First Public Data Presented from Gritstone Oncology's Tumor Antigen Identification Platform for Personalized Cancer Immunotherapy

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Achieving a Breakthrough in Predictive Accuracy for Tumor Neoantigens

Gritstone's Novel Approach Presented at the American Association for Cancer Research Annual Meeting

EMERYVILLE, CA, March 31, 2017 —Gritstone Oncology, a next-generation personalized cancer immunotherapy company, today announced the first reported data supporting its novel approach to tumor-specific neoantigen (TSNA) identification through integrated tumor tissue analysis and deep learning. The data are being presented in the Tumor Antigens and Adaptive Immunity poster session on Sunday, April 2 from 1:00 – 5:00 PM EDT at the American Association for Cancer Research (AACR) Annual Meeting 2017 in Washington, D.C.

"For years, cancer immunotherapy has been one of the most exciting fields in oncology research, yet it also poses some of the greatest challenges," said Andrew Allen, M.D., Ph.D., co-founder, president and chief executive officer of Gritstone Oncology. "We believe these early data underscore the significant impact our approach could make in advancing this field. By leveraging our best-in-class genomics, proteomics, and computational platform, we are working toward personalized immunotherapies to address difficult-to-treat cancers – because every cancer and every patient is unique."

Gritstone performed deep tumor exome and transcriptome next-generation sequencing (NGS) and mass spectrometry human leukocyte antigen (HLA) class I peptide sequencing on tumor specimens from 22 non-small cell lung cancer (NSCLC) patients. A median of 286 nonsynonymous somatic mutations were found per patient, with 62% transcribed in mRNA. Down-sampling tumor NGS data to a more typical lower average coverage revealed a 20% loss of candidate neoantigens, demonstrating the importance of NGS sequencing depth.

Gene expression measurement at the RNA level was strongly predictive of HLA presentation, with peptides from genes detected in RNA found presented >20X more often than peptides from non-detected genes. With this and public datasets, a deep learning model was created to predict HLA presentation and compared to standard binding affinity prediction. While a binding affinity-based approach gave a positive predictive value (PPV) of only ~3%, Gritstone's platform showed ~30% PPV, a near ten-fold gain. Initial *in vitro* results also indicated that HLA presented TSNA can prime T cells from HLA-matched donors.

ABOUT GRITSTONE ONCOLOGY

Gritstone Oncology is a privately-held, next-generation personalized cancer immunotherapy company. Gritstone brings together distinguished scientific founders, an experienced and diverse management team, a seasoned and successful board of directors, and deep financial backing to tackle fundamental challenges at the intersection of cancer genomics, immunology, and immunotherapy design. The company's initial goal is to identify and deploy therapeutic neoantigens from individual patients' tumor to develop novel treatments for lung cancer. Gritstone Oncology is headquartered in the San Francisco Bay Area with certain key functions located in Cambridge, MA. The company launched in October 2015 with a Series A financing of $102 million from leading blue-chip biotechnology investors, including Versant Ventures, The Column Group, and Clarus Ventures. More information can be found at www.gritstoneoncology.com.

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