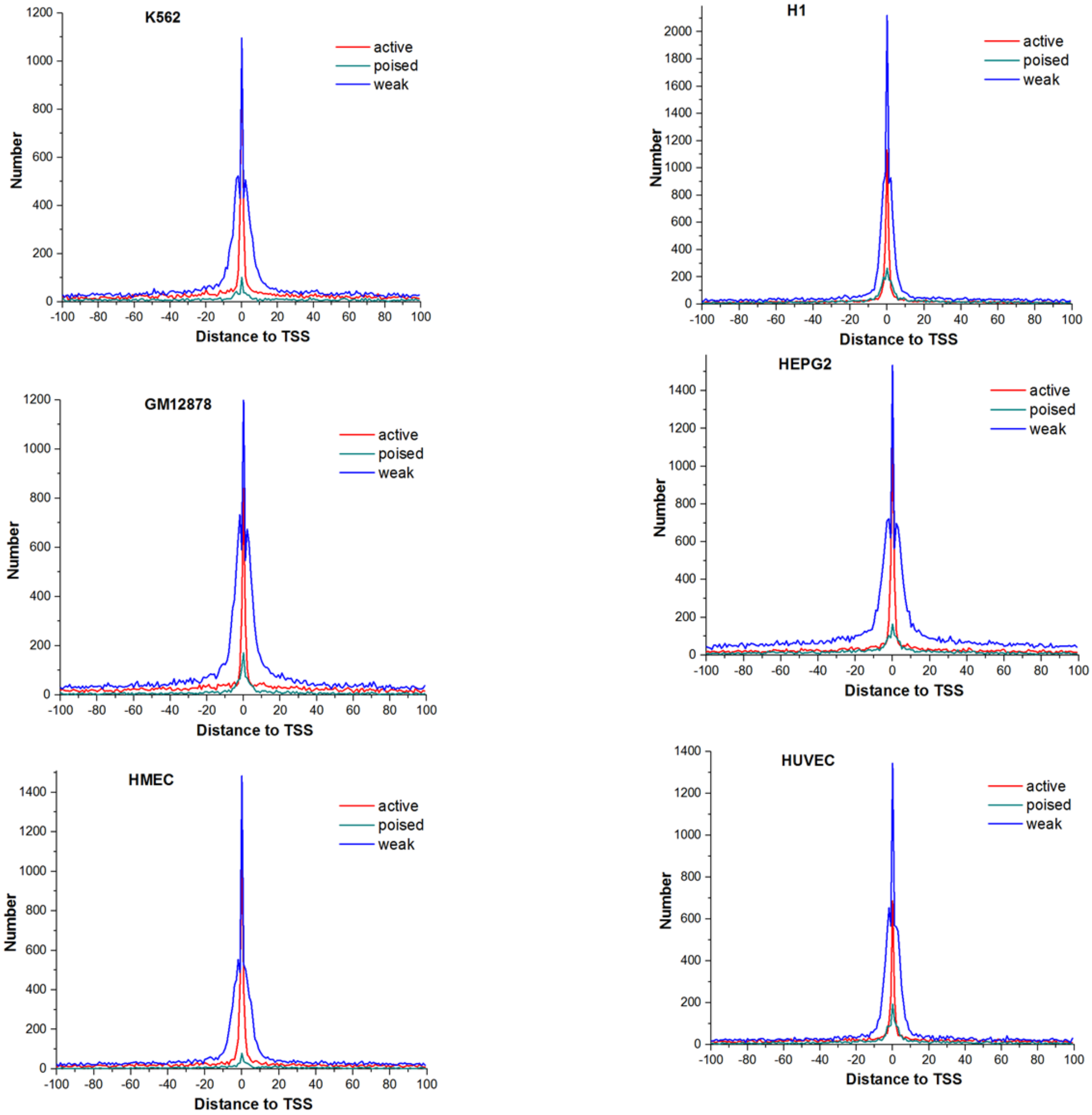
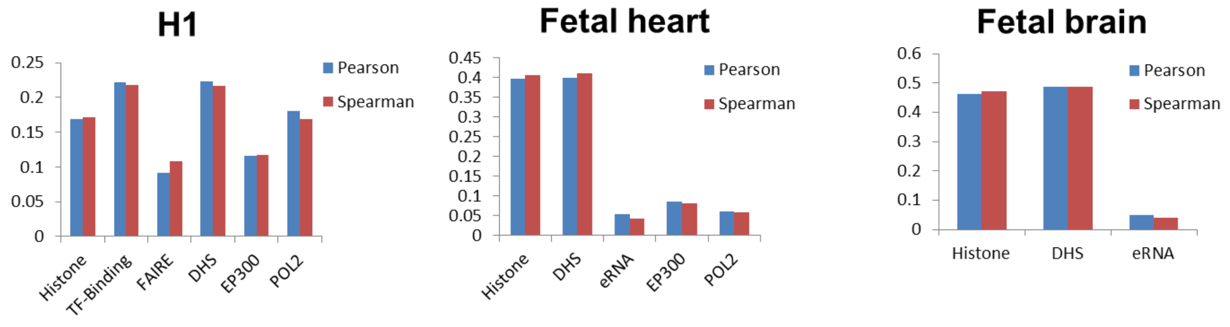
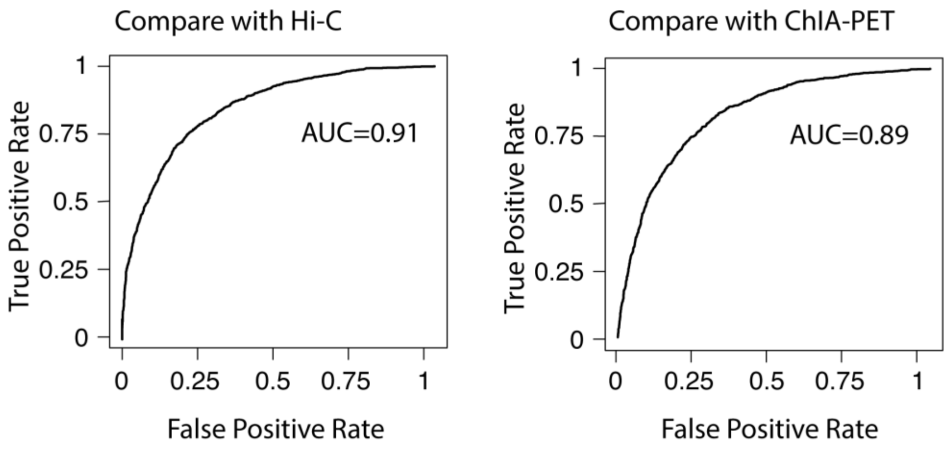


Supplementary Fig. 1: relative genomic positions of promoters to TSS in six cell lines. Three types of promoters (active, poised and weak) are extracted from genome annotation based on histone modifications (http://ucscbrowser.genap.ca/cgi-bin/hgTrackUi?db=hg19&g=wgEncodeBroadHmm). Most promoters (99.5% of all) are within 5Kb (i.e. 25 bin, 1 bin=200bp) upstream of TSS.



Supplementary Fig. 2: comparison of the relative weights for all tracks between the rank-based Spearman and Pearson. Three cell types with different numbers of tracks were selected for analysis. The relative weight for each track was calculated based on Spearman and Pearson correlation respectively. It is clear that both approaches yielded very similar relative weights for these cell types.



Supplementary Fig. 3: Comparison of predictions between IM-PET and Hi-C or CHIA-PET methods. The reported EP interaction in CD4+, GM12878, CD34, Hela, HMEC, HUVEC, IMR90 and NHEK cells are used as the gold standard to assess the quality of our IM-PET prediction. Specifically, we first identified EP pairs in which enhancers overlap with the interacting fragments reported by the 3C-based methods. Those EP pairs are regarded as eligible for comparison with ChIA-PET/Hi-C data. Then the ROC curves were computed based on using either Hi-C or ChIA-PET data. The AUC values for the predictions in these new cell types (~0.9) are similar the predictions we evaluated in the original IM-PET prediction.