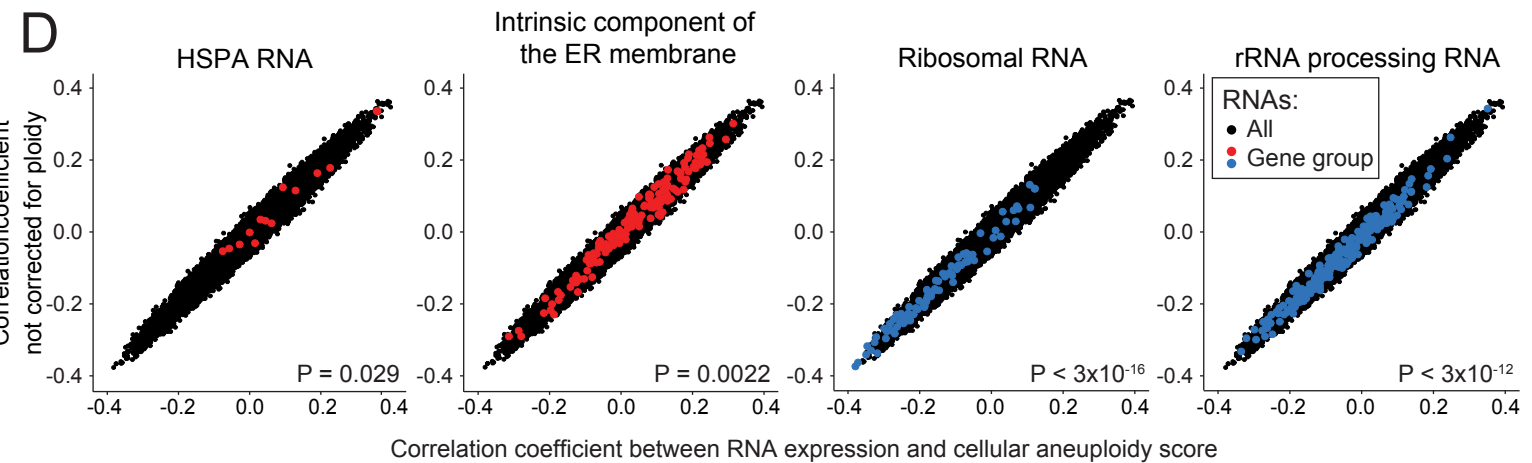
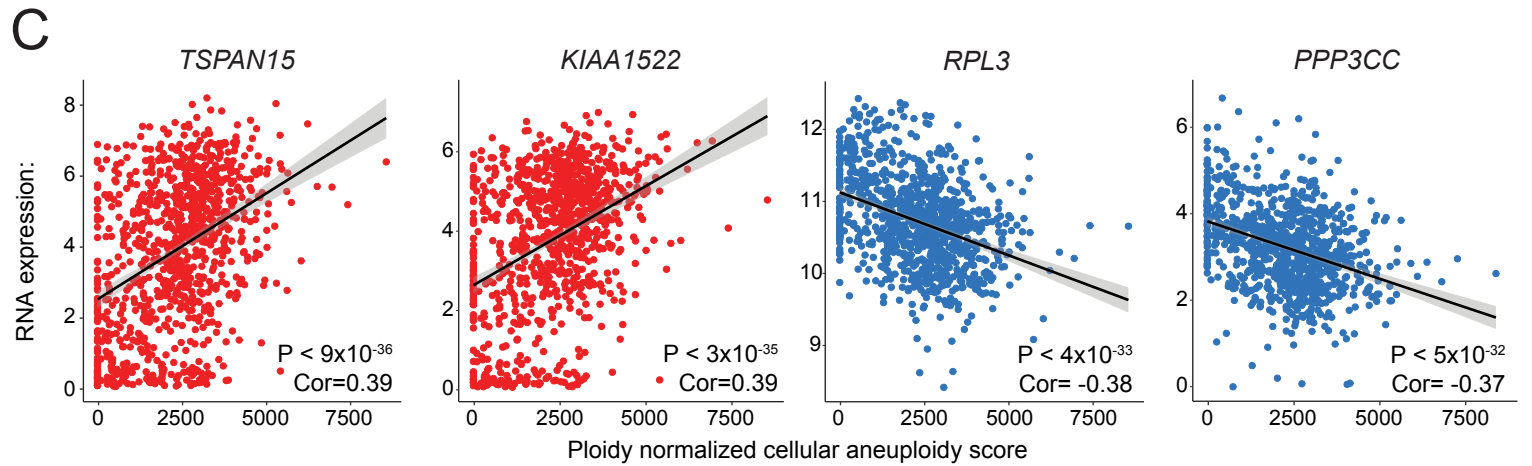
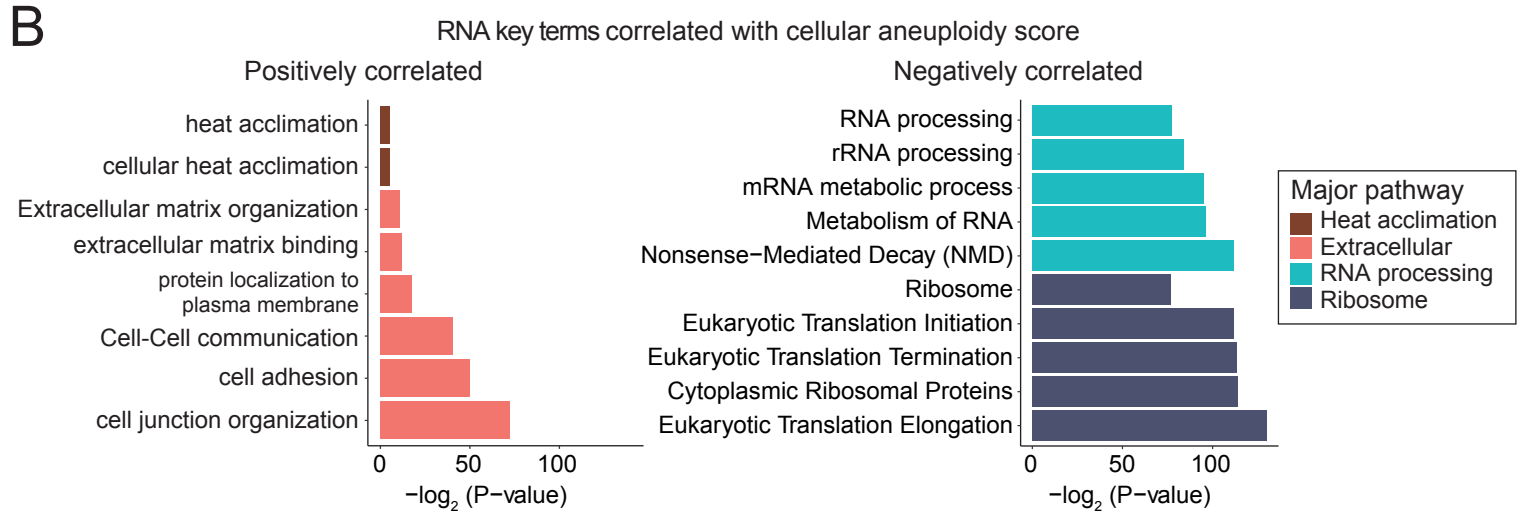
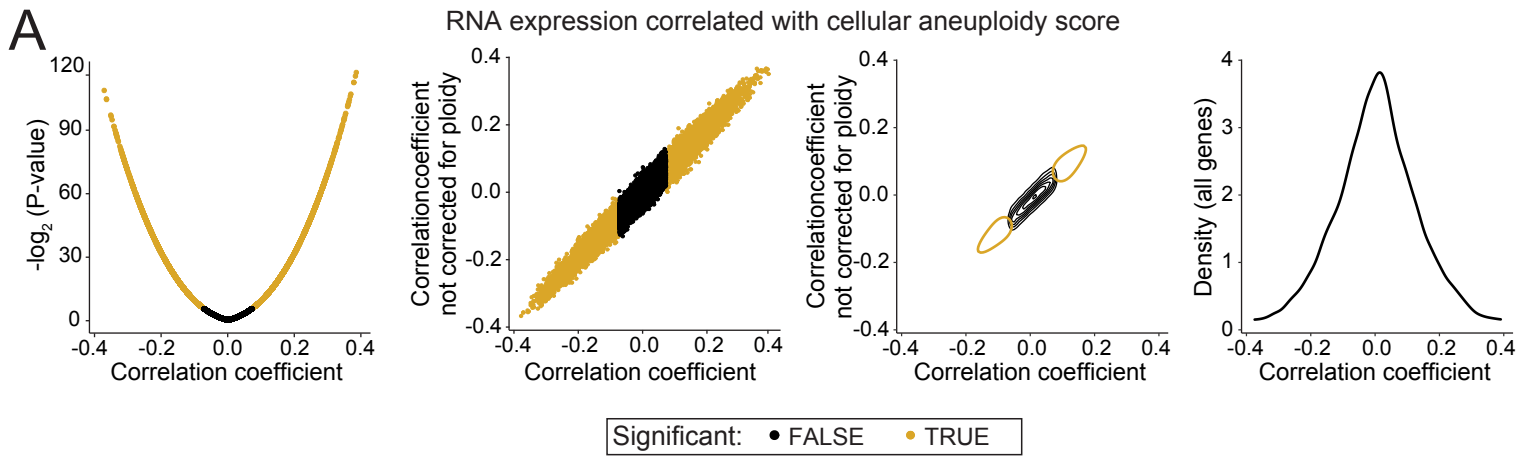


Supplemental Figure S7



Supplemental Figure S7. Specific RNA expression levels correlate with total cellular aneuploidy scores.

A) Pearson correlation coefficients between RNA expression levels and cellular aneuploidy score were calculated. To better view the distribution of this data, the data was plotted in four ways. The negative \log_2 of the uncorrected p-value was set relative to the correlation coefficient (left). Correlation coefficient between RNA expression and either cellular aneuploidy score (x axis), or the cellular aneuploidy score not corrected for cellular ploidy (y axis) was plotted in two ways (center two graphs). Finally, a one dimensional density plot of the correlation coefficient between RNA expression and cellular aneuploidy score (right). Genes that are significant at a $P < 0.05$ threshold after Benjamini Hochberg correction with a 5% FDR are labeled in gold.

B) Bar graphs displaying the GO terms enriched among RNAs that are positively or negatively correlated with cellular aneuploidy score. Terms are color-coded by their overarching pathway.

C) The two RNAs that are most significantly positively correlated (left, red, gene names: *TSPAN15* and *KIAA1522*), and negatively correlated (right, blue, gene names: *RPL3* and *PPP3CC*) with aneuploidy scores are displayed. RNA expression is plotted according to the aneuploidy score per cell line.

D) Scatter plots displaying the correlation coefficients between gene expression and cellular aneuploidy score and the cellular aneuploidy score not corrected for ploidy are displayed for all genes (black), as well as the indicated gene groups (red or blue). “HSPA” genes and “intrinsic component of the ER membrane” genes (red) are significantly more positively correlated with cellular aneuploidy scores than other genes. Ribosomal RNAs and rRNA processing genes (blue) are significantly more negatively correlated with aneuploidy scores than other genes. P-values from two-sided *t*-tests of RNA expression in gene groups vs all other genes are displayed.