Figure S4. Expression of DDR genes upon DSB induction or inactivation of RNA decay factors.

A, B Expression of DDR genes in wild type cells 60 minutes (A) and 240 minutes (B) after DSB induction relative to wild type cells at time zero. For each of the DDR genes, expression fold change and \( P \)-value from DESeq analysis were determined. Genes showing significant differential expression (fold change \( \leq 0.5 \) or \( \geq 2 \), \( P \)-value \( \leq 0.001 \)) are highlighted in red (list in Table S2).

C-E Expression of DDR genes in \( xrn1\Delta \), \( rrp6\Delta \) and \( trf4\Delta \) cells. As in (A) but showing \( xrn1\Delta \) (C), \( rrp6\Delta \) (D) and \( trf4\Delta \) (E) cells at time zero relative to wild type cells at time zero.

F-H Scatter plots of tag density (expressed in tag per nucleotide, log2 scale) for genes encoding proteins involved in histone modifications/chromatin remodeling (red dots), DNA damage checkpoint (green dots), DNA repair/recombination (blue dots) and all other protein-coding genes (grey dots) in \( xrn1\Delta \) (F), \( rrp6\Delta \) (G) and \( trf4\Delta \) (H) cells at time zero relative to wild type cells at time zero. Spearman’s correlation coefficients for each set of genes are indicated.