

Supplemental Materials

Supplemental Table 1. Detailed Case History

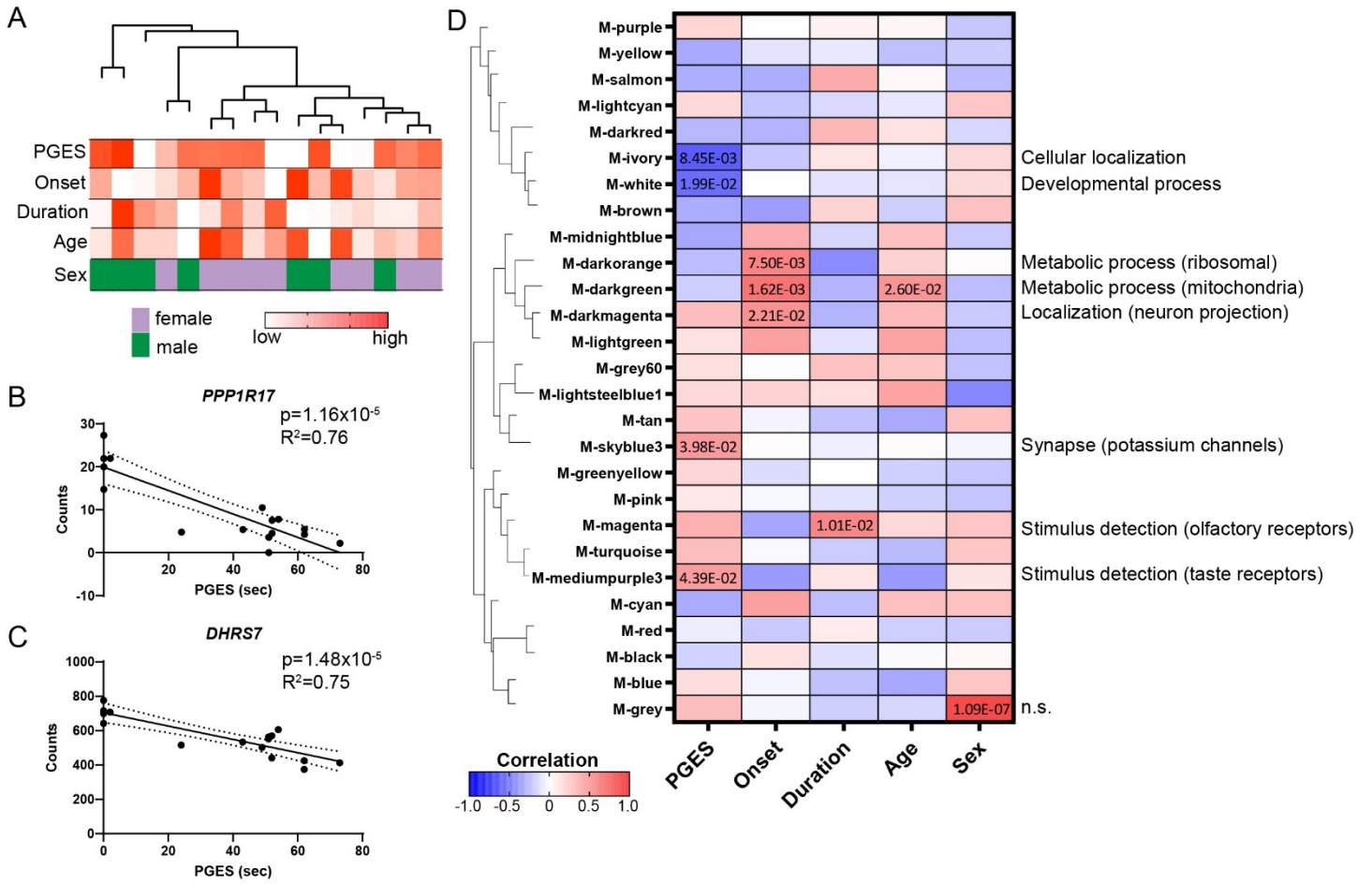
Supplemental Table 2. WGCNA RNAseq Gene and Module Correlations in Hippocampus

Supplemental Table 3. WGCNA RNAseq GOenRichment Analysis in Hippocampus

Supplemental Figure 1. WGCNA of RNAseq in the hippocampus. A) Clustering of TLE patients is indicated from RNAseq expression data in the hippocampus ($n = 16$) with the corresponding clinical history. PGES, epilepsy onset, epilepsy duration, and age are indicated from low (white) to high (red) values. Sex is indicated for females (purple) and males (green). **B)** After WGCNA, the top two transcripts that correlated with PGES duration were **B) *PPP1R17*** ($p < 0.0001$, $R^2 = 0.76$) and **C) *DHRS7*** ($p < 0.0001$, $R^2 = 0.75$) with negative correlations. **D)** WGCNA resulted in identification of 27 modules (M-color), with clustering indicated on the left by eigenprotein adjacency. Module trait analysis indicated 4 significant modules (p value is indicated) correlated with PGES duration, 3 modules with epilepsy onset, 1 module with epilepsy duration, and 1 module with age at surgery. Heatmap indicates correlation values, blue is a negative correlation and red is a positive correlation. Top GO annotations below 5% FDR are noted for the significant modules on the right.

Supplemental Figure 2. Potassium channel transcript expression from RNAseq in the hippocampus by PGES duration. A) Expression of potassium channel transcripts in the hippocampus ($n = 16$) that were identified by WGCNA in the M-skyblue3 module, with a positive correlation to PGES duration ($p = 3.98 \times 10^{-2}$, $\text{corr.} = 0.52$). Z-score is indicated on the heatmap, with higher values represented in red and lower values in blue.

Supplemental Figure 1.



Supplemental Figure 2.

