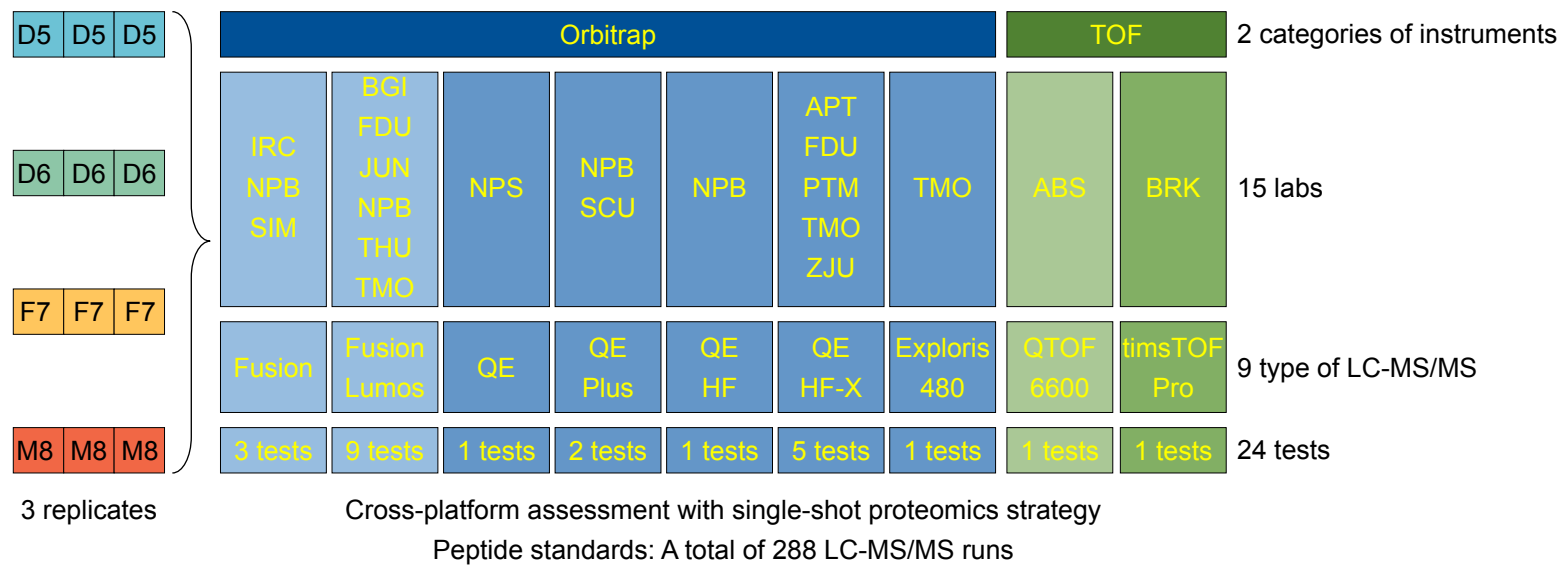
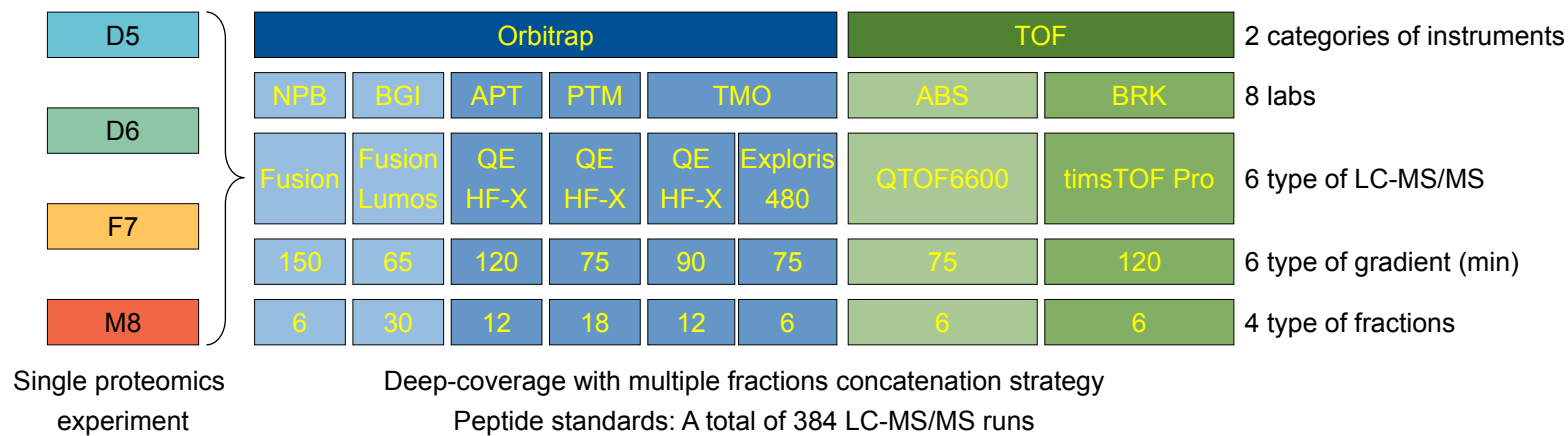


Fig. S1

A



B



C

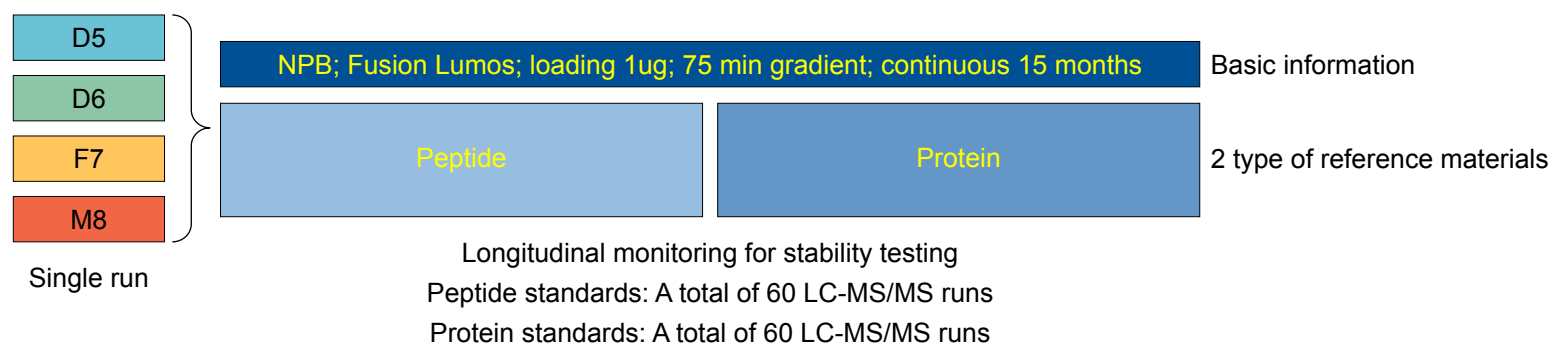


Fig. S2

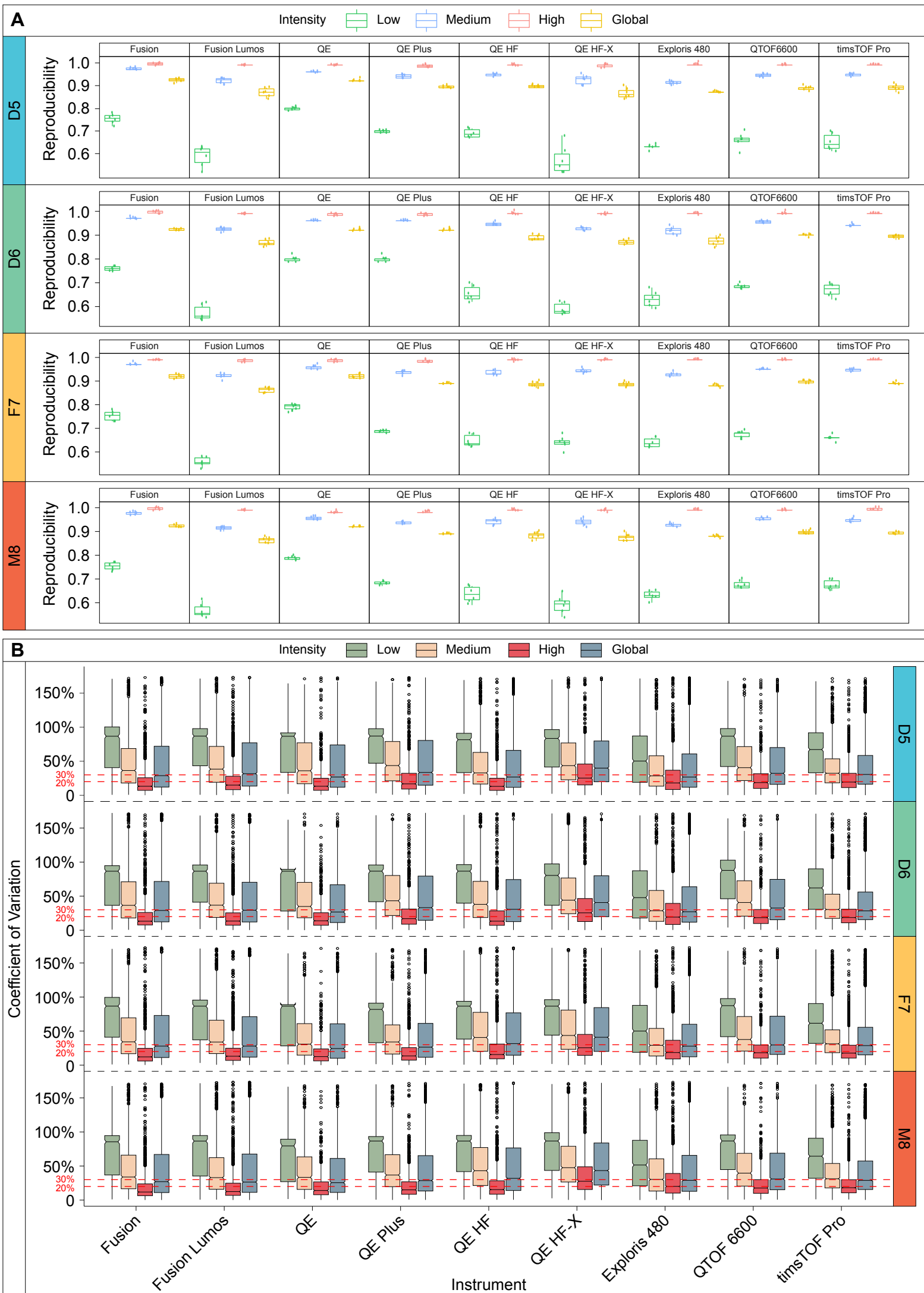


Fig. S3

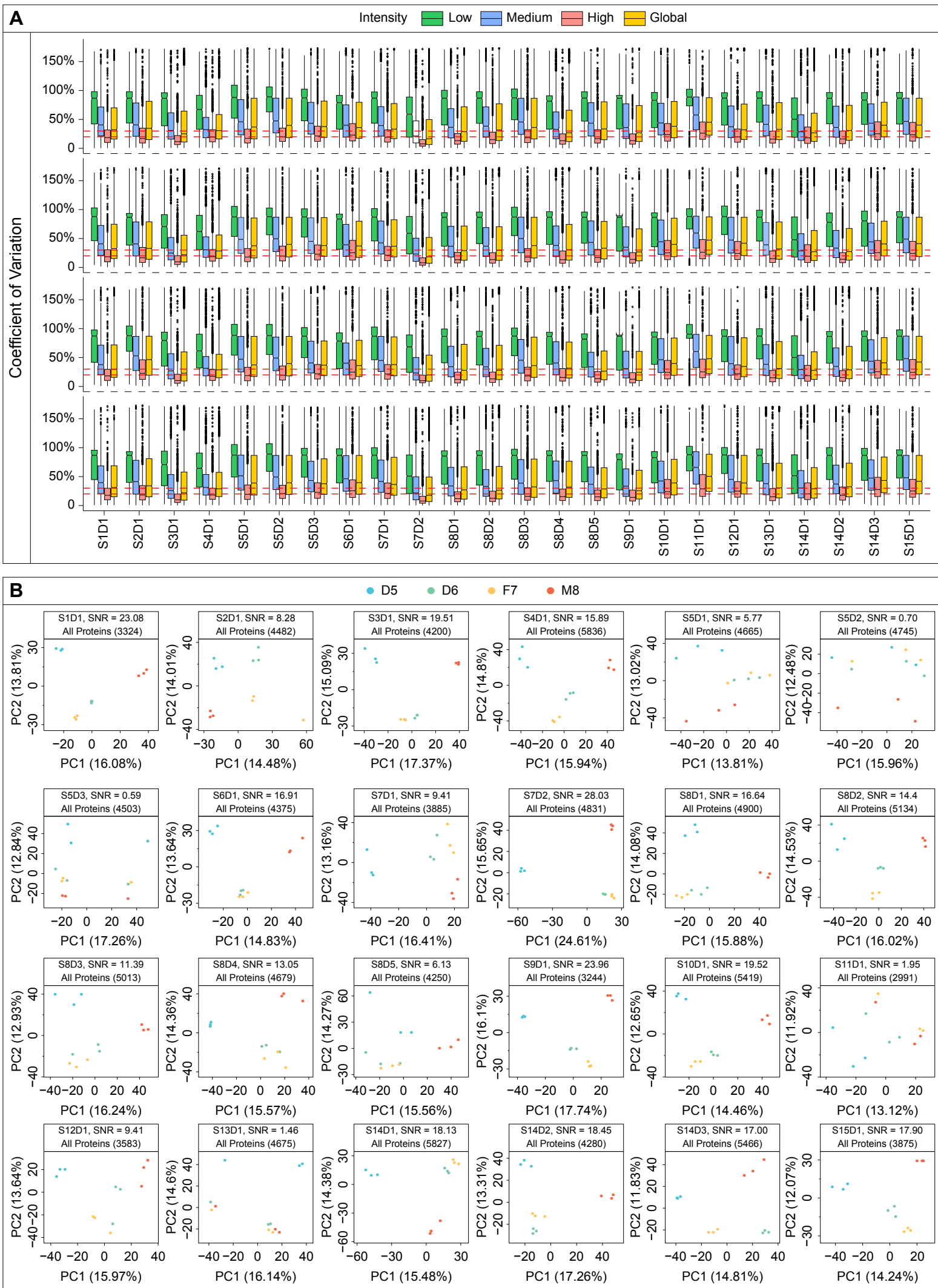


Fig. S4

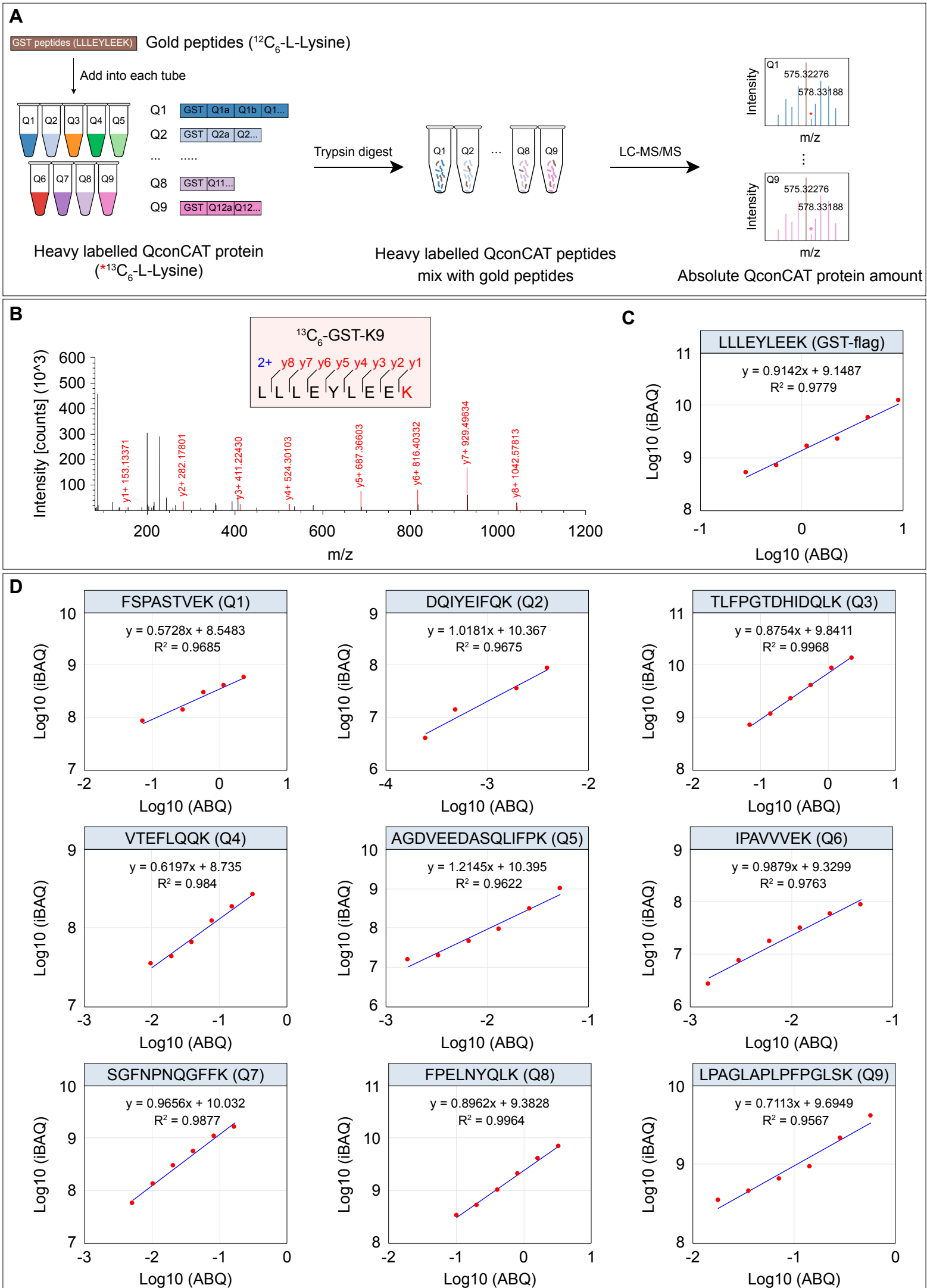


Fig. S5

A

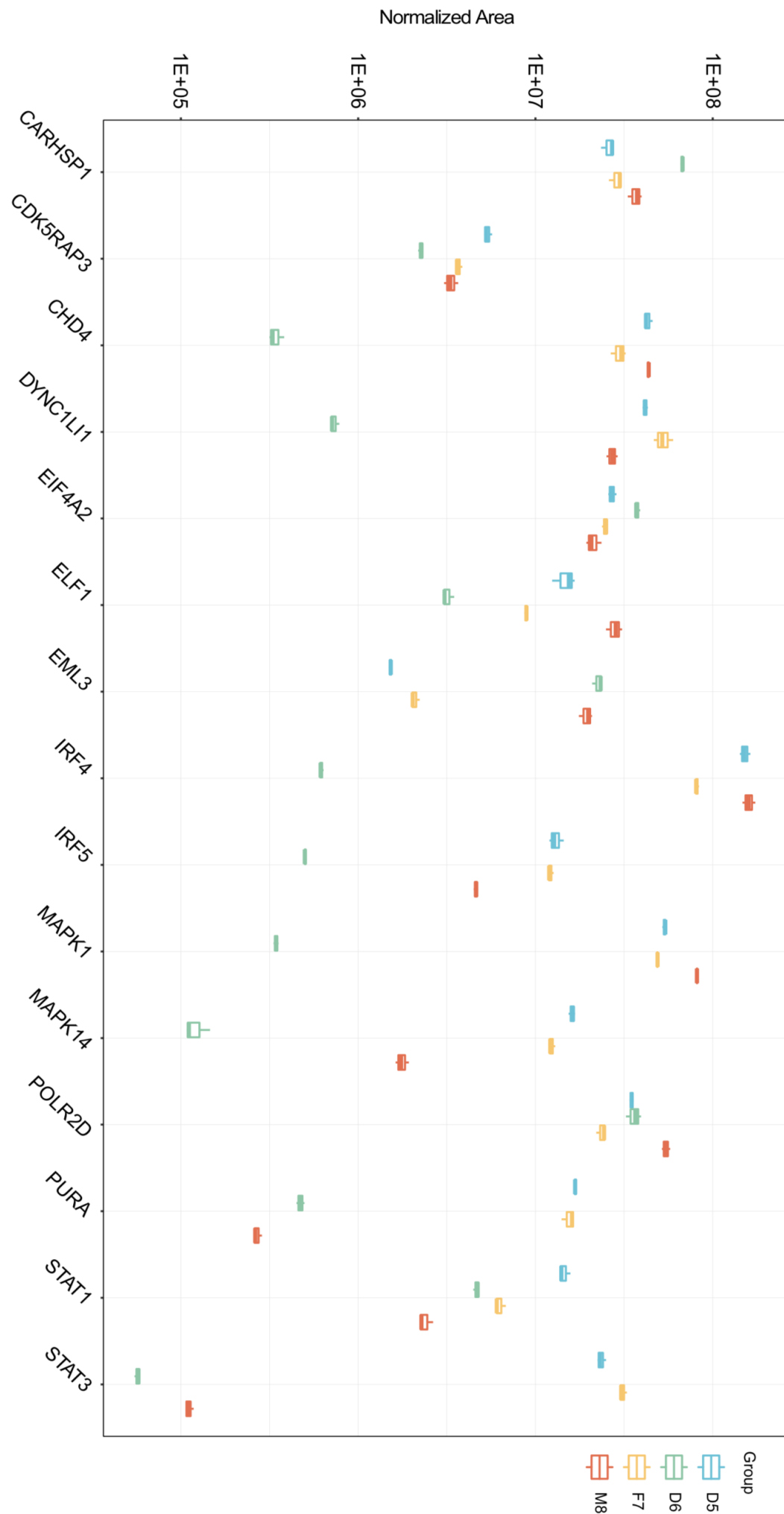


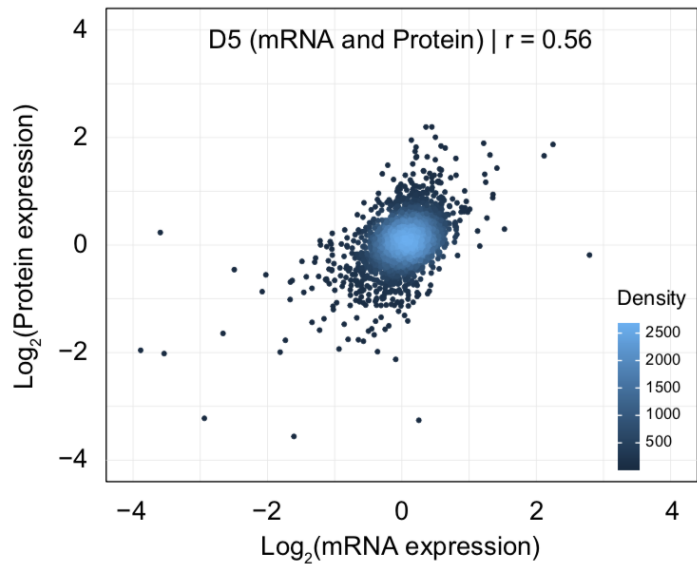
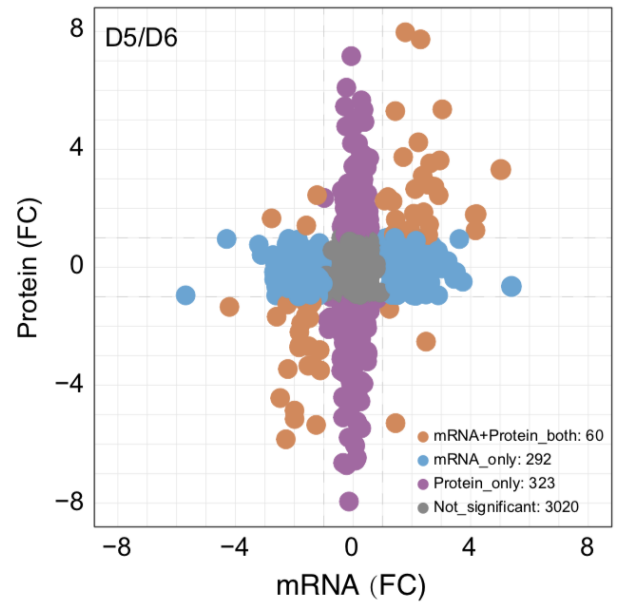
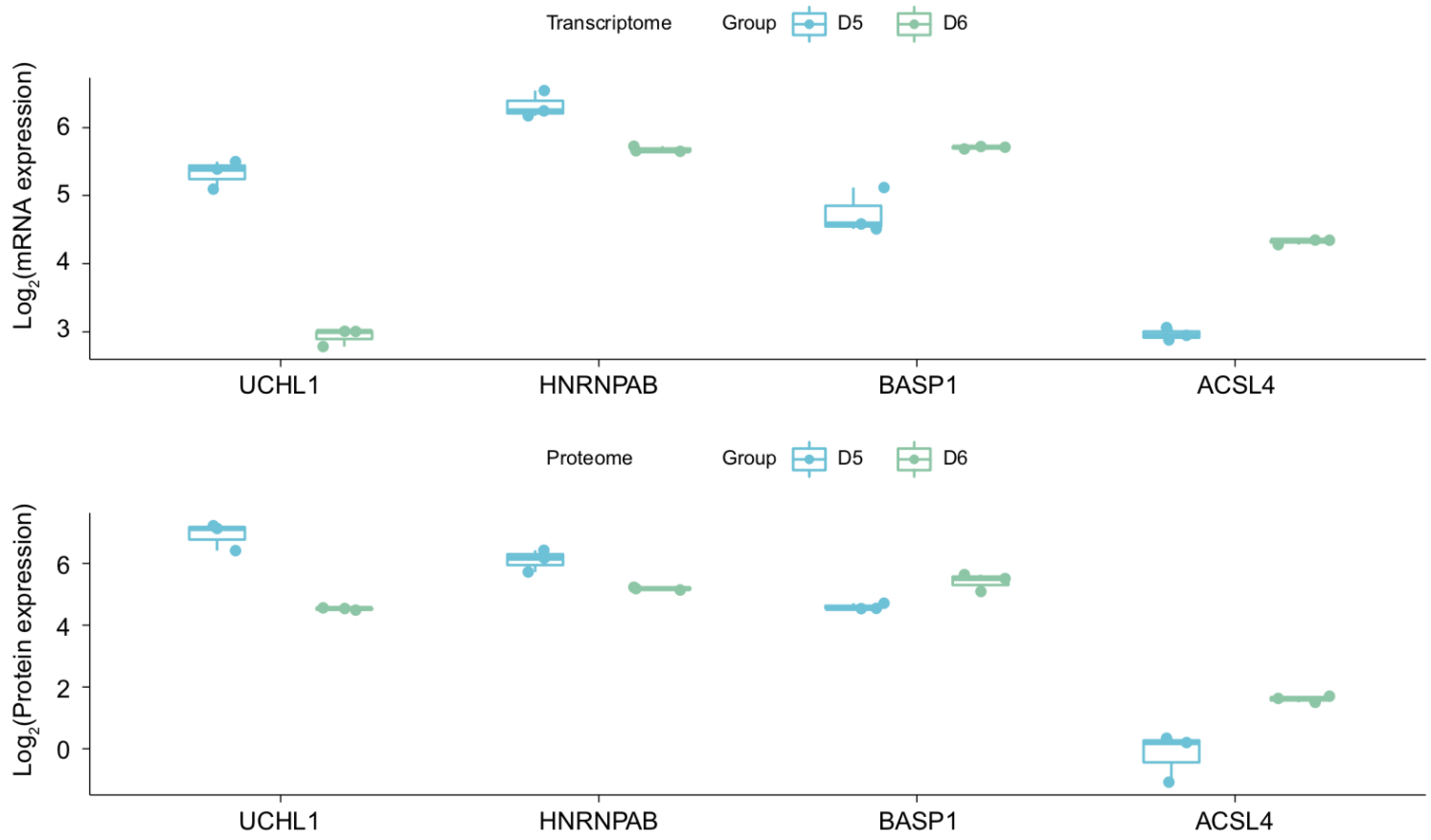
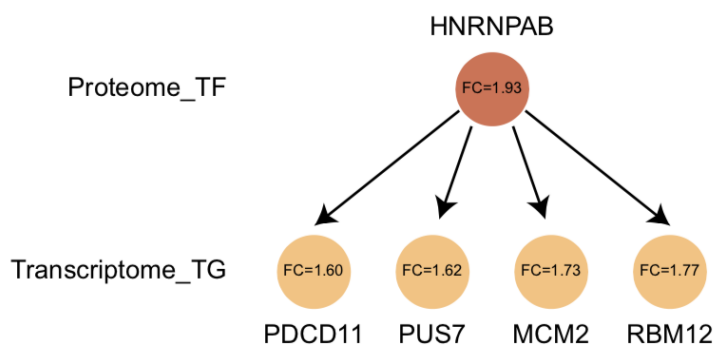
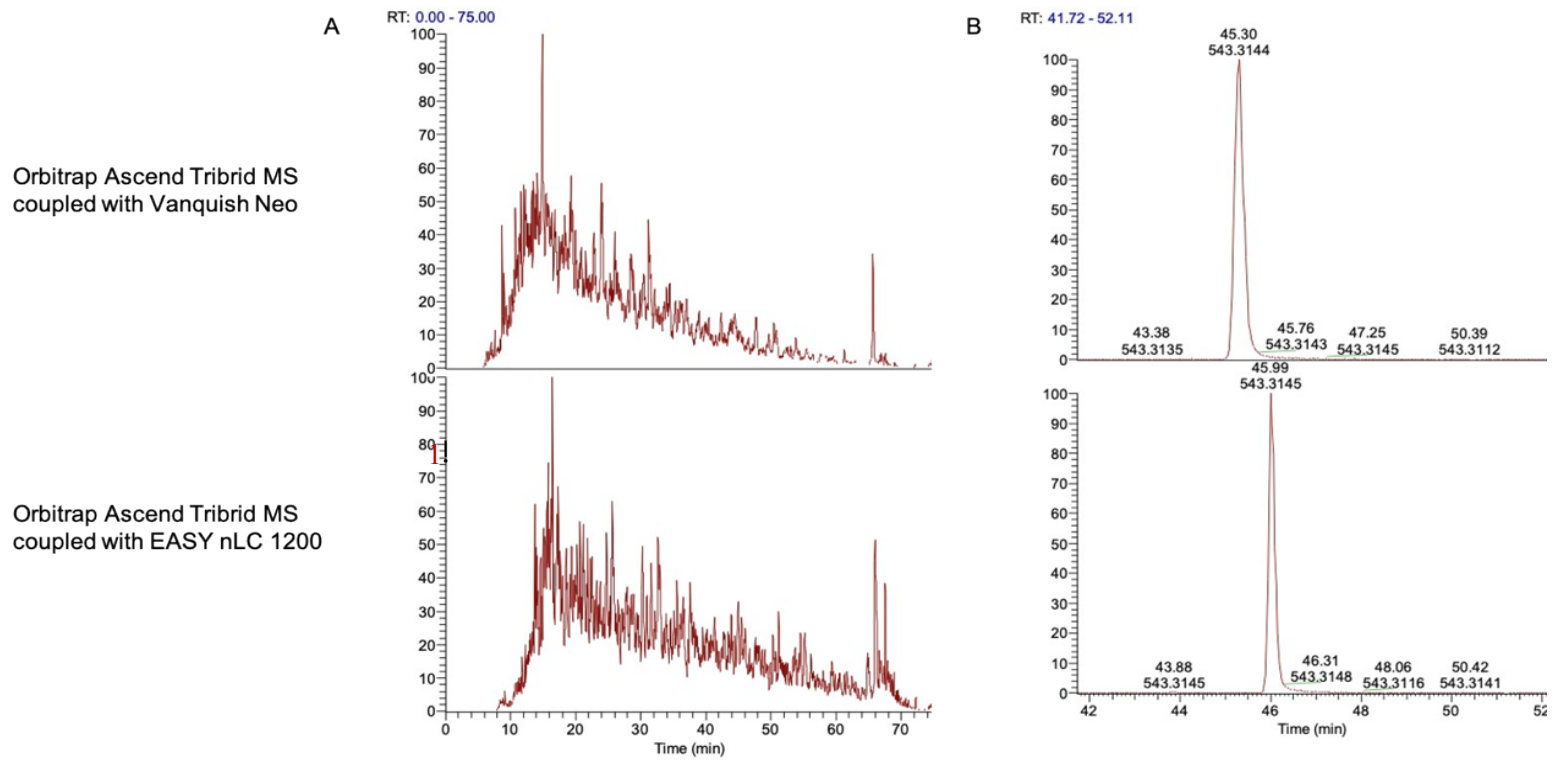
Fig. S6**A****B****C****D**

Fig. S7



Supplemental figure legends

Fig. S1 | MS files (N = 792) used to generate standard reference material datasets. **A**, Cross-platform assessment with the single-shot proteomics strategy (peptide standards with a total of 288 LC-MS/MS runs). **B**, Deep coverage with a multiple fraction concatenation strategy (peptide standards with a total of 384 LC-MS/MS runs). **C**, Longitudinal monitoring for stability testing (peptide standards: total of 60 LC-MS/MS runs; protein standards: total of 60 LC-MS/MS runs).

Fig. S2 | Quantitative reproducibility and variation analysis among nine conventional instruments. **A**, Reproducibility of detected proteins from a quantitative perspective (low-intensity, medium-intensity, high-intensity, and global groups) analyzed by nine conventional instruments in each sample of the Quartet. **B**, Quantitative variation of each sample of the Quartet in the low-intensity, medium-intensity, high-intensity, and global groups of nine conventional instruments (to facilitate overall comparison, the CVs of D5 among nine conventional instruments are repeated here).

Fig. S3 | Quantitative evaluation based on CVs and SNR. **A**, Quantitative variation of each sample of the Quartet in the low-intensity, medium-intensity, high-intensity, and global groups of 24 datasets produced by nine types of mass spectrometers across 15 laboratories (to facilitate overall comparison, the CVs of D5 among S8D2 and S3D1 are repeated here). **B**, Principal component analysis and SNR scoring of all proteins groups from 24 datasets produced by nine types of mass spectrometers across 15 laboratories (to facilitate overall comparison, the principal component analysis and SNR scoring in S8D2 and S3D1 are also repeated here).

Fig. S4 | Absolute quantification of the QconCAT proteins. **A**, Workflows for absolute quantification (ABQ) of the QconCAT proteins. **B**, MS/MS spectra (left panel) and dilution response curve (right panel) of the C13-labeled gold peptide (LLLEYLEEK) in GST-flag of the QconCAT proteins. **C**, Dilution response curve of the C13-labeled representative anchor peptide in every QconCAT protein.

Fig. S5 | Boxplot showing the expression of "anchor" proteins validated by PRM assay.

Fig. S6 | Analysis of transcriptome and proteome. **A**, the Pearson correlation coefficient between the transcriptome and proteome of the D5 sample is 0.56, which is consistent with previous research

findings ($r=0.36\sim0.60$). **B**, Gene products (GPs) expression pattern in D5 vs D6 at the transcriptome and proteome level. A total of 3,695 GPs were identified in D5 and D6, 292 GPs and 323 GPs were differentially expressed between D5 and D6, at the transcriptome and proteome levels, respectively. In which, 60 GPs were significantly differentially expressed on both transcriptome and proteome levels. **C**, The expression of UCHL1, HNRNPAB, BASP1, and ACSL4 in D5 and D6 at the transcriptome and proteome level (transcriptome level, top panel; proteome level, bottom panel). **D**, HNRNPAB and its target genes (PDCD11, PUS7, MCM2 and RBM12) in D5 sample were upregulated on both proteome and transcriptome levels, respectively.

Fig. S7 | Two different types of chromatographic instruments coupled with Ascend MS instrument for the detection of Quartet D5 samples. **A**, The total ion chromatogram (TIC) of the detection results of two different types of chromatographic instruments. **B**, The RT of the peptide of two different types of chromatographic instruments.