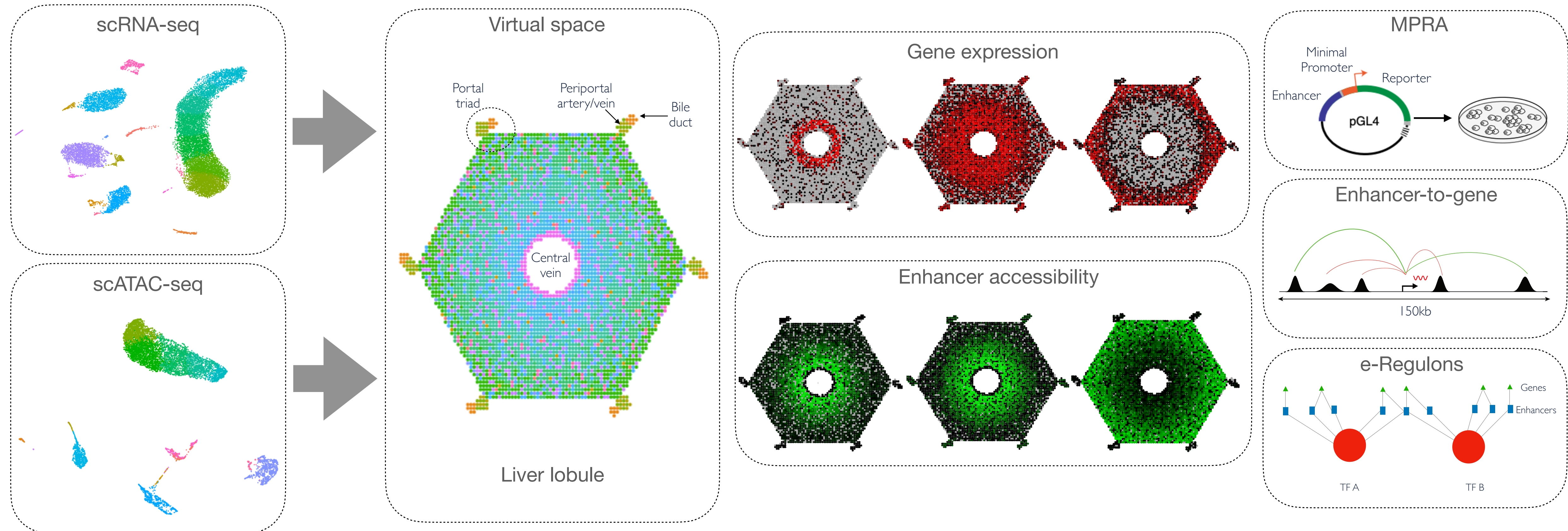


# Identification of genomic enhancers through spatial integration of single-cell omics in the mouse liver

Carmen Bravo González-Blas, Irina Matetovici, Leticia Sansores\*, Elizabeth Verboven\*, Suresh Poovathingal, Georg Halder\* and Stein Aerts

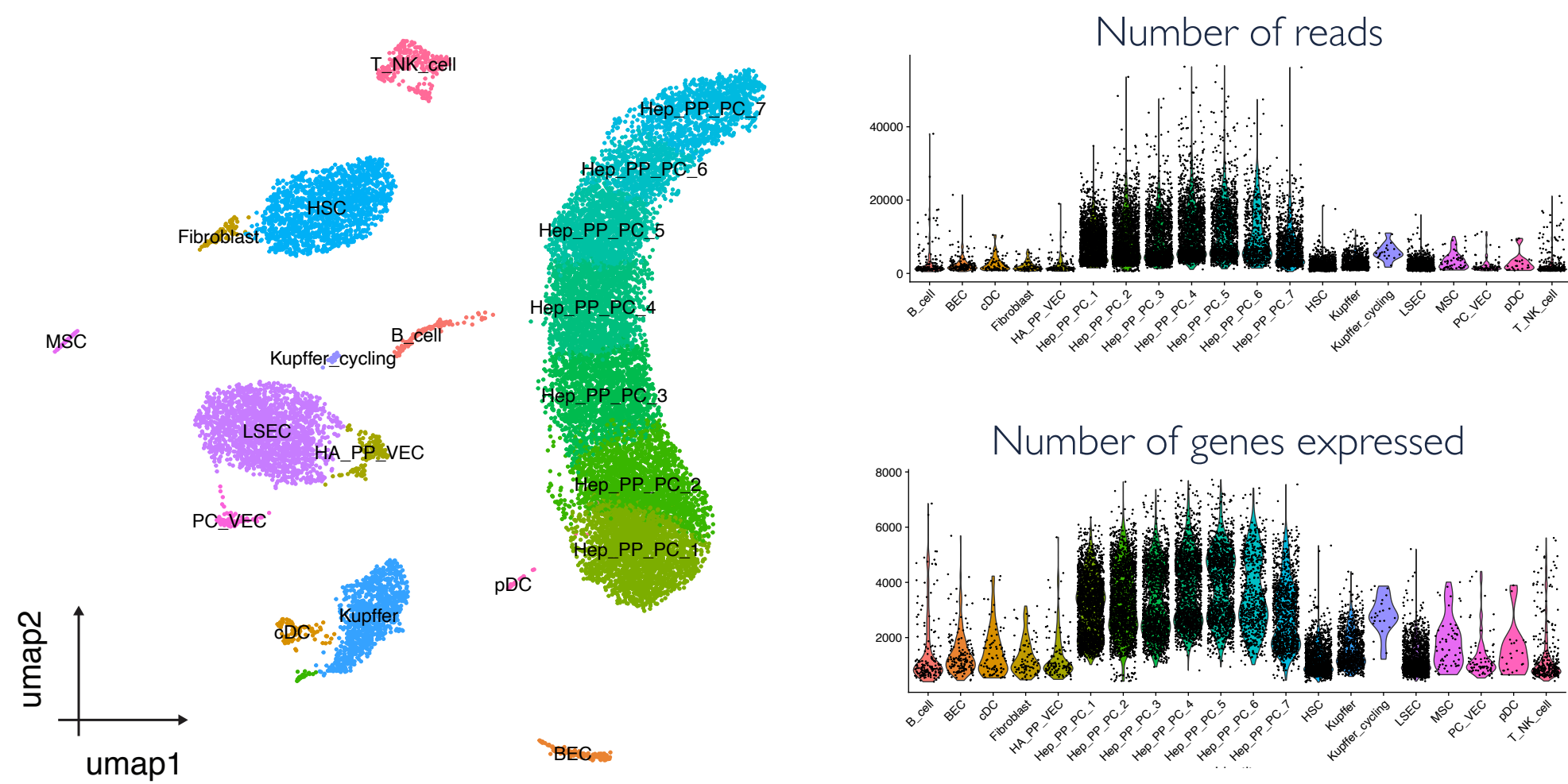
✉ carmen.bravogonzalezblas@kuleuven.vib.be





# Transcriptome and epigenome single-cell atlases of the mouse liver

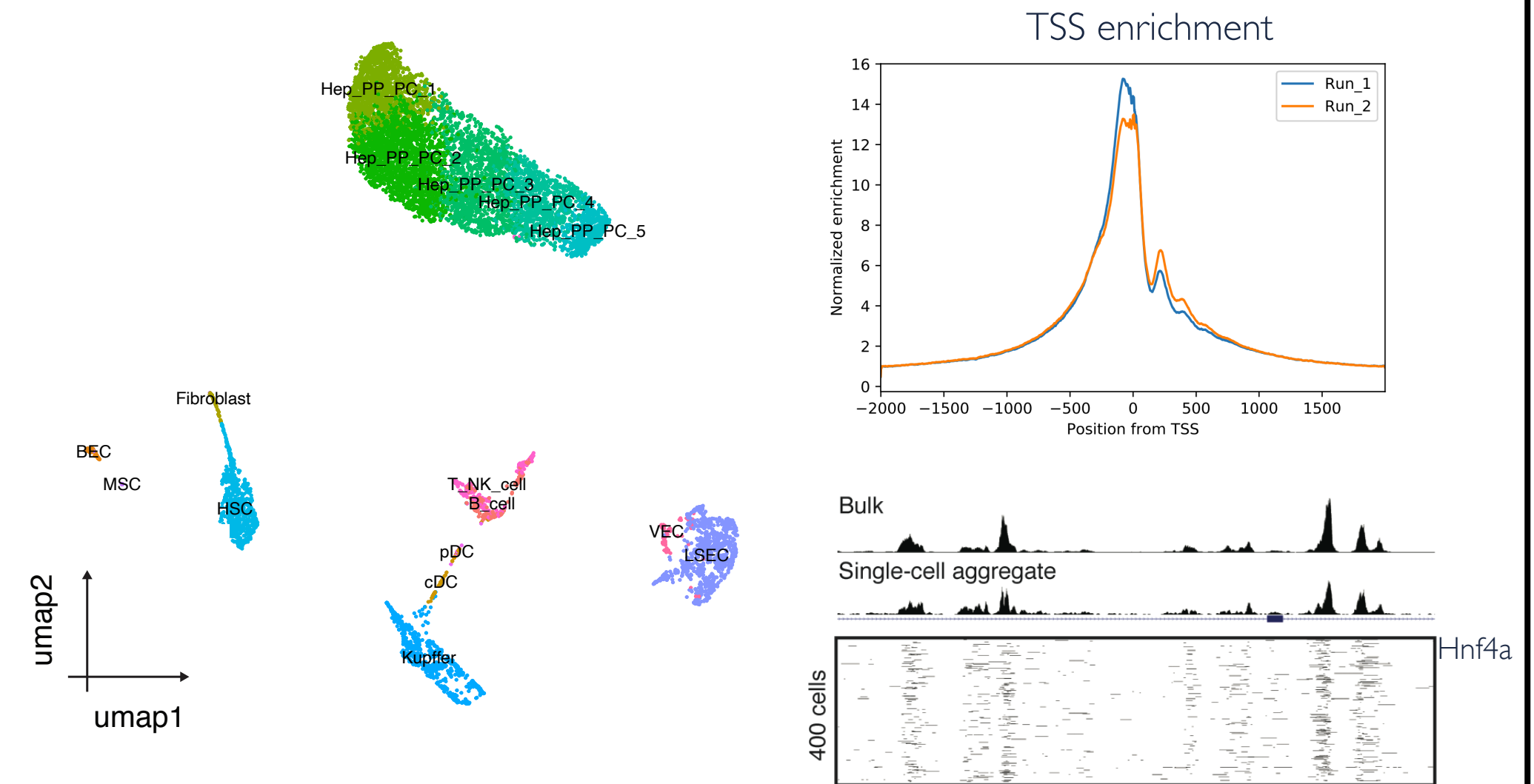
## Single-nuclei RNA-seq (16K cells)



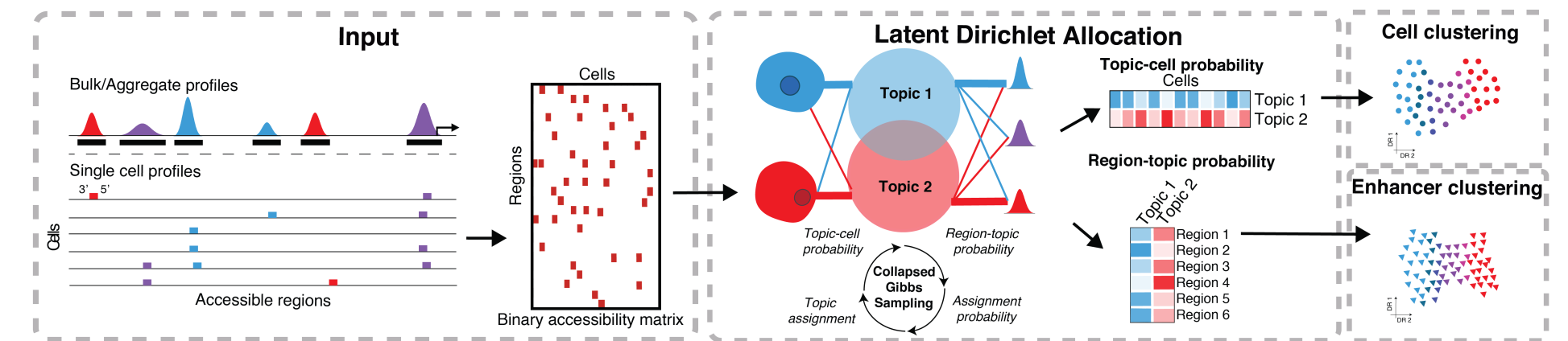
How to integrate independent assays?



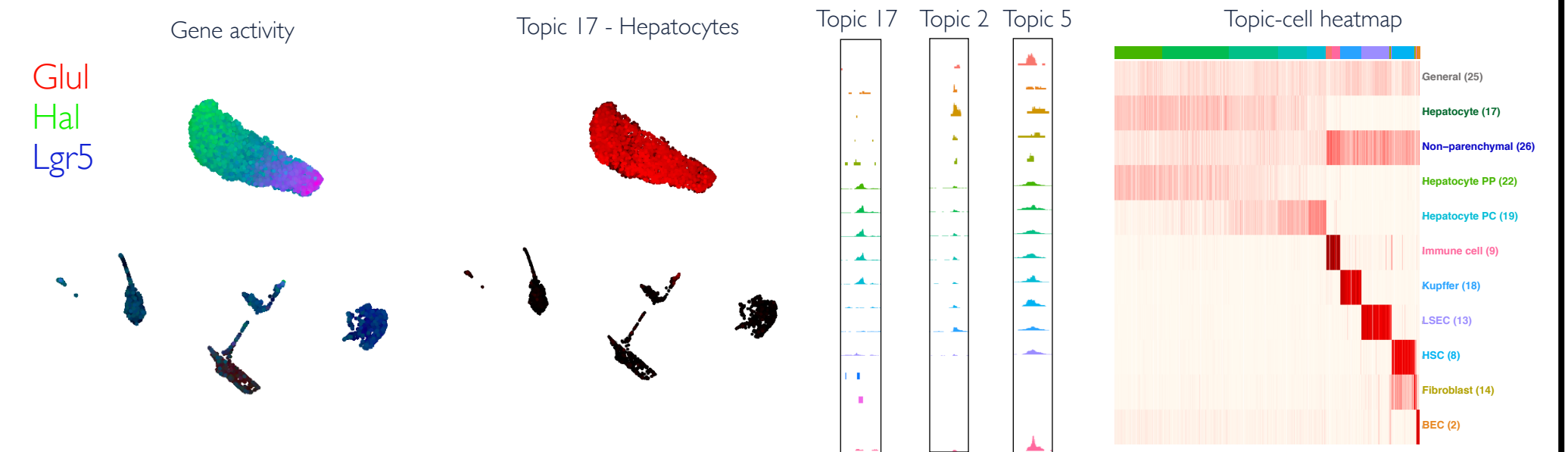
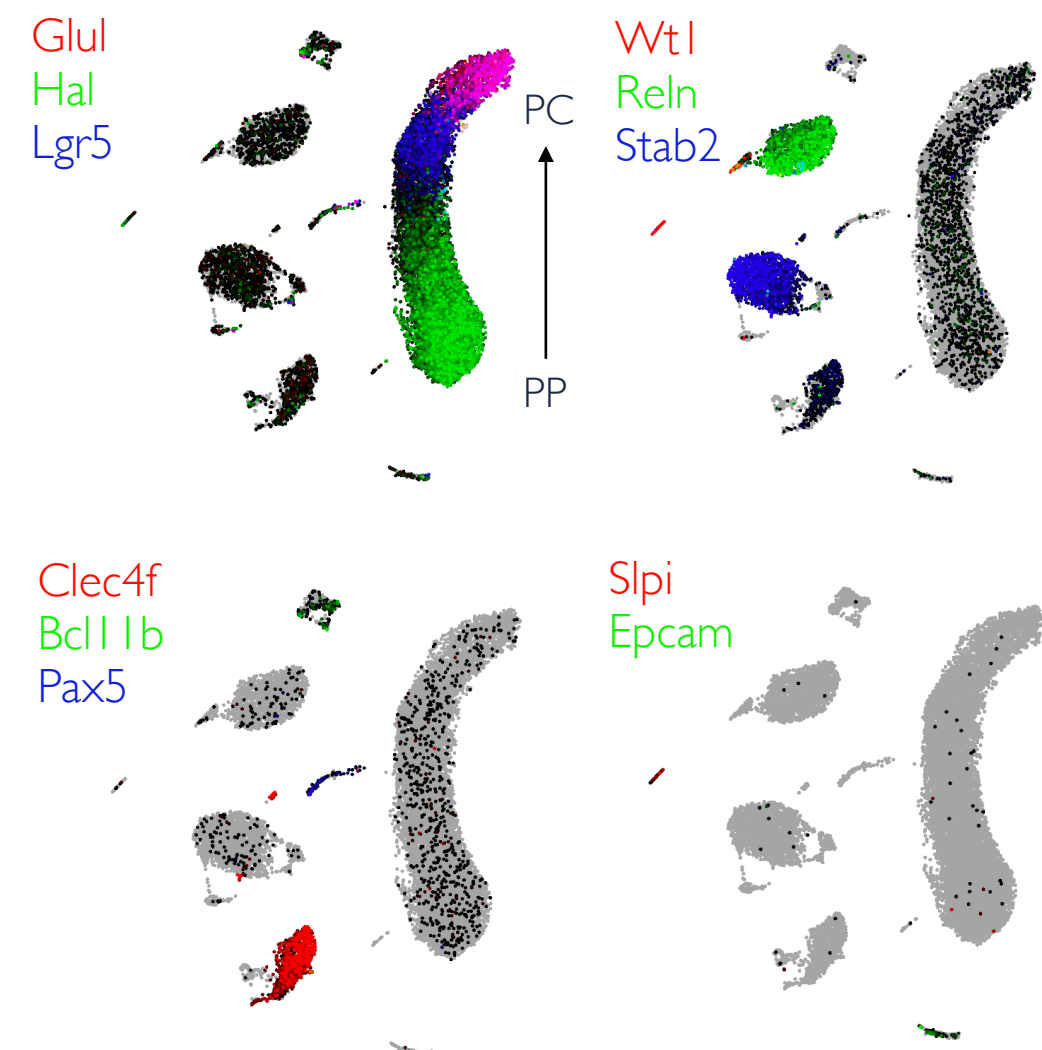
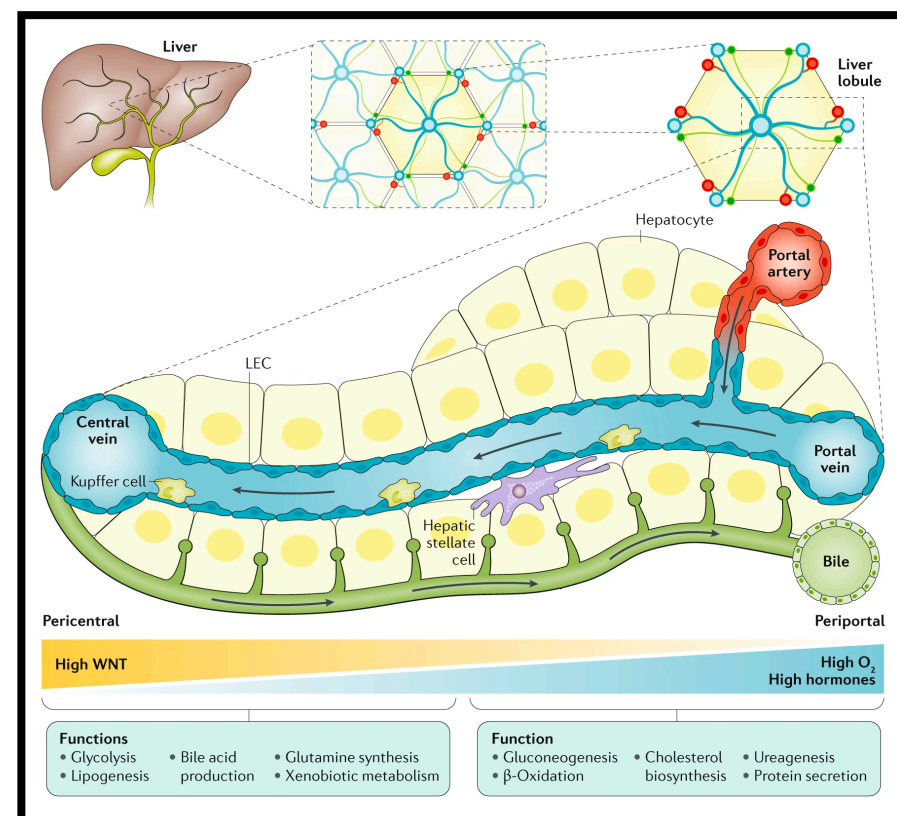
## Single-cell ATAC-seq (9K cells)



## cisTopic (Bravo et al., 2019)



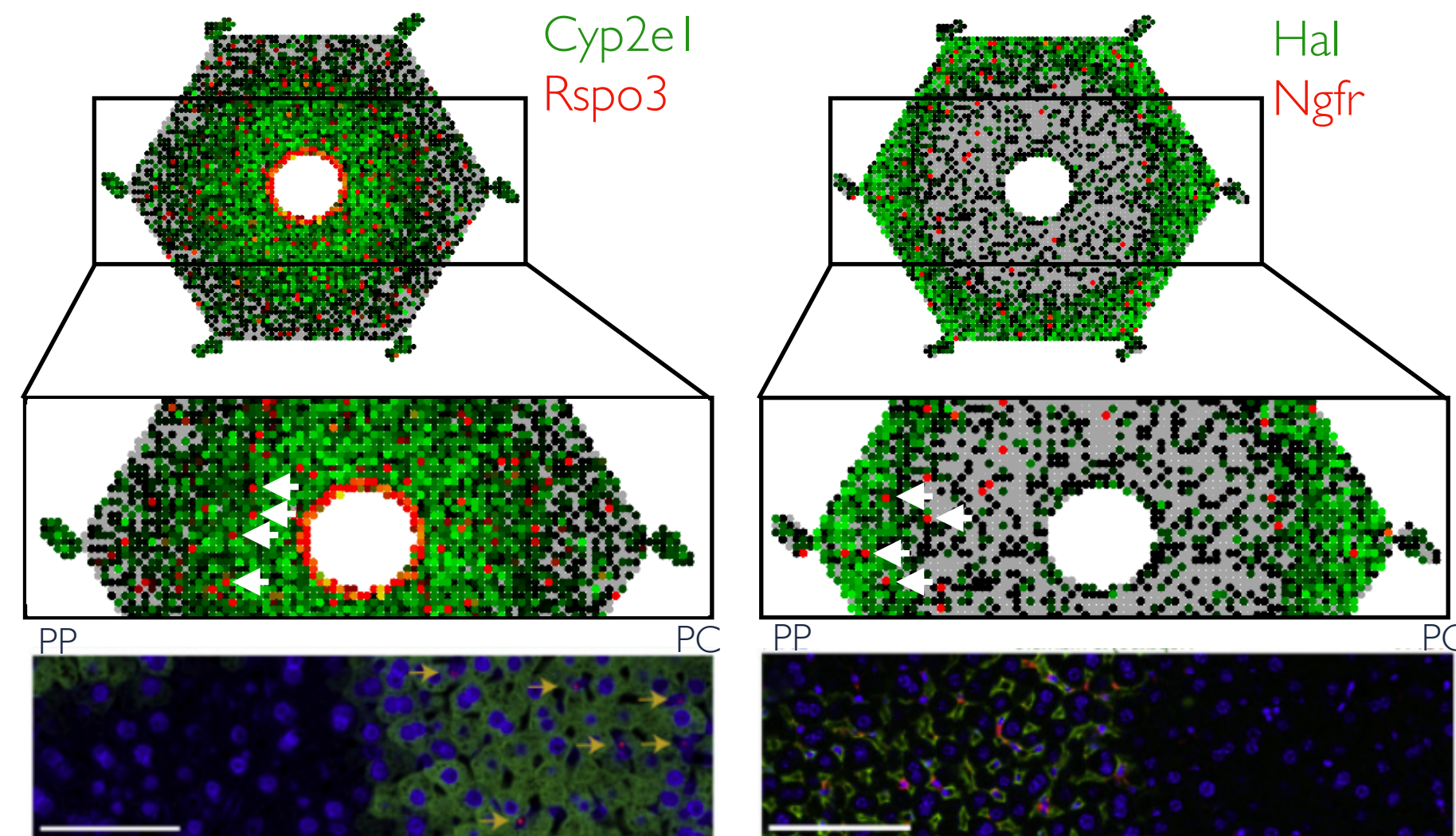
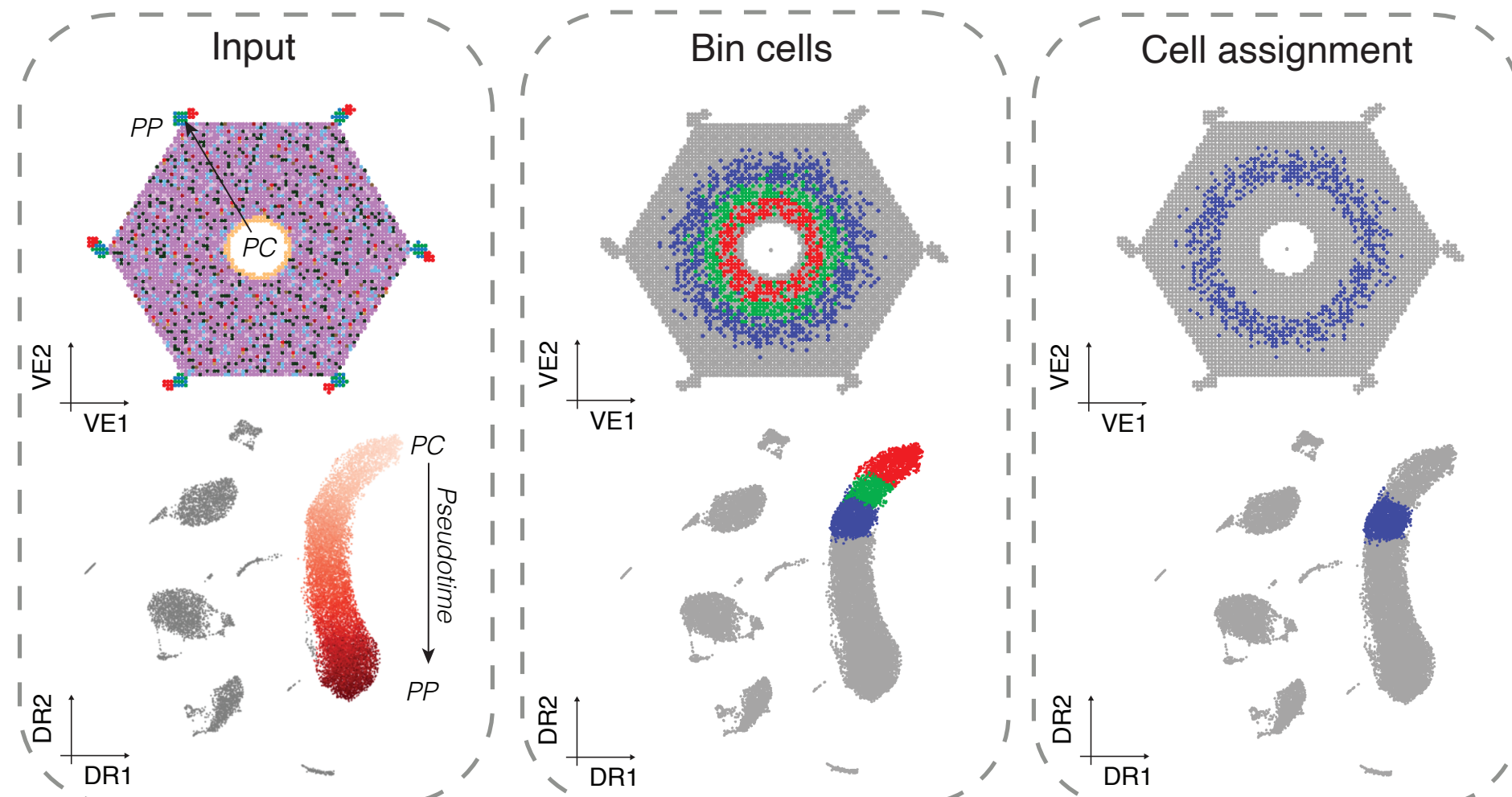
## Liver zonation





# Spatial integration of single-cell omics data using ScoMAP

## Mapping single-cell omics data into a virtual template



Dovie et al., 2019

## Inferring enhancer-to-gene links

