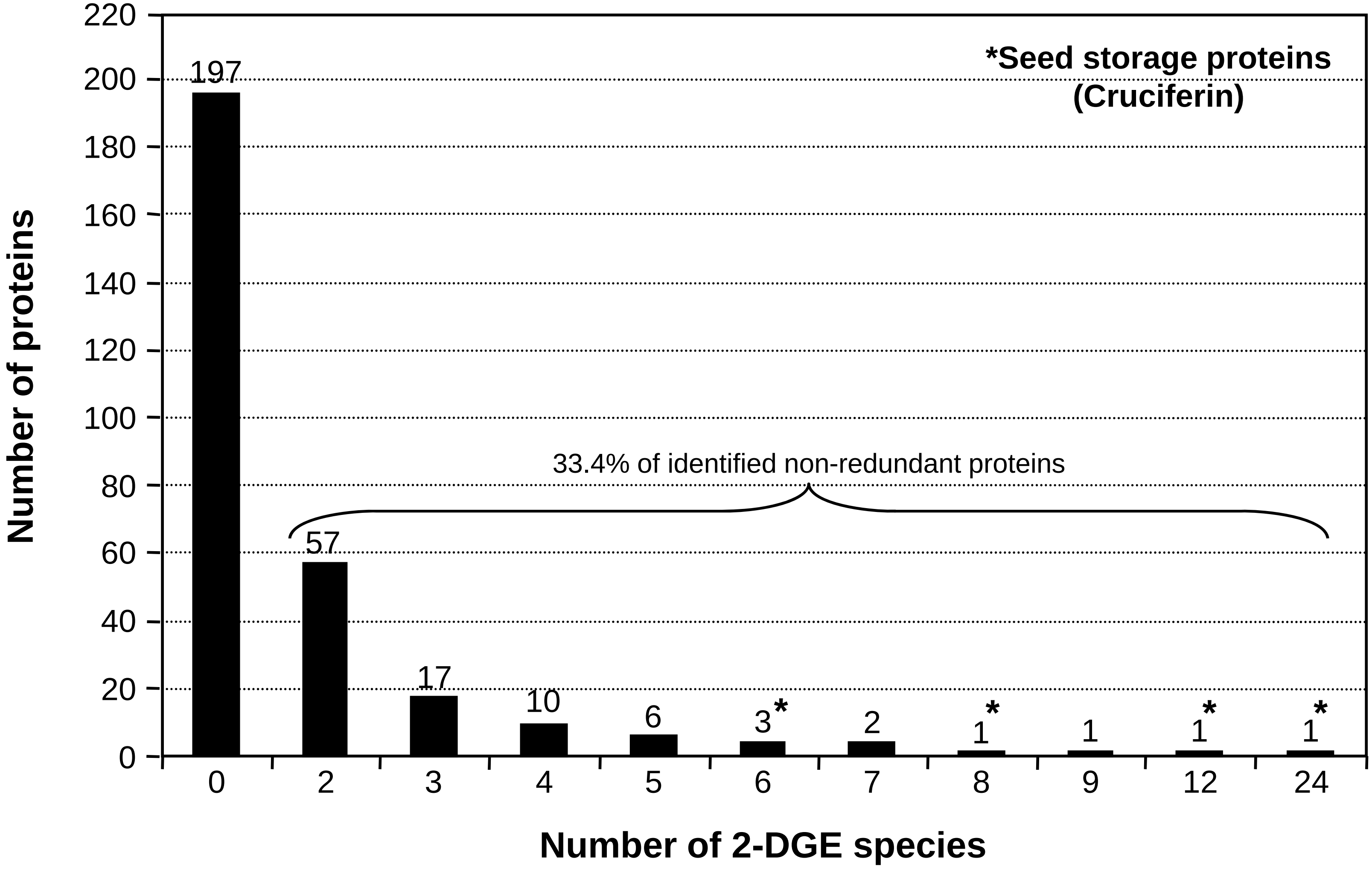

Figure S2. Distribution of 2-DGES in the seed-filling proteome of rapeseed. This analysis was conducted using the data previously published by Hajduch et al. (2006). In that data, differentially expressed proteins were identified by a combination of 2-DGE and mass spectrometry (MALDI-TOF-MS and nESI-LC-MS/MS) during seed filling in rapeseed (*Brassica napus* cv. Reston).

Supplementary Figure S2
Agrawal et al.