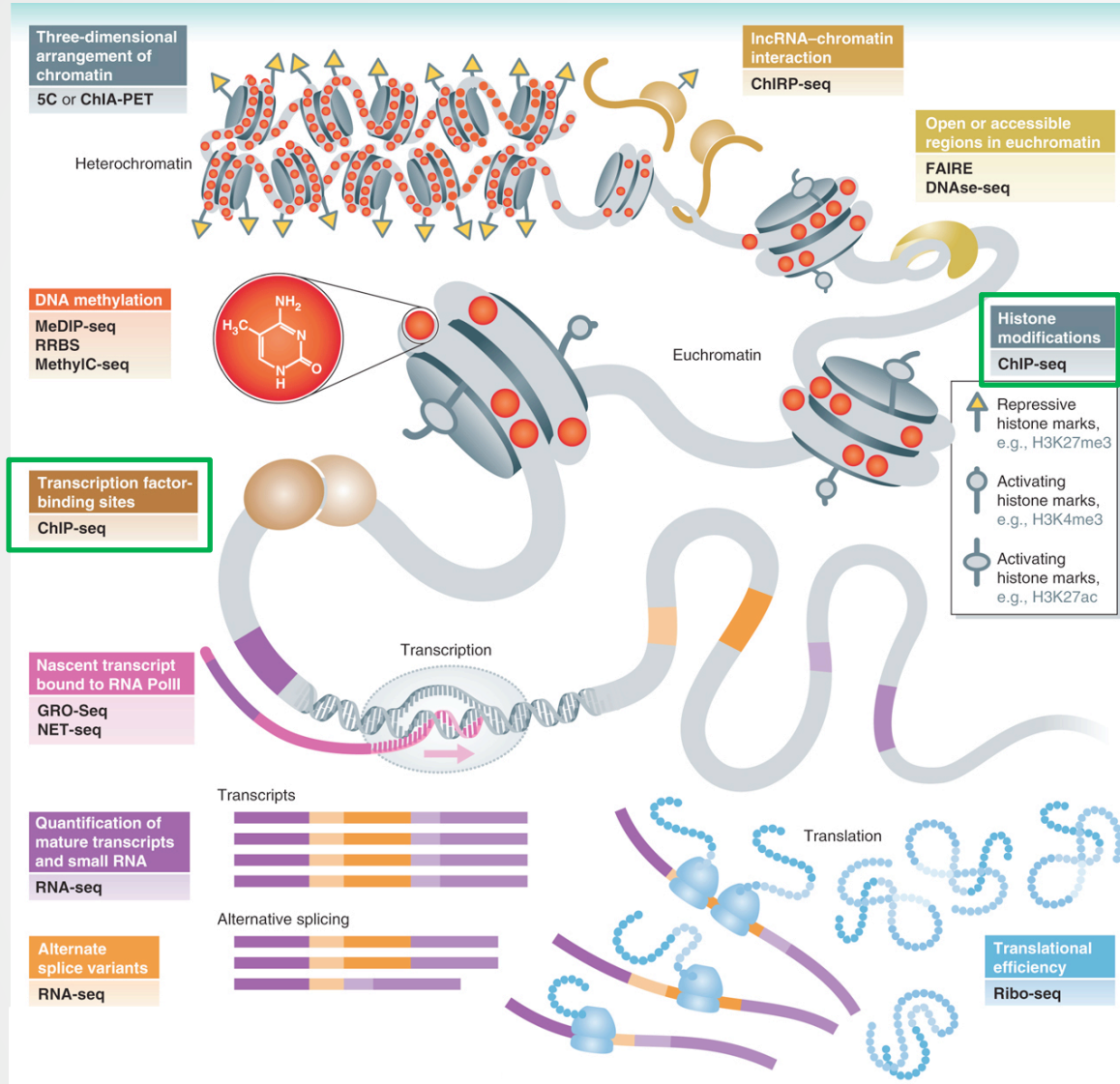


ChIP-sequencing: Library preparation and experimental design

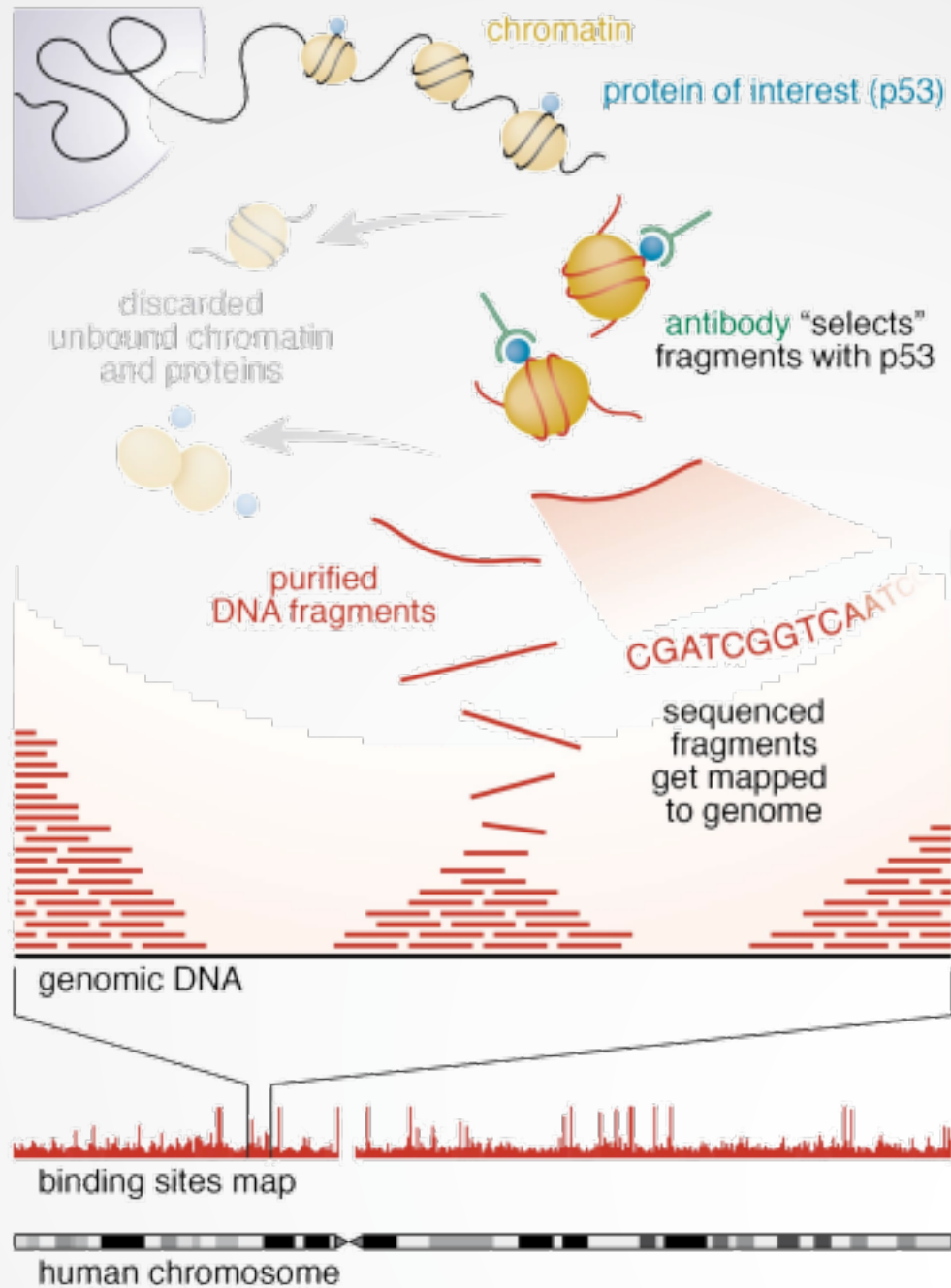
Stéphanie Le Gras
(slegras@igbmc.fr)

Sequencing technologies and their uses



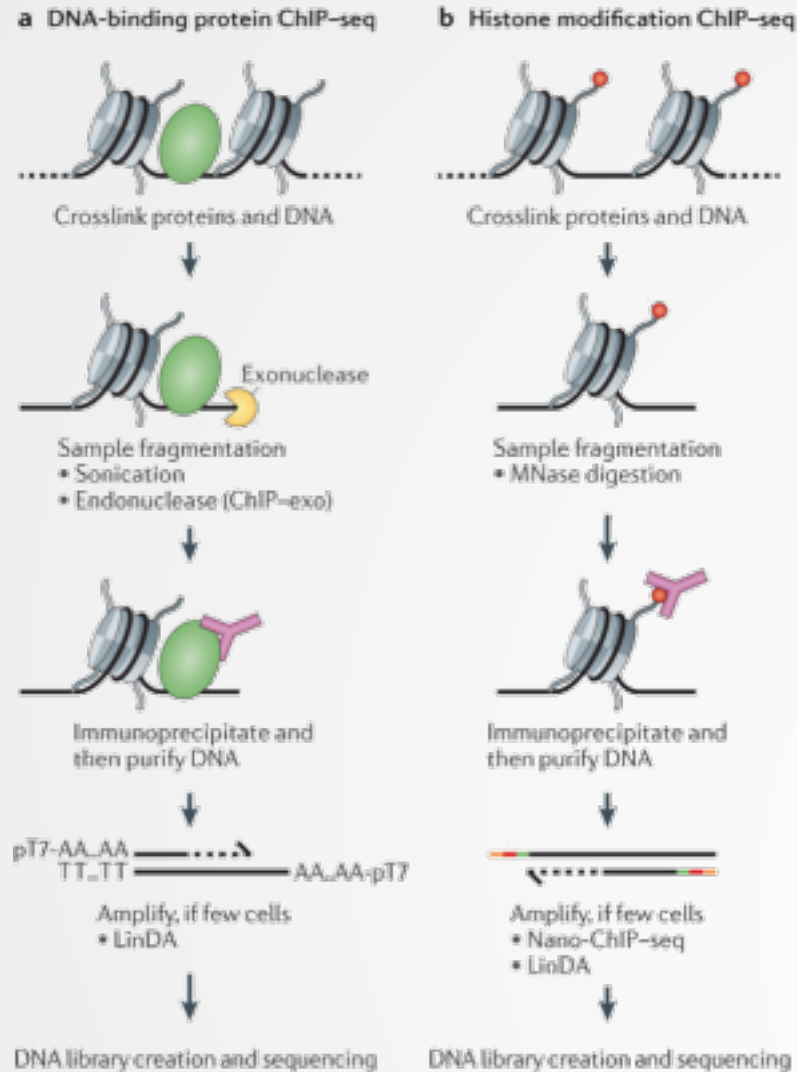
Soon et al, 2013

ChIP-seq



ChIP and library prep considerations

Chromatin ImmunoPrecipitation



Nature Reviews Genetics 13, 840-852
(December 2012) doi:10.1038/nrg3306

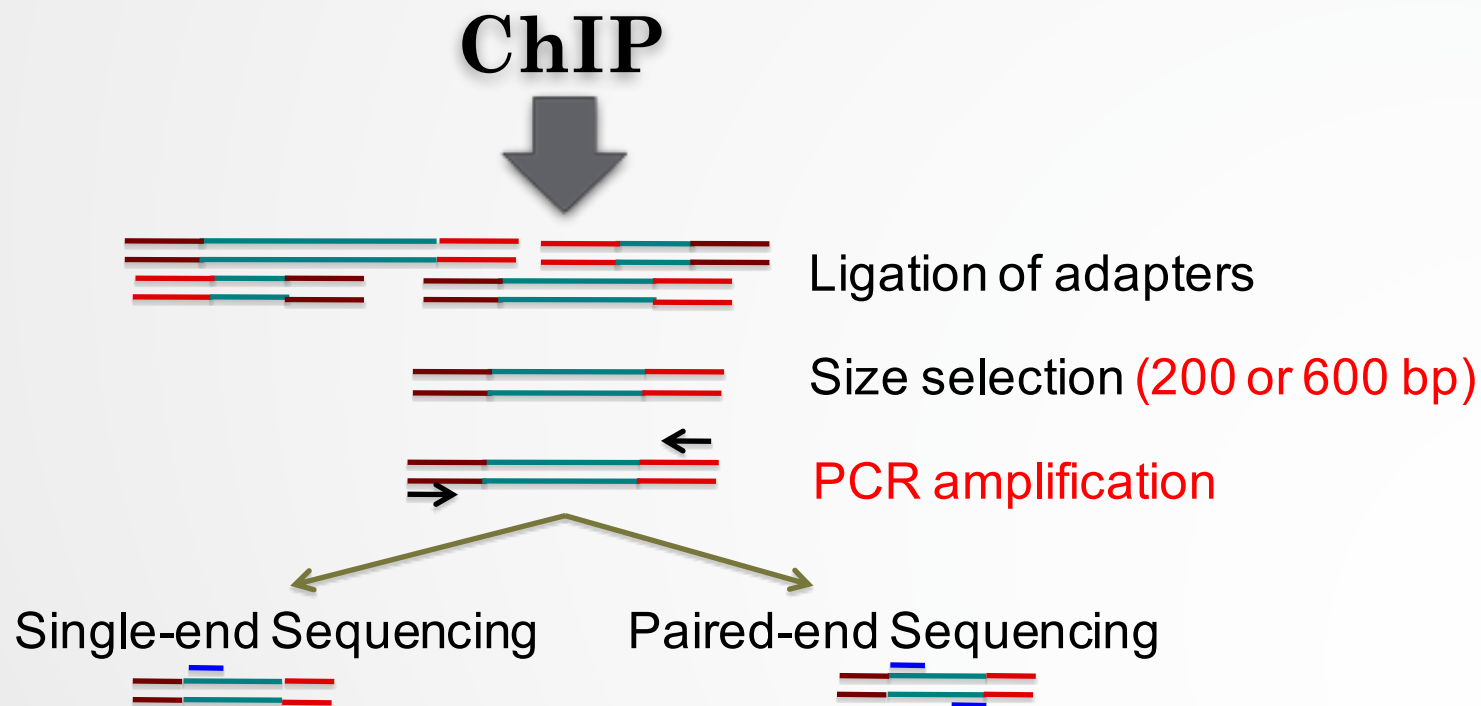
Considerations on chIP

- Antibody
 - Antibody quality varies, even between independently prepared lots of the same antibody (Egelhofer, T. A. *et al.* 2011)
- Number of cells
 - large number of cells are required for a ChIP experiment (limitation for small organisms)
 - Nano-ChIP-seq (Adli et al, 2011)
 - LinDA (Shankaranarayanan et al, 2011)
- Shearing of DNA (Mnase I, sonication, Covaris): trying to narrow down the size distribution of DNA fragments

————→ **Complexity in DNA fragments**

Library prep

- Step between ChIP and sequencing
- The goal is to prepare DNA for the sequencing
- Starting material: ChIP sample (1-10ng of sheared DNA)



Library prep

- PCR amplification : to increase amount of starting DNA
 - Number of PCR cycles as low as possible
 - Protocols with low quantity of starting material

Sequencing

- Sequencer : Illumina HiSeq 4000
- No. of reads per run, per sample :
 - 1st run on the GAIIx : 10-20 millions of reads per lane
 - (HiSeq 2500) 4 samples per lane :~41 millions per sample
 - (HiSeq 4000) 8 samples per lane :~43 millions per sample
- Length of DNA fragment : ~200-600bp
- No. of cycle per run : 50



Single end or paired end?

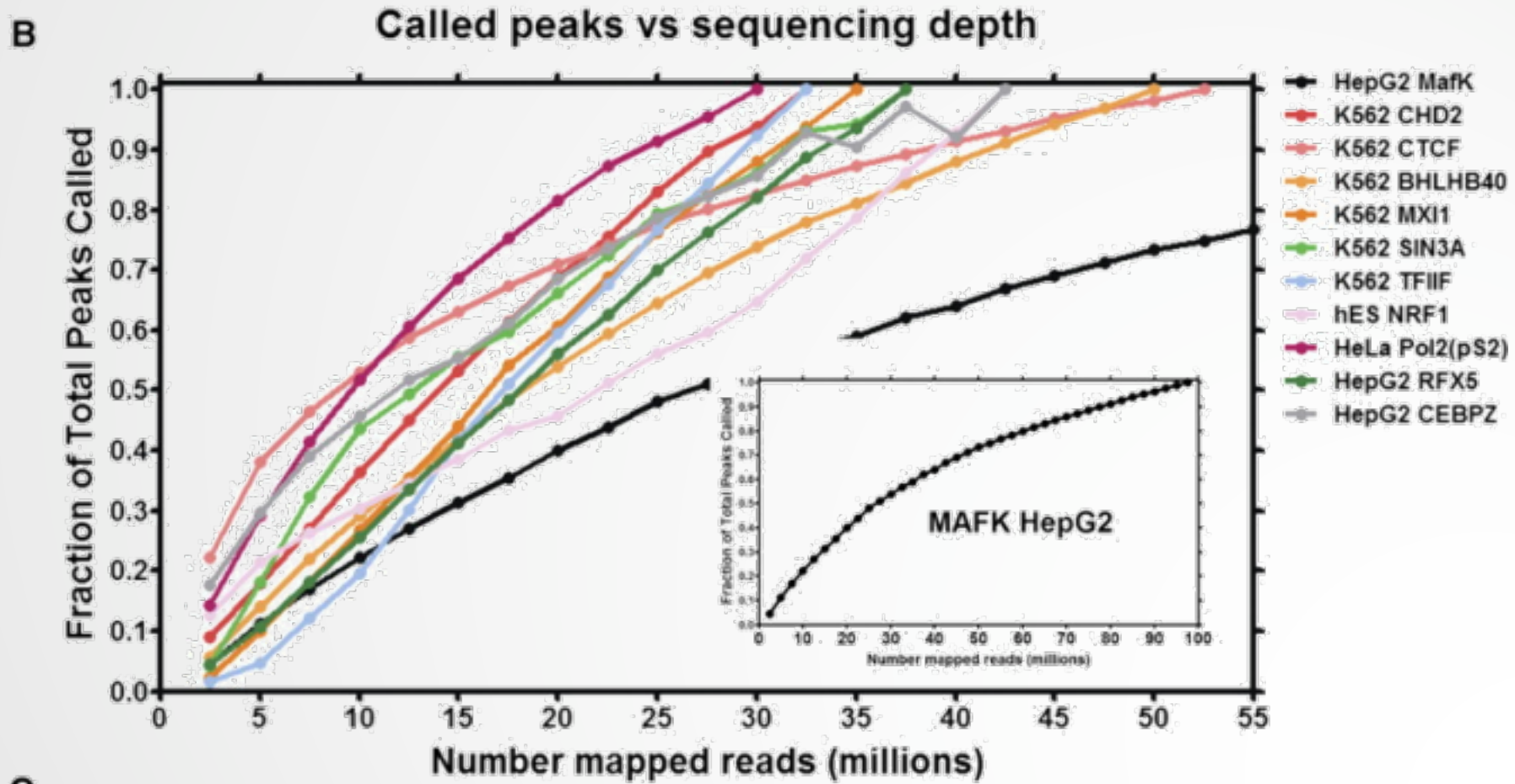
- Single end (most of the time)
- Paired-end sequencing
 - 😊 Improve identification of duplicated reads
 - 😊 Better estimation of the fragment size distribution
 - 😊 Increase the mapping efficiency to **repeat regions**
 - 😞 The price!

Sequencing depth

Consider the depth needed
depending on:

- chipped protein,

Sequencing depth



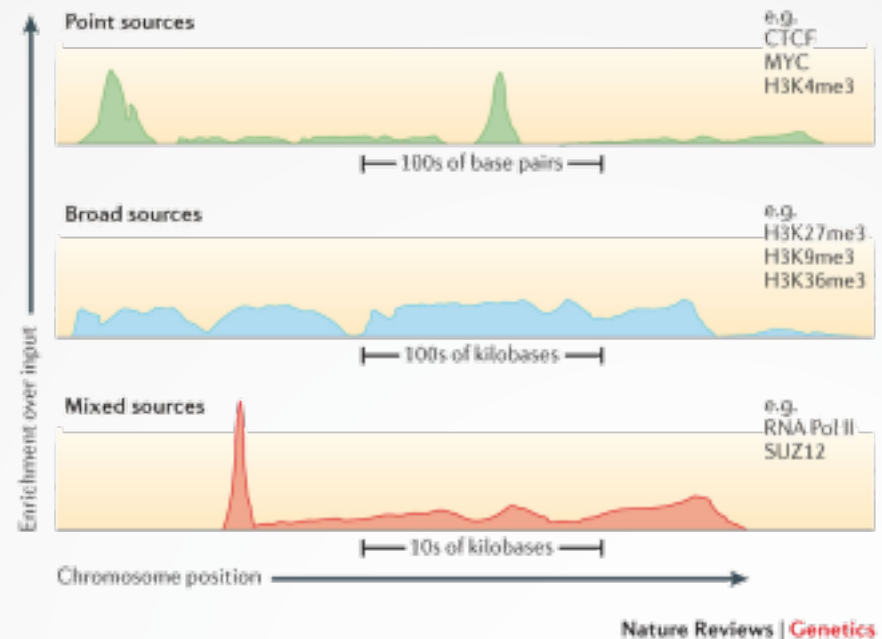
Sequencing depth

Consider the depth needed depending on:

- chipped protein,
- type of expected profile,
- number of expected binding sites,
- size of the genome of interest.

Ex:

- For human genomes, 20 million uniquely mapped read sequences are suggested for point-source peaks, or 40 million for broad-source peaks.
- For fly genome: 8 million reads
- For worm genome: 10 million reads



Controls

- Used mostly to filter out false positives (high level of noise)
 - Idea: potential false positive will be enriched in both treatment and control.
- A control will fail to filter out false positives if its enrichment profile is very different from the enrichment profile of false positive regions in the treatment sample
- 3 types of control are commonly used :
 - Input DNA : a portion of DNA sample removed prior to IP
 - DNA from non specific IP : DNA obtained from IP with an antibody not known to be involved in DNA binding or chromatin modification such as IgG
 - Mock IP DNA : DNA obtained from IP without antibodies
- Choice of control is extremely important
- It is recommended to cover the control in a higher extend than the IPs

Replicates

- A minimum of two replicates should be carried out per experiment.
- Each replicate should be a biological rather than a technical replicate; that is, it represents an independent cell culture, embryo pool or tissue sample.

ENCODE

- The Encyclopedia of DNA Elements (ENCODE) Consortium has carried out hundreds of ChIP–seq experiments and has used this experience to develop a set of working standards and guidelines

See: <https://www.encodeproject.org/about/experiment-guidelines/>

Data used in this course

Sample name	No. of raw reads
MITF	31,334,257
Ctrl	29,433,042
H3K4me3	11,192,622
polII	10,404,820