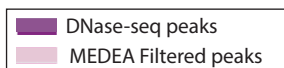


Accessible peaks overlapping with ChIP-seq peaks (%)



* Significant Decrease ($P < 0.01$)

* Significant Increase ($P < 0.01$)

Supplemental Figure S8

Supplemental Figure S8: MEDEA filtering sorts out accessible peaks associated with general transcriptional co-activators and chromatin binders. Similar to **Fig. 3A**, percentages of either the best 500 unfiltered DNase-seq peaks (purple bars) or the best 500 MEDEA-filtered DNase-seq peaks (pink bars, mean and SD within each MEDEA-filtered series is presented) that overlap with TF ChIP-seq peaks for the indicated chromatin binding factors (**Methods**). ChIP-seq datasets were obtained from ENCODE (**Supplemental Table S1.1**).