

Legends for figures in Supplementary Data

Fig. S1. Agilent Bioanalyser scans of aRNA from embryonic tissues. A. Size markers. B. aRNA from apical globular-stage samples. C. aRNA from apical heart-stage samples. D. aRNA from apical torpedo-stage samples.

Fig. S2. Cluster analysis of synexpressed genes during development of the apical domain of the embryo.

A. K-means clustal analysis was performed on the 1872 genes showing statistically significant changes in expression level. The number of clusters was defined as 10, represented as each of the datasets. Genes expressed to levels higher than the median values are indicated in yellow, while genes expressed to lower levels are indicated in green.

B. Diagrammatic representation of 7 identified distinct temporal expression patterns emerging from K-means clustal analysis of an apical developmental series. The % of the 1872 genes represented by each pattern is indicated. Horizontal axis: Developmental stage (g = globular, h = heart, t = torpedo). Vertical axis: Expression level.

Fig. S3. Cluster analysis of synexpressed genes during development of the basal domain of the embryo.

A. K-means clustal analysis was performed on the 1226 genes showing statistically significant changes in expression level. The number of clusters was defined as 10, represented as each of the datasets. Genes expressed to levels higher than the median values are indicated in yellow, while genes expressed to lower levels are indicated in green.

B. Diagrammatic representation of 7 identified distinct temporal expression patterns emerging from K-means clustal analysis of an apical developmental series. The % of the 1226 genes represented by each pattern is indicated. Horizontal axis: Developmental stage (g = globular, h = heart, t = torpedo). Vertical axis: Expression level.

Tables S1-S9: Signal values for all replicate ATH1 GeneChip® data, from globular- stage, heart-stage and torpedo-stage embryo tissues and seedling tissues, showing means and standard deviations of the replicate data, based on the use of 8 probe pairs. S1: Globular-stage apical tissue, S2: globular-stage basal tissue, S3: heart-stage apical tissue, S4: heart-stage basal tissue, S5: torpedo-stage SAM, S6: torpedo-stage cotyledonary tissue, S7: torpedo-stage basal tissue, S8: seedling apical tissue, S9: seedling basal tissue.

Table S10. Estimate of the number of genes expressed based on a signal value cut-off, based on the use of 8 probe pairs. An estimated number of expressed genes for cut-off values of 40 and 75 was calculated for the ATH1 GeneChip® data for torpedo stage embryonic tissue. The replicates for each tissue type (torpedo SAM, cotyledon and root) were collated and a mean signal value across the replicates calculated. The mean

signal values were ranked highest to lowest thus revealing the number of genes with an equal or greater value than the designated cut-offs.

Table S11. Differential expression of genes in the apical and basal region of the globular-stage embryo (1). All genes showing significant up-regulation in apical vs. basal domains, with a p value at or less than 0.05.

Table S12. Differential expression of genes in the apical and basal region of the globular-stage embryo (2). All genes showing significant up-regulation in basal vs. apical domains, with a p value at or less than 0.05.

Table S13. Differential expression of genes in the apical (cotyledon) region compared to the basal (root) region in the heart-stage embryo (1). All genes showing significant up-regulation in apical vs. basal domains, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S14. Differential expression of genes in the apical and basal region of the heart-stage embryo (2). All genes showing significant up-regulation in basal vs. apical domains, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Tables S15. Differential gene expression in the cotyledon region compared to the root region in the torpedo stage embryo (1). All genes showing significant up-regulation in apical vs. basal domains, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S16. Differential gene expression in the cotyledon region compared to the root region in the torpedo stage embryo (2). All genes showing significant up-regulation in basal vs. apical domains, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S17. Differential gene expression in the shoot apical meristem of the torpedo-stage embryo compared to the apical region of the globular-stage embryo (1). All genes showing significant up-regulation in torpedo-stage vs. globular-stage apical domains, with a p value at or less than 0.05. Normalized

values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S18. Differential gene expression in the shoot apical meristem of the torpedo-stage embryo compared to the apical region of the globular-stage embryo (2). All genes showing significant up-regulation in globular-stage vs. torpedo-stage apical domains, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S19. Differential gene expression in the 7 dpg seedling (1). All genes showing significant up-regulation in the cotyledon compared to the root, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S20. Differential gene expression in the 7 dpg seedling (2). All genes showing significant up-regulation in the root compared to the cotyledon, with a p value at or less than 0.05. Normalized values (column B) show the fold-change between samples. Standard deviations of the means of three samples (normalized and raw data) are given.

Table S21. *EMB* genes determined to show spatial differential expression during the torpedo-stage of embryogenesis.

Genes selected from expressed *EMB* genes (mean signal value >40) that show at least a fourfold difference in expression between embryo zones, filtered for outlier and inconsistent signal values. Cot = cotyledonary tissue, Meri = shoot apical meristem, Root = root tissue