Description of Data Objects

* R Objects:
  + Core Data Files
    - All\_QC.rds
      * This file contains all quality control information for each cell from STAR and RSEM metrics.
    - ASE.bygene.rds
      * This file contains the allele specific expression of each cell by gene determined by number of reads covering heterozygous SNPs using ASEreadcounter.
    - TPM.nolim.rds
      * The file contains expression (Transcripts Per Million) levels of each cell for all genes using RSEM.
    - TPM.bygene.rds
      * This file contains expression (Transcripts Per Million) levels of each cell for a subset of reliable genes using RSEM.
  + Meta Data and Annotations
    - controlSampleIDs.rds
      * This file contains a list of all control cells IDs.
    - geneRanges\_Nikos.rds
      * This file contains annotations of the genomic ranges of each gene.
    - grouped\_control\_aneuploidies.rds
      * This file contains a list of manually selected cells that demonstrate control aneuploid chromosomes.
    - armRanges.rds
      * This file contains annotations of the genomic ranges of each chromosome arm.
* CSVs:
  + annotation\_list.csv
    - This file contains experimental meta data and annotations for each cell.
  + centromeres.csv
    - This file contains annotations of genomic loci of centromeres.
  + manual\_review\_results.csv
    - This file is an annotation list that records our manual interpretations of each cell after analysis. This file is used only for summary visualizations.
* VCF and DAT files:
  + RPE-1.hets.chr1-X.BA.SNPs\_only.recode.vcf.gz
    - This file is a list of heterozygous SNPs.
  + RPE1\_Haplotype\_update.dat
    - This file is a list of haplotype assignments for each heterozygous SNP.
* Samples
  + Directory of txt files with the IDs of raw sequencing files that are read into the preprocessing pipeline.