Supplemental Figure S21. Coefficients for a lasso model that uses genomic annotations as well as LS-GKM scores to predict RNA/DNA ratios for MT (panel A), WT (panel B) and MT-WT (panel C). Models were fit as described in the methods and summarized in Fig. S17. In addition, the 64 HepG2 ChIP-seq derived LS-GKM model scores were included as predictors (Mod-prefix).