

Table S1. Top 14 clusters with their representative enriched terms (one per cluster). "Count" is the number of genes in the user-provided lists with membership in the given ontology term. "%" is the percentage of all of the user-provided genes that are found in the given ontology term (only input genes with at least one ontology term annotation are included in the calculation). "Log10 (P)" is the p-value in log base 10. "Log10 (q)" is the multi-test adjusted p-value in log base 10.

GO	Category	Description	Count	%	Log10(P)	Log10(q)
R-HSA-6809371	Reactome Gene Sets	Formation of the cornified envelope	15	18.07	-19.87	-15.53
GO:0003012	GO Biological Processes	muscle system process	13	15.66	-12.04	-8.64
GO:0030858	GO Biological Processes	positive regulation of epithelial cell differentiation	5	6.02	-6.00	-3.14
GO:0044597	GO Biological Processes	daunorubicin metabolic process	3	3.61	-5.78	-2.95
WP2840	WikiPathways	Hair follicle development: cytodifferentiation - part 3 of 3	5	6.02	-5.32	-2.58
GO:0019730	GO Biological Processes	antimicrobial humoral response	5	6.02	-4.83	-2.16
M277	Canonical Pathways	PID INTEGRIN A4B1 PATHWAY	3	3.61	-3.99	-1.45
WP2877	WikiPathways	Vitamin D receptor pathway	5	6.02	-3.78	-1.30
WP560	WikiPathways	TGF-beta receptor signaling	3	3.61	-3.26	-0.83
GO:2001259	GO Biological	positive regulation of cation channel	3	3.61	-2.90	-0.54

	Processes	activity				
GO:0045216	GO Biological Processes	cell-cell junction organization	4	4.82	-2.87	-0.52
GO:0001895	GO Biological Processes	retina homeostasis	3	3.61	-2.85	-0.50
GO:0030155	GO Biological Processes	regulation of cell adhesion	7	8.43	-2.23	-0.02
GO:0090596	GO Biological Processes	sensory organ morphogenesis	4	4.82	-2.23	-0.02

Table S2. Summary of enrichment analysis in COVID

GO	Description	Count	%	Log10(P)	Log10(q)
<u>COVID20</u> <u>2</u>	RNA_Vanderheiden_pHAE_48h_Down	6	7.20	-4.90	-1.90
<u>COVID00</u> <u>3</u>	RNA_Appelberg_Huh-7_48h_Down	3	3.60	-4.50	-1.70
<u>COVID02</u> <u>8</u>	RNA_Lamers_intestinal-organoid_expansion_Up	5	6.00	-4.00	-1.30
<u>COVID13</u> <u>5</u>	Proteome_Stukalov_A549-ACE2_24h_Up	4	4.80	-3.30	-0.84
<u>COVID03</u> <u>9</u>	RNA_Sun_Calu-3_24h_Down	5	6.00	-2.80	-0.54
<u>COVID04</u> <u>3</u>	RNA_Wyler_Caco-2_12h_Down	3	3.60	-2.30	-0.18
<u>COVID20</u> <u>3</u>	RNA_Vanderheiden_pHAE_48h_Up	3	3.60	-2.00	-0.01
<u>COVID00</u> <u>6</u>	RNA_Appelberg_Huh-7_72h_Up	4	4.80	-2.00	0.00
<u>COVID03</u> <u>6</u>	RNA_Sun_Calu-3_0h_Up	4	4.80	-2.00	0.00
<u>COVID19</u> <u>9</u>	Ubiquitinome_Stukalov_A549-ACE2_24h_Up	4	4.80	-2.00	0.00

Table S3. Summary of enrichment analysis in Cell Type Signatures

GO	Description	Count	%	Log10(P)	Log10(q)
<u>M40176</u>	DESCARTES FETAL EYE SKELETAL MUSCLE CELLS	12	14.00	-13.00	-9.40
<u>M40254</u>	DESCARTES FETAL MUSCLE SKELETAL MUSCLE CELLS	13	16.00	-13.00	-8.80
<u>M40093</u>	DESCARTES MAIN FETAL SKELETAL MUSCLE CELLS	11	13.00	-11.00	-7.50
<u>M40004</u>	BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS	8	9.60	-8.30	-4.90
<u>M39317</u>	CUI DEVELOPING HEART CARDIAC FIBROBLASTS	7	8.40	-7.70	-4.40
<u>M39299</u>	CUI DEVELOPING HEART C2 CARDIOMYOCYTE	6	7.20	-6.70	-3.50
<u>M41656</u>	TRAVAGLINI LUNG MUCOUS CELL	6	7.20	-5.90	-2.80
<u>M40237</u>	DESCARTES FETAL LUNG SQUAMOUS EPITHELIAL CELLS	7	8.40	-5.80	-2.70
<u>M39125</u>	AIZARANI LIVER C24 EPCAM POS BILE DUCT CELLS 3	6	7.20	-4.90	-2.00
<u>M40122</u>	DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS	5	6.00	-4.50	-1.70
<u>M40012</u>	BUSSLINGER GASTRIC IMMATURE PIT CELLS	5	6.00	-4.00	-1.30

<u>M39283</u>	DURANTE ADULT OLFACTORY NEUROEPITHELIUM BOWMANS GLAND	3	3.60	-4.00	-1.30
<u>M40220</u>	DESCARTES FETAL KIDNEY URETERIC BUD CELLS	6	7.20	-3.70	-1.10
<u>M39278</u>	DURANTE ADULT OLFACTORY NEUROEPITHELIUM SUSTENTACULAR CELLS	3	3.60	-3.50	-0.99
<u>M39111</u>	AIZARANI LIVER C7 EPCAM POS BILE DUCT CELLS 2	5	6.00	-3.50	-0.94
<u>M40299</u>	DESCARTES FETAL STOMACH SQUAMOUS EPITHELIAL CELLS	3	3.60	-3.10	-0.67
<u>M41666</u>	TRAVAGLINI LUNG CAPILLARY INTERMEDIATE 1 CELL	4	4.80	-3.00	-0.64
<u>M40033</u>	BUSSLINGER DUODENAL TUFT CELLS	3	3.60	-2.80	-0.54
<u>M39108</u>	AIZARANI LIVER C4 EPCAM POS BILE DUCT CELLS 1	4	4.80	-2.70	-0.45
<u>M41657</u>	TRAVAGLINI LUNG SEROUS CELL	3	3.60	-2.60	-0.40

Table S4. Summary of enrichment analysis in DisGeNET

GO	Description	Count	%	Log10(P)	Log10(q)
<u>C0037274</u>	Dermatologic disorders	15	18.00	-9.90	-6.20
<u>C0007193</u>	Cardiomyopathy, Dilated	13	16.00	-8.80	-5.20
<u>C0026848</u>	Myopathy	14	17.00	-8.70	-5.20
<u>C1449563</u>	Cardiomyopathy, Familial Idiopathic	15	18.00	-8.60	-5.00
<u>C0949658</u>	Cardiomyopathy, Hypertrophic, Familial	7	8.40	-8.50	-5.00
<u>C0011615</u>	Dermatitis, Atopic	14	17.00	-7.80	-4.40
<u>C4551675</u>	Keratoderma, Palmoplantar	8	9.60	-7.70	-4.40
<u>C0521158</u>	Recurrent tumor	13	16.00	-7.00	-3.70
<u>C0149721</u>	Left Ventricular Hypertrophy	10	12.00	-6.80	-3.50
<u>C0206157</u>	Myopathies, Nemaline	5	6.00	-6.70	-3.50
<u>C4551472</u>	Hypertrophic obstructive cardiomyopathy	8	9.60	-6.60	-3.40
<u>C0007194</u>	Hypertrophic Cardiomyopathy	11	13.00	-6.40	-3.30
<u>C0009917</u>	Contracture	6	7.20	-6.20	-3.10
<u>C0597124</u>	Obstructive asymmetric septal hypertrophy	3	3.60	-6.20	-3.10
<u>C0700053</u>	Idiopathic hypertrophic subaortic stenosis	3	3.60	-6.20	-3.10
<u>C1533847</u>	Disorder of skeletal muscle	4	4.80	-5.90	-2.90
<u>C0241005</u>	Creatine phosphokinase serum increased	7	8.40	-5.50	-2.50
<u>C0221270</u>	Acanthosis	4	4.80	-5.50	-2.50

<u>C0332615</u>	Myopathic facies	4	4.80	-5.20	-2.20
<u>C1837262</u>	Increased muscle lipid content	3	3.60	-5.10	-2.20

Table S5. Summary of enrichment analysis in PaGenBase

GO	Description	Count	%	Log10(P)	Log10(q)
PGB:00017	Tissue-specific: skin	17	20.00	-20.00	-15.00
PGB:00044	Tissue-specific: skeletal muscle	16	19.00	-14.00	-9.90
PGB:00005	Tissue-specific: tonsil	7	8.40	-9.50	-5.80
PGB:00156	Tissue-specific: Tongue	5	6.00	-7.40	-4.10
PGB:00071	Cell-specific: Vaginal Epithelial	4	4.80	-6.00	-2.90
PGB:00047	Cell-specific: THY+	5	6.00	-4.80	-1.90
PGB:00062	Cell-specific: Skeletal Muscle Stromal Cells	3	3.60	-4.30	-1.50
PGB:00053	Cell-specific: NHEK	7	8.40	-4.10	-1.40
PGB:00119	Cell-specific: Renal Epithelial	3	3.60	-3.50	-0.97
PGB:00120	Cell-specific: Cardiac Myocytes	3	3.60	-3.20	-0.76
PGB:00010	Tissue-specific: adipose tissue	4	4.80	-2.90	-0.55
PGB:00037	Tissue-specific: heart	5	6.00	-2.70	-0.45
PGB:00007	Tissue-specific: colon	5	6.00	-2.60	-0.38
PGB:00018	Tissue-specific: lung	6	7.20	-2.60	-0.37

Table S6. Summary of enrichment analysis in Transcription Factor Targets.

GO	Description	Count	%	Log10(P)	Log10(q)
<u>M16022</u>	CTAWWWATA RSRFC4 Q2	10	12.00	-7.20	-3.90
<u>M574</u>	RSRFC4 01	6	7.20	-4.20	-1.40
<u>M15966</u>	TTTNNANAGCYR UNKNOWN	4	4.80	-3.30	-0.82
<u>M11820</u>	TTGCWCAAY CEBPB 02	3	3.60	-3.20	-0.71
<u>M3150</u>	TATA 01	5	6.00	-3.10	-0.71
<u>M15183</u>	E12 Q6	5	6.00	-3.10	-0.67
<u>M572</u>	TGCCAAR NF1 Q6	7	8.40	-2.40	-0.22
<u>M11407</u>	MEF2 02	4	4.80	-2.40	-0.21
<u>M17420</u>	WGGAATGY TEF1 Q6	5	6.00	-2.40	-0.20
<u>M15929</u>	MEF2 Q6 01	4	4.80	-2.30	-0.16
<u>M11442</u>	HNF1 Q6	4	4.80	-2.30	-0.14
<u>M2814</u>	SREBP Q3	4	4.80	-2.20	-0.13
<u>M946</u>	GGATTA PITX2 Q2	6	7.20	-2.20	-0.12
<u>M13332</u>	HNF4 DR1 Q3	4	4.80	-2.20	-0.11
<u>M4803</u>	NF1 Q6	4	4.80	-2.20	-0.09
<u>M16178</u>	HOXA4 Q2	4	4.80	-2.20	-0.09
<u>M2501</u>	MEF2 01	3	3.60	-2.10	-0.04
<u>M14649</u>	FREAC4 01	3	3.60	-2.10	-0.02