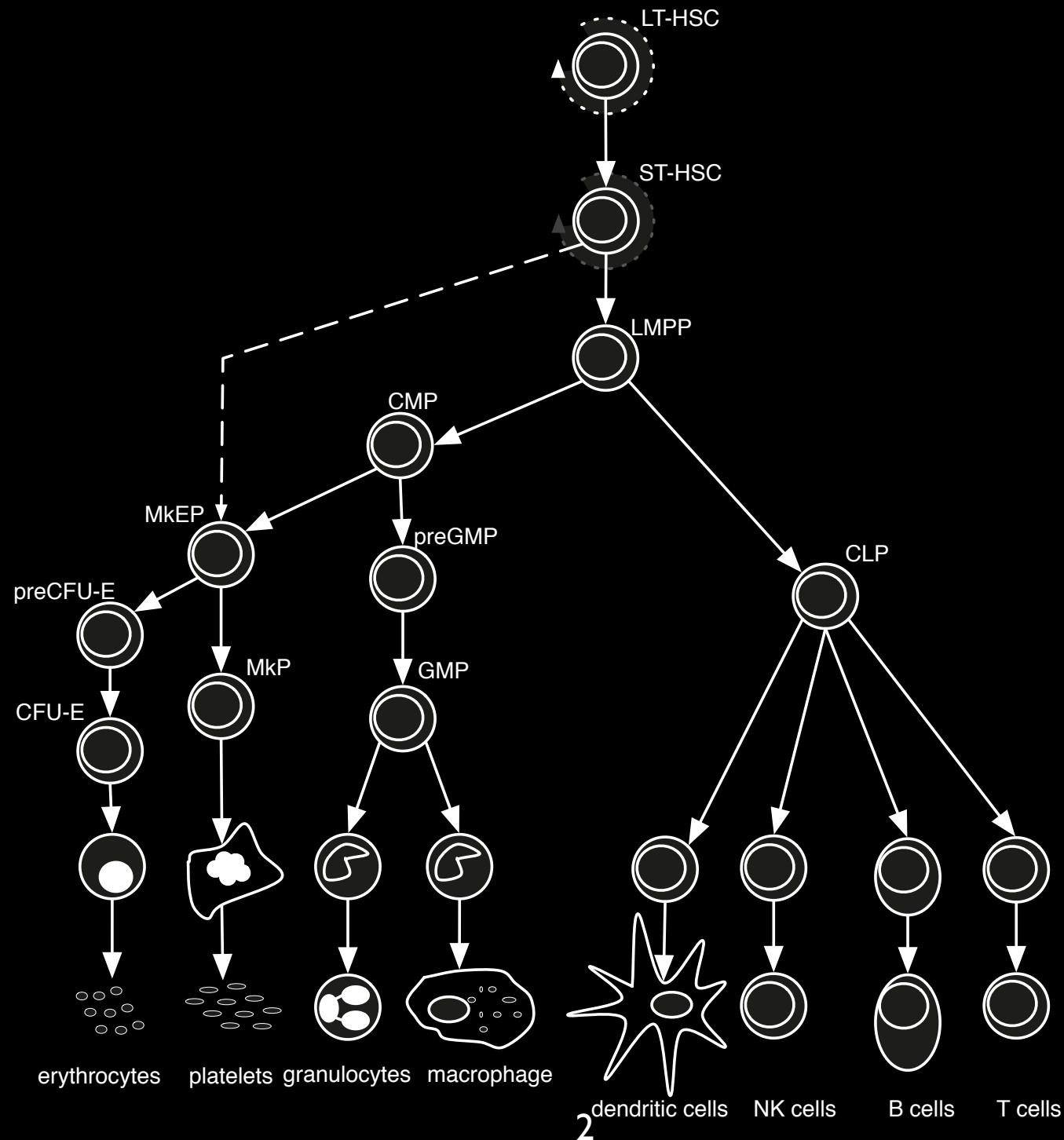


BloodSpot

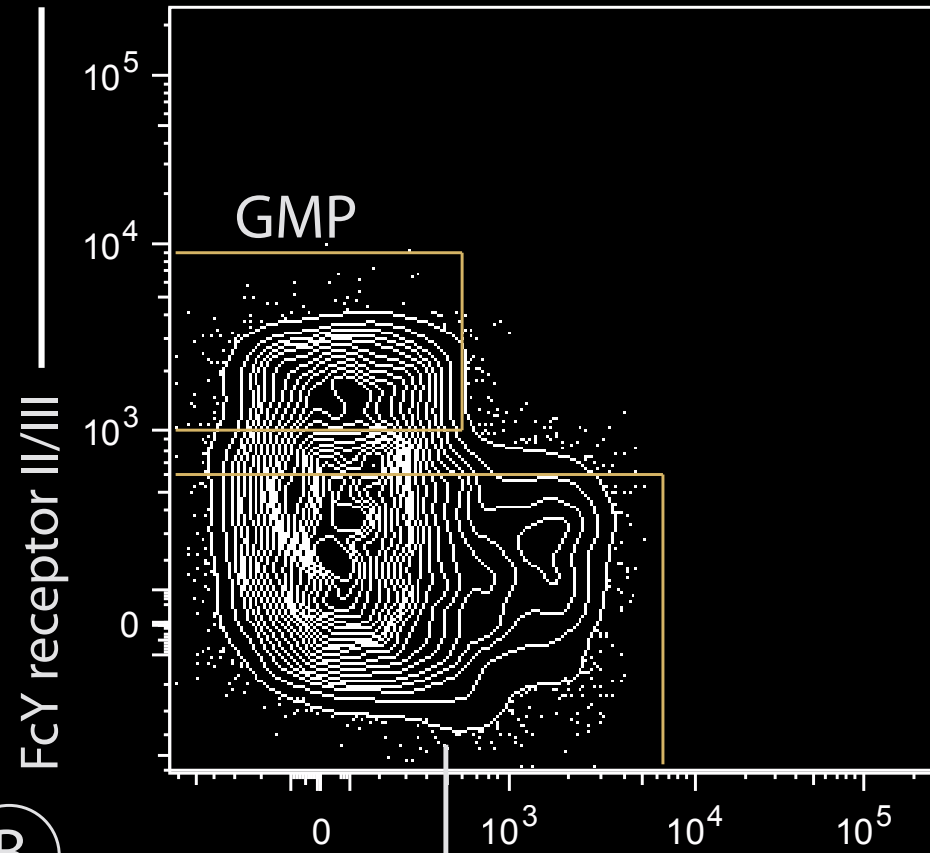
ELIXIR 25. nov. 2014

The hematopoietic system

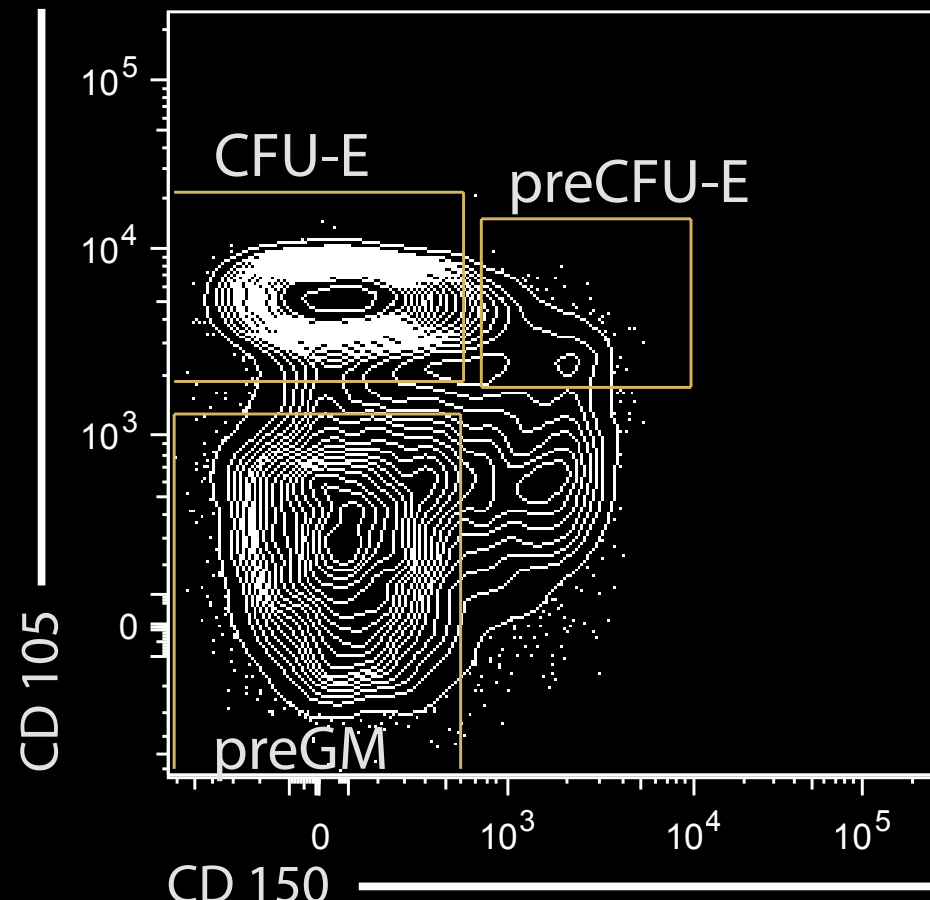


FlowJo output

A

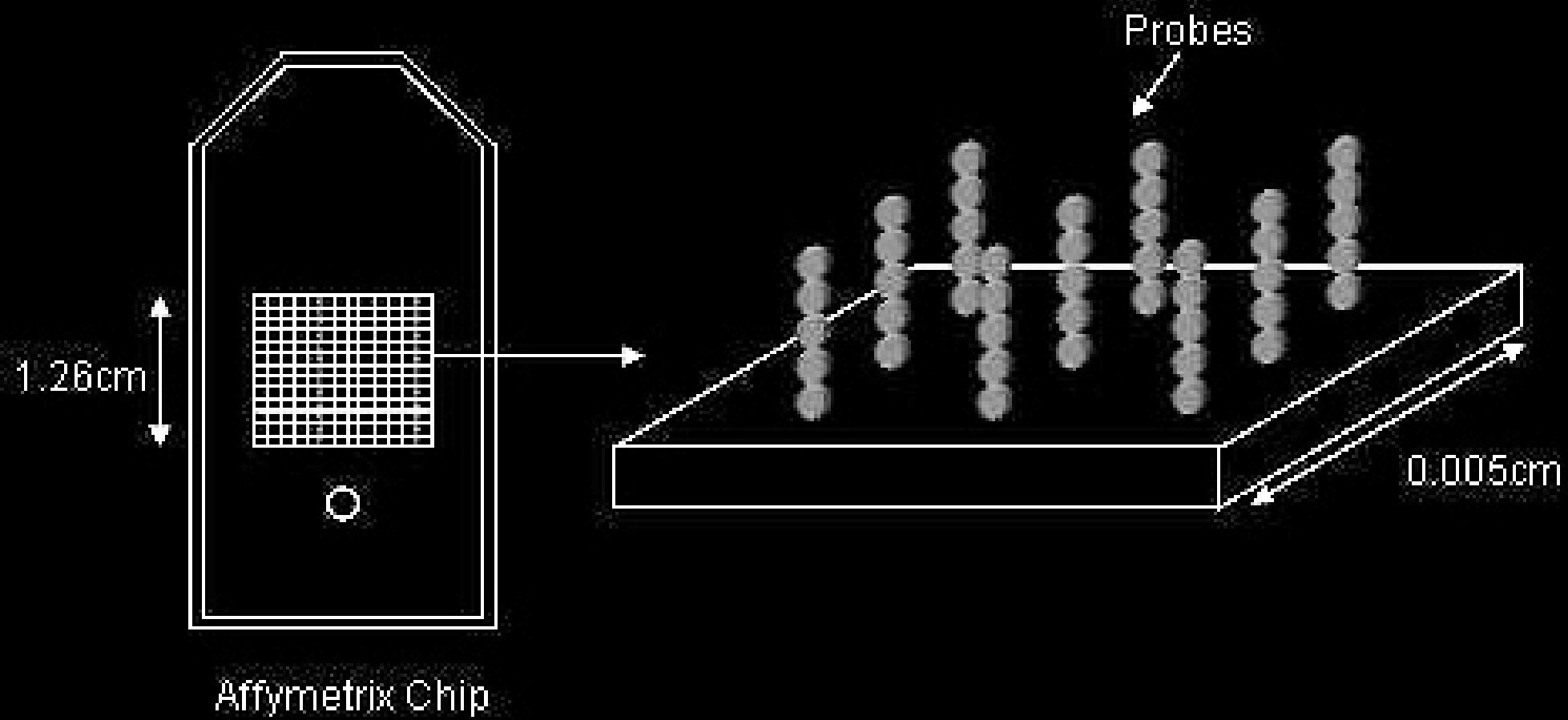


B



Microarrays

Microarrays



Microarrays



Microarray samples

- Find FACS sorted cells on the internet
(very cumbersome, very few cells)
 - Look at sorting strategies
 - Look at quality scores

Batch effects

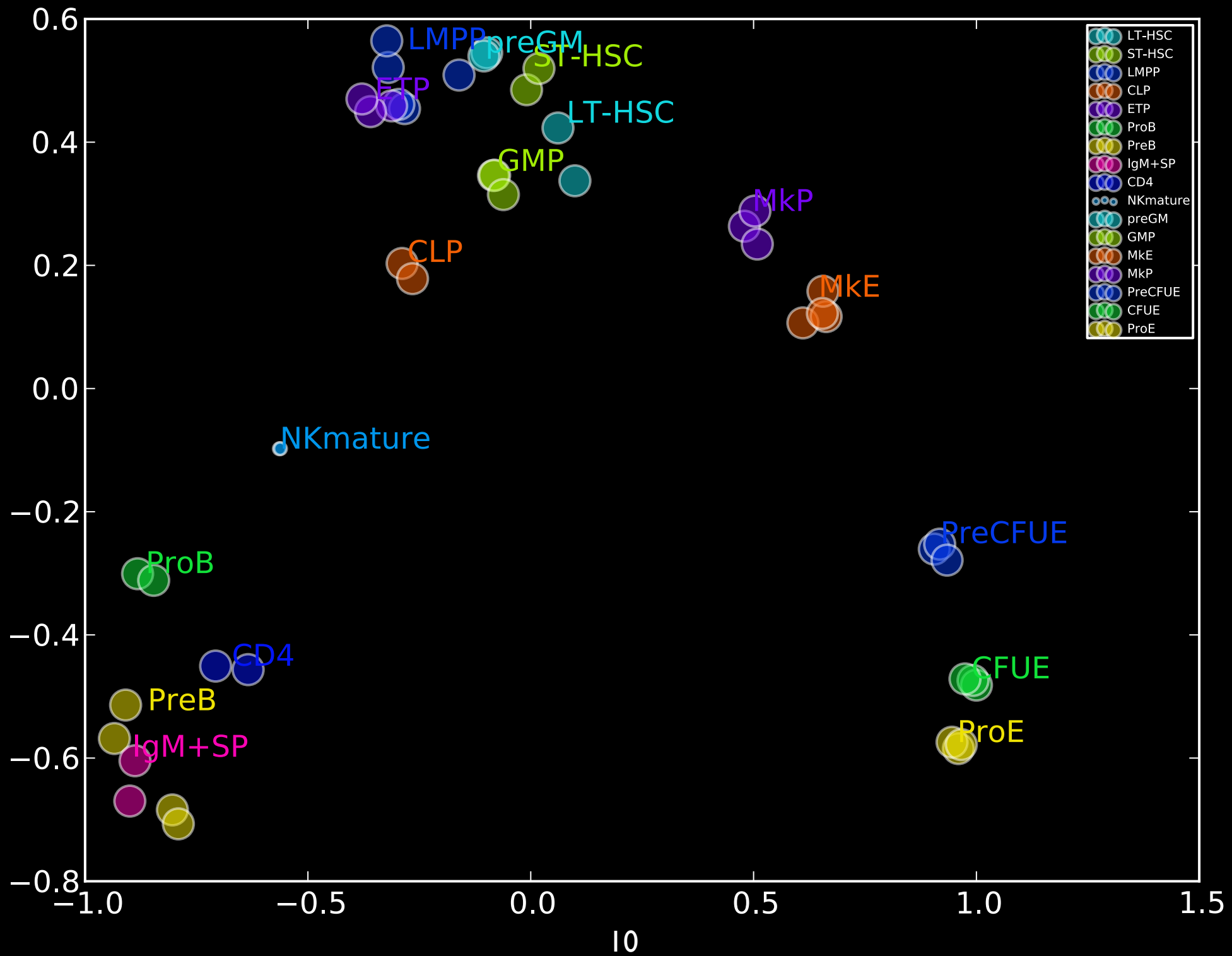
- Samples from 8 labs gives non-comparable probe sets
- Batch correction with ComBat:
 - Empirical Bayes method which uses prior information about batches and cell types

Batch effects

$$Y_{ijg} = \alpha_g + X\beta_g + \gamma_{ig} + \delta_{ig}\varepsilon_{ijg},$$

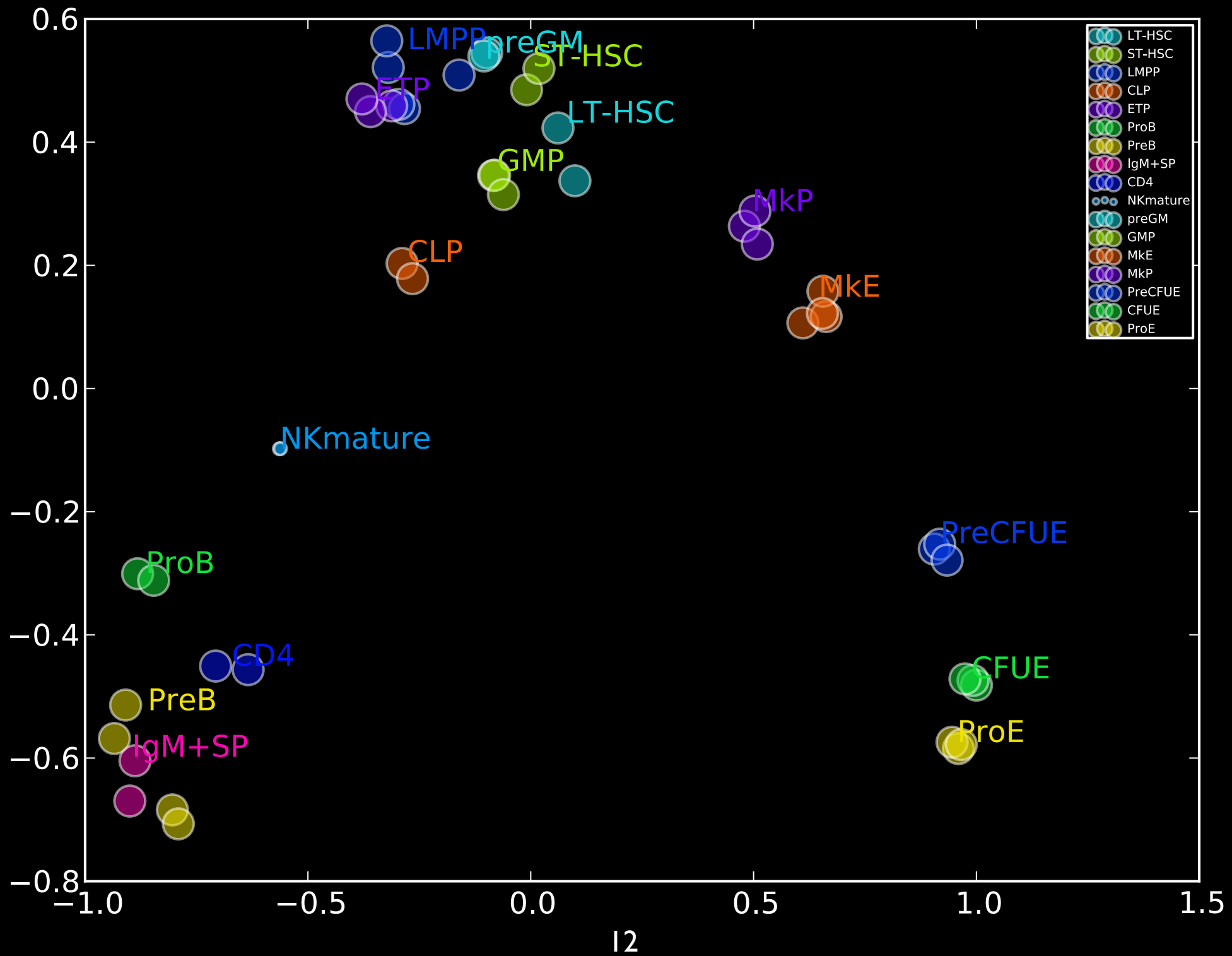
$$\gamma_{ijg}^* = \frac{\hat{\sigma}_g}{\hat{\delta}_{ig}^*} (Z_{ijg} - \hat{\gamma}_{ig}^*) + \hat{\alpha}_g + X\hat{\beta}_g.$$

PCA

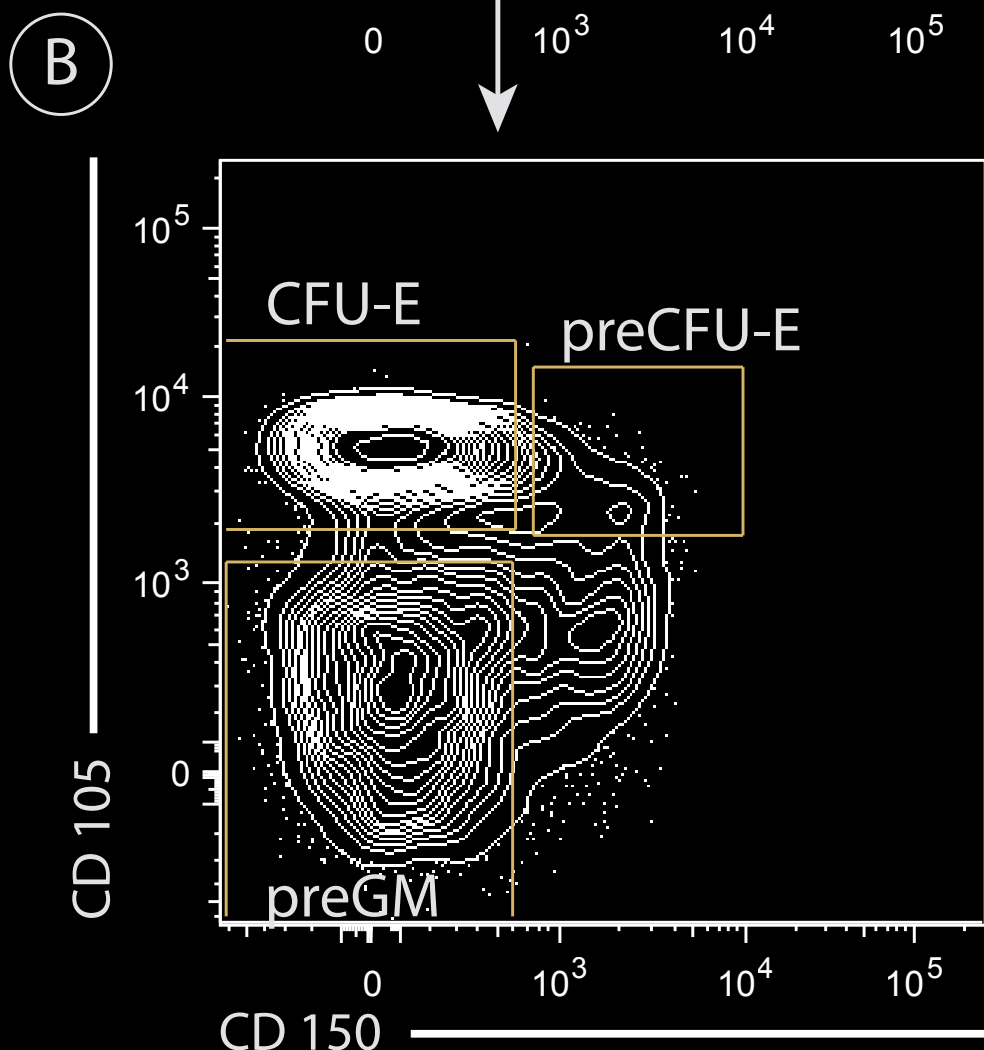
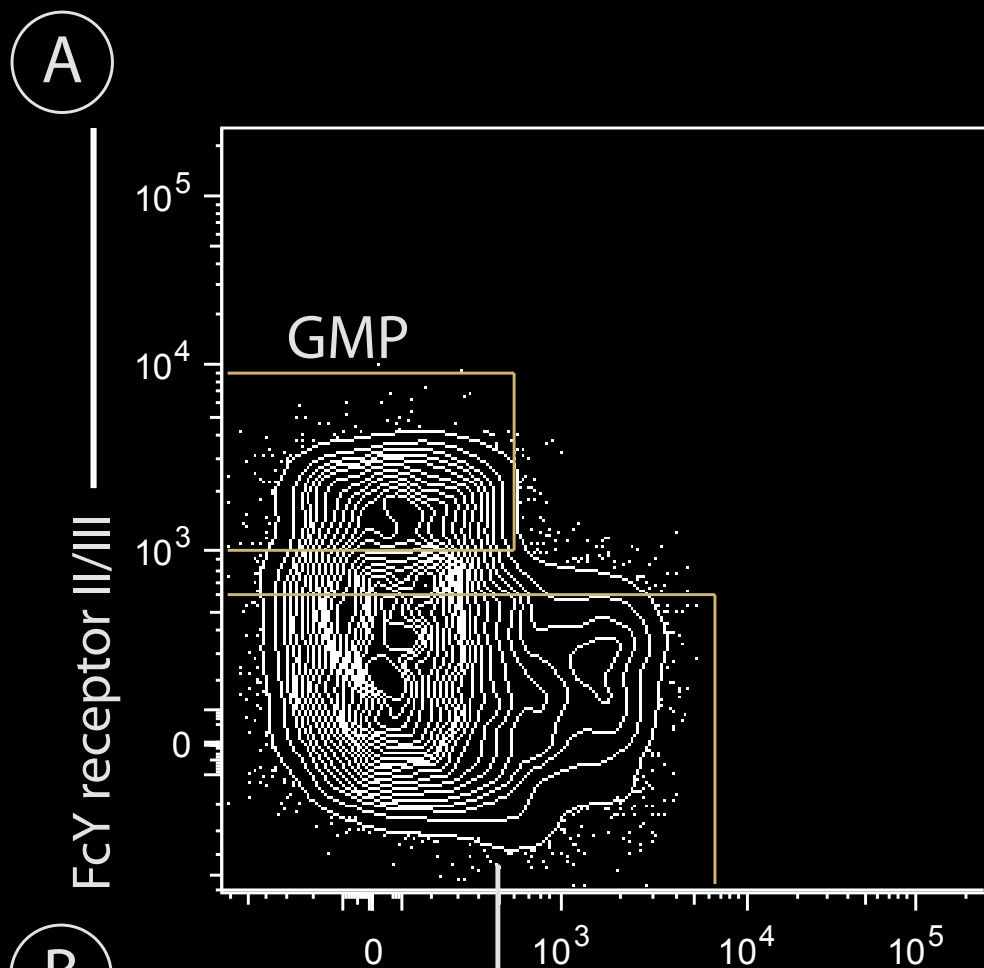




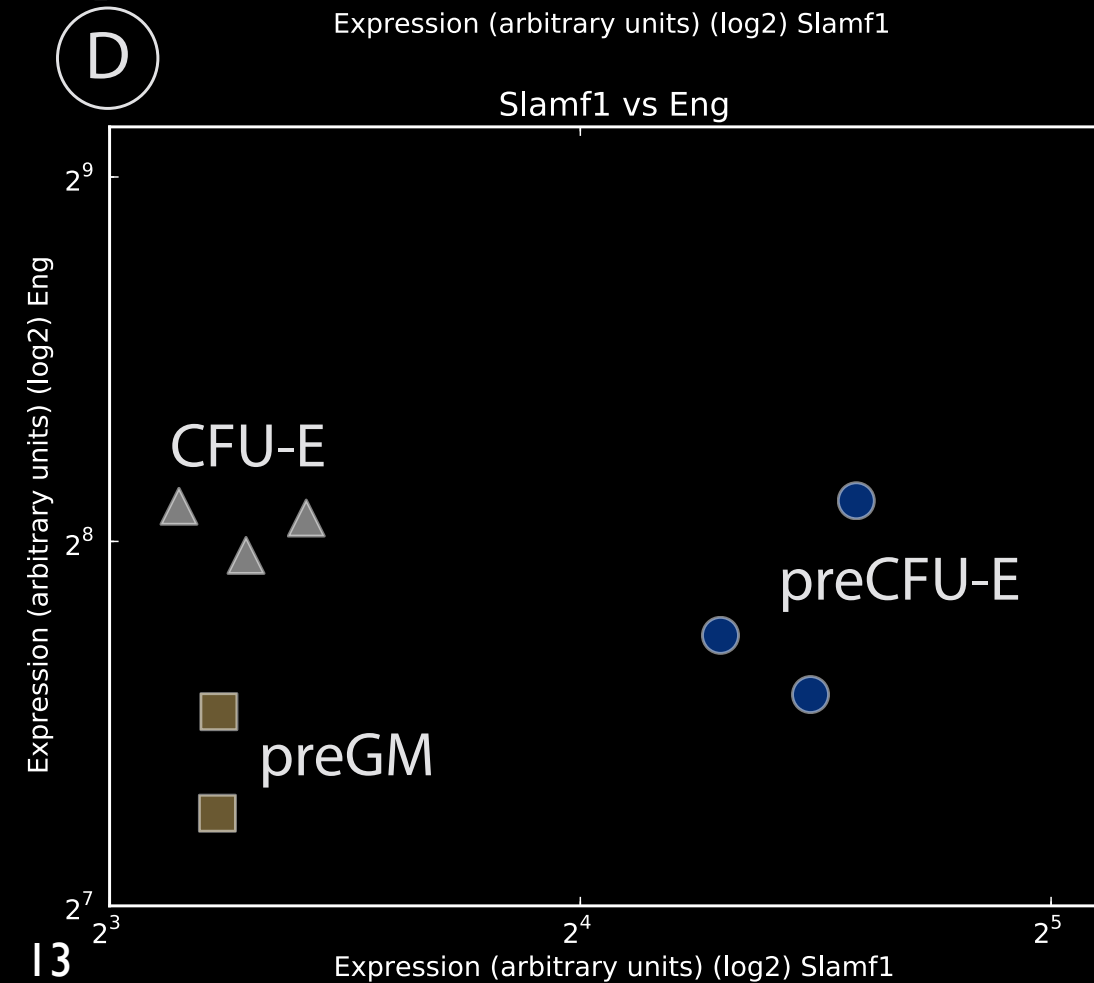
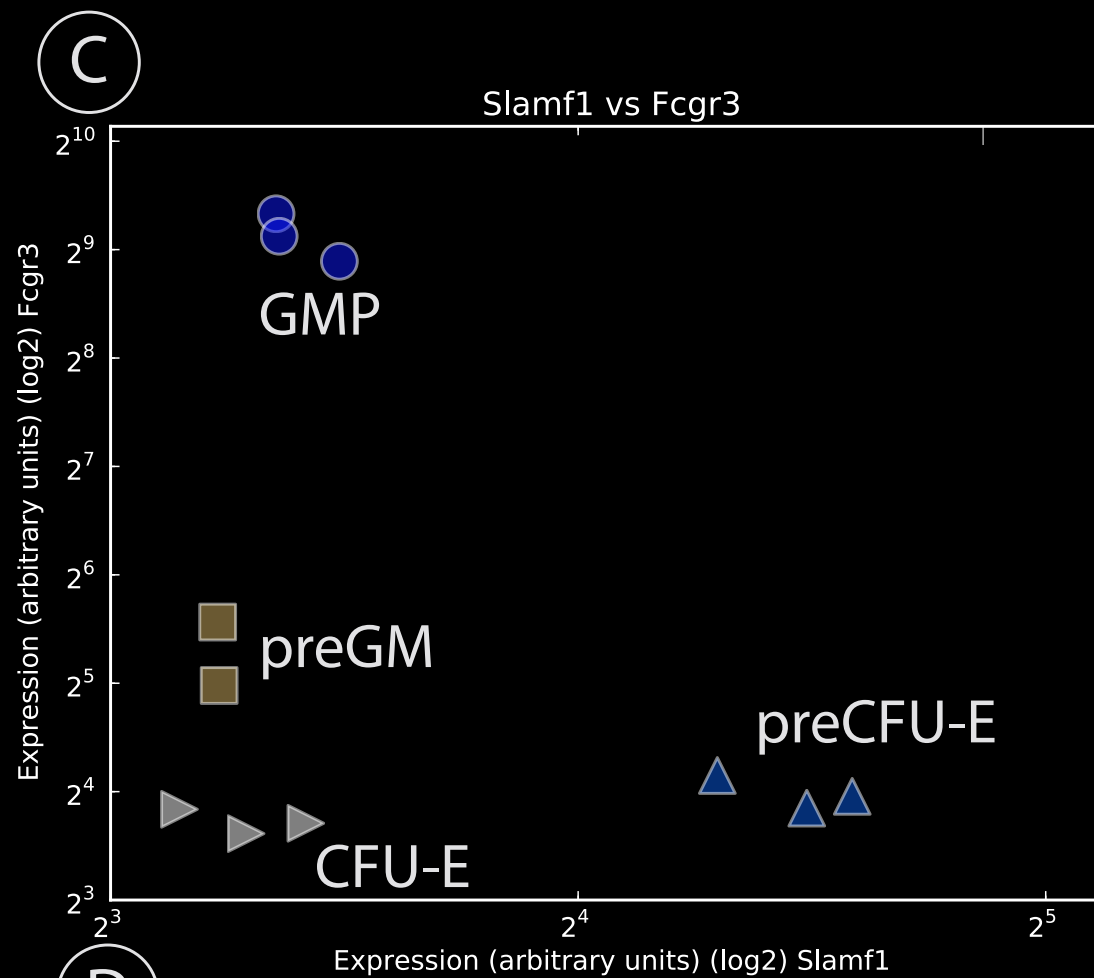
PCA



FlowJo output

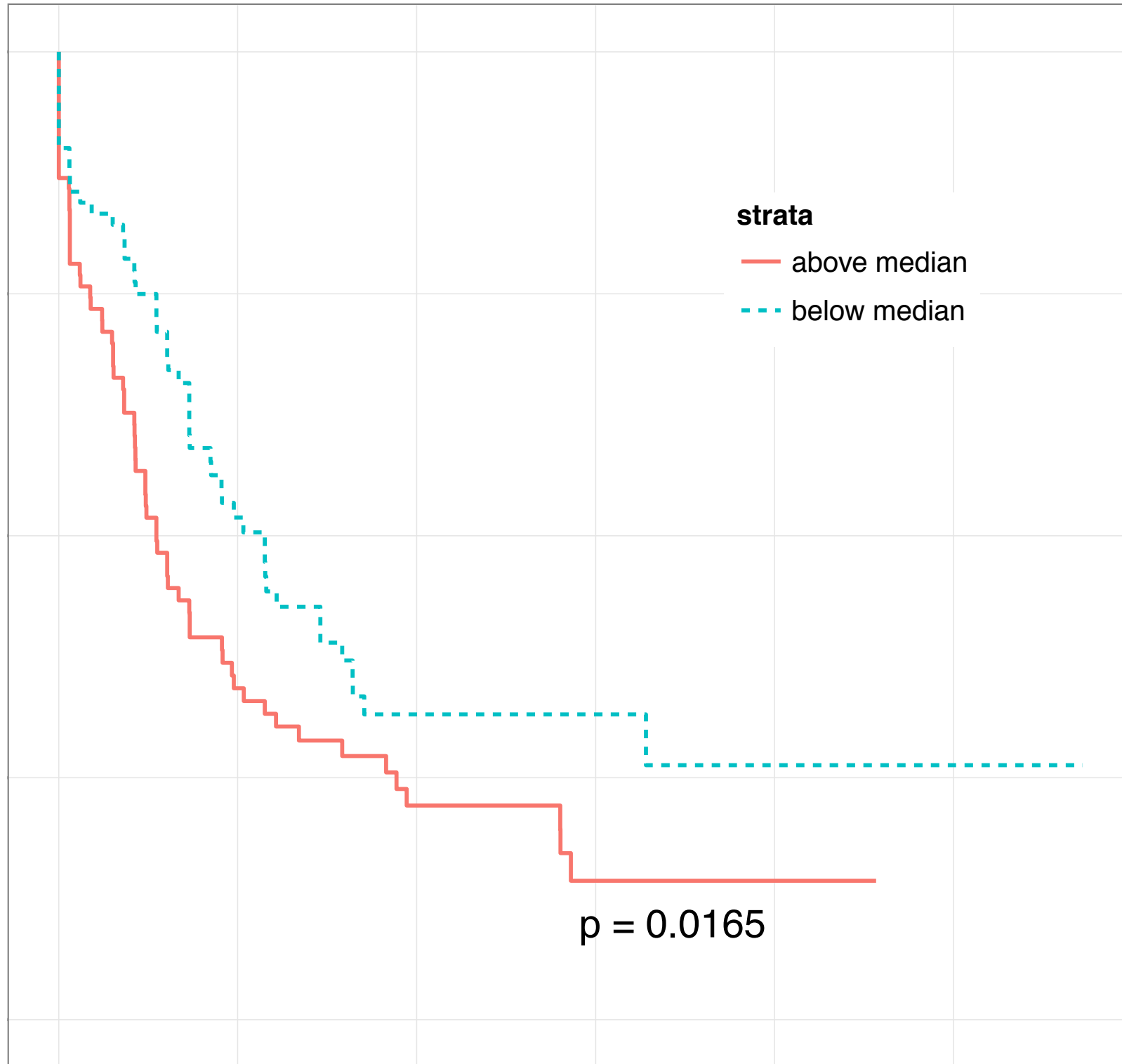


HemaExplorer output



Making data available

- We have build a nice integrated database with comparable expression between cell types of the hematopoietic system
- Feed the driver gene paradigm:
 - Single gene lookup



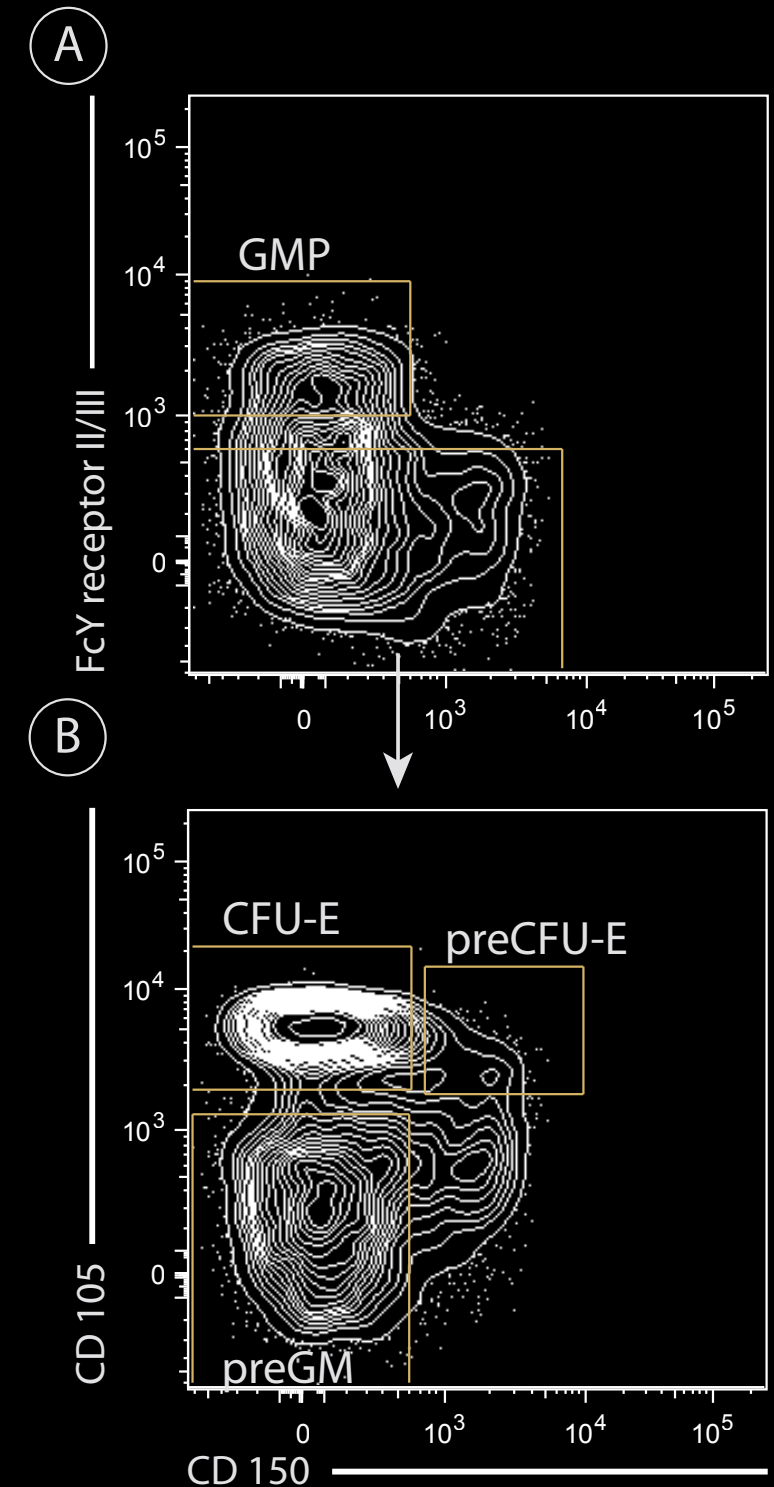
Normalizing AML in the context of the hematopoietic system

Using a novel two-step semi local rank-based
normalization algorithm

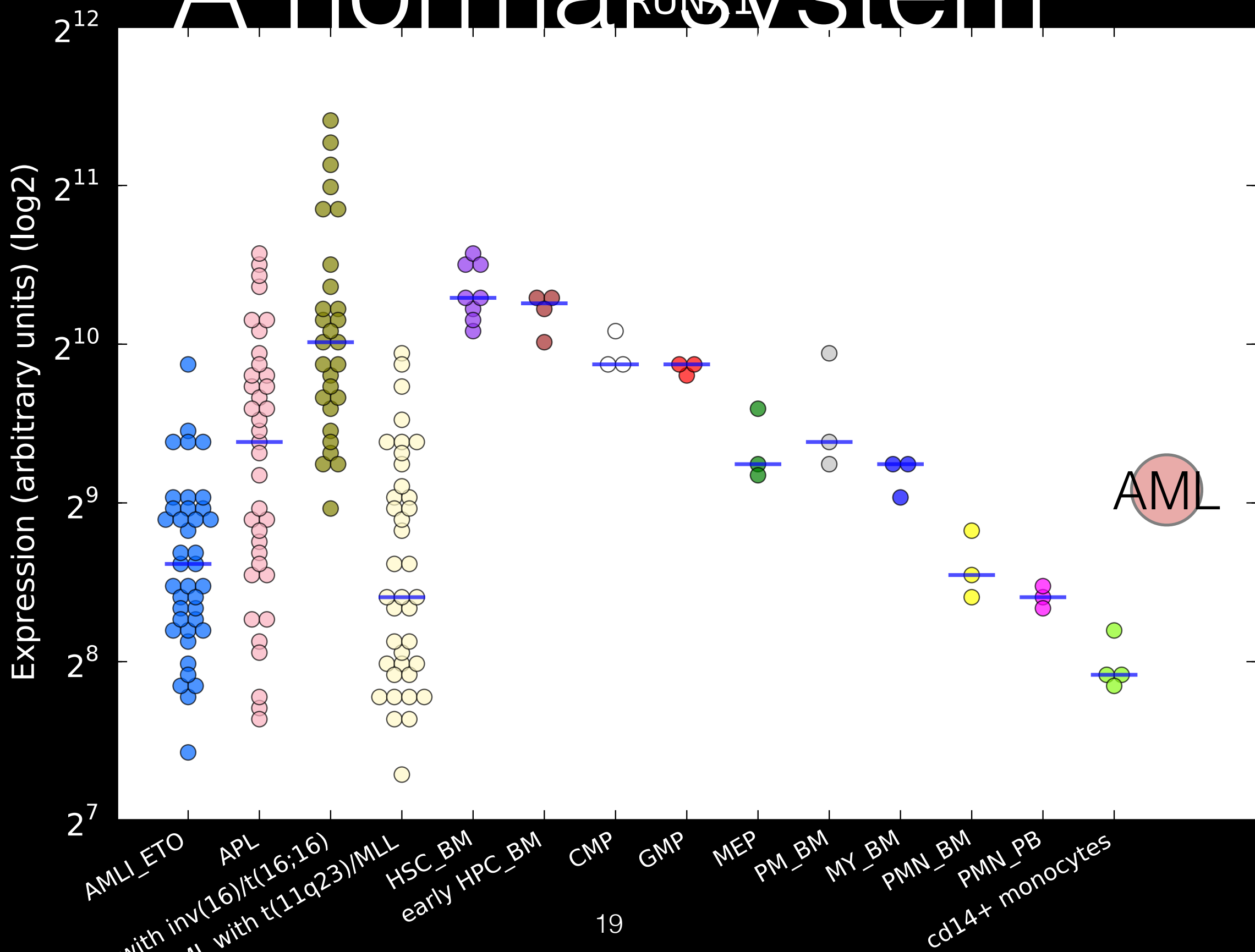
Extended database

FlowJo output

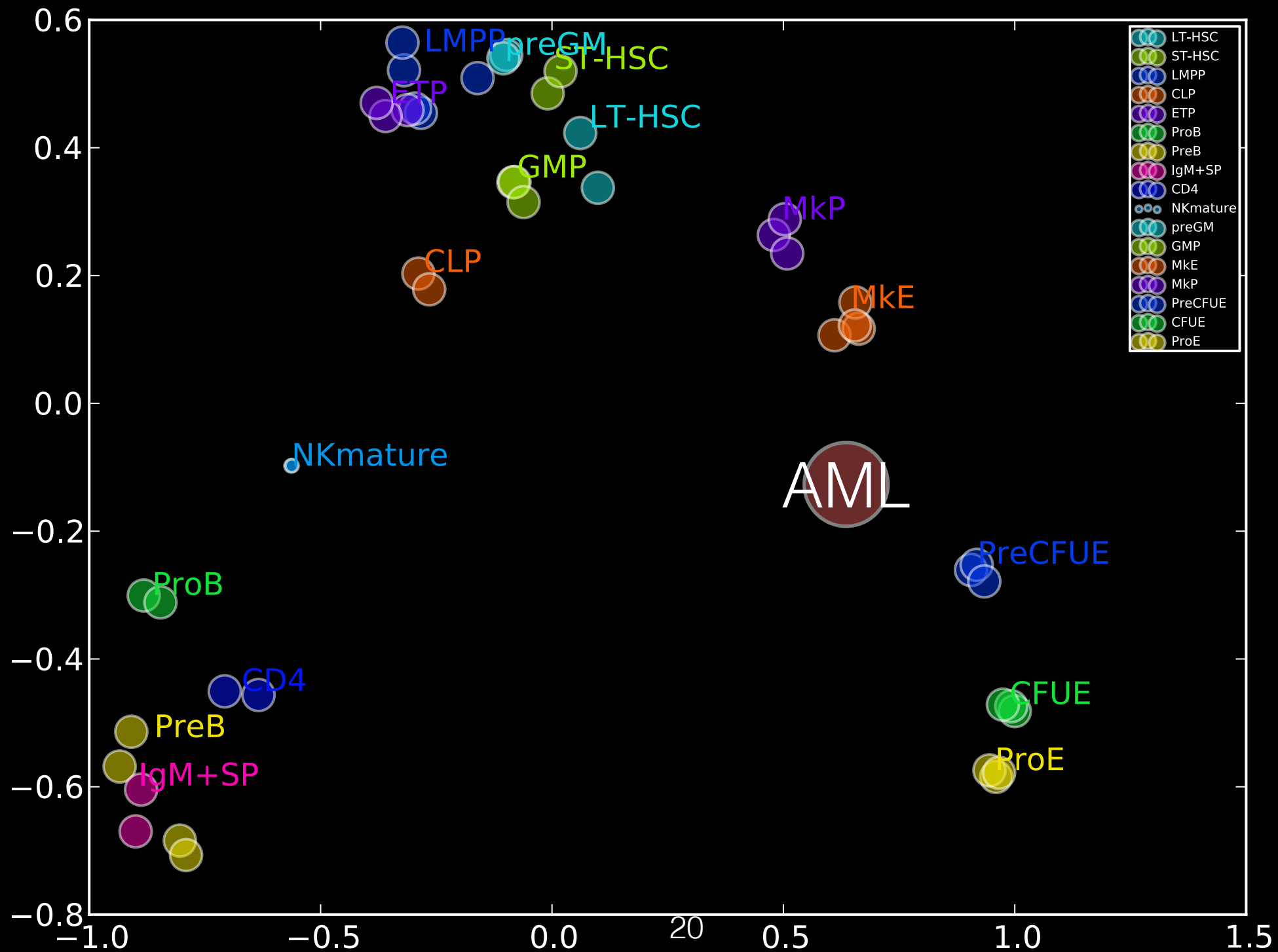
- Knowing what is normal



A normal system



A normal system



Does it work?

exercises