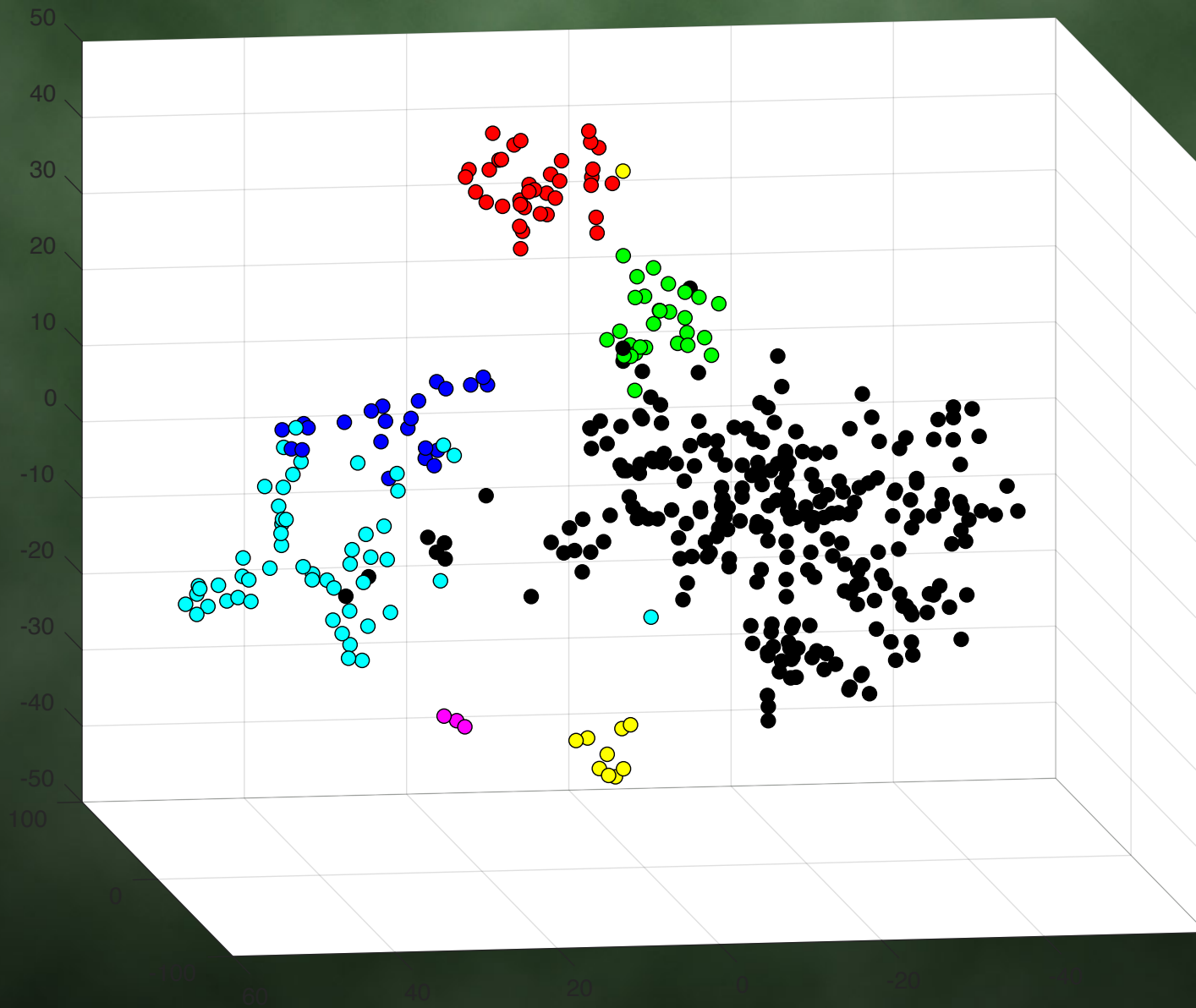
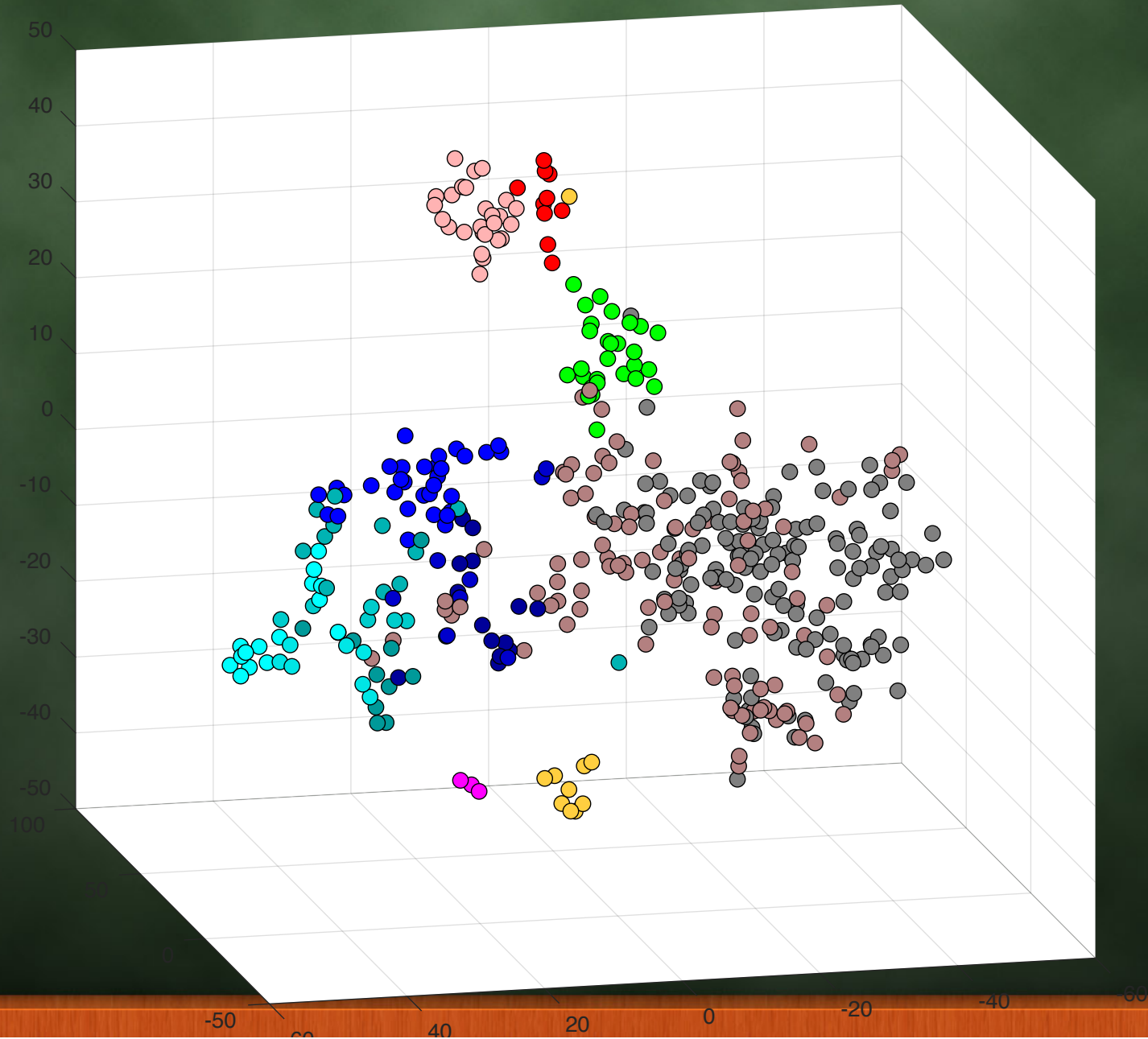


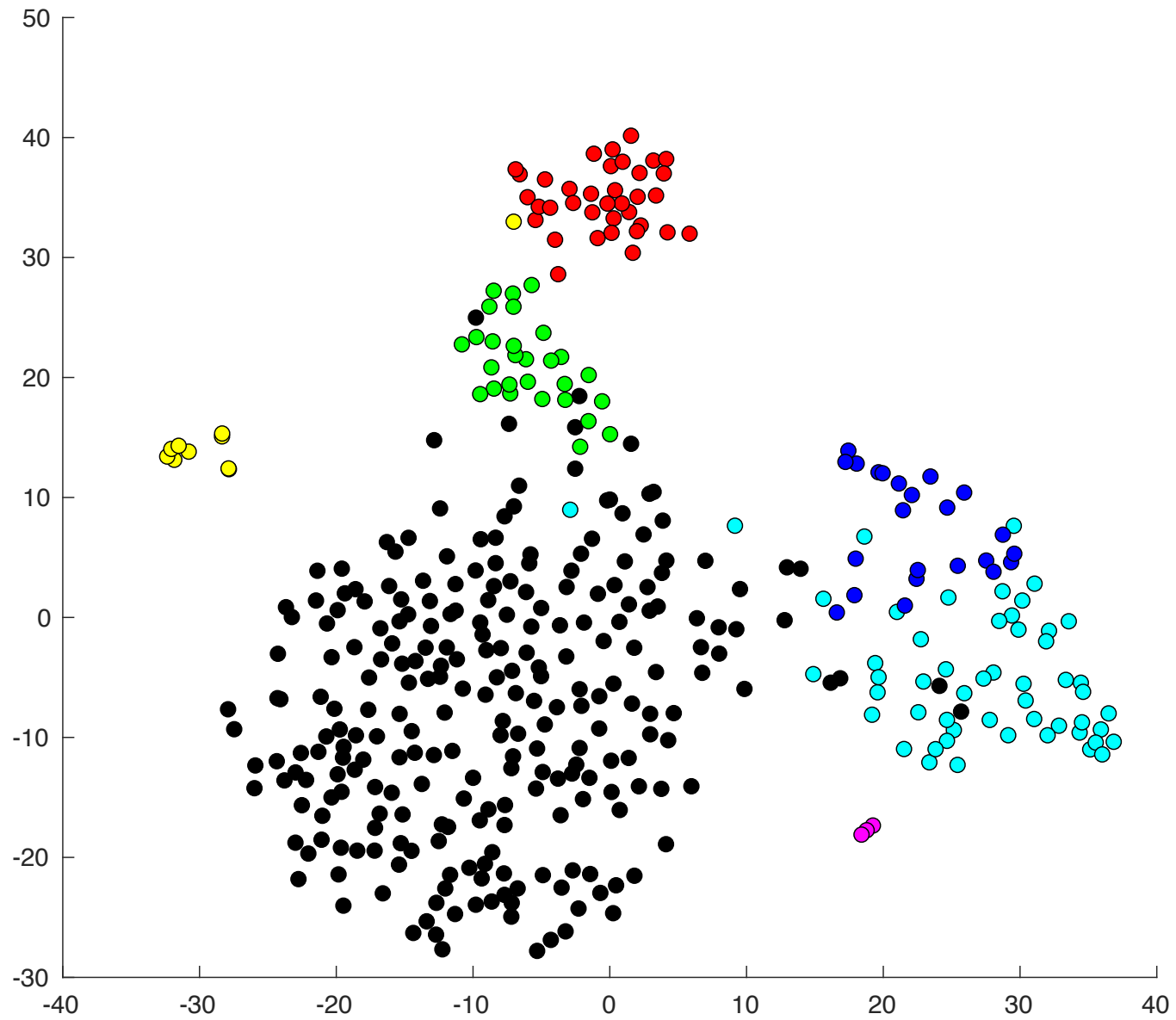
# Corrected colors



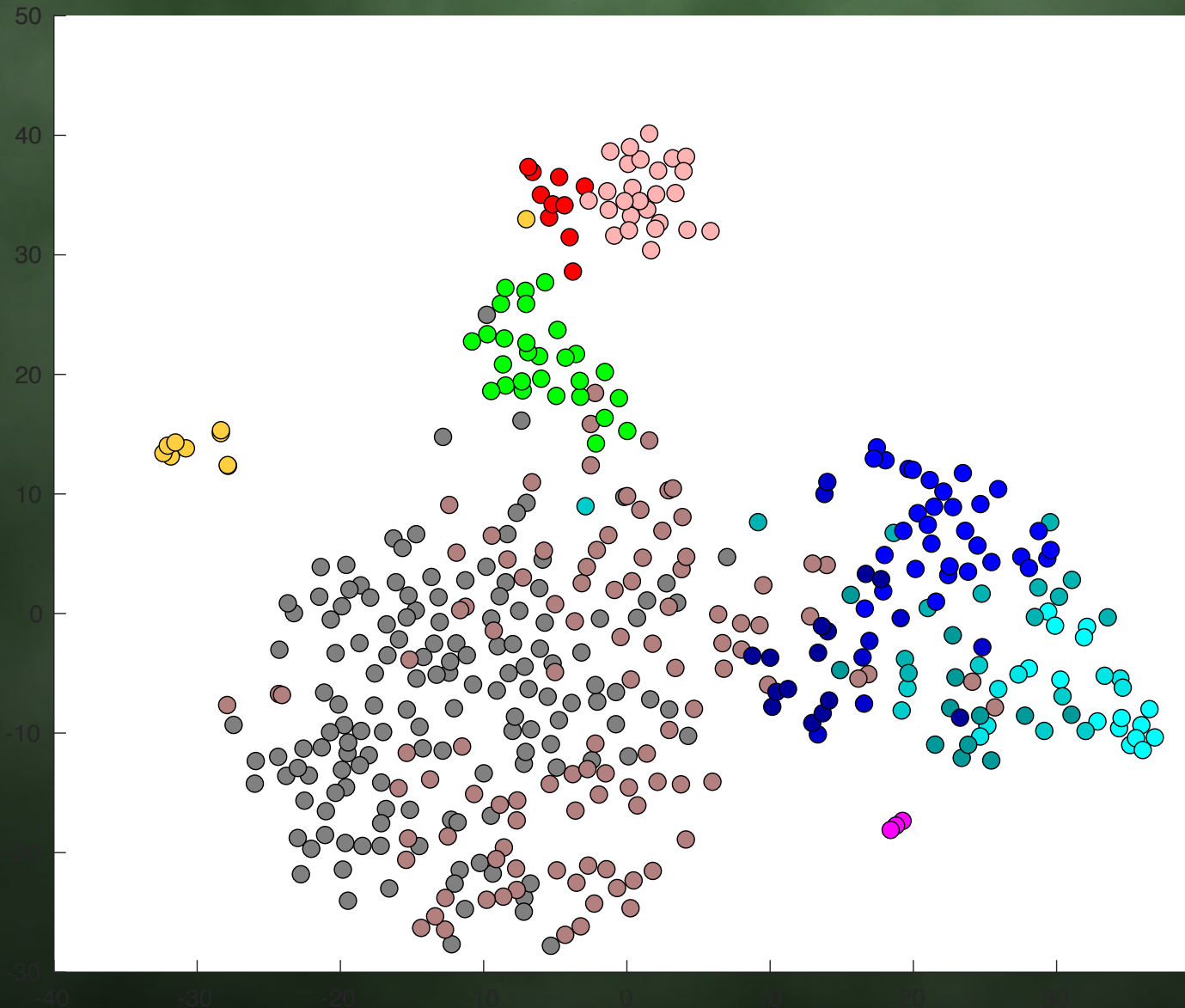
# Overannotated version



# 2D t-SNE

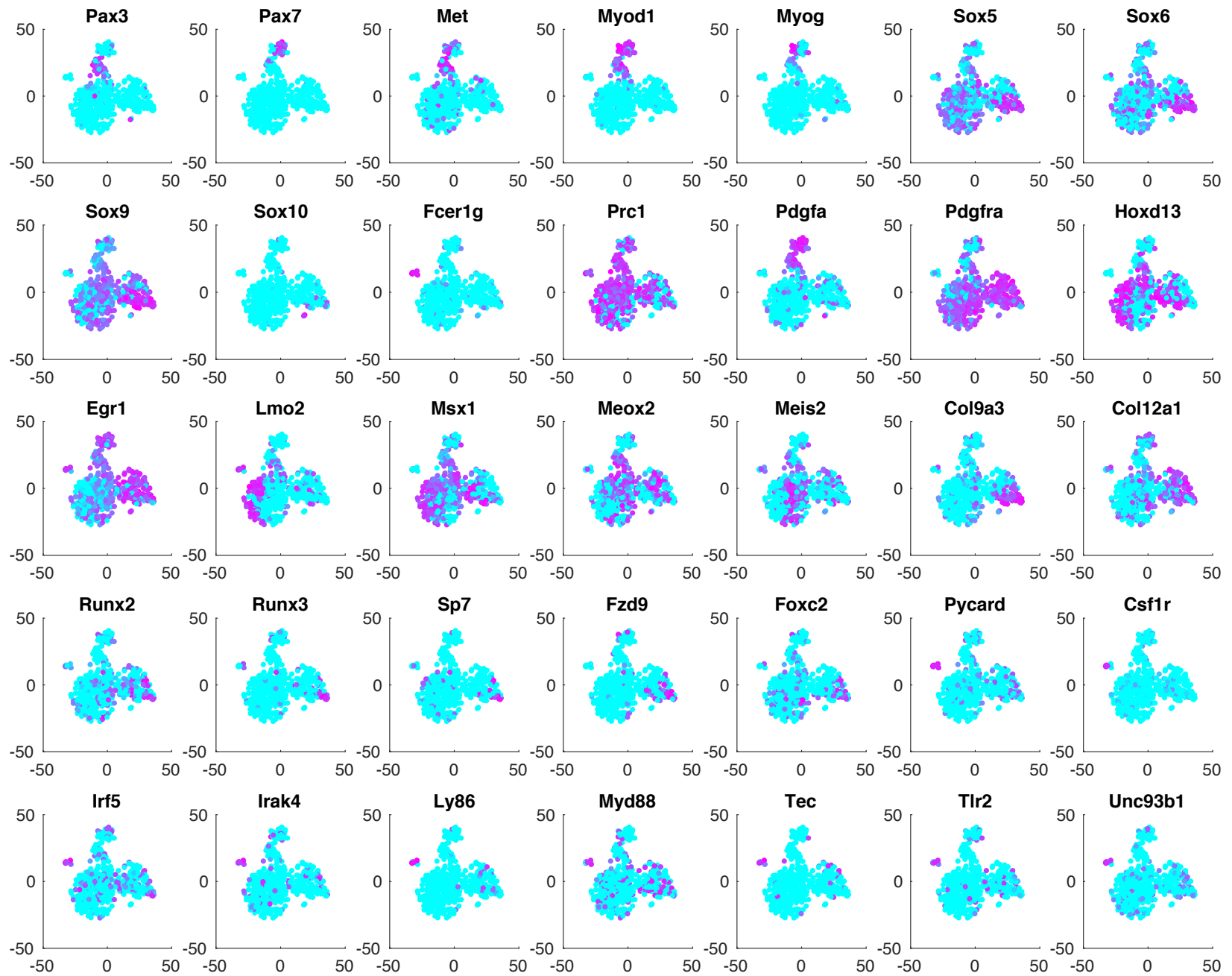


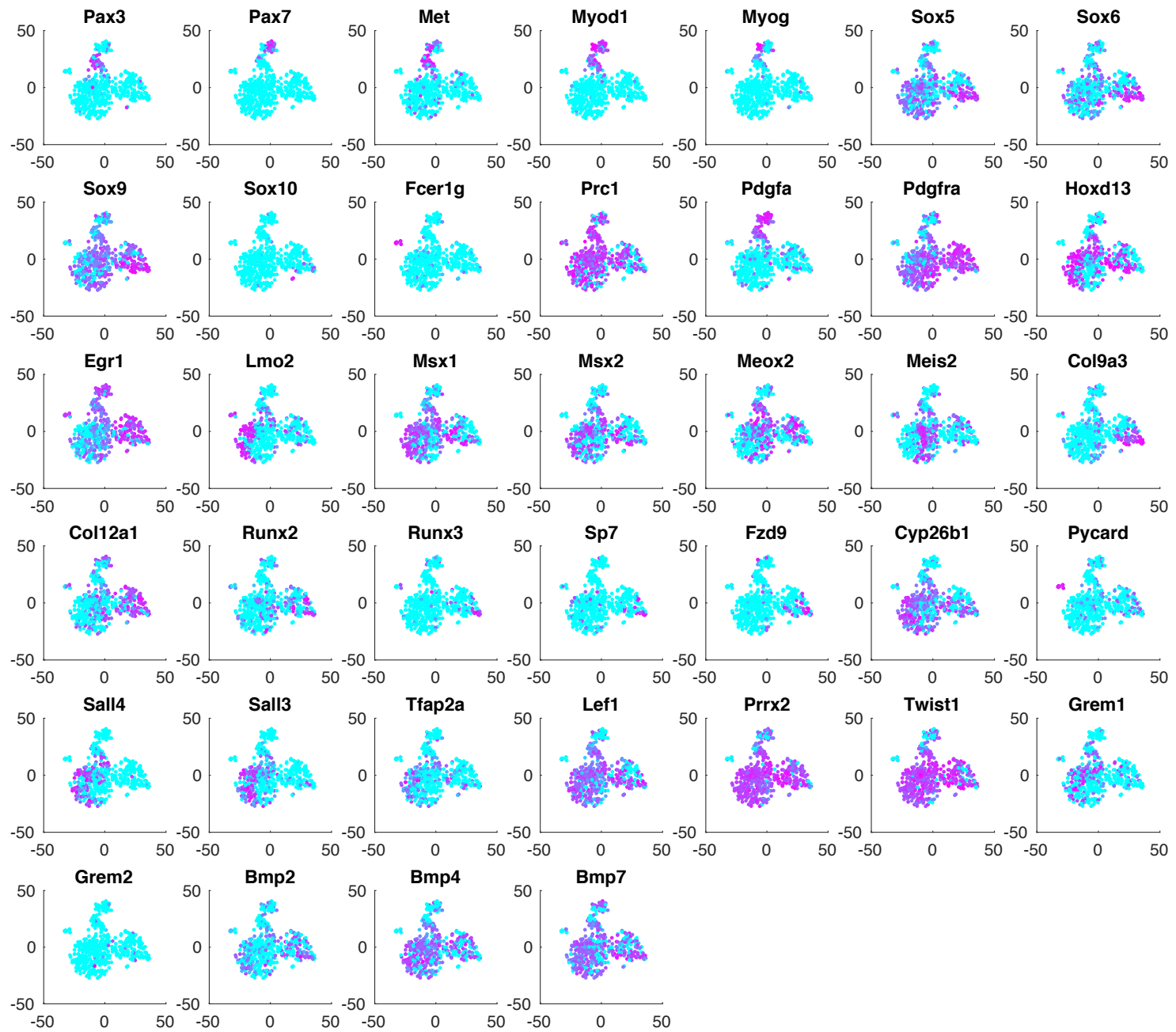
# Overannotated version



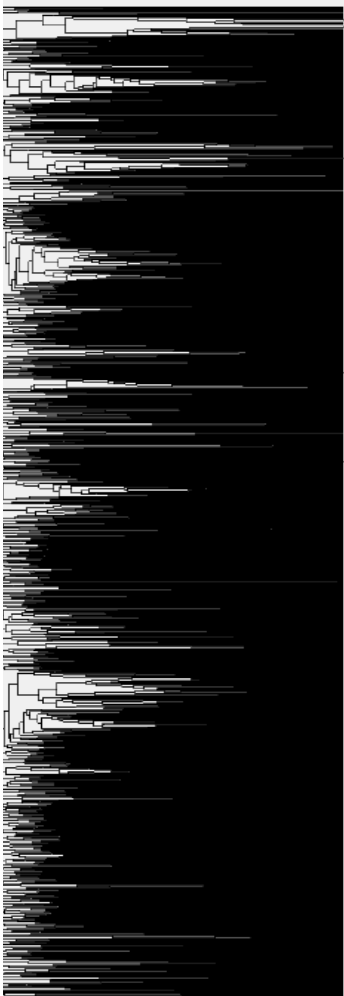
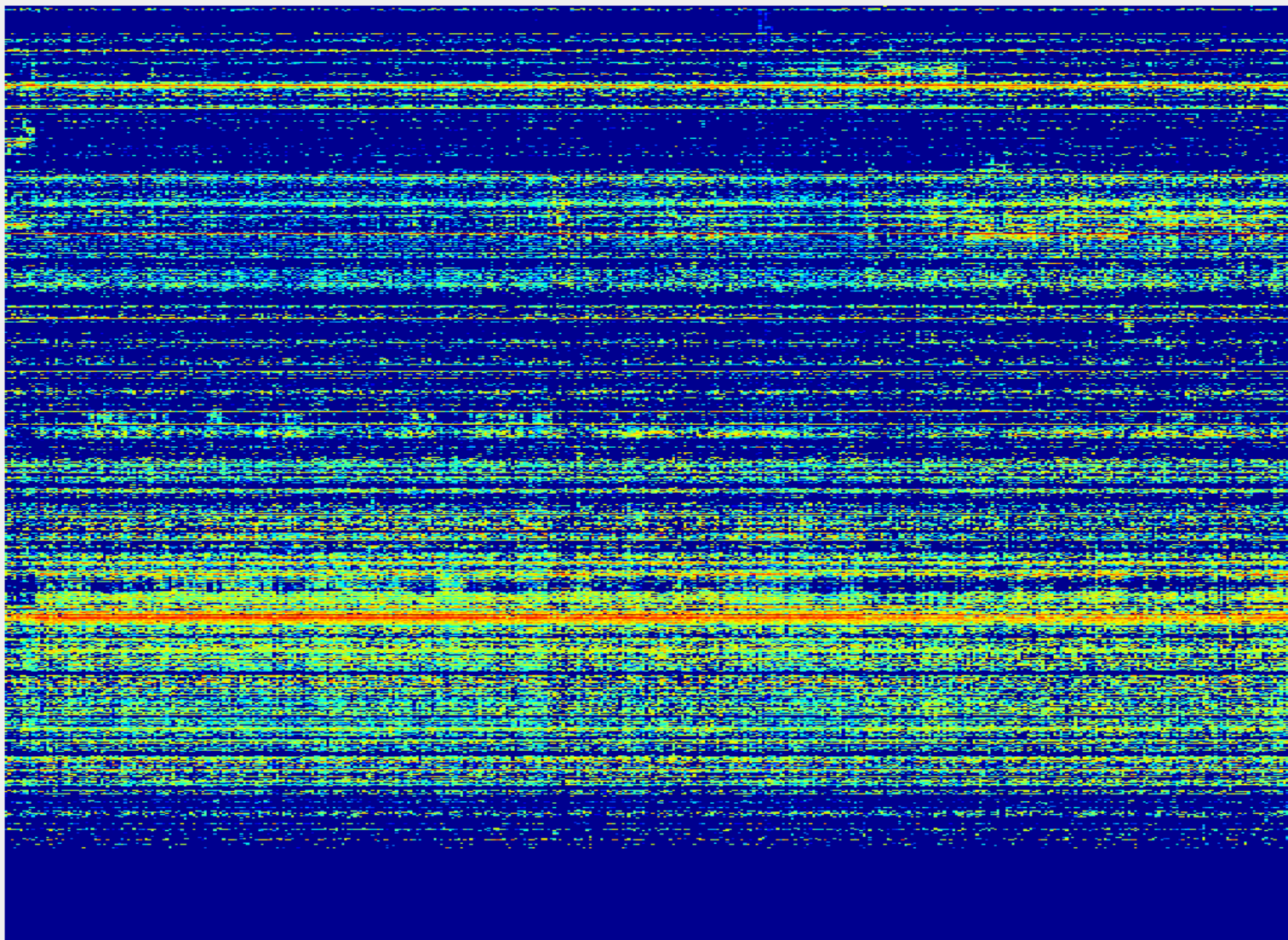
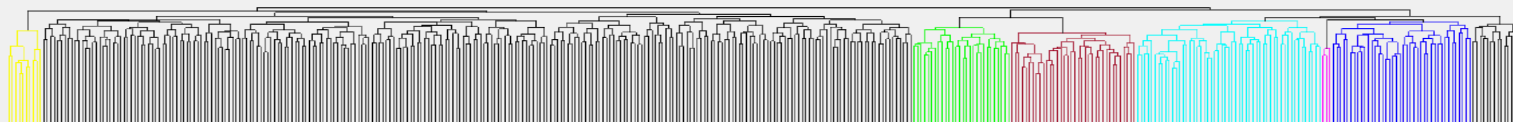


# All



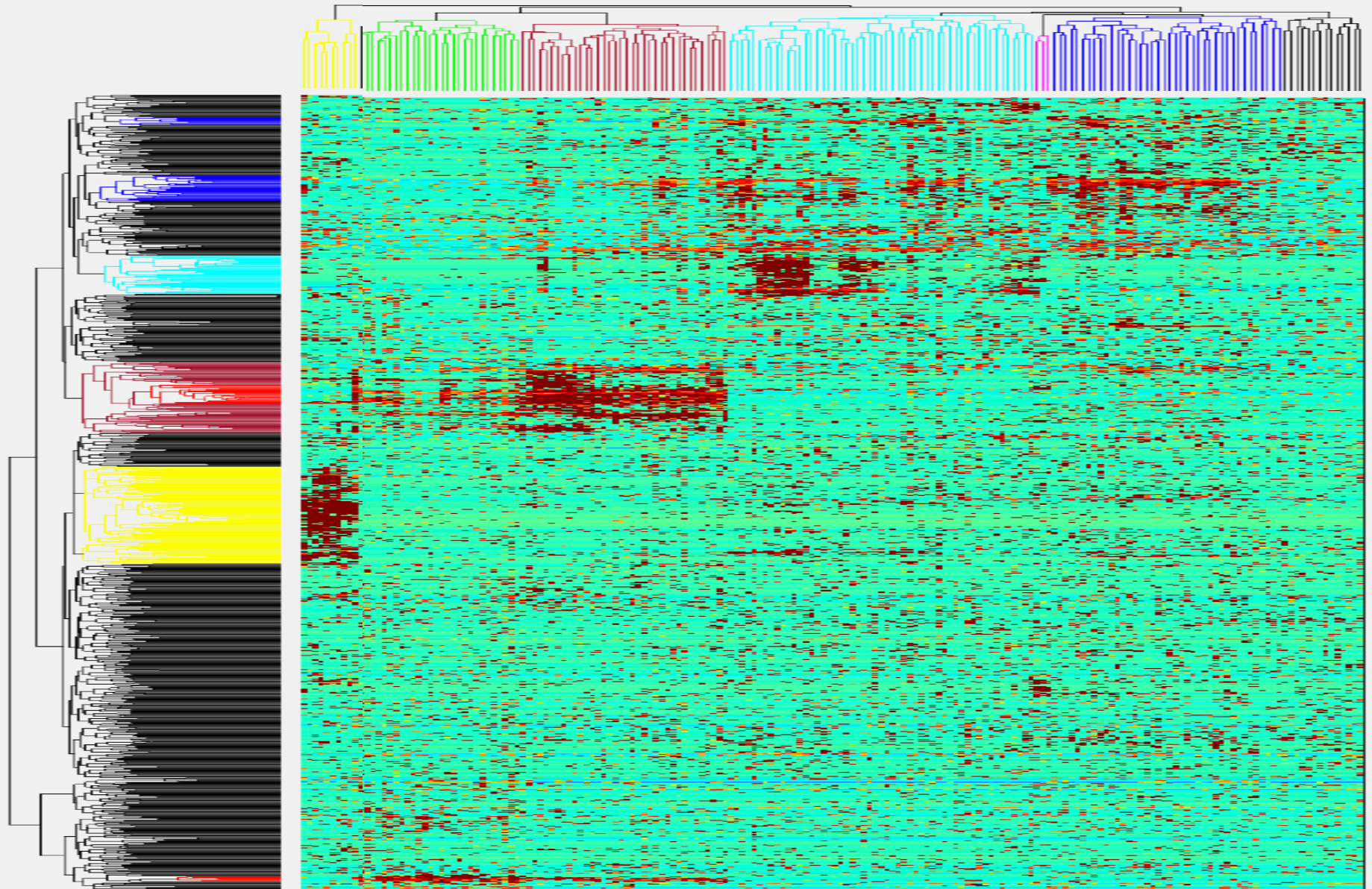


# TFs





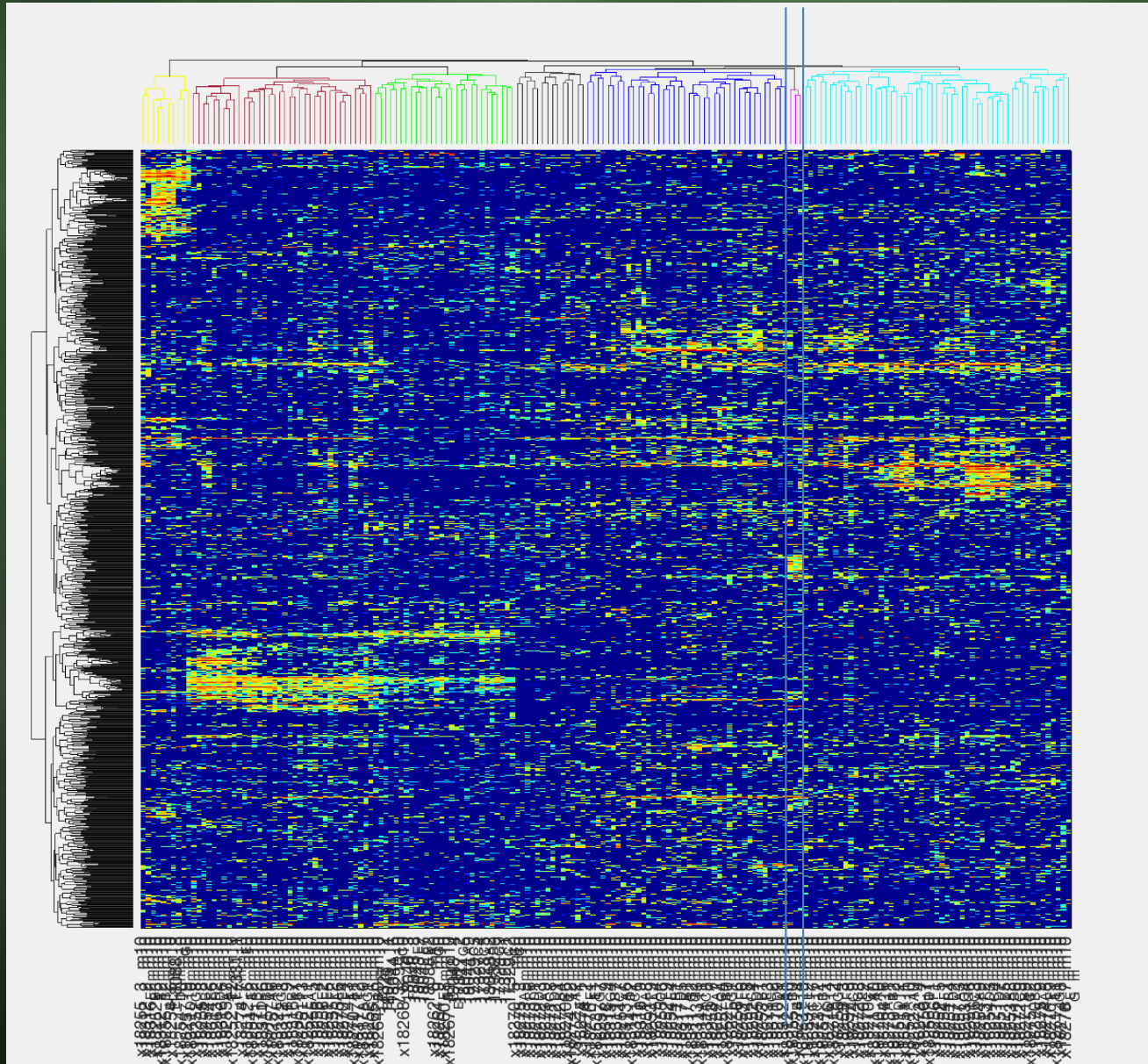
# 1037 genes – known universe (cropped)







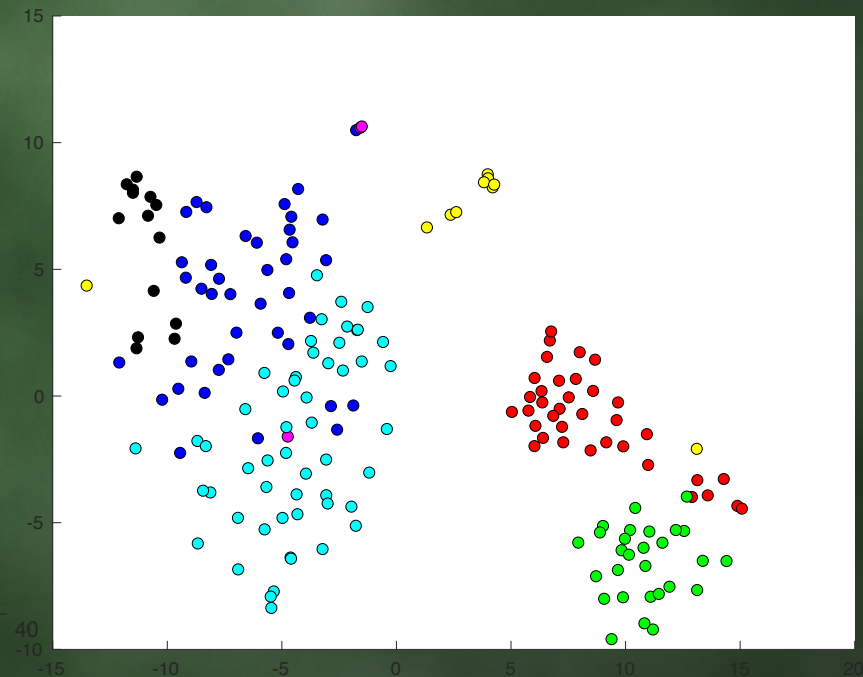
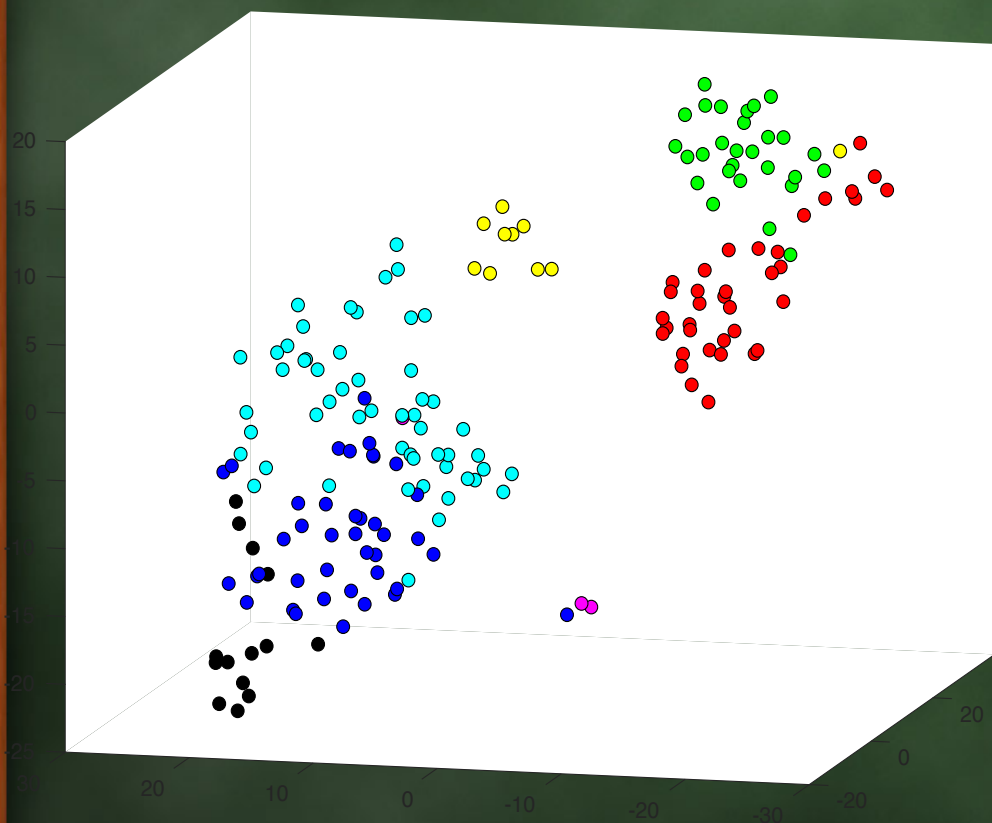
# 1037 genes – known universe (reclustered)



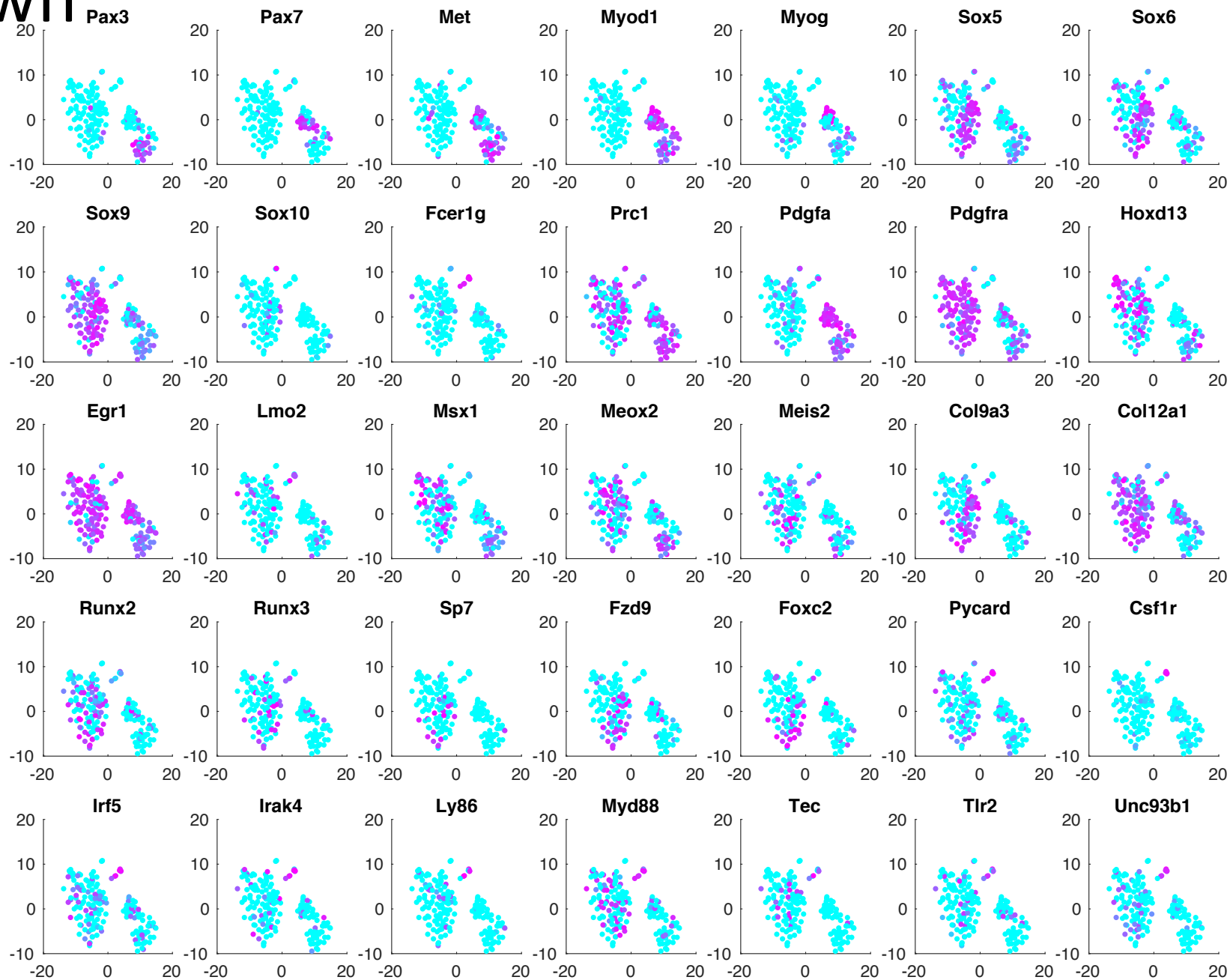




# tSNE for known universe

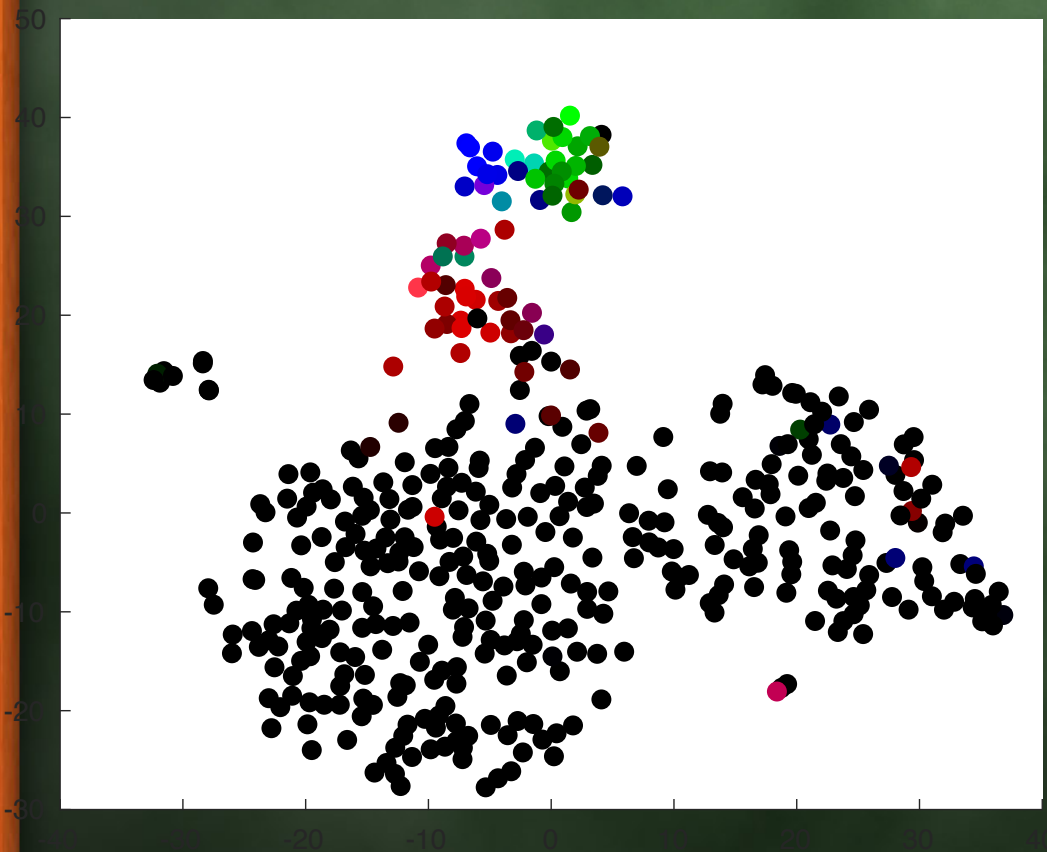


# Known

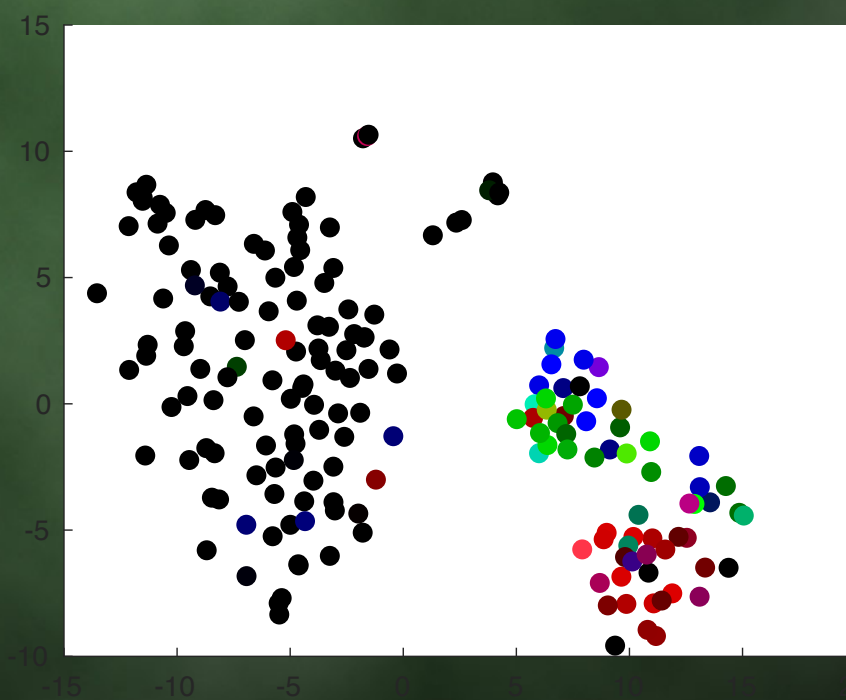


# RGB labeling of Pax3 Pax7 Myog

- Global



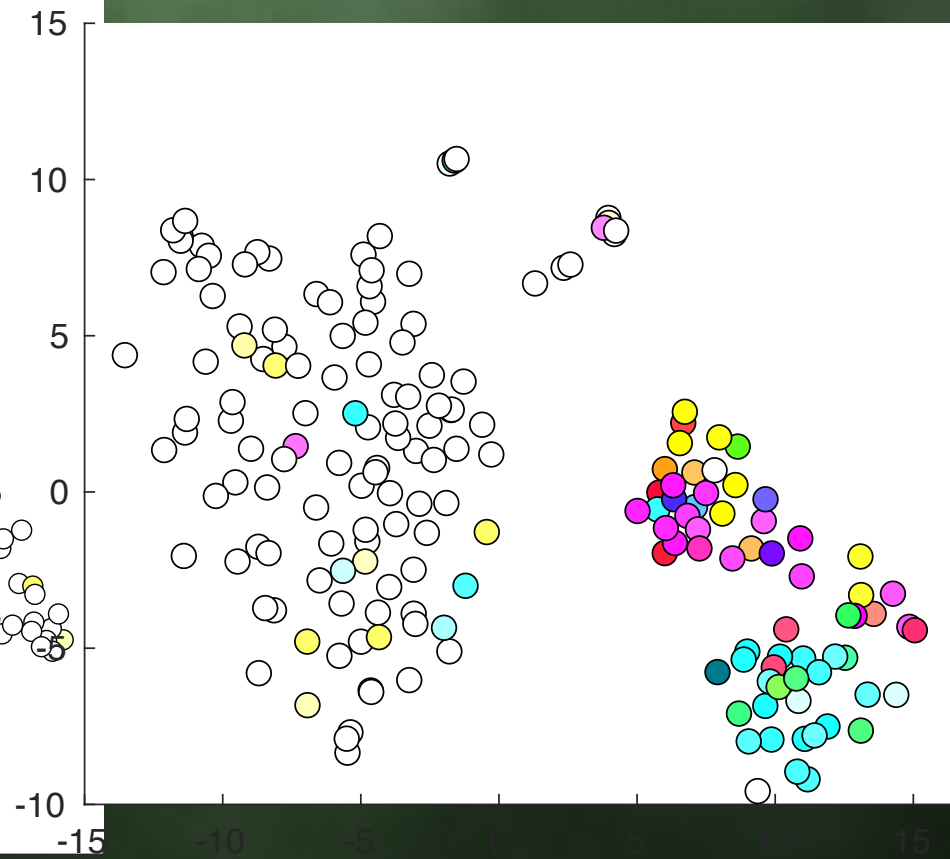
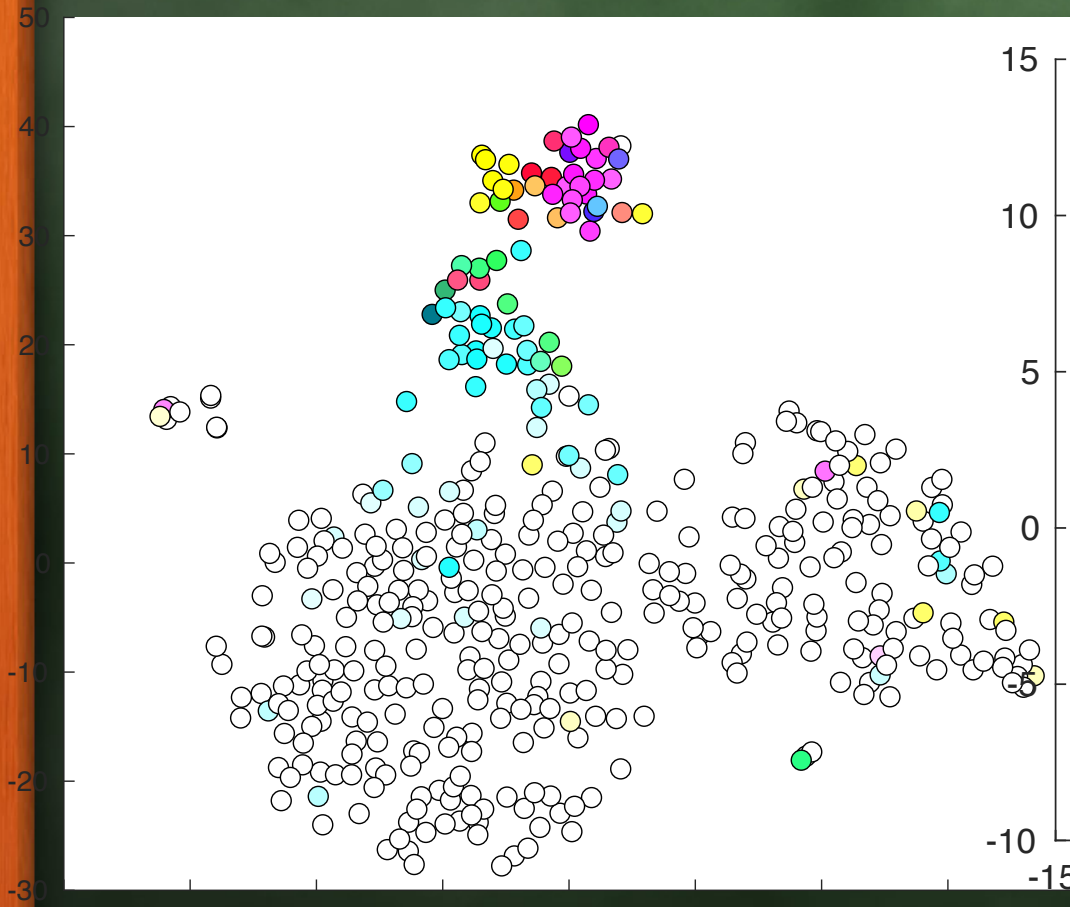
Known



# CMY labeling of Pax3 Pax7 Myog

- Global

Known

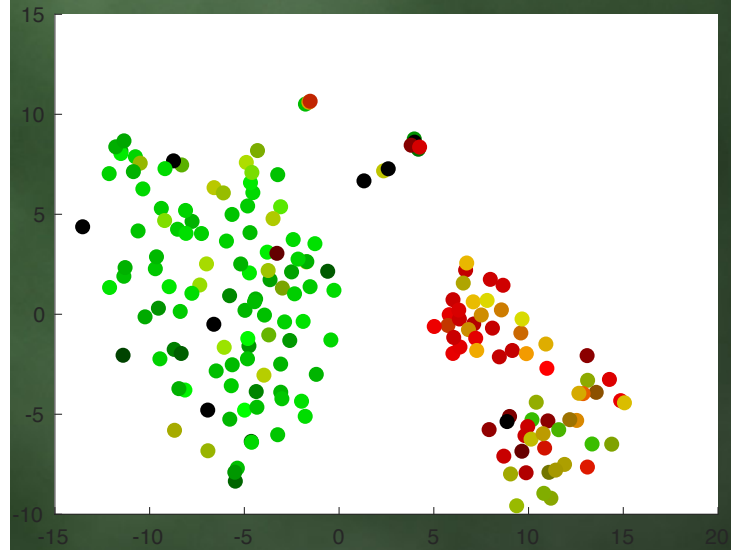
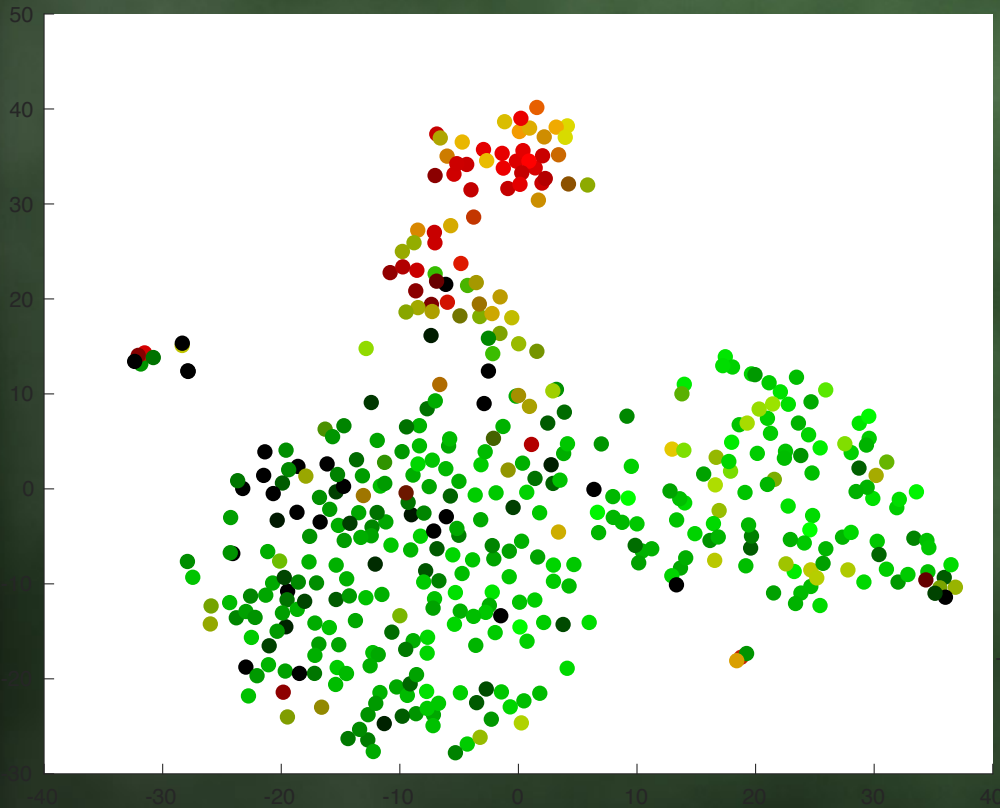




# RG labeling of Pdgfa and Pdgfra

- Global

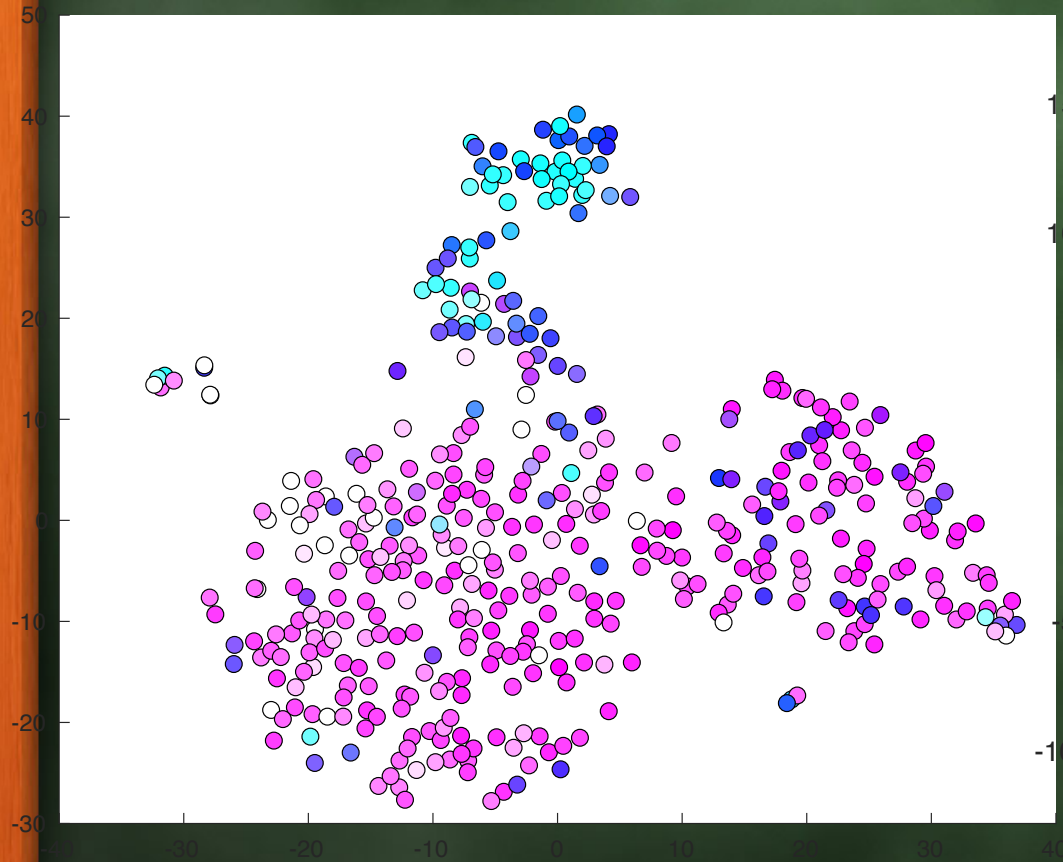
Known



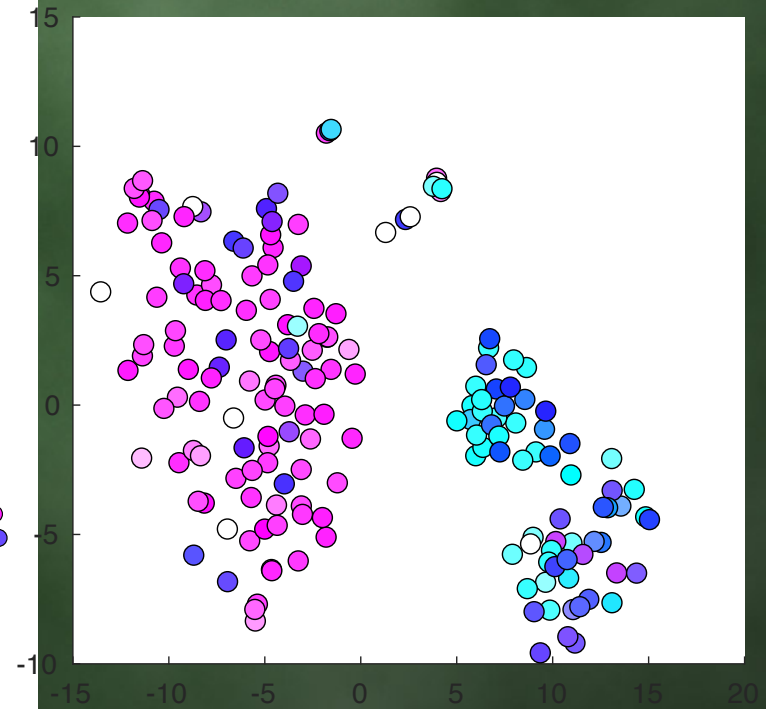


# CM labeling of Pdgfa and Pdgfra

- Global

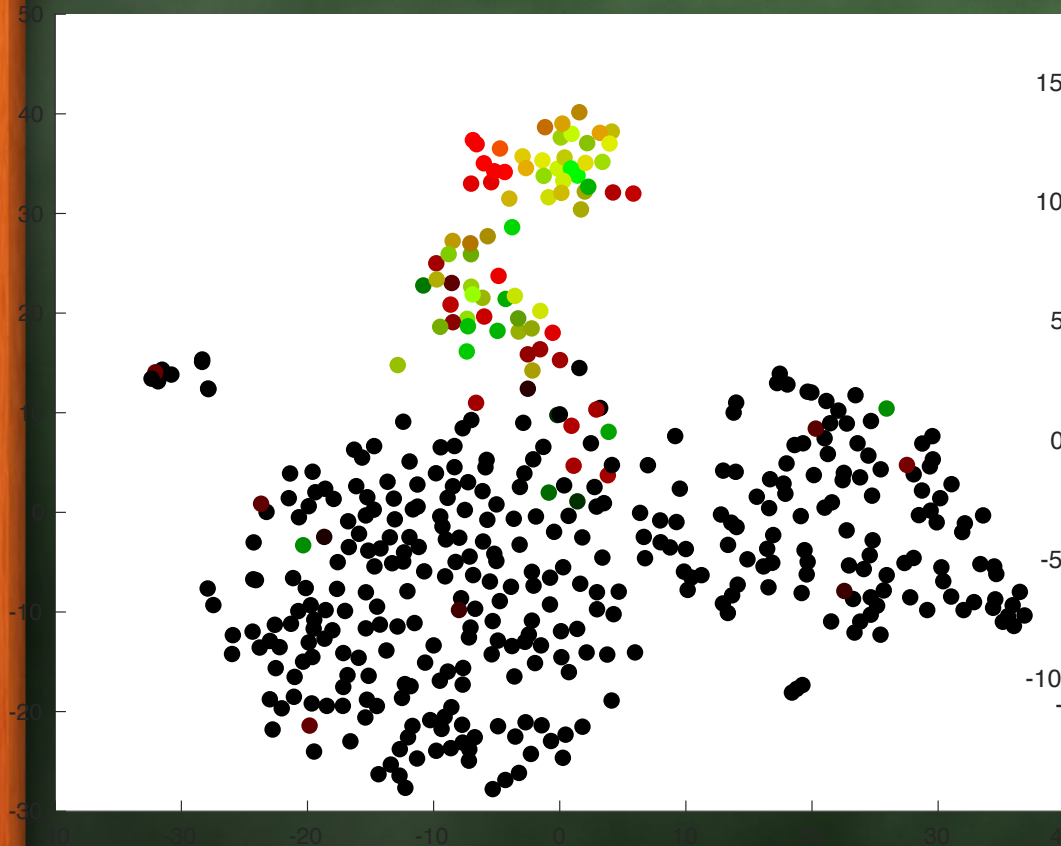


Known

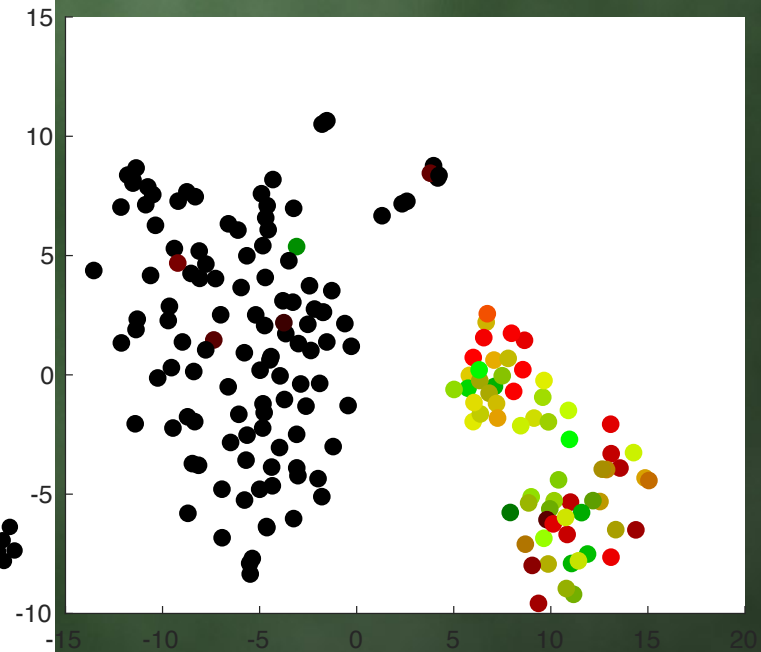


# RG labeling of Myod1 and Myf5

- Global



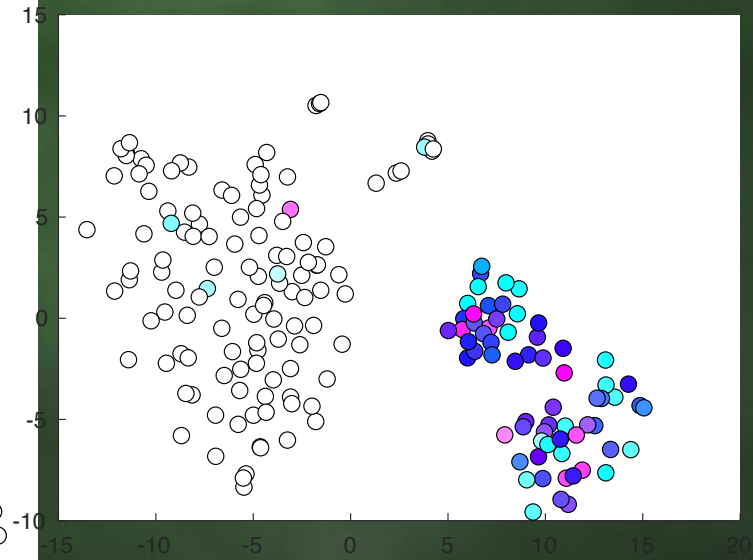
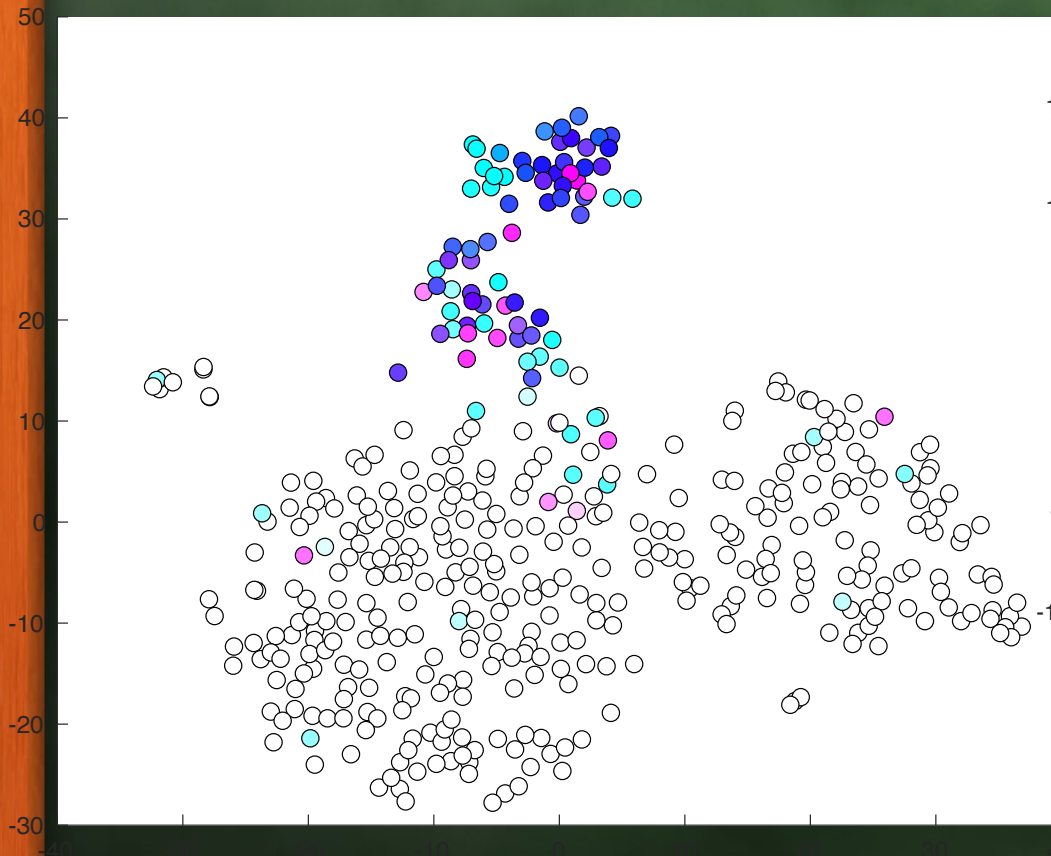
Known



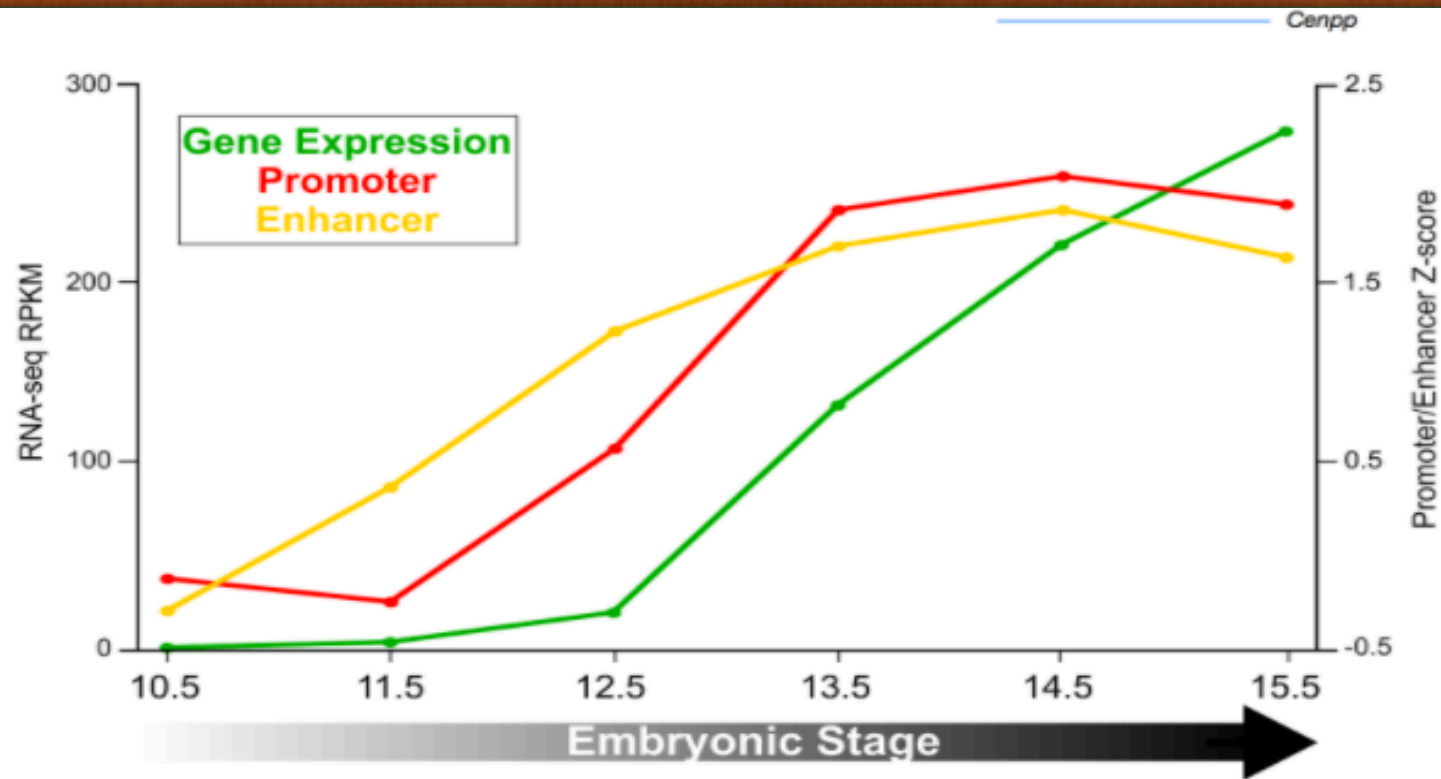
# CM labeling of Myod1 and Myf5

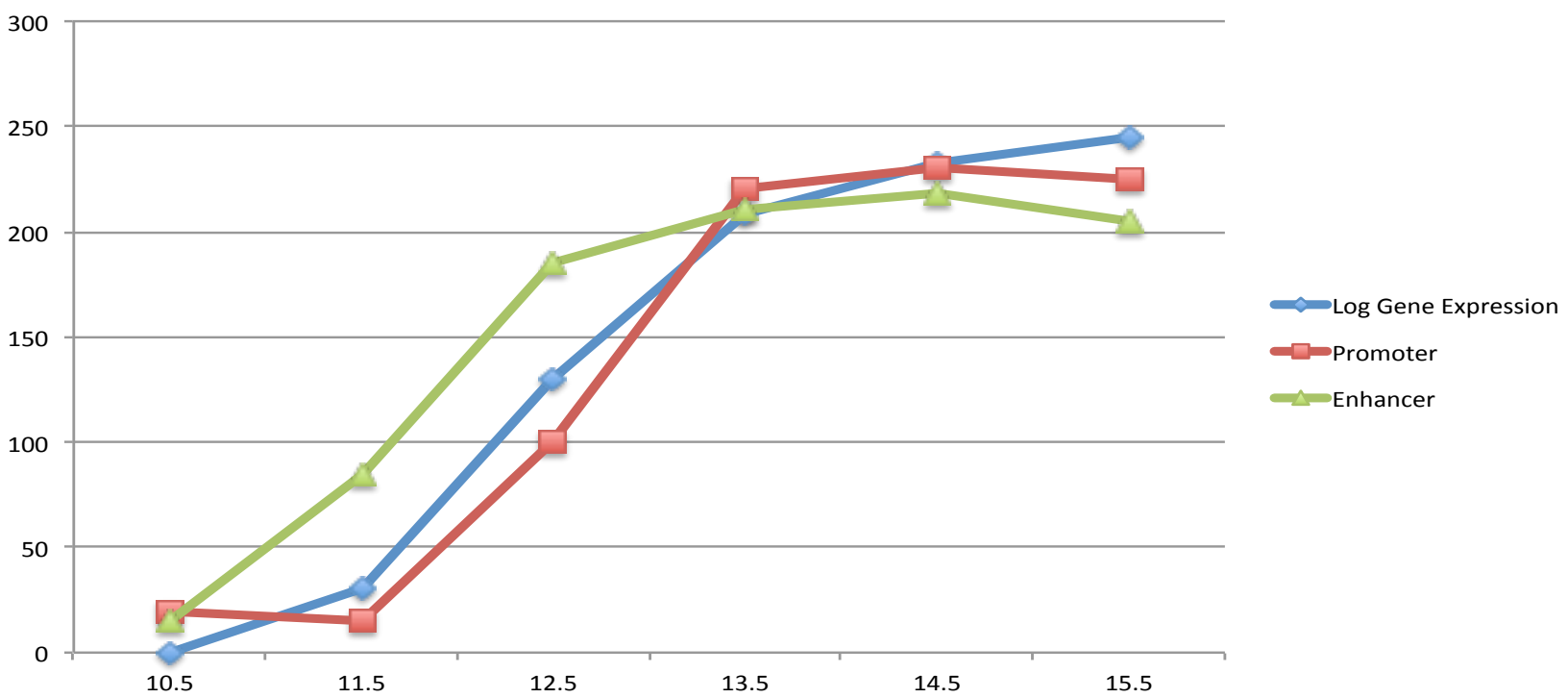
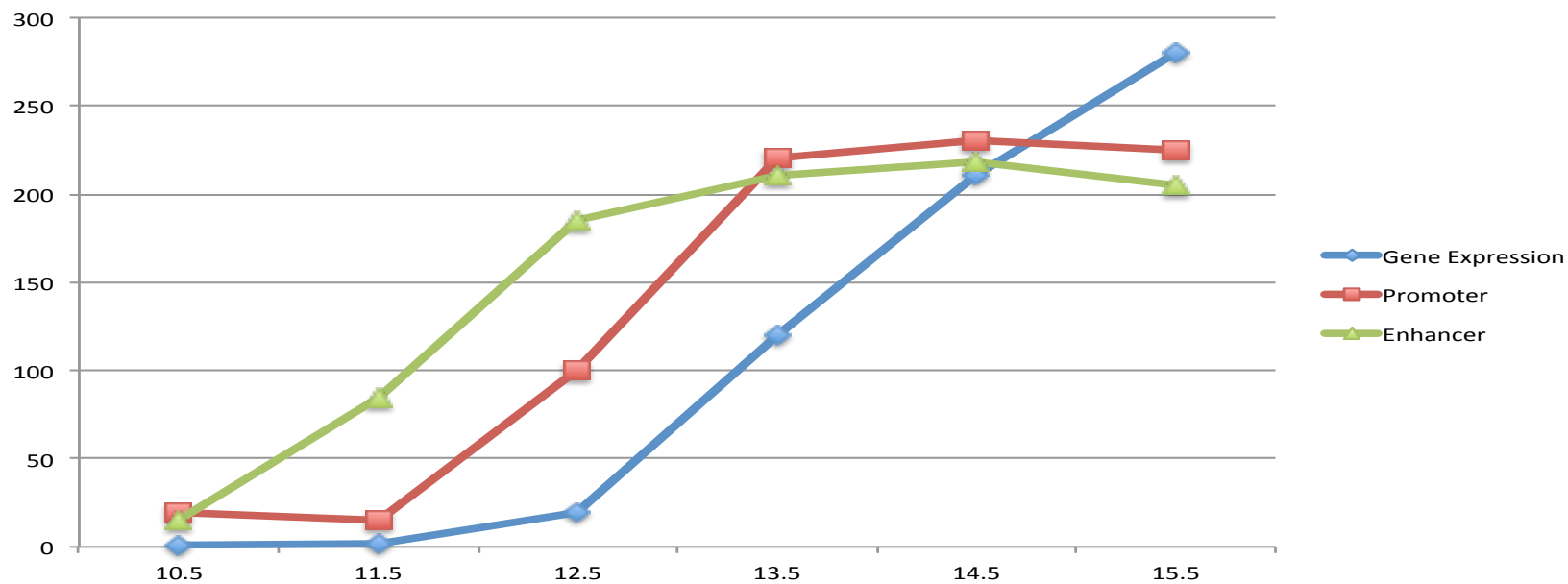
- Global

Known

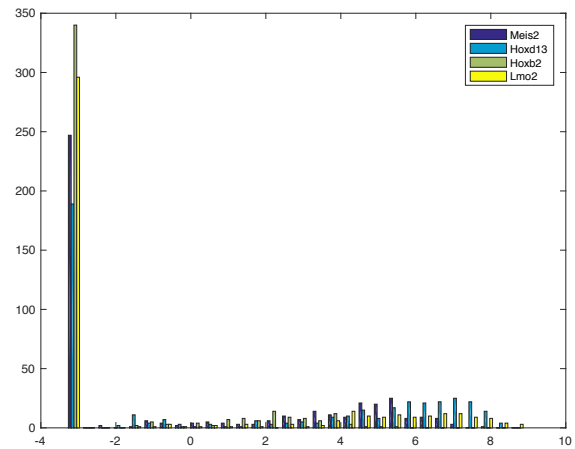
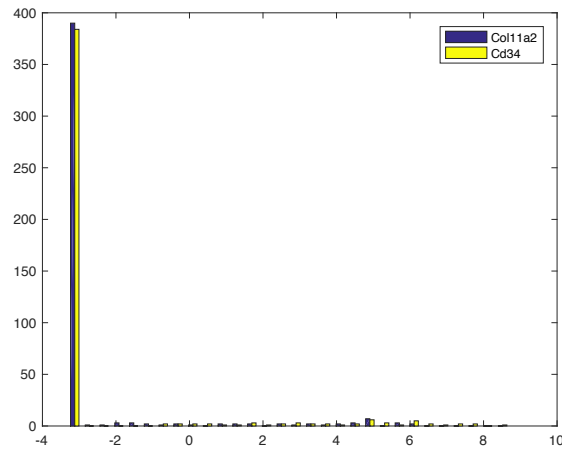
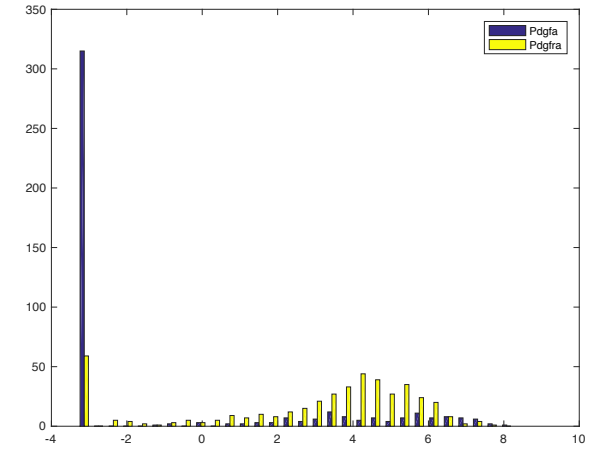
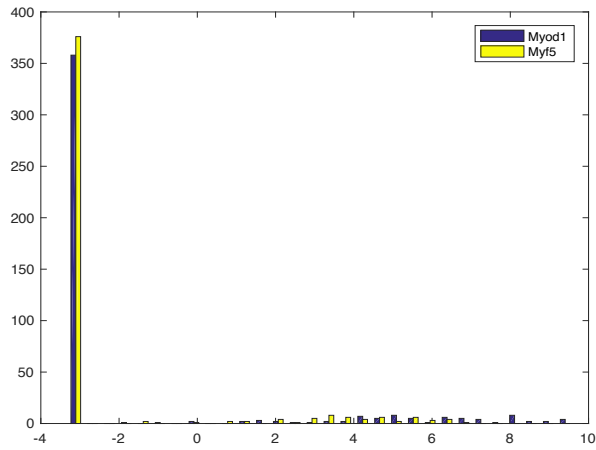
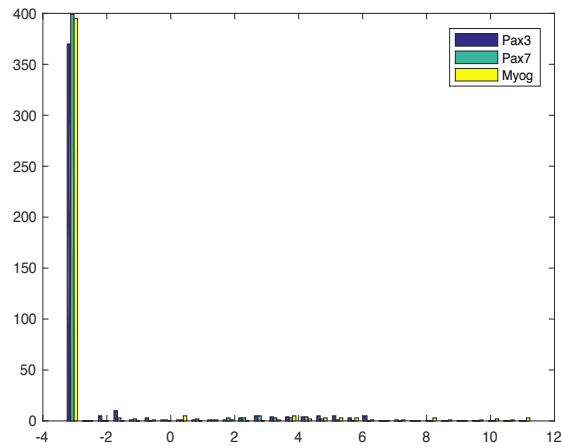


C



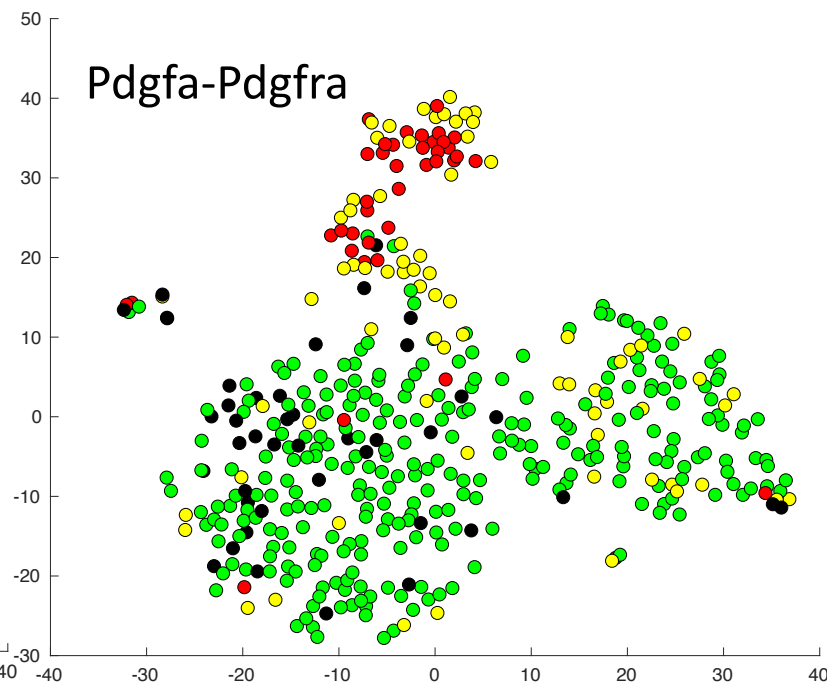
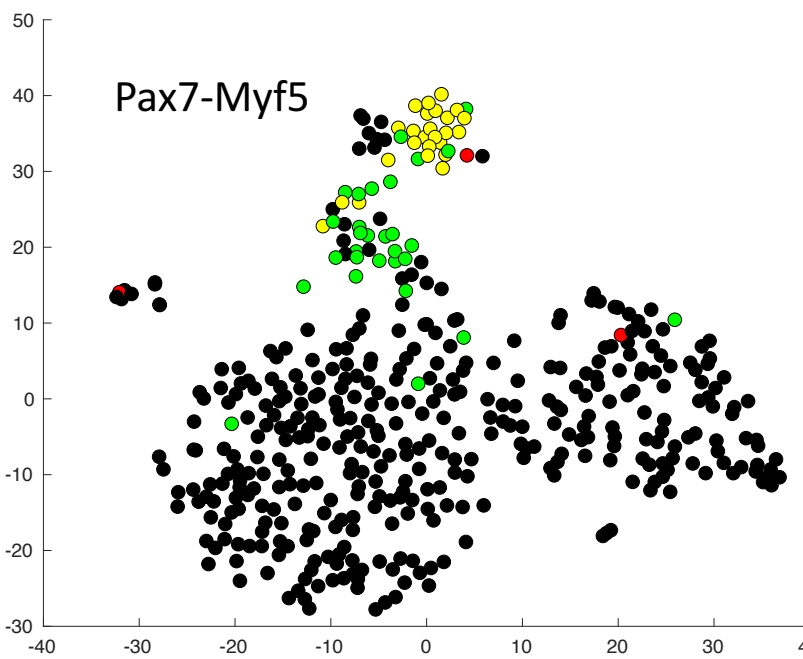
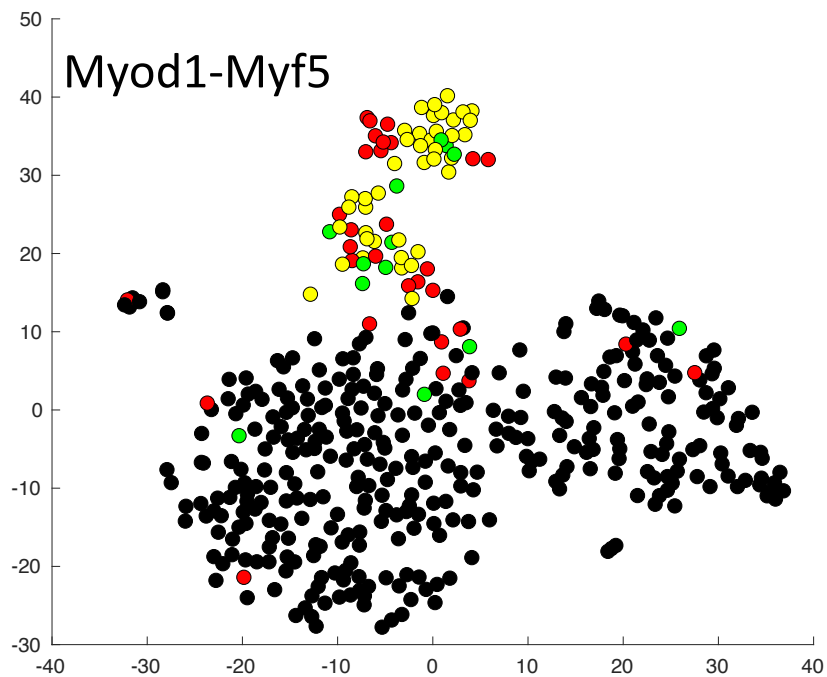
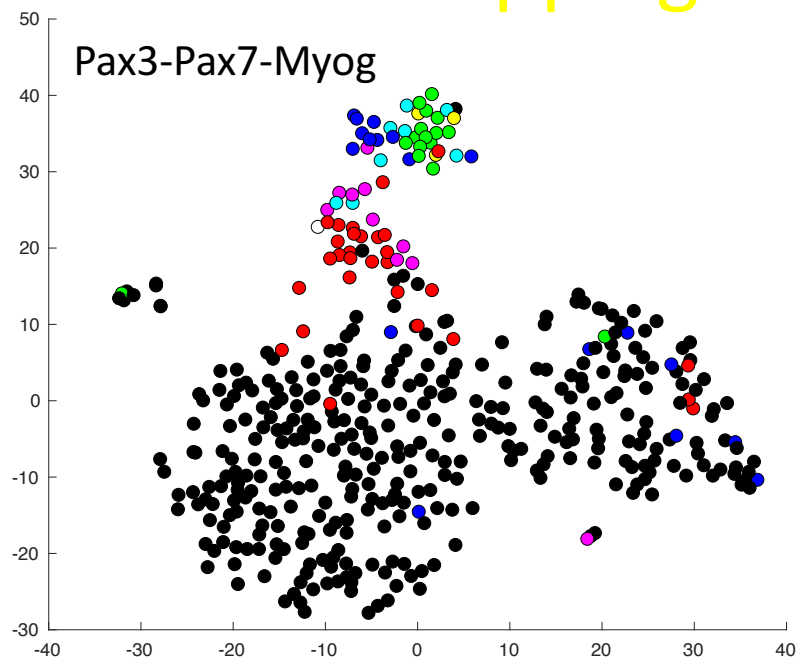


# Set FPKM > 1 as positive



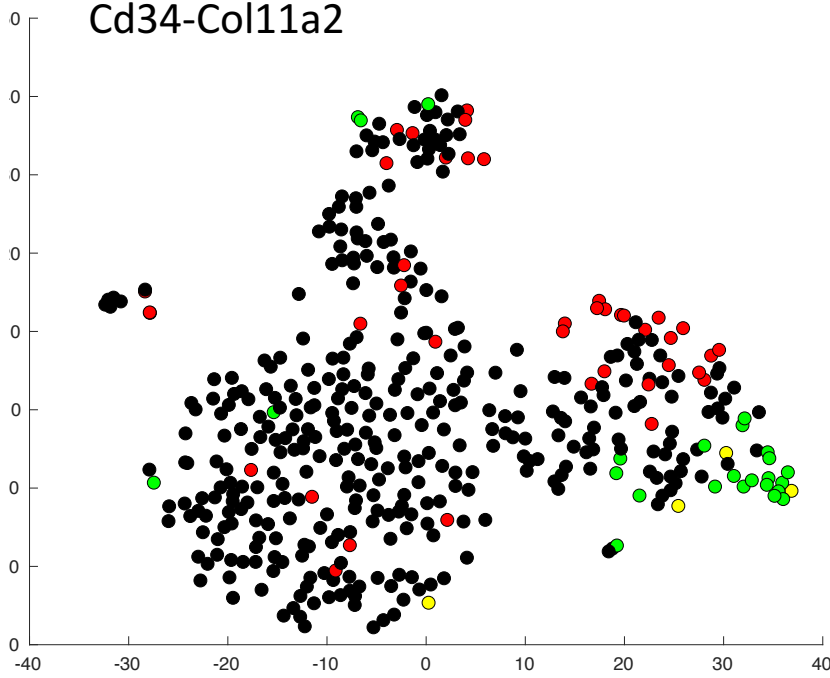


# Boolean mapping

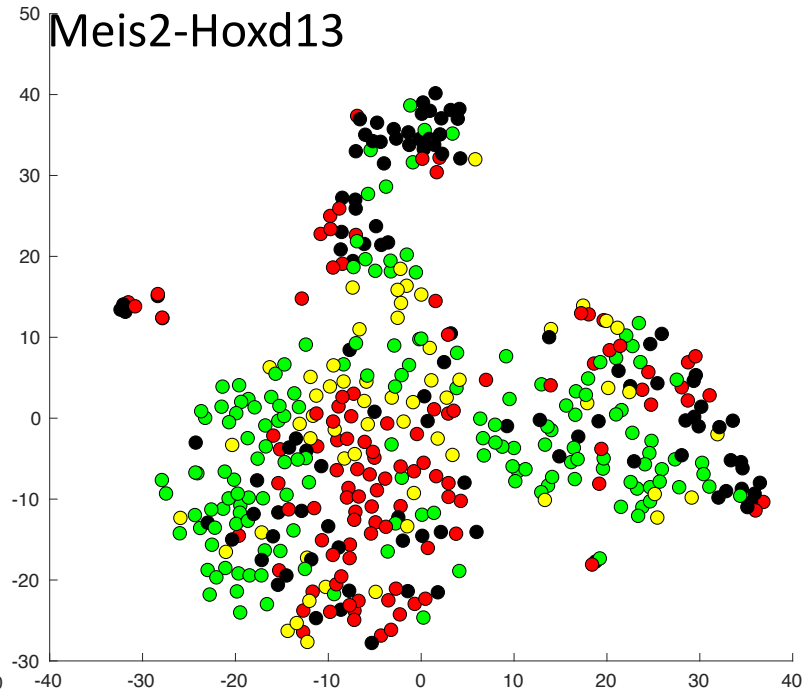


# Boolean mapping

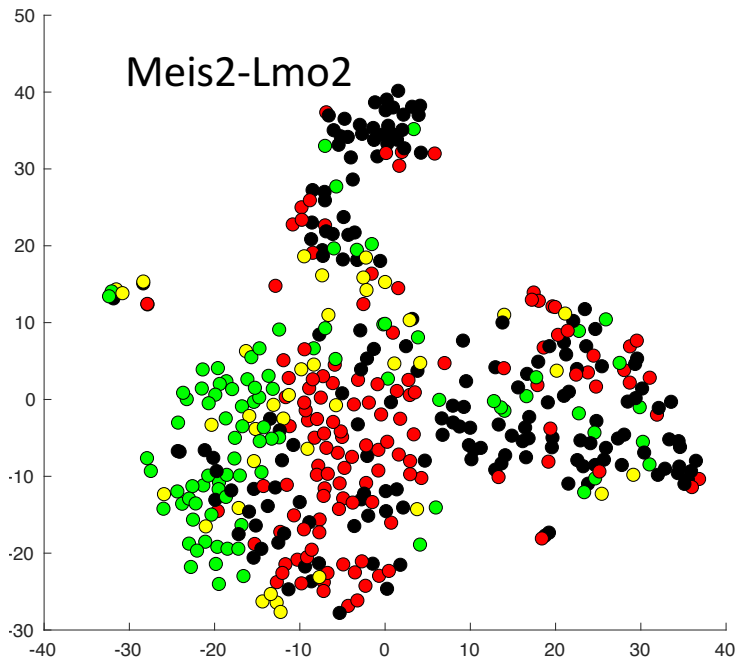
Cd34-Col11a2



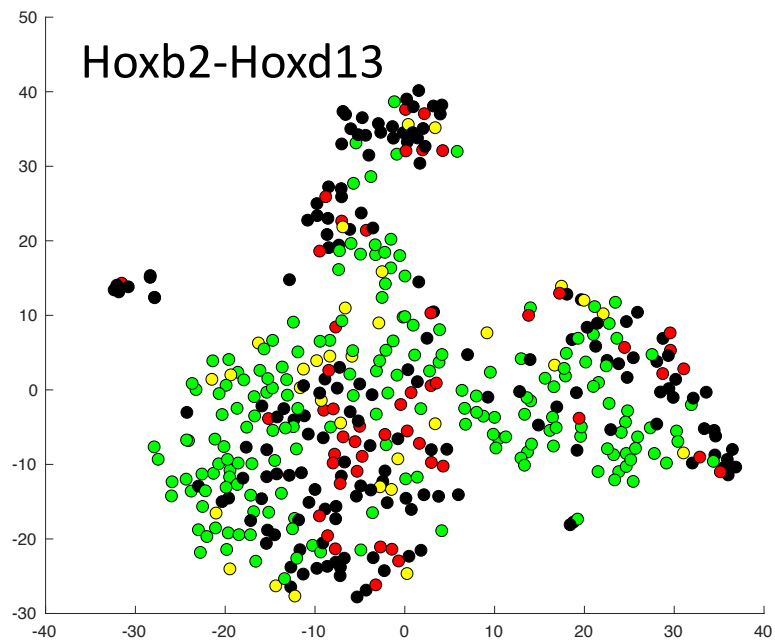
Meis2-Hoxd13



Meis2-Lmo2

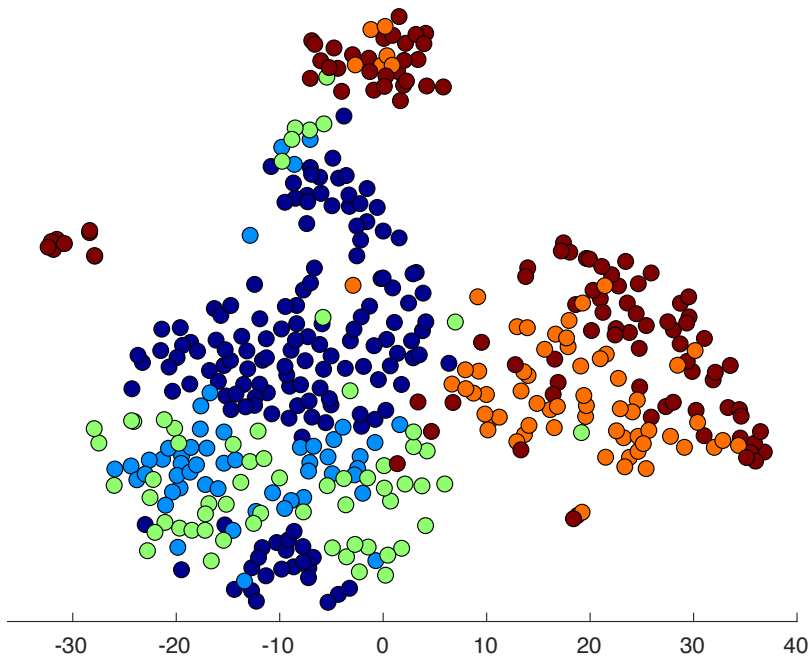


Hoxb2-Hoxd13

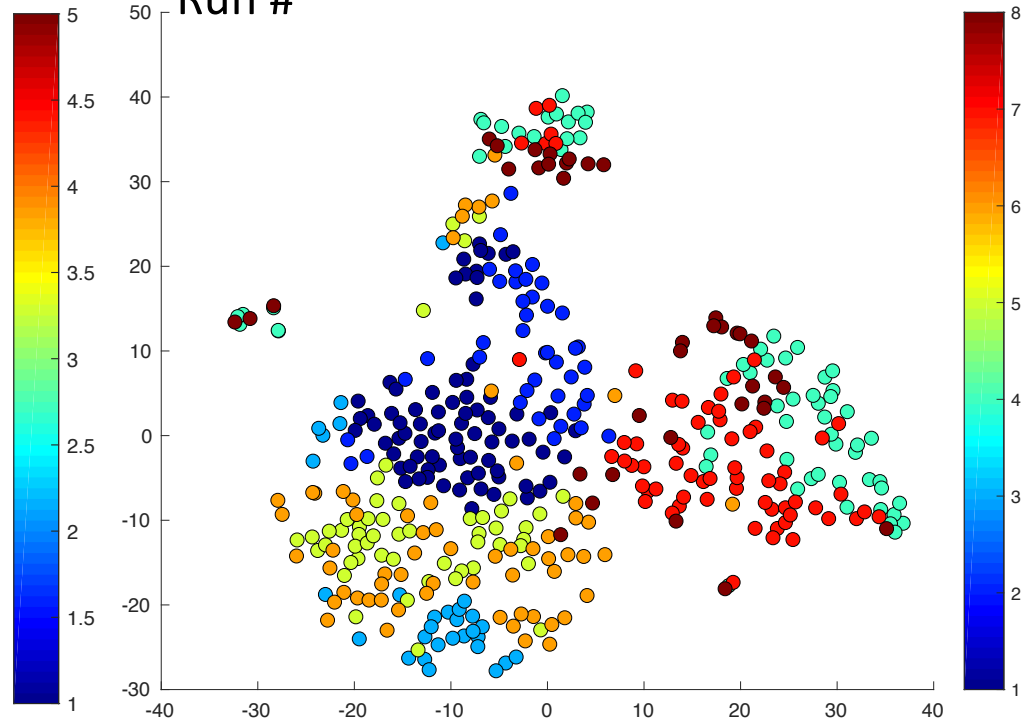


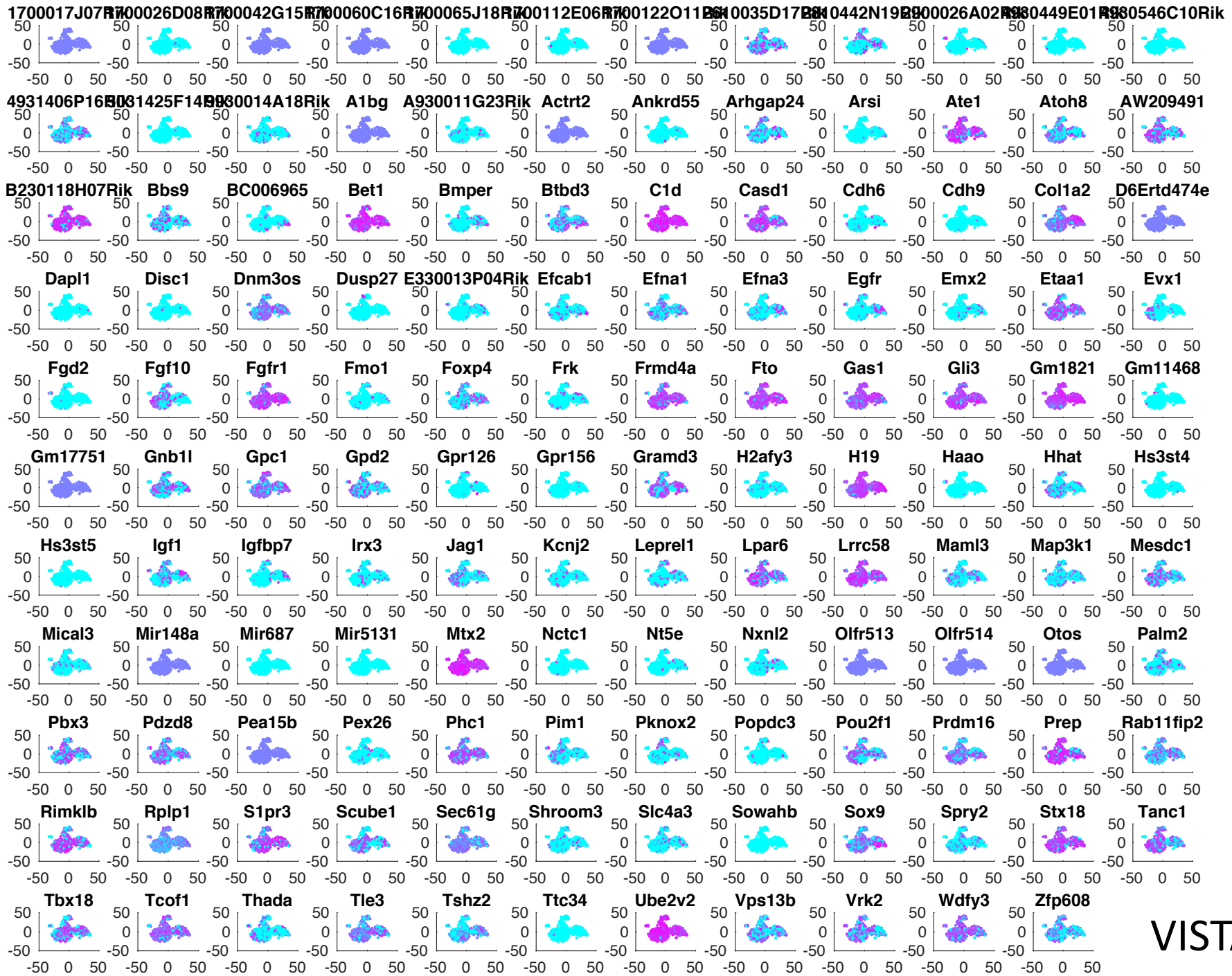
# Boolean mapping

Dissection Time



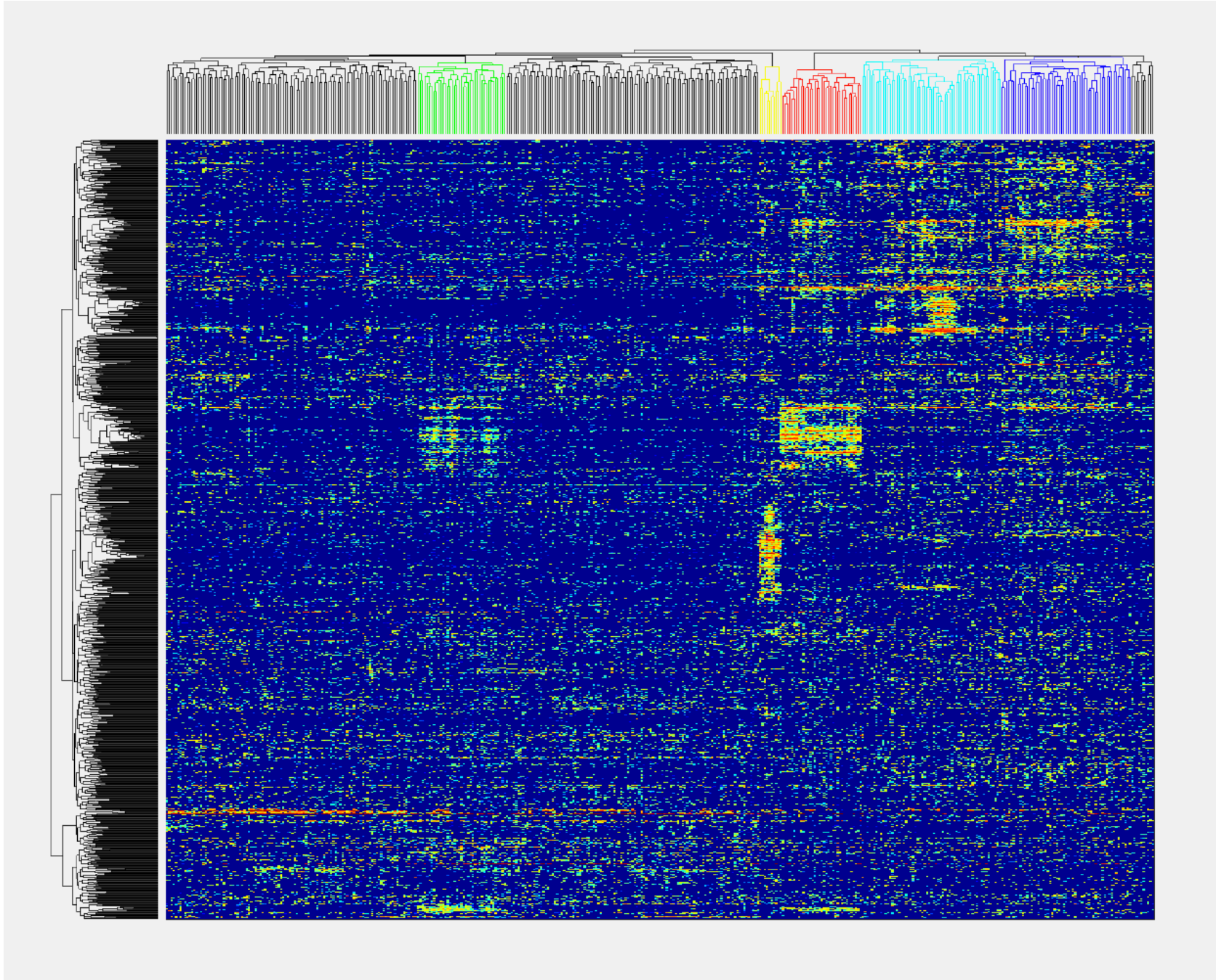
Run #





VISTA

# Dispersion Plus (1037), correlation





# tSNE k-means clustering (Euclidean)

