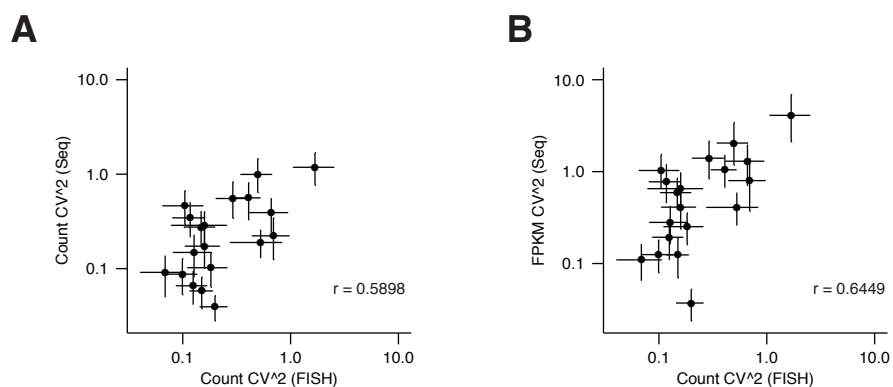


Supplementary Figure 21



Supplementary Fig. 21. Comparison of noise metrics through RNA FISH and single-cell sequencing.

A. Correspondence between CV^2 of RNA FISH counts and CV^2 of inferred counts from single-cell sequencing (transforming FPKM as in Supplementary Fig. 14 and Methods). Each data point represents a single gene.

B. Same as A, except using CV^2 of FPKM from single-cell sequencing instead. Correlation is slightly higher than in A.

For all plots, Nm is calculated by bootstrapping; error bars represent 95% confidence intervals, calculated by bootstrapping.