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Gritstone Oncology announces publication of Neoantigen Identification Capabilities of its AI Platform, EDGE

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Gritstone Oncology, Inc., a clinical-stage biotechnology company developing the next generation of cancer immunotherapies to fight multiple cancer types has announced that data demonstrating the predictive performance of its EDGE (Epitope Discovery in cancer GEnomes) platform in the identification of tumor-specific neoantigens (TSNA) and neoantigen-reactive T-cells was published in Nature Biotechnology.

Three distinct datasets were used in the manuscript to validate the EDGE platform as a robust machine-learning tool for neoantigen identification. First, the authors showed that EDGE increases the accuracy of predicting human leukocyte antigen (HLA)-presented peptides on tumor cells by up to nine-fold over industry-standard methods using relevant metrics. Second, independently validated neoantigens from published third-party studies (mostly from the U.S. National Cancer Institute) were used to compare the performance of EDGE versus public prediction tools. Using only patient tumor mutation data from these studies to predict neoantigens, EDGE correctly identified validated TSNA for 11 of 12 patients, versus only 4 of 12 patients identified with the standard approach. Finally, using routine blood samples obtained from nine non-small cell lung cancer patients receiving PD-(L)1 checkpoint inhibitors, EDGE enabled identification of circulating T-cells specific for true neoantigens in the majority of (5 of 9) patients.

“Neoantigens are critical targets of immunotherapy and can drive an effective anti-tumor T-cell response; yet, existing tools have had low success rates in identifying true neoantigens,” said Roman Yelensky, Ph.D., executive vice president and chief technology officer. “We built our EDGE platform to be a best-in-class machine-learning model using the largest dataset of HLA-presented peptides from human tumor samples. The data published in Nature Biotechnology support EDGE as a transformative tool for the development of the next generation of neoantigen-targeted cancer immunotherapies.”

“EDGE represents the cutting edge in personalized immunotherapy,” said Timothy Chan, M.D., Ph.D., co-founder and scientific advisory board member of Gritstone. “I am very excited to see this state-of-the-art technology used to improve

neoantigen vaccine development.”

EDGE’s prediction model was trained using a large dataset of human tumor and normal tissue samples with paired class I HLA-presented peptide sequences, HLA types and transcriptome RNA sequencing. A variety of tumor types, such as breast, lung, melanoma, colon and ovarian cancers were collected for sequencing, and combined with publicly available data. The training dataset for EDGE has since grown to now include more than 300 tumor and normal tissue samples, yielding over one million peptides, from patients of various ancestries with diverse HLA types. In addition to the training dataset, a key differentiator that contributed to improved performance was a novel integrated neural network model architecture. This neural network enabled EDGE to jointly model multiple key features, such as variable peptide length and the dependence of peptide presentation on gene expression level using RNA, essential for accurate prediction of true TSNA. The United States Patent Office issued Gritstone its first patent covering EDGE, on August 21, 2018 (Yelensky, et al., Neoantigen identification, manufacture and use, US 10,055,540.).