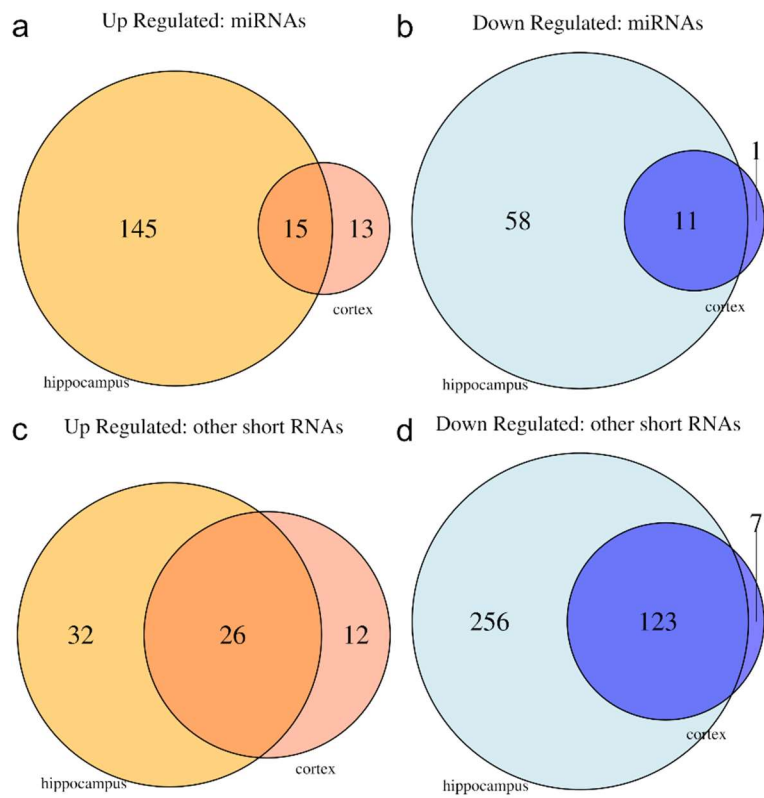


Supplementary Figure 1. RT-qPCR validation of RNA-Sequencing data. **A.** *CTSH* was up-regulated 4-fold in the MTLE-HS when compared to the control hippocampus (p-value=0.029). **B.** *IL1B* was up-regulated 135-fold in the MTLE-HS when compared to the control hippocampus (p-value=0.0019). **C.** *MMP14* was down-regulated 3.2-fold in the MTLE-HS when compared to the control hippocampus (p-value=0.0484). **D.** *MMP17* was down-regulated when the MTLE-HS was compared to the control hippocampus, however the down-regulation was not statistically significant. Data are expressed relative to levels observed in control groups; mRNA expression was normalized to the geometric mean of reference gene eEF1A1. Errors bars represent standard deviation. Mann-Whitney-U test. P-value; * <0.05 , ** <0.01 .



Supplementary Figure 2. Overlap of differentially expressed miRNAs and other small RNA species in different regions of the brain. a. Overlap of up-regulated miRNAs in the MTLE hippocampus and cortex. **b.** Overlap of down-regulated miRNAs in the MTLE hippocampus and cortex. **c.** Overlap of up-regulated other small RNAs in the MTLE hippocampus and cortex. **d.** Overlap of down-regulated other small RNAs in the MTLE hippocampus and cortex.