NantHealth and NantOmics to Present Data on Three-Fold Overestimation of Tumor Mutation Burden Using Gene Panel vs Whole Exome 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, the leader in molecular diagnostics and a member of the NantWorks ecosystem of families, will present data on three-fold overestimation of tumor mutation burden (TMB) using a 248 gene list as a panel to impute TMB 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.

The data presented here have significant implications on the use of immunotherapies such as Keytruda and Opdivo given previous data touting the effectiveness of these drugs in patients whose tumors bear high TMB. The NantWorks companies' data presented here caution against overestimation of TMB and thus immunotherapy overuse when extrapolating TMB from smaller panel tests (<500 genes) versus simply identifying all actual mutations by surveying the entire genome. Further, whether performing analysis on the entire genome or in a panel test, clinical validity for the use of immunotherapies is made appreciably more precise by confirming the expression of identified mutations. The patient's immune system recognizes and targets non-self proteins, not DNA, thus underscoring the need to append the mutated genomic data with expression data. Maximal accuracy as established in this presentation by the use of tumor-normal DNA interpretation of TMB from surveying all genes and further amplified by derivation of expressed TMB is what is required for future immunotherapies such as neoepitope vaccines.

"We're excited to share our data from our retrospective analysis, which may impact ICT prescription and expectation of clinical benefit," said Patrick Soon-Shiong, MD, founder of NantWorks. "Our analysis builds on our breadth of actionable insight and molecularly driven support for cancer patients and their providers, and we look forward to continuing to build upon our diagnostic capabilities."

Presentation Details

Three-fold overestimation of tumor mutation burden using 248 gene panel versus whole exome, Abstract, #12117
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

This study analyzed if actual TMB (aTMB), consisting of mutations across the exome, and expressed TMB (eTMB), consisting of expressed genes, would differ substantially from iTMB. Retrospective analysis of a database from a commercial DNA tumor:normal and RNAseq platform was carried out. 890 clinical samples were analyzed, composing of both primary and metastatic disease by whole genome sequencing (WGS) or WES and RNA sequencing (RNA-Seq), and compared true tumor mutational burden to a predicted tumor mutational burden from a list of 248 genes thought to drive cancer. The study showed an estimated tumor mutational burden based only on the list of 248 genes had an average of 15.79 mutations per megabase whereas WGS/WES derived TMB had an average of 5.09 mutations per megabase of coding DNA. As a result, the study indicates that a roughly 3-fold over-estimate of TMB was observed, which may impact ICT prescription and expectation of clinical benefit.

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.nanthealth.com.

About NantOmics

NantOmics, a member of the NantWorks ecosystem of companies, delivers molecular diagnostic 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 diagnostics 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 and follow Dr. Soon-Shiong on Twitter @DrPatSoonShiong.

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