Interestingly, canines display close clinical and molecular similarities to humans therefore are viewed as excellent models of human melanoma. Despite advances in melanoma therapeutics, resistance to treatment remains a problem for patients. Cancer-Associated stroma (CAS) is known to play a key role in cancer initiation, progression and response to treatment, however, understanding of the role of CAS in melanoma is limited, therefore presents an opportunity for further investigation.

For specific analysis of the stroma from archival patient samples, we have successfully established a protocol to isolate CAS and normal stroma from formalin-fixed paraffin embedded (FFPE) patient specimen using laser-capture microdissection (LCM) coupled with next-generation RNA sequencing (NGS). Using this powerful technique, we aim to analyse CAS, normal stroma and corresponding melanoma tumour cells from both human and canine melanoma patients to define a molecular landscape of gene expression signatures by NGS and to identify novel candidate genes that influence the growth and metastatic potential of melanoma by a series of comparative analyses. Finally, we intend to pursue our findings with functional studies to elucidate the genes role in melanoma progression.

The possibility to study gene expression signatures in specific small sections of archival FFPE tissue, which often entail large amounts of highly relevant clinical follow-up data, unlocks a new dimension of once difficult-to-analyse samples which now become amenable for investigation.

SPECIAL TECHNIQUES AND EQUIPMENT
Laser Capture Microdissection (LCM), RNA extraction, NGS, qPCR, IHC, ISH, Bioinformatics analysis, Conda, R