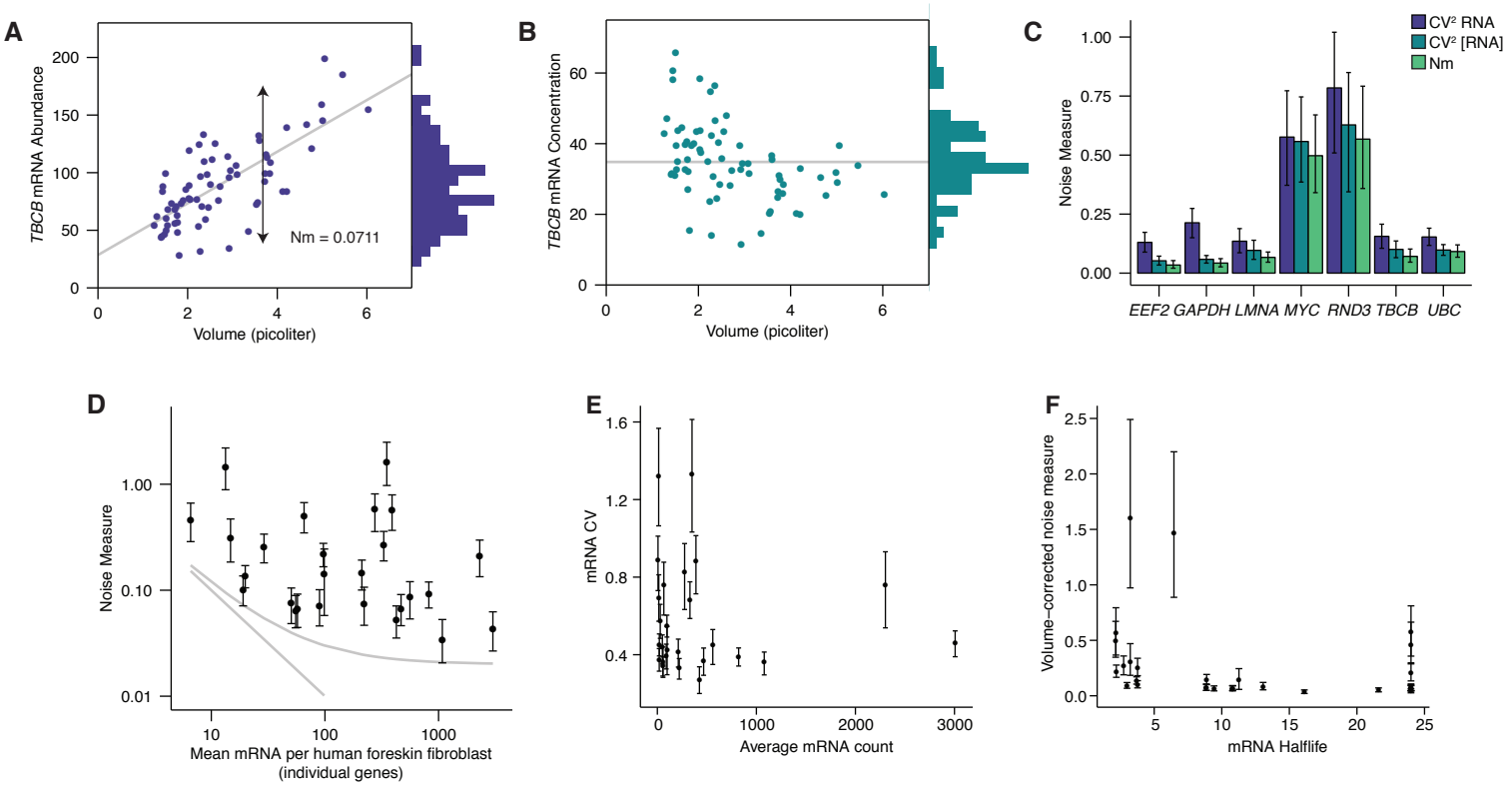
Supplementary Figure 17



Supplementary Fig. 17. Quantification of cell-to-cell variability in gene expression.
A. *TBCB* mRNA abundance and volume in hFF cells. Each point represents a single-cell measurement. Histogram indicates mRNA distribution. Arrow indicates volume-corrected noise measure, see (c). Gray line is best linear fit.
B. *TBCB* mRNA concentration vs. volume. These data are the same as in (a), but each is normalized by volume. Histogram indicates distribution of mRNA concentration. Gray line indicates average concentration. Data are from a combination of two biological replicates.
C. Comparison of squared coefficients of variation for mRNA abundance, concentration, and volume-corrected noise measure, Nm, for a sampling of genes in hFF cells. Nm is calculated by bootstrapping; error bars represent 95% confidence interval, calculated by bootstrapping.
D. Volume-corrected noise measure values for different genes in hFF cells. Each data point represents a collection of single-cell measurements for one gene. The straight gray line represents the Poisson limit. The curved gray line is the Poisson limit plus our experimental noise limit, a combination of the Poisson limit and a 15% measurement error.
Data for each gene is a combination of at least two biological replicates, with at least 30 cells per replicate.
E. We calculated the coefficient of variation (CV = standard deviation / mean) for mRNA counts in single CRL2097 cells and plotted against mean RNA count measured by RNA FISH. We find that CV does not scale with mean mRNA abundance.
F. We compared volume-corrected noise measure and mRNA half-life. We obtained half-life values from Tani et al., Genome Res. (2012). We find that volume-corrected noise measure does not depend strongly on half-life. (E,F) Each data point represents one gene. For each gene, we have at least two biological replicates with at least 30 cells per replicate. Error bars represent 95% confidence intervals, calculated by bootstrapping.