



Apple
(*Malus domestica*)



Alligator
(*Alligator mississippiensis*)



Cow
(*Bos taurus*)



Barrel Clover
(*Medicago truncatula*)



Chicken
(*Gallus gallus domesticus*)



Platypus
(*Ornithorhynchus anatinus*)



Salmon
(*Salmo salar*)



Rat
(*Rattus norvegicus*)



Mouse
(*Mus musculus*)

Epigenetics Services

Explore with Next-Gen Sequencing

Shown here are some of the diverse species analyzed by our team



Human
(*Homo sapien*)



Wheat
(*Triticum*)



Dog
(*Canis lupus familiaris*)



Opossum
(*Didelphimorphia*)



Soybean
(*Glycine max*)



Pig
(*Sus scrofa domestica*)



Bean
(*Phaseolus vulgaris*)



Wine Grape
(*Vitis vinifera*)



Fruit Fly
(*Drosophila melanogaster*)



Rockcress
(*Arabidopsis*)



Baboon
(*Papio anubis*)



Guinea Pig
(*Cavia porcellus*)



Earthworm
(*Lumbricina*)



Cod
(*Gadus morhua*)



Sheep
(*Ovis aries*)



Zebrafish
(*Danio rerio*)



Zebra Finch
(*Taeniopygia guttata*)



ZYMO RESEARCH

The Beauty of Science is to Make Things Simple

Overview

Epigenetic Analysis



Epigenetic Biomarker Discovery Program
Start to finish development for your diagnostic test



DNA Methylation
Platforms for genome-wide and targeted single-base resolution DNA methylation analysis



MethylCheck™ Bisulfite Sequencing
Validate epigenetic markers from a large sample cohort or specific gene region



DNA Hydroxymethylation: RRHP™
Single-base resolution platforms for detection of 5-hydroxymethylation in DNA



ChIP-Seq
Genome-wide analysis of protein-DNA interactions

Expression Services



RNA-Seq
Transcriptome-wide analysis of total RNA or small RNA (miRNA)

Epigenetic Aging Clock Service



Epigenetic Aging Clock
Gauge the biological age from a wide variety of human samples

Additional Services



Mass Spectrometry
Global quantitative analysis of DNA methylation and hydroxymethylation levels



Custom Bioinformatics
Fully customizable bioinformatics solutions for the analysis of raw data from any of your Next-Generation Sequencing experiments



Microbiomics Services
Next-Generation Sequencing services for microbiomics, including discovery, identification, and characterization of microbial communities

Epigenetic Biomarker Discovery Program



From Collection to Conclusion

Zymo Research offers a new Epigenetic Biomarker Discovery Program for the development of epigenetic lab diagnostic tests. Whether you are interested in developing epigenetic tests for cancer, developmental disorders, autoimmune diseases, obesity and other anomalies, Zymo Research provides a solution for sample collection through to commercial development. The experts at Zymo Research can help you at any step in the development pipeline by offering a portfolio of products and services for sample collection and purification, biomarker discovery, biomarker validation, platform selection and commercial development.

Sample Collection & Purification

Zymo Research offers specialized collection devices and purification kits for tissues, feces, urine, blood, and other biological specimens. Sample collection begins with DNA/RNA Shield™, which is an innovative stabilization reagent that allows samples to be stored and transported at ambient temperatures. DNA/RNA Shield™ does not require the need for refrigeration or specialized equipment, and makes shipping your precious specimens to Zymo Research easy.



Biomarker Discovery: Epigenetic NGS Services

With the latest Next-Generation Sequencing technologies for DNA methylation analysis, Zymo Research provides comprehensive services and bioinformatics analysis to help discover epigenetic biomarkers in your specific sample set. Zymo Research's Illumina® certified MethylSeq® platforms are each designed to suit your specific coverage needs.



Epigenetic Biomarker Validation

Zymo Research offers the simplest way to validate epigenetic biomarkers with our MethylCheck™ sequencing platform. Whether you have genome-wide DNA methylation (450K/EPIC array or RRBS) data or a particular gene region in mind, our scientists will design, validate, and evaluate site-specific DNA methylation changes.



Platform Selection

Once you have your specific biomarkers narrowed down and validated, Zymo Research will help you select the most sensitive and cost-effective platform for your lab diagnostic test. A wide range of citation-leading bisulfite and bisulfite-free methods are available to implement your test.

Commercial Development

Zymo Research's associates, Pangea™ CLIA-certified lab, will help you to bring your lab diagnostic test to the market.



Inquire about the Epigenetic Biomarker Discovery Program today at
www.zymoresearch.com/services

DNA Methylation Services

5-mC

Zymo Research offers three platforms for genome-wide DNA methylation analysis at single nucleotide resolution, each designed to suit your specific coverage needs. The main difference between the platforms is the percentage of the total genome actually being sequenced. All platforms accommodate a wide range of sample types, including any species with a reference genome, low-input (>10 ng), and FFPE samples.

Classic RRBS (Reduced Representation Bisulfite Sequencing) combines restriction enzyme digestion with bisulfite sequencing to enrich for a CpG-dense fraction of the genome. The Classic RRBS platform allows for a maximum amount of methylation data using a minimal amount of sequencing at a significantly reduced cost. This combination makes Classic RRBS the perfect platform for pilot studies. Classic RRBS covers $\geq 70\%$ all CpG islands, $>75\%$ all gene promoters, and detects 1.5-2 million unique CpG sites at 5-10x average minimum coverage*.

Methyl-MiniSeq[®] is an expanded version of Classic RRBS. The system is extremely robust and the read depth is impressive, making it ideal for biomarker discovery using identification of differentially methylated regions. The low cost of this platform relative to the sequence data it produces also makes Methyl-MiniSeq[®] a good platform for pilot studies. Methyl-MiniSeq[®] covers $\geq 85\%$ all CpG islands, $>80\%$ all gene promoters, and captures approximately 4 million unique CpG sites at 5-10x average minimum coverage*.

Methyl-MaxiSeq[®] is a whole-genome bisulfite sequencing (WGBS) option that provides DNA methylation information at single nucleotide resolution in a CpG context, as well as in the less common CHG and CHH contexts, across all regions of the genome.

The Basic Service package for each platform includes sample standardization, library construction, sequencing, and raw data alignment. The Full Service package offers additional down-stream bioinformatics processing and statistical analysis.

Service Option	Classic RRBS	Methyl-MiniSeq [®]	Methyl-MaxiSeq [®]
Capable with low DNA input?	Yes	Yes	Yes
Single-base Resolution?	Yes	Yes	Yes
Methylome Coverage*	1.5 - 2 million sites	3 - 4 million sites	Entire methylome
Quantitative Analysis?	Yes	Yes	Yes
Genomic Regions covered	Nearly all CpG islands and gene promoters	Twice as many unique CpG sites compared to Classic RRBS	Entire methylome
Notes	Efficient genome-wide analysis	Robust biomarker discovery	Complete methylation analysis

* coverage estimates based on the human genome

** depends on capture efficiency and methylation levels

Inquire about DNA Methylation Services today at
www.zymoresearch.com/services

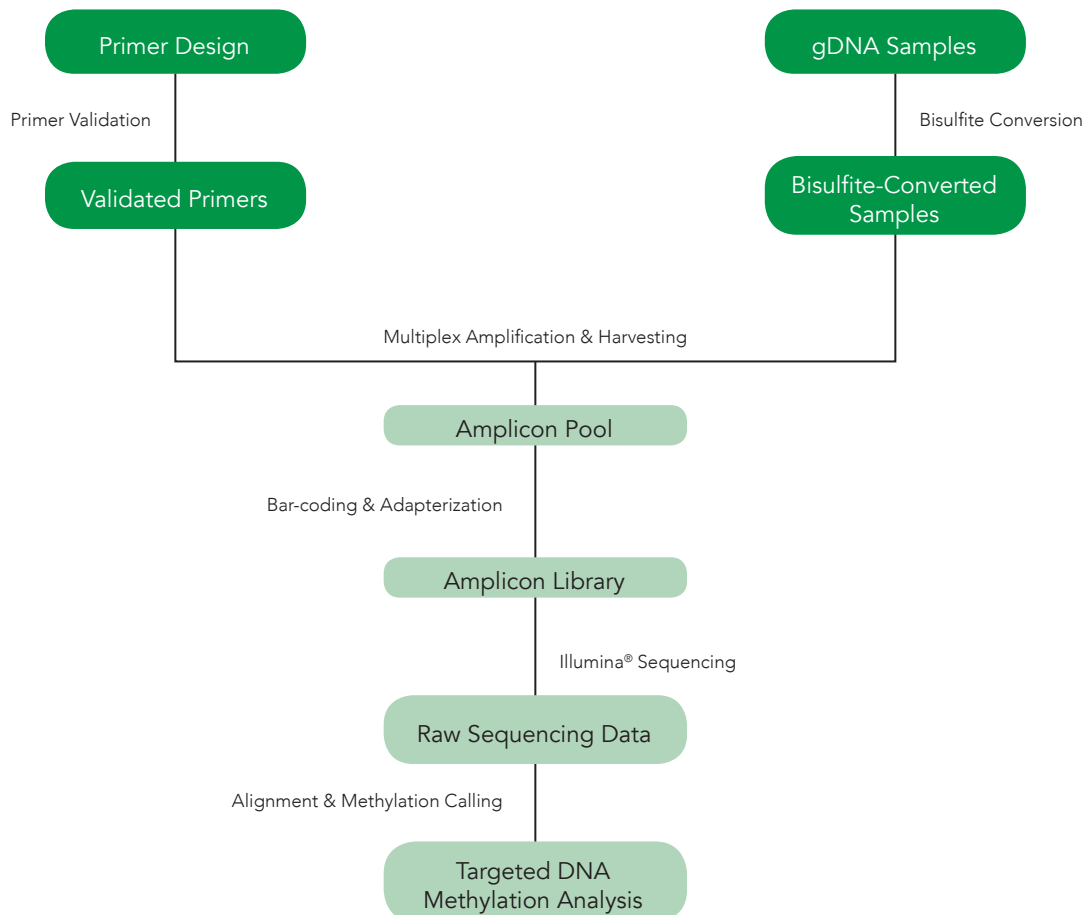
MethylCheck™



Zymo Research makes epigenetic biomarker validation simple with our MethylCheck™ platform. Whether you have methylation array (450K/EPIC) data that you would like to validate in a large sample cohort or have a specific gene region in mind, our scientists are available to design, validate, and evaluate site-specific DNA methylation changes. Simply send us your samples and regions of interest, and we will perform every step through data analysis, sending you back publication-quality graphs and figures.

The Targeted Bisulfite Sequencing service includes:

- Primer Design and Validation
- Targeted Amplification
- Adapterization and Barcoding
- Sequencing with Illumina® Technology
- Sequence Alignment to Reference Genome
- DNA Methylation Analysis



Inquire about MethylCheck™ Services today at www.zymoresearch.com/services

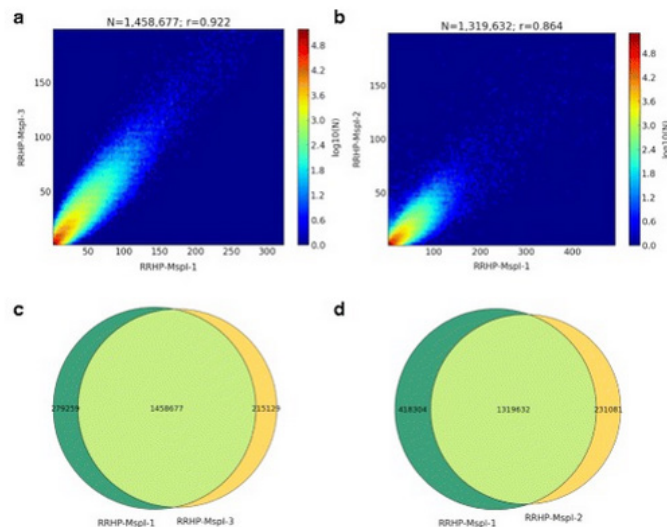
DNA Hydroxymethylation

5-hmC

Zymo Research's platform for the analysis of DNA hydroxymethylation have unparalleled sensitivity and coverage of 5-hydroxymethylcytosine (5-hmC). With traditional bisulfite-conversion methods, 5-hmC cannot be distinguished from 5-mC. Therefore, Zymo Research has developed Reduced Representation Hydroxymethylcytosine Profiling (RRHP®), combined with Next-Generation sequencing to ensure high coverage and sensitivity for the detection of 5-hmC at single-base resolution. RRHP® allows genome-wide profiling for 5-hmC with reduced sequencing requirements.

Reduced Representation Hydroxymethylation Profiling - RRHP®

This service is for genome-wide profiling of 5-hydroxymethylcytosine in DNA at single-nucleotide resolution. RRHP® also allows strand-specific determination of the location of the 5-hmC modification, as well as relative quantification of 5-hmC levels. Data from RRHP® can be combined with DNA methylation data from Methyl-MiniSeq®, allowing for direct comparison of DNA methylation and hydroxymethylation in the same sample. RRHP® is compatible with low DNA inputs and has the added advantage of providing read data for simultaneous SNP detection.



Replicate sample 5-hmC levels show very strong correlation when assessed using the RRHP® platform.

(Petterson A, Chung TH, Tan D, Sun X, Jia XY. Genome Biol. 2014 Sep 24;15(9):456.)

Inquire about DNA Hydroxymethylation Services today at
www.zymoresearch.com/services

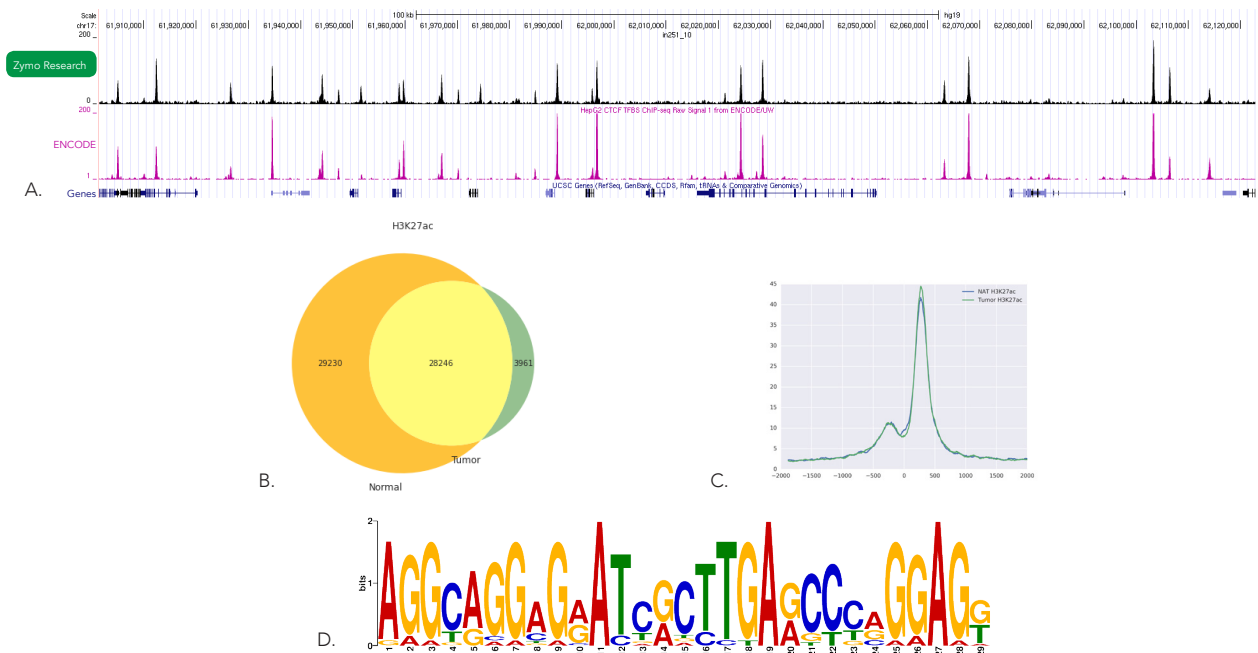
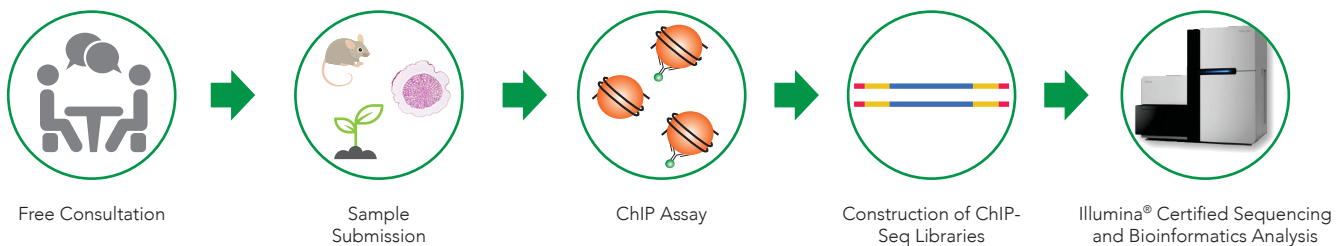
ChIP Seq



Chromatin Immunoprecipitation Sequencing (ChIP-Seq) is a technique that combines chromatin immunoprecipitation with the quantitative power and genome-wide coverage of Next-Generation Sequencing. It is a powerful tool for genome-wide mapping of DNA interactions with transcription factors, histone modifications, and chromatin binding proteins and is essential for understanding the effect of DNA-protein interactions on gene regulation.

With the ChIP-Seq service from Zymo Research, you can either perform the ChIP assay yourself and send us the enriched DNA for library construction and Next-Gen Sequencing, or we can process your samples using our proprietary chromatin shearing and enrichment procedures. We also perform the bioinformatics and statistical analyses, and send you the publication-ready results.

Simply send us your samples and we will handle the rest!



Example of Zymo Research's ChIP-Seq Services Data Output: A. Browser tracks for visualization of peak regions. B. Venn diagram showing sample comparison data. C. Peak density profile to analyze peak locations relative to transcriptional start sites. D. Motif analysis to analyze bound genomic regions.

Inquire about ChIP Seq Services today at
www.zymoresearch.com/services

RNA-Seq Services



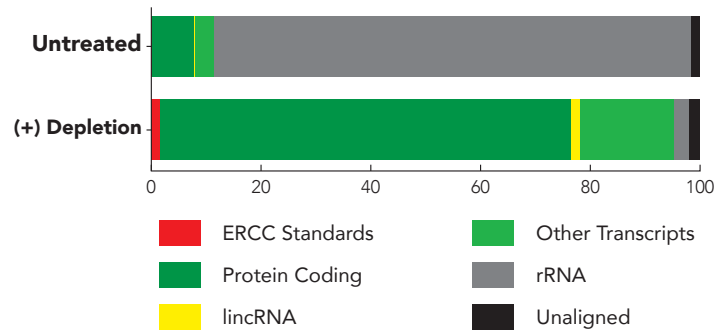
Zymo Research's RNA-Seq service makes transcriptome analysis available to every researcher, without the need for expensive equipment or bioinformatics expertise. Now you can achieve transcriptome-wide coverage of total RNA or small RNA with the latest Next-Gen Sequencing technology.

Let Zymo Research do the work for you!

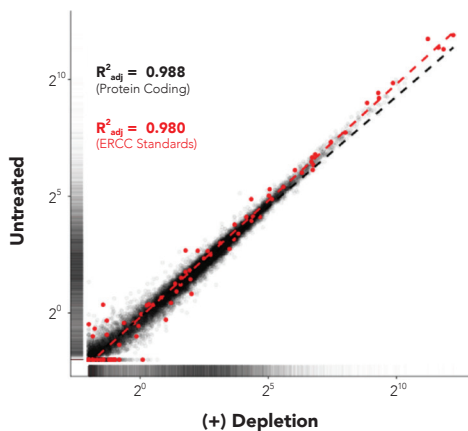
- **Simple and customizable:** All RNA purification, sample prep, sequencing, and bioinformatics analysis is included. Each project is customizable and delivers publication-ready figures.
- **Maximize Coverage:** Proprietary depletion method minimizes bias during rRNA removal, allowing for cost effective sequencing to increase coverage of relevant transcripts, no matter the sample type.
- **Stringent QC:** Each library is assessed using standards to ensure that quality data is generated.
- **Available Services:** Total RNA-Seq and miRNA-Seq.

Maximize Coverage

All RNA-Seq services projects use cutting-edge methods to prepare your libraries. Shown here is a proprietary depletion method to eliminate rRNA transcripts from your sample with virtually zero bias. Stacked bar plot represents read classification by gene biotype of Universal Human Reference RNA samples using the Zymo Research RNA-Seq analysis pipeline.

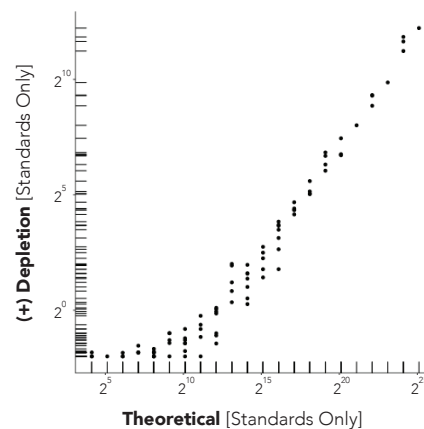


Unbiased Depletion



Have confidence in your data every time with increasing read depth of relevant transcript coverage. Scatterplot demonstrates that rRNA Depletion (Y-axis) vs Untreated (X-axis) RPKM show virtually no bias in both gene expression (black) and spike-in standards (red).

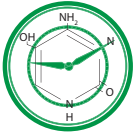
Stringent QC Using Standards



Empirical quality control ensures reliable data generation and interpretation. RNA-seq pipelines are optimized using spike-in standards to deliver data of the highest quality and rigor, with the lowest bias. Scatterplot comparing measured (Y-axis) vs theoretical (X-axis) RPKM for spike-in standards

Inquire about RNA-Seq Services today at
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Epigenetics Aging Clock



Highlights

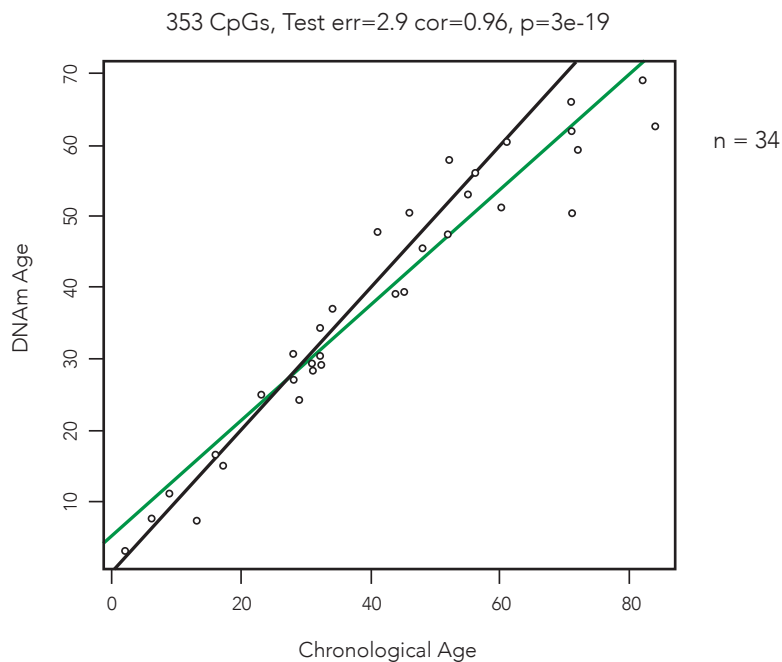
- Reliably determine the true biological age of any human sample.
- Quantify changes in biological age following lifestyle interventions or drug treatments.
- Identify disease associated aging alterations.

A growing number of studies have highlighted the strong correlation of DNA methylation changes with aging. Additionally, accelerated biological aging, as determined by DNA methylation profiling, has been associated with disease phenotypes including Down Syndrome and HIV-1-infection. DNA methylation-based biological age is a valuable surrogate biomarker of molecular aging.

The Epigenetic Aging Clock Service allows you to effectively gauge the biological age of any human tissue sample. With this easy to use service, the only thing you have to do is provide us with the sample. Starting with DNA purification all the way through bioinformatics analysis, Zymo Research scientists will do the work for you and provide you with an accurate biological age estimate along with a comprehensive report. Enhance any aging study or satisfy your intellectual curiosity with this multi-tissue age predictor.

This profiler is designed to:

- Detect methylation changes at highly informative CpG sites
- Use optimized data analysis workflow to provide an accurate biological age



Predicted epigenetic age of urine samples from healthy donors.

Inquire about Epigenetics Aging Clock Services today at
www.zymoresearch.com/services

Additional Services



Mass Spectrometry

Zymo Research offers DNA composition analysis with LC/MS analysis. Please inquire for more information.



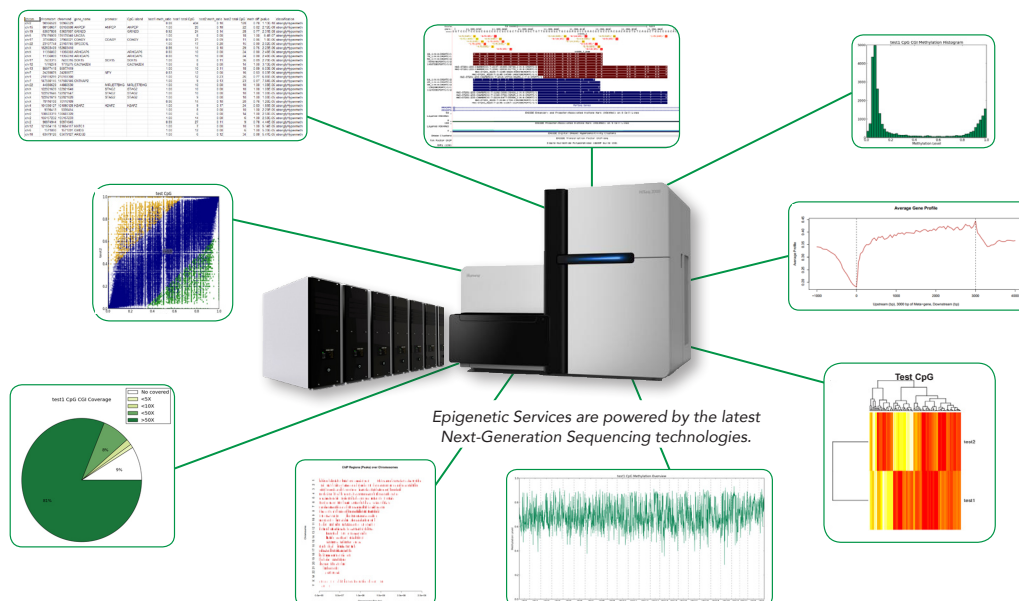
Custom Bioinformatics

Do you have Next-Generation Sequencing data that you need analyzed? Zymo Research offers complete bioinformatics solutions to fulfill your needs. Whether it is whole-genome bisulfite sequencing data or ChIP-Seq data, we can help make sense of your overwhelming data sets. We use established as well as customizable bioinformatic pipelines to transform raw sequence data into manageable and interpretable figures and data sets. Simply provide the raw (FASTQ) or aligned (SAM or BAM) data and we will provide you with your desired downstream analyses.

Service Packages

Basic Service Packages for all of the platforms include sample standardization, library construction, Next-Generation Sequencing, and raw data alignment.

Full Service Packages offer additional down-stream bioinformatic processing and statistical analysis specifically tailored to fit your needs.



Inquire about additional services today at
www.zymoresearch.com/services

Microbiomics Services

A Complete Solution for Unbiased Microbiome Profiling

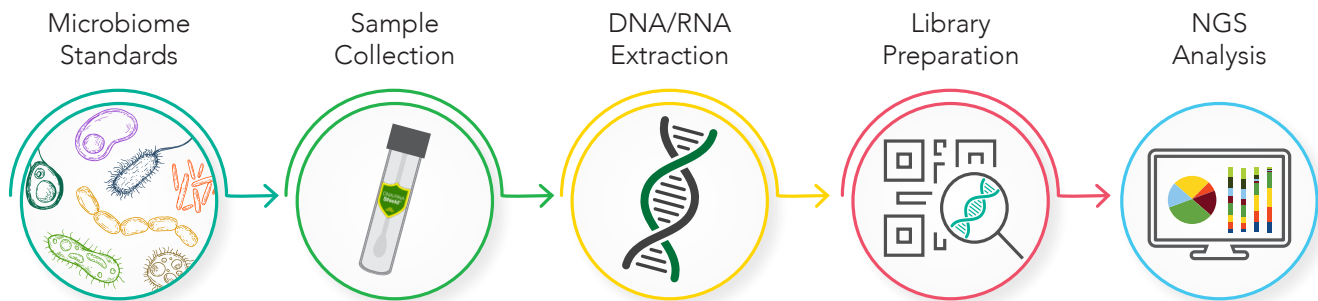
- Simply submit samples and receive a comprehensive, customizable, and user-friendly report
- Unbiased & contamination-free sample processing validated using microbial standards

Quick Turnaround

- Results in ≤ 2 weeks for 16S rRNA gene sequencing
- Results in ≤ 6 weeks for shotgun metagenomic sequencing

Superior Taxonomic Resolution

- Species-level resolution with 16S rRNA gene sequencing
- Strain-level resolution with shotgun metagenomic sequencing



All ZymoBIOMICS® Services include comprehensive bioinformatics and statistical analyses for each microbiomics project. The report can be customized according to each unique project or application. Let Zymo Research do the bioinformatics so that you don't have to!

Typical Analyses Include:

- Composition Barplots
- Taxonomy Heatmap
- Alpha-Diversity
- Beta-Diversity
- LEfSe Biomarker Discovery
- Taxa2SV Decomposer

Inquire about microbiomics services today at
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