

Supplementary Information For: *TFmapper*: A tool for searching putative factors regulating gene expression using ChIP-seq data

Jianming Zeng ¹, Gang Li ^{1*}

¹Faculty of Health Sciences, University of Macau, Macau, China

* To whom correspondence should be addressed: gangli@umac.mo

107 8097 8 79786977 79787130 3.61593 8875 CBX2 3' UTR (NM_005189, exon 5 of 5) chr17 GSM748532 H1 Embryonic Stem Cell Embryo POLR2A human TF H1_ES_PoIIi_REP1

H1_ES_PoIIi

Supplementary Table S3. The GEO accession numbers for selected datasets illustrated in Figure 4 and supplementary Figure S1

Factors	GSM
EZH2	GSM1003524
CHD7	GSM1003473
CTCF	GSM1267206
POU5F1	GSM803438
SRF	GSM803425
BRCA1	GSM935517
H3K27me3	GSM733748
H3K4me3	GSM733657
H3K4me1	GSM466739
POLR2A	GSM803366
EP300	GSM803542
SOX2	GSM456570
MAFK	GSM935292
MXI1	GSM935293
SP2	GSM101076
USF2	GSM935380
CTBP2	GSM935463

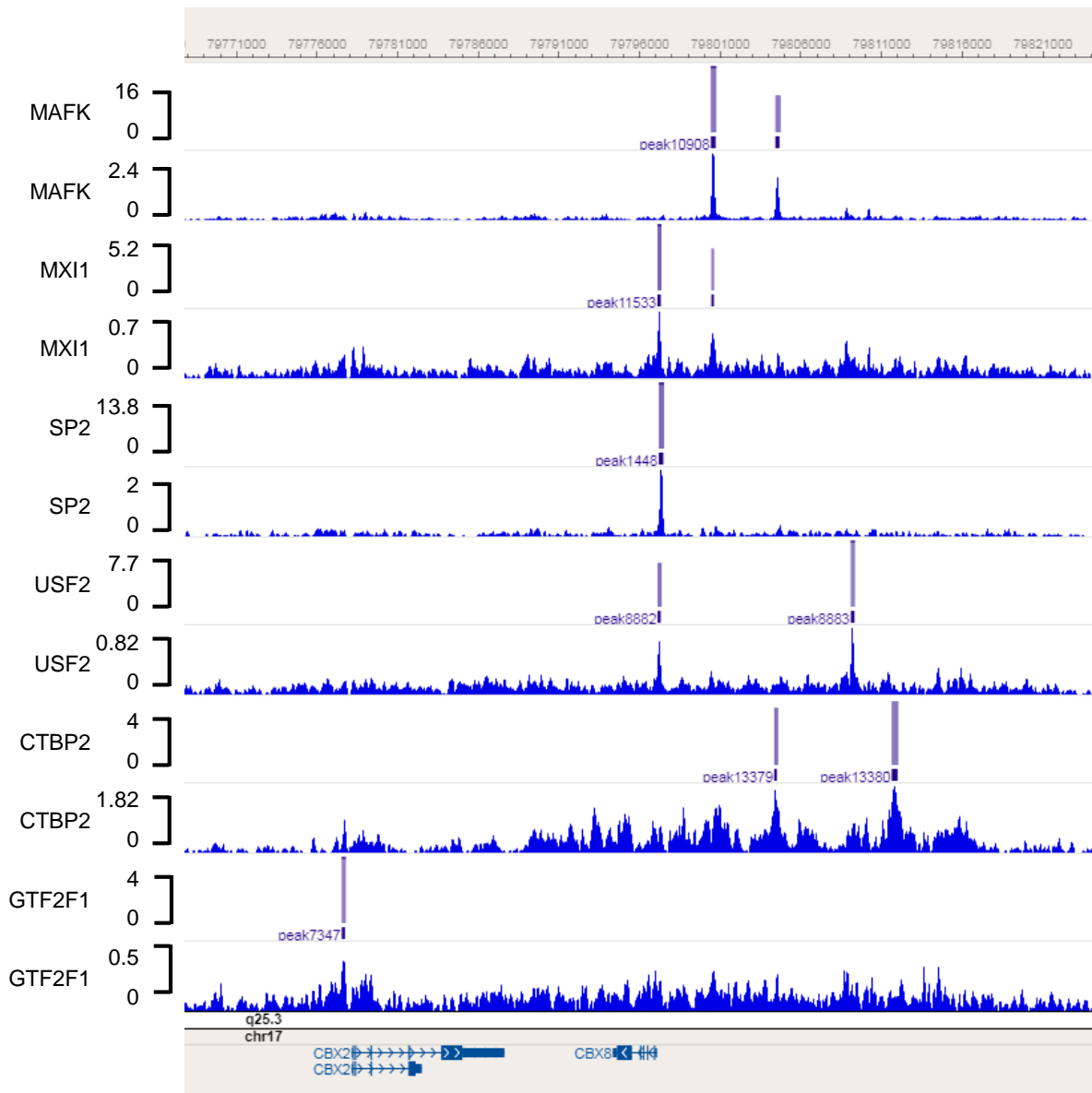


Figure S1. Binding profiles of selected trans-acting factors at the CBX2-CBX8 locus in hESC-H1 cells. The peaks are visualized with the WashU Epigenome Browser. The GEO accession number for each dataset can be found in the Supplementary Table S3. For each factor, the Y-axis of the top panel displays the enrichment score, the Y-axis of the bottom panel displays reads per million (RPM).