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Supplementary Information for

Cisplatin-DNA Adduct Repair of Transcribed Genes is Controlled by Two Circadian Programs in Mouse Tissues

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Supplementary Information

Methods

Cis-regulatory element annotation system (CEAS)

The distribution of XR-seq uniquely mapped reads on whole chromatin were determined with command line options ceas -g mm10 -b -w -name(1).

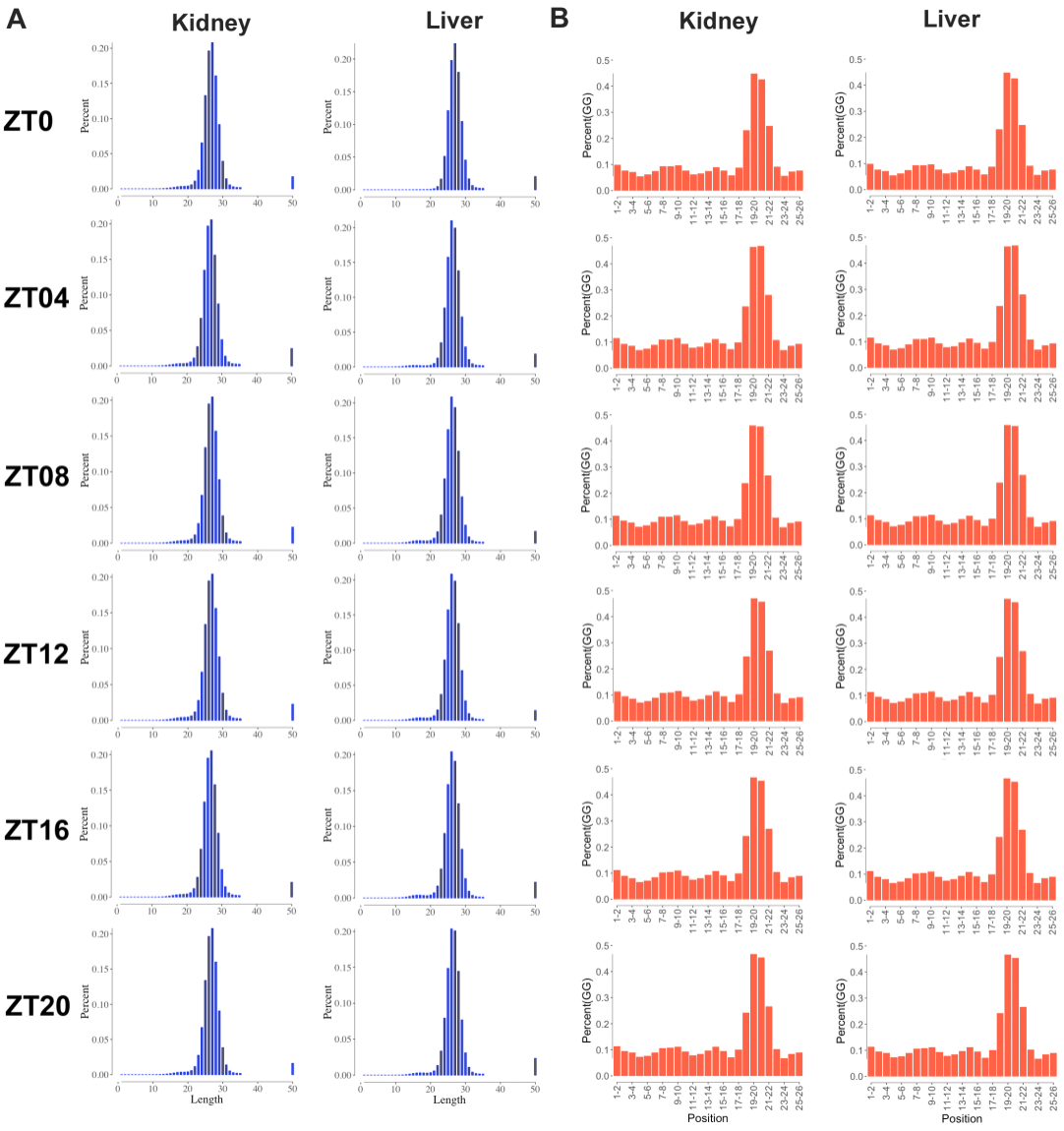

Fig. S1. Size distribution and Pt-GG adduct position in the excised oligomers. A) Size Distribution. Both in kidney and liver, fragments in the 24-30nt range account for > 95% of all excision products. **B)** Position of Pt-d(GpG) in the excised oligomers. Adducts from 19-20 to 20-21 from the 5' end of the 26-mer account for > 95% of all 26-mer excision products.

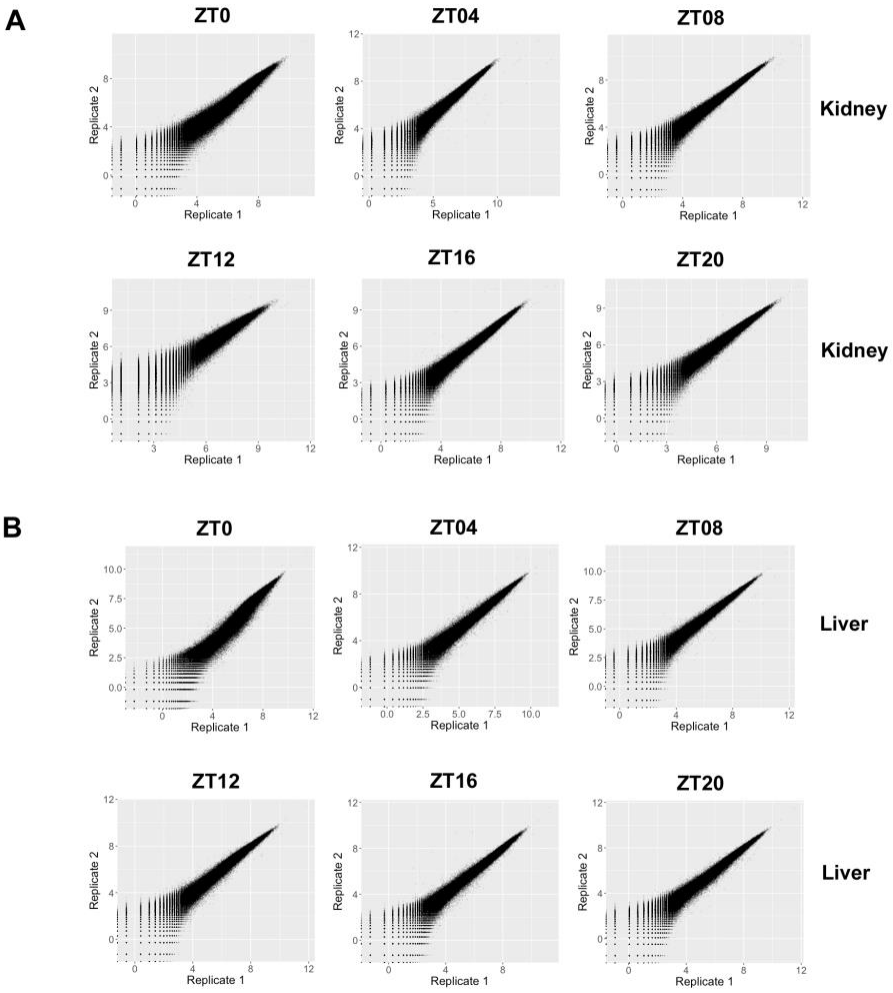

Fig. S2. **Reproducibility of XR-seq on A)** Kidney, **B)** Liver. The x and y axes represent Replicate 1 and Replicate 2, respectively. Axis values are the log2-transformed normalized read numbers (10 million). Pearson correlation coefficients for kidney are 0.979852 (ZT0), 0.8555965 (ZT04), 0.9918644 (ZT08), 0.9754492 (ZT12), 0.9903791(ZT16), 0.9914235(ZT20), and for liver are 0.9813121 (ZT0), 0.9901277 (ZT04), 0.9930494 (ZT08), 0.9910942 (ZT12), 0.992062 (ZT16) and 0.993173 (ZT20).

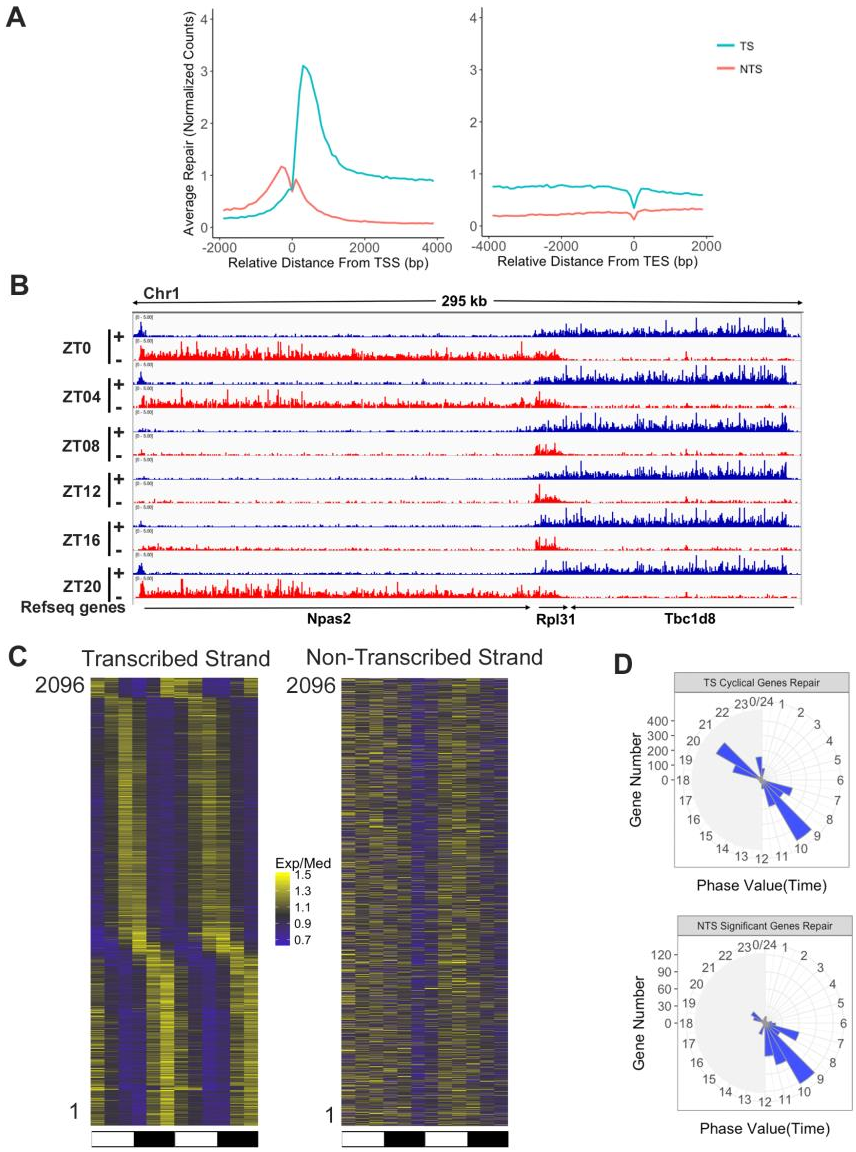

Fig. S3. **XR-seq results from liver A)** Repair in genes, showing separately TS and NTS repair within the TSS, gene body and TES. **B)** Screenshot showing repair maps of Npas2 and two neighboring genes over a circadian cycle. **C)** Heatmaps for TS and NTS repair. **D)** Repair phases of circadian clock-controlled genes for TS and NTS in the form of radial diagrams.

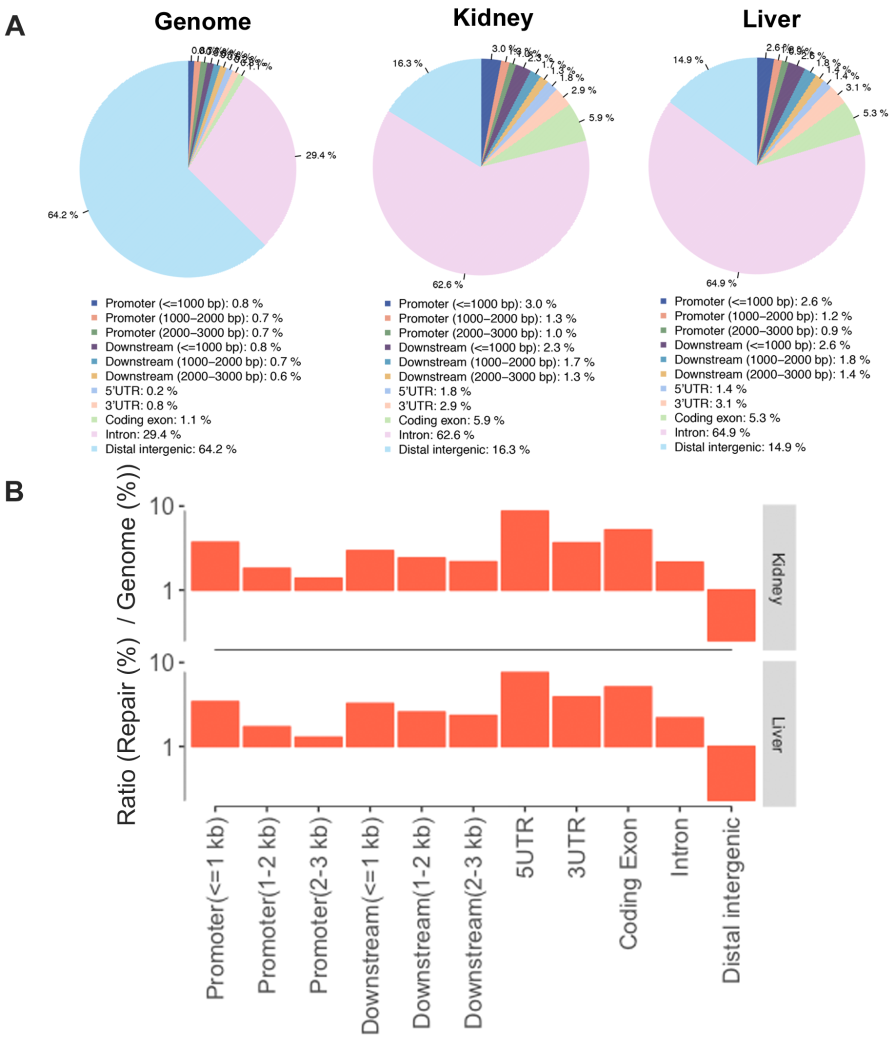

Fig. S4. **Distribution of XR-seq signals among genomic elements by CEAS analysis. A)** The Genome pie chart (left) shows how much of the chromosome (in %) each functional element comprises. Kidney and Liver charts show how much repair (in %) occurs in each functional region. **B)** Summary of XR-seq signals in different regions. Y-axis represents percent of repair in a region (**see Figure S4A Kidney, Liver**) divided by the relative amount of that region (%) in the genome (**see Figure S4A Genome**). Note that there is a higher level of repair in genes and gene-associated regions compared with intergenic DNA(2). This "gene-specific repair" is largely a consequence of highly efficient transcription-driven TS repair.

References

1. Shin H, Liu T, Manrai AK, & Liu XS (2009) CEAS: cis-regulatory element annotation system. *Bioinformatics* 25(19):2605-2606.
2. Hanawalt PC & Spivak G (2008) Transcription-coupled DNA repair: two decades of progress and surprises. *Nat Rev Mol Cell Biol* 9(12):958-970.