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Introduction to practical sessions

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Introduction to the biological question

- 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

- 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

■ mRNA-seq dataset

- Illumina TruSeq stranded mRNAseq protocol
- Illumina HiSeq2500 sequencer
- Single-end 50bp

Sample name	Condition
siLuc2	siLuc
siLuc3	siLuc
siMitf3	siMitf
siMitf4	siMitf

Introduction to the datasets

- **ChIP-seq dataset**
 - Illumina GAIIx sequencer
 - Single-end reads

Sample name	Read length (pb)
Mitf	54
Control	54
H3K4me3	40
poll	40

Data files available

- On your computer

- On Galaxy

- “NGS data analysis training Strasbourg” history
 - All files needed for the training on Galaxy
- “NGS data analysis training Strasbourg - RNAseq” and “NGS data analysis training Strasbourg - ChIPseq” histories
 - All datasets generated during the training
 - To be used only if you did not manage to perform an analysis step

RNAseq : <https://usegalaxy.fr/u/celine/h/ngs-data-analysis-training-strasbourg---rnaseq>

ChIPseq : <https://usegalaxy.fr/u/stephanie/h/ngs-data-analysis-training-strasbourg---chipseq>