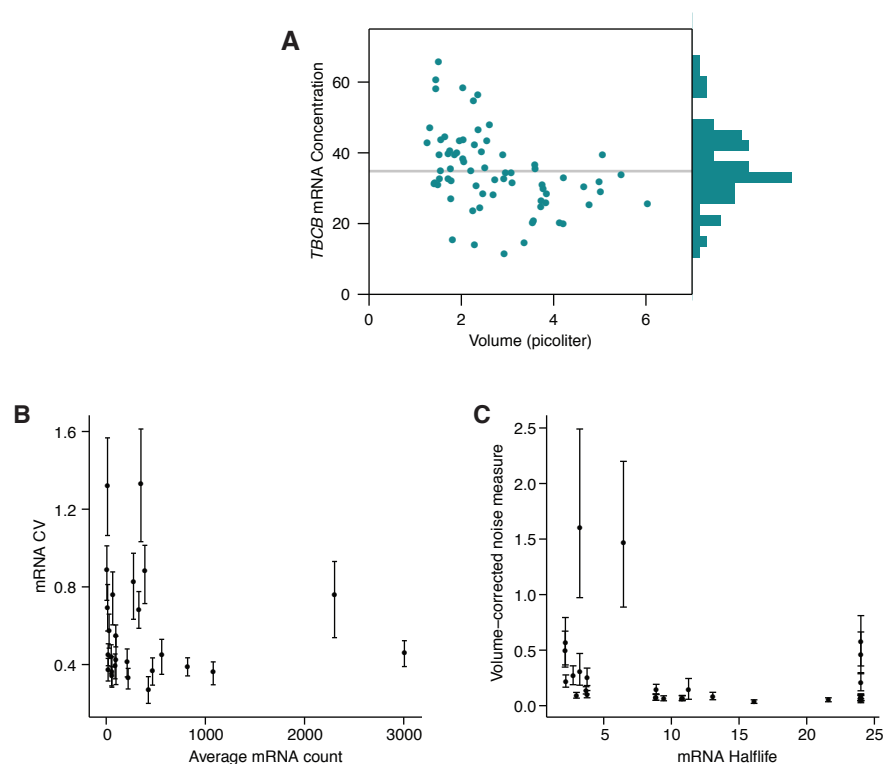


Supplementary Figure 18



Supplementary Fig. 18. Quantification of cell-to-cell variability in gene expression.

A. *TBCB* mRNA concentration vs. volume. These data are the same as in (Fig. 6C), 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.

B. We calculated the coefficient of variation ($CV = \text{standard deviation} / \text{mean}$) for mRNA counts in single human foreskin fibroblast cells and plotted against mean RNA count measured by RNA FISH. We find that CV does not scale with mean mRNA abundance.

C. 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.

(B,C) 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.