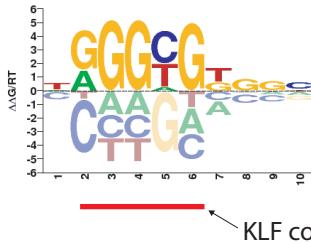
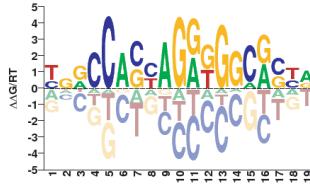
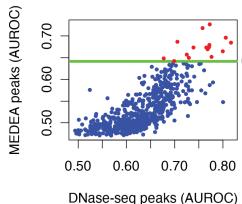
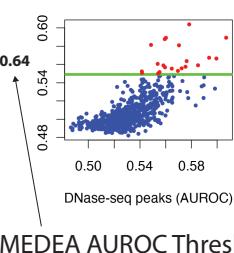
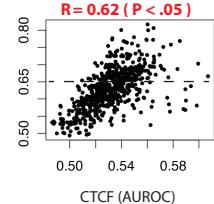
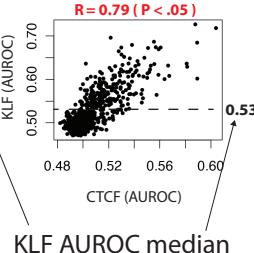


A**KLF12**

(PBM, M0443_1.02)

**CTCF**

(ChIP-seq, M1957_1.02)

**B****KLF motif****CTCF motif****C****DNase-seq peaks** $R = 0.62 (P < .05)$ **MEDEA peaks** $R = 0.79 (P < .05)$ **MEDEA AUROC Threshold****Supplemental Figure S12**

Supplemental Figure S12: MEDEA filtering reduces the bias in KLF motif enrichment due to CTCF motif similarity. (A) Position weight matrices for a representative KLF motif (*i.e.*, KLF12) and CTCF were obtained from the CIS-BP database. The red bars indicate the KLF core consensus regions shared by CTCF and KLF motifs. (B) Similar to **Fig. 4B** and **Supplemental Fig. S11**, AUROC values for the KLF and CTCF motifs. Red and blue points depict “high pool” and “low pool” of the MEDEA AUROC values. On the side, the values of the MEDEA thresholds (green line, **Supplemental Table S3.2, Methods**). (C) Correlation plots between KLF and CTCF motifs for AUROC values obtained without (left) and with (right) MEDEA filtering. On the side, the median AUROC values of the KLF motif.