NantHealth and NantOmics to Present Data on the Frequency of Non-Expressed Variants Tested by Standard NGS Panel 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 American Society of Clinical Oncology (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 17 percent of next generation sequencing (NGS) 50 gene panel variants are not expressed in RNA sequencing 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.

“By determining the frequency of non-expressed variants that would be tested by a standard NGS panel, our data shows that the identification of these genes can yield improved testing algorithms and treatment strategies,” said Patrick Soon-Shiong, MD, founder of NantWorks. “We’re excited to share this data and look forward to further exploring how NGS can be used for target therapy in oncology.”

Presentation Details

Seventeen percent of NGS 50 gene panel variants are not expressed in RNAseq, Abstract #12118
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 the frequency of non-expressed variants that would be tested by a standard NGS panel through retrospective analysis of a database from a commercial DNA tumor: normal and RNAseq platform. In the 992 samples that were identified with paired DNA (WGS or WES) / RNAseq NGS, a total of 225,727 SNVs were detected. Across 37 tumor types the range of expression was 57% (melanoma) – 100% (uterine). In this analysis, 17 percent of detected variants were not expressed in the RNA sequence. As a result, the lack of RNA expression may contribute to less than expected clinical benefit with molecularly targeted therapies. Since the distribution is non-uniform, identification of these genes can yield improved testing algorithms and treatment strategies.

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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Source: NantHealth, Inc.