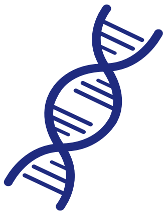
HOLOGIC®
Diagenode

Accelerating Biomarker Discovery with Epigenomics

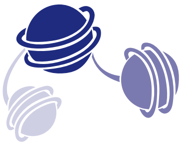
Our services in numbers

40,000+ samples	250+ projects	600+ projects
including liquid biopsies	Biotech & Pharma	Academia/Government/NFP



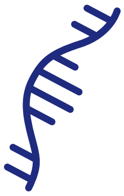
DNA methylation

- Whole genome methylation: bisulfite (WGBS) and enzymatic (EM-seq)
- Human methylome
- Infinium Methylation Arrays: for Human Cancer (EPIC V2.0), population epidemiology (MSA) and for Mouse (MMA)
- RRBS
- Targeted custom methyl-seq



Chromatin

- Histone modifications profiling (ChIP-seq and CUT&Tag)
- Transcription factors binding (ChIP-seq)
- Chromatin accessibility (ATAC-seq)



RNA

- Whole transcriptome (total RNA-seq)
- Messenger RNA (mRNA-seq)
- Small non coding and circulating RNA (D-Plex)

Bioinformatics & Data Analysis

- Statistical analysis
- Multi-omics integrative analysis
- AI and machine learning

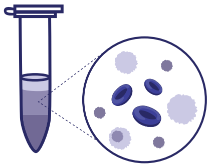
www.diagenode.com

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 (cfDNA) 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

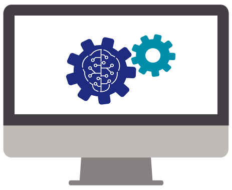
Once a pool of potential biomarkers was available, the best performers were identified.

> “With the help of Hologic Diagenode’s experts, we are developing blood tests that detect cancer in its earliest stages.”

AI and Epigenomics: Powering Biomarker Signature Identification

DNA methylation signatures are highly sensitive and specific, thus ideal for early detection, surveillance screening, and monitoring/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 analysis, such as our WGBS/EM-seq, Human Methylome and EPIC array.

AI and 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.

Last update: 09_2024

Learn more about our services:
www.diagenode.com

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