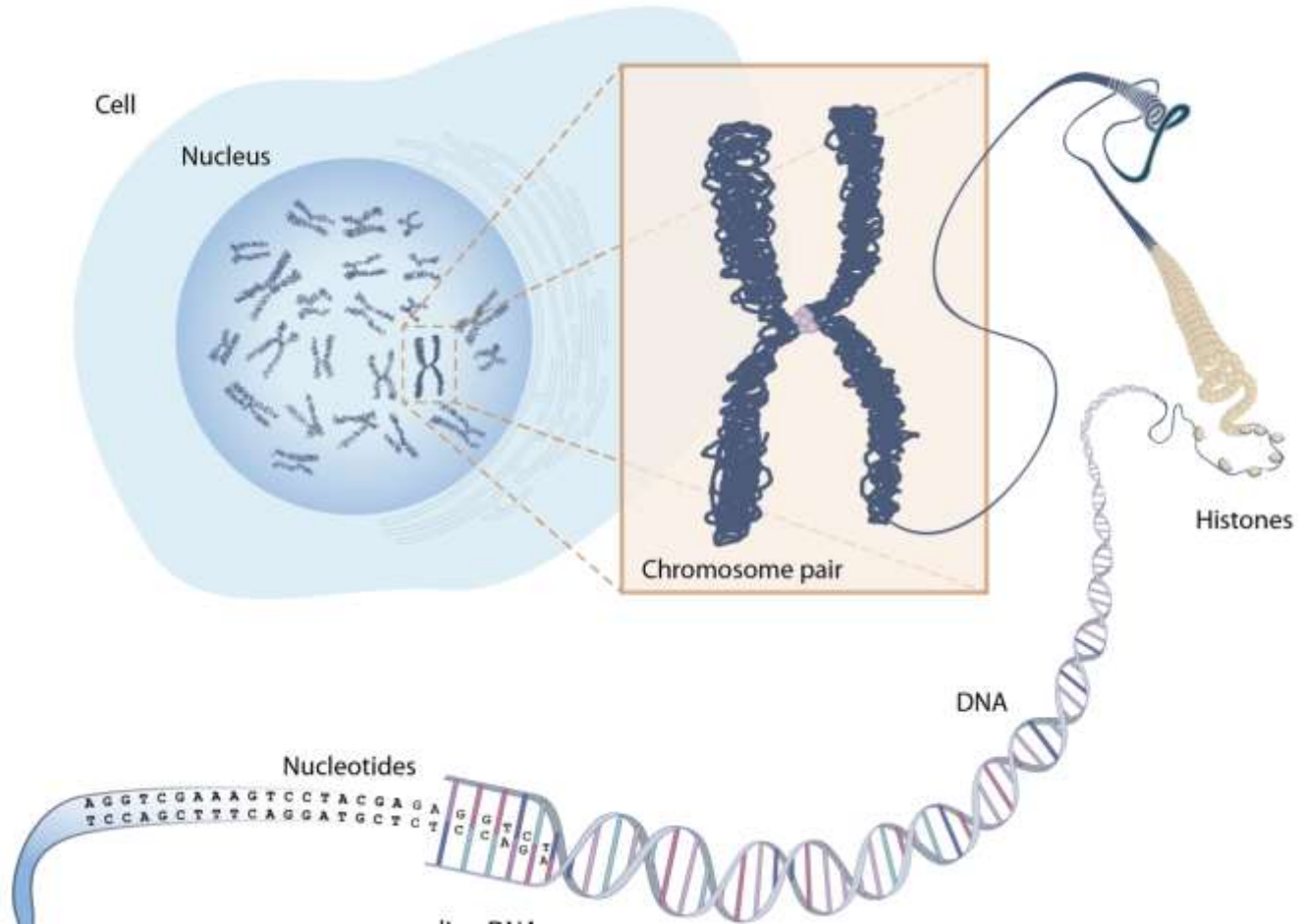


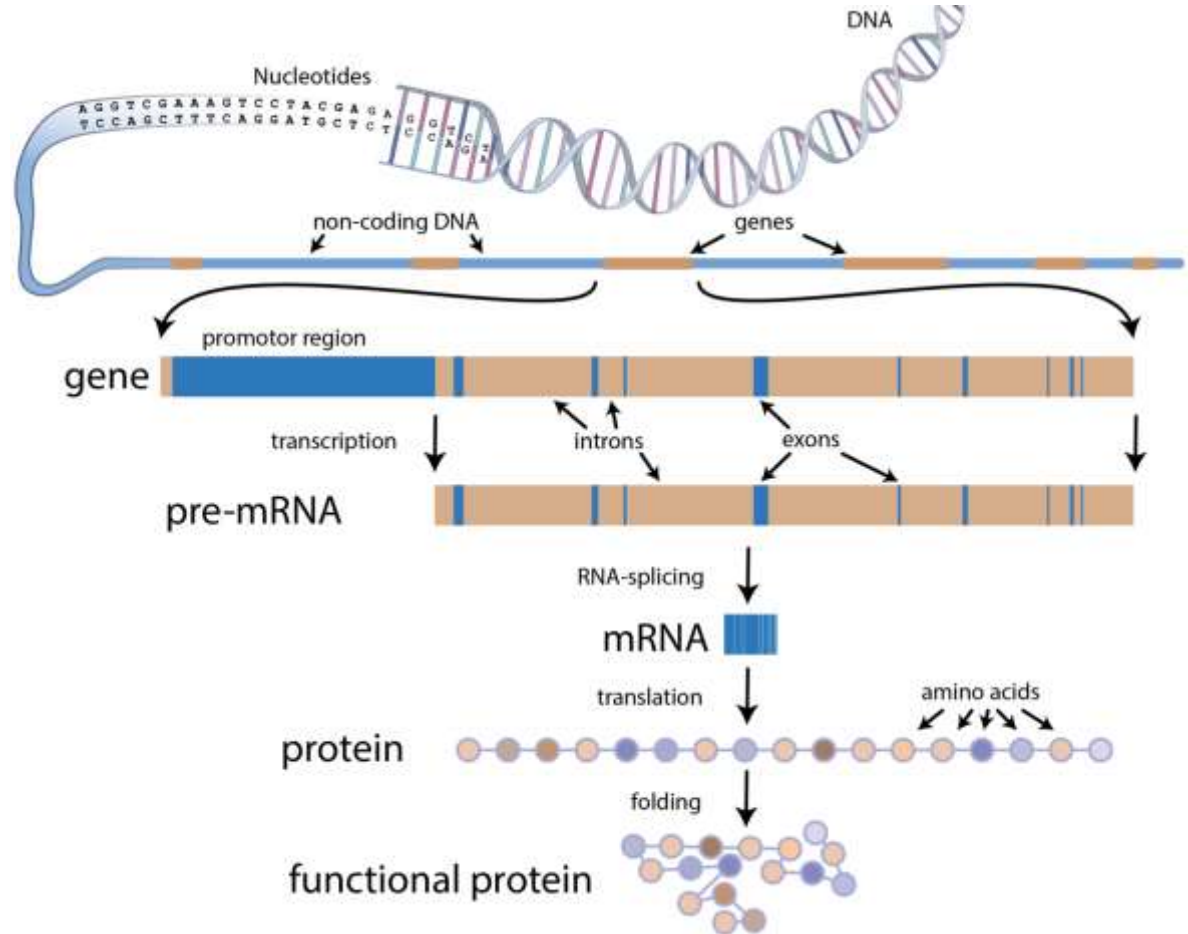
Why we did this project?

First, a minimum of molecular biology

The normal cell

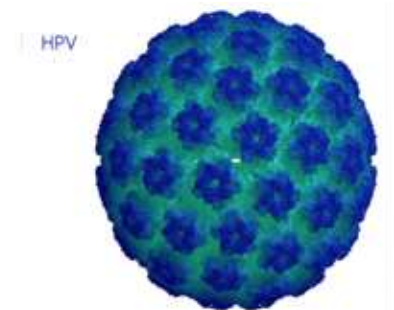


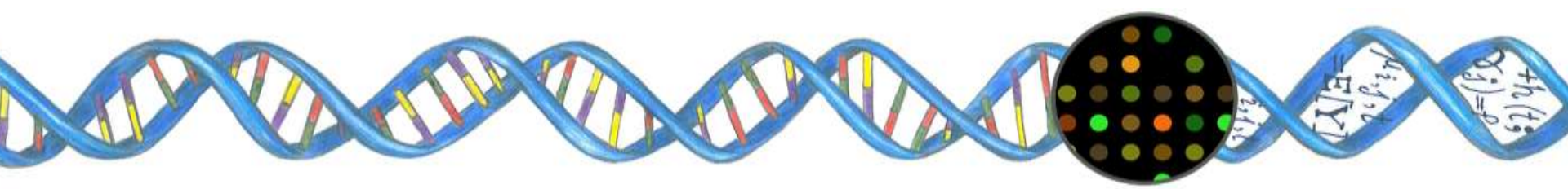
Central dogma of molecular biology



Cervical cancer

- One of the most diagnosed cancer in women
- Caused by HPV virus and (epi)genetic abnormalities
- HPV16 and HPV18 cause 70% of all cervical cancers

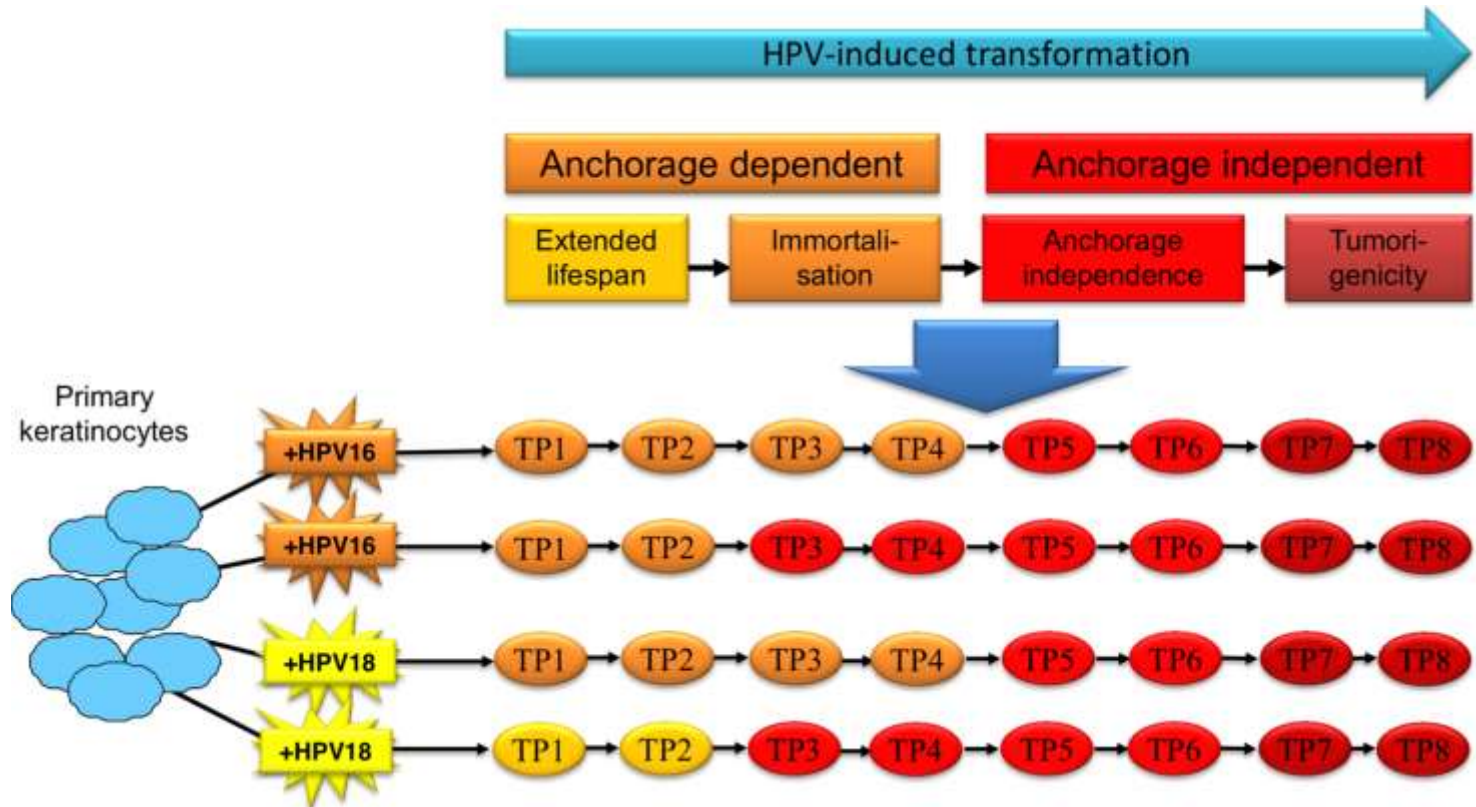




Gain more insights into the molecular mechanism driving cervical cancer

How we can do it?

The experiment



Differential expression analysis

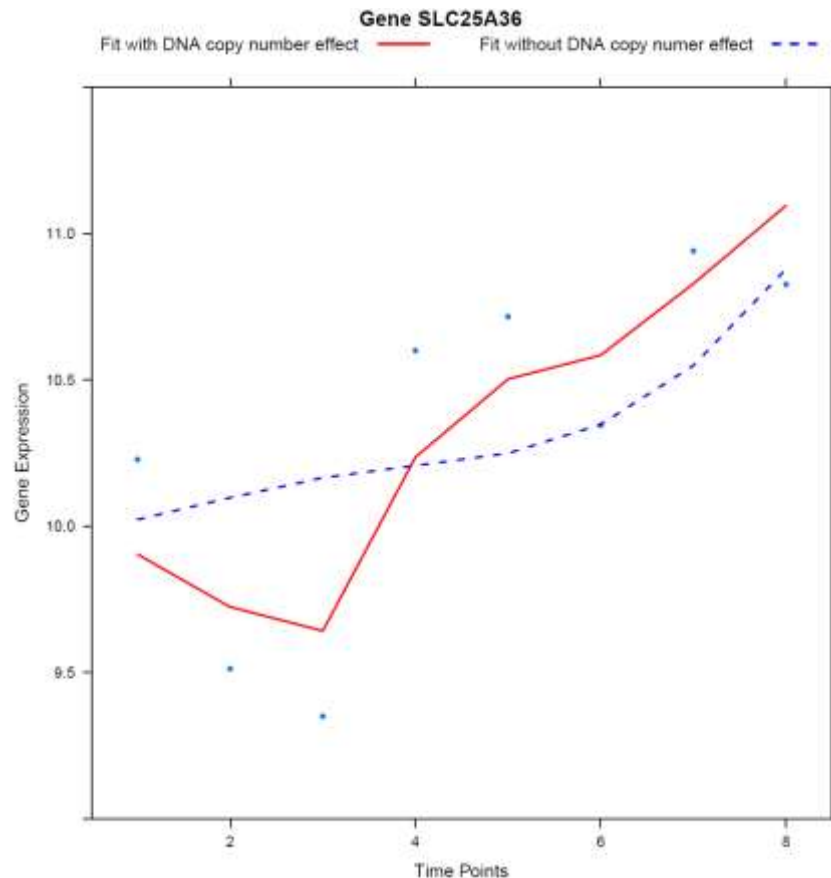
Which genes are changed during cervical cancer development?

Does DNA copy number drive gene expression?

GE **CL** **CN** **Time** **Error**

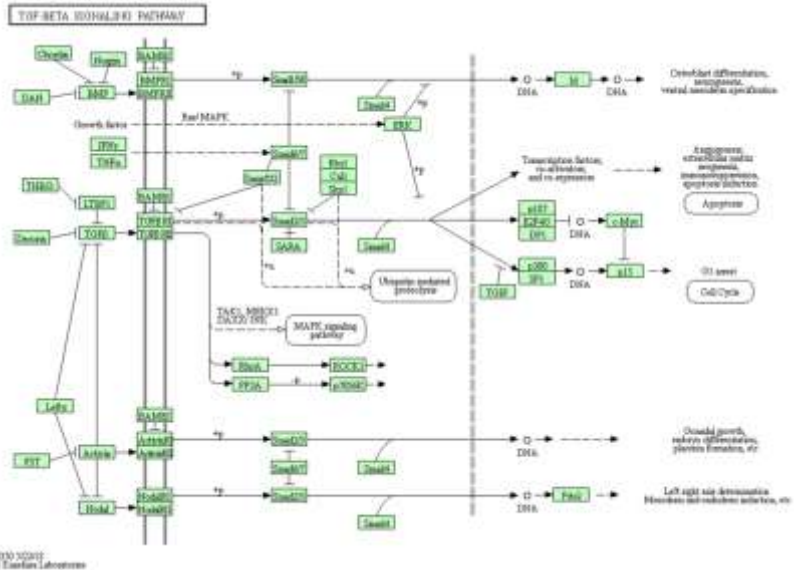
↓ ↓ ↓ ↓ ↓

$$Y_{i,j,t} = \alpha_{i,j} + \beta_j x_{i,j,t} + \tilde{Z}_t \tilde{\gamma}_j + \varepsilon_{i,j,t}$$

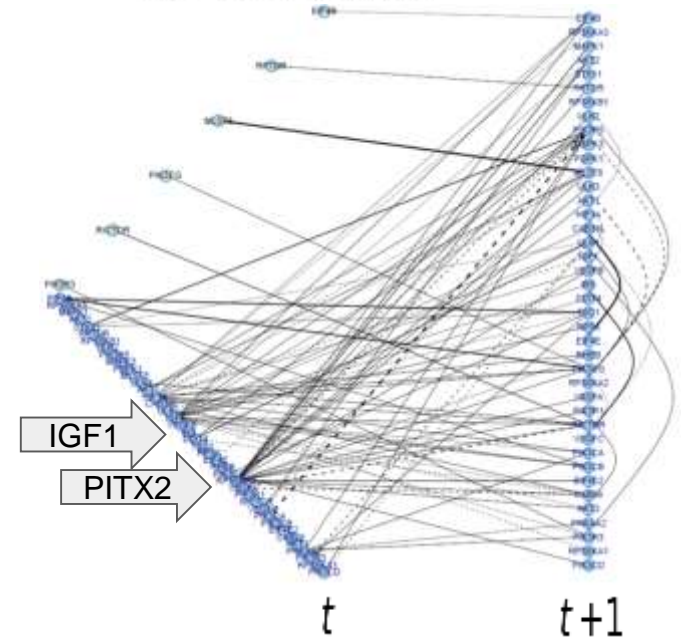


Pathway analysis

Pathways: set of genes which carry one function



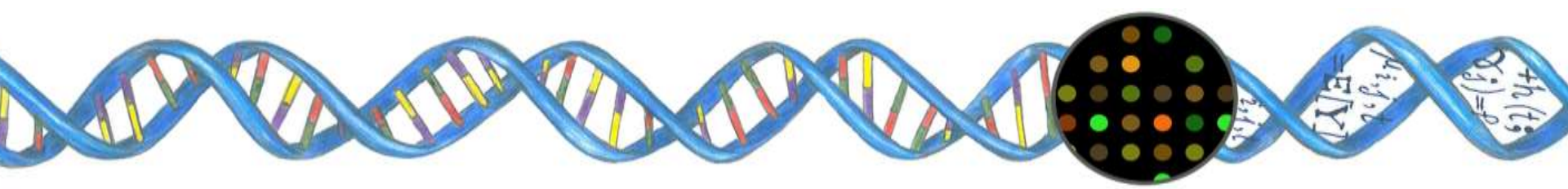
TGF- β signalling



Node: indicate a gene



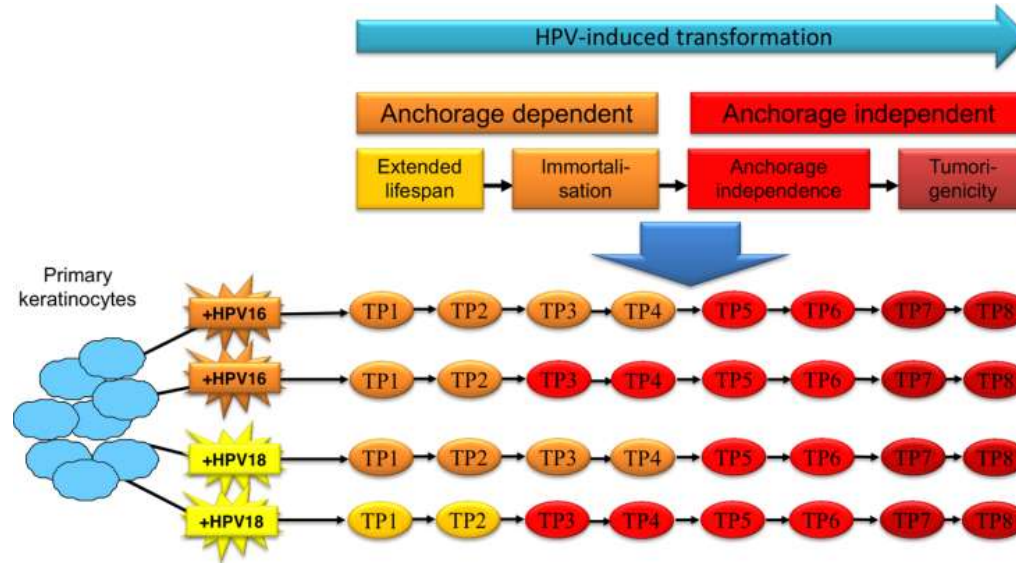
Edge: interaction between two genes



What we got out of it?

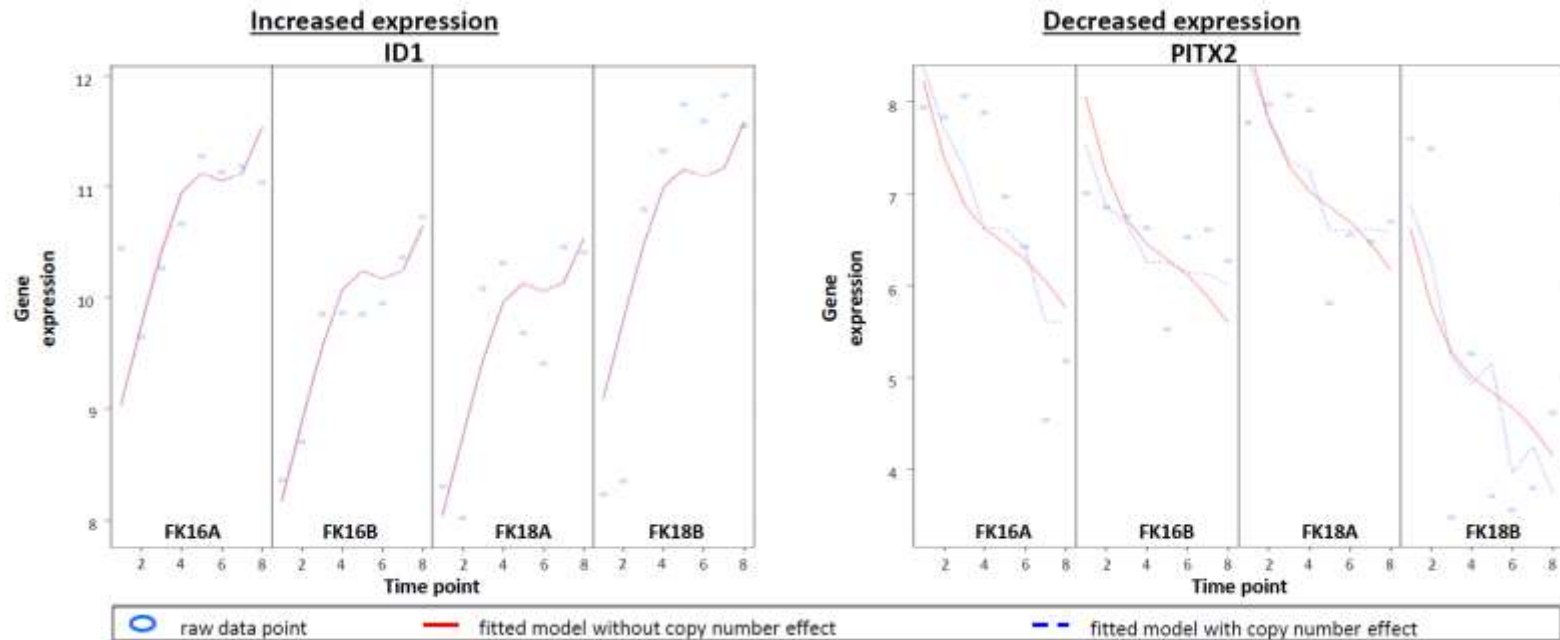
What we got out of it?

First comprehensive molecular profiling of HPV-induced transformation over time



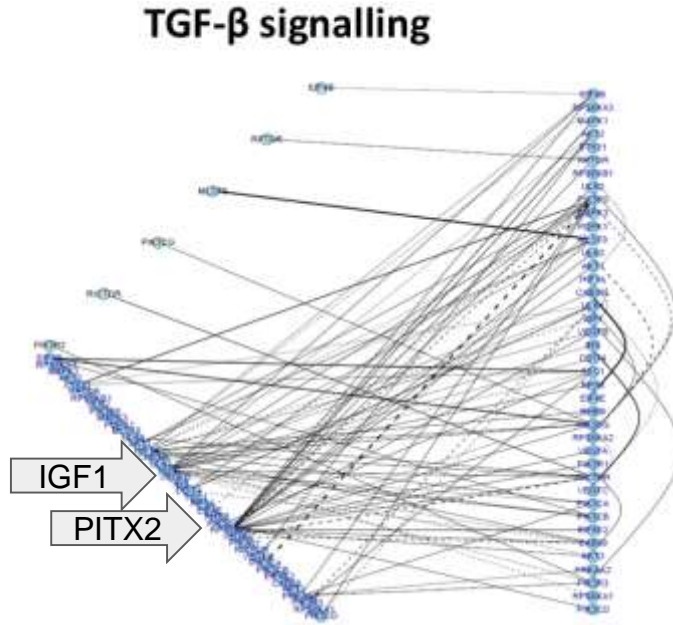
What we got out of it?

1/3rd of differentially expressed genes are associated with copy number changes



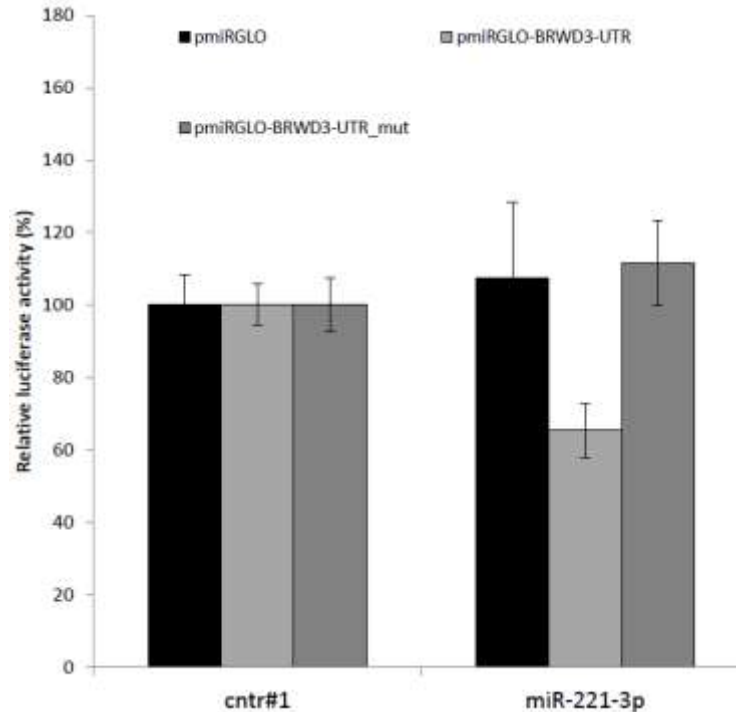
What we got out of it?

Among this genes in enriched pathways are identified key regulators



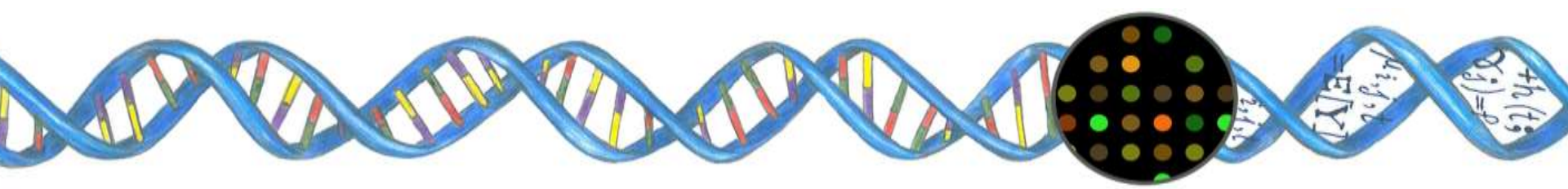
What we got out of it?

Identify the potential miRNA targets over time: miR-221-3p->BRWD3 validated



What we got out of it?

Functional studies on the identified key regulators and differentially expressed genes will result in many more potential therapeutic targets and disease markers in the future



Thank you for your attention!