1a. Thirteenth leaf (276, 279), and Whole Seed (283, 284)

1b. You can determine some information, like how it was sequenced and who sequenced. When clicking the project info it listed grant information but not experimental. Like I do know that it was a Buell sample.

2 I did not see a line in the log file specifically for transcripts other than removing duplicates. But there were 527,581 contigs and segments

3a.SRR940283

3b.I do all of them for >84%

3c. They could represent non-coding regions, or regions that are affected by a mutation. Also contaminations like I knew someone who accidentally sequenced dog hair. Unknown genese is another, or genes just not in the index.

4a.(outlier 43) 646-3417

4b. in SRR940283 using less I don't see any zeros. But if there was a zero it could be something that is not expressed

4c.I only see one TPM with not a whole number, I think this could be a partial match or partial expression. Not all genes are expressed all the time, so it could have been paritally read or something before the gene was surpressed or something.