**Supporting Information (**Investigating reproductive development in *Brachypodium distachyon* focussing on the *YABBY* family of transcription factors**)**

**Data S2.1. List of gene IDs for grain-specific, germination-specific and seedling-specific transcripts**. Genes represent the number of transcripts shown in Figure 2.3. Gene IDs are based on *Brachypodium disctachyon* v3.1 assembly available at Phytozome v12.0 (<https://phytozome.jgi.doe.gov/pz/portal.html> ).

**Data S2.2 Differentially expressed genes between intact mature grain (MG) and mature grain where the embryo has been removed (MG-Emb).** List of gene IDs with gene descriptions and GO annotations.

**Data S2.3. Fishers Exact Test (FET) for UP and DOWN regulation >2.0 L2FC between each stages.** List of overrepresented GO terms enriched in each pairwise comparison, extending the representative data from Table 2.2.

**Data S2.4.** **Clustering analysis of all genes expressed during *Brachypodium* grain development and germination**.  List of gene IDs that are included in each cluster in Figure 2.5, along with their gene description and GO term annotations.

**Data S2.5.** **Clustering analysis of transcription factors expressed during *Brachypodium* grain development and germination**. List of gene IDs that are included in each cluster in Figure 2.6, along with their gene description and GO term annotations.

**Data S2.6. List of protein Domains of Transcription Factors in Brachypodium**. Details gene list presented in Figure 2.6.

**Data S4.1. Gene sets for top 500 coexpressed genes related to each YABBY genes** **by Jenson Shannon Distance**. This list were used for enrichment GO terms latter.

**Data S4.2. Fishers Exact Test (FET) for coexpressed of individual YABBY genes**, presented in Figure 4.7.