Supporting Information

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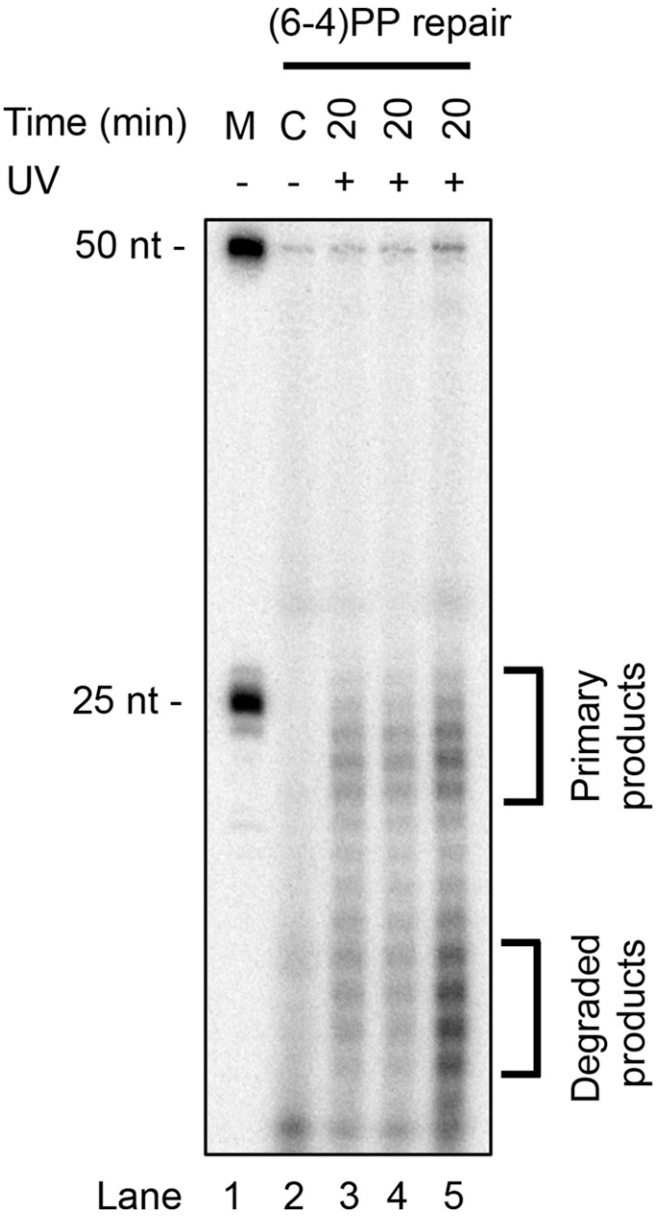

Fig. S1. Comparison and analysis of three different methods for isolation of the excised oligomers. After irradiation with 120 J/m^2 UV (254 nm), cells were incubated in the dark for 20 min to allow excision repair. For lanes 2 and 3, STES, phenol chloroform, and glass beads were used to disrupt the cell wall and separate the small DNA molecules. For lane 4, the whole procedure was the same as for lanes 2 and 3 except STET instead of STES was used. For lane 5, TEP and glass beads were used to disrupt the cell wall, and then a modified Hirt procedure was applied to isolate the excision products. The isolated excision products were further purified by a G-50 filtration column and immunoprecipitation with anti-(6-4)PP antibody, 3′ end-labeled with ^{32}P-Cordycepin, and resolved on an 11% denaturing sequencing gel.

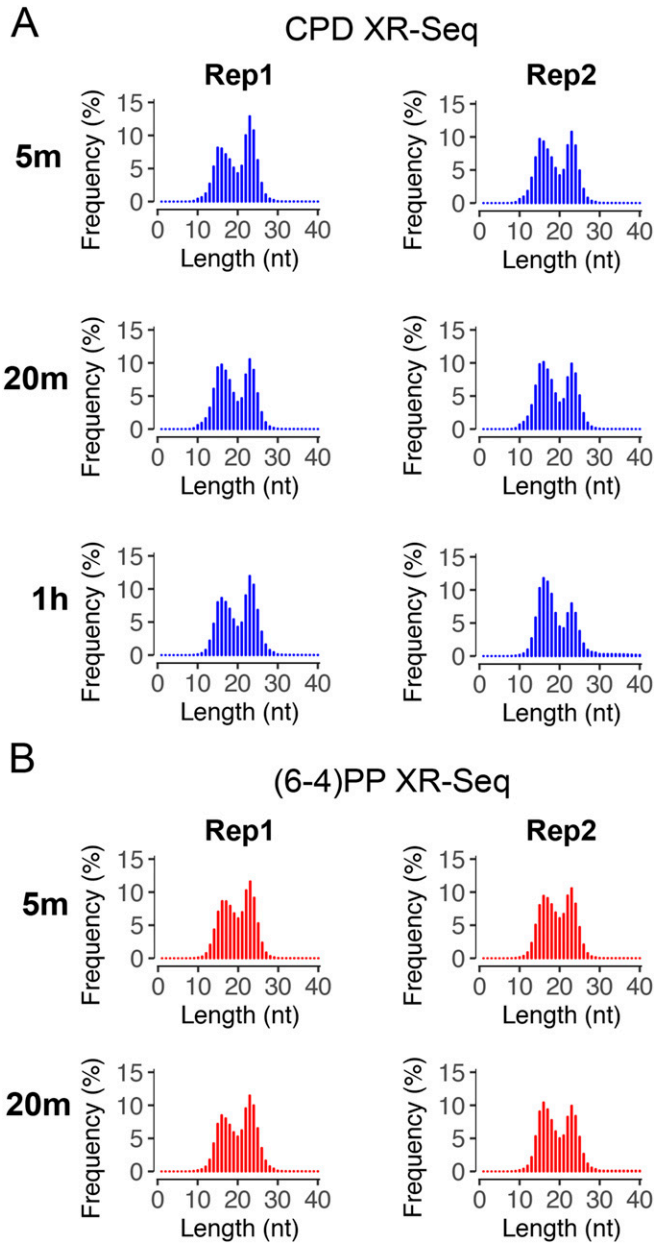

Fig. S2. Length distribution profiles of the excised oligomers from XR-seq. (*A*) The length distribution of the excised oligomers from CPD XR-seq at 5 min, 20 min, and 1 h. (*B*) The length distribution of the excised oligomers from (6-4)PP XR-seq at 5 and 20 min. Replicates (Reps) 1 and 2 are shown.

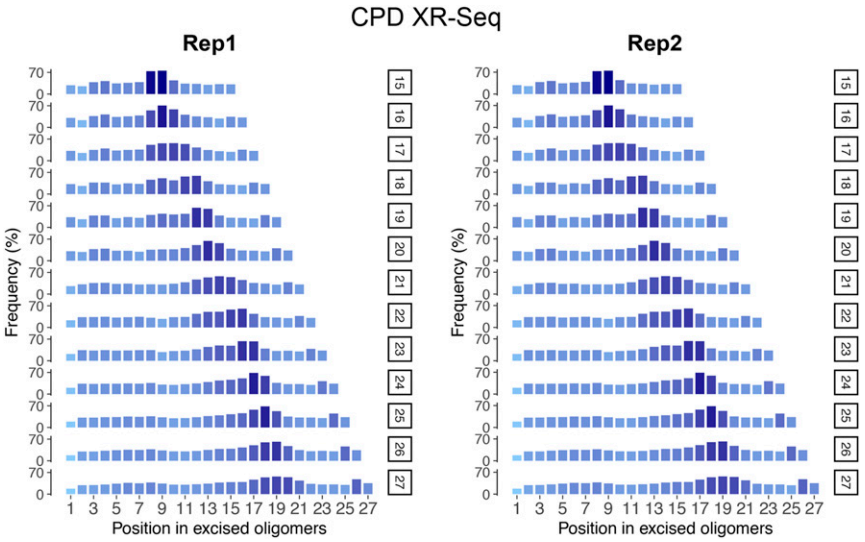

Fig. S3. Thymine frequencies at each position within the 15–27 mers obtained from CPD XR-seq at the 20-min time point. The color gradient from blue to dark blue and peak heights indicate the enrichment of TT from low to high, respectively.

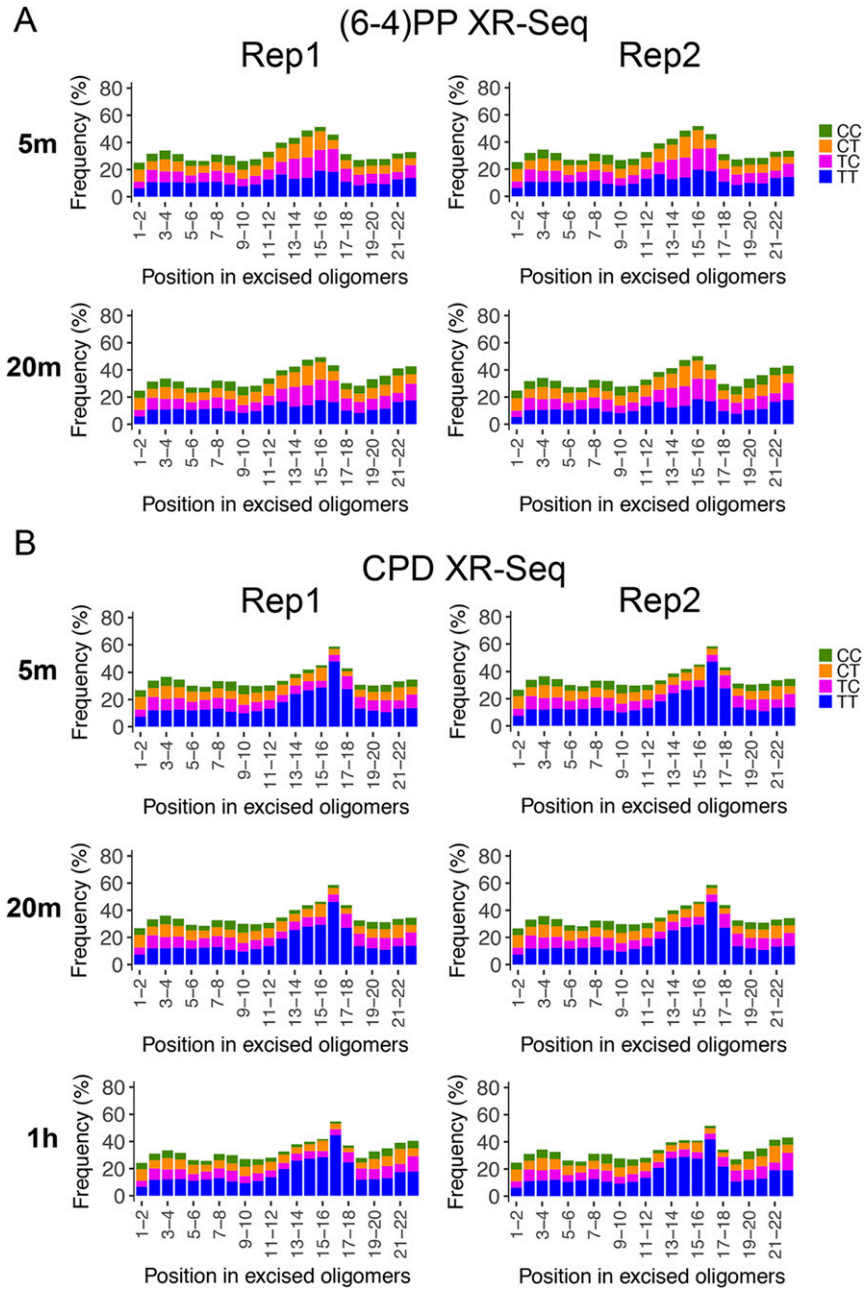

Fig. S4. Dipyrimidine frequency distribution at each position within the 23 mers obtained from XR-seq. (*A*) Frequencies of dipyrimidine at each position within 23 mers from (6-4)PP XR-seq at 5- and 20-min time points. The TC enrichment is at a position 6 nt from the 3′ end. (*B*) Frequencies of dipyrimidine at each position within 23 mers from CPD XR-seq at 5-min, 20-min, and 1-h time points. The TT enrichment is at the position 6 nt from the 3′ end. Replicates (Reps) 1 and 2 are shown.

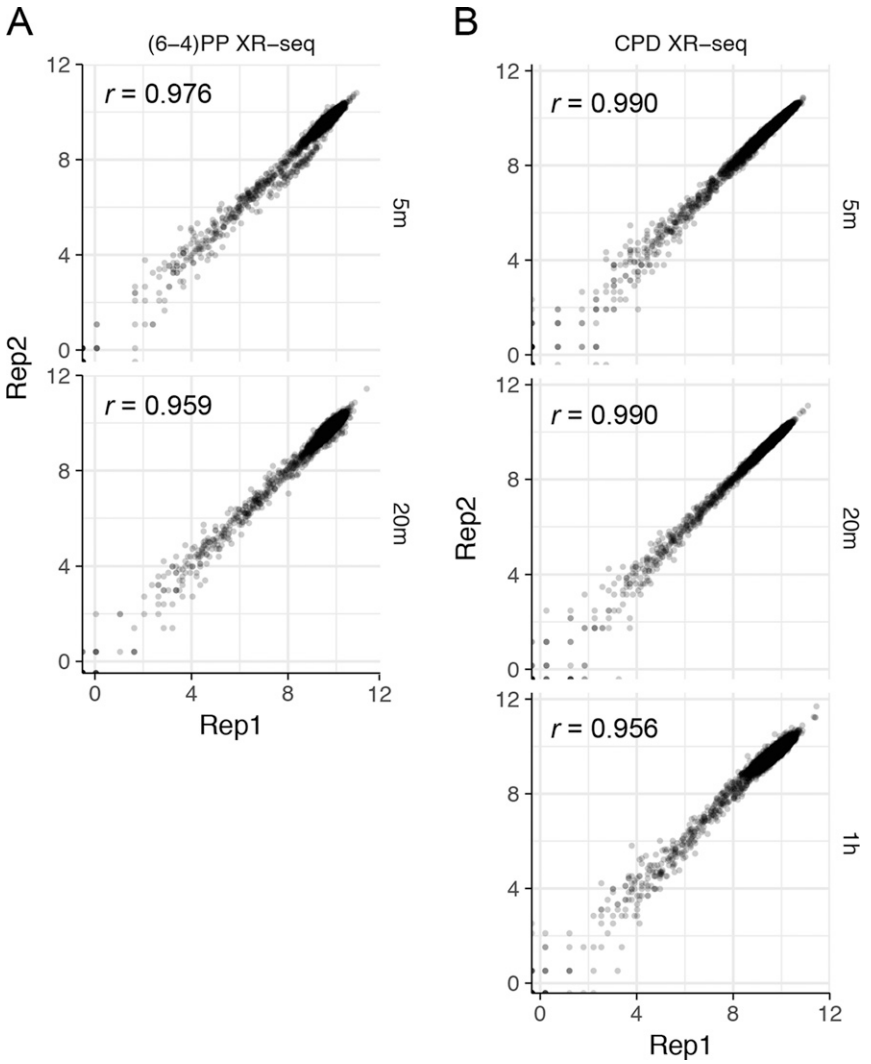

Fig. S5. Scatter plots showing correlation of excision repair signals between two biological replicates (Rep1 and Rep2). (*A*) (6-4)PP XR-seq. (*B*) CPD XR-seq. The values of *x* and *y* axes are the $\log_2$(normalized read counts). Values of Pearson's *r* are shown in the plots.

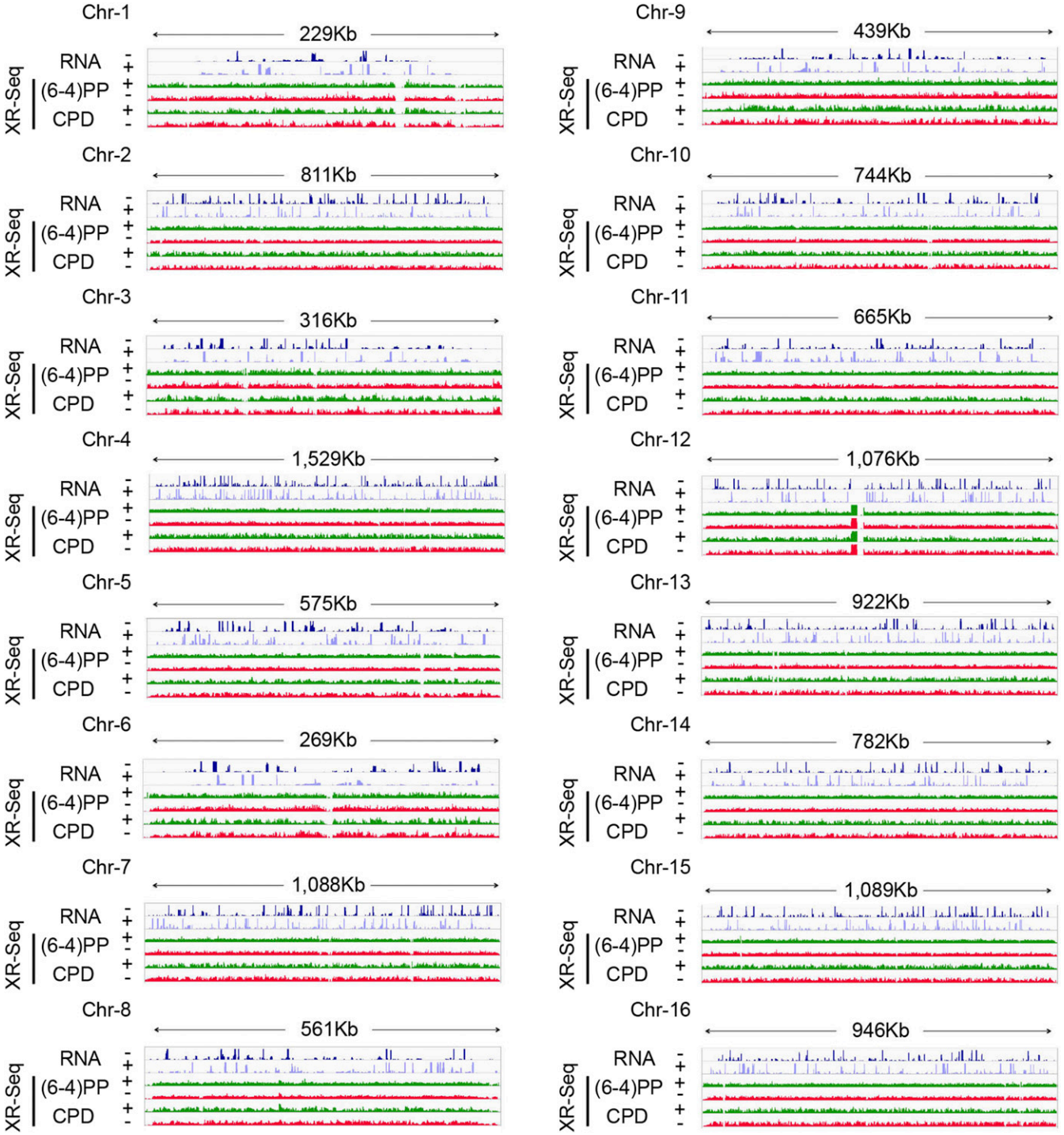

Fig. S6. Whole-genome map of (6-4)PP and CPD repair generated by XR-seq in yeast cells. The RNA-seq signals in blue, separated by strands, are plotted above the XR-seq tracks. The (6-4)PP and CPD repair data are from XR-seq at 5- and 20-min time points, respectively. For XR-seq signals, plus strands are shown in green, and minus strands are shown in red. The whole-genome repair map represents data from one biological replicate.

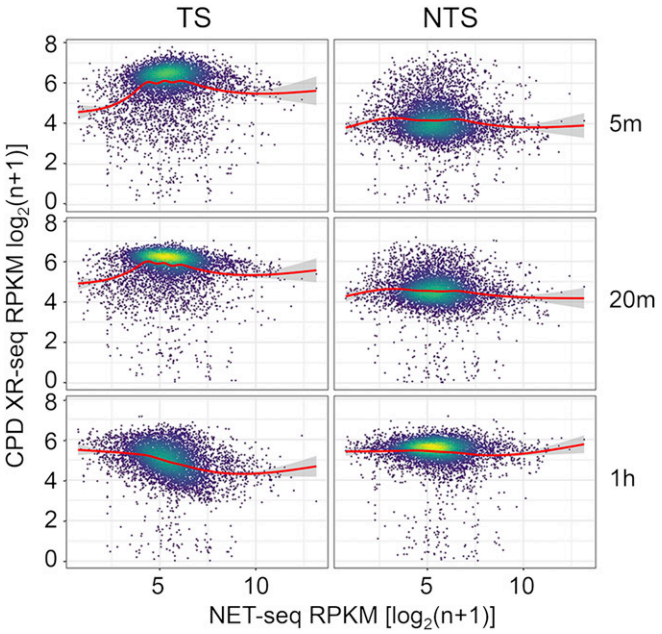

Fig. S7. Scatter plots for CPD repair as a function of expression level. XR-seq (*y* axis) for the two strands (TS and NTS) at 5 min, 20 min, and 1 h after UV irradiation and NET-seq (*x* axis) RPKM values for each gene are represented by points [$\log_2$(RPKM + 1)]. The color gradient of the points indicates density from low (purple) to high (yellow). The smoothed red curve was fitted using a generalized additive model. A single biological replicate was plotted.

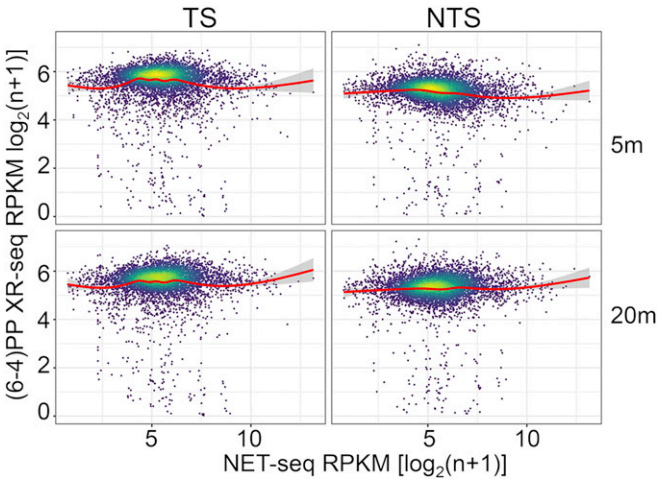

Fig. S8. Scatter plots for (6-4)PP repair as a function of expression level. Same as in Fig. S7 except for damage type [(6-4)PP] and time points (5 and 20 min).

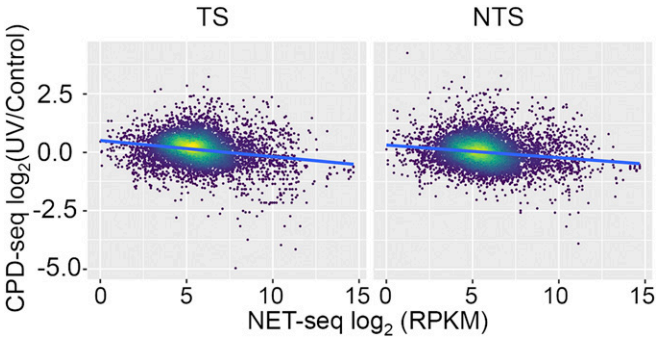

Fig. S9. Scatter plots for CPD-seq damage formation as a function of expression level. The $\log_2$-transformed values of CPD-seq to control (no UV) ratio were plotted for TS and NTS as a function of expression derived from the NET-seq dataset. The trend lines (blue) showing the negative correlations were plotted using generalized additive model fitting. The color gradient from purple to yellow indicates density of the data points from low to high, respectively.

Table S1. RPKM for individual genes representing the four quartiles

		Q4		Q3		Q2		Q1	
		PDC1		*TRX1*		*RIC1*		*YLR046C*	
XR-seq	Time	TS	NTS	TS	NTS	TS	NTS	TS	NTS
CPD	5 min	64	11	164	12	81	20	57	13
	20 min	45	12	84	22	88	25	61	25
	1 h	29	55	30	42	49	51	25	66
(6-4)PP	5 min	37	31	69	27	61	40	37	24
	20 min	53	54	61	38	52	35	48	41

The values are the average of the two biological replicates.