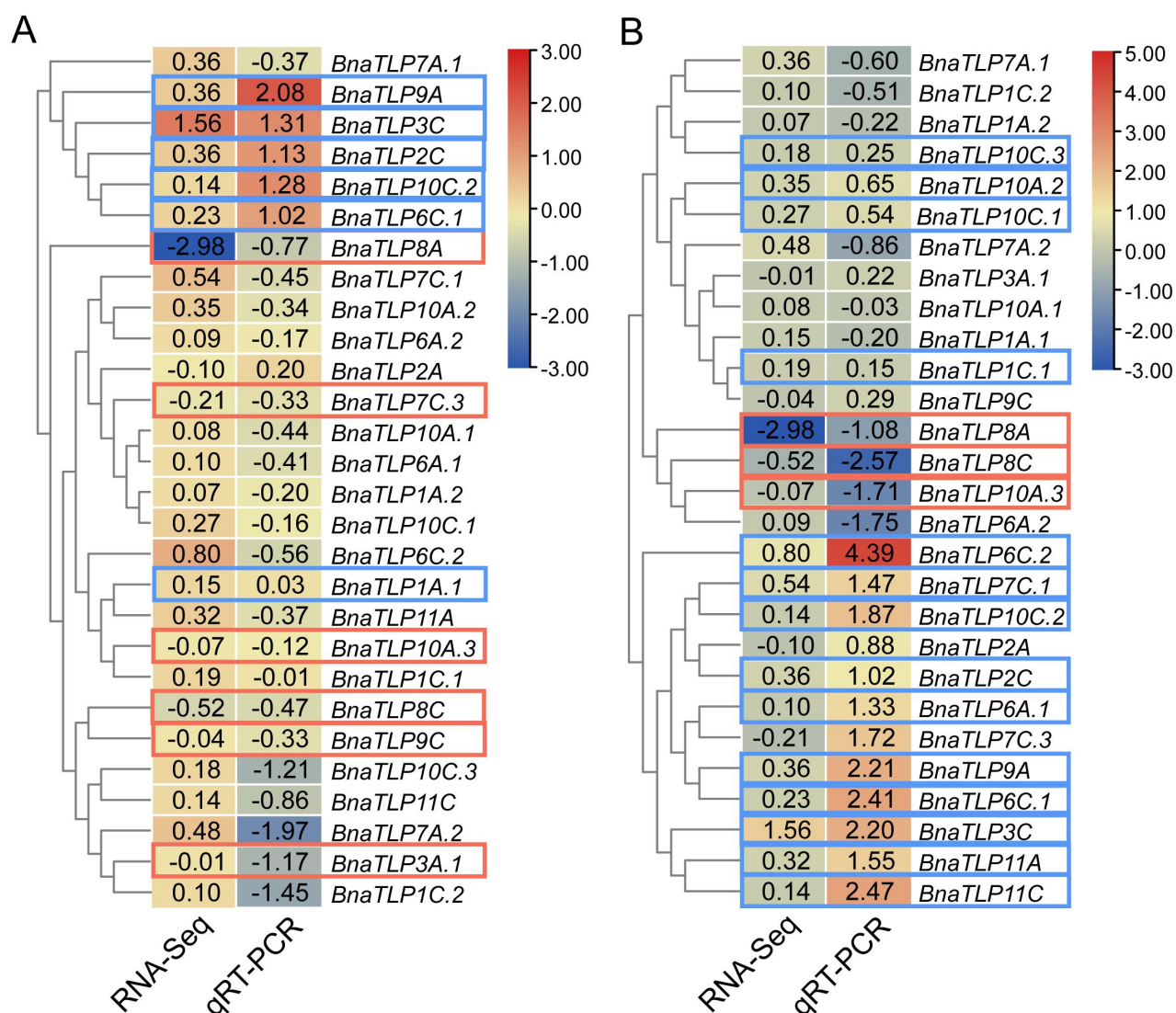




Supplementary Figure 6 | The transcriptome and qRT-PCR gene expression patterns analysis of *BnaTLPs* under NaCl treatment. Expression of *BnaTLPs* in *B.napus* shoots (**A**) and roots (**B**). RNA-Seq represents the log₂ fold change between the transcriptome data and control data after NaCl treatment for 12 hour; qRT-PCR represented the log₂ fold change between the Real-Time quantitative

PCR data after NaCl treatment for 12 hour and the 0 hour data after NaCl treatment. The black numbers in the heatmap are the values for each transcript. The abundance of each transcript is represented by a color bar. Red indicates a higher expression level, and blue indicates a lower expression level. (C) Expression of stress-responsive genes under NaCl treatment, up-regulated/down-regulated genes were marked with blue/red boxes in (A) and (B).