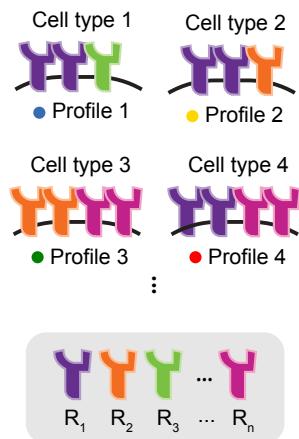


Figure 1: Pathway expression profiles could recur across diverse cell types

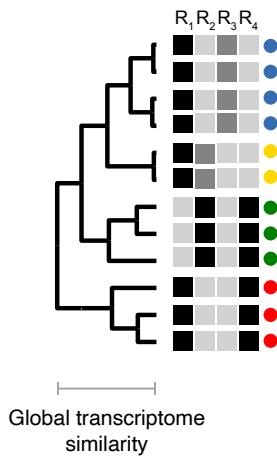
A

Receptor expression profiles

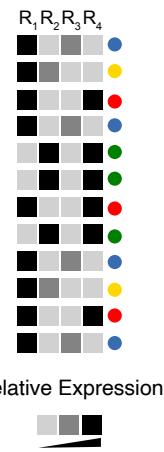


B

Regime 1:  
Similar cell types share  
similar pathway profiles



Regime 2:  
Pathway profiles recur  
in diverse cell types



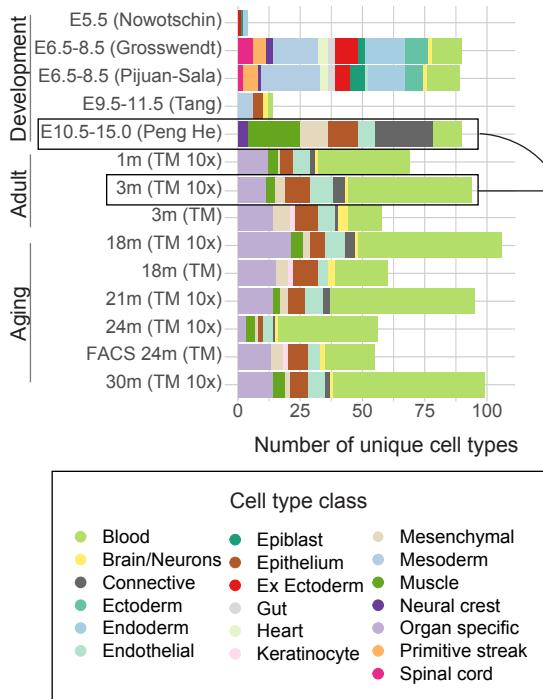
Relative Expression



Global transcriptome  
similarity

C

Multiple mouse cell atlas datasets

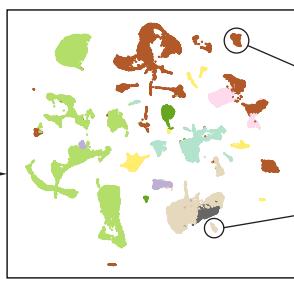


D

Individual cell atlases

1 dot = 1 cell

Tabula muris (3 month old mouse)

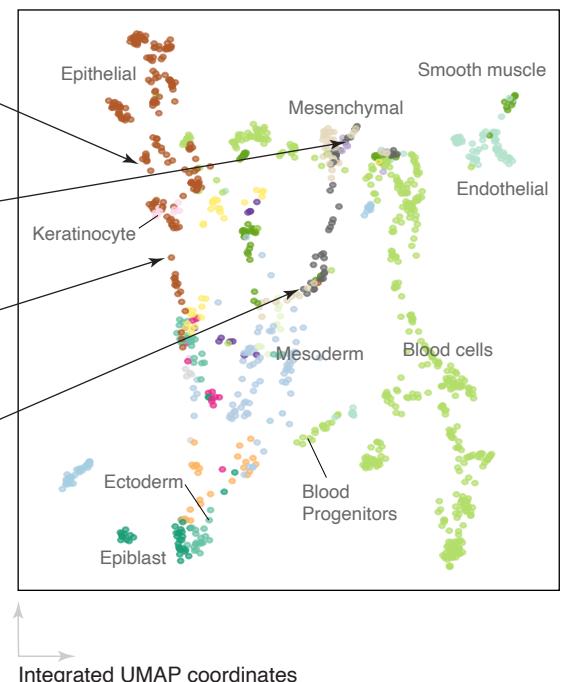


Forelimb (Days E10.5 - E15.0)

Integrated cell state atlas, cluster-averaged profiles

All data sets in (C)

1 dot = 1 cell cluster

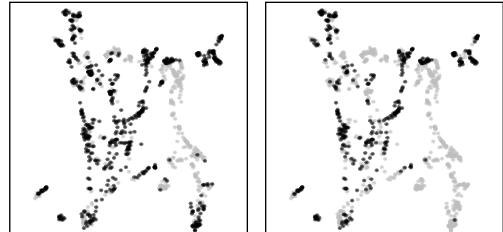


Dataset UMAP coordinates

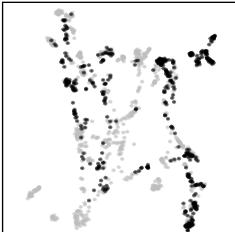
Integrated UMAP coordinates

E

TGF- $\beta$ : 52% of cell types    Wnt: 31% of cell types



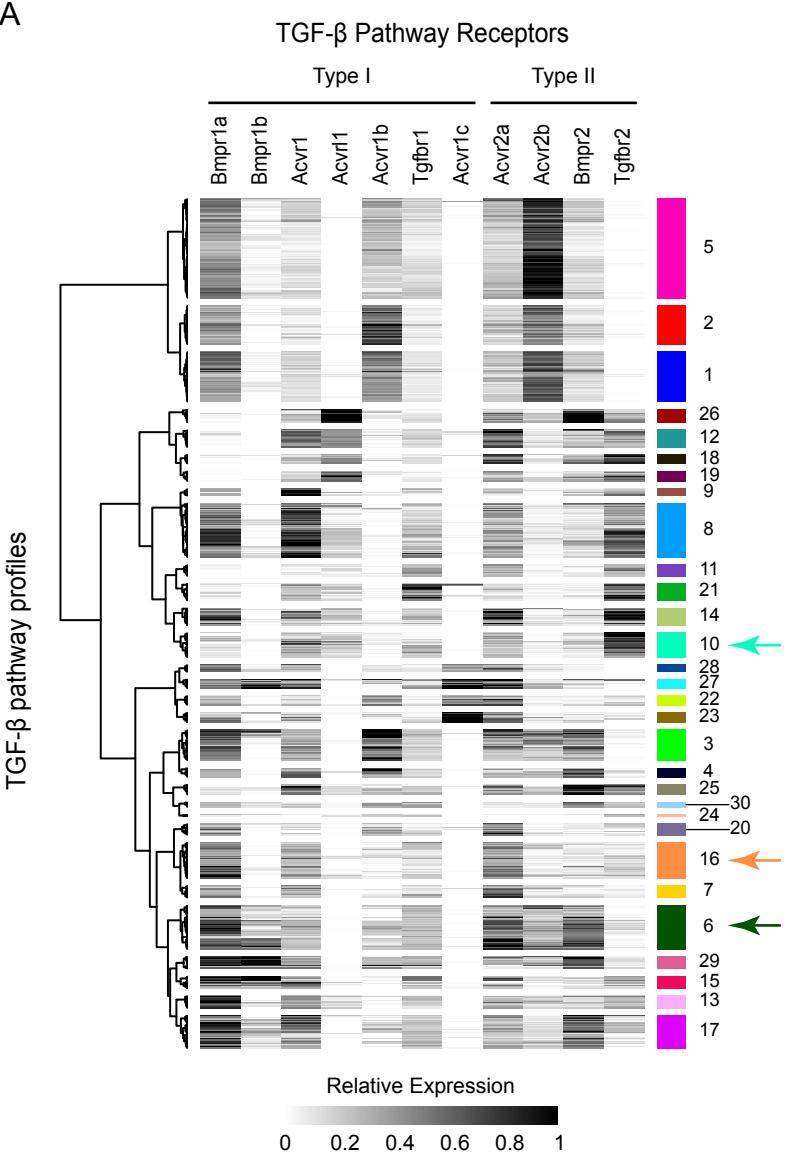
Notch: 37% of cell types



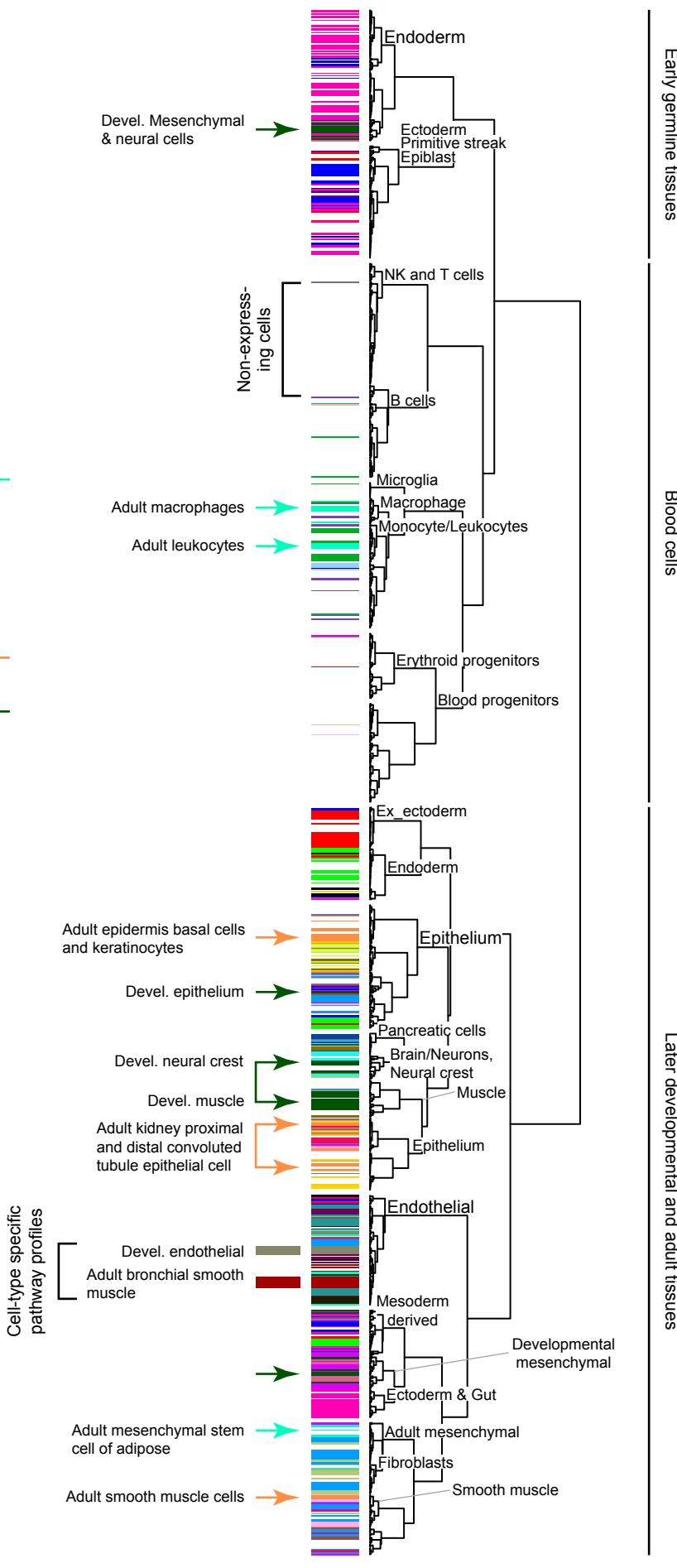
Dataset UMAP coordinates

Figure 2: TGF- $\beta$  Receptors exhibit distinct and recurrent pathway expression profiles

A



C Global distribution of pathway profiles



B

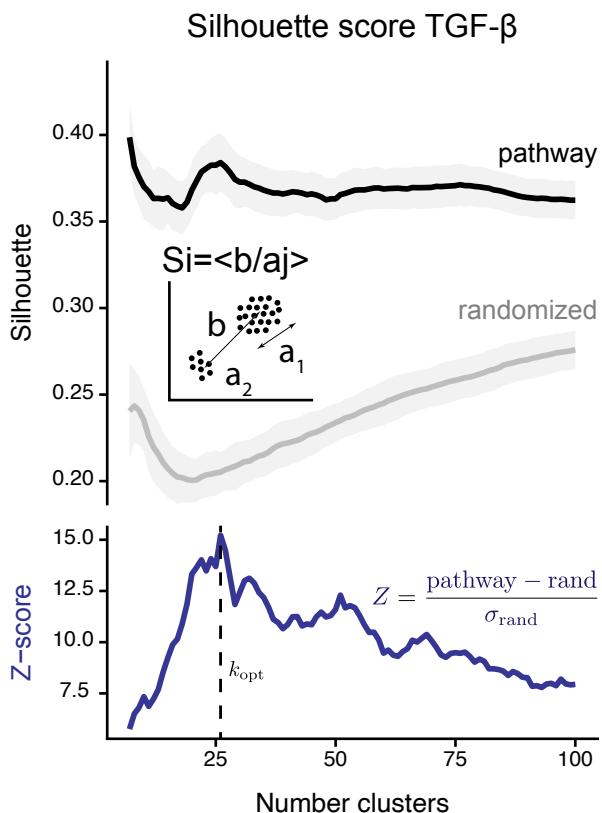
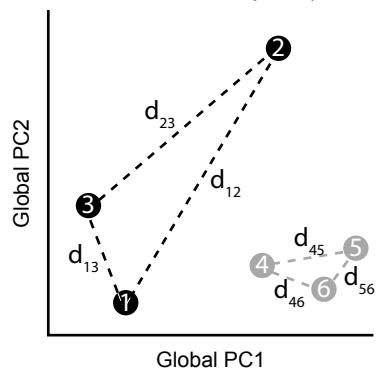


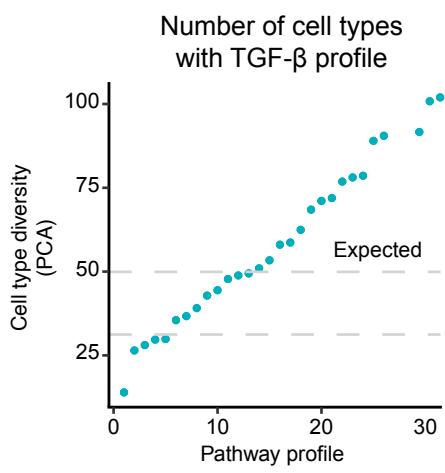
Figure 3: TGF- $\beta$  expression motifs are dispersed across cell types and organs

A

Pairwise distance computation (schematic)  
(Actual computation occurs in 100-dimensional PCA space)



B



Number of cell types with TGF- $\beta$  profile  
Cell type diversity (PCA)

Expected

Fraction of pathway profiles

motifs

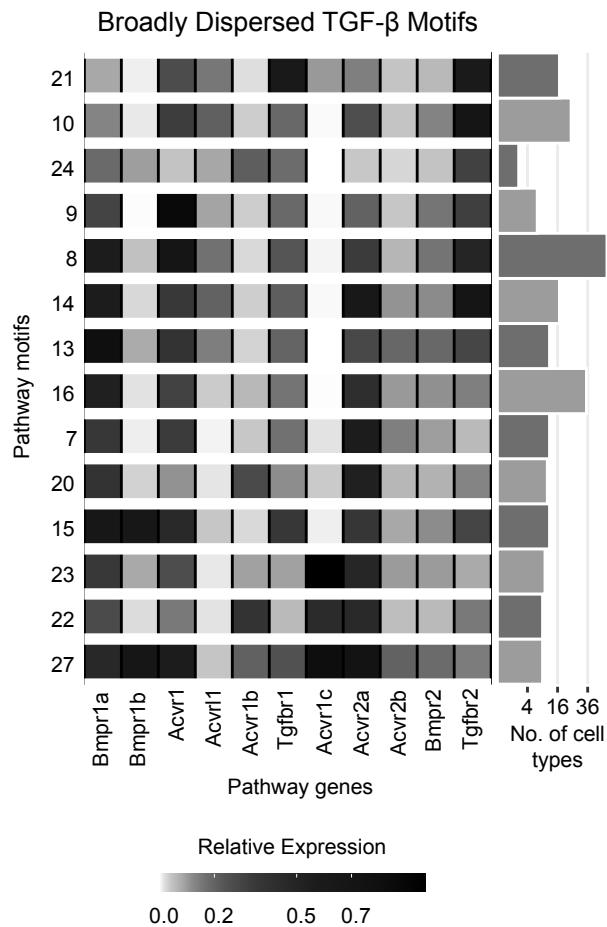
Actual pathway profile

Similar cell types (lower bound)

uncorrelated (upper bound)

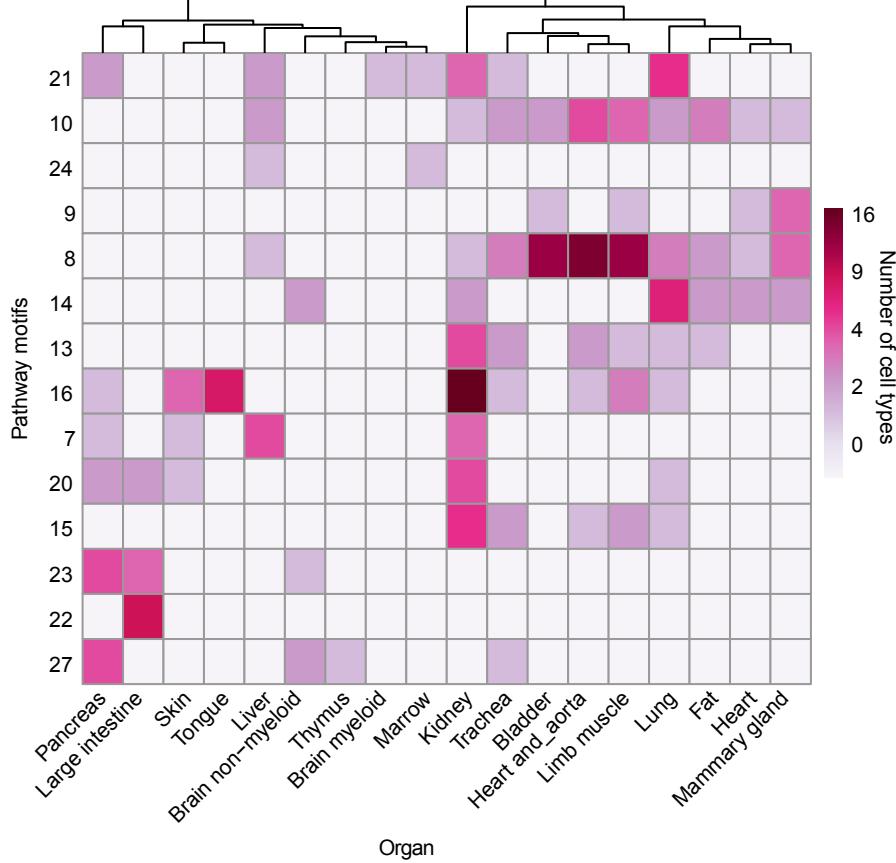
mean cell type dispersion within each pathway profile

D



E

Broadly Dispersed TGF- $\beta$  Motifs



Number of cell types

Add some cool examples?

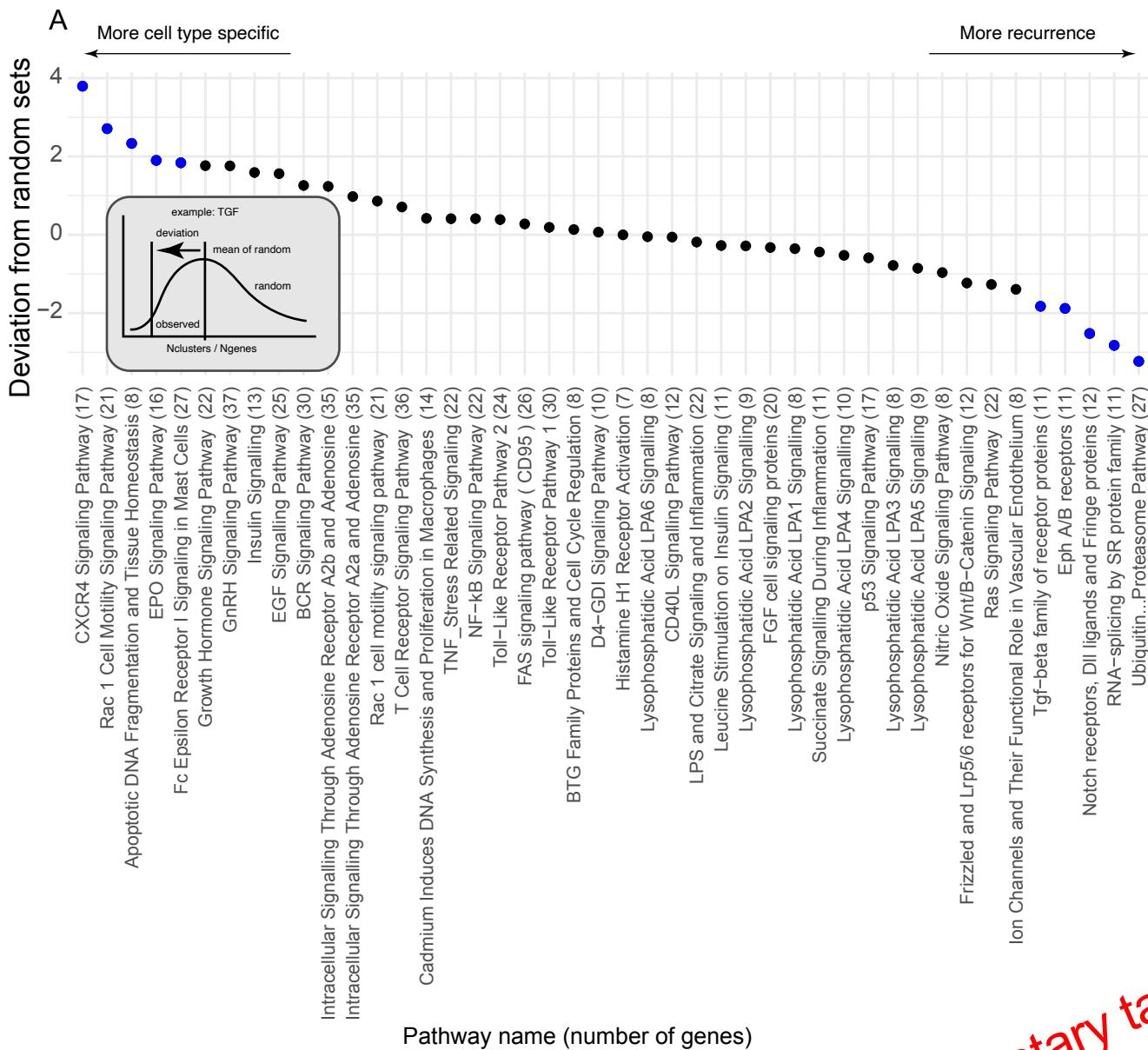
is it possible that epithelial or mesenchymal cells in different tissues tend to share the same profile?

Profile 16 is in a lot of epithelial cells (kidney, skin, bladder)

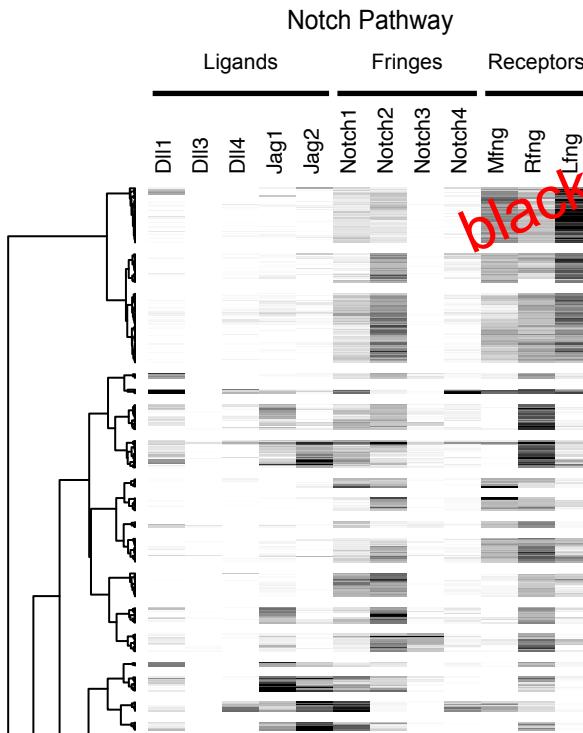
Barplot (w/ error bars) and listed cell types below for 2 interesting profiles (16 + 8?)

Figure 4: Wnt and Notch also show broadly dispersed recurrent pathway expression motifs

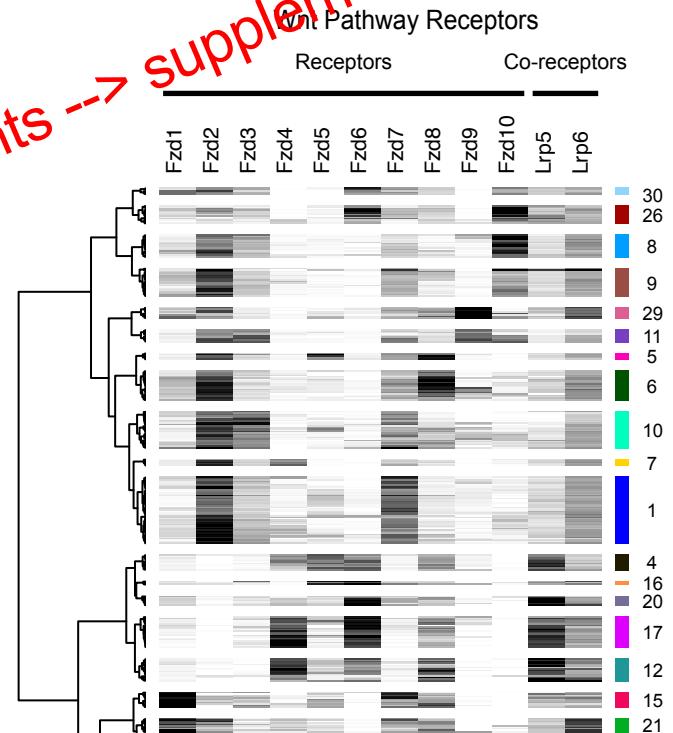
ofiles



B

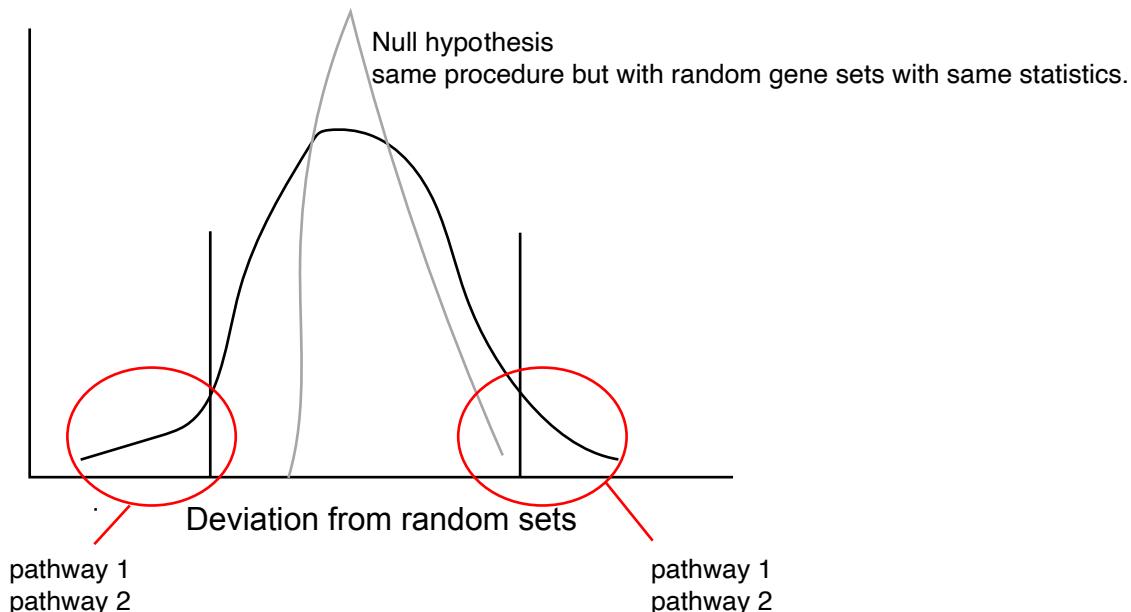


C



black points → supplementary table

Example of the statistic for TGF-->distribution of stat over pathways-->identification of the significantly recurrent or private pathways

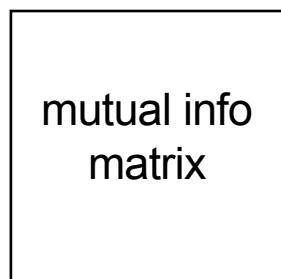
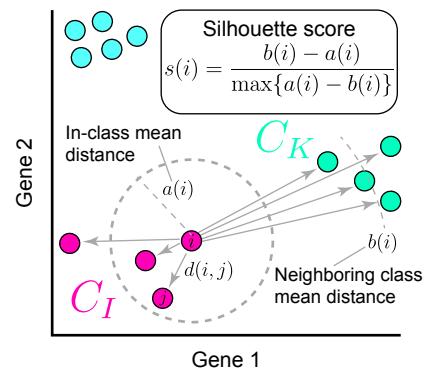


$$a(i) \text{ In-class mean distance}$$

$$a(i) = \frac{1}{|C_I| - 1} \sum_{j \in C_I, j \neq i} d(i, j)$$

$$b(i) \text{ Neighboring class mean distance}$$

$$b(i) = \min_{K \neq I} \frac{1}{|C_K|} \sum_{k \in C_K, k \neq i} d(i, k)$$



Pathway-pathway correlations

