



Figure SX. a) Transdifferentiation of human B-cell precursors into macrophages induced by CEBP α expression. RNA-seq and ChIP-seq data on nine histone post-translational modifications were obtained at twelve time points during the process. Data available through ENCODE portal. b) Log likelihood values for tHMM models computed with between 6 and 10 states; The selected 8 states are indicated with a vertical dashed line. c) cCREs' dynamism over time based on the amount of chromatin states each element displays during transdifferentiation. cCREs categories generated based on ENCODEv4's classification –CA/TF refers to a category comprising all cCREs that are not defined as dELSSs, pELSSs or PLSs–. d) Sankey plot representing transitions between states in consecutive time points, as well as the proportion of cCREs assigned to each state during transdifferentiation. e) Sankey plots representing state transitions between first and final time points dividing cCREs into three categories i) TSS-proximal –PLS and pELS–, ii) marked TSS-distal –dELS–, and iii) unmarked open chromatin regions/TF binding motifs –CA-H3K4me3, CA-CTCF, CA-TF, CA, and TF–; the number of elements belonging to each category is indicated. f) 88,150 accessible cCREs' dynamism over time based on the amount of chromatin states each element displays during transdifferentiation. cCREs categories generated based on ENCODEv4's classification –CA/TF refers to a category comprising all cCREs that are not defined as dELSSs, pELSSs or PLSs– (equivalent to panel c). Horizontal lines indicate the percentage of cCREs undergoing one chromatin state during transdifferentiation in the complete set of active cCREs for dELSSs (yellow), pELSSs (orange), and PLSs (red) (see panel c).