NantHealth Presented Clinical Data on Immunotherapy, Molecularly Targeted Agents and Tumor Biology at the American Society of Clinical Oncology (ASCO) 2020 Virtual Scientific Program

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Findings presented during the developmental therapeutics session at the ASCO 2020 Virtual Scientific Program

CULVER CITY, Calif.--(BUSINESS WIRE)--Jun. 18, 2020-- NantHealth, Inc. (NASDAQ: NH), a next-generation, evidence-based, personalized healthcare company, announced the publication of four abstracts on developmental therapeutics for immunotherapy, molecularly targeted agents and tumor biology during the American Society of Clinical Oncology (ASCO) 2020 Virtual Scientific Program.

The program, held virtually from May 29-31, 2020, gathered oncology physicians, biotechnology executives, researchers, patient advocates, and investment analysts to discuss cutting-edge clinical research and therapeutics in oncology, and to gain insights for improving cancer care.

Alongside ImmunityBio, LLC, and others, Dr. Sandeep K. Reddy, Chief Medical Officer at NantHealth, and Christopher Szeto, Director of Machine Learning at NantHealth, presented the data gathered from NantHealth's database which was used to advance findings in developmental therapeutics.

The details of NantHealth's ASCO posters are as follows:

Title: "Effect of chemokine signaling signatures on resolving discrepancy between TMB and checkpoint expression"
Authors: Saihitha Veerapaneni, Rahul Parulkar, Sandeep K. Reddy, Shahrooz Rabizadeh, Stephen Charles Benz and Christopher Szeto; ImmunityBio, LLC, Culver City, CA; NantHealth, Culver City, CA
Abstract Number: 3131
Session Title: Developmental Therapeutics—Immunotherapy

"In this study, 1,395 clinical samples from the NantHealth database with matched tumor normal whole exomes and deep whole-transcriptomic sequencing were analyzed to confirm previous findings that Tumor Mutation Burden (TMB) and PDL1 mRNA were not correlated," said Dr. Sandeep K. Reddy, Chief Medical Officer, NantHealth. "However, chemokine activity may be an alternative to TMB and PDL1 to identify patients appropriate for immunotherapy and can help resolve discordant cases."

Title: "Targetable immune checkpoint molecules may be significantly differentially expressed in minority ethnicities"
Authors: Jacob J. Adashek, Christopher Szeto, J. Zack Sanborn, Sandeep K. Reddy, Amir A. Toor, Stamatina Danielides, Steven Smith, Steven R. Grossman, Charles V Clevenger, Anthony Faber, Andrea Ferreira-Gonzalez, Sosipatros Alexandros Boikos; University of South Florida, H. Lee Moffitt Cancer Center & Research Institute, Tampa, FL; NantHealth, Culver City, CA
Abstract Number: 3576
Session Title: Developmental Therapeutics—Molecularly Targeted Agents and Tumor Biology

"The Cancer Genome Atlas (TCGA) data for 7,087 patients and about 2,700 patients in the NantHealth database were used to identify differential patterns of checkpoint gene expression across different ethnic groups," said Dr. Sandeep K. Reddy, Chief Medical Officer, NantHealth. "White breast cancer patients might be anticipated to exhibit reduced sensitivity to PD1/CTLA4 blockade, while Black colon cancer patients may exhibit reduced sensitivity to IDO1 therapies, such as epacadostat. Ethnicity may represent a significant factor for efficacy checkpoint blockade therapies."

Title: "Highly accurate automated tissue classification using deep learning on digital pathology images: A novel tool for resolving conflicts in diagnosis"
Authors: Liudmila Beziaeva, Mustafa Jaber, Stephen Charles Benz, Shahrooz Rabizadeh, and Christopher Szeto, ImmunityBio, LLC, Culver City, CA; NantHealth, Culver City, CA
Abstract Number: 3578
Session Title: Developmental Therapeutics—Molecularly Targeted Agents and Tumor Biology

"NantHealth combined whole slide imaging with deep neural networks to develop a tool which can identify which of 24 primary tumor types a sample is derived from with 94.6 percent accuracy," said Christopher Szeto, Director of Machine Learning, NantHealth. "This accuracy, which approaches that of a human pathologist, is achieved by focusing machine-vision attention on just tumor regions within bulk samples. Used in conjunction with molecular profiling, rates of Cancers of Unknown Primary (CUP) or misdiagnosis can feasibly be minimized to improve patient care."

Title: "High correlation between TMB, expressed TMB, and neoantigen load using tumor: Normal whole exome DNA and matched whole transcriptome RNA sequencing"
Authors: Christopher Szeto, Mrinal M. Gounder, Rahul Parulkar, Andrew Nguyen, Shahrooz Rabizadeh, Sandeep K. Reddy; Memorial Sloan Kettering Cancer Center, New York, NY; ImmunityBio, LLC, Culver City, CA; NantHealth, Culver City, CA
Abstract Number: e15238
Session Title: Publication Only: Developmental Therapeutics—Immunotherapy

"Surprisingly, we see minimal difference between the various biomarkers derived from mutational burden," said Christopher Szeto, Director of Machine Learning, NantHealth. "Tissue-specific TMB thresholds may be useful in patient with Sarcoma and Pancreatic cancers. Otherwise, additional data inputs such as microbiome, chemokine expression, and TME cell phenotyping may be required to improve upon TMB as a biomarker of immunotherapy response."

About NantHealth, Inc.

NantHealth, a member of the NantWorks ecosystem of companies, provides leading solutions across the continuum of care for physicians, payers, patients and biopharmaceutical organizations. NantHealth enables the use of cutting-edge data and technology toward the goals of empowering clinical decision support and improving patient outcomes. NantHealth's comprehensive product portfolio combines the latest technology in payer/provider platforms that exchange information in near-real time (NaviNet and Eviti), and molecular profiling services that combine comprehensive DNA & RNA tumor-normal profiling with pharmacogenomics analysis (GPS Cancer®). For more information, please visit nanthealth.com or follow us on Twitter, Facebook and LinkedIn.

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