Transcriptional Analysis of ASCL1 and the Effects of Neurogenesis in GABAergic Neurons [Logbook]

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Date	Objective(s)	Next Steps
10/06/2020	● Meeting with supervisor Dr Schubert to discuss ideas for the project and the next steps	**NEXT STEP:** Start research on the topic of neurogenesis **NEXT STEP**: Consider planning to change the project structure from a lab project to a computer-based project
25/07/2020	● Decide on what The approaches to use for the project idea and provide advantages and disadvantages to each approach Literature review ● (Advantage) easy to conduct ● (Disadvantage) very hard to get the standard of a first-class and requires critical analysis and as require a lot of journals and papers to review Bioinformatics ● (Advantage) Easier to get the first class as the supervisor is more experienced ● (Disadvantage) Requires learning bioinformatics programs and requires a lot more analysis Data Submitted by transcription of RNA molecules ● (Advantage) is in line with my project based on the comparative analysis of the expression of genes among different and similar cell clusters. The idea is dissociation from the cells to obtain a data sheet which is multidimensional which requires	**NEXT STEP**: Consider the approaches to computer-based projects and look at past projects

	mathematical methods to reduce the complexity of the data. This will result in the 2D graphical representation between the gene cluster and the clustering of the gene themselves	
07/10/2020	● Refine my introduction	**NEXT STEP**: Define my aims
15/10/2020	● The first group meeting with Dr Schubert on how to organise your project	**NEXT STEP**: Refine my introduction and how clear understanding of my aims
28/10/2020 - 21/11/20	● Refine my introduction ● Defined my aims	**NEXT STEP**: Begin to research the methodology that is going to be used in my project
22/11/2020	● Research on the methodology that is going to be used; RNA-seq analysis and choose my three primary datasets	**NEXT STEP**: Begin to learn how to use Galaxy for my project and to further define my methodology and include the use of Gene ontology in the methods **NEXT STEP**: Submit my project to Dr Schubert for feedback
30/11/2020	● Group meeting with Dr Schubert discussing how to deal with the technical aspects for gene lists and GO term analysis and STRING analysis	**NEXT STEP**: Practice how to use GO term analysis and practice string analysis
18/12/2020	● Submit my project to Dr Schubert for feedback	**NEXT STEP**: N/A
13/01/2021	● Created a defined title for the project. "The transcription analysis of ASCL1 and the effect of neurogenesis in GABAergic Neurons"	**NEXT STEP**: Reorganise the project into clearer sections with the result section, discussion and the conclusion being added
10/02/2021	● Refined my introduction	**NEXT STEP**: Plan to add diagrams and images into my project showing tangential migration, bHLH proteins and stem cell division
17/02/2021 - 18/02/2021	● Added diagrams of bHLH proteins and stem cell division	**NEXT STEP**: Plan to add diagrams and images into my project showing tangential migration

18/02/2021	● Added diagrams showing tangential migration	**NEXT STEP**: Sort out the methods section
19/02/201	● The first training session for data techniques with Dr Schubert. Using GEO2R. Comparing two or more samples. usually derived from microarray or NGS data, and typically is used for differential gene expression analysis	**NEXT STEP**: Obtain two more datasets to supplement the existing data **NEXT STEP**: Process the previous microarray data acquired early
5/03/2021	● Training session exploring with Dr Schubert through GO term analysis and String first and introducing Galaxy	**NEXT STEP**: Perform a preliminary GO term analysis
19/02/2021 - 10/03/2021	● Obtain preliminary results from the Venn diagram and the STRING analysis ● Constructed the methodology pipeline and accompanying diagram ● Project meeting with Dr Schubert discussing the poster and how to prepare for it	**NEXT STEP**: Sort out the methods section; replacing GeneVenn with InteriVenn **NEXT STEP**: Obtain two more datasets **NEXT STEP**: Sort out the methods section **NEXT STEP**: FInalising my poster **NEXT STEP**: Replace AmiGo2 with g:profiler
11/03/2021	● Preliminary Principal component analysis plot (PCA) and uniform manifold approximation and projection (UMAP) results ● Preliminary volcano plots	**NEXT STEP**: Reanalyse the STRING data **NEXT STEP**: Make a table in the methodology section which details of the datasets **NEXT STEP**: Refine the preliminary Principal component analysis plot (PCA) and uniform manifold approximation and projection (UMAP) results and the preliminary volcano plots

12/03/2021 - 24/03/2021	• Constructed a table in the methodology section which details of the datasets used in the present study and the biological function • Construct a GO Term enrichment analysis visualised as a Manhattan-like-bubble graph. • Replace AmiGo2 with g:profiler for the GO term analysis. Results of GO enrichment analysis for A, molecular function B, biological process and C, cellular component categories	**NEXT STEP**: Start the discussion based on the experiment data **NEXT STEP**: Construct a diagram displaying adult neurogenesis
16/03/2021 - 31/03/2021	• Project meeting with Dr Schubert discusses possible points for areas for the discussion area • Expanded the discussion section to include "limitations of experiment design" and "future research" section	**NEXT STEP**: Being to research various discussion points. **NEXT STEP**: Reanalyse the STRING data
05/04/2021 - 28/04/2021	• Identified specific factors associated with ASCL1 expression: Pixt2, FGFR1, GOT2, NeuroD6 and NOTCH2 were found and play roles in the brain development • Finalise the STRING analysis	**NEXT STEP**: Decided what genes to focus on my discussion
19/04/2021 - 23/04/2021	• Project group meeting with Dr Schubert discussing and focusing on the preparation of the actual project write-up	**NEXT STEP**: Reanalyse UMAP and volcano for GSE78949 **NEXT STEP**: To fine tune the methodology and results (and explain and summarise the meaning of the results)

02/05 2021	• Reanalyse UMAP and volcano for GSE78949 • Add details to Table 1	**NEXT STEP**: Annotate my bibliography **NEXT STEP**: Rework my stem cell diagram and clarify the terminology **NEXT STEP**: Create a second table to explain the justification of the used database being selected
13/05/2021	• Project meeting with Dr Schubert discussing and finalising the discussion and amending the diagrams and their captions parts of the results and general queries • Complete my annotated bibliography	**NEXT STEP**: Finalise conclusion and abstract **NEXT STEP**: explain and summarise the meaning of the of the STRING analysis **NEXT STEP**: Perform a final count