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Streamline ChIP-Seq and ATAC-Seq analysis

Unlock insights from gene regulation studies with intuitive tools from Partek™ Flow™ software

Powerful tools for genome-wide surveys of gene regulation, including ChIP-Seq and ATAC-Seq, deepen our understanding of how gene expression is influenced by transcription factor binding or chromatin packaging. Unlike most command line–based tools for analyzing ChIP-Seq and ATAC-Seq data, Partek Flow software offers a user-friendly bioinformatics solution to analyze and visualize data, empowering researchers of all skill levels to maximize insights from their gene regulation studies.

ChIP-Seq
Identifies DNA–protein interactions

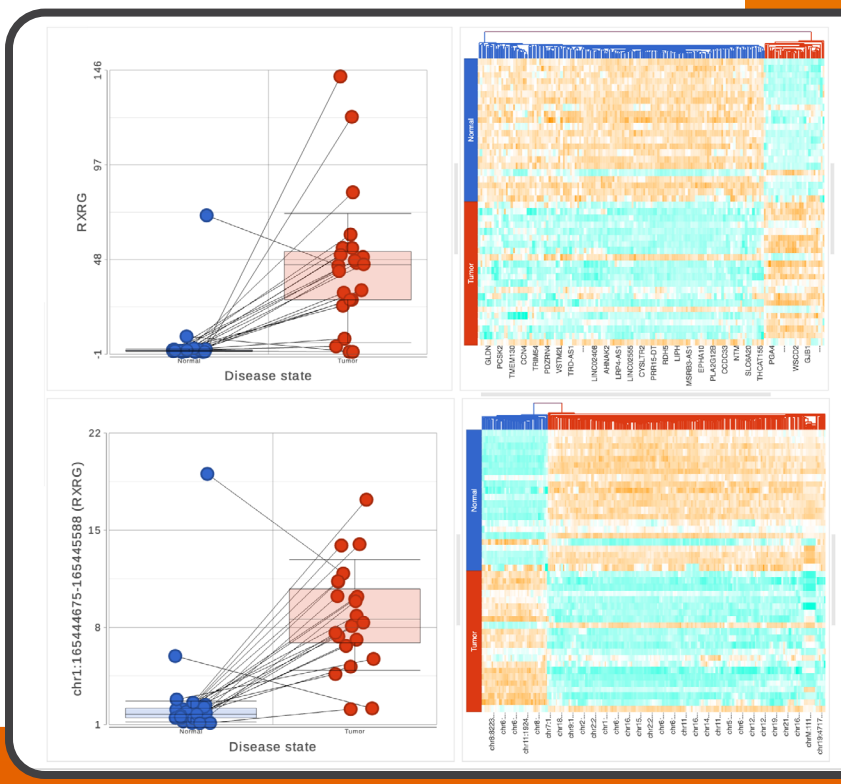
ATAC-Seq
Assesses chromatin accessibility

Point-and-click analysis
Analyze data easily with an intuitive, context-sensitive interface

Advanced visualization tools
Create informative, publication-ready visualizations with just a few clicks

Powerful statistics
Access industry-standard statistical algorithms for results you can trust

Customizable workflows
Build custom analysis pipelines visually and share with collaborators



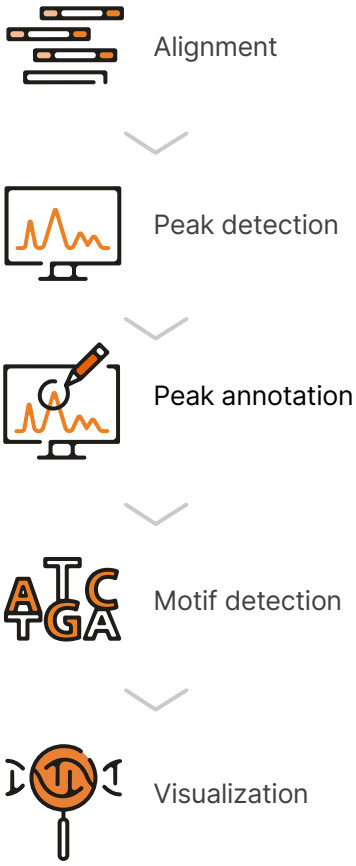
Powerful analysis and visualization tools

Whether looking for patterns of epigenetic changes in time series, exploring regulatory mechanisms in disease, mapping nucleosomes, or studying transcription factor binding, Partek Flow software has the tools you need for easy analysis and visualization of your ChIP-Seq and ATAC-Seq data.

Data to **biological insights in a single solution**

Start the ChIP-Seq or ATAC-Seq analysis pipeline with either unaligned or aligned reads, with tools for trimming adapter sequences and low-quality bases. Align reads to any reference genome using BWA, Bowtie 2, and other popular aligners. Detect and annotate peaks, discover motifs from regions of interest, and integrate results with RNA-Seq data to explore the regulatory effect of transcription factors on gene expression. QA and QC reports are available for key steps of the analysis workflow.

Steps in the **ChIP-Seq and ATAC-Seq workflow**

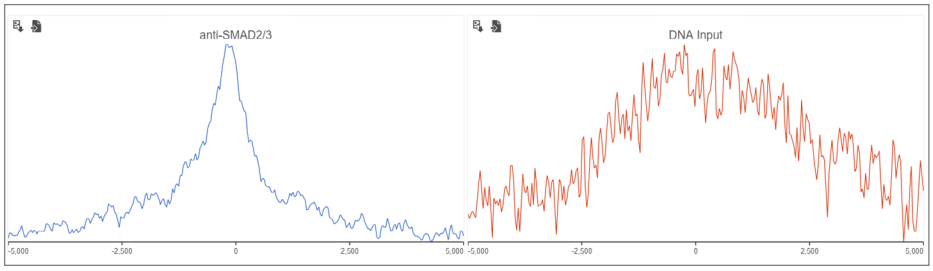


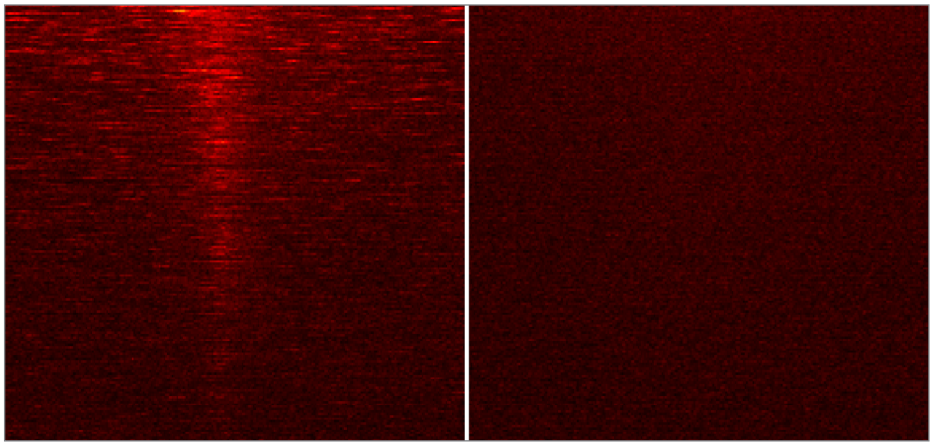
Partek Flow tools for ChIP-Seq/ATAC-Seq analysis

- Perform peak detection using MACS3
- Quantify read counts within detected regions
- Compare detected regions among groups
- Annotate peaks of interest with any gene annotation model
- Perform pathway enrichment analysis on genes related to the regions of interest
- Detect known motifs present in the JASPAR database
- Detect novel motifs
- Identify the peak region around the transcription start site with a TSS plot
- Visualize consensus binding sequences with the sequence logo

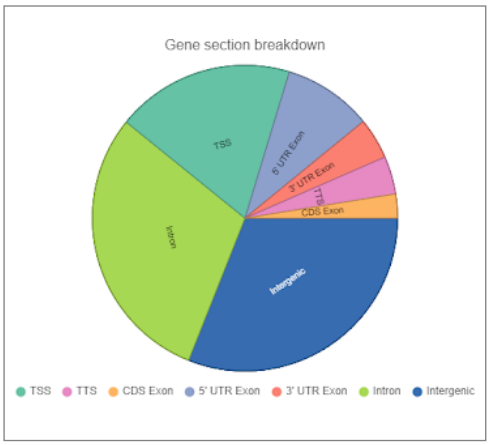
Multiple ways to **explore ChIP-Seq and ATAC-Seq data**

Transform ChIP-Seq and ATAC-Seq data into interactive figures to maximize biological insights from your epigenomics studies. The integrated genome browser in Partek Flow software simplifies visualizing peaks and consensus sequence motifs. Visualizations are then easily exported as publication-quality images.

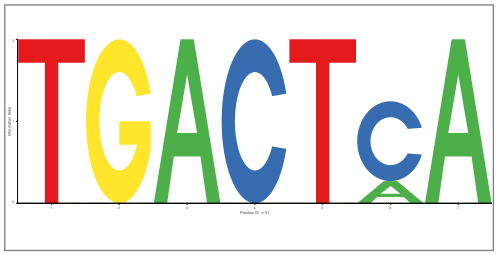




Map reads of interest to the transcription start site.



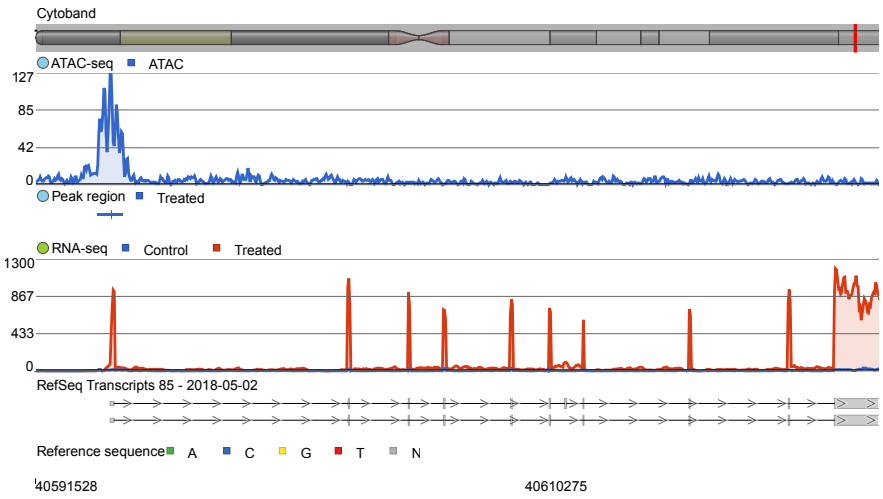
Summarize the annotation of enriched regions by genes using a pie chart.



Identify consensus sequence motifs from regions of interest with the sequence logo.

Cross-platform integration for multiomic insights

Analyzing multiple omics data sets in parallel provides a more complete view of the molecular mechanisms underlying phenotypes. Partek Flow software makes it easy to integrate data from ChIP-Seq or ATAC-Seq with RNA-Seq studies. Compare lists of target genes generated from ChIP-Seq data with lists of differentially expressed genes generated from RNA-Seq data using Venn diagrams. Visualize peaks and differentially expressed genes together with the chromosome view in the data viewer for a comprehensive picture of gene expression and regulation.



Integrate ChIP-Seq or ATAC-Seq data with RNA-Seq data for multiomic insights.

Learn more

Partek Flow software

Request a free 14-day trial

Abbreviations: ATAC-Seq, assay for transposase-accessible chromatin with sequencing; BWA, Burrows-Wheeler aligner; ChIP-Seq, chromatin immunoprecipitation with sequencing; MAC3, model-based analysis of ChIP-Seq; NGS, next-generation sequencing; QA, quality assurance; QC, quality control; RNA-Seq, RNA sequencing; TSS, transcription start site

illumina®

1.800.809.4566 toll-free (US) | +1.858.202.4566 tel
techsupport@illumina.com | www.illumina.com

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