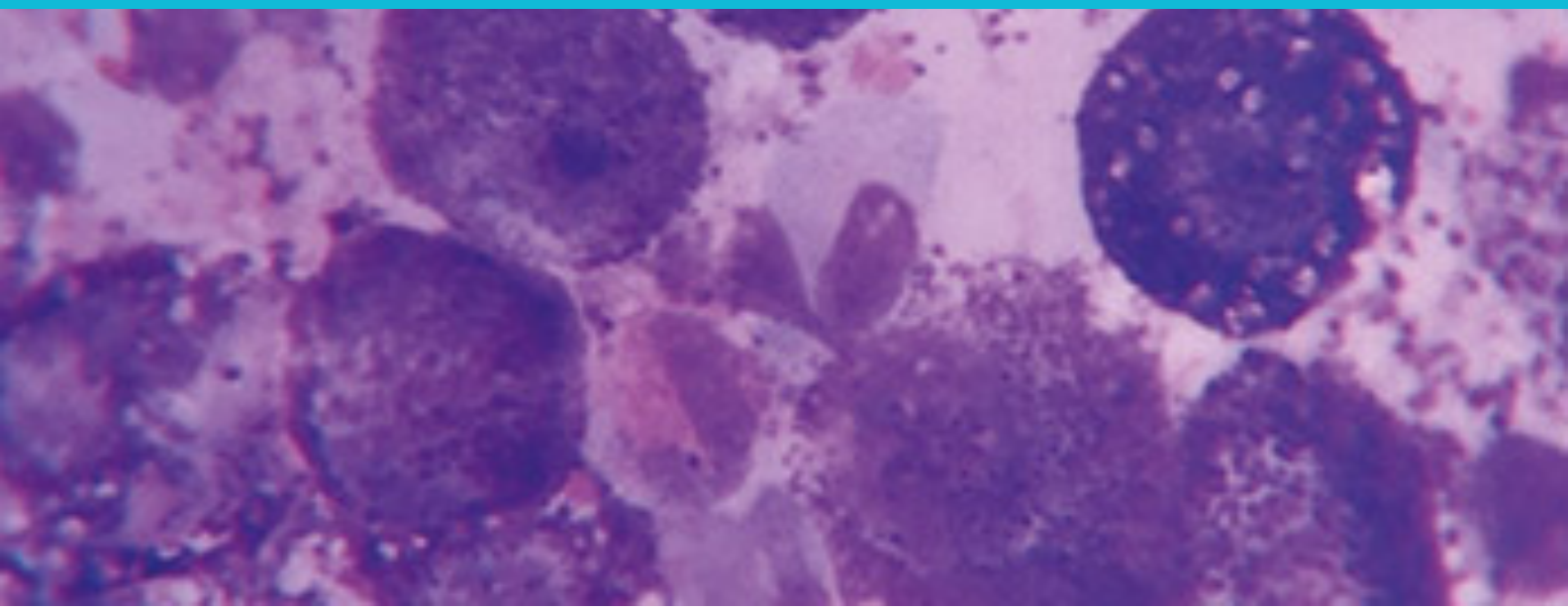


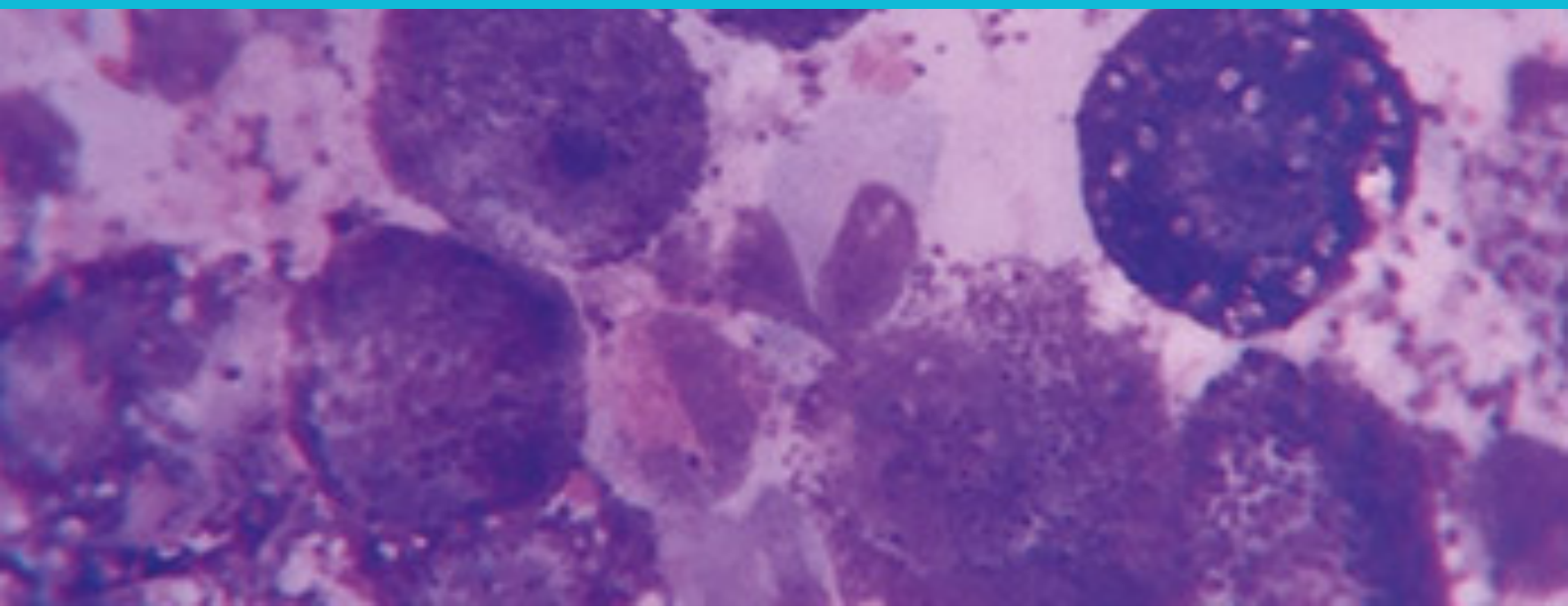
How do the specific expressions of cancer-associated genes compare between dog and human ?

Cases reported in the literature can be cited showing that several cancer-associated genes have been well preserved between dog and human.

One example that has been extensively studied in mammary cancers is the steroid receptor. Canine and human breast cancers share common histological types and have similar biological behavior. Histological subtype strongly influences oestradiol receptor α/Progesterone receptor expression. Simple and complex adenomas as well as simple tubular carcinomas exhibited the greatest expression, whereas the immunohistochemical labelling for these receptors was weaker in carcinoma and malignant myoepitheliomas, as well as in solid/anaplastic carcinomas and comedocarcinomas. Receptor expression was generally higher in benign relative to malignant neoplasms, and in the latter it was significantly lower in ovariectomised *vs*. intact bitches. Lymphatic invasion, mitotic index, nodule diameter, and tumor grade were significantly associated with ORα/PR expression. Tumors from dogs with <10% cells with ORα/PR expression had a poorer prognosis. Lymphatic invasion, the status of the margins of excision, and the mitotic index were found to be independent prognostic indicators. Like in human, the differences in histological subtype and whether or not a bitch has been ovariectomised (spayed) should be considered when evaluating the significance of ORα and PR expression in CMTs. The dog may be a useful model for hormonal studies and for the development of models of endocrine therapy and endocrine independent therapies for human breast cancer.

Bibliography : MacEwen et al; Cancer Research, 42, 2255-2259, June 1982. Estrogen Receptors in Canine Mammary Tumors

Mainenti et al, Vet J. 2014 Oct;202(1):62-8. Oestrogen and progesterone receptor expression in subtypes of canine mammary tumors in intact and ovariectomised dogs.



Spontaneous canine head and neck squamous cell carcinoma (HNSCC) represents an excellent model of human HNSCC but is greatly understudied. To better understand and utilize this valuable resource, a pilot study was performed to characterize the genome by investigating 12 canine HNSCC cases, of which 9 are oral, via high density array comparative genomic hybridization and RNA-seq. The analyses reveal that these canine cancers recapitulate many molecular features of human HNSCC. These include analogous genomic copy number abnormality landscapes and sequence mutation patterns, recurrent alteration of known HNSCC genes and pathways (e.g., cell cycle, PI3K/AKT signaling), and comparably extensive heterogeneity. Amplification or overexpression of protein kinase genes, matrix metalloproteinase genes, and epithelial-mesenchymal transition genes TWIST1 and SNAI1 are also prominent in these canine tumors. This pilot study, along with a rapidly growing body of literature on canine cancer, reemphasizes the potential value of spontaneous canine cancers in HNSCC basic and translational research.

Bibliography:
Liu D, PLOS Genetics, June 1, 2015; Canine Spontaneous Head and Neck Squamous Cell Carcinomas Represent Their Human Counterparts at the Molecular Level

In addition to the sense transcription, it is noteworthy that in dog, the antisense transcription has also been reported to facilitate a more fine-tuned regulation of gene expression, usually of the protein coding gene located sense to the antisense element. Using RNA-Seq data, 4,636 sequences were transcribed from the opposite strand of a protein-coding gene and which also overlapped with at least one sense exon have been reported in dog.

Hoeppner et al, An Improved Canine Genome and a Comprehensive Catalogue of Coding Genes and Non-Coding Transcripts. PLOS ONE, www.plosone.org 5 March 2014 | Volume 9 | Issue 3.