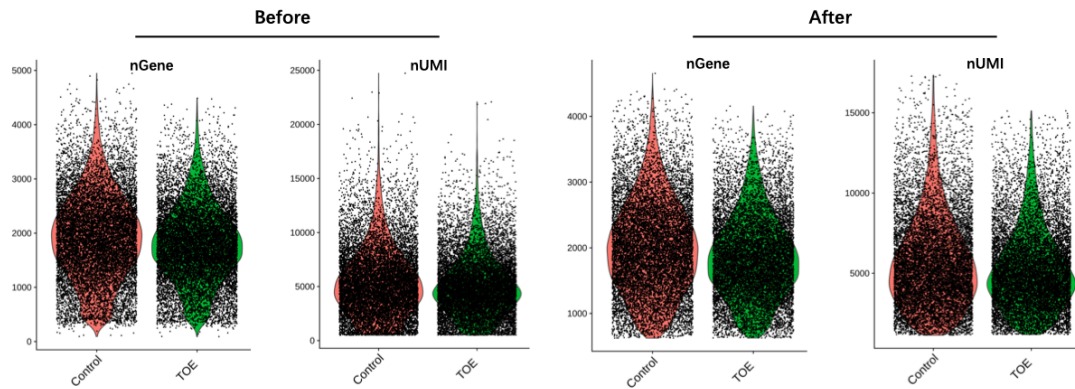
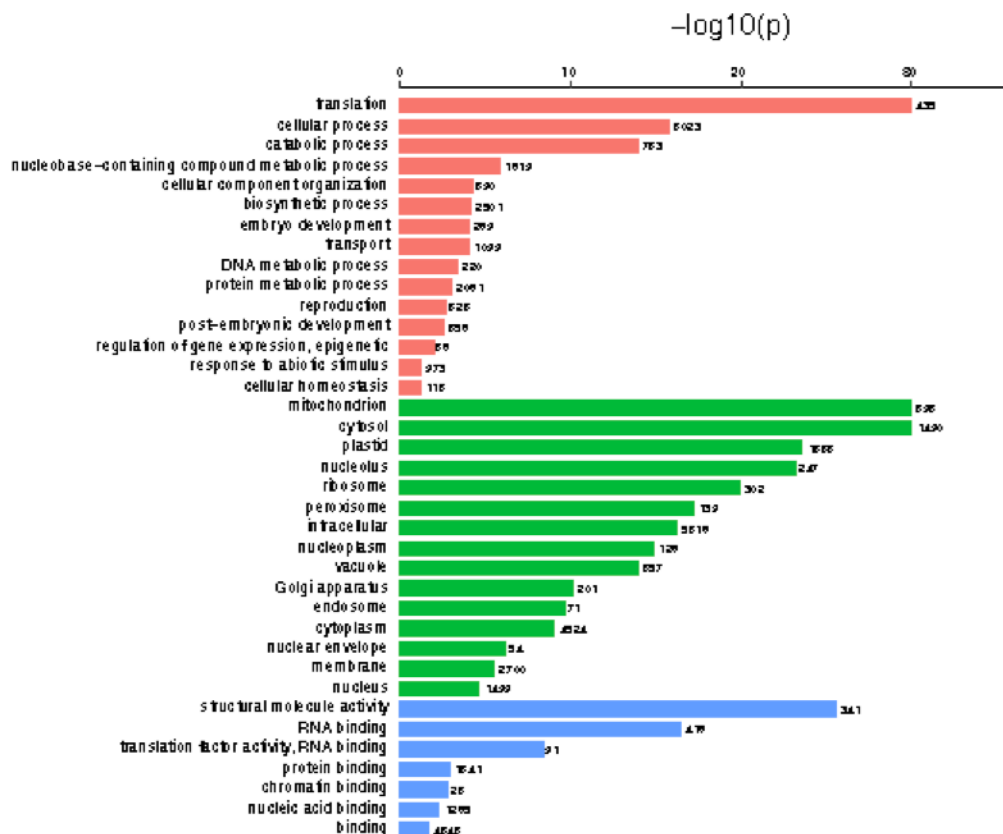


## Supplementary figures

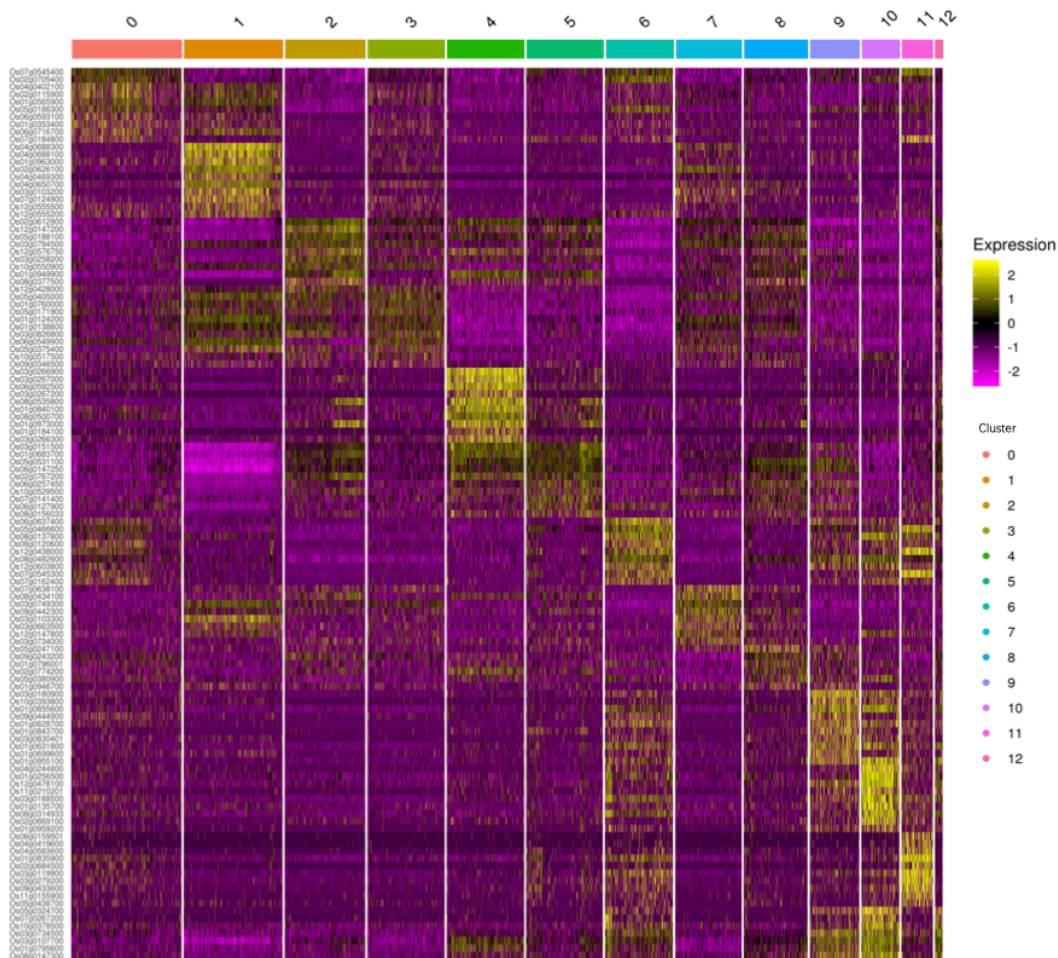


**Supplementary Figure S1.** Violin plot showing each cells' gene/UMI numbers in scRNA-seq samples before or after quality filtering. Each dot denotes a single cell.

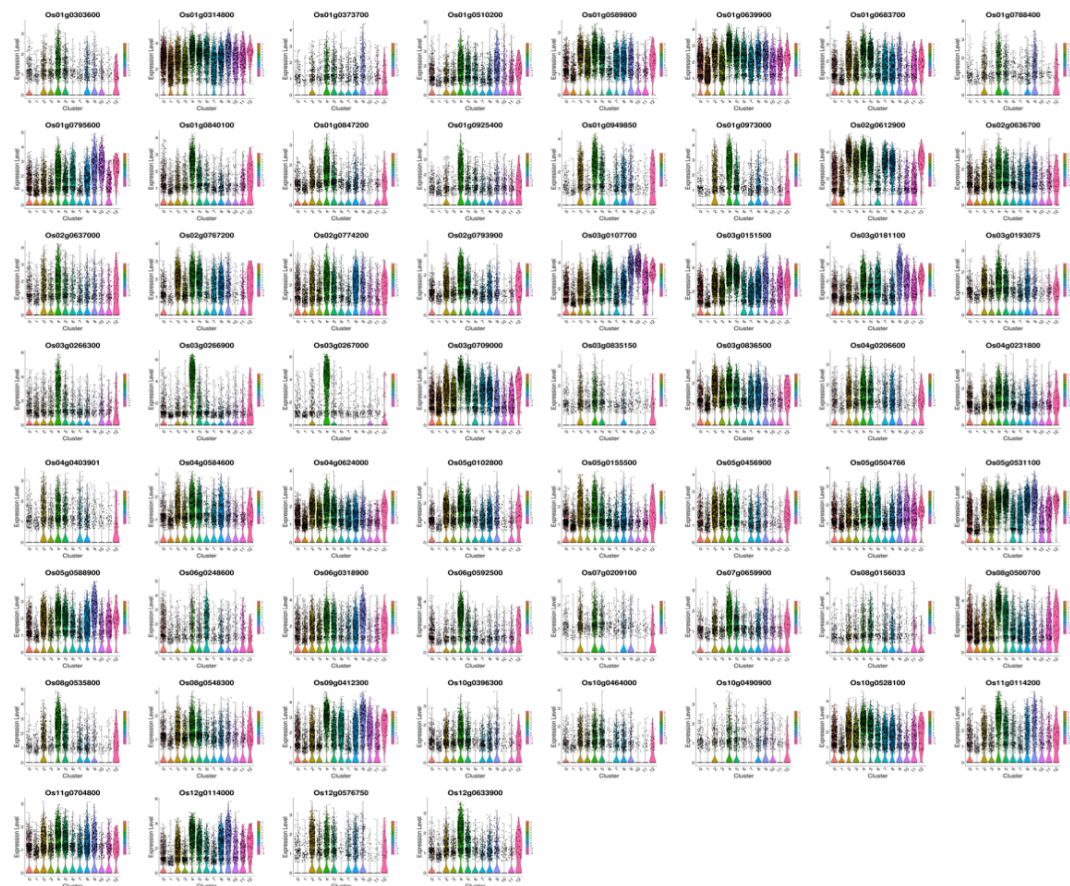


**Supplementary Figure S2.** Gene ontology analysis of detected genes in control and TOE sample. A GO term with a p-value < 0.05 was regarded

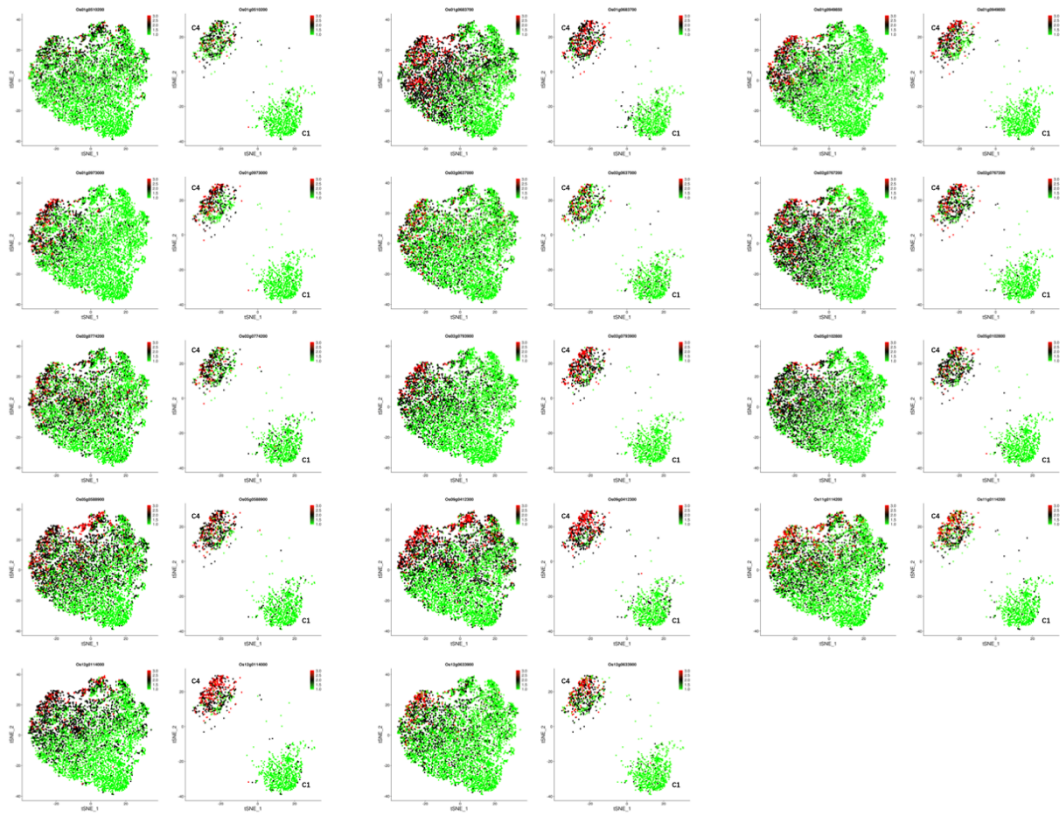
as significantly enriched. Gene ontology terms in biological process(red), cellular component(green) and molecular function(blue) were plotted.



**Supplementary Figure S3.** Heat map illustrating the transcript levels of top10 marker genes in each cluster of the TOE. The bars at the top of the heat map indicate the clusters in TOE.



**Supplementary Figure S4.** Violin plot showing the expression levels of 60 of the 65 candidate genes whose expression correlated with that of OsNAC78 in the TOE. Each dot denotes a single cell.



**Supplementary Figure S5.** t-SNE visualization of 14 of the 19 overlapping genes in the TOE and isolated from cluster 1 or 4. C1, cluster 1; C4, cluster 4. Each dot denotes a single cell. The depth of color indicates differences in expression levels.