Daniel Rotroff et al., J Mol Genet Med 2014, 8:3
http://dx.doi.org/10.4172/1747-0862.S1.002

OMICS Group Conferences
Accelerating Scientific Discovery

2nd International Conference on
Genomics & Pharmacogenomics
September 08-10, 2014 DoubleTree by Hilton Hotel Raleigh-Brownstone-University, USA

# Using DNA copy number aberrations in naturally occurring canine cancers to identify candidate drivers of carcinogenesis

**Daniel Rotroff**[1], **Rachael Thomas**[1], **Sarah Roode**[1], **Alison Motsinger-Reif**[1] and **Matthew Breen**[2]
[1]North Carolina State University, USA
[2]UNC Lineberger Comprehensive Cancer Center, USA

There are approximately 78 million domestic dogs residing in the USA. Cancer is one of the leading causes of death for domestic dogs, with popular breeds such as golden retrievers, Labrador retrievers and boxers, succumbing to cancer with frequencies of 50, 34 and 44%, respectively. Because canines exhibit a wide variety of spontaneous cancers that share clinicopathologic features with humans, we have a unique opportunity for comparative analysis of naturally occurring cancers toward advancing treatment strategies in both species. Furthermore, the recent development of a high-quality canine genome sequence assembly has opened the door for researchers to identify key drivers of disease that may impact both canine and human patients. We have developed tumor-associated genomic DNA copy number aberration profiles for 75 canine hemangiosarcomas and more than 200 canine leukemias and lymphosarcomas using an oligonucleotide array comparative genomic hybridization (oaCGH) platform. Using a variety of bioinformatic approaches we have mapped canine genes to available human homologues for pathway-based analyses, identified putative drivers of carcinogenesis, and have identified genes that may be useful as diagnostic tools for characterizing leukemia subtypes. Overall, these results demonstrate the potential for using spontaneously occurring canine cancers to improve diagnoses and develop novel therapies for both dogs and humans.

## Biography

Daniel Rotroff has completed his MSPH and his PhD from the University of North Carolina at Chapel Hill and is currently a Postdoctoral research scholar at North Carolina State University in the Department of Statistics. His graduate work was conducted within the ToxCast project at the National Center for Computational Toxicology at the US EPA and focused on predictive modeling of the estrogen receptor signaling pathway. He is currently focused on association mapping and predictive modeling for a wide range of pharmacogenomics applications.

daniel.rotroff@gmail.com