

# NantHealth and NantOmics to Present Patterns of Immune Checkpoint Molecules in Relation to PD-L1 Expression at the American Society of Clinical Oncology (ASCO) 2018 Annual Meeting

June 2, 2018

*Results to be presented during the tumor biology session at the ASCO 2018 Annual Meeting*

CHICAGO--(BUSINESS WIRE)-- [NantWorks, LLC](#) today announced that its affiliate companies, [NantHealth, Inc.](#), (NASDAQ: NH), a leading next-generation, evidence-based, personalized healthcare company and [NantOmics, LLC](#), the leader in molecular analysis and a member of the NantWorks ecosystem of companies, will present findings on how targeting immune checkpoints and employing combinations has led to clinical benefit across a variety of tumor types during the tumor biology session at the [American Society of Clinical Oncology \(ASCO\) 2018 Annual Meeting](#), an event bringing together 30,000 oncology professionals from June 1-5, 2018 at McCormick Place in Chicago, Illinois. NantWorks will be exhibiting at booth #7147 during the event.

“We are excited to share data on how profiling the tumor and associated microenvironment can help tailor rational combinations of immunotherapeutic strategies,” said Patrick Soon-Shiong, MD, founder of NantWorks. “This data is an important step in enhancing response rates through individualized immune checkpoints in PD-L1 expression, and we look forward to continued exploration and potential solutions for patients.”

## Presentation Details

**Co-expression patterns of immune checkpoint molecules in relation to PD-L1 expression, Abstract #12113**

**WHO:** NantHealth, LLC and NantOmics, LLC

**WHAT:** Tumor Biology Session

**WHEN:** June 4, 1:15-4:45 PM CST

**WHERE:** Hall A, McCormick Place

## Presentation Summary

In order to determine if tailored rational combinations of immunotherapeutic strategies can be achieved by profiling the tumor and associated microenvironment, whole transcriptomic sequencing of 1,880 unselected clinical cases, reflecting 38 distinct histologies, was performed. Cases were categorized as PD-L1-low, PD-L1-normal and PD-L1-high by cutoffs defined in TCGA expression profiles. The results found that high and low PD-L1 expression in the tumor and adjacent microenvironment are associated with variations in key checkpoint molecules. The results also found that low expression of PD-L1 may be an ideal setting for use of IDO- or TIM3-directed therapies.

**About NantHealth, Inc.**

NantHealth, Inc., a member of the NantWorks ecosystem of companies, is a next-generation, evidence-based, personalized healthcare company enabling improved patient outcomes and more effective treatment decisions for critical illnesses. NantHealth's unique systems-based approach to personalized healthcare applies novel diagnostics tailored to the specific molecular profiles of patient tissue and integrates this molecular data in a clinical setting with large-scale, real-time biometric signal and phenotypic data to track patient outcomes and deliver precision medicine. For nearly a decade, NantHealth has developed an adaptive learning system that integrates our unique molecular profiling solution, software and hardware. Our system infrastructure collects, indexes, analyzes and interprets billions of molecular, clinical, operational and financial data points derived from novel and traditional sources to continuously improve decision-making and optimize our clinical pathways and decision algorithms over time. For more information please visit [www.nanthhealth.com](http://www.nanthhealth.com).

### **About NantOmics**

NantOmics, a member of the NantWorks ecosystem of companies, delivers molecular analysis capabilities with the intent of providing actionable intelligence and molecularly driven decision support for cancer patients and their providers at the point of care. NantOmics is the first molecular analysis company to pioneer an integrated approach to unearthing the genomic and proteomic variances that initiate and drive cancer, by analyzing both normal and tumor cells from the same patient and following identified variances through from DNA to RNA to protein to drug. NantOmics has a highly scalable cloud-based infrastructure capable of storing and processing thousands of genomes a day, computing genomic variances in near real-time, and correlating proteomic pathway analysis with quantitative multi-plexed protein expression analysis from the same micro-dissected tumor sample used for genomic analysis. For more information please visit [www.nantomics.com](http://www.nantomics.com) and follow Dr. Soon-Shiong on Twitter [@DrPatSoonShiong](https://twitter.com/DrPatSoonShiong).

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