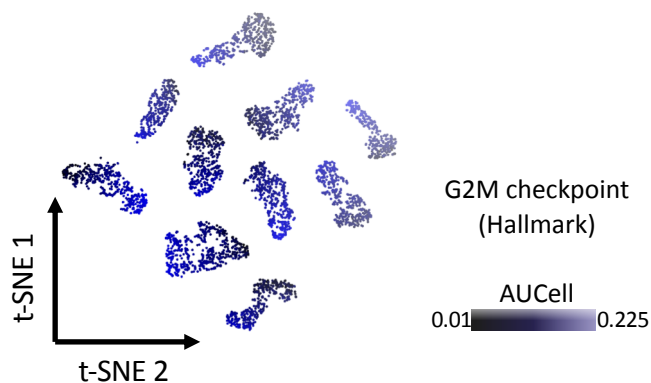


# Supplementary Figure S1

a

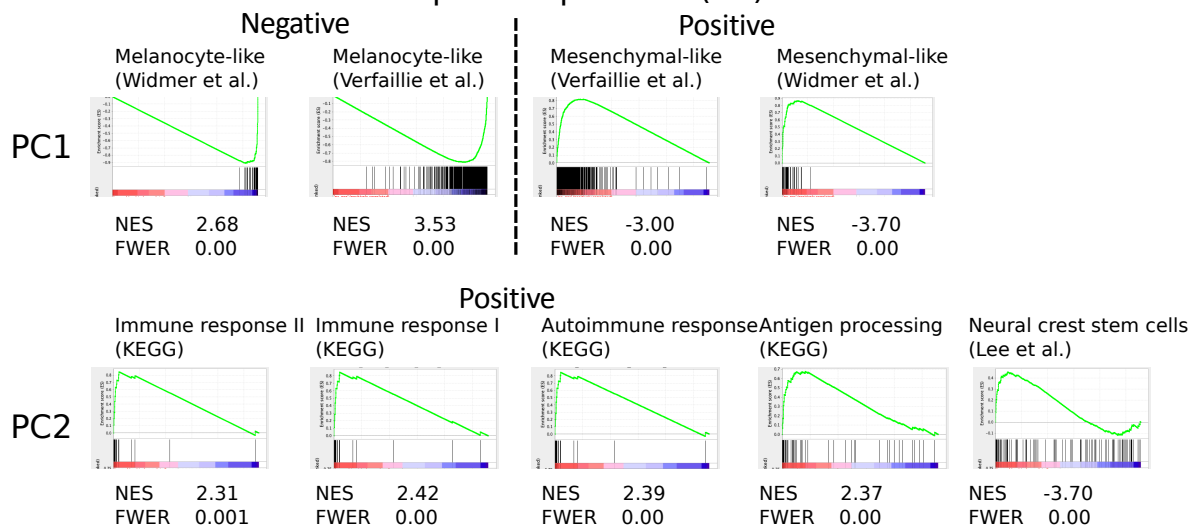


b



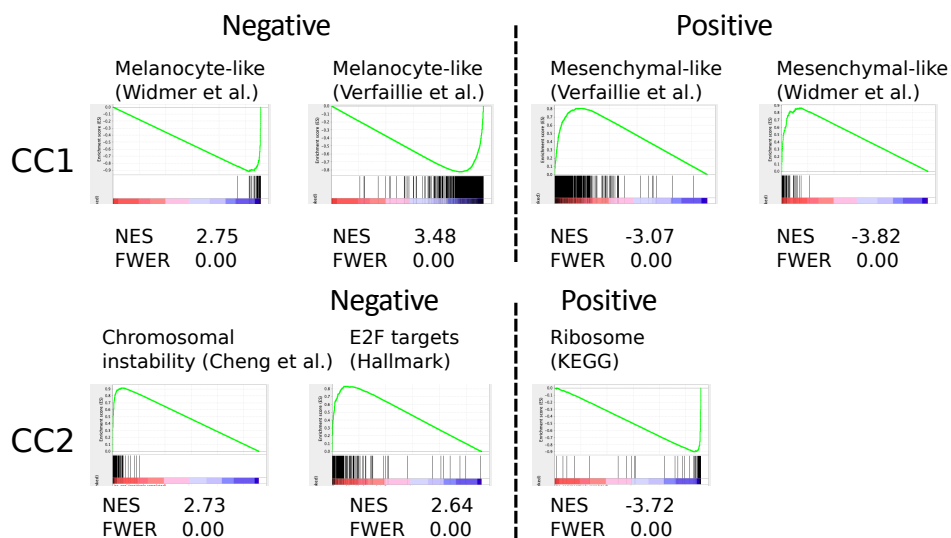
c

## Principal components (PC)



d

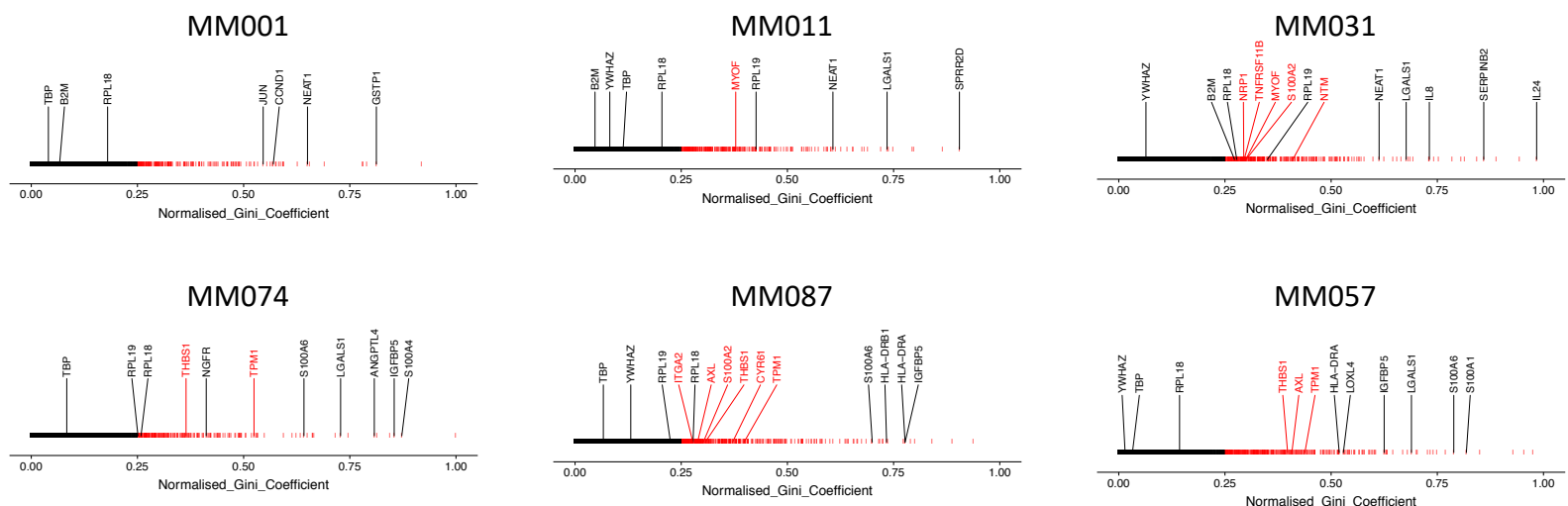
## Canonical correlations (CC)



# Supplementary Figure S2

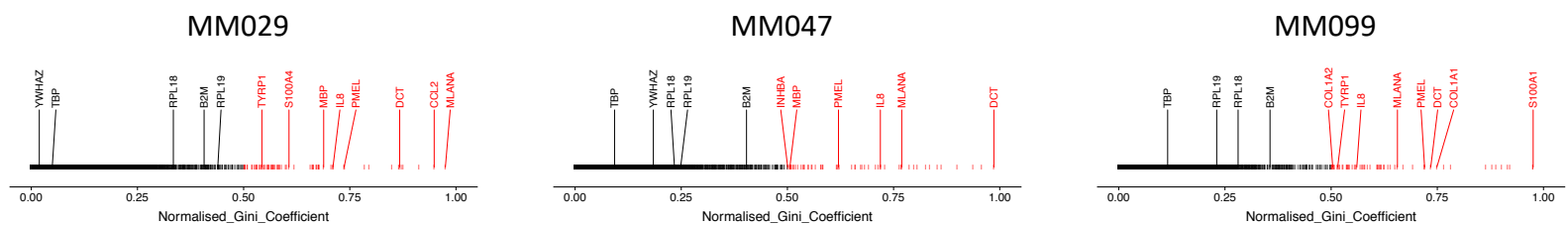
**a**

## Melanocyte-like cultures



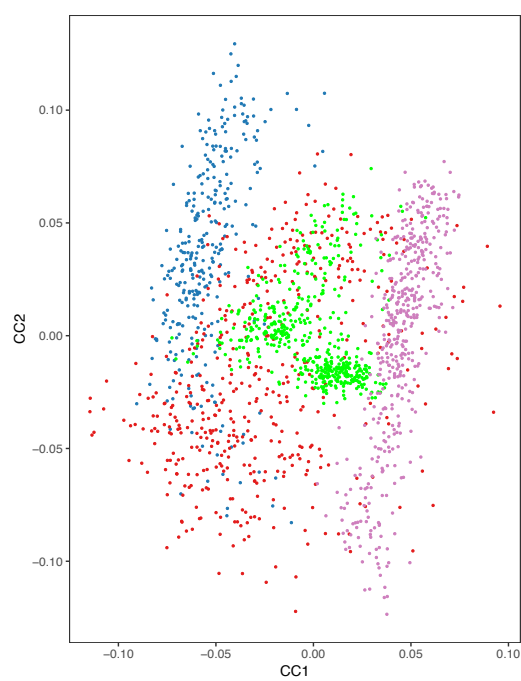
Gene name: present in mesenchymal-like gene signature

## Mesenchymal-like cultures

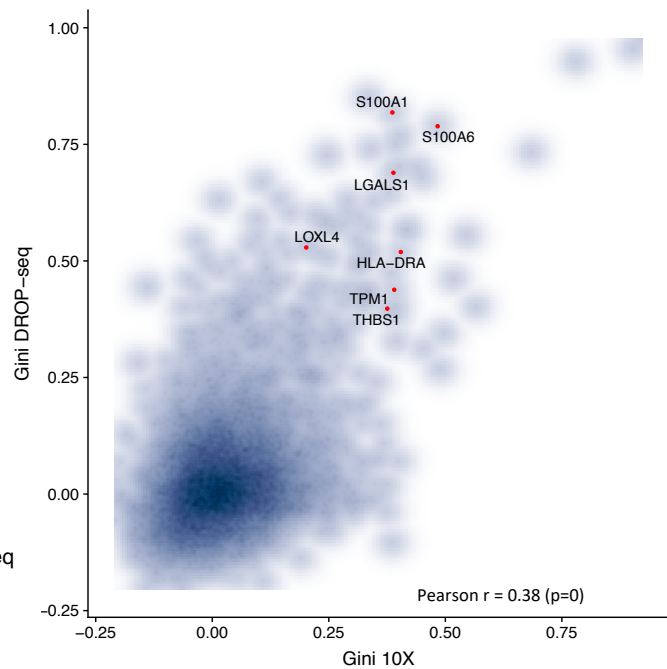


Gene name: present in melanocyte-like gene signature

**b**

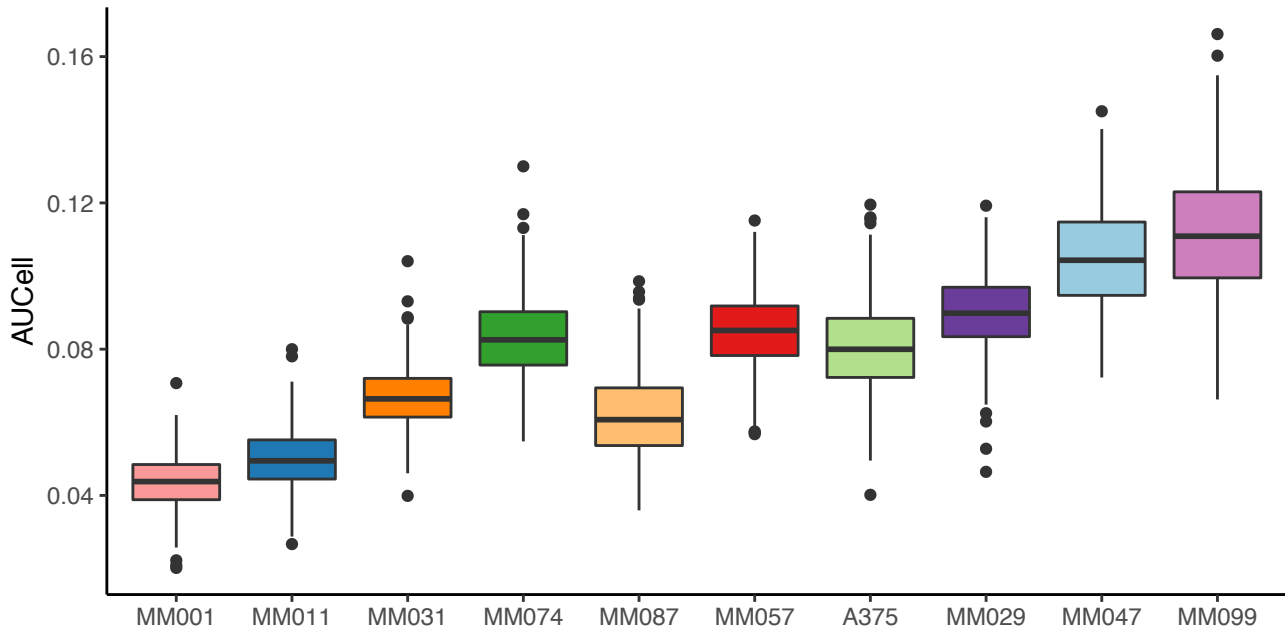


**c**

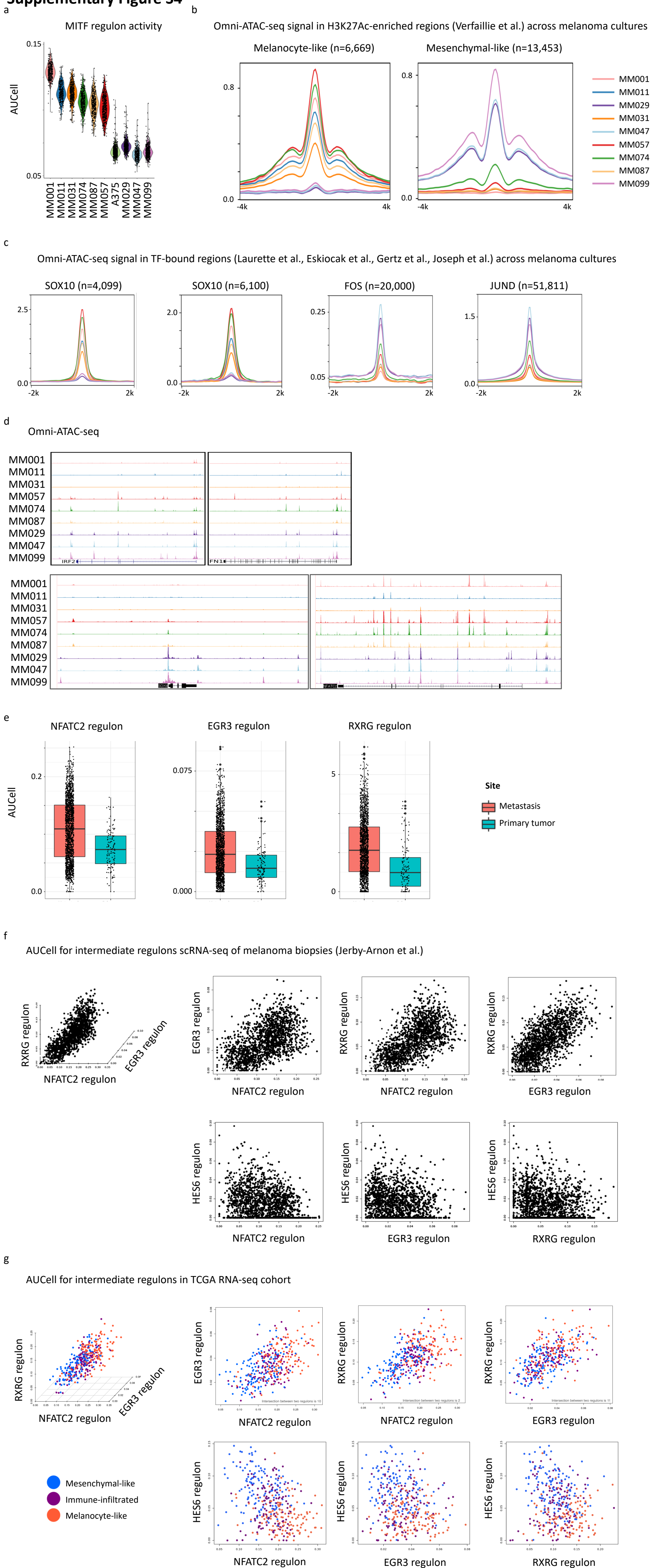


# Supplementary Figure S3

## Cell migration (Wu et al.; including MM074)

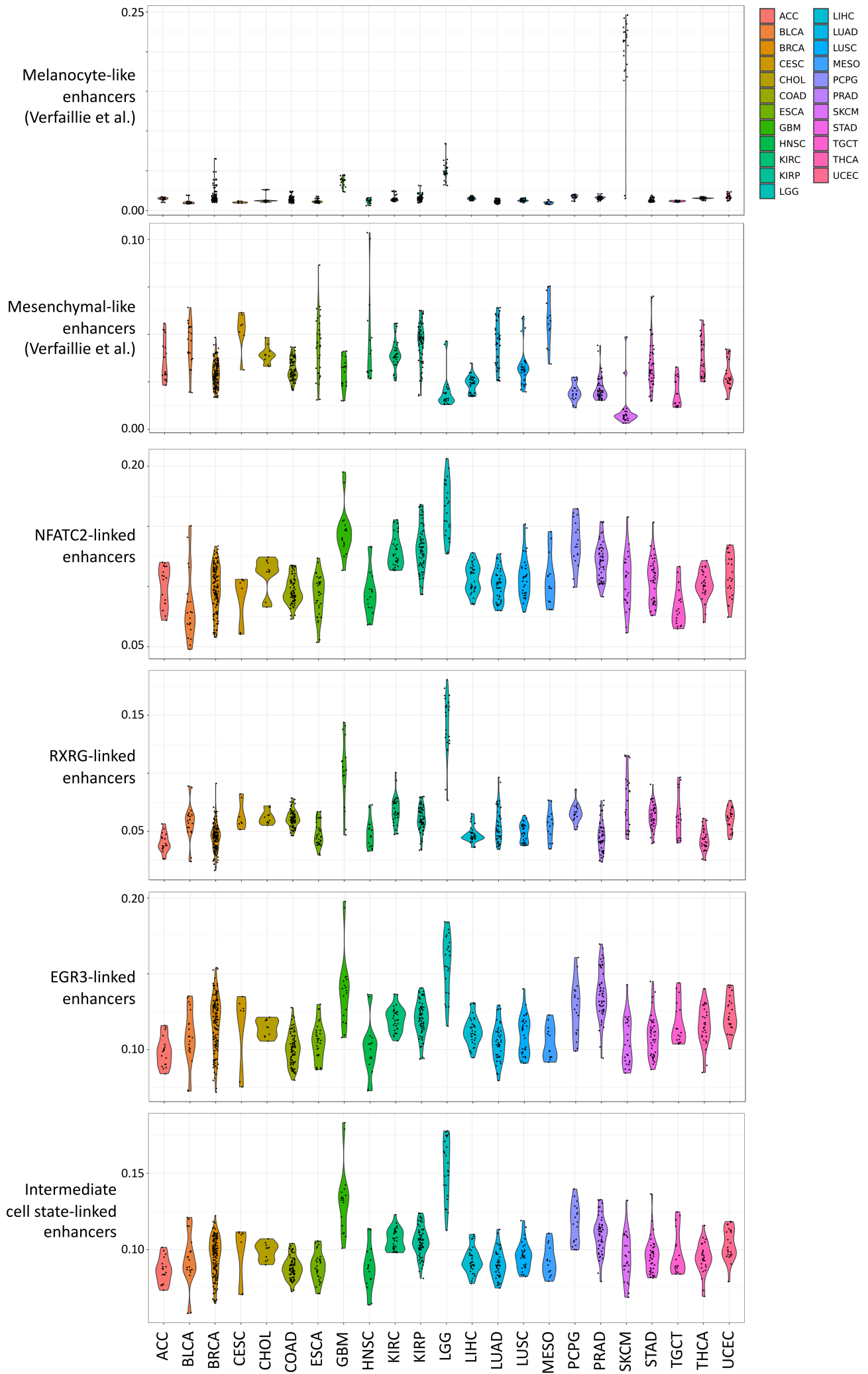


# Supplementary Figure S4



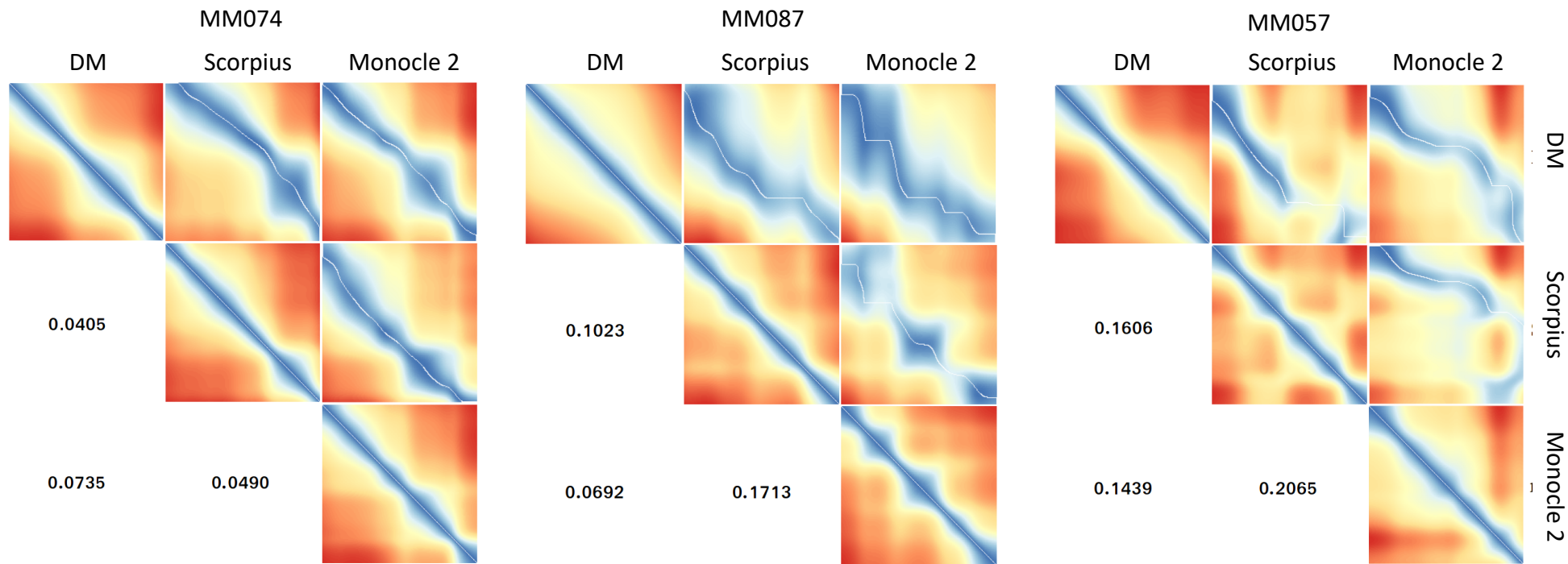
# Supplementary Figure S5

Normalized ATAC-seq signal in TCGA cohort (Corces et al. 2018)



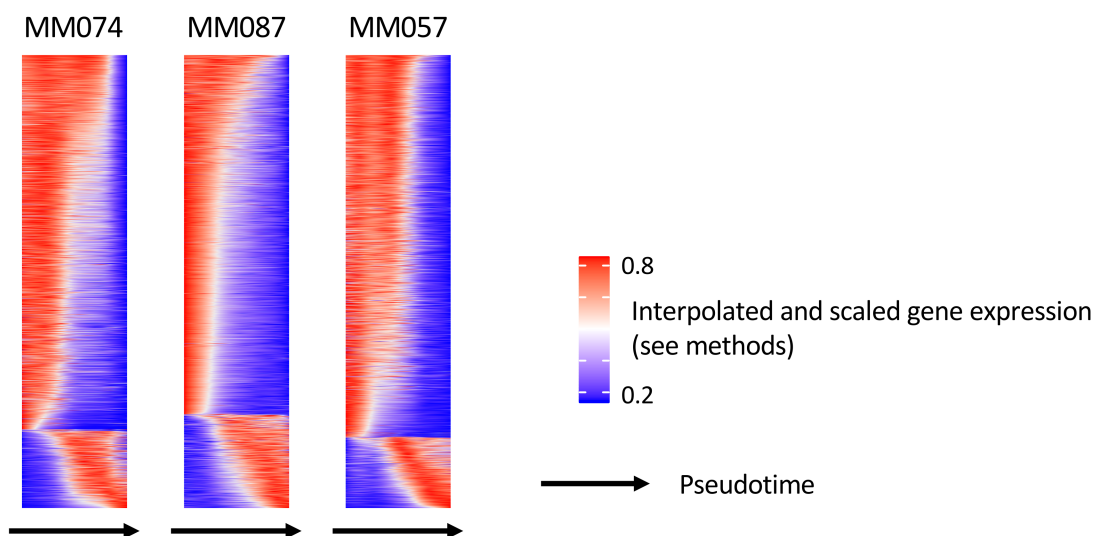
# Supplementary Figure S6

## Alignment of trajectory methods

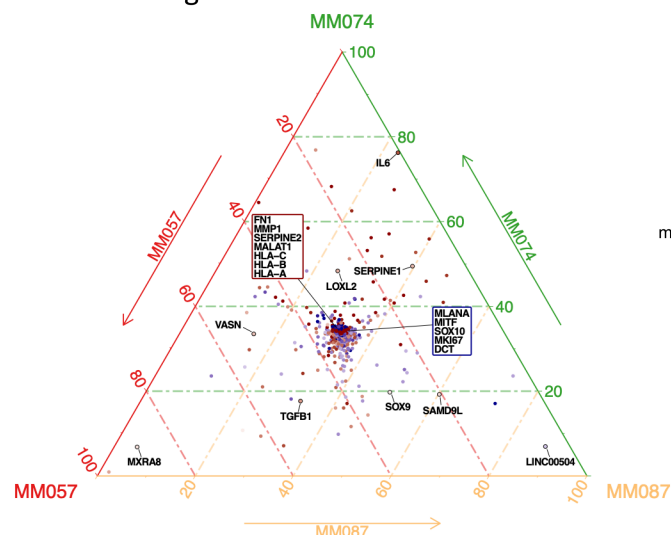


# Supplementary Figure S7

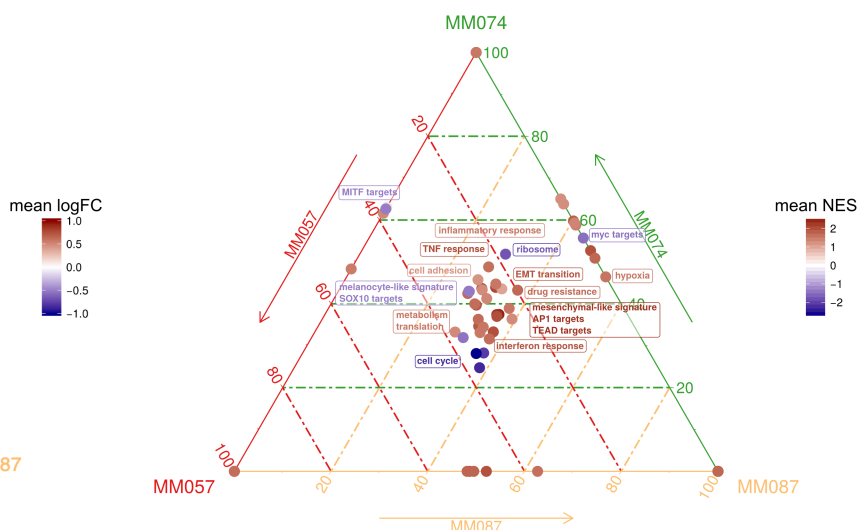
**a** Gene expression changes along pseudotime



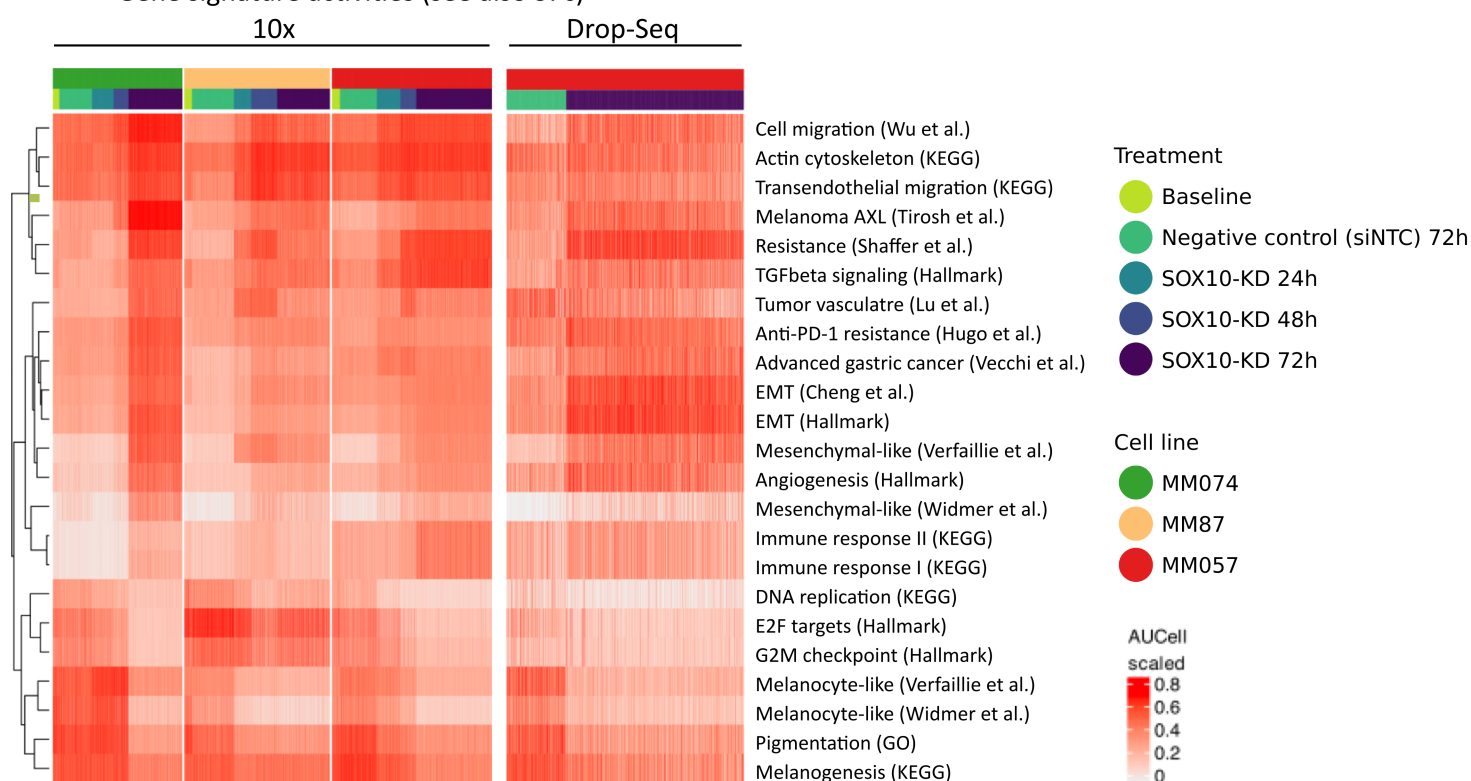
**b** Comparison of gene expression changes across melanoma cultures



**c** Comparison of gene signature activity changes across melanoma cultures

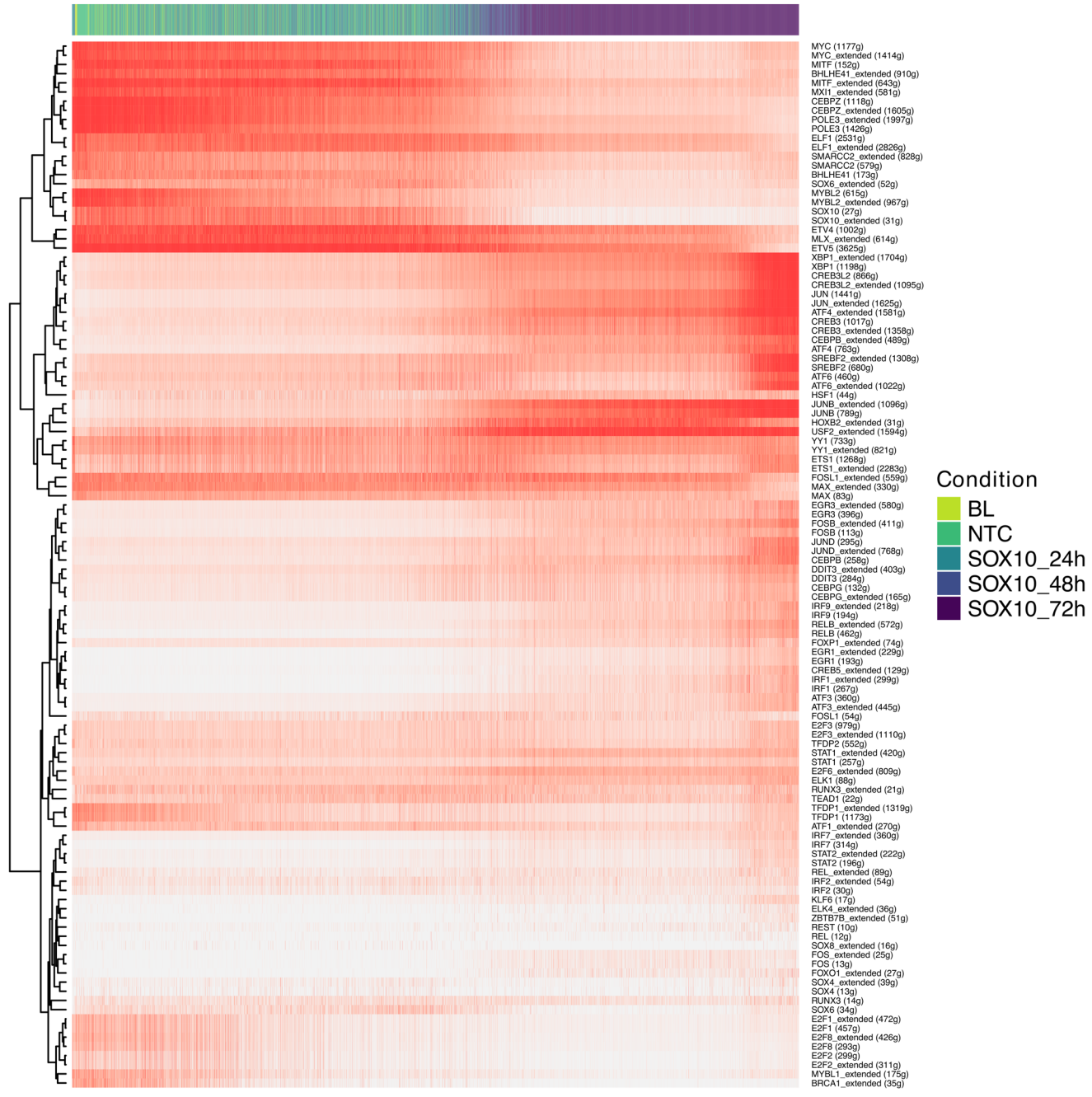


**d** Gene signature activities (see also S7c)



# Supplementary Figure S8

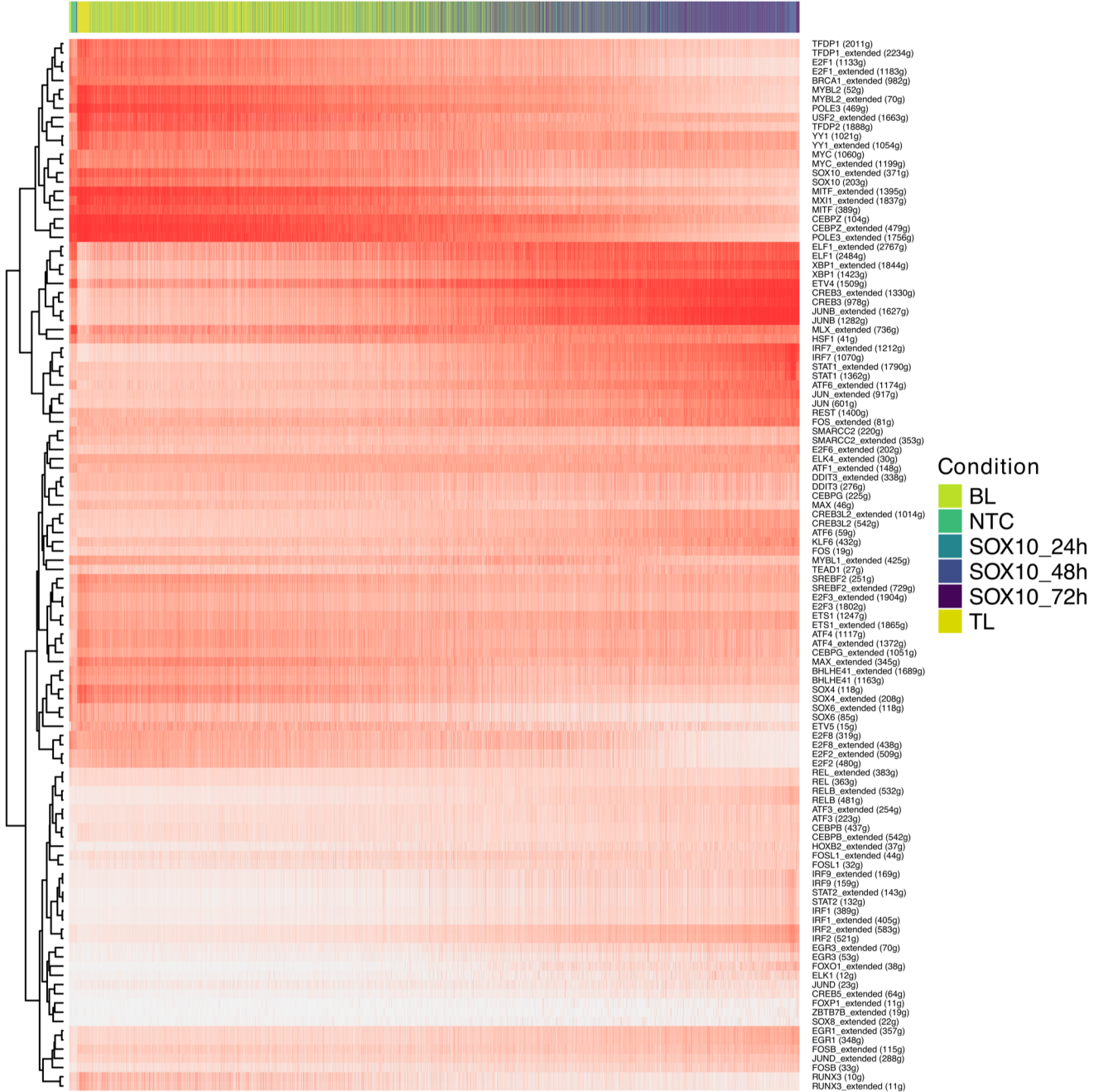
## MM074





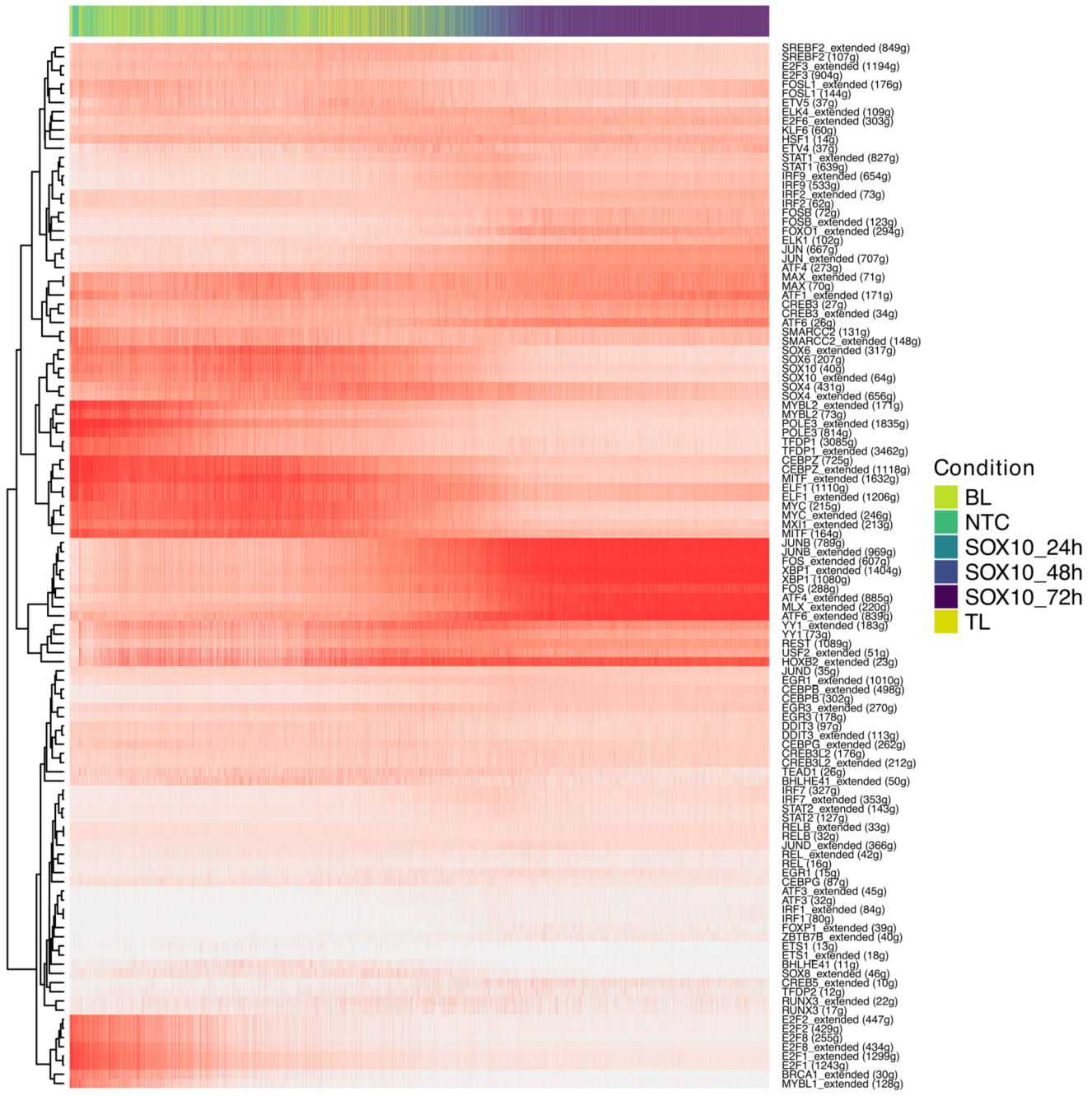
# Supplementary Figure S9

## MM087

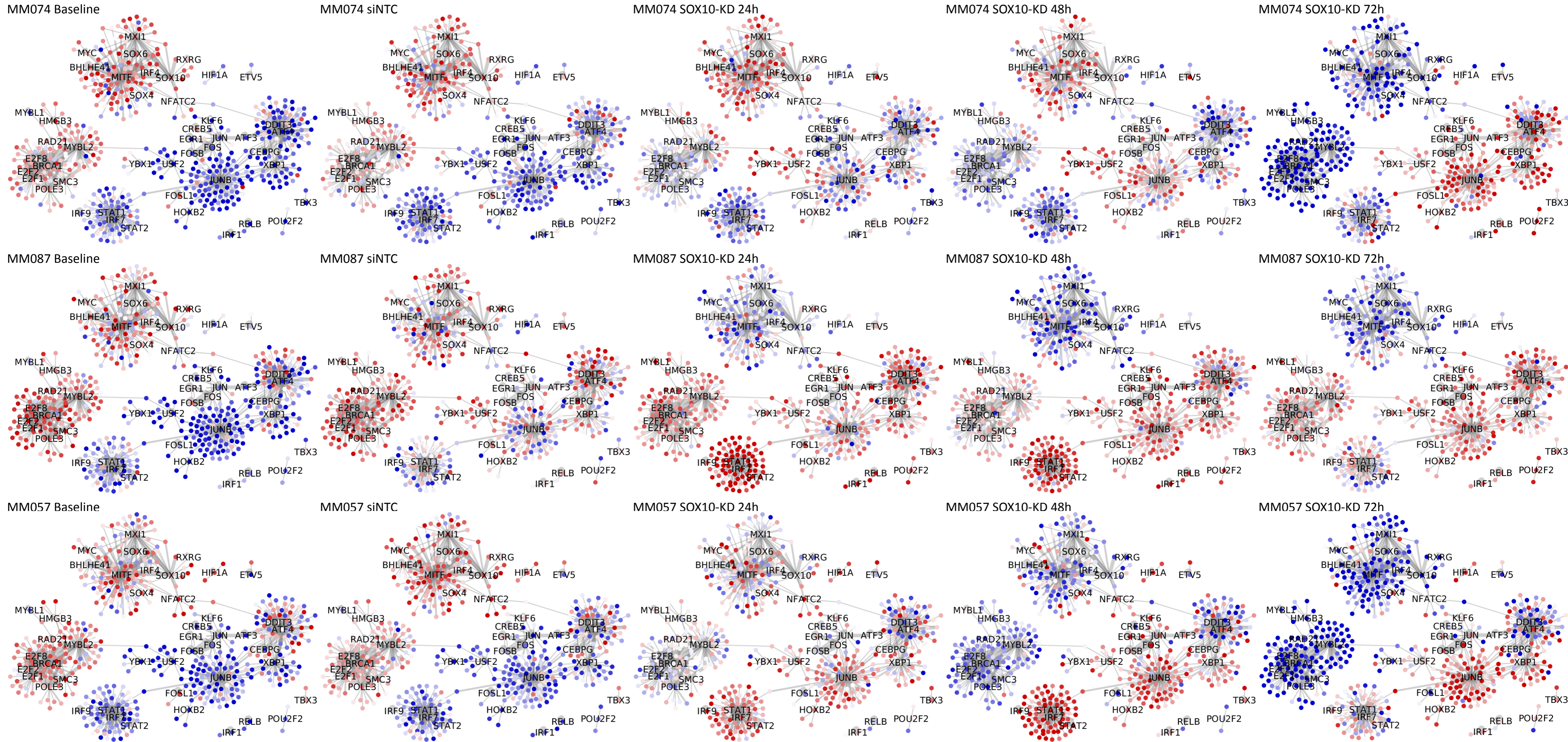


# Supplementary Figure S10

MM057



**Supplementary Figure S11**



# Supplementary Figure S12

## Comparison to public data

114 genes downregulated after 6h of THZ1 treatment

(Eliades et al., JID, 2018)

