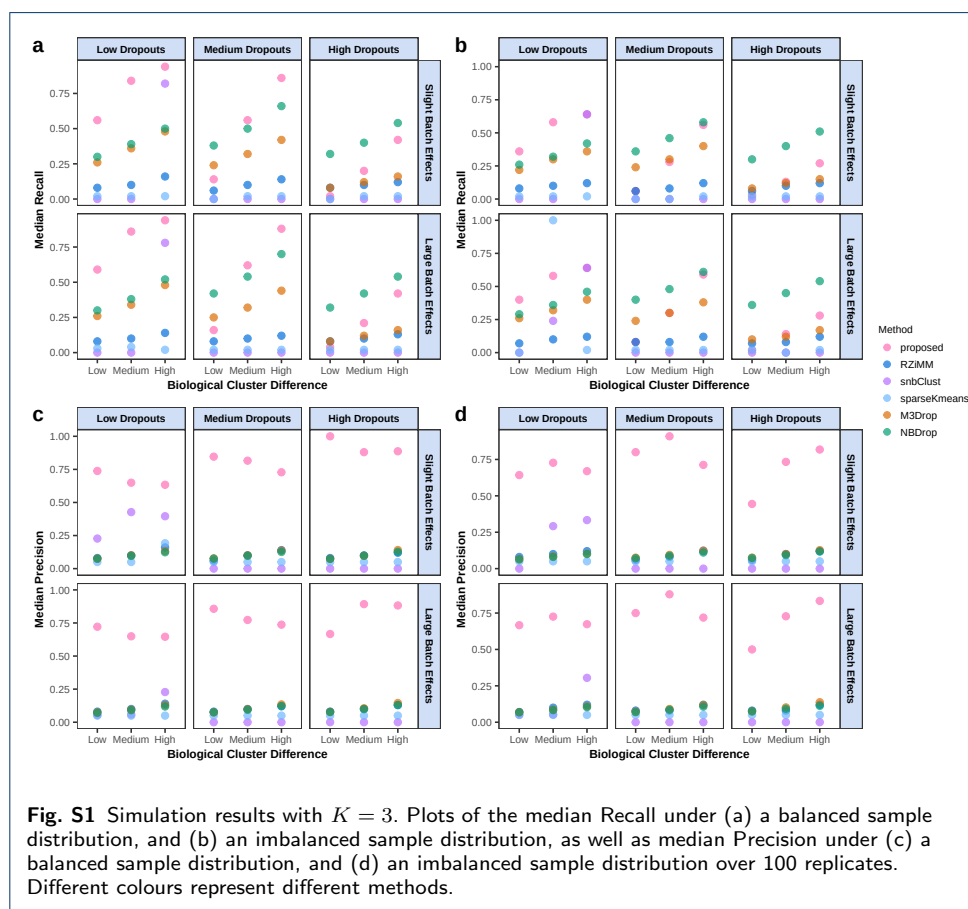
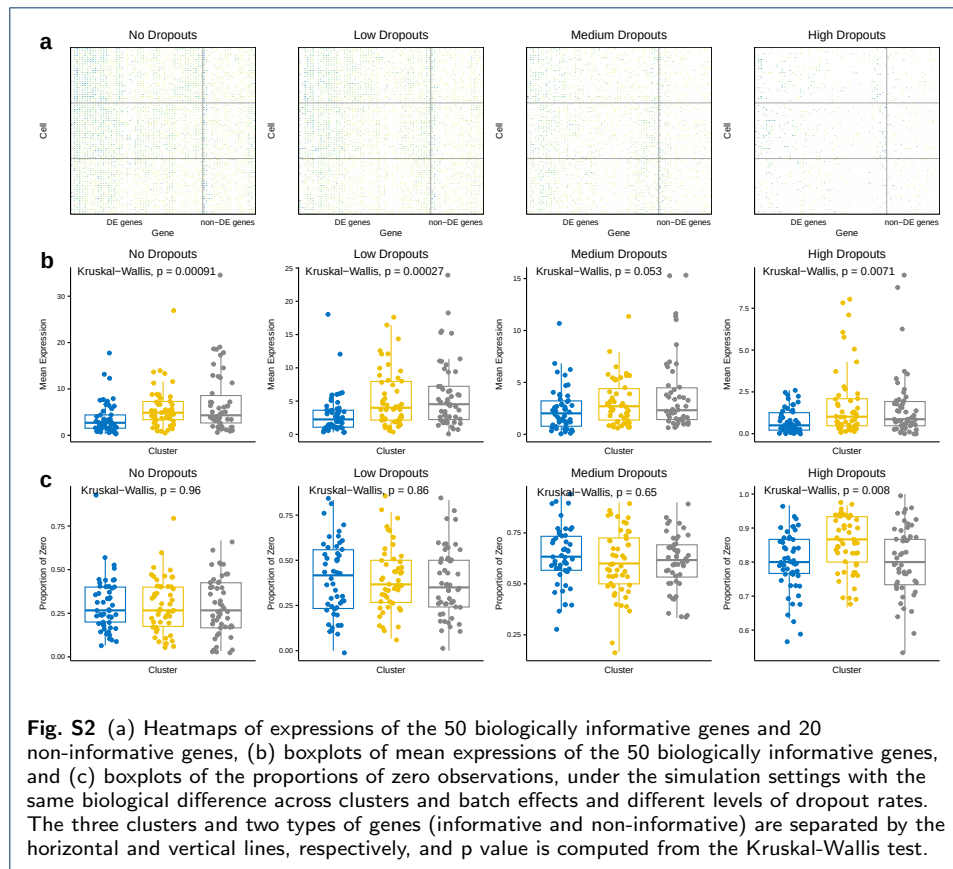
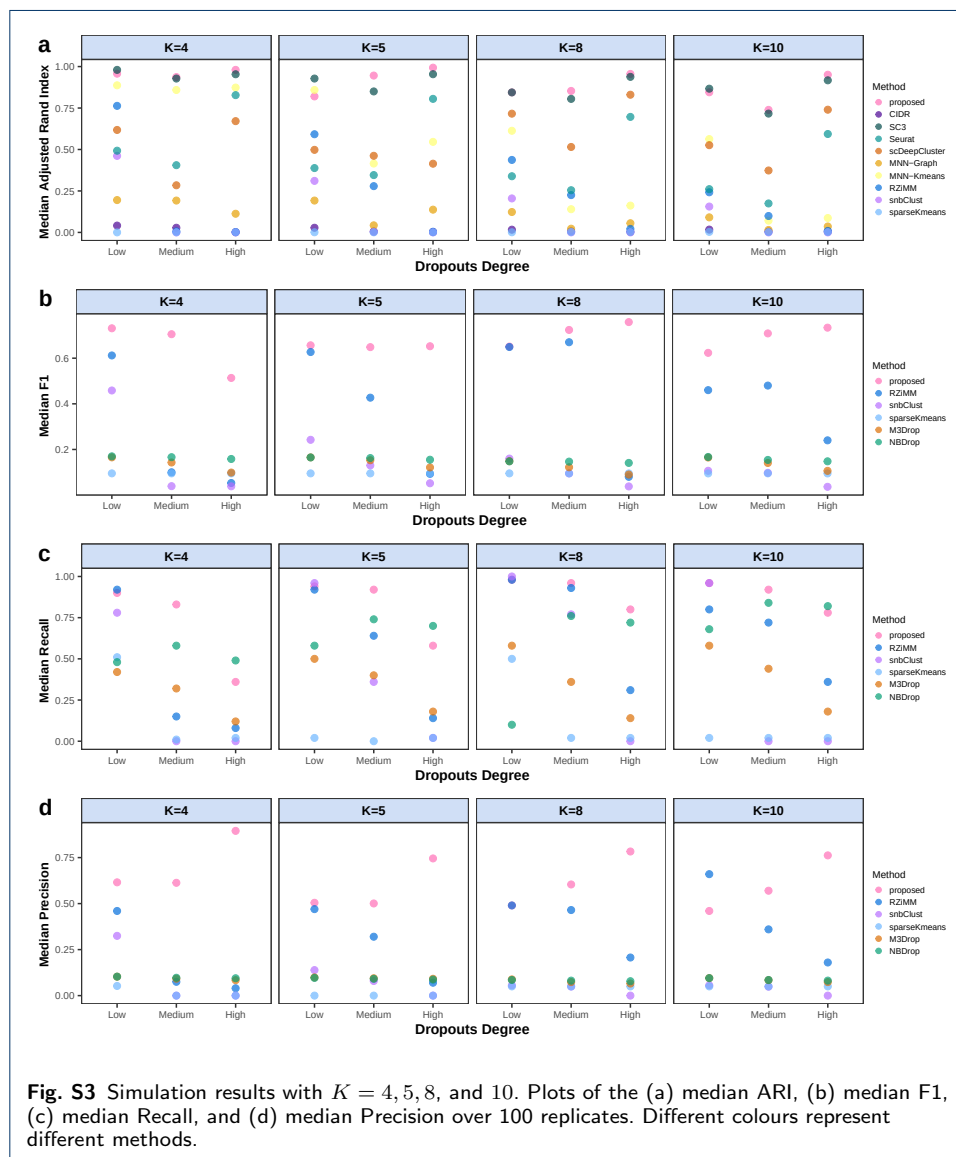








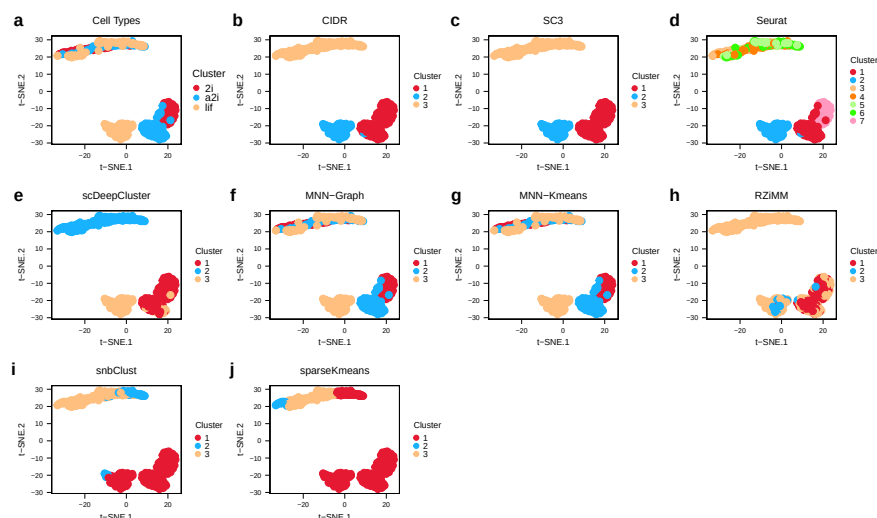


Fig. S4 Two-dimensional t-SNE projection of cells for the mouse embryonic stem cell dataset. The cells are coloured by (a) the annotated cell types, and clustering results identified using (b) CIDR, (c) SC3, (d) Seurat, (e) scDeepCluster, (f) MNN-Graph, (g) MNN-Kmeans, (h) RZIMM, (i) snbClust, and (j) sparseKmeans.

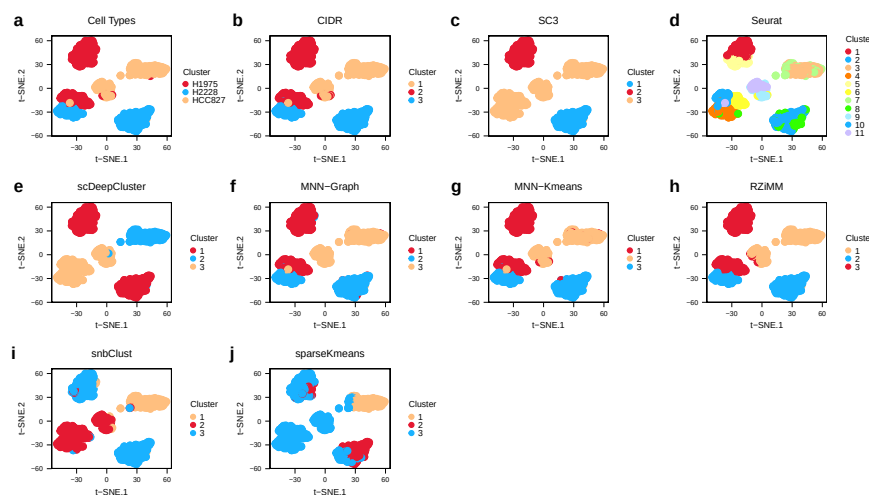
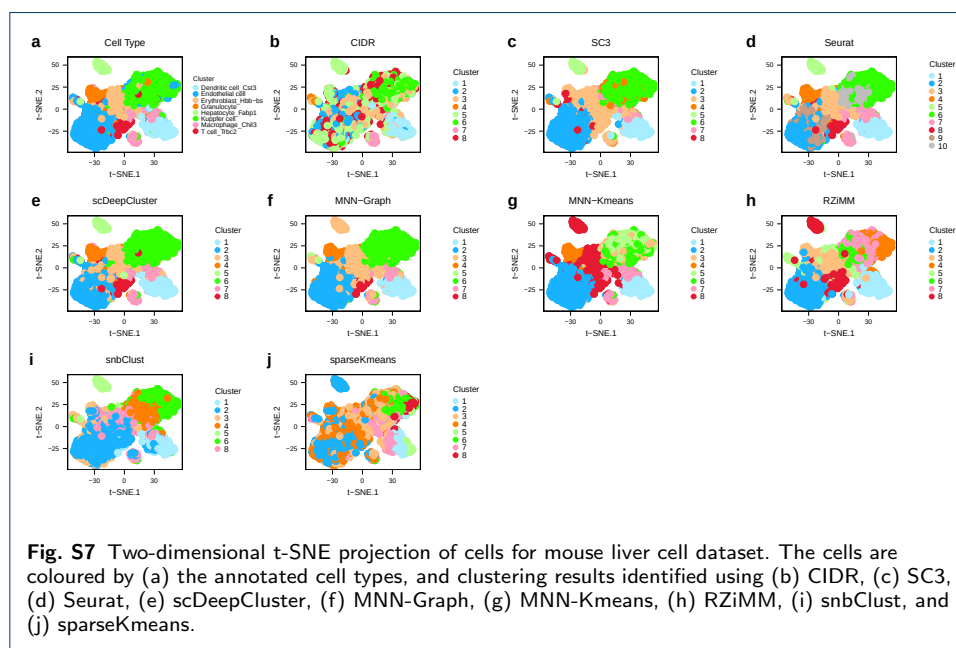
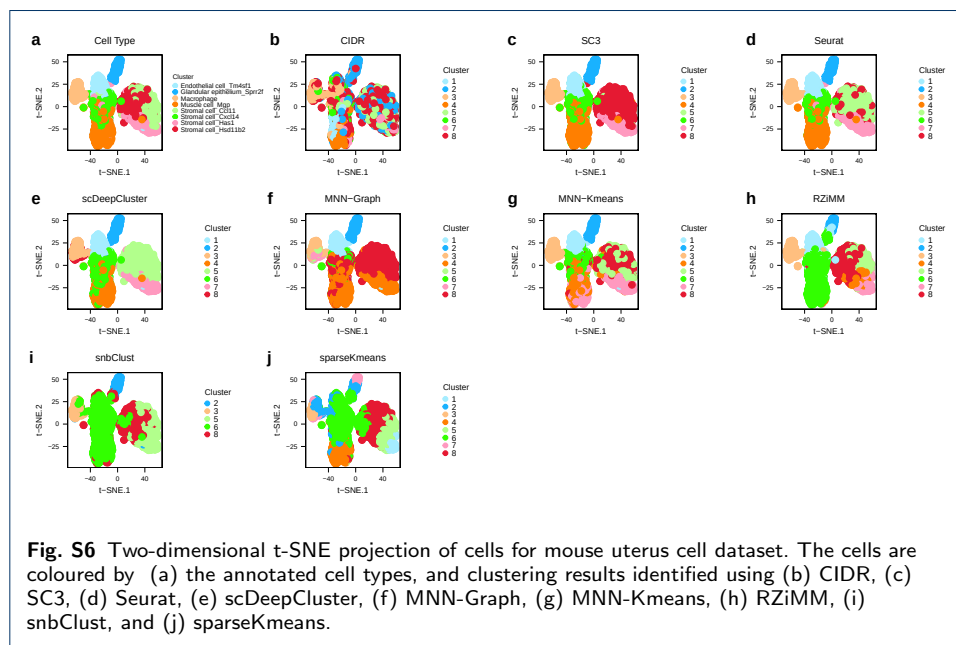
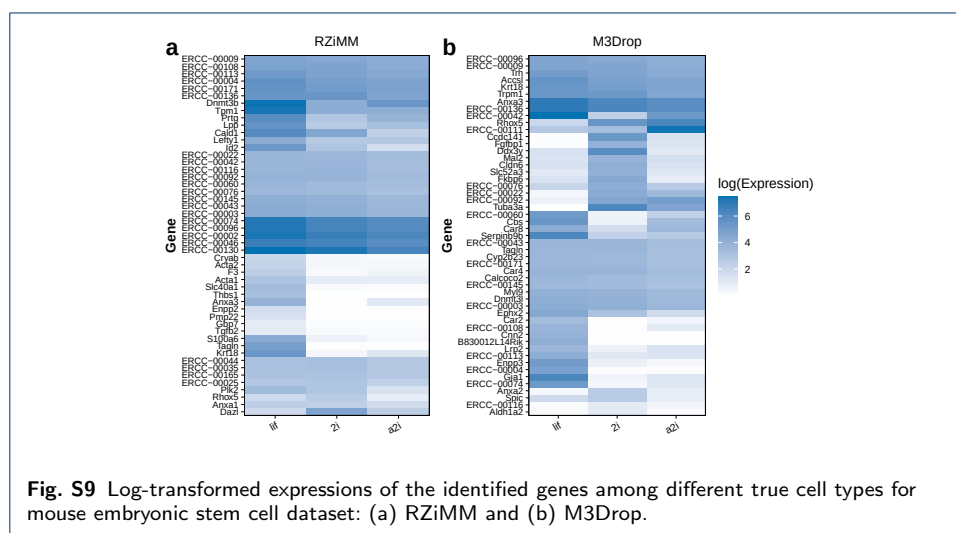
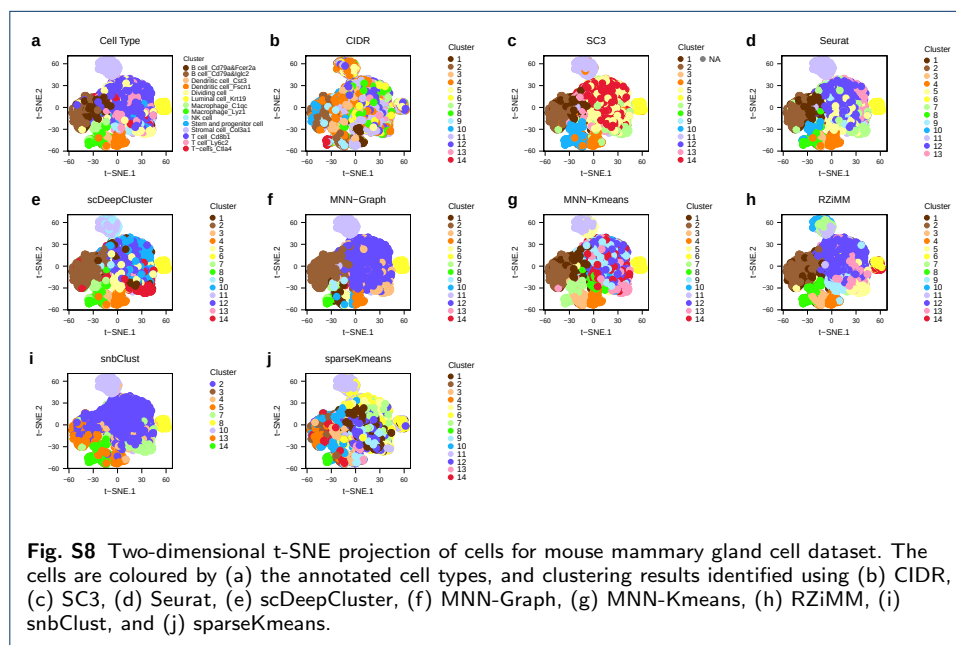


Fig. S5 Two-dimensional t-SNE projection of cells for human lung cell dataset. The cells are coloured by (a) the annotated cell types, and clustering results identified using (b) CIDR, (c) SC3, (d) Seurat, (e) scDeepCluster, (f) MNN-Graph, (g) MNN-Kmeans, (h) RZIMM, (i) snbClust, and (j) sparseKmeans.





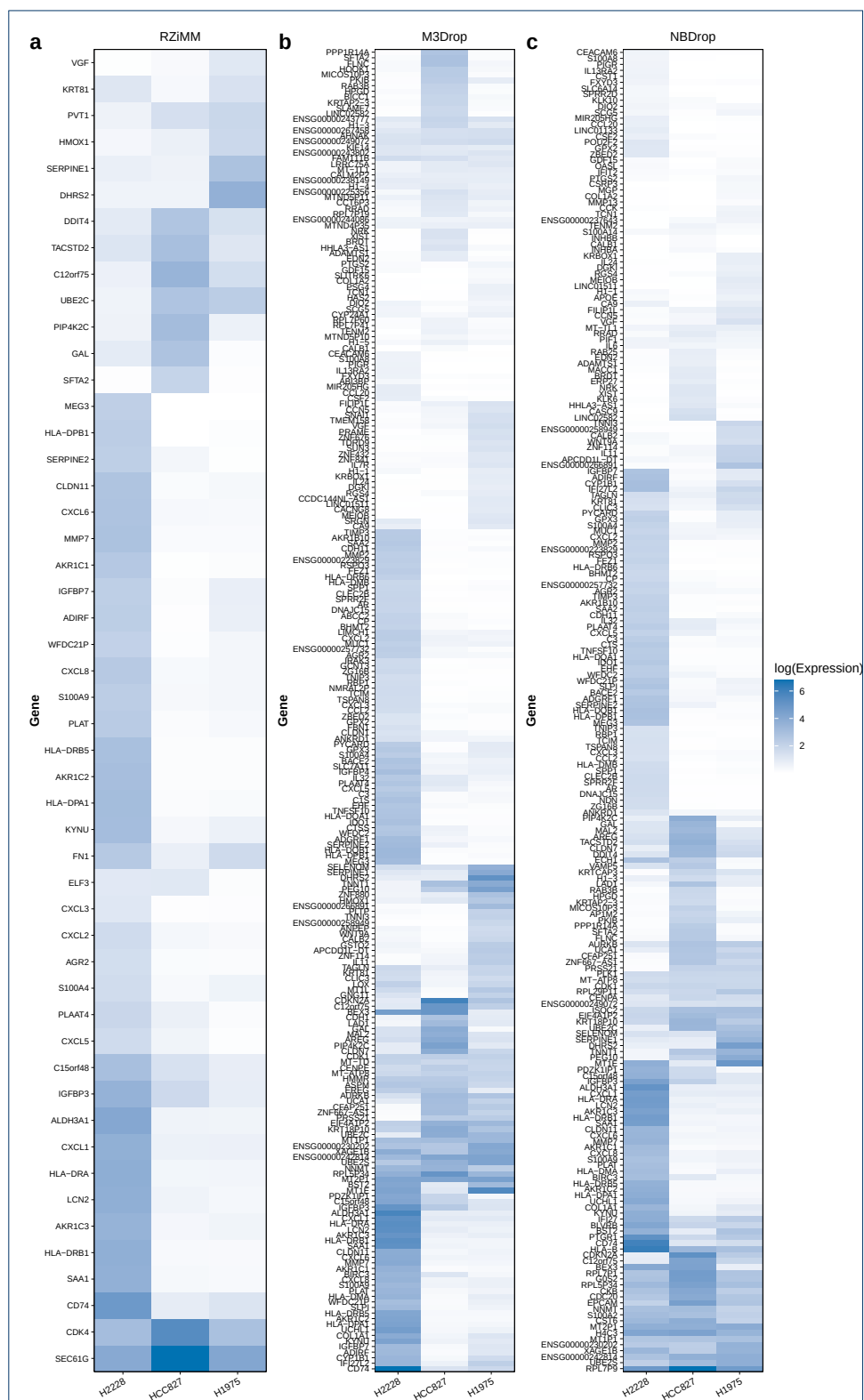


Fig. S10 Log-transformed expressions of the identified genes among different true cell types for human lung cancer cell dataset: (a) RZiMM , (b) M3Drop, and (c) NBDrop.

