Abuhashem_Figure S4

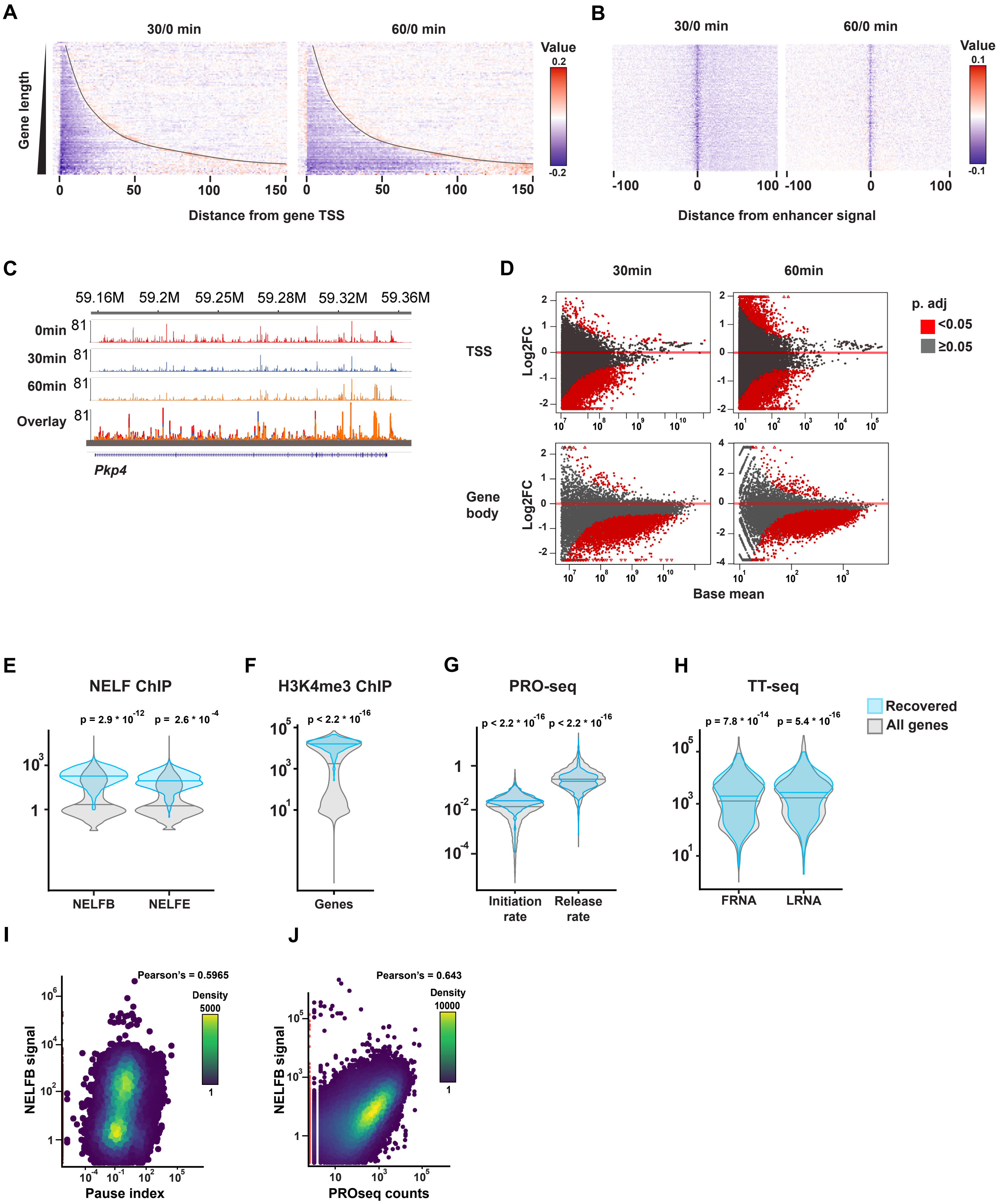

Fig S4. NELF stabilizes Pol II pausing and transcription at promoters and enhancers, related to Figure 4.

(A) Heatmaps of Log2 fold change of PRO-seq signal at genes ordered by gene length. Dashed lines represent poly A sites.

(B) Heatmaps of Log2 fold change of PRO-seq signal at enhancers.

(C) Genome browser shot of PRO-seq signal for a long gene, related to Figure 4E.

(D) MA plot of Log2 fold change with significantly changed genes highlighted. Related to Figure 4F and 4H.

(E) Transcription initiation and release rates from PRO-seq data at 0 mins of all genes vs. recovering TSS genes at 60 mins treatment.

(F) NELF ChIP signal at all genes vs. recovering TSS genes at 60 mins treatment.

(G) H3K4me3 signal at all genes vs. recovering TSS genes at 60 mins treatment.

(H) TT-seq signal at all genes vs. recovering TSS genes at 60 mins treatment.

(I) Correlation between NELFB ChIP-seq signal and pause index at all expressed genes.

(J) Correlation between NELFB ChIP-seq signal and gene body PRO-seq count at all expressed genes.