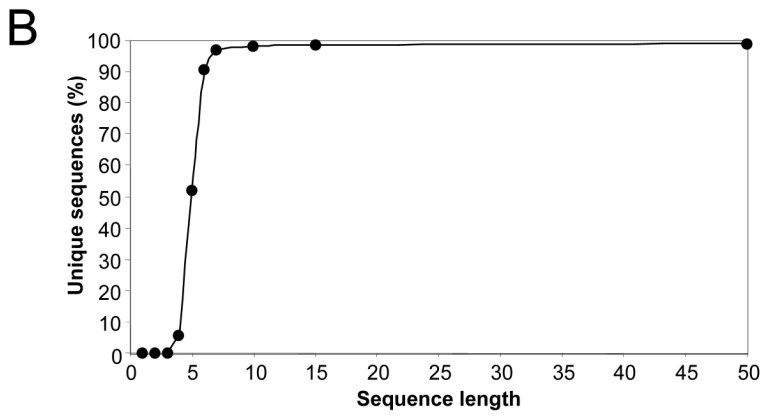
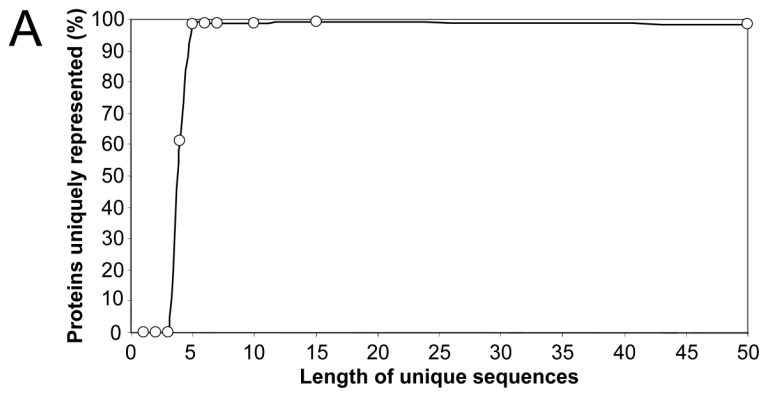


Type of file: figure

Label: 1

Filename: UStag_SupFig1_Shen.jpg



Supplementary Figure 1.

Type of file: figure

Label: 10

Filename: UStag_SupFig10_Shen.jpg

•Input:

1, ..., n //spectra (peaks)
1, ..., 10 //SEQUEST candidates
1, ..., m //list of residual replacements used in RRF
Mp //molecular mass error threshold
Ms //residual sequencing error threshold

•Processing:

for every candidate

 if correct parent mass (within the Mp of expected)

 generate b and y fragment masses

 identify fragments (within the Ms of expected residue mass)

 use consecutive fragments to produce sequence tags

 for every tag

 use RRF to determine if UStag

 if at least one tag is UStag

 candidate is identified

 else

 explore modifications with obtained Stags and delta mass

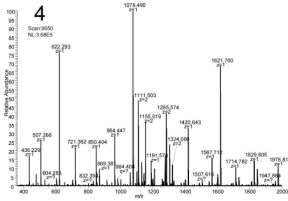
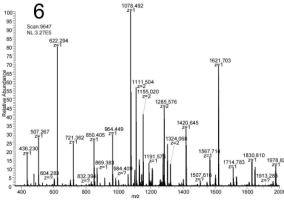
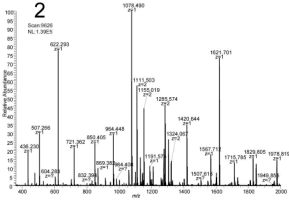
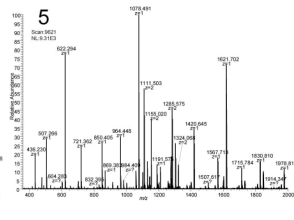
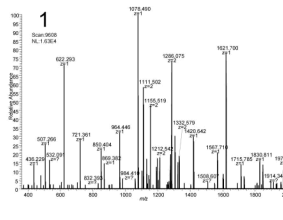
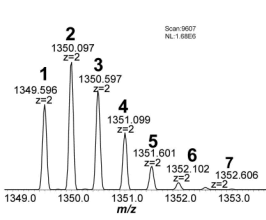
•Output:

UStags-based unambiguous identifications

Type of file: figure

Label: 2

Filename: UStag_SupFig2_Shen.jpg

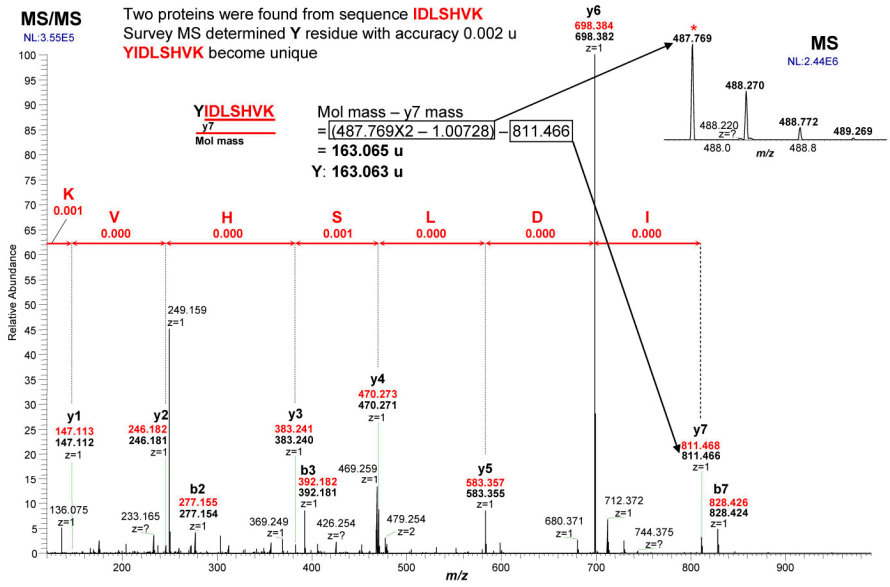


Supplementary Figure 2.

Type of file: figure

Label: 3

Filename: UStag_SupFig3_Shen.jpg

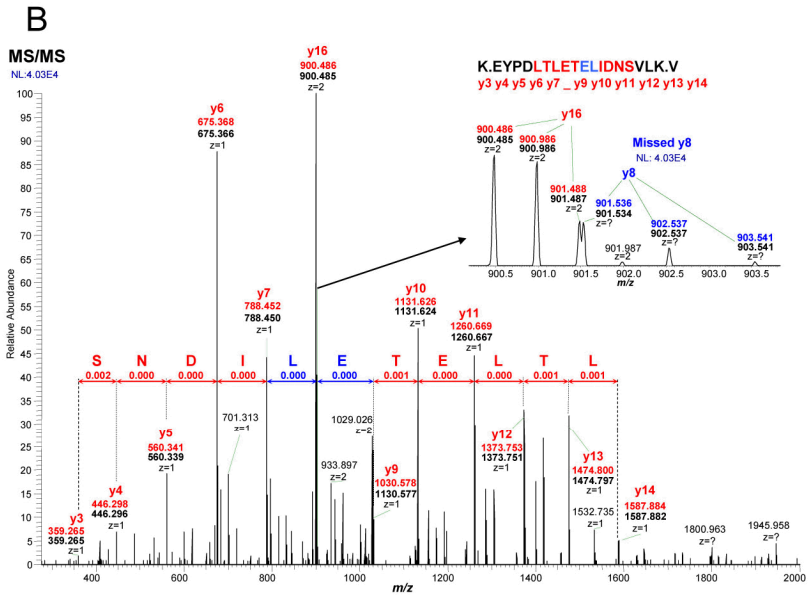
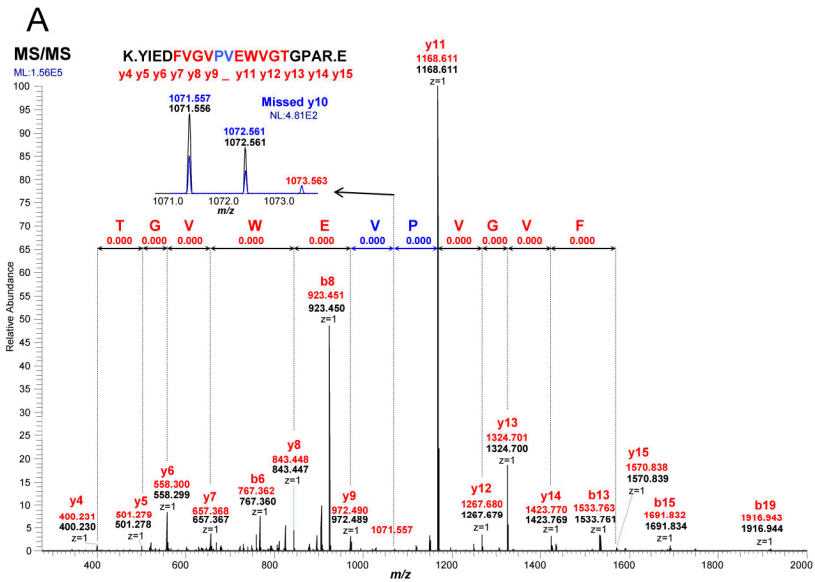


Supplementary Figure 3.

Type of file: figure

Label: 4

Filename: UStag_SupFig4_Shen.jpg

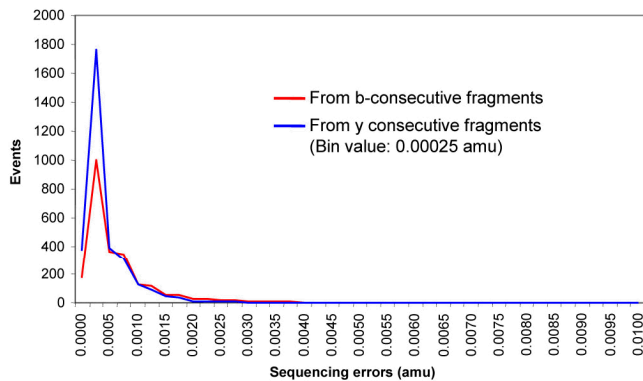
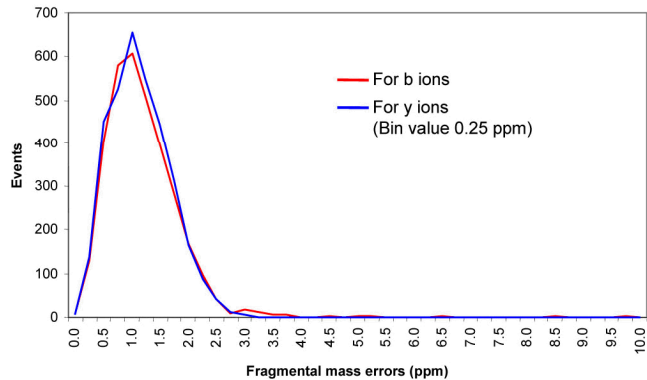
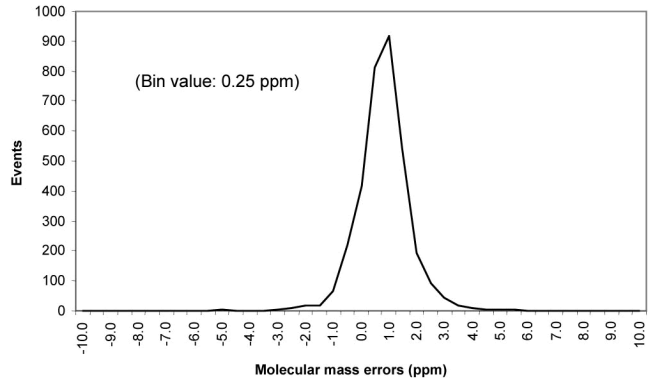


Supplementary Figure 4.

Type of file: figure

Label: 5

Filename: UStag_SupFig5_Shen.jpg

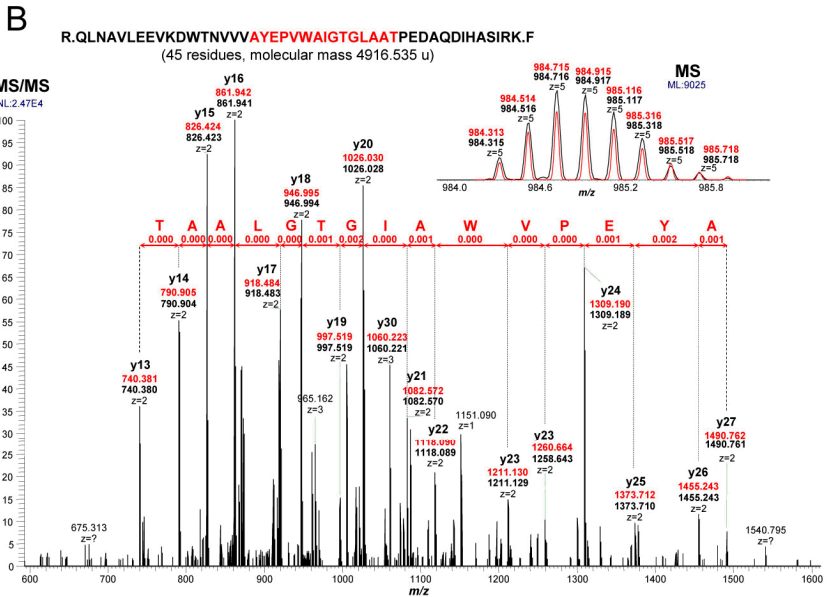
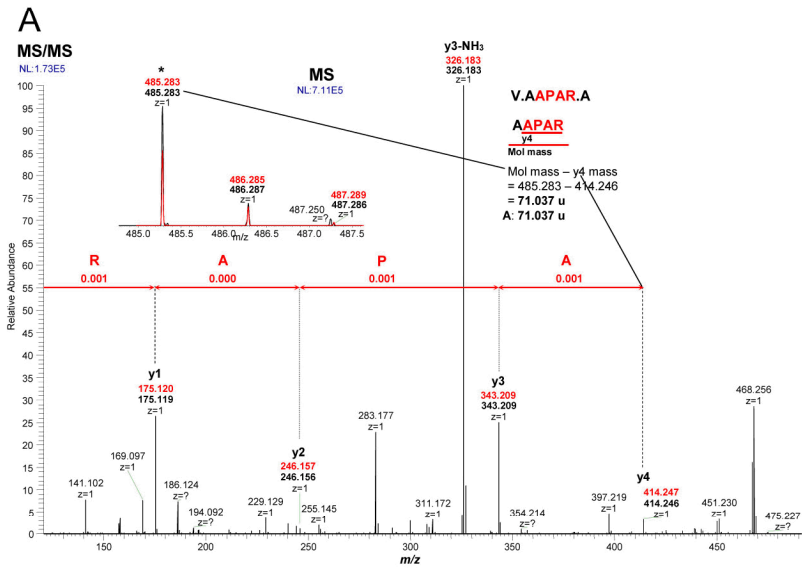


Supplementary Figure 5.

Type of file: figure

Label: 6

Filename: UStag_SupFig6_Shen.jpg



Supplementary Figure 6.

Type of file: figure

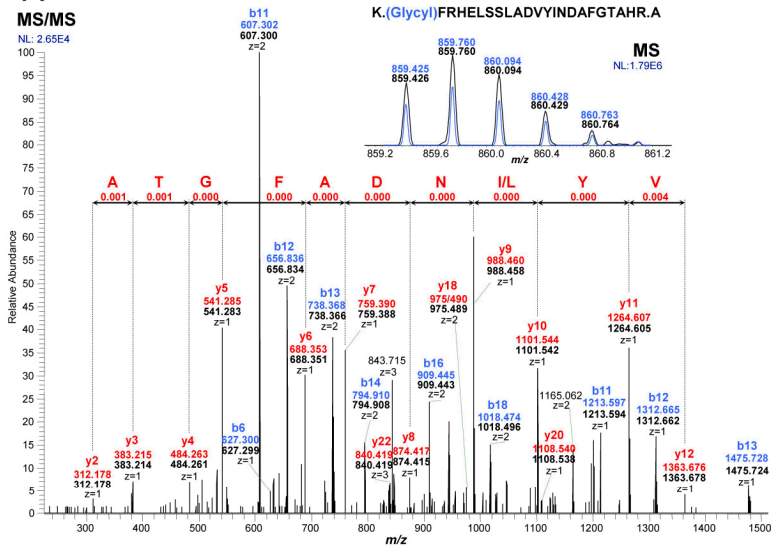
Label: 7

Filename: UStag_SupFig7_Shen.jpg

A

MS/MS

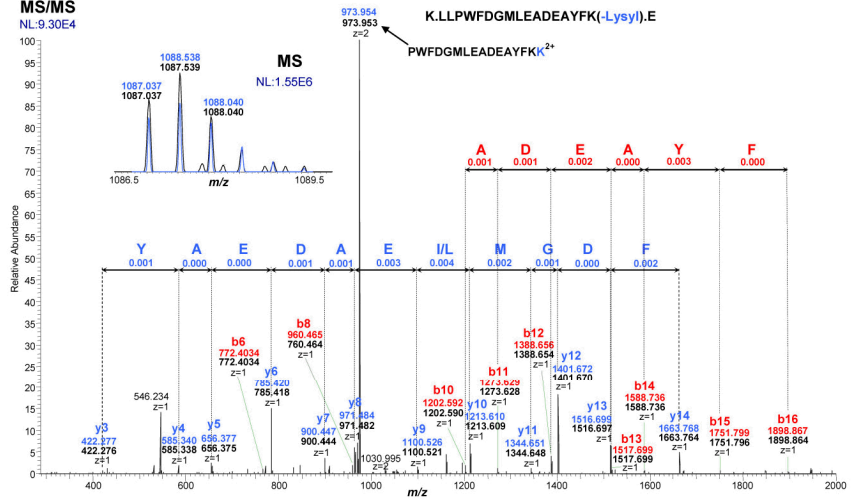
NL: 2.65E4



B

MS/MS

NL: 9.30E4

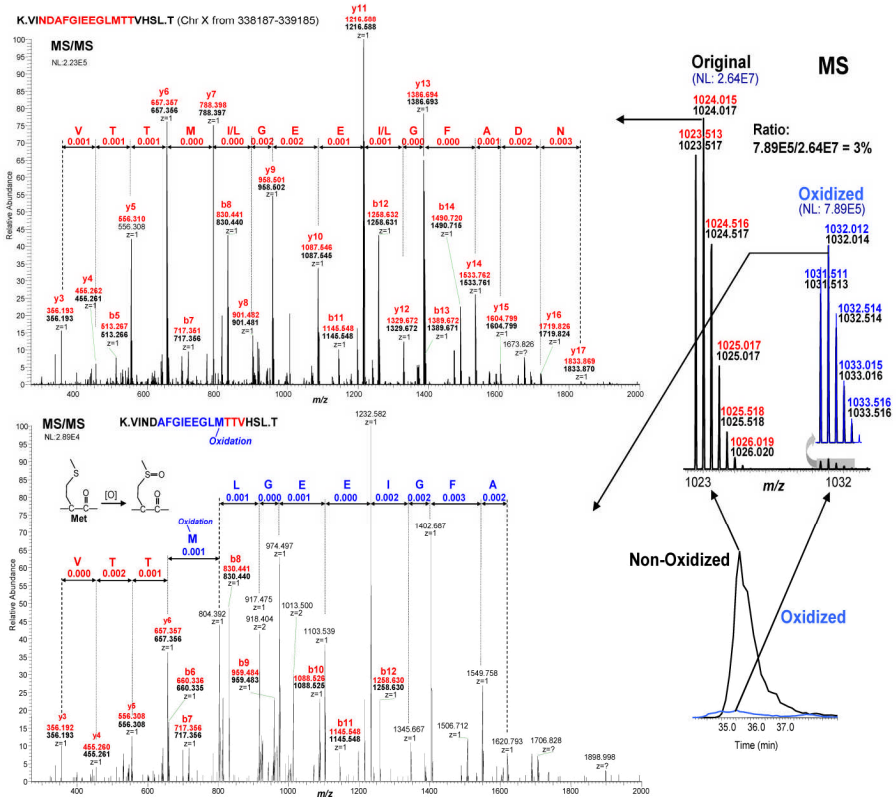


Supplementary Figure 7.

Type of file: figure

Label: 8

Filename: UStag_SupFig8_Shen.jpg



Supplementary Figure 8.

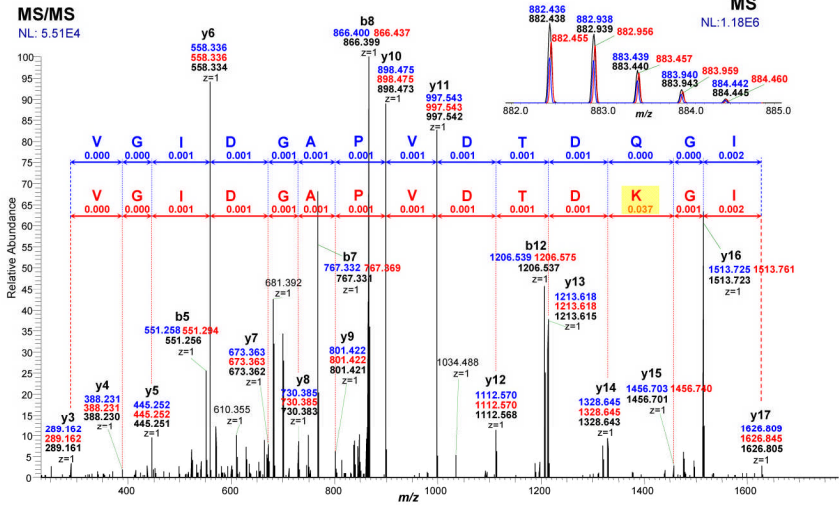
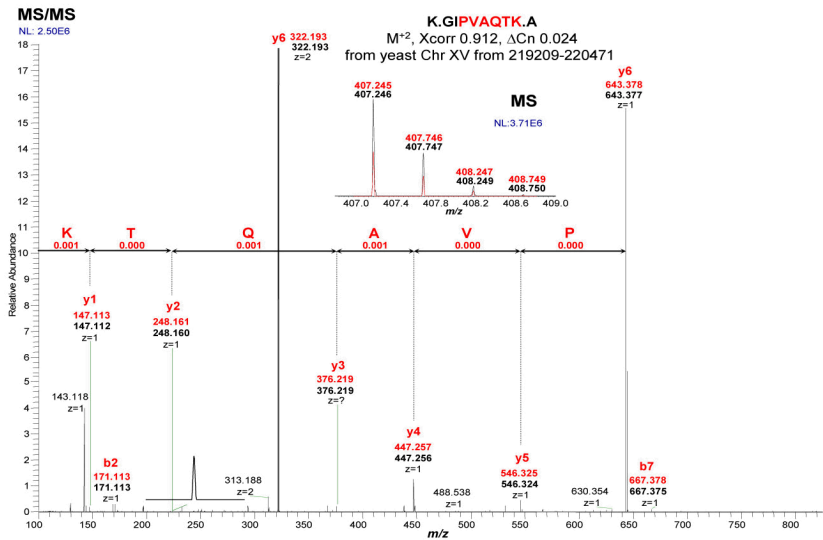
Type of file: figure

Label: 9

Filename: UStag_SupFig9_Shen.jpg

A

R.HIGKDTDVPAGDIGVGGRR.E (M⁺, Xcorr 5.108, 1st, from yeast Chr I from 31568-32941)
 R.HIGQDTPVAGDIGVGGRR.E (M⁺, Xcorr 5.108, 1st, from yeast Chr XV from 1043038-1041674) } ΔCn = 0

**B**

Supplementary Figure 9.