**Explanation of Data from Pelch 2015 TAAP**

**ALL qPCR Stats.pzfx**

* Contains Prism file with statistical analysis of all qPCR data showing in Table 2, Figures 1-5 and Supplemental Figure 1

**Figures 1-5:**

1. No data to show. This figure just shows where CpG sites are in the amplicon. I can provide sequence files if you think I need to though (they are PDFs, but are not annotated as to where the PCR primers are).
2. COBRA Data
   * For some of the genes, there is more than 1 amplicon per gene. (Note, S100P and Nes amplicon names in the paper may not match the raw data. This is because all the raw data was stored using the names I originally gave them when I started the experiments. When preparing the manuscript though it became necessary to re-name amplicons to improve clarity for the reader).
     + S100P#2 became S100P#1 in the paper
     + S100P#3 became S100P#2 in the paper
     + Nes#1 became Nes#2 in the paper
     + Nes#2 became Nes#1 in the paper
   * There is a folder for the PCR data. Most folders contain:
     + Excel sheet where band size was determined
     + An annotated tiff of the PCR product run on a gel prior to enzymatic digestion (confirmation that a PCR product was present)
     + A bip file of above (used by the analysis program)
     + A tif file of above (high quality image not annotated)
   * There is a folder for the data generated during enzymatic digestion. Most amplicons were digested by more than one enzyme (BstUI, Hpy99I, HpyCH4IV, or TaqI). In each digestion folder you will find:
     + Excel sheet where band size was determined
     + An annotated tiff of the digested PCR products
     + A bip file of above (used by the analysis program)
     + A tif file of above (high quality image not annotated)
     + A tif file cropped in on the gel of interest (this is what is actually shown in **B**)
3. Sequencing Data
   * The same is true regarding multiple amplicons and the naming issues discussed above for the COBRA data
   * 6 files – 1/cell type.
     + Contain individual edited fasta sequences files that can be uploaded into the analysis program
     + A file called epi-files. The analysis program generates this. It is the output of the analysis
       - There are several different .png files that are used to crease the figures in **C**
       - The .html file is the overall results for that cell type
   * A file or two labelled as RAW SEQUENCES
     + This is the raw, unedited sequence file provided by the sequencing core/GeneWiz.
     + There is also an Excel file or two that describes the naming of the sequences and the results/outcomes of the sequencing reads
4. 5-aza Data
   * An Excel sheet that contains raw CT values and data analysis
   * A RAW DATA file that contains
     + Word document with amplification and dissociation curve figures
     + Excel sheets named “.melt” containing the melting temperatures generated during dissociation curve
     + Excel sheets named “.results” containing the raw results as they come off the BioRad machine
     + Excel sheet named “.setup” showing the plate setup.

**Supplemental Figure 1**

* Associated Raw Data contains a file for each of the TaqMan qPCR assays for different miRNAs
  + Excel sheet with the setup for the generation of the cDNA
  + Excel sheet with the raw data as they come off the BioRad machine
* Final Analysis Sheets contains a file for each of analysis of each of the miRNA qPCR runs.
* Excel sheet that describes how the plates were setup
* Excel sheet that describes how RNA was diluted to equal concentration prior to generating cDNA

**Supporting Data for Various Experiments**

* Background Data Supporting QAQC of qPCR Results
  + 5-aza Data:
    - A file that has the information for the housekeeping gene Nono
    - A file that contains the results from Nanodrop quantitation of RNA and jpb and bip files showing the RNA quality
    - An Excel sheet showing the setup for generating cDNA
  + Untreated cells/Table 2:
    - qPCR Primer Validation contains:
      * Excel sheets from generating cDNA that was used to validate qPCR primers
      * Files that contain qPCR associated data generated while validating primers (document with amplification and dissociation curves, analysis worksheet, raw results, plate setup sheet, and raw melting curve results)
    - RNA Isolation
      * Excel sheet with quantitation of RNA from Nanodrop
      * Associated image files showing quality of isolated RNA
* DNA Isolation, Conversion & Primer Validation for COBRA
  + Bisulfite Conversions contains two folders:
    - Excel sheet with results of DNA quantitation and dilution calculations
    - Excel sheet with results from Nanodrop
    - Excel sheet for setup of PCR
    - Excel sheet for setup of COBRA enzymatic digestion
  + COBRA PCR
  + DNA Isolation – Excel sheet with results from Nanodrop quantitation of DNA
  + Primer Validation & Optimization Steps – contains work from when COBRA/Bisulfite sequencing primers were being validated

**Table 2**

* Associated Raw Data
  + Files containing amplification and dissociation curves, raw melting curve and results from BioRad program, and plate setup
* cDNA Generation
  + Excel sheets showing how cDNA was generated
* Final Analysis Sheets

**Table 3**

* Excel sheet summarizing data. The actual data is derived from looking at files in the Figures 1-5 folders.