Supplemental Figure S17. Correlation (Pearson/p-rho and Spearman/s-rho) of MT and WT RNA/DNA ratios fit in linear models derived from all genomic annotations with and without HepG2 gkm-SVM scores. SRES and other control sequences were excluded from this analysis as genomic annotations are mostly missing for those. WT linear models correlate better with the WT ratios than do MT linear models for the MT ratios (e.g. Spearman R^2 of 0.271 WT vs. 0.148 for MT / Pearson R^2 of 0.314 for WT vs. 0.194 for MT). Gapped-k-mer SVM scores further improve R^2 values especially for WT ratios (Spearman R^2 0.302 for WT vs. 0.156 for MT / Pearson R^2 0.341 for WT vs. 0.203 for MT).