**iCLIP data analysis**

The iCLIP data were processed from raw reads to RBP binding sites by the pipeline as previously described 1. Briefly, the barcode regions in the reads are filtered by FASTX-Toolkit (http://hannonlab.cshl.edu/fastx\_toolkit/). The demultiplexing and adapter trimming are performed by Flexbar 2. Only trimmed reads with at least 15 nt are kept for further analysis. The individual FASTQ files for each sample are mapped to human reference genome (GRCh38) by STAR 3⁠. The technical duplicates are removed using UMI-tools 4⁠. After deduplication, the crosslink events are transformed from the mapped reads by extracting the position upstream of the 5’end of the reads with BEDTools 5⁠. The crosslink sites with significantly enriched crosslink events are identified by PureCLIP 6⁠ and post-processed by the steps as previously described 1⁠.

**RNAmap**

The crosslink events located within only one annotated gene were normalized by the total count of the respective gene and the gene length 7⁠. The total number of normalized crosslink events relative to the 3’ splicing site (3SS) and 5’ splicing site (5SS) of the enhanced and silenced SE events were shown in the RNAmap. We used a 30 nt sliding window with 1 nt step to detect the regions in which crosslink events were significantly different between WT and KO samples. In each step, we performed t-test with the number of crosslink events of two samples, and calculated the fold-change. The windows with Bonferroni adjusted *p-*value < 0.01 and fold-change > 2 were merged and shown as a red box in the RNAmap.

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