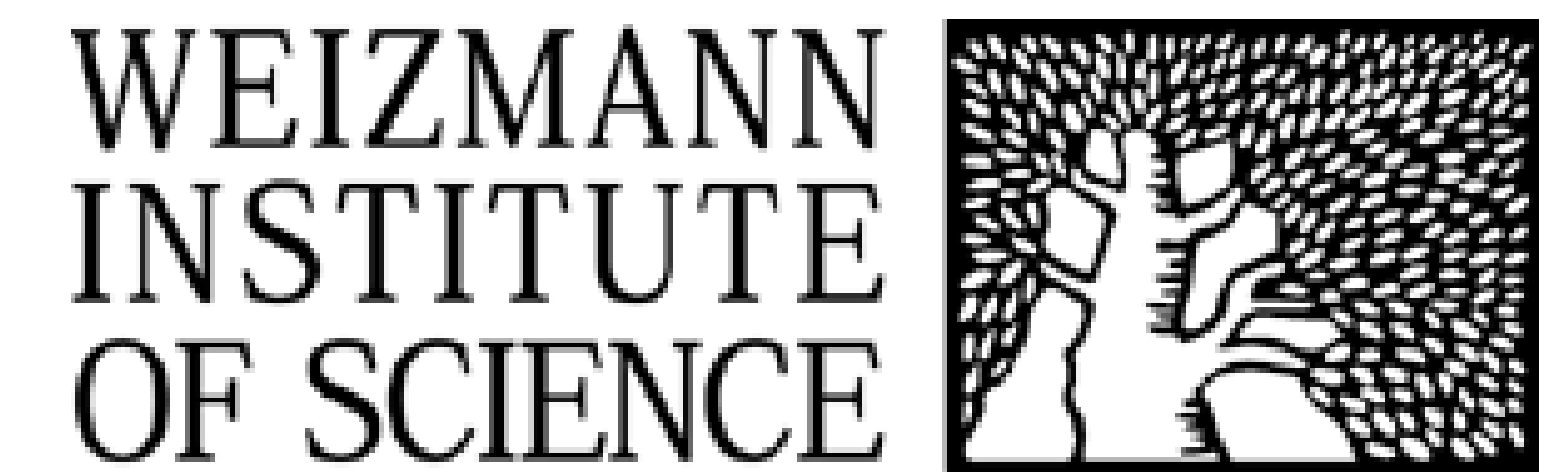


Dissecting neuroendocrine mixed tumors by single cell RNA-seq

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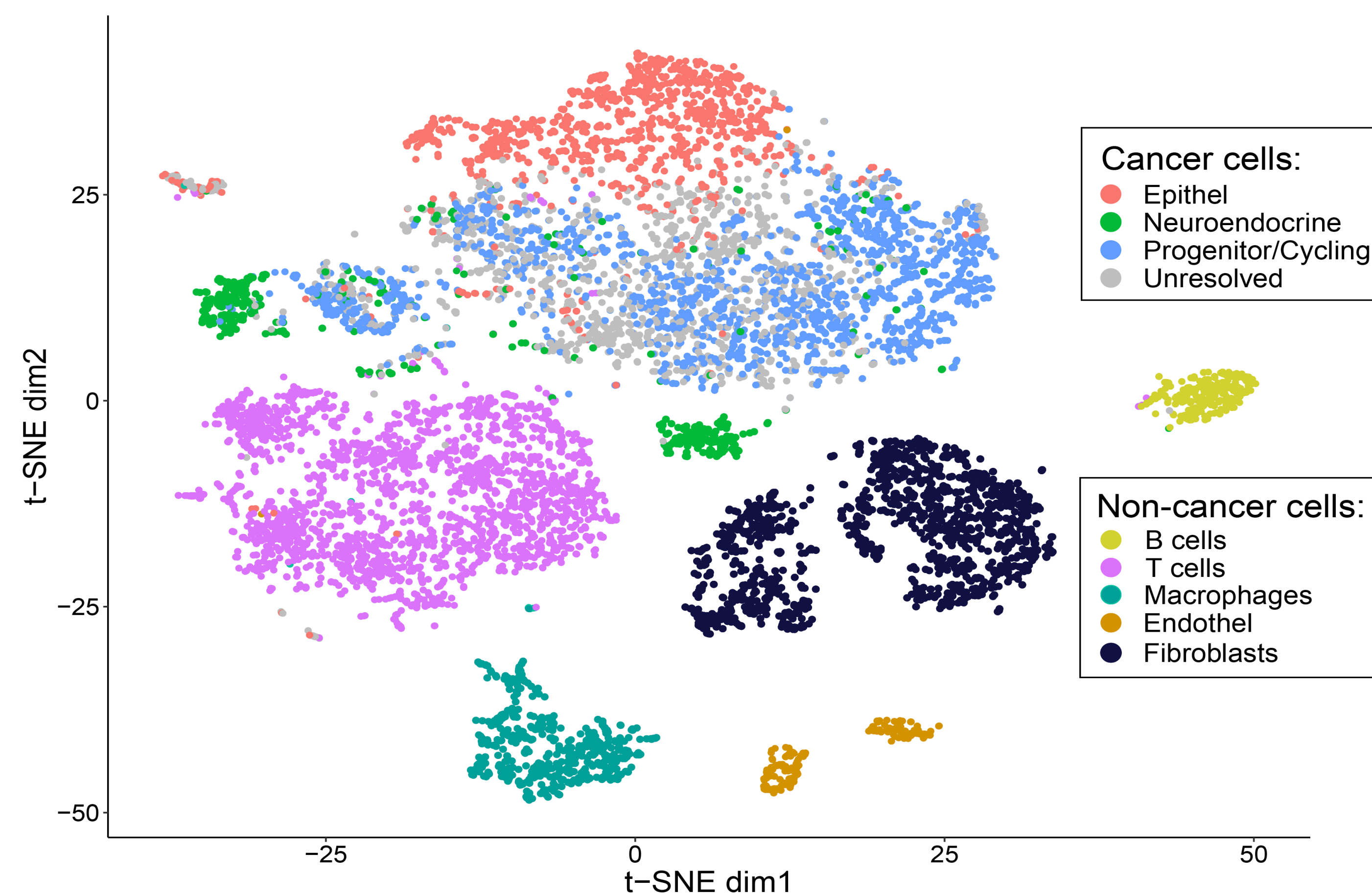
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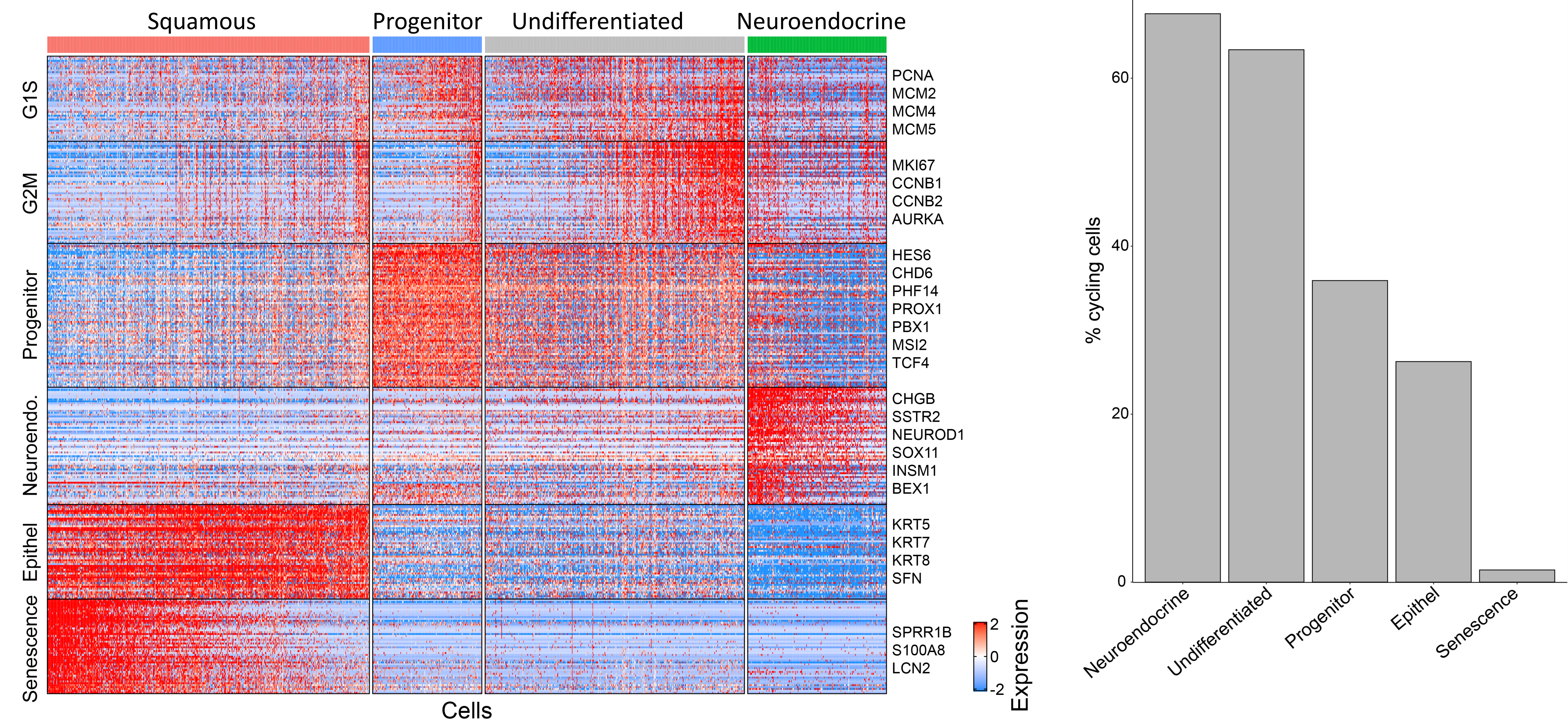
(1) Abstract

We use single cell RNA-seq to comprehensively characterize the cellular diversity of “mixed” tumors that contain both a neuroendocrine and a non-neuroendocrine component. Here, we analyze a large cell neuroendocrine carcinoma (LCNEC) combined with squamous cell carcinoma. We identify the two expected cancer components - neuroendocrine and squamous – but also populations of undifferentiated/progenitor cells that may give rise to both of the differentiated components.

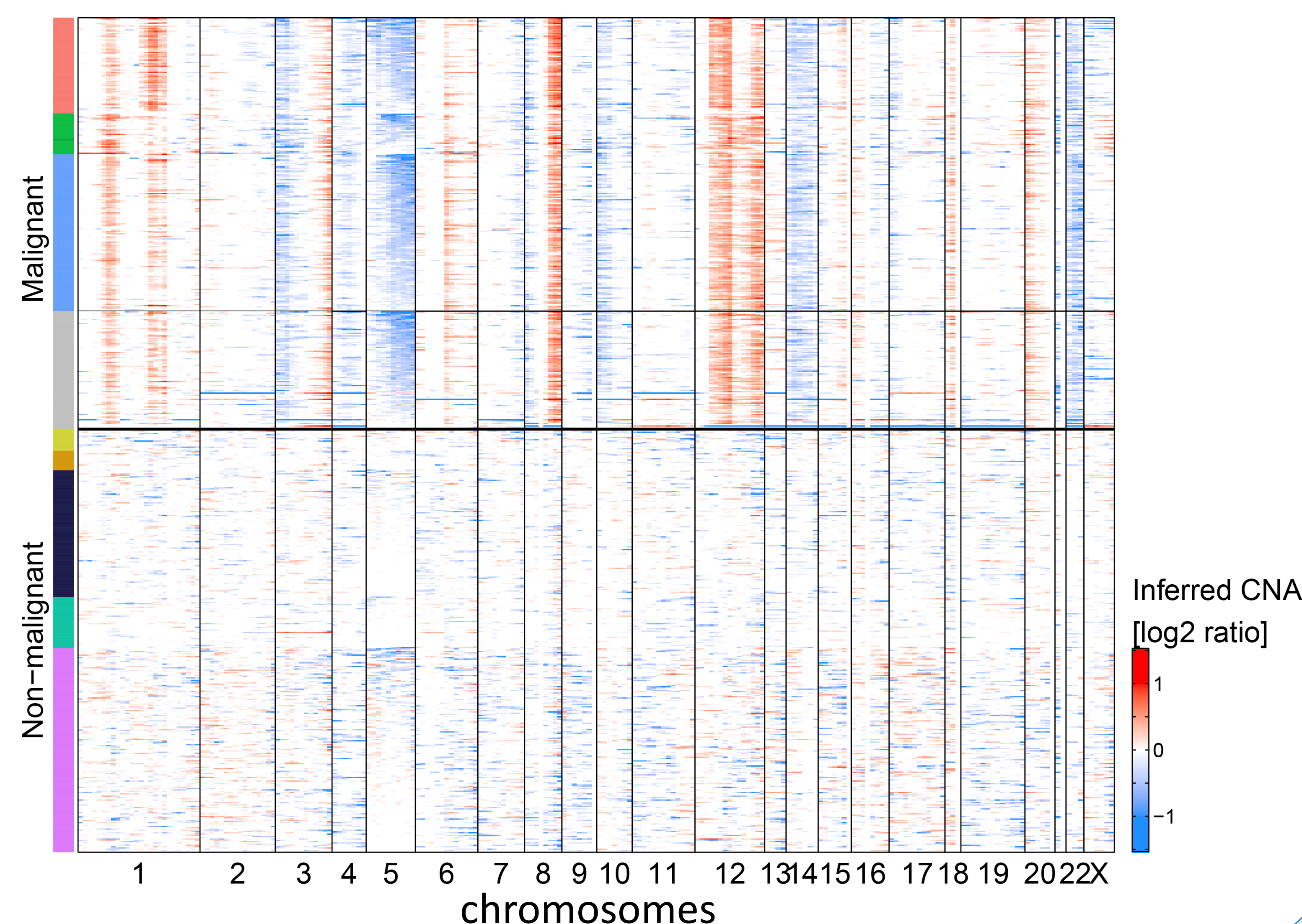
(2) Global classifications of cell types



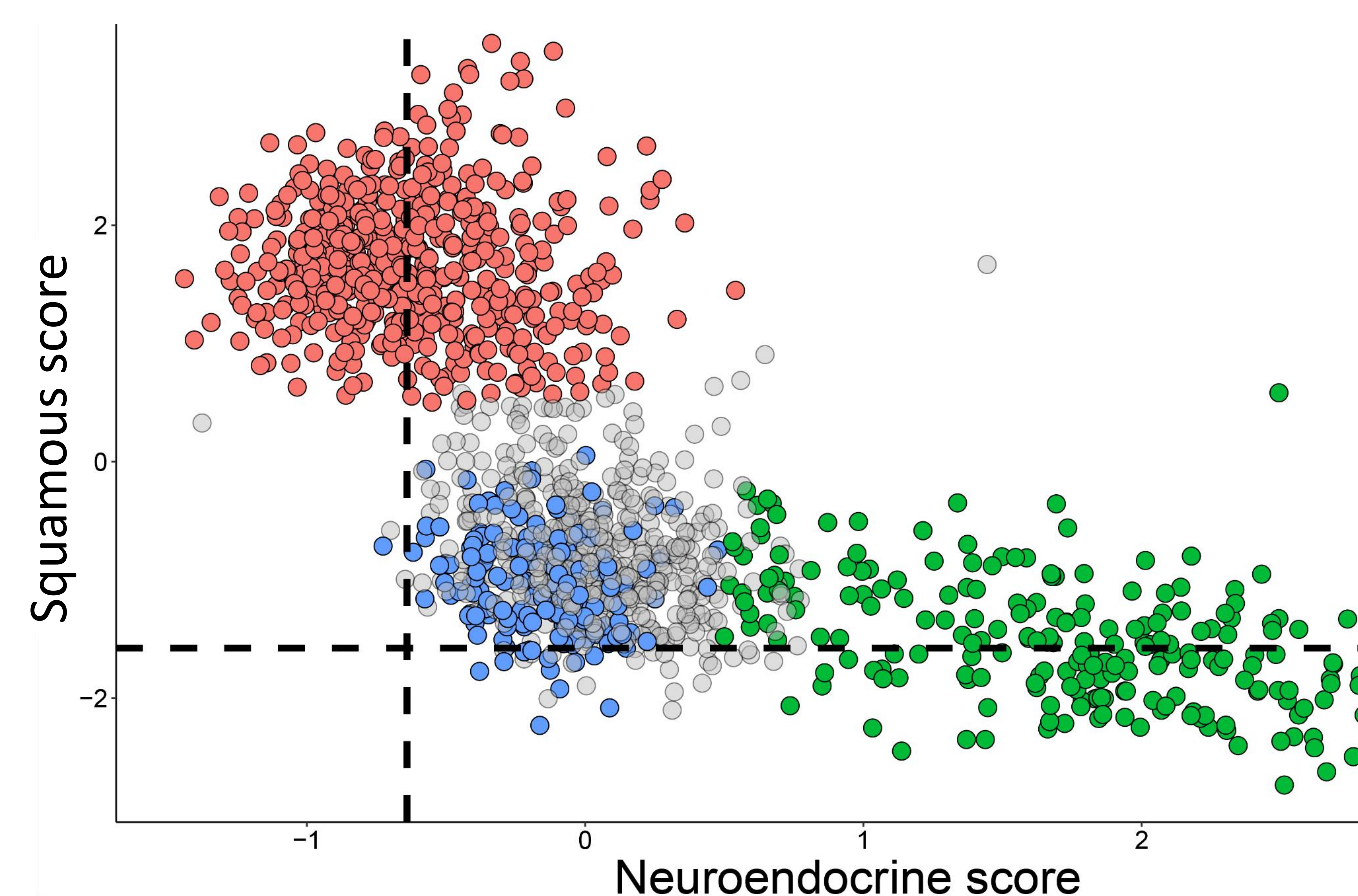
(4) Distinct populations of cancer cells by differentiation and cell cycle programs



(3) Inference of copy-number aberrations (CNAs)



(5) Progenitors retain partial expression of differentiation programs



(6) Conclusions

- Single cell RNA-seq may be used to improve our understanding of tumors with poorly understood biology, such as “mixed” tumors.
- A single tumor with combined LCNEC and squamous histology was examined. This tumor harbors a third population of progenitor-like cells that we do not yet understand but appears to reflect an intermediate between the two differentiated states.
- Further work is needed to examine the function of the progenitors, their presence in additional tumors and the clinical implications

References

Suvà ML, Tirosh I (2019). “Single-Cell RNA Sequencing in Cancer: Lessons Learned and Emerging Challenges”. *Mol Cell*. 2019 Jul 11;75(1):7-12.