Supporting Data

Supplemental Table I - Individual expression data for the 409 retained protein spots. The table includes the Id which is the spot number on the 2D reference map (Méchin et al., 2004) and the normalized volume for each spot at each developmental stage in the three replicates corresponding to the three independent protein extracts

Supplemental Table II - The 302 identified protein spots with their allocation to functional categories and cluster membership. Protein Id is the spot number on the 2D reference map (Méchin et al., 2004), protein similarity gives the characteristics of the protein matching the spot in the databases (with the NCBI gi identifier), function category follows Schoof et al. (2002) definition, function description provides details about the function, cluster assignation of the spot (1: "Early accumulation" cluster, 2: "Midstage accumulation" cluster, 3: "Mid-late accumulation" cluster, 4 : "Late accumulation" cluster, and X: not included in the clusters).

Supplemental Table III - Proteins presented on figure 7 with their subcellular localization prediction. Protein Id is the spot number on the 2D reference map (Méchin et al., 2004), protein similarity gives the characteristics of the protein matching the spot in the databases (with the NCBI gi identifier), function category follows Schoof et al. (2002) definition, function description provides details about the function, localization prediction was incorporated in this table if at least three programs predicted the same subcellular destination , and protein number on figure 7 is the number attributed to the considered protein in figure 7.

Supplemental Table IV - Summary of all proteins processed in the reference 2D map, with allocation to functional categories. Protein Id is the spot number on our 2D reference map (Méchin et al., 2004), supplementary identifications: a re-interrogation of databases allowed 14 supplementary identifications compared to identification accessible in Méchin et al. (2004), protein similarity gives the characteristics of the protein matching the spot in the databases (with the NCBI gi identifier), function category follows Schoof et al (2002) definition, function description provides details about the function when possible, pI is the isoelectric point, Mr the apparent molecular mass and peptides identified with the number of times they are found (indicated in parenthesis) are listed. NI: non identified protein spot, NYC: function not yet clear cut.

Supplemental Figure - The 2D reference map. The 2D reference map presented in Méchin et al. (2004) with a specific focus on the 302 functionally identified protein spots included in the analysis. Each of the 302 protein spots is pointed out by its Id on the 2D map.