diagenode

Innovating Epigenetics Solutions

WELCOME TO DIAGENODE

ChIP Workshop

Jessica Apulei & Juri Kazakevych

16-17 February 2021

Jessica Apulei

WHO AM I?

- Inside sales representative and technical support specialist at Diagenode
- PhD at Collège de France, Paris , France 2015-2019
- Postdoc at Harvard University, Cambridge, Boston MA 2019-2020

Juri Kazakevych

WHO AM I?

- Inside sales representative and technical support specialist at Diagenode since 2019
- PhD in Mainz, Germany 2012-2016
- Postdoc in Cambridge, UK 2016-2019

OBJECTIVES

Day 1

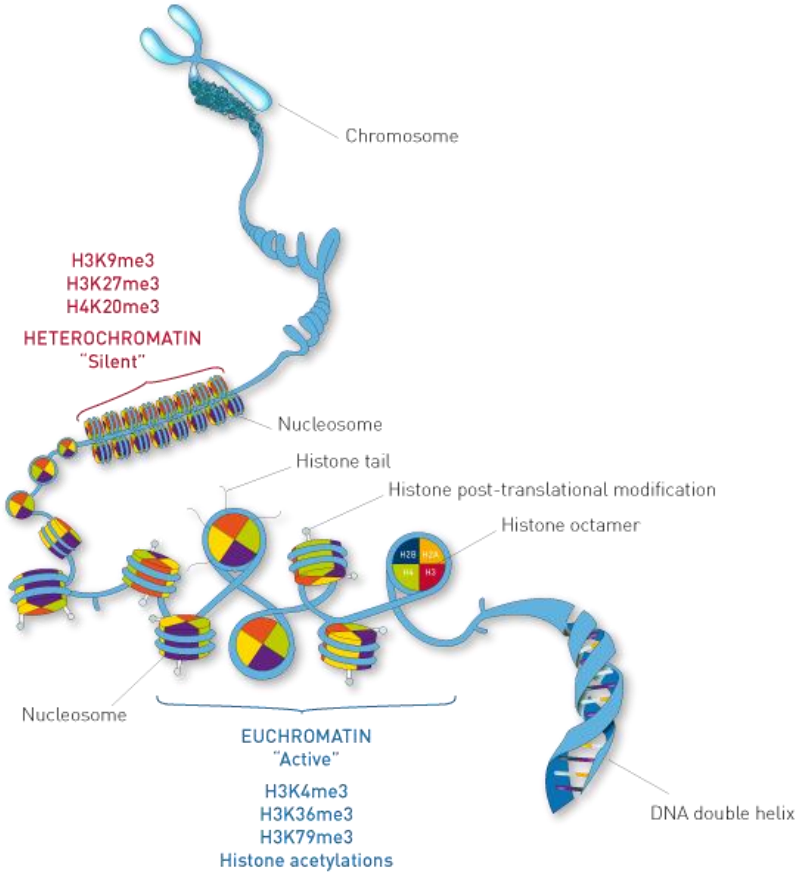
- ChIP overview
  - Chip-qPCR vs. ChIP-Seq
- Chromatin preparation
  - Fixation, Cell lysis and Chromatin shearing
- Setting up IP
  - Antibodies, Replicates, inputs, controls

Day 2

- ChIP-qPCR
- ChIP-seq: library prep & sequencing
- ChIP-seq: analysis
- Overview of Alternate methods

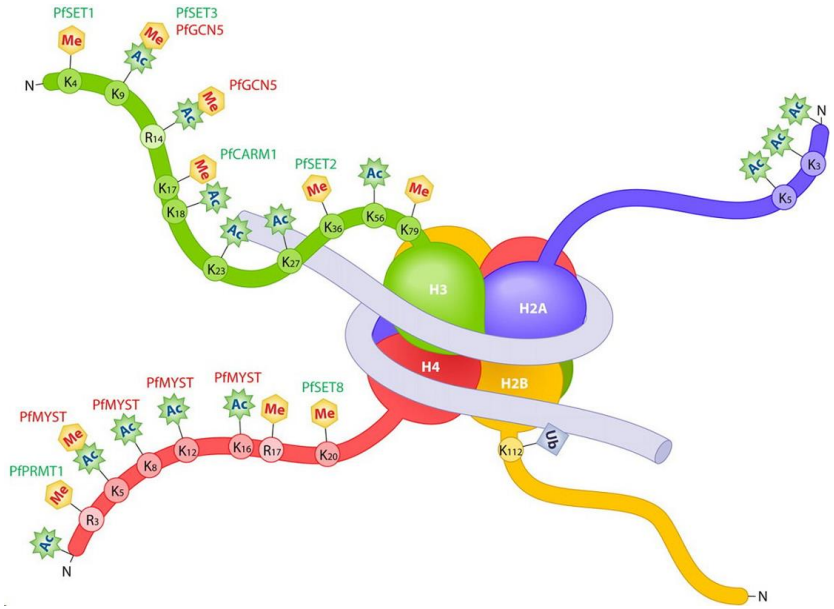
What is Chromatin?

A complex of DNA and proteins found in eukaryotic cells



What is Chromatin?

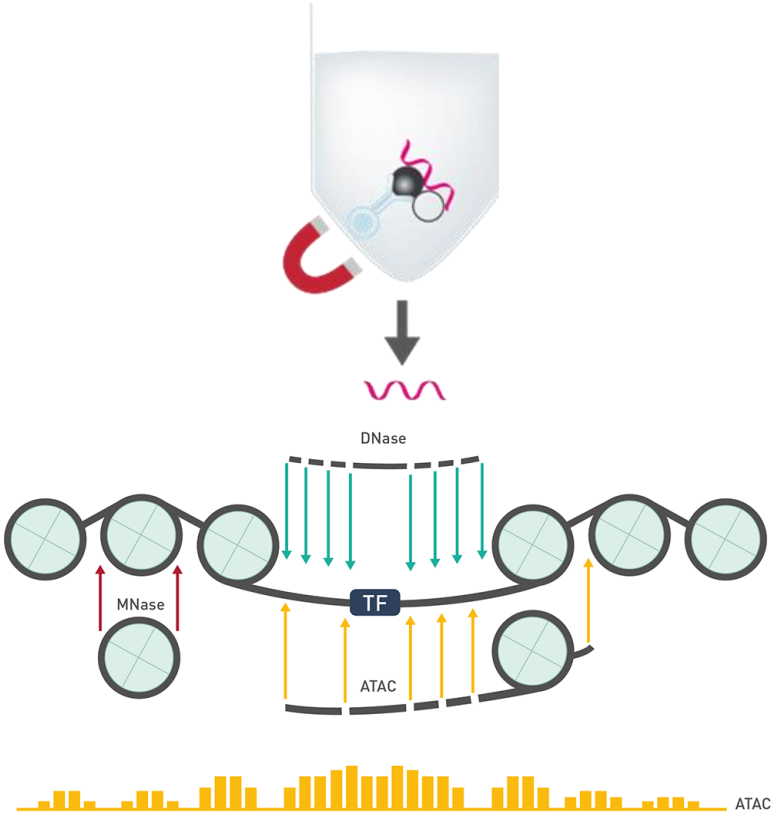
- Identifying genome-wide DNA binding sites for histones, transcription factors and other proteins
- Defines transcription factor (TF) binding sites
- Reveals gene regulatory networks in combination with RNA sequencing and methylation analysis



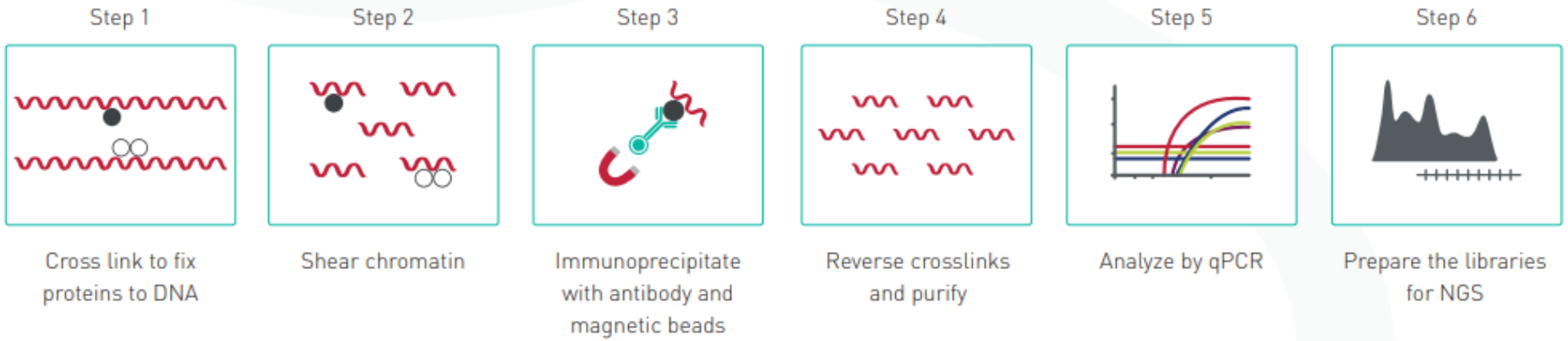
CHROMATIN ANALYSIS

- Interaction between proteins and DNA (immuno- assays)
  - ChIP-qPCR
  - ChIP-Seq
  - Cut&Run and Cut&TAG

- Methods to study chromatin accessibility (non-immuno assays)
  - ATAC-seq



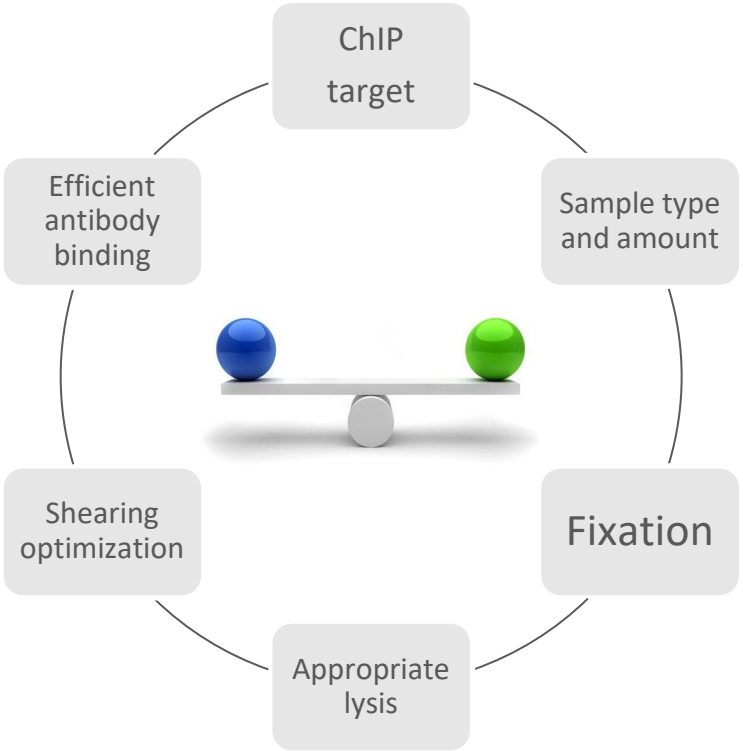
Workflow: Chromatin ImmunoPrecipitation (ChIP):



ChIP-qPCR or ChIP-Seq?

ChIP-qPCR	ChIP-Seq
Single-locus data QC step for ChIP-seq	Genome-wide data suitable for exploratory analysis
Low-cost Fast	High sequencing costs Longer protocol High sequencing turnaround time

Summary – Tips to Prepare Good Chromatin



Guide for successful chromatin preparation using the Bioruptor® Pico

https://www.diagenode.com/files/protocols/bioruptor-pico-chromatin-preparation-guide.pdf

Starting material: Cells and Tissues

- **Cells**
  ChIP: 1 million/IP for histones, 4 million/IP for TF (less depending on histone/TF)
  low-input ChIP: 10k/IP for histones

- **Tissues**
  Amount – 20-30 mg/IP
  Dounce homogenization for soft tissues (e.g. liver or brain)
  Bead beater like TissueLyser for hard fibrous frozen tissues (e.g. muscles)

- **FFPE tissue**
  Challenging due to extensive crosslinking
  Heptane instead of xylene for de-paraffinization -> easier, non-toxic workflow

Fixation

- Covalent stabilization of protein-DNA interactions; Reversible
  - Directly in medium for weak or rare protein-DNA interaction
  - For histone marks, cells can be resuspended by trypsinization before fixation

- Common fixative: Formaldehyde
  - Fresh
  - Methanol-free not mandatory

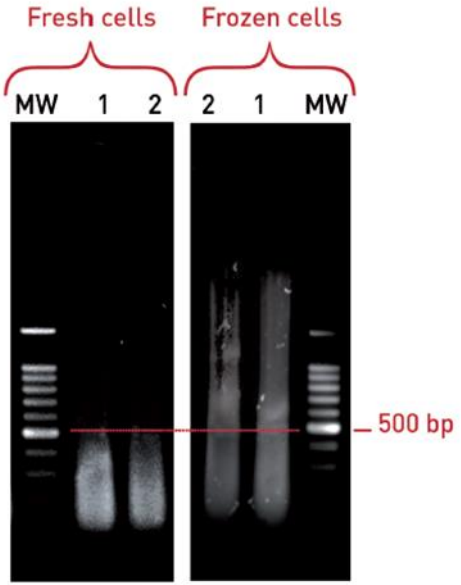
Target / Fixator	Formaldehyde	ChIP Cross-link Gold C01019021
Histones	Yes (8-10 min)	No need
Transcriptional factors directly bound to DNA	Yes (10-20 min)	No need
Indirect higher order and/or dynamic interactions	Yes (10-15 min)	Yes (30-45 min)

Cell Lysis

- One step lysis – for low cell numbers
  - Lyse cells directly with an SDS-containing buffer

- Two step lysis – standard protocol, difficult cells
  - Remove soluble cytosolic proteins first
  - Improves sonication efficiency
  - Reduces background

- Tips/Tricks/Critical steps:
  - Incubate on ice to start lysis and get narrower fragments size
  - Centrifuge to remove soluble membranes and cytosol
  - Avoid freezing chromatin if possible



Stopping Points

Cells

- Fix cells, lyse, isolate & shear chromatin -> freeze
- Fix cells, lyse, isolate chromatin -> freeze
- Fix cells -> freeze

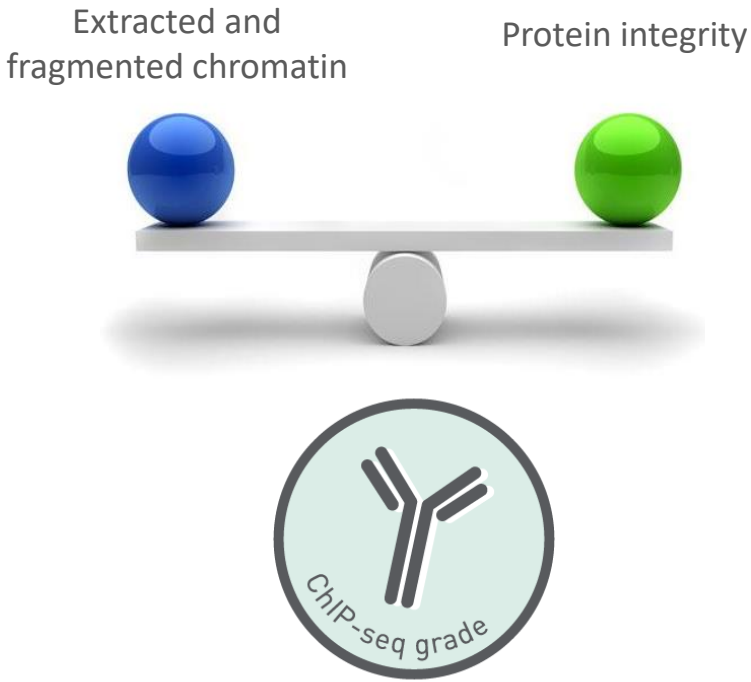
Tissues

- Fix tissue, lyse, isolate & shear chromatin -> freeze
- Freeze prior fixation

Optimal: Perform ChIP workflow directly, without freezing

Secrets of ChIP Success

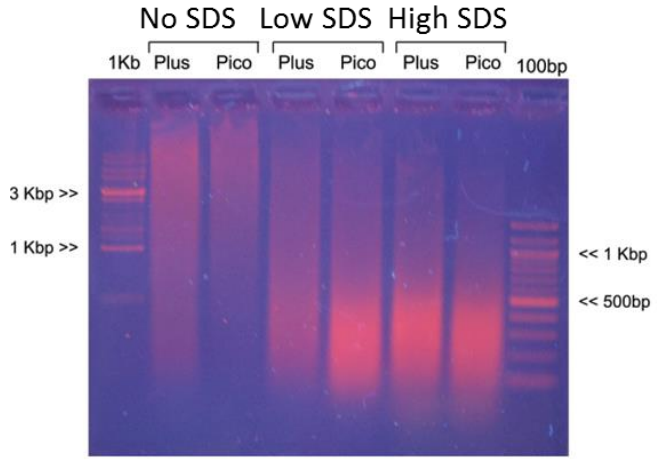
- Prepare “good” chromatin
  - Suitable fragment size and available epitopes
- Use a good antibody at the right concentration
- Optimize for highest specific signal and the lowest background

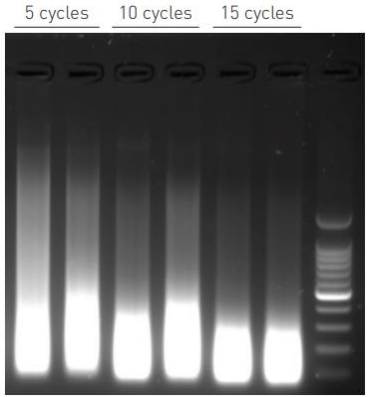


Chromatin Shearing

- 100-800 bp fragments, peak 200-500bp
- Use a good sonicator
  - Gentle - not to dislodge protein
  - Uniform and reproducible energy
  - Temperature control at 4°C
  - Multiplex and easy to use

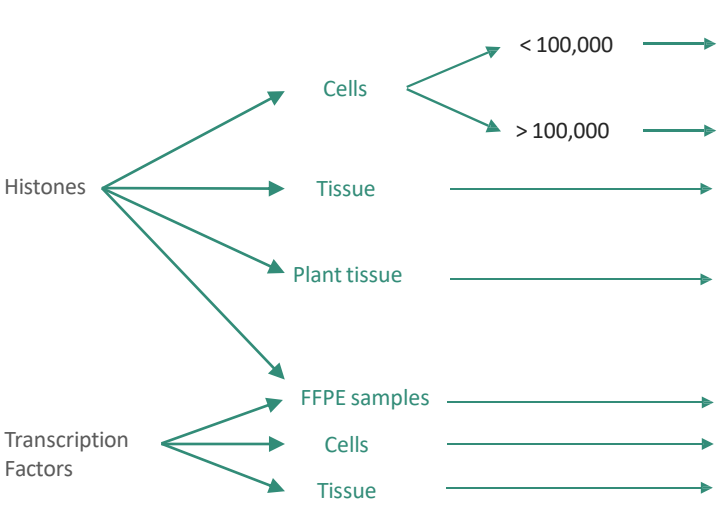
- Shearing buffer with detergents, preferably SDS
  - Increase sonication efficiency and chromatin yield
  - Improve epitope availability
  - Balance shearing and downstream IP
- Sample concentration
- Select the shortest time resulting in efficient shearing





Bioruptor Pico

Chromatin Shearing



Chromatin prep for ChIP on	*Sample type*	*Sample input*	*Kit*	*SDS concentration*	*Nuclei isolation*	*Compatible with ChIP kits*
Histones	Cells	< 100,000	**Chromatin EasyShear Kit High SDS**	**1%**	No	True MicroChIP Kit µChipmentation for Histones Kit
Histones	Cells	> 100,000	**Chromatin EasyShear Kit Ultra Low SDS**	**< 0.1%**	**Yes**	iDeal ChIP-seq for Histones Kit ChIPmentation for Histones Kit
Histones	Tissue					
Histones	Plant tissue		**Chromatin EasyShear Kit for Plant**	**0.5%**	**Yes**	Universal Plant ChIP-seq Kit
Transcription Factors	FFPE samples		**Chromatin EasyShear Kit Low SDS**	**0.2%**	**Yes**	iDeal ChIP-seq for TF Kit iDeal ChIP-qPCR Kit iDeal ChIP-FFPE Kit
Transcription Factors	Cells					
Transcription Factors	Tissue					

Chromatin Shearing

Chromatin EasyShear Kits

Kit of choice for:

- **Chromatin prep with Bioruptor**

Chromatin EasyShear Kit

+

Bioruptor

- **Chromatin optimization** prior to **ChIP kits**

Chromatin EasyShear Kit

+

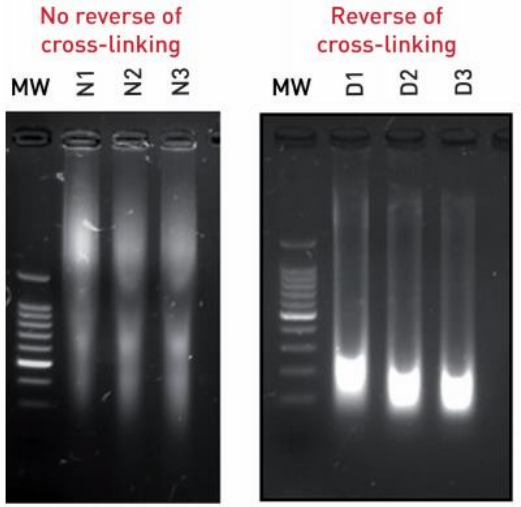
Diagenode's ChIP Kit

Features & Benefits

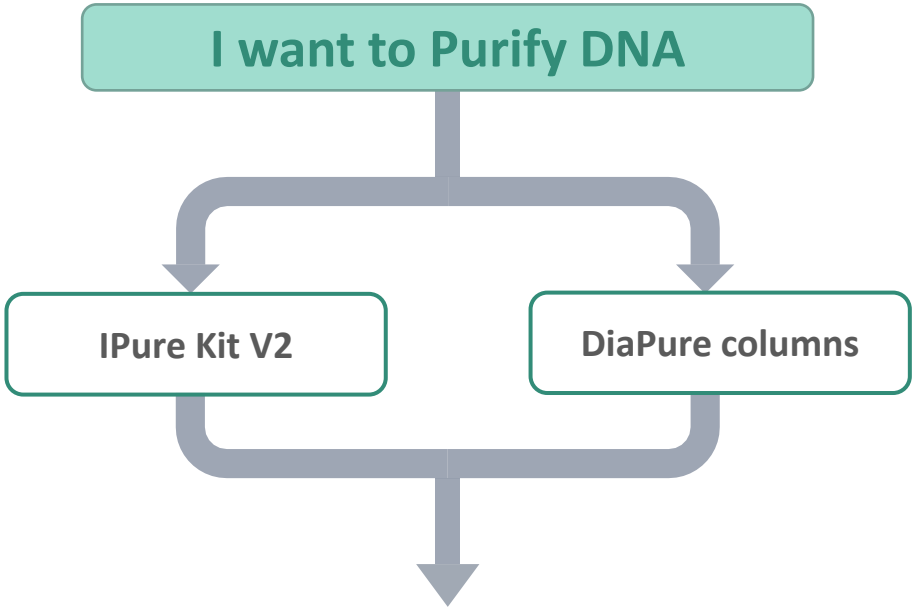
- Highly optimized for chromatin preparation
- Preserves epitope integrity
- Recommended for the optimization of the chromatin shearing of a new cell line/new sample type prior to ChIP
- Validated: Kit performance has been validated in ChIP-seq

Analyzing Fragment Size

- **De-crosslink**
  - Residual crosslinking retards migration
- **RNase treatment**
  - reduces background
- **DNA purification**
  - IPure beads + DiaMag magnetic rack
  - **Low inputs:** DiaPure columns (eluted in 6 µl)
- **Electrophoretic analysis**
  - 1.2 - 1.8% agarose gel
  - 300 ng or 60k cells per lane
  - **Low inputs:** FragmentAnalyzer, 2k cells



DNA Purification



Provides pure DNA for any downstream application (e. g. NGS)

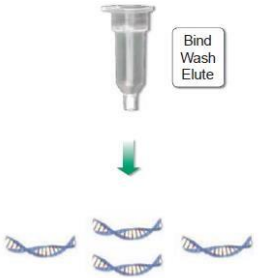
DNA Purification

IPure Kit v2

- Best yields
- Recovery of small amounts of DNA
- No toxic reagents (e.g. phenol/chloroform)
- Compatible with automation

MicroChIP DiaPure columns

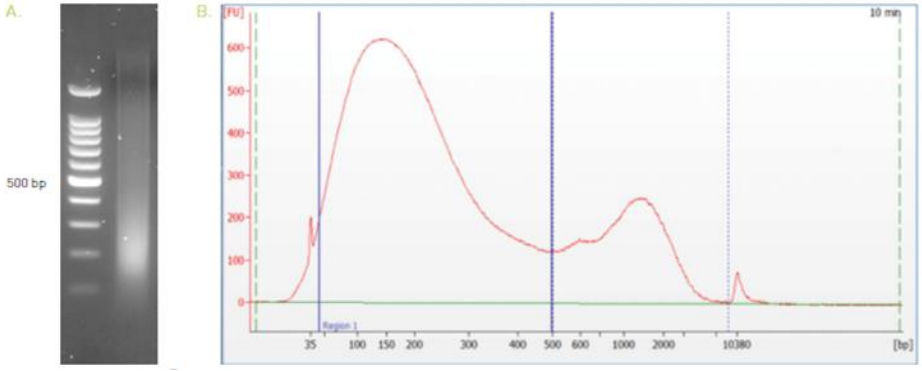
- Perfect for low concentrated samples (elution from 6 µl)
- DNA recovery 70-90% (50bp - 10kB)
- No toxic reagents (e.g. phenol/chloroform)



Analyzing fragment size

- Use agarose gel or fragment analyzer

- Bioanalyzer or Tapestation:
  - Over-representation of HMW fragments
  - Log-based -> visual misinterpretation of fragment distribution
  - More sensitive to overloading, incomplete reverse crosslinking and residual contaminants



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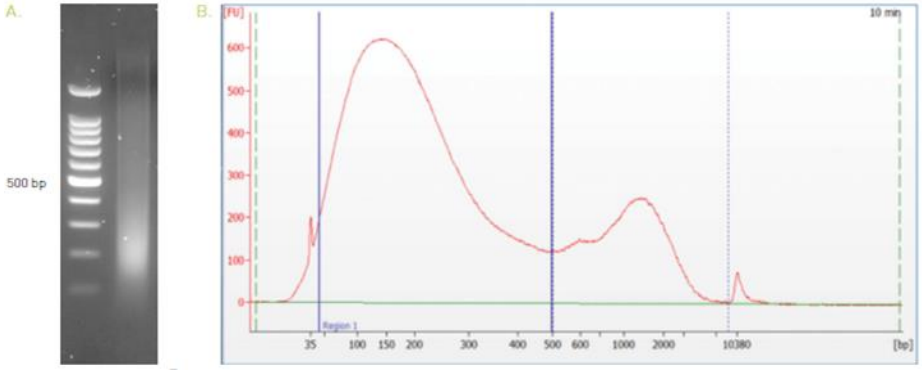
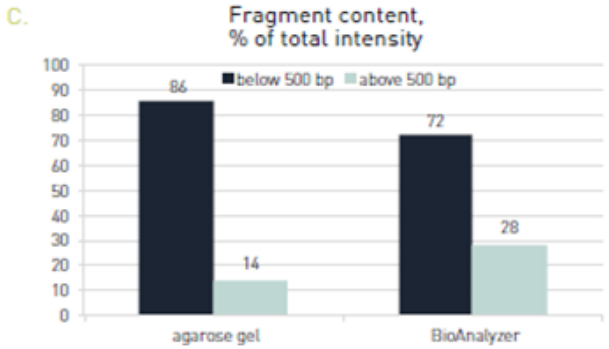
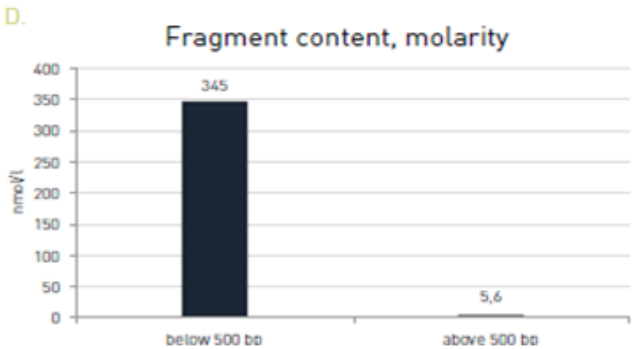


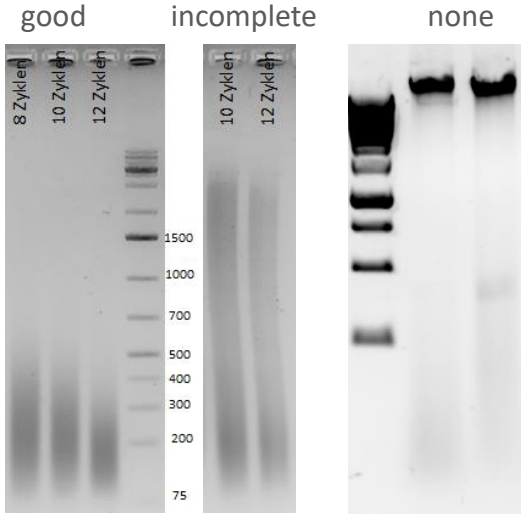




Troubleshooting Chromatin Shearing

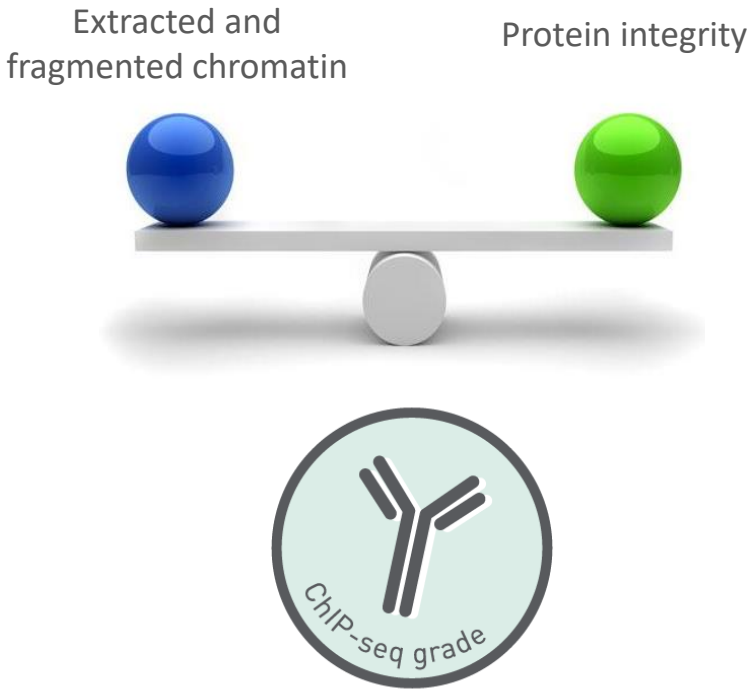
- **No shearing at all**
  - Incomplete lysis – check buffer composition
  - Check instrument efficiency - QC test on sonicator

- **Incomplete shearing**
  - Over-fixation: check fixative and duration
  - Too high cell density
  - Changes in sample require adjustment of shearing protocol
    - Fresh vs. Frozen chromatin
    - Different sample types
  - Wrong consumables (tubes)
  - Sample out of sonication focus
    - droplets on walls/lid of tube
    - Wrong sample volume
  - Wrong temperature (should be 4°C for chromatin)
  - None of the above? -> Check instrument efficiency - QC test on sonicator

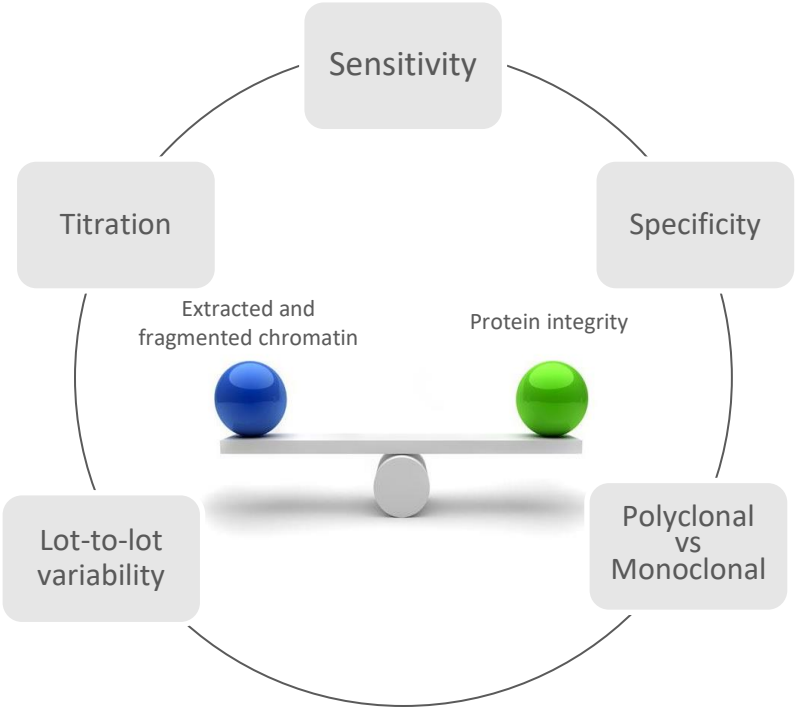


Secrets of ChIP Success

- Prepare “good” chromatin
  - Suitable fragment size and available epitopes
- Use a good antibody at the right concentration
- Optimize for highest specific signal and the lowest background



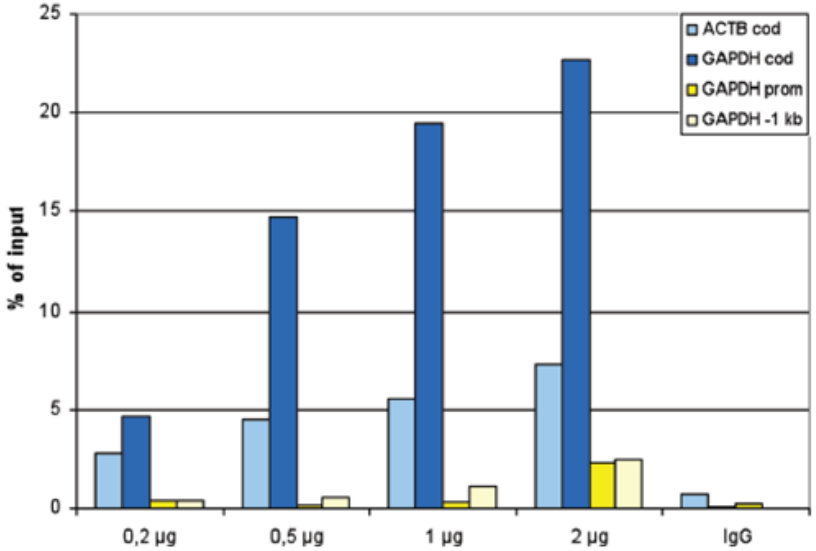
Antibodies for ChIP

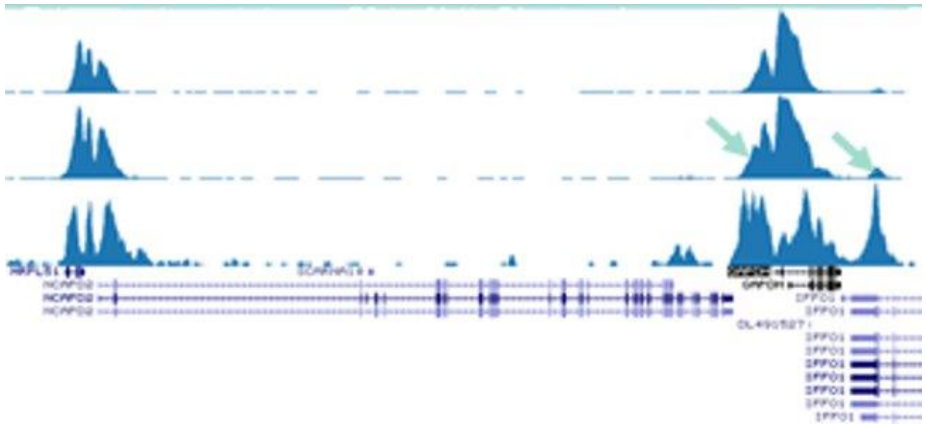


https://www.diagenode.com/en/categories/chip-seq-grade-antibodies

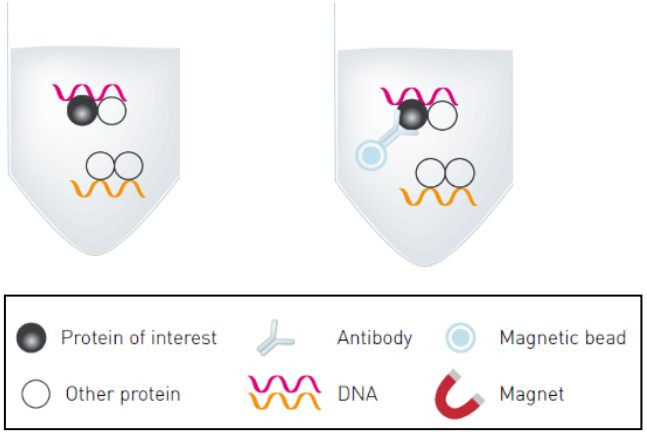
Antibodies for ChIP

Polyclonal H3K36me3 antibody titration (Diagenode C15410192)
1µg IgG as negative IP control
Chromatin from 100.000 cells





Setting up IP



Components:

- Sheared chromatin
- **ChIP grade antibodies**
  -> optimized quantity
- ProteinA/G magnetic beads
- ChIP buffer
- Protease inhibitor cocktail

Antibodies for ChIP – What beads?

Agarose beads

Required: centrifuge

Sensitive to handling

High background

Risk of carry-over

Magnetic beads

Required: magnetic rack

Robust

Low background

Easy separation

Limit antibody amounts to bead capacity!

Protein G or A beads

- Both bind to IgG antibodies and are structurally similar
- Slightly different affinities for IgG subclasses across different species.
- Use appropriate depending on the IgG subtype you are using:

Protein A

Rabbit
Pig
Dog
Cat

Protein G

Mouse
Rat
Human

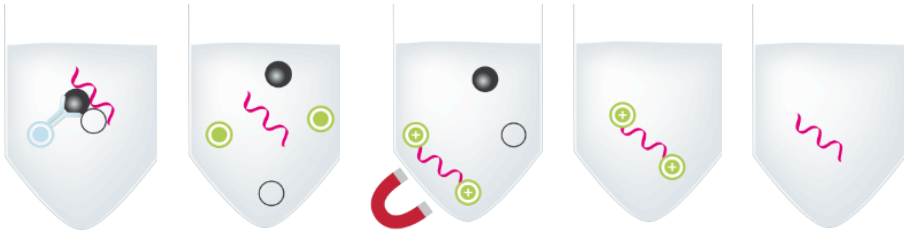
Setting up IP: Input Sample

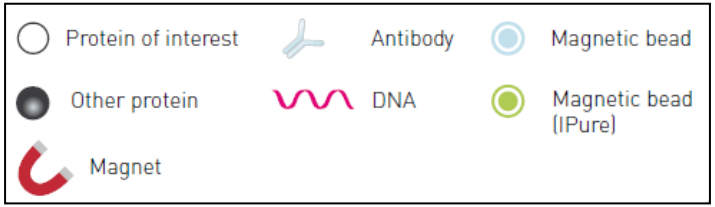
- Fraction of sheared chromatin is kept aside as INPUT
  - Processed in parallel with IP-samples from reversed crosslinking
  - Include one input for each chromatin sample
- Key reference for ChIP-qPCR and ChIP-seq analysis
- ChIP-qPCR: used to calculate the recovery (% of input)
- ChIP-seq: mandatory for bio-informatics analysis
  - Normalization for mappability of a region, avoid duplication bias etc.
  - Input pooling can be considered for ChIP-seq on very similar samples

Setting Up IP: Additional Controls

- Positive control (H3K4me3, CTCF):
  - Confirm overall efficiency of ChIP workflow
  - ChIP optimization for new target
- Negative Control (IgG)
  - Measure of non specific IP background
  - Include one negative IgG control in each series of ChIP reactions
- Not necessary to sequence these but good control for qPCR
- Biological Replicates
  - ChIP-qPCR ≥3
  - ChIP-seq ≥2

ChIP Protocol – Elution, de-crosslinking and DNA isolation



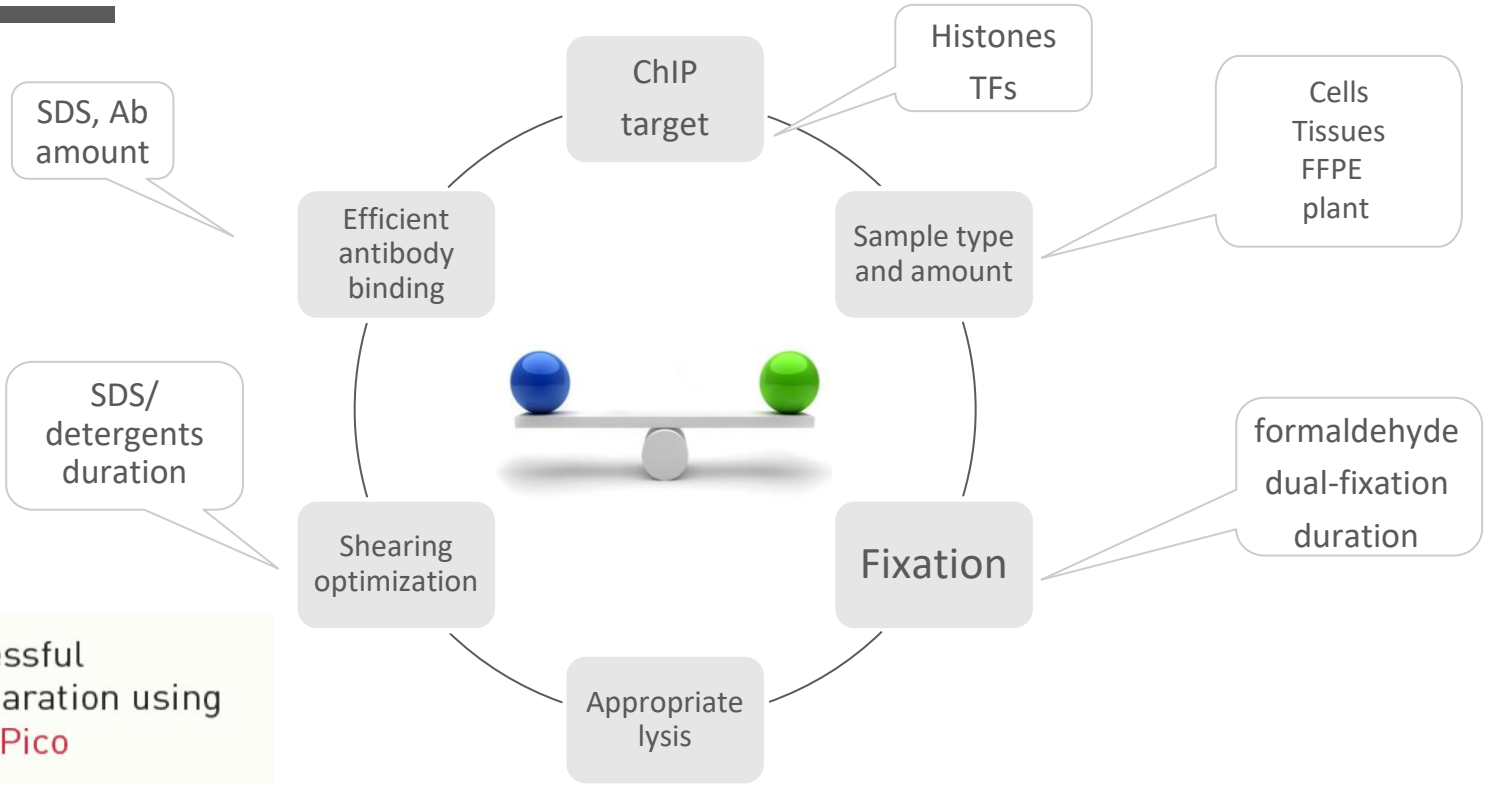


- Elution of the chromatin complexes from protein A/G-bound magnetic beads:
  elution buffer 30 min at RT

- Reversal of cross-links:
  Incubation for at least 4h at 65°C

- Isolation of the ChIP'd DNA:
  IPure magnetic beads
  Column purification (DiaPure columns for low elution volumes >6µl)

Summary – Tips to Prepare Good Chromatin



Guide for successful chromatin preparation using the Bioruptor® Pico

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Fastest Fingers Quiz

Fastest Fingers Quiz

Can I use formaldehyde that has been open for 3 months for fixing cells?

A. Yes, it is not an issue as long as you make a fresh dilution

B. No, open fresh bottle

Fastest Fingers Quiz

I am working with tissues, but I do not have time to shear chromatin today. What should I do?

A. Fix tissues, lyse and freeze chromatin - shear later

B. Fix tissues and freeze - lyse and shear chromatin later

C. Freeze fresh tissue - fix, lyse and shear chromatin later

Fastest Fingers Quiz

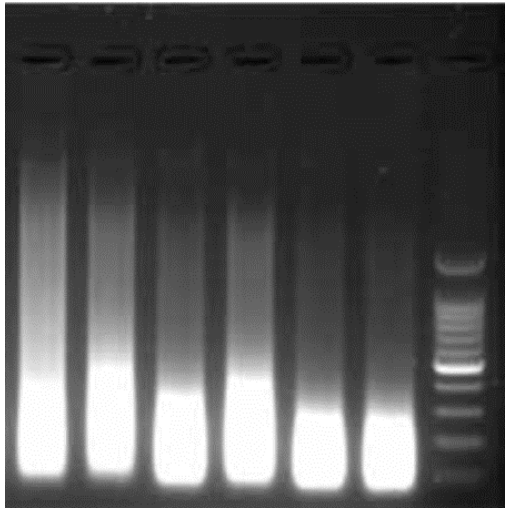
Which cycle in the image would you use for chromatin shearing?

A. 5 cycles

B. 10 cycles

C. 15 cycles

5 cycles 10 cycles 15 cycles



500 bp

First correct answer in the chat box wins

diagenode

Innovating Epigenetics Solutions

WELCOME TO DIAGENODE

ChIP Workshop

Jessica Apulei & Juri Kazakevych

16-17 February 2021

OBJECTIVES

Day 1

- ChIP overview
  - Chip-qPCR vs. ChIP-Seq
  - Chromatin preparation
    - Fixation, Cell lysis and Chromatin shearing
- Setting up IP
  - Antibodies, Replicates, inputs, controls

Day 2

- ChIP-qPCR: set-up
- ChIP-qPCR: analysis
- ChIP-seq: library prep & sequencing
- ChIP-seq: analysis
- Overview of Alternate methods

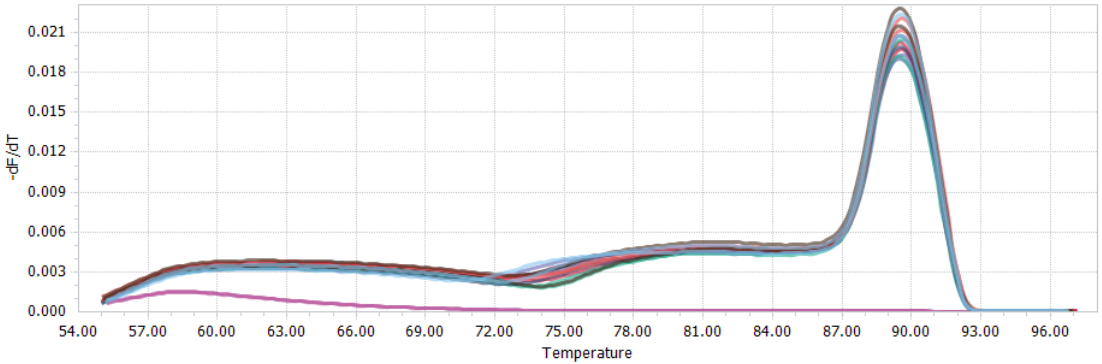
ChIP-qPCR

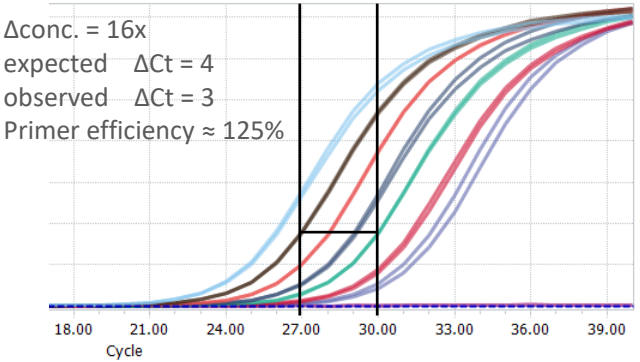
- Target & Primer selection is key for ChIP-qPCR
- Predict qPCR-targets from ChIP-seq data
- qPCR as QC prior ChIP-seq
- If no ChIP-seq data:
  estimate binding from similar data, biological function etc.
  -use multiple regions
- PCR program depends on Master Mix, qPCR system and primer pairs

Setting up ChIP-qPCR

- **Target primer design:**
  - Place primers around binding site
  - 50-150bp amplicons
  - 20-30 bp primers with a similar Tm between 55° and 60°C

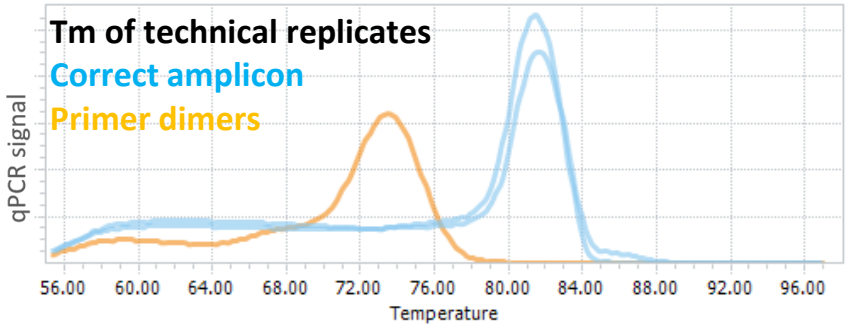
- **Primer pair validation:**
  - Check on gDNA/input for T_m profile
  - Check efficiency (95-105% acceptable)





Setting up ChIP-qPCR

- **QC**
  - T_m: no second peaks, no primer dimers
  - technical replicates within 0.3 Ct
  - Ct values >>30 are often not reliable



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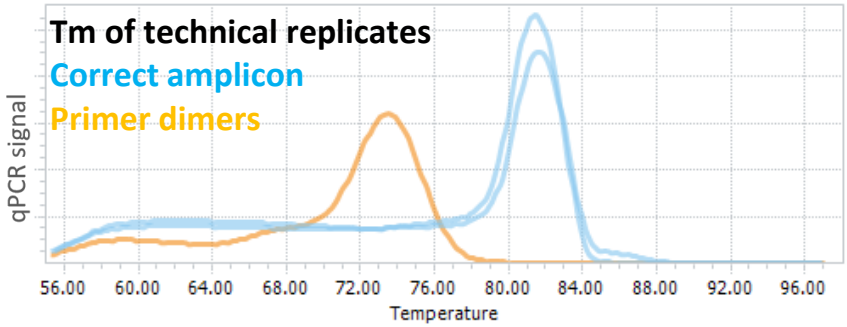
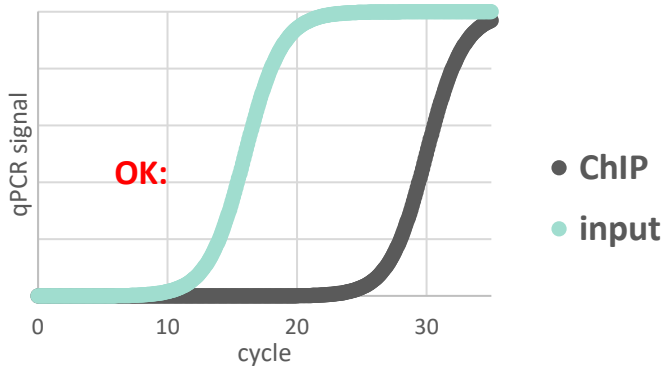
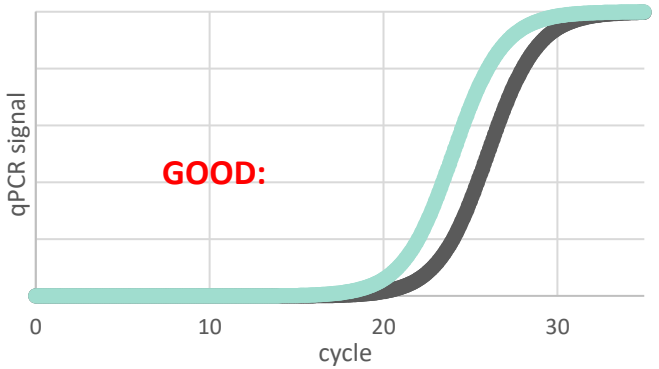


- **ChIP and input samples**
  - Adjust amount of ChIP-sample/input to obtain comparable Ct values
  - Consider primer efficiency for high ΔCt





ChIP-qPCR analysis

ChIP recovery *R*:

- chromatin recovery as % of Input
- R should be minimal for the IgG control and high for the epitope of interest

$$R = \frac{2^{Ct\,(input)} - Ct(ChIP)}{100\,(input\ fraction)}$$

-> for each target separately

Input fraction is often corrected with a logarithmic compensatory factor, e.g. -6.64 Ct for 1% input

ChIP fold-enrichment *F* with ΔΔCt method:

- fold-enrichment of bound vs. epitope-"free" regions
- S varies depending on regions analyzed

$$F = \frac{R(positive\ region)}{R(negative\ region)}$$

-> main success parameter

Successful ChIP?

- If wrong regions targeted – risk of false negative result
- ***F*** > 2 for ChIP-qPCR analysis
- ***F*** > 4 for ChIP-seq

ChIP-qPCR Exercise

Conditions: untreated (A), treated (B)
Targets: positive control (e.g. GAPDH) (P), genes of interest (G1, G2) intergenic region (N)
Antibodies: IgG, H3K4me3

Ct values

A

	IgG		H3K4me3		Input (1% of sample)	
P	34.0	36.0	26.0	26.1	27.0	27.1
G1	35.0	35.0	27.0	27.2	26.0	25.7
G2	-	37.0	33.0	34.0	29.0	29.6
N	34.0	35.0	33.0	33.5	28.0	28.1

B

	IgG		H3K4me3		Input (1% of sample)	
	-	36.4	25.4	25.5	26.5	26.6
	35.4	36.4	26.4	26.6	25.4	25.1
	34.4	33.4	28.7	28.5	28.6	28.7
	35.4	-	32.4	33.4	27.4	27.5

ChIP-qPCR Exercise

Conditions: untreated (A), treated (B)
Targets: positive control (e.g. GAPDH) (P), genes of interest (G1, G2) intergenic region (N)
Antibodies: IgG, H3K4me3

Ct values

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G2	-	37.0	33.0	34.0	29.0	29.6
N	34.0	35.0	33.0	33.5	28.0	28.1

B

	IgG		H3K4me3		Input (1% of sample)	
	-	36.4	25.4	25.5	26.5	26.6
	35.4	36.4	26.4	26.6	25.4	25.1
	34.4	33.4	28.7	28.5	28.6	28.7
	35.4	-	32.4	33.4	27.4	27.5

1. Technical sanity check

- values out of range
- high Ct-variation (>0.3) between technical replicates
- A/B inputs shifted
- Ct(H3K4me3) ≈ Ct(input)

ChIP-qPCR Exercise

Conditions: untreated (A), treated (B)
Targets: positive control (e.g. GAPDH) (P), genes of interest (G1, G2) intergenic region (N)
Antibodies: IgG, H3K4me3

2. **Averaging Technical replicates**

	A			B		
	IgG	H3K4me3	Input (1% of sample)	IgG	H3K4me3	Input
P	35.0	26.1	27.1	36.4	25.5	26.6
G1	35.0	27.1	25.9	35.9	26.5	25.3
G2	37.0	33.5	29.3	33.9	28.6	28.7
N	34.5	33.3	28.1	35.4	32.9	27.5

3. **Biological Sanity Check**

- Ct(P) < Ct(N) for H3K4me3
- Ct(H3K4me3) << Ct(IgG)

ChIP-qPCR Exercise

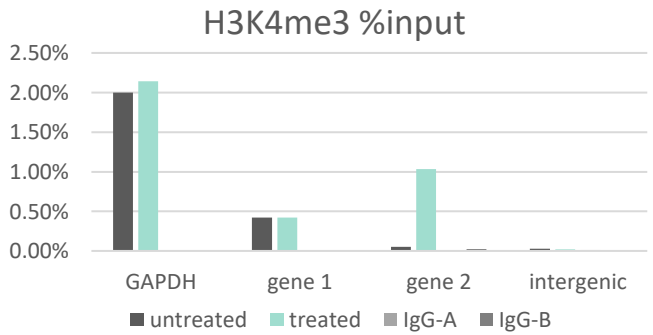
Conditions: untreated (A), treated (B)
Targets: positive control (e.g. GAPDH) (P), genes of interest (G1, G2) intergenic region (N)
Antibodies: IgG, H3K4me3

	A			B		
	IgG	H3K4me3	Input (1% of sample)	IgG	H3K4me3	Input
P	35.0	26.1	27.1	36.4	25.5	26.6
G1	35.0	27.1	25.9	35.9	26.5	25.3
G2	37.0	33.5	29.3	33.9	28.6	28.7
N	34.5	33.3	28.1	35.4	32.9	27.5

4. **Recovery (% of input)**

$$R = \frac{2^{Ct\,(input)} - Ct(ChIP)}{100\,(input\ fraction)}$$

	A	IgG-A	B	IgG-B
P	2.00%	0.00%	2.14%	0.00%
G1	0.42%	0.00%	0.42%	0.00%
G2	0.05%	0.00%	1.04%	0.03%
N	0.03%	0.01%	0.02%	0.00%



ChIP-qPCR Exercise

Conditions: untreated (A), treated (B)
Targets: positive control (e.g. GAPDH) (P), genes of interest (G1, G2) intergenic region (N)
Antibodies: IgG, H3K4me3

H3K4me3 % of input

	A	B
P	2.00%	2.14%
N	0.03%	0.02%

5. **ChIP fold-enrichment**

$$F_A = \frac{R(P_A)}{R(N_A)} = 74x\ enrichment$$

$$F_B = \frac{R(P_B)}{R(N_B)} = 94x\ enrichment$$

ChIP-qPCR Exercise

Conditions: untreated (A), treated (B)
Targets: positive control (e.g. GAPDH) (P), genes of interest (G1, G2) intergenic region (N)
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H3K4me3 % of input

	A	B
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$$F_B = \frac{R(P_B)}{R(N_B)} = 94x\ enrichment$$

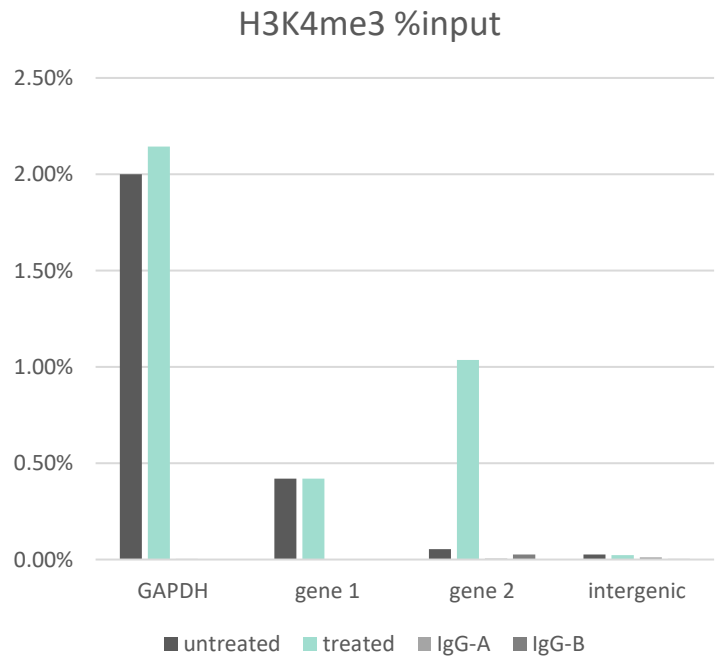
6. **Assessment**
   - ***F***>2 ChIP-qPCR qualified
   - ***F***>4 ChIP-seq qualified

7. **Optimization**
   - if ***R*** or ***F*** are low, optimize ChIP parameters

DIAGENODE

ChIP-qPCR Analysis summary

- Determine ChIP-recovery and fold-enrichment
- input used as reference to calculate ChIP-recovery
- Each ChIP-target requires specific control regions
- Suitable control regions can vary among samples



Fastest Fingers Quiz

Fastest Fingers Quiz

You did a histone ChIP-qPCR and got 1.5-fold enrichment. Should you go forward with seq?

A. Yes

B. No

Fastest Fingers Quiz

You performed a ChIP on a novel Transcription factor. You do not see an enrichment of positive control regions over negative (intergenic) ones. Which could be the reasons? (select all applicable)

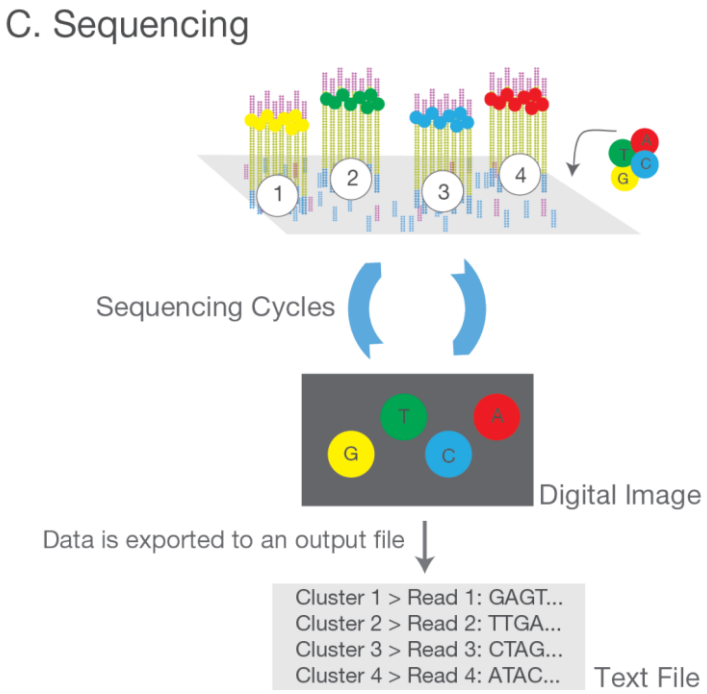
A. antibody used is not suitable for ChIP

B. ChIP ok but positive control regions are not bound by the TF

C. fixation protocol not adequate for targeted TF

D. Covid19

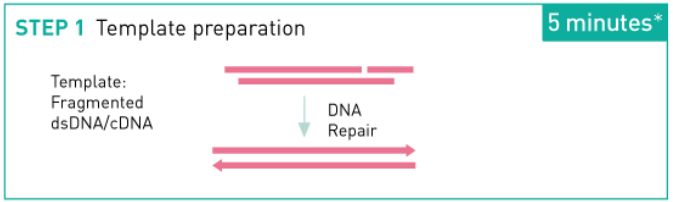
ChIP-seq: library prep

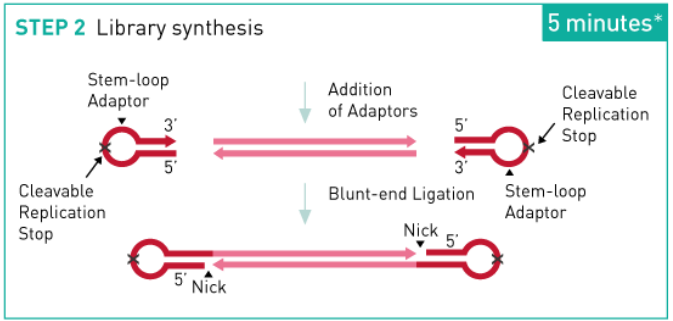


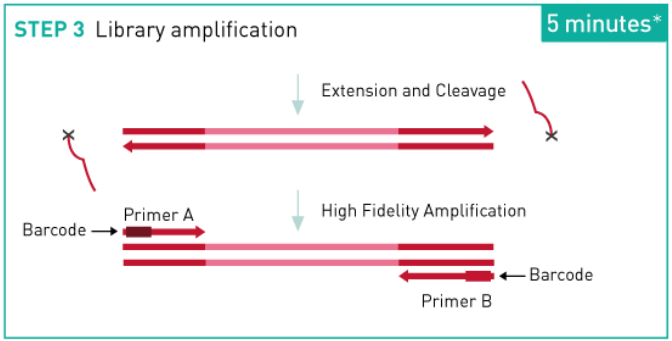
ChIP-seq: Library Prep

- Low input
- Minimal steps
  - To maximize recovery
- Sensitive
  - Minimal PCR amplification
- Suitable for pooling

MicroPlex kit workflow







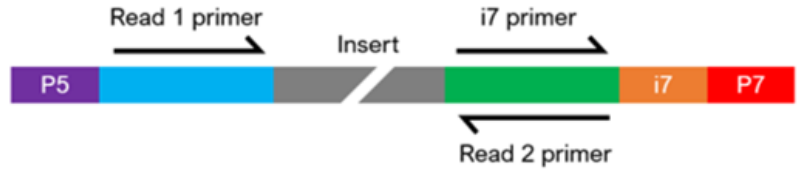
* hands-on-time

Benefits of Multiplexing

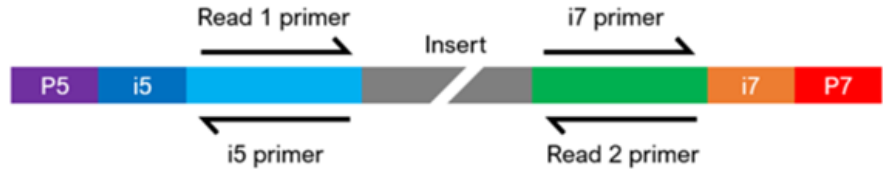
- **Fast High-Throughput Strategy:**
  - Large sample numbers can be simultaneously sequenced
- **Cost-Effective Method:**
  - Reduces time and reagent use
  - Cluster detection more efficient with different bases in beginning of read
- **Simplified Analysis:**
  - Automatic sample identification with "**barcodes**“ using Illumina software

Single and Dual-indexed Libraries

- **Single-index sequencing**
  - Low level of multiplexing
- **Dual indexing**
  - Higher multiplexing - more samples per lane possible
  - Higher accuracy of sample identification
- **Unique dual indexing (UDI)**
  - Allows filtering of index-hopping events

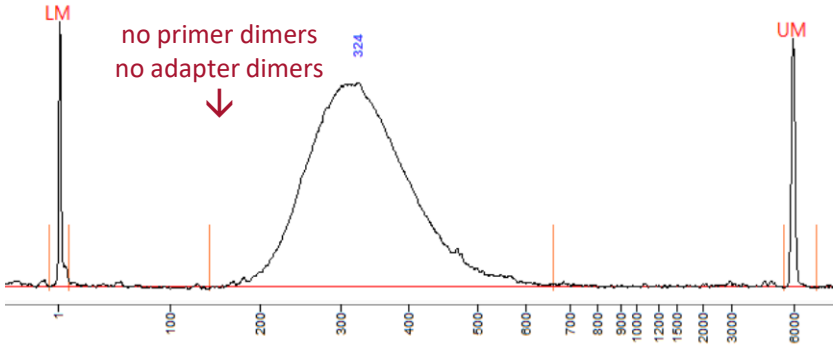


Dual-Indexed Sequencing



Library Pooling

- **Determine library size**
  - Bioanalyzer or Fragment Analyzer
  - Identify adapter dimers or unexpected library sizes
- **Quantify**
  - Qubit
  - qPCR –quantify sequencable library
  - Convert from ng/µl to nM using average library size
- **Dilute and Pool normalized libraries**
  - Same size for best clustering



ChIP-seq: Sequencing Settings

Read length

- 50 bp sufficient for most ChIPs
- adjust fragment-size to read length

Sequencing depth

- mainly set by samples/flow cell and flow cell type
- 30 M reads for sharp peaking targets e.g. H3K4me3, H3K27ac
- 50 M for broadly distributed and abundant targets e.g. H3K27me3
- use same depth for input

Replicates

- ≥ duplicates
- increased replicate number will improve sensitivity of the downstream analysis

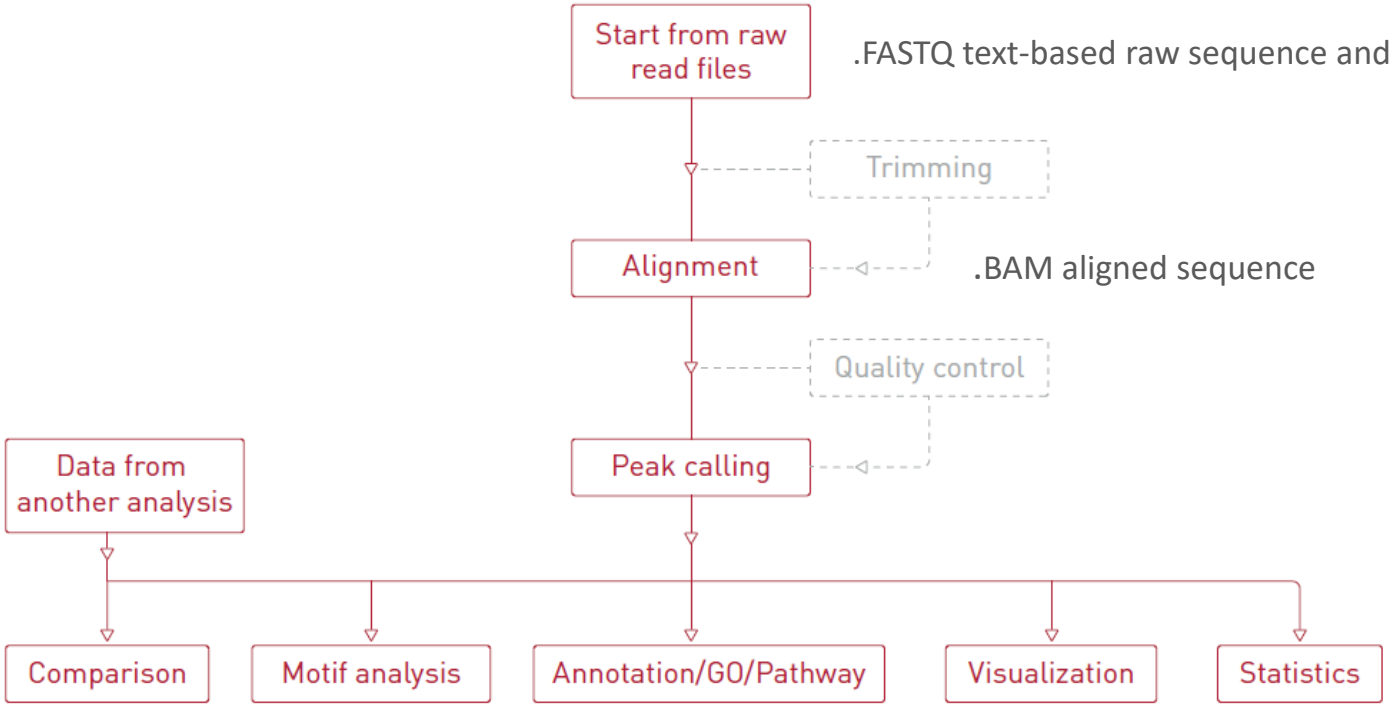
Input sequencing

- one input per sample is gold standard
- pooling inputs from replicates can often be considered

ChIP-seq: Analysis

Bioinformatician	R	https://www.r-project.org/
	free-ware and online tool kits	www.bioinformatics.babraham.ac.uk/projects/seqmonk/ biit.cs.ut.ee/gprofiler/gost
Wet-lab expert with free time	standard bio-informatic services	https://www.diagenode.com/en/categories/Services Comprehensive Multi-Omic and bio-info services
	free-ware and online tool kits	www.bioinformatics.babraham.ac.uk/projects/seqmonk/ initial & advanced data analysis, genome browser, graphical presentation of data https://biit.cs.ut.ee/gprofiler/gost Functional profiling tool
No expertise or no free time	advanced bio-informatic services	https://www.diagenode.com/en/categories/Services Comprehensive Multi-Omic and bio-info services

ChIP-seq: Analysis



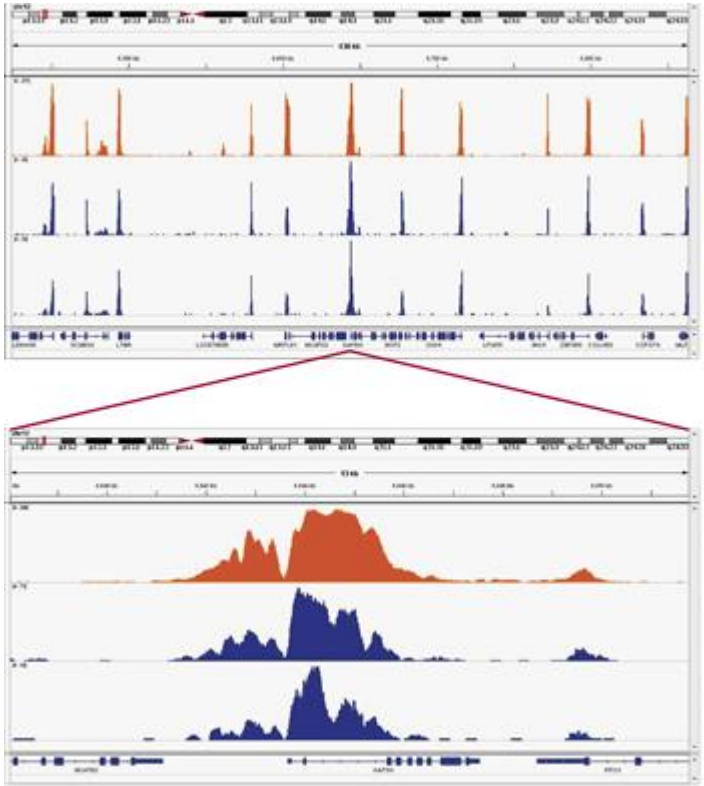
ChIP-seq: Analysis

Standard bioinformatic analysis:

- **alignment to reference genome**
- **peak calling**

Advanced bioinformatic analysis:

- **annotation of peaks and genes**
- differential analysis of peak/gene lists
- unsupervised analysis (PCA, clustering)
- functional enrichment analysis
  (e.g. Pathway analysis, Gene ontology)
- Machine learning
- integrative analysis
  (RNA-seq, ATAC-seq, more ChIP-seq targets)
- publication-ready Visualization of genomic regions



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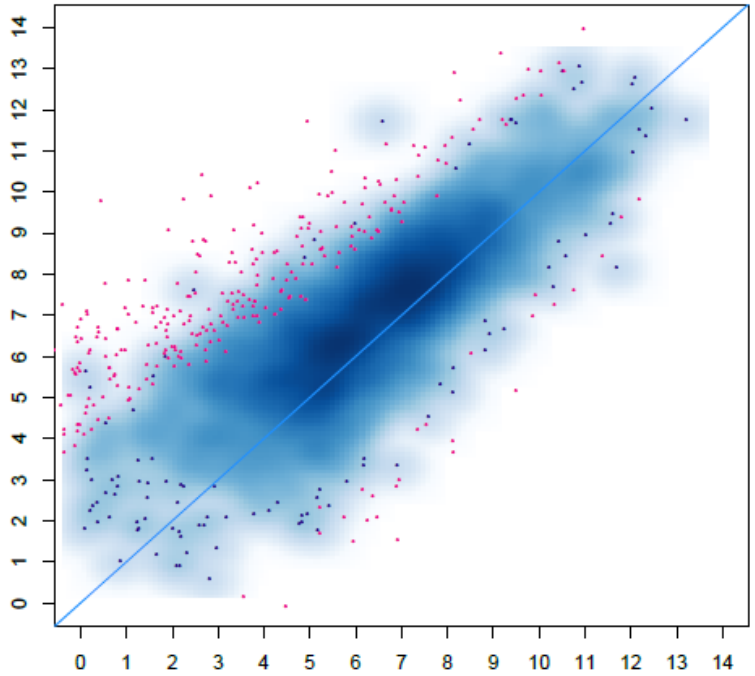

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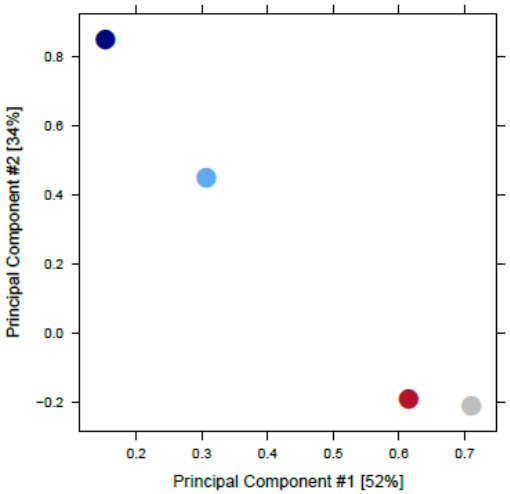

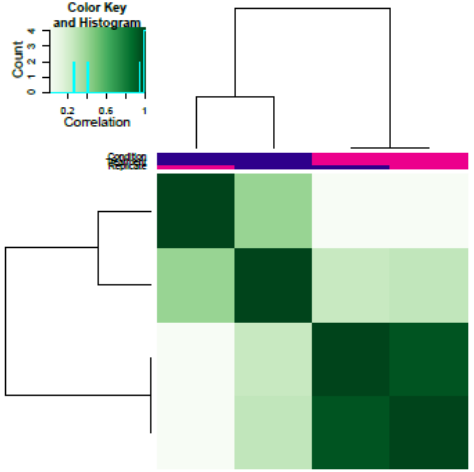

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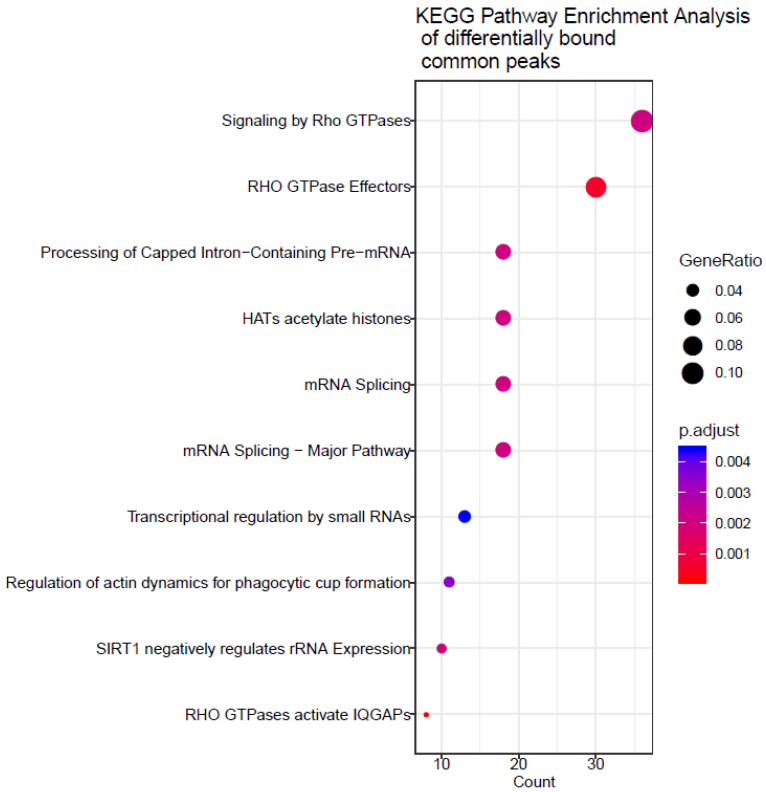
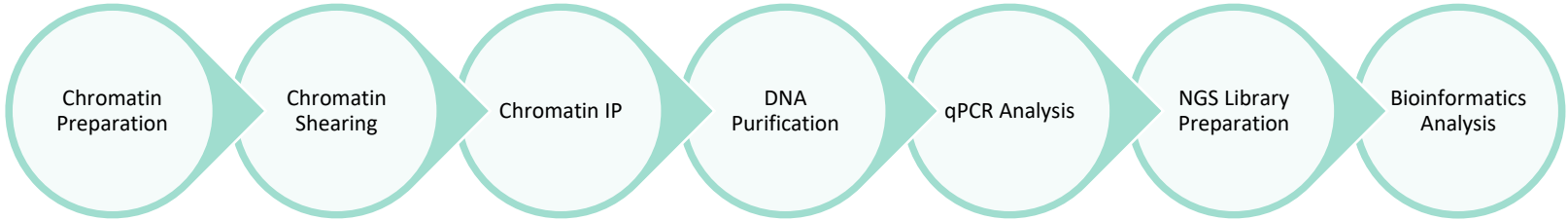


Summary



Hardware:		Bioruptor	IP-Star			IP-Star
Reagents:	Cross-link Gold		ChIP-seq grade antibodies	IPure kit MicroChIP DiaPure columns	Primer Pairs	
Kits:	EasyShear kits					
	iDeal ChIP kits					MicroPlex kit or TAG kits
	True MicroChIP kit					
	ChIPmentation kits					
Services:	Epigenomic Profiling Services					
						Data Analysis Service

Other Methods to Study Chromatin

- Interaction between proteins and DNA (immuno- assays)
  - ChIPmentation
  - Cut&Run and Cut&TAG

- Methods to study chromatin accessibility (non-immuno assays)
  - ATAC-seq

ChIPmentation™ & µChIPmentation™

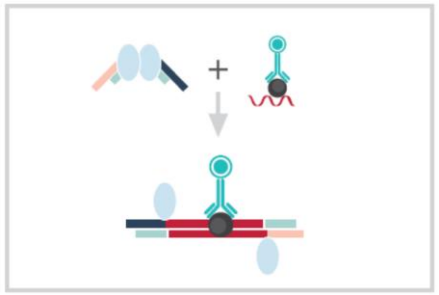
Easier and faster than classical ChIP-seq

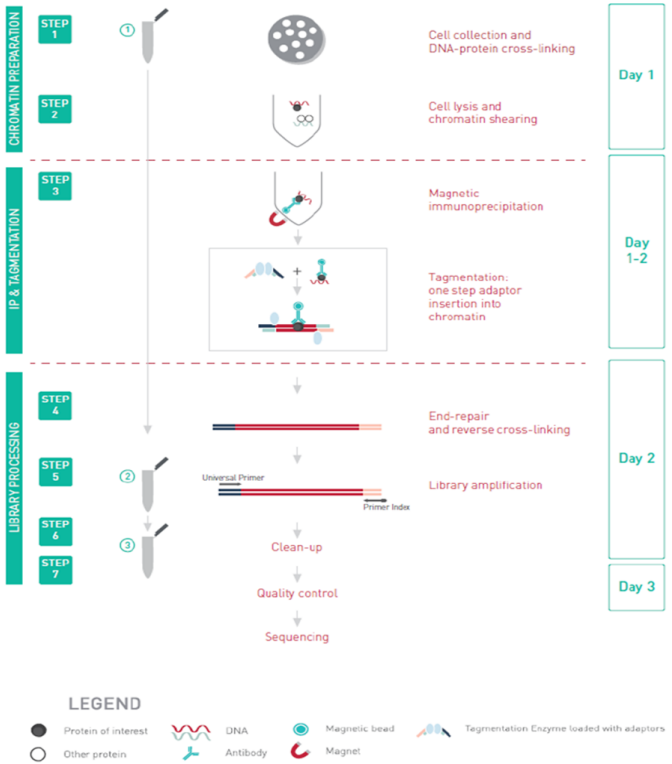
Validated for various histone marks

Ideal for analysis of large cohorts of samples (easy and fast)

Ideal for analysis of large number of marks on a unique sample

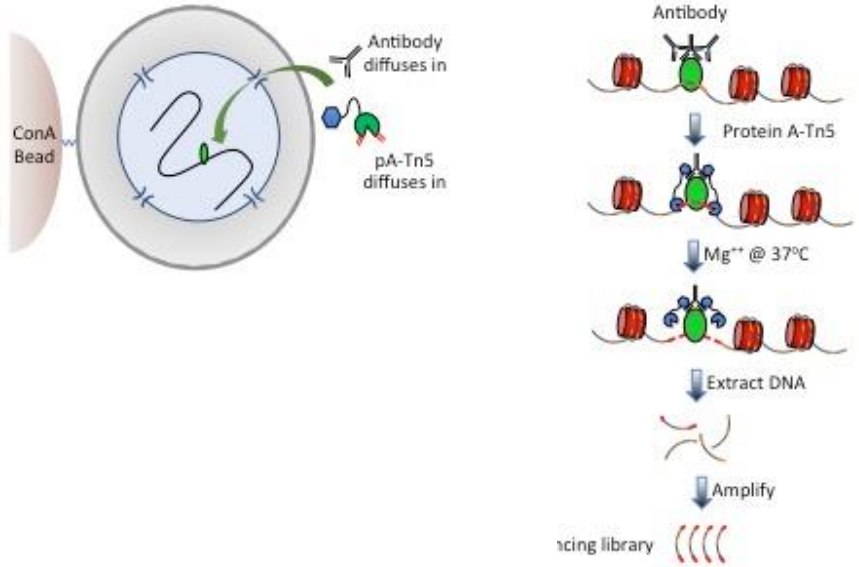
µChipmentation for 10,000 cells





CUT&Tag: Cleavage Under Targets and Tagmentation

CUT&Tag (Cleavage Under Targets & Tagmentation)

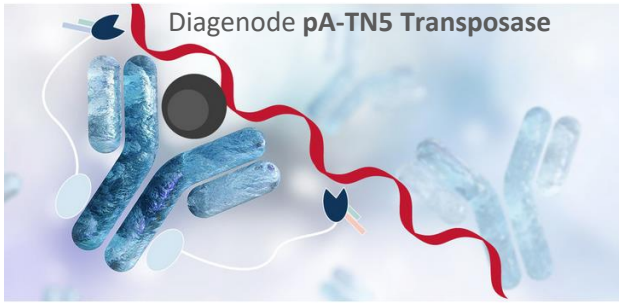


Key features:

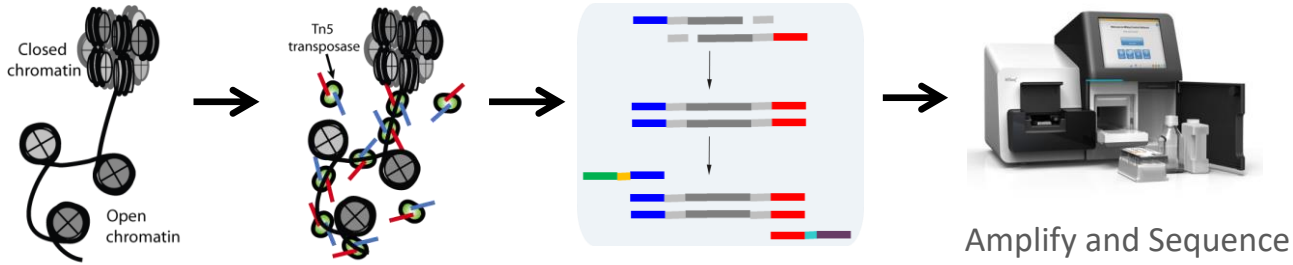
Crucial reagent:
- proteinA-Tn5

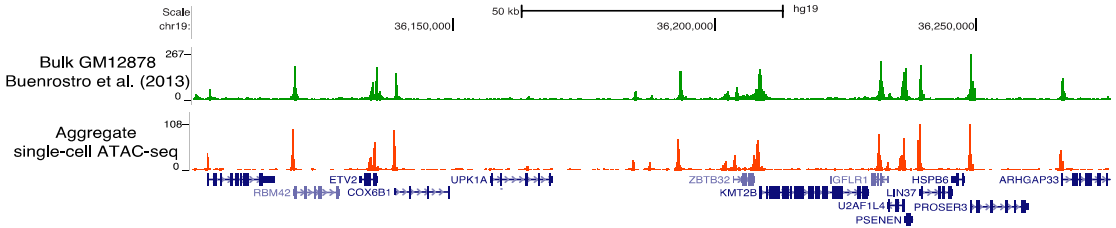
Fast and easy protocol:
- fast tagmentation-based library prep
- No chromatin prep

Suitable for low cell numbers



Assay for Transposase-Accessible Chromatin





50,000 cells

254 single-cells

Buenrostro et al., Nature, 2013

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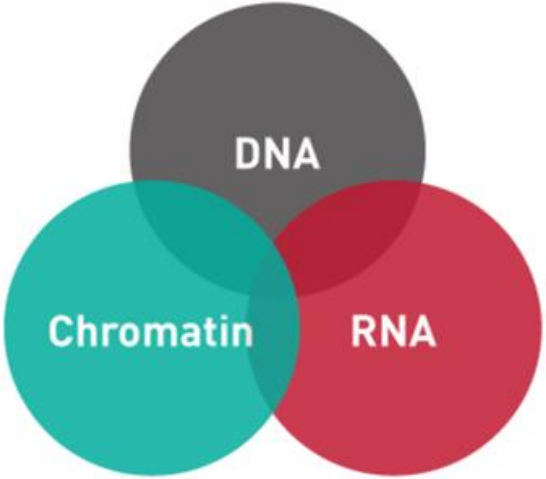
- Presentation-quality data and graphs



Sample Shipment | Processing | Data Delivery

CHIP WORKSHOP

THANK YOU!

Thank you for taking part in our ChIP workshops! (more coming)

Presentation will be sent to each participant

Watch for a little survey in your inbox – your feedback is invaluable

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