***Next***

***3***

***weeks***

*For CODIG SEQUENCES (genes):*

* *Cross-checking with exome-seq genes* 🡪 ***with Kriti/Charlotte***
* *Cross-checking with GWAS data* 🡪 ***with Kriti***
* *Candidate gene selection + prioritization:*

1. *Detailed check the phenotypes of involved patients*
2. *Check of their functions/pathways (GeneCards and others)*
3. *Check of their expression in embrional mouse palate* 🡪 ***with Kriti***
4. ***Check them using ENDEAVOUR and DAVID***
5. *Check the availability of mouse models*

**Comparing all these results, we will draw the first conclusions (August, 20th)**

New patients from ECARUCA

***Now***

List of candidate genes

*New 17 ECARUCA patients added to my dataset:*

*new overlapping regions and their gene lists*

*For NON-CODIG SEQUENCES:*

* *Cross-checking using p63 binding site profile*
* *Cross-checking using p63 binding motifs (with SNPs in their important positions)* 🡪 ***with Kriti***
* *Cross-checking with GWAS data* 🡪 ***with Kriti***
* *Oligo pulldown assay (Mass Spec)* 🡪***with******NingQing and Luan***

***Already done***

***ONLY DECIPHER PATIENTS***

2nd prioritization of genes (contained in overlapping regions), according to phenotypes (*quick check*)

1st prioritization of genes (contained in overlapping regions), according to the number of genes

List of prioritized regions (DEL/DUP)

Prioritization of overlapping regions

(number of overlaps)

Comparison of all regions to identify the overlapping regions

(overlapping DEL and overlapping DUP)

1st division:

Type of CNV

(DEL/DUP)

Patients selection

(Decipher)

Data collection