**Starting Point**

Transcriptome data assembled by Trinity. Three females:

1128\_SWS - Super white ZAL2M/ZAL2M

1131\_WS - White ZAL2M/ZAL2

1150\_TS - Tan ZAL2 /ZAL2

There was a potential name swap between 1131 and 1150.

in a readme from Jim: "note that 1128=1128 but 1131=1150 and 1150=1131. ie, some kind of switch occurred, probably when samples run or prepped"

The files contain sequences and claim to match them to chromosome, but Dr. Yi says don't trust that information.

For now we are comparing Super White to Tan, i.e. 1128 to 1150.

**Blast**

To use blast, I added it to my biocluster account by adding this line to .pacemodules:

module load ncbi\_blast/2.2.28

To use it, I mostly followed these directions:

<http://www.blaststation.com/freestuff/en/howtoNCBIBlastMac.html>

To make databases for blast use, see makeDB.sh

blast - make a database, use it

blastn -query small\_1128\_rearranged.fasta -db db\_1128 -out blastTestOut -outfmt 10

future plans:

How many sequences in each file?

grep ">" $1 | wc -l

1128\_SWS has 298,236 sequences

1150\_TS has 343,164 sequences

How many with reciprocal matches?

compare outputs, find sequences that match, examine differences