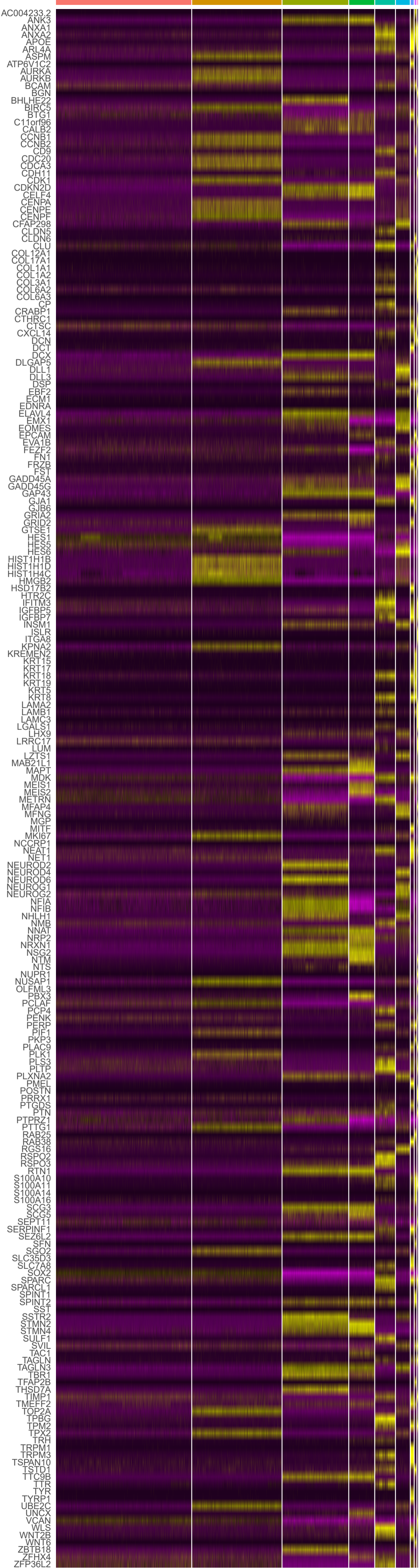


Suppl. Fig. 3: Gene expression patterns in 9 cell types (clusters) of hiPSC-derived human cortical neuronal cultures on day 38 of differentiation.

Differential gene expression (DEG) was performed for all binary comparison of expression levels of all genes in cells of any cluster vs every other individual cluster by edgeR analysis. The differentially expressed genes were ranked by FDR. The top 20 most significant genes were pulled out for gene expression analysis by heat map. This resulted in 720 genes (20 genes *36 comparisons). Some of the genes were identified as significant genes in more than one comparison. At the end, we obtained 214 unique genes, which are displayed in the heatmap of the expression of these genes ordered by name (rows), across single cells (sub-columns) in each of the 9 identified clusters (main column) as shown. Color keys to cluster identity and color-coded expression levels are provided in the figure itself.

0 1 2 3 4 5 6 7 8



Identity

- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8

Expression

2

1

0

-1

-2