

Molecular characterisation of lung neuroendocrine tumours through innovative technologies

A. Sexton-Oates, E. Mathian, C. Voegele, N. Alcalá, M. Foll, L. Fernandez-Cuesta

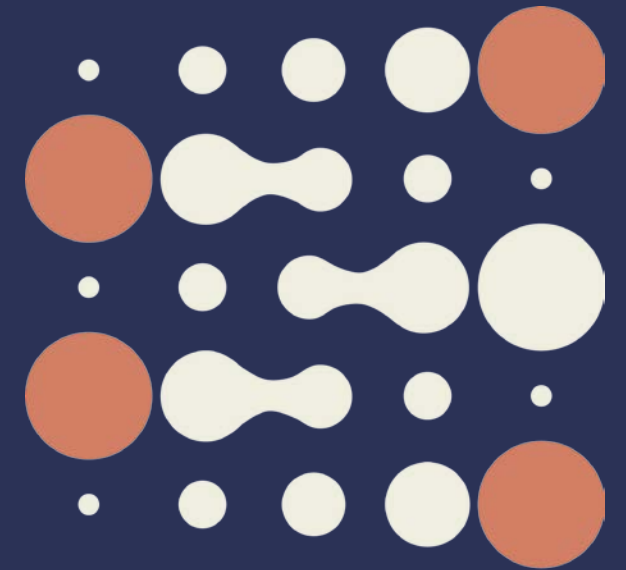
Rare Cancers Genomics Team, Genomic Epidemiology Branch

SextonoatesA@iarc.who.int

International Agency
for Research on Cancer



www.rarecancersgenomics.com



Introduction

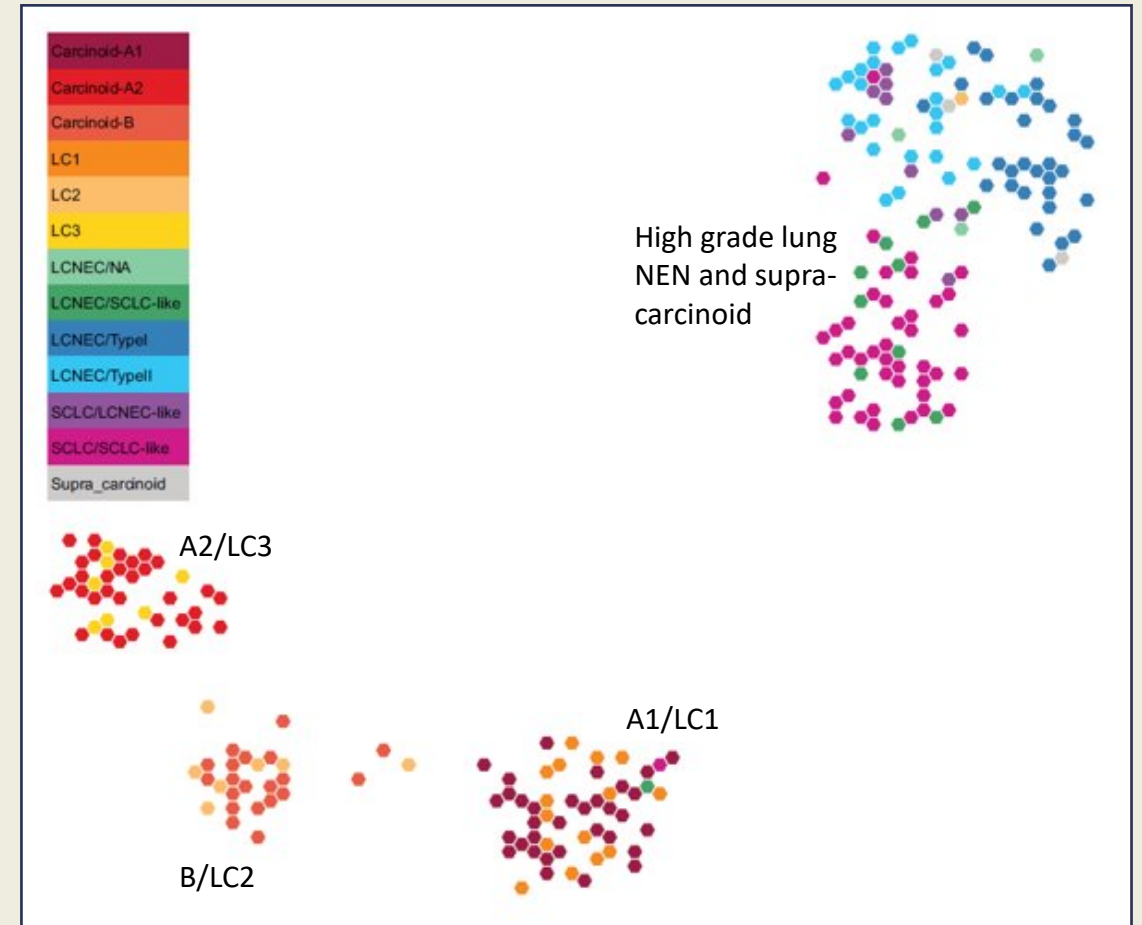
	Atypical pulmonary carcinoid	Typical pulmonary carcinoid
WHO grade	G2	G1
Epidemiology	Female 50s	Female 50s
Necrosis	Focal, if any	No
Mitosis per 2mm²	2-10	<2
10-year OS	51% (38-74)	89% (60-100)

Lung neuroendocrine Tumours (LNETs)

DATA NOTE

A molecular map of lung neuroendocrine neoplasms

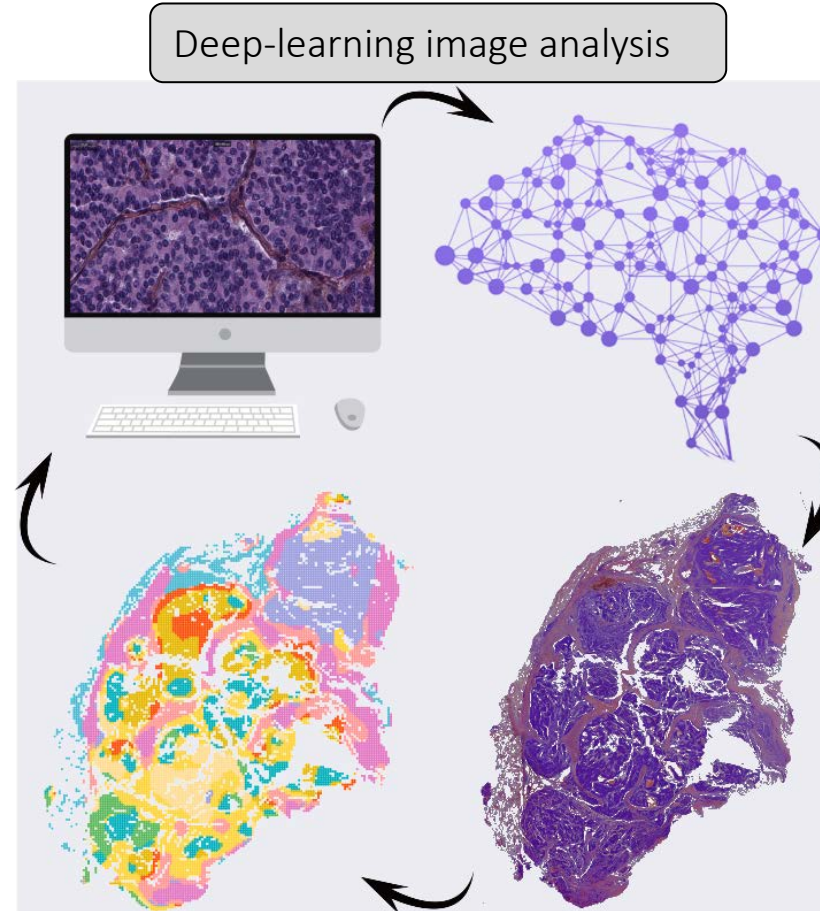
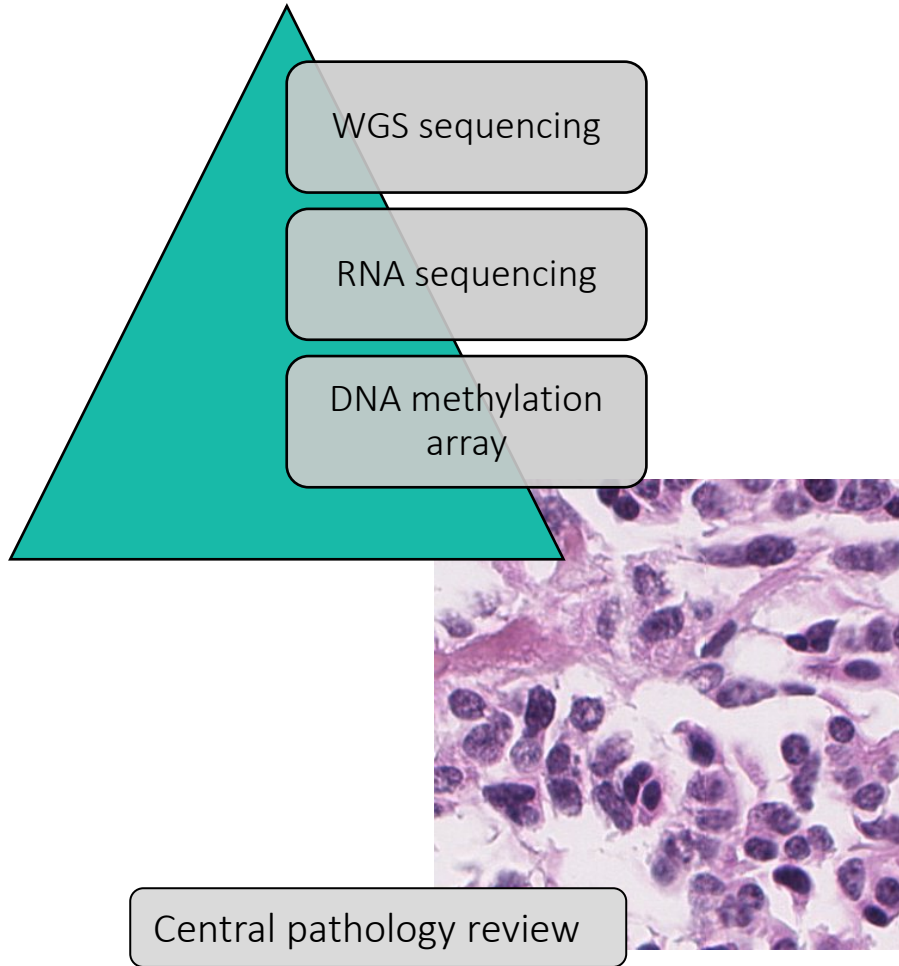
Aur lie AG Gabriel ^{1,†}, Emilie Mathian ^{1,†}, Lise Mangiante ¹, Catherine Voegel  ¹, Vincent Cahais ², Akram Ghantous ², James D. McKay ¹, Nicolas Alcala ¹, Lynnette Fernandez-Cuesta ^{1,‡} and Matthieu Foll ^{1,*‡}



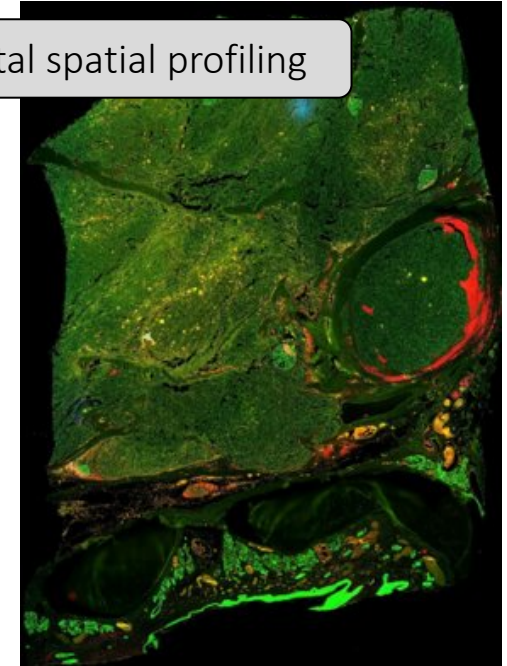


lungNENomics

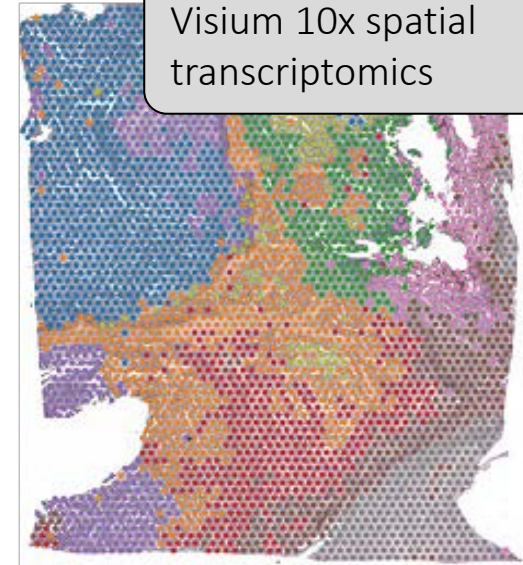
Unveiling the molecular pathways underlying the development of lung neuroendocrine neoplasms



Digital spatial profiling

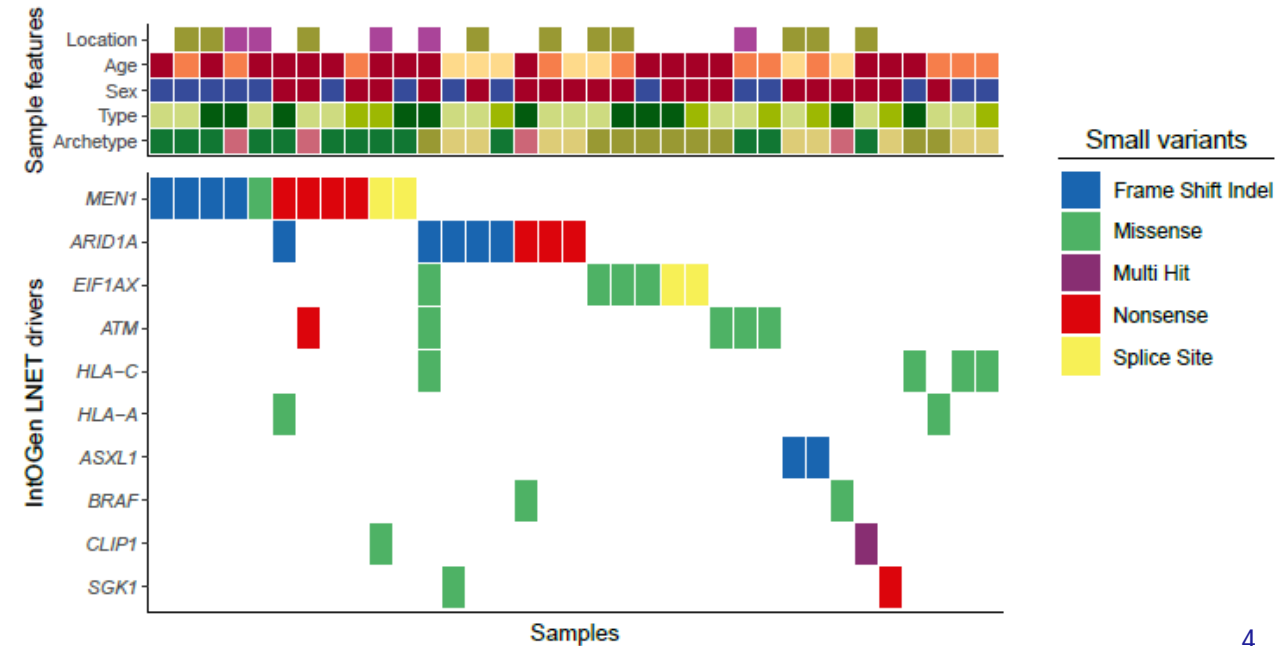
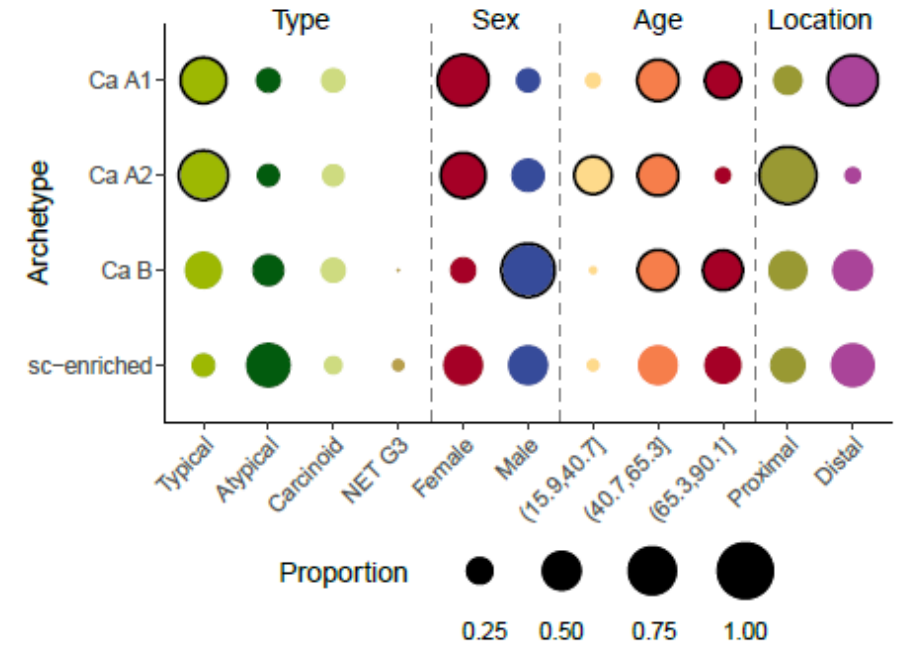
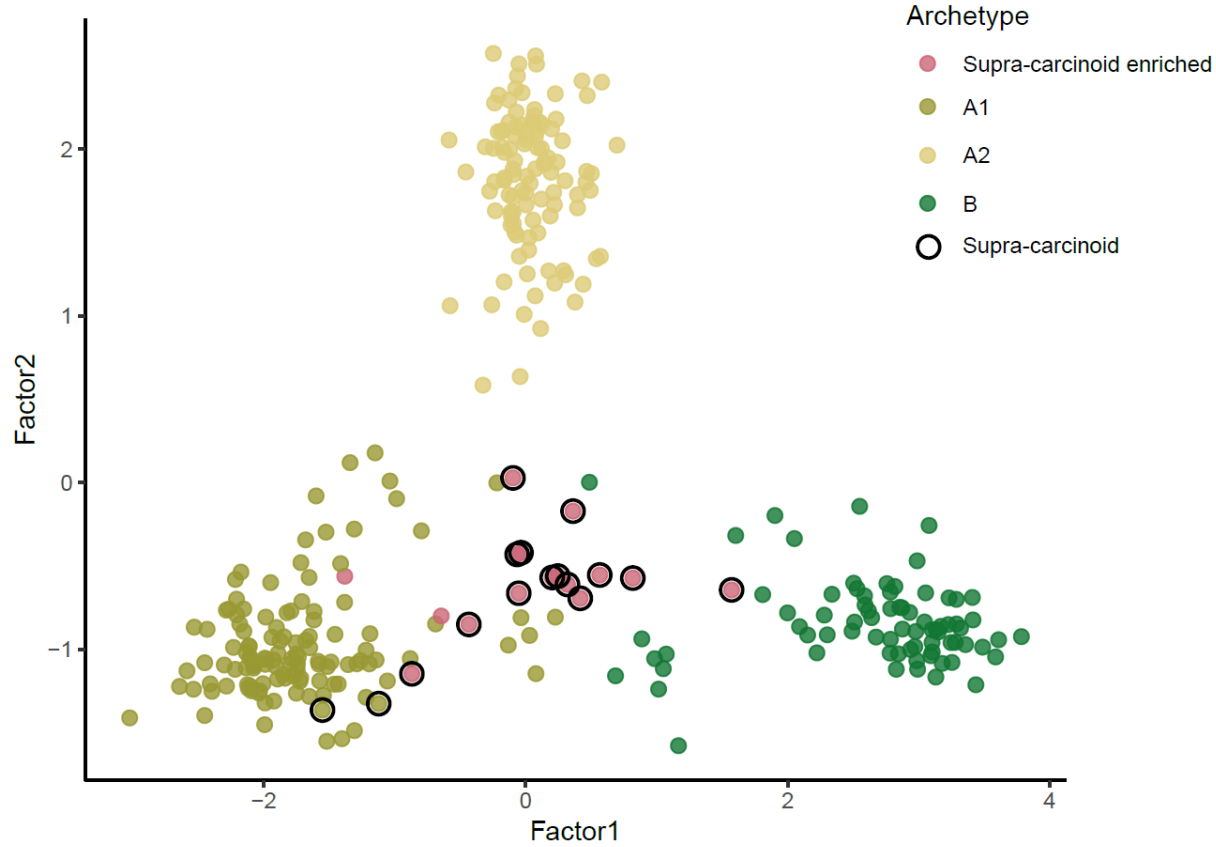


Visium 10x spatial transcriptomics



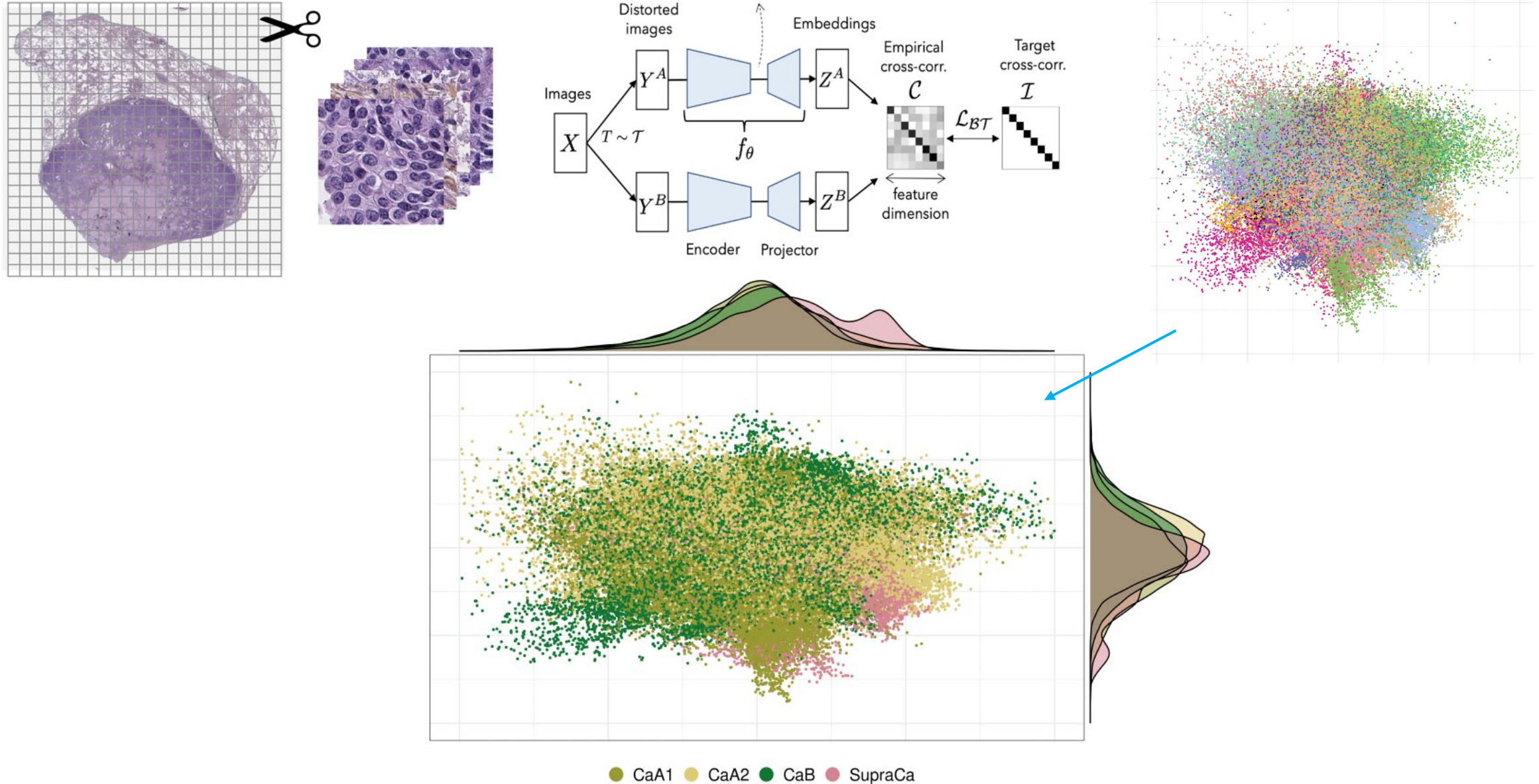
Results: Identification of molecular groups with distinct epidemiological and genomic features

Sexton-Oates A, Mathian E, *et al.* In preparation.



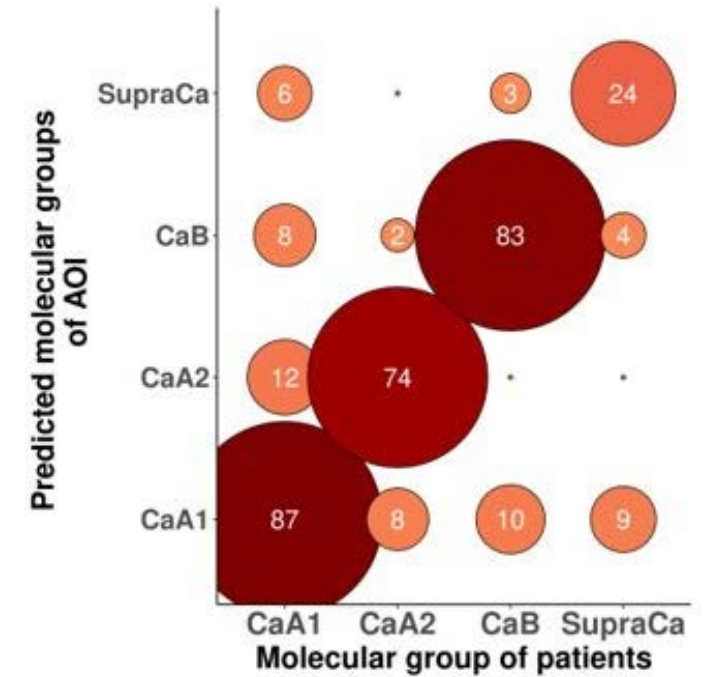
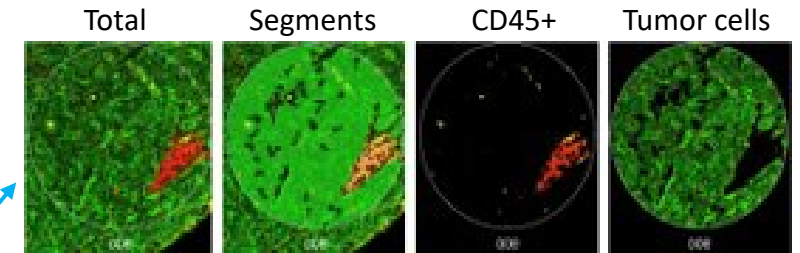
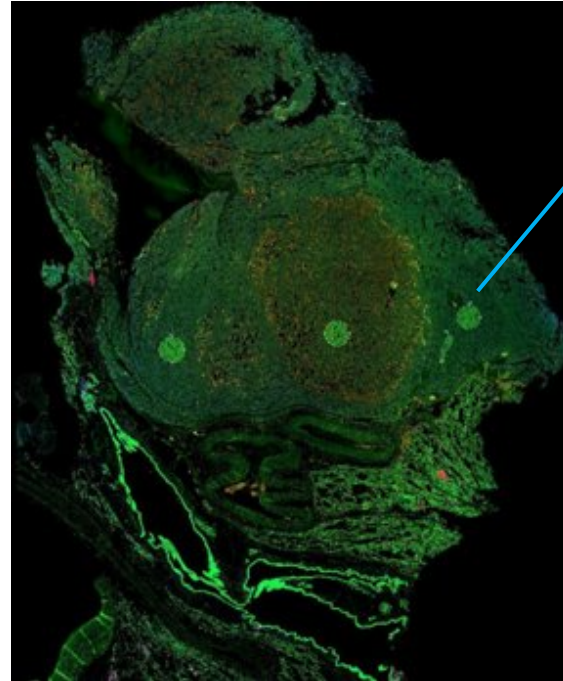
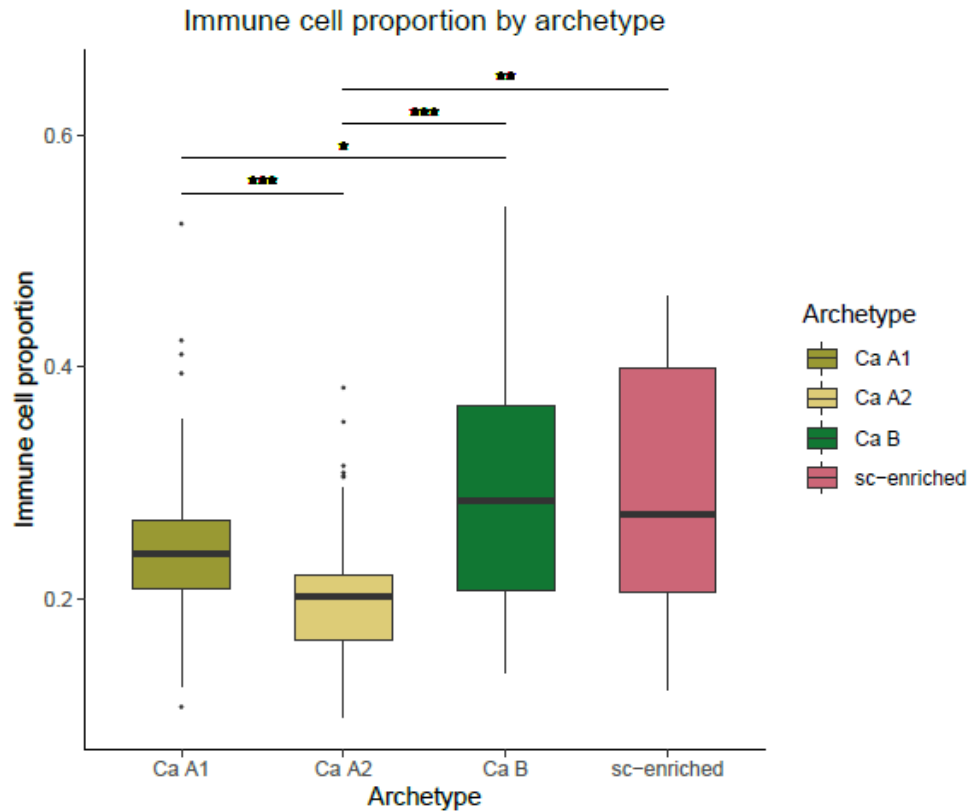
Results: Deep-learning image analysis better identifies distinct morphological communities between molecular groups than between tumour types

Mathian E, *et al.* Under Review



Results: Immune micro-environment is variable between molecular groups, and particularly heterogeneous in supra-carcinoids

Sexton-Oates A, Mathian E, *et al.* In preparation.



Discussion and Conclusions

Existence of four molecular groups of lung neuroendocrine tumours with variable:

- Epidemiology
- Genetics
- Morphology
- Immune micro-environment

New model systems can teach us more about their development

Cancer Cell Article

Druggable growth dependencies and tumor evolution analysis in patient-derived organoids of neuroendocrine neoplasms from multiple body sites

Graphical abstract **Authors**

The graphical abstract illustrates a research workflow. It starts with a 'Cohort' of 'x27' patients. From this cohort, 'Resection or biopsy' leads to 'Patient-Derived Tumor organoid' models. These organoids are used to create 'Organoid models of Neuroendocrine Neoplasms'. The organoids are then subjected to 'Longitudinal sequencing', which includes 'Genome Whole-genome sequencing' and 'Transcriptome RNA-seq'.

Authors
Talya L. Dayton, Nicolas Alcalá, Laura Moonen, ..., Matthieu Foll, Lynnette Fernández-Cuesta, Hans Clevers

Potential to impact public health through improving classification systems, intercepting tumours at an early stage, and putting patients on the right path for personalised cancer management

Key take-home messages

Integration of multi-omic and spatial data analysed with cancer evolution approaches, coupled with whole-image deep learning analyses, provides a comprehensive molecular and morphological understanding of lung neuroendocrine tumours.