

Canine Normal Tissue Database

Our understanding of disease is increasingly informed by changes in gene expression between normal and abnormal tissues. The release of the canine genome sequence in 2005 provided an opportunity to better understand human health and disease using the dog as clinically relevant model. Accordingly, we now present the first genome-wide, canine normal tissue gene expression compendium with corresponding human cross-species analysis.

The database is now available. [Click here](#) to download the .cel files.

The [oncogenomics website](#) is also available. This allows for the comparison of canine normal tissue individual gene expression with human normal and tumor tissue gene expression.

For more information regarding the Comparative Oncology Program's microarray work, please contact Christina Mazcko at mazckoc@mail.nih.gov