Small-rna data analysis

- Running ABI small-rna pipeline on TACC
  - About the pipeline- how it works, advantages and disadvantages.
  - Issues faced - restrictions on data, setting up configuration files, things we tried.
  - Parallelizing the pipeline (way around interactive processes)
  - Results
- Quantifying mature miRNAs from small-rna pipeline results
  - Our scripts and what they do Normalization ??* Conversion of pipeline output to SAM format (viewing the reads in base space)
- Looking for novel miRNA, siRNA, moRNA
  - Generating coverage graphs around each miRNA
  - Could we get Rodney to talk about how they identified that antisense miRNA?