

NantHealth and NantOmics Present Four Research Papers Demonstrating Advancements in Cancer Diagnostics with NantHealth's GPS Cancer® and Liquid GPS™

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NantHealth's Liquid GPS™ technology shows promise in the monitoring of key biomarkers in metastatic colorectal cancer

MUNICH & CULVER CITY, Calif.--(BUSINESS WIRE)-- Significant developments in cancer research were presented by NantHealth (NASDAQ: NH) and NantOmics at the ESMO conference in Munich, Germany this week. NantHealth, a leader in breakthrough cancer research and solutions to improve patient care and lower healthcare costs, in conjunction with NantOmics, a leader in molecular diagnostic testing, conducted one oral presentation and four papers, including a few demonstrating the promise of the company's Liquid GPS™, a blood-based molecular test that provides oncologists with a powerful tool for non-invasive tumor profiling and quantitative monitoring of treatment response. ESMO is the world's second largest cancer symposium where researchers and clinicians come together to study the latest breakthroughs in treatment.

"We continue to be on the cutting edge of cancer research and that, coupled with the advancements we're making in all areas of cancer diagnostics, treatment plans and provider solutions, are all important steps in supporting physicians and patients," said Dr. Sandeep Reddy, Chief Medical Officer, NantHealth. "Our researchers and scientists are working very hard to tackle some of the toughest challenges in cancer research and sharing them as quickly as possible. Our Liquid GPS™ tumor profiling is dramatically changing the way that physicians identify and treat different types of cancer."

The oral presentation, Gene mutation status in circulating tumor DNA (ctDNA) and first-line FOLFOXIRI plus bevacizumab (bev) in metastatic colorectal cancer (mCRC) harboring RAS mutation, authored by Y. Sunakawa, et al, includes investigational data suggesting that circulating DNA markers may predict outcomes in mCRC and can guide treatment decisions for these patients.

Additional papers were reviewed showing breakthroughs in immune oncology, including:

Title: Differential expression of PD-L1 and immune biomarkers by age: Decreased expression in pediatric/AYA patients with advanced cancer

Author: Dr. Omid Hamid, et al

Description: Whole exome and RNA sequencing of 1,467 patients highlights younger patients (age < 24) with advanced cancer appear to have lower levels of CTLA4 and PD-L1 expression.

Key Takeaway: Immune checkpoint drugs have not yet been approved in pediatric and adolescent/young adult patients. Large dataset results show it may be necessary to employ new combinations to be used in younger patients such as Nant's Cancer Vaccine, immunotherapy that combines the delivery of metronomic, low-dose chemotherapy and radiation therapy with natural killer (NK) cell-based technology to enhance patient's immune system response against cancer cells.

Title: PD-L1 expression is strongly associated with TIGIT, FOXP3 and LAG3 across advanced cancers, but not OX40, TIM3 and IDO

Author: Dr. Sumanta K. Pal, et al

Description: RNA sequencing reveals immune checkpoint gene expression was not significantly different in TMB high versus low groups. In patients demonstrating the highest PD-L1 expression, higher expression of CTLA4, TIGIT, FOXP3 and LAG3 were also observed.

Key Takeaway: While researchers are focused on TMB as a more promising biomarker for Immuno-Oncology (IO) therapy than PDL1, this research shows PDL1 may be a marker of generalized tumor inflammation and could be the reason those tumors respond to IO drugs.

Title: Predicting survival benefit of capecitabine plus cisplatin in patients with metastatic gastric cancer using quantitative proteomics

Author: D. Yan, et al

Description: Targeted proteomic analysis of metabolic enzymes required for intracellular activation of the chemotherapeutic drug capecitabine identifies specific enzymes and expression cutoffs which are significantly associated with extended survival in metastatic gastric cancer patients given this drug regimen.

Key Takeaway: Clinical tissue analysis of specific proteomic biomarkers could be used to better personalize the usage of chemotherapeutic agents.

Title: Development and validation of neuroendocrine tumor marker panel in small biopsies using multiplexed mass spectrometry

Author: S. Thyparambil, et al

Description: Immunohistochemical analysis of neuroendocrine tumor markers is performed on only a small subset of cancer. In spite of the approval of several new agents with specific activity against neuroendocrine tumors. A multiplexed clinical tissue proteomics assay was developed to add analysis of neuroendocrine markers into a larger diagnostic panel in order to better identify candidates for neuroendocrine specific therapy.

Key Takeaway: A three protein targeted proteomics assay can identify neuroendocrine tumors with high sensitivity and specificity. The expanded use of this technology may efficiently identify patients for optimal therapy.

About NantHealth

NantHealth, Inc., a member of the NantWorks ecosystem of companies, uses personalized data to improve patient care and lower healthcare costs. NantHealth leads the way in providing oncologists with unprecedented insights that enable cancer treatment tailored to the individual characteristics of each patient. NantHealth solutions reduce the cost of care by connecting patient data and streamlining the accurate collection and sharing of that data--starting from a patient's bedside, extending to payers and providers. NantHealth improves clinical decision support, eliminates unwarranted care and seeks to enhance. For more information please visit www.nanthealth.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 multiplexed protein expression analysis from the same micro-dissected tumor sample used for genomic analysis. For more information please visit www.nantomics.com.

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