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 Processes | positive regulation of cation channel      | 3     | 3.61   | -2.90    | -0.54     |
| 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) |
|----------|-----------------------------------------------------------------------------|-------|-----|----------|----------|
| COVID20  | RNA_Vanderheiden_pHAE_48h_Down                                              | 6     | 7.2 | -4.90    | -1.90    |
| 2        |                                                                            |       | 0   |          |          |
| COVID00  | RNA_Appelberg_Huh-7_48h_Down                                               | 3     | 3.6 | -4.50    | -1.70    |
| 3        |                                                                            |       | 0   |          |          |
| COVID02  | RNA_Lamers_intestinal-organoid_expansion_Up                                 | 5     | 6.0 | -4.00    | -1.30    |
| 8        |                                                                            |       | 0   |          |          |
| COVID13  | Proteome_Stukalov_A549-ACE2_24h_Up                                          | 4     | 4.8 | -3.30    | -0.84    |
| 5        |                                                                            |       | 0   |          |          |
| COVID03  | RNA_Sun_Calu-3_24h_Down                                                    | 5     | 6.0 | -2.80    | -0.54    |
| 9        |                                                                            |       | 0   |          |          |
| COVID04  | RNA_Wyler_Caco-2_12h_Down                                                  | 3     | 3.6 | -2.30    | -0.18    |
| 3        |                                                                            |       | 0   |          |          |
| COVID20  | RNA_Vanderheiden_pHAE_48h_Up                                                | 3     | 3.6 | -2.00    | -0.01    |
| 2        |                                                                            |       | 0   |          |          |
| COVID00  | RNA_Appelberg_Huh-7_72h_Up                                                  | 4     | 4.8 | -2.00    | 0.00     |
| 6        |                                                                            |       | 0   |          |          |
| COVID03  | RNA_Sun_Calu-3_0h_Up                                                       | 4     | 4.8 | -2.00    | 0.00     |
| 6        |                                                                            |       | 0   |          |          |
| COVID19  | Ubiquitinome_Stukalov_A549-ACE2_24h_Up                                      | 4     | 4.8 | -2.00    | 0.00     |
| 9        |                                                                            |       | 0   |          |          |
Table S3. Summary of enrichment analysis in Cell Type Signatures

| GO   | Description                                                      | Count | %   | Log10(P) | Log10(q) |
|------|------------------------------------------------------------------|-------|-----|----------|----------|
| M40176 | DESCARTES FETAL EYE SKELETAL MUSCLE CELLS                         | 12    | 14.00 | -13.00   | -9.40    |
| M40254 | DESCARTES FETAL MUSCLE SKELETAL MUSCLE CELLS                      | 13    | 16.00 | -13.00   | -8.80    |
| M40093 | DESCARTES MAIN FETAL SKELETAL MUSCLE CELLS                       | 11    | 13.00 | -11.00   | -7.50    |
| M40004 | BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS                       | 8     | 9.60  | -8.30    | -4.90    |
| M39317 | CUI DEVELOPING HEART CARDIAC FIBROBLASTS                          | 7     | 8.40  | -7.70    | -4.40    |
| M39299 | CUI DEVELOPING HEART C2 CARDIOMYOCYTE                             | 6     | 7.20  | -6.70    | -3.50    |
| M41656 | TRAVAGLINI LUNG MUCOUS CELL                                       | 6     | 7.20  | -5.90    | -2.80    |
| M40237 | DESCARTES FETAL LUNG SQUAMOUS EPITHELIAL CELLS                    | 7     | 8.40  | -5.80    | -2.70    |
| M39125 | AIZARANI LIVER C24 EPCAM POS BILE DUCT CELLS 3                    | 6     | 7.20  | -4.90    | -2.00    |
| M40122 | DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS                    | 5     | 6.00  | -4.50    | -1.70    |
| M40012 | BUSSLINGER GASTRIC IMMATURE PIT CELLS                             | 5     | 6.00  | -4.00    | -1.30    |
| Code   | Description                                                                 | Type | Value1 | Value2 | Value3 |
|--------|-----------------------------------------------------------------------------|------|--------|--------|--------|
| M39283 | DURANTE ADULT OLFACTORY NEUROEPITHELIIUM BOWMANS GLAND                      | 3    | 3.60   | -4.00  | -1.30  |
| M40220 | DESCARTES FETAL KIDNEY URETERIC BUD CELLS                                   | 6    | 7.20   | -3.70  | -1.10  |
| M39278 | DURANTE ADULT OLFACTORY NEUROEPITHELIIUM SUSTENTACULAR CELLS               | 3    | 3.60   | -3.50  | -0.99  |
| M39111 | AIZARANI LIVER C7 EPCAM POS BILE DUCT CELLS 2                               | 5    | 6.00   | -3.50  | -0.94  |
| M40299 | DESCARTES FETAL STOMACH SQUAMOUS EPITHELIAL CELLS                           | 3    | 3.60   | -3.10  | -0.67  |
| M41666 | TRAVAGLINI LUNG CAPILLARY INTERMEDIATE 1 CELL                              | 4    | 4.80   | -3.00  | -0.64  |
| M40033 | BUSSLINGER DUODENAL TUFT CELLS                                              | 3    | 3.60   | -2.80  | -0.54  |
| M39108 | AIZARANI LIVER C4 EPCAM POS BILE DUCT CELLS 1                               | 4    | 4.80   | -2.70  | -0.45  |
| M41657 | 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) |
|--------|---------------------------------------------------------|-------|------|----------|----------|
| C0037274 | Dermatologic disorders                                  | 15    | 18.00| -9.90    | -6.20    |
| C0007193 | Cardiomyopathy, Dilated                                 | 13    | 16.00| -8.80    | -5.20    |
| C0026848 | Myopathy                                                | 14    | 17.00| -8.70    | -5.20    |
| C1449563 | Cardiomyopathy, Familial Idiopathic                     | 15    | 18.00| -8.60    | -5.00    |
| C0949658 | Cardiomyopathy, Hypertrophic, Familial                  | 7     | 8.40 | -8.50    | -5.00    |
| C0011615 | Dermatitis, Atopic                                      | 14    | 17.00| -7.80    | -4.40    |
| C4551675 | Keratoderma, Palmoplantar                               | 8     | 9.60 | -7.70    | -4.40    |
| C0521158 | Recurrent tumor                                         | 13    | 16.00| -7.00    | -3.70    |
| C0149721 | Left Ventricular Hypertrophy                            | 10    | 12.00| -6.80    | -3.50    |
| C0206157 | Myopathies, Nemaline                                    | 5     | 6.00 | -6.70    | -3.50    |
| C4551472 | Hypertrophic obstructive cardiomyopathy                 | 8     | 9.60 | -6.60    | -3.40    |
| C0007194 | Hypertrophic Cardiomyopathy                             | 11    | 13.00| -6.40    | -3.30    |
| C0009917 | Contracture                                             | 6     | 7.20 | -6.20    | -3.10    |
| C0597124 | Obstructive asymmetric septal hypertrophy               | 3     | 3.60 | -6.20    | -3.10    |
| C0700053 | Idiopathic hypertrophic subaortic stenosis              | 3     | 3.60 | -6.20    | -3.10    |
| C1533847 | Disorder of skeletal muscle                             | 4     | 4.80 | -5.90    | -2.90    |
| C0241005 | Creatine phosphokinase serum increased                  | 7     | 8.40 | -5.50    | -2.50    |
| C0221270 | Acanthosis                                              | 4     | 4.80 | -5.50    | -2.50    |
|        | Description                           | Value | Change 1 | Change 2 |
|--------|---------------------------------------|-------|----------|----------|
| C0332615 | Myopathic facies                      | 4     | 4.80     | -5.20    | -2.20    |
| C1837262 | Increased muscle lipid content        | 3     | 3.60     | -5.10    | -2.20    |
| 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) |
|------|--------------------------------------|-------|-----|----------|----------|
| M16022 | CTAWWWATA RSRFC4 Q2                | 10    | 12.00 | -7.20    | -3.90    |
| M574 | RSRFC4 01                           | 6     | 7.20  | -4.20    | -1.40    |
| M15966 | TTTNNANAGCYR UNKNOWN            | 4     | 4.80  | -3.30    | -0.82    |
| M11820 | TTGCWCAAY CEBPB 02            | 3     | 3.60  | -3.20    | -0.71    |
| M3150 | TATA 01                             | 5     | 6.00  | -3.10    | -0.71    |
| M15183 | E12 Q6                              | 5     | 6.00  | -3.10    | -0.67    |
| M572 | TGCCAAR NF1 Q6                     | 7     | 8.40  | -2.40    | -0.22    |
| M11407 | MEF2 02                             | 4     | 4.80  | -2.40    | -0.21    |
| M17420 | WGGAATGY TEF1 Q6                 | 5     | 6.00  | -2.40    | -0.20    |
| M15929 | MEF2 06 Q2                        | 4     | 4.80  | -2.30    | -0.16    |
| M11442 | HNF1 Q6                            | 4     | 4.80  | -2.30    | -0.14    |
| M2814 | SREBP Q3                           | 4     | 4.80  | -2.20    | -0.13    |
| M946  | GGATTA PITX2 Q2                    | 6     | 7.20  | -2.20    | -0.12    |
| M13332 | HNF4 DR1 Q3                      | 4     | 4.80  | -2.20    | -0.11    |
| M4803 | NF1 Q6                             | 4     | 4.80  | -2.20    | -0.09    |
| M16178 | HOXA4 Q2                          | 4     | 4.80  | -2.20    | -0.09    |
| M2501 | MEF2 01                            | 3     | 3.60  | -2.10    | -0.04    |
| M14649 | FREAC4 01                         | 3     | 3.60  | -2.10    | -0.02    |