

Supplemental Figure S8. Expressed *Alu* elements are enriched near highly expressed genes and in the motifs of master TFs.

A. Specifically expressed *Alu* elements were close to highly expressed genes. Only biosamples with more than 50 expressed *Alu* elements were compared. Wilcoxon rank-sum test FDR adjusted *p*-values are reported.

B. Nearby genes of specifically expressed *Alu* elements showed higher DNase-seq signals than nearby genes of unexpressed *Alu* elements. Wilcoxon rank-sum test FDR adjusted *p*-values are reported.

C. Enriched motifs of master transcription factors at tissue-specific expressed *Alu* elements. All of these transcription factors were previously demonstrated to play key roles in the biology of the respective tissues.

D. POLR2A ChIP-seq signals are shown around the TSSs of *Alu* elements that do (solid yellow line) or do not overlap cCREs-ELS (solid green line) in the corresponding biosample, *Alu* elements expressed in other biosamples (solid grey line) and unexpressed *Alu* elements (dashed grey line) in K562 (left) and GM12878 (right) cells. The signals were averaged over all *Alu* elements in each set.