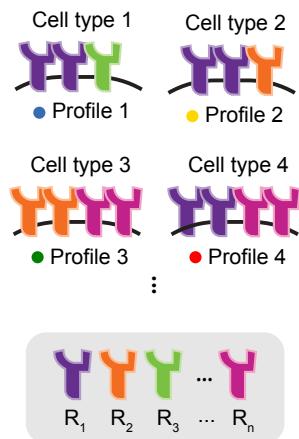


Figure 1: Pathway expression profiles could recur across diverse cell types

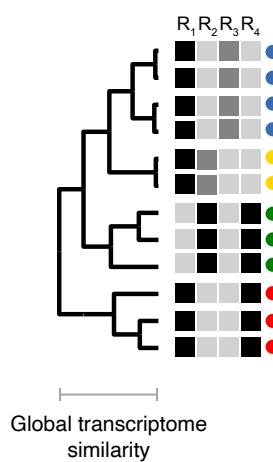
A

Receptor expression profiles

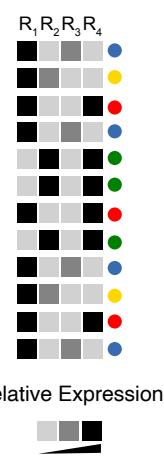


B

Regime 1:
Similar cell types share
similar pathway profiles

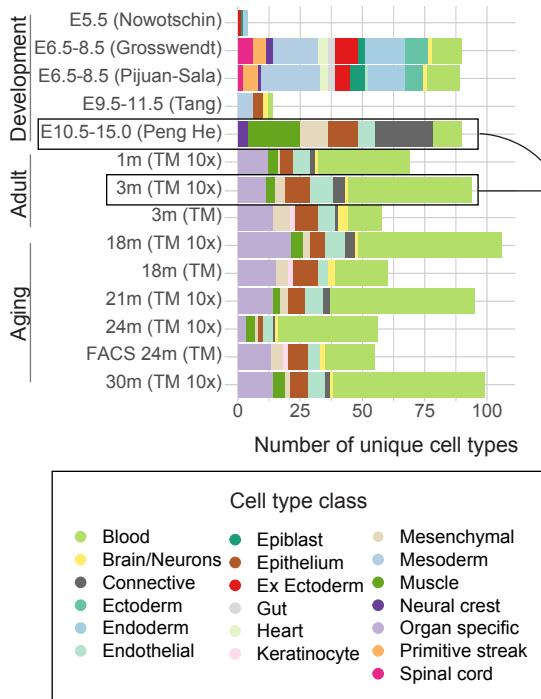


Regime 2:
Pathway profiles recur
in diverse cell types



C

Multiple mouse cell atlas datasets

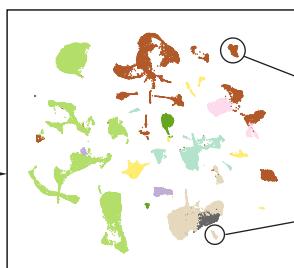


D

Individual cell atlases

1 dot = 1 cell

Tabula muris (3 month old mouse)

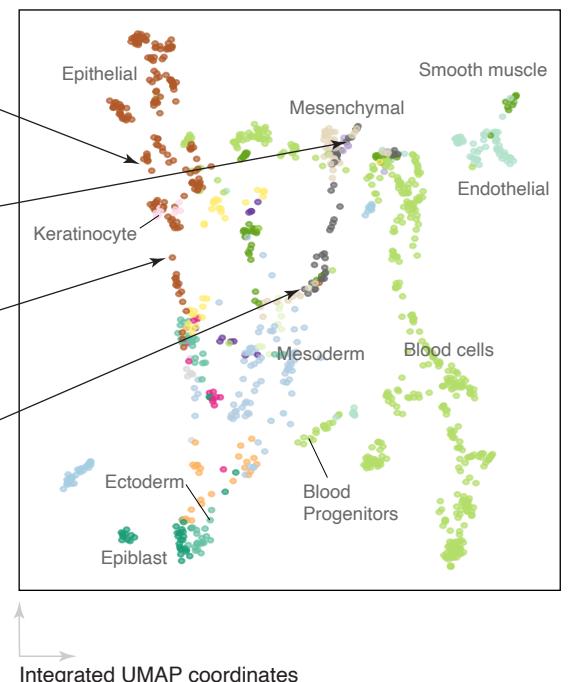


Forelimb (Days E10.5 - E15.0)

Integrated cell state atlas, cluster-averaged profiles

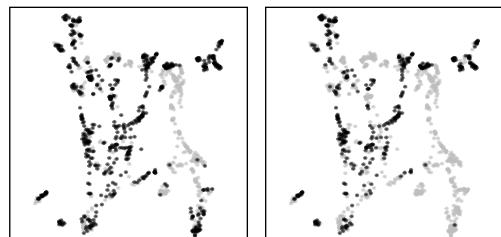
All data sets in (C)

1 dot = 1 cell cluster



E

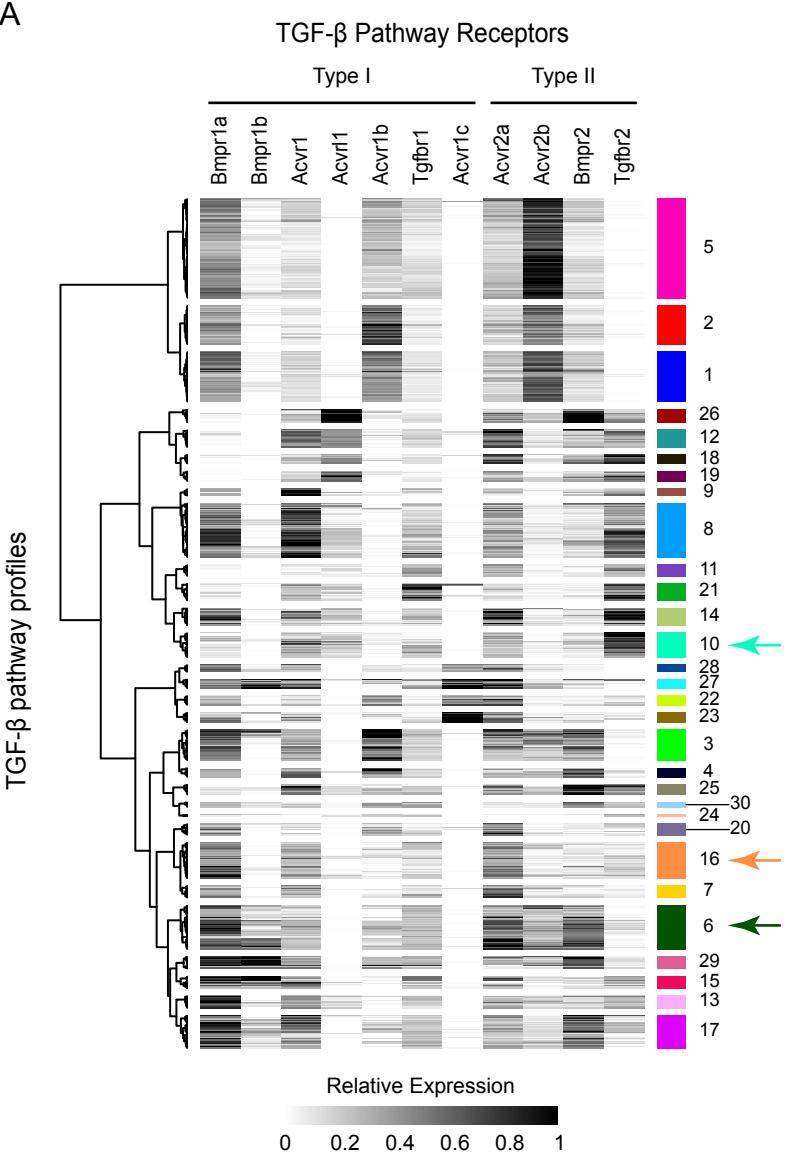
TGF- β : 52% of cell types Wnt: 31% of cell types



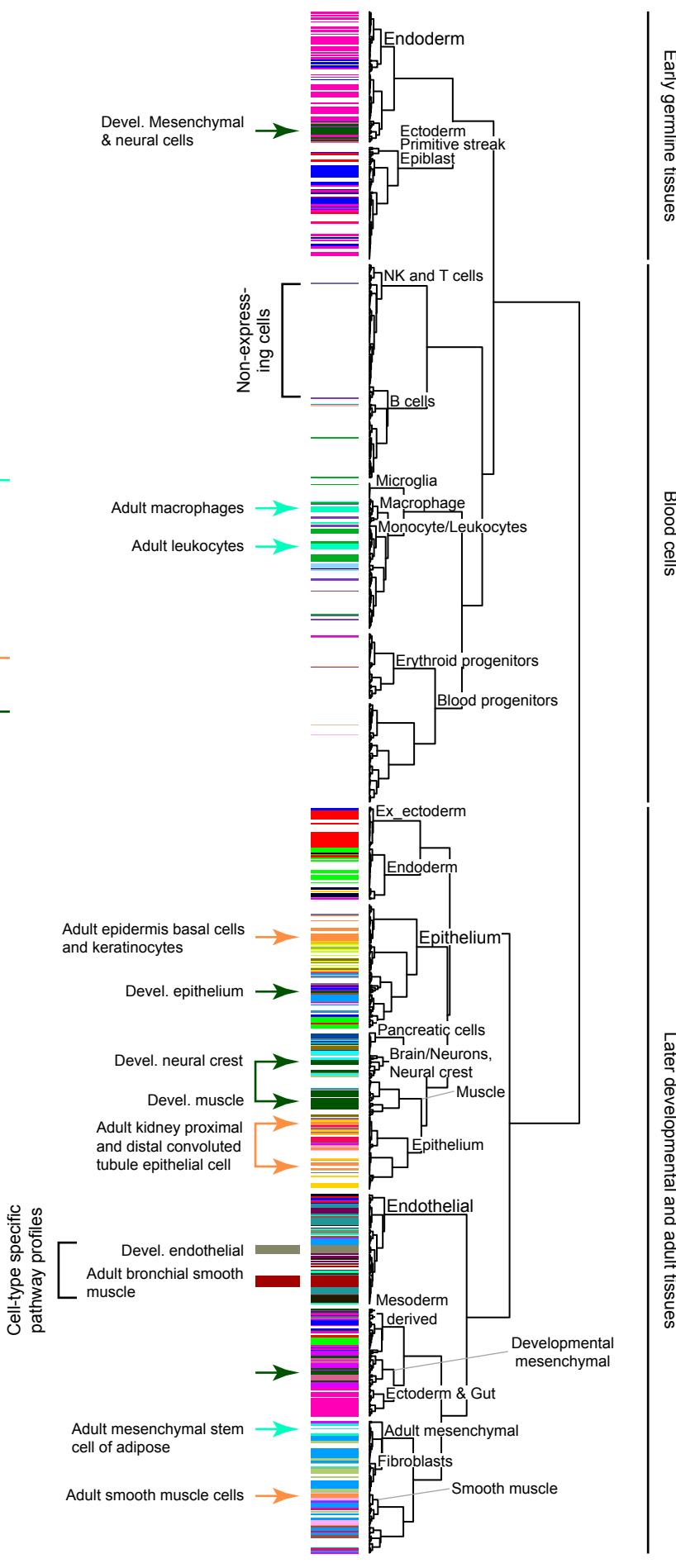
Dataset UMAP coordinates

Figure 2: TGF- β Receptors exhibit distinct and recurrent pathway expression profiles

A



C Global distribution of pathway profiles



B

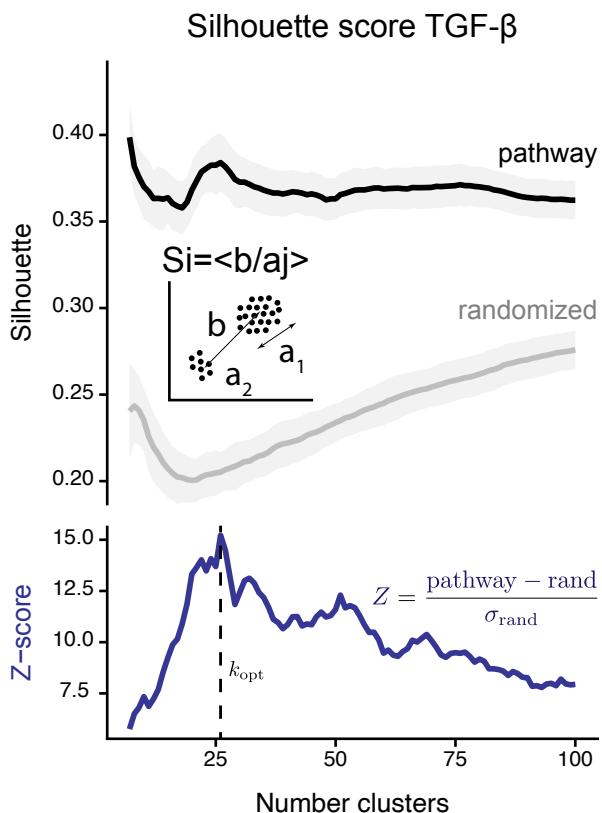
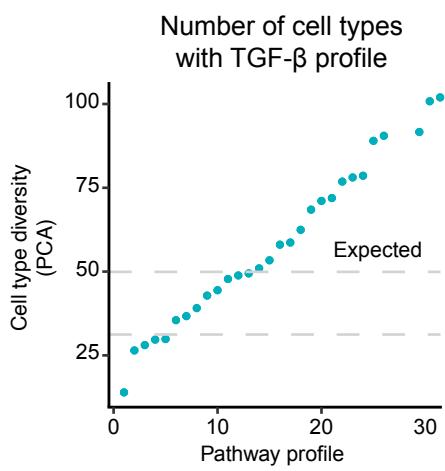
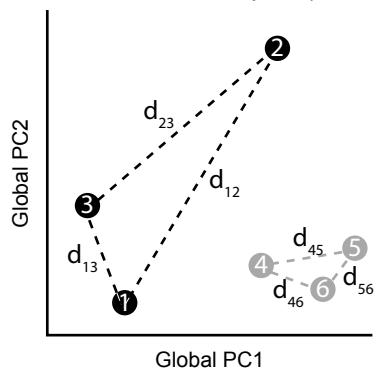


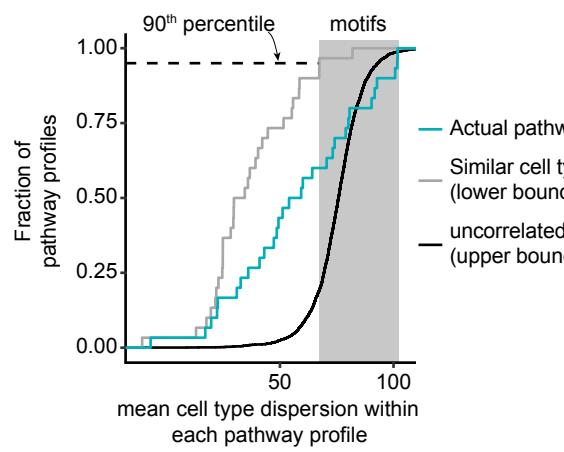
Figure 3: TGF- β expression motifs are dispersed across cell types and organs

A

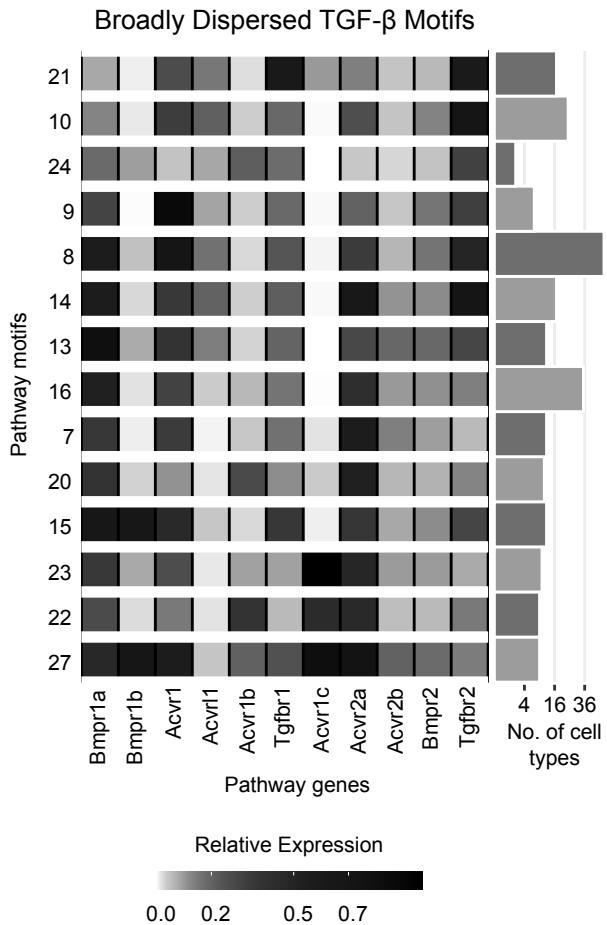
Pairwise distance computation (schematic)
(Actual computation occurs in 100-dimensional PCA space)



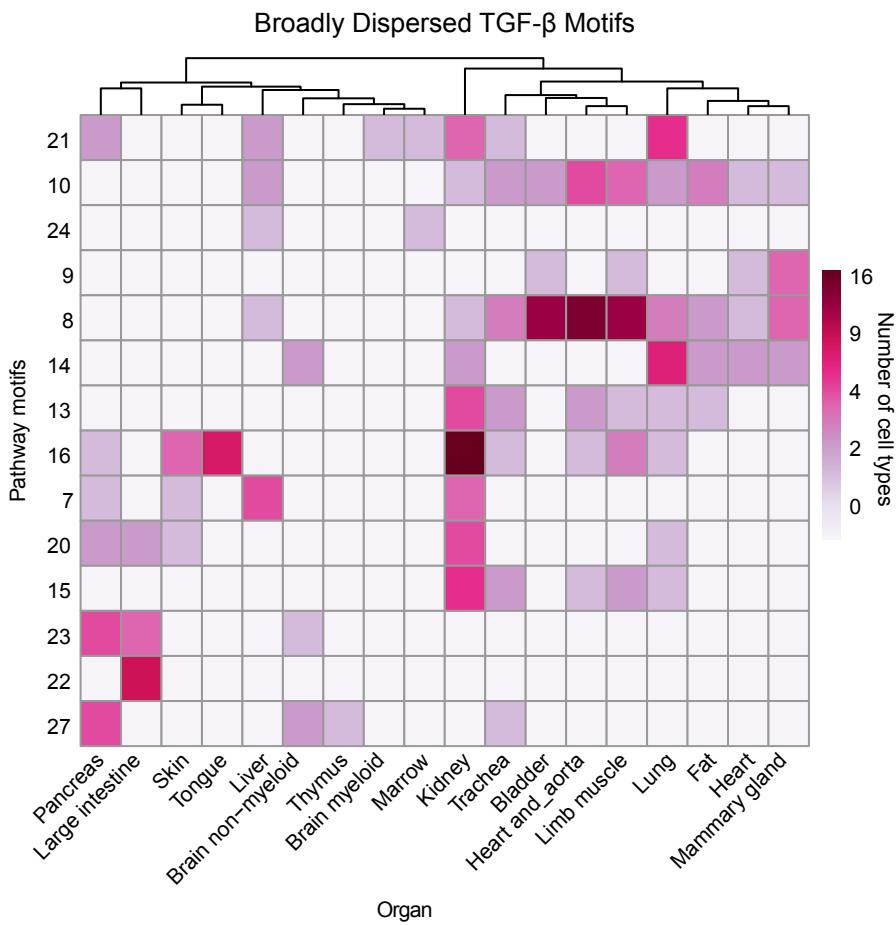
B



D



E



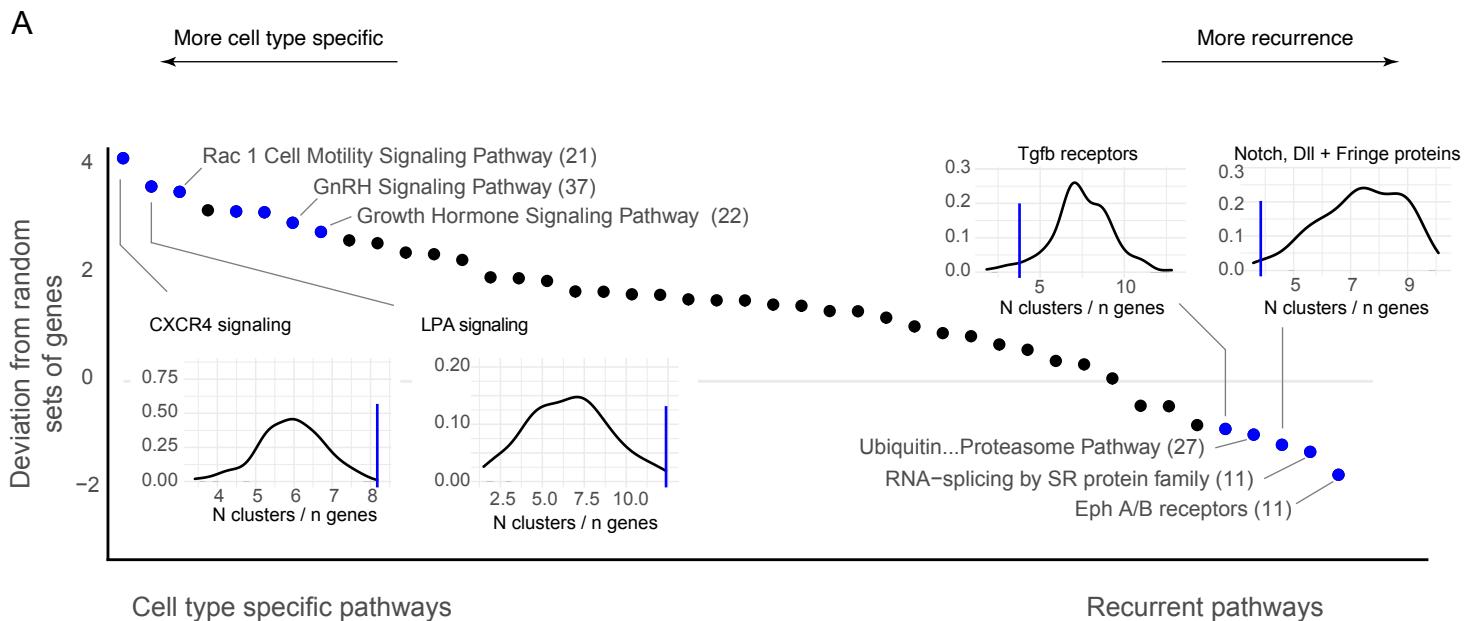
Add some cool examples?

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

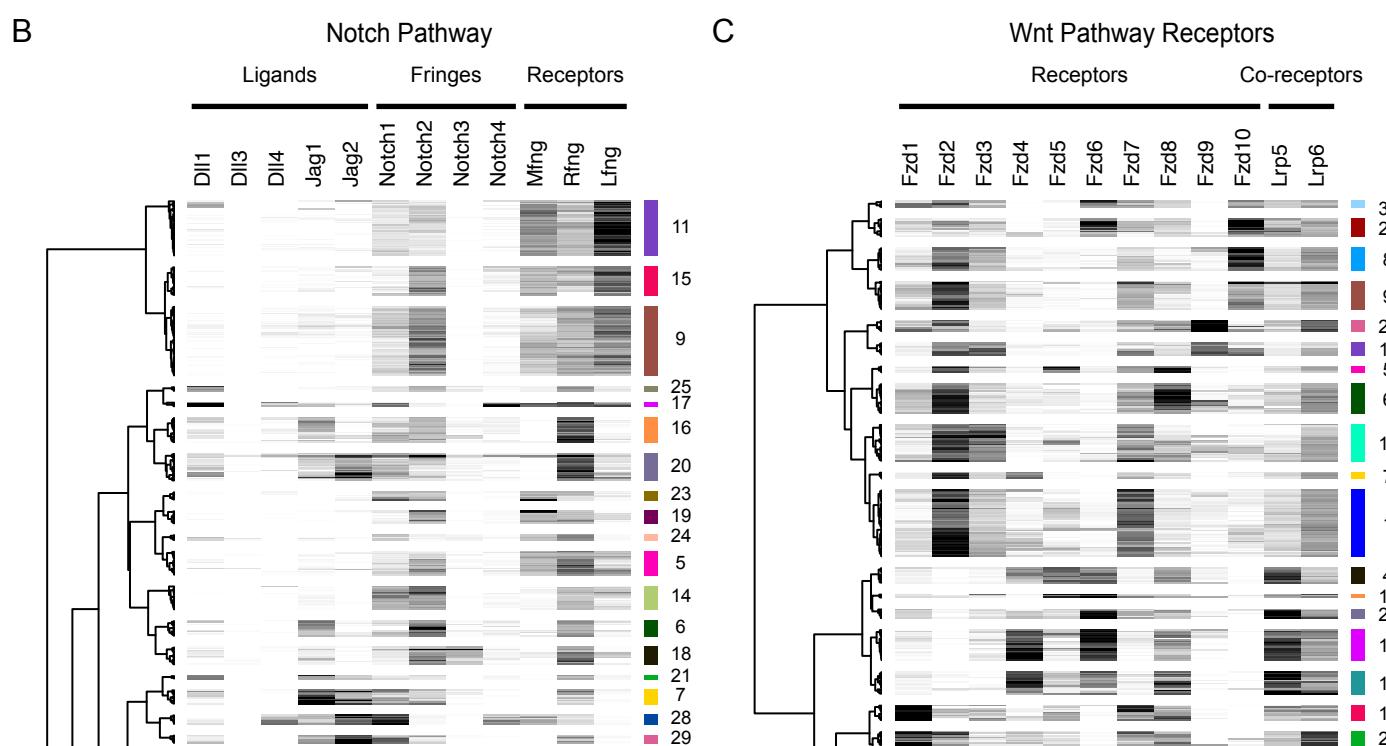
Profile 16 is in a lot of epithelial cells (kidney, skin, bladder)

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

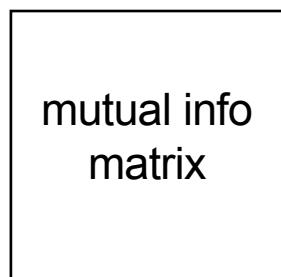
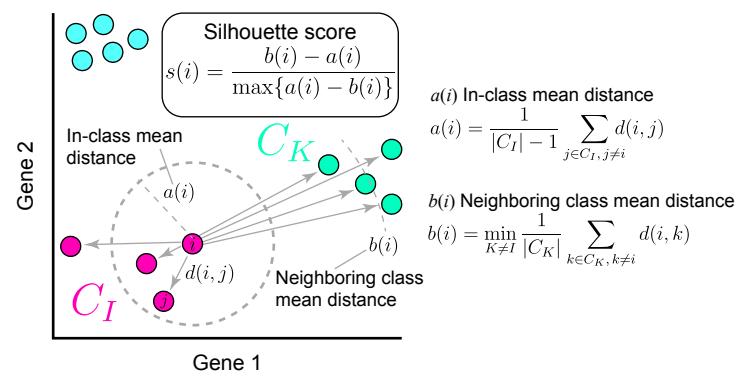
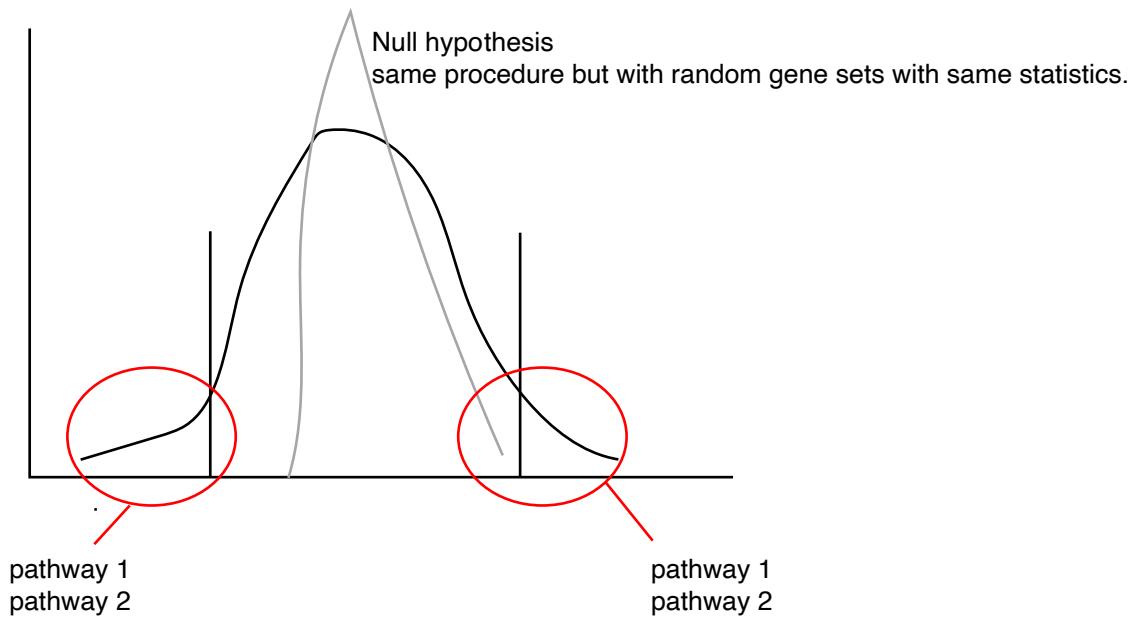
Figure 4: Wnt and Notch also show broadly dispersed recurrent pathway expression motifs



black points → supplementary table



example of the statistic for TGF-->distribution of stat over pathways-->identification of the significantly recurrent



Pathway-pathay correlations

private pathways