Utilization of the dog as a naturally occurring comparative oncology and pathology model is emerging as an important study mechanism to understand the pathogenesis, progression, and response to treatment for numerous neoplasms. Intracranial neoplasia represents approximately 3-4% of all tumors in the dog with meningioma and glioma most commonly reported. Canine meningioma (~40-50% of intracranial tumors) recapitulates many of the histologic features seen in human meningioma with subtypes like meningothelial, transitional, and atypical commonly represented. A validated grading scheme of canine meningioma has not been developed and features of malignancy like invasion and high mitotic rate are often relied on for subjective determination of grade. Molecular abnormalities in pathways associated with DNA repair, cell cycle progression, and apoptosis are similar between canine and human patients; however, alterations in tumor suppressor genes NF2 and 4.1B are not important in canine meningioma tumorigenesis. Canine glioma (~30% of intracranial tumors) is heavily skewed toward oligodendroglioma over astrocytoma and undefined glioma. Canine gliomas are graded based on the presence/absence of microvascular proliferation, necrosis, mitoses, and invasion; however, the utilization of molecular phenotypes to determine prognosis is not currently utilized in veterinary medicine. Molecular features of canine glioma include alterations in major components of the RB1, TP53, and RTK-RAS-PI3K pathways; however, important molecular feature of human glioma, like IDH1 mutation, do not exist in the dog. Overexpression of PDGFRα, EGFR, and IGFBP2 are well documented in canine glioma. Due to similarities between human and canine intracranial neoplasia, the dog is an important model system to study the pathogenesis, progression, and treatment of these tumors. This talk will review what is known regarding the pathologic basis of canine meningioma and glioma and note future directions of study.