Cure First and SEngine Precision Medicine Scientists Join Global Pan-Cancer Atlas Research Collaboration:

Discover Common Link in Nearly 30% of All Cancers

*Research from the Fred Hutch spin-outs expected to bring scientists closer to developing targeted and less-toxic cancer therapies for cancer patients*

SEATTLE, April 5, 2018 – Seattle scientists from Cure First [curefirst.org], a non-profit research organization, and SEngine Precision Medicine [senginemedicine.com], a biotech developing targeted, more effective, and less toxic cancer therapeutics, co-authored one of 27 high-profile papers published today by *Cell Press.*

The paper entitled, *Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across The Cancer Genome Atlas,* details a multiyear in-depth analysis of the MYC cancer gene family. For the first time, it was possible to use the data from 11,000 cancer samples across 33 tumor types which are part of The Cancer Genome Atlas (TCGA) [https://cancergenome.nih.gov]. During the last two years, SEngine Precision Medicine, Cure First, MYC gene experts from academic institutions, and scientists at the Institute for Systems Biology carefully interpreted, visualized and integrated the data with existing knowledge. The TCGA data set uses 2.5 petabytes of storage, that’s more data than all U.S. academic research libraries combined.

The results were striking. Researchers discovered 28% of all cancer samples analyzed show the Myc family of cancer genes had increased the number of gene copies showing the gene is “amplified” and thus hyperactivated.

SEngine Precision Medicine Founder and CEO, Dr. Carla Grandori, who co-authored the paper, says “This paper is going to help the pharmaceutical and research community develop drugs and biomarkers for Myc gene driven cancers which are currently often incurable.”

The coordinated release of the peer-reviewed paper is the culmination of a multi-year collaboration between the National Cancer Institute, the National Human Genome Research Institute, and researchers associated with The Cancer Genome Atlas (TCGA) Research Network.

Cure First Scientist, Franz Schaub, also a co-author on the paper says, "This project was a two-year marathon of computational analysis and development of novel bioinformatics approaches, driven by the speed of biocomputing through the Google Cloud, specifically the Institute for Systems Biology Cancer Genomics Cloud. The findings will help us prioritize which drugs we believe offer the most hope to patients and move them quickly to patients’ bedsides."

The Myc cancer gene has been the subject of research for the past 30 years as a recognized and powerful cancer-causing gene.

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