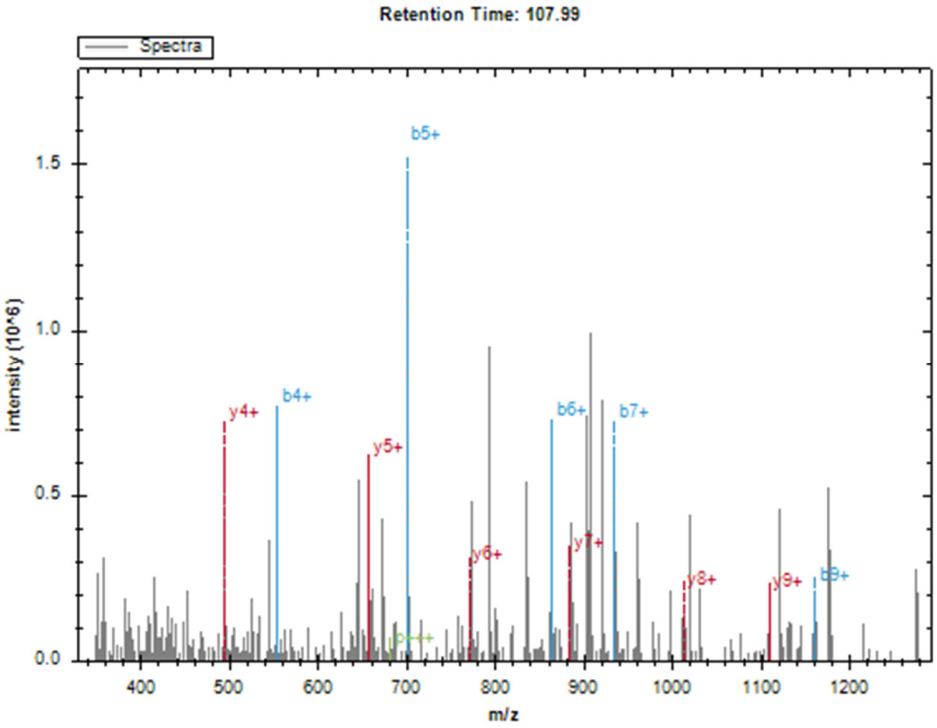
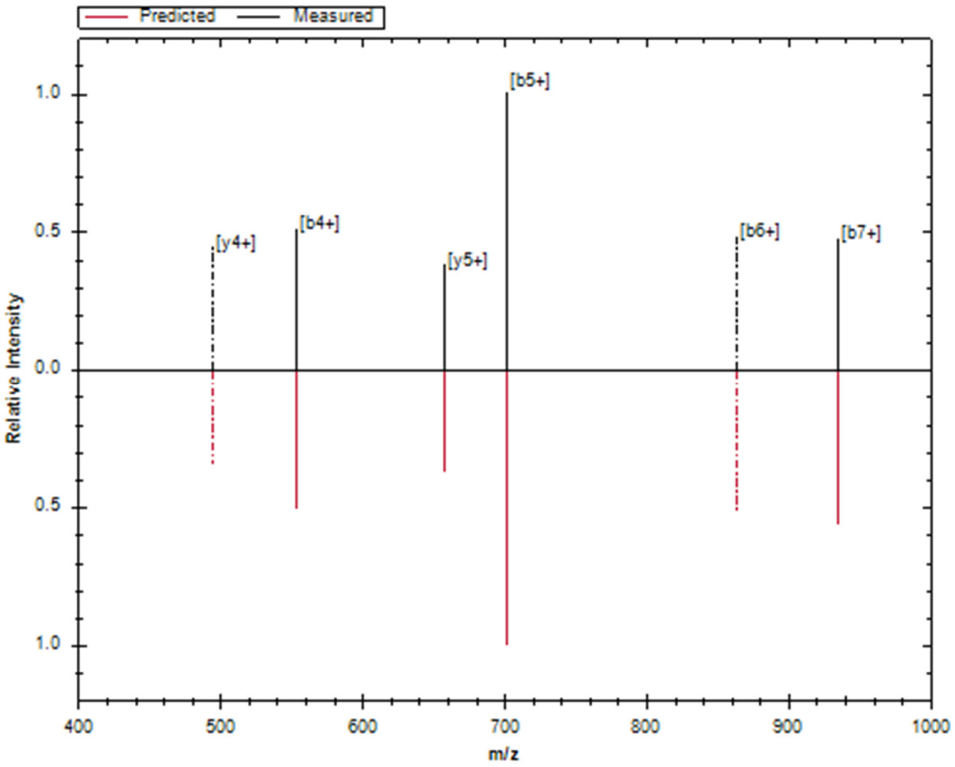
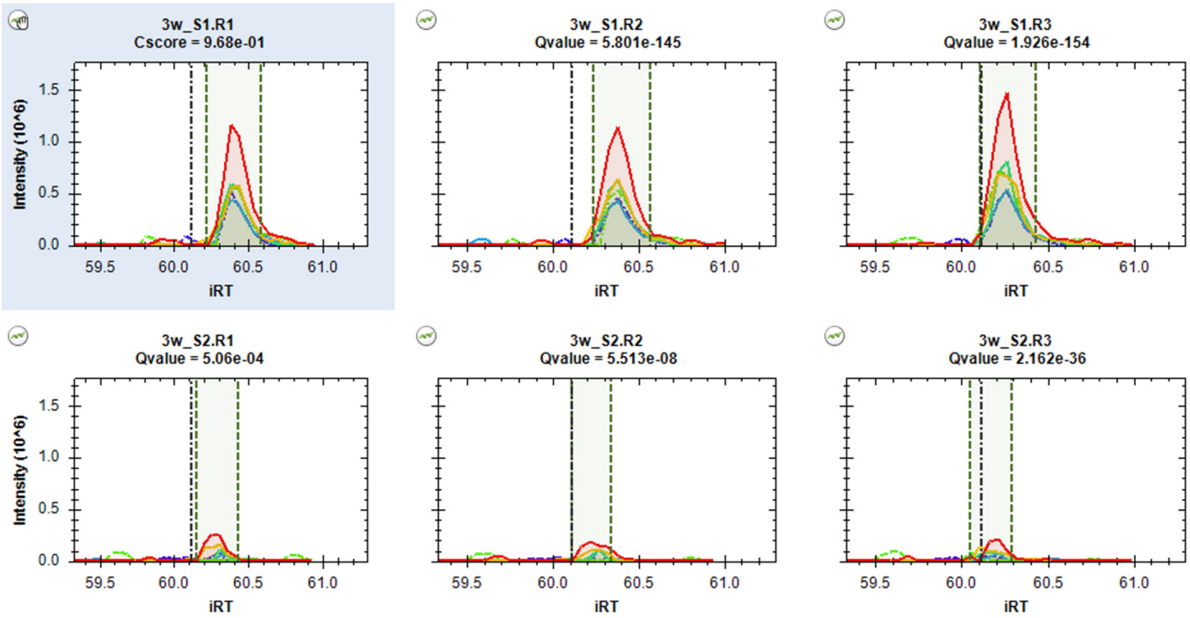
Supplementary material 1, Example shows how DIA-MS identified and quantified one peptide of ALBU_BOVIN.

1). DIA-MS spectra matching with spectral library and identified a peptide sequence RHPYFYAPELLYYANK (z = 3+) which belongs to the protein ALBU-BOVIN.

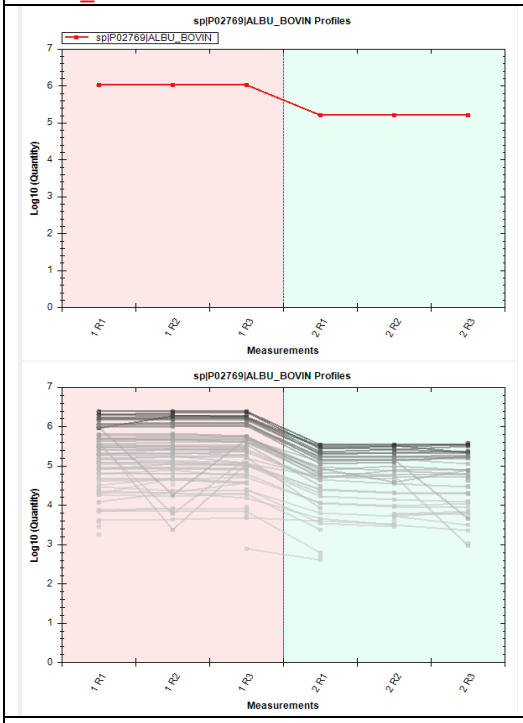
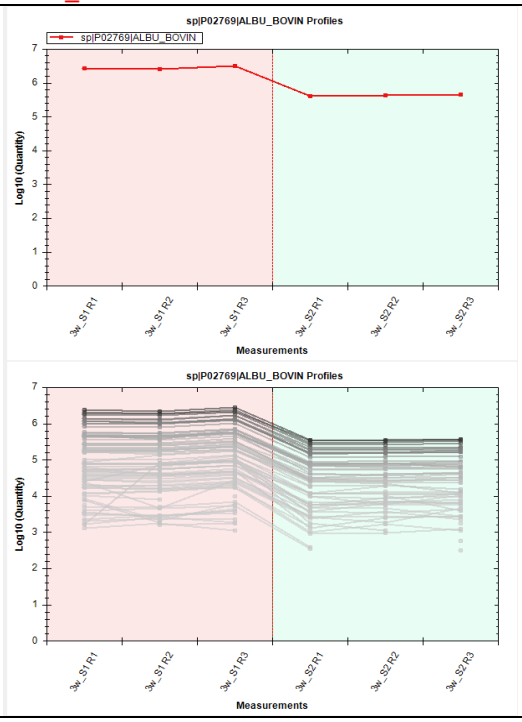
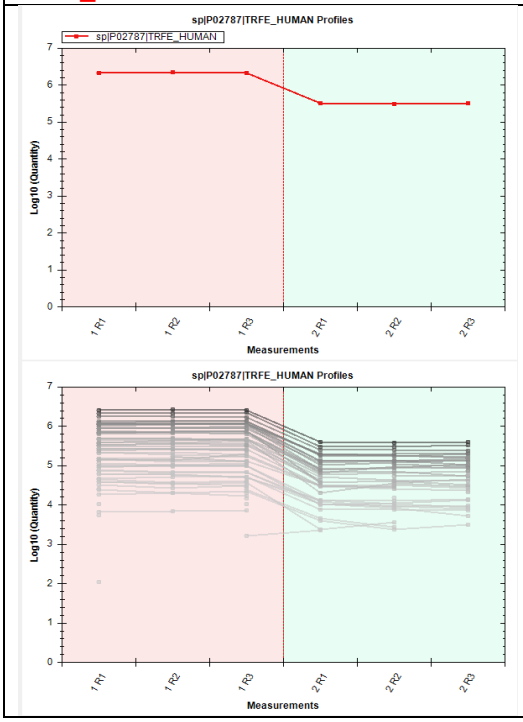
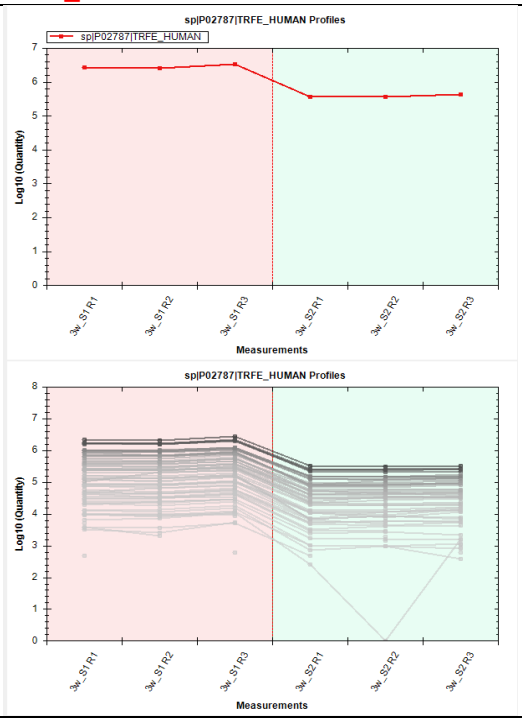




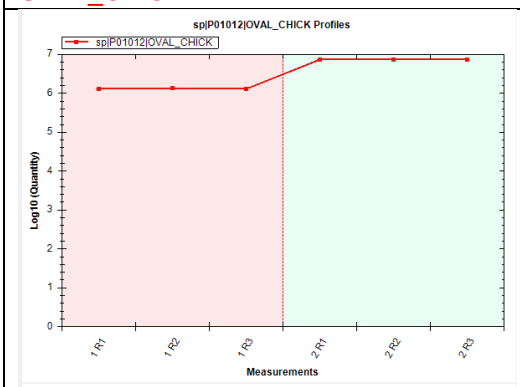
2). MS2 XIC across all runs to generate quantitation information

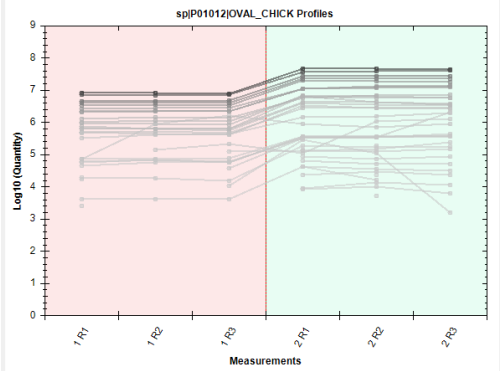


Supplementary material 2. Quantitation of spike-in proteins using cDIA-MS and cGPF-DIA-MS. The upper figure indicates protein quantitation, and the lower panel indicates peptide quantitation for the protein (the dot in the same line represents a same analyte).

Protein quantitation using cDIA-MS	Protein quantitation using cGPF-DIA-MS
ALBU_BOVIN	ALBU_BOVIN
	
TRFE_HUMAN	TRFE_HUMAN
	

OVAL_CHICK





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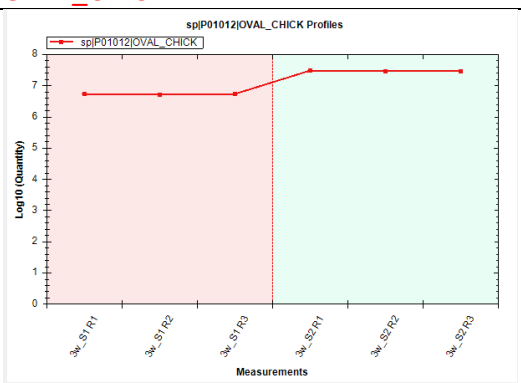
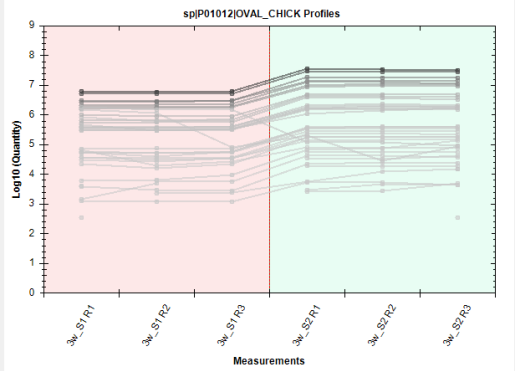
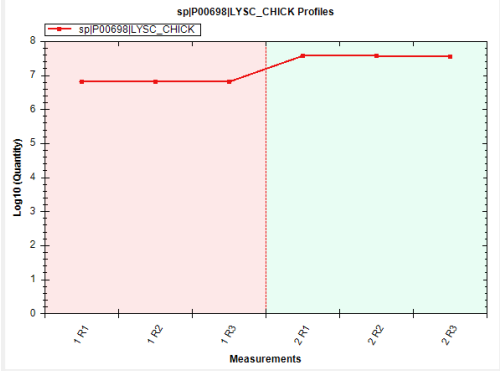
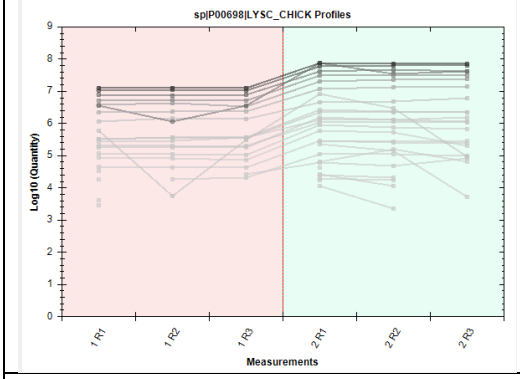




LYSC__CHICK





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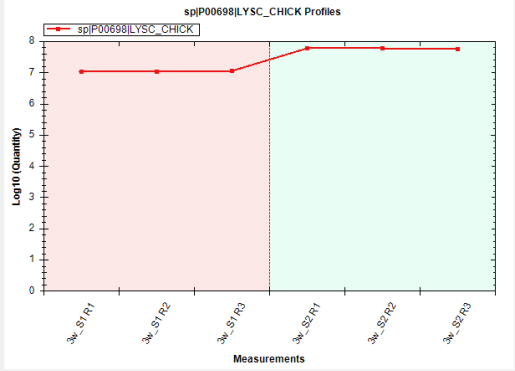
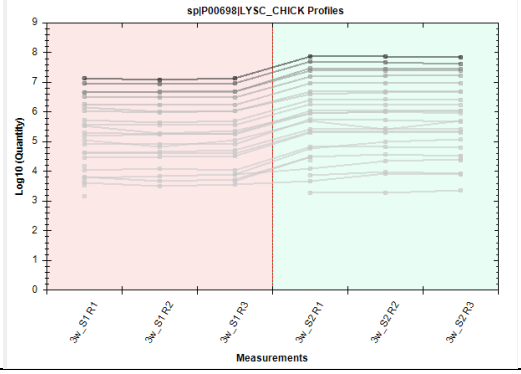
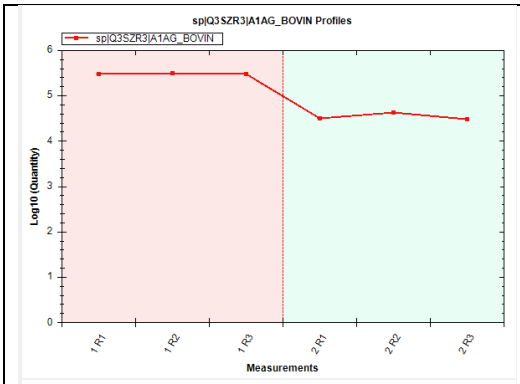
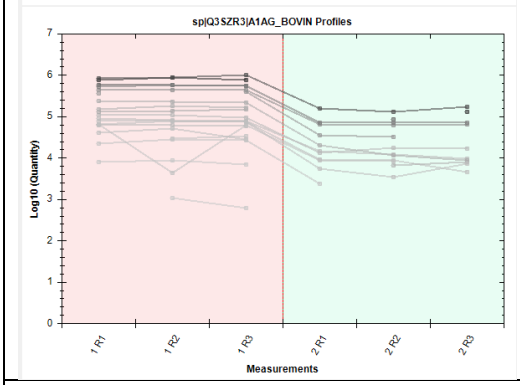


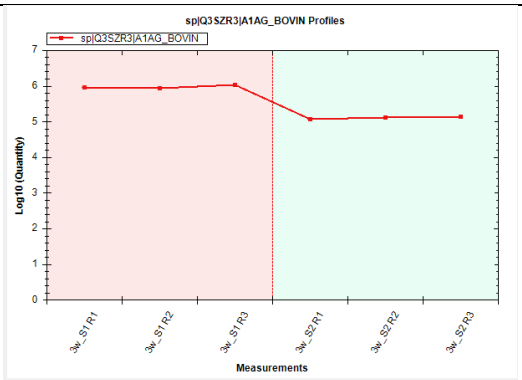


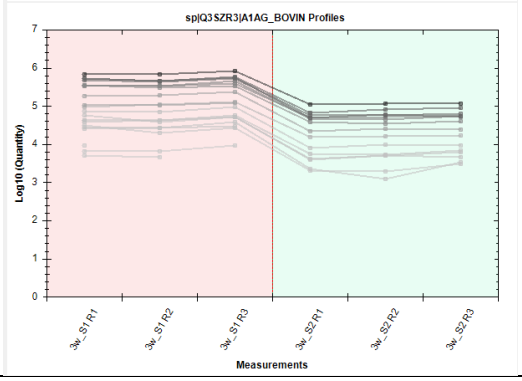
A1AG_BOVIN

A1AG_BOVIN





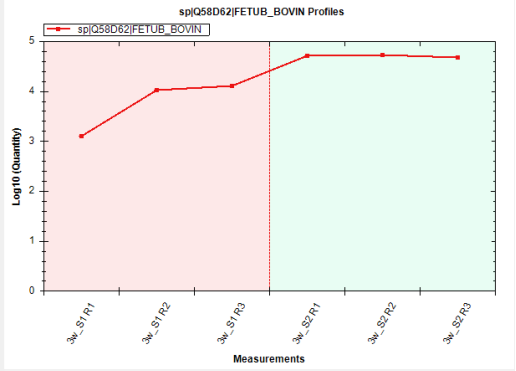


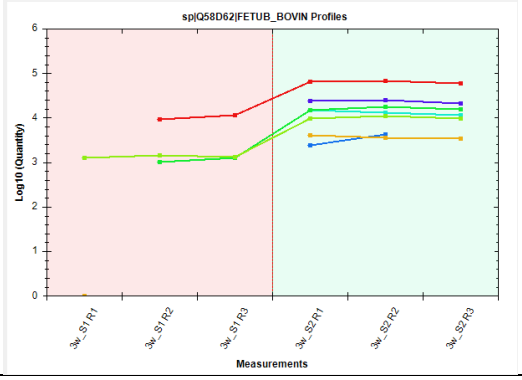
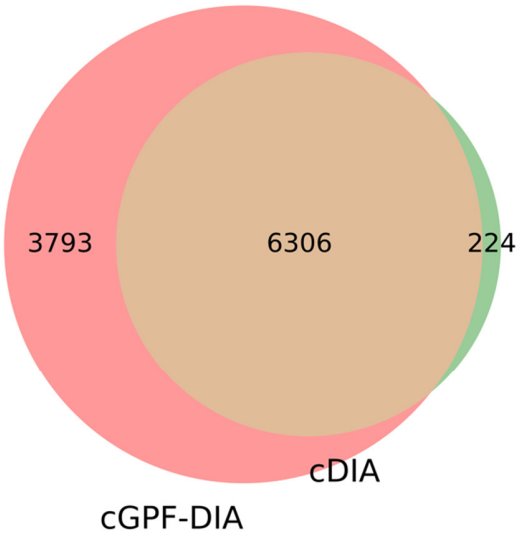


FETUB_BOVIN

FETUB_BOVIN

Not detected as significant change





Supplementary material 3, venn diagram shows the protein identified from cGPF-DIA-MS and cDIA-MS analysis.