**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.