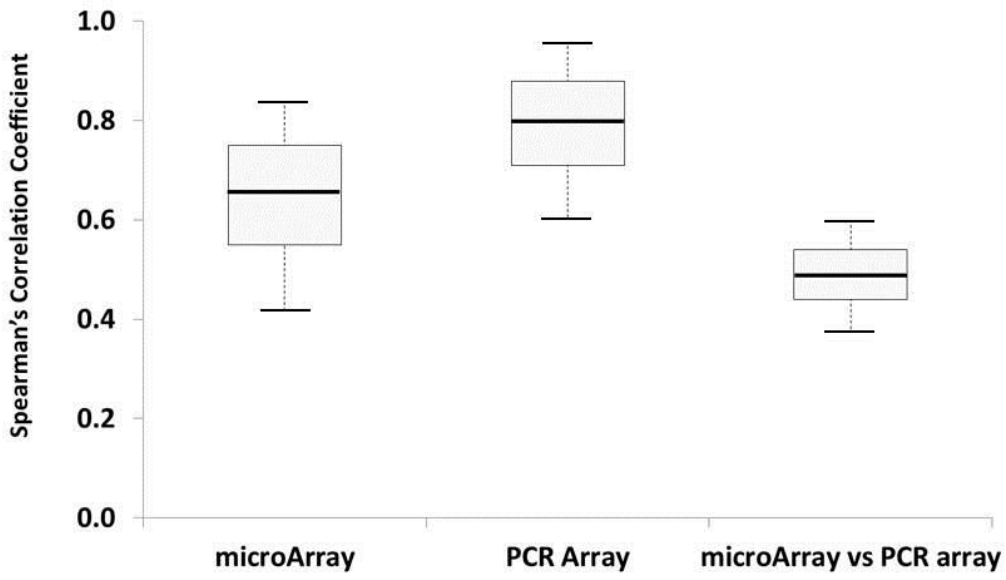
SUPPLEMENTARY FIGURE LEGENDS

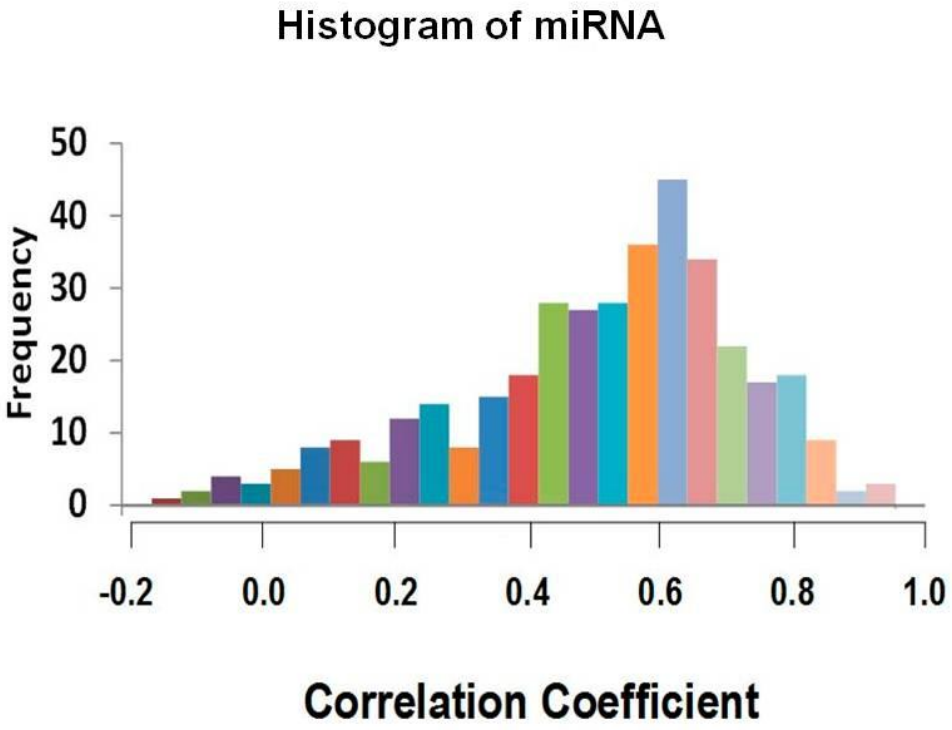
Supplementary Figure 1: microArray and PCR array platform reproducibility comparisons.

The Spearman's correlation coefficients were employed to evaluate the intra- and inter-platform reproducibility as illustrated in 3 box plots. **Panel A** shows the coefficients between the training set (n=5) and the testing set (n=5) between the two platforms (microarray and PCR array). Left box plot is based on Spearman's correlation coefficients between the microarray profiles using half comparisons (n=5) as the training set and the other half comparisons as testing set (n=5). The second plot is for the PCR array. The 3rd box plot is constructed based on the Spearman's correlation coefficients between the 2 profiles obtained by microarray and PCR array based on the same sample under the same condition for all samples (n=10). Even though PCR array has the higher intra-platform reproducibility than microArray, the intra-platform reproducibilities of both platforms are acceptable and have no significant differences. **Panel B:** Distribution of correlations between testing set and training set for miRNA expression by microarray. Spearman's rank correlation coefficients and histograms were computed and plotted for each miRNA using r value. Distribution of correlations between testing set (n=5) and training set (n=5) by microArray for miRNA expression is presented in histogram format. Only 39% of miRNAs demonstrate a correlation coefficient ≤0.5. When filtered based on expression level, the percentage of miRNAs with correlations of ≤0.5 saturated to 32%. Overall, our data indicates acceptable reproducibility and the microarray displays relatively good intra- inter-platform reproducibility with the PCR array. We found that correlation coefficients for ~61% of miRNAs profiled in between testing and training datasets were ≥ 0.5 indicating relatively good reproducibility. miR-199a/miR-199b are among the most correlated miRNAs with the median Spearman correlations of 0.8233/0.7947 and the standard deviation of 0.0453/0.0421, respectively.

Supplementary Figure 1A

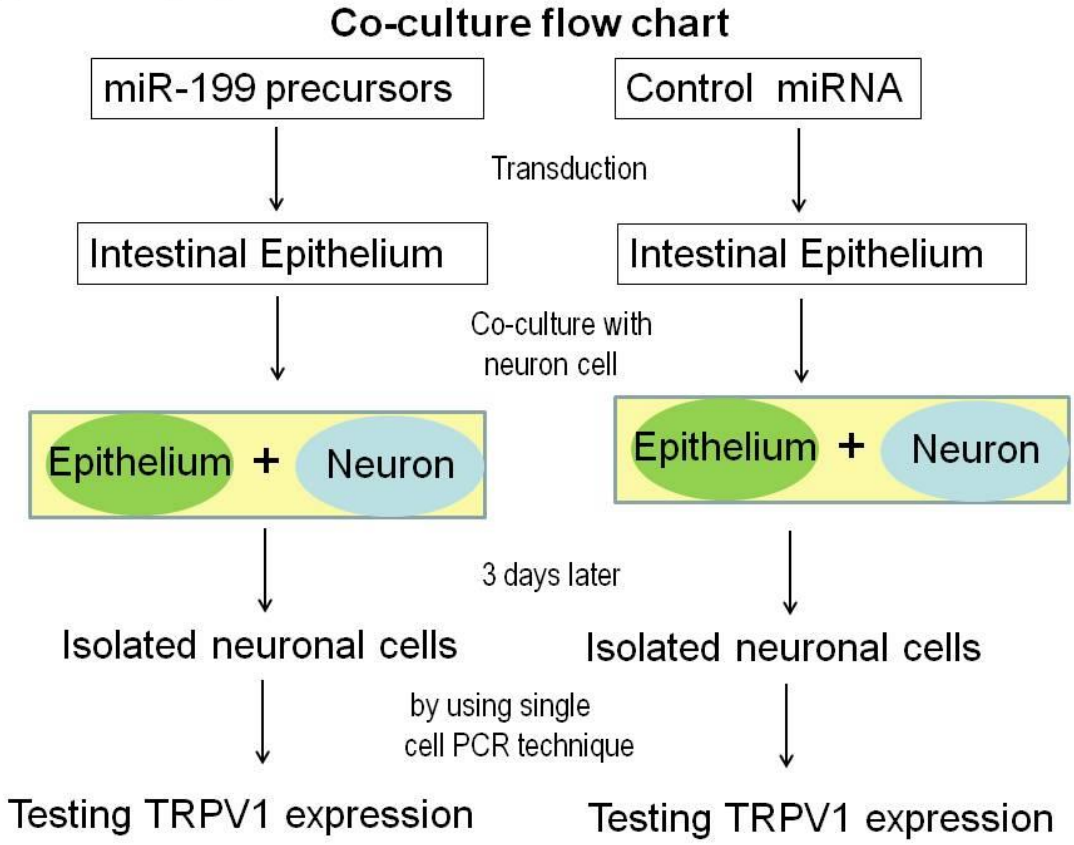


Supplementary Figure 1B

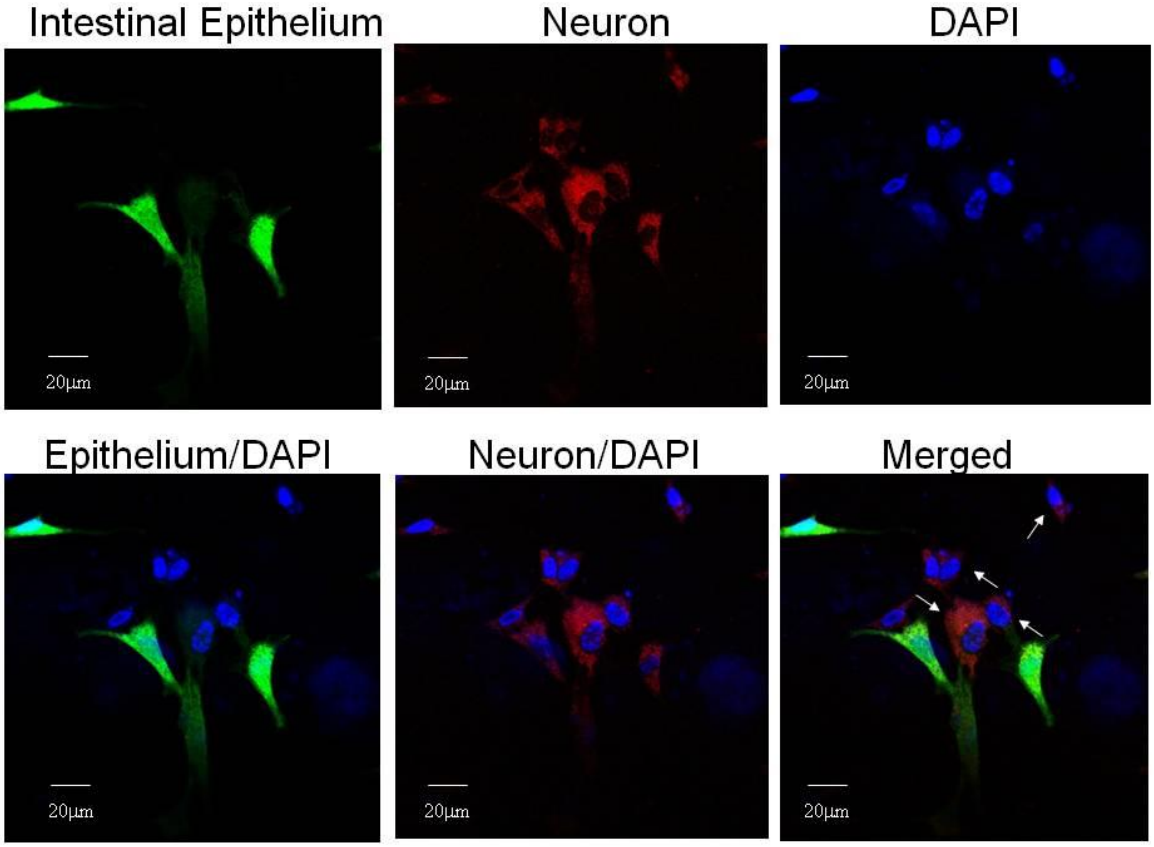


Supplementary Figure 2: In vitro intercellular communications between neuronal and intestinal epithelial cells via cell culture: **Panel A** Illustrates a flow chart for the experiment design in order to indicate the communication between neuronal and intestinal epithelial cells. A co-culture of intestinal epithelial cells and neuronal cells was performed. Intestinal epithelial cells were either transfected with a miR-199a precursor or with a control-miR, and then co-cultured with naïve neuronal cells for 3 days. **Panel B** shows the condition of the co-culture of intestinal epithelial cells with miR-199a-*GFGP*-epithelia cells and *RFP*-neuronal cells. The white arrow demonstrates the neuron cells we isolated after 3 days of co-culture with intestinal epithelium that was pre-transfected with mR-199a precursor. **Panel C** shows a significantly diminished TRPV1 expression in neuronal cells followed by co-cultured intestinal epithelial cells which were transfected with miR-199a and miR-199b precursors compared to transfected cells with a control miRNA (*p<0.05).

Supplementary Figure 2A



Supplementary Figure 2B



Supplementary Figure 2C