

Figure S1. Variations in the total isoflavone contents in soybean seeds across 3 years. DB, Danbaek; HG, Hwanggeum.

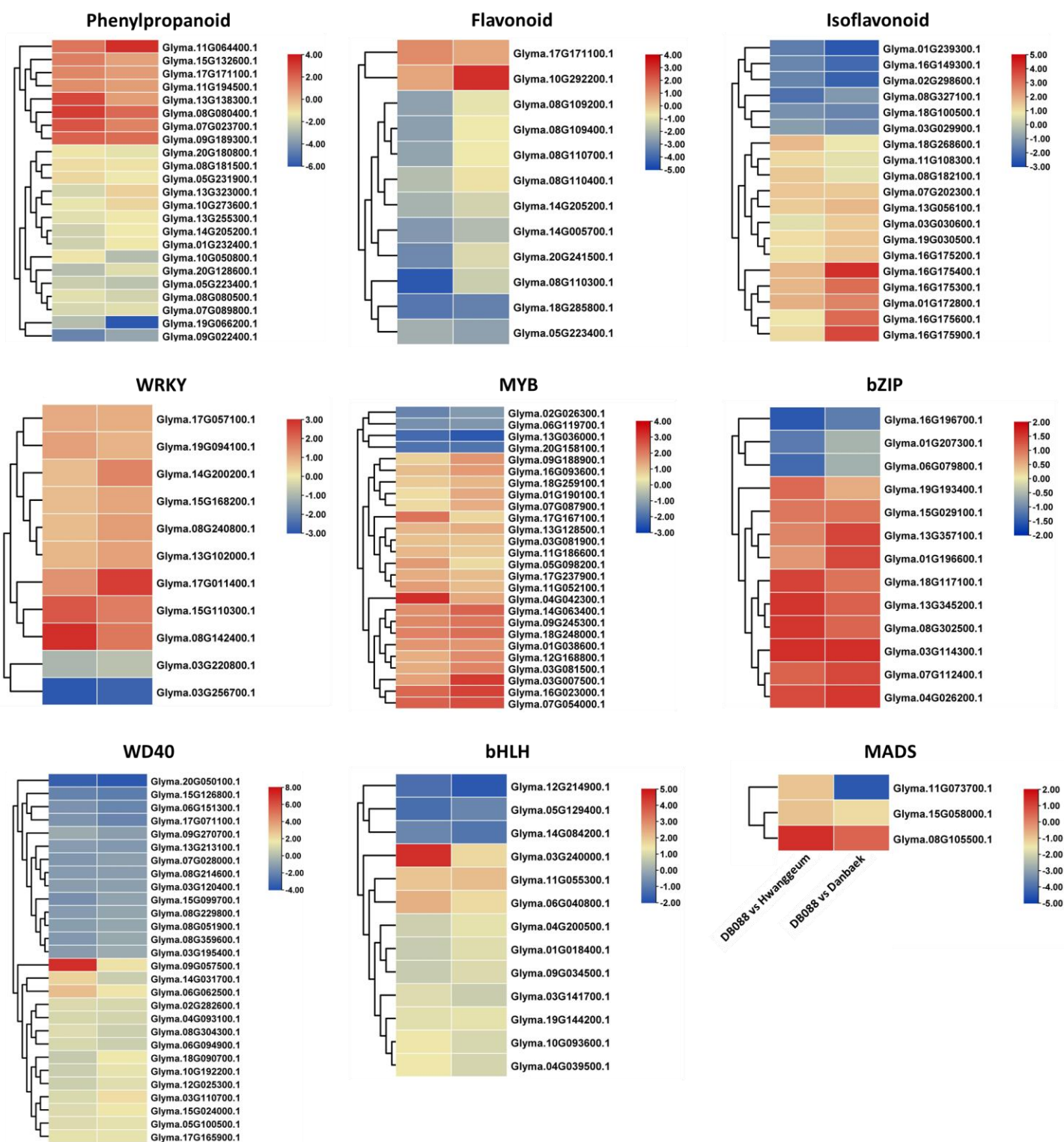


Figure S2. Heatmap depicting the expression patterns of the DEGs related to isoflavone biosynthesis and TFs according to KEGG pathways. Gene expression levels are presented as \log_2 (fold-change) values. The results for Hwanggeum and Danbaek are presented on the left and right, respectively.

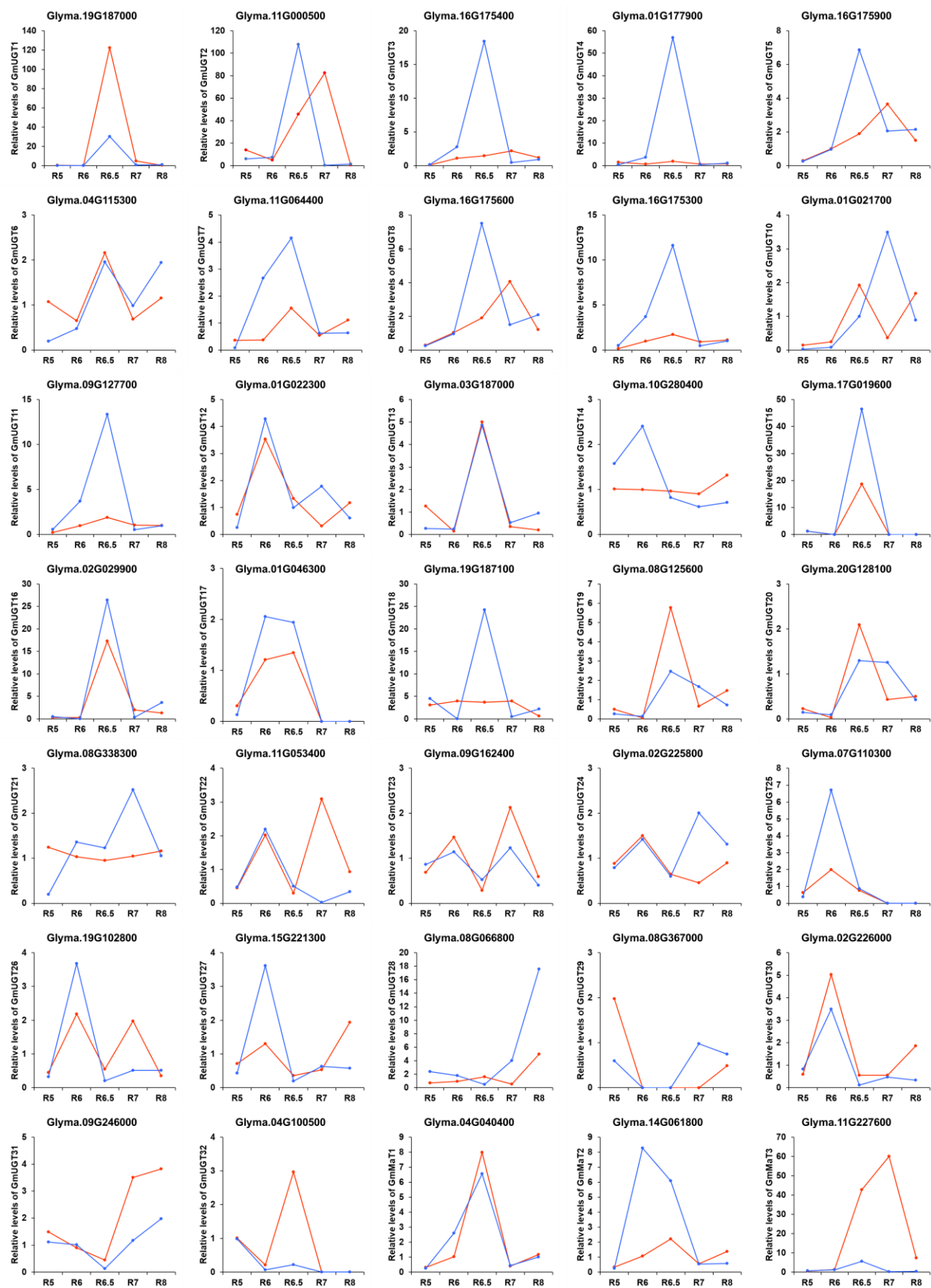


Figure S3. Relative expression patterns of the downstream genes involved in isoflavone biosynthesis in different seed developmental stages according to the RNA-seq data and the findings of earlier research. The red and blue lines represent the results of the DB-088 vs Hwanggeum and DB-088 vs Danbaek comparisons, respectively. The heatmap presents relative gene expression levels, which were normalized against the expression of the internal reference gene *F-box*.

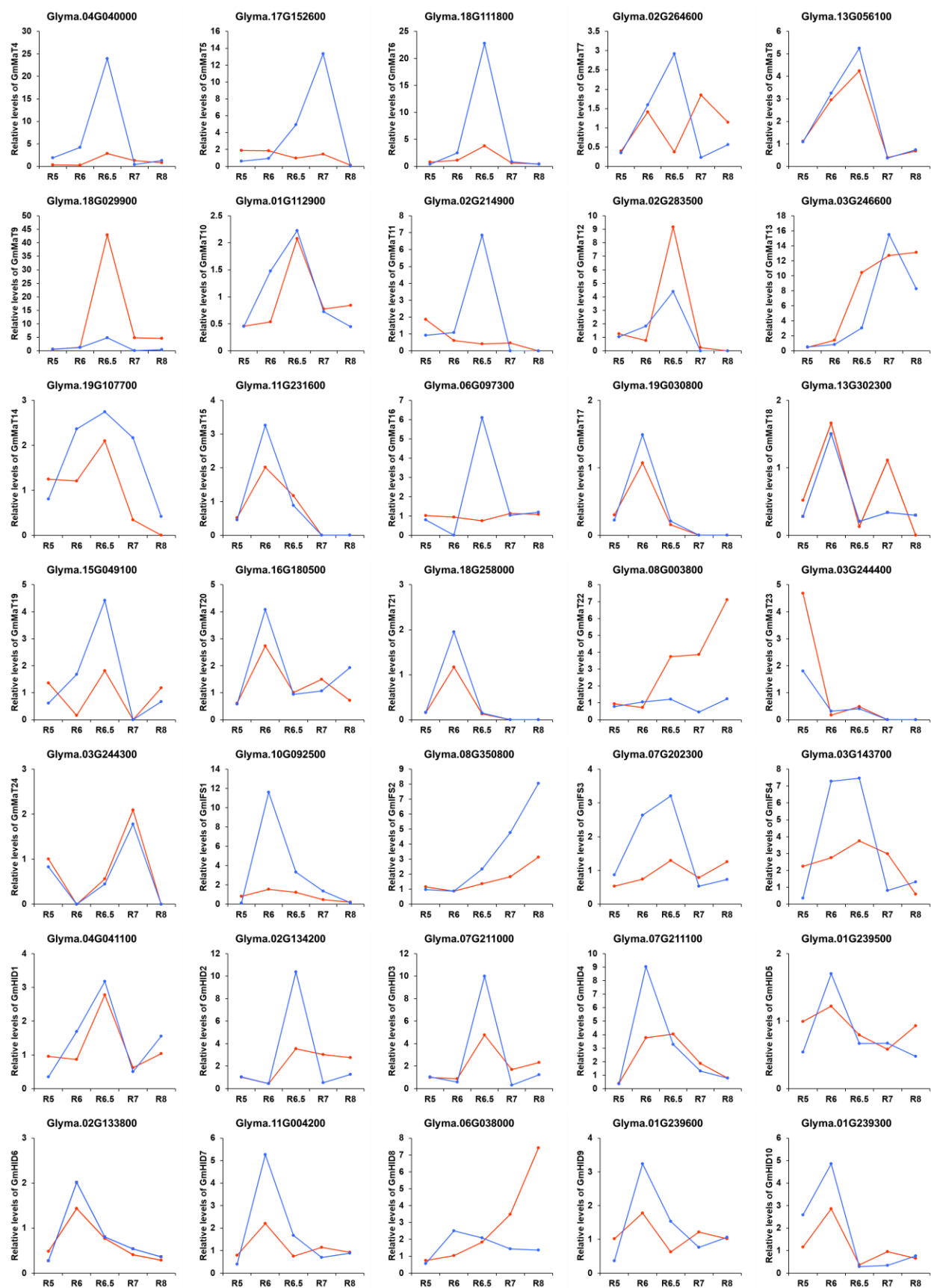


Figure S3. continued.

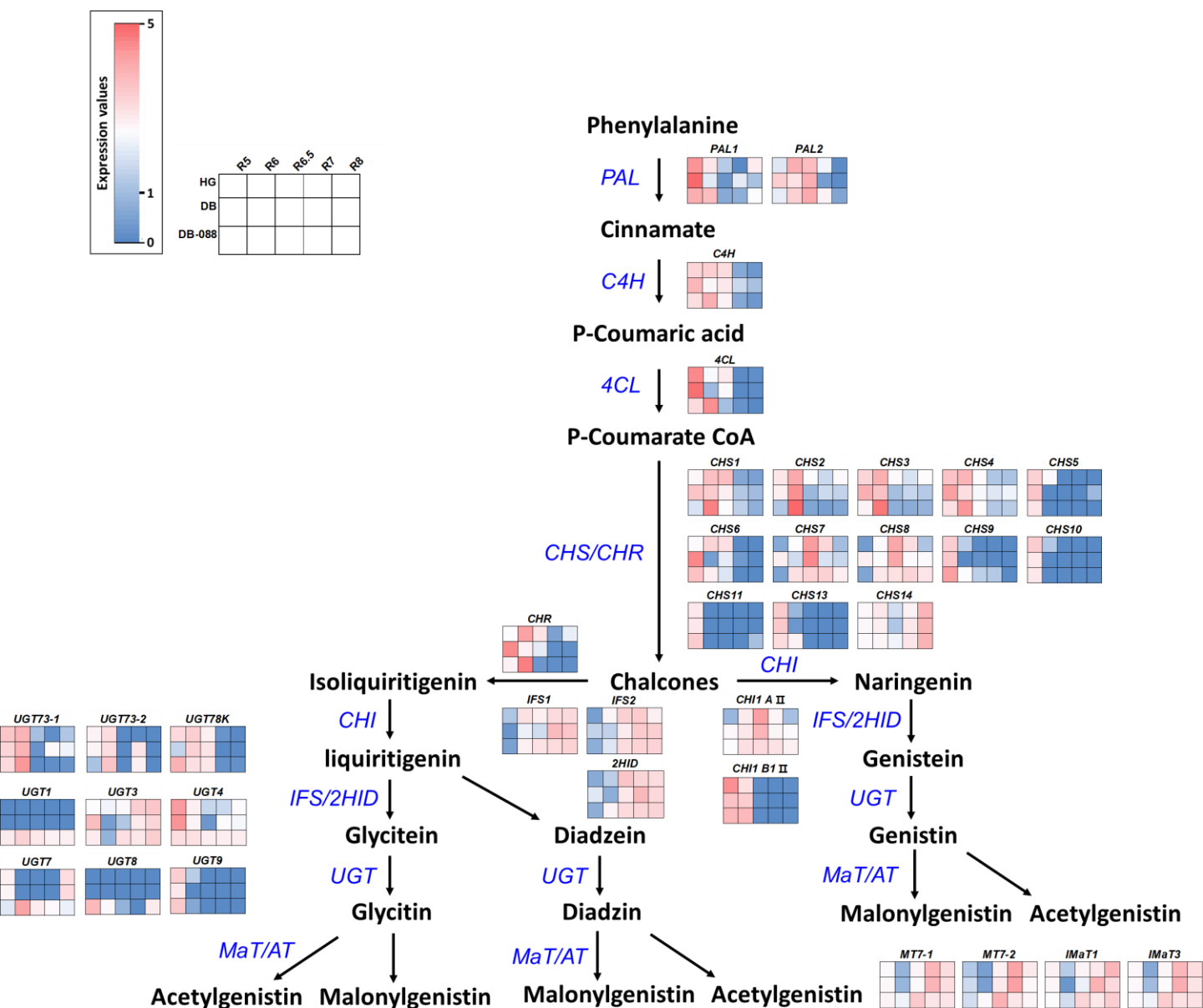


Figure S4. Overview of the expression patterns of previously reported genes involved in isoflavone biosynthesis across seed developmental stages. The heatmap presents relative gene expression levels, which were normalized against the expression of the internal reference gene *F-box*.

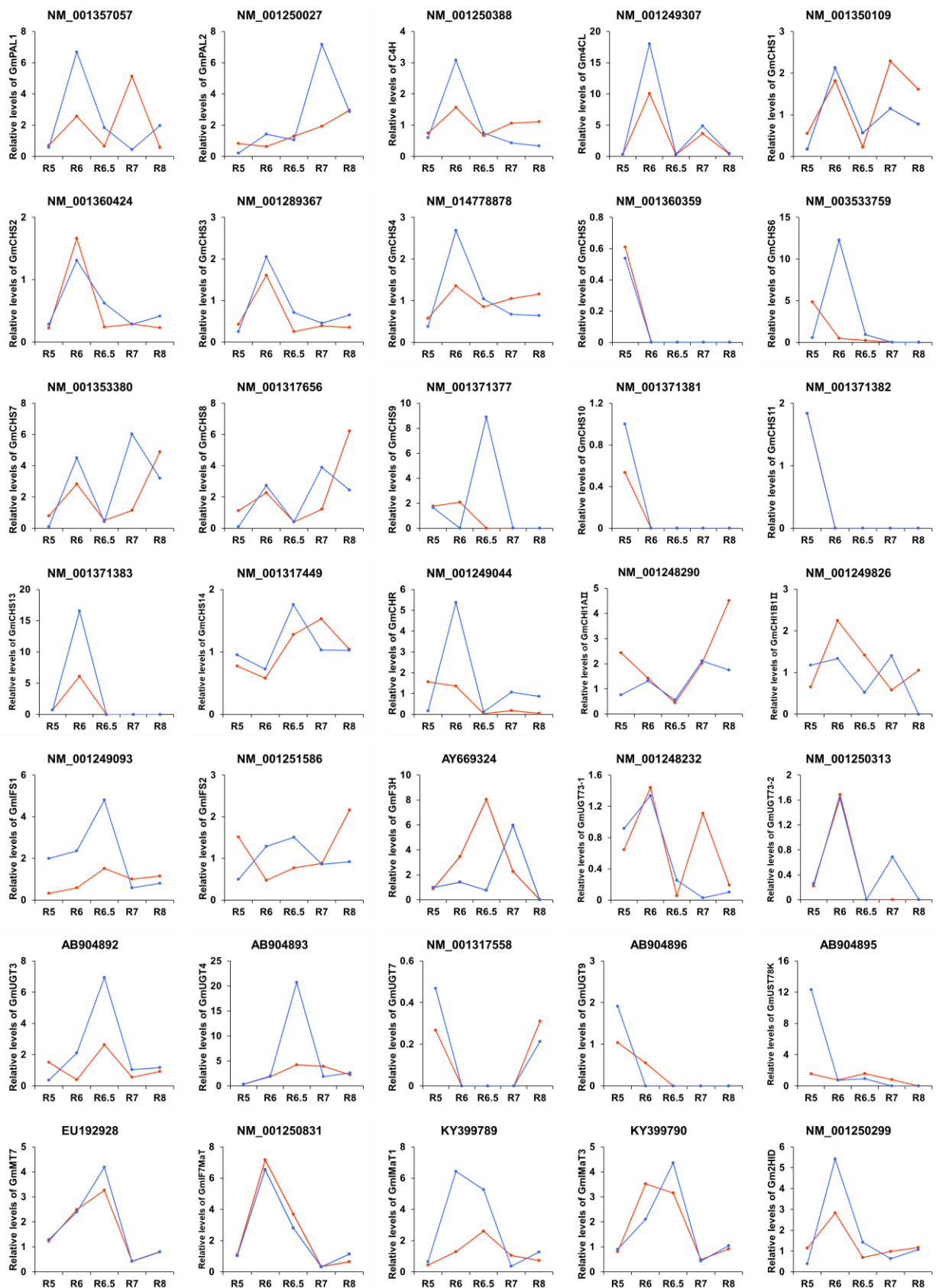


Figure S5. Relative expression patterns of previously reported genes involved in isoflavone biosynthesis across seed developmental stages. The results of the comparisons between DB-088 and Hwanggeum (red line) and Danbaek (blue line) are presented. The heatmap presents relative gene expression levels, which were normalized against the expression of the internal reference gene *F-box*.

