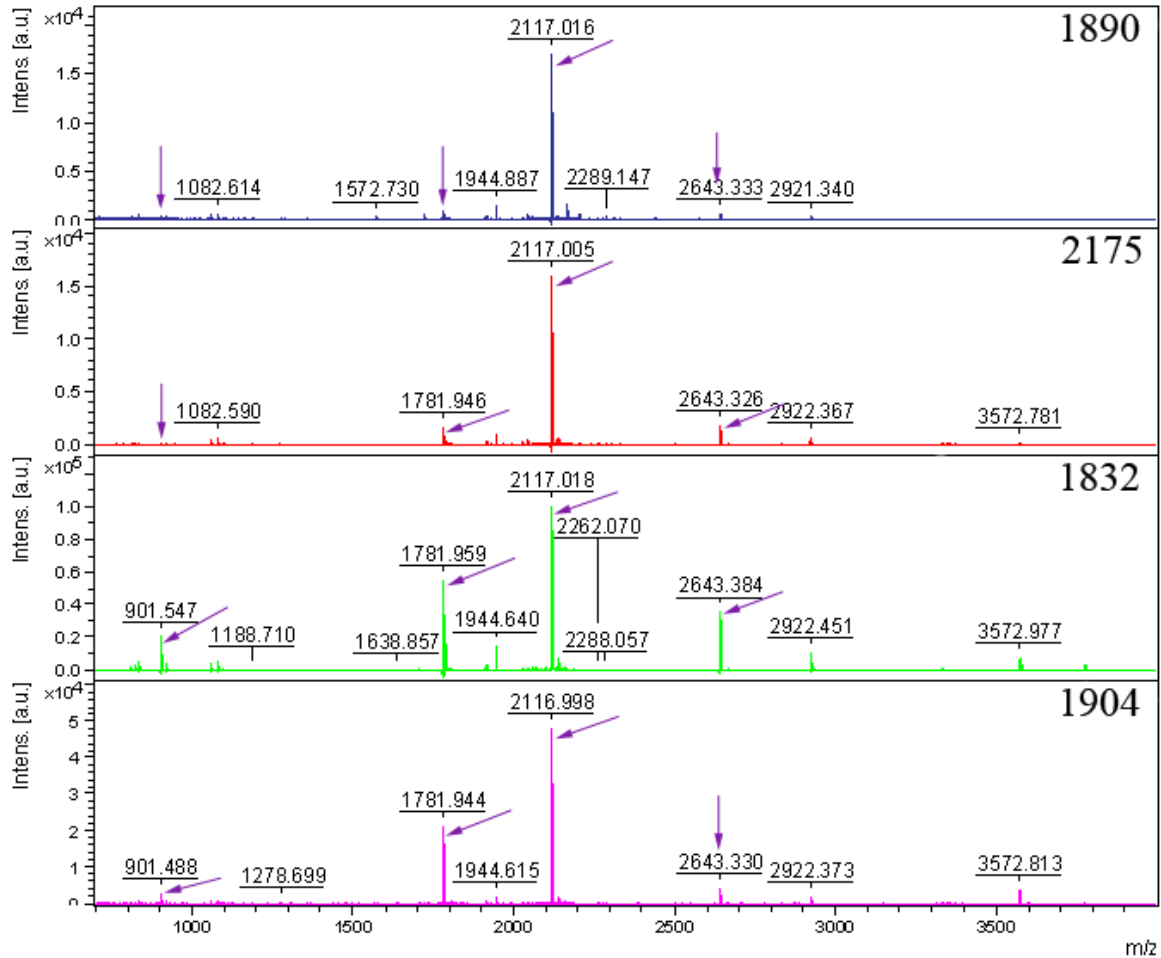


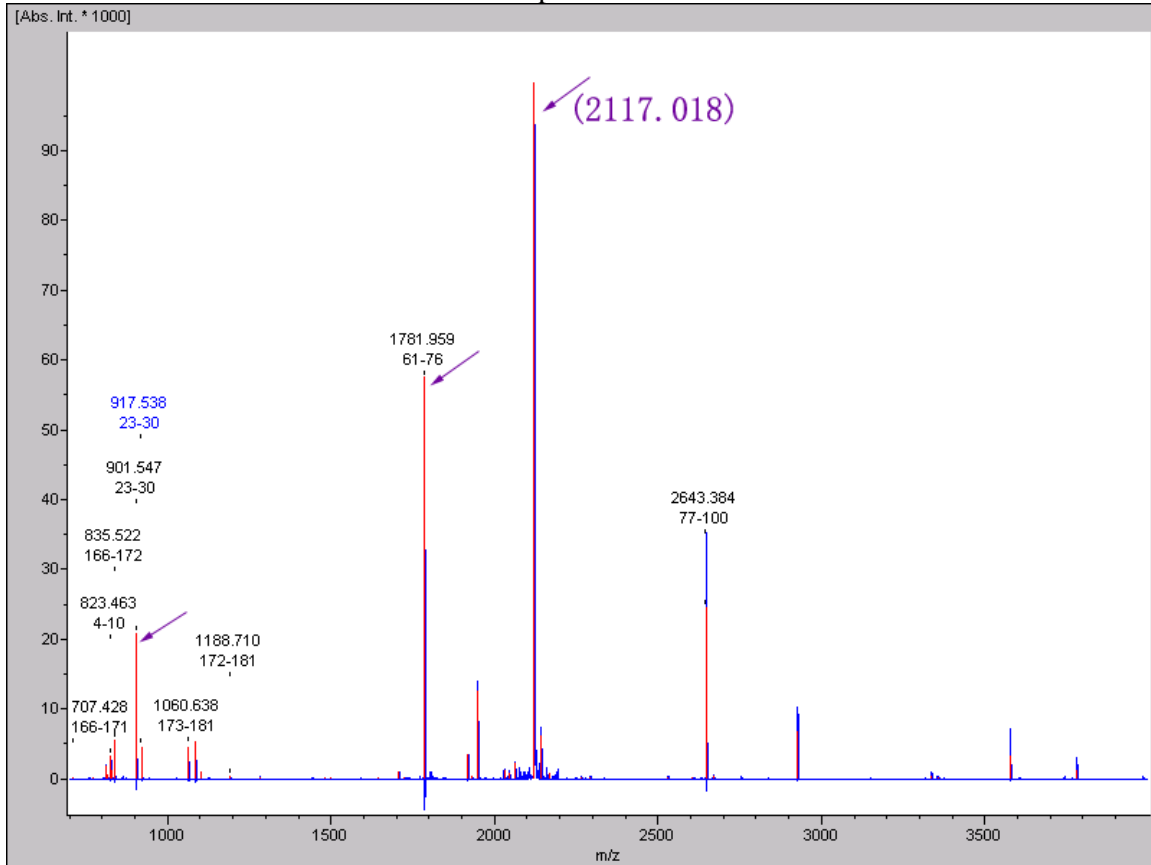
Figure S3. MS/MS identifications.

a. Four similar spectrum derived from PMF-based identification. The spots 1890 and 2175 were identified as germin-like protein 3 firstly, however, they have the lower score, and the remarkable peak 2117.010 (± 6 ppm) didn't match to the candidate proteins. So the protein might need further confirm by MS/MS. Therefore, when spot 1832 and 1904 were identifying, three peptides fragments were selected for MS/MS analysis.

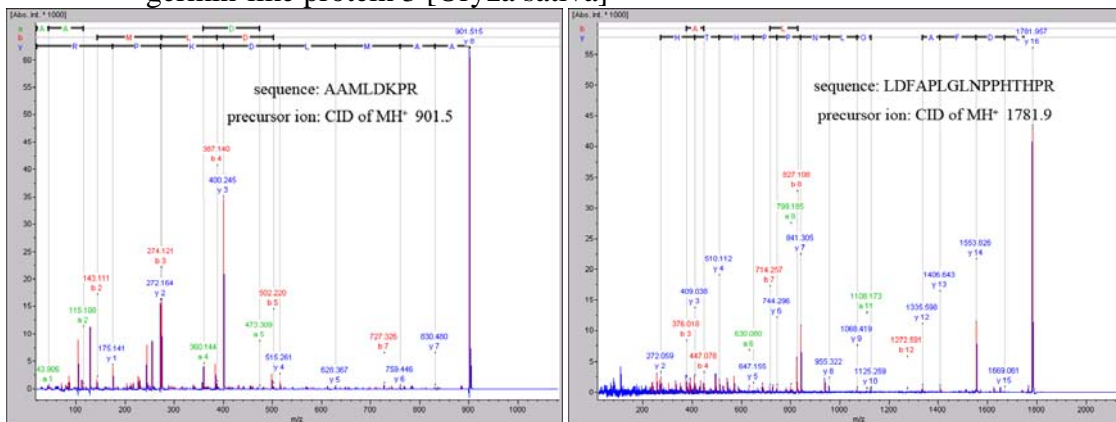


b. MS/MS analysis

Spot 1832



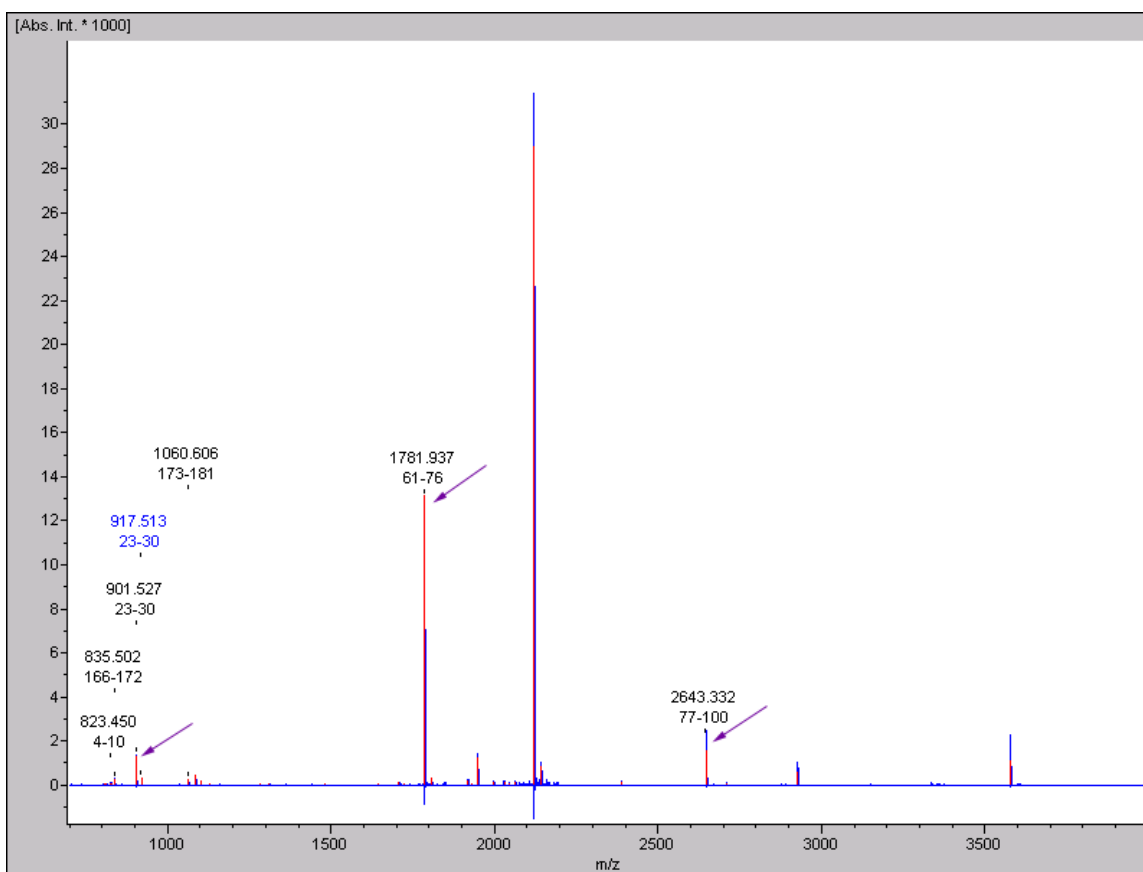
MS result: gi|2655289; Mass:19629; Score:95; Expect:4.4e-05; Queries matched: 9
germin-like protein 3 [*Oryza sativa*]



m/z	error[Da]	Hit protein	Peptide	Score
901.5018	0.32	germin-like protein 3	AAMLDKPR	47
1781.9557	0.26	germin-like protein 3	LDFAPLGLNPPHTHPR	74
2117.018	0.41	OsL_34178	ALDSLQWLSLLVIYGRGR	13

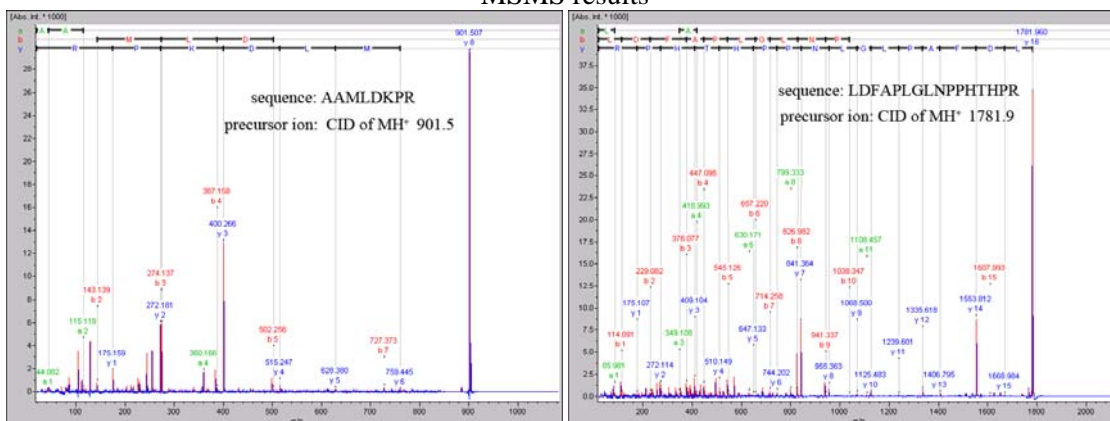
Individual ions scores > 44 indicate identity or extensive homology (p<0.01).

Spot 1904



MS result: gi|2655289; Mass:19629; Score:74; Expect:0.0051; Queries matched: 7
germin-like protein 3 [*Oryza sativa*]

MSMS results



m/z	error[Da]	Hit protein	Peptide	Score
901.5018	0.25	germin-like protein 3	AAMLDKPR	48
1781.9557	0.37	germin-like protein 3	LDFAPLGLNPPHTHPR	73

2463.332	0.71	germin-like protein 3	ATEIFTVLEGTLYVGFVTSNPDNR	25
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Individual ions scores > 44 indicate identity or extensive homology (p<0.01)

Conclusion: the MS/MS results support the results of MS although the remarkable peak (2117.009 ± 20 ppm) didn't match to the germin-like protein 3.