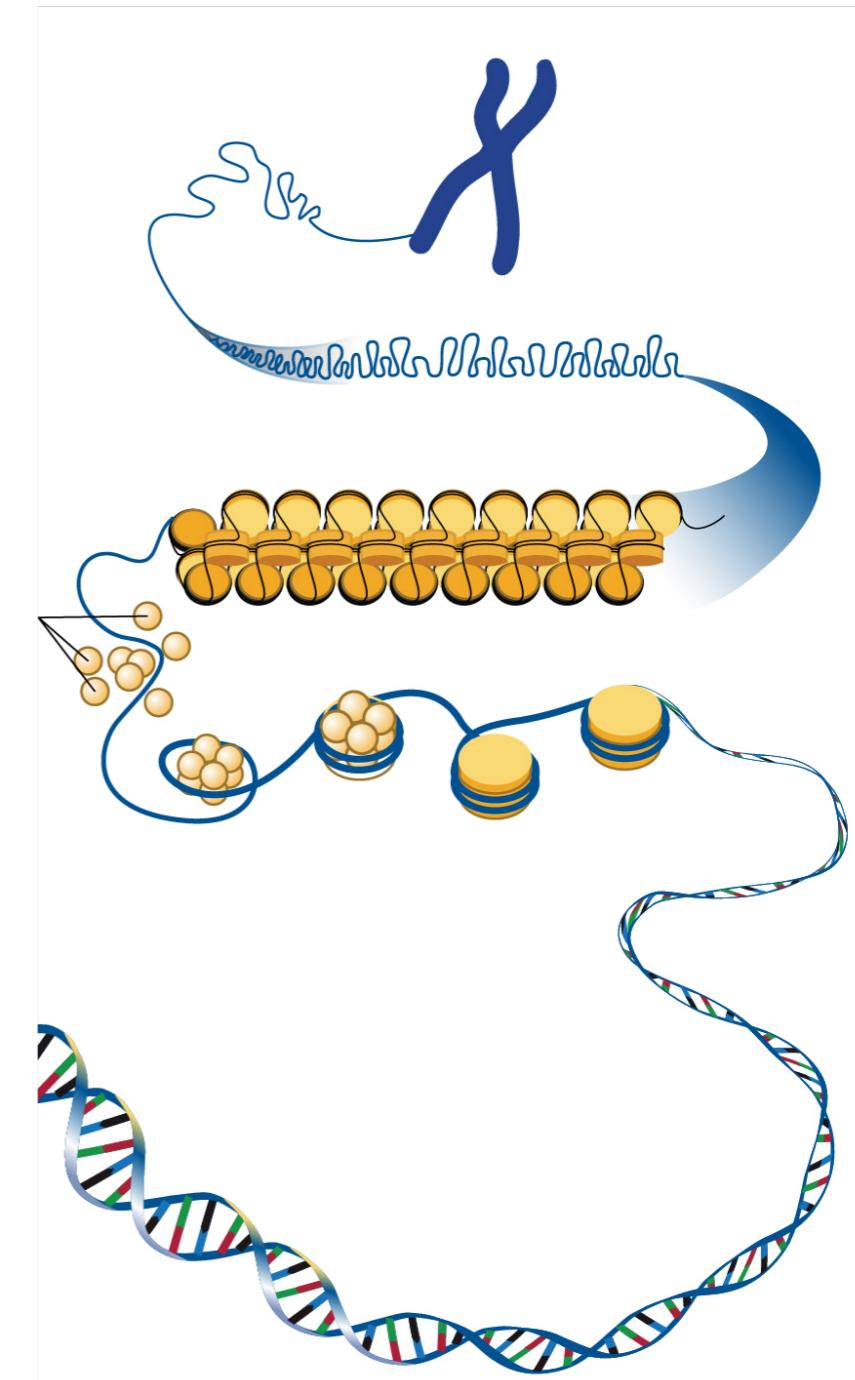


Understanding chromatin biology using high throughput sequencing methods

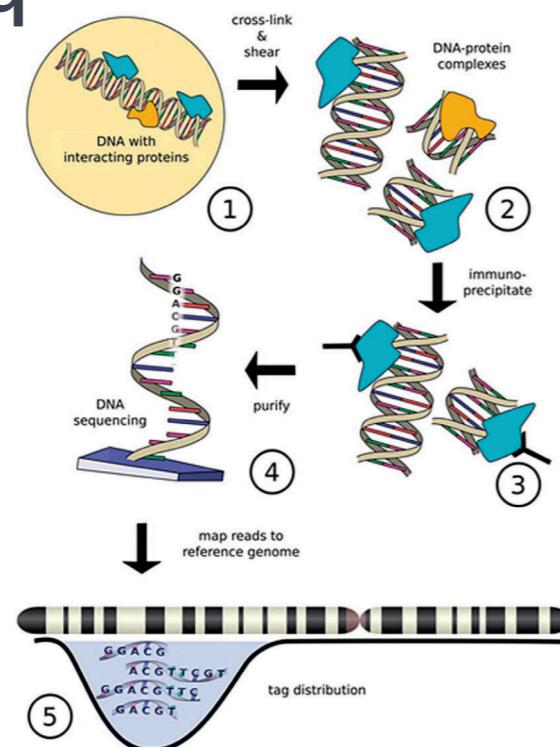
Harvard Chan Bioinformatics Core
in collaboration with
HMS Research Computing

<https://tinyurl.com/hbc-chipseq>



Genomic methods for profiling chromatin

ChIP-seq



CUT&RUN

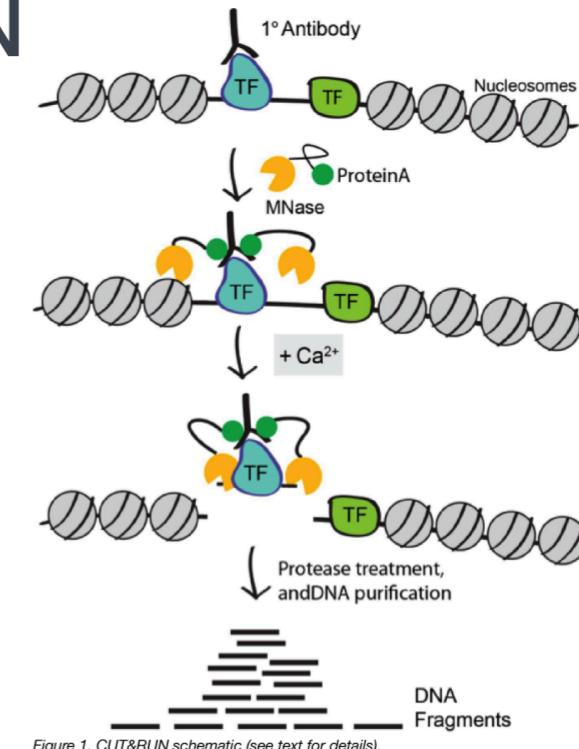
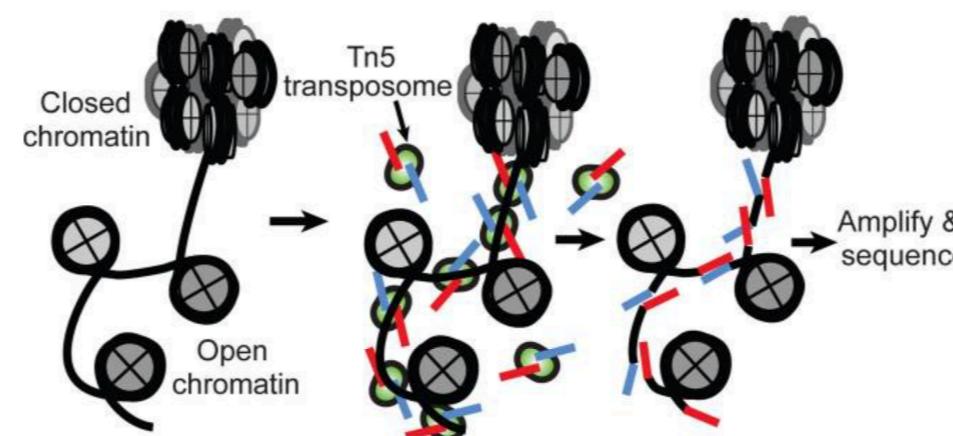
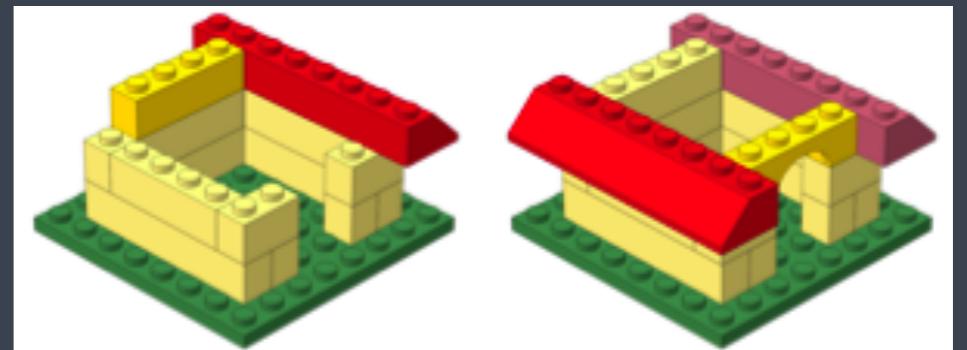


Figure 1. CUT&RUN schematic (see text for details).

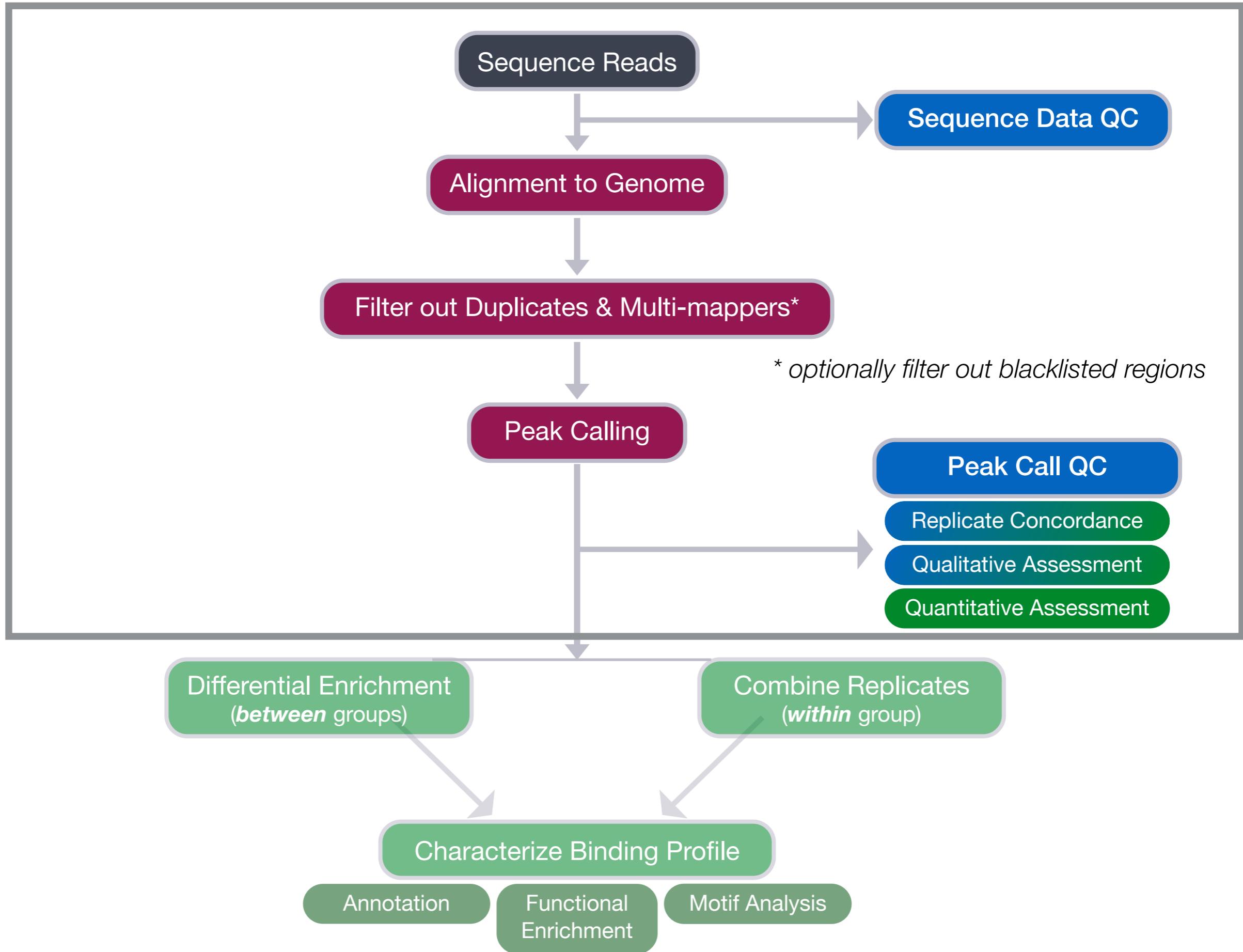
ATAC-seq

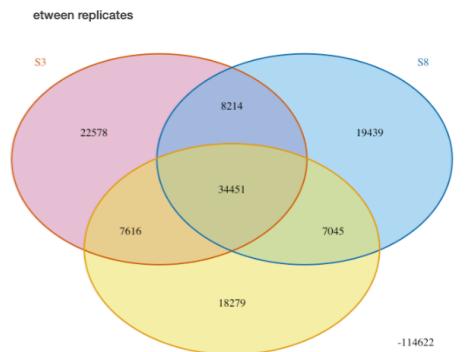
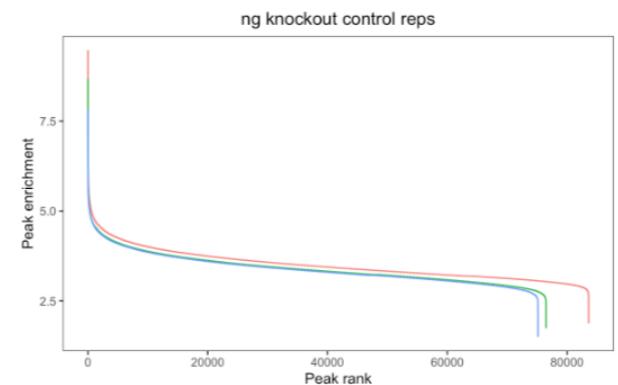
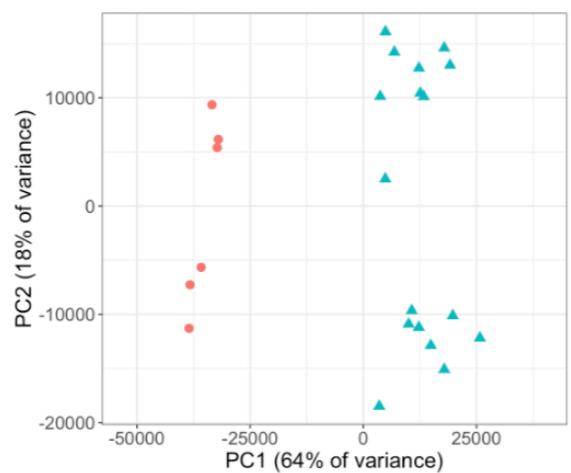
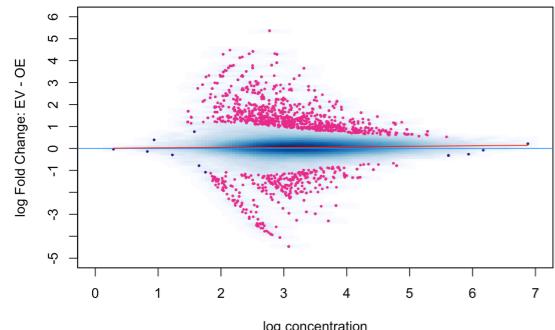


Learning Objectives



- ✓ Describe important considerations for setting up a successful ChIP-seq, CUT&RUN or ATAC-seq experiment
- ✓ Describe the steps in an ChIP-seq analysis workflow (from sequence data to peak calls) and contrast any differences for CUT&RUN and ATAC-seq analyses
- ✓ Learn how to handle various file formats encountered when analyzing ChIP-seq and related data
- ✓ Implement shell scripts on a high-performance compute cluster to perform the above steps





Differential Enrichment
(between groups)

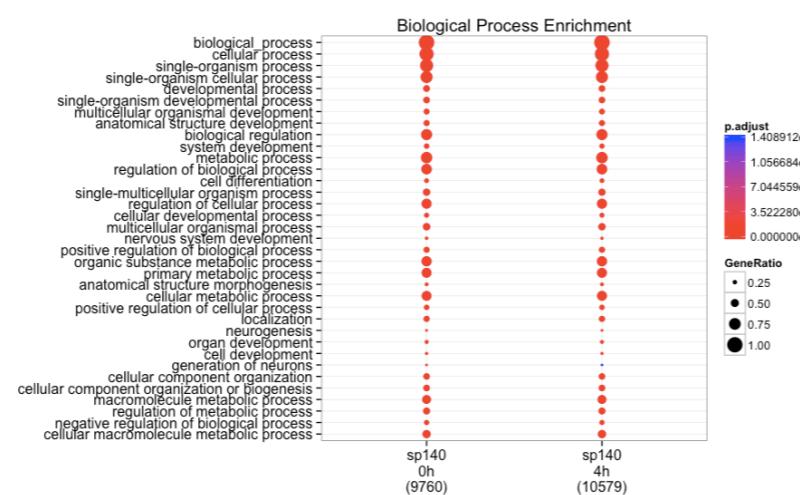
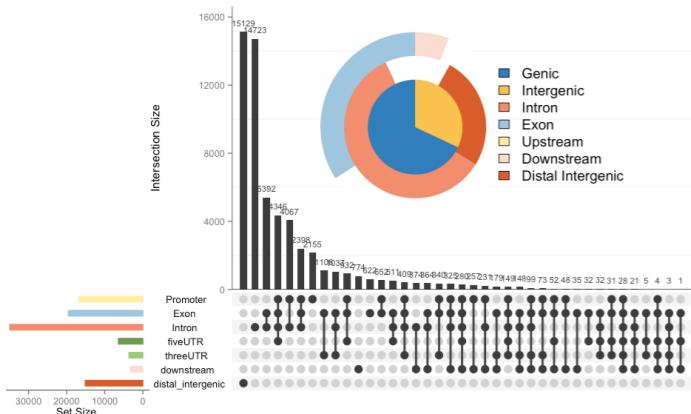
Combine Replicates
(within group)

Characterize Binding Profile

Annotation

Functional
Enrichment

Motif Analysis



For further information on how to interpret these results or to get a copy of the MEME software please access <http://meme.nbcr.net>.

If you use DREME in your research please cite the following paper:
Timothy L. Bailey, "DREME: Motif discovery in transcription factor ChIP-seq data", *Bioinformatics*, 27(12):1653-1659, 2011. [\[full text\]](#)

[DISCOVERED MOTIFS](#) | [INPUTS & SETTINGS](#) | [PROGRAM INFORMATION](#)

DISCOVERED MOTIFS

Motif	Logo	RC Logo	E-value	Unerased E-value	More	Submit/Download
1. CYWTTGTB			4.2e-299	4.2e-299	↓	...
2. ATGBWAAT			8.4e-179	1.1e-179	↓	...
3. CCMCDCCC			1.3e-130	1.1e-131	↓	...

Downstream of peak calls

We would love your feedback!

<http://tinyurl.com/hbc-chromatin-bio-exitsurvey>

Thanks!

- Shannan Ho Sui (HBC)
- Andy Bergman (HMS-RC)
- Kathleen Keating (HMS-RC)
- Data Carpentry

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Questions?

HBC training team: hbctraining@hsph.harvard.edu

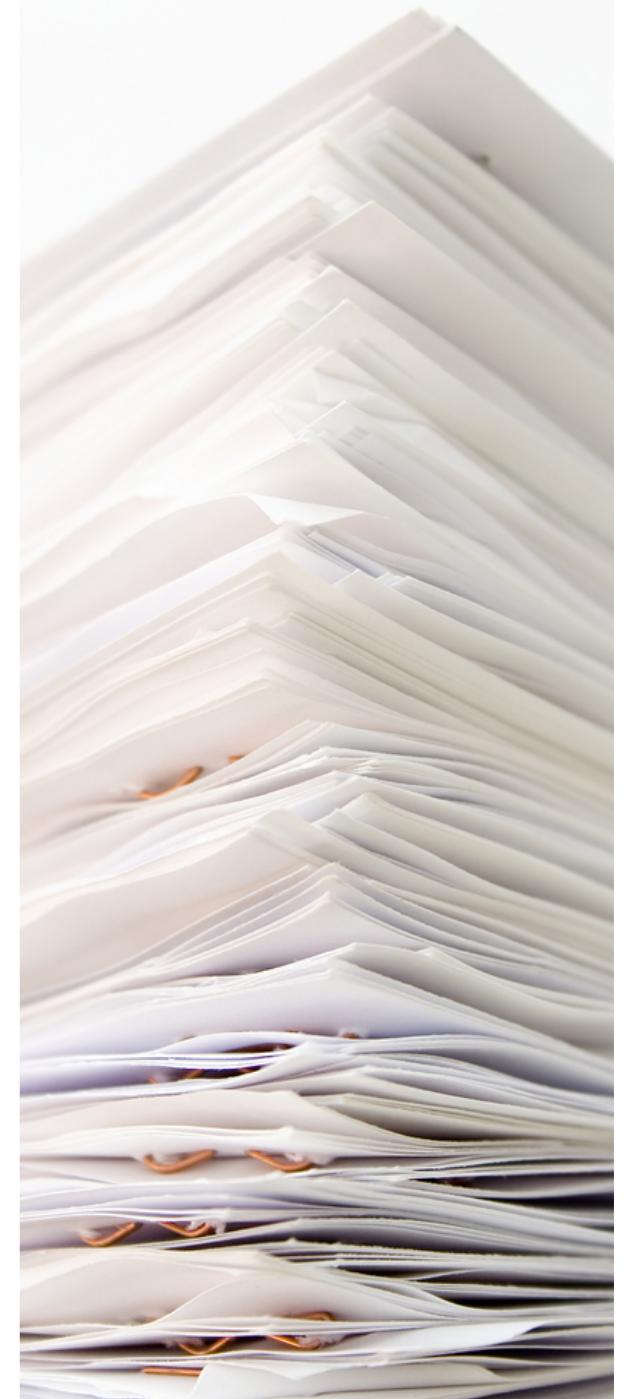
HBC consulting: bioinformatics@hsph.harvard.edu

O2 (HMS-RC): rchelp@hms.harvard.edu



Talk to us early

Involvement in study design to optimize experiments



More information

HBC training materials: <https://hbctraining.github.io/main>

HBC website: <http://bioinformatics.sph.harvard.edu>

O2 Wiki (HMS-RC): <https://wiki.rc.hms.harvard.edu/display/O2>

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