

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Distribution of the number of distinct mRNA transcripts per cell for each treatment condition.

File Name: Supplementary Data 2

Description: Coefficient of variations (CV) of mean transcript numbers.

File Name: Supplementary Data 3

Description: The data of the heatmap for DE genes corresponding to the 4 samples; each number corresponds to the normalized expression level in a single cell.

File Name: Supplementary Data 4

Description: List of marker genes corresponding to each subcluster from the 4 treatment conditions identified by AUROC.

File Name: Supplementary Data 5

Description: The data of the Heatmap for DE genes corresponding to the 8 sub-clusters identified by SC3; each number corresponds to the normalized expression level in a single cell.

File Name: Supplementary Data 6

Description: List of marker genes corresponding to the 4 treatment conditions identified by Wilcoxon test.

File Name: Supplementary Data 7

Description: List of marker genes corresponding to the subclusters of the 4 treatment conditions identified by Wilcoxon Test.

File Name: Supplementary Data 8

Description: List of marker genes corresponding to the SC3 clusters identified by Wilcoxon test.

File Name: Supplementary Data 9

Description: Gene ontology analysis of the 4 conditions.

File Name: Supplementary Data 10

Description: Gene ontology analysis of the subclusters corresponding to 4 conditions.