Quantify extractions using plate reader:

Per the JBP method, using large bottle of the 1xTE to keep on shelf

(opened new package, 24mL \* 20X = 1X \* 480mL

1. Is TX STD#1 in fridge? Make TX STD #1: in a 15mL falcon tube, combine 3992µL TE+ 8µL DNA, vortex well
2. Make Pico dilution (1/200) for all wells - 200 sample wells + 24 standard wells = 225 wells, need 100µL per well = 22500µL or 23mL (23000/200=115); combine 115µL pico and 22mL + 885µL TE in 50mL falcon tube.
3. Make the rest of the standards (TX) in 1.5mL tubes: #2 - combine 900µL TE with 100µL STD#1 = 0.2µg/mL final 0.1µg/mL; #3 - combine 990µL TE with 10µL STD#1 = 0.02µg/mL final 0.01µg/mL; #4 is the blank - 1mL TE
4. Add 99µL TE to **sample wells** of plate
5. Add 100µL STDs to first free column of plate
6. Add 1µL sample to sample wells
7. Add 100µL 1/200 pico dilution to all wells; pipet up and down to mix
8. Incubate at room temp 5 minutes in the dark

At the Bidle plate reader:

* Turn on the unit and let warm up for at least 5 min
* Open SoftMax Pro
* Open Michelle's folder (Desktop>bidle>My Documents>Michelle) and open the saved protocol "Pico"
* Double check that the standards are correct by clicking on the Plate in the navigation tree, clicking on the "plate" icon (just after the wand and the orange bubbles), clicking on the blue standard wells and making sure the values match the way you set up the plate.
* Click Read - if it isn't there, make sure the spectramax is detected
* It will ask you if you want to replace data in plate 1, click OK
* When it is done, check standard curves to make sure the plate ran ok, if you can eliminate a bad standard and re-run, do so.
* click save as...and then export...and then pop in your new plate and hit read again.

Back at the lab, processing the data:

* Upload files to Plate Reader folder in Google Drive (you cannot work with them through Google Drive, this is just for storage)
* Open .txt files in Numbers (or even better, Excel)
* Open Sample\_Data file in Google Drive
* Copy AdjConc column from the Numbers file into the appropriate sample’s Quant\_ng/ul column