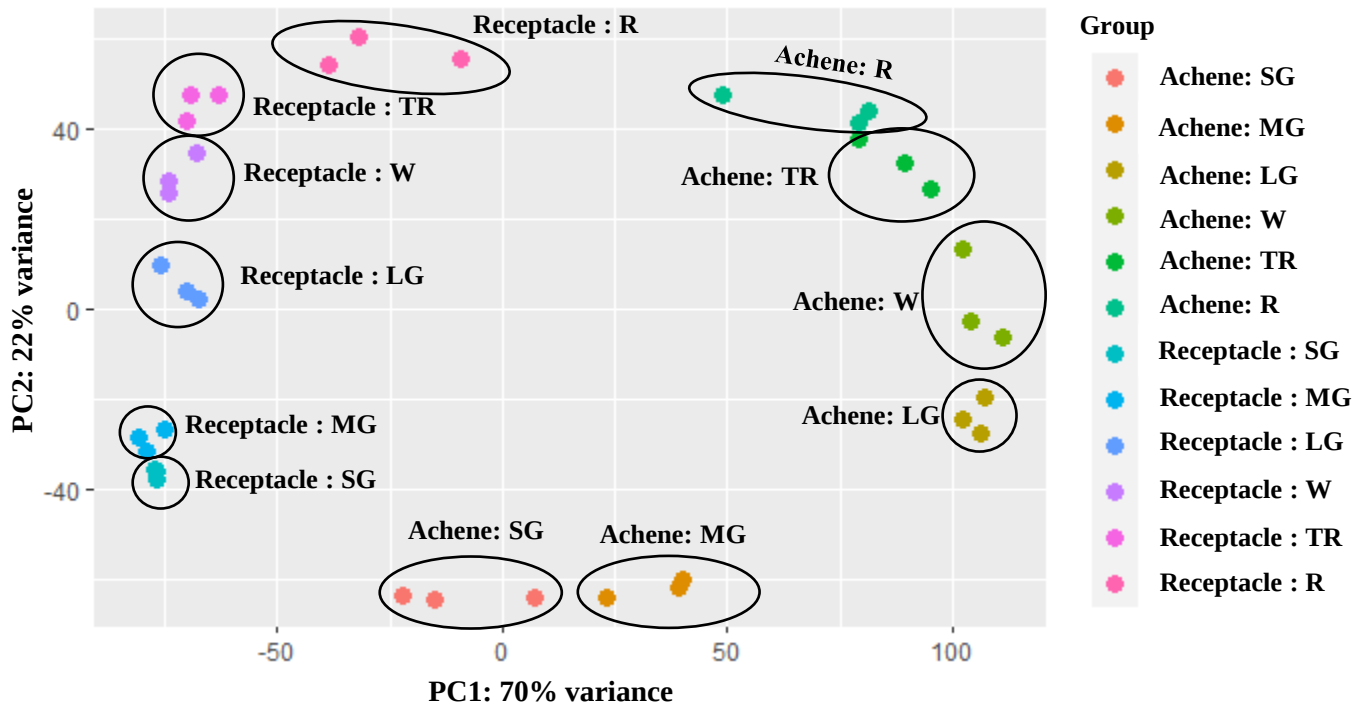
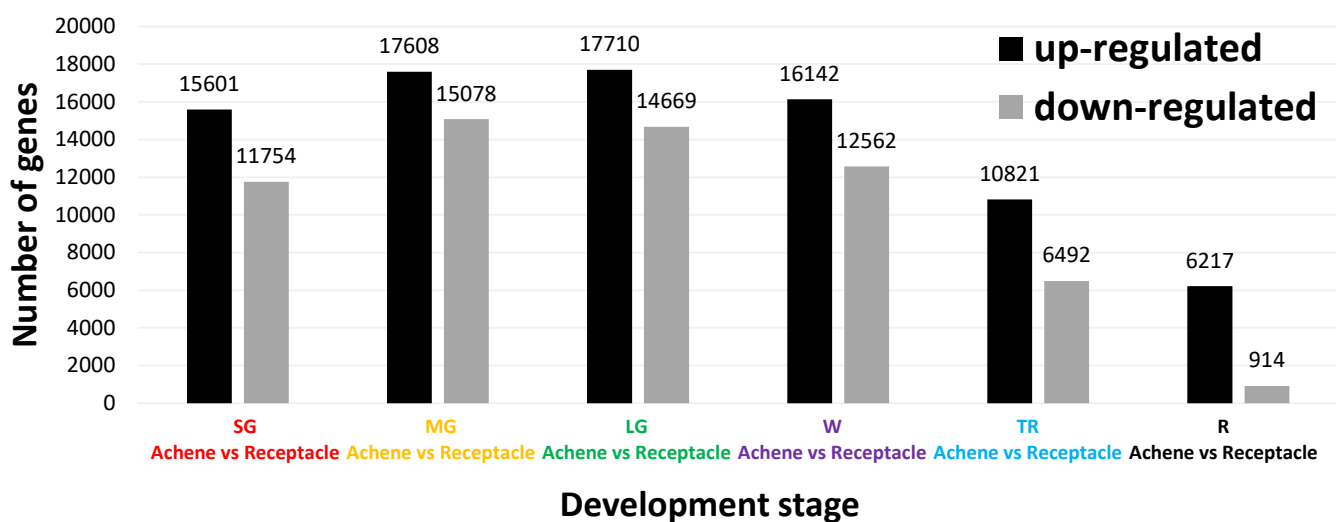




Supplemental Fig. 1. Principal component analysis (PCA) of transcriptome data from 36 samples.

Each colored prototype demonstrates the distinct separation of developmental samples into different stages throughout the entire time course. Furthermore, the analysis includes 36 samples, encompassing different tissue types, namely achene and receptacle, as well as 3 biological replicates for each stage.



Supplemental Fig. 2. Comparison of vesicular and receptor differentially expressed genes via DESeq2