

Sapiient tumor proteomics

Unmatched protein capture, **robust** measures, **deep** insights

Sapiient's mass spectrometry-based tumor proteomics workflows offer an in-depth, dynamic, and unbiased view of molecular effectors within cancer cells, delivering high-specificity, quantitative measures to **characterize proteins and their modifications expressed in individual tumors**.

Our tumor proteomics method measures **12,000+ protein groups, comprising ~226,500 peptides**, in as little as 200k tumor cells or 5mg of tissue. This includes deep characterization of **cell surface protein (antigen) expression as well as intracellular proteins** central to cellular function, structure, and signaling. In addition, Sapiient's mass spectrometry workflows enable **capture of key protein variants and isoforms (proteoforms)** including established and novel post-translational modifications (PTMs) as well as emerging non-canonical proteins that are highly specific to the cancer state.

Coupled with Sapiient's plasma proteomics workflows, we have the ability to not only characterize the tumor proteome, but also to **develop targeted liquid biopsies that assay tumor-derived proteins and peptides** in blood circulation (Figure 1).

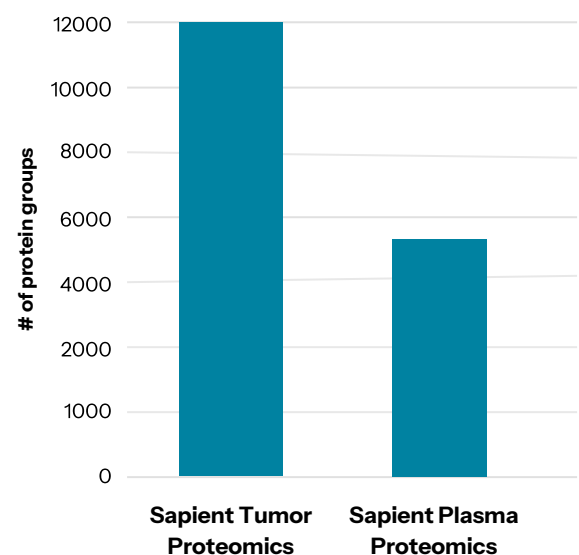


Figure 1. Protein groups captured in patient samples by Sapiient's proteomics workflows.

Our fully automated pipeline uses nanoflow chromatography coupled to Bruker timsTOF HT mass spectrometers for comprehensive, **label-free quantitative DIA proteomics** at a high throughput of 30 samples per day per instrument (**30 SPD**). These established workflows are also leveraged to assay normal tissue adjacent to the tumor site as well as remote normal tissues, as a means for **deep interrogation of proteins and proteoforms that are differentially expressed between tumor and normal tissue**. This provides a path to identify robust drug targets and assess potential on-target, off-tissue side effects.

Our method leverages **single fraction-single injection processing to achieve exceptional quantitative reproducibility and high throughput**. Automated workflows limit sample-to-sample and prep-to-prep variance to maintain a protein group median technical variance (% coefficient of variance, CV) **of ~6%**.

Biological insights from deep tumor profiling

Sapient's expertise is centered not only on generating robust proteomics data, but also *leveraging* it for **key actionable insight**, illuminating the complex interactions of proteins and signaling pathways that **drive tumorigenesis, and identifying key protein targets for emerging therapeutics**.

Within these efforts, Sapient has annotated hundreds of key pathways and processes that are well represented in tumor proteomics data. This mapping **captures hundreds of proteins across core signaling pathways and cascades** (Figure 2A). It also allows for examination of proteins of **oncogenes and tumor suppressors** with altered expression in both tumor and normal samples (Figure 2B).

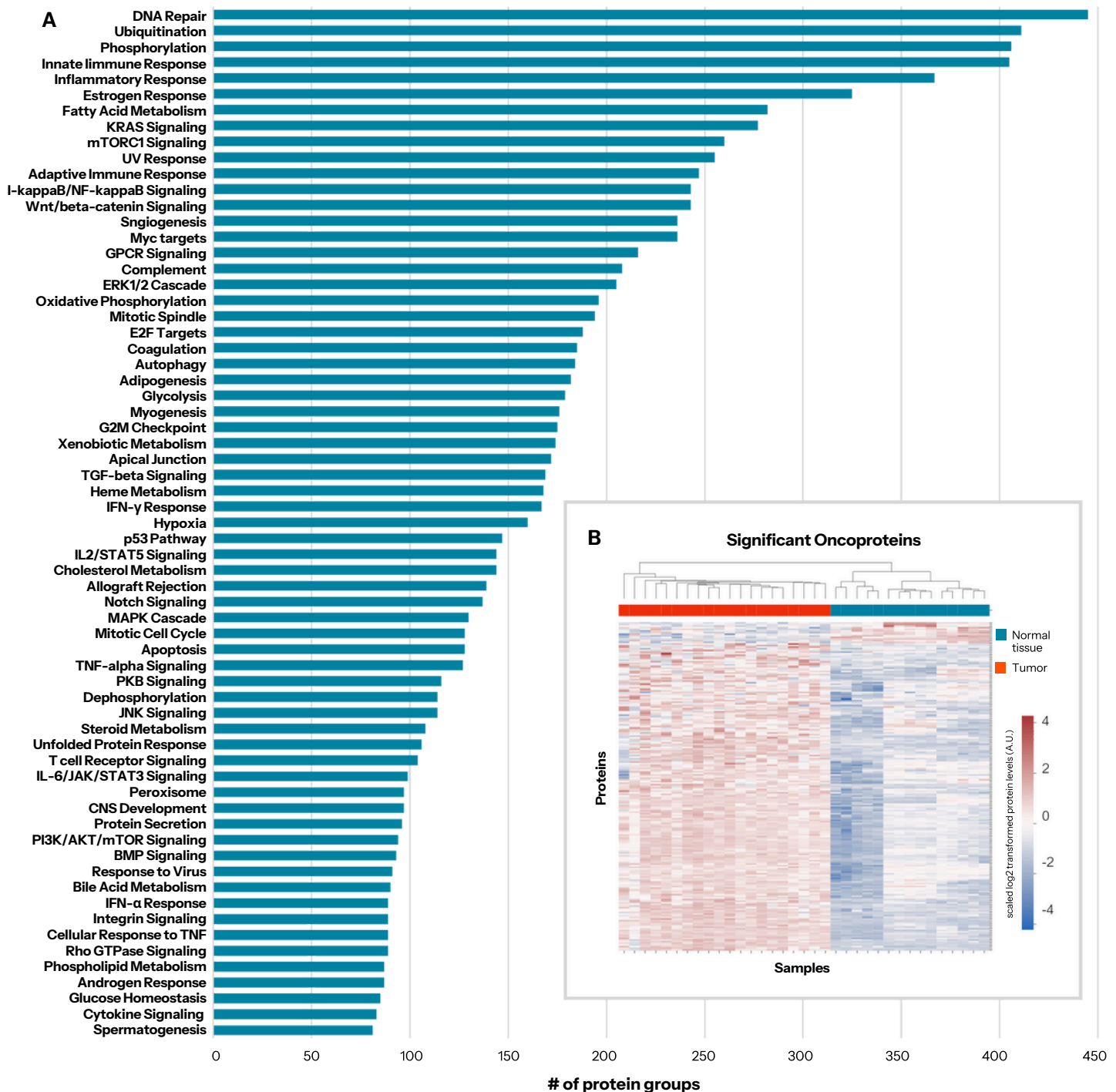


Figure 2. Proteins measured by Sapient's tumor proteomics method mapped by (A) signaling pathways and (B) proteins of oncogenes.

To further enable our clients' studies, Sapiient has established our **DynamiQ™ tumor and tissue database containing comprehensive proteomics measures across a key panel of normal human tissues** (Figure 3). We use these measures to identify differentially expressed proteins and proteoforms in tumors and enable discovery and/or validation of key drug targets.

Analysis of tumors and normal tissues using Sapiient's tumor proteomics workflows finds that **greater than 50% of proteins have significant differential expression in tumor samples** (Figure 4A). These proteomics datasets also capture **more than 1,000 known and emerging drug targets**, including **300+ proteins targets with existing approved therapeutic agents** (Figure 4B), as well as hundreds of differentially expressed proteins in tumors that may represent robust novel targets, highlighting the **significant discovery potential** of these approaches.

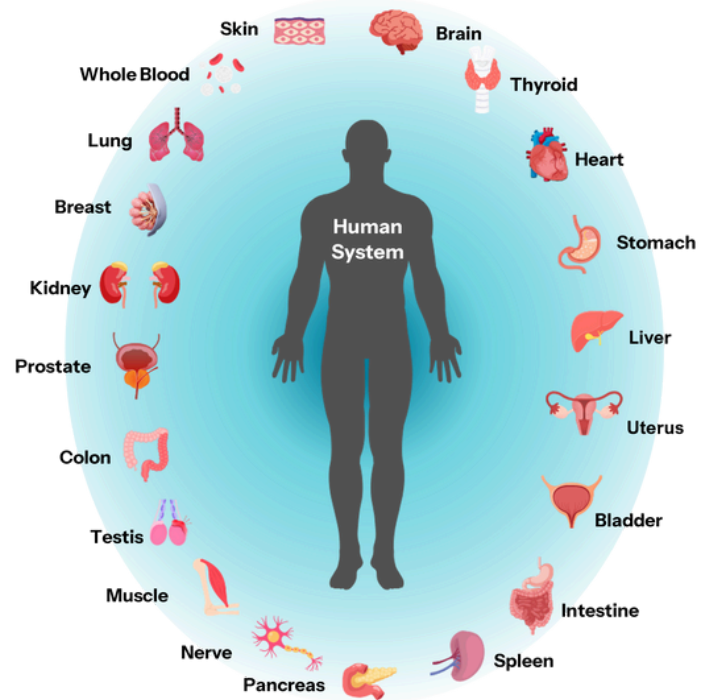


Figure 3. Normal tissues represented in Sapiient's DynamiQ tumor and tissue database for which discovery proteomics data has been generated.

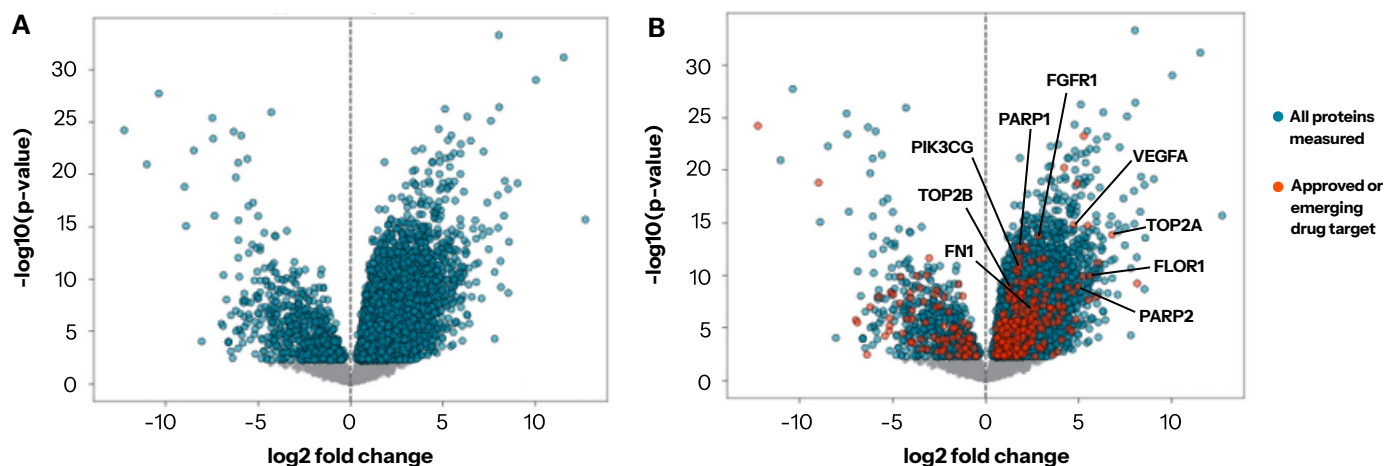


Figure 4. Proteins measured by Sapiient's tumor proteomics method that A) are significantly changed in tumor samples and B) represent approved and emerging drug targets.

Sapiient's tumor proteomics data can also be integrated with other proteomics, metabolomics, lipidomics, RNA sequencing, and cytokine measurements via Sapiient's **multi-omics platform**, enabling deeper biological insights to drive drug development programs forward.

To request a tumor proteomics study, email discover@sapiient.bio today.

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