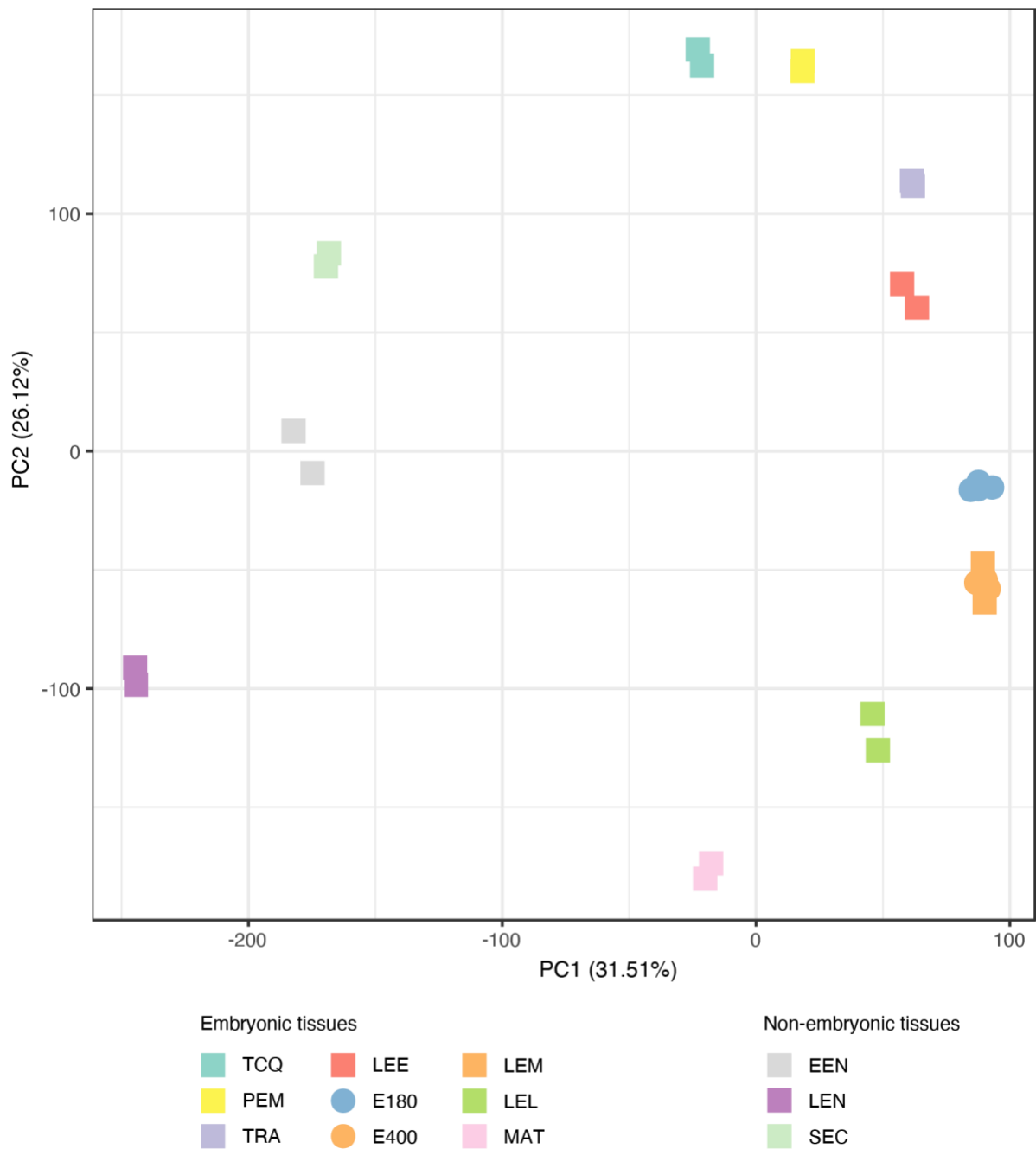
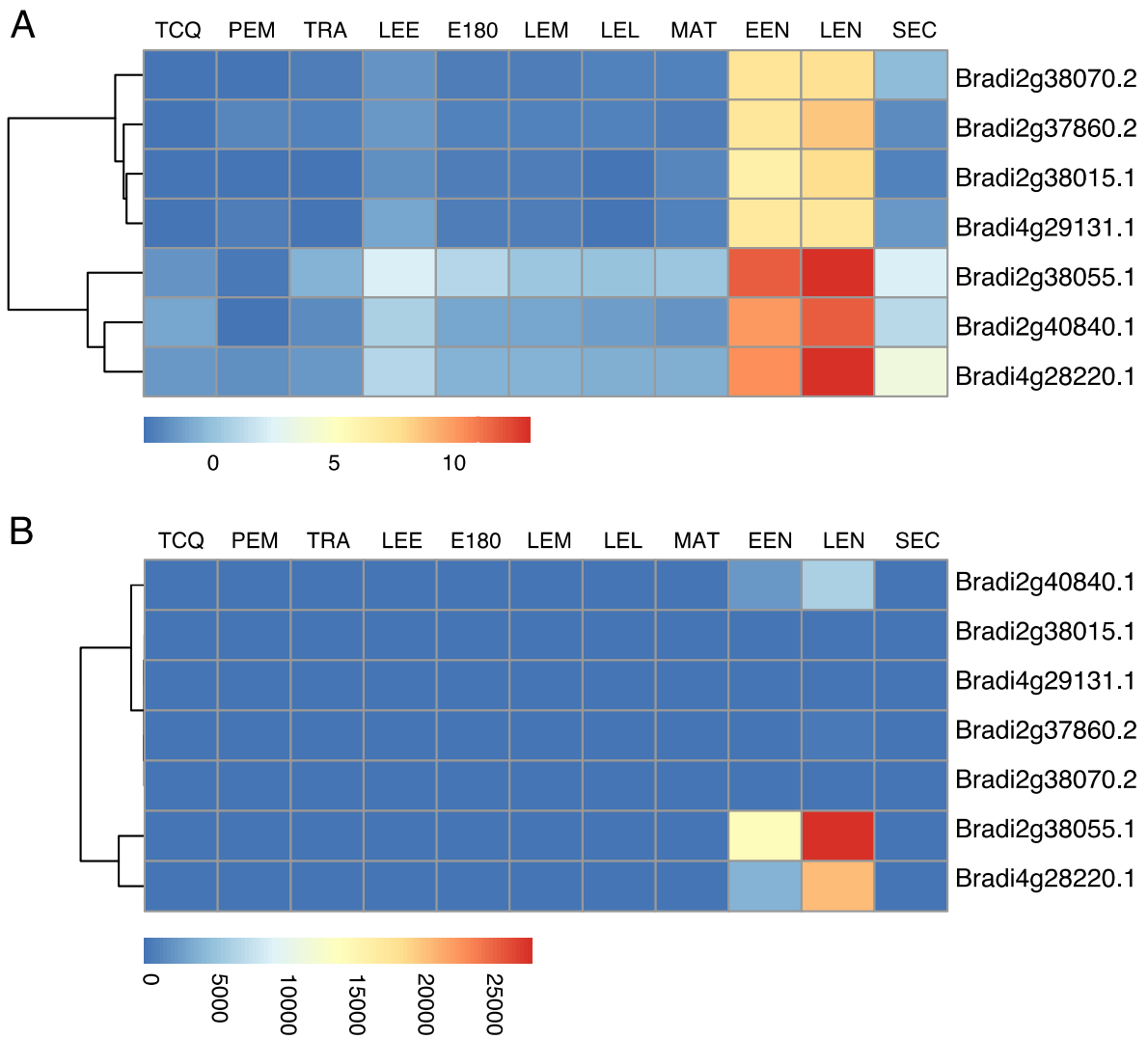




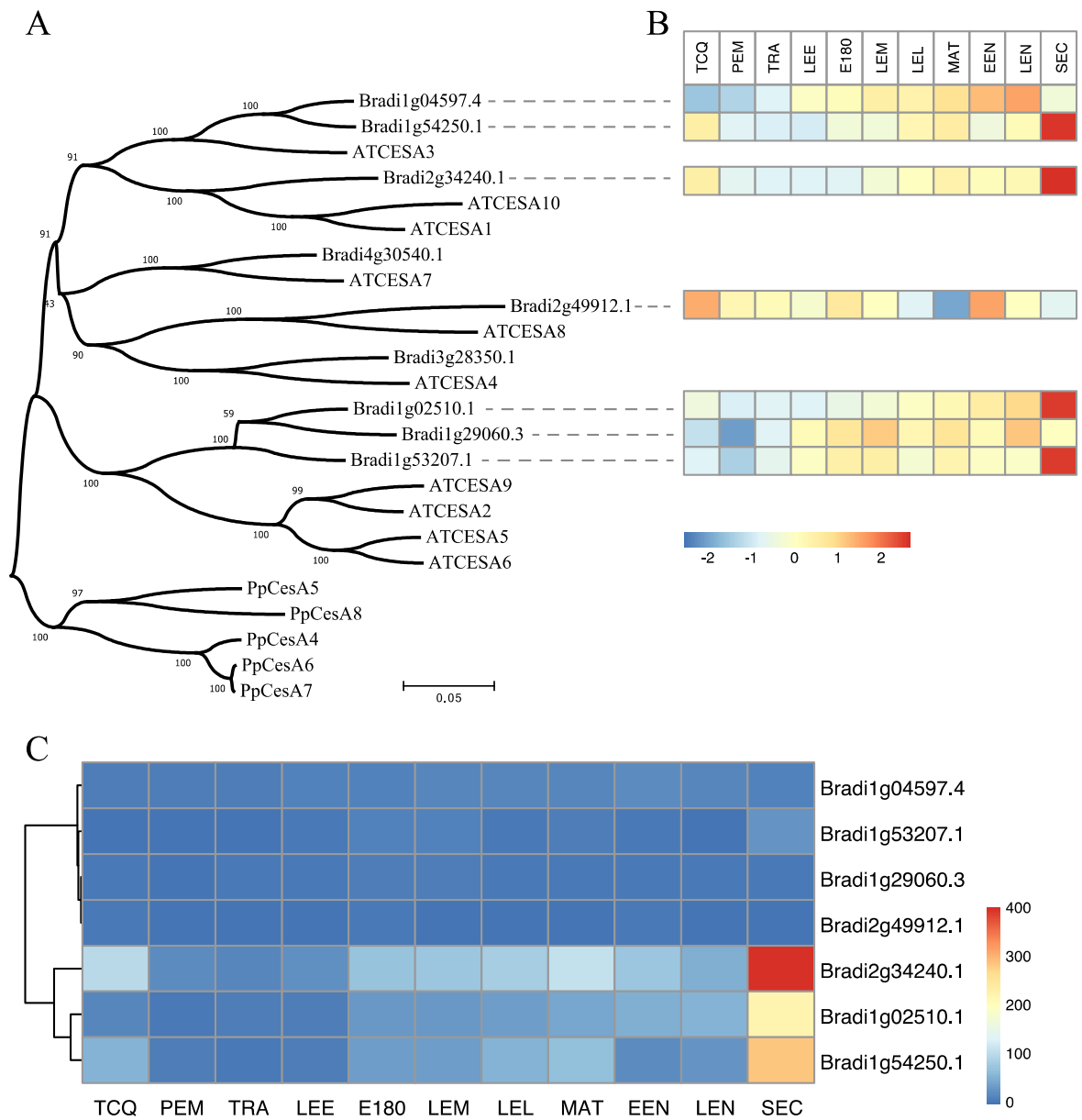
Supplementary Figure 1. Transcriptome profiling of *B. distachyon* embryogenesis. Hierarchical clustering of differential gene expression. Embryonic tissues cover eight successive developmental stages (TCQ, PEM, TRA, LEE, E180, LEM, LEL and MAT), two endosperm tissues correspond to embryonic TRA stage (EEN) and LEL stage (LEN), respectively, and the seed coat (SEC) corresponds to the embryonic LEL stage. Color scale show relative expression.



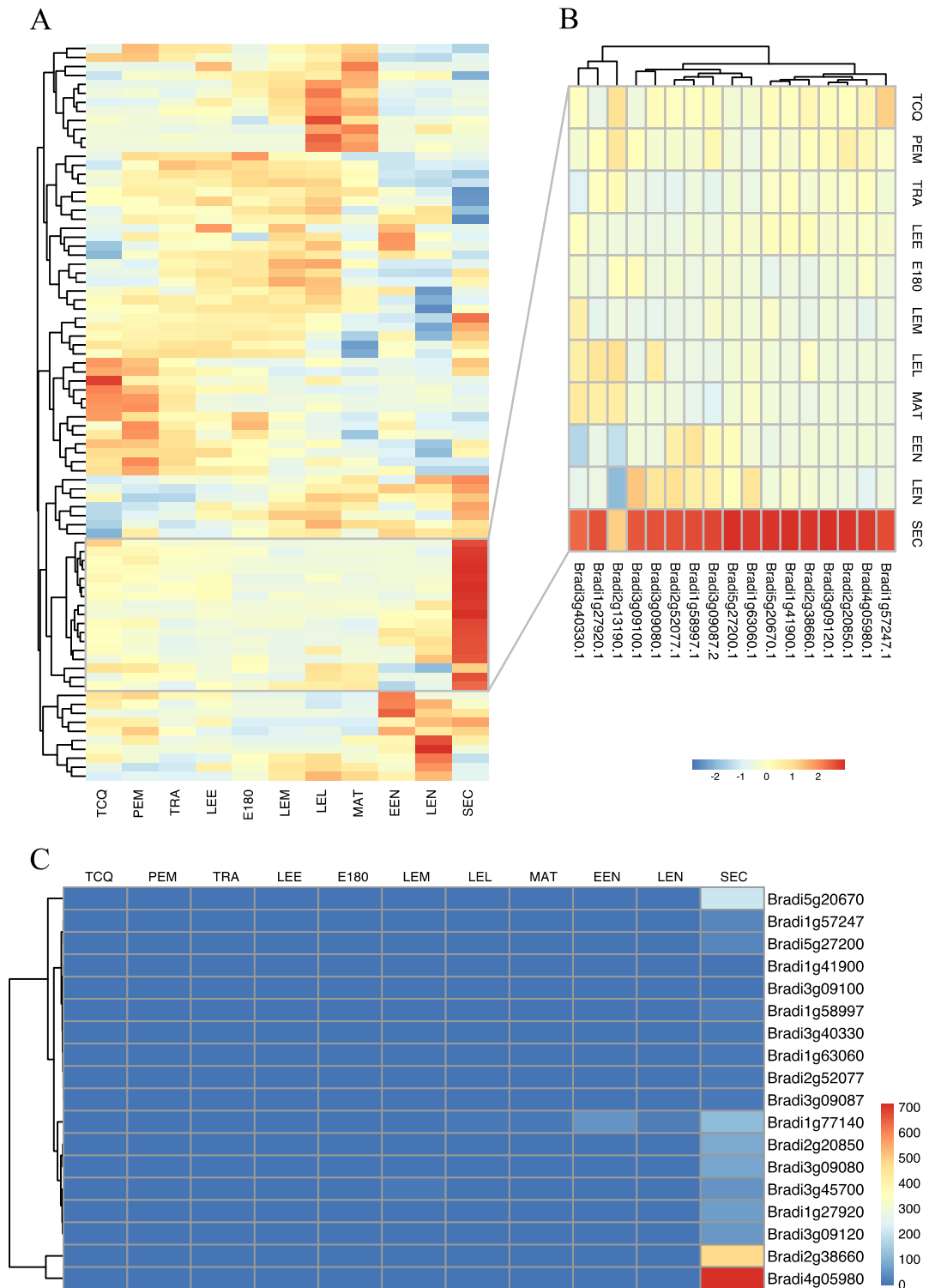
Supplementary Figure 2. Principal Component Analysis of *Brachypodium* transcriptome samples. PCA plot depicting the variance among replicates of each embryo sample. PC1 and PC2 explain 31.51% and 21.62% of the total variance, respectively. Each stage or tissue has two replicates, except for E180 and E400 which both have four replicates. For each sample, replicates are all clustered very closely and separated from all other samples. In addition, there is a clear distinction between embryonic and non-embryonic tissues. Among embryonic tissues, there is clear separation of successive stages through PC1 and PC2.



Supplementary Figure 3. Glutelin gene expression in embryo and non-embryo samples. The relative expression of 7 *Brachypodium* glutelin genes is plotted across the 8 embryonic stages, and in the 3 non-embryo samples. Absolute gene expression is shown in color scale with the expression unit being the logCPM (A) and TPM (B).

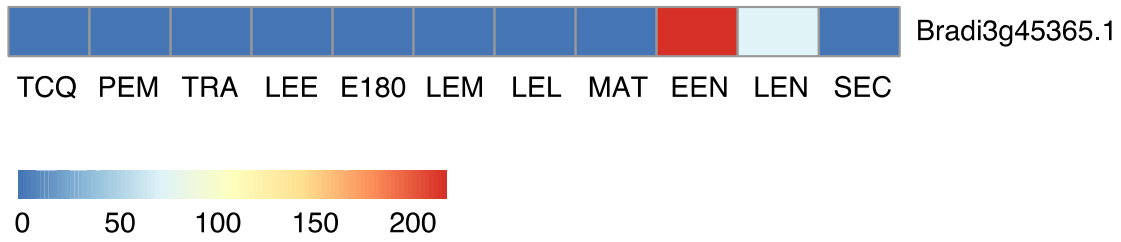


Supplementary Figure 4. *CESA* gene expression during *Brachypodium* embryogenesis. (A) Phylogenetic tree of *CESA* genes from *Arabidopsis*, *Brachypodium* and *Physcomitrium patens* and (B) heatmap of *CESA* gene expression in 7 *Brachypodium* embryo and 3 non-embryo samples. Relative expression is shown in color scale. (C) The absolute expression profiles of *CESA* genes in 7 *Brachypodium* embryo and 3 non-embryo samples. Absolute expression is shown in color scale with the expression unit being the TPM.

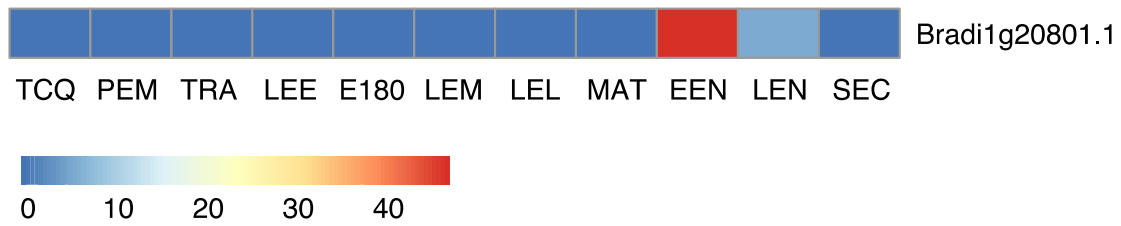


Supplementary Figure 5. Peroxidase genes expression during *Brachypodium* embryogenesis. (A) Hierarchical clustering of 82 genes encoding peroxidases that are expressed during *Brachypodium* embryogenesis, along with relative expression in embryo and non-embryo samples. (B) Detailed heatmap of peroxidases that are highly expressed in seed coat samples. Relative expression is shown in color scale. (C) The absolute expression profiles of peroxidases that are highly expressed in seed coat samples. Absolute expression is shown in color scale with the expression unit being the TPM.

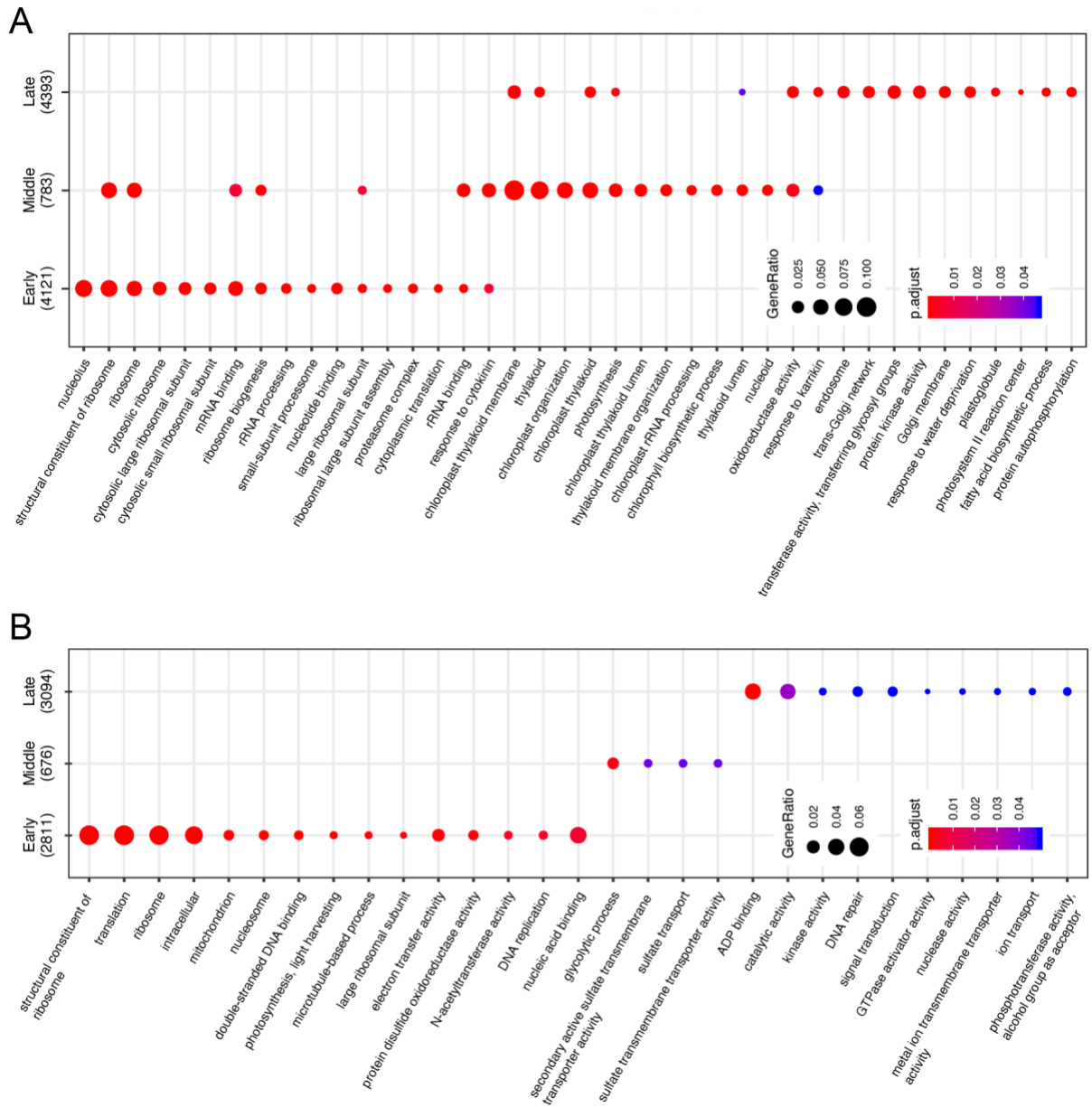
A



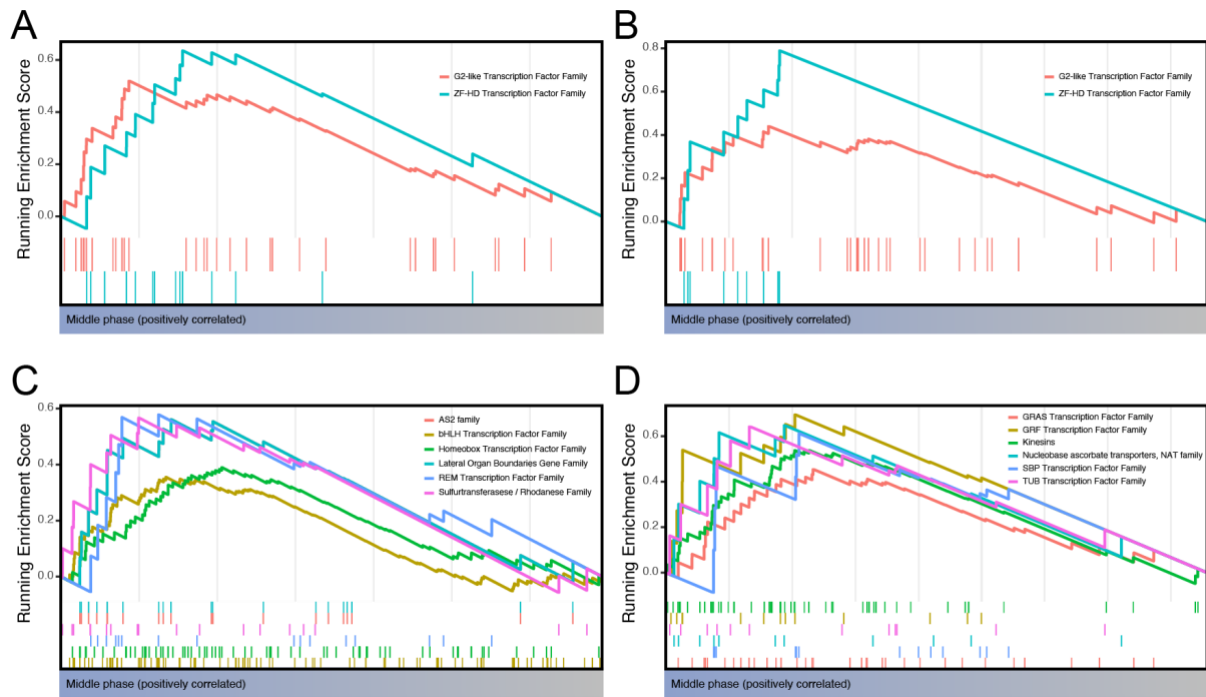
B



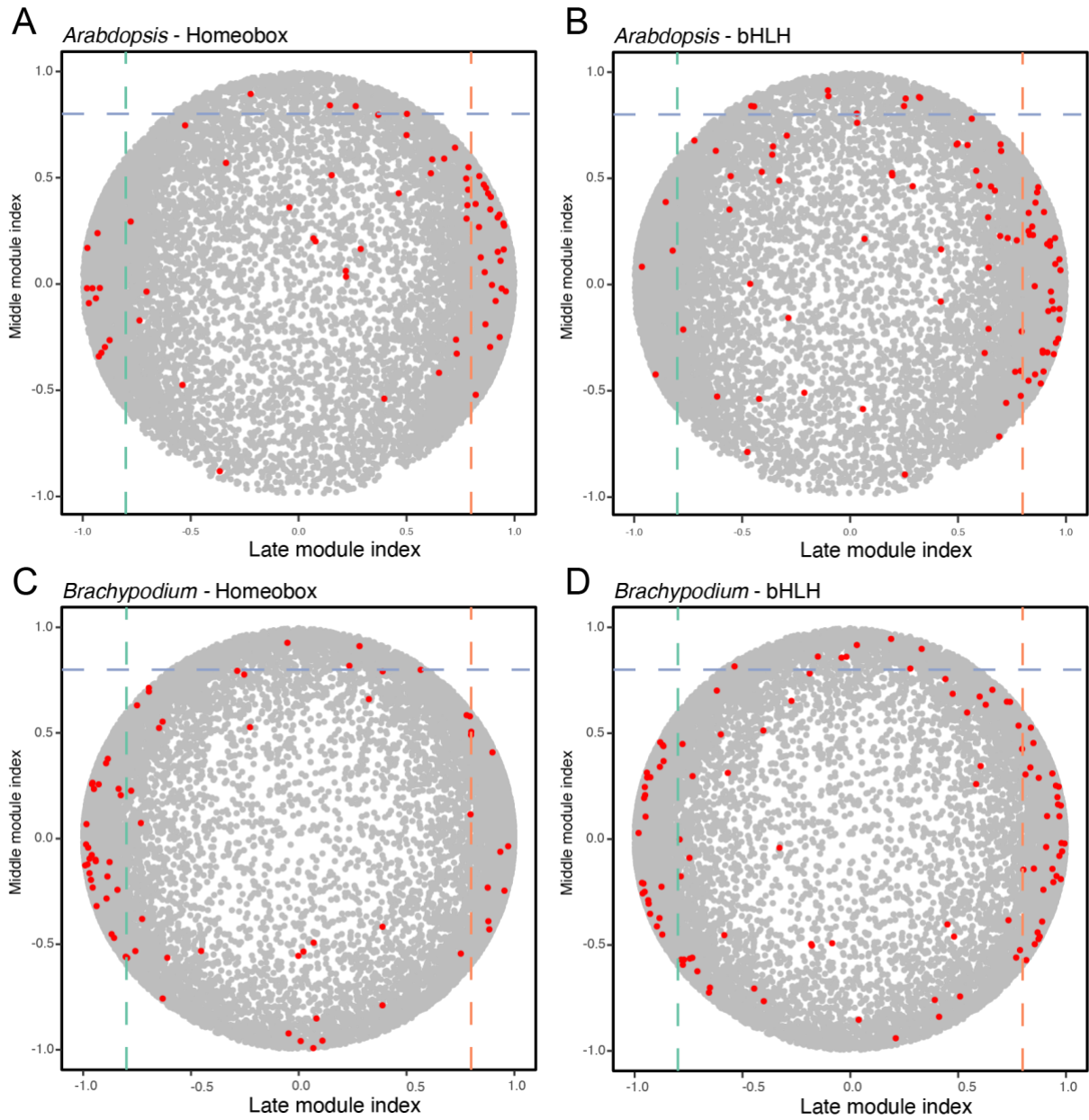
Supplementary Figure 6. *ZOU* and *NAC019* expression during *Brachypodium* embryogenesis. The absolute expression profiles of putative orthologs of *AtZOU* (A) and *TaNAC019* (B) in 7 *Brachypodium* embryo and 3 non-embryo samples. Absolute expression is shown in color scale with the expression unit being the TPM.



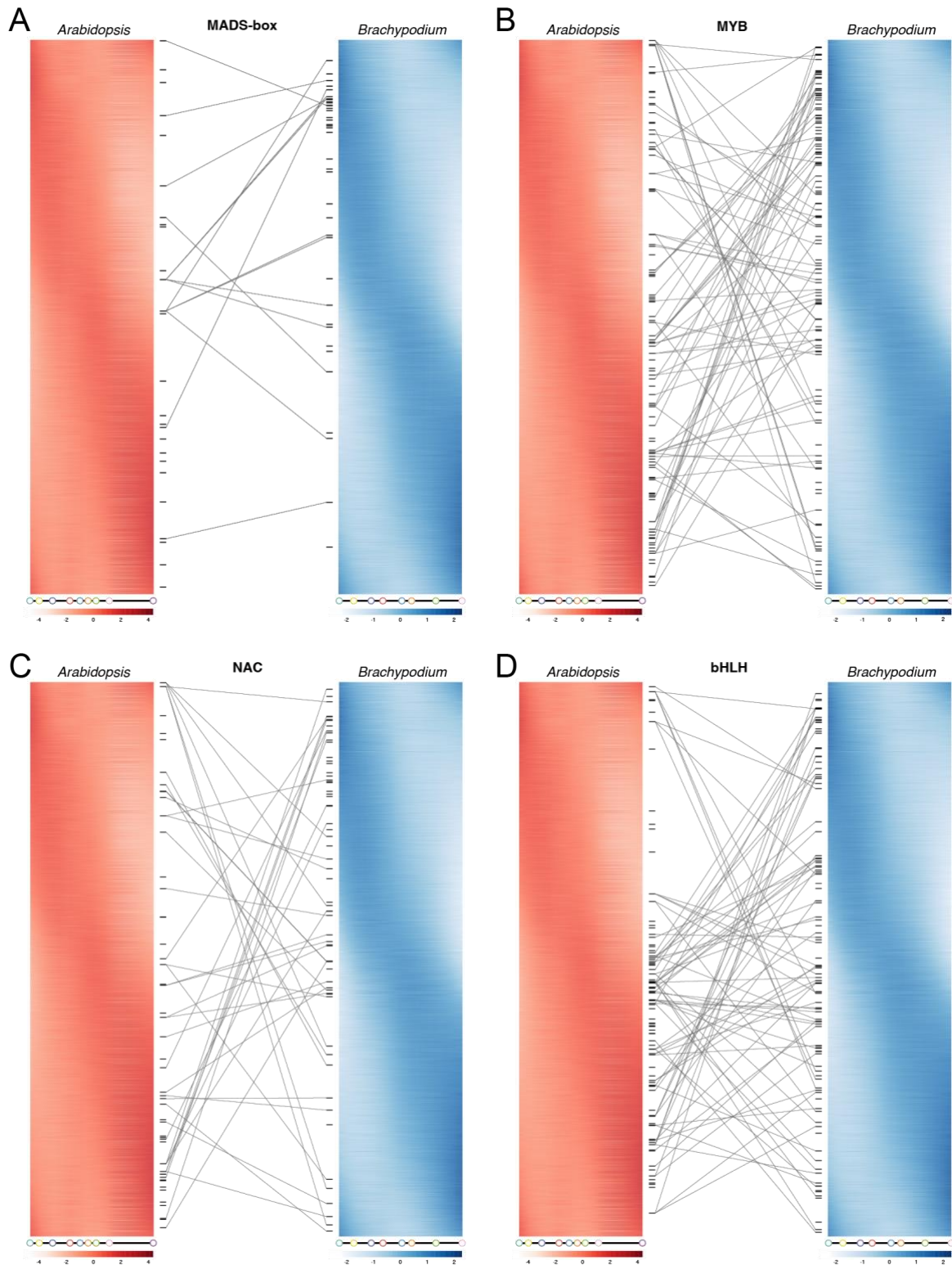
Supplementary Figure 7. Gene Ontology (GO) enrichment analyses of embryo phases. Plots show the enrichment (gene ratio indicated by size of circle; adjusted p-value indicated by color scale) of functional annotations in gene sets that are highly expressed during early, middle or late embryogenesis in *Arabidopsis* (a) or *Brachypodium* (b).



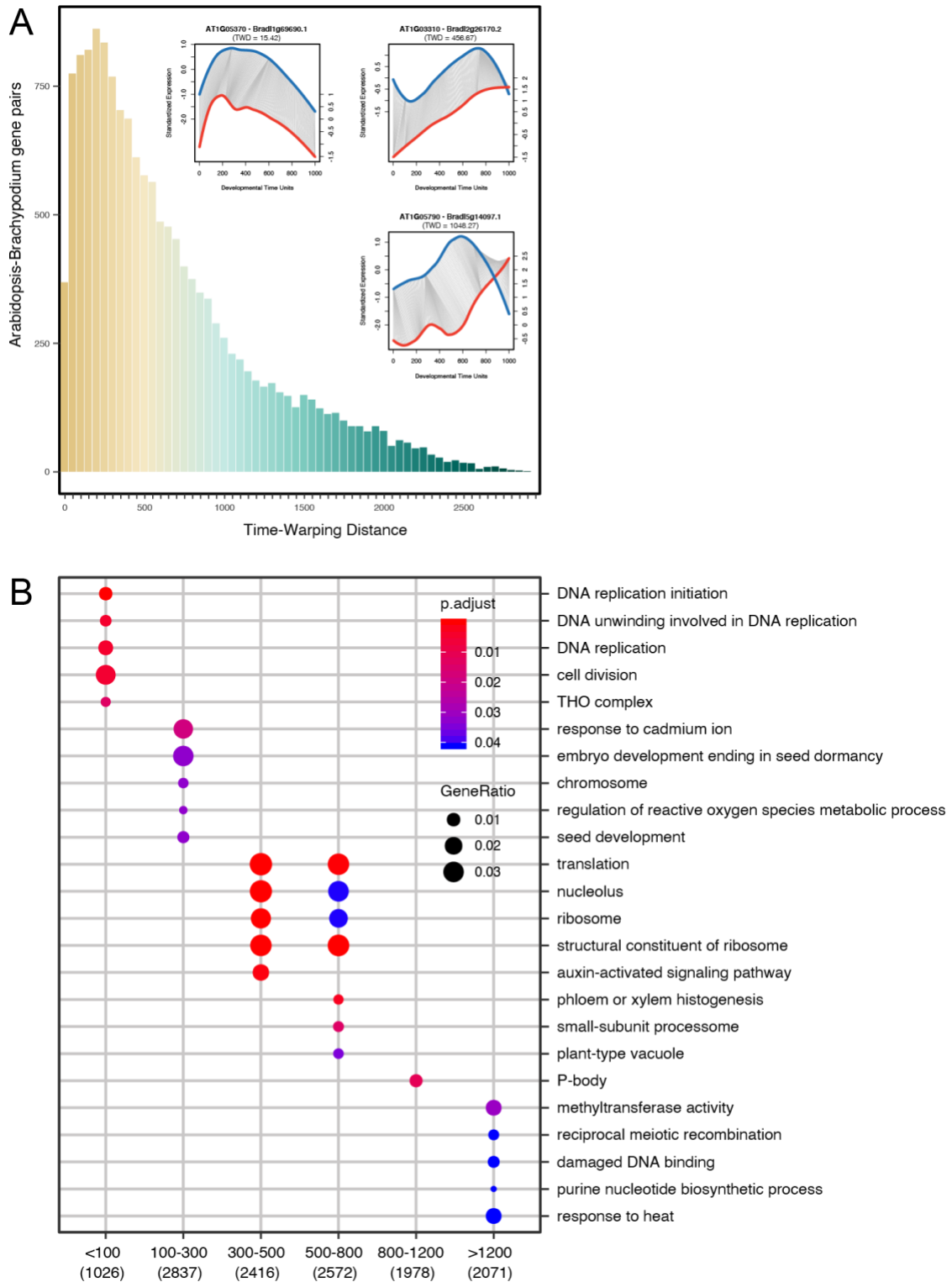
Supplementary Figure 10. Gene set enrichment analysis (GSEA) of middle embryonic developmental genes. Both *Arabidopsis* (a) and *Brachypodium* (b) middle phases during embryogenesis are enriched in ZF-HD transcription factor family and G2-like transcription factor family. Except for these two common gene families, the middle phases of *Arabidopsis* (c) and *Brachypodium* (d) are enriched in various but different gene families.



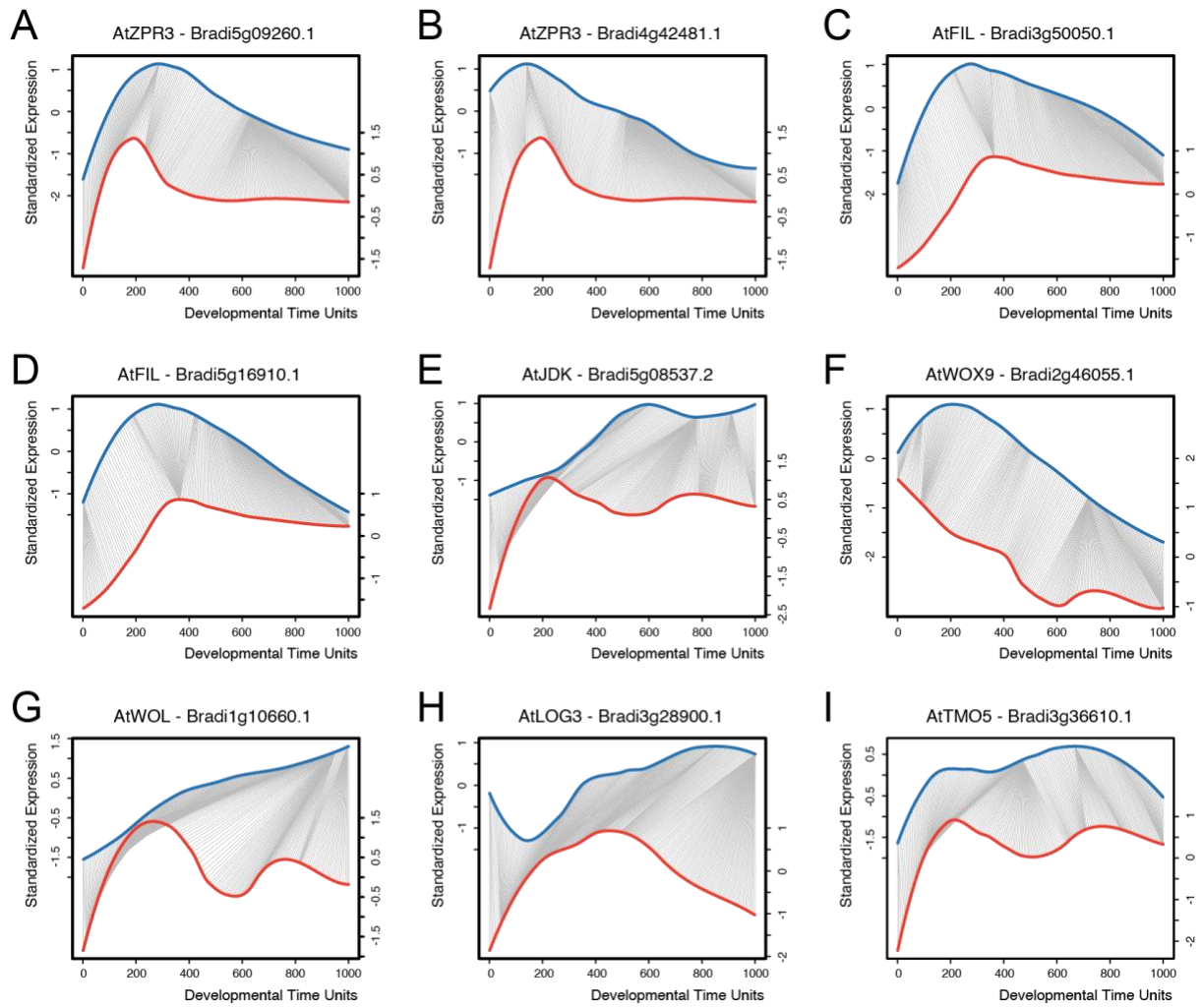
Supplementary Figure 11. HD and bHLH expression profiles across *Arabidopsis* and *Brachypodium* embryogenesis. Members of the HD (a,c) or bHLH (b,d) transcription factor families are plotted on the middle/late module index plot for *Arabidopsis* (a,b) or *Brachypodium* (c,d). Each TF gene is represented by a red dot.



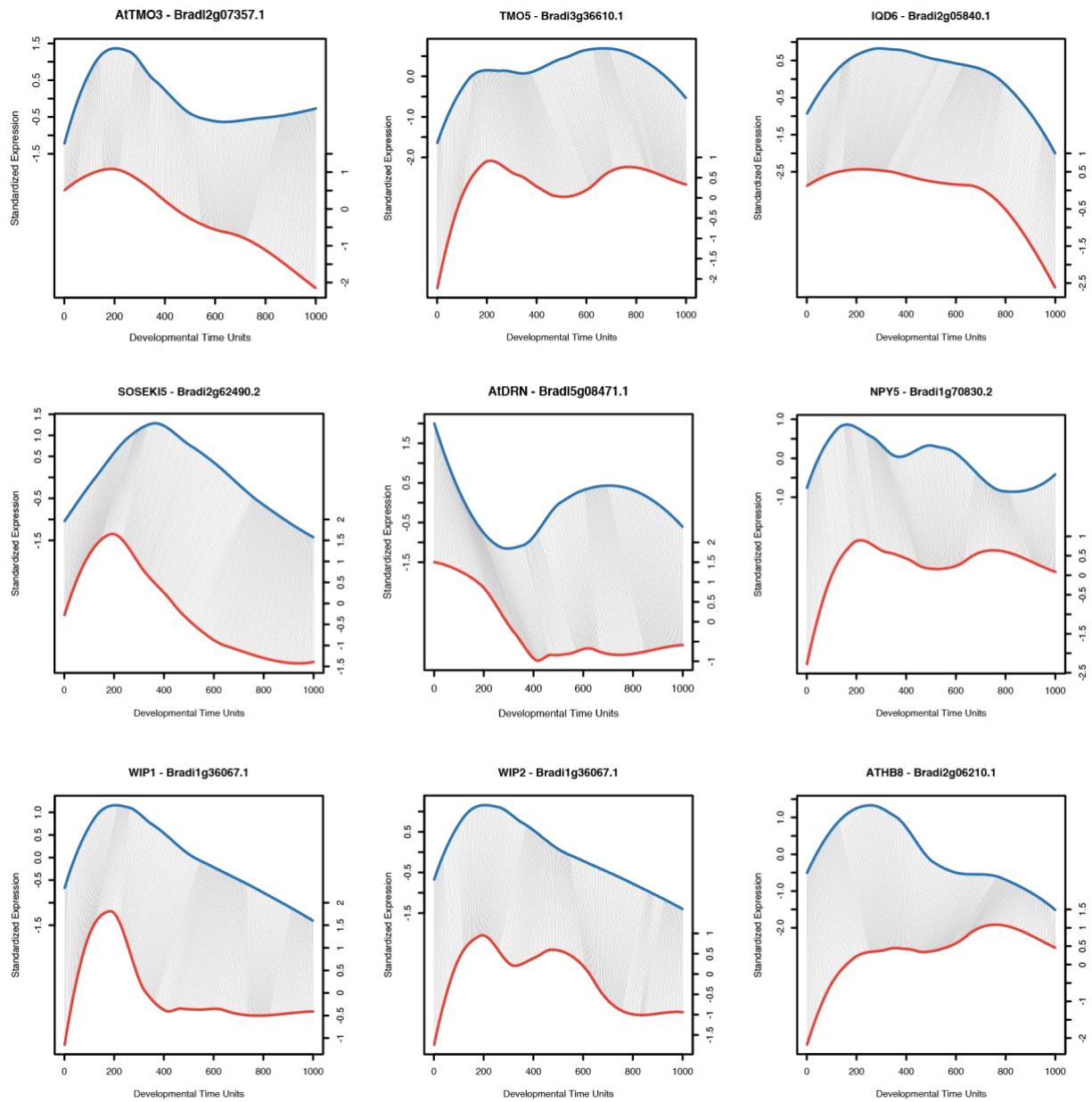
Supplementary Figure 12. Phased gene expression and gene family mapping. All members of the *Arabidopsis* (red) and *Brachypodium* (blue) MADS-box (a), MYB (b), NAC (c) and bHLH (d) gene families are sorted by their expression peaks along embryonic development. relative expression is shown in white (low) to red or blue (high) scale, and DTU plots below each phasigram indicate developmental progression. Orthology relationships between *Arabidopsis* and *Brachypodium* genes are indicated by connecting lines.



Supplementary Figure 13. Dynamic time warping analysis of *Arabidopsis* and *Brachypodium* embryogenesis. (a) Examples of expression time warping plots for orthologous gene pairs between *Arabidopsis* and *Brachypodium* throughout embryogenesis (insets; including time warp distance [TWD]), and distribution of TWD distance scores for all *Arabidopsis-Brachypodium* gene pairs. (b) Gene Ontology analysis of gene sets binned by time warping distance score (x-axis). Plot shows the enrichment (gene ratio indicated by size of circle; adjusted p-value indicated by color scale).



Supplementary Figure 14. DTW expression profile alignments of gene pairs between *Arabidopsis* and *Brachypodium*.



Supplementary Figure 15. DTW expression profile alignments of *Arabidopsis*-*Brachypodium* gene pairs, of which *Arabidopsis* counterparts are well-characterized auxin-responsive (output) genes during embryogenesis.