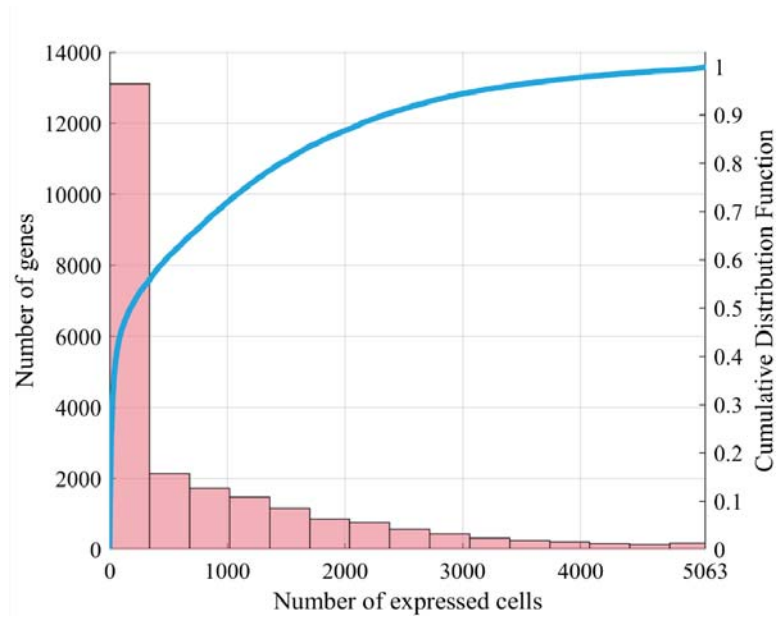# Supplementary Figures

Figure S1. Low dimension embedding visualization of recovered single cell expression profile with different number of pools. Sparse genes were selected for classification with different threshold, represents the number of cells that one gene expressed in.

Figure S2. Low dimension embedding visualization of recovered single cell expression profile with different number of pools. Sparse genes were selected for classification with different threshold, represents the number of cells that one gene expressed in.
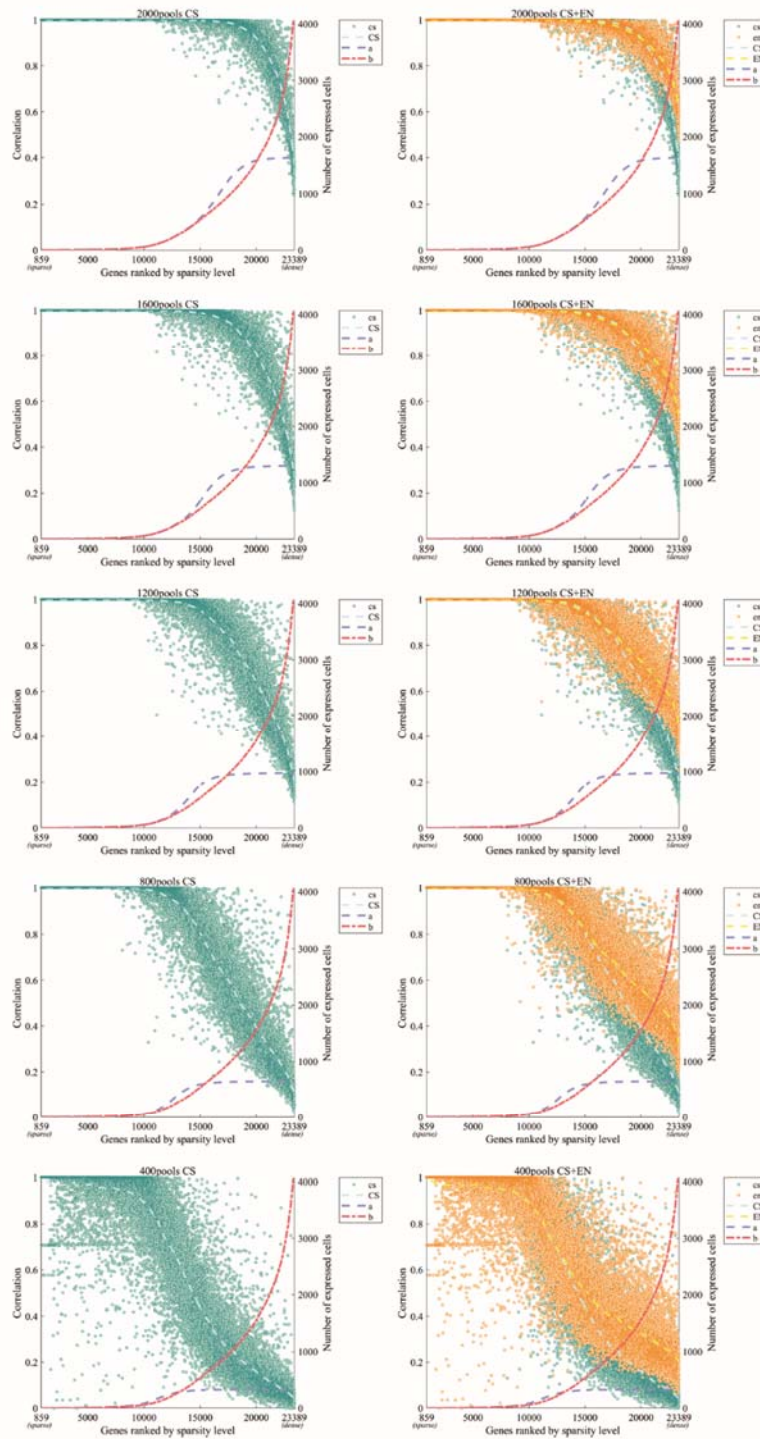
Figure S3. Comparison between compressed sensing only method (left column) with combined model (right column). Each dot represents a gene defined by it's sparse level and recovery accuracy. We exclude genes that not expressed in any cells (858 genes). *b* line indicates the sparsity level in original data and the *a* line is for recovered data.
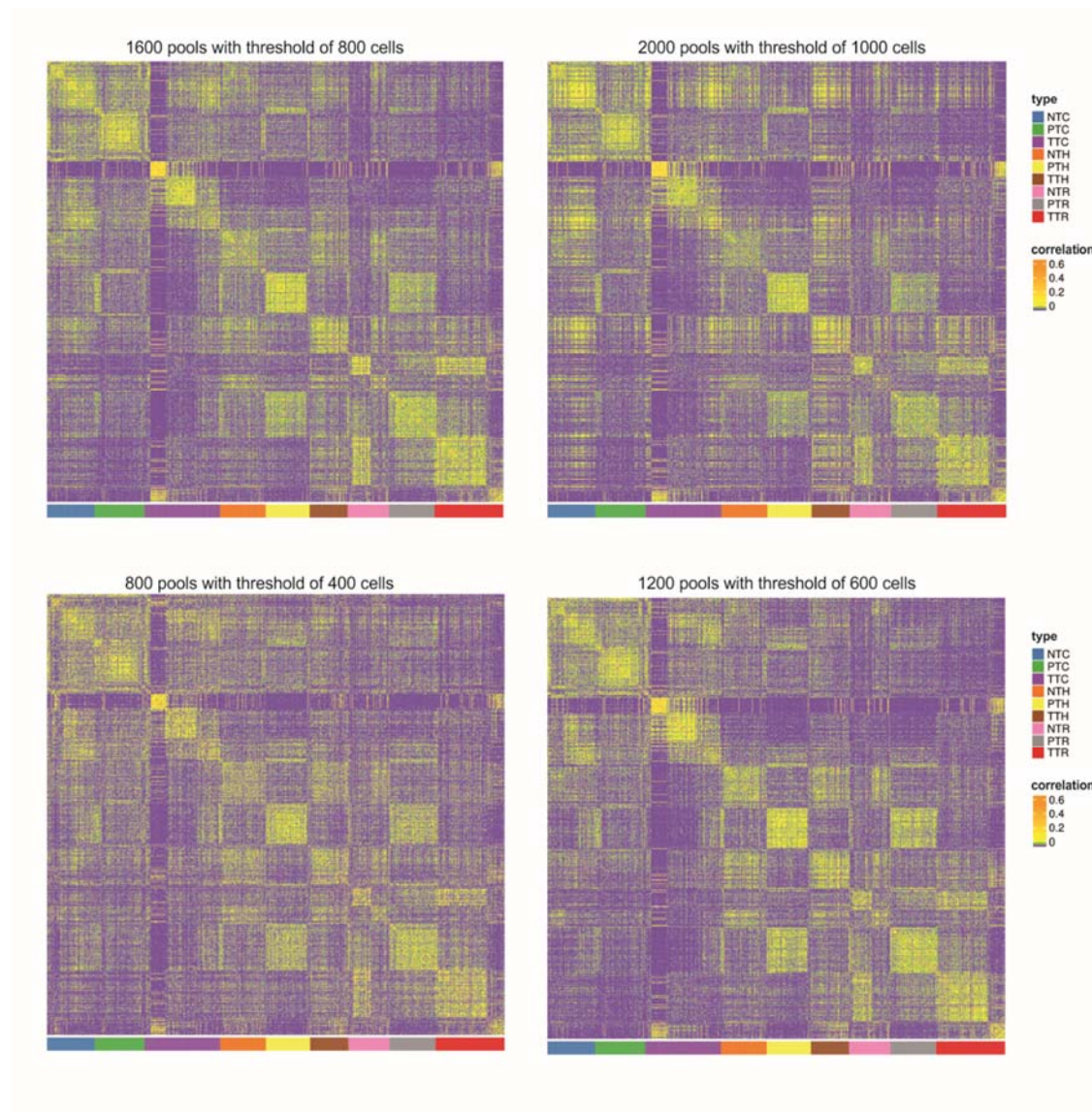
Figure S4. Cell-cell Pearson correlation heatmap. 818 cells in 9 different cell types.
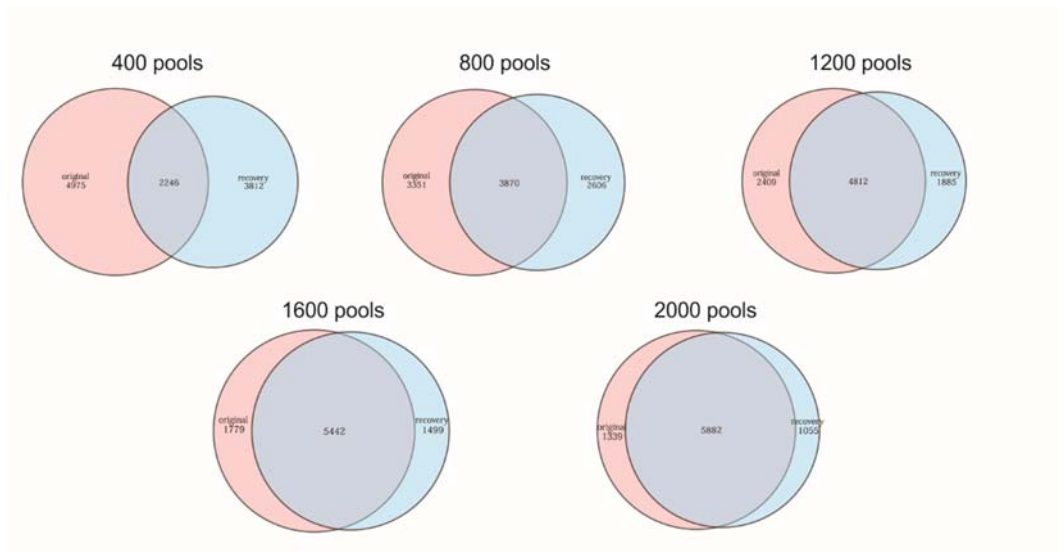
Figure S5. Venn plot for highly variable genes from two sets. Blue circle indicates the number of variable genes selected from recovery data while pink circle indicates original data. Thresholds were the same for all sets and described in methods.