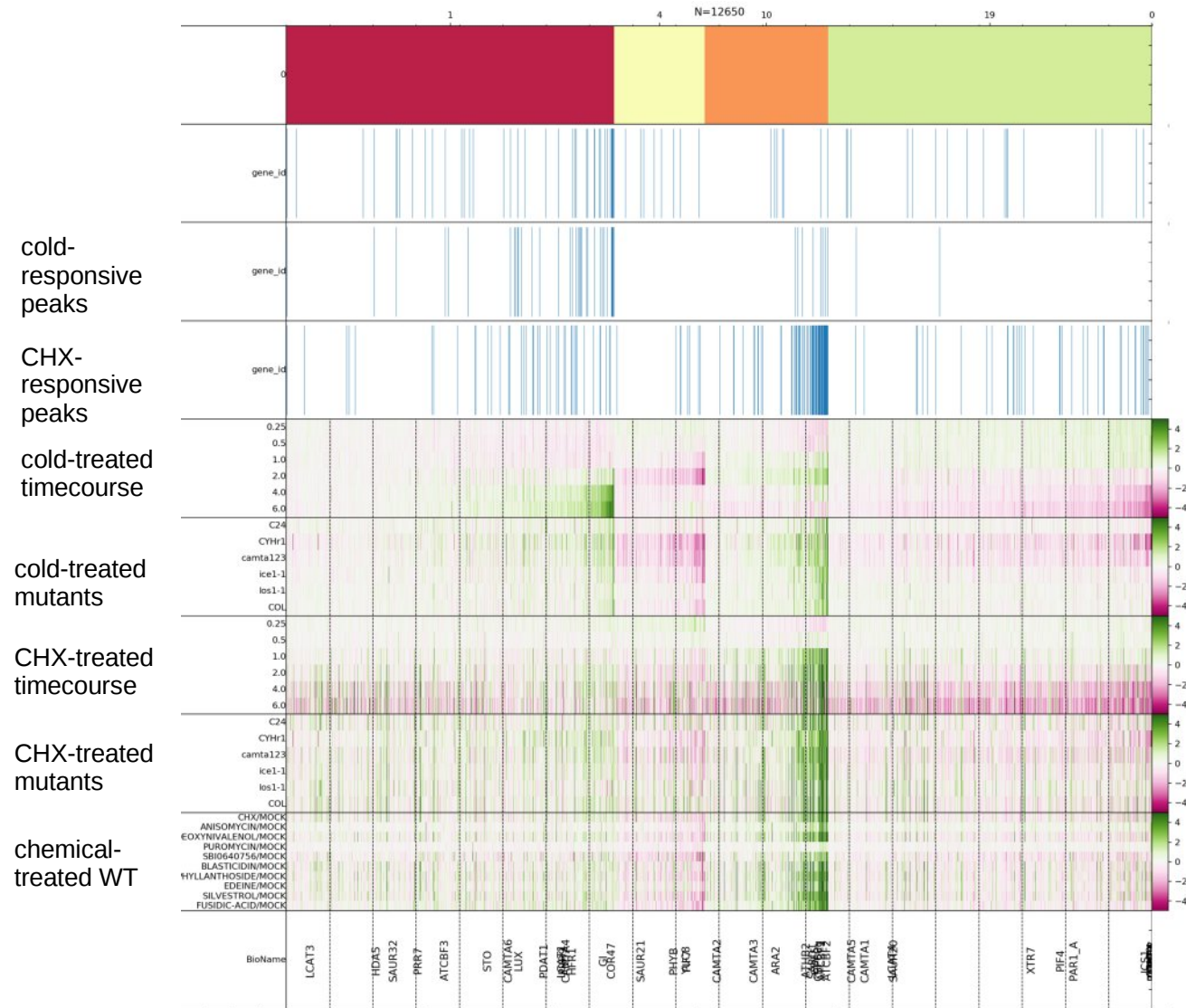


# Lab Meeting

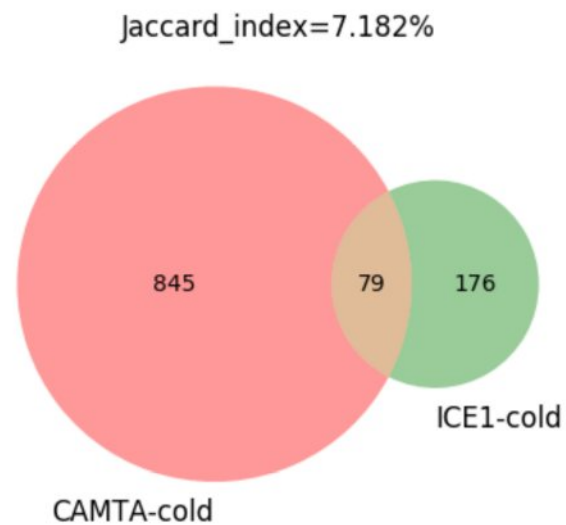
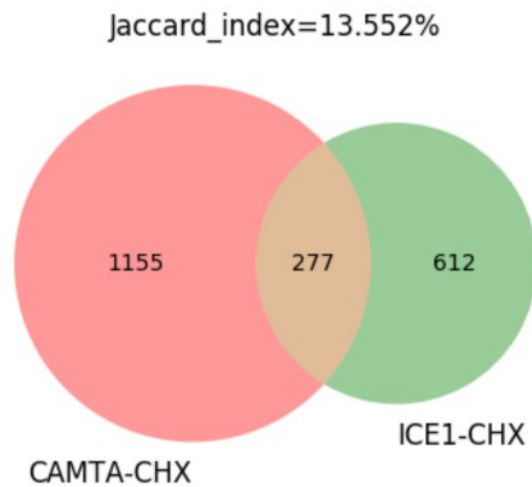
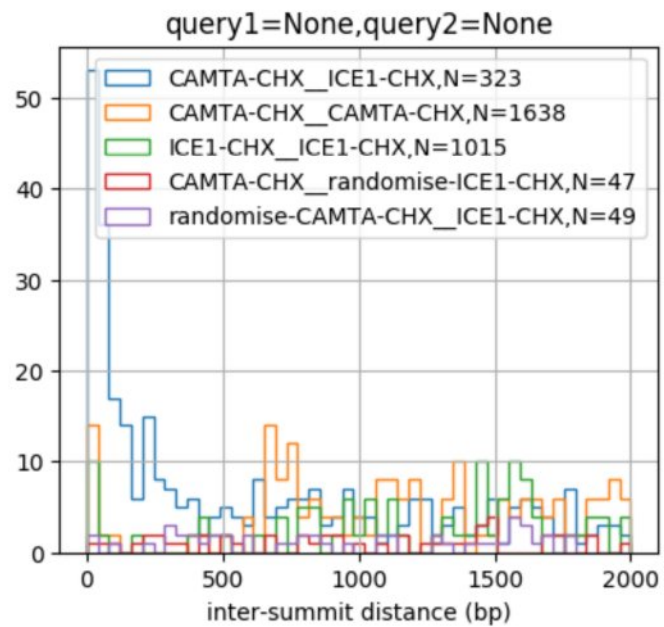
Feng Geng  
2019.02.10

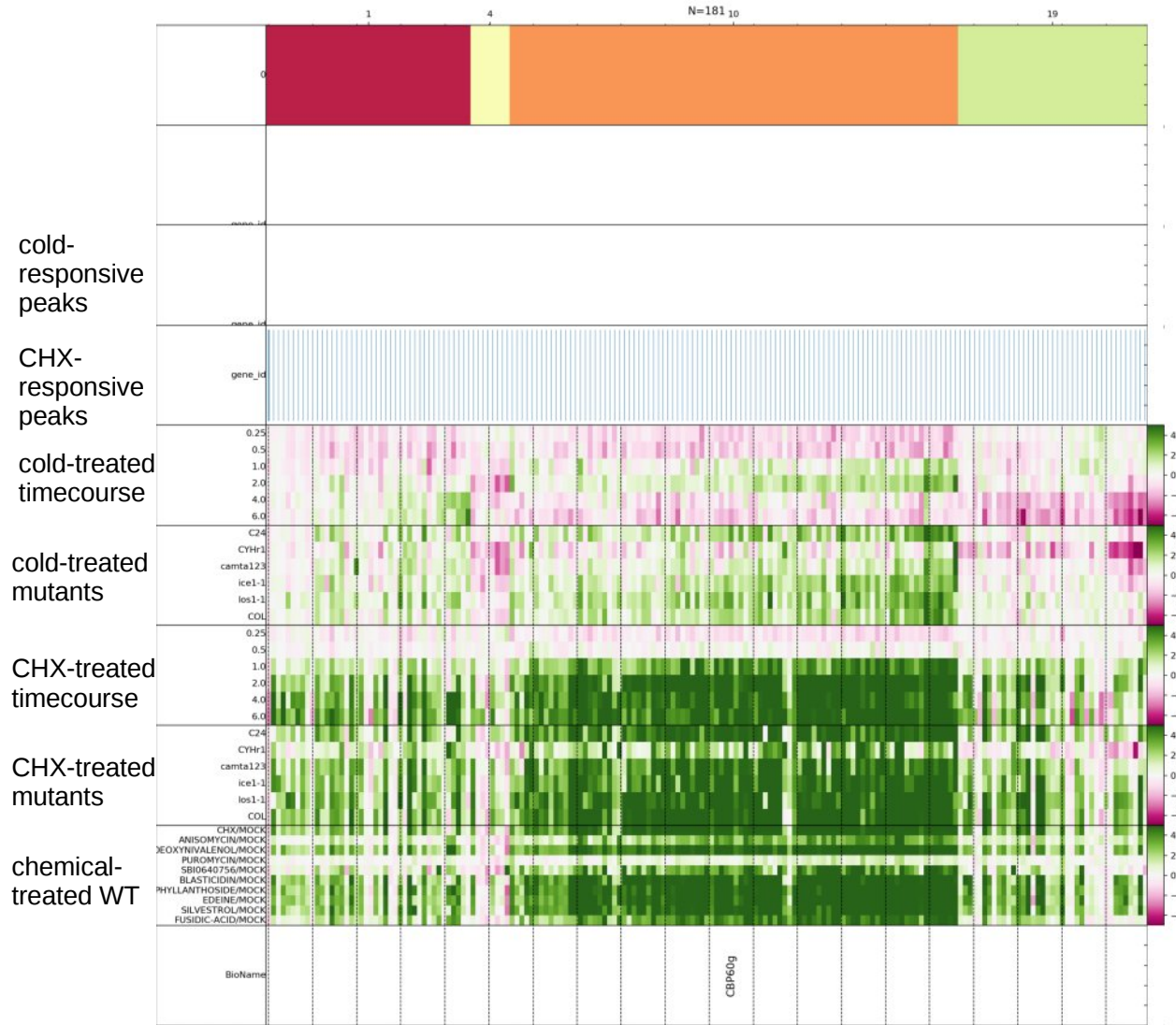
- Update on cold-responsive genes.
- Meta analysis of transcriptome data

Update on cold-responsive genes

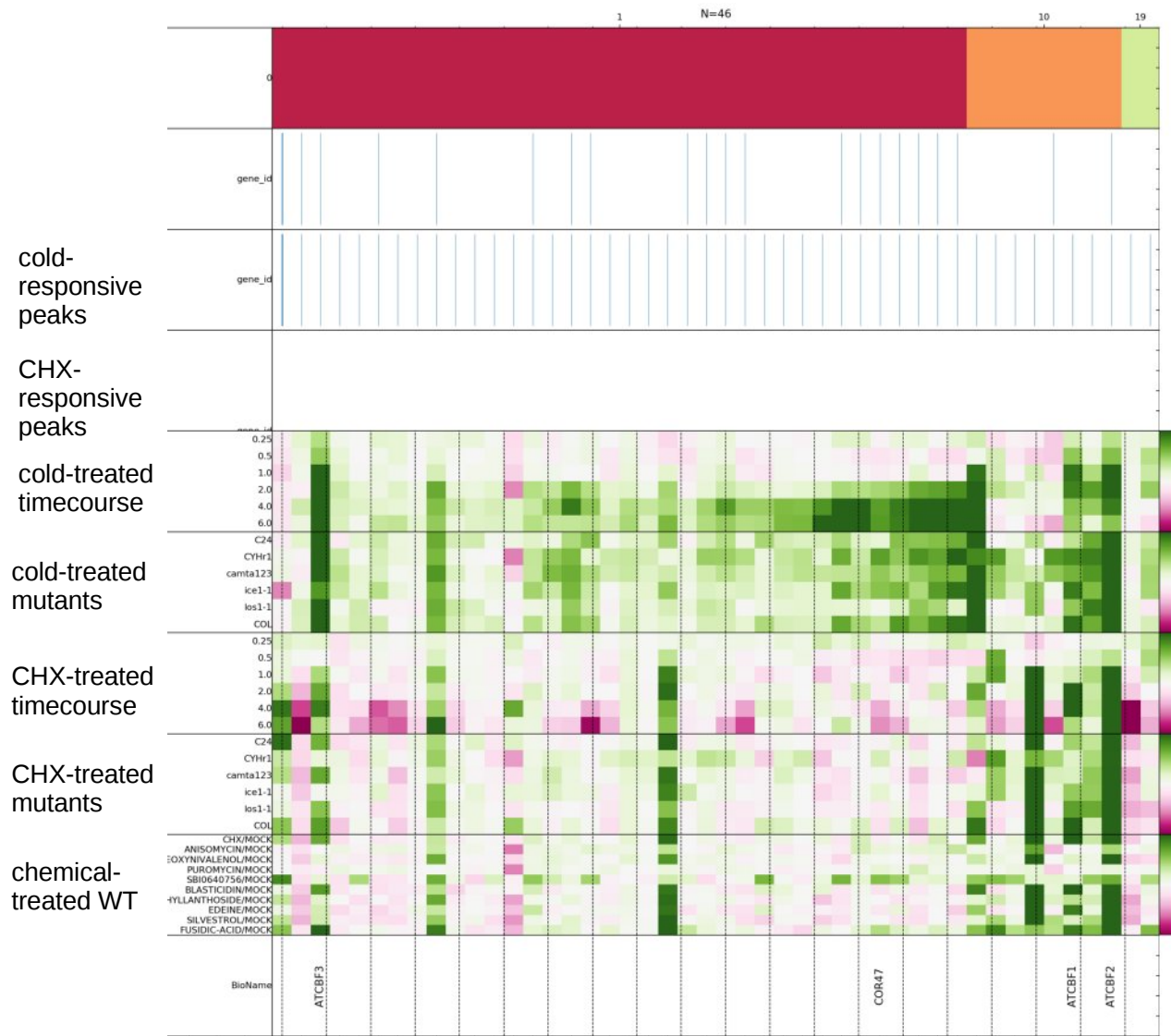


- CHX induces an early response (1.0hr onwards)
- This response is early but transient in cold treatment



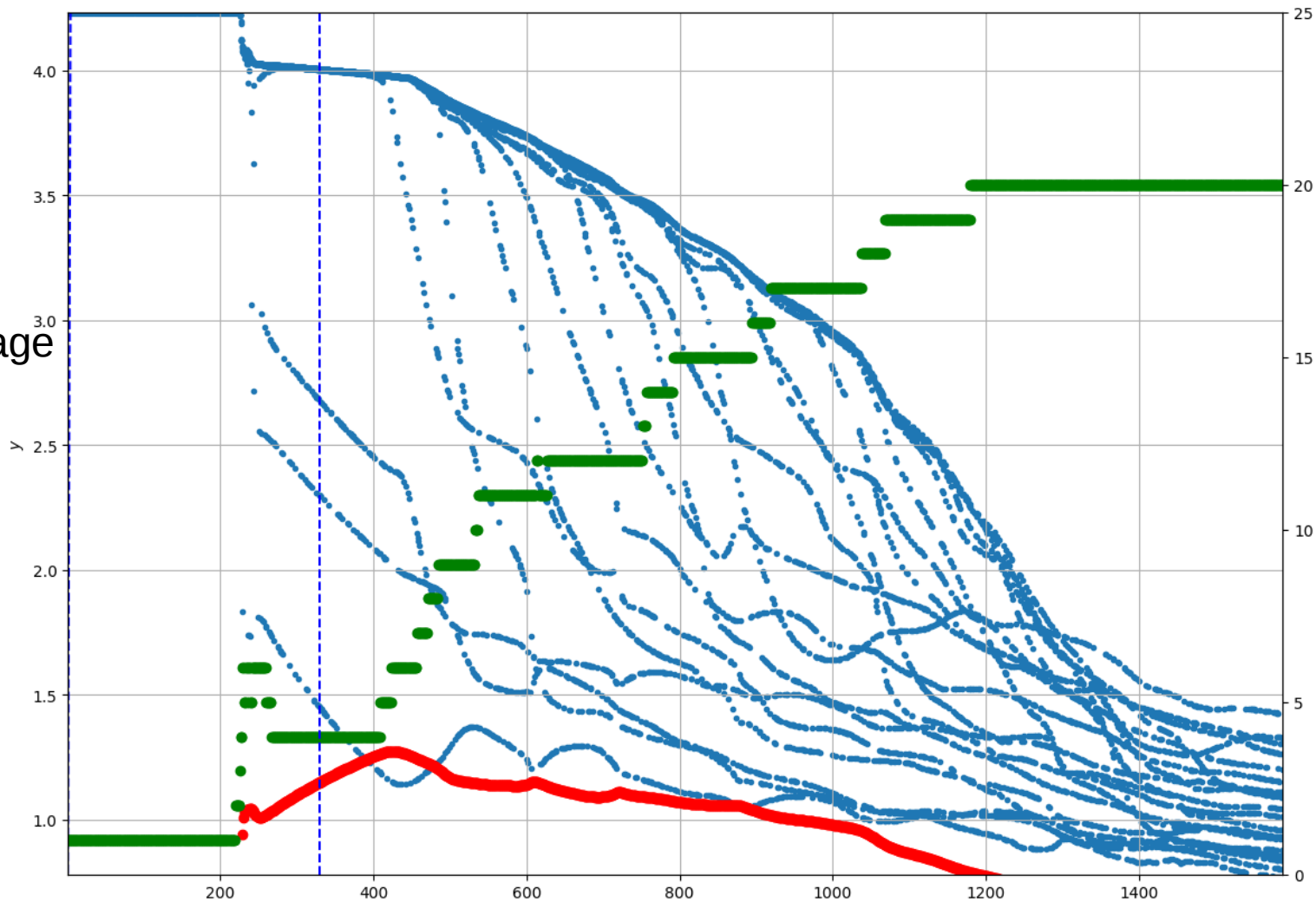


- A closer look at the CHX target
- CYHr1-1.0hr, ANISOMYCIN-1.0hr PUROMYCIN-1.0hr shows a reduced response
- GO term: response to organonitrogen compound



- A closer look at the cold targets
- *los1-1\_\_1.0hr* shows a reduced response
- Go-term: response to cold, cold acclimation

(blue):Average  
entropy of a  
cluster



(green):  
number of  
active  
cluster

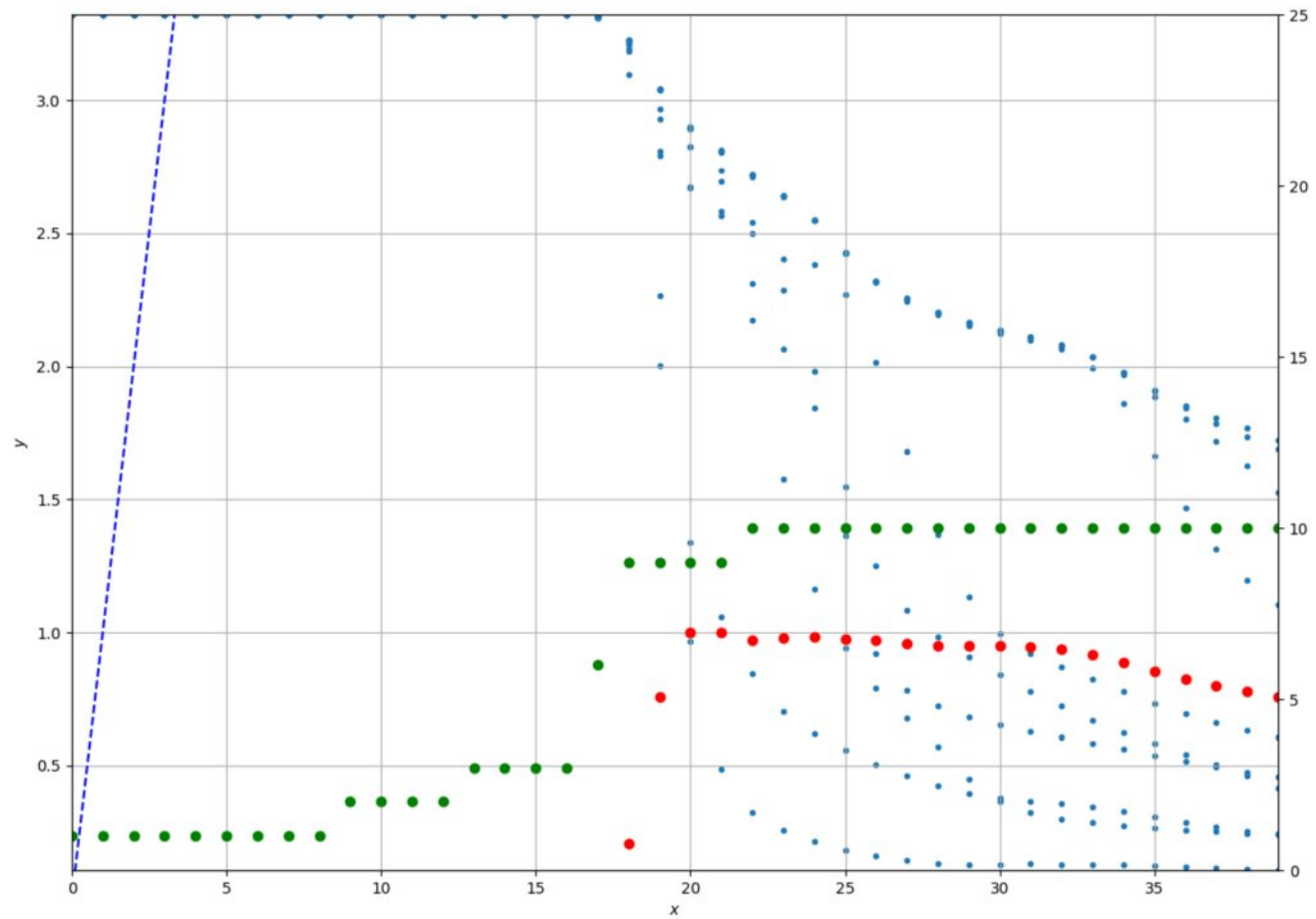
Concentration of component distributions

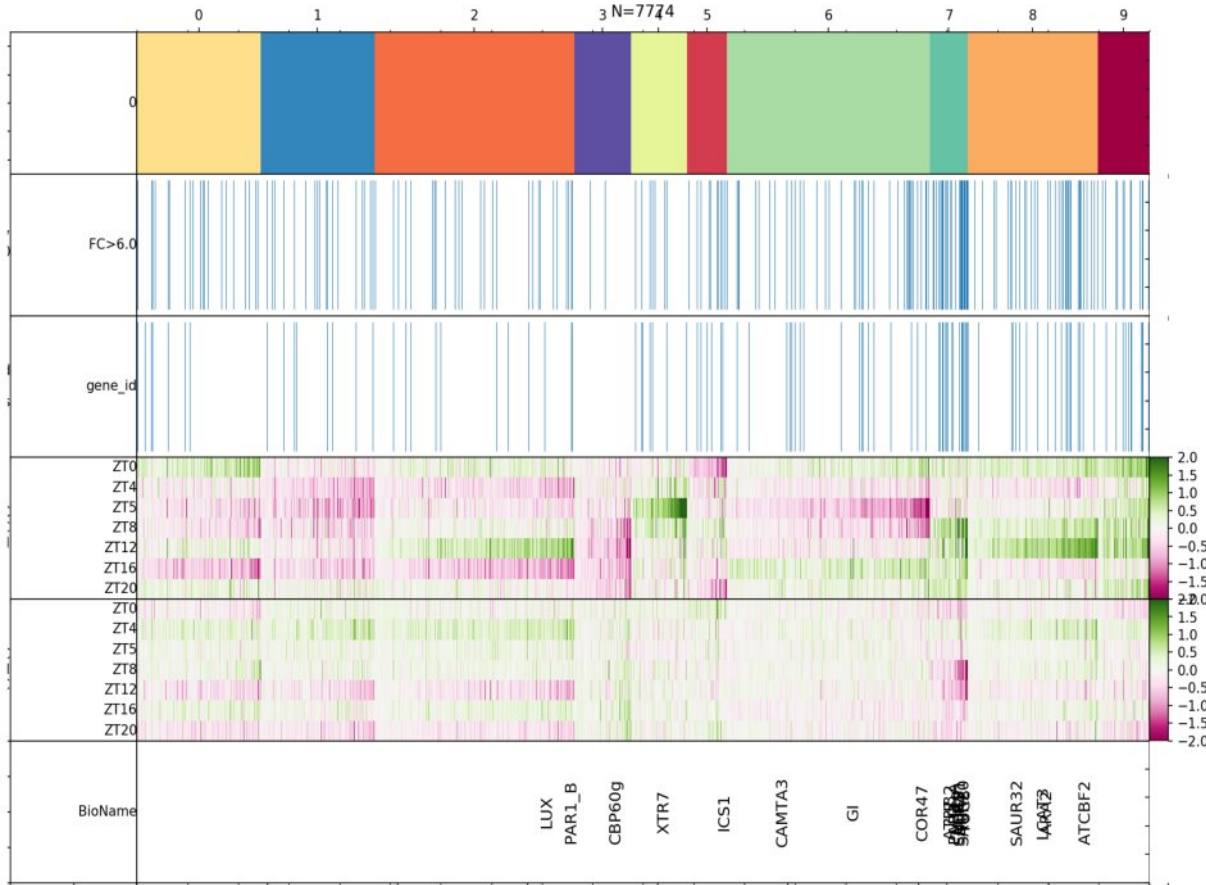


# Meta analysis of transcriptome data

- Species: *Arabidopsis thaliana*
- 558 in-house mapped transcriptomes (test set)
- 770 external transcriptomes from ArrayExpress (training set)







- Expectation maximisation specifies a deterministic dynamics on the responsibility matrix (that specifies cluster-assignment)
- Possible to feed random-subset of full data.
- Information can be extracted from cluster-average entropy. Potentially useful for quality control.
- Highly confident cluster should remain highly confident if the clustering is real.