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# Introduction to practical sessions

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# Introduction to the biological question

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- For all further practical sessions we will use data from Thomas Strub et al. (IGBMC, Davidson team)
- Main biological question
  - What is the role of MITF in melanoma ?
  - MITF = Microphthalmia Transcription Factor
  - Why study MITF ?
    - Essential for the survival of melanocytes  
Regulates multiple aspects of normal melanocyte function
    - Important role in regulating the proliferative and invasive properties of melanoma cells

# Introduction to the datasets

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- In order to have a comprehensive view of MITF role in human melanoma cells
  - Generation of a human melanoma cell line stably expressing HA-tagged MITF
    - **Anti-HA ChIP-Seq on the tagged and native cells**
  - Use of siRNAs to knockdown MITF expression in melanoma cells
    - 3'end RNA-Seq on RNA from siMITF and control cells  
*Strub et al. Oncogene 2011*
    - **mRNA-Seq on RNA from siMITF and control cells**

# Introduction to the datasets

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- mRNA-seq dataset
  - Illumina Hiseq2500 sequencer
  - Single-end 50bp
  - 4 samples per lane

| Sample name | Condition |
|-------------|-----------|
| siLuc2      | siLuc     |
| siLuc3      | siLuc     |
| siMitf3     | siMitf    |
| siMitf4     | siMitf    |

- Data available in GalaxEast
  - Shared Data → Data Libraries → CNRS training → RNAseq

# Introduction to the datasets

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- **ChIP-seq dataset**
  - Illumina GAIIx sequencer
  - Single-end 50bp
  - 1 sample per line

| Sample name    | Condition |
|----------------|-----------|
| MITF (flag HA) | Mitf      |
| CTRL           | Control   |

- **Data available in GalaxEast**
  - Shared Data → Data Libraries → CNRS training → ChIPseq