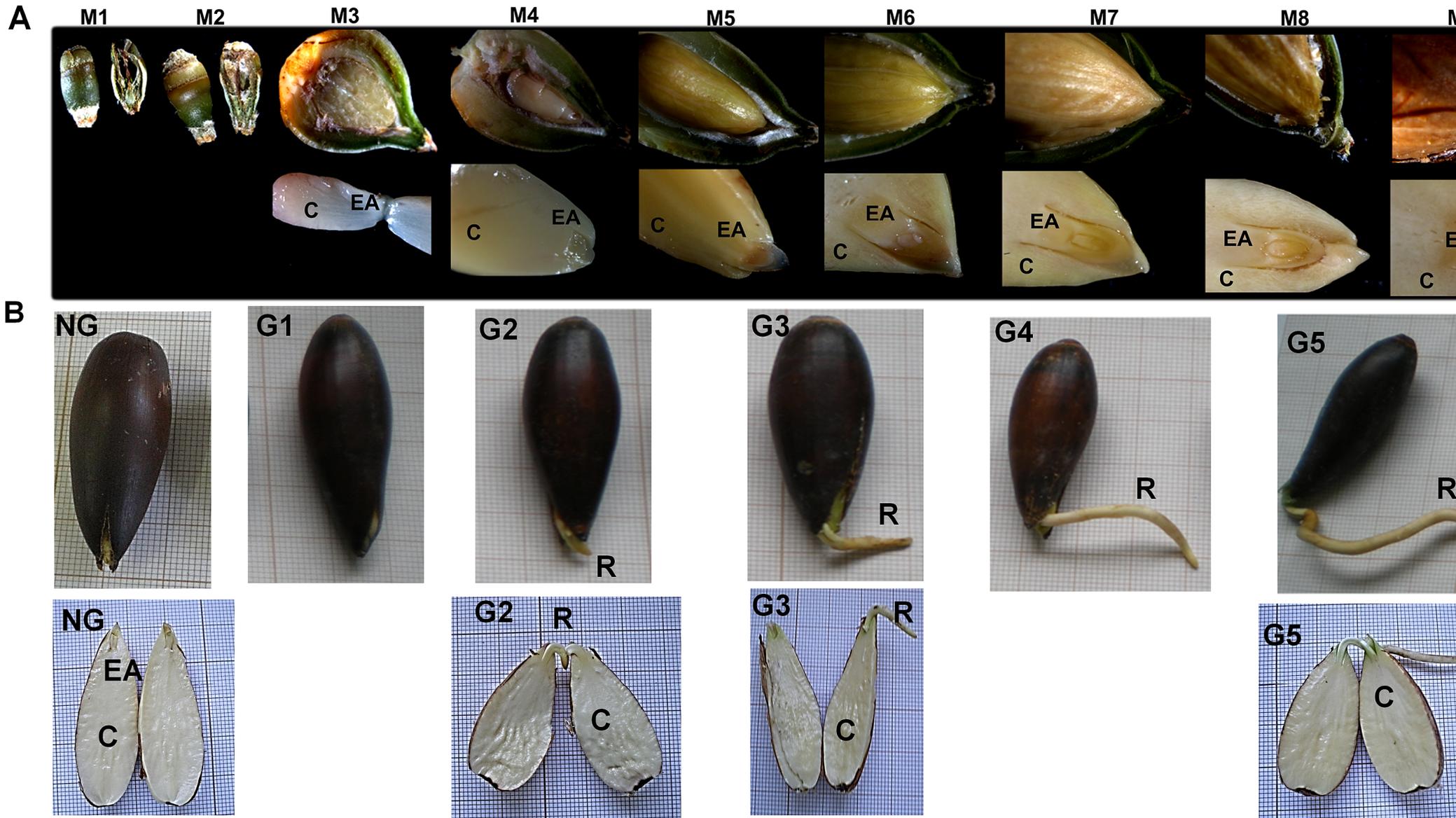


Figure S1. Photos of the Holm oak acorns at the different collected stages, from M1 to M9. The date of fruit collection is indicated. M9 corresponds to the mature acorns

Developmental stages

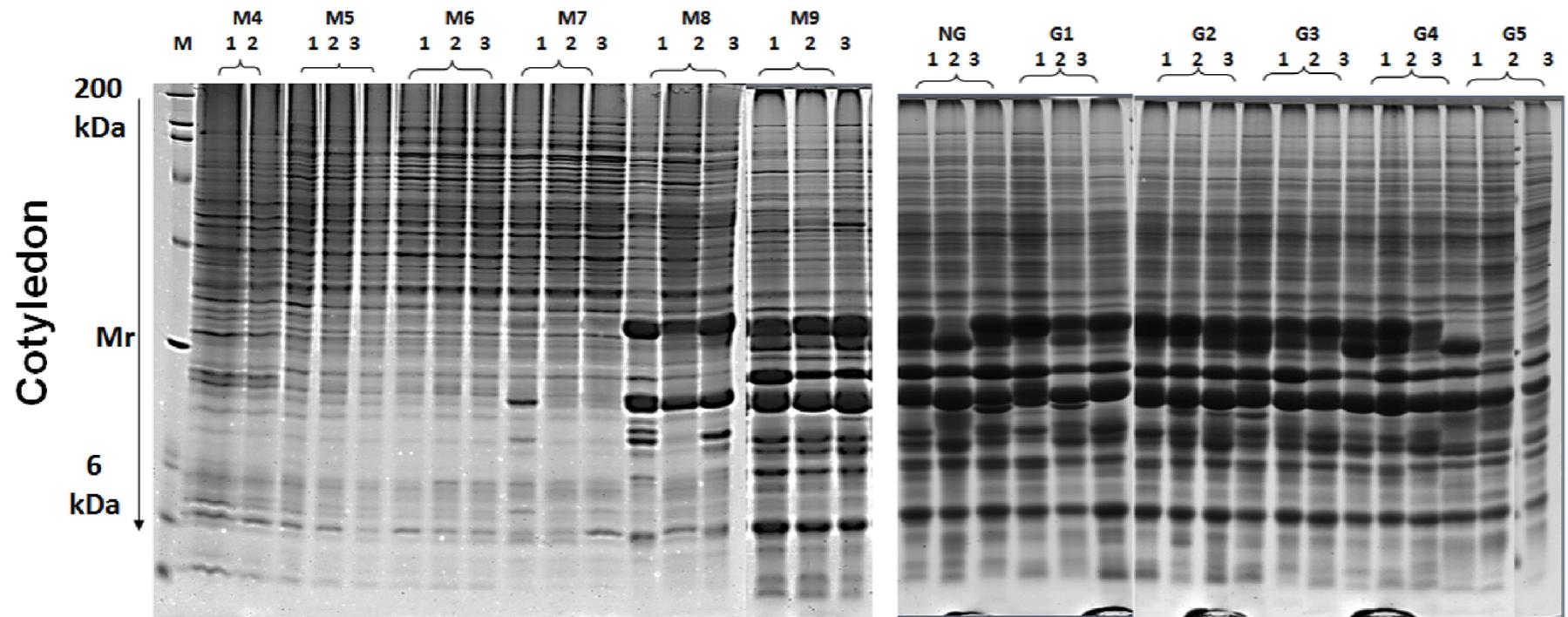


Figure S2. Photos of the Holm oak seeds during the different developmental stages (maturation and germination). A; maturation stages of the entire acorn from stage M1 to M9, with the median longitudinal section of the acorn showing the position of the cotyledon surrounded by the pericarp and localizing the embryonic axis (EA) inside the cotyledon (C). B; photo of non-germinating (NG) and germinating acorns of Holm oak during different stages (from G1 to G5), showing the emersion of the radicle (R). EA, embryo axis, C; cotyledon, NG; non-germinating and R; radicle



Maturation

Germination



Maturation

Germination

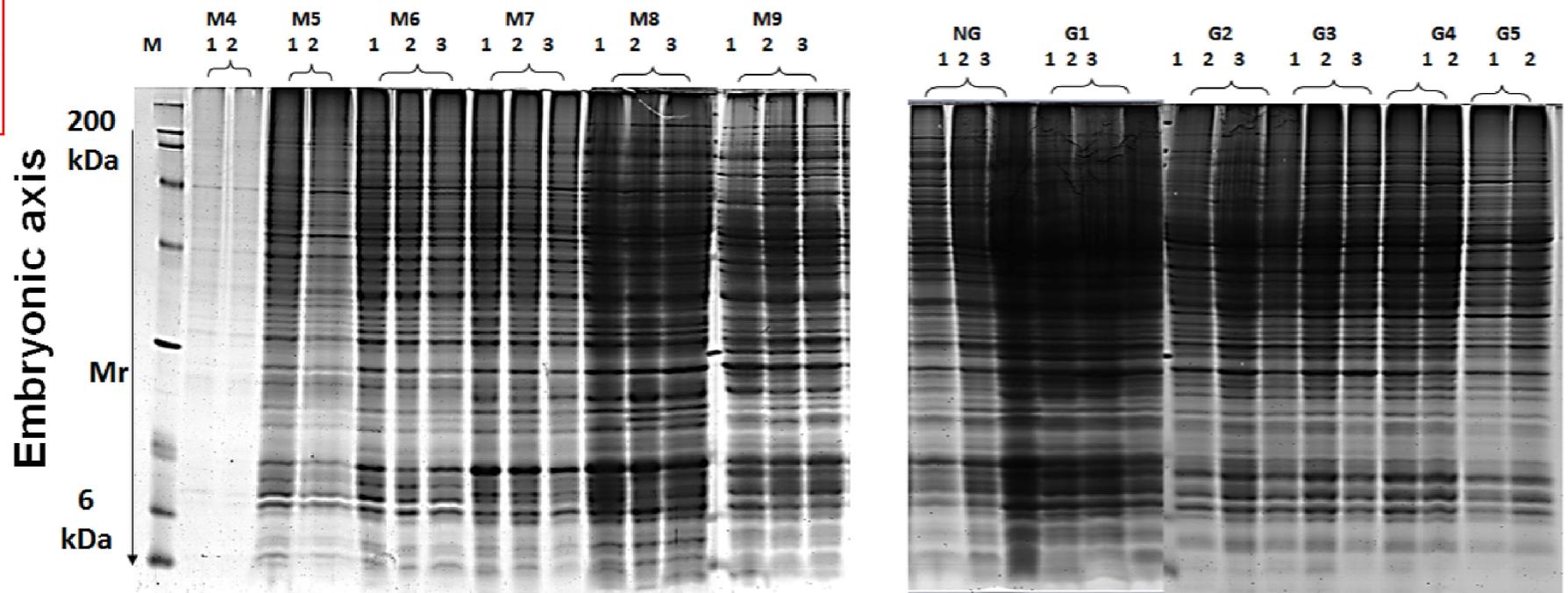


Figure S3. Protein profiles, as visualized by 1-D gel electrophoresis. Top images correspond to cotyledon and bottom ones to embryo. On the left maturation (M4-M9), and on the right germination (G1-G5). Lines correspond to the different stages and replicates.

Figure S4. Representative 2-DE gel images of embryonic axis and cotyledon during different maturation (M6-M9) and germination (G3 and G5) stages, including non-germinating acorns (NG). Molecular marker (*Mr*) was given on the left and *pI* on top.

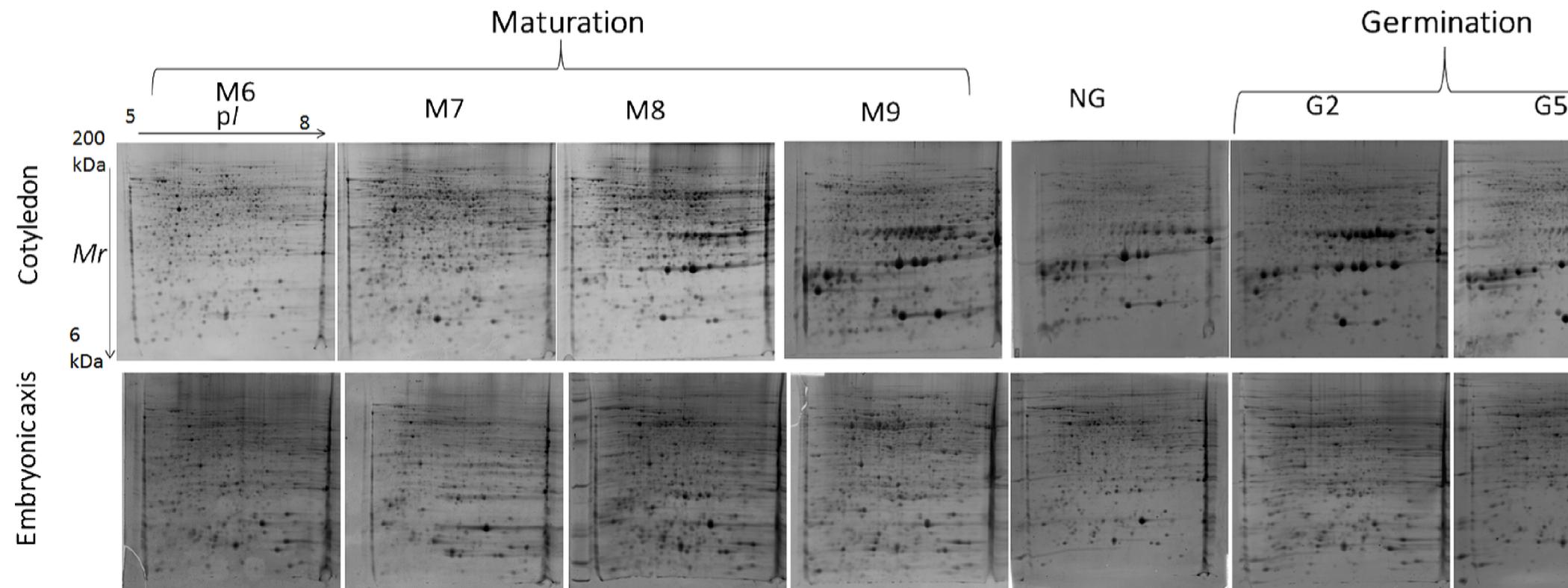
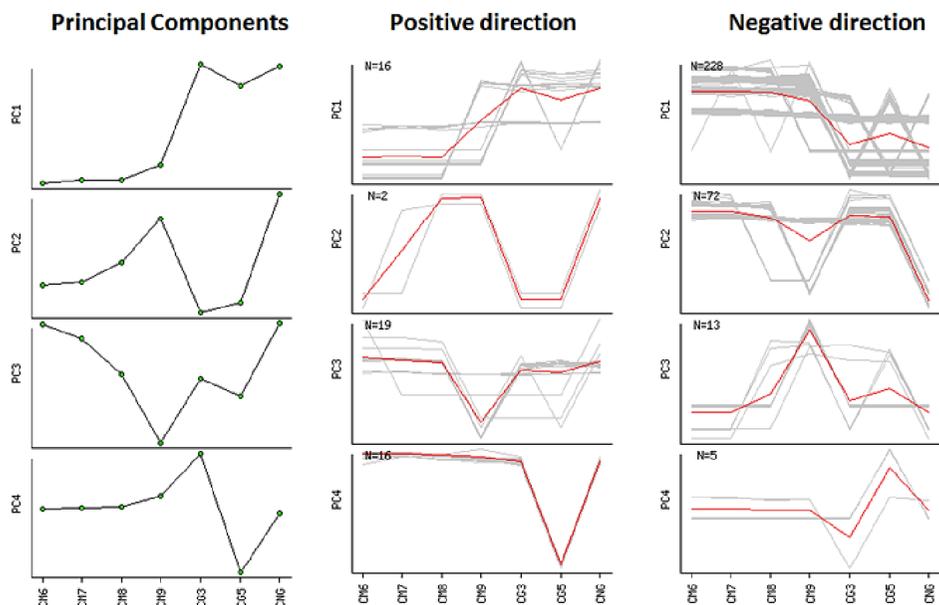
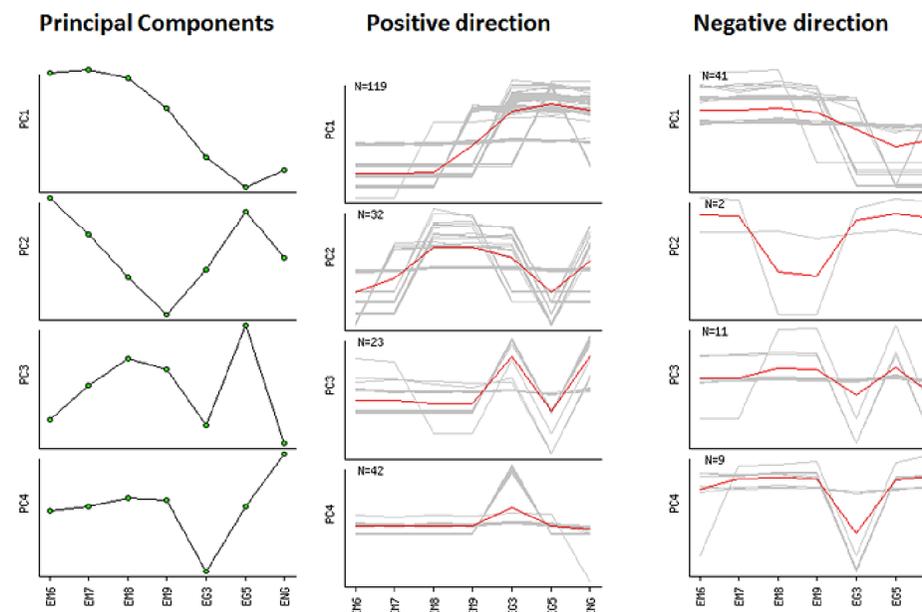


Figure S5. Tendencies in protein spots evolution along the maturation and germination stages, as determined by PCA analysis. (A) Cotyledons; (B) Embryo; (C) Maturation; (D) Germination

A

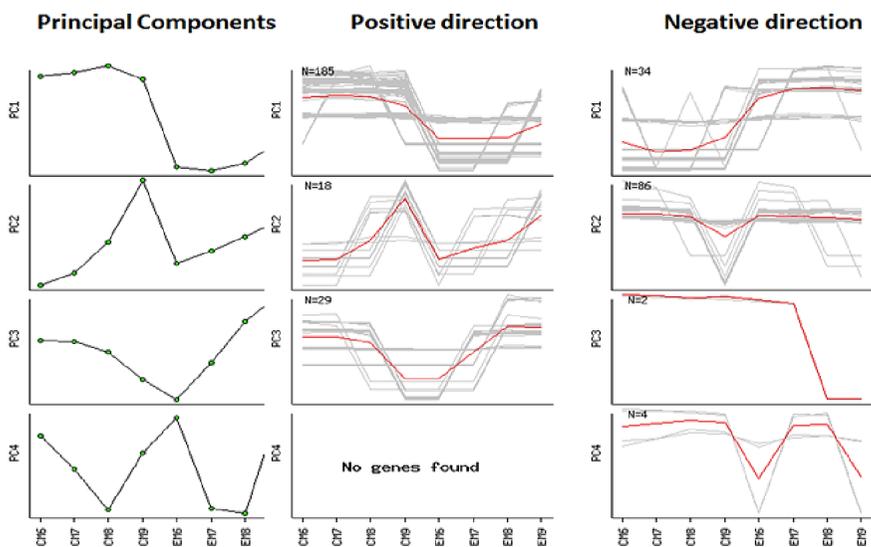


B



C

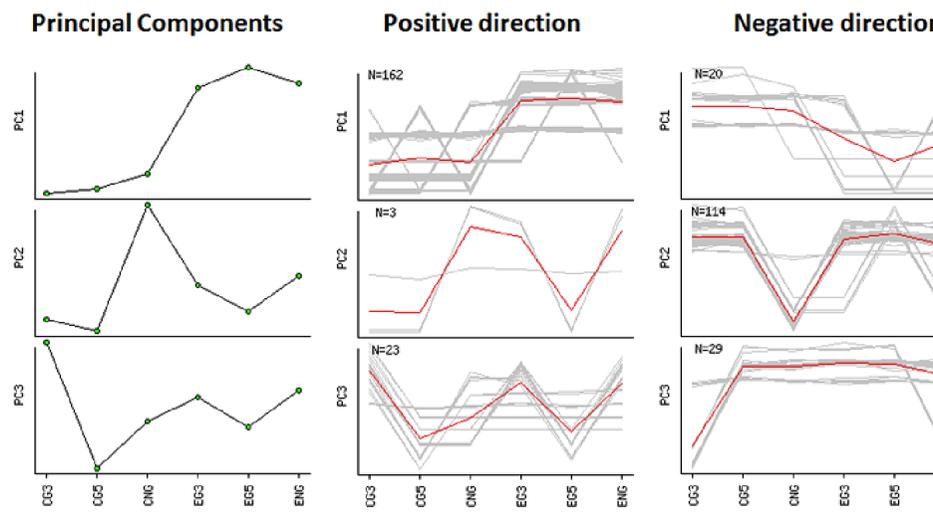
Gray lines = centered gene intensity, Red line = average



Gray lines = centered gene intensity, Red line = average

D

Gray lines = centered gene intensity, Red line = average



Gray lines = centered gene intensity, Red line = average

Figure S6. Dendrogram showing hierarchical clustering of different samples of cotyledon and embryonic during maturation (M6-M9) and germination (G3 and G5). The replicates (three) for each sample were numbered 1, 2 and 3. A short distance between samples and protein spots in the component space is indicative of similarity in expression profiles. Statistical protein expression cluster analysis of embryonic axis and cotyledon using the ANOVA-based NIA array analysis tool, p-value ≤ 0.05 (Sharov, Dudekula, & Ko, 2005).

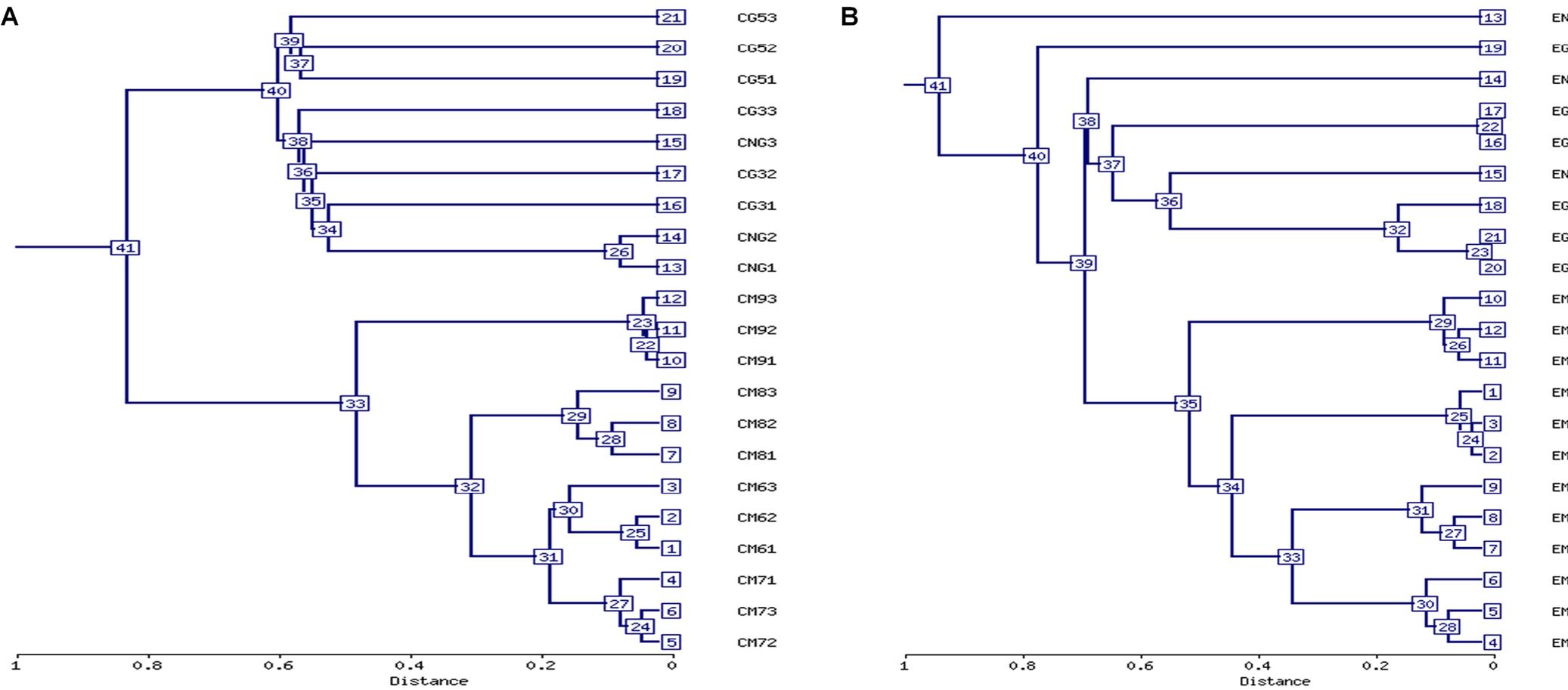


Figure S7. Photography of the acorns seeds placed on humid perlite (50 seeds/replicate, three replicates) in a plant growth chamber under 12/12 h photoperiod (25/20 °C) for germination.

