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Genomenon Announces First Automated, Evidence-Based Blood Cancer Panel

Genomenon Presents the Details of a Pan-Hematopoietic Malignancy Gene Panel with Supporting Evidence at AMP 2017 Conference

ANN ARBOR, Michigan – November 14, 2017 – Genomenon will announce the first comprehensive, evidence-based cancer panel produced using automated machine learning techniques at the Association for Molecular Pathologist (AMP) 2017 Annual Conference this week. Dr. Mark Kiel, Founder and Chief Science Officer at Genomenon, led his team of scientists in the development of an automated process to mine proven disease-gene associations from millions of scientific articles.

The panel design algorithm developed by Dr. Kiel and his team uses the Mastermind Genomic Search Engine software to objectively correlate genes and genetic variants with the quality and frequency of citations from the scientific literature. This approach automatically produces a list of candidate biomarkers associated with a specific disease with reference citations that can then be reviewed by specialists for final approval.

Using this method, what used to take months of meticulous effort to create an *ad hoc* diagnostic gene panel design from manually selected research publications, can now be done comprehensively for any disease within days in a highly systematized way. Furthermore, Genomenon's algorithm points physicians to relevant gene-specific therapeutic, prognostic and diagnostic information in the literature, empowering them to make fully informed, confident, evidence-based treatment decisions for their patients.

The new method of systematized panel design allows physicians to redirect time and energy that was formerly spent searching for and synthesizing information from literature review to examining and assessing the assembled evidence. In contrast to commercially available gene panels, Genomenon's panel design is supported by a comprehensive understanding of the scientific literature and can be automated for any condition, opening the door for more rapid and accurate diagnostic assay development.

Genomenon's gene panel for pan-hematopoietic malignancies is the first such panel to be published using this approach. The result is a highly comprehensive listing of over 300 genes with all associated variants supported by specific literature citations from thousands of research publications.

The new cancer panel, including the gene list and literature citations will be presented at Genomenon's Corporate Workshop at the AMP 2017 Conference on Wednesday Nov. 15 at 4:00 p.m. A white paper on the pan-hematopoietic malignancy gene panel will be available at the Genomenon Exhibitor Booth #1503 throughout conference and available on Genomenon's website after the conference. The panel was reviewed by Dr. Kojo Elenitoba-Johnson, chair of the Department of Pathology and Laboratory Medicine at the Perelman School of Medicine, University of Pennsylvania and an internationally recognized leader in hematopathology, molecular pathology and mass spectrometry- driven proteomics. Dr. Elenitoba-Johnson is also a co-founder of Genomenon.

About Genomenon:

Genomenon is helping doctors, clinicians and researchers make sense of patients' DNA data. With the world's only comprehensive genomic-specific search engine, Genomenon helps doctors connect diseases and patients' DNA profiles to the most impactful scientific genomic research to diagnose and treat patients. Our web-based search engine has indexed millions of medical articles cataloguing the genetic relationships between DNA and human diseases, including cancer. Genomenon's solutions lower the cost of genetic tests, deliver faster diagnoses and help assure that no data is missed that could save a patient's life.

For more information, visit www.genomenon.com or email sales@genomenon.com.

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