**microRNA editing in wildtype and ADAR mutant in *C.elegans***

Introduction:

**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 matches to the 3’ end of an mRNA molecule, preventing it’s translation.

**RNA editing**

RNA editing is the process of post-transcriptional modification of the nucleotide sequence of RNA molecules. RNA editing is vital to the proper development of many organisms. The gene ADAR mediates Adenosine to Inosine editing in RNA molecules, the most prominent form of RNA editing.

The aim of the project is to find differences between miRNA expression between cell lines of *C.elegans* with and without mutations in ADAR, as well as sites of miRNA editing, by comparing sequenced miRNAs from these cell lines.

Data:

BB21 cells: ADAR mutants, with no RNA editing

N2 cells: Wildtype

Results:

**Differential Expression Between Wildtype and Mutant Cells:**

Small RNA sequencing data from embryonic C. elegans cells was first pre-processed (filtered to reads between 15-25 nucleotides, to avoid non-mirna sequences), then N2 and BB21 read libraries were aligned to version 35 of the miRDB mirna reference database, containing sequences of known miRNAs. The alignment files were converted into the pileup format using samtools, and gene counts were generated using these files. Using BiSEK(1) and R, differential expression was done, comparing gene counts between BB21 and N2 cell lines.

Biological repeat 11311 was discarded to being a statistical outlier to the other 3 biological repeats, leaving us with 3 repeats to test for editing.

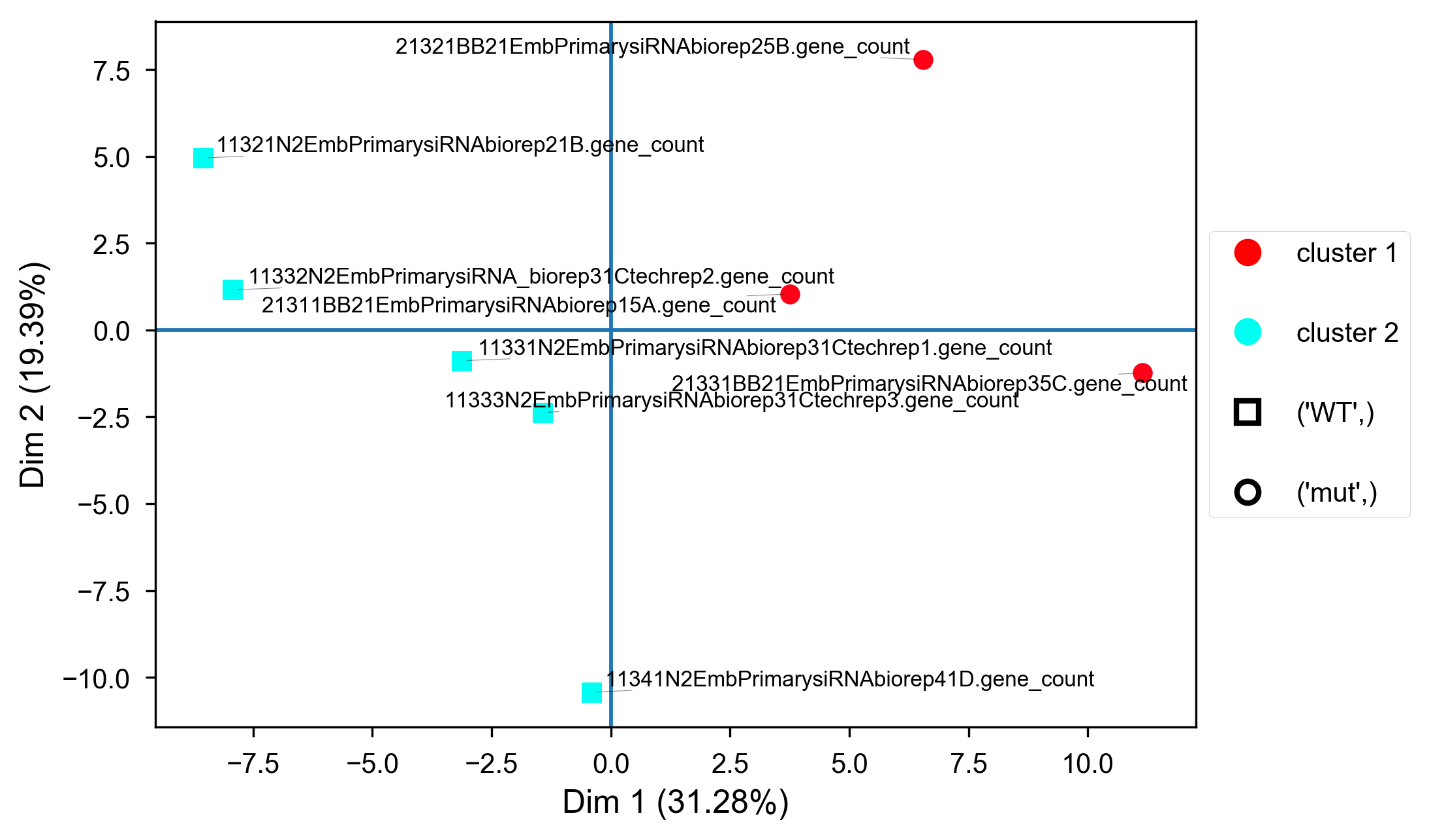


Figure 1: PCA plot representing differences in miRNA expression. WT and mutant sequences are divided into different clusters, showing that there are significant differences in mirna expression.

**microRNA Editing:**

The pileup files created from alignment files for the N2 reads were combined into consensus files containing only reads that were in 2/3 biological repeats at least. The resulting consensus file was compared to each of the BB21 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, a file containing only the mismatches was created, mismatches were sorted by type, and counted.

The results were not conclusive, as A->I editing is done by the missing ADAR, and there were not significant differences in the percentage/amount of A->I (which is detected as A->G in sequencing) edits, and other types of editing. There were 24 miRNAs found to have statistically significant differences in expression between the cell lines, however.

(1): BiSEK is a tool developed in Ayelet Lamm’s lab for differential expression analysis