

NEW: nCounter[®] Vantage 3D[™] Heme Panel

Despite the great diversity in cell of origin and other clinical features, hematologic malignancies share a core set of pathways and processes that drive tumorigenesis. Pathways critical to the normal growth and development of the hematopoietic compartment, such as MAPK, MYC signaling, NF-κB, PI3K-AKT, and B cell and T cell receptor signaling are frequently mutated and disrupted. Additionally, dysregulation of cytokines, apoptosis, the DNA damage response, and epigenetic factors are frequently seen in gene expression as well as mutational profiles across a variety of these cancers. Seminal publications focused on hematologic oncology research and signature development were collated and scored to develop a curated 192-plex gene set that measures the conserved and crucial pathways underlying hematologic malignancies.

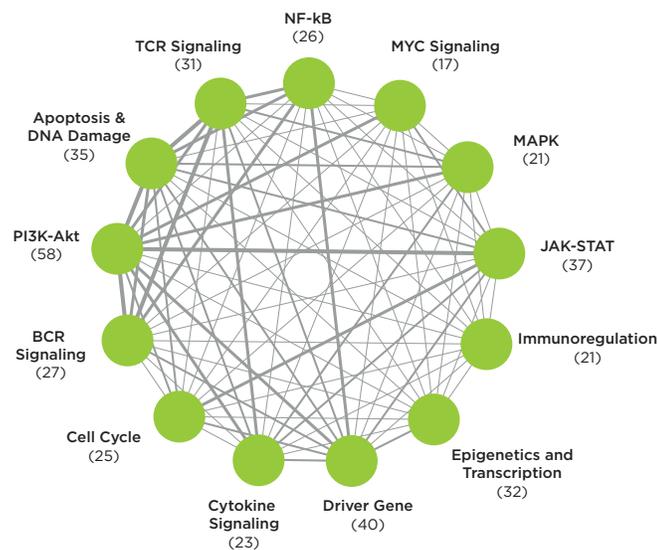


FIGURE 1 Number of genes representing each annotation. Panel includes 180 genes plus 12 internal controls.

The Vantage 3D RNA Heme panel is also designed with the application of 3D Biology[™] Technology in mind. As part of our Vantage 3D RNA panel line up, this content is compatible with the Vantage 3D Protein heme panel to simplify your workflow and data analysis by comparing gene and protein expression in a single view.

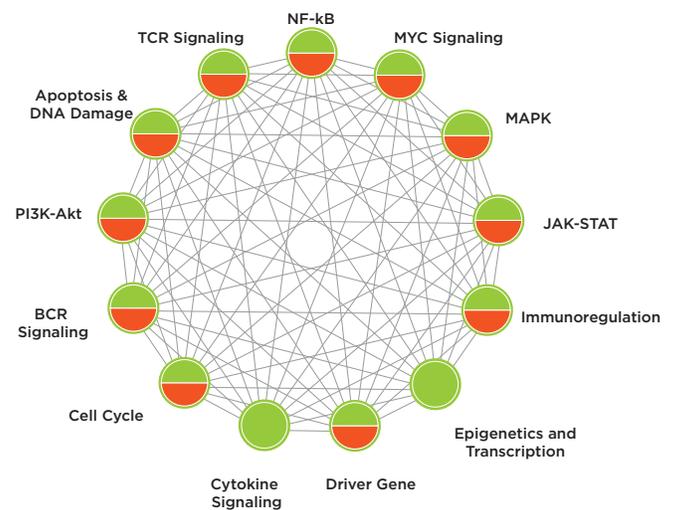


FIGURE 2 Multi-analyte representation of canonical pathways underlying hematologic malignancies. Green = Vantage 3D RNA Heme; Orange = Vantage 3D Protein Heme

For more information, visit nanosttring.com

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