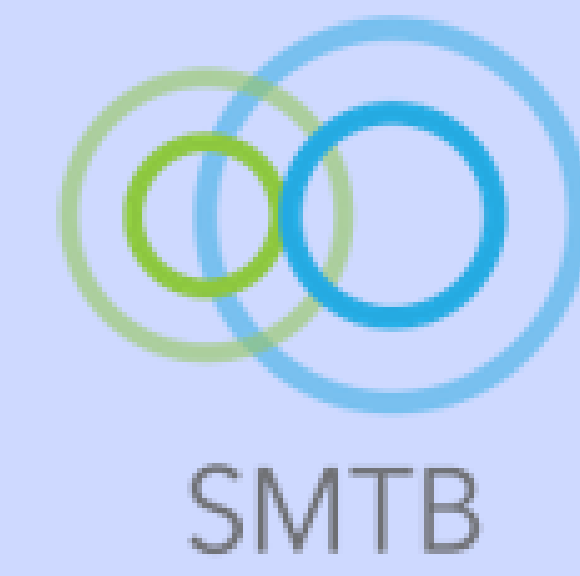


Transposon expression study in the neuronal cells



Anna Doroshenko, Yana Diachkova, Daryna Sizon, Anastasia Kolos, Larisa Okorokova

Introduction

Transposons - parts of the genome capable of moving and reproducing inside the genome. For example, in the human genome, about 50% of DNA is represented by a different range of mobile elements (ME). The mosaic insertions of the ME cause somatic genomic variations and are highly capable of producing phenotypic diversity, including in the brain. Transposon insertions can involve disruption of the coding sequence of genes through splicing disruption or frameshift, but generally, they appear in non-coding parts of the genome, and it is complicated to predict the impact of the insertion in this case. When this occurs, it is likely that the transcriptional programs in the cells are damaged, which, in turn, can lead to the development of diseases such as autism spectrum disorders. Exploring transposon expression using RNA sequencing data from single cells of brain organoids treated with valproic acid (a factor that increases the risk of developing RAS) would help to explain the mechanisms behind this phenomenon.

Methods

Collection and selection of brain organoid RNA sequencing data from inducible pluripotent stem cells

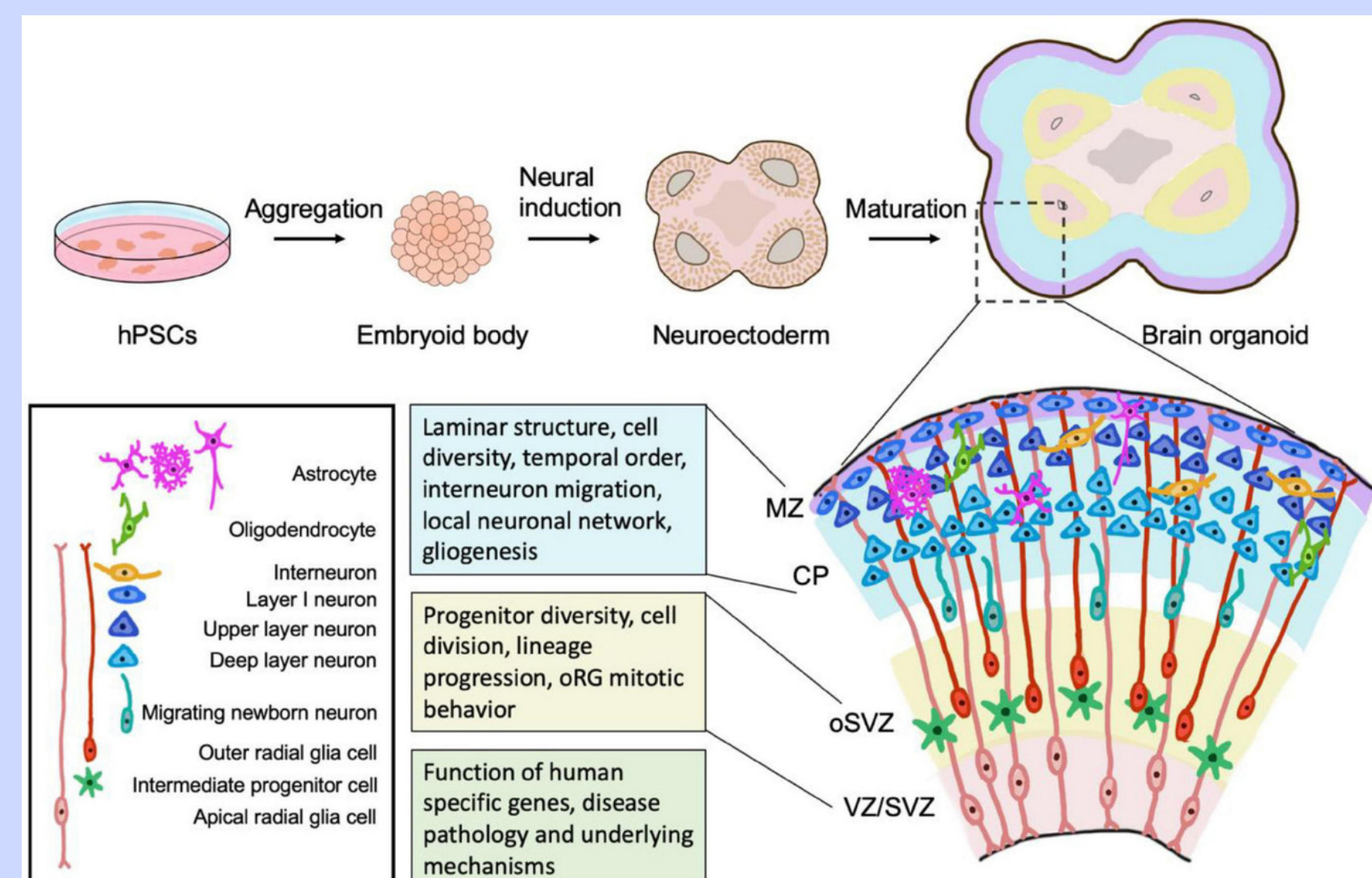


Fig.1

Aligning reads to the genome in **STARsolo**

Counting gene expression and transposons in single cells using **scTE**

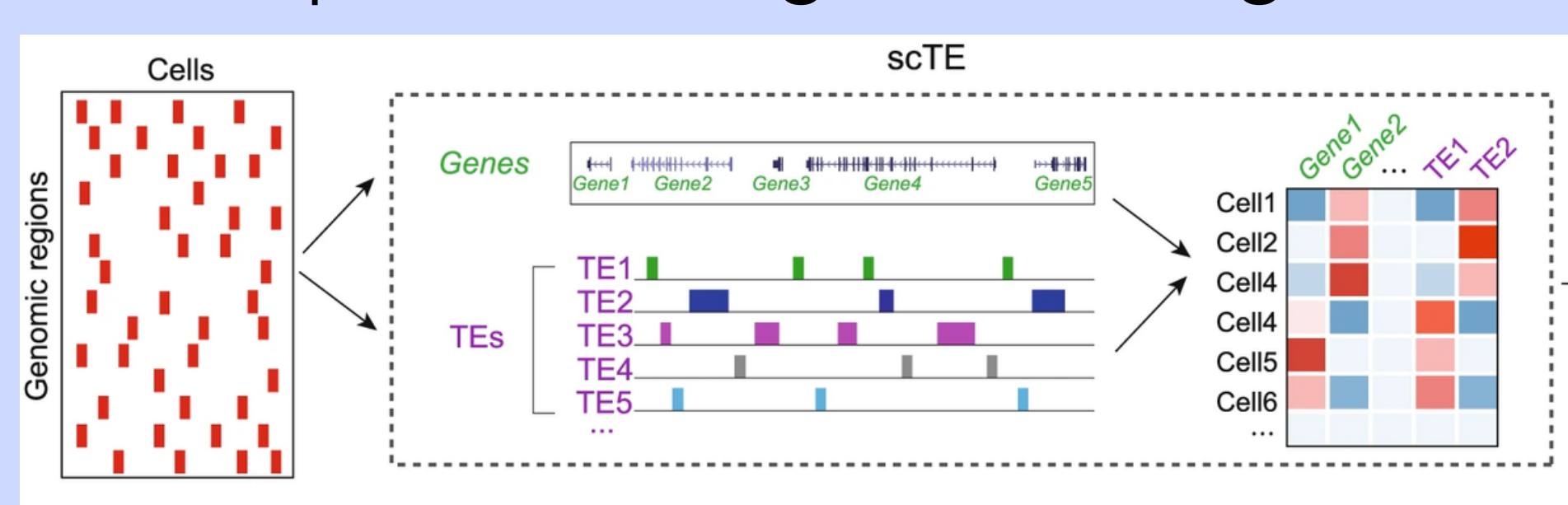


Fig.2

Processing the generated expression matrices in **R**

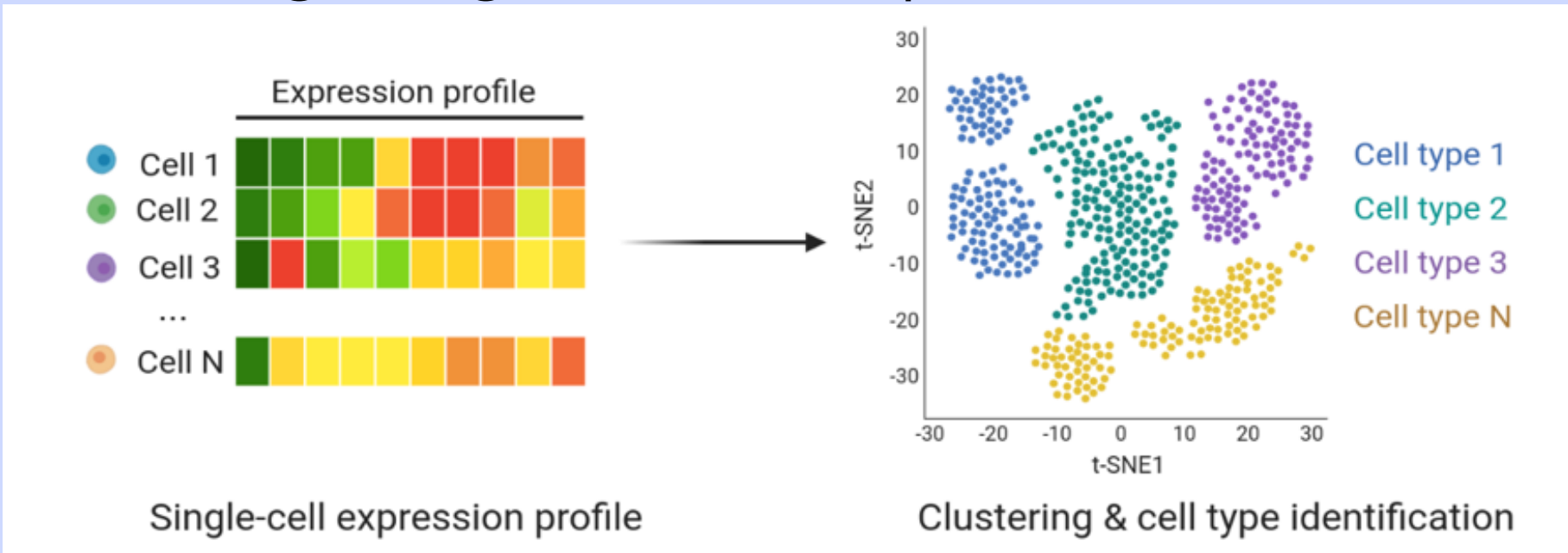
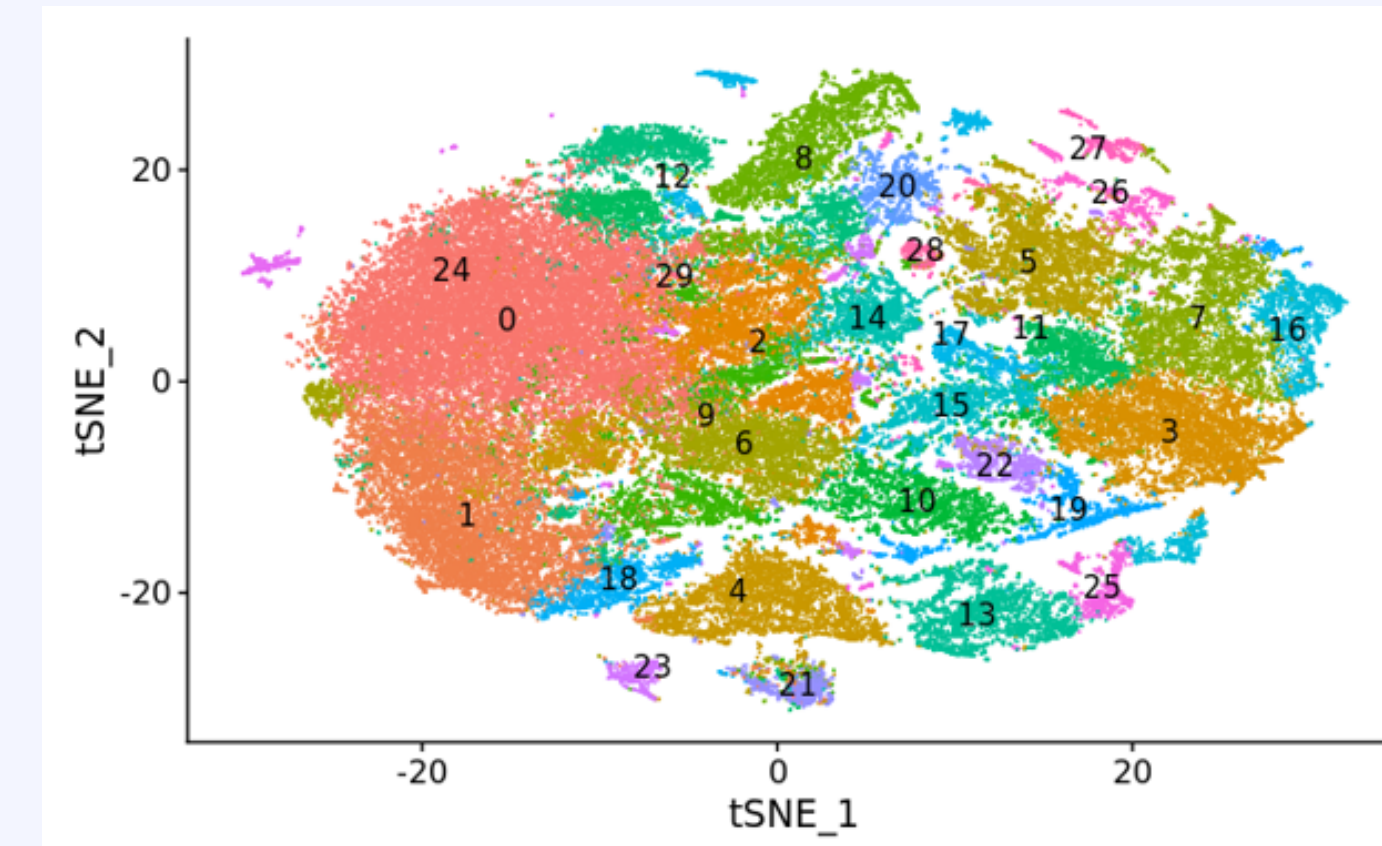


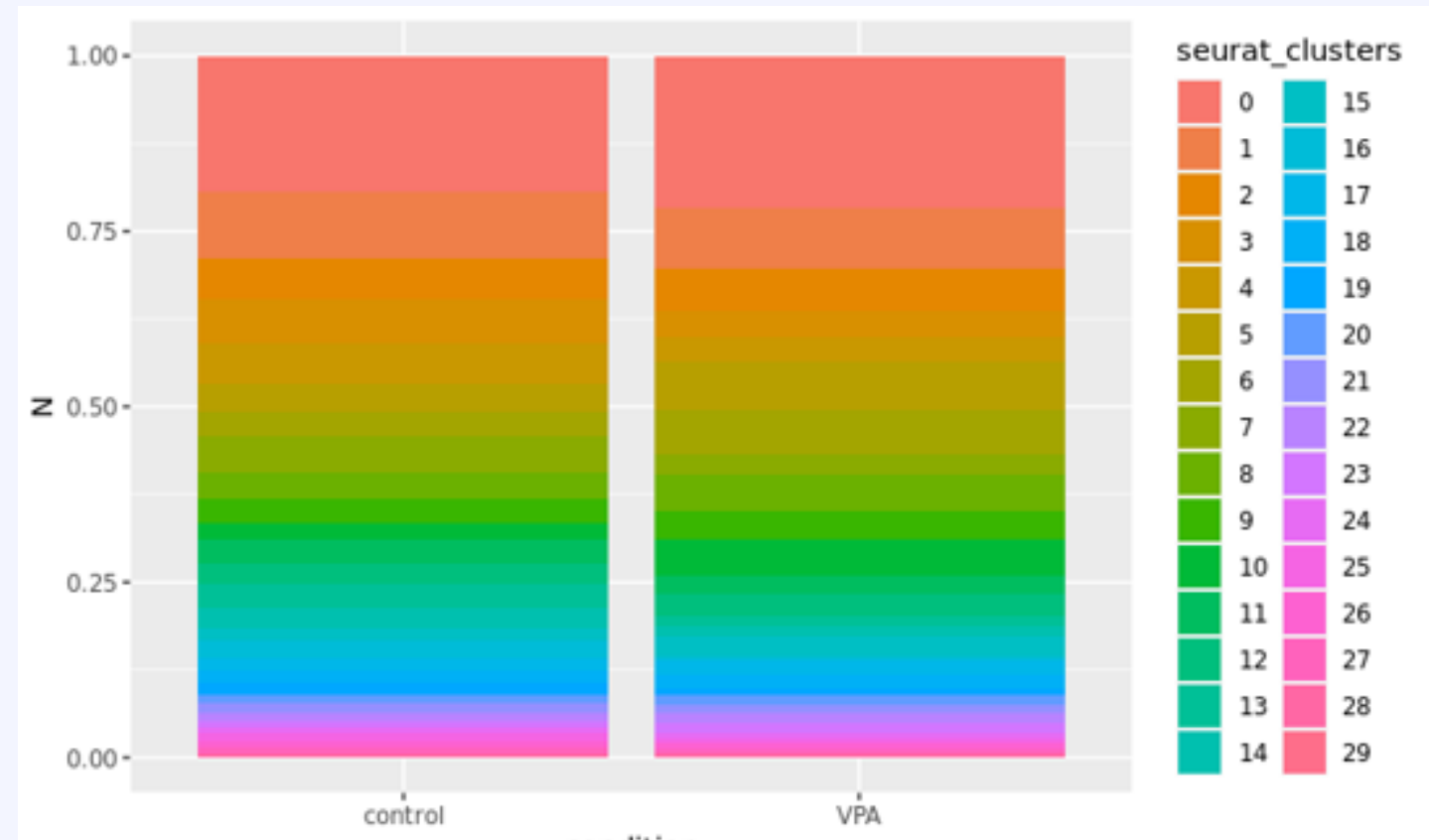
Fig.3

Results

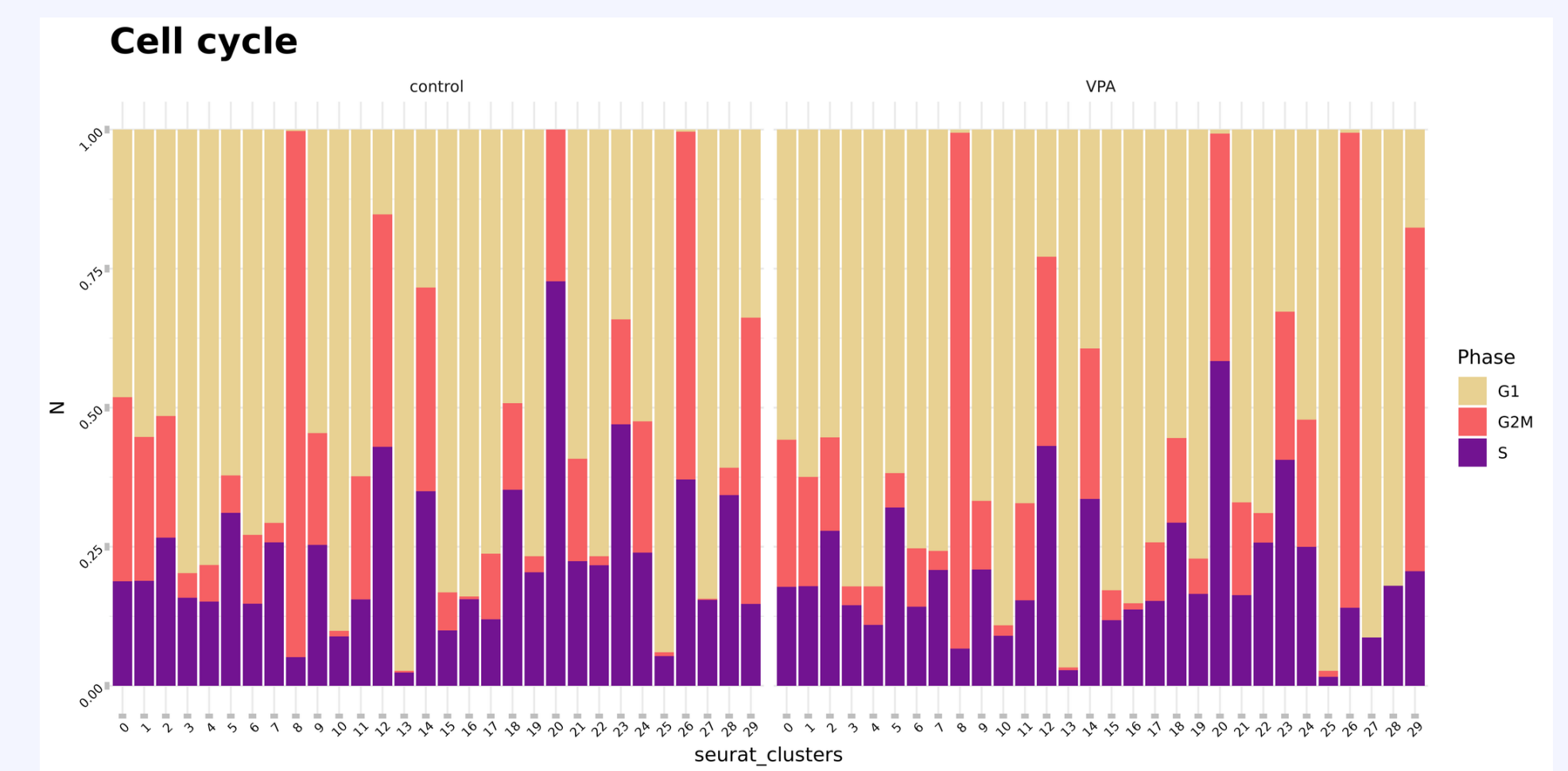
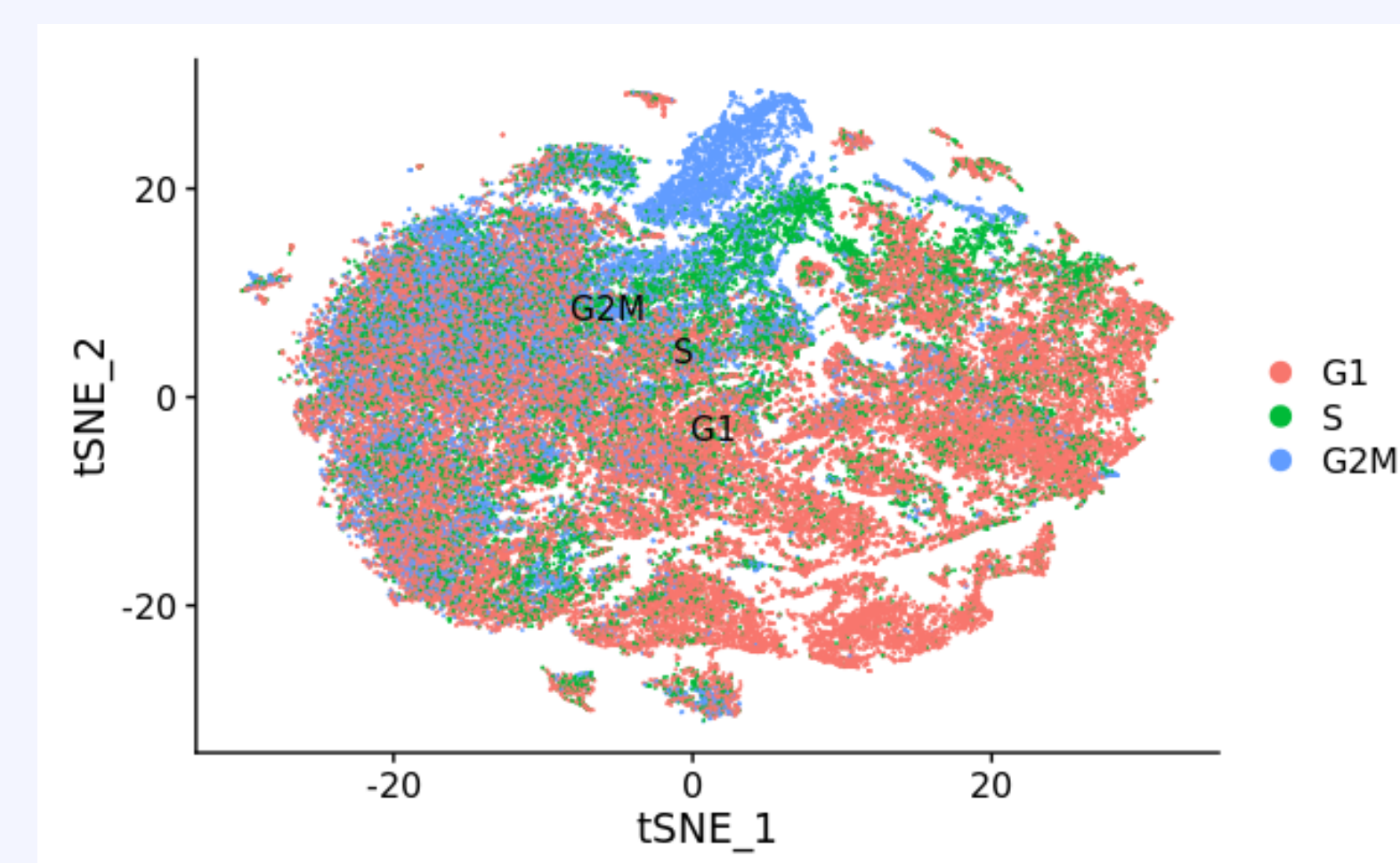
1. We combined cells from 4 samples: 2 controls and 2 treated with valproic acid, created an object, and isolated 29 clusters of cell types.



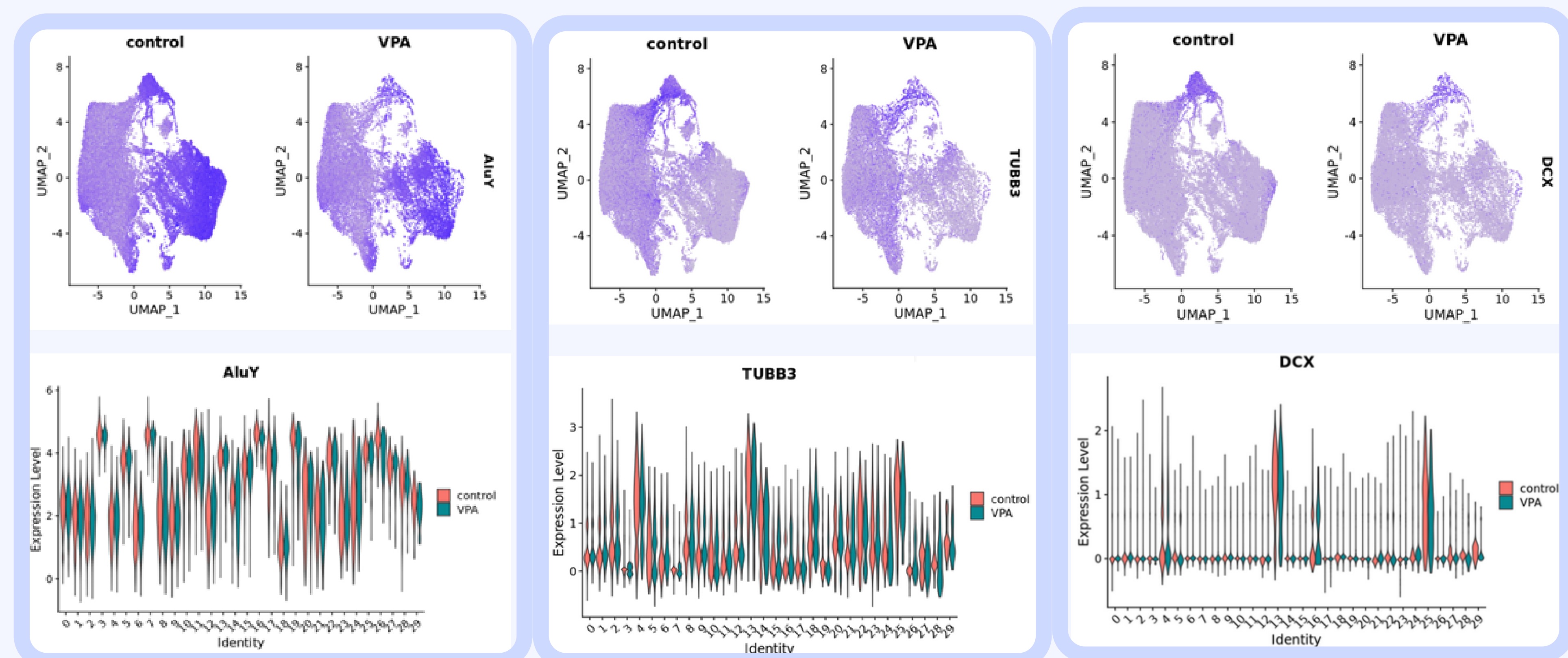
2. Then, we analyzed the structure of the cell populations under the VPA treatment. The relative population density did not change significantly.



3. The organoid cells are in different stages of the cell cycle. The exposure of the VPA had no impact on it.



4. Next, we identified the expression levels of nonautonomous elements and risk genes.



5. Among the markers in the cell clusters are alu-elements, which refer to nonautonomous elements. Furthermore, HERVK.int, which is related to human endogenous retroviruses, is also found.

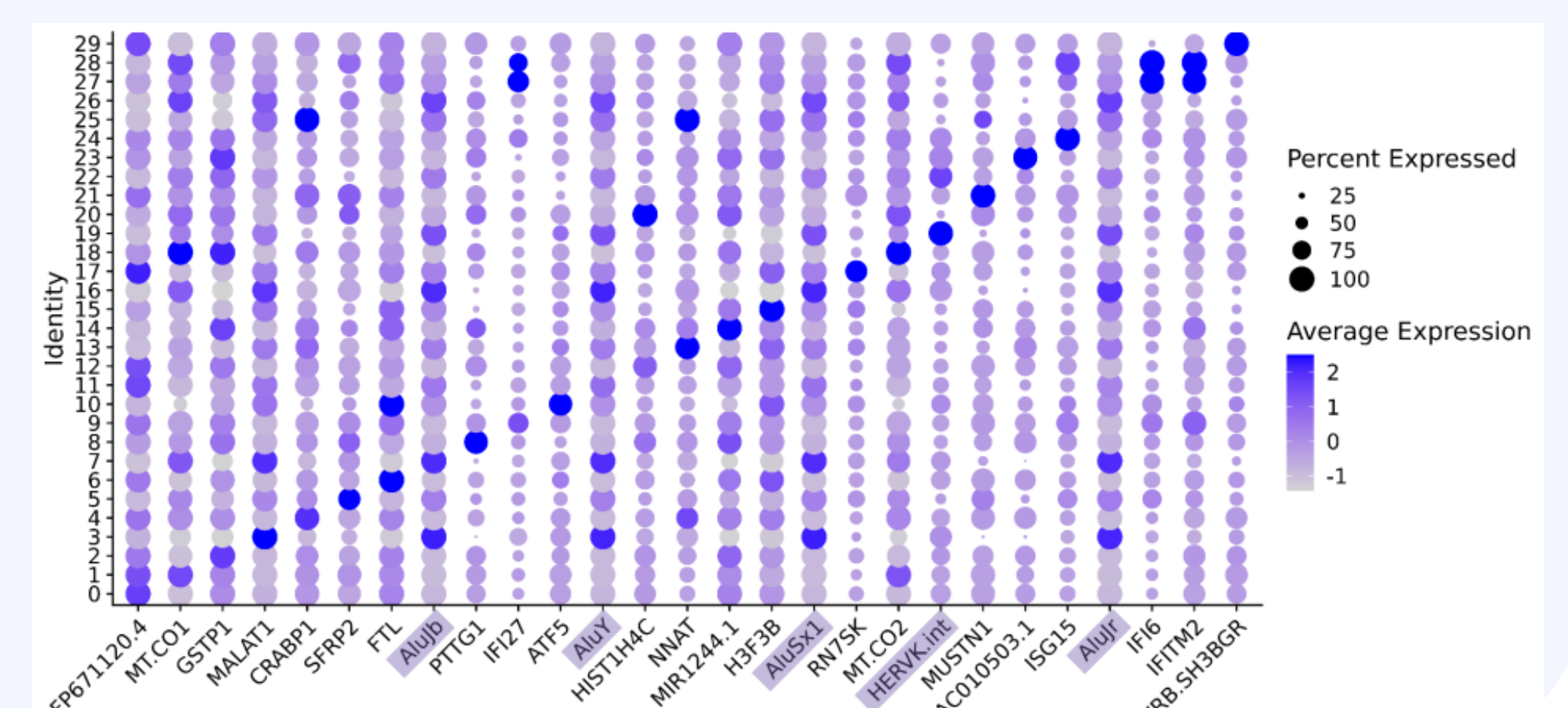


Fig.1: <https://doi.org/10.3389/fnins.2022.872794>

Fig.2: <https://doi.org/10.1038/s41467-021-21808-x>

Fig.3: <https://doi.org/10.3390/cancers13184627>