

Results

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1: GO: Molecular Function [\[Display Chart\]](#) 1835 input genes in category / 2191 annotations before applied cutoff / 19912 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0019904	protein domain specific binding		1.906E-10	2.925E-7	2.419E-6	4.176E-7	140	893
2	GO:0008092	cytoskeletal protein binding		2.677E-10	2.925E-7	2.419E-6	5.866E-7	168	1135
3	GO:0005102	signaling receptor binding		4.561E-10	2.925E-7	2.419E-6	9.993E-7	237	1756
4	GO:0030695	GTPase regulator activity		5.340E-10	2.925E-7	2.419E-6	1.170E-6	91	510
5	GO:0060589	nucleoside-triphosphatase regulator activity		8.069E-10	3.536E-7	2.924E-6	1.768E-6	91	514

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2: GO: Biological Process [\[Display Chart\]](#) 1840 input genes in category / 9613 annotations before applied cutoff / 20649 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0007155	cell adhesion		3.242E-19	3.117E-15	3.038E-14	3.117E-15	264	1735
2	GO:0048666	neuron development		3.523E-17	1.693E-13	1.651E-12	3.386E-13	252	1691
3	GO:0000902	cell morphogenesis		3.672E-16	1.177E-12	1.147E-11	3.530E-12	210	1356
4	GO:0009887	animal organ morphogenesis		1.035E-15	2.155E-12	2.101E-11	9.951E-12	250	1720
5	GO:0044057	regulation of system process		1.121E-15	2.155E-12	2.101E-11	1.077E-11	143	813

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3: GO: Cellular Component [\[Display Chart\]](#) 1856 input genes in category / 1098 annotations before applied cutoff / 20915 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0070161	anchoring junction		5.148E-17	5.653E-14	4.284E-13	5.653E-14	168	987
2	GO:0098590	plasma membrane region		3.357E-15	1.426E-12	1.080E-11	3.686E-12	230	1565
3	GO:0043025	neuronal cell body		4.193E-15	1.426E-12	1.080E-11	4.604E-12	145	845
4	GO:0005911	cell-cell junction		5.193E-15	1.426E-12	1.080E-11	5.702E-12	113	596
5	GO:0044297	cell body		1.517E-14	3.330E-12	2.524E-11	1.665E-11	155	940

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4: Human Phenotype [\[Display Chart\]](#) 645 input genes in category / 7292 annotations before applied cutoff / 5088 genes in category

No results to display

5: Mouse Phenotype [\[Display Chart\]](#) 1552 input genes in category / 7518 annotations before applied cutoff / 13846 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	MP:0001533	abnormal skeleton physiology		3.427E-6	2.577E-2	2.448E-1	2.577E-2	108	630
2	MP:0002113	abnormal skeleton development		1.231E-5	4.628E-2	4.397E-1	9.255E-2	80	446

6: Domain [\[Display Chart\]](#) 1804 input genes in category / 5984 annotations before applied cutoff / 18677 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	2.30.29.30	-	Gene3D	9.305E-10	1.114E-6	1.033E-5	5.568E-6	77	391
2	2.30.42.10	-	Gene3D	6.133E-9	4.588E-6	4.255E-5	3.670E-5	39	150
3	2.60.40.10	-	Gene3D	3.438E-5	4.115E-3	3.816E-2	2.057E-1	96	663
4	3.30.505.10	-	Gene3D	1.466E-4	1.393E-2	1.291E-1	8.773E-1	24	112
5	2.120.10.30	-	Gene3D	2.078E-4	1.829E-2	1.696E-1	1.000E0	12	39

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	IPR001452	SH3 domain	InterPro	2.642E-10	1.114E-6	1.033E-5	1.581E-6	53	220
2	IPR011993	PH dom-like	InterPro	8.329E-10	1.114E-6	1.033E-5	4.984E-6	82	426

3	IPR001478	PDZ	InterPro	9.171E-9	4.989E-6	4.627E-5	5.488E-5	39	152
4	IPR013098	Ig I-set	InterPro	8.750E-8	3.740E-5	3.469E-4	5.236E-4	43	190
5	IPR017441	Protein kinase ATP BS	InterPro	1.740E-7	6.198E-5	5.748E-4	1.041E-3	69	379

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PS50002	SH3	PROSITE	3.994E-10	1.114E-6	1.033E-5	2.390E-6	52	216
2	PS50106	PDZ	PROSITE	7.508E-9	4.989E-6	4.627E-5	4.493E-5	39	151
3	PS00022	EGF 1	PROSITE	9.002E-9	4.989E-6	4.627E-5	5.387E-5	55	255
4	PS01186	EGF 2	PROSITE	3.664E-8	1.827E-5	1.694E-4	2.193E-4	55	265
5	PS50026	EGF 3	PROSITE	1.726E-7	6.198E-5	5.748E-4	1.033E-3	49	235

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PF00595	PDZ	Pfam	8.906E-10	1.114E-6	1.033E-5	5.330E-6	39	141
2	PF07679	I-set	Pfam	8.750E-8	3.740E-5	3.469E-4	5.236E-4	43	190
3	PF00018	SH3 1	Pfam	2.555E-7	8.494E-5	7.878E-4	1.529E-3	38	164
4	PF07974	EGF 2	Pfam	4.243E-7	1.188E-4	1.102E-3	2.539E-3	20	60
5	PF00169	PH	Pfam	1.231E-6	2.946E-4	2.732E-3	7.365E-3	46	229

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	SM00326	SH3	SMART	3.600E-9	3.474E-6	3.222E-5	2.154E-5	50	216
2	SM00228	PDZ	SMART	4.064E-9	3.474E-6	3.222E-5	2.432E-5	39	148
3	SM00181	EGF	SMART	4.369E-7	1.188E-4	1.102E-3	2.614E-3	48	235
4	SM00233	PH	SMART	2.454E-6	5.439E-4	5.045E-3	1.469E-2	52	278
5	SM00179	EGF CA	SMART	3.775E-6	7.059E-4	6.547E-3	2.259E-2	29	122

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7: Pathway [\[Display Chart\]](#) 1363 input genes in category / 4662 annotations before applied cutoff / 13850 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M7253	KEGG FOCAL ADHESION	KEGG Legacy Pathways	8.743E-6	8.152E-3	7.357E-2	4.076E-2	40	199
2	M5539	KEGG AXON GUIDANCE	KEGG Legacy Pathways	1.675E-5	8.183E-3	7.384E-2	7.809E-2	29	129
3	M1979	KEGG GNRH SIGNALING PATHWAY	KEGG Legacy Pathways	3.366E-5	9.809E-3	8.852E-2	1.569E-1	24	101
4	M2164	KEGG LEUKOCYTE TRANSENDOTHELIAL MIGRATION	KEGG Legacy Pathways	1.291E-4	2.050E-2	1.850E-1	6.018E-1	25	116
5	M10792	KEGG MAPK SIGNALING PATHWAY	KEGG Legacy Pathways	2.267E-4	3.020E-2	2.726E-1	1.000E0	45	267

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M47510	KEGG MEDICUS VARIANT MUTATION INACTIVATED ATP1A1 TO ANGIOTENSIN ALDOSTERONE SIGNALING PATHWAY	KEGG Medicus Pathways	6.747E-5	1.430E-2	1.290E-1	3.145E-1	10	25
2	M47508	KEGG MEDICUS VARIANT MUTATION ACTIVATED CACNA1D H TO ANGIOTENSIN ALDOSTERONE SIGNALING PATHWAY	KEGG Medicus Pathways	2.802E-4	3.530E-2	3.186E-1	1.000E0	9	24
3	M47509	KEGG MEDICUS VARIANT MUTATION ACTIVATED KCNJ5 TO ANGIOTENSIN ALDOSTERONE SIGNALING PATHWAY	KEGG Medicus Pathways	3.998E-4	4.236E-2	3.823E-1	1.000E0	9	25

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M68	PID RHOA REG PATHWAY	PID Pathways	3.511E-4	3.992E-2	3.603E-1	1.000E0	13	46

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M5485	REACTOME MUSCLE CONTRACTION	Reactome Pathways	2.431E-6	8.152E-3	7.357E-2	1.133E-2	42	203
2	M27870	REACTOME SIGNALING BY RECEPTOR TYROSINE KINASES	Reactome Pathways	7.657E-6	8.152E-3	7.357E-2	3.570E-2	83	524
3	M27078	REACTOME RHO GTPASE CYCLE	Reactome Pathways	1.176E-5	8.183E-3	7.384E-2	5.484E-2	73	450

4	M41808	REACTOME CDC42 GTPASE CYCLE	Reactome Pathways	1.524E-5	8.183E-3	7.384E-2	7.106E-2	33	155
5	M610	REACTOME EXTRACELLULAR MATRIX ORGANIZATION	Reactome Pathways	1.755E-5	8.183E-3	7.384E-2	8.183E-2	53	300

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M39329	WP CALCIUM REGULATION IN CARDIAC CELLS	WikiPathways	8.543E-6	8.152E-3	7.357E-2	3.983E-2	33	151
2	M39402	WP FOCAL ADHESION	WikiPathways	8.743E-6	8.152E-3	7.357E-2	4.076E-2	40	199
3	MM15854	WP CALCIUM REGULATION IN CARDIAC CELLS	WikiPathways	1.267E-5	8.183E-3	7.384E-2	5.907E-2	32	147
4	MM15913	WP FOCAL ADHESION	WikiPathways	2.698E-5	9.677E-3	8.733E-2	1.258E-1	37	187
5	M39681	WP CARDIAC PROGENITOR DIFFERENTIATION	WikiPathways	3.096E-5	9.769E-3	8.816E-2	1.443E-1	16	53

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8: Pubmed [\[Display Chart\]](#) 1871 input genes in category / 221736 annotations before applied cutoff / 34794 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	24952961	A high-resolution spatiotemporal atlas of gene expression of the developing mouse brain.	Pubmed	7.486E-46	1.660E-40	2.139E-39	1.660E-40	264	1937
2	28611215	Genome-wide CRISPR screen identifies HNRNPL as a prostate cancer dependency regulating RNA splicing.	Pubmed	1.666E-41	1.847E-36	2.381E-35	3.695E-36	216	1489
3	35914814	Chr21 protein-protein interactions: enrichment in proteins involved in intellectual disability, autism, and late-onset Alzheimer's disease.	Pubmed	4.360E-32	3.222E-27	4.152E-26	9.667E-27	179	1285
4	36931259	A central chaperone-like role for 14-3-3 proteins in human cells.	Pubmed	7.418E-29	4.112E-24	5.299E-23	1.645E-23	134	861
5	15840001	Characterization of an exchangeable gene trap using pU-17 carrying a stop codon-beta geo cassette.	Pubmed	2.319E-27	1.029E-22	1.325E-21	5.143E-22	99	536

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9: Interaction [\[Display Chart\]](#) 1830 input genes in category / 16356 annotations before applied cutoff / 20081 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	int:YWHAQ	YWHAQ interactions		6.671E-15	1.091E-10	1.122E-9	1.091E-10	178	1095
2	int:YWHAH	YWHAH interactions		1.324E-13	1.082E-9	1.113E-8	2.165E-9	174	1097
3	int:YWHAB	YWHAB interactions		3.226E-12	1.759E-8	1.808E-7	5.277E-8	157	994
4	int:YWHAZ	YWHAZ interactions		1.112E-11	4.545E-8	4.672E-7	1.818E-7	188	1275
5	int:YWHAG	YWHAG interactions		3.169E-11	1.037E-7	1.066E-6	5.183E-7	182	1238

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10: Cytoband [\[Display Chart\]](#) 1873 input genes in category / 1078 annotations before applied cutoff / 45858 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1p36.13	1p36.13		2.186E-6	1.178E-3	8.907E-3	2.356E-3	12	56
2	17q22	17q22		8.771E-6	2.364E-3	1.787E-2	9.455E-3	10	44
3	12p13.3	12p13.3		1.995E-5	4.302E-3	3.253E-2	2.151E-2	8	30
4	12q24	12q24		4.710E-5	8.463E-3	6.398E-2	5.078E-2	7	25
5	5q33.1	5q33.1		6.219E-5	9.577E-3	7.240E-2	6.704E-2	7	26

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	chr1p36	Ensembl 110 genes in cytogenetic band chr1p36	MSigDB C1	8.094E-7	8.726E-4	6.597E-3	8.726E-4	56	683
2	chr17q25	Ensembl 110 genes in cytogenetic band chr17q25	MSigDB C1	4.032E-6	1.449E-3	1.095E-2	4.346E-3	31	307
3	chr20q11	Ensembl 110 genes in cytogenetic band chr20q11	MSigDB C1	7.148E-5	9.632E-3	7.282E-2	7.706E-2	24	244
4	chr20q13	Ensembl 110 genes in cytogenetic band chr20q13	MSigDB C1	9.642E-5	1.083E-2	8.188E-2	1.039E-1	34	412
5	chr6p21	Ensembl 110 genes in cytogenetic band chr6p21	MSigDB C1	5.540E-4	3.981E-2	3.010E-1	5.972E-1	36	489

Show 3 more annotations

11: Transcription Factor Binding Site [\[Display Chart\]](#) 1803 input genes in category / 1087 annotations before applied cutoff / 26909 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M40710	HMGB1 TARGET GENES	MSigDB	2.559E-20	2.782E-18	2.105E-17	2.782E-17	200	1535

2	M30400	ZNF92 TARGET GENES	MSigDB	2.775E-16	2.011E-14	1.522E-13	3.016E-13	180	1448
3	M40811	ZSCAN4 TARGET GENES	MSigDB	4.463E-16	3.032E-14	2.295E-13	4.851E-13	140	1026
4	M30087	NFKBIA TARGET GENES	MSigDB	9.653E-14	5.246E-12	3.971E-11	1.049E-10	161	1327
5	M30386	ZNF768 TARGET GENES	MSigDB	2.612E-13	1.352E-11	1.023E-10	2.839E-10	162	1354

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	CAGGTG V\$E12 Q6	CAGGTG V\$E12 Q6	TFBS	6.366E-38	6.920E-35	5.237E-34	6.920E-35	285	1950
2	AACTTT UNKNOWN	AACTTT UNKNOWN	TFBS	1.331E-37	7.234E-35	5.476E-34	1.447E-34	242	1529
3	GGGAGGRR V\$MAZ Q6	GGGAGGRR V\$MAZ Q6	TFBS	9.027E-32	3.271E-29	2.476E-28	9.812E-29	259	1836
4	CAGCTG V\$AP4 Q5	CAGCTG V\$AP4 Q5	TFBS	9.532E-30	2.590E-27	1.961E-26	1.036E-26	189	1184
5	CTTTGT V\$LEF1 Q2	CTTTGT V\$LEF1 Q2	TFBS	3.722E-29	8.092E-27	6.124E-26	4.046E-26	224	1543

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12: Gene Family [\[Display Chart\]](#) 1235 input genes in category / 481 annotations before applied cutoff / 18080 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1220 Ankyrin repeat domain containing Sterile alpha motif domain containing PDZ domain containing	genenames.org	3.008E-13	1.121E-10	7.571E-10	1.447E-10	39	152
2	593 Fibronectin type III domain containing I-set domain containing Protein tyrosine phosphatases, receptor type	genenames.org	4.661E-13	1.121E-10	7.571E-10	2.242E-10	40	161
3	682 Pleckstrin homology domain containing	genenames.org	4.382E-10	7.027E-8	4.746E-7	2.108E-7	41	206
4	594 I-set domain containing Immunoglobulin like domain containing	genenames.org	2.978E-7	3.553E-5	2.400E-4	1.432E-4	34	193
5	555 Fibronectin type III domain containing	genenames.org	3.693E-7	3.553E-5	2.400E-4	1.777E-4	30	160

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13: Coexpression [\[Display Chart\]](#) 1864 input genes in category / 10491 annotations before applied cutoff / 26205 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M45001 LIU OVARIAN CANCER TUMORS AND XENOGRAPHS XDGS DN	C2:CGP: Chemical and Genetic Perturbations	8.357E-31	2.922E-27	2.874E-26	8.767E-27	255	1716
2	M1941 MEISSNER BRAIN HCP WITH H3K4ME3 AND H3K27ME3	C2:CGP: Chemical and Genetic Perturbations	1.295E-30	3.396E-27	3.340E-26	1.358E-26	186	1074
3	M4391 PEREZ TP53 TARGETS	C2:CGP: Chemical and Genetic Perturbations	4.720E-27	8.253E-24	8.117E-23	4.952E-23	192	1201
4	M157 GRYDER PAX3FOXO1 ENHANCERS IN TADS	C2:CGP: Chemical and Genetic Perturbations	6.033E-24	7.912E-21	7.782E-20	6.330E-20	164	1009
5	M2369 GOBERT OLIGODENDROCYTE DIFFERENTIATION DN	C2:CGP: Chemical and Genetic Perturbations	1.581E-22	1.382E-19	1.360E-18	1.659E-18	169	1087

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M2882 KRAS.600 UP.V1 UP	C6: Oncogenic Signature	3.657E-9	1.884E-7	1.853E-6	3.836E-5	49	279
2	M2681 ATF2 S UP.V1 DN	C6: Oncogenic Signature	1.160E-8	5.072E-7	4.988E-6	1.217E-4	37	187
3	M2820 IL2 UP.V1 DN	C6: Oncogenic Signature	2.785E-8	1.124E-6	1.105E-5	2.922E-4	37	193
4	M2670 MTOR UP.V1 DN	C6: Oncogenic Signature	1.915E-7	6.144E-6	6.043E-5	2.009E-3	34	182
5	M2886 KRAS.600.LUNG.BREAST UP.V1 UP	C6: Oncogenic Signature	2.315E-7	6.960E-6	6.845E-5	2.429E-3	45	280

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M9285 GSE39110 UNTREATED VS IL2 TREATED CD8 TCELL DAY6 POST IMMUNIZATION DN	C7:IMMUNESIGDB: ImmuneSigDB	3.348E-12	3.860E-10	3.796E-9	3.512E-8	45	200
2	M6690 GSE3920 IFNA VS IFNG TREATED FIBROBLAST UP	C7:IMMUNESIGDB: ImmuneSigDB	3.136E-11	2.861E-9	2.814E-8	3.290E-7	40	175
3	M7490 GSE21774 CD62L POS CD56 BRIGHT VS CD62L NEG CD56 DIM NK CELL UP	C7:IMMUNESIGDB: ImmuneSigDB	1.780E-10	1.297E-8	1.275E-7	1.867E-6	42	200
4	M7526 GSE21546 SAP1A KO VS SAP1A KO AND ELK1 KO ANTI CD3 STIM DP THYMOCYTES DN	C7:IMMUNESIGDB: ImmuneSigDB	1.780E-10	1.297E-8	1.275E-7	1.867E-6	42	200
5	M7839 GSE24210 RESTING TREG VS TCONV UP	C7:IMMUNESIGDB: ImmuneSigDB	1.780E-10	1.297E-8	1.275E-7	1.867E-6	42	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M41018	NAKAYA PLASMACYTOID DENDRITIC CELL FLUMIST AGE 18 50YO 7DY DN	C7:VAX: HIPC Vaccine Response	2.341E-15	5.581E-13	5.489E-12	2.456E-11	132	909
2	M41099	HARALAMBIEVA PBMC FLUARIX AGE 50 74YO CORR WITH 28D MEM B CELL RESPONSE AT 28DY POSITIVE	C7:VAX: HIPC Vaccine Response	2.083E-14	4.277E-12	4.207E-11	2.186E-10	163	1250
3	M41202	HARALAMBIEVA PBMC M M R II AGE 11 22YO VACCINATED VS UNVACCINATED 7YR DN	C7:VAX: HIPC Vaccine Response	2.753E-13	4.376E-11	4.304E-10	2.888E-9	109	740
4	M41080	HARALAMBIEVA PBMC M M R II AGE 11 22YO VACCINATED VS UNVACCINATED 7YR UP	C7:VAX: HIPC Vaccine Response	1.914E-12	2.383E-10	2.343E-9	2.008E-8	130	973
5	M40868	ZAK PBMC MRKAD5 HIV 1 GAG POL NEF AGE 20 50YO 1DY UP	C7:VAX: HIPC Vaccine Response	3.786E-8	1.471E-6	1.447E-5	3.972E-4	119	1012

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M39071	MANNO MIDBRAIN NEUROTYPES HGABA	C8: Cell Type Signature	3.263E-32	1.712E-28	1.683E-27	3.423E-28	193	1106
2	M39224	LAKE ADULT KIDNEY C5 PROXIMAL TUBULE EPITHELIAL CELLS STRESS INFLAM	C8: Cell Type Signature	6.871E-26	1.030E-22	1.013E-21	7.208E-22	97	417
3	M39173	MURARO PANCREAS DUCTAL CELL	C8: Cell Type Signature	5.080E-23	5.921E-20	5.824E-19	5.329E-19	190	1276
4	M39222	LAKE ADULT KIDNEY C3 PROXIMAL TUBULE EPITHELIAL CELLS S1 S2	C8: Cell Type Signature	6.709E-23	7.039E-20	6.923E-19	7.039E-19	64	221
5	M39068	MANNO MIDBRAIN NEUROTYPES HDA1	C8: Cell Type Signature	8.134E-23	7.757E-20	7.630E-19	8.533E-19	113	584

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M5909	HALLMARK MYOGENESIS	H: Hallmark	1.296E-11	1.271E-9	1.250E-8	1.360E-7	44	200
2	M5930	HALLMARK EPITHELIAL MESENCHYMAL TRANSITION	H: Hallmark	4.874E-11	4.157E-9	4.089E-8	5.113E-7	43	200
3	M5915	HALLMARK APICAL JUNCTION	H: Hallmark	7.319E-8	2.577E-6	2.534E-5	7.679E-4	37	200
4	M5953	HALLMARK KRAS SIGNALING UP	H: Hallmark	2.218E-7	6.688E-6	6.578E-5	2.327E-3	36	200
5	M5942	HALLMARK UV RESPONSE DN	H: Hallmark	2.891E-7	8.472E-6	8.333E-5	3.033E-3	29	144

Show 23 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	MM1335	LIU OVARIAN CANCER TUMORS AND XENOGRAFTS XDGS DN	M2:CGP: Chemical and Genetic Perturbations	1.835E-37	1.925E-33	1.893E-32	1.925E-33	254	1556
2	MM457	LAZARO GENETIC MOUSE MODEL HIGH GRADE SMALL CELL NEUROENDOCRINE LUNG CARCINOMA DN	M2:CGP: Chemical and Genetic Perturbations	1.028E-28	2.156E-25	2.121E-24	1.078E-24	259	1809
3	MM1070	GOBERT OLIGODENDROCYTE DIFFERENTIATION DN	M2:CGP: Chemical and Genetic Perturbations	1.998E-21	1.577E-18	1.551E-17	2.096E-17	169	1113
4	MM1018	CUI TCF21 TARGETS 2 DN	M2:CGP: Chemical and Genetic Perturbations	5.617E-20	3.274E-17	3.220E-16	5.893E-16	141	883
5	MM1082	LIM MAMMARY STEM CELL UP	M2:CGP: Chemical and Genetic Perturbations	2.910E-17	1.053E-14	1.035E-13	3.053E-13	90	484

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	MM3634	DESCARTES ORGANOGENESIS ENDOTHELIAL CELLS	M8: Cell Type Signature	3.615E-17	1.223E-14	1.203E-13	3.792E-13	63	272
2	MM3641	DESCARTES ORGANOGENESIS WHITE BLOOD CELLS	M8: Cell Type Signature	9.348E-14	1.635E-11	1.608E-10	9.807E-10	97	615
3	MM3826	TABULA MURIS SENIS SUBCUTANEOUS ADIPOSE TISSUE MYELOID CELL AGEING	M8: Cell Type Signature	3.182E-8	1.264E-6	1.244E-5	3.338E-4	40	219
4	MM3689	TABULA MURIS SENIS BRAIN NON MYELOID NEURON AGEING	M8: Cell Type Signature	1.038E-6	2.468E-5	2.428E-4	1.088E-2	108	954
5	MM3637	DESCARTES ORGANOGENESIS CARDIAC MUSCLE LINEAGES	M8: Cell Type Signature	1.360E-5	1.776E-4	1.747E-3	1.426E-1	30	182

Show 29 more annotations

14: Coexpression Atlas [Display Chart] 1839 input genes in category / 4555 annotations before applied cutoff / 21234 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	BM Top 100 - spleen	Body Map	9.734E-4	4.681E-3	4.213E-2	1.000E0	14	64
2	BM Top 100 - endometrium	Body Map	1.337E-3	6.116E-3	5.505E-2	1.000E0	14	66
3	BM Top 100 - cerebellum	Body Map	1.809E-3	7.952E-3	7.158E-2	1.000E0	14	68
4	BM Top 100 - hippocampus	Body Map	2.571E-3	1.063E-2	9.573E-2	1.000E0	15	78
5	BM Top 100 - mammary gland	Body Map	4.108E-3	1.590E-2	1.431E-1	1.000E0	14	74

Show 6 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	Facebase RNAseq e10.5 Olfactory Pit 1000	FacebaseRNAseq e10.5 Olfactory Pit top-relative-expression-ranked 1000	FaceBase_RNAseq	1.012E-13	1.590E-11	1.431E-10	4.611E-10	155	984
2	Facebase RNAseq ratio e10.5 MaxillaryArch vs Mandibular 1000	FacebaseRNAseq ratio e10.5 MaxillaryArch vs Mandibular top-relative-expression-ranked 1000	FaceBase_RNAseq	7.248E-13	8.465E-11	7.619E-10	3.301E-9	151	973
3	Facebase RNAseq e8.5 Paraxial Mesoderm 1000	FacebaseRNAseq e8.5 Paraxial Mesoderm top-relative-expression-ranked 1000	FaceBase_RNAseq	1.830E-12	1.853E-10	1.668E-9	8.337E-9	149	967
4	Facebase RNAseq e9.5 Olfactory Placode 1000	FacebaseRNAseq e9.5 Olfactory Placode top-relative-expression-ranked 1000	FaceBase_RNAseq	8.742E-11	5.381E-9	4.844E-8	3.982E-7	144	973
5	Facebase RNAseq ratio e9.5 MandibularArch vs MaxillaryArch 1000	FacebaseRNAseq ratio e9.5 MandibularArch vs MaxillaryArch top-relative-expression-ranked 1000	FaceBase_RNAseq	3.922E-10	1.963E-8	1.767E-7	1.786E-6	141	967

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	Facebase ST1 e9.5 OticVesic 500	e9.5 OticVesic top-relative-expression-ranked 500	FaceBase_ST1	1.546E-8	4.575E-7	4.119E-6	7.042E-5	69	396
2	Facebase ST1 e10.5 MandibArch 500 1	e10.5 MandibArch top-relative-expression-ranked 500 1	FaceBase_ST1	2.225E-5	1.904E-4	1.714E-3	1.013E-1	37	209
3	Facebase ST1 e9.5 OticVesic 250	e9.5 OticVesic top-relative-expression-ranked 250	FaceBase_ST1	1.336E-4	8.874E-4	7.987E-3	6.087E-1	33	194
4	Facebase ST1 e10.5 Nasal Pit 500 2	e10.5 Nasal Pit top-relative-expression-ranked 500 2	FaceBase_ST1	3.048E-4	1.805E-3	1.625E-2	1.000E0	31	186
5	Facebase ST1 e9.5 MaxilArch 500 2	e9.5 MaxilArch top-relative-expression-ranked 500 2	FaceBase_ST1	2.580E-3	1.066E-2	9.591E-2	1.000E0	32	220

Show 6 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	gudmap developingKidney e15.5 Endothelial cells 1000	DevelopingKidney e15.5 Endothelial cells emap-29965 top-relative-expression-ranked 1000	Gudmap Mouse MOE430.2	3.698E-23	8.421E-20	7.580E-19	1.684E-19	152	761
2	DevelopingKidney e15.5 Endothelial cells emap-29977 1000	DevelopingKidney e15.5 Endothelial cells emap-29977 top-relative-expression-ranked 1000	Gudmap Mouse MOE430.2	1.158E-21	1.319E-18	1.187E-17	5.276E-18	149	764
3	gudmap developingKidney e15.5 Endothelial cells 500	DevelopingKidney e15.5 Endothelial cells emap-29965 top-relative-expression-ranked 500	Gudmap Mouse MOE430.2	1.125E-14	2.697E-12	2.428E-11	5.125E-11	82	384
4	gudmap kidney P0 JuxtaGlom Ren1 1000	kidney P0 JuxtaGlom Ren1 top-relative-expression-ranked 1000	Gudmap Mouse MOE430.2	1.750E-14	3.640E-12	3.277E-11	7.972E-11	148	905
5	gudmap developingKidney e13.5 podocyte cells 1000	DevelopingKidney e13.5 podocyte cells emap-27773 top-relative-expression-ranked 1000	Gudmap Mouse MOE430.2	1.758E-14	3.640E-12	3.277E-11	8.009E-11	142	855

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	gudmap dev gonad e13.5 F gudmap devVascOvary Flk 1000	dev gonad e13.5 F DevVascOvary Flk top-relative-expression-ranked 1000	Gudmap Mouse ST 1.0	6.269E-21	5.711E-18	5.141E-17	2.856E-17	156	831
2	gudmap dev gonad e12.5 M gudmap devVasTestis Flk 1000	dev gonad e12.5 M DevVasTestis Flk top-relative-expression-ranked 1000	Gudmap Mouse ST 1.0	1.084E-19	7.053E-17	6.349E-16	4.937E-16	155	847
3	gudmap dev gonad e12.5 F gudmap devVasOvary Flk 1000	dev gonad e12.5 F DevVasOvary Flk top-relative-expression-ranked 1000	Gudmap Mouse ST 1.0	2.901E-17	1.321E-14	1.189E-13	1.321E-13	145	817
4	gudmap dev gonad e13.5 F VascAssocMesenchStromOvary Sma 1000	dev gonad e13.5 F VascAssocMesenchStromOvary Sma top-relative-expression-ranked 1000	Gudmap Mouse ST 1.0	2.573E-16	8.807E-14	7.927E-13	1.172E-12	140	797

5	gudmap dev gonad e13.5 M gudmap devVasTestis Fik 1000	dev gonad e13.5 M DevVasTestis Fik top- relative-expression-ranked 1000	Gudmap Mouse ST 1.0	2.707E- 16	8.807E- 14	7.927E- 13	1.233E-12	146	846
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[Show 45 more annotations](#)

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	gudmap RNAseq e15.5 Podocytes 2500	gudmap RNAseq e15.5 Podocytes 2500	Gudmap RNAseq	2.506E-25	1.141E-21	1.027E-20	1.141E-21	292	1860
2	gudmap RNAseq e11.5 Ureteric bud 2500	gudmap RNAseq e11.5 Ureteric bud 2500	Gudmap RNAseq	4.738E-22	7.194E-19	6.475E-18	2.158E-18	262	1685
3	facebase RNAseq e14.5 palate poster proximal ERK2 WT 2500	facebase RNAseq e14.5 palate poster proximal ERK2 WT 2500	Gudmap RNAseq	9.022E-21	6.849E-18	6.165E-17	4.110E-17	258	1685
4	facebase RNAseq e14.5 palate poster nasal Tgfb2 WT 2500	facebase RNAseq e14.5 palate poster nasal Tgfb2 WT 2500	Gudmap RNAseq	2.583E-19	1.471E-16	1.324E-15	1.177E-15	248	1638
5	gudmap RNAseq e11.5 Ureteric stalks 2500	gudmap RNAseq e11.5 Ureteric stalks 2500	Gudmap RNAseq	9.444E-19	4.780E-16	4.302E-15	4.302E-15	275	1897

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	cerebral cortex	Human Protein Atlas	2.378E-13	3.385E-11	3.047E-10	1.083E-9	204	1428
2	skeletal muscle	Human Protein Atlas	1.542E-5	1.397E-4	1.258E-3	7.026E-2	51	320
3	lymph node	Human Protein Atlas	5.912E-5	4.393E-4	3.955E-3	2.693E-1	43	268
4	placenta	Human Protein Atlas	8.058E-5	5.799E-4	5.219E-3	3.670E-1	52	349
5	spleen	Human Protein Atlas	8.554E-5	6.069E-4	5.463E-3	3.896E-1	48	315

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GSM538245 500 Myeloid Cells, DC.4+ SLN, CD11b-FITC CD4-PE CD11c-Alexa750 CD8a-PacificBlue, Lymph Node, avg-3	Immgen.org, GSE15907	4.795E-15	1.213E-12	1.092E-11	2.184E-11	86	407
2	GSM538303 500 NK cells, NK.H+.MCMV7.Sp, NK1.1+ TCRb- Ly49H+, Spleen, avg-3	Immgen.org, GSE15907	2.653E-13	3.554E-11	3.199E-10	1.208E-9	83	413
3	GSM777037 500 Stromal Cells, BEC.SLN, gp38- CD31+, Lymph Node, avg-4	Immgen.org, GSE15907	8.140E-13	8.828E-11	7.947E-10	3.708E-9	88	459
4	GSM476678 500 gamma delta T cells, Tgd.vg2+.act.Sp, TCRd+ Vg2+ CD44+, Spleen, avg-3	Immgen.org, GSE15907	1.300E-12	1.346E-10	1.211E-9	5.922E-9	79	395
5	GSM777032 500 Stromal Cells, BEC.MLN, gp38- CD31+, Lymph Node, avg-5	Immgen.org, GSE15907	9.498E-12	7.866E-10	7.080E-9	4.326E-8	85	456

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PCBC ratio EB vs SC 1000	ratio EmbryoidBody vs StemCell top-relative-expression-ranked 1000	PCBC	5.798E-11	3.773E-9	3.396E-8	2.641E-7	147	994
2	PCBC EB 1000	Progenitor-Cell-Biology-Consortium EmbryoidBody top-relative-expression-ranked 1000	PCBC	5.798E-11	3.773E-9	3.396E-8	2.641E-7	147	994
3	PCBC ctl geo-heart 1000	geo heart top-relative-expression-ranked 1000	PCBC	8.295E-11	5.248E-9	4.723E-8	3.778E-7	146	990
4	geo heart 1000 K5	geo heart top-relative-expression-ranked 1000 k-means-cluster#5	PCBC	3.234E-10	1.674E-8	1.507E-7	1.473E-6	77	424
5	JC hmvEC 2500 K1	JC hmvEC top-relative-expression-ranked 2500 k-means-cluster#1	PCBC	6.583E-9	2.343E-7	2.109E-6	2.999E-5	133	936

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PCBC ratio CardioEndothel vs SC cfr-2X-p05	Cardiovascular Endothelial Cells vs Pluripotent Stem Cells-Confounder removed-fold2.0 adjp0.05	PCBC_AltAnalyze	3.084E-11	2.230E-9	2.007E-8	1.405E-7	232	1767
2	PCBC ratio EB vs SC cfr-2X-p05	Embryoid Body Cells vs Pluripotent Stem Cells-Confounder removed-fold2.0 adjp0.05	PCBC_AltAnalyze	5.328E-11	3.569E-9	3.212E-8	2.427E-7	234	1796
3	PCBC ratio MESO-30 vs SC cfr-2X-p05	Mesoderm Day 30 vs Pluripotent Stem Cells-Confounder removed-fold2.0 adjp0.05	PCBC_AltAnalyze	1.194E-10	6.974E-9	6.277E-8	5.440E-7	215	1630
4	PCBC ratio Lung Fibroblast vs SC cfr-2X-p05	Lung Fibroblast vs Pluripotent Stem Cells-Confounder removed-fold2.0 adjp0.05	PCBC_AltAnalyze	3.716E-9	1.434E-7	1.291E-6	1.692E-5	236	1899
5	PCBC ratio MESO-30 from-OSKM - NLT vs MESO-30 from-ESC cfr-2X-p05	Mesoderm Day 30-reprogram OSKM - NLT vs Mesoderm Day 30-reprogram NA-Confounder removed-fold2.0 adjp0.05	PCBC_AltAnalyze	1.365E-8	4.201E-7	3.782E-6	6.218E-5	82	501

[Show 45 more annotations](#)**15: ToppCell Atlas [Display Chart] 1874 input genes in category / 32773 annotations before applied cutoff / 44991 genes in category**

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 0bc97a9a78aaafd1554ae6a61356ed9ea4983fa5	ASK452-Endothelial ASK452 / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	4.286E-19	1.410E-17	1.548E-16	1.404E-14	43	199
2 2b777a2026b56839112fd179f2db482c49f4594a	ASK454-Endothelial-Endothelium ASK454 / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	1.529E-18	4.391E-17	4.819E-16	5.010E-14	42	196
3 e282769f5fa1765bccce79a0ed9d761bf2e14b012	ASK452-Endothelial-Endothelium ASK452 / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	1.434E-17	3.153E-16	3.460E-15	4.698E-13	41	198
4 56b746e5791b47fe33a7872f0942ae0747b13d4a	Transplant Alveoli and parenchyma-Endothelial Transplant Alveoli and parenchyma / Tissue, Lineage and Cell class of Lung Cells from 10X	A Cellular Census of Human Lungs (Vieira Braga et al)	1.434E-17	3.153E-16	3.460E-15	4.698E-13	41	198
5 4d0bf2a4bd97e5a3bfe4570a201cc21bb9c4c1f6	ASK452-Mesenchymal-Fibroblast ASK452 / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	1.734E-17	3.721E-16	4.084E-15	5.682E-13	41	199

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 1996373bdccc55aac347d349bd22f6aad6d0c668	Parenchymal-NucSeq Parenchymal / Cell types per location group and 10X technology with lineage, and cell group designations	A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche	6.209E-38	5.087E-34	5.583E-33	2.035E-33	63	198
2 ab53c742866945545a92e2e61850d63c80d9a2a6	Bronchial-NucSeq Bronchial / Cell types per location group and 10X technology with lineage, and cell group designations	A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche	3.491E-37	2.288E-33	2.511E-32	1.144E-32	62	196
3 8872d5fa101d413fb43b4231d476878678543035	Bronchial-NucSeq-Immune Myeloid-Monocytic NucSeq / Cell types per location group and 10X technology with lineage, and cell group designations	A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche	1.471E-33	3.013E-30	3.307E-29	4.822E-29	59	200
4 7ee2805fd9143eba11bf6832267b62189683608b	Parenchymal-NucSeq-Immune Myeloid NucSeq / Cell types per location group and 10X technology with lineage, and cell group designations	A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche	1.073E-32	1.674E-29	1.837E-28	3.515E-28	58	199
5 d3af0a706baf66e3f32e67b17dcfc31e5b32ce0e	Tracheal-NucSeq-Epithelial NucSeq / Cell types per location group and 10X technology with lineage, and cell group designations	A spatial multi-omics atlas of the human lung reveals a novel immune cell survival niche	1.198E-29	7.273E-27	7.982E-26	3.927E-25	55	200

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 b1bb0f846d2865efdd9bc8842b16b9d069785882	PCW 13-14-Mesenchymal-	A topographic atlas defines	1.607E-27	5.375E-25	5.899E-24	5.268E-23	52	194

		Mesenchymal fibroblastic-mes immature5 (6) PCW 13-14 / Celltypes from embryonic and fetal-stage human lung	developmental origins of cell heterogeneity in the human embryonic lung							
2	0e55fa5b3cbeb7baee3d4ac272a3bf80381ec937	PCW 10-12- Mesenchymal- Mesenchymal fibroblastic-mes immature5 (6) PCW 10-12 / Celltypes from embryonic and fetal-stage human lung	A topographic atlas defines developmental origins of cell heterogeneity in the human embryonic lung	2.105E-27	6.829E-25	7.495E-24	6.897E-23	52	195	
3	3004e961d214919e08c7cd5f10c3de5cf85b35a3	PCW 07-8.5- Mesenchymal- Mesenchymal myocytic-mes immature ASM2 (12) PCW 07-8.5 / Celltypes from embryonic and fetal-stage human lung	A topographic atlas defines developmental origins of cell heterogeneity in the human embryonic lung	1.359E-23	1.525E-21	1.674E-20	4.453E-19	47	188	
4	e84539978ab4de42e19186aed00f24bb50cbc21f	PCW 05-06- Mesenchymal- Mesenchymal myocytic-mes immature ASM2 (12) PCW 05-06 / Celltypes from embryonic and fetal-stage human lung	A topographic atlas defines developmental origins of cell heterogeneity in the human embryonic lung	3.142E-23	3.130E-21	3.435E-20	1.030E-18	46	183	
5	b66f1f08827dd6c48583d871f9f3ea41e48bfb2	PCW 13-14-Endothelial- Endothelial immature-endo immature arterial2 (6) PCW 13-14 / Celltypes from embryonic and fetal-stage human lung	A topographic atlas defines developmental origins of cell heterogeneity in the human embryonic lung	1.062E-22	9.404E-21	1.032E-19	3.479E-18	46	188	

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	73459ee062ae1f1a3bb9719dc0b89aae10600e22	CTRL-Myeloid-Monocyte Macrophage Myeloid / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	7.482E-24	8.982E-22	9.857E-21	2.452E-19	48	194
2	927480f56cccd3940b689f3c40ee132fe3e63745	CTRL-Myeloid-Monocyte Macrophage CTRL / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	1.533E-19	5.556E-18	6.097E-17	5.023E-15	43	194
3	14f3a8c0f4f057ad4e6839b4c3eeaf956d6dc92e	CTRL-Lymphoid-B cell Lymphoid / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	1.580E-17	3.440E-16	3.776E-15	5.178E-13	40	189
4	70b89a930709fdb91fde6f96106add8455b11618	CTRL-Myeloid CTRL / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	1.053E-16	1.831E-15	2.009E-14	3.452E-12	40	199
5	7ebf20344a9a154fd2cfa281526867fcf0aded3	CF-Lymphoid-B cell Lymphoid / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	2.098E-16	3.390E-15	3.721E-14	6.876E-12	39	193

Show 36 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	68eadc91c2d89edd2412e86dfe134dd7c0ef6ee9	LAM-Endothelial-LymEndo LAM / Condition, Lineage and Cell class	Atlas of Lymphangiomiomatosis (LAM)	5.431E-18	1.335E-16	1.465E-15	1.780E-13	41	193
2	ba64b1c95dfaa995045239d412e725596f6c482e	LAM-Endothelial-LymEndo Endothelial / Condition, Lineage and Cell class	Atlas of Lymphangiomiomatosis (LAM)	1.657E-14	1.679E-13	1.842E-12	5.432E-10	37	198
3	050911dcce17dee539bbaf79295e614ad84e1dae	LAM-Myeloid LAM / Condition, Lineage and Cell class	Atlas of Lymphangiomiomatosis (LAM)	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197
4	92bccaec01f1dbb17d5efcba30f7f800f674ca96	LAM-Endothelial-VasEndo-2 Endothelial / Condition, Lineage and Cell class	Atlas of Lymphangiomiomatosis (LAM)	8.913E-14	7.442E-13	8.167E-12	2.921E-9	36	198

5	3457e15d1e9b36a78363d46b320c4ec46b40290a	LAM-Epithelial-AT1 Epithelial / Condition, Lineage and Cell class	Atlas of Lymphangioma myomatosis (LAM)	1.540E-13	1.193E-12	1.309E-11	5.047E-9	35	191
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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1c69395c9305b6ecb0a826d46c8e8ec95795ad6d	10x3'2.3-week 14-16-Endothelial-stroma-tip EC week 14-16 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	1.840E-22	1.523E-20	1.671E-19	6.031E-18	47	199
2	997d37ca2af661c92a56add888762724dfccc890	10x3'2.3-week 14-16-Endothelial-stroma-proliferating EC week 14-16 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	1.493E-21	9.465E-20	1.039E-18	4.893E-17	44	182
3	473b01c9162b12b90a617c600238436177a0d18d	10x5'v1-week 12-13-Mesenchymal fibro-stroma-endosteal fibroblast week 12-13 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	3.644E-19	1.227E-17	1.347E-16	1.194E-14	42	189
4	77ac1aa73c16a4f595ff01c6b4e171e0b8fed1e6	10x5'v1-week 14-16-Endothelial-stroma-tip EC week 14-16 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	5.242E-19	1.671E-17	1.834E-16	1.718E-14	43	200
5	cf1a67b7c0d5c0dc5d4d59faf9d9b1a3a1fb00e0	10x5'v1-week 12-13-Endothelial-stroma-tip EC week 12-13 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	3.648E-18	9.327E-17	1.024E-15	1.196E-13	41	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	a7c01df7623aa6cee4ed4a341545ba240194ca8b	Mild-Lymphoid-T-Treg Mild / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	1.155E-13	9.386E-13	1.030E-11	3.785E-9	34	179
2	2cbaef86af870a228cb46895dd765ea8894c83c5	Mild-Myeloid-Macrophages-FCN1+SPP1+ Mild / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	2.697E-12	1.551E-11	1.702E-10	8.837E-8	34	199
3	7437bc48a803ab8f153e5516a0aa0391ae3d97c7	Healthy Control-Myeloid-Macrophages-FCN1-SPP1+ Healthy Control / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	2.697E-12	1.551E-11	1.702E-10	8.837E-8	34	199
4	29d4db6816fead2ad9136ef824e0775463b02159	Severe-Lymphoid-T-Treg Severe / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	8.494E-12	4.360E-11	4.785E-10	2.784E-7	33	196
5	7765a5b04ac117d525201f8eb08e1754e55942ff	Healthy Control-Lymphoid-T-Treg Healthy Control / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	5.398E-11	2.312E-10	2.537E-9	1.769E-6	30	176

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9ad844d9d5aac39d133ae8ab9c4839300f08064c	COVID-19-Lymphoid-Tregs Lymphoid / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	1.003E-14	1.073E-13	1.177E-12	3.286E-10	37	195
2	228f641d79282cc3dc51b95a1f4b0cccf200735	COVID-19 World / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	1.403E-14	1.453E-13	1.595E-12	4.599E-10	37	197
3	7e6f089e71e70190ff8486341ab06719d7741467	COVID-19-Epithelial-AT2, AT1 cells COVID-19 / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	1.657E-14	1.679E-13	1.842E-12	5.432E-10	37	198
4	96400477d130b2403ed81c229e4e4182cc2cdc14	Control-Myeloid-MoAM5, CCL3L1 Myeloid /	Bronchoalveolar Lavage (BAL) Atlas of	4.664E-14	4.178E-13	4.585E-12	1.529E-9	36	194

		Condition, Lineage and Cell class	Severe COVID-19 Patients (Grant et al.)						
5	52b8578699325b0d35a2d3ba36772096130ccc0c	COVID-19-Myeloid-TRAM1 COVID-19 / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	1.809E-13	1.381E-12	1.515E-11	5.927E-9	35	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ba958f731de6c9eff60103d483e020e2c0c7af7c	RSV-Healthy-5 RSV / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	7.627E-10	2.545E-9	2.793E-8	2.500E-5	29	184
2	1e282d619ef8035437fabe0fd2aefda1c142f7f6	RSV-Healthy-5 Healthy / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	7.627E-10	2.545E-9	2.793E-8	2.500E-5	29	184
3	f121b009d64704177f73f2da3848f0ad6ed6bf1f	CV-Healthy-5 Healthy / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	1.390E-8	3.602E-8	3.953E-7	4.555E-4	28	196
4	4a3ce0c603c2ffe11f0f00775b6af4f6d9a6070a	CV-Moderate-4 Moderate / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	1.577E-8	4.032E-8	4.425E-7	5.169E-4	27	185
5	9fe3d53346a95c1bbb0fc6a2f2e974889873424b	CD8+ Memory T cell-CV-3 CD8+ Memory T cell / cell class, Virus stimulation and cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	6.042E-8	1.387E-7	1.522E-6	1.980E-3	27	197

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	2f00d0b7b2ffce8eb3eb5bbae49a0d425b23c982	COVID-19-kidney-VWF+PLVAP+EC COVID-19 / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	9.117E-33	1.494E-29	1.640E-28	2.988E-28	57	191
2	f09675cd472200363c458952f00d2e41990800ee	COVID-19-Heart-Macrophage Heart / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	2.307E-32	3.287E-29	3.608E-28	7.561E-28	57	194
3	a436483fec137584611f86b7a498a4dc2aa19cd3	COVID-19-kidney-PLVAP+EC kidney / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	3.043E-31	3.562E-28	3.909E-27	9.973E-27	56	195
4	27ff3621e177e7932dd44dd6baa81551ea75a874	COVID-19-kidney-AQP1+PLVAP+EC COVID-19 / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.198E-30	1.047E-27	1.149E-26	3.928E-26	55	192
5	60b1312e84f6d6448365a952469c506c00b5fe93	COVID-19-Heart-Fib + EC + Pericyte Heart / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.198E-30	1.047E-27	1.149E-26	3.928E-26	55	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	0a3221e4d1fa31a35868bdda0f0cc873c233b407	Mild/Remission-B naive-8 Mild/Remission / disease group and sub cluster of B and Plasma cells(res = 0.5)	COVID-19 B cell and Plasma cell Atlas in PBMC and BAL	1.489E-12	9.215E-12	1.011E-10	4.879E-8	34	195
2	925bf0d38e4ce279fa45f455546ebd199282c0df	Control-B naive-8 World / disease group and sub cluster of B and Plasma cells(res = 0.5)	COVID-19 B cell and Plasma cell Atlas in PBMC and BAL	9.799E-12	4.962E-11	5.445E-10	3.211E-7	33	197

3	224bd958369ba8fa0d7be2126f7dc61c9f6ac19d	Control-B intermediate-10 Control / disease group and sub cluster of B and Plasma cells(res = 0.5)	COVID-19 B cell and Plasma cell Atlas in PBMC and BAL	2.304E-11	1.062E-10	1.166E-9	7.550E-7	32	192
4	278064c9f0582463b83bf156d34e77f60187613b	Mild/Remission-B intermediate-10 Mild/Remission / disease group and sub cluster of B and Plasma cells(res = 0.5)	COVID-19 B cell and Plasma cell Atlas in PBMC and BAL	3.060E-11	1.377E-10	1.511E-9	1.003E-6	31	183
5	54074da84000e4749ade8acc542f05a275bf829f	Control-B naive-8 Control / disease group and sub cluster of B and Plasma cells(res = 0.5)	COVID-19 B cell and Plasma cell Atlas in PBMC and BAL	8.077E-10	2.671E-9	2.932E-8	2.647E-5	30	196

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	c8c9343c19198b6534f8f07e74405e29b3a164bf	Severe COVID-19-T/NK-CD4+ T2 Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	1.657E-14	1.679E-13	1.842E-12	5.432E-10	37	198
2	bc6b983fdb9547ef8a9e693bc15fcd1b73e101f	Severe COVID-19-T/NK-CD4+ T1 Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	1.657E-14	1.679E-13	1.842E-12	5.432E-10	37	198
3	43e33d28d9de5033bd00d39be953542a225236ed	Severe COVID-19-Epithelial-AT1 AT2 Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	1.657E-14	1.679E-13	1.842E-12	5.432E-10	37	198
4	1da7c303a2e36af4a9d8ec30a11380d9b1897922	Control-Myeloid-MoAM4 Control / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	3.351E-14	3.108E-13	3.411E-12	1.098E-9	36	192
5	05867b96199a46a415848409130697c810d18937	Severe COVID-19-Myeloid-TRAM3 Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	1.540E-13	1.193E-12	1.309E-11	5.047E-9	35	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	445a1aab962673dcc926c33ce9bed5ede9c41c57	COVID-mono1- COVID / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200
2	bd002c54305c746c07b7418a2084195e9c852ec5	COVID-mono1 COVID / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200
3	fa88ceb336e30de3585e62608527a0d44df74190	VE-Treg-CD4 Treg VE / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	5.049E-13	3.494E-12	3.834E-11	1.655E-8	34	188
4	ef048517dfe2fc995d13eb1f08106a487354a4cc	VE-Treg VE / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	2.606E-12	1.515E-11	1.663E-10	8.542E-8	33	188
5	6b00a393ad06ae91bf135a54a53ad4de68956193	VE-CD4-exh CD4 VE / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	2.697E-12	1.551E-11	1.702E-10	8.837E-8	34	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9c753043024871b1f1436fc39defac4da85e10cd	Parenchyma Control (B.)-Endothelial-TX-Bronchial vessel Parenchyma Control (B.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	9.407E-21	4.765E-19	5.229E-18	3.083E-16	45	199
2	e1d50556ca116ef4b65ec29ab2ef7341f0d21451	Biopsy Control (H.)-Immune Biopsy Control (H.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	7.931E-20	3.137E-18	3.443E-17	2.599E-15	44	200
3	e0beacb8bbdc353a3e883171613027feafcf1ef	Bronchus Control (B.)-Immune-TX-DCs Bronchus Control (B.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	5.242E-19	1.671E-17	1.834E-16	1.718E-14	43	200

4	88f33b8dcd837abfa1d12c28719e073a7da6e979	Parenchyma COVID-19-Endothelial-TX-Lymphatic Parenchyma COVID-19 / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199
5	471738f2059e20407572d9c4cbd11812068333ea	Parenchyma Control (B.)-Stromal-TX-Smooth muscle-2 Parenchyma Control (B.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	1.734E-17	3.721E-16	4.084E-15	5.682E-13	41	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	fb847f2277609c31ffcdf49517243ce0684facf	COVID-19-Fibroblasts COVID-19 / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	5.300E-36	2.171E-32	2.383E-31	1.737E-31	61	197
2	f1c8936986123a3151140c374fcd62d6705c530b	COVID-19-Fibroblasts-Intermediate pathological FB COVID-19 / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	5.828E-33	1.005E-29	1.103E-28	1.910E-28	58	197
3	603050beeb33c331d4b2e3fa46cae3f3e0e4bdc7	COVID-19-Fibroblasts-Alveolar FB COVID-19 / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	3.130E-32	4.274E-29	4.691E-28	1.026E-27	57	195
4	a6b3bd01e585e2e3f9e9bf693a2e385773123f8e	Control-Myeloid-Monocyte-derived macrophages Control / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	1.508E-29	8.827E-27	9.688E-26	4.943E-25	54	193
5	92d468dde81125d51daf7abd4703741abe1ab91c	Control-Fibroblasts-Alveolar FB Control / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	2.308E-28	9.954E-26	1.092E-24	7.566E-24	52	187

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	b17ab094cdc7050c2997e24ed474779b5d6f6146	Control-Non-classical Monocyte- Control / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	3.628E-16	5.588E-15	6.132E-14	1.189E-11	39	196
2	404064ccfe2cb73df7a7f88aa65d86b97dcef9d4	Control-Non-classical Monocyte Control / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	3.628E-16	5.588E-15	6.132E-14	1.189E-11	39	196
3	c9250c80dd5bc3d27c6065b99119ff7dcf392e84	COVID-19 Convalescent-Non-classical Monocyte COVID-19 Convalescent / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	1.955E-14	1.938E-13	2.126E-12	6.408E-10	37	199
4	996a207b8b91e10dd018dc07aaf5ecd473bfeaad	COVID-19 Convalescent-Non-classical Monocyte- COVID-19 Convalescent / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	1.955E-14	1.938E-13	2.126E-12	6.408E-10	37	199
5	d70b9039fd2fef3e4be086513b94fb7e9bc1f670	COVID-19 Severe-Non-classical Monocyte- COVID-19 Severe / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	4.664E-14	4.178E-13	4.585E-12	1.529E-9	36	194

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	16359a56297f0558fc93fa52563cce0c53def167	COVID-19 Severe-Neu 2 World / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	1.390E-8	3.602E-8	3.953E-7	4.555E-4	28	196
2	945f19475905cdedf232315eea1076ca0b753b67	COVID-19 Severe-Neu 2 COVID-19 Severe / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	1.556E-8	3.992E-8	4.381E-7	5.100E-4	28	197
3	5ef9eb806fb2c8ee5aae0a75503d244b08ee10d4	COVID-19 Mild-Neu 4 World / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	9.557E-7	1.801E-6	1.976E-5	3.132E-2	19	124
4	f5fd08b42c002d4693646b27e7b708eceb49524f	COVID-19 Mild-Neu 2 COVID-19 Mild / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	3.150E-6	5.479E-6	6.013E-5	1.032E-1	22	172
5	eb8d8303c1a8f8f8cf9f8c2180406c06624690af	Control-Neu 1 Control / 5 Neutrophil clusters in	COVID-19 PBMC	1.314E-5	2.088E-5	2.292E-4	4.306E-1	8	28

	COVID-19 patients	Neutrophil Atlas						
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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 f595eba81911eb860dce964f1d8269287f50d3ea	Control-PLT 1 World / Disease Group and Platelet Clusters	COVID-19 PBMC Platelet Atlas	1.078E-10	4.306E-10	4.725E-9	3.532E-6	31	192
2 90c61e10c7860bfa6ccfe6f37671c8924637f7b	COVID-19 Mild World / Disease Group and Platelet Clusters	COVID-19 PBMC Platelet Atlas	4.507E-8	1.062E-7	1.166E-6	1.477E-3	26	182
3 cd4ed3fa3cd8b159ab10cf9b2ad5cd05640530d0	COVID-19 Severe-PLT 3 COVID-19 Severe / Disease Group and Platelet Clusters	COVID-19 PBMC Platelet Atlas	6.441E-8	1.473E-7	1.617E-6	2.111E-3	24	161
4 c86cb4b2df5102af904c362f3cbd24fe4462ba6c	COVID-19 Mild-PLT 1 World / Disease Group and Platelet Clusters	COVID-19 PBMC Platelet Atlas	1.344E-7	2.912E-7	3.196E-6	4.405E-3	26	192
5 f07654b215279abaf1c0882cdf41fbe31580a2ca	Control World / Disease Group and Platelet Clusters	COVID-19 PBMC Platelet Atlas	1.187E-6	2.191E-6	2.405E-5	3.892E-2	24	188

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 742c4d6016cfa48444a5919a885ab8d02cad7e18	COVID-19 Severe-NK COVID-19 Severe / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	2.328E-12	1.364E-11	1.497E-10	7.630E-8	34	198
2 f3316fb97c6065286ffd22a0ad9fe7aa5b3b5650	Control-NK Control / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	6.049E-11	2.559E-10	2.809E-9	1.982E-6	32	199
3 b586b0f1127293c2f8529be16b24229359041da2	COVID-19 Mild-NK COVID-19 Mild / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	6.916E-11	2.856E-10	3.135E-9	2.266E-6	32	200
4 f0fceb5f87ca260bfe038c0db3487a6d2e1b0a6e	COVID-19 Mild-Treg COVID-19 Mild / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	7.150E-11	2.939E-10	3.226E-9	2.343E-6	31	189
5 06fdd76ea13b93e29959c745698b57af6746aaeb	COVID-19 Severe-Treg COVID-19 Severe / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	9.409E-11	3.794E-10	4.164E-9	3.084E-6	31	191

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 e669fd95278e145f55126d0e6be8fb2d6184dbbd	Mild-Treg Mild / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	2.876E-15	3.528E-14	3.872E-13	9.426E-11	36	178
2 0a80b8c317e8da4d4722cfd13cdabc32b58021eb	Severe-Treg World / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	4.092E-12	2.249E-11	2.468E-10	1.341E-7	33	191
3 3a9a8ac2aa278adde848608f9bb92a002dbb9bcc	Control-Treg Control / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	4.746E-12	2.564E-11	2.814E-10	1.555E-7	33	192
4 6df099f37875f2cd63502b732a2e07ebfec50e47	Mild-CD4+ T Exhausted Mild / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	9.270E-12	4.743E-11	5.205E-10	3.038E-7	31	175
5 dc6b0291714e2b9501c0796a63678bf9d1b1052	Severe-CD4+ T Exhausted Severe / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	1.300E-11	6.385E-11	7.007E-10	4.261E-7	33	199

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 fb873b7636bb1c7b119dd5b23d7a20f518e6c6da	PBMC-Mild-cDC 0 Mild / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	2.982E-15	3.605E-14	3.956E-13	9.773E-11	38	198
2 4b5a7450fed912f340da16065c1e65d626dbe8d1	PBMC-Control-cDC 10 Control / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	8.340E-12	4.303E-11	4.722E-10	2.733E-7	32	185
3 4518ffa51ead9da1ddf07bf048b18602e50f0f84	BAL-Control-cDC 0 Control / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	6.049E-11	2.559E-10	2.809E-9	1.982E-6	32	199

4	ebf03979ef56e978d72db475bb635b43b9cbe402	PBMC-Control-cDC 0 Control / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	6.049E-11	2.559E-10	2.809E-9	1.982E-6	32	199
5	6d1e524f000b71c935359afc801a1d31f218fec8	PBMC-Severe-cDC 1 Severe / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	6.950E-10	2.340E-9	2.568E-8	2.278E-5	19	81

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1f35efb0765e05f7f9c881849953bef3965be25a	3'-GW trimst-1-LargeIntestine-Endothelial-blood vessel EC-Fetal arterial EC GW trimst-1 / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	1.444E-20	6.959E-19	7.637E-18	4.732E-16	44	192
2	b15304d3d3f6c254969b54a61bee3d9f368840b2	3'-GW trimst-1.5-SmallIntestine-Endothelial-blood vessel EC-Fetal arterial EC GW trimst-1.5 / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	6.443E-20	2.655E-18	2.913E-17	2.111E-15	44	199
3	98e34e8612f111bb667a574de1faaa785d318ca4	3'-GW trimst-1-SmallIntestine-Endothelial-blood vessel EC-Fetal arterial EC GW trimst-1 / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	2.852E-19	9.871E-18	1.083E-16	9.348E-15	43	197
4	ff8a9adc1302a4679ccdf9ef95ef53e4c7a5391	3'-GW trimst-1-SmallIntestine-Endothelial GW trimst-1 / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	3.499E-19	1.193E-17	1.309E-16	1.147E-14	43	198
5	ec74ff85d6b61013b1f785b2fca343759feb7843	3'-Pediatric IBD-SmallIntestine-Mesenchymal-fibroblastic-Stromal 2 (NPY+) Pediatric IBD / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	4.286E-19	1.410E-17	1.548E-16	1.404E-14	43	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ab0b32c077ac26d32a293dcf686af6984980793f	Caecum-T cell-Treg Caecum / Region, Cell class and subclass	Colon Immune Atlas	6.204E-16	8.914E-15	9.782E-14	2.033E-11	39	199
2	90a2a75ca078f7088b8739795a9b396113bcbe23	Caecum-T cell-Treg T cell / Region, Cell class and subclass	Colon Immune Atlas	2.982E-15	3.605E-14	3.956E-13	9.773E-11	38	198
3	b7a1637e4baadd657f6279f4aa96cd590c9cd8c9	Transverse-T cell-Treg T cell / Region, Cell class and subclass	Colon Immune Atlas	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197
4	3779489d57ebda33277c79cba037f4c73128c8ba	mLN-T cell-Treg T cell / Region, Cell class and subclass	Colon Immune Atlas	3.972E-13	2.811E-12	3.085E-11	1.302E-8	35	197
5	caa37ec509b54e842564d754f100ab1b2a77a7c1	mLN-T cell mLN / Region, Cell class and subclass	Colon Immune Atlas	5.400E-13	3.694E-12	4.054E-11	1.770E-8	35	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	12c22b07a231c9dc548e9dc37e0a60296a4a6273	Caecum-(1) T cell-(15) Treg Caecum / shred on region, Cell type, and subtype	Colon Immune Atlas from Gut Cell Atlas	6.204E-16	8.914E-15	9.782E-14	2.033E-11	39	199
2	6e7723e8b977be35c60cc11ac7cfa4f71339441e	(1) T cell-(15) Treg (1) T cell / shred on Cell type and subtype	Colon Immune Atlas from Gut Cell Atlas	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197
3	4bf2641409c543c2167bff71efa95b00dd7bfe19	mLN-(1) T cell mLN / shred on region, Cell type, and subtype	Colon Immune Atlas from Gut Cell Atlas	5.400E-13	3.694E-12	4.054E-11	1.770E-8	35	199
4	d519adeb8290fcce107e81a439ba3bf1e231b55b	(50) cDC2 World / shred on Cell type and subtype	Colon Immune Atlas	1.530E-12	9.443E-12	1.036E-10	5.015E-8	35	206

			from Gut Cell Atlas						
5	528520dc98775aca6cc7568fedf5906ea55e0bea	Transverse-(3) ILC-(30) ILC Transverse / shred on region, Cell type, and subtype	Colon Immune Atlas from Gut Cell Atlas	3.120E-12	1.747E-11	1.918E-10	1.023E-7	34	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	b9763ac9857a60db6f1f104fe1e9ea2266cf931b	Non-neuronal-Postmitotic-Endothelial World / Primary Cells by Cluster	Comparison of human cortex and organoids	3.218E-24	4.202E-22	4.612E-21	1.055E-19	49	199
2	0b4edf3e359749827ef978a77b5267dde732d71	Non-neuronal-Postmitotic-Endothelial-Endothelial-24 World / Primary Cells by Cluster	Comparison of human cortex and organoids	3.218E-24	4.202E-22	4.612E-21	1.055E-19	49	199
3	9e01eee126247a0696c71b019f855a8a41a0ede3	Non-neuronal-Postmitotic-Endothelial-Endothelial World / Primary Cells by Cluster	Comparison of human cortex and organoids	3.218E-24	4.202E-22	4.612E-21	1.055E-19	49	199
4	00d756bc0231e1b3b88430214338c1059cb11106	Neuron-Postmitotic-Excitatory Neuron -Deep Layer-37 World / Primary Cells by Cluster	Comparison of human cortex and organoids	1.184E-17	2.663E-16	2.922E-15	3.880E-13	41	197
5	61749ccafeb938c310cff1de5ff924a1c794325a	Non-neuronal-Non-dividing-Radial Glia-tRG World / Primary Cells by Cluster	Comparison of human cortex and organoids	1.184E-17	2.663E-16	2.922E-15	3.880E-13	41	197

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e16035b3328f9b1b2e28d234c62ba88387540550	10x5'-lymph-node spleen-Lymphocytic Invariant-Inducer-like-ILC3 lymph-node spleen / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	4.454E-18	1.117E-16	1.226E-15	1.460E-13	41	192
2	2ffe44edf2b02d11a7c10513692eb697a10f911e	3' v3-blood-Lymphocytic T CD4-Tregs blood / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	1.243E-15	1.646E-14	1.807E-13	4.074E-11	38	193
3	2cbafcb03df3c9aca68371df500d18ab8dcc416c	10x5'-lymph-node spleen-Lymphocytic T CD4 lymph-node spleen / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	2.982E-15	3.605E-14	3.956E-13	9.773E-11	38	198
4	04bd6e135733570e877af9460f87379ed0a5c5f8	10x5'-lymph-node spleen-Lymphocytic T CD4-Tregs lymph-node spleen / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	6.001E-15	6.736E-14	7.392E-13	1.967E-10	37	192
5	479e60f76c191253e23699c9dd7ef7efc08c59ad	3' v3-lymph-node spleen-Lymphocytic Invariant-Inducer-like-ILC3 lymph-node spleen / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	8.500E-15	9.230E-14	1.013E-12	2.786E-10	36	184

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	f374cb3ec31c6eef2cef9e07547bfd1e380553af	10x 3' v2v3-Non-neoplastic-Glial-Neuronal-OPC-OPC 10x 3' v2v3 / Platform, Oncotype, Lineage, Cell class, celltype (level4), mutation group	Harmonized single-cell landscape, intercellular crosstalk and tumor architecture of glioblastoma	1.927E-25	3.759E-23	4.126E-22	6.316E-21	50	196
2	671c380b58d7f634b4bec38c357d357ea4f3535	10x 3' v2v3-Non-neoplastic-Glial-Neuronal-OPC 10x 3' v2v3 / Platform, Oncotype, Lineage, Cell class, celltype (level4), mutation group	Harmonized single-cell landscape, intercellular crosstalk and tumor architecture of glioblastoma	1.927E-25	3.759E-23	4.126E-22	6.316E-21	50	196

3	19a97e27a4758e794ce7246d295e112b47931a48	Smart-start-Cell-Wel seq-Non-neoplastic-Glial-Neuronal-OPC-OPC-G Smart-start-Cell-Wel seq / Platform, Oncotype, Lineage, Cell class, celltype (level4), mutation group	Harmonized single-cell landscape, intercellular crosstalk and tumor architecture of glioblastoma	2.467E-23	2.617E-21	2.872E-20	8.087E-19	48	199
4	ad777683adeb2ce45ade570386235e311fa7ea2d	Smart-start-Cell-Wel seq-Non-neoplastic-Glial-Neuronal-OPC-OPC-F Smart-start-Cell-Wel seq / Platform, Oncotype, Lineage, Cell class, celltype (level4), mutation group	Harmonized single-cell landscape, intercellular crosstalk and tumor architecture of glioblastoma	3.117E-23	3.124E-21	3.429E-20	1.022E-18	48	200
5	218f33e068eb126458ec33176de3cfa6fc06ddf0	Smart-start-Cell-Wel seq-Non-neoplastic-Endothelial-Endothelial mature Smart-start-Cell-Wel seq / Platform, Oncotype, Lineage, Cell class, celltype (level4), mutation group	Harmonized single-cell landscape, intercellular crosstalk and tumor architecture of glioblastoma	1.464E-22	1.233E-20	1.353E-19	4.797E-18	47	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	dc344b3ec51d506952e38f0b3a7795d65f9dd4eb	Hematolymphoid-Microglia-TYROBP-- Hematolymphoid / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	1.309E-30	1.047E-27	1.149E-26	4.291E-26	56	200
2	21bcca3b670fe9bac034aef2275d3de4a9a73e2b	Hematolymphoid-Microglia Hematolymphoid / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	1.309E-30	1.047E-27	1.149E-26	4.291E-26	56	200
3	33036d21c1c82109284473a515c4f890b33dd5c	Hematolymphoid-Microglia-TYROBP Hematolymphoid / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	1.309E-30	1.047E-27	1.149E-26	4.291E-26	56	200
4	a20dce14f94777687aad57d6fbc3258ad376f63f	Hematolymphoid-Microglia-TYROBP----L1-3 Hematolymphoid / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	1.309E-30	1.047E-27	1.149E-26	4.291E-26	56	200
5	3bba5219453322198e8fdb0921d5f8c403598751	Hematolymphoid-Microglia-TYROBP- Hematolymphoid / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	1.309E-30	1.047E-27	1.149E-26	4.291E-26	56	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	5b7a1edee602e55d3400dc17dbb6b8aaa26defc0	Primary Visual cortex (V1C)-Non-neuronal-Macrogial-Oligo-OPC-OPC L1-6 MYT1 Primary Visual cortex (V1C) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	6.384E-22	4.568E-20	5.013E-19	2.092E-17	45	187
2	daff7ccd3f1924cf2b34d3aca3eccde245aaf371	Primary Visual cortex (V1C)-Non-neuronal-Macrogial-Oligo-OPC Primary Visual cortex (V1C) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	6.384E-22	4.568E-20	5.013E-19	2.092E-17	45	187
3	2e1766f1a972fec670daaaf7eb2d3a404f121e7	Mid-temporal gyrus (MTG)-Non-neuronal-Macrogial-Oligo-OPC-OPC L1-6 MYT1 Mid-temporal gyrus (MTG) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	3.001E-21	1.747E-19	1.917E-18	9.834E-17	44	185
4	7aaa8335b40927e3e8fcdced807cd521fc213a0d	Mid-temporal gyrus (MTG)-Non-neuronal-Macrogial-Oligo-OPC Mid-temporal gyrus (MTG) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	3.001E-21	1.747E-19	1.917E-18	9.834E-17	44	185

5	6d18b45eda4014759e6dd282d78ffd28df8a6044	primary auditory cortex (A1C)-Neuron primary auditory cortex (A1C) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	7.581E-21	3.963E-19	4.349E-18	2.485E-16	45	198
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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	4240d0b3cf264f51dcf0cb4d0a18641d85d38638	(0) Myeloid-(001) CD16+ Monocyte (0) Myeloid / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	4.148E-17	8.073E-16	8.859E-15	1.359E-12	40	194
2	89cb262e04d7105012e957e0add44c73de6c1ed0	(0) Myeloid-(00) Monocyte-(001) CD16+ Monocyte (00) Monocyte / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	1.485E-15	1.931E-14	2.119E-13	4.865E-11	38	194
3	33843d550cbca03c044d593b1f6972e4d3871f7f	(001) CD16+ Monocyte World / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	2.109E-15	2.659E-14	2.918E-13	6.912E-11	38	196
4	4aabb3f5ce70100e4d98d7fa9f8d12e84fb9fe3d	(010) cDC World / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	2.910E-13	2.131E-12	2.339E-11	9.536E-9	35	195
5	08dc0c019c594da7b9944db8fd706aa7780e6ae9	(210) NKT cell World / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	4.746E-12	2.564E-11	2.814E-10	1.555E-7	33	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	aeeadfeb01827dbc7de6576c76fb2e41a3c59247	myeloid-CD16+ Monocyte myeloid / Lineage and Cell class	Human Bone Marrow Atlas	4.664E-14	4.178E-13	4.585E-12	1.529E-9	36	194
2	3ff06100deee9bee852a52078666999a9f7beaf1	B cell maturation-CD34+ pre-plasma World / Lineage and Cell class	Human Bone Marrow Atlas	1.258E-11	6.254E-11	6.863E-10	4.124E-7	31	177
3	117abdafd294c85ccb5d8ea907e3c0491b7200b2	hematopoetic progenitors-CD34+ CLP hematopoetic progenitors / Lineage and Cell class	Human Bone Marrow Atlas	1.732E-11	8.175E-11	8.972E-10	5.678E-7	32	190
4	b1c630ca2189d9d49402a5621b57618976fba5c	megakaryocytic World / Lineage and Cell class	Human Bone Marrow Atlas	3.534E-11	1.571E-10	1.724E-9	1.158E-6	31	184
5	4ee160a863d4fb9c4c9449633b9f337db8871992	B cell maturation-CD34+ pre-plasma B cell maturation / Lineage and Cell class	Human Bone Marrow Atlas	9.409E-11	3.794E-10	4.164E-9	3.084E-6	31	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	3f78eddeaa67d3b767aa38de765632166b09a4f0	(02) MMP9/10+ World / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199
2	8194777d367405a7840787e977854b5c07e3bd6b	(07) Ionocytes World / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	6.204E-16	8.914E-15	9.782E-14	2.033E-11	39	199
3	f2e33cb569c25fc2732722cac295647e9bd8738f	(08) Brush+PNEC World / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	2.697E-12	1.551E-11	1.702E-10	8.837E-8	34	199
4	c773b9180dbfec9c19d4098dd43332e6f6050372	(06) OLFM4+ World / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	2.713E-10	9.872E-10	1.083E-8	8.890E-6	31	199
5	501420901bf3ec1b050e0d14596a9f9f3dfc928	(01) IL1RL1+ World / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	1.324E-9	4.112E-9	4.513E-8	4.340E-5	30	200

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 779276e775cb2492e8dd36436295a536084a6415	nucseq World / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	1.377E-28	6.184E-26	6.787E-25	4.514E-24	53	193
2 53f3e49e91b1096f3226010e2de767efb490dfe4	nucseq-Epithelial-Epithelial Alveolar nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	1.383E-26	3.535E-24	3.880E-23	4.531E-22	51	194
3 9406866f99555198a9be311fbd65751b70f35446	nucseq-Epithelial nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	1.495E-25	3.043E-23	3.340E-22	4.900E-21	50	195
4 6688cee34beee4f151ac17fccbc9c26a9aad72e1	nucseq-Mesenchymal-Fibroblastic-Fibroblastic 2-AF1 nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	4.427E-25	7.365E-23	8.083E-22	1.451E-20	49	191
5 99ce9e3c4c50cf64ebb62145f2b5420efa0db309	nucseq-Mesenchymal-Fibroblastic-Fibroblastic 2 nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	5.708E-25	9.037E-23	9.917E-22	1.871E-20	49	192

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 23138e579f07d5a6f20d41457cb573b4ac95a4ef	lymphoid-B cell-pro-B World / Lineage, cell class and subclass	Human Cord Blood Atlas	2.809E-11	1.280E-10	1.404E-9	9.207E-7	29	161
2 42a4d706382be33d552ece1d0598d073857a8d4e	lymphoid-T cell-Regulatory T cell World / Lineage, cell class and subclass	Human Cord Blood Atlas	4.023E-11	1.773E-10	1.945E-9	1.318E-6	32	196
3 352cd442b6e62f09b6d22a139774067873644594	Megakaryocytic-erythropoietic-Megakaryo-cells-Megakaryocyte World / Lineage, cell class and subclass	Human Cord Blood Atlas	1.233E-10	4.879E-10	5.355E-9	4.042E-6	31	193
4 06ddaeb2fd32895181e23f3f1bb3e9103e79752c	Megakaryocytic-erythropoietic-Megakaryo-cells-Platelet Megakaryocytic-erythropoietic / Lineage, cell class and subclass	Human Cord Blood Atlas	5.522E-10	1.885E-9	2.068E-8	1.810E-5	30	193
5 b8b05894e811e431d797ac4fa3ccff4963a154e7	lymphoid-B cell-Naive B cell lymphoid / Lineage, cell class and subclass	Human Cord Blood Atlas	1.642E-9	5.028E-9	5.518E-8	5.381E-5	29	190

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 ac0e48b0c09a7f57d30dff321b0c30a4c5e16ad9	15-Airway-Endothelial Airway / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	4.148E-17	8.073E-16	8.859E-15	1.359E-12	40	194
2 f3851337a2d17f4acef2cd812a766eb0b503748b	15-Airway-Endothelial-Endothelial Airway / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	4.148E-17	8.073E-16	8.859E-15	1.359E-12	40	194
3 a737061703af06cfa1acd9f5f77b9d42b3cd7c33	15-Airway-Immune Airway / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	1.053E-16	1.831E-15	2.009E-14	3.452E-12	40	199
4 1a8c77d241bd817a195e1532fd25f51358cb1ff1	11.5-Airway-Mesenchymal-Airway Smooth Muscle Airway / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	1.053E-16	1.831E-15	2.009E-14	3.452E-12	40	199
5 c294cd421f277992b56ae9c40b8f3948e33148fe	15-Distal-Immune-Hematopoietic, B Cells Distal / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	2.374E-16	3.808E-15	4.179E-14	7.779E-12	38	184

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
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1	b070a0667f1ee9b825b267b6c389b7c42fc436f9	human hepatoblastoma-Tumor cells-T5 Tumor cells / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	3.532E-33	6.431E-30	7.058E-29	1.158E-28	57	188
2	1d874608aa2062024323512f68889219471b2f00	pdx-Tumor cells-T0 Tumor cells / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	9.279E-26	1.977E-23	2.170E-22	3.041E-21	49	185
3	e6fb0bfab1779ec64a8c35d01519eaa6bf62e977	background-Endothelial cells background / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	1.927E-25	3.759E-23	4.126E-22	6.316E-21	50	196
4	e09f609fed033a25baacaf4a07bbbae1076da366	human hepatoblastoma-Endothelial cells human hepatoblastoma / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	3.587E-23	3.541E-21	3.886E-20	1.176E-18	47	192
5	503a979328c68b096680b71359a26f02fafdf35	human hepatoblastoma-Tumor cells human hepatoblastoma / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	3.437E-22	2.675E-20	2.936E-19	1.126E-17	46	193

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	d787b7cdb8c3f677ac9c4934a5df9cc194df3987	Paneth cell World / shred on cell type and cluster	Human Ileal Epithelial cells from Crohn's Disease	1.318E-8	3.435E-8	3.770E-7	4.319E-4	25	160
2	b7c5a8a1c85da92e1945721b6887b32fad7b76b8	C 07 World / shred on cell type and cluster	Human Ileal Epithelial cells from Crohn's Disease	1.318E-8	3.435E-8	3.770E-7	4.319E-4	25	160
3	5cb42e09f380c4468cdc603ec0c3de35eadd3213	C 06 World / shred on cell type and cluster	Human Ileal Epithelial cells from Crohn's Disease	1.656E-7	3.544E-7	3.890E-6	5.426E-3	26	194
4	d82d3204f24c95771c1496c28e3fbc6e2442199b	Goblet cell World / shred on cell type and cluster	Human Ileal Epithelial cells from Crohn's Disease	2.742E-6	4.825E-6	5.295E-5	8.986E-2	24	197
5	885604356e19a850b0e601c3167ad26b8180bcec	C 04 World / shred on cell type and cluster	Human Ileal Epithelial cells from Crohn's Disease	2.742E-6	4.825E-6	5.295E-5	8.986E-2	24	197

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	084c88f08ce0ecd6c9f433caed370eb2154f896	ILEUM-inflamed-(8) Smooth muscle cells inflamed / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	2.521E-21	1.491E-19	1.636E-18	8.261E-17	45	193
2	97052c28e354833901f28d339b09f97f50a5b752	ILEUM-inflamed-(7) Endothelial cell inflamed / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199
3	3368c0a90a47c4dcdfe70be3192550df0744e508	ILEUM-non-inflamed-(8) Smooth muscle cells non-inflamed / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199
4	5c799115a6e95bcd896e4ad10bd272705c9a4e2c	ILEUM-inflamed-(7) ACKR1+ endothelial cells inflamed / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	1.053E-16	1.831E-15	2.009E-14	3.452E-12	40	199
5	1fe3417dfd1cf1758fd82c9ac13dbd88bdf0b548	ILEUM-inflamed-(1) Tregs inflamed / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	1.743E-16	2.873E-15	3.152E-14	5.713E-12	39	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	069c8949b33ecfdb6da32992002d4060ff6082bc	distal-mesenchymal-Myofibroblast-3 distal / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	1.664E-21	1.025E-19	1.125E-18	5.454E-17	46	200

2	61854a459385cd9295be37157a8f81a2c227dff3	distal-mesenchymal-Myofibroblast distal / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	7.931E-20	3.137E-18	3.443E-17	2.599E-15	44	200
3	00fdee373eaa43c9ce897f2ba2ecbe94cedea93a	distal-3-Endothelial-Bronchial Vessel 1 3 / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	3.499E-19	1.193E-17	1.309E-16	1.147E-14	43	198
4	1f20addc0d138fec02ed6ca4c518169c568de263	distal-3-mesenchymal-Myofibroblast 3 / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	4.286E-19	1.410E-17	1.548E-16	1.404E-14	43	199
5	7f4840ae6a888380feca722543e5e52783f3e35d	proximal-mesenchymal-Alveolar Fibroblast proximal / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9bfd7b88aa646eaf5eddb15cf985c7ca910cb35e	Adult-Immune Adult / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	7.355E-36	2.562E-32	2.811E-31	2.410E-31	61	198
2	98b8ee42b89d97e4c9db01740e0c193503c68f2c	Children (3 yrs)-Epithelial-alveolar epithelial cell type 2 Club-like (AT2 Club-like) Children (3 yrs) / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.247E-34	3.144E-31	3.450E-30	4.087E-30	58	185
3	efb962a5fd3b9bdfd8cf8d13c435e29c8271713e	Adult-Epithelial Adult / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.245E-32	1.855E-29	2.036E-28	4.081E-28	57	192
4	881ab995c90d75fd987d6e8f1f926a4bfcc4235f	Children (3 yrs)-Immune-monocyte-D139 Children (3 yrs) / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.309E-30	1.047E-27	1.149E-26	4.291E-26	56	200
5	81cc8435b2704a9a8287b3f54acaae0f11dd4ac7	Epithelial-alveolar epithelial cell type 2 Club-like (AT2 Club-like) World / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	2.604E-30	1.816E-27	1.993E-26	8.534E-26	54	187

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e0e47cf65774191981840b22905b2094b95abe0f	normal Lung-Fibroblasts-COL13A1+ matrix FBs Fibroblasts / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	4.672E-27	1.389E-24	1.525E-23	1.531E-22	52	198
2	5228c4bf2513186140c2c4eaa67a268c732bdc84	tumor Lung-Endothelial cells-Tumor ECs tumor Lung / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	5.226E-20	2.189E-18	2.403E-17	1.713E-15	44	198
3	bfdde765bf05c5bff88bc3ab5175bfe61e79ed60	normal Lung-Endothelial cells-EPCs Endothelial cells / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	1.184E-17	2.663E-16	2.922E-15	3.880E-13	41	197
4	d551bc29afef071adf4c9bb80345352ec33441d8	metastatic Lymph Node-Endothelial cells-Lymphatic ECs metastatic Lymph Node / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	3.297E-17	6.621E-16	7.266E-15	1.081E-12	38	174
5	7ee98acda030366ac6cf3890a6d93fd0426712ed	normal Lung-Endothelial cells-Tumor ECs normal Lung / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	2.374E-16	3.808E-15	4.179E-14	7.779E-12	38	184

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	dcf453e22dba90c0ae349fa6c3d4c20758bb95af	wk 15-18-Endothelial wk 15-18 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and	2.274E-18	6.225E-17	6.832E-16	7.451E-14	42	198

			fetal stage lung cell atlas						
2	dfc5da514fb34a2c318a5c4c61f44049fa43960e	wk 15-18-Endothelial-Blood vessel endothelial-Late cap wk 15-18 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	8.040E-18	1.881E-16	2.064E-15	2.635E-13	41	195
3	70e05d7c0c68c28754ce0e72434b205aed6287ae	wk 20-22-Endothelial-Blood vessel endothelial-Venous endo wk 20-22 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	1.053E-16	1.831E-15	2.009E-14	3.452E-12	40	199
4	4986ef70a665fdfa1df86f7f8a15117487eae159	wk 15-18-Endothelial-Blood vessel endothelial-Early cap wk 15-18 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	1.743E-16	2.873E-15	3.152E-14	5.713E-12	39	192
5	a27aa97aa6508a3ffe92c2b6bb0511a95650a390	wk 08-11-Endothelial-Blood vessel endothelial-GRIA2+ arterial endo wk 08-11 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	4.172E-16	6.375E-15	6.996E-14	1.367E-11	38	187

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	d70b49f6b9c6c4422adb2936c837a1af7569fb0a	10x 3' v3-lymph node (10x 3' v3)-lymphocytic-innate lymphocytic-innate lymphoid cell lymph node (10x 3' v3) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.	8.040E-18	1.881E-16	2.064E-15	2.635E-13	41	195
2	b69709323a9f1b368b5a4f87295b9f7fd9c9be8e	10x 3' v3-lymph node (10x 3' v3)-lymphocytic-T lymphocytic-regulatory T cell lymph node (10x 3' v3) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.	1.199E-16	2.050E-15	2.250E-14	3.929E-12	39	190
3	3fafb1d36c5f98a29d20a5ce5192c83d6f03514	Smart-seq2-tissue-resident (Smart-seq2)-myeloid-myeloid granulocytic-mast cell tissue-resident (Smart-seq2) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.	1.734E-15	2.228E-14	2.445E-13	5.683E-11	37	185
4	de55471dd5c842026b409cfefb67fe32f079a011	Smart-seq2-tissue-resident (Smart-seq2)-myeloid-myeloid granulocytic tissue-resident (Smart-seq2) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.	1.207E-14	1.260E-13	1.383E-12	3.955E-10	36	186
5	b2f4d7c301c0b24003374923b31d6d058e40b213	10x 3' v3-tissue-resident (10x 3' v3)-myeloid-myeloid monocytic-monocyte tissue-resident (10x 3' v3) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	8ef9810ee99082a9c803c7ecad6ceb5710d16b54	Influenza Severe-Non-classical Monocyte World / Disease group and Cell class	Influenza Atlas	1.187E-14	1.248E-13	1.370E-12	3.890E-10	37	196
2	197edf6feb1cfc71d88e532d74f77305a42a3486	Influenza Severe-Non-classical Monocyte Influenza Severe / Disease group and Cell class	Influenza Atlas	4.092E-12	2.249E-11	2.468E-10	1.341E-7	33	191
3	c2d31b2a560309264e846271430a846f09a73ef8	Influenza Severe-CD8+ Tem Influenza Severe / Disease group and Cell class	Influenza Atlas	4.023E-11	1.773E-10	1.945E-9	1.318E-6	32	196

4	6218e6cbe44d92bb98d42ef2f5e18ab7a683b100	Healthy/Control-CD4+ T naive World / Disease group and Cell class	Influenza Atlas	1.233E-10	4.879E-10	5.355E-9	4.042E-6	31	193
5	e7fd91080fca7c31a2d48433791da3c2a4adf14d	Healthy/Control-NK Healthy/Control / Disease group and Cell class	Influenza Atlas	2.713E-10	9.872E-10	1.083E-8	8.890E-6	31	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e8cc4d08fcfceab75a02558817e4ccd7dbafe3a	renal cortex nuclei World / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	6.502E-40	2.090E-35	2.294E-34	2.131E-35	64	192
2	7002937e8903e037332a215d00fbc7c7843b33f2	renal cortex nuclei-CKD+DKD normotensive-Epithelial CKD+DKD normotensive / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	1.339E-39	2.090E-35	2.294E-34	4.387E-35	64	194
3	6477e6e7be5bd8eb99119a12ae16334ccddec43	renal medulla nuclei-CKD+DKD normotensive-Epithelial CKD+DKD normotensive / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	1.913E-39	2.090E-35	2.294E-34	6.271E-35	64	195
4	eea66711a16134f86e6c533a5a837ff2e0d7ca7f	renal medulla nuclei-Adult normal reference-Epithelial Adult normal reference / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	3.810E-36	1.784E-32	1.958E-31	1.249E-31	61	196
5	6ce74aa3f0ce3ca284b67e5a4660ffd2cc9611e0	renal medulla nuclei-Renal AKI (acute kidney injury)-Epithelial Renal AKI (acute kidney injury) / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	3.810E-36	1.784E-32	1.958E-31	1.249E-31	61	196

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	bf6f72a489c62cbf1a679552d8c5eaaaa0b99d33	COVID-19 Mild-Lymphoid B-B intermediate COVID-19 Mild / Disease group, lineage and cell class	Integration of 5 COVID-19 PBMC Datasets	4.664E-14	4.178E-13	4.585E-12	1.529E-9	36	194
2	9c943d18f8e6cb0ce9f2158d50796fafae5c81d4	COVID-19 Mild-Myeloid-Non-classical Monocyte COVID-19 Mild / Disease group, lineage and cell class	Integration of 5 COVID-19 PBMC Datasets	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197
3	85d92bc226cc28384c30991cc4ebb02ec2e3ec99	Control-Myeloid-cDC Control / Disease group, lineage and cell class	Integration of 5 COVID-19 PBMC Datasets	3.402E-13	2.452E-12	2.691E-11	1.115E-8	35	196
4	ae0a51e63e2751a6d9dc0c8a3852680949173523	Control-Myeloid-Non-classical Monocyte Control / Disease group, lineage and cell class	Integration of 5 COVID-19 PBMC Datasets	2.328E-12	1.364E-11	1.497E-10	7.630E-8	34	198
5	42553fdc127e5f613ffd5067620a768a40f1a8a1	COVID-19 Mild-Lymphoid T/NK-Treg COVID-19 Mild / Disease group, lineage and cell class	Integration of 5 COVID-19 PBMC Datasets	2.606E-12	1.515E-11	1.663E-10	8.542E-8	33	188

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	0eccf41edefc3b8b5d0316f57d5ba572949aec2b	Fetal brain-organoid Tanaka cellReport-GW23-Mesenchymal GW23 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	4.093E-24	5.220E-22	5.728E-21	1.341E-19	49	200

2	01d707c4f8ee0daac635b7260937b1baebc6fc23	Fetal brain-organoid Tanaka cellReport-GW23-Mesenchymal-BMP responsible cell GW23 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	4.093E-24	5.220E-22	5.728E-21	1.341E-19	49	200
3	cd0d69f973ca3204b500d12031b403a1f4593431	Fetal brain-organoid Tanaka cellReport-GW26-Mesenchymal-BMP responsible cell GW26 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	1.664E-21	1.025E-19	1.125E-18	5.454E-17	46	200
4	604a88633d4162337e394155c7346dbdef8b9f5a	Fetal brain-organoid Tanaka cellReport-GW10-Mesenchymal-BMP responsible cell GW10 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	5.242E-19	1.671E-17	1.834E-16	1.718E-14	43	200
5	5c638c80661017c85f9390f1b398ac7728c8f001	Fetal brain-organoid Tanaka cellReport-GW10-Mesenchymal GW10 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	5.242E-19	1.671E-17	1.834E-16	1.718E-14	43	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	53b6a661d381b1ed3ea96e61e8bd1750de7d9fda	Lung Parenchyma-Control-Endothelial-Endothelial-Bronchial vessel Control / Location, Disease Group, Cell group, Cell class (2021.03.09)	Integration of Multiple Sampling Location of COVID-19 Patients	9.407E-21	4.765E-19	5.229E-18	3.083E-16	45	199
2	d017dd91f9b10038f1f83753a766e534da2dbe89	Lung Parenchyma-Control-Endothelial-Endothelial-Bronchial vessel- Control / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.01)	Integration of Multiple Sampling Location of COVID-19 Patients	9.407E-21	4.765E-19	5.229E-18	3.083E-16	45	199
3	64b19aff72e2a109cb5857cb248bd4712dd49b43	Lung Parenchyma-Severe-Endothelial-Endothelial-Lymphatic Severe / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.01)	Integration of Multiple Sampling Location of COVID-19 Patients	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199
4	2b9e1e069b36b3a61cc3e384f4523687b0e03905	Lung Parenchyma-Severe-Endothelial-Endothelial-Lymphatic- Severe / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.01)	Integration of Multiple Sampling Location of COVID-19 Patients	2.767E-18	7.367E-17	8.085E-16	9.069E-14	42	199
5	706b7de777f86eb22e538ccd5c2987ceb6be308	Lung Parenchyma-Control-Mesenchymal-Mesenchymal-Smooth muscle-2 Control / Location, Disease Group, Cell group, Cell class (2021.03.09)	Integration of Multiple Sampling Location of COVID-19 Patients	1.734E-17	3.721E-16	4.084E-15	5.682E-13	41	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1c6a08d01f6c1a2a4b6587d3a4522efbd03275e1	COVID-19-COVID-19 Mild-Lymphocyte-B-B intermediate COVID-19 Mild / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	6.204E-16	8.914E-15	9.782E-14	2.033E-11	39	199
2	5c0eb14bdf1bfeaf93f6c3d521529bd5a4de50ce	COVID-19-COVID-19 Mild-Myeloid-CD16+ Monocyte COVID-19 Mild / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200
3	1375d199320feb85ba06e74b10df6521e790addf	Control-Control-Myeloid-cDC Control / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200
4	f661e1737be736c62ffb04a45667a65fc3d11e2a	Sepsis-ICU-NoSEP-Myeloid-CD16+ Monocyte ICU-	Integration of immune-mediated diseases (COVID-	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200

		NoSEP / Disease, condition lineage and cell class	19 + Influenza + Sepsis + Multiple Sclerosis)						
5	1efdcfd86e99fbe03db19a2a5ab10808eec282d	Influenza-Influenza Severe-Myeloid-CD16+ Monocyte Influenza Severe / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	5cd72330c9d9bb21b6c9d5d35085eade101486d1	PBMC fresh-frozen-Severe-critical progression d12-22 no-steroids-Lymphocytic-Lymphocytic B-B cell-B c02-MS4A1-CD27 Severe-critical progression d12-22 no-steroids / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	4.148E-17	8.073E-16	8.859E-15	1.359E-12	40	194
2	a44be2f021cfdd0fcdc698c3f04d66db7a1aa6c2	PBMC fresh-frozen-Mild-Moderate progression d12-25-Lymphocytic-Lymphocytic T-mature alpha-beta T cell Mild-Moderate progression d12-25 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	4.148E-17	8.073E-16	8.859E-15	1.359E-12	40	194
3	446c61c0d6ba89c619efe87ee495951299953981	PBMC fresh-frozen-Severe-critical progression d03-09-Lymphocytic-Lymphocytic B-B cell Severe-critical progression d03-09 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	1.743E-16	2.873E-15	3.152E-14	5.713E-12	39	192
4	bbea475d2c4c7b29674ff302529f8f83dd666dcb	PBMC fresh-frozen-Severe-critical progression d03-09-Lymphocytic-Lymphocytic B-B cell-B c02-MS4A1-CD27 Severe-critical progression d03-09 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	2.098E-16	3.390E-15	3.721E-14	6.876E-12	39	193
5	0c49d22c348aec6d8a1a976e7c88d0a3b48a4244	PBMC fresh-frozen-Severe-critical progression d03-09-Lymphocytic-Lymphocytic B Severe-critical progression d03-09 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	1.771E-15	2.268E-14	2.489E-13	5.803E-11	38	195

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	2cec938caf6ffd031cea37277071487e59b2c71c	P03-Mesenchymal-myocytic cell aortic smooth muscle cell P03 / developmental time, Lineage, Cell group, Cell type, Cell type cellcyc-phase	LungMAP — Genomic, epigenomic and biophysical cues controlling the emergence of the gas exchange niche in the mouse lung	1.980E-24	2.761E-22	3.031E-21	6.489E-20	49	197
2	079db904a08743b3c555cb7b3f5fb5c978dde25a	P03-Mesenchymal-myocytic cell P03 / developmental time, Lineage, Cell group, Cell type, Cell type cellcyc-phase	LungMAP — Genomic, epigenomic and biophysical cues controlling the emergence of the gas exchange niche in the mouse lung	1.980E-24	2.761E-22	3.031E-21	6.489E-20	49	197
3	f3a54038cde58326f1caed96ecca33c141bcc8b3	P03-Epithelial-airway epithelial cell-ciliated cell of airway P03 / developmental time, Lineage, Cell group, Cell type, Cell type cellcyc-phase	LungMAP — Genomic, epigenomic and biophysical cues controlling the emergence of the gas exchange niche in the mouse lung	5.289E-24	6.566E-22	7.206E-21	1.733E-19	46	176
4	01a750d660993017af00736215cbcff2de5909c1	E17.5-Mesenchymal-myocytic cell E17.5 / developmental time,	LungMAP — Genomic, epigenomic and biophysical cues	7.299E-23	6.758E-21	7.416E-20	2.392E-18	47	195

		Lineage, Cell group, Cell type, Cell type cellcyc-phase	controlling the emergence of the gas exchange niche in the mouse lung						
5	b1135378d768fbb62a75747d1e8653d35252187	P07-Mesenchymal-myocytic cell-aortic smooth muscle cell P07 / developmental time, Lineage, Cell group, Cell type, Cell type cellcyc-phase	LungMAP — Genomic, epigenomic and biophysical cues controlling the emergence of the gas exchange niche in the mouse lung	1.163E-22	1.003E-20	1.100E-19	3.810E-18	47	197

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ea9e4f461dda34c0ebc707d7dbefc7a49ce5bb55	Posterior cortex-Hematopoietic Posterior cortex / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	3.290E-20	1.491E-18	1.637E-17	1.078E-15	42	178
2	5122fc794509492afde4af8b1b76d51e3070ef05	Posterior cortex-Hematopoietic-MICROGLIA Posterior cortex / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	2.057E-18	5.718E-17	6.275E-16	6.741E-14	40	179
3	12301d823338bf829475905c66c5f08f7159d29f	Striatum-Hematopoietic Striatum / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	2.713E-17	5.539E-16	6.079E-15	8.890E-13	36	155
4	e34ea7014c5a059a7db38f78bd903cf02616ddd3	Striatum-Neuronal-Excitatory-eN3(Slc17a7 Gad1Gad2) Striatum / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	8.201E-17	1.483E-15	1.627E-14	2.688E-12	39	188
5	7d319a112b9062efee428bef6f4534d2ce782e04	Cerebellum-Endothelial-ENDOTHELIAL STALK Cerebellum / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	1.495E-15	1.939E-14	2.128E-13	4.901E-11	35	165

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	6baa9a74560121cc008bb8fa9b2b7a335b3ae0	Neuroendocrine-neuroendo-2-Calca World / Class top	Mouse Adult Trachea	2.022E-14	1.985E-13	2.179E-12	6.627E-10	36	189
2	4b68bcb4b5fc3cd2db23cd4edace7444aa2d605c	Ionocyte-iono-1 World / Class top	Mouse Adult Trachea	1.165E-13	9.436E-13	1.036E-11	3.817E-9	33	169
3	f4d83f15ab7b49c0920a322cd832413ece7c9948	Tuft World / Class top	Mouse Adult Trachea	3.669E-13	2.630E-12	2.886E-11	1.202E-8	34	186
4	0199da3ef9ddb6673e9aa41f346f374838aec182	Neuroendocrine World / Class top	Mouse Adult Trachea	9.429E-13	6.089E-12	6.683E-11	3.090E-8	34	192
5	4584de577d3736c89187e522497498e58d381c46	Club-club-14 World / Class top	Mouse Adult Trachea	2.237E-12	1.324E-11	1.453E-10	7.333E-8	33	187

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	38a815abf0ac5cac6071737cad54a514f62d37d	fac-Limb Muscle- ForelimbandHindlimb-3m- Endothelial-endothelial cell Limb Muscle / Tongue Heart Limb Muscle Aorta Diaphragm - method, tissue, subtissue, age, lineage, cell ontology and free annotation	Mouse Aging Atlas- Tabula Muris Senis	5.904E- 29	2.804E- 26	3.077E- 25	1.935E-24	53	190
2	d180205c70b5ca9bc5a01a2e6cb42fceb7f630d	fac-Limb Muscle- ForelimbandHindlimb-3m- Endothelial-nan Limb Muscle / Tongue Heart Limb Muscle Aorta Diaphragm - method, tissue, subtissue, age, lineage, cell ontology and free annotation	Mouse Aging Atlas- Tabula Muris Senis	5.904E- 29	2.804E- 26	3.077E- 25	1.935E-24	53	190
3	bb1476b44dd49e1dd52a636a91c4600b6d4fbe2e	fac-Limb Muscle- ForelimbandHindlimb-3m-	Mouse Aging	5.904E- 29	2.804E- 26	3.077E- 25	1.935E-24	53	190

		Endothelial Limb Muscle / Tongue Heart Limb Muscle Aorta Diaphragm - method, tissue, subtissue, age, lineage, cell ontology and free annotation	Atlas- Tabula Muris Senis						
4	df8cdbc26443e55a203cbafa21b0952a2a55b9bf	facs-Lung-Endomucin -18m- Endothelial-Capillary Aerocyte endothelial cell Lung / Lung Trachea - method, tissue, subtissue, age, lineage, cell ontology and free annotation	Mouse Aging Atlas- Tabula Muris Senis	5.320E- 26	1.211E- 23	1.329E- 22	1.743E-21	50	191
5	30c75761079fa1e1a3b84d23c88a222f459d5ce5	facs-Heart-RA-18m- Endothelial Heart / Tongue Heart Limb Muscle Aorta Diaphragm - method, tissue, subtissue, age, lineage, cell ontology and free annotation	Mouse Aging Atlas- Tabula Muris Senis	1.495E- 25	3.043E- 23	3.340E- 22	4.900E-21	50	195

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	bc4a93dc5f37829799c37877e751ff3bc122e4ab	facs-Lung-18m-Hematologic-myeloid-non-classical monocyte 18m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	6.306E-27	1.829E-24	2.007E-23	2.067E-22	47	160
2	a8a7b135d86701ab9acac8273061debf8cce79a0	facs-Lung-3m-Hematologic 3m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	9.292E-26	1.977E-23	2.170E-22	3.045E-21	48	177
3	121d63b8e2e37107467b170e5b2c798a7dbf6325	facs-Lung-18m-Hematologic-myeloid-non-classical monocyte-nonclassical monocyte l4 18m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	3.237E-25	5.766E-23	6.328E-22	1.061E-20	45	158
4	52213cd2a6a20772d4f49ba9ac0407abafa528db	facs-Lung-3m-Endothelial-capillary endothelial-capillary endothelial cell-capillary aerocyte endothelial cell 3m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	3.428E-25	5.944E-23	6.523E-22	1.123E-20	49	190
5	40e617d3c93f03ae87baf6c0b2304b617f5fe782	facs-Lung-24m-Endothelial-capillary endothelial-capillary endothelial cell-capillary aerocyte endothelial cell 24m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	4.427E-25	7.365E-23	8.083E-22	1.451E-20	49	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e401f06843528a75693ce455bbeff2a98b8c24e5	HSPCs-LMPs World / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	3.142E- 23	3.130E- 21	3.435E- 20	1.030E-18	46	183
2	38f0c52de252101d4bc8633af80002061635e487	EC-Arteriolar ECs World / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	1.533E- 19	5.556E- 18	6.097E- 17	5.023E-15	43	194
3	478866dd5b0d6ff3a76d07a17c4b5989dd7a27bb	EC World / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	4.454E- 18	1.117E- 16	1.226E- 15	1.460E-13	41	192
4	f7392645d38da7285e797aa0e4625751af83ebd7	HSPCs-LMPs HSPCs / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	4.734E- 18	1.179E- 16	1.294E- 15	1.551E-13	40	183
5	e899b906409f3fad69cb3d3c6432c3fd862ae3c1	Mesenchymal cells-Ng2+ MSCs Mesenchymal cells / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	4.172E- 16	6.375E- 15	6.996E- 14	1.367E-11	38	187

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 67b59defdd1ed3608229cc5e2a3b480d92312afa	(5) Pericytes-(50) Pericytes World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	3.774E-21	2.133E-19	2.340E-18	1.237E-16	44	186
2 acbca8cc048d87faf859b3e77bdb38d0a3dad71c	(5) Pericytes World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	3.774E-21	2.133E-19	2.340E-18	1.237E-16	44	186
3 4428b472c2042f88eae028b1770767512a515b75	(4) Endothelial cells-(42) EC-sinusoidal World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	2.230E-20	1.032E-18	1.133E-17	7.309E-16	44	194
4 d00cb2fab25f2026a9668a7f0686938a2e7155e2	(3) Chondrocytes-(34) Chondro-progen World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	1.888E-19	6.689E-18	7.341E-17	6.187E-15	43	195
5 718c83046668a7c33bd8319b45c56f8edb34cf7	(4) Endothelial cells-(41) EC-arteriolar World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	5.529E-19	1.739E-17	1.908E-16	1.812E-14	42	191

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 6b5d3ecec0c00ebfc889dc6235390ff53b5c0b6a	(1) Control (PBS)-(1) VE-Cad+ vascular cells World / Stress and Cell class	Mouse Bone Marrow Niche (Tikhonova et al)	2.765E-20	1.257E-18	1.380E-17	9.063E-16	44	195
2 56ae86072858c156681507aecdd1bc6cb0a3372d2	(2) 5-FU-(4) COL2.3+ osteoblasts (2) 5-FU / Stress and Cell class	Mouse Bone Marrow Niche (Tikhonova et al)	3.130E-18	8.233E-17	9.036E-16	1.026E-13	40	181
3 4077282c45a37403f47e8d1b9ac102e6b1ba2cf9	(0) Normal/No Treatment World / Stress and Cell class	Mouse Bone Marrow Niche (Tikhonova et al)	1.334E-16	2.241E-15	2.460E-14	4.370E-12	38	181
4 e16e49b302019474232ef4cc0ff217d33afe34cf	(1) Control (PBS)-(1) VE-Cad+ vascular cells (1) Control (PBS) / Stress and Cell class	Mouse Bone Marrow Niche (Tikhonova et al)	1.743E-16	2.873E-15	3.152E-14	5.713E-12	39	192
5 6b391b8a3ffcbdec3acaf242bc52fc3fc9da77c8	(2) 5-FU-(1) VE-Cad+ vascular cells World / Stress and Cell class	Mouse Bone Marrow Niche (Tikhonova et al)	4.236E-15	4.882E-14	5.357E-13	1.388E-10	37	190

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 9af9d22a130ff97a9c37142a65e841b056d08640	(07) Brush World / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	2.122E-13	1.593E-12	1.749E-11	6.953E-9	35	193
2 2ee37155c03cd5009427a4bffe6c80ed2ac6939e	(08) PNEC World / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	3.402E-13	2.452E-12	2.691E-11	1.115E-8	35	196
3 237b9b646513ca6e4b754c0da95d24015b3661f7	(09) Ionocytes World / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	1.836E-9	5.605E-9	6.151E-8	6.018E-5	24	135
4 cb7b1945788196ca79007f0768b6576ec885a0e5	(03) Secretory World / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	9.093E-8	2.012E-7	2.208E-6	2.980E-3	25	176
5 e95d34170f5053678e0dd9793e68d93c03b05822	(08) PNEC-(2) 48hpi (08) PNEC / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	1.120E-7	2.457E-7	2.696E-6	3.670E-3	22	142

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 e044b3428b7eacfdc72d0f57cdabaa1de04c74cd	E16.5-samps-Mesenchymal-Myofibroblast E16.5-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	8.275E-24	9.862E-22	1.082E-20	2.712E-19	47	186

2	427176ad9ab8d9511200fb0a132cfd1e835fe35c	PND07-28-samps-Mesenchymal-Myofibroblast-myofibroblast - mature - C PND07-28-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	2.193E-20	1.027E-18	1.127E-17	7.186E-16	43	185
3	60d3fe1f5cec4285b8774ff078ebcc6bfaec26ed	E18.5-samps-Myeloid-Macrophage-macrophage - intermediate - unactivated E18.5-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	4.399E-20	1.872E-18	2.055E-17	1.442E-15	40	162
4	18e4a807e25f754a69e9eaaddfde40f8de9b8512	E18.5-samps-Myeloid E18.5-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	4.399E-20	1.872E-18	2.055E-17	1.442E-15	40	162
5	0970e4eda60e3f015335e2726e6d565fb2f43372	E18.5-samps-Myeloid-Macrophage E18.5-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	4.399E-20	1.872E-18	2.055E-17	1.442E-15	40	162

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9790340c25f446ec655f5a0b64ec3bb44ed2e1bd	PND03-Epithelial-Epithelial Alveolar-Epithelial Alveolar-AT1-AT1 mature PND03 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	9.220E-23	8.233E-21	9.035E-20	3.022E-18	47	196
2	b9ceceeeacbcf81976ce92adf044f0d0aa132632b	PND03-Epithelial-Epithelial Alveolar-Epithelial Alveolar-AT1 PND03 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	9.220E-23	8.233E-21	9.035E-20	3.022E-18	47	196
3	090a251194da3e2806989d9a522588f83f52da7f	PND03-Mesenchymal-Mesenchymal myocytic-Myofibroblast airway-SCMF PND03 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	8.543E-22	5.809E-20	6.375E-19	2.800E-17	46	197
4	490745024730df6357f6c2b81d7a64e21557c0d5	PND10-Endothelial-Endothelial blood-vessel-Microvascular EC-CAP2-CAP2 prolif PND10 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	1.043E-21	6.947E-20	7.624E-19	3.418E-17	43	172
5	9d7b631f24a19a7dc7a28f28525d4019fc8fc8a	PND01-Mesenchymal-Mesenchymal myocytic-Myofibroblast airway PND01 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	4.903E-21	2.705E-19	2.969E-18	1.607E-16	45	196

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	87c1f52ab19b105bae3f315496c620c226a77a7f	IIF-Myeloid-CD16 Mono IIF / Disease, Lineage and Cell Type	Multiple Sclerosis	7.355E-12	3.821E-11	4.193E-10	2.410E-7	33	195

2	2e480dde7ecb2f88ff005f86ef732a1cf0209d45	Multiple Sclerosis-Other-Platelet Multiple Sclerosis / Disease, Lineage and Cell Type	Multiple Sclerosis	8.340E-12	4.303E-11	4.722E-10	2.733E-7	32	185
3	fa53f1aab2f5923e90f090e10e3560b583441dc4	Multiple Sclerosis-Lymphocyte-T NK-CD8 TEM Multiple Sclerosis / Disease, Lineage and Cell Type	Multiple Sclerosis	3.050E-11	1.376E-10	1.511E-9	9.997E-7	32	194
4	83011b56780295dff5ded57064b07dcd2f19ea26	Multiple Sclerosis-Myeloid-CD16 Mono Multiple Sclerosis / Disease, Lineage and Cell Type	Multiple Sclerosis	4.023E-11	1.773E-10	1.945E-9	1.318E-6	32	196
5	529c0d2159e539546876246122f2e999170a6b20	IIF-Other-Platelet IIF / Disease, Lineage and Cell Type	Multiple Sclerosis	6.786E-9	1.853E-8	2.034E-7	2.224E-4	27	178

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	256c557fa11414c9d2cbb1fcff33f482ee1c78ac	COVID-19 Moderate-Non-classical Monocyte COVID-19 Moderate / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	6.462E-14	5.630E-13	6.178E-12	2.118E-9	36	196
2	af9e8f5ef9d03862f707e105857309b55595b1b9	COVID-19 Severe-Non-classical Monocyte COVID-19 Severe / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	6.462E-14	5.630E-13	6.178E-12	2.118E-9	36	196
3	60fee75b12451206bb2c07b61651a73c59ec6ade	COVID-19 Severe-Non-classical Monocyte World / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197
4	5f94310f1470487816fce697ffcdc2627fc66878	COVID-19 Moderate-CD4+ Tcm World / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	1.809E-13	1.381E-12	1.515E-11	5.927E-9	35	192
5	394e5fa8998c46c6f7cd57b53f347d2029c75ae1	Healthy-Non-classical Monocyte Healthy / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	4.634E-13	3.233E-12	3.549E-11	1.519E-8	35	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	049d995986c20ce066bd64fcc2d2f1c2f8899883	remission-Non-classical Monocyte remission / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	1.730E-12	1.053E-11	1.156E-10	5.669E-8	34	196
2	1c170655070acca00520b7cf9c510a04c0a90a8f	remission-Non-classical Monocyte World / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	1.129E-11	5.632E-11	6.180E-10	3.701E-7	33	198
3	f1e4b8fcb422727f665f22b48f34bee23f0fad52	remission-CD8+ Tem remission / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	6.916E-11	2.856E-10	3.135E-9	2.266E-6	32	200
4	8f59e51ca50bef4753f67cd1efdb02665805a120	severe-B intermediate severe / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	1.837E-10	6.985E-10	7.666E-9	6.020E-6	31	196
5	78556b60c84c7bbffa1c8bf8684b3c427512da44	remission-B intermediate World / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	6.274E-10	2.120E-9	2.327E-8	2.056E-5	30	194

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	f1b370d2869ad29c9d8ff41fdcc486ffa781ee2	control-HLA-DR+ CD83+ Monocyte control / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	1.053E-16	1.831E-15	2.009E-14	3.452E-12	40	199
2	9e3e13a68bc1110fa000ec2d80f4c654ddbce17e	control-HLA-DR- S100A+ Monocyte control / Cohort 1 (10x PBMC) with disease	PBMC Atlas of COVID-19 Patients	1.264E-16	2.131E-15	2.338E-14	4.144E-12	40	200

		condition, cell group and cell class	(Schulte-Schrepping et al.)						
3	4a6d17a4225be38537d3dd8a39512051f597f4e0	control-cDC control / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	4.196E-15	4.875E-14	5.350E-13	1.375E-10	38	200
4	6cc7190a4ffc6c06335072f3b5b5f98eae36e2ce	severe-Non-classical Monocyte severe / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	1.224E-13	9.678E-13	1.062E-11	4.011E-9	36	200
5	692b48da9fd56bafcb3c8b33b0fe369160881c45	mild-Non-classical Monocyte mild / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	1.224E-13	9.678E-13	1.062E-11	4.011E-9	36	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	69330689b6e353c8ee9ea1b63a5eac6ab38d456f	mild COVID-19-Treg World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	8.165E-14	6.904E-13	7.577E-12	2.676E-9	33	167
2	790ee20abc9666b8095675b0d445c0914ee70ea3	severe influenza-Non-classical Monocyte World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	8.913E-14	7.442E-13	8.167E-12	2.921E-9	36	198
3	7630e223666fb65743e21e045478f687dd739a54	severe influenza-Non-classical Monocyte severe influenza / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	1.280E-12	8.036E-12	8.819E-11	4.195E-8	34	194
4	72928a1d987a3a5361c666f3972292aefec5f548	severe COVID-19-Non-classical Monocyte World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	1.489E-12	9.215E-12	1.011E-10	4.879E-8	34	195
5	eb809331557f8c40de45b1208cbc49b621930a4b	mild COVID-19 (asymptomatic)-Non-classical Monocyte World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	1.489E-12	9.215E-12	1.011E-10	4.879E-8	34	195

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	621af09aae34226902c03edf556562f3ab35a7d8	COVID vent-Myeloid COVID vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	4.196E-15	4.875E-14	5.350E-13	1.375E-10	38	200
2	b0a5bee87700ce38f26f95a6f491da7e27cade51	COVID vent-Myeloid-Monocytic COVID vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200
3	63a5cdd3f60681762a218be32db84be8f29b88fd	COVID vent-Myeloid-Dendritic COVID vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	6.771E-14	5.858E-13	6.429E-12	2.219E-9	35	186
4	39457a7b43537f2c3e221f9375c95d4515424d7d	COVID vent-Myeloid-Dendritic-cDC COVID vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	6.771E-14	5.858E-13	6.429E-12	2.219E-9	35	186
5	836061acd7f0d5de89b16f52ec679bdf09eac9db	COVID non-vent-Lymphocytic-T cell-CD8+ Memory T cell COVID non-vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	7.593E-14	6.474E-13	7.105E-12	2.489E-9	36	197

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
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1	4235005c49fc2b29ad3a0ee6b608f0109d04f775	Epithelial cells-Basal cells Epithelial cells / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	1.950E-23	2.109E-21	2.315E-20	6.390E-19	48	198
2	c2ebc0b33bda9b35b9ef26d69e5d2c6acfdb6ff1	Fibroblasts-Pericytes Fibroblasts / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	1.251E-18	3.686E-17	4.046E-16	4.099E-14	42	195
3	3b66f3a79b3f2ebacb4ad646f179e505ab38d6f0	Basal cells-Myositis-ILD 01 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	1.529E-18	4.391E-17	4.819E-16	5.010E-14	42	196
4	febe0b99a6a815ce687160a0e7af55228b1d5beb	Endothelial-A-SSc-ILD 02 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	6.769E-17	1.251E-15	1.373E-14	2.218E-12	39	187
5	24360b66000bdfb999d58bf4e29585a97e1785	Basal cells World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	7.284E-17	1.336E-15	1.466E-14	2.387E-12	40	197

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	45df8fee00f8949937863159d7aa042e72748d9b	PretermPrimateLungAtlas	4.090E-26	9.507E-24	1.043E-22	1.340E-21	50	190
2	327ff3ac8d2fecdd5d242bdc34f0dfdb1c59a68b	PretermPrimateLungAtlas	6.047E-25	9.528E-23	1.046E-21	1.982E-20	48	184
3	89b706af2b25991fc2707eb24f49ba6ff3ae01f7	PretermPrimateLungAtlas	9.436E-25	1.445E-22	1.586E-21	3.093E-20	49	194
4	4780af76237d7af2abbe2d8d5530cdf53e3ed0b7	PretermPrimateLungAtlas	1.015E-24	1.540E-22	1.690E-21	3.325E-20	48	186
5	9af14a056eb6d88c6f11b09f6d4c0d3448d647d5	PretermPrimateLungAtlas	6.862E-24	8.360E-22	9.175E-21	2.249E-19	46	177

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
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1	f304d42fc4936fe20996e07c8dccc698a6e5e5ef	IPF-Stromal-Myofibroblast Stromal / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	5.786E-34	1.264E-30	1.387E-29	1.896E-29	59	197
2	62904f94dfce430456f05066522cbf9bd29f4d7e	COPD-Stromal-Myofibroblast Stromal / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	1.237E-31	1.622E-28	1.780E-27	4.055E-27	56	192
3	d84ed1ea4a03edaa18c804f75afb03bd7b1f0e16	Control-Epithelial-Club Control / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	6.907E-26	1.529E-23	1.678E-22	2.264E-21	50	192
4	5896242f713ae5f1a4ebb63827f15d7279dced2	Control-Stromal-Myofibroblast Stromal / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	8.950E-26	1.943E-23	2.132E-22	2.933E-21	50	193
5	9798428691408e17ff2af2fe2d1b345f074d67e4	Control-Epithelial-Club World / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	1.015E-24	1.540E-22	1.690E-21	3.325E-20	48	186

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	c6729a207526ff4aa48176207b9353176f631fea	Basal World / shred by cell class for mouse tongue	Respiratory Tissues from Nasal Brushing to Parenchyma	3.097E-17	6.223E-16	6.830E-15	1.015E-12	39	183
2	f0e46e859f7a9bdead3203889f7e20fa21f76ff0	Endothelial World / shred by cell class for bronchial biopsy	Respiratory Tissues from Nasal Brushing to Parenchyma	5.011E-17	9.498E-16	1.042E-14	1.642E-12	40	195
3	1526a130565a97c291a25a7a988089bffc1515c1	FF-Differ-KC World / shred by cell class for mouse tongue	Respiratory Tissues from Nasal Brushing to Parenchyma	9.013E-17	1.611E-15	1.768E-14	2.954E-12	38	179
4	07530bbeffd5951880ed6ea50a962c102b05ccc2	T cell World / shred by cell class for nasal brushing	Respiratory Tissues from Nasal Brushing to Parenchyma	7.130E-15	7.886E-14	8.655E-13	2.337E-10	37	193
5	dec9ce1bc2571197003596f32e5f742ede72aa79	Fibroblast World / shred by cell class for parenchyma	Respiratory Tissues from Nasal Brushing to Parenchyma	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	b4088128f5acf53f43244c9af9fe44e033f1a57a	Fibroblasts-CD55+ Fibroblasts Fibroblasts / Immune cells in Rheumatoid Arthritis Joint Synovial Tissues	Rheumatoid Arthritis and Lupus Nephritis Atlas	6.558E-20	2.663E-18	2.923E-17	2.149E-15	43	190
2	5e12201ce7ba912e7faa123ca200e609252ba288	Monocytes-NUPR1+ Monocytes World / Immune cells in Rheumatoid Arthritis Joint Synovial Tissues	Rheumatoid Arthritis and Lupus Nephritis Atlas	1.888E-19	6.689E-18	7.341E-17	6.187E-15	43	195
3	2de34e20915a247bee75aa40495e23c20bb23e18	T cells-CTLs World / Immune cells in Kidney/Urine in Lupus Nephritis	Rheumatoid Arthritis and Lupus Nephritis Atlas	1.866E-18	5.248E-17	5.760E-16	6.114E-14	42	197
4	24d64b67aa9b0e8215ad06f9101c1314b3483620	Fibroblasts-DKK3+ Fibroblasts Fibroblasts / Immune cells in Rheumatoid Arthritis Joint Synovial Tissues	Rheumatoid Arthritis and Lupus Nephritis Atlas	9.762E-18	2.244E-16	2.462E-15	3.199E-13	41	196
5	e2ae43e5ec31de6197f2cbd6089f944adb0a163	T cells-TFH-like cells T cells / Immune cells in Kidney/Urine in Lupus Nephritis	Rheumatoid Arthritis and Lupus Nephritis Atlas	1.127E-17	2.567E-16	2.818E-15	3.695E-13	39	178

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	a549aa08aeefe905653266dae3936094ff55f8e4	Calu 3 World / Cell line, Condition and Strain	SARS-CoV-2 Infected Human Cell Lines	2.304E-14	2.206E-13	2.421E-12	7.550E-10	37	200
2	8f7f5000645f24f20a8d7700c4df1f8953a1780b	Calu 3-infected Calu 3 / Cell line, Condition and Strain	SARS-CoV-2 Infected Human Cell Lines	7.264E-7	1.398E-6	1.534E-5	2.381E-2	24	183
3	a689d5955ecf10bf88c886197d4f7bf9be6c586	Calu 3-infected-SARSCoV1 infected / Cell line, Condition and Strain	SARS-CoV-2 Infected Human Cell Lines	5.592E-3	6.586E-3	7.228E-2	1.000E0	16	188

4	f7bfeefc0f30f81710a5ddd979f19b0c910c4a42	H1299-infected-SARSCoV1 infected / Cell line, Condition and Strain	SARS-CoV-2 Infected Human Cell Lines	6.178E-3	7.252E-3	7.959E-2	1.000E0	16	190
5	2da876d26f37a00dbdf1ee79d724306e8b20f304	Calu 3-infected-SARSCoV2 infected / Cell line, Condition and Strain	SARS-CoV-2 Infected Human Cell Lines	6.490E-3	7.604E-3	8.345E-2	1.000E0	16	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	b15abb1c5396d038bab92b048795020199370f44	ICU-NoSEP-Myeloid-CD16 Mono ICU-NoSEP / Disease, Lineage and Cell Type	Sepsis Atlas	1.187E-14	1.248E-13	1.370E-12	3.890E-10	37	196
2	c5056605e1a61d165adba9cbee53b7cc0d41ec98	Bac-SEP-Myeloid-CD16 Mono Bac-SEP / Disease, Lineage and Cell Type	Sepsis Atlas	3.972E-13	2.811E-12	3.085E-11	1.302E-8	35	197
3	3e6f262ec71e99a5dadbaaeaff1b4f1894907c7d	ICU-SEP-Myeloid-CD16 Mono ICU-SEP / Disease, Lineage and Cell Type	Sepsis Atlas	4.634E-13	3.233E-12	3.549E-11	1.519E-8	35	198
4	a37e75be248ff28f6647e4e690629f82c1fb7370	Control-Myeloid-CD16 Mono Control / Disease, Lineage and Cell Type	Sepsis Atlas	1.489E-12	9.215E-12	1.011E-10	4.879E-8	34	195
5	142b7db0c2b686c8f2704ff7bcd9b44dfcb07403	URO-Lymphocyte-T NK-CD8 Naive URO / Disease, Lineage and Cell Type	Sepsis Atlas	2.943E-10	1.067E-9	1.170E-8	9.644E-6	25	134

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	741d79c10cb87fa7f14080c6fccb1553c3a20bad	primary visual cortex-Neuronal-GABAergic neuron-Sst-Sst Myh8 Fbin primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	1.279E-20	6.236E-19	6.844E-18	4.191E-16	40	157
2	f59ca572556c17c606604da1b0331710d4751e54	primary visual cortex-Non-neuronal-macrophage-Macrophage-Microglia Siglech primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	6.239E-20	2.582E-18	2.833E-17	2.045E-15	39	155
3	60a8a8584d3c80c4ceb433cb820de914e33e3500	primary visual cortex-Non-neuronal-macrophage primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	7.988E-20	3.137E-18	3.443E-17	2.618E-15	39	156
4	4b6b59a1638a7218a9ed9bd702c04d9f51dbc7aa	primary visual cortex-Non-neuronal-macrophage-Macrophage primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	7.988E-20	3.137E-18	3.443E-17	2.618E-15	39	156
5	cbe9b4c4b2e42e9f92a57ed66758af93434db5bb	frontal cortex-Non-neuronal-macrophage-Macrophage frontal cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	4.252E-19	1.410E-17	1.548E-16	1.394E-14	39	163

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	d91bd26e499637949768587603cad3c03dcc56e7	normal-na-Myeloid-non-classical monocyte-female normal / PBMC cell types (v2) per disease, treatment status, and sex	Single-cell RNA-seq reveals the cell-type-specific molecular and genetic associations to lupus	2.274E-18	6.225E-17	6.832E-16	7.451E-14	42	198
2	f5a12861e2b8ff8309f3e4d0ad83d4f6860cc616	normal-na-Myeloid-non-classical monocyte normal / PBMC cell types (v2) per disease, treatment status, and sex	Single-cell RNA-seq reveals the cell-type-specific molecular and genetic	2.274E-18	6.225E-17	6.832E-16	7.451E-14	42	198

			associations to lupus						
3	053adc7ed9f997b503e12239a684bb9f5896e10c	normal-na-Myeloid-non-classical monocyte-male normal / PBMC cell types (v2) per disease, treatment status, and sex	Single-cell RNA-seq reveals the cell-type-specific molecular and genetic associations to lupus	7.130E-15	7.886E-14	8.655E-13	2.337E-10	37	193
4	8de49c62ab533031936db4cee50ff13b259ecc22	systemic lupus erythematosus-managed-Myeloid-non-classical monocyte-female systemic lupus erythematosus / PBMC cell types (v2) per disease, treatment status, and sex	Single-cell RNA-seq reveals the cell-type-specific molecular and genetic associations to lupus	4.634E-13	3.233E-12	3.549E-11	1.519E-8	35	198
5	60e5bd8dfe27c43ce5f4da19b65270c41577ef4f	systemic lupus erythematosus-managed-Myeloid-non-classical monocyte systemic lupus erythematosus / PBMC cell types (v2) per disease, treatment status, and sex	Single-cell RNA-seq reveals the cell-type-specific molecular and genetic associations to lupus	4.634E-13	3.233E-12	3.549E-11	1.519E-8	35	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1e6526fc9e9381b7ace864588cc7bd80194338d6	TCGA-Kidney-Primary Tumor-Renal Cell Carcinoma-Kidney Clear Cell Renal Carcinoma-2 TCGA-Kidney / Sample Type by Project: Shred V9	TCGA OncoMap	1.316E-18	3.861E-17	4.237E-16	4.312E-14	41	186
2	5562665dd3beb70e2358aa32611a337bef5731c1	TCGA-Prostate-Primary Tumor-Prostate Adenocarcinoma-Acinar Adenocarcinoma-4 TCGA-Prostate / Sample Type by Project: Shred V9	TCGA OncoMap	3.027E-16	4.762E-15	5.226E-14	9.919E-12	39	195
3	55b97095a7a17a312c616703d291738a0f806339	TCGA-Head and Esophagus-Primary Tumor-Head and Neck Carcinoma-Squamous Cell Carcinoma-8 TCGA-Head and Esophagus / Sample Type by Project: Shred V9	TCGA OncoMap	1.485E-15	1.931E-14	2.119E-13	4.865E-11	38	194
4	194e7fa00a50cc4e026987b715323d125d79594e	TCGA-Colorectal-Primary Tumor-Colorectal Adenocarcinoma-Colon Adenocarcinoma-10 TCGA-Colorectal / Sample Type by Project: Shred V9	TCGA OncoMap	3.956E-14	3.609E-13	3.961E-12	1.296E-9	36	193
5	a96495803ba13fcadd1d83b3cf5774f3fed0a20	TCGA-Breast-Primary Tumor-Breast Carcinoma-Infiltrating Ductal Carcinoma-6 TCGA-Breast / Sample Type by Project: Shred V9	TCGA OncoMap	8.000E-14	6.770E-13	7.429E-12	2.622E-9	35	187

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	49441ca0a8fa34cb847fecbb4b809dd01d879ebb	3'-Broncho-tracheal-Immune Myeloid-Myeloid monocytic-non-classical monocyte-Non-classical monocytes 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	4.326E-22	3.229E-20	3.544E-19	1.418E-17	46	194
2	16c6fcbd36d473b883fb5361caca86eb134767ab	3'-Broncho-tracheal-Immune Myeloid-Myeloid monocytic-non-classical monocyte-Non-classical monocytes-Non-classical monocytes L.1.2.2.0 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	4.326E-22	3.229E-20	3.544E-19	1.418E-17	46	194
3	de9c7c602d886d0cd8bbd1d7e7744f84df951238	3'-Broncho-tracheal-Immune Myeloid-Myeloid monocytic-non-classical monocyte 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	4.326E-22	3.229E-20	3.544E-19	1.418E-17	46	194
4	d5c22b43531414951666ee7542a66ed9380e2d14	5'-Parenchyma lung-Immune Myeloid-Myeloid macrophage-alveolar macrophage-Alveolar	The Integrated	9.711E-20	3.727E-18	4.090E-17	3.183E-15	41	174

		macrophages-Alveolar macrophages L.1.0.5.0 5' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	Human Lung Cell Atlas						
5	71ee440b1ac566db63d0b415c50a0ad064d14f15	3'-Parenchyma lung-Endothelial-Blood vessel EC-vein endothelial cell 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	2.274E-18	6.225E-17	6.832E-16	7.451E-14	42	198

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	d9eec28fa7b255c0ec023276dd955f1e276e7159	368C-Fibroblasts-Fibroblast-G- Fibroblasts / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	3.151E-21	1.793E-19	1.968E-18	1.033E-16	45	194
2	e4d7e9709ce42d4610e44d3445927eefbcb9eff	368C-Fibroblasts-Fibroblast-G Fibroblasts / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	3.151E-21	1.793E-19	1.968E-18	1.033E-16	45	194
3	6730743cf088c419ccc2d28765769fc09d3ba6a7	367C-Fibroblasts-Fibroblast-C (Myofibroblast)- Fibroblasts / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	3.424E-20	1.516E-18	1.664E-17	1.122E-15	44	196
4	21dab89f3699037138a9c7a0e4dc98739a9fad9c	367C-Fibroblasts-Fibroblast-C (Myofibroblast) Fibroblasts / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	3.424E-20	1.516E-18	1.664E-17	1.122E-15	44	196
5	a21a710c824f9e5c7ef1674168d1ce5aef85bd35	(5) Fibroblasts-(5) Fibroblast-G (5) Fibroblasts / Lung cell shreds - cell class (v4) and cell subclass (v4)	Tissue Stability Cell Atlas - Lung Cells	2.852E-19	9.871E-18	1.083E-16	9.348E-15	43	197

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ba289658777a2669fda9da9128e87adb60fd8430	(0) T CD4 World / Oesophagus cell shreds on cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Oesophagus Cells	5.045E-15	5.753E-14	6.314E-13	1.653E-10	37	191
2	6b3afc2ae870ff73e30a60ce84fcee0eb365d809	(4) Lymph vessel World / Oesophagus cell shreds on cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Oesophagus Cells	1.207E-14	1.260E-13	1.383E-12	3.955E-10	36	186
3	59b87beec2b12ad0a35d86f911423e3a0a3f4701	(0) T CD8 World / Oesophagus cell shreds on cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Oesophagus Cells	2.835E-14	2.671E-13	2.931E-12	9.292E-10	36	191
4	f0818821c495022569aef2c1886d9f2446dc027e	(6) Stroma World / Oesophagus cell shreds on cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Oesophagus Cells	6.286E-13	4.191E-12	4.599E-11	2.060E-8	35	200
5	f9baef67dde62f1c161a9408a78f635ea70ea9d3	(6) Stroma World / Oesophagus cell shreds on cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Oesophagus Cells	6.286E-13	4.191E-12	4.599E-11	2.060E-8	35	200

Show 32 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	713991025bb92d38cb0507ff01fd91b48c8af45a	(0) NK CD160pos World / Spleen cell shreds - cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Spleen Cells	3.033E-12	1.735E-11	1.904E-10	9.939E-8	33	189
2	de7cb273899d0e0748c85f45c6b5e7f0642ab057	(6) ILC World / Spleen cell shreds - cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Spleen Cells	1.297E-11	6.385E-11	7.007E-10	4.252E-7	32	188
3	f4734d5b703678670ece204a0519cf015e180a6e	(6) ILC World / Spleen cell shreds - cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Spleen Cells	1.297E-11	6.385E-11	7.007E-10	4.252E-7	32	188

4	28f28672fd260bb2a8d64152737a7242347c3174	(1) T CD4 reg World / Spleen cell shreds - cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Spleen Cells	1.500E-11	7.154E-11	7.851E-10	4.916E-7	32	189
5	6cbeceb52bb207f3c074e57b5b3f7cfb24fd5877	(0) NK cells-(0) NK CD160pos (0) NK cells / Spleen cell shreds - cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Spleen Cells	3.505E-11	1.563E-10	1.715E-9	1.149E-6	32	195

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	5d1b674eb7703830b7ce8bbeac3363cabd0e6ae9	LA-03. Atrial Cardiomyocyte LA / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	7.817E-36	2.562E-32	2.811E-31	2.562E-31	60	191
2	c3535f7cc0076653c72db582047cff053c322397	RA-03. Atrial Cardiomyocyte RA / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	2.115E-35	5.776E-32	6.339E-31	6.931E-31	60	194
3	89812fb164065041357bb37a3c2d87028ec3de4e	RA-03. Atrial Cardiomyocyte World / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	2.297E-33	4.429E-30	4.861E-29	7.529E-29	58	194
4	d4bf89437216baf489ea0239136dcedf3b6714af	LA World / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	1.674E-31	2.031E-28	2.229E-27	5.485E-27	56	193
5	e7a0bc46ba9ba772636a583f3387748418e18832	LV-08. Macrophage World / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	8.906E-31	9.729E-28	1.068E-26	2.919E-26	55	191

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	4b9b55154a79992112c1c467e8752c3cdbb541d9	NS-control-d 0-4-Lymphoid-B cell d 0-4 / Location, Severity, dps group, Lineage and Cell class of Upper airway (combined)	Upper Airway and Bronchi Atlas of COVID-19 Patients	2.450E-23	2.617E-21	2.872E-20	8.029E-19	46	182
2	e414303bb90e5fe7b667c2acf9a50f8694b90e54	control-Lymphoid-B cell control / Severity, Lineage and Cell class of Nasopharyngeal (NS) Samples from Patients and Controls	Upper Airway and Bronchi Atlas of COVID-19 Patients	6.464E-20	2.655E-18	2.913E-17	2.118E-15	42	181
3	a5284adca931a78b1c4592925c4860853ebd24f1	control-Lymphoid-B cell Lymphoid / Severity, Lineage and Cell class of Nasopharyngeal (NS) Samples from Patients and Controls	Upper Airway and Bronchi Atlas of COVID-19 Patients	1.533E-19	5.556E-18	6.097E-17	5.023E-15	43	194
4	22a19365782003c18ec8dddcdbfdaa82c4e330f6	moderate-Lymphoid-NK Lymphoid / Severity, Lineage and Cell class of Nasopharyngeal (NS) Samples from Patients and Controls	Upper Airway and Bronchi Atlas of COVID-19 Patients	1.580E-17	3.440E-16	3.776E-15	5.178E-13	40	189
5	05a2c3549b68f49081723bf35db14974274419d5	critical-Epithelial-Ionocyte Epithelial / Severity, Lineage and Cell class of Nasopharyngeal (NS) Samples from Patients and Controls	Upper Airway and Bronchi Atlas of COVID-19 Patients	1.922E-17	4.068E-16	4.465E-15	6.298E-13	40	190

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	f8d7bd81e031d09a557722627c2f6180811cc6ab	Endothelial-Endothelial-B Endothelial / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	2.013E-21	1.211E-19	1.329E-18	6.598E-17	45	192
2	a8d6416518f226e1ec2d6bdc9d4b90cef5cb1365	Fibroblast-B (Myofibroblast) World / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	2.765E-20	1.257E-18	1.380E-17	9.063E-16	44	195
3	38ea0eaf42f95c321ca23570d0d7752980cf00f8	MatrixFB-Fibroblast-B (Myofibroblast) MatrixFB / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	3.424E-20	1.516E-18	1.664E-17	1.122E-15	44	196
4	484bbc6b1f58bc260964babb949d14f5df101393	Epithelial-A (AT1) World / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	1.529E-18	4.391E-17	4.819E-16	5.010E-14	42	196

5	2777eb7689b271c199021fe7d9db88ccebff14de	Endothelial-Endothelial-E Endothelial / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	1.987E-18	5.534E-17	6.073E-16	6.513E-14	41	188
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Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	8a3039de45b8087f8319e2e37329acf7278219b7	lung-Type II Pneumocytes lung / shred on tissue and cell subclass	scRNA-seq of ileum and lung epithelial cells in macaque.	2.214E-9	6.664E-9	7.314E-8	7.256E-5	25	147
2	a8ed48cbd1e207fd1aaad454da9f329eb22aa83	ileum-Epithelial Stem Cells ileum / shred on tissue and cell subclass	scRNA-seq of ileum and lung epithelial cells in macaque.	2.330E-9	6.998E-9	7.680E-8	7.637E-5	23	126
3	6023212a51f8b3e05e6c3dcf4e8bf53ba696fb2	lung-Type I Pneumocytes lung / shred on tissue and cell subclass	scRNA-seq of ileum and lung epithelial cells in macaque.	6.943E-6	1.150E-5	1.262E-4	2.275E-1	14	82
4	9f1211bd4287620e19a59f21e6ecdca3e42e0260	ileum World / shred on tissue and cell subclass	scRNA-seq of ileum and lung epithelial cells in macaque.	9.046E-6	1.475E-5	1.618E-4	2.965E-1	21	170
5	b12cacd499b18b96120ca6d14646aebeaed41d10	lung-Club Cells lung / shred on tissue and cell subclass	scRNA-seq of ileum and lung epithelial cells in macaque.	1.772E-5	2.772E-5	3.043E-4	5.806E-1	20	164

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16: Computational [Display Chart] 1174 input genes in category / 951 annotations before applied cutoff / 10746 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GAVISH 3CA METAPROGRAM ENDOTHELIAL ENDO 1	Genes upregulated in subsets of cells of a given type within various tumors	C4:3CA: Curated Cancer Cell Atlas gene sets	6.801E-4	4.975E-2	3.699E-1	6.467E-1	14	50

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation	
1	MODULE 38	Placenta genes.	C4:CM: Cancer Modules	1.008E-7	9.589E-5	7.129E-4	9.589E-5	88	463
2	MODULE 100	Genes in the cancer module 100.	C4:CM: Cancer Modules	2.952E-6	9.890E-4	7.353E-3	2.807E-3	94	543
3	MODULE 66	Genes in the cancer module 66.	C4:CM: Cancer Modules	3.120E-6	9.890E-4	7.353E-3	2.967E-3	95	551
4	MODULE 137	CNS genes.	C4:CM: Cancer Modules	6.186E-6	1.273E-3	9.468E-3	5.883E-3	93	545
5	MODULE 11	Genes in the cancer module 11.	C4:CM: Cancer Modules	6.875E-6	1.273E-3	9.468E-3	6.538E-3	92	539

Show 7 more annotations

17: MicroRNA [Display Chart] 1873 input genes in category / 8193 annotations before applied cutoff / 57445 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ACCAAAG,MIR-9:MSigDB	ACCAAAG,MIR-9:MSigDB	MSigDB	6.712E-30	4.688E-29	4.495E-28	5.499E-26	75	471
2	TGTTTAC,MIR-30B:MSigDB	TGTTTAC,MIR-30B:MSigDB	MSigDB	1.714E-29	1.150E-28	1.103E-27	1.404E-25	80	542
3	TGTTTAC,MIR-30C:MSigDB	TGTTTAC,MIR-30C:MSigDB	MSigDB	1.714E-29	1.150E-28	1.103E-27	1.404E-25	80	542
4	TGTTTAC,MIR-30E-5P:MSigDB	TGTTTAC,MIR-30E-5P:MSigDB	MSigDB	1.714E-29	1.150E-28	1.103E-27	1.404E-25	80	542
5	TGTTTAC,MIR-30A-5P:MSigDB	TGTTTAC,MIR-30A-5P:MSigDB	MSigDB	1.714E-29	1.150E-28	1.103E-27	1.404E-25	80	542

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-670:mirSVR lowEffct	hsa-miR-670:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	2.276E- 71	3.107E- 68	2.979E- 67	1.864E-67	225	1734
2	hsa-miR-484:mirSVR lowEffct	hsa-miR-484:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	3.371E- 70	3.452E- 67	3.310E- 66	2.762E-66	230	1833
3	hsa-miR-1266:mirSVR lowEffct	hsa-miR-1266:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	6.715E- 69	6.113E- 66	5.861E- 65	5.501E-65	239	1999
4	hsa-miR-3155:mirSVR lowEffct	hsa-miR-3155:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	7.072E- 68	5.794E- 65	5.556E- 64	5.794E-64	236	1977
5	hsa-miR-148a*:mirSVR lowEffct	hsa-miR-148a*:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	2.224E- 67	1.519E- 64	1.456E- 63	1.822E-63	234	1958

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-4728-5p	MirDB	7.883E-80	6.458E-76	6.193E-75	6.458E-76	223	1540
2	hsa-miR-520d-5p	MirDB	4.286E-76	1.756E-72	1.683E-71	3.511E-72	241	1868
3	hsa-miR-524-5p	MirDB	1.263E-75	3.448E-72	3.306E-71	1.035E-71	241	1878
4	hsa-miR-6785-5p	MirDB	8.715E-73	1.785E-69	1.712E-68	7.141E-69	203	1397
5	hsa-miR-8485	MirDB	1.622E-72	2.657E-69	2.548E-68	1.329E-68	227	1739

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-590-3p:PITA	hsa-miR-590-3p:PITA TOP	PITA	4.652E-44	1.086E-42	1.041E-41	3.811E-40	166	1476
2	hsa-miR-30a:PITA	hsa-miR-30a:PITA TOP	PITA	3.839E-41	6.526E-40	6.257E-39	3.146E-37	120	861
3	hsa-miR-30c:PITA	hsa-miR-30c:PITA TOP	PITA	3.839E-41	6.526E-40	6.257E-39	3.146E-37	120	861
4	hsa-miR-30d:PITA	hsa-miR-30d:PITA TOP	PITA	3.839E-41	6.526E-40	6.257E-39	3.146E-37	120	861
5	hsa-miR-30b:PITA	hsa-miR-30b:PITA TOP	PITA	3.839E-41	6.526E-40	6.257E-39	3.146E-37	120	861

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-325-3p:TargetScan	hsa-miR-325-3p	TargetScan	3.730E-61	1.019E-58	9.766E-58	3.056E-57	209	1722
2	hsa-miR-30a-5p:TargetScan	hsa-miR-30a-5p	TargetScan	2.401E-59	4.014E-57	3.849E-56	1.967E-55	166	1143
3	hsa-miR-30c-5p:TargetScan	hsa-miR-30c-5p	TargetScan	2.401E-59	4.014E-57	3.849E-56	1.967E-55	166	1143
4	hsa-miR-30e-5p:TargetScan	hsa-miR-30e-5p	TargetScan	2.401E-59	4.014E-57	3.849E-56	1.967E-55	166	1143
5	hsa-miR-30d-5p:TargetScan	hsa-miR-30d-5p	TargetScan	2.401E-59	4.014E-57	3.849E-56	1.967E-55	166	1143

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-124-3p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	2.538E-62	8.316E-60	7.974E-59	2.079E-58	192	1446
2	hsa-miR-218-5p:Non-Functional MTI	Non-Functional MTI	miRTarbase	3.998E-37	4.933E-36	4.730E-35	3.275E-33	111	816
3	hsa-miR-26b-5p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	8.207E-36	8.859E-35	8.494E-34	6.724E-32	175	1873
4	hsa-miR-8485:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	1.040E-33	9.430E-33	9.042E-32	8.525E-30	110	874
5	hsa-miR-16-5p:Functional MTI	Functional MTI	miRTarbase	2.980E-33	2.579E-32	2.472E-31	2.442E-29	152	1557

[Show 45 more annotations](#)**18: Drug [Display Chart] 1858 input genes in category / 40668 annotations before applied cutoff / 22768 genes in category**

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	4001 DN Ethambutol dihydrochloride [1070-11-7]; Down 200; 14.4uM; PC3; HT HG-U133A	Broad Institute CMAP Down	5.445E-13	1.476E-9	1.652E-8	2.214E-8	49	194
2	3641 DN Finasteride [98319-26-7]; Down 200; 10.8uM; MCF7; HT HG-U133A	Broad Institute CMAP Down	2.083E-11	3.531E-8	3.951E-7	8.471E-7	47	199
3	7535 DN irinotecan HCl; Down 200; 100uM; PC3; HT HG-U133A	Broad Institute CMAP Down	2.391E-10	2.262E-7	2.531E-6	9.725E-6	41	171
4	2667 DN Rapamycin; Down 200; 0.1uM; HL60; HT HG-U133A	Broad Institute CMAP Down	1.721E-9	1.147E-6	1.284E-5	6.997E-5	43	196
5	4102 DN Tenoxicam [59804-37-4]; Down 200; 11.8uM; PC3; HT HG-U133A	Broad Institute CMAP Down	2.030E-9	1.251E-6	1.400E-5	8.254E-5	43	197

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	5793 UP Quinidine hydrochloride monohydrate [6151-40-2]; Up 200; 10.6uM; PC3; HT HG-U133A	Broad Institute CMAP Up	4.276E-11	5.912E-8	6.616E-7	1.739E-6	46	196
2	6163 UP haloperidol; Up 200; 10uM; HL60; HT HG-U133A	Broad Institute CMAP Up	6.178E-11	7.851E-8	8.785E-7	2.512E-6	46	198
3	3997 UP Cefotetan [69712-56-7]; Up 200; 7uM; PC3; HT HG-U133A	Broad Institute CMAP Up	2.150E-10	2.133E-7	2.387E-6	8.745E-6	45	198
4	3324 UP Liothyronine [6893-02-3]; Up 200; 6.2uM; MCF7; HT HG-U133A	Broad Institute CMAP Up	2.150E-10	2.133E-7	2.387E-6	8.745E-6	45	198
5	4525 UP Nialamide [51-12-7]; Up 200; 13.4uM; PC3; HT HG-U133A	Broad Institute CMAP Up	2.150E-10	2.133E-7	2.387E-6	8.745E-6	45	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ctd:D002737	Chloroprene	CTD	2.371E-21	9.644E-17	1.079E-15	9.644E-17	212	1349
2	ctd:C548651	2-(1'H-indolo-3'-carbonyl)thiazole-4-carboxylic acid methyl ester	CTD	1.351E-19	2.748E-15	3.075E-14	5.495E-15	144	807
3	ctd:C029938	nickel sulfate	CTD	3.957E-19	5.365E-15	6.003E-14	1.609E-14	233	1600
4	ctd:D012906	Smoke	CTD	4.433E-17	4.507E-13	5.044E-12	1.803E-12	153	937
5	ctd:C041786	palm oil	CTD	6.156E-16	5.007E-12	5.603E-11	2.503E-11	235	1720

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	DB00398	Sorafenib	Drug Bank	6.572E-5	1.451E-3	1.624E-2	1.000E0	5	7
2	DB01268	Sunitinib	Drug Bank	1.634E-4	2.728E-3	3.053E-2	1.000E0	5	8
3	DB00568	Cinnarizine	Drug Bank	3.429E-4	4.601E-3	5.149E-2	1.000E0	5	9
4	DB00270	Isradipine	Drug Bank	1.265E-3	1.219E-2	1.364E-1	1.000E0	4	7
5	DB00155	L-Citrulline	Drug Bank	1.750E-3	1.488E-2	1.665E-1	1.000E0	5	12

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	CID000002524	1-alpha-25-dihydroxycholecalciferol	Stitch	2.409E-12	5.762E-9	6.448E-8	9.795E-8	136	909
2	CID000004792	phorbol acetate myristate	Stitch	1.846E-9	1.211E-6	1.355E-5	7.506E-5	177	1399
3	CID000000806	D-myo-inositol-1,4,5-triphosphate	Stitch	1.637E-8	5.791E-6	6.480E-5	6.659E-4	86	568
4	CID000006410	tert-butyl hydroperoxide	Stitch	1.768E-8	5.992E-6	6.706E-5	7.191E-4	122	902
5	CID000002551	carbamol	Stitch	1.945E-8	6.263E-6	7.008E-5	7.912E-4	99	688

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19: Disease [Display Chart] 1843 input genes in category / 12907 annotations before applied cutoff / 29490 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	DOID:10763 (biomarker via orthology)	hypertension (biomarker via orthology)	AllianceGenome	3.894E-17	2.513E-13	2.524E-12	5.027E-13	53	227
2	DOID:162 (implicated via orthology)	cancer (implicated via orthology)	AllianceGenome	3.602E-8	5.224E-6	5.247E-5	4.649E-4	42	268
3	DOID:10652 (is marker for)	Alzheimer's disease (is marker for)	AllianceGenome	9.131E-8	1.240E-5	1.245E-4	1.179E-3	40	257
4	DOID:10763 (is implicated in)	hypertension (is implicated in)	AllianceGenome	3.460E-7	3.988E-5	4.005E-4	4.466E-3	24	120
5	DOID:3312 (is implicated in)	bipolar disorder (is implicated in)	AllianceGenome	6.673E-7	7.300E-5	7.331E-4	8.613E-3	11	29

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	cv:CN043650	Nonsyndromic Hearing Loss and Deafness, Autosomal Recessive	Clinical Variations	5.539E-5	2.705E-3	2.716E-2	7.149E-1	12	51
2	cv:C0686353	Limb-girdle muscular dystrophy	Clinical Variations	1.295E-4	5.297E-3	5.320E-2	1.000E0	8	26
3	cv:CN033288	Wilms tumor 1	Clinical Variations	2.059E-4	7.604E-3	7.637E-2	1.000E0	4	6
4	cv:C0037052	Sick sinus syndrome	Clinical Variations	2.437E-4	8.666E-3	8.703E-2	1.000E0	3	3
5	cv:C0340491	Familial sick sinus syndrome	Clinical Variations	2.437E-4	8.666E-3	8.703E-2	1.000E0	3	3

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	C0036341	Schizophrenia	DisGeNET Curated	1.035E-16	3.765E-13	3.781E-12	1.336E-12	122	883
2	C0005586	Bipolar Disorder	DisGeNET Curated	1.834E-16	3.765E-13	3.781E-12	2.368E-12	81	477
3	C0006142	Malignant neoplasm of breast	DisGeNET Curated	5.848E-14	4.193E-11	4.211E-10	7.548E-10	132	1074
4	C0009402	Colorectal Carcinoma	DisGeNET Curated	1.562E-13	8.400E-11	8.436E-10	2.016E-9	97	702
5	C0376358	Malignant neoplasm of prostate	DisGeNET Curated	2.173E-12	9.671E-10	9.712E-9	2.805E-8	86	616

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	EFO 0004464	brain measurement	GWAS	7.520E-23	9.707E-19	9.748E-18	9.707E-19	210	1674
2	EFO 0000694, MONDO 0100096	severe acute respiratory syndrome, COVID-19	GWAS	1.221E-16	3.765E-13	3.781E-12	1.576E-12	78	446
3	MONDO 0100096	COVID-19	GWAS	1.674E-16	3.765E-13	3.781E-12	2.160E-12	201	1790
4	EFO 0004312	vital capacity	GWAS	2.042E-16	3.765E-13	3.781E-12	2.636E-12	153	1232
5	EFO 0004343	waist-hip ratio	GWAS	2.589E-16	4.177E-13	4.195E-12	3.342E-12	152	1224

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	194070	WILMS TUMOR 1	OMIM MedGen	2.059E-4	7.604E-3	7.637E-2	1.000E0	4	6
2	201300	NEUROPATHY, HEREDITARY SENSORY AND AUTONOMIC, TYPE IIA	OMIM MedGen	9.292E-4	2.338E-2	2.348E-1	1.000E0	3	4