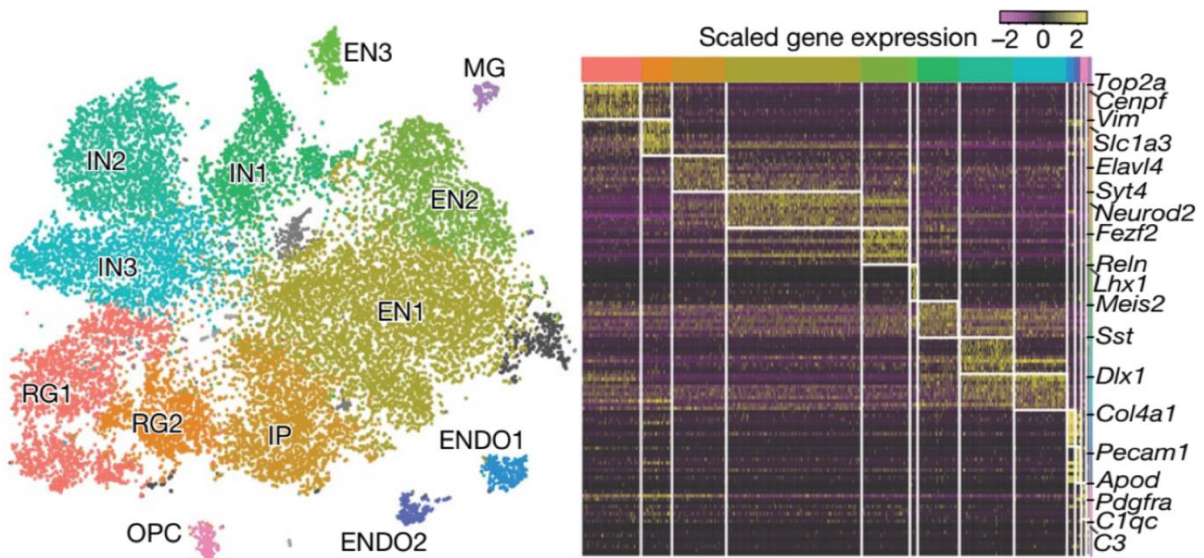


Single cell gene expression in the developing brain

We are interested in understanding how distinct cell types in the brain develop and what makes them unique in both health and disease. To do so, we are studying which genes are expressed in different cell types throughout brain development.

By studying gene expression in neural progenitor cells and mature neurons in the cortex, we found that alternative exon use due to splicing differentiates the transcriptomic profiles in these cells. We also reported an intronic mutation in *FLNA* that disrupts normal splicing in neural progenitor cells which can lead to brain malformations in humans (Xiaochang *et al.* 2016).

Using single cell RNA-sequencing, we have uncovered the heterogeneity of gene expression that is found in human cortical radial glial cells when compared to mouse radial glial cells in the developing brain (Johnson *et al.* 2015). We have also used single cell RNA sequencing to study cell type gene expression in the developing ferret (Johnson *et al.* 2015) and in a ferret model of microcephaly (Johnson *et al.* 2018). This work has shown that the ferret might be a more accurate model of human cortical development than the mouse and has revealed cell type specific changes in disease.



Single cell RNA-sequencing from the ferret brain at E35 identifies major cell types and cell type specific gene expression markers (Johnson *et al.* 2018).

~Rebeca Borges Monroy