

Supplementary information to the article

Changes to the TDP-43 and FUS Interactomes Induced by DNA Damage

Tetsuya Kawaguchi¹, Matthew G. Rollins¹, Mahta Moinpour¹, Andres A. Morera^{1,2}, Christopher C. Ebmeier³, William M. Old³, Jacob C. Schwartz^{1,}*

¹ Department of Chemistry and Biochemistry and ² Department of Molecular and Cellular Biology, University of Arizona, Tucson AZ 85721, USA

³ Department of Molecular and Cellular Biology, University of Colorado, Boulder CO 80309, USA

* Corresponding author:

E-mail: jcschwartz@email.arizona.edu

Table of contents

Supplementary Figures and Tables:

Table S1. Fluorescence microscopy and LFQ analysis of AE-MS experiments.

Table S2. IR profile for AE-MS.

Figure S1. Changes to interactions after DNA damage.

Figure S2. Entire images for Figure 1A westerns.

Figure S3. Entire images for Figure 2B westerns.

Figure S4. Entire images for Figure 4 westerns of LAP-FUS IP experiments.

Figure S5. Entire images for Figure 4 westerns of LAP-TDP43 IP experiments.

Table S1. Sums of LFQ analysis for the four replicates of AE-MS experiments for FUS, TDP-43, and controls, before and after DNA damage. For each sheet, data for FUS is highlighted in blue and that for TDP-43 is highlighted in red. The first sheet includes genes bound to both TDP-43 and FUS, the second is bound only to TDP-43, and the third is bound only to FUS.

Table S2. IR profile for AE-MS experiment, including protein accession, gene name, and spectral counts.

Figure S1. Changes to interactions of TDP-43 and FUS after DNA damage. **(A)** Fluorescence microscopy of GFP for GFP-FUS or GFP-TDP43 (green), Hoechst stain (blue), and combined with phase contrast. Volcano plots with the \log_{10} of the fold change after etoposide treatment (x-axis) versus the \log_{10} of p-values of the change for interactors of FUS only **(B)** or TDP-43 only **(C)**. For FUS, the first plot is all interactors unique to FUS in blue. Below that shows RNAi and hnRNP proteins, then paraspeckle and nuclear speckle proteins, and last is snRNP proteins and transcription factors. Other than paraspeckle proteins that did not change, most FUS specific interactions tended to be decreased after DNA damage. For TDP-43, those uniquely interacting with TDP-43 are shown in red and heterotrimeric G-protein complex associated proteins, which mostly trended to be increased after DNA damage.

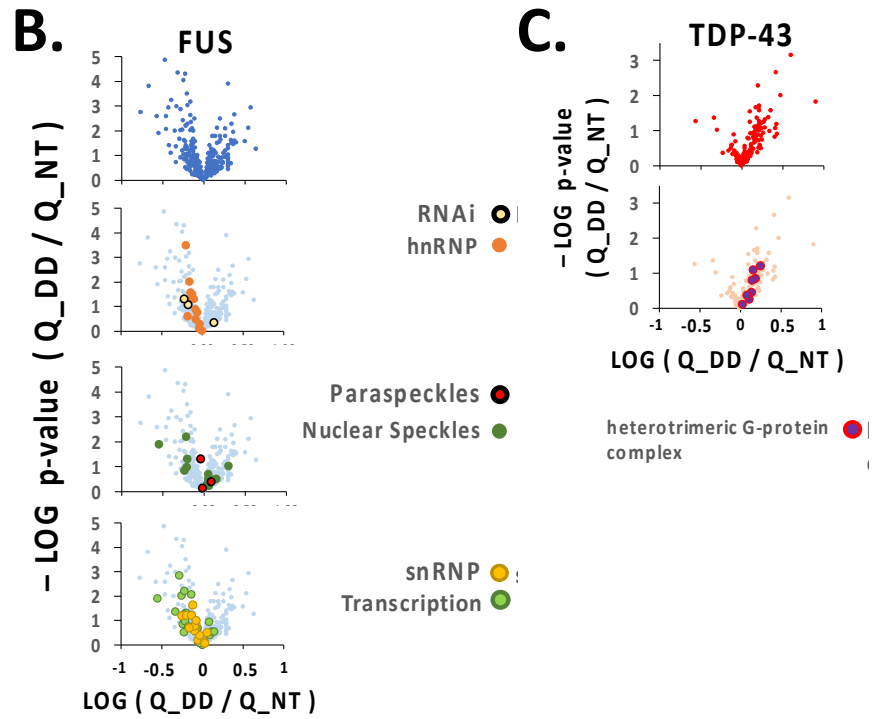
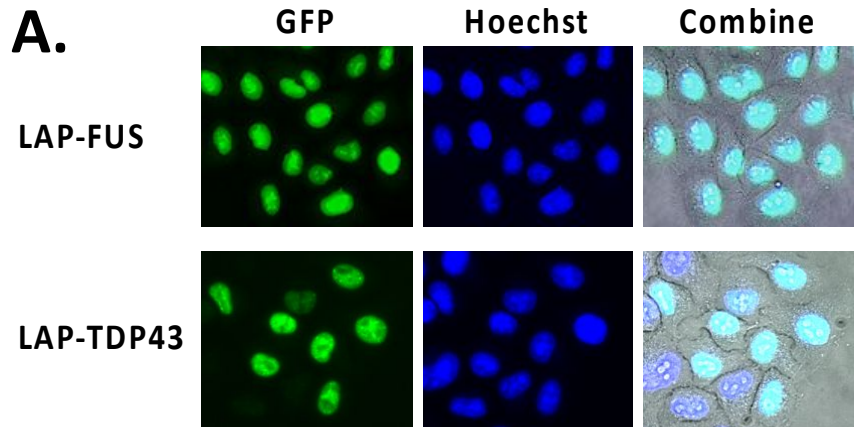
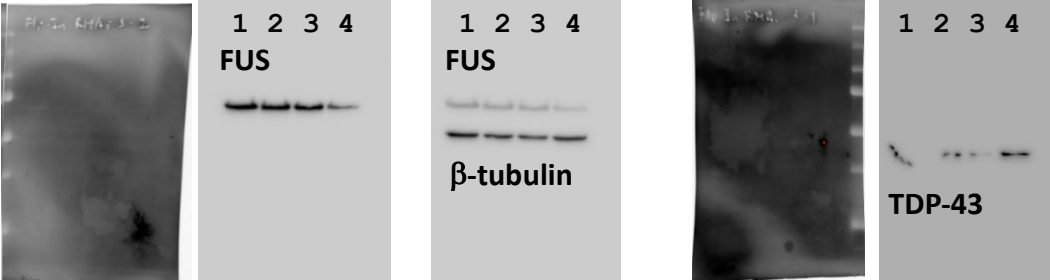


Figure S2. Westerns for three TDP-43 and FUS knockdown experiments for comet tail assays and indicated as replicates 1, 2, and 3, with replicate 1 shown in Figure 1A.

Replicate 1



Replicate 2



Replicate 3

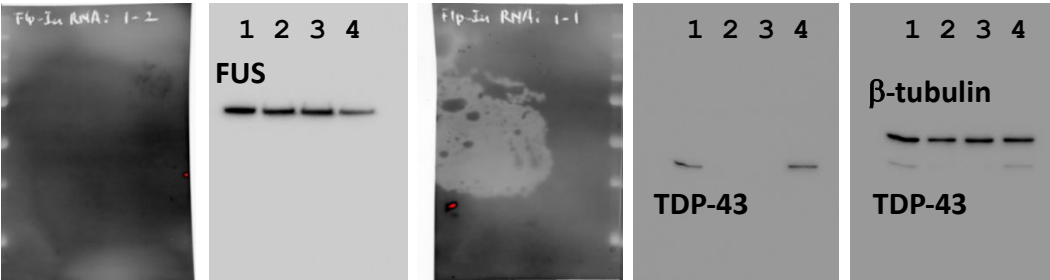


Figure S3. Westerns showing relative expression of LAP-TDP43 and LAP-FUS from Figure 2B. Etoposide treatment is indicated by "+" and vehicle DMSO control is indicated by "-". HeLa-Kyoto cells expressed LAP-FUS in (A) and LAP-TDP43 (B).

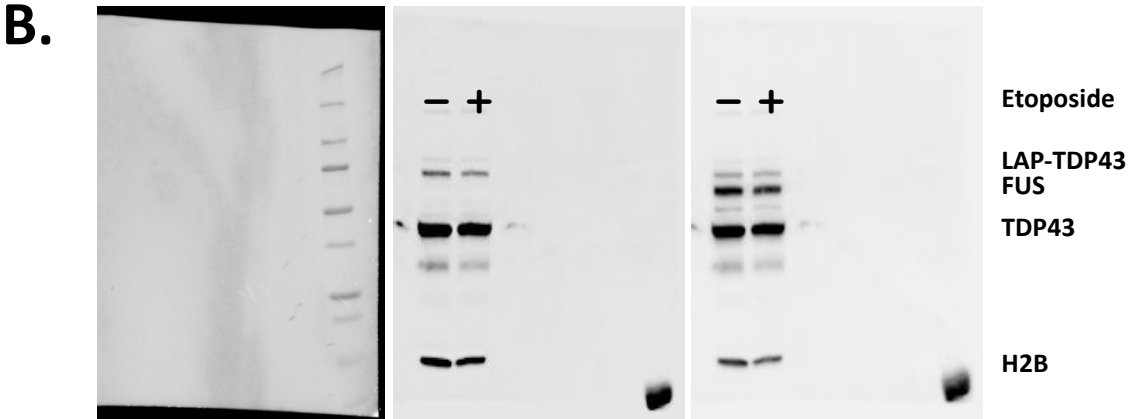
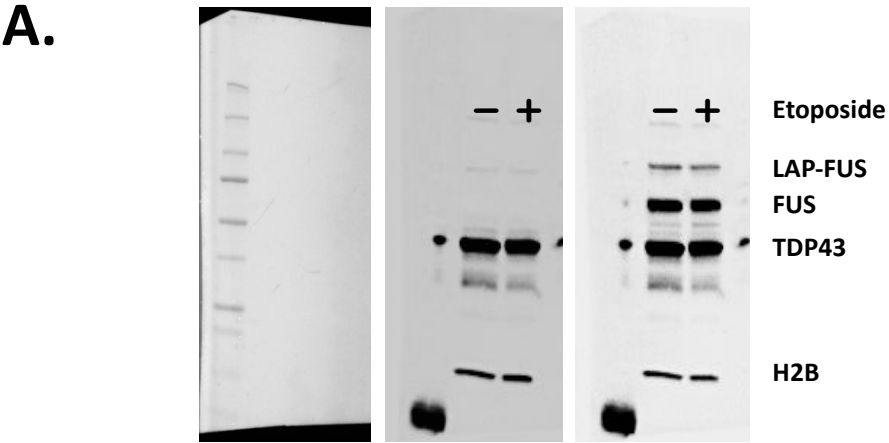


Figure S4. Westerns used to quantify LAP-FUS co-IP experiments and shown in Figure 4. Five replicate experiments are shown, indicated as 1, 2, 3, 4, and 5. Etoposide treatment is indicated by "+" and vehicle DMSO control is indicated by "-". Experiments including a lane for the negative IgG control are indicated by "I". For blots that were re-probed, the identities of bands still visible from the previous western are also indicated.

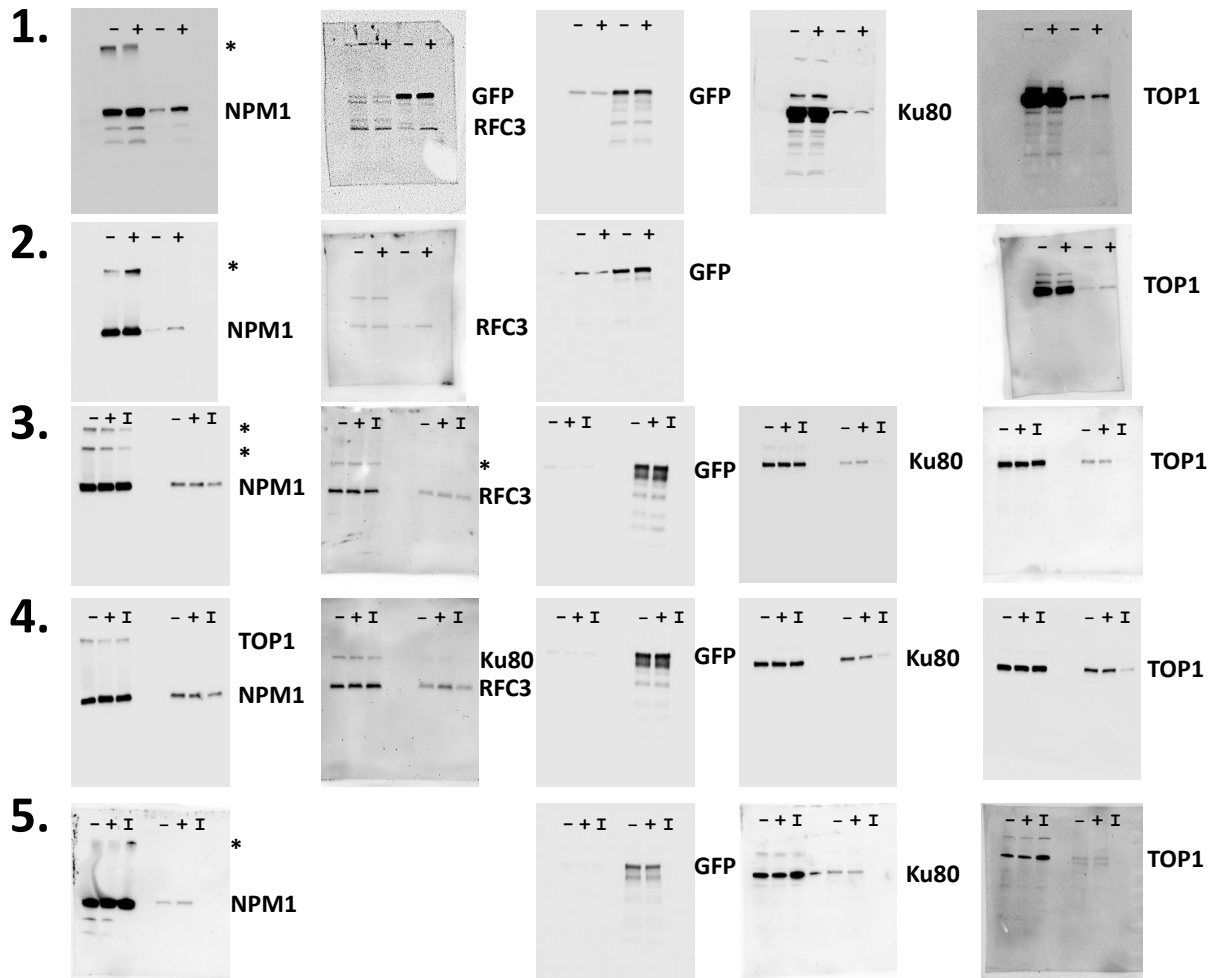


Figure S5. Westerns used to quantify LAP-TDP43 co-IP experiments and shown in Figure 4. Four replicate experiments are shown, indicated as 1, 2, 3, and 4. Etoposide treatment is indicated by "+" and vehicle DMSO control is indicated by "-". Experiments including a lane for the negative IgG control are indicated by "I" and a lane loaded with material boiled from the beads are labeled as "B". For blots that were re-probed, the identities of bands still visible from the previous western are also indicated. Two blots were also probed for hnRNPA1 and are indicated as "A1", though this data was not included in the analysis for this study.

