

Supplemental Figure S18. Coefficients for lasso models to predict RNA/DNA for MT (panel A), WT (panel B) and MT-WT (panel C) using genomic annotations, without including gkm-SVM score. The R glmnet package was used to fit the models, and the tuning parameter for each model was selected via 10-fold cross-validation. All annotation features were scaled and centered before fitting the lasso model. Categorical features were coded as K-1 binary columns, where K is the number of levels of the categorical feature. We excluded ZNF274 and EZH2 annotations from the model, because none of the inserts overlapped with these ChIP-seq tracks

