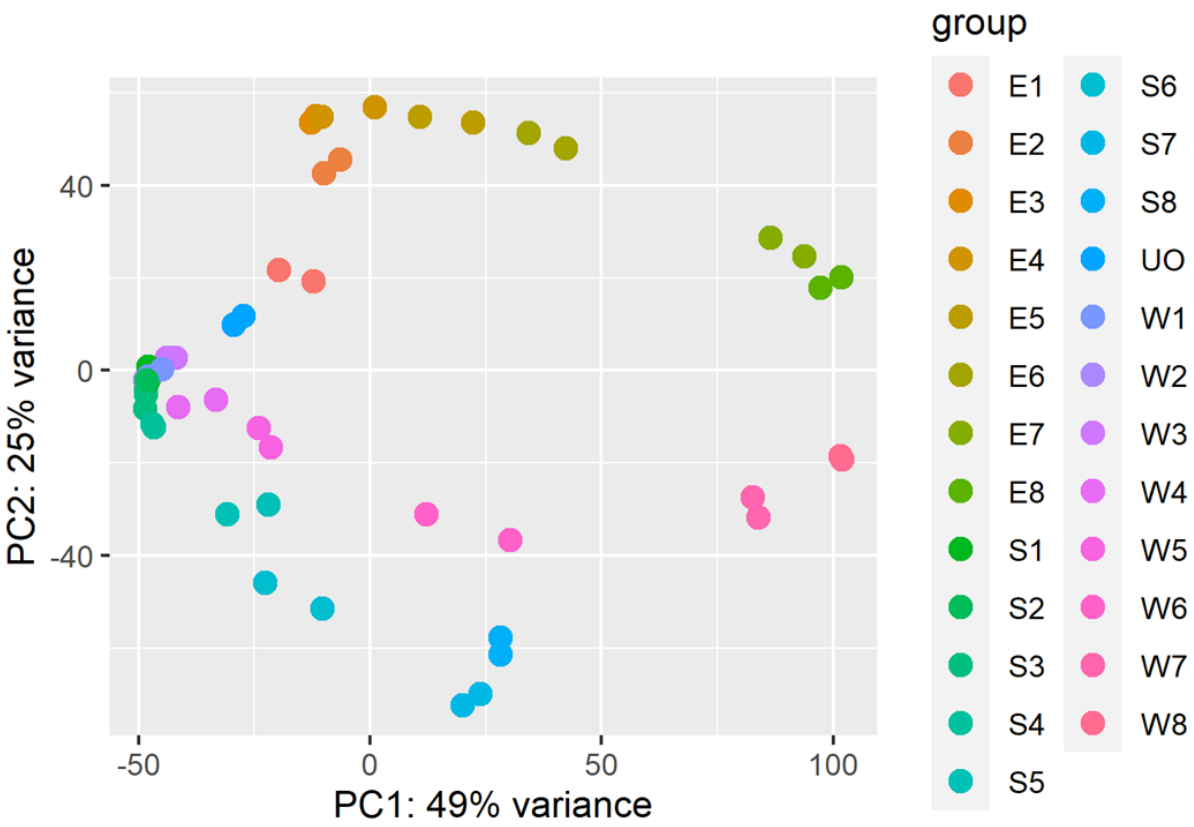

Figure S1. 2-D Principal component analysis (PCA) of lentil embryo, seed coat and whole seed samples from different stages of seed development. This is a 2-D reflection of Fig. 2a. X-axis and Y-axis indicate PC1 and PC2, respectively, and the proportion of variance explained by each principal component. The samples of two replicates are indicated with the dots of the same color. UO, unfertilized ovule; E, embryo; S, seed coat; W, whole seed; 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8).

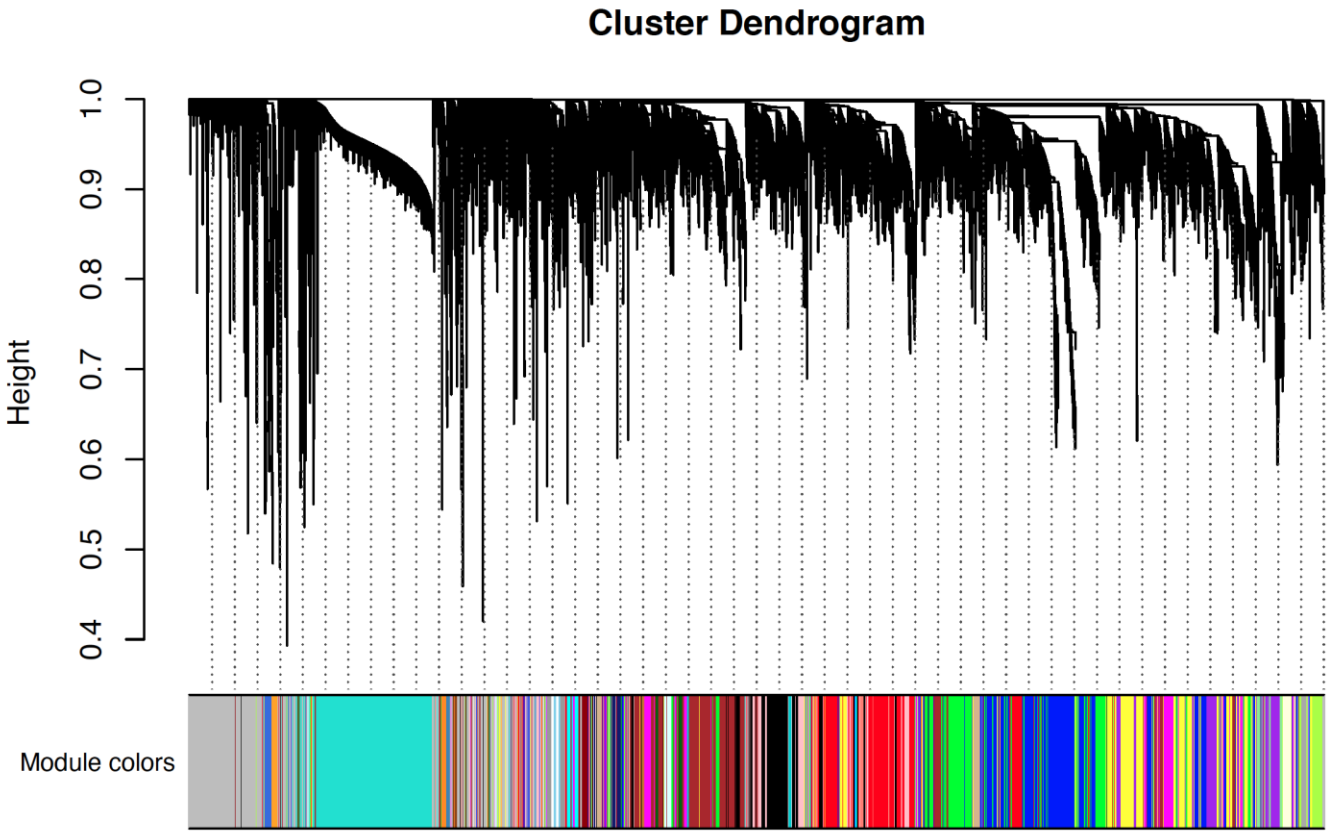

Figure S2. Weighted gene co-expression network analysis (WGCNA) modules (Clusters) dendrogram. The color row below the dendrogram indicates module membership.

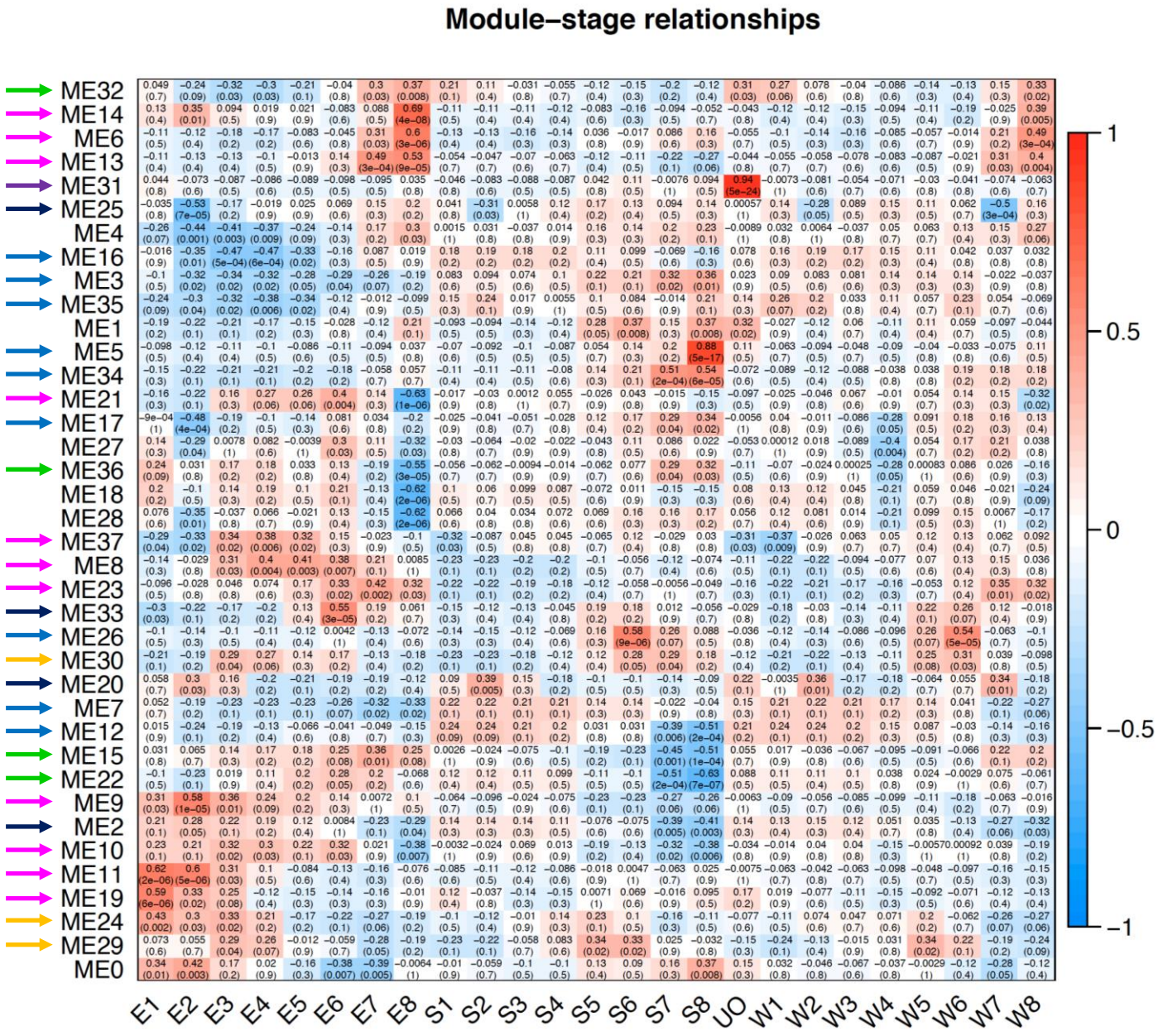

Figure S3. Weighted gene co-expression network analysis (WGCNA) module and stage relationship. UO, unfertilized ovule; E, embryo; S, seed coat; W, whole seed; 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8). Arrows with different colors indicate different categories of modules. Pink, dominant in different stages in embryo, repressed in seed coat. Blue, dominant in different stages in seed coat, repressed in embryo. Black, similar expression between embryo and seed coat. Green, opposite expression pattern between embryo and seed coat. Orange, genes with delayed activation in seed coat compared to embryo. Purple, dominant expressed in unfertilized ovule, repressed in both embryo and seed coat. Colors (red to blue) indicate the values of the Pearson's correlations, where red is positively correlated and blue is negatively correlated.

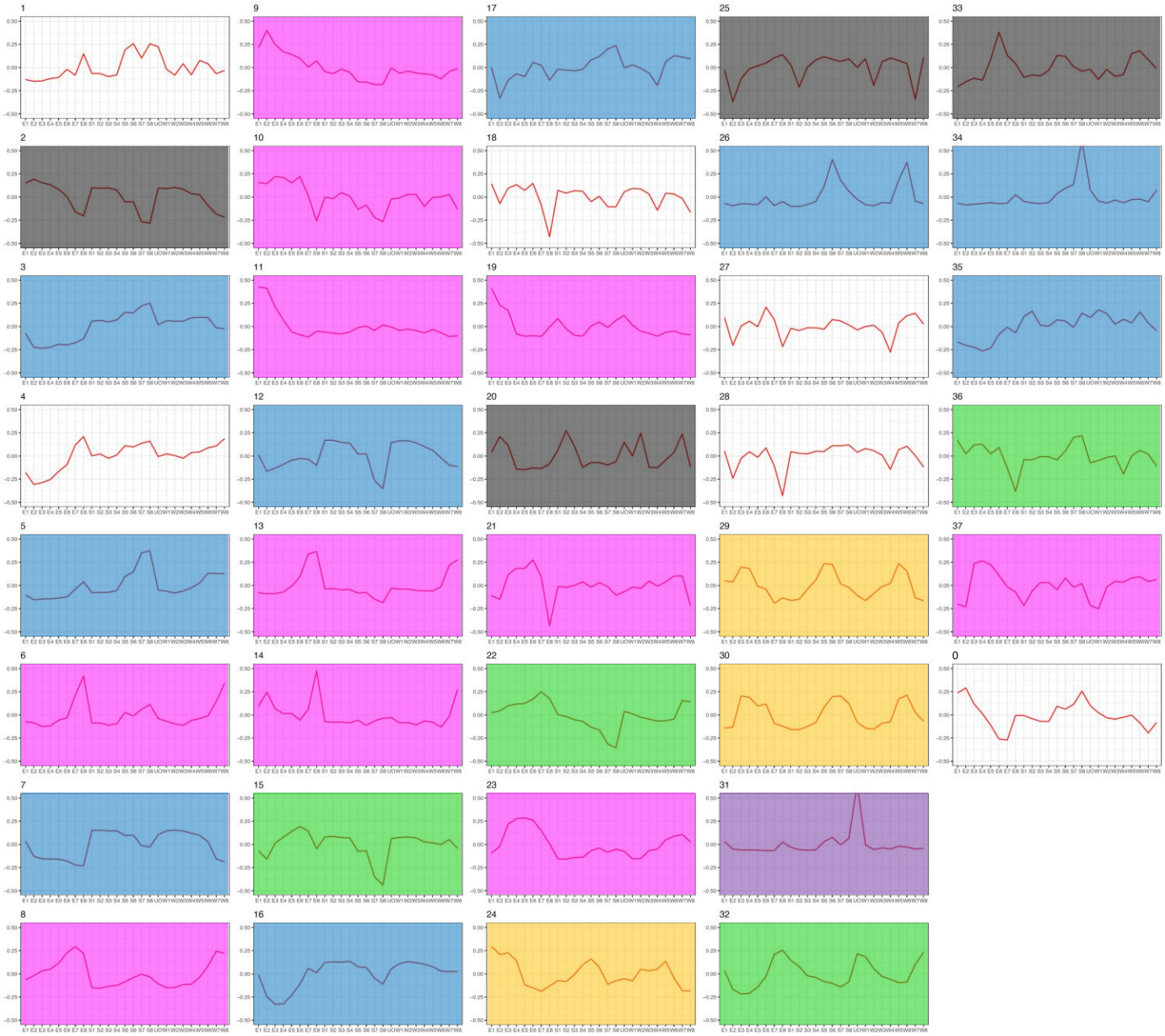

Figure S4. Weighted gene co-expression network analysis (WGCNA) modules. UO, unfertilized ovule; E, embryo; S, seed coat; W, whole seed; 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8). Different background colors indicate different categories of modules. Pink, dominant in different stages in embryo, repressed in seed coat. Blue, dominant in different stages in seed coat, repressed in embryo. Black, similar expression between embryo and seed coat. Green, opposite expression pattern between embryo and seed coat. Orange, genes with delayed activation in seed coat compared to embryo. Purple, dominant expressed in unfertilized ovule, repressed in both embryo and seed coat.

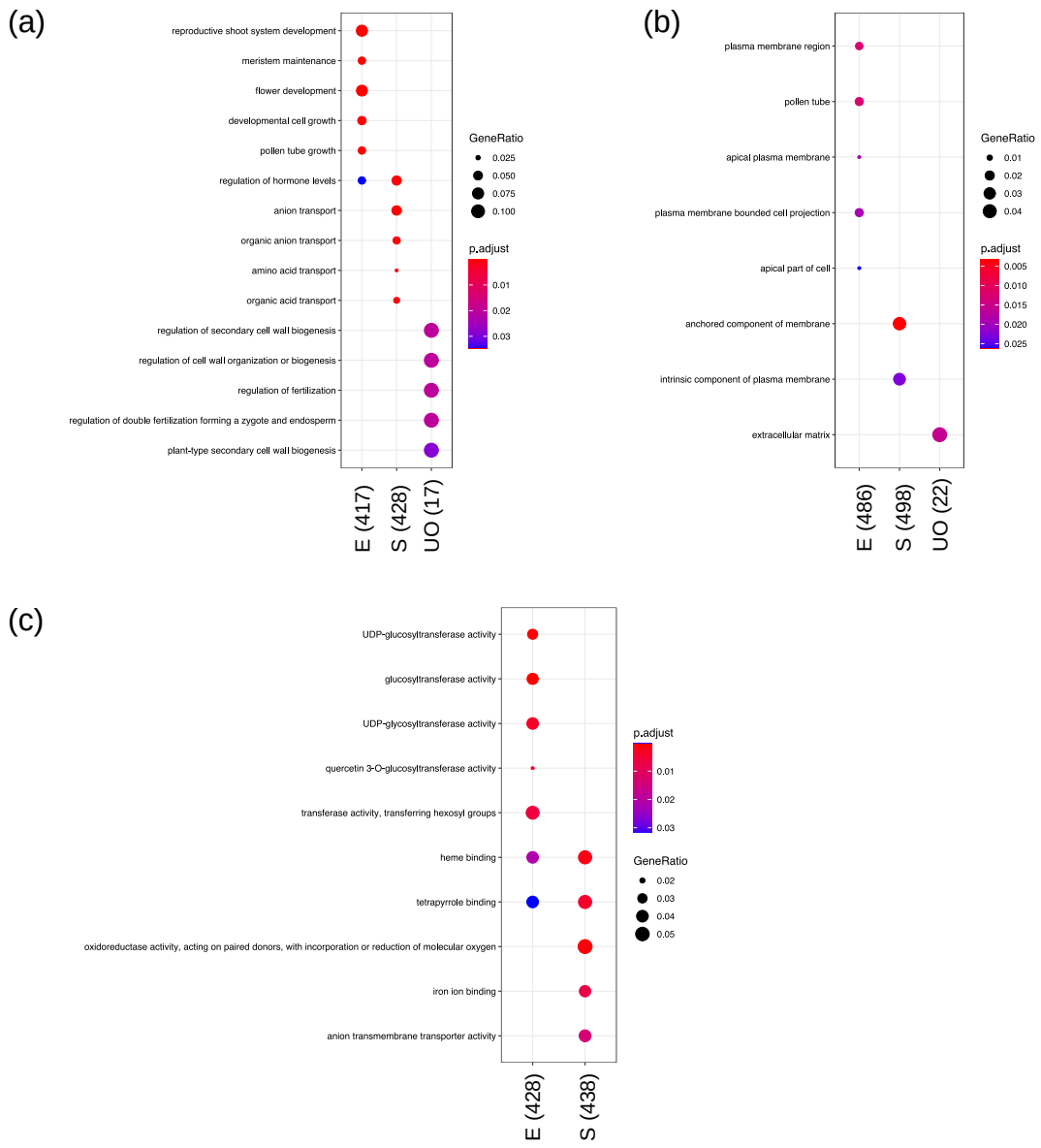

Figure S5. Gene Ontology (GO) of tissue-specific genes. (a) Biological process; (b) Cellular component; (c) Molecular function. E, embryo; S, seed coat; UO, unfertilized ovule. The number of genes was shown in the parenthesis.

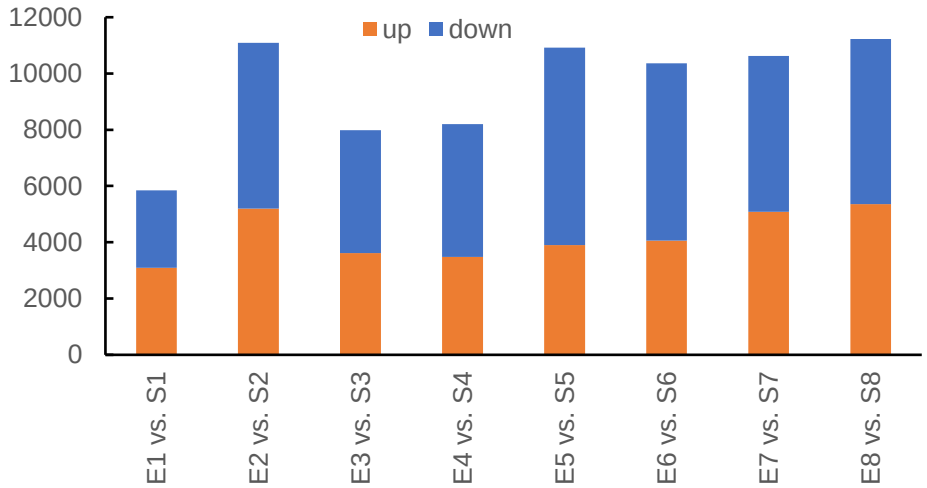

Figure S6. Differentially expressed genes (DEGs) in embryo vs. seed coat at each developmental stage of lentil seed. E, embryo; S, seed coat; 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8)**.**

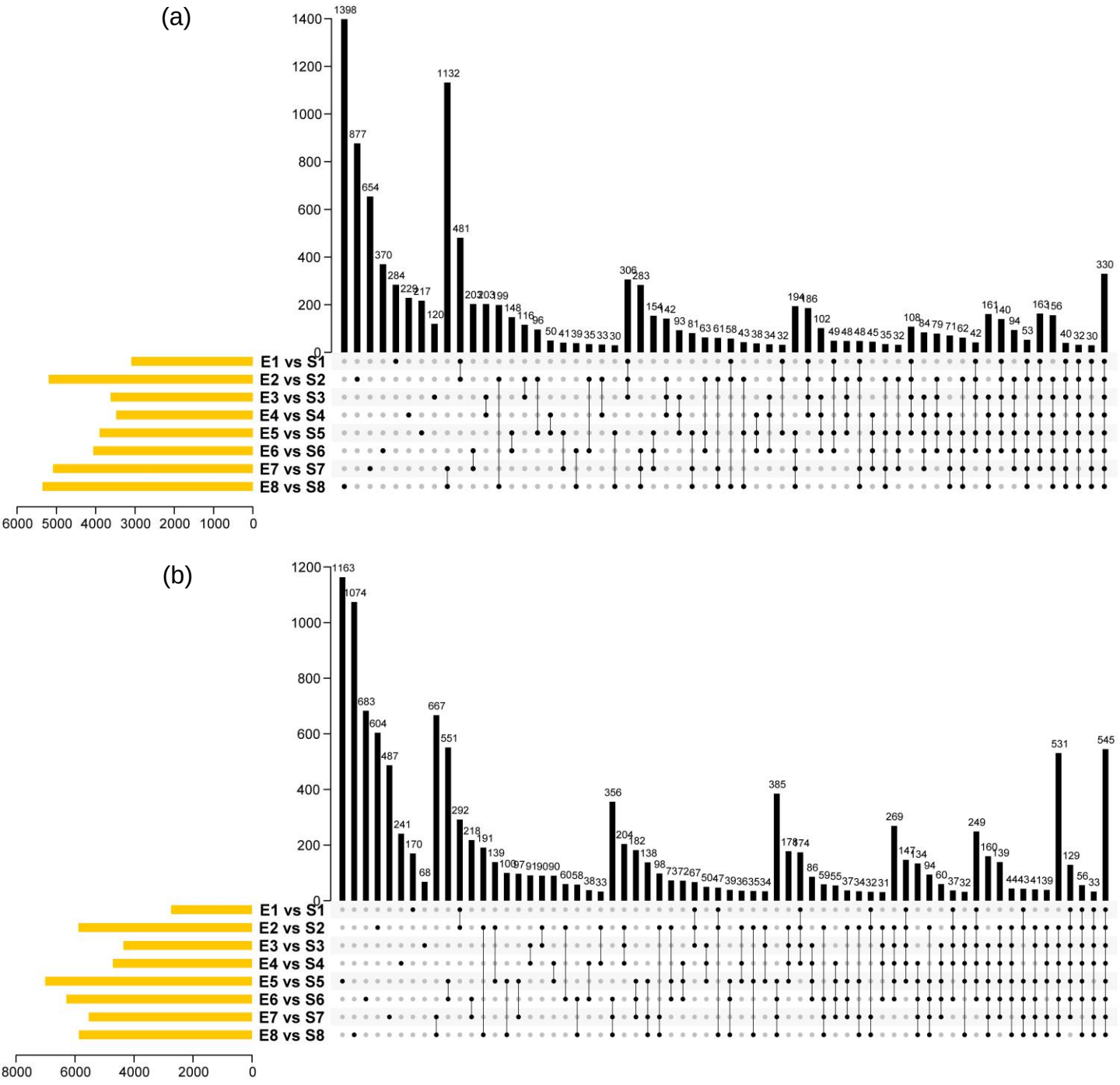

Figure S7. UpSet plot showing the number of differentially expressed genes (DEGs) in embryo vs. seed coat at each development stage. (a) Up-regulated genes; (b) Down-regulated genes. The number of DEG for each of comparisons is given by set size (horizontal bars). Unique DEG for each pair of comparisons is marked by a single black dot. Common (overlapping) DEGs between comparisons are indicated by a line connecting black points and also by intersection size (vertical bars). The corresponding DEG number is shown by the bar and number above the dot. E, embryo; S, seed coat.

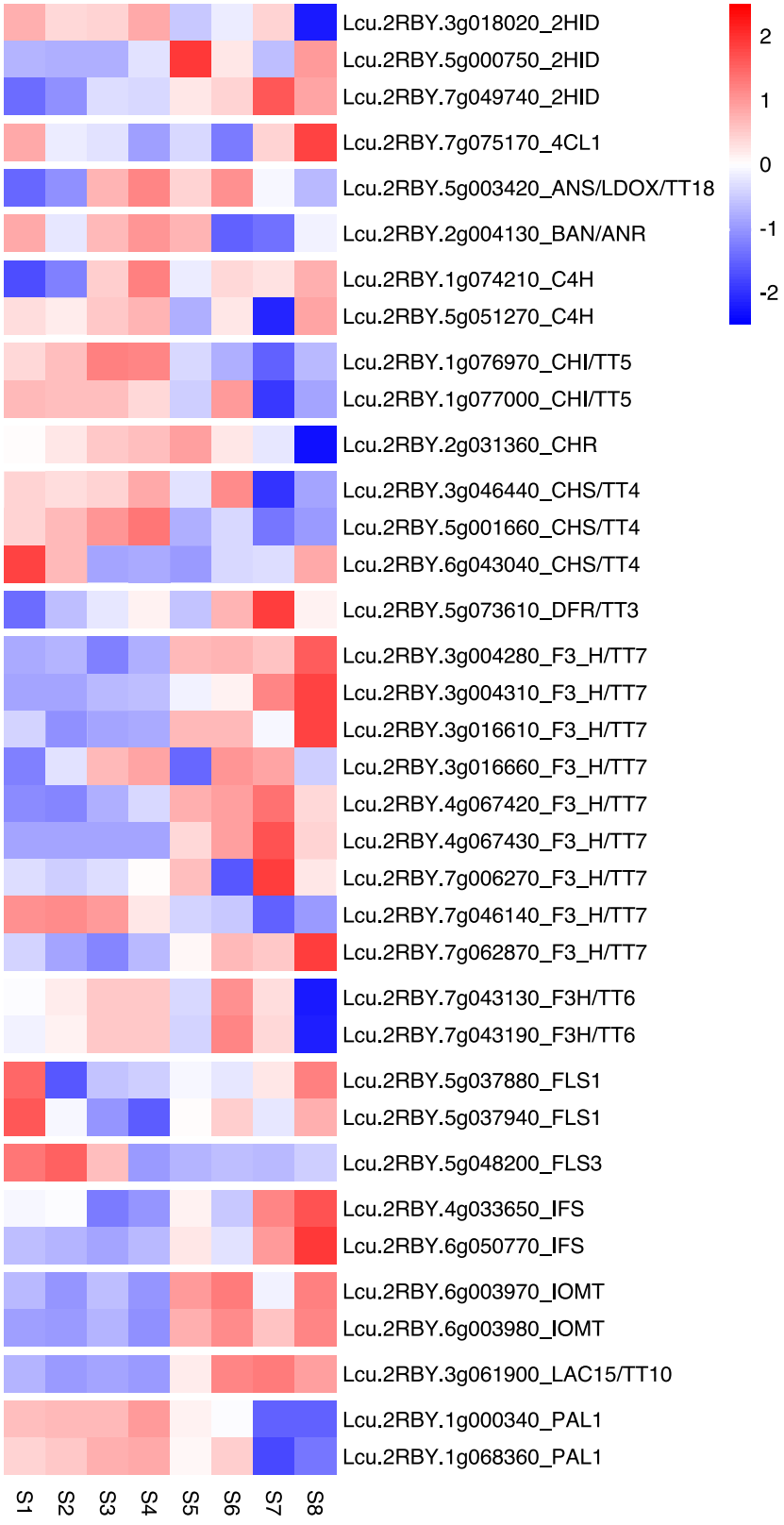

Figure S8. Heatmap of putative flavonoid biosynthetic gene expression in lentil seed coat. 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8). The standard scores (*z* –scores) of gene expression were used. Red color indicates up-regulated genes and blue color indicates down-regulated genes.

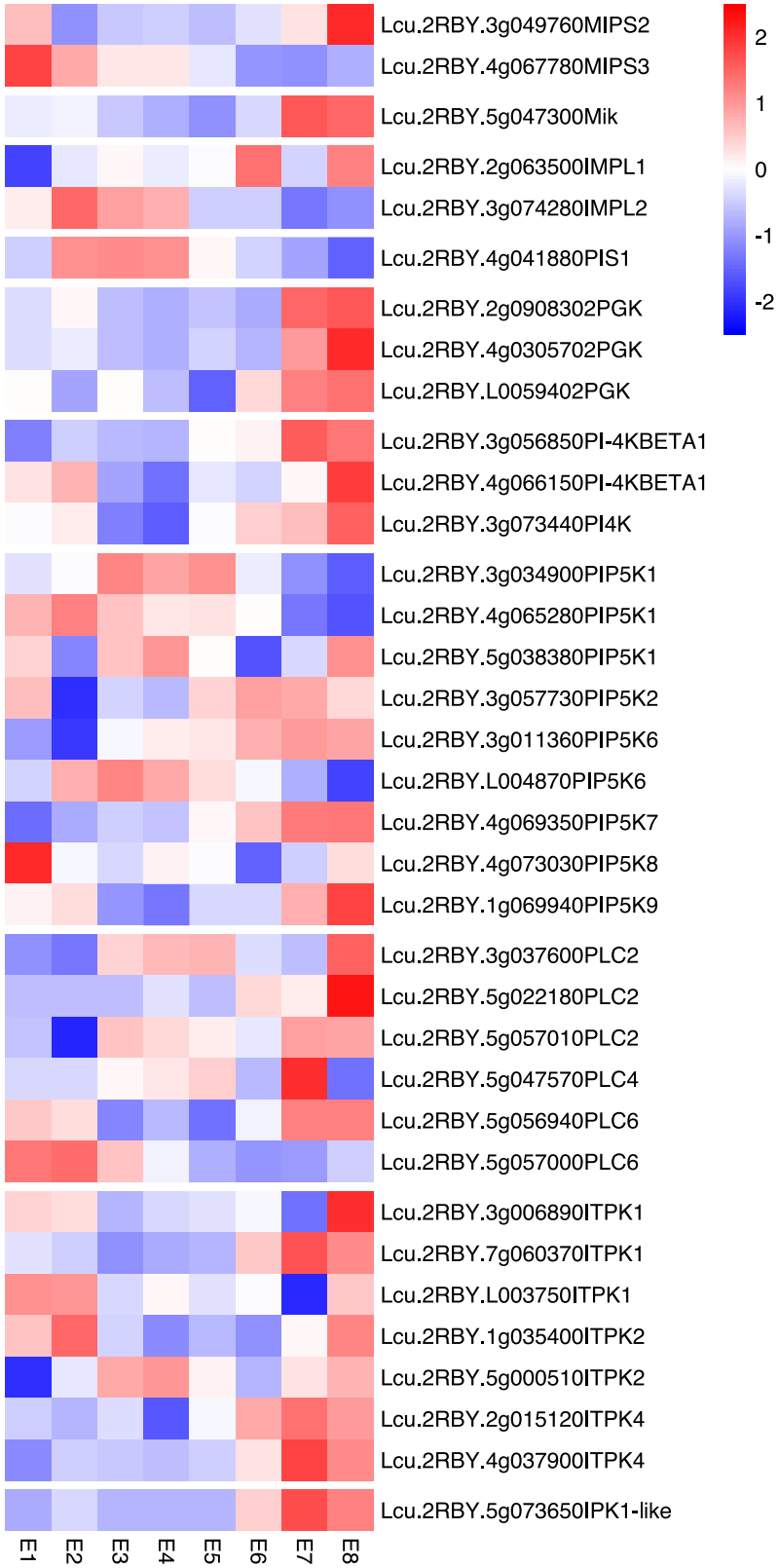

Figure S9. Heatmap of putative InsP6 biosynthetic gene expression in lentil embryo. 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8). The standard scores (*z* –scores) of gene expression were used. Red color indicates up-regulated genes and blue color indicates down-regulated genes.

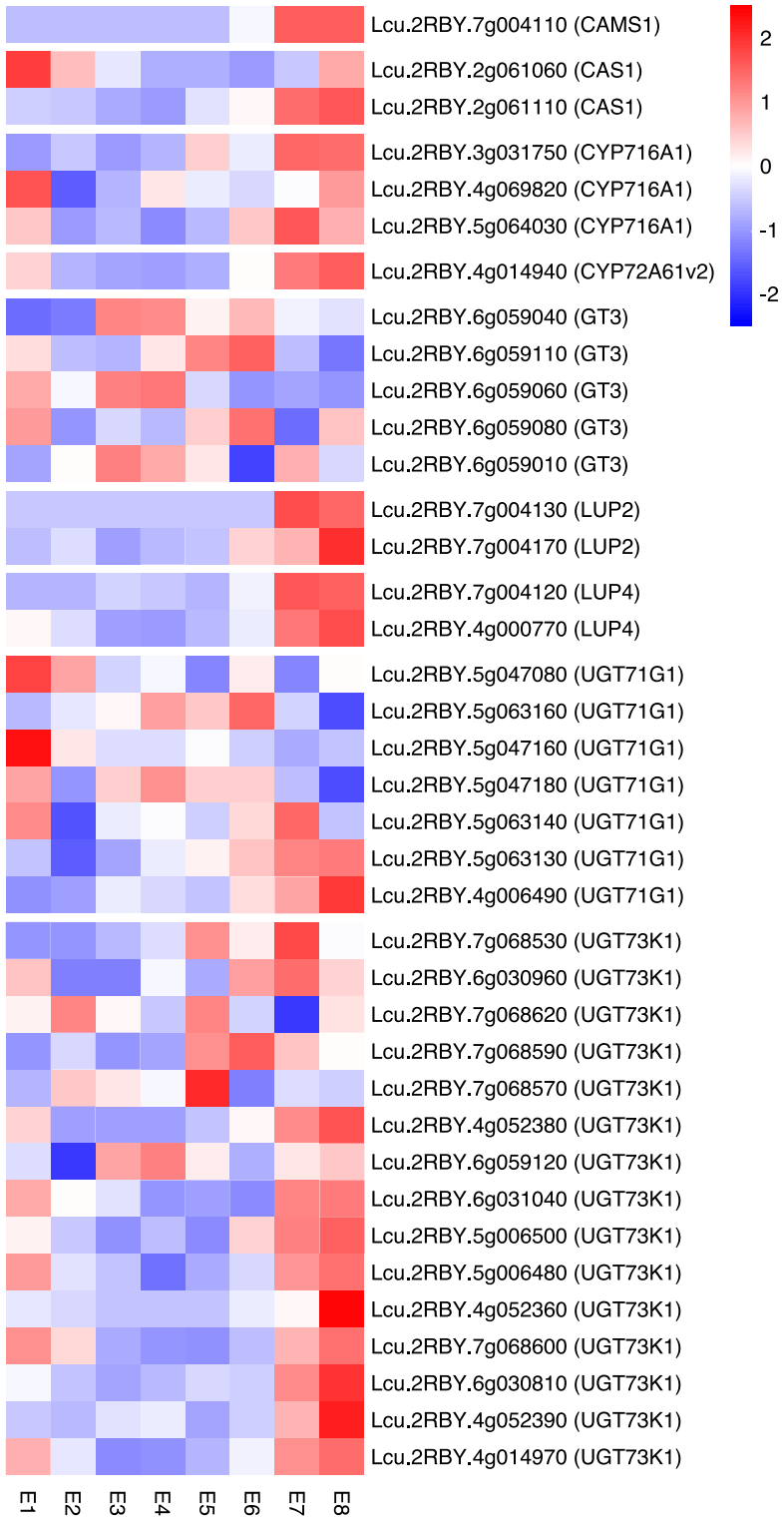

Figure S10. Heatmap of putative saponin biosynthetic gene expression in lentil embryo. 1-8 indicates sequential stages: zygote (1), quadrant (2), globular (3), heart (4), torpedo (5), early cotyledon (6), late cotyledon (7) and mature (8). The standard scores (*z* –scores) of gene expression were used. Red color indicates up-regulated genes and blue color indicates down-regulated genes.