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Figure S1. A. Original KEGG pathway image of Hippo signaling pathway. B. Network extracted from the original KGML file. C. Network after automated and further manual curation with the PSF toolkit (18 fixes with automatic error correction during parsing, 24 fixes with manual curation). Nodes with a blue border are terminal (sink) nodes. Red and blue lines between the nodes are activation and inhibition interactions, respectively. Purple and yellow lines are manually curated interactions.



Figure S2. AMPK signaling pathway detected with only PSF. Differentially expressed genes/nodes are highlighted with red borders. According to the PSF algorithm, the blue highlighted branch was downregulated 10-fold due to the activation of the AMPK gene through the Leptin Receptor which represses growth arrest.



Figure S3. Chemokine signaling pathway color-coded with pathway activity values. The pathway is classified as activated with the SPIA algorithm, while there are three terminal nodes that are inhibited with the AKT3 gene.







Figure S4. Two KEGG signaling pathways deregulated in lung cells. The first pathway is detected with both the PSF and ORA methods, while the second is only detected with the PSF algorithm. Differentially expressed genes/nodes are highlighted with red borders and deregulated terminal nodes with blue (yellow if the node is both differentially expressed and deregulated by the PSF algorithm). **A)** Fc gamma R mediated phagocytosis pathway,

detected with ORA where 33 genes are differentially expressed out of 91. The proportion of deregulated terminal nodes over the total is 0.9 (9 nodes out of 10). **B**) Toll-like receptor signaling pathway detected only with the PSF method where 16 genes were differentially expressed out of 104. The proportion of deregulated terminal nodes over the total is 0.27 (5 nodes out of 18). This demonstrates the sensitivity of the PSF algorithm to detect part of a deregulated pathway.

Supplementary table1. Top 5 cluster-associated features for each tissue type from gene and pathway activity clustering and top 5 enriched pathways based on gene level cluster specific significant genes.

Cluster/Tissue	Top genes	Top psf branches	Top enriched pathways
skeletalmuscle	MYF6	51-FoxO-signaling-pathway	Focal adhesion
skeletalmuscle	PPP1R27	56-FoxO-signaling-pathway	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
skeletalmuscle	CACNG1	88-FoxO-signaling-pathway	Rap1 signaling pathway
skeletalmuscle	CHRNA1	27-PI3K-Akt-signaling-pathway	Endocytosis
skeletalmuscle	DDIT4L	50-FoxO-signaling-pathway	Regulation of actin cytoskeleton
breast	SLC7A10	8-ErbB-signaling-pathway	Focal adhesion
breast	LGALS12	7-JAK-STAT-signaling-pathway	Dilated cardiomyopathy (DCM)
breast	OXTR	52-Hedgehog-signaling-pathway	AMPK signaling pathway
breast	ANGPTL8	50-Hedgehog-signaling-pathway	Hypertrophic cardiomyopathy (HCM)
breast	ADIPOQ	24-ErbB-signaling-pathway	Cardiac muscle contraction
esophagusmuc osa	CRNN	27-JAK-STAT-signaling-pathway	Rap1 signaling pathway
esophagusmuc osa	SPRR3	29-B-cell-receptor-signaling-pathway	Focal adhesion
esophagusmuc osa	SPRR2A	44-T-cell-receptor-signaling-pathway	Dilated cardiomyopathy (DCM)
esophagusmuc osa	SPRR2D	60-cAMP-signaling-pathway	Axon guidance
esophagusmuc osa	KRT6C	48-Rap1-signaling-pathway	Adherens junction
esophagusmus cularis	NKX6-1	27-p53-signaling-pathway	Hypertrophic cardiomyopathy (HCM)
esophagusmus cularis	IL6	110-cAMP-signaling-pathway	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
esophagusmus cularis	SPP2	118-cAMP-signaling-pathway	Focal adhesion
esophagusmus cularis	FAM83D	61-Complement-and-coagulation-ca scades	Dilated cardiomyopathy (DCM)
esophagusmus cularis	FOXF2	62-Complement-and-coagulation-ca scades	PI3K-Akt signaling pathway
heart	NPPB	26-cAMP-signaling-pathway	Focal adhesion
heart	MYL7	7-cAMP-signaling-pathway	Cardiac muscle contraction
heart	TNNI3	8-Calcium-signaling-pathway	Alzheimer disease

TBX20	5 AMD signaling pathway	A
/ 0	o-came-signaling-pathway	Axon guidance
ACTC1	20-Calcium-signaling-pathway	Regulation of actin cytoskeleton
SFTPA1	15-Hedgehog-signaling-pathway	Focal adhesion
NKX2-1	26-Hedgehog-signaling-pathway	Dilated cardiomyopathy (DCM)
SFTPA2	33-Hedgehog-signaling-pathway	PI3K-Akt signaling pathway
SFTPC	114-cAMP-signaling-pathway	Phospholipase D signaling pathway
NGB	15-AMPK-signaling-pathway	Hypertrophic cardiomyopathy (HCM)
PRAC1	69-cAMP-signaling-pathway	Focal adhesion
KLK4	60-AMPK-signaling-pathway	Protein processing in endoplasmic reticulum
HOXB13	31-Wnt-signaling-pathway	Axon guidance
KLK3	100-cAMP-signaling-pathway	Prostate cancer
KLK2	26-TGF-beta-signaling-pathway	Proteoglycans in cancer
KRT2	47-ErbB-signaling-pathway	Dilated cardiomyopathy (DCM)
KRT1	48-ErbB-signaling-pathway	Hypertrophic cardiomyopathy (HCM)
CLEC2A	20-NOD-like-receptor-signaling-path way	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
DCD	79-Ras-signaling-pathway	Fluid shear stress and atherosclerosis
WFDC5	64-Complement-and-coagulation-ca scades	GnRH signaling pathway
	ACTC1 SFTPA1 NKX2-1 SFTPA2 SFTPC NGB PRAC1 KLK4 HOXB13 KLK3 KLK2 KRT2 KRT1 CLEC2A DCD	ACTC120-Calcium-signaling-pathwayACTC120-Calcium-signaling-pathwaySFTPA115-Hedgehog-signaling-pathwayNKX2-126-Hedgehog-signaling-pathwaySFTPA233-Hedgehog-signaling-pathwaySFTPC114-cAMP-signaling-pathwayNGB15-AMPK-signaling-pathwayPRAC169-cAMP-signaling-pathwayKLK460-AMPK-signaling-pathwayHOXB1331-Wnt-signaling-pathwayKLK226-TGF-beta-signaling-pathwayKLK226-TGF-beta-signaling-pathwayKLK247-ErbB-signaling-pathwayKRT148-ErbB-signaling-pathwayCLEC2A20-NOD-like-receptor-signaling-path wayWFDC564-Complement-and-coagulation-ca scades