University of Massachusetts Medical School

ATACseqQC for quality assessment of ATACseq dataset
NADfinder for identifying Nucleoli Associated Domain (NAD)

July 26th 2017

Lihua Julie Zhu and Jianhong Ou
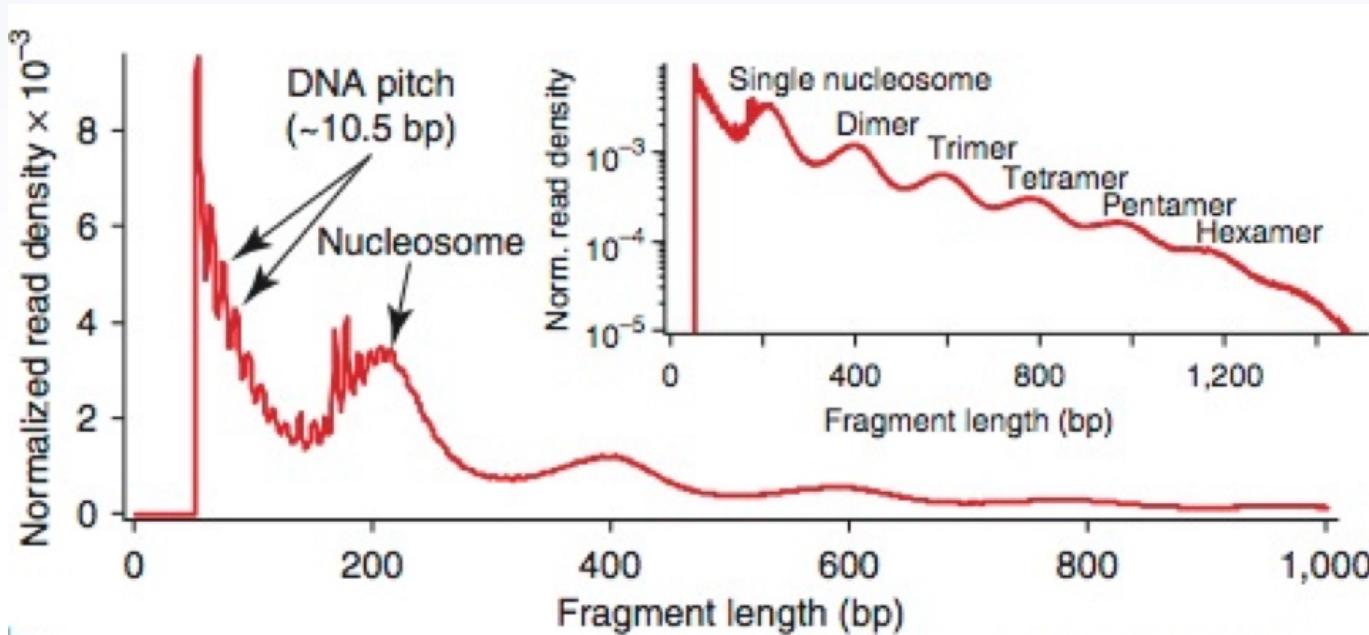
Assay for Transposase-Accessible Chromatin using Sequencing (ATAC-seq)

Adapted from *Nature Methods* 10, 1213–1218, *2013* *By* Buenrostro and *Greenleaf et al.*
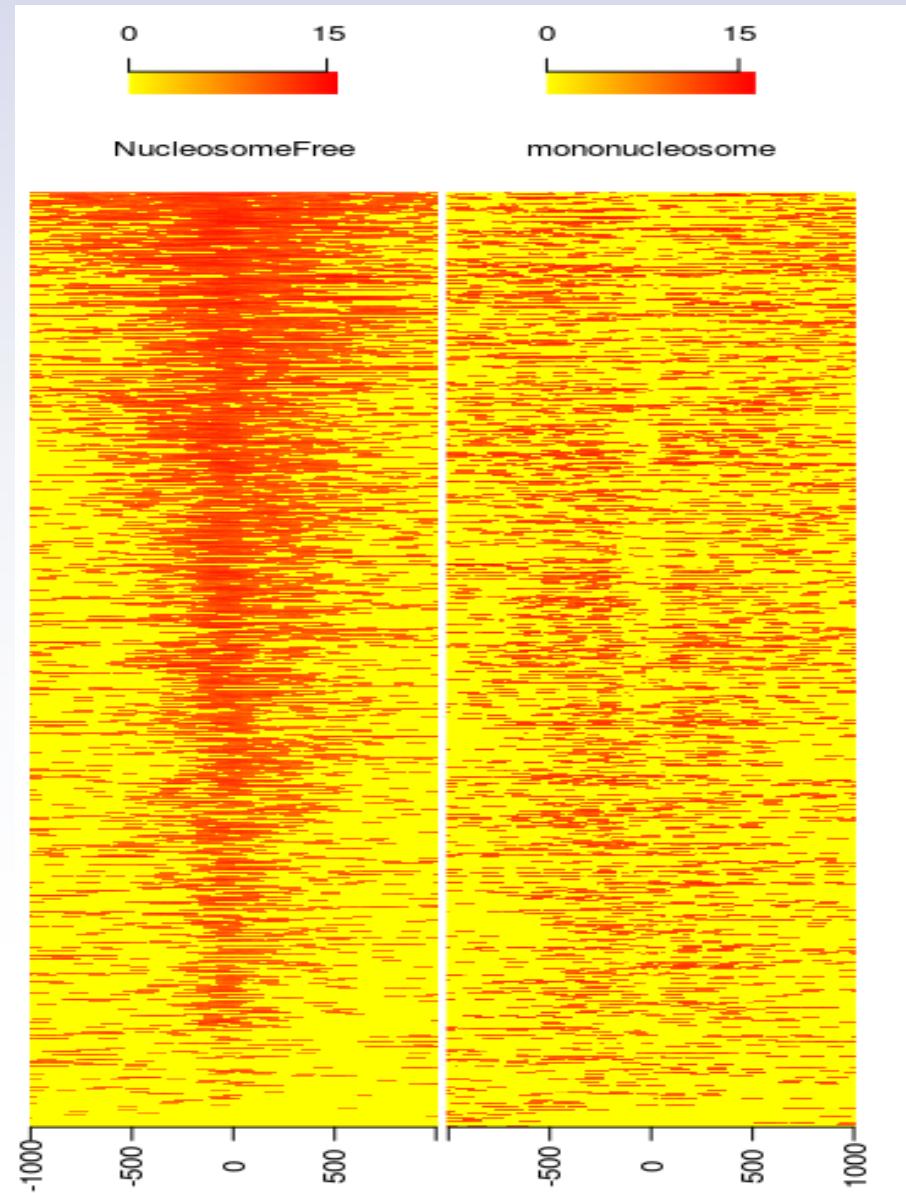
ATACseqQC Package

- **Provide quick assessment of the quality of the ATAC-seq data**

  - **diagnostic plot of insert size distribution of sequenced fragments (periodicity)**

  - proportion of mitochondria reads (< 5%)

  - genome-wide nucleosome positioning pattern at TSS

  - CTCF or other Transcript Factor footprints (depleted signals)
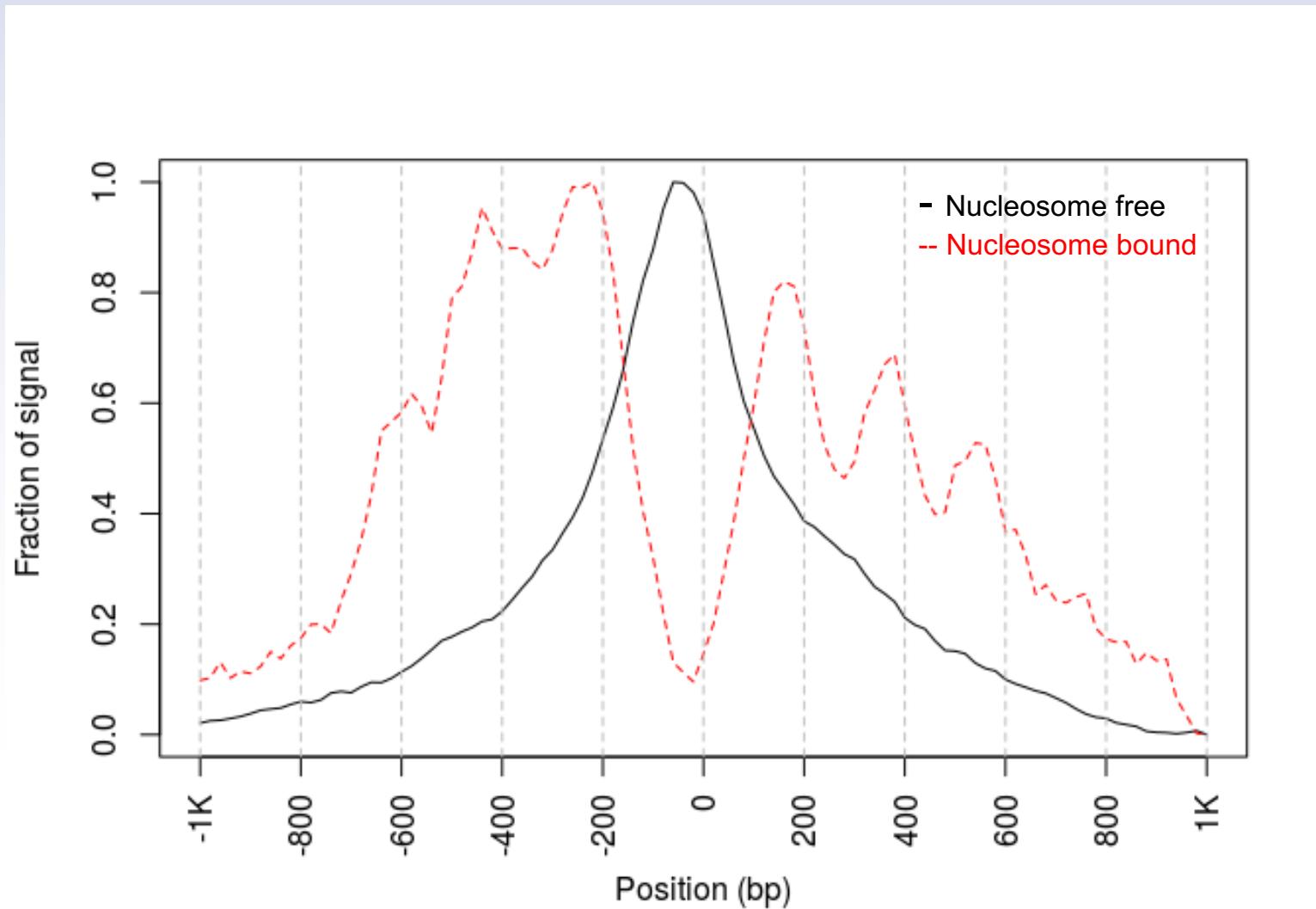

Adapted from
Nature Methods
10, 1213–1218, 2013
By Buenrostro and
Greenleaf et al.

University of
Massachusetts
Medical School
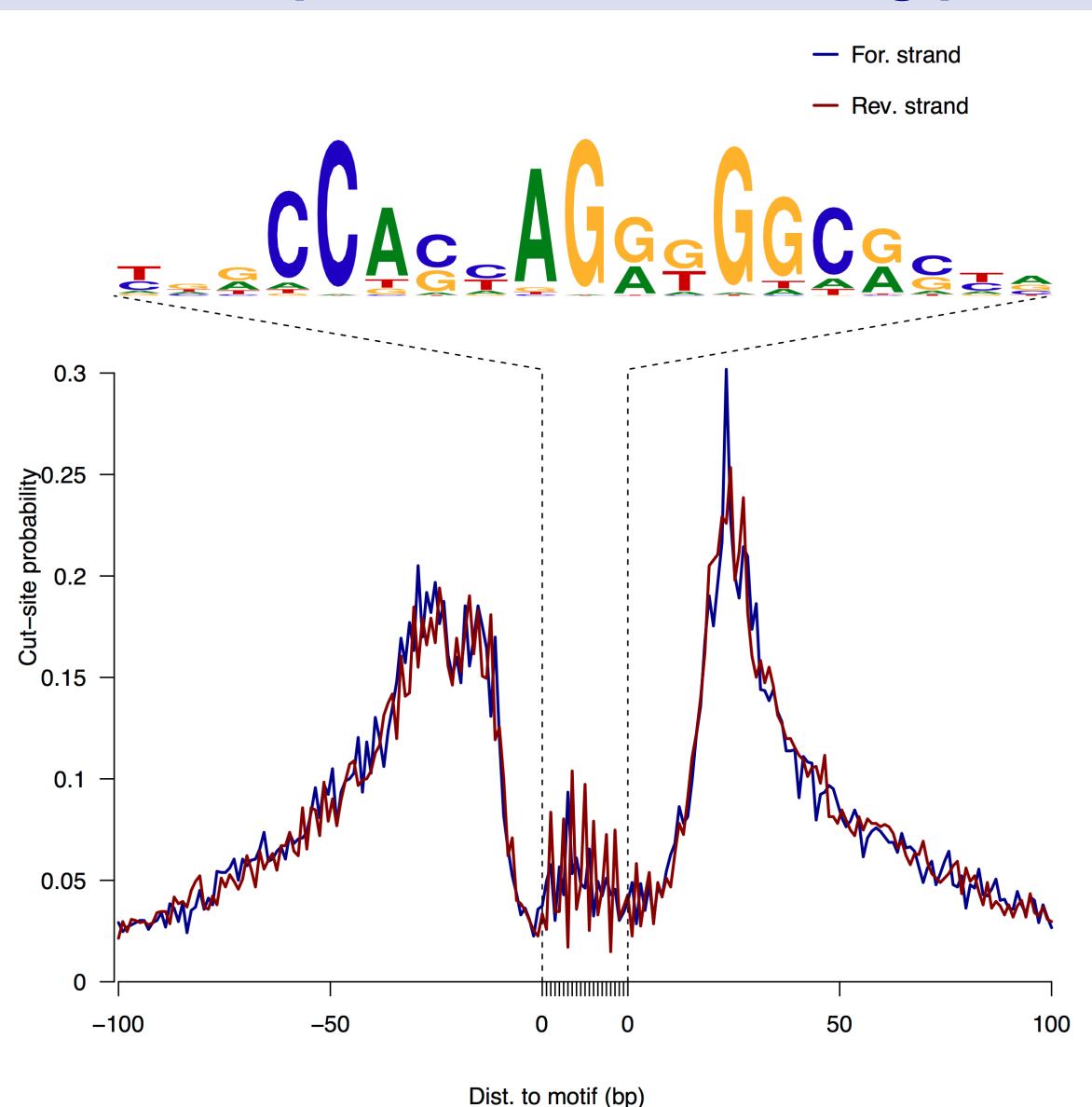
Expected patterns of nucleosome occupancy and depletion at the TSS

Density Plot Flanking TSS
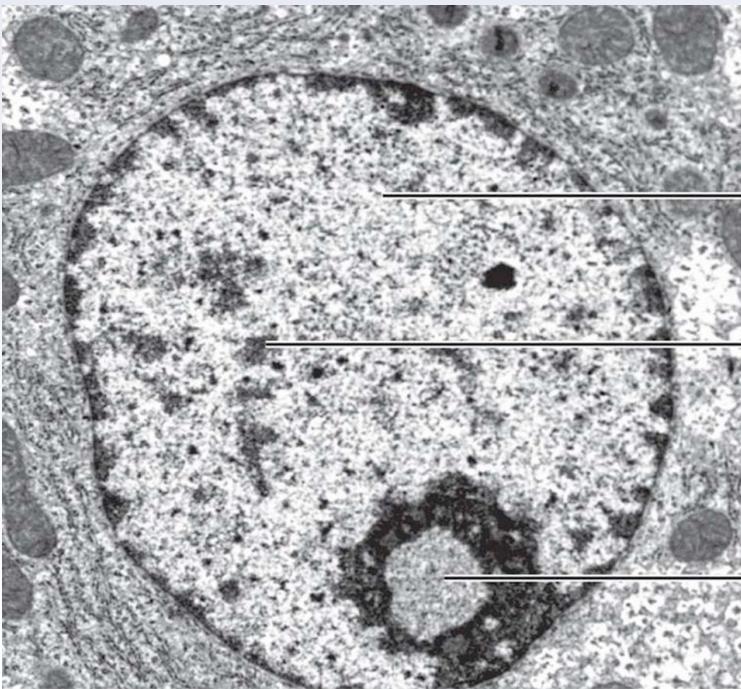
Generate footprints for DNA-binding proteins
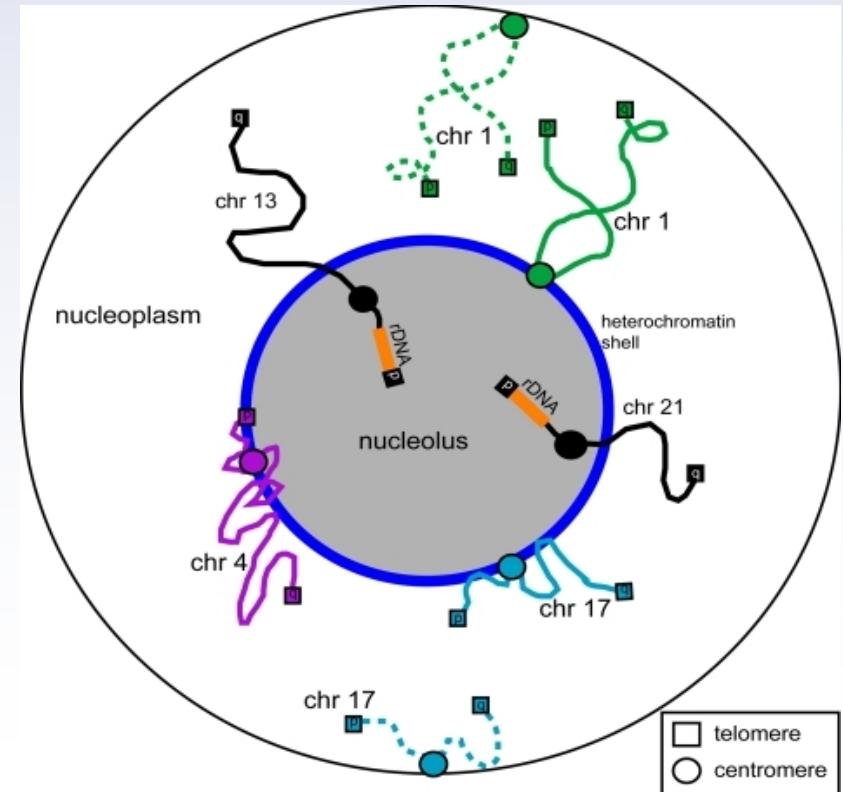
NADFINDER
NUCLEOLI ARE THE LARGEST NUCLEAR BODIES AND ARE SURROUNDED BY HETEROCHROMATIN
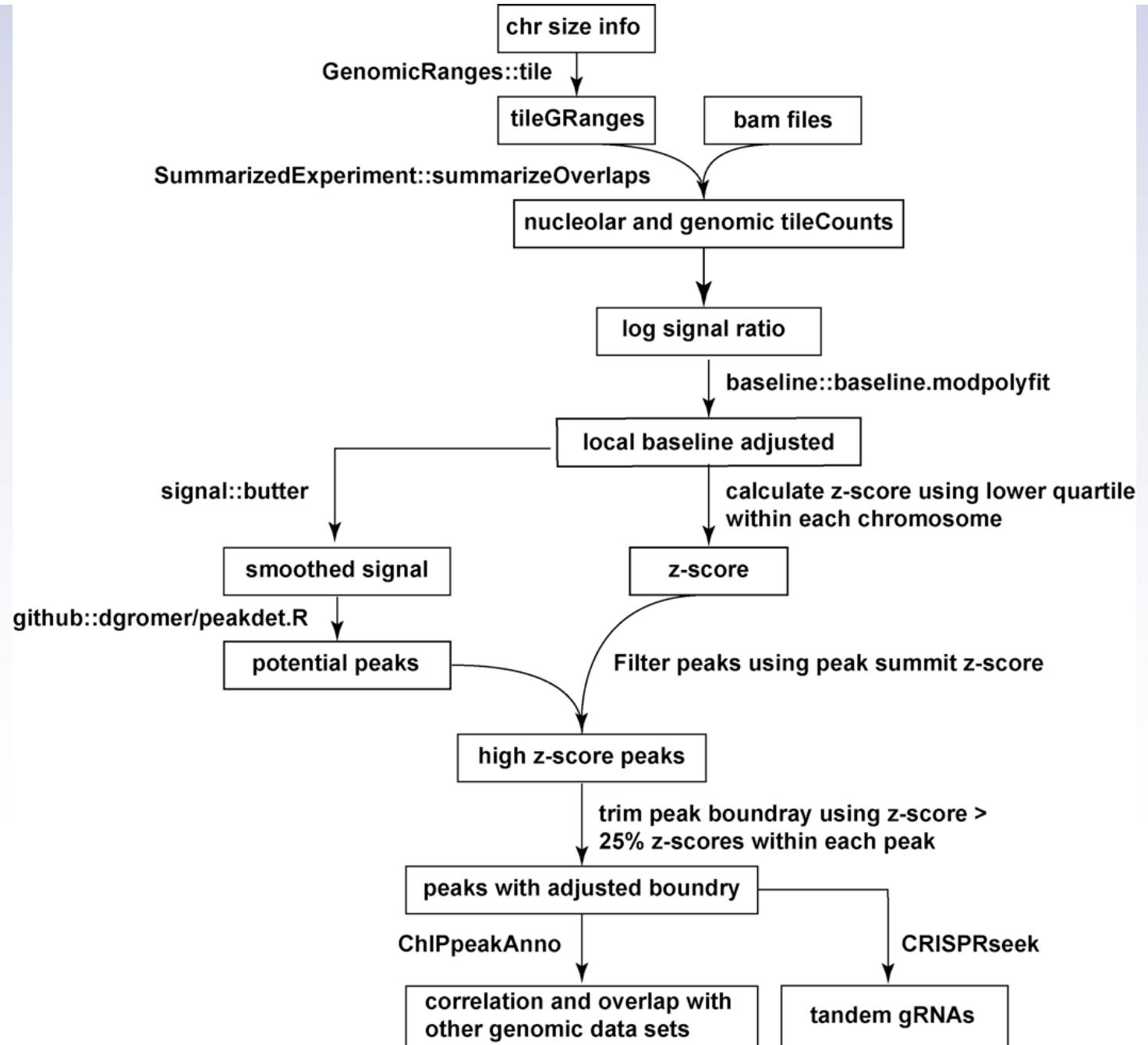
http://schoolbag.info/chemistry/mcat_biochemistry/mcat_
biochemistry.files/image140.jpg
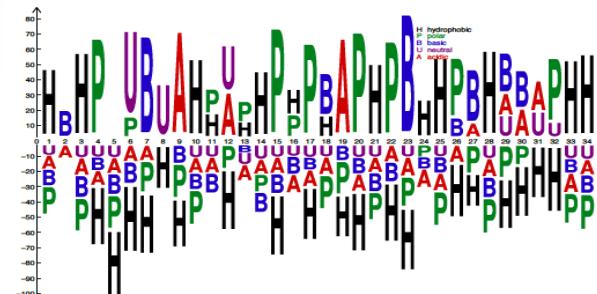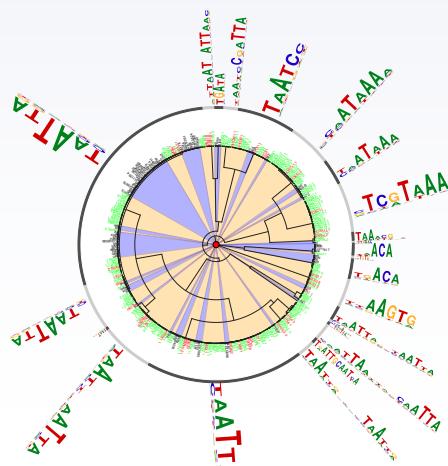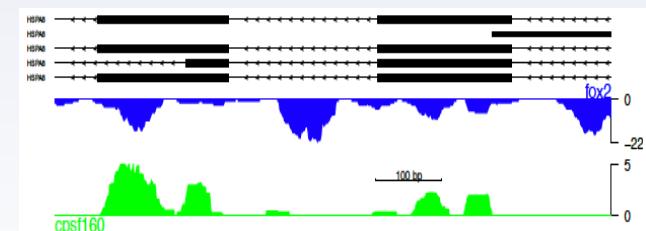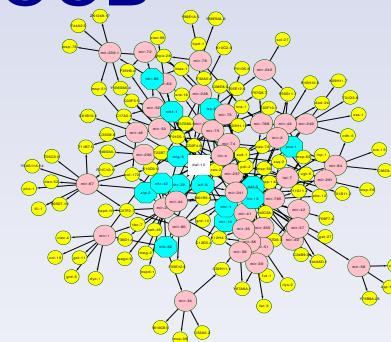
van Koningsbruggen et al… Lamond, *MBoC* 2010

University of Massachusetts Medical School

NADfinder Workflow

Bioconductor Packages By MCCB

- **Workshop By J Ou and LJ Zhu on July 28th, 3:15 - 5:00 Smith 309**
  - **ChIPpeakAnno** (BMC Bioinformatics 2010)
  - **GeneNetworkBuilder**
  - **TrackViewer**
- **Workshop by LJ Zhu on July 27th , 1-2:45pm Smith 309**
  - **CRISPRseek** (PLoS One 2014)
  - **GUIDEseq** (BMC Genomics 2017)
- **NADFinder (Poster)**
- **ATACseqQC**
- cleanUpdTseq (Bioinformatics 2013)
- REDseq (BMC Genomics 2014)
- MotifStack (in prep)
- InPAS
- dagLogo

Acknowledgement

- University of Massachusetts Medical School
  - Usha Acharya & Niraj Nirala (dagLogo)
  - Neil Aronin (CRISPRseek)
  - Michael Brodsky (CRISPRseek & MotifStack)
  - Tom Fazio and Benson Chen (REDseq)
  - Claude Gazin & Chris Hull (ChIPpeakAnno)
  - Michael Green (ChIPpeakAnno & InPAS)
  - Alper Kucukural & Manuel Garber (GUIDEseq)
  - **Nathan Lawson** (ChIPpeakAnno, **ATACseqQC** & cleanUpdTSeq)
  - **Jianhong Ou** (ChIPpeakAnno, dagLogo, NADfinder, **ATACseqQC**, GeneNetworkBuilder, MotifStack, TrackViewer, InPAS)
  - Sungmi Park (InPAS)   **Lucio Castilla (ATACseqQC)**
  - Sarah Sheppard (cleanUpdTSeq)   Paul Kaufman (NADfinder)
  - Heidi Tissenbaum (GeneNetworkBuilder)
  - Yongxu Wang (TrackViewer) **Michelle Kelliher (ATACseqQC)**
  - Scot Wolfe (GUIDEseq and motifStack)
  - **Jun Yu** (ChIPpeakAnno, NADfinder, **ATACseqQC**)

- Broad Institute of MIT and Harvard
  - Feng Zhang (CRISPRseek)
    - Benjamin Holmes
- Genentech
  - Michael Lawrence(GUIDEseq)
- The Bioconductor core members
  - Hervé Pagès (ChIPpeakAnno, CRISPRseek & GUIDEseq)
  - Martin Morgan (CRISPRseek)
  - Valerie Obenchain
  - Dan Tenenbaum
- The Bioconductor community
  - Ryan Thompson (ChIPpeakAnno)
- Nationwide Children's Hospital
  - Simon Lin (ChIPpeakAnno)
- Tufts University
  - David Lapointe (ChIPpeakAnno)

University of Massachusetts Medical School