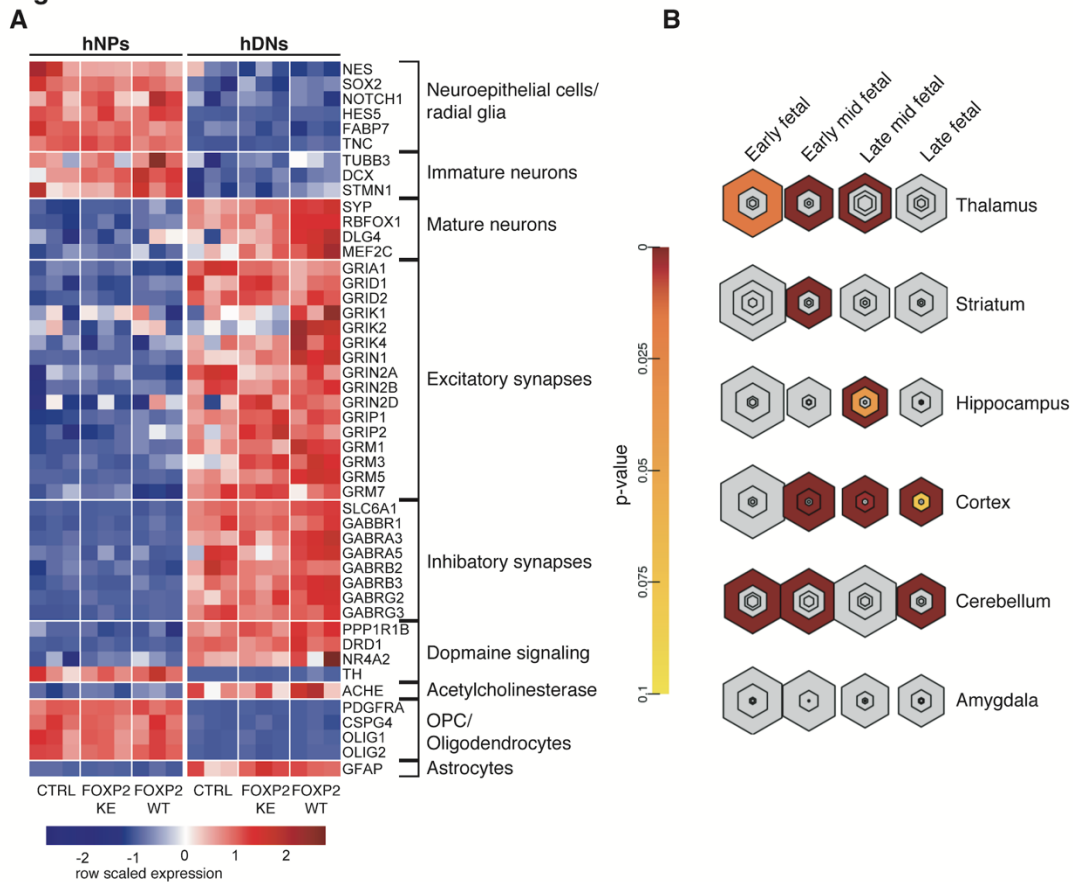


**Figure S1**



**Figure S1:** Related to Figure 1

**(A)** Heat map comparing the expression of genes across hNP and hDN from each condition. Expression of each gene is scaled across samples with the mean expression equaling zero. Negative values reflect expression below the mean and do not indicate a lack of expression. **(B)** Specific expression analysis (SEA tool) (Xu et al., 2014) was used to identify the enrichment of genes with significantly increased expression in CTRL hDNs compared to CTRL hNPs among genes with region specific expression in the human fetal brain. P-value is calculated with a Fisher's exact test with Benjamini-Hochberg correction. Genes with varying stringencies for enrichment are represented by the size of the hexagons going from least specific lists (outer hexagons) to most specific (center). Hexagons are scaled to the size of the gene lists.