SUPPLEMENTARY DATA

Methods

Alignment of Mob1A and Mob1B protein sequences

Amino acid sequences were aligned by Clustal W method (Gonnet protein weight matrix, gap penalty = 10, gap length penalty = 0.2, delay divergent seqs = 30%) using the MegAlign software (DNASTAR).

In silico analyses of gene expression

Co-regulated genes to Mob1A were identified using the Co-expression tool from Genevestigator V3 (Hruz *et al.*, 2008) for perturbation and anatomy data sets. Enriched GO terms were found using VirtualPlant 1.3 (http://virtualplant.bio.nyu.edu/cgi-bin/vpweb/) applying BioMaps function with a 0.05 p-value cutoff (Katari *et al.*, 2010).

Reference

Katari MS, Nowicki SD, Aceituno FF, *et al*. 2010. VirtualPlant: a software platform to support systems biology research. *Plant Physiol* **152**: 500-515.