**microRNA editing in wildtype and ADAR1- *C.Elegans***

**microRNA**

microRNAs are short sequences of RNA, usually around 21-25bp in length. microRNAs serve an important function in gene regulation, by creating near-perfect(perfect?) matches to the 3’ end of an mRNA molecule, preventing it’s translation.

Create alignments for WT and mut

Create pileups from aligned files

Create genecounts files

Look at expression, differential expression changes, plots, tables,

BB21 cells: ADAR1 mutants, significantly reduced/no (mi?)rna editing

N2 cells: Wildtype

Differential Expression Between Wildtype and Mutant Cells:

RNA(i?) sequencing data from embryonic C. elegans cells was pre-processed(aligned, filtered to reads between 15-25 nucleotides), aligned to version 35 of the mirnaDB mirna reference transcriptome(?)/genome, containing known mirna sequences. The alignment files were converted into gene counts, and using Bisek(1) and R, differential expression was done.

Biological repeat 113311(?) was discarded to being a statistic outlier, leaving us with 3 other biological repeats

(images of differential expression, bisek explanation?, include R script? In git(?)), heatmap

microRNA Editing:

Alignment files for the N2 reads were combined to mirnas detected in at least 2/3 of the biological repeats. The resulting consensus file was compared to each of the mutant repeats, and reads that appeared in both the BB21 and N2 sequences were removed (e.g an A->G mutation in position 5 on a certain mirna that appears in both WT and mutant cells was discarded). After discarding such reads, mutations in the wildtype were compared to the total amount of reads, and edit percents were produced. (differentiate between editing types?)