Fig. S1. MS/MS/MS of y_6 ion observed in the MS/MS of the di-methylated form of the peptide $_1$APKKRPE$_7$

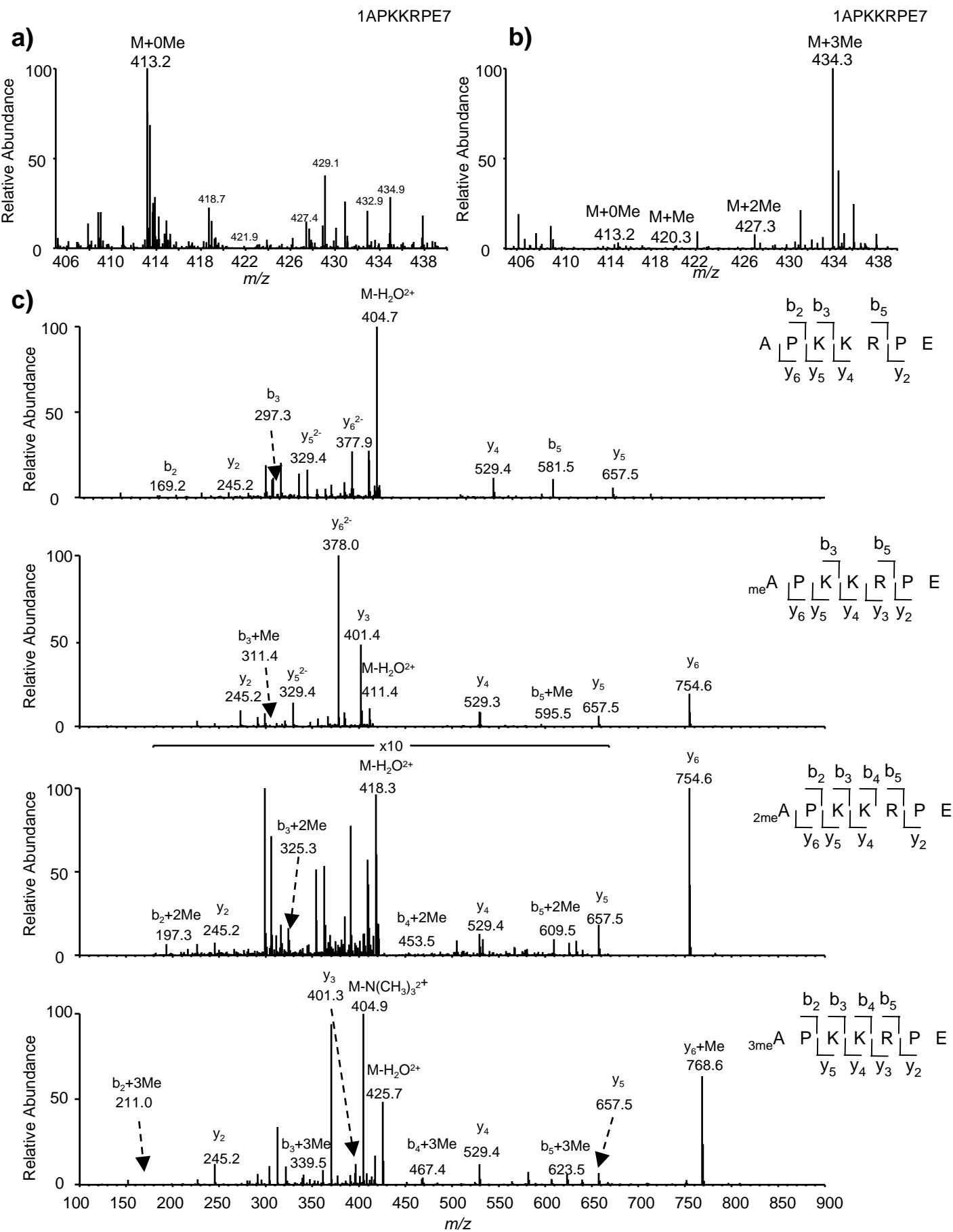**a)**

b)

c)

Fig. S2. ESI-MS/MS of unmodified, mono-, di-, tri-α-N-methylated forms of the peptide $_1$APKKRPE$_7$ from X-factor-cleaved recombinant DDB2: (a) without the addition of NRMT, (b) with the addition of NRMT. (c) ESI-MS/MS of unmodified, mono-, di-, tri-α-N-methylated forms of the peptide $_1$AAKKRPE$_7$ arising from Glu-C digestion of X-factor-cleaved recombinant DDB2 with incubation with NRMT. Certain regions of the spectra were amplified to visualize better the peaks for some fragment ions.
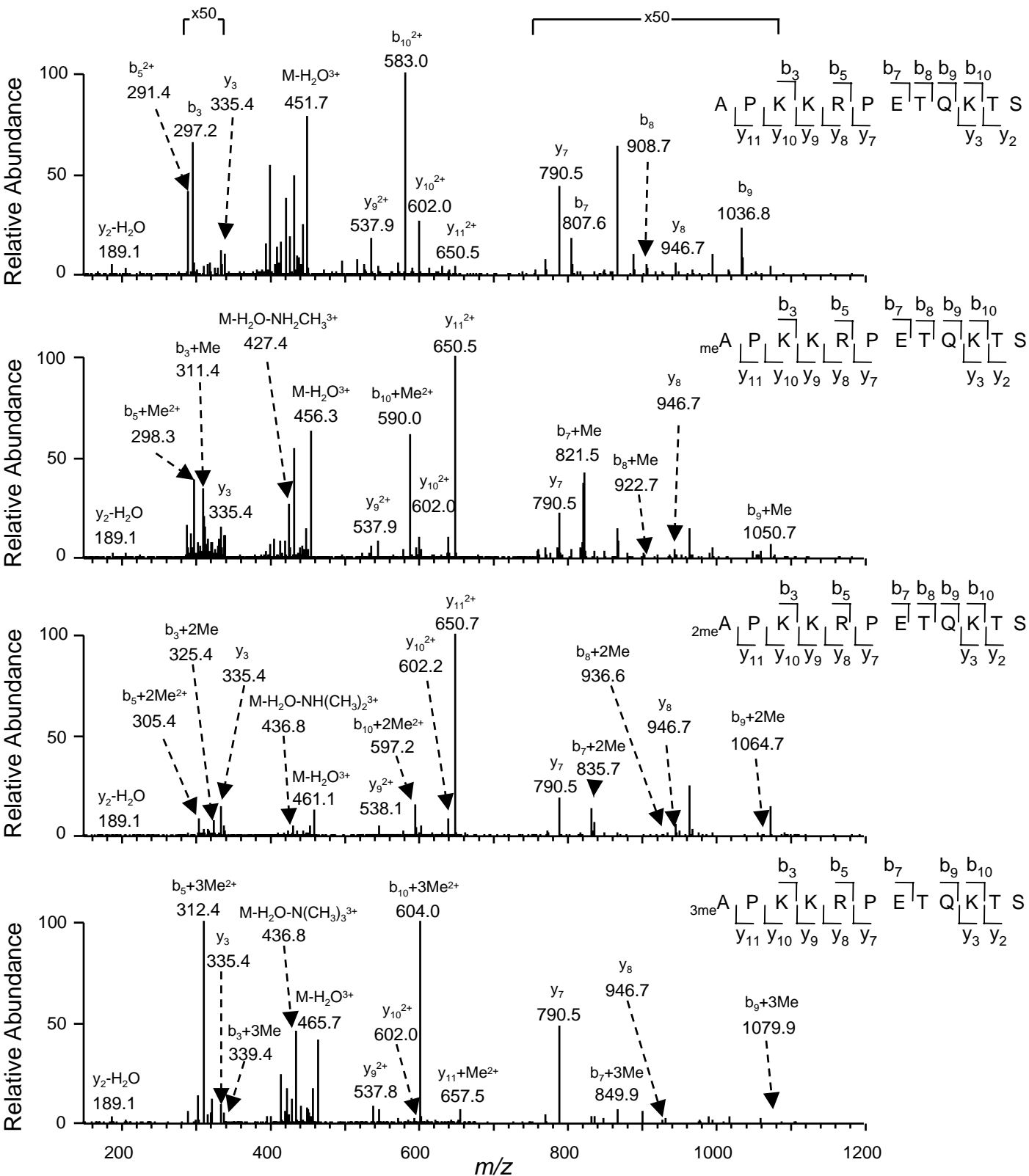
Fig. S3. ESI-MS/MS of unmodified as well as mono-, di-, tri-α-N-methylated forms of the peptide $_1$APKKRPETQKTS$_{12}$. Certain regions of the spectra were amplified to visualize better the peaks for some fragment ions.
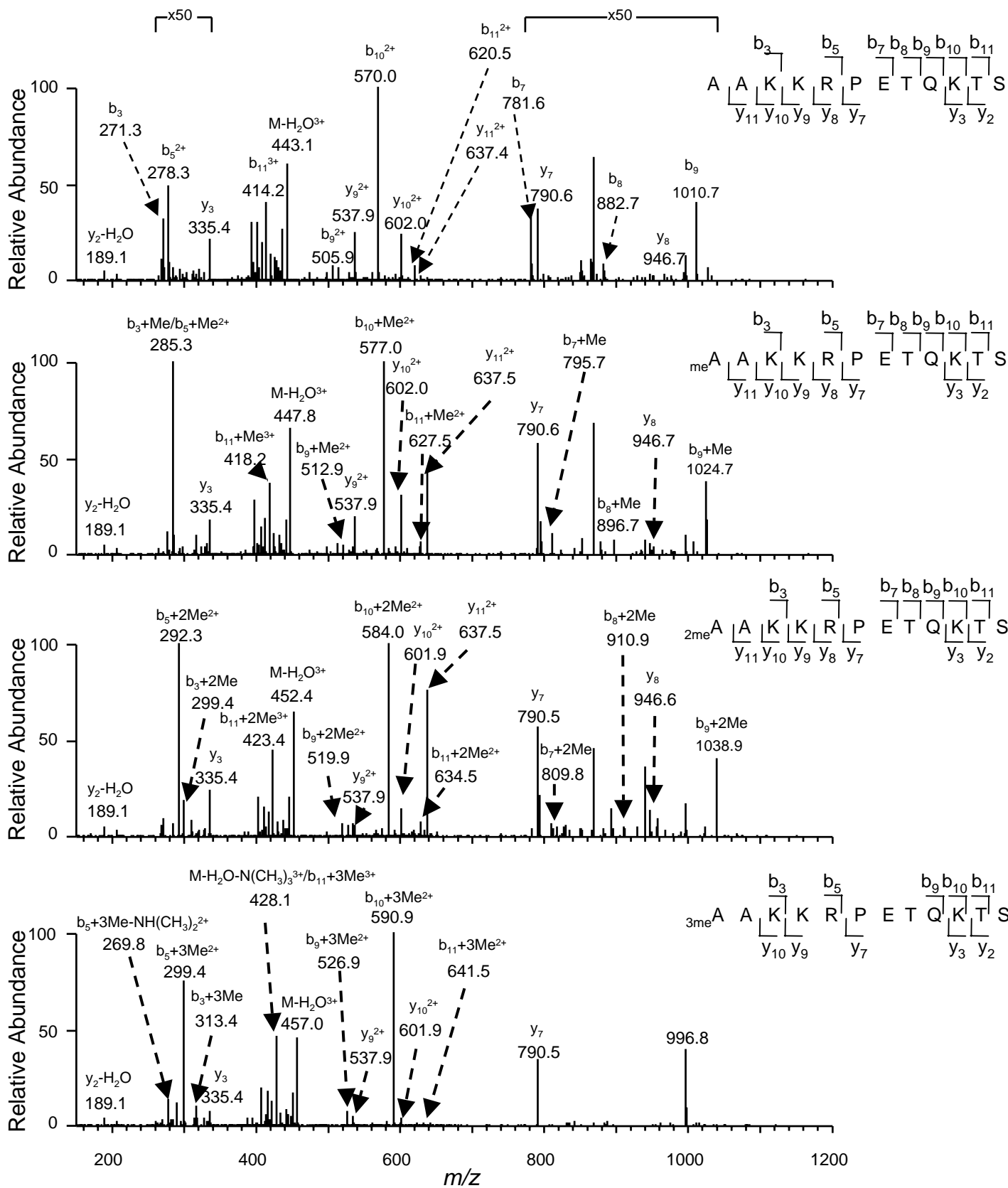
Fig. S4. ESI-MS/MS of unmodified as well as mono-, di-, tri-α-N-methylated forms of the peptide $_1$AAKKRPETQKTS$_{12}$. Certain regions of the spectra were amplified to visualize better the peaks for some fragment ions.
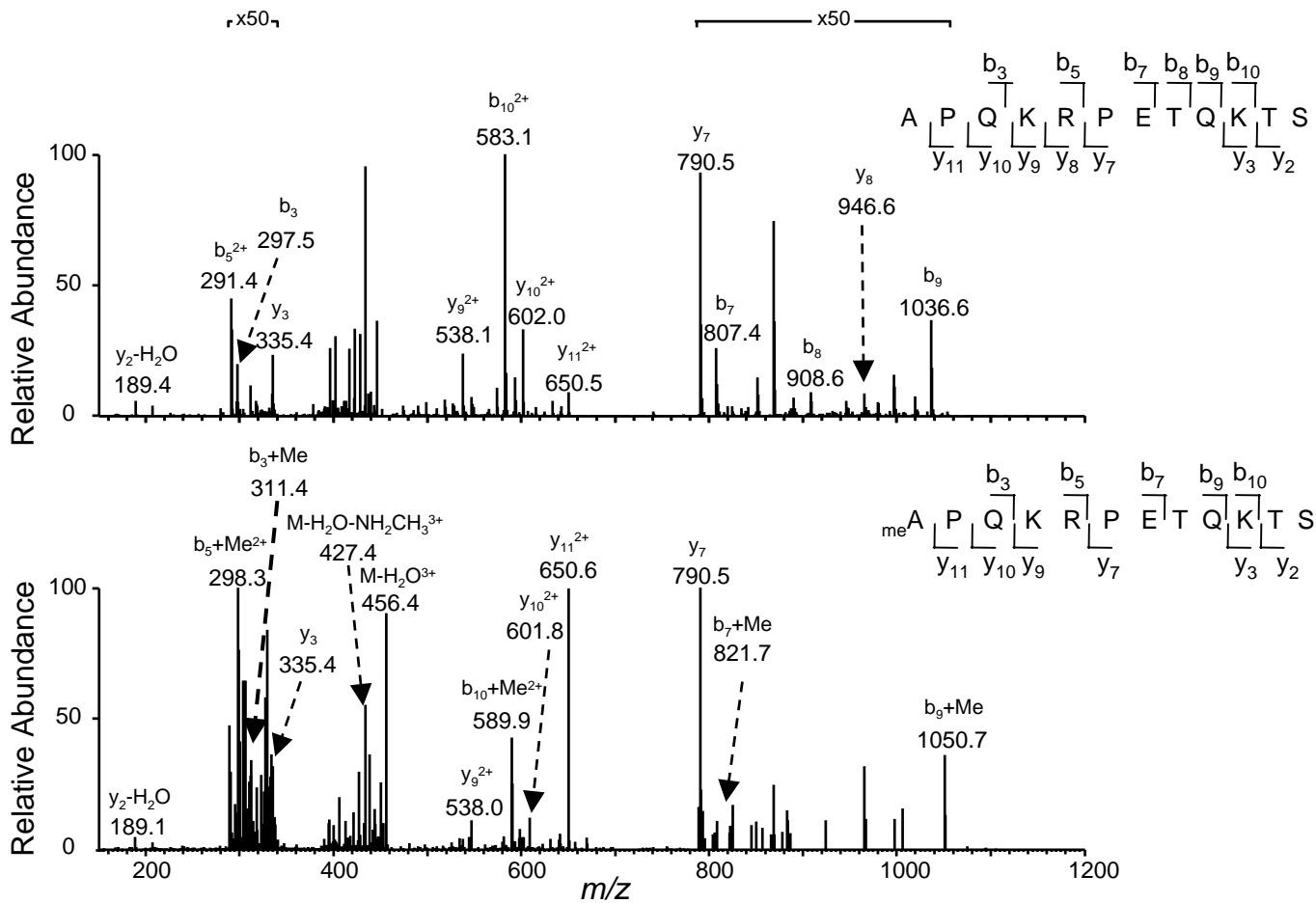
Fig. S5. ESI-MS/MS of unmodified and monomethylated forms of the peptide
$_1$APQKRPETQKTS$_{12}$. Certain regions of the spectrum were amplified to visualize better
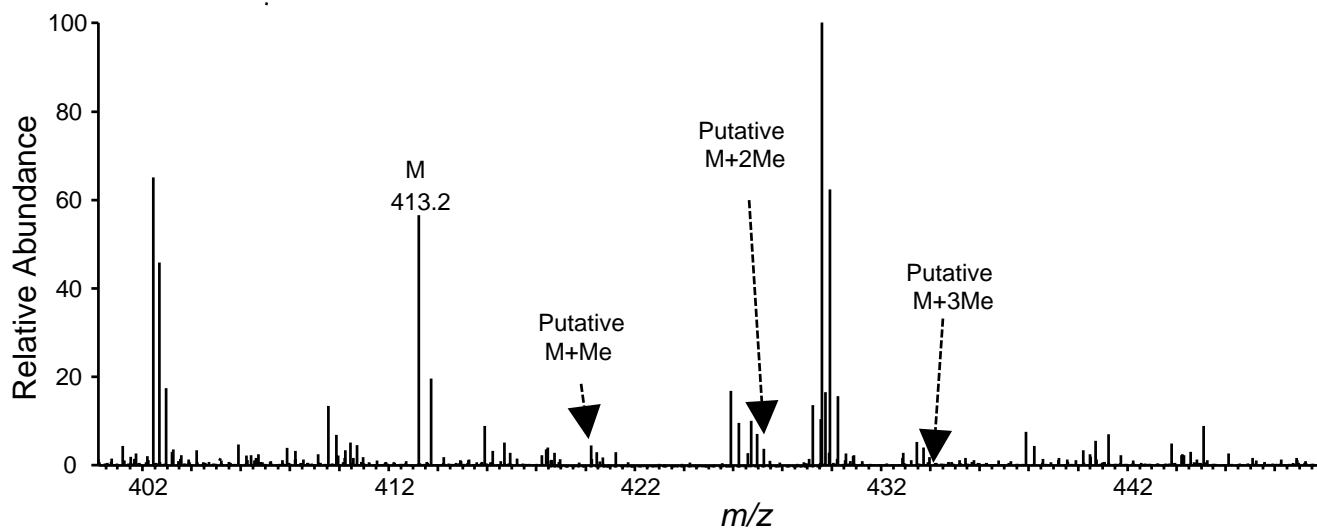the peaks for some fragment ions.

Fig. S6. ESI-MS of unmodified forms of the peptide $_1$APQKRPE$_7$.