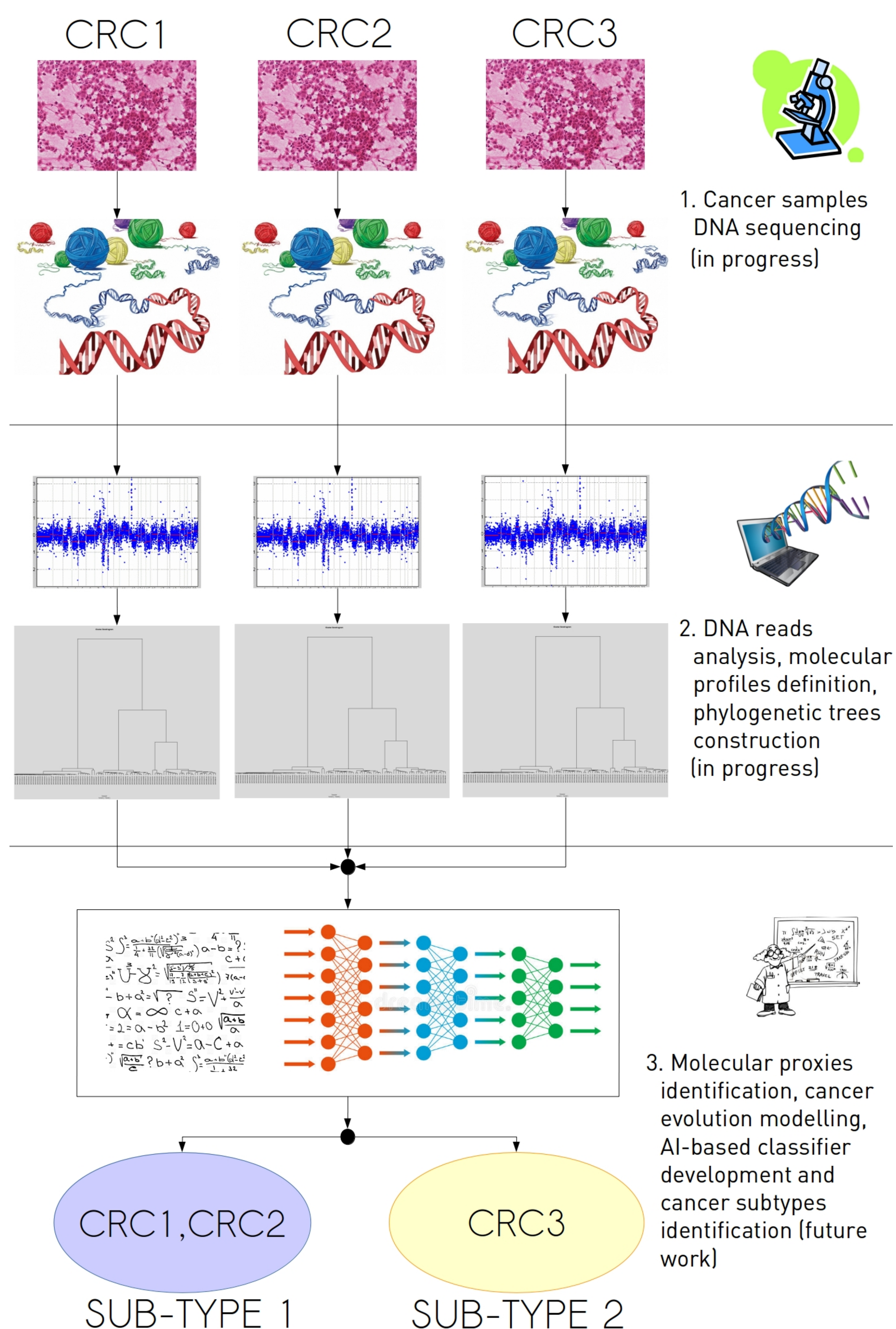


Motivation and background

Cancer is an evolving entity and the evolutionary properties of each tumor are likely to play a critical role in shaping its natural behaviour and how it responds to therapy.

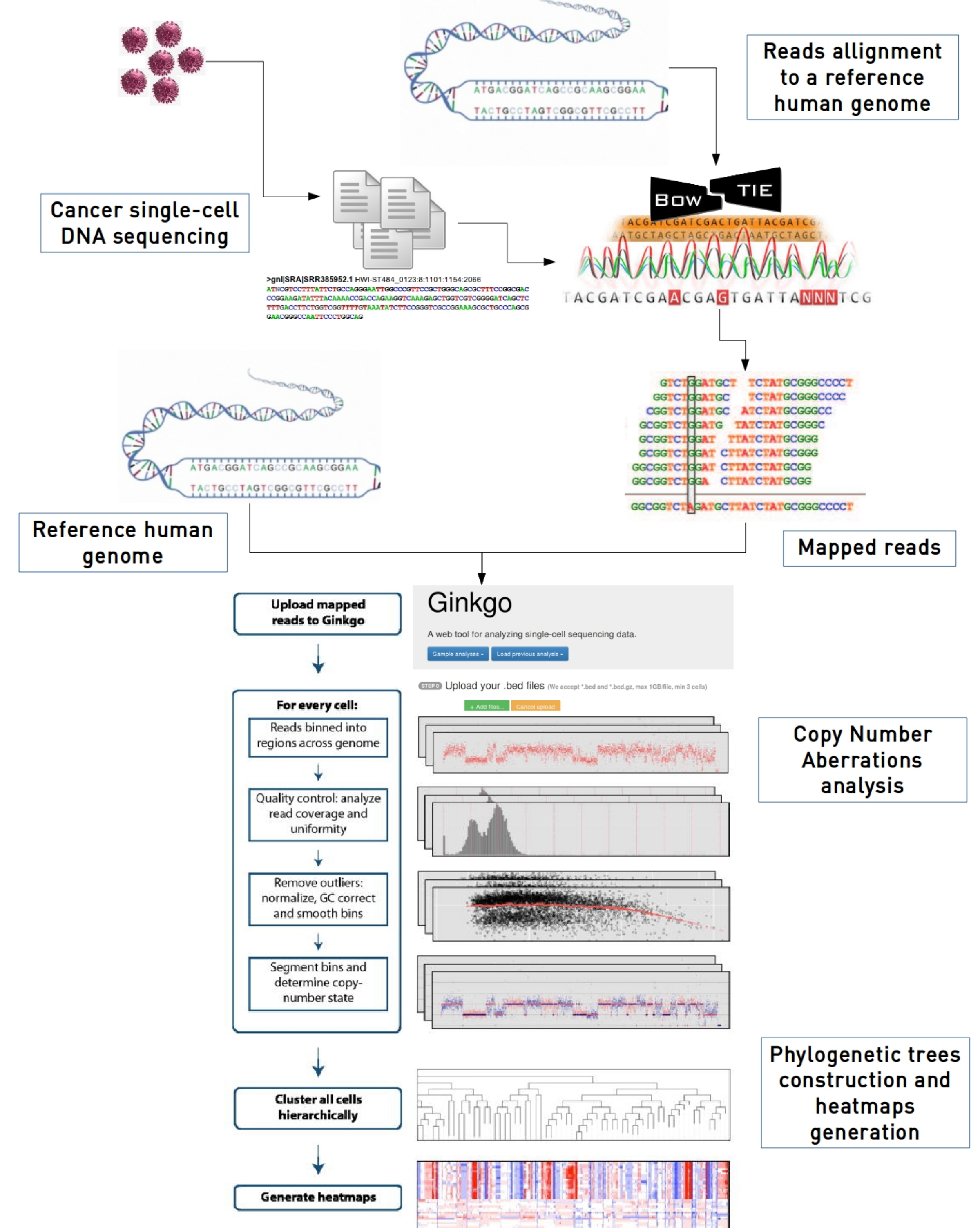
The main goal of the present work is to combine mathematical modelling and AI-based approaches to develop a new generation of **cancer classifiers** based on **tumor evolutionary properties** and **proxy data**.

Addressed problem



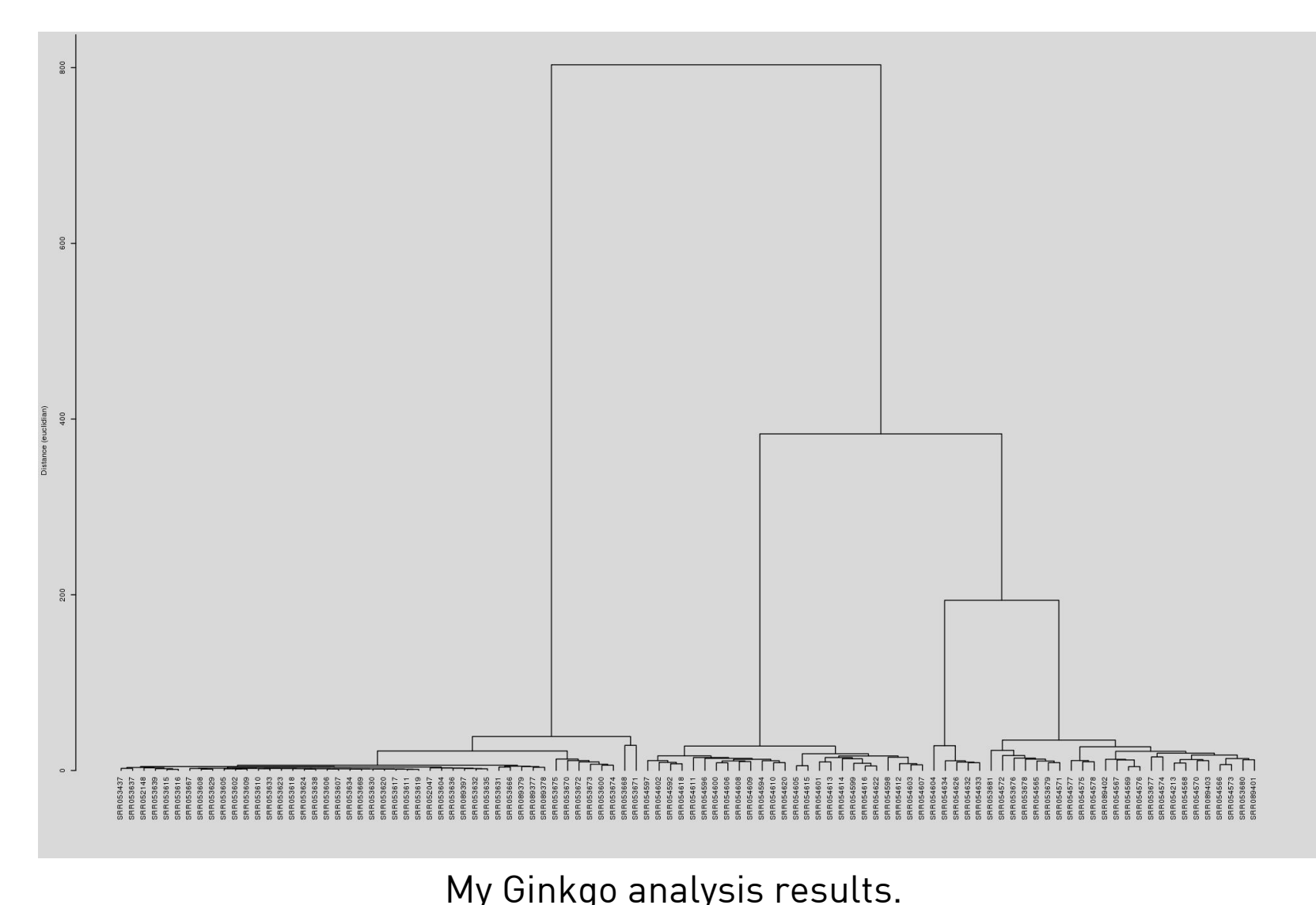
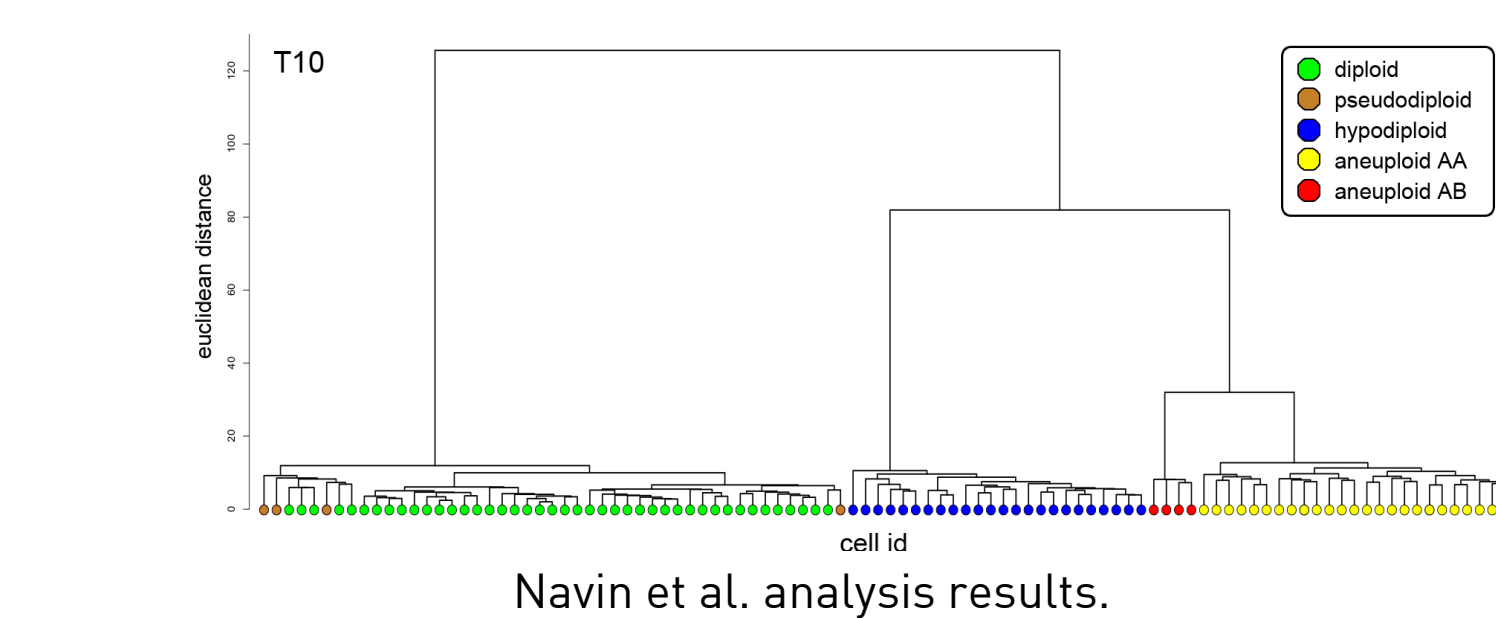
Materials and methods

Pipeline to build cancer sample phylogenetic trees from **single-cell DNA sequencing** data and **CNA's** profiles.



Preliminary analysis results

I tested Ginkgo over a public dataset related to a breast tumor study conducted by Navin et al.³



References

- Garvin T et al. *Interactive analysis and assessment of single-cell copy-number variations.*
- Bowtie2. <http://bowtie-bio.sourceforge.net/bowtie2/index.shtml>
- Navin N et al. *Tumor Evolution Inferred by Single Cell Sequencing.* Nature.