

**Supplemental Figure S22.** The results of 440 single-feature linear models predicting log2 RNA/DNA ratios using a single genomic annotation. The two-tailed p-value corresponding to the t-ratio based on a Student-t distribution (Table S7) is plotted for the inclusion of each coefficient in a single coefficient plus intercept linear model for predicting log2 RNA/DNA ratios for MT and WT experiments. For plotting purposes, p-values smaller than  $10^{-10}$  were set to this threshold and p-values were log10 transformed. Highlighted in red are coefficients passing a p-value threshold of 0.05 (0.00012 after Bonferroni correction) in MT or WT while failing it in the other experiments. We also require a minimum p-value difference (0.0025) between MT and WT to account for stochasticity in the p-value estimates.

