

# Results

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1: GO: Molecular Function [\[Display Chart\]](#) 35 input genes in category / 234 annotations before applied cutoff / 19912 genes in category

No results to display

2: GO: Biological Process [\[Display Chart\]](#) 34 input genes in category / 1376 annotations before applied cutoff / 20649 genes in category

No results to display

3: GO: Cellular Component [\[Display Chart\]](#) 35 input genes in category / 162 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:0035976	transcription factor AP-1 complex		2.712E-5	4.393E-3	2.490E-2	4.393E-3	2	5

4: Human Phenotype [\[Display Chart\]](#) 14 input genes in category / 1050 annotations before applied cutoff / 5088 genes in category

No results to display

5: Mouse Phenotype [\[Display Chart\]](#) 31 input genes in category / 1334 annotations before applied cutoff / 13846 genes in category

No results to display

**6: Domain** [Display Chart] 35 input genes in category / 299 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	1.25.40.150	-	Gene3D	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1
2	3.40.630.30	-	Gene3D	2.545E-3	3.729E-2	2.341E-1	7.609E-1	2	40
3	3.30.70.590	-	Gene3D	5.612E-3	3.729E-2	2.341E-1	1.000E0	1	3
4	1.10.12.10	-	Gene3D	7.475E-3	3.921E-2	2.462E-1	1.000E0	1	4

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	IPR000182	GNAT dom	InterPro	9.961E-4	2.949E-2	1.852E-1	2.978E-1	2	25
2	IPR003277	K chnl inward-rec Kir3.4	InterPro	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1
3	IPR032957	SAT1	InterPro	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1
4	IPR031293	Anoctamin-4	InterPro	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1
5	IPR033583	BEND3	InterPro	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PS51186	GNAT	PROSITE	9.961E-4	2.949E-2	1.852E-1	2.978E-1	2	25
2	PS00554	TEA 1	PROSITE	7.475E-3	3.921E-2	2.462E-1	1.000E0	1	4
3	PS51088	TEA 2	PROSITE	7.475E-3	3.921E-2	2.462E-1	1.000E0	1	4
4	PS51303	PET	PROSITE	1.119E-2	4.236E-2	2.660E-1	1.000E0	1	6

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PF00583	Acetyltransf 1	Pfam	8.420E-4	2.949E-2	1.852E-1	2.518E-1	2	23
2	PF15926	RNF220	Pfam	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1
3	PF11698	V-ATPase H C	Pfam	1.874E-3	2.949E-2	1.852E-1	5.603E-1	1	1
4	PF16545	CCM2 C	Pfam	3.745E-3	3.729E-2	2.341E-1	1.000E0	1	2
5	PF15246	NCKAP5	Pfam	3.745E-3	3.729E-2	2.341E-1	1.000E0	1	2

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	SM00426	TEA	SMART	7.475E-3	3.921E-2	2.462E-1	1.000E0	1	4
2	SM01062	Ca chan IQ	SMART	1.305E-2	4.536E-2	2.848E-1	1.000E0	1	7

**7: Pathway** [Display Chart] 23 input genes in category / 451 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	MM15854	WP CALCIUM REGULATION IN CARDIAC CELLS	WikiPathways	9.219E-5	2.307E-2	1.543E-1	4.158E-2	4	147
2	M39329	WP CALCIUM REGULATION IN CARDIAC CELLS	WikiPathways	1.023E-4	2.307E-2	1.543E-1	4.614E-2	4	151

**8: Pubmed** [Display Chart] 35 input genes in category / 4580 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	15146197	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation.	Pubmed	2.331E-6	3.390E-3	3.053E-2	1.068E-2	9	1215
2	27637333	Identification of Novel Nuclear Factor of Activated T Cell (NFAT)-associated Proteins in T Cells.	Pubmed	3.063E-5	3.390E-3	3.053E-2	1.403E-1	4	178
3	12297500	G protein-coupled receptors form stable complexes with inwardly rectifying potassium channels and adenylyl cyclase.	Pubmed	3.523E-5	3.390E-3	3.053E-2	1.614E-1	2	9
4	22077140	Transcriptional control of HIV replication by multiple modulators and their implication for a novel antiviral therapy.	Pubmed	3.523E-5	3.390E-3	3.053E-2	1.614E-1	2	9
5	9060410	Mutations in the Cacn1a4 calcium channel gene are associated with seizures, cerebellar degeneration, and ataxia in tottering and leaner mutant mice.	Pubmed	4.401E-5	3.390E-3	3.053E-2	2.016E-1	2	10

Show 45 more annotations

**9: Interaction** [Display Chart] 35 input genes in category / 2215 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:NFATC1	NFATC1 interactions		1.023E-5	2.266E-2	1.876E-1	2.266E-2	5	168

**10: Cytoband** [Display Chart] 35 input genes in category / 62 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	12q13.12	12q13.12		3.910E-4	1.856E-2	8.746E-2	2.424E-2	2	38
2	12q12	12q12		5.987E-4	1.856E-2	8.746E-2	3.712E-2	2	47
3	8q11.2	8q11.2		3.050E-3	4.195E-2	1.977E-1	1.891E-1	1	4
4	Xp22.1	Xp22.1		5.331E-3	4.195E-2	1.977E-1	3.305E-1	1	7
5	12q12-q13	12q12-q13		6.090E-3	4.195E-2	1.977E-1	3.776E-1	1	8

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	chr12q12	Ensembl 110 genes in cytogenetic band chr12q12	MSigDB C1	1.107E-3	2.289E-2	1.079E-1	6.866E-2	2	64
2	chr12q13	Ensembl 110 genes in cytogenetic band chr12q13	MSigDB C1	4.044E-3	4.195E-2	1.977E-1	2.507E-1	3	421

**11: Transcription Factor Binding Site [Display Chart]** 35 input genes in category / 507 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	M30363	ZNF596 TARGET GENES	MSigDB	1.913E-5	9.700E-3	6.602E-2	9.700E-3	7	660
2	M30308	ZNF362 TARGET GENES	MSigDB	1.464E-4	3.710E-2	2.525E-1	7.421E-2	6	630

**12: Gene Family [Display Chart]** 26 input genes in category / 31 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	1134	GCN5 related N-acetyltransferases	genenames.org	5.383E-4	1.669E-2	6.720E-2	1.669E-2	2	24
2	1257	Basic leucine zipper proteins Jun transcription factor family	genenames.org	4.308E-3	3.175E-2	1.279E-1	1.336E-1	1	3
3	1033	SCY1 like pseudokinases	genenames.org	4.308E-3	3.175E-2	1.279E-1	1.336E-1	1	3
4	1184	Prickle planar cell polarity proteins LIM domain containing	genenames.org	5.740E-3	3.175E-2	1.279E-1	1.779E-1	1	4
5	1183	TEA domain transcription factors	genenames.org	5.740E-3	3.175E-2	1.279E-1	1.779E-1	1	4

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**13: Coexpression [Display Chart]** 35 input genes in category / 3138 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	M7072	GSE12198 NK VS NK ACT EXPANSION SYSTEM DERIVED NK CELL UP	C7:IMMUNESIGDB: ImmuneSigDB	6.638E-6	2.083E-2	1.797E-1	2.083E-2	5	200

**14: Coexpression Atlas [Display Chart]** 35 input genes in category / 1145 annotations before applied cutoff / 21234 genes in category

No results to display

**15: ToppCell Atlas [Display Chart]** 35 input genes in category / 12920 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	9e275c4a70f9866f770fdbb0fe14a577287fe290	ASK428-Epithelial-Secretory ASK428 / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	3.174E-4	1.282E-2	1.287E-1	1.000E0	3	170
2	48cafe44951908d03f3c6f3e185e9cbb86fb5b3b	ASK452-Epithelial-Type 1 Epithelial / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	5.026E-4	1.282E-2	1.287E-1	1.000E0	3	199
3	127559d1a083c68cda9fce143afcc3eec168df17	ASK440-Immune-B cell Immune / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	7.606E-3	4.623E-2	4.643E-1	1.000E0	2	168
4	66074a288501c136b4e83b883db5f0d8269ee326	ASK428-Epithelial-Secretory Epithelial / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	8.409E-3	4.623E-2	4.643E-1	1.000E0	2	177
5	316c857dec9383823e09f966bca62d52d933b141	ASK454-Endothelial-Lymphatic Endothelial / Donor, Lineage and Cell class of Lung cells from Dropseq	A Cellular Census of Human Lungs (Vieira Braga et al)	9.535E-3	4.623E-2	4.643E-1	1.000E0	2	189

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 c72ef2ddcbb6dacbed4c6200d89e17d57314dcdc	Tracheal-10x5prime-Stromal-Chondrocytic 10x5prime / 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	1.712E-5	3.950E-3	3.967E-2	2.212E-1	4	198
2 55f013e9e6587d9ece59751fa131b1d22d6ccee	Tracheal-10x5prime-Stromal-Chondrocytic 10x5prime / 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	1.712E-5	3.950E-3	3.967E-2	2.212E-1	4	198
3 5c82dad416938d5c460069796d808170e7dbc8d9	Tracheal-NucSeq-Endothelial-Endothelia vascular-VE systemic venous 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	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
4 9ce9b3721fb8a154667211c29e60133412134c76	Bronchial-NucSeq-Immune Lymphocytic-T-T CD3-NKT 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	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
5 3c23fb8a84d4e4a20f7fa60055c7b37fc45a29d5	Bronchial-NucSeq-Immune Lymphocytic-T-T CD3 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	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 33db879e629821fb75684e60f8f0749cf9623bdd	PCW 10-12-Immune Lymphocytic-Immune Lymphocytic NK/ILC-im ILC2 (21) 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	4.000E-4	1.282E-2	1.287E-1	1.000E0	3	184
2 c227da59dc7beb73f84405bf13356bdeb59d9338	PCW 13-14-Endothelial-Endothelial mature-endo arterial (9) 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	8.500E-3	4.623E-2	4.643E-1	1.000E0	2	178
3 5861b44acfb8fe92c281c8355bf19c059b3dcd64	PCW 05-06-Endothelial-Endothelial mature-endo arterial (9) 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	8.684E-3	4.623E-2	4.643E-1	1.000E0	2	180
4 1fa882ee66e6f835acf3f293fd24dc7f8b1eff99	PCW 07-8.5-Immune Lymphocytic-Immune Lymphocytic NK/ILC-im ILC2 (21) 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	8.777E-3	4.623E-2	4.643E-1	1.000E0	2	181
5 f7f9be9c7ef8da9864d6aefe20043b26e1bb8697	PCW 05-06-Neuronal-Neuronal SCP-neuro proliferating SCP2 (1) 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	8.870E-3	4.623E-2	4.643E-1	1.000E0	2	182

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 a8dfc59a3974e3433f434676b7c2749d0fcfc8b2	CF-Lymphoid-T cell & NK cell CF / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	3.874E-4	1.282E-2	1.287E-1	1.000E0	3	182
2 bfa01571516a0b24476ae06cb07f56c5579dbd70	CTRL-Myeloid-Monocyte Myeloid / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	7.870E-3	4.623E-2	4.643E-1	1.000E0	2	171
3 e73d8e78a96b63e27a8a7694c62b3c44ec7ecfe6	CTRL-Lymphoid-T cell & NK cell CTRL / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	8.409E-3	4.623E-2	4.643E-1	1.000E0	2	177
4 26fb2c4e6cb9950c27eb15428e7e74e5abb4397d	CTRL-Lymphoid CTRL / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	9.058E-3	4.623E-2	4.643E-1	1.000E0	2	184
5 15057036b46c9df621ec4955aa94ca3036245d45	CF-Lymphoid-T cell & NK cell Lymphoid / Disease state, Lineage and Cell class	Airway Inflammation in Cystic Fibrosis (CF)	9.439E-3	4.623E-2	4.643E-1	1.000E0	2	188

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 9495134779bce4997f8b21d8921bfd5af17f050b	LAM-Lymphoid LAM / Condition, Lineage and Cell class	Atlas of Lymphangioleiomyomatosis (LAM)	9.925E-3	4.623E-2	4.643E-1	1.000E0	2	193
2 8165e0b5953b3639a56ebe96bb020ae52b7dbd89	LAM-Myeloid-Monocyte Myeloid / Condition, Lineage and Cell class	Atlas of Lymphangioleiomyomatosis (LAM)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
3 ba64b1c95dfaa995045239d412e725596f6c482e	LAM-Endothelial-LymEndo Endothelial / Condition, Lineage and Cell class	Atlas of Lymphangioleiomyomatosis (LAM)	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
4 cd2169b09626aa6257fd7cb3f951fcb7c59f88c	LAM-Lymphoid-NK Lymphoid / Condition, Lineage and Cell class	Atlas of Lymphangioleiomyomatosis (LAM)	1.062E-2	4.623E-2	4.643E-1	1.000E0	2	200

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 a126dacd94939851de1403d30f0b63eaaad48bfa1	10x3'2.3-week 12-13-Lymphocytic NK-T NK-NK progenitor week 12-13 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	3.284E-4	1.282E-2	1.287E-1	1.000E0	3	172
2 9befd44bce43eb5dc1fe3d2e44608f442cf74a47	10x5'v1-week 12-13-Myeloid macrophage-stroma-monocytoid macrophage week 12-13 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	7.958E-3	4.623E-2	4.643E-1	1.000E0	2	172
3 0a98d21fec67a890e75ebf0e2d23adddd77da214	10x3'2.3-week 17-19-Lymphocytic NK-T NK week 17-19 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	8.684E-3	4.623E-2	4.643E-1	1.000E0	2	180
4 1c8398342d3fa4d5ca9a8a63626cc497c5291446	10x3'2.3-week 17-19-Lymphocytic NK week 17-19 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	8.684E-3	4.623E-2	4.643E-1	1.000E0	2	180
5 ddbab26b05f057bd78b78773381cd447bd2e2726	10x3'2.3-week 17-19-Lymphocytic NK-T NK-CD56 bright NK week 17-19 / cell types per 3 fetal stages;per 3',per 5'	Blood and immune development in human fetal bone marrow	8.684E-3	4.623E-2	4.643E-1	1.000E0	2	180

Show 33 more annotations

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 5788e1158fde036937d41708e9db3222ca351eb1	Severe-Lymphoid-T- Severe / Condition,	Bronchoalveolar Lavage (BAL) Atlas of	3.174E-4	1.282E-2	1.287E-1	1.000E0	3	170

		Lineage, Cell class and cell subclass	COVID-19 Patients (Liao et al.)						
2	50ab8562552339d97e4f19aa6ae49fd797da492e	Severe-Lymphoid-T-innate T Severe / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	3.812E-4	1.282E-2	1.287E-1	1.000E0	3	181
3	769b52073a0f0543a72e9f32772321194b70cb2f	Severe-Myeloid-Macrophages- Severe / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	4.325E-4	1.282E-2	1.287E-1	1.000E0	3	189
4	36b6ea21b0b1342f2dcac4dcaf359b6c772203f7	Healthy Control-Lymphoid-T-CD8 T Healthy Control / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192
5	0489e0b08f3c3ef90b166ea2f26a0b2b12bd2077	Severe-Lymphoid-T-CCR7+ T Severe / Condition, Lineage, Cell class and cell subclass	Bronchoalveolar Lavage (BAL) Atlas of COVID-19 Patients (Liao et al.)	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	68d68ec9254f0fb9f1a1f5f98ef0ef736989b308	Control-Lymphoid-CD8 T cells Control / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
2	dad6479caac07c1536f2b3082a51d61ae08beca0	Control-Lymphoid-CD4 T cells Control / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
3	5aa3ce2eaed62f341abf47895d651aec5e14e729	Control-Lymphoid Control / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
4	4408304fd43c6e329b0d7e131f1759e7f2932299	COVID-19-Lymphoid COVID-19 / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
5	6e5140527437193f441ca96893b9a00d346614f3	Control-Myeloid-MoAM1, IL1R2 Myeloid / Condition, Lineage and Cell class	Bronchoalveolar Lavage (BAL) Atlas of Severe COVID-19 Patients (Grant et al.)	7.519E-3	4.623E-2	4.643E-1	1.000E0	2	167

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	76f39935763848ea6e7917b2f9f1432c543063d9	CD8+ Memory T cell-FLU-1 CD8+ Memory T cell / cell class, Virus stimulation and cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	7.092E-3	4.623E-2	4.643E-1	1.000E0	2	162
2	1e285c31823d3e1a18d8c01748cc3604f400c954	CV-Healthy-6 CV / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	9.925E-3	4.623E-2	4.643E-1	1.000E0	2	193
3	b50cfd87c5b67806450cb8b3c6860ab97f6d3b1	CV-Moderate-1 Moderate / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
4	e3d00d850b4d191f9592ef993c0eaadfe5710b5f	CV-Moderate-1 CV / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197
5	4b078714c49e7befb7b113d72485e712236d35fa	CV-Mild-1 CV / Virus stimulation, Condition and Cluster	CD8+ Memory T cells (PBMC) of COVID-19 Patients	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	5a4ad5ae5c2dbfb225158cb598ef649c26a48350	COVID-19-lung-CD4+ Treg COVID-19 / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191
2	73ea3078c1f55cd47e4d99e77b3ce4ff17549d49	COVID-19-lung-CD4+ Treg lung / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191



3	326fd2ce2c4b51e5a38f2a7a09f22f8f0e92735a	COVID-19-lung-CD4+ T cells metabolically active COVID-19 / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.549E-5	3.950E-3	3.967E-2	2.001E-1	4	193
4	780e23e2705fc5c1b70e37568b79731ced5038bd	COVID-19-lung-CD8+ T cells lung / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.549E-5	3.950E-3	3.967E-2	2.001E-1	4	193
5	5b84fa640cf30dea55fde53b810f850ff946d253	COVID-19-kidney-T-cells-1 COVID-19 / Disease (COVID-19 only), tissue and cell type	COVID-19 Autopsy Atlas (Lung, Liver, Kidney, Heart)	1.549E-5	3.950E-3	3.967E-2	2.001E-1	4	193

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	694d02c4d2dc2de4b344544f9124fec40fcf7d8f	Mild/Remission-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	3.340E-4	1.282E-2	1.287E-1	1.000E0	3	173
2	382686d62f7b8576c44bb9726a4e10dc26fd348e	Mild/Remission-B activate-7 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	4.460E-4	1.282E-2	1.287E-1	1.000E0	3	191
3	01c97543972159a9468272da06e7e611e2c21fae	Mild/Remission-B activate-7 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	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
4	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	4.737E-4	1.282E-2	1.287E-1	1.000E0	3	195
5	6f7e0b8bc06368d6e7026d69473ddd42dd41cfcb	Control-B intermediate-0 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	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	908cc9a3b0b99aea28a24bbd27667c824743e967	Control-T/NK-CD4+ T 1 Control / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
2	98fca0a2e2f66525c5c9d6cdaebcad14b4d53da4	Mild COVID-19-T/NK-CD4+ T 1 Mild COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
3	bc6b983fdb9547ef8a9e693bc15fed1b73e101f	Severe COVID-19-T/NK-CD4+ T 1 Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
4	584f0dc6f22bb13956a5f6950698599e382907e9	Severe COVID-19-T/NK-CD8+ T Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
5	c8c9343c19198b6534f8f07e74405e29b3a164bf	Severe COVID-19-T/NK-CD4+ T 2 Severe COVID-19 / Disease group,lineage and cell class (2021.01.30)	COVID-19 BAL Atlas	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	dd40dfc5b1211d31607e16d9b433a5c1796e7edf	COVID-CD4-proli CD4 COVID / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	6.192E-3	4.623E-2	4.643E-1	1.000E0	2	151
2	c6722bf142c84ccedd99c1a3344085aebc4cbab4	MS-Treg-exh CD4 MS / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192

3	b579a447d5c40bde5152ed0e5d3c442c4186749f	MS-CD4 MS / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	9.925E-3	4.623E-2	4.643E-1	1.000E0	2	193
4	a4fb3abf3c38928da9e8281dee8a304e8fd55eab	COVID-CD4-memory CD4 COVID / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
5	d6c92c91e17230a6ef0cfaea476d560691ed5d98	IIH-CD4 IIH / Condition, Cell class and T cell subcluster	COVID-19 Cerebrospinal Fluid-derived (CSF) Leukocytes	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196

Show 6 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	3545706d133b29df61affe8ac47b6c9fe85f7775	Biopsy Control (H.)-Immune-T cells Biopsy Control (H.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
2	6231c44a909dd06f85c8210814e976a5f29148d0	Bronchus Control (B.)-Immune-TX-B cells Bronchus Control (B.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
3	45ab554e6d0399b3182f089a25b2adf96de1144b	Parenchyma COVID-19 World / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
4	91985d01bc11dca8325aa3a02e5039db4fed04dd	Biopsy Other PF-Immune-T cells Biopsy Other PF / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	1.052E-2	4.623E-2	4.643E-1	1.000E0	2	199
5	cd581d7330b471431ef427f8a4f5be553f70e068	Bronchus Control (B.)-Epithelial-TX-Transitional AT2 Bronchus Control (B.) / Sample group, Lineage and Cell type	COVID-19 Lung Atlas	1.052E-2	4.623E-2	4.643E-1	1.000E0	2	199

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	0646cca78e24aeb6baa9934d3c439b797c567997	COVID-19-T cells-CD4+ T cells COVID-19 / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191
2	7f64add931b64b8d35836fa6bee9ebab593844d3	COVID-19-T cells COVID-19 / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191
3	02ab64c0166c0646d1d4c6ed110ef0b75a1096d0	Control-T cells-CD8+ T cells Control / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	4.063E-4	1.282E-2	1.287E-1	1.000E0	3	185
4	755c0998c729f462399f1d5e88adf4bfae31be30	Control-T cells-NK cells Control / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	4.063E-4	1.282E-2	1.287E-1	1.000E0	3	185
5	f4e8e0eba58da89b56587667555a5d4754e108c7	Control-T cells Control / group, cell type (main and fine annotations)	COVID-19 Lung Autopsy Data (SCP1219)	4.193E-4	1.282E-2	1.287E-1	1.000E0	3	187

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	3729d1444c65cad640377894decc64129bc3fd5b	COVID-19 Mild-Classical Monocyte-cMono 4 COVID-19 Mild / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
2	b17ab094cdc7050c2997e24ed474779b5d6f6146	Control-Non-classical Monocyte- Control / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
3	404064ccfe2cb73df7a7f88aa65d86b97dcef9d4	Control-Non-classical Monocyte Control / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
4	e666f6580e9a20b5e550f02125706db17eec8510	COVID-19 Mild-Classical Monocyte-cMono 4 Classical Monocyte / Disease condition and Cell class	COVID-19 PBMC Myeloid Cell Atlas	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197
5	c9250c80dd5bc3d27c6065b99119ff7dcf392e84	COVID-19 Convalescent-Non-classical Monocyte COVID-19	COVID-19 PBMC	1.052E-2	4.623E-2	4.643E-1	1.000E0	2	199



		Convalescent / Disease condition and Cell class	Myeloid Cell Atlas						
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Show 1 more annotation

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ce7f044956613118ee2e9fb6af2455c3166cb414	Control-Neu 4 World / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	9.058E-3	4.623E-2	4.643E-1	1.000E0	2	184
2	4831243fcd680cf4821fa0246e758c3e7c13a962	COVID-19 Severe-Neu 0 COVID-19 Severe / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
3	4fdea41ac7d84f0c52d102d87a5fce620480985e	COVID-19 Severe-Neu 0 World / 5 Neutrophil clusters in COVID-19 patients	COVID-19 PBMC Neutrophil Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	bb54bb81b450462ad521b57e1a07a80ce1678e67	COVID-19 Convalescent-PLT 3 World / Disease Group and Platelet Clusters	<a href="#">COVID-19 PBMC Platelet Atlas</a>	5.128E-3	4.623E-2	4.643E-1	1.000E0	2	137
2	f07654b215279abaf1c0882cdf41fbe31580a2ca	Control World / Disease Group and Platelet Clusters	<a href="#">COVID-19 PBMC Platelet Atlas</a>	9.439E-3	4.623E-2	4.643E-1	1.000E0	2	188
3	8e2794a20c96e4b87f3e779c7b01c8d3983b4a86	COVID-19 Severe-PLT 2 COVID-19 Severe / Disease Group and Platelet Clusters	<a href="#">COVID-19 PBMC Platelet Atlas</a>	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195
4	ad43efdd4d73b6615f65f06a315b33576e317473	COVID-19 Severe-PLT 4 World / Disease Group and Platelet Clusters	<a href="#">COVID-19 PBMC Platelet Atlas</a>	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
5	abfddbee99ef8c7719e6e6f62571e9be030e4acf	COVID-19 Severe-PLT 4 COVID-19 Severe / Disease Group and Platelet Clusters	<a href="#">COVID-19 PBMC Platelet Atlas</a>	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	728d81405fdcd137097433dd676b26519185e916	COVID-19 Severe-CD4+ CTL COVID-19 Severe / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	9.248E-3	4.623E-2	4.643E-1	1.000E0	2	186
2	e834d7a6aa7bb4f194b203d351e53bf5d95175d6	COVID-19 Mild-MAIT COVID-19 Mild / Disease condition and Cell class	COVID-19 T Cell Atlas (PBMC)	9.729E-3	4.623E-2	4.643E-1	1.000E0	2	191

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	7a92e0d6a021be23125495927b8571e25c83204a	Severe-MAIT World / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	9.632E-3	4.623E-2	4.643E-1	1.000E0	2	190
2	1c063dc1b62d9f9912aaf8d0297555a6545f5550	Severe-MAIT Severe / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	9.632E-3	4.623E-2	4.643E-1	1.000E0	2	190
3	daa1c3322d81e649161e889e1d78451d2d425d09	Mild-CD4+ T activated Mild / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
4	5e4ed4a5a437cfa002b92775992a791e27aa4c27	Mild World / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
5	79632190e44cfef9d7c11d9b9e37f2ebf0e6e255	Mild-CD8+ T activated World / Disease group and Cell class	COVID-19 T cell Atlas (BAL)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	58f66f35646f281e64d634e6c26adbd1d4e6c830	PBMC-Mild-cDC 7 Mild / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	5.497E-3	4.623E-2	4.643E-1	1.000E0	2	142

2	0121d08cc527aed9b3e11ff62bb9012916f5c56b	BAL-Control-cDC 12 Control / Compartment, Disease Groups and Clusters	COVID-19 cDC Atlas	6.431E-3	4.623E-2	4.643E-1	1.000E0	2	154
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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	62abaaaf48cabd1423f17fb27c33b75ea88867f4	5'-Adult-Distal Rectal-Hematopoietic-Plasma cells Adult / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	3.340E-4	1.282E-2	1.287E-1	1.000E0	3	173
2	09cd878c33534bd476d6a4880f5582076189da8c	5'-Adult-Distal Rectal-Hematopoietic-Plasma cells-IgA plasma cell Adult / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	3.340E-4	1.282E-2	1.287E-1	1.000E0	3	173
3	87f90834c7278516beff7814b78f7c75732d9bf0	3'-GW trimst-2-LargeIntestine-Hematopoietic-Myeloid-cDC1 GW trimst-2 / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	3.513E-4	1.282E-2	1.287E-1	1.000E0	3	176
4	6b06da40eb97ea2db09f3a769494738b3e5fe3fa	5'-Adult-Appendix-Hematopoietic-T cells-CX3CR1+ CD8 Tmem Adult / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	3.513E-4	1.282E-2	1.287E-1	1.000E0	3	176
5	50d5730e2cd4951d3ad0641fc81ae9f6ddabafe7	3'-GW trimst-1-SmallIntestine-Endothelial-blood vessel EC-arterial capillary GW trimst-1 / Celltypes from developing, pediatric, Crohn's, & adult GI tract	Cells of the human intestinal tract mapped across space and time	4.193E-4	1.282E-2	1.287E-1	1.000E0	3	187

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	82af19cc3e7c97300a5cbcd1bbcbcc9226c8db01	Caecum-Macrophage-Macrophage Macrophage / Region, Cell class and subclass	Colon Immune Atlas	6.980E-3	4.623E-2	4.643E-1	1.000E0	1	9
2	bb16e135b6ae0d66615420b61edd6f62f2a3233c	Sigmoid-Macrophage-Macrophage Macrophage / Region, Cell class and subclass	Colon Immune Atlas	7.606E-3	4.623E-2	4.643E-1	1.000E0	2	168
3	20822fce311326765b71337ce501ba44ea14f58f	mLN-B cell-B cell IgA Plasma mLN / Region, Cell class and subclass	Colon Immune Atlas	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197
4	04905f62941b193864704a10ad692faf777fa51d	mLN-T cell-Th17 mLN / Region, Cell class and subclass	Colon Immune Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
5	efdc9515dd9fb20ef9c8ddc106d88cbdde7d6ea2	mLN-T cell-Th17 T cell / Region, Cell class and subclass	Colon Immune Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	356978d2ee61e7042d7a9ad3bc744d3e7a7f76c0	(6) Macrophage-(60) Macrophage (6) Macrophage / shred on Cell type and subtype	Colon Immune Atlas from Gut Cell Atlas	1.533E-3	3.839E-2	3.855E-1	1.000E0	2	74
2	a39b384ee9824a08c3b544a9c3c7f0f95f08d6a7	mLN-(2) B cell-(20) B cell IgA Plasma mLN / shred on region, Cell type, and subtype	Colon Immune Atlas from Gut Cell Atlas	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197
3	c575e9ae4e034e8c4d171fe754403652343731	mLN-(1) T cell-(13) Th17 mLN / shred on region, Cell type, and subtype	Colon Immune Atlas from Gut Cell Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
4	a3ac65295da7baed447786a302b01db1cc824db2	(1) T cell-(13) Th17 (1) T cell / shred on Cell type and subtype	Colon Immune Atlas from Gut Cell Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
5	4d189df1db5b41306e9653436d7d7e75ff5afa06	mLN-(2) B cell-(22) B cell memory mLN / shred on region, Cell type, and subtype	Colon Immune Atlas from Gut Cell Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	93bce9741dec4e60dd470acca87cd4c8074f8876	Non-neuronal-Postmitotic-Microglia-Microglia-8 World / Primary Cells by Cluster	Comparison of human cortex and organoids	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
2	76bcd96e311fe80504e32e9b5fef0b6510c54b6	Non-neuronal-Postmitotic-Microglia-Microglia World / Primary Cells by Cluster	Comparison of human cortex and organoids	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
3	907ba412166bcb0526c5be0b06a76b6bd37c5a35	Neuron-Postmitotic-Inhibitory Neuron-SST-MGE1-3 World / Primary Cells by Cluster	Comparison of human cortex and organoids	9.058E-3	4.623E-2	4.643E-1	1.000E0	2	184
4	4dd9c8117c4499ed9bde127baf2598603a82080d	Neuron-Postmitotic-Inhibitory Neuron World / Primary Cells by Cluster	Comparison of human cortex and organoids	9.729E-3	4.623E-2	4.643E-1	1.000E0	2	191
5	bcc499f4c7ba2898ecd9c47bf68c92ed359b81ba	Neuron-Postmitotic-Inhibitory Neuron-SST-MGE1 World / Primary Cells by Cluster	Comparison of human cortex and organoids	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	f43960506ed3e699e910ec7711c1113e2e9b80d1	3' v3-Lung-Lymphocytic T CD4-Trm Th1/Th17 Lung / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	4.325E-4	1.282E-2	1.287E-1	1.000E0	3	189
2	c1db871e8e8e8b8d6a5798bc43eaf54e102b75eb	10x5'-blood-Lymphocytic NK blood / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	4.737E-4	1.282E-2	1.287E-1	1.000E0	3	195
3	480cc62ee1e5b1aaf6b62be6e5afd7a81236a1b0	10x5'-Liver-Lymphocytic T CD4-Trm Th1/Th17 Liver / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	4.737E-4	1.282E-2	1.287E-1	1.000E0	3	195
4	a54ec174461944229c98a0b48b4822a556191ccb	3' v3-GI small-bowel-Lymphocytic T CD4/8-lo GI small-bowel / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	4.808E-4	1.282E-2	1.287E-1	1.000E0	3	196
5	84cab9390794fe50203834b745722bf11c208ebd	3' v3-GI small-bowel-Lymphocytic T CD4/8-lo-Trm Tgd GI small-bowel / Manually curated celltypes from each tissue	Cross-tissue immune cell analysis reveals tissue-specific features in humans	4.808E-4	1.282E-2	1.287E-1	1.000E0	3	196

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e6dfbd2652b67577c8834c05348f62150637f348	Smart-start-Cell-Wel seq-Non-neoplastic-Lymphoid-CD4/CD8-CD4 INF-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	3.229E-4	1.282E-2	1.287E-1	1.000E0	3	171
2	ddaeb96ce9c9c3bf232b4a42266fa2ee7e8f3f41	Smart-start-Cell-Wel seq-Non-neoplastic-Lymphoid-CD4/CD8-CD4 INF 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	3.229E-4	1.282E-2	1.287E-1	1.000E0	3	171
3	e1fe07652c10c37191d1471ddaea500f74269e0c	Smart-start-Cell-Wel seq-Non-neoplastic-Lymphoid-CD4/CD8-CD4 rest-G Smart-start-Cell-Wel seq / Platform, Oncotype,	Harmonized single-cell landscape, intercellular crosstalk and tumor	3.229E-4	1.282E-2	1.287E-1	1.000E0	3	171

		Lineage, Cell class, celltype (level4), mutation group	architecture of glioblastoma							
4	6be74e4ba631b0c46cef2c580553f4c1ed29579e	10x 3' v2v3-Non-neoplastic-Lymphoid-CD4/CD8-CD8 NK sig-C 10x 3' v2v3 / Platform, Oncotype, Lineage, Cell class, celltype (level4), mutation group	Harmonized single-cell landscape, intercellular crosstalk and tumor architecture of glioblastoma	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194	
5	032ccc91e604113da9bc34a6f9ddb1d45dea1892	Smart-start-Cell-Wel seq-Non-neoplastic-Glial-Neuronal-Oligodendrocyte-B 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	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197	

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	48fd48990a6833066be314dc5b66b90893f7ea8f	Neuronal-Excitatory-eE(FEZF2 SLC17A7)-eE 2-SLC17A7 IL15- Neuronal / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	4.809E-7	6.213E-4	6.240E-3	6.213E-3	5	200
2	012dd2180f6f596d6e55e864be2e62b53c15edb2	Neuronal-Excitatory-eE(FEZF2 SLC17A7)-eE 2-SCUBE1 Neuronal / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	4.809E-7	6.213E-4	6.240E-3	6.213E-3	5	200
3	9103e6f72a04f66f2b7069b0d71a719e9b10026b	Neuronal-Excitatory-eE(FEZF2 SLC17A7)-eE 2-SLC17A7 IL15--L5-6 Neuronal / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	4.809E-7	6.213E-4	6.240E-3	6.213E-3	5	200
4	06f949c81eecba00203f0716d0c5854724871184	Neuronal-Excitatory-eE(FEZF2 SLC17A7)-eE 2-SCUBE1- Neuronal / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	4.809E-7	6.213E-4	6.240E-3	6.213E-3	5	200
5	d31e26387d879ee30731c497cea6aaf4746e40d9	Neuronal-Excitatory-eE(FEZF2 SLC17A7)-eE 2 Neuronal / cells hierarchy compared to all cells using T-Statistic	Human Adult Brain MTG	4.809E-7	6.213E-4	6.240E-3	6.213E-3	5	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	3d6295fe25e3b1fb4b6e83704c5dbf86dc639b3	Mid-temporal gyrus (MTG)-Neuronal-Glutamatergic Excit-Glut A (CT)-Glut CT2 L6 FEZF2-Exc L6 FEZF2 TBC1D26 Mid-temporal gyrus (MTG) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	1.494E-7	6.213E-4	6.240E-3	1.931E-3	5	158
2	1c9e54e7b14eb99996590fb93b257cf881a9f184	Mid-temporal gyrus (MTG)-Neuronal-Glutamatergic Excit-Glut A (CT)-Glut CT2 L6 FEZF2-Exc L6 FEZF2 SLITRK6 Mid-temporal gyrus (MTG) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	2.088E-7	6.213E-4	6.240E-3	2.698E-3	5	169
3	a6ff7a3d9b80839c0efa91658836812e868561fa	Mid-temporal gyrus (MTG)-Neuronal-Glutamatergic Excit-Glut A (CT)-Glut CT2 L6 FEZF2 Mid-temporal gyrus (MTG) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	3.012E-4	1.282E-2	1.287E-1	1.000E0	3	167
4	2abdd8ae9a5d88aac30992142d1b502c959bc015	Anterior Cingulate gyrus (CgG)-Neuronal-Glutamatergic Excit-Glut A (CT)-Glut CT2 L6 FEZF2-Exc L6 FEZF2 TBC1D26 Anterior Cingulate gyrus (CgG) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	3.119E-4	1.282E-2	1.287E-1	1.000E0	3	169

5	5de2f7d16a05af74ebfb1ca42d0f9c3c3524692d	Somatosensory Cortex (S1)-Neuronal-Glutamatergic Excit-Glut C-D (RORB)-Glut D (IT RORB THEMIS LINC00507) 2-Exc L3-4 RORB SEMA6D Somatosensory Cortex (S1) / Sample groups (6 Anatomical region groups), with 5 level hierarchy of cell types	Human Adult Multiple Cortical Areas SMART-seq	3.174E-4	1.282E-2	1.287E-1	1.000E0	3	170
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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	08dc0c019c594da7b9944db8fd706aa7780e6ae9	(210) NKT cell World / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192
2	b0a573ddde2978485a857b8261ee1ee5ef68ecf	(21) NKT cell World / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192
3	e9718642ee2751c9d46a1b968547bdc59cdfd30	(0) Myeloid-(000) CD14+ Monocyte  (0) Myeloid / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
4	9c17589ef0f6583c4c106c06936877fd74c258ce	(0) Myeloid-(00) Monocyte (0) Myeloid / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198
5	cd1548fc27779ada721ca00c72ebd3b6c9b15a19	(2) NK/T-(23) CD4+ T cell-(231) CD4+/CD45RO+ Memory T cell  (23) CD4+ T cell / immune cells in Peripheral Blood (logTPM normalization)	Human Blood Atlas	1.042E-2	4.623E-2	4.643E-1	1.000E0	2	198

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	3b061dbc10918be7cbdd4453311d2c1ebf18c6b2	hematopoietic progenitors-CD34+ MEP 2 hematopoietic progenitors / Lineage and Cell class	Human Bone Marrow Atlas	4.460E-4	1.282E-2	1.287E-1	1.000E0	3	191
2	4f55da763f63d1bf6379582e9d85796a797c5b76	T/NK cells-Regulatory T cell World / Lineage and Cell class	Human Bone Marrow Atlas	1.002E-2	4.623E-2	4.643E-1	1.000E0	2	194
3	aeeadfeb01827dbc7de6576c76fb2e41a3c59247	myeloid-CD16+ Monocyte myeloid / Lineage and Cell class	Human Bone Marrow Atlas	1.002E-2	4.623E-2	4.643E-1	1.000E0	2	194
4	60fab0c24c827567fb42bbd7eb165bf45178c198	myeloid-CD14+ Monocyte myeloid / Lineage and Cell class	Human Bone Marrow Atlas	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195
5	9bb1281e63daf6aca2817f9cc1f55463b069909f	T/NK cells-CD8+ Effector T cell T/NK cells / Lineage and Cell class	Human Bone Marrow Atlas	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	4ac33e7d11b8b0fff6ee2e9dacad49c21d63b818	(07) Ionocytes-(0) Reference (07) Ionocytes / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
2	c773b9180dbfec9c19d4098dd43332e6f6050372	(06) OLFM4+ World / shred by cell type by condition	Human Bronchial Epithelial Cells (HBEC)	1.052E-2	4.623E-2	4.643E-1	1.000E0	2	199

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e237384b02be460d44eeada3026a5691c66f6fc1	nucseq-Immune-Immune Myeloid-pMON-pMON nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
2	0bc83ae79873a5e473e6e1e3111924cd003986a1	nucseq-Immune-Immune Myeloid-pMON nucseq / Celltype	Human Cell Ref	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194

		signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	v1.1						
3	ffb40486f8097b2c08e8f3b3685d0b8cb8d1bc66	nucseq-Immune-Lymphocytic T/NK-Lymphocytic T/NK nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	4.737E-4	1.282E-2	1.287E-1	1.000E0	3	195
4	b8124e8a23e6d37b40023608674e67285c6ffe84	nucseq-Immune-Lymphocytic T/NK nucseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	4.737E-4	1.282E-2	1.287E-1	1.000E0	3	195
5	3b5f76a1f7b1ef6820742345af61d7afd0d73f41	cellseq-Immune-Lymphocytic T/NK-Lymphocytic T/NK cellseq / Celltype signatures by Technology, Lineage, Lineage subclass, Celltype group, Cell type2	Human Cell Ref v1.1	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	f215435aee15f0ed254104bfd55670144b6d2ac3	lymphoid-T cell-unlabelled(multiplets) T cell / Lineage, cell class and subclass	Human Cord Blood Atlas	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
2	a224c0a010489ad043bd2ad1385eef33c3b6b792	lymphoid-T cell-unlabelled(multiplets) lymphoid / Lineage, cell class and subclass	Human Cord Blood Atlas	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	8eb8b086c38960200578a9fe8853ca6e894ddee4	21-Trachea-Epithelial Trachea / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	1.746E-5	3.958E-3	3.976E-2	2.256E-1	4	199
2	409e12d2bb26b6d2ed025304ca6ace07df16638a	15-Trachea-Epithelial-Submucosal gland basal Trachea / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	4.460E-4	1.282E-2	1.287E-1	1.000E0	3	191
3	f0557920b9b3e7c4f39938d1b524aa58711af4d2	15-Trachea-Epithelial-Goblet-like secretory Trachea / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	8.500E-3	4.623E-2	4.643E-1	1.000E0	2	178
4	f8cddad28896f0edf10a8645fa49a011b22b120d	21-Trachea-Epithelial-Goblet-like secretory Trachea / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	9.248E-3	4.623E-2	4.643E-1	1.000E0	2	186
5	c1ea2dc44cf5340378e56e0ffc2e6f64e6c95a58	18-Airway-Epithelial-Submucosal gland Airway / Age, Tissue, Lineage and Cell class	Human Fetal Lung in Development	9.535E-3	4.623E-2	4.643E-1	1.000E0	2	189

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	de8e538c8767d41b8a52f5e58ba1affd4e7244c4	pdx World / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	9.248E-3	4.623E-2	4.643E-1	1.000E0	2	186
2	0b88a87158a9ca8de3bf40a4ff1687150707a5f0	pdx-Tumor cells World / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	9.248E-3	4.623E-2	4.643E-1	1.000E0	2	186
3	e785135262f4c9cc66c403bf362bb34643b212c5	human hepatoblastoma-Tumor cells-T8 Tumor cells / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192
4	f8d6eff1e04926f85d265ec39fe66897fe29574d	background-NK cells background / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	9.925E-3	4.623E-2	4.643E-1	1.000E0	2	193
5	b60db71f419caf3705e391e7b6dcf29b406cda9a	background-T cells background / Sample and Cell Type and Tumor Cluster (all cells)	Human Hepatoblastoma Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196



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	6.924E-3	4.623E-2	4.643E-1	1.000E0	2	160
2 b7c5a8a1c85da92e1945721b6887b32fad7b76b8	C 07 World / shred on cell type and cluster	Human Ileal Epithelial cells from Crohn's Disease	6.924E-3	4.623E-2	4.643E-1	1.000E0	2	160

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 0099def970fbc828756fbf853eca2ce77b8cd342	ILEUM-inflamed-(3) MNP-(3) moDC (3) MNP / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	4.193E-4	1.282E-2	1.287E-1	1.000E0	3	187
2 4395dbd18c14d491f5066a2ddac438a16b1fd7c3	ILEUM World / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	4.392E-4	1.282E-2	1.287E-1	1.000E0	3	190
3 b7a792a7c0c22d8b703509f134115f0e394d7de0	ILEUM-non-inflamed-(3) MNP-(3) moDC (3) MNP / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	4.984E-3	4.623E-2	4.643E-1	1.000E0	2	135
4 cef3ee2a4a0af961aa3b4c92150d423e841ae8c1	ILEUM-inflamed-(1) T cell-(1) CD8 Trm (1) T cell / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	9.058E-3	4.623E-2	4.643E-1	1.000E0	2	184
5 a77d7ae44f47410bd92fb3aa0f44dce891752b63	ILEUM-inflamed-(1) CD8 Trm inflamed / shred on tissue, inflammation status, cell class(v3), cell subclass (v2)	Human Ileal Immune cells from Crohn's Disease	9.343E-3	4.623E-2	4.643E-1	1.000E0	2	187

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 f30c866e5f41ee79bdc6b6e08af962d62b199835	distal-1-Hematologic-IGSF21+ Dendritic 1 / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	1.002E-2	4.623E-2	4.643E-1	1.000E0	2	194
2 f1cbf82484f489fe7e0b5de6a49ea28d69f04e1a	proximal-Endothelial-Capillary Aerocyte proximal / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195
3 13168c9632b58dd65ecb365df3832d95e7325919	proximal-Endothelial-Capillary Aerocyte-3 proximal / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195
4 36b2e754ed7ff138ac05fb51f4494e5339669828	proximal-3-Endothelial-Capillary Aerocyte 3 / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195
5 252e15a4ea54d872c5b910711941dcdf359c0492	medial-Hematologic-CD8+ Memory/Effector T-2 medial / Location, Lineage, Cell class (ontology) and Donor from 10X sequencing (macrophage renamed)	Human Lung Cell Atlas (HLCA)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 06c371d0f0c5a7b234dd143e98800e19af95a8b5	Adult-Immune-T lymphocyte-D122 Adult / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.177E-5	3.950E-3	3.967E-2	1.521E-1	4	180
2 df30478b288084a1bd48f660409dcc784040897c	Children (3 yrs)-Immune-T lymphocyte-D032 Children (3 yrs) / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.426E-5	3.950E-3	3.967E-2	1.843E-1	4	189
3 0b84fd1dc68146d9f72422b102744d2847f5ecb2	Adult-Immune-T lymphocyte-D175 Adult / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191

4	c7be771543089fc94e5c62fd22f745189642aec3	Children (3 yrs)-Immune-T lymphocyte-D046 Children (3 yrs) / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191
5	26df0c4c8a2355dd5503fadd07e368eb9a2bf06a	Adult-Immune-T lymphocyte Adult / Lineage, Cell type, age group and donor	Human Lung Cells in 3 Age Groups (Wang et al.)	1.549E-5	3.950E-3	3.967E-2	2.001E-1	4	193

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	b732c6a423c28856211002107d8c611dcfb6f265	metastatic Brain-T/NK cells-Exhausted Tfh metastatic Brain / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	3.455E-4	1.282E-2	1.287E-1	1.000E0	3	175
2	5228c4bf2513186140c2c4eaa67a268c732bdc84	tumor Lung-Endothelial cells-Tumor ECs tumor Lung / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
3	fbd72ebaba73cc30e79dc8a8c3d46b6f863c1494	normal Lung-Myeloid cells-mo-Mac Myeloid cells / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
4	204e5a675f4684c9570c24c8d34bbf632fd8164a	tumor Lymph Node / Brain-B lymphocytes-MALT B cells tumor Lymph Node / Brain / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	6.841E-3	4.623E-2	4.643E-1	1.000E0	2	159
5	fed9e4120c758fdcc23bb248d1801002b0e0d485	tumor Lymph Node / Brain-Fibroblasts-Smooth muscle cells tumor Lymph Node / Brain / Location, Cell class and cell subclass	Human Metastatic Lung Adenocarcinoma (Nayoung Kim et al)	8.227E-3	4.623E-2	4.643E-1	1.000E0	2	175

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9534c4f4e950bb1498c1737ca1713e7f37d0aff2	wk 20-22-Epithelial-Proximal epithelial-basal proximal wk 20-22 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	8.500E-3	4.623E-2	4.643E-1	1.000E0	2	178
2	c630a121aedd09a51ea18cc6e8552eb979e5b555	wk 15-18-Hematologic-Myeloid-APOE+ Mac2 wk 15-18 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	8.684E-3	4.623E-2	4.643E-1	1.000E0	2	180
3	9e5f98f9113e5e38bdadba6d9d2c346177fb35fe	wk 15-18-Epithelial-Proximal epithelial-intermediate neuroendocrine wk 15-18 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	9.058E-3	4.623E-2	4.643E-1	1.000E0	2	184
4	7b3d30a54bec66ca6b0209c86448f4fff97ed75c	wk 15-18-Endothelial-Blood vessel endothelial-Aerocyte wk 15-18 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	9.153E-3	4.623E-2	4.643E-1	1.000E0	2	185
5	ac1d2a94674bd15885e70502abad3a2ff3c21d73	wk 20-22-Hematologic Lymphocytic-T & ILC-ILC3 wk 20-22 / Celltypes from embryonic and fetal-stage human lung	Human embryonic and fetal stage lung cell atlas	9.248E-3	4.623E-2	4.643E-1	1.000E0	2	186

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	5024d43b4cf7dea305ed911f1e123ca7fd44e990	10x 3' v3-tissue-resident (10x 3' v3)-lymphocytic 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.	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
2	1fa0ea06453d6b979039f63454e7f9c69323a350	10x 3' v3-tissue-resident (10x 3' v3)-lymphocytic-T	Immune and Hematologic Cells	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198

		lymphocytic tissue-resident (10x 3' v3) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.						
3	34c564ece9a2b94dcf646e3c95b5be9c5ecfaafe	10x 3' v3-blood (10x 3' v3)-lymphocytic-T lymphocytic-CD8-positive, alpha-beta cytokine secreting effector T cell blood (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.	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
4	b340b6acf675c75adffb98e560080f966571f594	10x 3' v3-spleen (10x 3' v3)-lymphocytic spleen (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.	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
5	b0511ce81c446482339def3a0945fcbba6da35d0	10x 3' v3-tissue-resident (10x 3' v3)-lymphocytic-T lymphocytic-effector CD8-positive, alpha-beta T cell 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.	6.594E-3	4.623E-2	4.643E-1	1.000E0	2	156

Show 33 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	70680b29428b6bf882b1fae36f924b775961176b	Healthy/Control-CD8+ T naive World / Disease group and Cell class	Influenza Atlas	6.758E-3	4.623E-2	4.643E-1	1.000E0	2	158
2	e1386c21fcbbf57fa32d8bdfba3cb1887477ff73	Healthy/Control-CD8+ T naive Healthy/Control / Disease group and Cell class	Influenza Atlas	6.924E-3	4.623E-2	4.643E-1	1.000E0	2	160
3	de802ff96b52d28550a7854fc915f813c76ea271	Influenza Severe-NK CD56bright World / Disease group and Cell class	Influenza Atlas	7.008E-3	4.623E-2	4.643E-1	1.000E0	2	161
4	98c95b1b85d5427415af2ca8fb14849e97f6e8b5	Influenza Severe-Neutrophil Influenza Severe / Disease group and Cell class	Influenza Atlas	7.008E-3	4.623E-2	4.643E-1	1.000E0	2	161
5	7748d5709e8cf6673f5a8370108309f76cd830f4	Influenza Severe-NK CD56bright Influenza Severe / Disease group and Cell class	Influenza Atlas	7.176E-3	4.623E-2	4.643E-1	1.000E0	2	163

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	2c51850f5c559d665b8a27a12b75af9ed58dffe1	renal cortex nuclei-Adult normal reference-Mesenchymal-Fibroblast-kidney interstitial fibroblast-Adaptive / Maladaptive / Repairing Fibroblast 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	1.487E-5	3.950E-3	3.967E-2	1.921E-1	4	191
2	28eb3a5728e8901bcb5ba12f6b009f41b065fa37	renal medulla nuclei-Hypertensive with+without-CKD-Endothelial-blood vessel endothelial cell of kidney-arteriolar vasa-recta endothelial Hypertensive with+without-CKD / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	1.517E-5	3.950E-3	3.967E-2	1.960E-1	4	192
3	8ad8efb631164b46f0c082572270188e5ead20bf	renal medulla nuclei-Hypertensive with+without-CKD-Endothelial Hypertensive with+without-CKD / Celltypes from Cells and Nuclei per compartment and clinical group	Integrated Single-nucleus and Single-cell RNA-seq of the Adult Human Kidney	1.645E-5	3.950E-3	3.967E-2	2.126E-1	4	196

4	ab7be3858deabbdb1fc44e8b9da8ff49a50bf1fb1	renal cortex nuclei-Renal AKI (acute kidney injury)-Endothelial-blood vessel endothelial cell of kidney-capillary-immature endothelial cell-Peritubular Capillary Endothelial Cell  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	1.645E-5	3.950E-3	3.967E-2	2.126E-1	4	196
5	b8f89a50114932c08fc5daac4b549adfe9df8e66	renal medulla nuclei-Adult normal reference-Endothelial-blood vessel endothelial cell of kidney 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	1.645E-5	3.950E-3	3.967E-2	2.126E-1	4	196

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	6aea5d00c417708f05b6d2dfe5a962d80864f8eb	COVID-19 Mild-Lymphoid T/NK-gd T COVID-19 Mild / Disease group, lineage and cell class	<a href="#">Integration of 5 COVID-19 PBMC Datasets</a>	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
2	94b2693a8378b9b2c58c6aebb2c6658d75b2e3de	Control-Lymphoid T/NK-NK Control / Disease group, lineage and cell class	<a href="#">Integration of 5 COVID-19 PBMC Datasets</a>	5.026E-4	1.282E-2	1.287E-1	1.000E0	3	199
3	b5d5eead192a22c6b5ea699fe36873809fe6e3e2	Control-Lymphoid T/NK Control / Disease group, lineage and cell class	<a href="#">Integration of 5 COVID-19 PBMC Datasets</a>	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
4	7717fce227b4e02ed41baad8ae7dd2e22bd7c13e	COVID-19 Mild-Lymphoid T/NK-CD4+ T activated COVID-19 Mild / Disease group, lineage and cell class	<a href="#">Integration of 5 COVID-19 PBMC Datasets</a>	8.964E-3	4.623E-2	4.643E-1	1.000E0	2	183
5	ca138cc2224b32dd08cf98ead00188bcfb1a9b69	COVID-19 Severe-Lymphoid T/NK-CD4+ CTL COVID-19 Severe / Disease group, lineage and cell class	<a href="#">Integration of 5 COVID-19 PBMC Datasets</a>	9.729E-3	4.623E-2	4.643E-1	1.000E0	2	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	cf592d93612023a13de21e0fb8c6b13714f9af71	Fetal brain-organoid Tanaka cellReport-GW10-Neuronal-Intermediate GW10 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	5.026E-4	1.282E-2	1.287E-1	1.000E0	3	199
2	0f4b8b0868bda406fe6bf01d1b722510dfd0168	Fetal brain-organoid Tanaka cellReport-GW13-Mesenchymal-Mesoderm GW13 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
3	306926cb7a847871641f02e03d52dc56fd55711c	Fetal brain-organoid Tanaka cellReport-GW26-Neuronal GW26 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
4	1f94622186d8329357fa06785e03eeacf29ab1ce	Brain organoid-organoid Kanton Nature-Organoid-1M-Neuronal-cortical neurons 1 Organoid-1M / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	6.758E-3	4.623E-2	4.643E-1	1.000E0	2	158
5	4d7b2d0980fb4f47721fa2891151e2bd892ccb91	Fetal brain-fetalBrain Zhong nature-GW16-Neuronal-GABAergic neurons GW16 / Sample Type, Dataset, Time group, and Cell type.	Integration of Four Brain Organoid Datasets and One Fetal Brain Dataset	7.261E-3	4.623E-2	4.643E-1	1.000E0	2	164

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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	300edc4aa3ce55f309005c02c315fa0102ea9da7	PBMC-Control-Lymphocyte-T/NK-CD4+ T-Treg-Treg 0 Control / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.09)	Integration of Multiple Sampling Location of COVID-19 Patients	4.000E-4	1.282E-2	1.287E-1	1.000E0	3	184
2	c30b6d1fd5fabd99e25857f7486d6dc9c054f552	BAL-Control-Lymphocyte-T/NK-CD4+ T-CD4+ T 1- Control / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.09)	Integration of Multiple Sampling Location of COVID-19 Patients	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
3	749cc39cbe5d68372fc43f7dbdbe5004cd01ace8	BAL-Control-Lymphocyte-T/NK-CD4+ T-CD4+ T 1 Control / Location, Disease Group, Cell group, Cell class (2021.03.09)	Integration of Multiple Sampling Location of COVID-19 Patients	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
4	a7f11ac46965b3fc21c9d04870ce0bd2b3868cec	BAL-Control-Lymphocyte-T/NK-CD4+ T Control / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.09)	Integration of Multiple Sampling Location of COVID-19 Patients	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
5	068210aa57e733cbcb54a0b20616f0cb2a1ff639	BAL-Mild-Lymphocyte-T/NK-CD4+ T-CD4+ T Mild / Location, Disease Group, Cell group, Cell class and sub cluster (2021.03.01)	Integration of Multiple Sampling Location of COVID-19 Patients	4.737E-4	1.282E-2	1.287E-1	1.000E0	3	195

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	c53405a8d082fbd10131a6ec88b69fdd835f2925	Sepsis-URO-Lymphocyte-T/NK-CD4+ CTL URO / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
2	8c7d00d8c27fb47954d8ac53eebc4582e92b970c	Sepsis-Int-URO-Lymphocyte-T/NK-CD8+ T naive Int-URO / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
3	6560753d3df2f87860b52052d4881aa45410f666	COVID-19-COVID-19 Mild-Lymphocyte-T/NK-gd T COVID-19 Mild / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
4	31859b8db7ea17e48b7b54e92f0d76aeb755e7ca	COVID-19-COVID-19 Severe-Lymphocyte-T/NK-CD8+ Tem COVID-19 Severe / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
5	fddb3df5b90eb97ef8ed80fac320c1a90903f012	Control-Control-Lymphocyte-T/NK-CD8+ Tem Control / Disease, condition lineage and cell class	Integration of immune-mediated diseases (COVID-19 + Influenza + Sepsis + Multiple Sclerosis)	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	8e2b51d7b42e0b6e62641efdbbc73d31561d6a3e	saliva-Severe-critical progression d12-22 no-steroids-Lymphocytic-Lymphocytic T-CD8-positive, alpha-beta T cell-T CD8 c03-GZMK 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.)	2.657E-4	1.282E-2	1.287E-1	1.000E0	3	160
2	8f3255d7f67890389a768453492243ea982eb38a	PBMC fresh-frozen-Severe-critical progression d12-22 no-steroids-Lymphocytic-Lymphocytic T-mature alpha-beta T cell-T CD4 c04-ANXA2 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.)	2.857E-4	1.282E-2	1.287E-1	1.000E0	3	164
3	ceb0a48c0d853448fd45ac31dde046df9a178571	saliva-Severe-critical progression d28-40-Lymphocytic-Lymphocytic T-	Large Scale COVID-19 Single Cell	2.960E-4	1.282E-2	1.287E-1	1.000E0	3	166



		CD8-positive, alpha-beta T cell-T CD8 c02-GPR183 Severe-critical progression d28-40 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Data (Ren et al.)						
4	986c036e656f24fe374807e2711cec9e3c83c892	saliva-Severe-critical progression d28-40-Lymphocytic-Lymphocytic T-CD8-positive, alpha-beta T cell Severe-critical progression d28-40 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	3.812E-4	1.282E-2	1.287E-1	1.000E0	3	181
5	f8e6247bedc0ba494c5bb551539cb8ba5a97f557	PBMC fresh-frozen-Severe-critical convalescent d42-56-Lymphocytic-Lymphocytic T-CD8-positive, mature gamma-delta T cell-T gdT c14-TRDV2 Severe-critical convalescent d42-56 / Compartment, severity and other cell annotations on 10x 3' data (130k)	Large Scale COVID-19 Single Cell Data (Ren et al.)	4.259E-4	1.282E-2	1.287E-1	1.000E0	3	188

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	8ed22b1af04a711203293e7a8b3df6fb9222fad5	P28-Endothelial-large vessel endothelial cell-endothelial cell of artery P28 / 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	4.000E-4	1.282E-2	1.287E-1	1.000E0	3	184
2	a54045cac65a66197e3ad2b002fa6c511102834a	P15-Hematopoietic-Immune P15 / 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	6.192E-3	4.623E-2	4.643E-1	1.000E0	2	151
3	6b905d309f2a9b8828399b36f4942aec8696bee6	P15-Hematopoietic-Immune-immune cell unspecified P15 / 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	6.192E-3	4.623E-2	4.643E-1	1.000E0	2	151
4	9703b7e67d9fadb6129cad166bd01be915042e44	E15.5-Mesenchymal-mesenchymal fibroblast-tracheal fibroblast E15.5 / 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	7.008E-3	4.623E-2	4.643E-1	1.000E0	2	161
5	4ee59a6147bbe7e4a03cc2d6fe9d6c10b18a3a06	P28 World / 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	7.606E-3	4.623E-2	4.643E-1	1.000E0	2	168

Show 10 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	58bfff3284ae21150e4619511bd58622c16c5dde	Thalamus-Endothelial-ENDOTHELIAL STALK-Flt1 2-Endothelial Stalk.Flt1.Pi16 (Pi16) Thalamus / BrainAtlas - Mouse McCarroll V32	<a href="#">Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)</a>	1.871E-4	1.282E-2	1.287E-1	1.000E0	3	142
2	5fd737c1fee9d97aee8955f1bf378ead3fce138d	Thalamus-Endothelial-ENDOTHELIAL STALK-Flt1 2-Endothelial Stalk.Flt1.Pi16 (Pi16)-- Thalamus / BrainAtlas - Mouse McCarroll V32	<a href="#">Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)</a>	1.871E-4	1.282E-2	1.287E-1	1.000E0	3	142



3	16f9945e835c3506b12d904778560d065a50f059	Thalamus-Endothelial- ENDOTHELIAL STALK-Flt1 2- Endothelial Stalk.Flt1.Pi16 (Pi16)- Thalamus / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	1.871E- 4	1.282E- 2	1.287E- 1	1.000E0	3	142
4	172f1c6fdc8005a6f21d68a4dc0f8631c265d9e5	Hippocampus-Neuronal- Excitatory-eN1(Slc17a7)-eN1 1- Fibcd1-Excitatory Neuron.Slc17a7.Fibcd1-Nrip3 (CA1 Principal cells) Hippocampus / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	9.783E- 4	2.454E- 2	2.465E- 1	1.000E0	2	59
5	355a6793e2828728da62357bd2250735b0fd76b1	Hippocampus-Neuronal- Excitatory-eN2(Slc17a7 Slc17a6)-Nxph3-Excitatory Neuron.Slc17a7- Slc17a6.Nxph3-Nts (Subiculum)-  Hippocampus / BrainAtlas - Mouse McCarroll V32	Mouse Adult Brain Overview (690k cells, 9 regions, 565 cell clusters)	1.616E- 3	4.031E- 2	4.048E- 1	1.000E0	2	76

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	d6f306ebf66061bf9e9742000bfdce12d277452	Tuft-tuft-4 World / Class top	Mouse Adult Trachea	1.030E- 5	3.950E- 3	3.967E- 2	1.331E-1	4	174
2	3653cf20b1b312578a54ffd33e75a8b92874f9bf	Club-club-6 World / Class top	Mouse Adult Trachea	1.658E- 3	4.128E- 2	4.146E-1	1.000E0	2	77
3	4fadfc58102b21bf9db9d0092f3437aa78fddd99	Basal-basal-10 World / Class top	Mouse Adult Trachea	1.052E- 2	4.623E- 2	4.643E-1	1.000E0	2	199

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	7278a1a1bf9bb27aeb03852134defb31b62f30d6	facts-Brain Non-Myeloid-Cortex-24m Brain Non-Myeloid / Brain Non-Myeloid Brain Myeloid - method, tissue, subtissue, age, lineage, cell ontology and free annotation	<a href="#">Mouse Aging Atlas-Tabula Muris Senis</a>	3.359E-7	6.213E-4	6.240E-3	4.339E-3	5	186
2	a74e5a390cbeaca9de1fdb7b2a0e50783bd202dd	facts-Brain Non-Myeloid-Striatum-24m-Neuronal-neuron Brain Non-Myeloid / Brain Non-Myeloid Brain Myeloid - method, tissue, subtissue, age, lineage, cell ontology and free annotation	<a href="#">Mouse Aging Atlas-Tabula Muris Senis</a>	1.127E-5	3.950E-3	3.967E-2	1.456E-1	4	178
3	1bddbc083c36657bd6910f7466126ab325e88176	facts-Brain Non-Myeloid-Striatum-24m-Neuronal-nan Brain Non-Myeloid / Brain Non-Myeloid Brain Myeloid - method, tissue, subtissue, age, lineage, cell ontology and free annotation	<a href="#">Mouse Aging Atlas-Tabula Muris Senis</a>	1.127E-5	3.950E-3	3.967E-2	1.456E-1	4	178
4	a3922476f33d2e4137a12dbda21a1703dff79684	facts-Brain Non-Myeloid-Striatum-24m-Neuronal Brain Non-Myeloid / Brain Non-Myeloid Brain Myeloid - method, tissue, subtissue, age, lineage, cell ontology and free annotation	<a href="#">Mouse Aging Atlas-Tabula Muris Senis</a>	1.152E-5	3.950E-3	3.967E-2	1.488E-1	4	179
5	e78ba2c5cae480c16a596ce7c3bf2d480becacf4	droplet-Marrow-nan-3m-Hematologic-nan Marrow / Spleen Marrow Thymus - method, tissue, subtissue, age, lineage, cell ontology and free annotation	<a href="#">Mouse Aging Atlas-Tabula Muris Senis</a>	1.230E-5	3.950E-3	3.967E-2	1.589E-1	4	182

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	a8adce007ff4c713f71f2359b40cb3575b28c98d	droplet-Lung-30m- Hematologic-lymphocytic- CD4-positive, alpha-beta T cell-CD4-positive, alpha-beta T cell l21 30m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	3.229E- 4	1.282E- 2	1.287E- 1	1.000E0	3	171
2	8bab8be68611e49c8aad39b4df0ba0f1c143d118	droplet-Lung-18m- Hematologic-lymphocytic- CD4-positive, alpha-beta T cell-CD4-positive, alpha-beta	Mouse Aging Atlas- Tabula Muris Senis	3.812E- 4	1.282E- 2	1.287E- 1	1.000E0	3	181

		T cell I5 18m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	(Lung and Trachea)						
3	c7f2d24697affa530b748ab32b1d40bdc1bdc20a	droplet-Lung-21m-Endothelial-arterial endothelial-pulmonary artery endothelial cell 21m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	3.874E-4	1.282E-2	1.287E-1	1.000E0	3	182
4	d95635b74e8cd8bc00bfe40340806b59fb9bee43	droplet-Lung-21m-Endothelial-arterial endothelial 21m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	3.874E-4	1.282E-2	1.287E-1	1.000E0	3	182
5	087666ba949b129c53d7ace40f9e543e3875a7de	droplet-Lung-21m-Endothelial-arterial endothelial-pulmonary artery endothelial cell-pulmonary artery endothelial cell I25 21m / method, tissue, age, lineage, sublineage, cell ontologies, cell type and subtype	Mouse Aging Atlas- Tabula Muris Senis (Lung and Trachea)	4.000E-4	1.282E-2	1.287E-1	1.000E0	3	184

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	c5afdb5e7700bbd3ee8276910f9c4b4b3bcc3266	Immune cells-T cells World / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	7.176E-3	4.623E-2	4.643E-1	1.000E0	2	163
2	b646894b691a99bf2742bd9da8e578dff0e87f1f	Immune cells-B cell Immune cells / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	7.958E-3	4.623E-2	4.643E-1	1.000E0	2	172
3	e173adb5f5789dfa20f3cbc668efde5f0992ac219	Immune cells-pro-B World / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	8.137E-3	4.623E-2	4.643E-1	1.000E0	2	174
4	af420242277e2a4e2524002a2914b0538f79a134	Immune cells-T cells Immune cells / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	8.500E-3	4.623E-2	4.643E-1	1.000E0	2	178
5	f5322429963257cfd3fd813d7b7d273d3d12d622	Mesenchymal cells-Myofibroblasts Mesenchymal cells / Lineage and Cell class	Mouse Bone Marrow Niche (Baccin et al)	9.535E-3	4.623E-2	4.643E-1	1.000E0	2	189

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9f9dcf23ffb333105263132d87b90095642294cf	(1) Osterolineage cells-(11) OLC-2 (1) Osterolineage cells / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
2	394b153393904c3dba51a6bfe338afd554e66649	(3) Chondrocytes-(31) Chondrohyper World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	9.535E-3	4.623E-2	4.643E-1	1.000E0	2	189
3	ff774faf3f12759d11e50ed7d189288bb79e22e1	(4) Endothelial cells-(40) EC-arterial (4) Endothelial cells / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	9.632E-3	4.623E-2	4.643E-1	1.000E0	2	190
4	5d2b4830d025d3dbdf5623ce1c28d1036e1984a8	(3) Chondrocytes World / Cell class and subclass of bone marrow stroma cells in homeostatis	Mouse Bone Marrow Niche (Baryawno et al)	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192
5	4428b472c2042f88eae028b1770767512a515b75	(4) Endothelial cells-(42) EC-sinusoidal World / Cell class	Mouse Bone Marrow Niche	1.002E-2	4.623E-2	4.643E-1	1.000E0	2	194

and subclass of bone marrow  
stroma cells in homeostatis(Baryawno et  
al)

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 06b52f85baa31b55bb31477244892b6da79fe2c9	(03) Secretory-(4) 1wkpi  (03) Secretory / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	8.227E-3	4.623E-2	4.643E-1	1.000E0	2	175
2 bf82ba905e5eee1c39a2731702071d3de10a78b8	(00) Basal-(4) 1wkpi (00) Basal / shred by cell type and Timepoint	Mouse Trachea Epithelial Cells (MTECs)	9.153E-3	4.623E-2	4.643E-1	1.000E0	2	185

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 461a971f3e8047c727b7c6e00d2d64e97d50c6de	PND07-28-samps-Lymphocyte-T cells-T cells 1 PND07-28-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	3.835E-3	4.623E-2	4.643E-1	1.000E0	2	118
2 b5fed0e0295aa8ad323c318b59bf23cde3e758c8	E18.5-samps-Epithelial-Alveolar epithelial-AT2 progenitor E18.5-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	4.291E-3	4.623E-2	4.643E-1	1.000E0	2	125
3 9bfdbc102cdd861996b3c4eac35b606be8af97eb	PND01-03-samps-Mesenchymal-Matrix fibroblast-matrix - mature 3 PND01-03-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	5.128E-3	4.623E-2	4.643E-1	1.000E0	2	137
4 574f761962a7dd3308bd41fc529dd3ea1b8625f8	PND07-28-samps-Mesenchymal-Mesothelial PND07-28-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	6.594E-3	4.623E-2	4.643E-1	1.000E0	2	156
5 605d95a900e1443d3f6aae163ef2e893d3293203	PND07-28-samps-Mesenchymal-Mesothelial-Mesothelial PND07-28-samps / Age Group, Lineage, Cell class and subclass	Mouse_Lung_DevAtlas	6.594E-3	4.623E-2	4.643E-1	1.000E0	2	156

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1 55fe16d98ea284d05fb899888e4569c685644c7b	E16.5-Endothelial-Endothelial blood-vessel-Macrovacular EC-AEC-AEC prolifer E16.5 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	3.174E-4	1.282E-2	1.287E-1	1.000E0	3	170
2 9da012fd9a8d488cab7110a463a1d70e89f990c	PND07-Endothelial-Endothelial blood-vessel-Macrovacular EC-AEC-AEC mature PND07 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	4.325E-4	1.282E-2	1.287E-1	1.000E0	3	189
3 d87b9e9ca863270a9c7f61674271a6440c97d1f4	PND03-Endothelial-Endothelial blood-vessel-Macrovacular EC-AEC PND03 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	4.392E-4	1.282E-2	1.287E-1	1.000E0	3	190

4	3307dbccadb09c62b0e1c0235ec89bb294d748c3	PND07-Endothelial-Endothelial blood-vessel-Macrovacular EC-AEC PND07 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	4.460E-4	1.282E-2	1.287E-1	1.000E0	3	191
5	285a9d332a1e07b94f222d4b518dd56928b9e075	PND03-Endothelial-Endothelial blood-vessel-Macrovacular EC-AEC-AEC mature PND03 / Age group by Lineage, Lineage subclass, Cell type, subtypes-by-prolif	Mouse_Lung_DropSeq_E16-P28	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	87806883330ad56cf1dfd564734c0c1b64152e7c	Multiple Sclerosis-Lymphocyte-T NK Multiple Sclerosis / Disease, Lineage and Cell Type	Multiple Sclerosis	1.052E-2	4.623E-2	4.643E-1	1.000E0	2	199
2	50f2ae32e8792e2292e0113b7b27450b8dc33080	IIF-Lymphocyte-T NK IIF / Disease, Lineage and Cell Type	Multiple Sclerosis	1.062E-2	4.623E-2	4.643E-1	1.000E0	2	200

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	e22bfcd170ba23e313512f0f07c658fc6ae1b97	Healthy-Treg World / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	4.597E-4	1.282E-2	1.287E-1	1.000E0	3	193
2	6a623eeb2ba8d4e16543820bcbb41eecd00ed2	Healthy-CD4+ CTL World / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	4.808E-4	1.282E-2	1.287E-1	1.000E0	3	196
3	afdc025fa75e7926b1cc182c4a33654a2186abb1	COVID-19 Moderate-multiplets World / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	6.594E-3	4.623E-2	4.643E-1	1.000E0	2	156
4	7a81652406332afd03a9b3b529e9b5e6c0b54c28	COVID-19 Moderate-CD4+ T activated COVID-19 Moderate / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192
5	9d3795a64bf0c62f460d80730c5615869fc46933	Healthy-Treg Healthy / disease group, cell group and cell class	PBMC Atlas of COVID-19 Patients (Arunachalam et al.)	9.827E-3	4.623E-2	4.643E-1	1.000E0	2	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	9456a5879948e25bc483a7233c274da841ef2c68	severe-CD8+ Tem severe / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
2	db7367210b5480b53002407f3e66988e85a5c22f	severe World / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197
3	320cb0d79adaa1b43d90d027a876cd74f8b55ec3	severe-NK World / disease stage, cell group and cell class	PBMC Atlas of COVID-19 Patients (Guo et al.)	1.062E-2	4.623E-2	4.643E-1	1.000E0	2	200

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
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1	cbe1fb6d2c5fca7a1baf1ad20afcdf8e8e11bd84	mild-MAIT World / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	5.026E-4	1.282E-2	1.287E-1	1.000E0	3	199
2	a11fb1d7e124c352eb73fea0e0ec0fed577c97f7	mild-NK World / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	5.100E-4	1.282E-2	1.287E-1	1.000E0	3	200
3	8e96a9dd70814cb0925776613b3a12026d455cad	control-Treg World / Cohort 1 (10x PBMC) with disease condition, cell group and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	8.870E-3	4.623E-2	4.643E-1	1.000E0	2	182
4	61688846d398fbf086ea66a7b88cdf632f9d8c25	mild-Lymphocytic-CD4 T cells 3 mild / Cohort 2 (Rhapsody WB + PBMC) with disease condition, lineage and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	8.964E-3	4.623E-2	4.643E-1	1.000E0	2	183
5	aff6bfae9a2f1e17d2731315e7fe63c4601679f	severe-Lymphocytic-CD4 T cells 3 Lymphocytic / Cohort 2 (Rhapsody WB + PBMC) with disease condition, lineage and cell class	PBMC Atlas of COVID-19 Patients (Schulte-Schrepping et al.)	9.729E-3	4.623E-2	4.643E-1	1.000E0	2	191

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	97fead264e986d922669a6006cbcec530c697df7	mild COVID-19-CD8+ Tem World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
2	03c01fc384d46eec55ff730edbab8a3fde618ed8	mild COVID-19 (asymptomatic)-CD4+ CTL World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	4.953E-4	1.282E-2	1.287E-1	1.000E0	3	198
3	a9b7465ecd9fd7c5ad35970ff7c3c93b4ec2c4c3	mild COVID-19 (asymptomatic)-CD4+ CTL mild COVID-19 (asymptomatic) / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	5.026E-4	1.282E-2	1.287E-1	1.000E0	3	199
4	c7f696e55e2d959c58ec32640c71ef86ee25203c	severe COVID-19-B cell severe COVID-19 / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	5.648E-3	4.623E-2	4.643E-1	1.000E0	2	144
5	8a61395af33132783a0a37956c6f821aba5d3b1e	Healthy donor-CD8+ T naive World / disease group, cell group and cell class (v2)	PBMC Atlas of COVID-19 and Influenza Patients (Lee et al.)	7.008E-3	4.623E-2	4.643E-1	1.000E0	2	161

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	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.)	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
2	d4dfb3b561d0783cdbee4e8d27009ad81df695cb	COVID vent-Lymphocytic-T cell-CD8+ Memory T cell COVID vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	4.880E-4	1.282E-2	1.287E-1	1.000E0	3	197
3	b133d3d198360269cc449a75d34c29be377d91e0	COVID vent-Myeloid-Monocytic-CD16+ Monocyte COVID vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	1.002E-2	4.623E-2	4.643E-1	1.000E0	2	194
4	af00c31612e4fe068e5fccae05368edba46bbd20	healthy donor-Lymphocytic-T cell-CD8+ Memory T cell healthy donor / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilk et al.)	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196

5	c672915f8c8c1e948d251f6eaf9f84a5600c1193	COVID non-vent-Lymphocytic COVID non-vent / Disease condition, Lineage, Cell class and subclass	PBMC Atlas of COVID-19 patients (Wilik et al.)	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197
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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	45d52a086ced8d58e01ac51ac4a90338e8649b16	AT1-AT2 cells-Donor 04 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	5.348E-3	4.623E-2	4.643E-1	1.000E0	2	140
2	e089bf197ed60e7243160521d4390d4b40a3832b	Dendritic Cells-IPF 03 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	6.192E-3	4.623E-2	4.643E-1	1.000E0	2	151
3	3afca2a429c634af0220c1aa19ce4cf4ee3e8b3e	AT1 cells-Donor 03 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	8.048E-3	4.623E-2	4.643E-1	1.000E0	2	173
4	d2cd081bdda0eba9f6f6473c4d3939e4bee3440e	Dendritic Cells-Cryobiopsy 01 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	8.409E-3	4.623E-2	4.643E-1	1.000E0	2	177
5	e4224b2e9c4ae7da62cf670adf811f4112c7d060	-Donor 06 World / lung cells shred on cell class, cell subclass, sample id	Pathobiology of Pulmonary Fibrosis (Reyfman et al., 2019)	8.592E-3	4.623E-2	4.643E-1	1.000E0	2	179

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	3b750d4023a0a09d86113aae5a97d84391f7b482	LPS-antiTNF-Endothelial-Mes-Like-Gen Cap LPS-antiTNF / V2 postpublication: Rhesus Genome Updated; Treatment groups by lineage, cell type level1, cell type level2	PretermPrimateLungAtlas	2.960E-4	1.282E-2	1.287E-1	1.000E0	3	166
2	9e7b4b9b977e90e083f5164013e79df8bc2d492e	LPS-antiTNF-Epithelial alveolar-Mes-like-AT2 Progenitor LPS-antiTNF / V2 postpublication: Rhesus Genome Updated; Treatment groups by lineage, cell type level1, cell type level2	PretermPrimateLungAtlas	3.066E-4	1.282E-2	1.287E-1	1.000E0	3	168
3	539ea88acc6f948efdeae8b69e5c5ffaee29f1d9	LPS-IL1RA-Lymphocytic NKT-T cells-T-cells LPS-IL1RA / V2 postpublication: Rhesus Genome Updated; Treatment groups by lineage, cell type level1, cell type level2	PretermPrimateLungAtlas	3.229E-4	1.282E-2	1.287E-1	1.000E0	3	171
4	0fc692be845d4225ff8b63bf9195724fc8510c2c	LPS-IL1RA-Lymphocytic NKT-T cells LPS-IL1RA / V2 postpublication: Rhesus Genome Updated; Treatment groups by lineage, cell type level1, cell type level2	PretermPrimateLungAtlas	3.284E-4	1.282E-2	1.287E-1	1.000E0	3	172
5	9d4a4dfeebb5a8a0f3ab18c37c8ddc2cd2158575	LPS-IL1RA+antiTNF-Lymphocytic NKT-T cells-T-cells LPS-IL1RA+antiTNF / V2 postpublication: Rhesus Genome Updated; Treatment groups by lineage, cell type level1, cell type level2	PretermPrimateLungAtlas	3.513E-4	1.282E-2	1.287E-1	1.000E0	3	176



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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	186fe1ea328c942910190a4240262c0d8642ea3b	COPD-Multiplet-Multiplet World / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	4.259E-4	1.282E-2	1.287E-1	1.000E0	3	188
2	e5d0186bfb416a3eda76ac12b9379650afb6f409	IPF-Lymphoid-T Cytotoxic IPF / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	4.392E-4	1.282E-2	1.287E-1	1.000E0	3	190
3	5bfd9f5d47511441eb2d3cc3c4d7ed330ffd0bd1	COPD-Lymphoid-T Cytotoxic World / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192
4	064fefb8212fadab0ff441f4bf643559b7fdb25d	COPD-Lymphoid COPD / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192
5	58e94fe2e89cdafc6974938f97a4c162061a437d	COPD-Lymphoid-T Cytotoxic COPD / Disease state, Lineage and Cell class	Resident Cell Populations in IPF and COPD	4.597E-4	1.282E-2	1.287E-1	1.000E0	3	193

[Show 39 more annotations](#)

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	f0e46e859f7a9bdead3203889f7e20fa21f76ff0	Endothelial World / shred by cell class for bronchial biopsy	Respiratory Tissues from Nasal Brushing to Parenchyma	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	dc2b00e920efa1dcc2a6265cd1024e3249c9974f	B cells-IGG-high B cells World / Immune cells in Kidney/Urine in Lupus Nephritis	Rheumatoid Arthritis and Lupus Nephritis Atlas	8.964E-3	4.623E-2	4.643E-1	1.000E0	2	183
2	13dc3a0aaa554f63eabac37726bd1f11b66fb3dd	T cells-Effector memory CD4+ T cells World / Immune cells in Kidney/Urine in Lupus Nephritis	Rheumatoid Arthritis and Lupus Nephritis Atlas	9.632E-3	4.623E-2	4.643E-1	1.000E0	2	190
3	003ea7ddec6c1c98d2f6470bb51ebd97450eb936	T cells-GZMK+ T cells T cells / Immune cells in Rheumatoid Arthritis Joint Synovial Tissues	Rheumatoid Arthritis and Lupus Nephritis Atlas	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195
4	24d64b67aa9b0e8215ad06f9101c1314b3483620	Fibroblasts-DKK3+ Fibroblasts Fibroblasts / Immune cells in Rheumatoid Arthritis Joint Synovial Tissues	Rheumatoid Arthritis and Lupus Nephritis Atlas	1.022E-2	4.623E-2	4.643E-1	1.000E0	2	196
5	904430779c42b51d3eec62cf0cdd501b17058d8b	T cells-CCR7+ T cells World / Immune cells in Rheumatoid Arthritis Joint Synovial Tissues	Rheumatoid Arthritis and Lupus Nephritis Atlas	1.032E-2	4.623E-2	4.643E-1	1.000E0	2	197

[Show 5 more annotations](#)

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1afeeb17e263cf625a4f285203cf82f973735193	URO-Lymphocyte-T NK-CD4 CTL URO / Disease, Lineage and Cell Type	Sepsis Atlas	2.756E-4	1.282E-2	1.287E-1	1.000E0	3	162
2	15016a73c953d8d3e7c32a05ead5e7261f9914ca	Int-URO-Lymphocyte-T NK-gdT Int-URO / Disease, Lineage and Cell Type	Sepsis Atlas	3.513E-4	1.282E-2	1.287E-1	1.000E0	3	176
3	1a7948eb86ee1da607db4d0576312b2859d94523	Control-Lymphocyte-T NK-CD8 TCM Control / Disease, Lineage and Cell Type	Sepsis Atlas	3.513E-4	1.282E-2	1.287E-1	1.000E0	3	176
4	2787b52546eedada4aa413025b86841c351273f4	Leuk-UTI-Lymphocyte-T NK-CD8 TEM Leuk-UTI / Disease, Lineage and Cell Type	Sepsis Atlas	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192
5	ee99b58462f955b96d036aa67e343db047d66f64	ICU-SEP-Lymphocyte-T NK-Treg ICU-SEP / Disease, Lineage and Cell Type	Sepsis Atlas	5.724E-3	4.623E-2	4.643E-1	1.000E0	2	145

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	d05556ea185c15815a4f8643f1c01185badbeece	frontal cortex-Neuronal-GABAergic neuron-Sst-Sst Chrna2 Ptgdr frontal cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	1.284E-4	1.282E-2	1.287E-1	1.000E0	3	125
2	71107275767a0728541a3695715c44874b3e5efc	primary visual cortex-Neuronal-GABAergic neuron-Sst-Sst Chrna2 Ptgdr primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	1.949E-4	1.282E-2	1.287E-1	1.000E0	3	144
3	95b28c5bd10ffb74c0993ebd565038b9818e4bd2	primary visual cortex-Non-neuronal-astrocyte primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	2.330E-4	1.282E-2	1.287E-1	1.000E0	3	153
4	b09f8def40a1ea56722f3398f61a036667b61cd9	primary visual cortex-Non-neuronal-astrocyte-Astro primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	2.330E-4	1.282E-2	1.287E-1	1.000E0	3	153
5	3ab9d55b3db51715c1d61eca142384195ce4b54f	primary visual cortex-Non-neuronal-astrocyte-Astro-Aqp4 primary visual cortex / Per Region, Lineage, Cell class, Cell type, Cell subtype	Shared and distinct transcriptomic cell types across neocortical areas	2.330E-4	1.282E-2	1.287E-1	1.000E0	3	153

Show 31 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	40a280c1e35963dd45d1809a3e85b568344dd1f5	normal-na-Lymphocytic B-plasmablast-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	8.500E-3	4.623E-2	4.643E-1	1.000E0	2	178
2	4fe87c713770173336177e3488f7b4a3be54f71b	normal-na-Lymphocytic B-plasmablast 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	8.500E-3	4.623E-2	4.643E-1	1.000E0	2	178
3	b1a8a8c4d0fc7605eabc17dcb6bd9e8ab4fd578c	normal-na-Lymphocytic NK-NK dim-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	9.153E-3	4.623E-2	4.643E-1	1.000E0	2	185
4	1634a6044dce4e026a63976031a498c7460e3dce	systemic lupus erythematosus-treated-Lymphocytic T-T4 em 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	9.632E-3	4.623E-2	4.643E-1	1.000E0	2	190
5	08813c2f9321b82f0ec66854bb7a383aa1171780	systemic lupus erythematosus-treated-Lymphocytic T-T4 em-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	9.632E-3	4.623E-2	4.643E-1	1.000E0	2	190

Show 33 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	519a474238e370fe2a8b51460c28b39c1b01c0c9	TCGA-Thyroid-Primary Tumor-Thyroid Papillary Carcinoma-Follicular-8 TCGA-Thyroid / Sample Type by Project: Shred V9	TCGA OncoMap	4.291E-3	4.623E-2	4.643E-1	1.000E0	2	125
2	b49b15ba1458488f98d54e87100257a12ee34076	TCGA-Lung-Primary Tumor-Lung Carcinoma-Lung Adenocarcinoma	TCGA OncoMap	4.358E-3	4.623E-2	4.643E-1	1.000E0	2	126

		Mixed Subtype-6 TCGA-Lung / Sample Type by Project: Shred V9							
3	0219d0d5d21df08f816569c7eb34f1bfa095d29a	TCGA-Lung-Primary Tumor-Lung Carcinoma-Lung Acinar Adenocarcinoma-7 TCGA-Lung / Sample Type by Project: Shred V9	TCGA OncoMap	4.631E-3	4.623E-2	4.643E-1	1.000E0	2	130
4	f9aa7f2401e26f1e8cec1112a71c16e1c2784893	TCGA-Peripheral Nervous System-Primary Tumor-Paraganglioma-Paraganglioma-2 TCGA-Peripheral Nervous System / Sample Type by Project: Shred V9	TCGA OncoMap	5.724E-3	4.623E-2	4.643E-1	1.000E0	2	145
5	85501c636cd04f15ba1be24df1ba7ac909633ce8	TCGA-Mesothelium-Primary Tumor-Mesothelioma-Biphasic-6 TCGA-Mesothelium / Sample Type by Project: Shred V9	TCGA OncoMap	6.841E-3	4.623E-2	4.643E-1	1.000E0	2	159

Show 4 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ac601d53e20ca2edd022764cf2c239461ec119c7	3'-Distal airway-Immune Lymphocytic-Lymphocytic T/NK-CD8-positive, alpha-beta T cell 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	1.645E-5	3.950E-3	3.967E-2	2.126E-1	4	196
2	2d55f5a683e574873aee908da0b02b450d9340df	3'-Distal airway-Immune Lymphocytic-Lymphocytic T/NK-CD8-positive, alpha-beta T cell-CD8 T cells-CD8 T cells L.1.1.0.0 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	1.645E-5	3.950E-3	3.967E-2	2.126E-1	4	196
3	756e76440a92fa35ec8f6ad4900110ab202810cf	3'-Distal airway-Immune Lymphocytic-Lymphocytic T/NK-CD8-positive, alpha-beta T cell-CD8 T cells 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	1.645E-5	3.950E-3	3.967E-2	2.126E-1	4	196
4	1921226196b2ab7919d9f843e60d9f4bd9ec9c57	3'-Distal airway-Endothelial-Blood vessel EC-vein endothelial cell-EC venous systemic-EC venous systemic L.2.2.0.0 3' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	3.571E-4	1.282E-2	1.287E-1	1.000E0	3	177
5	d153a0bdedcd6865e6ee19575234a78b5d859ff1	5'-Parenchyma lung-Immune Lymphocytic-Lymphocytic T/NK-CD8-positive, alpha-beta T cell-CD8 T cells-CD8 T cells L.1.1.4.0 5' / 5'-vs-3', Tissue groups, Lineages, Lineage subclass, Cell type2, Cell subtype2 L4.5	The Integrated Human Lung Cell Atlas	4.392E-4	1.282E-2	1.287E-1	1.000E0	3	190

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	11ff53a748160570d2908ea9eb9779c038e5b676	356C-Myeloid-Macrophage-M2-like Macrophage (MARCO negative) Macrophage / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	4.667E-4	1.282E-2	1.287E-1	1.000E0	3	194
2	065177aaa63c0441d312260b43ecdac78c84ad03	356C-Lymphocytic-CD8+ Cytotoxic T-cell-CD8+ Cytotoxic T cell 0.5 Lymphocytic / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	5.956E-3	4.623E-2	4.643E-1	1.000E0	2	148
3	b0ed8cb6000ce8bf94444307e4b7b3574fa3fab2	367C-Epithelial cells-Epithelial-A (AT2) Epithelial cells / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	7.261E-3	4.623E-2	4.643E-1	1.000E0	2	164
4	3aea6207a011ad55a1aeb2ed9fb54d31b23694b5	367C-Epithelial cells-Epithelial-A (AT2)- Epithelial cells / Donor, Lineage, Cell class and subclass (all cells)	Tissue Stability Cell Atlas - Lung Cells	7.261E-3	4.623E-2	4.643E-1	1.000E0	2	164
5	f416d8a322f086c769659a9fab6b460a2d546ab1	367C-Myeloid-Macrophage-FABP4+ Macrophage 3 Myeloid /	Tissue Stability	7.433E-3	4.623E-2	4.643E-1	1.000E0	2	166

	Donor, Lineage, Cell class and subclass (all cells)	Cell Atlas - Lung Cells							
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[Show 40 more annotations](#)

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation	
1	d2476956ca13f9234d7e77c3ee432dd54eebeac4	(1) B cells-(1) B CD27pos  (1) B cells / Oesophagus cell shreds on cell class (v1) and cell subclass (v1)	Tissue Stability Cell Atlas - Oesophagus Cells	8.777E-3	4.623E-2	4.643E-1	1.000E0	2	181

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	8448b645508342dd0b9c81a3212d348c7cdee63c	(5) Plasma-(5) Plasma IgM  (5) Plasma / Spleen cell shreds - cell class (v1) and cell subclass (v1)	<a href="#">Tissue Stability Cell Atlas - Spleen Cells</a>	4.061E-4	1.282E-2	1.287E-1	1.000E0	2	38
2	47c0f7a1c39ba0836e40ea3ca8066457c0951575	(5) Plasma IgM World / Spleen cell shreds - cell class (v1) and cell subclass (v1)	<a href="#">Tissue Stability Cell Atlas - Spleen Cells</a>	1.002E-2	4.623E-2	4.643E-1	1.000E0	2	194
3	d3fa551bc6f5ee5890af1040415e61ecd5d46201	(1) T cells-(1) T CD4 naive  (1) T cells / Spleen cell shreds - cell class (v1) and cell subclass (v1)	<a href="#">Tissue Stability Cell Atlas - Spleen Cells</a>	1.012E-2	4.623E-2	4.643E-1	1.000E0	2	195

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	29c9b4770d0e73d59cfc7937b179484c76b6dcc	RV-13. Vascular Smooth Muscle World / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	7.401E-6	3.950E-3	3.967E-2	9.562E-2	4	160
2	e99ecae66530d1ae09330cee408c8f3950b87e67	LV-13. Vascular Smooth Muscle LV / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	9.621E-6	3.950E-3	3.967E-2	1.243E-1	4	171
3	47b3b7662cbb671ccc086dc0a0cabd65f63eb5a1	RV-13. Vascular Smooth Muscle RV / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	2.706E-4	1.282E-2	1.287E-1	1.000E0	3	161
4	f37fd95adc95d7753cf6e55ae819976513c7ec77	LV-13. Vascular Smooth Muscle World / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	2.908E-4	1.282E-2	1.287E-1	1.000E0	3	165
5	e1ea621184014415870e00d511386b8cc3e0833b	RV-17. Lymphocyte RV / Chamber and Cluster Paper	Transcriptional and Cellular Diversity of the Human Heart	6.351E-3	4.623E-2	4.643E-1	1.000E0	2	153

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	fb70918867fbd111bb192a797dcafed5f39ea299	BL-critical-LOC-Lymphoid-CTL LOC / Location, Severity, dps group, Lineage and Cell class of Upper airway (combined)	Upper Airway and Bronchi Atlas of COVID-19 Patients	1.678E-5	3.950E-3	3.967E-2	2.169E-1	4	197
2	f478dfa231fc1b12ead0183cc9d22077cdf43d1f	NS-critical-d 0-4-Lymphoid-Treg d 0-4 / Location, Severity, dps group, Lineage and Cell class of Upper airway (combined)	Upper Airway and Bronchi Atlas of COVID-19 Patients	3.937E-4	1.282E-2	1.287E-1	1.000E0	3	183
3	fb7572fb4c7c43886d57a025decad076f32a14c4	NS-critical-d 0-4-Lymphoid-CTL d 0-4 / Location, Severity, dps group, Lineage and Cell class of Upper airway (combined)	Upper Airway and Bronchi Atlas of COVID-19 Patients	4.325E-4	1.282E-2	1.287E-1	1.000E0	3	189
4	8c83050c1578d43ca0398ff920f30ea63f092a83	critical-Lymphoid-CTL critical / Severity, Lineage and Cell class of Nasopharyngeal (NS) Samples from Patients and Controls	Upper Airway and Bronchi Atlas of COVID-19 Patients	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192
5	e7e5ba94ee8fd3c04bb4c358c86d0227c563e9dc	NS-critical-d 07-13-Lymphoid-CTL d 07-13 / Location, Severity, dps group, Lineage and Cell class of Upper airway (combined)	Upper Airway and Bronchi Atlas of COVID-19 Patients	4.528E-4	1.282E-2	1.287E-1	1.000E0	3	192

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	2777eb7689b271c199021fe7d9db88ccebff14de	Endothelial-Endothelial-E Endothelial / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	9.439E-3	4.623E-2	4.643E-1	1.000E0	2	188
2	bf203931f973098b79ec681d1dd0854419819e98	Endothelial-C World / shred on cell class and cell subclass (v4)	mouse_P3_lung_dropseq (2716 cells)	9.729E-3	4.623E-2	4.643E-1	1.000E0	2	191

**16: Computational [Display Chart] 21 input genes in category / 164 annotations before applied cutoff / 10746 genes in category**

No results to display

**17: MicroRNA [Display Chart] 35 input genes in category / 4081 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	AATGTGA,MIR-23A:MSigDB	AATGTGA,MIR-23A:MSigDB	MSigDB	9.739E-5	5.445E-3	4.841E-2	3.975E-1	4	395
2	AATGTGA,MIR-23B:MSigDB	AATGTGA,MIR-23B:MSigDB	MSigDB	9.739E-5	5.445E-3	4.841E-2	3.975E-1	4	395
3	TAATGTG,MIR-323:MSigDB	TAATGTG,MIR-323:MSigDB	MSigDB	1.053E-4	5.450E-3	4.846E-2	4.298E-1	3	149
4	CTTGAT,MIR-381:MSigDB	CTTGAT,MIR-381:MSigDB	MSigDB	2.190E-4	6.927E-3	6.159E-2	8.935E-1	3	191
5	AAAGGGA,MIR-204:MSigDB	AAAGGGA,MIR-204:MSigDB	MSigDB	2.932E-4	8.022E-3	7.133E-2	1.000E0	3	211

Show 23 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-363:mirSVR highEffect	hsa-miR-363:mirSVR conserved highEffect-0.5	MicroRNA.org	5.799E-9	1.951E-5	1.735E-4	2.367E-5	9	984
2	hsa-miR-367:mirSVR highEffect	hsa-miR-367:mirSVR conserved highEffect-0.5	MicroRNA.org	1.110E-8	1.951E-5	1.735E-4	4.529E-5	9	1061
3	hsa-miR-4302:mirSVR lowEffect	hsa-miR-4302:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	1.434E-8	1.951E-5	1.735E-4	5.854E-5	11	1966
4	hsa-miR-668:mirSVR lowEffect	hsa-miR-668:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	6.421E-8	4.201E-5	3.735E-4	2.620E-4	9	1303
5	hsa-miR-92a:mirSVR highEffect	hsa-miR-92a:mirSVR conserved highEffect-0.5	MicroRNA.org	6.629E-8	4.201E-5	3.735E-4	2.705E-4	8	918

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-7108-5p		MirDB	3.779E-6	6.855E-4	6.095E-3	1.542E-2	4	172
2	hsa-let-7c-3p		MirDB	4.236E-6	6.855E-4	6.095E-3	1.729E-2	7	1114
3	hsa-miR-25-3p		MirDB	5.621E-6	7.169E-4	6.374E-3	2.294E-2	6	748
4	hsa-miR-363-3p		MirDB	5.621E-6	7.169E-4	6.374E-3	2.294E-2	6	748
5	hsa-miR-367-3p		MirDB	5.839E-6	7.221E-4	6.420E-3	2.383E-2	6	753

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-206:PITA	hsa-miR-206:PITA TOP	PITA	3.028E-6	5.961E-4	5.300E-3	1.236E-2	5	371
2	hsa-miR-1:PITA	hsa-miR-1:PITA TOP	PITA	3.028E-6	5.961E-4	5.300E-3	1.236E-2	5	371
3	hsa-miR-613:PITA	hsa-miR-613:PITA TOP	PITA	3.067E-6	5.961E-4	5.300E-3	1.252E-2	5	372
4	hsa-miR-199a-5p:PITA	hsa-miR-199a-5p:PITA TOP	PITA	1.894E-5	1.644E-3	1.462E-2	7.728E-2	4	259
5	hsa-miR-199b-5p:PITA	hsa-miR-199b-5p:PITA TOP	PITA	1.894E-5	1.644E-3	1.462E-2	7.728E-2	4	259

Show 45 more annotations

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-137:TargetScan	hsa-miR-137	TargetScan	1.405E-6	3.584E-4	3.187E-3	5.735E-3	7	942
2	hsa-miR-30a-5p:TargetScan	hsa-miR-30a-5p	TargetScan	5.011E-6	6.855E-4	6.095E-3	2.045E-2	7	1143
3	hsa-miR-30b-5p:TargetScan	hsa-miR-30b-5p	TargetScan	5.011E-6	6.855E-4	6.095E-3	2.045E-2	7	1143
4	hsa-miR-30c-5p:TargetScan	hsa-miR-30c-5p	TargetScan	5.011E-6	6.855E-4	6.095E-3	2.045E-2	7	1143
5	hsa-miR-30e-5p:TargetScan	hsa-miR-30e-5p	TargetScan	5.011E-6	6.855E-4	6.095E-3	2.045E-2	7	1143

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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	hsa-miR-6508-3p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	1.304E-5	1.330E-3	1.183E-2	5.320E-2	3	74
2	hsa-miR-6780b-3p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	2.270E-5	1.816E-3	1.615E-2	9.263E-2	3	89
3	hsa-miR-4726-5p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	5.404E-5	3.738E-3	3.324E-2	2.206E-1	3	119
4	hsa-miR-4640-5p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	5.541E-5	3.769E-3	3.351E-2	2.261E-1	3	120
5	hsa-miR-378c:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	2.635E-4	7.657E-3	6.808E-2	1.000E0	2	39

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**18: Drug** [Display Chart] 35 input genes in category / 7502 annotations before applied cutoff / 22768 genes in category

No results to display

**19: Disease** [Display Chart] 35 input genes in category / 680 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:0050951 (implicated via orthology)	hereditary ataxia (implicated via orthology)	AllianceGenome	2.863E-5	1.947E-3	1.382E-2	1.947E-2	2	7
2	DOID:0110654 (is implicated in)	long QT syndrome 13 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
3	DOID:0050990 (is implicated in)	episodic ataxia type 2 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
4	DOID:0070397 (is implicated in)	hypomyelinating leukodystrophy 23 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
5	DOID:0080454 (is implicated in)	developmental and epileptic encephalopathy 42 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
6	DOID:0111448 (is implicated in)	progressive myoclonus epilepsy 1B (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
7	DOID:0111674 (is implicated in)	intellectual developmental disorder with short stature and behavioral abnormalities (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
8	DOID:0111634 (is implicated in)	autosomal recessive nonsyndromic deafness 99 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
9	DOID:0111155 (is implicated in)	autosomal recessive spinocerebellar ataxia 21 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
10	DOID:0050704 (implicated via orthology)	childhood electroclinical syndrome (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
11	DOID:0050214 (implicated via orthology)	Lambert-Eaton myasthenic syndrome (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
12	DOID:0050990 (implicated via orthology)	episodic ataxia type 2 (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
13	DOID:0070309 (implicated via orthology)	absence epilepsy (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
14	DOID:0110002 (is implicated in)	3-methylglutaconic aciduria type 1 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
15	DOID:0070397 (implicated via orthology)	hypomyelinating leukodystrophy 23 (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
16	DOID:0111448 (implicated via orthology)	progressive myoclonus epilepsy 1B (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
17	DOID:0050956 (implicated via orthology)	spinocerebellar ataxia type 6 (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
18	DOID:0111181 (is implicated in)	familial hemiplegic migraine 1 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
19	DOID:0111155 (implicated via orthology)	autosomal recessive spinocerebellar ataxia 21 (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
20	DOID:0111979 (is implicated in)	immunodeficiency 49 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
21	DOID:0050835 (implicated via orthology)	generalized dystonia (implicated via orthology)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
22	DOID:0050956 (is implicated in)	spinocerebellar ataxia type 6 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1



23	DOID:0081210 (is implicated in)	autosomal recessive intellectual developmental disorder 46 (is implicated in)	AllianceGenome	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
24	DOID:447 (is implicated in)	renal tubular transport disease (is implicated in)	AllianceGenome	2.372E-3	1.551E-2	1.101E-1	1.000E0	1	2
25	DOID:0060764 (implicated via orthology)	autosomal recessive Robinow syndrome (implicated via orthology)	AllianceGenome	2.372E-3	1.551E-2	1.101E-1	1.000E0	1	2
26	DOID:0111181 (implicated via orthology)	familial hemiplegic migraine 1 (implicated via orthology)	AllianceGenome	3.556E-3	2.103E-2	1.493E-1	1.000E0	1	3
27	DOID:5408 (implicated via orthology)	Paget's disease of bone (implicated via orthology)	AllianceGenome	3.556E-3	2.103E-2	1.493E-1	1.000E0	1	3
28	DOID:12716 (implicated via orthology)	newborn respiratory distress syndrome (implicated via orthology)	AllianceGenome	3.556E-3	2.103E-2	1.493E-1	1.000E0	1	3
29	DOID:6364 (implicated via orthology)	migraine (implicated via orthology)	AllianceGenome	4.739E-3	2.498E-2	1.774E-1	1.000E0	1	4
30	DOID:446 (is implicated in)	primary hyperaldosteronism (is implicated in)	AllianceGenome	5.921E-3	2.939E-2	2.086E-1	1.000E0	1	5
31	DOID:4451 (biomarker via orthology)	renal carcinoma (biomarker via orthology)	AllianceGenome	5.921E-3	2.939E-2	2.086E-1	1.000E0	1	5
32	DOID:1825 (implicated via orthology)	childhood absence epilepsy (implicated via orthology)	AllianceGenome	7.101E-3	3.376E-2	2.397E-1	1.000E0	1	6
33	DOID:10024 (is implicated in)	migraine with aura (is implicated in)	AllianceGenome	7.101E-3	3.376E-2	2.397E-1	1.000E0	1	6
34	DOID:0060178 (implicated via orthology)	familial hemiplegic migraine (implicated via orthology)	AllianceGenome	8.279E-3	3.586E-2	2.546E-1	1.000E0	1	7
35	DOID:0060558 (is implicated in)	lethal congenital contracture syndrome (is implicated in)	AllianceGenome	8.279E-3	3.586E-2	2.546E-1	1.000E0	1	7
36	DOID:0050753 (implicated via orthology)	cerebellar ataxia (implicated via orthology)	AllianceGenome	9.457E-3	3.851E-2	2.734E-1	1.000E0	1	8
37	DOID:13139 (biomarker via orthology)	crescentic glomerulonephritis (biomarker via orthology)	AllianceGenome	9.457E-3	3.851E-2	2.734E-1	1.000E0	1	8
38	DOID:6364 (is implicated in)	migraine (is implicated in)	AllianceGenome	1.063E-2	4.039E-2	2.868E-1	1.000E0	1	9
39	DOID:12583 (implicated via orthology)	velocardiofacial syndrome (implicated via orthology)	AllianceGenome	1.063E-2	4.039E-2	2.868E-1	1.000E0	1	9
40	DOID:3328 (implicated via orthology)	temporal lobe epilepsy (implicated via orthology)	AllianceGenome	1.063E-2	4.039E-2	2.868E-1	1.000E0	1	9
41	DOID:0060041 (implicated via orthology)	autism spectrum disorder (implicated via orthology)	AllianceGenome	1.405E-2	4.935E-2	3.504E-1	1.000E0	2	152
42	DOID:3827 (implicated via orthology)	congenital diaphragmatic hernia (implicated via orthology)	AllianceGenome	1.415E-2	4.935E-2	3.504E-1	1.000E0	1	12

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	cv:C1832884 Migraine, familial hemiplegic, 1	Clinical Variations	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
2	cv:C5231462 Intellectual developmental disorder with short stature and behavioral abnormalities	Clinical Variations	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
3	cv:C5569084 Acute infantile liver failure-cerebellar ataxia-peripheral sensory motor neuropathy syndrome	Clinical Variations	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
4	cv:C4310716 Developmental and epileptic encephalopathy, 42	Clinical Variations	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
5	cv:C4748152 Intellectual developmental disorder with speech delay, dysmorphic facies, and t-cell abnormalities	Clinical Variations	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1

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ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	C0087012 Ataxia, Spinocerebellar	DisGeNET Curated	8.935E-6	7.378E-4	5.238E-3	6.076E-3	3	34
2	C0752121 Spinocerebellar Ataxia Type 2	DisGeNET Curated	8.935E-6	7.378E-4	5.238E-3	6.076E-3	3	34
3	C0752120 Spinocerebellar Ataxia Type 1	DisGeNET Curated	8.935E-6	7.378E-4	5.238E-3	6.076E-3	3	34
4	C0752123 Spinocerebellar Ataxia Type 5	DisGeNET Curated	8.935E-6	7.378E-4	5.238E-3	6.076E-3	3	34
5	C0752125 Spinocerebellar Ataxia Type 7	DisGeNET Curated	8.935E-6	7.378E-4	5.238E-3	6.076E-3	3	34

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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	EFO 0003060, EFO 0005937	longitudinal BMI measurement, non-small cell lung carcinoma	GWAS	8.198E-6	7.378E-4	5.238E-3	5.575E-3	2	4
2	EFO 0004842, EFO 0005090	basophil count, eosinophil count	GWAS	9.292E-6	7.378E-4	5.238E-3	6.319E-3	5	241
3	EFO 0004229	Dupuytren Contracture	GWAS	2.871E-4	8.407E-3	5.969E-2	1.952E-1	3	108
4	HP 0000964	Eczema	GWAS	4.850E-4	8.407E-3	5.969E-2	3.298E-1	4	310
5	EFO 0001357	sporadic amyotrophic lateral sclerosis	GWAS	6.132E-4	8.407E-3	5.969E-2	4.170E-1	3	140

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	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	613485	LONG QT SYNDROME 13	OMIM MedGen	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
2	616116	INTELLECTUAL DEVELOPMENTAL DISORDER, AUTOSOMAL RECESSIVE 46	OMIM MedGen	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
3	614063	N-ACETYLASPARTATE DEFICIENCY	OMIM MedGen	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
4	616287	LETHAL CONGENITAL CONTRACTURE SYNDROME 8	OMIM MedGen	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1
5	617106	DEVELOPMENTAL AND EPILEPTIC ENCEPHALOPATHY 42	OMIM MedGen	1.187E-3	8.407E-3	5.969E-2	8.071E-1	1	1

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