**Protocol for analyzing RT PCR data:**

First transfer all of your data to an excel worksheet.

There will be excessive information, you want to KEEP the columns that have “identifier” , “threshold”, “starting quantity (SQ)” and “SQ mean”

**Normalizing data:**

Calculation 1: you will be using the starting quantity for this calculation

use your gene of interest and divide it by a standard gene.

Ex: gene of interest is GILZ standard gene is GADPH

GILZ/GADPH

if you have 3 samples that are in duplicate, after calculation 1, average the duplicates.

**Calculation 2: normalization**

Once you have complete calculation 1 figure out which set of data is your “control”

Ex: if your samples are, cells only, cells during an infection, and cells after an infection, your control is cells only.

Take your averaged control data and divide all your samples by it.

Sample/control sample