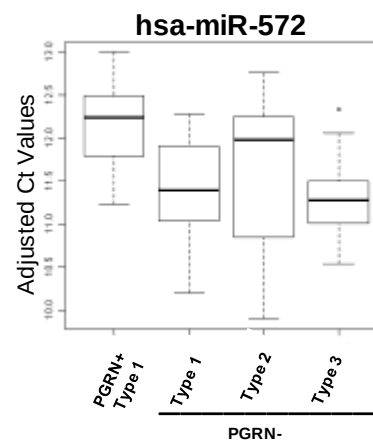
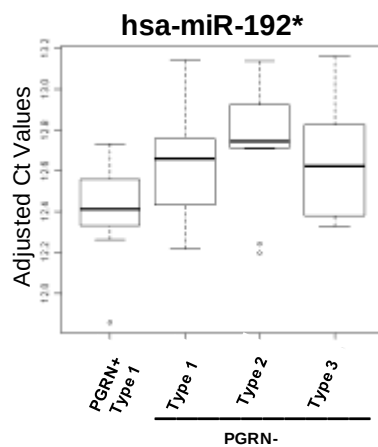
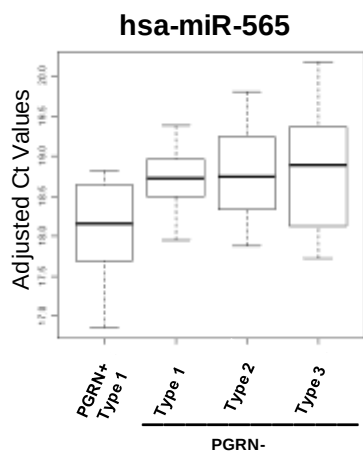
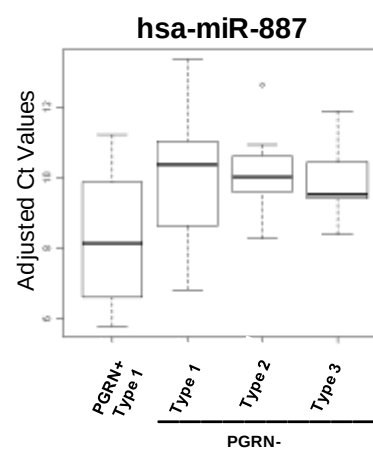
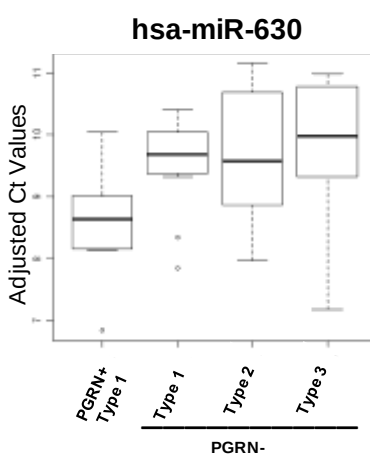
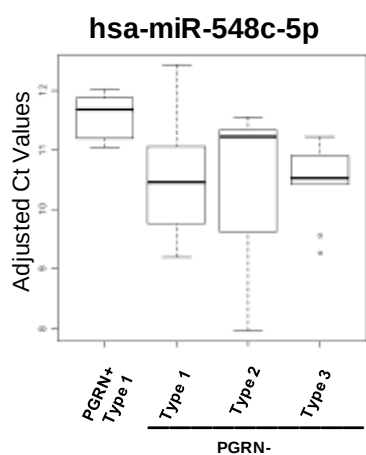
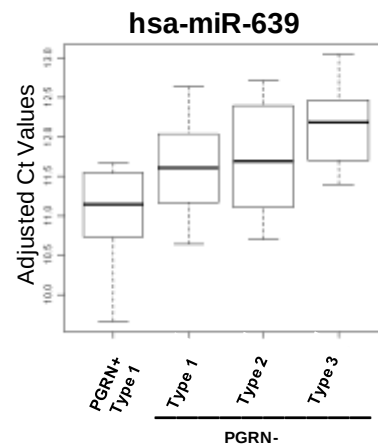
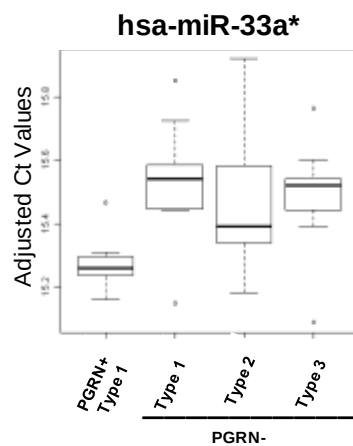
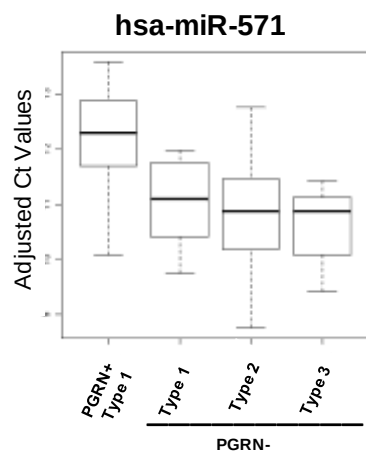
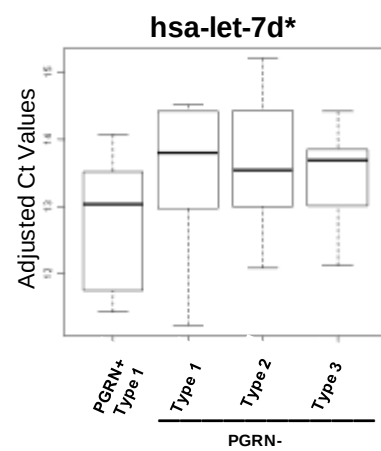
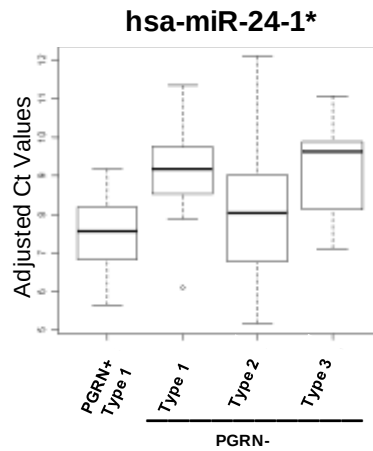
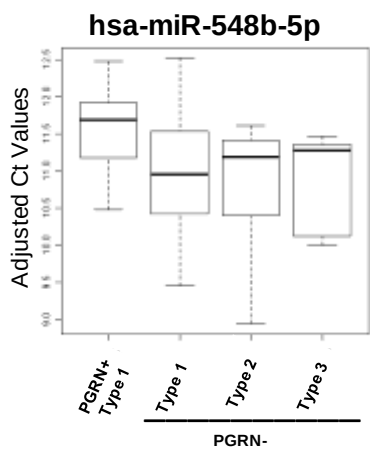
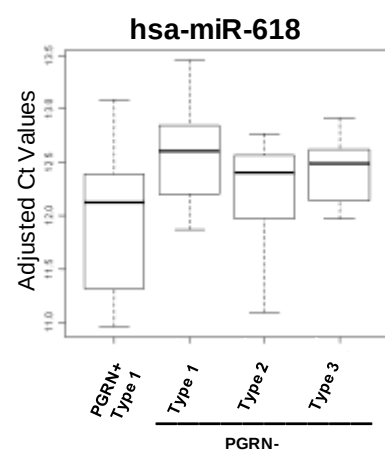
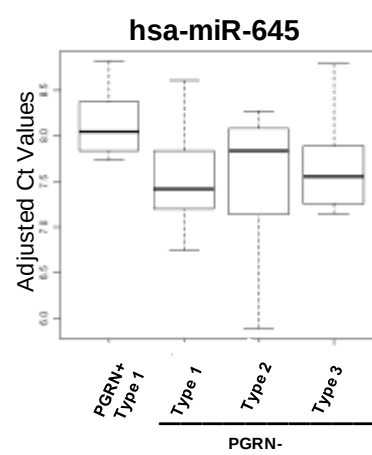
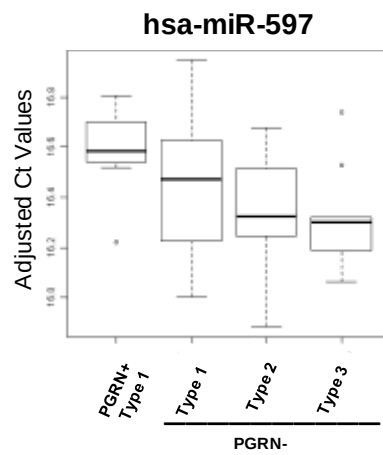
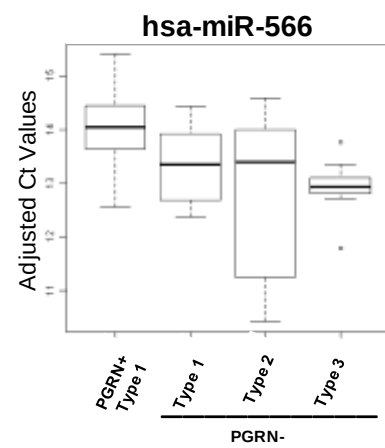
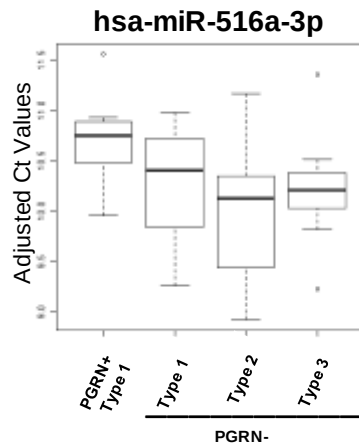
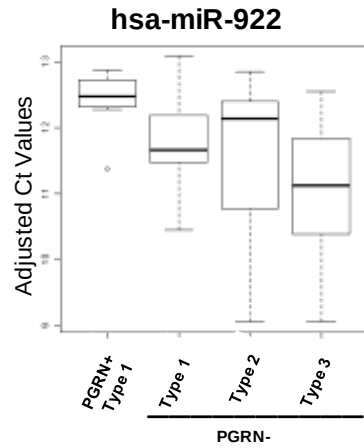
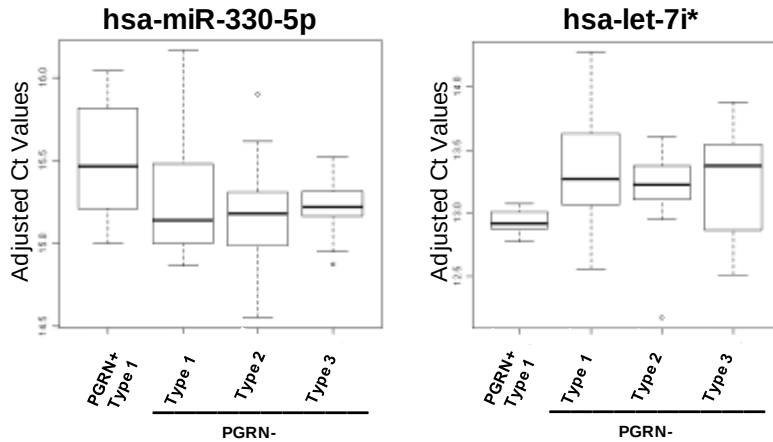








Additional file 2 - Comparative Box and Whisker plots of significant miRNAs from array profiling. Box and Whisker plots comparing miRNA expression (adjusted Ct values) between the various FTLT-TDP subtypes were generated using the built-in function in R library (R Statistical Software, Version 2.11.1). Specifically, we examined the top 20 miRNAs which were significantly dysregulated from frontal cortex tissue in the array profiling. The central line, upper and lower end of the box, represents the median, upper and lower quartile values of the miRNA expression data respectively. The bars represent the maximum and minimum values and circles denote the outlier values in the miRNA expression data. Values that are greater than 1.5 times the inter-quartile range from the upper or lower quartile were classified as outliers.