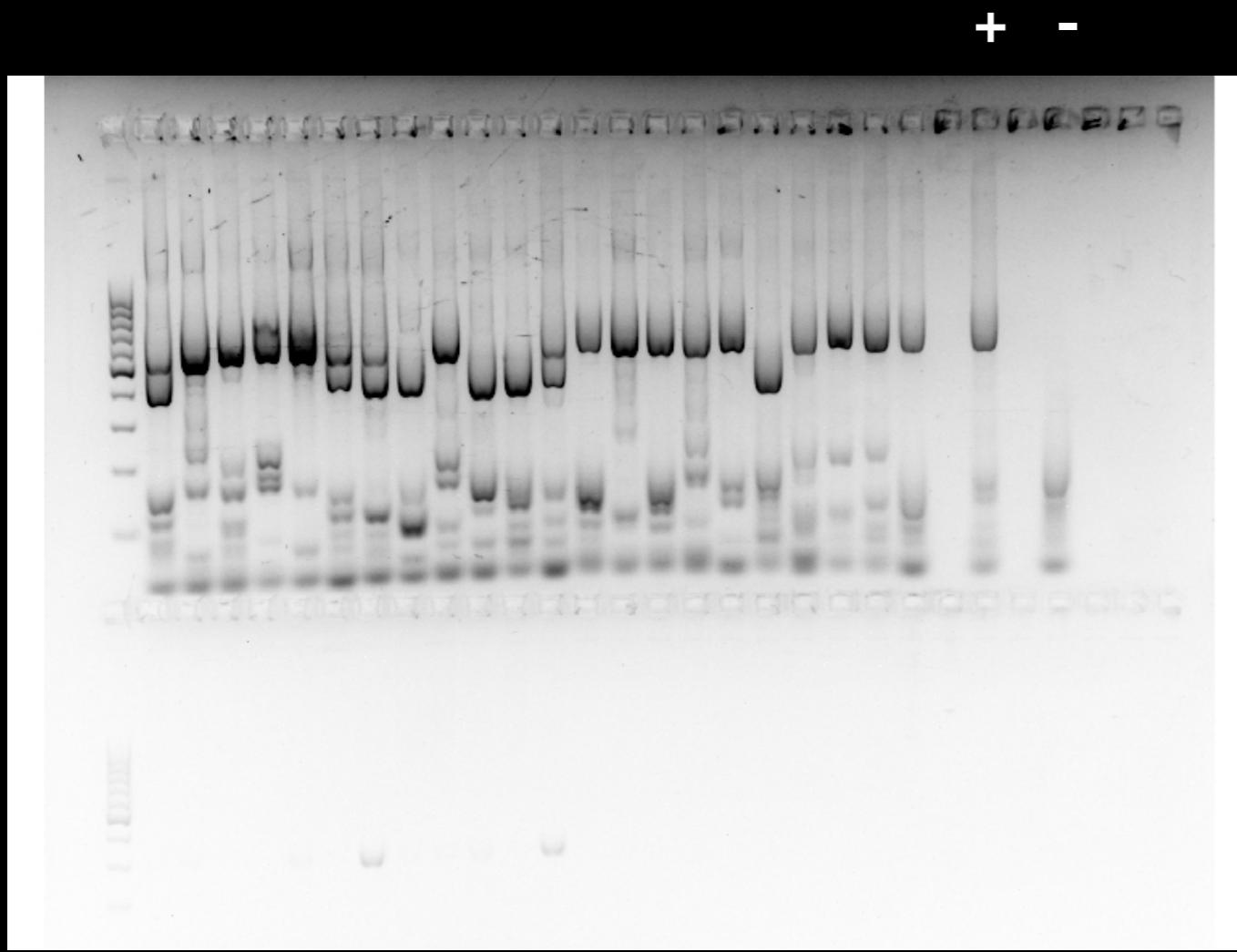


Lab Update

29.08.2019

Genotyping



Sirt1cko - 40 cycles

Bandsize : 750bp - mutant band
550bp - wild type band

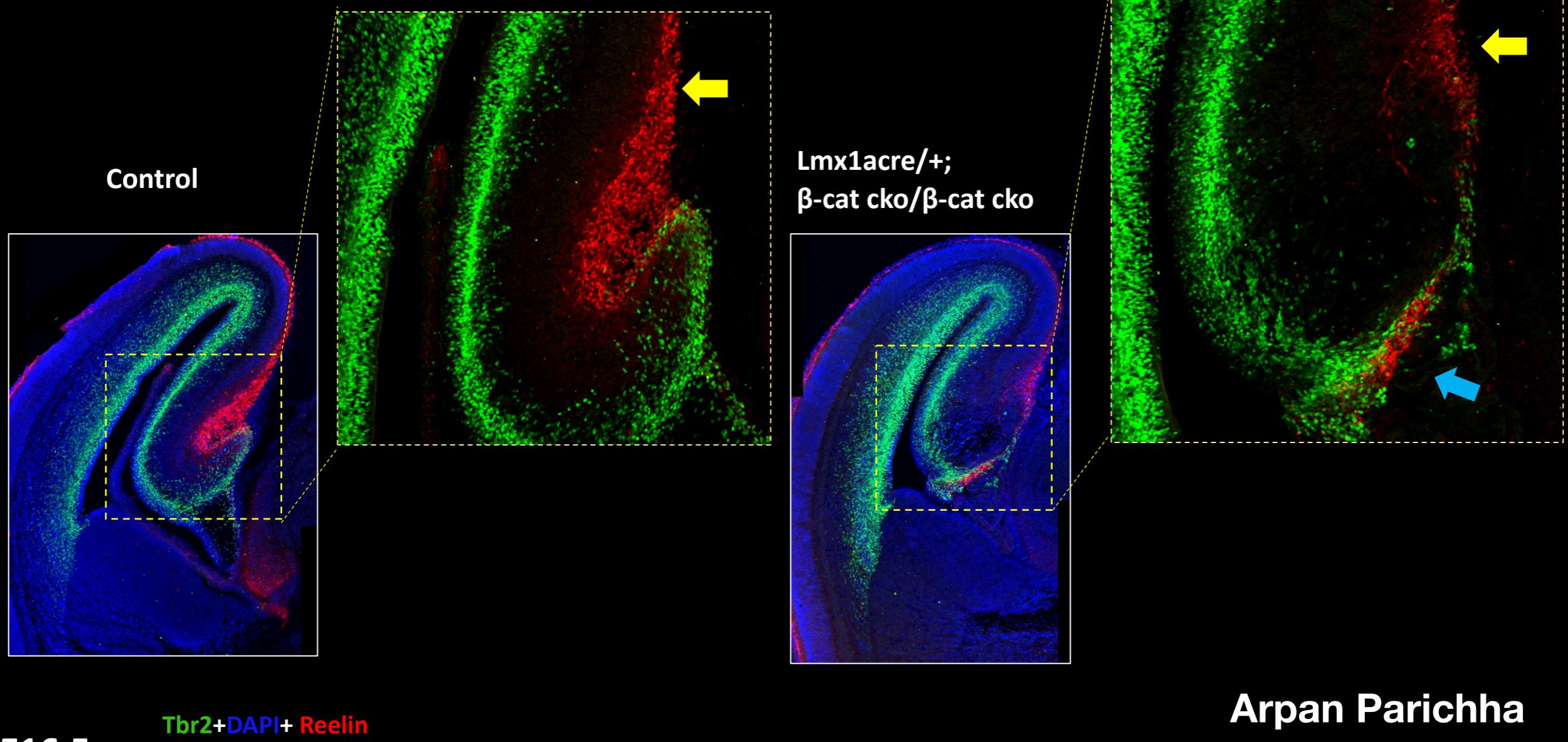


Sirt1cko - 35 cycles

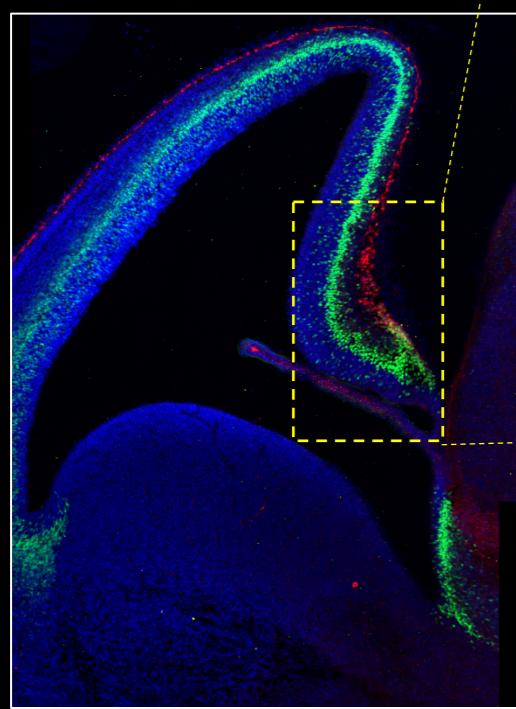
Hem-Seq data analysis

- Transcriptome of the hem at E12.5, in the LOF condition(*Lmx1* acre/+; β -cat cko/ β -cat cko) was sequenced.
- Corresponds to the mis-migration of Cajal-Retzius cells phenotype in our Wnt study.
- Analysed the data using two algorithms: EdgeR and Deseq2

Recap



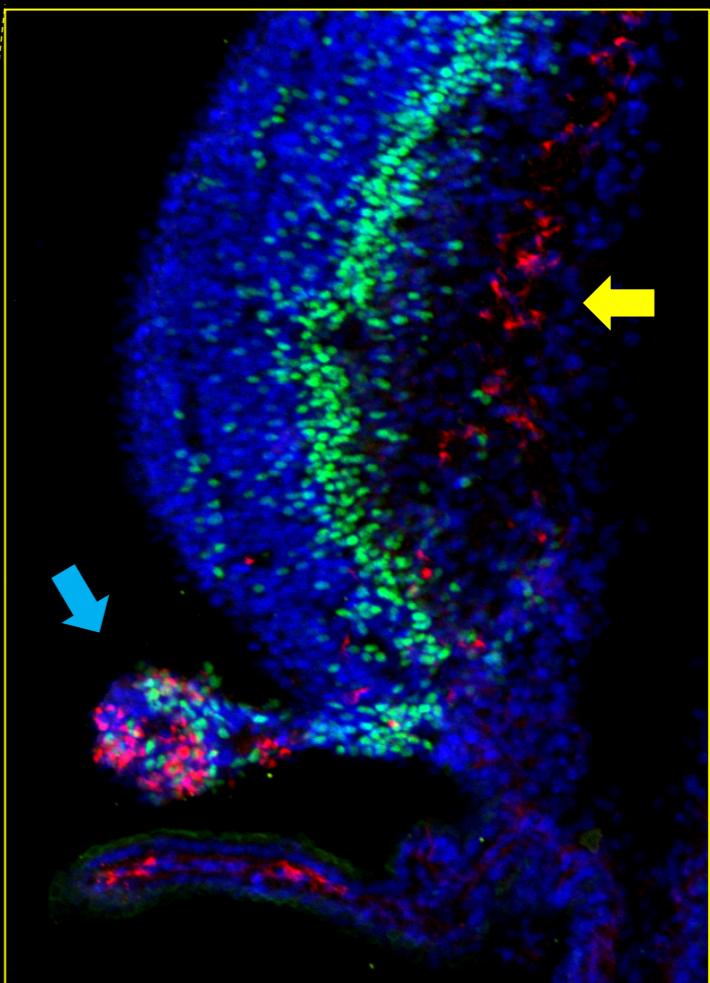
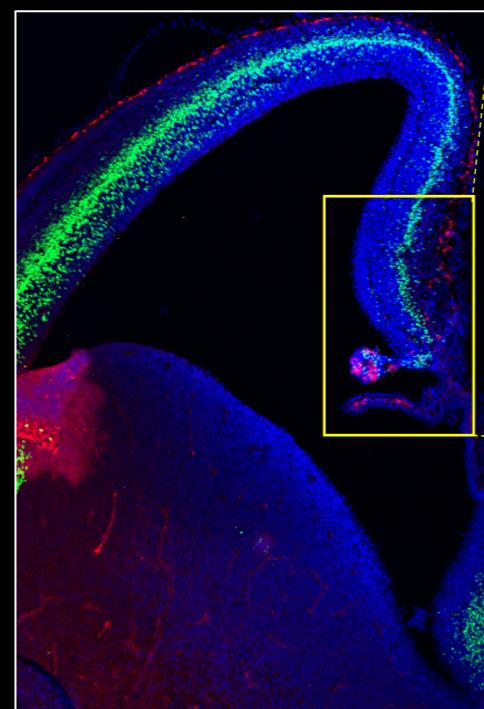
Control



E14.5

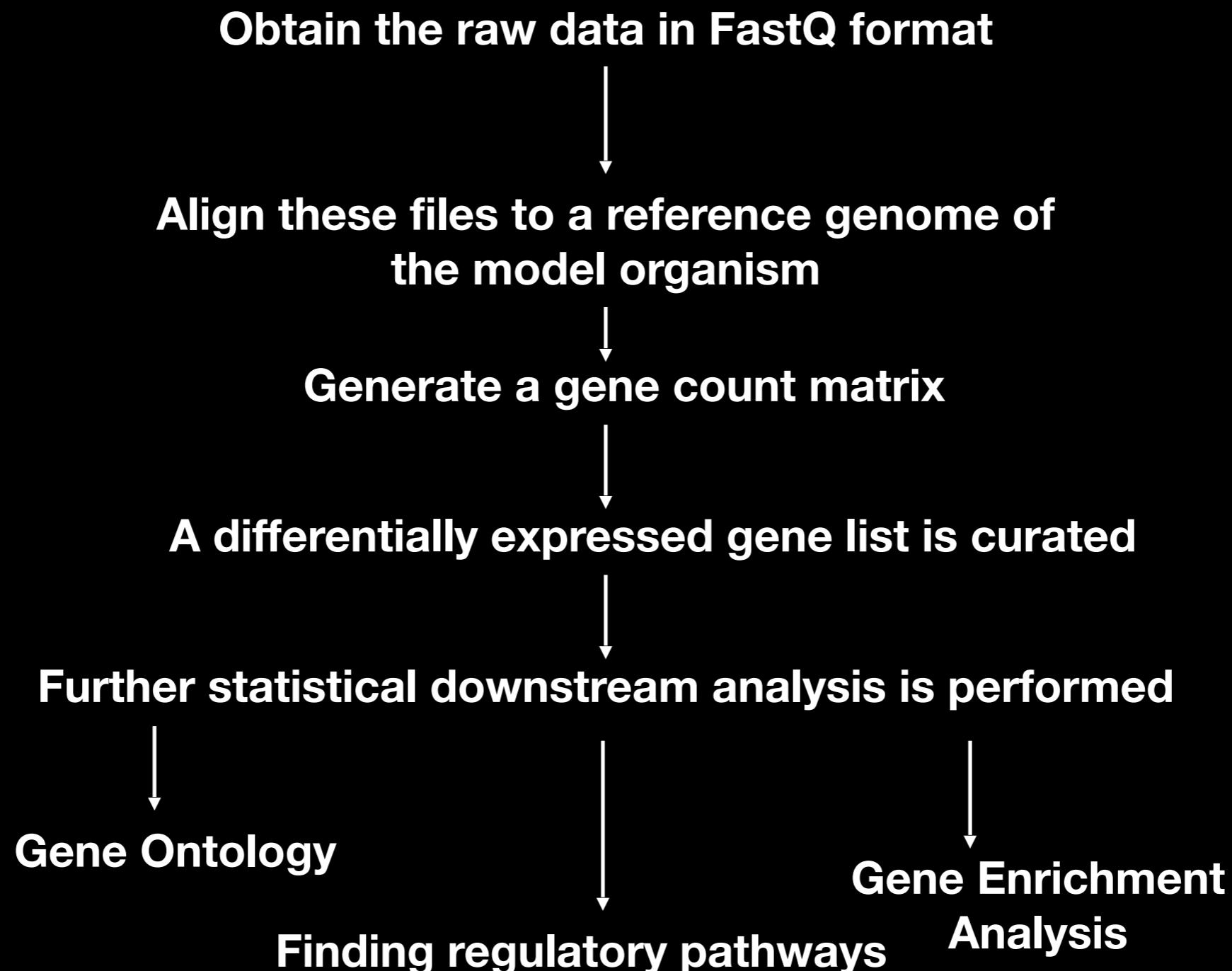
Tbr2+DAPI+ Reelin

Lmx1acre/+;
 β -cat cko/ β -cat cko



Arpan Parichha

Standard RNA-Seq workflow



Differential gene expression analysis

	Deseq2	EdgeR
Method	Null hypothesis	Null hypothesis
Key difference: Normalisation Strategy	Geometric mean	Weighted mean of log ratios
Distribution	Negative binomial	Over-dispersed Poisson
Complexity of the code	Complex and extensive	Comparably less than deseq2
Number of DEGs in our dataset	16261 131 up regulated 233 down regulated	23421 *work in progress*

Preliminary findings...

Up regulated pathways	Down regulated pathways
Nervous system development	Nucleosome assembly
Neuron development	Nucleosome organisation
Positive regulation of synapse assembly	Chromatin organisation
Neuron projection development	DNA conformation change
Neurogenesis	protein-DNA complex assembly
Dendrite development	Cellular component organisation
Neuron différentiation	Pattern specification process
Axiogenesis	Chromatin assembly or disassembly
Behavior	System development

Future goals

- Gene Enrichment analysis for hem seq
- Generate necessary plots and graphs
- Generate and analyse data with edgeR
- Other downstream analysis with edgeR
- Compare all the results finally
- Start with single cell seq data mining

Thank You

