Figure S1

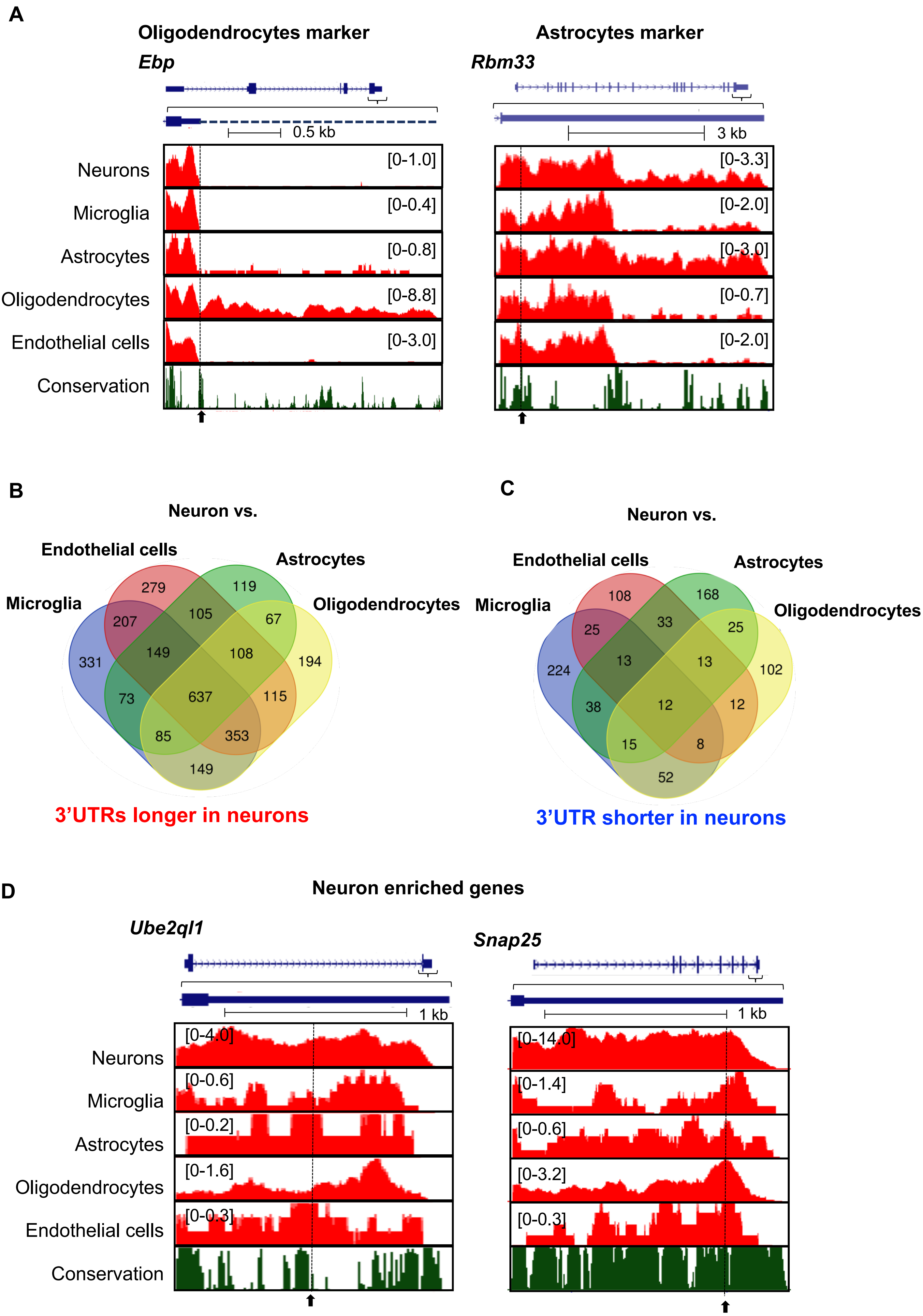

Figure S1. Distinct APA profile of neuronal cells. (A) Example genes *Ebp* and *Rbm33* shown in UCSC genome browser. *Ebp* showed a longer 3'UTR in oligodendrocytes than other cell types, and *Rbm33* showed a longer 3'UTR in astrocytes. See Figure 2D for figure format. **(B)** & **(C)** Venn diagrams showing overlaps of significantly lengthened (B) or shortened (C) genes in neurons vs. other cell types. **(C)** Example neuron-enriched genes *Ube2ql1* and *Snap25* shown in UCSC genome browser. See Figure 2D for figure format.

Figure S2

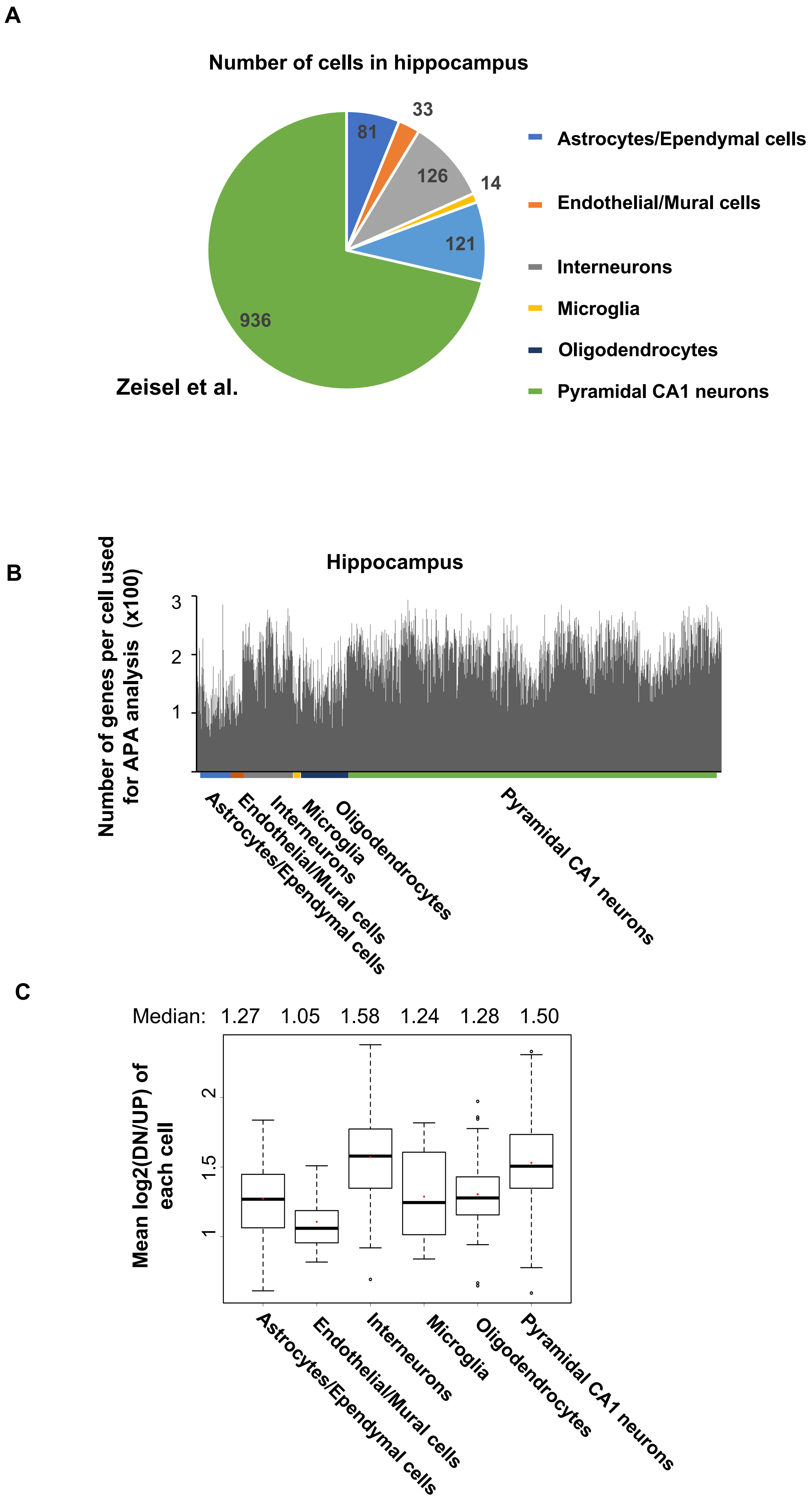

Figure S2. Analysis of APA events using single cell RNA-seq data. (A) A pie chart showing number of cells for each cell type in hippocampus used in the analysis. **(B)** Bar graph showing number of genes in each cell used. Genes that had at least 1 read in either UP or DN region are shown. Cell types are indicated at the bottom. **(C)** Box plots showing mean log2(DN/UP) of all single cells for each cell type in hippocampus.

Figure S3

A

BP	**P-value**
peptide metabolic process	5.2E-06
RNA processing	8.1E-06
cellular nitrogen compound metabolic process	1.1E-05
cellular macromolecular complex assembly	1.6E-05
ribonucleoprotein complex biogenesis	5.1E-05

CC	**P-value**
intracellular part	1.7E-09
intracellular ribonucleoprotein complex	1.1E-08
mitochondrial part	8.4E-07
small ribosomal subunit	1.8E-06
mitochondrial ribosome	4.6E-06

B

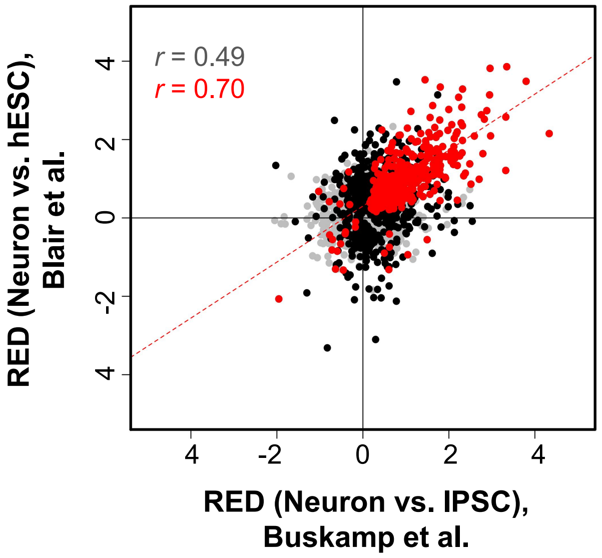

Figure S3. APA in human and mouse neurogenesis. (A) Top GO terms enriched for genes showing significant 3'UTR lengthening in mouse neurogenesis. BP, biological process; CC, cellular component. **(B)** Scatter plot comparing RED values of human neurogenesis (differentiated neurons vs. ESC or IPSC) from Busskamp et al. (x-axis, n=2) and Blair et al. (y-axis, n=2). Genes with significantly regulated 3'UTR APA (P < 0.01, Fisher's Exact Test) in only one of the data sets are shown in black (1,378), and those significant in both data sets are in red (421). Pearson correlation coefficient (r) for each gene group is indicated.

Figure S4

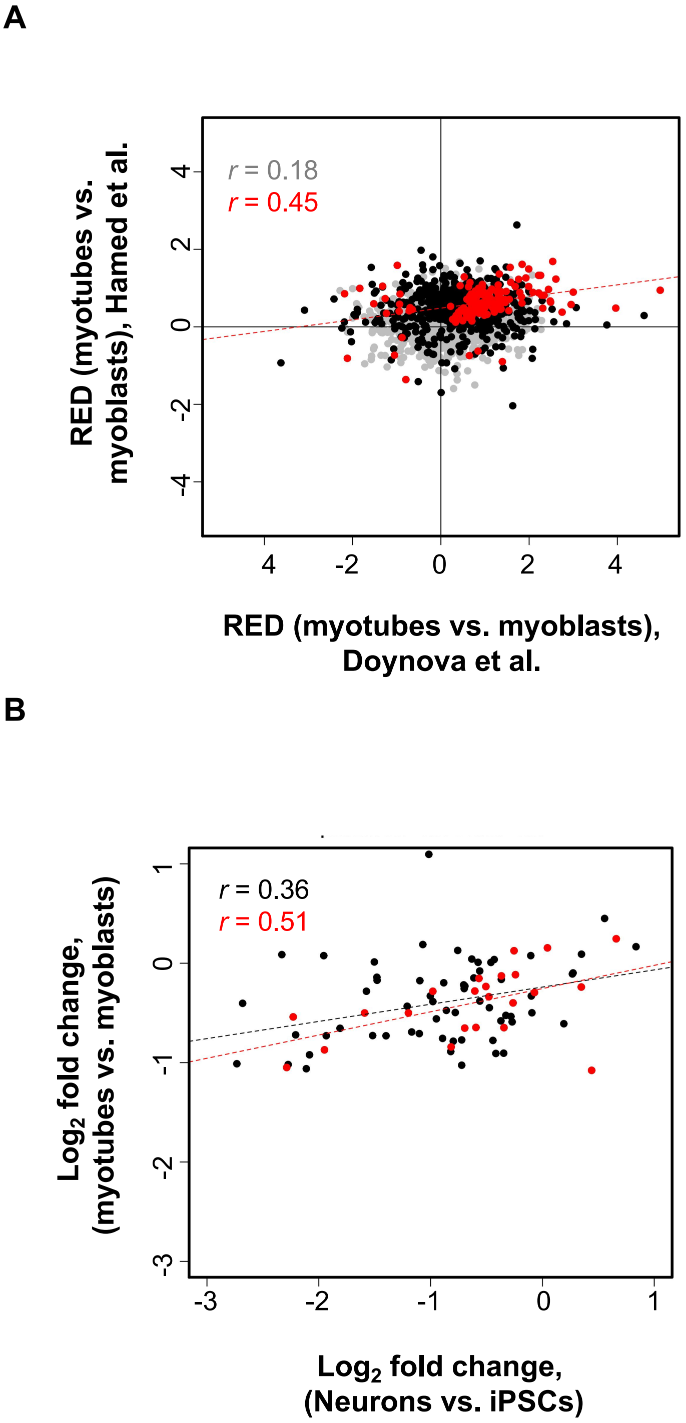

Figure S4. APA regulation in myogenesis. (A) Scatter plot comparing RED values of myogenesis (differentiated C2C12 cells vs. proliferating C2C12 cells) from Doynova et al. (x-axis, n=2) and Hamed et al. (y-axis, n=2). Genes with significantly regulated 3'UTR APA ($P < 0.01$, Fisher's Exact Test) in only one of the data sets are shown in black (897), and those significant in both data sets are in red (180). Pearson correlation coefficient (*r*) is indicated. **(B)** Scatter plot showing $\log_2$ fold change of 87 C/P factor genes expressed in both neurogenesis and myogenesis. Core C/P factor genes are in red. Pearson correlation coefficient (*r*) is indicated for all C/P factor genes and core factor genes.