CUSTOM SERVICES
for epigenetics and gene regulation research

- Histone Analysis
- ATAC-Seq
- ChIP-Seq
- DNA Methylation
- Gene Regulation
CUSTOM SERVICES
for epigenetics and gene regulation research

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.

- Total Histone Modification Analysis
- ATAC-Seq
- ChIP-Seq
- ChIP Antibody Validation
- RNA-Seq
- Transcription CoFactor Recruitment (RIME)
- DNA Methylation Assays
- LightSwitch™ Custom Cloning & Mutagenesis
- LightSwitch™ Custom Stable Cell Line Development

For a complete list of available products, please visit us at www.activemotif.com.
MOD SPEC®
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.

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

For more information about Mod Spec® Services, please visit us at www.activemotif.com/services.
HISTONE PTM QUANTITATION

quantify histone modifications in multiplex using Luminex® xMAP® technology

Active Motif now offers Custom Services for our Histone H3 PTM Multiplex Assay. The service uses Luminex® xMAP® magnetic bead-based multiplexing technology to simultaneously measure multiple histone modification targets in a single reaction. This first-of-its-kind multiplex epigenetic assay generates more data with less sample than traditional Western blot or ELISA methods.

The **Histone H3 PTM Quantitation Service** gives you access to ground-breaking technology that enables high-throughput multiplexed screening of histone modifications. The end-to-end, customizable service includes sample preparation, assay design and execution, data analysis and support. Our expert scientists will consult with you on project-specific details and outline an appropriate experimental design.

**SHOULD I CHOOSE MOD-SPEC OR LUMINEX HISTONE PTM QUANTITATION?**

Mod Spec is a great first step for those exploring the possible role of epigenetics in their cell system. A comprehensive screen of more than 80 histone modifications will identify global differences in histone states across samples.

Luminex Histone PTM Quantitation can be used as a follow-up to Mod Spec™. The multiplex panel detects 13 histone PTMs. It is a cost effective, higher throughput method ideal for processing more samples for time point optimization, dose optimization, or patient sample comparisons.

**ASSAY FEATURES**

- **MULTIPLEX**: perform multiple histone modification assays on one or many samples at the same time
- **EFFICIENT**: use less input amounts than WB or ELISAs
- **SENSITIVE**: 250K cells required to multiplex all modifications
- **HIGH CONTENT**: simultaneously measure specific & off-target effects

**AVAILABLE TARGETS**

<table>
<thead>
<tr>
<th>H3K4me3</th>
<th>H3 pan-ac</th>
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<tr>
<td>H3K9ac</td>
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For more information, please visit us at [www.activemotif.com/services-luminex](http://www.activemotif.com/services-luminex).
HISTONE PTM MULTIPLEX ASSAY WORKFLOW

Histone-specific modifications on the N-terminus are captured using antibodies conjugated to fluorescent-labeled magnetic beads. Each bead emits a unique fluorescent signal to enable detection of multiple targets within the same well. A biotinylated H3 C-terminal antibody is used to capture histones. Streptavidin-phycoerythrin is then added to bind biotin and produce a signal. A Luminex instrument is used to read signals and decipher both the bead identity and the number of binding events pertaining to each histone modification.

PROFILE CHANGES IN HISTONE MODIFICATIONS IN CLINICAL AND COMPOUND-TREATED SAMPLES

The Histone H3 PTM Service’s multiplexing and sample throughput capabilities are ideally suited for screening and profiling epigenetic variances caused by disease or compound treatment. Multiplexing has the added advantage of enabling simultaneous analysis of both specific and off-target effects.

FIGURE: The Histone H3 PTM Multiplex Assay shows increased histone acetylation in response to SAHA-mediated HDAC inhibition. HeLa cells treated with increasing concentrations of the HDAC inhibitor SAHA, were evaluated in a multiplex of H3 pan-acetyl, H3S10ph, H3K9ac, H3K4me3, H3K27me2 & H3 Total Ab-conjugated beads using the Histone H3 PTM Multiplex Assay. Total H3 beads were used for normalization. The results demonstrate the ability of the assay to simultaneously assess specific and off-target effects of the treatment on histone modification levels. The dashed lines represent IC50 values, 4.0 μM and 4.6 μM, determined for pan-acetyl and H3K9ac, respectively.
ATAC-Seq

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.

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 1: 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.

To learn more, visit www.activemotif.com/services.

FIGURE 2: 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.
CHOOSE THE GLOBAL LEADER IN END-TO-END ChIP SERVICES

Active Motif offers the most diverse portfolio for ChIP Services. We bring over a decade of experience providing services, with over 15,000 samples processed, and the highest level of expertise of any service provider.

ChIP SERVICES

- ChIP-Seq
  map protein-DNA interactions and histone modifications
- ChIP Antibody Validation
  verify that your antibody performs in ChIP
- ChIP-Seq Spike-in
  a novel data normalization strategy
- Super-enhancer Profiling
  choose from our validated super-enhancer targets
- RNA Pol II ChIP-Seq
  measure transcription rates using ChIP-Seq
- ChIP-qPCR
  custom analysis of any gene

For more information and a complete list of available genome-wide services, please visit us at www.activemotif.com/services.

“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.
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.

ChIP ANTIBODY VALIDATION services to test the suitability of your antibody for ChIP applications

ChIP ANTIBODY VALIDATION SERVICES

1 Customer submits fixed cells or frozen tissue
2 Chromatin preparation
3 ChIP reactions
4 ChIP-Seq library construction
5 Next-Generation Sequencing
6 Data analysis and delivery

PEAKS Antibody passed its validation.

NO PEAKS Antibody failed its validation.

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

For more complete information, visit us at www.activemotif.com/ab-val
ChIP-SEQ SPIKE-IN

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.

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, please visit us at www.activemotif.com/services-normalize

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.

**CHIP-SEQ NORMALIZATION ADVANTAGE**

- Uncover latent or subtle biological effects
- Monitor consistency between samples
- Reduce effects of technical variation
- Reduce sample bias
A standard ChIP reaction is set up using experimental chromatin and an antibody of interest. *Drosophila* Spike-in chromatin and a Spike-in antibody that recognizes the *Drosophila* chromatin are also added to the reaction. Since variation introduced during the ChIP procedure will also occur with the immunoprecipitated Spike-in chromatin, the Spike-in signal can serve as a reference to normalize the test sample signals.

**Available separately:**

<table>
<thead>
<tr>
<th>Product</th>
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<tr>
<td>Spike-in Antibody</td>
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</table>

**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.

*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

**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.**

**SPIKE-IN NORMALIZATION UNVEILS BIOLOGICAL EFFECTS OF COMPOUND TREATMENTS**

**CHIP-SEQ NORMALIZATION WORKFLOW**

A standard ChIP reaction is set up using experimental chromatin and an antibody of interest. *Drosophila* Spike-in chromatin and a Spike-in antibody that recognizes the *Drosophila* chromatin are also added to the reaction. Since variation introduced during the ChIP procedure will also occur with the immunoprecipitated Spike-in chromatin, the Spike-in signal can serve as a reference to normalize the test sample signals.

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**FIGURE:**

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.
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.

FIGURE 1: 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 2: 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.

USE SUPER-ENHANCER SERVICES TO IDENTIFY:
- Master regulators of cell identity
- Regulatory regions associated with disease
- Mechanisms of BRD4 inhibitors

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

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

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 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

To learn more, visit www.activemotif.com/services-expression.
INTERACTOME PROFILING
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.

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

RIME identifies interacting TFs and cofactors

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

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.

For more information about RIME Services, visit www.activemotif.com/rime.

sales@activemotif.com
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, 5fC and 5-caC localization. Targeted bisulfite sequencing is well suited for those who are interested in DNA methylation at a handful of genomic locations.

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

For a complete list of services, visit www.activemotif.com/services-methylation.

FIGURE 1: MeDIP DNA methylation data correlates with CpG density.

FIGURE 2: Genome-wide profiling of DNA variants.

FIGURE 3: 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.
RRBS
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.

WHY IS RRBS THE RIGHT CHOICE?
RRBS is significantly less expensive than Whole Genome Bisulfite Sequencing, while still providing the methylation status of more than 4 million CpGs at biologically relevant positions such as promoters and CpG islands. You need only to provide 1 μg of purified DNA, or may also provide cells or tissues.

WHY USE RRBS FOR BIOMARKER IDENTIFICATION?
• 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: RRBS data using biopsied human kidney tumor and adjacent normal kidney. The displayed region is a representative region from the genome wide data set and shows differential DNA methylation at the promoter of the LAT1 gene. Each block is a separate data point with red representing a methylated cytosine and blue representing the unmethylated base.
BIOINFORMATIC SOLUTIONS

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.

For more information, please visit us at www.activemotif.com/services.
GENE REGULATION SERVICES

LightSwitch™ comprehensive suite of services to accelerate your functional genomics research

The LightSwitch™ Reporter Assay System provides a comprehensive genome-wide approach for studying gene element function and identifying gene regulatory networks on a high-throughput scale. In addition to over 30,000 ready-to-use promoter & 3’UTR reporter constructs, Active Motif offers services for custom cloning and mutagenesis, and custom stable cell line development.

LIGHTSWITCH™ REPORTER ASSAY SYSTEM

THE OPTIMAL SOLUTION FOR GENE REGULATION HIGH-THROUGHPUT SCREENS

The LightSwitch™ Reporter Assay System is a complete solution for performing gene regulation studies and/or high-throughput screening. All LightSwitch vectors utilize our RenSP luciferase engineered for gene regulation experiments to produce higher levels of luminescence with a shorter half-life than other Renilla luciferases. LightSwitch™ reporter vectors provide industry leading sensitivity and dynamic range, which not only enables you to assess the activity of regulatory elements, but also map functional motifs or characterize the effects of sequence variation on gene expression.

Measure luciferase activity to determine the functional effects of TF binding, treatments, sequence variations and/or translation of miRNA binding to the hybrid luciferase-3’UTR mRNA.
LIGHTSWITCH™ CUSTOM SERVICES

assess the activity of regulatory elements using the LightSwitch system engineered to provide industry-leading sensitivity and dynamic range

CUSTOM CLONING & MUTAGENESIS SERVICE

In addition to the 30,000 human regulatory elements available as pre-cloned LightSwitch reporter vectors, Active Motif offers custom services to clone and/or mutate any human, mouse or rat genomic element into any LightSwitch reporter vector. Services include cloning and sequence validation of every reporter construct. LightSwitch vectors are engineered to provide optimal kinetics from your reporter assays, Figure 1, previous page.

SERVICE FEATURES

- Clone any genomic element of interest
- Promoter, long-range, 3’UTR, and 5’UTR reporter vectors available
- Ideal for gene regulation studies or validation of ChIP binding events
- Create sequence variants of any genomic sequence
- Custom vectors ready in 6-8 weeks

INSERT ANY ELEMENT...

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For more on Custom Cloning & Mutagenesis Services or to place an order, please visit www.activemotif.com/ls-services.

IDENTIFY SEQUENCE MOTIFS NECESSARY FOR FUNCTION

RIMS1

WT seed seq | Mutant seed seq
-------------|-----------------|
ACACTCC     | AGTCTCC

GNPDA2

ACACTCCA | AGTCTCCA

ANKR1D13C

ACACTCC | ACAGAACC

G6PC3

ACACTCCA | ACAGAACA

G3BP2

ACACTCC | GGGTCTCC

ALDOA

ACACTCCA | AGTCTCCA

FIGURE 2: LightSwitch 3’ UTR Reporter constructs containing the 3’ UTRs of 6 genes known to be miR-122 target sites were subjected to site-directed mutagenesis. Constructs were co-transfected in cells with an miR-122 miRNA mimic or non-targeting control and then assayed to identify seed sequences necessary for miR-122 function. Wild-type miRNAs reduce luciferase expression through 3’ UTR interactions. miRNA mutations in the seed sequence disrupt miRNA targeting and reduce the functional effect.
TRANSCRIPTIONAL REGULATION
• Assess promoter and enhancer response to transcription factor (TF) modulation
• Confirm functionality of binding sites identified in ChIP-Seq experiments
• Measure functional effects of mutated motifs
• Validate computational predictions and add biological relevance to microarray or NGS data

POST-TRANSCRIPTIONAL REGULATION
• Validate the 3’UTR targets of any miRNA, Figure 2
• Measure the effect of miRNA or siRNA on transcript stability or translation efficiency
• Quantify the impact of a 3’UTR in post-transcriptional gene regulation
• Assess miRNA function in response to various stimuli

HIGH-THROUGHPUT SCREENING (HTS)
• Primary screens using the LightSwitch stable cell lines (agonist or antagonist mode)
• Secondary screens using our collection of over 18,000 promoters, TF response elements, and validated biomarkers
• Investigate MOA, specificity, and off-target effects
• Dose response analysis

CUSTOM STABLE CELL LINE SERVICE
Simplify the task of measuring the response of specific pathways to treatment with various compounds or growth conditions! Choose any regulatory element or biomarker from our collection of over 30,000 targets to create a reporter cell line of your choice. LightSwitch™ reporter cell lines are ideal for both primary and secondary HTS in many different plate-based formats. Use a panel of reporter cell lines to characterize the effect of your compounds on a variety of biological pathways and targets.

VALIDATED PATHWAY REPORTER CELL LINES

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FIGURE 3: Response of the LightSwitch SYT8 Promoter GoClone (Product ID S714388) in HT1080 cells co-transfected with an ER cDNA expression plasmid, upon treatment with five estrogen compounds at different doses for 24 hours before the luminescence was measured using the LightSwitch Luciferase Assay Kit.