**Analysis of isotopic labeling in peptide fragments by tandem mass spectrometry**

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**File S7: Fragment Abundances Contribute to Variability**

The relative abundances for three fragments from the same peptide obtained from 13C-labeled soybean protein were measured in multiple scan events (*m*/*z* 990.5, n=3). Greater fragment ion intensities resulted in improved precision, as indicated by reduced standard deviations for y adducts consistent with previous findings.



