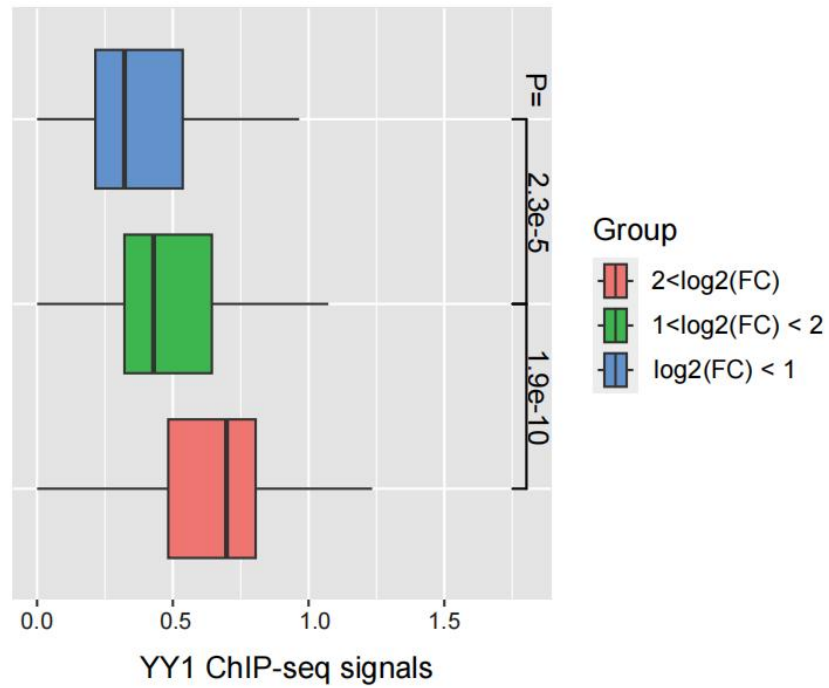


Supplementary Figure S1. Analysis of the CRISPRa data. (A) Pie chart displaying the genomic distribution of different reads from RNA-seq peaks. (B) Heat map representing Pearson correlations between control and dCas9-VP64 L02 cell lines, based on two replicates.



Supplementary Figure 2. The correlation between the YY1 ChIP-seq signals and the L1 expression. The young L1s after CRISPRa are divided into 3 groups: lowly expressed (\log_2 fold change < 1); medially expressed ($1 < \log_2$ fold change < 2); and highly expressed (\log_2 fold change > 2).