Personalis to Present Data Demonstrating Breadth of NeXT Platform for Oncology at AACR Annual Meeting 2022

March 23, 2022

MENLO PARK, Calif.--(BUSINESS WIRE)--Mar. 23, 2022--Personalis, Inc. (Nasdaq: PSNL), a leader in advanced genomics for precision oncology, announced it is presenting new data in scientific posters at the American Association for Cancer Research (AACR) Annual Meeting 2022, which will be held in-person and online, April 8-13, 2022.

“These abstracts demonstrate the full range of our capabilities in advancing the field of oncology, from a rich understanding of molecular-level interactions through clinical applications in multiple disease indications. The work also builds on the company’s strong foundation of genomic data generated with solid tumor tissue and expands into liquid biopsy with a unique, exome-wide approach,” said Richard Chen, M.D., Chief Medical Officer and SVP of R&D of Personalis.

Personalis is presenting five posters, outlined below. Further details can be found at this link.

Title: Applying NeXT Liquid Biopsy™, an exome-scale platform, to monitor and discover somatic variants in a broad set of cancer types
Overview: Circulating tumor cell-free DNA (ctDNA) has become a biomarker for prognosis and disease monitoring. However, studies typically utilize assays limited to a small set of genes that may miss biologically important and clinically actionable mutations. To address this limitation, we have developed a whole-exome scale cfDNA platform, NeXT Liquid Biopsy, that enables sensitive detection and tracking of somatic mutations in plasma samples across ~20,000 genes. The NeXT Liquid Biopsy platform monitors tumor variants and discovers novel mutations in the plasma, through analysis of tumor, normal and plasma samples from the same patient. The NeXT Liquid Biopsy platform enables the identification of somatic variants in liquid biopsy samples, following interventions such as surgery and treatment therapies. Here, we have applied NeXT Liquid Biopsy to profile the shedding of somatic mutations from more than 100 pan-cancer patients on an exome scale, detecting variants in well-characterized cancer driver genes and many events outside of traditional panel footprints.

Title: Accurate quantification of infiltrating B cell composition and clone diversity in tumor samples
Overview: The role of B cells as a prognostic biomarker remains elusive. For instance, infiltrating B cells in colorectal cancer have both positive and negative prognostic value. Thus, a scalable approach to quantify B cells and the B-cell receptor repertoire could yield novel insights into the role of B cells in tumor biology. To address this, we have developed immune cell quantification (InfiltrateID™) and immune receptor repertoire profiling (RepertoireID™) methods as part of the ImmunoID NeXT Platform®, an augmented, immuno-oncology-optimized exome/transcriptome platform. We show that InfiltrateID and RepertoireID accurately capture the composition and clone diversity of infiltrating B cells in tumor samples. Furthermore, we apply the two methods to explore B cell infiltration and BCR repertoires across a set of more than 650 pan-cancer samples.

Title: Exome-scale longitudinal tracking of emerging therapeutic resistance in GIST via analysis of circulating tumor DNA
Overview: Gastrointestinal stromal tumors (GIST) are lethal tumors characterized by constitutively activating mutations to KIT or PDGFRA. Transient disease control in the first-line setting is achieved via inhibition of tyrosine kinase signaling using the KIT inhibitor imatinib. As patients progress through subsequent lines of therapy, a molecularly heterogeneous disease evolves, characterized by distinct subtypes and shifting repertoires of exon-specific KIT variants that directly impact treatment outcomes. This study uses tumor-informed exome-scale liquid biopsy to identify and track the evolution of multiple resistance mechanisms in patients receiving tyrosine kinase inhibitors (TKIs) to address the unmet need of comprehensive understanding of GIST evolution in response to therapy.

Title: A high sensitivity, tumor-informed liquid biopsy platform, designed to detect minimal residual disease at part per million resolution
Overview: Tumor-informed liquid biopsy approaches have proven promising for detecting minimal residual disease (MRD) and recurrence of cancer following surgical resection or other therapy. However, current liquid biopsy MRD assays typically detect ctDNA in a range above 30 to 300 parts per million (PPM), leaving a significant fraction of MRD cases undetected, particularly soon after surgery and in early-stage cancers where ctDNA can be at very low levels. To address this, Personalis has developed NeXT Personal™, a tumor-informed liquid biopsy assay that achieves sensitivity down to 1 PPM, therefore enabling earlier detection of MRD and recurrence.

Title: Mono-allelic immunopeptidomics data from 109 MHC-I alleles reveals variability in binding preferences and improves neoantigen prediction algorithm
Overview: This study extends the previously published MHC-I, pan-allelic neoantigen prediction algorithm, SHERPA™, with immunopeptidomics from 84 additional mono-allelic transfected cell lines, totaling data from 109 unique alleles. SHERPA achieves model generalizability and 98% population allelic coverage by integrating nearly 500 additional public immunopeptidomics samples. As a result, SHERPA identifies 1.38-fold more immunogenic epitopes than either NetMHCPan-4.1 and MHCFlurry-2.0 and reveals strong correlations between evolutionary divergence and influential binding pocket positions in the MHC allele.

About Personalis

Personalis, Inc. is a leader in advanced cancer genomics for enabling the next generation of precision cancer therapies and diagnostics. The Personalis NeXT Platform® is designed to adapt to the complex and evolving understanding of cancer, providing its biopharmaceutical customers and clinicians with information on all of the approximately 20,000 human genes, together with the immune system, from a single tissue sample. To enable cancer sequencing, Personalis' Clinical Laboratory was built with a focus on clinical accuracy, quality, big data, scale, and efficiency. The laboratory is GxP-aligned as well as Clinical Laboratory Improvement Amendments of 1988-certified and College of American Pathologists-accredited. For more information, visit the Personalis website and follow Personalis on LinkedIn and Twitter.

Forward-Looking Statements

All statements in this press release that are not historical are “forward-looking statements” within the meaning of U.S. securities laws, including statements relating to attributes or advantages of the ImmunoID NeXT or NeXT Liquid Biopsy platforms, the NeXT Personal assay or the SHERPA algorithm, Personalis’ business opportunities, leadership, plans or expectations, or other future events. Such forward-looking statements involve risks and uncertainties that could cause actual results to differ materially from any anticipated results or expectations expressed or implied by such statements. Factors that could materially affect actual results can be found in Personalis’ filings with the U.S. Securities and Exchange Commission, including Personalis’ most recent reports on Forms 8-K, 10-K and 10-Q, the company’s registration statement on Form S-3 filed on December 30, 2020, and the company’s prospectus supplement filed on January 3, 2022, and include those listed under the caption “Risk Factors.” Personalis disclaims any obligation to update such forward-looking statements.

View source version on businesswire.com: https://www.businesswire.com/news/home/20220323005254/en/

Investor Relations Contact for Personalis:
Caroline Corner
investors@personalis.com
www.westwicke.com
415-202-5678

Media Contact for Personalis:
Jennifer Temple
pr@personalis.com
www.personalis.com
650-752-1300

Source: Personalis, Inc.