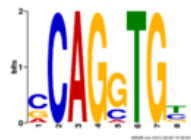**A** H1-hESC - Myers - ENCSR000BIT **TCF12**

1.
436 / 500
1.4e-412
CCAGGTGT

TCF12 Motif

2.
100 / 500
7.4e-91
TTTTGTTATGCAAAT

POU5F1 Motif

B GM12878 - Weissman - ENCSR000EYV **JUND**

2.
122 / 500
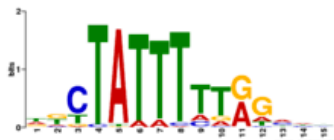2.0e-42
TGAGTCAT

JUN motif

3.
69 / 500
1.1e-18
AAGAACTGAAA

SPI1-IRF motif

GM12878 - Myers - ENCSR000BKB **Mef2A**

1.
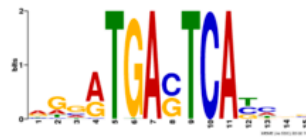484 / 500
2.0e-459
TGCTATTTTGGAAT

MEF motif
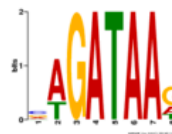
2.
129 / 500
1.1e-65
GGAACTGAAAG

SPI1-IRF motif

C K562 - Snyder - ENCSR000EGN **JUND**

1.
412 / 500
6.7e-817
AGGATGACTCATCGG

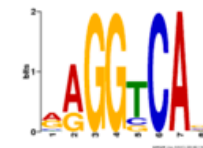JUN motif

5.
110 / 500
3.6e-22
CAGATAAG

GATA motif

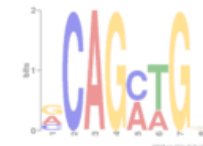K562 - Myers - ENCSR000BRS **NR2F2**

1.
397 / 500
1.1e-282
ACAGATAAGG

GATA motif

2.
343 / 500
7.3e-138
AAGGTCAG

NR motif

3.
219 / 500
7.4e-31
GCAGCTGT

E-BOX/TAL motif

Supplemental Figure S9

Supplemental Figure S9: FactorBook analysis of motif enrichment. For the indicated combinations of TFs and cell types, which had a mean fold-change of DFP overlap in MEDEA-filtered peaks above 2 (**Fig. 3B**), we checked the motif enrichment predicted by FactorBook (http://www.factorbook.org/human/chipseq/tf/) in the associated ChIP-seq peaks. The panels collect the enriched motifs that show the predicted specificity of either the ChIPed factors or other lineage specifiers. Transparent panels indicate that the enriched motifs were not found significantly centered toward the peak summits.