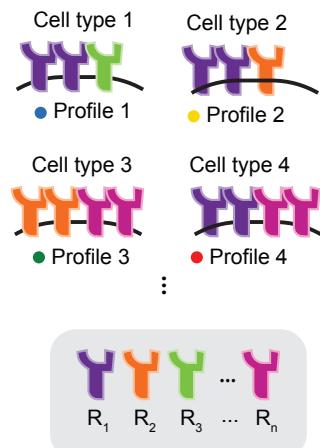


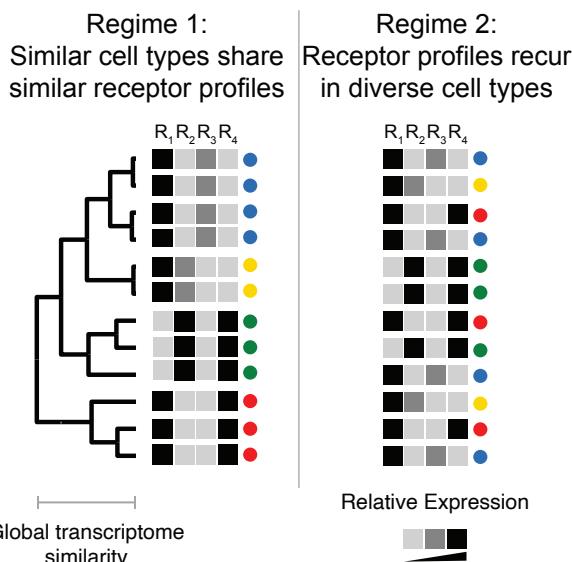
Figure 1: Pathway expression profiles could recur across diverse cell types

A

Receptor expression profiles

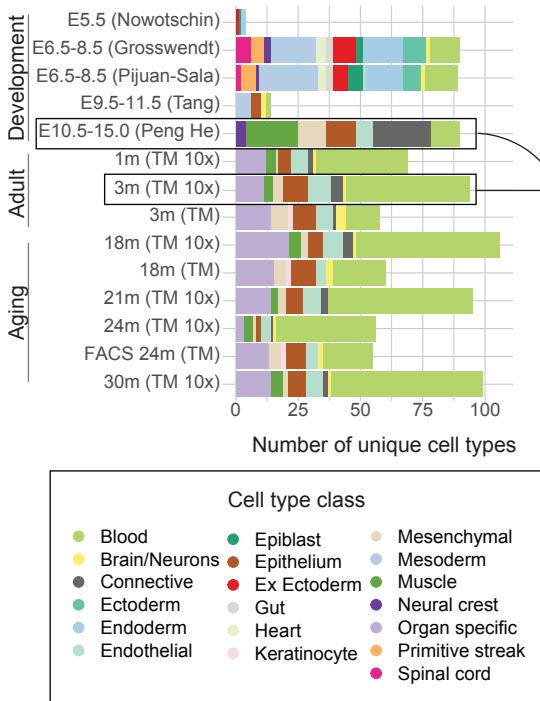


B



C

Multiple mouse cell atlas datasets

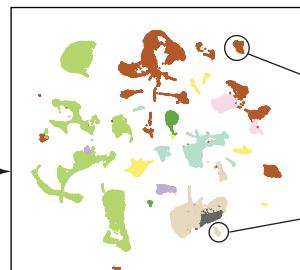


D

Individual cell atlases

1 dot = 1 cell

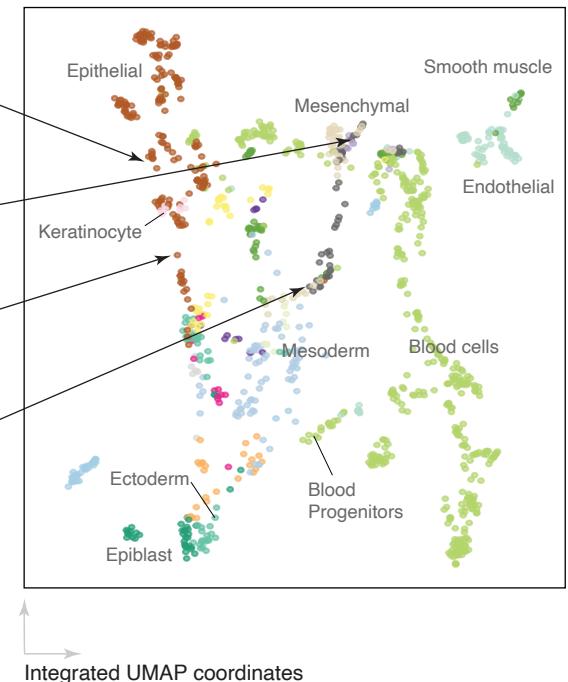
Tabula muris (3 month old mouse)



Integrated cell state atlas, cluster-averaged profiles

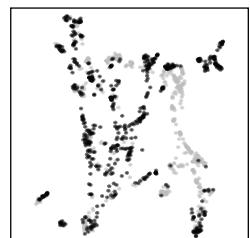
All data sets in (C)

1 dot = 1 cell cluster



E

TGF- β : 52% of cell types



Wnt: 31% of cell types



Notch: 37% of cell types



Dataset UMAP coordinates

F

cluster of cell types

Gene 2

Gene 1

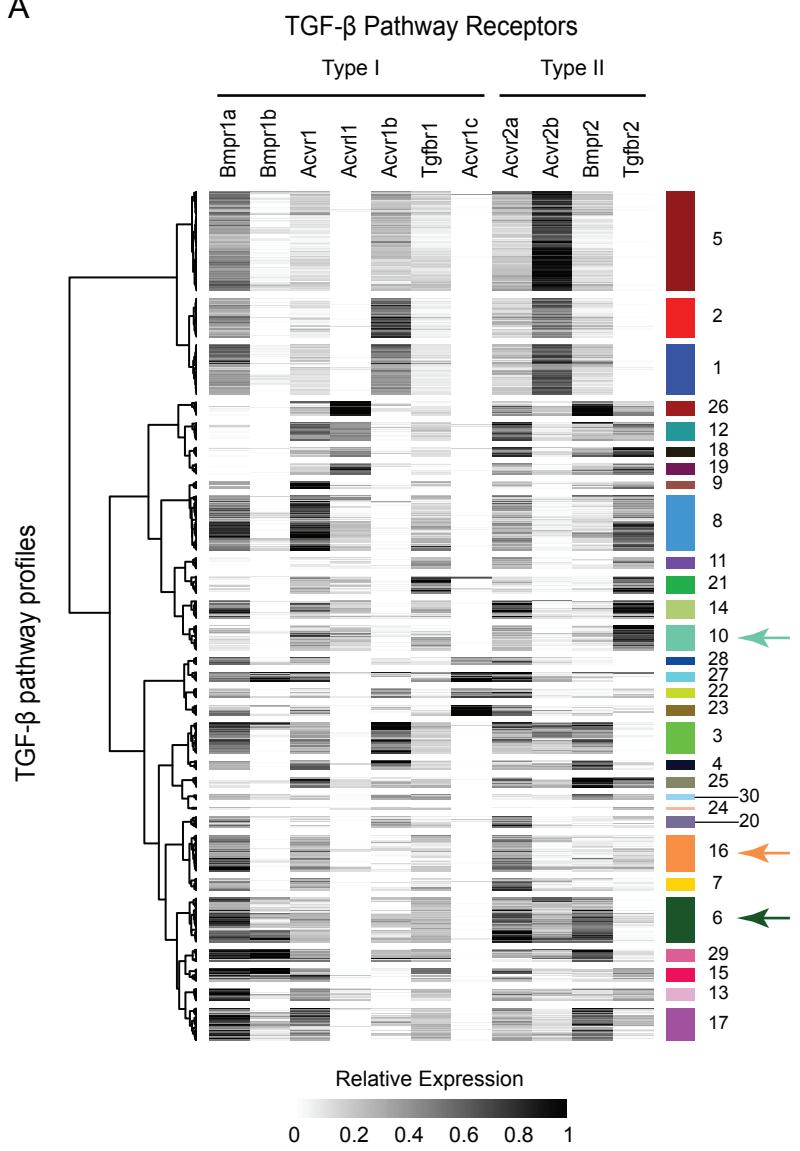
$$\text{In-class mean distance: } a(i) = \frac{1}{|C_I| - 1} \sum_{j \in C_I, j \neq i} d(i, j)$$

$$\text{Neighboring class mean distance: } b(i) = \min_{K \neq I} \frac{1}{|C_K|} \sum_{k \in C_K} d(i, k)$$

$$\text{Silhouette score: } s(i) = \frac{b(i) - a(i)}{\max\{a(i) - b(i)\}}$$

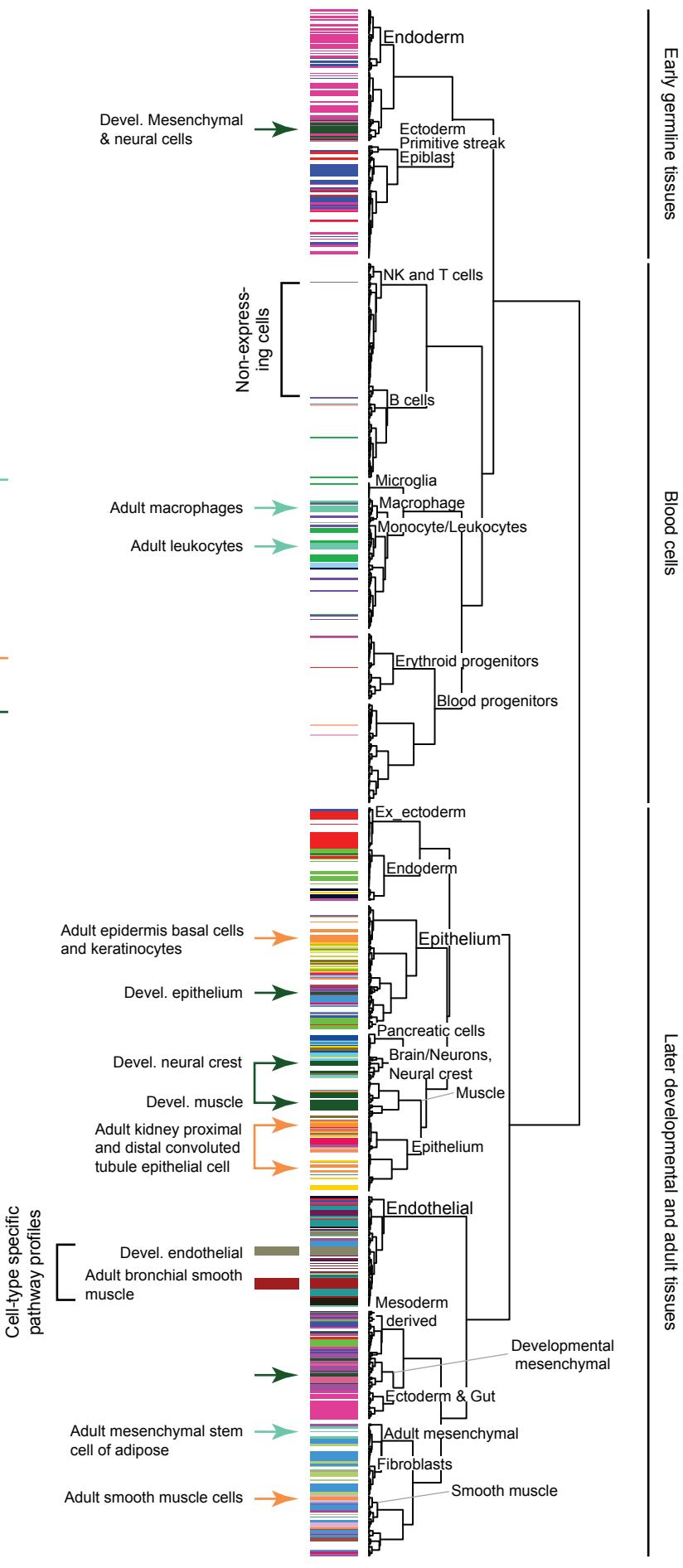
Figure 2: TGF- β Receptors exhibit distinct and recurrent pathway expression profiles

A



C

Global distribution of pathway profiles



B

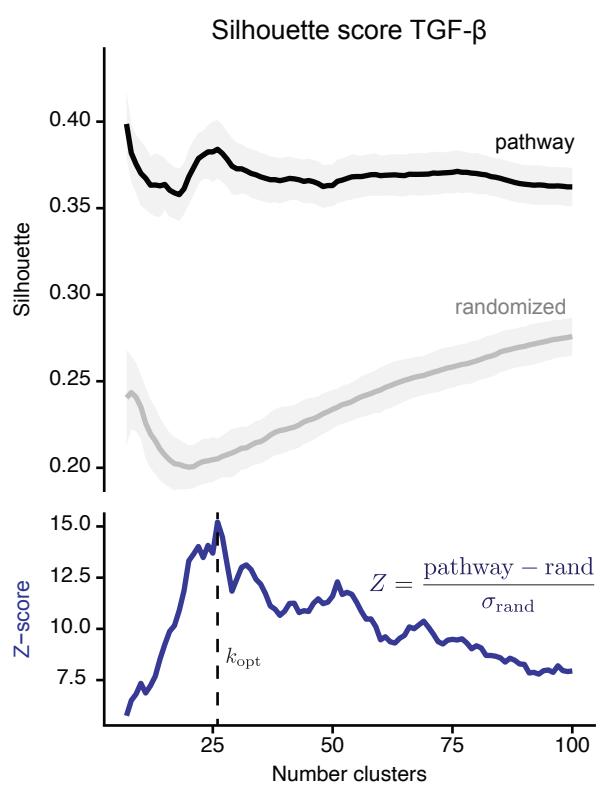
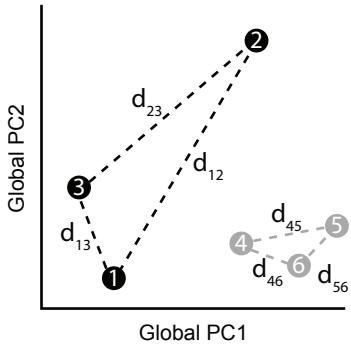


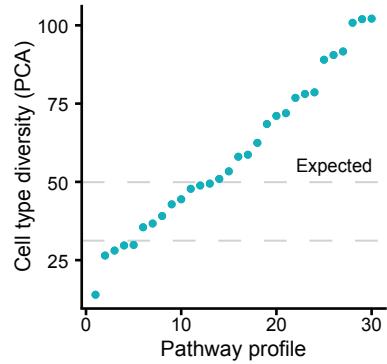
Figure 3: TGF- β expression motifs are dispersed across cell types and organs

A

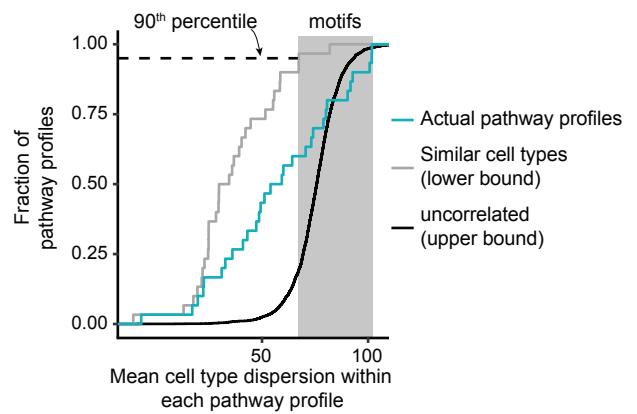
Pairwise distance computation (schematic)
 (Actual computation occurs in 100-dimensional PCA space)



Number of cell types with
 TGF- β profile

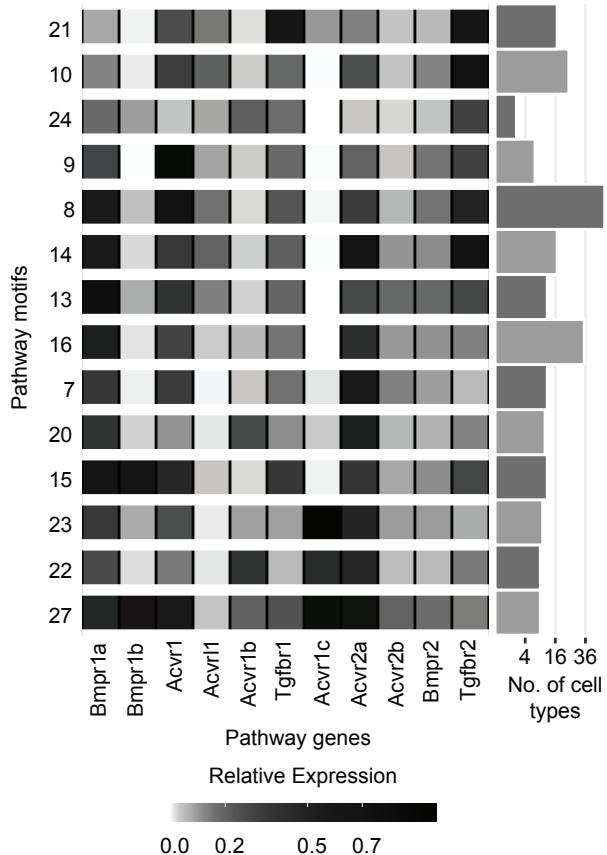


B



D

Broadly Dispersed TGF- β Motifs



E

Broadly Dispersed TGF- β Motifs

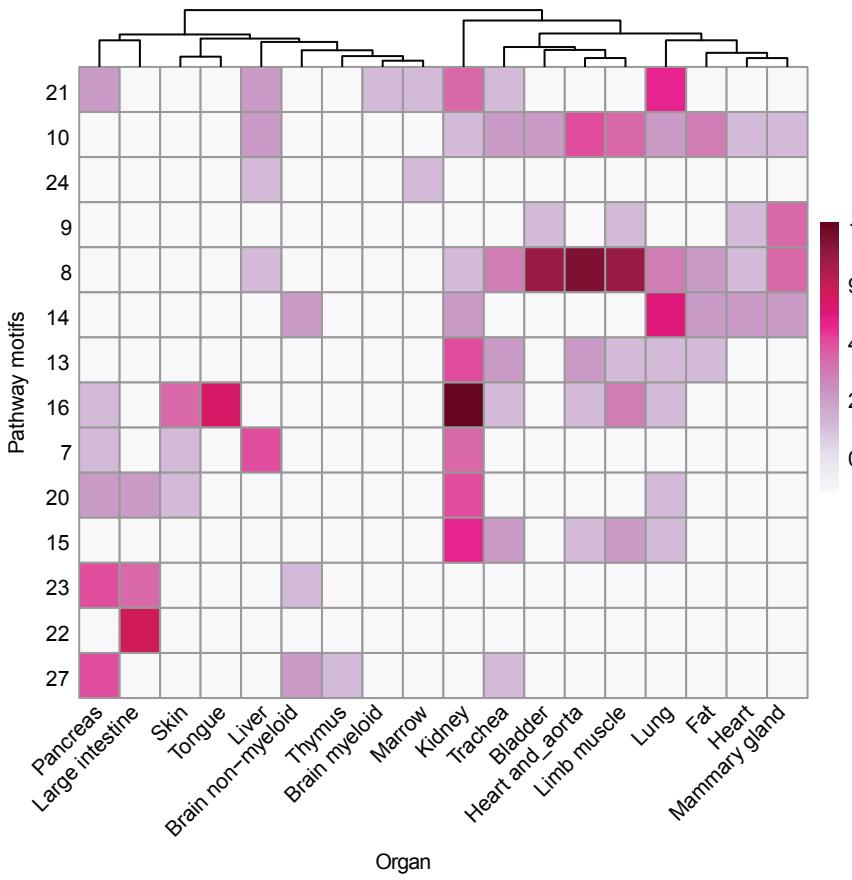
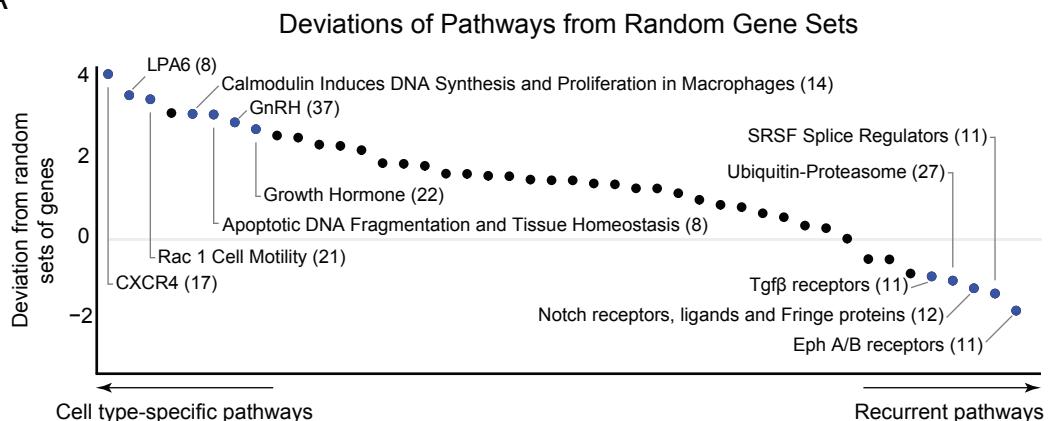
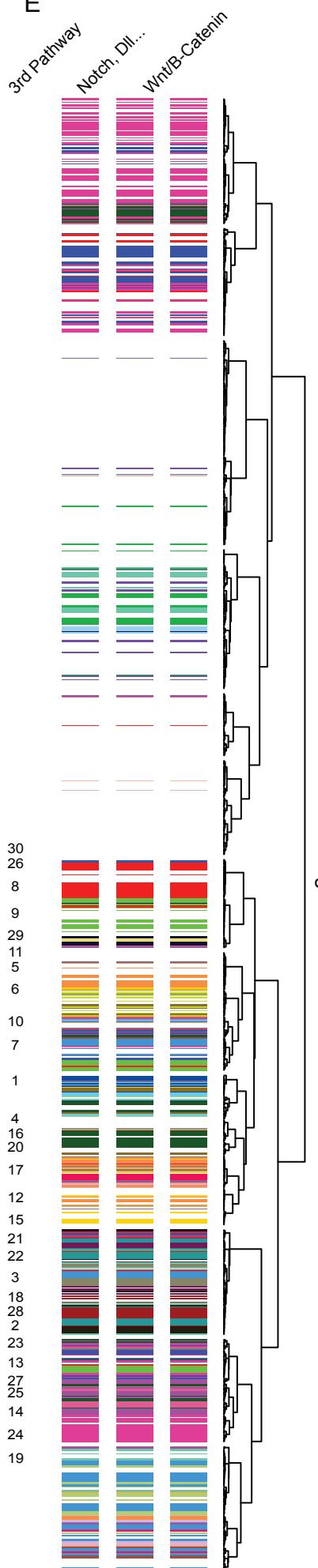


Figure 4: Wnt and Notch also show broadly dispersed recurrent pathway expression motifs

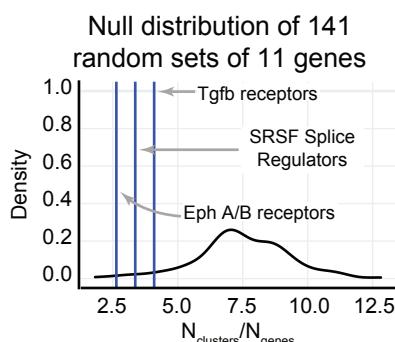
A



E

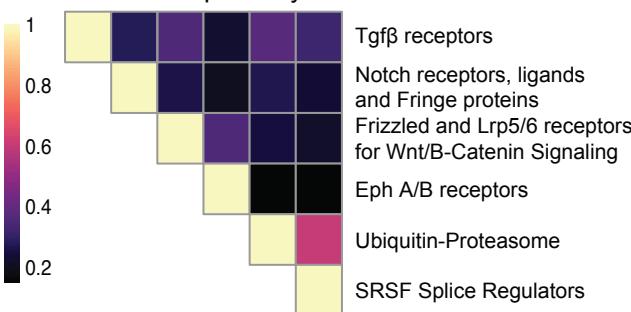


B

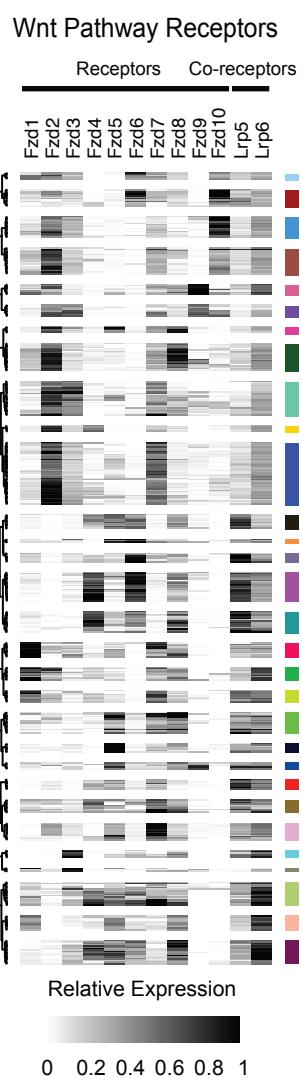
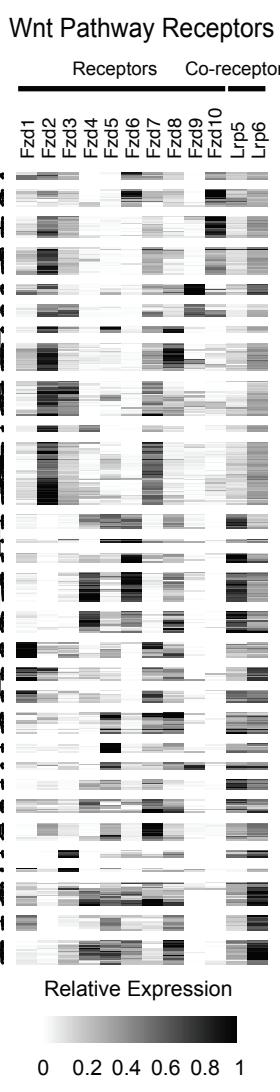
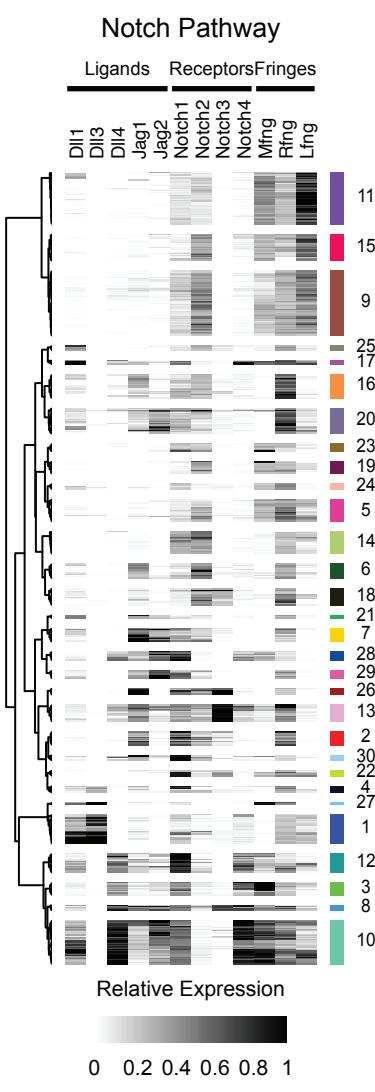


C

Mutual information between recurrent pathways



D



Global dendrogram

