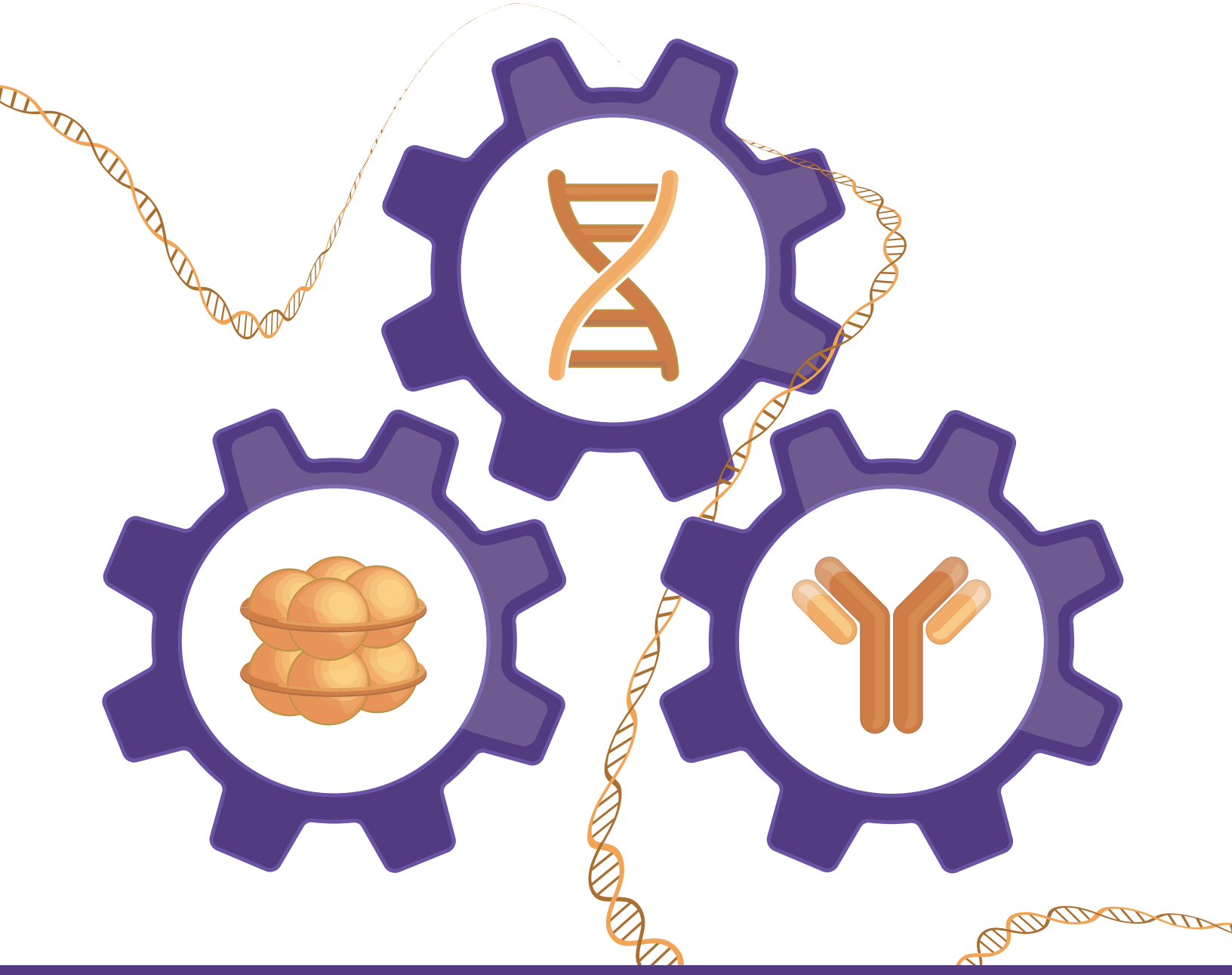
ACTIVE MOTIF®

Enabling Epigenetics Research

Custom Services

for Epigenetic and Gene Regulation Research



activemotif.com

Custom Services
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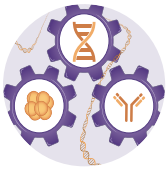
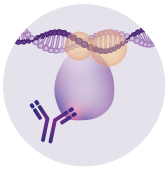


Custom Services
Overview

The Active Motif Custom Services team makes cutting-edge research accessible to the wider life science community. We provide services for state-of-the-art epigenetics and gene regulation analysis techniques to accelerate your research.

- ChIP-Seq and CUT&Tag
- DNA Methylation Sequencing
- Chromatin Structure
- Histone Modification Analysis
- RNA-Seq
- IP-Mass Spec
- Single-Cell Assays



ChIP-Seq

end-to-end services for genome-wide mapping of protein-DNA interactions

Chromatin immunoprecipitation (ChIP-Seq) combined with Next-Generation Sequencing is the most widely utilized technique to study protein-DNA interactions and histone modification localization across the genome. Given the importance of ChIP-Seq data sets for development and disease research, obtaining the highest quality data is crucial.

Choose the Global Leader in End-to-end ChIP Services

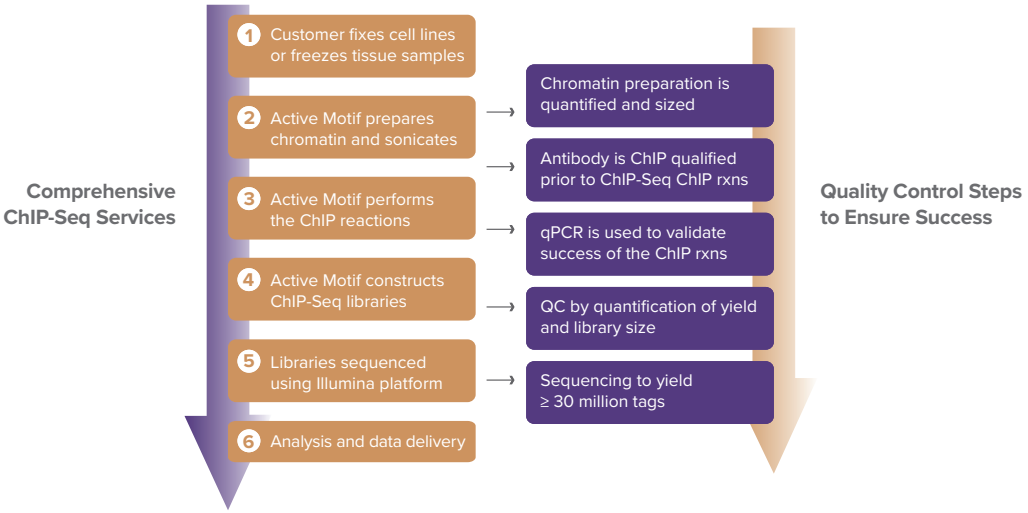
Active Motif offers the most diversified portfolio of ChIP Services. We bring over a decade of experience providing services, with over 10,000 samples processed, and the highest level of expertise of any service provider.

> "I have been using Active Motif's ChIP-Seq Services for several years, for histone tail modifications, epigenetic regulators, and transcription factors. I have been consistently impressed with the professional customer service, as well as the speed of turnaround and the quality of data obtained from frozen human tumor specimens. I would not hesitate to recommend that people try the service for themselves."
>
> – Dr. David T. W. Jones
> German Research Center (DKFZ),
> Heidelberg, Germany

ChIP Services

activemotif.com/services-chipseq

- Histone mark ChIP-Seq
- Transcription factor ChIP-Seq
- ChIP Antibody Validation – verify that your antibody works in ChIP
- Super-enhancer Profiling – choose from our validated super-enhancer targets
- RNA Pol II ChIP-Seq – measure transcription rates
- ChIP-qPCR



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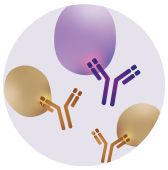


ChIP Antibody Validation
services to test the suitability of your antibody for ChIP applications

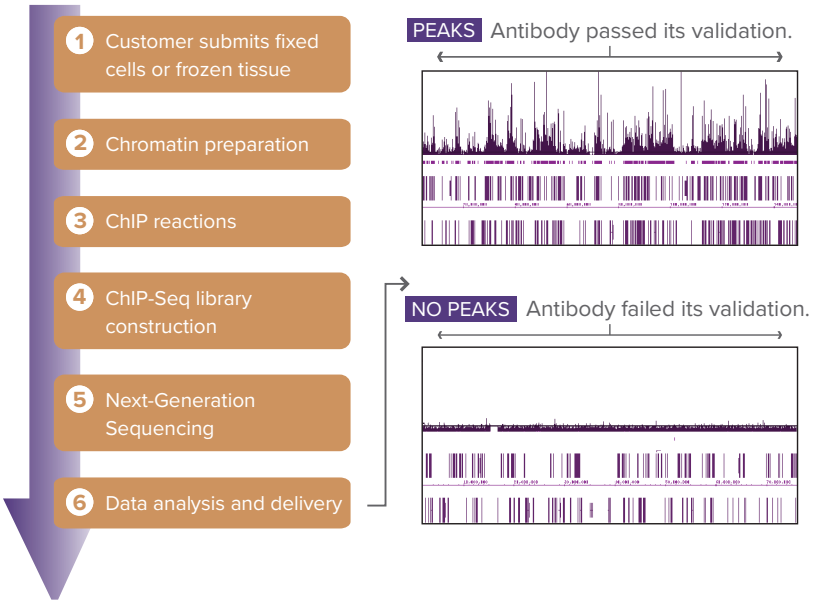
One of the greatest challenges in ChIP experiments is the lack of available antibodies that can recognize fixed, target-bound proteins and that function in immunoprecipitation. Active Motif's ChIP Antibody Validation Service makes this process simple, fast, and convenient.

Let the ChIP Experts® do the work for you.

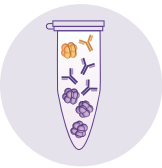
Only 30% of all antibodies work in ChIP-Seq. Therefore, identification of a good ChIP-Seq antibody presents a significant barrier to project initiation and completion. Our Epigenetic Services team has validated antibodies to over 350 targets. If your target of interest is on our list, we can start your project immediately. Otherwise, submit an antibody to us and our Antibody Validation Service can give you an answer in as little as 4 weeks.

Learn more at: activemotif.com/ab-val

ChIP Antibody Validation Services



- Submit any antibody for testing
- 'Yes' or 'No' results for ChIP-Seq functionality
- Results in 4-5 weeks
- Hundreds of antibodies already validated



ChIP-Seq Spike-In Normalization

a novel ChIP-Seq normalization strategy to reveal hidden biological effects

As a leader in ChIP innovation, Active Motif has developed ChIP-Seq Spike-In, a technical advancement in ChIP that enables more accurate sample comparisons. The normalization strategy is universally applicable to any ChIP experimental set-up.

Advanced ChIP-Seq Normalization

ChIP is a multi-step process in which the effects of sample loss, uneven sequencing read depth, or technical variation often lead to uninterpretable results or conceal subtle biological effects in your samples.

ChIP-Seq Normalization Advantage

- Uncover latent or subtle biological effects
- Monitor consistency between samples
- Reduce effects of technical variation
- Reduce sample bias

Active Motif's Services team has developed a ChIP-Seq Spike-in Normalization strategy that can correct for variance. Spike-in is available as part of our end-to-end ChIP-Seq Service.

How Does It Work?

ChIP-Seq reactions:

- A standard ChIP-Seq reaction is set up using your experimental chromatin and antibody of interest.
- *Drosophila melanogaster* chromatin is "spiked in" to each reaction as a minor fraction of total chromatin.
- An antibody recognizing the *Drosophila*-specific histone variant, H2Av, is added to the reaction to reliably pull down a small fraction of *Drosophila* chromatin.
- Following ChIP, immunoprecipitated DNA sequences are analyzed by Next-Generation Sequencing (NGS).

Normalization:

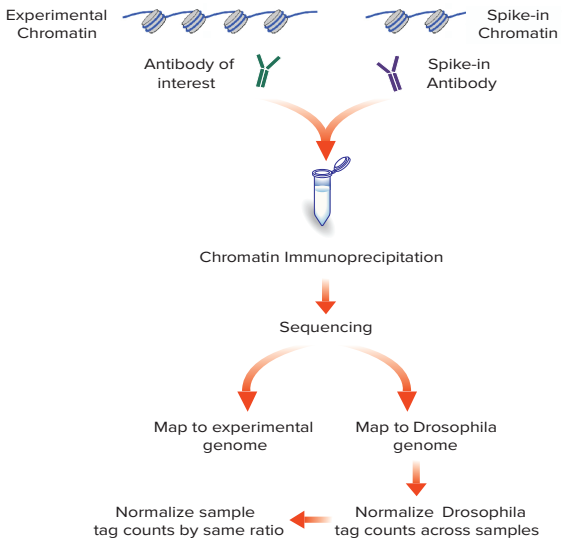
- Following NGS, sequence tags are aligned to the experimental reference genome (e.g. human) and the *Drosophila* genome.
- Variances in *Drosophila* tag counts are equalized across samples.
- The same ratio used to equalize *Drosophila* tag counts is applied to human tag counts for normalization.

Results:

Biases introduced during ChIP and Next-Generation library amplification and sequencing also occur in the *Drosophila* Spike-in chromatin. Normalization using our Spike-in strategy corrects for these biases to enable the observation of any significant biological changes in your ChIP-Seq samples (see ChIP-Seq Normalization Workflow, opposite page). To learn more, visit activemotif.com/services-normalize.

ChIP-Seq Spike-In Normalization (continued)
a novel ChIP-Seq normalization strategy to reveal hidden biological effects

ChIP-Seq Normalization Workflow



Global ELISA-based DNA methylation assays are used to investigate the overall levels of 5-mC or 5-hmC in samples to determine whether treatment conditions or disease phenotypes change epigenetic profiles. Clinical researchers use these high-throughput assays when screening large numbers of patient samples from their study cohorts.

Available separately:

Product	Format	Catalog Number
Spike-in Chromatin	15 rxns	53083
Spike-in Antibody	50 µg	61686

SPIKE-IN NORMALIZATION UNVEILS BIOLOGICAL EFFECTS OF COMPOUND TREATMENTS

Active Motif's ChIP-Seq Spike-in Normalization strategy reveals EZH2 inhibitor-induced changes in H3K27me3 levels that were previously undetected using a standard ChIP-Seq protocol.*

WHY?

Without Spike-in normalization (-), uneven amplification of the ChIP DNA during preparation of Next-Gen sequencing libraries led to loss of differences between samples. With Spike-in normalization (+) the bias in PCR amplification was corrected and the difference between samples is clearly visible.

Figure 1: Cells treated with a small molecule inhibitor of EZH2 methyltransferase have dramatic reductions in global H3K27me3 levels. However, H3K27me3 ChIP-Seq using standard ChIP-Seq protocols (-) does not detect these differences. Incorporation of Active Motif's ChIP-Seq Spike-in Strategy (+) reveals the expected decrease in H3K27me3 ChIP-Seq signal.

*Egan, B. *et al.* An alternative approach to ChIP-Seq normalization enables detection of genome-wide changes in histone H3 lysine 27 trimethylation upon EZH2 inhibition. PLoS One. 11:e0166438

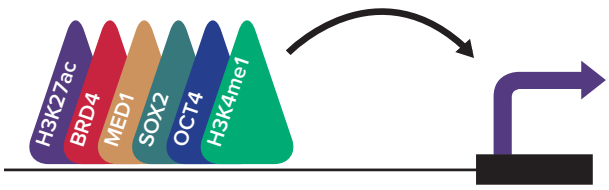
Super Enhancer Profiling

specialized ChIP-Seq data generation and analysis services for genome-wide super-enhancer profiling

Most genes that are considered master regulators are transcription factors. Super-Enhancers are regulatory regions that control the expression of these master transcription factors. Active Motif offers a specialized ChIP-Seq service to identify Super-Enhancers which helps define the master regulators of any given cell type or disease sample.

There are many proteins that assemble into Super-Enhancers, however H3K27ac is a universal marker of Super-Enhancers. Active Motif can generate a Super-Enhancer profile from any sample by simply performing an H3K27ac ChIP-Seq experiment.

To learn more, visit activemotif.com/services-superenhancer.



USE SUPER-ENHANCER SERVICES TO IDENTIFY:

- Master regulators of cell identity
- Regulatory regions associated with disease
- Mechanisms of BRD4 inhibitors

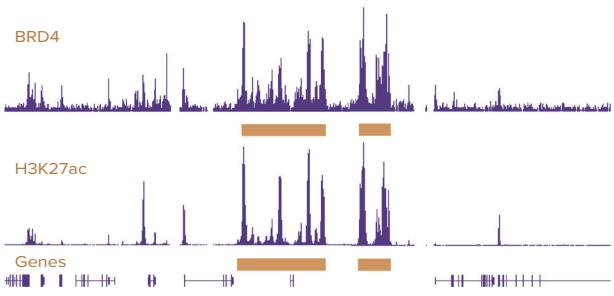


Figure 2: BRD4 and H3K27ac ChIP-Seq data identify Super-Enhancers. The Super-Enhancer is defined by the clustering of high intensity peaks (copper hashes). This Super-Enhancer is marked by high intensity BRD4 and H3K27ac ChIP-Seq signal.

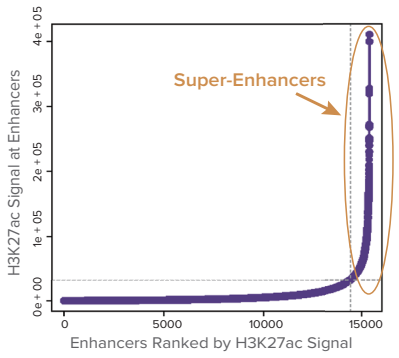


Figure 3: Identification of Super-Enhancers. Enhancers are plotted in increasing order based on ChIP-Seq peak intensity. Super-Enhancers are the population above the inflection point of the curve.

Custom Services
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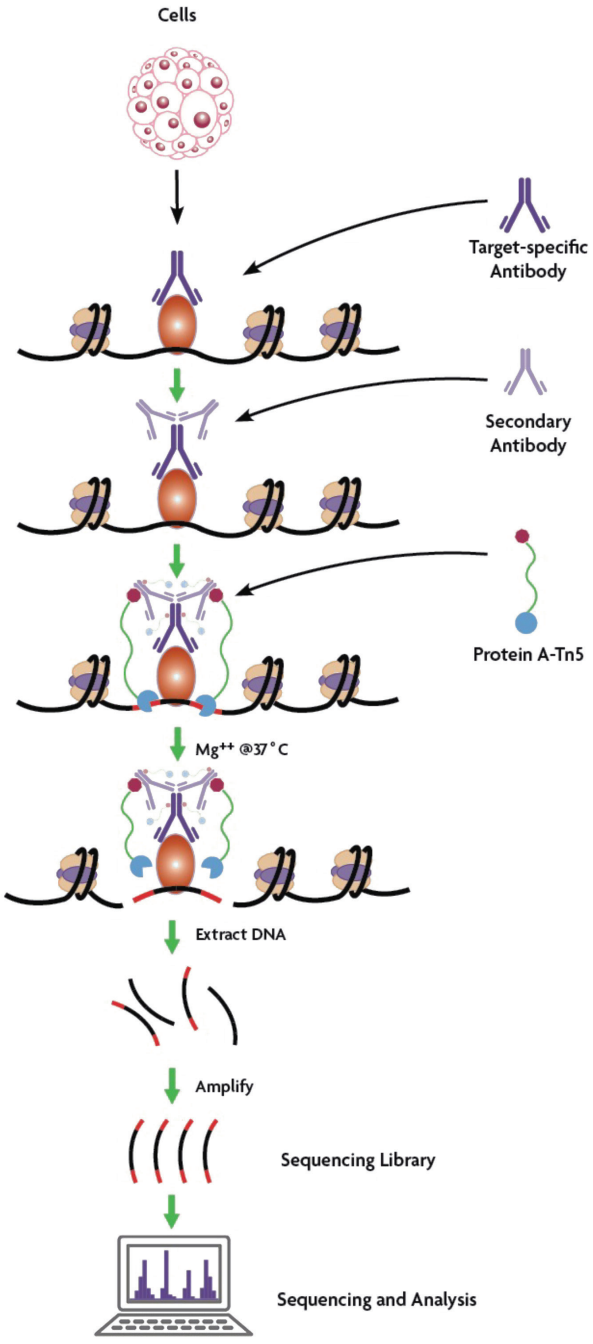
CUT&Tag-IT®* Service
Tn5 Transposase assisted chromatin profiling

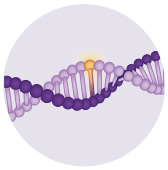


Cleavage Under Targets and Tagmentation (CUT&Tag) is a method to map genomic localization of histone modifications that reveals interactions between proteins and DNA or identifies DNA binding sites for proteins of interest. CUT&Tag utilizes antibody-directed Tn5 Transposase tagmentation* to target specific histone modifications to create genome-wide maps. Tn5 tagmentation sharpens resolution and decreases the sequencing depth requirement compared to ChIP-Seq.

To learn more, visit activemotif.com/services-cut-and-tag.

Figure 4: Our CUT&Tag-IT®* Service is based on the same principles as ChIP-Seq, but with several improvements advantageous for mapping histone marks. Instead of the sonication of fixed chromatin and immunoprecipitation steps performed in ChIP-Seq protocols, in CUT&Tag, unfixed cells are bound to concanavalin A beads and the antibody incubation is performed with cells in their native state. Directly following antibody binding, the chromatin is digested and NGS libraries are prepared in a single step by tagmentation using the protein A-Tn5 (pA-Tn5) transposase enzyme that has been pre-loaded with sequencing adapters.

*Our Tn5 Transposase mediated chromatin tagmentation methods are covered by these patents: US9938524, US10689643B2, EP2783001B1, EP2999784B1.



DNA Methylation Services

services for whole-genome and gene-targeted DNA methylation analysis

Active Motif offers a range of DNA methylation services, each fulfilling a different role depending on experimental needs. RRBS detects 5-methylcytosine genome-wide at single base pair-resolution. MeDIP, as well as our other antibody enrichment assays, generate genome-wide profiles of 5-mc, 5-hmc, 5-fC and 5-caC localization. Targeted bisulfite sequencing is well suited for those who are interested in DNA methylation at a handful of genomic locations.

To learn more, visit activemotif.com/services-methylation.

Targeted Bisulfite Sequencing

Once differentially methylated regions are identified as potential biomarker candidates or regions of interest, these regions require further validation across larger populations. Active Motif's Targeted Next-Generation Bisulfite Sequencing Service offers a single base-pair, high-throughput solution for targeted validation of these regions. Services include:

- Bisulfite conversion
- Primer design and testing
- PCR amplification
- Barcoded library generation
- DNA sequencing
- Data analysis

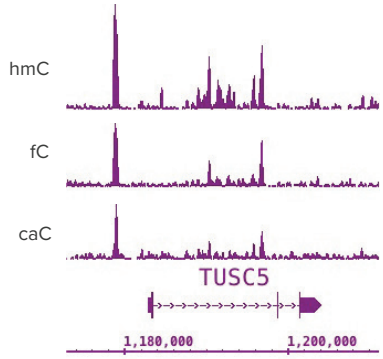


Figure 5: Genome-wide profiling of DNA variants.

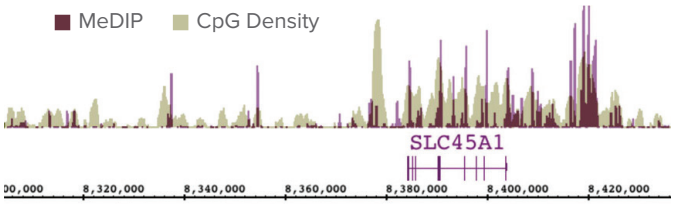


Figure 6: MeDIP DNA methylation data correlates with CpG density.

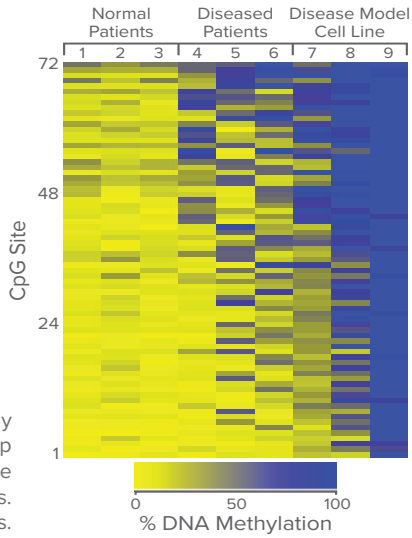


Figure 7: Single base-pair validation of differentially methylated sites identified by MeDIP. Heat map represents Targeted Next-Generation Bisulfite Sequencing data of 72 CpGs from nine samples. Differential methylation is observed across the samples.

Custom Services
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RRBS Services
Reduced Representation Bisulfite Sequencing

DNA methylation patterns are cell-type specific, and alterations in these patterns can be indicative of disease. RRBS is a bisulfite dependent method that provides single base pair resolution of cytosine methylation at millions of locations and allowing for sample-to-sample comparisons of DNA methylation patterns. Comparing DNA methylation profiles from normal and diseased patient samples can facilitate novel biomarker discovery. To learn more, visit activemotif.com/services-rrbs.

Why is RRBS the right choice?

RRBS is significantly less expensive than Whole Genome Bisulfite Sequencing, while still providing the methylation status of up to 5 million CpGs at biologically relevant positions such as promoters and CpG islands. You need only to provide 100 ng of purified DNA, or may also provide cells or tissues.

Why use RRBS for biomarker identification?

Services include:

- Single base resolution
- Quantitation at each base
- Data at millions of locations across the genome
- Data enriched at promoters and CpG islands
- Dramatically less expensive than Whole Genome Bisulfite Sequencing

FEATURES:

- Low starting material requirements
- Data provided on millions of CpGs
- Data from biologically relevant regions
  - Promoters
  - CpG Islands

RRBS Service

Customers submit DNA, cell pellets or frozen tissue then we perform:

1. DNA purification
2. DNA digestion
3. Sequencing adaptor ligation
4. Bisulfite conversion
5. PCR amplification
6. Sequencing on Illumina platform
7. Bioinformatic analysis

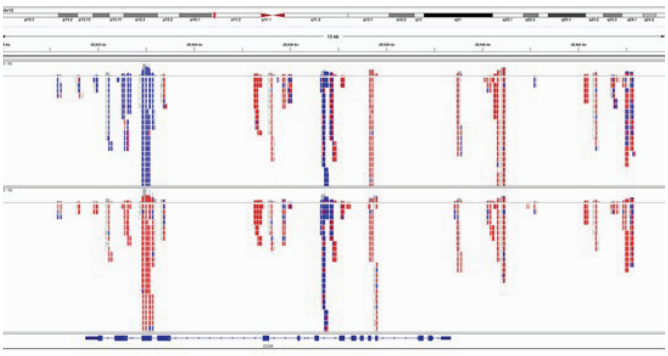


Figure 8 – RRBS data from human samples: The displayed regions are representative regions from the genome-wide data set and shows differential DNA methylation at an exon of CD19. Each block is a separate data point with red representing a methylated cytosine and blue representing an unmethylated base.

ATAC-Seq Services

genome-wide identification of open chromatin regions

Assay for Transposase Accessible Chromatin Sequencing (ATAC-Seq) is designed to study open chromatin, which is known to contain active gene regulatory elements including promoters, enhancers, and insulators. This assay provides data to enable identification of accessible chromatin regions across the genome that are distinct to individual cell types. ATAC-Seq is a perfect first step for those exploring the role of epigenetics in cell systems or disease models for which little information is available on mechanisms of gene regulation.

To learn more, visit activemotif.com/services-atacseq.

Determine if Epigenetic Mechanisms are at Work

- Gain mechanistic insight into gene regulation in response to treatment
- Identify which transcription factors are driving disease or response
- Generate genome-wide profiles from patient samples (cells or tissues)
- Only 50,000 cells required

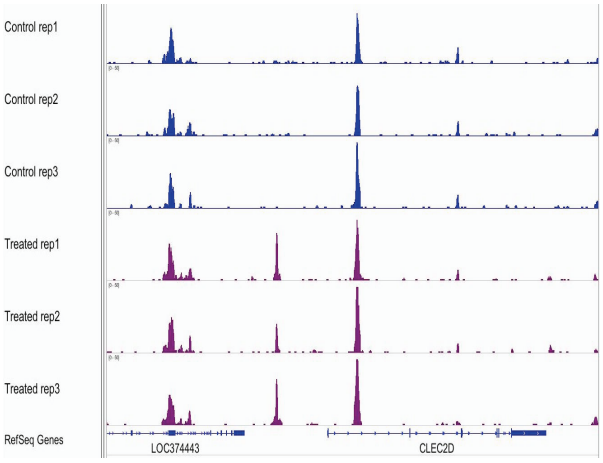


Figure 9: Active Motif's ATAC-Seq assay was performed on control and treated cells, each in triplicate. Hundreds of differential peaks were detected. The one depicted is in an intergenic region.

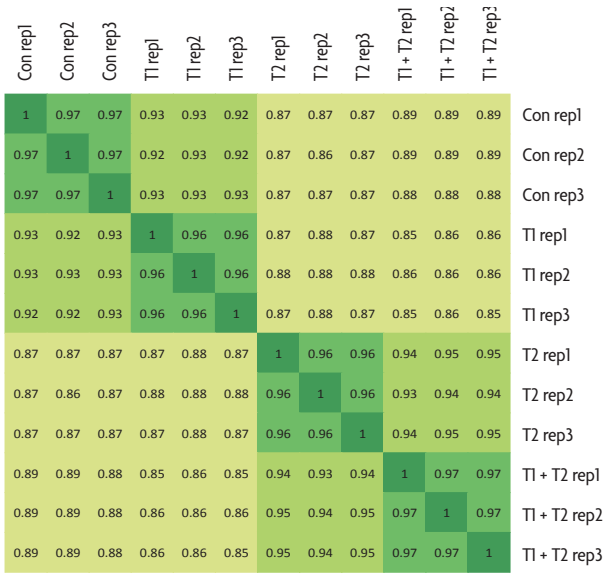
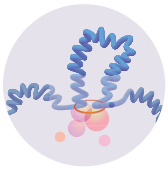


Figure 10: Active Motif's ATAC-Seq assay was performed under four different cellular conditions, each condition in triplicate. The Pearson correlation coefficients were generated and graphed for each pair-wise comparison. The data demonstrates the assay is highly reproducible with correlation coefficients near 1 for replicates. Four separate groups are clearly visible in the heat map, showing that triplicates are more similar to each other than to other samples and indicating differences between sample types.

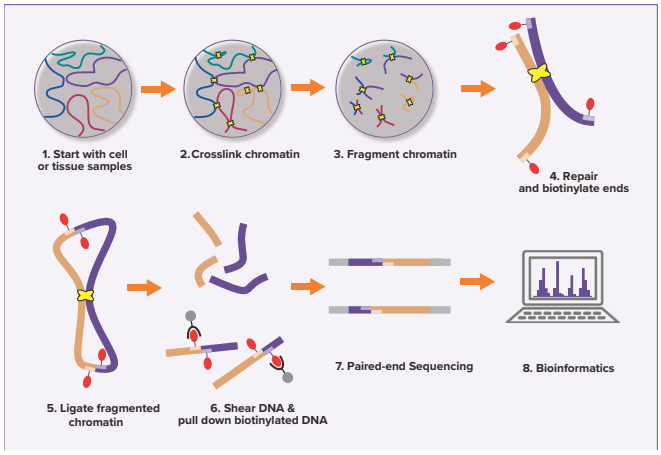


Hi-C Services

map genome-wide chromatin-chromatin interactions using our Hi-C service

Functional elements such as enhancers can influence gene expression by interacting directly with promoters and other loci that may be thousands of kilobases away. Use our end-to-end Hi-C service to map these interactions and get a 3D view of genome organization. Elements detected include A/B compartments, topologically associated domains (TADs), and chromatin loops.

To learn more, visit activemotif.com/services-hi-c.



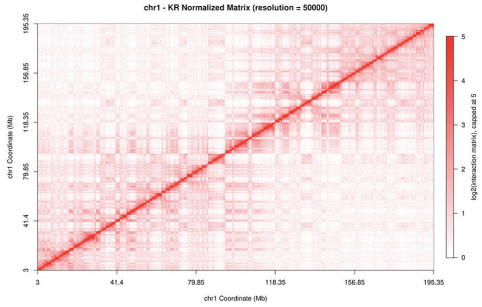


Figure 11: Observe high level chromosome interactions by using Hi-C. Hi-C contact maps of mouse uterine tissue reveal interactions among chromosome 1. Dark red boxes plotted diagonally are the interaction values. A point directly on the diagonal shows the score for how proximal a region is to itself.

ELEMENTS DETECTED INCLUDE:

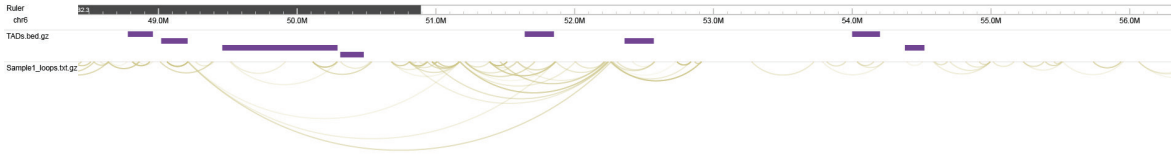


Figure 12. Hi-C enables identification of complex chromatin interactions like chromatin looping and Topological Associating Domains (TADs). Hi-C was performed using mouse uterine tissue. Snapshot of WashU Epigenome Browser looking at a 6.8 Mb region of chromosome 6. Topologically Associating Domains (TADs) are represented as purple bars. Chromatin loops are indicated by brown arcs.

Mod Spec® Services

histone modification detection service

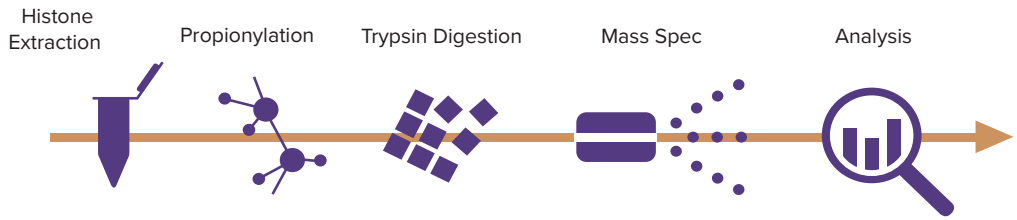
Total nuclear levels of histone post-translational modifications (PTM) may differ under varying conditions – disease vs normal, DMSO vs inhibitor, or WT vs KO. Active Motif's Mod Spec® service can verify expected differences, and more importantly, identify unexpected changes in histone PTM levels. This service uses mass spectrometry for relative quantitation of over 80 histone modifications.

To learn more, visit activemotif.com/modspec.

Quantify Histone Modifications Using Mass Spec

- Optimized to detect over 80 different histone states
- Measure acetylation, methylation, ubiquitination, and unmodified peptides
- Analyze histone modifications on H1, H2, H3.1, H3.3, and H4
- More quantitative and comprehensive than western blots or ELISA
- **No hassle.** Send your cells to Active Motif and receive data

How Does Mod Spec® Work?



Cell pellets or tissues are sent to Active Motif and processed.

1. Histones are acid extracted
2. Lysines are blocked to prevent trypsin cleavage at all lysine amino acids
3. Histones are digested using trypsin
4. Peptide masses are measured using mass spectrometry
5. Data is analyzed to determine modifications on each histone peptide

Custom Services
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Gene Expression Services

RNA-Seq for steady state mRNA levels
RNA Pol II ChIP-Seq for transcription rate measurements

Active Motif transcriptome analysis services include RNA-Seq for identification and quantitation of RNA transcripts and RNA Pol II ChIP-Seq for quantitation of transcription rates to enable rapid profiling of changes in gene expression associated with transcription factor (TF) and histone modification occupancy.

To learn more, visit activemotif.com/rna-seq.

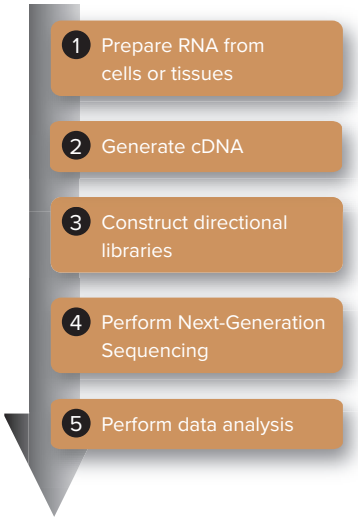
FEATURES:

- PolyA enrichment
- Directional library preparation
- Paired-end sequencing on Illumina sequencing platform
- QC performed using Bioanalyzer
- Data analysis pipelines include differential analysis and GSEA

RNA-Seq Services

Simply submit RNA, cell or tissue samples. Order RNA-Seq alone or combine with ChIP-Seq data to uncover contextual information about:

- Differential gene expression
- Changes in gene structure or splicing patterns
- Effects of TF binding on gene expression



RNA Pol II ChIP-Seq Services

Analysis of RNA Pol II occupancy as a proxy measurement of transcription rates offers the advantage of enabling you to:

- Measure transcription without the influence of RNA half-life
- Identify genes poised for transcriptional activation
- Generate gene expression data from cells used for ChIP-Seq
- Measure changes at early time points post-treatment

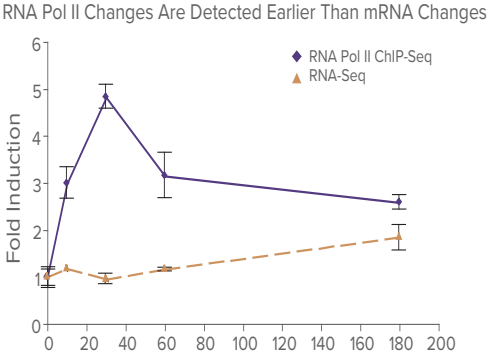


Figure 13: Gene expression profiles vary depending on the analysis method. Data for Igf1r was extracted from RNA–Seq and RNA Pol II ChIP-Seq data sets. Cell treatment resulted in induced gene expression that was measured at various time points. The cumulative data show that transcription, as measured by RNA Pol II ChIP-Seq, is induced immediately, while mRNA levels only accumulate over time.

Interactome Profiling (RIME)

mass spectrometry identifies co-factor recruitment into transcriptional complexes

RIME (Rapid Immunoprecipitation Mass Spectrometry of Endogenous Proteins) sheds light on the complex process of gene regulation by enabling capture and identification of chromatin associated proteins that interact with an endogenous protein of interest. To learn more, visit activemotif.com/rime.

Why RIME?

Gene regulation is often oversimplified when the focus is on one particular transcription factor in any given cell model. In reality, differential gene expression is greatly influenced by co-factors and other protein interactions within chromatin. RIME clarifies this complexity by providing a means to identify the protein interactions that are important for gene regulation.

RIME ADVANTAGES:

- Targets DNA/chromatin associated proteins
- Enables capture of low affinity interactions
- Allows more stringent wash conditions resulting in less non-specific interactions

Experimental Design

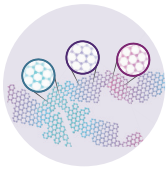
- Antibody validation is performed on a single sample to show that the target protein is detected
- IP-mass spec using the target antibody is performed in duplicate
- IP-mass spec using anti-IgG is performed in duplicate
- IgG interactions are removed from the target antibody specific interaction list

How Does RIME Work?

- Targeted TF
- DNA binding direct interactor
- Non-DNA binding direct interactor
- Indirect interactor

Ligand 1	Ligand 2
Estrogen Receptor	Estrogen Receptor
Nuclear receptor co-activator 3	Vang-like protein 1
Nuclear receptor interacting protein 1	Pericentriolar material 1 protein
Pericentriolar material 1 protein	Centrosomal protein of 131 kDa
Centrosomal protein of 131 kDa	Protein GREB1
CREB-binding protein	E3 ubiquitin-protein ligase TRIM33
E3 ubiquitin-protein ligase TRIM33	Nuclear receptor interacting protein 1

Example data from RIME: Different Estrogen Receptor (ER) binding profiles have been observed depending on the ligand used to stimulate ER binding. Our RIME data shows differential recruitment of co-factors to DNA bound estrogen receptor after ligand 1 and ligand 2 treatment. Grey indicates recruited proteins with similar rank order for both ligands. Red indicates common proteins detected, but with change in order. Purple indicates unique interacting proteins.



Single-Cell ATAC-Seq Services

end-to-end service to identify open chromatin regions at single-cell resolution

Active Motif's scATAC-Seq service enables examination of genome-wide chromatin accessibility of thousands of cells in parallel, allowing examination of subpopulations of cells within a heterogenous population that would otherwise be lost in standard bulk ATAC-Seq.

To learn more, visit activemotif.com/scatac-seq.

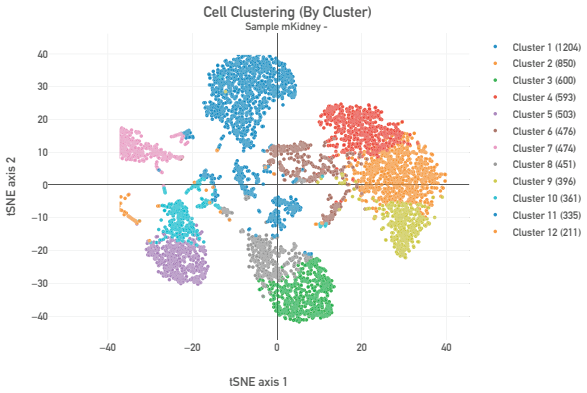


Figure 14: Identify variations in chromatin accessibility across different cell populations within a single sample

ACTIVE MOTIF'S END-TO-END scATAC-SEQ SERVICE INCLUDES:

- Cell preparation
- Transposase reaction
- Sample processed using 10X Genomics Chromium platform
- Library generation
- Sequencing
- Bioinformatic analysis and GSEA

Active Motif's scATAC-Seq service enables examination of genome-wide chromatin accessibility of thousands of cells in parallel, allowing examination of subpopulations of cells within a heterogeneous population that would otherwise be lost in standard bulk ATAC-Seq.

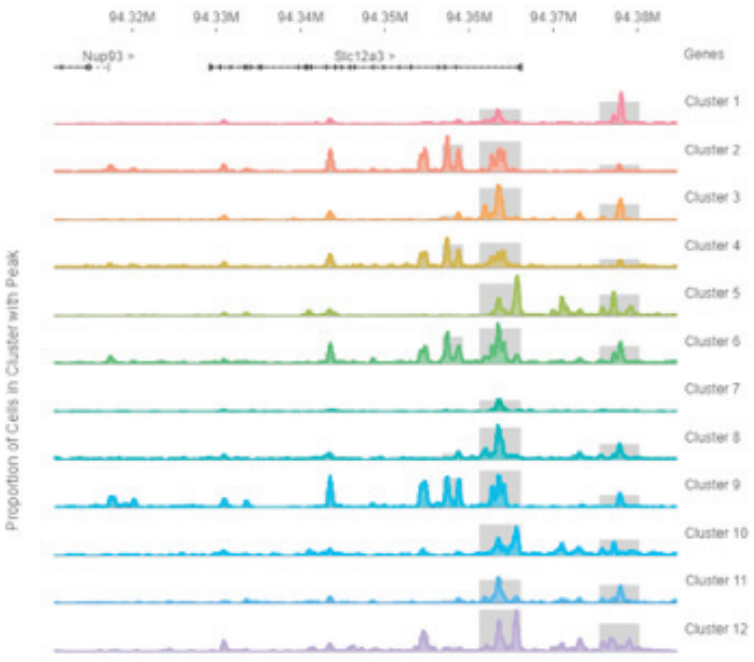


Figure 15: Analysis of individual cell population using scATAC-Seq can reveal cell subpopulation specific data that would not be captured by "bulk" ATAC-Seq.

Representative region using mouse kidney tissue. Each cell cluster is displayed as a unique peak track. scATAC-Seq provides the resolution to identify unique open chromatin peak profiles for each cell population, allowing for the identification of cells that are driving a specific phenotype.

Single-Cell RNA-Seq Services

measure gene expression in heterogeneous populations at single-cell resolution

Single-Cell RNA-Seq enables transcriptome analysis at the single-cell level. scRNA-Seq can be used to identify cell subpopulations with different transcriptome profiles within complex samples, eliminating the need for isolation strategies like FACS or magnetic sorting that could alter the biology of the sample due to sample manipulation.

To learn more, visit activemotif.com/services-scrna-seq.

ACTIVE MOTIF'S END-TO-END scRNA-SEQ SERVICE INCLUDES:

- Cell preparation
- Sample processed using 10X Genomics Chromium platform
- Library generation
- Sequencing
- Bioinformatic analysis

2_4428AM_PBMC-B_scRNA_hg38 Cluster UMAP

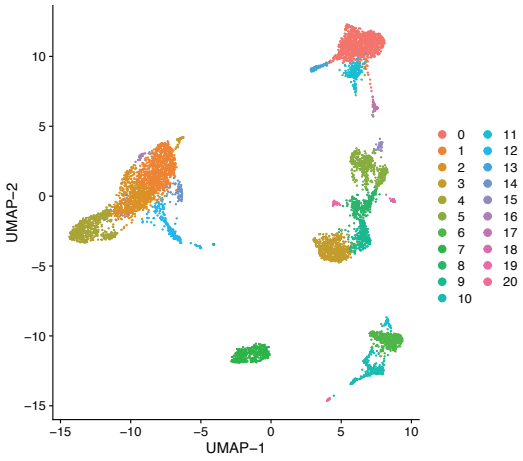


Figure 16: Identify unique subpopulations of cells within a single sample. Single-Cell RNA-Seq data generated from human PBMCs. Each color-coded cluster on the UMAP plot represents populations of cells that have the same gene expression profile. 20 refined clusters were identified.

2_4428AM_PBMC-B_scRNA_hg38 Marker Heatmap

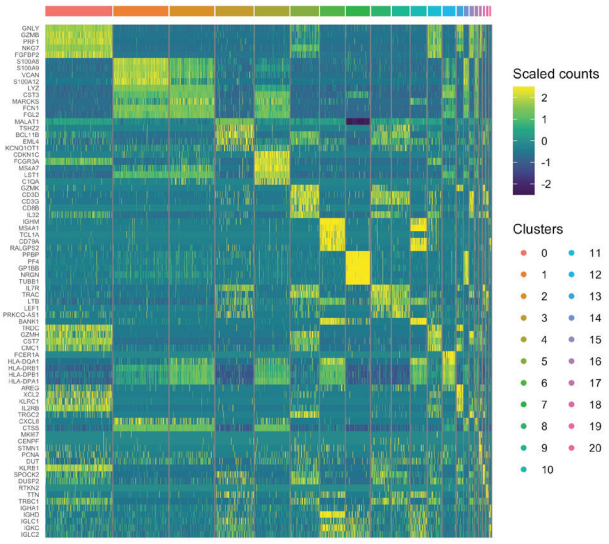
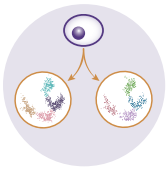


Figure 17: Heatmap of differentially expressed genes per cluster.



Single-Cell Multiome Service

end-to-end service to measure gene expression and open chromatin states from the same cell

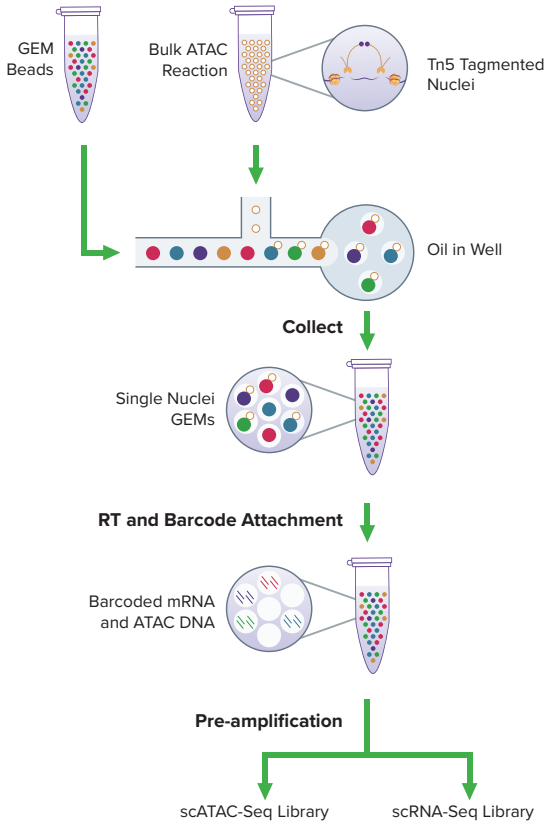


Figure 18: Single-Cell Multiome measures gene expression and open chromatin from the same cell. Tn5 tagmentation is performed on nuclei, which are loaded onto the 10X Genomics Chromium Controller and met with GEMs (gel bead-in-emulsion) containing reverse transcriptase and sequencing adapters. Open chromatin fragments and cDNAs are barcoded, creating two unique libraries per cell.

Single-Cell Multiome allows for both transcriptome analysis and genome-wide detection of open chromatin at the single cell level. Understanding both the gene expression profile and the chromatin state at single-cell resolution can help identify how epigenetic changes instruct gene expression in distinct cell populations.

To learn more, visit activemotif.com/services-scmultiome.

What are the advantages of using Single-Cell Multiome?

Single-Cell Multiome can be used to identify cell subpopulations with different transcriptomal and epigenetic profiles within complex samples, eliminating the need for isolation strategies like FACS or magnetic sorting that could alter the biology due to sample manipulatiaon.

For example:

- Identifying novel cell subpopulations that modulate response to drug treatments (e.g., responders vs. resistant cells)
- Identifying subpopulations of cells with variations in gene expression that can provide insight into developmental trajectories (e.g., brain development, T-helper cell development, B-cell differentiation)

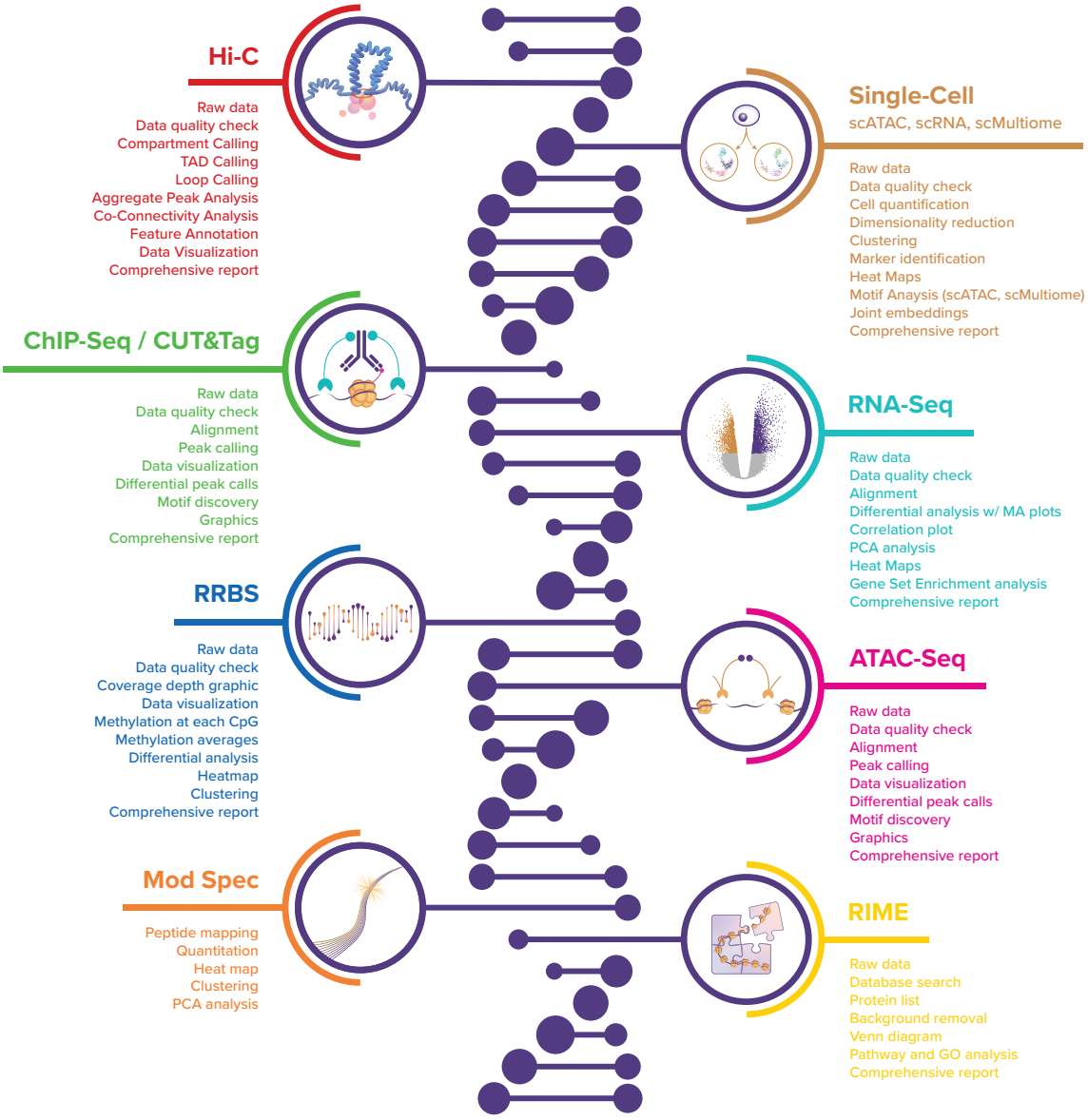
ACTIVE MOTIF'S END-TO-END SINGLE-CELL MULTIOME SERVICE INCLUDES:

- Preparation of nuclei
- Barcoding of mRNA and Tn5-tagmented open chromatin regions in the same nucleus
- Sample processed using 10x Genomics Chromium platform
- Library generation
- Sequencing
- Bioinformatic analysis

Bioinformatics

comprehensive and customizable data analysis and support from our expert team of scientists

To help our clients interpret large and highly complex whole-genome data sets, our Services team provides complete bioinformatic analysis and support for all services. We leverage our extensive experience and background to extract relevant information embedded within complex data sets and provide you with the most meaningful and highest quality data analysis.



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Enabling Epigenetics Research

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- **Publications which cite Active Motif services** – activemotif.com/publications
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