General:

- Is the data already trimmed?

- Which pathway/genes are you focussed on? Cathacyc for pathway info

- Planning

- Group tasks

- Which samples used?

- In the transcript paper, are all the samples completely clear?

- Do a quick clustering of the samples, to see if the samples cluster together

- Additional mapping later in case of using different mappers

Related to us:

- Suspension culture sample; most appropriate? *no*

- Complete pipeline earlier than 11th of December

To do:

* identify pathways using KEGG
* checking the transcriptome/genome
* look at the paper with 3 samples/transcriptome → check wether we can do other analysis