Supplemental Figures and Legends

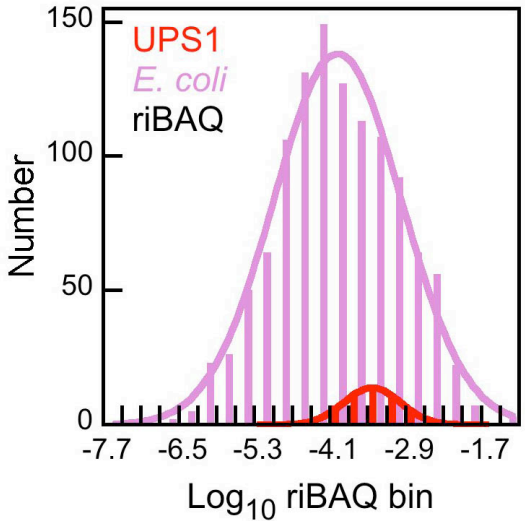

Figure S1. Distribution of UPS1 and *E. coli* riBAQ values. The UPS1 data are replotted from Fig. 2A. The peaks for Gaussian fits were $\log_{10}$ riBAQ of -3.88 and -3.22 (UPS1 proteins); the *E. coli* data did not appear normally distributed, however, with greater representation by high abundance proteins.

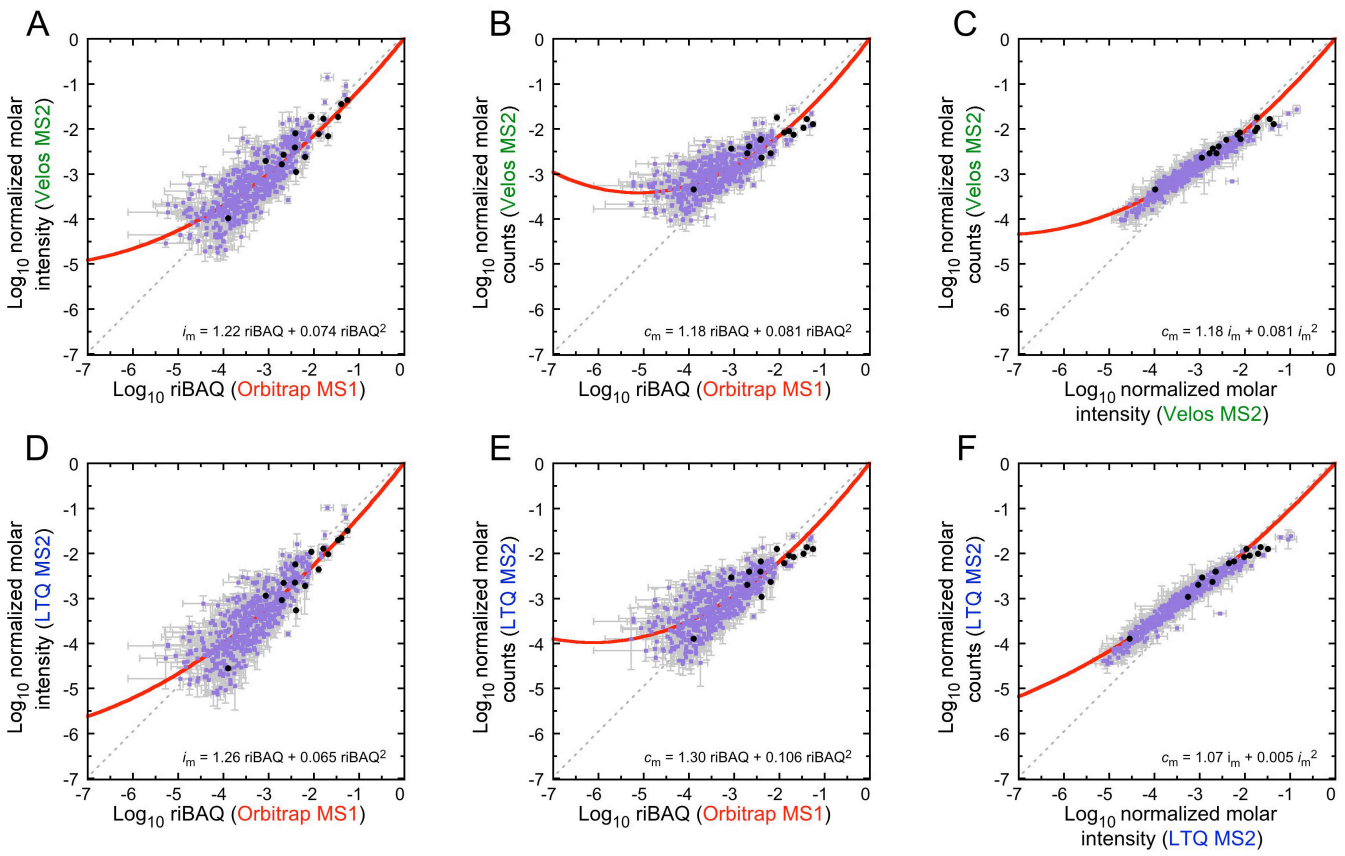

Figure S2. Comparison of label-free quantitation of UPS2 and *E. coli* proteins on the Velos and LTQ mass spectrometers: comparison to Orbitrap riBAQ. Lavender points, *E. coli* proteins; black points, UPS2 proteins. Mean ± SD is indicated for each; fits are second-order polynomials with equations indicated. (A) riBAQ and Velos normalized molar intensity. (B) riBAQ and Velos normalized molar counts. (C) Velos normalized molar intensity and normalized molar counts. (D) riBAQ and LTQ normalized molar intensity. (E) riBAQ and LTQ normalized molar counts. (F) LTQ normalized molar intensity and normalized molar counts.

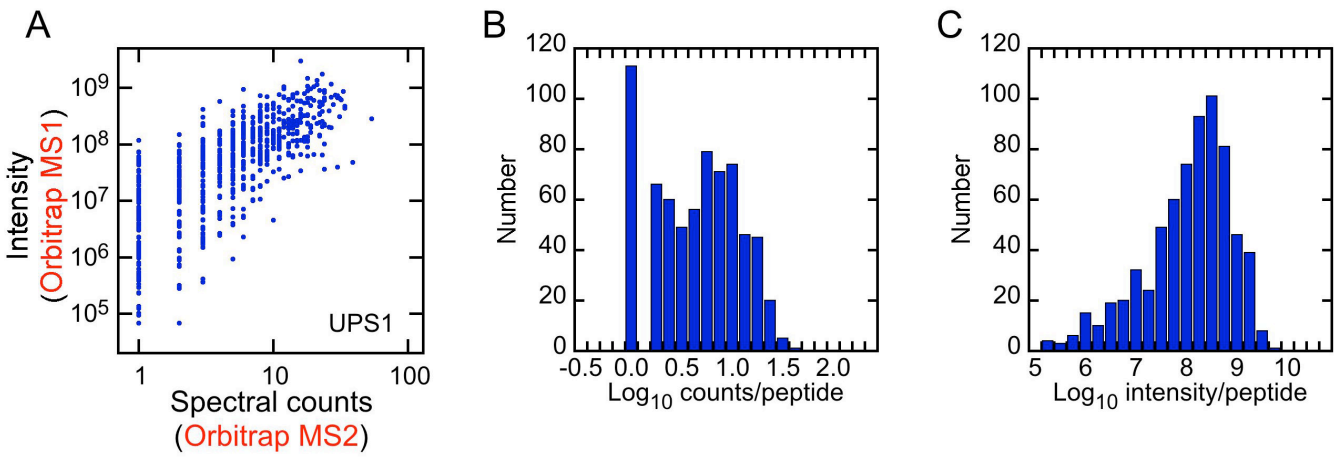

Figure S3. Distribution of spectral counts and intensities from Orbitrap experiments. (A) Relationship between the number of times a UPS1 peptide was identified in MS2 scans and the MS1 intensity of the peptide. (B) Distribution of $\log_{10}$ spectral count frequency of UPS1 peptides. (C) Distribution of $\log_{10}$ intensity per UPS1 peptide frequency.