

SUPPLEMENTAL FIGURE LEGENDS:

Supplemental Figure S1. Gene Ontology (GO) term enrichment status for the putative rice stigma-specific genes. The graph displayed term enrichment levels along with the GO term hierarchy within the "biological process" branch, and the analysis was performed using EasyGO. The classification terms and their serial numbers are represented as rectangles. The numbers in brackets represent the total number of genes that may be involved in the corresponding biological processes. The graph displays the classification term enrichment status and term hierarchy. The color scale shows the *p*-value cutoff levels for each biological process. The deeper colors represent the more significant biological processes in the putative stigma pathway.

Supplemental Figure S2. Hierarchical clustering of the stigma-preferential genes from the three clusters with the eight tested organs or tissues and suspension culture cells. A, Cluster I. B, Cluster II. C, Cluster III. The genes in the three clusters were preferentially and/or highly expressed in stigma and the correlation coefficients of the three clusters were 0.9277, 0.9389 and 0.8263, respectively. 1: Unpollinated stigmas at anthesis. 2: Mature anthers. 3: Seedling shoots. 4: Seedling roots. 5: Seeds of 5 days after pollination. 6: Endosperms derived from 10-day-old seed. 7: Ovaries at anthesis. 8: Embryos derived from 10-day-old seed. 9: Suspension culture cells. The color scale shows the gene signal intensities in 57K Affymetrix rice GeneChip.