



! Service Alert: Planned Maintenance beginning July 25th

Most services will be unavailable for 24+ hours starting 9 PM EDT. [Learn more about the maintenance.](#)

Use GEO2R to compare two or more groups of Samples in order to identify genes that are differentially expressed across experimental conditions. Results are presented as a table of genes ordered by significance. [Full instructions](#) [YouTube](#)

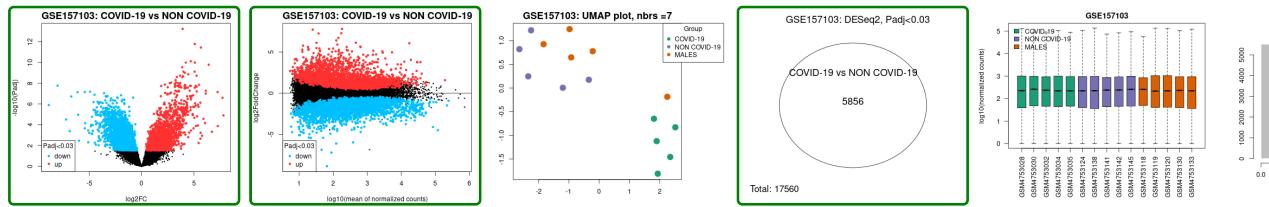
GEO accession **GSE157103** [X](#) Set Large-scale Multi-omic Analysis of COVID-19 Severity RNA-seq Series analysis [BETA](#)

[Samples](#) [Define groups](#) Selected 15 out of 126 samples

[GEO2R](#) Options Profile graph R script

[Reanalyze](#) if you changed any options.

Visualization [?](#)



Top differentially expressed genes [?](#)

[Download full table](#) [Select columns](#)

GenelD	padj	pvalue	stat	baseMean	Symbol	Description	GOFunction...	GOProcessID	GOCompo...
3000	6.34e-13	3.62e-17	75.7	200.2	GUCY2D	guanylate cyclase	GO:0001653/...	GO:0006182/...	GO:0001750/...
148534	4.01e-12	4.58e-16	70.6	144	TLCD4	TLC domain protein	GO:0003674/...	GO:0008150/...	GO:0005575/...
1063	1.48e-11	2.53e-15	67.2	138.2	CENPF	centromere protein F	GO:0003682/...	GO:0000278/...	GO:0000775/...
7704	2.98e-10	6.80e-14	60.6	2081.6	ZBTB16	zinc finger ankyrin repeat containing 16	GO:0000978/...	GO:0000122/...	GO:0001673/...
154664	4.54e-10	1.56e-13	59	625.7	ABCA13	ATP binding cassette A13	GO:0005319/...	GO:0006869/...	GO:0005886/...
4756	4.54e-10	1.35e-13	59.3	181.7	NEO1	neogenin 1	GO:0005515/...	GO:0001764/...	GO:0005654/...
89890	9.79e-10	4.44e-13	56.9	703	KBTBD6	kelch repeat domain containing 6	GO:0003674/...	GO:0006986/...	GO:0005634/...
8120	9.79e-10	4.47e-13	56.9	301.1	AP3B2	adaptor related protein 3B2	GO:0006886/...	GO:0005769/...	
4072	1.90e-09	9.76e-13	55.3	24.3	EPCAM	epithelial cell adhesion molecule	GO:0005515/...	GO:0001657/...	GO:0005886/...
144455	2.32e-09	1.32e-12	54.7	18.8	E2F7	E2F transcription factor 7	GO:0000978/...	GO:0000122/...	GO:0000785/...
56992	2.32e-09	1.46e-12	54.5	65.9	KIF15	kinesin family member 15	GO:0003774/...	GO:0000278/...	GO:0005813/...
85320	3.14e-09	2.15e-12	53.7	23.4	ABCC11	ATP binding cassette C11	GO:0005524/...	GO:0015698/...	GO:0005774/...
222389	7.23e-09	5.66e-12	51.8	207.3	BEND7	BEN domain containing 7	GO:0003677/...		GO:0070062
57522	7.23e-09	5.78e-12	51.8	36.1	SRGAP1	SLIT-ROBO gene family member 1	GO:0005096/...	GO:0007165/...	GO:0005737/...
699	7.37e-09	6.31e-12	51.6	140.2	BUB1	BUB1 mitotic kinase	GO:0004672/...	GO:0006468/...	GO:0000776/...
3643	8.87e-09	8.10e-12	51.1	378.6	INSR	insulin receptor	GO:0001540/...	GO:0001934/...	GO:0005635/...
54443	9.88e-09	1.00e-11	50.7	118.2	ANLN	anillin, actin binding protein	GO:0003779/...	GO:0000281/...	GO:0005654/...
247	9.88e-09	1.01e-11	50.6	290.8	ALOX15B	arachidonate 15-lipoxygenase	GO:0005506/...	GO:0006629/...	GO:0005634/...
9697	1.30e-08	1.48e-11	49.9	344.8	TRAM2	translocation-associated membrane protein 2	GO:0005515	GO:0006616/...	GO:0005789
55852	1.30e-08	1.43e-11	49.9	777.5	TEX2	testis expressed gene 2	GO:0003674/...	GO:0006665/...	GO:0005783/...
7153	1.30e-08	1.56e-11	49.8	296.5	TOP2A	DNA topoisomerase 2A	GO:0000287/...	GO:0000712/...	GO:0000228/...
7272	1.77e-08	2.22e-11	49.1	57	TTK	TTK protein kinase	GO:0004674/...	GO:0007051/...	GO:0000776/...
5187	1.77e-08	2.33e-11	49	1426.5	PER1	period circadian clock 1	GO:0000976/...	GO:0000122/...	GO:0005634/...
28414	1.85e-08	2.54e-11	48.8	37.1	IGHV3-64	immunoglobulin heavy chain variable 3-64	GO:0003823/...	GO:0006910/...	GO:0009897/...
342035	1.92e-08	2.74e-11	48.6	32.2	GLDN	gliomedin	GO:0086080	GO:0007165/...	GO:0005581/...
160851	1.98e-08	2.93e-11	48.5	1050.6	DGKH	diacylglycerol kinase	GO:0004143/...	GO:0006654/...	GO:0005737/...
4751	2.08e-08	3.44e-11	48.2	37.6	NEK2	NIMA related kinase 2	GO:0004672/...	GO:0000070/...	GO:0000776/...
2335	2.08e-08	3.40e-11	48.2	35.7	FN1	fibronectin 1	GO:0002020/...	GO:0001525/...	GO:0005576/...

GenelD	padj	pvalue	stat	baseMean	Symbol	Description	GOFunction...	GOProcessID	GOCompo...
28395	2.08e-08	3.26e-11	48.3	355.5	IGHV4-34	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0005576/...
497189	2.70e-08	4.77e-11	47.5	12.4	TIFAB	TIFA inhibitor	GO:0005515	GO:0007249/...	
28401	2.70e-08	4.70e-11	47.6	170.2	IGHV4-4	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
10721	2.79e-08	5.09e-11	47.4	54.9	POLQ	DNA polymer...	GO:0003682/...	GO:0006261/...	GO:0005654/...
3624	2.82e-08	5.31e-11	47.3	123.1	INHBA	inhibin subuni...	GO:0005125/...	GO:0001541/...	GO:0005576/...
101928377	3.37e-08	6.54e-11	46.9	78.9	JDP2-AS1	JDP2 antisen...			
105379321	4.17e-08	8.56e-11	46.4	75.6	LOC105379321	uncharacteriz...			
37	4.17e-08	8.54e-11	46.4	6299.9	ACADVL	acyl-CoA deh...	GO:0000062/...	GO:0001659/...	GO:0005654/...
64151	4.78e-08	1.01e-10	46	127.5	NCAPG	non-SMC con...	GO:0005515	GO:0007076/...	GO:0000779/...
63967	4.83e-08	1.05e-10	46	74.2	CLSPN	claspin	GO:0000217/...	GO:0000076/...	GO:0005634/...
105369565	4.84e-08	1.08e-10	45.9	20.8	LOC105369565	uncharacteriz...			
259266	5.41e-08	1.24e-10	45.6	97.5	ASPM	assembly fact...	GO:0005516	GO:0001764/...	GO:0005634/...
4288	5.99e-08	1.43e-10	45.3	322.8	MKI67	marker of prol...	GO:0003677/...	GO:0007049/...	GO:0000793/...
9787	5.99e-08	1.44e-10	45.3	93.2	DLGAP5	DLG associat...	GO:0005515/...	GO:0007052/...	GO:0005634/...
105372252	6.20e-08	1.52e-10	45.2	18.7	LOC105372252	uncharacteriz...			
105377068	8.37e-08	2.10e-10	44.6	249.2	LINC02009	long intergeni...			
100130698	9.78e-08	2.51e-10	44.2	51.1	LOC100130698	uncharacteriz...			
9833	1.09e-07	2.87e-10	43.9	39.7	MELK	maternal emb...	GO:0004674/...	GO:0000086/...	GO:0005737/...
4837	1.35e-07	3.62e-10	43.5	32.4	NNMT	nicotinamide ...	GO:0008112//...	GO:0006769/...	GO:0005829
56670	1.45e-07	4.24e-10	43.2	144.5	SUCNR1	succinate rec...	GO:0004930/...	GO:0002001/...	GO:0005886/...
1062	1.45e-07	4.11e-10	43.2	108.6	CENPE	centromere p...	GO:0003777/...	GO:0000278/...	GO:0000775/...
105377682	1.45e-07	4.32e-10	43.1	13.4	LINC01932	long intergeni...			
79733	1.45e-07	4.21e-10	43.2	43.6	E2F8	E2F transcrip...	GO:0000978/...	GO:0000122/...	GO:0000785/...
11065	1.45e-07	4.28e-10	43.1	124.2	UBE2C	ubiquitin conj...	GO:0004842/...	GO:0000209/...	GO:0000151/...
55176	1.65e-07	5.00e-10	42.8	474.1	SEC61A2	SEC61 transl...	GO:0003674/...	GO:0006616/...	GO:0005784
4430	1.73e-07	5.32e-10	42.7	90.2	MYO1B	myosin IB	GO:0000146/...	GO:0006892/...	GO:0005737/...
1058	1.79e-07	5.63e-10	42.6	30.2	CENPA	centromere p...	GO:0003677/...	GO:0000132/...	GO:0000775/...
83903	2.06e-07	6.60e-10	42.3	22.1	HASPIN	histone H3 as...	GO:0004672/...	GO:0000278/...	GO:0005634/...
3832	2.12e-07	6.91e-10	42.2	181.4	KIF11	kinesin family...	GO:0003777/...	GO:0000070/...	GO:0000922/...
28773	2.47e-07	8.19e-10	41.8	79.2	IGLV9-49	immunoglobu...		GO:0002250/...	GO:0005615/...
10635	3.19e-07	1.09e-09	41.3	64.2	RAD51AP1	RAD51 assoc...	GO:0000217/...	GO:0000724/...	GO:0000781/...
57082	3.19e-07	1.09e-09	41.3	90.3	KNL1	kinetochore s...	GO:0005515	GO:0001675/...	GO:0000776/...
983	4.11e-07	1.43e-09	40.7	161.3	CDK1	cyclin depend...	GO:0001618/...	GO:0000086/...	GO:0000307/...
105372270	4.11e-07	1.46e-09	40.7	12.5	LOC105372270	uncharacteriz...			
9837	4.32e-07	1.55e-09	40.6	41.8	GINS1	GINS comple...		GO:0001833/...	GO:0000811//...
112268252	4.46e-07	1.63e-09	40.5	569.2	LOC112268252	uncharacteriz...			
55536	4.56e-07	1.69e-09	40.4	633.4	CDCA7L	cell division c...	GO:0005515	GO:0006355/...	GO:0001650/...
83540	5.58e-07	2.10e-09	40	75.7	NUF2	NUF2 compo...	GO:0003674/...	GO:0007052/...	GO:0000775/...
701	6.08e-07	2.33e-09	39.8	72.1	BUB1B	BUB1 mitotic ...	GO:0004672/...	GO:0006915/...	GO:0000776/...
140606	6.50e-07	2.52e-09	39.6	82.3	SELENOM	selenoprotein M	GO:0005515/...	GO:0010269/...	GO:0005788/...
3161	6.85e-07	2.70e-09	39.5	65.9	HMMR	hyaluronan m...	GO:0005515/...	GO:0006898/...	GO:0005813/...
5357	6.99e-07	2.79e-09	39.4	33.1	PLS1	plastin 1	GO:0005200/...	GO:0001951/...	GO:0005737/...
440603	7.23e-07	2.96e-09	39.3	234.5	BCL2L15	BCL2 like 15	GO:0005515	GO:0006915/...	GO:0005634/...
157313	7.23e-07	2.97e-09	39.3	40.2	CDCA2	cell division c...		GO:0007049/...	GO:0005634/...
57650	7.33e-07	3.10e-09	39.2	75	CIP2A	cellular inhibit...	GO:0005515/...		GO:0005737/...
83752	7.33e-07	3.08e-09	39.2	1341.1	LONP2	Ion peptidase...	GO:0002020/...	GO:0006515/...	GO:0005634/...
89797	7.79e-07	3.34e-09	39	23.2	NAV2	neuron navig...	GO:0005515/...	GO:0003025/...	GO:0005614/...
5318	7.97e-07	3.46e-09	39	62.9	PKP2	plakophilin 2	GO:0005080/...	GO:0002159/...	GO:0001533/...
55355	8.12e-07	3.57e-09	38.9	83	HJURP	Holliday juncti...	GO:0003677/...	GO:0007049/...	GO:0000775/...
962	8.30e-07	3.74e-09	38.8	13827.9	CD48	CD48 molecule	GO:0003823/...	GO:0002819/...	GO:0005886/...
10733	8.30e-07	3.72e-09	38.8	79.5	PLK4	polo like kina...	GO:0004674/...	GO:0000278/...	GO:0000922/...
2334	8.54e-07	3.90e-09	38.7	98.1	AFF2	ALF transcript...	GO:0002151/...	GO:0006397/...	GO:0016607/...
54821	8.80e-07	4.07e-09	38.6	30.7	ERCC6L	ERCC excisio...	GO:0003677/...	GO:0006338/...	GO:0000776/...
79801	1.12e-06	5.23e-09	38.1	119.1	SHCBP1	SHC binding ...	GO:0005515/...	GO:0008543/...	GO:0005737/...
11169	1.12e-06	5.31e-09	38.1	71.5	WDHD1	WD repeat an...	GO:0003677/...	GO:0000278/...	GO:0005654/...
85413	1.13e-06	5.44e-09	38.1	73.8	SLC22A16	solute carrier ...	GO:0005275/...	GO:0007283/...	GO:0005829/...
9133	1.17e-06	5.68e-09	38	84.2	CCNB2	cyclin B2	GO:0005515/...	GO:0000079/...	GO:0000307/...
84296	1.23e-06	6.06e-09	37.8	50.5	GINS4	GINS comple...	GO:0005515	GO:0000727/...	GO:0000811//...
28467	1.25e-06	6.22e-09	37.8	248.6	IGHV1-24	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
4680	1.37e-06	6.88e-09	37.6	1499.9	CEACAM6	CEA cell adh...	GO:0005515/...	GO:0006915/...	GO:0005615/...
28882	1.46e-06	7.43e-09	37.4	86.2	IGKV2D-29	immunoglobu...		GO:0002250/...	GO:0005615/...
28878	1.48e-06	7.64e-09	37.4	31.9	IGKV2D-40	immunoglobu...			
55165	1.48e-06	7.67e-09	37.4	76.8	CEP55	centrosomal ...	GO:0005515/...	GO:0000281/...	GO:0005737/...
112268263	1.52e-06	8.07e-09	37.3	12.4	LOC112268263	uncharacteriz...			
259197	1.52e-06	8.15e-09	37.3	436.2	NCR3	natural cytoto...	GO:0005515/...	GO:0002429/...	GO:0005886

GenelD	padj	pvalue	stat	baseMean	Symbol	Description	GOFunction...	GOProcessID	GOCompo...
11135	1.52e-06	8.05e-09	37.3	20.2	CDC42EP1	CDC42 effect...	GO:0005515/...	GO:0007266/...	GO:0005737/...
11001	2.19e-06	1.20e-08	36.5	72.8	SLC27A2	solute carrier ...	GO:0004467/...	GO:0001561/...	GO:0005778/...
1675	2.19e-06	1.19e-08	36.5	830.8	CFD	complement f...	GO:0004252/...	GO:0006508/...	GO:0005576/...
81930	2.21e-06	1.22e-08	36.4	26.8	KIF18A	kinesin family...	GO:0003777/...	GO:0000070/...	GO:0000776/...
28424	2.33e-06	1.31e-08	36.3	202.3	IGHV3-48	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0005576/...
6576	2.43e-06	1.38e-08	36.2	556.6	SLC25A1	solute carrier ...	GO:0015137/...	GO:0006094/...	GO:0005634/...
105378751	2.52e-06	1.44e-08	36.1	25.1	LOC105378751	uncharacteriz...			
1088	2.53e-06	1.46e-08	36.1	2778	CEACAM8	CEA cell adh...	GO:0005515/...	GO:0006955/...	GO:0005615/...
28913	2.63e-06	1.53e-08	36	1429.5	IGKV3-15	immunoglobu...	GO:0003823	GO:0002250/...	GO:0005576/...
1397	2.70e-06	1.59e-08	35.9	122.6	CRIP2	cysteine rich ...	GO:0005515/...	GO:0008284/...	GO:0005938
10161	2.74e-06	1.63e-08	35.9	2111.3	LPAR6	lysophosphati...	GO:0004930/...	GO:0001835/...	GO:0005886
79630	2.81e-06	1.68e-08	35.8	62.2	C1orf54	chromosome ...			GO:0005576
54438	2.81e-06	1.72e-08	35.8	419.5	GFOD1	glucose-fruct...	GO:0000166/...		GO:0005576
55388	2.81e-06	1.73e-08	35.7	37	MCM10	minichromos...	GO:0003688/...	GO:0006270/...	GO:0005634/...
84326	2.81e-06	1.70e-08	35.8	515	METTL26	methyltransfe...			
28875	3.02e-06	1.91e-08	35.5	465.4	IGKV3D-15	immunoglobu...		GO:0002250/...	GO:0005615/...
28595	3.02e-06	1.91e-08	35.5	44.1	TRBV7-3	T cell recepto...		GO:0002250/...	GO:0005886/...
23659	3.02e-06	1.90e-08	35.6	418.5	PLA2G15	phospholipas...	GO:0004622/...	GO:0006629/...	GO:0005576/...
28449	3.11e-06	1.99e-08	35.5	142.7	IGHV3-13	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0005576/...
513	3.19e-06	2.08e-08	35.4	414.4	ATP5F1D	ATP synthase...	GO:0005515/...	GO:0009060/...	GO:0000275/...
2078	3.19e-06	2.08e-08	35.4	146.7	ERG	ETS transcrip...	GO:0000978/...	GO:0006357/...	GO:0000785/...
203260	3.20e-06	2.10e-08	35.4	308.3	CCDC107	coiled-coil do...	GO:0005515		GO:0016020
112483	3.25e-06	2.15e-08	35.3	1366.9	SAT2	spermidine/s...	GO:0004145/...	GO:0006596/...	GO:0005737/...
5746	3.26e-06	2.17e-08	35.3	33.6	PTH2R	parathyroid h...	GO:0004991/...	GO:0007166/...	GO:0005886
5790	3.45e-06	2.32e-08	35.2	820.7	PTPRCAP	protein tyrosi...	GO:0005515	GO:0006952	GO:0005886
28386	3.50e-06	2.37e-08	35.1	99.7	IGHV5-10-1	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
28803	3.61e-06	2.48e-08	35	400.6	IGLV3-10	immunoglobu...		GO:0002250/...	GO:0005615/...
10695	3.74e-06	2.58e-08	34.9	10842.3	CNPY3	canopy FGF ...	GO:0005102/...	GO:0045087	GO:0005788
22974	4.04e-06	2.81e-08	34.8	139.7	TPX2	TPX2 microtu...	GO:0005515/...	GO:0000278/...	GO:0000922/...
28393	4.26e-06	2.99e-08	34.7	57.6	IGHV4-55	immunoglobu...			
4173	4.30e-06	3.04e-08	34.6	269.7	MCM4	minichromos...	GO:0003678/...	GO:0000727/...	GO:0000781/...
102724971	4.43e-06	3.16e-08	34.5	32.2	LOC102724971	putative V-set...			
6241	4.55e-06	3.30e-08	34.5	443.1	RRM2	ribonucleotid...	GO:0004748/...	GO:0001824/...	GO:0005634/...
9055	4.55e-06	3.28e-08	34.5	169.6	PRC1	protein regula...	GO:0005515/...	GO:0000022/...	GO:0000922/...
53827	4.72e-06	3.47e-08	34.4	7573.6	FXYD5	FXYD domai...	GO:0003779/...	GO:0006811//...	GO:0016020
28799	4.72e-06	3.48e-08	34.3	67.4	IGLV3-16	immunoglobu...		GO:0002250/...	GO:0005615/...
55076	4.78e-06	3.57e-08	34.3	86.2	TMEM45A	transmembra...	GO:0005515		GO:0016020
8447	4.78e-06	3.58e-08	34.3	186.2	DOC2B	double C2 do...	GO:0005509/...	GO:0006887/...	GO:0005737/...
63898	4.84e-06	3.67e-08	34.2	47.8	SH2D4A	SH2 domain ...	GO:0005515/...		GO:0005737/...
283870	4.84e-06	3.65e-08	34.3	69.8	BRICD5	BRICHOS do...	GO:0005515	GO:0042127	GO:0005615/...
101928517	4.89e-06	3.74e-08	34.2	317	LOC101928517	uncharacteriz...			
6181	4.91e-06	3.79e-08	34.2	13570.1	RPLP2	ribosomal pro...	GO:0003735/...	GO:0002181/...	GO:0005737/...
653820	5.16e-06	4.07e-08	34	39.4	FAM72B	family with se...			GO:0005829/...
102723170	5.16e-06	4.05e-08	34	51.8	IGHV3-64D	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
28450	5.16e-06	4.05e-08	34	193.5	IGHV3-11	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0005576/...
6319	5.41e-06	4.30e-08	33.9	240.4	SCD	stearoyl-CoA ...	GO:0004768/...	GO:0006636/...	GO:0005730/...
7380	5.41e-06	4.32e-08	33.9	50.9	UPK3A	uroplakin 3A	GO:0005515	GO:0000902/...	GO:0005789/...
1942	5.62e-06	4.52e-08	33.8	56.7	EFNA1	ephrin A1	GO:0005102/...	GO:0000122/...	GO:0005576/...
58155	5.83e-06	4.76e-08	33.7	568.6	PTBP2	polypyrimidin...	GO:0003723/...	GO:0006376/...	GO:0005634/...
990	5.83e-06	4.75e-08	33.7	98.1	CDC6	cell division c...	GO:0000166/...	GO:0000076/...	GO:0000922/...
857	5.89e-06	4.87e-08	33.7	26.4	CAV1	caveolin 1	GO:0005102/...	GO:0000122/...	GO:0000139/...
120425	5.89e-06	4.87e-08	33.7	43698.6	JAML	junction adhe...	GO:0005178/...	GO:0007157/...	GO:0005654/...
28638	5.91e-06	4.99e-08	33.6	5465.4	TRBC2	T cell recepto...	GO:0003823/...	GO:0002250/...	GO:0009897/...
1368	5.91e-06	4.94e-08	33.6	472.4	CPM	carboxypepti...	GO:0004180/...	GO:0006518/...	GO:0005576/...
116840	5.91e-06	4.99e-08	33.6	731.8	CNTROB	centrobin, ce...	GO:0005515/...	GO:0007099/...	GO:0005737/...
6518	6.29e-06	5.35e-08	33.5	291.4	SLC2A5	solute carrier ...	GO:0005353/...	GO:0003044/...	GO:0005886/...
28791	6.31e-06	5.40e-08	33.5	139	IGLV3-27	immunoglobu...	GO:0003823	GO:0002250/...	GO:0005576/...
6491	6.43e-06	5.54e-08	33.4	42.4	STIL	STIL centriola...	GO:0005515/...	GO:0000578/...	GO:0005737/...
728377	6.49e-06	5.63e-08	33.4	39.3	ARHGEF34P	Rho guanine ...			
54855	6.54e-06	5.71e-08	33.4	1032.8	TENT5C	terminal nucl...	GO:0003723/...	GO:0001701/...	GO:0005634/...
28426	6.67e-06	5.86e-08	33.3	86.5	IGHV3-43	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
84266	6.85e-06	6.06e-08	33.2	231.7	ALKBH7	alkB homolog 7	GO:0005515/...	GO:0006631/...	GO:0005739/...
112268097	6.91e-06	6.16e-08	33.2	4404.4	MYG1-AS1	MYG1 antise...			
105369593	7.05e-06	6.32e-08	33.2	12.7	LOC105369593	uncharacteriz...			
23397	7.13e-06	6.43e-08	33.1	70.1	NCAPH	non-SMC con...	GO:0003682/...	GO:0007076/...	GO:0000794/...

GenelD	padj	pvalue	stat	baseMean	Symbol	Description	GOFunction...	GOProcessID	GOCompo...
28560	7.25e-06	6.58e-08	33.1	73	TRBV27	T cell recepto...		GO:0002250/...	GO:0005886/...
5013	7.28e-06	6.65e-08	33.1	131	OTX1	orthodenticle ...	GO:0000978/...	GO:0006357/...	GO:000785/...
81544	7.51e-06	6.91e-08	33	316.5	GDPD5	glycerophosp...	GO:0004435/...	GO:0006629/...	GO:0005886/...
102723168	7.61e-06	7.08e-08	32.9	75.5	IGHV2-70D	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
102724638	7.61e-06	7.04e-08	32.9	125.2	LOC102724638	uncharacteriz...			
6415	7.77e-06	7.28e-08	32.9	1730.8	SELENOW	selenoprotein...	GO:0016209	GO:0010269/...	GO:0005829
146909	8.01e-06	7.54e-08	32.8	31.5	KIF18B	kinesin family...	GO:0003774/...	GO:0000070/...	GO:0000235/...
4681	8.27e-06	7.84e-08	32.7	44.5	NBL1	NBL1, DAN f...	GO:0005515/...	GO:0007165/...	GO:0005615
81610	8.33e-06	7.94e-08	32.7	17.5	FAM83D	family with se...	GO:0005515/...	GO:0001837/...	GO:0005737/...
8045	8.52e-06	8.17e-08	32.6	341.8	RASSF7	Ras associati...	GO:0005515	GO:0006915/...	GO:0005737/...
2829	8.57e-06	8.32e-08	32.6	242.3	XCR1	X-C motif che...	GO:0004950/...	GO:0006935/...	GO:0005886/...
11113	8.57e-06	8.31e-08	32.6	46.2	CIT	citron rho-inte...	GO:0001223/...	GO:0000086/...	GO:0005634/...
28455	8.58e-06	8.43e-08	32.6	92.8	IGHV2-26	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
8938	8.58e-06	8.38e-08	32.6	222.2	BAIAP3	BAI1 associat...	GO:0000149/...	GO:0001956/...	GO:0005829/...
57447	8.67e-06	8.56e-08	32.5	143.8	NDRG2	NDRG family ...	GO:0003674/...	GO:0001818/...	GO:0005634/...
729178	8.80e-06	8.74e-08	32.5	121.3	STXBP5-AS1	STXBP5 anti...			
2650	8.80e-06	8.79e-08	32.5	647.1	GCNT1	glucosaminyl ...	GO:0003829/...	GO:0009101/...	GO:0000139/...
29028	8.92e-06	8.96e-08	32.5	303.5	ATAD2	ATPase famil...	GO:0003682/...	GO:0006325/...	GO:0005634/...
3040	8.98e-06	9.07e-08	32.4	118573.3	HBA2	hemoglobin s...	GO:0004601/...	GO:0010942/...	GO:0005576/...
647135	9.06e-06	9.31e-08	32.4	418.7	SRGAP2B	SLIT-ROBO ...		GO:0007399/...	GO:0005737
128239	9.06e-06	9.23e-08	32.4	57.1	IQGAP3	IQ motif cont...	GO:0005096/...	GO:0000082/...	GO:0005737/...
116931	9.06e-06	9.31e-08	32.4	88	MED12L	mediator com...	GO:0003713/...	GO:0006351/...	GO:0016592
55486	9.24e-06	9.55e-08	32.3	1165.5	PARL	presenilin ass...	GO:0004175/...	GO:0006465/...	GO:0005634/...
112268460	9.40e-06	9.77e-08	32.3	921.9	LOC112268460	uncharacteriz...			
28622	1.02e-05	1.07e-07	32.1	41.6	TRBJ2-7	T cell recepto...		GO:0002250	GO:0042101
100526836	1.04e-05	1.10e-07	32.1	1619.9	BLOC1S5-TX...	BLOC1S5-TX...			
79803	1.05e-05	1.11e-07	32	529.2	HPS6	HPS6 biogen...	GO:0005515/...	GO:0006996/...	GO:0005765/...
8444	1.12e-05	1.19e-07	31.9	32.4	DYRK3	dual specificit...	GO:0000287/...	GO:0006468/...	GO:0000242/...
100133941	1.12e-05	1.20e-07	31.9	3716.8	CD24	CD24 molecule	GO:0005515/...	GO:0001666/...	GO:0009897/...
57175	1.13e-05	1.21e-07	31.8	1582.1	CORO1B	coronin 1B	GO:0005515/...	GO:0007015/...	GO:0001725/...
993	1.15e-05	1.24e-07	31.8	42.2	CDC25A	cell division c...	GO:0004721/...	GO:0000079/...	GO:0005634/...
196385	1.15e-05	1.27e-07	31.8	103.9	DNAH10	dynein axone...	GO:0005524/...	GO:0007018	GO:0005874/...
102724977	1.15e-05	1.26e-07	31.8	41	LOC102724977	uncharacteriz...			
28409	1.15e-05	1.28e-07	31.7	39.4	IGHV3-73	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
100288637	1.15e-05	1.27e-07	31.8	56.2	LOC100288637	OTU deubiqui...			
55049	1.15e-05	1.28e-07	31.7	243.9	REX1BD	required for e...	GO:0005515		
54923	1.15e-05	1.28e-07	31.7	445.5	LIME1	Lck interactin...	GO:0005515/...	GO:0002250/...	GO:0005615/...
105373262	1.15e-05	1.29e-07	31.7	185.7	LOC105373262	uncharacteriz...			
6023	1.17e-05	1.32e-07	31.7	96.9	RMRP	RNA compon...	GO:0000171/...	GO:0001172/...	GO:0000172/...
146722	1.19e-05	1.35e-07	31.6	4220.2	CD300LF	CD300 molec...	GO:0001786/...	GO:0033004/...	GO:0005886
3004	1.19e-05	1.35e-07	31.6	242.4	GZMM	granzyme M	GO:0004252/...	GO:0001913/...	GO:0005576/...
55225	1.19e-05	1.36e-07	31.6	879.8	RAVER2	ribonucleopro...	GO:0003723/...	GO:0000381	GO:0005634/...
9928	1.19e-05	1.37e-07	31.6	39.4	KIF14	kinesin family...	GO:0003777/...	GO:0001558/...	GO:0005634/...
28793	1.20e-05	1.38e-07	31.6	1463.2	IGLV3-25	immunoglobu...	GO:0003823	GO:0002250/...	GO:0005576/...
28937	1.23e-05	1.44e-07	31.5	294.5	IGKV1-17	immunoglobu...	GO:0003823	GO:0002250/...	GO:0005576/...
81567	1.23e-05	1.44e-07	31.5	1578.1	TXNDC5	thioredoxin d...	GO:0003756/...	GO:0006457/...	GO:0005576/...
24137	1.29e-05	1.51e-07	31.4	53.4	KIF4A	kinesin family...	GO:0003677/...	GO:0000281/...	GO:0005654/...
102723407	1.35e-05	1.59e-07	31.3	463.5	LOC102723407	immunoglobu...			
915	1.39e-05	1.64e-07	31.2	2436.1	CD3D	CD3 delta su...	GO:0004888/...	GO:0002250/...	GO:0005737/...
105378539	1.42e-05	1.69e-07	31.2	473.7	LOC105378539				
102724843	1.43e-05	1.70e-07	31.2	22.9	LOC102724843	uncharacteriz...			
1719	1.50e-05	1.81e-07	31	538.6	DHFR	dihydrofolate ...	GO:0000900/...	GO:0006545/...	GO:0005739/...
376497	1.50e-05	1.81e-07	31.1	336.4	SLC27A1	solute carrier ...	GO:0000166/...	GO:0001579/...	GO:0005743/...
113655	1.54e-05	1.87e-07	31	76	MFSD3	major facilitat...	GO:0005515/...	GO:1902600	GO:0016020
51203	1.54e-05	1.87e-07	31	252.8	NUSAP1	nucleolar and...	GO:0003677/...	GO:0000070/...	GO:0005694/...
4050	1.55e-05	1.89e-07	31	4938.1	LTB	lymphotoxin b...	GO:0005102/...	GO:0006955/...	GO:0005575/...
28923	1.56e-05	1.91e-07	30.9	234.1	IGKV2-24	immunoglobu...		GO:0002250/...	GO:0005615/...
90313	1.58e-05	1.94e-07	30.9	431.3	TP53I13	tumor protein ...	GO:0003674/...	GO:0009410/...	GO:0005737/...
728833	1.61e-05	1.99e-07	30.9	37.3	FAM72D	family with se...	GO:0005515		GO:0005829/...
5032	1.62e-05	2.02e-07	30.8	162.9	P2RY11	purinergic rec...	GO:0030594/...	GO:0006952/...	GO:0005886
6137	1.63e-05	2.04e-07	30.8	24682	RPL13	ribosomal pro...	GO:0003723/...	GO:0001824/...	GO:0005634/...
653464	1.66e-05	2.09e-07	30.8	391.4	SRGAP2C	SLIT-ROBO ...	GO:0042803/...	GO:0021816/...	GO:0005737
8928	1.69e-05	2.13e-07	30.7	227.4	FOXH1	forkhead box ...	GO:0000976/...	GO:0000122/...	GO:0000785/...
6142	1.69e-05	2.14e-07	30.7	10018.5	RPL18A	ribosomal pro...	GO:0003723/...	GO:0002181/...	GO:0005737/...
28907	1.71e-05	2.17e-07	30.7	40.8	IGKV5-2	immunoglobu...	GO:0003823	GO:0002250/...	GO:0005576/...

GenelD	padj	pvalue	stat	baseMean	Symbol	Description	GOFunctio...	GOProcessID	GOCompo...
101928383	1.71e-05	2.18e-07	30.7	26.7	LOC101928383				
445328	1.74e-05	2.23e-07	30.6	31.5	ARHGEF35	Rho guanine ...			
140467	1.79e-05	2.30e-07	30.6	111.3	ZNF358	zinc finger pr...	GO:0000978/...	GO:0006357/...	GO:0005634
105374925	1.81e-05	2.37e-07	30.5	171.6	LOC105374925	uncharacteriz...			
375704	1.81e-05	2.35e-07	30.5	65.3	ENHO	energy home...	GO:0005179	GO:0007165/...	GO:0005576/...
10233	1.81e-05	2.36e-07	30.5	100.6	LRRC23	leucine rich r...	GO:0003674/...	GO:0008150	GO:0005575/...
28444	1.85e-05	2.43e-07	30.5	412.1	IGHV3-21	immunoglobu...	GO:0003823/...	GO:0006910/...	GO:0009897/...
728658	1.88e-05	2.48e-07	30.4	6877.2	RPL13AP5	ribosomal pro...			
28941	1.93e-05	2.56e-07	30.4	354.4	IGKV1-9	immunoglobu...		GO:0002250/...	GO:0005615/...
401551	1.94e-05	2.58e-07	30.3	207.4	WDR38	WD repeat do...		GO:0002244	
4574	1.94e-05	2.59e-07	30.3	9999.6	TRNS1	tRNA-Ser			
5168	1.95e-05	2.61e-07	30.3	28.5	ENPP2	ectonucleotid...	GO:0003676/...	GO:0006897/...	GO:0005615/...
5806	1.95e-05	2.64e-07	30.3	324.5	PTX3	pentraxin 3	GO:0001849/...	GO:0001550/...	GO:0005576/...
112267953	1.95e-05	2.65e-07	30.3	364.3	LOC112267953				
2003	1.95e-05	2.65e-07	30.3	69.4	ELK2AP	ETS transcrip...			
131540	1.96e-05	2.68e-07	30.3	793.5	ZDHHC19	zinc finger D...	GO:0019706	GO:0006612/...	GO:0000139/...
123099	1.96e-05	2.68e-07	30.3	238.9	DEGS2	delta 4-desat...	GO:0000170/...	GO:0006667/...	GO:0005789
55789	2.01e-05	2.77e-07	30.2	55	DEPDC1B	DEP domain ...	GO:0005096	GO:0016477/...	
126789	2.02e-05	2.80e-07	30.2	140.1	PUSL1	pseudouridin...	GO:0003723/...	GO:0031119	GO:0005739/...
105373422	2.04e-05	2.84e-07	30.1	16.1	LOC105373422	uncharacteriz...			
4353	2.04e-05	2.84e-07	30.1	1830.2	MPO	myeloperoxid...	GO:0003682/...	GO:0001878/...	GO:0005576/...
2731	2.08e-05	2.91e-07	30.1	41.4	GLDC	glycine decar...	GO:0004375/...	GO:0006546/...	GO:0005654/...
26271	2.09e-05	2.93e-07	30.1	122.9	FBXO5	F-box protein 5	GO:0005515/...	GO:0001556/...	GO:0005634/...
1936	2.14e-05	3.03e-07	30	10746.1	EEF1D	eukaryotic tra...	GO:0003677/...	GO:0006414/...	GO:0001650/...
286204	2.14e-05	3.02e-07	30	129.5	CRB2	crumbs cell p...	GO:0005509/...	GO:0001707/...	GO:0005737/...
54972	2.15e-05	3.05e-07	30	99.1	TMEM132A	transmembra...	GO:0003674	GO:0008150	GO:0000139/...
401399	2.16e-05	3.08e-07	30	160	PRRT4	proline rich tr...			GO:0016020

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