

Figure S1: Relationship between the mean of protein amount and standard deviation of spots before (a) and after (b) transformation of normalized spot values.

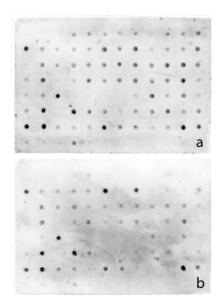


Figure S2: Representative dot blot hybridization of array 2 employing immature (a) or mature (b) testers obtained from total RNA, which shows differential expression of tested probes.

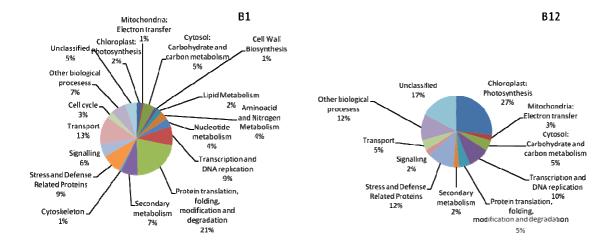


Figure S3: Classification of the non redundant genes present in immature (B1) and mature (B12) needles subtractive libraries; the ontology classification was determined for biological process/metabolic pathway according to KEGG. Relative proportions of each ontology terms are expressed.

Figure S4: Single-peptide spectra corresponding to de identification of spot 0109.

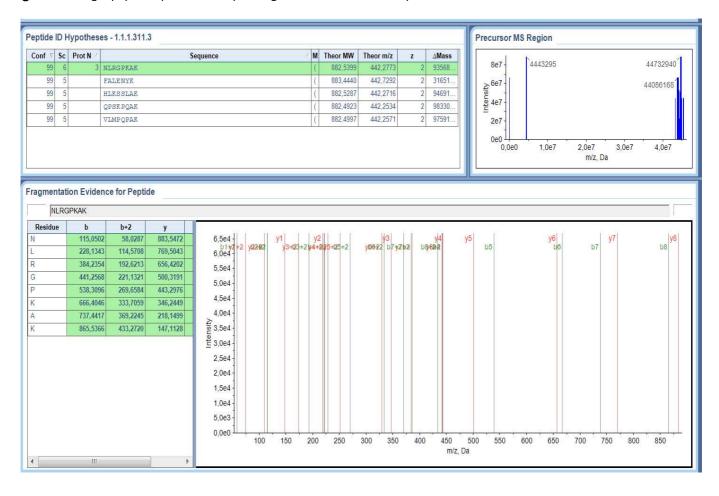


Figure S5: Single-peptide spectra corresponding to de identification of spot 2006.

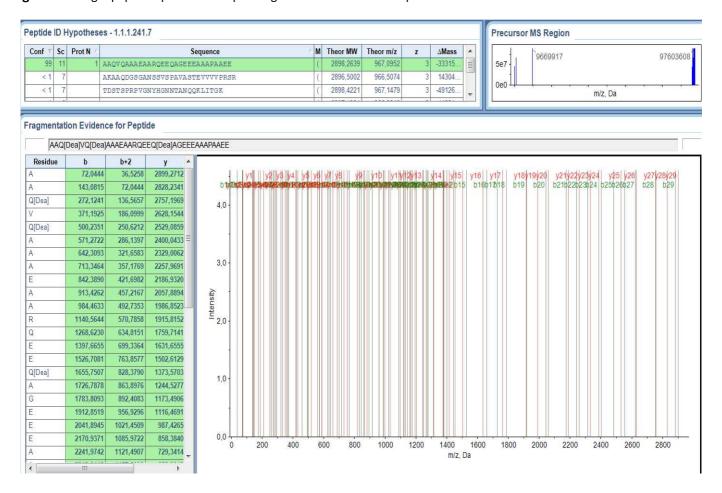


Figure S6: Single-peptide spectra corresponding to de identification of spot 2007.

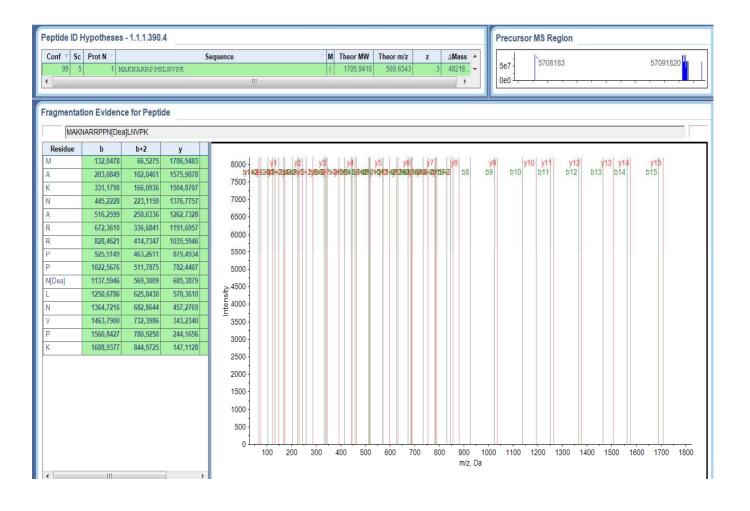


Figure S7: Single-peptide spectra corresponding to de identification of spot 3611.

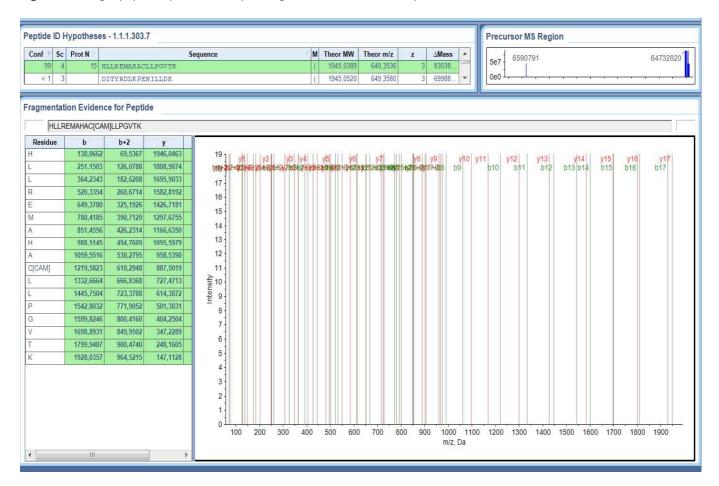


Figure S8: Single-peptide spectra corresponding to de identification of spot 5404.

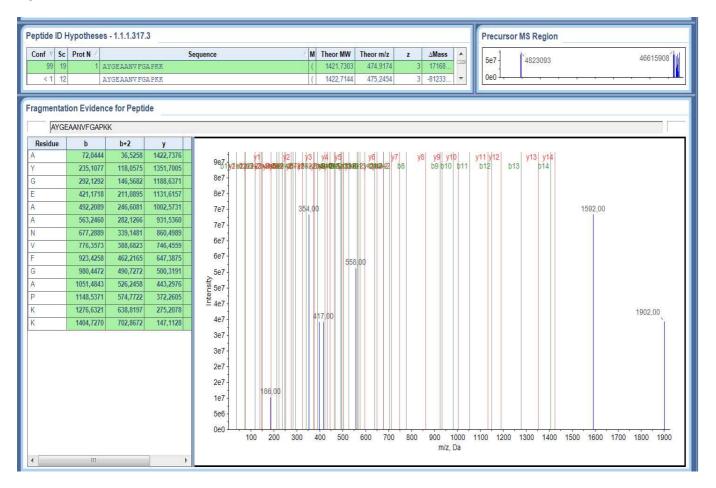


Figure S9: Single-peptide spectra corresponding to de identification of spot 6001.

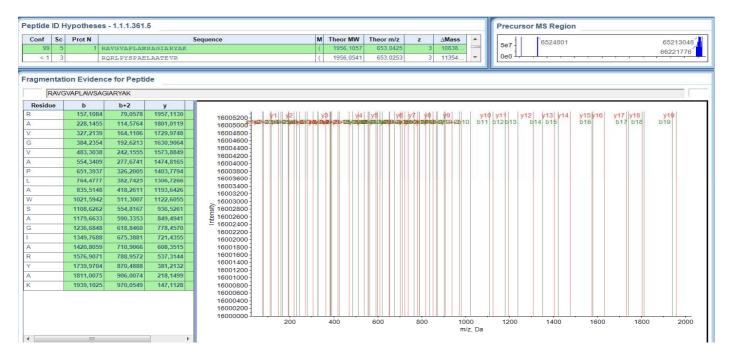


Figure S10: Single-peptide spectra corresponding to de identification of spot 6307.

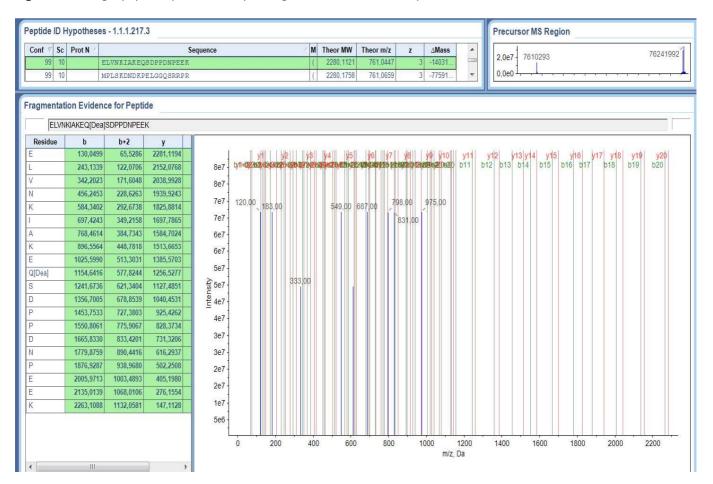


Figure S11: Single-peptide spectra corresponding to de identification of spot 6804.

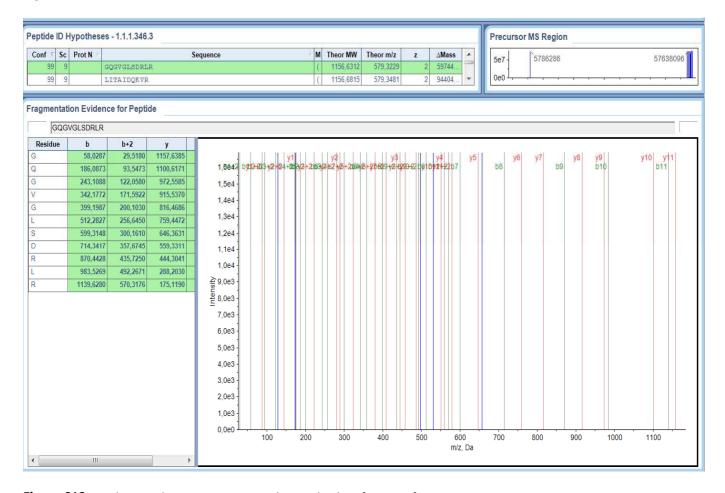


Figure S12: Single-peptide spectra corresponding to de identification of spot 8803.

