

Supplementary Table 1 Enriched GO and KEGG pathways of genes in the PTR-GUS set

A ID	GO-BP Description	Count in geneset	pvalue	p.adjust
GO:0051607	defense response to virus	48	1.26E-18	3.42E-15
GO:0140546	defense response to symbiont	48	1.45E-18	3.42E-15
GO:0009615	response to virus	55	6.66E-18	1.05E-14
GO:0045071	negative regulation of viral genome	20	1.97E-15	2.32E-12
GO:0048525	negative regulation of viral process	23	4.79E-14	4.51E-11
GO:0050792	regulation of viral process	29	3.61E-13	2.83E-10
GO:1903900	regulation of viral life cycle	27	5.26E-13	3.28E-10
GO:0008544	epidermis development	44	5.58E-13	3.28E-10
GO:0045069	regulation of viral genome replication	21	1.61E-12	8.00E-10
GO:0043588	skin development	39	1.79E-12	8.00E-10
GO:0002237	response to molecule of bacterial origin	43	1.87E-12	8.00E-10
GO:0045787	positive regulation of cell cycle	43	2.26E-12	8.85E-10
GO:0032496	response to lipopolysaccharide	41	4.14E-12	1.47E-09
GO:0140014	mitotic nuclear division	40	4.37E-12	1.47E-09
GO:0000280	nuclear division	50	5.59E-12	1.76E-09
GO:0031424	keratinization	20	7.21E-12	2.12E-09
GO:0019221	cytokine-mediated signaling pathway	50	1.73E-11	4.69E-09
GO:0032103	positive regulation of response to external stimulus	48	1.79E-11	4.69E-09
GO:0019079	viral genome replication	24	2.00E-11	4.95E-09
GO:0000070	mitotic sister chromatid segregation	30	2.61E-11	6.15E-09
GO:0030216	keratinocyte differentiation	27	4.28E-11	9.59E-09
GO:0007059	chromosome segregation	42	5.04E-11	1.08E-08
GO:0000819	sister chromatid segregation	32	7.03E-11	1.44E-08
GO:0007088	regulation of mitotic nuclear division	22	1.13E-10	2.18E-08
GO:0002831	regulation of response to biotic stimulus	40	1.16E-10	2.18E-08
GO:0090068	positive regulation of cell cycle process	33	1.49E-10	2.68E-08
GO:0052548	regulation of endopeptidase activity	44	1.57E-10	2.68E-08
GO:0019058	viral life cycle	37	1.59E-10	2.68E-08
GO:0051983	regulation of chromosome segregation	23	1.77E-10	2.88E-08
GO:0009913	epidermal cell differentiation	31	2.04E-10	3.21E-08
GO:0051783	regulation of nuclear division	24	2.15E-10	3.27E-08
GO:1905818	regulation of chromosome separation	21	2.25E-10	3.31E-08
GO:0051304	chromosome separation	23	2.83E-10	4.03E-08
GO:0001819	positive regulation of cytokine production	47	2.91E-10	4.03E-08
GO:0016032	viral process	43	3.13E-10	4.21E-08
GO:0034340	response to type I interferon	18	4.24E-10	5.54E-08
GO:0052547	regulation of peptidase activity	45	4.55E-10	5.78E-08
GO:0050777	negative regulation of immune response	27	5.69E-10	7.05E-08
GO:0071216	cellular response to biotic stimulus	32	6.91E-10	8.35E-08
GO:0098813	nuclear chromosome segregation	36	7.20E-10	8.47E-08
GO:0031349	positive regulation of defense response	35	8.00E-10	9.04E-08
GO:0071219	cellular response to molecule of bacterial origin	30	8.06E-10	9.04E-08
GO:0071357	cellular response to type I interferon	17	9.65E-10	1.06E-07
GO:0071222	cellular response to lipopolysaccharide	29	9.93E-10	1.06E-07
GO:0019730	antimicrobial humoral response	21	2.19E-09	2.29E-07
GO:0032479	regulation of type I interferon production	19	3.55E-09	3.56E-07
GO:0032606	type I interferon production	19	3.55E-09	3.56E-07
GO:0060337	type I interferon signaling pathway	16	5.12E-09	5.02E-07

GO:1902850	microtubule cytoskeleton organization involved in mitosis	23	1.23E-08	1.18E-06
GO:0060759	regulation of response to cytokine stimulus	24	1.65E-08	1.56E-06
GO:0002697	regulation of immune effector process	37	1.86E-08	1.71E-06
GO:0001959	regulation of cytokine-mediated signaling pathway	23	1.97E-08	1.78E-06
GO:0050727	regulation of inflammatory response	39	2.04E-08	1.81E-06
GO:0045088	regulation of innate immune response	28	2.42E-08	2.11E-06
GO:0032481	positive regulation of type I interferon production	14	2.68E-08	2.29E-06
GO:0010965	regulation of mitotic sister chromatid separation	17	4.54E-08	3.82E-06
GO:0045824	negative regulation of innate immune response	15	5.65E-08	4.67E-06
GO:0002683	negative regulation of immune system process	40	6.23E-08	5.06E-06
GO:0042742	defense response to bacterium	36	7.11E-08	5.66E-06
GO:0051306	mitotic sister chromatid separation	17	7.21E-08	5.66E-06
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	28	8.92E-08	6.85E-06
GO:0044772	mitotic cell cycle phase transition	41	9.02E-08	6.85E-06
GO:0050729	positive regulation of inflammatory response	21	9.65E-08	7.21E-06
GO:0031348	negative regulation of defense response	29	1.00E-07	7.36E-06
GO:0030071	regulation of mitotic metaphase/anaphase transition	16	1.09E-07	7.88E-06
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	15	1.15E-07	8.17E-06
GO:0033046	negative regulation of sister chromatid segregation	12	1.35E-07	9.24E-06
GO:0033048	negative regulation of mitotic sister chromatid segregation	12	1.35E-07	9.24E-06
GO:2000816	negative regulation of mitotic sister chromatid separation	12	1.35E-07	9.24E-06
GO:0033045	regulation of sister chromatid segregation	17	1.72E-07	1.13E-05
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	16	1.73E-07	1.13E-05
GO:1902099	regulation of metaphase/anaphase transition of cell cycle	16	1.73E-07	1.13E-05
GO:0007052	mitotic spindle organization	19	1.87E-07	1.20E-05
GO:0051985	negative regulation of chromosome segregation	12	2.13E-07	1.34E-05
GO:1905819	negative regulation of chromosome separation	12	2.13E-07	1.34E-05
GO:1901987	regulation of cell cycle phase transition	39	2.23E-07	1.38E-05
GO:0033044	regulation of chromosome organization	27	2.49E-07	1.53E-05
GO:0044784	metaphase/anaphase transition of cell cycle	16	2.69E-07	1.63E-05
GO:0006260	DNA replication	29	2.93E-07	1.74E-05
GO:0043616	keratinocyte proliferation	12	3.29E-07	1.94E-05
GO:0007249	I-kappaB kinase/NF-kappaB signaling	29	3.39E-07	1.97E-05
GO:0007094	mitotic spindle assembly checkpoint	11	3.79E-07	2.12E-05
GO:0071173	spindle assembly checkpoint signaling	11	3.79E-07	2.12E-05
GO:0071174	mitotic spindle checkpoint signaling	11	3.79E-07	2.12E-05
GO:0033047	regulation of mitotic sister chromatid segregation	12	4.06E-07	2.22E-05

GO:0045839	negative regulation of mitotic nuclear	12	4.06E-07	2.22E-05
GO:0034341	response to interferon-gamma	19	4.22E-07	2.29E-05
GO:0031577	spindle checkpoint signaling	11	4.79E-07	2.56E-05
GO:0032608	interferon-beta production	12	4.98E-07	2.60E-05
GO:0032648	regulation of interferon-beta production	12	4.98E-07	2.60E-05
GO:0002832	negative regulation of response to biotic stimulus	17	5.66E-07	2.93E-05
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	11	6.02E-07	3.08E-05
GO:0071621	granulocyte chemotaxis	18	6.28E-07	3.18E-05
GO:0032102	negative regulation of response to external stimulus	37	6.49E-07	3.23E-05
GO:0051383	kinetochore organization	8	6.52E-07	3.23E-05
GO:0002221	pattern recognition receptor signaling pathway	22	6.60E-07	3.24E-05
GO:0002833	positive regulation of response to biotic stimulus	22	7.24E-07	3.49E-05
GO:0002718	regulation of cytokine production involved in immune response	17	7.25E-07	3.49E-05
GO:0002367	cytokine production involved in immune response	17	9.24E-07	4.39E-05
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	11	9.34E-07	4.40E-05
GO:1901990	regulation of mitotic cell cycle phase transition	32	9.56E-07	4.46E-05
GO:0035456	response to interferon-beta	9	9.96E-07	4.60E-05
GO:0007051	spindle organization	22	1.35E-06	6.17E-05
GO:0071347	cellular response to interleukin-1	16	1.52E-06	6.89E-05
GO:0051784	negative regulation of nuclear division	12	1.55E-06	6.95E-05
GO:0008608	attachment of spindle microtubules to kinetochore	10	1.70E-06	7.55E-05
GO:0007093	mitotic cell cycle checkpoint signaling	18	2.09E-06	9.22E-05
GO:0002700	regulation of production of molecular mediator of immune response	21	2.52E-06	0.00011
GO:0097530	granulocyte migration	19	2.72E-06	0.00012
GO:0018149	peptide cross-linking	9	2.95E-06	0.00013
GO:0071706	tumor necrosis factor superfamily cytokine production	21	2.99E-06	0.00013
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	21	2.99E-06	0.00013
GO:0010950	positive regulation of endopeptidase activity	20	3.04E-06	0.00013
GO:0032760	positive regulation of tumor necrosis factor production	15	3.61E-06	0.00015
GO:0007159	leukocyte cell-cell adhesion	34	3.80E-06	0.00016
GO:0030593	neutrophil chemotaxis	15	4.07E-06	0.00017
GO:0002699	positive regulation of immune effector process	25	5.33E-06	0.00021
GO:0006275	regulation of DNA replication	17	5.35E-06	0.00021
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	15	5.79E-06	0.00023
GO:0032728	positive regulation of interferon-beta production	9	6.05E-06	0.00024
GO:0010466	negative regulation of peptidase activity	25	6.10E-06	0.00024

GO:2001251	negative regulation of chromosome organization	14	6.71E-06	0.00026
GO:0032640	tumor necrosis factor production	20	7.15E-06	0.00027
GO:0032680	regulation of tumor necrosis factor	20	7.15E-06	0.00027
GO:0061082	myeloid leukocyte cytokine production	10	7.31E-06	0.00028
GO:0046637	regulation of alpha-beta T cell differentiation	12	7.77E-06	0.00029
GO:0000075	cell cycle checkpoint signaling	20	8.41E-06	0.00031
GO:0010951	negative regulation of endopeptidase activity	24	9.02E-06	0.00033
GO:0050863	regulation of T cell activation	31	9.37E-06	0.00034
GO:0060338	regulation of type I interferon-mediated signaling pathway	9	9.39E-06	0.00034
GO:0032731	positive regulation of interleukin-1 beta production	11	1.02E-05	0.00037
GO:1990266	neutrophil migration	16	1.23E-05	0.00044
GO:0050830	defense response to Gram-positive	15	1.54E-05	0.00055
GO:0010952	positive regulation of peptidase activity	20	1.58E-05	0.00055
GO:0002720	positive regulation of cytokine production involved in immune response	12	1.79E-05	0.00062
GO:1903046	meiotic cell cycle process	21	1.79E-05	0.00062
GO:0045861	negative regulation of proteolysis	29	1.83E-05	0.00063
GO:0097193	intrinsic apoptotic signaling pathway	26	1.84E-05	0.00063
GO:0044771	meiotic cell cycle phase transition	5	1.98E-05	0.00067
GO:0051988	regulation of attachment of spindle microtubules to kinetochore	6	2.30E-05	0.00077
GO:0006959	humoral immune response	27	2.33E-05	0.00078
GO:0051092	positive regulation of NF-kappaB transcription factor activity	17	2.80E-05	0.00093
GO:0032722	positive regulation of chemokine production	11	2.87E-05	0.00095
GO:0070269	pyroptosis	7	2.96E-05	0.00097
GO:0032611	interleukin-1 beta production	14	3.22E-05	0.00104
GO:0032651	regulation of interleukin-1 beta production	14	3.22E-05	0.00104
GO:0070555	response to interleukin-1	16	3.41E-05	0.00109
GO:0032642	regulation of chemokine production	13	3.58E-05	0.00114
GO:0030595	leukocyte chemotaxis	22	3.80E-05	0.0012
GO:0046631	alpha-beta T cell activation	18	3.95E-05	0.00124
GO:0032602	chemokine production	13	3.99E-05	0.00124
GO:0033260	nuclear DNA replication	8	4.09E-05	0.00127
GO:0097529	myeloid leukocyte migration	22	4.31E-05	0.00133
GO:0060339	negative regulation of type I interferon-mediated signaling pathway	6	4.51E-05	0.00138
GO:0046634	regulation of alpha-beta T cell activation	14	4.80E-05	0.00145
GO:0045089	positive regulation of innate immune response	16	4.81E-05	0.00145
GO:0097421	liver regeneration	7	4.89E-05	0.00146
GO:0032732	positive regulation of interleukin-1	11	4.89E-05	0.00146
GO:0140013	meiotic nuclear division	19	5.19E-05	0.00154
GO:0051346	negative regulation of hydrolase activity	29	5.30E-05	0.00156
GO:0022407	regulation of cell-cell adhesion	35	5.38E-05	0.00158
GO:0071900	regulation of protein serine/threonine kinase activity	30	6.08E-05	0.00175
GO:0042454	ribonucleoside catabolic process	6	6.13E-05	0.00175
GO:0071605	monocyte chemotactic protein-1 production	6	6.13E-05	0.00175
GO:0071637	regulation of monocyte chemotactic protein-1 production	6	6.13E-05	0.00175

GO:0071346	cellular response to interferon-gamma	14	6.39E-05	0.0018
GO:0002702	positive regulation of production of molecular mediator of immune response	15	6.39E-05	0.0018
GO:1903037	regulation of leukocyte cell-cell adhesion	29	6.41E-05	0.0018
GO:0051321	meiotic cell cycle	24	6.73E-05	0.00188
GO:0051231	spindle elongation	5	7.87E-05	0.00215
GO:0031100	animal organ regeneration	10	7.95E-05	0.00215
GO:0032613	interleukin-10 production	10	7.95E-05	0.00215
GO:0032653	regulation of interleukin-10 production	10	7.95E-05	0.00215
GO:0060760	positive regulation of response to cytokine stimulus	10	7.95E-05	0.00215
GO:2000116	regulation of cysteine-type endopeptidase activity	21	8.18E-05	0.00219
GO:0032069	regulation of nuclease activity	6	8.19E-05	0.00219
GO:0044786	cell cycle DNA replication	8	8.73E-05	0.00231
GO:0050691	regulation of defense response to virus by host	8	8.73E-05	0.00231
GO:0002698	negative regulation of immune effector process	14	9.21E-05	0.00242
GO:0002274	myeloid leukocyte activation	21	9.23E-05	0.00242
GO:0006066	alcohol metabolic process	28	9.82E-05	0.00255
GO:0070661	leukocyte proliferation	27	9.84E-05	0.00255
GO:0002224	toll-like receptor signaling pathway	14	0.0001	0.00259
GO:0000302	response to reactive oxygen species	19	0.0001	0.00261
GO:0009620	response to fungus	10	0.0001	0.00263
GO:0050670	regulation of lymphocyte proliferation	21	0.0001	0.00263
GO:1903039	positive regulation of leukocyte cell-cell adhesion	23	0.00011	0.00265
GO:0032943	mononuclear cell proliferation	25	0.00011	0.00266
GO:0010838	positive regulation of keratinocyte	5	0.00011	0.00283
GO:0071639	positive regulation of monocyte chemotactic protein-1 production	5	0.00011	0.00283
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	5	0.00011	0.00283
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	18	0.00012	0.00285
GO:0007143	female meiotic nuclear division	7	0.00012	0.00289
GO:0009394	2'-deoxyribonucleotide metabolic process	8	0.00012	0.00298
GO:0045862	positive regulation of proteolysis	28	0.00012	0.00298
GO:0044839	cell cycle G2/M phase transition	16	0.00012	0.003
GO:0001836	release of cytochrome c from mitochondria	9	0.00013	0.00303
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	9	0.00013	0.00303
GO:0032944	regulation of mononuclear cell proliferation	21	0.00013	0.00311
GO:1903706	regulation of hemopoiesis	30	0.00013	0.00318
GO:1902105	regulation of leukocyte differentiation	25	0.00014	0.0032
GO:0010948	negative regulation of cell cycle process	25	0.00014	0.00334
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	7	0.00014	0.00334
GO:0009262	deoxyribonucleotide metabolic process	8	0.00015	0.00334
GO:0019692	deoxyribose phosphate metabolic process	8	0.00015	0.00334
GO:0060326	cell chemotaxis	25	0.00015	0.00345
GO:0051225	spindle assembly	14	0.00015	0.00352

GO:0045930	negative regulation of mitotic cell cycle	21	0.00016	0.00353
GO:0045931	positive regulation of mitotic cell cycle	14	0.00017	0.00377
GO:0001961	positive regulation of cytokine-mediated signaling pathway	9	0.00017	0.00377
GO:0051310	metaphase plate congression	10	0.00017	0.00379
GO:0010389	regulation of G2/M transition of mitotic cell cycle	12	0.00017	0.0038
GO:0022409	positive regulation of cell-cell adhesion	25	0.00017	0.00385
GO:0051984	positive regulation of chromosome segregation	6	0.00018	0.00391
GO:0032612	interleukin-1 production	14	0.00018	0.00396
GO:0032652	regulation of interleukin-1 production	14	0.00018	0.00396
GO:0042542	response to hydrogen peroxide	14	0.00018	0.00396
GO:0046651	lymphocyte proliferation	24	0.00019	0.00412
GO:0043903	regulation of biological process involved in symbiotic interaction	9	0.00019	0.00412
GO:0051785	positive regulation of nuclear division	9	0.00019	0.00412
GO:0006575	cellular modified amino acid metabolic process	17	0.0002	0.0042
GO:0070663	regulation of leukocyte proliferation	22	0.0002	0.00431
GO:0050870	positive regulation of T cell activation	21	0.00021	0.00435
GO:0009119	ribonucleoside metabolic process	7	0.00021	0.00444
GO:0002886	regulation of myeloid leukocyte mediated immunity	9	0.00022	0.0046
GO:0009164	nucleoside catabolic process	6	0.00022	0.00463
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	13	0.00023	0.00463
GO:0046632	alpha-beta T cell differentiation	13	0.00023	0.00463
GO:0071887	leukocyte apoptotic process	13	0.00023	0.00463
GO:1901988	negative regulation of cell cycle phase transition	22	0.00024	0.00486
GO:0050688	regulation of defense response to virus	10	0.00024	0.00491
GO:0048144	fibroblast proliferation	12	0.00025	0.00506
GO:0010934	macrophage cytokine production	7	0.00025	0.00509
GO:0010935	regulation of macrophage cytokine	7	0.00025	0.00509
GO:0070665	positive regulation of leukocyte proliferation	16	0.00026	0.00512
GO:0001960	negative regulation of cytokine-mediated signaling pathway	11	0.00027	0.00529
GO:0050000	chromosome localization	11	0.00027	0.00529
GO:0002696	positive regulation of leukocyte activation	31	0.00027	0.00532
GO:0061436	establishment of skin barrier	6	0.00028	0.00549
GO:1905820	positive regulation of chromosome	6	0.00028	0.00549
GO:1904029	regulation of cyclin-dependent protein kinase activity	13	0.00029	0.00566
GO:0033033	negative regulation of myeloid cell apoptotic process	5	0.0003	0.00579
GO:0051382	kinetochore assembly	5	0.0003	0.00579
GO:1904872	regulation of telomerase RNA localization to Cajal body	5	0.0003	0.00579
GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	6	0.00035	0.00665
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	8	0.00036	0.00684
GO:0050900	leukocyte migration	28	0.00038	0.00716

GO:0008637	apoptotic mitochondrial changes	12	0.00039	0.00729
GO:2000106	regulation of leukocyte apoptotic process	11	0.00039	0.00729
GO:0051797	regulation of hair follicle development	5	0.0004	0.00729
GO:0090670	RNA localization to Cajal body	5	0.0004	0.00729
GO:0090671	telomerase RNA localization to Cajal body	5	0.0004	0.00729
GO:0090672	telomerase RNA localization	5	0.0004	0.00729
GO:0090685	RNA localization to nucleus	5	0.0004	0.00729
GO:0039530	MDA-5 signaling pathway	4	0.0004	0.00729
GO:0044848	biological phase	4	0.0004	0.00729
GO:0051256	mitotic spindle midzone assembly	4	0.0004	0.00729
GO:0090085	regulation of protein deubiquitination	4	0.0004	0.00729
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	10	0.00041	0.00751
GO:0032607	interferon-alpha production	6	0.00042	0.00763
GO:0032647	regulation of interferon-alpha production	6	0.00042	0.00763
GO:0045619	regulation of lymphocyte differentiation	18	0.00043	0.0077
GO:0060761	negative regulation of response to cytokine stimulus	11	0.00043	0.00771
GO:0000086	G2/M transition of mitotic cell cycle	14	0.00046	0.00811
GO:0034605	cellular response to heat	9	0.00046	0.00811
GO:1902749	regulation of cell cycle G2/M phase	12	0.00046	0.00813
GO:1901136	carbohydrate derivative catabolic process	16	0.00046	0.00813
GO:0006690	icosanoid metabolic process	13	0.00047	0.00819
GO:0046638	positive regulation of alpha-beta T cell differentiation	8	0.00047	0.00819
GO:1901991	negative regulation of mitotic cell cycle phase transition	17	0.00048	0.0083
GO:0032733	positive regulation of interleukin-10	7	0.00049	0.00848
GO:2001056	positive regulation of cysteine-type endopeptidase activity	14	0.00049	0.00848
GO:0050867	positive regulation of cell activation	31	0.00051	0.00869
GO:0046394	carboxylic acid biosynthetic process	24	0.00051	0.00869
GO:0035455	response to interferon-alpha	5	0.00051	0.00869
GO:0071243	cellular response to arsenic-containing substance	5	0.00051	0.00869
GO:0070498	interleukin-1-mediated signaling pathway	6	0.00051	0.00869
GO:0009636	response to toxic substance	20	0.00052	0.00869
GO:0002275	myeloid cell activation involved in immune response	11	0.00052	0.00869
GO:0044403	biological process involved in symbiotic interaction	23	0.00052	0.00869
GO:0042572	retinol metabolic process	8	0.00053	0.00893
GO:0016053	organic acid biosynthetic process	24	0.00055	0.00923
GO:0045580	regulation of T cell differentiation	16	0.00056	0.00925
GO:0051303	establishment of chromosome localization	10	0.00056	0.00926
GO:0034142	toll-like receptor 4 signaling pathway	7	0.00057	0.00942
GO:0000022	mitotic spindle elongation	4	0.00058	0.00959
GO:0002819	regulation of adaptive immune response	17	0.0006	0.00986
GO:0050671	positive regulation of lymphocyte	14	0.0006	0.00988
GO:1990868	response to chemokine	11	0.00062	0.0099
GO:1990869	cellular response to chemokine	11	0.00062	0.0099
GO:0002230	positive regulation of defense response to virus by host	6	0.00062	0.0099
GO:0033561	regulation of water loss via skin	6	0.00062	0.0099

GO:0034656	nucleobase-containing small molecule catabolic process	6	0.00062	0.0099
GO:1902751	positive regulation of cell cycle G2/M phase transition	6	0.00062	0.0099
GO:1903131	mononuclear cell differentiation	31	0.00063	0.00999
GO:0002526	acute inflammatory response	12	0.00064	0.0101
GO:0045109	intermediate filament organization	9	0.00064	0.0101
GO:0045622	regulation of T-helper cell differentiation	7	0.00066	0.01044
GO:0006979	response to oxidative stress	29	0.00068	0.0107
GO:0009116	nucleoside metabolic process	8	0.00068	0.0107
GO:0033559	unsaturated fatty acid metabolic process	12	0.00069	0.0107
GO:0042303	molting cycle	12	0.00069	0.0107
GO:0042633	hair cycle	12	0.00069	0.0107
GO:0006261	DNA-templated DNA replication	15	0.00073	0.01127
GO:1901992	positive regulation of mitotic cell cycle phase transition	11	0.00073	0.01127
GO:0034508	centromere complex assembly	6	0.00074	0.01127
GO:0043304	regulation of mast cell degranulation	6	0.00074	0.01127
GO:0032946	positive regulation of mononuclear cell proliferation	14	0.00074	0.01127
GO:2000377	regulation of reactive oxygen species metabolic process	14	0.00074	0.01127
GO:0098586	cellular response to virus	12	0.00074	0.01131
GO:0045840	positive regulation of mitotic nuclear division	7	0.00076	0.01154
GO:0090329	regulation of DNA-templated DNA	8	0.00077	0.01165
GO:0002548	monocyte chemotaxis	9	0.00079	0.01184
GO:0051701	biological process involved in interaction with host	17	0.0008	0.01194
GO:0007144	female meiosis I	4	0.00082	0.01208
GO:0070486	leukocyte aggregation	4	0.00082	0.01208
GO:1900262	regulation of DNA-directed DNA polymerase activity	4	0.00082	0.01208
GO:1900264	positive regulation of DNA-directed DNA polymerase activity	4	0.00082	0.01208
GO:0051767	nitric-oxide synthase biosynthetic process	5	0.00082	0.01208
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	5	0.00082	0.01208
GO:0050673	epithelial cell proliferation	31	0.00082	0.01208
GO:0033003	regulation of mast cell activation	7	0.00088	0.01278
GO:0033032	regulation of myeloid cell apoptotic process	6	0.00088	0.01278
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	17	0.00089	0.01288
GO:0001523	retinoid metabolic process	10	0.00089	0.01288
GO:0048145	regulation of fibroblast proliferation	10	0.00089	0.01288
GO:1900182	positive regulation of protein localization to nucleus	10	0.00089	0.01288
GO:0032609	interferon-gamma production	12	0.00093	0.01337
GO:0032649	regulation of interferon-gamma production	12	0.00093	0.01337
GO:0046635	positive regulation of alpha-beta T cell activation	9	0.00096	0.01377
GO:0043367	CD4-positive, alpha-beta T cell	10	0.00098	0.01391
GO:0001906	cell killing	16	0.001	0.01413
GO:0010837	regulation of keratinocyte proliferation	7	0.001	0.01413
GO:0031640	killing of cells of another organism	7	0.001	0.01413

GO:0032401	establishment of melanosome localization	5	0.00102	0.01428
GO:0032727	positive regulation of interferon-alpha production	5	0.00102	0.01428
GO:0033006	regulation of mast cell activation involved in immune response	6	0.00103	0.01439
GO:0039528	cytoplasmic pattern recognition receptor signaling pathway in response to virus	6	0.00103	0.01439
GO:0090307	mitotic spindle assembly	9	0.00107	0.01478
GO:0045786	negative regulation of cell cycle	27	0.00107	0.01478
GO:0006643	membrane lipid metabolic process	17	0.0011	0.01518
GO:0007100	mitotic centrosome separation	4	0.00111	0.0152
GO:0009158	ribonucleoside monophosphate catabolic process	4	0.00111	0.0152
GO:0051255	spindle midzone assembly	4	0.00111	0.0152
GO:1902969	mitotic DNA replication	4	0.00111	0.0152
GO:0051091	positive regulation of DNA-binding transcription factor activity	20	0.00112	0.0152
GO:0002701	negative regulation of production of molecular mediator of immune response	7	0.00114	0.01551
GO:0010639	negative regulation of organelle organization	25	0.00115	0.01556
GO:1901989	positive regulation of cell cycle phase transition	12	0.00116	0.01563
GO:0016101	diterpenoid metabolic process	10	0.00116	0.01563
GO:0070098	chemokine-mediated signaling pathway	10	0.00116	0.01563
GO:0002719	negative regulation of cytokine production involved in immune response	6	0.00121	0.0161
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	6	0.00121	0.0161
GO:1901658	glycosyl compound catabolic process	6	0.00121	0.0161
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	5	0.00125	0.01645
GO:0035458	cellular response to interferon-beta	5	0.00125	0.01645
GO:0051905	establishment of pigment granule	5	0.00125	0.01645
GO:0060907	positive regulation of macrophage cytokine production	5	0.00125	0.01645
GO:0001942	hair follicle development	10	0.00127	0.01664
GO:0002444	myeloid leukocyte mediated immunity	11	0.00129	0.01681
GO:0044409	entry into host	14	0.00131	0.0171
GO:0032635	interleukin-6 production	15	0.00133	0.01722
GO:0032675	regulation of interleukin-6 production	15	0.00133	0.01722
GO:0043030	regulation of macrophage activation	8	0.00136	0.01755
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	12	0.00144	0.01853
GO:0043300	regulation of leukocyte degranulation	7	0.00147	0.01871
GO:0000212	meiotic spindle organization	4	0.00148	0.01871
GO:0043455	regulation of secondary metabolic process	4	0.00148	0.01871
GO:0048021	regulation of melanin biosynthetic process	4	0.00148	0.01871
GO:0048820	hair follicle maturation	4	0.00148	0.01871
GO:0051299	centrosome separation	4	0.00148	0.01871
GO:1900376	regulation of secondary metabolite biosynthetic process	4	0.00148	0.01871
GO:0042116	macrophage activation	11	0.0015	0.01888
GO:0071356	cellular response to tumor necrosis factor	18	0.0015	0.01892

GO:0031663	lipopolysaccharide-mediated signaling pathway	8	0.00151	0.01892
GO:0032400	melanosome localization	5	0.00152	0.01897
GO:0051446	positive regulation of meiotic cell cycle	5	0.00152	0.01897
GO:0034612	response to tumor necrosis factor	19	0.00156	0.01942
GO:0051656	establishment of organelle localization	28	0.00157	0.01955
GO:0022404	molting cycle process	10	0.00163	0.02006
GO:0022405	hair cycle process	10	0.00163	0.02006
GO:0071897	DNA biosynthetic process	16	0.00163	0.02006
GO:0022616	DNA strand elongation	6	0.00163	0.0201
GO:0042180	cellular ketone metabolic process	17	0.00174	0.02128
GO:0030217	T cell differentiation	21	0.00175	0.02129
GO:0046683	response to organophosphorus	12	0.00176	0.02129
GO:0032088	negative regulation of NF-kappaB transcription factor activity	10	0.00176	0.02129
GO:0032465	regulation of cytokinesis	10	0.00176	0.02129
GO:0098773	skin epidermis development	10	0.00176	0.02129
GO:0006665	sphingolipid metabolic process	14	0.00176	0.02129
GO:0045785	positive regulation of cell adhesion	30	0.00181	0.02184
GO:0035821	modulation of process of another organism	5	0.00183	0.02184
GO:0051875	pigment granule localization	5	0.00183	0.02184
GO:0060333	interferon-gamma-mediated signaling pathway	5	0.00183	0.02184
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	15	0.00185	0.02198
GO:0042129	regulation of T cell proliferation	15	0.00185	0.02198
GO:0042060	wound healing	28	0.00186	0.02198
GO:0070227	lymphocyte apoptotic process	9	0.00186	0.02198
GO:0051251	positive regulation of lymphocyte activation	26	0.00187	0.02204
GO:0009263	deoxyribonucleotide biosynthetic process	4	0.00192	0.02245
GO:0009265	2'-deoxyribonucleotide biosynthetic process	4	0.00192	0.02245
GO:0046385	deoxyribose phosphate biosynthetic process	4	0.00192	0.02245
GO:1901657	glycosyl compound metabolic process	9	0.00203	0.02369
GO:0002703	regulation of leukocyte mediated immunity	18	0.00208	0.02426
GO:0006636	unsaturated fatty acid biosynthetic process	7	0.00209	0.02433
GO:0033028	myeloid cell apoptotic process	6	0.00216	0.02508
GO:0006760	folic acid-containing compound metabolic process	5	0.00218	0.02515
GO:0090200	positive regulation of release of cytochrome c from mitochondria	5	0.00218	0.02515
GO:0031638	zymogen activation	8	0.00225	0.02581
GO:0045576	mast cell activation	8	0.00225	0.02581
GO:0044282	small molecule catabolic process	25	0.00229	0.02621
GO:0035710	CD4-positive, alpha-beta T cell activation	11	0.0023	0.02621
GO:1990748	cellular detoxification	11	0.0023	0.02621
GO:0048146	positive regulation of fibroblast proliferation	7	0.00234	0.02655
GO:0052372	modulation by symbiont of entry into host	7	0.00234	0.02655
GO:0140694	non-membrane-bounded organelle	25	0.00237	0.02687
GO:0032755	positive regulation of interleukin-6	10	0.0024	0.0271
GO:0000910	cytokinesis	15	0.00241	0.02716
GO:0042307	positive regulation of protein import into nucleus	6	0.00247	0.02776

GO:0046718	viral entry into host cell	13	0.00248	0.02783
GO:0042634	regulation of hair cycle	5	0.00258	0.02878
GO:0001776	leukocyte homeostasis	10	0.00258	0.02878
GO:0002532	production of molecular mediator involved in inflammatory response	10	0.00258	0.02878
GO:0033674	positive regulation of kinase activity	30	0.00262	0.02905
GO:0009410	response to xenobiotic stimulus	27	0.00268	0.02967
GO:0051090	regulation of DNA-binding transcription factor activity	28	0.00272	0.0301
GO:0006721	terpenoid metabolic process	10	0.00278	0.03068
GO:0051302	regulation of cell division	15	0.00281	0.03084
GO:0036297	interstrand cross-link repair	6	0.00281	0.03084
GO:0000281	mitotic cytokinesis	9	0.00283	0.03098
GO:0002448	mast cell mediated immunity	7	0.0029	0.03169
GO:0071902	positive regulation of protein serine/threonine kinase activity	17	0.00291	0.03171
GO:0000723	telomere maintenance	13	0.00295	0.03206
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	10	0.00299	0.03244
GO:0090025	regulation of monocyte chemotaxis	5	0.00303	0.03262
GO:0009125	nucleoside monophosphate catabolic	4	0.00305	0.03262
GO:0046040	IMP metabolic process	4	0.00305	0.03262
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	4	0.00305	0.03262
GO:0072567	chemokine (C-X-C motif) ligand 2	4	0.00305	0.03262
GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	4	0.00305	0.03262
GO:0016485	protein processing	18	0.00309	0.03301
GO:0061982	meiosis I cell cycle process	12	0.00311	0.03313
GO:0002685	regulation of leukocyte migration	17	0.00318	0.03382
GO:0050832	defense response to fungus	7	0.00322	0.03412
GO:0002440	production of molecular mediator of immune response	22	0.00332	0.03517
GO:0006720	isoprenoid metabolic process	11	0.00342	0.03613
GO:0030098	lymphocyte differentiation	26	0.0035	0.03685
GO:0007080	mitotic metaphase plate congression	7	0.00356	0.03733
GO:0010332	response to gamma radiation	7	0.00356	0.03733
GO:0071548	response to dexamethasone	6	0.00359	0.03759
GO:0045860	positive regulation of protein kinase activity	26	0.00361	0.03769
GO:0002283	neutrophil activation involved in immune response	4	0.00376	0.03862
GO:0007076	mitotic chromosome condensation	4	0.00376	0.03862
GO:0009148	pyrimidine nucleoside triphosphate biosynthetic process	4	0.00376	0.03862
GO:0032695	negative regulation of interleukin-12 production	4	0.00376	0.03862
GO:0060340	positive regulation of type I interferon-mediated signaling pathway	4	0.00376	0.03862
GO:0097202	activation of cysteine-type endopeptidase activity	4	0.00376	0.03862
GO:1901978	positive regulation of cell cycle checkpoint	4	0.00376	0.03862
GO:0072593	reactive oxygen species metabolic process	17	0.00379	0.03887
GO:0043462	regulation of ATP-dependent activity	8	0.00386	0.03939

GO:0071677	positive regulation of mononuclear cell migration	8	0.00386	0.03939
GO:0045104	intermediate filament cytoskeleton organization	9	0.00386	0.03939
GO:0007292	female gamete generation	13	0.00388	0.03939
GO:0097237	cellular response to toxic substance	11	0.00388	0.03939
GO:0001889	liver development	12	0.00393	0.03981
GO:0042102	positive regulation of T cell proliferation	10	0.00395	0.03993
GO:2000316	regulation of T-helper 17 type immune response	5	0.00409	0.04122
GO:0045103	intermediate filament-based process	9	0.00416	0.04177
GO:0006672	ceramide metabolic process	10	0.00423	0.04177
GO:0002138	retinoic acid biosynthetic process	3	0.00423	0.04177
GO:0002775	antimicrobial peptide production	3	0.00423	0.04177
GO:0009128	purine nucleoside monophosphate catabolic process	3	0.00423	0.04177
GO:0009155	purine deoxyribonucleotide catabolic process	3	0.00423	0.04177
GO:0009169	purine ribonucleoside monophosphate catabolic process	3	0.00423	0.04177
GO:0010496	intercellular transport	3	0.00423	0.04177
GO:0060075	regulation of resting membrane potential	3	0.00423	0.04177
GO:0060368	regulation of Fc receptor mediated stimulatory signaling pathway	3	0.00423	0.04177
GO:0072330	monocarboxylic acid biosynthetic process	16	0.00425	0.0419
GO:0042306	regulation of protein import into nucleus	7	0.00433	0.04245
GO:0051653	spindle localization	7	0.00433	0.04245
GO:0034308	primary alcohol metabolic process	10	0.00452	0.04421
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	6	0.00453	0.04421
GO:0051546	keratinocyte migration	4	0.00457	0.04452
GO:0061008	hepaticobiliary system development	12	0.00466	0.0453
GO:0051054	positive regulation of DNA metabolic process	20	0.00468	0.0454
GO:0006221	pyrimidine nucleotide biosynthetic process	5	0.00471	0.04544
GO:0046685	response to arsenic-containing substance	5	0.00471	0.04544
GO:0051642	centrosome localization	5	0.00471	0.04544
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	7	0.00475	0.04578
GO:0046822	regulation of nucleocytoplasmic transport	10	0.00482	0.04633
GO:0010822	positive regulation of mitochondrion organization	8	0.00495	0.04743
GO:0062197	cellular response to chemical stress	22	0.00504	0.04808
GO:0044000	movement in host	14	0.00505	0.04808
GO:0046006	regulation of activated T cell proliferation	6	0.00505	0.04808
GO:0046596	regulation of viral entry into host cell	6	0.00505	0.04808
GO:0046456	icosanoid biosynthetic process	7	0.00521	0.04949
GO:0070585	protein localization to mitochondrion	11	0.00525	0.04971
B	GO-CC			
ID	Description	Count in geneset	pvalue	p.adjust
GO:0001533	cornified envelope	19	3.38E-14	1.75E-11
GO:0034774	secretory granule lumen	40	1.18E-12	2.51E-10
GO:0060205	cytoplasmic vesicle lumen	40	1.59E-12	2.51E-10
GO:0031983	vesicle lumen	40	1.94E-12	2.51E-10
GO:0005819	spindle	42	5.63E-10	5.82E-08
GO:0035580	specific granule lumen	13	1.20E-07	1.03E-05

GO:1904813	ficolin-1-rich granule lumen	18	1.89E-07	1.39E-05
GO:0072686	mitotic spindle	22	2.61E-07	1.69E-05
GO:0000922	spindle pole	20	1.54E-06	8.85E-05
GO:0098687	chromosomal region	32	3.42E-06	0.00018
GO:0000793	condensed chromosome	25	6.67E-06	0.00031
GO:0000779	condensed chromosome, centromeric	19	7.09E-06	0.00031
GO:0042599	lamellar body	6	1.31E-05	0.00049
GO:1904724	tertiary granule lumen	10	1.34E-05	0.00049
GO:0000775	chromosome, centromeric region	23	1.44E-05	0.00049
GO:0101002	ficolin-1-rich granule	19	1.71E-05	0.00055
GO:0000307	cyclin-dependent protein kinase holoenzyme complex	9	3.93E-05	0.00119
GO:0000776	kinetochore	17	4.17E-05	0.0012
GO:0035578	azurophil granule lumen	12	5.49E-05	0.00149
GO:0030496	midbody	19	6.21E-05	0.0016
GO:0042581	specific granule	16	0.00011	0.00263
GO:0005874	microtubule	32	0.00013	0.00297
GO:0000502	proteasome complex	9	0.00015	0.00338
GO:0005876	spindle microtubule	11	0.00016	0.00352
GO:0045171	intercellular bridge	11	0.0002	0.00415
GO:0031617	NMS complex	4	0.00023	0.00458
GO:1902554	serine/threonine protein kinase complex	13	0.00025	0.00475
GO:0005775	vacuolar lumen	16	0.00032	0.00575
GO:0000228	nuclear chromosome	20	0.00032	0.00575
GO:1904090	peptidase inhibitor complex	4	0.00035	0.00606
GO:1905369	endopeptidase complex	10	0.00043	0.00711
GO:0005839	proteasome core complex	5	0.00044	0.00711
GO:0000940	outer kinetochore	4	0.00051	0.00805
GO:0030665	clathrin-coated vesicle membrane	13	0.00054	0.00814
GO:0030669	clathrin-coated endocytic vesicle membrane	9	0.00069	0.01019
GO:1902911	protein kinase complex	13	0.00071	0.01022
GO:0030136	clathrin-coated vesicle	17	0.00085	0.01192
GO:0051233	spindle midzone	6	0.00119	0.01619
GO:0070820	tertiary granule	14	0.00137	0.01821
GO:0005657	replication fork	8	0.0015	0.01939
GO:0046930	pore complex	5	0.00158	0.0199
GO:0005766	primary lysosome	13	0.00235	0.02823
GO:0042582	azurophil granule	13	0.00235	0.02823
GO:0061702	inflammasome complex	4	0.0027	0.03176
GO:0045334	clathrin-coated endocytic vesicle	9	0.00335	0.03851
GO:0034399	nuclear periphery	12	0.00379	0.04237
GO:0070938	contractile ring	3	0.00385	0.04237
GO:0030135	coated vesicle	20	0.00451	0.04859
GO:0043596	nuclear replication fork	5	0.00469	0.04948
C	GO-MF			
ID	Description	Count in geneset	pvalue	p.adjust
GO:0061134	peptidase regulator activity	27	1.05E-07	8.52E-05
GO:0004252	serine-type endopeptidase activity	21	1.50E-06	0.00047
GO:0008236	serine-type peptidase activity	22	2.05E-06	0.00047
GO:0061135	endopeptidase regulator activity	22	2.44E-06	0.00047
GO:0017171	serine hydrolase activity	22	2.89E-06	0.00047
GO:0030414	peptidase inhibitor activity	21	4.80E-06	0.00065
GO:0004866	endopeptidase inhibitor activity	20	9.44E-06	0.00109
GO:0004867	serine-type endopeptidase inhibitor activity	14	1.21E-05	0.00123

GO:0002020	protease binding	16	4.70E-05	0.00424
GO:0004175	endopeptidase activity	32	9.40E-05	0.00763
GO:0004869	cysteine-type endopeptidase inhibitor	9	0.00017	0.01285
GO:0042379	chemokine receptor binding	10	0.00024	0.01607
GO:0050786	RAGE receptor binding	4	0.00031	0.01888
GO:0016229	steroid dehydrogenase activity	7	0.00033	0.01888
GO:0003725	double-stranded RNA binding	10	0.00042	0.02258
GO:0004745	NAD-retinol dehydrogenase activity	5	0.00048	0.02427
GO:0035325	Toll-like receptor binding	4	0.00068	0.031
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as	13	0.00069	0.031
GO:0008017	microtubule binding	21	0.00098	0.03947
GO:0030295	protein kinase activator activity	12	0.00099	0.03947
GO:0005546	phosphatidylinositol-4,5-bisphosphate	10	0.00102	0.03947
GO:0019887	protein kinase regulator activity	18	0.00107	0.03954
GO:0015631	tubulin binding	26	0.00135	0.04573
GO:0004857	enzyme inhibitor activity	27	0.00135	0.04573
GO:0019209	kinase activator activity	12	0.00154	0.04991
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	13	0.0016	0.04991
D	KEGG			
ID	Description	Count in geneset	pvalue	p.adjust
hsa05164	Influenza A	30	3.25E-11	9.48E-09
hsa04621	NOD-like receptor signaling pathway	27	1.15E-08	1.68E-06
hsa04110	Cell cycle	20	2.63E-07	2.56E-05
hsa04657	IL-17 signaling pathway	17	3.95E-07	2.61E-05
hsa05169	Epstein-Barr virus infection	26	4.46E-07	2.61E-05
hsa05162	Measles	19	6.79E-06	0.00033
hsa05160	Hepatitis C	20	1.15E-05	0.00048
hsa00480	Glutathione metabolism	10	0.00013	0.00484
hsa04623	Cytosolic DNA-sensing pathway	10	0.00031	0.01013
hsa05134	Legionellosis	9	0.00065	0.0176
hsa03050	Proteasome	8	0.00066	0.0176
hsa05417	Lipid and atherosclerosis	20	0.0009	0.02154
hsa05171	Coronavirus disease - COVID-19	21	0.00096	0.02154

Abbreviations: GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes; BP, Biological process; CC, Cellular component; MF, Molecular Function