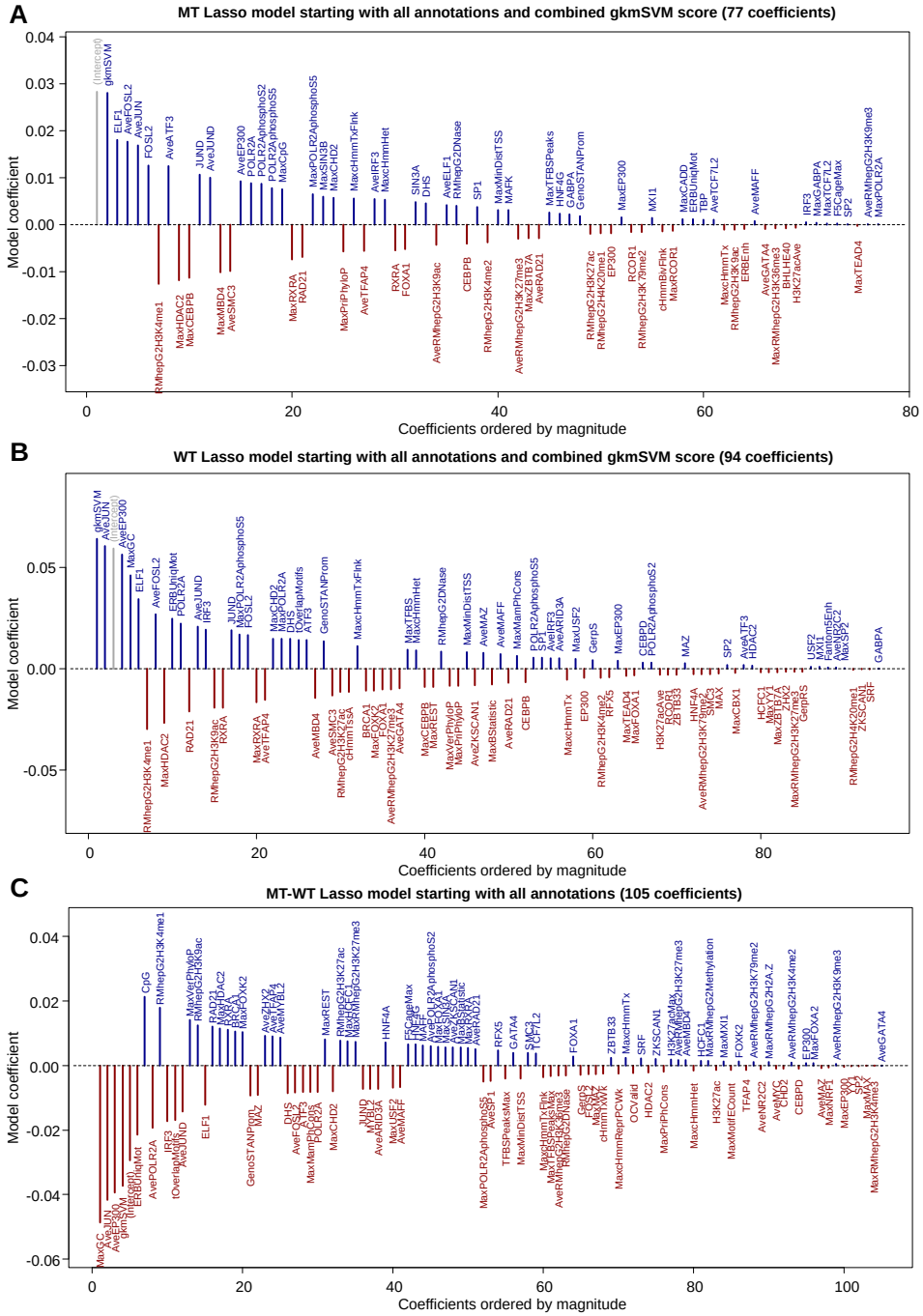Supplemental Figure S19. Coefficients for lasso models to predict RNA/DNA for MT (panel A), WT (panel B) and MT-WT (panel C) using genomic annotations and the combined HepG2 gkm-SVM score as predictors. Additional details are as in Figure S17. In the resulting models, the sequence based gkm-SVM score is assigned the highest model coefficient.