

Figure S1. Laser microdissection of early embryo.

(A) Whole embryo at 2 DAP. (B) Whole embryo at 3 DAP. (C) Whole embryo at 4 DAP. (D) Apical half of the embryo at 3 DAP. (E) Basal half of the embryo at 3 DAP. (F) Ventral half of the embryo at 3 DAP. (G) Dorsal half of the embryo at 3 DAP. Top, middle and bottom are images of before dissection, after dissection, and a collected sample, respectively.

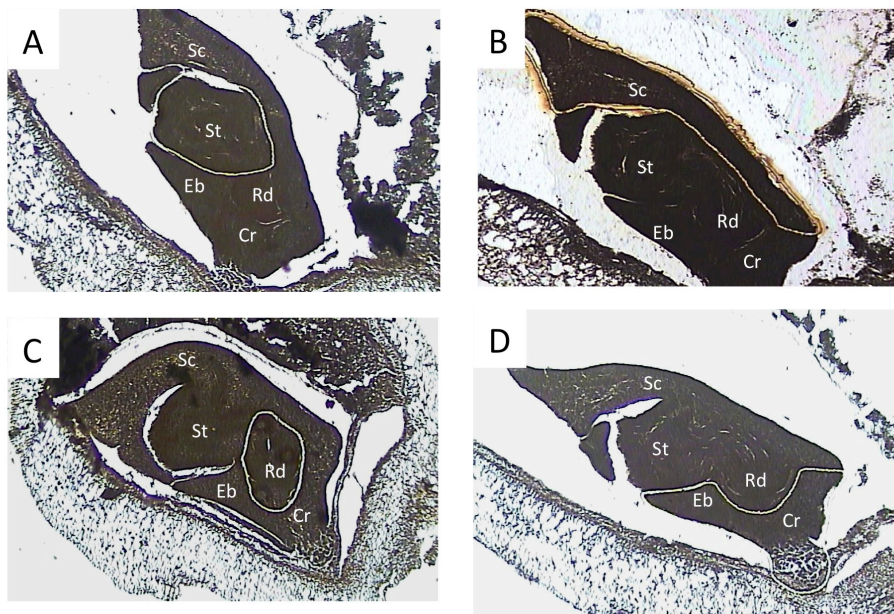


Figure S2. Laser microdissection of 7-DAP embryo.

(A) Separation of shoot containing tissue. (B) Scutellum. (C) Radicle (Root). (D) Epiblast/coleorhizae.
Ct: coleoptile, Sc: scutellum, Rd: radicle, St: shoot, Eb: epiblast, Cr: coleorhiza

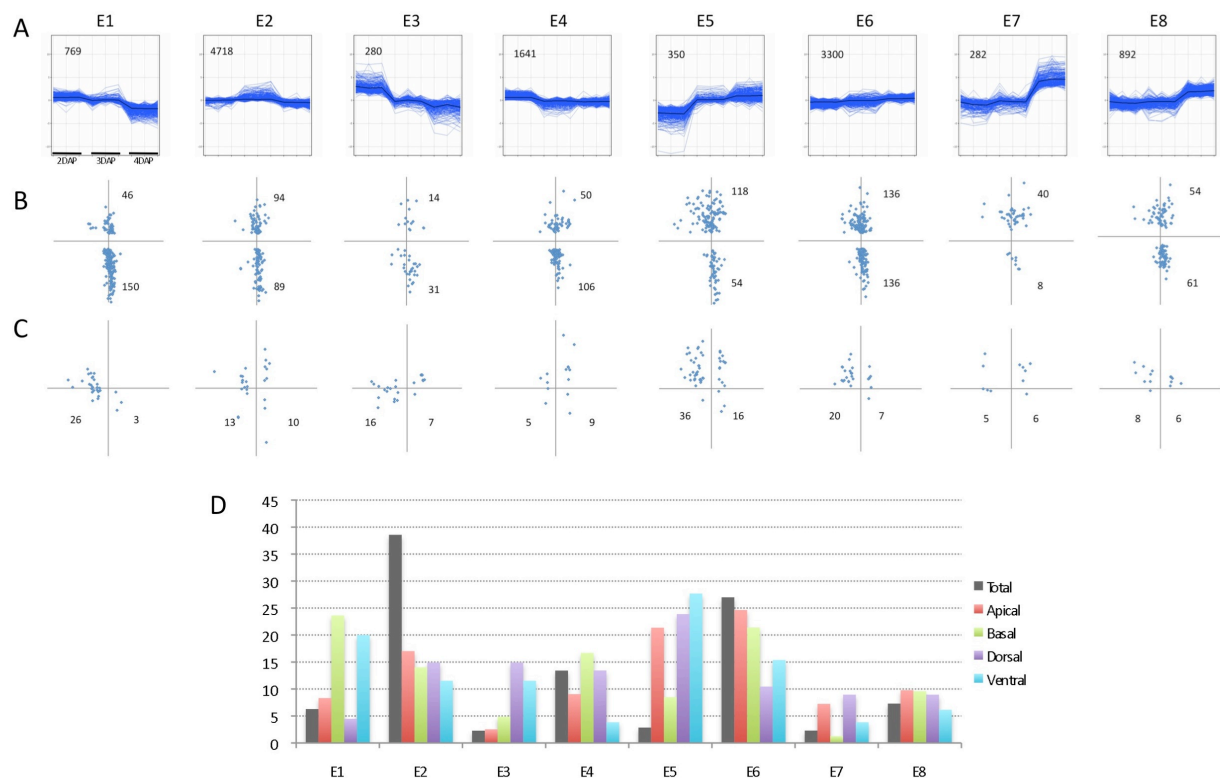


Figure S3. K-means clustering of gene expression in 3-DAP embryos.

(A) Changes in the expression levels of genes in the eight clusters. The X-axis represents 2-, 3-, and 4-DAP samples in triplicate. Y-axis represents the relative expression value of each probe. The number of probes categorized in the cluster is indicated in the upper left. (B) Expression sites of genes significantly biased along the apical-basal axis of 3-DAP embryos in each cluster. X- and Y-axes indicate the relative expression values (\log_2) along the dorsal-ventral and apical-basal axes, respectively. Numbers of genes preferentially expressed in the apical and basal regions are indicated. (C) Expression sites of genes significantly biased along the dorsal-ventral axis of 3-DAP embryos in each cluster. Numbers of genes preferentially expressed in the dorsal and ventral regions are indicated. (D) Percentages of genes contained in each cluster and region. Gray bar indicates the percentage of clustered genes compared to the total number of expressed genes. Red, green, purple and blue bars indicate the percentage of preferentially expressed genes in the apical, basal, dorsal and ventral regions compared to the total number of genes expressed in those regions.

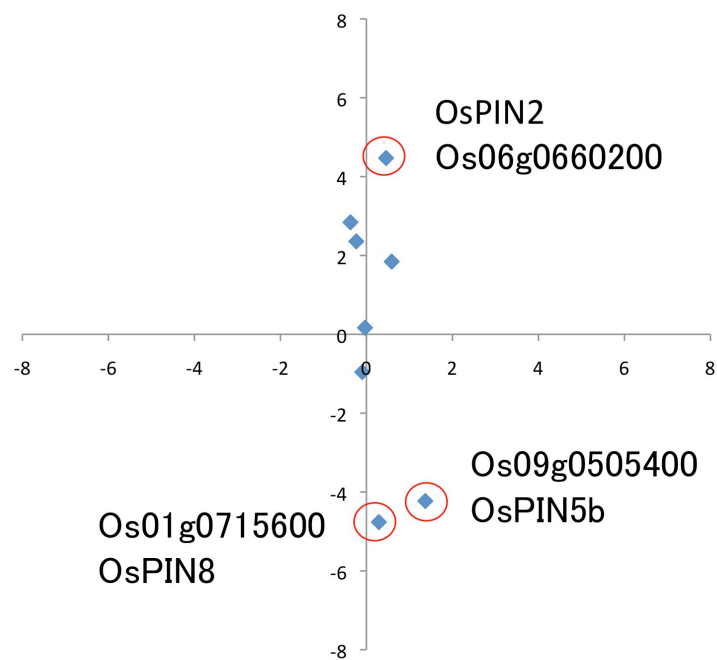


Figure S4. Spatial distribution of PIN-like genes in 3-DAP embryo.

Expression sites of PIN-like genes expressed in the 3DAP embryo in the scatter diagram. X- and Y-axis indicate the relative expression values (log2) along the dorsal-ventral and the apical-basal axis, respectively. Red circles indicate probes that showed conspicuously biased expression along the dorsal-ventral and/or the apical-basal axis as outliers. The RAP-ID and the annotation of the outliers are represented.

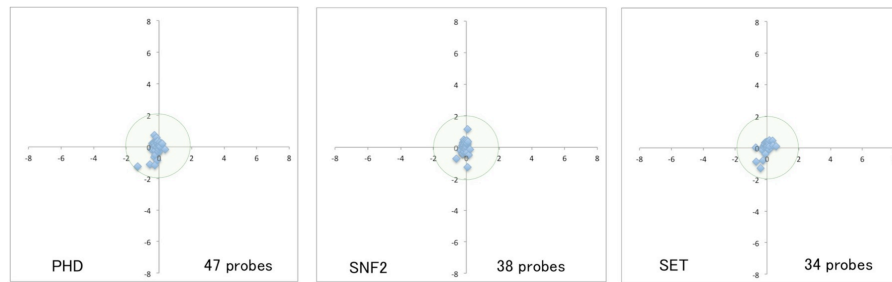


Figure S5. Spatial distribution of transcriptional factor and transcriptional regulator genes categorized into Type III.

Sites of transcription factor (TF) and transcriptional regulator (TR) genes expression in 3-DAP embryos in the scatter diagram. X- and Y-axes indicate the relative expression values (log2) along the dorsal-ventral and apical-basal axes, respectively. Data points inside the green circle represent probes with absolute relative expression values of less than 2.

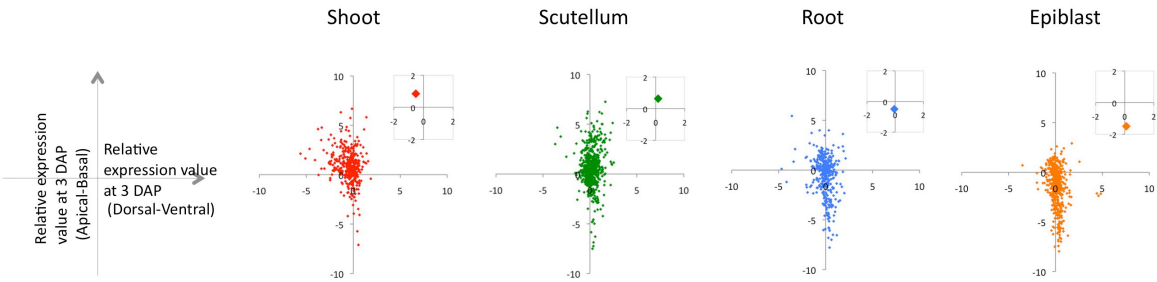


Figure S6. Spatial correlation between expression profiles in globular embryo and in embryonic organs at the later stage. Spatial expression pattern of genes upregulated in specific tissues of 7DAP embryos at 3DAP. Titles of the X- and Y-axes are presented in the leftmost diagram. Insets indicate the barycenters of the data points. Red, green, blue, and orange points represent the shoot, scutellum, root, and epiblast samples, respectively, of 7-DAP embryos.

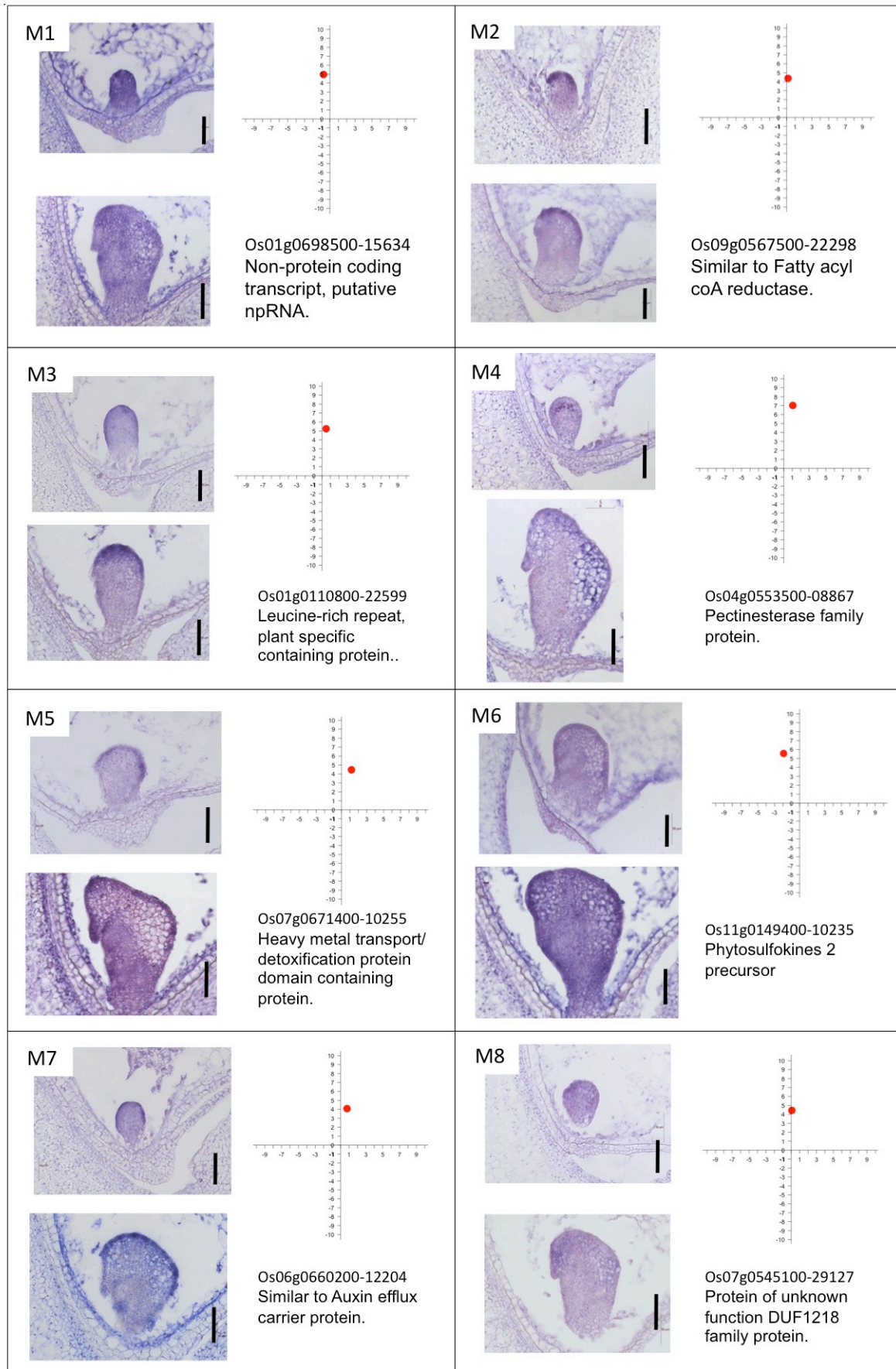


Figure S7. *In situ* expression pattern of the selected genes that are not included in the Figure 5. On the left of the upper and lower images of each panel are the expression patterns of 3- and 4-DAP embryos, respectively. The right scatter diagram indicates the predicted expression site of the corresponding probe based on microarray analysis. The RAP-ID, probe number, annotations and marker ID (see supplementary material Table S10) of the genes are indicated. Scale bars = 50 μ m.

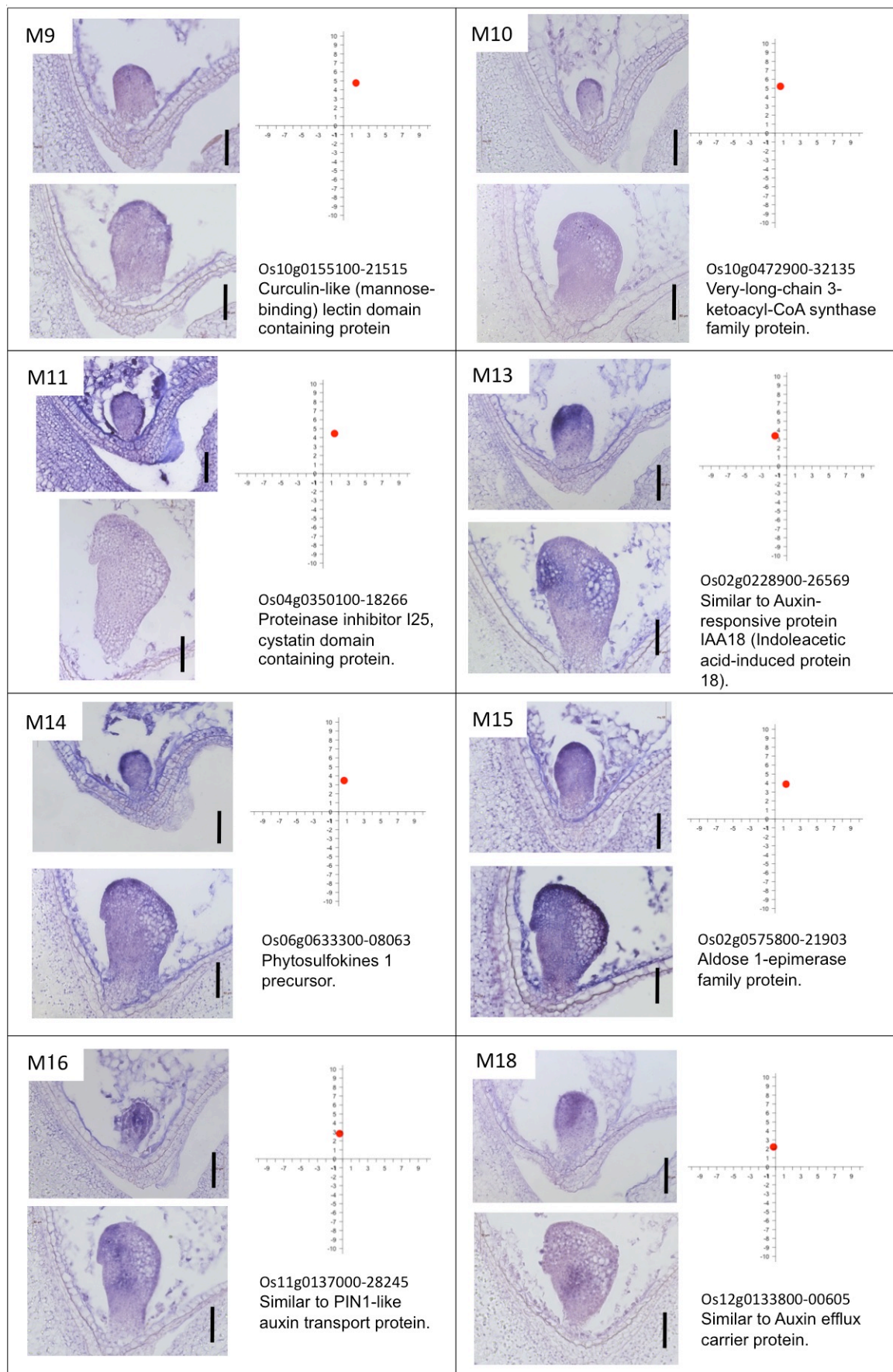


Figure S7. Cont'd.

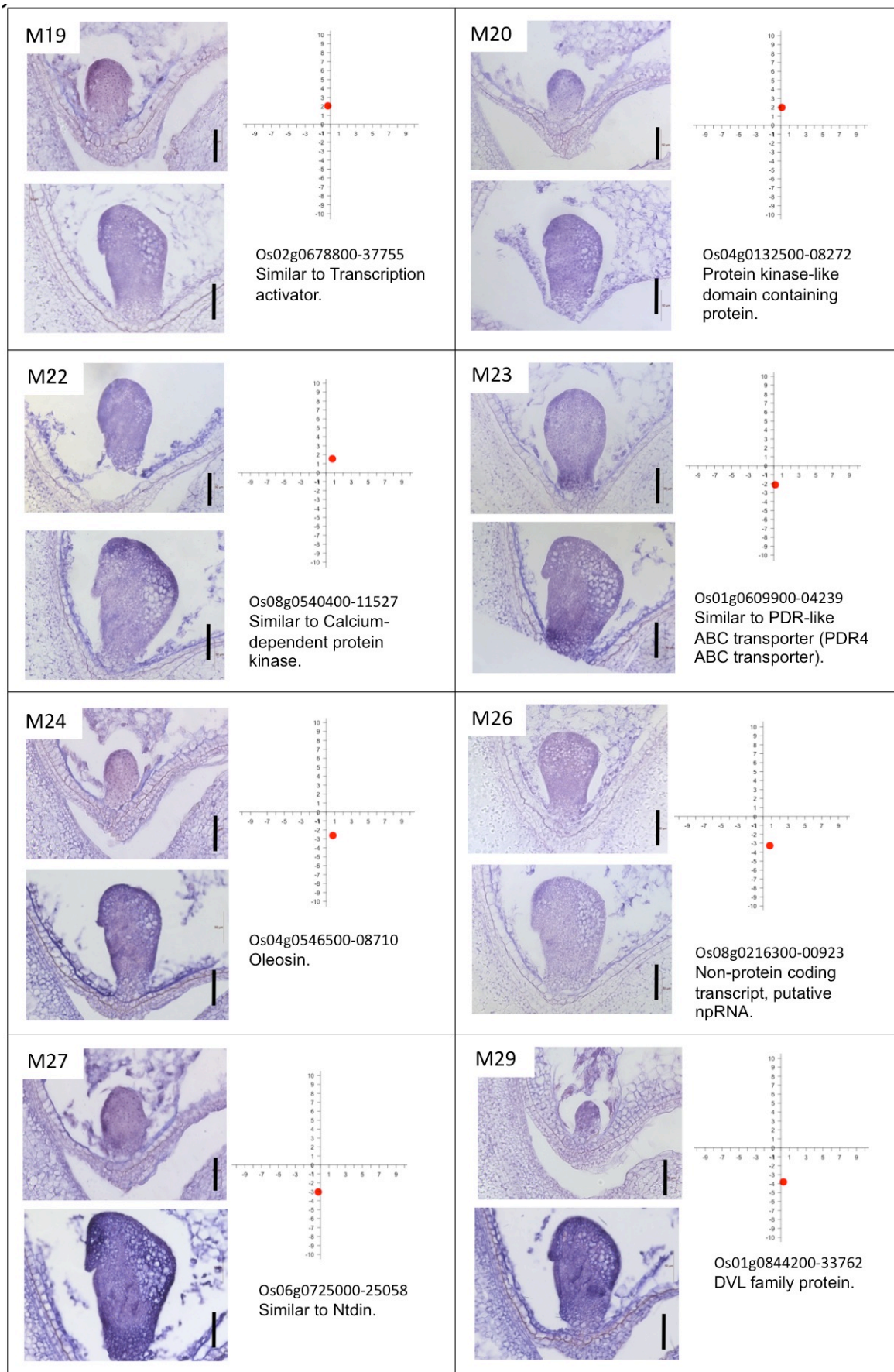


Figure S7. Cont'd.

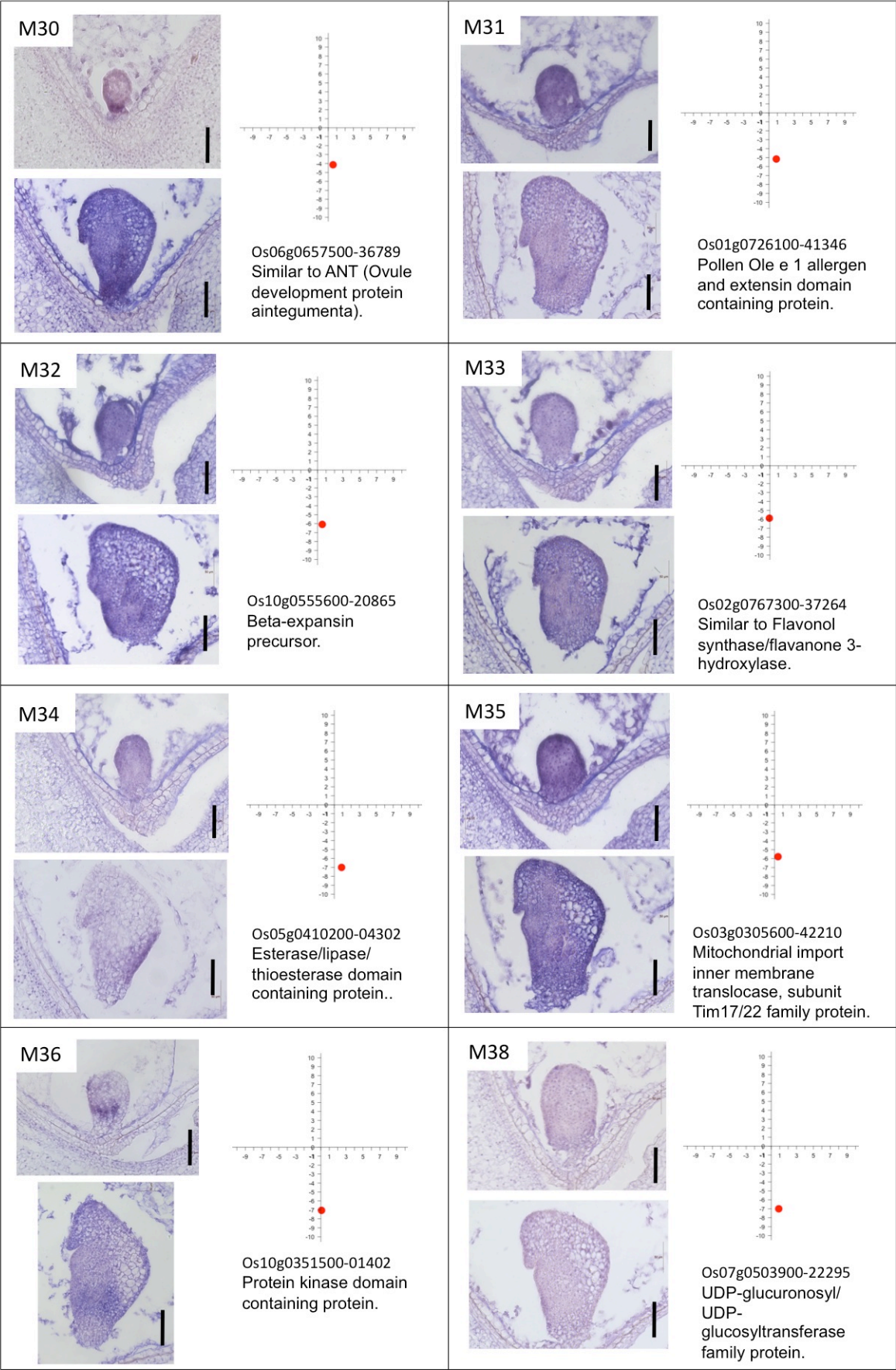


Figure S7. Cont'd.

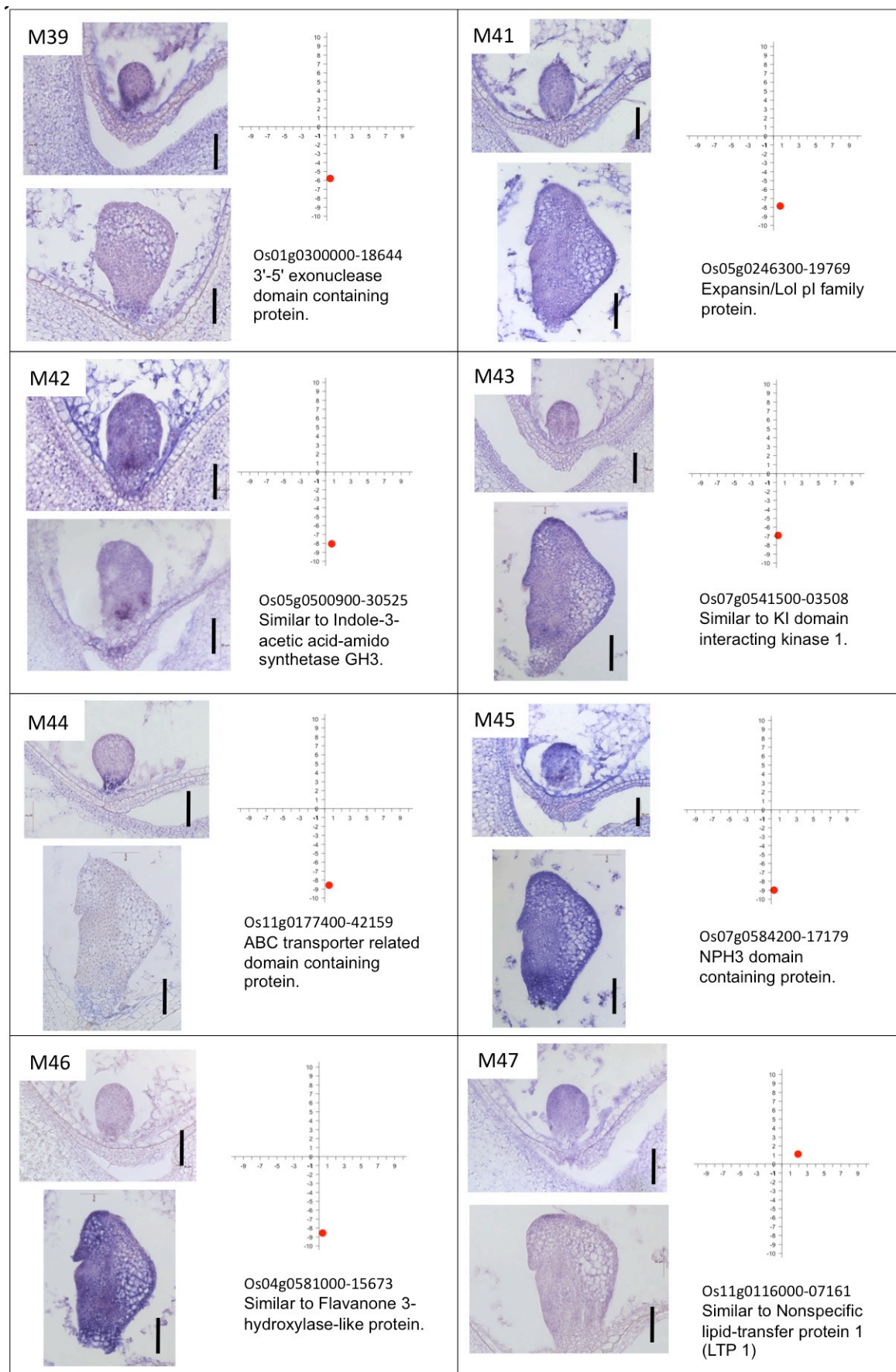


Figure S7. Cont'd.

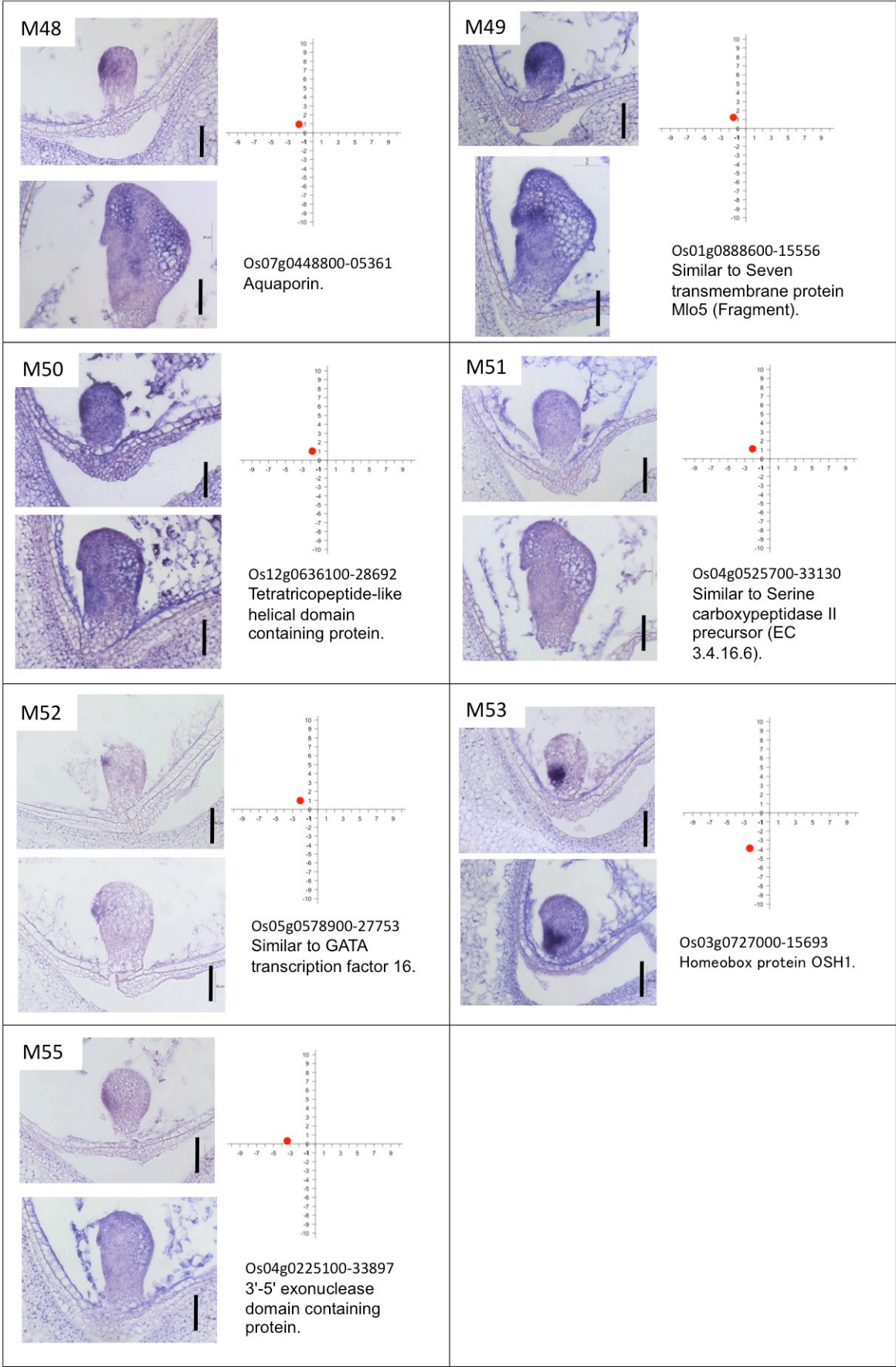


Figure S7. Cont'd.

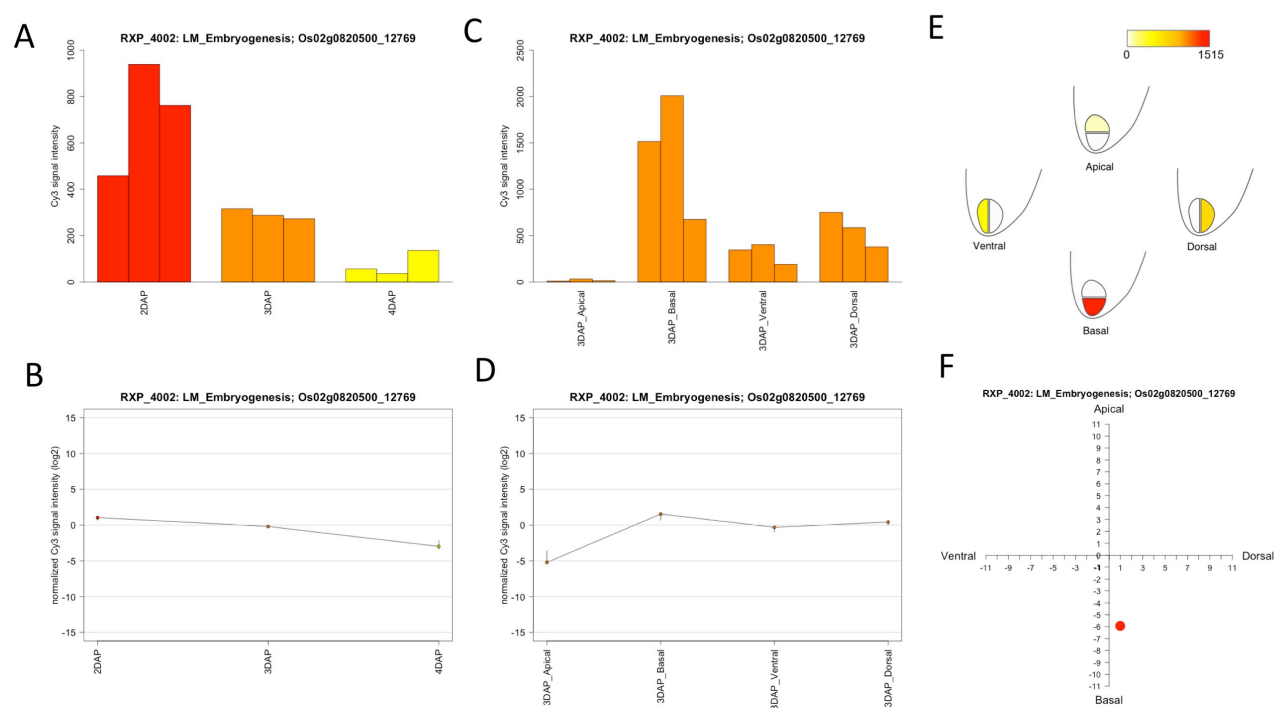


Figure S8. Gene expression profiles during early embryogenesis, as shown in the RiceXPro database. Schematic of the expression pattern of Os02g0820500 in the ‘temporal’ and ‘spatial’ data sets. (A) Raw signal intensity of whole embryos at 2, 3 and 4 DAP. Three replicates are shown. (B) Normalized signal intensity of whole embryos at 2, 3 and 4 DAP. (C) Raw signal intensity of the apical, basal, ventral and dorsal embryonic regions at 3 DAP. (D) Normalized signal intensity of the four embryonic regions at 3 DAP. (E) Pictograph of expression intensity among the four embryonic regions. (F) Scatter diagram of expression sites in 3-DAP embryos.

Table S1. Pearson correlation coefficient among the entire set of normalized data.

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Table S2. The list of the genes that are preferentially expressed in the apical and basal region of 3-DAP embryo.

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Table S3. The list of the genes that are preferentially expressed in the dorsal and ventral region of 3-DAP embryo.

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Table S4. The list of the genes that are preferentially expressed in the apical-dorsal, apical-ventral, basal-dorsal and basal-ventral regions of 3-DAP embryo.

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Table S5. The list of the genes that are categorized by K-means clustering of 3-DAP embryo.

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Table S6. The list of the genes that are preferentially expressed in the apical, basal, dorsal and ventral region in each cluster.

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Table S7. The list of the genes and their expression profiles of phytohormone-related genes in 3-DAP embryo.

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Table S8. The list of the genes and their expression profiles of transcriptional factor and transcriptional regulator genes in 3-DAP embryo.

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Table S9. The list of the genes that are preferentially expressed in the shoot, epiblast, scutellum and root containing tissues of 7-DAP embryos.

[Click here to Download Table S9](#)

Table S10. The list of the selected genes as markers of *in situ* hybridization for early embryogenesis.

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