Tempus Announces Abstracts to be Presented at the American Association for Cancer Research Annual Meeting 2021

April 7, 2021

Tempus, a leader in artificial intelligence and precision medicine, today announced abstracts accepted for poster presentation at the American Association for Cancer Research (AACR) Annual Meeting 2021, which will convene virtually on April 10-15 and May 17-21. The research leverages Tempus' unparalleled library of multi-modal data to facilitate discovery, development, and delivery of optimized therapeutic options for patients.

"We're proud to present our recent research that demonstrates the power and depth of our database," said Dr. Kim Blackwell, Chief Medical Officer at Tempus. "As evidenced by the collection of abstracts, we are utilizing data-driven tools that empower physicians to optimize patient care."

Tempus will present eight posters; including two in collaboration with outside investigators from Baylor College of Medicine, Harris Health Ben Taub Hospital, and the Dan L Duncan Comprehensive Cancer Center. Four of the abstracts accepted for poster presentation at AACR 2021 are highlighted below and the complete list can be found at www.tempus.com/publications.

- **Incidence of Molecular Alterations in *KRAS* and Other Known Cancer Genes in Patients With Pancreatic Cancer Assessed With a Commercial Genomic Profiling Panel Compared to TCGA Results**
  - **Overview**: Tempus' xT LDT assay detected common alterations in genes such as *KRAS, TP53,* and *SMAD4* in a Baylor College of Medicine pancreatic cancer cohort at a similar incidence to The Cancer Genome Atlas Program. Approximately 13% of pancreatic cancer patients had an alteration in the homologous recombination repair pathway. Lens, Tempus' next-generation data exploration and analysis platform, allowed researchers to identify the incidence of targetable molecular alterations landscape in patients with pancreatic cancer.

- **Genomic Characterization and Monitoring Molecular Response to Treatment in African Americans (AA) Advanced Prostate Cancer (PC) Patients (Pts) via Next-Generation Sequencing (NGS); Real-world Experience in a Safety Net Hospital Oncology Clinic**
  - **Overview**: Tempus' xF liquid biopsy LDT assay allows for longitudinal monitoring of treatment response and resistance in patients with advanced prostate cancer. This study reported the incidence of key prostate cancer driver gene alterations, including *TP53*, *SPOP*, *AR* and *BRCA2*, in both the Ben Taub Hospital cohort and Tempus database, and revealed the value of longitudinal xF monitoring in 4 case studies: (1) Response to first line hormonal therapy, (2) Nonresponse to third line darolutamide, and (3) Two cases of response to pembrolizumab in MSI-H metastatic prostate cancer.

- **Comprehensive Validation of RNA Sequencing for Clinical NGS Fusion Genes and RNA Expression Reporting**
  - **Overview**: Tempus sequenced both DNA and the whole-transcriptome RNA to improve coverage and provide the most comprehensive patient molecular profile. This study reported results from the clinical and analytical validation of fusion calling for improved gene rearrangement detection, and the analytical validation of RNA expression for research purposes. The orthogonal testing concordance for targeted fusions was 100%, with 99.9% sensitivity and 99.9% specificity, and for untargeted fusions, the overall concordance was 97%, with 97% sensitivity. The enhanced RNA-sequencing assay offers unbiased detection of common and novel fusions, as well as validated gene expression data for comprehensive research analyses.
- **Leveraging Clinical RNA Sequencing for Scalable Tumor Immune Repertoire Profiling**
  - **Overview**: Characterizing tumor-infiltrating lymphocytes (TILs) by repertoire sequencing

(rep-seq) at scale can help maximize patient benefit from data-driven treatment options. This study presents a scalable method for TIL rep-seq from whole-transcriptome RNA data in approximately 500 tumors from 38 cancer types. Results of this study were consistent with an orthogonal DNA-seq method and confirmed expected trends in receptor profiles across the cohort, including monoclonality of lymphocyte receptors in T-cell/B-cell-driven malignancies, high repertoire richness in TIL-high cancers (e.g., NSCLC) and low in TIL-low cancers (e.g., multiforme glioblastoma). This method can be seamlessly integrated for improved TIL characterization from routine RNA-sequencing.

About Tempus

Tempus is a technology company advancing precision medicine through the practical application of artificial intelligence in healthcare. With one of the world's largest libraries of clinical and molecular data, and an operating system to make that data accessible and useful, Tempus enables physicians to make real-time, data-driven decisions to deliver personalized patient care and in parallel facilitates discovery, development and delivery of optimal therapeutics. The goal is for each patient to benefit from the treatment of others who came before by providing physicians with tools that learn as the company gathers more data. For more information, visit tempus.com.