



VANDERBILT

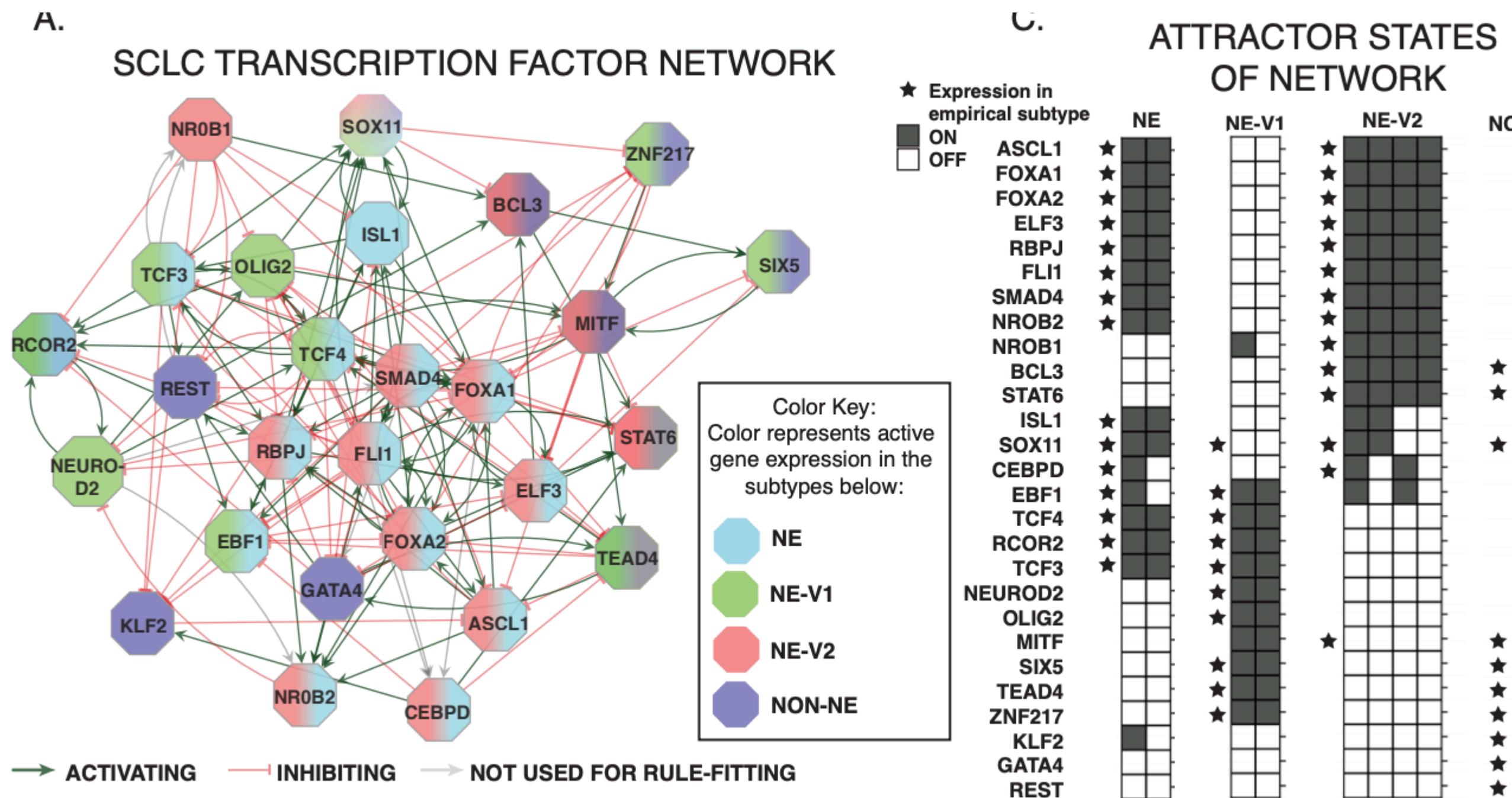
Vanderbilt's U54 Center

Project 1: Modeling the SCLC Phenotypic Space

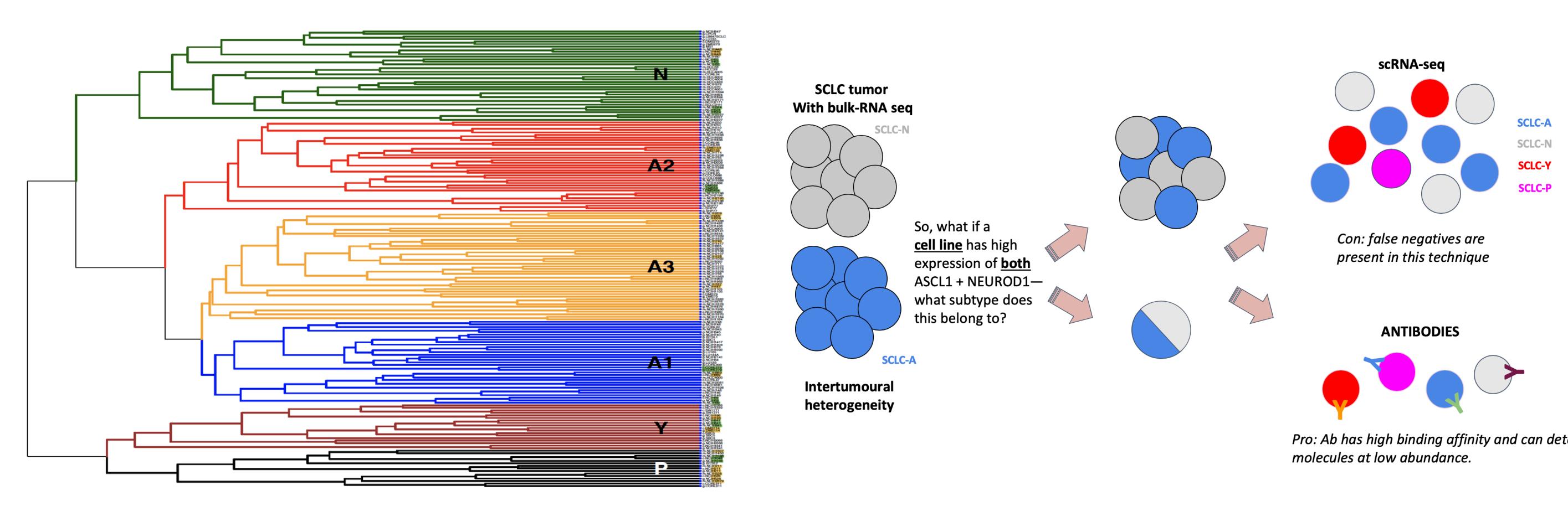
Aim 1:

Identify core SCLC tumor phenotypes

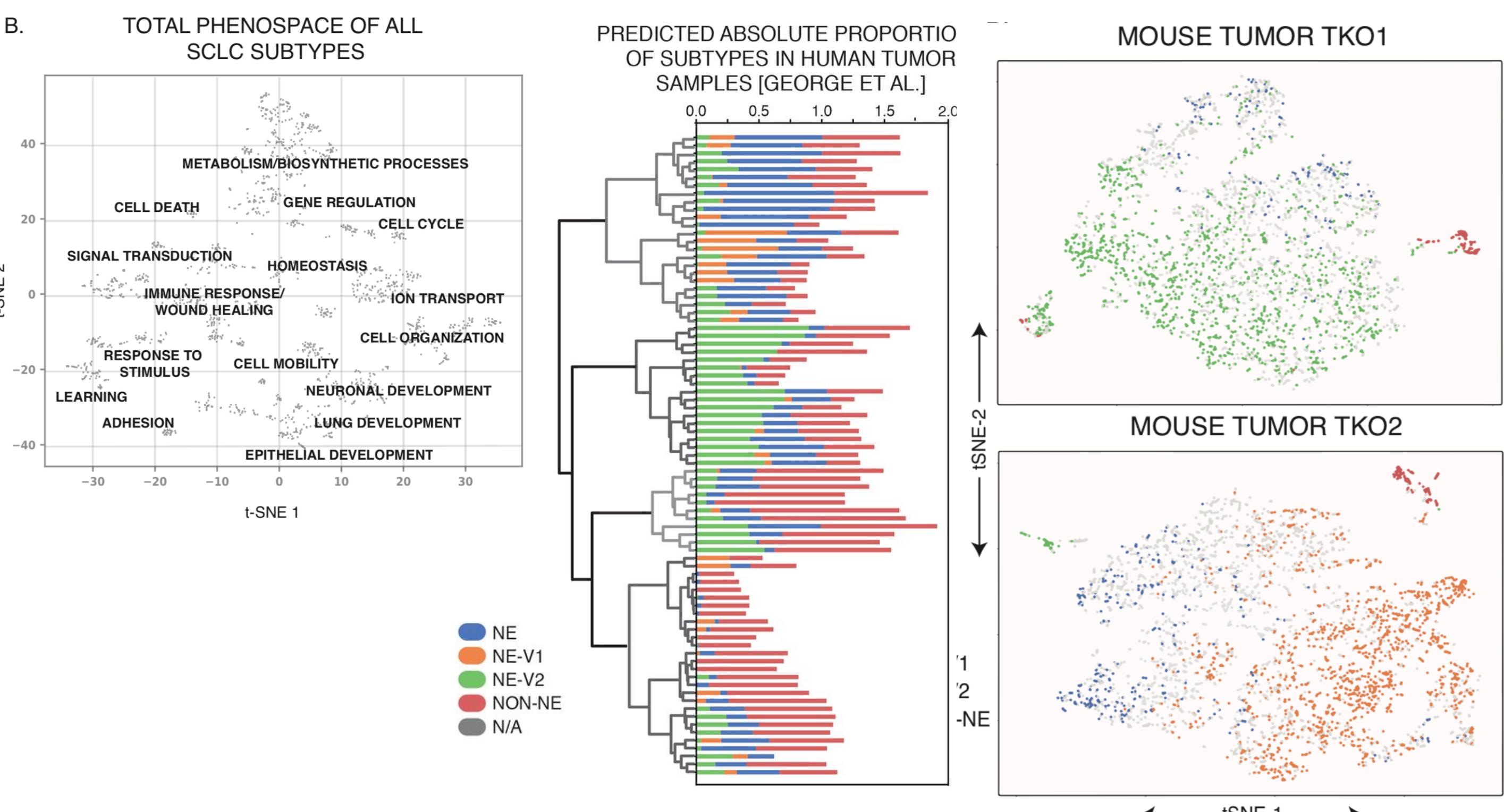
We identified 4 transcriptional subtypes of SCLC that depend on a network of transcription factors.



More recent evidence suggests additional phenotypes may exist at the cell line level, and we are developing biomarkers to distinguish these phenotypes.

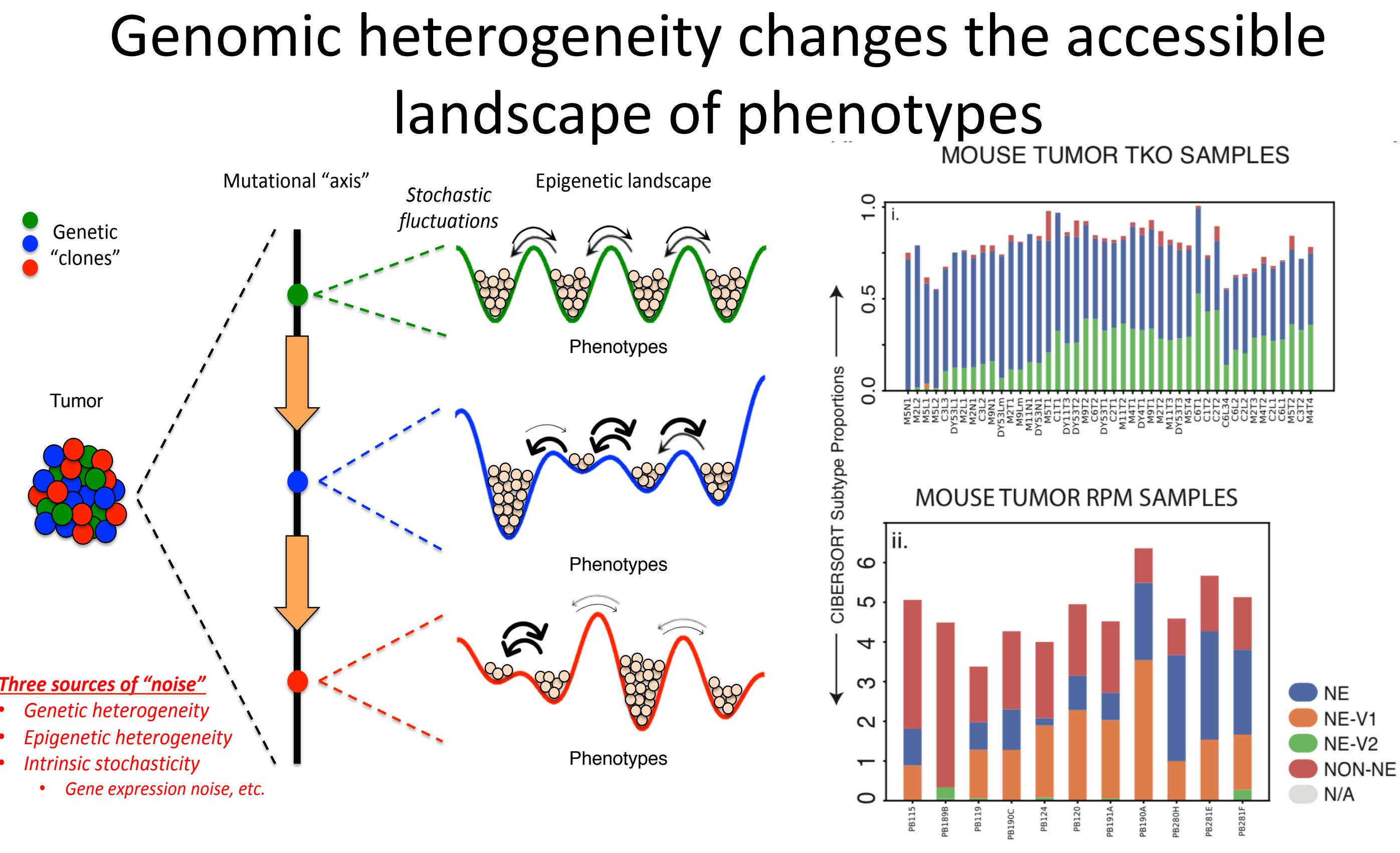


Gene ontology analysis describes the character of each subtype, and allows us to compare human and mouse phenotypes.



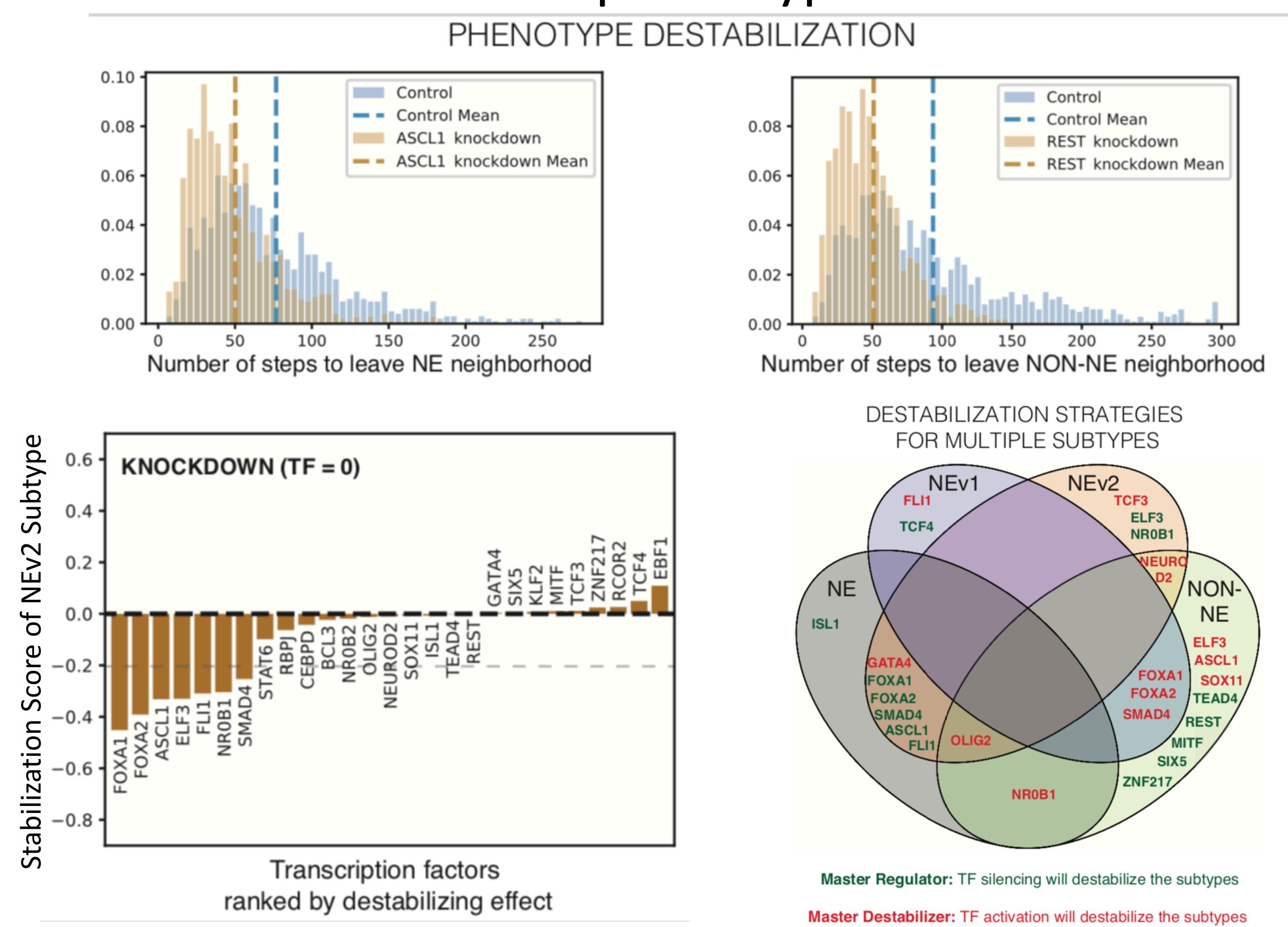
Aim 2:

Phenotype bias from genomic alterations



Our central hypothesis that there are *core single-cell SCLC phenotypes present in most or all SCLC tumors, which are biologically important, and control the overall tumor response to therapy.*

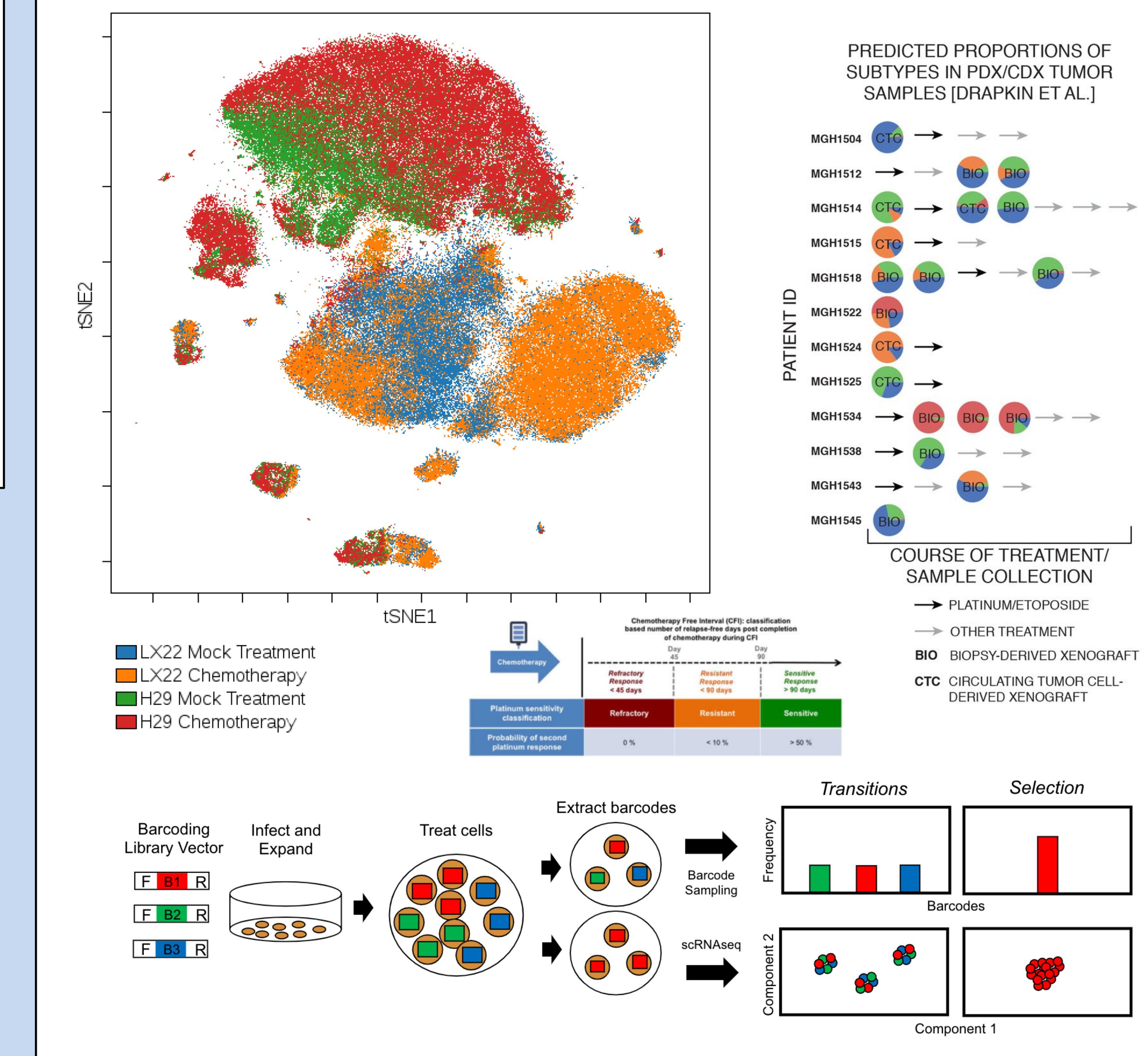
Using an *in silico* knockdown/deletion experiment, we found that knockdown of key transcription factors can shift phenotype



Aim 3:

Phenotype plasticity in response to treatment

Mass cytometry and barcoded single cell sequencing experiments can track tumor population dynamics before and after treatment



Cell free DNA collection follows tumor progression over course of treatment and may be useful for tracking phenotypic changes in human patients

