



Supplemental Figure S1 (related to Figure 1). Features of the zebrafish MZT mRNA-bound proteome. (A, B) Clustered heat maps displaying the abundance of quantified proteins in samples from the indicated embryonic stages. Columns refer to three independent experiments of UV-irradiated (UV+) and non-irradiated (UV-) samples. Rows represent individual proteins. Color-coded bar below each heat map shows log transformed LFQ intensity (white-red and white-blue color bars for preZGA and ZGA stages, respectively). LFQ, label-free quantification. **(C, D, E, F)** Five the most represented molecular function, biological process, cellular component GO terms and PFAM protein domains are shown. Numbers of identified and all annotated proteins with respective GO terms and PFAM domains are indicated above each bar. X axis, - log transformed adjusted p values. **(G)** Scatterplot showing translational efficiencies of the mRNAs encoding MZT mRBPome components during MZT. X axis, translation efficiency at preZGA (2 hpf); y axis, translation efficiency at late ZGA (4 hpf). **(H)** Boxplot showing fold change in translational efficiencies for different protein groups (grey, MZT mRNA-bound proteome; red, preZGA-specific proteins; blue, ZGA-specific proteins) between 2 and 4 hpf.