Supplementary table

Table S1. List of the identified proteins by LC-ESI-MS/MS and bioinformatics analyses. The table shows the sequence of all the peptides identified by MS/MS fragmentation and the associated statistical information obtained from database searches conducted by BioworksBrowser using TurboSEQUEST® software. For each identified protein, statistical information related to alignment analysis of identified peptides by FASTS software is reported. **Spot ID**: spot identifier number. **Protein A.N.**: protein NCBI accession number (version). **DB**: database used for the search; NR= protein non-redundant database downloaded from NCBI (*5947209 entries*); EST= subset of *Lolium* EST sequences downloaded from NCBI (*13919 entries*). The searches against the two corresponding sequence-reversed databases didn't identify any positive hit. **n. pep**.: number of the peptides used to identify the protein, computed counting peptides with the same primary sequence, even if they present different modification or charge states, as one. **a.a. cov. (%)**: sequence coverage %. **FASTS (*E*) value**: FASTS expectation (*E*) values of the entry resulting from the alignment of peptides against NR. **Hom. Protein A.N**.: homologous protein accession number (version)**. EST A.N.**: EST NCBI accession number (version). **Peptide**: sequence of the identified peptides; the symbol M* indicates oxidized methionine. **MH+**: molecular mass of the peptide; **z**: charge state of the peptide**. Sf:** SEQUEST Sf score. **Xcorr**: SEQUEST cross-correlation value. **ΔCn**: delta correlation value. **Sp**: SEQUEST preliminary score. **(a)**: value referred to the mature form of the protein.