BioMAP®
Oncology Panels

*In Vivo* Insights with the Speed and Ease of an *In Vitro* Assay

Tumors do not propagate in isolation, but as part of a complex interaction of stroma, vasculature, immune cells, and the tumor itself. This intricate microenvironment is much more than the sum of its parts, which explains why it is so difficult to broadly predict the behavior of a cancer drug candidate based simply on the effect it has on isolated tumor cells or cell monoculture. Xenograft models attempt to look at potential drug effects on a tumor *in situ*, however, the tumor microenvironment and immune response is predominantly mouse and not representative of a human patient. The BioMAP Oncology Panels were built to assess the effect of drug candidates in a complex human tumor-host microenvironment. By modeling the tumor-mediated immuno-suppression that is seen *in vivo*, the BioMAP platform recapitulates the clinical effects of both candidate and standard-of-care drugs.

Phenotypic Profiling That Captures the Complexity of the Human Tumor Microenvironment

The BioMAP Oncology Panels are complex co-cultures of tumor cell lines and early passage human primary cell types. These cell-based assay systems model the solid tumor-host microenvironment in a platform that simplifies compound screening. Leaders in immuno-oncology drug discovery are using BioMAP Oncology Panels to:

- Study the impact of novel molecules on tumor mediated immuno-suppression

- Guide dosing, identify clinical biomarkers, and differentiate against current standards of care

- Track efficacy and identify potential synergy as part of combination therapies

Pembrolizumab and Nivolumab Show Similar Profiles in BioMAP Oncology Panel
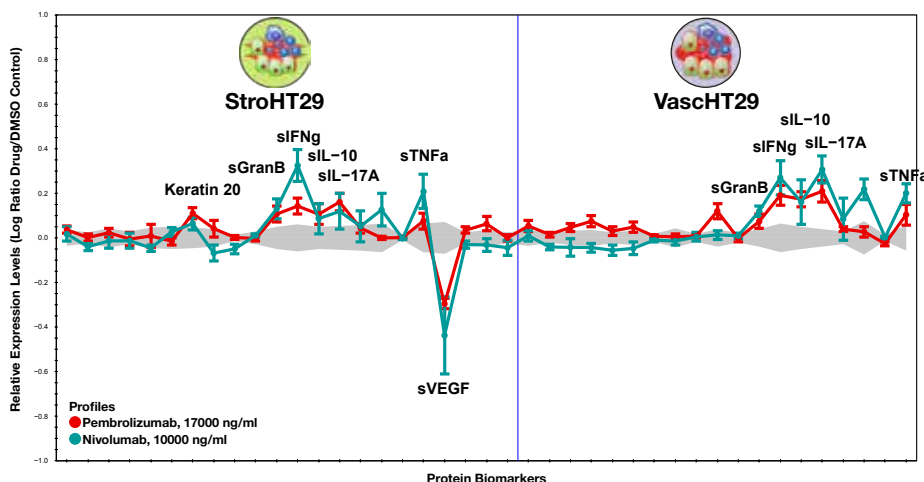
Profiles of Pembrolizumab (red) and Nivolumab (blue) in the BioMAP Colorectal Cancer Oncology Panel. Biomarker readouts are displayed along the x-axis and log expression ratio (drug/vehicle control) is displayed along the y-axis. Annotated peaks represent biomarkers that are statistically changed as compared to vehicle controls and demonstrated activity that was common to both Pembrolizumab and Nivolumab. The grey area around the axis represents the range of activities of all historical controls.

Better Tools in Immuno-Oncology Drug Development

No matter what stage of the development pathway your compound is in, the BioMAP® Oncology Panels are the ideal tools to help you make better decisions about your drug candidates, faster. By modeling the complex interactions of compounds in the context of an intact tumor microenvironment, this service is able to provide reliable information on efficacy, dosing, and mechanism of action. The utilization of human primary cells to produce readouts on clinically relevant protein biomarkers means better preclinical design and easier translation into human patients.

The BioMAP Oncology Panels will accelerate your compound from discovery through to the clinic.

A few examples of the reference compounds that have been run through the BioMAP Oncology Panels include Pembrolizumab, Paclitaxel, Ipilimumab, Erlotinib, anti-CD73, and many more!

BioMAP Oncology Panels Service

Service	Compound profiling (chemicals or biologics) in 2 model systems of the human tumor microenvironment at 4 concentrations in triplicate.
Examples of Analysis Performed	Identification and biological interpretation of relevant biomarker activities that are increased or decreased in comparison to vehicle control. Benchmarking (optional). A direct comparison of test compound to a specified Oncology Panel reference from the BioMAP Database.
Report Details	DiscoverX provides a study report that includes: Annotation of biomarker activities with respect to biological significance, profile plots, graphical overlays of test and reference compound profiles, and expert data interpretation and analysis.

Human Biology Modeled by Oncology Panels

Panel	System			Description
Colorectal Cancer (CRC) Panel	StroHT29		Colorectal Cancer - Stro	The Colorectal Cancer - Stro (StroHT29) system models the host stromal-tumor microenvironment by capturing the complex interactions between tumor cells, the host stromal network, and infiltrating immune cells recruited into the tumor mass.
	VascHT29		Colorectal Cancer - Vasc	The Colorectal Cancer - Vasc (VascHT29) system models host vascular-tumor microenvironment by capturing the complex interactions between tumor cells, the host vascular network, and infiltrating immune cells associated with angiogenesis.
Non-Small Cell Lung Cancer (NSCLC) Panel	StroNSCLC		Lung Cancer - Stro	The Lung Cancer - Stro (StroNSCLC) host-NSCLC tumor microenvironment model system consists of human primary fibroblasts co-cultured with a NSCLC cell line, NCI-H1299, and human peripheral blood mononuclear cells. These conditions model the host stromal-tumor microenvironment by capturing the complex interactions between tumor cells, the host stromal network, and infiltrating immune cells recruited into the tumor mass.
	VascNSCLC		Lung Cancer - Vasc	The Lung Cancer - Vasc (VascNSCLC) host-NSCLC tumor microenvironment model system consists of human primary vascular endothelial cells co-cultured with a NSCLC cell line, NCI-H1299, and human peripheral blood mononuclear cells. These conditions model the host vascular-tumor microenvironment by capturing the complex interactions between tumor cells, the host vascular network, and infiltrating immune cells associated with angiogenesis.

To learn more about how to characterize compounds in the context of a human tumor microenvironment visit us at discoverx.com/oncologypanel