



**Supplemental Figure S3: Percentage of raw ChIP-seq reads that overlap with *Alu* sequences.** The percentage of raw ChIP-seq reads that overlap with *Alu* sequences is plotted for TFs that bind to 20% or more of the *Alu* sequences tested by eY1H assays (red) and TFs for which we did not detect binding to *Alu* sequences (blue). ChIP-seq data was obtained from the ENCODE Project for the K562 and HepG2 cell lines. Violin plots are shown, and the median is indicated by a solid black line. Statistical significance evaluated by one-tailed Mann-Whitney *U* test.