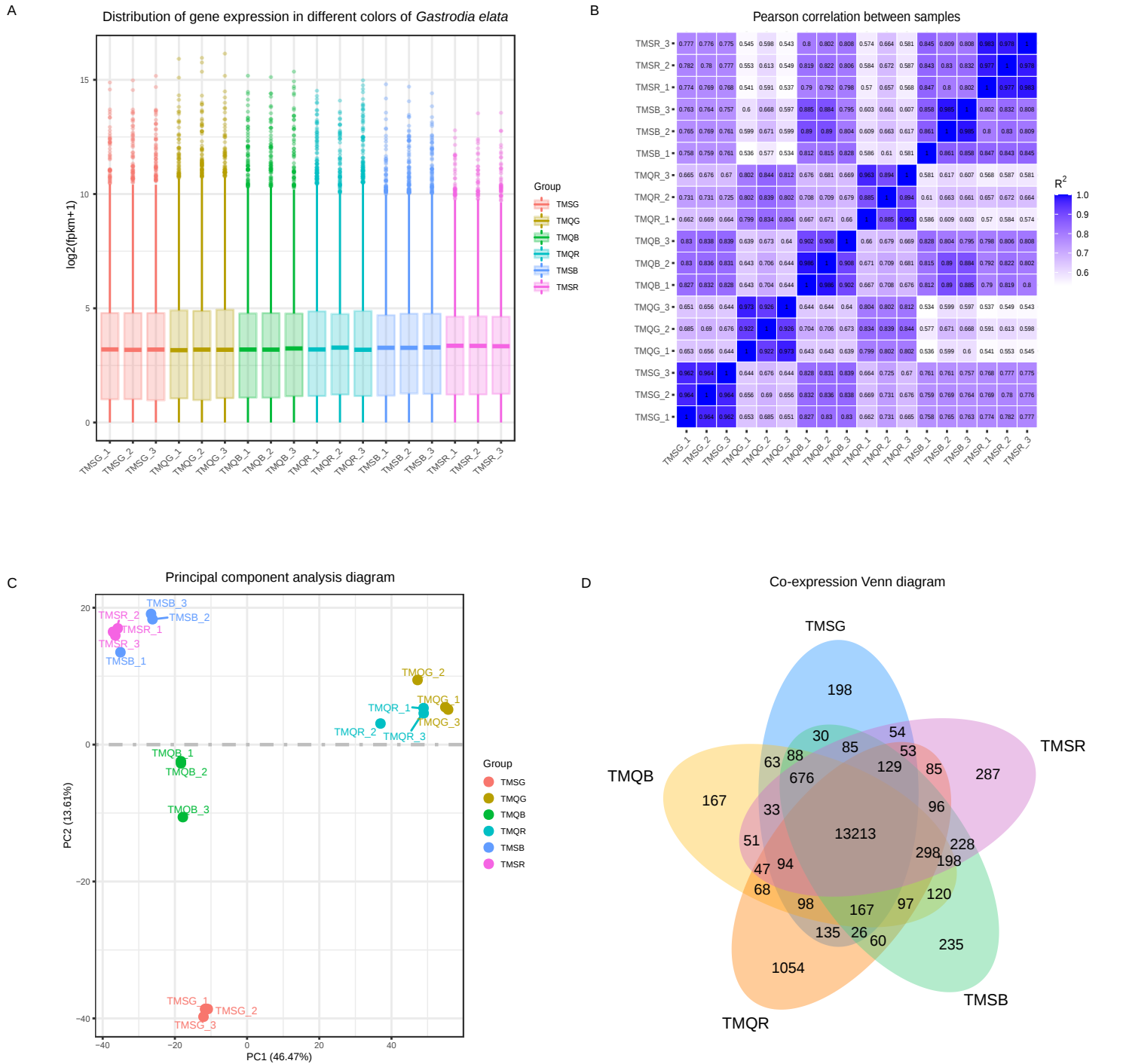




Supplementary figure 3. Quantitative genetic analysis of different color forms of *G. elata*. (A) RNA-seq gene expression quantification, adjusted for sequencing depth and gene length using FPKM (Fragments Per Kilobase Million), illustrated by box plots showing expression levels across samples. X-axis: sample names; Y-axis: $\log_2(\text{FPKM} + 1)$. (B) Heatmap depicting correlation coefficients between samples based on FPKM values, highlighting group differences and sample repetition. (C) PCA plot evaluating inter-group differences and intra-group consistency using gene expression values (FPKM). Samples between groups ideally disperse, while within-group samples cluster. (D) Co-expression Venn diagram showing uniquely expressed genes per sample and co-expressed genes across samples. TMSG: dark green *G. elata*, TMQG: light green *G. elata*, TMSR: dark red *G. elata*, TMQR: light red *G. elata*, TMSB: dark brown *G. elata*, TMQB: light brown *G. elata*.