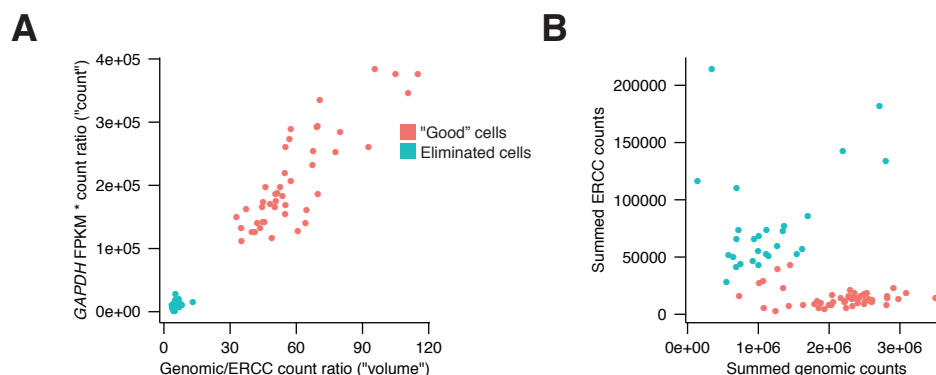


Supplementary Figure 17



Supplementary Fig. 17. Classification of cells to eliminate from sequencing analysis.

A. "Count" vs. "volume" for GAPDH from single-cell sequencing data. We define "volume" as the ratio between genomic reads and ERCC reads for each cell. This quantity is more representative of total RNA, which we know to be roughly proportional to volume, although the relationship is not exactly proportional due to volume-independent transcription (see Supplementary Fig. 10). We observed two clearly distinct classes of cells, those with a volume range that matches what we see by imaging and RNA FISH and those that have very low volumes. For unknown reasons, these cells ended up with a considerably higher ratio of ERCC reads than genomic reads, and we eliminated them from our subsequent analyses.

B. ERCC counts vs. genomic counts for the cells that we kept and those we eliminated.