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Supplemental figure legends

Figure S1. Venn diagram for identification of proteome and phosphoproteome at 0/2h after 0/20/80/160 (A-D) Gy irradiation.

Figure S2. Comparison of proteome and phosphoproteome identification results and quality control (A-C).

(A, B) Violin diagram shows the comparison of expression levels between (phospho)proteome sample in each irradiation state. (C) The correlation between two experiment repeats of the proteome.

Figure S3. Analysis of differently expressed proteins at each irradiation dose and time point (A-F).

Volcanic plot to show the DEPs screened by $log_2FC > 1$, FDR < 0.05. 20 Gy, 80 Gy and 160 Gy were all compared with 0 Gy at the corresponding time point.

Figure S4. Analysis of differential phosphosites at each irradiation dose and time point (A-F).

Volcanic plot to show the differential phosphosites screened by $log_2FC > 1$, FDR < 0.05. 20 Gy, 80 Gy and 160 Gy were all compared with 0 Gy at the corresponding time point.

Figure S5. A comparison of the upregulated proteins between our proteome dataset and the published datasets.

Venn diagram shows comparison with other irradiation proteomics datasets, 740 upregulated proteins were identified only in this dataset.

Figure S6. Protein domain enrichment analysis of upregulated proteins in different time points.

The time points are distinguished by different colors, and the size of the circle in the

figure indicates the number of genes with that domain.

Figure S7. Motif analysis of irradiation sensitive phosphopeptides (A-C).

Analysis of motifs upstream and downstream of differential phosphosites. Distinguish between serine (S), threonine (T) and tyrosine (Y).

Figure S8. Site disorder analysis.

Whether the phosphosites and other AA sites are located in a disordered region. Phosphosites tend to be disordered, the difference is significant (fisher exact t test, P = 3.98e-84).

Figure S1. Venn diagram for identification of proteome and phosphoproteome at 0/2h after 0/20/80/160 (A-D) Gy irradiation.

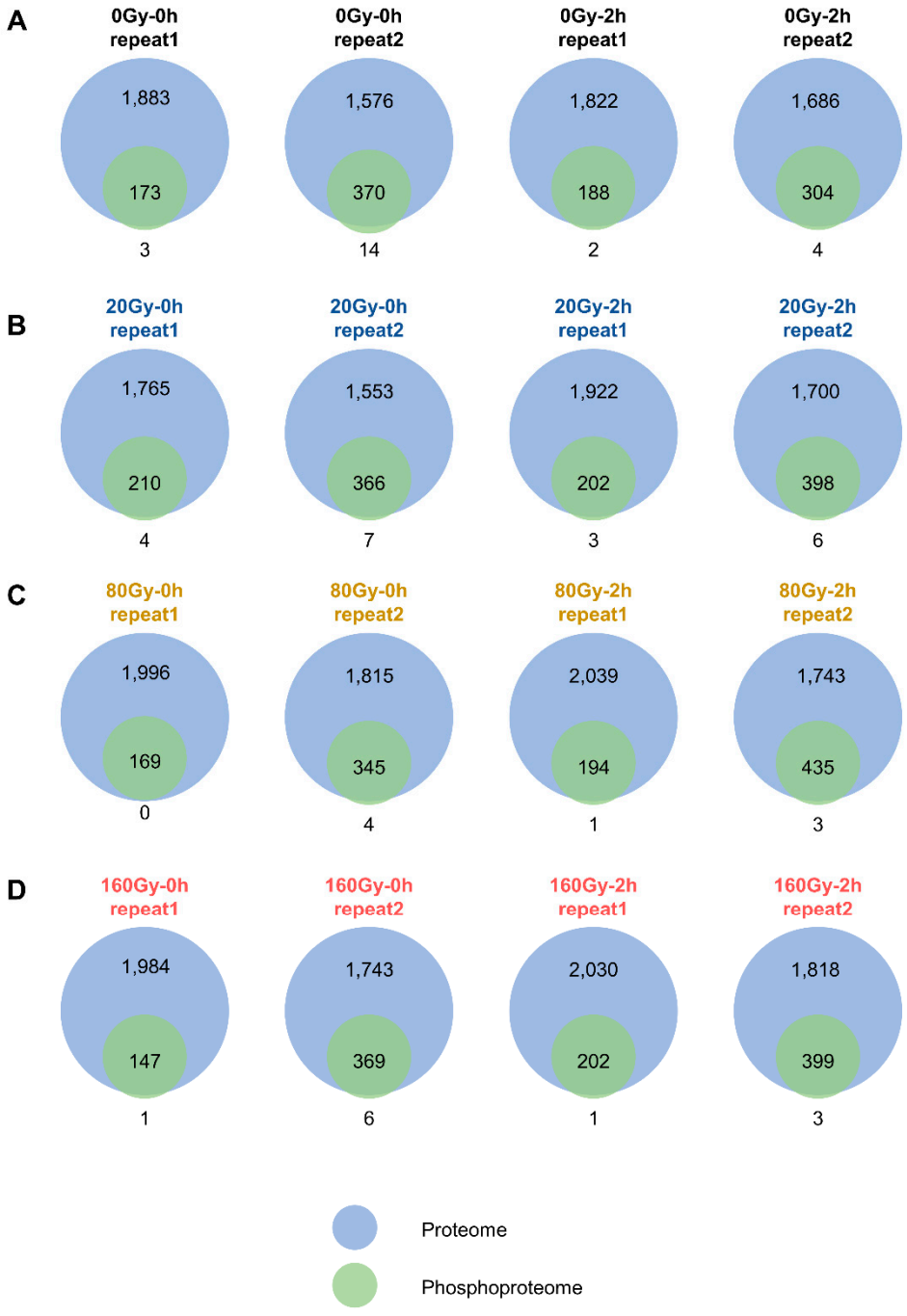
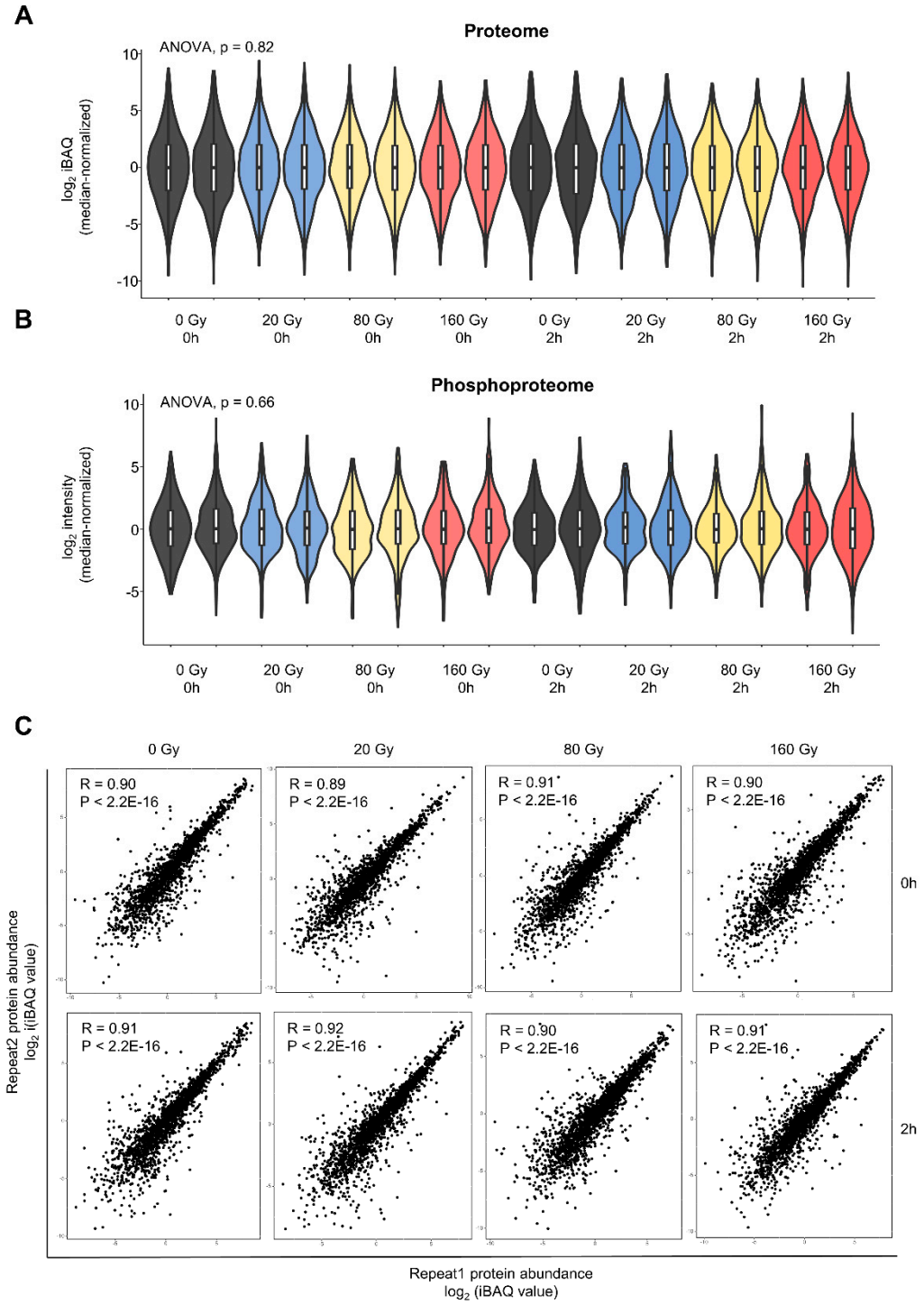


Figure S2. Comparison of proteome and phosphoproteome identification results and quality control (A-C).



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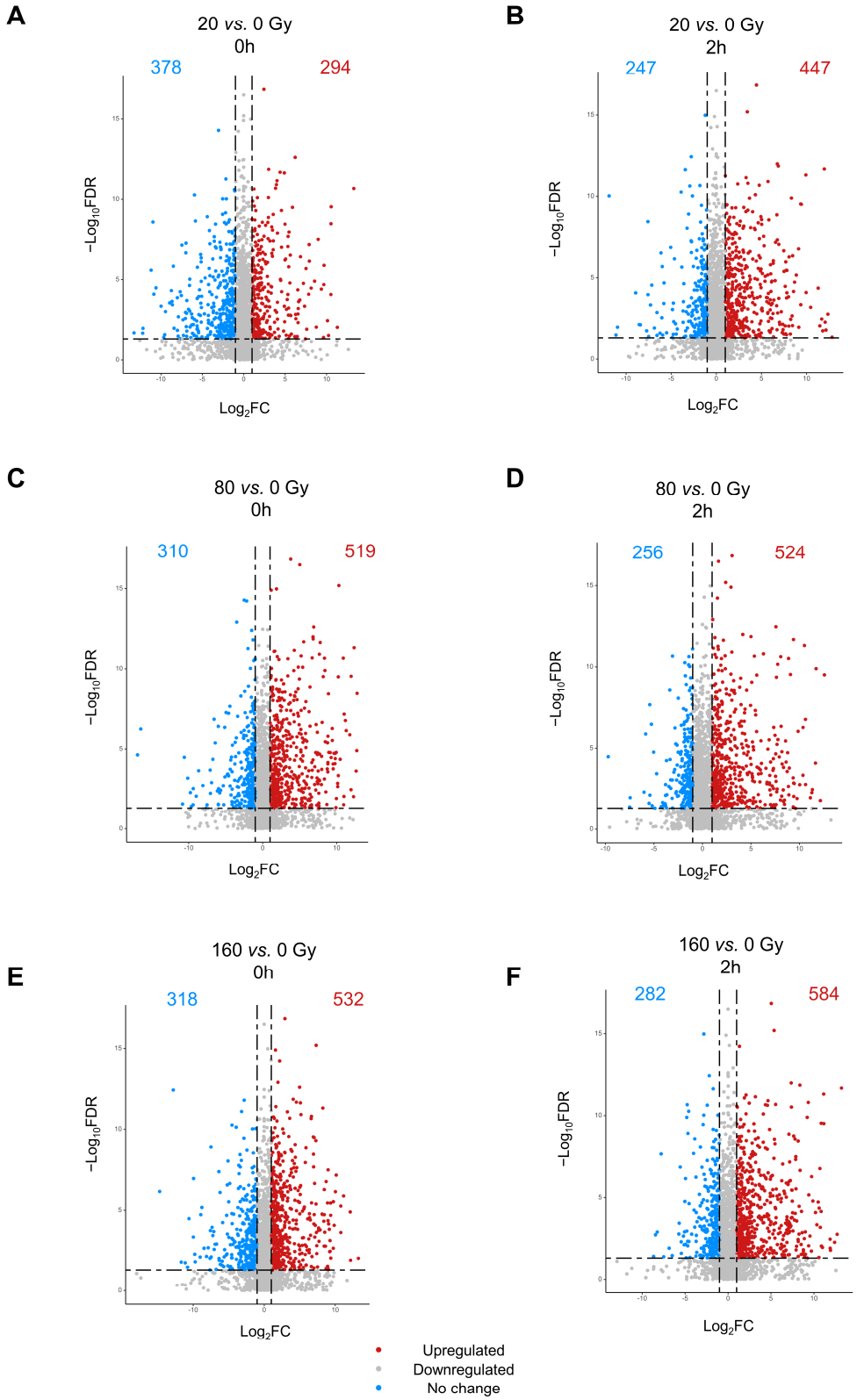


Figure S4. Analysis of differential phosphosites at each irradiation dose and time point (A-F).

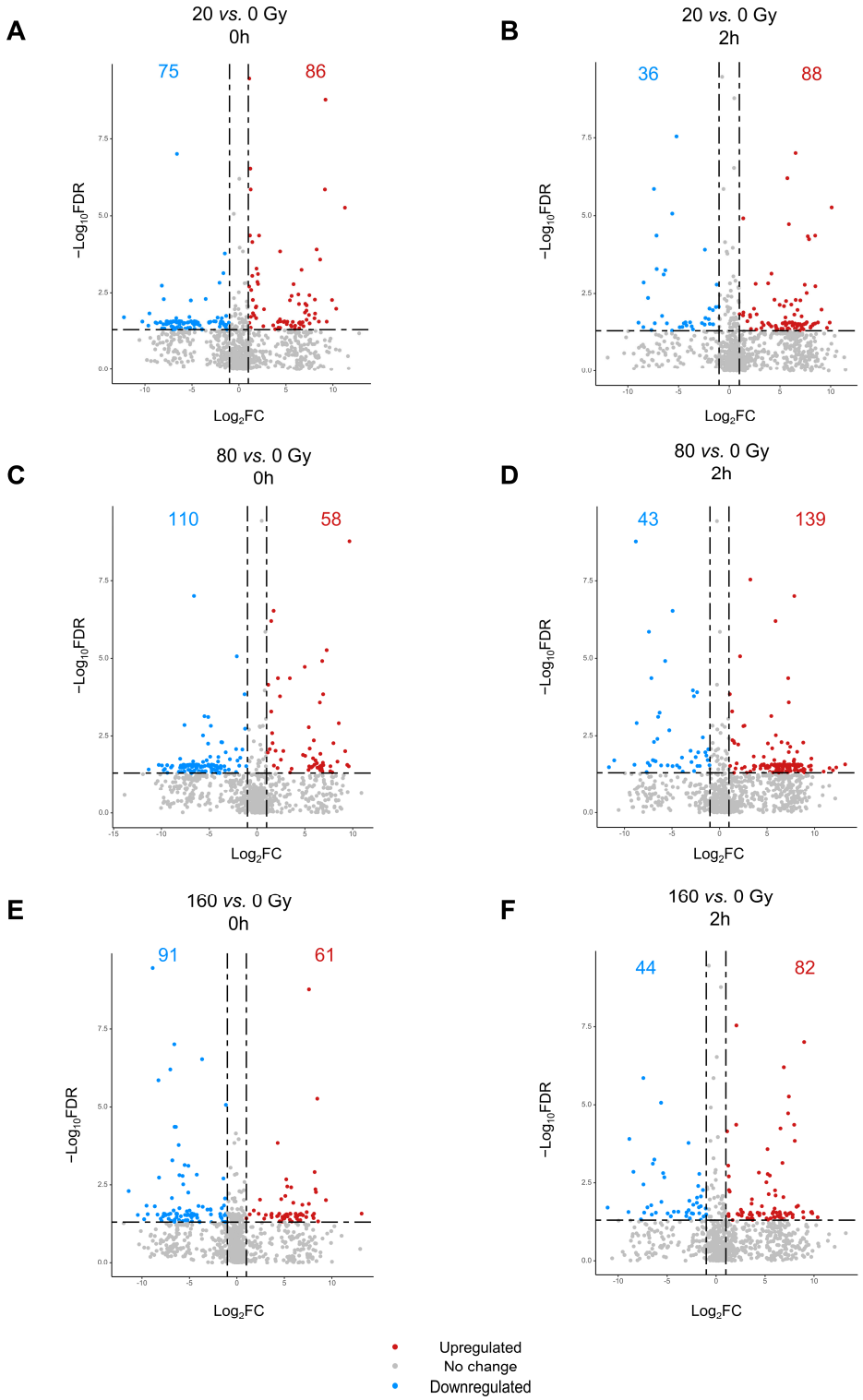
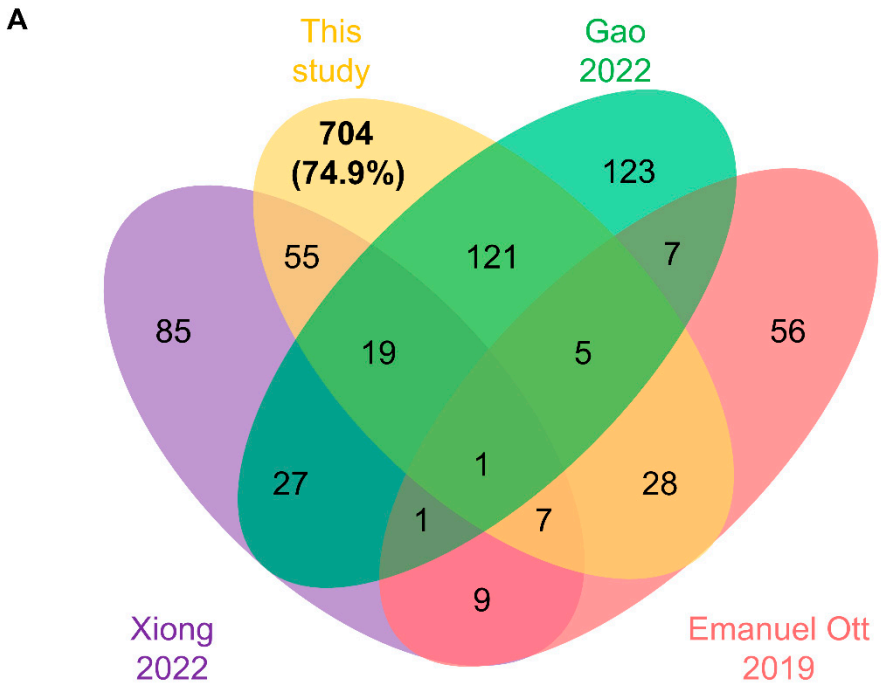
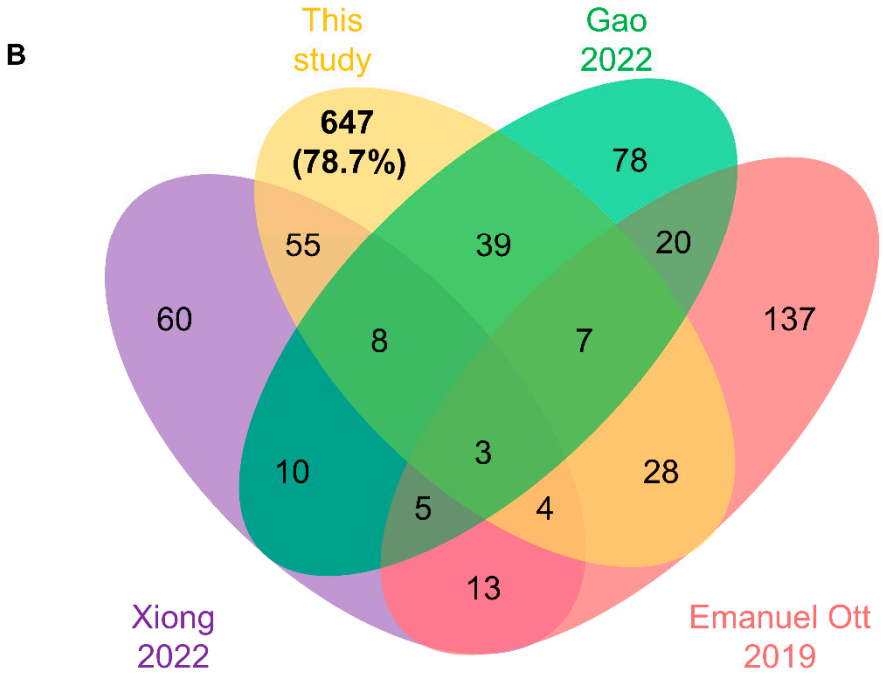


Figure S5. A comparison of the upregulated (A) and downregulated (B) proteins between our proteome dataset and the published datasets.





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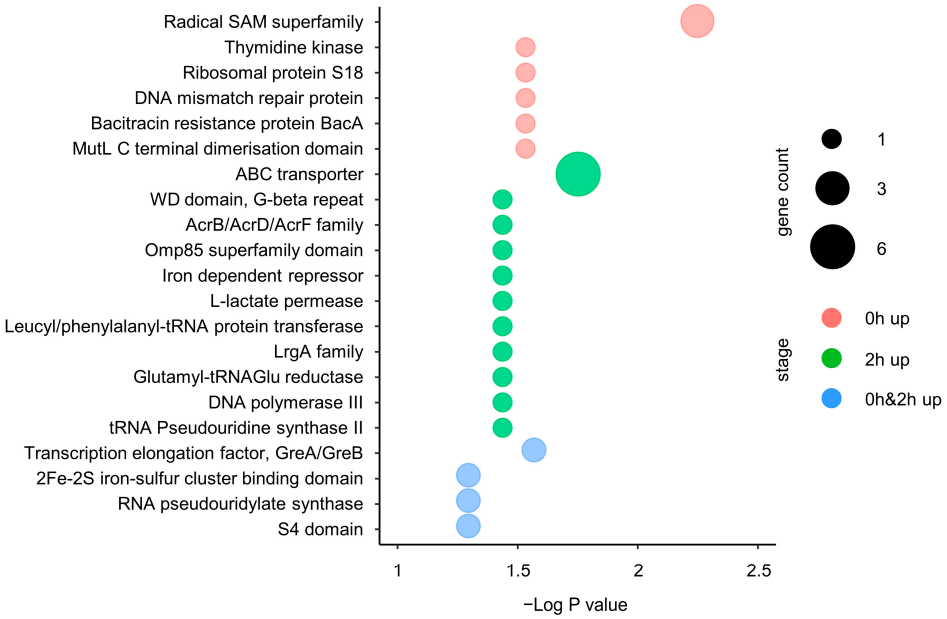

Figure S7. Motif analysis of irradiation sensitive phosphopeptides (A-C).

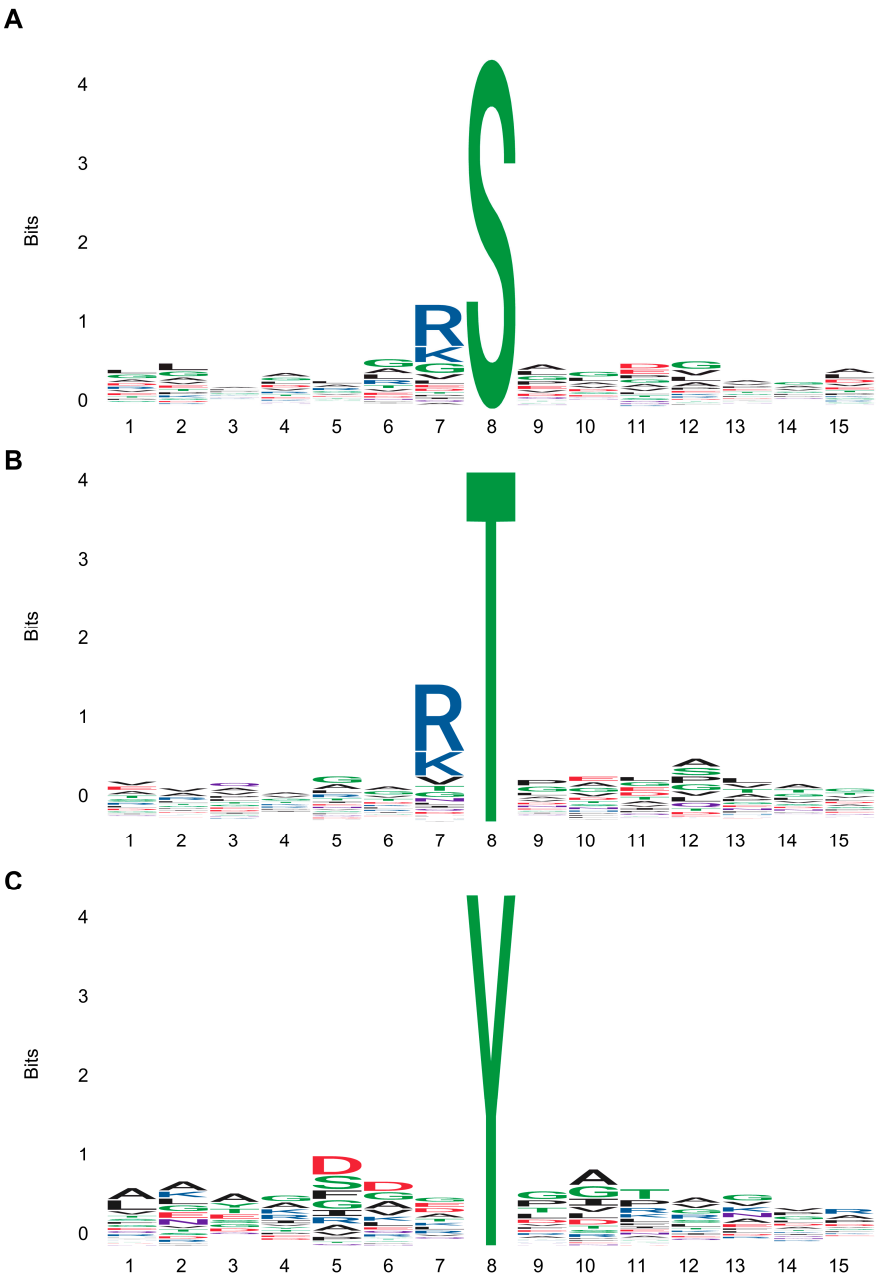

Figure S8. Site disorder analysis.