HOLOGIC®
Diagenode

Accelerating Biomarker Discovery with Epigenomics

Our Services by the Numbers

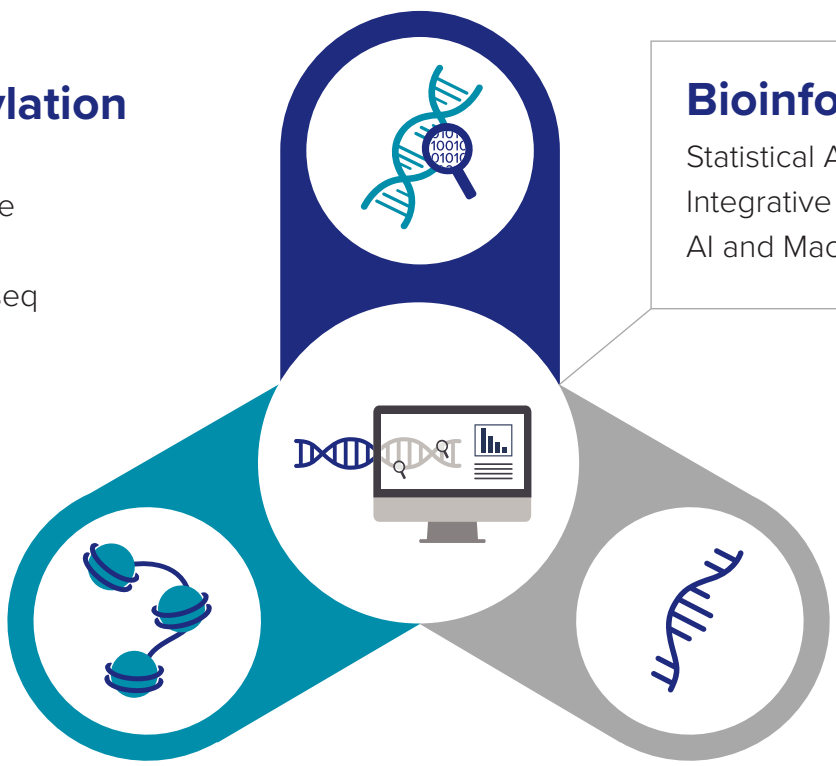
40,000+ samples
including liquid biopsies

250+ projects
Biotech & Pharma

600+ projects
Academia/Government/
Nonprofit Organization (NPO)

DNA Methylation
WGBS/EM-seq
Human Methylome
Infinium Arrays
Targeted Methyl-seq
RRBS

Bioinformatics
Statistical Analysis
Integrative Multi-omics
AI and Machine Learning



Chromatin
ChIP-seq
ATAC-seq
CUT&Tag

RNA
Total RNA-seq
mRNA-seq
Small RNA-seq

Our Service Laboratory Facilities:

USA: San Diego, CA
CLIA environment*

Europe: Liège, Belgium

***Note:** Epigenomic testing services are research use only and do not necessarily comply with all CLIA requirements.*

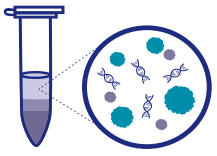
For more information: **diagenode.com**

Epigenomics Meets Diagnostics: Case-Studies

DNA Methylation in Liquid Biopsies: Overcoming Early Detection Challenges in Cancer

We leveraged our 20 years of epigenomic expertise to help Universal Diagnostics (UDx) develop a customized early-detection workflow for colorectal cancer (CRC), integrating liquid biopsies with DNA methylation technologies for biomarker discovery and validation.

Our Approach



Capturing Biomarkers in Real-Time with Liquid Biopsy

Using cell-free DNA isolated from plasma, biomarkers were monitored in real-time in the risk population.

DNA Methylation for Cancer Classification

Genome-wide methylation profiles from healthy and cancer patients were created to identify potential biomarkers.

Biomarker Validation

Once a pool of potential biomarkers was available, the best performers were identified.

"With the help of Hologic Diagenode's experts, we are developing blood tests that detect cancer in its earliest stages."

Kristi Kruusmaa, Chief Scientific Officer, Universal Diagnostics

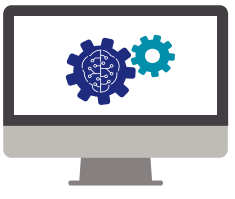
AI and Epigenomics: Powering Biomarker Signature Identification

DNA methylation signatures are highly sensitive and specific, making them ideal for early detection, surveillance screening, and monitoring of minimal residual disease (MRD) for cancer and beyond.

Our Approach

DNA Methylation Profiling

Tissue-specific and cancer-specific DNA methylation profiles can be found in previously published and publicly available databases or via genome-wide *de novo* analyses, such as our WGBS/EM-seq, Human Methylome and EPIC array.



AI and Machine Learning (ML)

Biomarker signatures can be identified bioinformatically using AI and ML analysis approaches.

Biomarker Validation

Biomarkers could then be validated on an independent cohort, publicly available or via new data generated from our custom Targeted Methyl-seq.

Learn more about our services:
www.diagenode.com

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Last update: 01_2025