

Table1: Identification of spots using MALDI-TOF or LC-MSMS. Difference in spot expression between genotypes in EW were annotated + (-) when fold change of normalised volume was >1.80 (<1.80) respectively. (-): spot absent and present (+) (supplemental data 1)

Spot number	Database	Taxonomy	Name of protein	Mass spectrometry method	Theoretical pI/MW(Da)	Experimental pI/MW (kDa)	DV92 2006	DV92 2007
Metabolism								
Carbohydrate metabolism								
1264	UniP_Viridiplantae	Triticum aestivum	Aldose reductase	MALDI-TOF	6,51/35784	7,08/53037	+	-
Metabolism of other amino acid								
2605	UniP_Viridiplantae	Oryza sativa	Glyoxalase family protein	LC-MSMS	5,00/36001	5,97/16094	-	+
Carbohydrate metabolism								
Storage protein								
2184	TaESTpartCDS	Triticum aestivum	Globulin 3C	MALDI-TOF	8,96/38272	6,30/22000	-	+
2249	UniP_Viridiplantae	Triticum aestivum	Globulin 3	MALDI-TOF	7,78/66652	4,77/20879	-	+
2313	TaESTpartCDS	Triticum aestivum	Globulin 3	MALDI-TOF	7,78/66652	5,50/20352	-	+
2369	TaESTpartCDS	Triticum aestivum	Globulin 3B	MALDI-TOF	7,36/56931	6,11/19266	-	+
2370	UniP_Viridiplantae	Triticum aestivum	Globulin 3	LC-MSMS	7,78/66652	6,19/19266	-	+
3387	UniP_Viridiplantae	Triticum aestivum	Globulin 3	MALDI-TOF	7,78/66652	6,41/19673	-	+
3390	UniP_Viridiplantae	Triticum aestivum	Globulin 3	MALDI-TOF	7,78/66652	5,20/21000	-	+
Stress/defense								
1717	UniP_Viridiplantae	Triticum aestivum	1-Cys-peroxiredoxine	MALDI-TOF	6,08/23965	6,06/37447	-	+