

# Supplementary Information

## Site-Specific Quantification of Protein Ubiquitination on MS2 Fragment Ion Level via Isobaric Peptide Labeling

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Table S-1. SILAC labeling efficiency of MCF-7 cells.

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Excel S-2. Peptides identified in supernatant proteome.

Excel S-3. K-ε-GG peptides quantified in ubiquitinated proteome.

Excel S-4. Peptides quantified in supernatant proteome.

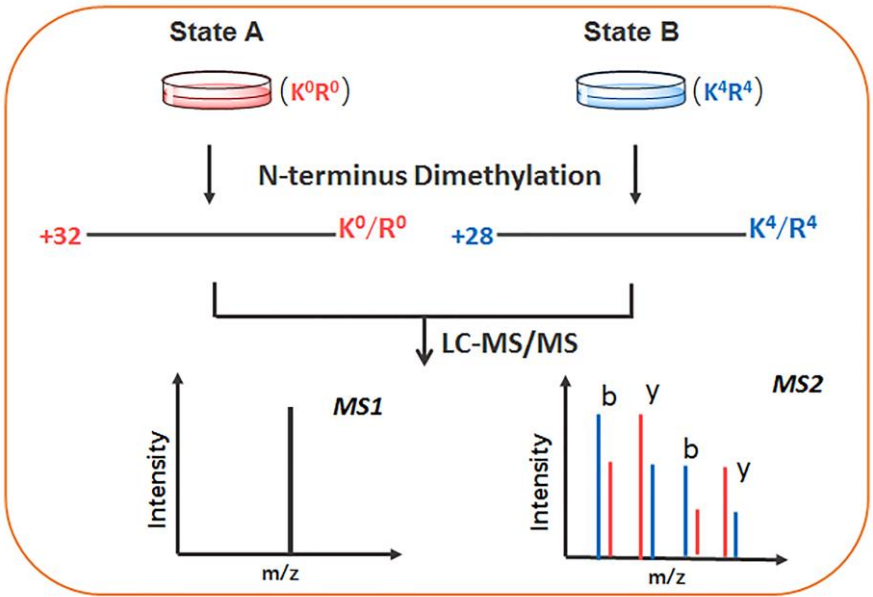


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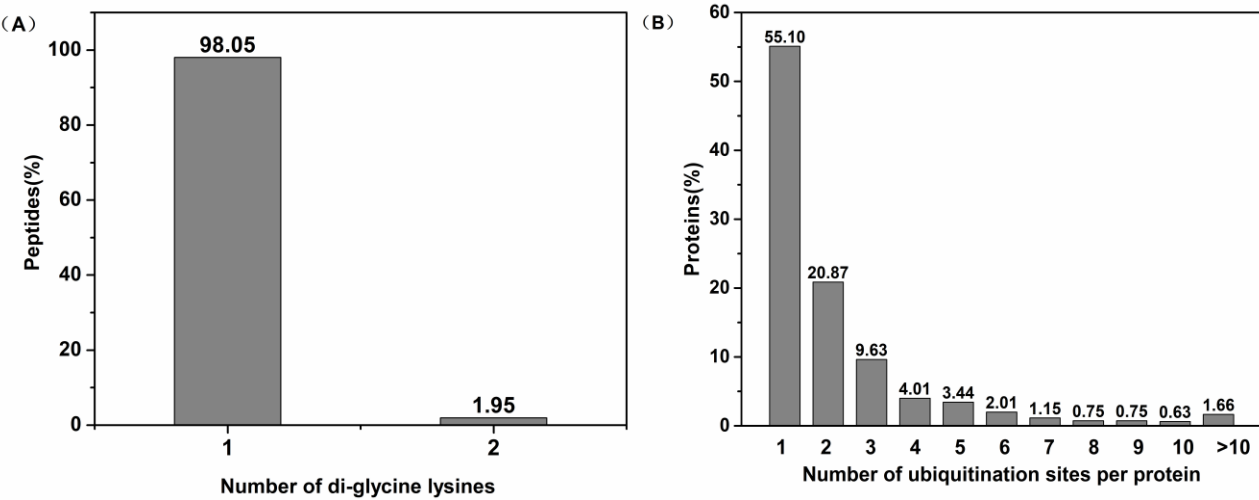


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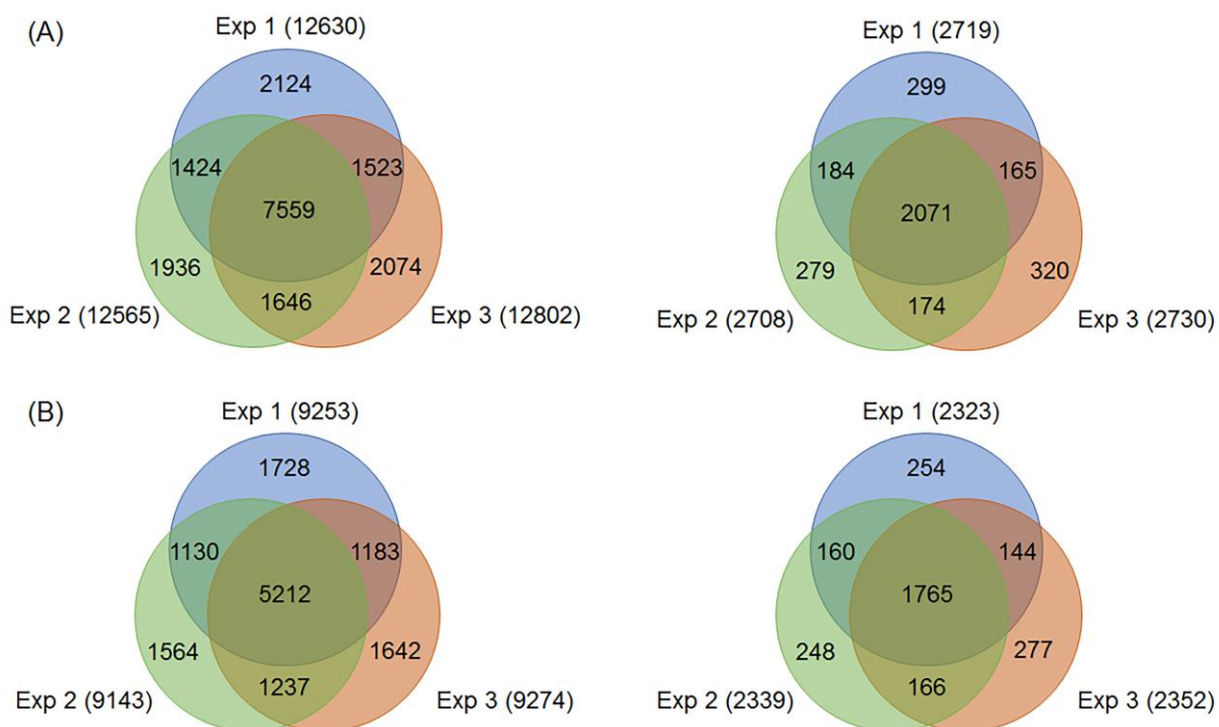


Figure S-3 Identification and quantification of supernatant proteome. Venn diagram showing the overlap of identified peptides (A, left) and proteins (A, right), quantified peptides (B, left) and proteins (B, right).



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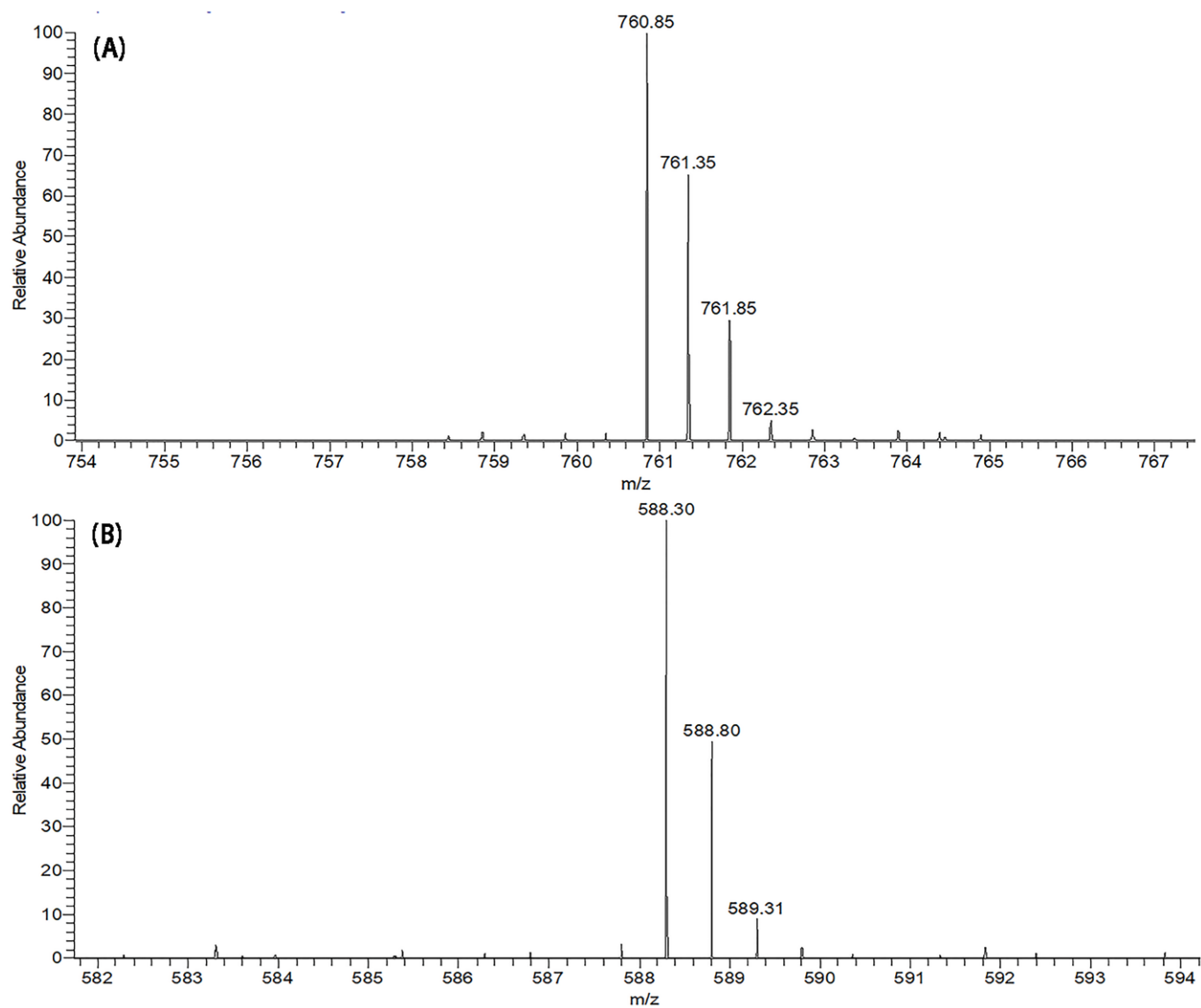


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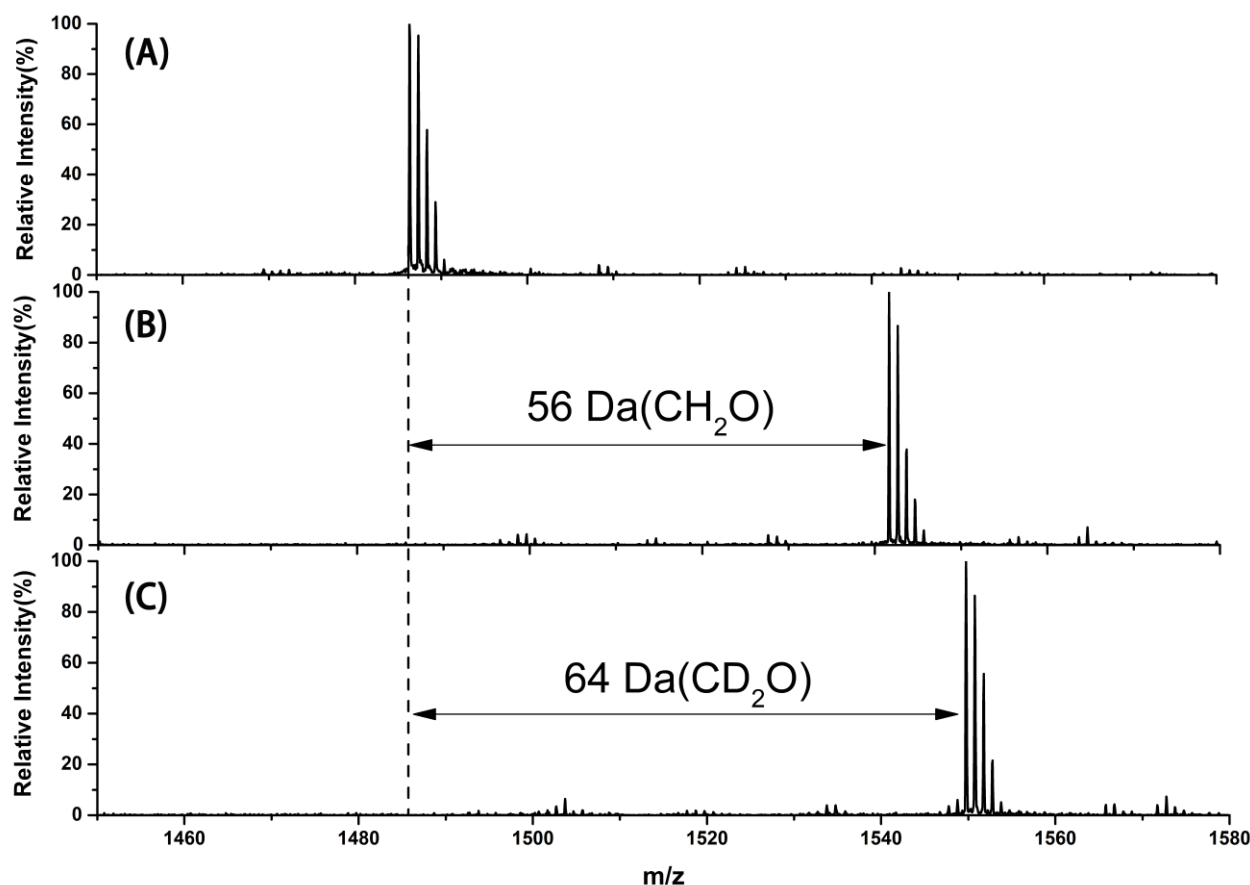


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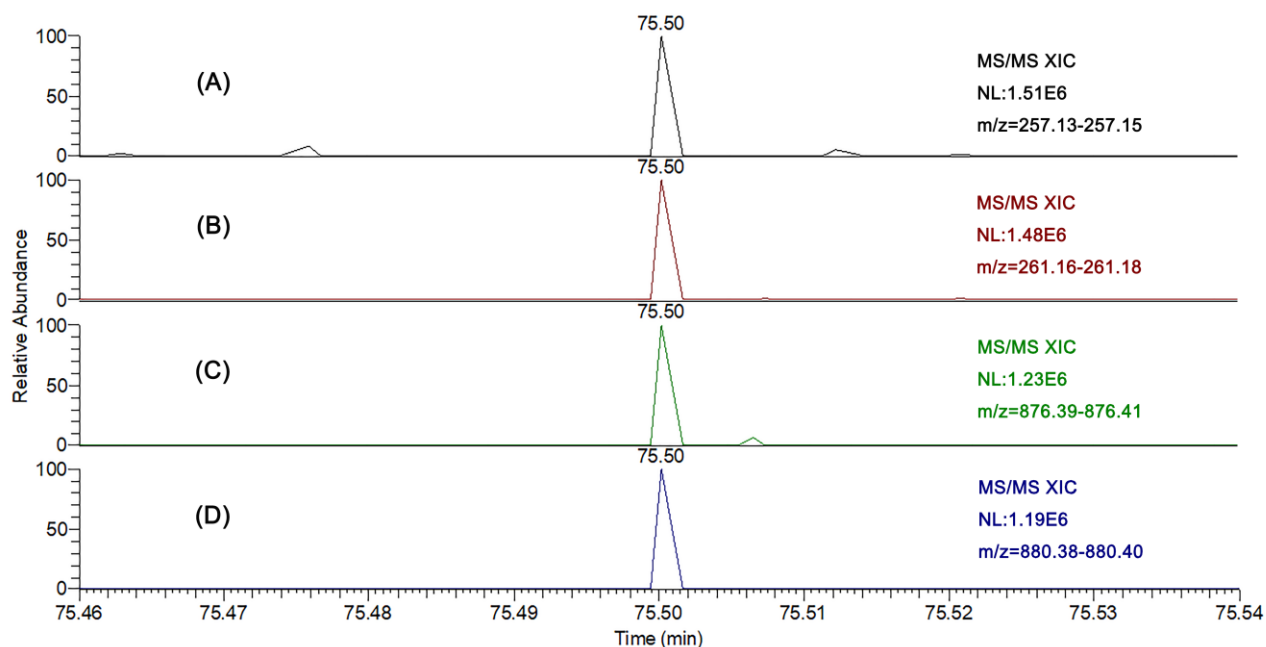


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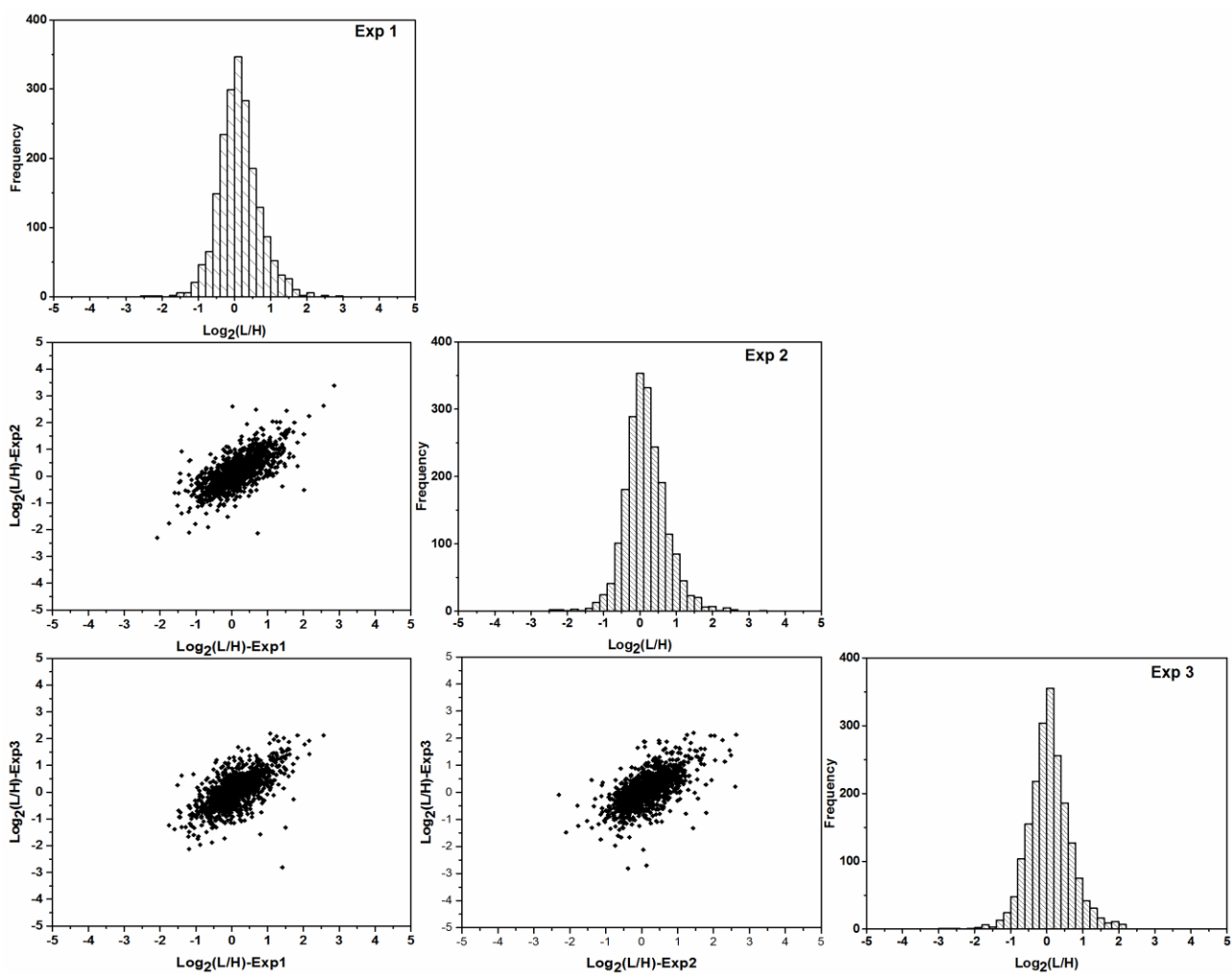


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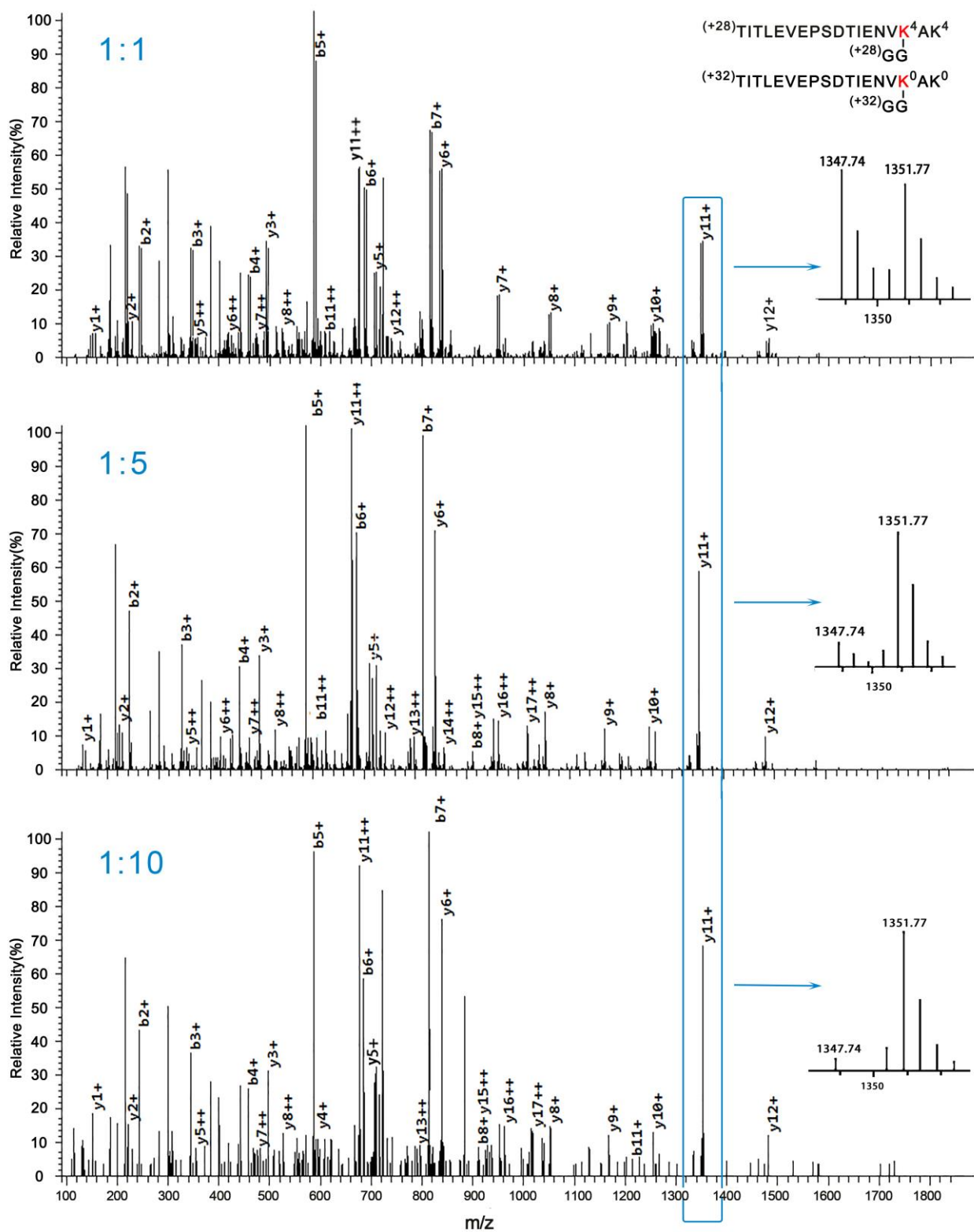


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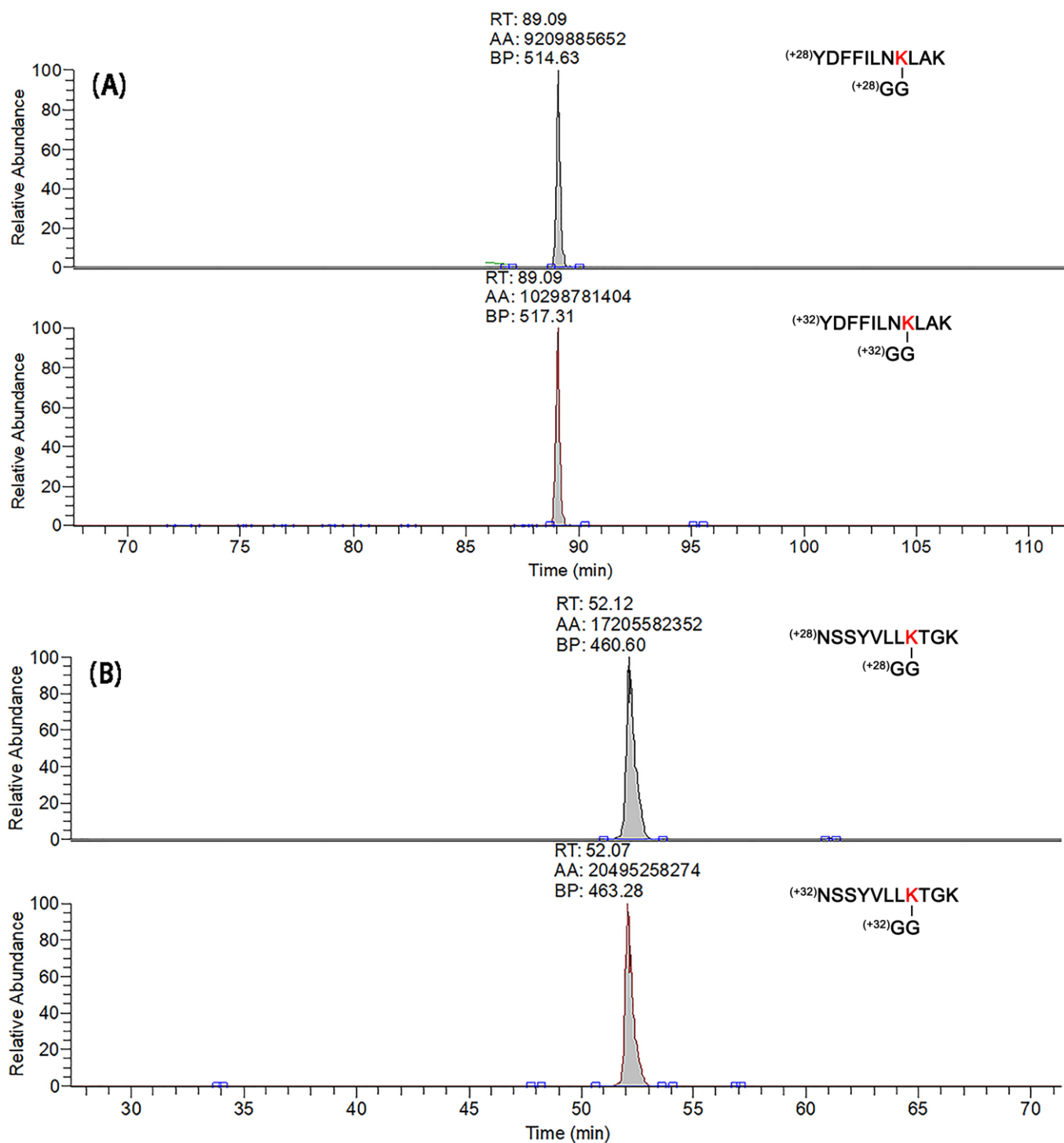


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Table S-1. SILAC labeling efficiency of MCF-7 cells.

Identified peptides	Identified peptides with R <sup>4</sup> or K <sup>4</sup>	Labeled ratio (%)
12147	12088	99.5

Table S-2. Labeling efficiency of peptide N-terminus dimethylation.

	Labeled N-terminus	Non-labeled N-terminus	Labeled ratio (%)
Supernatant 1	11857	80	99.3
Supernatant 2	11797	71	99.4
Supernatant 3	12106	94	99.2
Elute 1	2381	22	99.1
Elute 2	2511	18	99.3
Elute 3	2218	21	99.1