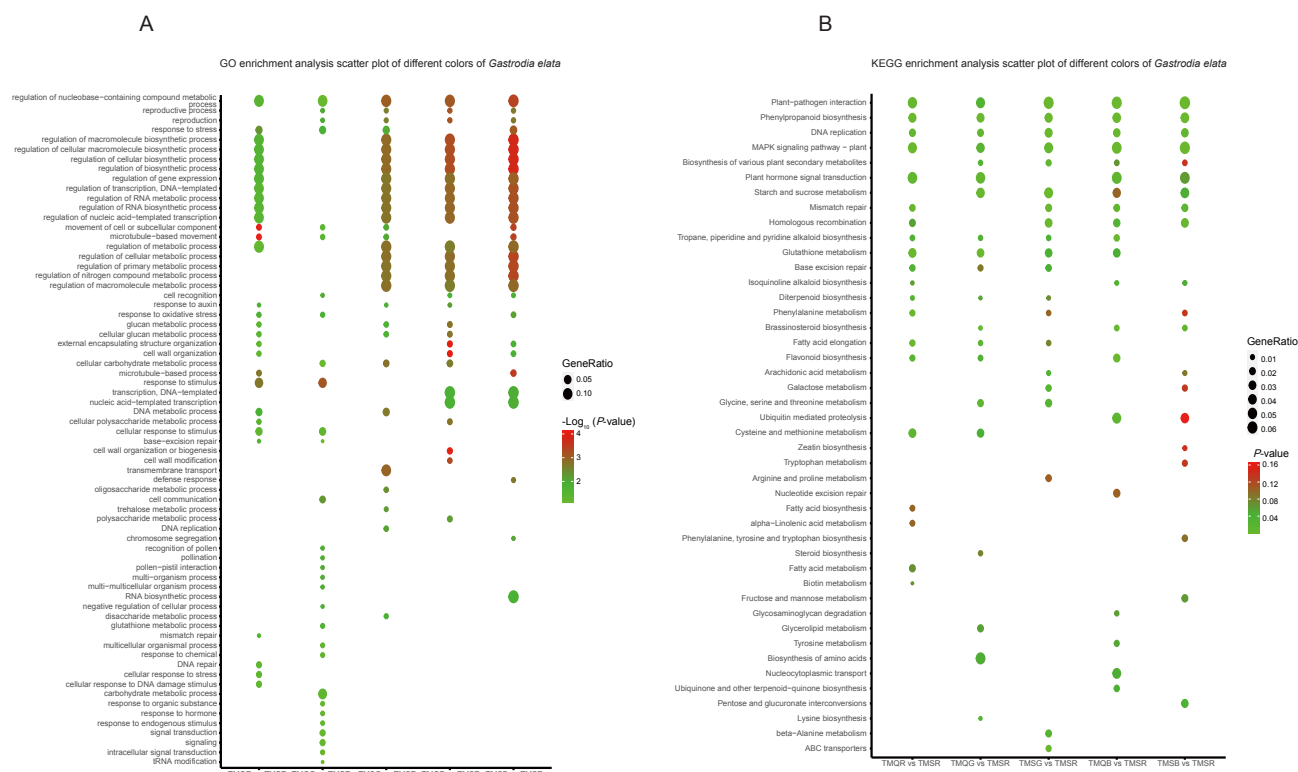




Supplementary figure 5. GO and KEGG functional enrichment analyses in different color stems of *G. elata* transcriptome. (A) Scatter plots displaying the top 30 statistically significant GO terms from GO enrichment analysis. (B) Scatter plots showcasing the 20 most significant KEGG pathways from KEGG enrichment analysis. The horizontal axis represents sample comparisons, and the vertical axis lists GO terms/pathways. Point size reflects the number of annotated genes, and the color gradient (from green to red) indicates enrichment significance; if raw P-values are shown, lower P-values indicate stronger significance, whereas if $-\log_{10}(P\text{-value})$ is shown, higher values indicate stronger significance.