

TRUE DISCOVERY™

BIOFLUID BIOMARKER DISCOVERY

Case Study

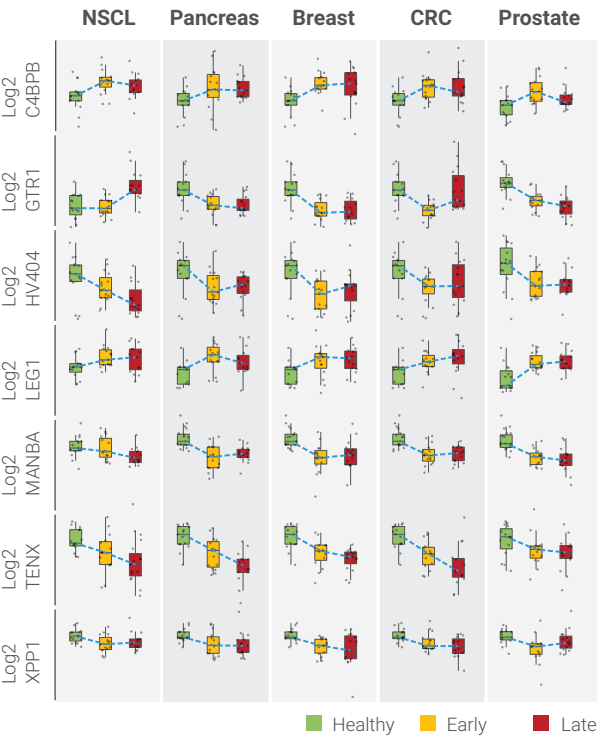
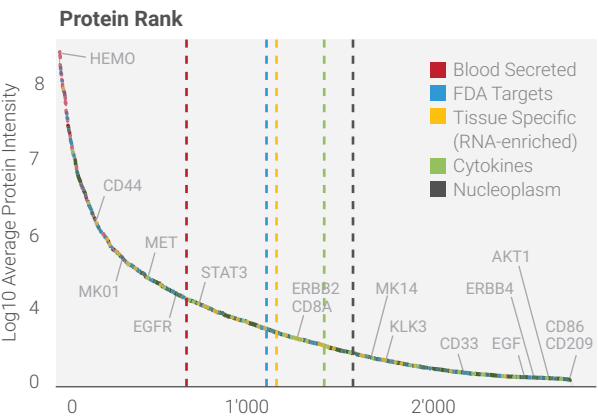
BIOMARKER CANDIDATES FOR TUMORS
IDENTIFIED FROM DEEP PROFILED PLASMA
STEM PREDOMINANTLY FROM THE LOW
ABUNDANT AREA

Marco Tognetti, Kamil Sklodowski, Sebastian Müller, Dominique Kamber,
Jan Muntel, Roland Bruderer and Lukas Reiter

DEEPER BIOLOGICAL INSIGHTS FOR TRUE, UNBIASED PLASMA BIOMARKER DISCOVERY

Mass spectrometry offers the possibility to study the unexplored, looking at the total proteome with a 360° view. In this case study, we show the results of a clinical study of 180 plasma samples from lung, breast, colorectal, pancreatic and prostate cancer, performed using our next-generation Plasma Biomarker Discovery workflow.

	Stage I-II	Stage III
NSCL squamous cell	n=15	n=15
Pancreas adenocarcinoma	n=15	n=15
Breast infiltrating ductal carcinoma	n=15	n=15
CRC adenocarcinoma	n=15	n=15
Prostate adenocarcinoma	n=15	n=15
Control Group Cancer-free	n=30	



Robust Workflow

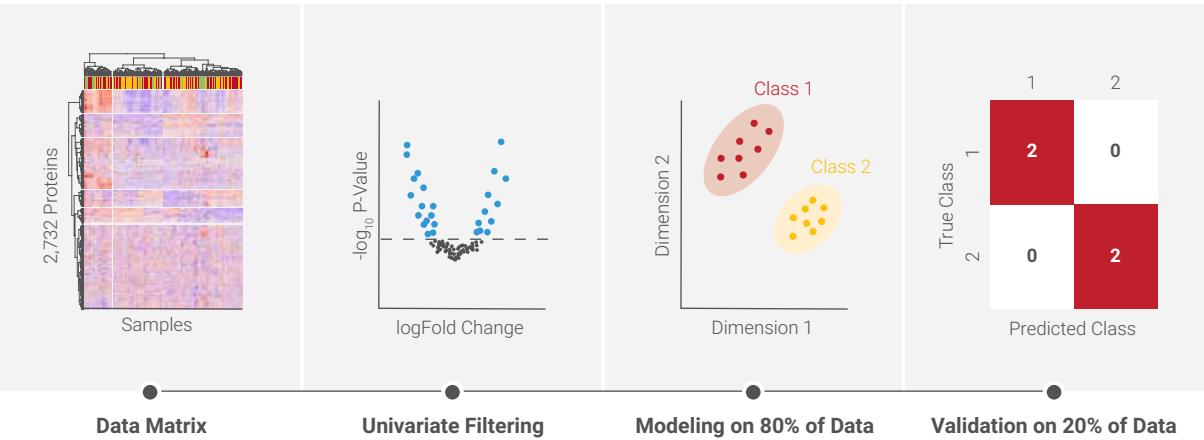
We identified 2,732 proteins, demonstrating a 257% increase in protein identification and a 263% increase in significantly differentially abundant proteins over neat plasma. In addition, we discovered novel biomarker candidates and developed models that classify the disease state. Biomarker candidates came predominantly from the low abundance region, demonstrating the need for deep, unbiased profiling to identify potential novel biomarkers. In the study, depletion led to a 362% increase in true hits.

Unprecedented Depth

Our analysis captured an extensive proportion of the proteome, including:

- tissue leakage proteome
- interleukins
- signaling proteins
- tissue-specific proteins coming from the diseased organs
- cytokines and nucleoplasm

The detected hits included 190 targets for FDA-approved drugs, 66% of which were detected in the lower intensity range. The final dataset recapitulates biological features of intra-patient heterogeneity while providing a deep unbiased view of the plasma proteome.



Post-processing Steps

The post-processing steps include univariate testing for filtering, machine learning on 80% of the data and classification performance accuracy on the hold-out 20% validation data.

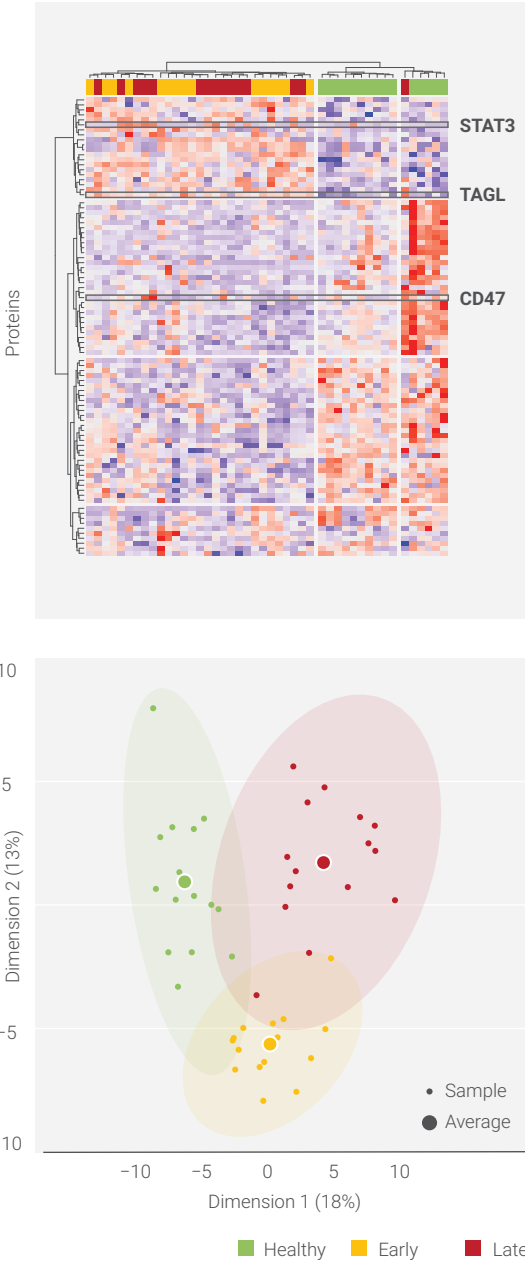
Protein Signature in Colorectal Cancer

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.

Protein Signature in Pancreatic Cancer

We identified 436 proteins that were significantly altered between healthy, early, and late stages of pancreatic cancer. Of these, seven have previously been suggested as possible pancreatic cancer biomarkers. In addition, we achieved an efficient separation between healthy, early, and late-stage disease. This separation was primarily driven by the three cancer-related proteins CD9, TENX, and DIAC and additionally by the recently proposed therapeutic target CNN261 and the prognostic marker GTR162. Finally, we identified sequestration of zinc ions which was downregulated mainly in cancer samples.

Reference: Biomarker Candidates for Tumors Identified from Deep-Profiled Plasma Stem Predominantly from the Low Abundant Area, Marco Tognetti, Kamil Sklodowski, Sebastian Müller, Dominique Kamber, Jan Muntel, Roland Bruderer, Lukas Reiter, bioRxiv 2021.10.05.463153; doi: <https://doi.org/10.1101/2021.10.05.463153>



«Biognosys' biomarker discovery solutions are supported by a constantly improving platform and can be run in large-scale studies while maintaining high data quality.»

Kanna Palaniappan, PhD
Staff Scientist, Freenome

Benefits

**Unbiased Analysis with
Unprecedented Depth**

**Unparalleled Specificity and
Quantitative Precision**

**Plasma and
Serum Profiling**

**Indication-agnostic
Approach**

**End-to-end Solutions
and Support**

Features

We search the complete proteome to quantify more than 4,000 of the most relevant proteins, including an unlimited number of proteoforms such as PTMs

Tens of thousands of peptide-level data points assure high quantitative precision and unbeatable specificity

Dynamic view of a subject's health status at any given point in time, without relying on invasive tissue biopsies

We gain insights across the intricacy of different conditions' phenotypes and uncover true connections between genotype and phenotype

Drive your research from early-stage discovery to clinical biomarkers and diagnostics

Contact us at services@biognosys.com to discuss your specific study needs with one of our scientific consultants.

At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that can dramatically improve human health. We enable life science researchers and drug hunters to look at the proteome from every angle with our versatile portfolio of proprietary proteomics services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types. Through advanced data analytics, Biognosys translates data into actionable insights for R&D and clinical research.