



**Supplemental Figure S6. Comparing tested PIC binding-regions identified by ChIP-exo to GRO-cap measurements.** (A) Hypergeometric distribution of the probabilities to obtain the same site in the genome by both ChIP-exo and GRO-cap measurements.  $M$  is the number of potential binding sites in the human genome calculated as the size of the human genome ( $3 \times 10^9$  bp) divided by 200bp;  $n$  is the number of total TSSs identified in K562 cells by Core *et al.* (Core *et al.* 2014) using GRO-cap;  $N$  is the number of PIC binding-regions that we included in our study identified by ChIP-exo measurements by Venters *et al.* (Venters and Pugh 2013);  $k$  is the number of sequences that were identified by both ChIP-exo and GRO-cap methods. Shown is the probability to obtain the same sites number in both methods by chance ( $\sim 4$ ). (B) same as (A) but with only 5% of the potential binding sites. Shown is the probability to obtain the same sites number in both methods by chance ( $\sim 100$ ). (C) Comparison of promoter activity levels measured in our library for PIC binding-regions that were also identified by GRO-cap measurements or not ( $p < 10^{-18}$ , Wilcoxon rank-sum test). (D) Comparison of promoter activity of sequences from promoters and enhancers for 160 PIC binding-regions that were by ChIP-exo and GRO-cap assays ( $p < 10^{-4}$ , Wilcoxon rank-sum test). (E-F) Promoter activity measurements of the two orientations of sequences from promoters (E) and enhancers (F) for 160 PIC binding-regions that were by ChIP-exo and GRO-cap assays.