

domain	term.id	term name	term.size(T)	query.size(Q)	overlap.size(Q&T)	adjusted.p.value	(Q∩T)/T	(Q∩T)/Q	local.hierarchy.depth	participated_genes
BP	GO:0032088	negative regulation of NF-kappaB transcription factor activity	66	442	9	0.0203	0.02	0.136	1	NLRCS, PYCARD, TLR9, HAVCR2, PARP10, TRIM21, TNFAIP3, CMKLR1, ZC3H12A
BP	GO:0071725	response to triacyl bacterial lipopeptide	3	289	3	0.00707	0.01	1	1	TLR1, TLR2, CD14
BP	GO:0071727	cellular response to triacyl bacterial lipopeptide	3	289	3	0.00707	0.01	1	2	TLR1, TLR2, CD14
BP	GO:0050852	T cell receptor signaling pathway	81	321	9	0.00893	0.028	0.113	1	PI3K, TNF, TNFR, TRAF3, TRAF2, TRAF1, TRAF4, TRAF5, TRAF6, TRAF7, TRAF8, TRAF9, TRAF10, TRAF11, TRAF12, TRAF13, TRAF14, TRAF15, TRAF16, TRAF17, TRAF18, TRAF19, TRAF20, TRAF21, TRAF22, TRAF23, TRAF24, TRAF25, TRAF26, TRAF27, TRAF28, TRAF29, TRAF30, TRAF31, TRAF32, TRAF33, TRAF34, TRAF35, TRAF36, TRAF37, TRAF38, TRAF39, TRAF40, TRAF41, TRAF42, TRAF43, TRAF44, TRAF45, TRAF46, TRAF47, TRAF48, TRAF49, TRAF50, TRAF51, TRAF52, TRAF53, TRAF54, TRAF55, TRAF56, TRAF57, TRAF58, TRAF59, TRAF60, TRAF61, TRAF62, TRAF63, TRAF64, TRAF65, TRAF66, TRAF67, TRAF68, TRAF69, TRAF70, TRAF71, TRAF72, TRAF73, TRAF74, TRAF75, TRAF76, TRAF77, TRAF78, TRAF79, TRAF80, TRAF81, TRAF82, TRAF83, TRAF84, TRAF85, TRAF86, TRAF87, TRAF88, TRAF89, TRAF90, TRAF91, TRAF92, TRAF93, TRAF94, TRAF95, TRAF96, TRAF97, TRAF98, TRAF99, TRAF100, TRAF101, TRAF102, TRAF103, TRAF104, TRAF105, TRAF106, TRAF107, TRAF108, TRAF109, TRAF110, TRAF111, TRAF112, TRAF113, TRAF114, TRAF115, TRAF116, TRAF117, TRAF118, TRAF119, TRAF120, TRAF121, TRAF122, TRAF123, TRAF124, TRAF125, TRAF126, TRAF127, TRAF128, TRAF129, TRAF130, TRAF131, TRAF132, TRAF133, TRAF134, TRAF135, TRAF136, TRAF137, TRAF138, TRAF139, TRAF140, TRAF141, TRAF142, TRAF143, TRAF144, TRAF145, TRAF146, TRAF147, TRAF148, TRAF149, TRAF150, TRAF151, TRAF152, TRAF153, TRAF154, TRAF155, TRAF156, TRAF157, TRAF158, TRAF159, TRAF160, TRAF161, TRAF162, TRAF163, TRAF164, TRAF165, TRAF166, TRAF167, TRAF168, TRAF169, TRAF170, TRAF171, TRAF172, TRAF173, TRAF174, TRAF175, TRAF176, TRAF177, TRAF178, TRAF179, TRAF180, TRAF181, TRAF182, TRAF183, TRAF184, TRAF185, TRAF186, TRAF187, TRAF188, TRAF189, TRAF190, TRAF191, TRAF192, TRAF193, TRAF194, TRAF195, TRAF196, TRAF197, TRAF198, TRAF199, TRAF200, TRAF201, TRAF202, TRAF203, TRAF204, TRAF205, TRAF206, TRAF207, TRAF208, TRAF209, TRAF210, TRAF211, TRAF212, TRAF213, TRAF214, TRAF215, TRAF216, TRAF217, TRAF218, TRAF219, TRAF220, TRAF221, TRAF222, TRAF223, TRAF224, TRAF225, TRAF226, TRAF227, TRAF228, TRAF229, TRAF230, TRAF231, TRAF232, TRAF233, TRAF234, TRAF235, TRAF236, TRAF237, TRAF238, TRAF239, TRAF240, TRAF241, TRAF242, TRAF243, TRAF244, TRAF245, TRAF246, TRAF247, TRAF248, TRAF249, TRAF250, TRAF251, TRAF252, TRAF253, TRAF254, TRAF255, TRAF256, TRAF257, TRAF258, TRAF259, TRAF260, TRAF261, TRAF262, TRAF263, TRAF264, TRAF265, TRAF266, TRAF267, TRAF268, TRAF269, TRAF270, TRAF271, TRAF272, TRAF273, TRAF274, TRAF275, TRAF276, TRAF277, TRAF278, TRAF279, TRAF280, TRAF281, TRAF282, TRAF283, TRAF284, TRAF285, TRAF286, TRAF287, TRAF288, TRAF289, TRAF290, TRAF291, TRAF292, TRAF293, TRAF294, TRAF295, TRAF296, TRAF297, TRAF298, TRAF299, TRAF300, TRAF301, TRAF302, TRAF303, TRAF304, TRAF305, TRAF306, TRAF307, TRAF308, TRAF309, TRAF310, TRAF311, TRAF312, TRAF313, TRAF314, TRAF315, TRAF316, TRAF317, TRAF318, TRAF319, TRAF320, TRAF321, TRAF322, TRAF323, TRAF324, TRAF325, TRAF326, TRAF327, TRAF328, TRAF329, TRAF330, TRAF331, TRAF332, TRAF333, TRAF334, TRAF335, TRAF336, TRAF337, TRAF338, TRAF339, TRAF340, TRAF341, TRAF342, TRAF343, TRAF344, TRAF345, TRAF346, TRAF347, TRAF348, TRAF349, TRAF350, TRAF351, TRAF352, TRAF353, TRAF354, TRAF355, TRAF356, TRAF357, TRAF358, TRAF359, TRAF360, TRAF361, TRAF362, TRAF363, TRAF364, TRAF365, TRAF366, TRAF367, TRAF368, TRAF369, TRAF370, TRAF371, TRAF372, TRAF373, TRAF374, TRAF375, TRAF376, TRAF377, TRAF378, TRAF379, TRAF380, TRAF381, TRAF382, TRAF383, TRAF384, TRAF385, TRAF386, TRAF387, TRAF388, TRAF389, TRAF390, TRAF391, TRAF392, TRAF393, TRAF394, TRAF395, TRAF396, TRAF397, TRAF398, TRAF399, TRAF400, TRAF401, TRAF402, TRAF403, TRAF404, TRAF405, TRAF406, TRAF407, TRAF408, TRAF409, TRAF410, TRAF411, TRAF412, TRAF413, TRAF414, TRAF415, TRAF416, TRAF417, TRAF418, TRAF419, TRAF420, TRAF421, TRAF422, TRAF423, TRAF424, TRAF425, TRAF426, TRAF427, TRAF428, TRAF429, TRAF430, TRAF431, TRAF432, TRAF433, TRAF434, TRAF435, TRAF436, TRAF437, TRAF438, TRAF439, TRAF440, TRAF441, TRAF442, TRAF443, TRAF444, TRAF445, TRAF446, TRAF447, TRAF448, TRAF449, TRAF450, TRAF451, TRAF452, TRAF453, TRAF454, TRAF455, TRAF456, TRAF457, TRAF458, TRAF459, TRAF460, TRAF461, TRAF462, TRAF463, TRAF464, TRAF465, TRAF466, TRAF467, TRAF468, TRAF469, TRAF470, TRAF471, TRAF472, TRAF473, TRAF474, TRAF475, TRAF476, TRAF477, TRAF478, TRAF479, TRAF480, TRAF481, TRAF482, TRAF483, TRAF484, TRAF485, TRAF486, TRAF487, TRAF488, TRAF489, TRAF490, TRAF491, TRAF492, TRAF493, TRAF494, TRAF495, TRAF496, TRAF497, TRAF498, TRAF499, TRAF500, TRAF501, TRAF502, TRAF503, TRAF504, TRAF505, TRAF506, TRAF507, TRAF508, TRAF509, TRAF510, TRAF511, TRAF512, TRAF513, TRAF514, TRAF515, TRAF516, TRAF517, TRAF518, TRAF519, TRAF520, TRAF521, TRAF522, TRAF523, TRAF524, TRAF525, TRAF526, TRAF527, TRAF528, TRAF529, TRAF530, TRAF531, TRAF532, TRAF533, TRAF534, TRAF535, TRAF536, TRAF537, TRAF538, TRAF539, TRAF540, TRAF541, TRAF542, TRAF543, TRAF544, TRAF545, TRAF546, TRAF547, TRAF548, TRAF549, TRAF550, TRAF551, TRAF552, TRAF553, TRAF554, TRAF555, TRAF556, TRAF557, TRAF558, TRAF559, TRAF560, TRAF561, TRAF562, TRAF563, TRAF564, TRAF565, TRAF566, TRAF567, TRAF568, TRAF569, TRAF570, TRAF571, TRAF572, TRAF573, TRAF574, TRAF575, TRAF576, TRAF577, TRAF578, TRAF579, TRAF580, TRAF581, TRAF582, TRAF583, TRAF584, TRAF585, TRAF586, TRAF587, TRAF588, TRAF589, TRAF590, TRAF591, TRAF592, TRAF593, TRAF594, TRAF595, TRAF596, TRAF597, TRAF598, TRAF599, TRAF600, TRAF601, TRAF602, TRAF603, TRAF604, TRAF605, TRAF606, TRAF607, TRAF608, TRAF609, TRAF610, TRAF611, TRAF612, TRAF613, TRAF614, TRAF615, TRAF616, TRAF617, TRAF618, TRAF619, TRAF620, TRAF621, TRAF622, TRAF623, TRAF624, TRAF625, TRAF626, TRAF627, TRAF628, TRAF629, TRAF630, TRAF631, TRAF632, TRAF633, TRAF634, TRAF635, TRAF636, TRAF637, TRAF638, TRAF639, TRAF640, TRAF641, TRAF642, TRAF643, TRAF644, TRAF645, TRAF646, TRAF647, TRAF648, TRAF649, TRAF650, TRAF651, TRAF652, TRAF653, TRAF654, TRAF655, TRAF656, TRAF657, TRAF658, TRAF659, TRAF660, TRAF661, TRAF662, TRAF663, TRAF664, TRAF665, TRAF666, TRAF667, TRAF668, TRAF669, TRAF670, TRAF671, TRAF672, TRAF673, TRAF674, TRAF675, TRAF676, TRAF677, TRAF678, TRAF679, TRAF680, TRAF681, TRAF682, TRAF683, TRAF684, TRAF685, TRAF686, TRAF687, TRAF688, TRAF689, TRAF690, TRAF691, TRAF692, TRAF693, TRAF694, TRAF695, TRAF696, TRAF697, TRAF698, TRAF699, TRAF700, TRAF701, TRAF702, TRAF703, TRAF704, TRAF705, TRAF706, TRAF707, TRAF708, TRAF709, TRAF710, TRAF711, TRAF712, TRAF713, TRAF714, TRAF715, TRAF716, TRAF717, TRAF718, TRAF719, TRAF720, TRAF721, TRAF722, TRAF723, TRAF724, TRAF725, TRAF726, TRAF727, TRAF728, TRAF729, TRAF730, TRAF731, TRAF732, TRAF733, TRAF734, TRAF735, TRAF736, TRAF737, TRAF738, TRAF739, TRAF740, TRAF741, TRAF742, TRAF743, TRAF744, TRAF745, TRAF746, TRAF747, TRAF748, TRAF749, TRAF750, TRAF751, TRAF752, TRAF753, TRAF754, TRAF755, TRAF756, TRAF757, TRAF758, TRAF759, TRAF760, TRAF761, TRAF762, TRAF763, TRAF764, TRAF765, TRAF766, TRAF767, TRAF768, TRAF769, TRAF770, TRAF771, TRAF772, TRAF773, TRAF774, TRAF775, TRAF776, TRAF777, TRAF778, TRAF779, TRAF780, TRAF781, TRAF782, TRAF783, TRAF784, TRAF785, TRAF786, TRAF787, TRAF788, TRAF789, TRAF790, TRAF791, TRAF792, TRAF793, TRAF794, TRAF795, TRAF796, TRAF797, TRAF798, TRAF799, TRAF800, TRAF801, TRAF802, TRAF803, TRAF804, TRAF805, TRAF806, TRAF807, TRAF808, TRAF809, TRAF810, TRAF811, TRAF812, TRAF813, TRAF814, TRAF815, TRAF816, TRAF817, TRAF818, TRAF819, TRAF820, TRAF821, TRAF822, TRAF823, TRAF824, TRAF825, TRAF826, TRAF827, TRAF828, TRAF829, TRAF830, TRAF831, TRAF832, TRAF833, TRAF834, TRAF835, TRAF836, TRAF837, TRAF838, TRAF839, TRAF840, TRAF841, TRAF842, TRAF843, TRAF844, TRAF845, TRAF846, TRAF847, TRAF848, TRAF849, TRAF850, TRAF851, TRAF852, TRAF853, TRAF854, TRAF855, TRAF856, TRAF857, TRAF858, TRAF859, TRAF860, TRAF861, TRAF862, TRAF863, TRAF864, TRAF865, TRAF866, TRAF867, TRAF868, TRAF869, TRAF870, TRAF871, TRAF872, TRAF873, TRAF874, TRAF875, TRAF876, TRAF877, TRAF878, TRAF879, TRAF880, TRAF881, TRAF882, TRAF883, TRAF884, TRAF885, TRAF886, TRAF887, TRAF888, TRAF889, TRAF890, TRAF891, TRAF892, TRAF893, TRAF894, TRAF895, TRAF896, TRAF897, TRAF898, TRAF899, TRAF900, TRAF901, TRAF902, TRAF903, TRAF904, TRAF905, TRAF906, TRAF907, TRAF908, TRAF909, TRAF910, TRAF911, TRAF912, TRAF913, TRAF914, TRAF915, TRAF916, TRAF917, TRAF918, TRAF919, TRAF920, TRAF921, TRAF922, TRAF923, TRAF924, TRAF925, TRAF926, TRAF927, TRAF928, TRAF929, TRAF930, TRAF931, TRAF932, TRAF933, TRAF934, TRAF935, TRAF936, TRAF937, TRAF938, TRAF939, TRAF940, TRAF941, TRAF942, TRAF943, TRAF944, TRAF945, TRAF946, TRAF947, TRAF948, TRAF949, TRAF950, TRAF951, TRAF952, TRAF953, TRAF954, TRAF955, TRAF956, TRAF957, TRAF958, TRAF959, TRAF960, TRAF961, TRAF962, TRAF963, TRAF964, TRAF965, TRAF966, TRAF967, TRAF968, TRAF969, TRAF970, TRAF971, TRAF972, TRAF973, TRAF974, TRAF975, TRAF976, TRAF977, TRAF978, TRAF979, TRAF980, TRAF981, TRAF982, TRAF983, TRAF984, TRAF985, TRAF986, TRAF987, TRAF988, TRAF989, TRAF990, TRAF991, TRAF992, TRAF993, TRAF994, TRAF995, TRAF996, TRAF997, TRAF998, TRAF999, TRAF1000

BP	GO:0002440	production of molecular mediator of immune response	278	326	18	0.000659	0.055	0.065	2	CD74,H2-AB1,B2M,SLC11A1,BST2,H2-T23,TLR2,TNFSF13B,FCER1G,TLR9,SASH3,ICOSL,FAS,CD37,PTPN22,RSAD2,BTK,IL4RA
BP	GO:0019882	antigen processing and presentation	105	318	29	9.93E-26	0.091	0.276	2	H2-M2,H2-Q7,CD74,H2-AB1,H2-AA,H2-Q6,H2-EB1,H2-OA,H2-Q4,H2-K1,PSMB8,H2-D1,TAP1,B2M,SLC11A1,H2-DMB1,H2-T23,CTSS,ICAM1,PCYARD,FCGR1,WAS,FCER1G,H2-M3,H2-DMA,TRIM2,TAP2,H2-T22
BP	GO:0002475	antigen processing and presentation via MHC class Ib	6	305	4	0.00168	0.013	0.667	3	B2M,H2-T23,H2-M3,TAP2
BP	GO:0019884	antigen processing and presentation of exogenous antigen	19	305	10	6.02E-11	0.033	0.526	3	CD74,H2-AB1,H2-AA,H2-OA,H2-K1,B2M,FCGR1,FCER1G,H2-M3,TAP2
BP	GO:0048002	antigen processing and presentation of peptide antigen	58	318	23	4.01E-24	0.072	0.397	3	H2-M2,H2-Q7,CD74,H2-AB1,H2-AA,H2-Q6,H2-OA,H2-Q4,H2-K1,H2-D1,TAP1,B2M,SLC11A1,H2-T23,CTSS,PCYARD,FCGR1,FCER1G,H2-M3,H2-DMA,TRIM2,TAP2,H2-T22
BP	GO:0002478	antigen processing and presentation of exogenous peptide antigen	14	305	10	6.94E-13	0.033	0.714	4	CD74,H2-AB1,H2-AA,H2-OA,H2-K1,B2M,FCGR1,FCER1G,H2-M3,TAP2
BP	GO:0002428	antigen processing and presentation of peptide antigen via MHC class I	4	305	4	0.000115	0.013	1	4	B2M,H2-T23,H2-M3,TAP2
BP	GO:0002477	antigen processing and presentation of exogenous peptide antigen via 3	3	305	3	0.00832	0.01	1	5	B2M,H2-M3,TAP2
BP	GO:0002481	antigen processing and presentation of exogenous protein antigen via 3	3	305	3	0.00832	0.01	1	6	B2M,H2-M3,TAP2
BP	GO:0002474	antigen processing and presentation of peptide antigen via MHC class 4	3	318	14	2.29E-12	0.044	0.326	4	H2-M2,H2-Q7,H2-Q6,H2-Q4,H2-K1,H2-D1,TAP1,B2M,H2-T23,FCGR1,FCER1G,H2-M3,TAP2,H2-T22
BP	GO:0042590	antigen processing and presentation of exogenous peptide antigen via 4	162	3	0.00483	0.019	0.75	5	H2-K1,FCGR1,FCER1G	
BP	GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	19	283	10	2.82E-11	0.035	0.526	3	CD74,H2-AB1,H2-AA,H2-EB1,H2-OA,H2-DMB1,PCYARD,FCER1G,H2-DMA,TRIM2
BP	GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	15	283	8	1.29E-08	0.028	0.533	4	CD74,H2-AB1,H2-AA,H2-OA,PCYARD,FCER1G,H2-DMA,TRIM2
BP	GO:0002586	regulation of antigen processing and presentation of peptide antigen 4	283	3	0.0263	0.011	0.75	5	H2-OA,PCYARD,TRIM2	
BP	GO:0019886	antigen processing and presentation of exogenous peptide antigen via 9	162	5	0.00000771	0.031	0.556	5	CD74,H2-AB1,H2-AA,H2-OA,FCER1G	
BP	GO:0019883	antigen processing and presentation of endogenous antigen	11	305	7	9.23E-08	0.023	0.636	3	H2-K1,H2-D1,TAP1,B2M,H2-T23,H2-M3,TAP2
BP	GO:0002483	antigen processing and presentation of endogenous peptide antigen	10	305	7	0.00000034	0.023	0.7	4	H2-K1,H2-D1,TAP1,B2M,H2-T23,H2-M3,TAP2
BP	GO:0019885	antigen processing and presentation of endogenous peptide antigen 8	73	4	0.0000237	0.055	0.5	5	H2-K1,H2-D1,TAP1,B2M	
BP	GO:0002484	antigen processing and presentation of endogenous peptide antigen via 3	305	3	0.00832	0.01	1	6	H2-K1,H2-D1,TAP2	
BP	GO:0002476	antigen processing and presentation of endogenous peptide antigen 3	305	3	0.00832	0.01	1	7	H2-K1,H2-D1,TAP2	
BP	GO:0005007	biological regulation	12115	406	283	0.00000117	0.697	0.023	1	H2-K1,H2-D1,TAP2
BP	GO:0065008	regulation of biological quality	3138	371	89	0.00129	0.24	0.028	2	H2-K1,H2-D1,TAP2
BP	GO:0042592	homeostatic process	1561	377	59	0.0000279	0.156	0.038	3	H2-K1,H2-D1,TAP2
BP	GO:0048872	homeostasis of number of cells	275	362	20	0.000114	0.055	0.073	4	H2-K1,H2-D1,TAP2
BP	GO:0002262	myeloid cell homeostasis	146	362	14	0.000462	0.039	0.096	5	H2-K1,H2-D1,TAP2
BP	GO:0001776	leukocyte homeostasis	99	494	13	0.00102	0.026	0.131	5	H2-K1,H2-D1,TAP2
BP	GO:0050878	regulation of body fluid levels	322	371	19	0.0088	0.051	0.059	3	H2-K1,H2-D1,TAP2
BP	GO:0007599	hemostasis	179	362	13	0.0291	0.036	0.073	4	H2-K1,H2-D1,TAP2
BP	GO:0065009	regulation of molecular function	2674	419	94	0.00000547	0.224	0.035	2	H2-K1,H2-D1,TAP2
BP	GO:0044093	positive regulation of molecular function	1610	342	58	0.00000537	0.17	0.036	3	H2-K1,H2-D1,TAP2
BP	GO:0050790	regulation of catalytic activity	2101	342	69	0.00000579	0.202	0.033	3	H2-K1,H2-D1,TAP2
BP	GO:0051336	regulation of hydrolase activity	1215	406	54	0.00000549	0.133	0.044	4	H2-K1,H2-D1,TAP2
BP	GO:0043085	positive regulation of catalytic activity	1305	323	48	0.0000137	0.149	0.037	4	H2-K1,H2-D1,TAP2
BP	GO:0051345	positive regulation of hydrolase activity	775	419	36	0.00261	0.086	0.046	5	H2-K1,H2-D1,TAP2
BP	GO:0072511	divalent inorganic cation transport	416	321	20	0.0118	0.062	0.048	1	H2-K1,H2-D1,TAP2
BP	GO:0070838	divalent metal ion transport	413	321	20	0.0106	0.062	0.048	2	H2-K1,H2-D1,TAP2
BP	GO:0006816	calcium ion transport	359	321	18	0.0204	0.056	0.05	3	H2-K1,H2-D1,TAP2

BP	GO:0044699	single-organism process	13775	481	347	0.00868	0.721	0.025	1	HCAR2,CLEC4D,CLEC4E,GZMB,CCL1,CCL5,C3,CXCL9,H2-Q7,CD74,CCL8,IFIT204,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,ITGAX,TSPAN32,PIRB,LV9,AOAH,NLRCS,CXCL10,ZBP1,CSF2RB2,LRG1,CD4,CC-L12,CSF2RB2,IGF1,H2-OA,MYD16,IL2RG,BCL2A18,H2-N1,IL12RB1,LGALS3,ITGAL,PSMB8,H2-D1,TAP1,SPINT1,SLFN2,B2M,SLC11A1,IRF7,ACAP1,BST2,TLR1,H2-T23,CTSS,TAGAP,A2M,FYB,C3AR1,CD84,ELF4,LAT,ITGB2,ST14,CD48,ARHGAP9,S100A9,OASL2,CCR2,S100A8,RAC2,CRYBA4,SULT1A1,RASAL3,ITGB7,TLR2,HCK,NAIP2,GBP5,PLAC8,THEMIS5,XDH,CSAR1,IL2LR,LTB,TLR12,CD274,MYO1F,CD300C2,ICAM1,TLR7,CSF3R,TLR13,TTR,OAS2,NCF1,PYCARD,PTPRC,TNFAIP2,GBP4,OAS1A,CCL6,PLD4,TRIM30A,CXCL16,FCGR1,ICP2,TNFSF13B,WAS,CD44,C1QB,ADGRE1,FCER1G,APOBEC3,TLR9,DLK1,RHOH,SP110,IL1ORA,GALNT15,TRPV4,CH25H,P2RY6,HCL1,C1QC,LST1,RTN4,SP11,SA-SH3,APOBEC1,ACPS,ICOSL,IRF1,PTPN6,GSDMD,FERMT3,ADCV7,TNFRSF18,UGT1A7C,H2-M3,NGP,IKZF1,CTSC,AIF1,LAG3,CYP26B1,CD86,CLEC10A,VAV1,ARHGAP30,PIK3RS,PTAFR,HIF3A,LCP1,CAPG,DOCK2,ARHGAP45,HAVCR2,TNFAIP8L2,S100A4,FAS,ALOX5AP,STAT1,LV86,PLCG2,BLNK,NLAK2,CD37,RAE32,CP,F13A1,ARHGAP25,HK2,DDX60,GFAP,ADAP2,CCDC88B,PLA1A,CTSH,UNC93B1,SEPT1,ADORA3,HYCK1,ASPS,TSP0,HIST1HH4,KNK6,LSP1,MAFB,PIK3CG,DHX58,RNF213,PARP3,IKBK,ICF2,PRKCD,IL1A,PIK3AP1,CAPN3,SERPING1,FGD2,INPP5D,PARV6,MAFF,PTPN22,TREM2,BIRC3,TIFAB,LGALS9,CD14,PHYHD1,TGFB1,CARD9,NCKAP1L,CD300A,TYROBP,FGFBP1,MAP3K6,ACER2,CBR2,RHBQF2,RSAD2,PARP10,PRODH,TAP2,XAF1,IFIT2L2A,VWF,PLAU,TRIM21,KLHL6,IL6RA,PIK3R6,CCRS,LPXN,LCK,BTK,CSF1R,IL1LR1,IL4RA,IFIT3,CBPBA,ISG15,NFAM1,APOC1,IRF9,RAB20,OSMR,IFITM3,ECM1,CMTM7,TMEM173,SP100,RIN3,CD53,ADM,RASD1,FOLH1,TG-M2,GUPIR2,CTSZ,DNASE2A,FAM107A,MT2,NFKBIE,PIM1,GGTA1,MERTK,ITIH3,CYTH4,CCDC3,COL1A1,NPAS4,APLN,NGFR,ATF5,UGT8A,FOS,MYOC,KLK6,STOML3,OMP,GKN3,CY-P21,FCRL5,CFB,HP,GPR84,FBUM1,ARL11,EBI3,CCL9,PRRS5,ANG,CD180,SLC2A18,L
BP	GO:1902578	single-organism localization	2699	348	81	0.0000255	0.233	0.03	2	HCAR2,CLEC4E,CCL5,C3,CXCL9,CD74,LCN2,CXCL10,CD4,MYO1G,ITGAL,TAP1,SLC11A1,TLR1,H2-T23,FYB,CD84,LAT,S100A9,CCR2,S100A8,RAC2,TLR2,HCK,GBP5,XDH,CD274,CD300C2,TLR7,TTR,PCYARD,TNFAIP2,GBP4,PLD4,FCGR1,ICP2,TNFSF13B,WAS,FCER1G,TLR9,TRPV4,P2RY6,HCL1,APOBEC1,PTPN6,GSDMD,AIF1,VAV1,PTAFR,DOCK2,HAVCR2,PLCG2,H2-2,GFAP,HVCN1,TSP0,KCNK6,PRKCD,IL1A,CAPN3,PTPN22,TREM2,TIFAB,LGALS9,CD14,NCKAP1L,CD300A,RHBF2,RSAD2,PARP10,TAP2,CCR5,LCK,BTK,CSF1R,IL4RA,APOC1,RAB20,TMEM173,ADM,TGM2
BP	GO:0044765	single-organism transport	2554	348	80	0.0000046	0.23	0.031	3	HCAR2,CLEC4E,CCL5,C3,CXCL9,CD74,LCN2,CXCL10,CD4,MYO1G,ITGAL,TAP1,SLC11A1,TLR1,H2-T23,CD84,LAT,S100A9,CCR2,S100A8,RAC2,TLR2,HCK,GBP5,XDH,CD274,CD300C2,TLR7,TTR,PCYARD,TNFAIP2,GBP4,PLD4,FCGR1,ICP2,TNFSF13B,WAS,FCER1G,TLR9,TRPV4,P2RY6,HCL1,APOBEC1,PTPN6,GSDMD,AIF1,VAV1,PTAFR,DOCK2,HAVCR2,PLCG2,H2,GFAP,HVCN1,TSP0,KCNK6,PRKCD,IL1A,CAPN3,PTPN22,TREM2,TIFAB,LGALS9,CD14,NCKAP1L,CD300A,RHBF2,RSAD2,PARP10,TAP2,CCR5,LCK,BTK,CSF1R,IL4RA,APOC1,RAB20,TMEM173,ADM,TGM2
BP	GO:0046903	secretion	965	490	54	0.00000143	0.11	0.056	4	HCAR2,CLEC4E,CCL5,CD74,MYO1G,TLR1,H2-T23,CD84,LAT,S100A9,CCR2,S100A8,RAC2,TLR2,HCK,GBP5,XDH,CD274,CD300C2,PCYARD,TNFAIP2,GBP4,PLD4,FCGR1,ICP2,TNFSF13B,WAS,FCER1G,TLR9,TRPV4,P2RY6,HCL1,APOBEC1,PTPN6,GSDMD,AIF1,VAV1,PTAFR,DOCK2,HAVCR2,PLCG2,H2,GFAP,HVCN1,TSP0,KCNK6,PRKCD,IL1A,CAPN3,PTPN22,TREM2,TIFAB,LGALS9,CD14,NCKAP1L,CD300A,RHBF2,RSAD2,PARP10,TAP2,CCR5,LCK,BTK,CSF1R,IL4RA,APOC1,RAB20,TMEM173,ADM,TGM2
BP	GO:0008283	cell proliferation	1817	412	84	1.53E-11	0.204	0.046	2	CCL5,CXCL9,CD74,TSPAN32,CXCL10,LRG1,CD4,CCL12,IL12RB1,LGALS3,ITGAL,SPINT1,SLFN2,SLC11A1,H2-T23,ELF4,CCR2,RAC2,RASAL3,TLR2,HCK,PLAC8,XDH,CSAR1,CD274,NCF1,PCYARD,TNFSF13B,HCL1,LST1,SASH3,APOBEC1,ICOSL,IRF1,PTPN6,TNFRSF18,H2-M3,AIF1,CD86,PTAFR,DOCK2,HAVCR2,FAS,STAT1,CD37,GFAP,CCDC88B,CTSH,TSP0,PRKCD,IL1A,INPP5D,PTPN22,LGALS9,TGFB1,NCKAP1L,CD300A,FGFBP1,ACER2,PARP10,PLAU,IL6RA,LCK,BTK,CSF1R,IL4RA,IFIT3,CBPBA,OSMR,IFITM3,ECM1,ADM,TGM2,CTSZ,PI-M3,APLN,NGFR,ATF5,GKN3,CFB,EBI3,ANG,CD180,TNFAIP3
BP	GO:0070661	leukocyte proliferation	291	295	33	1.49E-17	0.112	0.113	3	CCL5,CD74,CD4,CCL12,IL12RB1,LGALS3,ITGAL,SLC11A1,H2-T23,ELF4,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,DOCK2,HAVCR2,CCDC88B,PRKCD,INPP5D,PTPN22,LGALS9,NCKAP1L,CD300A
BP	GO:0032943	mononuclear cell proliferation	277	295	32	3.45E-17	0.108	0.116	4	CCL5,CD74,CD4,IL12RB1,LGALS3,ITGAL,SLC11A1,H2-T23,ELF4,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,DOCK2,HAVCR2,CCDC88B,PRKCD,INPP5D,PTPN22,LGALS9,NCKAP1L,CD300A
BP	GO:0044707	single-multicellular organism process	5693	379	160	9.92E-09	0.422	0.028	2	HCAR2,CLEC4D,CLEC4E,CCL5,C3,H2-Q7,CD74,IFIT204,FCGR4,H2-AB1,H2-AA,CYBB,TSPAN32,PIRB,LV9,CXCL10,LRG1,CD4,CCL12,H2-OA,IL2RG,H2-N1,IL12RB1,H2-D1,SPINT1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,CTSS,C3AR1,CD84,ITGB2,ST14,S100A9,CCR2,S100A8,RAC2,CRYBA4,TLR2,GBP5,PLAC8,XDH,CSAR1,LTB,CD274,CD300C2,ICAM1,TLR7,CSF3R,NCF1,PCYARD,TNFAIP2,GBP4,PLD4,TRIM30A,ICP2,CD44,C1QB,FCER1G,APOBEC3,TLR9,RHOH,TRPV4,HCL1,C1QC,LST1,SP11,SASH3,ACPS,ICOSL,IRF1,PTPN6,GSDMD,FERMT3,TNFRSF18,H2-M3,NGP,IKZF1,AIF1,LAG3,CYP26B1,CD86,CLEC10A,VAV1,PTAFR,HIF3A,LCP1,DOCK2,HAVCR2,FAS,ALOX5AP,STAT1,PLCG2,F13A1,HK2,DDX60,GFAP,ADAP2,CCDC88B,CTSH,TSFQ,HIST1HH4,MAFB,PIK3CG,DHX58,RNF213,PRKCD,IL1A,CAPN3,SERPING1,INPP5D,MAFF,PTPN22,TREM2,TIFAB,LGALS9,CD14,TGFB1,CARD9,NCKAP1L,CD300A,TYROBP,RSAD2,VVWF,PLAU,IL6RA,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,APOC1,IRF9,ECM1,CMTM7,TMEM173,SP100,ADM,TGM2,GUPIR2,CTSZ,DNASE2A,MT2,PIM1,MERTK,COL1A1,NPAS4,APLN,NGFR,ATF5,UGT8A,FOS,MYOC,KLK6
BP	GO:0050817	coagulation	181	362	13	0.0328	0.036	0.072	3	TSPAN32,S100A9,FCER1G,PTPN6,FERMT3,VAV1,F13A1,PRKCD,SERPING1,MAFF,VWF,PLAU,MERTK
BP	GO:0001816	cytokine production	594	340	62	7.34E-30	0.182	0.104	3	CLEC4E,CCL5,C3,CD74,CYBB,LV9,CD4,IL12RB1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,C3AR1,CD84,CCR2,TLR2,GBP5,CSAR1,LTB,CD274,CD300C2,TLR7,PCYARD,GBP4,TRIM30A,ICP2,FCER1G,TLR9,TRPV4,SASH3,ACPS,ICOSL,IRF1,GSDMD,H2-M3,LAG3,PTAFR,HAVCR2,PLCG2,DDX60,CCDC88B,TSP0,DHX58,PRKCD,IL1A,INPP5D,PTPN22,LGALS9,CD14,CARD9,NCKAP1L,RSAD2,IL6RA,BTK,CSF1R,IL4RA,ISG15,NFAM1,IRF9,TMEM173
BP	GO:0071706	tumor necrosis factor superfamily cytokine production	112	480	23	8.26E-13	0.048	0.205	4	CYBB,TLR1,H2-T23,CCR2,CD274,PCYARD,TRIM30A,FCER1G,TLR9,SASH3,ACPS,PTAFR,HAVCR2,TSP0,PTPN22,LGALS9,CD14,CARD9,TNFAIP3,ZC3H12A,BCL3,SPN,CCL2
BP	GO:0032640	tumor necrosis factor production	109	480	22	5.46E-12	0.046	0.202	5	CYBB,TLR1,H2-T23,CCR2,PCYARD,TRIM30A,FCER1G,TLR9,SASH3,ACPS,PTAFR,HAVCR2,TSP0,PTPN22,LGALS9,CD14,CARD9,TNFAIP3,ZC3H12A,BCL3,SPN,CCL2
BP	GO:0032606	type I interferon production	64	340	13	4.82E-08	0.038	0.203	4	IRF7,TLR7,PCYARD,GBP4,TLR9,IRF1,HAVCR2,PLCG2,DHX58,PTPN22,CD14,IRF9,TMEM173
BP	GO:0032608	interferon-beta production	44	340	7	0.0149	0.021	0.159	5	IRF7,TLR7,PCYARD,TLR9,IRF1,PTPN22,TMEM173
BP	GO:0032607	interferon-alpha production	23	281	6	0.0011	0.021	0.261	5	IRF7,TLR7,GBP4,TLR9,HAVCR2,PTPN22
BP	GO:0032612	interleukin-1 production	66	442	9	0.0203	0.02	0.136	4	GBP5,PCYARD,ACPS,GSDMD,HAVCR2,LGALS9,TNFAIP3,CASP4,ZC3H12A
BP	GO:0032602	chemokine production	74	326	13	0.000000198	0.04	0.176	4	CCL5,CD74,TLR2,TLR7,PCYARD,TLR9,TRPV4,HAVCR2,IL1A,LGALS9,IL6RA,CSF1R,IL4RA
BP	GO:0032609	interferon-gamma production	103	330	14	0.0000015	0.042	0.136	4	IL12RB1,SLC11A1,CCR2,CD274,TLR7,PCYARD,TLR9,SASH3,H2-M3,HAVCR2,PTPN22,LGALS9,CD14,ISG15
BP	GO:0032635	interleukin-6 production	114	313	17	1.82E-09	0.054	0.149	4	TLR1,TLR2,TLR7,PCYARD,TRIM30A,FCER1G,TLR9,TRPV4,PTAFR,HAVCR2,IL1A,INPP5D,PTPN22,LGALS9,CARD9,NCKAP1L,IL6RA
BP	GO:0032623	interleukin-2 production	58	412	8	0.0366	0.019	0.138	4	SLC11A1,CCR2,SASH3,LAG3,HAVCR2,IL1A,CARD9,TNFAIP3
BP	GO:0032621	interleukin-18 production	5	165	3	0.0127	0.018	0.6	4	CD84,GBP5,TLR9
BP	GO:0032613	interleukin-10 production	46	286	8	0.000401	0.028	0.174	4	TLR2,CD274,PCYARD,FCER1G,TLR9,SASH3,PRKCD,LGALS9

BP	GO:0050896	response to stimulus	8893	344	254	3.54E-33	0.738	0.029	1	HICAR2,CLEC4D,CLEC4E,CD8B1,GZMB,CCL1,CCL5,C3,CHL3,CXCL9,H2-Q7,CD74,CCL8,IFITM2,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,ITGAX,TSPAN32,H2-EB1,PIR8,LY9,AOAH,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,LY22,CD4,IGTP,P,CCL12,CSF2RB,ITGIP1,IL2RG,IL12RB1,IL2RG,IFI47,SPINT1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,B2T2,TLR1,IRGM1,CTSS,GBP6,CCR2,S100A8,SULT1A1,TLR2,NAIP2,GBP5,XDH,CSAR1,IL12R1,LTB,CD274,C1QA,ICAM1,CSF3R,NCF1,PCYARD,GBP4,OSAS1,CCL6,C1S1,TRIM30A,CXCL16,FCGR1,LC2P,TNFSF13B,WAS,CD44,C1QB,ADGRE1,FCER1G,APOBEC3,TLR9,DLK1,RHOH,SP110,IL10RA,TRPV4,CH25H,P2RY6,HCL5,C1QC,LST1,RTPA,SP11,SASH3,APC,BECL1,USP18,ACPS,ICOSL,IRF1,PTPN6,GSDMD,FERM13,ADCY7,TNFRSF1B,CD163,UGT1A7C,H2-M3,NGP,CTSC,AIF1,LAG3,CYP26B1,CD86,CLEC10A,VAV1,ARHGAP30,PIK3RS,PTAFR,GBP3,HIF3A,LCPI,DOCK2,H2-DMA,ARHGAP45,HAVERC2,TNFAIP8L2,S100A8,FAS,ALOX5AP,STAT1,LY86,PLCG2,BLANK,NUAK2,CD37,RAB32,F13A1,ARHGAP25,HK2,DDX60,GFAP,CD68,ADAP2,CCDC88B,CTSH,GBP7,UNC93B1,ADORA3,GBP9,HVCN1,TSP0,ISP1,PIK3CG,DHX58,RFN213,PARP3,IKBK,E,PRKCD,IL1A,PIK3AP1,CAPN3,SERPING1,FGD2,INPP5D,MAFF,PTPN22,PARP9,TREM2,IFAB,IGALS9,DTX3L,CD14,CARD9,NCKAP1L,CD300A,TYROBP,FGFBP1,MAP3K6,ACER2,RHBD2,RSAD2,TAP2,XAF1,IFI27L2A,VWF,PLAU,TRIM21,KHLH6,IL6RA,TRIM12A,PIK3R,C,CCR5,LPXN,LCK,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,CEBPA,ISG15,NFAM1,OSMR,IFITM3,ECM1,CMTM7,TMEM173,SP100,RIN3,CD53,ADM
BP	GO:0042221	response to chemical	4662	340	138	1.07E-12	0.406	0.03	2	CCL1,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,CCL12,CSF2RB,TGTP2,ITGIP1,IL2RG,IL12RB1,IL2RG,IFI47,SPINT1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,B2T2,TLR1,IRGM1,CTSS,GBP6,CCR2,S100A8,SULT1A1,TLR2,NAIP2,GBP5,XDH,CSAR1,IL12R1,LTB,CD274,C1QA,ICAM1,CSF3R,NCF1,PCYARD,GBP4,CCL6,CXCL16,FCGR1,CD44,FCER1G,TLR9,IL10RA,TRPV4,CH25H,P2RY6,HCL5,RTPA,SP11,APOBEC1,USP18,ACPS,IRF1,PTPN6,ADCY7,TNFRSF1B,UGT1A7C,H2-M3,CTSC,AIF1,CYP26B1,CD86,VAV1,PTAFR,GBP3,DOCK2,HAVCR2,FAS,ALOX5AP,STAT1,LY86,PLCG2,CD68,CTSH,GBP7,GBP9,HVCN1,TSP0,ISP1,PIK3CG,IKBKE,PRKCD,IL1A,CAPN3,PTPN22,PARP9,TREM2,IGALS9,CD14,CARD9,NCKAP1L,FGFBP1,ACER2,TAP2,XAF1,TRIM21,IL6RA,CCR5,LCK,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,CEBPA,ISG15,OSMR,IFITM3,ECM1,CMTM7,TMEM173
BP	GO:1901700	response to oxygen-containing compound	1466	492	70	0.00000388	0.142	0.048	3	CCL5,CXCL9,FCGR4,LCN2,CYBB,CXCL10,CD4,CCL12,SLC11A1,GBP2,GBP6,S100A8,TLR2,CSAR1,ICAM1,NCF1,PCYARD,CXCL16,FCGR1,TLR9,IL10RA,TRPV4,P2RY6,SP11,APOBEC1,ACPS,PTPN6,ADCY7,TNFRSF1B,AIF1,CYP26B1,CD86,PTAFR,HAVERC2,FAS,LY86,PLCG2,CTSH,TSP0,PIK3CG,PRKCD,PTPN22,TREM2,IGALS9,CD14,CARD9,ACER2,CCR5,BTK,ADM,PIM1,COL1A1,NPAS4,FOS,CYP2E1,HP,CD180,TNFAIP3,CASP4,PTGER4,GLRA4,GBP10,ZC3H12A,MMP2,NPPC,CRHR2,CCL2,CAMP,BGLAP2,MA51
BP	GO:0010033	response to organic substance	2758	492	151	1.16E-23	0.307	0.055	3	CCL1,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,CCL12,CSF2RB,TGTP2,ITGIP1,IL2RG,IL12RB1,IL2RG,IFI47,SPINT1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,B2T2,TLR1,IRGM1,CTSS,GBP6,CCR2,S100A8,SULT1A1,TLR2,GBP5,XDH,CSAR1,IL12R1,LTB,CD274,ICAM1,CSF3R,PCYARD,GBP4,CCL6,CXCL16,FCGR1,CD44,FCER1G,TLR9,IL10RA,TRPV4,P2RY6,HCL5,SP11,APOBEC1,USP18,ACPS,IRF1,PTPN6,ADCY7,TNFRSF1B,H2-M3,CTSC,AIF1,CYP26B1,CD86,PTAFR,GBP3,HAVERC2,FAS,STAT1,LY86,PLCG2,CD68,CTSH,GBP7,GBP9,TSP0,PIK3CG,IKBKE,PRKCD,IL1A,PTPN22,PARP9,TREM2,IGALS9,CD14,CARD9,FGFBP1,ACER2,TAP2,XAF1,TRIM21,IL6RA,CCR5,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,CEBPA,ISG15,OSMR,IFITM3,ECM1,TMEM173,ADM,MT2,PIM1,CDCDC3,COL1A1,NPAS4,FOS,CYP2E1,EBI3,CCL9,ANG,CD180,TNFAIP3,CASP4,CCR2,PTGER4,IL3RA,GLRA4,GBP10,ZC3H12A,GBP8,CCL17,MMP2,NPPC,CNMD,CRHR2,GPR35,CCL2,CAMP,CASP12,BGLAP2,MA51
BP	GO:0034097	response to cytokine	719	484	95	2.24E-43	0.196	0.132	4	CCL1,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,H2-AB1,LCN2,H2-AA,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,CCL12,CSF2RB,TGTP2,ITGIP1,IL2RG,IL12RB1,IL2RG,IFI47,SPINT1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,B2T2,TLR1,IRGM1,CTSS,GBP6,CCR2,S100A8,SULT1A1,TLR2,GBP5,XDH,CSAR1,IL12R1,LTB,CD274,ICAM1,CSF3R,PCYARD,GBP4,CCL6,CXCL16,CD44,IL10RA,HCL5,ACPS,IRF1,PTPN6,TNFRSF1B,AIF1,CD86,GBP3,FAS,STAT1,GBP7,GBP9,IKBKE,IL1A,PARP9,TREM2,CD14,XAF1,TRIM21,IL6RA,CCR5,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,CEBPA,ISG15,OSMR,IFITM3,ECM1,TMEM173,ADM,MT2,PIM1,CDCDC3,COL1A1,NPAS4,FOS,CYP2E1,EBI3,CCL9,ANG,CD180,TNFAIP3,CASP4,CCR2,PTGER4,IL3RA,GLRA4,GBP10,ZC3H12A,GBP8,CCL17,GPR35,CCL2,CAMP
BP	GO:0034612	response to tumor necrosis factor	196	484	22	0.00000129	0.045	0.112	5	CCL1,CCL5,CCL8,LCN2,CCL12,LTB,ICAM1,PCYARD,CCL6,CXCL16,TNFRSF1B,FAS,STAT1,CD14,CEBPA,CD3,COL1A1,CCL9,ZC3H12A,CCL17,CCL2,CAMP
BP	GO:0035455	response to interferon-alpha	23	337	6	0.00319	0.018	0.261	5	TGTP2,TGTP1,B2T2,IFIT1,IFIT3,IFITM3
BP	GO:0070555	response to interleukin-1	124	484	15	0.000294	0.031	0.121	5	CCL1,CCL5,CCL8,LCN2,CCL12,ICAM1,PCYARD,CCL6,IL1A,IL1R1,CCL9,ZC3H12A,CCL17,CCL2,CAMP
BP	GO:0035456	response to interferon-beta	45	340	22	7.34E-25	0.065	0.489	5	IFI204,IFI209,GM4951,IGTP,TGTP2,ITGIP1,IFI47,TGTP1,IRGM2,GBP2,B2T2,IRGM1,GBP6,IRF1,GBP3,STAT1,IKBKE,XAF1,IFIT1,IFIT3,IFITM3,TMEM173
BP	GO:0033993	response to lipid	893	442	51	5.74E-08	0.115	0.057	4	CCL1,CCL5,CXCL9,FCGR4,LCN2,CYBB,CXCL10,CD4,CCL12,SLC11A1,GBP2,GBP6,S100A8,SULT1A1,TLR2,CSAR1,ICAM1,PCYARD,CXCL16,FCGR1,TLR9,IL10RA,P2RY6,ACPS,TNFRSF1B,AIF1,CYP26B1,CD86,PTAFR,HAVERC2,FAS,LY86,PLCG2,CTSH,TSP0,PTPN22,TREM2,IGALS9,CD14,ACER2,CCR5,ADM,PIM1,COL1A1,NPAS4,FOS,CD180,TNFAIP3,PTGER4,GBP10,ZC3H12A
BP	GO:0010035	response to inorganic substance	493	412	25	0.0224	0.061	0.051	3	LCN2,CYBB,B2M,S100A8,C1QA,ICAM1,NCF1,TLR9,APOBEC1,CD86,FAS,ALOX5AP,HVCN1,TSP0,PRKCD,IL1A,CAPN3,CD14,CEBPA,MT2,COL1A1,FOS,CYP2E1,HP,TNFAIP3
BP	GO:0010038	response to metal ion	317	375	19	0.00819	0.051	0.06	4	CYBB,B2M,S100A8,C1QA,ICAM1,NCF1,TLR9,APOBEC1,CD86,FAS,ALOX5AP,HVCN1,TSP0,IL1A,CAPN3,CD14,CEBPA,MT2,FOS
BP	GO:0009605	response to external stimulus	2107	484	157	4.98E-42	0.324	0.075	2	CLEC4D,CLEC4E,CCL1,CCL5,C3,CXCL9,CD74,CCL8,FCGR4,LCN2,CYBB,ITGAX,TSPAN32,AOAH,NLRCS,CXCL10,ZBP1,LY22,CD4,CCL12,TGTP2,ITGIP1,H2-K1,IL12RB1,IGALS9,TGTP1,IRGM2,B2M,SLC11A1,GBP2,B2T2,TLR1,H2-T3,CT55,TAGAP,GBP6,A2M,CSAR1,S100A8,OAS2,CCR2,S100A8,RAC2,TLR2,HCK,NAIP2,GBP5,PLAC8,OAS1,CSAR1,TLR12,ICAM1,TLR7,CSF3R,TLR13,OAS2,NCF1,PCYARD,GBP4,OSAS1,CCL6,FCGR1,FCER1G,APOBEC3,TLR9,SP110,IL10RA,TRPV4,CH25H,APOBEC1,ACPS,IRF1,GSDMD,TNFRSF1B,H2-M3,AIF1,CD86,VAV1,PTAFR,GBP3,DOCK2,HAVCR2,TNFAIP8L2,FAS,ALOX5AP,LY86,PLCG2,NUAK2,CD37,RAB32,DDX60,CCDC88B,GBP7,GBP9,TSP0,ISP1,PIK3CG,DHX58,IKBKE,PRKCD,PIK3AP1,CAPN3,SERPING1,PTPN22,TREM2,IFAB,IGALS9,CD14,CARD9,NCKAP1,RSAD2,TAP2,IFI27L2A,PLAU,TRIM12A,CCR5,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,ISG15,IFITM3,CMTM7,TMEM173,ADM,TGM2,PIM1,COL1A1,FOS,HP,ISG20,CCL9,CD180,TNFAIP3,CMKLR1,CASP4,CCR2,PTGER4,RETNLG,BATF2,SIGLEC6,GBP10,ZC3H12A,CLEC4N,UPPP1,STAB1,CCL17,IL16,BCL3,C2,UNC13D,SPN,CCL2,CAMP
BP	GO:0009607	response to biotic stimulus	963	484	107	3.56E-42	0.221	0.111	2	CLEC4D,CLEC4E,CCL5,CXCL9,FCGR4,LCN2,ITGAX,TSPAN32,NLRCS,CXCL10,ZBP1,LY22,CD4,CCL12,TGTP2,ITGIP1,H2-K1,IL12RB1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,B2T2,TLR1,H2-T3,TAGAP,GBP6,OAS2,S100A8,TLR2,HCK,NAIP2,PLAC8,OAS1,CSAR1,TLR12,ICAM1,TLR7,TLR13,OAS2,NCF1,PCYARD,GBP4,OSAS1,CXCL16,FCGR1,FCER1G,APOBEC3,TLR9,SP110,IL10RA,APOBEC1,ACPS,IRF1,GSDMD,TNFRSF1B,H2-M3,CD86,PTAFR,GBP3,HAVERC2,FAS,LY86,PLCG2,CD37,DDX60,CCDC88B,GBP7,GBP9,TSP0,DHX58,IKBKE,PRKCD,PTPN22,TREM2,IGALS9,CD14,CARD9,RSAD2,TAP2,IFI27L2A,TRIM12A,BTK,IFIT1,IL4RA,IFIT3,ISG15,IFITM3,TMEM173,ADM,FOS,HP,ISG20,CD180,TNFAIP3,PTGER4,BATF2,GBP10,ZC3H12A,CLEC4N,STAB1,BCL3,UNC13D,SPN,CCL2,CAMP
BP	GO:0043207	response to external biotic stimulus	917	484	107	3.11E-44	0.221	0.117	3	CLEC4D,CLEC4E,CCL5,CXCL9,FCGR4,LCN2,ITGAX,TSPAN32,NLRCS,CXCL10,ZBP1,LY22,CD4,CCL12,TGTP2,ITGIP1,H2-K1,IL12RB1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,B2T2,TLR1,H2-T3,TAGAP,GBP6,OAS2,S100A8,TLR2,HCK,NAIP2,PLAC8,OAS1,CSAR1,TLR12,ICAM1,TLR7,TLR13,OAS2,NCF1,PCYARD,GBP4,OSAS1,CXCL16,FCGR1,FCER1G,APOBEC3,TLR9,SP110,IL10RA,APOBEC1,ACPS,IRF1,GSDMD,TNFRSF1B,H2-M3,CD86,PTAFR,GBP3,HAVERC2,FAS,LY86,PLCG2,CD37,DDX60,CCDC88B,GBP7,GBP9,TSP0,DHX58,IKBKE,PRKCD,PTPN22,TREM2,IGALS9,CD14,CARD9,RSAD2,TAP2,IFI27L2A,TRIM12A,BTK,IFIT1,IL4RA,IFIT3,ISG15,IFITM3,TMEM173,ADM,FOS,HP,ISG20,CD180,TNFAIP3,PTGER4,BATF2,GBP10,ZC3H12A,CLEC4N,STAB1,BCL3,UNC13D,SPN,CCL2,CAMP

BP	GO:0051707	response to other organism	913	484	107	2.03E-44	0.221	0.117	4	CLEC4D,CLEC4E,CCL5,CXCL9,FCGR4,LCN2,ITGAX,TSPAN32,NLRCS,CXCL10,ZBP1,LVZ2,CD4,CCL12,TGTP2,IIGP1,H2-K1,IL12RB1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,BST2,TLR1,H2-T23,TAGAP,GBP6,0ASL2,S100A8,TLR2,HCK,NAIP2,PLAC8,0ASL1,CSAR1,TLR12,ICAM1,TLR7,TLR13,0AS2,NCF1,PYCARD,GBP4,0AS1A,CXCL16,FCGR1,FCER1G,APOBEC3,TLR9,SP110,IL10RA,APOBEC1,ACPS,IRF1,GSDMD,TNFRSF18,H2-M3,CD86,PTAFR,GBP3,HAVCR2,FAS,LY86,PLCG2,CD37,DDX60,CCDC888,GBP7,GBP9,TSPO,DHX58,IKBKE,PRKCD,PTPN22,TREM2,LGALS9,CD14,CARD9,RSAD2,TAP2,IFI27L2A,TRIM12A,BTK,IFIT1,IL4RA,IFIT3,ISG15,IFITM3,TEMEM173,ADM,FOS,HP,ISG20,CD180,TNFAIP3,PTGERA,BATF2,GBP10,ZC3H12A,CLEC4N,STAB1,BCL3,UNC13D,SPN,CCL2,CAMP
BP	GO:0009615	response to virus	268	340	41	3.38E-25	0.121	0.153	5	CCL5,CXCL9,FCGR4,LCN2,ITGAX,TSPAN32,NLRCS,CXCL10,ZBP1,TGTP2,IL12RB1,TGTP1,BST2,TAGAP,0ASL2,0ASL1,TLR7,TLR13,0AS2,PYCARD,GBP4,0AS1A,APOBEC3,TLR9,APOBEC1,IRF1,CD86,CD37,DDX60,DHX58,IKBKE,PTPN22,LGALS9,CARD9,RSAD2,IFI27L2A,TRIM12A,IFIT3,ISG15,IFITM3,TEMEM173
BP	GO:0001562	response to protozoan	30	479	17	1.15E-17	0.035	0.567	5	TSPAN32,IIGP1,IRGM2,SLC11A1,GBP2,GBP6,TLR12,GBP3,CD37,CCDC888,GBP7,GBP9,IL4RA,BATF2,GBP10,BCL3,SPN
BP	GO:0009617	response to bacterium	662	484	70	9.74E-25	0.145	0.106	5	CLEC4D,CLEC4E,CCL5,CXCL9,FCGR4,LCN2,CXCL10,LVZ2,CD4,CCL12,IIGP1,H2-K1,IRGM2,B2M,SLC11A1,GBP2,TLR1,H2-T23,GBP6,S100A8,TLR2,HCK,NAIP2,PLAC8,CSAR1,TLR12,ICAM1,NCF1,PYCARD,CXCL16,FCGR1,FCER1G,TLR9,SP110,IL10RA,ACPS,GSDMD,TNFRSF18,H2-M3,CD86,PTAFR,GBP3,HAVCR2,FAS,LY86,PLCG2,GBP7,GBP9,TSPO,PRKCD,PTPN22,TREM2,LGALS9,CD14,CARD9,TAP2,ISG15,ADM,FOS,HP,CD180,TNFAIP3,PTGERA,GBP10,ZC3H12A,STAB1,BCL3,SPN,CCL2,CAMP
BP	GO:0002237	response to molecule of bacterial origin	332	484	44	2.35E-18	0.091	0.133	4	CCL5,CXCL9,FCGR4,LCN2,CXCL10,CCL12,B2M,SLC11A1,GBP2,TLR1,GBP6,S100A8,TLR2,CSAR1,ICAM1,PYCARD,CXCL16,TLR9,IL10RA,ACPS,TNFRSF18,H2-M3,CD86,PTAFR,HAVCR2,FAS,LY86,PLCG2,TSPO,PTPN22,TREM2,LGALS9,CD14,CARD9,TAP2,ADM,FOS,CD180,TNFAIP3,PTGERA,GBP10,ZC3H12A,CCL2,CAMP
BP	GO:0032496	response to lipopolysaccharide	318	484	39	8.59E-15	0.081	0.123	5	CCL5,CXCL9,FCGR4,LCN2,CXCL10,CCL12,SLC11A1,GBP2,GBP6,S100A8,TLR2,CSAR1,ICAM1,PYCARD,CXCL16,TLR9,IL10RA,ACPS,TNFRSF18,H2-M3,CD86,PTAFR,HAVCR2,FAS,LY86,PLCG2,TSPO,PTPN22,TREM2,LGALS9,CD14,ADM,FOS,CD180,TNFAIP3,PTGERA,GBP10,ZC3H12A,CCL2,CAMP
BP	GO:0006950	response to stress	3285	330	164	3.3E-47	0.497	0.05	2	CLEC4D,CLEC4E,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,ITGAX,TSPAN32,LV9,ADAAH,NLRCS,CXCL10,GM4951,ZBP1,LVZ2,CD4,IGTP,CCL12,TGTP2,IIGP1,H2-K1,IL12RB1,IFI47,TAP1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,BST2,TLR1,H2-T23,IRGM1,CTSS,TAGAP,GBP6,A2M,C3AR1,C4B,CLEC4A2,ELF4,C1RA,LAT,ITGB2,S100A9,0ASL2,CCR2,S100A8,TLR2,HCK,NAIP2,GBPS,PLAC8,THEMIS2,XDH,0ASL1,CSAR1,TLR12,C1QA,ICAM1,TLR7,TLR13,0AS2,NCF1,PYCARD,GBP4,0AS1A,CCL6,TRIM30A,CXCL16,FCGR1,FCER1G,CD14,C1QB,FCER1G,APOBEC3,TLR9,SP110,TRPV4,C1QC,APOBEC1,ACPS,IRF1,PTPN6,GSDMD,FERMT3,TNFRSF18,CD163,H2-M3,NGP,AIF1,LAG3,CYP26B1,CD86,CLEC10A,VAV1,PTAFR,GBP3,HAVCR2,TNFAIP8L2,FAS,ALOX5AP,STAT1,LY86,PLCG2,NUAK2,CD37,F13A1,HK2,DDX60,GFAP,CCDC888,GBP7,UNC93B1,GBP9,TSPO,LSPI1,PIK3CG,DHX58,PARP3,IKBKE,PRKCD,IL1A,PIK3AIP1,CAPN3,SERPING1,FGD2,MAFF,PTPN22,PARP9,TREM2,LGALS9,DTX3L,CD14,CARD9,CD300A,TYROBP,RSAD2,VWF,PLAU,TRIM21,TRIM12A,PIK3R6,CCRS,LCK,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,ISG15
BP	GO:0006952	defense response	1353	340	148	9.87E-85	0.435	0.109	3	CLEC4D,CLEC4E,CCL5,CXCL9,H2-Q7,CD74,CCL8,H2-AB1,LCN2,H2-AA,CYBB,ITGAX,TSPAN32,LV9,ADAAH,NLRCS,CXCL10,GM4951,ZBP1,LVZ2,CD4,IGTP,CCL12,TGTP2,IIGP1,H2-K1,IL12RB1,IFI47,TAP1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,BST2,TLR1,H2-T23,IRGM1,CTSS,TAGAP,GBP6,A2M,C3AR1,C4B,CLEC4A2,ELF4,C1RA,LAT,ITGB2,S100A9,0ASL2,CCR2,S100A8,TLR2,HCK,NAIP2,GBPS,PLAC8,THEMIS2,0ASL1,CSAR1,TLR12,C1QA,ICAM1,TLR7,TLR13,0AS2,NCF1,PYCARD,GBP4,0AS1A,CCL6,TRIM30A,CXCL16,FCGR1,C1QB,FCER1G,APOBEC3,TLR9,SP110,TRPV4,C1QC,APOBEC1,ACPS,IRF1,PTPN6,GSDMD,TNFRSF18,CD163,H2-M3,NGP,AIF1,LAG3,CYP26B1,CD86,CLEC10A,VAV1,PTAFR,GBP3,HAVCR2,TNFAIP8L2,FAS,ALOX5AP,STAT1,LY86,PLCG2,CD37,DDX60,CCDC888,GBP7,UNC93B1,GBP9,LSPI1,PIK3CG,DHX58,IKBKE,PRKCD,IL1A,PIK3AIP1,SERPING1,PTPN22,PARP9,TREM2,LGALS9,CD14,CARD9,CD300A,TYROBP,RSAD2,TRIM21,TRIM12A,PIK3R6,CCRS,LCK,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,ISG15
BP	GO:0006954	inflammatory response	576	492	79	5.92E-36	0.161	0.137	4	CCL1,CCL5,C3,CHIL3,CXCL9,CCL8,CYBB,ADAAH,CXCL10,CCL12,SLC11A1,TLR1,CTSS,A2M,C3AR1,C4B,LAT,ITGB2,S100A8,CCR2,S100A8,TLR2,HCK,NAIP2,GBPS,THEMIS2,CSAR1,TLR12,ICAM1,TLR7,TLR13,NCF1,PYCARD,CCL6,FCGR1,FCER1G,TLR9,TRPV4,ACPS,GSDMD,TNFRSF18,CD163,AIF1,CYP26B1,CLEC10A,PTAFR,HAVCR2,TNFAIP8L2,FAS,ALOX5AP,LY86,PIK3CG,IL1A,PIK3AIP1,SERPING1,LGALS9,CD14,CD300A,CCRS,BTK,CSF1R,IL1R1,IL4RA,ECM1,TGMD2,HP,CCL9,CD180,TNFAIP3,CASPA,CCR2,PTGERA,SLGCEC,ZC3H12A,CCL17,UNC13D,SPN,CCL2,MAST1
BP	GO:0002526	acute inflammatory response	111	322	12	0.000276	0.037	0.108	5	C3,A2M,S100A8,ICAM1,FCGR1,FCER1G,CD163,ALOX5AP,PIK3CG,IL1A,SERPING1,BTK
BP	GO:0002438	acute inflammatory response to antigenic stimulus	25	479	6	0.0395	0.013	0.24	6	C3,ICAM1,FCGR1,FCER1G,BTK,SPN
BP	GO:0002524	hypersensitivity	11	479	5	0.00612	0.01	0.455	7	C3,FCGR1,FCER1G,BTK,SPN
BP	GO:0006968	cellular defense response	15	141	4	0.0064	0.028	0.267	4	B2M,LAT,CCR2,NCF1
BP	GO:0009842	defense response to other organism	570	484	77	5.41E-35	0.159	0.135	4	CLEC4D,CLEC4E,CCL5,CXCL9,ITGAX,TSPAN32,NLRCS,CXCL10,ZBP1,LVZ2,CD4,IIGP1,H2-K1,IL12RB1,IRGM2,SLC11A1,GBP2,BST2,TLR1,H2-T23,TAGAP,GBP6,0ASL2,TLR2,HCK,NAIP2,PLAC8,0ASL1,CSAR1,TLR12,TLR7,0AS2,NCF1,PYCARD,GBP4,0AS1A,FCGR1,FCER1G,APOBEC3,TLR9,APOBEC1,ACPS,IRF1,GSDMD,H2-M3,CD86,GBP3,HAVCR2,CD37,DDX60,CCDC888,GBP7,GBP9,DHX58,PRKCD,PTPN22,LGALS9,CARD9,RSAD2,TRIM12A,IFIT1,IL4RA,IFIT3,ISG15,IFITM3,TEMEM173,HP,ISG20,BATF2,GBP10,ZC3H12A,CLEC4N,STAB1,BCL3,UNC13D,SPN,CAMP
BP	GO:0042742	defense response to bacterium	362	293	32	8.49E-14	0.109	0.088	5	CLEC4D,CLEC4E,LVZ2,CD4,IIGP1,H2-K1,IRGM2,SLC11A1,GBP2,TLR1,H2-T23,GBP6,TLR2,HCK,NAIP2,PLAC8,CSAR1,NCF1,PYCARD,FCGR1,FCER1G,TLR9,ACPS,GSDMD,H2-M3,GBP3,HAVCR2,GBP7,GBP9,PRKCD,LGALS9,CARD9
BP	GO:0050830	defense response to Gram-positive bacterium	71	293	15	7.81E-11	0.051	0.211	6	LVZ2,GBP2,H2-LVZ2,GBP6,TLR2,HCK,CSAR1,NCF1,ACPS,GSDMD,GBP3,HAVCR2,GBP7,GBP9,CARD9
BP	GO:0050829	defense response to Gram-negative bacterium	42	190	7	0.000208	0.037	0.167	6	LVZ2,CD4,IIGP1,SLC11A1,PYCARD,TLR9,GSDMD
BP	GO:0042832	defense response to protozoan	27	470	16	4.55E-17	0.034	0.593	5	TSPAN32,IIGP1,IRGM2,SLC11A1,GBP2,GBP6,TLR12,GBP3,CD37,CCDC888,GBP7,GBP9,IL4RA,BATF2,GBP10,BCL3
BP	GO:0051607	defense response to virus	201	340	34	6.33E-22	0.1	0.169	5	CCL5,CXCL9,ITGAX,TSPAN32,NLRCS,CXCL10,ZBP1,IL12RB1,BST2,TAGAP,0ASL2,0ASL1,TLR7,0AS2,PYCARD,GBP4,0AS1A,APOBEC3,TLR9,APOBEC1,IRF1,CD86,CD37,DDX60,DHX58,PTPN22,CARD9,RSAD2,TRIM12A,IFIT1,IFIT3,ISG15,IFITM3,TEMEM173
BP	GO:0009611	response to wounding	479	369	26	0.000593	0.07	0.054	3	FCGR4,TSPAN32,SLC11A1,S100A9,CCR2,S100A8,FCER1G,PTPN6,FERMT3,AIF1,CLEC10A,VAV1,IF13A1,GFAP,TSPO,PRKCD,IL1A,CAPN3,SERPING1,MAFF,VWF,PLAU,ADM,MERTK,COL1A1
BP	GO:0042060	wound healing	379	369	21	0.00659	0.057	0.055	4	FCGR4,TSPAN32,SLC11A1,S100A9,CCR2,S100A8,FCER1G,PTPN6,FERMT3,CLEC10A,VAV1,IF13A1,PRKCD,IL1A,CAPN3,SERPING1,MAFF,VWF,PLAU,MERTK,COL1A1
BP	GO:0007596	blood coagulation	177	362	13	0.0258	0.036	0.073	5	TSPAN32,S100A9,FCER1G,PTPN6,FERMT3,VAV1,IF13A1,PRKCD,SERPING1,MAFF,VWF,PLAU,MERTK
BP	GO:0006955	immune response	1362	340	161	2.86E-99	0.474	0.118	2	CLEC4D,CLEC4E,CDB81,G2MB,CCL1,CCL5,C3,CXCL9,H2-Q7,CD74,CCL8,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,H2-EB1,PIR8,LV9,NLRCS,CXCL10,ZBP1,CD4,CCL12,TGTP2,IIGP1,H2-QA,MYO1G,H2-K1,IL12RB1,ITGAL,H2-D1,TAP1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,BST2,H2-DMB1,TLR1,H2-T23,IRGM1,CTSS,GBP6,A2M,FYB,C3AR1,C4B,CD84,CLEC4A2,ELF4,C1RA,LAT,CD48,S100A9,0ASL2,CCR2,S100A8,RAC2,TLR2,HCK,NAIP2,GBPS,THEMIS2,0ASL1,CSAR1,LTB,TLR12,CD274,C1QA,ICAM1,TLR7,TLR13,0AS2,PYCARD,PTPRC,GBP4,0AS1A,CCL6,C1S1,TRIM30A,CXCL16,FCGR1,LCP2,TNFRSF13B,WAS,C1QB,ADGRE1,FCER1G,APOBEC3,TLR9,SP110,C1QC,LSL1,SASH3,ICOSL,IRF1,PTPN6,GSDMD,TNFRSF18,H2-M3,CTSC,AIF1,LAG3,CD86,VAV1,PTAFR,GBP3,LCP1,DOCK2,H2-DMA,HAVCR2,TNFAIP8L2,FAS,STAT1,LY86,PLCG2,BLNK,CD37,DDX60,CTSH,GBP7,UNC93B1,GBP9,DHX58,IKBKE,PRKCD,IL1A,PIK3AIP1,SERPING1,PTPN22,PARP9,TREM2,LGALS9,CD14,CARD9,NCKAIP1,CD300A,TYROBP,RSAD2,TAP2,TRIM21,KHLH6,TRIM12A,PIK3R6,CCRS,LPXN,LCK,BTK,CSF1R,IFIT1,IL4RA,IFIT3,ISG15,NFAM1,IFITM3,ECM1,TEMEM173
BP	GO:0006959	humoral immune response	256	189	12	0.00723	0.063	0.047	3	C3,H2-AB1,H2-T23,A2M,C4B,C1RA,CCR2,C1QA,C1S1,C1QB,C1QC,PTPN6
BP	GO:0002250	adaptive immune response	441	326	53	5.21E-29	0.163	0.12	3	CLEC4D,CDB81,G2MB,C3,CD74,H2-AB1,PIR8,LV9,CD4,MYO1G,H2-K1,IL12RB1,H2-D1,TAP1,B2M,SLC11A1,IRF7,H2-T23,CTSS,C4B,CLEC4A2,C1RA,LAT,CD48,CCR2,C1QA,ICAM1,PYCARD,FCGR1,TNFRSF13B,WAS,C1QB,ADGRE1,FCER1G,C1QC,SASH3,ICOSL,IRF1,PTPN6,H2-M3,CTSC,CD86,HAVCR2,FAS,CTSH,PRKCD,SERPING1,INPP5D,RSAD2,TAP2,KHLH6,BTK,IL4RA
BP	GO:0002460	adaptive immune response based on somatic recombination of immu	336	326	43	4.57E-24	0.132	0.128	4	G2MB,C3,CD74,H2-AB1,PIR8,LV9,CD4,MYO1G,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,IRF7,H2-T23,C4B,C1RA,CCR2,C1QA,ICAM1,FCGR1,TNFRSF13B,WAS,C1QB,FCER1G,C1QC,SASH3,ICOSL,IRF1,PTPN6,H2-M3,CTSC,HAVCR2,FAS,CTSH,PRKCD,SERPING1,INPP5D,RSAD2,TAP2,KHLH6,BTK,IL4RA
BP	GO:0042088	T-helper 1 type immune response	40	470	8	0.00526	0.017	0.2	5	H2-AB1,IL12RB1,SLC11A1,CCR2,IRF1,HAVCR2,IL4RA,BCL3

BP	GO:0002456	T cell mediated immunity	78	305	15	6.18E-10	0.049	0.192	5	GZMB, MYO1G, H2-K1, H2-D1, B2M, SLC11A1, H2-T23, ICAM1, WAS, SASH3, H2-M3, CTSC, CTSH, RSAD2, TAP2
BP	GO:0001913	T cell mediated cytotoxicity	31	305	9	0.00000832	0.03	0.29	6	GZMB, H2-K1, H2-D1, B2M, H2-T23, H2-M3, CTSC, CTSH, TAP2
BP	GO:0019724	B cell mediated immunity	219	326	20	0.00000363	0.061	0.091	5	C3, CD74, H2-AB1, IRF7, IRF7, C4B, C1RA, C1QA, FCGR1, C1QB, FCER1G, C1QC, ICOSL, PTPN6, FAS, PRKCD, SERPING1, INPP5D, BTK, IL4RA
BP	GO:0016064	immunoglobulin mediated immune response	217	326	18	0.0000147	0.055	0.083	6	C3, CD74, H2-AB1, IRF7, C4B, C1RA, C1QA, FCGR1, C1QB, FCER1G, C1QC, ICOSL, PTPN6, PRKCD, SERPING1, INPP5D, BTK, IL4RA
BP	GO:0002445	type II hypersensitivity	3	162	3	0.00121	0.019	1	7	C3, FCGR1, FCER1G
BP	GO:0001794	type III hypersensitivity	3	162	3	0.00121	0.019	1	8	C3, FCGR1, FCER1G
BP	GO:0001802	type III hypersensitivity	3	322	3	0.00981	0.009	1	7	FCGR1, FCER1G, BTK
BP	GO:0042092	type 2 immune response	34	470	7	0.0194	0.015	0.206	3	CD74, CCR2, IRF1, RSAD2, IL4RA, EGM1, BCL3
BP	GO:0045087	innate immune response	708	484	119	6.24E-68	0.246	0.168	3	CLEC4D, CLEC4E, CCL1, CCL5, C3, H2-Q7, CD74, CCL8, H2-AB1, LCN2, H2-AA, CYBB, LY9, NLRCS, ZBP1, CCL12, TGTP2, IIGP1, IL12RB1, TGTP1, IRGM2, SLC11A1, GBP2, IRF7, BST2, IL1R1, H2-T23, IRGM1, GBP6, AZM, C4B, CLEC4A2, ELF4, C1RA, S100A9, OASL2, S100A8, TLR2, HCK, NAI1, P2, GBP5, OASL1, TLR12, C1QA, ICAM1, TLR7, TLR13, OAS2, PYCARD, GBP4, OAS1A, CCL6, TRIM30A, CXCL16, FCGR1, C1QB, FCER1G, APOBEC3, TLR9, SP110, C1QC, IRF1, PTPN6, GSDMD, H2-M3, AIF1, LAG3, CD86, VAV1, GBP3, HAVCR2, TNFAIP81, STAT1, LY86, PLCG2, DDX60, GBP7, UNC93B1, GBP9, DHX58, IKKKE, PIK3AP1, SERPING1, PTPN22, PARP9, TREM2, LGALS9, CD14, CARD9, CD300A, TYROBP, RSAD2, TRIM21, TRIM12A, PIK3R6, LCK, BTK, CSF1R, IFIT1, IFIT3, JSG15, IFITM3, TMEM173, CFB, ISG20, CCL9, CD180, TNFAIP3, CASP4, GBP10, CLEC4N, GBP8, CCL17, MMP2, TRIM14, C2, UNCL3D, CCL2, CAMP
BP	GO:0034341	response to interferon-gamma	110	480	37	1.43E-30	0.077	0.336	4	CCL1, CCL5, H2-Q7, CCL8, H2-AB1, H2-AA, NLRCS, CXCL12, TGTP2, IL12RB1, TGTP1, IRGM2, SLC11A1, GBP2, BST2, GBP6, GBP5, ICAM1, GBP4, CCL6, CXCL16, IRF1, PTPN6, AIF1, CD86, GBP3, STAT1, GBP7, GBP9, PARP9, TRIM21, IFITM3, CCL9, GBP10, GBP8, CCL17, CCL2
BP	GO:0034340	response to type I interferon	30	337	6	0.0172	0.018	0.2	4	NLRCS, ZBP1, IRF7, IKKKE, ISG15, IFITM3
BP	GO:0002228	natural killer cell mediated immunity	49	317	8	0.00147	0.025	0.163	4	H2-T23, PTPN6, H2-M3, LAG3, VAV1, HAVCR2, LGALS9, PIK3R6
BP	GO:0042267	natural killer cell mediated cytotoxicity	47	317	8	0.00105	0.025	0.17	5	H2-T23, PTPN6, H2-M3, LAG3, VAV1, HAVCR2, LGALS9, PIK3R6
BP	GO:0002367	cytokine production involved in immune response	77	182	8	0.000751	0.044	0.104	3	CD74, B2M, SLC11A1, BST2, TLR2, FCER1G, TLR9, SASH3
BP	GO:0040011	locomotion	1468	468	70	0.000000436	0.15	0.048	1	CCL1, CCL5, CXCL9, CD74, CCL8, CXCL10, CCL12, MYO1G, LGALS3, BST2, C3AR1, ITGB2, ST14, S100A9, CCR2, S100A8, RAC2, ITGB7, HCK, CSAR1, CD274, ICAM1, CSF3R, PYCARD, CCL6, CXCL16, WAS, FCER1G, TRPV4, CH25H, P2RY6, FERMT3, AIF1, VAV1, PTAFR, LCP1, DOCK2, CTSH, TSP0, LSP1, PIK3CG, PRKCD, IL1A, PTPN22, LGALS9, NCKAP1, CD300A, PLAU, TRIM21, CCR5, LCK, CSF1R, IL1R1, EGM1, CMTM7, SP100, GUPR2, COL1A1, MYOC, CCL9, PRRS5, ANK, CMKLR1, CCR2, PTGER4, RETNLG, ZC3H12A, CCL17, HTR6, IL16
BP	GO:0042330	taxis	496	480	39	1.54E-08	0.081	0.079	2	CCL1, CCL5, CXCL9, CD74, CCL8, CXCL10, CCL12, LGALS3, C3AR1, S100A9, CCR2, S100A8, RAC2, CSAR1, CSF3R, CCL6, CXCL16, FCER1G, TRPV4, CH25H, AIF1, VAV1, PTAFR, DOCK2, LSP1, IK3CG, PRKCD, LGALS9, NCKAP1, CCR5, CSF1R, CMTM7, CCL9, CMKLR1, CCR2, RETNLG, CCL17, IL16, CCL2
BP	GO:0006935	chemotaxis	494	480	39	1.36E-08	0.081	0.079	3	CCL1, CCL5, CXCL9, CD74, CCL8, CXCL10, CCL12, LGALS3, C3AR1, S100A9, CCR2, S100A8, RAC2, CSAR1, CSF3R, CCL6, CXCL16, FCER1G, TRPV4, CH25H, AIF1, VAV1, PTAFR, DOCK2, LSP1, IK3CG, PRKCD, LGALS9, NCKAP1, CCR5, CSF1R, CMTM7, CCL9, CMKLR1, CCR2, RETNLG, CCL17, IL16, CCL2
BP	GO:0032502	developmental process	5720	379	136	0.045	0.359	0.024	1	CLEC4D, CLEC4E, C3, CXCL9, H2-Q7, CD74, CCL8, IFI202, H2-AB1, H2-AA, CYBB, PI8B, LY9, CXCL10, LRG1, CD4, CCL12, H2-QA, IL2RG, H2-K1, LGALS3, PSMB8, H2-D1, SPINT1, B2M, H2-T23, AZM, C3AR1, ELF4, ITGB2, ST14, S100A9, CCR2, S100A8, CRYBA4, ITGB7, TLR2, HCK, PLA2, XDH, CSAR1, LTB, ICAM1, CSF3R, TNFAIP2, PLD4, TNFSF13B, CD44, C1QB, FCER1G, APOBEC3, TLR9, DLK1, RHOH, TRPV4, HCL51, C1QC, LST1, SP11, SASH3, ACPS, ICOSL, IRF1, PTPN6, FERMT3, TNFRSF18, H2-M3, NKG, IKZF1, CTSC, CYP26B1, CD86, VAV1, HIF3A, LCP1, DOCK2, HAVCR2, FAS, STAT1, PLCG2, RAB32, HK2, GFAP, ADAP2, CTSH, TSP0, HIST1H4H, MAFB, PIK3CG, RNF213, PRKCD, IL14, CAPN3, SERPING1, INPP5D, MAFF, PTPN22, TREM2, TIFAB, LGALS9, TGFBI, NCKAP1, TYROBP, RSAD2, IFI7L2A, KLHL6, IL6RA, PIK3R6, LCK, BTK, CSF1R, IL4RA, CEBPA, ISG15, NFAM1, E, CM1, CMTM7, SP100, CD53, ADM, TGM2, GUPR2, CTS2, DNASE2A, MT2, PIM1, MERTK, CDC3, COL1A1, NPAS4, NGRF, ATF5, UGT8A, FOS, MYOC, KLK6
BP	GO:0022610	biological adhesion	1220	326	66	9.05E-17	0.202	0.054	1	CCL5, CD74, H2-AB1, H2-AA, ITGAX, TSPAN32, LY9, CD4, H2-OA, MYO1G, IL2RG, IL12RB1, LGALS3, ITGAL, GBP2, H2-T23, GBP6, CD74, ITGB2, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, LGALS3BP, CD274, ICAM1, CSF3R, PYCARD, TNFSF13B, CD44, TRPV4, SASH3, ICOSL, IRF1, PTPN6, FERMT3, H2-M3, AIF1, LAG3, CYP26B1, CD86, VAV1, PTAFR, HAVCR2, TNFAIP81, C, CDC8B8, PRKCD, GBP9, PRKCD, PARVG, CD33, PTPN22, LGALS9, TGFBI, NCKAP1, CD300A, ACER2, VWF, PLAU, PIK3R6, LPXN, LCK, IL4RA
BP	GO:0007155	cell adhesion	1209	326	61	8.97E-14	0.187	0.05	2	CCL5, CD74, H2-AB1, H2-AA, ITGAX, TSPAN32, LY9, CD4, H2-OA, MYO1G, IL2RG, IL12RB1, LGALS3, ITGAL, H2-T23, LAT, ITGB2, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, LGALS3BP, CD274, ICAM1, CSF3R, PYCARD, TNFSF13B, CD44, TRPV4, SASH3, ICOSL, IRF1, PTPN6, FERMT3, H2-M3, AIF1, LAG3, CYP26B1, CD86, VAV1, PTAFR, HAVCR2, TNFAIP81, C, CDC8B8, PRKCD, PARVG, CD33, PTPN22, LGALS9, TGFBI, NCKAP1, CD300A, ACER2, VWF, PLAU, PIK3R6, LPXN, LCK, IL4RA
BP	GO:0098602	single organism cell adhesion	592	326	49	3.15E-19	0.15	0.083	3	CCL5, CD74, H2-AB1, H2-AA, ITGAX, TSPAN32, CD4, H2-OA, IL2RG, IL12RB1, LGALS3, ITGAL, H2-T23, LAT, ITGB2, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, CD274, ICAM1, PYCARD, TNFSF13B, CD44, TRPV4, SASH3, ICOSL, IRF1, PTPN6, FERMT3, H2-M3, AIF1, LAG3, CYP26B1, CD86, PTAFR, HAVCR2, TNFAIP81, C, CDC8B8, PRKCD, PTPN22, LGALS9, NCKAP1, CD300A, PIK3R6, LCK, IL4RA
BP	GO:0033627	cell adhesion mediated by integrin	52	320	8	0.00254	0.025	0.154	3	CCL5, ICAM1, PTPN6, FERMT3, NCKAP1, ACER2, PLAU, LPXN
BP	GO:0098609	cell-cell adhesion	740	326	49	4.04E-15	0.15	0.066	3	CCL5, CD74, H2-AB1, H2-AA, ITGAX, TSPAN32, CD4, H2-OA, IL2RG, IL12RB1, LGALS3, ITGAL, H2-T23, LAT, ITGB2, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, CD274, ICAM1, PYCARD, TNFSF13B, CD44, TRPV4, SASH3, ICOSL, IRF1, PTPN6, FERMT3, H2-M3, AIF1, LAG3, CYP26B1, CD86, PTAFR, HAVCR2, TNFAIP81, C, CDC8B8, PRKCD, PTPN22, LGALS9, NCKAP1, CD300A, PIK3R6, LCK, IL4RA
BP	GO:0016337	single organismal cell-cell adhesion	538	326	49	4.67E-21	0.15	0.091	4	CCL5, CD74, H2-AB1, H2-AA, ITGAX, TSPAN32, CD4, H2-OA, IL2RG, IL12RB1, LGALS3, ITGAL, H2-T23, LAT, ITGB2, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, CD274, ICAM1, PYCARD, TNFSF13B, CD44, TRPV4, SASH3, ICOSL, IRF1, PTPN6, FERMT3, H2-M3, AIF1, LAG3, CYP26B1, CD86, PTAFR, HAVCR2, TNFAIP81, C, CDC8B8, PRKCD, PTPN22, LGALS9, NCKAP1, CD300A, PIK3R6, LCK, IL4RA
BP	GO:0007159	leukocyte cell-cell adhesion	310	326	45	9.75E-28	0.138	0.145	5	CCL5, CD74, H2-AB1, H2-AA, CD4, H2-OA, IL2RG, IL12RB1, LGALS3, ITGAL, H2-T23, LAT, ITGB2, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, CD274, ICAM1, PYCARD, TNFSF13B, CD44, SASH3, ICOSL, IRF1, PTPN6, FERMT3, H2-M3, AIF1, LAG3, CYP26B1, CD86, PTAFR, HAVCR2, TNFAIP81, C, CDC8B8, PRKCD, PTPN22, LGALS9, NCKAP1, CD300A, PIK3R6, LCK, IL4RA
BP	GO:0070486	leukocyte aggregation	14	159	4	0.00767	0.025	0.286	6	S100A9, S100A8, RAC2, CD44
BP	GO:0044406	adhesion of symbiont to host	14	252	6	0.0000187	0.024	0.429	2	GBP2, GBP6, ICAM1, GBP3, GBP9
BP	GO:0023052	signaling	6618	492	220	6.28E-09	0.447	0.033	1	HCA2, CLEC4D, CLEC4E, GZMB, CCL1, CCL5, C3, CXCL9, CD74, CCL8, IFI204, FCGR4, LCN2, CYBB, ITGAX, TSPAN32, PI8B, NLRCS, CXCL10, ZBP1, CSF2R2, LRG1, CD4, CCL12, CSF2R8, IIGP1, MYO1G, IL2RG, IL12RB1, LGALS3, ITGAL, SLC11A1, IRF7, ACAP1, BST2, TLR1, TAGAP, VAV, C3AR1, LAT, ITGB2, CD48, ARHGAP9, S100A9, CCR2, S100A8, RAC2, SASAL3, ITGB7, TLR2, HCK, NAIIP2, THEMIS2, XDH, CSAR1, IL21R, LTB, TLR12, CD274, ICAM1, TLR7, CSF3R, TLR13, NCF1, PYCARD, PTPRC, CCL6, TRIM30A, FCGR1, LCP2, WAS, CD44, ADGRE1, FCER1G, TLR9, DLK1, RHOH, IL10RA, TRPV4, P2RY6, HCL51, ICOSL, IRF1, PTPN6, FERMT3, ADCY7, TNFRSF18, H2-M3, CTSC, AIF1, LAG3, CYP26B1, CD86, VAV1, ARHGAP30, PIK3R5, PTAFR, LCP1, DOCK2, ARHGAP45, HAVCR2, S100A4, FAS, STAT1, LY86, PLCG2, BLNK, NUA2, CD37, ARHGAP25, DDX60, GFAP, ADAP2, CTSH, UNC93B1, ADORA3, TSP0, LSP1, PIK3CG, DHX58, RNF213, IKKKE, PRKCD, IL1A, PIK3AP1, CAPN3, FGD2, INPP5D, PTPN22, TREM2, TIFAB, LGALS9, CD14, CARD9, NCKAP1, CD300A, TYROBP, FCGBP1, MAAP3K6, RHBO2, RSAD2, PLAU, KLHL6, IL6RA, PIK3R6, CCR5, LPXN, LCK, BTK, CSF1R, IL1R1, IL4RA, CEBPA, NFAM1, OSMR, IFITM3, EGM1, SP100, RIN2, CD53, ADM, RASD1, TGM2, GUPR2, MIT2, PIM1, MERTK, CYTH4, CDC3, COL1A1, NPAS4, API, N, NGRF, FOS, MYOC, KLG6, STOML3, OMP, FCRL3, HP, GPR84, ARL11, EB1, CCL9, PRRS5, CD180, TNFAIP3, CMKLR1, CASP4, GPR65, CCR2, PTGER4, DOK1, IL3RA, SIGLEC, GLRA4, ZC3H3, 2A, CLEC4N, DUSP2, DOK2, PLAU, STAB1, LAT2, CCL17, HTR6, CD247, F10, BCL3, NPCC, CN, MD, CRRH2, GPR35, SPN, CCL2, UPK18, PSD4, CASP12, BGLAP2, RAPS5, MAS1

BP	GO:0044700	single organism signaling	6606	492	220	5.16E-09	0.447	0.033	2	HCR2,CLEC4D,CLEC4E,GZMB,CCL1,CCL5,C3,CD4,CD74,CCL8,IFIT204,FCGR4,LCN2,CYBB,ITGAX,TSKAN2,P1RB,NLRCS,CXCL10,ZBP1,CSF2RB2,LRG1,CD4,CCL12,CSF2R8,IL6,MYO1G,IL2RG,IL12RB1,IGALS3,ITGAL,SLC11A1,IRF7,ACAP1,BST2,TLR1,TAGAP,FYB,C3AR1,LAT,ITGB2,CD48,ARHGAP9,S100A9,CCR2,S100A8,RAC2,RASAL3,ITGB7,TLR2,KNAP2,TNFRSF2,XDH,CSAR1,IL18,IL1B,TLR2,CD274,ICAM1,TLR7,CSF3R,TLR13,NCF1,LYCARD,PTPRC,CCL6,TRIM30A,FCGR1,LCP2,WAS,CD4,ADGRE1,FCER1G,TLR9,DLK1,RHOH,IL10RA,TRPV4,P2RY6,HCLS1,ICOSL,IRF1,PTPN6,FERM13,ADCV7,TNFRSF18,H2-M3,CTSC,AIF1,LAG3,CYP26B1,CD86,VAV1,ARHGAP30,PIK3R5,PTAFR,LCP1,DOCK2,ARHGAP45,HAVCR2,S100A4,FAS,STAT1,LY86,PLCG2,BLNK,NUAK2,CD37,ARHGAP25,DDX6,GFAP,ADAP2,CTSH,UNC93B1,ADORA3,TSP0,LP1,PIK3CG,DHX58,RFN213,IKKBE,PRKC,DIJL1A,PIK3AP1,CAPN3,FGD2,INPP5D,PTPN22,TREM2,TIFAB,IGALS9,CD14,CARD9,NCAP1L,CD300A,TYROBP,FGBP1,MAP3K6,RHBD2,RSAD2,PLAU,KLHL6,IL6RA,PIK3R6,CCR5,LPXN,LCK,BTK,CSF1R,IL1R1,IL1RA,CEBPA,NFAM1,OSMR,IFITM3,ECM1,SP100,RIN3,CD53,ADM,RASD1,TGM2,GLIPR2,MT2,PIM1,MERTK,CYTH4,CCDC3,COL1A1,NPAS4,APLN,NGFR,FOS,MYOC,KLK6,STOML3,OMP,FCRL5,HP,GPR84,ARL11,EBI3,CCL9,PRR5L,CD180,TNFAIP3,CMKLR1,CASP4,GPR65,CCR2,PTGER4,DOCK1,IL3RA,SIGLEC6,GLRA4,ZC3H2A,CLECAN,DUSP2,DOCK2,PLAUR,STAB1,LAT2,CCL17,HTB6,CD247,F10,BCL3,NPPC,CNMD,CRHR2,GPR35,SPN,CCL2,UPK1B,P504,CASP12,BGLAP2,RAFSM,MSA1
BP	GO:0044763	single-organism cellular process	9764	448	257	0.0000376	0.574	0.026	1	HCR2,CLEC4D,CLEC4E,GZMB,CCL1,CCL5,C3,CD4,CD74,CCL8,IFIT204,FCGR4,H2-AB1,LCN2,H2-AA,TSKAN2,P1RB,LY9,AOAH,CXCL10,LRG1,CD4,CCL12,CSF2R8,H2-OA,MYO1G,IL2RG,BCL2A1B,H2-K1,IL12RB1,IGALS3,ITGAL,PSMB8,H2-D1,SPINT1,B2M,SLC11A1,BST2,TLR1,H2-T23,CTSS,A2M,FYB,C3AR1,CD84,ELF4,LAT,ITGB2,ST14,CD48,S100A9,OASL2,CCR2,S100A8,RAC2,SULT1A1,RASAL3,ITGB7,TLR2,HCK,NAIP2,GBP5,PLAC8,XDH,CSAR1,CD274,MTO13,CD300C,ICAM1,TLR7,CSF3R,TLR13,TTR,OAS2,NCF1,LYCARD,TNFAIP2,OAS1A,CC16,PLD4,CXCL16,FCGR1,LCP2,TNFSF13B,WAS,CD44,FCER1G,APOBEC3,TLR9,DLK1,RHOH,SP110,IL10RA,GALNT15,TRPV4,CH25H,P2RY6,FERMT3,AIF1,AV1,PTAFR,LCP1,CTSH,TSP0,POBEC1,ICOSL,IRF1,PTPN6,GSDMD,FERM13,ADCV7,TNFRSF18,UGT1A7,H2-M3,IJZF1,C2C,AIF1,LAG3,CYP26B1,CD86,VAV1,PIK3R5,PTAFR,HIF3A,LCP1,CAP6,DOC2,H2,HAVCR2,TNFAIP8L2,FAS,ALOX5AP,STAT1,PLCG2,BLNK,NUAK2,CD37,RAB32,CP,HK2,GFAP,CDC88B,CTSH,SEPT1,ASP,PTPN6,HIST1H4H,KCNK6,LP1,MAFB,PIK3CG,RFN213,PARP3,IKKBE,NCF2,PRKC,DIJL1A,CAPN3,FGD2,INPP5D,PARVG,MAFF,PTPN22,TREM2,BCR3,IGALS9,CD14,TGFB1,CARD9,NCAP1L,CD300A,TYROBP,MAP3K6,ACER2,CBR2,RHEDF2,RSAD2,PARP10,PRODH,XAF1,VWF,PLAU,TRIM21,IL6RA,PIK3R6,CCR5,LCK,BTK,CSF1R,IL1R1,IL4RA,IFIT3,CEBPA,ISG15,NFAM1,APOC1,RAB20,ECM1,CMTM7,TM6SF13,SP100,CD53,ADM,FOLH1,TGM2,GLIPR2,CTSD,DNASE2A,FAM107A,MT2,PIM1,GGTA1,ME,RTK,ITIH3,CCDC3,COL1A1,NPAS4,APLN,NGFR,ATFS,UGT8A,FOS,MYOC,KLK6,OMP,CYP2E1,HP,FBLN1,ARL11,EBI3,CCL9,PRR5L,ANG,CD180,LTBP2,TNFAIP3,CMKLR1,CASP4,S,TEAP4,GPR65,MNDAL,PTGER4,HKS,DOCK1,IL3RA,CYP4F18,RETNLG,XLR,ICOS,BATF2,GBGT1,GLRA4,ZC3H12A,CLE4N,B3GN13,UPP1,DUSP2,DOCK2,PLAUR
BP	GO:006928	movement of cell or subcellular component	1616	214	37	0.00283	0.173	0.023	2	CCL1,CCL5,CXCL9,CD74,CCL8,CXCL10,CCL12,MYO1G,IGALS3,BST2,C3AR1,ITGB2,ST14,S100A9,CCR2,S100A8,RAC2,ITGB7,HCK,CSAR1,CD274,MYO1F,ICAM1,CSF3R,LYCARD,CCL6,CXCL16,WAS,FCER1G,TRPV4,CH25H,P2RY6,FERMT3,AIF1,AV1,PTAFR,LCP1,CTSH,TSP0,RKCD,IL1A,PTPN22,IGALS9,NCAP1L,CD300A,PLAU,LCK,CSF1R,IL1R1,ECM1,SP100,HLF,PR2,COL1A1,MYOC,CCL9,PRR5L,ANG,CMKLR1,PTGER4,RETNLG,ZC3H12A,CCL17,HTR6,IL16
BP	GO:0048870	cell motility	1269	468	63	0.00000837	0.135	0.05	3	CCL1,CCL5,CXCL9,CD74,CCL8,CXCL10,CCL12,MYO1G,IGALS3,BST2,C3AR1,ITGB2,ST14,S100A9,CCR2,S100A8,RAC2,ITGB7,HCK,CSAR1,CD274,ICAM1,CSF3R,LYCARD,CCL6,CXCL16,WAS,FCER1G,TRPV4,CH25H,P2RY6,FERMT3,AIF1,AV1,PTAFR,LCP1,CTSH,TSP0,RKCD,IL1A,PTPN22,IGALS9,NCAP1L,CD300A,PLAU,LCK,CSF1R,IL1R1,ECM1,SP100,HLF,PR2,COL1A1,MYOC,CCL9,PRR5L,ANG,CMKLR1,PTGER4,RETNLG,ZC3H12A,CCL17,HTR6,IL16
BP	GO:0016477	cell migration	1154	468	62	4.76E-08	0.132	0.054	4	CCL1,CCL5,CXCL9,CD74,CCL8,CXCL10,CCL12,MYO1G,IGALS3,BST2,C3AR1,ITGB2,ST14,S100A9,CCR2,S100A8,RAC2,ITGB7,HCK,CSAR1,CD274,ICAM1,CSF3R,LYCARD,CCL6,CXCL16,FCER1G,TRPV4,CH25H,P2RY6,FERMT3,AIF1,AV1,PTAFR,LCP1,CTSH,TSP0,PRKC,DIJL1A,PTPN22,IGALS9,NCAP1L,CD300A,PLAU,LCK,CSF1R,IL1R1,ECM1,SP100,HLIPR2,DO1A1,MYOC,CCL9,PRR5L,ANG,CMKLR1,PTGER4,RETNLG,ZC3H12A,CCL17,HTR6,IL16
BP	GO:0050900	leukocyte migration	297	480	43	1.46E-19	0.09	0.145	5	CCL1,CCL5,CXCL9,CD74,CCL8,CXCL10,CCL12,MYO1G,IGALS3,C3AR1,ITGB2,S100A9,CCR2,S100A8,RAC2,ITGB7,CSAR1,ICAM1,CSF3R,LYCARD,CCL6,CXCL16,FCER1G,TRPV4,CH25H,AIF1,AV1,PTAFR,LCP1,PTPN22,IGALS9,NCAP1L,CD300A,IL1R1,ECM1,CCL9,ANG,CMKLR1,PTGER4,RETNLG,CCL17,IL16,CCL2
BP	GO:0097529	myeloid leukocyte migration	164	480	29	7.58E-15	0.06	0.177	6	CCL1,CCL5,CD74,CCL8,CXCL10,CCL12,IGALS3,C3AR1,S100A9,CCR2,S100A8,RAC2,CSAR1,CSF3R,CCL6,FCER1G,TRPV4,AIF1,AV1,PTAFR,LCP1,PTPN22,IGALS9,NCAP1L,CD300A,IL1R1,CCL9,CMKLR1,PTGER4,RETNLG,CCL17,CCL2
BP	GO:0097530	granulocyte migration	117	480	25	1.48E-14	0.052	0.214	7	CCL1,CCL5,CD74,CCL8,CCL12,IGALS3,C3AR1,S100A9,S100A8,RAC2,CSAR1,CSF3R,CCL6,FCER1G,TRPV4,VAV1,IL1A,NCAP1L,CD300A,IL1R1,CCL9,CMKLR1,PTGER4,CCL17,CC12
BP	GO:1990266	neutrophil migration	96	480	21	4.28E-12	0.044	0.219	8	CCL1,CCL5,CD74,CCL8,CCL12,IGALS3,C3AR1,S100A9,S100A8,RAC2,CSAR1,CSF3R,CCL6,FCER1G,VAV1,IL1A,NCAP1L,IL1R1,CCL9,CCL17,CCL2
BP	GO:0072677	eosinophil migration	14	480	5	0.0254	0.01	0.357	8	CCL5,IGALS3,CD300A,PTGER4,CCL2
BP	GO:1905517	macrophage migration	35	172	6	0.000868	0.035	0.171	7	CCL5,CCL12,IGALS3,C3AR1,TRPV4
BP	GO:0071674	mononuclear cell migration	80	201	12	2.64E-08	0.06	0.15	6	CCL1,CCL5,CCL8,CXCL10,CCL12,IGALS3,C3AR1,CCR2,CSAR1,CCL6,TRPV4,AIF1
BP	GO:0072676	lymphocyte migration	89	480	19	1.57E-10	0.04	0.213	6	CCL1,CCL5,CXCL9,CCL8,CXCL10,CCL12,MYO1G,CCR2,ITGB7,LYCARD,CCL6,CXCL16,CH25H,AIF1,IGALS9,FCM1,CCL9,CCL17,CCL2
BP	GO:0072678	T cell migration	50	338	11	0.00000608	0.033	0.22	7	CCL5,CXCL9,CXCL10,MYO1G,CCR2,ITGB7,LYCARD,CCL16,AIF1,IGALS9,ECM1
BP	GO:0045123	cellular extravasation	44	480	9	0.00114	0.019	0.205	6	ITGB2,CCR2,ITGB7,ICAM1,PTAFR,IL1A,IL1R1,PTGER4,CCL2
BP	GO:0001775	cell activation	948	339	81	4.75E-34	0.239	0.085	2	CLEC4D,CLEC4E,CCL5,CD74,FCGR4,H2-AB1,H2-AA,TSKAN2,P1RB,LY9,CXCL10,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,B2M,SLC11A1,TLR1,H2-T23,CD84,ELF4,LAT,ITGB2,CD48,CCR2,RAC2,RASAL3,TLR2,CD274,ICAM1,TLR7,PTAFR,D,LCP2,TNFSF13B,WAS,FCER1G,TLR9,RHOH,ST1,SP1,SASH3,ICOSL,IRF1,PTPN6,FERM13,H2-M3,IJZF1,AIF1,LAG3,CYP26B1,CD86,VAV1,PTAFR,LCP1,DOCK2,HAVCR2,TNFAIP8L2,FAS,PLCG2,BLNK,CD37,CDC88B,MAFB,PRKC,DIJL1A,CAPN3,INPP5D,PTPN22,IGALS9,NCAP1L,CD300A,TYROBP,RSAD2,VWF,PIK3R6,LCK,BTK,IL4RA,NFAM1,CMTM7
BP	GO:0045321	leukocyte activation	832	339	77	1.54E-34	0.227	0.093	3	CLEC4D,CLEC4E,CCL5,CD74,FCGR4,H2-AB1,H2-AA,TSKAN2,P1RB,LY9,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,B2M,SLC11A1,TLR1,H2-T23,CD84,ELF4,LAT,ITGB2,CD48,CCR2,RAC2,RASAL3,TLR2,CD274,ICAM1,TLR7,PTAFR,D,LCP2,TNFSF13B,WAS,FCER1G,TLR9,RHOH,ST1,SP1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,IJZF1,AIF1,LAG3,CYP26B1,CD86,VAV1,PTAFR,LCP1,DOCK2,HAVCR2,TNFAIP8L2,FAS,PLCG2,BLNK,CD37,CDC88B,MAFB,PRKC,DIJL1A,CAPN3,INPP5D,PTPN22,IGALS9,NCAP1L,CD300A,TYROBP,RSAD2,VWF,PIK3R6,LCK,BTK,IL4RA,NFAM1,CMTM7
BP	GO:0002274	myeloid leukocyte activation	154	326	31	9.75E-23	0.095	0.201	4	CCL5,FCGR4,TSKAN2,P1RB,SLC11A1,TLR1,CD84,LAT,CD48,CCR2,RAC2,TLR2,TLR7,PTAFR,LCP2,FCER1G,TLR9,RHOH,SP1,AIF1,CD86,PTAFR,DOCK2,HAVCR2,CD37,PRKC,DIJL1A,AL9,CD300A,TYROBP,BTK,IL4RA
BP	GO:0036230	granulocyte activation	27	296	8	0.00000555	0.027	0.296	5	CCL5,FCGR4,CCR2,FCER1G,PTAFR,PRKC,DIJL1A,TYROBP
BP	GO:0042119	neutrophil activation	21	296	7	0.0000234	0.024	0.333	6	CCL5,FCGR4,FCER1G,PTAFR,PRKC,DIJL1A,TYROBP
BP	GO:0042116	macrophage activation	54	326	10	0.000193	0.031	0.185	5	SLC11A1,TLR1,TLR2,TLR7,TLR9,AIF1,HAVCR2,IGALS9,TYROBP,IL4RA
BP	GO:0001774	microglial cell activation	17	201	4	0.0457	0.02	0.235	6	TLR2,TLR7,TLR9,AIF1
BP	GO:0045576	mast cell activation	54	487	13	0.00000382	0.027	0.241	5	CD84,LAT,CD48,RAC2,LCP2,FCER1G,RHOH,CD300A,BTK,IL4RA,LAT2,UNC13D,MILR1
BP	GO:0001773	myeloid dendritic cell activation	32	232	8	0.0000036	0.034	0.25	5	TSKAN2,P1RB,PTAFR,SP11,CD86,DOCK2,HAVCR2,CD37
BP	GO:0046649	lymphocyte activation	728	339	66	2.05E-28	0.195	0.091	4	CLEC4D,CLEC4E,CCL5,CD74,H2-AB1,H2-AA,LY9,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,B2M,SLC11A1,H2-T23,ELF4,LAT,ITGB2,CD48,CCR2,RAC2,RASAL3,CD274,ICAM1,LYCARD,TNFSF13B,WAS,FCER1G,TLR9,RHOH,ST1,SP1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,IJZF1,AIF1,LAG3,CYP26B1,CD86,VAV1,LCP1,DOCK2,HAVCR2,TNFAIP8L2,FAS,PLCG2,BLNK,CD37,CDC88B,MAFB,PRKC,DIJL1A,CAPN3,INPP5D,PTPN22,IGALS9,NCAP1L,CD300A,RSAD2,PIK3R6,LCK,BTK,IL4RA,NFAM1,CMTM7
BP	GO:0042110	T cell activation	436	326	54	2.65E-30	0.166	0.124	5	CLEC4D,CLEC4E,CCL5,CD74,H2-AB1,H2-AA,LY9,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,B2M,SLC11A1,H2-T23,ELF4,LAT,CD48,CCR2,RAC2,RASAL3,CD274,ICAM1,LYCARD,TNFSF13B,WAS,FCER1G,RHOH,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LAG3,CYP26B1,CD86,VAV1,LCP1,DOCK2,HAVCR2,TNFAIP8L2,FAS,PLCG2,BLNK,CD37,CDC88B,MAFB,PRKC,DIJL1A,CAPN3,INPP5D,PTPN22,IGALS9,NCAP1L,CD300A,RSAD2,PIK3R6,LCK,BTK,IL4RA,NFAM1,CMTM7
BP	GO:0046631	alpha-beta T cell activation	124	326	17	1.43E-08	0.052	0.137	6	CLEC4D,CLEC4E,CCL5,CD74,H2-AB1,H2-AA,LY9,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,B2M,SLC11A1,H2-T23,ELF4,LAT,CD48,CCR2,RAC2,RASAL3,CD274,ICAM1,LYCARD,TNFSF13B,WAS,FCER1G,RHOH,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LAG3,CYP26B1,CD86,VAV1,LCP1,DOCK2,HAVCR2,TNFAIP8L2,FAS,PLCG2,BLNK,CD37,CDC88B,MAFB,PRKC,DIJL1A,CAPN3,INPP5D,PTPN22,IGALS9,NCAP1L,CD300A,RSAD2,PIK3R6,LCK,BTK,IL4RA,NFAM1,CMTM7
BP	GO:0035710	CD4-positive, alpha-beta T cell activation	74	470	11	0.00142	0.023	0.149	7	LY9,IL2RG,CCR2,SASH3,IRF1,IGALS9,NCAP1L,RSAD2,IL4RA,PTGER4,BCL3
BP	GO:0042113	B cell activation	352	470	23	0.00701	0.049	0.065	5	CD74,H2-AB1,IL2RG,TNFSF13B,TLR9,SASH3,ICOSL,PTPN6,CD86,FAS,PLCG2,BLNK,PRKC,DIJL1A,NCAP1L,CD300A,BTK,NFAM1,CMTM7,CD180,TNFAIP3,LAT2,BCL3
BP	GO:0046651	lymphocyte proliferation	276	295	32	3.09E-17	0.108	0.116	5	CCL5,CD74,CD4,IL12RB1,IGALS3,ITGAL,SLC11A1,H2-T23,ELF4,CCR2,RAC2,RASAL3,CD274,LYCARD,TNFSF13B,ST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,DOCK2,HAVCR2,CDC88B,PRKC,DIJL1A,INPP5D,PTPN22,IGALS9,NCAP1L,CD300A

BP	GO:0042098	T cell proliferation	181	294	27	4.34E-17	0.092	0.149	6	CCL5,CD4,IL12RB1,ILGALS3,ITGAL,SLC11A1,H2-T23,ELF4,CCR2,RAC2,RASAL3,CD274,PPYCARD,TNFRSF13B,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,DOCK2,HAVCR2,CCDC88B,PTPN22,LGALS9,NCKAP1L
BP	GO:0050798	activated T cell proliferation	43	204	6	0.00844	0.029	0.14	7	IL12RB1,ITGAL,CD274,PPYCARD,ICOSL,CD86
BP	GO:0046633	alpha-beta T cell proliferation	31	286	8	0.0000143	0.028	0.258	7	H2-T23,ELF4,CCR2,RASAL3,IRF1,DOCK2,PTPN22,LGALS9
BP	GO:0002263	cell activation involved in immune response	233	487	33	5.73E-14	0.068	0.142	3	CLEC4D,CLEC4E,LY9,ITGAL,SLC11A1,CCR2,LAT2,CCR2,RAC2,ICAM1,PPYCARD,FCER1G,ICOSL,IRF1,H2-M3,CD86,PTAFR,LCP1,DOCK2,HAVCR2,PLCG2,LGALS9,CD300A,TYROBP,BTK,IL4RA,CD180,TNFAIP3,PTGER4,LAT2,BCL3,UNC13D,MILR1
BP	GO:0002366	leukocyte activation involved in immune response	231	487	33	4.4E-14	0.068	0.143	4	CLEC4D,CLEC4E,LY9,ITGAL,SLC11A1,CCR2,LAT2,CCR2,RAC2,ICAM1,PPYCARD,FCER1G,ICOSL,IRF1,H2-M3,CD86,PTAFR,LCP1,DOCK2,HAVCR2,PLCG2,LGALS9,CD300A,TYROBP,BTK,IL4RA,CD180,TNFAIP3,PTGER4,LAT2,BCL3,UNC13D,MILR1
BP	GO:0002285	lymphocyte activation involved in immune response	170	477	22	5.88E-08	0.046	0.129	5	CLEC4D,CLEC4E,LY9,ITGAL,SLC11A1,CCR2,ICAM1,FCER1G,ICOSL,IRF1,H2-M3,CD86,LCP1,HAVCR2,PLCG2,LGALS9,IL4RA,CD180,TNFAIP3,PTGER4,BCL3,UNC13D
BP	GO:0002286	T cell activation involved in immune response	101	220	13	8.26E-08	0.059	0.129	6	CLEC4D,CLEC4E,LY9,ITGAL,SLC11A1,CCR2,ICAM1,FCER1G,IRF1,H2-M3,CD86,LCP1,HAVCR2
BP	GO:0002291	T cell activation via T cell receptor contact with antigen bound to MHC	4	220	3	0.0123	0.014	0.75	7	ITGAL,ICAM1,HAVCR2
BP	GO:0002275	myeloid cell activation involved in immune response	69	487	16	5.07E-09	0.033	0.232	5	CD84,LAT,CCR2,RAC2,PPYCARD,FCER1G,PTAFR,DOCK2,HAVCR2,CD300A,TYROBP,BTK,IL4RA,LAT2,UNC13D,MILR1
BP	GO:0002279	mast cell activation involved in immune response	41	487	10	0.0000475	0.021	0.244	6	CD84,LAT,RAC2,FCER1G,CD300A,BTK,IL4RA,LAT2,UNC13D,MILR1
BP	GO:0008219	cell death	1826	379	67	0.00000946	0.177	0.037	2	H2M3,CD86,LCP1,HAVCR2
BP	GO:0012501	programmed cell death	1717	373	66	0.000000967	0.177	0.038	3	H2M3,CD86,LCP1,HAVCR2
BP	GO:0006915	apoptotic process	1690	373	62	0.0000221	0.166	0.037	4	H2M3,CD86,LCP1,HAVCR2
BP	GO:0071887	leukocyte apoptotic process	105	362	10	0.03	0.028	0.095	5	H2M3,CD86,LCP1,HAVCR2
BP	GO:0032940	secretion by cell	828	490	47	0.0000134	0.096	0.057	2	H2M3,CD86,LCP1,HAVCR2
BP	GO:0007154	cell communication	6673	492	222	4.07E-09	0.451	0.033	1	H2M3,CD86,LCP1,HAVCR2
BP	GO:0050789	regulation of biological process	11548	406	274	0.000000666	0.675	0.024	1	H2M3,CD86,LCP1,HAVCR2
BP	GO:0031341	regulation of cell killing	60	317	11	0.00000276	0.035	0.183	2	H2M3,CD86,LCP1,HAVCR2
BP	GO:0001910	regulation of leukocyte mediated cytotoxicity	52	317	11	0.000000539	0.035	0.212	3	H2M3,CD86,LCP1,HAVCR2
BP	GO:0043900	regulation of multi-organism process	326	484	38	1.34E-13	0.079	0.117	2	H2M3,CD86,LCP1,HAVCR2
BP	GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	180	484	21	0.00000158	0.043	0.117	3	H2M3,CD86,LCP1,HAVCR2
BP	GO:0050792	regulation of viral process	151	469	20	0.000000236	0.043	0.132	4	H2M3,CD86,LCP1,HAVCR2
BP	GO:1903900	regulation of viral life cycle	116	442	15	0.0000364	0.034	0.129	5	H2M3,CD86,LCP1,HAVCR2
BP	GO:0045069	regulation of viral genome replication	71	442	11	0.000505	0.025	0.155	6	H2M3,CD86,LCP1,HAVCR2
BP	GO:0048519	negative regulation of biological process	4599	496	166	7.63E-08	0.335	0.036	2	H2M3,CD86,LCP1,HAVCR2
BP	GO:0043901	negative regulation of multi-organism process	152	484	20	0.000000468	0.041	0.132	3	H2M3,CD86,LCP1,HAVCR2
BP	GO:0048525	negative regulation of viral process	78	469	15	0.00000026	0.032	0.192	4	H2M3,CD86,LCP1,HAVCR2
BP	GO:1903901	negative regulation of viral life cycle	62	442	12	0.00000993	0.027	0.194	5	H2M3,CD86,LCP1,HAVCR2
BP	GO:0045071	negative regulation of viral genome replication	41	442	11	0.00000107	0.025	0.268	6	H2M3,CD86,LCP1,HAVCR2

BP	GO:0032879	regulation of localization	2407	377	88	1.33E-08	0.233	0.037	2	HCAR2,CLEC4E,CCL1,CCL5,C3,CXCL9,CD74,CYBB,ITGAX,CXCL10,CD4,CCL12,IGALS3,B2M,SLC11A1,BST2,TLR1,H2-T23,CTSS,C3AR1,CD84,S100A9,CCR2,S100A8,RAC2,TLR2,HCK,CSAR1,CD274,CD300C2,CAM1,TLR7,PTCARD,GBP4,CXCL16,FCGR1,WAS,FCER1G,TLR9,TRPV4,P2RY6,HCL51,PTPN6,GSDMD,FERMT3,AIF1,PTAFR,LC1,DOCK2,HAVCR2,PLCG2,HK2,GFAP,CTSH,HVCN1,TSP0,PIK3CG,IKBKE,PRKCD,IL1A,CAPN3,PTPN22,TREM2,TIFAB,IGALS9,CD14,NCKAP1L,CD300A,RHBD2,RSAD2,PARP10,PLAU,CCR5,LCK,CSF1R,IL1R1,IL4RA,APOC1,RAB20,ECM1,TMEM173,SP100,GLIPR2,MERTK,COL1A1,APLN,NRFR,MYOC
BP	GO:0051049	regulation of transport	1716	341	66	0.00000016	0.194	0.038	3	HCAR2,CLEC4E,CCL5,C3,CXCL9,CD74,CYBB,ITGAX,CXCL10,CD4,CCL12,IGALS3,B2M,SLC11A1,BST2,TLR1,H2-T23,CTSS,CD84,S100A9,CCR2,S100A8,RAC2,TLR2,HCK,CD274,CD300C2,CAM1,TLR7,PTCARD,GBP4,FCGR1,FCER1G,TLR9,TRPV4,HCL51,PTPN6,GSDMD,PTAFR,LC1,DOCK2,HAVCR2,PLCG2,HK2,GFAP,HVCN1,TSP0,PIK3CG,IKBKE,PRKCD,IL1A,CAPN3,PTPN22,TIFAB,IGALS9,CD14,NCKAP1L,CD300A,RHBD2,RSAD2,PARP10,CSF1R,IL4RA,APOC1,RAB20,TMEM173,SP100
BP	GO:0051046	regulation of secretion	666	443	38	0.0000276	0.086	0.057	4	HCAR2,CLEC4E,CCL5,CD74,TLR1,H2-T23,CTSS,S100A9,CCR2,S100A8,RAC2,TLR2,CD274,CD300C2,PTCARD,FCER1G,TLR9,TRPV4,GSDMD,PTAFR,HAVCR2,IL1A,PTPN22,TIFAB,IGALS9,CD14,CD300A,RHBD2,RSAD2,CSEF1R,IL4RA,APLN,ANG,CASP4,PTGER4,CYP4F18,ZC3H12A,CLEC4N
BP	GO:0048583	regulation of response to stimulus	3221	480	178	1.46E-31	0.371	0.055	2	CLEC4D,CLEC4E,CCL1,CCL5,C3,CXCL9,CD74,CCL8,FCGR4,H2-AB1,TSPAN32,AOAH,NLRCS,CXCL10,ZBP1,LRG1,CD4,CCL12,MYO1G,H2-K1,IL12RB1,IGALS3,ITGAL,H2-D1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,CTSS,A2M,FYB,C3AR1,C4B,CD84,C1RA,IAT,CD48,S100A9,CCR2,S100A8,RAC2,RASAL3,TLR2,NAIP2,GBP5,THEMIS2,XDH,CSAR1,TLR12,C1QA,ICAM1,TLR7,TLR13,NCF1,PTCARD,PTPRC,GBP4,CCL6,C1S1,TRIM30A,FCGR1,LC2,TNFSF13B,WAS,CD44,C1QB,FCER1G,APOBEC3,TLR9,DLK1,RHOH,TRPV4,HCL51,C1QC,SASH3,ACPS,IRF1,PTPN6,TNFRSF18,H2-M3,CTSC,AIF1,LGALS3,CYP26B1,CD86,VAV1,PIK3RS,PTAFR,DOCK2,HAVCR2,TNFAIP8L2,S100A4,FAS,ALOX5AP,STAT1,LY86,PLCG2,BLNK,CD37,DDX60,CTSH,UNC93B1,PIK3CC,D,HXS8,RNF213,IKBKE,PRKCD,PIK3AP1,CAPN3,SERPING1,FGD2,INPP5D,PTPN22,PARP9,TREM2,IGALS9,CD14,CARD9,NCKAP1L,CD300A,FGFBP1,MAP3K6,RHBD2,RSAD2,TAP2,PLAU,KLHL6,IL6RA,PIK3R6,LPXN,LCK,BTK,CSF1R,IL1R1,IL4RA,NFAM1,ECM1,TMEM173,SP100,ADM,TGM2,GLIPR2,CYTH4,CCDC3,COL1A1,MYOC,KLK6,FCRL5,CFB,CCL9,PRR5L,CD180,TNFAIP3,CMKLR1,CASP4,PTGER4,SIGLECE,ZC3H12A,CLEC4N,DUSP2,PLAU,LA,T2,CCL17,HTR6,MMP2,CD247,F10,IL16,BCL3,CNMD,CHRHR2,C,GNPR35,UNC13D,SPN,CCL2
BP	GO:0002831	regulation of response to biotic stimulus	118	479	18	0.000000276	0.038	0.153	3	CCL5,TSPAN32,IL12RB1,PTCARD,GBP4,APOBEC3,HAVCR2,LY86,CD37,DDX60,DHX58,PTPN22,IGALS9,TMEM173,CD180,TNFAIP3,ZC3H12A,SPN
BP	GO:0060759	regulation of response to cytokine stimulus	89	366	12	0.0000921	0.033	0.135	3	CCL5,CD74,NLRCS,ZBP1,IRF7,PTCARD,PTPN6,PARP9,TREM2,IL1R1,ECM1,CCDC3
BP	GO:0080134	regulation of response to stress	1054	324	66	2.34E-20	0.204	0.063	3	CCL5,C3,CD74,TSPAN32,AOAH,NLRCS,ZBP1,IL12RB1,IRF7,TLR1,H2-T23,CTSS,A2M,S100A9,CCR2,S100A8,TLR2,GBP5,XDH,TLR12,TLR7,TLR13,NCF1,PTCARD,GBP4,TRIM30A,FCGR1,CD44,FCER1G,APOBEC3,TLR9,TRPV4,ACPS,IRF1,PTPN6,TNFRSF18,H2-M3,LAG3,CD86,VAV1,HAVCR2,TNFAIP8L2,FAS,ALOX5AP,PLCG2,CD37,DDX60,UNC93B1,PIK3CG,DHX58,PRKCD,PIK3AP1,CAPN3,SERPING1,FGD2,PTPN22,PARP9,IGALS9,CD14,CARD9,CD300A,RSAD2,PLAU,PIK3R6,BTK,IL1R1
BP	GO:0031347	regulation of defense response	468	443	67	5.62E-34	0.151	0.143	4	CCL5,C3,CD74,TSPAN32,AOAH,NLRCS,ZBP1,IL12RB1,IRF7,TLR1,H2-T23,CTSS,A2M,S100A9,CCR2,S100A8,TLR2,GBP5,TLR12,TLR7,TLR13,PTCARD,GBP4,TRIM30A,FCGR1,FCER1G,APOBEC3,TLR9,TRPV4,ACPS,IRF1,PTPN6,TNFRSF18,H2-M3,LAG3,CD86,VAV1,HAVCR2,TNFAIP8L2,ALOX5AP,PLCG2,CD37,DDX60,UNC93B1,PIK3CG,DHX58,PIK3AP1,SERPING1,PTPN22,PARP9,IGALS9,CD14,CARD9,CD300A,RSAD2,PIK3R6,BTK,IL1R1,TMEM173,TGM2,CD180,TNFAIP3,CASP4,PTGER4,SIGLECE,ZC3H12A,CLEC4N
BP	GO:0032101	regulation of response to external stimulus	610	492	61	1.75E-19	0.124	0.1	3	CCL1,CCL5,C3,CXCL9,CD74,TSPAN32,AOAH,CXCL10,CCL12,IL12RB1,CTSS,A2M,C3AR1,S100A9,CCR2,S100A8,RAC2,TLR2,GBP5,CSAR1,PTCARD,GBP4,FCGR1,FCER1G,APOBEC3,TLR9,TRPV4,ACPS,TNFRSF18,AIF1,HAVCR2,TNFAIP8L2,ALOX5AP,LY86,CD37,DDX60,PIK3CG,DHX58,PRKCD,PIK3AP1,CAPN3,SERPING1,PTPN22,IGALS9,NCKAP1L,PLAU,BTK,IL1R1,TMEM173,TGM2,CD180,TNFAIP3,CMKLR1,CASP4,PTGER4,SIGLECE,ZC3H12A,IL16,SPN,CCL2,MA51
BP	GO:0050727	regulation of inflammatory response	249	492	32	4.19E-12	0.065	0.129	4	C3,AOAH,CTSS,A2M,S100A9,CCR2,S100A8,TLR2,GBP5,PTCARD,FCGR1,FCER1G,TLR9,TRPV4,ACPS,TNFRSF18,TNFAIP8L2,ALOX5AP,PIK3CG,PIK3AP1,SERPING1,IGALS9,BTK,IL1R1,TGM2,TNFAIP3,CASP4,PTGER4,SIGLECE,ZC3H12A,SPN,MA51
BP	GO:0002673	regulation of acute inflammatory response	50	322	8	0.00195	0.025	0.16	5	C3,A2M,FCGR1,FCER1G,ALOX5AP,PIK3CG,SERPING1,BTK
BP	GO:0048585	negative regulation of response to stimulus	1301	479	54	0.0117	0.113	0.042	3	CCL5,CD74,AOAH,NLRCS,CCL12,IGALS3,BST2,H2-T23,A2M,CD84,CCR2,RASAL3,XDH,ICAM1,PTCARD,TRIM30A,CD44,TLR9,DLK1,RHOH,ACPS,IRF1,PTPN6,TNFRSF18,AIF1,CYP26B1,HAVCR2,TNFAIP8L2,STAT1,DHX58,RNF213,PRKCD,SERPING1,INPP5D,PTPN22,IGALS9,CD300A,PLAU,LPXN,IL4RA,ECM1,ADM,CCDC3,MYOC,PRR5L,TNFAIP3,PTGER4,SIGLECE,ZC3H12A,DUSP2,PLAU,CNMD,CHRHR2,SPN,IGAP2,RAPSN,MA51
BP	GO:0031348	negative regulation of defense response	154	479	16	0.000809	0.033	0.104	4	AOAH,NLRCS,H2-T23,A2M,ACPS,TNFRSF18,HAVCR2,TNFAIP8L2,DHX58,SERPING1,IGALS9,TNFAIP3,PTGER4,SIGLECE,ZC3H12A,SPN
BP	GO:0040012	regulation of locomotion	776	422	40	0.000466	0.095	0.052	2	CCL1,CCL5,CXCL9,CD74,CXCL10,CCL12,IGALS3,BST2,C3AR1,CCR2,RAC2,CSAR1,CD274,ICAM1,PTCARD,CXCL16,WAS,TRPV4,P2RY6,FERMT3,AIF1,PTAFR,CTSH,IL1A,PTPN22,IGALS9,NCKAP1L,CD300A,PLAU,TRIM21,CSF1R,IL1R1,ECM1,SP100,GLIPR2,COL1A1,MYOC,PRR5L,CMKLR1,PTGER4
BP	GO:0050920	regulation of chemotaxis	173	122	10	0.000142	0.082	0.058	3	CCL1,CCL5,CXCL9,CD74,CXCL10,CCL12,C3AR1,CCR2,RAC2,CSAR1
BP	GO:0023051	regulation of signaling	2741	492	116	1.13E-08	0.236	0.042	2	HCAR2,CCL1,CCL5,C3,CXCL9,CD74,CXCL8,NLRCS,CXCL10,ZBP1,LRG1,CD4,CCL12,IGALS3,ITGAL,IRF7,BST2,TLR1,LAT,S100A9,S100A8,RASAL3,TLR2,NAIP2,XDH,CSAR1,CAM1,TRPV4,HCL51,C1QC,SP1,SASH3,IRF1,PTPN6,H2-M3,NGP,CYP26B1,CD86,HAVCR2,FAS,STAT1,GFAP,CTSH,PTSO,HIST1H4H,MAFB,IL1A,CAPN3,INPP5D,MAFF,TIFAB,IGALS9,NCKAP1L,TYROBP,PIK3R6,LCK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,ECM1,SP100,CD53,ADM,GLIPR2,CTSZ,PIM1,CCDC3,COL1A1,NGFR,FOS,MYOC,KLK6
BP	GO:0050793	regulation of developmental process	2275	379	75	0.0000921	0.198	0.033	2	C3,CXCL9,CD74,CCL8,IF204,H2-AA,CYBB,CXCL10,LRG1,CD4,CCL12,H2-OA,IL2RG,H2-K1,H2-D1,SPIN1,B2M,C3AR1,ITGB2,CCR2,TLR2,HCK,PLAC8,XDH,CSAR1,ICAM1,CSF3R,TNFRSF13B,TRPV4,HCL51,C1QC,SP1,SASH3,IRF1,PTPN6,H2-M3,NGP,CYP26B1,CD86,HAVCR2,FAS,STAT1,GFAP,CTSH,PTSO,HIST1H4H,MAFB,IL1A,CAPN3,INPP5D,MAFF,TIFAB,IGALS9,NCKAP1L,TYROBP,PIK3R6,LCK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,ECM1,SP100,CD53,ADM,GLIPR2,CTSZ,PIM1,CCDC3,COL1A1,NGFR,FOS,MYOC,KLK6
BP	GO:0002682	regulation of immune system process	1188	340	121	4.73E-63	0.356	0.102	2	HCAR2,CLEC4D,CLEC4E,CCL1,CCL5,C3,CXCL9,CD74,FCGR4,H2-AB1,H2-AA,TSPAN32,NLRCS,CXCL10,ZBP1,CD4,CCL12,H2-OA,MYO1G,IL2RG,H2-K1,IL12RB1,IGALS3,ITGAL,H2-D1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,CTSS,A2M,FYB,C3AR1,C4B,CD84,C1RA,IAT,CD48,CCR2,RAC2,RASAL3,TLR2,GBP5,THEMIS2,CSAR1,TLR12,CD274,C1QA,ICAM1,TLR7,CSF3R,TLR13,PTCARD,PTPRC,GBP4,C1S1,TIFAB,IGALS9,FCGR1,LC2,TNFSF13B,WAS,C1QB,FCER1G,APOBEC3,TLR9,TRPV4,HCL51,C1C,C1S1,SP1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LGALS3,CYP26B1,CD86,VAV1,PTAFR,HAVCR2,TNFAIP8L2,FAS,STAT1,PLCG2,CD37,DDX60,CCDC88B,CTSH,UNC93B1,HIST1H4H,MAFB,DHX58,IL1A,PIK3AP1,SERPING1,INPP5D,PTPN22,PARP9,TREM2,IGALS9,CD14,CARD9,NCKAP1L,CD300A,TYROBP,RSAD2,TAP2,KLHL6,PIK3R6,LPXN,LCK,BTK,IL1R1,IL4RA,ISG15,NFAM1,ECM1,TMEM173
BP	GO:0002577	regulation of antigen processing and presentation	19	283	7	0.00000759	0.025	0.368	3	CD74,H2-AB1,H2-OA,SLC11A1,PTCARD,WAS,TREM2
BP	GO:0002697	regulation of immune effector process	300	340	42	2.76E-24	0.124	0.14	3	CCL5,C3,CD74,TSPAN32,H2-K1,IL12RB1,H2-D1,B2M,BST2,H2-T23,A2M,CD84,CCR2,RAC2,PTCARD,GBP4,FCGR1,WAS,FCER1G,APOBEC3,TLR9,SASH3,IRF1,PTPN6,H2-M3,LAG3,VAV1,PTAFR,HAVCR2,CD37,DDX60,DHX58,SERPING1,PTPN22,IGALS9,CD300A,RSAD2,TAP2,PIK3R6,BTK,IL4RA,TMEM173
BP	GO:0002703	regulation of leukocyte mediated immunity	161	326	27	2.76E-17	0.083	0.168	4	C3,H2-K1,H2-D1,B2M,BST2,H2-T23,CD84,CCR2,RAC2,FCGR1,WAS,FCER1G,TLR9,SASH3,PTPN6,H2-M3,LAG3,VAV1,PTAFR,HAVCR2,IGALS9,CD300A,RSAD2,TAP2,PIK3R6,BTK,IL4RA
BP	GO:0002706	regulation of lymphocyte mediated immunity	124	322	19	7.73E-11	0.059	0.153	5	C3,H2-K1,H2-D1,B2M,H2-T23,FCGR1,WAS,FCER1G,SASH3,PTPN6,H2-M3,LAG3,VAV1,HAVCR2,IGALS9,RSAD2,TAP2,PIK3R6,BTK
BP	GO:0002886	regulation of myeloid leukocyte mediated immunity	39	326	10	0.000000624	0.031	0.256	5	C3,CD84,CCR2,RAC2,FCGR1,FCER1G,PTAFR,CD300A,BTK,IL4RA
BP	GO:0002700	regulation of production of molecular mediator of immune response	118	326	11	0.00482	0.034	0.093	4	CD74,B2M,BST2,H2-T23,FCER1G,TLR9,SASH3,CD37,PTPN22,RSAD2,IL4RA
BP	GO:0043300	regulation of leukocyte degranulation	38	326	8	0.000227	0.025	0.211	4	CD84,CCR2,RAC2,FCER1G,PTAFR,IGALS9,CD300A,IL4RA
BP	GO:0050688	regulation of defense response to virus	63	479	13	0.00000246	0.027	0.206	4	CCL5,TSPAN32,IL12RB1,PTCARD,GBP4,APOBEC3,CD37,DDX60,DHX58,PTPN22,TMEM173,ZC3H12A,SPN
BP	GO:0002683	negative regulation of immune system process	391	326	36	7.04E-15	0.11	0.092	3	CD74,TSPAN32,NLRCS,CCL12,H2-OA,BST2,H2-T23,A2M,CD84,CCR2,CD274,TRIM30A,FCER1G,TLR9,C1QC,LST1,IRF1,PTPN6,H2-M3,LAG3,CD86,HAVCR2,TNFAIP8L2,FAS,CD37,HIST1H4H,MAFB,DHX58,SERPING1,INPP5D,PTPN22,IGALS9,CD300A,LPXN,BTK,IL4RA
BP	GO:0002698	negative regulation of immune effector process	106	326	13	0.0000197	0.04	0.123	4	BST2,H2-T23,A2M,CD84,CCR2,IRF1,PTPN6,HAVCR2,DHX58,SERPING1,IGALS9,CD300A,IL4RA
BP	GO:0002704	negative regulation of leukocyte mediated immunity	44	295	8	0.000354	0.027	0.182	5	BST2,H2-T23,CD84,CCR2,PTPN6,HAVCR2,IGALS9,CD300A

BP	GO:0043301	negative regulation of leukocyte degranulation	11	295	4	0.0307	0.014	0.364	5	CD84,CCR2,IGALS9,CD300A
BP	GO:0050776	regulation of immune response	693	340	84	2.42E-47	0.247	0.121	3	CLEC4D,CLEC4E,C3,CD74,FCGR4,H2-AB1,NLRCS,ZBP1,CD4,MYO1G,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,A2M,FYB,C3AR1,C4B,CD84,C1RA,CD48,CCR2,RAC2,TLR2,GBP5,THEMIS2,CSAR1,TLR12,C1QA,TLR7,TLR13,PCYCARD,PTPRC,C151,TRIM30A,FCGR1,ICP2,TNFSF13B,WAS,C1QB,FCER1G,TLR8,C1QC,SASH3,IRF1,PTPN6,H2-M3,LAG3,CD86,VAV1,PTAFR,HAVCR2,PLCG2,CD37,DDX60,CTSH,LUNC93B1,DHX58,PIK3AP1,SERPING1,INPP5D,PTPN22,PARR9,IGALS9,CD14,CARD9,NCKAP1L,CD300A,RSAD2,TAP2,KLHL6,PIK3R6,LPXN,LCK,BTK,IL4RA,NFAM1,ECM1,TMEM173
BP	GO:0002828	regulation of type 2 immune response	28	338	6	0.0114	0.018	0.214	4	CD74,CCR2,IRF1,RSAD2,IL4RA,ECM1
BP	GO:0002819	regulation of adaptive immune response	140	326	27	5.78E-19	0.083	0.193	4	C3,CD74,H2-AB1,CD4,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,IRF7,H2-T23,CD48,CCR2,PCYCARD,FCGR1,TNFSF13B,WAS,FCER1G,SASH3,IRF1,PTPN6,H2-M3,HAVCR2,RSAD2,TAP2,BTK,IL4RA
BP	GO:0002822	regulation of adaptive immune response based on somatic recombination	129	326	23	5.31E-15	0.071	0.178	5	C3,H2-AB1,CD4,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,H2-T23,CCR2,FCGR1,TNFSF13B,WAS,FCER1G,SASH3,IRF1,PTPN6,H2-M3,HAVCR2,RSAD2,TAP2,BTK,IL4RA
BP	GO:0002825	regulation of T helper 1 type immune response	26	326	7	0.000243	0.021	0.269	6	H2-AB1,IL12RB1,SLC11A1,CCR2,IRF1,HAVCR2,IL4RA
BP	GO:0002715	regulation of natural killer cell mediated immunity	51	305	9	0.000984	0.03	0.176	6	H2-K1,H2-D1,B2M,H2-T23,WAS,SASH3,H2-M3,RSAD2,TAP2
BP	GO:0001914	regulation of T cell mediated cytotoxicity	20	305	6	0.000707	0.02	0.3	7	H2-K1,H2-D1,B2M,H2-T23,H2-M3,TAP2
BP	GO:0050777	negative regulation of immune response	121	326	15	0.00000113	0.046	0.124	4	NLRCS,BST2,H2-T23,A2M,CD84,CCR2,IRF1,PTPN6,HAVCR2,DHX58,SERPING1,INPP5D,IGALS9,CD300A,IL4RA
BP	GO:0045088	regulation of innate immune response	220	340	38	3.65E-25	0.112	0.173	4	CD74,NLRCS,ZBP1,IRF7,TLR1,H2-T23,A2M,TLR2,GBP5,TLR12,TLR7,TLR13,PCYCARD,TRIM30A,FCER1G,TLR9,IRF1,PTPN6,H2-M3,LAG3,CD86,VAV1,HAVCR2,PLCG2,DDX60,LUNC93B1,DHX58,PIK3AP1,SERPING1,PTN22,PARR9,CD300A,RSAD2,PIK3R6,TMEM173
BP	GO:0045824	negative regulation of innate immune response	39	412	8	0.0016	0.019	0.205	5	NLRCS,H2-T23,A2M,HAVCR2,DHX58,SERPING1,IGALS9,TNFAIP3
BP	GO:0002709	regulation of T cell mediated immunity	35	317	7	0.00183	0.022	0.2	5	H2-T23,H2-M3,LAG3,VAV1,HAVCR2,IGALS9,PIK3R6
BP	GO:0004269	regulation of natural killer cell mediated cytotoxicity	34	317	7	0.00148	0.022	0.206	6	H2-T23,H2-M3,LAG3,VAV1,HAVCR2,IGALS9,PIK3R6
BP	GO:0030155	regulation of cell adhesion	600	326	47	2.51E-17	0.144	0.078	2	CCL5,CD74,H2-AB1,H2-AA,CD4,H2-0A,IL2RG,IL12RB1,IGALS3,ITGAL,H2-T23,LAT,CCR2,RAC2,RASAL3,CD274,ICAM1,PCYCARD,TNFSF13B,CD44,TRPV4,SASH3,ICOSL,IRF1,PTPN6,FERM3,H2-M3,AIF1,LAG3,CYP26B1,CD86,VAV1,PTAFR,HAVCR2,TNFAIP82,CDC88B,PRKCD,PTP,N22,IGALS9,NCKAP1L,CD300A,ACER2,PLAU,PIK3R6,LPXN,LCK,IL4RA
BP	GO:0033628	regulation of cell adhesion mediated by integrin	36	320	7	0.00239	0.022	0.194	3	CCL5,PTPN6,FERM3,NCKAP1L,ACER2,PLAU,LPXN
BP	GO:0022407	regulation of cell-cell adhesion	359	326	43	7.07E-23	0.132	0.12	3	CCL5,CD74,H2-AB1,H2-AA,CD4,H2-0A,IL2RG,IL12RB1,IGALS3,ITGAL,H2-T23,LAT,CCR2,RAC2,RASAL3,CD274,ICAM1,PCYCARD,TNFSF13B,CD44,TRPV4,SASH3,ICOSL,IRF1,PTPN6,FERM3,H2-M3,AIF1,LAG3,CYP26B1,CD86,PTAFR,HAVCR2,TNFAIP82,CDC88B,PRKCD,PTPN22,IGALS9,NCKAP1L,CD300A,PIK3R6,LCK,IL4RA
BP	GO:1903037	regulation of leukocyte cell-cell adhesion	285	326	40	9.45E-24	0.123	0.14	4	CCL5,CD74,H2-AB1,H2-AA,CD4,H2-0A,IL2RG,IL12RB1,IGALS3,ITGAL,H2-T23,LAT,CCR2,RAC2,RASAL3,CD274,ICAM1,PCYCARD,TNFSF13B,CD44,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LAG3,CYP26B1,CD86,PTAFR,HAVCR2,TNFAIP82,CDC88B,PTPN22,IGALS9,NCKAP1L,CD300A,PIK3R6,LCK,IL4RA
BP	GO:0032844	regulation of homeostatic process	474	377	24	0.00877	0.064	0.051	2	H2AR2,CXCL9,CD74,FCGR4,CXCL10,CD4,B2M,FCER1G,TRPV4,SP11,PTPN6,STAT1,PLCG2,TSP0,MAFB,CAPN3,INPP5D,NCKAP1L,CCRS,LCK,CSF1R,ISG15,APLN,MYOC
BP	GO:0051239	regulation of multicellular organismal process	2551	379	114	5.61E-19	0.301	0.045	1	H2AR2,CLEC4E,CCL5,C3,CD74,IFI204,FCGR4,H2-AA,CYBB,LV9,CXCL10,LRG1,CD4,H2-0A,IL2RG,H2-K1,IL12RB1,H2-D1,SPINT1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,C3AR1,CD84,ITGB2,S100A9,CCR2,TLR2,GBP5,PLAC8,XDH,CSAR1,LTB,CD274,CD300C,ICAM1,TLR7,CSF3R,NCF1,PCYCARD,GBP4,TRIM30A,FCER1G,H2-ICQ,SP11,SASH3,ADCP5,ICOSL,IRF1,PTPN6,GSDMD,H2-M3,NGP,AIF1,LAG3,CYP26B1,CD86,PTAFR,HAVCR2,FAS,STAT1,PLCG2,DDX60,GFAP,CCDC88B,TGIF1,H4H,MAFB,DHX58,PRKCD,IL1A,CAPN3,SERPING1,INPP5D,MAFF,PTPN22,TIFAB,IGALS9,CD14,CARD9,NCKAP1L,TYROBP,RSAD2,PLAU,L6RA,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,APOC1,ECM1,TMEM173,SP100,ADM,GUPR2,CTSZ,PIM1,MERTK,COL1A1,APLN,NGFR,FOS,KLK6
BP	GO:2000026	regulation of multicellular organismal development	1699	379	62	0.0000503	0.164	0.036	2	C3,CD74,H2-AA,CYBB,CXCL10,LRG1,CD4,H2-0A,IL2RG,H2-K1,H2-D1,SPINT1,B2M,C3AR1,ITGB2,CCR2,TLR2,XDH,CSAR1,CSF3R,TRPV4,HCL5,C1QC,SP11,SASH3,IRF1,PTPN6,H2-M3,NGP,CYP26B1,CD86,HAVCR2,FAS,STAT1,GFAP,TSPO,HIST1H4H,MAFB,IL1A,CAPN3,INPP5D,MAFF,TIFAB,IGALS9,NCKAP1L,TYROBP,PIK3R6,LCK,IL4RA,ISG15,NFAM1,ECM1,SP100,ADM,GUPR2,CTSZ,PIM1,COL1A1,NGFR,FOS,KLK6
BP	GO:0051241	negative regulation of multicellular organismal process	1027	480	63	3.08E-10	0.131	0.061	2	CD74,CXCL10,H2-K1,H2-D1,B2M,SLC11A1,BST2,CD84,CCR2,PLAC8,XDH,CD274,NCF1,PCYCARD,GBP4,TRIM30A,TLR9,TRPV4,C1QC,ACPS,IRF1,H2-M3,NGP,LAG3,CD86,HAVCR2,STAT1,GFAP,TSPO,HIST1H4H,MAFB,DHX58,PRKCD,CAPN3,SERPING1,INPP5D,PTPN22,TIFAB,IGALS9,NCKAP1L,PLAU,IL6RA,BTK,IL4RA,APOC1,ECM1,SP100,ADM,CTSZ,MERTK,APLN,NGFR,TNFAIP3,CMKLR1,PTGER4,ZC3H12A,STAB1,BCL3,NPPC,CNMD,CRHR2,GPR35,CCL2
BP	GO:0001817	regulation of cytokine production	534	480	68	4.37E-29	0.142	0.127	2	CLEC4E,CCL5,C3,CD74,CYBB,LV9,IL12RB1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,C3AR1,CD84,CCR2,TLR2,GBP5,CSAR1,LTB,CD274,CD300C2,TLR7,PCYCARD,GBP4,TRIM30A,FCER1G,TLR9,TRPV4,SASH3,ADCP5,ICOSL,IRF1,GSDMD,H2-M3,LAG3,PTAFR,HAVCR2,PLCG2,DDX60,CDC88B,TSP0,DHX58,IL1A,INPP5D,PTPN22,IGALS9,CD14,CARD9,NCKAP1L,RSAD2,IL6RA,BTK,CSF1R,IL4RA,ISG15,NFAM1,TMEM173,MERTK,TNFAIP3,CMKLR1,CASP4,PTGER4,ZC3H12A,CLEC4E,BCL3,SPN,CCL2
BP	GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	110	480	23	5.42E-13	0.048	0.209	3	CYBB,TLR1,H2-T23,CCR2,CD274,PCYCARD,TRIM30A,FCER1G,TLR9,SASH3,ADCP5,PTAFR,HAVCR2,TSP0,PTPN22,IGALS9,CD14,CARD9,TNFAIP3,ZC3H12A,BCL3,SPN,CCL2
BP	GO:0032680	regulation of tumor necrosis factor production	108	480	22	4.44E-12	0.046	0.204	4	CYBB,TLR1,H2-T23,CCR2,PCYCARD,TRIM30A,FCER1G,TLR9,SASH3,ADCP5,PTAFR,HAVCR2,TSP0,PTPN22,IGALS9,CD14,CARD9,TNFAIP3,ZC3H12A,BCL3,SPN,CCL2
BP	GO:0032479	regulation of type I interferon production	62	340	12	0.000000538	0.035	0.194	3	IRF7,TLR7,PCYCARD,GBP4,TLR9,IRF1,HAVCR2,PLCG2,DHX58,PTPN22,CD14,TMEM173
BP	GO:0032647	regulation of interferon-alpha production	22	281	6	0.00082	0.021	0.273	4	IRF7,TLR7,GBP4,TLR9,HAVCR2,PTPN22
BP	GO:0032653	regulation of Interleukin-10 production	43	286	7	0.004	0.024	0.163	3	TLR2,CD274,PCYCARD,FCER1G,TLR9,SASH3,IGALS9
BP	GO:0032652	regulation of interleukin-1 production	56	442	8	0.0469	0.018	0.143	3	PCYCARD,ACPS,GSDMD,HAVCR2,IGALS9,TNFAIP3,CASP4,ZC3H12A
BP	GO:0032642	regulation of chemokine production	69	326	13	7.82E-08	0.04	0.188	3	CCL5,CD74,TLR2,TLR7,PCYCARD,TLR9,TRPV4,HAVCR2,IL1A,IGALS9,IL6RA,CSF1R,IL4RA
BP	GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	9	14	2	0.043	0.143	0.222	4	CCL5,CD74
BP	GO:0032649	regulation of interferon-gamma production	94	330	14	0.000000429	0.042	0.149	3	IL12RB1,SLC11A1,CCR2,CD274,TLR7,PCYCARD,TLR9,SASH3,H2-M3,HAVCR2,PTPN22,IGALS9,CD14,ISG15
BP	GO:0032675	regulation of interleukin-6 production	109	313	17	8.54E-10	0.054	0.156	3	TLR1,TLR2,TLR7,PCYCARD,TRIM30A,FCER1G,TLR9,TRPV4,PTAFR,HAVCR2,IL1A,INPP5D,PTPN22,IGALS9,CARD9,NCKAP1L,IL6RA
BP	GO:0001818	negative regulation of cytokine production	201	470	24	2.96E-08	0.051	0.119	3	SLC11A1,BST2,CD84,CD274,PCYCARD,GBP4,TRIM30A,TLR9,ACPS,LAG3,HAVCR2,TSP0,DHX58,INPP5D,PTPN22,IGALS9,NCKAP1L,BTK,MERTK,TNFAIP3,CMKLR1,PTGER4,ZC3H12A,BCL3
BP	GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	46	470	9	0.00143	0.019	0.196	4	CD274,TRIM30A,ACPS,HAVCR2,TSP0,PTPN22,TNFAIP3,ZC3H12A,BCL3
BP	GO:0032720	negative regulation of tumor necrosis factor production	44	470	8	0.0112	0.017	0.182	5	TRIM30A,ACPS,HAVCR2,TSP0,PTPN22,TNFAIP3,ZC3H12A,BCL3
BP	GO:0032715	negative regulation of interleukin-6 production	40	442	8	0.00336	0.018	0.2	4	TRIM30A,TLR9,HAVCR2,INPP5D,PTPN22,NCKAP1L,TNFAIP3,ZC3H12A
BP	GO:0002718	regulation of cytokine production involved in immune response	62	182	6	0.0383	0.033	0.097	3	CD74,B2M,BST2,FCER1G,TLR9,SASH3
BP	GO:0048518	positive regulation of biological process	5180	379	184	4.63E-23	0.485	0.036	1	H2AR2,CLEC4E,CCL1,CCL5,C3,CXCL9,CD74,CCL8,IFI204,FCGR4,H2-AB1,LGN2,H2-AA,CYBB,ITGAX,LV9,NLRCS,CXCL10,ZBP1,LRG1,CD4,CCL12,MYO1G,IL2RG,H2-K1,IL12RB1,IGALS3,ITGAL,H2-D1,SPINT1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,CTSS,A2M,FYB,C3AR1,C4B,CD84,ELF4,C1RA,LAT,ITGB2,S100A9,CCR2,S100A8,RAC2,RASAL3,TLR2,HCK,NAIP2,GBP5,PLAC8,THEMIS2,XDH,CSAR1,LTB,TLR12,CD274,C1QA,CD300C2,ICAM1,TLR7,TLR13,NCF1,PCYCARD,PTPRC,CCL6,C151,TRIM30A,CXCL16,FCGR1,ICP2,TNFSF13B,WAS,CD44,C1QB,FCER1G,TLR9,SP110,TRPV4,P2RY6,HCL51,C1QC,SP11,SASH3,ADPBE1,C1QSI,IRF1,PTPN6,GSDMD,FERM3,TADCY7,TNFSF1B,H2-M3,CTSS,AIF1,LAG3,CYP26B1,CD86,VAV1,PIK3R5,PTAFR,HF3A,LCF3,DOC2B,HAVCR2,CD300A,FAS,ALOX5,STAT1,LV96,BLX2,ILK,CD37,H2,DDX60,GFAP,CDC88B,CTSH,LUNC93B1,TSP0,HIST1H4H,MAFB,PIK3CG,DHX58,PARR9,WKKE,PRKCD,IL1A,PIK3AP1,CAPN3,SERPING1,FGD2,INPP5D,PTPN22,TREM2,BIRC3,IGALS9,CD14,CARD9,NCKAP1L,CD300A,FGFBP1,MAP3K6,ACER2,RSAD2,TAP2,PLAU,TRIM21,KLHL6,IL6RA,PIK3R6,LPXN,LCK,BTK,CSF1R,IL1R1,IL4RA,CEBPA,ISG15,NFAM1,OSMR,ECM1,TMEM173,CD53,ADM,TGM2,GUPR2,CTSZ,PIM1,MERTK,CCDC3,COL1A1,NPASA,APLN,NGFR,ATF5,FOS,MYOC,KLK6
BP	GO:0051240	positive regulation of multicellular organismal process	1447	375	78	1.84E-16	0.208	0.054	2	H2AR2,CLEC4E,CCL5,C3,CD74,IFI204,FCGR4,H2-AB1,B2M,SLC11A1,IRF7,TLR1,H2-T23,C3AR1,ITGB2,S100A9,CCR2,TLR2,GBP5,CSAR1,LTB,CD274,CD300C2,ICAM1,TLR7,PCYCARD,FCER1G,TLR9,TRPV4,HCL51,SASH3,ICOSL,IRF1,GSDMD,H2-M3,AIF1,CYP26B1,PTAFR,HAVCR2,STAT1,PLCG2,DDX60,GFAP,CDC88B,CTSH,LUNC93B1,TSP0,HIST1H4H,MAFB,PIK3CG,DHX58,PARR9,WKKE,PRKCD,IL1A,PIK3AP1,CAPN3,SERPING1,FGD2,INPP5D,PTPN22,TREM2,BIRC3,IGALS9,CD14,CARD9,NCKAP1L,CD300A,FGFBP1,MAP3K6,ACER2,RSAD2,TAP2,PLAU,TRIM21,KLHL6,IL6RA,PIK3R6,LPXN,LCK,BTK,CSF1R,IL1R1,IL4RA,CEBPA,ISG15,NFAM1,OSMR,ECM1,TMEM173,CD53,ADM,TGM2,GUPR2,CTSZ,PIM1,MERTK,CCDC3,COL1A1,NPASA,APLN,NGFR,ATF5,FOS,MYOC,KLK6

BP	GO:0001819	positive regulation of cytokine production	359	340	47	3.39E-26	0.138	0.131	3	CLEC4E,CCL5,C3,CD74,CYBB,LY9,IL12RB1,B2M,SLC11A1,IRF7,TLR1,H2-T23,C3AR1,CCR2,TLR2,GBP5,CSAR1,LTB,CD274,CD300C2,TLR7,PCYARD,FCER1G,TLR9,TRPV4,SASH3,ICOSL,IRF1,GSDMD,H2-M3,PTAFR,HAVCR2,PLCG2,DDX60,CDC88B,DHX58,IL1A,PTPN22,LGALS9,CD14,CARD9,RSAD2,IL6RA,CSF1R,IL4RA,NFAM1,TMEM173
BP	GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine prod	63	293	13	5.92E-09	0.044	0.206	4	CYBB,TLR1,H2-T23,CCR2,PCYARD,FCER1G,TLR9,SASH3,PTAFR,HAVCR2,LGALS9,CD14,CARD9
BP	GO:0032760	positive regulation of tumor necrosis factor production	62	293	13	4.76E-09	0.044	0.21	5	CYBB,TLR1,H2-T23,CCR2,PCYARD,FCER1G,TLR9,SASH3,PTAFR,HAVCR2,LGALS9,CD14,CARD9
BP	GO:0032729	positive regulation of interferon-gamma production	65	289	11	0.0000255	0.038	0.169	4	IL12RB1,SLC11A1,CCR2,TLR7,PCYARD,TLR9,SASH3,H2-M3,HAVCR2,PTPN22,CD14
BP	GO:0032733	positive regulation of interleukin-10 production	31	286	7	0.000373	0.024	0.226	4	TLR2,CD274,PCYARD,FCER1G,TLR9,SASH3,LGALS9
BP	GO:0032722	positive regulation of chemokine production	49	326	13	6.93E-10	0.04	0.265	4	CCL5,CD74,TLR2,TLR7,PCYARD,TLR9,TRPV4,HAVCR2,IL1A,LGALS9,IL6RA,CSF1R,IL4RA
BP	GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	6	14	2	0.0179	0.143	0.333	5	CCL5,CD74
BP	GO:0032481	positive regulation of type I interferon production	41	340	9	0.0000331	0.026	0.22	4	IRF7,TLR7,TLR9,IRF1,PLCG2,DHX58,PTPN22,CD14,TMEM173
BP	GO:0032755	positive regulation of interleukin-6 production	68	313	12	0.00000645	0.038	0.176	4	TLR1,TLR2,TLR7,PCYARD,FCER1G,TLR9,TRPV4,PTAFR,IL1A,LGALS9,CARD9,IL6RA
BP	GO:0048584	positive regulation of response to stimulus	1881	480	143	5.93E-39	0.298	0.076	2	CCL1,CCL5,C3,CXCL9,CD74,CCL8,H2-AB1,NLRCS,CXCL10,ZBP1,IRF1,IRF7,CD4,CCL12,MYO1G,H2-K1,IL12RB1,ITGAL,H2-D1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,CTSS,A2M,FYB,C3AR1,C4B,C1RA,LAT,S100A9,CCR2,S100A8,RAC2,TLR2,NAIP2,GBP5,THEMIS2,XDH,CSAR1,TLR12,C1QA,CAM1,TLR7,TLR13,NC1,PCYARD,PTPRC,CCL6,C1S1,TRIM30A,FCGR1,LC2P2,TNFSF13B,WAS,CD44,C1QB,FCER1G,TLR9,TRPV4,HCL5,C1QC,SASH3,IRF1,PTPN6,H2-M3,CTSC,AIF1,LAG3,CD86,VAV1,PIK3R5,PTAFR,DOCK2,HAVCR2,S100A4,FAS,ALOX5AP,LY86,PLCG2,BLNK,DDX60,CTSH,UNC93B1,PIK3CG,DHX58,IKBKE,PRKCD,PIK3AP1,CAPN3,SERPING1,FGD2,PTPN22,TREM2,LGALS9,CD14,CARD9,NCKAP1,CD300A,FGFBP1,MAP3K6,RSAD2,TAP2,KLHL6,IL6RA,PIK3R6,LPXN,LCK,BTK,CSF1R,IL1R1,IL4RA,NFAM1,ECM1,TMEM173,TGM2,GLIPR2,COL1A1,MYOC,KLK6,FCRL5,CFL1,PRRS1,CD180,TNFAIP3,CMKLR1,PTGER4,ZC3H12A,CLEC4N,PLAUR,LAT2,CCL17,HTB6,MMP2,CD247,F10,IL16,CH2CH2,C3,GPR35,CCL2
BP	GO:0032103	positive regulation of response to external stimulus	242	480	35	1.87E-15	0.073	0.145	3	CCL1,CCL5,C3,CXCL9,CD74,CXCL10,CTSS,C3AR1,S100A9,CCR2,S100A8,RAC2,TLR2,GBP5,CSAR1,FCGR1,FCER1G,TLR9,TRPV4,AIF1,HAVCR2,ALOX5AP,LY86,DDX60,PIK3CG,DHX58,LGALS9,NCKAP1,BTK,TGM2,CD180,CMKLR1,PTGER4,IL16,CCL2
BP	GO:0031349	positive regulation of defense response	262	463	49	1.06E-28	0.106	0.187	3	C3,CD74,H2-AB1,NLRCS,ZBP1,IRF7,TLR1,H2-T23,CTSS,S100A9,CCR2,S100A8,TLR2,GBP5,TLR12,TLR7,TLR13,PCYARD,TRIM30A,FCGR1,FCER1G,TLR9,TRPV4,IRF1,H2-M3,LAG3,CD86,VAV1,HAVCR2,ALOX5AP,PLCG2,DDX60,UNC93B1,PIK3CG,DHX58,PIK3P1,PTPN22,LGALS9,CD14,CARD9,CD300A,RSAD2,BTK,TMEM173,TGM2,CD180,TNFAIP3,PTGER4,CLEC4N,MMP2
BP	GO:0050729	positive regulation of inflammatory response	83	348	15	1.09E-08	0.043	0.181	4	C3,CTSS,S100A9,CCR2,S100A8,TLR2,GBP5,FCGR1,FCER1G,TLR9,TRPV4,ALOX5AP,PIK3CG,BTK,TGM2
BP	GO:0002675	positive regulation of acute inflammatory response	23	322	6	0.00245	0.019	0.261	5	C3,FCGR1,FCER1G,ALOX5AP,PIK3CG,BTK
BP	GO:0060760	positive regulation of response to cytokine stimulus	32	79	4	0.0158	0.051	0.125	3	CD74,NLRCS,ZBP1,IRF7
BP	GO:0051094	positive regulation of developmental process	1216	377	45	0.00353	0.119	0.037	2	C3,CXCL9,CD74,CCL8,IFI202,H2-AA,CYBB,LRG1,CD4,IL2RG,SPINT1,C3AR1,ITGB2,CCR2,TLR2,CSAR1,TNFSF13B,HCL51,SASH3,IRF1,H2-M3,CYP26B1,STAT1,GFAP,CTSH,TSPO,IL1A,CAPN3,INPP5D,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA,CBPBA,ISG15,ECM1,CD53,ADM,GLIPR2,PIM1,CDC3,COL1A1,FOS,MYOC
BP	GO:0031343	positive regulation of cell killing	41	305	8	0.000255	0.026	0.195	2	H2-K1,H2-D1,B2M,H2-T23,H2-M3,LAG3,VAV1,TAP2
BP	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	36	305	8	0.000859	0.026	0.222	3	H2-K1,H2-D1,B2M,H2-T23,H2-M3,LAG3,VAV1,TAP2
BP	GO:0002684	positive regulation of immune system process	854	331	98	2.36E-55	0.296	0.115	2	H2-K1,H2-D1,B2M,H2-T23,H2-M3,LAG3,VAV1,TAP2
BP	GO:0002579	positive regulation of antigen processing and presentation	13	283	5	0.00127	0.018	0.385	3	CD74,H2-AB1,SLC11A1,PCYARD,TREM2
BP	GO:0002699	positive regulation of immune effector process	174	326	26	2.97E-15	0.08	0.149	3	C3,CD74,H2-K1,H2-D1,B2M,H2-T23,CD84,CCR2,RAC2,FCGR1,FCER1G,SASH3,IRF1,H2-M3,LAG3,VAV1,PTAFR,CD37,DDX60,DHX58,PTPN22,CD300A,RSAD2,TAP2,BTK,IL4RA
BP	GO:0002702	positive regulation of production of molecular mediator of immune re	81	326	9	0.0101	0.028	0.111	4	CD74,B2M,H2-T23,FCER1G,SASH3,CD37,PTPN22,RSAD2,IL4RA
BP	GO:0002705	positive regulation of leukocyte mediated immunity	99	326	16	4.58E-09	0.049	0.162	4	C3,H2-K1,H2-D1,B2M,H2-T23,FCGR1,FCER1G,SASH3,H2-M3,LAG3,VAV1,PTAFR,RSAD2,TAP2,BTK,IL4RA
BP	GO:0002888	positive regulation of myeloid leukocyte mediated immunity	20	326	6	0.00105	0.018	0.3	5	C3,FCGR1,FCER1G,PTAFR,BTK,IL4RA
BP	GO:0002708	positive regulation of lymphocyte mediated immunity	85	322	14	0.000000076	0.043	0.165	5	C3,H2-K1,H2-D1,B2M,H2-T23,FCGR1,FCER1G,SASH3,H2-M3,LAG3,VAV1,RSAD2,TAP2,BTK
BP	GO:0050778	positive regulation of immune response	574	340	71	8.65E-40	0.209	0.124	3	C3,CD74,H2-AB1,NLRCS,ZBP1,CD4,MYO1G,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,IRF7,TLR1,H2-T23,A2M,FYB,C3AR1,C4B,C1RA,CCR2,TLR2,GBP5,THEMIS2,CSAR1,TLR12,C1QA,TLR7,TLR13,PCYARD,PTPRC,C1S1,TRIM30A,FCGR1,LC2P2,TNFSF13B,WAS,C1QB,FCER1G,TLR9,TRPV4,HCL5,C1QC,SASH3,IRF1,PTPN6,H2-M3,LAG3,CD86,VAV1,PTAFR,HAVCR2,STAT1,PLCG2,CD37,DDX60,CDC88B,UNC93B1,DHX58,IL1A,PIK3AP1,SERPING1,INPP5D,PTPN22,TREM2,LGALS9,CD14,CARD9,NCKAP1,CD300A,RSAD2,TAP2,KLHL6,PIK3R6,LPXN,LCK,BTK,IL1R1,IL4RA,ISG15,NFAM1
BP	GO:0002253	activation of immune response	424	340	47	5.86E-23	0.138	0.111	4	C3,MYO1G,IRF7,TLR1,A2M,FYB,C3AR1,C4B,C1RA,TLR2,THEMIS2,CSAR1,TLR12,C1QA,TLR7,TLR13,PCYARD,PTPRC,C1S1,TRIM30A,LC2P2,WAS,C1QB,FCER1G,TLR9,C1QC,IRF1,PTPN6,CD86,HAVCR2,PLCG2,DDX60,UNC93B1,DHX58,PIK3AP1,SERPING1,PTPN22,CD14,CARD9,NCKAP1,CD300A,RSAD2,KLHL6,LPXN,LCK,NFAM1,TMEM173
BP	GO:0002821	positive regulation of adaptive immune response	95	197	18	1.16E-15	0.091	0.189	4	C3,CD74,H2-AB1,CD4,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,H2-T23,CCR2,PCYARD,FCGR1,TNFSF13B,FCER1G,SASH3,IRF1,H2-M3
BP	GO:0002824	positive regulation of adaptive immune response based on somatic re	90	322	19	1.52E-13	0.059	0.211	5	C3,H2-AB1,CD4,H2-K1,IL12RB1,H2-D1,B2M,SLC11A1,H2-T23,CCR2,FCGR1,TNFSF13B,FCER1G,SASH3,IRF1,H2-M3,RSAD2,TAP2,BTK
BP	GO:0002827	positive regulation of T-helper 1 type immune response	20	187	5	0.00182	0.027	0.25	6	H2-AB1,IL12RB1,SLC11A1,CCR2,IRF1
BP	GO:0002711	positive regulation of T cell mediated immunity	33	305	8	0.0000409	0.026	0.242	6	H2-K1,H2-D1,B2M,H2-T23,SASH3,H2-M3,RSAD2,TAP2
BP	GO:0001916	positive regulation of T cell mediated cytotoxicity	15	305	6	0.0000969	0.02	0.4	7	H2-K1,H2-D1,B2M,H2-T23,H2-M3,TAP2
BP	GO:0045089	positive regulation of innate immune response	182	302	32	1.16E-22	0.106	0.176	4	CD74,NLRCS,ZBP1,IRF7,TLR1,H2-T23,TLR2,GBP5,TLR12,TLR7,TLR13,PCYARD,TRIM30A,FCER1G,TLR9,IRF1,H2-M3,LAG3,CD86,VAV1,HAVCR2,PLCG2,DDX60,UNC93B1,DHX58,PIK3AP1,PTPN22,LGALS9,CD14,CARD9,CD300A,RSAD2
BP	GO:0002218	activation of innate immune response	135	443	27	5.51E-16	0.061	0.2	5	IRF7,TLR1,TLR2,TLR12,TLR7,TLR13,PCYARD,TRIM30A,FCER1G,TLR9,IRF1,CD86,HAVCR2,PLCG2,DDX60,UNC93B1,DHX58,PIK3AP1,PTPN22,CD14,CARD9,CD300A,RSAD2,TMEM173,CD180,TNFAIP3,CLEC4N
BP	GO:0040017	positive regulation of locomotion	445	377	30	0.000000709	0.08	0.067	2	CCL1,CCL5,CXCL9,CD74,CXCL10,CCL12,LGALS3,C3AR1,CCR2,RAC2,CSAR1,CD274,ICAM1,PCYARD,CXCL16,TRPV4,P2RY6,FERMT3,AIF1,PTAFR,CTSH,IL1A,LGALS9,NCKAP1,PLAUR,CSF1R,IL1R1,GLIPR2,COL1A1,MYOC
BP	GO:0050921	positive regulation of chemotaxis	127	201	11	0.0000772	0.055	0.087	3	CCL1,CCL5,CXCL9,CD74,CXCL10,C3AR1,CCR2,RAC2,CSAR1,TRPV4,AIF1
BP	GO:0045785	positive regulation of cell adhesion	346	348	34	6.69E-14	0.098	0.098	2	CCL5,CD74,H2-AB1,H2-AA,CD4,IL2RG,IL12RB1,ITGAL,H2-T23,CCR2,RASAL3,CD274,ICAM1,PCYARD,TNFSF13B,CD44,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,VAV1,PTAFR,HAVCR2,CDC88B,PTPN22,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA,TGM2
BP	GO:0022409	positive regulation of cell-cell adhesion	203	326	31	6.11E-19	0.095	0.153	3	CCL5,CD74,H2-AB1,H2-AA,CD4,IL2RG,IL12RB1,ITGAL,H2-T23,CCR2,RASAL3,CD274,ICAM1,PCYARD,TNFSF13B,CD44,SASH3,ICOSL,IRF1,H2-M3,AIF1,CD86,VAV1,PTAFR,HAVCR2,CDC88B,PTPN22,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA
BP	GO:1903039	positive regulation of leukocyte cell-cell adhesion	177	326	31	8.44E-21	0.095	0.175	4	CCL5,CD74,H2-AB1,H2-AA,CD4,IL2RG,IL12RB1,ITGAL,H2-T23,CCR2,RASAL3,CD274,ICAM1,PCYARD,TNFSF13B,CD44,SASH3,ICOSL,IRF1,H2-M3,AIF1,CD86,VAV1,PTAFR,HAVCR2,CDC88B,PTPN22,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA
BP	GO:0023056	positive regulation of signaling	1439	492	89	2.89E-15	0.181	0.062	2	H2-K1,H2-D1,B2M,H2-T23,H2-M3,TAP2
BP	GO:0051050	positive regulation of transport	888	490	56	6.51E-09	0.114	0.063	2	H2-K1,H2-D1,B2M,H2-T23,H2-M3,TAP2

BP	GO:0051047	positive regulation of secretion	363	490	27	0.000157	0.055	0.074	3	HCA2R2,CLEC4E,H2-T23,S100A9,S100A8,CD274,CD300C2,PYCARD,FCER1G,TRPV4,GSDMD,PTAFR,HAVCR2,IL1A,PTPN22,IGALS9,CD14,CSF1R,IL4RA,APLN,ANG,CASP4,CYP4F18,CLEC4N,UNC130,BGLAP2
BP	GO:0010959	regulation of metal ion transport	318	281	16	0.0119	0.057	0.05	1	CC15,CXCL9,CXCL10,CD4,CC112,IGALS3,B2M,CD84,ICAM1,TLR9,PTPN6,PLCG2,TSPO,PIK3CG,CAPN3,PTPN22
BP	GO:0051924	regulation of calcium ion transport	197	281	15	0.000126	0.053	0.076	2	CC15,CXCL9,CXCL10,CD4,CC112,IGALS3,CD84,ICAM1,TLR9,PTPN6,PLCG2,TSPO,PIK3CG,CAPN3,PTPN22
BP	GO:0090087	regulation of peptide transport	764	490	44	0.0000281	0.09	0.058	1	HCA2R2,CLEC4E,CCL5,CD74,ITGAX,TLR1,H2-T23,S100A9,S100A8,RAC2,TLR2,CD274,CD300C2,TLR7,PYCARD,GBP4,TLR9,TRPV4,HCL51,GSDMD,ICP1,HAVCR2,PRKCD,IL1A,PTPN22,IGALS9,CD14,RHBD2,RSAD2,PARP10,SF1R,IL4RA,TMEM173,SP100,APLN,PRR5L,ANG,CASP4,PTGER4,ZC3H12A,CLEC4N,BCL2,CC12,BGLAP2
BP	GO:0002864	regulation of acute inflammatory response to antigenic stimulus	14	479	5	0.0251	0.01	0.357	1	C3,FCGR1,FCER1G,BTK,SPN
BP	GO:0002883	regulation of hypersensitivity	9	479	5	0.00173	0.01	0.556	2	C3,FCGR1,FCER1G,BTK,SPN
BP	GO:0001803	regulation of type III hypersensitivity	3	322	3	0.00981	0.009	1	3	FCGR1,FCER1G,BTK
BP	GO:0002892	regulation of type II hypersensitivity	3	162	3	0.00121	0.019	1	3	C3,FCGR1,FCER1G
BP	GO:0001796	regulation of type IIA hypersensitivity	3	162	3	0.00121	0.019	1	4	C3,FCGR1,FCER1G
BP	GO:0051716	cellular response to stimulus	7406	485	263	6.38E-18	0.542	0.036	1	HCA2R2,CLEC4E,CLEC4E,GZMB,CCL1,CCL5,C3,CXCL9,H2-Q7,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,CYBB,ITGAX,TSPAN32,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,CCL12,CSF2R8,TGTP2,IGP1,IL2RG,IL12RB1,IGALS3,IFI47,SPINT1,TGTP1,IRGM2,B2M,SLC11A1,GBP2,IRF7,ACAP1,BST2,TLR1,IRGM1,CTSS,TAGA P,GBP6,FBY,C3AR1,LAT,ITGB2,CD48,ARHGAP9,S100A9,CCR2,S100A8,RAC2,SULT1A1,RSAL3,ITGB7,TLR2,HCK,NAIP2,GBP5,THEMIS2,XDH,CSAR1,IL21R,LTB,TLR12,CD274,ICAM1,TLR7,CSF3R,TLR13,NCF1,PYCARD,PTPRC,GBP4,CCL6,TRIM30A,CXCL6,FCGR1,ICP2,WAS,CD44,ADGRE1,FCER1G,TLR9,DLK1,RHOH,IL10RA,TRPV4,CH25H,P2RY6,HCL51,SP1,APOBEC1,COSL,IRF1,PTPN6,GSDMD,FERMT3,ADCY7,TNFRSF1B,UGT1A7C,H2-M3,CTSC,AIF1,LAG3,CYP26B1,CD86,VAV1,ARHGAP20,PIK3R5,PTAFR,GBP3,ICP1,DOCK2,ARHGAP45,HAVCR2,S100A4,FAS,ALOX5AP,STAT1,LY86,PLCG2,BLNK,NUAK2,CD37,RA B2,ARHGAP25,HK2,DDX60,GFAP,CD68,ADAP2,CTSH,GBP7,UNC93B1,ADORA3,GBP9,HVCN1,TSPO,ISP1,PIK3CG,DHX58,RNF113,PARP3,IKBKE,PRKCD,IL1A,PIK3A1,CAPN3,FGD2,INPP5D,PTPN22,PARP9,TREM2,TIFAB,IGALS9,DTX3L,CD14,CARD9,NCKAP1,CD300A,TYROBP,FGFBP1,MAP3K6,ACER2,RHBD2,RSAD2,PLAU,KLHL6,IL6RA,PIK3R6,CCR5,LRXN,CLK,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,CEBPA,NFAM1,OSMR,IFITM3,ECM1,TMEM173,SP100,RIN3,CD53,ADM,RASD1,TGM2,GUPR2,MT2,PIM1,MERTK,CYTH4,CCDC3,COL1A1,NP4A,APLN,NGFR,FOS,MYOC,KLK6,STOML3,OMP,CYP2E1,FCRL5,HP,GR84,ARL11,EBI3,CCL9,PRR5L,CD180,TNFAIP3,CMKLR1,CASP4,GRP65,CCR2,PTGER4,DOCK1,IL3RA,RETNLG,SIGLECE,GLRA4,GBP10,ZC3H12A,CLEC4N,UPP1,DUSP2,DDK2,PLAUR,PON3,LAT2,BG8B,CCL17,HTR6,MMP2,CD247,F10,IL16,BCL3,NPPC,CNMD,CRHR2,GPR35,SPN,CCL2,UPK1B,CAMP,PSD4
BP	GO:0070887	cellular response to chemical stimulus	2414	492	146	3.29E-27	0.297	0.06	2	CCL1,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,CYBB,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,CCL12,CSF2R8,TGTP2,IGP1,IL2RG,IL12RB1,IGALS3,IFI47,SPINT1,TGTP1,IRGM2,B2M,GBP2,IRF7,IRGM1,CTSS,GBP6,C3AR1,S100A9,CCR2,S100A8,RAC2,SULT1A1,TLR2,NAIP2,GBP5,XDH,CSAR1,IL21R,LTB,ICAM1,CSF3R,NCF1,PYCARD,GBP4,CCL6,CXCL16,CD44,FCE R1G,TLR9,IL10RA,TRPV4,CH25H,P2RY6,HCL51,SP1,APOBEC1,IRF1,PTPN6,ADCY7,TNFR SF1B,UGT1A7C,AIF1,CYP26B1,CD86,VAV1,PTAFR,GBP3,HAVCR2,FAS,ALOX5AP,STAT1,LY86,CD68,CTSH,GBP7,GBP9,HVCN1,TSPO,PIK3CG,PRKCD,IL1A,CAPN3,PTPN22,TREM2,CD14,NCKAP1,FGFBP1,ACER2,IL6RA,CCR5,BTK,CSF1R,IL1R1,IFIT1,IL4RA,IFIT3,CEBPA,OSMR,IFITM3,ECM1,TMEM173,MT2,PIM1,CCDC3,COL1A1,NP4A,FOS,CYP2E1,FCRL5,PRR5L,CD180,TNFAIP3,CMKLR1,CASP4,CCR2,PTGER4,IL3RA,RETNLG,GBP10,ZC3 H12A,PON3,GBP8,CCL17,MMP2,IL16,CNMD,CRHR2,GPR35,CCL2,CAMP,CASP12,BGLA P2,MA51
BP	GO:1901701	cellular response to oxygen-containing compound	920	492	49	0.0000545	0.1	0.053	3	CCL5,FCGR4,LCN2,CYBB,CXCL10,CCL12,GBP2,GBP6,TLR2,ICAM1,NCF1,PYCARD,CXCL1 6,TLR9,P2RY6,SP1,APOBEC1,PTPN6,ADCY7,TNFRSF1B,AIF1,CYP26B1,CD86,PTAFR, HAVCR2,LY86,TSPO,PIK3CG,PRKCD,PTPN22,TREM2,CD14,BTK,PIM1,COL1A1,NP4A,FOS, CD180,TNFAIP3,CASP4,PTGER4,GBP10,ZC3H12A,MMP2,CRHR2,CCL2,CAMP,BGLAP2,MA 51
BP	GO:0071241	cellular response to inorganic substance	169	375	13	0.0228	0.035	0.077	3	CYBB,B2M,NCF1,TLR9,CD86,FAS,ALOX5AP,HVCN1,TSPO,CAPN3,CEBPA,MT2,FOS
BP	GO:0071248	cellular response to metal ion	145	375	13	0.00415	0.035	0.09	4	CYBB,B2M,NCF1,TLR9,CD86,FAS,ALOX5AP,HVCN1,TSPO,CAPN3,CEBPA,MT2,FOS
BP	GO:0071310	cellular response to organic substance	1998	492	120	5.47E-21	0.244	0.06	3	CCL1,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,CYBB,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,C CL12,CSF2R8,TGTP2,IGP1,IL2RG,IL12RB1,IGALS3,IFI47,SPINT1,TGTP1,IRGM2,GBP2,IRF 7,IRGM1,CTSS,GBP6,CCR2,GBP5,XDH,IL21R,LTB,ICAM1,CSF3R,PTAFR,GBP4,CCL6,CXCL16, CD44,FCER1G,TLR9,IL10RA,P2RY6,HCL51,SP1,APOBEC1,IRF1,PTPN6,ADCY7,TNFRSF1 B,AIF1,CYP26B1,CD86,PTAFR,GBP3,HAVCR2,FAS,STAT1,LY86,CD68,CTSH,GBP7,GBP9,TS PO,PIK3CG,PRKCD,IL1A,PTPN22,TREM2,CD14,FGFBP1,IL6RA,CCR5,BTK,CSF1R,IL1R1,IF IT1,IL4RA,IFIT3,CEBPA,OSMR,IFITM3,ECM1,TMEM173,MT2,PIM1,CCDC3,COL1A1,NP4 A,FOS,EBI3,CCL9,CD180,TNFAIP3,CASP4,CCR2,PTGER4,IL3RA,GBP10,ZC3H12A,GBP8, CCL17,MMP2,CNMD,CRHR2,GPR35,CCL2,CAMP,CASP12,BGLAP2,MA51
BP	GO:0071345	cellular response to cytokine stimulus	604	484	82	1.06E-37	0.169	0.136	4	CCL1,CCL5,CXCL9,H2-Q7,CD74,CCL8,IFI204,H2-AB1,LCN2,PIR8,NLRCS,CXCL10,IFI209,GM4951,ZBP1,CSF2RB2,LRG1,CD4,IGTP,CCL12,CSF2R B,TGTP2,IGP1,IL2RG,IL12RB1,IFI47,TGTP1,IRGM2,GBP2,IRF7,IRGM1,CTSS,GBP6,CCR 2,GBP5,IL21R,LTB,ICAM1,CSF3R,PTAFR,GBP4,CCL6,CXCL16,CD44,FCER1G,TLR9,IL10RA, P2RY6,HCL51,SP1,APOBEC1,IRF1,PTPN6,ADCY7,TNFRSF1B,AIF1,CYP26B1,CD86,PTAFR, GBP3,HAVCR2,FAS,STAT1,LY86,CD68,CTSH,GBP7,GBP9,TSPO,PIK3CG,PRKCD,IL1A,PTPN22,TREM2,CD14,FGFBP1,IL6RA,CCR5,BTK,CSF1R,IL1R1,IFIT 1,IL4RA,IFIT3,CEBPA,OSMR,IFITM3,ECM1,TMEM173,MT2,PIM1,CCDC3,COL1A1,NP4 A,FOS,EBI3,CCL9,CD180,TNFAIP3,CASP4,CCR2,PTGER4,IL3RA,GBP10,ZC3H12A,GBP8, CCL17,MMP2,CNMD,CRHR2,GPR35,CCL2,CAMP,CASP12,BGLAP2,MA51
BP	GO:0071356	cellular response to tumor necrosis factor	178	484	20	0.00000794	0.041	0.112	5	CCL1,CCL5,CCL8,LCN2,CCL12,LTB,ICAM1,PYCARD,CCL6,TNFRSF1B,FAS,STAT1,CEBPA, CCDC3,COL1A1,CCL9,ZC3H12A,CCL17,CCL2,CAMP
BP	GO:0071347	cellular response to interleukin-1	98	484	15	0.0000114	0.031	0.153	5	CCL1,CCL5,CCL8,LCN2,CCL12,ICAM1,PYCARD,CCL6,IL1A,IL1R1,CCL9,ZC3H12A,CCL17, CCL2,CAMP
BP	GO:0035458	cellular response to interferon-beta	37	340	18	7.27E-20	0.053	0.486	5	IFI204,IFI209,GM4951,IGTP,TGTP2,IGP1,IFI47,TGTP1,IRGM2,GBP2,IRGM1,GBP6,IRF1, GBP3,STAT1,IFIT1,IFIT3,TMEM173
BP	GO:0071346	cellular response to interferon-gamma	85	480	26	1.45E-19	0.054	0.306	5	CCL1,CCL5,H2-Q7,CCL8,H2-AB1,NLRCS,CCL12,IL2RB1,GBP2,GBP6,GBP5,ICAM1,GBP4,CCL6,IFIT1,PTPN6,AIF1,GBP 3,STAT1,GBP7,GBP9,CCL9,GBP10,GBP9,CCL17,CCL2
BP	GO:0071396	cellular response to lipid	530	484	32	0.000867	0.066	0.06	4	CCL5,FCGR4,LCN2,CXCL10,CCL12,GBP2,GBP6,ICAM1,PYCARD,CXCL16,TLR9,P2RY6,TN FRSF1B,CYP26B1,CD86,PTAFR,HAVCR2,LY86,TSPO,PTPN22,TREM2,CD14,PIM1,COL1A 1,NP4A,CD180,TNFAIP3,PTGER4,GBP10,ZC3H12A,CCL2,CAMP
BP	GO:0060326	cell chemotaxis	251	206	22	7.74E-12	0.107	0.088	3	CCL1,CCL5,CXCL9,CD74,CCL8,CXCL10,CCL12,IGALS3,C3AR1,S100A9,CCR2,S100A8,RA C2,CSAR1,CSF3R,CCL6,CXCL16,FCER1G,TRPV4,CH25H,AIF1,VAV1
BP	GO:0030595	leukocyte chemotaxis	186	206	22	1.27E-14	0.107	0.118	4	CCL1,CCL5,CXCL9,CD74,CCL8,CXCL10,CCL12,IGALS3,C3AR1,S100A9,CCR2,S100A8,RA C2,CSAR1,CSF3R,CCL6,CXCL16,FCER1G,TRPV4,CH25H,AIF1,VAV1
BP	GO:0048247	lymphocyte chemotaxis	60	173	10	0.000000114	0.058	0.167	5	CCL1,CCL5,CXCL9,CCL8,CXCL10,CCL12,CCR2,CCL6,CXCL16,CH25H
BP	GO:0010818	T cell chemotaxis	23	153	5	0.00142	0.033	0.217	6	CCL5,CXCL9,CXCL10,CCR2,CXCL16
BP	GO:0002548	monocyte chemotaxis	57	201	9	0.0000071	0.045	0.158	5	CCL1,CCL5,CXCL10,CCL12,IGALS3,CCR2,CCL6,AIF1
BP	GO:0048246	macrophage chemotaxis	32	172	6	0.000494	0.035	0.188	5	CCL5,CCL12,IGALS3,C3AR1,CSAR1,TRPV4
BP	GO:0071621	granulocyte chemotaxis	106	206	16	1.06E-11	0.078	0.151	5	CCL1,CCL5,CD74,CCL8,CCL12,IGALS3,C3AR1,S100A9,S100A8,RAC2,CSAR1,CSF3R,CCL 6,FCER1G,TRPV4,VAV1
BP	GO:0030593	neutrophil chemotaxis	88	162	14	9.35E-12	0.086	0.159	6	CCL1,CCL5,CD74,CCL8,CCL12,IGALS3,C3AR1,S100A9,S100A8,RAC2,CSAR1,CSF3R,CCL 6,FCER1G
BP	GO:0071216	cellular response to biotic stimulus	188	484	29	4.38E-13	0.06	0.154	2	CCL5,FCGR4,LCN2,CXCL10,CCL12,GBP2,TLR1,GBP6,TLR2,ICAM1,PTAFR,CXCL16,TLR9 ,TNFRSF1B,CD86,PTAFR,HAVCR2,LY86,TSPO,PTPN22,TREM2,CD14,BTK,CD180,TNFAIP 3,GBP10,ZC3H12A,CCL2,CAMP
BP	GO:0071219	cellular response to molecule of bacterial origin	167	484	28	1.57E-13	0.058	0.168	3	CCL5,FCGR4,LCN2,CXCL10,CCL12,GBP2,TLR1,GBP6,TLR2,ICAM1,PTAFR,CXCL16,TLR9 ,TNFRSF1B,CD86,PTAFR,HAVCR2,LY86,TSPO,PTPN22,TREM2,CD14,CD180,TNFAIP3,GB P10,ZC3H12A,CCL2,CAMP
BP	GO:0071222	cellular response to lipopolysaccharide	161	484	26	5.37E-12	0.054	0.161	4	CCL5,FCGR4,LCN2,CXCL10,CCL12,GBP2,GBP6,ICAM1,PTAFR,CXCL16,TLR9,TNFRSF1B ,CD86,PTAFR,HAVCR2,LY86,TSPO,PTPN22,TREM2,CD14,CD180,TNFAIP3,GBP10,ZC3H 2A,CCL2,CAMP

BP	GO:0050794	regulation of cellular process	10955	406	255	0.000127	0.628	0.023	1	HCAR2,CLEC4D,CLEC4E,GZMB,CC11,CC5,C3,CXCL9,CD74,CCL8,IFI204,FCGR4,H2-AB1,LCN2,H2-AA,CYBB,ITGAX,TSPAN32,PIR8,NLRCS,CXCL10,IFI207,ZBP1,CSF2RB2,LRG1,CD4,CCL12,CSF2RB,IGF1,H2-OA,MYO1G,IL2RG,BCL2A18,H2-N1,IL12RB1,IGALS3,ITGAL,H2-D1,SPINT1,SLFN2,B2M,SLC11A1,IRF7,ACAP1,BST2,TLR1,H2-T23,TAGAP,A2M,FYB,CSAR1,C4B,CD84,ELF4,LAT,ITGB2,CD48,ARHGAP9,S100A9,CCR2,S100A8,RAC2,RASAL3,ITGB7,TLR2,HCK,NAIP2,GBP5,PLAC8,THEMIS2,XDH,CSAR1,IL21B,LTB,TLR12,CD274,CD300C2,ICAM1,TLR7,WFDIC17,CF3R,TLR13,NCF1,PCYARD,PTPRC,GBP4,CCL6,TRIM30A,CXCL16,FCGR1,LCP2,TNFSF13B,WAS,CD44,ADGRE1,FCER1G,AP0BEC3,TLR9,DLK1,RHOH,SP110,IL10RA,TRPV4,P2RY6,HCLS1,C1QC,LST1,SP11,SASH3,AP0BEC1,ACPS,ICOSL,IRF1,PTPN6,GSDMD,FERM13,ADCV7,TNFRSF18,H2-M3,NGP,IKZF1,CTSC,AIF1,LAG3,CYP26B1,CD86,VAWI,PARP14,ARHGAP30,PIK3R5,PTAFR,HIF3A,LCP1,CAPG,DOCK2,ARHGAP45,HAVCR2,TNFAIP8L2,S100A4,FAS,STAT1,LY86,PLCG2,BLNK,NUAK2,CD37,ARHGAP25,HK2,DDX60,GFAP,ADAP2,CCDC88B,CTSH,UNC93B1,ADORA3,TSP0,HIST1H4H,ISP1,CTLA2B,MAFB,PIK3CG,DHX58,RNF213,PARP3,IKBKE,PRKCD,IL1A,PIK3A1,CAPN3,SERPIN3,FGD2,INPP5D,MAFF,PTPN22,TREM2,BIRC3,ITGAL,IGALS9,CD14,CARD9,NCKAP1L,CD300A,TYROBP,FGFBP1,MAP3K6,ACER2,RHBD2,RSAD2,PARP10,XAF1,PLAU,TRIM21,KLHL6,IL6RA,PIK3R6,CCRS,LPXN,LCK,BTK,CSF1R,IL1R1,IL4RA,IFIT3,CEBPA,ISG15,NFAM1,APOC1,IRF9,RAB20,OSMR,IFITM3,ECM1,TMEM173,SP100,RIN3,CD53,ADM,RASD1,TGM2,GLP2R,CTSZ,FAM107A,MT2,NFKBIE,PIM1,MYO1G,ITGAX,CD3C,COL1A1,NPASA,APLN,NGFR,ATF5,FOS,EGFR4,MYOC,KLK6,CDL28A1,STOML3,OMP,GKN3,FCRL5,GM15446,CS77,HP,PHF11D,GPR84,FBUM1,ARL11,FBIB3,CCL9,PRRS1,LANG
BP	GO:0048522	positive regulation of cellular process	4656	379	154	1.72E-14	0.406	0.033	2	HCAR2,CLEC4E,CCL1,CC5,C3,CXCL9,CD74,CCL8,IFI204,H2-AB1,LCN2,H2-AA,CYBB,ITGAX,NLRCS,CXCL10,ZBP1,LRG1,CD4,CCL12,IL2RG,IL12RB1,IGALS3,ITGALS,PTN1,B2M,SLC11A1,IRF7,BST2,TLR1,H2-T23,CSAR1,ELF4,LAT,ITGB2,S100A9,CCR2,S100A8,RAC2,RASAL3,TLR2,HCK,NAIP2,GBP5,PLAC8,XDH,CSAR1,LTB,CD274,CD300C2,ICAM1,TLR7,NCF1,PCYARD,CCL6,CXCL16,FCGR1,LCP2,TNFSF13B,WAS,CD44,FCER1G,TLR9,SP110,TRPV4,P2RY6,HCLS1,SP11,SASH3,AP0BEC1,ICOSL,IRF1,PTPN6,GSDMD,FERM13,ADCV7,TNFRSF18,H2-M3,CTSC,AIF1,CYP26B1,CD86,PIK3R5,PTAFR,HIF3A,LCP1,DOCK2,HAVCR2,S100A4,FAS,STAT1,LY86,PLCG2,BLNK,HK2,DDX60,GFAP,CCDC88B,CTSH,TSP0,MAFB,PIK3CG,DHX58,PARP3,IKBKE,PRKCD,IL1A,PIK3A1,CAPN3,FGD2,INPP5D,PTPN22,TREM2,BIRC3,IGALS9,CD14,CARD9,NCKAP1L,CD300A,FGFBP1,MAP3K6,ACER2,RSAD2,PLAU,TRIM21,KLHL6,IL6RA,PIK3R6,LCK,CSF1R,IL1R1,IL4RA,CEBPA,ISG15,NFAM1,OSMR,ECM1,TMEM173,CD53,ADM,TGM2,GLP2R,CTSZ,PIM1,MERTK,CCDC3,COL1A1,NPASA,APLN,NGFR,ATF5,FOS,MYOC,KLK6
BP	GO:1903530	regulation of secretion by cell	610	443	33	0.000928	0.074	0.054	2	HCAR2,CLEC4E,CCL5,TLR1,H2-T23,CD84,CCR2,RAC2,TLR2,CD274,CD300C2,PCYARD,FCER1G,TLR9,TRPV4,GSDMD,PTAFR,HAVCR2,IL1A,PTPN22,IGALS9,CD14,CD300A,RHBD2,RSAD2,CSF1R,IL4RA,APLN,ANG,CASP4,PTGER4,ZC3H12A,CLEC4N
BP	GO:1903532	positive regulation of secretion by cell	334	490	24	0.00164	0.049	0.072	3	HCAR2,CLEC4E,H2-T23,CD274,CD300C2,PCYARD,FCER1G,TRPV4,GSDMD,PTAFR,HAVCR2,IL1A,PTPN22,IGALS9,CD14,CSF1R,IL4RA,APLN,ANG,CASP4,PTGER4,CLEC4N,UNC13D,BGLAP2
BP	GO:0010646	regulation of cell communication	2717	492	116	6.33E-09	0.236	0.043	2	HCAR2,CCL1,CC5,C3,CXCL9,CD74,CCL8,NLRCS,CXCL10,ZBP1,LRG1,CD4,CCL12,IGALS3,ITGAL,IRF7,BST2,TLR1,LAT,S100A9,S100A8,RASAL3,TLR2,NAIP2,XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYARD,CCL6,TRIM30A,CD44,TLR9,DLK1,RHOH,TRPV4,HCLS1,IRF1,PTPN6,CTSC,CYP26B1,VAWI,PIK3R5,DOCK2,HAVCR2,S100A4,FAS,STAT1,LY86,BLNK,DDX60,GFAP,CTSH,PIK3CG,DHX58,RNF213,IKBKE,PRKCD,PIK3A1,CAPN3,FGD2,INPP5D,PTPN22,TREM2,IGALS9,CD14,CARD9,CD300A,FGFBP1,MAP3K6,RHBD2,RSAD2,PLAU,IL4RA,PIK3R6,LPXN,LCK,CSF1R,IL1R1,NFAM1,ECM1,SP100,ADM,TGM2,GLP2R,CYTH4,CCDC3,COL1A1,NPASA,APLN,MYOC,KLK6,FCRL5,CCL9,PRRS1,CD180,TNFAIP3,CMKLK1,ZC3H12A,CLEC4N,DUSP2,PLAUR,CCL17,HTR6,F10,BCL3,CNMD,CRHR2,GPR35,CCL2,PSD4,BGLAP2,RAPSN,MAS1
BP	GO:0010647	positive regulation of cell communication	1430	492	89	1.94E-15	0.181	0.062	3	HCAR2,CCL1,CC5,C3,CXCL9,CD74,CCL8,NLRCS,CXCL10,ZBP1,LRG1,CD4,CCL12,ITGAL,IRF7,BST2,TLR1,LAT,S100A9,S100A8,TLR2,NAIP2,XDH,CSAR1,ICAM1,TLR7,NCF1,PCYARD,CCL6,CD44,TLR9,TRPV4,HCLS1,PTPN6,CTSC,PIK3R5,DOCK2,HAVCR2,S100A4,FAS,LY86,BLNK,DDX60,GFAP,CTSH,PIK3CG,DHX58,IKBKE,PRKCD,PIK3A1,FGD2,PTPN22,TREM2,IGALS9,CD14,CARD9,CD300A,FGFBP1,MAP3K6,RSAD2,IL6RA,PIK3R6,LCK,CSF1R,IL1R1,NFAM1,ECM1,TGM2,GLP2R,COL1A1,APLN,MYOC,KLK6,FCRL5,CCL9,PRRS1,CD180,ZC3H12A,CLEC4N,PLAUR,CCL17,HTR6,F10,CRHR2,GPR35,CCL2,BGLAP2,RAPSN,MAS1
BP	GO:0042127	regulation of cell proliferation	1491	373	72	1.73E-12	0.193	0.048	2	CCL5,CXCL9,CD74,TSPAN32,CXCL10,LRG1,CD4,CCL12,IL12RB1,IGALS3,ITGAL,SPINT1,SLFN2,H2-T23,CCR2,RAC2,RASAL3,TLR2,HCK,PLAC8,XDH,CSAR1,CD274,PCYARD,TNFSF13B,HCLS1,1,ST1,SASH3,AP0BEC1,ICOSL,IRF1,PTPN6,TNFRSF18,H2-M3,AIF1,CD86,PTAFR,HAVCR2,FAS,STAT1,CD37,GFAP,CCDC88B,CTSH,TSP0,IL1A,INPP5D,PTPN22,IGALS9,NCKAP1L,CD300A,FGFBP1,ACER2,PARP10,PLAU,IL6RA,LCK,BTK,CSF1R,IL4RA,IFIT3,CEBPA,OSMR,IFITM3,ECM1,ADM,TGM2,CTSZ,PIM1,APLN,NGFR,ATF5
BP	GO:0070663	regulation of leukocyte proliferation	206	322	30	8.59E-18	0.093	0.146	3	CCL5,CD74,CD4,CCL12,IL12RB1,IGALS3,ITGAL,H2-T23,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,HAVCR2,CCDC88B,INPP5D,PTPN22,IGALS9,NCKAP1L,CD300A,BTK
BP	GO:0032944	regulation of mononuclear cell proliferation	197	322	29	2.98E-17	0.09	0.147	4	CCL5,CD74,CD4,IL12RB1,IGALS3,ITGAL,H2-T23,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,CD86,HAVCR2,CCDC88B,INPP5D,PTPN22,IGALS9,NCKAP1L,CD300A,BTK
BP	GO:0008284	positive regulation of cell proliferation	849	371	42	0.00000168	0.113	0.049	3	CCL5,CD74,CXCL10,LRG1,CD4,IL12RB1,ITGAL,H2-T23,CCR2,RAC2,RASAL3,HCK,PLAC8,CSAR1,CD274,PCYARD,TNFSF13B,HCLS1,SASH3,ICOSL,PTPN6,AIF1,CD86,PTAFR,HAVCR2,GFAP,CCDC88B,CTSH,TSP0,PTPN22,NCKAP1L,FGFBP1,ACER2,IL6RA,CSF1R,OSMR,ECM1,ADM,TGM2,CTSZ,PIM1,APLN
BP	GO:0070665	positive regulation of leukocyte proliferation	133	294	19	5.52E-11	0.065	0.143	4	CCL5,CD74,CD4,IL12RB1,ITGAL,H2-T23,CCR2,RASAL3,CD274,PCYARD,TNFSF13B,SASH3,ICOSL,AIF1,CD86,HAVCR2,CCDC88B,PTPN22,NCKAP1L
BP	GO:0032946	positive regulation of mononuclear cell proliferation	127	294	19	2.31E-11	0.065	0.15	5	CCL5,CD74,CD4,IL12RB1,ITGAL,H2-T23,CCR2,RASAL3,CD274,PCYARD,TNFSF13B,SASH3,ICOSL,AIF1,CD86,HAVCR2,CCDC88B,PTPN22,NCKAP1L
BP	GO:0010941	regulation of cell death	1467	373	48	0.0326	0.129	0.033	2	HCAR2,CCL5,CD74,CCL12,BCL2A1B,IGALS3,S100A9,S100A8,HCK,NAIP2,PLAC8,XDH,CSAR1,CD274,ICAM1,PCYARD,CD44,FCER1G,SP110,HCLS1,TNFRSF18,CTSC,AIF1,FAS,PLCG2,NUAK2,CTSH,TSP0,PIK3CG,PRKCD,CAPN3,INPP5D,BIRC3,CARD9,NCKAP1L,ACER2,CCR5,LCK,CSF1R,IFIT3,SP100,ADM,TGM2,CTSZ,PIM1,MERTK,NGFR,ATF5
BP	GO:0043067	regulation of programmed cell death	1370	373	48	0.00514	0.129	0.035	3	HCAR2,CCL5,CD74,CCL12,BCL2A1B,IGALS3,S100A9,S100A8,HCK,NAIP2,PLAC8,XDH,CSAR1,CD274,ICAM1,PCYARD,CD44,FCER1G,SP110,HCLS1,TNFRSF18,CTSC,AIF1,FAS,PLCG2,NUAK2,CTSH,TSP0,PIK3CG,PRKCD,CAPN3,INPP5D,BIRC3,CARD9,NCKAP1L,ACER2,CCR5,LCK,CSF1R,IFIT3,SP100,ADM,TGM2,CTSZ,PIM1,MERTK,NGFR,ATF5
BP	GO:0042981	regulation of apoptotic process	1356	373	47	0.00893	0.126	0.035	4	HCAR2,CCL5,CD74,CCL12,BCL2A1B,IGALS3,S100A9,S100A8,HCK,NAIP2,PLAC8,XDH,CSAR1,CD274,ICAM1,PCYARD,CD44,FCER1G,SP110,HCLS1,TNFRSF18,CTSC,AIF1,FAS,NUAK2,CTSH,TSP0,PIK3CG,PRKCD,CAPN3,INPP5D,BIRC3,CARD9,NCKAP1L,ACER2,CCR5,LCK,CSF1R,IFIT3,SP100,ADM,TGM2,CTSZ,PIM1,MERTK,NGFR,ATF5
BP	GO:2000106	regulation of leukocyte apoptotic process	87	362	10	0.00541	0.028	0.115	5	HCAR2,CCL5,CD74,IGALS3,CD274,FCER1G,HCLS1,FAS,CCRS,MERTK
BP	GO:0050865	regulation of cell activation	574	331	50	2.28E-20	0.151	0.087	2	CCL5,CD74,H2-AB1,H2-AA,TSPAN32,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,H2-T23,CD84,LAT,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,FCER1G,TLR9,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LAG3,CYP26B1,CD86,PTAFR,HAVCR2,TNFAIP8L2,FAS,CD37,CCDC88B,PRKCD,CAPN3,INPP5D,PTPN22,IGALS9,NCKAP1L,CD300A,PIK3R6,LCK,BTK,IL4RA,NFAM1
BP	GO:0002694	regulation of leukocyte activation	544	331	48	1.14E-19	0.145	0.088	3	CCL5,CD74,H2-AB1,H2-AA,TSPAN32,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,H2-T23,CD84,LAT,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,FCER1G,TLR9,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LAG3,CYP26B1,CD86,PTAFR,HAVCR2,TNFAIP8L2,FAS,CD37,CCDC88B,INPP5D,PTPN22,IGALS9,NCKAP1L,CD300A,PIK3R6,LCK,BTK,IL4RA,NFAM1
BP	GO:0051249	regulation of lymphocyte activation	486	331	43	2.31E-17	0.13	0.088	4	CCL5,CD74,H2-AB1,H2-AA,CD4,H2-OA,IL2RG,IL12RB1,IGALS3,ITGAL,H2-T23,LAT,CCR2,RAC2,RASAL3,CD274,PCYARD,TNFSF13B,TLR9,LST1,SASH3,ICOSL,IRF1,PTPN6,H2-M3,AIF1,LAG3,CYP26B1,CD86,HAVCR2,TNFAIP8L2,FAS,CCDC88B,INPP5D,PTPN22,IGALS9,NCKAP1L,CD300A,PIK3R6,LCK,BTK,IL4RA,NFAM1

BP	GO:0050670	regulation of lymphocyte proliferation	196	322	29	2.58E-17	0.09	0.148	5	CCL5, CD74, CD4, IL12RB1, LGALS3, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, LST1, SASH3, ICOSL, IRF1, PTPN6, H2-M3, AIF1, CD86, HAVCR2, CCR2, CCR8, INPP5D, PTPN22, LGALS9, NCKAP1L, CD300A, BTK
BP	GO:0050863	regulation of T cell activation	268	326	37	1.67E-21	0.113	0.138	5	CCL5, CD74, H2-AB1, H2-AA, CD4, H2-DA, IL2RG, IL12RB1, LGALS3, ITGAL, H2-T3, LAT, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, IRF1, PTPN6, H2-M3, AIF1, LAG3, CYP26B1, CD86, HAVCR2, TNFAIP812, CCR2, CCR8, PTPN22, LGALS9, NCKAP1L, CD300A, PIK3R6, LCK, IL4RA
BP	GO:0046634	regulation of alpha-beta T cell activation	79	326	12	0.00000626	0.037	0.152	6	H2-AB1, IL2RG, H2-T3, CCR2, RASAL3, SASH3, IRF1, PTPN22, LGALS9, NCKAP1L, CD300A, IL4RA
BP	GO:2001185	regulation of CD8-positive, alpha-beta T cell activation	9	294	4	0.0118	0.014	0.444	7	H2-T3, IRF1, PTPN22, NCKAP1L
BP	GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	46	326	7	0.0153	0.021	0.152	7	IL2RG, CCR2, SASH3, IRF1, LGALS9, NCKAP1L, IL4RA
BP	GO:0042129	regulation of T cell proliferation	149	294	24	9.91E-16	0.082	0.161	6	CCL5, CD4, IL12RB1, LGALS3, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, IRF1, PTPN6, H2-M3, AIF1, CD86, HAVCR2, CCR2, CCR8, INPP5D, PTPN22, LGALS9, NCKAP1L
BP	GO:0046640	regulation of alpha-beta T cell proliferation	27	286	6	0.00342	0.021	0.222	7	H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, IRF1, H2-M3, AIF1, CD86, HAVCR2, CCR2, CCR8, INPP5D, PTPN22, LGALS9, NCKAP1L
BP	GO:0030885	regulation of myeloid dendritic cell activation	5	232	3	0.0357	0.013	0.6	4	TSKAN32, HAVCR2, CD37
BP	GO:0033003	regulation of mast cell activation	36	487	7	0.0366	0.014	0.194	4	CD84, RAC2, FCER1G, CD300A, IL4RA, IJUNC130, MIMR1
BP	GO:0050867	positive regulation of cell activation	384	326	32	1.04E-11	0.098	0.083	3	CCL5, CD74, H2-AB1, H2-AA, CD4, IL2RG, IL12RB1, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, FCEIR1G, SASH3, ICOSL, IRF1, H2-M3, AIF1, CD86, PTAFR, HAVCR2, CCR2, CCR8, CAPN3, INPP5D, PTPN22, LGALS9, NCKAP1L, PIK3R6, LCK, IL4RA
BP	GO:0002696	positive regulation of leukocyte activation	375	326	31	3.59E-11	0.095	0.083	4	CCL5, CD74, H2-AB1, H2-AA, CD4, IL2RG, IL12RB1, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, FCEIR1G, SASH3, ICOSL, IRF1, H2-M3, AIF1, CD86, PTAFR, HAVCR2, CCR2, CCR8, INPP5D, PTPN22, LGALS9, NCKAP1L, PIK3R6, LCK, IL4RA
BP	GO:0051251	positive regulation of lymphocyte activation	350	326	29	2.54E-10	0.089	0.083	5	CCL5, CD74, H2-AB1, H2-AA, CD4, IL2RG, IL12RB1, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, IRF1, H2-M3, AIF1, CD86, HAVCR2, CCR2, CCR8, INPP5D, PTPN22, LGALS9, NCKAP1L, PIK3R6, LCK, IL4RA
BP	GO:0050671	positive regulation of lymphocyte proliferation	126	294	19	1.99E-11	0.065	0.151	6	CCL5, CD74, CD4, IL12RB1, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, AIF1, CD86, HAVCR2, CCR2, CCR8, PTPN22, NCKAP1L
BP	GO:0050870	positive regulation of T cell activation	168	326	28	6.15E-18	0.086	0.167	6	CCL5, CD74, H2-AB1, H2-AA, CD4, IL2RG, IL12RB1, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, IRF1, H2-M3, AIF1, CD86, HAVCR2, CCR2, CCR8, INPP5D, PTPN22, LGALS9, NCKAP1L, PIK3R6, LCK, IL4RA
BP	GO:0046635	positive regulation of alpha-beta T cell activation	55	326	10	0.0000232	0.031	0.182	7	H2-AB1, IL2RG, H2-T3, CCR2, RASAL3, SASH3, IRF1, PTPN22, NCKAP1L, IL4RA
BP	GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	29	326	6	0.0115	0.018	0.207	8	IL2RG, CCR2, SASH3, IRF1, NCKAP1L, IL4RA
BP	GO:0042102	positive regulation of T cell proliferation	92	294	18	8.65E-13	0.061	0.196	7	CCL5, CD4, IL12RB1, ITGAL, H2-T3, CCR2, RASAL3, CD274, PYCARD, TNFSF13B, SASH3, ICOSL, AIF1, CD86, HAVCR2, CCR2, CCR8, PTPN22, NCKAP1L
BP	GO:0051270	regulation of cellular component movement	778	422	39	0.00015	0.092	0.05	2	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, BST2, C3AR1, CCR2, RAC2, CSAR1, CD274, ICAM1, PYCARD, CXCL16, WAS, TRPV4, P2RY6, FERMT3, AIF1, PTAFR, CTSH, IL1A, PTPN22, LGALS9, NCKAP1L, CD300A, PLAU, CSF1R, IL1R1, ECM1, SP100, GLP2R, COL1A1, MYOC, PRR5, LCMKLR1, PTGER4
BP	GO:0051272	positive regulation of cellular component movement	425	377	30	0.000000232	0.08	0.071	3	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, C3AR1, CCR2, RAC2, CSAR1, CD274, ICAM1, PYCARD, CXCL16, TRPV4, P2RY6, FERMT3, AIF1, PTAFR, CTSH, IL1A, LGALS9, NCKAP1L, PLAU, CSF1R, IL1R1, GLP2R, COL1A1, MYOC
BP	GO:2000145	regulation of cell motility	708	422	39	0.0000117	0.092	0.055	3	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, BST2, C3AR1, CCR2, RAC2, CSAR1, CD274, ICAM1, PYCARD, CXCL16, WAS, TRPV4, P2RY6, FERMT3, AIF1, PTAFR, CTSH, IL1A, PTPN22, LGALS9, NCKAP1L, CD300A, PLAU, CSF1R, IL1R1, ECM1, SP100, GLP2R, COL1A1, MYOC, PRR5, LCMKLR1, PTGER4
BP	GO:0030334	regulation of cell migration	670	422	38	0.00000845	0.09	0.057	4	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, BST2, C3AR1, CCR2, RAC2, CSAR1, CD274, ICAM1, PYCARD, CXCL16, TRPV4, P2RY6, FERMT3, AIF1, PTAFR, CTSH, IL1A, PTPN22, LGALS9, NCKAP1L, CD300A, PLAU, CSF1R, IL1R1, ECM1, SP100, GLP2R, COL1A1, MYOC, PRR5, LCMKLR1, PTGER4
BP	GO:0002685	regulation of leukocyte migration	162	338	23	2.22E-12	0.068	0.142	5	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, C3AR1, CCR2, RAC2, CSAR1, ICAM1, PYCARD, TRPV4, AIF1, PTAFR, IL1A, PTPN22, LGALS9, NCKAP1L, CD300A, IL1R1, ECM1
BP	GO:0002691	regulation of cellular extravasation	22	480	7	0.000886	0.015	0.318	6	CCR2, ICAM1, PTAFR, IL1A, IL1R1, PTGER4, CCL2
BP	GO:0071675	regulation of mononuclear cell migration	44	201	9	0.00000062	0.045	0.205	6	CCL1, CCL5, CXCL10, LGALS3, C3AR1, CCR2, CSAR1, TRPV4, AIF1
BP	GO:1905521	regulation of macrophage migration	25	480	6	0.04	0.013	0.24	6	CCL5, C3AR1, CSAR1, TRPV4, CMLKLR1, CCL2
BP	GO:2000401	regulation of lymphocyte migration	47	338	8	0.00171	0.024	0.17	6	CCL5, CXCL10, CCL2, CCR2, PYCARD, AIF1, LGALS9, ECM1
BP	GO:2000404	regulation of T cell migration	36	338	7	0.00346	0.021	0.194	7	CCL5, CXCL10, CCR2, PYCARD, AIF1, LGALS9, ECM1
BP	GO:1902622	regulation of neutrophil migration	37	324	7	0.00317	0.022	0.189	6	CD74, C3AR1, RAC2, CSAR1, IL1A, NCKAP1L, IL1R1
BP	GO:0002688	regulation of leukocyte chemotaxis	104	201	12	0.00000626	0.06	0.115	6	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, C3AR1, CCR2, RAC2, CSAR1, TRPV4, AIF1
BP	GO:1901623	regulation of lymphocyte chemotaxis	22	106	4	0.0109	0.038	0.182	7	CCL5, CXCL10, CCL2, CCR2
BP	GO:0071622	regulation of granulocyte chemotaxis	47	480	9	0.00207	0.019	0.191	7	CCL5, CD74, C3AR1, RAC2, CSAR1, TRPV4, NCKAP1L, CMLKLR1, CCL2
BP	GO:0010758	regulation of macrophage chemotaxis	23	480	6	0.0236	0.013	0.261	7	CCL5, C3AR1, CSAR1, TRPV4, CMLKLR1, CCL2
BP	GO:0090025	regulation of monocyte chemotaxis	21	201	5	0.00341	0.025	0.238	7	CCL1, CCL5, CXCL10, CCR2, AIF1
BP	GO:2000147	positive regulation of cell motility	414	377	30	0.000000122	0.08	0.072	4	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, C3AR1, CCR2, RAC2, CSAR1, CD274, ICAM1, PYCARD, CXCL16, TRPV4, P2RY6, FERMT3, AIF1, PTAFR, CTSH, IL1A, LGALS9, NCKAP1L, PLAU, CSF1R, IL1R1, GLP2R, COL1A1, MYOC
BP	GO:0030335	positive regulation of cell migration	399	377	30	4.89E-08	0.08	0.075	5	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, C3AR1, CCR2, RAC2, CSAR1, CD274, ICAM1, PYCARD, CXCL16, TRPV4, P2RY6, FERMT3, AIF1, PTAFR, CTSH, IL1A, LGALS9, NCKAP1L, PLAU, CSF1R, IL1R1, GLP2R, COL1A1, MYOC
BP	GO:0002687	positive regulation of leukocyte migration	119	324	20	2.8E-12	0.062	0.168	6	CCL1, CCL5, CXCL9, CD74, CXCL10, CCL12, LGALS3, C3AR1, CCR2, RAC2, CSAR1, ICAM1, PYCARD, TRPV4, AIF1, PTAFR, IL1A, PTPN22, LGALS9, NCKAP1L, CD300A, IL1R1, ECM1
BP	GO:2000403	positive regulation of lymphocyte migration	34	286	6	0.0144	0.021	0.176	7	CCL5, CXCL10, CCR2, PYCARD, AIF1, LGALS9
BP	GO:2000406	positive regulation of T cell migration	30	286	6	0.00663	0.021	0.2	8	CD74, C3AR1, RAC2, CSAR1, IL1A, NCKAP1L, IL1R1
BP	GO:1902624	positive regulation of neutrophil migration	30	324	7	0.000685	0.022	0.233	7	CCL5, CXCL10, CCR2, PYCARD, AIF1, LGALS9
BP	GO:0071677	positive regulation of mononuclear cell migration	25	201	6	0.000258	0.03	0.24	7	CCL1, CCL5, CXCL10, LGALS3, CCR2, AIF1
BP	GO:0002693	positive regulation of cellular extravasation	14	480	6	0.000831	0.013	0.429	7	CCR2, ICAM1, PTAFR, IL1A, IL1R1, CCL2
BP	GO:1905523	positive regulation of macrophage migration	18	480	6	0.00477	0.013	0.333	7	CCL5, C3AR1, CSAR1, TRPV4, CMLKLR1, CCL2
BP	GO:0002690	positive regulation of leukocyte chemotaxis	85	201	11	0.00000103	0.055	0.129	7	CCL1, CCL5, CXCL9, CD74, CXCL10, C3AR1, CCR2, RAC2, CSAR1, TRPV4, AIF1
BP	GO:0090026	positive regulation of monocyte chemotaxis	17	201	5	0.00107	0.025	0.294	8	CCL1, CCL5, CXCL10, CCR2, AIF1
BP	GO:0010759	positive regulation of macrophage chemotaxis	17	480	6	0.00324	0.013	0.353	8	CCL5, C3AR1, CSAR1, TRPV4, CMLKLR1, CCL2
BP	GO:0006027	regulation of vesicle-mediated transport	421	480	26	0.00654	0.054	0.062	2	C3, LGALS3, B2M, SLC11A1, CD84, CCR2, RAC2, HCK, PYCARD, FCGR1, FCER1G, PTAFR, DOCK2, PLCG2, LGALS9, CD14, NCKAP1L, CD300A, IL4RA, APO1, RAB20, MERTK, SIGLEC2, C2, UNCE130, CCL2 HCAR2, CLEC4D, CLEC4E, G2MB, CCL1, CCL5, CXCL9, CD74, CCL8, FCGR4, LCN2, ITGAX, TSPAN32, PI3R, NLRCS, CXCL10, ZBP1, CSF2RB2, LRG1, CD4, CCL12, CSF2RB, IIGP1, MYO10, IL2RG, IL12RB1, LGALS3, ITGAL, SLC11A1, IRF7, ACAP1, BST2, TLR1, TAGAP, FYB, C3AR1, LAT, ITGB2, CD48, ARHGAP9, S100A9, CCR2, S100A8, RAC2, RASAL3, ITGB7, TLR2, HCK, NAIIP2, THEMIS2, XDH, CSAR1, IL2IR, LTB, TLR12, CD274, ICAM1, TLR7, CSF3R, TLR13, NCF1, PYCARD, PTPRC, CCL6, TRIM30A, FCGR1, LCP2, WAS, CD4, ADGRE1, FCER1G, TLR9, DLK1, RHOF, IL10RA, TRPV4, P2RY6, HCL5, ICOSL, IRF1, PTPN6, FERMT3, ADCY7, TNFSF18, H2-M3, CTC5, AIF1, LAG3, CYP26B1, CD86, VAV1, ARHGAP30, PIK3R5, PTAFR, LCP1, DOCK2, ARHGAP45, HAVCR2, S100A4, FAS, STAT1, LY86, PLCG2, BLNK, NUA2, CD37, ARHGAP25, DDX60, ADAP2, CTSH, UNC93B1, ADORA3, TSP1, LSP1, PIK3CG, DHX58, RNF213, IKK8I, PRKCD, IL1A, PIK3AP1, CAPN3, FGD2, INPP5D, PTPN22, TREM2, TRAF6, LGALS9, CD14, CARD9, NCKAP1L, CD300A, TYROBP, FGFBP1, MAAP3K6, RHBD2, RSAD2, PLAU, KLHL6, IL6RA, PIK3R6, CCR5, LPM, N, LCK, BTK, CSF1R, IL1R1, IL4RA, CE3PA, NFAM1, OSMR, JFTM3, EGM1, SP100, RIN3, CD53, 4DM, RASD1, TGM2, GLP2R, MT2, PIM1, MERTK, CYTH4, CDDC3, COL1A1, NPAS4, APLN, NCF1, R, FOS, MYOC, KLK6, STOML3, DMP, FCRL5, HP, GPR84, ARL11, EB13, CCL9, PRR5L, CD180, TNFAIP3, CMLKLR1, CASP4, GPR65, CCR12, PTGER4, DOK1, IL3RA, SIGLEC4, GLRA4, ZC3H12A, CLEC4N, DUSP2, DOK2, PLAU, LAT2, CCL17, HTR6, CD247, F10, BCL3, NPPC, CNMD, CRRH2, GPR35, SPN, CCL2, UPK18
BP	GO:0007165	signal transduction	6196	481	213	3.41E-11	0.443	0.034	2	H2-AB1, IL2RG, H2-T3, CCR2, RASAL3, SASH3, IRF1, PTPN22, LGALS9, NCKAP1L, IL4RA
BP	GO:0007166	cell surface receptor signaling pathway	2372	481	129	5.35E-20	0.268	0.054	3	H2-AB1, IL2RG, H2-T3, CCR2, RASAL3, SASH3, IRF1, PTPN22, LGALS9, NCKAP1L, IL4RA
BP	GO:0007229	integrin-mediated signaling pathway	92	206	9	0.000643	0.044	0.098	4	ITGAX, TSPAN32, ITGAL, ITGB2, ITGB7, FCER1G, FERMT3, VAV1
BP	GO:0019221	cytokine-mediated signaling pathway	396	480	49	1.46E-19	0.102	0.124	4	CCL1, CCL5, CXCL9, CD74, CCL8, PI3R, NLRCS, CXCL10, ZBP1, CSF2RB2, CD4, CCL12, CSF2RB1, IIGP1, IL2RG, IL12RB1, IRF7, CCR2, IL21R, LTB, CSF3R, PYCARD, CCL6, CD44, IL10RA, IRF1, PTPN6, TNFSF18, FAS, STAT1, IL1A, TREM2, IL6RA, CCR5, CSF1R, IL1R1, IL4RA, CE3PA, OSMR, IFTM3, EGM1, SP100, CD53, CDDC3, COL1A1, NPAS4, FOS, MYOC, HP, EB13, CCL9, CD180, TNFAIP3, CCR12, DOK1, IL3RA, GLRA4, CLEC4N, DOK2, PLAU, LAT2, CCL17, HTR6, CD247, F10, BCL3, NPPC, CNMD, CRRH2, GPR35, SPN, CCL2, UPK18
BP	GO:0070098	chemokine-mediated signaling pathway	79	480	15	0.000000437	0.031	0.19	5	CCL1, CCL5, CXCL9, CCL8, CXCL10, CCL12, CCR2, CCL6, TREM2, CCR5, CCL9, CCR12, CCL17, GPR35, CCL2
BP	GO:0031663	lipopolysaccharide-mediated signaling pathway	47	412	9	0.000576	0.022	0.191	4	CCL5, CCL12, PTAFR, LY86, PTPN22, TREM2, CD14, CD180, TNFAIP3

BP	GO:0035556	intracellular signal transduction	2244	492	110	3.04E-12	0.224	0.049	3	CC11,CC15,CCX19,CD74,CCL8,IF204,CCX110,CD4,CCL12,ITGAL,SLC11A1,BST2,TLR1,LA T,S100A9,S100A8,RAC2,RASAL3,TLR2,XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYCARD,C CL6,LCF2,WAS,CD44,TLR9,RHOH,TRPV4,HCL51,PTPN6,ADCY7,TNFRSF1B,AIF1,VAV1,PI K3R5,PTAFR,LCP1,DOCK2,ARHGAP45,HAVER2,S100A4,FAS,STAT1,PLCG2,BLNK,NUAK2, DDX60,ADAP2,CTSH,PIK3CG,DHX58,IKBKE,PRKCD,PIK3AP1,CAPN3,FGD2,INPP5D,PTPN 22,TREM2,TIFAB,CD14,CARD9,CD300A,MAP3K6,IL6RA,PIK3R6,CCR5,LCK,BTK,CSF1R,N FAM1,ECM1,ADM,RASD1,TGM2,GLI2R2,MT2,MERTK,CYTH4,NGFR,MYOC,ARL11,CC19, PRRSL,TNFAIP3,CMKLR1,CASP4,PTGER4,DOX1,ZC3H12A,CLEC4N,DUSP2,DOX2,PLAUR, LAT2,CCL17,HTF6,F10,BCL3,CRHR2,GPR35,CCL2,PSD4,CASP12,MAS1
BP	GO:0048017	inositol lipid-mediated signaling	136	404	13	0.00435	0.032	0.096	4	CC15,NCF1,HCL51,PTPN6,PIK3R5,PTAFR,ADAP2,PIK3CG,PIK3AP1,PIK3R6,CSF1R,MYOC, PRRSL
BP	GO:0048015	phosphatidylinositol-mediated signaling	132	404	12	0.0187	0.03	0.091	5	CC15,NCF1,HCL51,PTPN6,PIK3R5,PTAFR,PIK3CG,PIK3AP1,PIK3R6,CSF1R,MYOC,PRRSL
BP	GO:0007249	I-kappaB kinase/NF-kappaB signaling	236	470	21	0.000122	0.045	0.089	4	CD74,CD4,BST2,TLR2,TLR7,PCYCARD,TLR9,RHOH,S100A4,STAT1,IKBKE,CAPN3,TIFAB,CA RD9,BTK,ECM1,TGM2,TNFAIP3,ZC3H12A,CLEC4N,BCL3
BP	GO:0009966	regulation of signal transduction	2422	485	109	4.82E-10	0.225	0.045	3	CC11,CC15,C3,CCX19,CD74,CCL8,NLRCS,CCX110,ZBP1,IRG1,CD4,CCL12,I,IGALS3,ITGAL, IRF7,BS2,TLR1,LAT,S100A9,S100A8,RASAL3,TLR2,MAP2,XDH,CSAR1,ICAM1,TLR7,TLR 13,NCF1,PCYCARD,CCL6,TRIM30A,CD44,TLR9,DLK1,RHOH,TRPV4,HCL51,IRF1,PTPN6,CT SC,CYP26B1,VAV1,PIK3R5,DOCK2,HAVER2,S100A4,FAS,STAT1,LY86,BLNK,DDX60,CTSH, PIK3CG,DHX58,RNF213,IKBKE,PRKCD,PIK3AP1,CAPN3,FGD2,INPP5D,PTPN22,TREM2,I GALS9,CD14,CARD9,CD300A,FGFBP1,MAP3K6,RHBD2,RSAD2,PLAU,IL6RA,PIK3R6,LPX N,LCK,CSF1R,IL1R1,NFAM1,ECM1,SP100,ADM,TGM2,GLI2R2,CYTH4,CCDC3,COL1A1,M YOC,KLK6,FCLRS,CCL9,PRRSL,CD180,TNFAIP3,CMKLR1,ZC3H12A,CLEC4N,DUSP2,PLAU R,CCL17,HTF6,F10,BCL3,CNMD,CRHR2,GPR35,CCL2,PSD4
BP	GO:1902531	regulation of intracellular signal transduction	1488	492	76	0.000000028	0.154	0.051	4	CC11,CC15,CCX19,CD74,CCL8,CCX110,CD4,CCL12,ITGAL,BST2,TLR1,S100A9,S100A8,RA SAL3,TLR2,XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYCARD,CCL6,CD44,TLR9,RHOH,TRP V4,HCL51,PTPN6,VAV1,PIK3R5,DOCK2,HAVER2,S100A4,FAS,STAT1,DDX60,PIK3CG,DHX 58,IKBKE,PRKCD,PIK3AP1,CAPN3,FGD2,PTPN22,TREM2,CD14,CARD9,CD300A,MAP3K6, IL6RA,PIK3R6,LCK,CSF1R,ECM1,TGM2,GLI2R2,CYTH4,MYOC,CC19,PRRSL,TNFAIP3,CM KLR1,ZC3H12A,CLEC4N,DUSP2,PLAU,CC117,HTF6,F10,BCL3,CRHR2,GPR35,CCL2,PSD 4,MAS1
BP	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	215	470	19	0.000605	0.04	0.088	5	CD74,CD4,BST2,TLR2,TLR7,PCYCARD,TLR9,RHOH,S100A4,STAT1,IKBKE,CAPN3,CARD9,E CM1,TGM2,TNFAIP3,ZC3H12A,CLEC4N,BCL3
BP	GO:0001959	regulation of cytokine-mediated signaling pathway	82	366	11	0.000369	0.03	0.134	4	CC15,CD74,NLRCS,ZBP1,IRF7,PCYCARD,PTPN6,TREM2,IL1R1,ECM1,CCDC3
BP	GO:0002764	immune response-regulating signaling pathway	397	331	43	7.94E-21	0.13	0.108	3	CLEC4D,CLEC4E,FCGR4,MYO1G,IRF7,TLR1,FYB,C3AR1,TLR2,THEMIS2,CSAR1,TLR12,TL R7,TLR13,PTPRC,TRIM30A,FCGR1,LC2,WAS,FCER1G,TLR9,IRF1,PTPN6,H2- M3,CD86,HAVER2,PLCG2,DDX60,CTSH,UNC93B1,DHX58,PIK3AP1,PTPN22,CD14,CARD 9,NCKAP1,CD300A,RSAD2,KHLH6,LPXN,LCK,BTK,NFAM1
BP	GO:0002768	immune response-regulating cell surface receptor signaling pathway	283	331	24	3.23E-08	0.073	0.085	4	CLEC4D,CLEC4E,FCGR4,MYO1G,FYB,C3AR1,THEMIS2,CSAR1,PTPRC,FCGR1,LC2,WAS, FCER1G,PTPN6,H2-M3,PLCG2,PTPN22,NCKAP1,CD300A,KHLH6,LPXN,LCK,BTK,NFAM1
BP	GO:0038093	Fc receptor signaling pathway	25	162	7	0.00000136	0.043	0.28	5	CLEC4D,CLEC4E,FCGR4,MYO1G,FCGR1,WAS,FCER1G
BP	GO:0038094	Fc-gamma receptor signaling pathway	12	162	7	2.42E-09	0.043	0.583	6	CLEC4D,CLEC4E,FCGR4,MYO1G,FCGR1,WAS,FCER1G
BP	GO:0002757	immune response-activating signal transduction	379	331	36	4.21E-15	0.109	0.095	4	MYO1G,IRF7,TLR1,FYB,C3AR1,TLR2,THEMIS2,CSAR1,TLR12,TLR7,TLR13,PTPRC,TRIM3 0A,LC2,WAS,FCER1G,TLR9,IRF1,PTPN6,CD86,HAVER2,PLCG2,DDX60,UNC93B1,DHX5 8,PIK3AP1,PTPN22,CD14,CARD9,NCKAP1,CD300A,RSAD2,KHLH6,LPXN,LCK,NFAM1
BP	GO:0002758	innate immune response-activating signal transduction	128	302	22	1.32E-14	0.073	0.172	5	IRF7,TLR1,TLR2,TLR12,TLR7,TLR13,TRIM30A,FCER1,TLR9,IRF1,CD86,HAVER2,PLCG2, DDX60,UNC93B1,DHX58,PIK3AP1,PTPN22,CD14,CARD9,CD300A,RSAD2
BP	GO:0002221	pattern recognition receptor signaling pathway	120	302	20	8.48E-13	0.066	0.167	6	IRF7,TLR1,TLR2,TLR12,TLR7,TLR13,TRIM30A,IRF9,IRF1,CD86,HAVER2,DDX60,UNC93 B1,DHX58,PIK3AP1,PTPN22,CD14,CARD9,CD300A,RSAD2
BP	GO:0002224	toll-like receptor signaling pathway	84	412	19	3.2E-12	0.046	0.226	7	IRF7,TLR1,TLR2,TLR12,TLR7,TLR13,TRIM30A,TLR9,IRF1,CD86,HAVER2,DDX60,UNC93 B1,DHX58,PIK3AP1,PTPN22,CD14,CARD9,CD300A,RSAD2
BP	GO:0034162	toll-like receptor 9 signaling pathway	12	302	6	0.0000175	0.02	0.5	8	TLR9,HAVER2,UNC93B1,PIK3AP1,PTPN22,RSAD2
BP	GO:0002755	MyD88-dependent toll-like receptor signaling pathway	19	295	8	0.00000202	0.027	0.421	8	IRF7,TLR1,TLR2,TLR7,TLR13,TLR9,IRF1,CD300A
BP	GO:0034138	toll-like receptor 3 signaling pathway	15	412	5	0.0178	0.012	0.333	8	CD86,HAVER2,UNC93B1,PTPN22,TNFAIP3
BP	GO:0034154	toll-like receptor 7 signaling pathway	6	302	6	2.03E-08	0.02	1	8	TLR7,HAVER2,UNC93B1,PIK3AP1,PTPN22,RSAD2
BP	GO:0034121	regulation of toll-like receptor signaling pathway	47	412	9	0.000576	0.022	0.191	8	IRF7,TLR1,TRIM30A,TLR9,IRF1,PTPN22,CD300A,RSAD2,TNFAIP3
BP	GO:0034124	regulation of MyD88-dependent toll-like receptor signaling pathway	4	295	3	0.0298	0.01	0.75	9	IRF7,IRF1,CD300A
BP	GO:0002429	immune response-activating cell surface receptor signaling pathway	267	331	18	0.000453	0.054	0.067	5	MYO1G,FYB,C3AR1,THEMIS2,CSAR1,PTPRC,LC2,WAS,FCER1G,PTPN6,PLCG2,PTPN22 NCKAP1,CD300A,KHLH6,LPXN,LCK,NFAM1
BP	GO:0009967	positive regulation of signal transduction	1289	480	83	9.72E-16	0.173	0.064	3	CC11,CC15,C3,CCX19,CD74,CCL8,NLRCS,CCX110,ZBP1,IRG1,CD4,CCL12,ITGAL,IRF7,BS T2,TLR1,LAT,S100A9,S100A8,TLR2,NAIP2,XDH,CSAR1,ICAM1,TLR7,NCF1,PCYCARD,CCL 6,CD44,TLR9,TRPV4,HCL51,PTPN6,ADCY7,TNFRSF1B,AIF1,VAV1,BLNK,DDX60,CTSH, PIK3CG,DHX58,IKBKE,PRKCD,PIK3AP1,FCG2,PTPN22,TREM2,IGALS9,CD14, CARD9,CD300A,FGFBP1,MAP3K6,RSAD2,IL6RA,PIK3R6,LCK,CSF1R,IL1R1,NFAM1,EC M1,TGM2,GLI2R2,COL1A1,MYOC,KLK6,FCLRS,CCL9,PRRSL,CD180,ZC3H12A,CLEC4N,P LAUR,CCL17,HTF6,F10,CRHR2,GPR35,CCL2
BP	GO:1902533	positive regulation of intracellular signal transduction	839	492	61	1.2E-12	0.124	0.073	4	CC11,CC15,CCX19,CD74,CCL8,CCX110,CD4,CCL12,ITGAL,BST2,TLR1,S100A9,S100A8,LA R2,XDH,CSAR1,ICAM1,TLR7,NCF1,PCYCARD,CCL6,CD44,TLR9,TRPV4,HCL51,PTPN6,PIK 3R5,DOCK2,HAVER2,S100A4,DDX60,PIK3CG,DHX58,IKBKE,PIK3AP1,FGD2,PTPN22,TREM 2,CD14,CARD9,CD300A,MAP3K6,IL6RA,PIK3R6,LCK,CSF1R,ECM1,TGM2,GLI2R2,MYOC CCL9,PRRSL,ZC3H12A,CLEC4N,CCL17,HTF6,F10,CRHR2,GPR35,CCL2,MAS1
BP	GO:0001961	positive regulation of cytokine-mediated signaling pathway	30	79	4	0.0121	0.051	0.133	4	CD74,NLRCS,ZBP1,IRF7
BP	GO:0048646	anatomical structure formation involved in morphogenesis	974	484	53	0.00000361	0.11	0.054	1	C3,CCX19,CCL8,TRIM30A,CCX110,LARG1,CCL12,SPINT1,C3AR1,THEMIS2,BTB1,CCR2,TLR2,CSA R1,CSF1R,TNFAIP2,TNFSF13B,PTPN6,NGP,HIF3A,STAT1,CTSH,MAFB,PIK3CG,RNF213,IL 1A,CAPN3,TIFAB,TGFB1,KHLH6,PIK3R6,IL6RA,ECM1,SP100,CD53,ADM,TGM2,PIM1,COL 1A1,NGFR,UGT8A,ANG,TNFAIP3,ZC3H12A,DUSP2,STAB1,MM2P,BCL3,CNMD,CRHR2,I NCL3D,CCL2,CAMP
BP	GO:0002467	germinal center formation	14	477	5	0.0246	0.01	0.357	2	TNFSF13B,KHLH6,TNFAIP3,BCL3,UNC13D
BP	GO:0006793	phosphorus metabolic process	2955	458	94	0.0416	0.205	0.032	1	CC11,CC15,C3,CCX19,CD74,CCL8,NLRCS,CCX110,CD4,CCL12,IL12RB1,SLC11A1,TLR1,L AT,OSL2,RAC2,TLR2,HCK,XDH,CSAR1,ICAM1,TLR7,TLR13,OSL2,NCF1,PCYCARD,PTPRC GBP4,OAS1A,CCL6,PLD4,LC2,CD44,TLR9,RHOH,TRPV4,HCL51,ACPS,PTPN6,ADCY7,AIF 1,PIK3R5,PTAFR,HAVER2,FAS,PLCG2,NUAK2,HK2,CTSH,TSP0,PIK3CG,IKBKE,NCF2,PRK D,FGD2,INPP5D,PTPN22,TREM2,IGALS9,CARD9,NCKAP1,CD300A,TYROBP,MAP3K6,C BR2,PLAU,IL6RA,PIK3R6,LCK,BTK,CSF1R,APOC1,ADM,GLI2R2,PIM1,MERTK,APLN,MYO C,CCL9,PRRSL,ANG,TNFAIP3,GPR65,PTGER4,HK3,DOX1,PTPN18,ZC3H12A,UPPP1,DUSP 2,DOX2,PLAUR,PN3,CCL17
BP	GO:0006796	phosphate-containing compound metabolic process	2889	458	94	0.0165	0.205	0.033	2	CC11,CC15,C3,CCX19,CD74,CCL8,NLRCS,CCX110,CD4,CCL12,IL12RB1,SLC11A1,TLR1,L AT,OSL2,RAC2,TLR2,HCK,XDH,CSAR1,ICAM1,TLR7,TLR13,OSL2,NCF1,PCYCARD,PTPRC GBP4,OAS1A,CCL6,PLD4,LC2,CD44,TLR9,RHOH,TRPV4,HCL51,ACPS,PTPN6,ADCY7,AIF 1,PIK3R5,PTAFR,HAVER2,FAS,PLCG2,NUAK2,HK2,CTSH,TSP0,PIK3CG,IKBKE,NCF2,PRK D,FGD2,INPP5D,PTPN22,TREM2,IGALS9,CARD9,NCKAP1,CD300A,TYROBP,MAP3K6,C BR2,PLAU,IL6RA,PIK3R6,LCK,BTK,CSF1R,APOC1,ADM,GLI2R2,PIM1,MERTK,APLN,MYO C,CCL9,PRRSL,ANG,TNFAIP3,GPR65,PTGER4,HK3,DOX1,PTPN18,ZC3H12A,UPPP1,DUSP 2,DOX2,PLAUR,PN3,CCL17
BP	GO:0016310	phosphorylation	2081	448	72	0.016	0.161	0.035	3	CC11,CC15,C3,CD74,CCL8,NLRCS,CD4,CCL12,IL12RB1,SLC11A1,TLR1,LAT,RAC2,TLR2,H CK,XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYCARD,GBP4,CCL6,LC2,CD44,TLR9,RHOH,T RPV4,HCL51,PTPN6,AIF1,PIK3R5,HAVER2,FAS,NUAK2,CTSH,PIK3CG,IKBKE,PRKCD,FGD2, PTPN22,TREM2,IGALS9,CARD9,NCKAP1,CD300A,TYROBP,MAP3K6,PLAU,IL6RA,PIK3R6, LCK,BTK,CSF1R,GLI2R2,PIM1,MERTK,APLN,MYOC,CCL9,PRRSL,ANG,TNFAIP3,P TGER4,HK3,DOX1,ZC3H12A,DUSP2,DOX2,PLAUR
BP	GO:0006468	protein phosphorylation	1732	492	70	0.0027	0.142	0.04	4	CC11,CC15,C3,CD74,CCL8,CD4,CCL12,IL12RB1,SLC11A1,TLR1,LAT,RAC2,TLR2,HCK,XD H,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYCARD,GBP4,CCL6,LC2,CD44,TLR9,TRPV4,HCL51 ,PTPN6,AIF1,PIK3R5,HAVER2,FAS,NUAK2,CTSH,PIK3CG,IKBKE,PRKCD,FGD2,PTPN22,TR EM2,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,IL6RA,PIK3R6,LCK,BTK,CSF1R,GLI2R2, PIM1,MERTK,MYOC,CCL9,PRRSL,ANG,TNFAIP3,PTGER4,DOX1,ZC3H12A,DUSP2,DOX2, PLAUR,CCL17,SPN,CCL2,CAMP,MAS1
BP	GO:0018108	peptidyl-tyrosine phosphorylation	324	323	18	0.00532	0.056	0.056	5	CCL5,CD74,CD4,IL12RB1,HCK,ICAM1,NCF1,CD44,HCL51,PTPN6,PRKCD,PTPN22,TREM 2,CD300A,IL6RA,LCK,BTK,CSF1R
BP	GO:0023014	signal transduction by protein phosphorylation	735	458	42	0.0000114	0.092	0.057	5	CC11,CC15,CD74,CCL8,CD4,CCL12,SLC11A1,XDH,CSAR1,ICAM1,TLR13,NCF1,PCYCARD,C CL6,CD44,TLR9,TRPV4,PTPN6,PIK3R5,HAVER2,FAS,CTSH,PIK3CG,PRKCD,FGD2,PTPN22, TREM2,CARD9,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R,GLI2R2,MYOC,CCL9,PTGER4,DO X1,ZC3H12A,DUSP2,DOX2,CCL17
BP	GO:0000165	MAPK cascade	698	458	42	0.00000247	0.092	0.06	6	CC11,CC15,CD74,CCL8,CD4,CCL12,SLC11A1,XDH,CSAR1,ICAM1,TLR13,NCF1,PCYCARD,C CL6,CD44,TLR9,TRPV4,PTPN6,PIK3R5,HAVER2,FAS,CTSH,PIK3CG,PRKCD,FGD2,PTPN22, TREM2,CARD9,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R,GLI2R2,MYOC,CCL9,PTGER4,DO X1,ZC3H12A,DUSP2,DOX2,CCL17
BP	GO:0070371	ERK1 and ERK2 cascade	275	480	23	0.00013	0.048	0.084	7	CC11,CC15,CD74,CCL8,CD4,CCL12,CSAR1,ICAM1,PCYCARD,CCL6,CD44,TRPV4,PTPN6,H AVER2,CTSH,PTPN22,TREM2,CSF1R,GLI2R2,CCL9,PTGER4,CCL17,CCL2
BP	GO:0051174	regulation of phosphorus metabolic process	1563	492	69	0.000122	0.14	0.044	2	CC11,CC15,C3,CCX19,CD74,CCL8,NLRCS,CCX110,CD4,CCL12,SLC11A1,TLR1,LAT,RAC2, XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYCARD,GBP4,CCL6,LC2,CD44,TLR9,RHOH,TRP V4,HCL51,PTPN6,ADCY7,AIF1,PIK3R5,PTAFR,HAVER2,FAS,TSP0,PIK3CG,PRKCD,FGD2, PTPN22,TREM2,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R,APOC1, ADM,GLI2R2,APLN,MYOC,CCL9,PRRSL,ANG,TNFAIP3,GPR65,ZC3H12A,DUSP2,PLAUR,C CL17,NPPC,SPN,CCL2,CAMP,MAS1

BP	GO:0019220	regulation of phosphate metabolic process	1558	492	69	0.000107	0.14	0.044	3	CC11,CC15,C3,CXCL9,CD74,CCL8,NLRCS,CXCL10,CD4,CCL12,SLC11A1,TLR1,LAT,RAC2,XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYARD,GBP4,CCL6,PCP2,CD44,TLR9,RHOH,TRPV4,HCL1,PTPN6,ADCV7,AIF1,PIK3R5,PTAFR,HAVCR2,FAS,TSPO,PIK3CG,PRKCD,FGD2,PTPN22,TREM2,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R,APOC1,ADM,GULP2,APLN,MYOC,CCL3,PRRS1,ANG,TNFAIP3,GNP65,ZC3H12A,DUSP2,PLAUR,CL17,NPPC,SPN,CC12,CAMP,MAS1
BP	GO:0042325	regulation of phosphorylation	1335	323	45	0.000563	0.139	0.034	4	CC11,CC15,C3,CD74,CCL8,NLRCS,CD4,CCL12,SLC11A1,TLR1,LAT,RAC2,XDH,CSAR1,ICAM1,TLR7,TLR13,NCF1,PCYARD,GBP4,CCL6,PCP2,CD44,TLR9,RHOH,TRPV4,HCL1,PTPN6,AIF1,PIK3R5,HAVCR2,FAS,PIK3CG,PRKCD,FGD2,PTPN22,TREM2,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R
BP	GO:0032418	lysosome localization	57	487	10	0.00133	0.021	0.175	1	CD84,LAT,RAC2,FCER1G,CD300A,BTK,IL4RA,LAT2,UNC13D,MILR1
BP	GO:0043303	mast cell degranulation	41	487	10	0.000475	0.021	0.244	2	CD84,LAT,RAC2,FCER1G,CD300A,BTK,IL4RA,LAT2,UNC13D,MILR1
BP	GO:0006897	endocytosis	647	480	37	0.000317	0.077	0.057	1	C3,MYO1G,IGALS3,ITGAL,B2M,SLC11A1,CCR2,HCK,IGALS3BP,PCYARD,PLD4,CXCL16,FGFR1,WAS,FCER1G,CD163,AIF1,VAV1,DOCK2,PLCG2,PIK3CG,TREM2,CD14,NCKAP1,CD300A,APOC1,RAB20,IFITM3,ADM,TGM2,MERTK,FCRL5,SIGLECE,STAB1,C2,UNC13D,CCL2
BP	GO:0006909	phagocytosis	267	480	24	0.0000161	0.05	0.09	2	C3,MYO1G,ITGAL,SLC11A1,CCR2,HCK,PCYARD,PLD4,FCGR1,WAS,FCER1G,AIF1,VAV1,DOCK2,TREM2,NCKAP1,CD300A,RAB20,TGM2,MERTK,SIGLECE,C2,UNC13D,CCL2
BP	GO:0048523	negative regulation of cellular process	4218	406	124	0.0000512	0.305	0.029	1	CCL5,C3,CXCL9,CD74,IF1204,TSPAN32,NLRCS,CXCL10,IF1209,IF1207,CCL12,BCL2A1B,H2-K1,IGALS3,H2-D1,SPINT1,SLFN2,B2M,BST2,A2M,C4B,CD84,CCR2,RASAL3,TLR2,HCK,NAIP2,PLAC8,XDH,CSAR1,CD274,ICAM1,WFC17,PCYARD,GBP4,TRIM30A,WAS,CD44,FCER1G,APOBEC3,TLR9,DLK1,RHOH,TRPV4,HCL1,C1QC,LST1,SP1,APOBEC1,ACPS,IRF1,PTPN6,H2-M3,NGP,IKZF1,AIF1,LAG3,CYP26B1,HIF3A,CAPG,HAVCR2,TNFAIP8L2,FAS,STAT1,PLCG2,NUAK2,CD37,HK2,GFAP,CTSH,TSH,SP1,H1H4,CTLA2B,MAFB,PIK3CG,DHX58,RNF213,PRKCD,IL1A,CAPN3,SERPINC1,INPP5D,PTPN22,IGALS9,NCKAP1,CD300A,ACER2,RHBD,F2,RSAD2,PARP10,XAF1,TRIM21,CCRS,LPXN,LCK,BTK,CSF1R,IL4RA,IFIT3,CEBPA,ISG15,APOC1,IFITM3,ECM1,SP100,ADM,RASD1,CTS2,NFKBIE,PIM1,MERTK,ITIH3,CCDC3,COL1A1,NGFR,ATF5,MYOC,COL28A1,GKN3,CS17,HP,CC19,PRRS1,ANG
BP	GO:0050866	negative regulation of cell activation	161	487	25	5.57E-11	0.051	0.155	2	CD74,TSPAN32,CD84,CCR2,CD274,LST1,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,FAS,CD37,PRKCD,INPP5D,PTPN22,IGALS9,CD300A,BTK,IL4RA,MERTK,TNFAIP3,SPN,MILR1
BP	GO:0002695	negative regulation of leukocyte activation	146	487	24	5.05E-11	0.049	0.164	3	CD74,TSPAN32,CD84,CCR2,CD274,LST1,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,FAS,CD37,INPP5D,PTPN22,IGALS9,CD300A,BTK,IL4RA,MERTK,TNFAIP3,SPN,MILR1
BP	GO:0051250	negative regulation of lymphocyte activation	125	412	18	6.35E-08	0.044	0.144	4	CD74,CD274,LST1,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,FAS,INPP5D,PTPN22,IGALS9,CD300A,BTK,IL4RA,MERTK,TNFAIP3
BP	GO:0030886	negative regulation of myeloid dendritic cell activation	4	232	3	0.0144	0.013	0.75	4	TSPAN32,HAVCR2,CD37
BP	GO:0007162	negative regulation of cell adhesion	223	412	19	0.00014	0.046	0.085	2	CD74,CD274,TRPV4,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,PRKCD,PTPN22,IGALS9,CD300A,ACER2,LPXN,IL4RA,COL1A1,MYOC,TNFAIP3
BP	GO:0022408	negative regulation of cell-cell adhesion	145	326	14	0.000115	0.043	0.097	3	CD74,CD274,TRPV4,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,PRKCD,PTPN22,IGALS9,CD300A,IL4RA
BP	GO:1903038	negative regulation of leukocyte cell-cell adhesion	103	326	12	0.000136	0.037	0.117	4	CD74,CD274,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,PTPN22,IGALS9,CD300A,IL4RA
BP	GO:0050868	negative regulation of T cell activation	94	326	12	0.0000478	0.037	0.128	5	CD74,CD274,IRF1,PTPN6,H2-M3,LAG3,HAVCR2,TNFAIP8L2,PTPN22,IGALS9,CD300A,IL4RA
BP	GO:0008285	negative regulation of cell proliferation	582	412	32	0.000186	0.078	0.055	2	TSPAN32,CCL12,SPINT1,SLFN2,TLR2,XDH,CD274,LST1,IRF1,PTPN6,H2-M3,AIF1,HAVCR2,STAT1,CD37,TSPO,IL1A,INPP5D,IGALS9,CD300A,PARP10,BTK,CSF1R,IFIT3,CEBPA,IFITM3,ADM,NGFR,ATF5,GKN3,ANG,TNFAIP3,CCL12,CD274,LST1,PTPN6,H2-M3,HAVCR2,INPP5D,IGALS9,CD300A,BTK
BP	GO:0070664	negative regulation of leukocyte proliferation	72	322	10	0.000204	0.031	0.139	3	CD274,LST1,PTPN6,H2-M3,HAVCR2,INPP5D,IGALS9,CD300A,BTK
BP	GO:0032945	negative regulation of mononuclear cell proliferation	68	322	9	0.00204	0.028	0.132	4	CD274,LST1,PTPN6,H2-M3,HAVCR2,INPP5D,IGALS9,CD300A,BTK
BP	GO:0050672	negative regulation of lymphocyte proliferation	68	322	9	0.00204	0.028	0.132	5	CD274,LST1,PTPN6,H2-M3,HAVCR2,INPP5D,IGALS9,CD300A,BTK
BP	GO:0009893	positive regulation of metabolic process	2989	375	92	0.0000267	0.245	0.031	1	CC11,CC15,C3,CXCL9,CD74,CCL8,LCN2,CYBB,NLRCS,CXCL10,CD4,CCL12,SLC11A1,IRF7,TLR1,ELF4,LAT,ITGB2,S100A9,CCR2,S100A8,TLR2,PLAC8,XDH,CSAR1,LTB,ICAM1,TLR7,NCF1,PCYARD,CCL6,TRIM30A,PCP2,CD44,TLR9,TRPV4,HCL1,SP1,APOBEC1,ICOSL,IRF1,ADCV7,TNFRSF1B,H2-M3,CTSC,AIF1,CYP26B1,PIK3R5,PTAFR,HIF3A,HAVCR2,FAS,STAT1,PLCG2,HK2,CTSH,TSPO,HIST1H4H,MAFB,PIK3CG,PARP3,PRKCD,IL1A,CAPN3,FGD2,PTPN22,TREM2,BIRC3,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,ACER2,KLHL6,IL6RA,PIK3R6,LCK,CSF1R,CEBPA,TMEM173,ADM,GULP2,CCDC3,COL1A1,NPAS4,APLN,NGFR,ATF5,FOS
BP	GO:0010604	positive regulation of macromolecule metabolic process	2760	323	73	0.000113	0.226	0.026	2	CCL1,CC15,C3,CXCL9,CD74,CCL8,LCN2,CYBB,NLRCS,CXCL10,CD4,CCL12,SLC11A1,IRF7,TLR1,ELF4,LAT,ITGB2,S100A9,CCR2,S100A8,PLAC8,XDH,CSAR1,LTB,ICAM1,TLR7,NCF1,PCYARD,CCL6,TRIM30A,PCP2,CD44,TLR9,TRPV4,HCL1,SP1,APOBEC1,ICOSL,IRF1,ADCV7,TNFRSF1B,H2-M3,CTSC,AIF1,PIK3R5,PTAFR,HIF3A,HAVCR2,FAS,STAT1,CTSH,MAFB,PIK3CG,PARP3,PRKCD,IL1A,CAPN3,FGD2,PTPN22,TREM2,BIRC3,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,ACER2,KLHL6,IL6RA,PIK3R6,LCK,CSF1R,CEBPA,TMEM173,ADM,GULP2,COL1A1,NPAS4,NGFR,ATF5,FOS
BP	GO:0051173	positive regulation of nitrogen compound metabolic process	2662	375	81	0.000451	0.216	0.03	2	CC11,CC15,C3,CXCL9,CD74,CCL8,CYBB,NLRCS,CXCL10,CD4,CCL12,SLC11A1,IRF7,TLR1,ELF4,LAT,ITGB2,S100A9,CCR2,S100A8,PLAC8,XDH,CSAR1,LTB,ICAM1,TLR7,NCF1,PCYARD,CCL6,TRIM30A,PCP2,CD44,TLR9,TRPV4,HCL1,SP1,APOBEC1,ICOSL,IRF1,ADCV7,TNFRSF1B,H2-M3,CTSC,AIF1,PIK3R5,PTAFR,HIF3A,HAVCR2,FAS,STAT1,CTSH,MAFB,PIK3CG,PARP3,PRKCD,IL1A,CAPN3,FGD2,PTPN22,TREM2,BIRC3,IGALS9,CARD9,NCKAP1,CD300A,MAP3K6,ACER2,KLHL6,IL6RA,PIK3R6,LCK,CSF1R,CEBPA,TMEM173,ADM,GULP2,COL1A1,NPAS4,NGFR,ATF5,FOS
BP	GO:0048869	cellular developmental process	3994	434	114	0.0416	0.263	0.029	1	CLEC4D,CLEC4E,CXCL9,CD74,CCL8,IF1204,H2-AB1,H2-AA,PIRB,LY9,CXCL10,LRG1,CD4,CCL12,H2-OA,IL2RG,H2-K1,IGALS3,PSMB8,H2-D1,SPINT1,B2M,A2M,ELF4,ST14,S100A9,CCR2,S100A8,ITGB7,TLR2,HCK,PLAC8,XDH,ICAM1,CSF3R,TNFAIP2,PLD4,FCER1G,APOBEC3,TLR9,DLK1,RHOH,TRPV4,HCL1,C1QC,LS1,SP1,SASH3,IRF1,PTPN6,FERMT3,H2-M3,IKZF1,CYP26B1,CD86,VAV1,DOCK2,FAS,STAT1,PLCG2,RAB32,GFAP,TSPO,HIST1H4H,MAFB,PRKCD,IL1A,CAPN3,INPP5D,MAFF,PTPN22,TREM2,IGALS9,TGFB1,NCKAP1,TYROBP,RSAD2,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,CMTM7,CD53,ADM,GULP2,CITSD,DNASE2,MT2,MERTK,CCDC3,COL1A1,NPAS4,ATF5,UGT8A,FOS,MYOC,KLK6,OMPA,ARL11,ARL11,CCL9,ANG,TNFAIP3,CMKLR1,CASP4,STEAP4,PTGER4,IL3RA,XLR,BATF2
BP	GO:0030154	cell differentiation	3816	481	122	0.0129	0.254	0.032	2	CLEC4D,CLEC4E,CXCL9,CD74,CCL8,IF1204,H2-AB1,H2-AA,PIRB,LY9,CXCL10,LRG1,CD4,CCL12,H2-OA,IL2RG,H2-K1,IGALS3,PSMB8,H2-D1,SPINT1,B2M,A2M,ELF4,ST14,S100A9,CCR2,S100A8,ITGB7,TLR2,HCK,PLAC8,XDH,ICAM1,CSF3R,TNFAIP2,PLD4,FCER1G,APOBEC3,TLR9,DLK1,RHOH,TRPV4,HCL1,C1QC,LS1,SP1,SASH3,IRF1,PTPN6,FERMT3,H2-M3,IKZF1,CYP26B1,CD86,VAV1,DOCK2,FAS,STAT1,PLCG2,RAB32,GFAP,TSPO,HIST1H4H,MAFB,PRKCD,IL1A,CAPN3,INPP5D,MAFF,PTPN22,TREM2,IGALS9,TGFB1,NCKAP1,TYROBP,RSAD2,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,CMTM7,CD53,ADM,GULP2,CITSD,DNASE2,MT2,MERTK,CCDC3,COL1A1,NPAS4,ATF5,UGT8A,FOS,MYOC,KLK6,OMPA,ARL11,ARL11,CCL9,ANG,TNFAIP3,CMKLR1,CASP4,STEAP4,PTGER4,IL3RA,XLR,BATF2,ZC3H12A,CCL17,MMP2,BCL3,NPPC,CNMD,UNC13D,SPN,CCL2,UPK1B
BP	GO:0045595	regulation of cell differentiation	1597	379	53	0.0114	0.14	0.033	3	CXCL9,CD74,CCL8,IF1204,H2-AA,CXCL10,CD4,H2-OA,IL2RG,H2-K1,H2-D1,SPINT1,B2M,CCR2,TLR2,XDH,CSF3R,TRPV4,HCL1,C1QC,SP1,SASH3,IRF1,PTPN6,H2-M3,CYP26B1,FAS,STAT1,GFAP,TSPO,HIST1H4H,MAFB,CAPN3,INPP5D,MAFF,IGALS9,NCKAP1,TYROBP,PIK3R6,LCK,IL4RA,CEBPA,ISG15,NFAM1,CD53,ADM,GULP2,CITSD,CCDC3,COL1A1,FOS,MYOC,KLK6
BP	GO:0048731	system development	4283	379	114	0.00157	0.301	0.027	1	CLEC4D,CLEC4E,C3,CD74,IF1204,H2-AB1,H2-AA,PIRB,LY9,CXCL10,LRG1,CD4,CCL12,H2-OA,IL2RG,H2-K1,H2-D1,SPINT1,B2M,H2-T23,CSAR1,ITGB2,ST14,S100A9,CCR2,S100A8,CRYBA4,TLR2,XDH,CSAR1,LTB,ICAM1,CSF3R,TNFAIP2,PLD4,CD44,C1QB,FCER1G,APOBEC3,TLR9,RHOH,TRPV4,HCL1,C1QC,LST1,SP1,SASH3,ACPS,ICOSL,IRF1,PTPN6,H2-M3,NGP,IKZF1,CYP26B1,CD86,VAV1,HIF3A,LCPI,DOCK2,HAVCR2,FAS,STAT1,PLCG2,H2-GFAP,ADAP2,CTSH,TSPO,HIST1H4H,MAFB,PIK3CG,RNF213,IL1A,CAPN3,INPP5D,MAFF,PTPN22,TREM2,TIFAB,IGALS9,TGFB1,NCKAP1,TYROBP,RSAD2,IL6RA,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,ECM1,CMTM7,SP100,ADM,TGM2,GULP2,CITSD,NASE2A,MT2,PIM1,MERTK,COL1A1,NPAS4,NGFR,ATF5,UGT8A,FOS,MYOC,KLK6
BP	GO:0048513	animal organ development	3197	377	86	0.0365	0.228	0.027	2	CLEC4D,CLEC4E,CD74,IF1204,H2-AB1,H2-AA,PIRB,LY9,CD4,H2-OA,IL2RG,H2-K1,SPINT1,B2M,H2-T23,ST14,CCR2,CRYBA4,XDH,CSAR1,LTB,ICAM1,CSF3R,PLD4,CD44,C1QB,FCER1G,APOBEC3,TLR9,RHOH,HCL1,C1QC,SP1,SASH3,ACPS,IRF1,PTPN6,H2-M3,IKZF1,CYP26B1,CD86,VAV1,LCPI,DOCK2,FAS,STAT1,PLCG2,H2-ADAP2,CTSH,TSPO,HIST1H4H,MAFB,CAPN3,INPP5D,MAFF,PTPN22,TREM2,TIFAB,IGALS9,TGFB1,NCKAP1,TYROBP,RSAD2,IL6RA,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,ECM1,CMTM7,SP100,ADM,TGM2,GULP2,CITSD,NASE2A,MT2,PIM1,MERTK,COL1A1,NPAS4,NGFR,ATF5,UGT8A,FOS,MYOC,KLK6

BP	GO:0002520	immune system development	888	434	62	1E-14	0.143	0.07	2	CLEC4D,CLEC4E,CD74,H2-AB1,H2-AA,PIRB,LY9,CD4,H2-OA,IL2RG,B2M,CCR2,LTB,CSF3R,PLD4,FCER1G,APOBEC3,RHOH,HCL1,C1QC,SP1,SAS H3,ICOSL,IRF1,PTPN6,H2-M3,IKZF1,CYP26B1,CD86,NAV1,DOCK2,HAVCR2,FAS,STAT1,PLCG2,HIST1H4H,MAFB,INPP5D,PTN22,TREM2,LGALS9,NCKAP1,TYROBP,RSAD2,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,ISG15,NFAM1,CMTM7,DNASE2A,MERTK,FOS,ARL11,TNFAIP3,PTGER4,IL3RA,IC OS,BATF2
BP	GO:0048534	hematopoietic or lymphoid organ development	846	434	59	7.59E-14	0.136	0.07	3	CLEC4D,CLEC4E,CD74,H2-AB1,H2-AA,PIRB,LY9,CD4,H2-OA,IL2RG,B2M,CCR2,LTB,CSF3R,PLD4,FCER1G,APOBEC3,RHOH,HCL1,C1QC,SP1,SAS H3,IRF1,PTPN6,H2-M3,IKZF1,CYP26B1,CD86,NAV1,DOCK2,FAS,STAT1,PLCG2,HIST1H4H,MAFB,INPP5D,PTN22,TREM2,LGALS9,NCKAP1,TYROBP,RSAD2,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,IS G15,NFAM1,CMTM7,DNASE2A,MERTK,FOS,ARL11,TNFAIP3,PTGER4,IL3RA,BATF2
BP	GO:0030097	hemopoiesis	801	434	58	2.6E-14	0.134	0.072	4	CLEC4D,CLEC4E,CD74,H2-AB1,H2-AA,PIRB,LY9,CD4,H2-OA,IL2RG,B2M,CCR2,CSF3R,PLD4,FCER1G,APOBEC3,RHOH,HCL1,C1QC,SP1,SASH3,IR F1,PTPN6,H2-M3,IKZF1,CYP26B1,CD86,NAV1,DOCK2,FAS,STAT1,PLCG2,HIST1H4H,MAFB,INPP5D,PT N22,TREM2,LGALS9,NCKAP1,TYROBP,RSAD2,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,IS G15,NFAM1,CMTM7,DNASE2A,MERTK,FOS,ARL11,TNFAIP3,PTGER4,IL3RA,BATF2
BP	GO:0030099	myeloid cell differentiation	354	434	25	0.000133	0.058	0.071	5	CD74,PIRB,CD4,B2M,CSF3R,HCL1,C1QC,SP1,PTPN6,IKZF1,CD86,FAS,STAT1,HIST1H4H ,MAFB,INPP5D,NCKAP1,TYROBP,CSF1R,CEBPA,ISG15,DNASE2A,FOS,IL3RA,BATF2
BP	GO:0030218	erythrocyte differentiation	106	352	10	0.0255	0.028	0.094	6	B2M,HCL1,SP1,IKZF1,STAT1,MAFB,INPP5D,NCKAP1,ISG15,DNASE2A
BP	GO:0002521	leukocyte differentiation	498	434	50	6.74E-18	0.115	0.1	5	CLEC4D,CLEC4E,CD74,H2-AB1,H2-AA,PIRB,LY9,CD4,H2-OA,IL2RG,B2M,CCR2,FCER1G,RHOH,HCL1,C1QC,SP1,SASH3,IRF1,PTPN6,H2-M3,IKZF1,CYP26B1,CD86,NAV1,DOCK2,FAS,PLCG2,MAFB,INPP5D,PTN22,TREM2,LGA S9,NCKAP1,TYROBP,RSAD2,PIK3R6,LCK,BTK,CSF1R,IL4RA,CEBPA,NFAM1,CMTM7,ME RTK,FOS,TNFAIP3,PTGER4,IL3RA,BATF2
BP	GO:0002573	myeloid leukocyte differentiation	191	434	15	0.0193	0.035	0.079	6	CD74,PIRB,CD4,HCL1,C1QC,SP1,CD86,MAFB,INPP5D,TYROBP,CSF1R,CEBPA,FOS,IL3R A,BATF2
BP	GO:0030098	lymphocyte differentiation	342	339	36	3.14E-16	0.106	0.105	6	CLEC4D,CLEC4E,CD74,H2-AB1,H2-AA,LY9,CD4,H2-OA,IL2RG,B2M,CCR2,FCER1G,RHOH,SP1,SASH3,IRF1,PTPN6,H2-M3,IKZF1,CYP26B1,NAV1,DOCK2,FAS,PLCG2,MAFB,INPP5D,PTN22,LGALS9,NCKAP1,RSAD2,PIK3R6,LCK,BTK,IL4RA,NFAM1,CMTM7
BP	GO:0030217	T cell differentiation	231	326	27	3.86E-13	0.083	0.117	7	CLEC4D,CLEC4E,CD74,H2-AA,LY9,CD4,H2-OA,IL2RG,B2M,CCR2,FCER1G,RHOH,SASH3,IRF1,H2-M3,CYP26B1,NAV1,DOCK2,FAS,MAFB,PTN22,LGALS9,NCKAP1,RSAD2,PIK3R6,LCK,IL4 RA
BP	GO:0002292	T cell differentiation involved in immune response	59	470	9	0.0127	0.019	0.153	8	CLEC4D,CLEC4E,LY9,CCR2,FCER1G,IRF1,IL4RA,PTGER4,BCL3
BP	GO:1903706	regulation of hemopoiesis	352	331	29	4.34E-10	0.088	0.082	5	CD74,H2-AA,CD4,H2-OA,IL2RG,B2M,CCR2,CSF3R,HCL1,C1QC,SP1,SASH3,IRF1,PTPN6,H2-M3,CYP26B1,FAS,STAT1,HIST1H4H,MAFB,INPP5D,LGALS9,NCKAP1,TYROBP,PIK3R6,L CK,IL4RA,ISG15,NFAM1
BP	GO:1902105	regulation of leukocyte differentiation	253	331	23	2.13E-08	0.069	0.091	6	CD74,H2-AA,CD4,H2-OA,IL2RG,CCR2,HCL1,C1QC,SASH3,IRF1,PTPN6,H2-M3,CYP26B1,FAS,MAFB,INPP5D,LGALS9,NCKAP1,TYROBP,PIK3R6,LCK,IL4RA,NFAM1
BP	GO:0045619	regulation of lymphocyte differentiation	154	331	18	6.74E-08	0.054	0.117	7	CD74,H2-AA,CD4,H2-OA,IL2RG,CCR2,SASH3,IRF1,PTPN6,H2-M3,CYP26B1,FAS,INPP5D,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA,NFAM1
BP	GO:0045580	regulation of T cell differentiation	126	326	14	0.000188	0.043	0.111	8	CD74,H2-AA,H2-OA,IL2RG,CCR2,SASH3,IRF1,H2-M3,CYP26B1,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA
BP	GO:1903708	positive regulation of hemopoiesis	177	330	17	0.00000513	0.052	0.096	6	CD74,H2-AA,CD4,IL2RG,CCR2,HCL1,SASH3,IRF1,H2-M3,STAT1,INPP5D,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA,ISG15
BP	GO:1902107	positive regulation of leukocyte differentiation	144	375	16	0.000116	0.043	0.111	7	CD74,H2-AA,CD4,IL2RG,CCR2,HCL1,SASH3,IRF1,H2-M3,INPP5D,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA,FOS
BP	GO:0045621	positive regulation of lymphocyte differentiation	92	326	13	0.00000332	0.04	0.141	8	CD74,H2-AA,IL2RG,CCR2,SASH3,IRF1,H2-M3,INPP5D,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA
BP	GO:0045582	positive regulation of T cell differentiation	79	326	12	0.00000626	0.037	0.152	9	CD74,H2-AA,IL2RG,CCR2,SASH3,IRF1,H2-M3,LGALS9,NCKAP1,PIK3R6,LCK,IL4RA
BP	GO:0045637	regulation of myeloid cell differentiation	196	375	16	0.00091	0.043	0.082	6	CD74,CD4,B2M,CSF3R,HCL1,C1QC,SP1,FAS,STAT1,HIST1H4H,MAFB,INPP5D,NCKAP1 ,LYROBP,ISG15,FOS
BP	GO:0045646	regulation of erythrocyte differentiation	43	330	7	0.0104	0.021	0.163	7	B2M,SP1,STAT1,MAFB,INPP5D,NCKAP1,ISG15
BP	GO:0042107	cytokine metabolic process	109	333	15	0.000000338	0.045	0.138	1	CYBB,IRF7,TLR1,CCR2,LTB,TLR7,TLR9,ICOSL,IRF1,LAG3,PTAFR,IL1A,INPP5D,CARD9,IRF 9
BP	GO:0042089	cytokine biosynthetic process	105	333	15	0.000000195	0.045	0.143	2	CYBB,IRF7,TLR1,CCR2,LTB,TLR7,TLR9,ICOSL,IRF1,LAG3,PTAFR,IL1A,INPP5D,CARD9,IRF 9
BP	GO:0042533	tumor necrosis factor biosynthetic process	18	479	6	0.00471	0.013	0.333	3	CYBB,TLR1,CCR2,CARD9,BCL3,SPN
BP	GO:0070201	regulation of establishment of protein localization	786	490	40	0.00341	0.082	0.051	1	HCAR2,CLEC4E,CCL5,ITGAX,TLR1,H2-T23,RAC2,TLR2,CD274,CD300C2,TLR7,PCYARD,GBP4,TLR9,TRPV4,HCL1,GSDMD,LCPI ,HAVCR2,PRKCD,IL1A,PTPN22,LGALS9,CD14,RHBD2,RSAD2,PARP10,CSF1R,IL4RA,TM EM173,SP100,PRRS1,ANG,CASP4,PTGER4,ZC3H12A,CLEC4N,BCL3,CCL2,BGLAP2
BP	GO:0051223	regulation of protein transport	732	490	40	0.000555	0.082	0.055	2	HCAR2,CLEC4E,CCL5,ITGAX,TLR1,H2-T23,RAC2,TLR2,CD274,CD300C2,TLR7,PCYARD,GBP4,TLR9,TRPV4,HCL1,GSDMD,LCPI ,HAVCR2,PRKCD,IL1A,PTPN22,LGALS9,CD14,RHBD2,RSAD2,PARP10,CSF1R,IL4RA,TM EM173,SP100,PRRS1,ANG,CASP4,PTGER4,ZC3H12A,CLEC4N,BCL3,CCL2,BGLAP2
BP	GO:0072358	cardiovascular system development	623	484	35	0.00132	0.072	0.056	1	C3,CYBB,CXCL10,LRG1,CCL12,SPINT1,C3AR1,ITGB2,CCR2,XDH,CSAR1,TNFAIP2,SPIL,N GP,HIF3A,STAT1,CTSH,PIK3CG,RNF213,IL1A,TFEB,PIK3R6,ECM1,SP100,ADM,COL1A1,NGFR,ANG,ZC3H12A,STAB1,MMP2,CNMD,CHRR2,CCL2,CAMP
BP	GO:0001944	vasculature development	610	484	35	0.000803	0.072	0.057	2	C3,CYBB,CXCL10,LRG1,CCL12,SPINT1,C3AR1,ITGB2,CCR2,XDH,CSAR1,TNFAIP2,SPIL,N GP,HIF3A,STAT1,CTSH,PIK3CG,RNF213,IL1A,TFEB,PIK3R6,ECM1,SP100,ADM,COL1A1,NGFR,ANG,ZC3H12A,STAB1,MMP2,CNMD,CHRR2,CCL2,CAMP
BP	GO:1901342	regulation of vasculature development	233	484	24	0.00000122	0.05	0.103	3	C3,CYBB,CXCL10,LRG1,C3AR1,ITGB2,CCR2,XDH,CSAR1,NGF,STAT1,CTSH,IL1A,PIK3R6, ECM1,SP100,ADM,NGFR,ZC3H12A,STAB1,CNMD,CHRR2,CCL2,CAMP
BP	GO:1904018	positive regulation of vasculature development	134	484	13	0.0257	0.027	0.097	4	C3,CYBB,LRG1,C3AR1,ITGB2,CCR2,XDH,CSAR1,CTSH,IL1A,PIK3R6,ECM1,ADM,ZC3H12A,CAMP
BP	GO:1904951	positive regulation of establishment of protein localization	495	490	31	0.000792	0.063	0.063	1	HCAR2,CLEC4E,ITGAX,H2-T23,RAC2,TLR2,CD274,CD300C2,TLR7,PCYARD,TLR9,TRPV4,HCL1,GSDMD,HAVCR2,P RKCD,IL1A,PTPN22,LGALS9,CD14,CSF1R,IL4RA,TMEM173,PRRS1,ANG,CASP4,PTGER4,Z C3H12A,CLEC4N,CCL2,BGLAP2
BP	GO:0051222	positive regulation of protein transport	462	490	31	0.000171	0.063	0.067	2	HCAR2,CLEC4E,ITGAX,H2-T23,RAC2,TLR2,CD274,CD300C2,TLR7,PCYARD,TLR9,TRPV4,HCL1,GSDMD,HAVCR2,P RKCD,IL1A,PTPN22,LGALS9,CD14,CSF1R,IL4RA,TMEM173,PRRS1,ANG,CASP4,PTGER4,Z C3H12A,CLEC4N,CCL2,BGLAP2
BP	GO:0001568	blood vessel development	585	484	35	0.000295	0.072	0.06	1	C3,CYBB,CXCL10,LRG1,CCL12,SPINT1,C3AR1,ITGB2,CCR2,XDH,CSAR1,TNFAIP2,SPIL,N GP,HIF3A,STAT1,CTSH,PIK3CG,RNF213,IL1A,TFEB,PIK3R6,ECM1,SP100,ADM,COL1A1,NGFR,ANG,ZC3H12A,STAB1,MMP2,CNMD,CHRR2,CCL2,CAMP
BP	GO:0043270	positive regulation of ion transport	219	86	8	0.00709	0.093	0.037	1	CCL5,CXCL9,CXCL10,CD4,CCL12,LGALS3,B2M,CTSS
BP	GO:0051928	positive regulation of calcium ion transport	95	57	6	0.000555	0.105	0.063	2	CCL5,CXCL9,CXCL10,CD4,CCL12,LGALS3,B2M,CTSS
BP	GO:0031325	positive regulation of cellular metabolic process	2772	375	85	0.000142	0.227	0.031	1	CCL5,CXCL9,CXCL10,CD4,CCL12,LGALS3
BP	GO:0010562	positive regulation of phosphorus metabolic process	988	492	57	0.000000164	0.116	0.058	3	CCL1,CCL5,C3,CXCL9,CD74,CCL8,CYBB,NLRCS,CXCL10,CD4,CCL12,SLC11A1,IRF7,TLR1,ELF4,LAT,ITGB2,S100A9,CCR2,S100A8,PLA2G8,ADAM10,CSAR1,ITB,ICAM1,TLR7,NCF1,PCY ARD,CCL6,ICP2,CD44,TLR9,TRPV4,HCL1,SP1,APOBEC1,ICOSL,IRF1,ADCY7,TNFRSF18,H2-M3,CTSC,AIF1,PIK3RS,PTAFR,HIF3A,HAVCR2,FAS,STAT1,PLCG2,HK2,CTSH,TSP0,MAFB,PIK3CG,PARP3,PRKCD,IL1A,CAPN3,FGD2,PTPN22,TREM2,BIRC3,LGALS9,CARD9,NCKAP1,CD300A,MAP3K6,ACER2,TRIM21,KLHL6,IL6RA,PIK3R6,LCK,CSF1R,CEBPA,TMEM173,ADM,GLI2,COL1A1,NPAS4,APLN,NGFR,ATF5,FOS
BP	GO:0045937	positive regulation of phosphate metabolic process	988	492	57	0.000000164	0.116	0.058	3	CCL1,CCL5,C3,CXCL9,CD74,CCL8,CYBB,NLRCS,CXCL10,CD4,CCL12,SLC11A1,IRF7,TLR1,ELF4,LAT,ITGB2,S100A9,CCR2,S100A8,PLA2G8,ADAM10,CSAR1,ITB,ICAM1,TLR7,NCF1,PCY ARD,CCL6,ICP2,CD44,TLR9,TRPV4,HCL1,SP1,APOBEC1,ICOSL,IRF1,ADCY7,TNFRSF18,H2-M3,CTSC,AIF1,PIK3RS,PTAFR,HIF3A,HAVCR2,FAS,STAT1,PLCG2,HK2,CTSH,TSP0,MAFB,PIK3CG,PARP3,PRKCD,FGD2,PTPN22,TREM2,LGALS9,CARD9,NCKAP1,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R,ADM,GLI2,APLN,CCL9,PRRS1,ANG,GPR65,ZC3H12A,PLA UR,CCL17,NPPC,SPN,CCL2,CAMP,MA51
BP	GO:0042327	positive regulation of phosphorylation	870	492	50	0.00000315	0.102	0.057	4	CCL1,CCL5,C3,CD74,CCL8,CD4,CCL12,SLC11A1,TLR1,LAT,XDH,CSAR1,ICAM1,NCF1,PCY ARD,CCL6,ICP2,CD44,TLR9,TRPV4,HCL1,AIF1,PIK3RS,HAVCR2,FAS,PIK3CG,PRKCD,FG D2,PTPN22,TREM2,LGALS9,CARD9,NCKAP1,CD300A,MAP3K6,IL6RA,PIK3R6,CSF1R,GI IPR2,APLN,CCL9,PRRS1,ANG,ZC3H12A,PLAUR,CCL17,SPN,CCL2,CAMP,MA51
BP	GO:0002790	peptide secretion	507	443	33	0.0000116	0.074	0.065	1	HCAR2,CLEC4E,CCL5,CD74,TLR1,H2-T23,S100A9,S100A8,TLR2,GBP5,CD274,CD300C2,PCYARD,LCP2,TNFSF13B,TLR9,TRPV4 ,GSDMD,HAVCR2,IL1A,PTPN22,LGALS9,CD14,RHBD2,RSAD2,CSF1R,IL4RA,APLN,ANG,CASP4,PTGER4,ZC3H12A,CLEC4N
BP	GO:0002791	regulation of peptide secretion	417	443	30	0.00000608	0.068	0.072	2	HCAR2,CLEC4E,CCL5,CD74,TLR1,H2-T23,S100A9,S100A8,TLR2,CD274,CD300C2,PCYARD,TLR9,TRPV4,GSDMD,HAVCR2,IL1A ,PTPN22,LGALS9,CD14,RHBD2,RSAD2,CSF1R,IL4RA,APLN,ANG,CASP4,PTGER4,ZC3H1 2A,CLEC4N

BP	GO:0009306	protein secretion	471	443	29	0.000346	0.065	0.062	2	HRCAR2, CLEC4E, CCL5, TLR1, H2-T23, TLR2, GBP5, CD274, CD300C2, PYCARD, LCP2, TNFSF138, TLR9, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, RHBD2, RSAD2, CSF1R, IL4RA, ANG, CASP4, PTGER4, ZC3H12A, CLEC4N
BP	GO:0050663	cytokine secretion	175	443	22	2.56E-08	0.05	0.126	3	CLEC4E, TLR1, TLR2, GBP5, CD274, CD300C2, PYCARD, LCP2, TLR9, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, CSF1R, IL4RA, CASP4, PTGER4, ZC3H12A, CLEC4N
BP	GO:0050708	regulation of protein secretion	386	443	26	0.000278	0.059	0.067	3	HRCAR2, CLEC4E, CCL5, TLR1, H2-T23, TLR2, CD274, CD300C2, PYCARD, TLR9, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, RHBD2, RSAD2, CSF1R, IL4RA, ANG, CASP4, PTGER4, ZC3H12A, CLEC4N
BP	GO:0050707	regulation of cytokine secretion	154	443	20	0.00000127	0.045	0.13	4	CLEC4E, TLR1, TLR2, CD274, CD300C2, PYCARD, TLR9, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, CSF1R, IL4RA, CASP4, PTGER4, ZC3H12A, CLEC4N
BP	GO:0002793	positive regulation of peptide secretion	240	443	22	0.0000118	0.05	0.092	2	HRCAR2, CLEC4E, H2-T23, S100A9, S100A8, CD274, CD300C2, PYCARD, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, CSF1R, IL4RA, APLN, ANG, CASP4, PTGER4, CLEC4N
BP	GO:0050714	positive regulation of protein secretion	218	490	20	0.000308	0.041	0.092	3	HRCAR2, CLEC4E, H2-T23, CD274, CD300C2, PYCARD, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, CSF1R, IL4RA, ANG, CASP4, PTGER4, CLEC4N, BGLAP2
BP	GO:0050715	positive regulation of cytokine secretion	106	443	16	0.00000119	0.036	0.151	4	CLEC4E, CD274, CD300C2, PYCARD, TRPV4, GSDMD, HAVCR2, IL1A, PTPN22, LGALS9, CD14, CSF1R, IL4RA, CASP4, PTGER4, CLEC4N
BP	GO:0051246	regulation of protein metabolic process	2450	323	78	0.000000085	0.241	0.032	1	CCL1, CCL5, C3, CD74, CCL8, CYBB, CD4, CCL12, PSM88, SPINT1, PSM89, SLC11A1, BST2, TLR1, A2M, CAB, LAT, S100A9, CCR2, S100A8, RAC2, NAIIP2, XDH, CSAR1, LTB, ICAM1, TLR7, WFDCL17, TR13, NCF1, PYCARD, GBP4, CCL6, TRIM30A, LCP2, CD44, TLR9, TRPV4, HCL51, SPI1, ICOSL, IIRF1, PTPN6, TNFRSF18, NGP, CTSC, AIF1, LAG3, PIK3R5, PTAFR, HAVCR2, FAS, GFAP, CTSH, TSP0, CTLA2B, PIK3CG, PRKCD, IL1A, CAPN3, SERPING1, FGD2, INPP5D, PTPN22, TREM2, BIRC3, LGALS9, CARD9, NCKAP1, CD300A, MAP3K6, ACER2, PARP10, TRIM21, IL6RA, PIK3R6, LCK, CSF1R
BP	GO:0048514	blood vessel morphogenesis	491	484	33	0.0000449	0.068	0.067	1	C3, CYBB, CXCL10, LRG1, CCL12, C3AR1, ITGB2, CCR2, XDH, CSAR1, TNFAIP2, SPI1, NGP, HIF3A, STAT1, CTSH, PIK3CG, RNF213, IL1A, TGFBI, PIK3R6, ECM1, SP100, ADM, NGFR, ANG, ZC3H12A, STAB1, MMP2, CNMD, CRRH2, CCL2, CAMP
BP	GO:2000181	negative regulation of blood vessel morphogenesis	84	480	10	0.0442	0.021	0.119	2	CXCL10, CCR2, XDH, NGP, STAT1, NGFR, STAB1, CNMD, CRRH2, CCL2
BP	GO:0030100	regulation of endocytosis	202	480	19	0.000315	0.04	0.094	1	C3, LGALS9, B2M, SLC11A1, HCK, PYCARD, FCGR1, FCER1G, DOCK2, PLCG2, CD14, NCKAP1L, CD300A, APOC1, RAB20, MERTK, SIGLEC2, C2, CCL2
BP	GO:0050764	regulation of phagocytosis	72	480	13	0.0000143	0.027	0.181	2	C3, SLC11A1, HCK, PYCARD, FCGR1, FCER1G, DOCK2, NCKAP1L, CD300A, MERTK, SIGLEC2, C2, CCL2
BP	GO:0030162	regulation of proteolysis	678	390	31	0.00563	0.079	0.046	1	C3, PSM88, SPINT1, PSM89, BST2, A2M, CAB, S100A9, S100A8, NAIIP2, XDH, WFDCL17, PYCARD, CD44, TNFRSF18, NGP, CTSC, FAS, CTSH, CTLA2B, CAPN3, SERPING1, ACER2, TRIM21, LCK, ECM1, CTSH, ITIH3, NGFR, COL28A1, CST7
BP	GO:0052547	regulation of peptidase activity	420	390	26	0.000134	0.067	0.062	2	C3, PSM88, SPINT1, PSM89, BST2, A2M, CAB, S100A9, S100A8, NAIIP2, XDH, WFDCL17, PYCARD, CD44, NGP, FAS, CTSH, CTLA2B, SERPING1, ACER2, LCK, ECM1, ITIH3, NGFR, COL28A1, CST7
BP	GO:0052548	regulation of endopeptidase activity	391	390	25	0.000131	0.064	0.064	3	C3, PSM88, SPINT1, PSM89, BST2, A2M, CAB, S100A9, S100A8, NAIIP2, XDH, WFDCL17, PYCARD, CD44, NGP, FAS, CTSH, CTLA2B, SERPING1, ACER2, LCK, ECM1, ITIH3, NGFR, COL28A1, CST7
BP	GO:0001525	angiogenesis	405	484	31	0.00000596	0.064	0.077	1	C3, CYBB, CXCL10, LRG1, CCL12, C3AR1, ITGB2, CCR2, CCR5, TNFAIP2, NGP, HIF3A, STAT1, CTSH, PIK3CG, RNF213, IL1A, TGFBI, PIK3R6, ECM1, SP100, ADM, NGFR, ANG, ZC3H12A, STAB1, MMP2, CNMD, CRRH2, CCL2, CAMP
BP	GO:0045765	regulation of angiogenesis	212	484	23	0.00000102	0.048	0.108	2	C3, CYBB, CXCL10, LRG1, C3AR1, ITGB2, CCR2, CCR5, TNFAIP2, NGP, STAT1, CTSH, IL1A, PIK3R6, ECM1, SP100, ADM, NGFR, ZC3H12A, STAB1, CNMD, CRRH2, CCL2, CAMP
BP	GO:0045766	positive regulation of angiogenesis	118	484	13	0.0062	0.027	0.11	2	C3, CYBB, LRG1, C3AR1, ITGB2, CCR5, TNFAIP2, NGP, STAT1, CTSH, IL1A, PIK3R6, ECM1, SP100, ADM, NGFR, ZC3H12A, STAB1, CNMD, CRRH2, CCL2, CAMP
BP	GO:0051247	positive regulation of protein metabolic process	1409	323	56	2.85E-08	0.173	0.04	1	CCL1, CCL5, C3, CD74, CCL8, CYBB, CD4, CCL12, SLC11A1, TLR1, LAT, S100A9, CCR2, S100A8, XDH, CSAR1, LTB, ICAM1, TLR7, NCF1, PYCARD, CCL6, TRIM30A, LCP2, CD44, TLR9, TRPV4, HCL51, ICOSL, IIRF1, PTPN6, TNFRSF18, CTSC, AIF1, PIK3R5, PTAFR, HAVCR2, FAS, GFAP, CTSH, TSP0, CTLA2B, PIK3CG, PRKCD, CAPN3, SERPING1, FGD2, PTPN22, TREM2, BIRC3, LGALS9, CARD9, NCKAP1, CD300A, MAP3K6, ACER2, PARP10, TRIM21, IL6RA, PIK3R6, LCK, CSF1R
BP	GO:0045807	positive regulation of endocytosis	116	480	13	0.00465	0.027	0.112	1	C3, B2M, SLC11A1, PYCARD, FCGR1, FCER1G, DOCK2, CD14, NCKAP1L, MERTK, C2, CCL2
BP	GO:0050766	positive regulation of phagocytosis	47	480	10	0.00017	0.021	0.213	2	C3, SLC11A1, PYCARD, FCGR1, FCER1G, DOCK2, NCKAP1L, MERTK, C2, CCL2
BP	GO:0032268	regulation of cellular protein metabolic process	2259	412	79	0.0000893	0.192	0.035	1	CCL1, CCL5, C3, CD74, CCL8, CD4, CCL12, SPIN1, SLC11A1, BST2, TLR1, A2M, CAB, LAT, S100A9, S100A8, RAC2, NAIIP2, XDH, CSAR1, ICAM1, TLR7, WFDCL17, TR13, NCF1, PYCARD, GBP4, CCL6, LCP2, CD44, TLR9, TRPV4, HCL51, SPI1, PTPN6, TNFRSF18, NGP, CTSC, AIF1, PIK3R5, PTAFR, HAVCR2, FAS, CTSH, TSP0, CTLA2B, PIK3CG, PRKCD, CAPN3, SERPING1, FGD2, PTPN22, TREM2, BIRC3, LGALS9, CARD9, NCKAP1, CD300A, MAP3K6, ACER2, PARP10, TRIM21, IL6RA, PIK3R6, LCK, CSF1R
BP	GO:0031399	regulation of protein modification process	1546	330	51	0.000304	0.155	0.033	2	CCL1, CCL5, C3, CD74, CCL8, CD4, CCL12, SLC11A1, TLR1, LAT, RAC2, XDH, CSAR1, ICAM1, TLR7, TLR13, NCF1, PYCARD, GBP4, CCL6, LCP2, CD44, TLR9, TRPV4, HCL51, SPI1, PTPN6, AIF1, PIK3R5, HAVCR2, FAS, TSP0, PIK3CG, PRKCD, CAPN3, FGD2, PTPN22, TREM2, BIRC3, LGALS9, CARD9, NCKAP1L, CD300A, MAP3K6, ACER2, PARP10, TRIM21, IL6RA, PIK3R6, CSF1R, ISG15
BP	GO:0001932	regulation of protein phosphorylation	1239	323	43	0.000493	0.133	0.035	3	CCL1, CCL5, C3, CD74, CCL8, CD4, CCL12, SLC11A1, TLR1, LAT, RAC2, XDH, CSAR1, ICAM1, TLR7, TLR13, NCF1, PYCARD, GBP4, CCL6, LCP2, CD44, TLR9, TRPV4, HCL51, PTPN6, AIF1, PIK3R5, HAVCR2, FAS, PIK3CG, PRKCD, FGD2, PTPN22, TREM2, CARD9, CD300A, MAP3K6, IL6RA, PIK3R6, CSF1R
BP	GO:0050730	regulation of peptidyl-tyrosine phosphorylation	203	323	14	0.00642	0.043	0.069	4	CCL5, CD74, CD4, ICAM1, NCF1, CD44, HCL51, PTPN6, PRKCD, PTPN22, TREM2, CD300A, IL6RA, CSF1R
BP	GO:0043408	regulation of MAPK cascade	633	323	31	0.0000176	0.096	0.049	4	CCL1, CCL5, CD74, CCL8, CD4, CCL12, XDH, CSAR1, ICAM1, TLR13, NCF1, PYCARD, CCL6, CD44, TLR9, TRPV4, PTPN6, PIK3R5, HAVCR2, FAS, PIK3CG, PRKCD, FGD2, PTPN22, TREM2, CARD9, CD300A, MAP3K6, IL6RA, PIK3R6, CSF1R
BP	GO:0070372	regulation of ERK1 and ERK2 cascade	260	350	18	0.000701	0.051	0.069	5	CCL1, CCL5, CD74, CCL8, CD4, CCL12, CSAR1, ICAM1, PYCARD, CCL6, CD44, TRPV4, PTPN6, HAVCR2, PTPN22, TREM2, CSF1R, GLIPR2
BP	GO:0032270	positive regulation of cellular protein metabolic process	1310	323	48	0.0000155	0.149	0.037	2	CCL1, CCL5, C3, CD74, CCL8, CD4, CCL12, SLC11A1, TLR1, LAT, S100A9, S100A8, XDH, CSAR1, ICAM1, NCF1, PYCARD, CCL6, LCP2, CD44, TLR9, TRPV4, HCL51, TNFRSF18, CTSC, AIF1, PIK3R5, PTAFR, HAVCR2, FAS, CTSH, PIK3CG, PRKCD, CAPN3, FGD2, PTPN22, TREM2, BIRC3, LGALS9, CARD9, NCKAP1, CD300A, MAP3K6, ACER2, IL6RA, PIK3R6, LCK, CSF1R
BP	GO:0031401	positive regulation of protein modification process	1019	323	39	0.000161	0.121	0.038	3	CCL1, CCL5, C3, CD74, CCL8, CD4, CCL12, SLC11A1, TLR1, LAT, XDH, CSAR1, ICAM1, NCF1, PYCARD, CCL6, LCP2, CD44, TLR9, TRPV4, HCL51, AIF1, PIK3R5, HAVCR2, FAS, PIK3CG, PRKCD, FGD2, PTPN22, TREM2, BIRC3, LGALS9, CARD9, NCKAP1, CD300A, MAP3K6, IL6RA, PIK3R6, CSF1R
BP	GO:0001934	positive regulation of protein phosphorylation	829	492	49	0.00000184	0.1	0.059	4	CCL1, CCL5, C3, CD74, CCL8, CD4, CCL12, SLC11A1, TLR1, LAT, XDH, CSAR1, ICAM1, NCF1, PYCARD, CCL6, LCP2, CD44, TLR9, TRPV4, HCL51, AIF1, PIK3R5, HAVCR2, FAS, PIK3CG, PRKCD, FGD2, PTPN22, TREM2, LGALS9, CARD9, NCKAP1, CD300A, MAP3K6, IL6RA, PIK3R6, CSF1R, GLIPR2, CCL9, PRRS1, ANG, ZC3H12A, PLAU, CCL17, SPN, CCL2, CAMP, MASI
BP	GO:0043410	positive regulation of MAPK cascade	432	323	26	0.00000478	0.08	0.06	5	CCL1, CCL5, CD74, CCL8, CD4, CCL12, XDH, CSAR1, ICAM1, NCF1, PYCARD, CCL6, CD44, TLR9, TRPV4, PIK3R5, HAVCR2, PIK3CG, FGD2, PTPN22, TREM2, CARD9, MAP3K6, IL6RA, PIK3R6, CSF1R
BP	GO:0070374	positive regulation of ERK1 and ERK2 cascade	180	480	20	0.00000837	0.042	0.111	6	CCL1, CCL5, CD74, CCL8, CD4, CCL12, CSAR1, ICAM1, PYCARD, CCL6, CD44, TRPV4, HAVCR2, PTPN22, TREM2, CSF1R, GLIPR2, CCL9, CCL17, CCL2
BP	GO:0043367	CD4-positive, alpha-beta T cell differentiation	65	470	10	0.00342	0.021	0.154	1	UV9, IL2RG, CCR2, SASH3, IIRF1, NCKAP1L, RSAD2, IL4RA, PTGER4, BCL3
BP	GO:0033674	positive regulation of kinase activity	441	323	20	0.0307	0.062	0.045	1	CCL5, CD74, CD4, SLC11A1, TLR1, LAT, NCF1, LCP2, TLR9, PIK3R5, PIK3CG, PRKCD, FGD2, LGALS9, NCKAP1, CD300A, MAP3K6, IL6RA, PIK3R6, CSF1R
BP	GO:0045860	positive regulation of protein kinase activity	408	323	20	0.00968	0.062	0.049	2	CCL5, CD74, CD4, SLC11A1, TLR1, LAT, NCF1, LCP2, TLR9, PIK3R5, PIK3CG, PRKCD, FGD2, LGALS9, NCKAP1, CD300A, MAP3K6, IL6RA, PIK3R6, CSF1R
BP	GO:0002866	positive regulation of acute inflammatory response to antigenic stimulus	9	322	4	0.017	0.012	0.444	1	C3, FCGR1, FCER1G, BTK
BP	GO:0002885	positive regulation of hypersensitivity	7	322	4	0.00482	0.012	0.571	2	C3, FCGR1, FCER1G, BTK
BP	GO:0002894	positive regulation of type II hypersensitivity	3	162	3	0.00121	0.019	1	3	C3, FCGR1, FCER1G
BP	GO:0001798	positive regulation of type IIA hypersensitivity	3	162	3	0.00121	0.019	1	4	C3, FCGR1, FCER1G
BP	GO:0001805	positive regulation of type III hypersensitivity	3	322	3	0.00981	0.009	1	3	FCGR1, FCER1G, BTK
BP	GO:0042035	regulation of cytokine biosynthetic process	93	293	13	0.00000103	0.044	0.14	1	CYBB, TLR1, CCR2, LTB, TLR7, TLR9, ICOSL, IIRF1, LAG3, PTAFR, IL1A, INPP5D, CARD9
BP	GO:0042534	regulation of tumor necrosis factor biosynthetic process	18	479	6	0.00471	0.013	0.333	2	CYBB, TLR1, CCR2, CARD9, BCL3, SPN
BP	GO:0042108	positive regulation of cytokine biosynthetic process	59	269	10	0.00000747	0.037	0.169	2	CYBB, TLR1, CCR2, LTB, TLR7, TLR9, ICOSL, IIRF1, PTAFR, IL1A
BP	GO:0060340	positive regulation of type I interferon-mediated signaling pathway	11	79	3	0.0223	0.038	0.273	1	NLRX5, ZBP1, IIRF7
BP	GO:0009023	positive regulation of neutrophil chemotaxis	27	122	4	0.0449	0.033	0.148	1	CD74, CSAR1, RAC2, CSAR1
BP	GO:2001181	positive regulation of interleukin-10 secretion	4	286	3	0.0271	0.01	0.75	1	CD274, PYCARD, LGALS9
BP	GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	25	326	6	0.0045	0.018	0.24	1	IL2RG, CCR2, SASH3, IIRF1, NCKAP1L, IL4RA
BP	GO:0042554	superoxide anion generation	26	453	6	0.0371	0.013	0.231	1	CYBB, NCF1, ACPS, NCF2, PRKCD, PON3