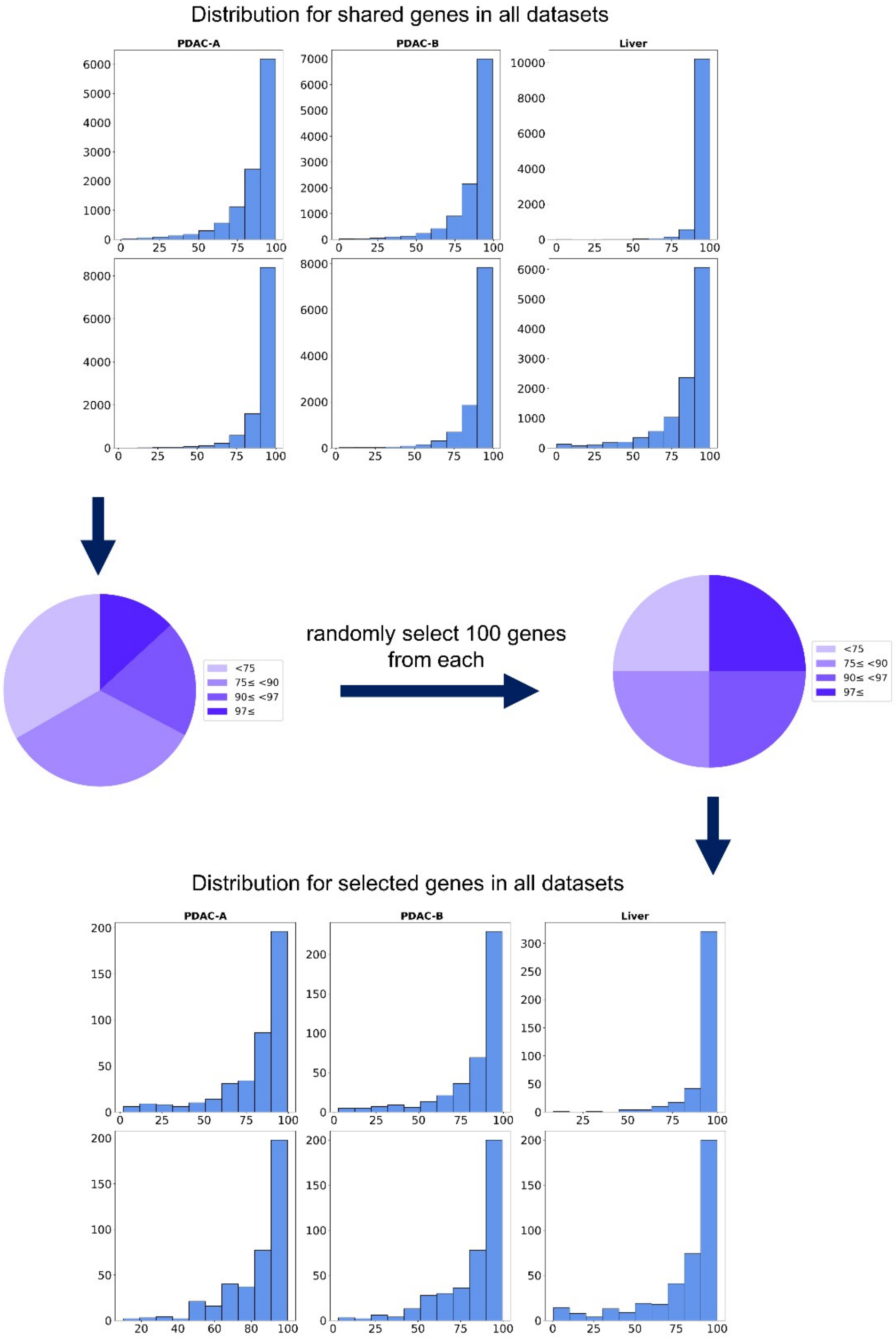
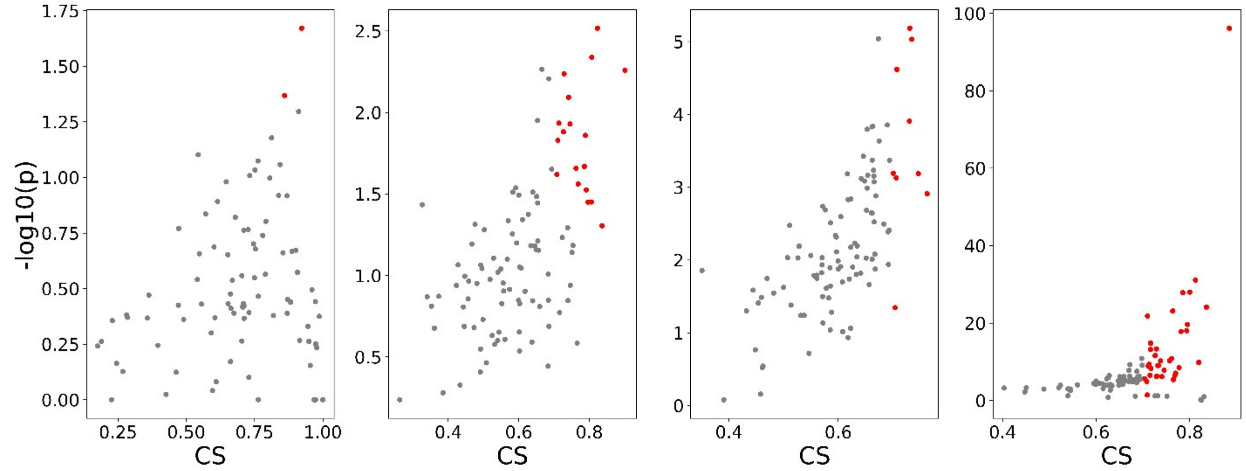
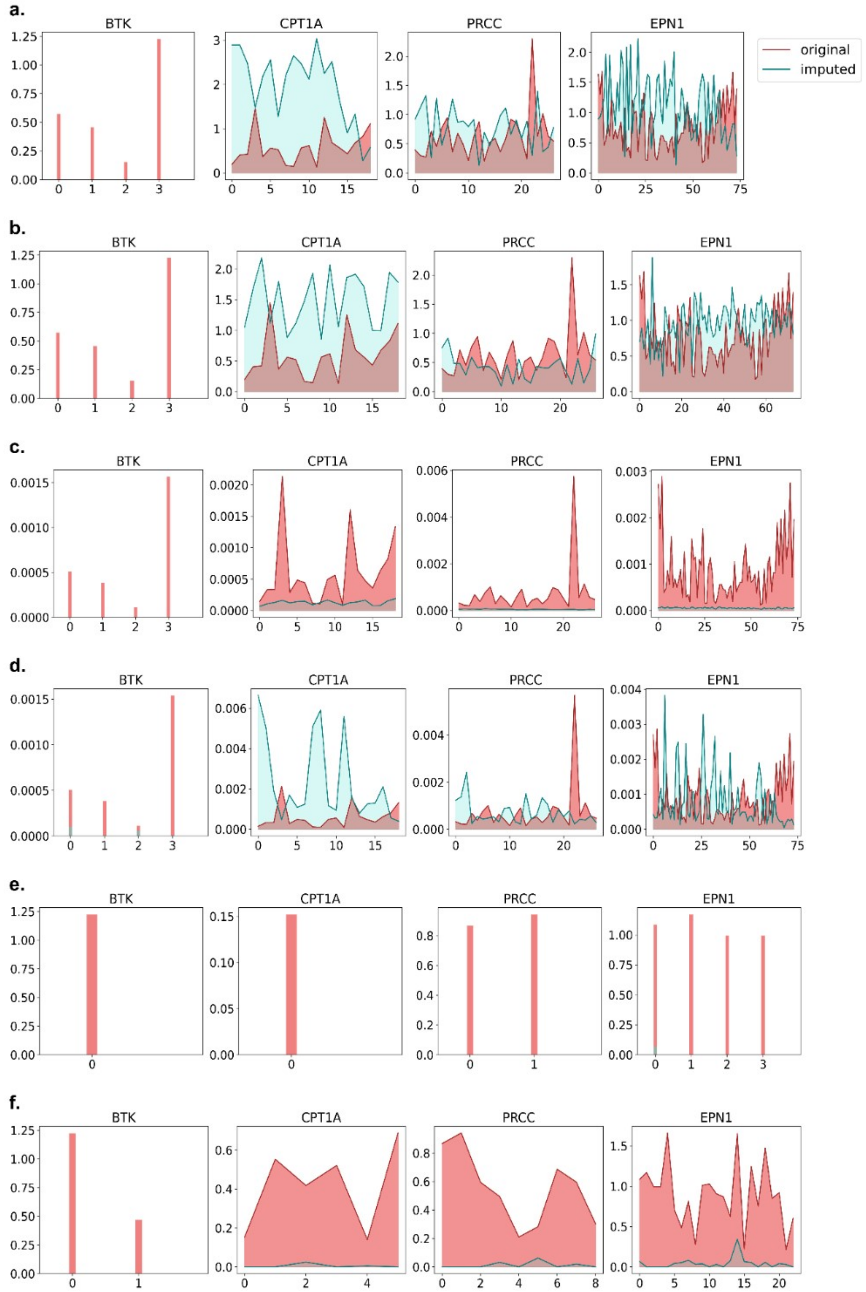
Supplementary Material



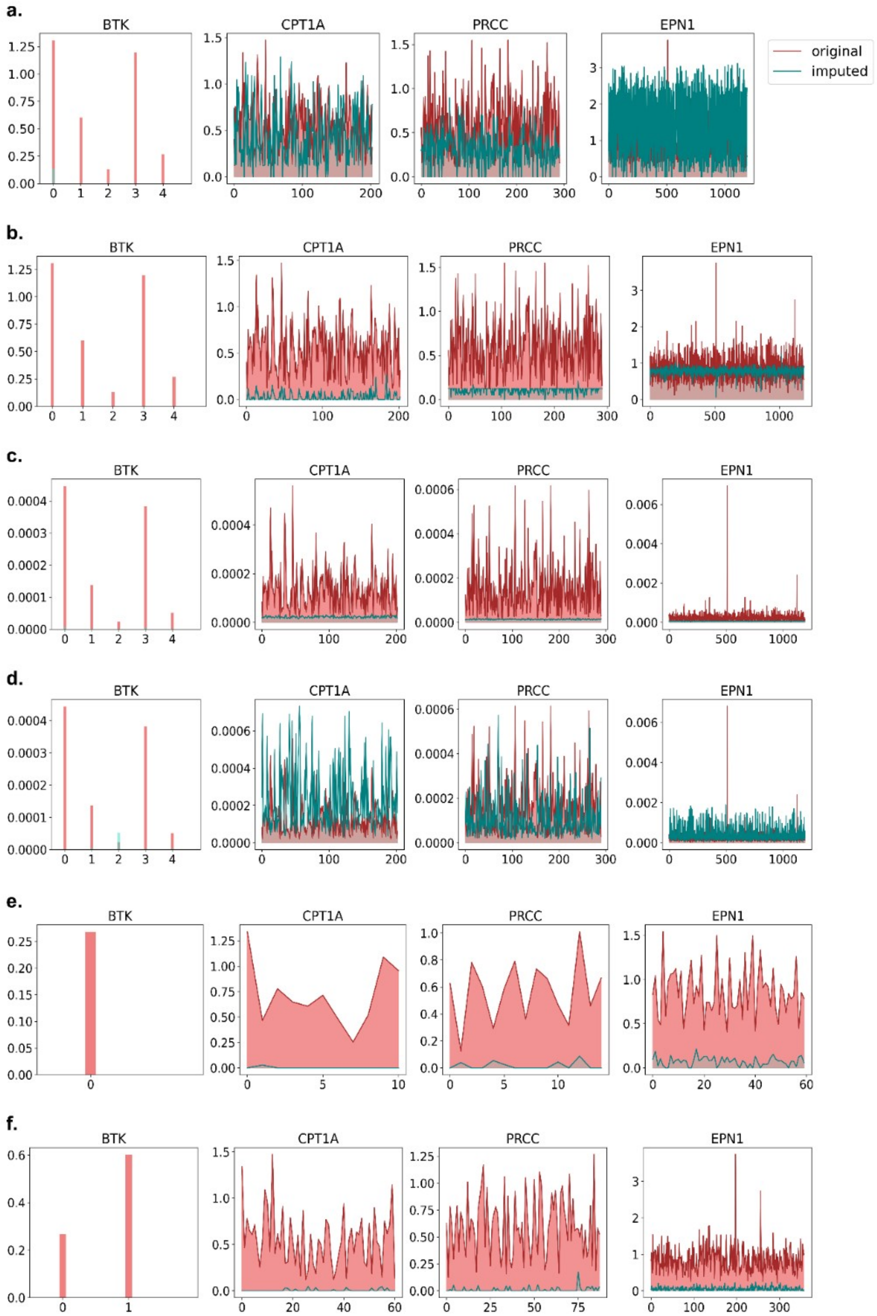
Supplementary Figure 1: The steps of selection of genes for the imputation. In each distribution plot, the upper row refers the scRNA-seq and the lower rows indicates the SRT datasets.



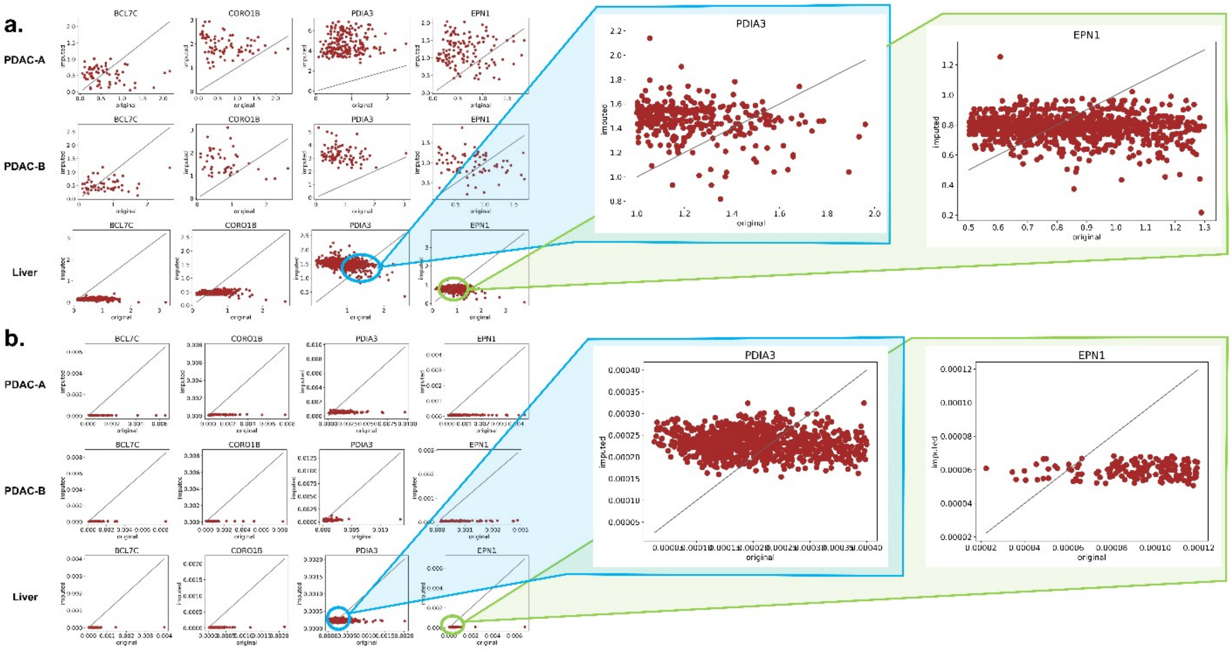
Supplementary Figure 2: Calculated CS of originally non-zero counts and the corresponding predicted values for Liver dataset by gimVI. The columns represent the genes with very-high sparsity, high sparsity, moderate sparsity, and low sparsity from left to right, respectively. The statistically significant high similarities ($p<0.05$ and $CS\geq0.7$) indicated as red.



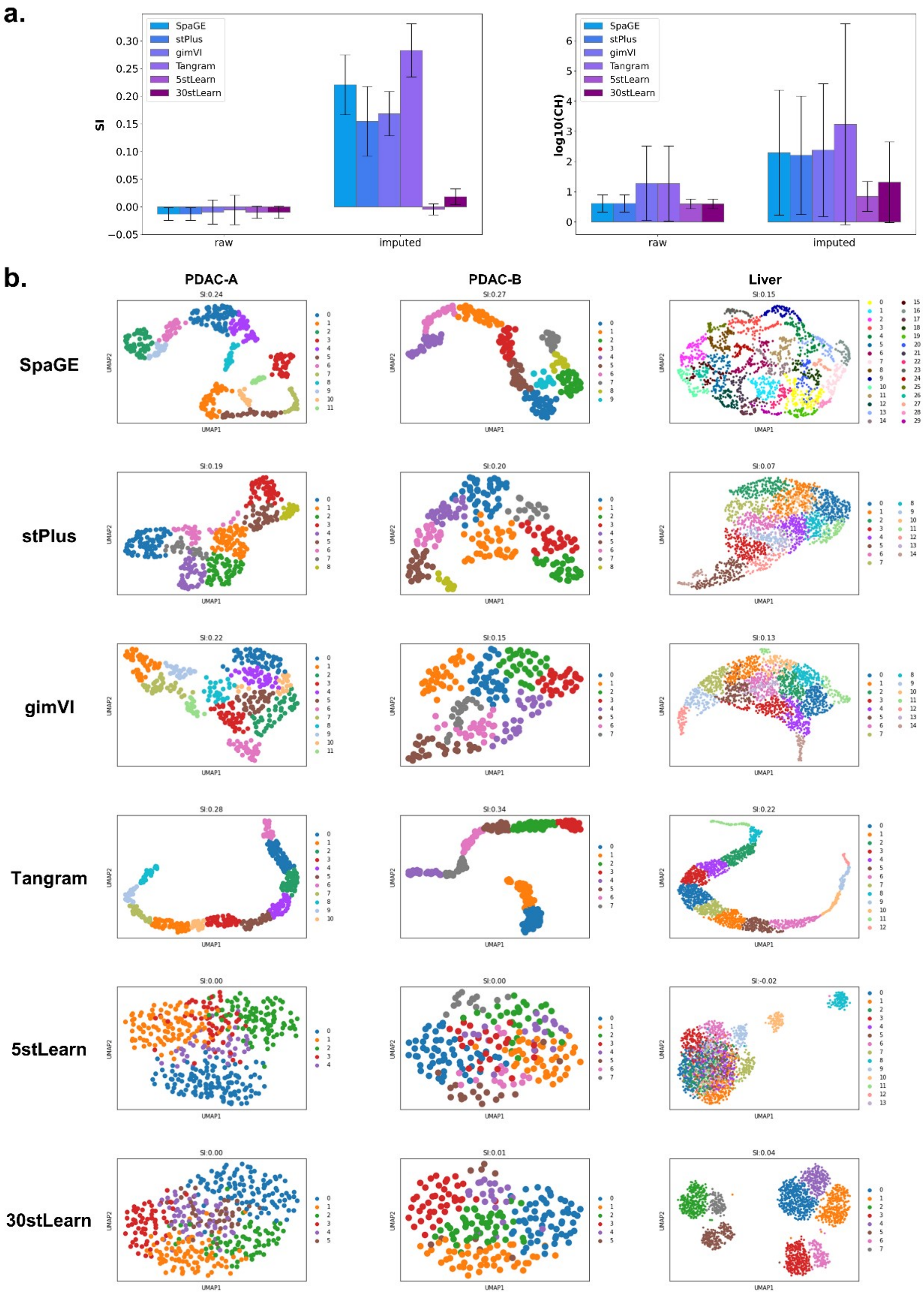
Supplementary Figure 3: Visualization of the original non-zero counts and their predicted values for PDAC-B sample with **a.** SpaGE, **b.** stPlus, **c.** gimVI, **d.** Tangram, **e.** 5stLearn and **f.** 30stLearn. The rows indicate the different groups of genes with very-high sparsity, high sparsity, moderate sparsity and low sparsity, respectively. (The colors represent the original and the imputed values for red and turquoise, respectively.)



Supplementary Figure 4: Visualization of the original non-zero counts and their predicted values for Liver sample with **a.** SpaGE, **b.** stPlus, **c.** gimVI, **d.** Tangram, **e.** 5stLearn and **f.** 30stLearn. The rows indicate the different groups of genes with very-high sparsity, high sparsity, moderate sparsity, and low sparsity, respectively. (The colors represent the original and the imputed values for red and turquoise, respectively.)



Supplementary Figure 5: Comparison of originally non-zero counts and the corresponding predicted values of randomly chosen genes (OAZ1 and EIF1) in the low sparsity group with **a.** stPlus, **b.** gimVI in the Liver sample. The black line represents the location where the original value and its predicted value are equal.



Supplementary Figure 6: Clustering performance evaluation with **a.** SI and CH, and **b.** projection of the clusters after imputation.