Cellecta, Inc. Launches DriverMap[™] Adaptive Immune Receptor (AIR) Human RNA Spike-In Controls to Ensure Consistent Quality and Optimal Performance of TCR and BCR Profiling Assays

The first-to-market DriverMap[™] AIR RNA TCR/BCR spike-in controls measure the accuracy, sensitivity, and linear range of sequencing-based immune repertoire profiling assays.

MOUNTAIN VIEW, CA—(PR Newswire)—Apr. 4, 2024—Cellecta, Inc. today announced the launch of the DriverMap[™] Adaptive Immune Receptor (AIR) Human RNA Spike-In Premixed Controls, the first commercially available collection of synthetic mRNA constructs that can serve as universal controls for commercial or home-brewed AIR repertoire sequencing (AIR-Seq, TCR-seq and BCR-seq) assays based on multiplex RT-PCR or 5' RACE PCR techniques.

While AIR-Seq assays have been increasingly adopted in recent years to gain insight into the adaptive immune response, the lack of readily available controls has limited their utility and made harmonization of data across platforms next to impossible. Now, the possibility of adding validated RNA spike-in controls to an AIR assay provides a way to measure and check biases introduced by PCR, next-generation sequencing (NGS), cross-contamination and batch-to-batch experimental variation.

"We are pleased to offer the research community a new tool to optimize performance of different AIR-Seq assays and improve the quality of immune receptor repertoire profiling data," affirmed Alex Chenchik, Ph.D., president and chief scientific officer of Cellecta. "This should increase the utility of these assays for discovery of novel biomarkers and ensure reliable results that will afford greater insights into immunity mechanisms for a wide range of human diseases."

The DriverMap[™] AIR RNA Spike-In Controls key characteristics include:

- These controls consist of 48 B-Cell Receptor (BCR) and 39 T-Cell Receptor (TCR) synthetic mRNA constructs designed to mimic all the different and most abundant TCR and BCR genes.
- When introduced into the sample, the synthetic controls are amplified and sequenced along with the endogenous TCRs and BCRs, thus presenting a defined copy number of RNA transcripts for calibration and QC of NGS data.
- The ability to standardize results across samples with these RNA spike-in constructs ensures the accuracy of sequencing data and eliminates bias caused by PCR and sequencing.

These standards and controls will help attain the goal of more reliable and reproducible AIR sequencing (AIR-Seq) data harmonization, interpretation, and sharing.

In addition to offering the DriverMap AIR RNA Spike-In Controls, which are useful on all AIR-Seq assay platforms, Cellecta offers its own workflow, including AIR-DNA and AIR-RNA kits, a full TCR/BCR profiling service and a data analysis pipeline.

For more information on the DriveMap AIR RNA Spike-In Controls, including introductory pricing, visit www.cellecta.com/DriverMapAIR or email info@cellecta.com/DriverMapAIR or email www.cellecta.com/DriverMapAIR or email www.cellecta.com/DriverMapAIR or email www.cellecta.com/DriverMapAIR or email www.cellecta.com/DriverMapAIR or email www.cellecta.com

About Cellecta:

Cellecta, Inc. is a trusted provider of genomic products and services that advance researchers' drug target and biomarker discovery efforts. Since 2006, we have collaborated with the world's leading pharma, biotech, government, and academic institutions. Numerous scientific papers have been published utilizing Cellecta's expertise in viral vector production, phenotypic screening, custom cell engineering and multiplex RT-qPCR.

Cellecta, Inc. is headquartered in Mountain View, California. More information about the company and its products and services may be found at <u>www.cellecta.com</u>

Cellecta, Inc.

Paul Diehl, 650-938-4050 pauld@cellecta.com

or

Media: Ruth Mercado, 650-938-4080 rmercado@cellecta.com

###