ChIP-sequencing: Library preparation and experimental design
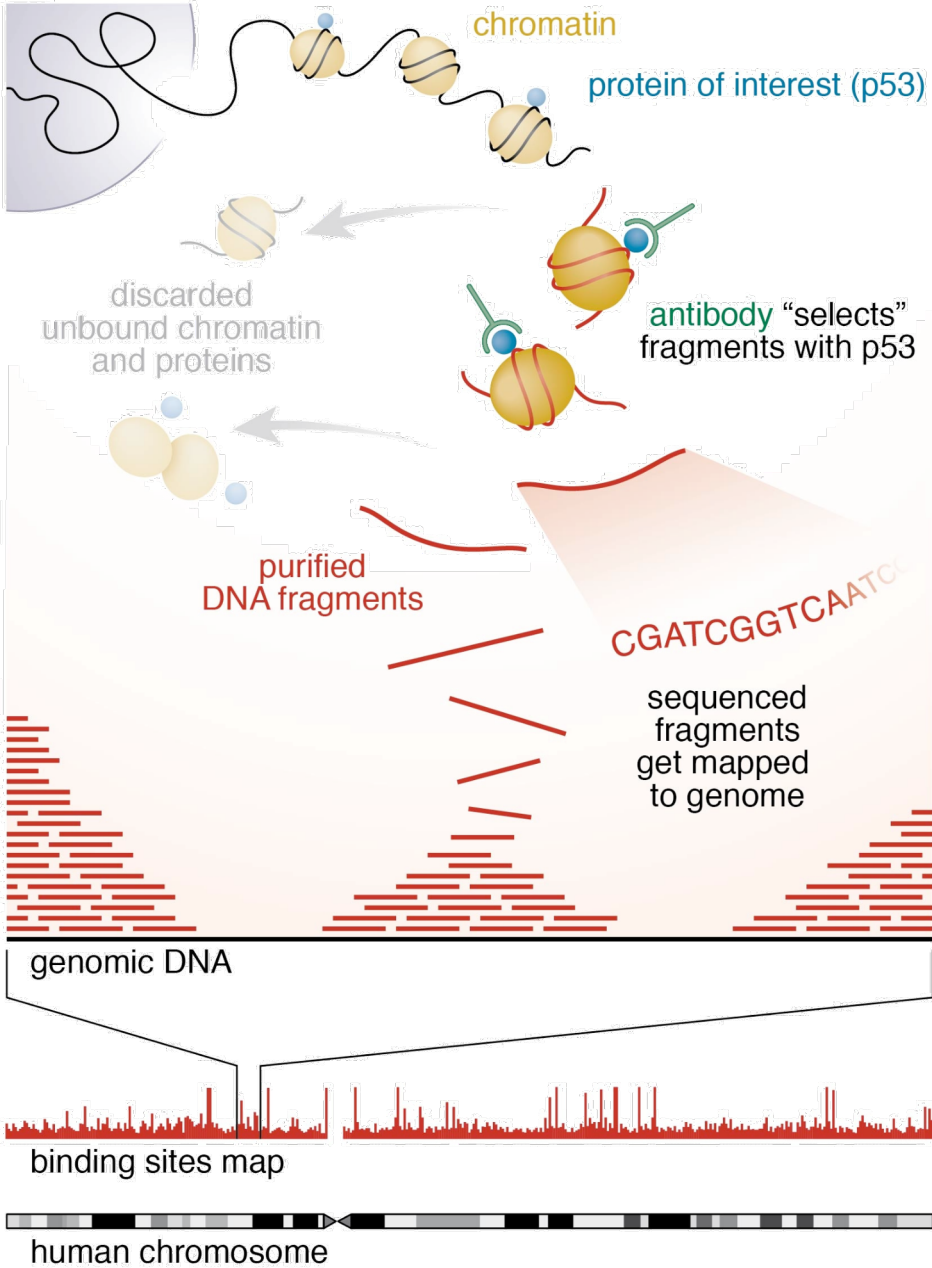
Stéphanie Le Gras
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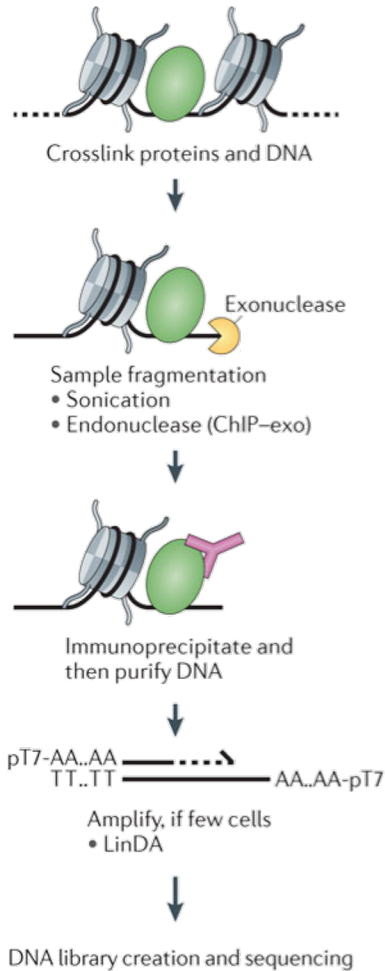
ChIP-seq
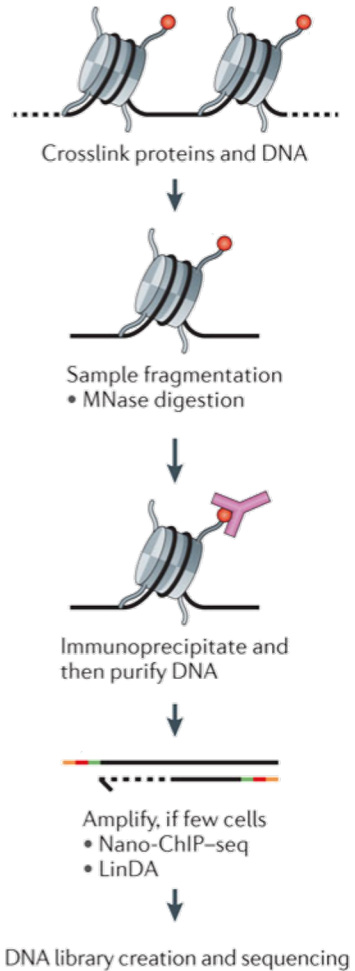

chromatin

protein of interest (p53)

discarded unbound chromatin and proteins

antibody "selects" fragments with p53

purified DNA fragments

CGATCGGTCAATC

sequenced fragments get mapped to genome

genomic DNA

binding sites map

human chromosome

ChIP and library prep considerations

Chromatin ImmunoPrecipitation

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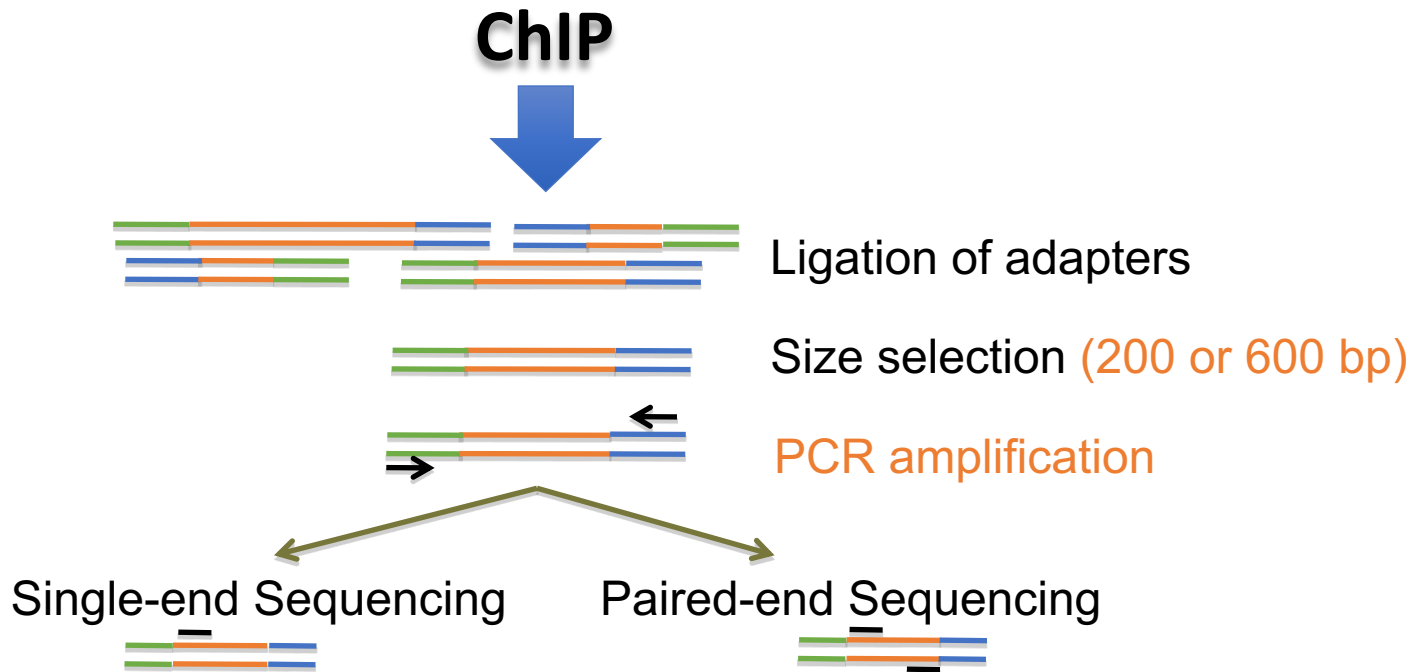(December 2012) doi:10.1038/nrg3306

Considerations on chIP

Complexity in DNA fragments ++

- 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

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)

ChIP

Ligation of adapters

Size selection (200 or 600 bp)

PCR amplification

Single-end Sequencing   Paired-end Sequencing

Sequencing

- Sequencer : Illumina HiSeq 4000
- No. of reads per run, per sample :
  - HiSeq 4000: 300-350 millions reads per lane
  - Multiplexing 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**
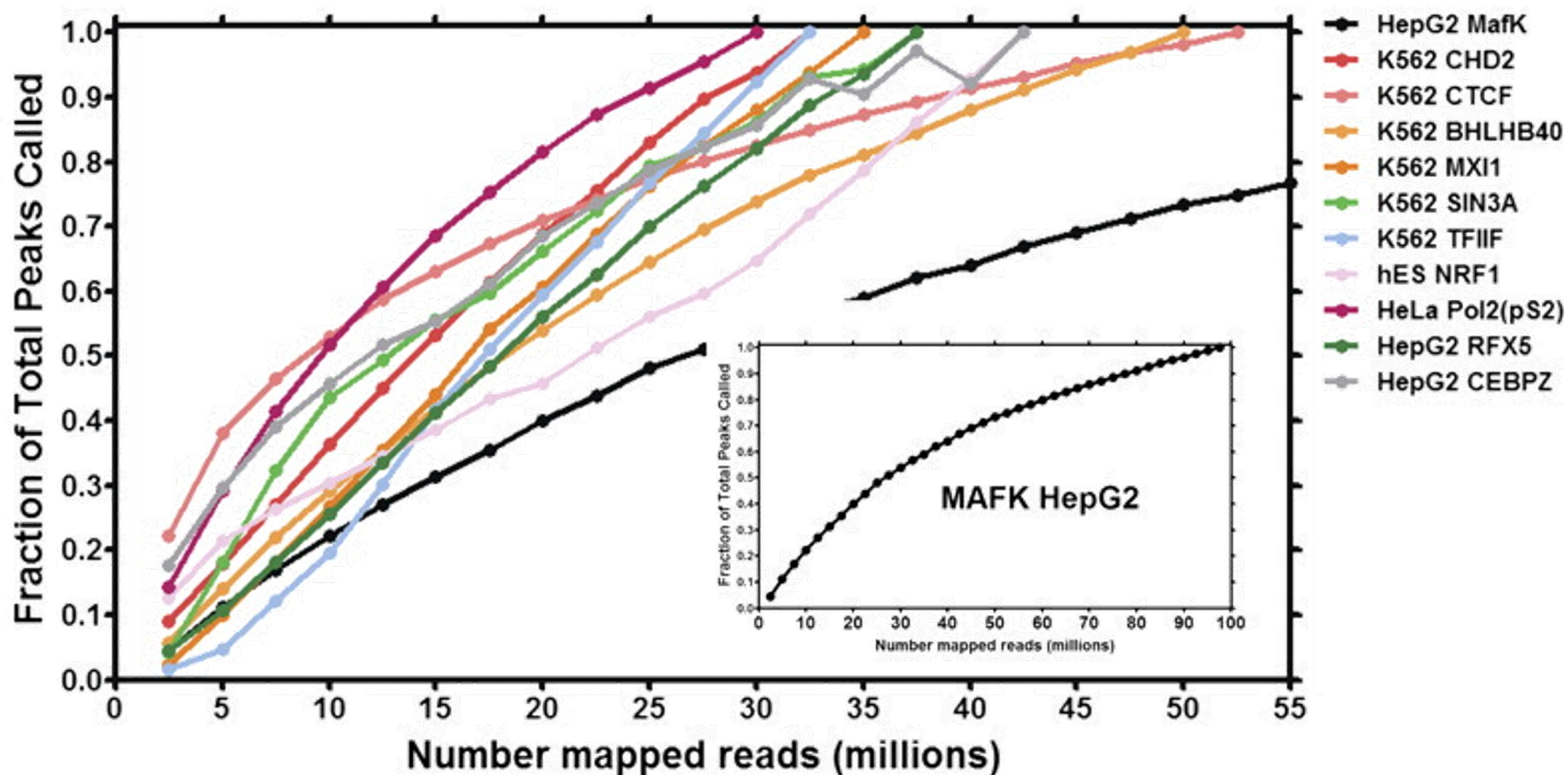   - 🙁 The price!

Sequencing depth

Consider the depth needed depending on:

- chipped protein,

Sequencing depth

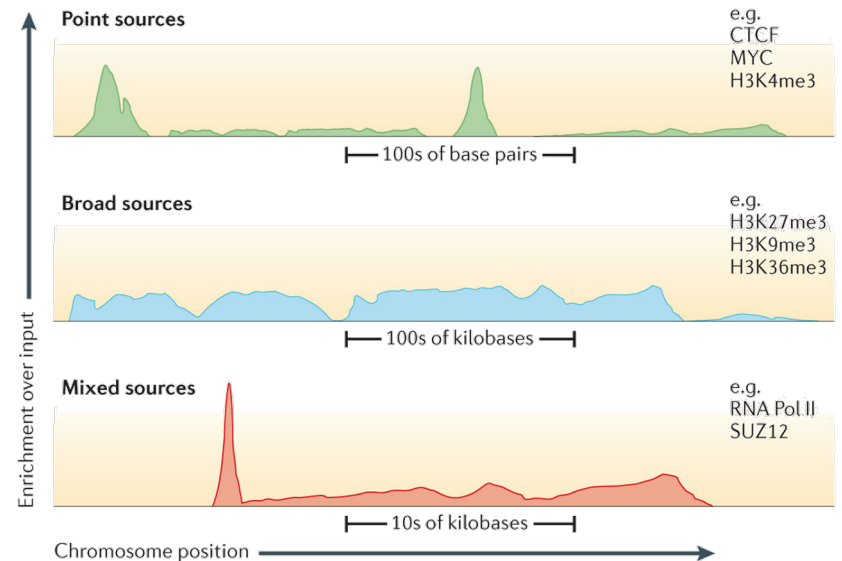Called peaks vs sequencing depth

Landt et al, 2012

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

Point sources — e.g. CTCF MYC H3K4me3 — 100s of base pairs

Broad sources — e.g. H3K27me3 H3K9me3 H3K36me3 — 100s of kilobases

Mixed sources — e.g. RNA Pol II SUZ12 — 10s of kilobases

Enrichment over input

Chromosome position

Nature Reviews | Genetics

Controls

- Used mostly to filter out false positives
  - Idea: potential false positive will be enriched in both the treatment and the 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