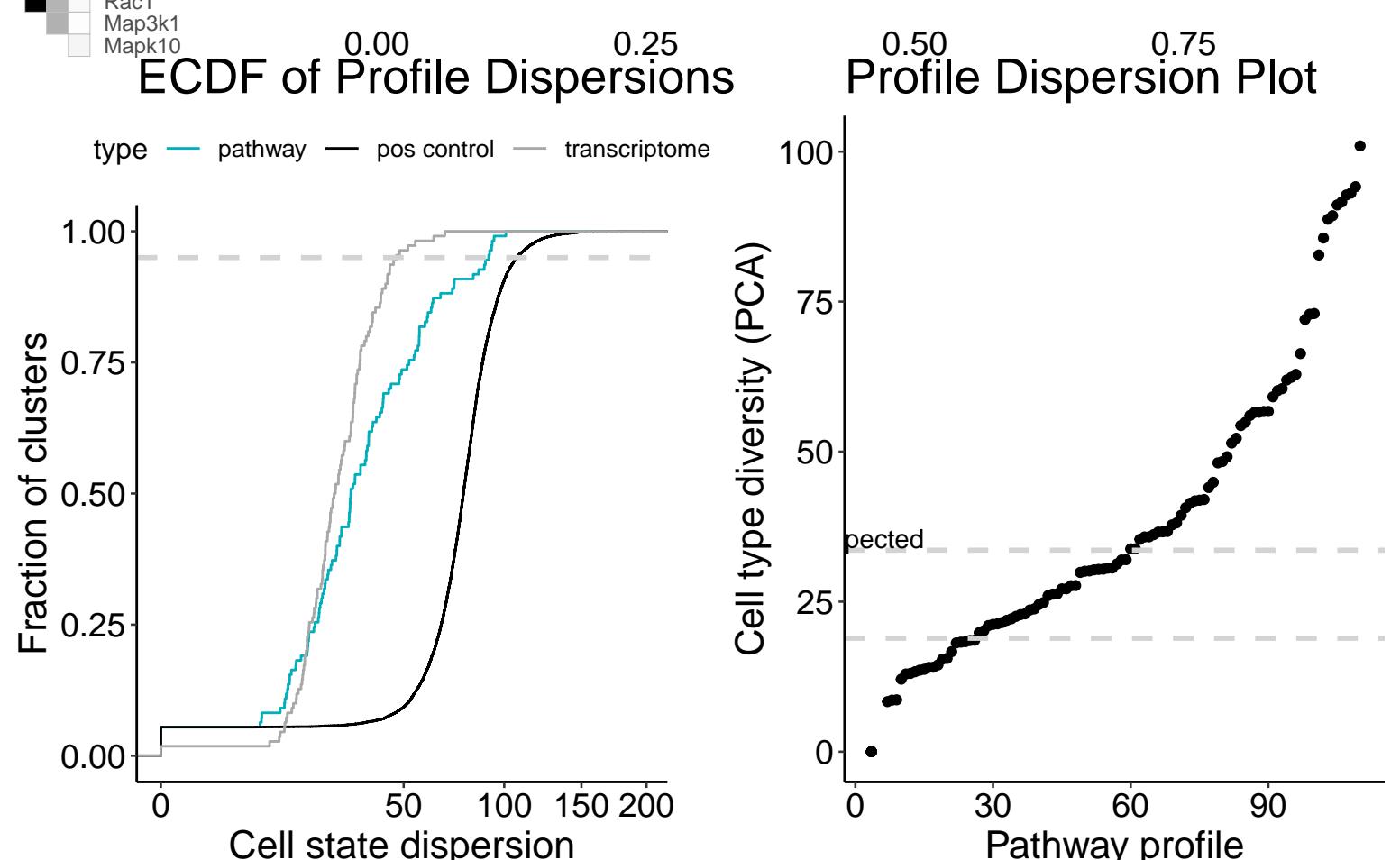
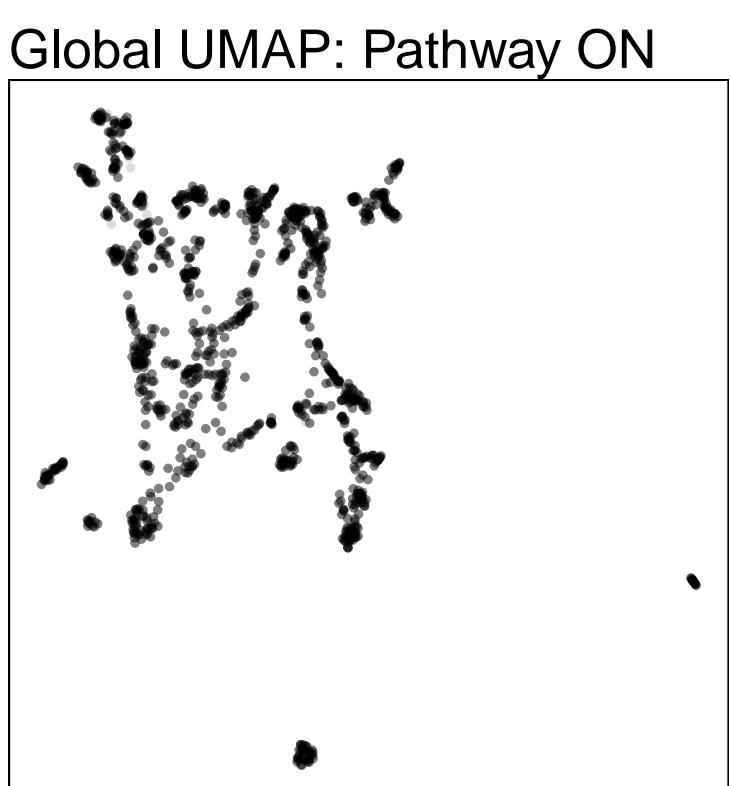
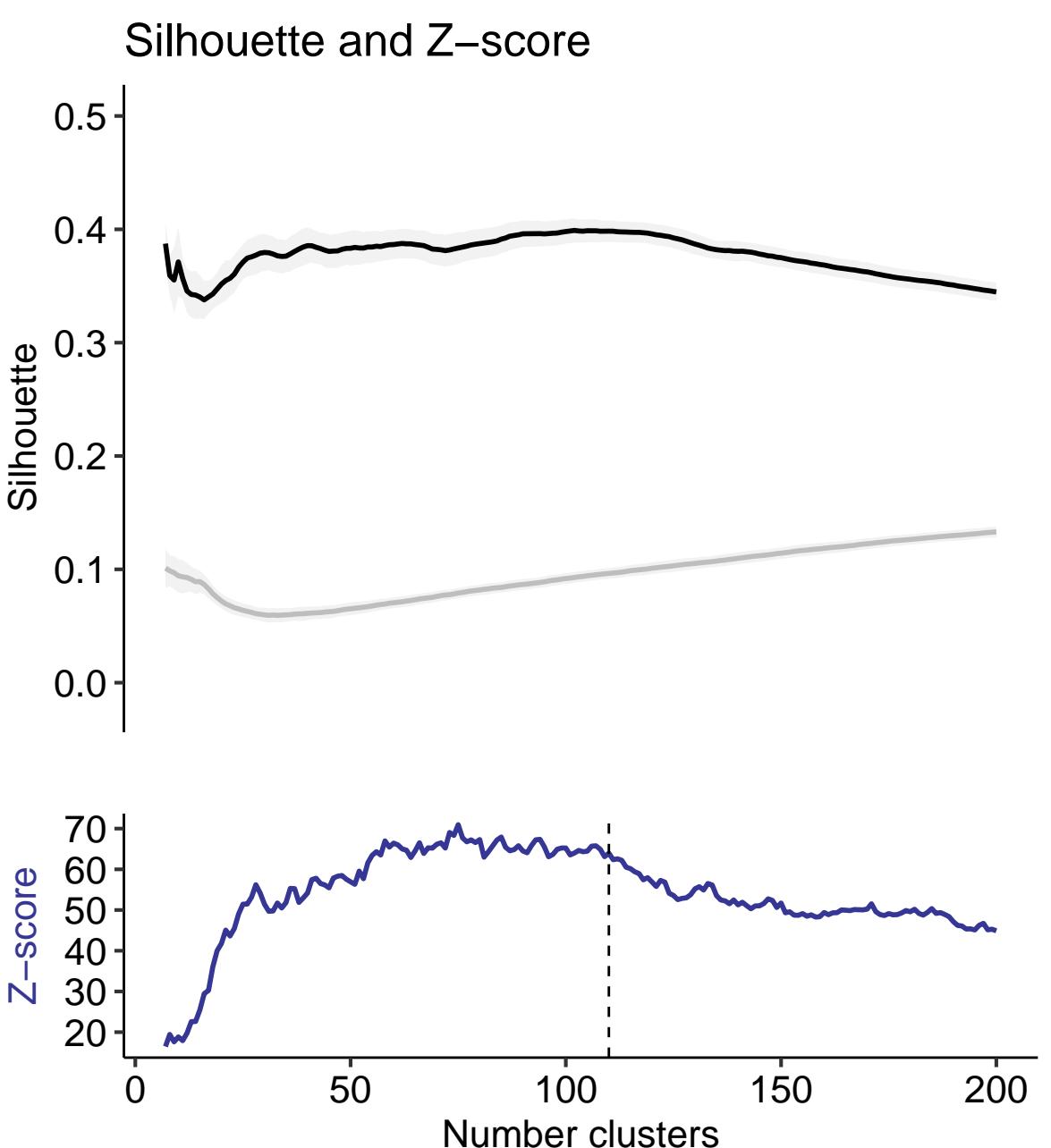
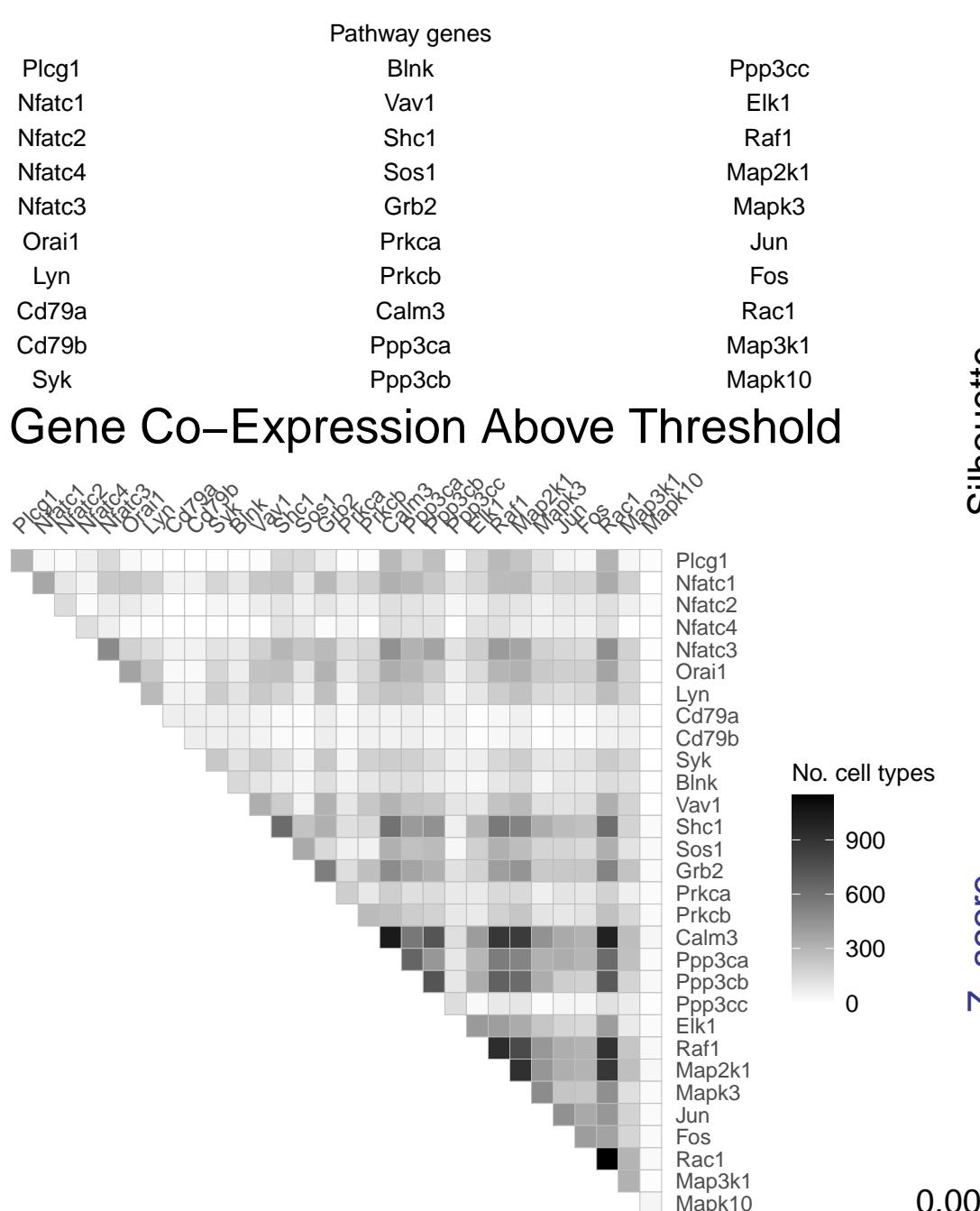
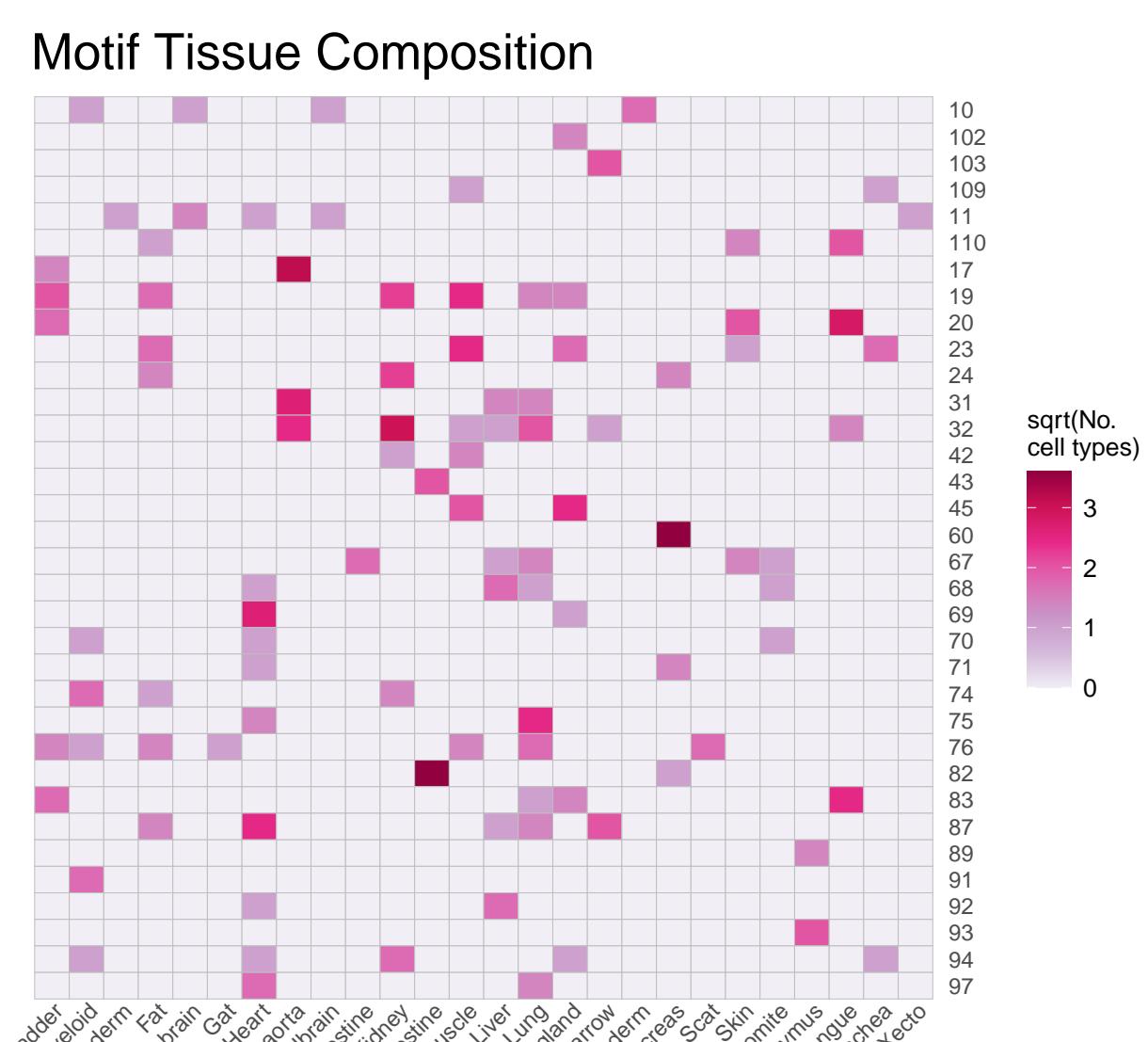
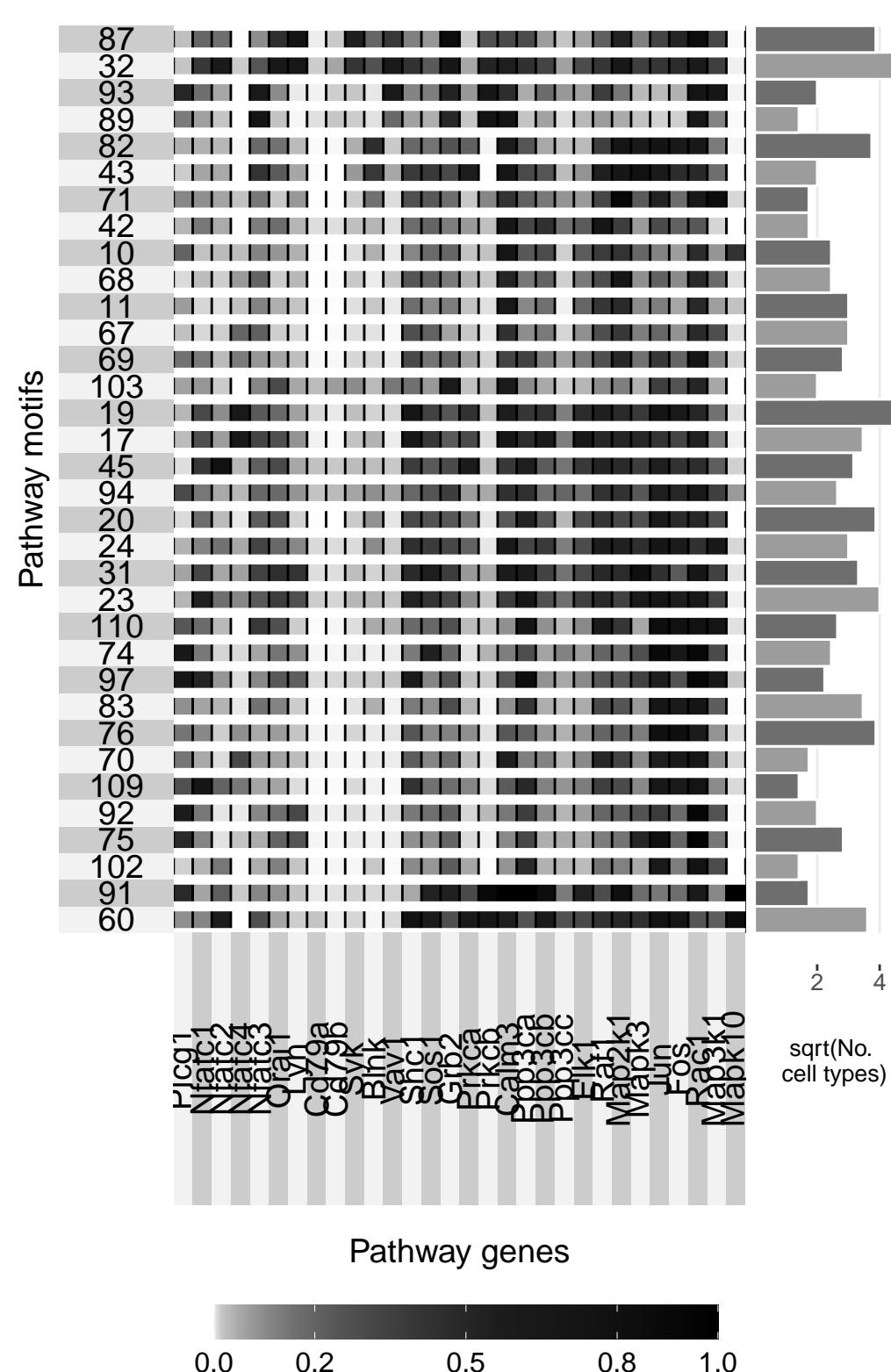


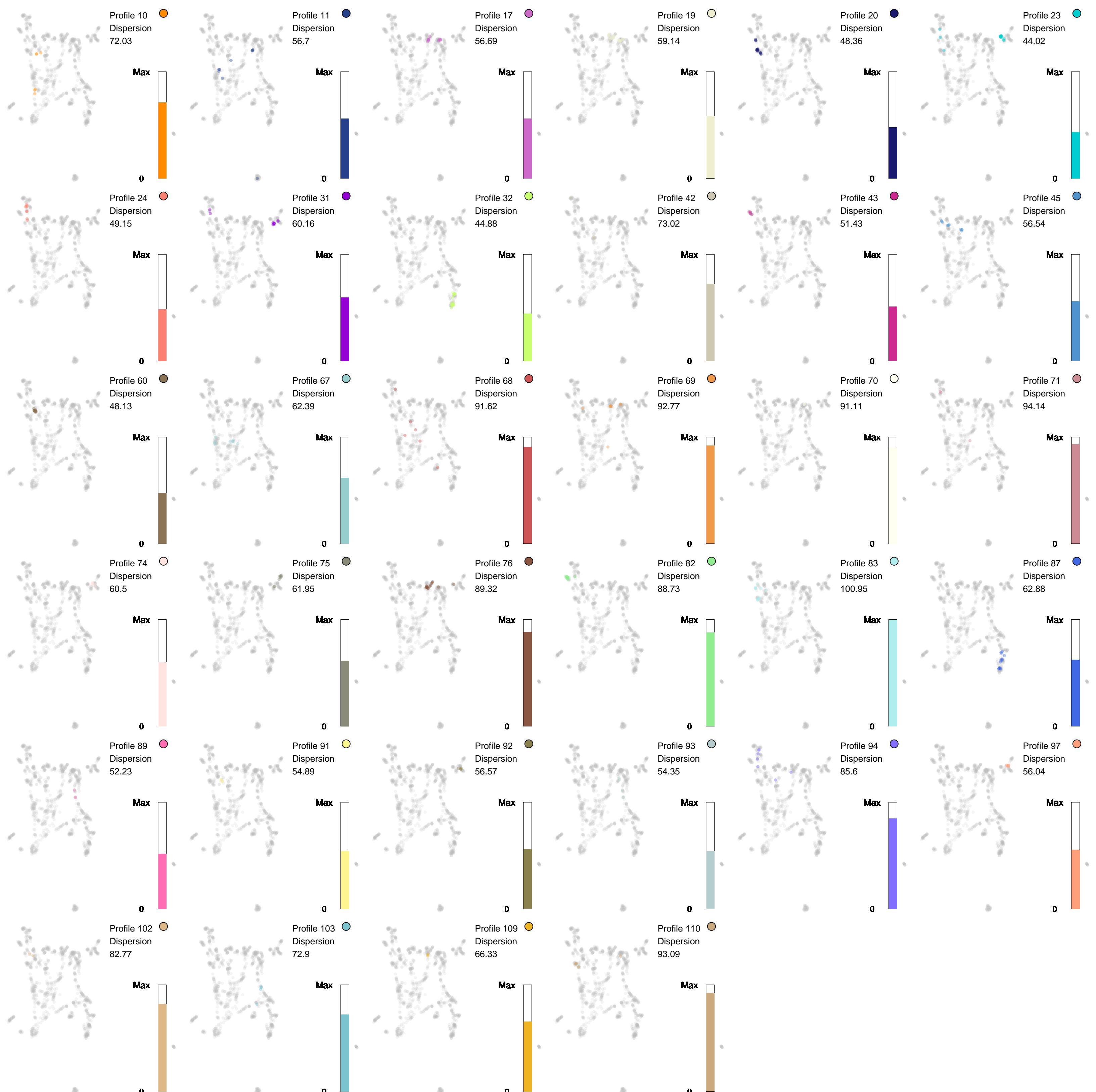
BCR Signaling Pathway (k_opt = 110)



Motifs, Dispersion \geq 90th percentile



BCR Signaling Pathway (k_opt = 110)



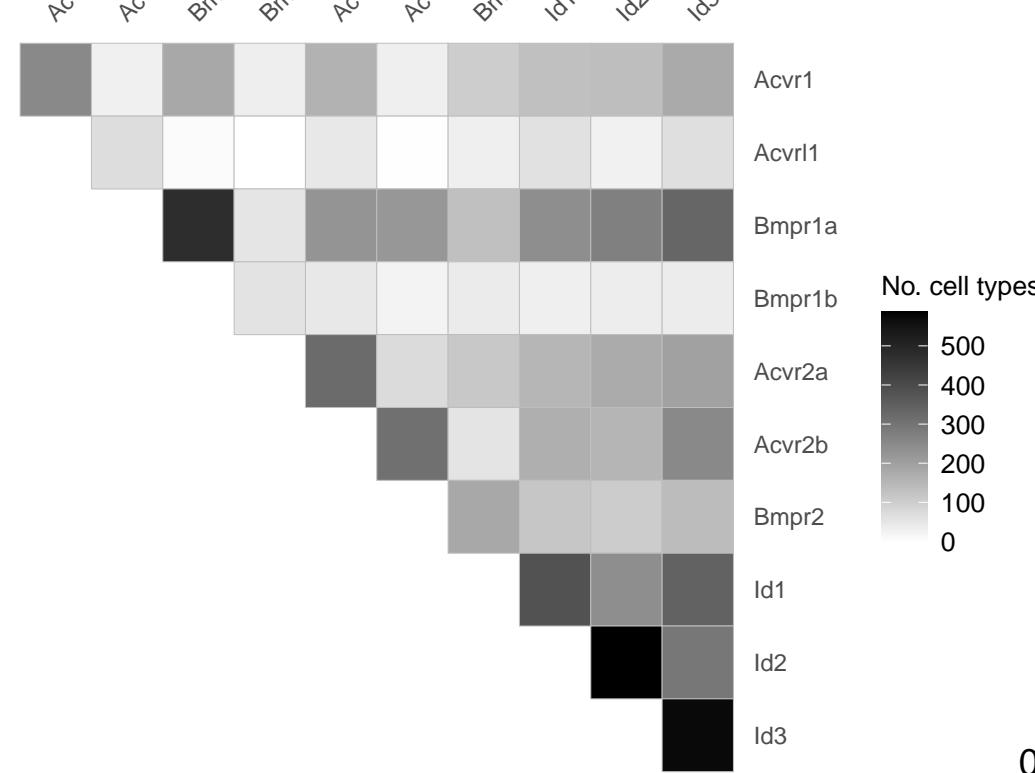
Bmp_down (k_opt = 50)

Pathway genes
Acvr1a
Acvr1b
Bmpr1a
Bmpr1b

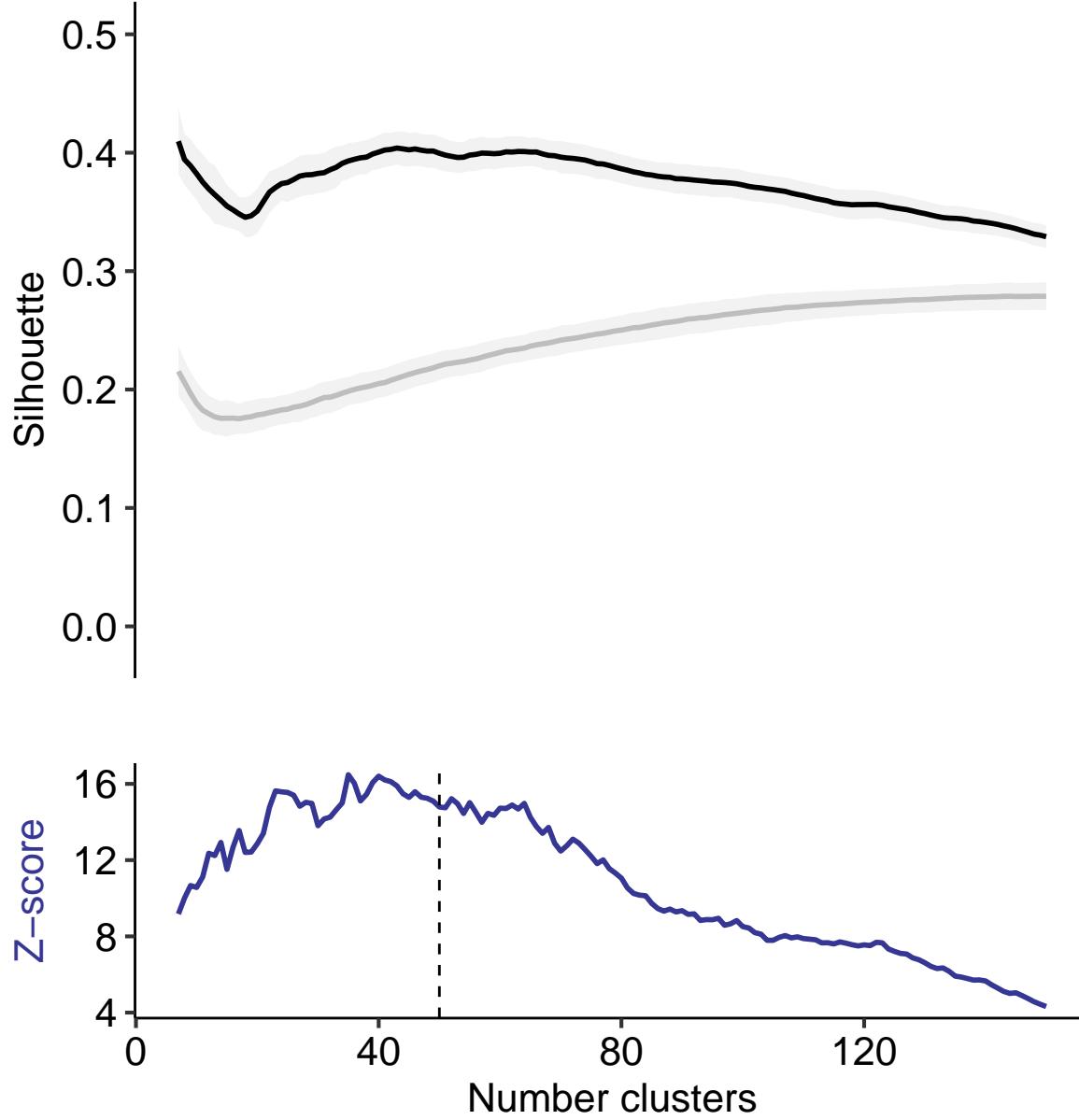
Pathway genes
Acvr2a
Acvr2b
Bmpr2

Id1
Id2
Id3

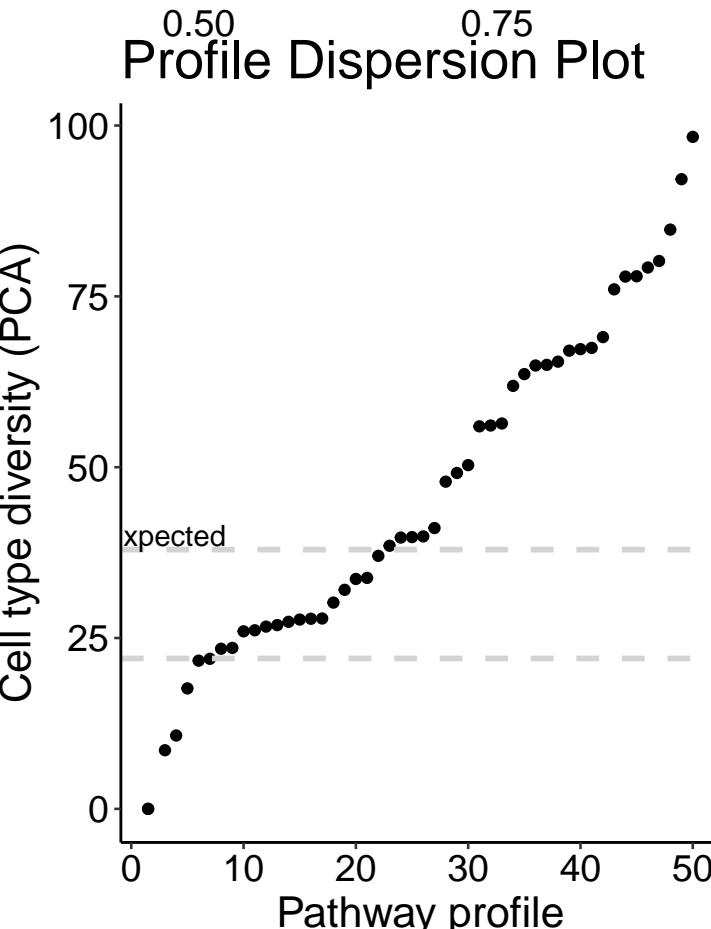
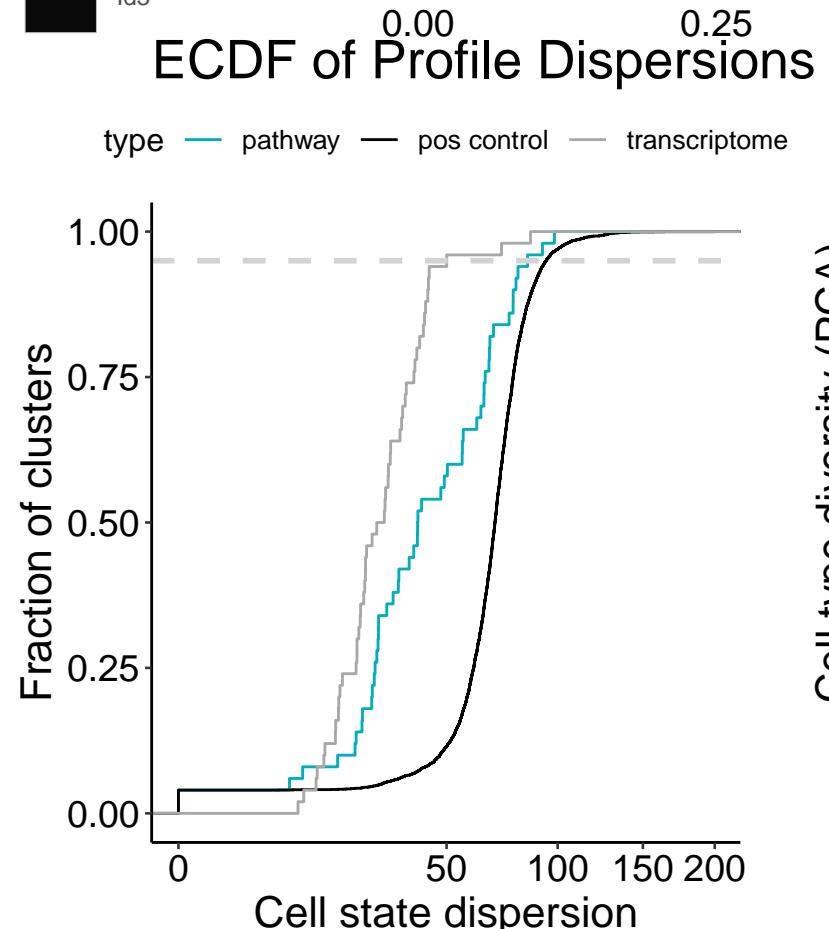
Gene Co-Expression Above Threshold



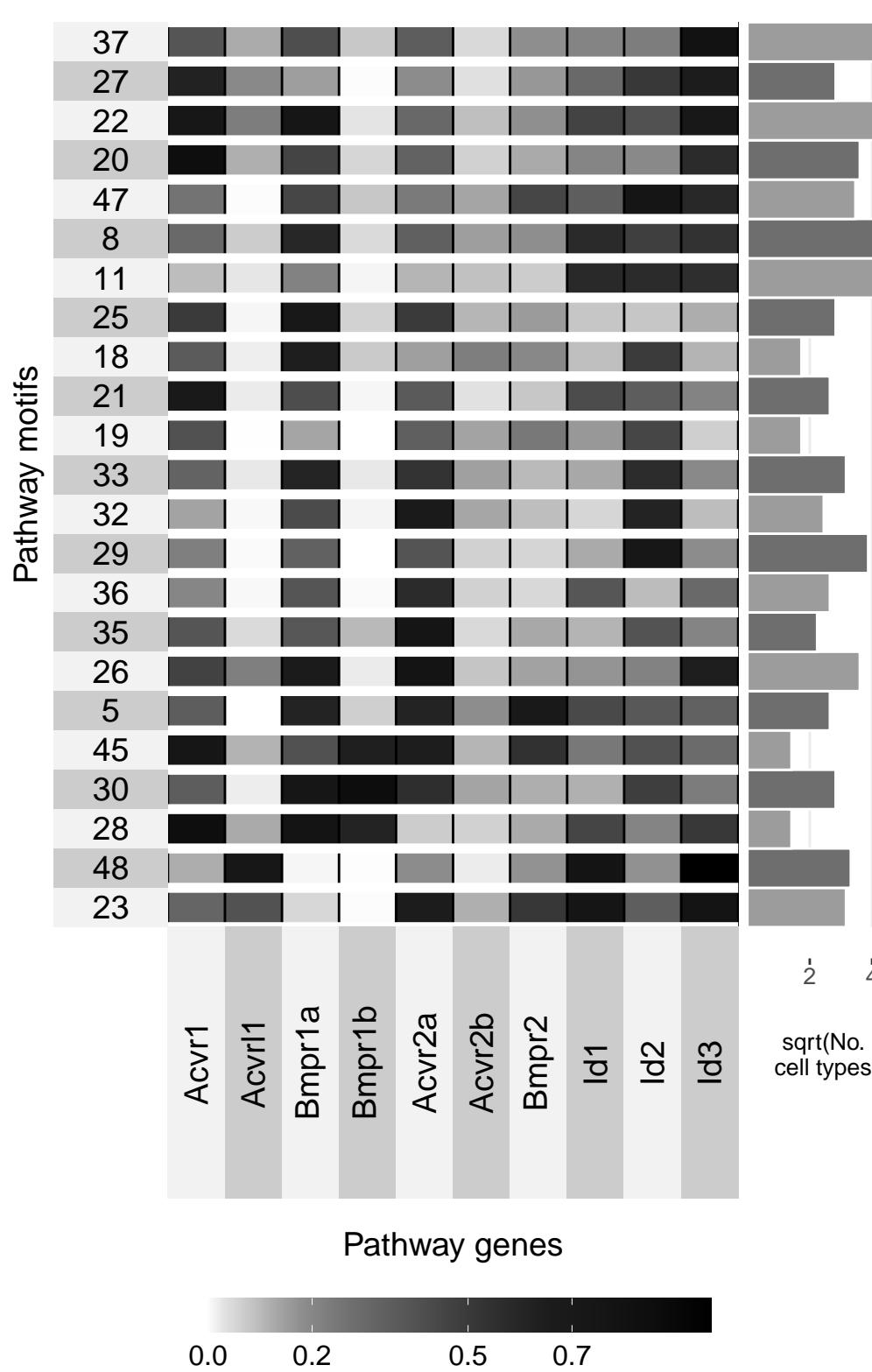
Silhouette and Z-score



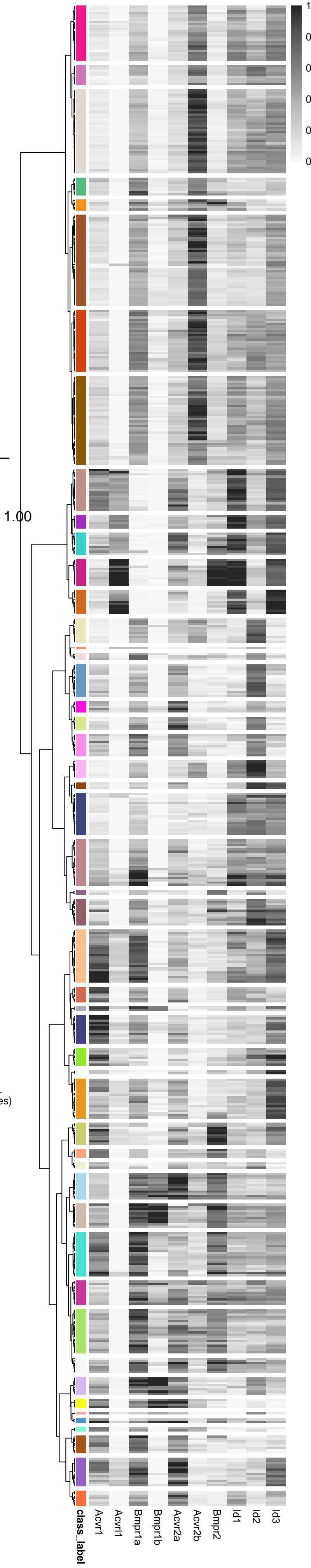
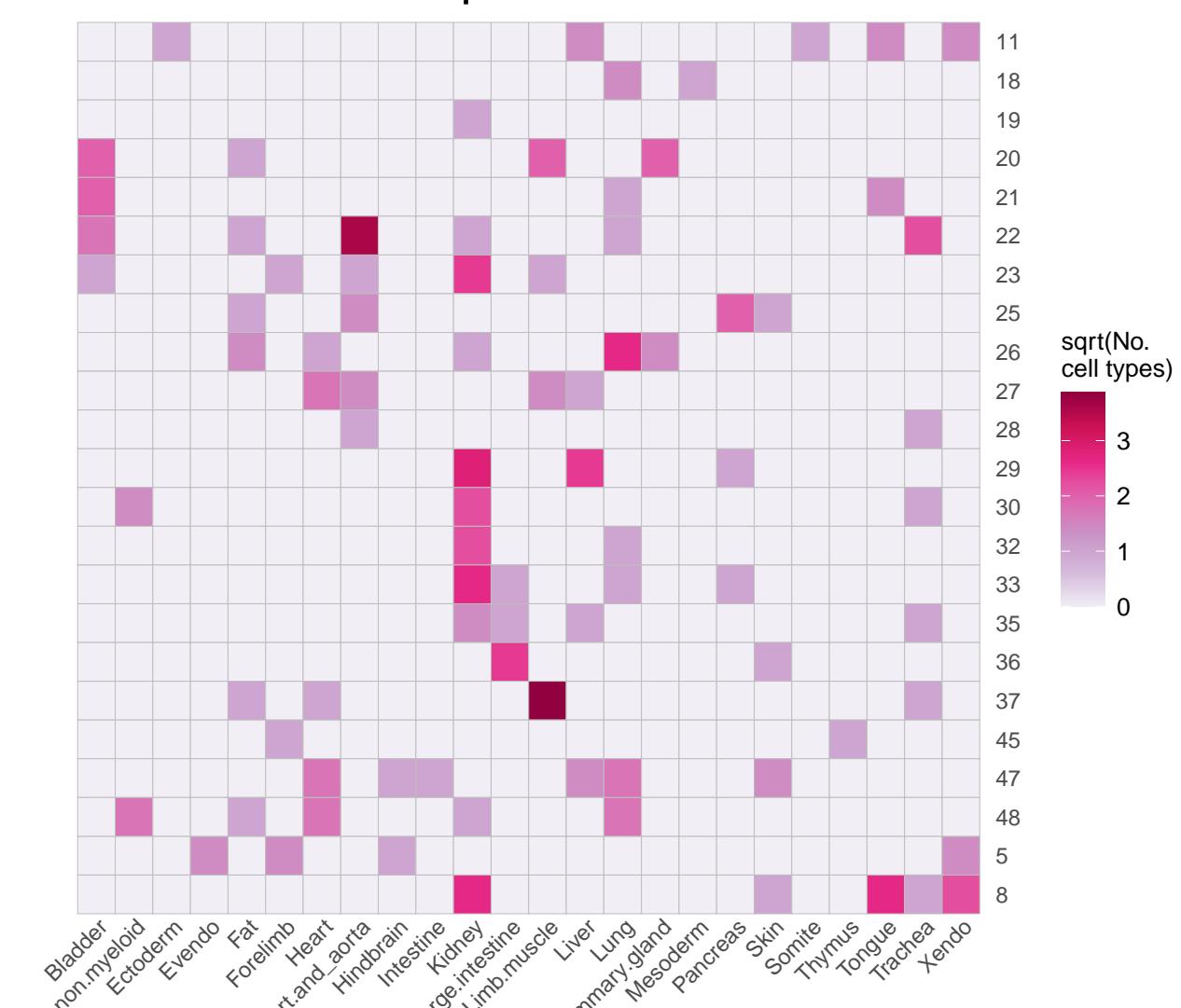
Global UMAP: Pathway ON



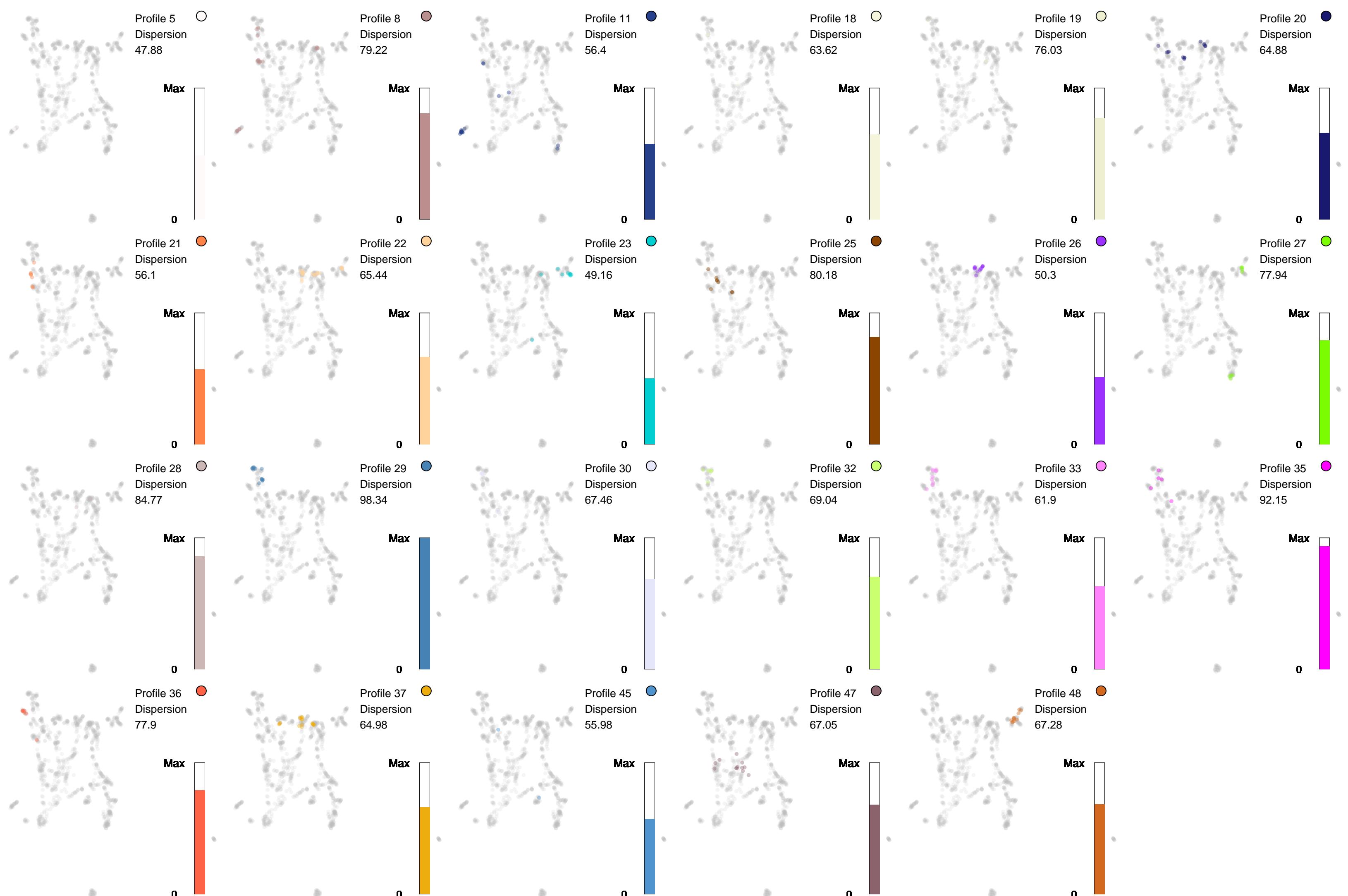
Motifs, Dispersion $\geq 90^{\text{th}}$ percentile



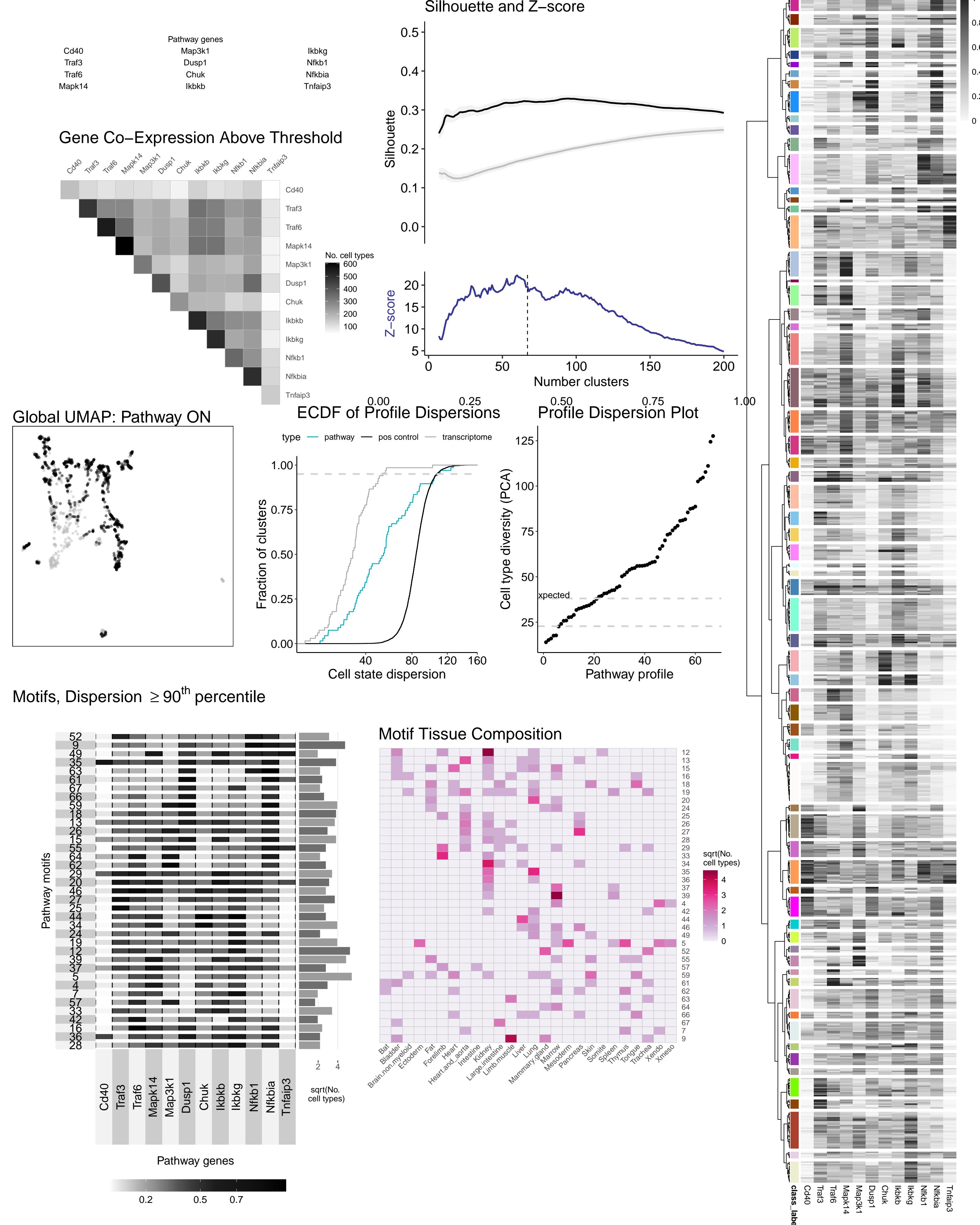
Motif Tissue Composition



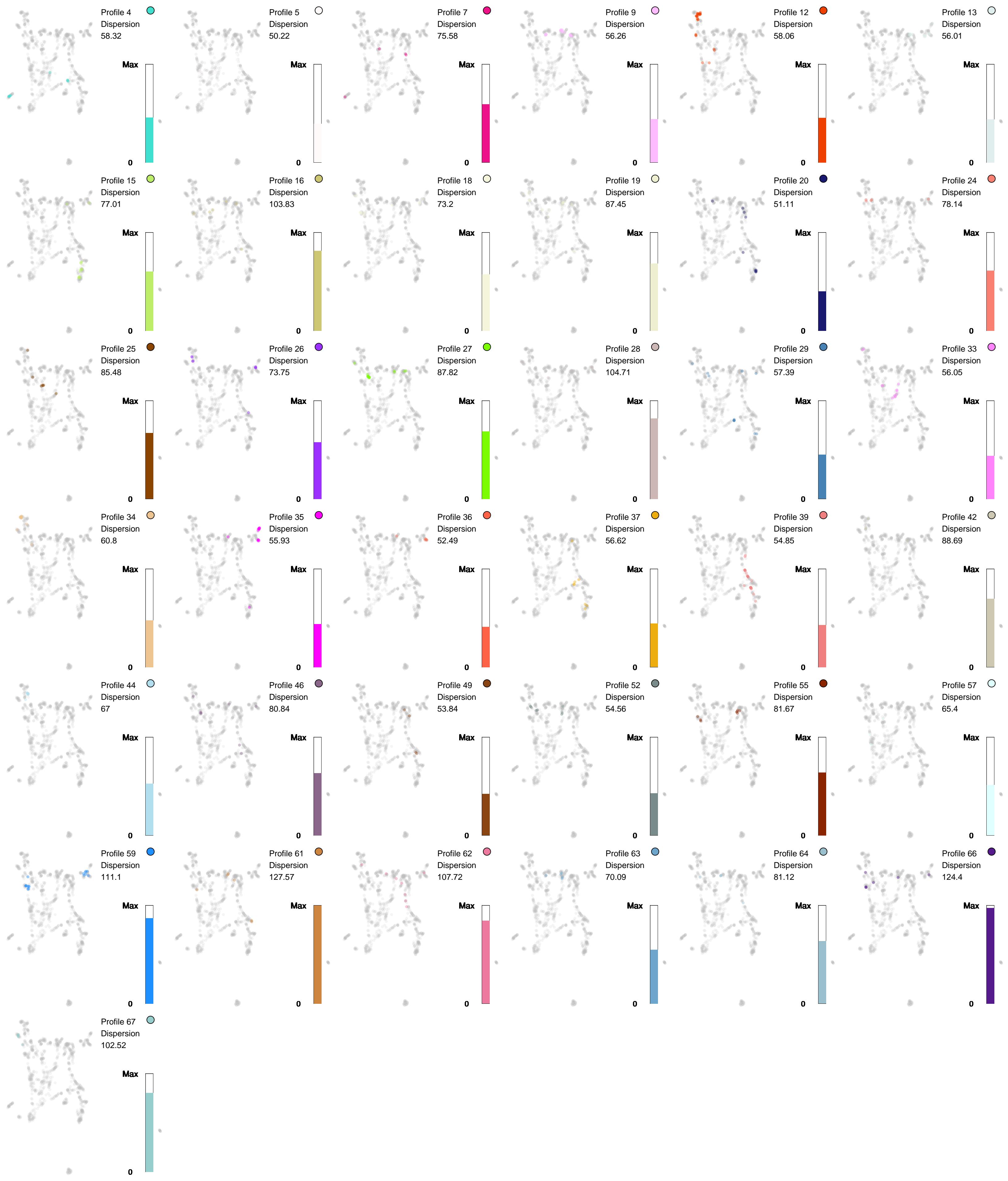
Bmp_down (k_opt = 50)



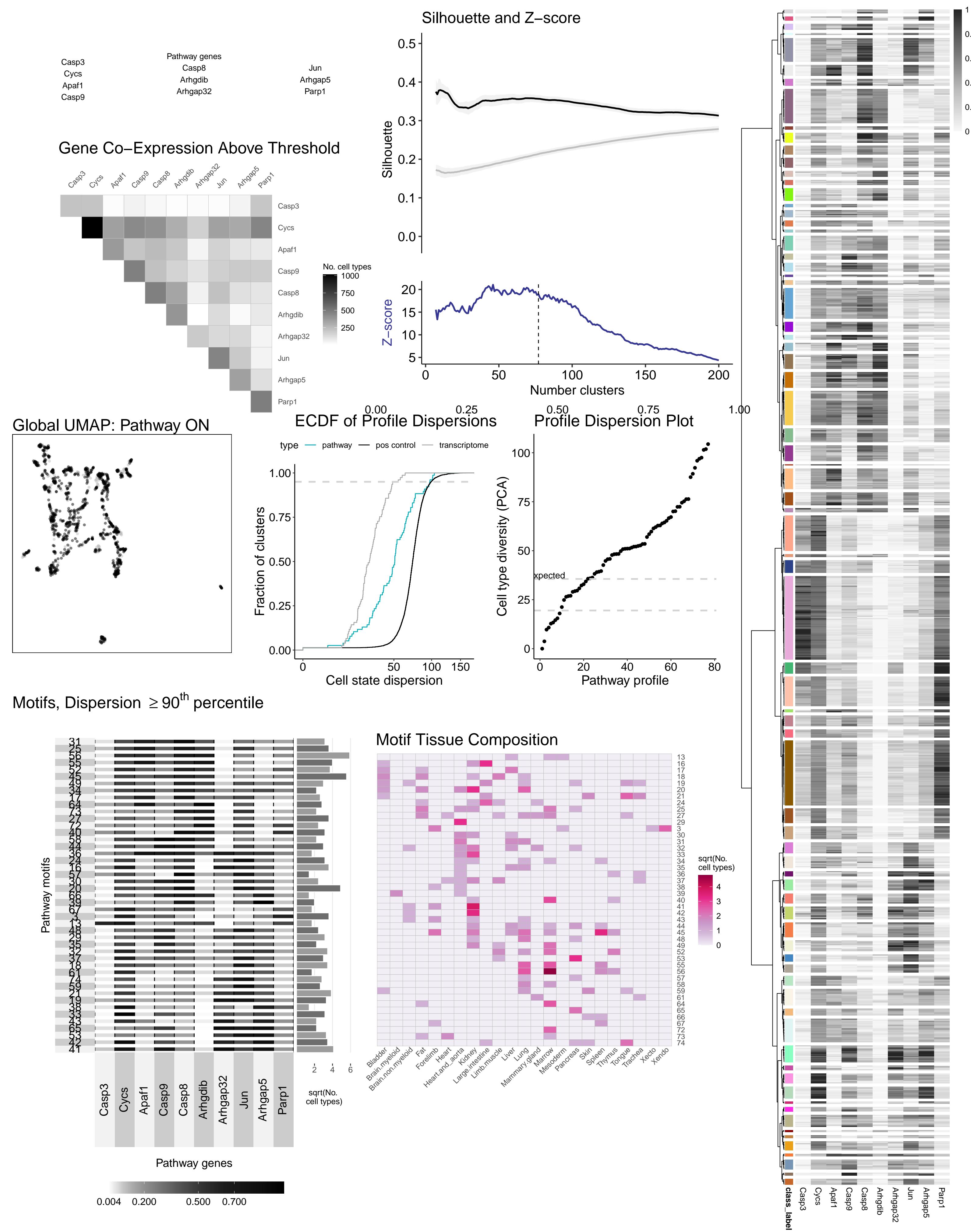
CD40L Signalling Pathway ($k_{opt} = 67$)



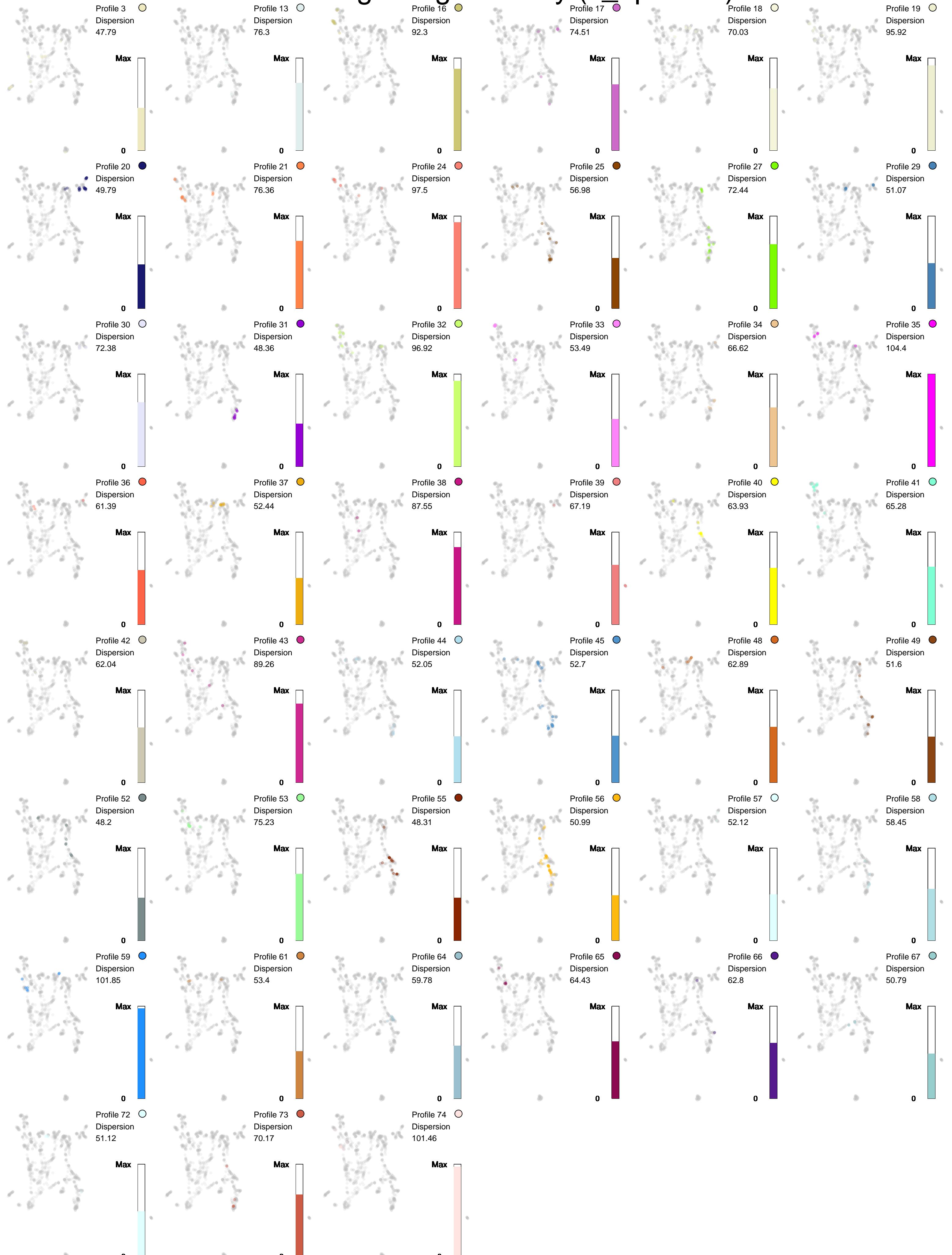
CD40L Signalling Pathway (k_opt = 67)



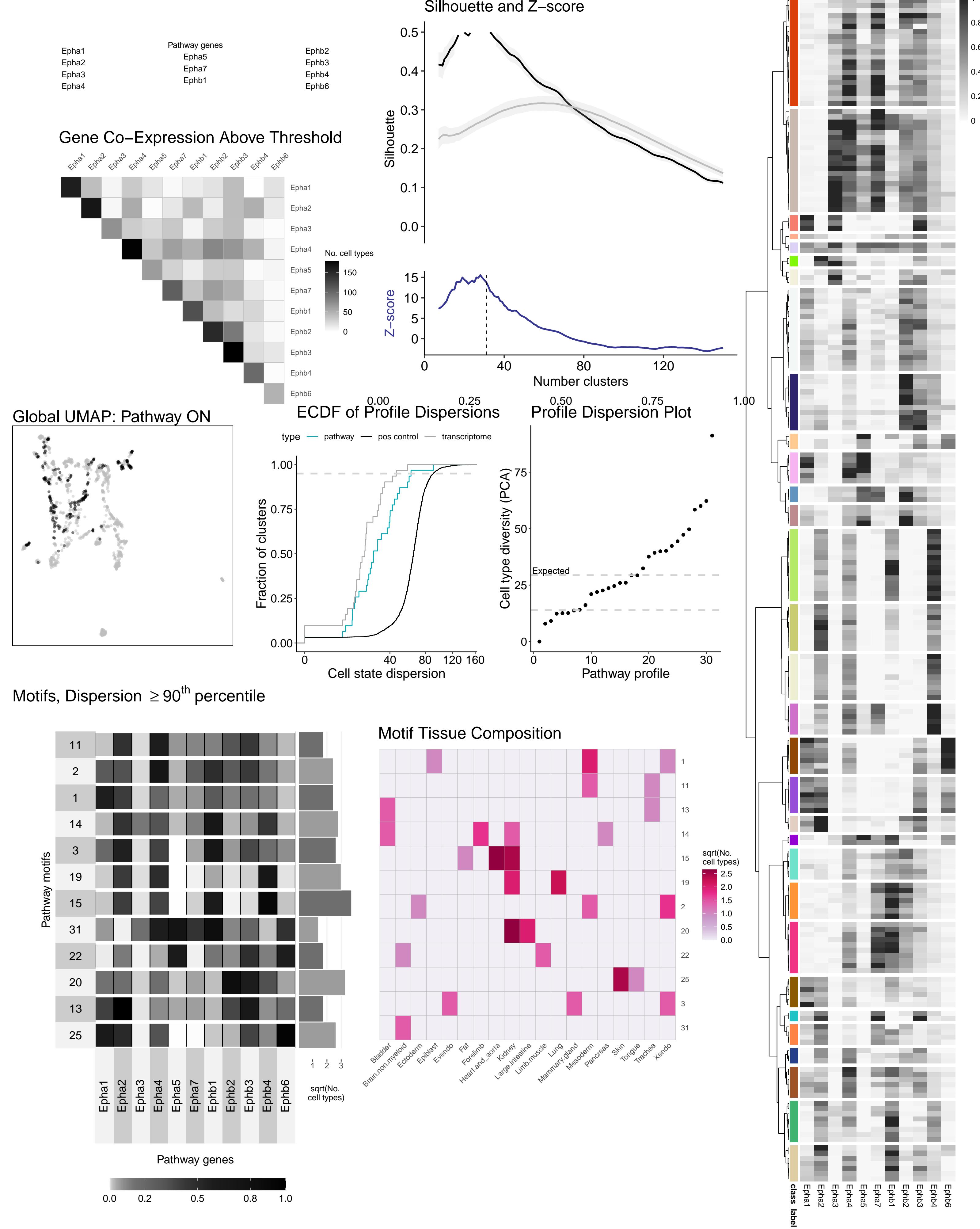
D4-GDI Signaling Pathway (k_opt = 77)



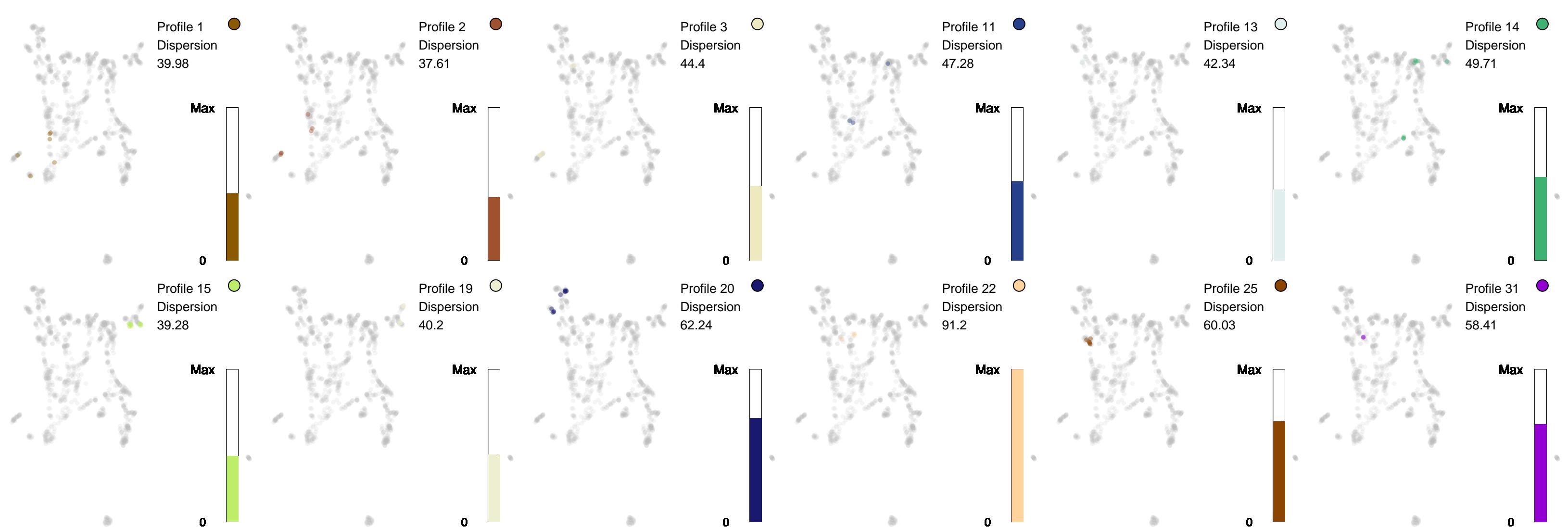
D4-GDI Signaling Pathway ($k_{opt} = 77$)



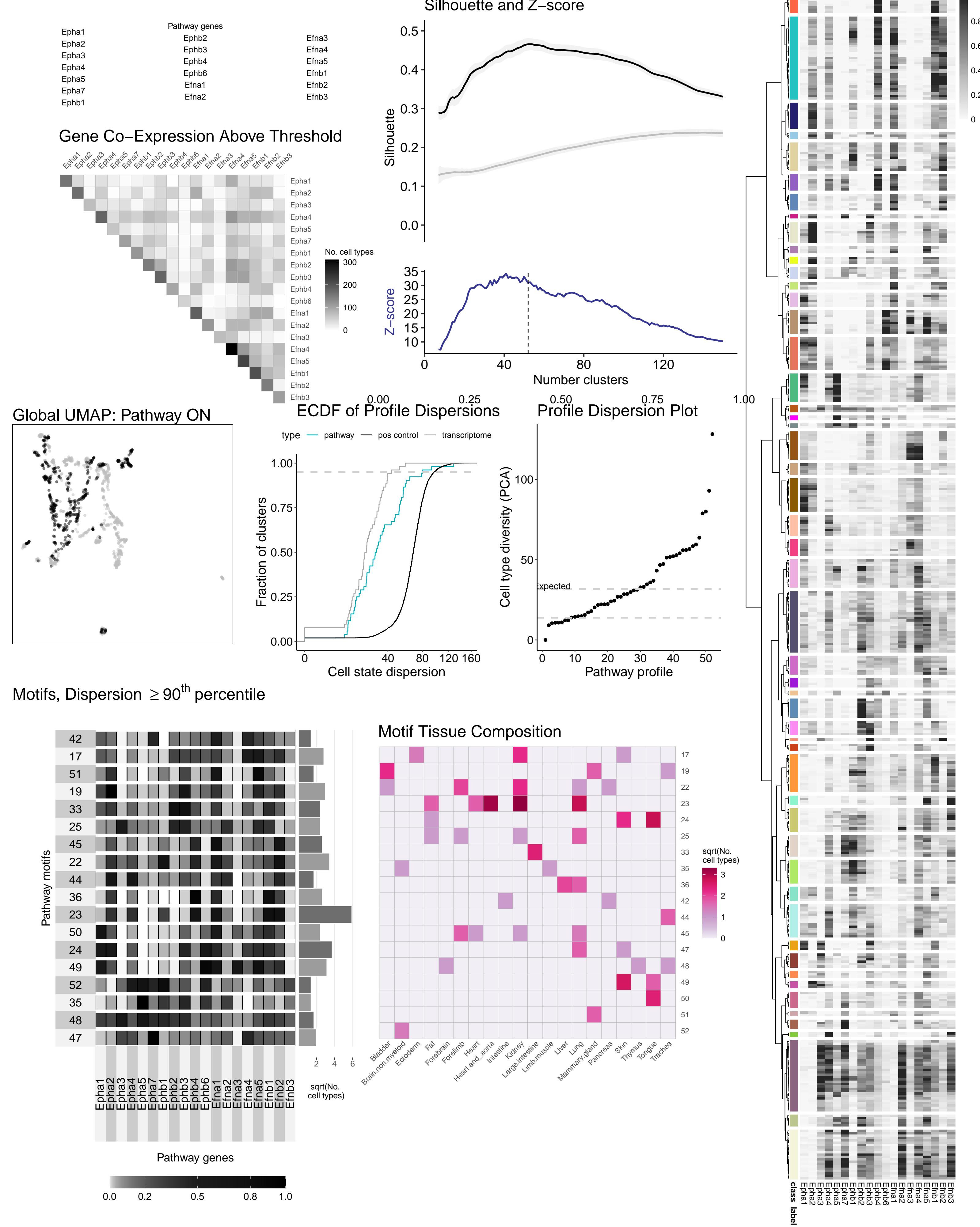
Eph A-B receptors ($k_{opt} = 31$)



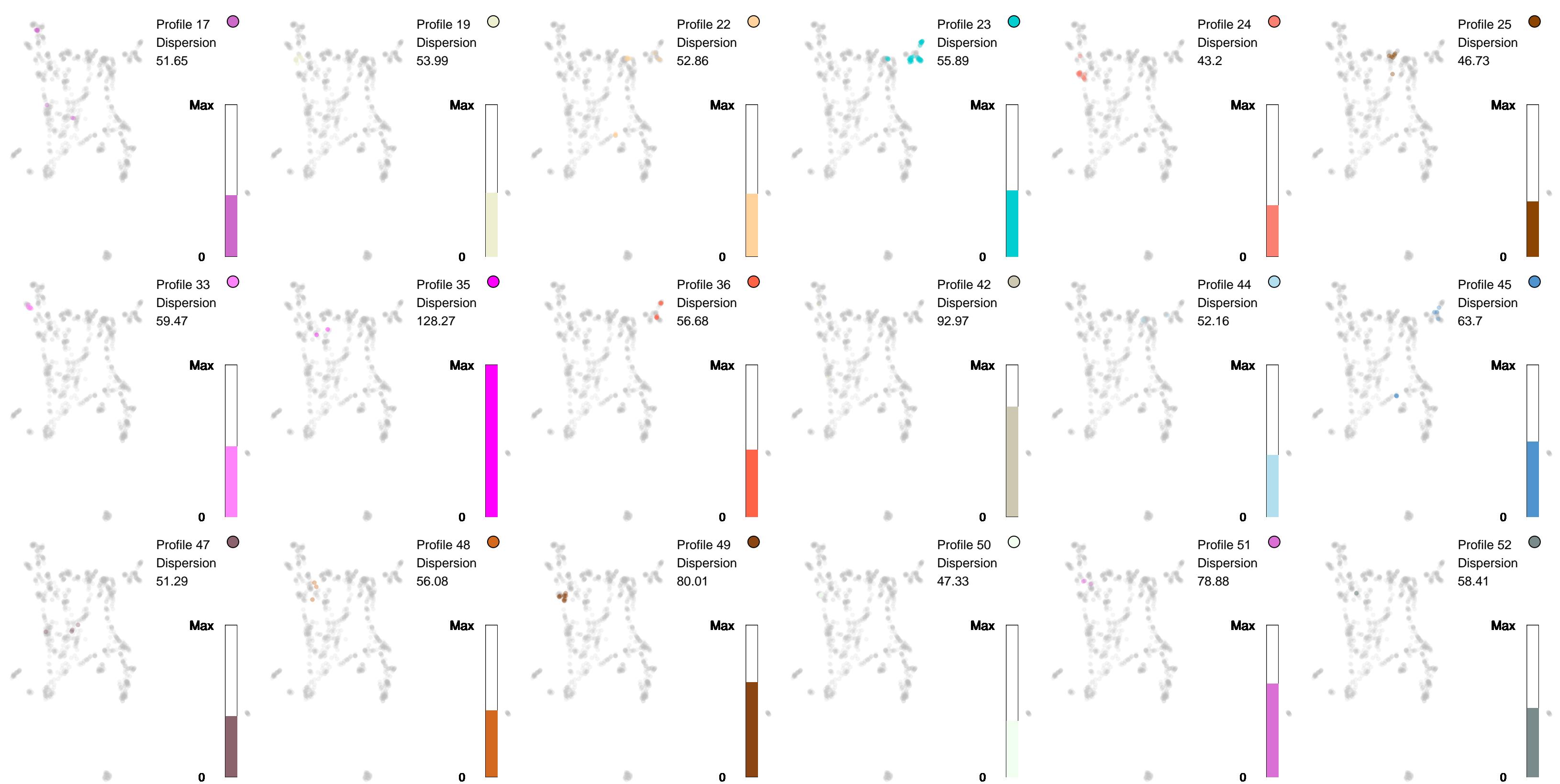
Eph A–B receptors ($k_{opt} = 31$)



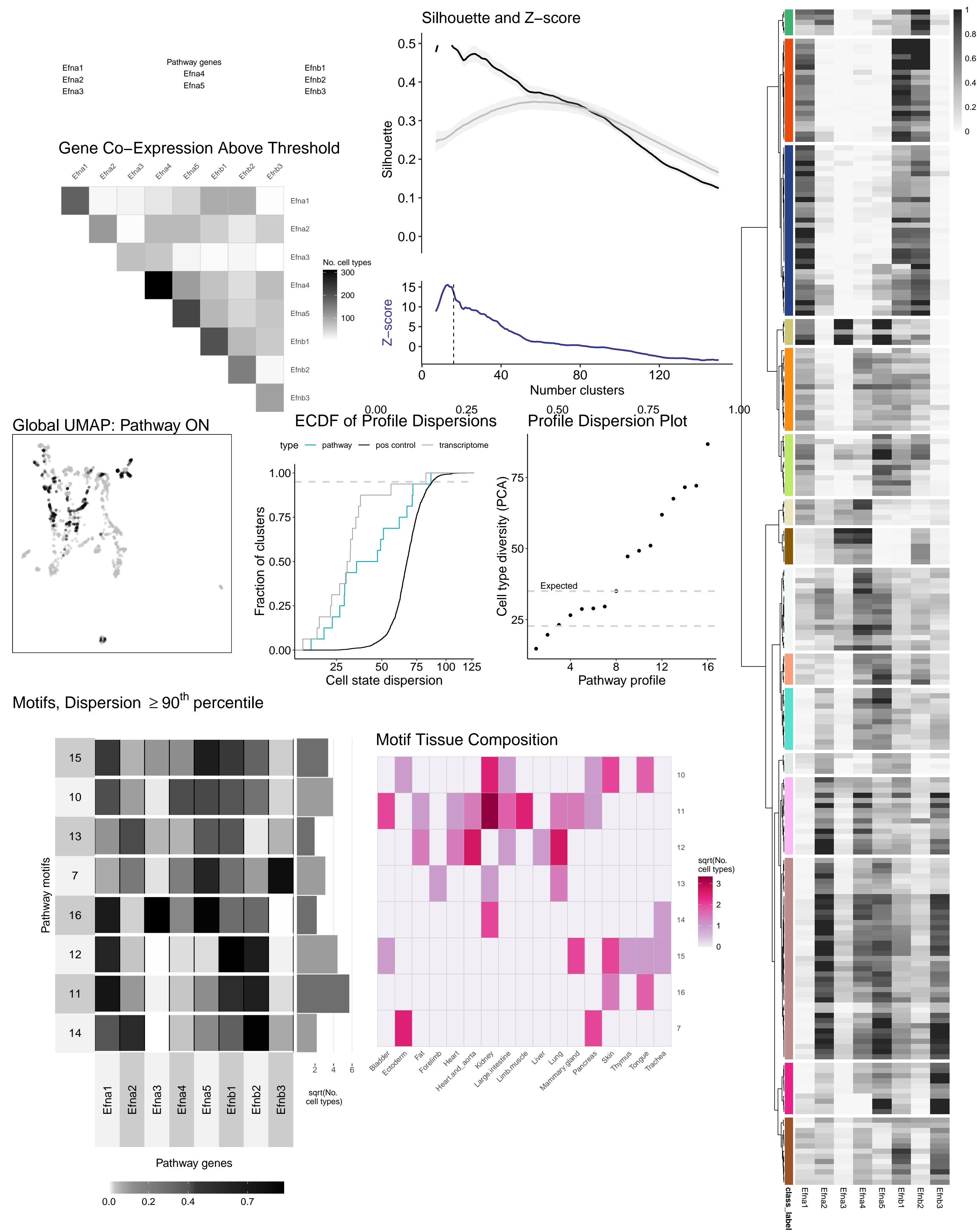
Eph receptors and ligands ($k_{opt} = 52$)



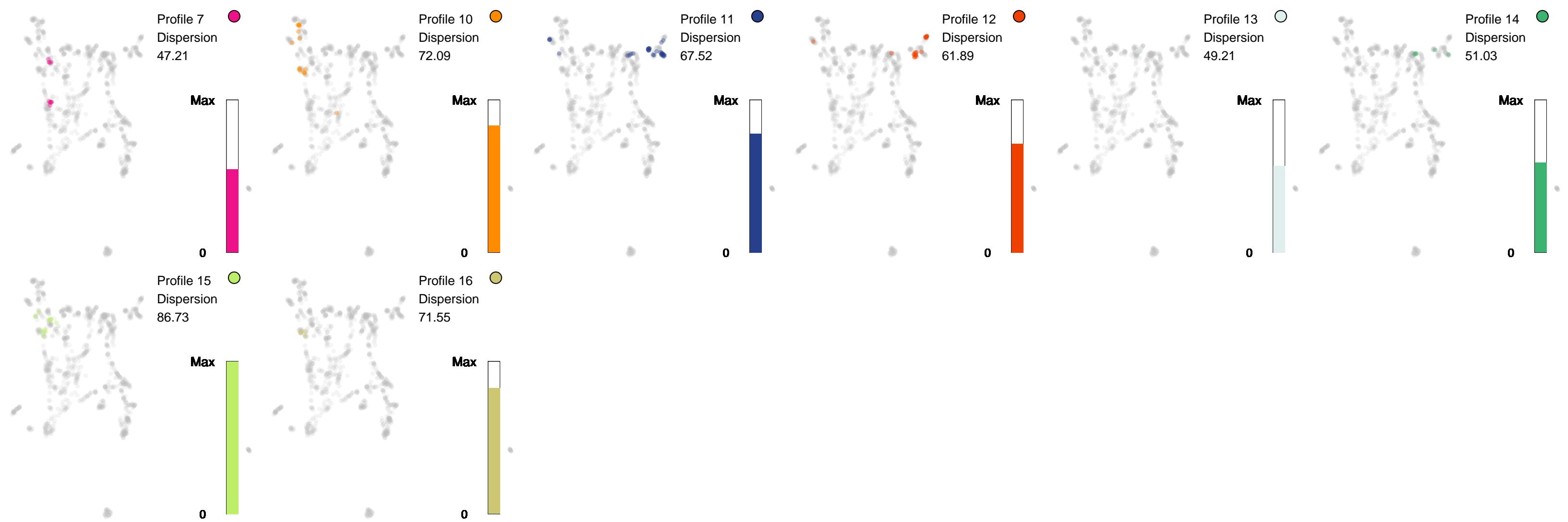
Eph receptors and ligands (k_opt = 52)



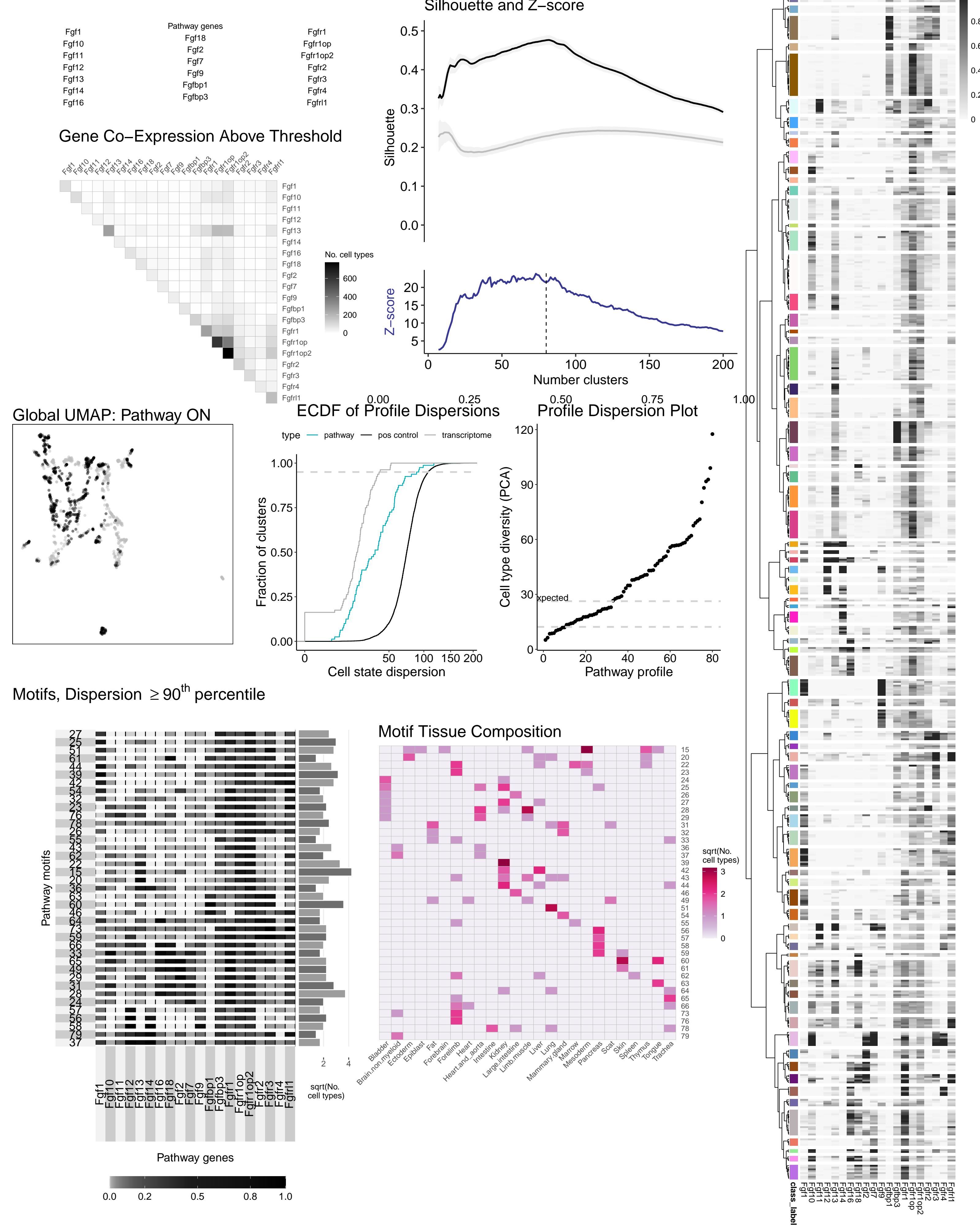
Eph_I (k_opt = 16)



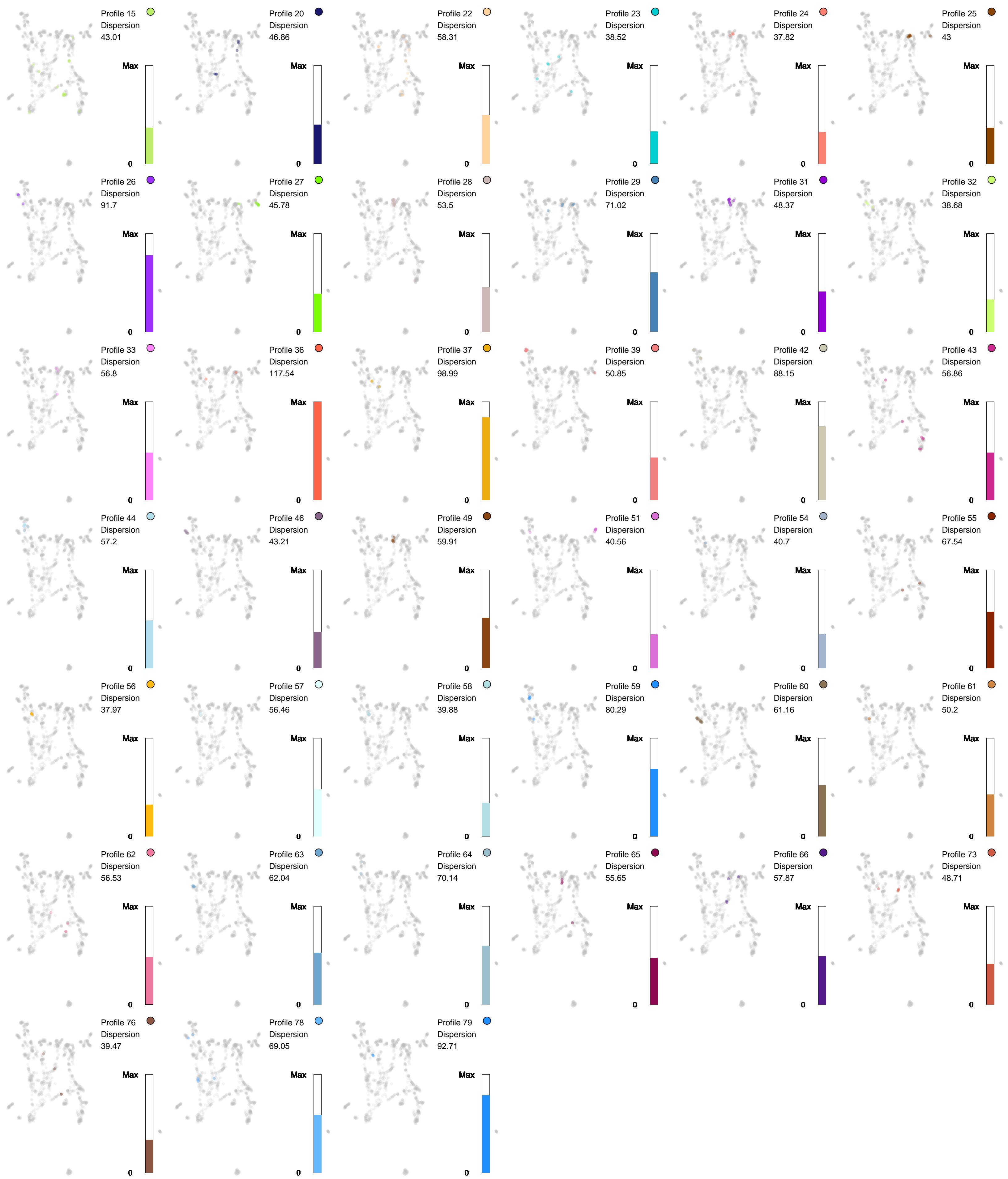
Eph_I (k_opt = 16)



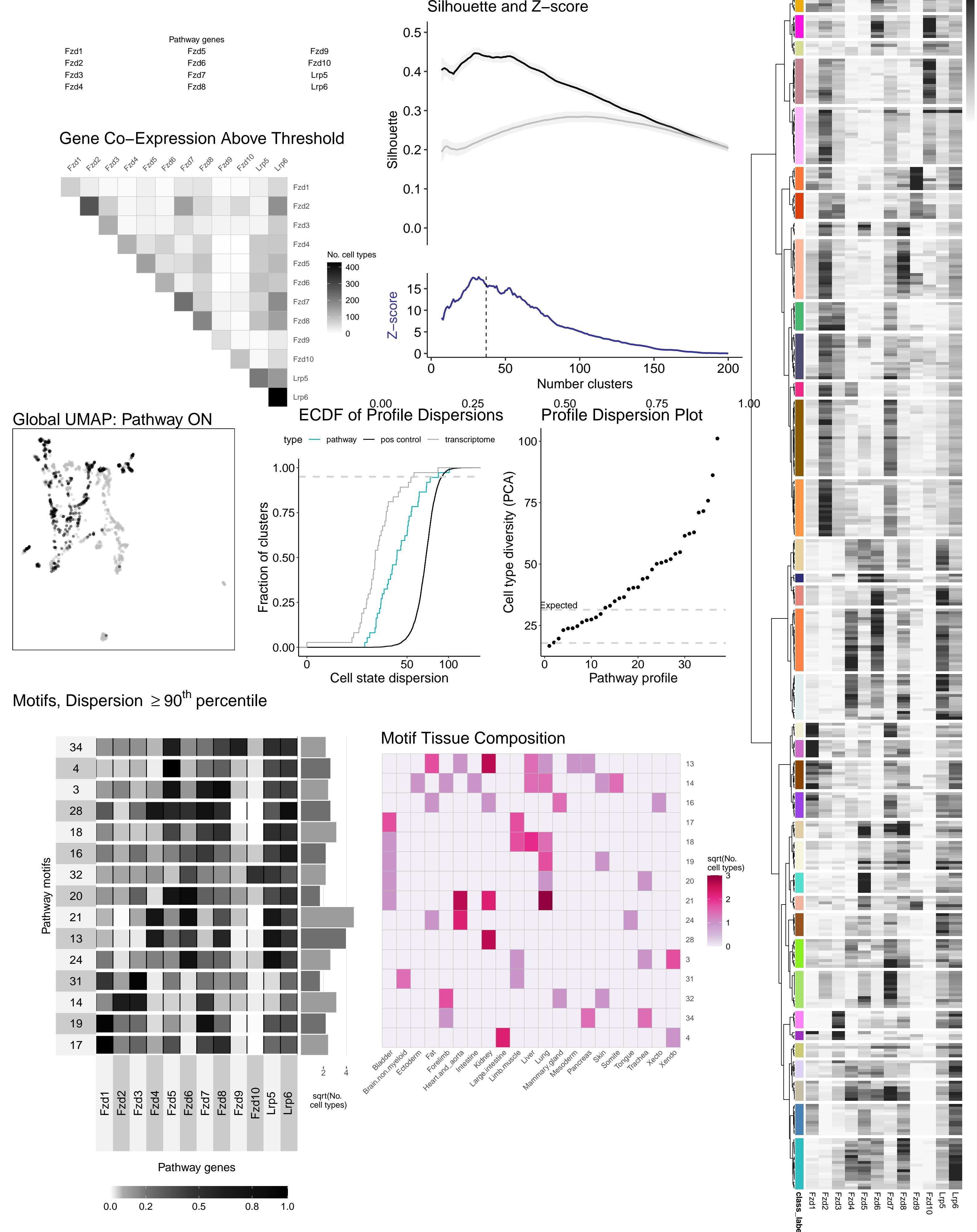
FGF cell signaling proteins ($k_{opt} = 80$)



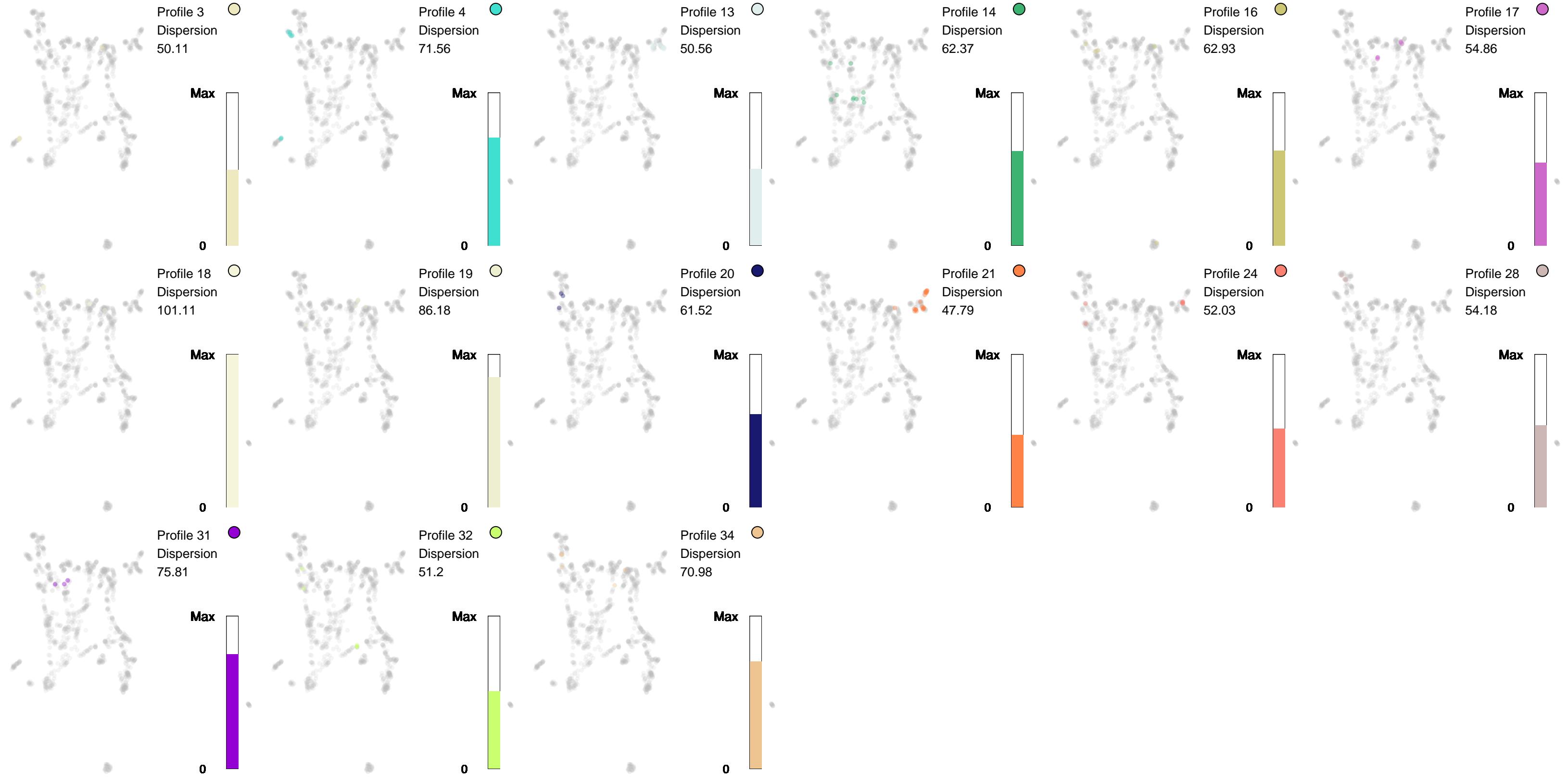
FGF cell signaling proteins (k_opt = 80)



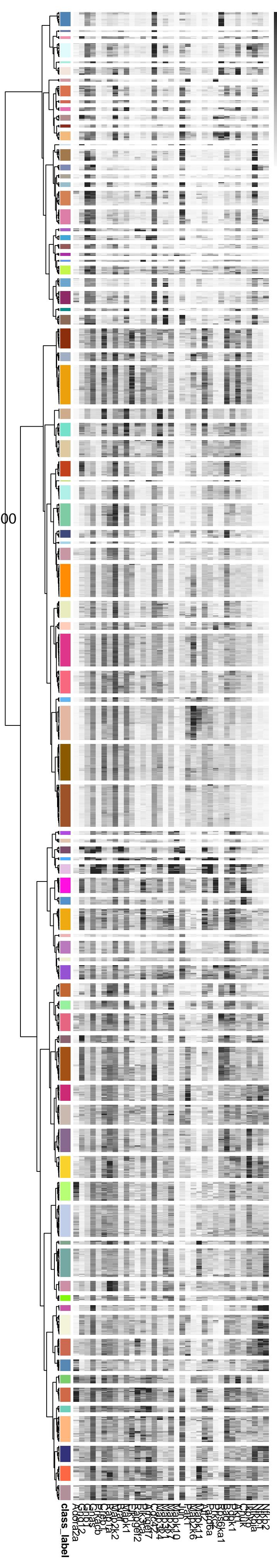
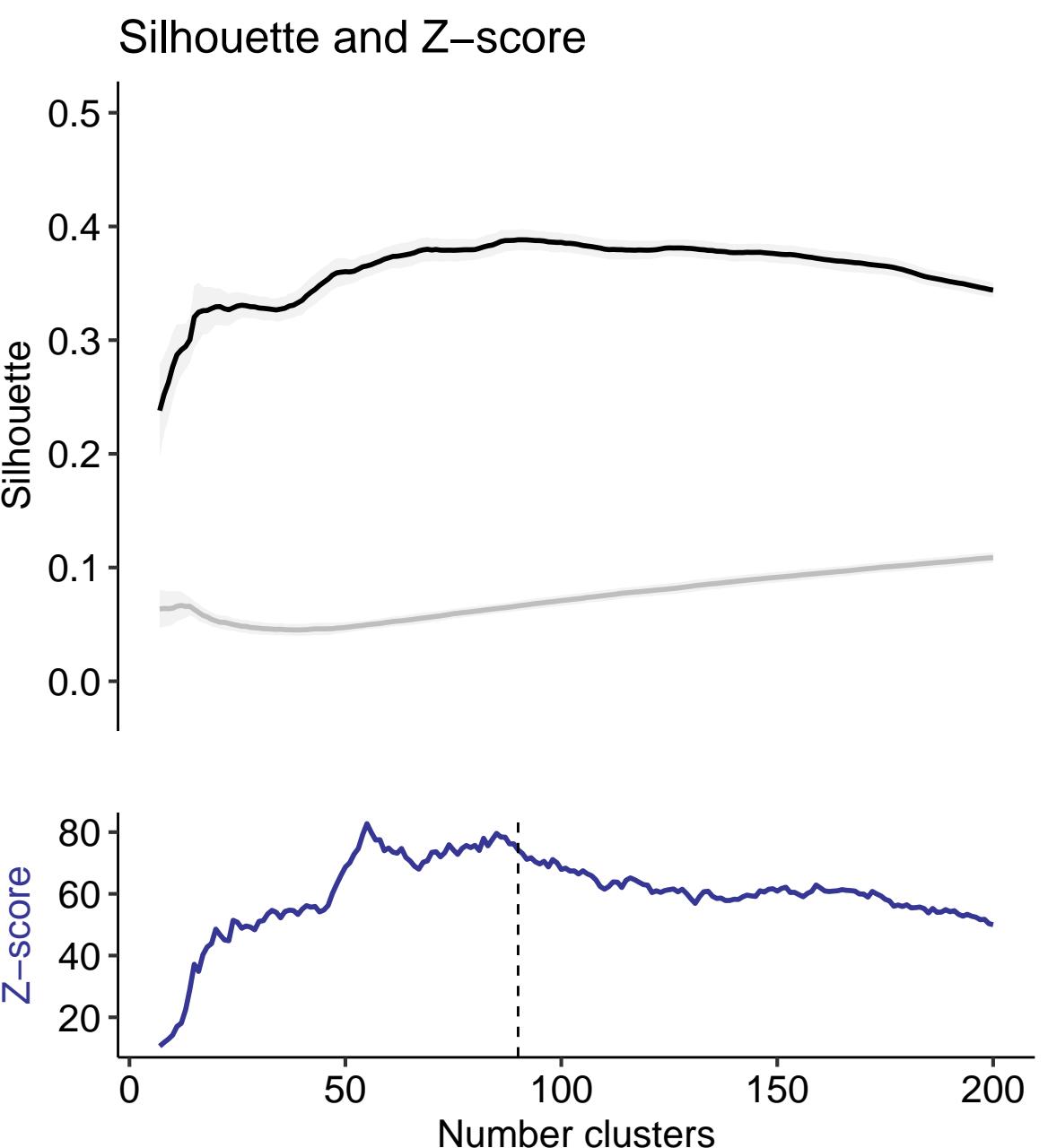
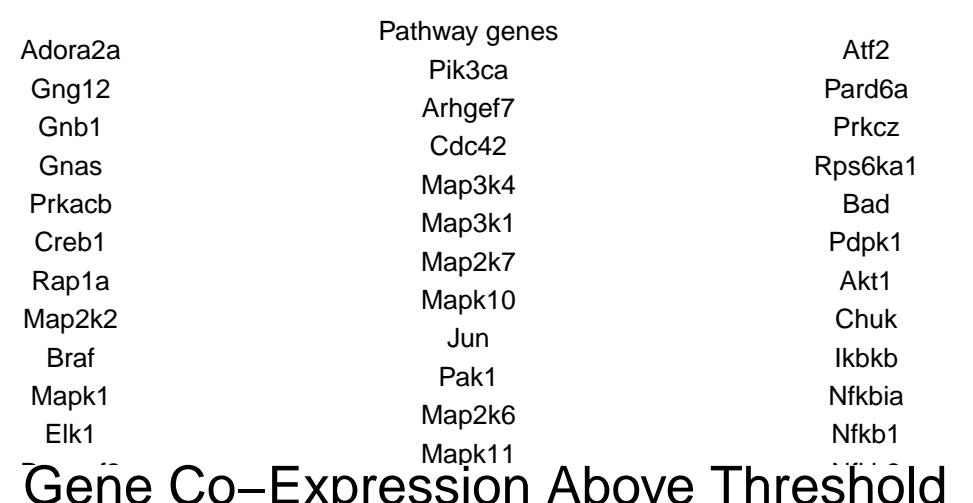
Frizzled and Lrp5 6 receptors for Wnt B Catenin Signaling ($k_{opt} = 37$)



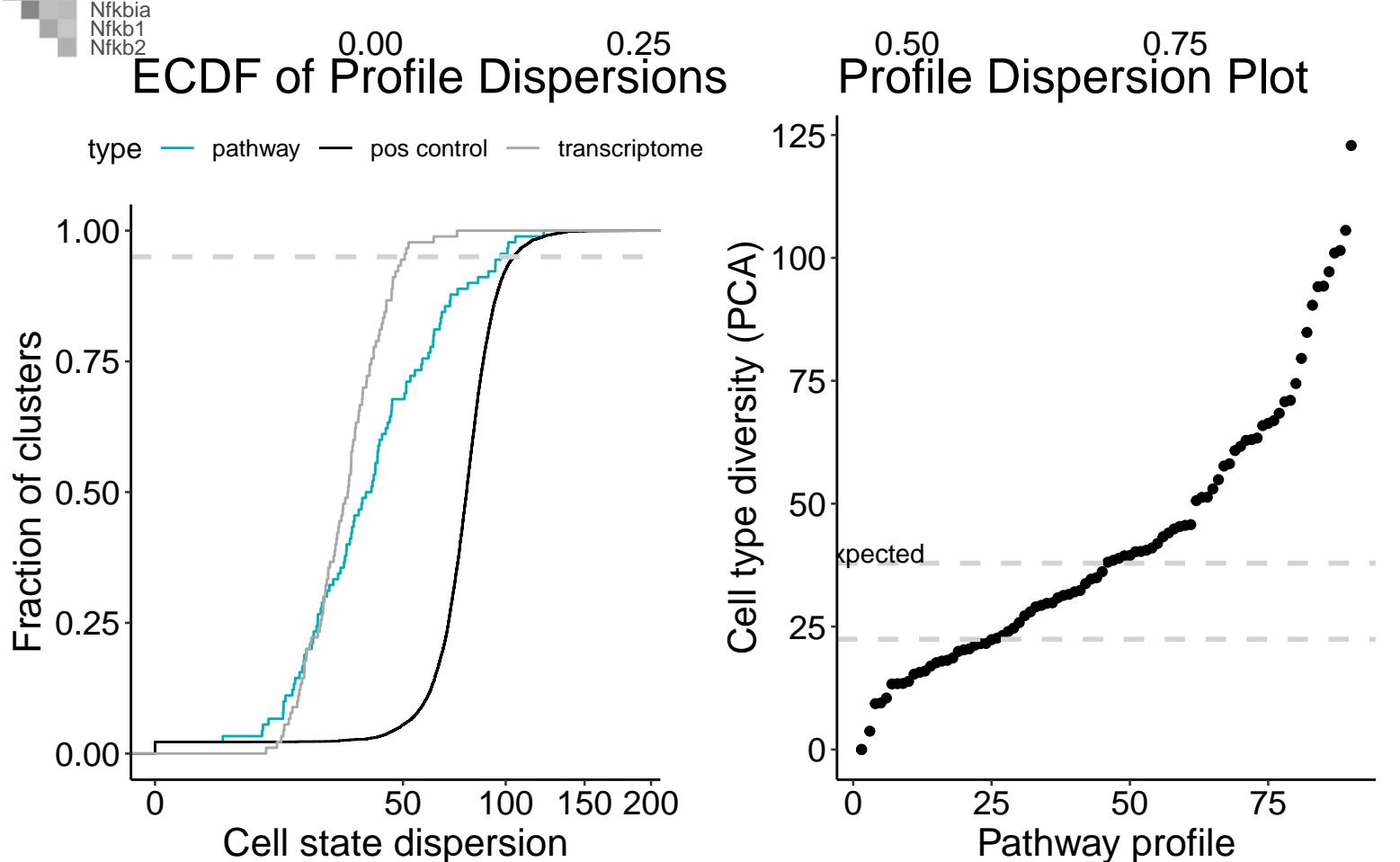
Frizzled and Lrp5 6 receptors for Wnt B Catenin Signaling (k_opt = 37)



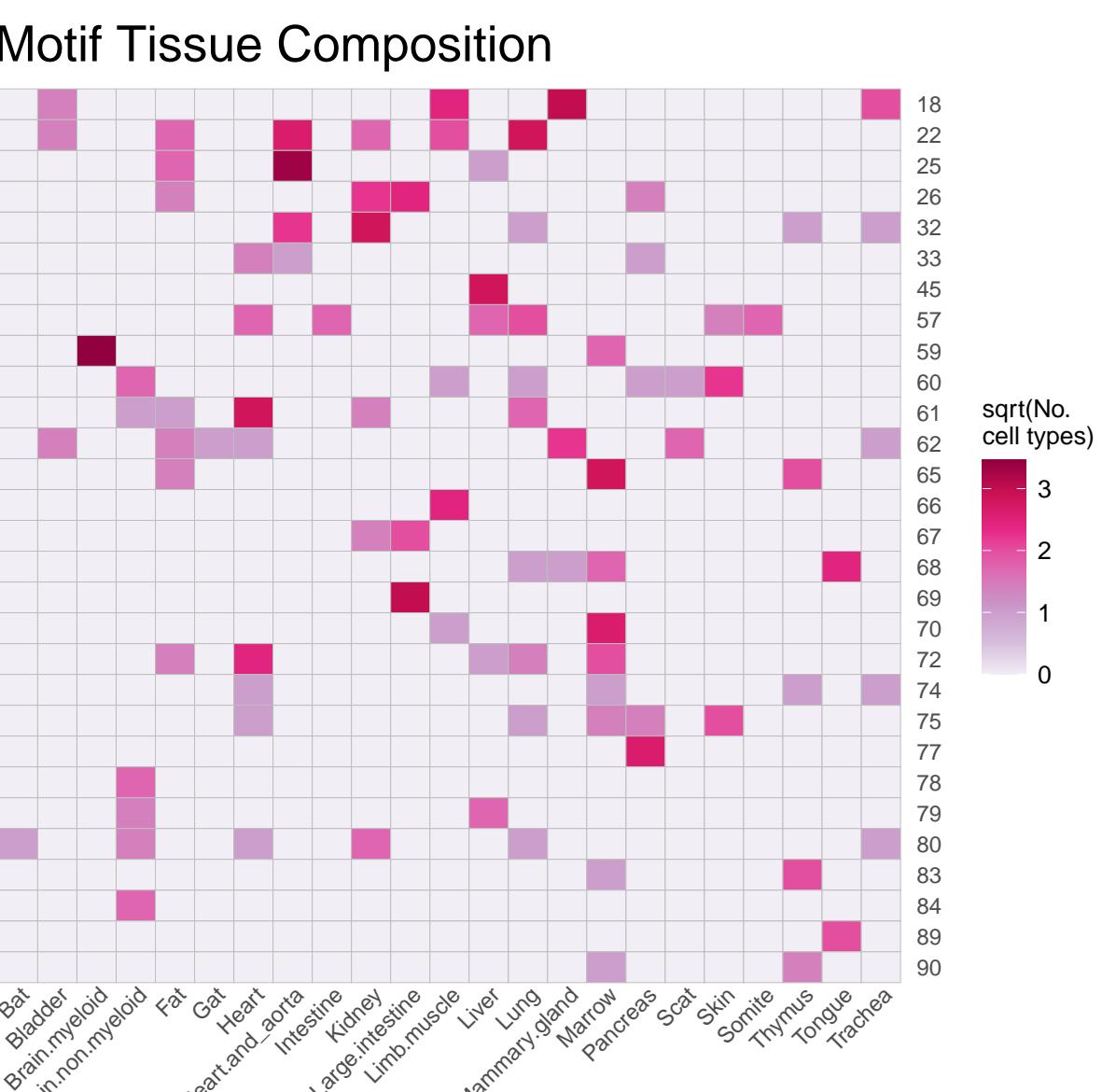
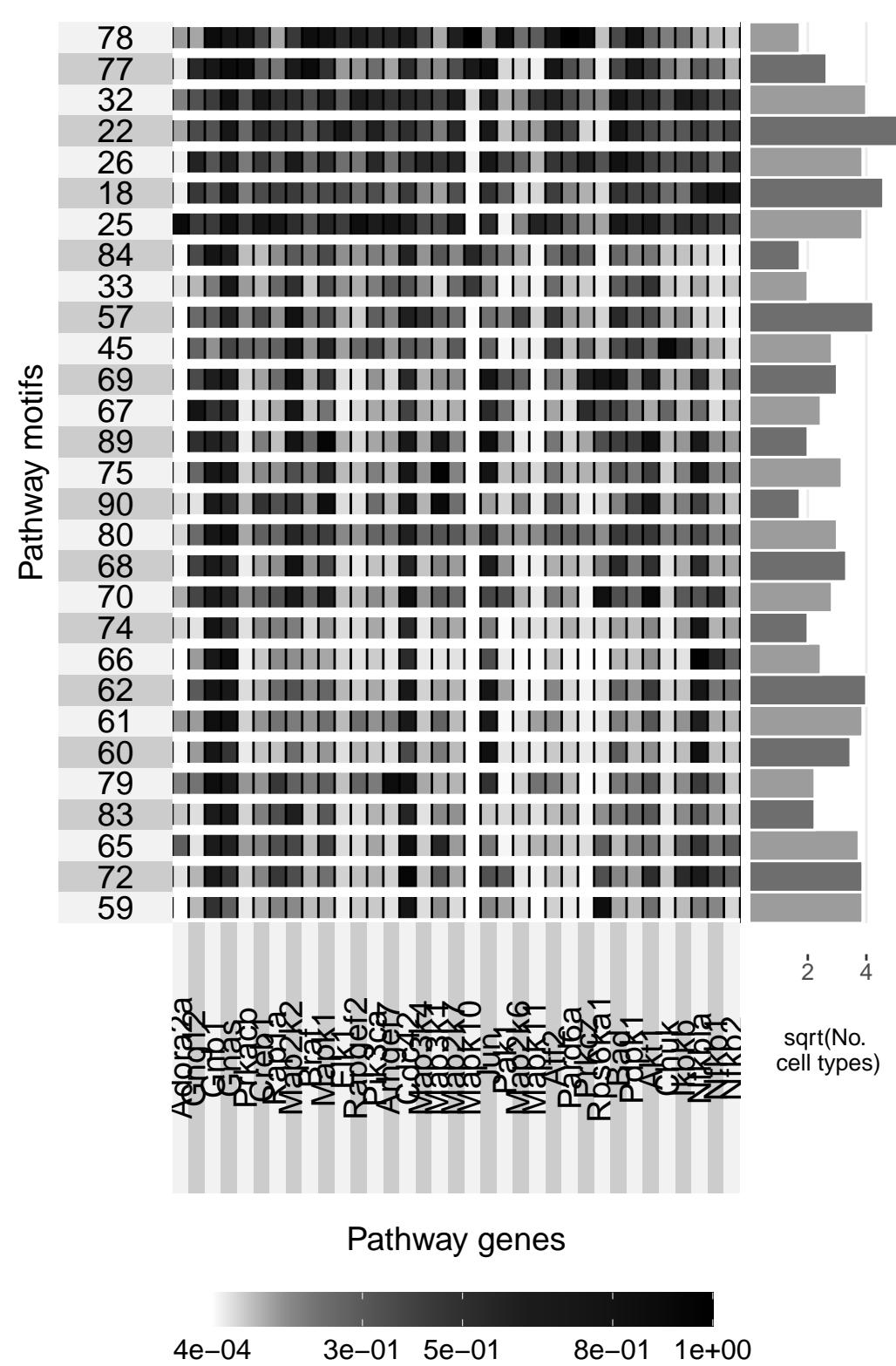
Intracellular Signalling Through Adenosine Receptor A2a and Adenosine (k_opt =



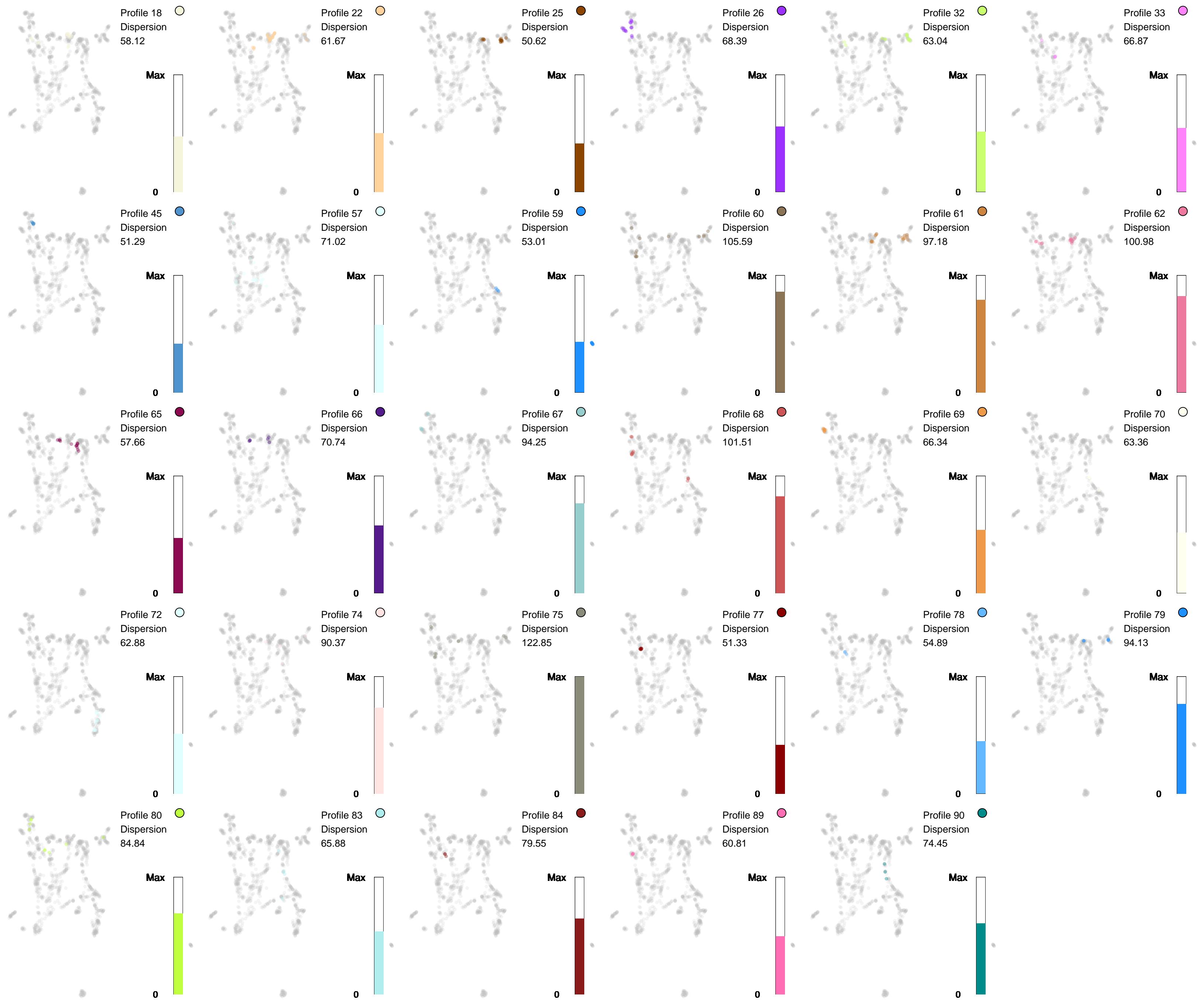
Global UMAP: Pathway ON



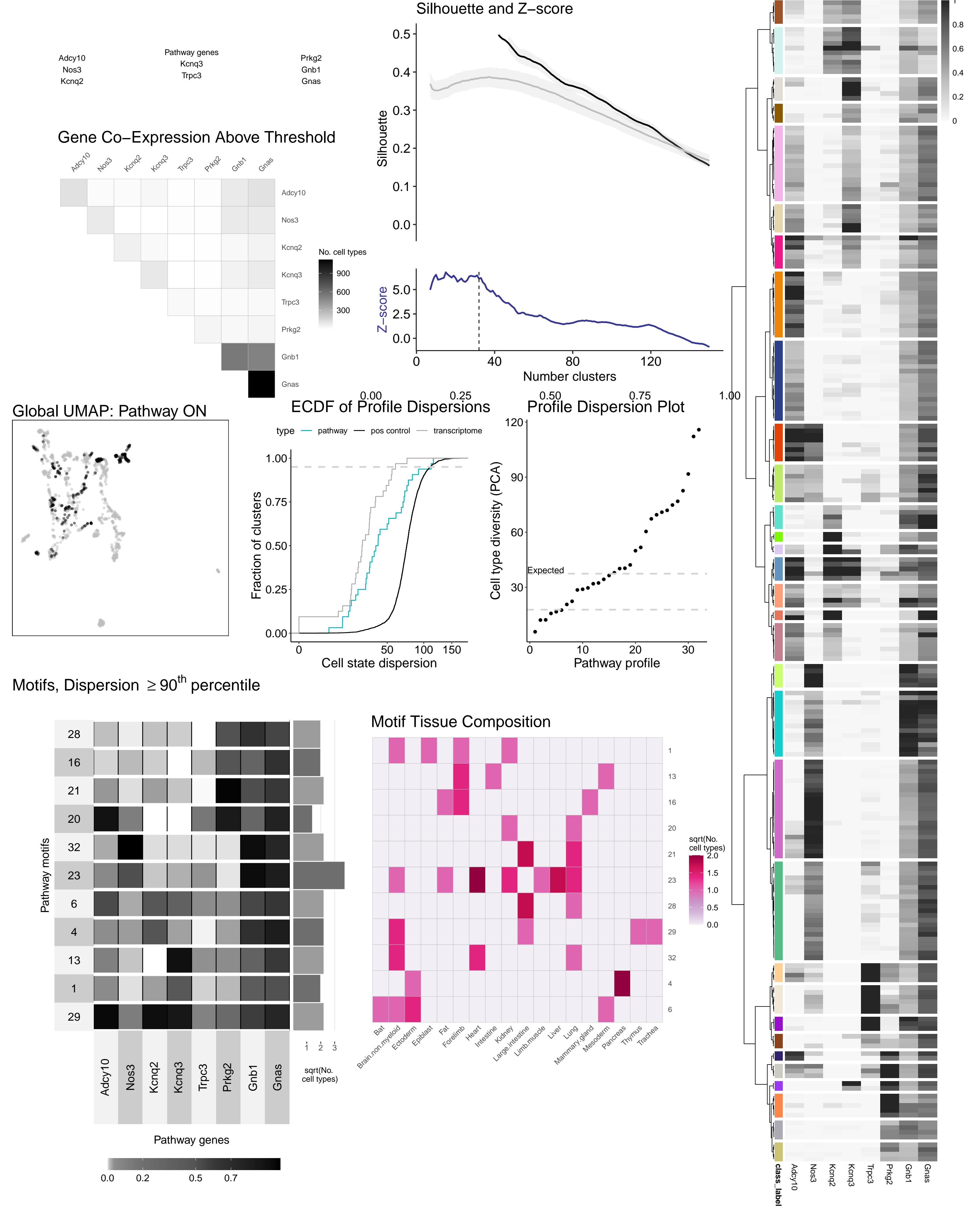
Motifs, Dispersion $\geq 90^{\text{th}}$ percentile



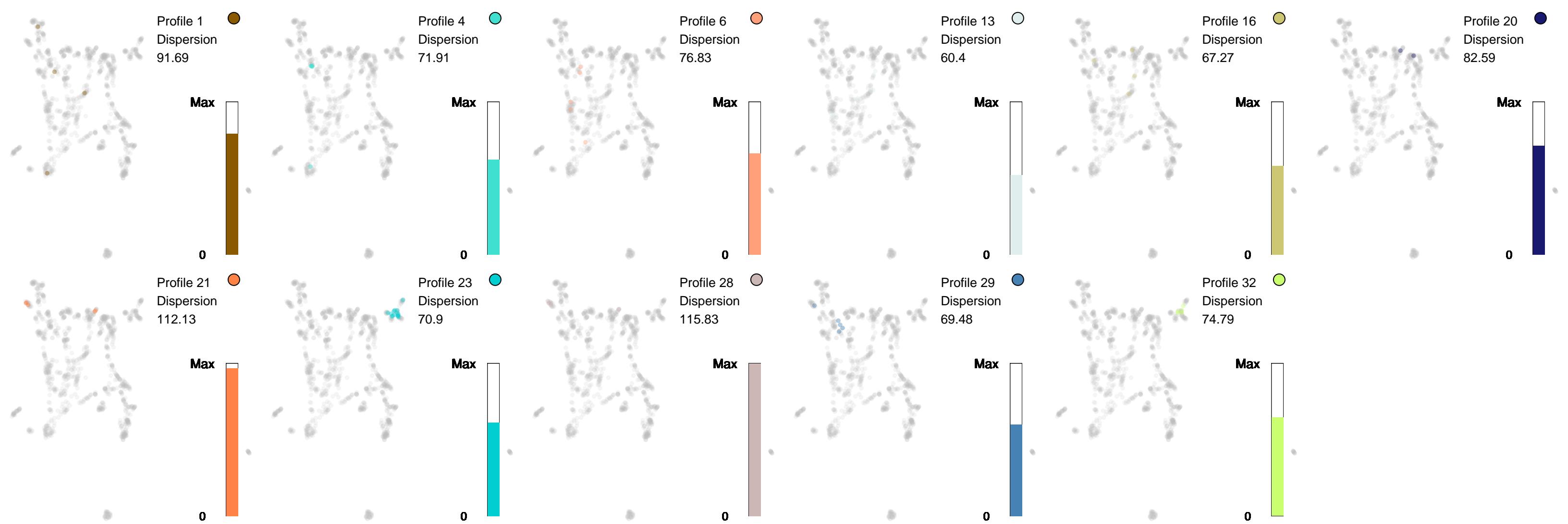
Intracellular Signalling Through Adenosine Receptor A2a and Adenosine ($k_{opt} =$



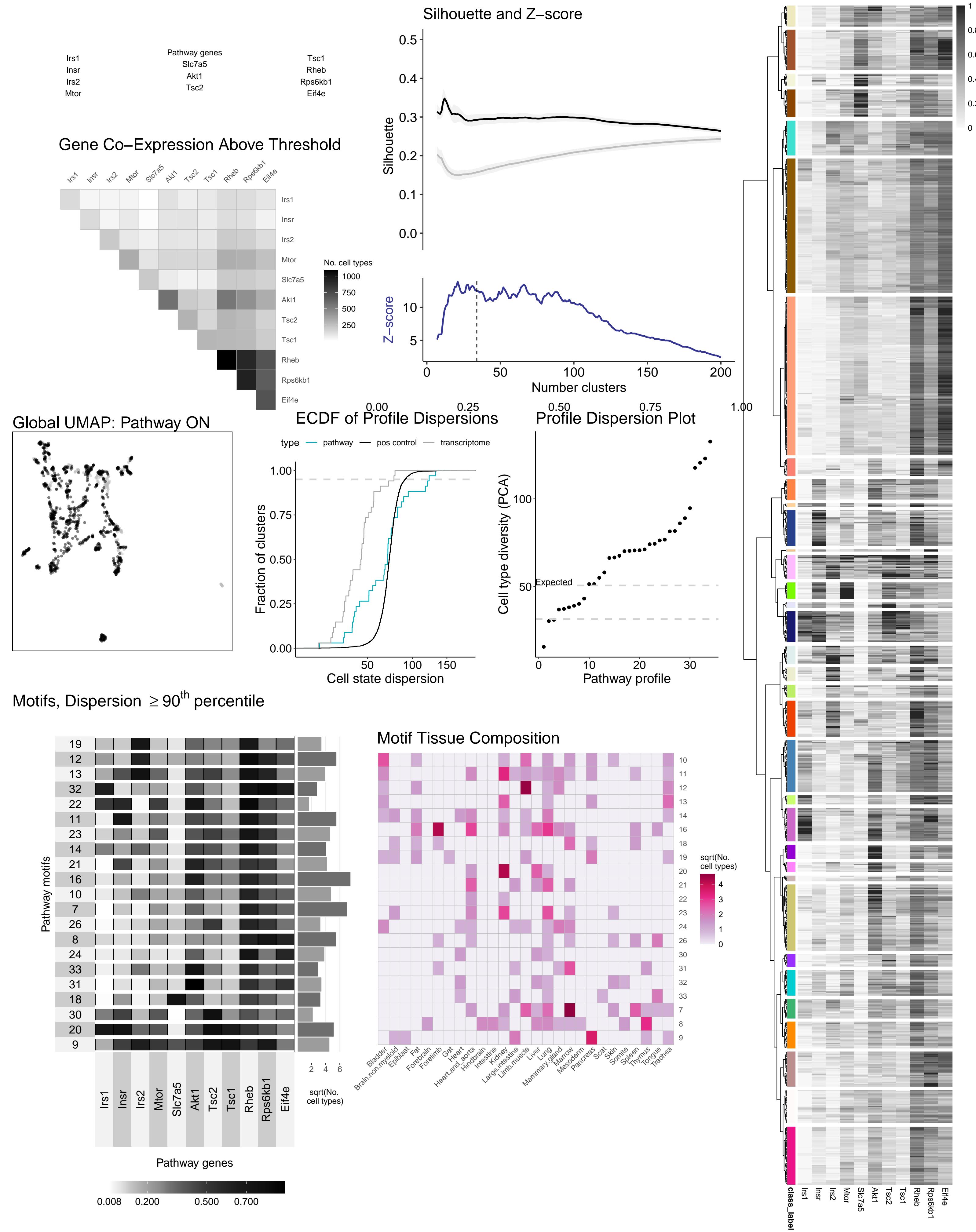
Ion Channels and Their Functional Role in Vascular Endothelium ($k_{opt} = 32$)



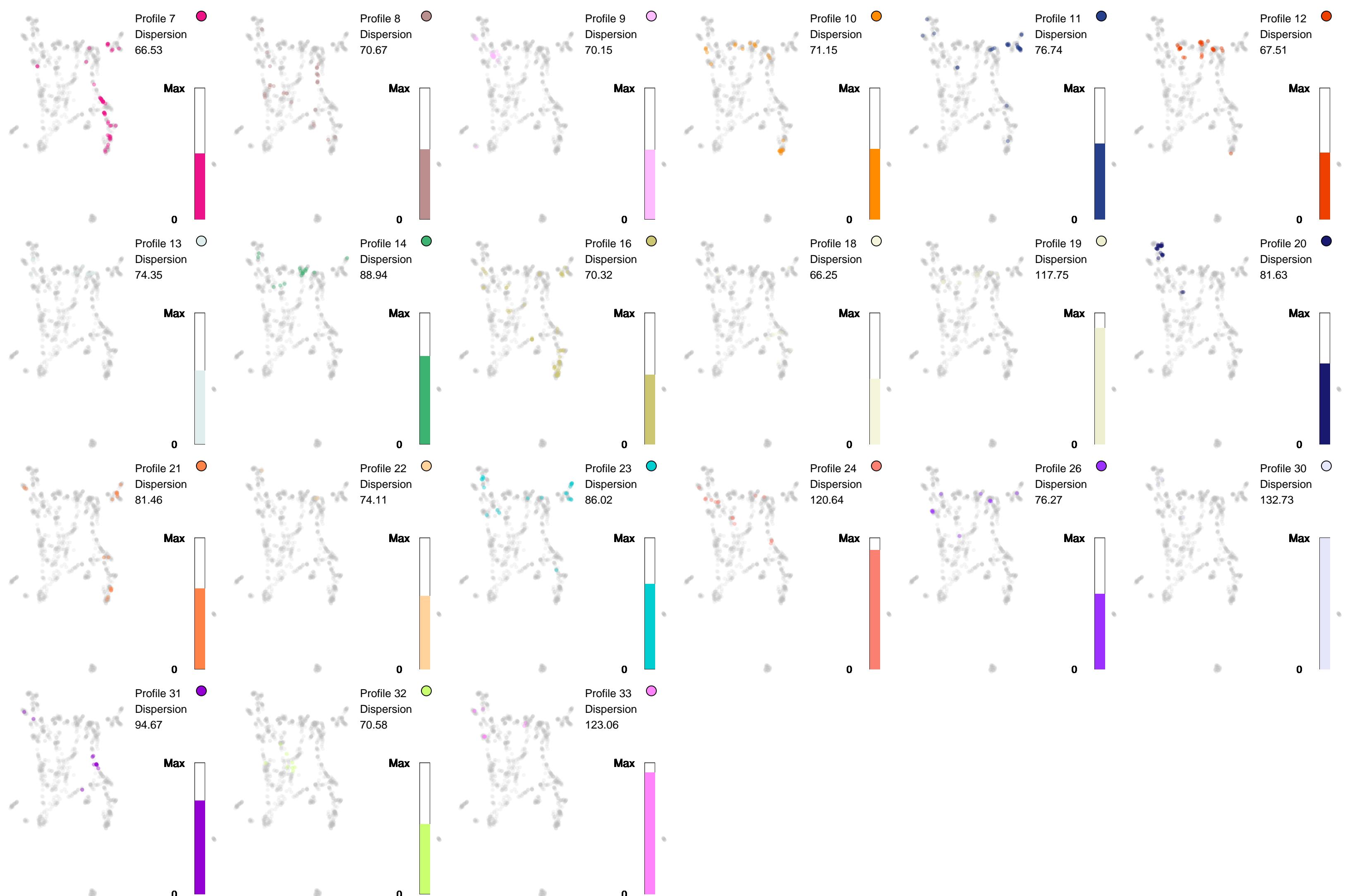
Ion Channels and Their Functional Role in Vascular Endothelium (k_opt = 32)



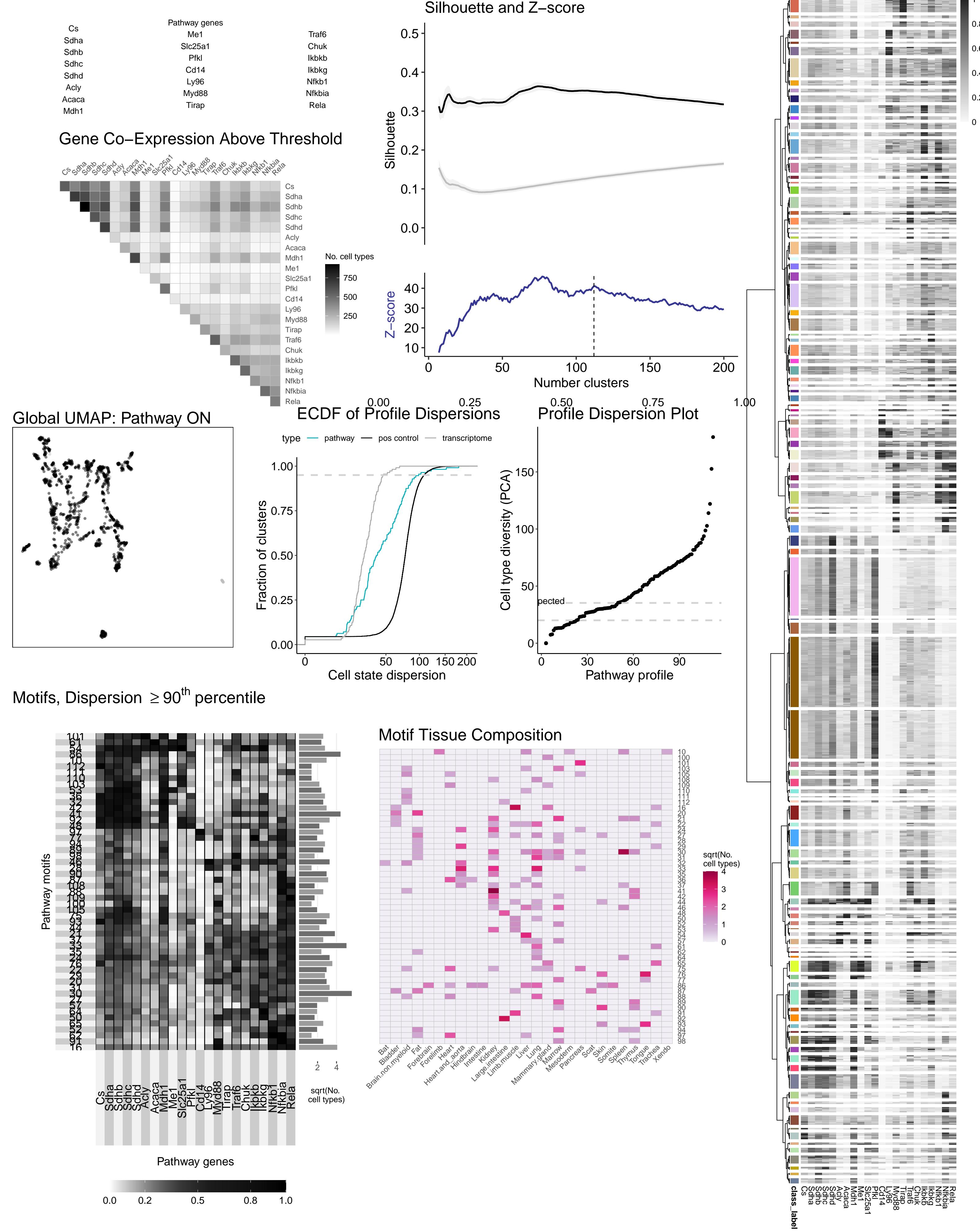
Leucine Stimulation on Insulin Signaling ($k_{opt} = 34$)



Leucine Stimulation on Insulin Signaling ($k_{opt} = 34$)



LPS and Citrate Signaling and Inflammation ($k_{opt} = 112$)



LPS and Citrate Signaling and Inflammation ($k_{opt} = 112$)



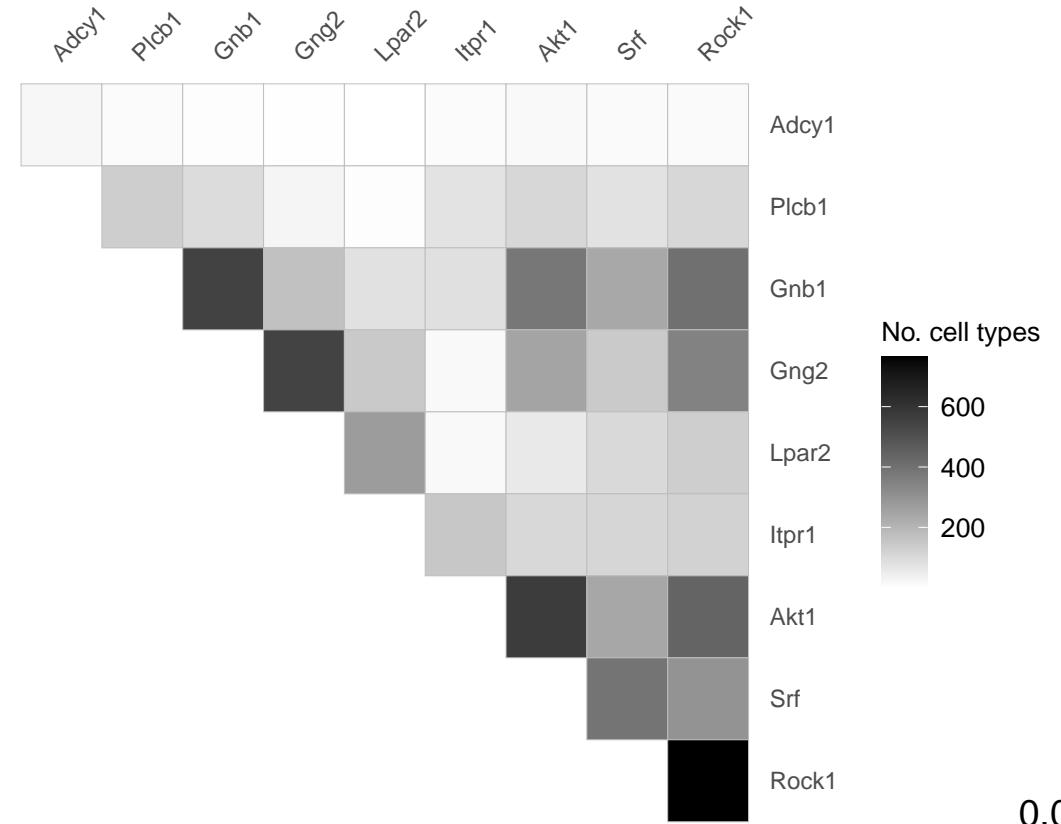
Lysophosphatidic Acid LPA2 Signalling ($k_{opt} = 31$)

Pathway genes
Adcy1
Plcb1
Gnb1

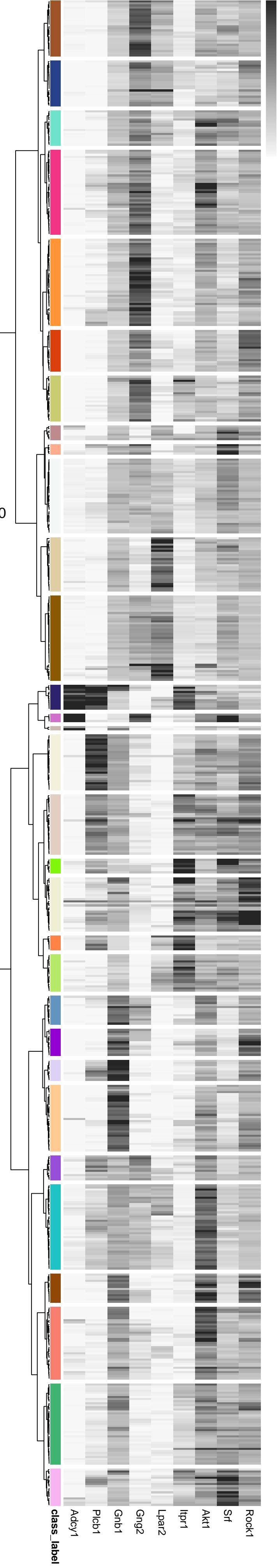
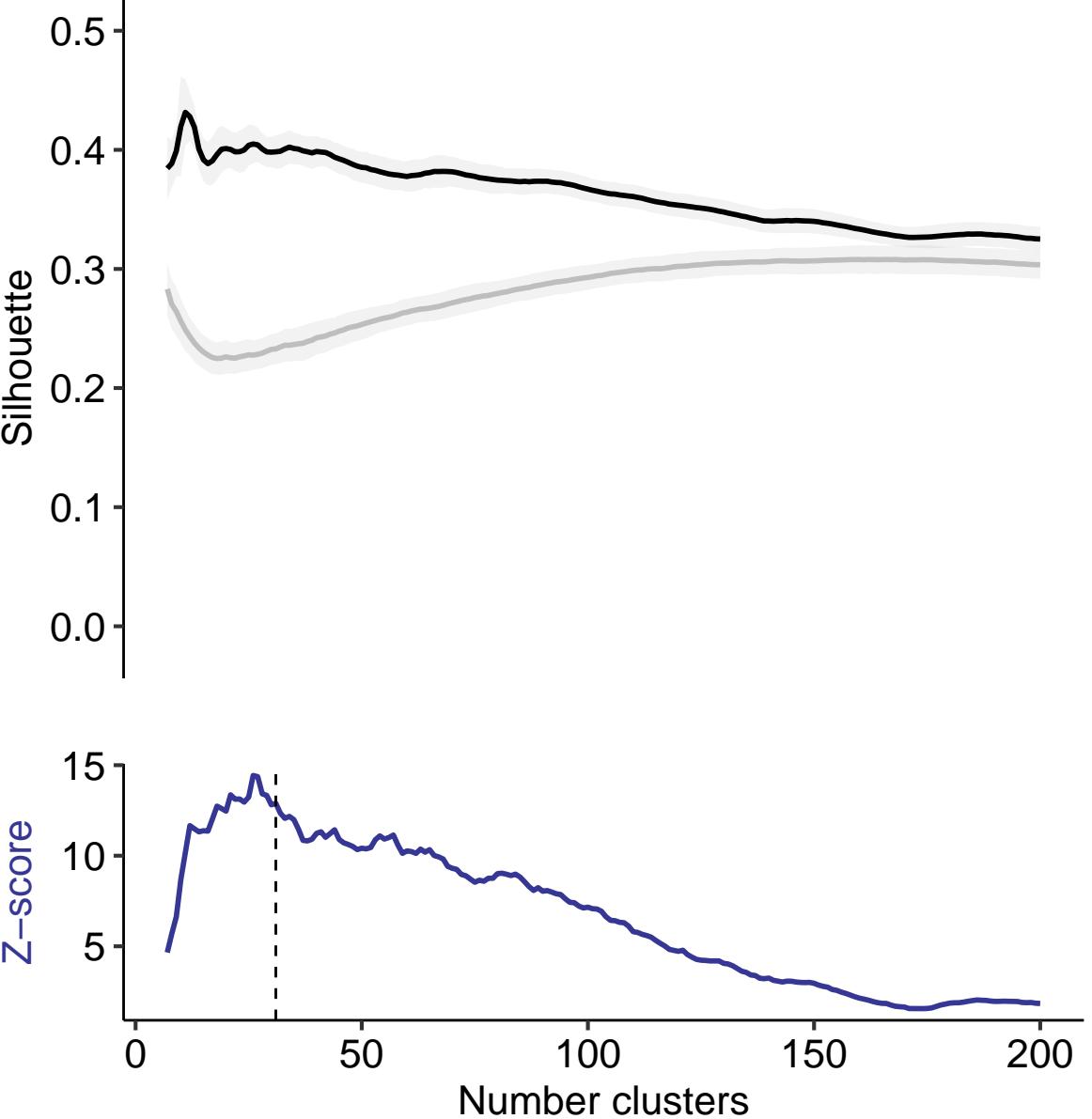
Gng2
Lpar2
Itpr1

Akt1
Srf
Rock1

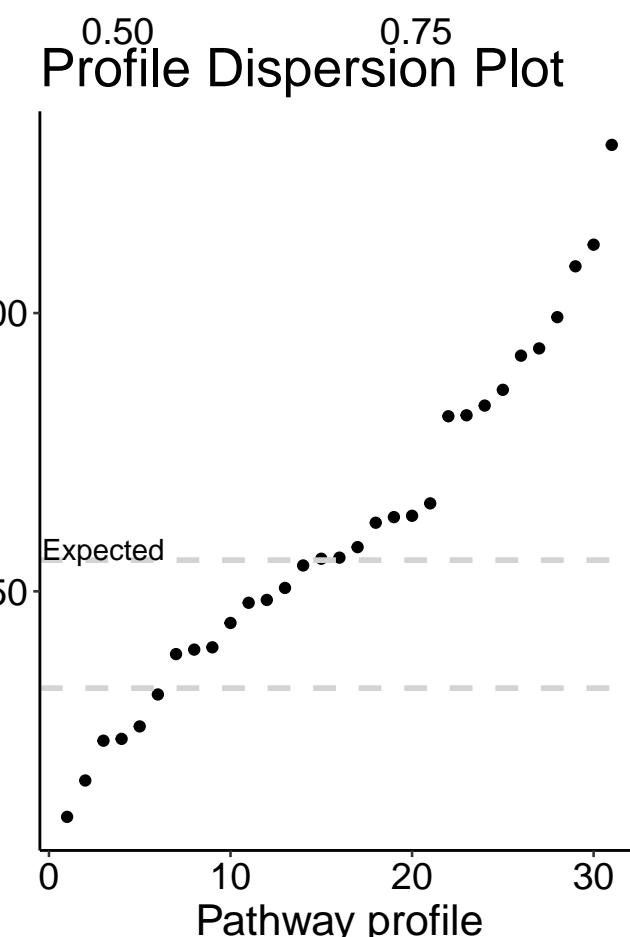
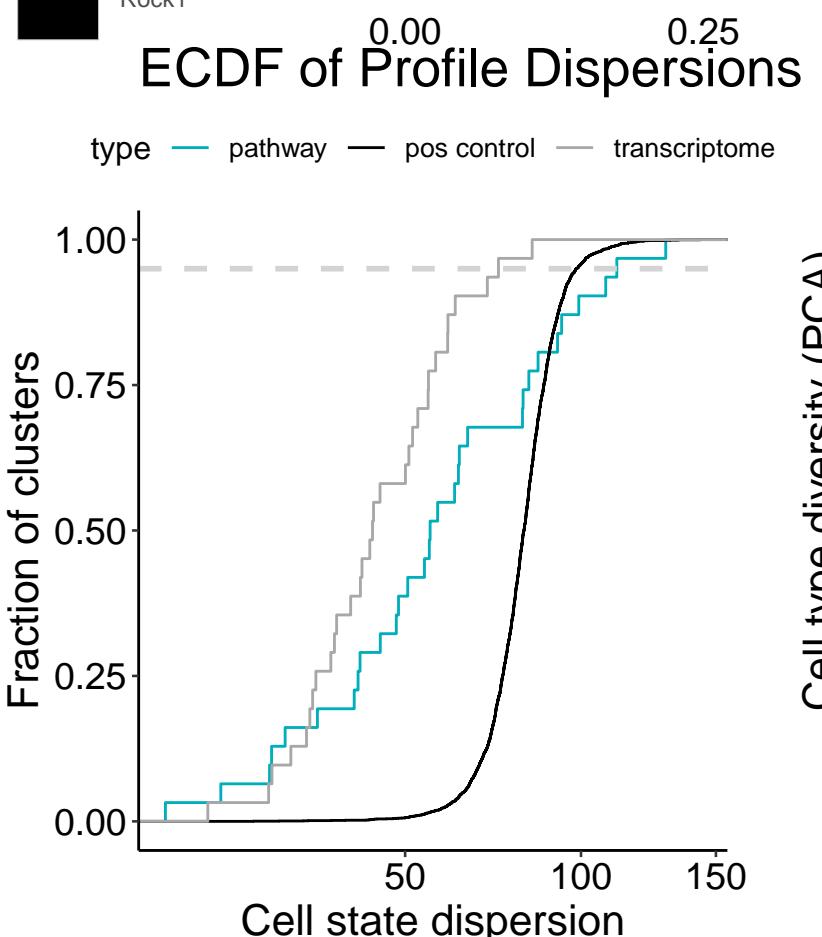
Gene Co-Expression Above Threshold



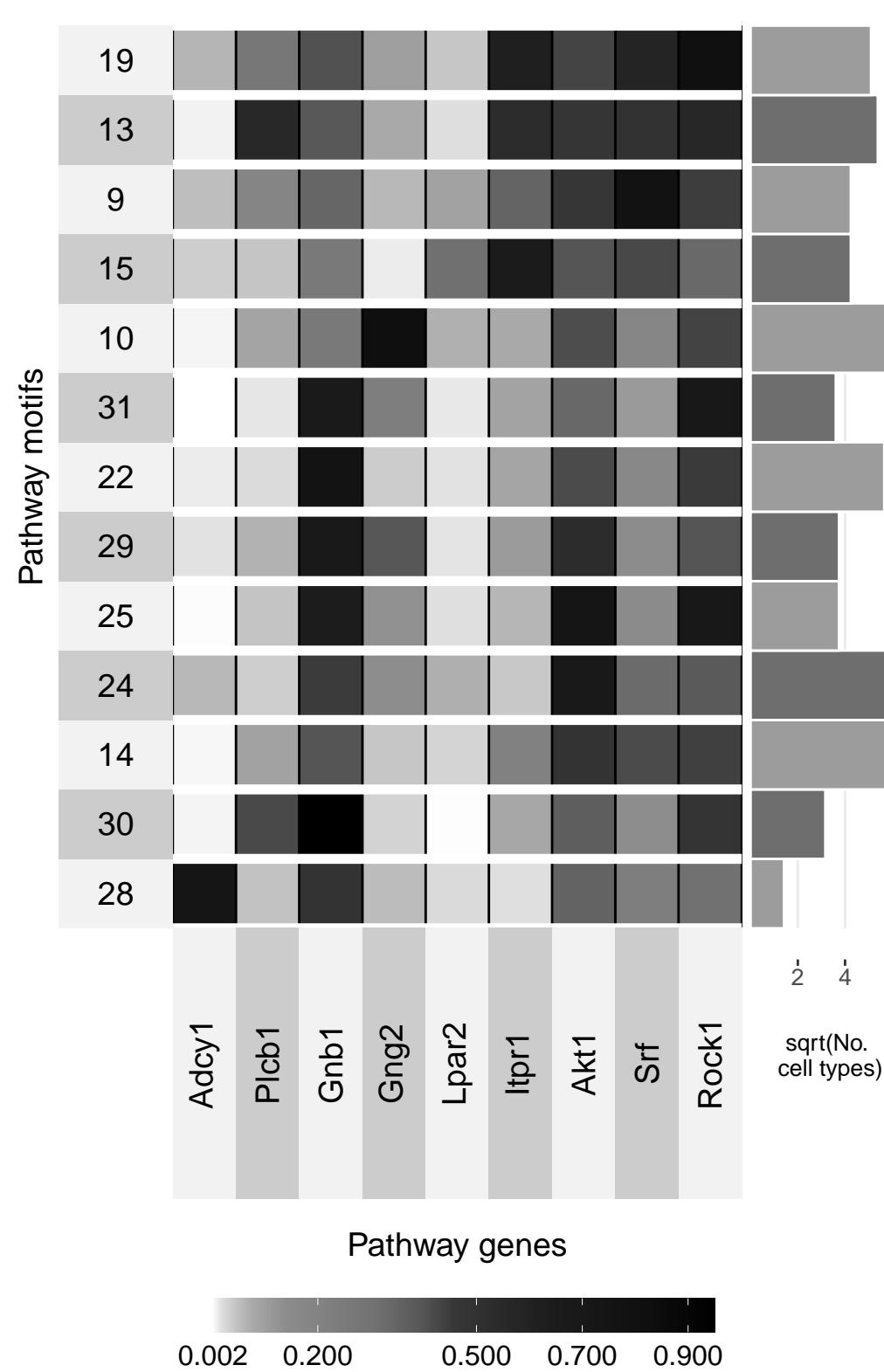
Silhouette and Z-score



Global UMAP: Pathway ON

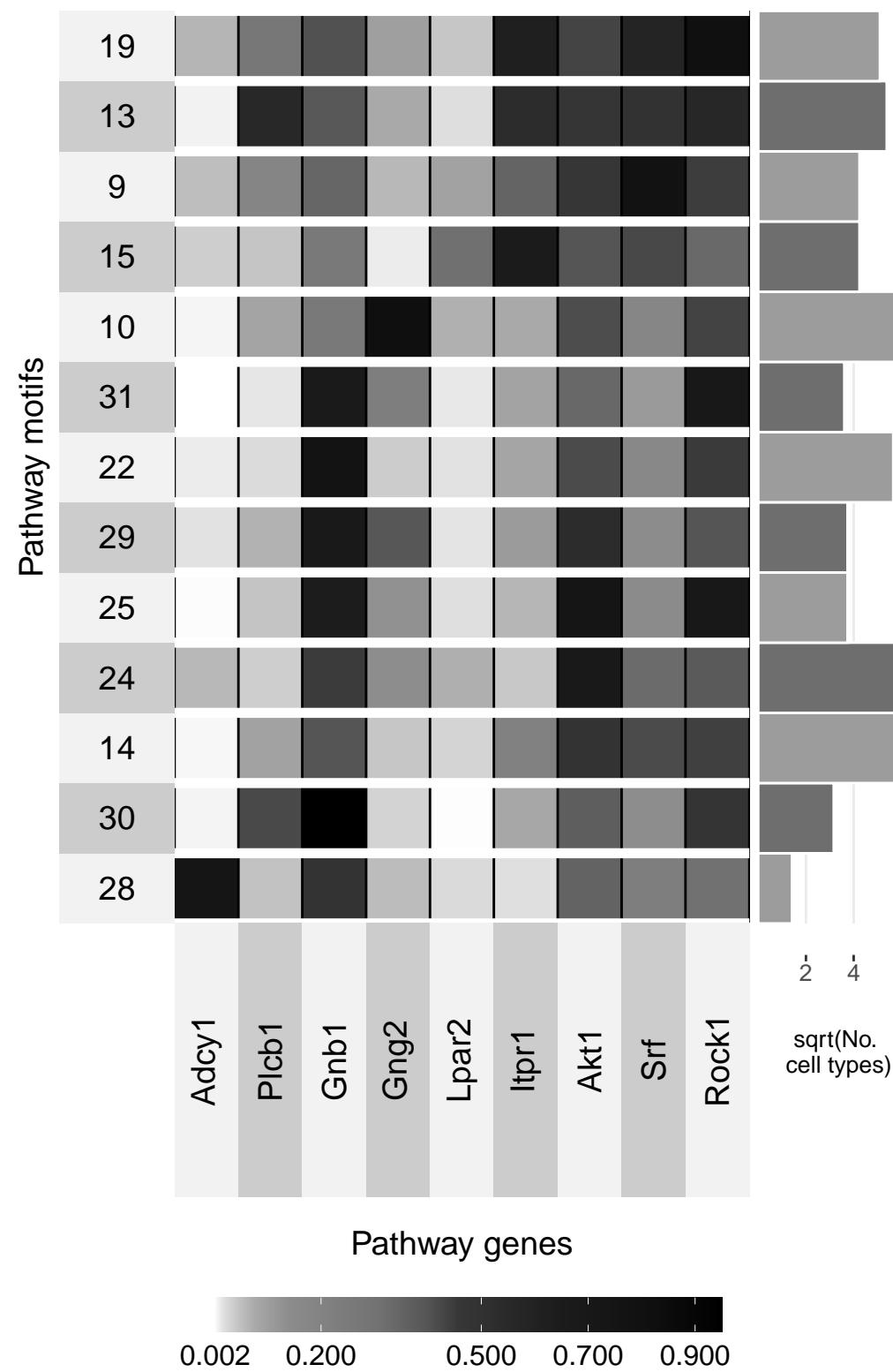


Motifs, Dispersion $\geq 90^{\text{th}}$ percentile



Motif Tissue Composition

Pathway motifs



Pathway genes

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

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0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

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0.002 0.200 0.500 0.700 0.900

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0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

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0.002 0.200 0.500 0.700 0.900

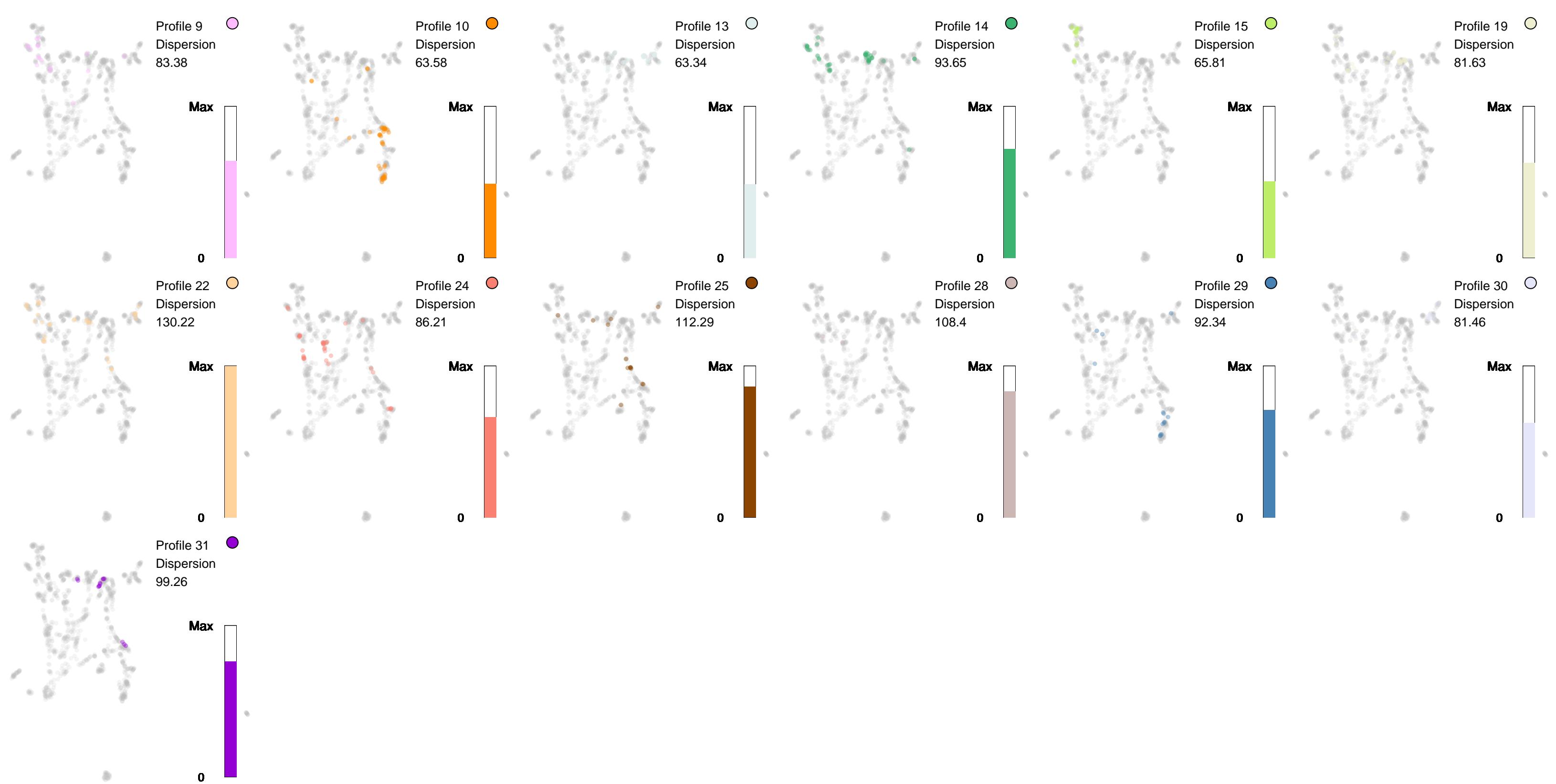
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0.002 0.200 0.500 0.700 0.900

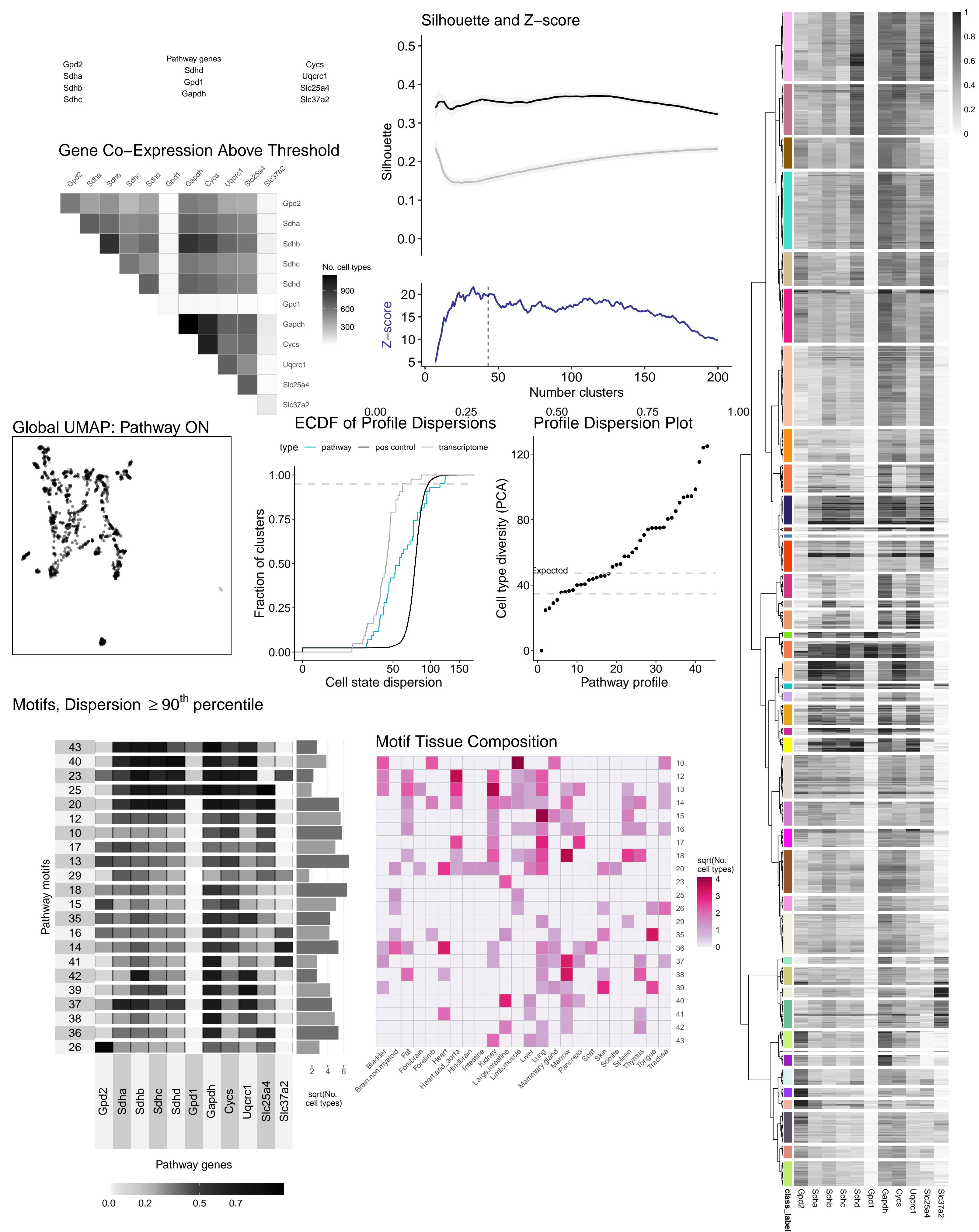
0.002 0.200 0.500 0.700 0.900

0.002 0.200 0.500 0.700 0.900

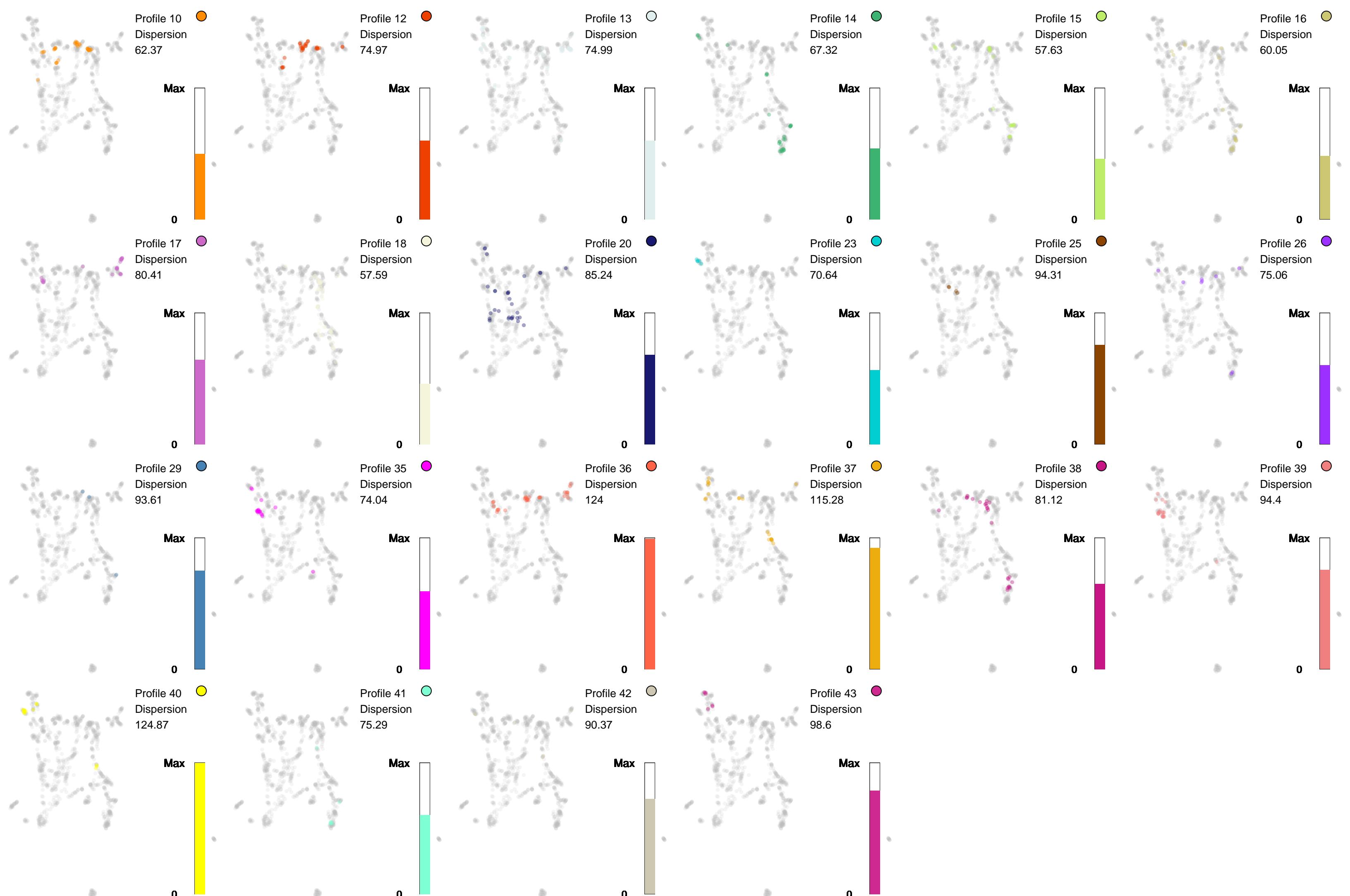
Lysophosphatidic Acid LPA2 Signalling ($k_{opt} = 31$)



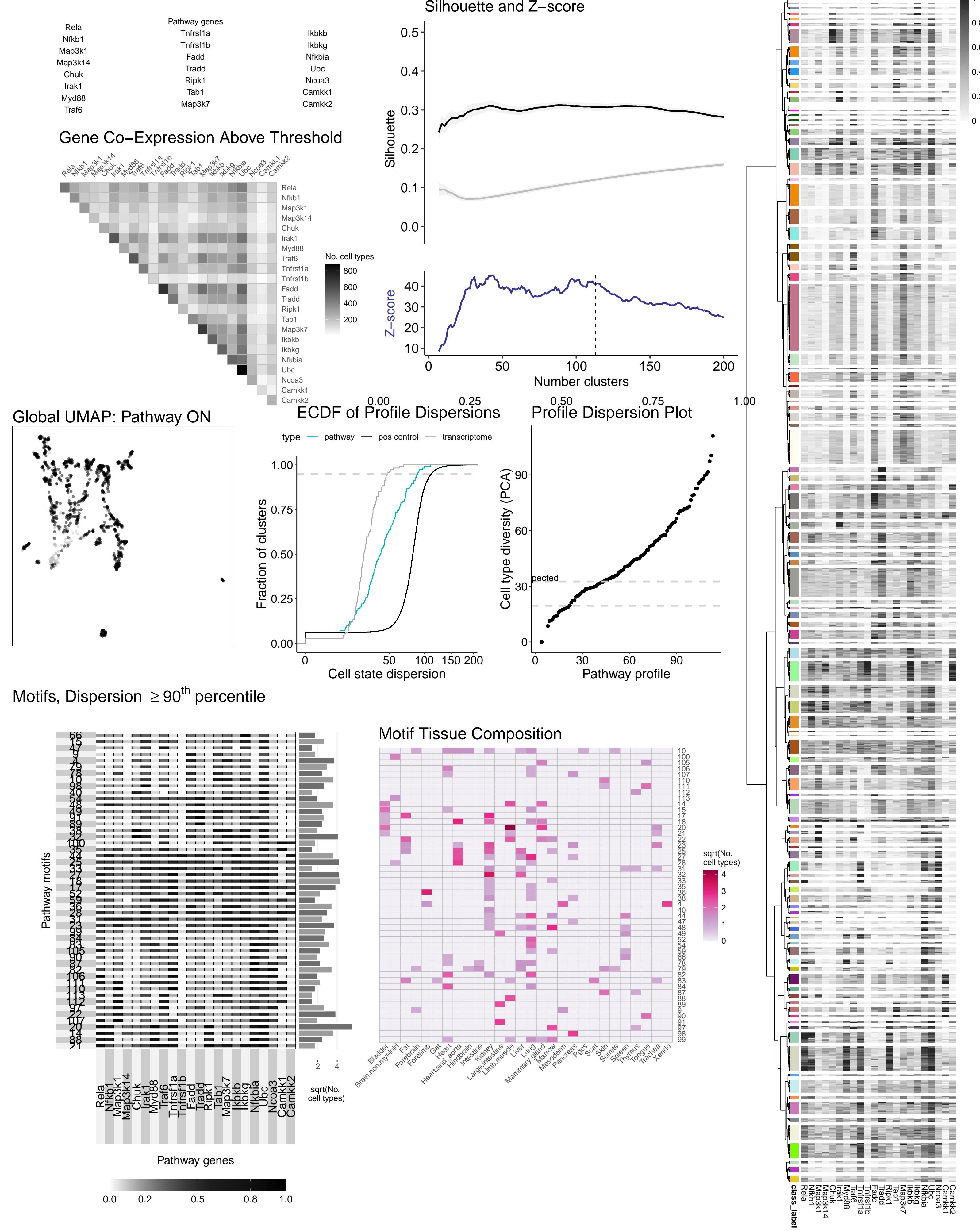
Mitochondrial Electron Transport Chain (k_opt = 43)



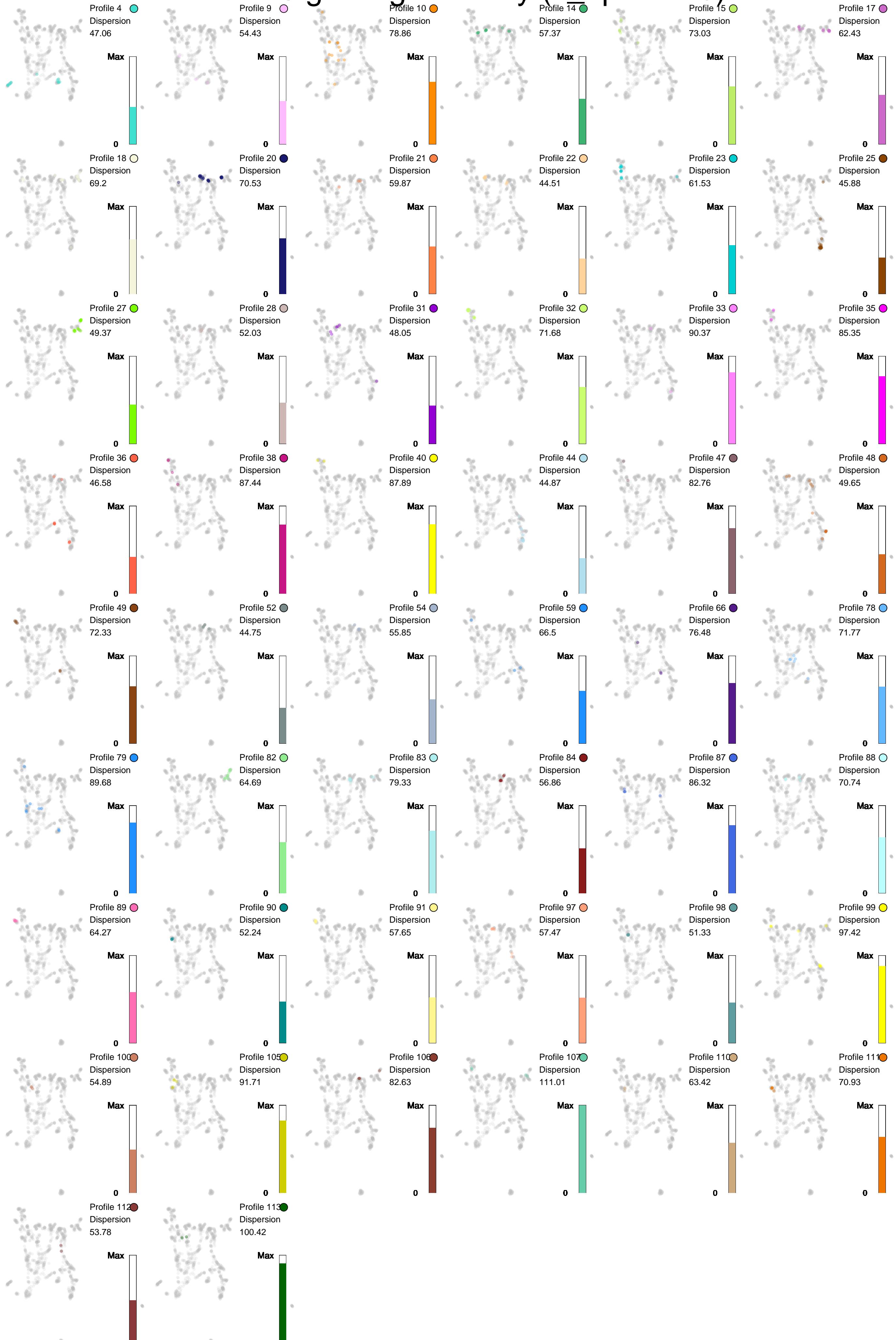
Mitochondrial Electron Transport Chain (k_opt = 43)



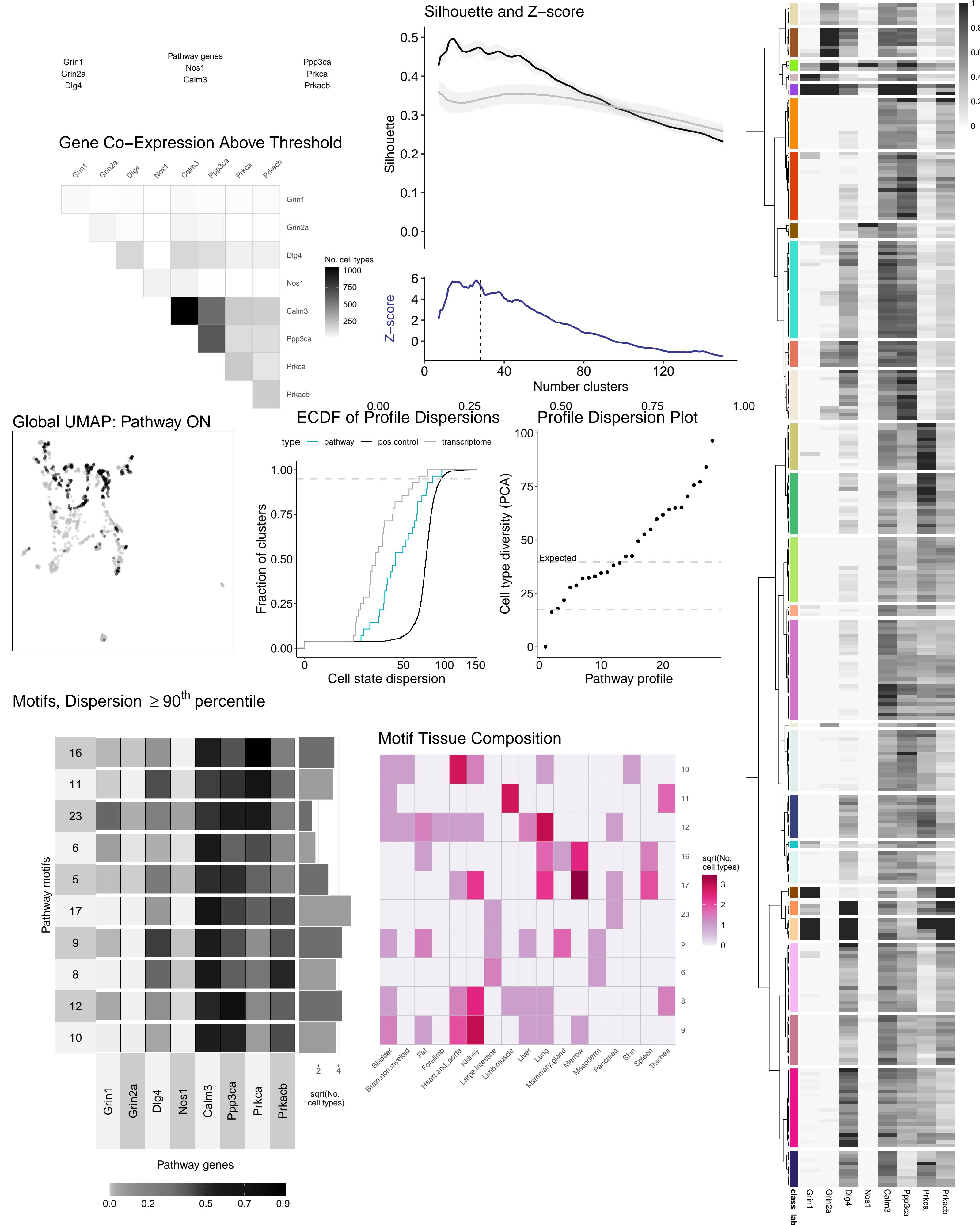
NF- κ B Signaling Pathway ($k_{\text{opt}} = 113$)



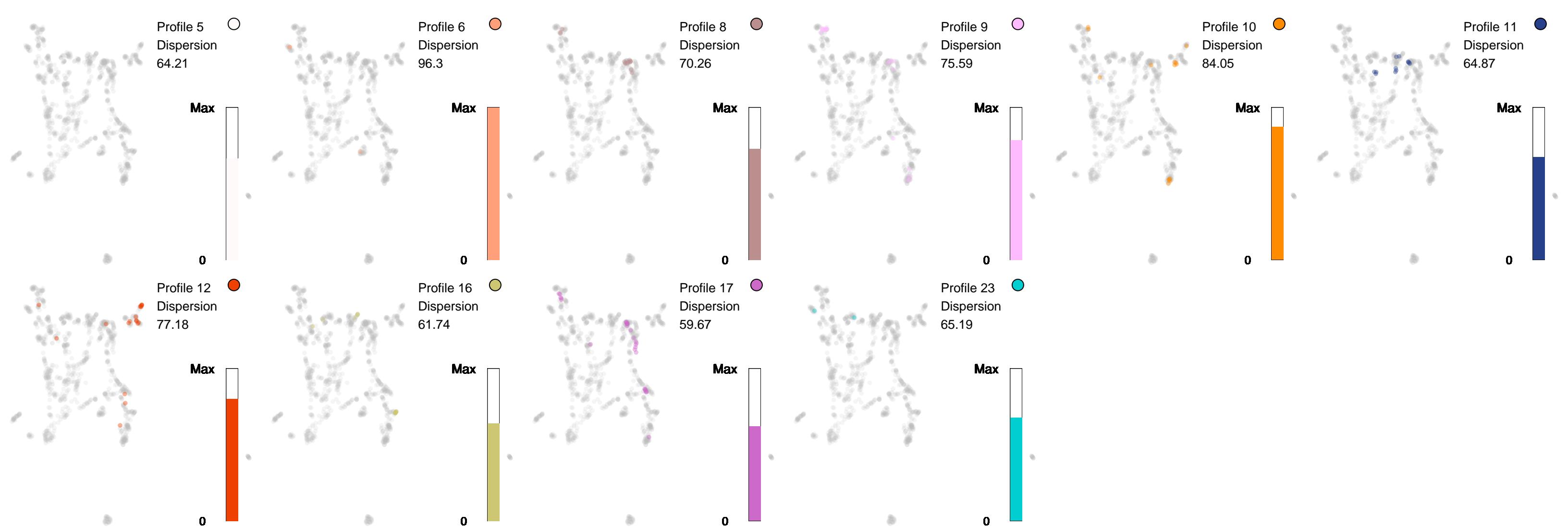
NF- κ B Signaling Pathway ($k_{\text{opt}} = 113$)



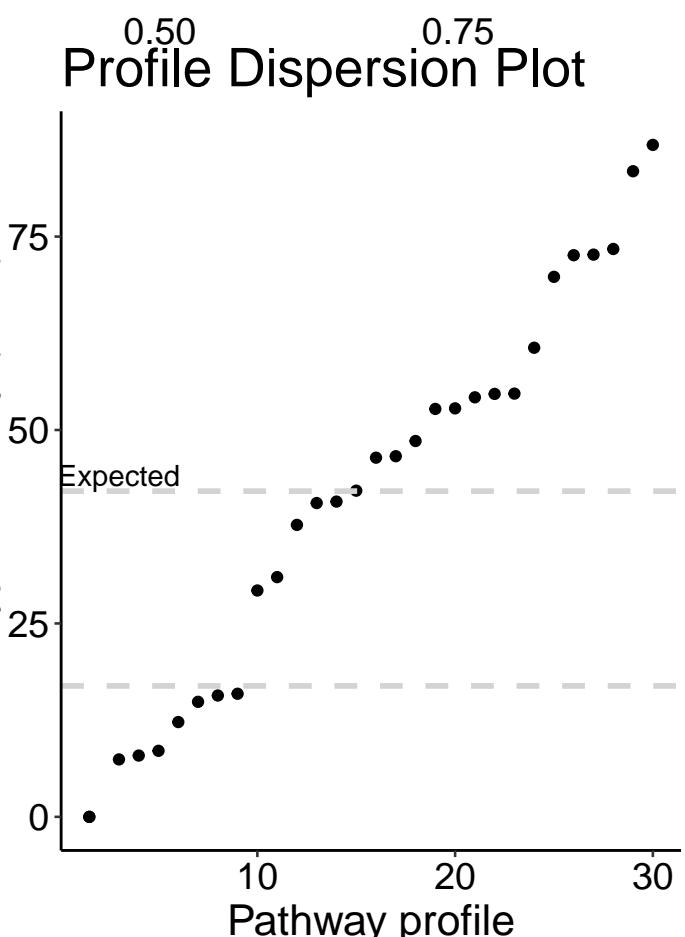
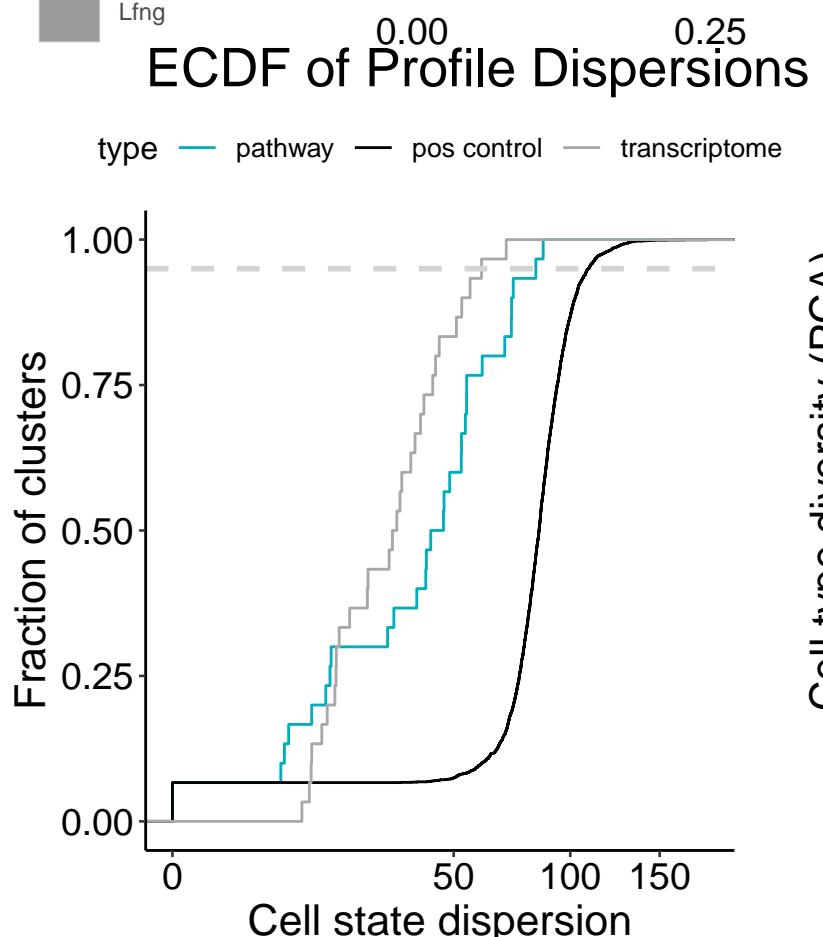
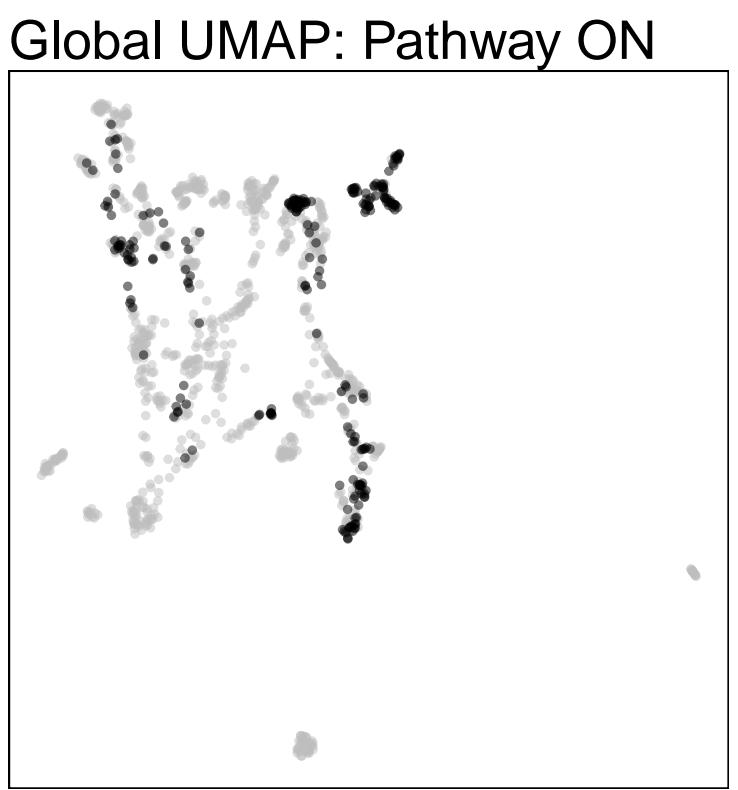
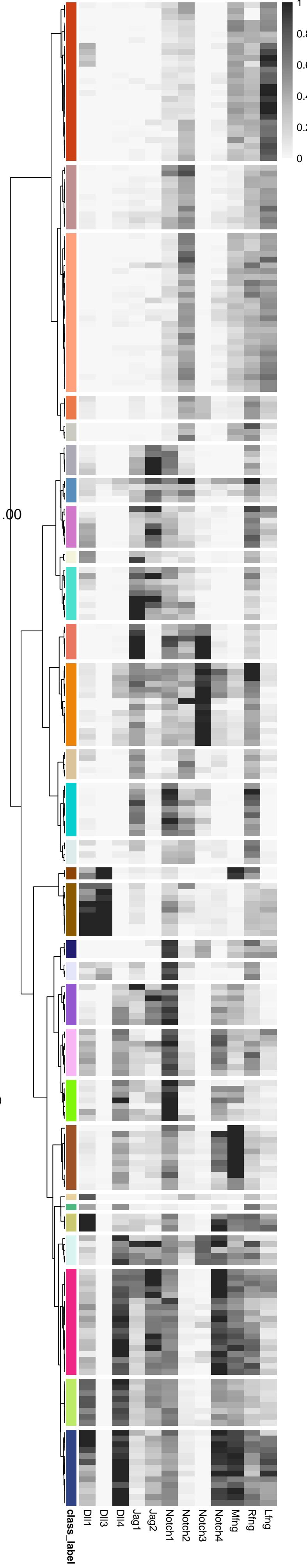
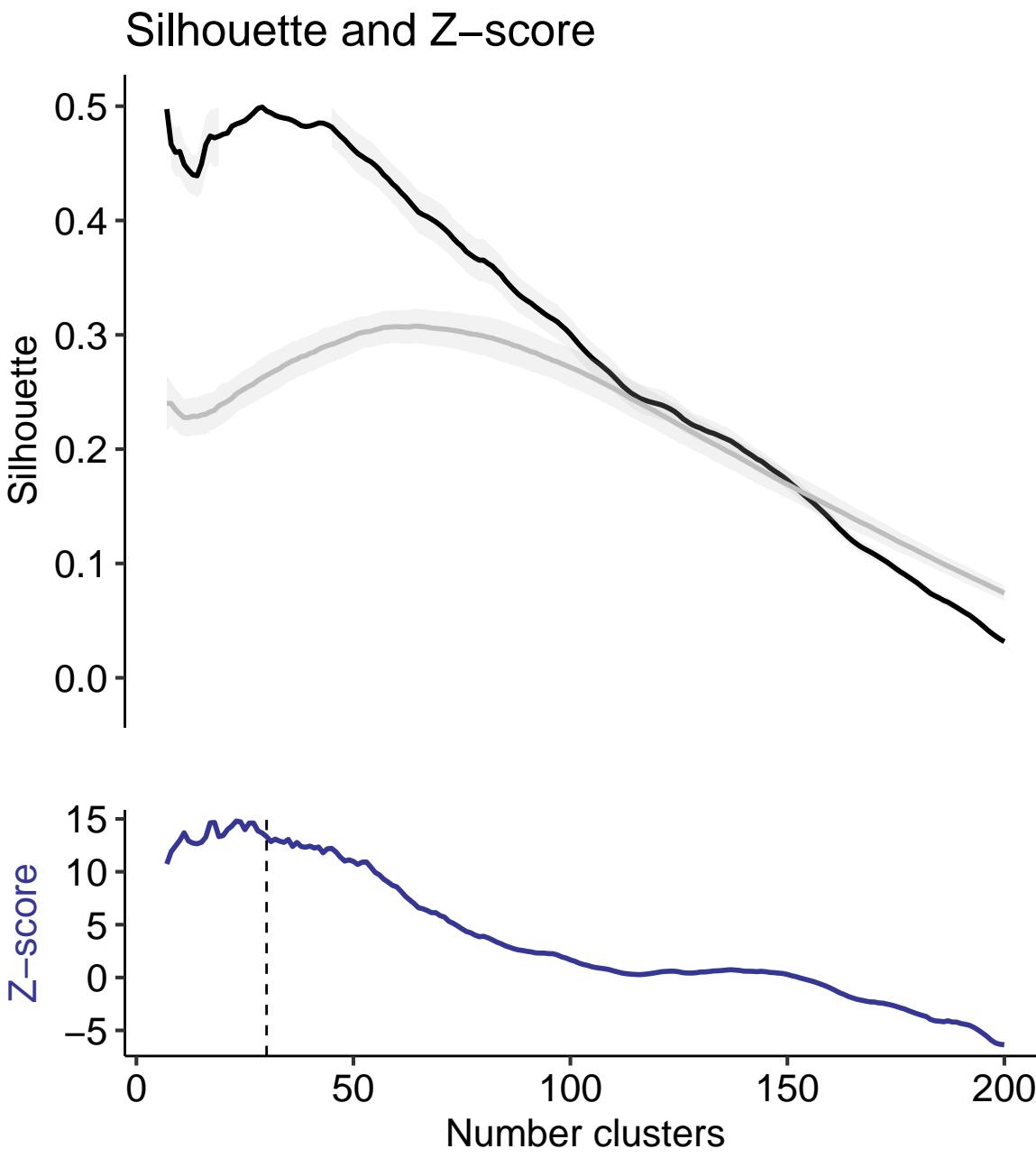
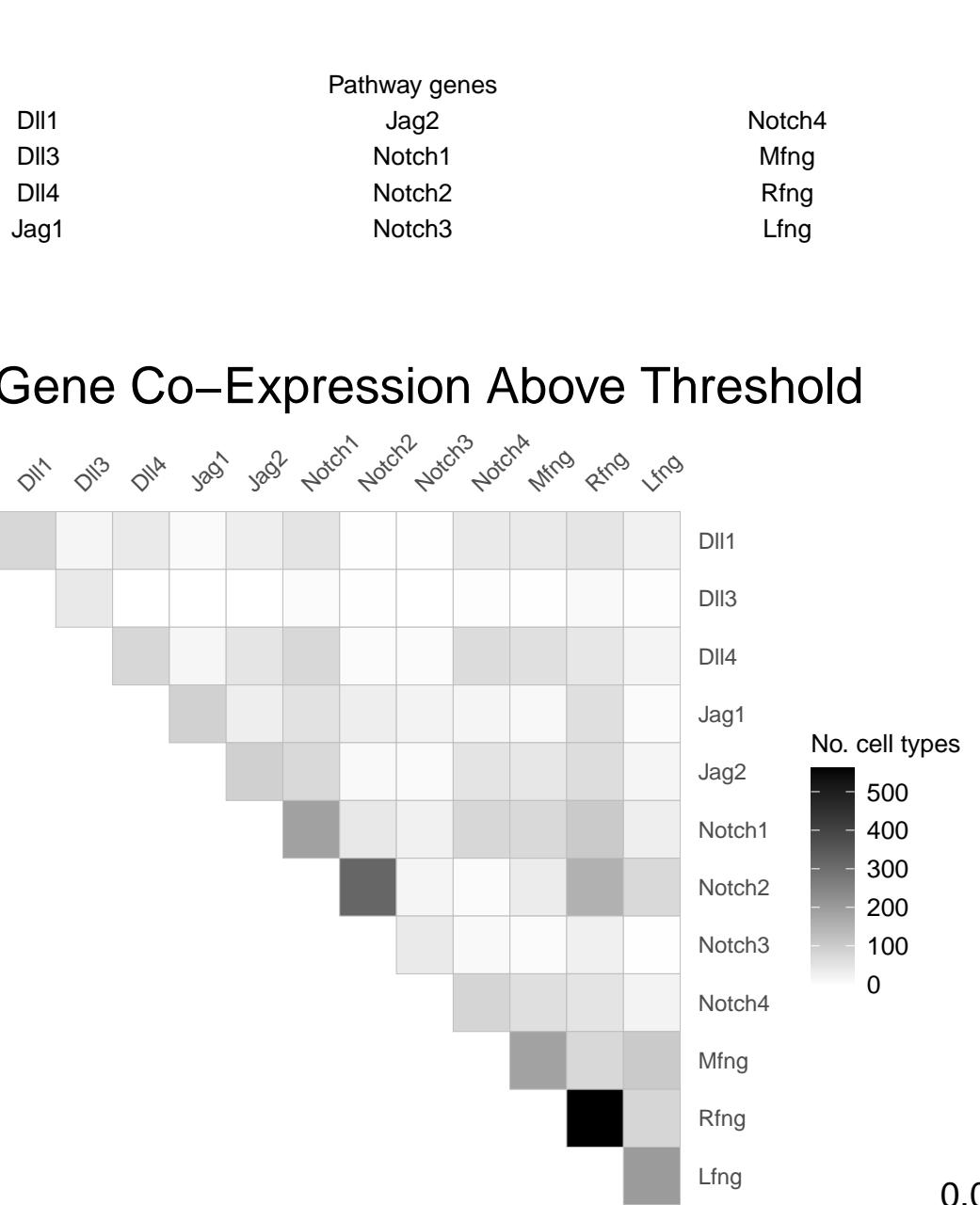
Nitric Oxide Signaling Pathway ($k_{opt} = 28$)



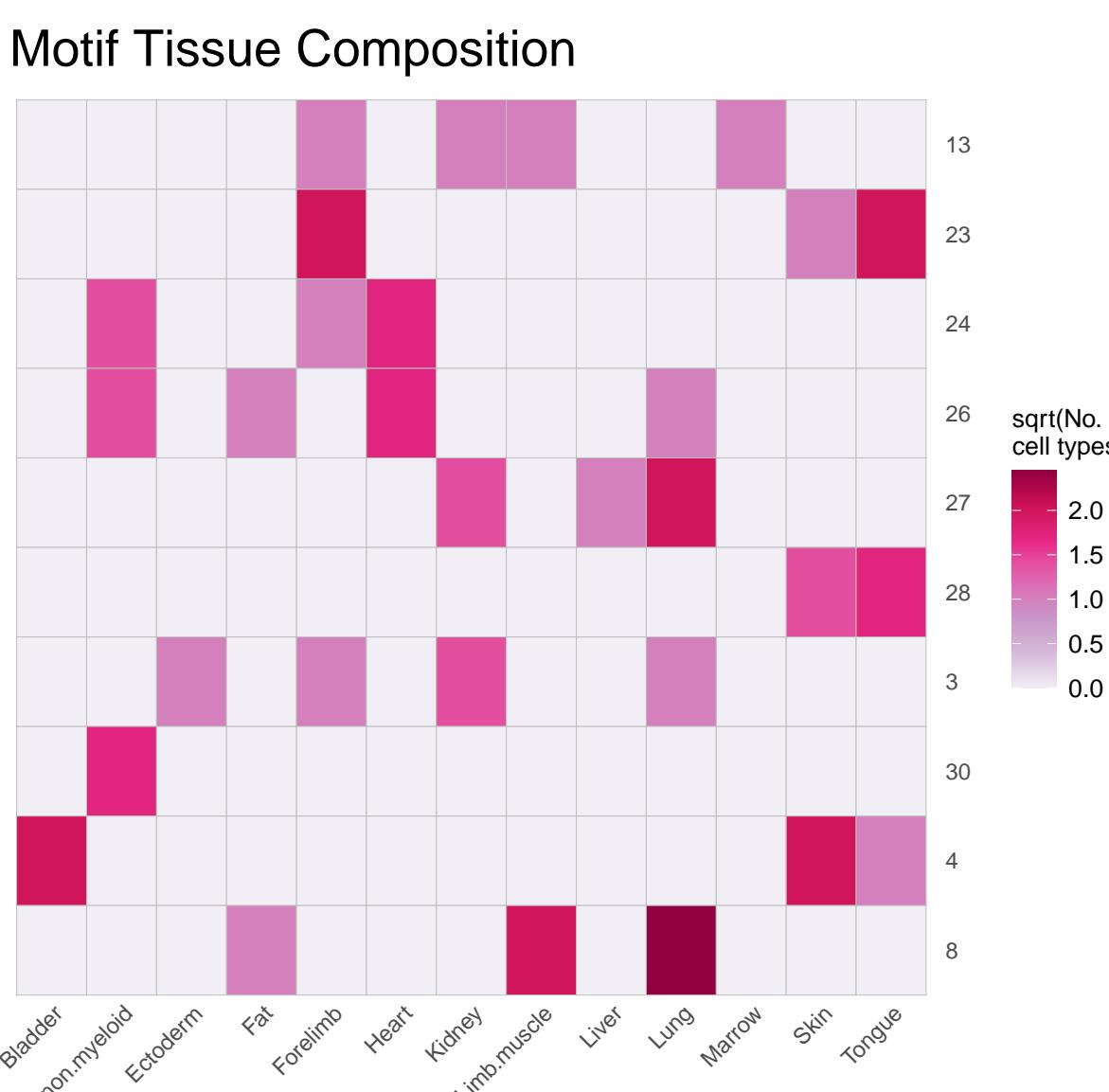
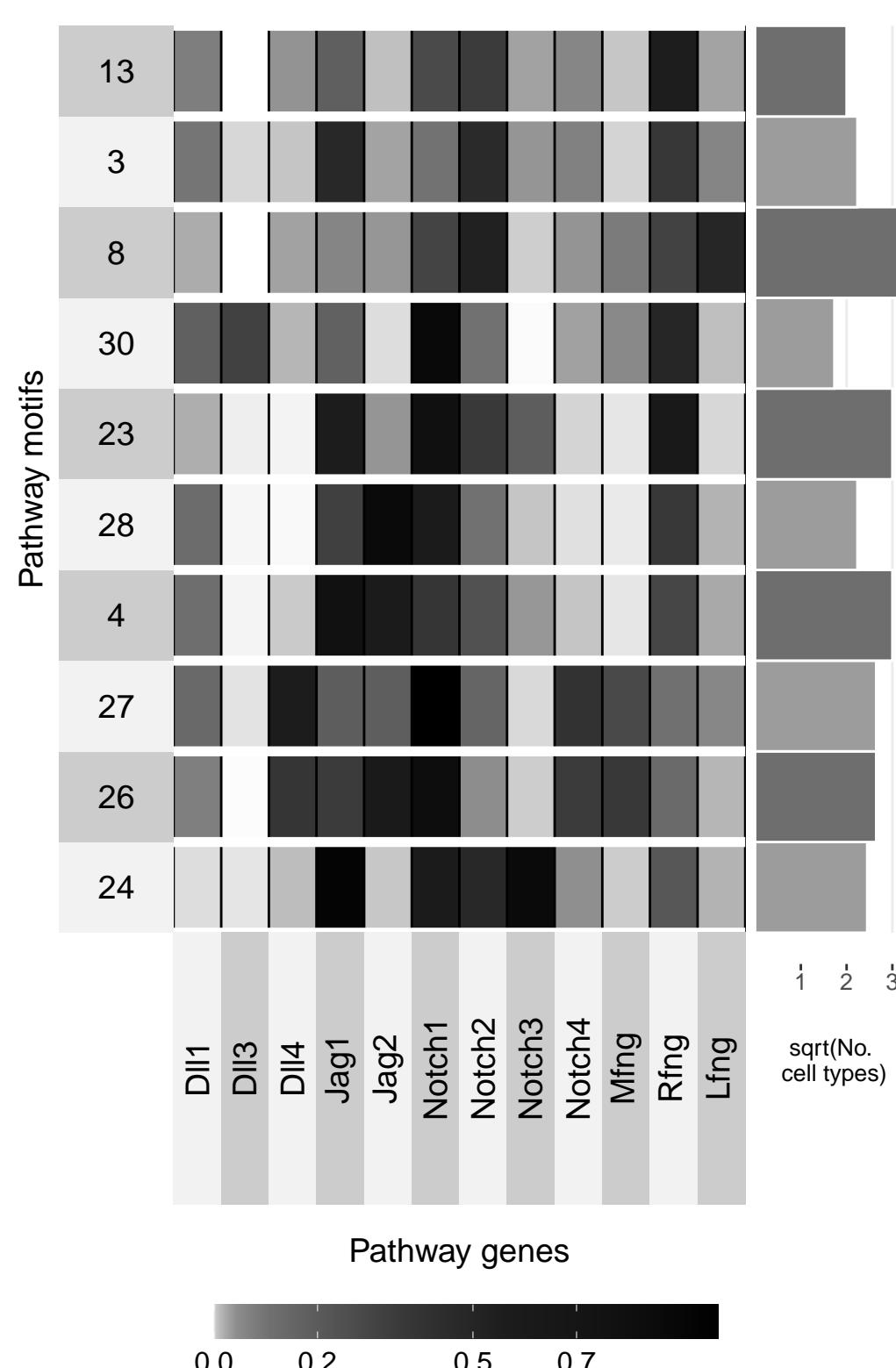
Nitric Oxide Signaling Pathway ($k_{opt} = 28$)



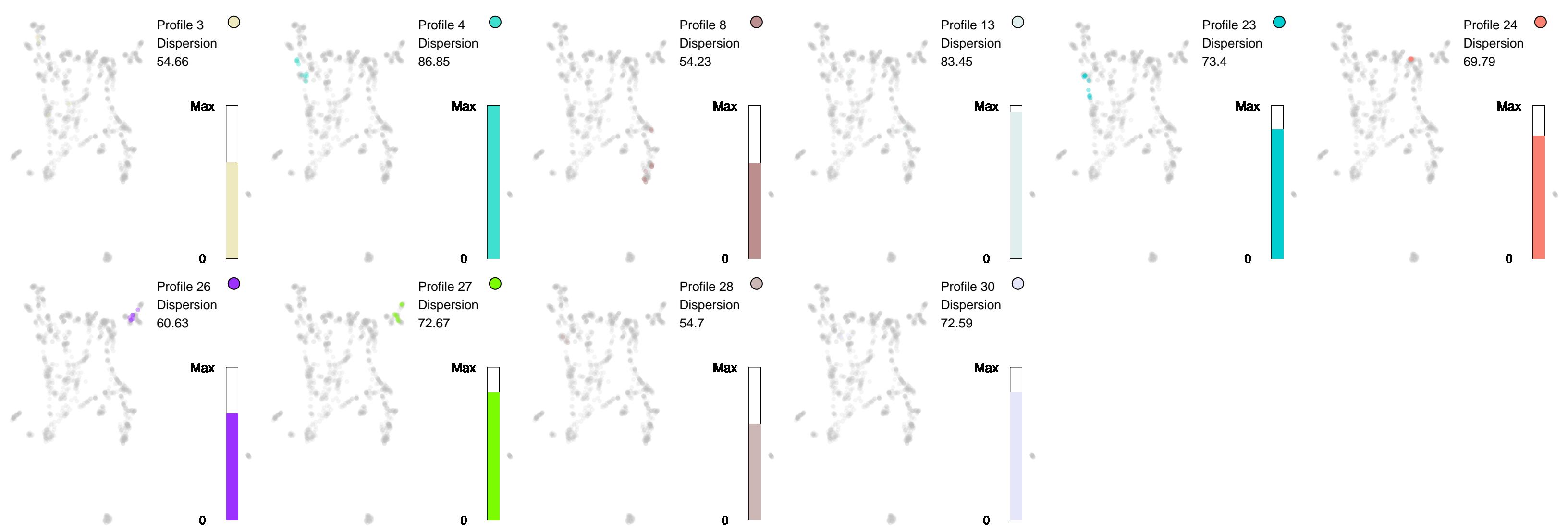
Notch receptors, Dll ligands and Fringe proteins ($k_{opt} = 30$)



Motifs, Dispersion \geq 90th percentile



Notch receptors, DII ligands and Fringe proteins ($k_{opt} = 30$)

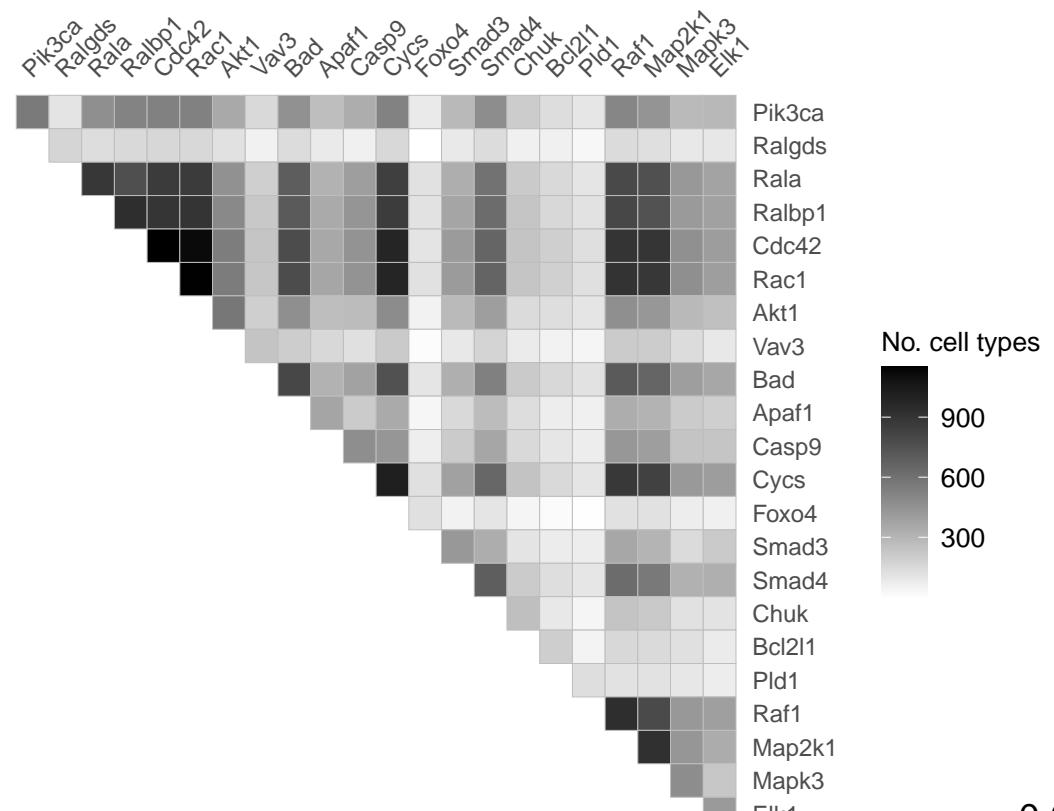


Ras Signaling Pathway (k_opt = 83)

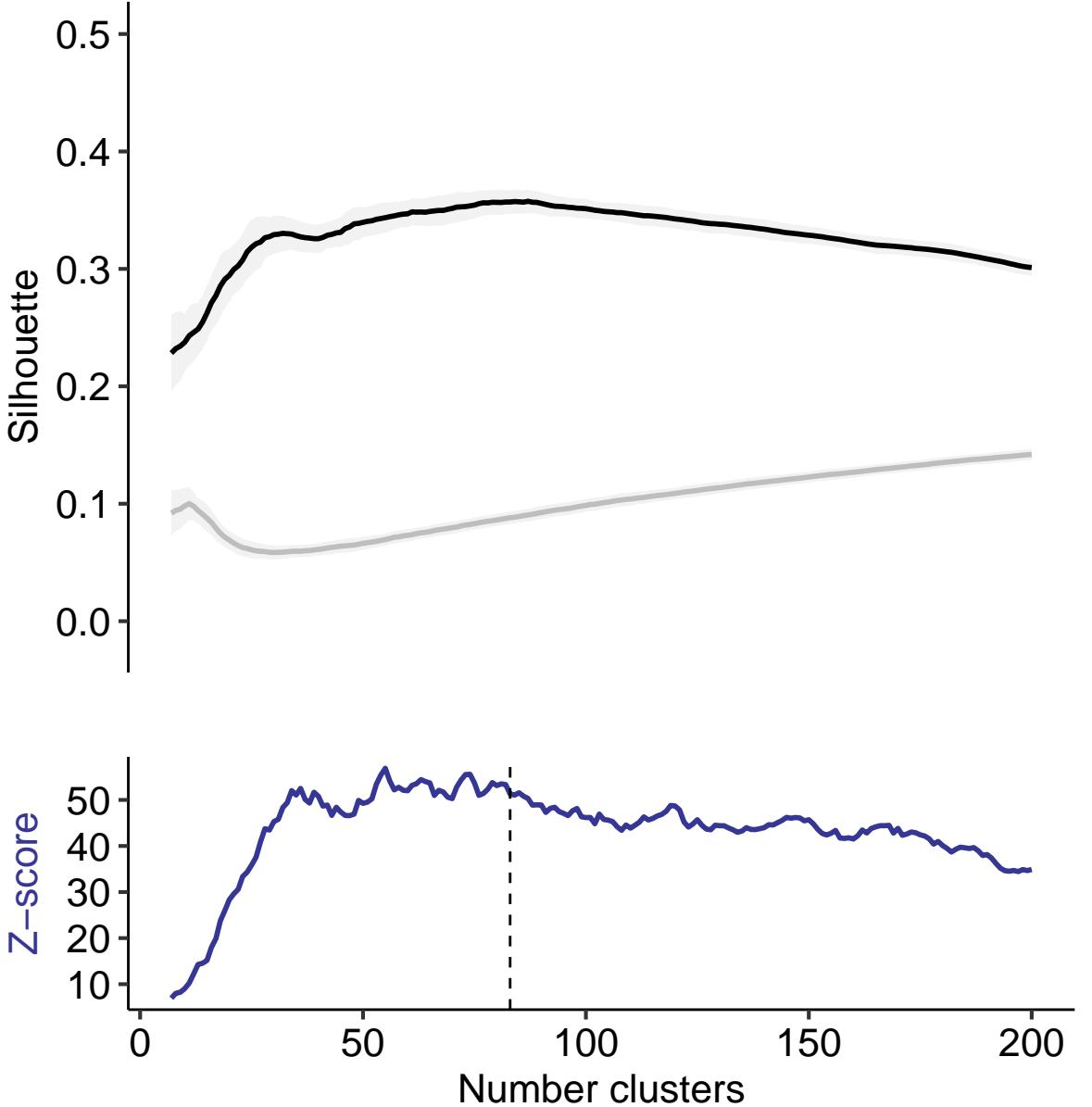
Pathway genes

Pik3ca	Bad	Chuk
Ralgds	Apa1f	Bcl2l1
Rala	Casp9	Pld1
Ralbp1	Cycs	Raf1
Cdc42	Foxo4	Map2k1
Rac1	Smad3	Mapk3
Akt1	Smad4	Elk1
Vav3		

Gene Co-Expression Above Threshold



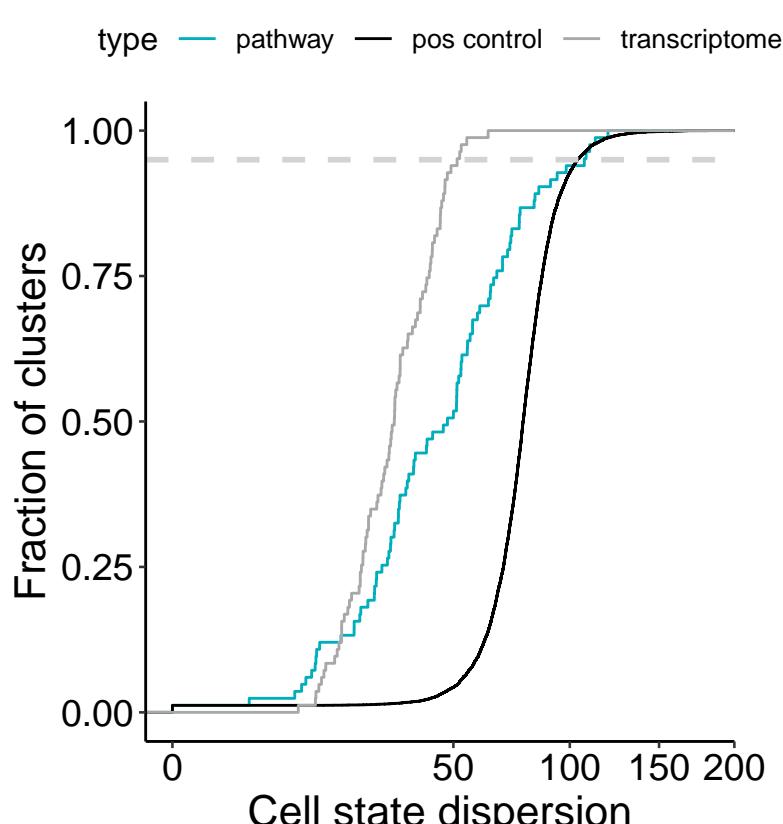
Silhouette and Z-score



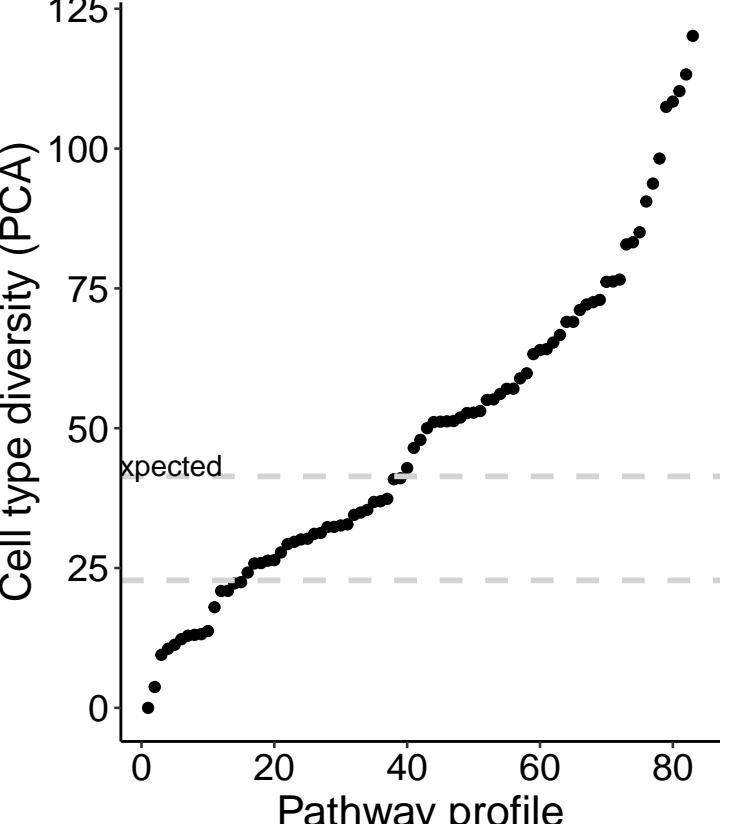
Global UMAP: Pathway ON



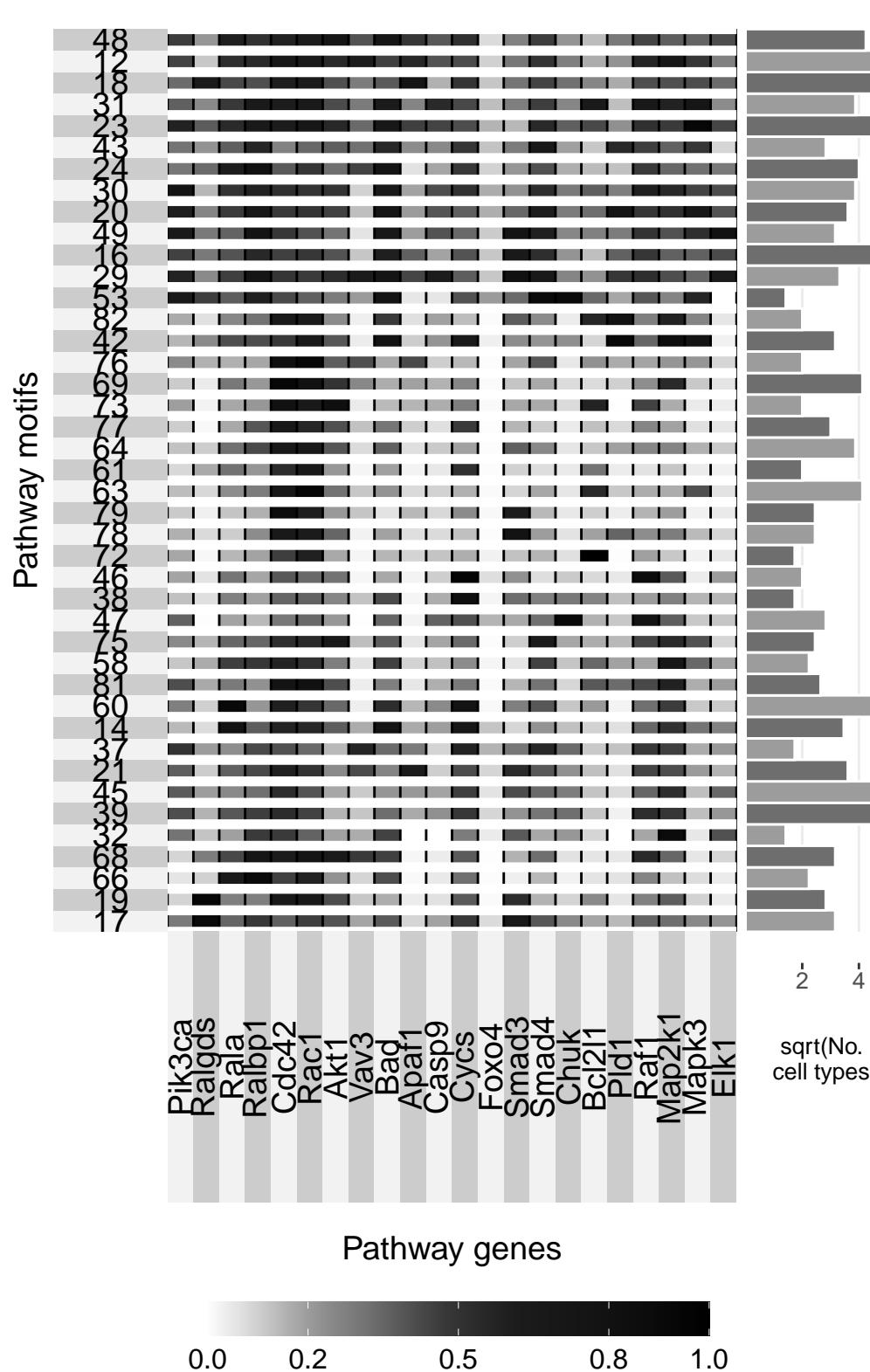
ECDF of Profile Dispersion



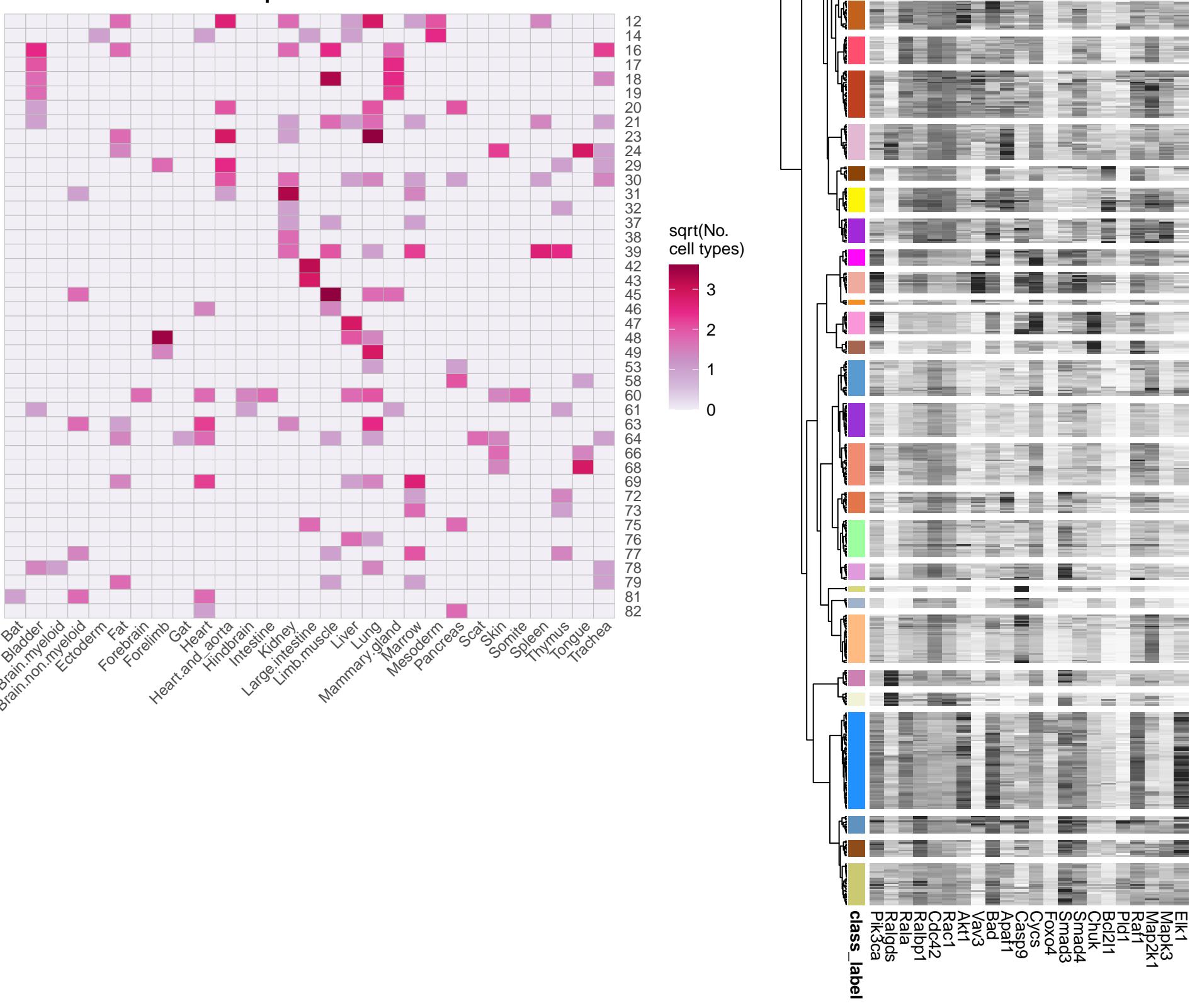
Profile Dispersion Plot



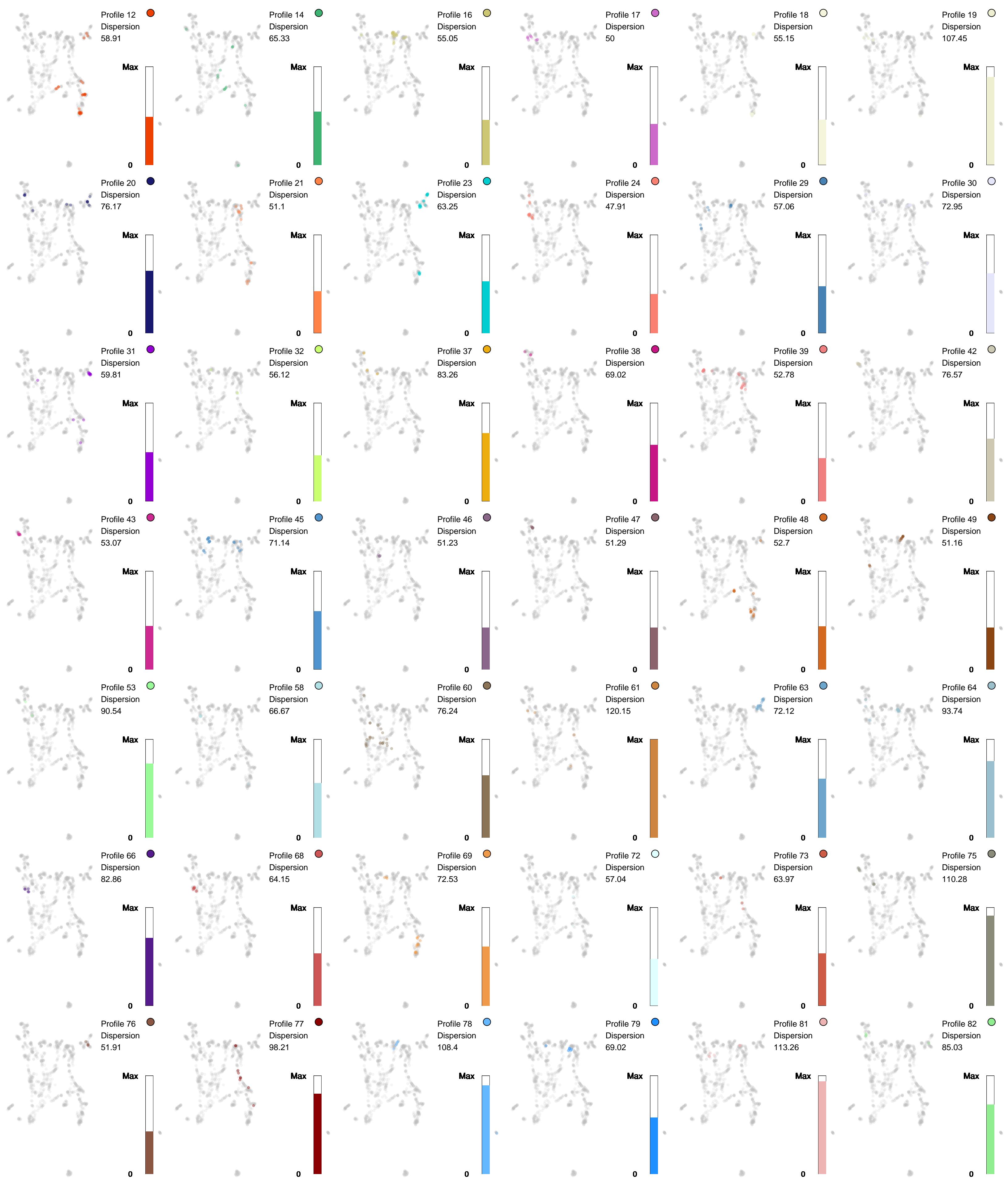
Motifs, Dispersion $\geq 90^{\text{th}}$ percentile



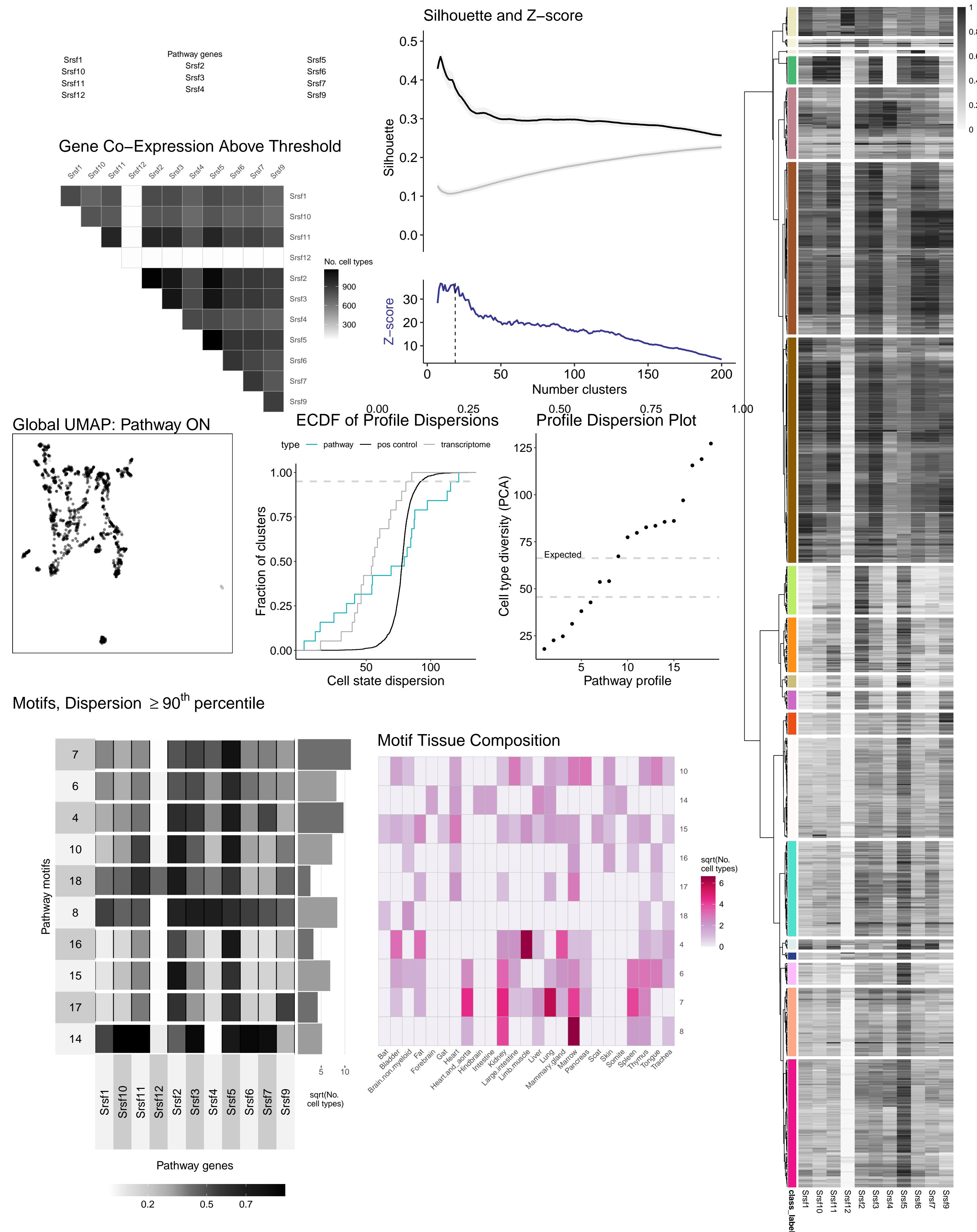
Motif Tissue Composition



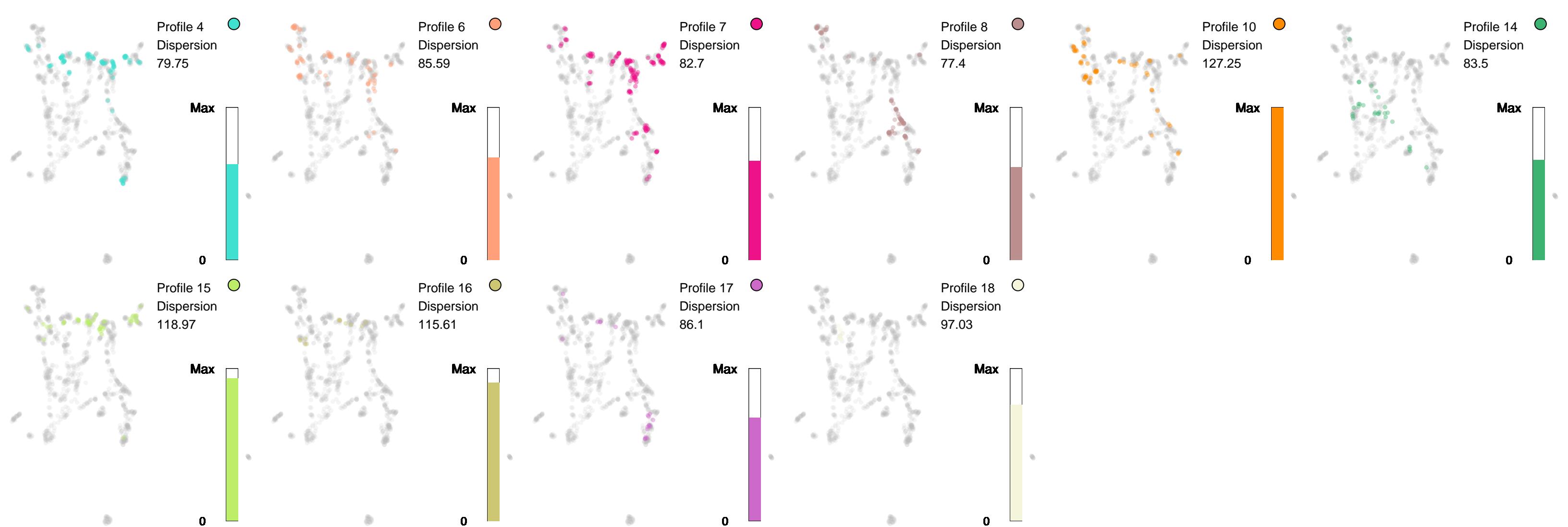
Ras Signaling Pathway (k_opt = 83)



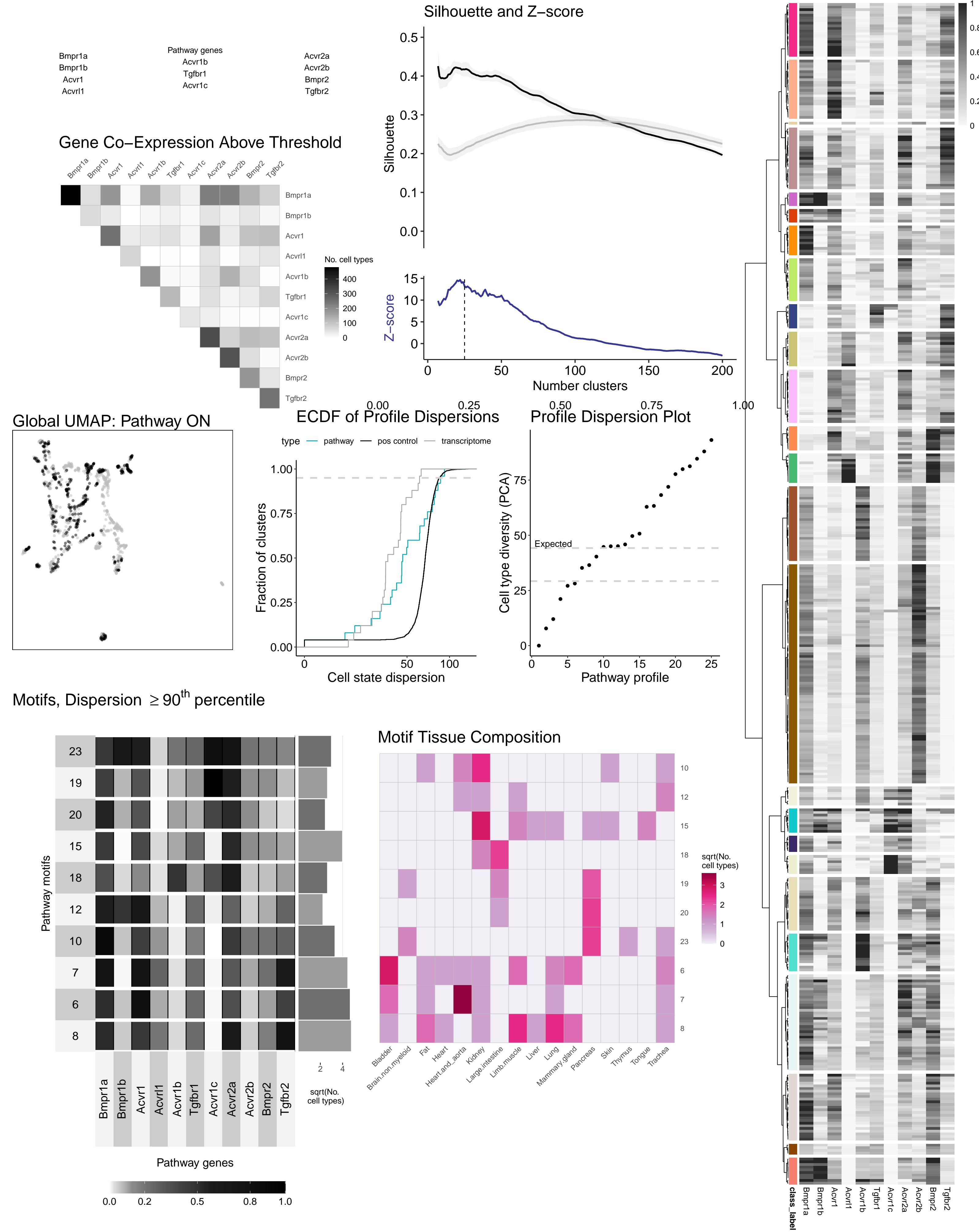
RNA-splicing by SR protein family ($k_{opt} = 19$)



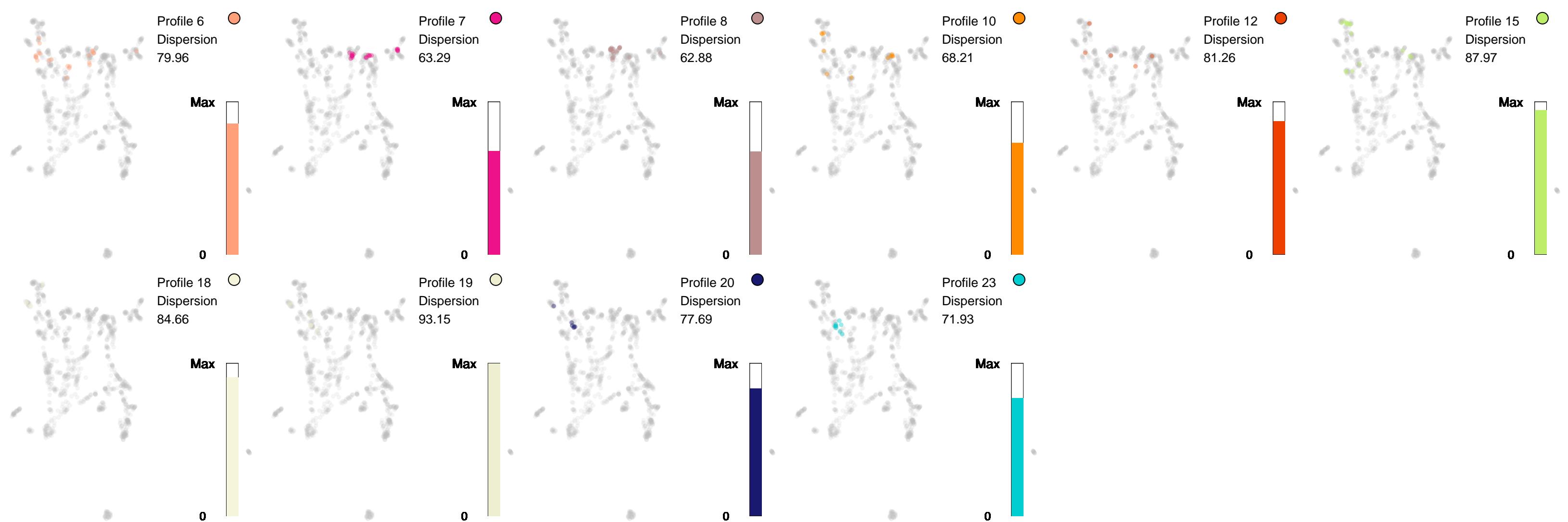
RNA-splicing by SR protein family ($k_{opt} = 19$)



Tgf-beta family receptors (k_opt = 25)



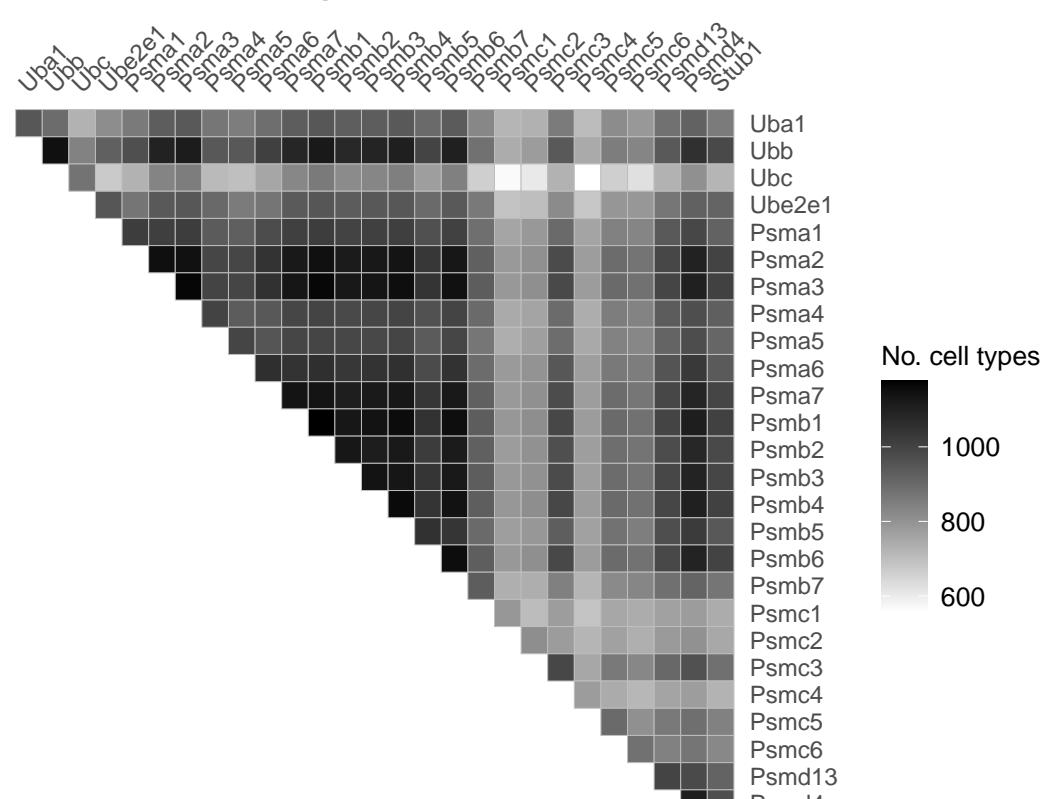
Tgf–beta family receptors (k_opt = 25)



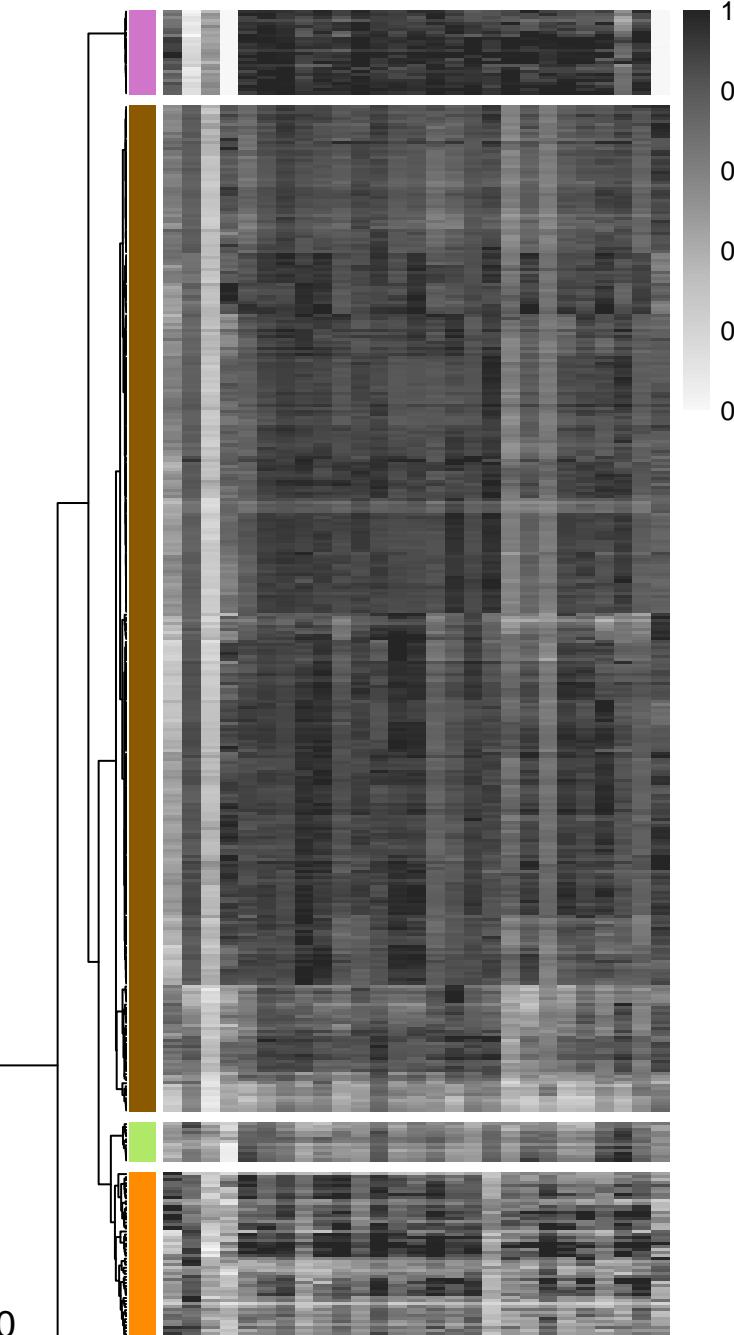
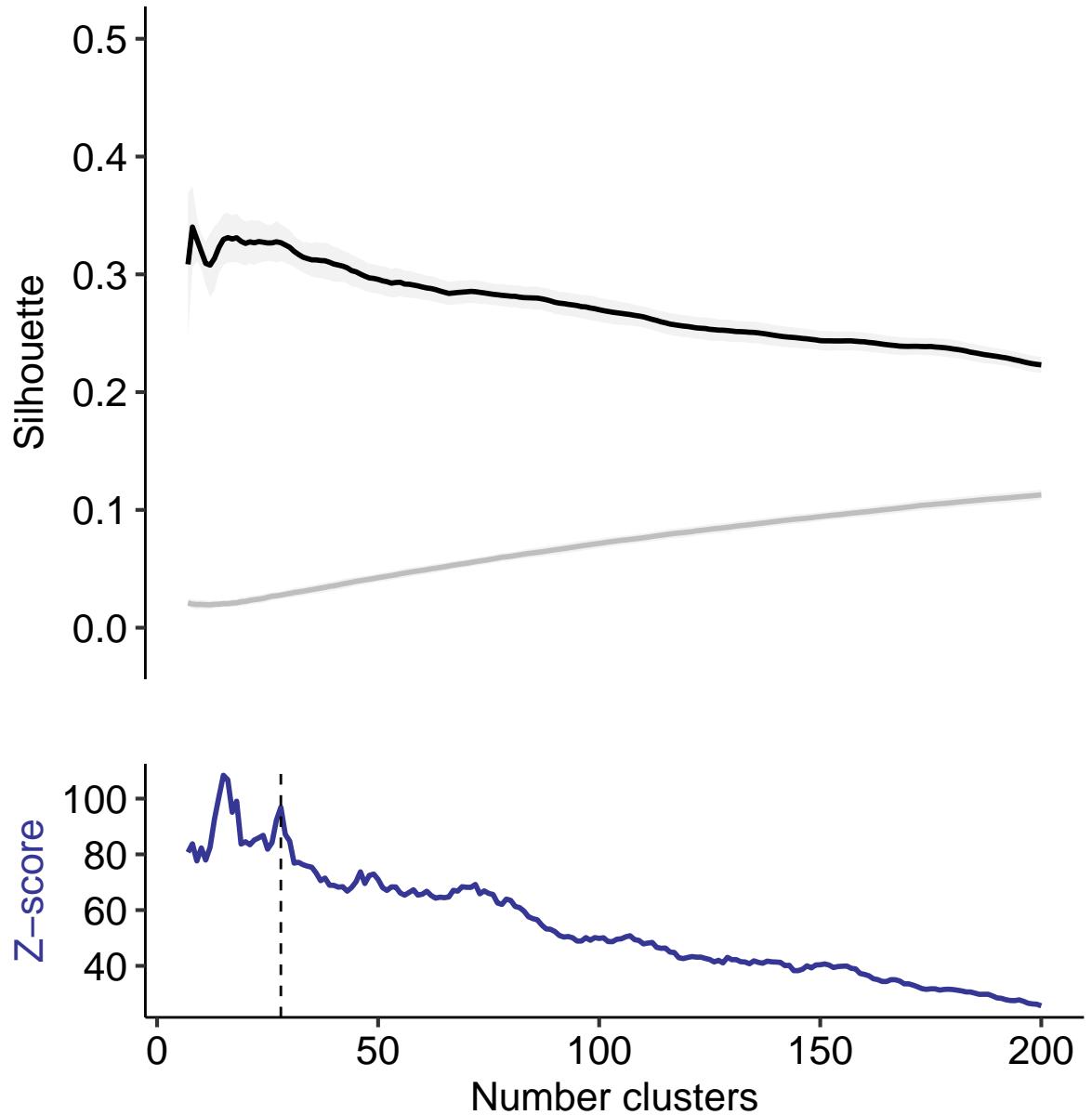
Ubiquitin–Proteasome Pathway (k_{opt} = 28)

Pathway genes		
Uba1	Psma6	Psmc1
Ubb	Psma7	Psmc2
Ubc	Psmb1	Psmc3
Ube2e1	Psmb2	Psmc4
Psma1	Psmb3	Psmc5
Psma2	Psmb4	Psmc6
Psma3	Psmb5	Psmd13
Psma4	Psmb6	Psmd4
Psma5	Psmb7	Stub1

Gene Co-Expression Above Threshold



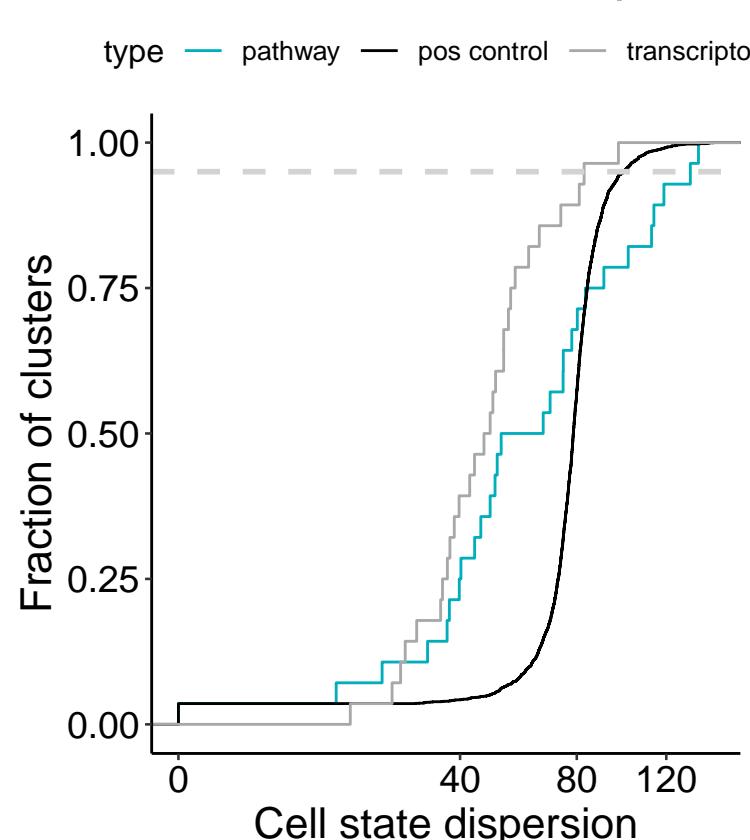
Silhouette and Z-score



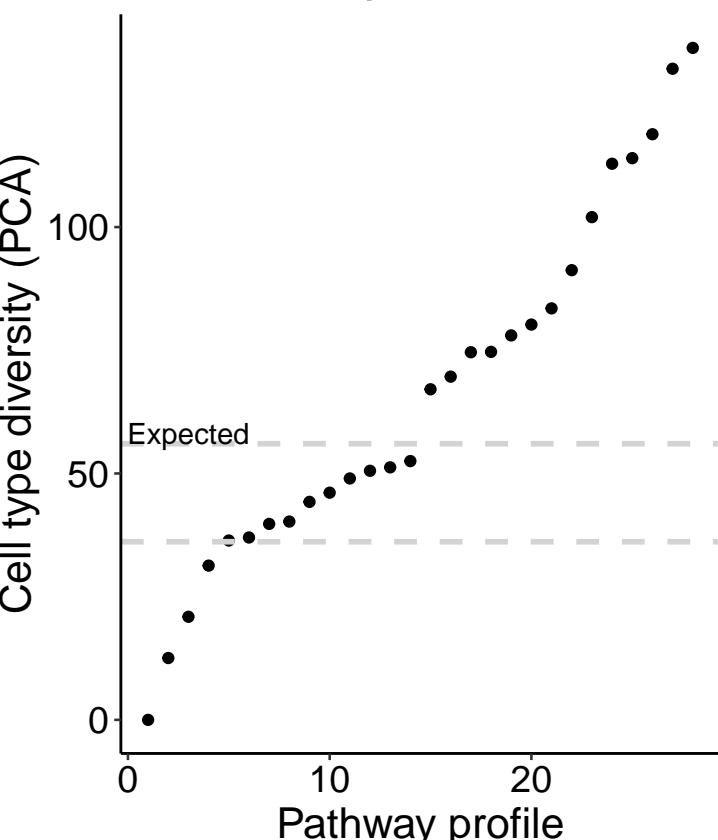
Global UMAP: Pathway ON



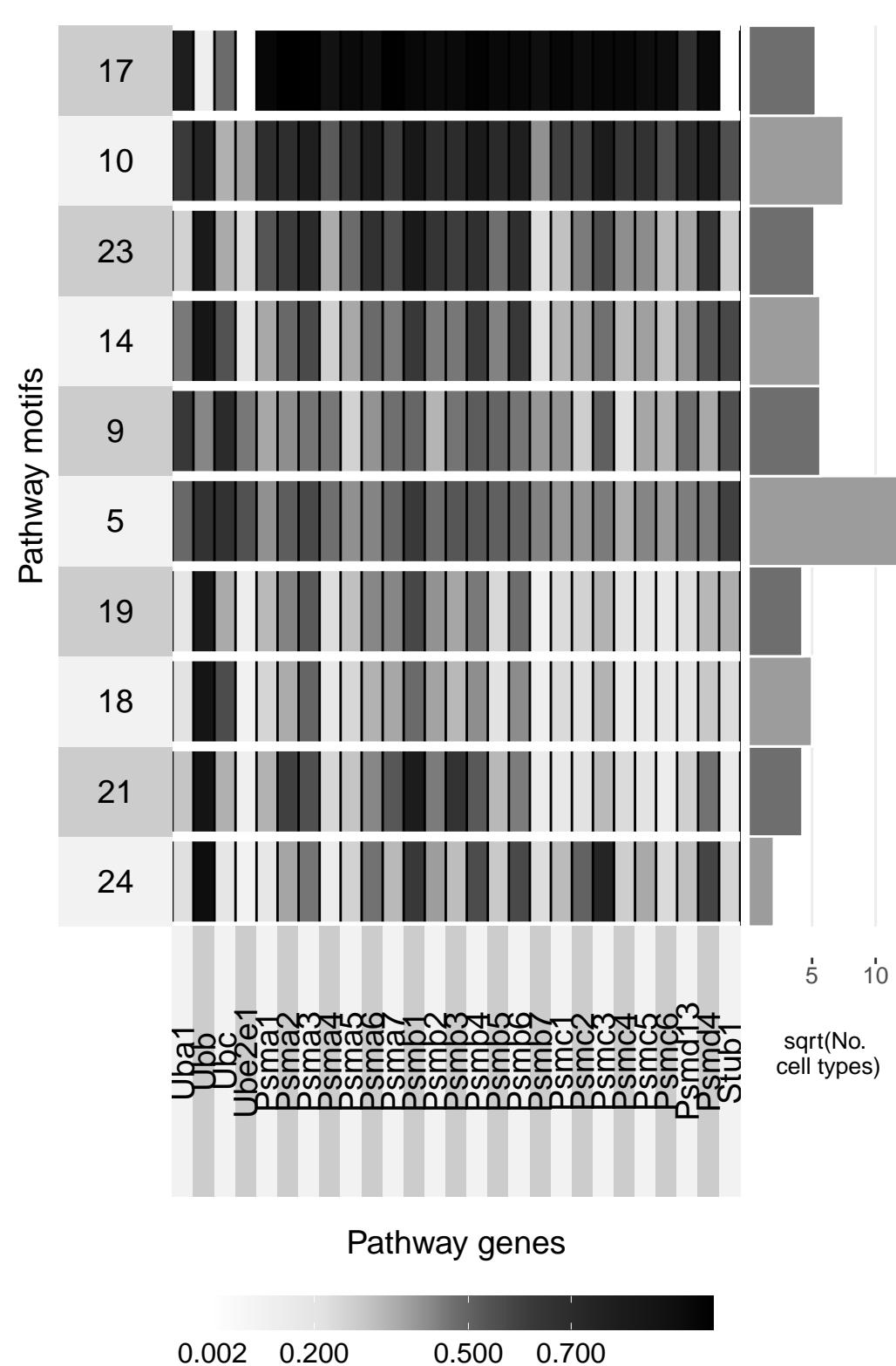
ECDF of Profile Dispersion



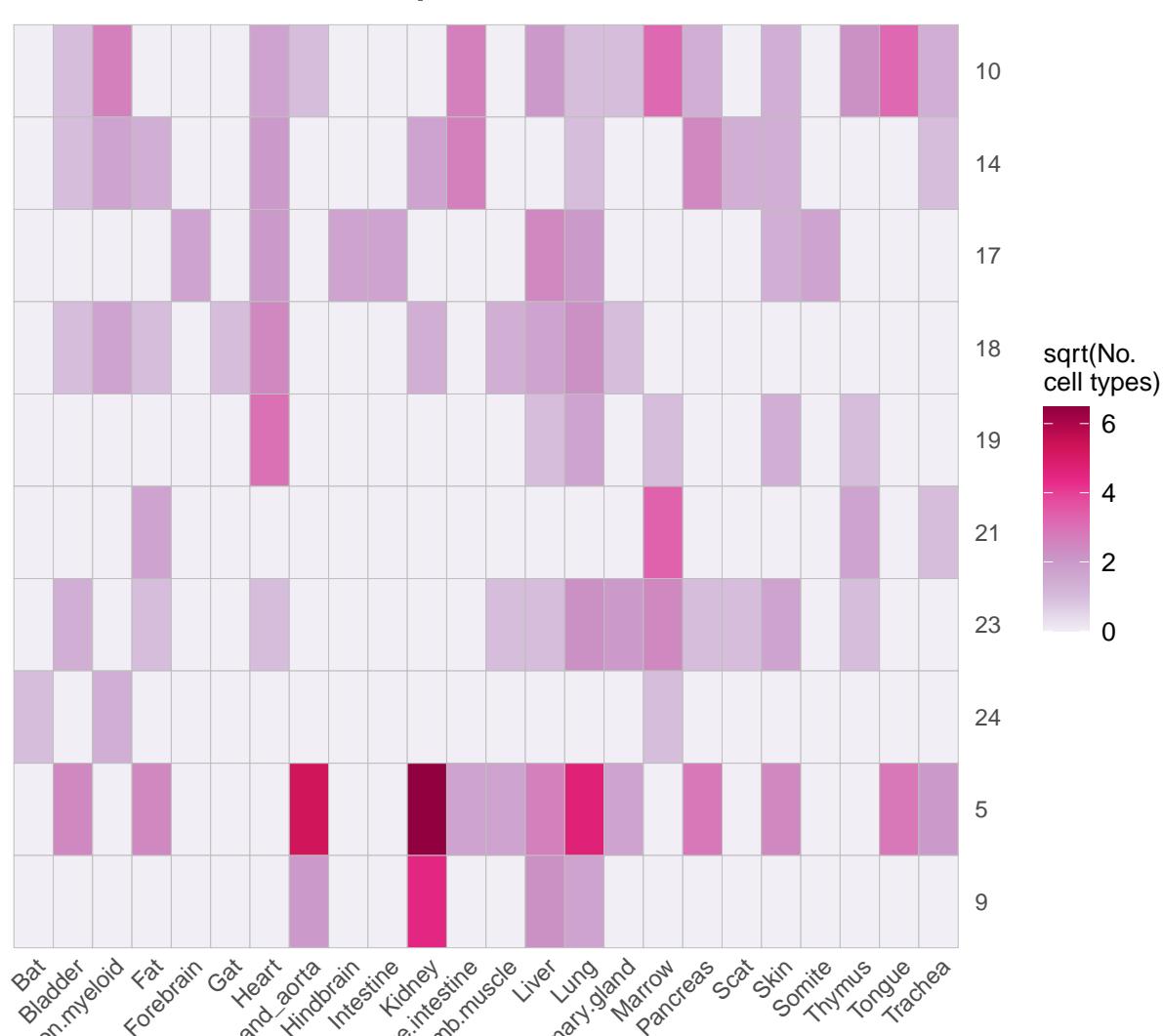
Profile Dispersion Plot



Motifs, Dispersion $\geq 90^{\text{th}}$ percentile



Motif Tissue Composition



Ubiquitin–Proteasome Pathway (k_opt = 28)

