Supplementary Table 1. List of genes comprising Cluster 1 from Figure 2.

ISG15
IFI44L
IFI44
TTF2
FCGR1A
HIST2H2AA4
IFI16
RGS1
ANO7L1
IFI6
RNF19B
GBP1
GBP2
GBP4
CD58
XCL2
TNFSF4
SNORA36B
SRGN
IFIT2
IFIT3
IFIT1
EGR2
PPA1
RGS10
IFITM1
TRIM22
MDK
RARRES3
BIRC3
OR52E8
AMBRA1
UBE2L6
SLC15A3
UNC93B1
CASP1
KLRD1

RASSF3
OAS1
OAS3
OAS2
TESPA1
OASL
LMO7DN-IT1
EPSTI1
IRF9
IFI27
WARS
B2M
TRIM69
PML
ISG20
BCL2A1
TNFRSF12A
SOCS1
XAF1
CCL4
IFI35
KPNA2
SYNGR2
RNF213
CCL3L3
MIR924
GNA15
JUNB
IFI30
HCST
ZFP36
TYROBP
RSAD2
CCL20
SP100
NRIR
CMPK2
EIF2AK2
LOC101927070

NMI
IFIH1
STAT1
SP110
ZNF831
DSN1
SAMHD1
ZNFX1
HELZ2
MX2
MX1
APOL6
APOBEC3G
TYMP
ODF3B
LOC105373098
ECT2
LINC00888
RTP4
SHISA5
PLSCR1
LAMP3
RPL39L
NCAPG
MRPS18C
HERC6
HERC5
TLR3
CXCL9
CXCL10
CXCL11
DDX60
LINC01667
C5orf56
SMAD5-AS1
SMIM13
CD83
HIST1H2BF
HIST1H2AG

OR2B6
HLA-F
NA
HLA-L
PSMB8-AS1
CENPW
HIST1H3B
HIST1H3D
HIST1H3J
TAP1
ETV7
TREM2
NFKBIE
DYNLT1
TRIM31
HLA-E
HCG26
PSMB9
UBD
HLA-G
HLA-A
TAP2
HCP5
HLA-C
ORAI2
ATP6V1F
NT5C3A
SAMD9
SAMD9L
PARP12
MSRA
MIR3926-2
IDO1
LOC105375753
TDRD7
LOC105376208
DDX58
LOC105373318
GBP1P1

LOC100288175
LGALS9
LINC00487
MIR4435-2HG
TRANK1

Supplementary Table 2: List of 408 differentially expressed genes comparing week2/4 on treatment liver biopsy to baseline liver biopsy

SYMBOL	GENE	Fold Change	P value
ISG15	ISG15 ubiquitin-like modifier	-4.084118186	3.57E-09
IFITM1	interferon induced transmembrane protein 1	-1.789282969	3.60E-08
OASL	2'-5'-oligoadenylate synthetase like	-4.538084295	6.29E-08
ODF3B	outer dense fiber of sperm tails 3B	-1.499396384	3.84E-07
LINC00487	long intergenic non-protein coding RNA 487	-2.866622293	8.14E-07
CMPK2	cytidine/uridine monophosphate kinase 2	-2.91695621	1.05E-06
HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	-2.87404025	1.47E-06
CXCL11	C-X-C motif chemokine ligand 11	-2.790076471	1.83E-06
MX1	MX dynamin like GTPase 1	-3.433429014	2.62E-06
NRIR	negative regulator of interferon response (non-protein coding)	-2.18991233	2.92E-06
EPSTI1	epithelial stromal interaction 1 (breast)	-2.599603995	3.14E-06
DDX60	DEXD/H-box helicase 60	-2.936424136	3.42E-06
IFI35	interferon induced protein 35	-1.635350735	4.83E-06
CXCL10	C-X-C motif chemokine ligand 10	-4.782268615	5.87E-06
OAS3	2'-5'-oligoadenylate synthetase 3	-2.861678472	9.71E-06
SOCS1	suppressor of cytokine signaling 1	-1.481346731	1.28E-05
STAT1	signal transducer and activator of transcription 1	-2.206781852	1.33E-05
IFI44L	interferon induced protein 44 like	-3.865389456	1.40E-05
RTP4	receptor transporter protein 4	-2.259017307	2.54E-05
TSSK2	testis specific serine kinase 2	1.346865488	2.85E-05
CMTM4	CKLF like MARVEL transmembrane domain containing 4	1.541485445	2.86E-05
IFI6	interferon alpha inducible protein 6	-4.380653218	3.80E-05
PLSCR1	phospholipid scramblase 1	-1.587591103	3.84E-05
UNC119B	unc-119 lipid binding chaperone B	1.390173092	3.96E-05
TAP2	transporter 2, ATP binding cassette subfamily B member	-1.318580458	4.62E-05
HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	-2.599314365	5.83E-05
PPA1	pyrophosphatase (inorganic) 1	-1.400670164	5.84E-05
MDK	midkine (neurite growth-promoting factor 2)	-1.657301129	6.11E-05
OAS2	2'-5'-oligoadenylate synthetase 2	-2.848102776	7.98E-05
UBE2L6	ubiquitin conjugating enzyme E2 L6	-1.641916274	8.21E-05
TRIM69	tripartite motif containing 69	-1.329986293	8.83E-05
IFIT3	interferon induced protein with tetratricopeptide repeats 3	-2.409943325	8.95E-05

GPC5-AS2	GPC5 antisense RNA 2	1.248301794	0.000107112
MIR320E	microRNA 320e	-1.49041472	0.000109682
HIST1H3D	histone cluster 1 H3 family member d	-1.402539674	0.000114783
LOC105373318	uncharacterized LOC105373318	-1.480000675	0.00011553
B2M	beta-2-microglobulin	-1.251693724	0.000124783
SLC15A3	solute carrier family 15 member 3	-1.467205042	0.000129326
RSAD2	radical S-adenosyl methionine domain containing 2	-2.534805615	0.000130468
HLA-G	major histocompatibility complex, class I, G	-1.276770294	0.000131691
PSMB9	proteasome subunit beta 9	-1.349720303	0.000137667
IFI44	interferon induced protein 44	-2.508178277	0.000137843
LOC101927942	uncharacterized LOC101927942	1.633982299	0.000147473
IQSEC1	IQ motif and Sec7 domain 1	1.249858695	0.000153783
FCGR1A	Fc fragment of IgG receptor Ia	-1.77772631	0.000155293
WBSCR27	Williams Beuren syndrome chromosome region 27	1.2179421	0.00018273
LAMP3	lysosomal associated membrane protein 3	-2.15734409	0.000188927
IFI27	interferon alpha inducible protein 27	-1.903885042	0.000188962
FAM149A	family with sequence similarity 149 member A	1.299004526	0.000189032
LINC01534	long intergenic non-protein coding RNA 1534	1.378072946	0.000192563
IFI30	IFI30, lysosomal thiol reductase	-1.429611907	0.000201026
CXCL9	C-X-C motif chemokine ligand 9	-2.499027019	0.000202519
SP110	SP110 nuclear body protein	-1.473734731	0.00020986
DDX58	DEXD/H-box helicase 58	-1.755213616	0.000223119
HIST1H2BF	histone cluster 1 H2B family member f	-1.633757785	0.000234856
HCP5	HLA complex P5 (non-protein coding)	-1.813193437	0.000235264
PARP12	poly(ADP-ribose) polymerase family member 12	-1.602124803	0.000249442
ESR1	estrogen receptor 1	1.406039973	0.000257248
ISM1	isthmin 1	1.391467238	0.000276503
OAS1	2'-5'-oligoadenylate synthetase 1	-2.116599739	0.000276514
ARSD	arylsulfatase D	1.45719898	0.000281214
ISG20	interferon stimulated exonuclease gene 20	-1.589310188	0.000342715
WARS	tryptophanyl-tRNA synthetase	-1.256789751	0.000343771
CDK14	cyclin dependent kinase 14	1.267986803	0.000353517
EEF2	eukaryotic translation elongation factor 2	1.283595477	0.000366083
RNF19B	ring finger protein 19B	-1.218425966	0.000402113
EIF3L	eukaryotic translation initiation factor 3 subunit L	1.25129337	0.000409995
SLC46A1	solute carrier family 46 member 1	1.437252517	0.000410035
IRF9	interferon regulatory factor 9	-1.550630683	0.000412971

KIF12	kinesin family member 12	1.592543631	0.000425764
GBP1P1	guanylate binding protein 1 pseudogene 1	-1.393890072	0.000427544
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	1.301563841	0.0004369
HDLBP	high density lipoprotein binding protein	1.204505042	0.000466716
EIF4B	eukaryotic translation initiation factor 4B	1.41354455	0.000468452
RNASE13	ribonuclease A family member 13 (inactive)	1.309608536	0.000491023
LOC105375753	uncharacterized LOC105375753	-1.257477152	0.000505051
TDRD7	tudor domain containing 7	-1.459946351	0.000531538
SPATA33	spermatogenesis associated 33	1.326668112	0.00053207
MIR924	microRNA 924	-1.406071033	0.00054886
CERK	ceramide kinase	1.303698557	0.000553821
TAP1	transporter 1, ATP binding cassette subfamily B member	-1.514233832	0.00056765
UBE4B	ubiquitination factor E4B	1.253367072	0.000587016
LOC101927070	uncharacterized LOC101927070	-1.260497734	0.000591263
IFI27L1	interferon alpha inducible protein 27 like 1	-1.322781726	0.000600939
CENPW	centromere protein W	-1.407574923	0.000617066
NMI	N-myc and STAT interactor	-1.409033684	0.000650526
DANCR	differentiation antagonizing non-protein coding RNA	1.350322818	0.000717876
SNRPN	small nuclear ribonucleoprotein polypeptide N	1.654522647	0.000719874
IFIT1	interferon induced protein with tetratricopeptide repeats 1	-2.328918851	0.000741899
TRIM22	tripartite motif containing 22	-1.49562576	0.000768763
NMNAT1	nicotinamide nucleotide adenylyltransferase 1	1.336008166	0.000806324
DYNLT1	dynein light chain Tctex-type 1	-1.324415449	0.000809257
KIR2DL3	killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3	-1.240001076	0.000810983
TARP	TCR gamma alternate reading frame protein	-1.428842348	0.000812516
OR4C15	olfactory receptor family 4 subfamily C member 15	-1.257084846	0.00084982
TENM1	teneurin transmembrane protein 1	1.585773066	0.000851129
IFI16	interferon gamma inducible protein 16	-1.451595036	0.00085949
IFIT2	interferon induced protein with tetratricopeptide repeats 2	-1.932594154	0.000881979
TYMP	thymidine phosphorylase	-1.252558969	0.0009105
HIST1H3B	histone cluster 1 H3 family member b	-1.21843228	0.000940249
HOGA1	4-hydroxy-2-oxoglutarate aldolase 1	1.511972579	0.000948252

LOC105374177	uncharacterized LOC105374177	1.499613721	0.000959977
ETV7	ETS variant 7	-1.488907792	0.000973949
ZNRF3-AS1	ZNRF3 antisense RNA 1	1.264252585	0.000991298
C12orf43	chromosome 12 open reading frame 43	1.213964114	0.00099694
SP100	SP100 nuclear antigen	-1.311904246	0.001006411
PML	promyelocytic leukemia	-1.29205157	0.001015788
DRC3	dynein regulatory complex subunit 3	1.203884744	0.001060388
MAVS	mitochondrial antiviral signaling protein	1.228603568	0.001072166
MIR3689E	microRNA 3689e	1.95326426	0.00108346
SMAD5-AS1	SMAD5 antisense RNA 1	-1.358138068	0.001098434
BCL2A1	BCL2 related protein A1	-1.537452439	0.001099632
SNORD116-11	small nucleolar RNA, C/D box 116-11	-1.293026999	0.001107458
HIST1H3J	histone cluster 1 H3 family member j	-1.357159102	0.00115336
WASH3P	WAS protein family homolog 3 pseudogene	1.273180119	0.001154403
MLEC	malectin	1.393681936	0.001178088
VIPR1	vasoactive intestinal peptide receptor 1	1.248229977	0.001192851
LILRA2	leukocyte immunoglobulin like receptor A2	-1.288869636	0.001210621
ACSS3	acyl-CoA synthetase short-chain family member 3	1.369816704	0.001232621
NEK6	NIMA related kinase 6	1.26119547	0.001243334
TTF2	transcription termination factor 2	-1.322371941	0.001259094
SCN3A	sodium voltage-gated channel alpha subunit 3	1.215028628	0.001270737
SSRP1	structure specific recognition protein 1	1.209983664	0.001291043
CYP20A1	cytochrome P450 family 20 subfamily A member 1	1.314294427	0.001292872
IFIH1	interferon induced with helicase C domain 1	-1.867668889	0.001297286
LOC100129034	uncharacterized LOC100129034	1.276927304	0.001328882
PLS3-AS1	PLS3 antisense RNA 1	1.253472616	0.001416321
ZFP36	ZFP36 ring finger protein	-1.338703554	0.001419856
GCSHP3	glycine cleavage system protein H pseudogene 3	1.720280873	0.001426852
PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	1.301597718	0.001450373
MYCL	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived homolog	1.262941875	0.001473967
MIR3926-2	microRNA 3926-2	-1.274712088	0.001520833
RPL39L	ribosomal protein L39 like	-1.394602625	0.00152438
MSRA	methionine sulfoxide reductase A	-1.295340013	0.001551104
LOC105379013	uncharacterized LOC105379013	2.003091813	0.001576357

RNF213	ring finger protein 213	-1.374217119	0.001589072
BIRC3	baculoviral IAP repeat containing 3	-1.6407883	0.00158945
CFAP126	cilia and flagella associated protein 126	1.556067581	0.001654795
GHR	growth hormone receptor	1.38337482	0.001703927
MIR181A1HG	MIR181A1 host gene	-1.284185752	0.001708261
NFKBIE	NFKB inhibitor epsilon	-1.222779931	0.001766892
HLA-C	major histocompatibility complex, class I, C	-1.338706788	0.001785695
LOC101927542	uncharacterized LOC101927542	1.290834919	0.001789819
LOC101928462	uncharacterized LOC101928462	1.342306142	0.001838053
DPF3	double PHD fingers 3	1.228181561	0.001862071
HMHB1	histocompatibility minor HB-1	-1.23385538	0.001868774
KPNA2	karyopherin subunit alpha 2	-1.385126122	0.001872084
PSMB8-AS1	PSMB8 antisense RNA 1 (head to head)	-1.254616604	0.001873093
NCAPG	non-SMC condensin I complex subunit G	-1.231274097	0.001909829
SAMD9L	sterile alpha motif domain containing 9 like	-1.642119408	0.001917832
UQCRHL	ubiquinol-cytochrome c reductase hinge protein like	-1.235246608	0.001941006
NT5C3A	5'-nucleotidase, cytosolic IIIA	-1.397272152	0.001946086
MIR576	microRNA 576	-1.215030382	0.001948058
LOC105370524	uncharacterized LOC105370524	1.26924875	0.001953529
BHLHE40	basic helix-loop-helix family member e40	1.409678884	0.001965467
MRPS18C	mitochondrial ribosomal protein S18C	-1.228741733	0.002024079
PPARA	peroxisome proliferator activated receptor alpha	1.564675351	0.002068441
XAGE-4	XAGE-4 protein	-1.294201768	0.002147185
LCMT1	leucine carboxyl methyltransferase 1	-1.216466335	0.002167662
DDX11L9	DEAD/H-box helicase 11 like 9	-1.26505878	0.002207783
MID1IP1-AS1	MID1IP1 antisense RNA 1	1.391618186	0.002214971
GBP1	guanylate binding protein 1	-1.477206485	0.002227865
SAMD9	sterile alpha motif domain containing 9	-1.935997983	0.002231845
RUSC1-AS1	RUSC1 antisense RNA 1	1.286957242	0.002249435
TBL1X	transducin beta like 1X-linked	1.282845804	0.002271253
LINC01358	long intergenic non-protein coding RNA 1358	-1.218769113	0.002308708
MAP2K1	mitogen-activated protein kinase kinase 1	1.31746141	0.002379995
IFITM4P	interferon induced transmembrane protein 4 pseudogene	-1.316011344	0.002405186
ANO1	anoctamin 1	1.537418921	0.00244399
CYP3A43	cytochrome P450 family 3 subfamily A member 43	1.961188997	0.00246213

GBP4	guanylate binding protein 4	-1.483740455	0.002482125
LOC399886	uncharacterized LOC399886	-1.208874876	0.002534518
KLHDC3	kelch domain containing 3	1.262336738	0.002559868
ZC2HC1B	zinc finger C2HC-type containing 1B	-1.283663755	0.00257745
HIST1H2AG	histone cluster 1 H2A family member g	-1.628412873	0.002627372
LOC105370700	uncharacterized LOC105370700	1.232440555	0.002635332
ANXA2P3	annexin A2 pseudogene 3	-1.224898136	0.002644719
LOC100506302	uncharacterized LOC100506302	1.308979049	0.00268818
ATP6V1F	ATPase H+ transporting V1 subunit F	-1.262617039	0.002734717
CMBL	carboxymethylenebutenolidase homolog	1.524545841	0.002736704
DEPTOR	DEP domain containing MTOR-interacting protein	1.265151043	0.002783557
TRIM31	tripartite motif containing 31	-1.491904208	0.002845391
PGP	phosphoglycolate phosphatase	-1.257901084	0.002900176
FLJ37453	uncharacterized LOC729614	1.26825923	0.002952173
LOC105369656	uncharacterized LOC105369656	-1.574963318	0.003009843
UNC93B1	unc-93 homolog B1 (C. elegans)	-1.215908262	0.003033978
ACOX1	acyl-CoA oxidase 1	1.278328008	0.003076003
RAB32	RAB32, member RAS oncogene family	-1.280065188	0.003096829
LOC105373098	uncharacterized LOC105373098	-1.326629328	0.003109043
LDLR	low density lipoprotein receptor	1.330227261	0.003115179
LOC105379011	uncharacterized LOC105379011	1.499606759	0.003142483
LOC374890	uncharacterized LOC374890	-1.207661444	0.00316429
TYROBP	TYRO protein tyrosine kinase binding protein	-1.269285847	0.003170133
ZC3H7B	zinc finger CCCH-type containing 7B	1.239929668	0.00319539
LOC554223	histocompatibility antigen-related	-1.203054582	0.003223417
WWP1	WW domain containing E3 ubiquitin protein ligase 1	1.281187961	0.003290126
SRGN	serglycin	-1.337020553	0.003369667
APOL6	apolipoprotein L6	-1.3037033	0.003393877
MIR4636	microRNA 4636	-1.285582133	0.003436268
EGR2	early growth response 2	-1.248301318	0.003449068
LOC105378668	uncharacterized LOC105378668	1.27779994	0.003558404
FDPS	farnesyl diphosphate synthase	1.526675409	0.003559337
LOC102723878	uncharacterized LOC102723878	-1.210681594	0.00355934
MPP6	membrane palmitoylated protein 6	1.222769623	0.003590771
CYP3A4	cytochrome P450 family 3 subfamily A member 4	1.603137442	0.003604739
CCNE1	cyclin E1	-1.241740126	0.003631135
ATXN1	ataxin 1	1.217850847	0.003632137
SLC25A23	solute carrier family 25 member 23	1.249966945	0.003647021
MIR548A3	microRNA 548a-3	-1.273565858	0.003653685
LAIR2	leukocyte associated immunoglobulin like receptor 2	-1.376651384	0.003691653

GNG7	G protein subunit gamma 7	1.368838028	0.003700575
LOC100507663	uncharacterized LOC100507663	-1.218476555	0.003728062
ARMCX4	armadillo repeat containing, X-linked 4	1.269737694	0.003795093
PRTN3	proteinase 3	-1.291776889	0.003810882
C6orf226	chromosome 6 open reading frame 226	-1.364160902	0.003829972
LINC00888	long intergenic non-protein coding RNA 888	-1.348448296	0.003835249
IDO1	indoleamine 2,3-dioxygenase 1	-1.222615139	0.003901111
PRR29	proline rich 29	-1.228666649	0.003916443
TLR3	toll like receptor 3	-1.35624191	0.003938373
PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	1.229064269	0.003941582
HIST2H2AA4	histone cluster 2 H2A family member a4	-1.401945632	0.003953029
TRANK1	tetratricopeptide repeat and ankyrin repeat containing 1	-1.378954601	0.003992168
APOBEC3G	apolipoprotein B mRNA editing enzyme catalytic subunit 3G	-1.3677342	0.003997702
XAF1	XIAP associated factor 1	-1.857863286	0.004065363
ORAI2	ORAI calcium release-activated calcium modulator 2	-1.235657154	0.004118105
RFESD	Rieske Fe-S domain containing	1.23575838	0.004133803
NTHL1	nth like DNA glycosylase 1	1.344501525	0.004135177
MELK	maternal embryonic leucine zipper kinase	-1.270599953	0.004162355
C5orf56	chromosome 5 open reading frame 56	-1.26769588	0.004222265
SETD7	SET domain containing lysine methyltransferase 7	1.362158793	0.004231582
HIST1H2BN	histone cluster 1 H2B family member n	-1.305096878	0.00430468
PAQR9-AS1	PAQR9 antisense RNA 1	1.443605398	0.004311734
BBOF1	basal body orientation factor 1	1.283433343	0.004343393
XCL2	X-C motif chemokine ligand 2	-1.381601304	0.004366952
RGS1	regulator of G-protein signaling 1	-1.299380103	0.004393236
LOC101929959	ribosome biogenesis protein BMS1 homolog	-1.415708053	0.004467535
SYNGR2	synaptogyrin 2	-1.215228001	0.004475543
HELZ2	helicase with zinc finger 2	-1.250800246	0.004477477
SORD	sorbitol dehydrogenase	1.764826446	0.004483391
PRORY	proline rich, Y-linked	1.204220001	0.004536783
PAIP2B	poly(A) binding protein interacting protein 2B	1.453698457	0.004564292
CD58	CD58 molecule	-1.279450379	0.00457066
CD83	CD83 molecule	-1.408890497	0.004604445
TRIM48	tripartite motif containing 48	-1.348486192	0.004627254
STARD4-AS1	STARD4 antisense RNA 1	1.27576853	0.004640711

ZBTB48	zinc finger and BTB domain containing 48	1.277542832	0.004643501
SEPHS1	selenophosphate synthetase 1	1.205175564	0.004643516
LOC100129518	uncharacterized LOC100129518	1.450309835	0.004683515
ZNF132	zinc finger protein 132	1.207498586	0.004699149
TREM2	triggering receptor expressed on myeloid cells 2	-1.412290564	0.004702685
MIR4435-2HG	MIR4435-2 host gene	-1.42287971	0.004864498
ARRDC3	arrestin domain containing 3	1.525821114	0.004870807
SRPRA	SRP receptor alpha subunit	1.258799261	0.004936924
SMIM13	small integral membrane protein 13	-1.238113535	0.004978011
EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2	-1.551096801	0.00499379
NDRG2	NDRG family member 2	1.307878222	0.004996449
SLC16A2	solute carrier family 16 member 2	1.536833131	0.005006588
ALAD	aminolevulinate dehydratase	1.482128032	0.005016007
RARRES3	retinoic acid receptor responder 3	-1.418744428	0.005070548
PRAMEF18	PRAME family member 18	-1.549068501	0.005110224
CCL4	C-C motif chemokine ligand 4	-1.696267974	0.005183547
TPPP2	tubulin polymerization promoting protein family member 2	1.416332901	0.005261439
VAMP5	vesicle associated membrane protein 5	-1.335151013	0.00530427
LOC105376208	uncharacterized LOC105376208	-1.207361584	0.005318808
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1.563133961	0.005323788
HLA-F	major histocompatibility complex, class I, F	-1.390839003	0.005358091
ZNFX1	zinc finger NFX1-type containing 1	-1.461233984	0.00537676
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2	1.253273483	0.005458683
LOC105379551	uncharacterized LOC105379551	-1.436276454	0.005465952
CCNB1IP1	cyclin B1 interacting protein 1	1.395048654	0.005514291
IL6	interleukin 6	-1.270253581	0.005524365
LGALS9	galectin 9	-1.568597133	0.0055249
BMP1	bone morphogenetic protein 1	1.251848674	0.00556441
REN	renin	1.304966552	0.005594698
MLK4	mixed lineage kinase 4	1.266981683	0.00559891
HLA-E	major histocompatibility complex, class I, E	-1.283497019	0.005612347
CHRNA3	cholinergic receptor nicotinic alpha 3 subunit	-1.208986425	0.005642546
MX2	MX dynamin like GTPase 2	-1.635144141	0.005728397
LOC101927331	uncharacterized LOC101927331	1.796962698	0.005776355
MGC39584	uncharacterized LOC441058	-1.232427535	0.005812997
CASP1	caspase 1	-1.247790578	0.005842726
PACSIN3	protein kinase C and casein kinase substrate in neurons 3	1.303242192	0.005854873

HN1L	hematological and neurological expressed 1 like	1.213234397	0.005858388
PSMG2	proteasome assembly chaperone 2	-1.236460493	0.005864651
HLA-L	major histocompatibility complex, class I, L (pseudogene)	-1.266271091	0.005911388
AMBRA1	autophagy and beclin 1 regulator 1	-1.204998222	0.005911957
MIR133B	microRNA 133b	-1.218028505	0.005916678
ASB18	ankyrin repeat and SOCS box containing 18	1.202284559	0.005923613
TERB2	telomere repeat binding bouquet formation protein 2	1.401341969	0.005975481
HCG26	HLA complex group 26 (non-protein coding)	-1.659636625	0.005986847
CHID1	chitinase domain containing 1	1.220593816	0.006012616
OR2B6	olfactory receptor family 2 subfamily B member 6	-1.276656329	0.006084408
KIR2DL2	killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2	-1.281725124	0.00611361
ANO7L1	anoctamin 7 like 1	-1.342735059	0.0061154
LIPC	lipase C, hepatic type	1.826616422	0.006127694
SUCLG2	succinate-CoA ligase GDP-forming beta subunit	1.262917252	0.006131551
BCL7A	BCL tumor suppressor 7A	1.230928446	0.006143985
UBD	ubiquitin D	-2.004222519	0.006152245
CLEC4E	C-type lectin domain family 4 member E	-1.21704847	0.006168402
ALDH1L1	aldehyde dehydrogenase 1 family member L1	1.526589627	0.006256383
ERCC2	ERCC excision repair 2, TFIIH core complex helicase subunit	1.238176159	0.006256751
MEIS2	Meis homeobox 2	1.278637623	0.00627205
LOC105378616	uncharacterized LOC105378616	1.231641653	0.006313276
AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	1.403392866	0.006315592
SYCE2	synaptonemal complex central element protein 2	1.346245123	0.006429066
HOMER2	homer scaffolding protein 2	1.526450868	0.006442758
SLC47A1	solute carrier family 47 member 1	1.83978459	0.006469699
CAPN5	calpain 5	1.346405199	0.006482182
MSX2P1	msh homeobox 2 pseudogene 1	-1.210186795	0.006543386
IYD	iodotyrosine deiodinase	1.563297255	0.006558549
SLC17A2	solute carrier family 17 member 2	1.87333544	0.006594012
TNFSF4	tumor necrosis factor superfamily member 4	-1.267240435	0.006675711
LINC00266-1	long intergenic non-protein coding RNA 266-1	-1.289336601	0.006715458
HLA-A	major histocompatibility complex, class I, A	-1.251511963	0.00677024

GNA15	G protein subunit alpha 15	-1.27362254	0.006780472
PCSK6	proprotein convertase subtilisin/kexin type 6	1.389755445	0.006849857
BPHL	biphenyl hydrolase like	1.42519753	0.006852611
JUNB	JunB proto-oncogene, AP-1 transcription factor subunit	-1.396322759	0.006907598
SFXN2	sideroflexin 2	1.458475308	0.006928705
SPRR2A	small proline rich protein 2A	-1.360696328	0.006944558
MIR891A	microRNA 891a	-1.27878609	0.00695483
CCL20	C-C motif chemokine ligand 20	-1.549720118	0.006998927
TOM1L1	target of myb1 like 1 membrane trafficking protein	1.388152541	0.007041118
UNC13B	unc-13 homolog B	1.207284449	0.00705907
LOC105369360	uncharacterized LOC105369360	1.330929888	0.007063914
CCL3L3	C-C motif chemokine ligand 3 like 3	-1.259379398	0.007089751
HDAC1	histone deacetylase 1	1.220983173	0.007114559
FAM160A1	family with sequence similarity 160 member A1	1.213546732	0.007116067
PHYH	phytanoyl-CoA 2-hydroxylase	1.360604343	0.007142084
PTMS	parathymosin	1.249433073	0.007146879
LOC105374780	uncharacterized LOC105374780	-1.303074519	0.007147094
SULT1E1	sulfotransferase family 1E member 1	1.810122983	0.007154936
DSN1	DSN1 homolog, MIS12 kinetochore complex component	-1.223236157	0.007162669
TM7SF2	transmembrane 7 superfamily member 2	1.334647113	0.007243289
SHISA5	shisa family member 5	-1.219692039	0.007380629
ADGRA3	adhesion G protein-coupled receptor A3	1.540157819	0.00739376
SNORA36B	small nucleolar RNA, H/ACA box 36B	-1.629939069	0.007405847
LOC105378020	uncharacterized LOC105378020	-1.249063493	0.007420739
ATE1-AS1	ATE1 antisense RNA 1	1.213922469	0.007427835
PBLD	phenazine biosynthesis like protein domain containing	1.469844409	0.007449371
FADS2	fatty acid desaturase 2	1.334591392	0.007467437
FAM185A	family with sequence similarity 185 member A	1.264939516	0.00749023
KLRD1	killer cell lectin like receptor D1	-1.247592525	0.007493583
IVD	isovaleryl-CoA dehydrogenase	1.493466855	0.007498082
PROS1	protein S (alpha)	1.435835309	0.007554003
C3orf14	chromosome 3 open reading frame 14	-1.223603397	0.007567907
ABHD1	abhydrolase domain containing 1	1.352775765	0.00763734
ELOVL6	ELOVL fatty acid elongase 6	1.438574551	0.007654384
ANO1-AS2	ANO1 antisense RNA 2 (head to head)	1.389367145	0.00766423
LMO7DN-IT1	LMO7DN intronic transcript 1	-1.234702854	0.007737194
SLC5A12	solute carrier family 5 member 12	1.375561552	0.007852778

LOC100288175	uncharacterized LOC100288175	-1.526219179	0.007865938
LOC100129917	uncharacterized LOC100129917	1.271960267	0.007868999
R3HDM2	R3H domain containing 2	1.235294553	0.0079272
PCYOX1	prenylcysteine oxidase 1	1.258830281	0.007966075
ABHD14B	abhydrolase domain containing 14B	1.237336979	0.008004708
LOC105379049	uncharacterized LOC105379049	1.243169983	0.00813725
SRD5A2	steroid 5 alpha-reductase 2	2.397823302	0.008212711
LINC01093	long intergenic non-protein coding RNA 1093	1.921583425	0.00822248
THNSL1	threonine synthase like 1	1.408205606	0.008277976
SOWAHC	sosondowah ankyrin repeat domain family member C	1.254095212	0.008297998
ACAD10	acyl-CoA dehydrogenase family member 10	1.289939639	0.008311685
RGS10	regulator of G-protein signaling 10	-1.408559971	0.008311959
TMEM97	transmembrane protein 97	1.603922542	0.008326666
HIST1H2AI	histone cluster 1 H2A family member i	-1.350579183	0.008348313
ACSM3	acyl-CoA synthetase medium-chain family member 3	2.055359242	0.008354682
HCST	hematopoietic cell signal transducer	-1.428042783	0.008356231
TESPA1	thymocyte expressed, positive selection associated 1	-1.228171013	0.008367879
SEC14L3	SEC14 like lipid binding 3	1.607784424	0.008371875
SYT4	synaptotagmin 4	-1.209813914	0.00837907
MORF4L2-AS1	MORF4L2 antisense RNA 1	1.316278614	0.008396699
PROSC	proline synthetase cotranscribed homolog (bacterial)	1.205674442	0.008408021
SAMHD1	SAM and HD domain containing deoxynucleoside triphosphate triphosphohydrolase 1	-1.302498274	0.008501254
OR4C45	olfactory receptor family 4 subfamily C member 45	-1.342829153	0.008595854
CFHR4	complement factor H related 4	1.475266802	0.008600195
BOLA3	bolA family member 3	-1.255423616	0.008646903
ZNF831	zinc finger protein 831	-1.441661015	0.008661497
GCAT	glycine C-acetyltransferase	1.387108984	0.008705845
ECT2	epithelial cell transforming 2	-1.244759693	0.008713631
ANXA9	annexin A9	1.637898023	0.008744376
TCEB3-AS1	TCEB3 antisense RNA 1	1.352048388	0.008767114
ANKRD26	ankyrin repeat domain 26	1.387504316	0.008822369
CRAT	carnitine O-acetyltransferase	1.278012103	0.008869568
OR52E8	olfactory receptor family 52 subfamily E member 8	-1.22282658	0.00900289
BET1L	Bet1 golgi vesicular membrane trafficking protein like	1.247046417	0.009016676
ZNF691	zinc finger protein 691	1.292141043	0.009034144

ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1	1.348007564	0.009074879
MAP7	microtubule associated protein 7	1.259774633	0.009081484
TNFRSF12A	TNF receptor superfamily member 12A	-1.566284432	0.009143382
CYB5R1	cytochrome b5 reductase 1	1.215687132	0.009196959
IGLL1	immunoglobulin lambda like polypeptide 1	1.20206444	0.009248116
RASSF3	Ras association domain family member 3	-1.352593238	0.009248297
MIR4672	microRNA 4672	-1.200910775	0.009330249
KCTD3	potassium channel tetramerization domain containing 3	1.267392423	0.009335937
THSD4	thrombospondin type 1 domain containing 4	1.222595416	0.009386692
MRPS31P5	mitochondrial ribosomal protein S31 pseudogene 5	-1.228905363	0.009413175
FOXRED1	FAD dependent oxidoreductase domain containing 1	1.357140662	0.009425564
CSH1	chorionic somatomammotropin hormone 1	-1.238215675	0.009434576
ABCA6	ATP binding cassette subfamily A member 6	1.335715871	0.009454323
LOC105374716	uncharacterized LOC105374716	1.51870564	0.009541017
CYP2A6	cytochrome P450 family 2 subfamily A member 6	1.881674877	0.009636942
C8orf4	chromosome 8 open reading frame 4	1.260575782	0.009675907
GBP2	guanylate binding protein 2	-1.282198343	0.009722857
STAB2	stabilin 2	1.511845294	0.009732577
RNF123	ring finger protein 123	1.248576511	0.009735419
MIR4692	microRNA 4692	1.441297781	0.009809468
SVBP	small vasohibin binding protein	-1.317650993	0.009907199
SLC29A2	solute carrier family 29 member 2	1.227970488	0.009939249

Supplementary Table 3: List of significantly downregulated pathways

Pathway	Database	Genes in list	Genes in pathway	pval	adj pval	Genes
immune system process	GO	80	2418	<1E-18	<1E-18	ISG15 IFITM1 OASL HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI44L IFI6 PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 BIRC3 HLA-C HMHB1 GBP1 TRIM31 UNC93B1 RAB32 TYROBP PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 DSN1 KLRD1 SAMHD1 GBP2
Immune System	REACTOME	80	2050	<1E-18	<1E-18	ISG15 IFITM1 OASL HERC6 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 TAP2 HERC5 OAS2 UBE2L6 TRIM69 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 RNF19B IRF9 TAP1 IFIT1 TRIM22 DYNLT1 KIR2DL3

						IFI16 IFIT2 SP100 PML LILRA2 IFIH1 RNF213 BIRC3 NFKBIE HLA-C KPNA2 GBP1 GBP4 ATP6V1F TRIM31 UNC93B1 TYROBP LAIR2 PRTN3 TLR3 XAF1 ORAI2 CD58 TRIM48 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 KIR2DL2 CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 DSN1 KLRD1 HCST SAMHD1 CSH1 GBP2
immune response	GO	71	1492	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI6 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 HLA-G FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 HLA-C HMHB1 GBP1 TRIM31 UNC93B1 TYROBP PRTN3 TLR3 XAF1 XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 DSN1 KLRD1 SAMHD1 GBP2
defense response	GO	67	1247	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI44L IFI6

						PLSCR1 HERC5 MDK OAS2 IFIT3 B2M RSAD2 HLA-G FCGR1A IFI27 IFI30 CXCL9 DDX58 HCP5 OAS1 ISG20 IRF9 TAP1 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 HLA-C GBP1 TRIM31 UNC93B1 TYROBP IDO1 TLR3 XAF1 XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 KLRD1 SAMHD1 GBP2
response to cytokine	GO	57	762	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 TRIM31 CCNE1 TLR3 XAF1 XCL2 CD58 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1 GBP2
Cytokine Signaling in Immune system	REACTOME	55	741	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 HERC5 OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 DDX58

						OAS1 ISG20 IRF9 IFIT1 TRIM22 IFIT2 SP100 PML BIRC3 HLA-C KPNA2 GBP1 GBP4 TRIM31 PRTN3 XAF1 TRIM48 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1 CSH1 GBP2
innate immune response	GO	54	611	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 IFI35 OAS3 STAT1 IFI6 HERC5 OAS2 IFIT3 B2M RSAD2 HLA-G FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML IFIH1 HLA-C GBP1 TRIM31 UNC93B1 TYROBP TLR3 XAF1 XCL2 CD58 TREM2 EIF2AK2 CCL4 HLA-F LGALS9 HLA-E MX2 UBD CLEC4E HLA-A CCL20 CCL3L3 KLRD1 SAMHD1 GBP2
response to biotic stimulus	GO	51	921	<1E-18	<1E-18	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 ZFP36 GBP1 UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4

response to external biotic stimulus	GO	51	889	<1E-18	<1E-18	HLA-A JUNB CCL20 SAMHD1 ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 ZFP36 GBP1 UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1
response to other organism	GO	51	886	<1E-18	<1E-18	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 ZFP36 GBP1 UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1
cellular response to cytokine stimulus	GO	51	657	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9

						NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 TRIM31 TLR3 XAF1 XCL2 CD58 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 TNFSF4 HLA-A CCL20 CCL3L3 SAMHD1 GBP2
multi-organism cellular process	GO	47	967	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1
interspecies interaction between organisms	GO	47	963	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1
symbiosis, encompassing mutualism through parasitism	GO	47	960	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3

						B2M RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1
cytokine-mediated signaling pathway	GO	47	473	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML BIRC3 HLA-C GBP1 TRIM31 XAF1 XCL2 CCL4 HLA-F IL6 HLA-E MX2 TNFSF4 HLA-A CCL20 CCL3L3 SAMHD1 GBP2
viral process	GO	46	811	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1

immune effector process	GO	43	927	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 FCGR1A CXCL9 DDX58 OAS1 ISG20 RNF19B IRF9 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TYROBP PRTN3 TLR3 CD58 EIF2AK2 IL6 MX2 CLEC4E TNFSF4 DSN1 KLRD1 SAMHD1
Interferon Signaling	REACTOME	42	197	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 SOCS1 STAT1 IFI6 HERC5 OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFIT2 SP100 PML HLA-C KPNA2 GBP1 GBP4 TRIM31 XAF1 TRIM48 EIF2AK2 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
defense response to other organism	GO	38	497	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TLR3 EIF2AK2 IL6 HLA-E MX2 CLEC4E TNFSF4 HLA-A CCL20 SAMHD1
response to virus	GO	37	250	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L

						PLSCR1 HERC5 OAS2 IFIT3 RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 SAMHD1 ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L
defense response to virus	GO	32	164	<1E-18	<1E-18	PLSCR1 HERC5 OAS2 IFIT3 RSAD2 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TLR3 EIF2AK2 IL6 MX2 SAMHD1
response to interferon-gamma	GO	30	145	<1E-18	<1E-18	IFITM1 OASL OAS3 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 NMI TRIM22 SP100 PML HLA-C GBP1 TRIM31 TLR3 XCL2 CD58 CCL4 HLA-F LGALS9 HLA-E UBD HLA-A CCL20 CCL3L3 GBP2
cellular response to interferon-gamma	GO	28	123	<1E-18	<1E-18	OASL OAS3 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 NMI TRIM22 SP100 PML HLA-C GBP1 TRIM31 TLR3 XCL2 CD58 CCL4 HLA-F LGALS9 HLA-E HLA-A CCL20 CCL3L3 GBP2
response to type I interferon	GO	27	69	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 SP100 HLA-C XAF1

						HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
Interferon alpha/beta signaling	REACTOME	27	68	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
type I interferon signaling pathway	GO	27	65	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 SP100 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
cellular response to type I interferon	GO	27	65	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 SP100 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
Interferon gamma signaling	REACTOME	23	92	<1E-18	<1E-18	OASL OAS3 SOCS1 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 TRIM22 SP100 PML HLA-C GBP1 GBP4 TRIM31 TRIM48 HLA-F HLA-E HLA-A GBP2
interferon-gamma-mediated signaling pathway	GO	21	70	<1E-18	<1E-18	OASL OAS3 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 NMI TRIM22 SP100 PML HLA-C GBP1 TRIM31 HLA-F HLA-E HLA-A GBP2
regulation of viral process	GO	29	387	<1E-18	2E-18	ISG15 IFITM1 OASL MX1 DDX60 OAS3

						STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 LAMP3 DDX58 OAS1 ISG20 TAP1 IFIT1 DYNLT1 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EIF2AK2 CCL4 LGALS9 HLA-A
cellular response to organic substance	GO	60	2004	<1E-18	6E-18	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 EGR2 CCNE1 TLR3 XAF1 XCL2 CD58 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1 CSH1 GBP2
regulation of symbiosis, encompassing mutualism through parasitism	GO	29	415	<1E-18	1.3E-17	ISG15 IFITM1 OASL MX1 DDX60 OAS3 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 LAMP3 DDX58 OAS1 ISG20 TAP1 IFIT1 DYNLT1 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EIF2AK2 CCL4 LGALS9 HLA-A
response to organic substance	GO	70	2728	<1E-18	2.3E-17	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 MDK OAS2 IFIT3

						B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 EGR2 CCNE1 IDO1 TLR3 XAF1 XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 UBD TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 RGS10 SAMHD1 CSH1 GBP2
response to stress	GO	79	3384	<1E-18	3.7E-17	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI44L IFI6 PLSCR1 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 DDX58 HCP5 OAS1 ISG20 IRF9 TAP1 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 MSRA HLA-C GBP1 TRIM31 UNC93B1 TYROBP PRTN3 IDO1 TLR3 XAF1 MELK XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 AMBRA1 UBD CLEC4E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 SHISA5 KLRD1

						SAMHD1 ECT2 GBP2
regulation of immune system process	GO	51	1546	<1E-18	4.1E-17	ISG15 IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 NMI IFIT1 KIR2DL3 IFI16 PML IFIH1 ZFP36 BIRC3 HLA-C GBP1 UNC93B1 TYROBP LAIR2 IDO1 TLR3 XCL2 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E KIR2DL2 CLEC4E TNFSF4 HLA-A CCL20 KLRD1 HCST TESPA1 SAMHD1
negative regulation of viral life cycle	GO	17	89	<1E-18	1.12E-16	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4
negative regulation of viral process	GO	18	111	<1E-18	1.37E-16	ISG15 IFITM1 OASL MX1 OAS3 STAT1 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4
cellular response to chemical stimulus	GO	65	2550	1E-18	3.56E-16	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 EGR2 CCNE1 TLR3

						XAF1 MELK XCL2 CD58 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 RGS10 SAMHD1 ECT2 CSH1 GBP2
Type II interferon signaling (IFNG)	WikiPathw	13	36	3E-18	1.238E-15	ISG15 CXCL10 SOCS1 STAT1 IFI6 PSMB9 CXCL9 OAS1 IRF9 TAP1 IFIT2 GBP1 EIF2AK2
Herpes simplex infection	KEGG	20	182	3E-18	1.472E-15	OAS3 STAT1 TAP2 OAS2 HLA-G DDX58 OAS1 IRF9 TAP1 IFIT1 SP100 PML IFIH1 HLA-C TLR3 EIF2AK2 HLA-F IL6 HLA-E HLA-A
regulation of immune response	GO	38	943	3E-18	1.474E-15	IFITM1 DDX60 SOCS1 STAT1 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A DDX58 TAP1 NMI KIR2DL3 IFI16 IFIH1 BIRC3 HLA-C GBP1 UNC93B1 TYROBP LAIR2 IDO1 TLR3 TREM2 HLA-F IL6 LGALS9 HLA-E KIR2DL2 CLEC4E TNFSF4 HLA-A KLRD1 HCST TESPA1 SAMHD1
regulation of cytokine production	GO	31	603	5E-18	1.974E-15	ISG15 DDX60 SOCS1 HERC5 UBE2L6 B2M RSAD2 HLA-G DDX58 NMI IFI16 PML IFIH1 ZFP36 BIRC3 GBP1 SRGN IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL20

regulation of multi-organism process	GO	29	522	7E-18	2.888E-15	ISG15 IFITM1 OASL MX1 DDX60 OAS3 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 LAMP3 DDX58 OAS1 ISG20 TAP1 IFIT1 DYNLT1 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EIF2AK2 CCL4 LGALS9 HLA-A
multi-organism process	GO	66	2778	1.1E-17	4.418E-15	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 FCGR1A LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TDRD7 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 ZFP36 RPL39L BIRC3 HLA-C KPNA2 GBP1 ATP6V1F UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1 GBP2
cell surface receptor signaling pathway	GO	57	2171	1.5E-17	6.181E-15	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML BCL2A1 BIRC3 HLA-

						C GBP1 ATP6V1F TRIM31 TYROBP CCNE1 TLR3 XAF1 XCL2 CCL4 HLA-F IL6 HLA-E CHRNA3 MX2 CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 KLRD1 SAMHD1 CSH1 GBP2
regulation of viral life cycle	GO	19	197	1.94E-16	7.589E-14	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 LAMP3 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4 LGALS9
negative regulation of multi-organism process	GO	18	169	2.3E-16	8.8355E-14	ISG15 IFITM1 OASL MX1 OAS3 STAT1 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4
response to external stimulus	GO	59	2491	3.58E-16	1.34654E-13	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 TYMP PML IFIH1 ZFP36 GBP1 UNC93B1 RAB32 TYROBP EGR2 CCNE1 PRTN3 IDO1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 AMBRA1 CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1
Immunoregulatory interactions	REACTOME	16	124	6.17E-16	2.27354E-13	IFITM1 B2M HLA-G FCGR1A KIR2DL3 LILRA2 HLA-C

between a Lymphoid and a non-Lymphoid cell						TYROBP LAIR2 TREM2 HLA-F HLA-E KIR2DL2 HLA-A KLRD1 HCST
positive regulation of immune system process	GO	36	1005	6.64E-16	2.39724E-13	ISG15 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 IFI16 IFIH1 BIRC3 HLA-C UNC93B1 IDO1 TLR3 XCL2 CD83 TREM2 CCL4 HLA-F IL6 LGALS9 HLA-E CLEC4E TNFSF4 HLA-A CCL20 TESPA1
regulation of defense response	GO	33	864	1.561E-15	5.5289E-13	DDX60 SOCS1 STAT1 PLSCR1 HERC5 B2M RSAD2 PSMB9 FCGR1A DDX58 TAP1 NMI IFIT1 IFI16 PML IFIH1 ZFP36 BIRC3 UNC93B1 IDO1 TLR3 XCL2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL3L3 SAMHD1
response to chemical	GO	81	4360	3.395E-15	1.17995E-12	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFIT2 TYMP SP100 PML ZFP36 BIRC3 HLA-C KPNA2 GBP1 ATP6V1F TRIM31

						EGR2 CCNE1 IDO1 TLR3 XAF1 MELK XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 UBD TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 RGS10 SAMHD1 OR4C45 ECT2 OR52E8 CSH1 GBP2
negative regulation of viral genome replication	GO	12	51	3.957E-15	1.34961E-12	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 EIF2AK2
Influenza A	KEGG	16	169	5.1051E-14	1.67903E-11	MX1 CXCL10 OAS3 STAT1 OAS2 RSAD2 DDX58 OAS1 IRF9 PML IFIH1 KPNA2 TLR3 EIF2AK2 IL6 CASP1
signal transduction	GO	82	4737	7.7947E-14	2.51866E-11	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 CCL20 CCL3L3

						SHISA5 KLRD1 RGS10 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
Adaptive Immune System	REACTOME	29	799	2.02191E-13	6.20661E-11	IFITM1 HERC6 SOCS1 TAP2 HERC5 UBE2L6 TRIM69 B2M HLA-G PSMB9 FCGR1A IFI30 RNF19B TAP1 KIR2DL3 LILRA2 RNF213 NFKBIE HLA-C TYROBP LAIR2 ORAI2 TREM2 HLA-F HLA-E KIR2DL2 HLA-A KLRD1 HCST
Antigen processing and presentation	KEGG	12	74	1.98835E-13	6.20661E-11	TAP2 B2M HLA-G IFI30 TAP1 KIR2DL3 HLA-C HLA-F HLA-E KIR2DL2 HLA-A KLRD1
positive regulation of cytokine production	GO	21	389	2.5409E-13	7.67185E-11	DDX60 B2M RSAD2 HLA-G DDX58 IFI16 IFIH1 IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL20
regulation of viral genome replication	GO	12	81	5.20521E-13	1.54628E-10	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 EIF2AK2
cell communication	GO	85	5274	1.1322E-12	3.30997E-10	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C GBP1

						ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 AMBRA1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
regulation of T cell mediated immunity	GO	11	67	1.71839E-12	4.94519E-10	TAP2 B2M RSAD2 HLA-G TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
signaling	GO	90	5795	1.78214E-12	4.97324E-10	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C KPNA2 GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6

						CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
single organism signaling	GO	90	5795	1.78214E-12	4.97324E-10	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C KPNA2 GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
positive regulation of lymphocyte mediated immunity	GO	12	95	2.85975E-12	7.74571E-10	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A

positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO	12	95	2.85975E-12	7.74571E-10	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
positive regulation of adaptive immune response	GO	12	99	4.44729E-12	1.18711E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
positive regulation of immune response	GO	25	690	7.47348E-12	1.96638E-09	DDX60 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A DDX58 TAP1 IFI16 IFIH1 BIRC3 HLA-C UNC93B1 IDO1 TLR3 HLA-F IL6 LGALS9 HLA-E CLEC4E TNFSF4 HLA-A TESPA1
antigen processing and presentation of exogenous peptide antigen via MHC class I	GO	11	78	7.58312E-12	1.96712E-09	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C HLA-F HLA-E HLA-A
regulation of immune effector process	GO	21	473	8.33145E-12	2.13123E-09	DDX60 TAP2 HERC5 B2M RSAD2 HLA-G FCGR1A DDX58 TAP1 IFIT1 PML BIRC3 HLA-C TLR3 EIF2AK2 HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
regulation of lymphocyte mediated immunity	GO	13	138	1.10986E-11	2.8002E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A

modification of morphology or physiology of other organism involved in symbiotic interaction	GO	20	436	1.42319E-11	3.41803E-09	ISG15 STAT1 TAP2 RSAD2 PSMB9 SP110 DDX58 TAP1 IFIT1 TRIM22 DYNLT1 SP100 PML IFIH1 HLA-C KPNA2 TLR3 EIF2AK2 CCL4 HLA-A
negative regulation of reproductive process	GO	12	110	1.37495E-11	3.41803E-09	IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 IFIT1 IFI16 SP100 EIF2AK2 CCL4
Graft-versus-host disease	KEGG	9	40	1.42897E-11	3.41803E-09	HLA-G KIR2DL3 HLA-C HLA-F IL6 HLA-E KIR2DL2 HLA-A KLRD1
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	REACTOME	8	25	1.73803E-11	4.10398E-09	TAP2 B2M HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
positive regulation of leukocyte mediated immunity	GO	12	114	2.01598E-11	4.70004E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
modification of morphology or physiology of other organism	GO	20	452	2.61222E-11	6.01398E-09	ISG15 STAT1 TAP2 RSAD2 PSMB9 SP110 DDX58 TAP1 IFIT1 TRIM22 DYNLT1 SP100 PML IFIH1 HLA-C KPNA2 TLR3 EIF2AK2 CCL4 HLA-A
regulation of leukocyte mediated immunity	GO	14	186	3.05477E-11	6.94602E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C TLR3 HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
response to stimulus	GO	110	8044	3.33652E-11	7.49414E-09	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2

						UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 HCP5 OAS1 ISG20 RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 MSRA BIRC3 HLA-C HMHB1 KPNA2 GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
positive regulation of defense response	GO	20	461	3.63718E-11	8.07102E-09	DDX60 PLSCR1 RSAD2 PSMB9 FCGR1A DDX58 IFI16 IFIH1 BIRC3 UNC93B1 IDO1 TLR3 XCL2 CCL4 IL6 LGALS9 HLA-E CLEC4E TNFSF4 CCL3L3
negative regulation of cytokine production	GO	15	232	4.71932E-11	1.03477E-08	ISG15 HERC5 UBE2L6 DDX58 NMI PML IFIH1 ZFP36 GBP1 SRGN IDO1

						CD83 IL6 LGALS9 TNFSF4
positive regulation of immune effector process	GO	14	197	6.21722E-11	1.34716E-08	DDX60 TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
antigen processing and presentation of peptide antigen via MHC class I	GO	11	98	7.12001E-11	1.52484E-08	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C HLA-F HLA-E HLA-A
response to bacterium	GO	21	538	7.90976E-11	1.67451E-08	ISG15 CMPK2 CXCL11 CXCL10 SOCS1 B2M CXCL9 ZFP36 IDO1 TLR3 TREM2 EIF2AK2 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20
cellular response to stimulus	GO	89	6172	9.11081E-11	1.90685E-08	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 AMBRA1

						OR2B6 CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
ISG15 antiviral mechanism	REACTOME	10	74	9.63838E-11	1.97244E-08	ISG15 MX1 STAT1 HERC5 UBE2L6 DDX58 IFIT1 KPNA2 EIF2AK2 MX2
Antiviral mechanism by IFN-stimulated genes	REACTOME	10	74	9.63838E-11	1.97244E-08	ISG15 MX1 STAT1 HERC5 UBE2L6 DDX58 IFIT1 KPNA2 EIF2AK2 MX2
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	GO	10	75	1.08631E-10	2.19864E-08	TAP2 B2M HLA-G PSMB9 FCGR1A TAP1 HLA-C HLA-F HLA-E HLA-A
phagocytic vesicle	GO	11	104	1.27653E-10	2.55556E-08	TAP2 B2M HLA-G TAP1 HLA-C UNC93B1 RAB32 HLA-F HLA-E AMBRA1 HLA-A
regulation of innate immune response	GO	19	445	1.37077E-10	2.71471E-08	DDX60 SOCS1 STAT1 PLSCR1 RSAD2 PSMB9 DDX58 TAP1 NMI IFI16 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 HLA-E CLEC4E HLA-A SAMHD1
regulation of adaptive immune response based on somatic recombination of immune receptors built from	GO	12	139	1.68253E-10	3.29669E-08	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A

immunoglobulin superfamily domains						
response to interferon-alpha	GO	7	20	1.90436E-10	3.65709E-08	IFITM1 IFIT3 LAMP3 OAS1 IFIT2 EIF2AK2 MX2
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	GO	6	9	1.90618E-10	3.65709E-08	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
Class I MHC mediated antigen processing & presentation	REACTOME	17	365	3.32768E-10	6.31847E-08	HERC6 SOCS1 TAP2 HERC5 UBE2L6 TRIM69 B2M HLA-G PSMB9 FCGR1A RNF19B TAP1 RNF213 HLA-C HLA-F HLA-E HLA-A
regulation of adaptive immune response	GO	12	150	3.79195E-10	7.12654E-08	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
MHC class I protein complex	GO	6	11	4.66539E-10	8.6795E-08	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
receptor binding	GO	34	1504	4.98404E-10	9.1796E-08	OASL CXCL11 CXCL10 SOCS1 STAT1 RTP4 PLSCR1 TAP2 MDK HLA-G CXCL9 TAP1 TYMP SP100 HLA-C UNC93B1 TYROBP CCNE1 XCL2 CD58 PRAMEF1 CCL4 HLA-F IL6 HLA-E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 KLRD1 HCST TESPA1 CSH1
regulation of response to stimulus	GO	64	4092	6.2881E-10	1.14148E-07	IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 TAP2

						HERC5 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 SP100 PML BCL2A1 IFIH1 ZFP36 RNF213 BIRC3 HLA-C GBP1 UNC93B1 TYROBP LAIR2 IDO1 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 HLA-F IL6 LGALS9 HLA-E CASP1 AMBRA1 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SAMHD1 ECT2
response to lipopolysaccharide	GO	16	331	6.32158E-10	1.14148E-07	CMPK2 CXCL11 CXCL10 SOCS1 B2M CXCL9 ZFP36 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CASP1 TNFSF4 JUNB CCL20
Endosomal/Vacuolar pathway	REACTOME	6	12	6.9623E-10	1.24497E-07	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
double-stranded RNA binding	GO	9	66	7.57877E-10	1.34217E-07	OASL DDX60 OAS3 OAS2 DDX58 OAS1 IFIH1 TLR3 EIF2AK2
response to molecule of bacterial origin	GO	16	345	1.11167E-09	1.94998E-07	CMPK2 CXCL11 CXCL10 SOCS1 B2M CXCL9 ZFP36 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CASP1 TNFSF4 JUNB CCL20
NOD-like receptor signaling pathway	KEGG	12	168	1.2652E-09	2.17779E-07	OAS3 STAT1 OAS2 OAS1 IRF9 IFI16 BIRC3 GBP1 GBP4 IL6 CASP1 GBP2
Antigen processing-	REACTOME	10	99	1.2958E-09	2.20982E-07	TAP2 B2M HLA-G PSMB9 FCGR1A

						TAP1 HLA-C HLA-F HLA-E HLA-A
Cross presentation phagocytic vesicle membrane	GO	9	71	1.36168E-09	2.30087E-07	TAP2 B2M HLA-G TAP1 HLA-C RAB32 HLA-F HLA-E HLA-A
Measles	KEGG	11	133	1.42547E-09	2.36526E-07	MX1 OAS3 STAT1 OAS2 DDX58 OAS1 IRF9 IFIH1 CCNE1 EIF2AK2 IL6
antigen processing and presentation of endogenous peptide antigen	GO	6	15	2.00409E-09	3.29565E-07	TAP2 B2M TAP1 HLA-C HLA-E HLA-A
antigen processing and presentation of exogenous peptide antigen	GO	12	183	3.1274E-09	5.09739E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 HLA-F HLA-E HLA-A
regulation of response to stress	GO	34	1635	3.57856E-09	5.78157E-07	DDX60 SOCS1 STAT1 PLSCR1 HERC5 B2M RSAD2 PSMB9 FCGR1A DDX58 TAP1 NMI IFIT1 IFI16 PML IFIH1 ZFP36 BIRC3 UNC93B1 IDO1 TLR3 XCL2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 AMBRA1 CLEC4E TNFSF4 HLA-A CCL3L3 SAMHD1
positive regulation of response to stimulus	GO	42	2320	4.02055E-09	6.43917E-07	CXCL11 DDX60 CXCL10 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 TRIM22 IFI16 PML IFIH1 BIRC3 HLA-C UNC93B1 IDO1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CASP1 AMBRA1 UBD CLEC4E

						TNFSF4 HLA-A CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
antigen processing and presentation	GO	13	232	4.30375E-09	6.83332E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 RAB32 HLA-F HLA-E HLA-A
antigen processing and presentation of exogenous antigen	GO	12	190	4.64602E-09	7.31371E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 HLA-F HLA-E HLA-A
ER-Phagosome pathway	REACTOME	9	83	4.77812E-09	7.45791E-07	TAP2 B2M HLA-G PSMB9 TAP1 HLA-C HLA-F HLA-E HLA-A
antigen processing and presentation of endogenous antigen	GO	6	18	4.89512E-09	7.57633E-07	TAP2 B2M TAP1 HLA-C HLA-E HLA-A
TAP binding	GO	5	7	5.13907E-09	7.88762E-07	TAP2 TAP1 HLA-C HLA-F HLA-A
antigen processing and presentation of peptide antigen	GO	12	196	6.44375E-09	9.72795E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 HLA-F HLA-E HLA-A
antigen binding	GO	9	91	1.00161E-08	1.4998E-06	HLA-G TAP1 KIR2DL3 LILRA2 HLA-C HLA-F HLA-E HLA-A KLRD1
inflammatory response	GO	17	480	1.61112E-08	2.39304E-06	CXCL11 CXCL10 PLSCR1 FCGR1A CXCL9 NMI IFI16 SP100 IDO1 TLR3 XCL2 CCL4 IL6 LGALS9 TNFSF4 CCL20 CCL3L3
regulation by virus of viral protein levels in host cell	GO	5	11	2.77868E-08	4.09422E-06	STAT1 TAP2 TAP1 IFIT1 DYNLT1
negative regulation of biological process	GO	70	5225	3.37306E-08	4.93056E-06	ISG15 IFITM1 OASL MX1 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 HERC5

						MDK UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 LAMP3 IFI27 IFI30 DDX58 OAS1 ISG20 WARS TAP1 NMI IFIT1 TRIM22 DYNLT1 IFI16 ETV7 SP100 PML BCL2A1 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE LCMT1 GBP1 TRIM31 PGP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 RGS1 CD83 EIF2AK2 RARRES3 PRAMEF1 CCL4 IL6 LGALS9 HLA-E PSMG2 AMBRA1 TNFSF4 HLA-A JUNB CCL3L3 RGS10 SYT4 ZNF831 SVBP
chemokine activity	GO	7	48	3.75659E-08	5.44795E-06	CXCL11 CXCL10 CXCL9 XCL2 CCL4 CCL20 CCL3L3
MHC protein complex	GO	6	27	3.84679E-08	5.53517E-06	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
antigen processing and presentation of endogenous peptide antigen via MHC class I	GO	5	13	5.3968E-08	7.70529E-06	TAP2 B2M TAP1 HLA-C HLA-A
Allograft Rejection	WikiPathw	8	80	5.99151E-08	8.48859E-06	CXCL11 STAT1 HLA-G CXCL9 HLA-C HLA-F HLA-E HLA-A
peptide antigen binding	GO	6	30	6.66206E-08	9.36655E-06	HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
positive regulation of T cell cytokine production	GO	5	15	9.66946E-08	1.33904E-05	B2M RSAD2 IL6 TNFSF4 HLA-A
regulation of cytokine secretion	GO	10	162	1.02683E-07	1.41135E-05	SOCS1 PML GBP1 SRGN CD58 IL6 LGALS9 CASP1 CLEC4E TNFSF4

regulation of multicellular organismal process	GO	46	3013	1.1156E-07	1.52201E-05	ISG15 IFITM1 DDX60 CXCL10 SOCS1 STAT1 HERC5 UBE2L6 B2M RSAD2 HLA-G PSMB9 DDX58 WARS NMI DYNLT1 IFI16 TYMP SP100 PML IFIH1 ZFP36 BIRC3 GBP1 TYROBP SRGN EGR2 IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CHRNA3 CASP1 CLEC4E TNFSF4 HLA-A CCL20 TESPA1 SYT4 ECT2 SVBP
early endosome	GO	13	311	1.12468E-07	1.52312E-05	B2M HLA-G FCGR1A LAMP3 PML HLA-C SAMD9L SAMD9 RAB32 TLR3 HLA-F HLA-E HLA-A
response to tumor necrosis factor	GO	12	260	1.21314E-07	1.63093E-05	STAT1 PSMB9 ZFP36 BIRC3 XCL2 CD58 CCL4 IL6 UBD TNFSF4 CCL20 CCL3L3
regulation of response to external stimulus	GO	24	1072	1.31495E-07	1.75498E-05	CXCL11 DDX60 CXCL10 HERC5 B2M FCGR1A CXCL9 DDX58 IFIT1 PML ZFP36 BIRC3 IDO1 TLR3 XCL2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 AMBRA1 TNFSF4 HLA-A CCL3L3
endocytic vesicle membrane	GO	10	167	1.34068E-07	1.77645E-05	TAP2 B2M HLA-G FCGR1A TAP1 HLA-C RAB32 HLA-F HLA-E HLA-A
chemokine receptor binding	GO	7	59	1.36094E-07	1.79042E-05	CXCL11 CXCL10 CXCL9 XCL2 CCL4 CCL20 CCL3L3
regulation of reproductive process	GO	12	265	1.47428E-07	1.88565E-05	IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 IFIT1 IFI16 SP100 EIF2AK2 CCL4

positive regulation of T cell mediated immunity	GO	6	35	1.49911E-07	1.90417E-05	B2M RSAD2 IL6 HLA-E TNFSF4 HLA-A
Innate Immune System	REACTOME	26	1247	1.6215E-07	2.00192E-05	ISG15 SOCS1 HERC5 UBE2L6 B2M PSMB9 FCGR1A DDX58 DYNLT1 IFI16 IFIH1 BIRC3 HLA-C ATP6V1F UNC93B1 TYROBP PRTN3 TLR3 CD58 TREM2 HLA-E CASP1 CLEC4E HLA-A DSN1 KLRD1
Natural killer cell mediated cytotoxicity	KEGG	9	129	1.64128E-07	2.00192E-05	HLA-G KIR2DL3 HLA-C TYROBP HLA-E KIR2DL2 HLA-A KLRD1 HCST
Hepatitis C	KEGG	9	130	1.74541E-07	2.10111E-05	OAS3 STAT1 OAS2 DDX58 OAS1 IRF9 IFIT1 TLR3 EIF2AK2
endocytic vesicle	GO	12	277	2.31582E-07	2.76966E-05	TAP2 B2M HLA-G FCGR1A TAP1 HLA-C UNC93B1 RAB32 HLA-F HLA-E AMBRA1 HLA-A
negative regulation of cellular process	GO	62	4693	2.44625E-07	2.90678E-05	ISG15 IFITM1 OASL MX1 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 MDK IFIT3 B2M RSAD2 HLA-G PSMB9 LAMP3 IFI27 IFI30 OAS1 ISG20 WARS NMI IFIT1 TRIM22 DYNLT1 IFI16 ETV7 SP100 PML BCL2A1 ZFP36 RNF213 BIRC3 NFKBIE LCMT1 GBP1 TRIM31 PGP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 RGS1 EIF2AK2 RARRES3 PRAMEF1 CCL4 IL6 LGALS9 PSMG2 AMBRA1 TNFSF4 JUNB CCL3L3

						RGS10 SYT4 ZNF831 SVBP ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE HLA-C KPNA2 SAMD9L LCMT1 GBP1 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST
regulation of biological process	GO	122	11240	2.9252 2E-07	3.4324 3E-05	TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2

						OR52E8 RASSF3 CSH1 GBP2 SVBP
regulation of cysteine-type endopeptidase activity	GO	11	231	2.92589E-07	3.43243E-05	IFI6 PSMB9 LAMP3 IFI27 IFI16 PML BIRC3 TLR3 IL6 LGALS9 CASP1
negative regulation of immune system process	GO	14	401	3.10051E-07	3.61425E-05	HLA-G TAP1 NMI IFIT1 IFI16 ZFP36 GBP1 IDO1 TLR3 EIF2AK2 LGALS9 HLA-E TNFSF4 HLA-A
Toll-like receptor signaling pathway	KEGG	8	102	3.39576E-07	3.90894E-05	CXCL11 CXCL10 STAT1 CXCL9 TLR3 CCL4 IL6 CCL3L3
cellular response to tumor necrosis factor	GO	11	236	3.58048E-07	4.09598E-05	STAT1 PSMB9 ZFP36 BIRC3 XCL2 CD58 CCL4 IL6 TNFSF4 CCL20 CCL3L3
positive regulation of innate immune response	GO	13	348	3.81356E-07	4.33569E-05	DDX60 PLSCR1 RSAD2 PSMB9 DDX58 IFI16 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 HLA-E CLEC4E
regulation of cellular process	GO	116	10629	4.44176E-07	4.9959E-05	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE HLA-C KPNA2 LCMT1 GBP1 ATP6V1F TRIM31 PGP

						UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
negative regulation of innate immune response	GO	6	43	4.47564E-07	4.9959E-05	TAP1 NMI IFI16 LGALS9 HLA-E HLA-A
lymphocyte chemotaxis	GO	6	43	4.47564E-07	4.9959E-05	CXCL11 CXCL10 CXCL9 XCL2 CCL20 CCL3L3
regulation of hemopoiesis	GO	13	355	4.72454E-07	5.24196E-05	ISG15 STAT1 B2M HLA-G ZFP36 TYROBP TLR3 CD83 EIF2AK2 IL6 LGALS9 TNFSF4 TESPA1
negative regulation of multicellular organismal process	GO	24	1160	5.01878E-07	5.43741E-05	ISG15 CXCL10 STAT1 HERC5 UBE2L6 B2M HLA-G DDX58 NMI DYNLT1 SP100 PML IFIH1 ZFP36 GBP1 SRGN IDO1 TLR3 CD83 IL6 LGALS9 TNFSF4 SYT4 SVBP
negative regulation of type I interferon production	GO	6	44	5.06007E-07	5.45008E-05	ISG15 HERC5 UBE2L6 DDX58 NMI IFIH1

chemokine-mediated signaling pathway	GO	7	73	5.15926E-07	5.5246E-05	CXCL11 CXCL10 CXCL9 XCL2 CCL4 CCL20 CCL3L3
protein binding	GO	117	10853	5.49617E-07	5.81773E-05	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 DDX58 OAS1 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L LCMT1 GBP1 SAMD9 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 LAIR2 PRTN3 TLR3 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4

						SAMHD1 ECT2 RASSF3 CSH1 GBP2
Viral carcinogenesis	KEGG	10	198	5.90561E-07	6.11065E-05	HLA-G IRF9 SP100 HLA-C EGR2 CCNE1 EIF2AK2 HLA-F HLA-E HLA-A
regulation of T cell cytokine production	GO	5	23	5.89178E-07	6.11065E-05	B2M RSAD2 IL6 TNFSF4 HLA-A
response to interferon-beta	GO	5	23	5.89178E-07	6.11065E-05	IFITM1 STAT1 PLSCR1 TLR3 XAF1
Phagosome	KEGG	9	153	6.35135E-07	6.49884E-05	TAP2 HLA-G FCGR1A TAP1 HLA-C ATP6V1F HLA-F HLA-E HLA-A
positive regulation of T cell differentiation	GO	7	76	6.63816E-07	6.75479E-05	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
regulation of protein transport	GO	19	787	7.56874E-07	7.6594E-05	SOCS1 RSAD2 IFI27 DDX58 SP100 PML NFKBIE GBP1 SRGN TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
regulation of protein localization	GO	22	1027	7.98759E-07	7.9954E-05	SOCS1 RSAD2 IFI27 DDX58 TRIM22 SP100 PML NFKBIE GBP1 SRGN CCNE1 TLR3 CD58 TREM2 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
regulation of type I interferon production	GO	8	116	8.46856E-07	8.43102E-05	ISG15 HERC5 UBE2L6 DDX58 NMI IFI16 IFIH1 TLR3
negative regulation of defense response	GO	9	161	9.48796E-07	9.39512E-05	TAP1 NMI IFIT1 IFI16 ZFP36 EIF2AK2 LGALS9 HLA-E HLA-A
cytoplasmic part	GO	102	9320	9.57082E-07	9.42649E-05	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 PPA1 OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2

						HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 DDX58 OAS1 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 CD58 EIF2AK2 RARRES3 VAMP5 HLA-F LGALS9 HLA-E MX2 CASP1 PSMG2 AMBRA1 HLA-A GNA15 SPRR2A DSN1 SHISA5 RGS10 TESPA1 SYT4 BOLA3 ECT2 RASSF3 CSH1 GBP2
early endosome membrane	GO	8	119	1.01471E-06	9.94091E-05	B2M HLA-G FCGR1A PML HLA-C HLA-F HLA-E HLA-A
cytokine activity	GO	10	215	1.20028E-06	0.000116967	CXCL11 CXCL10 CXCL9 SP100 XCL2 CCL4 IL6 TNFSF4 CCL20 CCL3L3
positive regulation of response to external stimulus	GO	14	453	1.23343E-06	0.000119565	CXCL11 DDX60 CXCL10 FCGR1A CXCL9 IDO1 TLR3 XCL2 CCL4 IL6 LGALS9 AMBRA1 TNFSF4 CCL3L3

positive regulation of alpha-beta T cell activation	GO	6	53	1.37041E-06	0.000132148	CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A
single-organism cellular process	GO	133	12938	1.38812E-06	0.000133158	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A

					GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP ISG15 IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 TAP2 MDK B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 CXCL9 DDX58 WARS RNF19B TAP1 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML BCL2A1 IFIH1 ZFP36 BIRC3 HLA-C TRIM31 UNC93B1 EGR2 CCNE1 PRTN3 IDO1 TLR3 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 PRAMEF1 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 CASP1 AMBRA1 UBD CLEC4E TNFSF4 HLA-A
positive regulation of biological process	GO	71	5953	1.43431E-06	0.000136393	JUNB CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
positive regulation of inflammatory response	GO	8	125	1.43665E-06	0.000136393	FCGR1A IDO1 TLR3 XCL2 CCL4 IL6 TNFSF4 CCL3L3
leukocyte chemotaxis	GO	8	126	1.51976E-06	0.000143543	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 CCL20 CCL3L3
biological regulation	GO	123	11844	1.62102E-06	0.000150788	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2

						HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE HLA-C KPNA2 SAMD9L LCMT1 GBP1 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
integral component of lumenal side of endoplasmic reticulum membrane	GO	5	29	1.61942E-06	0.000150788	HLA-G HLA-C HLA-F HLA-E HLA-A

lumenal side of endoplasmic reticulum membrane	GO	5	29	1.61942E-06	0.000150788	HLA-G HLA-C HLA-F HLA-E HLA-A
positive regulation of lymphocyte differentiation	GO	7	88	1.6594E-06	0.000153582	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
Osteoclast differentiation	KEGG	8	128	1.6983E-06	0.000155618	SOCS1 STAT1 FCGR1A IRF9 LILRA2 TYROBP TREM2 JUNB
positive regulation of leukocyte migration	GO	8	129	1.79405E-06	0.000163578	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9 CCL20
lymphocyte migration	GO	6	56	1.84138E-06	0.000167066	CXCL11 CXCL10 CXCL9 XCL2 CCL20 CCL3L3
negative regulation of immune response	GO	8	130	1.89435E-06	0.00017103	HLA-G TAP1 NMI IFI16 LGALS9 HLA-E TNFSF4 HLA-A
regulation of peptide transport	GO	19	842	1.94587E-06	0.000174825	SOCS1 RSAD2 IFI27 DDX58 SP100 PML NFKBIE GBP1 SRGN TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
positive regulation of intracellular signal transduction	GO	20	927	2.09287E-06	0.000187119	CXCL11 DDX60 CXCL10 CXCL9 TRIM22 BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST ECT2
positive regulation of multicellular organismal process	GO	28	1626	2.13366E-06	0.000189844	ISG15 IFITM1 DDX60 STAT1 B2M RSAD2 HLA-G DDX58 IFI16 PML IFIH1 IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL20 TESPA1 SYT4 ECT2

regulation of apoptotic process	GO	26	1446	2.18238E-06	0.000193245	STAT1 IFI6 MDK IFIT3 LAMP3 IFI27 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 LCMT1 IDO1 TLR3 MELK EIF2AK2 PRAMEF1 IL6 LGALS9 CASP1 PSMG2 AMBRA1 UBD ECT2 RASSF3
adaptive immune response	GO	11	287	2.21202E-06	0.000194933	TAP2 FCGR1A LAMP3 RNF19B TAP1 LILRA2 HMHB1 UNC93B1 IL6 HLA-E TNFSF4
ER to Golgi transport vesicle membrane	GO	6	58	2.22299E-06	0.000194967	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
pyrophosphatase activity	GO	19	851	2.25353E-06	0.000196709	MX1 DDX60 TAP2 PPA1 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
side of membrane	GO	14	479	2.29509E-06	0.000199392	CXCL10 B2M HLA-G FCGR1A CXCL9 HLA-C RGS1 CD83 HLA-F IL6 HLA-E HLA-A GNA15 KLRD1
hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	GO	19	853	2.3276E-06	0.000201267	MX1 DDX60 TAP2 PPA1 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
hydrolase activity, acting on acid anhydrides	GO	19	855	2.40387E-06	0.000206596	MX1 DDX60 TAP2 PPA1 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
cell surface	GO	18	776	2.41167E-06	0.000206596	CXCL10 RTP4 B2M CXCL9 HLA-C TYROBP TLR3 CD58 CD83 VAMP5 HLA-F IL6 HLA-E TNFSF4

						HLA-A KLRD1 HCST ECT2
regulation of protein secretion	GO	13	415	2.47168E-06	0.000210757	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4
regulation of programmed cell death	GO	26	1462	2.63E-06	0.000222199	STAT1 IFI6 MDK IFIT3 LAMP3 IFI27 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 LCMT1 IDO1 TLR3 MELK EIF2AK2 PRAMEF1 IL6 LGALS9 CASP1 PSMG2 AMBRA1 UBD ECT2 RASSF3
recycling endosome membrane	GO	6	60	2.66667E-06	0.000224268	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of establishment of protein localization	GO	19	866	2.86513E-06	0.000237702	SOCS1 RSAD2 IFI27 DDX58 SP100 PML NFKBIE GBP1 SRGN TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
positive regulation of interleukin-12 production	GO	5	33	2.86417E-06	0.000237702	HLA-G IDO1 TLR3 LGALS9 TNFSF4
lumenal side of membrane	GO	5	33	2.86417E-06	0.000237702	HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of cell death	GO	27	1570	3.17096E-06	0.000261895	STAT1 IFI6 MDK IFIT3 LAMP3 IFI27 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 LCMT1 IDO1 TLR3 MELK EIF2AK2 PRAMEF1 IL6 LGALS9 CASP1 PSMG2 AMBRA1 UBD JUNB ECT2 RASSF3
Regulation of toll-like receptor signaling pathway	WikiPathw	8	140	3.1887E-06	0.000262185	CXCL11 CXCL10 SOCS1 STAT1 CXCL9 TLR3 CCL4 IL6

Negative regulators of RIG-I/MDA5 signaling	REACTOME	5	34	3.26921E-06	0.00026761	ISG15 HERC5 UBE2L6 DDX58 IFIH1
membrane fusion	GO	9	190	3.45628E-06	0.000281672	MX1 TAP2 TAP1 BCL2A1 SAMD9L SAMD9 VAMP5 MX2 SYT4
Toll-like Receptor Signaling Pathway	WikiPathw	7	100	3.67835E-06	0.000298449	CXCL11 CXCL10 STAT1 CXCL9 TLR3 CCL4 IL6
Proteasome Degradation	WikiPathw	6	64	3.77066E-06	0.000304597	HLA-G PSMB9 HLA-C HLA-F HLA-E HLA-A
nucleoside-triphosphatase activity	GO	18	807	4.03984E-06	0.000323503	MX1 DDX60 TAP2 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
regulation of defense response to virus	GO	9	195	4.22546E-06	0.000331168	DDX60 HERC5 B2M DDX58 IFIT1 PML BIRC3 EIF2AK2 HLA-A
positive regulation of cytokine production involved in immune response	GO	5	36	4.21341E-06	0.000331168	B2M RSAD2 IL6 TNFSF4 HLA-A
regulation of cytokine production involved in immune response	GO	6	66	4.44768E-06	0.000347107	B2M RSAD2 TLR3 IL6 TNFSF4 HLA-A
regulation of cellular localization	GO	19	901	4.9127E-06	0.000380863	CXCL11 CXCL10 IFI27 CXCL9 DDX58 SP100 PML ZFP36 NFKBIE GBP1 CCNE1 TLR3 TREM2 IL6 LGALS9 CHRNA3 MX2 SYT4 ECT2
Epstein-Barr virus infection	KEGG	9	199	4.94224E-06	0.000380863	HLA-G DDX58 NFKBIE HLA-C CD58 EIF2AK2 HLA-F HLA-E HLA-A

Allograft rejection	KEGG	5	38	5.35902E-06	0.000407862	HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of inflammatory response	GO	11	321	6.13348E-06	0.000464882	FCGR1A ZFP36 BIRC3 IDO1 TLR3 XCL2 CCL4 IL6 CASP1 TNFSF4 CCL3L3
response to lipid	GO	19	920	6.50662E-06	0.000491143	CMPK2 CXCL11 CXCL10 SOCS1 MDK B2M CXCL9 SP100 ZFP36 CCNE1 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CASP1 TNFSF4 JUNB CCL20
regulation of leukocyte chemotaxis	GO	7	111	7.02318E-06	0.000525825	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9
vacuole	GO	20	1011	7.09883E-06	0.000529337	B2M SLC15A3 HLA-G FCGR1A LAMP3 IFI30 RNF19B PML HLA-C ATP6V1F UNC93B1 RAB32 SRGN PRTN3 TLR3 HLA-F HLA-E AMBRA1 HLA-A DSN1
negative regulation of immune effector process	GO	7	112	7.42341E-06	0.000551308	TAP1 IFIT1 EIF2AK2 LGALS9 HLA-E TNFSF4 HLA-A
negative regulation of protein transport	GO	9	210	7.47305E-06	0.000552765	RSAD2 SP100 PML NFKBIE GBP1 SRGN IL6 TNFSF4 SYT4
monocyte chemotaxis	GO	5	41	7.51939E-06	0.000553968	XCL2 CCL4 IL6 CCL20 CCL3L3
negative regulation of protein secretion	GO	7	114	8.28073E-06	0.000607627	RSAD2 PML GBP1 SRGN IL6 TNFSF4 SYT4
positive regulation of T cell activation	GO	9	213	8.33018E-06	0.000608831	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
cytokine receptor binding	GO	10	272	8.76311E-06	0.00063794	CXCL11 CXCL10 STAT1 CXCL9 XCL2 CCL4 IL6 TNFSF4 CCL20 CCL3L3

regulation of molecular function	GO	43	3257	8.83697E-06	0.000640784	CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 HERC5 B2M PSMB9 LAMP3 IFI27 DDX58 OAS1 WARS IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML ZFP36 BIRC3 LCMT1 TRIM31 CCNE1 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 AMBRA1 TNFSF4 GNA15 CCL20 CCL3L3 RGS10 ECT2
immune system development	GO	15	618	8.95277E-06	0.00064411	HERC6 B2M RSAD2 PSMB9 IFI16 PML PRTN3 MELK TREM2 IL6 LGALS9 UBD CLEC4E TNFSF4 JUNB
regulation of cysteine-type endopeptidase activity involved in apoptotic process	GO	9	215	8.94707E-06	0.00064411	IFI6 LAMP3 IFI27 PML BIRC3 TLR3 IL6 LGALS9 CASP1
single-organism process	GO	135	13821	9.14638E-06	0.000652938	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2

					TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
regulation of peptide secretion	GO	13	471	9.11259E-06	0.000652938	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4
cellular response to molecule of bacterial origin	GO	8	163	9.20263E-06	0.000653835	CMPK2 CXCL10 B2M ZFP36 TREM2 IL6 TNFSF4 CCL20
mononuclear cell migration	GO	5	43	9.30095E-06	0.000653835	XCL2 CCL4 IL6 CCL20 CCL3L3
Type I diabetes mellitus	KEGG	5	43	9.30095E-06	0.000653835	HLA-G HLA-C HLA-F HLA-E HLA-A

ER to Golgi transport vesicle	GO	6	77	1.01607E-05	0.000711559	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
cytoplasm	GO	112	11152	1.06642E-05	0.00073563	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 CD58 EIF2AK2 RARRES3 VAMP5 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A GNA15 SPRR2A DSN1 SHISA5 RGS10 TESPA1 SYT4 BOLA3 ECT2 RASSF3 CSH1 GBP2

regulation of production of molecular mediator of immune response	GO	7	120	1.1359E-05	0.000771992	B2M RSAD2 TLR3 IL6 HLA-E TNFSF4 HLA-A
positive regulation of cellular process	GO	63	5503	1.19148E-05	0.000806787	ISG15 IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 MDK B2M RSAD2 HLA-G PSMB9 IFI27 CXCL9 DDX58 WARS RNF19B NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 TRIM31 EGR2 CCNE1 PRTN3 IDO1 TLR3 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 HLA-E CHRNA3 CASP1 AMBRA1 UBD CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
regulation of nucleocytoplasmic transport	GO	9	224	1.22291E-05	0.000825039	IFI27 DDX58 SP100 NFKBIE TLR3 IL6 LGALS9 MX2 ECT2
negative regulation of peptide secretion	GO	7	122	1.25742E-05	0.000842152	RSAD2 PML GBP1 SRGN IL6 TNFSF4 SYT4
regulation of T cell differentiation	GO	7	122	1.25742E-05	0.000842152	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
negative regulation of establishment of protein localization	GO	9	225	1.26501E-05	0.000844163	RSAD2 SP100 PML NFKBIE GBP1 SRGN IL6 TNFSF4 SYT4
cytoplasmic vesicle membrane	GO	16	719	1.31587E-05	0.000871788	TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 HLA-C RAB32 TYROBP SYNGR2

regulation of cytoplasmic transport	GO	13	493	1.44569E-05	0.000950955	CD58 VAMP5 HLA-F HLA-E HLA-A SYT4 CXCL11 CXCL10 IFI27 CXCL9 DDX58 SP100 PML NFKBIE TLR3 IL6 LGALS9 MX2 ECT2
cell chemotaxis	GO	8	174	1.44425E-05	0.000950955	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 CCL20 CCL3L3
regulation of leukocyte migration	GO	8	175	1.50231E-05	0.000984678	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9 CCL20
positive regulation of production of molecular mediator of immune response	GO	6	83	1.5174E-05	0.000986324	B2M RSAD2 IL6 HLA-E TNFSF4 HLA-A
Chemokine receptors bind chemokines	REACTOME	5	48	1.52088E-05	0.000986324	CXCL11 CXCL10 CXCL9 XCL2 CCL20
Interleukin-10 signaling	REACTOME	5	48	1.52088E-05	0.000986324	CXCL10 CCL4 IL6 CCL20 CCL3L3
response to interleukin-1	GO	7	126	1.53282E-05	0.000990575	PSMB9 XCL2 CCL4 IL6 LGALS9 CCL20 CCL3L3
positive regulation of leukocyte cell-cell adhesion	GO	9	231	1.5444E-05	0.000994572	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
transport vesicle membrane	GO	8	176	1.5623E-05	0.001002597	B2M HLA-G HLA-C SYNGR2 HLA-F HLA-E HLA-A SYT4
apoptotic process	GO	18	902	1.68654E-05	0.001071129	MX1 STAT1 IFI6 PLSCR1 TRIM69 IFI27 IFI16 IFIT2 PML BCL2A1 BIRC3 SRGN TLR3 XAF1 MELK IL6 CASP1 SHISA5
regulation of hydrolase activity	GO	25	1543	1.72891E-05	0.001094266	OAS3 IFI6 PLSCR1 PSMB9 LAMP3 IFI27 OAS1 IFIT1 DYNLT1 IFI16 PML BIRC3 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CASP1 GNA15 CCL20

						CCL3L3 RGS10 ECT2
vesicle membrane	GO	16	738	1.78273E-05	0.001121153	TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 HLA-C RAB32 TYROBP SYNGR2 CD58 VAMP5 HLA-F HLA-E HLA-A SYT4
hematopoietic or lymphoid organ development	GO	14	579	1.78357E-05	0.001121153	HERC6 B2M RSAD2 PSMB9 IFI16 PML PRTN3 MELK TREM2 IL6 LGALS9 UBD CLEC4E JUNB
negative regulation of cytokine secretion	GO	5	50	1.82564E-05	0.001139817	PML GBP1 SRGN IL6 TNFSF4
response to oxygen-containing compound	GO	28	1810	1.95679E-05	0.001213473	CMPK2 CXCL11 CXCL10 SOCS1 STAT1 B2M PSMB9 CXCL9 SP100 ZFP36 ATP6V1F EGR2 CCNE1 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CHRNA3 CASP1 TNFSF4 GNA15 JUNB CCL20 RGS10 ECT2 CSH1 GBP2
regulation of alpha-beta T cell activation	GO	6	87	1.95042E-05	0.001213473	CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A
positive regulation of I-kappaB kinase/NF-kappaB signaling	GO	8	182	1.96614E-05	0.001215182	TRIM22 BIRC3 TLR3 LGALS9 CASP1 UBD SHISA5 ECT2
regulation of I-kappaB kinase/NF-kappaB signaling	GO	9	239	1.99718E-05	0.001230237	STAT1 TRIM22 BIRC3 TLR3 LGALS9 CASP1 UBD SHISA5 ECT2
cellular response to biotic stimulus	GO	8	184	2.1188E-05	0.001296478	CMPK2 CXCL10 B2M ZFP36 TREM2 IL6 TNFSF4 CCL20
positive regulation of signal transduction	GO	24	1469	2.15709E-05	0.001313945	CXCL11 DDX60 CXCL10 RSAD2 PSMB9 CXCL9 TRIM22 PML BIRC3 TLR3 XCL2 TREM2

						EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
regulation of interleukin-12 production	GO	5	52	2.17588E-05	0.001313945	HLA-G IDO1 TLR3 LGALS9 TNFSF4
Autoimmune thyroid disease	KEGG	5	52	2.17588E-05	0.001313945	HLA-G HLA-C HLA-F HLA-E HLA-A
positive regulation of leukocyte chemotaxis	GO	6	89	2.20142E-05	0.001325028	CXCL11 CXCL10 CXCL9 CCL4 IL6 LGALS9
binding	GO	135	14140	2.28774E-05	0.001350497	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L NT5C3A LCMT1 GBP1 SAMD9 GBP4 ZC2HC1B ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3

						TRANK1 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 TRIM48 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 ZNF831 ECT2 RASSF3 CSH1 GBP2
interaction with host	GO	8	186	2.28125E-05	0.001350497	TAP2 LAMP3 TAP1 IFIT1 DYNLT1 KPNA2 TLR3 EIF2AK2
positive regulation of hemopoiesis	GO	8	186	2.28125E-05	0.001350497	ISG15 STAT1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
negative regulation of secretion by cell	GO	8	187	2.36631E-05	0.001389841	RSAD2 PML GBP1 SRGN IL6 LGALS9 TNFSF4 SYT4
regulation of leukocyte mediated cytotoxicity	GO	5	53	2.36948E-05	0.001389841	B2M TAP1 LGALS9 HLA-E HLA-A
cytoplasmic vesicle part	GO	23	1393	2.63636E-05	0.001533997	TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 DYNLT1 PML HLA-C RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E HLA-A DSN1 SYT4 CSH1
leukocyte differentiation	GO	10	311	2.64023E-05	0.001533997	B2M RSAD2 IFI16 PRTN3 TREM2 IL6 LGALS9 UBD CLEC4E JUNB

programmed cell death	GO	19	1025	2.6923E-05	0.001559335	MX1 STAT1 IFI6 PLSCR1 TRIM69 IFI27 IFI16 IFIT2 PML BCL2A1 BIRC3 SRGN TLR3 XAF1 MELK IL6 CASP1 SPRR2A SHISA5
hemopoiesis	GO	13	525	2.70699E-05	0.001562925	HERC6 B2M RSAD2 IFI16 PML PRTN3 MELK TREM2 IL6 LGALS9 UBD CLEC4E JUNB
regulation of T cell activation	GO	10	315	2.92923E-05	0.001675483	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
Hepatitis B	KEGG	7	142	3.17967E-05	0.001807504	STAT1 DDX58 IFIH1 EGR2 CCNE1 TLR3 IL6
integral component of endoplasmic reticulum membrane	GO	7	143	3.31808E-05	0.001880379	TAP2 HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
regulation of response to biotic stimulus	GO	9	256	3.34274E-05	0.001888547	DDX60 HERC5 B2M DDX58 IFIT1 PML BIRC3 EIF2AK2 HLA-A
regulation of catalytic activity	GO	35	2628	3.43816E-05	0.001935709	CXCL10 OAS3 SOCS1 IFI6 PLSCR1 HERC5 PSMB9 LAMP3 IFI27 OAS1 WARS IFIT1 DYNLT1 IFI16 PML ZFP36 BIRC3 LCMT1 CCNE1 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 AMBRA1 GNA15 CCL20 CCL3L3 RGS10 ECT2
regulation of endopeptidase activity	GO	11	390	3.44724E-05	0.001935709	IFI6 PSMB9 LAMP3 IFI27 IFI16 PML BIRC3 TLR3 IL6 LGALS9 CASP1
identical protein binding	GO	23	1426	3.69934E-05	0.002070955	MX1 STAT1 IFIT3 B2M HLA-G DDX58 WARS TAP1 NMI DYNLT1 IFI16 TYMP

						SP100 PML BCL2A1 IFIH1 GBP1 TYROBP TLR3 CCL4 SYT4 ECT2 RASSF3
Viral myocarditis	KEGG	5	59	3.82826E-05	0.002136631	HLA-G HLA-C HLA-F HLA-E HLA-A
positive regulation of cell-cell adhesion	GO	9	261	3.86053E-05	0.002148133	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
cellular response to interleukin-1	GO	6	99	3.87511E-05	0.00214975	PSMB9 XCL2 CCL4 IL6 CCL20 CCL3L3
bounding membrane of organelle	GO	28	1926	4.10013E-05	0.00224377	TAP2 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 TAP1 PML BCL2A1 HLA-C GBP1 GBP4 ATP6V1F UNC93B1 RAB32 TYROBP SRGN TLR3 SYNGR2 CD58 HLA-F HLA-E AMBRA1 HLA-A SYT4 GBP2
intrinsic component of endoplasmic reticulum membrane	GO	7	148	4.08639E-05	0.00224377	TAP2 HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
vesicle fusion	GO	6	100	4.08688E-05	0.00224377	TAP2 TAP1 SAMD9L SAMD9 VAMP5 SYT4
G-protein coupled receptor binding	GO	9	264	4.20251E-05	0.002289997	CXCL11 CXCL10 RTP4 CXCL9 XCL2 CCL4 GNA15 CCL20 CCL3L3
organelle fusion	GO	7	149	4.25627E-05	0.002312446	TAP2 TAP1 BCL2A1 SAMD9L SAMD9 VAMP5 SYT4
Cytokine-cytokine receptor interaction	KEGG	9	265	4.32204E-05	0.002334408	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 TNFSF4 CCL20 CCL3L3
cell death	GO	19	1066	4.43911E-05	0.002358454	MX1 STAT1 IFI6 PLSCR1 TRIM69 IFI27 IFI16 IFIT2 PML BCL2A1 BIRC3 SRGN TLR3 XAF1 MELK IL6 CASP1 SPRR2A SHISA5

regulation of lymphocyte differentiation	GO	7	150	4.43189E-05	0.002358454	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
regulation of interleukin-1 production	GO	5	61	4.44339E-05	0.002358454	IFI16 PML LGALS9 CASP1 CCL20
Cytosolic DNA-sensing pathway	KEGG	5	61	4.44339E-05	0.002358454	CXCL10 DDX58 CCL4 IL6 CASP1
IL12-mediated signaling events	Pathway I	5	61	4.44339E-05	0.002358454	SOCS1 STAT1 B2M CCL4 HLA-A
protein modification by small protein conjugation	GO	16	803	4.67656E-05	0.002460938	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 RNF19B TRIM22 SP100 PML IFIH1 RNF213 BIRC3 TRIM31 EGR2 UBD
response to nitrogen compound	GO	20	1165	4.78098E-05	0.002508723	SOCS1 STAT1 PSMB9 DDX58 IFIT1 ATP6V1F EGR2 CCNE1 TLR3 TREM2 EIF2AK2 IL6 CHRNA3 CASP1 UBD TNFSF4 GNA15 JUNB RGS10 CSH1
intracellular transport of virus	GO	5	63	5.13222E-05	0.002685373	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
regulation of leukocyte cell-cell adhesion	GO	10	338	5.17102E-05	0.002690391	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
multi-organism cellular localization	GO	5	64	5.5061E-05	0.002840653	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
multi-organism intracellular transport	GO	5	64	5.5061E-05	0.002840653	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
negative regulation of secretion	GO	8	212	5.5354E-05	0.002847792	RSAD2 PML GBP1 SRGN IL6 LGALS9 TNFSF4 SYT4
single-organism membrane fusion	GO	7	156	5.61457E-05	0.002872479	TAP2 TAP1 BCL2A1 SAMD9L SAMD9 VAMP5 SYT4
positive regulation of	GO	7	156	5.61457E-05	0.002872479	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1

leukocyte differentiation						
cellular response to lipopolysaccharide	GO	7	157	5.83465E-05	0.002968577	CMPK2 CXCL10 B2M ZFP36 IL6 TNFSF4 CCL20
regulation of leukocyte differentiation	GO	9	277	5.99496E-05	0.003041741	SOCS1 HLA-G TYROBP TLR3 CD83 IL6 LGALS9 TNFSF4 TESPA1
regulation of T cell proliferation	GO	7	158	6.06171E-05	0.003067158	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
regulation of peptidase activity	GO	11	417	6.14205E-05	0.003099294	IFI6 PSMB9 LAMP3 IFI27 IFI16 PML BIRC3 TLR3 IL6 LGALS9 CASP1
regulation of localization	GO	35	2681	6.16793E-05	0.003103851	IFITM1 CXCL11 CXCL10 SOCS1 B2M RSAD2 IFI27 CXCL9 DDX58 TRIM22 SP100 PML ZFP36 NFKBIE GBP1 SRGN CCNE1 PRTN3 TLR3 XCL2 CD58 TREM2 CCL4 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 CLEC4E TNFSF4 CCL20 SYT4 ECT2 SVBP
transport of virus	GO	5	66	6.31661E-05	0.003170011	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
vacuolar part	GO	16	828	6.59036E-05	0.003298403	B2M SLC15A3 HLA-G FCGR1A LAMP3 IFI30 PML HLA-C ATP6V1F RAB32 PRTN3 TLR3 HLA-F HLA-E HLA-A DSN1
regulation of cell differentiation	GO	25	1645	6.65358E-05	0.00332102	ISG15 IFITM1 CXCL10 STAT1 B2M HLA-G CXCL9 DYNLT1 PML ZFP36 GBP1 TYROBP CCNE1 TLR3 CD83 EIF2AK2 PRAMEF1 IL6 LGALS9 CHRNA3 TNFSF4 JUNB TESPA1 SYT4 ECT2

molecular transducer activity	GO	30	2192	6.82929E-05	0.003390349	IFITM1 STAT1 HLA-G FCGR1A SP110 KIR2DL3 OR4C15 LILRA2 HLA-C TYROBP LAIR2 TLR3 RGS1 TREM2 CCL4 HLA-F LGALS9 HLA-E CHRNA3 OR2B6 KIR2DL2 CLEC4E HLA-A GNA15 SHISA5 KLRD1 RGS10 OR4C45 ECT2 OR52E8
cellular process	GO	139	15083	6.92692E-05	0.003429572	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3

						XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
regulation of cell killing	GO	5	68	7.21604E-05	0.003544132	B2M TAP1 LGALS9 HLA-E HLA-A
nucleotide metabolic process	GO	19	1110	7.36757E-05	0.003608934	CMPK2 MX1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
activation of innate immune response	GO	9	285	7.38863E-05	0.003609652	PSMB9 DDX58 IFI16 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
endosome	GO	16	837	7.43068E-05	0.003620588	B2M HLA-G FCGR1A LAMP3 PML HLA-C SAMD9L SAMD9 UNC93B1 RAB32 TLR3 VAMP5 HLA-F HLA-E HLA-A CSH1
negative regulation of cell proliferation	GO	14	670	8.05005E-05	0.003912027	IFITM1 STAT1 IFIT3 HLA-G IFI30 WARS PML IDO1 EIF2AK2 RARRES3 IL6 LGALS9 AMBRA1 CCL3L3
multi-organism transport	GO	5	70	8.21087E-05	0.003969232	TAP2 TAP1 IFIT1 DYNLT1 KPNA2

multi-organism localization	GO	5	70	8.21087E-05	0.003969232	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
nucleoside catabolic process	GO	14	672	8.2956E-05	0.003999694	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
coated vesicle membrane	GO	7	167	8.44856E-05	0.004041705	B2M HLA-G FCGR1A HLA-C HLA-F HLA-E HLA-A
defense response to bacterium	GO	8	226	8.48916E-05	0.004050606	ISG15 B2M TLR3 IL6 HLA-E CLEC4E HLA-A CCL20
apoptotic signaling pathway	GO	9	292	8.82186E-05	0.004198477	IFI6 IFI27 IFI16 PML BCL2A1 SRGN TLR3 MELK SHISA5
regulation of cell communication	GO	41	3393	8.93465E-05	0.004241196	CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 RSAD2 PSMB9 CXCL9 TRIM22 DYNLT1 TYMP SP100 PML BCL2A1 RNF213 BIRC3 GBP1 EGR2 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 CHRNA3 CASP1 AMBRA1 UBD CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
positive regulation of interleukin-6 production	GO	5	72	9.30783E-05	0.004406981	DDX58 TLR3 IL6 LGALS9 TNFSF4
Signaling by Interleukins	REACTOME	12	516	9.40241E-05	0.004440347	CXCL10 SOCS1 STAT1 PSMB9 PRTN3 CCL4 IL6 LGALS9 CASP1 JUNB CCL20 CCL3L3
cellular nitrogen compound catabolic process	GO	19	1134	9.5946E-05	0.004519525	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2

						GNA15 SAMHD1 GBP2
glycosyl compound catabolic process	GO	14	682	9.6232E-05	0.004521431	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
RNA binding	GO	24	1583	9.72796E-05	0.004547452	OASL DDX60 OAS3 HERC5 OAS2 IFIT3 DDX58 PARP12 OAS1 ISG20 TDRD7 IFIT1 IFI16 IFIT2 IFIH1 ZFP36 RPL39L KPNA2 TLR3 HELZ2 EIF2AK2 ZNFX1 HLA-A SAMHD1
organelle membrane fusion	GO	6	118	9.76792E-05	0.0045457	TAP2 TAP1 SAMD9L SAMD9 VAMP5 SYT4
regulation of cell proliferation	GO	24	1588	9.93125E-05	0.004607399	IFITM1 CXCL11 CXCL10 STAT1 IFIT3 HLA-G IFI30 CXCL9 WARS PML ZFP36 PRTN3 IDO1 EIF2AK2 RARRES3 PRAMEF1 IL6 LGALS9 HLA-E AMBRA1 TNFSF4 HLA-A JUNB CCL3L3
heterocycle catabolic process	GO	19	1137	9.91089E-05	0.004607399	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
aromatic compound catabolic process	GO	19	1140	0.000102363	0.004716269	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
positive regulation of lymphocyte activation	GO	9	298	0.00010229	0.004716269	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1

positive regulation of apoptotic process	GO	13	604	0.000105395	0.004828749	IFI27 IFIT2 PML BCL2A1 IDO1 TLR3 MELK EIF2AK2 IL6 LGALS9 CASP1 UBD ECT2
regulation of secretion by cell	GO	14	693	0.000112923	0.005122706	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CHRNA3 CASP1 CLEC4E TNFSF4 SYT4
positive regulation of programmed cell death	GO	13	610	0.000115745	0.005237828	IFI27 IFIT2 PML BCL2A1 IDO1 TLR3 MELK EIF2AK2 IL6 LGALS9 CASP1 UBD ECT2
positive regulation of sequence-specific DNA binding transcription factor activity	GO	8	237	0.000116341	0.005251899	DDX58 TRIM22 SP100 TRIM31 TLR3 EIF2AK2 IL6 LGALS9
pattern recognition receptor signaling pathway	GO	6	123	0.000121326	0.005436937	DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9
nucleoside phosphate metabolic process	GO	19	1157	0.000122637	0.00548235	CMPK2 MX1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
endosomal part	GO	11	454	0.000126209	0.005614777	B2M HLA-G FCGR1A PML HLA-C RAB32 TLR3 HLA-F HLA-E HLA-A CSH1
carbohydrate derivative binding	GO	30	2239	0.000132094	0.005820351	OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 IFI44L TAP2 MDK OAS2 B2M DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 TREM2 EIF2AK2 MX2

						GNA15 SAMHD1 GBP2
Chemokine signaling pathway	KEGG	7	180	0.000131954	0.005820351	CXCL11 CXCL10 STAT1 CXCL9 CCL4 CCL20 CCL3L3
cellular response to oxygen-containing compound	GO	19	1169	0.000138991	0.006099507	CMPK2 CXCL10 SOCS1 STAT1 B2M PSMB9 ZFP36 ATP6V1F EGR2 TREM2 IL6 CHRNA3 TNFSF4 GNA15 CCL20 RGS10 ECT2 CSH1 GBP2
regulation of intracellular transport	GO	13	622	0.000139092	0.006099507	CXCL11 CXCL10 IFI27 CXCL9 DDX58 SP100 PML NFKBIE TLR3 IL6 LGALS9 MX2 ECT2
intrinsic component of organelle membrane	GO	9	312	0.000142553	0.006221659	TAP2 HLA-G TAP1 HLA-C VAMP5 HLA-F HLA-E HLA-A SYT4
leukocyte migration	GO	9	312	0.000142553	0.006221659	CXCL11 CXCL10 CXCL9 XCL2 CD58 CCL4 IL6 CCL20 CCL3L3
nucleobase-containing compound catabolic process	GO	18	1083	0.000154852	0.006726559	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
regulation of signal transduction	GO	35	2825	0.000155601	0.006728573	CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 RSAD2 PSMB9 CXCL9 TRIM22 DYNLT1 SP100 PML RNF213 BIRC3 GBP1 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 ECT2
organic cyclic compound	GO	19	1180	0.000155629	0.006728573	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213

catabolic process						NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	REACTOME	5	81	0.000156998	0.006771854	ISG15 HERC5 UBE2L6 DDX58 IFIH1
regulation of signaling	GO	39	3254	0.000164512	0.007079382	CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 RSAD2 PSMB9 CXCL9 TRIM22 DYNLT1 TYMP SP100 PML RNF213 BIRC3 GBP1 EGR2 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 CHRNA3 CASP1 UBD CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
protein modification by small protein conjugation or removal	GO	17	996	0.00016916	0.007262465	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 DDX58 RNF19B TRIM22 SP100 PML IFIH1 RNF213 BIRC3 TRIM31 EGR2 UBD
regulation of transport	GO	27	1984	0.000169951	0.007279427	CXCL11 CXCL10 SOCS1 B2M RSAD2 IFI27 CXCL9 DDX58 SP100 PML NFKBIE GBP1 SRGN PRTN3 TLR3 CD58 CCL4 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 CLEC4E TNFSF4 SYT4 ECT2
negative regulation of response to stimulus	GO	23	1561	0.000171054	0.007309664	SOCS1 STAT1 IFI6 HLA-G PSMB9 TAP1 NMI IFIT1 IFI16 BCL2A1 ZFP36 RNF213 GBP1 TLR3 RGS1 EIF2AK2 PRAMEF1 IL6 LGALS9 HLA-E

						TNFSF4 HLA-A RGS10
positive regulation of ERK1 and ERK2 cascade	GO	7	189	0.000175982	0.007468307	XCL2 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
carbohydrate derivative catabolic process	GO	15	815	0.00017768	0.007523019	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
purine nucleoside triphosphate catabolic process	GO	13	640	0.000181643	0.007638148	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
HTLV-I infection	KEGG	8	255	0.000188143	0.007875479	HLA-G ZFP36 HLA-C EGR2 HLA-F IL6 HLA-E HLA-A
positive regulation of chemotaxis	GO	6	134	0.000189319	0.007906754	CXCL11 CXCL10 CXCL9 CCL4 IL6 LGALS9
nucleoside triphosphate catabolic process	GO	13	645	0.000195274	0.008118625	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
positive regulation of cell death	GO	13	649	0.000206798	0.008559128	IFI27 IFIT2 PML BCL2A1 IDO1 TLR3 MELK EIF2AK2 IL6 LGALS9 CASP1 UBD ECT2
positive regulation of leukocyte activation	GO	9	329	0.000208387	0.008586306	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
regulation of ERK1 and ERK2 cascade	GO	8	259	0.000208224	0.008586306	GBP1 XCL2 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
ligase activity	GO	10	406	0.000218038	0.008943909	HERC6 HERC5 TRIM69 WARS RNF19B TRIM22 RNF213 BIRC3 TRIM31 EGR2
positive regulation of signaling	GO	24	1725	0.000231133	0.009439051	CXCL11 DDX60 CXCL10 RSAD2 PSMB9 CXCL9 TRIM22 PML BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6

						LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
intracellular membrane-bounded organelle	GO	99	10581	0.000258371	0.010412853	ISG15 OASL CMPK2 HERC6 MX1 IFI35 OAS3 SOCS1 STAT1 IFI44L IFI6 PLSCR1 TAP2 HERC5 OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 SP110 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI TRIM22 DYNLT1 IFI16 IFIT2 ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG UQCRHL NT5C3A MRPS18C GBP1 SAMD9 GBP4 ATP6V1F TRIM31 UNC93B1 RAB32 SRGN EGR2 CCNE1 PRTN3 TLR3 XAF1 MELK HELZ2 TREM2 EIF2AK2 VAMP5 HLA-F ZNFX1 LGALS9 HLA-E MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A JUNB DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1 BOLA3 ZNF831 ECT2 CSH1 GBP2
regulation of cell-cell adhesion	GO	10	415	0.000257906	0.010412853	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1

nucleobase-containing small molecule metabolic process	GO	19	1232	0.000260094	0.010459394	CMPK2 MX1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
Cell adhesion molecules (CAMs)	KEGG	6	143	0.000264707	0.01059864	HLA-G HLA-C CD58 HLA-F HLA-E HLA-A
molecular_function	GO	146	16545	0.000267154	0.010673403	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ZC2HC1B ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3

						TRANK1 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 TRIM48 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 BOLA3 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
nucleoside triphosphate metabolic process	GO	15	851	0.000275852	0.010973293	CMPK2 MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
purine-containing compound metabolic process	GO	17	1043	0.000281597	0.011177682	MX1 TAP2 OAS2 OAS1 TAP1 TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
positive regulation of cell activation	GO	9	344	0.00028574	0.011293486	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
regulation of chemotaxis	GO	7	206	0.000291167	0.011466224	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9
negative regulation of cysteine-type endopeptidase activity	GO	5	94	0.000302598	0.011883247	IFI6 LAMP3 IFI16 BIRC3 IL6

regulation of homeostatic process	GO	11	505	0.000303951	0.011910989	ISG15 CXCL11 CXCL10 STAT1 IFI6 B2M CXCL9 PML ZFP36 IL6 LGALS9
regulation of lymphocyte proliferation	GO	7	208	0.000307962	0.011991621	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
negative regulation of transport	GO	11	507	0.000313868	0.012195815	RSAD2 SP100 PML NFKBIE GBP1 SRGN PRTN3 IL6 LGALS9 TNFSF4 SYT4
humoral immune response	GO	7	209	0.000316645	0.012277831	B2M PRTN3 CD83 TREM2 IL6 HLA-E HLA-A
cytoplasmic vesicle	GO	28	2170	0.000321716	0.012448263	SOCS1 TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 DYNLT1 PML HLA-C SAMD9L SAMD9 UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E AMBRA1 HLA-A DSN1 SYT4 CSH1
regulation of secretion	GO	14	772	0.00032424	0.012493409	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CHRNA3 CASP1 CLEC4E TNFSF4 SYT4
regulation of leukocyte activation	GO	11	509	0.000324055	0.012493409	SOCS1 PLSCR1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
intracellular vesicle	GO	28	2173	0.000325561	0.012518114	SOCS1 TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 DYNLT1 PML HLA-C SAMD9L SAMD9 UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E AMBRA1 HLA-A DSN1 SYT4 CSH1

innate immune response-activating signal transduction	GO	8	279	0.000336715	0.01278684	PSMB9 DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
recycling endosome	GO	6	150	0.000338167	0.012815574	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of multicellular organismal development	GO	25	1857	0.000339906	0.012855008	ISG15 CXCL10 STAT1 B2M HLA-G PSMB9 WARS DYNLT1 TYMP SP100 PML ZFP36 TYROBP SRGN IDO1 TLR3 CD83 EIF2AK2 IL6 LGALS9 CHRNA3 TNFSF4 TESPA1 SYT4 ECT2
regulation of developmental process	GO	31	2538	0.000357668	0.013496633	ISG15 IFITM1 CXCL10 STAT1 B2M HLA-G PSMB9 CXCL9 WARS DYNLT1 TYMP SP100 PML ZFP36 GBP1 TYROBP SRGN CCNE1 IDO1 TLR3 CD83 EIF2AK2 PRAMEF1 IL6 LGALS9 CHRNA3 TNFSF4 JUNB TESPA1 SYT4 ECT2
purine-containing compound catabolic process	GO	13	690	0.000362503	0.013596917	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
positive regulation of T cell proliferation	GO	5	98	0.000363214	0.013596917	IL6 LGALS9 HLA-E TNFSF4 HLA-A
regulation of lymphocyte activation	GO	10	435	0.000368628	0.013771601	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
positive regulation of cell communication	GO	25	1876	0.000372521	0.013886097	CXCL11 DDX60 CXCL10 RSAD2 PSMB9 CXCL9 TRIM22 PML BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1

						AMBRA1 UBD CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
chemotaxis	GO	11	518	0.000373395	0.013886097	CXCL11 CXCL10 CXCL9 TYMP EGR2 XCL2 CCL4 IL6 LGALS9 CCL20 CCL3L3
regulation of interferon-gamma production	GO	5	99	0.000379704	0.014042946	ISG15 TLR3 LGALS9 TNFSF4 HLA-A
Golgi membrane	GO	13	695	0.000386969	0.014282938	B2M HLA-G HLA-C GBP1 GBP4 UNC93B1 SRGN TLR3 HLA-F HLA-E HLA-A SYT4 GBP2
regulation of cellular protein localization	GO	12	607	0.000391541	0.014422798	IFI27 DDX58 SP100 PML NFKBIE GBP1 CCNE1 TLR3 TREM2 IL6 LGALS9 ECT2
positive regulation of cytoplasmic transport	GO	8	286	0.000394571	0.014505389	CXCL11 CXCL10 CXCL9 DDX58 TLR3 IL6 LGALS9 ECT2
myeloid leukocyte differentiation	GO	5	100	0.000396752	0.014527576	IFI16 PRTN3 LGALS9 UBD JUNB
regulation of cytokine biosynthetic process	GO	5	100	0.000396752	0.014527576	NMI ZFP36 TLR3 IL6 CCL20
helicase activity	GO	6	155	0.000399731	0.014591687	DDX60 DDX58 TTF2 IFIH1 TRANK1 HELZ2
response to organic cyclic compound	GO	16	980	0.000402913	0.014665716	CXCL10 SOCS1 STAT1 MDK PSMB9 DDX58 IFIT1 ZFP36 CCNE1 TLR3 CD83 EIF2AK2 IL6 CHRNA3 CASP1 JUNB
regulation of mononuclear cell proliferation	GO	7	218	0.000403951	0.014674508	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
purine nucleotide binding	GO	25	1898	0.000417856	0.015115055	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58

						OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 SAMHD1 GBP2
regulation of intracellular signal transduction	GO	24	1756	0.00041854	0.015115055	CXCL11 DDX60 CXCL10 SOCS1 STAT1 CXCL9 TRIM22 PML BIRC3 GBP1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST ECT2
phosphate-containing compound metabolic process	GO	32	2657	0.000440475	0.015876056	CMPK2 MX1 PLSCR1 TAP2 PPA1 OAS2 PSMB9 OAS1 TAP1 TYMP PML TTF2 ZFP36 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F PGP RAB32 CCNE1 TLR3 MELK EIF2AK2 RARRES3 LGALS9 MX2 GNA15 HCST SAMHD1 GBP2
positive regulation of protein import into nucleus	GO	5	103	0.000451366	0.016236821	DDX58 TLR3 IL6 LGALS9 ECT2
purine ribonucleoside triphosphate binding	GO	24	1783	0.000461788	0.016547111	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
organelle membrane	GO	34	2895	0.000472939	0.016913785	MX1 TAP2 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 TAP1 PML BCL2A1 HLA-C UQCRHL MRPS18C GBP1 GBP4 ATP6V1F UNC93B1

						RAB32 TYROBP SRGN TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E MX2 AMBRA1 HLA-A SHISA5 SYT4 GBP2
organophosphate metabolic process	GO	22	1606	0.00048371	0.017265444	CMPK2 MX1 PLSCR1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F PGP RAB32 RARRES3 MX2 GNA15 SAMHD1 GBP2
positive regulation of cell differentiation	GO	15	902	0.000492392	0.017373333	ISG15 IFITM1 STAT1 HLA-G CXCL9 ZFP36 CCNE1 CD83 IL6 LGALS9 TNFSF4 JUNB TESPA1 SYT4 ECT2
regulation of leukocyte proliferation	GO	7	227	0.000509457	0.017739808	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
myeloid leukocyte migration	GO	5	106	0.000511447	0.017739808	XCL2 CCL4 IL6 CCL20 CCL3L3
positive regulation of protein import	GO	5	106	0.000511447	0.017739808	DDX58 TLR3 IL6 LGALS9 ECT2
positive regulation of transport	GO	16	1006	0.000527294	0.018255079	CXCL11 CXCL10 B2M CXCL9 DDX58 TLR3 CD58 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
positive regulation of protein secretion	GO	7	229	0.000535632	0.01850895	CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4
regulation of cellular protein metabolic process	GO	32	2716	0.000541517	0.018677275	ISG15 CXCL10 SOCS1 IFI6 HERC5 PSMB9 LAMP3 IFI27 WARS RNF19B NMI IFI16 PML ZFP36 BIRC3 LCMT1 GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9

						CHRNA3 CASP1 PSMG2 CCL20 CCL3L3 ECT2 SVBP
TNF signaling pathway	KEGG	5	108	0.000554708	0.019025349	CXCL10 BIRC3 IL6 JUNB CCL20
purine ribonucleotide binding	GO	24	1827	0.000565389	0.019355653	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
Antigen processing: Ubiquitination & Proteasome degradation	REACTOME	8	303	0.000569113	0.019438979	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 RNF19B RNF213
regulation of sequence-specific DNA binding transcription factor activity	GO	9	380	0.000571274	0.019448651	DDX58 TRIM22 SP100 TRIM31 TLR3 EIF2AK2 IL6 LGALS9 TNFSF4
regulation of interleukin-6 production	GO	5	109	0.000577339	0.019618864	DDX58 TLR3 IL6 LGALS9 TNFSF4
purine ribonucleoside binding	GO	24	1833	0.000583003	0.019774865	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
regulation of cell activation	GO	11	548	0.000585515	0.019823559	SOCS1 PLSCR1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
intracellular part	GO	123	13993	0.000590206	0.019829329	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2

						HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 HELZ2 CD58 TREM2 EIF2AK2 RARRES3 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A GNA15 JUNB SPRR2A DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1 BOLA3 ZNF831 ECT2 RASSF3 CSH1 GBP2
purine nucleoside binding	GO	24	1836	0.000592145	0.019829329	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2

ribonucleoside binding	GO	24	1836	0.000592145	0.019829329	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
ribonucleoside triphosphate catabolic process	GO	12	637	0.000589305	0.019829329	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
purine ribonucleoside triphosphate catabolic process	GO	12	637	0.000589305	0.019829329	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
plasma membrane protein complex	GO	7	233	0.000591179	0.019829329	B2M HLA-G HLA-C HLA-F HLA-E HLA-A GNA15
nucleoside binding	GO	24	1843	0.000614364	0.020461774	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
regulation of proteolysis	GO	14	826	0.000613454	0.020461774	IFI6 PSMB9 LAMP3 IFI27 RNF19B IFI16 PML BIRC3 LCMT1 TLR3 IL6 LGALS9 CASP1 PSMG2
ribonucleotide binding	GO	24	1844	0.000617641	0.020533786	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
intracellular	GO	125	14282	0.000642712	0.021290411	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2

						HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 HELZ2 CD58 TRIM48 TREM2 EIF2AK2 RARRES3 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A GNA15 JUNB SPRR2A CCL20 DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1 BOLA3 ZNF831 ECT2 RASSF3 CSH1 GBP2
purine nucleoside triphosphate	GO	14	830	0.000641589	0.021290411	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F

metabolic process						RAB32 MX2 GNA15 SAMHD1 GBP2 ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L IFI6 PLSCR1 TAP2 HERC5 OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI TRIM22 DYNLT1 IFI16 IFIT2 ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C GBP1 SAMD9 GBP4 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK SYNGR2 HELZ2 CD58 TREM2 EIF2AK2 VAMP5 HLA-F ZNFX1 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A JUNB DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1 BOLA3 ZNF831 ECT2
intracellular organelle	GO	109	12230	0.000650546	0.021472676	RASSF3 CSH1 GBP2

membrane	GO	83	8951	0.000685283	0.022369431	IFITM1 OASL MX1 CXCL10 OAS3 RTP4 IFI6 PLSCR1 TAP2 OAS2 TRIM69 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 RNF19B TAP1 IFI27L1 KIR2DL3 OR4C15 IFI16 PML BCL2A1 LILRA2 MSRA RNF213 BIRC3 HLA-C KPNA2 NCAPG UQCRHL MRPS18C GBP1 GBP4 ATP6V1F UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 ORAI2 MELK RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 SMIM13 EIF2AK2 RARRES3 VAMP5 HLA-F IL6 HLA-E CHRNA3 MX2 AMBRA1 OR2B6 KIR2DL2 CLEC4E TNFSF4 HLA-A GNA15 SPRR2A SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 OR52E8 RASSF3 GBP2
nucleotide catabolic process	GO	13	741	0.00068535	0.022369431	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
guanyl nucleotide binding	GO	9	390	0.00068252	0.022369431	MX1 IFI44L GBP1 GBP4 RAB32 MX2 GNA15 SAMHD1 GBP2
regulation of protein modification by small protein	GO	8	312	0.000684016	0.022369431	ISG15 PSMB9 NMI PML BIRC3 LCMT1 PSMG2 SVBP

conjugation or removal						
Golgi apparatus part	GO	15	934	0.000691557	0.0225037	B2M HLA-G HLA-C GBP1 GBP4 UNC93B1 RAB32 SRGN TLR3 VAMP5 HLA-F HLA-E HLA-A SYT4 GBP2
immune response-regulating signaling pathway	GO	10	475	0.000709563	0.023048893	HLA-G PSMB9 FCGR1A DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
nucleoside phosphate catabolic process	GO	13	746	0.000727081	0.023521831	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
regulation of tumor necrosis factor superfamily cytokine production	GO	5	115	0.000727953	0.023521831	ZFP36 TLR3 CCL4 LGALS9 HLA-E
regulation of locomotion	GO	14	843	0.000740665	0.023890678	IFITM1 CXCL11 CXCL10 CXCL9 DDX58 SP100 PML TRIM31 XCL2 CCL4 IL6 LGALS9 CCL20 SVBP
zinc ion binding	GO	17	1143	0.000748501	0.024101225	OAS2 TRIM69 SP110 DDX58 OAS1 RNF19B TRIM22 PML TTF2 IFIH1 RNF213 BIRC3 TRIM31 XAF1 TRIM48 ZNFX1 SAMHD1
Transcriptional misregulation in cancer	KEGG	6	176	0.000759148	0.024358863	FCGR1A ETV7 PML BCL2A1 BIRC3 IL6
cellular_component	GO	149	17527	0.000768571	0.024532999	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M

SLC15A3 RSAD2
HLA-G PSMB9 IFI44
FCGR1A LAMP3
IFI27 IFI30 CXCL9
SP110 DDX58
PARP12 OAS1
ISG20 WARS
RNF19B IRF9
TDRD7 TAP1
IFI27L1 CENPW NMI
IFIT1 TRIM22
DYNLT1 KIR2DL3
OR4C15 IFI16 IFIT2
TYMP ETV7 SP100
PML BCL2A1 LILRA2
TTF2 IFIH1 ZFP36
RPL39L MSRA
RNF213 BIRC3
NFKBIE HLA-C
KPNA2 NCAPG
SAMD9L UQCRHL
NT5C3A MRPS18C
LCMT1 GBP1
SAMD9 GBP4
ATP6V1F TRIM31
PGP UNC93B1
RAB32 TYROBP
SRGN APOL6 EGR2
CCNE1 LAIR2
PRTN3 IDO1 TLR3
XAF1 ORAI2 MELK
XCL2 RGS1
SYNGR2 HELZ2
CD58 CD83 TRIM48
TREM2 SMIM13
EIF2AK2 RARRES3
CCL4 VAMP5 HLA-F
ZNFX1 IL6 LGALS9
HLA-E CHRNA3 MX2
CASP1 PSMG2
AMBRA1 OR2B6
KIR2DL2 UBD
CLEC4E TNFSF4
HLA-A GNA15 JUNB
SPRR2A CCL20
CCL3L3 DSN1
SHISA5 KLRD1
RGS10 HCST
TESPA1 SYT4
SAMHD1 OR4C45
BOLA3 ZNF831

						ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
positive regulation of homeostatic process	GO	7	245	0.000785636	0.024991091	ISG15 CXCL11 CXCL10 STAT1 CXCL9 PML LGALS9
ribonucleoside catabolic process	GO	12	661	0.000802246	0.025431616	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
perinuclear region of cytoplasm	GO	12	661	0.000802246	0.025431616	MX1 STAT1 HERC5 OAS2 LAMP3 NFKBIE GBP4 EIF2AK2 VAMP5 AMBRA1 SYT4 GBP2
cell activation	GO	16	1049	0.000804697	0.025465481	CXCL10 PLSCR1 B2M RSAD2 DYNLT1 TYROBP PRTN3 TLR3 CD58 IL6 HLA-E UBD CLEC4E TNFSF4 GNA15 DSN1
positive regulation of protein transport	GO	10	484	0.000814128	0.025675693	DDX58 TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 ECT2
negative regulation of cell differentiation	GO	12	663	0.000822557	0.025897181	CXCL10 STAT1 B2M HLA-G DYNLT1 ZFP36 GBP1 TLR3 PRAMEF1 IL6 TNFSF4 SYT4
phosphorus metabolic process	GO	32	2739	0.00083905	0.026371364	CMPK2 MX1 PLSCR1 TAP2 PPA1 OAS2 PSMB9 OAS1 TAP1 TYMP PML TTF2 ZFP36 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F PGP RAB32 CCNE1 TLR3 MELK EIF2AK2 RARRES3 LGALS9 MX2 GNA15 HCST SAMHD1 GBP2
extracellular region	GO	47	4559	0.000867403	0.027031861	ISG15 CXCL11 CXCL10 OAS3 PLSCR1 TAP2 PPA1 MDK B2M PSMB9

						IFI30 CXCL9 OAS1 WARS TAP1 IFIT1 DYNLT1 LILRA2 MSRA HLA-C GBP1 ATP6V1F SRGN APOL6 LAIR2 PRTN3 XCL2 SYNGR2 CD58 TREM2 CCL4 VAMP5 IL6 LGALS9 HLA-E CASP1 TNFSF4 HLA-A CCL20 CCL3L3 DSN1 SHISA5 SYT4 BOLA3 CSH1 GBP2 SVBP
organic substance catabolic process	GO	28	2333	0.000879328	0.027311056	ISG15 HERC6 MX1 TAP2 HERC5 OAS2 UBE2L6 PSMB9 ISG20 RNF19B TAP1 TYMP PML TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 RARRES3 MX2 UBD GNA15 SAMHD1 GBP2
regulation of protein modification process	GO	25	1973	0.000879246	0.027311056	ISG15 CXCL10 SOCS1 HERC5 PSMB9 WARS NMI PML BIRC3 LCMT1 GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 PSMG2 CCL20 CCL3L3 ECT2 SVBP
positive regulation of cell adhesion	GO	9	405	0.000881876	0.027344085	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
organonitrogen compound catabolic process	GO	16	1061	0.000901215	0.027473553	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
taxis	GO	14	860	0.000889378	0.027473553	CXCL11 CXCL10 PSMB9 CXCL9

						TYMP TYROBP EGR2 XCL2 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
ribonucleotide catabolic process	GO	12	670	0.00089704	0.027473553	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
vesicle organization	GO	8	326	0.000899122	0.027473553	TAP2 TAP1 SAMD9L SAMD9 RAB32 SRGN VAMP5 SYT4
positive regulation of peptide secretion	GO	7	251	0.00090011	0.027473553	CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4
regulation of protein import into nucleus	GO	6	182	0.000897399	0.027473553	DDX58 NFKBIE TLR3 IL6 LGALS9 ECT2
nucleoside metabolic process	GO	15	967	0.000964433	0.028835908	MX1 TAP2 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
regulation of cell adhesion	GO	12	677	0.000977034	0.029165339	SOCS1 HLA-G PML GBP1 IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
endosome membrane	GO	9	414	0.001022522	0.03022922	B2M HLA-G FCGR1A PML HLA-C TLR3 HLA-F HLA-E HLA-A
positive regulation of nucleocytoplasmic transport	GO	5	125	0.001041579	0.030703294	DDX58 TLR3 IL6 LGALS9 ECT2
protein ubiquitination	GO	12	684	0.001062848	0.031270812	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 RNF19B TRIM22 RNF213 BIRC3 TRIM31 UBD
regulation of protein import	GO	6	189	0.001082267	0.031791374	DDX58 NFKBIE TLR3 IL6 LGALS9 ECT2
activation of immune response	GO	10	504	0.001092068	0.032028186	PSMB9 FCGR1A DDX58 IFI16 IFIH1 BIRC3 UNC93B1

						TLR3 LGALS9 CLEC4E
cellular response to nitrogen compound	GO	13	785	0.001131582	0.03297702	SOCS1 STAT1 PSMB9 IFIT1 ATP6V1F TLR3 TREM2 IL6 CHRNA3 TNFSF4 GNA15 RGS10 CSH1
peptide binding	GO	7	263	0.00116816	0.033828872	HLA-G TAP1 HLA-C KPNA2 HLA-F HLA-E HLA-A
mitochondrion	GO	22	1712	0.001194963	0.034550737	CMPK2 MX1 IFI6 OAS2 IFIT3 RSAD2 IFI27 OAS1 TDRD7 TAP1 BCL2A1 MSRA UQCRHL NT5C3A MRPS18C TRIM31 RAB32 XAF1 MX2 CASP1 AMBRA1 BOLA3
whole membrane	GO	27	2266	0.001200466	0.034655447	PLSCR1 TAP2 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 DDX58 TAP1 PML BCL2A1 BIRC3 HLA-C ATP6V1F RAB32 TYROBP TLR3 SYNGR2 CD58 HLA-F HLA-E CHRNA3 AMBRA1 HLA-A SYT4
coated vesicle	GO	7	265	0.001218321	0.035060988	B2M HLA-G FCGR1A HLA-C HLA-F HLA-E HLA-A
guanosine-containing compound catabolic process	GO	7	265	0.001218321	0.035060988	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
glycosyl compound metabolic process	GO	15	992	0.001226961	0.035254557	MX1 TAP2 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
organophosphate catabolic process	GO	13	793	0.001234214	0.035407704	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2

cellular catabolic process	GO	29	2505	0.001290165	0.036940719	ISG15 HERC6 MX1 TAP2 HERC5 OAS2 UBE2L6 PSMB9 ISG20 RNF19B TAP1 IFI16 TYMP PML TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 AMBRA1 UBD GNA15 SAMHD1 GBP2
regulation of myeloid cell differentiation	GO	6	196	0.001294945	0.036940719	ISG15 STAT1 B2M ZFP36 TYROBP TLR3
myeloid cell differentiation	GO	6	197	0.001327751	0.037680291	IFI16 PML PRTN3 LGALS9 UBD JUNB
positive regulation of macromolecule metabolic process	GO	35	3220	0.001348446	0.038208733	CXCL10 STAT1 PLSCR1 MDK PSMB9 LAMP3 IFI27 DDX58 WARS RNF19B NMI TRIM22 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EGR2 CCNE1 TLR3 XCL2 HELZ2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 TNFSF4 JUNB CCL20 CCL3L3 ECT2
positive regulation of lymphocyte proliferation	GO	5	133	0.001356817	0.038328012	IL6 LGALS9 HLA-E TNFSF4 HLA-A
positive regulation of cysteine-type endopeptidase activity	GO	5	133	0.001356817	0.038328012	IFI27 IFI16 PML LGALS9 CASP1
positive regulation of molecular function	GO	26	2133	0.001389462	0.039130132	STAT1 PLSCR1 B2M PSMB9 IFI27 DDX58 TRIM22 IFI16 SP100 PML TRIM31 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 AMBRA1 GNA15 CCL20

						CCL3L3 RGS10 ECT2
positive regulation of mononuclear cell proliferation	GO	5	135	0.001445514	0.040194512	IL6 LGALS9 HLA-E TNFSF4 HLA-A
purine nucleoside catabolic process	GO	7	274	0.00146521	0.040398553	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
purine ribonucleoside catabolic process	GO	7	274	0.00146521	0.040398553	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
regulation of phosphorylation	GO	19	1427	0.001480216	0.040751301	CXCL10 SOCS1 HERC5 WARS PML GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 AMBRA1 CCL20 CCL3L3 ECT2
positive regulation of NF-kappaB transcription factor activity	GO	5	136	0.001491424	0.040998587	TRIM22 TLR3 EIF2AK2 IL6 LGALS9
intracellular signal transduction	GO	21	1623	0.00151093	0.041472885	SOCS1 STAT1 PSMB9 DDX58 NMI IFI16 SP100 PML BCL2A1 IFIH1 ZFP36 BIRC3 RAB32 TYROBP TLR3 MELK LGALS9 CCL20 SHISA5 ECT2 CSH1
GTPase activity	GO	7	276	0.001525006	0.041734851	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
positive regulation of protein localization to nucleus	GO	5	137	0.001538396	0.04203885	DDX58 TLR3 IL6 LGALS9 ECT2
purine ribonucleoside metabolic process	GO	14	917	0.001582614	0.043183083	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2

purine nucleoside metabolic process	GO	14	920	0.001628915	0.044376297	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
regulation of cell migration	GO	12	723	0.001662801	0.045103772	IFITM1 CXCL11 CXCL10 CXCL9 DDX58 SP100 XCL2 CCL4 IL6 LGALS9 CCL20 SVBP
purine ribonucleoside triphosphate metabolic process	GO	13	824	0.001707575	0.046250167	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
regulation of protein metabolic process	GO	32	2899	0.001753234	0.047347595	ISG15 CXCL10 SOCS1 IFI6 HERC5 PSMB9 LAMP3 IFI27 WARS RNF19B NMI IFI16 PML ZFP36 BIRC3 LCMT1 GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 CCL20 CCL3L3 ECT2 SVBP
regulation of protein phosphorylation	GO	18	1334	0.001752488	0.047347595	CXCL10 SOCS1 HERC5 WARS PML GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CCL20 CCL3L3 ECT2
positive regulation of intracellular transport	GO	8	364	0.001763452	0.047440687	CXCL11 CXCL10 CXCL9 DDX58 TLR3 IL6 LGALS9 ECT2
immune response-activating signal transduction	GO	9	450	0.001776751	0.047564234	PSMB9 FCGR1A DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
endomembrane system	GO	43	4267	0.001806778	0.048297889	MX1 PLSCR1 TAP2 OAS2 TRIM69 B2M RSAD2 HLA-G FCGR1A LAMP3 IFI27 OAS1 TAP1

						DYNLT1 IFIT2 PML NFKBIE HLA-C KPNA2 SAMD9L NT5C3A GBP1 SAMD9 GBP4 UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E MX2 HLA-A DSN1 SHISA5 TESPA1 SYT4 CSH1 GBP2
ribonucleoside triphosphate metabolic process	GO	13	830	0.001814528	0.048434752	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
positive regulation of establishment of protein localization	GO	10	542	0.001831578	0.048819095	DDX58 TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 ECT2
regulation of cytokine-mediated signaling pathway	GO	5	143	0.00184334	0.049061616	SOCS1 STAT1 BIRC3 TREM2 IL6
locomotion	GO	20	1516	0.001865367	0.049576231	CXCL11 CXCL10 STAT1 MDK PSMB9 LAMP3 CXCL9 DYNLT1 TYMP PML TYROBP EGR2 XCL2 CD58 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
GTP binding	GO	8	368	0.001883164	0.049833504	MX1 IFI44L GBP1 GBP4 RAB32 MX2 GNA15 GBP2

Supplementary Table 4: List of significantly upregulated pathways

Pathway	Database	Genes in list	Genes in pathway	P value	Adj pval	Genes
immune system process	GO	80	2418	<1E-18	<1E-18	ISG15 IFITM1 OASL HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI44L IFI6 PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 BIRC3 HLA-C HMHB1 GBP1 TRIM31 UNC93B1 RAB32 TYROBP PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 DSN1 KLRD1 SAMHD1 GBP2
Immune System	REACTOME	80	2050	<1E-18	<1E-18	ISG15 IFITM1 OASL HERC6 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 TAP2 HERC5 OAS2 UBE2L6 TRIM69 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 RNF19B IRF9 TAP1 IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 RNF213 BIRC3

						NFKBIE HLA-C KPNA2 GBP1 GBP4 ATP6V1F TRIM31 UNC93B1 TYROBP LAIR2 PRTN3 TLR3 XAF1 ORAI2 CD58 TRIM48 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 KIR2DL2 CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 DSN1 KLRD1 HCST SAMHD1 CSH1 GBP2
immune response	GO	71	1492	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI6 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 HLA-G FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 HLA-C HMHB1 GBP1 TRIM31 UNC93B1 TYROBP PRTN3 TLR3 XAF1 XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 DSN1 KLRD1 SAMHD1 GBP2
defense response	GO	67	1247	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI44L IFI6 PLSCR1 HERC5 MDK OAS2 IFIT3 B2M RSAD2 HLA-G FCGR1A IFI27 IFI30

						CXCL9 DDX58 HCP5 OAS1 ISG20 IRF9 TAP1 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML LILRA2 IFIH1 HLA-C GBP1 TRIM31 UNC93B1 TYROBP IDO1 TLR3 XAF1 XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 KLRD1 SAMHD1 GBP2
response to cytokine	GO	57	762	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 TRIM31 CCNE1 TLR3 XAF1 XCL2 CD58 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 UBD TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1 GBP2
Cytokine Signaling in Immune system	REACTOME	55	741	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 HERC5 OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFIT2 SP100 PML BIRC3 HLA-C KPNA2 GBP1 GBP4 TRIM31 PRTN3 XAF1 TRIM48

						EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1 CSH1 GBP2 ISG15 IFITM1 OASL MX1 DDX60 IFI35 OAS3 STAT1 IFI6 HERC5 OAS2 IFIT3 B2M RSAD2 HLA-G FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML IFIH1 HLA-C GBP1 TRIM31 UNC93B1 TYROBP TLR3 XAF1 XCL2 CD58 TREM2
innate immune response	GO	54	611	<1E-18	<1E-18	EIF2AK2 CCL4 HLA-F LGALS9 HLA-E MX2 UBD CLEC4E HLA-A CCL20 CCL3L3 KLRD1 SAMHD1 GBP2 ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 ZFP36 GBP1 UNC93B1 PRTN3 IDO1 TLR3 TREM2
response to biotic stimulus	GO	51	921	<1E-18	<1E-18	EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1
response to external biotic stimulus	GO	51	889	<1E-18	<1E-18	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3

						B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 ZFP36 GBP1 UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1
response to other organism	GO	51	886	<1E-18	<1E-18	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 ZFP36 GBP1 UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1
cellular response to cytokine stimulus	GO	51	657	<1E-18	<1E-18	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 TRIM31 TLR3 XAF1 XCL2 CD58 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 TNFSF4 HLA-A CCL20 CCL3L3 SAMHD1 GBP2

multi-organism cellular process	GO	47	967	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1
interspecies interaction between organisms	GO	47	963	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1
symbiosis, encompassing mutualism through parasitism	GO	47	960	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6

						LGALS9 MX2
cytokine-mediated signaling pathway	GO	47	473	<1E-18	<1E-18	TNFSF4 HLA-A SAMHD1 ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML BIRC3 HLA-C GBP1 TRIM31 XAF1 XCL2 CCL4 HLA-F IL6 HLA-E MX2 TNFSF4 HLA-A CCL20 CCL3L3 SAMHD1 GBP2
viral process	GO	46	811	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 RSAD2 PSMB9 IFI44 LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TAP1 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 HLA-C KPNA2 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 HLA-A SAMHD1
immune effector process	GO	43	927	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 FCGR1A CXCL9 DDX58 OAS1 ISG20 RNF19B IRF9 IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TYROBP PRTN3 TLR3 CD58

						EIF2AK2 IL6 MX2 CLEC4E TNFSF4 DSN1 KLRD1 SAMHD1
Interferon Signaling	REACTOME	42	197	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 SOCS1 STAT1 IFI6 HERC5 OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G FCGR1A IFI27 IFI30 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFIT2 SP100 PML HLA-C KPNA2 GBP1 GBP4 TRIM31 XAF1 TRIM48 EIF2AK2 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
defense response to other organism	GO	38	497	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TLR3 EIF2AK2 IL6 HLA-E MX2 CLEC4E TNFSF4 HLA-A CCL20 SAMHD1
response to virus	GO	37	250	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TLR3 EIF2AK2 CCL4 IL6 LGALS9 MX2 TNFSF4 SAMHD1
defense response to virus	GO	32	164	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 DDX60 CXCL10 OAS3 STAT1 IFI44L PLSCR1 HERC5

						OAS2 IFIT3 RSAD2 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 PML IFIH1 GBP1 UNC93B1 TLR3 EIF2AK2 IL6 MX2 SAMHD1
response to interferon-gamma	GO	30	145	<1E-18	<1E-18	IFITM1 OASL OAS3 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 NMI TRIM22 SP100 PML HLA-C GBP1 TRIM31 TLR3 XCL2 CD58 CCL4 HLA-F LGALS9 HLA-E UBD HLA-A CCL20 CCL3L3 GBP2
cellular response to interferon-gamma	GO	28	123	<1E-18	<1E-18	OASL OAS3 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 NMI TRIM22 SP100 PML HLA-C GBP1 TRIM31 TLR3 XCL2 CD58 CCL4 HLA-F LGALS9 HLA-E HLA-A CCL20 CCL3L3 GBP2
response to type I interferon	GO	27	69	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 SP100 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
Interferon alpha/beta signaling	REACTOME	27	68	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
type I interferon	GO	27	65	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 STAT1 IFI6 OAS2

signaling pathway						IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 SP100 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
cellular response to type I interferon	GO	27	65	<1E-18	<1E-18	ISG15 IFITM1 OASL MX1 IFI35 OAS3 STAT1 IFI6 OAS2 IFIT3 RSAD2 HLA-G IFI27 OAS1 ISG20 IRF9 IFIT1 IFIT2 SP100 HLA-C XAF1 HLA-F HLA-E MX2 HLA-A SAMHD1 GBP2
Interferon gamma signaling	REACTOME	23	92	<1E-18	<1E-18	OASL OAS3 SOCS1 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 TRIM22 SP100 PML HLA-C GBP1 GBP4 TRIM31 TRIM48 HLA-F HLA-E HLA-A GBP2
interferon-gamma-mediated signaling pathway	GO	21	70	<1E-18	<1E-18	OASL OAS3 STAT1 OAS2 B2M HLA-G FCGR1A IFI30 OAS1 IRF9 NMI TRIM22 SP100 PML HLA-C GBP1 TRIM31 HLA-F HLA-E HLA-A GBP2
regulation of viral process	GO	29	387	<1E-18	2E-18	ISG15 IFITM1 OASL MX1 DDX60 OAS3 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 LAMP3 DDX58 OAS1 ISG20 TAP1 IFIT1 DYNLT1 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EIF2AK2 CCL4 LGALS9 HLA-A
cellular response to organic substance	GO	60	2004	<1E-18	6E-18	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9

						OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 EGR2 CCNE1 TLR3 XAF1 XCL2 CD58 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1 CSH1 GBP2
regulation of symbiosis, encompassing mutualism through parasitism	GO	29	415	<1E-18	1.3E-17	ISG15 IFITM1 OASL MX1 DDX60 OAS3 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 LAMP3 DDX58 OAS1 ISG20 TAP1 IFIT1 DYNLT1 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EIF2AK2 CCL4 LGALS9 HLA-A
response to organic substance	GO	70	2728	<1E-18	2.3E-17	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 EGR2 CCNE1 IDO1 TLR3 XAF1 XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 UBD TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 RGS10 SAMHD1 CSH1 GBP2

response to stress	GO	79	3384	<1E-18	3.7E-17	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 STAT1 IFI44L IFI6 PLSCR1 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 DDX58 HCP5 OAS1 ISG20 IRF9 TAP1 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 MSRA HLA-C GBP1 TRIM31 UNC93B1 TYROBP PRTN3 IDO1 TLR3 XAF1 MELK XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 AMBRA1 UBD CLEC4E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 SHISA5 KLRD1 SAMHD1 ECT2 GBP2
regulation of immune system process	GO	51	1546	<1E-18	4.1E-17	ISG15 IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 NMI IFIT1 KIR2DL3 IFI16 PML IFIH1 ZFP36 BIRC3 HLA-C GBP1 UNC93B1 TYROBP LAIR2 IDO1 TLR3 XCL2 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E KIR2DL2 CLEC4E TNFSF4 HLA-A CCL20 KLRD1 HCST TESPA1 SAMHD1

negative regulation of viral life cycle	GO	17	89	<1E-18	1.12E-16	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4
negative regulation of viral process	GO	18	111	<1E-18	1.37E-16	ISG15 IFITM1 OASL MX1 OAS3 STAT1 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4
cellular response to chemical stimulus	GO	65	2550	1E-18	3.56E-16	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 EGR2 CCNE1 TLR3 XAF1 MELK XCL2 CD58 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 RGS10 SAMHD1 ECT2 CSH1 GBP2
Type II interferon signaling (IFNG)	WikiPathw	13	36	3E-18	1.238E-15	ISG15 CXCL10 SOCS1 STAT1 IFI6 PSMB9 CXCL9 OAS1 IRF9 TAP1 IFIT2 GBP1 EIF2AK2
Herpes simplex infection	KEGG	20	182	3E-18	1.472E-15	OAS3 STAT1 TAP2 OAS2 HLA-G DDX58 OAS1 IRF9 TAP1 IFIT1 SP100 PML IFIH1 HLA-C TLR3 EIF2AK2 HLA-F IL6 HLA-E HLA-A

regulation of immune response	GO	38	943	3E-18	1.474E-15	IFITM1 DDX60 SOCS1 STAT1 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A DDX58 TAP1 NMI KIR2DL3 IFI16 IFIH1 BIRC3 HLA-C GBP1 UNC93B1 TYROBP LAIR2 IDO1 TLR3 TREM2 HLA-F IL6 LGALS9 HLA-E KIR2DL2 CLEC4E TNFSF4 HLA-A KLRD1 HCST TESPA1 SAMHD1
regulation of cytokine production	GO	31	603	5E-18	1.974E-15	ISG15 DDX60 SOCS1 HERC5 UBE2L6 B2M RSAD2 HLA-G DDX58 NMI IFI16 PML IFIH1 ZFP36 BIRC3 GBP1 SRGN IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL20
regulation of multi-organism process	GO	29	522	7E-18	2.888E-15	ISG15 IFITM1 OASL MX1 DDX60 OAS3 STAT1 PLSCR1 TAP2 HERC5 B2M RSAD2 LAMP3 DDX58 OAS1 ISG20 TAP1 IFIT1 DYNLT1 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EIF2AK2 CCL4 LGALS9 HLA-A
multi-organism process	GO	66	2778	1.1E-17	4.418E-15	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 TAP2 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 FCGR1A LAMP3 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 TDRD7 TAP1 IFIT1 TRIM22

						DYNLT1 IFI16 IFIT2 SP100 PML IFIH1 ZFP36 RPL39L BIRC3 HLA-C KPNA2 GBP1 ATP6V1F UNC93B1 PRTN3 IDO1 TLR3 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20 SAMHD1 GBP2
cell surface receptor signaling pathway	GO	57	2171	1.5E-17	6.181E-15	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 IFIT2 SP100 PML BCL2A1 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 TYROBP CCNE1 TLR3 XAF1 XCL2 CCL4 HLA-F IL6 HLA-E CHRNA3 MX2 CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 KLRD1 SAMHD1 CSH1 GBP2
regulation of viral life cycle	GO	19	197	1.94E-16	7.589E-14	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 LAMP3 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4 LGALS9
negative regulation of multi-organism process	GO	18	169	2.3E-16	8.8355E-14	ISG15 IFITM1 OASL MX1 OAS3 STAT1 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 SP100 PML ZFP36 TRIM31 EIF2AK2 CCL4

response to external stimulus	GO	59	2491	3.58E-16	1.34654E-13	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 SOCS1 STAT1 IFI44L PLSCR1 HERC5 OAS2 IFIT3 B2M RSAD2 PSMB9 IFI44 CXCL9 DDX58 OAS1 ISG20 IRF9 IFIT1 TRIM22 IFI16 IFIT2 TYMP PML IFIH1 ZFP36 GBP1 UNC93B1 RAB32 TYROBP EGR2 CCNE1 PRTN3 IDO1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E MX2 CASP1 AMBRA1 CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 SAMHD1
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	REACTOME	16	124	6.17E-16	2.27354E-13	IFITM1 B2M HLA-G FCGR1A KIR2DL3 LILRA2 HLA-C TYROBP LAIR2 TREM2 HLA-F HLA-E KIR2DL2 HLA-A KLRD1 HCST
positive regulation of immune system process	GO	36	1005	6.64E-16	2.39724E-13	ISG15 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 IFI16 IFIH1 BIRC3 HLA-C UNC93B1 IDO1 TLR3 XCL2 CD83 TREM2 CCL4 HLA-F IL6 LGALS9 HLA-E CLEC4E TNFSF4 HLA-A CCL20 TESPA1
regulation of defense response	GO	33	864	1.561E-15	5.5289E-13	DDX60 SOCS1 STAT1 PLSCR1 HERC5 B2M RSAD2 PSMB9 FCGR1A DDX58 TAP1 NMI IFIT1 IFI16 PML IFIH1

						ZFP36 BIRC3 UNC93B1 IDO1 TLR3 XCL2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL3L3 SAMHD1
response to chemical	GO	81	4360	3.395E-15	1.17995E-12	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFIT2 TYMP SP100 PML ZFP36 BIRC3 HLA-C KPNA2 GBP1 ATP6V1F TRIM31 EGR2 CCNE1 IDO1 TLR3 XAF1 MELK XCL2 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 UBD TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 RGS10 SAMHD1 OR4C45 ECT2 OR52E8 CSH1 GBP2
negative regulation of viral genome replication	GO	12	51	3.957E-15	1.34961E-12	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 EIF2AK2
Influenza A	KEGG	16	169	5.1051E-14	1.67903E-11	MX1 CXCL10 OAS3 STAT1 OAS2 RSAD2 DDX58 OAS1 IRF9 PML IFIH1 KPNA2 TLR3 EIF2AK2 IL6 CASP1
signal transduction	GO	82	4737	7.7947E-14	2.51866E-11	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3

						SOCS1 STAT1 IFI6 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 SHISA5 KLRD1 RGS10 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
Adaptive Immune System	REACTOME	29	799	2.02191E-13	6.20661E-11	IFITM1 HERC6 SOCS1 TAP2 HERC5 UBE2L6 TRIM69 B2M HLA-G PSMB9 FCGR1A IFI30 RNF19B TAP1 KIR2DL3 LILRA2 RNF213 NFKBIE HLA-C TYROBP LAIR2 ORAI2 TREM2 HLA-F HLA-E KIR2DL2 HLA-A KLRD1 HCST
Antigen processing and presentation	KEGG	12	74	1.98835E-13	6.20661E-11	TAP2 B2M HLA-G IFI30 TAP1 KIR2DL3 HLA-C HLA-F HLA-E KIR2DL2 HLA-A KLRD1
positive regulation of cytokine production	GO	21	389	2.5409E-13	7.67185E-11	DDX60 B2M RSAD2 HLA-G DDX58 IFI16 IFIH1 IDO1 TLR3 CD58 CD83 EIF2AK2

						CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL20
regulation of viral genome replication	GO	12	81	5.20521E-13	1.54628E-10	ISG15 IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 ISG20 IFIT1 IFI16 EIF2AK2
cell communication	GO	85	5274	1.1322E-12	3.30997E-10	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 AMBRA1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
regulation of T cell mediated immunity	GO	11	67	1.71839E-12	4.94519E-10	TAP2 B2M RSAD2 HLA-G TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
signaling	GO	90	5795	1.78214E-12	4.97324E-10	ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M

						RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C KPNA2 GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN
single organism signaling	GO	90	5795	1.78214E-12	4.97324E-10	EGR2 CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 ISG15 IFITM1 OASL CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C KPNA2 GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD83 EIF2AK2

						CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
positive regulation of lymphocyte mediated immunity	GO	12	95	2.85975E-12	7.74571E-10	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO	12	95	2.85975E-12	7.74571E-10	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
positive regulation of adaptive immune response	GO	12	99	4.44729E-12	1.18711E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
positive regulation of immune response	GO	25	690	7.47348E-12	1.96638E-09	DDX60 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A DDX58 TAP1 IFI16 IFIH1 BIRC3 HLA-C UNC93B1 IDO1 TLR3 HLA-F IL6 LGALS9 HLA-E CLEC4E TNFSF4 HLA-A TESPA1

antigen processing and presentation of exogenous peptide antigen via MHC class I	GO	11	78	7.58312E-12	1.96712E-09	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C HLA-F HLA-E HLA-A
regulation of immune effector process	GO	21	473	8.33145E-12	2.13123E-09	DDX60 TAP2 HERC5 B2M RSAD2 HLA-G FCGR1A DDX58 TAP1 IFIT1 PML BIRC3 HLA-C TLR3 EIF2AK2 HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
regulation of lymphocyte mediated immunity	GO	13	138	1.10986E-11	2.8002E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
modification of morphology or physiology of other organism involved in symbiotic interaction	GO	20	436	1.42319E-11	3.41803E-09	ISG15 STAT1 TAP2 RSAD2 PSMB9 SP110 DDX58 TAP1 IFIT1 TRIM22 DYNLT1 SP100 PML IFIH1 HLA-C KPNA2 TLR3 EIF2AK2 CCL4 HLA-A
negative regulation of reproductive process	GO	12	110	1.37495E-11	3.41803E-09	IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 IFIT1 IFI16 SP100 EIF2AK2 CCL4
Graft-versus-host disease	KEGG	9	40	1.42897E-11	3.41803E-09	HLA-G KIR2DL3 HLA-C HLA-F IL6 HLA-E KIR2DL2 HLA-A KLRD1
Antigen Presentation: Folding, assembly and peptide loading of class I MHC	REACTOME	8	25	1.73803E-11	4.10398E-09	TAP2 B2M HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
positive regulation of leukocyte	GO	12	114	2.01598E-11	4.70004E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F

mediated immunity						IL6 HLA-E TNFSF4 HLA-A
modification of morphology or physiology of other organism	GO	20	452	2.61222E-11	6.01398E-09	ISG15 STAT1 TAP2 RSAD2 PSMB9 SP110 DDX58 TAP1 IFIT1 TRIM22 DYNLT1 SP100 PML IFIH1 HLA-C KPNA2 TLR3 EIF2AK2 CCL4 HLA-A
regulation of leukocyte mediated immunity	GO	14	186	3.05477E-11	6.94602E-09	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C TLR3 HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
response to stimulus	GO	110	8044	3.33652E-11	7.49414E-09	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 HCP5 OAS1 ISG20 RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 MSRA BIRC3 HLA-C HMHB1 KPNA2 GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A

positive regulation of defense response	GO	20	461	3.63718E-11	8.07102E-09	GNA15 JUNB CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 DDX60 PLSCR1 RSAD2 PSMB9 FCGR1A DDX58 IFI16 IFIH1 BIRC3 UNC93B1 IDO1 TLR3 XCL2 CCL4 IL6 LGALS9 HLA-E CLEC4E TNFSF4 CCL3L3
negative regulation of cytokine production	GO	15	232	4.71932E-11	1.03477E-08	ISG15 HERC5 UBE2L6 DDX58 NMI PML IFIH1 ZFP36 GBP1 SRGN IDO1 CD83 IL6 LGALS9 TNFSF4
positive regulation of immune effector process	GO	14	197	6.21722E-11	1.34716E-08	DDX60 TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 LGALS9 HLA-E TNFSF4 HLA-A
antigen processing and presentation of peptide antigen via MHC class I	GO	11	98	7.12001E-11	1.52484E-08	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C HLA-F HLA-E HLA-A
response to bacterium	GO	21	538	7.90976E-11	1.67451E-08	ISG15 CMPK2 CXCL11 CXCL10 SOCS1 B2M CXCL9 ZFP36 IDO1 TLR3 TREM2 EIF2AK2 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A JUNB CCL20
cellular response to stimulus	GO	89	6172	9.11081E-11	1.90685E-08	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9

						FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 IRF9 NMI IFIT1 TRIM22 OR4C15 IFI16 IFIT2 SP100 PML BCL2A1 LILRA2 IFIH1 ZFP36 BIRC3 HLA-C GBP1 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 TLR3 XAF1 MELK XCL2 RGS1 CD58 CD83 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 AMBRA1 OR2B6 CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2
ISG15 antiviral mechanism	REACTOME	10	74	9.63838E-11	1.97244E-08	ISG15 MX1 STAT1 HERC5 UBE2L6 DDX58 IFIT1 KPNA2 EIF2AK2 MX2
Antiviral mechanism by IFN-stimulated genes	REACTOME	10	74	9.63838E-11	1.97244E-08	ISG15 MX1 STAT1 HERC5 UBE2L6 DDX58 IFIT1 KPNA2 EIF2AK2 MX2
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	GO	10	75	1.08631E-10	2.19864E-08	TAP2 B2M HLA-G PSMB9 FCGR1A TAP1 HLA-C HLA-F HLA-E HLA-A
phagocytic vesicle	GO	11	104	1.27653E-10	2.55556E-08	TAP2 B2M HLA-G TAP1 HLA-C UNC93B1 RAB32

regulation of innate immune response	GO	19	445	1.37077E-10	2.71471E-08	HLA-F HLA-E AMBRA1 HLA-A DDX60 SOCS1 STAT1 PLSCR1 RSAD2 PSMB9 DDX58 TAP1 NMI IFI16 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 HLA-E CLEC4E HLA-A SAMHD1
regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	GO	12	139	1.68253E-10	3.29669E-08	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F IL6 HLA-E TNFSF4 HLA-A
response to interferon-alpha	GO	7	20	1.90436E-10	3.65709E-08	IFITM1 IFIT3 LAMP3 OAS1 IFIT2 EIF2AK2 MX2
antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent	GO	6	9	1.90618E-10	3.65709E-08	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
Class I MHC mediated antigen processing & presentation	REACTOME	17	365	3.32768E-10	6.31847E-08	HERC6 SOCS1 TAP2 HERC5 UBE2L6 TRIM69 B2M HLA-G PSMB9 FCGR1A RNF19B TAP1 RNF213 HLA-C HLA-F HLA-E HLA-A
regulation of adaptive immune response	GO	12	150	3.79195E-10	7.12654E-08	TAP2 B2M RSAD2 HLA-G FCGR1A TAP1 HLA-C HLA-F

						IL6 HLA-E TNFSF4 HLA-A
MHC class I protein complex	GO	6	11	4.66539E-10	8.6795E-08	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
receptor binding	GO	34	1504	4.98404E-10	9.1796E-08	OASL CXCL11 CXCL10 SOCS1 STAT1 RTP4 PLSCR1 TAP2 MDK HLA-G CXCL9 TAP1 TYMP SP100 HLA-C UNC93B1 TYROBP CCNE1 XCL2 CD58 PRAMEF1 CCL4 HLA-F IL6 HLA-E TNFSF4 HLA-A GNA15 CCL20 CCL3L3 KLRD1 HCST TESPA1 CSH1
regulation of response to stimulus	GO	64	4092	6.2881E-10	1.14148E-07	IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 SP100 PML BCL2A1 IFIH1 ZFP36 RNF213 BIRC3 HLA-C GBP1 UNC93B1 TYROBP LAIR2 IDO1 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 HLA-F IL6 LGALS9 HLA-E CASP1 AMBRA1 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SAMHD1 ECT2
response to lipopolysaccharide	GO	16	331	6.32158E-10	1.14148E-07	CMPK2 CXCL11 CXCL10 SOCS1 B2M CXCL9 ZFP36 IDO1 TREM2 EIF2AK2 IL6

						LGALS9 CASP1 TNFSF4 JUNB CCL20
Endosomal/Vacuolar pathway	REACTOME	6	12	6.9623E-10	1.24497E-07	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
double-stranded RNA binding	GO	9	66	7.57877E-10	1.34217E-07	OASL DDX60 OAS3 OAS2 DDX58 OAS1 IFIH1 TLR3 EIF2AK2
response to molecule of bacterial origin	GO	16	345	1.11167E-09	1.94998E-07	CMPK2 CXCL11 CXCL10 SOCS1 B2M CXCL9 ZFP36 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CASP1 TNFSF4 JUNB CCL20
NOD-like receptor signaling pathway	KEGG	12	168	1.2652E-09	2.17779E-07	OAS3 STAT1 OAS2 OAS1 IRF9 IFI16 BIRC3 GBP1 GBP4 IL6 CASP1 GBP2
Antigen processing-Cross presentation	REACTOME	10	99	1.2958E-09	2.20982E-07	TAP2 B2M HLA-G PSMB9 FCGR1A TAP1 HLA-C HLA-F HLA-E HLA-A
phagocytic vesicle membrane	GO	9	71	1.36168E-09	2.30087E-07	TAP2 B2M HLA-G TAP1 HLA-C RAB32 HLA-F HLA-E HLA-A
Measles	KEGG	11	133	1.42547E-09	2.36526E-07	MX1 OAS3 STAT1 OAS2 DDX58 OAS1 IRF9 IFIH1 CCNE1 EIF2AK2 IL6
antigen processing and presentation of endogenous peptide antigen	GO	6	15	2.00409E-09	3.29565E-07	TAP2 B2M TAP1 HLA-C HLA-E HLA-A
antigen processing and presentation of exogenous peptide antigen	GO	12	183	3.1274E-09	5.09739E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 HLA-F HLA-E HLA-A
regulation of response to stress	GO	34	1635	3.57856E-09	5.78157E-07	DDX60 SOCS1 STAT1 PLSCR1 HERC5 B2M RSAD2

						PSMB9 FCGR1A DDX58 TAP1 NMI IFIT1 IFI16 PML IFIH1 ZFP36 BIRC3 UNC93B1 IDO1 TLR3 XCL2 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 AMBRA1 CLEC4E TNFSF4 HLA-A CCL3L3 SAMHD1
positive regulation of response to stimulus	GO	42	2320	4.02055E-09	6.43917E-07	CXCL11 DDX60 CXCL10 PLSCR1 TAP2 B2M RSAD2 HLA-G PSMB9 FCGR1A CXCL9 DDX58 TAP1 TRIM22 IFI16 PML IFIH1 BIRC3 HLA-C UNC93B1 IDO1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 HLA-F IL6 LGALS9 HLA-E CASP1 AMBRA1 UBD CLEC4E TNFSF4 HLA-A CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
antigen processing and presentation	GO	13	232	4.30375E-09	6.83332E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 RAB32 HLA-F HLA-E HLA-A
antigen processing and presentation of exogenous antigen	GO	12	190	4.64602E-09	7.31371E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 HLA-F HLA-E HLA-A
ER-Phagosome pathway	REACTOME	9	83	4.77812E-09	7.45791E-07	TAP2 B2M HLA-G PSMB9 TAP1 HLA-C HLA-F HLA-E HLA-A
antigen processing and presentation of endogenous antigen	GO	6	18	4.89512E-09	7.57633E-07	TAP2 B2M TAP1 HLA-C HLA-E HLA-A

TAP binding	GO	5	7	5.13907E-09	7.88762E-07	TAP2 TAP1 HLA-C HLA-F HLA-A
antigen processing and presentation of peptide antigen	GO	12	196	6.44375E-09	9.72795E-07	TAP2 B2M HLA-G PSMB9 FCGR1A IFI30 TAP1 HLA-C UNC93B1 HLA-F HLA-E HLA-A
antigen binding	GO	9	91	1.00161E-08	1.4998E-06	HLA-G TAP1 KIR2DL3 LILRA2 HLA-C HLA-F HLA-E HLA-A KLRD1
inflammatory response	GO	17	480	1.61112E-08	2.39304E-06	CXCL11 CXCL10 PLSCR1 FCGR1A CXCL9 NMI IFI16 SP100 IDO1 TLR3 XCL2 CCL4 IL6 LGALS9 TNFSF4 CCL20 CCL3L3
regulation by virus of viral protein levels in host cell	GO	5	11	2.77868E-08	4.09422E-06	STAT1 TAP2 TAP1 IFIT1 DYNLT1
negative regulation of biological process	GO	70	5225	3.37306E-08	4.93056E-06	ISG15 IFITM1 OASL MX1 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 HERC5 MDK UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 LAMP3 IFI27 IFI30 DDX58 OAS1 ISG20 WARS TAP1 NMI IFIT1 TRIM22 DYNLT1 IFI16 ETV7 SP100 PML BCL2A1 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE LCMT1 GBP1 TRIM31 PGP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 RGS1 CD83 EIF2AK2 RARRES3 PRAMEF1 CCL4 IL6 LGALS9 HLA-E PSMG2 AMBRA1 TNFSF4 HLA-A JUNB CCL3L3 RGS10 SYT4 ZNF831 SVBP

chemokine activity	GO	7	48	3.75659E-08	5.44795E-06	CXCL11 CXCL10 CXCL9 XCL2 CCL4 CCL20 CCL3L3
MHC protein complex	GO	6	27	3.84679E-08	5.53517E-06	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
antigen processing and presentation of endogenous peptide antigen via MHC class I	GO	5	13	5.3968E-08	7.70529E-06	TAP2 B2M TAP1 HLA-C HLA-A
Allograft Rejection	WikiPathw	8	80	5.99151E-08	8.48859E-06	CXCL11 STAT1 HLA-G CXCL9 HLA-C HLA-F HLA-E HLA-A
peptide antigen binding	GO	6	30	6.66206E-08	9.36655E-06	HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
positive regulation of T cell cytokine production	GO	5	15	9.66946E-08	1.33904E-05	B2M RSAD2 IL6 TNFSF4 HLA-A
regulation of cytokine secretion	GO	10	162	1.02683E-07	1.41135E-05	SOCS1 PML GBP1 SRGN CD58 IL6 LGALS9 CASP1 CLEC4E TNFSF4
regulation of multicellular organismal process	GO	46	3013	1.1156E-07	1.52201E-05	ISG15 IFITM1 DDX60 CXCL10 SOCS1 STAT1 HERC5 UBE2L6 B2M RSAD2 HLA-G PSMB9 DDX58 WARS NMI DYNLT1 IFI16 TYMP SP100 PML IFIH1 ZFP36 BIRC3 GBP1 TYROBP SRGN EGR2 IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CHRNA3 CASP1 CLEC4E TNFSF4 HLA-A CCL20 TESPA1 SYT4 ECT2 SVBP
early endosome	GO	13	311	1.12468E-07	1.52312E-05	B2M HLA-G FCGR1A LAMP3 PML HLA-C SAMD9L SAMD9

						RAB32 TLR3 HLA-F HLA-E HLA-A
response to tumor necrosis factor	GO	12	260	1.21314E-07	1.63093E-05	STAT1 PSMB9 ZFP36 BIRC3 XCL2 CD58 CCL4 IL6 UBD TNFSF4 CCL20 CCL3L3
regulation of response to external stimulus	GO	24	1072	1.31495E-07	1.75498E-05	CXCL11 DDX60 CXCL10 HERC5 B2M FCGR1A CXCL9 DDX58 IFIT1 PML ZFP36 BIRC3 IDO1 TLR3 XCL2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 AMBRA1 TNFSF4 HLA-A CCL3L3
endocytic vesicle membrane	GO	10	167	1.34068E-07	1.77645E-05	TAP2 B2M HLA-G FCGR1A TAP1 HLA-C RAB32 HLA-F HLA-E HLA-A
chemokine receptor binding	GO	7	59	1.36094E-07	1.79042E-05	CXCL11 CXCL10 CXCL9 XCL2 CCL4 CCL20 CCL3L3
regulation of reproductive process	GO	12	265	1.47428E-07	1.88565E-05	IFITM1 OASL MX1 OAS3 PLSCR1 RSAD2 OAS1 IFIT1 IFI16 SP100 EIF2AK2 CCL4
positive regulation of T cell mediated immunity	GO	6	35	1.49911E-07	1.90417E-05	B2M RSAD2 IL6 HLA-E TNFSF4 HLA-A
Innate Immune System	REACTOME	26	1247	1.6215E-07	2.00192E-05	ISG15 SOCS1 HERC5 UBE2L6 B2M PSMB9 FCGR1A DDX58 DYNLT1 IFI16 IFIH1 BIRC3 HLA-C ATP6V1F UNC93B1 TYROBP PRTN3 TLR3 CD58 TREM2 HLA-E CASP1 CLEC4E HLA-A DSN1 KLRD1
Natural killer cell mediated cytotoxicity	KEGG	9	129	1.64128E-07	2.00192E-05	HLA-G KIR2DL3 HLA-C TYROBP HLA-E KIR2DL2 HLA-A KLRD1 HCST

Hepatitis C	KEGG	9	130	1.74541E-07	2.10111E-05	OAS3 STAT1 OAS2 DDX58 OAS1 IRF9 IFIT1 TLR3 EIF2AK2
endocytic vesicle	GO	12	277	2.31582E-07	2.76966E-05	TAP2 B2M HLA-G FCGR1A TAP1 HLA-C UNC93B1 RAB32 HLA-F HLA-E AMBRA1 HLA-A
negative regulation of cellular process	GO	62	4693	2.44625E-07	2.90678E-05	ISG15 IFITM1 OASL MX1 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 MDK IFIT3 B2M RSAD2 HLA-G PSMB9 LAMP3 IFI27 IFI30 OAS1 ISG20 WARS NMI IFIT1 TRIM22 DYNLT1 IFI16 ETV7 SP100 PML BCL2A1 ZFP36 RNF213 BIRC3 NFKBIE LCMT1 GBP1 TRIM31 PGP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 RGS1 EIF2AK2 RARRES3 PRAMEF1 CCL4 IL6 LGALS9 PSMG2 AMBRA1 TNFSF4 JUNB CCL3L3 RGS10 SYT4 ZNF831 SVBP
regulation of biological process	GO	122	11240	2.92522E-07	3.43243E-05	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RNF213

						BIRC3 NFKBIE HLA-C KPNA2 SAMD9L LCMT1 GBP1 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
regulation of cysteine-type endopeptidase activity	GO	11	231	2.92589E-07	3.43243E-05	IFI6 PSMB9 LAMP3 IFI27 IFI16 PML BIRC3 TLR3 IL6 LGALS9 CASP1
negative regulation of immune system process	GO	14	401	3.10051E-07	3.61425E-05	HLA-G TAP1 NMI IFIT1 IFI16 ZFP36 GBP1 IDO1 TLR3 EIF2AK2 LGALS9 HLA-E TNFSF4 HLA-A
Toll-like receptor signaling pathway	KEGG	8	102	3.39576E-07	3.90894E-05	CXCL11 CXCL10 STAT1 CXCL9 TLR3 CCL4 IL6 CCL3L3
cellular response to tumor necrosis factor	GO	11	236	3.58048E-07	4.09598E-05	STAT1 PSMB9 ZFP36 BIRC3 XCL2 CD58 CCL4 IL6 TNFSF4 CCL20 CCL3L3
positive regulation of innate	GO	13	348	3.81356E-07	4.33569E-05	DDX60 PLSCR1 RSAD2 PSMB9 DDX58 IFI16 IFIH1

immune response						BIRC3 UNC93B1 TLR3 LGALS9 HLA-E CLEC4E
regulation of cellular process	GO	116	10629	4.44176E-07	4.9959E-05	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TAP1 NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE HLA-C KPNA2 LCMT1 GBP1 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
negative regulation of innate	GO	6	43	4.47564E-07	4.9959E-05	TAP1 NMI IFI16 LGALS9 HLA-E HLA-A

immune response						
lymphocyte chemotaxis	GO	6	43	4.47564E-07	4.9959E-05	CXCL11 CXCL10 CXCL9 XCL2 CCL20 CCL3L3
regulation of hemopoiesis	GO	13	355	4.72454E-07	5.24196E-05	ISG15 STAT1 B2M HLA-G ZFP36 TYROBP TLR3 CD83 EIF2AK2 IL6 LGALS9 TNFSF4 TESPA1
negative regulation of multicellular organismal process	GO	24	1160	5.01878E-07	5.43741E-05	ISG15 CXCL10 STAT1 HERC5 UBE2L6 B2M HLA-G DDX58 NMI DYNLT1 SP100 PML IFIH1 ZFP36 GBP1 SRGN IDO1 TLR3 CD83 IL6 LGALS9 TNFSF4 SYT4 SVBP
negative regulation of type I interferon production	GO	6	44	5.06007E-07	5.45008E-05	ISG15 HERC5 UBE2L6 DDX58 NMI IFIH1
chemokine-mediated signaling pathway	GO	7	73	5.15926E-07	5.5246E-05	CXCL11 CXCL10 CXCL9 XCL2 CCL4 CCL20 CCL3L3
protein binding	GO	117	10853	5.49617E-07	5.81773E-05	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 DDX58 OAS1 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L LCMT1

						GBP1 SAMD9 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 LAIR2 PRTN3 TLR3 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 ECT2 RASSF3 CSH1 GBP2
Viral carcinogenesis	KEGG	10	198	5.90561E-07	6.11065E-05	HLA-G IRF9 SP100 HLA-C EGR2 CCNE1 EIF2AK2 HLA-F HLA-E HLA-A
regulation of T cell cytokine production	GO	5	23	5.89178E-07	6.11065E-05	B2M RSAD2 IL6 TNFSF4 HLA-A
response to interferon-beta	GO	5	23	5.89178E-07	6.11065E-05	IFITM1 STAT1 PLSCR1 TLR3 XAF1
Phagosome	KEGG	9	153	6.35135E-07	6.49884E-05	TAP2 HLA-G FCGR1A TAP1 HLA-C ATP6V1F HLA-F HLA-E HLA-A
positive regulation of T cell differentiation	GO	7	76	6.63816E-07	6.75479E-05	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
regulation of protein transport	GO	19	787	7.56874E-07	7.6594E-05	SOCS1 RSAD2 IFI27 DDX58 SP100 PML NFKBIE GBP1 SRGN TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2

regulation of protein localization	GO	22	1027	7.98759E-07	7.9954E-05	SOCS1 RSAD2 IFI27 DDX58 TRIM22 SP100 PML NFKBIE GBP1 SRGN CCNE1 TLR3 CD58 TREM2 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
regulation of type I interferon production	GO	8	116	8.46856E-07	8.43102E-05	ISG15 HERC5 UBE2L6 DDX58 NMI IFI16 IFIH1 TLR3
negative regulation of defense response	GO	9	161	9.48796E-07	9.39512E-05	TAP1 NMI IFIT1 IFI16 ZFP36 EIF2AK2 LGALS9 HLA-E HLA-A
cytoplasmic part	GO	102	9320	9.57082E-07	9.42649E-05	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 PPA1 OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 DDX58 OAS1 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 CD58 EIF2AK2 RARRES3 VAMP5 HLA-F LGALS9 HLA-E MX2 CASP1 PSMG2

						AMBRA1 HLA-A GNA15 SPRR2A DSN1 SHISA5 RGS10 TESPA1 SYT4 BOLA3 ECT2 RASSF3 CSH1 GBP2
early endosome membrane	GO	8	119	1.01471E-06	9.94091E-05	B2M HLA-G FCGR1A PML HLA-C HLA-F HLA-E HLA-A
cytokine activity	GO	10	215	1.20028E-06	0.000116967	CXCL11 CXCL10 CXCL9 SP100 XCL2 CCL4 IL6 TNFSF4 CCL20 CCL3L3
positive regulation of response to external stimulus	GO	14	453	1.23343E-06	0.000119565	CXCL11 DDX60 CXCL10 FCGR1A CXCL9 IDO1 TLR3 XCL2 CCL4 IL6 LGALS9 AMBRA1 TNFSF4 CCL3L3
positive regulation of alpha-beta T cell activation	GO	6	53	1.37041E-06	0.000132148	CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A
single-organism cellular process	GO	133	12938	1.38812E-06	0.000133158	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL

						NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP ISG15 IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 TAP2 MDK B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 CXCL9 DDX58 WARS RNF19B TAP1 NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML BCL2A1 IFIH1 ZFP36 BIRC3 HLA-C TRIM31 UNC93B1 EGR2 CCNE1 PRTN3 IDO1 TLR3 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2
positive regulation of biological process	GO		71	5953	1.43431E-06	0.000136393	EIF2AK2 PRAMEF1 CCL4 HLA-F IL6 LGALS9 HLA-E CHRNA3 CASP1

						AMBRA1 UBD CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
positive regulation of inflammatory response	GO	8	125	1.43665E-06	0.000136393	FCGR1A IDO1 TLR3 XCL2 CCL4 IL6 TNFSF4 CCL3L3
leukocyte chemotaxis	GO	8	126	1.51976E-06	0.000143543	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 CCL20 CCL3L3
biological regulation	GO	123	11844	1.62102E-06	0.000150788	ISG15 IFITM1 OASL CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 TAP2 HERC5 MDK OAS2 UBE2L6 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RNF213 BIRC3 NFKBIE HLA-C KPNA2 SAMD9L LCMT1 GBP1 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3 XAF1 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 KIR2DL2 UBD

						CLEC4E TNFSF4 HLA-A GNA15 JUNB CCL20 CCL3L3 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
integral component of lumenal side of endoplasmic reticulum membrane	GO	5	29	1.61942E-06	0.000150788	HLA-G HLA-C HLA-F HLA-E HLA-A
lumenal side of endoplasmic reticulum membrane	GO	5	29	1.61942E-06	0.000150788	HLA-G HLA-C HLA-F HLA-E HLA-A
positive regulation of lymphocyte differentiation	GO	7	88	1.6594E-06	0.000153582	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
Osteoclast differentiation	KEGG	8	128	1.6983E-06	0.000155618	SOCS1 STAT1 FCGR1A IRF9 LILRA2 TYROBP TREM2 JUNB
positive regulation of leukocyte migration	GO	8	129	1.79405E-06	0.000163578	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9 CCL20
lymphocyte migration	GO	6	56	1.84138E-06	0.000167066	CXCL11 CXCL10 CXCL9 XCL2 CCL20 CCL3L3
negative regulation of immune response	GO	8	130	1.89435E-06	0.00017103	HLA-G TAP1 NMI IFI16 LGALS9 HLA-E TNFSF4 HLA-A
regulation of peptide transport	GO	19	842	1.94587E-06	0.000174825	SOCS1 RSAD2 IFI27 DDX58 SP100 PML NFKBIE GBP1 SRGN TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
positive regulation of	GO	20	927	2.09287E-06	0.000187119	CXCL11 DDX60 CXCL10 CXCL9

intracellular signal transduction						TRIM22 BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST ECT2
positive regulation of multicellular organismal process	GO	28	1626	2.13366E-06	0.000189844	ISG15 IFITM1 DDX60 STAT1 B2M RSAD2 HLA-G DDX58 IFI16 PML IFIH1 IDO1 TLR3 CD58 CD83 EIF2AK2 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 HLA-A CCL20 TESPA1 SYT4 ECT2
regulation of apoptotic process	GO	26	1446	2.18238E-06	0.000193245	STAT1 IFI6 MDK IFIT3 LAMP3 IFI27 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 LCMT1 IDO1 TLR3 MELK EIF2AK2 PRAMEF1 IL6 LGALS9 CASP1 PSMG2 AMBRA1 UBD ECT2 RASSF3
adaptive immune response	GO	11	287	2.21202E-06	0.000194933	TAP2 FCGR1A LAMP3 RNF19B TAP1 LILRA2 HMHB1 UNC93B1 IL6 HLA-E TNFSF4
ER to Golgi transport vesicle membrane	GO	6	58	2.22299E-06	0.000194967	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
pyrophosphatase activity	GO	19	851	2.25353E-06	0.000196709	MX1 DDX60 TAP2 PPA1 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
side of membrane	GO	14	479	2.29509E-06	0.000199392	CXCL10 B2M HLA-G FCGR1A CXCL9 HLA-C RGS1 CD83 HLA-F IL6 HLA-E HLA-A GNA15 KLRD1
hydrolase activity, acting on	GO	19	853	2.3276E-06	0.000201267	MX1 DDX60 TAP2 PPA1 DDX58 TAP1 DYNLT1 TTF2 IFIH1

acid anhydrides, in phosphorus-containing anhydrides						RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
hydrolase activity, acting on acid anhydrides	GO	19	855	2.40387E-06	0.000206596	MX1 DDX60 TAP2 PPA1 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
cell surface	GO	18	776	2.41167E-06	0.000206596	CXCL10 RTP4 B2M CXCL9 HLA-C TYROBP TLR3 CD58 CD83 VAMP5 HLA-F IL6 HLA-E TNFSF4 HLA-A KLRD1 HCST ECT2
regulation of protein secretion	GO	13	415	2.47168E-06	0.000210757	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4
regulation of programmed cell death	GO	26	1462	2.63E-06	0.000222199	STAT1 IFI6 MDK IFIT3 LAMP3 IFI27 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 LCMT1 IDO1 TLR3 MELK EIF2AK2 PRAMEF1 IL6 LGALS9 CASP1 PSMG2 AMBRA1 UBD ECT2 RASSF3
recycling endosome membrane	GO	6	60	2.66667E-06	0.000224268	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of establishment of protein localization	GO	19	866	2.86513E-06	0.000237702	SOCS1 RSAD2 IFI27 DDX58 SP100 PML NFKBIE GBP1 SRGN TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
positive regulation of interleukin-12 production	GO	5	33	2.86417E-06	0.000237702	HLA-G IDO1 TLR3 LGALS9 TNFSF4

lumenal side of membrane	GO	5	33	2.86417E-06	0.000237702	HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of cell death	GO	27	1570	3.17096E-06	0.000261895	STAT1 IFI6 MDK IFIT3 LAMP3 IFI27 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 LCMT1 IDO1 TLR3 MELK EIF2AK2 PRAMEF1 IL6 LGALS9 CASP1 PSMG2 AMBRA1 UBD JUNB ECT2 RASSF3
Regulation of toll-like receptor signaling pathway	WikiPathw	8	140	3.1887E-06	0.000262185	CXCL11 CXCL10 SOCS1 STAT1 CXCL9 TLR3 CCL4 IL6
Negative regulators of RIG-I/MDA5 signaling	REACTOME	5	34	3.26921E-06	0.00026761	ISG15 HERC5 UBE2L6 DDX58 IFIH1
membrane fusion	GO	9	190	3.45628E-06	0.000281672	MX1 TAP2 TAP1 BCL2A1 SAMD9L SAMD9 VAMP5 MX2 SYT4
Toll-like Receptor Signaling Pathway	WikiPathw	7	100	3.67835E-06	0.000298449	CXCL11 CXCL10 STAT1 CXCL9 TLR3 CCL4 IL6
Proteasome Degradation	WikiPathw	6	64	3.77066E-06	0.000304597	HLA-G PSMB9 HLA-C HLA-F HLA-E HLA-A
nucleoside-triphosphatase activity	GO	18	807	4.03984E-06	0.000323503	MX1 DDX60 TAP2 DDX58 TAP1 DYNLT1 TTF2 IFIH1 RNF213 GBP1 GBP4 ATP6V1F RAB32 TRANK1 HELZ2 MX2 GNA15 GBP2
regulation of defense response to virus	GO	9	195	4.22546E-06	0.000331168	DDX60 HERC5 B2M DDX58 IFIT1 PML BIRC3 EIF2AK2 HLA-A
positive regulation of cytokine production involved in	GO	5	36	4.21341E-06	0.000331168	B2M RSAD2 IL6 TNFSF4 HLA-A

immune response						
regulation of cytokine production involved in immune response	GO	6	66	4.44768E-06	0.000347107	B2M RSAD2 TLR3 IL6 TNFSF4 HLA-A
regulation of cellular localization	GO	19	901	4.9127E-06	0.000380863	CXCL11 CXCL10 IFI27 CXCL9 DDX58 SP100 PML ZFP36 NFKBIE GBP1 CCNE1 TLR3 TREM2 IL6 LGALS9 CHRNA3 MX2 SYT4 ECT2
Epstein-Barr virus infection	KEGG	9	199	4.94224E-06	0.000380863	HLA-G DDX58 NFKBIE HLA-C CD58 EIF2AK2 HLA-F HLA-E HLA-A
Allograft rejection	KEGG	5	38	5.35902E-06	0.000407862	HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of inflammatory response	GO	11	321	6.13348E-06	0.000464882	FCGR1A ZFP36 BIRC3 IDO1 TLR3 XCL2 CCL4 IL6 CASP1 TNFSF4 CCL3L3
response to lipid	GO	19	920	6.50662E-06	0.000491143	CMPK2 CXCL11 CXCL10 SOCS1 MDK B2M CXCL9 SP100 ZFP36 CCNE1 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CASP1 TNFSF4 JUNB CCL20
regulation of leukocyte chemotaxis	GO	7	111	7.02318E-06	0.000525825	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9
vacuole	GO	20	1011	7.09883E-06	0.000529337	B2M SLC15A3 HLA-G FCGR1A LAMP3 IFI30 RNF19B PML HLA-C ATP6V1F UNC93B1 RAB32 SRGN PRTN3 TLR3 HLA-F HLA-E AMBRA1 HLA-A DSN1
negative regulation of immune effector process	GO	7	112	7.42341E-06	0.000551308	TAP1 IFIT1 EIF2AK2 LGALS9 HLA-E TNFSF4 HLA-A

negative regulation of protein transport	GO	9	210	7.47305E-06	0.000552765	RSAD2 SP100 PML NFKBIE GBP1 SRGN IL6 TNFSF4 SYT4
monocyte chemotaxis	GO	5	41	7.51939E-06	0.000553968	XCL2 CCL4 IL6 CCL20 CCL3L3
negative regulation of protein secretion	GO	7	114	8.28073E-06	0.000607627	RSAD2 PML GBP1 SRGN IL6 TNFSF4 SYT4
positive regulation of T cell activation	GO	9	213	8.33018E-06	0.000608831	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
cytokine receptor binding	GO	10	272	8.76311E-06	0.00063794	CXCL11 CXCL10 STAT1 CXCL9 XCL2 CCL4 IL6 TNFSF4 CCL20 CCL3L3
regulation of molecular function	GO	43	3257	8.83697E-06	0.000640784	CXCL10 OAS3 SOCS1 STAT1 IFI6 PLSCR1 HERC5 B2M PSMB9 LAMP3 IFI27 DDX58 OAS1 WARS IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 SP100 PML ZFP36 BIRC3 LCMT1 TRIM31 CCNE1 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 AMBRA1 TNFSF4 GNA15 CCL20 CCL3L3 RGS10 ECT2
immune system development	GO	15	618	8.95277E-06	0.00064411	HERC6 B2M RSAD2 PSMB9 IFI16 PML PRTN3 MELK TREM2 IL6 LGALS9 UBD CLEC4E TNFSF4 JUNB
regulation of cysteine-type endopeptidase activity involved in apoptotic process	GO	9	215	8.94707E-06	0.00064411	IFI6 LAMP3 IFI27 PML BIRC3 TLR3 IL6 LGALS9 CASP1

single-organism process	GO	135	13821	9.14638E-06	0.000652938	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 IFI35 CXCL10 OAS3 SOCS1 STAT1 RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 SYT4

						SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
regulation of peptide secretion	GO	13	471	9.11259E-06	0.000652938	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4
cellular response to molecule of bacterial origin	GO	8	163	9.20263E-06	0.000653835	CMPK2 CXCL10 B2M ZFP36 TREM2 IL6 TNFSF4 CCL20
mononuclear cell migration	GO	5	43	9.30095E-06	0.000653835	XCL2 CCL4 IL6 CCL20 CCL3L3
Type I diabetes mellitus	KEGG	5	43	9.30095E-06	0.000653835	HLA-G HLA-C HLA-F HLA-E HLA-A
ER to Golgi transport vesicle	GO	6	77	1.01607E-05	0.000711559	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
cytoplasm	GO	112	11152	1.06642E-05	0.00073563	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 DDX58 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP

						UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 CD58 EIF2AK2 RARRES3 VAMP5 HLA-F IL6 LGALS9 HLA-E MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A GNA15 SPRR2A DSN1 SHISA5 RGS10 TESPA1 SYT4 BOLA3 ECT2 RASSF3 CSH1 GBP2
regulation of production of molecular mediator of immune response	GO	7	120	1.1359E-05	0.000771992	B2M RSAD2 TLR3 IL6 HLA-E TNFSF4 HLA-A
positive regulation of cellular process	GO	63	5503	1.19148E-05	0.000806787	ISG15 IFITM1 CXCL11 DDX60 CXCL10 SOCS1 STAT1 PLSCR1 MDK B2M RSAD2 HLA-G PSMB9 IFI27 CXCL9 DDX58 WARS RNF19B NMI IFIT1 TRIM22 IFI16 IFIT2 SP100 PML BCL2A1 ZFP36 BIRC3 TRIM31 EGR2 CCNE1 PRTN3 IDO1 TLR3 MELK XCL2 RGS1 HELZ2 CD58 CD83 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 HLA-E CHRNA3 CASP1 AMBRA1 UBD CLEC4E TNFSF4 HLA-A JUNB CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
regulation of nucleocytop	GO	9	224	1.22291E-05	0.000825039	IFI27 DDX58 SP100 NFKBIE TLR3 IL6 LGALS9 MX2 ECT2

lasmic transport						
negative regulation of peptide secretion	GO	7	122	1.25742E-05	0.000842152	RSAD2 PML GBP1 SRGN IL6 TNFSF4 SYT4
regulation of T cell differentiation	GO	7	122	1.25742E-05	0.000842152	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
negative regulation of establishment of protein localization	GO	9	225	1.26501E-05	0.000844163	RSAD2 SP100 PML NFKBIE GBP1 SRGN IL6 TNFSF4 SYT4
cytoplasmic vesicle membrane	GO	16	719	1.31587E-05	0.000871788	TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 HLA-C RAB32 TYROBP SYNGR2 CD58 VAMP5 HLA-F HLA-E HLA-A SYT4
regulation of cytoplasmic transport	GO	13	493	1.44569E-05	0.000950955	CXCL11 CXCL10 IFI27 CXCL9 DDX58 SP100 PML NFKBIE TLR3 IL6 LGALS9 MX2 ECT2
cell chemotaxis	GO	8	174	1.44425E-05	0.000950955	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 CCL20 CCL3L3
regulation of leukocyte migration	GO	8	175	1.50231E-05	0.000984678	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9 CCL20
positive regulation of production of molecular mediator of immune response	GO	6	83	1.5174E-05	0.000986324	B2M RSAD2 IL6 HLA-E TNFSF4 HLA-A
Chemokine receptors bind chemokines	REACTOME	5	48	1.52088E-05	0.000986324	CXCL11 CXCL10 CXCL9 XCL2 CCL20
Interleukin-10 signaling	REACTOME	5	48	1.52088E-05	0.000986324	CXCL10 CCL4 IL6 CCL20 CCL3L3
response to interleukin-1	GO	7	126	1.53282E-05	0.000990575	PSMB9 XCL2 CCL4 IL6 LGALS9 CCL20 CCL3L3
positive regulation of leukocyte	GO	9	231	1.5444E-05	0.000994572	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E

cell-cell adhesion						TNFSF4 HLA-A TESPA1
transport vesicle membrane	GO	8	176	1.5623E-05	0.001002597	B2M HLA-G HLA-C SYNGR2 HLA-F HLA-E HLA-A SYT4
apoptotic process	GO	18	902	1.68654E-05	0.001071129	MX1 STAT1 IFI6 PLSCR1 TRIM69 IFI27 IFI16 IFIT2 PML BCL2A1 BIRC3 SRGN TLR3 XAF1 MELK IL6 CASP1 SHISA5
regulation of hydrolase activity	GO	25	1543	1.72891E-05	0.001094266	OAS3 IFI6 PLSCR1 PSMB9 LAMP3 IFI27 OAS1 IFIT1 DYNLT1 IFI16 PML BIRC3 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CASP1 GNA15 CCL20 CCL3L3 RGS10 ECT2
vesicle membrane	GO	16	738	1.78273E-05	0.001121153	TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 HLA-C RAB32 TYROBP SYNGR2 CD58 VAMP5 HLA-F HLA-E HLA-A SYT4
hematopoietic or lymphoid organ development	GO	14	579	1.78357E-05	0.001121153	HERC6 B2M RSAD2 PSMB9 IFI16 PML PRTN3 MELK TREM2 IL6 LGALS9 UBD CLEC4E JUNB
negative regulation of cytokine secretion	GO	5	50	1.82564E-05	0.001139817	PML GBP1 SRGN IL6 TNFSF4
response to oxygen-containing compound	GO	28	1810	1.95679E-05	0.001213473	CMPK2 CXCL11 CXCL10 SOCS1 STAT1 B2M PSMB9 CXCL9 SP100 ZFP36 ATP6V1F EGR2 CCNE1 IDO1 TREM2 EIF2AK2 IL6 LGALS9 CHRNA3 CASP1 TNFSF4 GNA15 JUNB CCL20 RGS10 ECT2 CSH1 GBP2

regulation of alpha-beta T cell activation	GO	6	87	1.95042E-05	0.001213473	CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A
positive regulation of I-kappaB kinase/NF-kappaB signaling	GO	8	182	1.96614E-05	0.001215182	TRIM22 BIRC3 TLR3 LGALS9 CASP1 UBD SHISA5 ECT2
regulation of I-kappaB kinase/NF-kappaB signaling	GO	9	239	1.99718E-05	0.001230237	STAT1 TRIM22 BIRC3 TLR3 LGALS9 CASP1 UBD SHISA5 ECT2
cellular response to biotic stimulus	GO	8	184	2.1188E-05	0.001296478	CMPK2 CXCL10 B2M ZFP36 TREM2 IL6 TNFSF4 CCL20
positive regulation of signal transduction	GO	24	1469	2.15709E-05	0.001313945	CXCL11 DDX60 CXCL10 RSAD2 PSMB9 CXCL9 TRIM22 PML BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
regulation of interleukin-12 production	GO	5	52	2.17588E-05	0.001313945	HLA-G IDO1 TLR3 LGALS9 TNFSF4
Autoimmune thyroid disease	KEGG	5	52	2.17588E-05	0.001313945	HLA-G HLA-C HLA-F HLA-E HLA-A
positive regulation of leukocyte chemotaxis	GO	6	89	2.20142E-05	0.001325028	CXCL11 CXCL10 CXCL9 CCL4 IL6 LGALS9
binding	GO	135	14140	2.28774E-05	0.001350497	ISG15 IFITM1 OASL CMPK2 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M RSAD2 HLA-G PSMB9 FCGR1A

						IFI27 IFI30 CXCL9 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L NT5C3A LCMT1 GBP1 SAMD9 GBP4 ZC2HC1B ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3 TRANK1 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 TRIM48 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 ZNF831 ECT2 RASSF3 CSH1 GBP2
interaction with host	GO	8	186	2.28125E-05	0.001350497	TAP2 LAMP3 TAP1 IFIT1 DYNLT1 KPNA2 TLR3 EIF2AK2
positive regulation of hemopoiesis	GO	8	186	2.28125E-05	0.001350497	ISG15 STAT1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1

negative regulation of secretion by cell	GO	8	187	2.36631E-05	0.001389841	RSAD2 PML GBP1 SRGN IL6 LGALS9 TNFSF4 SYT4
regulation of leukocyte mediated cytotoxicity	GO	5	53	2.36948E-05	0.001389841	B2M TAP1 LGALS9 HLA-E HLA-A
cytoplasmic vesicle part	GO	23	1393	2.63636E-05	0.001533997	TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 DYNLT1 PML HLA-C RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E HLA-A DSN1 SYT4 CSH1
leukocyte differentiation	GO	10	311	2.64023E-05	0.001533997	B2M RSAD2 IFI16 PRTN3 TREM2 IL6 LGALS9 UBD CLEC4E JUNB
programmed cell death	GO	19	1025	2.6923E-05	0.001559335	MX1 STAT1 IFI6 PLSCR1 TRIM69 IFI27 IFI16 IFIT2 PML BCL2A1 BIRC3 SRGN TLR3 XAF1 MELK IL6 CASP1 SPRR2A SHISA5
hemopoiesis	GO	13	525	2.70699E-05	0.001562925	HERC6 B2M RSAD2 IFI16 PML PRTN3 MELK TREM2 IL6 LGALS9 UBD CLEC4E JUNB
regulation of T cell activation	GO	10	315	2.92923E-05	0.001675483	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
Hepatitis B	KEGG	7	142	3.17967E-05	0.001807504	STAT1 DDX58 IFIH1 EGR2 CCNE1 TLR3 IL6
integral component of endoplasmic reticulum membrane	GO	7	143	3.31808E-05	0.001880379	TAP2 HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A
regulation of response to biotic stimulus	GO	9	256	3.34274E-05	0.001888547	DDX60 HERC5 B2M DDX58 IFIT1 PML BIRC3 EIF2AK2 HLA-A

regulation of catalytic activity	GO	35	2628	3.43816E-05	0.001935709	CXCL10 OAS3 SOCS1 IFI6 PLSCR1 HERC5 PSMB9 LAMP3 IFI27 OAS1 WARS IFIT1 DYNLT1 IFI16 PML ZFP36 BIRC3 LCMT1 CCNE1 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 AMBRA1 GNA15 CCL20 CCL3L3 RGS10 ECT2
regulation of endopeptidase activity	GO	11	390	3.44724E-05	0.001935709	IFI6 PSMB9 LAMP3 IFI27 IFI16 PML BIRC3 TLR3 IL6 LGALS9 CASP1
identical protein binding	GO	23	1426	3.69934E-05	0.002070955	MX1 STAT1 IFIT3 B2M HLA-G DDX58 WARS TAP1 NMI DYNLT1 IFI16 TYMP SP100 PML BCL2A1 IFIH1 GBP1 TYROBP TLR3 CCL4 SYT4 ECT2 RASSF3
Viral myocarditis	KEGG	5	59	3.82826E-05	0.002136631	HLA-G HLA-C HLA-F HLA-E HLA-A
positive regulation of cell-cell adhesion	GO	9	261	3.86053E-05	0.002148133	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
cellular response to interleukin-1	GO	6	99	3.87511E-05	0.00214975	PSMB9 XCL2 CCL4 IL6 CCL20 CCL3L3
bounding membrane of organelle	GO	28	1926	4.10013E-05	0.00224377	TAP2 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 TAP1 PML BCL2A1 HLA-C GBP1 GBP4 ATP6V1F UNC93B1 RAB32 TYROBP SRGN TLR3 SYNGR2 CD58 HLA-F HLA-E AMBRA1 HLA-A SYT4 GBP2
intrinsic component of endoplasmi	GO	7	148	4.08639E-05	0.00224377	TAP2 HLA-G TAP1 HLA-C HLA-F HLA-E HLA-A

c reticulum membrane						
vesicle fusion	GO	6	100	4.08688E-05	0.00224377	TAP2 TAP1 SAMD9L SAMD9 VAMP5 SYT4
G-protein coupled receptor binding	GO	9	264	4.20251E-05	0.002289997	CXCL11 CXCL10 RTP4 CXCL9 XCL2 CCL4 GNA15 CCL20 CCL3L3
organelle fusion	GO	7	149	4.25627E-05	0.002312446	TAP2 TAP1 BCL2A1 SAMD9L SAMD9 VAMP5 SYT4
Cytokine-cytokine receptor interaction	KEGG	9	265	4.32204E-05	0.002334408	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 TNFSF4 CCL20 CCL3L3
cell death	GO	19	1066	4.43911E-05	0.002358454	MX1 STAT1 IFI6 PLSCR1 TRIM69 IFI27 IFI16 IFIT2 PML BCL2A1 BIRC3 SRGN TLR3 XAF1 MELK IL6 CASP1 SPRR2A SHISA5
regulation of lymphocyte differentiation	GO	7	150	4.43189E-05	0.002358454	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
regulation of interleukin-1 production	GO	5	61	4.44339E-05	0.002358454	IFI16 PML LGALS9 CASP1 CCL20
Cytosolic DNA-sensing pathway	KEGG	5	61	4.44339E-05	0.002358454	CXCL10 DDX58 CCL4 IL6 CASP1
IL12-mediated signaling events	Pathway I	5	61	4.44339E-05	0.002358454	SOCS1 STAT1 B2M CCL4 HLA-A
protein modification by small protein conjugation	GO	16	803	4.67656E-05	0.002460938	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 RNF19B TRIM22 SP100 PML IFIH1 RNF213 BIRC3 TRIM31 EGR2 UBD
response to nitrogen compound	GO	20	1165	4.78098E-05	0.002508723	SOCS1 STAT1 PSMB9 DDX58 IFIT1 ATP6V1F EGR2 CCNE1 TLR3 TREM2 EIF2AK2 IL6 CHRNA3 CASP1

						UBD TNFSF4 GNA15 JUNB RGS10 CSH1
intracellular transport of virus	GO	5	63	5.13222E-05	0.002685373	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
regulation of leukocyte cell-cell adhesion	GO	10	338	5.17102E-05	0.002690391	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
multi-organism cellular localization	GO	5	64	5.5061E-05	0.002840653	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
multi-organism intracellular transport	GO	5	64	5.5061E-05	0.002840653	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
negative regulation of secretion	GO	8	212	5.5354E-05	0.002847792	RSAD2 PML GBP1 SRGN IL6 LGALS9 TNFSF4 SYT4
single-organism membrane fusion	GO	7	156	5.61457E-05	0.002872479	TAP2 TAP1 BCL2A1 SAMD9L SAMD9 VAMP5 SYT4
positive regulation of leukocyte differentiation	GO	7	156	5.61457E-05	0.002872479	SOCS1 HLA-G CD83 IL6 LGALS9 TNFSF4 TESPA1
cellular response to lipopolysaccharide	GO	7	157	5.83465E-05	0.002968577	CMPK2 CXCL10 B2M ZFP36 IL6 TNFSF4 CCL20
regulation of leukocyte differentiation	GO	9	277	5.99496E-05	0.003041741	SOCS1 HLA-G TYROBP TLR3 CD83 IL6 LGALS9 TNFSF4 TESPA1
regulation of T cell proliferation	GO	7	158	6.06171E-05	0.003067158	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
regulation of peptidase activity	GO	11	417	6.14205E-05	0.003099294	IFI6 PSMB9 LAMP3 IFI27 IFI16 PML BIRC3 TLR3 IL6 LGALS9 CASP1
regulation of localization	GO	35	2681	6.16793E-05	0.003103851	IFITM1 CXCL11 CXCL10 SOCS1 B2M RSAD2 IFI27 CXCL9 DDX58 TRIM22 SP100 PML ZFP36 NFKBIE GBP1 SRGN CCNE1 PRTN3 TLR3

						XCL2 CD58 TREM2 CCL4 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 CLEC4E TNFSF4 CCL20 SYT4 ECT2 SVBP
transport of virus	GO	5	66	6.31661E-05	0.003170011	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
vacuolar part	GO	16	828	6.59036E-05	0.003298403	B2M SLC15A3 HLA-G FCGR1A LAMP3 IFI30 PML HLA-C ATP6V1F RAB32 PRTN3 TLR3 HLA-F HLA-E HLA-A DSN1
regulation of cell differentiation	GO	25	1645	6.65358E-05	0.00332102	ISG15 IFITM1 CXCL10 STAT1 B2M HLA-G CXCL9 DYNLT1 PML ZFP36 GBP1 TYROBP CCNE1 TLR3 CD83 EIF2AK2 PRAMEF1 IL6 LGALS9 CHRNA3 TNFSF4 JUNB TESPA1 SYT4 ECT2
molecular transducer activity	GO	30	2192	6.82929E-05	0.003390349	IFITM1 STAT1 HLA-G FCGR1A SP110 KIR2DL3 OR4C15 LILRA2 HLA-C TYROBP LAIR2 TLR3 RGS1 TREM2 CCL4 HLA-F LGALS9 HLA-E CHRNA3 OR2B6 KIR2DL2 CLEC4E HLA-A GNA15 SHISA5 KLRD1 RGS10 OR4C45 ECT2 OR52E8
cellular process	GO	139	15083	6.92692E-05	0.003429572	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 CXCL9 SP110 DDX58 OAS1

						ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 EIF2AK2 RARRES3 CCL4 VAMP5 HLA-F IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 SVBP
regulation of cell killing	GO	5	68	7.21604E-05	0.003544132	B2M TAP1 LGALS9 HLA-E HLA-A
nucleotide metabolic process	GO	19	1110	7.36757E-05	0.003608934	CMPK2 MX1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32

activation of innate immune response	GO	9	285	7.38863E-05	0.003609652	MX2 GNA15 SAMHD1 GBP2 PSMB9 DDX58 IFI16 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
endosome	GO	16	837	7.43068E-05	0.003620588	B2M HLA-G FCGR1A LAMP3 PML HLA-C SAMD9L SAMD9 UNC93B1 RAB32 TLR3 VAMP5 HLA-F HLA-E HLA-A CSH1
negative regulation of cell proliferation	GO	14	670	8.05005E-05	0.003912027	IFITM1 STAT1 IFIT3 HLA-G IFI30 WARS PML IDO1 EIF2AK2 RARRES3 IL6 LGALS9 AMBRA1 CCL3L3
multi-organism transport	GO	5	70	8.21087E-05	0.003969232	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
multi-organism localization	GO	5	70	8.21087E-05	0.003969232	TAP2 TAP1 IFIT1 DYNLT1 KPNA2
nucleoside catabolic process	GO	14	672	8.2956E-05	0.003999694	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
coated vesicle membrane	GO	7	167	8.44856E-05	0.004041705	B2M HLA-G FCGR1A HLA-C HLA-F HLA-E HLA-A
defense response to bacterium	GO	8	226	8.48916E-05	0.004050606	ISG15 B2M TLR3 IL6 HLA-E CLEC4E HLA-A CCL20
apoptotic signaling pathway	GO	9	292	8.82186E-05	0.004198477	IFI6 IFI27 IFI16 PML BCL2A1 SRGN TLR3 MELK SHISA5
regulation of cell communication	GO	41	3393	8.93465E-05	0.004241196	CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 RSAD2 PSMB9 CXCL9 TRIM22 DYNLT1 TYMP SP100 PML BCL2A1 RNF213 BIRC3 GBP1 EGR2 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 CHRNA3 CASP1

						AMBRA1 UBD CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
positive regulation of interleukin-6 production	GO	5	72	9.30783E-05	0.004406981	DDX58 TLR3 IL6 LGALS9 TNFSF4
Signaling by Interleukins	REACTOME	12	516	9.40241E-05	0.004440347	CXCL10 SOCS1 STAT1 PSMB9 PRTN3 CCL4 IL6 LGALS9 CASP1 JUNB CCL20 CCL3L3
cellular nitrogen compound catabolic process	GO	19	1134	9.5946E-05	0.004519525	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
glycosyl compound catabolic process	GO	14	682	9.6232E-05	0.004521431	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
RNA binding	GO	24	1583	9.72796E-05	0.004547452	OASL DDX60 OAS3 HERC5 OAS2 IFIT3 DDX58 PARP12 OAS1 ISG20 TDRD7 IFIT1 IFI16 IFIT2 IFIH1 ZFP36 RPL39L KPNA2 TLR3 HELZ2 EIF2AK2 ZNFX1 HLA-A SAMHD1
organelle membrane fusion	GO	6	118	9.76792E-05	0.00455457	TAP2 TAP1 SAMD9L SAMD9 VAMP5 SYT4
regulation of cell proliferation	GO	24	1588	9.93125E-05	0.004607399	IFITM1 CXCL11 CXCL10 STAT1 IFIT3 HLA-G IFI30 CXCL9 WARS PML ZFP36 PRTN3 IDO1 EIF2AK2 RARRES3 PRAMEF1 IL6 LGALS9 HLA-E AMBRA1 TNFSF4 HLA-A JUNB CCL3L3
heterocycle catabolic process	GO	19	1137	9.91089E-05	0.004607399	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4

						ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
aromatic compound catabolic process	GO	19	1140	0.000102363	0.004716269	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
positive regulation of lymphocyte activation	GO	9	298	0.00010229	0.004716269	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
positive regulation of apoptotic process	GO	13	604	0.000105395	0.004828749	IFI27 IFIT2 PML BCL2A1 IDO1 TLR3 MELK EIF2AK2 IL6 LGALS9 CASP1 UBD ECT2
regulation of secretion by cell	GO	14	693	0.000112923	0.005122706	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CHRNA3 CASP1 CLEC4E TNFSF4 SYT4
positive regulation of programmed cell death	GO	13	610	0.000115745	0.005237828	IFI27 IFIT2 PML BCL2A1 IDO1 TLR3 MELK EIF2AK2 IL6 LGALS9 CASP1 UBD ECT2
positive regulation of sequence-specific DNA binding transcription factor activity	GO	8	237	0.000116341	0.005251899	DDX58 TRIM22 SP100 TRIM31 TLR3 EIF2AK2 IL6 LGALS9
pattern recognition receptor signaling pathway	GO	6	123	0.000121326	0.005436937	DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9
nucleoside phosphate metabolic process	GO	19	1157	0.000122637	0.00548235	CMPK2 MX1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32

						MX2 GNA15 SAMHD1 GBP2
endosomal part	GO	11	454	0.000126209	0.005614777	B2M HLA-G FCGR1A PML HLA-C RAB32 TLR3 HLA-F HLA-E HLA-A CSH1
carbohydrate derivative binding	GO	30	2239	0.000132094	0.005820351	OASL CMPK2 CXCL11 MX1 DDX60 CXCL10 OAS3 IFI44L TAP2 MDK OAS2 B2M DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 TREM2 EIF2AK2 MX2 GNA15 SAMHD1 GBP2
Chemokine signaling pathway	KEGG	7	180	0.000131954	0.005820351	CXCL11 CXCL10 STAT1 CXCL9 CCL4 CCL20 CCL3L3
cellular response to oxygen-containing compound	GO	19	1169	0.000138991	0.006099507	CMPK2 CXCL10 SOCS1 STAT1 B2M PSMB9 ZFP36 ATP6V1F EGR2 TREM2 IL6 CHRNA3 TNFSF4 GNA15 CCL20 RGS10 ECT2 CSH1 GBP2
regulation of intracellular transport	GO	13	622	0.000139092	0.006099507	CXCL11 CXCL10 IFI27 CXCL9 DDX58 SP100 PML NFKBIE TLR3 IL6 LGALS9 MX2 ECT2
intrinsic component of organelle membrane	GO	9	312	0.000142553	0.006221659	TAP2 HLA-G TAP1 HLA-C VAMP5 HLA-F HLA-E HLA-A SYT4
leukocyte migration	GO	9	312	0.000142553	0.006221659	CXCL11 CXCL10 CXCL9 XCL2 CD58 CCL4 IL6 CCL20 CCL3L3
nucleobase-containing compound catabolic process	GO	18	1083	0.000154852	0.006726559	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
regulation of signal transduction	GO	35	2825	0.000155601	0.006728573	CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1

						RSAD2 PSMB9 CXCL9 TRIM22 DYNLT1 SP100 PML RNF213 BIRC3 GBP1 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 ECT2
organic cyclic compound catabolic process	GO	19	1180	0.000155629	0.006728573	MX1 TAP2 OAS2 ISG20 TAP1 TYMP TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways	REACTOME	5	81	0.000156998	0.006771854	ISG15 HERC5 UBE2L6 DDX58 IFIH1
regulation of signaling	GO	39	3254	0.000164512	0.007079382	CXCL11 DDX60 CXCL10 SOCS1 STAT1 IFI6 PLSCR1 RSAD2 PSMB9 CXCL9 TRIM22 DYNLT1 TYMP SP100 PML RNF213 BIRC3 GBP1 EGR2 TLR3 XCL2 RGS1 TREM2 EIF2AK2 PRAMEF1 CCL4 IL6 LGALS9 CHRNA3 CASP1 UBD CCL20 CCL3L3 SHISA5 RGS10 HCST TESPA1 SYT4 ECT2
protein modification by small protein conjugation or removal	GO	17	996	0.00016916	0.007262465	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 DDX58 RNF19B TRIM22 SP100 PML IFIH1 RNF213 BIRC3 TRIM31 EGR2 UBD
regulation of transport	GO	27	1984	0.000169951	0.007279427	CXCL11 CXCL10 SOCS1 B2M RSAD2 IFI27 CXCL9 DDX58 SP100 PML NFKBIE

						GBP1 SRGN PRTN3 TLR3 CD58 CCL4 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 CLEC4E TNFSF4 SYT4 ECT2
negative regulation of response to stimulus	GO	23	1561	0.000171054	0.007309664	SOCS1 STAT1 IFI6 HLA-G PSMB9 TAP1 NMI IFIT1 IFI16 BCL2A1 ZFP36 RNF213 GBP1 TLR3 RGS1 EIF2AK2 PRAMEF1 IL6 LGALS9 HLA-E TNFSF4 HLA-A RGS10
positive regulation of ERK1 and ERK2 cascade	GO	7	189	0.000175982	0.007468307	XCL2 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
carbohydrate derivative catabolic process	GO	15	815	0.00017768	0.007523019	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
purine nucleoside triphosphate catabolic process	GO	13	640	0.000181643	0.007638148	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
HTLV-I infection	KEGG	8	255	0.000188143	0.007875479	HLA-G ZFP36 HLA-C EGR2 HLA-F IL6 HLA-E HLA-A
positive regulation of chemotaxis	GO	6	134	0.000189319	0.007906754	CXCL11 CXCL10 CXCL9 CCL4 IL6 LGALS9
nucleoside triphosphate catabolic process	GO	13	645	0.000195274	0.008118625	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
positive regulation of cell death	GO	13	649	0.000206798	0.008559128	IFI27 IFIT2 PML BCL2A1 IDO1 TLR3 MELK EIF2AK2 IL6 LGALS9 CASP1 UBD ECT2
positive regulation of	GO	9	329	0.000208387	0.008586306	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E

leukocyte activation						TNFSF4 HLA-A TESPA1
regulation of ERK1 and ERK2 cascade	GO	8	259	0.000208224	0.008586306	GBP1 XCL2 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
ligase activity	GO	10	406	0.000218038	0.008943909	HERC6 HERC5 TRIM69 WARS RNF19B TRIM22 RNF213 BIRC3 TRIM31 EGR2
positive regulation of signaling	GO	24	1725	0.000231133	0.009439051	CXCL11 DDX60 CXCL10 RSAD2 PSMB9 CXCL9 TRIM22 PML BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
intracellular membrane-bounded organelle	GO	99	10581	0.000258371	0.010412853	ISG15 OASL CMPK2 HERC6 MX1 IFI35 OAS3 SOCS1 STAT1 IFI44L IFI6 PLSCR1 TAP2 HERC5 OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 SP110 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI TRIM22 DYNLT1 IFI16 IFIT2 ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG UQCRHL NT5C3A MRPS18C GBP1 SAMD9 GBP4 ATP6V1F TRIM31 UNC93B1 RAB32 SRGN EGR2 CCNE1 PRTN3 TLR3 XAF1 MELK HELZ2 TREM2 EIF2AK2 VAMP5

						HLA-F ZNFX1 LGALS9 HLA-E MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A JUNB DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1 BOLA3 ZNF831 ECT2 CSH1 GBP2
regulation of cell-cell adhesion	GO	10	415	0.000257906	0.010412853	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
nucleobase-containing small molecule metabolic process	GO	19	1232	0.000260094	0.010459394	CMPK2 MX1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
Cell adhesion molecules (CAMs)	KEGG	6	143	0.000264707	0.01059864	HLA-G HLA-C CD58 HLA-F HLA-E HLA-A
molecular_function	GO	146	16545	0.000267154	0.010673403	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A IFI27 IFI30 CXCL9 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 KIR2DL3 OR4C15 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 LILRA2 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG

						SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ZC2HC1B ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 LAIR2 PRTN3 IDO1 TLR3 TRANK1 XAF1 ORAI2 MELK XCL2 RGS1 SYNGR2 HELZ2 CD58 TRIM48 TREM2 EIF2AK2 RARRES3 PRAMEF1 CCL4 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 OR2B6 KIR2DL2 UBD CLEC4E TNFSF4 HLA-A GNA15 JUNB SPRR2A CCL20 CCL3L3 DSN1 SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 BOLA3 ZNF831 ECT2 OR52E8 RASSF3 CSH1 GBP2 CMPK2 MX1 TAP2 TAP1 TTF2 RNF213
nucleoside triphosphate metabolic process	GO	15	851	0.000275852	0.010973293	UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2 MX1 TAP2 OAS2 OAS1 TAP1 TTF2
purine-containing compound metabolic process	GO	17	1043	0.000281597	0.011177682	RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
positive regulation of cell activation	GO	9	344	0.00028574	0.011293486	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1

regulation of chemotaxis	GO	7	206	0.000291167	0.011466224	CXCL11 CXCL10 CXCL9 XCL2 CCL4 IL6 LGALS9
negative regulation of cysteine-type endopeptidase activity	GO	5	94	0.000302598	0.011883247	IFI6 LAMP3 IFI16 BIRC3 IL6
regulation of homeostatic process	GO	11	505	0.000303951	0.011910989	ISG15 CXCL11 CXCL10 STAT1 IFI6 B2M CXCL9 PML ZFP36 IL6 LGALS9
regulation of lymphocyte proliferation	GO	7	208	0.000307962	0.011991621	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
negative regulation of transport	GO	11	507	0.000313868	0.012195815	RSAD2 SP100 PML NFKBIE GBP1 SRGN PRTN3 IL6 LGALS9 TNFSF4 SYT4
humoral immune response	GO	7	209	0.000316645	0.012277831	B2M PRTN3 CD83 TREM2 IL6 HLA-E HLA-A
cytoplasmic vesicle	GO	28	2170	0.000321716	0.012448263	SOCS1 TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 DYNLT1 PML HLA-C SAMD9L SAMD9 UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E AMBRA1 HLA-A DSN1 SYT4 CSH1
regulation of secretion	GO	14	772	0.00032424	0.012493409	SOCS1 RSAD2 PML GBP1 SRGN CD58 IL6 LGALS9 HLA-E CHRNA3 CASP1 CLEC4E TNFSF4 SYT4
regulation of leukocyte activation	GO	11	509	0.000324055	0.012493409	SOCS1 PLSCR1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
intracellular vesicle	GO	28	2173	0.000325561	0.012518114	SOCS1 TAP2 B2M HLA-G FCGR1A LAMP3 TAP1 DYNLT1 PML HLA-C SAMD9L SAMD9

						UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E AMBRA1 HLA-A DSN1 SYT4 CSH1
innate immune response-activating signal transduction	GO	8	279	0.000336715	0.01278684	PSMB9 DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
recycling endosome	GO	6	150	0.000338167	0.012815574	B2M HLA-G HLA-C HLA-F HLA-E HLA-A
regulation of multicellular organismal development	GO	25	1857	0.000339906	0.012855008	ISG15 CXCL10 STAT1 B2M HLA-G PSMB9 WARS DYNLT1 TYMP SP100 PML ZFP36 TYROBP SRGN IDO1 TLR3 CD83 EIF2AK2 IL6 LGALS9 CHRNA3 TNFSF4 TESPA1 SYT4 ECT2
regulation of developmental process	GO	31	2538	0.000357668	0.013496633	ISG15 IFITM1 CXCL10 STAT1 B2M HLA-G PSMB9 CXCL9 WARS DYNLT1 TYMP SP100 PML ZFP36 GBP1 TYROBP SRGN CCNE1 IDO1 TLR3 CD83 EIF2AK2 PRAMEF1 IL6 LGALS9 CHRNA3 TNFSF4 JUNB TESPA1 SYT4 ECT2
purine-containing compound catabolic process	GO	13	690	0.000362503	0.013596917	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
positive regulation of T cell proliferation	GO	5	98	0.000363214	0.013596917	IL6 LGALS9 HLA-E TNFSF4 HLA-A
regulation of lymphocyte activation	GO	10	435	0.000368628	0.013771601	SOCS1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1

positive regulation of cell communication	GO	25	1876	0.000372521	0.013886097	CXCL11 DDX60 CXCL10 RSAD2 PSMB9 CXCL9 TRIM22 PML BIRC3 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 AMBRA1 UBD CCL20 CCL3L3 SHISA5 HCST TESPA1 ECT2
chemotaxis	GO	11	518	0.000373395	0.013886097	CXCL11 CXCL10 CXCL9 TYMP EGR2 XCL2 CCL4 IL6 LGALS9 CCL20 CCL3L3
regulation of interferon-gamma production	GO	5	99	0.000379704	0.014042946	ISG15 TLR3 LGALS9 TNFSF4 HLA-A
Golgi membrane	GO	13	695	0.000386969	0.014282938	B2M HLA-G HLA-C GBP1 GBP4 UNC93B1 SRGN TLR3 HLA-F HLA-E HLA-A SYT4 GBP2
regulation of cellular protein localization	GO	12	607	0.000391541	0.014422798	IFI27 DDX58 SP100 PML NFKBIE GBP1 CCNE1 TLR3 TREM2 IL6 LGALS9 ECT2
positive regulation of cytoplasmic transport	GO	8	286	0.000394571	0.014505389	CXCL11 CXCL10 CXCL9 DDX58 TLR3 IL6 LGALS9 ECT2
myeloid leukocyte differentiation	GO	5	100	0.000396752	0.014527576	IFI16 PRTN3 LGALS9 UBD JUNB
regulation of cytokine biosynthetic process	GO	5	100	0.000396752	0.014527576	NMI ZFP36 TLR3 IL6 CCL20
helicase activity	GO	6	155	0.000399731	0.014591687	DDX60 DDX58 TTF2 IFIH1 TRANK1 HELZ2
response to organic cyclic compound	GO	16	980	0.000402913	0.014665716	CXCL10 SOCS1 STAT1 MDK PSMB9 DDX58 IFIT1 ZFP36 CCNE1 TLR3 CD83 EIF2AK2 IL6 CHRNA3 CASP1 JUNB

regulation of mononuclear cell proliferation	GO	7	218	0.000403951	0.014674508	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
purine nucleotide binding	GO	25	1898	0.000417856	0.015115055	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 SAMHD1 GBP2
regulation of intracellular signal transduction	GO	24	1756	0.00041854	0.015115055	CXCL11 DDX60 CXCL10 SOCS1 STAT1 CXCL9 TRIM22 PML BIRC3 GBP1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CASP1 UBD CCL20 CCL3L3 SHISA5 HCST ECT2
phosphate-containing compound metabolic process	GO	32	2657	0.000440475	0.015876056	CMPK2 MX1 PLSCR1 TAP2 PPA1 OAS2 PSMB9 OAS1 TAP1 TYMP PML TTF2 ZFP36 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F PGP RAB32 CCNE1 TLR3 MELK EIF2AK2 RARRES3 LGALS9 MX2 GNA15 HCST SAMHD1 GBP2
positive regulation of protein import into nucleus	GO	5	103	0.000451366	0.016236821	DDX58 TLR3 IL6 LGALS9 ECT2
purine ribonucleoside triphosphate binding	GO	24	1783	0.000461788	0.016547111	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2

organelle membrane	GO	34	2895	0.000472939	0.016913785	MX1 TAP2 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 TAP1 PML BCL2A1 HLA-C UQCRHL MRPS18C GBP1 GBP4 ATP6V1F UNC93B1 RAB32 TYROBP SRGN TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E MX2 AMBRA1 HLA-A SHISA5 SYT4 GBP2
organophosphate metabolic process	GO	22	1606	0.00048371	0.017265444	CMPK2 MX1 PLSCR1 TAP2 OAS2 OAS1 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F PGP RAB32 RARRES3 MX2 GNA15 SAMHD1 GBP2
positive regulation of cell differentiation	GO	15	902	0.000492392	0.017373333	ISG15 IFITM1 STAT1 HLA-G CXCL9 ZFP36 CCNE1 CD83 IL6 LGALS9 TNFSF4 JUNB TESPA1 SYT4 ECT2
regulation of leukocyte proliferation	GO	7	227	0.000509457	0.017739808	HLA-G IDO1 IL6 LGALS9 HLA-E TNFSF4 HLA-A
myeloid leukocyte migration	GO	5	106	0.000511447	0.017739808	XCL2 CCL4 IL6 CCL20 CCL3L3
positive regulation of protein import	GO	5	106	0.000511447	0.017739808	DDX58 TLR3 IL6 LGALS9 ECT2
positive regulation of transport	GO	16	1006	0.000527294	0.018255079	CXCL11 CXCL10 B2M CXCL9 DDX58 TLR3 CD58 CCL4 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 SYT4 ECT2
positive regulation of protein secretion	GO	7	229	0.000535632	0.01850895	CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4
regulation of cellular	GO	32	2716	0.000541517	0.018677275	ISG15 CXCL10 SOCS1 IFI6 HERC5

protein metabolic process						PSMB9 LAMP3 IFI27 WARS RNF19B NMI IFI16 PML ZFP36 BIRC3 LCMT1 GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 CCL20 CCL3L3 ECT2 SVBP
TNF signaling pathway	KEGG	5	108	0.000554708	0.019025349	CXCL10 BIRC3 IL6 JUNB CCL20
purine ribonucleotide binding	GO	24	1827	0.000565389	0.019355653	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
Antigen processing: Ubiquitination & Proteasome degradation	REACTOME	8	303	0.000569113	0.019438979	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 RNF19B RNF213
regulation of sequence-specific DNA binding transcription factor activity	GO	9	380	0.000571274	0.019448651	DDX58 TRIM22 SP100 TRIM31 TLR3 EIF2AK2 IL6 LGALS9 TNFSF4
regulation of interleukin-6 production	GO	5	109	0.000577339	0.019618864	DDX58 TLR3 IL6 LGALS9 TNFSF4
purine ribonucleoside binding	GO	24	1833	0.000583003	0.019774865	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
regulation of cell activation	GO	11	548	0.000585515	0.019823559	SOCS1 PLSCR1 HLA-G IDO1 CD83 IL6 LGALS9 HLA-E

						TNFSF4 HLA-A TESPA1 ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 HELZ2 CD58 TREM2 EIF2AK2 RARRES3 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A GNA15 JUNB SPRR2A DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1 BOLA3
intracellular part	GO	123	13993	0.000590206	0.019829329	ZNF831 ECT2 RASSF3 CSH1 GBP2

purine nucleoside binding	GO	24	1836	0.000592145	0.019829329	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
ribonucleoside binding	GO	24	1836	0.000592145	0.019829329	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
ribonucleoside triphosphate catabolic process	GO	12	637	0.000589305	0.019829329	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
purine ribonucleoside triphosphate catabolic process	GO	12	637	0.000589305	0.019829329	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
plasma membrane protein complex	GO	7	233	0.000591179	0.019829329	B2M HLA-G HLA-C HLA-F HLA-E HLA-A GNA15
nucleoside binding	GO	24	1843	0.000614364	0.020461774	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1 TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2
regulation of proteolysis	GO	14	826	0.000613454	0.020461774	IFI6 PSMB9 LAMP3 IFI27 RNF19B IFI16 PML BIRC3 LCMT1 TLR3 IL6 LGALS9 CASP1 PSMG2
ribonucleotide binding	GO	24	1844	0.000617641	0.020533786	OASL CMPK2 MX1 DDX60 OAS3 IFI44L TAP2 OAS2 DDX58 OAS1 WARS TAP1

						TTF2 IFIH1 GBP1 GBP4 RAB32 TRANK1 MELK HELZ2 EIF2AK2 MX2 GNA15 GBP2 ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1 MDK OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 IFI44 FCGR1A LAMP3 IFI27 IFI30 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI IFIT1 TRIM22 DYNLT1 IFI16 IFIT2 TYMP ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C LCMT1 GBP1 SAMD9 GBP4 ATP6V1F TRIM31 PGP UNC93B1 RAB32 TYROBP SRGN APOL6 EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK RGS1 SYNGR2 HELZ2 CD58 TRIM48 TREM2 EIF2AK2 RARRES3 VAMP5 HLA-F ZNFX1 IL6 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A GNA15 JUNB SPRR2A
intracellular	GO	125	14282	0.000642712	0.021290411	CCL20 DSN1 SHISA5 RGS10 TESPA1

						SYT4 SAMHD1 BOLA3 ZNF831 ECT2 RASSF3 CSH1 GBP2
purine nucleoside triphosphate metabolic process	GO	14	830	0.000641589	0.021290411	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
intracellular organelle	GO	109	12230	0.000650546	0.021472676	ISG15 OASL CMPK2 HERC6 MX1 DDX60 IFI35 OAS3 SOCS1 STAT1 IFI44L IFI6 PLSCR1 TAP2 HERC5 OAS2 UBE2L6 TRIM69 IFIT3 B2M SLC15A3 RSAD2 HLA-G PSMB9 FCGR1A LAMP3 IFI27 IFI30 SP110 DDX58 PARP12 OAS1 ISG20 WARS RNF19B IRF9 TDRD7 TAP1 CENPW NMI TRIM22 DYNLT1 IFI16 IFIT2 ETV7 SP100 PML BCL2A1 TTF2 IFIH1 ZFP36 RPL39L MSRA RNF213 BIRC3 NFKBIE HLA-C KPNA2 NCAPG SAMD9L UQCRHL NT5C3A MRPS18C GBP1 SAMD9 GBP4 ATP6V1F TRIM31 UNC93B1 RAB32 TYROBP SRGN EGR2 CCNE1 PRTN3 IDO1 TLR3 XAF1 MELK SYNGR2 HELZ2 CD58 TREM2 EIF2AK2 VAMP5 HLA-F ZNFX1 LGALS9 HLA-E CHRNA3 MX2 CASP1 PSMG2 AMBRA1 UBD HLA-A JUNB DSN1 SHISA5 RGS10 TESPA1 SYT4 SAMHD1

membrane	GO	83	8951	0.000685283	0.022369431	BOLA3 ZNF831 ECT2 RASSF3 CSH1 GBP2 IFITM1 OASL MX1 CXCL10 OAS3 RTP4 IFI6 PLSCR1 TAP2 OAS2 TRIM69 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 IFI30 CXCL9 DDX58 RNF19B TAP1 IFI27L1 KIR2DL3 OR4C15 IFI16 PML BCL2A1 LILRA2 MSRA RNF213 BIRC3 HLA-C KPNA2 NCAPG UQCRHL MRPS18C GBP1 GBP4 ATP6V1F UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 ORAI2 MELK RGS1 SYNGR2 HELZ2 CD58 CD83 TREM2 SMIM13 EIF2AK2 RARRES3 VAMP5 HLA-F IL6 HLA-E CHRNA3 MX2 AMBRA1 OR2B6 KIR2DL2 CLEC4E TNFSF4 HLA-A GNA15 SPRR2A SHISA5 KLRD1 RGS10 HCST TESPA1 SYT4 SAMHD1 OR4C45 OR52E8 RASSF3 GBP2
nucleotide catabolic process	GO	13	741	0.00068535	0.022369431	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
guanyl nucleotide binding	GO	9	390	0.00068252	0.022369431	MX1 IFI44L GBP1 GBP4 RAB32 MX2 GNA15 SAMHD1 GBP2
regulation of protein modification	GO	8	312	0.000684016	0.022369431	ISG15 PSMB9 NMI PML BIRC3 LCMT1 PSMG2 SVBP

by small protein conjugation or removal						
Golgi apparatus part	GO	15	934	0.000691557	0.0225037	B2M HLA-G HLA-C GBP1 GBP4 UNC93B1 RAB32 SRGN TLR3 VAMP5 HLA-F HLA-E HLA-A SYT4 GBP2
immune response-regulating signaling pathway	GO	10	475	0.000709563	0.023048893	HLA-G PSMB9 FCGR1A DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
nucleoside phosphate catabolic process	GO	13	746	0.000727081	0.023521831	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
regulation of tumor necrosis factor superfamily cytokine production	GO	5	115	0.000727953	0.023521831	ZFP36 TLR3 CCL4 LGALS9 HLA-E
regulation of locomotion	GO	14	843	0.000740665	0.023890678	IFITM1 CXCL11 CXCL10 CXCL9 DDX58 SP100 PML TRIM31 XCL2 CCL4 IL6 LGALS9 CCL20 SVBP
zinc ion binding	GO	17	1143	0.000748501	0.024101225	OAS2 TRIM69 SP110 DDX58 OAS1 RNF19B TRIM22 PML TTF2 IFIH1 RNF213 BIRC3 TRIM31 XAF1 TRIM48 ZNFX1 SAMHD1
Transcriptional misregulation in cancer	KEGG	6	176	0.000759148	0.024358863	FCGR1A ETV7 PML BCL2A1 BIRC3 IL6
cellular_component	GO	149	17527	0.000768571	0.024532999	ISG15 IFITM1 OASL CMPK2 HERC6 CXCL11 MX1 DDX60 IFI35 CXCL10 OAS3 SOCS1 STAT1 IFI44L RTP4 IFI6 PLSCR1 TAP2 HERC5 PPA1

MDK OAS2 UBE2L6
TRIM69 IFIT3 B2M
SLC15A3 RSAD2
HLA-G PSMB9 IFI44
FCGR1A LAMP3
IFI27 IFI30 CXCL9
SP110 DDX58
PARP12 OAS1 ISG20
WARS RNF19B IRF9
TDRD7 TAP1 IFI27L1
CENPW NMI IFIT1
TRIM22 DYNLT1
KIR2DL3 OR4C15
IFI16 IFIT2 TYMP
ETV7 SP100 PML
BCL2A1 LILRA2 TTF2
IFIH1 ZFP36 RPL39L
MSRA RNF213
BIRC3 NFKBIE HLA-C KPNA2 NCAPG
SAMD9L UQCRHL
NT5C3A MRPS18C
LCMT1 GBP1 SAMD9
GBP4 ATP6V1F
TRIM31 PGP
UNC93B1 RAB32
TYROBP SRGN
APOL6 EGR2 CCNE1
LAIR2 PRTN3 IDO1
TLR3 XAF1 ORAI2
MELK XCL2 RGS1
SYNGR2 HELZ2
CD58 CD83 TRIM48
TREM2 SMIM13
EIF2AK2 RARRES3
CCL4 VAMP5 HLA-F
ZNFX1 IL6 LGALS9
HLA-E CHRNA3 MX2
CASP1 PSMG2
AMBRA1 OR2B6
KIR2DL2 UBD
CLEC4E TNFSF4
HLA-A GNA15 JUNB
SPRR2A CCL20
CCL3L3 DSN1
SHISA5 KLRD1
RGS10 HCST
TESPA1 SYT4
SAMHD1 OR4C45
BOLA3 ZNF831 ECT2

						OR52E8 RASSF3 CSH1 GBP2 SVBP
positive regulation of homeostatic process	GO	7	245	0.000785636	0.024991091	ISG15 CXCL11 CXCL10 STAT1 CXCL9 PML LGALS9
ribonucleoside catabolic process	GO	12	661	0.000802246	0.025431616	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
perinuclear region of cytoplasm	GO	12	661	0.000802246	0.025431616	MX1 STAT1 HERC5 OAS2 LAMP3 NFKBIE GBP4 EIF2AK2 VAMP5 AMBRA1 SYT4 GBP2
cell activation	GO	16	1049	0.000804697	0.025465481	CXCL10 PLSCR1 B2M RSAD2 DYNLT1 TYROBP PRTN3 TLR3 CD58 IL6 HLA-E UBD CLEC4E TNFSF4 GNA15 DSN1
positive regulation of protein transport	GO	10	484	0.000814128	0.025675693	DDX58 TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 ECT2
negative regulation of cell differentiation	GO	12	663	0.000822557	0.025897181	CXCL10 STAT1 B2M HLA-G DYNLT1 ZFP36 GBP1 TLR3 PRAMEF1 IL6 TNFSF4 SYT4
phosphorus metabolic process	GO	32	2739	0.00083905	0.026371364	CMPK2 MX1 PLSCR1 TAP2 PPA1 OAS2 PSMB9 OAS1 TAP1 TYMP PML TTF2 ZFP36 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F PGP RAB32 CCNE1 TLR3 MELK EIF2AK2 RARRES3 LGALS9 MX2 GNA15 HCST SAMHD1 GBP2
extracellular region	GO	47	4559	0.000867403	0.027031861	ISG15 CXCL11 CXCL10 OAS3 PLSCR1 TAP2 PPA1 MDK B2M PSMB9 IFI30 CXCL9 OAS1 WARS TAP1 IFIT1

						DYNLT1 LILRA2 MSRA HLA-C GBP1 ATP6V1F SRGN APOL6 LAIR2 PRTN3 XCL2 SYNGR2 CD58 TREM2 CCL4 VAMP5 IL6 LGALS9 HLA-E CASP1 TNFSF4 HLA-A CCL20 CCL3L3 DSN1 SHISA5 SYT4 BOLA3 CSH1 GBP2 SVBP
organic substance catabolic process	GO	28	2333	0.000879328	0.027311056	ISG15 HERC6 MX1 TAP2 HERC5 OAS2 UBE2L6 PSMB9 ISG20 RNF19B TAP1 TYMP PML TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 RARRES3 MX2 UBD GNA15 SAMHD1 GBP2
regulation of protein modification process	GO	25	1973	0.000879246	0.027311056	ISG15 CXCL10 SOCS1 HERC5 PSMB9 WARS NMI PML BIRC3 LCMT1 GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 PSMG2 CCL20 CCL3L3 ECT2 SVBP
positive regulation of cell adhesion	GO	9	405	0.000881876	0.027344085	SOCS1 HLA-G CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
organonitrogen compound catabolic process	GO	16	1061	0.000901215	0.027473553	MX1 TAP2 TAP1 TYMP TTF2 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 GNA15 SAMHD1 GBP2
taxis	GO	14	860	0.000889378	0.027473553	CXCL11 CXCL10 PSMB9 CXCL9 TYMP TYROBP EGR2 XCL2 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3

ribonucleotide catabolic process	GO	12	670	0.00089704	0.027473553	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
vesicle organization	GO	8	326	0.000899122	0.027473553	TAP2 TAP1 SAMD9L SAMD9 RAB32 SRGN VAMP5 SYT4
positive regulation of peptide secretion	GO	7	251	0.00090011	0.027473553	CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4
regulation of protein import into nucleus	GO	6	182	0.000897399	0.027473553	DDX58 NFKBIE TLR3 IL6 LGALS9 ECT2
nucleoside metabolic process	GO	15	967	0.000964433	0.028835908	MX1 TAP2 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
regulation of cell adhesion	GO	12	677	0.000977034	0.029165339	SOCS1 HLA-G PML GBP1 IDO1 CD83 IL6 LGALS9 HLA-E TNFSF4 HLA-A TESPA1
endosome membrane	GO	9	414	0.001022522	0.03022922	B2M HLA-G FCGR1A PML HLA-C TLR3 HLA-F HLA-E HLA-A
positive regulation of nucleocytoplasmic transport	GO	5	125	0.001041579	0.030703294	DDX58 TLR3 IL6 LGALS9 ECT2
protein ubiquitination	GO	12	684	0.001062848	0.031270812	HERC6 SOCS1 HERC5 UBE2L6 TRIM69 PSMB9 RNF19B TRIM22 RNF213 BIRC3 TRIM31 UBD
regulation of protein import	GO	6	189	0.001082267	0.031791374	DDX58 NFKBIE TLR3 IL6 LGALS9 ECT2
activation of immune response	GO	10	504	0.001092068	0.032028186	PSMB9 FCGR1A DDX58 IFI16 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
cellular response to	GO	13	785	0.001131582	0.03297702	SOCS1 STAT1 PSMB9 IFIT1

nitrogen compound						ATP6V1F TLR3 TREM2 IL6 CHRNA3 TNFSF4 GNA15 RGS10 CSH1
peptide binding	GO	7	263	0.00116816	0.033828872	HLA-G TAP1 HLA-C KPNA2 HLA-F HLA-E HLA-A
mitochondrion	GO	22	1712	0.001194963	0.034550737	CMPK2 MX1 IFI6 OAS2 IFIT3 RSAD2 IFI27 OAS1 TDRD7 TAP1 BCL2A1 MSRA UQCRHL NT5C3A MRPS18C TRIM31 RAB32 XAF1 MX2 CASP1 AMBRA1 BOLA3
whole membrane	GO	27	2266	0.001200466	0.034655447	PLSCR1 TAP2 B2M SLC15A3 RSAD2 HLA-G FCGR1A LAMP3 IFI27 DDX58 TAP1 PML BCL2A1 BIRC3 HLA-C ATP6V1F RAB32 TYROBP TLR3 SYNGR2 CD58 HLA-F HLA-E CHRNA3 AMBRA1 HLA-A SYT4
coated vesicle	GO	7	265	0.001218321	0.035060988	B2M HLA-G FCGR1A HLA-C HLA-F HLA-E HLA-A
guanosine-containing compound catabolic process	GO	7	265	0.001218321	0.035060988	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
glycosyl compound metabolic process	GO	15	992	0.001226961	0.035254557	MX1 TAP2 TAP1 TYMP TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
organophosphate catabolic process	GO	13	793	0.001234214	0.035407704	MX1 TAP2 TAP1 TTF2 RNF213 GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 SAMHD1 GBP2
cellular catabolic process	GO	29	2505	0.001290165	0.036940719	ISG15 HERC6 MX1 TAP2 HERC5 OAS2 UBE2L6 PSMB9 ISG20 RNF19B TAP1

						IFI16 TYMP PML TTF2 ZFP36 RNF213 NT5C3A GBP1 GBP4 ATP6V1F RAB32 IDO1 MX2 AMBRA1 UBD GNA15 SAMHD1 GBP2
regulation of myeloid cell differentiation	GO	6	196	0.001294945	0.036940719	ISG15 STAT1 B2M ZFP36 TYROBP TLR3
myeloid cell differentiation	GO	6	197	0.001327751	0.037680291	IFI16 PML PRTN3 LGALS9 UBD JUNB
positive regulation of macromolecule metabolic process	GO	35	3220	0.001348446	0.038208733	CXCL10 STAT1 PLSCR1 MDK PSMB9 LAMP3 IFI27 DDX58 WARS RNF19B NMI TRIM22 IFI16 SP100 PML ZFP36 BIRC3 TRIM31 EGR2 CCNE1 TLR3 XCL2 HELZ2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 TNFSF4 JUNB CCL20 CCL3L3 ECT2
positive regulation of lymphocyte proliferation	GO	5	133	0.001356817	0.038328012	IL6 LGALS9 HLA-E TNFSF4 HLA-A
positive regulation of cysteine-type endopeptidase activity	GO	5	133	0.001356817	0.038328012	IFI27 IFI16 PML LGALS9 CASP1
positive regulation of molecular function	GO	26	2133	0.001389462	0.039130132	STAT1 PLSCR1 B2M PSMB9 IFI27 DDX58 TRIM22 IFI16 SP100 PML TRIM31 TLR3 XCL2 RGS1 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 AMBRA1 GNA15 CCL20 CCL3L3 RGS10 ECT2
positive regulation of	GO	5	135	0.001445514	0.040194512	IL6 LGALS9 HLA-E TNFSF4 HLA-A

mononuclear cell proliferation						
purine nucleoside catabolic process	GO	7	274	0.00146521	0.040398553	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
purine ribonucleoside catabolic process	GO	7	274	0.00146521	0.040398553	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
regulation of phosphorylation	GO	19	1427	0.001480216	0.040751301	CXCL10 SOCS1 HERC5 WARS PML GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 AMBRA1 CCL20 CCL3L3 ECT2
positive regulation of NF-kappaB transcription factor activity	GO	5	136	0.001491424	0.040998587	TRIM22 TLR3 EIF2AK2 IL6 LGALS9
intracellular signal transduction	GO	21	1623	0.00151093	0.041472885	SOCS1 STAT1 PSMB9 DDX58 NMI IFI16 SP100 PML BCL2A1 IFIH1 ZFP36 BIRC3 RAB32 TYROBP TLR3 MELK LGALS9 CCL20 SHISA5 ECT2 CSH1
GTPase activity	GO	7	276	0.001525006	0.041734851	MX1 GBP1 GBP4 RAB32 MX2 GNA15 GBP2
positive regulation of protein localization to nucleus	GO	5	137	0.001538396	0.04203885	DDX58 TLR3 IL6 LGALS9 ECT2
purine ribonucleoside metabolic process	GO	14	917	0.001582614	0.043183083	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
purine nucleoside metabolic process	GO	14	920	0.001628915	0.044376297	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL NT5C3A GBP1 GBP4

						ATP6V1F RAB32 MX2 GNA15 GBP2
regulation of cell migration	GO	12	723	0.001662801	0.045103772	IFITM1 CXCL11 CXCL10 CXCL9 DDX58 SP100 XCL2 CCL4 IL6 LGALS9 CCL20 SVBP
purine ribonucleoside triphosphate metabolic process	GO	13	824	0.001707575	0.046250167	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
regulation of protein metabolic process	GO	32	2899	0.001753234	0.047347595	ISG15 CXCL10 SOCS1 IFI6 HERC5 PSMB9 LAMP3 IFI27 WARS RNF19B NMI IFI16 PML ZFP36 BIRC3 LCMT1 GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CASP1 PSMG2 CCL20 CCL3L3 ECT2 SVBP
regulation of protein phosphorylation	GO	18	1334	0.001752488	0.047347595	CXCL10 SOCS1 HERC5 WARS PML GBP1 CCNE1 TLR3 XCL2 TREM2 EIF2AK2 CCL4 IL6 LGALS9 CHRNA3 CCL20 CCL3L3 ECT2
positive regulation of intracellular transport	GO	8	364	0.001763452	0.047440687	CXCL11 CXCL10 CXCL9 DDX58 TLR3 IL6 LGALS9 ECT2
immune response-activating signal transduction	GO	9	450	0.001776751	0.047564234	PSMB9 FCGR1A DDX58 IFIH1 BIRC3 UNC93B1 TLR3 LGALS9 CLEC4E
endomembrane system	GO	43	4267	0.001806778	0.048297889	MX1 PLSCR1 TAP2 OAS2 TRIM69 B2M RSAD2 HLA-G FCGR1A LAMP3 IFI27 OAS1 TAP1 DYNLT1 IFIT2 PML NFKBIE HLA-C KPNA2 SAMD9L NT5C3A GBP1 SAMD9 GBP4

						UNC93B1 RAB32 TYROBP SRGN PRTN3 TLR3 SYNGR2 CD58 VAMP5 HLA-F HLA-E MX2 HLA-A DSN1 SHISA5 TESPA1 SYT4 CSH1 GBP2
ribonucleoside triphosphate metabolic process	GO	13	830	0.001814528	0.048434752	MX1 TAP2 TAP1 TTF2 RNF213 UQCRHL GBP1 GBP4 ATP6V1F RAB32 MX2 GNA15 GBP2
positive regulation of establishment of protein localization	GO	10	542	0.001831578	0.048819095	DDX58 TLR3 CD58 IL6 LGALS9 HLA-E CASP1 CLEC4E TNFSF4 ECT2
regulation of cytokine-mediated signaling pathway	GO	5	143	0.00184334	0.049061616	SOCS1 STAT1 BIRC3 TREM2 IL6
locomotion	GO	20	1516	0.001865367	0.049576231	CXCL11 CXCL10 STAT1 MDK PSMB9 LAMP3 CXCL9 DYNLT1 TYMP PML TYROBP EGR2 XCL2 CD58 TREM2 CCL4 IL6 LGALS9 CCL20 CCL3L3
GTP binding	GO	8	368	0.001883164	0.049833504	MX1 IFI44L GBP1 GBP4 RAB32 MX2 GNA15 GBP2

Supplementary Table 5. Intrahepatic expression of selected interferon-stimulated genes.

Gene	Intrahepatic Gene Expression Pre-treatment				Intrahepatic Gene Expression On-Treatment			
	Virological Breakthrough	Responders	Responders vs. Virological Breakthrough		Virological Breakthrough	Responders	Responders vs Virological Breakthrough	
	[Mean]	[Mean]	Fold change	P-value	[Mean]	[Mean]	Fold change	P-value
DDX60	6.733	8.304	-2.971	2.56E-06	5.938	6.316	-1.299	*n.s.*
IFIT1	7.135	8.776	-3.118	2.08E-04	7.049	6.908	1.102	*n.s.*
IRF9	7.380	8.082	-1.627	2.08E-04	7.095	7.251	-1.115	*n.s.*
ISG15	11.059	12.043	-1.978	2.05E-03	9.665	9.650	1.011	*n.s.*
MX1	6.777	8.250	-2.775	3.15E-03	5.766	6.031	-1.201	*n.s.*
OASL	7.629	8.899	-2.410	4.14E-04	6.196	6.288	-1.066	*n.s.*
SOCS1	5.019	4.943	1.054	2.43E-03	4.491	4.354	1.100	*n.s.*
USP18	6.193	7.320	-2.183	6.50E-01	6.199	6.455	-1.194	*n.s.*

Supplementary Table 6: Comparison of Microarray and Nanostring Gene Expression Data for the Top 46 Differentially Expressed Genes. (Ordered alphabetically)

Symbol	Gene	Microarray Fold Change	Microarray p value	Nanostring Fold Change	Nanostring p value
ACADSB	acyl-CoA dehydrogenase, short/branched chain	1.61	0.010517603	1.38	0.015613674
ACSM3	acyl-CoA synthetase medium-chain family member 3	2.06	0.008354682	1.70	0.000993563
ADH6	alcohol dehydrogenase 6 (class V)	1.70	0.086923493	1.23	0.089305591
ANXA9	annexin A9	1.64	0.008744376	1.36	0.003836942
APOA5	apolipoprotein A5	1.62	0.010371417	1.44	0.031966952
APOF	apolipoprotein F	1.78	0.07270472	1.47	0.062457893
BDH1	3-hydroxybutyrate dehydrogenase, type 1	1.51	0.026923968	1.18	0.261421616
CCL19	C-C motif chemokine ligand 19	-1.73	0.171879896	-2.60	0.022930136
CCL2	C-C motif chemokine ligand 2	-2.04	0.01985917	-1.61	0.035687669
CCL20	C-C motif chemokine ligand 20	-1.55	0.006998927	-2.67	0.00109496
CCL4	C-C motif chemokine ligand 4	-1.70	0.005183547	-1.74	0.001116588
CXCL10	C-X-C motif chemokine ligand 10	-4.78	5.87E-06	-9.69	2.43E-13
CXCL11	C-X-C motif chemokine ligand 11	-2.79	1.83E-06	-5.84	1.24E-11
CXCL9	C-X-C motif chemokine ligand 9	-2.50	0.000202519	-2.79	3.74E-05
CYP1A1	cytochrome P450 family 1 subfamily A member 1	2.10	0.029537442	1.63	0.027485863
CYP4A11	cytochrome P450 family 4 subfamily A member 11	1.53	0.068067419	1.38	0.12237672
DDX58	DEXD/H-box helicase 58	-1.76	0.000223119	-2.08	2.86E-05

DDX60	DEXD/H-box helicase 60	-2.94	3.42E-06	-4.29	1.21E-10
EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2	-1.55	0.00499379	-2.03	2.13E-05
FDPS	farnesyl diphosphate synthase	1.53	0.003559337	1.56	0.020802651
HMGCS2	3-hydroxy-3-methylglutaryl-CoA synthase 2	1.53	0.118530254	1.18	0.146653988
IFI27	interferon alpha inducible protein 27	-1.90	0.000188962	-6.45	1.59E-09
IFI44L	interferon induced protein 44 like	-3.87	1.40E-05	-6.33	2.69E-08
IFI6	interferon alpha inducible protein 6	-4.38	3.80E-05	-11.59	7.92E-09
IFIH1	interferon induced with helicase C domain 1	-1.87	0.001297286	-2.07	1.16E-05
IFIT1	interferon induced protein with tetratricopeptide repeats 1	-2.33	0.000741899	-4.16	3.42E-07
IFIT2	interferon induced protein with tetratricopeptide repeats 2	-1.93	0.000881979	-2.53	0.000168674
IFIT3	interferon induced protein with tetratricopeptide repeats 3	-2.41	8.95E-05	-3.29	2.98E-07
IFITM1	interferon induced transmembrane protein 1	-1.79	3.60E-08	-3.25	1.95E-08
IRF9	interferon regulatory factor 9	-1.55	0.000412971	-2.09	3.89E-06
ISG15	ISG15 ubiquitin-like modifier	-4.08	3.57E-09	-12.48	3.48E-12
ISG20	interferon stimulated exonuclease gene 20	-1.59	0.000342715	-2.14	0.001040931
LCAT	lecithin-cholesterol acyltransferase	1.54	0.048001038	1.17	0.193625174
LIPC	lipase C, hepatic type	1.83	0.006127694	1.69	0.001860569
LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	1.56	0.005323788	1.52	0.017610406
MX1	MX dynamin like GTPase 1	-3.43	2.62E-06	-6.46	1.00E-07

NPC1L1	NPC1 like intracellular cholesterol transporter 1	1.50	0.25345488	1.10	0.70849187
OAS1	2'-5'-oligoadenylate synthetase 1	-2.12	0.000276514	-2.95	1.86E-08
OAS2	2'-5'-oligoadenylate synthetase 2	-2.85	7.98E-05	-5.18	2.42E-09
OAS3	2'-5'-oligoadenylate synthetase 3	-2.86	9.71E-06	-5.34	9.93E-09
OASL	2'-5'-oligoadenylate synthetase like	-4.54	6.29E-08	-11.43	8.12E-14
PLSCR1	phospholipid scramblase 1	-1.59	3.84E-05	-2.12	4.02E-07
PPARA	peroxisome proliferator activated receptor alpha	1.56	0.002068441	1.27	0.068290148
PRKAB2	protein kinase AMP-activated non-catalytic subunit beta 2	1.53	0.014931816	1.29	0.11108575
RSAD2	radical S-adenosyl methionine domain containing 2	-2.53	0.000130468	-6.18	3.24E-07
STAT1	signal transducer and activator of transcription 1	-2.21	1.33E-05	-3.48	2.39E-09
TAP1	transporter 1, ATP binding cassette subfamily B member	-1.51	0.00056765	-2.13	1.07E-05

Supplementary Table 7: List of Genes at baseline with significantly different expression from microarray analysis among the 408 differentially expressed genes between patients who responded compared to those who experienced virological breakthrough to DAA therapy

Symbol	Gene	Fold Change	P value
IFI6	interferon alpha inducible protein 6	3.7555	0.001955355
OAS2	2'-5'-oligoadenylate synthetase 2	3.4108	5.36E-05
IFIT1	interferon induced protein with tetratricopeptide repeats 1	3.1177	0.000208439
DDX60	DEXD/H-box helicase 60	2.9706	2.56E-06
IFI44	interferon induced protein 44	2.9165	0.000185033
RSAD2	radical S-adenosyl methionine domain containing 2	2.8506	0.000340034
IFI44L	interferon induced protein 44 like	2.8218	0.005452927
IFIT3	interferon induced protein with tetratricopeptide repeats 3	2.7850	8.24E-05
MX1	MX dynamin like GTPase 1	2.7750	0.000413833
OAS3	2'-5'-oligoadenylate synthetase 3	2.7683	9.56E-05
HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	2.7376	0.000280182
XAF1	XIAP associated factor 1	2.6577	0.000491027
IFIH1	interferon induced with helicase C domain 1	2.6039	4.87E-05
OAS1	2'-5'-oligoadenylate synthetase 1	2.6009	8.14E-05
SAMD9	sterile alpha motif domain containing 9	2.5377	0.000862135
CMPK2	cytidine/uridine monophosphate kinase 2	2.4938	5.17E-05
IFIT2	interferon induced protein with tetratricopeptide repeats 2	2.4600	0.000242268
OASL	2'-5'-oligoadenylate synthetase like	2.4099	0.002430076
RTP4	receptor transporter protein 4	2.3386	9.60E-05
HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	2.3298	0.000335654
HCG26	HLA complex group 26 (non-protein coding)	2.2504	0.000619202
STAT1	signal transducer and activator of transcription 1	2.2296	6.04E-05
SORD	sorbitol dehydrogenase	2.1688	0.004258155
LAMP3	lysosomal associated membrane protein 3	2.1443	0.003479271
EPSTI1	epithelial stromal interaction 1 (breast)	2.1088	0.001113814
CXCL11	C-X-C motif chemokine ligand 11	2.1060	0.002126124
HCP5	HLA complex P5 (non-protein coding)	2.0959	0.000102935
CCL20	C-C motif chemokine ligand 20	2.0338	0.00111211
IFI27	interferon alpha inducible protein 27	2.0313	0.000768875
EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2	2.0112	0.000705207

SAMD9L	sterile alpha motif domain containing 9 like	2.0060	0.000720888
DDX58	DEXD/H-box helicase 58	1.9803	0.000187144
ISG15	ISG15 ubiquitin-like modifier	1.9784	0.003150921
GBP1	guanylate binding protein 1	1.8665	7.50E-05
TRIM31	tripartite motif containing 31	1.8628	0.000295083
NRIR	negative regulator of interferon response (non-protein coding)	1.8561	0.000924068
PARP12	poly(ADP-ribose) polymerase family member 12	1.8450	3.43E-05
GBP4	guanylate binding protein 4	1.8269	0.000272787
STAB2	stabilin 2	1.8098	0.007966073
ZNFX1	zinc finger NFX1-type containing 1	1.7527	0.002194265
BIRC3	baculoviral IAP repeat containing 3	1.7452	0.007702794
TAP1	transporter 1, ATP binding cassette subfamily B member	1.7292	0.000198839
PPARA	peroxisome proliferator activated receptor alpha	1.6750	0.008237206
UBE2L6	ubiquitin conjugating enzyme E2 L6	1.6467	0.000986465
TDRD7	tudor domain containing 7	1.6373	0.000238311
RNF213	ring finger protein 213	1.6344	3.84E-05
IRF9	interferon regulatory factor 9	1.6274	0.002048737
HLA-F	major histocompatibility complex, class I, F	1.5956	0.00384766
SLC46A1	solute carrier family 46 member 1	1.5371	0.000788678
SLC15A3	solute carrier family 15 member 3	1.5335	0.000376923
NT5C3A	5'-nucleotidase, cytosolic IIIA	1.5202	0.00322946
NMI	N-myc and STAT interactor	1.5105	0.001123907
PLSCR1	phospholipid scramblase 1	1.5049	0.001238307
ZNF691	zinc finger protein 691	1.5045	0.002348813
BHLHE40	basic helix-loop-helix family member e40	1.5022	0.004256359
SMAD5-AS1	SMAD5 antisense RNA 1	1.5013	0.000374862
KPNA2	karyopherin subunit alpha 2	1.4860	0.004835633
SP110	SP110 nuclear body protein	1.4791	0.002767034
NDRG2	NDRG family member 2	1.4576	0.003303144
IFI30	IFI30, lysosomal thiol reductase	1.4473	0.00227512
HLA-E	major histocompatibility complex, class I, E	1.4178	0.00462728
IFI35	interferon induced protein 35	1.4171	0.00472574
SP100	SP100 nuclear antigen	1.4129	0.001033798
PSMB9	proteasome subunit beta 9	1.3973	0.000358828
RNF123	ring finger protein 123	1.3914	0.005674182
PPIP5K1	diphosphoinositol pentakisphosphate kinase 1	1.3853	0.002705835
PSMB8-AS1	PSMB8 antisense RNA 1 (head to head)	1.3831	0.000430455

HLA-L	major histocompatibility complex, class I, L (pseudogene)	1.3798	0.006529507
KLRD1	killer cell lectin like receptor D1	1.3760	0.00512616
SRPRA	SRP receptor alpha subunit	1.3685	0.005093559
HDAC1	histone deacetylase 1	1.3616	0.002076623
PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	1.3563	0.00125254
IFITM1	interferon induced transmembrane protein 1	1.3519	0.005773255
ATXN1	ataxin 1	1.3417	0.000867161
AMBRA1	autophagy and beclin 1 regulator 1	1.3408	0.001109054
BCL7A	BCL tumor suppressor 7A	1.3134	0.008842616
SMIM13	small integral membrane protein 13	1.3104	0.009870538
TAP2	transporter 2, ATP binding cassette subfamily B member	1.2812	0.002447243
IQSEC1	IQ motif and Sec7 domain 1	1.2613	0.000840507
B2M	beta-2-microglobulin	1.2315	0.004438817
PRR29	proline rich 29	-1.2826	0.009919255
ZC2HC1B	zinc finger C2HC-type containing 1B	-1.3524	0.006132722
MIR133B	microRNA 133b	-1.3530	0.001263178
BOLA3	bolA family member 3	-1.3739	0.004947095
TRIM48	tripartite motif containing 48	-1.4629	0.008582016
LOC105369360	uncharacterized LOC105369360	-1.4768	0.008430766
LOC105374780	uncharacterized LOC105374780	-1.5878	0.000165173

Supplementary Table 8: List of Top 25 upregulated genes when comparing on-treatment to baseline biopsies

Symbol	Gene	Fold Change	P value
TSSK2	testis specific serine kinase 2	1.346865488	2.85E-05
CMTM4	CKLF like MARVEL transmembrane domain containing 4	1.541485445	2.86E-05
UNC119B	unc-119 lipid binding chaperone B	1.390173092	3.96E-05
GPC5-AS2	GPC5 antisense RNA 2	1.248301794	0.000107112
LOC101927942	uncharacterized LOC101927942	1.633982299	0.000147473
IQSEC1	IQ motif and Sec7 domain 1	1.249858695	0.000153783
WBSCR27	Williams Beuren syndrome chromosome region 27	1.2179421	0.00018273
FAM149A	family with sequence similarity 149 member A	1.299004526	0.000189032
LINC01534	long intergenic non-protein coding RNA 1534	1.378072946	0.000192563
ESR1	estrogen receptor 1	1.406039973	0.000257248
ISM1	isthmin 1	1.391467238	0.000276503
ARSD	arylsulfatase D	1.45719898	0.000281214
CDK14	cyclin dependent kinase 14	1.267986803	0.000353517
EEF2	eukaryotic translation elongation factor 2	1.283595477	0.000366083
EIF3L	eukaryotic translation initiation factor 3 subunit L	1.25129337	0.000409995
SLC46A1	solute carrier family 46 member 1	1.437252517	0.000410035
KIF12	kinesin family member 12	1.592543631	0.000425764
ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)	1.301563841	0.0004369
HDLBP	high density lipoprotein binding protein	1.204505042	0.000466716
EIF4B	eukaryotic translation initiation factor 4B	1.41354455	0.000468452
RNASE13	ribonuclease A family member 13 (inactive)	1.309608536	0.000491023
SPATA33	spermatogenesis associated 33	1.326668112	0.00053207
CERK	ceramide kinase	1.303698557	0.000553821
UBE4B	ubiquitination factor E4B	1.253367072	0.000587016
DANCR	differentiation antagonizing non-protein coding RNA	1.350322818	0.000717876

Legend to Supplementary Figures

Supplementary Figure 1: Flowchart indicating methods for identifying differentially expressed genes between on-treatment and baseline liver biopsies.

Raw files from Affymetrix Human Gene 2.0 array were preprocessed using RMA with quantile normalization in R (Bioconductor oligo package, v.1.34.2). Expression data for technical replicates were averaged for each sample and averages were used for further analysis. Differentially expressed genes were determined by linear mixed models using the Bioconductor limma package (v.3.26.8). Pathway enrichment analyses were performed using the hypergeometric distribution, using several databases (GO, Reactome, KEGG, WikiPathways).

Supplementary Figure 2: Similarity plot for gene expression at weeks 2 and 4 in treated subjects

Expression data for week 2 biopsies are shown in blue and week 4 biopsies are shown in green. The similarity plot for expression data from treated patients shows no separation in global expression between biopsies performed at week 2 or week 4.

Supplementary Figure 3: Fold change in expression data by NanoString for seven selected genes comparing pre-treatment to week 2/4 on-treatment biopsies

The mRNA expression level of 7 genes that represent different components of the intrahepatic immune response was determined by Nanostring analysis. Mean expression levels and p values are shown. Patients who responded to DAA therapy displayed a greater decline in intrahepatic ISG expression from baseline to on-treatment (week 2/4) compared to those who subsequently experience a virological breakthrough.

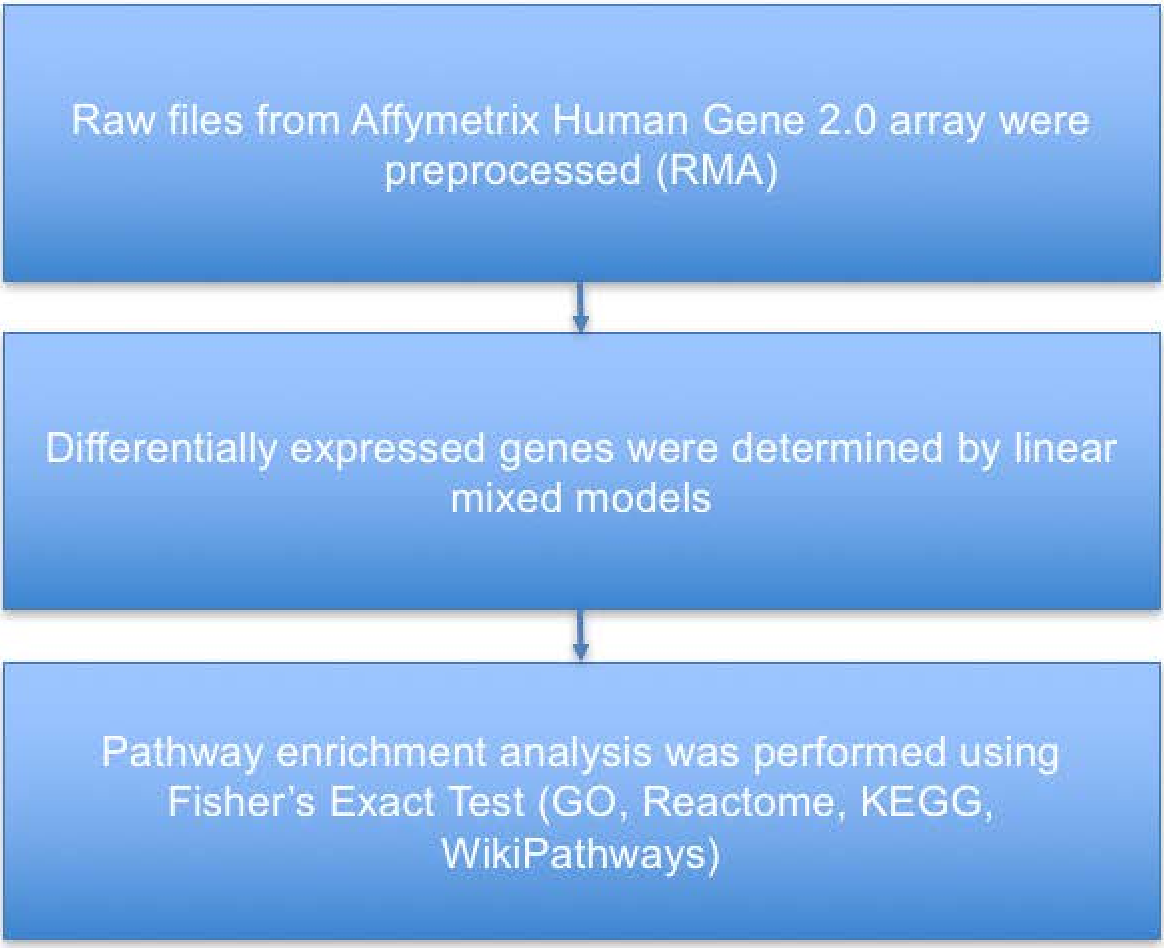
Supplementary Figure 4: Gating strategy to study NK cells by flow cytometry.

(A) Dot plots from left to right show gating on single cells in FSC area versus FSC height plots, gating on lymphocytes in FSC versus SSC plots, exclusion of EMA+ dead cells, CD14+ monocytes and CD19+ B cells, and gating on CD56+CD3- negative NK cells.

(B) Dot plots from left to right show gating on CD56^{dim} and CD56^{bright} NK cell subsets, NK cell degranulation (CD107a expression) after culture with or without K562 cells, and analysis of TRAIL expression. Percentages indicate the frequency of events in the red gate relative to the total number of events in the respective plot.

(C) Fluorescence minus one (FMO, pSTAT1 antibody excluded from the staining panel) and pSTAT1 staining of NK cells. Gating strategy as described in panel A except that cells were stained with anti-CD56-PE, anti-CD3-APC, anti-CD20-PerCP/Cy5.5 and anti-pSTAT1-Alexa488.

Suppl. Fig 1

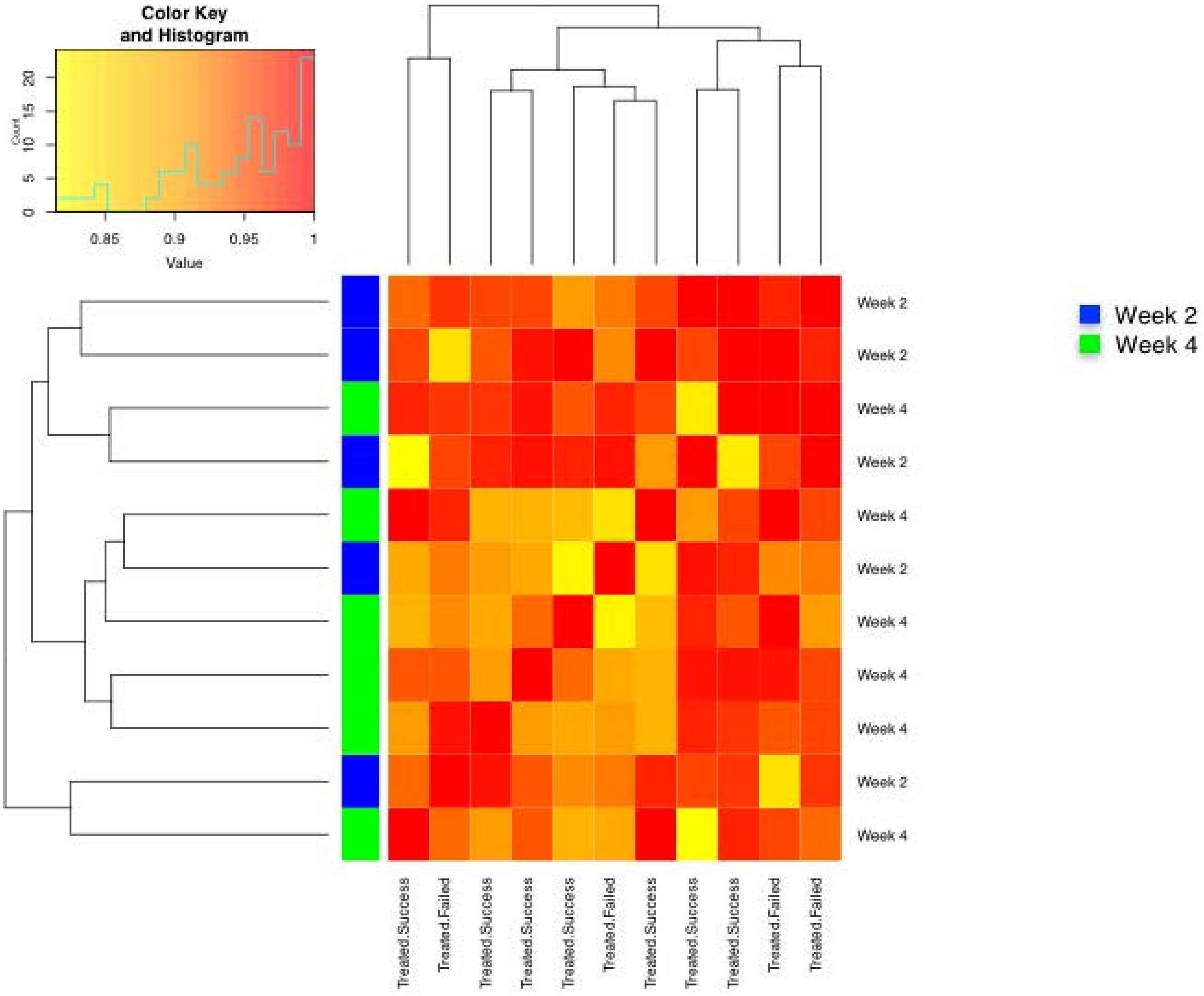


Raw files from Affymetrix Human Gene 2.0 array were preprocessed (RMA)

Differentially expressed genes were determined by linear mixed models

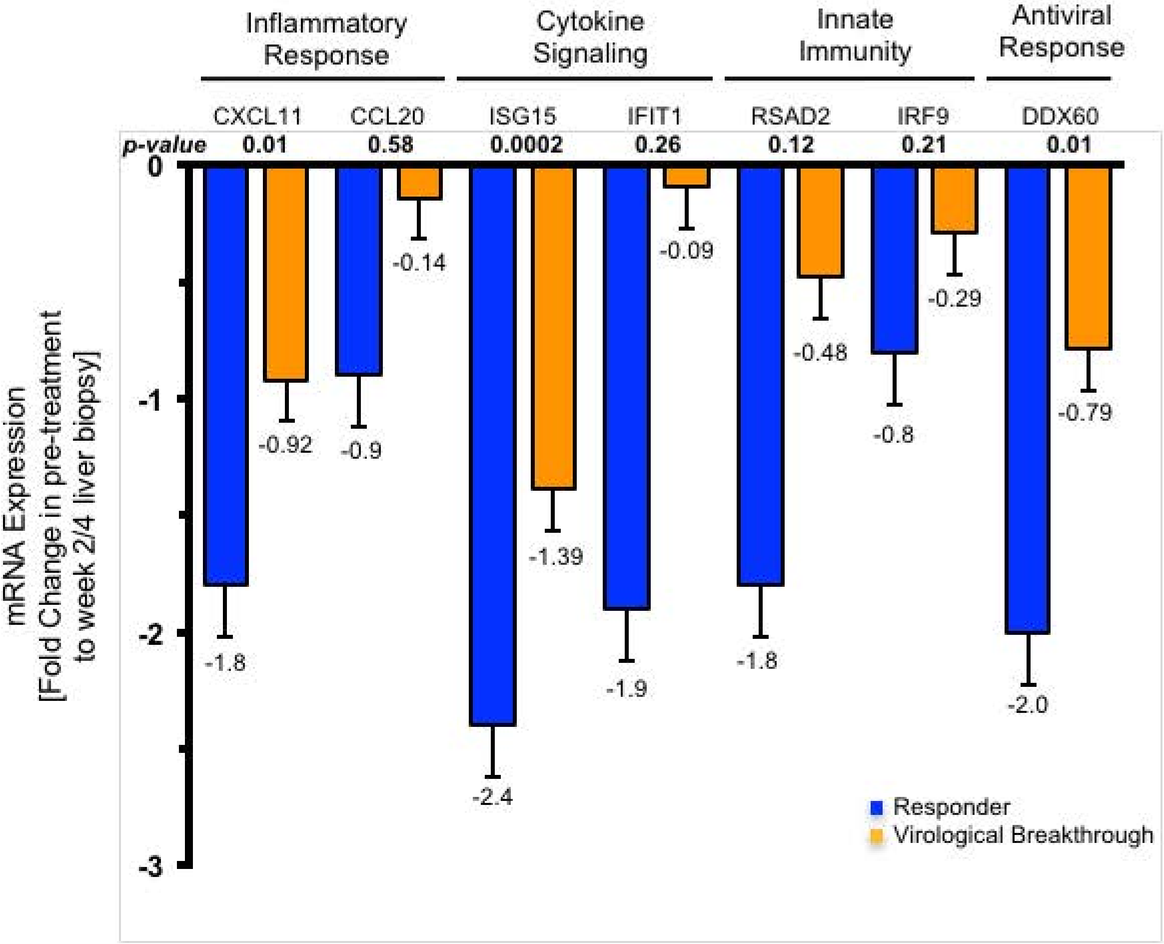
Pathway enrichment analysis was performed using Fisher’s Exact Test (GO, Reactome, KEGG, WikiPathways)

Suppl. Fig 2

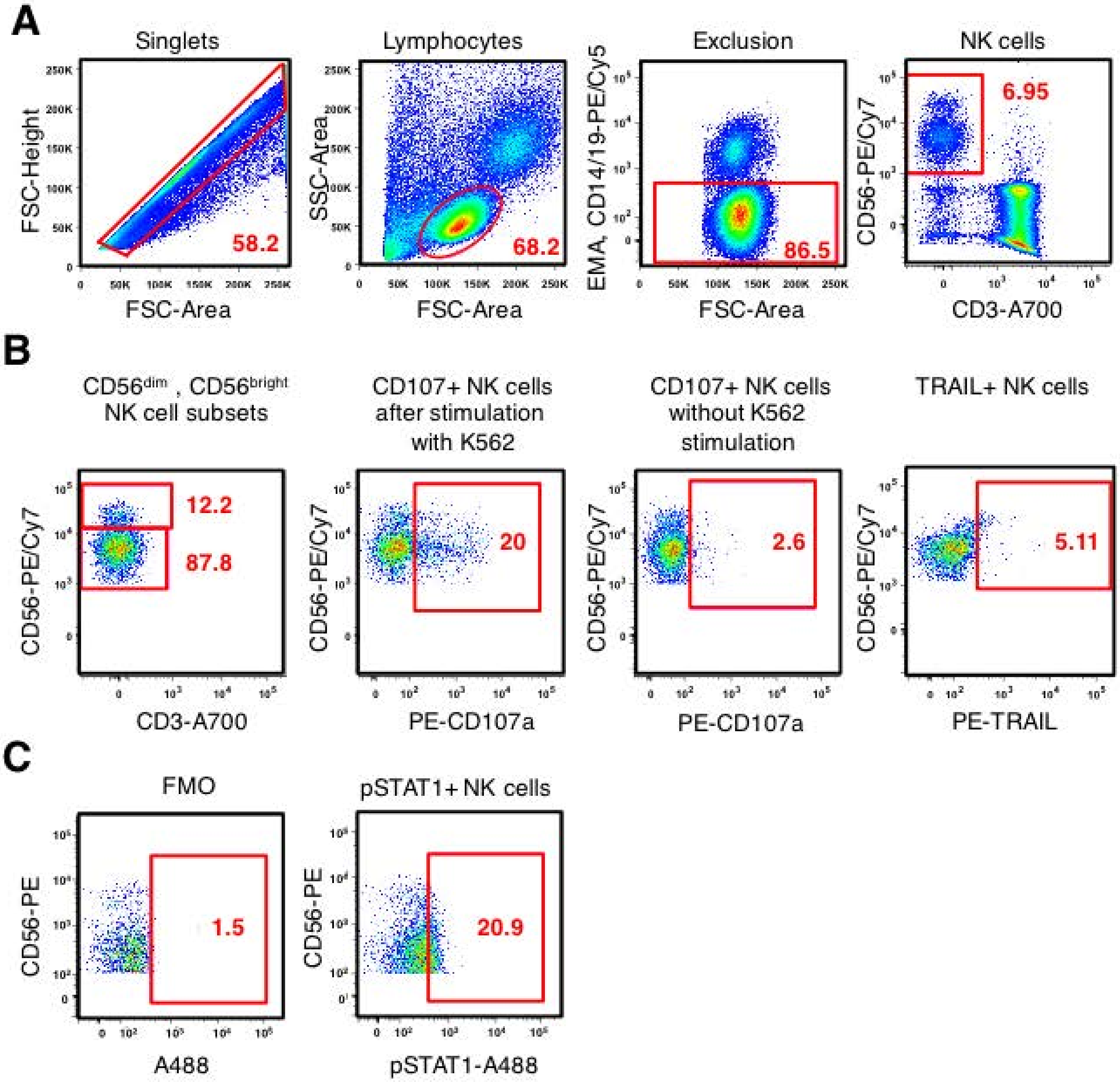


Color Key
and Histogram
Count
0
5
10
15
20
0.85
0.9
0.95
1
Value
Week 2
Week 2
Week 4
Week 2
Week 4
Week 2
Week 4
Week 4
Week 4
Week 2
Week 4
Treated.Success
Treated.Failed
Treated.Success
Treated.Success
Treated.Success
Treated.Failed
Treated.Success
Treated.Success
Treated.Success
Treated.Failed
Treated.Failed
Week 2
Week 4

Suppl. Fig 3


Inflammatory Response
Cytokine Signaling
Innate Immunity
Antiviral Response
CXCL11
CCL20
ISG15
IFIT1
RSAD2
IRF9
DDX60
p-value
0.01
0.58
0.0002
0.26
0.12
0.21
0.01
mRNA Expression [Fold Change in pre-treatment to week 2/4 liver biopsy]
0
-1
-2
-3
-1.8
-0.92
-0.9
-0.14
-2.4
-1.39
-1.9
-0.09
-1.8
-0.48
-0.8
-0.29
-2.0
-0.79
Responder
Virological Breakthrough

Suppl. Fig 4


A
Singlets
FSC-Height
FSC-Area
58.2
Lymphocytes
SSC-Area
FSC-Area
68.2
Exclusion
EMA, CD14/19-PE/Cy5
FSC-Area
86.5
NK cells
CD56-PE/Cy7
CD3-A700
6.95
B
CD56dim , CD56bright NK cell subsets
CD56-PE/Cy7
CD3-A700
12.2
87.8
CD107+ NK cells after stimulation with K562
CD56-PE/Cy7
PE-CD107a
20
CD107+ NK cells without K562 stimulation
CD56-PE/Cy7
PE-CD107a
2.6
TRAIL+ NK cells
CD56-PE/Cy7
PE-TRAIL
5.11
C
FMO
CD56-PE
A488
1.5
pSTAT1+ NK cells
CD56-PE
pSTAT1-A488
20.9