



# ICDC-Glioma01

## Summary

Sporadic gliomas in companion dogs provide a window on the interaction between tumorigenic mechanisms and host environment. We compared the molecular profiles of canine gliomas with those of human pediatric and adult gliomas to characterize evolutionarily conserved mammalian mutational processes in gliomagenesis. Employing whole genome-, exome-, transcriptome- and methylation-sequencing of 81 canine gliomas, our cross-species comparative genomic analysis provides unique insights into glioma etiology and the chronology of glioma-causing somatic alterations, and rationalizes sporadic canine glioma as a preclinical model tailored to measuring treatment efficacies in patients with canine or human glioma. Here, we provide high-throughput multi-omics sequencing data in binary alignment map (BAM) format for the largest canine glioma cohort to date.

This dataset includes baseline pathologic, MRI and genomic features of treatment-naive naturally-occurring canine glioma. Multi-omic data for all 81 subjects can be found in the [Integrated Canine Data Commons](#). Radiology imaging are available for 57 of these subjects, and pathology imaging for 76 subjects. The data were collected from 5 different veterinary institutions' patient populations. Clinical MRI are available prior to any treatment, and surgical biopsy and/or tissues collected at necropsy are provided as H&E stained sections. The tumors have been classified with a harmonized classification scheme developed by veterinary and physician neuropathologists. The genomic features were described using whole exome, whole genome, RNAseq and methylation profiling.

This is the first dataset of its kind to comprehensively describe and report the clinical, pathologic, imaging and genomic landscape of naturally-occurring canine glioma. This work serves the cancer research community by providing the necessary multi-parametric data to define the translational relevance of this canine tumor as a model for its human counterpart(s). Inclusion of appropriate canine glioma patients with similar and/or relevant features can be studied in the context of comparative oncology clinical trials to advance questions in cancer biology and drug development.

## About the Integrated Canine Data Commons

NCI's Division of Cancer Treatment and Diagnosis (DCTD) charged the Frederick National Laboratory for Cancer Research (FNLRC) to build the Integrated Canine Data Commons (ICDC), a cloud-based repository of spontaneously-arising canine cancer data. ICDC was established to further research on human cancers by enabling comparative analysis with canine cancer. The data in the ICDC is sourced from multiple different programs and projects; all focused on canine subjects. The data is harmonized into an integrated data model and then made available to the research community. The ICDC is part of the Cancer Research Data Commons (CRDC), an initiative from NCI's Center for Biomedical Informatics and Information Technology (CBIIT). Bioinformatic analysis of the ICDC data is accomplished using the CRDC's [Cloud Resources](#).

## Acknowledgements





We would like to acknowledge the individuals and institutions that have provided data for this collection:

- This work was funded in part by NCI funding to designated cancer centers through a competitive P30 supplement mechanism and through support of the COP, an intramural NCI/Center for Cancer Research program.

### Data Access

## Data Access

Click the **Download** button to save a ".tcia" manifest file to your computer, which you must open with the [NBIA Data Retriever](#) . Click the **Search** button to open our Data Portal, where you can browse the data collection and/or download a subset of its contents.

Data Type	Download all or Query/Filter
Images (DICOM, 5.1 GB)	 
Histopathology Images (SVS, 172 GB)	
Genomics (External)	

Click the Versions tab for more info about data releases.

### Detailed Description

## Detailed Description

	Radiology Image Statistics	Pathology Image Statistics
Modalities	MR	Pathology
Number of Participants	57	78
Number of Studies	58	N/A
Number of Series	650	N/A
Number of Images	17,797	84
Images Size (GB)	5.1 GB	172

### Citations & Data Usage Policy

## Citations & Data Usage Policy

Users of this data must abide by the [TCIA Data Usage Policy](#) and the [Creative Commons Attribution 4.0 International License](#) under which it has been published. Attribution should include references to the following citations:

### **i** Data Citation

Amin SB, Anderson KJ, Boudreau CE, Martinez-Ledesma E, Kocakavuk E, Johnson KC, Barthel FP, Varn FS, Kassab C, Ling X, Kim H, Barter M, Lau CC, Yee Ngan C, Chapman M, Koehler JW, Miller AD, Long JP, Miller CR, Porter BF, Rissi DR, Mazcko C, LeBlanc AK, Dickinson PJ, Packer RA, Taylor AR, Rossmeisl Jr. JH, Woolard KD, Heimberger AB, Levine JM, Verhaak RGW. Canine glioma characterization project for ICDC [Dataset]. The Cancer Imaging Archive; 2020. Available from: <https://doi.org/10.7937/TCIA.SVQT-Q016>

### **i** Publication Citation

Amin SB, Anderson KJ, Boudreau CE, Martinez-Ledesma E, Kocakavuk E, Johnson KC, Barthel FP, Varn FS, Kassab C, Ling X, Kim H, Barter M, Lau CC, Ngan CY, Chapman M, Koehler JW, Long JP, Miller AD, Miller CR, Porter BF, Rissi DR, Mazcko C, LeBlanc AK, Dickinson PJ, Packer RA, Taylor AR, Rossmeisl JH Jr, Woolard KD, Heimberger AB, Levine JM, Verhaak RGW. Comparative Molecular Life History of Spontaneous Canine and Human Gliomas. Cancer Cell [Internet]. Elsevier BV; 2020 Feb;37(2):243-257.e7. Available from: <http://dx.doi.org/10.1016/j.ccell.2020.01.004>

### **i** TCIA Citation

Clark K, Vendt B, Smith K, Freymann J, Kirby J, Koppel P, Moore S, Phillips S, Maffitt D, Pringle M, Tarbox L, Prior F. **The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository**, Journal of Digital Imaging, Volume 26, Number 6, December, 2013, pp 1045-1057. DOI: <https://doi.org/10.1007/s10278-013-9622-7>

## Other Publications Using This Data

TCIA maintains [a list of publications](#) which leverage TCIA data. If you have a manuscript you'd like to add please [contact the TCIA Helpdesk](#).

### Versions

#### **Version 1 (Current): Updated 2020/12/18**

Data Type	Download all or Query/Filter
Images (DICOM, 5.1 GB)	<div style="display: flex; justify-content: space-around;"> <div style="background-color: #007bff; color: white; padding: 5px 10px; border-radius: 3px; display: flex; align-items: center;"> <span style="font-size: 1em;">↓</span> Download         </div> <div style="background-color: #ffc107; color: white; padding: 5px 10px; border-radius: 3px; display: flex; align-items: center;"> <span style="font-size: 1em;">🔍</span> Search         </div> </div> <p>(Requires <a href="#">NBIA Data Retriever</a> .)</p>
Histopathology Images (SVS, 172 GB)	<div style="background-color: #007bff; color: white; padding: 5px 10px; border-radius: 3px; display: flex; align-items: center;"> <span style="font-size: 1em;">↓</span> Download         </div>

Genomics (External)

