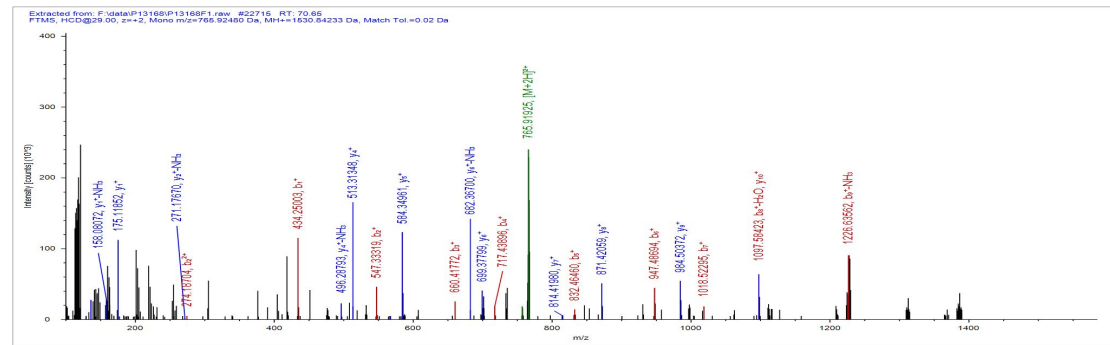


**Supplemental Figure S2** Annotated tandem mass spectra of the identified proteins based on a single high-confidence peptide assignment with 95% confidence of false discovery rate (FDR)  $\leq 1\%$  in roots of Hg-stressed wheat seedlings

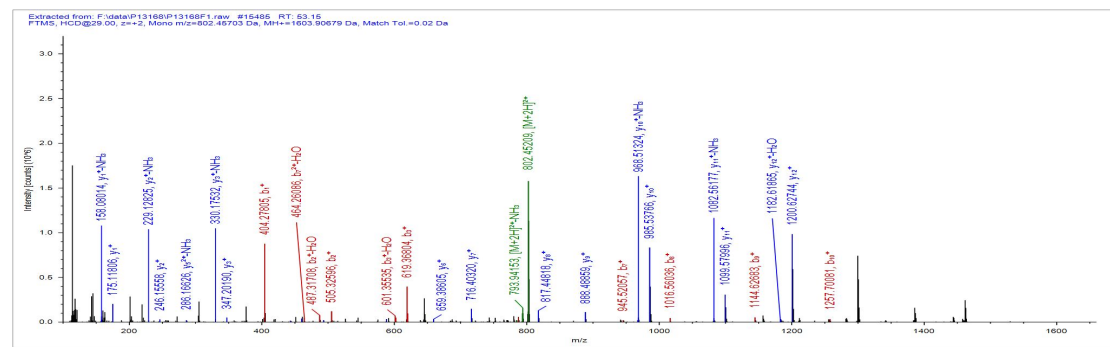
(1) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 765.92 with score 1.88

Protein description: Putative ADP-ribosylation factor GTPase-activating protein AGD14 OS=Triticum urartu GN=TRIUR3\_19703 PE=4 SV=1- [M8AIZ9\_TRIUA]



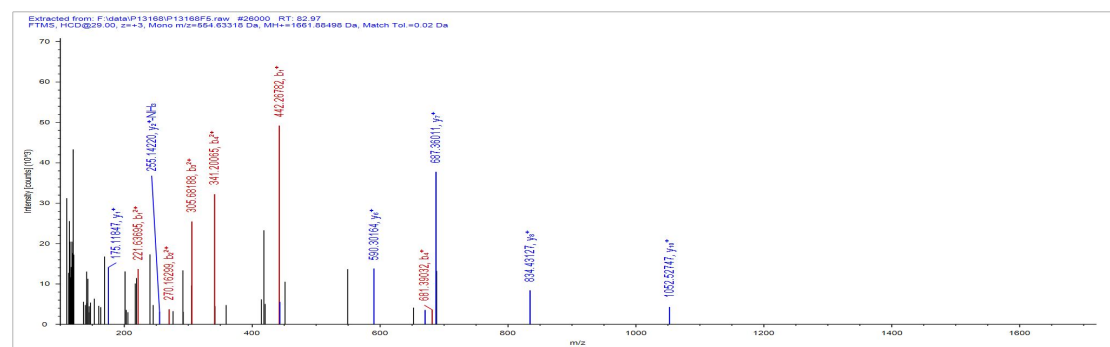
(2) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 802.45 with score 1.48

Protein description: PR-4 (Fragment) OS=Triticum aestivum PE=2 SV=1- [Q9SQG3\_WHEAT]



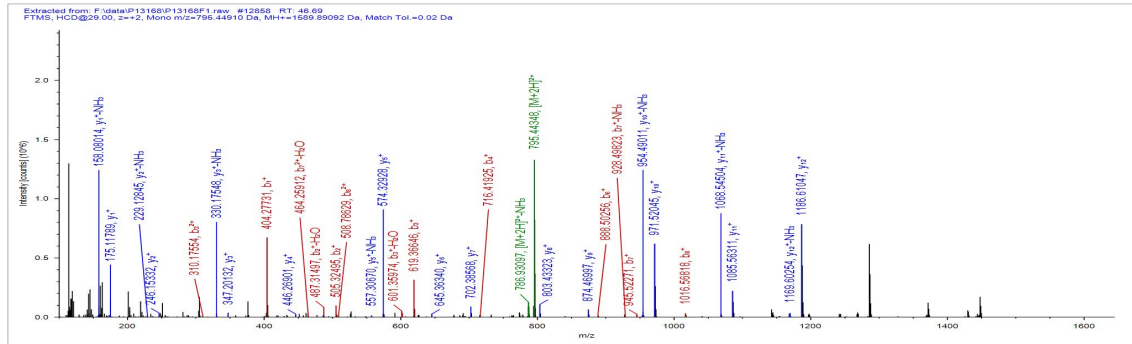
(3) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 554.63 with score 27.85

Protein description: Secologanin synthase OS=Triticum urartu GN=TRIUR3\_25996 PE=4 SV=1- [M8A608\_TRIUA]



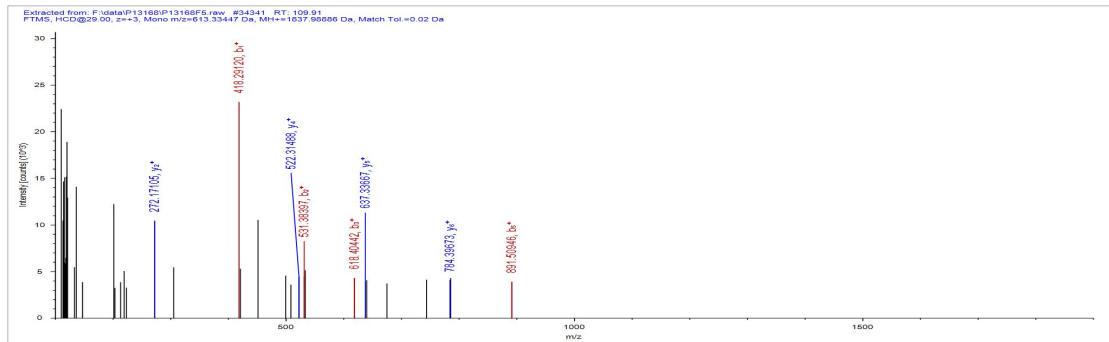
(4) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 795.45 with score 40.42

Protein description: Pathogenesis-related protein 4 (Fragment) OS=Triticum aestivum GN=PR4 PE=2 SV=1- [Q9SQG8\_WHEAT]



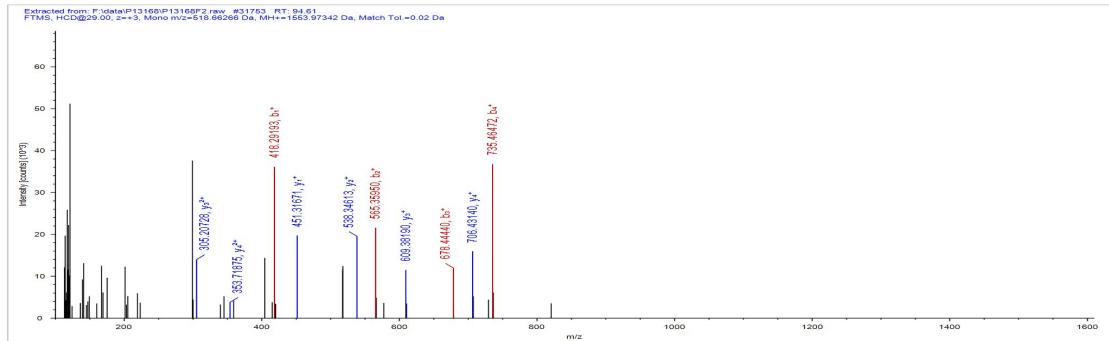
(5) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 613.33 with score 20.59

Protein description: Disease resistance RPP8-like protein 3 OS=Aegilops tauschii GN=F775\_08835 PE=4 SV=1-[M8B613\_AEGTA]



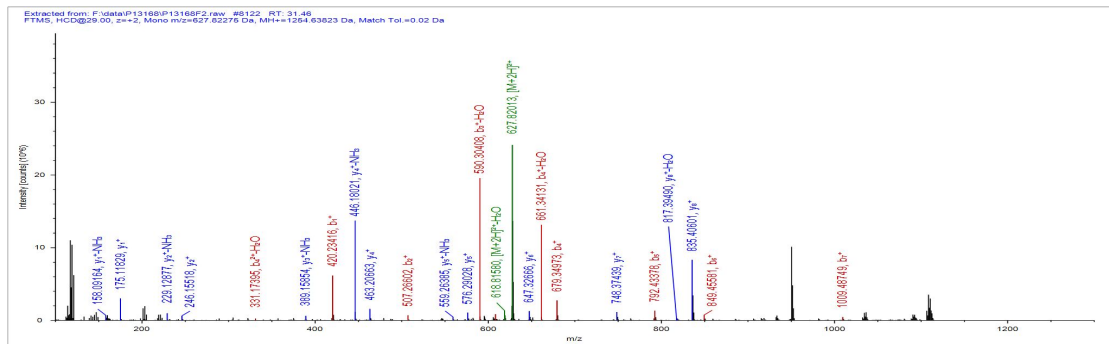
(6) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 518.67 with score 20.52;

Protein description: Acidic endochitinase OS=Aegilops tauschii GN=F775\_21686 PE=4 SV=1-[M8ASW4\_AEGTA]



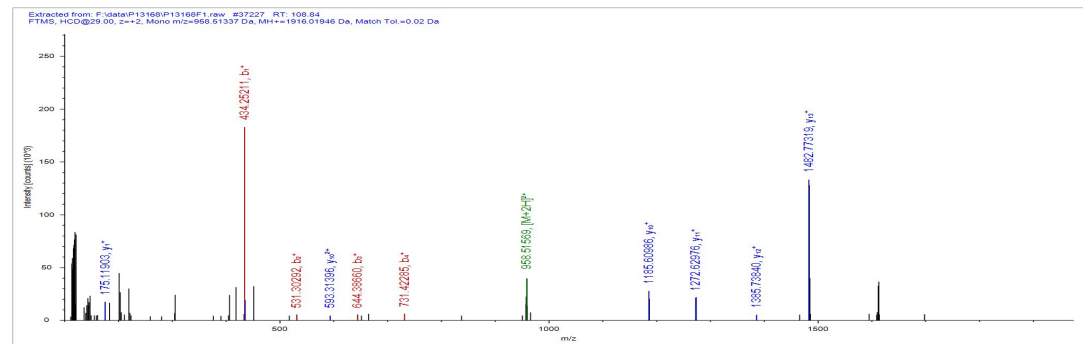
(7) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 627.82 with score 19.13

Protein description: Pathogenesis-related protein 1 OS=Aegilops tauschii GN=F775\_31533 PE=4 SV=1-[N1QT70\_AEGTA]



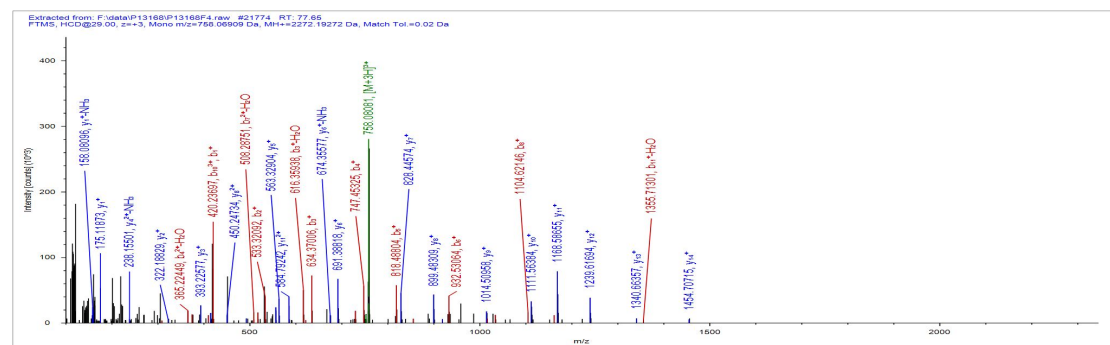
(8) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 958.52 with score 15.30

Protein description: NADH-ubiquinone oxidoreductase chain 1 (Fragment) OS=Phyllostachys edulis GN=nad1  
PE=2 SV=1- [B4XAP3\_9POAL]



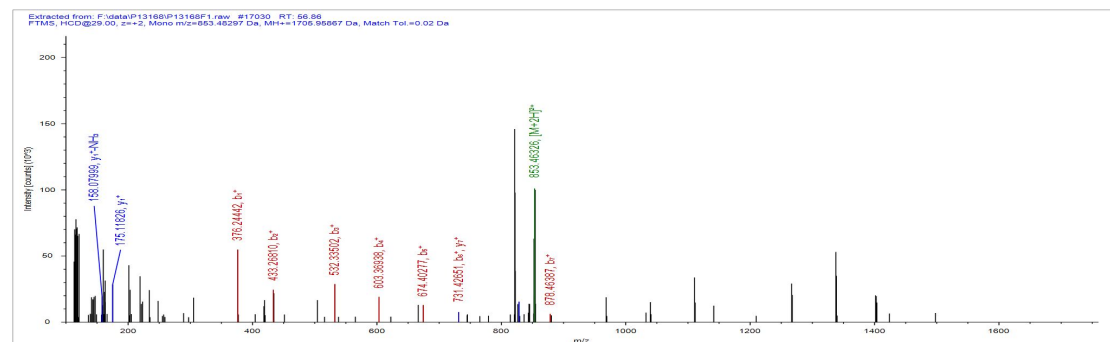
(9) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 758.07 with score 50.83

Protein description: Pectinesterase OS=Hordeum vulgare var. distichum PE=3 SV=1- [M0WJS2\_HORVD]



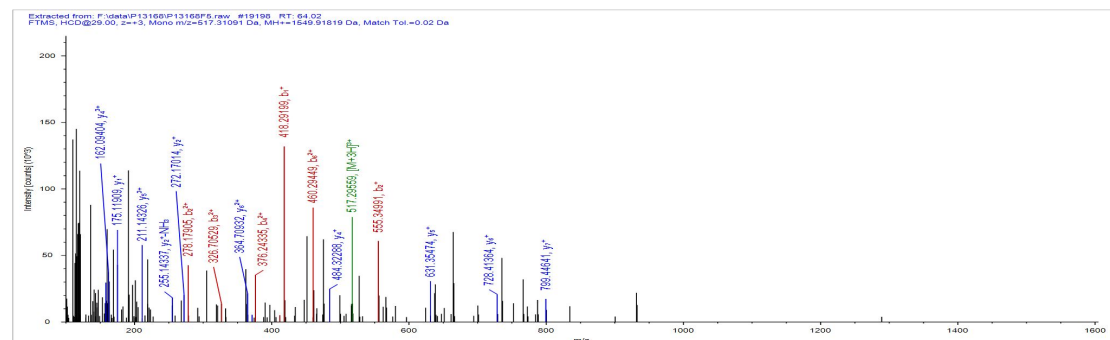
(10) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 853.48 with score 23.34

M8CYV8, Phosphorylated carbohydrates phosphatase OS=Aegilops tauschii GN=F775\_25876 PE=4 SV=1-  
[M8CYV8\_AEGTA]



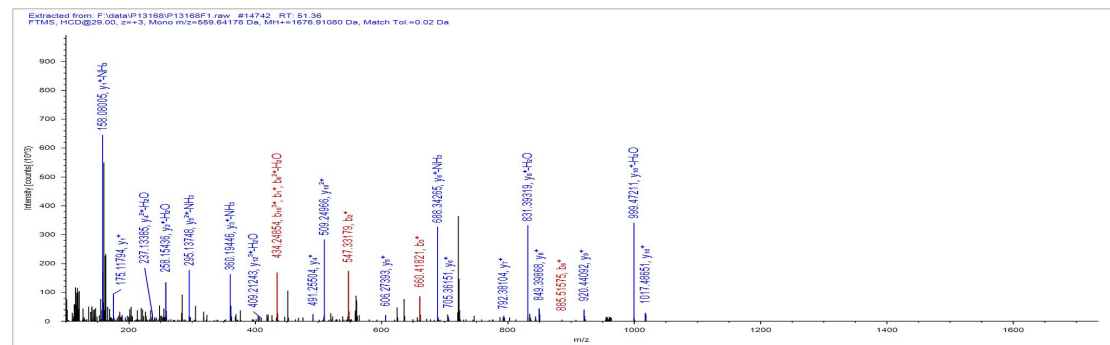
(11) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 517.31 with score 35.33

Protein description: Epidermal p-coumarate 3-hydroxylase (Fragment) OS=Triticum monococcum PE=2 SV=1-  
[B5KPW0\_TRIMO]



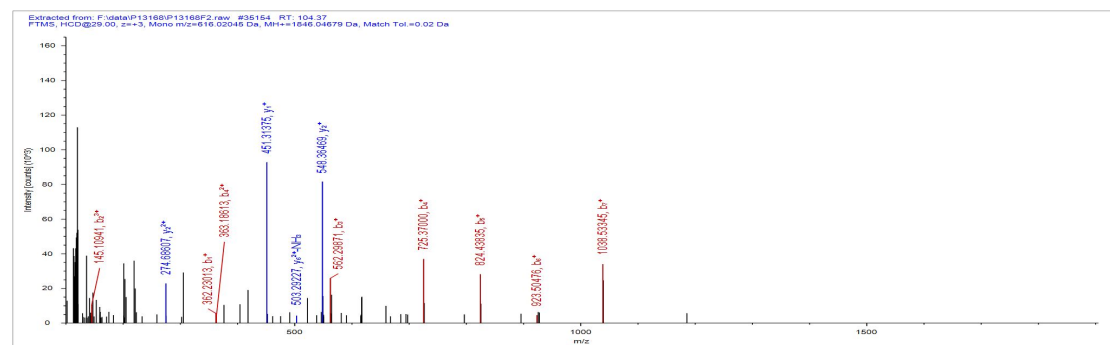
(12) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 559.64 with score 13.64

Protein description: Serpin-ZX OS=Aegilops tauschii GN=F775\_31803 PE=4 SV=1 - [M8BXN4\_AEGTA]



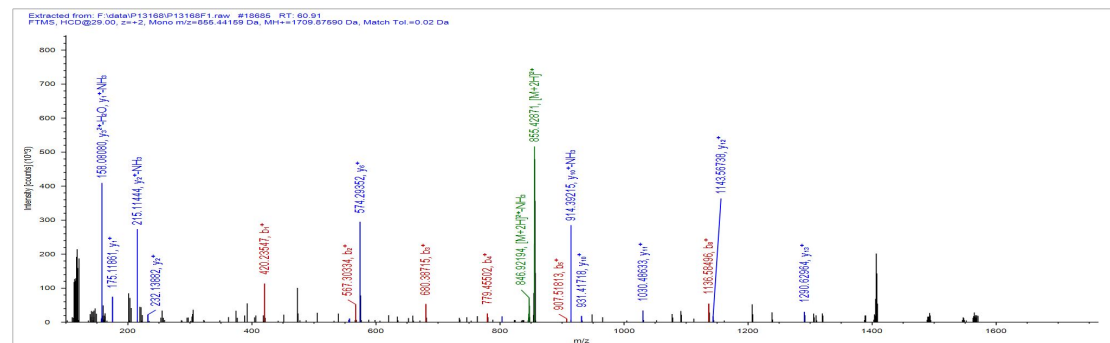
(13) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 616.02 with score 29.01

Protein description: Nitrogen regulatory protein P-II 2 OS=Aegilops tauschii GN=F775\_12533 PE=4 SV=1- [N1QP48\_AEGTA]



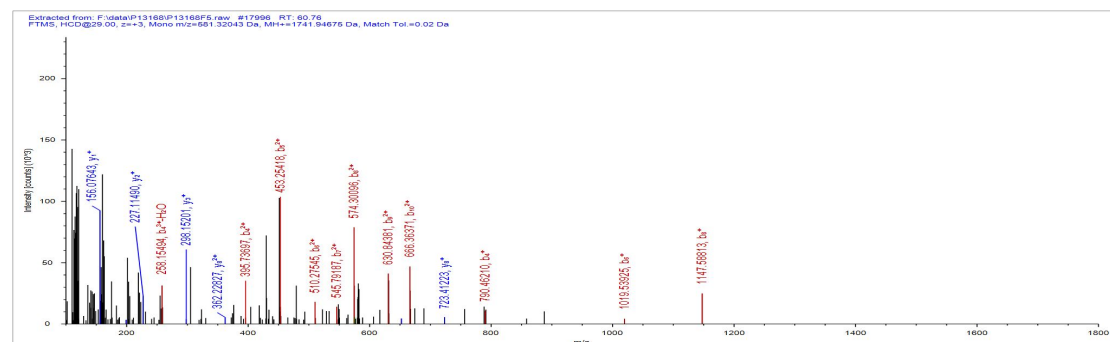
(14) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 855.44 with score 16.91

Protein description: Peptidyl-prolyl cis-trans isomerase OS=Hordeum vulgare var. distichum PE=3 SV=1- [M0W697\_HORVD]



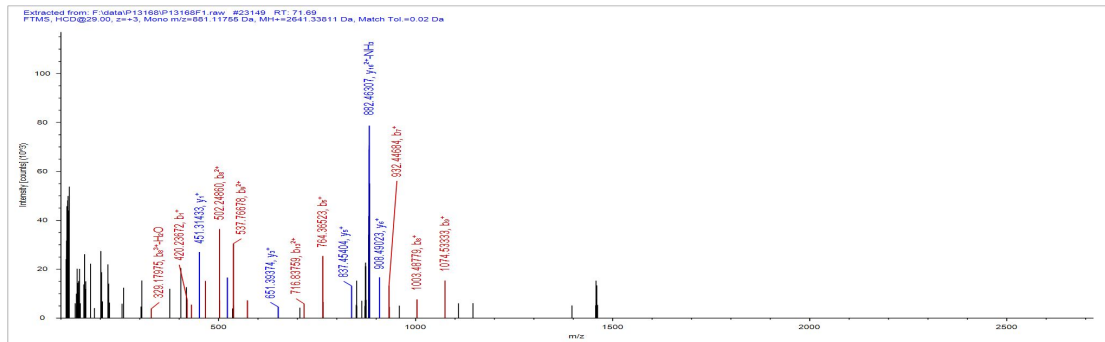
(15) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 581.32 with score 10.08

Protein description: 1, 2-dihydroxy-3-keto-5-methylthiopentene dioxygenase 4 OS=Triticum urartu GN=TRIUR3\_18280 PE=4 SV=1- [M8A347\_TRIUA]



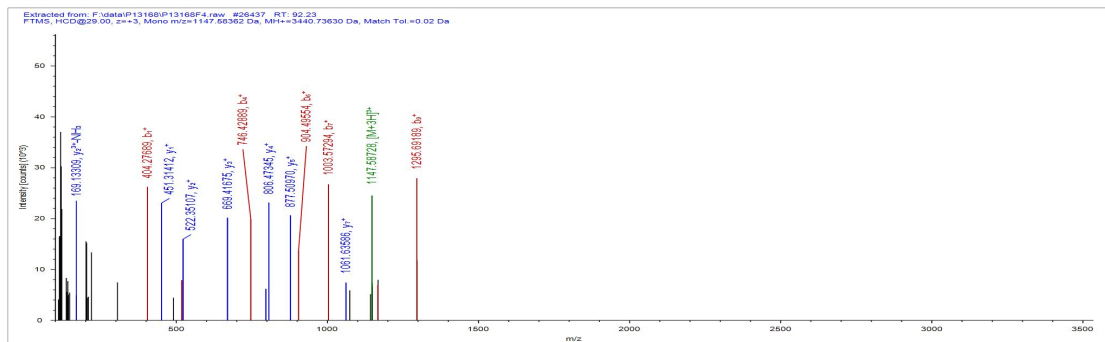
(16) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 881.12 with score 19.62

Protein description: H/ACA ribonucleoprotein complex subunit 4 OS=Aegilops tauschii GN=F775\_27812 PE=4 SV=1- [M8B1T7\_AEGTA]



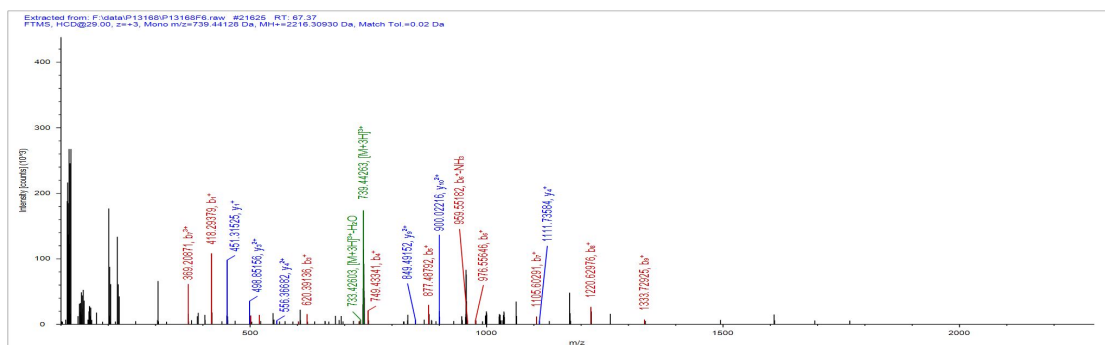
(17) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 1147.58 with score 51.73

Protein description: Patatin group M-3 OS=Triticum urartu GN=TRIUR3\_25915 PE=4 SV=1- [M7YQD5\_TRIUA]



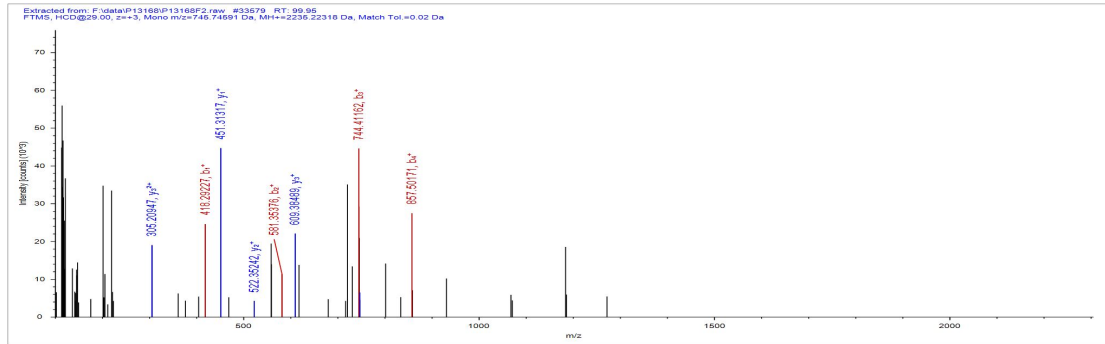
(18) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 793.44 with score 9.16

Protein description: Subtilisin-like protease OS=Triticum urartu GN=TRIUR3\_02213 PE=4 SV=1- [M7ZZZ8\_TRIUA]



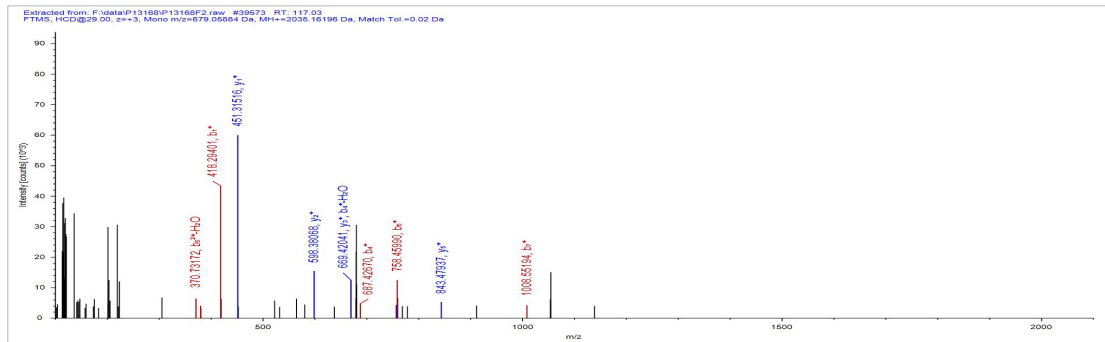
(19) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 745.74 with score 7.42

Protein description: SAP domain containing protein OS=Brachypodium distachyon GN=BRADI1G61000 PE=4 SV=1- [C3SA89\_BRADI]



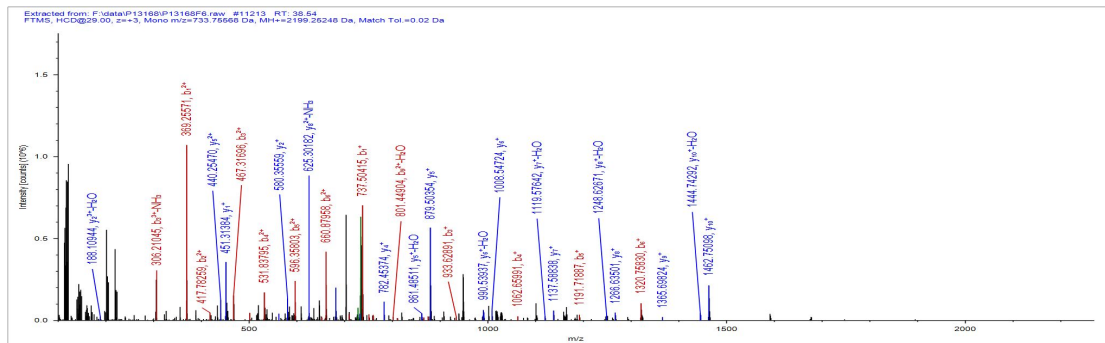
(20) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 679.06 with score 13.97

Protein description: Aspartic proteinase nepenthesin-2 OS=Triticum urartu GN=TRIUR3\_13924 PE=4 SV=1- [M8AQF1\_TRIUA]



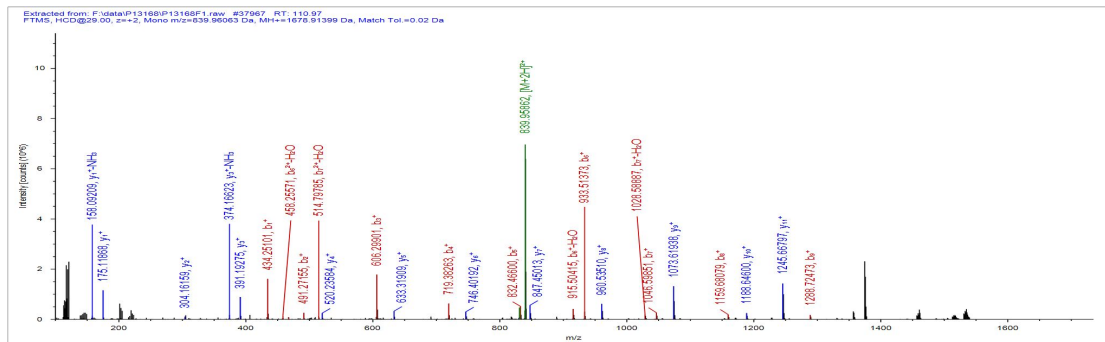
(21) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 733.76 with score 20.40

Protein description: Histone H2B-4 (Fragment) OS=Lolium perenne PE=2 SV=1- [Q94KK0\_LOLPR]



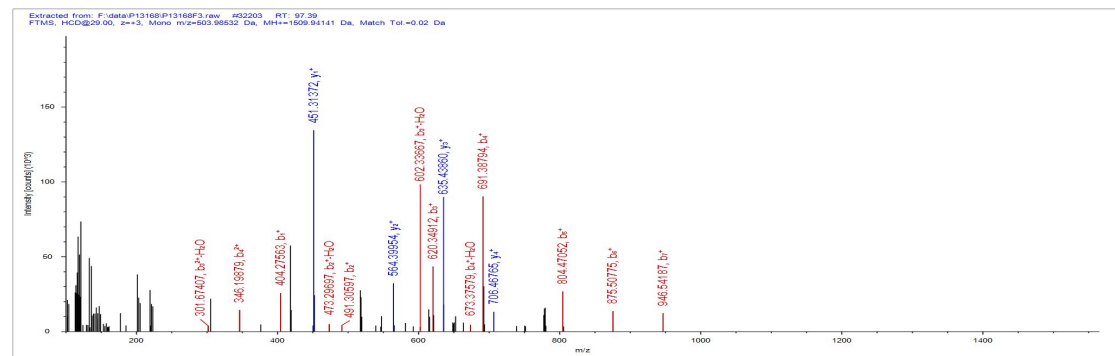
(22) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 839.96 with score 55.94

Protein description: 40S ribosomal protein S28 OS=Zea mays PE=4 SV=1- [B6SP50\_MAIZE]



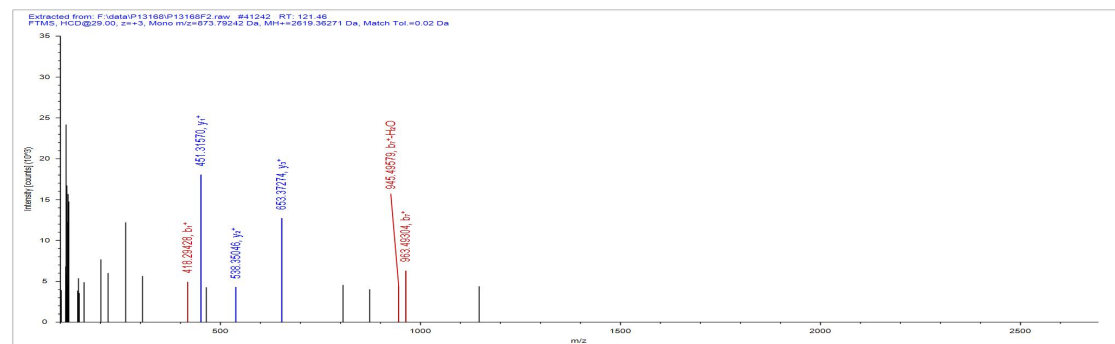
(23) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 503.98 with score 25.46

Protein description: Histone H1.1 (Fragment) OS=Triticum aestivum PE=1 SV=1- [H11\_WHEAT]



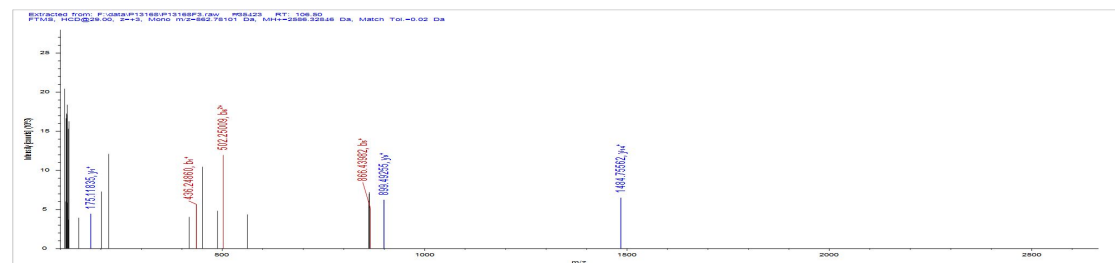
(24) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 873.79 with score 5.73

Protein description: Serine carboxypeptidase-like 51 OS=Triticum urartu GN=TRIUR3\_23998 PE=4 SV=1- [M7ZA68\_TRI]



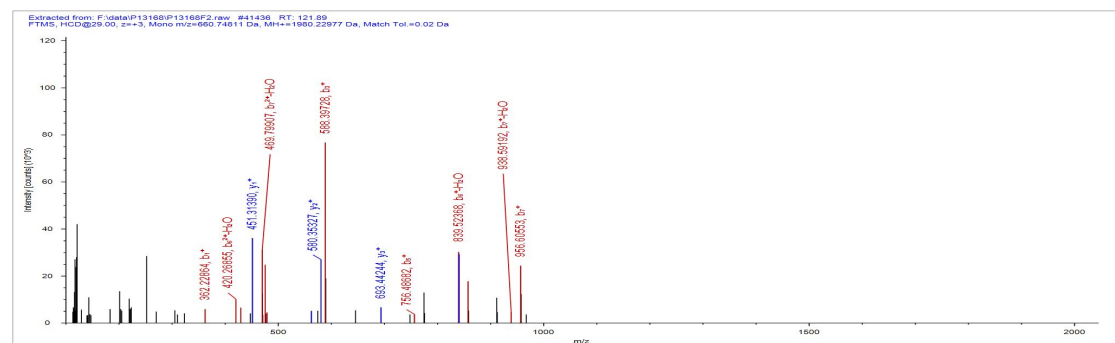
(25) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 862.78 with score 2.43;

Protein description: Alanine--glyoxylate aminotransferase 2-like protein 3, mitochondrial OS=Triticum urartu GN=TRIUR3\_23613 PE=4 SV=1- [M7YW64\_TRIUA]



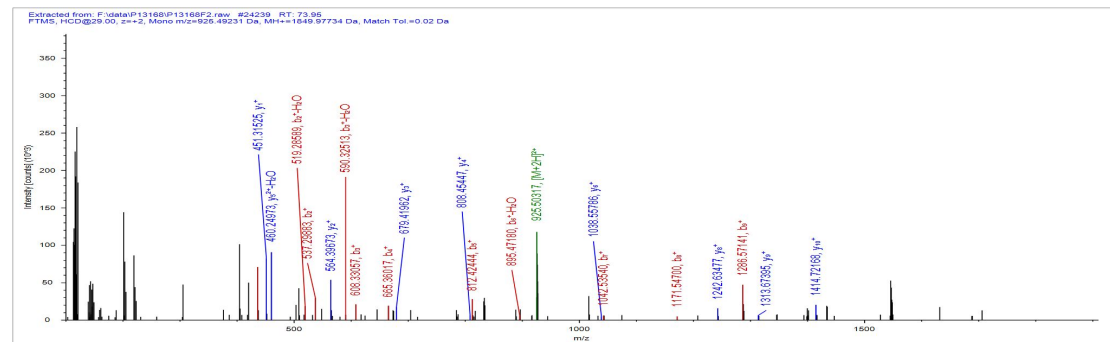
(26) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 660.75 with score 29.56

Protein description: Patatin group A-3 OS=Aegilops tauschii GN=F775\_12862 PE=4 SV=1- [M8BFN4\_AEGTA]



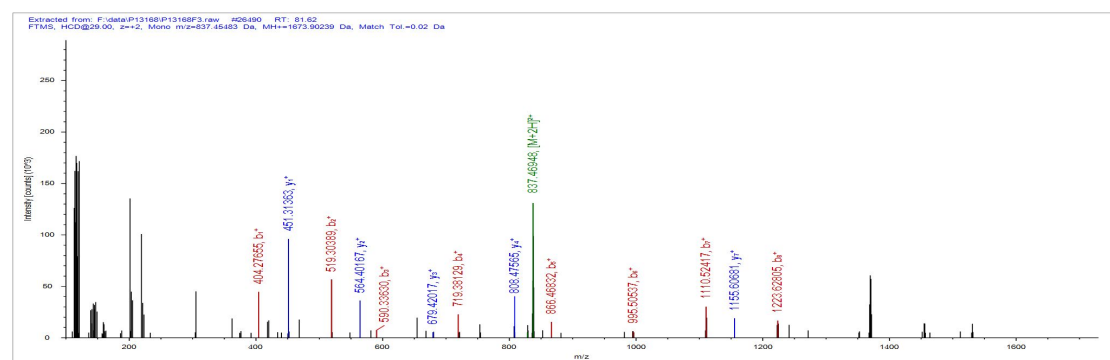
(27) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 925.49 with score 19.47

Protein description: Mitochondrial ATP synthase 6 kDa subunit (Fragment) OS=Aegilops crassa PE=2 SV=1- [D2K756\_AEGCR]



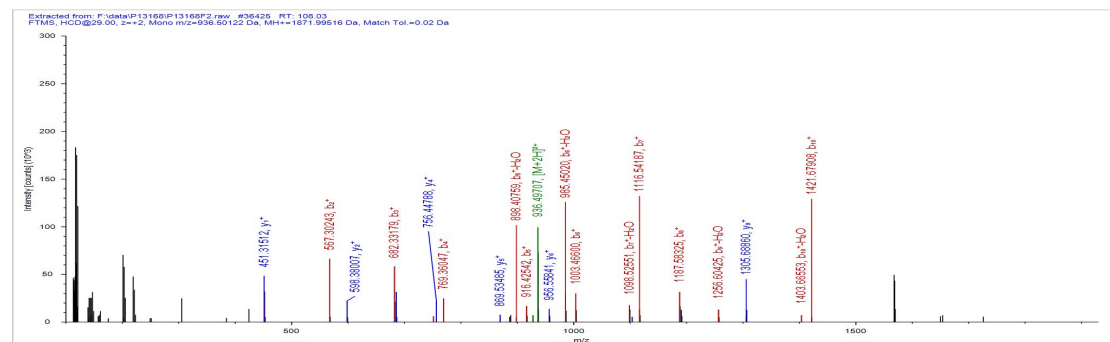
(28) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 837.45 with score 21.37

Protein description: Sugar transport protein 14 OS=Zea mays PE=2 SV=1- [B6T9F4\_MAIZE]



(29) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 936.50 with score 42.91

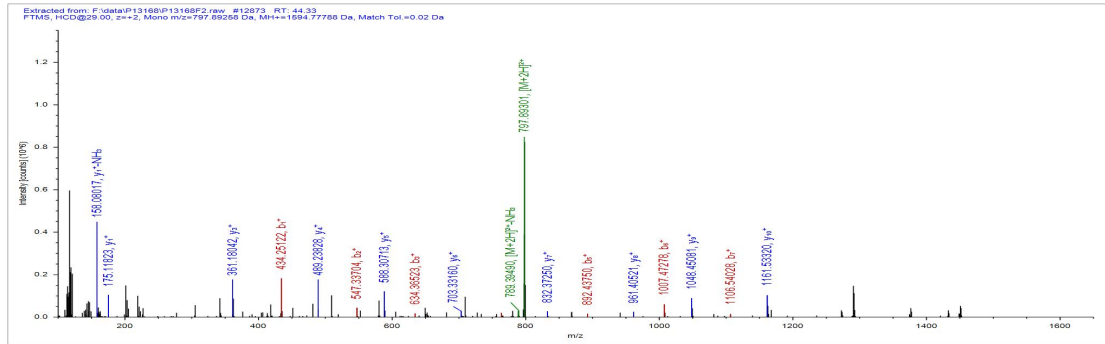
Protein description: Putative aquaporin TIP2-2 OS=Triticum urartu GN=TRIUR3\_24886 PE=4 SV=1- [M7Z4T9\_TRIUA]



(30) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 797.89 with score 25.43;

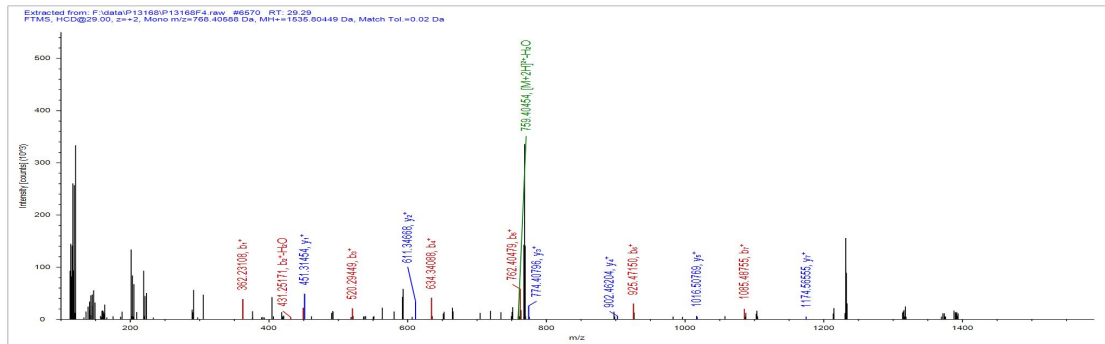
Protein description: Inorganic phosphate transporter (Fragment) OS=Triticum aestivum/Thinopyrum intermedium alien addition line GN=pt2 PE=2 SV=1- [Q93WQ8\_9POAL]





(31) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 768.41 with score 21.57

Protein description: Sugar transport protein 1 OS=Aegilops tauschii GN=F775\_26986 PE=4 SV=1-[M8B1H6\_AEGTA]



(32) MS/MS analysis of a single high-confidence peptide ions with a m/z ratio of 797.40 with score 32.81

Protein description: Inorganic phosphate transporter 1-2 OS=Triticum urartu GN=TRIUR3\_17227 PE=4 SV=1-[M8A5M8\_TRIUA]

