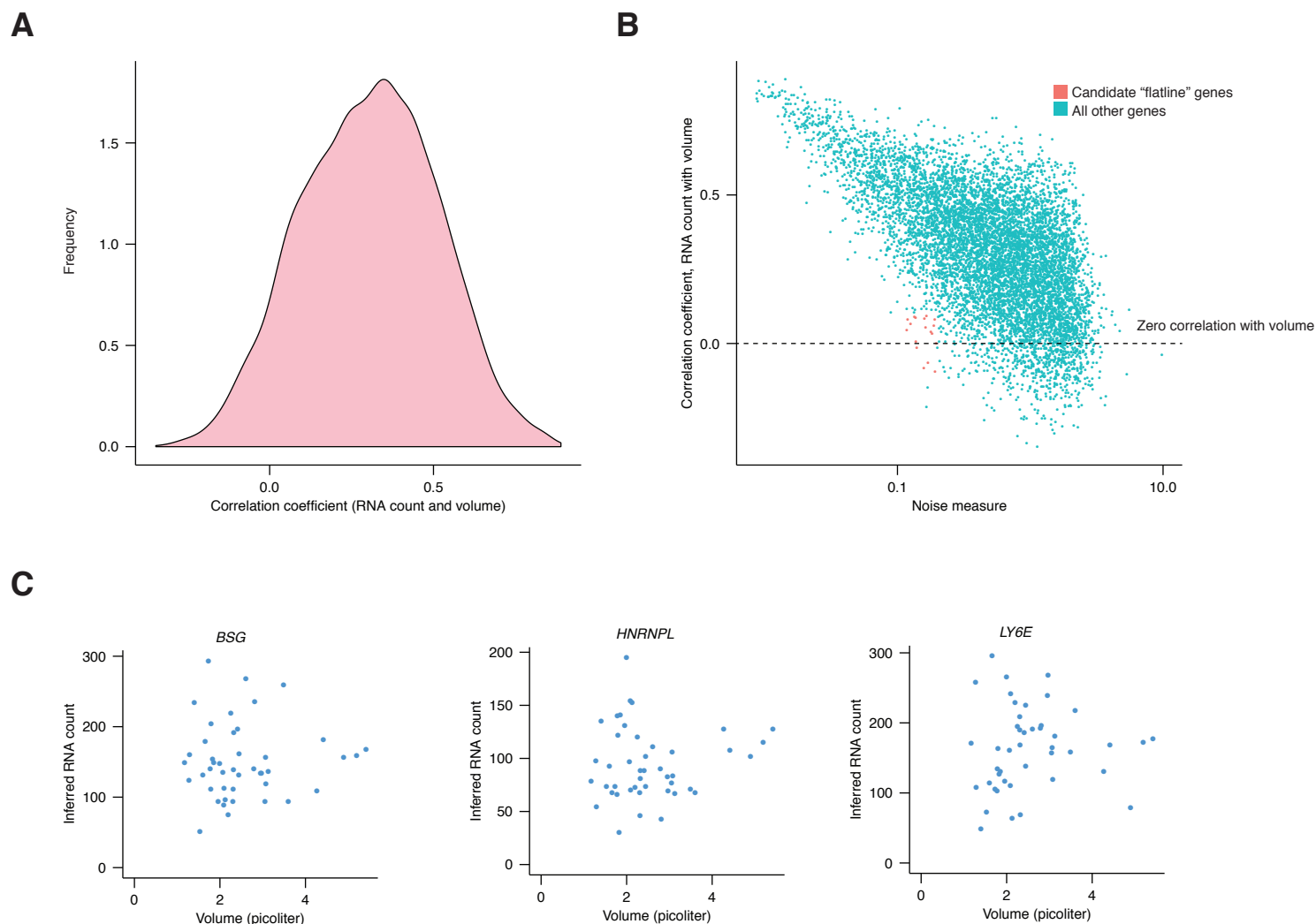


Supplementary Figure 16



Supplementary Fig. 16. There are likely no genes that have the same abundance at all volumes.

A. Histogram of correlation coefficients between RNA count and volume using single-cell RNA sequencing data. Here we chose genes with a median FPKM > 0, which left us with a pool of 8108 genes.

B. Identifying genes that may be candidate "flatline" genes that express at the same absolute level, regardless of volume. Our candidate genes were genes that had a low Nm ($Nm < 0.2$), and had correlation with volume close to zero ($-0.1 < r < 0.1$).

C. Representative plots of candidate flatline genes. While none of the genes we observed appeared to have the same abundance at all volumes, it is possible that there are flatline genes that we were unable to discern due to technical variability in RNA quantification via sequencing.