Supplementary Figures

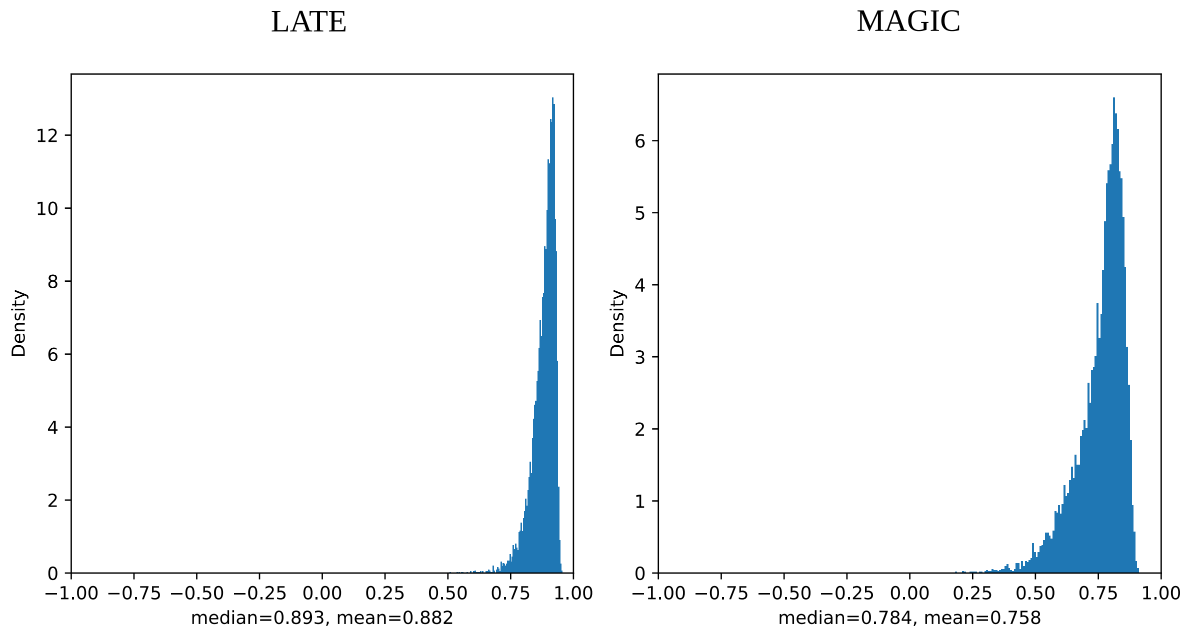


Figure S1: Histograms of Pearson correlations between the imputed gene expression profile and the ground truth in individual cells on the PBMC_G949_10K data (949 genes and 10K cells).

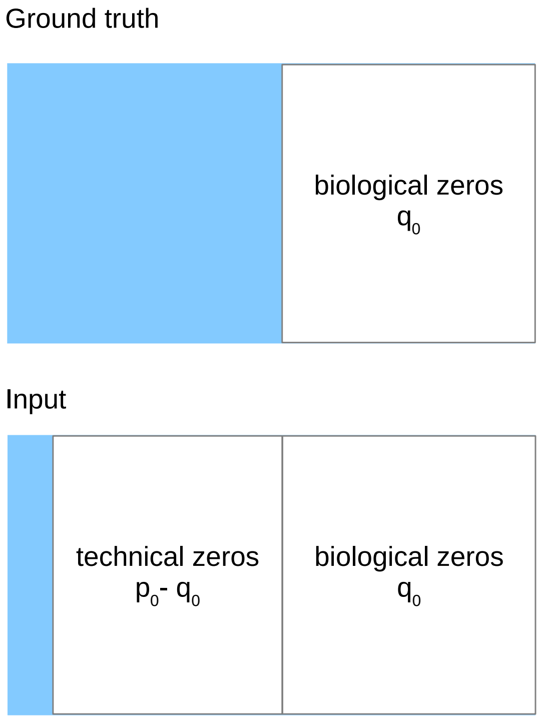


Figure S2: An illustration of biological and technical zeros in the ground truth and input. p_0 is the percentage of zeros in the input, and q_0 that in the ground truth.

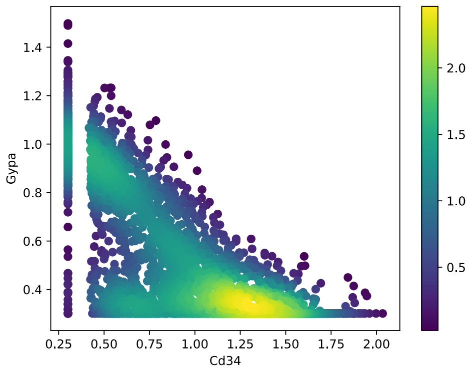


Figure S3: Two genes (*Cd34* vs *Gypa*) with a nonlinear relationship in the synthetic data based on the mouse bone marrow data (MAGIC_mouse; 16,114 genes and 2,576 cells) imputed by ALRA. Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

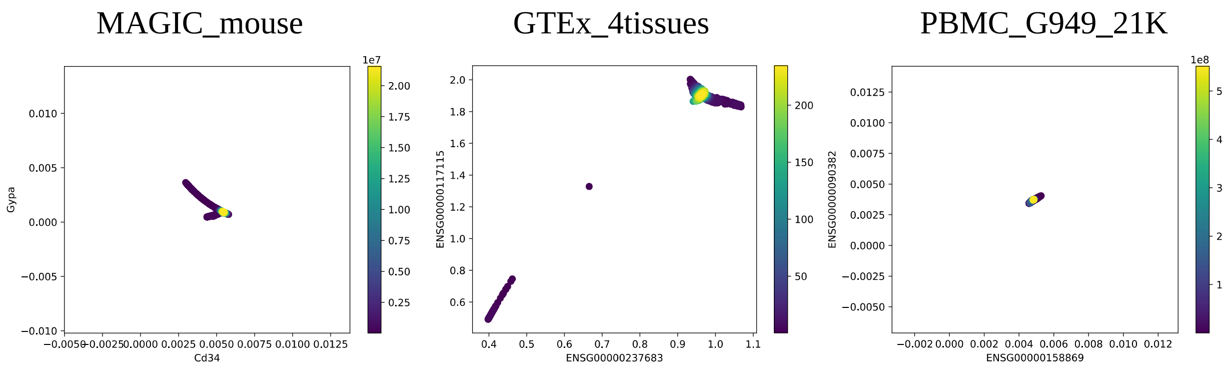
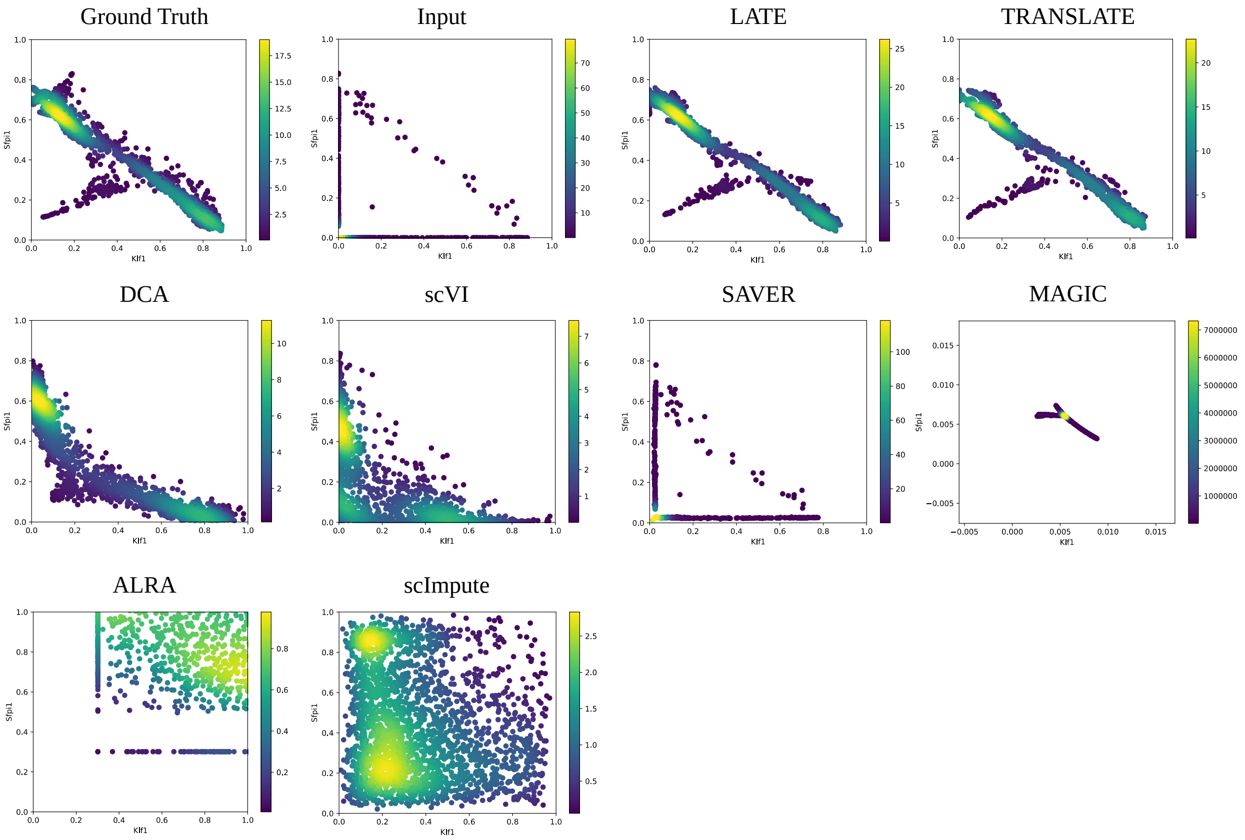


Figure S4: Nonlinear relationship results from MAGIC on the mouse bone marrow data (MAGIC_mouse; 16,114 genes and 2,576 cells), GTEx (GTEx_4tissues; 56,202 genes and 3,164 samples), and 10x Genomics PBMC data (PBMC_G949; 949 genes and 21,065 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.


Ground Truth

Input

LATE

TRANSLATE

DCA

scVI

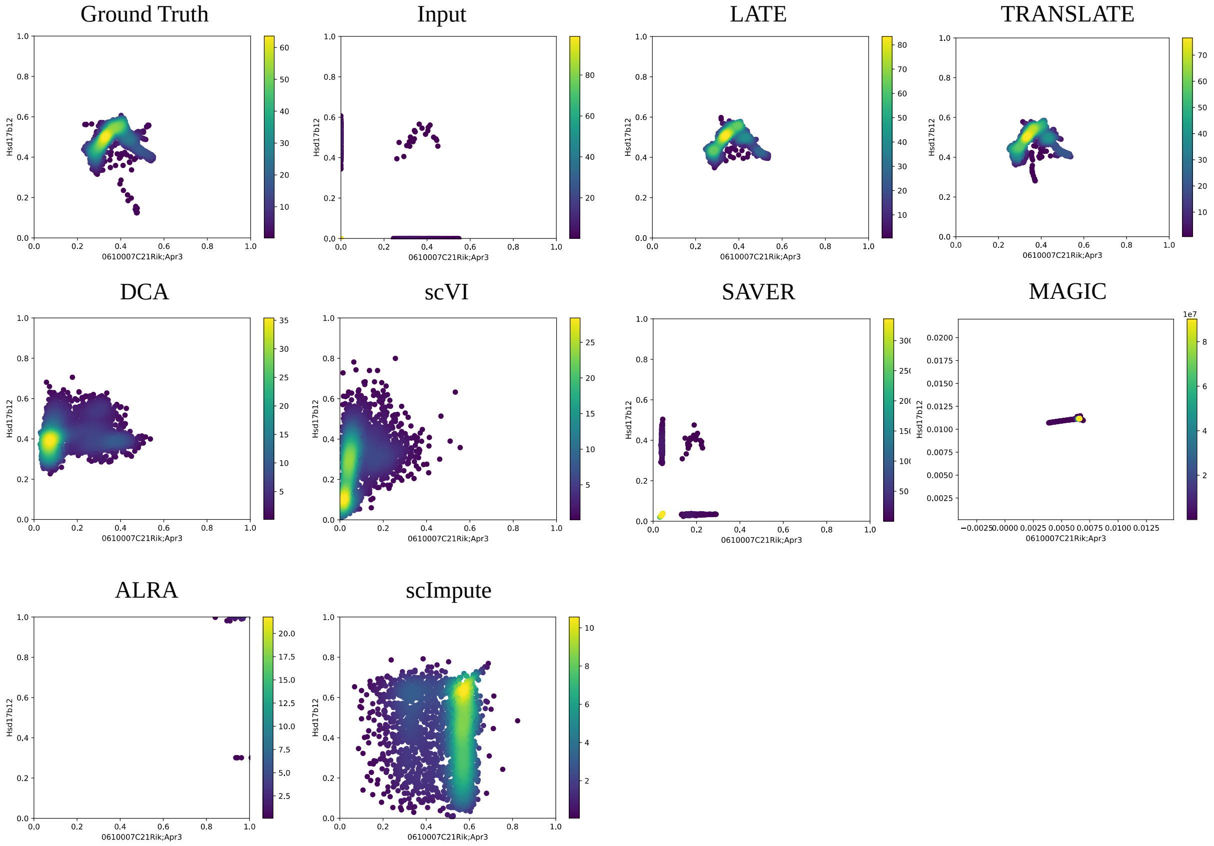
SAVER

MAGIC

ALRA

scImpute

Figure S5: Two genes (*Klf1* vs *Sfpi1*) with a nonlinear relationship in the synthetic data based on the mouse bone marrow data (MAGIC_mouse; 16,114 genes and 2,576 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.


Ground Truth

Input

LATE

TRANSLATE

DCA

scVI

SAVER

MAGIC

ALRA

scImpute

Figure S6: Two genes (*0610007C21Rik; Apr3* vs *Hsd17b12*) with a nonlinear relationship in the synthetic data based on the mouse bone marrow data (MAGIC_mouse; 16,114 genes and 2,576 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

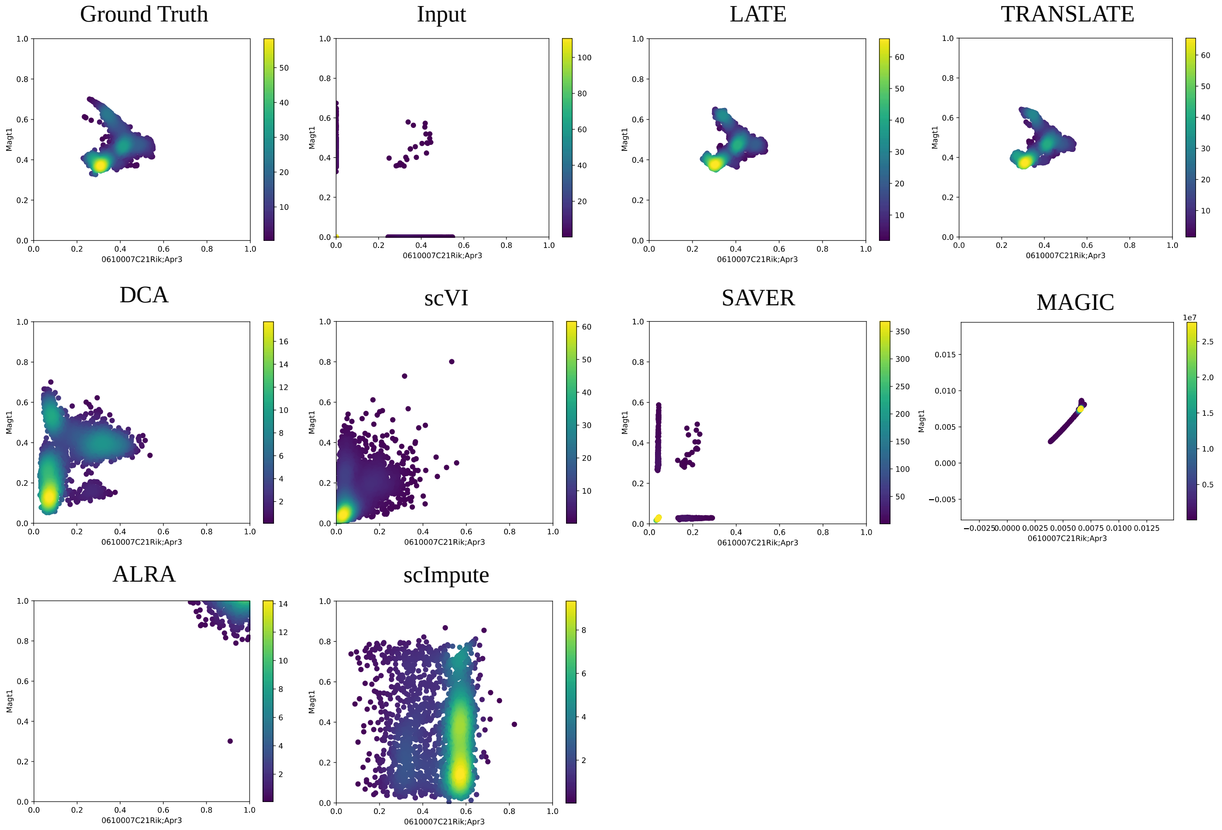


Figure S7: Two genes (*0610007C21Rik; Apr3* vs *Magt1*) with a nonlinear relationship in the synthetic data based on the mouse bone marrow data (MAGIC_mouse; 16,114 genes and 2,576 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

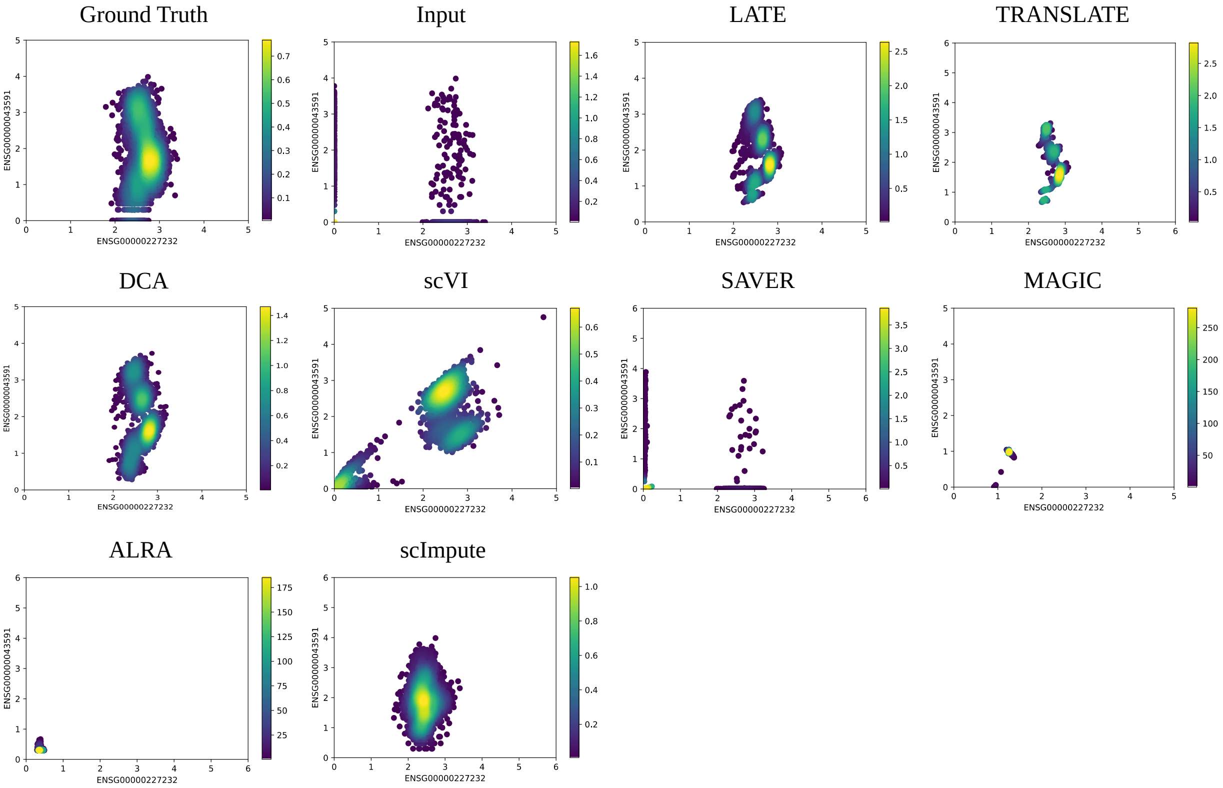


Figure S8: Two genes (*ENSG00000227232* vs *ENSG00000043591*) with a nonlinear relationship in the synthetic data based on GTEx (GTEx_4tissues; 56,202 genes and 3,164 samples). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

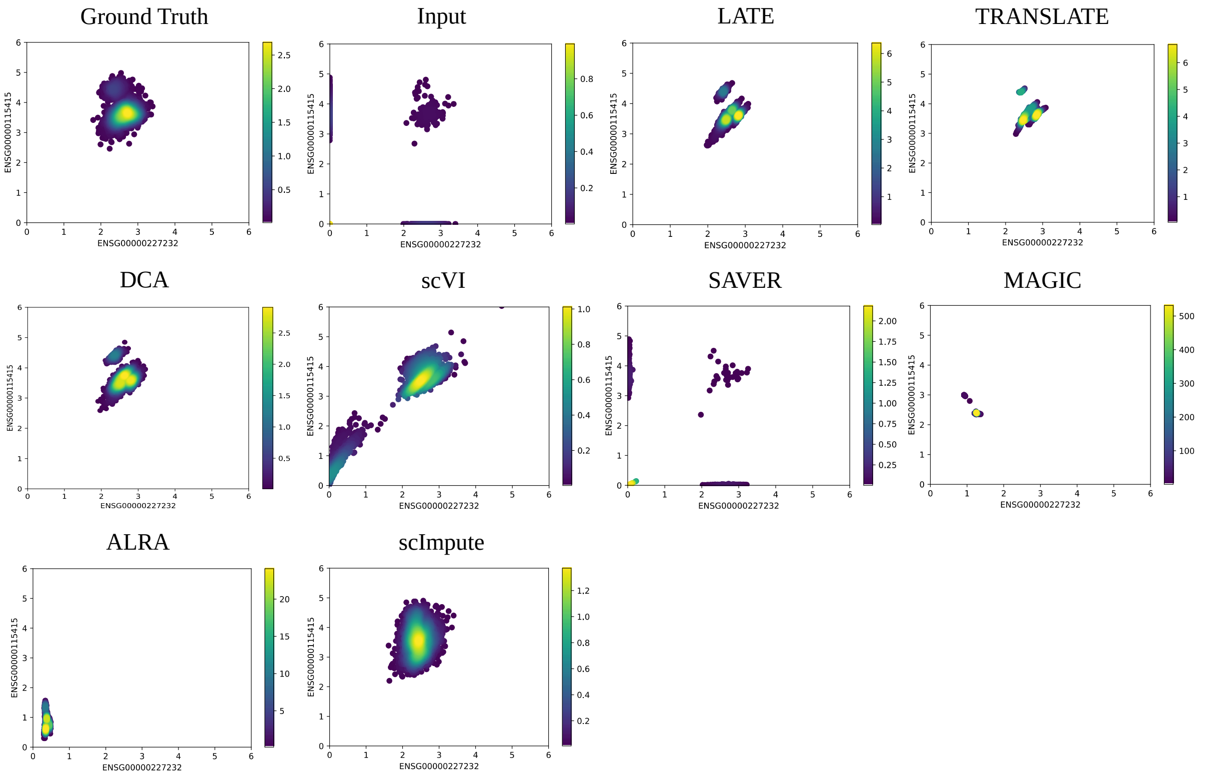


Figure S9: Two genes (*ENSG00000227232* vs *ENSG00000115415*) with a nonlinear relationship in the synthetic data based on GTEx (GTEx_4tissues; 56,202 genes and 3,164 samples). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

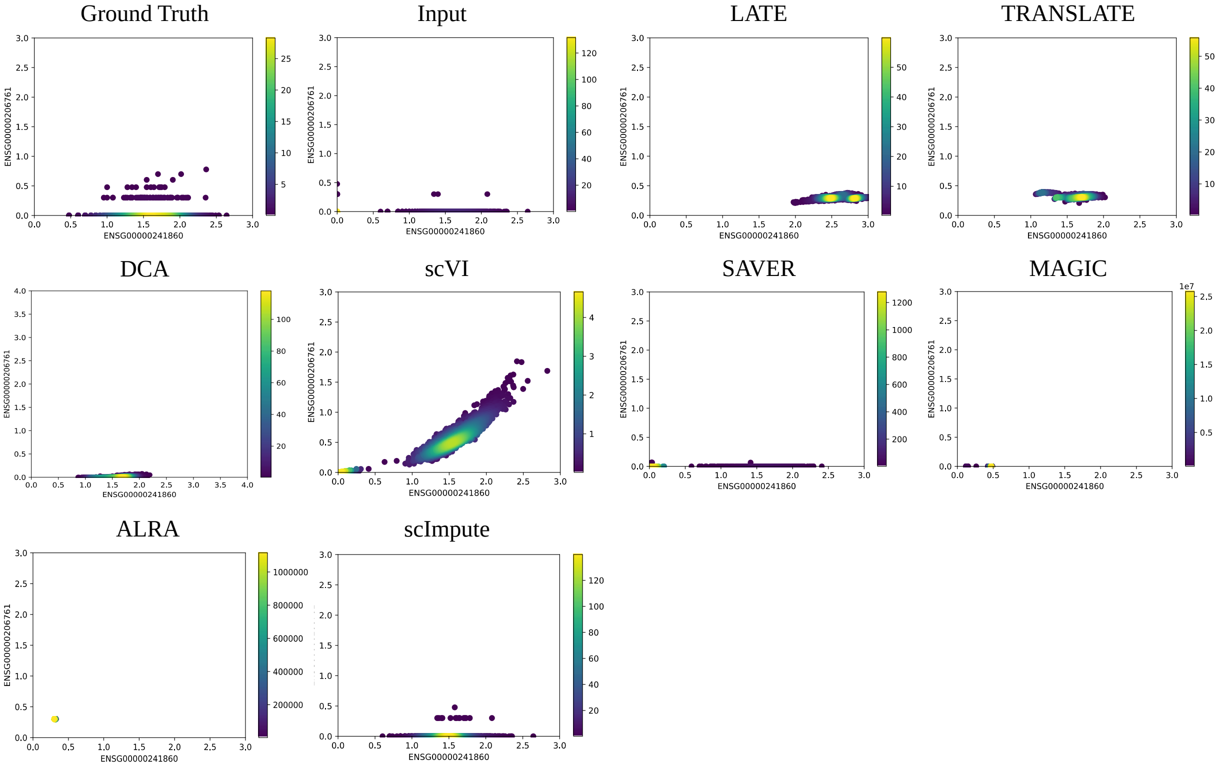


Figure S10: Two genes (*ENSG00000241860* vs *ENSG00000206761*) with a nonlinear relationship in the synthetic data based on GTEx (GTEx_4tissues; 56,202 genes and 3,164 samples). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

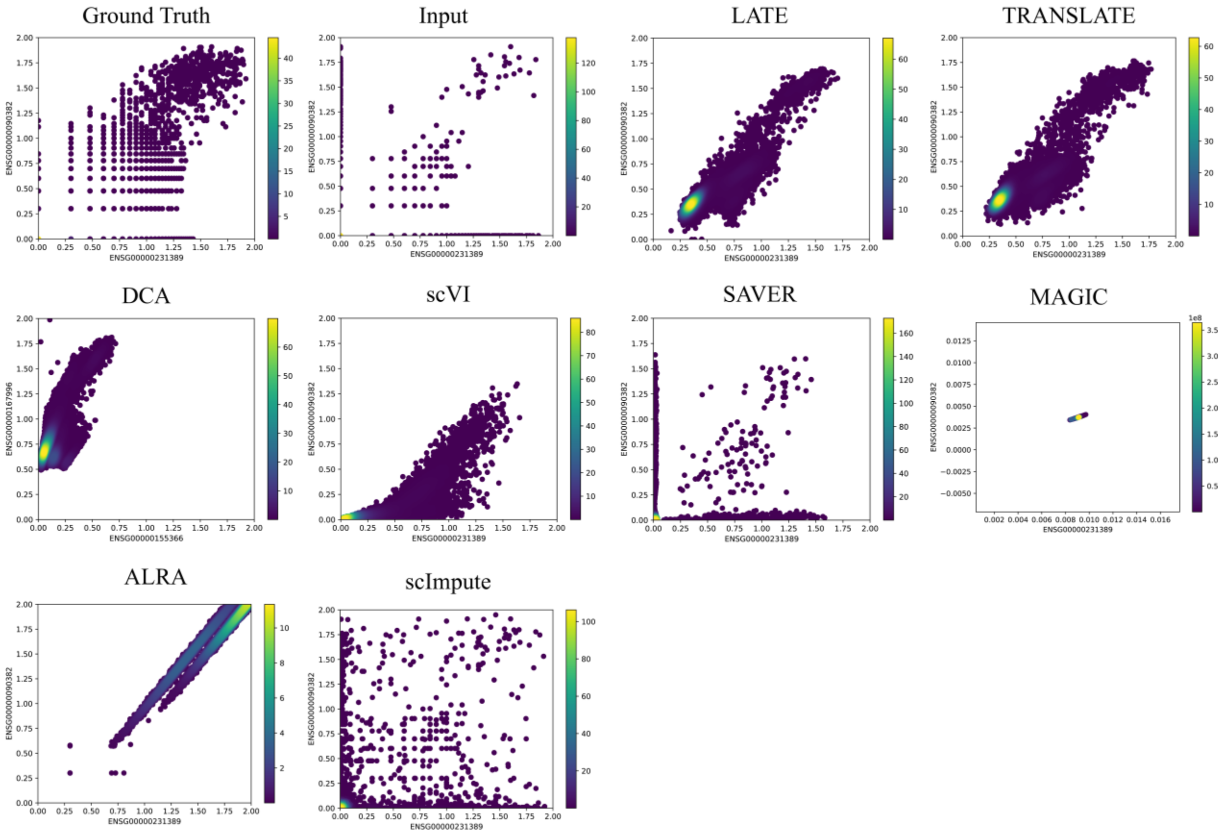


Figure S11: Two genes (*ENSG00000231389* vs *ENSG00000090382*) with a nonlinear relationship in the small synthetic data based on the 10x Genomics PBMC data (PBMC_G949; 949 genes and 21,065 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

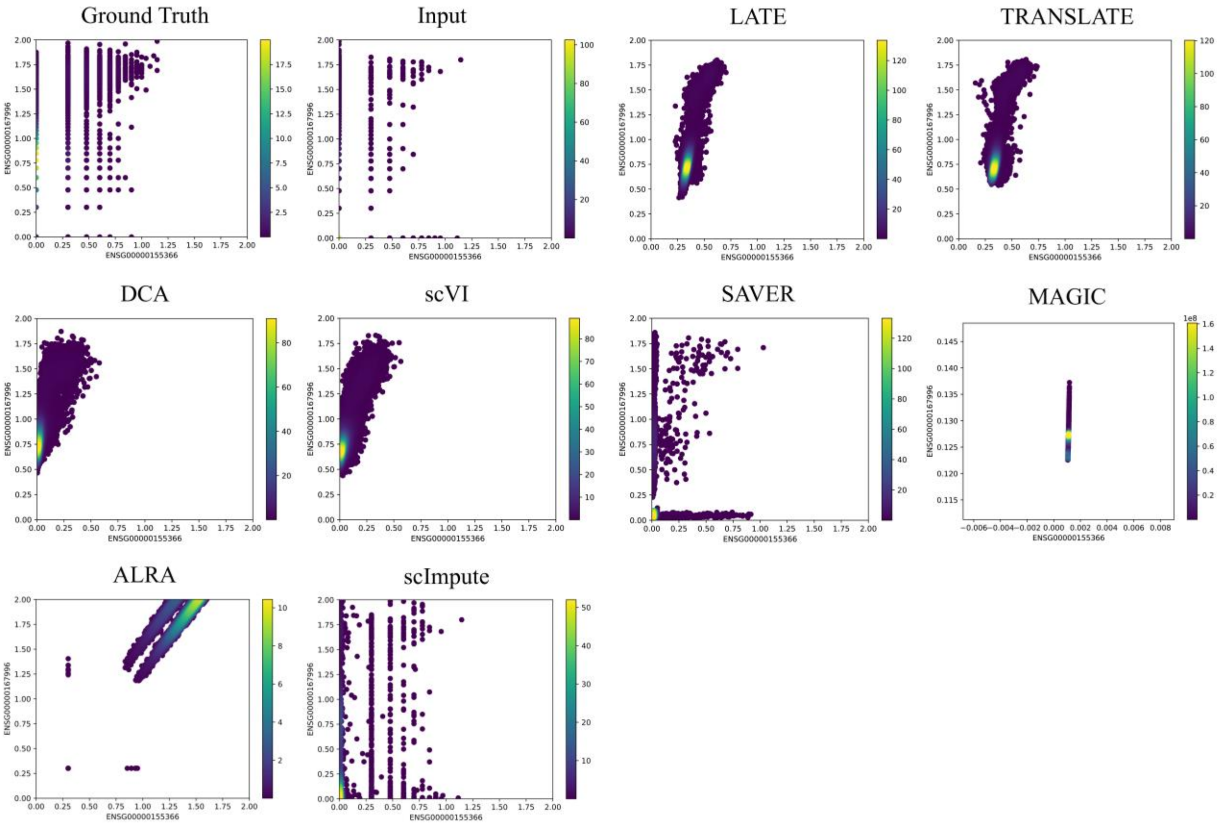


Figure S12: Two genes (*ENSG00000155366* vs *ENSG00000167996*) with a nonlinear relationship based on the 10x Genomics PBMC data (PBMC_G949; 949 genes and 21,065 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

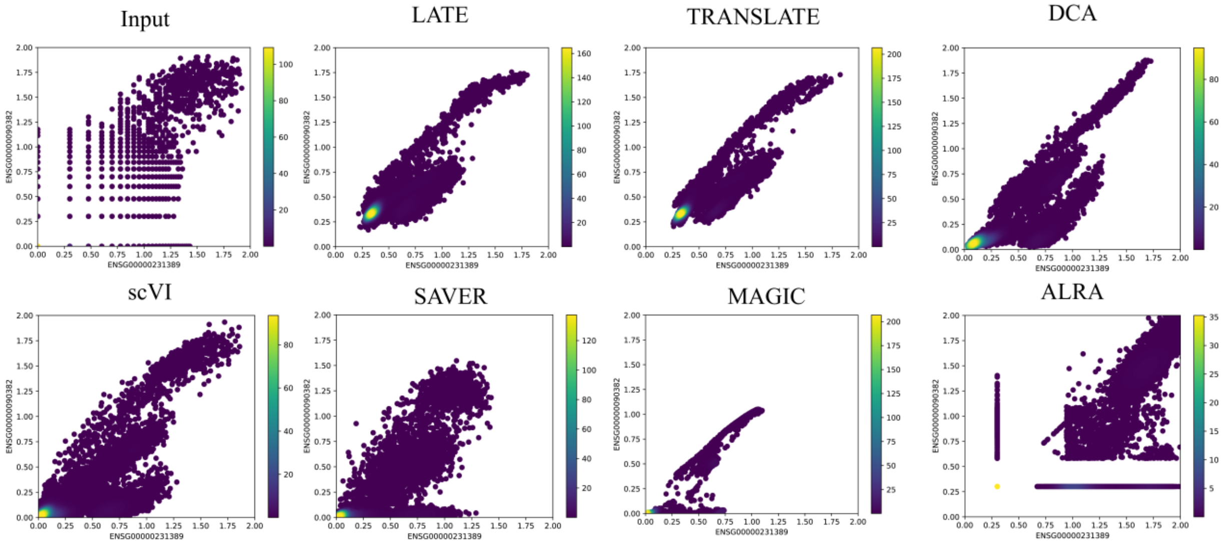


Figure S13: Two genes (*ENSG00000231389* vs *ENSG00000090382*) with a nonlinear relationship based on the 10x Genomics PBMC data (PBMC_G5561; 5,561 genes and 53,970 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

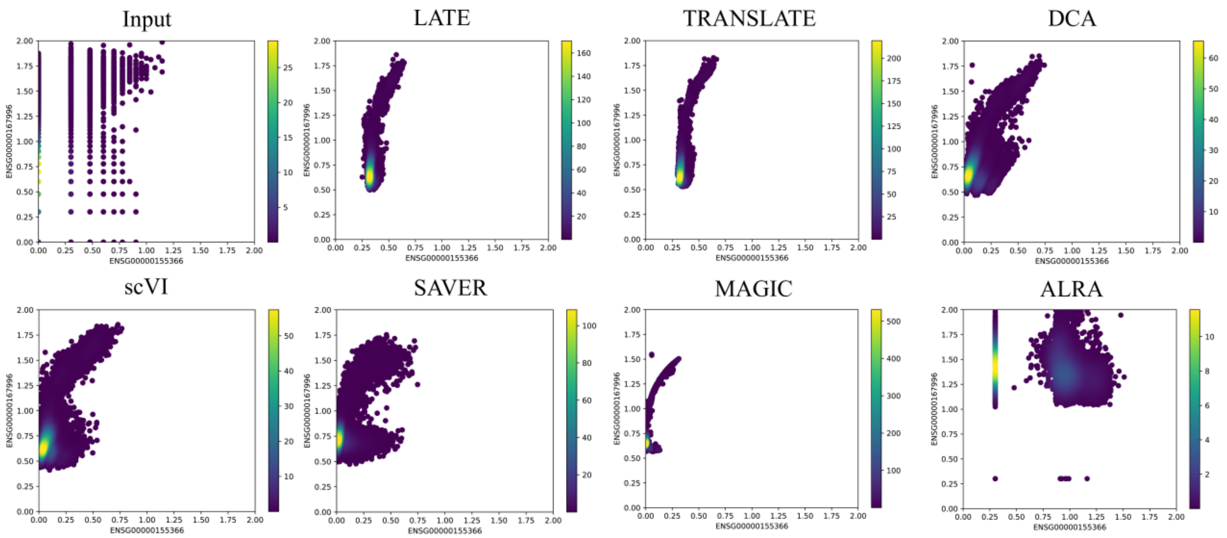


Figure S14: Two genes (*ENSG00000155366* vs *ENSG00000167996*) with a nonlinear relationship based on the 10x Genomics PBMC data (PBMC_G5561; 949 genes and 53,970 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

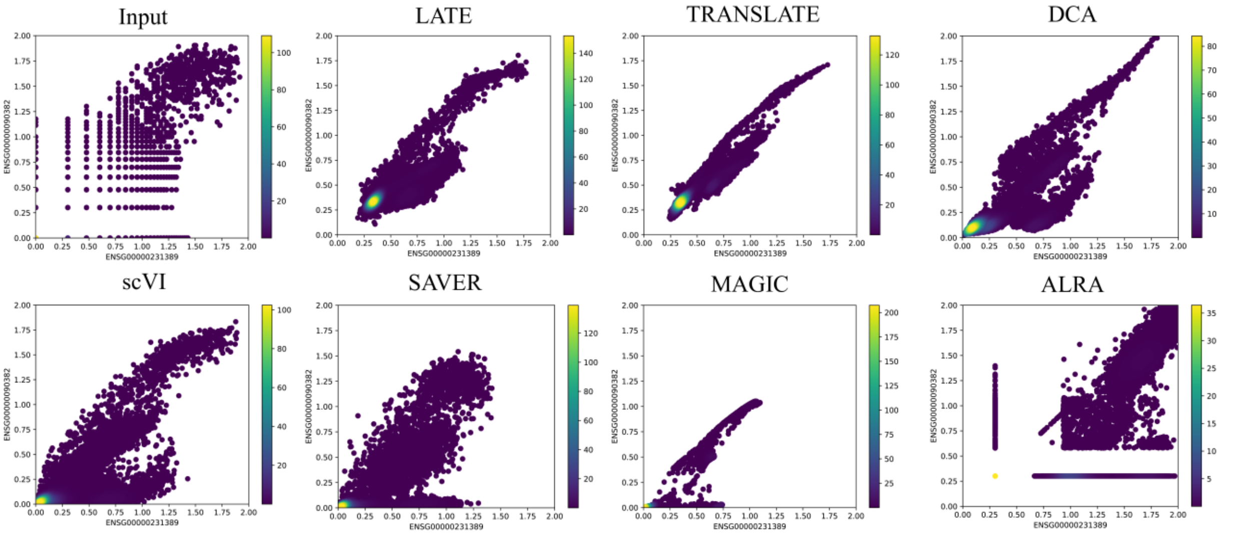


Figure S15: Two genes (*ENSG00000231389* vs *ENSG00000090382*) with a nonlinear relationship based on the 10x Genomics PBMC data (PBMC_G9987; 949 genes and 53,970 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

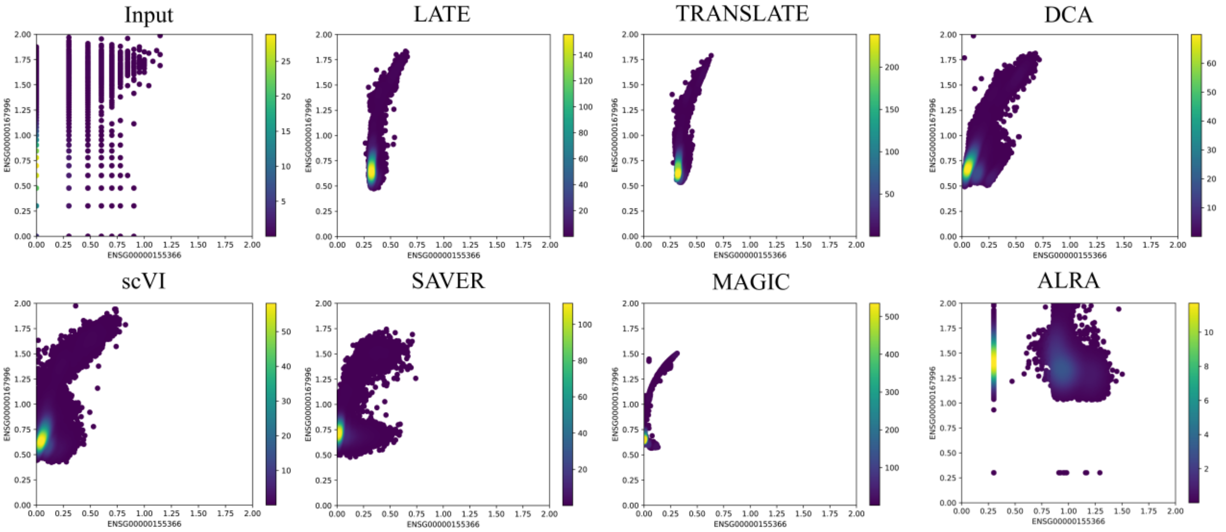


Figure S16: Two genes (*ENSG00000155366* vs *ENSG00000167996*) with a nonlinear relationship based on the 10x Genomics PBMC data (PBMC_G9987; 949 genes and 53,970 cells). Each dot is a single cell. The color bar indicates the Gaussian kernel density estimates of data points.

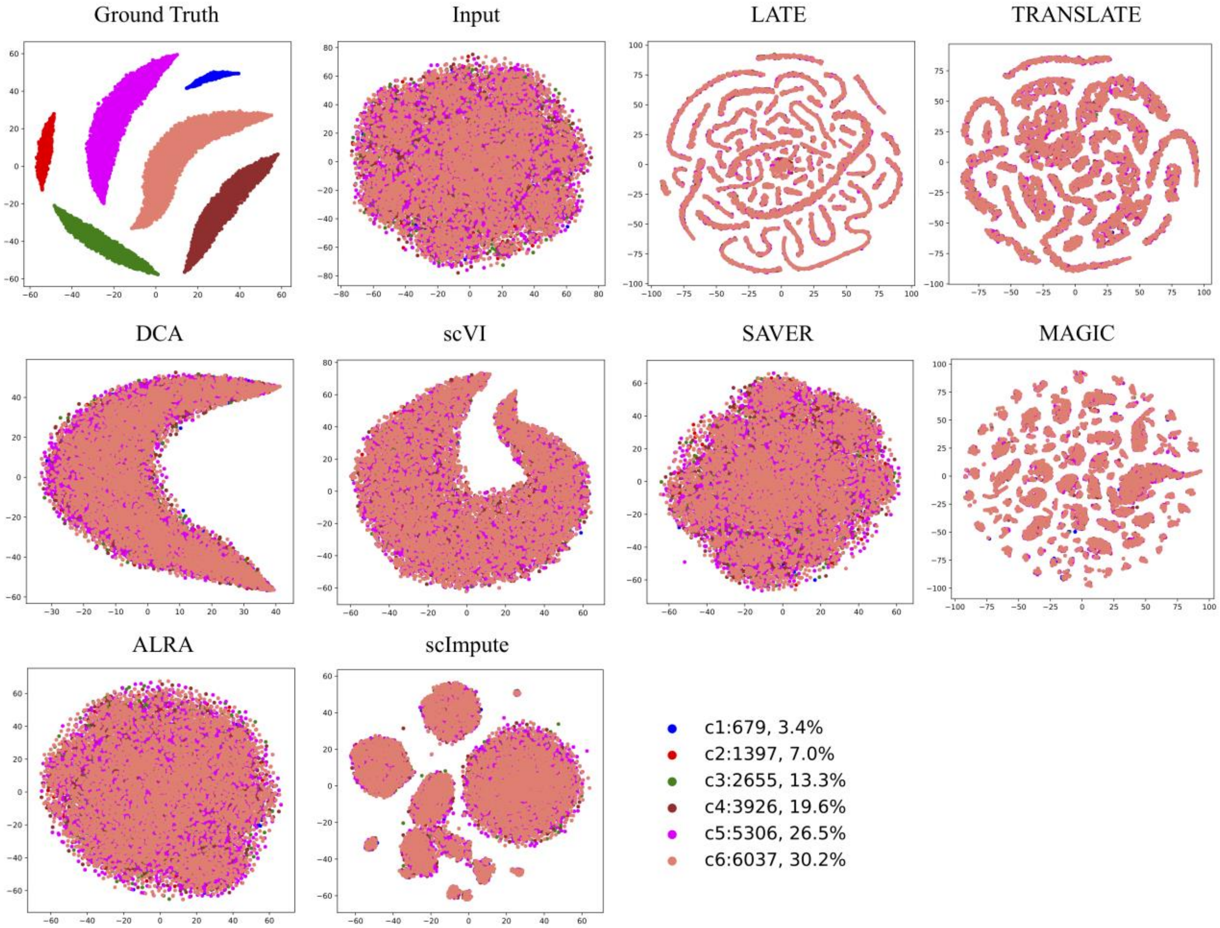


Figure S17. tSNE plots of cells from the synthetic data generated using the R package Splatter (1,000 genes, 20,000 cells, and 6 cell types). Each dot is a single cell, and each color indicates a cell type.

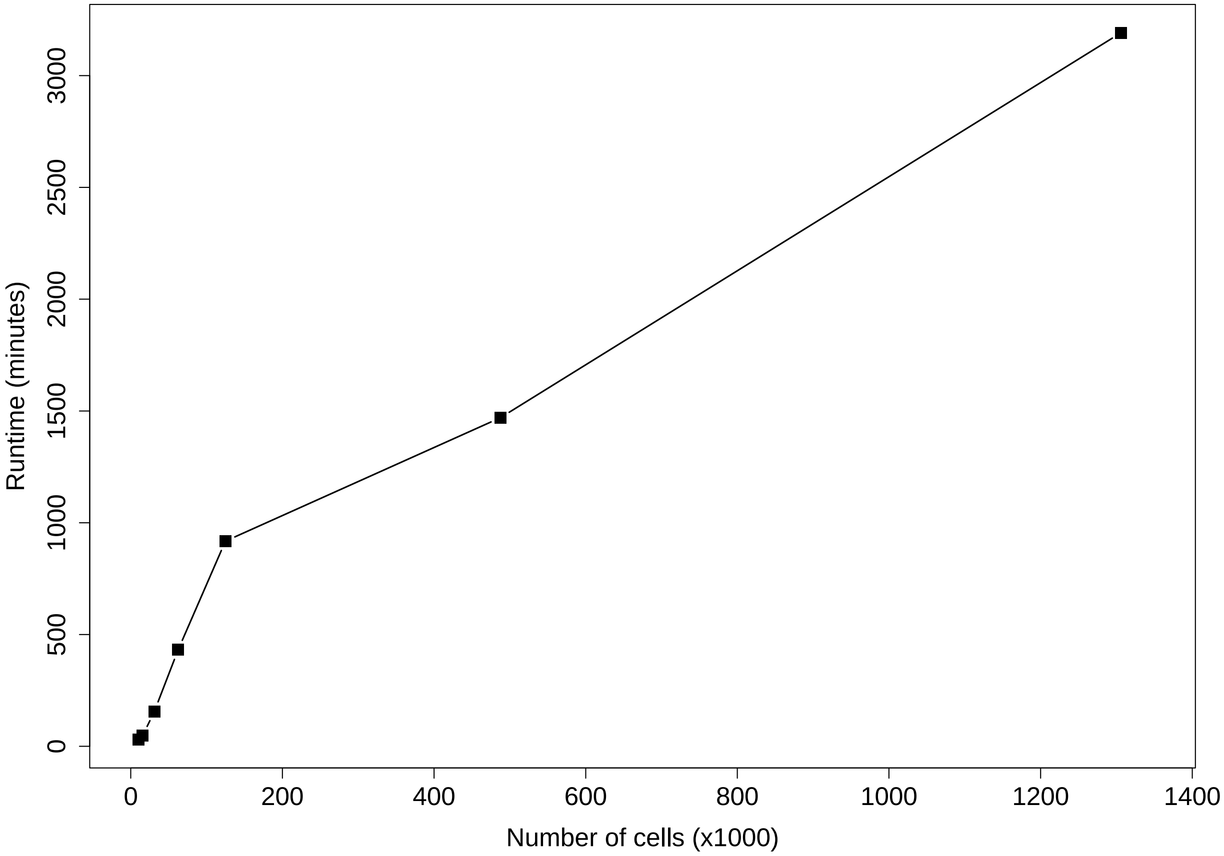


Figure S18: CPU runtime of LATE (genes as features) on multiple subsets of the mouse brain scRNA-seq data from 10x Genomics. The entire data set contains 28K genes and 1.3M cells. We sampled a subset of 10K genes with multiple subsets of cells as the input.