

**TRUE DISCOVERY™**

# IMMUNO PEPTIDOME PROFILING

## Case Study

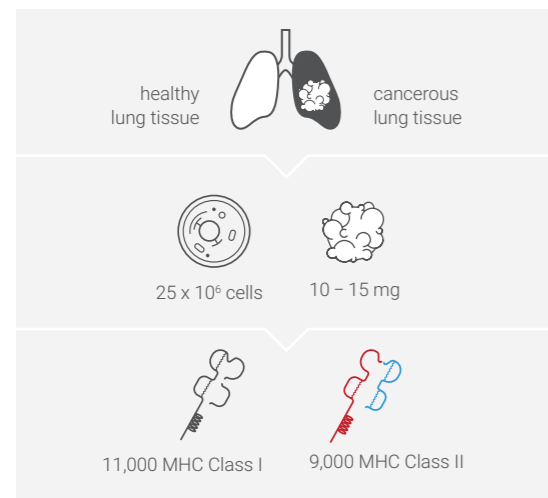
BIOGNOSYS IMMUNOPEPTIDOME  
PROFILING SOLUTION FOR MHC CLASS I  
AND CLASS II NEOANTIGENS DISCOVERY  
IN TUMOR BIOPSIES

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# A HIGH-THROUGHPUT SOLUTION FOR IMMUNOPEPTIDES ANALYSIS FROM NEEDLE-SIZED BIOPSIES

Mass spectrometry offers the possibility to identify more than **10,000 peptides** of each immunopeptide class (MHC-I and MHC-II) that are relevant for your drug discovery research.

## Study Overview



## About Immunopeptidomics

The immunopeptidome consists of peptides bound by the major histocompatibility complex (MHC) proteins. In humans these complexes are termed human leukocyte antigens (HLA). The immunopeptidome is involved in antigen-presentation pathways and plays an essential role in cell-mediated and humoral responses. Deep characterization of the immunopeptidome can support the development of new therapeutics for cancer, immunological diseases, and infectious diseases.

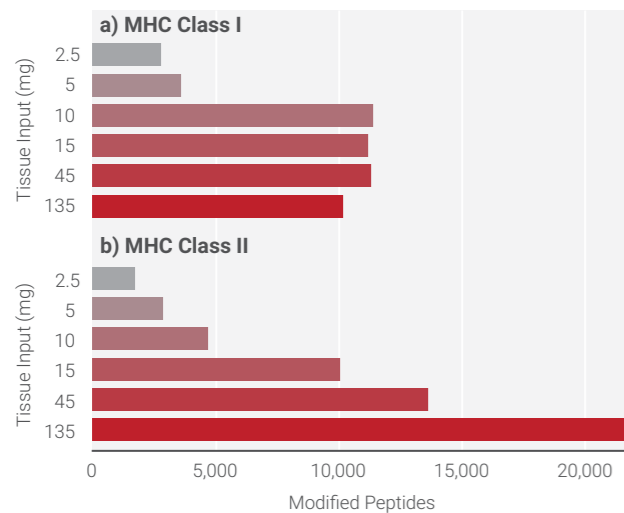
## Study Design

In this case study, we measured a cohort of 12 cancerous and matched healthy lung biopsies from as little as 15 mg of tissue. The immunopeptidomics analysis of MHC Class I and Class II peptides was conducted using Biognosys' Immunopeptidome Profiling solution, our proprietary pipeline for human cell line and tissues.

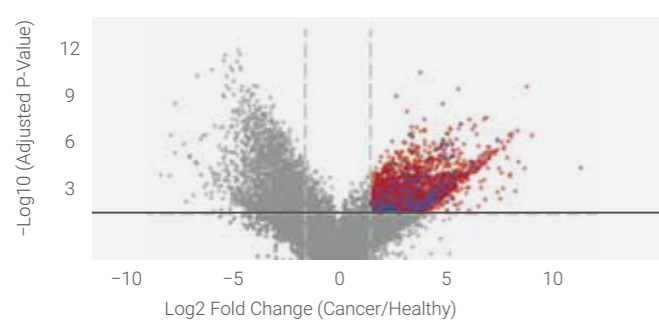
## High-quality Identifications

We identified > 11,000 Class I and > 9,000 Class II immunopeptides on average. The immunopeptide enrichment was extremely sensitive, even from small tissue amounts (e. g. 15 mg).

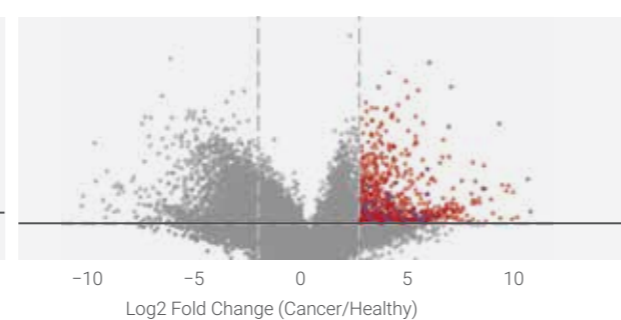
## Modified Peptides Found Per Tissue Input Amount



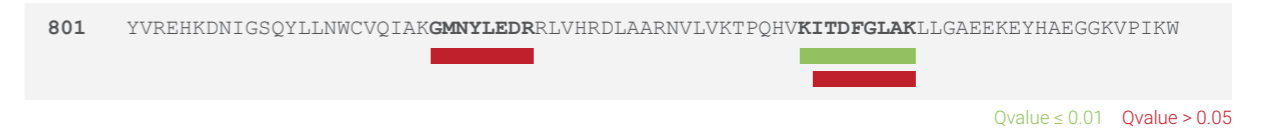
## Volcano Plot of Class I Peptides



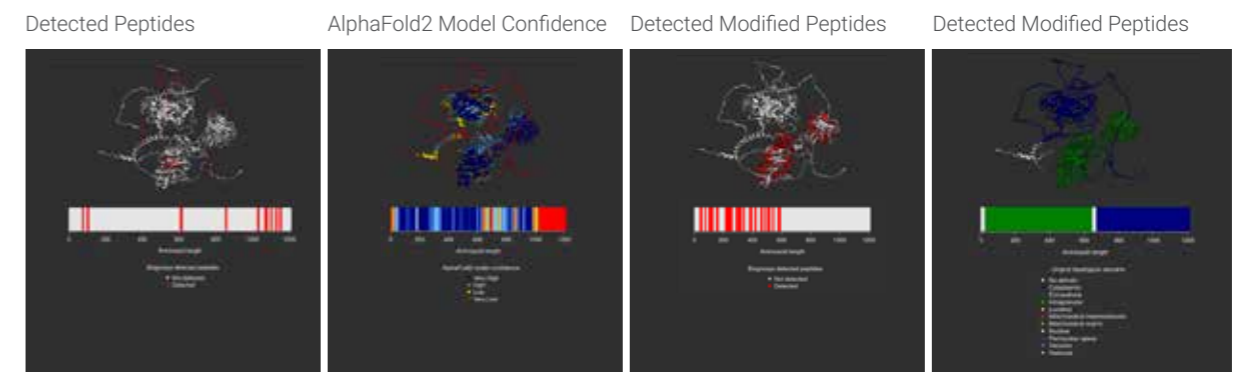
## Volcano Plot of Class II Peptides



## Mapping Of The Detected 9mer Class I Peptide



## Mapping of EGFR Immunopeptides Visualized Using Biognosys' 3D Protein Explorer



Class I peptide presentation is significantly modified in cancerous tissue, where more than 3,000 immunopeptides were found to be upregulated. Among them many were annotated as cancer-specific proteins. For Class II, more than 800 immunopeptides were upregulated in cancer tissue, with a significant enrichment for proteins associated with lung cancer.

## Tumor Associated Antigens MHC Class I

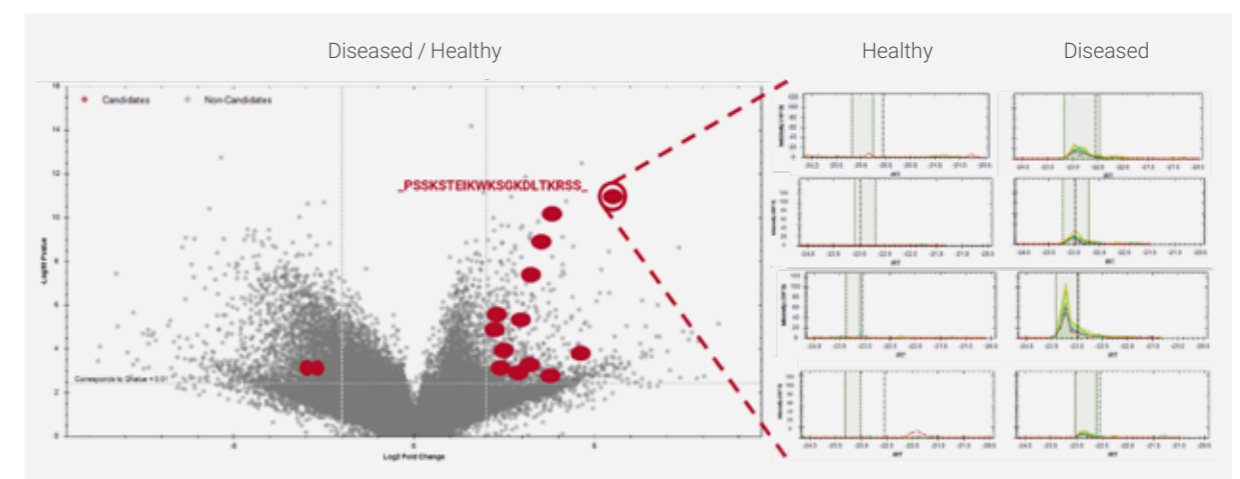
During the study, we identified 307 proteins that were significantly altered between healthy, early and late stages of colorectal cancer. Three of those proteins have a known role in the development of colorectal cancer: STAT3, TAGL, and CD47. In addition, gene ontology enrichment showed an increased response to leptin and regulation of proteolysis, along with

downregulation of cell-cell adhesion, leukocyte homeostasis, and response to hydrogen peroxide in patients with cancer.

## Tumor Associated Antigens MHC Class II

Focusing on MHC Class-II immunopeptides, an elegant example of the overexpression of a tumor-associated antigen is observed. Here we detect a significant upregulation of SET, a nuclear proto-oncogene that is known to be highly upregulated in lung tumors. Inspection of the peptide's intensities across samples clearly demonstrates this upregulation and highlights the ability of our workflow to characterize specific peptide regulation between conditions.

## Volcano plot of Class II peptides with peptide intensities for SET peptide highlighted across samples



# IMMUNO PEPTIDOME PROFILING

## Benefits

**Transformative insights**

**Unparalleled depth**

**Sensitive and reproducible**

**High throughput  
and scalability**

**End-to-end solutions  
and support**

## Features

Potential to enable personalized treatments, in cancers, vaccines, infectious, and autoimmune diseases

Industry-leading number of peptides identified from limited input material

Proprietary workflow optimized for high-quality identifications and performance

Only technology that can reliably measure and identify immunopeptide profiles of biological samples on a large scale

Gain insights to support your research from early discovery to clinical settings

*«We were really impressed at the depth of peptide identification for both HLA I and II complexes from a small amount of cancer patient tissue. Thanks to quantitative MS, we can link biological hypothesis to quantification of neoantigen of interest.»*

**Jonathan Woodsmith, PhD**

Director Advanced Analytics and AI,  
Indivumed

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Contact us at [services@biognosys.com](mailto:services@biognosys.com) to discuss your specific study needs with one of our scientific consultants.

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