Chip-seq - Analysis

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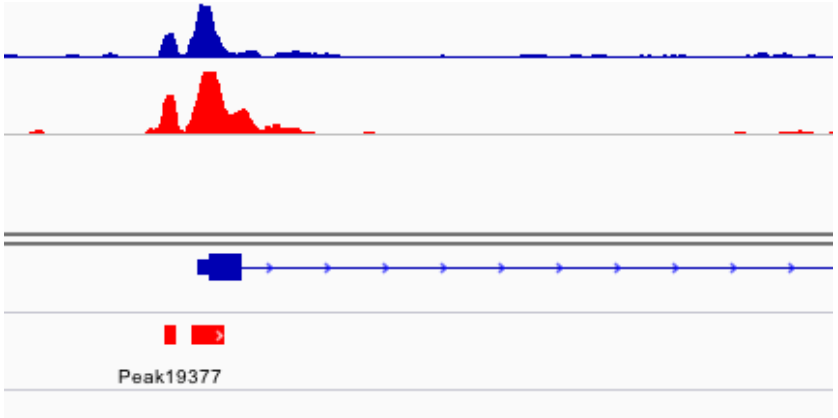
Bioinformatics analysis

Sequence file
fastq

```
@SRR038845.3 HWI-EAS038:6:1:0:1938 length=36
CAACGAGTTCACACCTTGGCCGACAGGCCCGGGTAA
+SRR038845.3 HWI-EAS038:6:1:0:1938 length=36
BA@7>B=>:>>7@7@>>9=BAA?;>52;>:9=8.=A
@SRR038845.41 HWI-EAS038:6:1:0:1474 length=36
CCAATGATTTTTTTCCGTGTTTCAGAATACGGTTAA
+SRR038845.41 HWI-EAS038:6:1:0:1474 length=36
BCCBA@BB@BBBBAB@B9B@=BABA@A:@693:@B=
@SRR038845.53 HWI-EAS038:6:1:1:360 length=36
GTTCAAAAAGAACTAAATTGTGTCAATAGAAAACTC
+SRR038845.53 HWI-EAS038:6:1:1:360 length=36
BBCBBBBBB@@BAB?BBBBCBC>BBBAA8>BBBAA@
```

Peak file



what this course is about

Steps

Filter poor-quality reads (optional)

- Remove sequences with poor-quality bases
- Remove sequences with adapter sequence or other contaminants

↓

Align reads to the genome

- Many aligners to choose from
- Allele-aware aligners
- Speed and memory considerations

↓

Filter artefacts and reads aligning to multiple locations

- Remove duplicate sequences
- PCR artefacts
- Eliminate non-unique aligning reads (but this masks segmental duplications)

↓

Call narrow/broad peaks (ChIP–seq, DNase–seq, FAIRE–seq)

- Settings may vary based on the type of peak
- Highly dependent on threshold settings

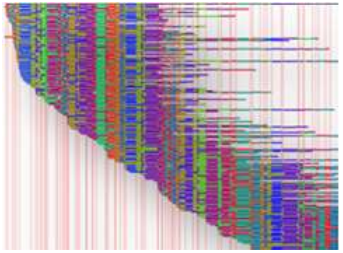
Furey 2012.
Nat. Genet. Rev.

Steps, graphics

Quality control

Cleaning

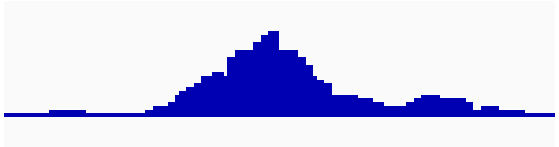
Mapping



Differential peak calling

Motif discovery

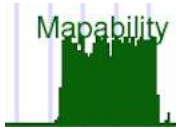
Peak calling

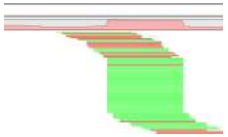


Signal normalization

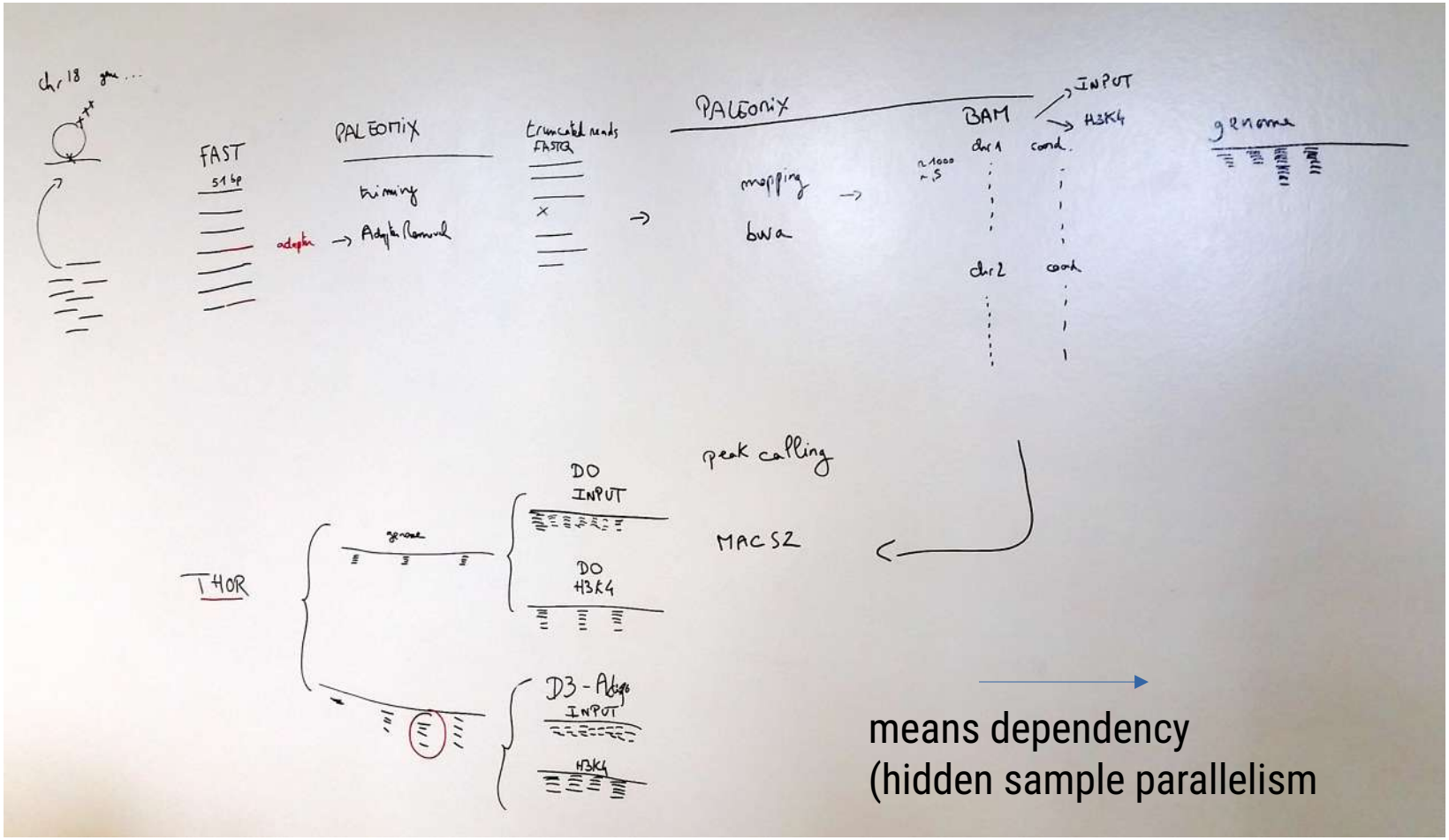
1 input / 1 IP

Controls





White board implementation



Computer implementation

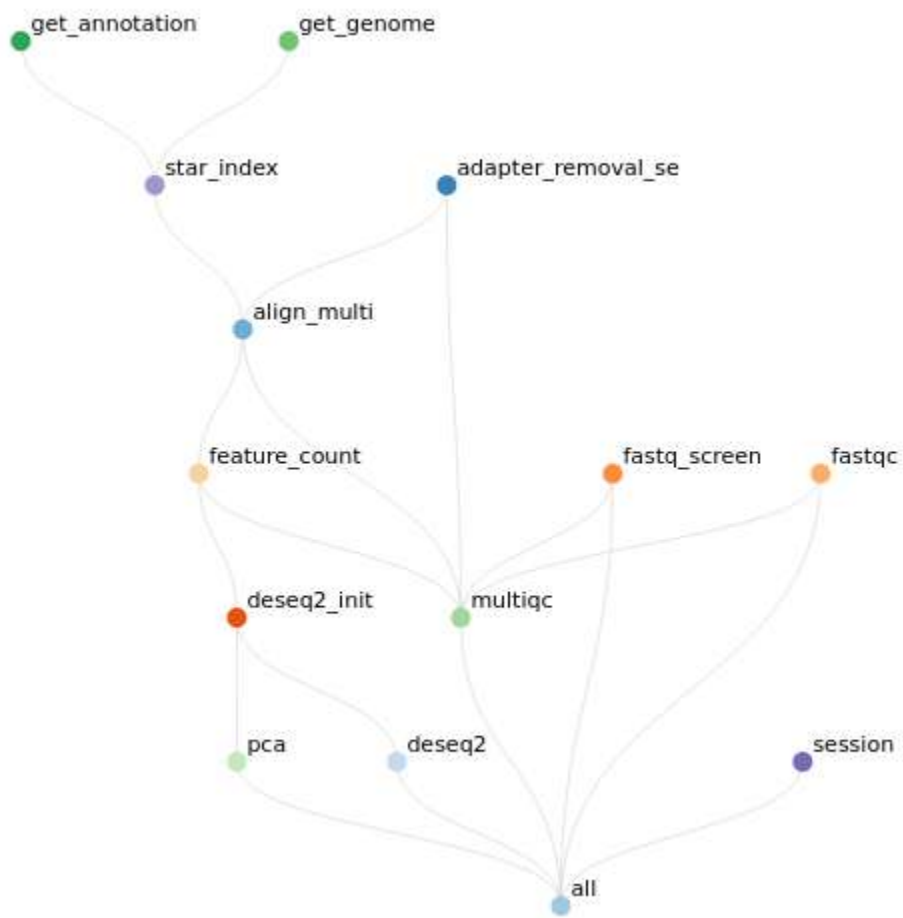
```
#!/bin/csh
# Created by: Chandra Sekhar Pedamallu @ DFCI, The Broad Ins
# Date: June 2016
# Full PathSeq pipeline
# time $pdir/FullPathSeq_June2016.sh $bamloc/SN218_Run0771_L
#
set start_time=`date +%s`

@ noargs=$#
##############################PLEASE SET THESE ENVIRONMENTAL
# Program Settings
set Institute="BROAD"
[...]
if($noargs < 4) then
    echo "Please check your argunments"
    echo "Usage : ./FullPathSeq_xxxx.sh <Input file in BAM c
    echo "Example : ./FullPathSeq_xxxx.sh unmappedreads.10K.
    exit
endif
####################INPUT FILES##############################
# Present Directory
set pdir = `pwd`
rm $pdir"/clean.files"
rm -r $pdir"/Commands/"
[...]
```

Issues

- mix of code and parameters
- common actions are mingled
- software/input defined as **absolute** paths
- comments are instructions
- software dependencies not included (`csh`!)
- on HPC, no admin rights
- any issue implies to start over
- version in filename (see the usage with **xxxx**)
- file management (here: `rm` recursive!)
- requires many effort to port over

Source: https://github.com/ChandraPedamallu/PathSeq/blob/4de7f350575404c9206b1e1c2d3f1fc81884908b/FullPathSeq_June2016.sh

What we need, dependencies



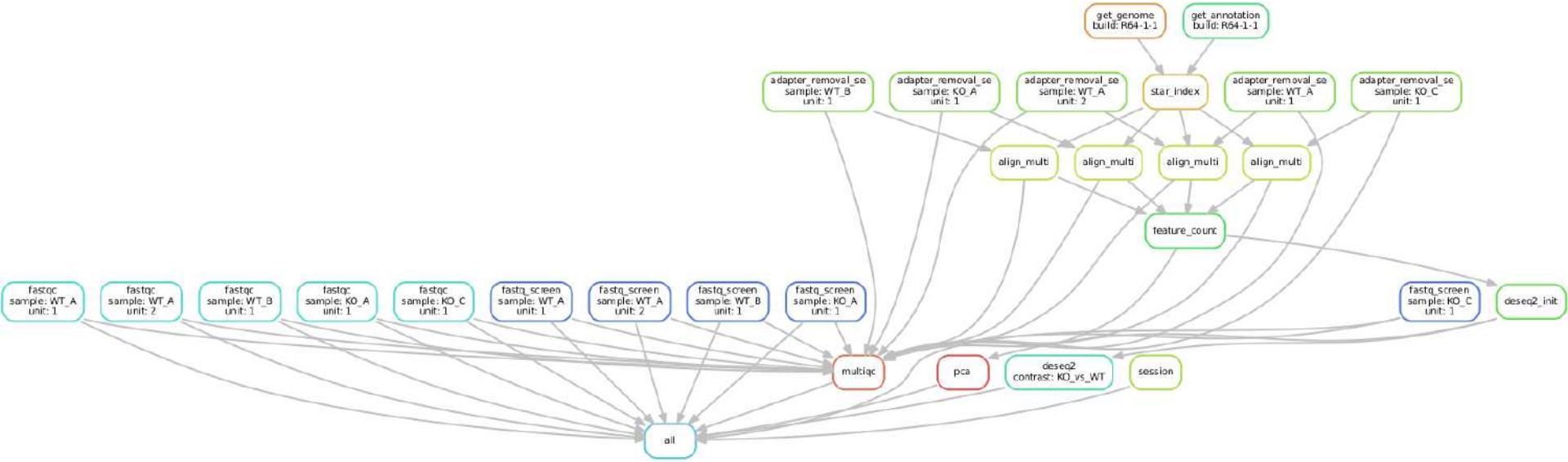
Source: Snakemake RNA-seq workflow,
https://gitlab.lcsb.uni.lu/aurelien.ginolhac/snakemake-rna-seq

Solved issues

- run only what needs to be, stop micromanaging your analyses
- use **relative** paths
- clear instructions in a `README`
- code in one folder, users edit 3 text files
- software installed in `singularity` image
- makes seamless deployment on HPC
- singularity images are versioned, code and reports too
- ongoing work in temporary folders
- multi-platform (Windows, MacOS, GNU/Linux)

Python

- This is the workflow being **used**: not just a diagram
- **Explicit** dependencies
- **Parallelization**: independent branches, like fastqc and adapter_removal and samples



Why you don't need/want to install any software?

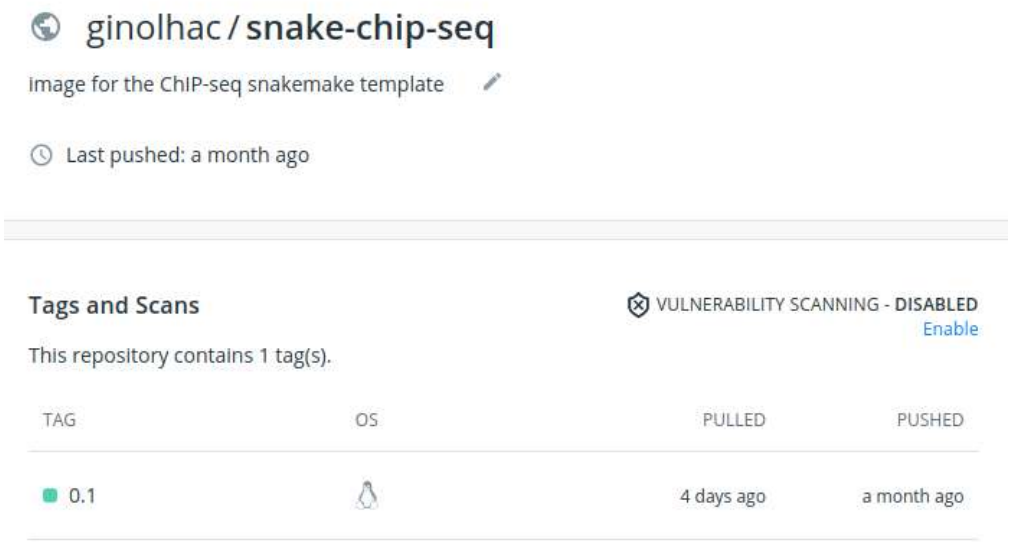
- it's boring
- On HPC one doesn't have admin rights
- modules prepared by the HPC teams are great, but more specific software are missing

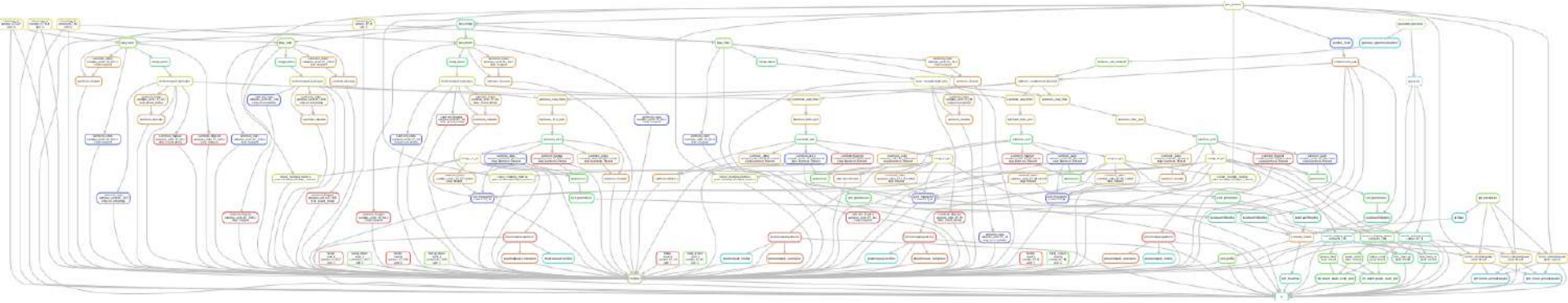
Docker

- is great but requires admin rights
- `singularity` is kind of docker for High Performance Computers

Of course, someone has to install software, it doesn't have to be you

— Aurélien adapted from **Jenny Bryan**





https://ginolhac.github.io/chip-seq/

ChIP-seq tutorials

Search

ChIP-seq tutorials

Home

Command line, basics

Setup snakemake

Workflow

Mapping

Peak calling

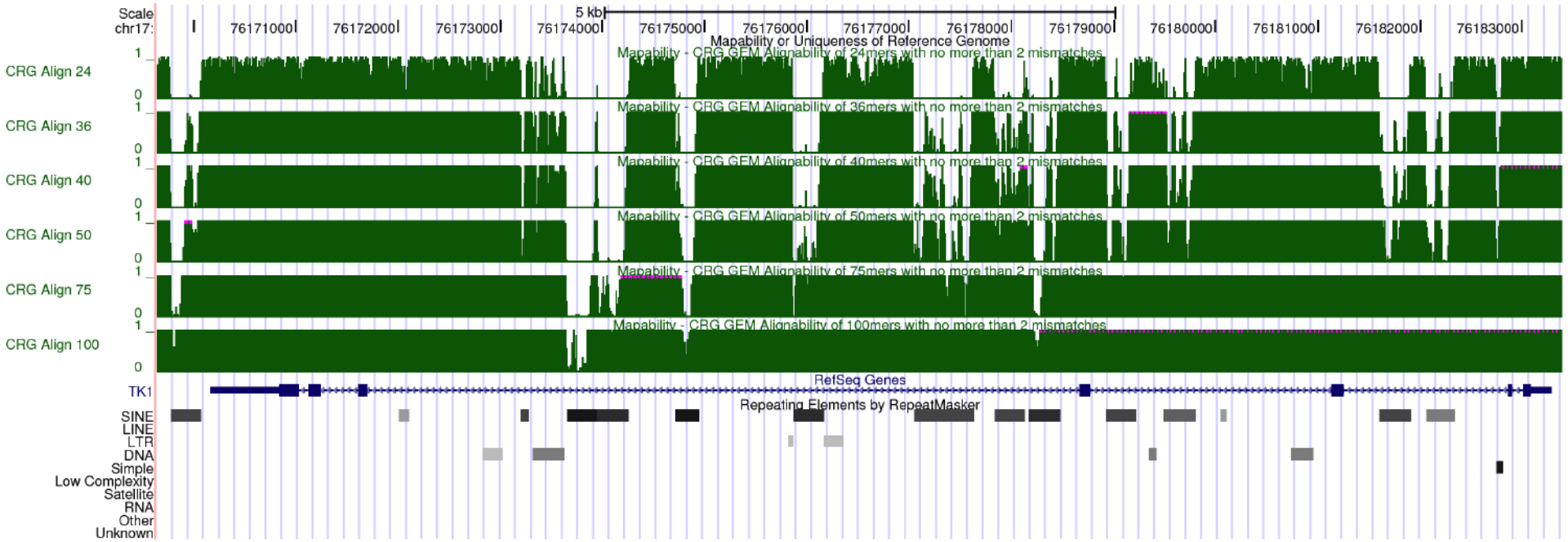
Contact

ChIP-seq practical session

Running all analyses is computationally intensive and despite the power of the current laptops, jobs should be run on high-performance clusters (HPC).

Moreover, bioinformatic analyses involve many inter-dependent steps that need to be coherently run by a workflow manager such as `snakemake`

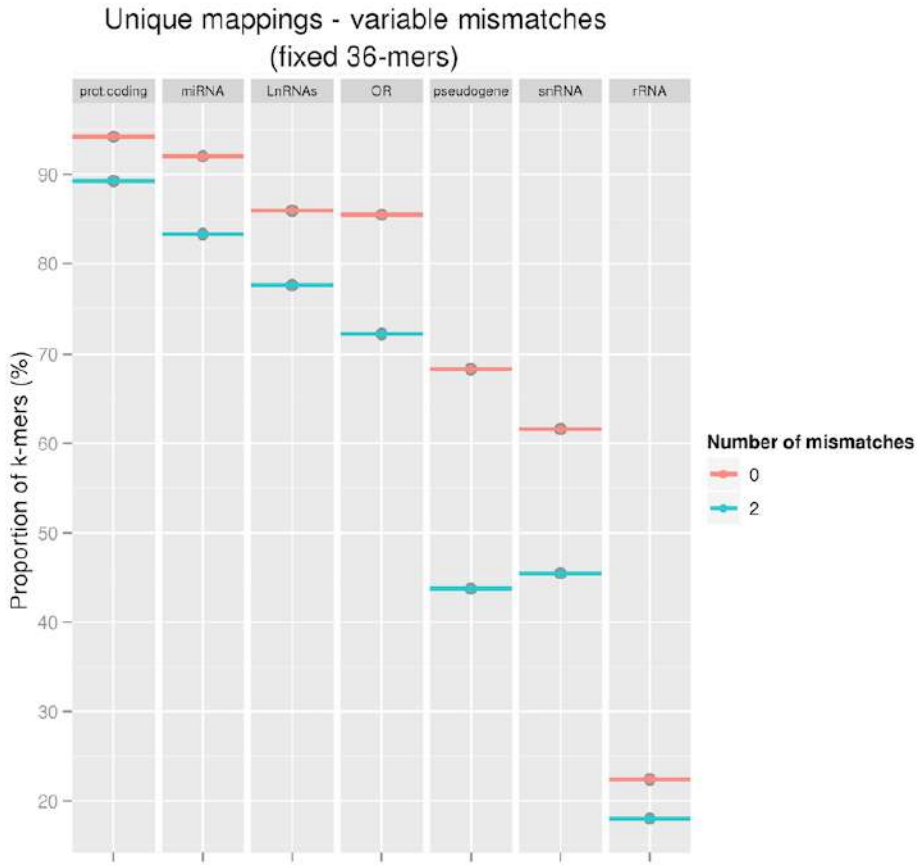
Mappability, causes



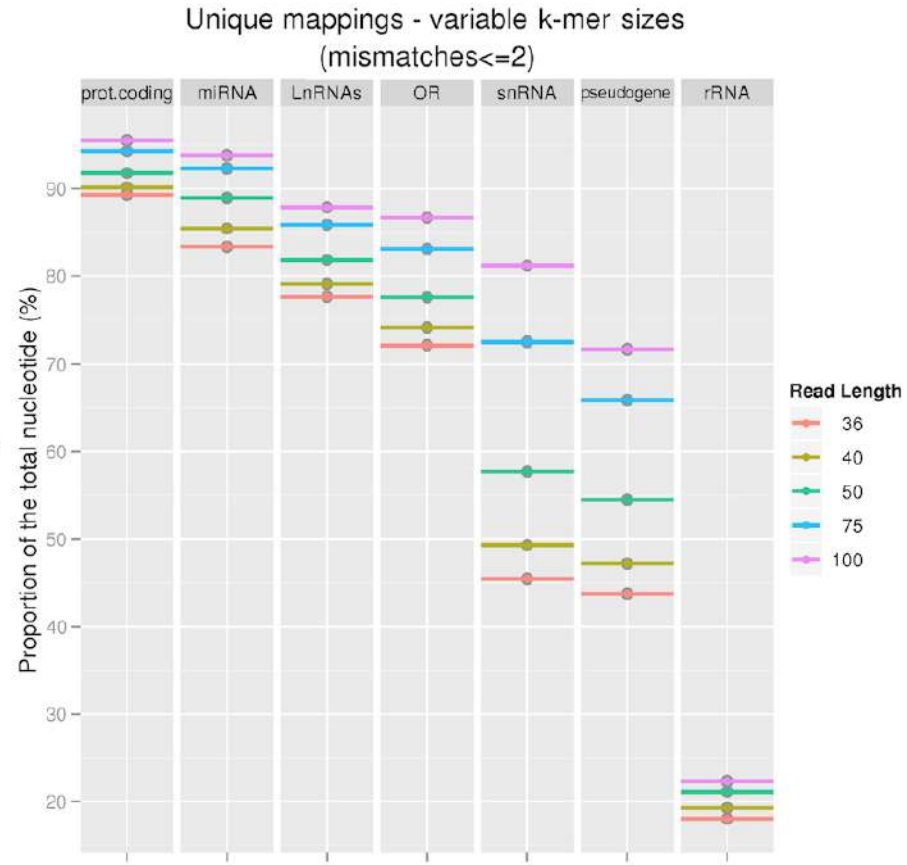
Mappability, consequences

Uniquely mapped

Mismatches

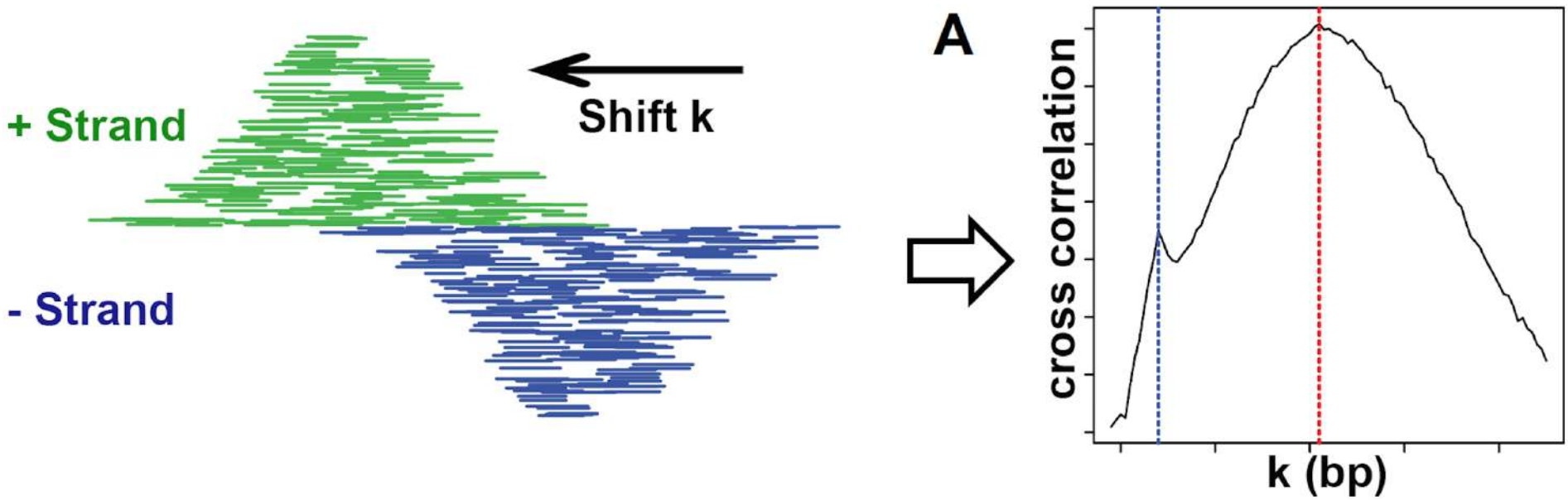


Read Length

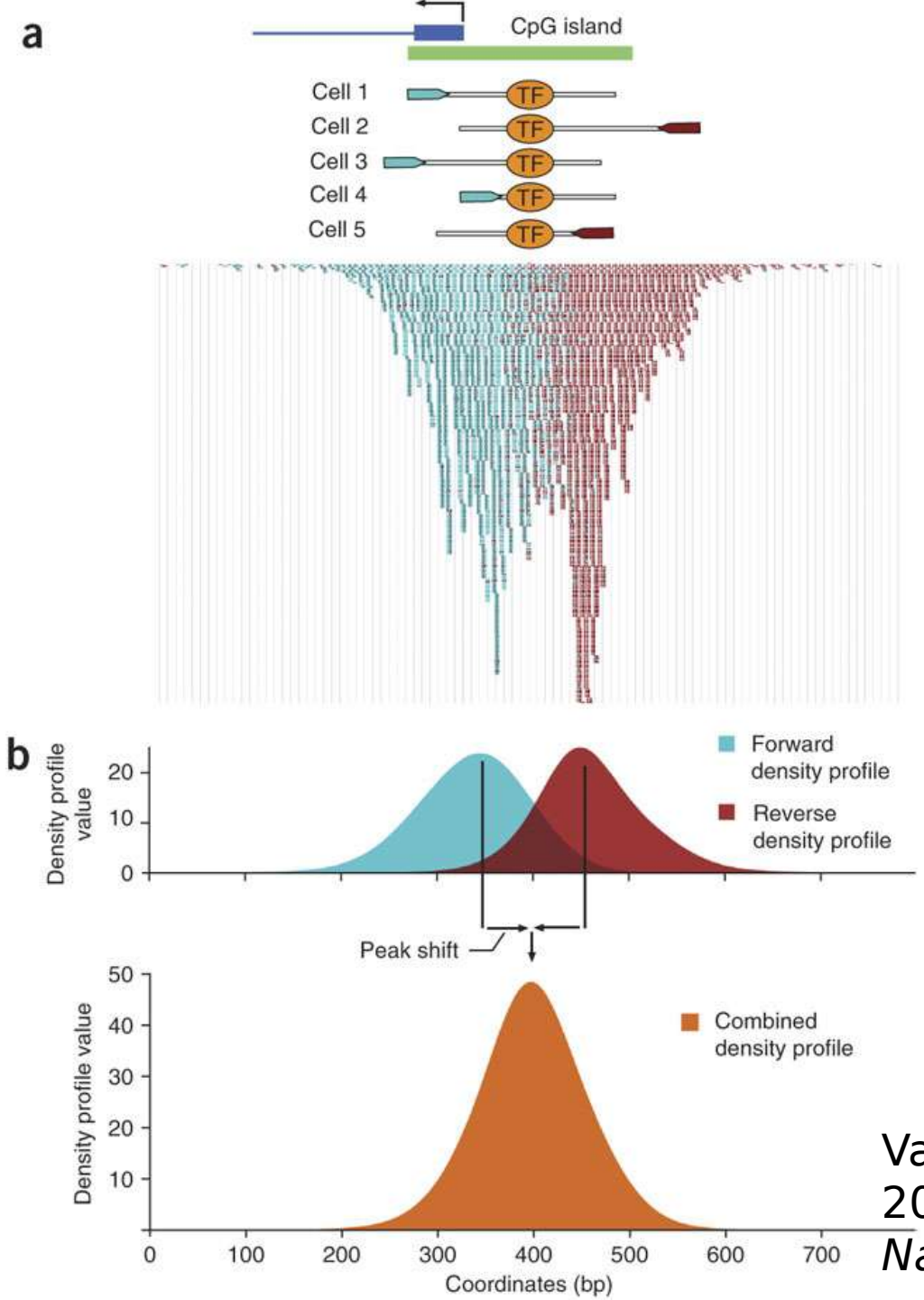


Derrien et al. 2013.
PLoS ONE

Peal calling, infer the shift size



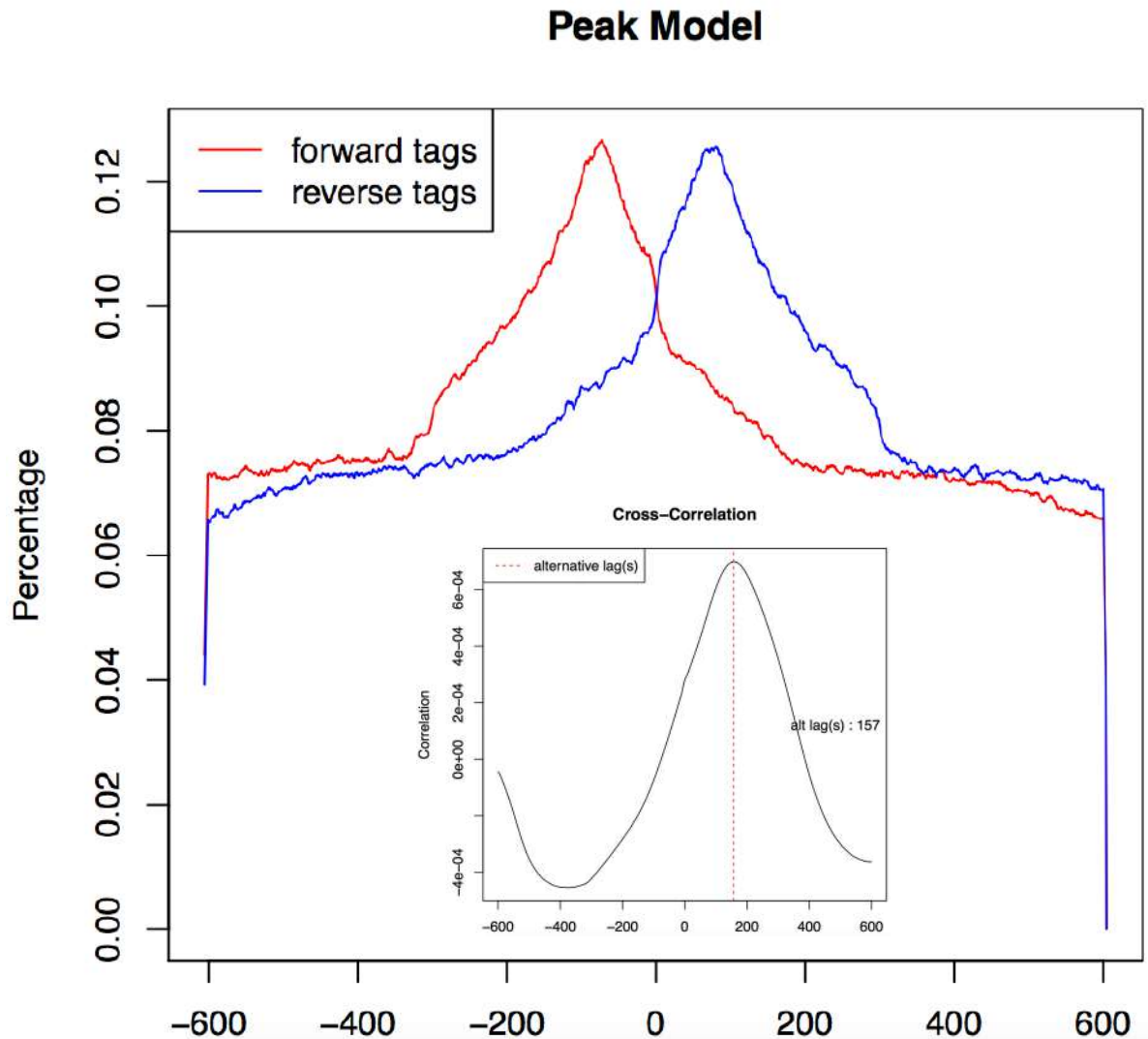
Bailey et al.
2013.
PLoS Comp. Biol.



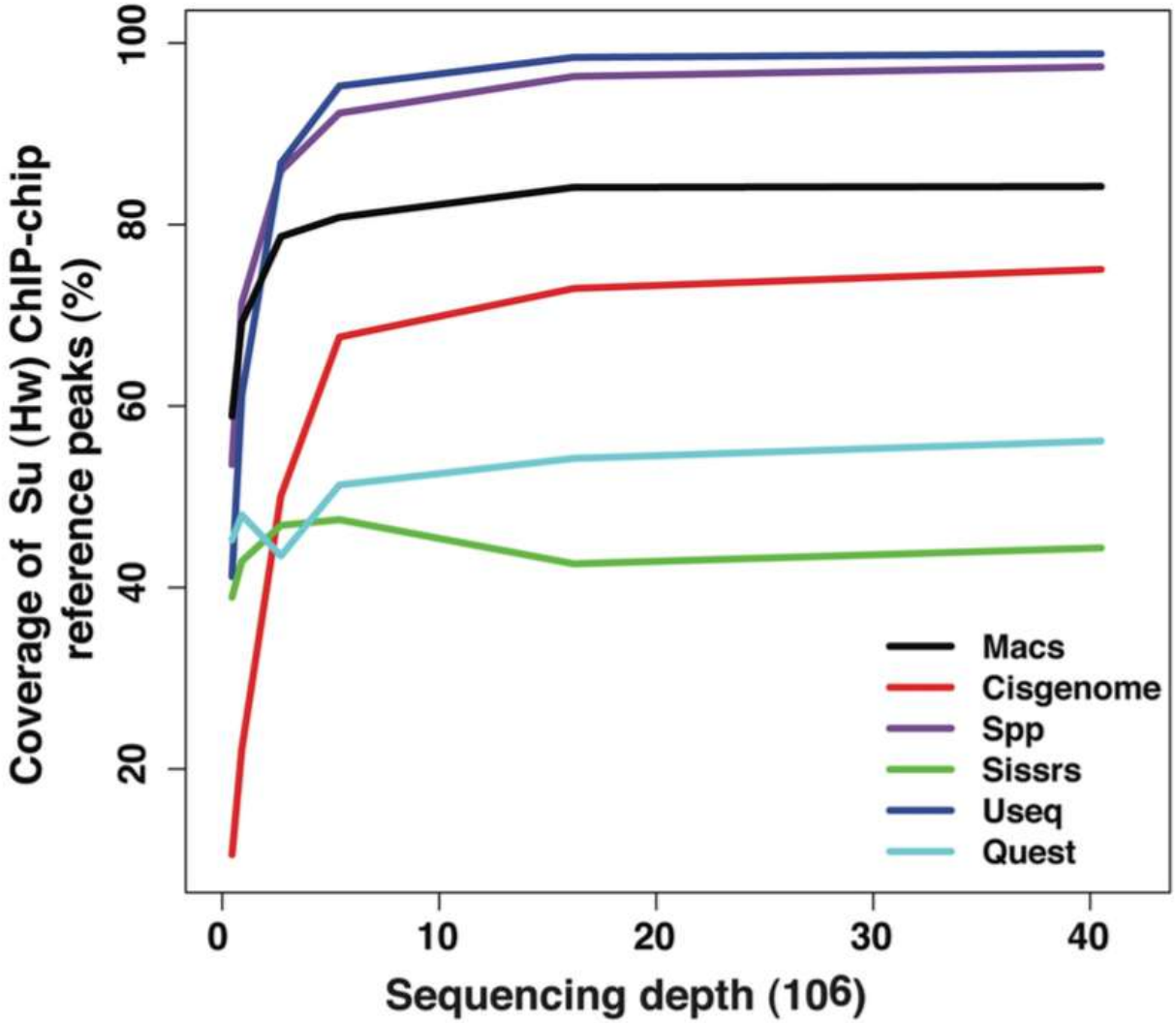
Valouev et al. 2008. *Nat. Methods*

Shift modeling: MACS2

Given a sonication size (*bandwidth*) and a high-confidence fold-enrichment (*mfold*), MACS slides *2bandwidth* windows across the genome to find regions with tags more than *mfold* enriched relative to a random tag genome distribution

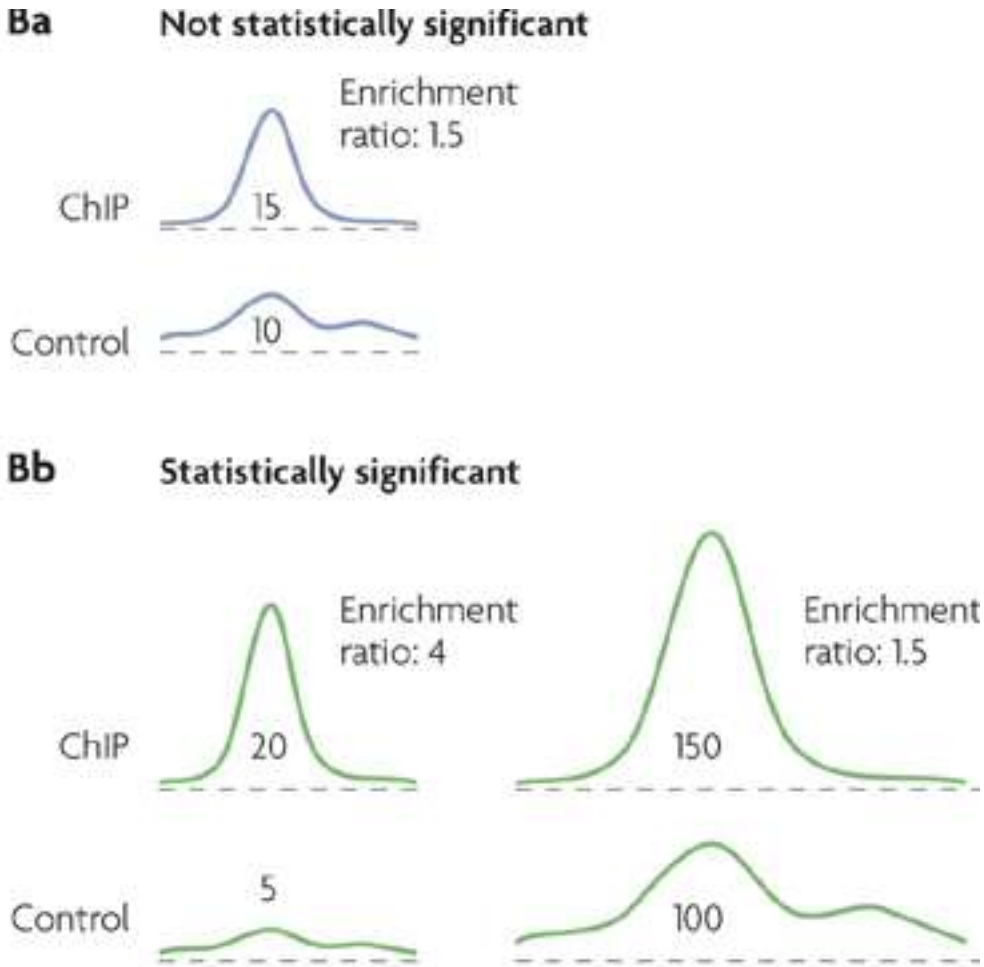


Sequencing depth

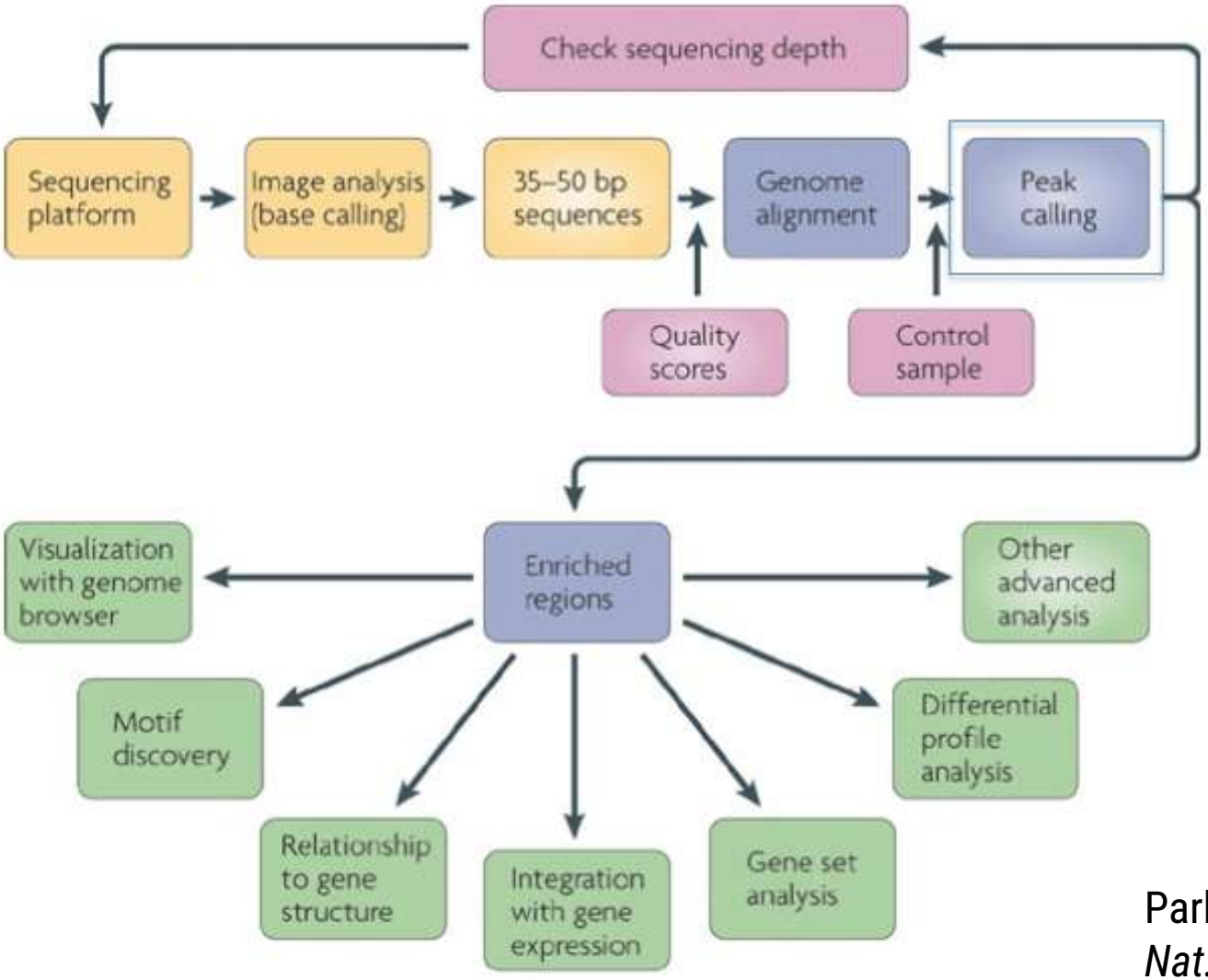


Chen et al. 2013.
Nat. Methods

Sequencing depth



Park et al. 2009.
Nat. Rev. Genet.



Park et al. 2009.
Nat. Rev. Genet.