



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

- 4 samples sequenced on an Illumina HiSeq2500 sequencer
 - 4 samples per lane

Sample ID	Condition
TSB-11_5_S1	siLuc
TSB-12_6_S1	siLuc
TSB-13_19_S2	siMitf
TSB-14_12_S2	siMitf

- Data available in directory D:\analyzeddata\rnaseq

Introduction to the datasets

- **ChIP-seq datasets**
 - 3 datasets sequenced on an Illumina GAIIx sequencer
 - 1 sample per line

Sample ID	Condition
MITF (flag HA)	Mitf
MITF_2 (flag HA)	Mitf
CTRL	Control

- Data available in directory D:\analyzeddata\chipseq

Exercise : quality analysis

- Launch quality analysis of the first mRNA-seq sample from previously described dataset, using FastQC software
 - Results will be discussed during QC course
- Run FastQC :
 - Double click on run_fastqc in FastQC directory
- In FastQC launch quality analysis of TSB-11_5_S1 sample :
 - File → Open
 - Choose TSB-11_5_S1_mrnaseq_noSpikes.fastq.gz located in directory D:\analyzeddata\rnaseq\fastq