Figure Legends:  
Figure 1: PCA plots show the quality of our reproducible RNA-seq datasets when assaying non-TE gene expression. Note that the vast majority of variance is on the X-axis. Also note the clustering of our Mature Pollen samples with those already published in the field.  
  
Figure 2: Compared to the baseline TE expression in seedlings, TEs are up-regulated in Tassel Primordia through Mature Pollen development. Most of these are not expressed in Sperm Cells. On the female side, we see many TEs up-regulated in ovules as well. We are only considering TEs farther than 2kb from genes and hence, read-through transcription from developmental changes in gene expression should not be an underlying cause for the observed dynamic behavior of TEs.  
  
Figure 3: There is significant overlap between the sets of TEs that are up-regulated at specific stages of maize reproductive development. This demonstrates that there are a class of TEs that are dynamically and specifically up-regulated on both the male and female side during maize reproduction.