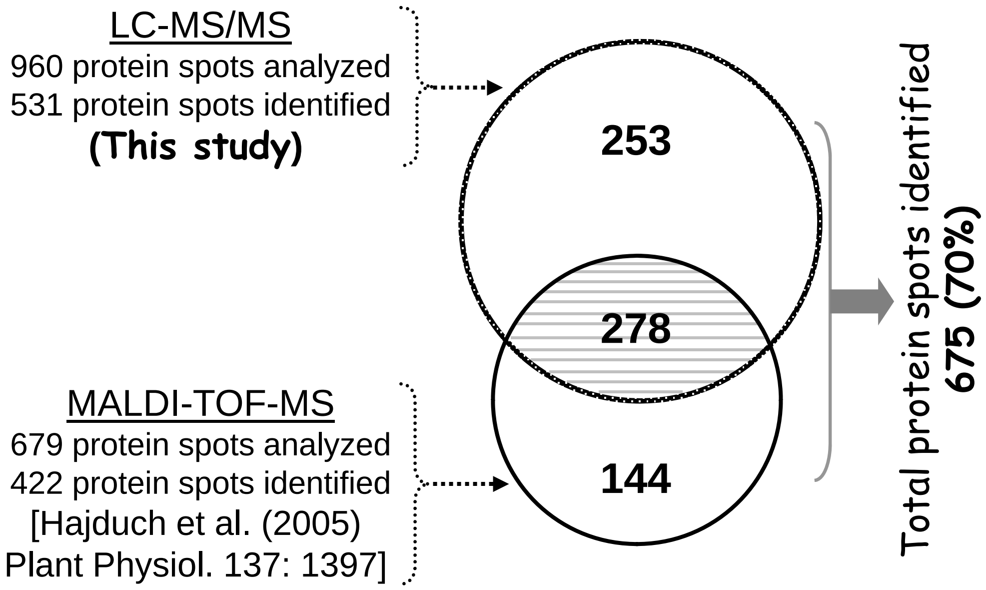

Figure S4. 2-DGE proteomics approach has unambiguously identified and mapped 675 protein spots on two high-resolution 2-D reference maps. The 2-DGE proteomics approach in combination with nESI-LC-MS/MS (this study) and MALDI-TOF-MS (Hajduch et al., 2005) led to an unambiguous identification of 675 protein spots out of 960 protein spots detected by ImageMaster software representing an identification efficiency of 70%. This study and Hajduch et al. (2005) identified 531 and 422 protein spots, respectively; 278 protein spots were common in these studies.

Supplementary Figure S4
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