

SUPPLEMENTARY MATERIALS

- Supplementary Table 1: CIBERSORT analysis of CT

Mixture	B cells naive	B cells memory	Plasma cells	T cells CD8	T cells CD4 naive	T cells CD4 memory resting	T cells CD4 memory activated	T cells follicular helper	T cells regulatory (Tregs)
C01	0	0,09759969	0,03025647	0,10614452	0,01422583	0,07655445	0,08173539	0	0
C02	0,00074342	0	0,01551462	0,04747407	0	0,19783052	0,06189349	0	0
C03	0	0	0,01472728	0,01432151	0	0,03603511	0,01460327	0	0,00405046
C04	0	0	0,04238577	0,03704544	0,03029847	0,06152255	0,04492482	0	0
C05	0,05954207	0	0,02394392	0,02113047	0	0,13539177	0,03812652	0	0
C06	0,13324385	0	0,04275435	0,06120088	0,02306937	0,10193796	0,03721102	0	0
C07	0,01624474	0	0,0311085	0,00809808	0,02626398	0	0	0,0289163	0
C08	0	0	0,03745579	0,04395936	0	0	0	0,02812074	0
C09	0	0	0,01705668	0,01499902	0	0,14373545	0,02398419	0	0
C10	0,01695705	0	0,01540567	0,04168429	0	0,22438786	0,01981674	0	0
C11	0,01594343	0,01039748	0,0097038	0,05155284	0	0,13142605	0,01750677	0	0
C12	0	0,00743274	0,0079163	0	0,02445247	0,05548639	0	0	0
C14	0,01697654	0	0,01413755	0,02966595	0	0,0597392	0,0349982	0	0
C16	0,03220421	0	0,01845315	0,01236729	0	0,16984381	0,0332128	0	0
C19	0,00065915	0	0,01300466	0,02442529	0	0,12806026	0,0725429	0	0
C21	0,00270602	0	0,03681365	0,06491407	0	0	0	0,08275854	0
C23	0,00510378	0	0,04673411	0,07963082	0	0,04023521	0	0,02164856	0,01343516
C24	0	0	0,03783332	0,02408513	0	0,11006461	0,04590342	0,01823363	0
C25	0,0939522	0	0,01664575	0,08055066	0	0,08283233	0,05092368	0	0
C26	0,01997065	0	0,01041481	0,02210731	0,00191913	0,14752175	0,05287914	0	0
C27	0	0	0,00055271	0,0121704	0,03233672	0,04073377	0,03436377	0	0
C28	0,06116088	0	0,03055621	0,0728951	0	0,11860397	0	0,03706395	0
C29	0	0,04705542	0,01582805	0,03839591	0	0,04689432	0,01639842	0	0
C30	0	0,04529186	0,01711406	0	0,03092673	0,07706219	0,0686093	0	0
C31	0,00583069	0	0,02730744	0,02479262	0,01463364	0	0,05249332	0	0
C32	0,0168608	0	0,0191942	0	0,10683442	0	0,03342975	0	0
C33	0	0	0,02248701	0,03562505	0	0,01440145	0	0,03096082	0
C37	0,01056263	0,00613915	0,01916831	0,05149463	0	0,12437905	0	0,02420848	0,00405276
C39	0	0	0,00785479	0,00447591	0,03992066	0	0	0	0,00626167
C40	0	0	0,0253407	0	0	0,05016456	0,02028743	0,00612037	0
C41	0,0022994	0,00907315	0	0	0	0,01176918	0,00538817	0,01506626	0,03213823
C42	0,00087421	0,01913844	0,02573961	0,01311985	0	0,10462921	0,02012387	0	0
C44	0	0	0,01195315	0	0,03014403	0	0,01719673	0	0
C54	0,05266968	0	0,02753544	0,044442	0,05160907	0	0,051592	0	0
C55	0,02231859	0	0,03850929	0,05160894	0	0,07149404	0	0,04346371	0
C57	0,00069928	0	0,06097069	0,04339145	0	0,12177634	0,03795041	0,00152024	0,00051959
C60	0	0,02213156	0,0180621	0,02346961	0	0,11075927	0,03006554	0	0
C61	0,03684879	0	0,01953546	0,03621726	0	0,1815402	0,06849592	0	0,00709377
C64	0,10934817	0	0,0297957	0,03163645	0	0,19933275	0,03058914	0	0
C65	0	0	0,02153487	0,03794246	0	0,15600123	0,01936591	0	0
C66	0	0,05202194	0,02390069	0	0	0,0474921	0	0,00109051	0
C68	0,11159397	0	0,04326253	0,05222102	0,03087659	0,13427693	0,04638238	0	0
C70	0	0	0,07044536	0,09172739	0	0,04131531	0,00648973	0,01047178	0,03496987
C71	0,05890081	0	0,01949055	0,02107703	0,00718747	0,26531895	0,0425027	0	0
C72	0,07531988	0	0,01325389	0,05368647	0	0,05994603	0	0,02478672	0,01847435
C73	0,00190865	0	0,03325793	0,03312694	0	0,08073367	0,02055202	0	0
C76	0	0,00054277	0,02336896	0	0,03194448	0,06606498	0	0	0
C78	0,00956775	0	0,02366551	0,0627396	0	0,07614491	0	0,01555234	0,01018107
C79	0,00561029	0	0,04308845	0,05249483	0	0,04917346	0	0,0130857	0,01164687
C81	0	0	0,04812639	0,03776692	0	0,05497806	0,05409008	0,01035497	0
C84	0,00804152	0,00190155	0,01704508	0	0,05978299	0,16150079	0,04040906	0	0
C85	0	0	0,04604347	0,09901258	0	0,04458287	0	0	0
C87	0	0	0,03628802	0,05299448	0	0,13719984	0	0,01883261	0,00136495
C89	0	0	0,02544766	0,03634452	0	0,002809	0	0,02933428	0
Average	0,01860487	0,00590233	0,02570353	0,03518938	0,01030419	0,08432748	0,02394348	0,00935788	0,00286192
SD	0,0326646	0,01724391	0,01422788	0,02708696	0,02019042	0,06511505	0,0234802	0,01676796	0,0072766

- Supplementary Table 2: CIBERSORT analysis of PB

Mixture	B cells naive	B cells memory	Plasma cells	T cells CD8	T cells CD4 naive	T cells CD4 memory resting	T cells CD4 memory activated	T cells follicular helper	T cells regulatory (Tregs)
M01	0	0,03821464	0	0	0,0554415	0,05567335	0,03732141	0	0
M02	0,02077476	0	0,00759692	0,00495705	0,00128332	0,17859528	0,04142263	0	0
M03	0	0,04081507	0,00085826	0	0,01428774	0,15374531	0,03205978	0	0
M04	0	0,00564814	0,0089421	0	0,08086346	0,05368823	0,04267107	0	0
M05	0,00752826	0,00635457	0,00280113	0	0,02852901	0,07235081	0,05058895	0	0
M06	0,01229107	0,01238306	0	0,07351141	0,0033826	0,13126636	0,0511956	0	0
M07	0	0	0,00416905	0	0	0	0,01299382	0,01850945	0
M08	0,00603513	0,00867205	0	0,00872764	0,0134585	0,11132127	0,0310822	0	0
M09	0,02122466	0,01172196	0	0,00546442	0,02637725	0,14996064	0,03135247	0	0
M10	0	0,02869588	0,00434564	0	0,03069455	0,06312064	0,03005627	0	0
M11	0	0,02497501	0,00739942	0,00918136	0,0186245	0,12573451	0,03662391	0	0
M12	0	0,02033872	0	0,04857601	0,0187459	0,05523952	0,07871766	0	0
M13	0,02318474	0	0,014572	0,12190711	0	0,11501687	0,06213469	0	0
M14	0	0,03164599	0,00866115	0,00422541	0,03411058	0,07415753	0,04648045	0	0
M15	0	0,01529533	0,01164647	0,00241953	0,03614555	0,08254585	0,03716961	0	0
M16	0	0,00797519	0,00882853	0	0,03801589	0,05123048	0,03587028	0	0
M22	0,02581112	0	0,01118027	0,00947512	0,01002861	0,10544917	0,06698519	0	0
M34	0	0,01625962	0,00220726	0,0240222	0,01293285	0,11137224	0,03291205	0	0
M35	0	0,01602918	0	0,09293933	0,007454	0,09655174	0,09966957	0	0
M36	0	0,02367385	0,00665671	0	0,03626724	0,05799095	0,03524056	0	0
M37	0,01094205	0	0,00502611	0	0,03267716	0,00664223	0,01402902	0	0
M38	0	0,02406465	0,00721816	0	0,01367369	0,08539733	0,03952285	0	0
M39	0	0,04342614	0	0	0,01488648	0,07875413	0,01218843	0	0
M40	0	0,01826036	0,01130981	0,07862478	0,00761279	0,14399911	0,0556977	0	0
M41	0,00599638	0,0084643	0	0,00123181	0,0281953	0,13673238	0,06573879	0	0
M42	0,00278018	0,01900492	0	0,01080024	0,05210208	0,10053379	0,04836273	0	0
M43	0,00075763	0,01097841	0,00010402	0	0,07029747	0,15770974	0,02341434	0	0
M44	0,01954192	0	0,00650565	0,00425051	0,06483157	0,19756966	0,03739689	0	0
M45	0,00465294	0	0,0002827	0	0,04785954	0	0,0076615	0	0
M46	0	0,03168775	0,00715013	0,00888507	0,00319412	0,18397642	0,03751456	0	0
M47	0,02163377	0	0,01157063	0,00028445	0,03920381	0,04879214	0,04487292	0	0
M48	0,0003863	0,00774385	0,00634404	0	0,01531804	0,10851209	0,03733944	0	0
M49	0	0,02384892	0,00477963	0,00063535	0,03076597	0,12314335	0,03490549	0	0
M50	0,02014232	0,00648995	0	0	0	0,13704372	0,04050277	0	0
M51	0	0,04850594	0,00160183	0	0,00024454	0,11795735	0,03648401	0	0
M53	0,01851324	0	0,00550065	0	0,03178425	0,10728791	0,04255282	0	0
Average	0,00617212	0,01531037	0,00464606	0,01416997	0,02553583	0,09941839	0,04085368	0,00051415	0
SD	0,0088523	0,01388418	0,00435534	0,02992238	0,02101577	0,04916843	0,01815718	0,00308491	0

Mixture	T cells gamma delta	NK cells resting	NK cells activated	Monocytes	Macrophages M0	Macrophages M1	Macrophages M2	Dendritic cells resting	Dendritic cells activated	Mast cells resting	Mast cells activated	Eosinophils	Neutrophils
M01	0,00476634	0,03898144	0	0	0	0	0,0019899	0,00665252	0,01611471	0,02066432	0	0	0,72417987
M02	0	0,05194803	0	0,00402868	0	0	0	0,00376832	0,01691336	0,01375164	0	0	0,65495999
M03	0	0,01747254	0	0	0	0	0	0,00202996	0,01485392	0,02720653	0	0	0,69667088
M04	0	0,04179996	0	0,01484659	0	0	0	0,00354964	0,01448171	0,02968997	0	0	0,70381913
M05	0,00504466	0,0224455	0	0	0	0	0	0,00433463	0,00815455	0,02203064	0	0	0,76983729
M06	0	0,0431777	0	0	0	0	0	0	0,00171849	0,01624074	0	0	0,65483298
M07	0,03913633	0,0263406	0	0,06312073	0,02486912	0	0	0	0,00919455	0,01705289	0	0	0,78461344
M08	0	0,07692073	0	0,08776941	0	0	0	0	0,0063803	0,01693381	0	0	0,63269895
M09	0	0,04921237	0	0	0	0	0	0,00723682	0,01886189	0,01364967	0	0	0,66493786
M10	0,00853237	0,02898335	0	0	0	0	0	0,00431384	0,01508709	0,03235753	0	0	0,75381285
M11	0	0,08407085	0	0	0	0	0	0	0,01768252	0,00503433	0	0	0,67067359
M12	0	0,13580972	0	0,02955646	0	0	0	0	0,00300025	0,02362757	0	0	0,5863882
M13	0	0,069655	0	0,01170353	0	0	0	0	0,02046944	0,03285001	0	0	0,52850662
M14	0	0,05240383	0	0,1204437	0	0	0	0,00501206	0,01524861	0,01849431	0	0	0,5891164
M15	0	0,04974823	0	0,10144294	0	0	0	0,0079706	0,01515261	0,01774426	0	0	0,62271903
M16	0,02822151	0,06389792	0	0	0,00486067	0	0	0	0,01629872	0,00999693	0	0	0,73480388
M22	0	0,0567371	0	0,01316605	0	0	0	0,00328958	0,01690633	0,02231566	0	0,00897335	0,64968246
M34	0	0,06162519	0	0,09978915	0	0	0	0	0,00705426	0,03268347	0	0	0,59914171
M35	0	0,24648195	0	0,02724375	0	0	0	0	0,00187731	0,0177038	0	0	0,39404936
M36	0,01080273	0,03132896	0	0	0	0	0	0	0,01095023	0,01292943	0	0	0,77415935
M37	0,04999475	0,0369987	0	0	0,02558673	0	0	0	0,00206938	0	0,00033521	0	0,81569866
M38	0,01971832	0,02365338	0	0	0	0	0	0,00521652	0,01252517	0,03903066	0	0	0,72997927
M39	0,03266333	0,05784856	0	0	0	0,00057605	0	0,00192824	0,00834111	0	0,03461147	0	0,71477608
M40	0	0,10071645	0	0,01340454	0	0	0	0	0,01480502	0,01951231	0	0	0,53605714
M41	0	0,12471267	0	0,04894187	0	0	0	0	0,00277777	0,01930151	0	0	0,55790721
M42	0	0,06514845	0	0,15013374	0	0	0	0	0,00226571	0,0095309	0	0	0,53933726
M43	0	0,05918562	0	0,11796257	0	0	0	0	0,00070775	0,00639475	0	0	0,55248769
M44	0	0,08044644	0	0	0	0	0	0	0,01466638	0,01520802	0	0	0,55958295
M45	0,04112032	0,01556168	0	0,0063577	0	0	0	0,00152427	0,01290297	0,01348164	0	0	0,84859474
M46	0	0,0775072	0	0,01803366	0	0	0	0	0,01733139	0,00636015	0	0	0,60835953
M47	0	0,03235991	0	0,0497096	0	0	0	0	0,01619227	0,02193727	0	0	0,71344324
M48	0	0,02900186	0	0,01541907	0	0	0	0,0018395	0,01676369	0,02018463	0	0	0,74114749
M49	0	0,04208758	0	0	0	0	0	0,00681442	0,01706656	0,01637187	0	0	0,69958087
M50	0	0,02728948	0	0	0	0	0	0,00229318	0,01761971	0,01906499	0	0	0,72955388
M51	0	0,02964383	0	0,00919156	0	0	0	0	0,01798742	0,02534096	0	0	0,71304257
M53	0	0,02186052	0	0	0	0	0	0	0,01582992	0,02747057	0	0	0,72920012
Average	0,00666668	0,05758509	0	0,0278407	0,00153657	1,60E-05	5,53E-05	0,00188261	0,01211814	0,01839299	0,00097074	0,00024926	0,66606535
SD	0,01374443	0,04301318	0	0,04238973	0,00588408	9,60E-05	0,00033165	0,00253636	0,00599853	0,00904614	0,00576725	0,00149556	0,0958405

- Supplementary Table 3: GO enrichment analysis in LAAVsCE comparison

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0001819	positive regulation of cytokine production	34/226	460/16686	5,94E-16	2,254E-12	1,61E-12	NDA/FFAR2/SORL1/STAT1/CLEC7A/PIK3CG/IFI16/TLR8/IL1B/CD46/PTGS2/EIF2AK2/	34
GO:0002764	immune response-regulating signaling pathway	32/226	441/16686	7,8E-15	1,481E-11	1,06E-11	PRKCB/PTPRJ/MNDA/FFAR2/LYN/CLEC7A/TLR8/WNK1/CREBBP/PTPRC/USP15/NAIP	32
GO:00031349	positive regulation of defense response	26/226	285/16686	1,51E-14	1,912E-11	1,37E-11	RK2/MNDA/FFAR2/LYN/CLEC7A/CASP4/PIK3CG/IFI16/TLR8/IL1B/CREBBP/PTGS2/NAIP	26
GO:1902532	negative regulation of intracellular signal transduction	33/226	492/16686	2,72E-14	2,578E-11	1,84E-11	IRK2/GSK3B/PTPRJ/SORL1/STAT1/UBR2/LYN/RASSF2/IL1B/STK38/PTGS2/PTPRC/H	33
GO:00032103	positive regulation of response to external stimulus	30/226	438/16686	2,63E-13	1,997E-10	1,43E-10	IRK2/MNDA/FFAR2/LYN/CLEC7A/CASP4/PIK3CG/IFI16/TLR8/IL1B/WNK1/CREBBP/PTC	30
GO:0042554	superoxide anion generation	11/226	42/16686	6,53E-12	3,54E-09	2,53E-09	FPR2/ITGAM/NCF4/CLEC7A/NCF1/NCF1C/CYBB/SOD2/PRKCD/NCF1B/TYROBP	11
GO:0046651	lymphocyte proliferation	23/226	288/16686	8,66E-12	4,109E-09	2,94E-09	MNDA/TGFBR2/LYN/PIK3CG/PRKAR1A/IL1B/LST1/CD46/PTPRC/HLA-G/MIR21/BCL6/	23
GO:0032943	mononuclear cell proliferation	23/226	295/16686	1,42E-11	5,373E-09	3,84E-09	MNDA/TGFBR2/LYN/PIK3CG/PRKAR1A/IL1B/LST1/CD46/PTPRC/HLA-G/MIR21/BCL6/	23
GO:0045088	regulation of innate immune response	20/226	221/16686	2,21E-11	6,986E-09	5E-09	CR1/HCK/MNDA/FFAR2/LYN/CLEC7A/IFI16/TLR8/CREBBP/NCF1/USP15/HLA-G/MIR2	20
GO:0050670	regulation of lymphocyte proliferation	20/226	225/16686	3,06E-11	8,946E-09	6,4E-09	EN/SOS2/MNDA/TGFBR2/LYN/PRKAR1A/IL1B/LST1/CD46/PTPRC/HLA-G/MIR21/BCL	20
GO:0070663	regulation of leukocyte proliferation	21/226	255/16686	4,1E-11	1,068E-08	7,64E-09	1/PTEN/SOS2/MNDA/TGFBR2/LYN/PRKAR1A/IL1B/LST1/CD46/PTPRC/HLA-G/MIR21	21
GO:0032944	regulation of mononuclear cell proliferation	20/226	229/16686	4,22E-11	1,068E-08	7,64E-09	EN/SOS2/MNDA/TGFBR2/LYN/PRKAR1A/IL1B/LST1/CD46/PTPRC/HLA-G/MIR21/BCL	20
GO:0002831	regulation of response to biotic stimulus	23/226	334/16686	1,72E-10	3,844E-08	2,75E-08	MNDA/FFAR2/STAT1/LYN/CLEC7A/IFI16/TLR8/IL1B/CREBBP/NCF1/USP15/HLA-G/M	23
GO:0019221	cytokine-mediated signaling pathway	27/226	469/16686	2,36E-10	4,977E-08	3,56E-08	IL17RA/HCK/CXCR1/ACSL1/PTPRJ/STAT1/LYN/CASP4/IL1B/FOXO3/IL13RA1/WNK1/PT	27
GO:1901652	response to peptide	27/226	486/16686	5,19E-10	9,001E-08	6,44E-08	IL1BTG2/MMP9/GSK3B/SORL1/STAT1/LYN/ROCK1/KLF2/CASP4/IL1B/FOXO3/PIPAK2A	27
GO:0002683	negative regulation of immune system process	25/226	418/16686	5,22E-10	9,001E-08	6,44E-08	MSN1/HCK/PTEN/PTPRJ/MNDA/LYN/IFI16/PRKAR1A/LST1/CD46/PTPRC/USP15/HLA-	25
GO:0045730	respiratory burst	9/226	35/16686	6,8E-10	1,076E-07	7,69E-08	HCK/NCF4/CLEC7A/PIK3CG/NCF1/NCF1C/CYBB/NCF1B/IGHA1	9
GO:0007159	leukocyte cell-cell adhesion	24/226	393/16686	7,8E-10	1,184E-07	8,47E-08	FBR2/ALOX5/LYN/ROCK1/PRKAR1A/IL1B/FOXO3/CD46/WNK1/PTPRC/HLA-G/MIR21	24
GO:0043065	positive regulation of apoptotic process	27/226	498/16686	8,86E-10	1,294E-07	9,25E-08	SF10/PTEN/IGF2R/MMP9/MNDA/LYN/RASSF2/FOXO3/PTGS2/PTPRC/HLA-G/MIR21	27
GO:0030595	leukocyte chemotaxis	18/226	217/16686	9,53E-10	1,339E-07	9,57E-08	IL1CR2/IL17RA/CXCR1/S100A12/ADGRE2/LYST/FFAR2/ALOX5/LYN/PIK3CG/IL1B/WNK1	18
GO:0050900	leukocyte migration	23/226	369/16686	1,21E-09	1,643E-07	1,17E-07	IL1A/HCK/CXCR1/S100A12/ADGRE2/MMP9/LYST/FFAR2/ALOX5/LYN/ROCK1/PIK3CG/IL	23
GO:0030099	myeloid cell differentiation	23/226	376/16686	1,74E-09	2,132E-07	1,52E-07	MMP9/TGFBR2/STAT1/LYN/KLF2/IFI16/RASSF2/FOXO3/PIPAK2A/BCL6/FAM210B/E	23
GO:0002274	myeloid leukocyte activation	18/226	228/16686	2,11E-09	2,425E-07	1,73E-07	IL1M/CXCR2/S100A12/ADGRE2/LRRK2/TGFBR2/LYN/DYSF/PIK3CG/PTPRC/ATM/PRKCC	18
GO:1903706	regulation of hemopoiesis	23/226	385/16686	2,74E-09	2,972E-07	2,13E-07	IL1SOS2/TGFBR2/STAT1/LYN/RASSF2/FOXO3/CD46/PTPRC/HLA-G/MIR21/BCL6/FAM2	23
GO:0071900	regulation of protein serine/threonine kinase activity	22/226	353/16686	2,84E-09	2,997E-07	2,14E-07	IL12/ACSL1/LRRK2/PTPRJ/SORL1/LYN/PIK3CG/PRKAR1A/DAZAP2/IL1B/STK38/PTPRC	22
GO:0051250	negative regulation of lymphocyte activation	15/226	155/16686	3,03E-09	3,108E-07	2,22E-07	SAMSN1/PTEN/MNDA/LYN/PRKAR1A/LST1/HLA-G/MIR21/BCL6/ATM/PTPN22/FGL	15
GO:0006909	phagocytosis	19/226	274/16686	6,4E-09	5,784E-07	4,14E-07	IL1M/HCK/LYST/NCF4/PTPRJ/LYN/DYSF/CLEC7A/IL1B/PTPRC/CRKCF/FCGR1A/BIN2/TY	19
GO:0051092	positive regulation of NF-kappaB transcription factor activity	14/226	144/16686	9,72E-09	8,384E-07	6E-07	IL1R2/S100A8/FLOT2/IRAK3/TLR4/IL18R1/PRKCB/S100A12/PRKCD/EIF2AK2/S10	14
GO:0042742	defense response to bacterium	20/226	315/16686	1,13E-08	9,342E-07	6,68E-07	FPR2/S100A8/TLR4/S100A12/LYST/CASP4/MPEG1/IL1B/NAIP/S100A9/PRKCD/FCGR	20
GO:0002443	leukocyte mediated immunity	23/226	415/16686	1,13E-08	9,342E-07	6,68E-07	RE2/LYST/LYN/CLEC7A/PIK3CG/TLR8/IL1B/TAP2/CD46/PTPRC/HLA-G/BCL6/PRKCD/F	23
GO:2000379	positive regulation of reactive oxygen species metabolic process	10/226	64/16686	1,36E-08	1,054E-06	7,54E-07	FPR2/TLR4/MAPK14/ITGAM/TGFBR2/CLEC7A/FOXO3/SOD2/PRKCD/TYROBP	10
GO:0002237	response to molecule of bacterial origin	20/226	336/16686	3,33E-08	2,255E-06	1,61E-06	IL1S100A8/IRAK3/TLR4/CSF2RB/MAPK14/FOS/HCK/LYN/IL1B/TAP2/PTGS2/MIR21/PT	20
GO:0045936	negative regulation of phosphate metabolic process	22/226	406/16686	3,59E-08	2,329E-06	1,67E-06	N/LRRK2/GSK3B/PTPRJ/SORL1/LYN/ROCK1/RASSF2/PRKAR1A/IL1B/PIPAK2A/STK38	22
GO:0042113	B cell activation	19/226	305/16686	3,62E-08	2,329E-06	1,67E-06	IL1R4/CR1/SAMSN1/PRKCB/PTEN/PTPRJ/MNDA/LYN/PTPRC/BCL6/ATM/KLF6/PRKCD	19
GO:0051348	negative regulation of transferase activity	17/226	245/16686	4,09E-08	2,545E-06	1,82E-06	IL1RGS2/PTEN/GSK3B/PTPRJ/SORL1/LYN/PRKAR1A/IL1B/PIPAK2A/STK38/PTPRC/PTP	17
GO:0002366	leukocyte activation involved in immune response	18/226	280/16686	5,21E-08	3,14E-06	2,25E-06	IL1TGAM/CR1/IL18R1/ADGRE2/LYN/DYSF/PIK3CG/CD46/PTPRC/MIR21/BCL6/FGL2/TY	18
GO:0009620	response to fungus	9/226	61/16686	1,23E-07	6,228E-06	4,45E-06	CLEC4D/CLEC4E/S100A8/TLR4/IL17RA/S100A12/CLEC7A/USP15/S100A9	9
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	19/226	333/16686	1,44E-07	7,116E-06	5,09E-06	IL1IL17RA/CLEC7A/TLR8/IL1B/TAP2/CD46/PTPRC/HLA-G/MIR21/BCL6/PRKCD/FCGR1	19
GO:0002696	positive regulation of leukocyte activation	21/226	406/16686	1,63E-07	7,931E-06	5,67E-06	IL14/ITGAM/CR1/LRRK2/TGFBR2/LYN/CLEC7A/IL1B/FOXO3/CD46/PTPRC/HLA-G/MIR21	21
GO:0050777	negative regulation of immune response	14/226	181/16686	1,76E-07	8,461E-06	6,05E-06	IL13/MAPK14/CR1/SAMSN1/HCK/LYN/IFI16/CD46/PTPRC/USP15/HLA-G/MIR21/BCL6/F	14
GO:0071214	cellular response to abiotic stimulus	18/226	316/16686	3,19E-07	1,389E-05	9,94E-06	IL1MAP3K1/YBX3/PTEN/MME/MMP9/SLC12A6/IFI16/TLR8/IL1B/CREBBP/PTGS2/MIR2	18
GO:0104004	cellular response to environmental stimulus	18/226	316/16686	3,19E-07	1,389E-05	9,94E-06	IL1MAP3K1/YBX3/PTEN/MME/MMP9/SLC12A6/IFI16/TLR8/IL1B/CREBBP/PTGS2/MIR2	18
GO:0150076	neuroinflammatory response	9/226	68/16686	3,22E-07	1,389E-05	9,94E-06	TLR2/ITGAM/MMP9/LRRK2/IL1B/PTGS2/PTPRC/ATM/TYROBP	9
GO:1901653	cellular response to peptide	19/226	355/16686	3,87E-07	1,614E-05	1,15E-05	IL1RKCB/GSK3B/SORL1/STAT1/LYN/ROCK1/KLF2/CASP4/IL1B/FOXO3/PIPAK2A/OSBP18	19
GO:1903037	regulation of leukocyte cell-cell adhesion	19/226	358/16686	4,4E-07	1,757E-05	1,26E-05	IL1/TGFBR2/ALOX5/LYN/PRKAR1A/IL1B/FOXO3/CD46/WNK1/PTPRC/HLA-G/MIR21/BCL	19
GO:0002532	production of molecular mediator involved in inflammatory response	10/226	93/16686	5,16E-07	2,017E-05	1,44E-05	IL1IL1R2/TLR4/MAPK14/IL17RA/ALOX5/LYN/CLEC7A/NCF1/MIR21/STAT3	10
GO:0050764	regulation of phagocytosis	10/226	97/16686	7,66E-07	2,794E-05	2E-05	TLR2/FPR2/HCK/PTPRJ/DYSF/CLEC7A/IL1B/PTPRC/FCGR1A/FCER1G	10
GO:0032612	interleukin-1 production	11/226	122/16686	8,29E-07	2,967E-05	2,12E-05	IL1IL1R2/CASP8/TLR4/SERPINB1/MNDA/CLEC7A/IFI16/TLR8/NAIP/TYROBP/STAT3	11
GO:0051346	negative regulation of hydrolase activity	18/226	346/16686	1,19E-06	4,073E-05	2,91E-05	IL1RGS2/MMP9/LRRK2/GSK3B/SORL1/ROCK1/IFI16/WNK1/PTGS2/NAIP/MIR21/PICAL	18

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0045785	positive regulation of cell adhesion	21/226	464/16686	1,44E-06	4,828E-05	3,45E-05	PRJ/TGFB2/ALOX5/LYN/ROCK1/IL1B/FOXO3/CD46/PTPRC/HLA-G/MIR21/BCL6/ATM	21
GO:0010950	positive regulation of endopeptidase activity	12/226	160/16686	1,88E-06	5,95E-05	4,25E-05	ASP8/S100A8/CR1/TNFSF10/LYN/CLEC7A/IFI16/MIR21/S100A9/PICALM/DDX3X/STAT3	12
GO:0052548	regulation of endopeptidase activity	19/226	396/16686	1,99E-06	6,143E-05	4,39E-05	B1/TNFSF10/MMP9/SORL1/LYN/ROCK1/CLEC7A/IFI16/PTGS2/NAIP/MIR21/S100A9/	19
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	5/226	17/16686	2,36E-06	7,061E-05	5,05E-05	TLR2/TLR4/LRRK2/STAT1/NAMPT	5
GO:1901216	positive regulation of neuron death	9/226	89/16686	3,25E-06	9,485E-05	6,78E-05	CASP8/TLR4/ITGAM/FOS/GSK3B/FOXO3/ATM/PICALM/TYROBP	9
GO:0033674	positive regulation of kinase activity	20/226	455/16686	4,02E-06	0,0001131	8,09E-05	FBR2/LYN/PIK3CG/RASSF2/DAZAP2/IL1B/OSBPL8/WNK1/NCF1/PTPRC/IQGAP1/MIR	20
GO:0018105	peptidyl-serine phosphorylation	16/226	304/16686	4,1E-06	0,0001143	8,17E-05	PRKCB/PTEN/LRRK2/GSK3B/TGFB2/ROCK1/RASSF2/STK38/WNK1/PTGS2/ATM/PR	16
GO:0002700	regulation of production of molecular mediator of immune response	12/226	174/16686	4,51E-06	0,0001241	8,88E-05	IRAK3/TLR4/CR1/IL18R1/FFAR2/CLEC7A/IL1B/PTPRC/HLA-G/BCL6/PTPN22/LITAF	12
GO:0002534	cytokine production involved in inflammatory response	8/226	71/16686	5,11E-06	0,0001359	9,72E-05	IL1R2/TLR4/MAPK14/IL17RA/ALOX5/CLEC7A/MIR21/STAT3	8
GO:0051767	nitric-oxide synthase biosynthetic process	5/226	20/16686	5,73E-06	0,0001445	0,000103	TLR2/TLR4/LRRK2/STAT1/NAMPT	5
GO:1903829	positive regulation of protein localization	19/226	427/16686	5,94E-06	0,0001484	0,000106	ITGAM/STOM/GSK3B/SORL1/ACSL4/EPB41/IL1B/PTGS2/PRKCD/OA	19
GO:2001233	regulation of apoptotic signaling pathway	17/226	352/16686	6,43E-06	0,0001574	0,000113	PTEN/MMP9/LRRK2/GSK3B/IL1B/PTGS2/PTPRC/MIR21/SOD2/S100A9/PRKCD/	17
GO:0007566	embryo implantation	7/226	53/16686	6,92E-06	0,0001661	0,000119	MMP9/VMP1/TGFB2/ARHGDB/IL1B/PTGS2/MIR21	7
GO:0062197	cellular response to chemical stress	16/226	323/16686	8,82E-06	0,0001993	0,000142	3X3/MMP9/LRRK2/ALOX5/SLC12A6/KLF2/FOXO3/NCF1/PTGS2/MIR21/ATM/SOD2/P	16
GO:0033002	muscle cell proliferation	13/226	221/16686	1,03E-05	0,000223	0,000159	23/TLR4/MAPK14/FOS/PTEN/MMP9/TGFB2/STAT1/PRKAR1A/PTGS2/MIR21/SOD2	13
GO:0055072	iron ion homeostasis	8/226	81/16686	1,38E-05	0,0002869	0,000205	STEAP4/FBXL5/NCOA4/SLC25A37/SOD2/PICALM/ALAS2/EGLN1	8
GO:0031663	lipopolysaccharide-mediated signaling pathway	7/226	60/16686	1,6E-05	0,0003245	0,000232	TLR2/TLR4/MAPK14/HCK/LYN/IL1B/PTPN22	7
GO:0009612	response to mechanical stimulus	12/226	204/16686	2,26E-05	0,0004446	0,000318	TXNIP/CASP8/TLR4/MAPK14/MAP3K1/FOS/BTG2/TGFB2/STAT1/TLR8/IL1B/PTGS2	12
GO:0070997	neuron death	16/226	349/16686	2,3E-05	0,000446	0,000319	ITGAM/FOS/BTG2/LRRK2/GSK3B/SORL1/ROCK1/FOXO3/NAIP/ATM/SOD2/PICALM/E	16
GO:0071216	cellular response to biotic stimulus	13/226	239/16686	2,36E-05	0,0004527	0,000324	NIP/MIR223/TLR2/TLR4/MAPK14/HCK/GSK3B/LYN/CLEC7A/IL1B/MIR21/PTPN22/LIT	13
GO:00097193	intrinsic apoptotic signaling pathway	14/226	276/16686	2,5E-05	0,0004694	0,000336	YBX3/MMP9/LRRK2/CASP4/IFI16/PTGS2/MIR21/ATM/SOD2/S100A9/PRKCD/DDX3	14
GO:0021782	glial cell development	9/226	115/16686	2,65E-05	0,0004958	0,000355	TLR2/S100A8/TLR4/B4GALT5/PTEN/DICER1/LYN/IL1B/S100A9	9
GO:0002367	cytokine production involved in immune response	9/226	116/16686	2,84E-05	0,0005203	0,000372	IRAK3/TLR4/IL18R1/FFAR2/CLEC7A/IL1B/HLA-G/BCL6/LITAF	9
GO:0032102	negative regulation of response to external stimulus	17/226	397/16686	3,04E-05	0,0005405	0,000386	RAK3/MAPK14/CR1/HCK/PTEN/ALOX5/LYN/IFI16/PTPRC/USP15/HLA-G/MIR21/PRK	17
GO:0001666	response to hypoxia	14/226	281/16686	3,05E-05	0,0005405	0,000386	FOS/PTEN/TGFB2/FOXO3/CREBBP/PTGS2/MIR21/CYBB/ATM/SOD2/ALAS2/EGLN1	14
GO:0019724	B cell mediated immunity	11/226	181/16686	3,69E-05	0,0006425	0,000459	CSF2RB/CR1/TLR8/CD46/PTPRC/HLA-G/BCL6/PRKCD/FCGR1A/FCER1G/IGHA1	11
GO:0009896	positive regulation of catabolic process	19/226	493/16686	4,38E-05	0,0007317	0,000523	6/PTEN/BTG2/AGTPBP1/LRRK2/GSK3B/SORL1/ROCK1/IL1B/FOXO3/PIP4K2A/ATM/	19
GO:0002269	leukocyte activation involved in inflammatory response	6/226	48/16686	4,41E-05	0,0007335	0,000525	TLR2/ITGAM/LRRK2/PTPRC/ATM/TYROBP	6
GO:0000302	response to reactive oxygen species	11/226	187/16686	4,97E-05	0,0008168	0,000584	TXNIP/FOS/MMP9/LRRK2/STAT1/KLF2/FOXO3/NCF1/MIR21/SOD2/PRKCD	11
GO:0009743	response to carbohydrate	12/226	223/16686	5,41E-05	0,0008809	0,000663	IRS2/TXNIP/PRKCB/TGFB2/LYN/SLC12A6/CLEC7A/IL1B/FOXO3/NCF1/PTGS2/SOD2	12
GO:2001057	reactive nitrogen species metabolic process	7/226	75/16686	6,92E-05	0,0011036	0,000789	TLR2/TLR4/KLF2/CLEC7A/IL1B/PTGS2/SOD2	7
GO:0034101	erythrocyte homeostasis	9/226	131/16686	7,4E-05	0,0011697	0,000836	MAPK14/STAT1/LYN/KLF2/FOXO3/BCL6/FAM210B/ALAS2/STAT3	9
GO:1990840	response to lectin	4/226	18/16686	8,64E-05	0,0013375	0,000956	LYN/CLEC7A/CREBBP/TYROBP	4
GO:1990858	cellular response to lectin	4/226	18/16686	8,64E-05	0,0013375	0,000956	LYN/CLEC7A/CREBBP/TYROBP	4
GO:1901342	regulation of vasculature development	14/226	311/16686	9,11E-05	0,0013906	0,000994	CXCR2/PRKCB/TGFB2/ALOX5/STAT1/ROCK1/KLF2/IL1B/HLA-G/MIR21/CYBB/EGLN	14
GO:0090066	regulation of anatomical structure size	18/226	477/16686	9,12E-05	0,0013906	0,000994	12/PTEN/LRRK2/GSK3B/ROCK1/SLC12A6/KLF2/PTGS2/MIR21/SOD2/PRKCD/PICALM/	18
GO:0035458	cellular response to interferon-beta	4/226	19/16686	0,000108	0,0016174	0,001157	MNDA/STAT1/IFI16/IFITM2	4
GO:0001906	cell killing	10/226	172/16686	0,000121	0,0017731	0,001268	ITGAM/S100A12/LYST/CLEC7A/TAP2/PTPRC/HLA-G/FCGR1A/TYROBP/KIF5B	10
GO:0051222	positive regulation of protein transport	13/226	282/16686	0,000128	0,0018716	0,001338	2/TLR2/TLR4/MAPK14/ITGAM/STOM/GSK3B/SORL1/ACSL4/IL1B/PTGS2/PRKCD/OA	13
GO:0009595	detection of biotic stimulus	5/226	37/16686	0,000133	0,0019319	0,001381	TLR2/TLR4/PTPRC/CLEC7A/NAIP	5
GO:0098543	detection of other organism	4/226	20/16686	0,000134	0,0019319	0,001381	TLR2/TLR4/CLEC7A/NAIP	4
GO:0031343	positive regulation of cell killing	6/226	61/16686	0,000172	0,0023102	0,001652	ITGAM/CLEC7A/TAP2/PTPRC/HLA-G/TYROBP	6
GO:0002902	regulation of B cell apoptotic process	4/226	22/16686	0,000198	0,0026076	0,001865	IRS2/PTEN/LYN/BCL6	4
GO:1904951	positive regulation of establishment of protein localization	13/226	296/16686	0,000207	0,0026951	0,001927	2/TLR2/TLR4/MAPK14/ITGAM/STOM/GSK3B/SORL1/ACSL4/IL1B/PTGS2/PRKCD/OA	13
GO:0045932	negative regulation of muscle contraction	4/226	23/16686	0,000237	0,0030184	0,002158	RG52/PIK3CG/PTGS2/DOCK5	4
GO:0060547	negative regulation of necrotic cell death	4/226	23/16686	0,000237	0,0030184	0,002158	PELI1/MIR223/CASP8/YBX3	4
GO:0048660	regulation of smooth muscle cell proliferation	9/226	155/16686	0,000266	0,0033504	0,002396	MIR223/TLR4/PTEN/MMP9/TGFB2/STAT1/PTGS2/MIR21/SOD2	9
GO:0032388	positive regulation of intracellular transport	10/226	190/16686	0,000271	0,0033903	0,002424	MAPK14/STOM/GSK3B/SORL1/IL1B/PTGS2/PRKCD/OA21/MSN	10
GO:0001909	leukocyte mediated cytotoxicity	8/226	124/16686	0,000286	0,003506	0,002507	ITGAM/LYST/TAP2/PTPRC/HLA-G/FCGR1A/TYROBP/KIF5B	8
GO:0071496	cellular response to external stimulus	13/226	308/16686	0,000304	0,0036822	0,002633	ASP8/TLR4/MAP3K1/FOS/LRRK2/LYN/IFI16/TLR8/IL1B/FOXO3/PTGS2/EIF2AK2/PTP	13
GO:0046620	regulation of organ growth	7/226	97/16686	0,000348	0,0040938	0,002927	MAPK14/RGS2/YBX3/PTEN/TGFB2/STK4/RBPJ	7
GO:0031331	positive regulation of cellular catabolic process	15/226	398/16686	0,000358	0,0041901	0,002995	23/ATF6/PTEN/BTG2/AGTPBP1/LRRK2/GSK3B/ROCK1/IL1B/FOXO3/PIP4K2A/ATM/P	15
GO:0006809	nitric oxide biosynthetic process	6/226	70/16686	0,000368	0,0042804	0,003061	TLR4/KLF2/CLEC7A/IL1B/PTGS2/SOD2	6
GO:0070673	response to interleukin-18	3/226	11/16686	0,000373	0,0043045	0,003078	IL18RAP/IL18R1/CASP4	3
GO:0071394	cellular response to testosterone stimulus	3/226	11/16686	0,000373	0,0043045	0,003078	NCOA4/NCF1/MSN	3

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0034612	response to tumor necrosis factor	11/226	236/16686	0,000385	0,0043969	0,003144	CASP8/MAPK14/FOS/YBX3/STAT1/KLF2/CASP4/FOXO3/PTGS2/NAIP/GBP2	11
GO:0035456	response to interferon-beta	4/226	26/16686	0,000388	0,0044042	0,003149	MNDA/STAT1/IFI16/IFITM2	4
GO:0070269	pyroptosis	4/226	26/16686	0,000388	0,0044042	0,003149	MIR223/CASP8/CASP4/NAIP	4
GO:0002437	inflammatory response to antigenic stimulus	6/226	71/16686	0,000397	0,0044857	0,003208	MAPK14/CXCR2/HCK/LYN/FCGR1A/RBPJ	6
GO:0010827	regulation of glucose transmembrane transport	6/226	71/16686	0,000397	0,0044857	0,003208	IRS2/MIR223/MAPK14/PRKCB/IL1B/OSBPL8	6
GO:0060759	regulation of response to cytokine stimulus	9/226	164/16686	0,000403	0,0045387	0,003245	IL1R2/TLR2/CASP8/IRAK3/TLR4/CASP4/PTPRC/NAIP/MIR21	9
GO:0002440	production of molecular mediator of immune response	12/226	279/16686	0,000436	0,0048693	0,003482	IRAK3/TLR4/CR1/IL18R1/FFAR2/CLEC7A/IL1B/PTPRC/HLA-G/BCL6/PTPN22/LITAF	12
GO:0001783	B cell apoptotic process	4/226	27/16686	0,00045	0,0049669	0,003552	IRS2/PTEN/LYN/BCL6	4
GO:0002645	positive regulation of tolerance induction	3/226	12/16686	0,000493	0,0053202	0,003804	IRAK3/TGFBF2/HLA-G	3
GO:0002679	respiratory burst involved in defense response	3/226	12/16686	0,000493	0,0053202	0,003804	HCK/PIK3CG/NCF1	3
GO:0044706	multi-multicellular organism process	10/226	205/16686	0,000495	0,0053202	0,003804	RGS2/FOS/MMP9/VMP1/TGFBF2/ACSL4/ARHGDB/IL1B/PTGS2/MIR21	10
GO:0002526	acute inflammatory response	7/226	106/16686	0,000597	0,00622	0,004448	S100A8/CXCR2/FFAR2/PIK3CG/IL1B/PTGS2/FCGR1A	7
GO:0006968	cellular defense response	5/226	51/16686	0,000617	0,0063964	0,004574	CXCR2/MNDA/NCF1/HLA-G/TYROBP	5
GO:0097746	blood vessel diameter maintenance	8/226	140/16686	0,000646	0,0066254	0,004738	HRH2/RGS2/ROCK1/KLF2/PTGS2/MIR21/SOD2/DOCK5	8
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	4/226	30/16686	0,000681	0,0068739	0,004915	TAP2/HLA-G/FCGR1A/FCER1G	4
GO:0071356	cellular response to tumor necrosis factor	10/226	216/16686	0,000742	0,0073564	0,00526	CASP8/MAPK14/FOS/YBX3/STAT1/KLF2/CASP4/FOXO3/NAIP/GBP2	10
GO:0071456	cellular response to hypoxia	8/226	143/16686	0,000743	0,0073564	0,00526	FOS/PTEN/FOXO3/PTGS2/MIR21/CYBB/EGLN1/RBPJ	8
GO:0090715	immunological memory formation process	3/226	14/16686	0,000799	0,0078579	0,005619	CD46/BCL6/FGL2	3
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	5/226	54/16686	0,000804	0,0078606	0,005621	ITGAM/TAP2/PTPRC/HLA-G/TYROBP	5
GO:1900407	regulation of cellular response to oxidative stress	6/226	82/16686	0,000858	0,0083531	0,005973	TLR4/LRRK2/ALOX5/FOXO3/MIR21/SOD2	6
GO:1901889	negative regulation of cell junction assembly	4/226	32/16686	0,000875	0,0084704	0,006057	TLR2/PTEN/ROCK1/IL1B	4
GO:0009895	negative regulation of catabolic process	12/226	303/16686	0,000902	0,0086659	0,006197	IRAK3/MAPK14/YBX3/LRRK2/SORL1/ROCK1/PIK3CG/IL1B/MIR21/PTPN22/WAC/STAT3	12
GO:0046456	icosanoid biosynthetic process	5/226	56/16686	0,00095	0,0090782	0,006492	ALOX5/IL1B/PTGS2/NAIP/LTA4H	5
GO:0055017	cardiac muscle tissue growth	6/226	84/16686	0,000974	0,0092915	0,006644	MAPK14/RGS2/PTEN/TGFBF2/PRKAR1A/RBPJ	6
GO:0097396	response to interleukin-17	3/226	15/16686	0,000989	0,0093375	0,006677	IL17RA/IL1B/STAT3	3
GO:0097398	cellular response to interleukin-17	3/226	15/16686	0,000989	0,0093375	0,006677	IL17RA/IL1B/STAT3	3
GO:0031330	negative regulation of cellular catabolic process	10/226	225/16686	0,001014	0,0095488	0,006828	MAPK14/YBX3/LRRK2/SORL1/ROCK1/PIK3CG/MIR21/PTPN22/WAC/STAT3	10
GO:0002711	positive regulation of T cell mediated immunity	5/226	57/16686	0,00103	0,0096247	0,006882	IL18R1/IL1B/TAP2/PTPRC/HLA-G	5
GO:0002712	regulation of B cell mediated immunity	5/226	57/16686	0,00103	0,0096247	0,006882	CR1/CD46/PTPRC/BCL6/FCGR1A	5
GO:0002889	regulation of immunoglobulin mediated immune response	5/226	57/16686	0,00103	0,0096247	0,006882	CR1/CD46/PTPRC/BCL6/FCGR1A	5
GO:0050994	regulation of lipid catabolic process	5/226	58/16686	0,001115	0,0101922	0,007288	IRS2/SORL1/PIK3CG/IL1B/PRKCD	5
GO:0007009	plasma membrane organization	8/226	153/16686	0,001152	0,0105089	0,007515	CR1/PTEN/VMP1/DYSF/PTPRC/S100A9/PRKCD/BIN2	8
GO:0006979	response to oxidative stress	14/226	402/16686	0,001202	0,0107876	0,007714	TLR4/FOS/MMP9/LRRK2/ALOX5/STAT1/KLF2/FOXO3/NCF1/PTGS2/MIR21/SOD2/FCGR1A	14
GO:0060263	regulation of respiratory burst	3/226	16/16686	0,001205	0,0107876	0,007714	CLEC7A/NCF1/IGHA1	3
GO:0090594	inflammatory response to wounding	3/226	16/16686	0,001205	0,0107876	0,007714	TLR4/ALOX5/MIR21	3
GO:1900034	regulation of cellular response to heat	3/226	16/16686	0,001205	0,0107876	0,007714	GSK3B/CREBBP/ATM	3
GO:0045444	fat cell differentiation	10/226	231/16686	0,001237	0,0109899	0,007859	STEAP4/MAPK14/RGS2/FFAR2/ALOX5/OSBPL8/PTGS2/MIR21/SOD2/STK4	10
GO:0034219	carbohydrate transmembrane transport	7/226	120/16686	0,001242	0,0109899	0,007859	IRS2/MIR223/MAPK14/PRKCB/IL1B/OSBPL8/AQP9	7
GO:0046686	response to cadmium ion	5/226	60/16686	0,0013	0,0114444	0,008184	FOS/MMP9/NCF1/CYBB/SOD2	5
GO:0070542	response to fatty acid	5/226	60/16686	0,0013	0,0114444	0,008184	TLR2/ACSL1/FFAR2/FOXO3/PTGS2	5
GO:0042982	amyloid precursor protein metabolic process	6/226	89/16686	0,001317	0,0115457	0,008256	FLOT2/SORL1/LYN/ROCK1/ITM2B/PICALM	6
GO:1902882	regulation of response to oxidative stress	6/226	89/16686	0,001317	0,0115457	0,008256	TLR4/LRRK2/ALOX5/FOXO3/MIR21/SOD2	6
GO:0090399	replicative senescence	3/226	17/16686	0,001449	0,0124409	0,008896	MME/MIR21/ATM	3
GO:0006606	protein import into nucleus	8/226	159/16686	0,001473	0,012616	0,009021	TXNIP/MAPK14/LRRK2/KPNB1/PTGS2/PRKCD/STK4/STAT3	8
GO:1903311	regulation of mRNA metabolic process	11/226	278/16686	0,001476	0,012616	0,009021	MIR223/MBNL3/MAPK14/YBX3/BTG2/ROCK1/SRPK1/DDX17/PAPOLA/PRKCD/RBM35	11
GO:0071276	cellular response to cadmium ion	4/226	37/16686	0,001524	0,0128829	0,009212	FOS/MMP9/NCF1/CYBB	4
GO:0097242	amyloid-beta clearance	4/226	37/16686	0,001524	0,0128829	0,009212	ITGAM/MME/ROCK1/PICALM	4
GO:0070265	necrotic cell death	5/226	63/16686	0,001619	0,0136218	0,009741	PELI1/MIR223/CASP8/YBX3/PYGL	5
GO:0001837	epithelial to mesenchymal transition	8/226	162/16686	0,001659	0,0137427	0,009827	PTEN/GSK3B/TGFBF2/ROCK1/IL1B/DDX17/MIR21/RBPJ	8
GO:0051170	import into nucleus	8/226	162/16686	0,001659	0,0137427	0,009827	TXNIP/MAPK14/LRRK2/KPNB1/PTGS2/PRKCD/STK4/STAT3	8
GO:0034341	response to interferon-gamma	7/226	129/16686	0,001884	0,0152154	0,01088	TLR2/TLR4/HCK/STAT1/GBP2/KIF5B/IFITM2	7
GO:0014812	muscle cell migration	6/226	96/16686	0,001944	0,0156272	0,011175	MIR223/TLR4/SORL1/ROCK1/MIR21/DOCK5	6
GO:0031333	negative regulation of protein-containing complex assembly	7/226	130/16686	0,001969	0,0157866	0,011289	SSH2/GSK3B/SORL1/PRKCD/CAPZA1/DDX3X/RIOK3	7
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	10/226	246/16686	0,001972	0,0157866	0,011289	MIR223/RGS2/BTG2/DDX6/GSK3B/ROCK1/EIF2AK2/MIR21/ITM2B/DDX3X	10
GO:0035265	organ growth	8/226	167/16686	0,002008	0,0158371	0,011325	MAPK14/RGS2/YBX3/PTEN/TGFBF2/PRKAR1A/STK4/RBPJ	8

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0036003	positive regulation of transcription from RNA polymerase II promoter in response to stress	3/226	19/16686	0,002024	0,0158371	0,011325	ATF6/KLF2/RBPJ	3
GO:0071800	podosome assembly	3/226	19/16686	0,002024	0,0158371	0,011325	HCK/BIN2/MSN	3
GO:1903978	regulation of microglial cell activation	3/226	19/16686	0,002024	0,0158371	0,011325	LRRK2/PTPRC/ATM	3
GO:0090398	cellular senescence	6/226	98/16686	0,002158	0,0167494	0,011977	MAPK14/PTEN/HLA-G/BCL6/ATM/PRKCD	6
GO:0034504	protein localization to nucleus	11/226	292/16686	0,002172	0,01682	0,012027	TXNIP/MAPK14/LRRK2/GSK3B/KPNB1/OSBPL8/PTGS2/PRKCD/GBP2/STK4/STAT3	11
GO:0010212	response to ionizing radiation	7/226	133/16686	0,002241	0,0171152	0,012239	MAPK14/NABP1/IFI16/PTPRC/MIR21/ATM/SOD2	7
GO:0009991	response to extracellular stimulus	15/226	483/16686	0,002491	0,0187958	0,01344	IRS2/ACSL1/LRRK2/SORL1/TGFBR2/STAT1/LYN/IFI16/FOXO3/PTGS2/EIF2AK2/PTPRC/	15
GO:1901655	cellular response to ketone	6/226	101/16686	0,002513	0,0189227	0,013531	FOS/KLF2/FOXO3/NCOA4/NCF1/MSN	6
GO:0030728	ovulation	3/226	21/16686	0,002723	0,0200669	0,014349	RGS2/FOXO3/PTGS2	3
GO:0035902	response to immobilization stress	3/226	21/16686	0,002723	0,0200669	0,014349	FOS/FOXO3/SOD2	3
GO:0044546	NLRP3 inflammasome complex assembly	3/226	21/16686	0,002723	0,0200669	0,014349	TLR4/EIF2AK2/DDX3X	3
GO:0009266	response to temperature stimulus	8/226	176/16686	0,002781	0,0202179	0,014457	CASP8/FOS/GSK3B/LYN/CREBBP/PTGS2/ATM/SOD2	8
GO:0003018	vascular process in circulatory system	10/226	259/16686	0,002863	0,020738	0,014829	HRH2/RGS2/CXCR2/PTPRJ/ROCK1/KLF2/PTGS2/MIR21/SOD2/DOCK5	10
GO:0040029	epigenetic regulation of gene expression	7/226	139/16686	0,002872	0,0207631	0,014847	HAT1/UBR2/KLF2/MSL1/BAZ1A/IFI16/SMCHD1	7
GO:0060284	regulation of cell development	15/226	495/16686	0,003139	0,0224771	0,016073	MME/DICER1/LRRK2/PLXNC1/GSK3B/SORL1/LYN/RNF10/ROCK1/CLEC7A/IL1B/TYR1	15
GO:0001890	placenta development	7/226	144/16686	0,003495	0,0247472	0,017696	CASP8/MAPK14/MME/PTGS2/EGLN1/STK4/RBPJ	7
GO:0008643	carbohydrate transport	7/226	144/16686	0,003495	0,0247472	0,017696	IRS2/MIR223/MAPK14/PRKCB/IL1B/OSBPL8/AQP9	7
GO:0002053	positive regulation of mesenchymal cell proliferation	3/226	23/16686	0,003555	0,0248431	0,017765	IRS2/TGFBR2/STAT1	3
GO:0035821	modulation of process of another organism	3/226	23/16686	0,003555	0,0248431	0,017765	CLEC7A/MPEG1/S100A9	3
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	3/226	23/16686	0,003555	0,0248431	0,017765	MAPK14/CD53/TYROBP	3
GO:0140632	inflammasome complex assembly	3/226	23/16686	0,003555	0,0248431	0,017765	TLR4/EIF2AK2/DDX3X	3
GO:0008360	regulation of cell shape	7/226	145/16686	0,003631	0,0253323	0,018114	HCK/PLXNC1/ARHGAP15/EPB41/LST1/MIR21/MSN	7
GO:0006939	smooth muscle contraction	6/226	109/16686	0,003673	0,0254708	0,018213	RGS2/ROCK1/PTGS2/MIR21/PROK2/DOCK5	6
GO:0046916	cellular transition metal ion homeostasis	6/226	109/16686	0,003673	0,0254708	0,018213	STEAP4/S100A8/NCOA4/S100A9/ALAS2/EGLN1	6
GO:0014910	regulation of smooth muscle cell migration	5/226	76/16686	0,003693	0,0254708	0,018213	MIR223/TLR4/SORL1/MIR21/DOCK5	5
GO:0043299	leukocyte degranulation	5/226	77/16686	0,003907	0,0267635	0,019138	ITGAM/HCK/ADGRE2/LYN/PIK3CG	5
GO:0032291	axon ensheathment in central nervous system	3/226	24/16686	0,004022	0,0272578	0,019491	TLR2/B4GALT5/PTEN	3
GO:0043393	regulation of protein binding	8/226	189/16686	0,004287	0,0288433	0,020625	MMP9/LRRK2/GSK3B/SORL1/ROCK1/EPB41/PRKCD/STK4	8
GO:0010543	regulation of platelet activation	4/226	49/16686	0,004309	0,0288433	0,020625	TLR4/LYN/PRKCD/FCER1G	4
GO:0010586	miRNA metabolic process	5/226	80/16686	0,004601	0,0302115	0,021603	FOS/DICER1/FOXO3/DDX17/STAT3	5
GO:0032092	positive regulation of protein binding	5/226	80/16686	0,004601	0,0302115	0,021603	MMP9/LRRK2/GSK3B/EPB41/STK4	5
GO:0042060	wound healing	13/226	419/16686	0,00479	0,0313955	0,02245	IRS2/TLR4/MAPK14/PTEN/TGFBR2/ALOX5/LYN/DYSF/CLEC7A/PIK3CG/PRKCD/FCER1G/	13
GO:0097479	synaptic vesicle localization	4/226	51/16686	0,004977	0,0323619	0,02141	PTEN/LRRK2/PICALM/KIF5B	4
GO:0050792	regulation of viral process	7/226	154/16686	0,005044	0,0327238	0,0234	STOM/STAT1/IFI16/SRPK1/EIF2AK2/DDX3X/IFITM2	7
GO:0006690	icosanoid metabolic process	6/226	119/16686	0,005634	0,035627	0,025476	TLR2/ALOX5/IL1B/PTGS2/NAIP/LTA4H	6
GO:0006898	receptor-mediated endocytosis	9/226	243/16686	0,005988	0,0375611	0,026859	ITGAM/CXCR2/CXCR1/IGF2R/SORL1/TGFBR2/FCGR1A/PICALM/FCER1G	9
GO:0019079	viral genome replication	6/226	121/16686	0,006103	0,0379729	0,027153	STOM/IFI16/SRPK1/EIF2AK2/DDX3X/IFITM2	6
GO:0042176	regulation of protein catabolic process	11/226	336/16686	0,006238	0,0383596	0,02743	IRAK3/FBXL5/LRRK2/GSK3B/SORL1/ROCK1/IL1B/OAZ1/WAC/EGLN1/MSN	11
GO:0043087	regulation of GTPase activity	11/226	336/16686	0,006238	0,0383596	0,02743	IRS2/SOS2/LRRK2/PLXNC1/ARHGAP15/GSK3B/WNK1/IQGAP1/MIR21/BCL6/PICALM	11
GO:0034063	stress granule assembly	3/226	28/16686	0,006257	0,0383596	0,02743	DDX6/DAZAP2/DDX3X	3
GO:0060479	lung cell differentiation	3/226	28/16686	0,006257	0,0383596	0,02743	KLF2/LTA4H/RBPJ	3
GO:0060487	lung epithelial cell differentiation	3/226	28/16686	0,006257	0,0383596	0,02743	KLF2/LTA4H/RBPJ	3
GO:0006470	protein dephosphorylation	9/226	245/16686	0,006308	0,0384845	0,027519	SSH2/PTEN/GSK3B/PTPRJ/ROCK1/PTPRC/PTPN22/PRKCD/PTPN12	9
GO:0010634	positive regulation of epithelial cell migration	7/226	162/16686	0,006617	0,0399206	0,028546	IRS2/MMP9/TGFBR2/PIK3CG/PTGS2/MIR21/DOCK5	7
GO:0046683	response to organophosphorus	6/226	124/16686	0,006859	0,0412505	0,029497	FOS/STAT1/PIK3CG/IL1B/AQP9/PTGS2	6
GO:0044264	cellular polysaccharide metabolic process	5/226	88/16686	0,006876	0,0412864	0,029523	IRS2/MGAM/B4GALT5/GSK3B/PYG1	5
GO:0034249	negative regulation of cellular amide metabolic process	9/226	249/16686	0,006986	0,0416205	0,029762	MIR223/RGS2/BTG2/DDX6/SORL1/ROCK1/EIF2AK2/MIR21/DDX3X	9
GO:0031647	regulation of protein stability	10/226	295/16686	0,007081	0,0421174	0,030117	FLOT2/B4GALT5/PTEN/LRRK2/RASSF2/DAZAP2/CREBBP/PRKCD/TYROBP/STK4	10
GO:0072091	regulation of stem cell proliferation	5/226	89/16686	0,007206	0,0427991	0,030604	IRS2/TGFBR2/EIF2AK2/PTPRC/RBPJ	5
GO:0043030	regulation of macrophage activation	4/226	57/16686	0,007388	0,0436703	0,031227	TLR4/LRRK2/PTPRC/ATM	4
GO:0046631	alpha-beta T cell activation	7/226	166/16686	0,007527	0,0441258	0,031553	IL18R1/TGFBR2/PTPRC/MIR21/BCL6/PTPN22/STAT3	7
GO:0051051	negative regulation of transport	13/226	443/16686	0,007527	0,0441258	0,031553	IRS2/TLR2/RGS2/PRKCB/PTEN/MMP9/LRRK2/DYSF/IL1B/WNK1/PTGS2/PICALM/OAZ	13
GO:0003056	regulation of vascular associated smooth muscle contraction	2/226	10/16686	0,007651	0,0441258	0,031553	MIR21/DOCK5	2
GO:0015911	long-chain fatty acid import across plasma membrane	2/226	10/16686	0,007651	0,0441258	0,031553	IRS2/ACSL1	2
GO:0140719	constitutive heterochromatin formation	2/226	10/16686	0,007651	0,0441258	0,031553	HAT1/SMCHD1	2
GO:1905065	positive regulation of vascular associated smooth muscle cell differentiation	2/226	10/16686	0,007651	0,0441258	0,031553	MIR21/SOD2	2
GO:0032091	negative regulation of protein binding	5/226	92/16686	0,008265	0,047259	0,033793	LRRK2/GSK3B/SORL1/ROCK1/PRKCD	5
GO:0050806	positive regulation of synaptic transmission	7/226	169/16686	0,008269	0,047259	0,033793	STX3/PTEN/MME/GSK3B/PTGS2/TYROBP/KIF5B	7
GO:2000191	regulation of fatty acid transport	3/226	31/16686	0,008334	0,0474154	0,033905	IRS2/ACSL1/IL1B	3
GO:0000768	syncytium formation by plasma membrane fusion	4/226	60/16686	0,008839	0,0498417	0,03564	MAPK14/CD53/TYROBP/DOCK5	4
GO:0140253	cell-cell fusion	4/226	60/16686	0,008839	0,0498417	0,03564	MAPK14/CD53/TYROBP/DOCK5	4

- Supplementary Table 4: REACTOME enrichment analysis in LAAVsCE comparison

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
R-HSA-6798695	Neutrophil degranulation	46/169	456/10164	4,41E-24	3,81E-21	3,20E-21	TOM/GMFG/ADGRE5/PTP
R-HSA-449147	Signaling by interleukins	34/169	441/10164	3,27E-14	1,41E-11	1,19E-11	IOA12/SOS2/MMP9/ALOX
R-HSA-5668599	RHO GTPases Activate NADPH Oxidases	8/169	24/10164	2,90E-09	8,36E-07	7,02E-07	/PRKCB/NCF4/NCF1/CYBE
R-HSA-9705462	Inactivation of CSF3 (G-CSF) signaling	7/169	21/10164	2,97E-08	6,41E-06	5,38E-06	D1/STAT1/LYN/UBA52/CSI
R-HSA-168898	Toll-like Receptor Cascades	15/169	160/10164	6,11E-08	1,06E-05	8,86E-06	APK14/ITGAM/MAP3K1/FC
R-HSA-166016	Toll Like Receptor 4 (TLR4) Cascade	14/169	141/10164	8,34E-08	1,20E-05	1,01E-05	/MAPK14/ITGAM/MAP3K1
R-HSA-9674555	Signaling by CSF3 (G-CSF)	7/169	26/10164	1,56E-07	1,93E-05	1,62E-05	D1/STAT1/LYN/UBA52/CSI
R-HSA-166058	MyD88: MAL (TRAP) cascade initiated on plasma membrane	12/169	109/10164	2,34E-07	2,25E-05	1,89E-05	{3/TLR4/MAPK14/MAP3K
R-HSA-168188	Toll Like Receptor TLR6:TLR2 Cascade	12/169	109/10164	2,34E-07	2,25E-05	1,89E-05	{3/TLR4/MAPK14/MAP3K
R-HSA-168179	Toll Like Receptor TLR1:TLR2 Cascade	12/169	112/10164	3,16E-07	2,48E-05	2,08E-05	{3/TLR4/MAPK14/MAP3K
R-HSA-181438	Toll Like Receptor 2 (TLR2) Cascade	12/169	112/10164	3,16E-07	2,48E-05	2,08E-05	{3/TLR4/MAPK14/MAP3K
R-HSA-1236975	Antigen processing-Cross presentation	11/169	102/10164	9,34E-07	6,73E-05	5,65E-05	/TAP2/NCF1/UBA52/HLA
R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	11/169	105/10164	1,25E-06	8,32E-05	6,98E-05	5/STAT1/IL1B/FOXO3/IL13
R-HSA-446652	Interleukin-1 family signaling	12/169	147/10164	5,80E-06	0,000358	0,000301	AK3/IL18R1/S100A12/ALC
R-HSA-5621481	C-type lectin receptors (CLRs)	11/169	135/10164	1,46E-05	0,000842	0,000707	!D1/LYN/CLEC7A/IL1B/CRI
R-HSA-5218859	Regulated Necrosis	7/169	52/10164	2,21E-05	0,001194	0,001002	3/FLOT2/TNFSF10/CASP4/
R-HSA-168181	Toll Like Receptor 7/8 (TLR7/8) Cascade	9/169	99/10164	3,77E-05	0,001917	0,001609	MAPK14/MAP3K1/FOS/S1
R-HSA-5213460	RIPK1-mediated regulated necrosis	5/169	26/10164	5,94E-05	0,002266	0,002266	/CASP8/FLOT2/TNFSF10/L
R-HSA-5675482	Regulation of necroptotic cell death	5/169	26/10164	5,94E-05	0,002266	0,002266	/CASP8/FLOT2/TNFSF10/L
R-HSA-5357801	Programmed Cell Death	12/169	195/10164	9,71E-05	0,004195	0,003521	!SF10/ROCK1/CASP4/IL1B
R-HSA-5602498	MyD88 deficiency (TLR2/4)	4/169	17/10164	0,000148	0,006099	0,00512	LR2/S100A8/TLR4/S100A
R-HSA-447115	Interleukin-12 family signaling	6/169	51/10164	0,000187	0,007035	0,005905	ALDO1/SOD2/CAPZ1/MS
R-HSA-5603041	IRAK4 deficiency (TLR2/4)	4/169	18/10164	0,000188	0,007035	0,005905	LR2/S100A8/TLR4/S100A
R-HSA-9711123	Cellular response to chemical stress	11/169	180/10164	0,000202	0,007035	0,005905	!1/CREBBP/NCF1/UBA52/
R-HSA-975138	TRAF6 mediated induction of NFKB and MAP kinases upon TLR7/8 or 9 activation	8/169	97/10164	0,000204	0,007035	0,005905	4/MAPK14/MAP3K1/FOS/
R-HSA-975155	MyD88 dependent cascade initiated on endosome	8/169	98/10164	0,000219	0,007263	0,006097	4/MAPK14/MAP3K1/FOS/
R-HSA-168138	Toll Like Receptor 9 (TLR9) Cascade	8/169	102/10164	0,000288	0,008956	0,007518	4/MAPK14/MAP3K1/FOS/
R-HSA-5686938	Regulation of TLR by endogenous ligand	4/169	20/10164	0,00029	0,008956	0,007518	LR2/S100A8/TLR4/S100A
R-HSA-982772	Growth hormone receptor signaling	4/169	23/10164	0,00051	0,015001	0,012592	IRS2/STAT1/LYN/STAT3
R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	17/169	414/10164	0,000521	0,015001	0,012592	!V/FOXO3/CREBBP/UBA52/
R-HSA-1236974	ER-Phagosome pathway	7/169	87/10164	0,000593	0,016539	0,013883	!S/TLR4/TAP2/UBA52/HLA
R-HSA-2029481	FCGR activation	3/169	11/10164	0,000675	0,018108	0,0152	HCK/LYN/FCGR1A
R-HSA-6783783	Interleukin-10 signaling	5/169	43/10164	0,000692	0,018108	0,0152	R2/FPR1/IL1B/PTGS2/STA
R-HSA-168142	Toll Like Receptor 10 (TLR10) Cascade	7/169	93/10164	0,000885	0,020775	0,017439	MAPK14/MAP3K1/FOS/S1
R-HSA-168176	Toll Like Receptor 5 (TLR5) Cascade	7/169	93/10164	0,000885	0,020775	0,017439	MAPK14/MAP3K1/FOS/S1
R-HSA-975871	MyD88 cascade initiated on plasma membrane	7/169	93/10164	0,000885	0,020775	0,017439	MAPK14/MAP3K1/FOS/S1
R-HSA-9027276	Erythropoietin activates Phosphoinositide-3-kinase (PI3K)	3/169	12/10164	0,00089	0,020775	0,017439	IRS2/LYN/PIK3CG
R-HSA-4420097	VEGFA-VEGFR2 Pathway	7/169	94/10164	0,000943	0,021272	0,017856	KCB/NCF4/ROCK1/NCF1/C
R-HSA-5621480	Dectin-2 family	4/169	27/10164	0,00096	0,021272	0,017856	EC4D/CLEC4E/LYN/FCER1
R-HSA-983169	Class I MHC mediated antigen processing & presentation	15/169	367/10164	0,001169	0,025254	0,021199	D1/NCF4/UBR2/TAP2/NCF
R-HSA-913531	Interferon Signaling	10/169	190/10164	0,001258	0,026506	0,02225	!BA52/HLA-G/PRKCD/FCG
R-HSA-194138	Signaling by VEGF	7/169	102/10164	0,001524	0,030706	0,025775	KCB/NCF4/ROCK1/NCF1/C
R-HSA-168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	6/169	76/10164	0,001616	0,030706	0,025775	!K1/UBE2D1/S100A12/CR
R-HSA-2871796	FCERI mediated MAPK activation	4/169	31/10164	0,001635	0,030706	0,025775	MAP3K1/FOS/LYN/FCER1G
R-HSA-5260271	Diseases of Immune System	4/169	31/10164	0,001635	0,030706	0,025775	LR2/S100A8/TLR4/S100A
R-HSA-5602358	Diseases associated with the TLR signaling cascade	4/169	31/10164	0,001635	0,030706	0,025775	LR2/S100A8/TLR4/S100A
R-HSA-9614657	FOXO-mediated transcription of cell death genes	3/169	15/10164	0,001774	0,031176	0,02617	FOXO3/CREBBP/BCL6
R-HSA-166166	MyD88-independent TLR4 cascade	7/169	105/10164	0,001802	0,031176	0,02617	MAPK14/FOS/UBE2D1/S1C
R-HSA-937061	TRIF (TICAM1)-mediated TLR4 signaling	7/169	105/10164	0,001802	0,031176	0,02617	MAPK14/FOS/UBE2D1/S1C
R-HSA-168643	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	5/169	53/10164	0,001804	0,031176	0,02617	/CASP8/MAPK14/CASP4/L
R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	4/169	32/10164	0,001844	0,031246	0,026229	ALDO1/SOD2/CAPZ1/MS
R-HSA-168638	NOD1/2 Signaling Pathway	4/169	33/10164	0,002072	0,034426	0,028898	SP8/MAPK14/CASP4/UBA
R-HSA-140534	Caspase activation via Death Receptors in the presence of ligand	3/169	16/10164	0,002156	0,035155	0,02951	CASP8/TLR4/TNFSF10
R-HSA-9020702	Interleukin-1 signaling	7/169	109/10164	0,002232	0,035708	0,029974	!CASP8/IRAK3/S100A12/
R-HSA-9018677	Biosynthesis of DHA-derived SPMs	3/169	17/10164	0,002587	0,040637	0,034112	ALOX5/PTGS2/LTA4H
R-HSA-9607240	FLT3 Signaling	4/169	36/10164	0,002869	0,044272	0,037163	HCK/PTPR1/FOXO3/UBA52
R-HSA-416700	Other semaphorin interactions	3/169	18/10164	0,003067	0,04629	0,038857	PLXNC1/PTPRC/TYROBP
R-HSA-3299685	Detoxification of Reactive Oxygen Species	4/169	37/10164	0,003176	0,04629	0,038857	NCF4/NCF1/CYBB/SOD2
R-HSA-9664323	FCGR3A-mediated IL10 synthesis	4/169	37/10164	0,003176	0,04629	0,038857	ICK/LYN/PRKAR1A/FCGR1
R-HSA-195258	RHO GTPase Effectors	11/169	252/10164	0,003215	0,04629	0,038857	!F4/ROCK1/NCF1/IOGAP1,
R-HSA-9705671	SARS-CoV-2 activates/modulates innate and adaptive immune responses	7/169	117/10164	0,003326	0,047116	0,039551	A/STAT1/TLR8/CREBBP/UE
R-HSA-9018678	Biosynthesis of specialized proresolving mediators (SPMs)	3/169	19/10164	0,003597	0,048724	0,0409	ALOX5/PTGS2/LTA4H
R-HSA-877300	Interferon gamma signaling	6/169	89/10164	0,0036	0,048724	0,0409	LA-G/PRKCD/FCGR1A/GBF
R-HSA-9614085	FOXO-mediated transcription	5/169	62/10164	0,003609	0,048724	0,0409	P/FOXO3/CREBBP/BCL6/S
R-HSA-373755	Semaphorin interactions	5/169	63/10164	0,003869	0,051422	0,043165	1/GSK3B/ROCK1/PTPRC/T
R-HSA-912631	Regulation of signaling by CBL	3/169	20/10164	0,004181	0,05146	0,043197	HCK/LYN/UBA52
R-HSA-9669938	Signaling by KIT in disease	3/169	20/10164	0,004181	0,05146	0,043197	STAT1/LYN/STAT3
R-HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	3/169	20/10164	0,004181	0,05146	0,043197	STAT1/LYN/STAT3
R-HSA-9671555	Signaling by PDGFR in disease	3/169	20/10164	0,004181	0,05146	0,043197	STAT1/BIN2/STAT3

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
R-HSA-9768919	NPAS4 regulates expression of target genes	3/169	20/10164	0,004181	0,05146	0,043197	FOS/CREBBP/NAMPT
R-HSA-9696264	RND3 GTPase cycle	4/169	40/10164	0,004229	0,05146	0,043197	LOT2/ROCK1/PICALM/CP1
R-HSA-9020591	Interleukin-12 signaling	4/169	41/10164	0,004626	0,055514	0,0466	ALDO1/SOD2/CAPZA1/MS
R-HSA-202427	Phosphorylation of CD3 and TCR zeta chains	3/169	21/10164	0,004819	0,055514	0,0466	PTPRJ/PTPRC/PTPN22
R-HSA-9008059	Interleukin-37 signaling	3/169	21/10164	0,004819	0,055514	0,0466	IL18R1/STAT3/PTPN12
R-HSA-937041	IKK complex recruitment mediated by RIP1	3/169	21/10164	0,004819	0,055514	0,0466	TLR4/UBE2D1/UBA52
R-HSA-5607764	CLEC7A (Dectin-1) signaling	6/169	95/10164	0,004964	0,056435	0,047373	3E2D1/CLEC7A/IL1B/UBA5
R-HSA-1433557	Signaling by SCF-KIT	4/169	42/10164	0,005048	0,056641	0,047546	MMP9/STAT1/LYN/STAT3
R-HSA-451927	Interleukin-2 family signaling	4/169	44/10164	0,005967	0,066098	0,055484	CSF2RB/SOS2/STAT1/STAT
R-HSA-909733	Interferon alpha/beta signaling	5/169	70/10164	0,006071	0,066396	0,055734	1/KPNB1/HLA-G/GBP2/IFI
R-HSA-168164	Toll Like Receptor 3 (TLR3) Cascade	6/169	101/10164	0,006674	0,07104	0,059632	PK14/FOS/UBE2D1/S100A
R-HSA-109581	Apoptosis	8/169	167/10164	0,006703	0,07104	0,059632	SF10/ROCK1/KPNB1/UBA
R-HSA-512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	4/169	46/10164	0,006992	0,07104	0,059632	CSF2RB/HCK/LYN/UBA52
R-HSA-75153	Apoptotic execution phase	4/169	46/10164	0,006992	0,07104	0,059632	ASP8/ROCK1/KPNB1/PRKC
R-HSA-9012852	Signaling by NOTCH3	4/169	46/10164	0,006992	0,07104	0,059632	TAT1/CREBBP/UBA52/RBF
R-HSA-2173788	Downregulation of TGF-beta receptor signaling	3/169	24/10164	0,007071	0,07104	0,059632	TGFBR2/UBA52/USP15
R-HSA-9013508	NOTCH3 Intracellular Domain Regulates Transcription	3/169	24/10164	0,007071	0,07104	0,059632	STAT1/CREBBP/RBPJ
R-HSA-5357769	Caspase activation via extrinsic apoptotic signalling pathway	3/169	25/10164	0,007938	0,076938	0,064583	CASP8/TLR4/TNFSF10
R-HSA-9006335	Signaling by Erythropoietin	3/169	25/10164	0,007938	0,076938	0,064583	IRS2/LYN/PIK3CG
R-HSA-9635486	Infection with Mycobacterium tuberculosis	3/169	25/10164	0,007938	0,076938	0,064583	TLR2/KPNB1/UBA52
R-HSA-9662851	Anti-inflammatory response favouring Leishmania parasite infection	5/169	75/10164	0,008103	0,076938	0,064583	14/HCK/LYN/PRKAR1A/FC
R-HSA-9664433	Leishmania parasite growth and survival	5/169	75/10164	0,008103	0,076938	0,064583	14/HCK/LYN/PRKAR1A/FC
R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	16/169	500/10164	0,009026	0,084386	0,070836	TPRJ/STAT1/LYN/ROCK1/F
R-HSA-9013149	RAC1 GTPase cycle	8/169	176/10164	0,009083	0,084386	0,070836	AP15/ARHGDI8/NCF1/IOC
R-HSA-2559582	Senescence-Associated Secretory Phenotype (SASP)	4/169	50/10164	0,009375	0,086172	0,072335	OS/UBE2D1/UBA52/STAT
R-HSA-9700206	Signaling by ALK in cancer	4/169	52/10164	0,010743	0,095039	0,079778	RKAR1A/KIF5B/MSN/STAT
R-HSA-9725370	Signaling by ALK fusions and activated point mutants	4/169	52/10164	0,010743	0,095039	0,079778	RKAR1A/KIF5B/MSN/STAT
R-HSA-2173795	Downregulation of SMAD2/3:SMAD4 transcriptional activity	3/169	28/10164	0,010904	0,095039	0,079778	UBE2D1/STAT1/UBA52
R-HSA-9634815	Transcriptional Regulation by NPAS4	3/169	28/10164	0,010904	0,095039	0,079778	FOS/CREBBP/NAMPT
R-HSA-9012999	RHO GTPase cycle	14/169	425/10164	0,011288	0,095039	0,079778	OCK1/ARHGDI8/STK38/NC
R-HSA-202403	TCR signaling	6/169	113/10164	0,011316	0,095039	0,079778	3E2D1/PTPRJ/PTPRC/RBPJ
R-HSA-2586552	Signaling by Leptin	2/169	10/10164	0,01133	0,095039	0,079778	IRS2/STAT3
R-HSA-450341	Activation of the AP-1 family of transcription factors	2/169	10/10164	0,01133	0,095039	0,079778	MAPK14/FOS
R-HSA-9020958	Interleukin-21 signaling	2/169	10/10164	0,01133	0,095039	0,079778	STAT1/STAT3
R-HSA-5663084	Diseases of carbohydrate metabolism	3/169	30/10164	0,013191	0,105667	0,088699	TALDO1/IDS/UBA52
R-HSA-1059683	Interleukin-6 signaling	2/169	11/10164	0,013698	0,105667	0,088699	STAT1/STAT3
R-HSA-3371378	Regulation by c-FLIP	2/169	11/10164	0,013698	0,105667	0,088699	CASP8/TNFSF10
R-HSA-5218900	CASP8 activity is inhibited	2/169	11/10164	0,013698	0,105667	0,088699	CASP8/TNFSF10
R-HSA-69416	Dimerization of procaspase-8	2/169	11/10164	0,013698	0,105667	0,088699	CASP8/TNFSF10
R-HSA-9020956	Interleukin-27 signaling	2/169	11/10164	0,013698	0,105667	0,088699	STAT1/STAT3
R-HSA-937039	IRAK1 recruits IKK complex	2/169	11/10164	0,013698	0,105667	0,088699	PEL1/UBA52
R-HSA-9637687	Suppression of phagosomal maturation	2/169	11/10164	0,013698	0,105667	0,088699	KPNB1/UBA52
R-HSA-975144	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	2/169	11/10164	0,013698	0,105667	0,088699	PEL1/UBA52
R-HSA-2559583	Cellular Senescence	6/169	121/10164	0,015457	0,117455	0,098595	1/FOS/UBE2D1/UBA52/ATI
R-HSA-170834	Signaling by TGF-beta Receptor Complex	5/169	88/10164	0,015498	0,117455	0,098595	1/TGFBR2/STAT1/UBA52/
R-HSA-9013423	RAC3 GTPase cycle	5/169	89/10164	0,016206	0,118049	0,099093	ARHGAP15/ARHGDI8/NCF
R-HSA-879415	Advanced glycosylation endproduct receptor signaling	2/169	12/10164	0,016259	0,118049	0,099093	S100A12/CAPZA1
R-HSA-8984722	Interleukin-35 Signalling	2/169	12/10164	0,016259	0,118049	0,099093	STAT1/STAT3
R-HSA-9673767	Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	2/169	12/10164	0,016259	0,118049	0,099093	STAT1/STAT3
R-HSA-9673770	Signaling by PDGFRA extracellular domain mutants	2/169	12/10164	0,016259	0,118049	0,099093	STAT1/STAT3
R-HSA-114604	GPVI-mediated activation cascade	3/169	33/10164	0,017096	0,122077	0,102475	LYN/PIK3CG/FCER1G
R-HSA-9013407	RHOH GTPase cycle	3/169	33/10164	0,017096	0,122077	0,102475	STOM/ROCK1/ARHGDI8
R-HSA-9658195	Leishmania infection	7/169	160/10164	0,017343	0,122819	0,103097	K14/HCK/LYN/PRKAR1A/IL
R-HSA-2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	2/169	13/10164	0,019008	0,129311	0,108547	TGFBR2/UBA52
R-HSA-75892	Platelet Adhesion to exposed collagen	2/169	13/10164	0,019008	0,129311	0,108547	LYN/FCER1G
R-HSA-8941856	RUNX3 regulates NOTCH signaling	2/169	13/10164	0,019008	0,129311	0,108547	CREBBP/RBPJ
R-HSA-9706369	Negative regulation of FLT3	2/169	13/10164	0,019008	0,129311	0,108547	PTPRJ/UBA52
R-HSA-975163	IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	2/169	13/10164	0,019008	0,129311	0,108547	TLR4/UBA52
R-HSA-2454202	Fc epsilon receptor (FCER) signaling	6/169	127/10164	0,019182	0,129478	0,108687	1/FOS/UBE2D1/LYN/UBA52
R-HSA-1222526	ROS and RNS production in phagocytes	3/169	35/10164	0,020021	0,134096	0,112564	NCF4/NCF1/CYBB
R-HSA-9755511	KEAP1-NFE2L2 pathway	5/169	95/10164	0,020909	0,138967	0,116652	1/TALDO1/CREBBP/UBA52/
R-HSA-5689896	Ovarian tumor domain proteases	3/169	36/10164	0,021581	0,141439	0,118727	PTEN/UBE2D1/UBA52
R-HSA-8983432	Interleukin-15 signaling	2/169	14/10164	0,021936	0,141439	0,118727	SOS2/STAT3
R-HSA-9027284	Erythropoietin activates RAS	2/169	14/10164	0,021936	0,141439	0,118727	IRS2/LYN
R-HSA-937072	TRAF6-mediated induction of TAK1 complex within TLR4 complex	2/169	14/10164	0,021936	0,141439	0,118727	TLR4/UBA52
R-HSA-1169408	ISG15 antiviral mechanism	4/169	66/10164	0,023939	0,153207	0,128606	AT1/KPNB1/EIF2AK2/UBA
R-HSA-111465	Apoptotic cleavage of cellular proteins	3/169	38/10164	0,024893	0,155632	0,130641	CASP8/ROCK1/PRKCD
R-HSA-210744	Regulation of gene expression in late stage (branching morphogenesis) pancreatic bud precursor cells	2/169	15/10164	0,025038	0,155632	0,130641	CREBBP/RBPJ
R-HSA-936964	Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	2/169	15/10164	0,025038	0,155632	0,130641	TLR4/UBA52
R-HSA-9694631	Maturation of nucleoprotein	2/169	15/10164	0,025038	0,155632	0,130641	GSK3B/SRPK1

- Supplementary Table 5: GO enrichment analysis in LAAvsCRYPTOGENIC comparison

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:1902532	negative regulation of intracellular signal transduction	27/155	492/16686	8,16E-14	2,77E-10	2,07E-10	TLR4/CASP8/RASSF2/YBX3/RGS2/LYN/PTEN/UBR2/MIR223/GSK3B/SORL1/PTPRJ/LRRK2/STAT1/PTPN22/STK38/LITAF/
GO:0070663	regulation of leukocyte proliferation	19/155	255/16686	2,73E-12	3,64E-09	2,71E-09	PEL1/IRS2/SOS2/TLR4/LYN/PTEN/LST1/TGFBR2/CD46/CR1/PTPN22/MNDA/CSF2RB/PTPRC/TYROBP/BCL6/PRKAR1A/A
GO:0050670	regulation of lymphocyte proliferation	18/155	225/16686	3,21E-12	3,64E-09	2,71E-09	PEL1/IRS2/SOS2/TLR4/LYN/PTEN/LST1/TGFBR2/CD46/CR1/PTPN22/MNDA/PTPRC/TYROBP/BCL6/PRKAR1A/ATM/MIR2
GO:0001819	positive regulation of cytokine production	24/155	460/16686	6,65E-12	4,52E-09	3,37E-09	PEL1/CLEC7A/TLR4/CASP8/SORL1/PTPRJ/CD46/LRRK2/STAT1/PTPN22/MNDA/IL17RA/IFI16/IRAK3/RIOK3/CLEC4E/PT
GO:0072593	reactive oxygen species metabolic process	17/155	207/16686	8,74E-12	4,95E-09	3,69E-09	FPR2/CLEC7A/TLR4/ALOX5/TGFBR2/NCF1B/NCF1C/NCF4/LRRK2/PRKCD/FOXO3/ITGAM/THBS1/SOD2/TYROBP/HBA2/
GO:0046651	lymphocyte proliferation	19/155	288/16686	2,31E-11	1,12E-08	8,34E-09	PEL1/IRS2/SOS2/TLR4/LYN/PTEN/LST1/TGFBR2/CD46/CR1/PTPN22/MNDA/PRKCD/PTPRC/TYROBP/BCL6/PRKAR1A/AT
GO:0070661	leukocyte proliferation	20/155	330/16686	3,08E-11	1,19E-08	8,85E-09	PEL1/IRS2/SOS2/TLR4/LYN/PTEN/LST1/TGFBR2/CD46/CR1/PTPN22/MNDA/CSF2RB/PRKCD/PTPRC/TYROBP/BCL6/PRK
GO:0043065	positive regulation of apoptotic process	24/155	498/16686	3,49E-11	1,19E-08	8,85E-09	IGF2R/STK17B/CASP8/RASSF2/LYN/PTEN/S100A8/CXCR2/MNDA/PRKCD/FOXO3/ITGAM/STK4/TXNIP/PTPRC/TNFSF10/
GO:0032943	mononuclear cell proliferation	19/155	295/16686	3,50E-11	1,19E-08	8,85E-09	PEL1/IRS2/SOS2/TLR4/LYN/PTEN/LST1/TGFBR2/CD46/CR1/PTPN22/MNDA/PRKCD/PTPRC/TYROBP/BCL6/PRKAR1A/AT
GO:0002683	negative regulation of immune system process	22/155	418/16686	4,61E-11	1,43E-08	1,06E-08	PEL1/TLR4/LYN/PTEN/LST1/MIR223/PTPRJ/CD46/CR1/USP15/PTPN22/FGL2/MNDA/IFI16/IRAK3/PTPRC/THBS1/TYRO
GO:1903706	regulation of hemopoiesis	21/155	385/16686	6,84E-11	1,94E-08	1,44E-08	SOS2/TLR4/CASP8/RASSF2/LYN/TGFBR2/MIR223/CD46/CR1/STAT1/EVI2B/FGL2/FOXO3/PTPRC/FAM210B/FOS/CSF3R/
GO:0071900	regulation of protein serine/threonine kinase activity	20/155	353/16686	1,03E-10	2,69E-08	2,00E-08	TLR4/RGS2/LYN/PTEN/DAZAP2/SORL1/PTPRJ/LRRK2/ACSL1/PTPN22/STK38/PRKCD/IRAK3/STK4/S100A12/PTPRC/IQG
GO:0002764	immune response-regulating signaling pathway	22/155	441/16686	1,29E-10	3,14E-08	2,33E-08	PEL1/CLEC4D/FPR2/CLEC7A/TLR4/LYN/FPR1/PTPRJ/CREBBP/CR1/WNK1/USP15/PTPN22/MNDA/PRKCD/IRAK3/RIOK3
GO:0045088	regulation of innate immune response	16/155	221/16686	2,44E-10	5,19E-08	3,86E-08	FPR2/CLEC7A/TLR4/CASP8/LYN/CREBBP/CR1/USP15/PTPN22/MNDA/IFI16/IRAK3/RIOK3/FFAR2/TYROBP/MIR21
GO:2000379	positive regulation of reactive oxygen species metabolic process	10/155	64/16686	3,52E-10	6,65E-08	4,95E-08	FPR2/CLEC7A/TLR4/TGFBR2/PRKCD/FOXO3/ITGAM/THBS1/SOD2/TYROBP
GO:0032103	positive regulation of response to external stimulus	21/155	438/16686	7,26E-10	1,23E-07	9,19E-08	FPR2/STX3/CLEC7A/TLR4/LYN/S100A8/CREBBP/CXCR2/WNK1/USP15/LRRK2/MNDA/IL17RA/IFI16/IRAK3/S100A12/S100A9
GO:0050866	negative regulation of cell activation	15/155	208/16686	9,65E-10	1,56E-07	1,16E-07	PEL1/LYN/PTEN/LST1/CR1/PTPN22/FGL2/MNDA/PRKCD/PTPRC/TYROBP/BCL6/PRKAR1A/ATM/MIR21
GO:0030595	leukocyte chemotaxis	15/155	217/16686	1,73E-09	2,68E-07	2,00E-07	FPR2/LYST/ALOX5/LYN/S100A8/MIR223/CXCR1/CXCR2/WNK1/IL17RA/S100A12/S100A9/CSF3R/FFAR2/THBS1
GO:0002831	regulation of response to biotic stimulus	18/155	334/16686	2,10E-09	2,77E-07	2,06E-07	FPR2/CLEC7A/TLR4/CASP8/LYN/CREBBP/CR1/USP15/STAT1/PTPN22/FGL2/MNDA/IFI16/IRAK3/RIOK3/FFAR2/TYROBP/
GO:0007159	leukocyte cell-cell adhesion	19/155	393/16686	4,37E-09	5,31E-07	3,95E-07	PEL1/ALOX5/LYN/PTEN/S100A8/TGFBR2/SELL/CD46/CR1/WNK1/FLOT2/PTPN22/FGL2/FOXO3/PTPRC/S100A9/BCL6/
GO:0009620	response to fungus	9/155	61/16686	4,68E-09	5,31E-07	3,95E-07	CLEC4D/CLEC7A/TLR4/S100A8/USP15/IL17RA/CLEC4E/S100A12/S100A9
GO:0002696	positive regulation of leukocyte activation	19/155	406/16686	7,43E-09	8,15E-07	6,07E-07	PEL1/IRS2/CLEC4D/CLEC7A/TLR4/LYN/TGFBR2/CD46/CR1/LRRK2/FLOT2/PTPN22/FOXO3/ITGAM/PTPRC/THBS1/TYRO
GO:0031349	positive regulation of defense response	16/155	285/16686	9,76E-09	1,01E-06	7,49E-07	FPR2/CLEC7A/TLR4/LYN/S100A8/CREBBP/LRRK2/MNDA/IL17RA/IFI16/IRAK3/S100A12/S100A9/FFAR2/TYROBP/MIR2
GO:0030099	myeloid cell differentiation	18/155	376/16686	1,34E-08	1,23E-06	9,16E-07	TLR4/CASP8/RASSF2/LYN/TGFBR2/MIR223/STAT1/PIP4K2A/EVI2B/IFI16/FOXO3/FAM210B/FOS/CSF3R/STAT3/ALAS2/T
GO:0010950	positive regulation of endopeptidase activity	12/155	160/16686	3,18E-08	2,46E-06	1,83E-06	CLEC7A/CASP8/LYN/S100A8/CR1/PICALM/IFI16/TNFSF10/S100A9/STAT3/DDX3X/MIR21
GO:0045936	negative regulation of phosphate metabolic process	18/155	406/16686	4,34E-08	3,07E-06	2,29E-06	IRS2/RASSF2/RGS2/LYN/PTEN/GSK3B/SORL1/PTPRJ/LRRK2/PIP4K2A/PTPN22/STK38/PRKCD/IRAK3/PTPRC/IQGAP1/ST
GO:0051348	negative regulation of transferase activity	14/155	245/16686	6,89E-08	4,42E-06	3,29E-06	IRS2/RGS2/LYN/PTEN/GSK3B/SORL1/PTPRJ/PIP4K2A/PTPN22/STK38/PRKCD/IRAK3/PTPRC/PRKAR1A
GO:0019221	cytokine-mediated signaling pathway	19/155	469/16686	7,42E-08	4,67E-06	3,48E-06	CASP8/LYN/CXCR1/PTPRJ/CXCR2/WNK1/STAT1/ACSL1/IL18RAP/IL17RA/CSF2RB/IL1R2/FOXO3/IRAK3/PTPRC/CSF3R/S
GO:1901216	positive regulation of neuron death	9/155	89/16686	1,38E-07	8,07E-06	6,01E-06	TLR4/CASP8/GSK3B/PICALM/FOXO3/ITGAM/FOS/TYROBP/ATM
GO:0002274	myeloid leukocyte activation	13/155	228/16686	2,12E-07	1,14E-05	8,52E-06	CLEC4D/TLR4/LYN/TGFBR2/CXCR2/LRRK2/PRKCD/ITGAM/S100A12/PTPRC/THBS1/TYROBP/ATM
GO:1903037	regulation of leukocyte cell-cell adhesion	16/155	358/16686	2,30E-07	1,22E-05	9,08E-06	PEL1/ALOX5/LYN/PTEN/TGFBR2/CD46/CR1/WNK1/FLOT2/PTPN22/FGL2/FOXO3/PTPRC/BCL6/PRKAR1A/MIR21
GO:0050900	leukocyte migration	16/155	369/16686	3,45E-07	1,80E-05	1,34E-05	FPR2/LYST/ALOX5/LYN/S100A8/MIR223/CXCR1/SELL/CXCR2/WNK1/IL17RA/S100A12/S100A9/CSF3R/FFAR2/THBS1
GO:0031348	negative regulation of defense response	13/155	245/16686	4,83E-07	2,31E-05	1,72E-05	FPR2/ALOX5/LYN/MIR223/CR1/USP15/FGL2/IFI16/PRKCD/IRAK3/RIOK3/PTPRC/MIR21
GO:0002237	response to molecule of bacterial origin	15/155	336/16686	5,67E-07	2,57E-05	1,91E-05	PEL1/TLR4/TAP2/CASP8/LYN/S100A8/MIR223/PTPN22/LITAF/CSF2RB/IRAK3/FOS/S100A9/SOD2/MIR21
GO:0051092	positive regulation of NF-kappaB transcription factor activity	10/155	144/16686	9,46E-07	4,07E-05	3,03E-05	CLEC7A/TLR4/S100A8/FLOT2/IL18RAP/IRAK3/S100A12/S100A9/STAT3/EIF2AK2
GO:0042113	B cell activation	14/155	305/16686	9,90E-07	4,21E-05	3,13E-05	PEL1/IRS2/TLR4/CASP8/LYN/PTEN/PTPRJ/CR1/MNDA/PRKCD/PTPRC/TYROBP/BCL6/ATM
GO:0045785	positive regulation of cell adhesion	17/155	464/16686	1,52E-06	5,93E-05	4,41E-05	STX3/ALOX5/LYN/TGFBR2/GSK3B/PTPRJ/CD46/CR1/FLOT2/PTPN22/FOXO3/STK4/DOCK5/PTPRC/BCL6/ATM/MIR21
GO:0002366	leukocyte activation involved in immune response	13/155	280/16686	2,16E-06	8,08E-05	6,02E-05	CLEC4D/TLR4/LYN/CD46/CR1/FGL2/ITGAM/CLEC4E/PTPRC/STAT3/TYROBP/BCL6/MIR21
GO:1904683	regulation of metalloendopeptidase activity	4/155	11/16686	2,25E-06	8,21E-05	6,12E-05	SORL1/PICALM/STAT3/MIR21
GO:0002532	production of molecular mediator involved in inflammatory resp	8/155	93/16686	2,42E-06	8,71E-05	6,48E-05	CLEC7A/TLR4/ALOX5/LYN/IL17RA/IL1R2/STAT3/MIR21
GO:0062207	regulation of pattern recognition receptor signaling pathway	8/155	95/16686	2,84E-06	9,75E-05	7,26E-05	PEL1/TLR4/LYN/USP15/PTPN22/IRAK3/RIOK3/DDX3X
GO:0055076	transition metal ion homeostasis	9/155	134/16686	4,43E-06	0,000137	0,000102	FBXL5/STEAP4/S100A8/NCOA4/PICALM/SLC25A37/S100A9/ALAS2/SOD2
GO:0032102	negative regulation of response to external stimulus	15/155	397/16686	4,48E-06	0,000137	0,000102	FPR2/ALOX5/LYN/PTEN/MIR223/CR1/USP15/FGL2/IFI16/PRKCD/IRAK3/RIOK3/PTPRC/THBS1/MIR21
GO:0032640	tumor necrosis factor production	10/155	172/16686	4,72E-06	0,000141	0,000105	CLEC7A/TLR4/PTPRJ/LRRK2/PTPN22/IRAK3/PTPRC/STAT3/THBS1/TYROBP
GO:2001233	regulation of apoptotic signaling pathway	14/155	352/16686	5,28E-06	0,000153	0,000114	YBX3/PTEN/S100A8/GSK3B/LRRK2/PRKCD/STK4/PTPRC/TNFSF10/S100A9/DDX3X/THBS1/SOD2/MIR21
GO:0033674	positive regulation of kinase activity	16/155	455/16686	5,30E-06	0,000153	0,000114	TLR4/RASSF2/LYN/TGFBR2/DAZAP2/WNK1/LRRK2/ACSL1/PRKCD/STK4/S100A12/PTPRC/IQGAP1/DDX3X/THBS1/MIR2
GO:0046777	protein autophosphorylation	11/155	217/16686	5,87E-06	0,000165	0,000123	STK17B/RASSF2/LYN/GSK3B/LRRK2/IRAK3/STK4/PTPRC/DDX3X/EIF2AK2/ATM
GO:0050777	negative regulation of immune response	10/155	181/16686	7,43E-06	0,000199	0,000148	LYN/CD46/CR1/USP15/FGL2/IFI16/IRAK3/PTPRC/BCL6/MIR21
GO:0006909	phagocytosis	12/155	274/16686	9,76E-06	0,000252	0,000187	FPR2/LYST/CLEC7A/TLR4/LYN/PTPRJ/NCF4/PRKCD/ITGAM/PTPRC/THBS1/TYROBP

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	4/155	17/16686	1,55E-05	0,000384	0,000286	TLR4/LRRK2/STAT1/NAMPT
GO:0042542	response to hydrogen peroxide	8/155	121/16686	1,71E-05	0,000416	0,00031	LRRK2/STAT1/PRKCD/FOXO3/TXNIP/SOD2/HBA2/MIR21
GO:1990840	response to lectin	4/155	18/16686	1,98E-05	0,000461	0,000343	CLEC7A/LYN/CREBBP/TYROBP
GO:1990858	cellular response to lectin	4/155	18/16686	1,98E-05	0,000461	0,000343	CLEC7A/LYN/CREBBP/TYROBP
GO:0034605	cellular response to heat	6/155	61/16686	2,12E-05	0,000488	0,000363	LYN/GSK3B/CREBBP/THBS1/SLU7/ATM
GO:0035458	cellular response to interferon-beta	4/155	19/16686	2,49E-05	0,000557	0,000415	STAT1/MNDA/IFI16/IFITM2
GO:1901653	cellular response to peptide	13/155	355/16686	2,77E-05	0,000607	0,000452	IRS2/FPR2/TLR4/LYN/GSK3B/SORL1/STAT1/PIP4K2A/PTPN22/PRKCD/FOXO3/FOS/STAT3
GO:0051767	nitric-oxide synthase biosynthetic process	4/155	20/16686	3,09E-05	0,000657	0,000489	TLR4/LRRK2/STAT1/NAMPT
GO:0002700	regulation of production of molecular mediator of immune response	9/155	174/16686	3,62E-05	0,00075	0,000559	CLEC7A/TLR4/CR1/PTPN22/LITAF/IRAK3/PTPRC/FFAR2/BCL6
GO:0033002	muscle cell proliferation	10/155	221/16686	4,18E-05	0,00083	0,000618	TLR4/PDEN/TGFBF2/MIR223/STAT1/FOS/THBS1/SOD2/PRKAR1A/MIR21
GO:0002902	regulation of B cell apoptotic process	4/155	22/16686	4,60E-05	0,000894	0,000665	IRS2/LYN/PDEN/BCL6
GO:1901652	response to peptide	15/155	486/16686	4,81E-05	0,000925	0,000689	IRS2/FPR2/TLR4/LYN/GSK3B/SORL1/LTA4H/STAT1/PIP4K2A/PTPN22/PRKCD/FOXO3/FOS/TNFSF10/STAT3
GO:0062197	cellular response to chemical stress	12/155	323/16686	4,95E-05	0,00094	0,0007	TLR4/ALOX5/YBX3/SLC12A6/LRRK2/PRKCD/FOXO3/FOS/DDX3X/SOD2/ATM/MIR21
GO:0060547	negative regulation of necrotic cell death	4/155	23/16686	5,53E-05	0,001027	0,000765	PEL1/CASP8/YBX3/MIR223
GO:0002460	adaptive immune response based on somatic recombination of immunoglobulin genes	12/155	333/16686	6,63E-05	0,001186	0,000883	CLEC7A/TLR4/TAP2/CD46/CR1/IL17RA/CSF2RB/PRKCD/PTPRC/STAT3/BCL6/MIR21
GO:0002269	leukocyte activation involved in inflammatory response	5/155	48/16686	8,04E-05	0,001395	0,001039	LRRK2/ITGAM/PTPRC/TYROBP/ATM
GO:0015911	long-chain fatty acid import across plasma membrane	3/155	10/16686	8,99E-05	0,001521	0,001133	IRS2/ACSL1/THBS1
GO:0035456	response to interferon-beta	4/155	26/16686	9,13E-05	0,001537	0,001144	STAT1/MNDA/IFI16/IFITM2
GO:0051346	negative regulation of hydrolase activity	12/155	346/16686	9,54E-05	0,00159	0,001184	RGS2/MIR223/GSK3B/SORL1/CR1/WNK1/LRRK2/PICALM/IFI16/DDX3X/THBS1/MIR21
GO:0048660	regulation of smooth muscle cell proliferation	8/155	155/16686	0,0001	0,001666	0,001241	TLR4/PDEN/TGFBF2/MIR223/STAT1/THBS1/SOD2/MIR21
GO:0070997	neuron death	12/155	349/16686	0,000103	0,001704	0,001268	TLR4/CASP8/GSK3B/SORL1/LRRK2/PICALM/FOXO3/ITGAM/FOS/SOD2/TYROBP/ATM
GO:0001783	B cell apoptotic process	4/155	27/16686	0,000106	0,001726	0,001285	IRS2/LYN/PDEN/BCL6
GO:0061900	glial cell activation	5/155	51/16686	0,000108	0,001739	0,001295	LRRK2/ITGAM/PTPRC/TYROBP/ATM
GO:1900407	regulation of cellular response to oxidative stress	6/155	82/16686	0,000114	0,00181	0,001363	TLR4/ALOX5/LRRK2/FOXO3/SOD2/MIR21
GO:0002443	leukocyte mediated immunity	13/155	415/16686	0,000135	0,002116	0,001576	LYST/CLEC7A/TLR4/TAP2/LYN/CD46/CR1/CSF2RB/PRKCD/ITGAM/PTPRC/TYROBP/BCL6
GO:0002262	myeloid cell homeostasis	8/155	163/16686	0,000142	0,002219	0,001652	LYN/CXCR2/STAT1/FOXO3/FAM210B/STAT3/ALAS2/BCL6
GO:1902882	regulation of response to oxidative stress	6/155	89/16686	0,00018	0,00269	0,002003	TLR4/ALOX5/LRRK2/FOXO3/SOD2/MIR21
GO:0071214	cellular response to abiotic stimulus	11/155	316/16686	0,000182	0,002696	0,002007	TLR4/CASP8/YBX3/PDEN/SLC12A6/CREBBP/IFI16/PRKCD/DDX3X/ATM/MIR21
GO:0104004	cellular response to environmental stimulus	11/155	316/16686	0,000182	0,002696	0,002007	TLR4/CASP8/YBX3/PDEN/SLC12A6/CREBBP/IFI16/PRKCD/DDX3X/ATM/MIR21
GO:0031333	negative regulation of protein-containing complex assembly	7/155	130/16686	0,000212	0,00304	0,002264	GSK3B/SSH2/SORL1/PRKCD/RIOK3/CAP2A1/DDX3X
GO:0009743	response to carbohydrate	9/155	223/16686	0,000241	0,003334	0,002483	IRS2/CLEC7A/LYN/TGFBF2/SLC12A6/FOXO3/TXNIP/THBS1/SOD2
GO:0031343	positive regulation of cell killing	5/155	61/16686	0,000254	0,003464	0,002579	CLEC7A/TAP2/ITGAM/PTPRC/TYROBP
GO:0090715	immunological memory formation process	3/155	14/16686	0,000265	0,003581	0,002667	CD46/FGL2/BCL6
GO:0070265	necrotic cell death	5/155	63/16686	0,000295	0,003921	0,00292	PEL1/CASP8/YBX3/MIR223/PYGL
GO:0045730	respiratory burst	4/155	35/16686	0,0003	0,003959	0,002948	CLEC7A/NCF1B/NCF1C/NCF4
GO:0001666	response to hypoxia	10/155	281/16686	0,0003	0,003959	0,002948	PTEN/TGFBF2/CREBBP/FOXO3/FOS/THBS1/ALAS2/SOD2/ATM/MIR21
GO:0071216	cellular response to biotic stimulus	9/155	239/16686	0,000401	0,005092	0,003791	CLEC7A/TLR4/LYN/MIR223/GSK3B/PTPN22/LITAF/TXNIP/MIR21
GO:0002713	negative regulation of B cell mediated immunity	3/155	16/16686	0,000403	0,005092	0,003791	CD46/CR1/BCL6
GO:0002890	negative regulation of immunoglobulin mediated immune response	3/155	16/16686	0,000403	0,005092	0,003791	CD46/CR1/BCL6
GO:0090594	inflammatory response to wounding	3/155	16/16686	0,000403	0,005092	0,003791	TLR4/ALOX5/MIR21
GO:0046621	negative regulation of organ growth	4/155	38/16686	0,000413	0,005187	0,003862	RGS2/PDEN/TGFBF2/STK4
GO:0031647	regulation of protein stability	10/155	295/16686	0,000441	0,005431	0,004044	RASSF2/PDEN/DAZAP2/CREBBP/LRRK2/FLOT2/PRKCD/STK4/B4GALT5/TYROBP
GO:0002544	chronic inflammatory response	3/155	19/16686	0,000683	0,007638	0,005687	S100A8/S100A9/THBS1
GO:1903978	regulation of microglial cell activation	3/155	19/16686	0,000683	0,007638	0,005687	LRRK2/PTPRC/ATM
GO:0009896	positive regulation of catabolic process	13/155	493/16686	0,000703	0,007829	0,005829	FBXL5/IRS2/AGTPBP1/PDEN/MIR223/GSK3B/SORL1/LRRK2/PIP4K2A/WAC/PRKCD/FOXO3/ATM
GO:0014910	regulation of smooth muscle cell migration	5/155	76/16686	0,000705	0,007829	0,005829	TLR4/MIR223/SORL1/DOCK5/MIR21
GO:0021782	glial cell development	6/155	115/16686	0,000714	0,007904	0,005885	TLR4/LYN/PDEN/S100A8/B4GALT5/S100A9
GO:0034248	regulation of cellular amide metabolic process	13/155	494/16686	0,000716	0,007904	0,005885	GSPT1/YBX3/RGS2/MIR223/SORL1/DDX6/PICALM/PRKCD/FOXO3/DDX3X/EIF2AK2/THBS1/MIR21
GO:0002367	cytokine production involved in immune response	6/155	116/16686	0,000747	0,008113	0,006041	CLEC7A/TLR4/LITAF/IRAK3/FFAR2/BCL6
GO:0002688	regulation of leukocyte chemotaxis	6/155	119/16686	0,000854	0,009044	0,006734	FPR2/LYN/MIR223/CXCR2/WNK1/THBS1
GO:0035902	response to immobilization stress	3/155	21/16686	0,000925	0,009704	0,007225	FOXO3/FOS/SOD2
GO:0044546	NLRP3 inflammasome complex assembly	3/155	21/16686	0,000925	0,009704	0,007225	TLR4/DDX3X/EIF2AK2
GO:0010506	regulation of autophagy	10/155	325/16686	0,00093	0,009733	0,007247	DCAF12/GSK3B/LRRK2/PIP4K2A/PTPN22/WAC/IFI16/FOXO3/STAT3/ATM
GO:0014909	smooth muscle cell migration	5/155	83/16686	0,001051	0,01093	0,008138	TLR4/MIR223/SORL1/DOCK5/MIR21
GO:0045069	regulation of viral genome replication	5/155	83/16686	0,001051	0,01093	0,008138	SRPK1/IFI16/DDX3X/EIF2AK2/IFITM2
GO:0032891	negative regulation of organic acid transport	3/155	22/16686	0,001063	0,011024	0,008208	IRS2/RGS2/THBS1
GO:0001906	cell killing	7/155	172/16686	0,001134	0,011576	0,008619	LYST/CLEC7A/TAP2/ITGAM/S100A12/PTPRC/TYROBP

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0016032	viral process	11/155	394/16686	0,001149	0,011665	0,008685	IGF2R/SRPK1/GSK3B/DDX6/CD46/CR1/STAT1/IFI16/DDX3X/EIF2AK2/IFITM2
GO:0043087	regulation of GTPase activity	10/155	336/16686	0,001196	0,012064	0,008982	SOS2/MIR223/GSK3B/WNK1/LRRK2/PICALM/PLXNC1/IQGAP1/BCL6/MIR21
GO:0002440	production of molecular mediator of immune response	9/155	279/16686	0,001205	0,012111	0,009018	CLEC7A/TLR4/CR1/PTPN22/LITAF/IRAK3/PTPRC/FFAR2/BCL6
GO:0002053	positive regulation of mesenchymal cell proliferation	3/155	23/16686	0,001215	0,012111	0,009018	IRS2/TGFBR2/STAT1
GO:0035821	modulation of process of another organism	3/155	23/16686	0,001215	0,012111	0,009018	MPEG1/CLEC7A/S100A9
GO:0140632	inflammasome complex assembly	3/155	23/16686	0,001215	0,012111	0,009018	TLR4/DDX3X/EIF2AK2
GO:0031331	positive regulation of cellular catabolic process	11/155	398/16686	0,001246	0,012388	0,009224	IRS2/AGTPBP1/PTEN/MIR223/GSK3B/LRRK2/PIP4K2A/WAC/PRKCD/FOXO3/ATM
GO:0006979	response to oxidative stress	11/155	402/16686	0,00135	0,013301	0,009904	TLR4/ALOX5/LRRK2/STAT1/PRKCD/FOXO3/TXNIP/FOS/SOD2/HBA2/MIR21
GO:0044264	cellular polysaccharide metabolic process	5/155	88/16686	0,001367	0,013397	0,009975	IRS2/GSK3B/PYGL/MGAM/B4GALT5
GO:0010332	response to gamma radiation	4/155	52/16686	0,001371	0,013397	0,009975	PTPRC/SOD2/ATM/MIR21
GO:0042982	amyloid precursor protein metabolic process	5/155	89/16686	0,001437	0,013964	0,010397	LYN/SORL1/FLOT2/PICALM/ITM2B
GO:0007566	embryo implantation	4/155	53/16686	0,001473	0,014223	0,01059	TGFBR2/VMP1/ARHGDI1/MIR21
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	4/155	54/16686	0,001579	0,014789	0,011012	TAP2/ITGAM/PTPRC/TYROBP
GO:0090066	regulation of anatomical structure size	12/155	477/16686	0,001678	0,015632	0,011639	RGS2/PTEN/GSK3B/SLC12A6/SSH2/LRRK2/PICALM/PRKCD/DOCK5/CAPZA1/SOD2/MIR21
GO:0009991	response to extracellular stimulus	12/155	483/16686	0,001862	0,017023	0,012675	LYN/TGFBR2/SORL1/LRRK2/STAT1/ACSL1/IFI16/FOXO3/PTPRC/FOS/EIF2AK2/SOD2
GO:0098657	import into cell	8/155	243/16686	0,001978	0,017652	0,013143	IRS2/RGS2/STEAP4/SLC12A6/WNK1/KCNJ15/ACSL1/THBS1
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	8/155	246/16686	0,002135	0,018806	0,014003	RGS2/MIR223/GSK3B/DDX6/ITM2B/DDX3X/EIF2AK2/MIR21
GO:0034063	stress granule assembly	3/155	28/16686	0,002172	0,018838	0,014026	DAZAP2/DDX6/DDX3X
GO:1903318	negative regulation of protein maturation	3/155	28/16686	0,002172	0,018838	0,014026	LRRK2/IL1R2/THBS1
GO:0098739	import across plasma membrane	7/155	194/16686	0,002256	0,019467	0,014495	IRS2/RGS2/SLC12A6/WNK1/KCNJ15/ACSL1/THBS1
GO:0005976	polysaccharide metabolic process	5/155	99/16686	0,0023	0,019799	0,014742	IRS2/GSK3B/PYGL/MGAM/B4GALT5
GO:0071496	cellular response to external stimulus	9/155	308/16686	0,00237	0,020344	0,015148	TLR4/CASP8/LYN/LRRK2/IFI16/FOXO3/PTPRC/FOS/EIF2AK2
GO:0002507	tolerance induction	3/155	29/16686	0,002406	0,020555	0,015305	LYN/TGFBR2/IRAK3
GO:0001937	negative regulation of endothelial cell proliferation	4/155	61/16686	0,002478	0,021011	0,015644	ALOX5/STAT1/THBS1/MIR21
GO:0009612	response to mechanical stimulus	7/155	204/16686	0,002987	0,024649	0,018353	TLR4/CASP8/TGFBR2/STAT1/TXNIP/FOS/THBS1
GO:0007009	plasma membrane organization	6/155	153/16686	0,00307	0,025274	0,018819	PTEN/VMP1/CR1/PRKCD/PTPRC/S100A9
GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	3/155	32/16686	0,0032	0,026031	0,019383	CREBBP/THBS1/MIR21
GO:1903846	positive regulation of cellular response to transforming growth factor beta	3/155	32/16686	0,0032	0,026031	0,019383	CREBBP/THBS1/MIR21
GO:0010810	regulation of cell-substrate adhesion	7/155	209/16686	0,003414	0,027314	0,020338	PTEN/GSK3B/PTPRJ/STK4/DOCK5/THBS1/BCL6
GO:0046916	cellular transition metal ion homeostasis	5/155	109/16686	0,00349	0,027842	0,020731	STEAP4/S100A8/NCOA4/S100A9/ALAS2
GO:0002604	regulation of dendritic cell antigen processing and presentation	2/155	10/16686	0,003674	0,028849	0,02148	FGL2/THBS1
GO:0003056	regulation of vascular associated smooth muscle contraction	2/155	10/16686	0,003674	0,028849	0,02148	DOCK5/MIR21
GO:1905065	positive regulation of vascular associated smooth muscle cell differentiation	2/155	10/16686	0,003674	0,028849	0,02148	SOD2/MIR21
GO:0007179	transforming growth factor beta receptor signaling pathway	7/155	213/16686	0,003789	0,029613	0,022049	TGFBR2/CREBBP/USP15/FOS/STAT3/THBS1/MIR21
GO:0050766	positive regulation of phagocytosis	4/155	70/16686	0,004083	0,031457	0,023422	FPR2/CLEC7A/PTPRJ/PTPRC
GO:0071356	cellular response to tumor necrosis factor	7/155	216/16686	0,004089	0,031457	0,023422	CASP8/YBX3/STAT1/FOXO3/FOS/THBS1/GBP2
GO:1903034	regulation of response to wounding	6/155	163/16686	0,004189	0,031897	0,02375	CLEC7A/ALOX5/PTEN/PRKCD/THBS1/MIR21
GO:0050920	regulation of chemotaxis	7/155	217/16686	0,004194	0,031897	0,02375	FPR2/STX3/LYN/MIR223/CXCR2/WNK1/THBS1
GO:0060759	regulation of response to cytokine stimulus	6/155	164/16686	0,004315	0,032676	0,02433	TLR4/CASP8/IL1R2/IRAK3/PTPRC/MIR21
GO:0046631	alpha-beta T cell activation	6/155	166/16686	0,004577	0,0339	0,025241	TGFBR2/PTPN22/PTPRC/STAT3/BCL6/MIR21
GO:0035265	organ growth	6/155	167/16686	0,004711	0,034748	0,025873	YBX3/RGS2/PTEN/TGFBR2/STK4/PRKAR1A
GO:0061045	negative regulation of wound healing	4/155	73/16686	0,004744	0,034911	0,025994	ALOX5/PTEN/PRKCD/THBS1
GO:0009595	detection of biotic stimulus	3/155	37/16686	0,004847	0,035362	0,02633	CLEC7A/TLR4/PTPRJ

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO:0031330	negative regulation of cellular catabolic process	7/155	225/16686	0,005101	0,037057	0,027592	YBX3/SORL1/LRRK2/PTPN22/WAC/STAT3/MIR21
GO:0010038	response to metal ion	9/155	347/16686	0,005182	0,037491	0,027915	CASP8/S100A8/LRRK2/LTA4H/TXNIP/FOS/IQGAP1/THBS1/SOD2
GO:0009410	response to xenobiotic stimulus	10/155	412/16686	0,00519	0,037491	0,027915	LYN/TGFBR2/STAT1/ACSL1/FOXO3/TXNIP/S100A12/FOS/THBS1/SOD2
GO:0032570	response to progesterone	3/155	38/16686	0,005227	0,037491	0,027915	TXNIP/FOS/THBS1
GO:0031589	cell-substrate adhesion	9/155	348/16686	0,005278	0,037628	0,028017	PTEN/GSK3B/MEGF9/PTPRJ/ITGAM/STK4/DOCK5/THBS1/BCL6
GO:0002638	negative regulation of immunoglobulin production	2/155	12/16686	0,005323	0,037628	0,028017	CR1/BCL6
GO:0002645	positive regulation of tolerance induction	2/155	12/16686	0,005323	0,037628	0,028017	TGFBR2/IRAK3
GO:2000008	regulation of protein localization to cell surface	3/155	39/16686	0,005624	0,039201	0,029188	STX3/PICALM/TYROBP
GO:0007041	lysosomal transport	5/155	122/16686	0,005626	0,039201	0,029188	IGF2R/LYST/NCOA4/SORL1/LRRK2
GO:0042060	wound healing	10/155	419/16686	0,005825	0,040339	0,030036	CLEC7A/TLR4/ALOX5/LYN/PTEN/S100A8/TGFBR2/PRKCD/JMJD1C/THBS1
GO:0033500	carbohydrate homeostasis	7/155	231/16686	0,005873	0,040419	0,030095	IRS2/ALOX5/SLC12A6/PYGL/FOXO3/STAT3/FFAR2
GO:0042593	glucose homeostasis	7/155	231/16686	0,005873	0,040419	0,030095	IRS2/ALOX5/SLC12A6/PYGL/FOXO3/STAT3/FFAR2
GO:0045444	fat cell differentiation	7/155	231/16686	0,005873	0,040419	0,030095	ALOX5/RGS2/STEAP4/STK4/FFAR2/SOD2/MIR21
GO:0001909	leukocyte mediated cytotoxicity	5/155	124/16686	0,006022	0,04128	0,030736	LYST/TAP2/ITGAM/PTPRC/TYROBP
GO:0002468	dendritic cell antigen processing and presentation	2/155	13/16686	0,006253	0,042099	0,031346	FGL2/THBS1
GO:0036166	phenotypic switching	2/155	13/16686	0,006253	0,042099	0,031346	SOD2/MIR21
GO:0042541	hemoglobin biosynthetic process	2/155	13/16686	0,006253	0,042099	0,031346	SLC25A37/ALAS2
GO:0045916	negative regulation of complement activation	2/155	13/16686	0,006253	0,042099	0,031346	CD46/CR1
GO:0016064	immunoglobulin mediated immune response	6/155	178/16686	0,006396	0,042895	0,031939	CD46/CR1/CSF2RB/PRKCD/PTPRC/BCL6
GO:0010586	miRNA metabolic process	4/155	80/16686	0,006558	0,043379	0,032299	FOXO3/DDX17/FOS/STAT3
GO:0032092	positive regulation of protein binding	4/155	80/16686	0,006558	0,043379	0,032299	EPB41/GSK3B/LRRK2/STK4
GO:0034612	response to tumor necrosis factor	7/155	236/16686	0,00658	0,043441	0,032345	CASP8/YBX3/STAT1/FOXO3/FOS/THBS1/GBP2
GO:0010463	mesenchymal cell proliferation	3/155	42/16686	0,006923	0,045095	0,033577	IRS2/TGFBR2/STAT1
GO:0006417	regulation of translation	10/155	431/16686	0,007055	0,045866	0,034151	GSPT1/YBX3/RGS2/MIR223/DDX6/FOXO3/DDX3X/EIF2AK2/THBS1/MIR21
GO:0001960	negative regulation of cytokine-mediated signaling pathway	4/155	82/16686	0,00715	0,045994	0,034246	IL1R2/IRAK3/PTPRC/MIR21
GO:0009251	glucan catabolic process	2/155	14/16686	0,007251	0,045994	0,034246	PYGL/MGAM
GO:0060628	regulation of ER to Golgi vesicle-mediated transport	2/155	14/16686	0,007251	0,045994	0,034246	SORL1/LRRK2
GO:1905288	vascular associated smooth muscle cell apoptotic process	2/155	14/16686	0,007251	0,045994	0,034246	SOD2/MIR21
GO:1905459	regulation of vascular associated smooth muscle cell apoptotic process	2/155	14/16686	0,007251	0,045994	0,034246	SOD2/MIR21
GO:0002920	regulation of humoral immune response	3/155	43/16686	0,007392	0,046544	0,034656	CD46/CR1/PTPRC
GO:0009895	negative regulation of catabolic process	8/155	303/16686	0,007443	0,046776	0,034829	YBX3/SORL1/LRRK2/PTPN22/WAC/IRAK3/STAT3/MIR21
GO:0045926	negative regulation of growth	7/155	242/16686	0,007511	0,047114	0,03508	RGS2/PTEN/TGFBR2/PTPRJ/STK4/DDX3X/BCL6
GO:0006898	receptor-mediated endocytosis	7/155	243/16686	0,007675	0,048055	0,035781	IGF2R/TGFBR2/CXCR1/SORL1/CXCR2/PICALM/ITGAM
GO:0055017	cardiac muscle tissue growth	4/155	84/16686	0,007776	0,048512	0,036121	RGS2/PTEN/TGFBR2/PRKAR1A
GO:0098869	cellular oxidant detoxification	4/155	84/16686	0,007776	0,048512	0,036121	S100A9/SOD2/HBA2/MIR21
GO:1902895	positive regulation of miRNA transcription	3/155	44/16686	0,00788	0,04898	0,036469	FOXO3/FOS/STAT3
GO:0006470	protein dephosphorylation	7/155	245/16686	0,008011	0,049431	0,036806	PTEN/GSK3B/SSH2/PTPRJ/PTPN22/PRKCD/PTPRC
GO:0031668	cellular response to extracellular stimulus	7/155	245/16686	0,008011	0,049431	0,036806	LYN/LRRK2/IFI16/FOXO3/PTPRC/FOS/EIF2AK2
GO:0048678	response to axon injury	4/155	85/16686	0,008102	0,049816	0,037092	LYN/PTEN/SOD2/TYROBP

- Supplementary Table 6: REACTOME enrichment analysis in LAAVsCRYPTOGENIC comparison

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
R-HSA-6798695	Neutrophil degranulation	33/120	456/10164	1,04E-17	8,21E-15	6,99E-15	3L/FCAR/MGAM/LTA4H/FGL2
R-HSA-449147	Signaling by Interleukins	25/120	441/10164	4,02E-11	1,59E-08	1,35E-08	/IL17RA/CSF2RB/IL1R2/FOXC
R-HSA-9705462	Inactivation of CSF3 (G-CSF) signaling	5/120	21/10164	3,69E-06	0,000646	0,00055	/N/STAT1/UBA52/CSF3R/STAT
R-HSA-166058	MyD88: MAL (TIRAP) cascade initiated on plasma membrane	9/120	109/10164	5,22E-06	0,000646	0,00055	/S100A8/IRAK3/S100A12/UE
R-HSA-168188	Toll Like Receptor TLR6:TLR2 Cascade	9/120	109/10164	5,22E-06	0,000646	0,00055	/S100A8/IRAK3/S100A12/UE
R-HSA-166016	Toll Like Receptor 4 (TLR4) Cascade	10/120	141/10164	6,07E-06	0,000646	0,00055	00A8/ITGAM/IRAK3/S100A12
R-HSA-168179	Toll Like Receptor TLR1:TLR2 Cascade	9/120	112/10164	6,53E-06	0,000646	0,00055	/S100A8/IRAK3/S100A12/UE
R-HSA-181438	Toll Like Receptor 2 (TLR2) Cascade	9/120	112/10164	6,53E-06	0,000646	0,00055	/S100A8/IRAK3/S100A12/UE
R-HSA-5213460	RIPK1-mediated regulated necrosis	5/120	26/10164	1,14E-05	0,000818	0,000697	1/CASP8/FLOT2/UBA52/TNFS
R-HSA-5675482	Regulation of necroptotic cell death	5/120	26/10164	1,14E-05	0,000818	0,000697	1/CASP8/FLOT2/UBA52/TNFS
R-HSA-9674555	Signaling by CSF3 (G-CSF)	5/120	26/10164	1,14E-05	0,000818	0,000697	/N/STAT1/UBA52/CSF3R/STAT
R-HSA-168898	Toll-like Receptor Cascades	10/120	160/10164	1,85E-05	0,001221	0,00104	00A8/ITGAM/IRAK3/S100A12
R-HSA-9711123	Cellular response to chemical stress	10/120	180/10164	5,10E-05	0,003103	0,002643	O1/NCF4/PRKCD/TXNIP/UBA5
R-HSA-446652	Interleukin-1 family signaling	9/120	147/10164	5,79E-05	0,003274	0,002788	5/IL18RAP/IL1R2/IRAK3/S100
R-HSA-982772	Growth hormone receptor signaling	4/120	23/10164	0,000138	0,007254	0,006178	IRS2/LYN/STAT1/STAT3
R-HSA-5668599	RHO GTPases Activate NADPH Oxidases	4/120	24/10164	0,000164	0,008086	0,006887	/S100A8/NCF4/PRKCD/S100A5
R-HSA-5621481	C-type lectin receptors (CLRs)	8/120	135/10164	0,00019	0,00883	0,00752	/CASP8/LYN/CREBBP/PRKCD,
R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	7/120	105/10164	0,000235	0,01032	0,008789	TAT1/FOXO3/ITGAM/FOS/STA
R-HSA-447115	Interleukin-12 family signaling	5/120	51/10164	0,000321	0,013371	0,011388	DO1/STAT1/CAPZA1/STAT3/SC
R-HSA-5218859	Regulated Necrosis	5/120	52/10164	0,000352	0,013923	0,011858	1/CASP8/FLOT2/UBA52/TNFS
R-HSA-9614657	FOXO-mediated transcription of cell death genes	3/120	15/10164	0,000658	0,024799	0,021121	CREBBP/FOXO3/BCL6
R-HSA-9614085	FOXO-mediated transcription	5/120	62/10164	0,000798	0,027629	0,023531	EBBP/FOXO3/TXNIP/SOD2/BC
R-HSA-140534	Caspase activation via Death Receptors in the presence of ligand	3/120	16/10164	0,000803	0,027629	0,023531	TLR4/CASP8/TNFSF10
R-HSA-5602498	MyD88 deficiency (TLR2/4)	3/120	17/10164	0,000967	0,031154	0,026533	TLR4/S100A8/S100A9
R-HSA-975138	TRAF6 mediated induction of Nfkb and MAP kinases upon TLR7/8 or 9 activation	6/120	97/10164	0,000985	0,031154	0,026533	/TLR4/CASP8/S100A12/UBA5
R-HSA-975155	MyD88 dependent cascade initiated on endosome	6/120	98/10164	0,001039	0,031384	0,02673	/TLR4/CASP8/S100A12/UBA5
R-HSA-168181	Toll Like Receptor 7/8 (TLR7/8) Cascade	6/120	99/10164	0,001095	0,031384	0,02673	/TLR4/CASP8/S100A12/UBA5
R-HSA-416700	Other semaphorin interactions	3/120	18/10164	0,001151	0,031384	0,02673	PLXNC1/PTPRC/TYROBP
R-HSA-5603041	IRAK4 deficiency (TLR2/4)	3/120	18/10164	0,001151	0,031384	0,02673	TLR4/S100A8/S100A9
R-HSA-1236975	Antigen processing-Cross presentation	6/120	102/10164	0,001279	0,032641	0,0278	AP2/S100A8/NCF4/UBA52/S
R-HSA-168138	Toll Like Receptor 9 (TLR9) Cascade	6/120	102/10164	0,001279	0,032641	0,0278	/TLR4/CASP8/S100A12/UBA5
R-HSA-5686938	Regulation of TLR by endogenous ligand	3/120	20/10164	0,00158	0,035709	0,030413	TLR4/S100A8/S100A9
R-HSA-9669938	Signaling by KIT in disease	3/120	20/10164	0,00158	0,035709	0,030413	LYN/STAT1/STAT3
R-HSA-9670439	Signaling by phosphorylated juxtamembrane, extracellular and kinase domain KIT mutants	3/120	20/10164	0,00158	0,035709	0,030413	LYN/STAT1/STAT3
R-HSA-9768919	NPAS4 regulates expression of target genes	3/120	20/10164	0,00158	0,035709	0,030413	CREBBP/FOS/NAMPT
R-HSA-451927	Interleukin-2 family signaling	4/120	44/10164	0,001742	0,038044	0,032401	SOS2/STAT1/CSF2RB/STAT3
R-HSA-9020702	Interleukin-1 signaling	6/120	109/10164	0,0018	0,038044	0,032401	CASP8/IL1R2/IRAK3/S100A12,
R-HSA-202427	Phosphorylation of CD3 and TCR zeta chains	3/120	21/10164	0,001828	0,038044	0,032401	PTPRJ/PTPN22/PTPRC
R-HSA-5357801	Programmed Cell Death	8/120	195/10164	0,002138	0,043365	0,036933	CASP8/FLOT2/PRKCD/UBA52/TI
R-HSA-2173788	Downregulation of TGF-beta receptor signaling	3/120	24/10164	0,002711	0,053601	0,045651	TGFBR2/USP15/UBA52
R-HSA-5357769	Caspase activation via extrinsic apoptotic signalling pathway	3/120	25/10164	0,003054	0,058917	0,050179	TLR4/CASP8/TNFSF10
R-HSA-5663202	Diseases of signal transduction by growth factor receptors and second messengers	12/120	414/10164	0,003515	0,066204	0,056385	/B/CREBBP/STAT1/FOXO3/UB,
R-HSA-1236974	ER-Phagosome pathway	5/120	87/10164	0,003608	0,066368	0,056525	4/TAP2/S100A8/UBA52/S100
R-HSA-5621480	Dectin-2 family	3/120	27/10164	0,003818	0,068632	0,058453	CLEC4D/LYN/CLEC4E
R-HSA-9634815	Transcriptional Regulation by NPAS4	3/120	28/10164	0,004239	0,074518	0,063466	CREBBP/FOS/NAMPT
R-HSA-9707564	Cytoprotection by HMOX1	4/120	57/10164	0,004508	0,077471	0,065981	CREBBP/TXNIP/STAT3/HBA2
R-HSA-168142	Toll Like Receptor 10 (TLR10) Cascade	5/120	93/10164	0,004799	0,077471	0,065981	11/CASP8/S100A12/UBA52/F
R-HSA-168176	Toll Like Receptor 5 (TLR5) Cascade	5/120	93/10164	0,004799	0,077471	0,065981	11/CASP8/S100A12/UBA52/F
R-HSA-975871	MyD88 cascade initiated on plasma membrane	5/120	93/10164	0,004799	0,077471	0,065981	11/CASP8/S100A12/UBA52/F

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
R-HSA-9755511	KEAP1-NFE2L2 pathway	5/120	95/10164	0,005252	0,083082	0,07076	B/CREBBP/TALDO1/PRKCD/U
R-HSA-5260271	Diseases of Immune System	3/120	31/10164	0,005669	0,085649	0,072946	TLR4/S100A8/S100A9
R-HSA-5602358	Diseases associated with the TLR signaling cascade	3/120	31/10164	0,005669	0,085649	0,072946	TLR4/S100A8/S100A9
R-HSA-2586552	Signaling by Leptin	2/120	10/10164	0,005847	0,085649	0,072946	IRS2/STAT3
R-HSA-9020958	Interleukin-21 signaling	2/120	10/10164	0,005847	0,085649	0,072946	STAT1/STAT3
R-HSA-8950505	Gene and protein expression by JAK-STAT signaling after Interleukin-12 stimulation	3/120	32/10164	0,006203	0,089038	0,075832	TALDO1/CAPZA1/SOD2
R-HSA-373755	Semaphorin interactions	4/120	63/10164	0,00644	0,089038	0,075832	SK3B/PLXNC1/PTPRC/TYROBI
R-HSA-1059683	Interleukin-6 signaling	2/120	11/10164	0,007092	0,089038	0,075832	STAT1/STAT3
R-HSA-3371378	Regulation by c-FLIP	2/120	11/10164	0,007092	0,089038	0,075832	CASP8/TNFSF10
R-HSA-5218900	CASP8 activity is inhibited	2/120	11/10164	0,007092	0,089038	0,075832	CASP8/TNFSF10
R-HSA-69416	Dimerization of procaspase-8	2/120	11/10164	0,007092	0,089038	0,075832	CASP8/TNFSF10
R-HSA-9020956	Interleukin-27 signaling	2/120	11/10164	0,007092	0,089038	0,075832	STAT1/STAT3
R-HSA-937039	IRAK1 recruits IKK complex	2/120	11/10164	0,007092	0,089038	0,075832	PEL1/UBA52
R-HSA-975144	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation	2/120	11/10164	0,007092	0,089038	0,075832	PEL1/UBA52
R-HSA-166166	MyD88-independent TLR4 cascade	5/120	105/10164	0,007977	0,095423	0,08127	R4/CASP8/S100A12/UBA52/F
R-HSA-937061	TRIF(TICAM1)-mediated TLR4 signaling	5/120	105/10164	0,007977	0,095423	0,08127	R4/CASP8/S100A12/UBA52/F
R-HSA-879415	Advanced glycosylation endproduct receptor signaling	2/120	12/10164	0,008444	0,095423	0,08127	S100A12/CAPZA1
R-HSA-8984722	Interleukin-35 Signalling	2/120	12/10164	0,008444	0,095423	0,08127	STAT1/STAT3
R-HSA-9027276	Erythropoietin activates Phosphoinositide-3-kinase (PI3K)	2/120	12/10164	0,008444	0,095423	0,08127	IRS2/LYN
R-HSA-9673767	Signaling by PDGFRA transmembrane, juxtamembrane and kinase domain mutants	2/120	12/10164	0,008444	0,095423	0,08127	STAT1/STAT3
R-HSA-9673770	Signaling by PDGFRA extracellular domain mutants	2/120	12/10164	0,008444	0,095423	0,08127	STAT1/STAT3
R-HSA-9607240	FLT3 Signaling	3/120	36/10164	0,008629	0,096136	0,081878	PTPRJ/FOXO3/UBA52
R-HSA-2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	2/120	13/10164	0,009903	0,105858	0,090158	TGFBR2/UBA52
R-HSA-9706369	Negative regulation of FLT3	2/120	13/10164	0,009903	0,105858	0,090158	PTPRJ/UBA52
R-HSA-975163	IRAK2 mediated activation of TAK1 complex upon TLR7/8 or 9 stimulation	2/120	13/10164	0,009903	0,105858	0,090158	TLR4/UBA52
R-HSA-9759194	Nuclear events mediated by NFE2L2	4/120	73/10164	0,010756	0,112063	0,095443	SK3B/CREBBP/TALDO1/UBA5
R-HSA-202403	TCR signaling	5/120	113/10164	0,010767	0,112063	0,095443	IN/PTPRJ/PTPN22/PTPRC/UBA
R-HSA-8983432	Interleukin-15 signaling	2/120	14/10164	0,011465	0,114109	0,097185	SOS2/STAT3
R-HSA-9027284	Erythropoietin activates RAS	2/120	14/10164	0,011465	0,114109	0,097185	IRS2/LYN
R-HSA-937072	TRAF6-mediated induction of TAK1 complex within TLR4 complex	2/120	14/10164	0,011465	0,114109	0,097185	TLR4/UBA52
R-HSA-9696264	RND3 GTPase cycle	3/120	40/10164	0,011541	0,114109	0,097185	FLOT2/PICALM/CPD
R-HSA-168928	DDX58/IFIH1-mediated induction of interferon-alpha/beta	4/120	76/10164	0,012343	0,117663	0,100212	ASP8/CREBBP/S100A12/UBA5
R-HSA-445989	TAK1-dependent IKK and NF-kappa-B activation	3/120	41/10164	0,012346	0,117663	0,100212	CASP8/S100A12/UBA52
R-HSA-9020591	Interleukin-12 signaling	3/120	41/10164	0,012346	0,117663	0,100212	TALDO1/CAPZA1/SOD2
R-HSA-936964	Activation of IRF3/IRF7 mediated by TBK1/IKK epsilon	2/120	15/10164	0,013128	0,121258	0,103274	TLR4/UBA52
R-HSA-9694631	Maturation of nucleoprotein	2/120	15/10164	0,013128	0,121258	0,103274	SRPK1/GSK3B
R-HSA-1433557	Signaling by SCF-KIT	3/120	42/10164	0,013184	0,121258	0,103274	LYN/STAT1/STAT3
R-HSA-5633008	TP53 Regulates Transcription of Cell Death Genes	3/120	43/10164	0,014052	0,124505	0,10604	CREBBP/BCL6/ATM
R-HSA-6783783	Interleukin-10 signaling	3/120	43/10164	0,014052	0,124505	0,10604	FPR1/IL1R2/STAT3
R-HSA-109581	Apoptosis	6/120	167/10164	0,014111	0,124505	0,10604	ASP8/PRKCD/UBA52/TNFSF10
R-HSA-1839117	Signaling by cytosolic FGFR1 fusion mutants	2/120	16/10164	0,014889	0,124505	0,10604	STAT1/STAT3
R-HSA-6804760	Regulation of TP53 Activity through Methylation	2/120	16/10164	0,014889	0,124505	0,10604	UBA52/ATM
R-HSA-9758274	Regulation of NF-kappa B signaling	2/120	16/10164	0,014889	0,124505	0,10604	CASP8/UBA52
R-HSA-2173789	TGF-beta receptor signaling activates SMADs	3/120	44/10164	0,014953	0,124505	0,10604	TGFBR2/USP15/UBA52
R-HSA-9645723	Diseases of programmed cell death	3/120	44/10164	0,014953	0,124505	0,10604	CASP8/FOXO3/SOD2
R-HSA-9707616	Heme signaling	3/120	44/10164	0,014953	0,124505	0,10604	TLR4/CREBBP/HBA2
R-HSA-9018677	Biosynthesis of DHA-derived SPMs	2/120	17/10164	0,016745	0,13601	0,115838	ALOX5/LTA4H
R-HSA-512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	3/120	46/10164	0,016851	0,13601	0,115838	LYN/CSF2RB/UBA52
R-HSA-9012852	Signaling by NOTCH3	3/120	46/10164	0,016851	0,13601	0,115838	CREBBP/STAT1/UBA52
R-HSA-977225	Amyloid fiber formation	3/120	49/10164	0,019939	0,159308	0,135681	SORL1/UBA52/ITM2B

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
R-HSA-170834	Signaling by TGF-beta Receptor Complex	4/120	88/10164	0,020153	0,159409	0,135766	TGFB2/USP15/STAT1/UBA52
R-HSA-6807004	Negative regulation of MET activity	2/120	19/10164	0,020734	0,160789	0,136942	PTPRJ/UBA52
R-HSA-9018678	Biosynthesis of specialized proresolving mediators (SPMs)	2/120	19/10164	0,020734	0,160789	0,136942	ALOX5/LTA4H
R-HSA-2559582	Senescence-Associated Secretory Phenotype (SASP)	3/120	50/10164	0,021033	0,161523	0,137567	UBA52/FOS/STAT3
R-HSA-8848021	Signaling by PTK6	3/120	51/10164	0,022159	0,162918	0,138755	LRRK2/UBA52/STAT3
R-HSA-9006927	Signaling by Non-Receptor Tyrosine Kinases	3/120	51/10164	0,022159	0,162918	0,138755	LRRK2/UBA52/STAT3
R-HSA-9006925	Intracellular signaling by second messengers	8/120	293/10164	0,022575	0,162918	0,138755	3B/PIP4K2A/PRKCD/FOXO3/L
R-HSA-2142691	Synthesis of Leukotrienes (LT) and Eoxins (EX)	2/120	20/10164	0,022862	0,162918	0,138755	ALOX5/LTA4H
R-HSA-5621575	CD209 (DC-SIGN) signaling	2/120	20/10164	0,022862	0,162918	0,138755	LYN/CREBBP
R-HSA-6803204	TP53 Regulates Transcription of Genes Involved in Cytochrome C Release	2/120	20/10164	0,022862	0,162918	0,138755	CREBBP/ATM
R-HSA-912631	Regulation of signaling by CBL	2/120	20/10164	0,022862	0,162918	0,138755	LYN/UBA52
R-HSA-9671555	Signaling by PDGFR in disease	2/120	20/10164	0,022862	0,162918	0,138755	STAT1/STAT3
R-HSA-168643	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways	3/120	53/10164	0,024509	0,173096	0,147423	CASP8/TXNIP/UBA52
R-HSA-913531	Interferon Signaling	6/120	190/10164	0,02493	0,173994	0,148189	RKCD/UBA52/EIF2AK2/GBP2
R-HSA-937041	IKK complex recruitment mediated by RIP1	2/120	21/10164	0,025076	0,173994	0,148189	TLR4/UBA52
R-HSA-432722	Golgi Associated Vesicle Biogenesis	3/120	54/10164	0,025733	0,174771	0,14885	IGF2R/PICALM/CPD
R-HSA-9694635	Translation of Structural Proteins	3/120	54/10164	0,025733	0,174771	0,14885	SRPK1/GSK3B/UBA52
R-HSA-5607764	CLEC7A (Dectin-1) signaling	4/120	95/10164	0,025851	0,174771	0,14885	CLEC7A/CASP8/PRKCD/UBA52
R-HSA-8862803	Deregulated CDK5 triggers multiple neurodegenerative pathways in Alzheimer's disease models	2/120	22/10164	0,027374	0,181957	0,154971	FOXO3/SOD2
R-HSA-8863678	Neurodegenerative Diseases	2/120	22/10164	0,027374	0,181957	0,154971	FOXO3/SOD2
R-HSA-983169	Class I MHC mediated antigen processing & presentation	9/120	367/10164	0,029486	0,189797	0,161648	R4/TAP2/UBR2/S100A8/NCF4
R-HSA-1834949	Cytosolic sensors of pathogen-associated DNA	3/120	57/10164	0,029597	0,189797	0,161648	CREBBP/IFI16/UBA52
R-HSA-1266695	Interleukin-7 signaling	2/120	23/10164	0,029753	0,189797	0,161648	IRS2/STAT3
R-HSA-6783589	Interleukin-6 family signaling	2/120	23/10164	0,029753	0,189797	0,161648	STAT1/STAT3
R-HSA-8982491	Glycogen metabolism	2/120	23/10164	0,029753	0,189797	0,161648	PYGL/UBA52
R-HSA-186797	Signaling by PDGF	3/120	58/10164	0,03095	0,19581	0,166769	STAT1/STAT3/THBS1
R-HSA-168164	Toll Like Receptor 3 (TLR3) Cascade	4/120	101/10164	0,031434	0,19581	0,166769	CASP8/S100A12/UBA52/FOS
R-HSA-449836	Other interleukin signaling	2/120	24/10164	0,032212	0,19581	0,166769	STX3/CSF3R
R-HSA-5674400	Constitutive Signaling by AKT1 E17K in Cancer	2/120	24/10164	0,032212	0,19581	0,166769	GSK3B/FOXO3
R-HSA-9013508	NOTCH3 Intracellular Domain Regulates Transcription	2/120	24/10164	0,032212	0,19581	0,166769	CREBBP/STAT1
R-HSA-9634638	Estrogen-dependent nuclear events downstream of ESR-membrane signaling	2/120	24/10164	0,032212	0,19581	0,166769	FOXO3/FOS
R-HSA-2219528	PI3K/AKT Signaling in Cancer	4/120	102/10164	0,032429	0,19581	0,166769	IRS2/PTEN/GSK3B/FOXO3
R-HSA-1368108	BMAL1:CLOCK,NPAS2 activates circadian gene expression	2/120	25/10164	0,034747	0,203593	0,173397	CREBBP/NAMPT
R-HSA-8854691	Interleukin-20 family signaling	2/120	25/10164	0,034747	0,203593	0,173397	STAT1/STAT3
R-HSA-9006335	Signaling by Erythropoietin	2/120	25/10164	0,034747	0,203593	0,173397	IRS2/LYN
R-HSA-9734009	Defective Intrinsic Pathway for Apoptosis	2/120	25/10164	0,034747	0,203593	0,173397	FOXO3/SOD2
R-HSA-400253	Circadian Clock	3/120	62/10164	0,036681	0,213342	0,181701	CREBBP/UBA52/NAMPT
R-HSA-9615017	FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	2/120	27/10164	0,040041	0,229509	0,19547	FOXO3/SOD2
R-HSA-9683701	Translation of Structural Proteins	2/120	27/10164	0,040041	0,229509	0,19547	GSK3B/UBA52
R-HSA-2173795	Downregulation of SMAD2/3:SMAD4 transcriptional activity	2/120	28/10164	0,042795	0,242483	0,206519	STAT1/UBA52
R-HSA-1169408	ISG15 antiviral mechanism	3/120	66/10164	0,042917	0,242483	0,206519	STAT1/UBA52/EIF2AK2
R-HSA-9772573	Late SARS-CoV-2 Infection Events	3/120	67/10164	0,044554	0,249947	0,212876	SRPK1/GSK3B/UBA52
R-HSA-1839124	FGFR1 mutant receptor activation	2/120	29/10164	0,045617	0,250579	0,213415	STAT1/STAT3
R-HSA-186763	Downstream signal transduction	2/120	29/10164	0,045617	0,250579	0,213415	STAT1/STAT3
R-HSA-9616222	Transcriptional regulation of granulopoiesis	2/120	29/10164	0,045617	0,250579	0,213415	CSF3R/STAT3
R-HSA-448424	Interleukin-17 signaling	3/120	68/10164	0,046222	0,25215	0,214753	IL17RA/UBA52/FOS
R-HSA-9006936	Signaling by TGFb family members	4/120	115/10164	0,047029	0,254796	0,217007	TGFB2/USP15/STAT1/UBA52
R-HSA-8939902	Regulation of RUNX2 expression and activity	3/120	69/10164	0,047921	0,257859	0,219615	GSK3B/STAT1/UBA52
R-HSA-5663084	Diseases of carbohydrate metabolism	2/120	30/10164	0,048507	0,25925	0,2208	TALDO1/UBA52
R-HSA-9705671	SARS-CoV-2 activates/modulates innate and adaptive immune responses	4/120	117/10164	0,049552	0,260085	0,221511	CREBBP/STAT1/IL17RA/UBA52
R-HSA-199992	trans-Golgi Network Vesicle Budding	3/120	70/10164	0,04965	0,260085	0,221511	IGF2R/PICALM/CPD
R-HSA-909733	Interferon alpha/beta signaling	3/120	70/10164	0,04965	0,260085	0,221511	STAT1/GBP2/IFITM2
R-HSA-2871796	FCERI mediated MAPK activation	2/120	31/10164	0,051461	0,267802	0,228083	LYN/FOS