

Cusanovich, Darren A., et al. "The functional consequences of variation in transcription factor binding." PLoS genetics 10.3 (2014): e1004226.

To evaluate the context of functional TF binding **we knocked down 59 TFs** and chromatin modifiers in **one HapMap lymphoblastoid cell line**. We then **identified genes whose expression was affected by the knockdowns**. We intersected the gene expression data with transcription factor binding data (based on ChIP-seq and DNase-seq) within 10 kb of the transcription start sites of expressed genes. This combination of data allowed us to infer functional TF binding.

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Knockdown effect on global gene expression levels :

...we identified **genes that were differentially expressed between the three knockdown replicates of each factor and the six controls.**

Depending on the factor targeted, the knockdowns resulted in between 39 and 3,892 **differentially expressed genes at an FDR of 5%** (Figure 1B; see **Table S3** for a summary of the results).

