Figure 3. Transcriptome analysis. (A) Principle component analysis (PCA) of transcriptome data derived from two treatments during three developmental stages under waterlogging stress (14, 21, 28d, with three biological replicates per point). (B) The number of differentially expressed genes (DEGs). DEGs were filed out using the DESeq2 R package with the parameter of | $\log_2$ (fold change)| > 1 and an adjusted *p* value < 0.05. (C) The Venn diagram of DEGs in C1-vs-C2 and C2-vs-C3. (D) The Venn diagram of DEGs in W1-vs-W2 and W2-vs-W3. (E) The Venn diagram of DEGs in C1-vs-W1, C2-vs-W2 and C3-vs-W3. C1, C2, and C3 represented 14, 21 and 28 days after after gynophores touched the ground in the control treatment; W1, W2, and W3 represented 14, 21 and 28 days after after gynophores touched the ground in the waterlogging treatment.