Harnessing the immune system to eliminate cancer and prevent its recurrence is proving to be a powerful therapeutic approach that has achieved unprecedented successes in hematological malignancies and some solid malignancies with a high tumor burden. Next generation immune therapies to improve clinical responses and widen the reach of immunotherapy are being designed at a rapid pace, and dogs represent a valuable resource that can be greatly facilitated using immune competent animals with spontaneous tumors. Pet dogs are immunologically outbred, immune competent and develop spontaneous situations such as non-Hodgkin's lymphoma, glioblastoma, osteosarcoma, uveal tract carcinoma and melanoma that share remarkable clinical, biological and genetic features with their human counterparts. As such, pre-clinical testing of immune therapeutic approaches in dogs with cancer goals to accurately inform human clinical trial design. For this comparative approach to provide maximum information to human clinical translation of next generation immunotherapeutics and identify correlative biomarkers of therapeutic response, it is necessary to develop research tools for deep interrogation of the canine immune response. Here we present work conducted through a year-long, multi-center, global collaboration resulting in the creation of a novel gene expression tool for studies of the immune response in dogs with immune competent and targeted therapies. This original approach utilizes NanoString’s nCounter® platform and is termed the Canine IO Panellist here described in this poster.

The Canine IO Panel has been uniquely designed with 800 genes for canine pan-cancer research studies. The panel represents a companion to the widely recognized nCounter Human IO 360® and Human PanCancer Immune Profiling panel currently in use with human clinical trials, with significant overlapping content designed for directly comparing human and canine immune responses. The customizable panel segments genes into 8 core components including: Cytokine & Chemokine Signaling, Interferon Signaling, Checkpoint Signaling, Complement Cascade, Immune Cell Abundance, Tumor Immunogenicity, Inhibitory Tumor Mechanisms, and Stromal Factors. Genes were selected based on their relevance for the study of oncology, their importance in human clinical studies as well as canine expression profiles from both RNA-Seq and nCounter experiments. Additionally, the canine reference transcriptome based on CanFam3.1, was utilized for designing the probes; the known genomic variability of dogs, canines and humans. Procuring adequate drug supplies and reagents for large animal studies is also essential. Finally, broad collaborations will always advance the field more effectively than any single institution. The Canine IO Panel has been uniquely designed with 800 genes for canine pan-cancer research studies. The panel represents a companion to the widely recognized nCounter Human IO 360® and Human PanCancer Immune Profiling panel currently in use with human clinical trials, with significant overlapping content designed for directly comparing human and canine immune responses. The customizable panel segments genes into 8 core components including: Cytokine & Chemokine Signaling, Interferon Signaling, Checkpoint Signaling, Complement Cascade, Immune Cell Abundance, Tumor Immunogenicity, Inhibitory Tumor Mechanisms, and Stromal Factors. Genes were selected based on their relevance for the study of oncology, their importance in human clinical studies as well as canine expression profiles from both RNA-Seq and nCounter experiments. Additionally, the canine reference transcriptome based on CanFam3.1, was utilized for designing the probes; the known genomic variability of dogs, canines and humans. Procuring adequate drug supplies and reagents for large animal studies is also essential. Finally, broad collaborations will always advance the field more effectively than any single institution. The Canine IO Panel has been uniquely designed with 800 genes for canine pan-cancer research studies. The panel represents a companion to the widely recognized nCounter Human IO 360® and Human PanCancer Immune Profiling panel currently in use with human clinical trials, with significant overlapping content designed for directly comparing human and canine immune responses. The customizable panel segments genes into 8 core components including: Cytokine & Chemokine Signaling, Interferon Signaling, Checkpoint Signaling, Complement Cascade, Immune Cell Abundance, Tumor Immunogenicity, Inhibitory Tumor Mechanisms, and Stromal Factors. Genes were selected based on their relevance for the study of oncology, their importance in human clinical studies as well as canine expression profiles from both RNA-Seq and nCounter experiments. Additionally, the canine reference transcriptome based on CanFam3.1, was utilized for designing the probes; the known genomic variability of dogs, canines and humans. Procuring adequate drug supplies and reagents for large animal studies is also essential. Finally, broad collaborations will always advance the field more effectively than any single institution.