Supplemental File

Table S1 Cell Group Details. Cell clusters identified in scRNAseq. Table shows the canonical markers and other genes that have been used to identify cells in each cluster and the cell group includes the presence of *SOX2*, *SOX5*, or *SOX9*.

Code	Cell Group	# of Control Cells	# of DPM cells	Markers used for Identity
A	S radial glia (SOX2,SOX9)	1213	577	*PAX6, LIX1, HMGA2, HES1, VIM, GLI3, LHX2, SOX3*
B	G1 radial glia (SOX2)	1135	395	
C	S radial glia (SOX2)	967	518	
D	G1 Glutamatergic Neurons (SOX5)	697	570	*GRIN2B, SLC17A7, NEUROD6, GRIA2, GRIA1, DLG4, GAP43, SYP, SOX12*
E	G1 Neurons	719	525	*NEFL, MAPT, NRN1, VAMP2, STMN3, STXBP1*
F	G2/M radial glia (SOX2,SOX9)	770	436	*VIM, HES1, GLI3, HMGA2*
G	G1 radial glia (SOX2,SOX9)	765	424	*VIM, HES1, FABP7, PAX6*
H	G1 Developing Neurons (SOX2,SOX9)	786	371	*MAP2, MAPT, INA, ELAV3, ELAV4*
I	G1 Outer Radial Glia (SOX2,SOX9)	992	160	*TTR, OTX2, RSPO2, HOPX, FAM107A, FABP7*
J	G1 Immature Neurons	556	511	*MAP2, RBFOX3, SYP, DCX, NEUROD1, TBR1, TUBB3, STMN1, SOX11*
K	G1 Unknown	388	510	*GRIA2, SYAP1*
L	G1 Stressed radial glia (SOX2,SOX9)	539	220	
M	G2/M radial glia (SOX2)	440	233	*PAX6, HES1, ASCL1*
N	S radial glia 2 (SOX2)	400	218	
O	G1/S Intermediate Progenitors (SOX2)	263	176	*EOMES, ASCL1*
P	Mesenchymal/Neural Crest	91	36	*COL3A1, DCN, COL1A2, FN1, SNAI2, VIM*
Q	G1/S Unknown (SOX2)	48	30	
R	G2/M Immature Neurons (SOX2,SOX5)	34	0	*TBR1, DCX, CDH2*
S	G1 Choroid Plexus (SOX2)	33	0	*TTR, PIFO, OTX2, SOX15*

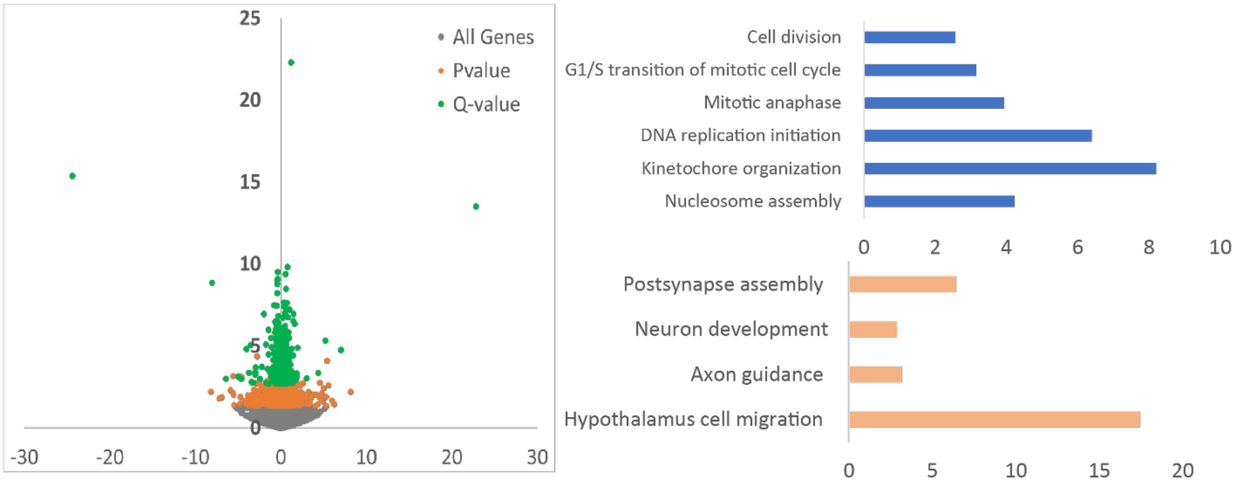

Figure S1 Ribosomal reduced RNAseq. Left shows the volcano plot of 6 control cerebral organoid vs 6 DPM treated ribosomal reduced RNAseq runs. The x-axis shows the log2 fold change of control over DPM and the y-axis is the -log10 of pvalue. Right shows enriched gene pathways for downregulated processes (blue) and upregulated processes (orange) suggesting mitotic processes and neural function are impacted by DPM exposure.

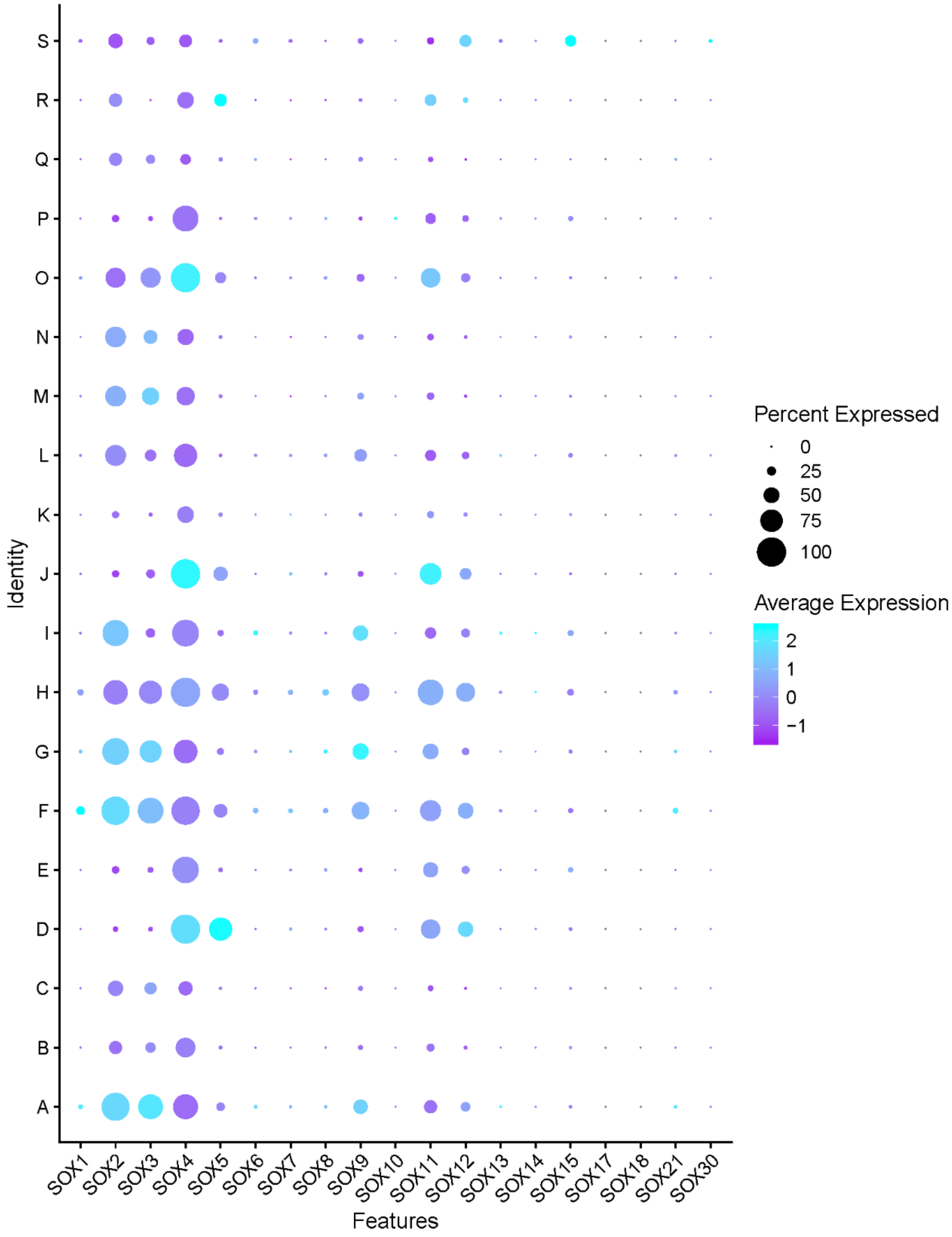

Figure S2 *SOX* gene expression in each identified cellular group. The changing expression of SOX genes are common markers of the transition from neural progenitors to mature neuron differentiation. Shown for each cell group (y-axis) is a dot plot of expression. The size of the circle corresponds to the percent of cells within the group expressing each factor and the color corresponds to the average expression level (cyan=high, purple-low).

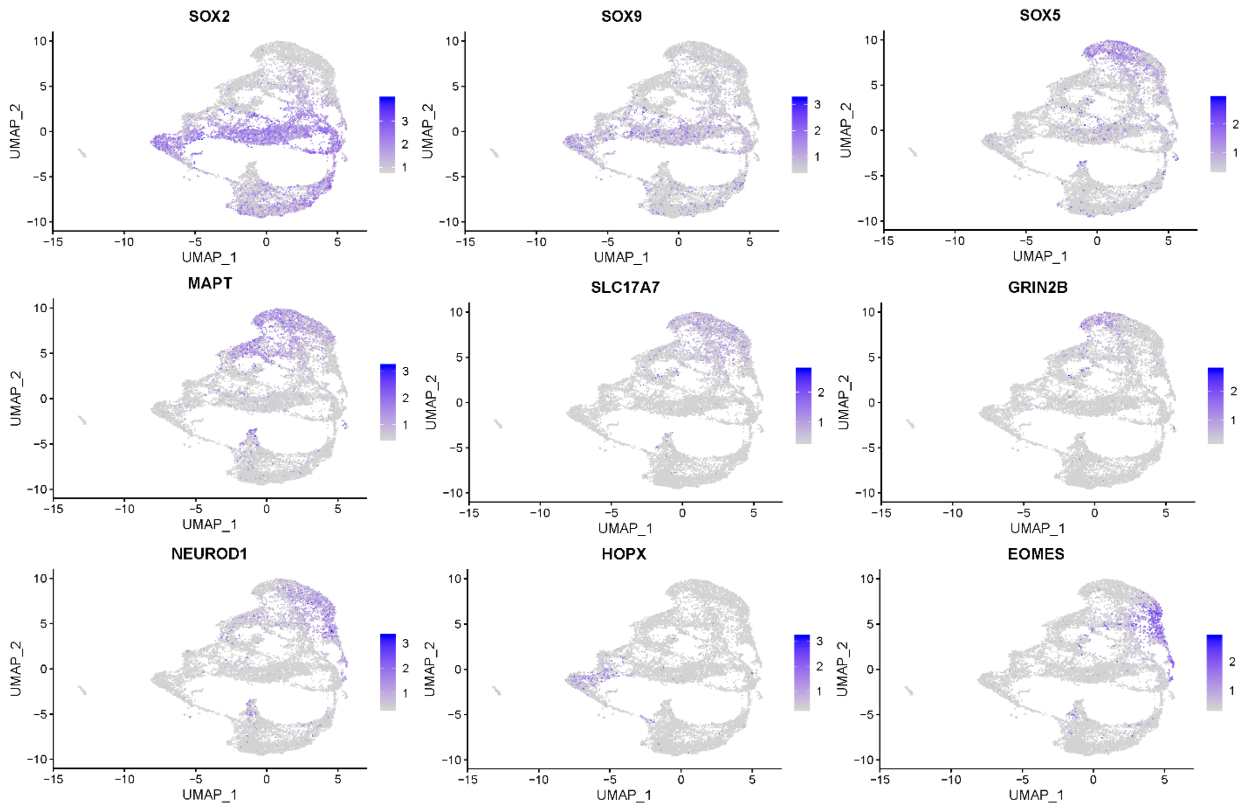

Figure S3 UMAP plot of top gene markers (*SOX2, SOX9, SOX5, MAPT, SLC17A7, GRIN2B, NEUROD1, HOPX, EOMES*). Normalized expression of the nine markers used for identification of the cellular group. The expression of these genes are highly regionalized, with the purple cells highlighting which cells express the marker genes. While gray indicates cells which do not express the gene of interest.

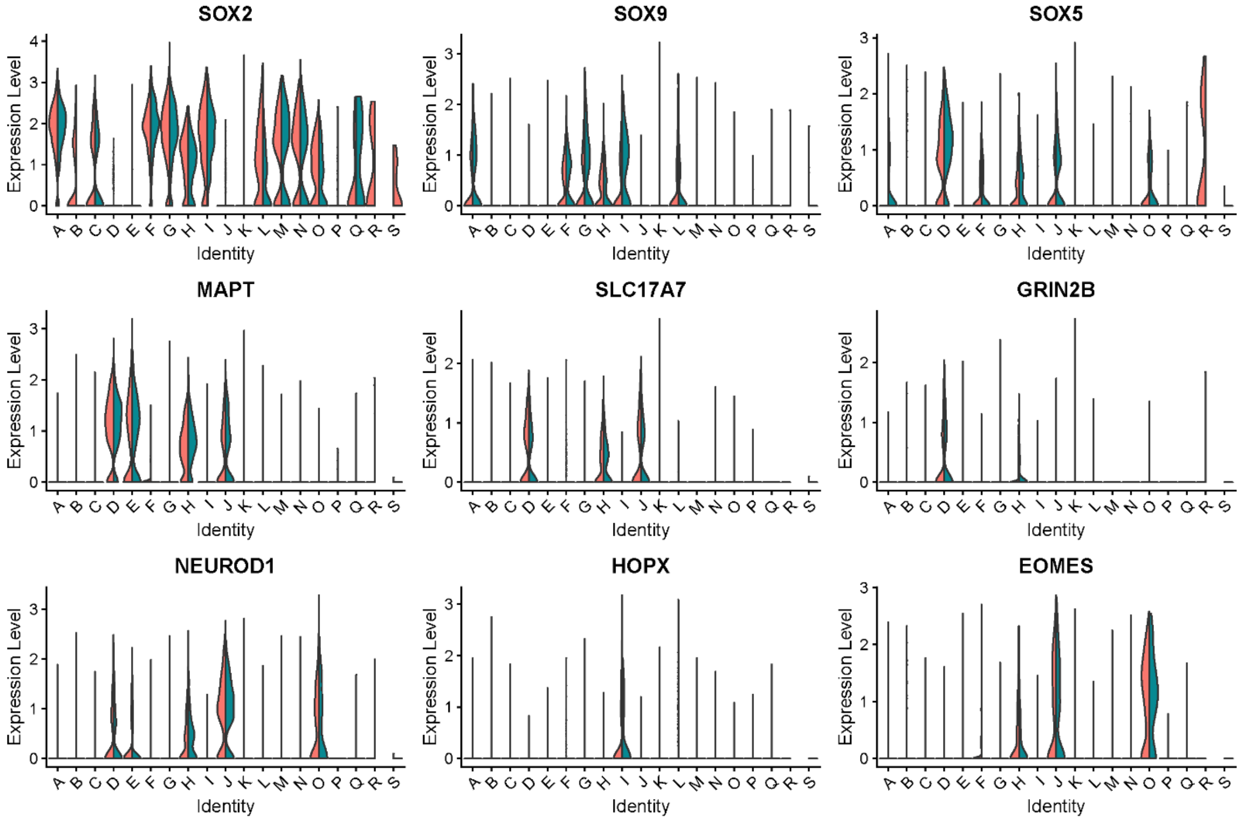

Figure S4 Violin plot of top gene markers (*SOX2, SOX9, SOX5, MAPT, SLC17A7, GRIN2B, NEUROD1, HOPX, EOMES*). Each plot for the different cell clusters A-S show the expression level (height of plot) in control (peach) or DPM (cyan) relative to the density of cells with that expression (width).

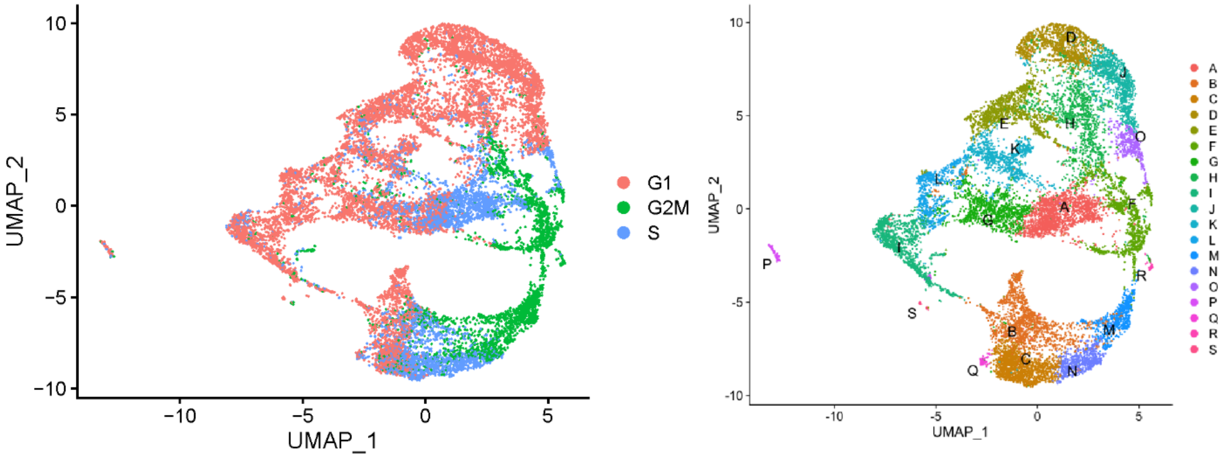

Figure S5 Cell cycle next to clustering. Panel to the right shows annotation for cell cycles, G1=red, G2/M=green, and S=blue. Cluster identity is shown on the right same as Figure 4A.

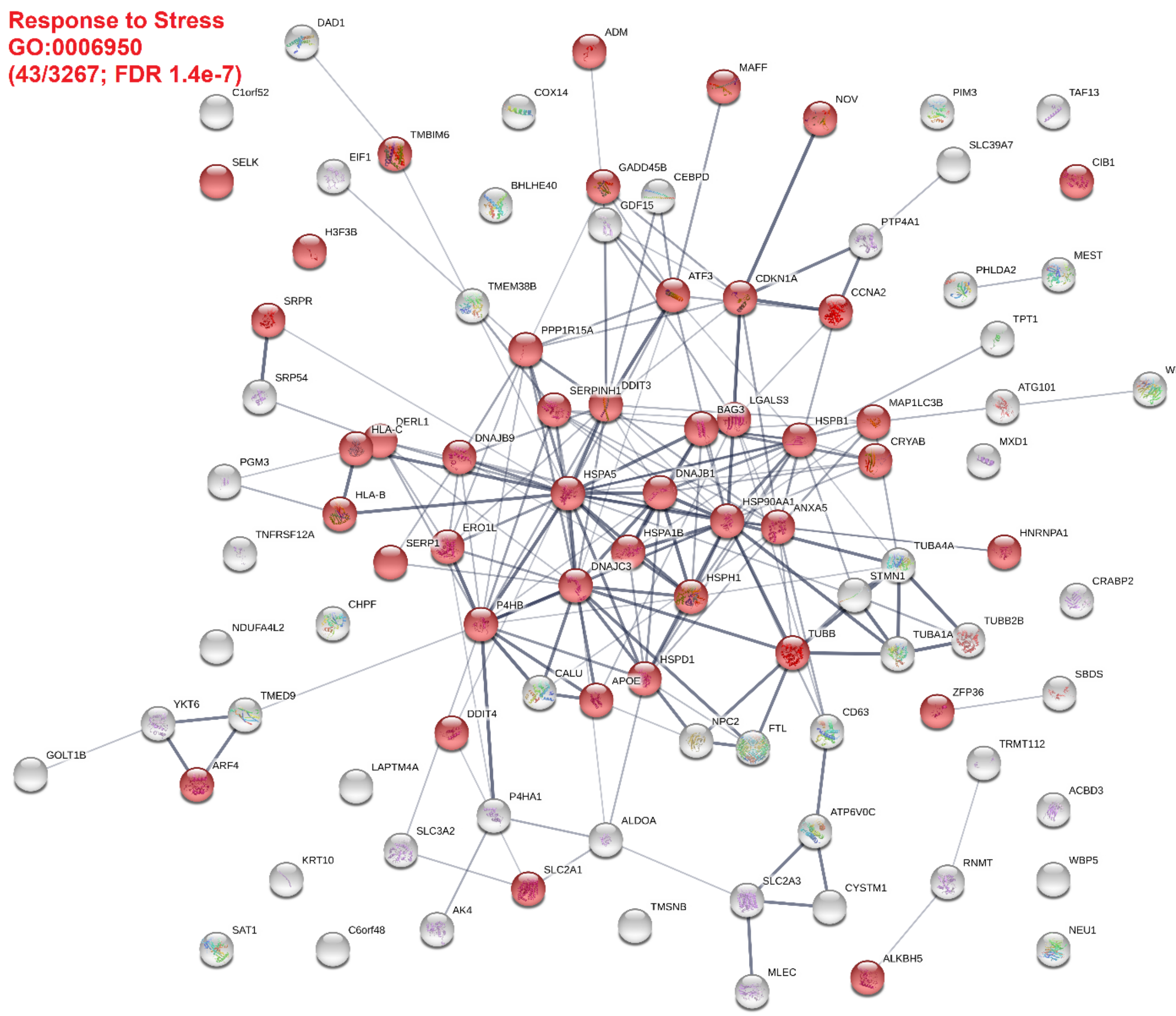

Figure S6 Genes enriched in group L relative to other genes. The top 100 genes of group L have a max_pval of groups from 8.38e-244 to 1.01e-54 and were fed into String analysis. Genes in red are significantly enriched for the GO term response to stress (FDR 1.4e-7).

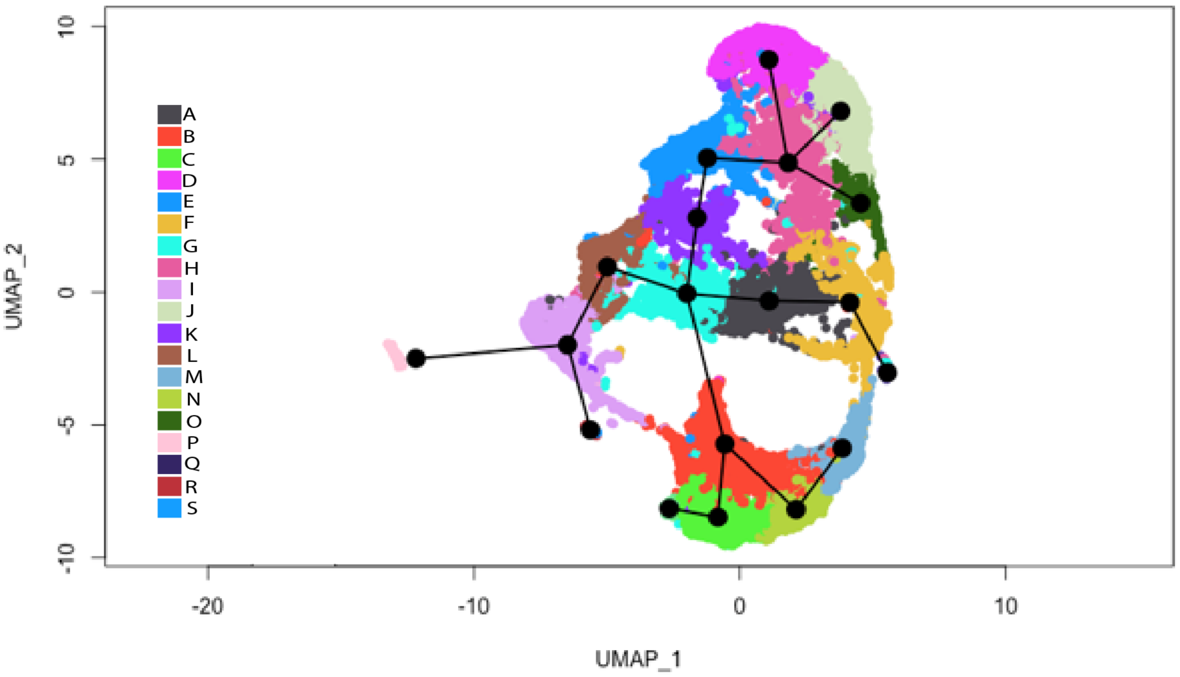

Figure S7 Pseudo time analysis plot of cerebral organoid scRNAseq. Analysis of the developmental trajectories of cells in cerebral organoids using slingshot. This show the different cell fates of the immature cells into mature neurons. Cells clustered in group A (dark gray) give rise to other cellular populations.

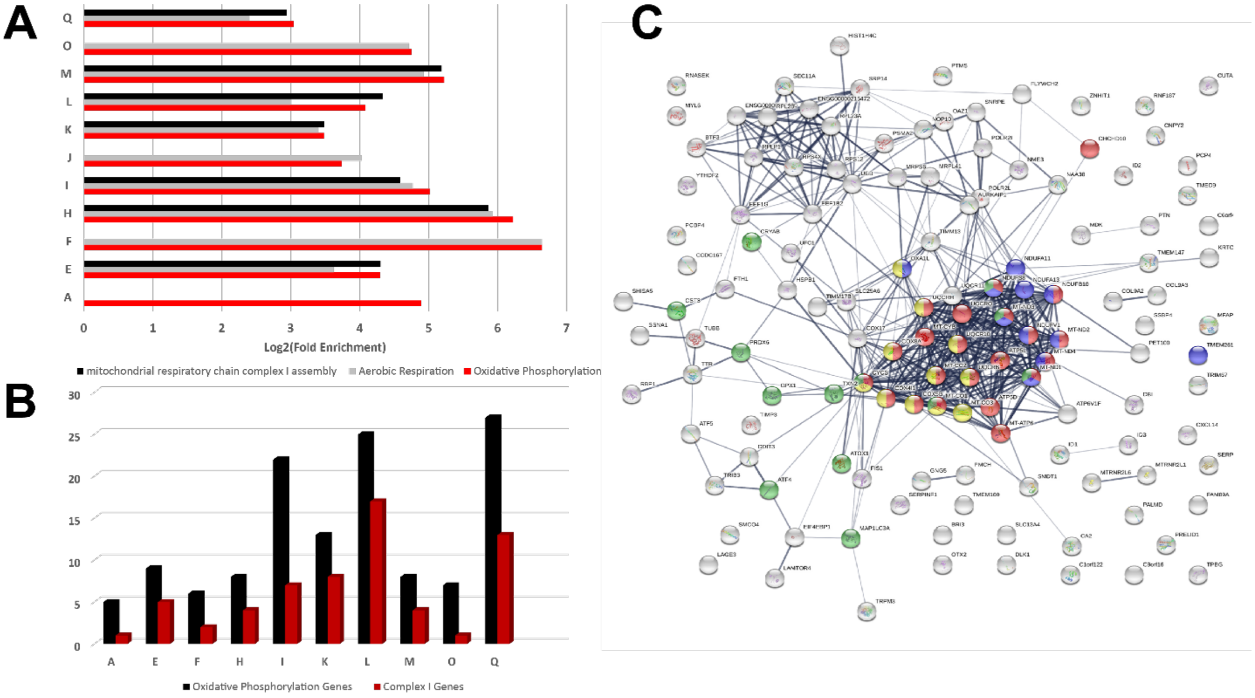

Figure S8 DPM treatment altered cellular processes. **A**). Biological processes in specific cell clusters are tied to cellular respiration. **B**) comparison between the number of genes in oxidative phosphorylation and electron transport complex genes. **C**) Sting analysis of Outer radial glia cell (group I) cluster and the specific biological processes that are enriched, oxidative phosphorylation (red), mitochondrial respiratory chain complex I assembly (blue), response to oxidative stress (green), aerobic respiration (yellow).

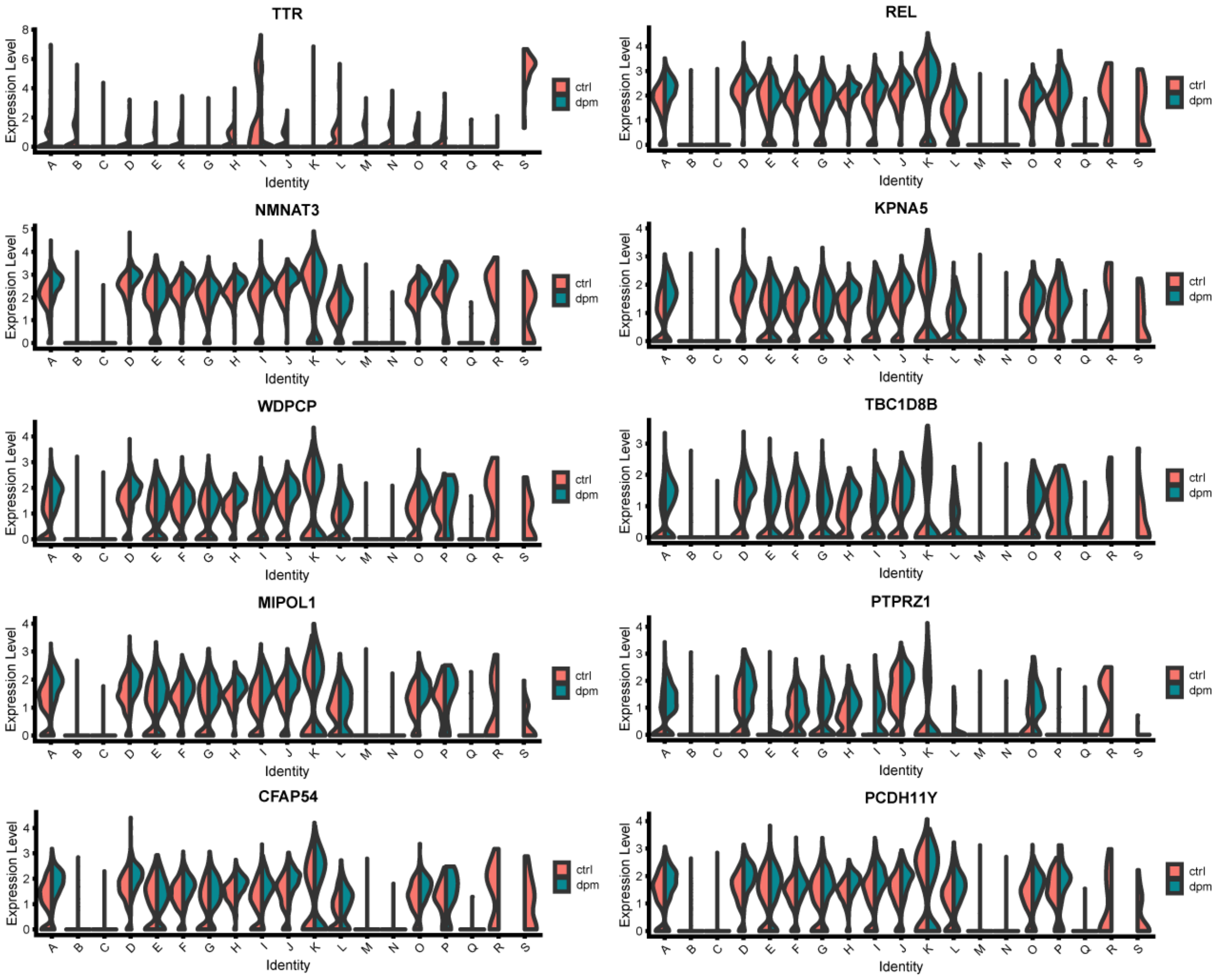

Figure S9 Differential Expression of the Top Genes Identified in multiple tissue types. Violin plots of the differential expression of the top 10 genes upon exposure to DPM. These genes occur in the majority of the cell clusters but also occur in multiple tissue types where the -log10 adjusted Pvalue < 0.0001.

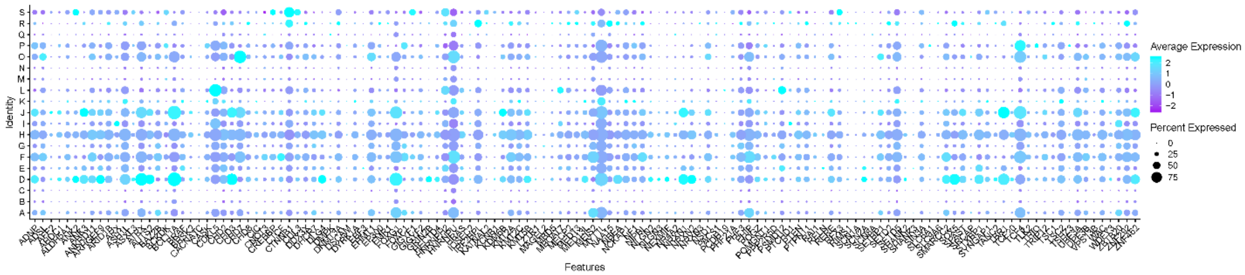

Figure S10 ASD SFARI gene expression. Dotplot of SFARI database genes with a score of 1 shows average cell expression in each cluster. Clusters that are identified as neurons (groups D, H, and J) and outer radial glia (group I) have the highest concentration of these ASD associated genes.