

# Gaining Insights into Tumor Cell Plasticity of Colorectal Cancer using Multi-omics Profiling

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## MOTIVATION

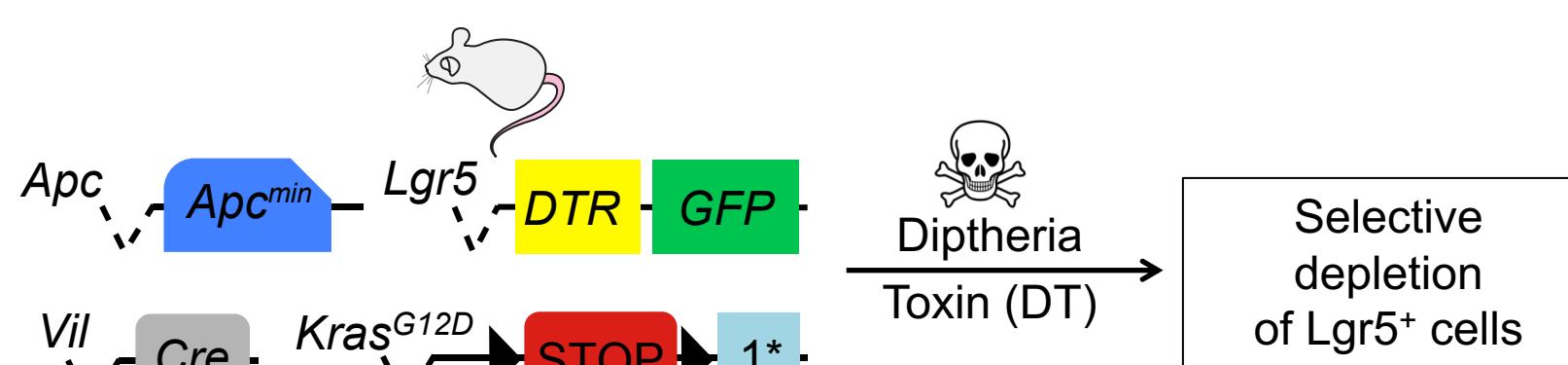
- Colorectal cancer (CRC) is a clinically diverse disease and a leading cause of cancer-related deaths
- Cancer stem cells (CSCs) play a key role in tumor maintenance and are thought to resist to therapy and cause relapse, therefore targeting CSCs may improve survival
- CSCs ablation through administration of diphtheria toxin (DT) has different impact on tumor growth: continuous growth in colon tumors versus tumor regression in liver metastases
- Discontinuation of DT treatment leads to re-initiation of tumor growth

## Questions:

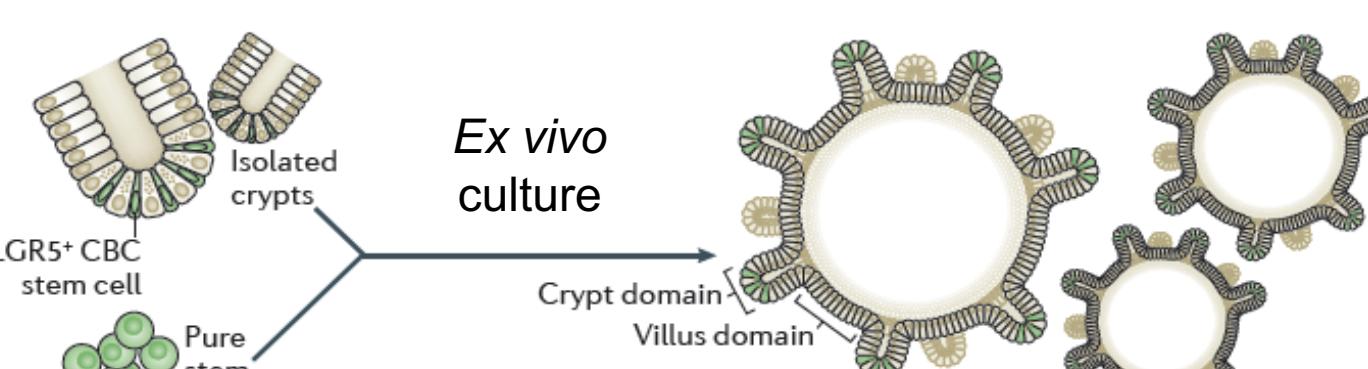
- What are the molecular mechanisms responding to CSC depletion?
- Are molecular features conserved between primary and metastatic tumors?

## RECAPITULATING HUMAN CRC IN MOUSE

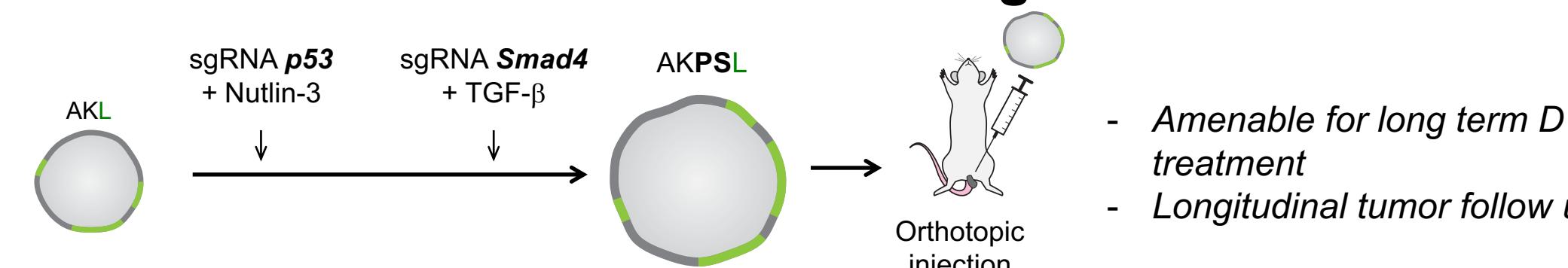
### 1. Model of intestinal tumorigenesis



### 2. Epithelial organoid culture

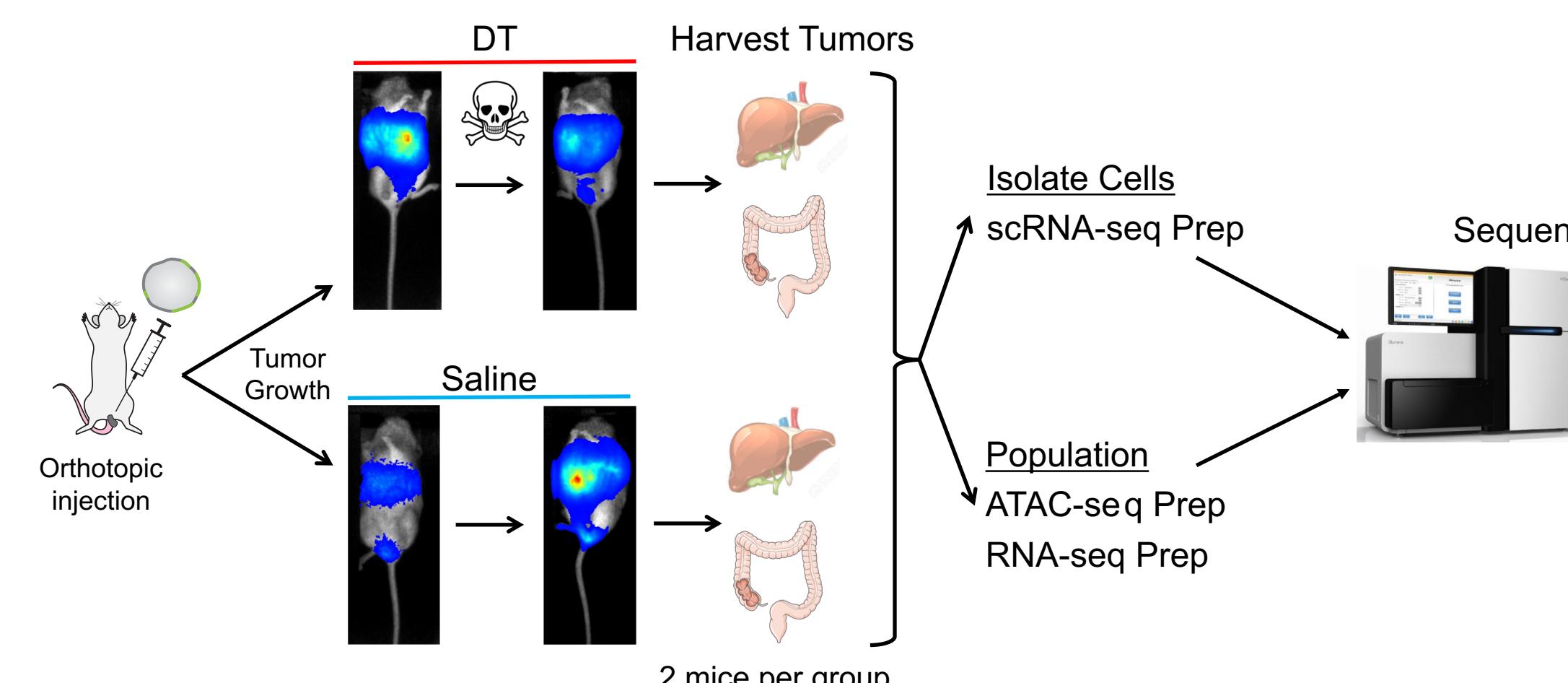


### 3. Generation of mutant cell lines using CRISPR/Cas9



## DATASET GENERATION

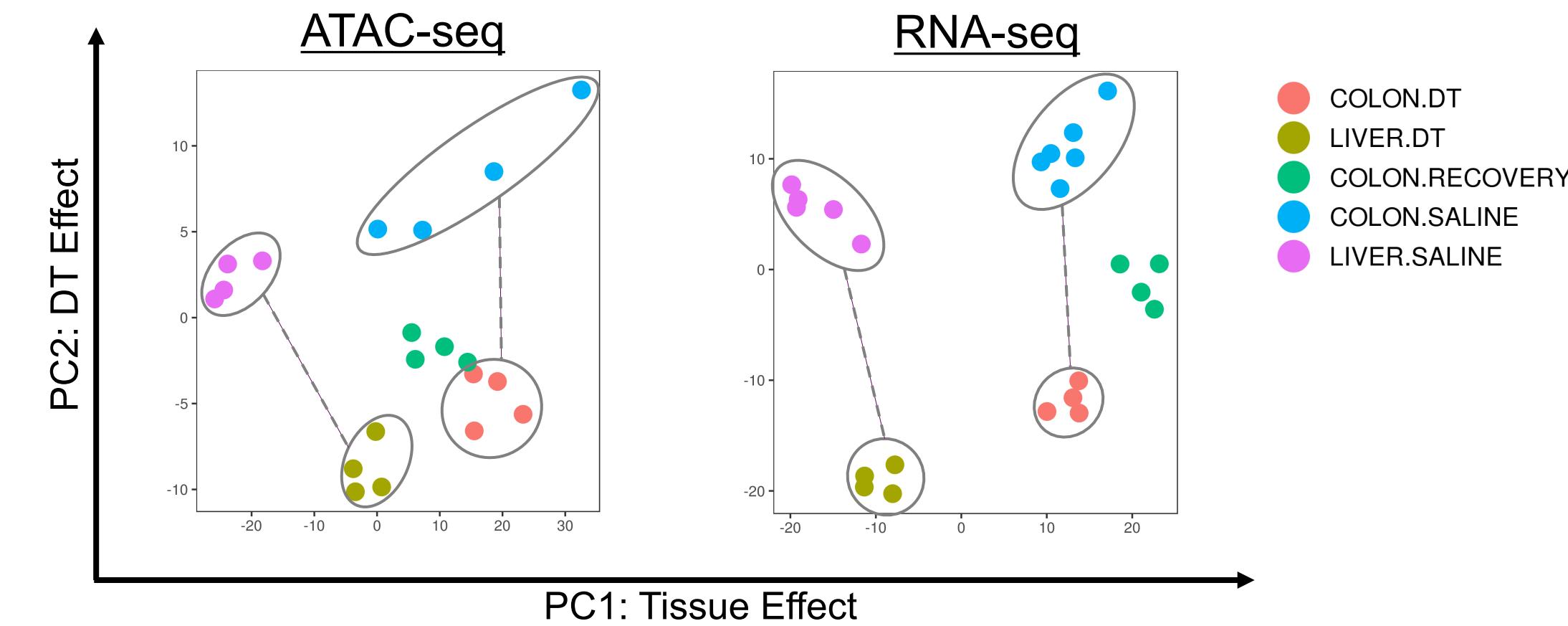
### 1. Utilizing a multi-omics approach to study CRC



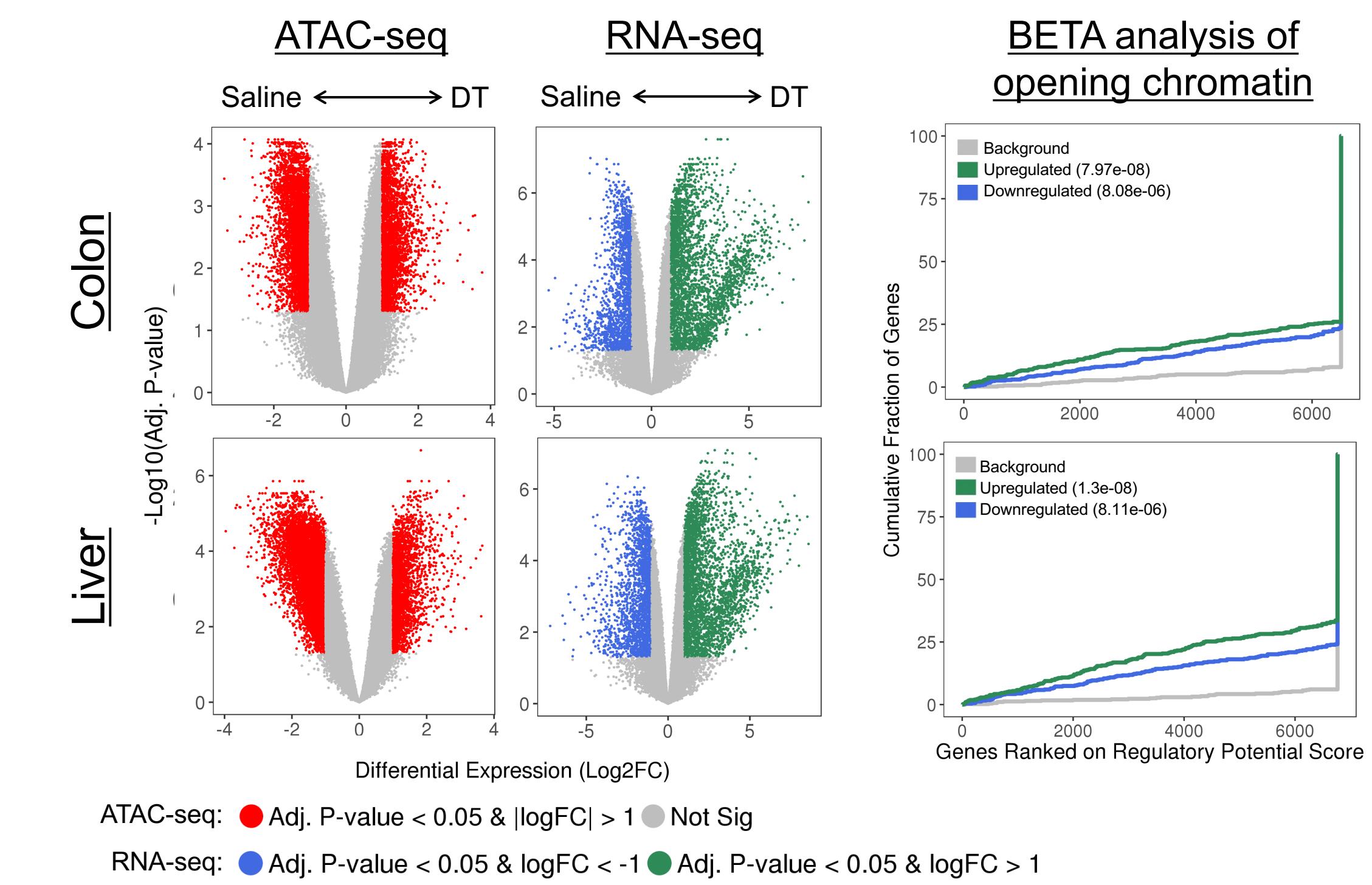
- To generate a rich representation of the landscape of metastatic CRC, we pair population-level transcriptional data (RNA-seq) with data that assays the chromatin landscape of the same tumors (ATAC-seq).
- Single cell RNA-seq will help tease out whether differences in the cellular composition of tumors at each site could explain the distinct tumor behavior.

## RESULTS

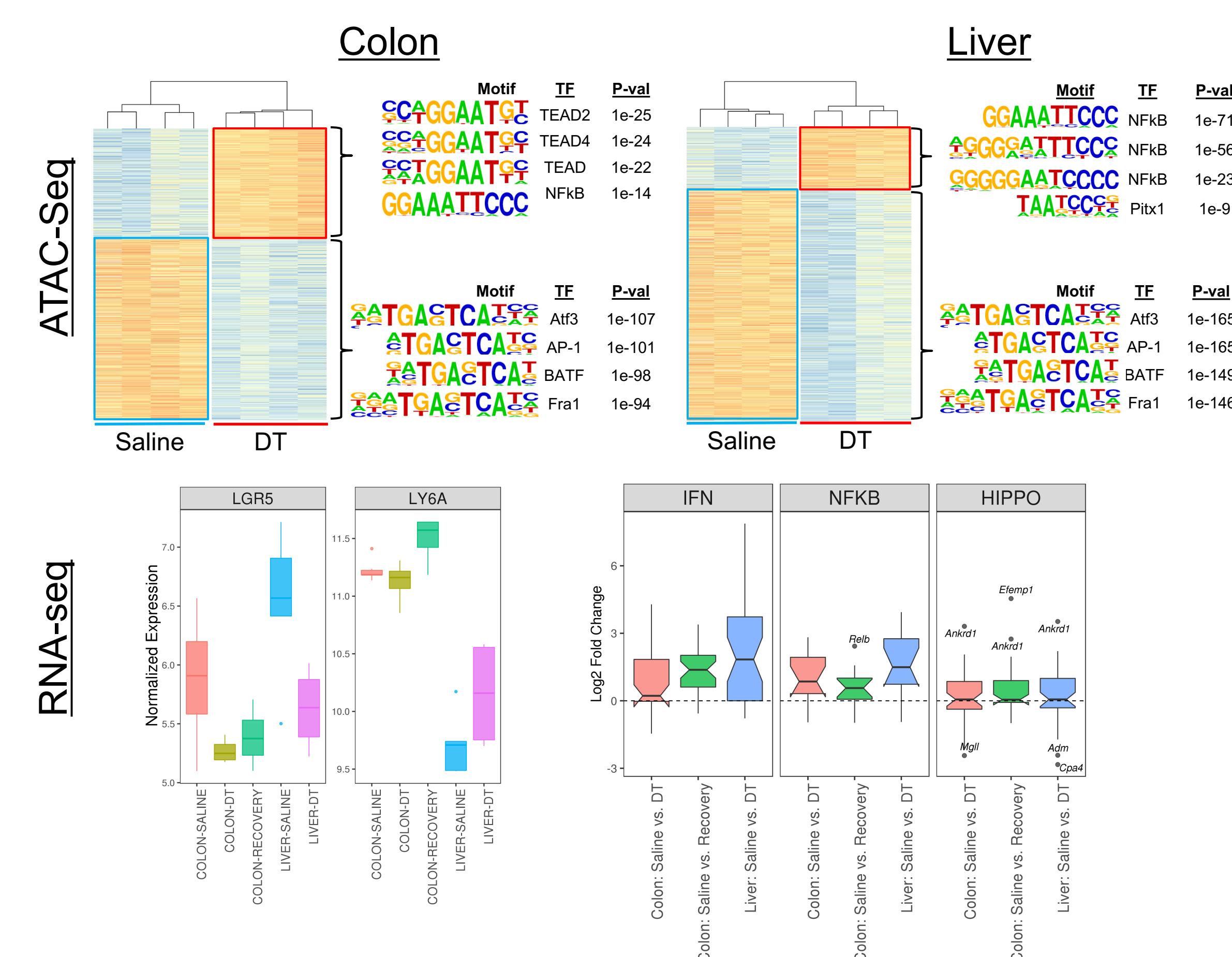
### 1. Strong changes in the transcriptional and chromatin landscapes are observed upon cancer stem cell depletion



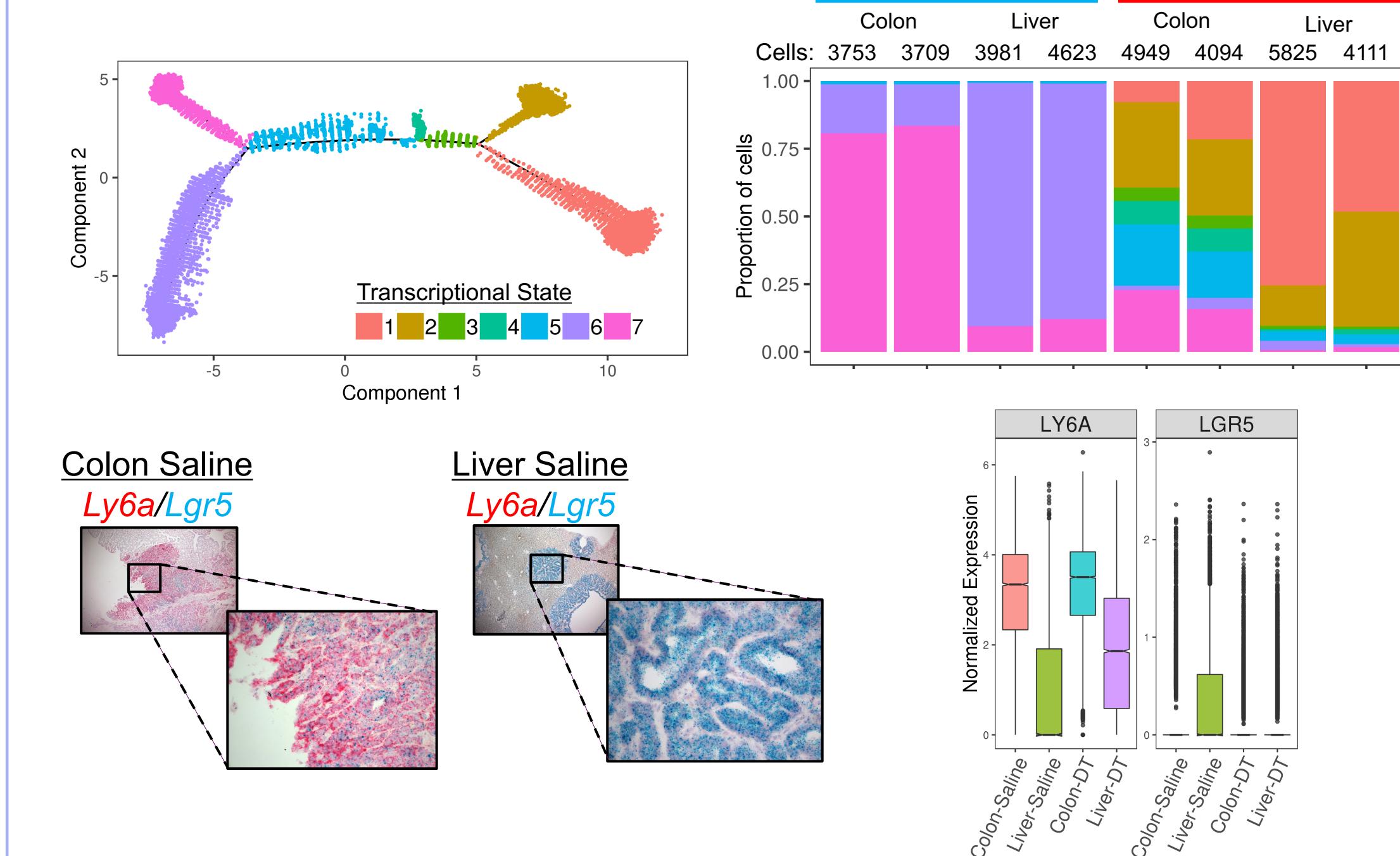
### 2. Changes of chromatin accessibility upon cancer stem cell depletion correlate with changes in gene expression



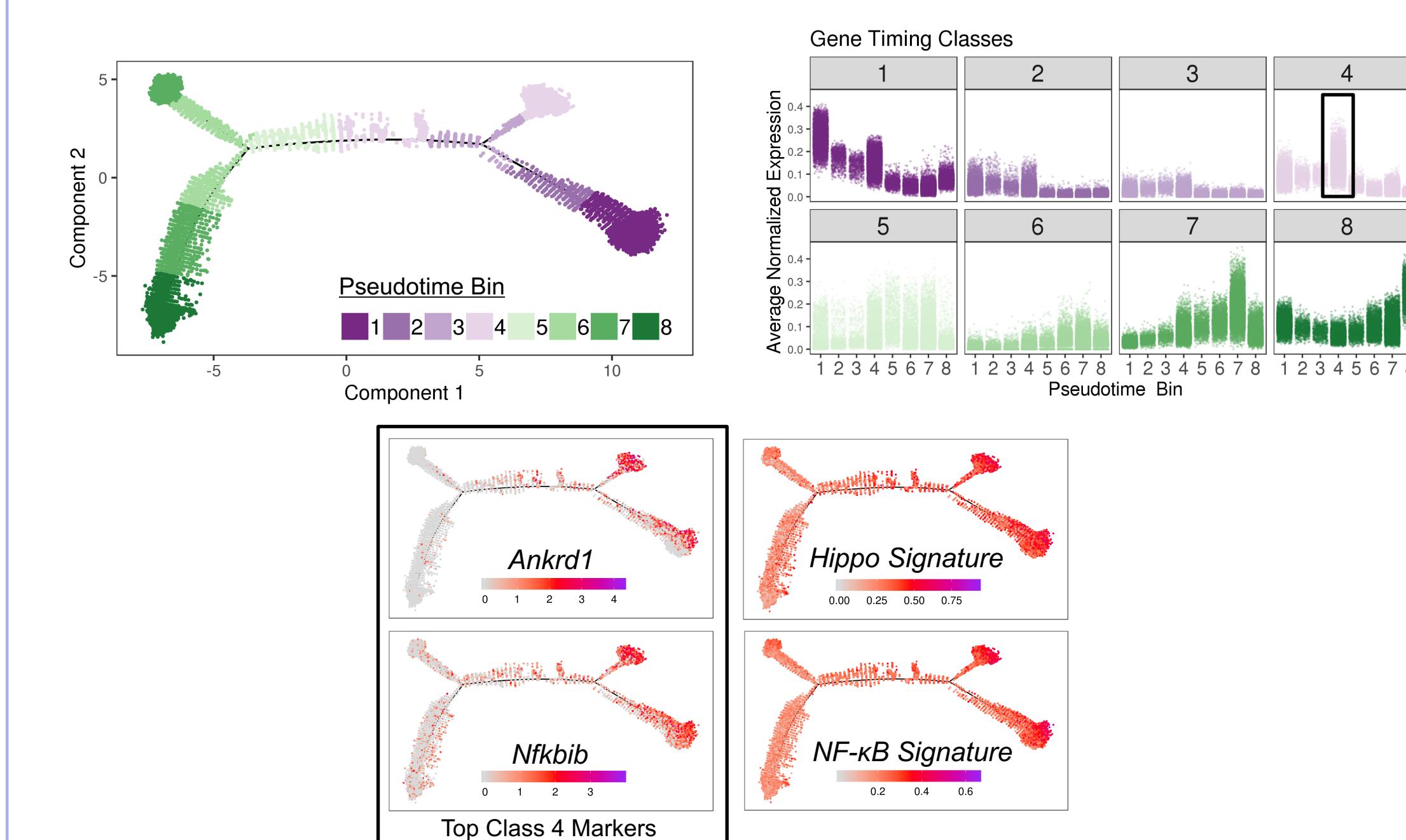
### 3. DT treatment induces NF-κB, Hippo and inflammatory response pathways



### 4. Colon tumors and liver metastases differ not only upon stem cell depletion but also at baseline and exhibit different responses to CSC depletion



### 5. Unbiased identification of gene timing classes suggests a role for Hippo and NF-κB pathways in CSC plasticity



## Conclusions

- Our results suggest that Interferon response, NF-κB and Hippo signaling pathways are induced upon DT treatment
- We identify shifts in cell composition of tumors at the primary and metastatic sites
- Our work offers insights into the mechanisms underlying tumor cell plasticity which represent a challenge for cancer treatment and opportunity for drug discovery

## Future Directions

- Better understand how primary tumors respond to stem cell depletion compared to the metastatic setting
- Address if the system returns to a steady state after DT treatment arrest

## Acknowledgements

- de Sauvage Lab
- Klijn Group
- Members of the Bioinformatics & Computational Biology Department