

Supplementary Materials for  
**Evolution of inflammation and immunity in a dengue virus 1 human  
infection model**

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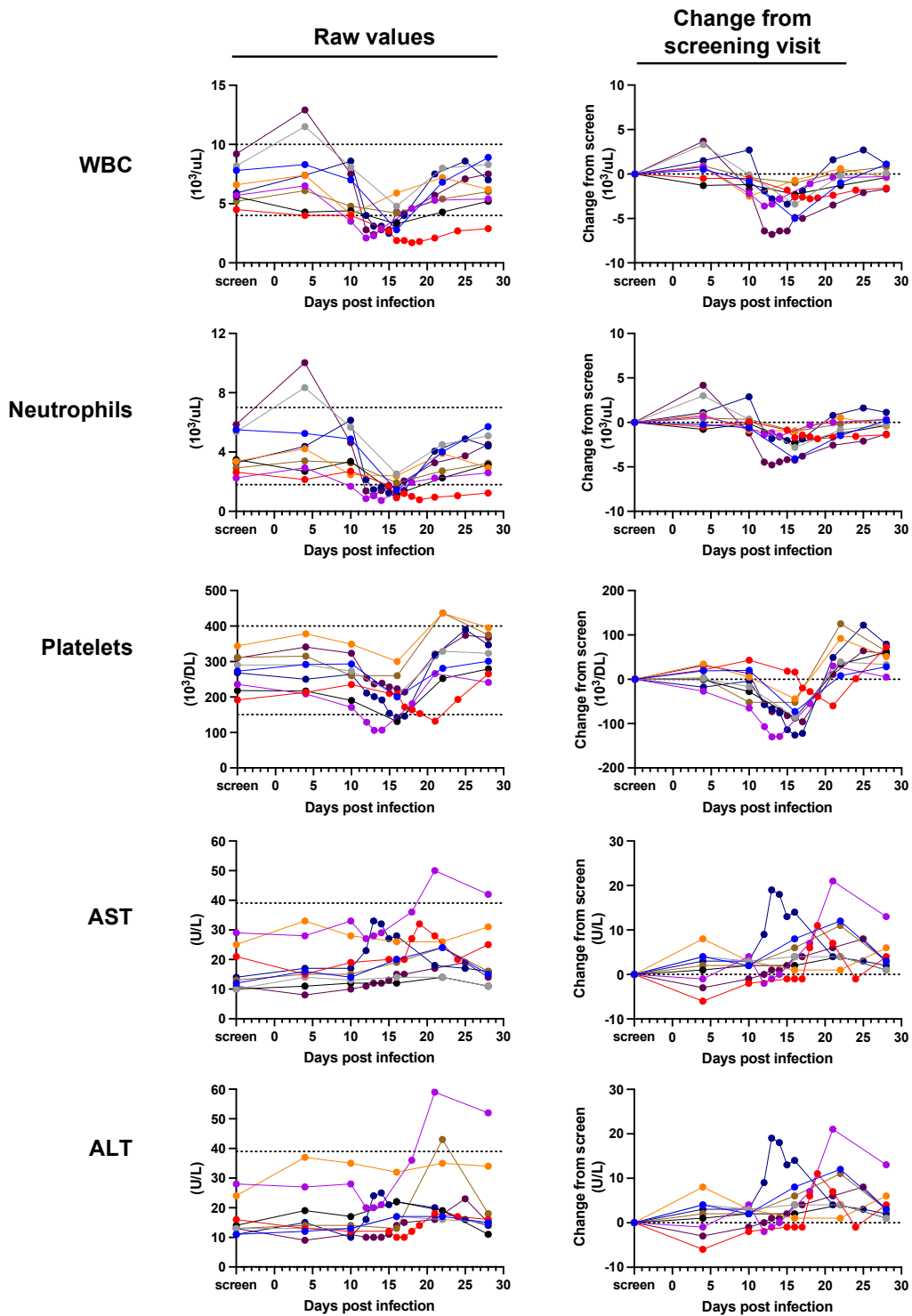
*Sci. Transl. Med.* **14**, eabo5019 (2022)  
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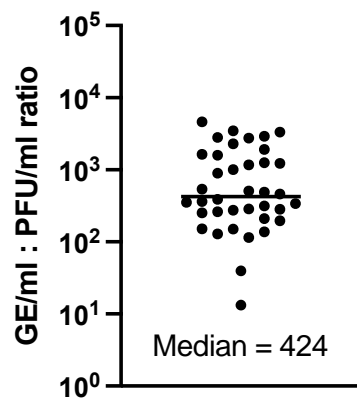
Figs. S1 to S4  
Tables S1 to S14

**Other Supplementary Material for this manuscript includes the following:**

MDAR Reproducibility Checklist



**Fig. S1. Select clinical labs from all study participants, screening day through day 28 post 45AZ5 challenge**



**Fig. S2. Ratio of viral RNA (GE/ml) to infectious virus (PFU/ml) in serum. Analysis from all time points with > 100 PFU/ml**

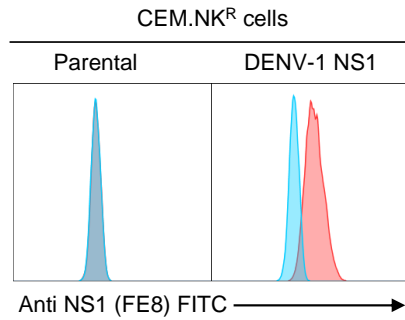
A)

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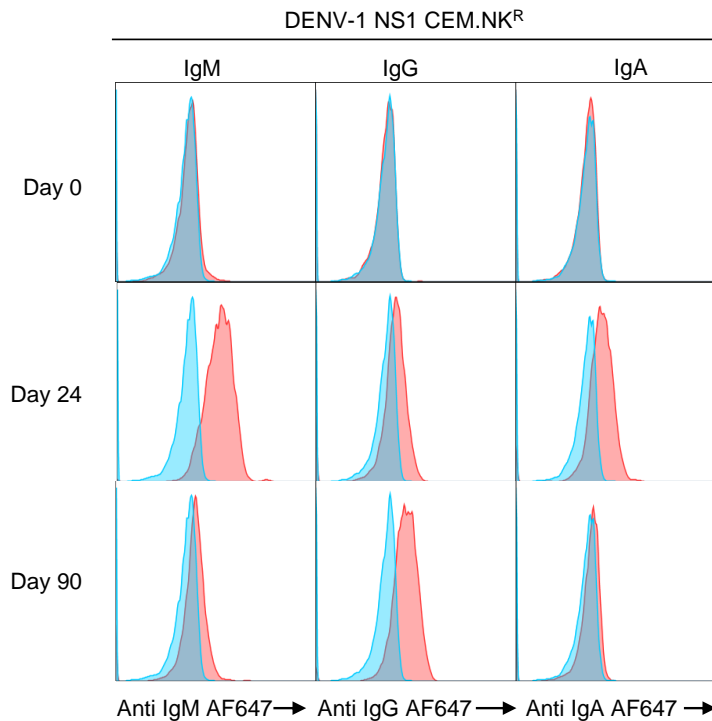
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GADVQNTTFIIDGPNTPECPDNQRAWNIWEVEDYGFGIPTTNIWLKLRDSYTVQCDHRLMSAAIKDSKAVHADMGY
WIESEKNETWKLARASFIEVKTCIWPKSHTLWSNGVLESEMIIPKRYGGPISQHNYPGYFTQTAGPWHLGKLELD
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GSGEVDSFSLGLLCISIMIEEVMRSRWSRKMLMTGTLAVFLLLTMGQLTWNDLIRLCIMVGANASDKMGMTTYLA
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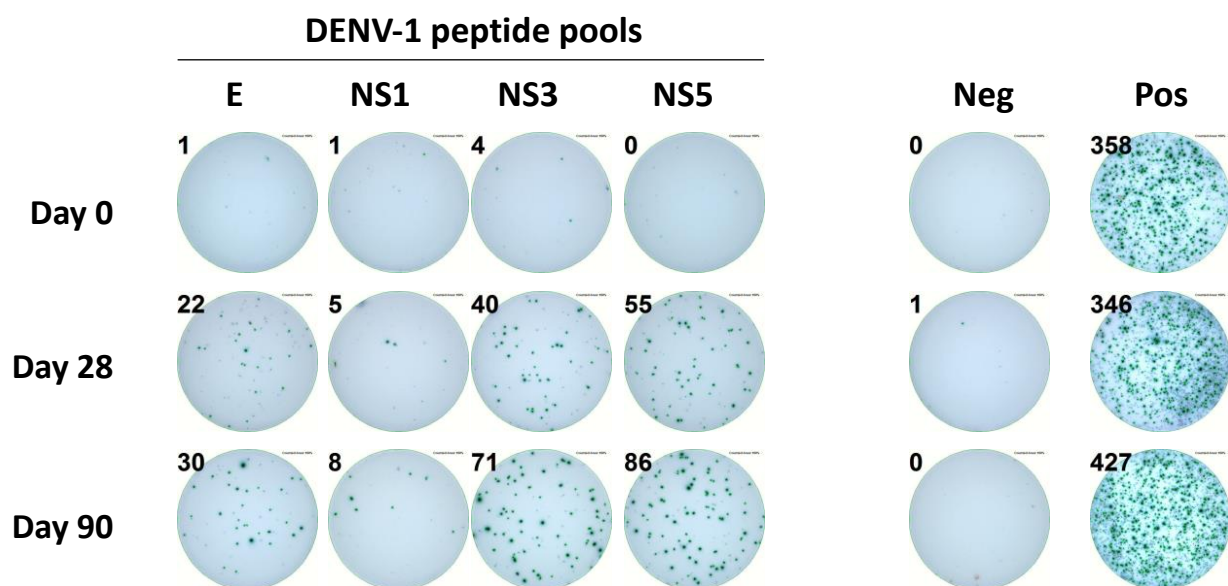
B)



C)



**Fig. S3. NS1 opsonization assay. A) Sequence and annotation of the DENV-1 NS1 expression construct used in this study. Yellow = signal peptide, green = NS1, blue = NS2A. Sequence derived from WestPac74 (U88535.1) B) Anti-NS1 staining mAb staining (clone FE8) of parental CEM.NKR cell line and DENV-1 NS1 expressing CEM.NKR cells. Unstained cells shown in blue, FE8 stained shown in red C) Representative NS1 opsonizing activity of serum collected at days 0, 24, and 90 days post DENV-1 challenge. Unstained cells shown in blue, serum stained shown in red**



**Fig. S4. Representative IFN-g ELISPOT assay images**

**Table S1. Study participants demographics**

	All Participants (N=9)
Age (years)	
Mean (SD)	34.6 (8.8)
Median	33.0
Min, Max	20, 45
Sex, n (%)	
Male	3 (33.3)
Female	6 (66.7)
Ethnicity, n (%)	
Hispanic or Latino	3 (33.3)
Non-Hispanic or Latino	6 (66.7)
Race, n (%)	
White	7 (77.8)
Black or African American	1 (11.1)
American Indian or Alaska Native	0 (0.0)
Asian	0 (0.0)
Native Hawaiian or Other Pacific Islander	0 (0.0)
Other or Multiple [1]	1 (11.1)

**Table S2. Summary of solicited Systemic Adverse Events reported within 28 days after inoculation or 7 days post hospitalization (whichever later)**

	Any	Mild/Moderate	Severe
Headache	9/9 (100%)	8/9 (88.8%)	1/9 (11.1%)
Rash	9/9 (100%)	5/9 (55.5%)	4/9 (44.4%)
Fever	7/9 (77.7%)	6/9 (66.6%)	1/9 (11.1%)
Eye pain	7/9 (77.7%)	6/9 (66.6%)	1/9 (11.1%)
Weakness/Fatigue	6/9 (66.6%)	3/9 (33.3%)	3/9 (33.3%)
Myalgia	7/9 (77.7%)	7/9 (77.7%)	0/9 (0%)

**Table S3. Summary of Lab Abnormalities**

Number of subjects experiencing at least one		Maximum intensity	All Subjects (N=9) n/M(%)
Lab abnormality			8/9(88.9)
		Mild	2/9(22.2)
		Moderate	3/9(33.3)
		Severe	2/9(22.2)
		Potentially life-threatening	1/9(11.1)
Blood and lymphatic system disorders			6/9(66.7)
		Moderate	5/9(55.6)
		Severe	1/9(11.1)
	Leukopenia		6/9(66.7)
		Mild	2/9(22.2)
		Moderate	4/9(44.4)
	Lymphopenia		3/9(33.3)
		Mild	2/9(22.2)
		Severe	1/9(11.1)
	Neutropenia		2/9(22.2)
		Moderate	2/9(22.2)
	Thrombocytopenia		1/9(11.1)
		Mild	1/9(11.1)
Investigations			8/9(88.9)
		Mild	4/9(44.4)
		Moderate	2/9(22.2)
		Severe	2/9(22.2)
	Activated partial thromboplastin time		1/9(11.1)
		Mild	1/9(11.1)
	Alanine aminotransferase increased		1/9(11.1)
		Mild	1/9(11.1)
	Aspartate aminotransferase increased		3/9(33.3)
		Mild	3/9(33.3)
	Blood alkaline phosphatase increased		1/9(11.1)
		Mild	1/9(11.1)
	Blood calcium increased		1/9(11.1)
		Mild	1/9(11.1)

Number of subjects experiencing at least one		Maximum intensity	All Subjects (N=9) n/M(%)
	Blood sodium decreased		1/9(11.1)
		Mild	1/9(11.1)
	Eosinophil count increased		1/9(11.1)
		Mild	1/9(11.1)
	Hemoglobin decreased		3/9(33.3)
		Mild	2/9(22.2)
		Moderate	1/9(11.1)
	Lymphocyte count decreased		4/9(44.4)
		Mild	2/9(22.2)
		Moderate	2/9(22.2)
	Neutrophil count decreased		4/9(44.4)
		Moderate	2/9(22.2)
		Severe	2/9(22.2)
	Platelet count decreased		3/9(33.3)
		Mild	2/9(22.2)
		Moderate	1/9(11.1)
	Protein total decreased		1/9(11.1)
		Mild	1/9(11.1)
	White blood cell count increased		2/9(22.2)
		Mild	2/9(22.2)
Metabolism and nutrition disorders			6/9(66.7)
		Mild	4/9(44.4)
		Moderate	1/9(11.1)
		Potentially life-threatening	1/9(11.1)
	Hypocalcemia		3/9(33.3)
		Mild	3/9(33.3)
	Hypoglycemia		2/9(22.2)
		Moderate	1/9(11.1)
		Potentially life-threatening	1/9(11.1)
	Hyponatremia		1/9(11.1)
		Mild	1/9(11.1)
	Hypoproteinemia		1/9(11.1)
		Mild	1/9(11.1)



**Table S4. Peptides used in IFN- $\gamma$  ELISPOT assay**

<b>Virus</b>	<b>Antigen</b>	<b>Supplier</b>	<b>Catalog #</b>
DENV-1: Singapore/S275/1990	E	BEI	NR-50710
DENV-1: Singapore/S275/1990	NS1	BEI	NR-2751
DENV-1: Singapore/S275/1990	NS3	BEI	NR-2752
DENV-1: Singapore/S275/1990	NS5	BEI	NR-4203

**Table S5: Day 10 upregulated DEGs**

<b>geneID</b>	<b>logFC</b>	<b>AveExpr</b>	<b>t</b>	<b>P.Value</b>	<b>adj.P.Val</b>	<b>B</b>
SIGLEC1	5.28933912	4.9170254	5.57008222	1.45E-06	4.88E-04	5.14181002
RSAD2	5.12713098	7.45523814	6.23112006	1.55E-07	1.86E-04	7.2244684
USP41	4.97810235	-0.3332919	4.14262612	1.54E-04	0.00761562	-0.0357048
IFI44L	4.89630162	7.86949929	6.51809444	5.87E-08	1.86E-04	8.11704845
USP18	4.78795711	4.06786798	4.97795746	1.04E-05	0.0015773	3.33039413
IFIT1	4.7806291	7.96079753	6.14184276	2.10E-07	1.88E-04	6.92851822
OAS3	4.35410419	8.45525895	6.18809519	1.80E-07	1.86E-04	7.06295287
CMPK2	4.34211562	6.30431638	6.15942995	1.98E-07	1.86E-04	7.03550612
SERPING1	4.33547355	5.10853182	6.01475457	3.23E-07	2.18E-04	6.56095313
IFI6	4.28717795	7.30993194	6.38353384	9.26E-08	1.86E-04	7.72871153
IFI44	4.24332021	6.48312526	6.17478727	1.88E-07	1.86E-04	7.08596531
IFIT3	4.24240159	8.51353137	6.18170763	1.83E-07	1.86E-04	7.03131762
OASL	4.13383203	6.65230664	6.06557972	2.72E-07	2.18E-04	6.74205204
EXOC3L1	4.08517533	1.57737062	4.32232158	8.71E-05	0.00563067	1.27047967
IFIT2	3.95768905	8.9735811	5.7238075	8.62E-07	3.84E-04	5.58321496
IFITM3	3.94580746	8.11792354	6.02510258	3.12E-07	2.18E-04	6.58410934
BATF2	3.93186641	4.5098331	5.21608921	4.73E-06	9.00E-04	4.07268239
HERC5	3.92934358	6.79190049	5.85009111	5.63E-07	3.02E-04	6.0617348
ATF3	3.91736562	2.14500789	4.19364889	1.31E-04	0.00705385	0.98340754
LAMP3	3.82469431	3.64792721	4.49226025	5.06E-05	0.0041574	1.88794784
ETV7	3.77868209	3.95378733	4.68829819	2.69E-05	0.00280203	2.46821467
OAS1	3.66964493	7.42875753	6.19344668	1.76E-07	1.86E-04	7.14092201
SPATS2L	3.60105974	5.24305999	5.20918701	4.83E-06	9.00E-04	4.05441889
MT2A	3.58791401	5.30056281	5.48705511	1.91E-06	5.53E-04	4.92239718
MX1	3.54868417	8.62072361	6.18756549	1.80E-07	1.86E-04	7.05207278
RP11-466G12.3	3.52138707	-0.420473	4.28550866	9.79E-05	0.00603748	0.65618487
RP4-641G12.3	3.49335065	0.00407114	4.71167228	2.49E-05	0.00270876	1.79151158
EPSTI1	3.40483944	6.79024856	6.86913068	1.79E-08	1.86E-04	9.29866305
CARD17	3.38974587	-0.4710274	4.69348239	2.64E-05	0.00277627	1.33701578
ZDHHC4P1	3.29123309	3.19294297	5.85414972	5.55E-07	3.02E-04	5.95634128
LY6E	3.29096159	8.27192948	6.04107531	2.95E-07	2.18E-04	6.64022358
FBXO39	3.11623692	1.19699362	5.48977715	1.89E-06	5.53E-04	4.27831017
OAS2	3.08162882	8.04770319	6.00227119	3.37E-07	2.18E-04	6.52288643
SMTNL1	2.90961277	4.80724124	5.32190721	3.32E-06	7.35E-04	4.40540173
RMI2	2.87018557	2.72868882	4.22400741	1.19E-04	0.00670342	1.11489591
ILIRN	2.86942241	7.29093357	4.66917458	2.86E-05	0.00288994	2.40043803
EIF2AK2	2.86661196	8.23836112	6.22919419	1.56E-07	1.86E-04	7.21898947
RTP4	2.86068258	4.69971644	5.41031669	2.47E-06	6.28E-04	4.68217208
LAP3	2.8578458	6.47855507	6.31916147	1.15E-07	1.86E-04	7.56553814
DHX58	2.84179357	5.59355218	5.37611892	2.77E-06	6.82E-04	4.57295317

IFI35	2.79696682	5.86924027	5.79975403	6.67E-07	3.30E-04	5.91350511
IFIH1	2.79295036	4.64938461	5.36988461	2.83E-06	6.82E-04	4.55541731
PLSCR2	2.79206355	2.74175719	5.44173739	2.22E-06	6.00E-04	4.71050799
PLSCR1	2.78667279	7.14933055	5.86936561	5.27E-07	3.02E-04	6.12773211
DDX60	2.77741734	6.84319897	6.69896506	3.18E-08	1.86E-04	8.76843931
TMPRSS2	2.76277301	-1.6361692	3.96963617	2.63E-04	0.0099939	-0.7484047
C1QB	2.75879546	1.04818111	4.5326293	4.45E-05	0.00383522	1.66260605
IRF7	2.74916201	7.13751945	5.70257159	9.26E-07	3.87E-04	5.6019334
DDX58	2.72662342	8.17224372	5.7090694	9.06E-07	3.87E-04	5.5980808
TNFAIP6	2.7110423	5.01580247	4.22364232	1.19E-04	0.00670342	1.05002071
GBP1	2.67649798	7.7556123	6.25580794	1.43E-07	1.86E-04	7.33849815
SAMD9L	2.67405473	8.53431501	6.19817362	1.73E-07	1.86E-04	7.10325287
ANKRD22	2.6621509	3.81398993	4.71365797	2.47E-05	0.00270876	2.54367511
IFIT5	2.65846346	6.76290143	5.73934207	8.18E-07	3.84E-04	5.72028608
AC007919.18	2.59468385	1.11313906	4.34630963	8.07E-05	0.00542228	1.32104624
UBE2L6	2.57609111	7.70048281	6.24474398	1.48E-07	1.86E-04	7.3017434
LIPA	2.57040806	6.30864899	6.17654797	1.87E-07	1.86E-04	7.11402157
PNPT1	2.56839029	5.45939854	5.4402196	2.24E-06	6.00E-04	4.77387191
RUFY4	2.56798385	2.08182909	4.1809425	1.36E-04	0.00708214	0.96546791
OR52M2P	2.56266818	-0.6309252	4.4075146	6.64E-05	0.00484142	0.78131702
LLpac-136A2.1	2.558184	-0.9240924	4.49301703	5.05E-05	0.0041574	1.06079828
AC007899.3	2.55502032	1.8636924	4.76276373	2.11E-05	0.0024314	2.60263196
TREX1	2.52256094	4.97323551	5.27924989	3.83E-06	7.92E-04	4.26900792
XAF1	2.51056562	8.38015327	6.48873778	6.49E-08	1.86E-04	8.02805586
TNFSF13B	2.51044741	7.09149607	5.07681897	7.50E-06	0.00122672	3.64248391
PARP14	2.49209437	9.57426596	6.00365384	3.35E-07	2.18E-04	6.4252801
TRIM6	2.48970255	2.6111843	5.42851012	2.32E-06	6.07E-04	4.66093925
AC003080.4	2.48752958	0.5368816	4.17916776	1.37E-04	0.00708214	0.76640666
FRMD3	2.48321788	4.33959254	4.62282128	3.32E-05	0.00318747	2.26094863
C1QC	2.45746823	0.24040917	4.16529332	1.43E-04	0.00726978	0.54163624
ZBP1	2.44186533	7.24901157	5.55903188	1.50E-06	4.88E-04	5.14871718
HERC6	2.43853919	6.1327843	5.86156199	5.42E-07	3.02E-04	6.11083487
SCO2	2.43733028	3.41575559	5.2131069	4.77E-06	9.00E-04	4.05485603
CD274	2.39357619	5.11770943	4.39045207	7.02E-05	0.00501851	1.53686814
RP11-820K3.2	2.3832536	1.44697259	4.48520469	5.18E-05	0.00421344	1.77202663
GBP4	2.36426952	7.58162532	5.55794533	1.51E-06	4.88E-04	5.14464536
TNFSF10	2.34513832	8.55380545	5.13142533	6.26E-06	0.00110015	3.80580503
PARP9	2.32844771	8.40541098	6.28634359	1.29E-07	1.86E-04	7.39561422
ACO1	2.31954731	7.13833425	5.45890697	2.10E-06	5.81E-04	4.8346327
TFEC	2.29603777	5.89552158	4.38625234	7.11E-05	0.00504463	1.51680605
TCN2	2.29510324	2.79259981	4.07342925	1.91E-04	0.00845425	0.69172565
SAMD4A	2.28626494	4.46504118	4.85439448	1.56E-05	0.00201151	2.95694848
RNA5SP39	2.28149067	1.07322946	4.01598103	2.28E-04	0.00925247	0.46867615
HELZ2	2.27785449	7.78274997	5.15008094	5.88E-06	0.00104384	3.87181563
AC074338.4	2.27066556	2.09771067	4.86550906	1.51E-05	0.00197997	2.94902764
RPL37P6	2.2608075	0.43198787	4.84870165	1.59E-05	0.0020215	2.36584541
STAT2	2.23860855	7.65709432	5.59106506	1.35E-06	4.78E-04	5.24702284
BST2	2.23841456	5.994799	5.64578523	1.12E-06	4.05E-04	5.4240373
STAT1	2.22743235	8.03222344	6.81241515	2.17E-08	1.86E-04	9.07584338
FBXO6	2.21469778	4.61604365	5.54829488	1.56E-06	4.96E-04	5.11614319
PML	2.20323024	7.91716837	5.64770958	1.11E-06	4.05E-04	5.41802096
C1QA	2.17987978	1.94303161	5.17782772	5.37E-06	9.80E-04	3.75029915
TDRD7	2.16817935	5.96333466	5.72681862	8.53E-07	3.84E-04	5.68172493
DDX60L	2.1641171	8.70357217	5.51104539	1.76E-06	5.43E-04	4.96787376
TTC26	2.13263162	3.36703253	4.5043839	4.87E-05	0.00405157	1.91924751
PARP12	2.12281677	7.23577109	5.6699239	1.03E-06	4.05E-04	5.49908191
NUDT19P5	2.11773239	-0.4214855	4.87649394	1.45E-05	0.00197659	1.97291785

AIM2	2.10535452	4.53893729	5.3577762	2.95E-06	6.89E-04	4.51681509
MTND4P26	2.09894625	1.56855523	4.41214469	6.55E-05	0.00479797	1.60028611
TOR1B	2.0858713	6.17430835	5.16725915	5.56E-06	9.95E-04	3.91357441
TTC21A	2.07430352	4.29185633	4.36766321	7.54E-05	0.00515801	1.48063394
ZCCHC2	2.072024	7.79786636	5.7182061	8.78E-07	3.84E-04	5.64252896
KIAA1958	2.06820903	4.8600693	4.82518502	1.72E-05	0.00211912	2.85497093
TRIM22	2.06430117	9.02455307	5.80842956	6.48E-07	3.29E-04	5.87180208
MS4A4A	2.06027982	2.69171556	4.85436158	1.56E-05	0.00201151	2.95676503
EPHB2	2.0596664	2.89674599	5.06652006	7.76E-06	0.00124757	3.59107029
SAMD9	2.03594466	8.32363289	4.31590608	8.89E-05	0.00566862	1.36751633
LGALS9	2.03326241	7.61471601	5.28604893	3.74E-06	7.92E-04	4.29358823
CCR1	2.03289549	7.57595165	4.71383975	2.47E-05	0.00270876	2.5342753
XXbac-BPG541D20.6	2.0174689	-0.1495043	4.76601447	2.09E-05	0.00242058	2.00609701

**Table S6: Day 10 downregulated DEGs**

geneID	logFC	AveExpr	t	P.Value	adj.P.Val	B
ADAMTS5	-2.5713877	-0.0678239	-4.2878975	9.72E-05	0.00603152	0.86656164
CXCL6	-2.0613406	-0.6719037	-4.2141531	1.23E-04	0.00676507	0.5176462

**Table S7: Day 14 upregulated DEGs**

geneID	logFC	AveExpr	t	P.Value	adj.P.Val	B
IFI27	7.93347021	4.73260463	6.341738	1.07E-07	4.27E-05	7.5798908
SIGLEC1	5.45400918	4.9170254	5.69134883	9.62E-07	1.56E-04	5.56889057
IFI44L	4.80809266	7.86949929	6.40070019	8.74E-08	4.01E-05	7.83929441
CXCL11	4.74554915	-1.799615	3.90327068	3.22E-04	0.00681958	-0.6997596
USP18	4.340308	4.06786798	4.52697666	4.53E-05	0.00175724	1.95715788
C1QC	4.21337769	0.24040917	7.62333764	1.42E-09	4.46E-06	10.3192292
SERPING1	4.2011929	5.10853182	5.82846665	6.06E-07	1.26E-04	6.00329553
RSAD2	4.14003508	7.45523814	5.3640527	2.88E-06	2.97E-04	4.51172107
PXT1	3.92190445	-0.6017883	3.95738208	2.73E-04	0.00606092	-0.0619256
C1QB	3.85243664	1.04818111	6.60362981	4.40E-08	2.67E-05	7.86615664
IFI44	3.83893165	6.48312526	5.69018305	9.65E-07	1.56E-04	5.5468332
NEURL3	3.71155614	-0.7379014	3.89810266	3.28E-04	0.00689636	-0.1366333
IFITM3	3.66232202	8.11792354	5.6663928	1.05E-06	1.65E-04	5.48526987
ATF3	3.64796173	2.14500789	3.89374333	3.32E-04	0.0069656	0.19599576
GBP1P1	3.62281344	2.29778179	5.03639548	8.58E-06	5.83E-04	3.51517375
KCTD14	3.62273191	-0.4284207	5.70427733	9.21E-07	1.56E-04	4.82134665
BATF2	3.59416766	4.5098331	4.77754478	2.01E-05	0.00106378	2.68675147
CDC25A	3.58666266	-0.4712332	4.48575326	5.17E-05	0.00193272	1.54067155
OAS3	3.58002207	8.45525895	5.35310664	2.99E-06	2.99E-04	4.49031733
CMPK2	3.54113036	6.30431638	5.23262184	4.47E-06	3.75E-04	4.0769934
LY6E	3.4745293	8.27192948	6.25290852	1.44E-07	5.21E-05	7.36538552
IFI6	3.42899215	7.30993194	5.38383309	2.70E-06	2.84E-04	4.56402743
FBXO39	3.42763138	1.19699362	6.14165384	2.10E-07	6.81E-05	6.57075929
ETV7	3.42189499	3.95378733	4.23683334	1.14E-04	0.00336633	1.07258835
CARD17	3.41525738	-0.4710274	4.76773145	2.07E-05	0.00108017	2.0629111
SPATS2L	3.40515225	5.24305999	4.93723177	1.19E-05	7.36E-04	3.15101832
OAS1	3.37912056	7.42875753	5.78209379	7.08E-07	1.34E-04	5.84596637
EPSTI1	3.34691563	6.79024856	6.73052023	2.86E-08	1.92E-05	8.91210078
HNRNPCP4	3.34193976	-2.3263868	4.13737686	1.56E-04	0.0041641	-0.1049377
IFIT1	3.29759912	7.96079753	4.68855623	2.68E-05	0.00126813	2.38961616
PBK	3.28709593	-1.3878625	5.15199892	5.85E-06	4.64E-04	2.9308033
MT2A	3.28352516	5.30056281	5.05332235	8.11E-06	5.67E-04	3.51374689
RMI2	3.27812218	2.72868882	4.91848449	1.27E-05	7.70E-04	3.16007102
LIF	3.22151501	-0.376349	4.33924292	8.26E-05	0.00268178	1.19308314

ANKRD22	3.20890316	3.81398993	5.73658967	8.26E-07	1.44E-04	5.7114729
IFIT3	3.20749187	8.51353137	5.00316486	9.57E-06	6.38E-04	3.3895502
HIST1H3G	3.20584982	3.29216642	6.09760875	2.44E-07	7.06E-05	6.8670601
HIST1H3C	3.20386106	2.45151343	5.42169592	2.38E-06	2.69E-04	4.71736987
RP4-641G12.3	3.17638213	0.00407114	4.26339543	1.05E-04	0.00318019	1.01365267
OASL	3.17530057	6.65230664	4.91288051	1.29E-05	7.74E-04	3.05844898
ZDHHC4P1	3.1599642	3.19294297	5.62013265	1.22E-06	1.81E-04	5.33676624
TMPRSS2	3.15885408	-1.6361692	4.68929343	2.68E-05	0.00126813	1.36984309
IGLV3-25	3.15557291	2.39379255	4.21099401	1.24E-04	0.00356262	1.03359306
IGLV3-1	3.14158154	3.31382776	4.62512564	3.30E-05	0.00143541	2.23506471
HIST1H2BM	3.0774712	1.84300985	5.54985098	1.55E-06	2.06E-04	5.0927266
CXCL9	3.02641038	-1.0610622	5.10144991	6.91E-06	5.22E-04	2.8215599
RUFY4	3.01924409	2.08182909	5.04843908	8.24E-06	5.72E-04	3.54287483
RRM2	2.99987922	2.90016402	5.27917218	3.83E-06	3.43E-04	4.25903124
NAT8	2.99563832	0.03652986	3.8592481	3.69E-04	0.0074414	0.04162973
HIST1H2AB	2.97167184	1.7752598	5.29866894	3.59E-06	3.32E-04	4.31915737
HIST1H2BO	2.95486391	3.25612525	7.460064	2.46E-09	4.62E-06	11.2114506
ANO5	2.9519081	-0.2939582	3.86882214	3.58E-04	0.00731429	-0.0676179
C1QA	2.92950279	1.94303161	7.25242186	4.93E-09	5.45E-06	10.263952
CDCA5	2.92737311	0.37438001	4.90432507	1.33E-05	7.86E-04	2.98669434
HIST1H3J	2.88517315	2.75115951	5.75240297	7.83E-07	1.44E-04	5.76319456
CDK1	2.85213247	0.60997238	4.98806735	1.01E-05	6.59E-04	3.25061427
NMRAL1P1	2.84927361	-1.0573799	5.25042851	4.21E-06	3.62E-04	3.41969183
SDC1	2.84626983	-1.9419671	3.77094498	4.82E-04	0.00883699	-0.5075626
E2F8	2.81706254	0.67739709	6.13297071	2.16E-07	6.89E-05	6.58332283
GBP1	2.80142465	7.7556123	6.45256126	7.33E-08	3.53E-05	8.01178897
IGLV3-21	2.79145015	3.10743434	4.16458389	1.43E-04	0.00392745	0.86439568
SMTNL1	2.78945799	4.80724124	5.09071078	7.17E-06	5.28E-04	3.62952385
OAS2	2.78100523	8.04770319	5.49332293	1.87E-06	0.00023297	4.92888067
RTP4	2.75688239	4.69971644	5.19953661	4.99E-06	4.10E-04	3.97563802
HMMR	2.75514391	0.38837942	5.2102837	4.82E-06	3.99E-04	3.86853945
HIST1H2AH	2.74593669	2.84712462	5.79223464	6.84E-07	1.31E-04	5.89011409
ELOVL3	2.74532657	-1.4171679	4.93821633	1.19E-05	7.36E-04	2.0831104
HIST1H3B	2.73439797	3.67190942	5.37937864	2.74E-06	2.86E-04	4.56053934
CDCA2	2.70995561	0.17140536	4.56272002	4.04E-05	0.00162129	2.01550843
IGLV6-57	2.70544753	1.24851897	5.09305269	7.11E-06	5.28E-04	3.65360665
HIST1H2AJ	2.68895199	3.13381681	5.00323027	9.57E-06	6.38E-04	3.39062359
HIST1H3F	2.66728673	2.9713132	5.27798958	3.84E-06	3.43E-04	4.25848239
CDC45	2.65694375	-0.5515261	3.93330133	2.94E-04	0.00635432	0.19530622
IGLC2	2.65576702	6.06964726	5.80951568	6.46E-07	1.29E-04	5.9195259
KIFC1	2.6512259	0.753573	4.56960938	3.95E-05	0.00159929	2.09018593
TCN2	2.6359242	2.79259981	4.77360945	2.03E-05	0.00107151	2.71327244
HIST1H2AL	2.63478516	2.87666973	5.80127195	6.64E-07	1.31E-04	5.91887865
DDX60	2.63160372	6.84319897	6.36235864	9.95E-08	4.16E-05	7.71588965
CEP55	2.62465002	0.24269623	4.49122592	5.08E-05	0.00191043	1.79725041
CENPA	2.62220982	-0.5000022	4.67130538	2.84E-05	0.0013116	2.05971841
LAP3	2.60636355	6.47855507	5.81354883	6.37E-07	1.29E-04	5.92928426
CCNB2	2.55281919	1.153791	5.17281437	5.46E-06	4.40E-04	3.87965304
ANXA10	2.55114597	-0.7950981	4.47423833	5.36E-05	0.00197026	1.3901627
IGHV5-51	2.52056322	2.23118049	3.98637889	2.50E-04	0.00566285	0.39277191
RPL37P6	2.50716098	0.43198787	5.48221105	1.94E-06	2.39E-04	4.4984345
SOCS1	2.48969411	3.20970579	3.73927734	5.31E-04	0.00925892	-0.3305986
HIST1H1B	2.48460985	4.67577083	5.08454689	7.31E-06	5.35E-04	3.59069491
IGLV8-61	2.48393278	0.92428013	3.96343543	2.68E-04	0.00600473	0.38820999
KIF4A	2.48250373	0.42739737	5.91421353	4.53E-07	1.05E-04	5.895672
MKI67	2.48119964	4.16898361	6.11135876	2.33E-07	7.06E-05	6.9054296
MX1	2.46365507	8.62072361	4.60071816	3.57E-05	0.00151829	2.14568607

SF3A3P2	2.44946737	-0.8549619	4.05696115	2.01E-04	0.00488035	0.24742754
HERC5	2.44786335	6.79190049	3.97596417	2.58E-04	0.00580581	0.19615984
FRMD3	2.43988735	4.33959254	4.53581959	4.40E-05	0.00172402	1.92180146
OR52M2P	2.42230052	-0.6309252	4.17685876	1.38E-04	0.00381462	0.64592261
IGLC1	2.4169643	4.89021051	4.66546751	2.89E-05	0.0013211	2.27118056
HIST2H3A	2.40927908	4.0064933	7.49847749	2.16E-09	4.51E-06	11.3801073
HIST2H3C	2.40927908	4.0064933	7.49847749	2.16E-09	4.51E-06	11.3801073
SCO2	2.4031521	3.41575559	5.15555476	5.78E-06	4.64E-04	3.87660083
PYCR1	2.39699261	-0.2487181	4.68348782	2.73E-05	0.00127843	2.1567944
TOP2A	2.39446444	2.21144413	5.05498626	8.06E-06	5.66E-04	3.5785904
MYBL2	2.38264305	3.54423285	6.40091402	8.73E-08	4.01E-05	7.84408517
IGKV2-28	2.37656221	2.10782537	4.06689602	1.95E-04	0.00480021	0.64360766
IGLV1-40	2.37181384	3.24791198	4.99299494	9.90E-06	6.53E-04	3.3604009
CXCR2P1	2.37114701	5.76999796	4.98088688	1.03E-05	6.73E-04	3.25297916
ASPM	2.36322039	2.54990206	5.97900808	3.64E-07	8.95E-05	6.4717111
IFIT2	2.36135241	8.9735811	3.79221646	4.52E-04	0.00850171	-0.2202673
DTL	2.35459427	1.77509196	5.45404192	2.13E-06	2.53E-04	4.79772738
IRF7	2.33647346	7.13751945	4.95194308	1.13E-05	7.17E-04	3.18148757
GBP4	2.32928409	7.58162532	5.44733441	2.18E-06	2.57E-04	4.77023735
HIST1H2BE	2.32485743	4.90197601	6.99492442	1.17E-08	1.00E-05	9.76920883
GBP5	2.29405186	8.80186475	5.75493002	7.76E-07	1.44E-04	5.77123863
HIST1H2BL	2.29154495	2.34535236	4.91319103	1.29E-05	7.74E-04	3.14018179
IGHV2-5	2.29138253	1.35632262	3.7513746	5.12E-04	0.00911483	-0.2018775
PDCD1LG2	2.27618761	1.33705307	5.46704388	2.04E-06	2.46E-04	4.77098672
BIRC5	2.26637619	1.33988256	5.1791195	5.34E-06	4.33E-04	3.92864161
RNASE1	2.26322099	-1.1156337	4.06399517	1.96E-04	0.0048164	0.28183219
IFI35	2.2533589	5.86924027	4.76502973	2.09E-05	0.00108277	2.57336139
NUSAP1	2.24772526	1.53053638	5.93417832	4.24E-07	9.96E-05	6.26675065
E2F1	2.23690526	2.14998264	6.48292796	6.61E-08	3.36E-05	8.04682839
TPX2	2.23638835	2.37656719	6.50932828	6.05E-08	3.25E-05	8.14986064
IGLV2-23	2.23109637	2.42257639	4.53240663	4.45E-05	0.00173585	1.9882958
IGLV2-8	2.22419485	2.72432305	4.30350599	9.25E-05	0.00290232	1.2753145
JCHAIN	2.21378639	6.67502835	4.56451743	4.01E-05	0.00161536	1.9884861
IGLV1-47	2.19944459	2.85653458	4.67781737	2.78E-05	0.00129048	2.4030072
XAF1	2.19179007	8.38015327	5.75195803	7.84E-07	1.44E-04	5.75923638
UBE2L6	2.18142464	7.70048281	5.39220281	2.63E-06	2.82E-04	4.59484
MCM10	2.17980912	1.90780566	5.65080497	1.10E-06	1.68E-04	5.42407355
MZB1	2.16448141	3.88358825	5.04184142	8.42E-06	5.78E-04	3.47682208
FBXO6	2.15631868	4.61604365	5.38798528	2.66E-06	2.83E-04	4.56970551
HIST1H2BI	2.15527456	3.40077437	5.25744822	4.12E-06	3.57E-04	4.17632757
IGLV1-51	2.15238909	3.04547045	3.89832205	3.27E-04	0.00689636	0.08069319
FAM72B	2.15158872	0.38083027	4.71775433	2.44E-05	0.00119523	2.38522852
IGKV1D-16	2.14357533	-1.5853255	4.16033336	1.45E-04	0.0039594	0.50064004
TYMS	2.13716394	2.20858967	5.30215444	3.55E-06	3.30E-04	4.34331106
AURKB	2.12675021	1.51096515	4.20416008	1.27E-04	0.00360699	1.05964053
PLSCR1	2.09710507	7.14933055	4.58688566	3.73E-05	0.00156202	2.04201501
EIF2AK2	2.09095881	8.23836112	4.75386743	2.17E-05	0.00109972	2.60240754
ANLN	2.08714183	1.96538302	7.00937931	1.12E-08	1.00E-05	9.5900875
STAT1	2.0851279	8.03222344	6.3906954	9.04E-08	4.05E-05	7.81200281
IGLV1-44	2.06923126	2.87436205	4.85862158	1.54E-05	8.70E-04	2.95966966
MT1E	2.06090682	0.86445192	4.72701158	2.37E-05	0.00116592	2.54088305
BUB1	2.05225794	2.31935214	8.6093627	5.54E-11	5.21E-07	14.6366238
NCAPG	2.03992264	2.20751672	6.36554892	9.84E-08	4.16E-05	7.69128653
IGHV4-39	2.02443772	1.79957613	4.36429848	7.63E-05	0.00253311	1.50861276
TMEM51	2.01862189	0.50255538	4.39776028	6.85E-05	0.00235149	1.53747578
GPR84	2.01809105	0.95403193	4.69483655	2.63E-05	0.0012583	2.43473106
MYOF	2.01584467	4.76808245	4.7990805	1.87E-05	0.00100277	2.69220592

HERC6	2.00908938	6.1327843	4.90685962	1.31E-05	7.86E-04	3.01214841
DHX58	2.00378908	5.59355218	3.89158561	3.34E-04	0.00697906	-0.0585073
SAMD4A	2.00215697	4.46504118	4.23424064	1.15E-04	0.00338337	0.99344984

**Table S8: Day 14 downregulated DEGs**

geneID	logFC	AveExpr	t	P.Value	adj.P.Val	B
ADAMTS5	-4.2703246	-0.0678239	-5.2398812	4.37E-06	3.68E-04	2.96553106
PHF24	-4.1281247	-0.4204843	-4.5273428	4.52E-05	0.00175724	1.07075856
RBM17P1	-3.6292412	0.45420766	-3.7529218	5.09E-04	0.00910743	-0.3592191
MTCYBP11	-3.1386321	0.41697961	-3.7791348	4.70E-04	0.00869732	-0.2378834
ENTPD2	-3.0014965	-1.0204361	-5.2609943	4.07E-06	3.56E-04	2.73274732
RP11-435F17.3	-2.8793972	0.17552539	-5.3132781	3.42E-06	3.21E-04	3.54846843
OTX1	-2.7834091	1.30226967	-5.3924835	2.62E-06	2.82E-04	4.33858156
ALPL	-2.7713125	6.55037767	-3.8102068	4.28E-04	0.00821479	-0.2659793
RSPH14	-2.7554649	-0.178196	-4.0774696	1.88E-04	0.00472545	0.41765881
SCRT2	-2.6695547	3.08530385	-7.3037573	4.15E-09	5.45E-06	10.5645698
TGM3	-2.6673512	1.30725345	-3.7247771	5.54E-04	0.00948169	-0.2547174
FABP6	-2.6555066	-0.0053424	-3.8588684	3.69E-04	0.0074414	-0.1282192
TSPEAR	-2.6398871	0.73919599	-4.4436994	5.92E-05	0.00211914	1.48180339
CXCL6	-2.4311896	-0.6719037	-4.6829926	2.73E-05	0.00127843	1.93745131
RAB36	-2.3856861	3.16647113	-5.9520915	3.99E-07	9.62E-05	6.3853719
RP4-673D20.4	-2.3473481	-1.1834619	-4.4931758	5.05E-05	0.0019023	0.99557874
AGMO	-2.336297	1.01712184	-4.1931112	1.31E-04	0.00366963	0.96538114
PDZD3	-2.3339129	0.19178061	-5.3585221	2.94E-06	2.97E-04	3.94552835
RP11-34P1.2	-2.2909288	-0.8387437	-5.0517082	8.15E-06	5.68E-04	2.40091969
SDC2	-2.2333407	0.18924219	-4.0618828	1.98E-04	0.00482498	0.50261328
THBD	-2.2104509	4.35362418	-6.4547159	7.28E-08	3.53E-05	8.01732434
CNTNAP3B	-2.1842551	4.25065745	-3.7345248	5.38E-04	0.00931394	-0.4111129
CNTNAP3	-2.14251	4.98229345	-4.0936799	1.79E-04	0.00457207	0.57497861
INHBB	-2.1030845	-0.7925172	-4.3931222	6.96E-05	0.00237789	0.9837876
ARHGEF40	-2.0702104	6.61822907	-6.620432	4.15E-08	2.67E-05	8.55084276
ANGPT1	-2.0062407	1.99811146	-4.444016	5.91E-05	0.00211914	1.74593849

**Table S9: GO term enrichment, day 10 post infection**

p_value	term_id	source	term_name
4.22E-18	GO:0009615	GO:BP	response to virus
2.09E-17	GO:0140546	GO:BP	defense response to symbiont
2.09E-17	GO:0051607	GO:BP	defense response to virus
1.86E-16	GO:0044419	GO:BP	biological process involved in interspecies interaction between organisms
5.66E-16	GO:0009607	GO:BP	response to biotic stimulus
3.20E-15	GO:0051707	GO:BP	response to other organism
3.20E-15	GO:0019058	GO:BP	viral life cycle
3.20E-15	GO:0019079	GO:BP	viral genome replication
3.20E-15	GO:0043207	GO:BP	response to external biotic stimulus
3.84E-14	GO:0098542	GO:BP	defense response to other organism
1.45E-13	GO:0045087	GO:BP	innate immune response
1.45E-13	GO:0016032	GO:BP	viral process
1.45E-13	GO:0045071	GO:BP	negative regulation of viral genome replication
2.01E-13	GO:1903900	GO:BP	regulation of viral life cycle
2.01E-13	GO:0048525	GO:BP	negative regulation of viral process
4.42E-13	GO:0006952	GO:BP	defense response
5.24E-13	GO:0034340	GO:BP	response to type I interferon

7.63E-13	GO:0050792	GO:BP	regulation of viral process
1.16E-12	GO:0009605	GO:BP	response to external stimulus
2.58E-12	GO:0034097	GO:BP	response to cytokine
3.77E-12	GO:0006955	GO:BP	immune response
4.38E-12	GO:0045069	GO:BP	regulation of viral genome replication
6.35E-12	GO:0071345	GO:BP	cellular response to cytokine stimulus
1.38E-11	GO:0071357	GO:BP	cellular response to type I interferon
3.92E-10	GO:0019221	GO:BP	cytokine-mediated signaling pathway
8.82E-10	GO:0060337	GO:BP	type I interferon signaling pathway
8.82E-10	GO:0002376	GO:BP	immune system process
1.47E-08	GO:0006950	GO:BP	response to stress
2.14E-08	GO:0070106	GO:BP	interleukin-27-mediated signaling pathway
2.75E-08	GO:0035455	GO:BP	response to interferon-alpha
3.99E-08	GO:0060700	GO:BP	regulation of ribonuclease activity
9.94E-07	GO:0140374	GO:BP	antiviral innate immune response
1.34E-06	GO:0071310	GO:BP	cellular response to organic substance
1.64E-06	GO:0010033	GO:BP	response to organic substance
1.64E-06	GO:0070887	GO:BP	cellular response to chemical stimulus
1.87E-06	GO:0060339	GO:BP	negative regulation of type I interferon-mediated signaling pathway
2.81E-06	GO:0032069	GO:BP	regulation of nuclease activity
8.65E-06	GO:0045824	GO:BP	negative regulation of innate immune response
1.22E-05	GO:0002831	GO:BP	regulation of response to biotic stimulus
1.32E-05	GO:0007166	GO:BP	cell surface receptor signaling pathway
1.49E-05	GO:0098586	GO:BP	cellular response to virus
2.12E-05	GO:0060338	GO:BP	regulation of type I interferon-mediated signaling pathway
3.16E-05	GO:0042221	GO:BP	response to chemical
3.88E-05	GO:0032728	GO:BP	positive regulation of interferon-beta production
3.95E-05	GO:0050896	GO:BP	response to stimulus
3.95E-05	GO:0032101	GO:BP	regulation of response to external stimulus
4.43E-05	GO:0035457	GO:BP	cellular response to interferon-alpha
5.85E-05	GO:0002832	GO:BP	negative regulation of response to biotic stimulus
1.30E-04	GO:0032648	GO:BP	regulation of interferon-beta production
1.30E-04	GO:0032608	GO:BP	interferon-beta production
1.47E-04	GO:0032481	GO:BP	positive regulation of type I interferon production
1.87E-04	GO:0048247	GO:BP	lymphocyte chemotaxis
2.48E-04	GO:0032102	GO:BP	negative regulation of response to external stimulus
2.80E-04	GO:0071659	GO:BP	negative regulation of IP-10 production
3.04E-04	GO:0009617	GO:BP	response to bacterium
3.13E-04	GO:0001960	GO:BP	negative regulation of cytokine-mediated signaling pathway
3.70E-04	GO:0048519	GO:BP	negative regulation of biological process
3.73E-04	GO:0060761	GO:BP	negative regulation of response to cytokine stimulus
4.15E-04	GO:0044403	GO:BP	biological process involved in symbiotic interaction
4.86E-04	GO:0071612	GO:BP	IP-10 production
4.86E-04	GO:2000342	GO:BP	negative regulation of chemokine (C-X-C motif) ligand 2 production
4.86E-04	GO:0071658	GO:BP	regulation of IP-10 production
5.57E-04	GO:0070098	GO:BP	chemokine-mediated signaling pathway
5.94E-04	GO:0050777	GO:BP	negative regulation of immune response
7.60E-04	GO:1990869	GO:BP	cellular response to chemokine
7.60E-04	GO:1990868	GO:BP	response to chemokine
7.60E-04	GO:0032606	GO:BP	type I interferon production
7.60E-04	GO:0032479	GO:BP	regulation of type I interferon production
0.00108886	GO:0030593	GO:BP	neutrophil chemotaxis
0.00108886	GO:0032020	GO:BP	ISG15-protein conjugation
0.00162984	GO:0072676	GO:BP	lymphocyte migration
0.00168113	GO:0031348	GO:BP	negative regulation of defense response
0.00176183	GO:0045088	GO:BP	regulation of innate immune response
0.0018814	GO:0051336	GO:BP	regulation of hydrolase activity

0.00215004	GO:0071621	GO:BP	granulocyte chemotaxis
0.00215004	GO:1990266	GO:BP	neutrophil migration
0.00271697	GO:0002683	GO:BP	negative regulation of immune system process
0.00296841	GO:0031347	GO:BP	regulation of defense response
0.00324332	GO:0001959	GO:BP	regulation of cytokine-mediated signaling pathway
0.00406204	GO:0012501	GO:BP	programmed cell death
0.00413264	GO:0060759	GO:BP	regulation of response to cytokine stimulus
0.00413264	GO:0097530	GO:BP	granulocyte migration
0.00500161	GO:0072678	GO:BP	T cell migration
0.00500161	GO:0002548	GO:BP	monocyte chemotaxis
0.0053133	GO:0071639	GO:BP	positive regulation of monocyte chemotactic protein-1 production
0.00571107	GO:0002221	GO:BP	pattern recognition receptor signaling pathway
0.00578837	GO:0002682	GO:BP	regulation of immune system process
0.00667471	GO:2000341	GO:BP	regulation of chemokine (C-X-C motif) ligand 2 production
0.00667471	GO:0072567	GO:BP	chemokine (C-X-C motif) ligand 2 production
0.00689766	GO:0051701	GO:BP	biological process involved in interaction with host
0.00715039	GO:0008219	GO:BP	cell death
0.00890189	GO:0071674	GO:BP	mononuclear cell migration
0.00897138	GO:0044827	GO:BP	modulation by host of viral genome replication
0.00897138	GO:0048245	GO:BP	eosinophil chemotaxis
0.00974818	GO:0071605	GO:BP	monocyte chemotactic protein-1 production
0.00974818	GO:0071637	GO:BP	regulation of monocyte chemotactic protein-1 production
0.00979237	GO:0051603	GO:BP	proteolysis involved in cellular protein catabolic process
0.01005662	GO:0071222	GO:BP	cellular response to lipopolysaccharide
0.01055134	GO:0006915	GO:BP	apoptotic process
0.01134889	GO:0046597	GO:BP	negative regulation of viral entry into host cell
0.01143386	GO:0071219	GO:BP	cellular response to molecule of bacterial origin
0.01205243	GO:0032682	GO:BP	negative regulation of chemokine production
0.01205243	GO:0072677	GO:BP	eosinophil migration
0.0120721	GO:0051716	GO:BP	cellular response to stimulus
0.0125326	GO:0032760	GO:BP	positive regulation of tumor necrosis factor production
0.01275983	GO:0042730	GO:BP	fibrinolysis
0.01297577	GO:0097529	GO:BP	myeloid leukocyte migration
0.01320038	GO:0044257	GO:BP	cellular protein catabolic process
0.01353707	GO:1903557	GO:BP	positive regulation of tumor necrosis factor superfamily cytokine production
0.0141843	GO:1903901	GO:BP	negative regulation of viral life cycle
0.0141843	GO:1901623	GO:BP	regulation of lymphocyte chemotaxis
0.0141843	GO:0030595	GO:BP	leukocyte chemotaxis
0.01602646	GO:0010818	GO:BP	T cell chemotaxis
0.01602646	GO:0071216	GO:BP	cellular response to biotic stimulus
0.01602646	GO:0039529	GO:BP	RIG-I signaling pathway
0.01604252	GO:0050790	GO:BP	regulation of catalytic activity
0.01605956	GO:0006816	GO:BP	calcium ion transport
0.01678783	GO:0065009	GO:BP	regulation of molecular function
0.01730814	GO:0042981	GO:BP	regulation of apoptotic process
0.0173304	GO:0044265	GO:BP	cellular macromolecule catabolic process
0.018363	GO:0050776	GO:BP	regulation of immune response
0.018363	GO:0044788	GO:BP	modulation by host of viral process
0.018363	GO:0035456	GO:BP	response to interferon-beta
0.01888328	GO:0051928	GO:BP	positive regulation of calcium ion transport
0.01888328	GO:0043067	GO:BP	regulation of programmed cell death
0.01972848	GO:0048583	GO:BP	regulation of response to stimulus
0.01972848	GO:1902362	GO:BP	melanocyte apoptotic process
0.01972848	GO:0075512	GO:BP	clathrin-dependent endocytosis of virus by host cell
0.01972848	GO:0035394	GO:BP	regulation of chemokine (C-X-C motif) ligand 9 production
0.01972848	GO:0035393	GO:BP	chemokine (C-X-C motif) ligand 9 production
0.01972848	GO:0035395	GO:BP	negative regulation of chemokine (C-X-C motif) ligand 9 production



0.02056542	GO:0039528	GO:BP	cytoplasmic pattern recognition receptor signaling pathway in response to virus
0.02182358	GO:0001819	GO:BP	positive regulation of cytokine production
0.02269272	GO:0071276	GO:BP	cellular response to cadmium ion
0.02379239	GO:0023052	GO:BP	signaling
0.02655641	GO:0007154	GO:BP	cell communication
0.02913417	GO:0030163	GO:BP	protein catabolic process
0.02913417	GO:0043065	GO:BP	positive regulation of apoptotic process
0.02922947	GO:0051281	GO:BP	positive regulation of release of sequestered calcium ion into cytosol
0.02922947	GO:0048523	GO:BP	negative regulation of cellular process
0.02922947	GO:0046718	GO:BP	viral entry into host cell
0.02922947	GO:1904064	GO:BP	positive regulation of cation transmembrane transport
0.02979019	GO:0080134	GO:BP	regulation of response to stress
0.02997642	GO:0060326	GO:BP	cell chemotaxis
0.0301151	GO:0010941	GO:BP	regulation of cell death
0.03021092	GO:0006959	GO:BP	humoral immune response
0.03021092	GO:0006233	GO:BP	dTDP biosynthetic process
0.03021092	GO:0009196	GO:BP	pyrimidine deoxyribonucleoside diphosphate metabolic process
0.03021092	GO:0009197	GO:BP	pyrimidine deoxyribonucleoside diphosphate biosynthetic process
0.03021092	GO:1905349	GO:BP	ciliary transition zone assembly
0.03021092	GO:0006227	GO:BP	dUDP biosynthetic process
0.03021092	GO:0019060	GO:BP	intracellular transport of viral protein in host cell
0.03021092	GO:0001869	GO:BP	negative regulation of complement activation, lectin pathway
0.03021092	GO:0001868	GO:BP	regulation of complement activation, lectin pathway
0.03021092	GO:0001581	GO:BP	detection of chemical stimulus involved in sensory perception of sour taste
0.03021092	GO:1901740	GO:BP	negative regulation of myoblast fusion
0.03021092	GO:0006954	GO:BP	inflammatory response
0.03021092	GO:0032640	GO:BP	tumor necrosis factor production
0.03021092	GO:0043068	GO:BP	positive regulation of programmed cell death
0.03021092	GO:0032680	GO:BP	regulation of tumor necrosis factor production
0.03021092	GO:0034341	GO:BP	response to interferon-gamma
0.03021092	GO:0048585	GO:BP	negative regulation of response to stimulus
0.03021092	GO:0046596	GO:BP	regulation of viral entry into host cell
0.03021092	GO:0046077	GO:BP	dUDP metabolic process
0.03021092	GO:2000502	GO:BP	negative regulation of natural killer cell chemotaxis
0.03021092	GO:0046072	GO:BP	dTDP metabolic process
0.03021092	GO:0061394	GO:BP	regulation of transcription from RNA polymerase II promoter in response to arsenic-containing substance
0.03021092	GO:0044409	GO:BP	entry into host
0.03021092	GO:0070371	GO:BP	ERK1 and ERK2 cascade
0.03021092	GO:0030581	GO:BP	symbiont intracellular protein transport in host
0.03021092	GO:0062208	GO:BP	positive regulation of pattern recognition receptor signaling pathway
0.03068357	GO:0032496	GO:BP	response to lipopolysaccharide
0.03099794	GO:0030195	GO:BP	negative regulation of blood coagulation
0.03127289	GO:0034767	GO:BP	positive regulation of ion transmembrane transport
0.03162907	GO:1903555	GO:BP	regulation of tumor necrosis factor superfamily cytokine production
0.03162907	GO:0071706	GO:BP	tumor necrosis factor superfamily cytokine production
0.03162907	GO:1900047	GO:BP	negative regulation of hemostasis
0.03162907	GO:0052126	GO:BP	movement in host environment
0.0326748	GO:0009057	GO:BP	macromolecule catabolic process
0.0346532	GO:0052372	GO:BP	modulation by symbiont of entry into host
0.0346532	GO:0050819	GO:BP	negative regulation of coagulation
0.03534872	GO:0065007	GO:BP	biological regulation
0.03534872	GO:0002237	GO:BP	response to molecule of bacterial origin
0.03842562	GO:0010942	GO:BP	positive regulation of cell death
0.03901068	GO:0010524	GO:BP	positive regulation of calcium ion transport into cytosol
0.03901068	GO:0042742	GO:BP	defense response to bacterium
0.03960354	GO:0007165	GO:BP	signal transduction

0.04000041	GO:1901624	GO:BP	negative regulation of lymphocyte chemotaxis
0.04000041	GO:1903487	GO:BP	regulation of lactation
0.04000041	GO:0010716	GO:BP	negative regulation of extracellular matrix disassembly
0.04000041	GO:1903984	GO:BP	positive regulation of TRAIL-activated apoptotic signaling pathway
0.04000041	GO:0034242	GO:BP	negative regulation of syncytium formation by plasma membrane fusion
0.04000041	GO:0035684	GO:BP	helper T cell extravasation
0.04000041	GO:0046686	GO:BP	response to cadmium ion
0.04092983	GO:0043903	GO:BP	regulation of biological process involved in symbiotic interaction
0.04092983	GO:0010628	GO:BP	positive regulation of gene expression
0.04207323	GO:0002753	GO:BP	cytoplasmic pattern recognition receptor signaling pathway
0.04486361	GO:0006508	GO:BP	proteolysis
0.04486361	GO:0050900	GO:BP	leukocyte migration
0.04555435	GO:2000401	GO:BP	regulation of lymphocyte migration
0.04673101	GO:0051851	GO:BP	modulation by host of symbiont process
0.04716357	GO:0042592	GO:BP	homeostatic process
0.04862041	GO:0009189	GO:BP	deoxyribonucleoside diphosphate biosynthetic process
0.04862041	GO:0009212	GO:BP	pyrimidine deoxyribonucleoside triphosphate biosynthetic process
0.04862041	GO:0010710	GO:BP	regulation of collagen catabolic process
0.04862041	GO:0032461	GO:BP	positive regulation of protein oligomerization
0.04862041	GO:0046075	GO:BP	dTTP metabolic process
0.04862041	GO:0060244	GO:BP	negative regulation of cell proliferation involved in contact inhibition
0.04862041	GO:0097325	GO:BP	melanocyte proliferation
0.04862041	GO:1903121	GO:BP	regulation of TRAIL-activated apoptotic signaling pathway
0.04862041	GO:0006235	GO:BP	dTTP biosynthetic process
0.04862041	GO:0030193	GO:BP	regulation of blood coagulation
0.04935862	GO:0048878	GO:BP	chemical homeostasis
0.04935862	GO:1900046	GO:BP	regulation of hemostasis

**Table S10: GO term enrichment, day 14 post infection**

p_value	term_id	source	term_name
1.09E-13	GO:0044419	GO:BP	biological process involved in interspecies interaction between organisms
2.07E-13	GO:0009607	GO:BP	response to biotic stimulus
9.66E-13	GO:0051707	GO:BP	response to other organism
9.66E-13	GO:0043207	GO:BP	response to external biotic stimulus
9.93E-12	GO:0006952	GO:BP	defense response
1.02E-11	GO:0098542	GO:BP	defense response to other organism
1.58E-11	GO:0009605	GO:BP	response to external stimulus
4.57E-10	GO:0009615	GO:BP	response to virus
4.57E-10	GO:0019079	GO:BP	viral genome replication
4.80E-10	GO:0045087	GO:BP	innate immune response
5.13E-10	GO:0006955	GO:BP	immune response
1.49E-09	GO:0019058	GO:BP	viral life cycle
1.99E-09	GO:0071357	GO:BP	cellular response to type I interferon
4.18E-09	GO:0034340	GO:BP	response to type I interferon
7.17E-09	GO:0140546	GO:BP	defense response to symbiont
7.17E-09	GO:0051607	GO:BP	defense response to virus
2.46E-08	GO:0016032	GO:BP	viral process
3.81E-08	GO:0048525	GO:BP	negative regulation of viral process
4.58E-08	GO:0002376	GO:BP	immune system process
7.42E-08	GO:0045071	GO:BP	negative regulation of viral genome replication
7.89E-08	GO:0060337	GO:BP	type I interferon signaling pathway
4.52E-07	GO:0006950	GO:BP	response to stress
4.78E-07	GO:1903900	GO:BP	regulation of viral life cycle

7.99E-07	GO:0045069	GO:BP	regulation of viral genome replication
1.13E-06	GO:0050792	GO:BP	regulation of viral process
1.35E-06	GO:0019221	GO:BP	cytokine-mediated signaling pathway
2.29E-06	GO:0060339	GO:BP	negative regulation of type I interferon-mediated signaling pathway
5.66E-06	GO:0009617	GO:BP	response to bacterium
6.52E-06	GO:0006959	GO:BP	humoral immune response
9.81E-06	GO:0045824	GO:BP	negative regulation of innate immune response
1.49E-05	GO:0071345	GO:BP	cellular response to cytokine stimulus
2.55E-05	GO:0060338	GO:BP	regulation of type I interferon-mediated signaling pathway
2.63E-05	GO:0032102	GO:BP	negative regulation of response to external stimulus
3.94E-05	GO:0034097	GO:BP	response to cytokine
7.19E-05	GO:0002832	GO:BP	negative regulation of response to biotic stimulus
9.59E-05	GO:0050896	GO:BP	response to stimulus
1.34E-04	GO:0140374	GO:BP	antiviral innate immune response
1.85E-04	GO:0031348	GO:BP	negative regulation of defense response
2.29E-04	GO:0048247	GO:BP	lymphocyte chemotaxis
2.79E-04	GO:0032101	GO:BP	regulation of response to external stimulus
3.47E-04	GO:0002682	GO:BP	regulation of immune system process
3.47E-04	GO:0071659	GO:BP	negative regulation of IP-10 production
3.74E-04	GO:0001960	GO:BP	negative regulation of cytokine-mediated signaling pathway
4.10E-04	GO:0002683	GO:BP	negative regulation of immune system process
4.42E-04	GO:0060761	GO:BP	negative regulation of response to cytokine stimulus
4.55E-04	GO:0098586	GO:BP	cellular response to virus
4.57E-04	GO:0044403	GO:BP	biological process involved in symbiotic interaction
5.82E-04	GO:0071612	GO:BP	IP-10 production
5.82E-04	GO:0071658	GO:BP	regulation of IP-10 production
5.82E-04	GO:2000342	GO:BP	negative regulation of chemokine (C-X-C motif) ligand 2 production
6.33E-04	GO:0070098	GO:BP	chemokine-mediated signaling pathway
6.57E-04	GO:0050777	GO:BP	negative regulation of immune response
8.62E-04	GO:0048583	GO:BP	regulation of response to stimulus
8.65E-04	GO:1990868	GO:BP	response to chemokine
8.65E-04	GO:1990869	GO:BP	cellular response to chemokine
9.94E-04	GO:0050776	GO:BP	regulation of immune response
0.00118878	GO:0006958	GO:BP	complement activation, classical pathway
0.00118878	GO:0030593	GO:BP	neutrophil chemotaxis
0.00118878	GO:0002831	GO:BP	regulation of response to biotic stimulus
0.00140835	GO:0042742	GO:BP	defense response to bacterium
0.00149686	GO:0032728	GO:BP	positive regulation of interferon-beta production
0.00171828	GO:0072676	GO:BP	lymphocyte migration
0.00174736	GO:0002455	GO:BP	humoral immune response mediated by circulating immunoglobulin
0.0018099	GO:0045088	GO:BP	regulation of innate immune response
0.00207899	GO:0060700	GO:BP	regulation of ribonuclease activity
0.00221263	GO:0006956	GO:BP	complement activation
0.00221316	GO:1990266	GO:BP	neutrophil migration
0.00221316	GO:0071621	GO:BP	granulocyte chemotaxis
0.0024203	GO:0048519	GO:BP	negative regulation of biological process
0.0025658	GO:0007166	GO:BP	cell surface receptor signaling pathway
0.00282269	GO:0031347	GO:BP	regulation of defense response
0.0032795	GO:0001959	GO:BP	regulation of cytokine-mediated signaling pathway
0.00331432	GO:0032608	GO:BP	interferon-beta production
0.00331432	GO:0032648	GO:BP	regulation of interferon-beta production
0.00352612	GO:0098883	GO:BP	synapse pruning
0.00357575	GO:0032481	GO:BP	positive regulation of type I interferon production
0.00400543	GO:0097530	GO:BP	granulocyte migration
0.00400543	GO:0060759	GO:BP	regulation of response to cytokine stimulus
0.00495189	GO:0072678	GO:BP	T cell migration
0.00495189	GO:0002548	GO:BP	monocyte chemotaxis

0.00531635	GO:0071639	GO:BP	positive regulation of monocyte chemotactic protein-1 production
0.00531635	GO:0070887	GO:BP	cellular response to chemical stimulus
0.00542924	GO:0002684	GO:BP	positive regulation of immune system process
0.00623776	GO:0006508	GO:BP	proteolysis
0.00628329	GO:0071310	GO:BP	cellular response to organic substance
0.00651646	GO:0072567	GO:BP	chemokine (C-X-C motif) ligand 2 production
0.00651646	GO:0051701	GO:BP	biological process involved in interaction with host
0.00651646	GO:2000341	GO:BP	regulation of chemokine (C-X-C motif) ligand 2 production
0.00686526	GO:0002449	GO:BP	lymphocyte mediated immunity
0.00748001	GO:0016064	GO:BP	immunoglobulin mediated immune response
0.00757426	GO:0002460	GO:BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
0.00775918	GO:0019724	GO:BP	B cell mediated immunity
0.00813126	GO:0071674	GO:BP	mononuclear cell migration
0.00814379	GO:0006954	GO:BP	inflammatory response
0.00848064	GO:0044827	GO:BP	modulation by host of viral genome replication
0.00848064	GO:0048245	GO:BP	eosinophil chemotaxis
0.00853222	GO:0051603	GO:BP	proteolysis involved in cellular protein catabolic process
0.00910357	GO:0071605	GO:BP	monocyte chemotactic protein-1 production
0.00910357	GO:0071222	GO:BP	cellular response to lipopolysaccharide
0.00910357	GO:0071637	GO:BP	regulation of monocyte chemotactic protein-1 production
0.00977801	GO:0032069	GO:BP	regulation of nuclease activity
0.00977801	GO:0150146	GO:BP	cell junction disassembly
0.01015746	GO:0048523	GO:BP	negative regulation of cellular process
0.01016259	GO:0071219	GO:BP	cellular response to molecule of bacterial origin
0.01016259	GO:0048585	GO:BP	negative regulation of response to stimulus
0.01024056	GO:0035455	GO:BP	response to interferon-alpha
0.01024056	GO:0046597	GO:BP	negative regulation of viral entry into host cell
0.01042351	GO:0032479	GO:BP	regulation of type I interferon production
0.01042351	GO:0032606	GO:BP	type I interferon production
0.01079834	GO:0032682	GO:BP	negative regulation of chemokine production
0.01079834	GO:0072677	GO:BP	eosinophil migration
0.01111606	GO:0044257	GO:BP	cellular protein catabolic process
0.01135786	GO:0097529	GO:BP	myeloid leukocyte migration
0.01145586	GO:0042730	GO:BP	fibrinolysis
0.01268732	GO:0030595	GO:BP	leukocyte chemotaxis
0.01291772	GO:0010033	GO:BP	response to organic substance
0.01300029	GO:1901623	GO:BP	regulation of lymphocyte chemotaxis
0.01300029	GO:1903901	GO:BP	negative regulation of viral life cycle
0.01408458	GO:0071216	GO:BP	cellular response to biotic stimulus
0.01483169	GO:0010818	GO:BP	T cell chemotaxis
0.01530979	GO:0002443	GO:BP	leukocyte mediated immunity
0.01773459	GO:0044788	GO:BP	modulation by host of viral process
0.01773459	GO:0035456	GO:BP	response to interferon-beta
0.01785532	GO:0051928	GO:BP	positive regulation of calcium ion transport
0.01878772	GO:0019941	GO:BP	modification-dependent protein catabolic process
0.01884674	GO:0019730	GO:BP	antimicrobial humoral response
0.01936395	GO:0035395	GO:BP	negative regulation of chemokine (C-X-C motif) ligand 9 production
0.01936395	GO:0035394	GO:BP	regulation of chemokine (C-X-C motif) ligand 9 production
0.01936395	GO:1902362	GO:BP	melanocyte apoptotic process
0.01936395	GO:0043632	GO:BP	modification-dependent macromolecule catabolic process
0.01936395	GO:0075512	GO:BP	clathrin-dependent endocytosis of virus by host cell
0.01936395	GO:0035393	GO:BP	chemokine (C-X-C motif) ligand 9 production
0.02379468	GO:0002250	GO:BP	adaptive immune response
0.02505475	GO:0051336	GO:BP	regulation of hydrolase activity
0.02618377	GO:0030163	GO:BP	protein catabolic process
0.02710278	GO:0080134	GO:BP	regulation of response to stress

0.02745622	GO:0051241	GO:BP	negative regulation of multicellular organismal process
0.02790162	GO:0046718	GO:BP	viral entry into host cell
0.02823599	GO:1904064	GO:BP	positive regulation of cation transmembrane transport
0.02838717	GO:0060326	GO:BP	cell chemotaxis
0.02838717	GO:0051281	GO:BP	positive regulation of release of sequestered calcium ion into cytosol
0.03035207	GO:0034341	GO:BP	response to interferon-gamma
0.03048412	GO:0007520	GO:BP	myoblast fusion
0.03048412	GO:0044409	GO:BP	entry into host
0.03058168	GO:0070371	GO:BP	ERK1 and ERK2 cascade
0.03126547	GO:0046596	GO:BP	regulation of viral entry into host cell
0.03192013	GO:0001869	GO:BP	negative regulation of complement activation, lectin pathway
0.03192013	GO:0030581	GO:BP	symbiont intracellular protein transport in host
0.03192013	GO:0006227	GO:BP	dUDP biosynthetic process
0.03192013	GO:0019060	GO:BP	intracellular transport of viral protein in host cell
0.03192013	GO:0001868	GO:BP	regulation of complement activation, lectin pathway
0.03192013	GO:0009197	GO:BP	pyrimidine deoxyribonucleoside diphosphate biosynthetic process
0.03192013	GO:0006233	GO:BP	dTDP biosynthetic process
0.03192013	GO:0009196	GO:BP	pyrimidine deoxyribonucleoside diphosphate metabolic process
0.03192013	GO:0032496	GO:BP	response to lipopolysaccharide
0.03192013	GO:0046072	GO:BP	dTDP metabolic process
0.03192013	GO:0046077	GO:BP	dUDP metabolic process
0.03192013	GO:2000502	GO:BP	negative regulation of natural killer cell chemotaxis
0.03192013	GO:1901740	GO:BP	negative regulation of myoblast fusion
0.03192013	GO:0061394	GO:BP	regulation of transcription from RNA polymerase II promoter in response to arsenic-containing substance
0.03197623	GO:0034767	GO:BP	positive regulation of ion transmembrane transport
0.03198698	GO:0030195	GO:BP	negative regulation of blood coagulation
0.03268021	GO:0052126	GO:BP	movement in host environment
0.03290093	GO:1900047	GO:BP	negative regulation of hemostasis
0.0330199	GO:0045861	GO:BP	negative regulation of proteolysis
0.03582025	GO:0002237	GO:BP	response to molecule of bacterial origin
0.03582025	GO:0002221	GO:BP	pattern recognition receptor signaling pathway
0.03586732	GO:0050819	GO:BP	negative regulation of coagulation
0.03586732	GO:0052372	GO:BP	modulation by symbiont of entry into host
0.04120765	GO:0010524	GO:BP	positive regulation of calcium ion transport into cytosol
0.04191399	GO:0050778	GO:BP	positive regulation of immune response
0.04191399	GO:0000768	GO:BP	syncytium formation by plasma membrane fusion
0.04191399	GO:0140253	GO:BP	cell-cell fusion
0.04275725	GO:1903984	GO:BP	positive regulation of TRAIL-activated apoptotic signaling pathway
0.04275725	GO:1901624	GO:BP	negative regulation of lymphocyte chemotaxis
0.04275725	GO:0110032	GO:BP	positive regulation of G2/M1 transition of meiotic cell cycle
0.04275725	GO:0034242	GO:BP	negative regulation of syncytium formation by plasma membrane fusion
0.04275725	GO:0035684	GO:BP	helper T cell extravasation
0.04275725	GO:0010716	GO:BP	negative regulation of extracellular matrix disassembly
0.04280627	GO:0044265	GO:BP	cellular macromolecule catabolic process
0.04284264	GO:0043903	GO:BP	regulation of biological process involved in symbiotic interaction
0.04486546	GO:0050900	GO:BP	leukocyte migration
0.04486546	GO:0042592	GO:BP	homeostatic process
0.04486546	GO:0022617	GO:BP	extracellular matrix disassembly
0.04486546	GO:0006949	GO:BP	syncytium formation
0.04735435	GO:2000401	GO:BP	regulation of lymphocyte migration
0.04856084	GO:0051851	GO:BP	modulation by host of symbiont process
0.04960877	GO:0002253	GO:BP	activation of immune response

**Table S11: Overlap in DEGs on days 10 and 14**

	Number	Genes
Unique Day 10	52	AC003080.4, AC007899.3, AC007919.18, AC074338.4, ACO1, AIM2, BST2, CCR1, CD274, DDX58, DDX60L, EPHB2, EXOC3L1, HELZ2, IFIH1, IFIT5, IL1RN, KIAA1958, LAMP3, LGALS9, LIPA, LLpac-136A2.1, MS4A4A, MTND4P26, NUDT19P5, PARP12, PARP14, PARP9, PLSCR2, PML, PNPT1, RNA5SP39, RP11-466G12.3, RP11-820K3.2, SAMD9, SAMD9L, STAT2, TDRD7, TFEC, TNFAIP6, TNFSF10, TNFSF13B, TOR1B, TREX1, TRIM22, TRIM6, TTC21A, TTC26, USP41, XXbac-BPG541D20.6, ZBP1, ZCCHC2
Shared Days 10 &14	60	ADAMTS5, ANKRD22, ATF3, BATF2, C1QA, C1QB, C1QC, CARD17, CMPK2, CXCL6, DDX60, DHX58, EIF2AK2, EPSTI1, ETV7, FBXO39, FBXO6, FRMD3, GBP1, GBP4, HERC5, HERC6, IFI35, IFI44, IFI44L, IFI6, IFIT1, IFIT2, IFIT3, IFITM3, IRF7, LAP3, LY6E, MT2A, MX1, OAS1, OAS2, OAS3, OASL, OR52M2P, PLSCR1, RMI2, RP4-641G12.3, RPL37P6, RSAD2, RTP4, RUFY4, SAMD4A, SCO2, SERPING1, SIGLEC1, SMTNL1, SPATS2L, STAT1, TCN2, TMPRSS2, UBE2L6, USP18, XAF1, ZDHHC4P1
Unique Day 14	117	AGMO, ALPL, ANGPT1, ANLN, ANO5, ANXA10, ARHGEF40, ASPM, AURKB, BIRC5, BUB1, CCNB2, CDC25A, CDC45, CDCA2, CDCA5, CDK1, CENPA, CEP55, CNTNAP3, CNTNAP3B, CXCL11, CXCL9, CXCR2P1, DTL, E2F1, E2F8, ELOVL3, ENTPD2, FABP6, FAM72B, GBP1P1, GBP5, GPR84, HIST1H1B, HIST1H2AB, HIST1H2AH, HIST1H2AJ, HIST1H2AL, HIST1H2BE, HIST1H2BI, HIST1H2BL, HIST1H2BM, HIST1H2BO, HIST1H3B, HIST1H3C, HIST1H3F, HIST1H3G, HIST1H3J, HIST2H3A, HIST2H3C, HMMR, HNRNPCP4, IFI27, IGHV2-5, IGHV4-39, IGHV5-51, IGKV1D-16, IGKV2-28, IGLC1, IGLC2, IGLV1-40, IGLV1-44, IGLV1-47, IGLV1-51, IGLV2-23, IGLV2-8, IGLV3-1, IGLV3-21, IGLV3-25, IGLV6-57, IGLV8-61, INHBB, JCHAIN, KCTD14, KIF4A, KIFC1, LIF, MCM10, MKI67, MT1E, MTCYBP11, MYBL2, MYOF, MZB1, NAT8, NCAPG, NEURL3, NMRAL1P1, NUSAP1, OTX1, PBK, PDCD1LG2, PDZD3, PHF24, PXT1, PYCR1, RAB36, RBM17P1, RNASE1, RP11-34P1.2, RP11-435F17.3, RP4-673D20.4, RRM2, RSPH14, SCRT2, SDC1, SDC2, SF3A3P2, SOCS1, TGM3, THBD, TMEM51, TOP2A, TPX2, TSPEAR, TYMS

**Table S12: Components of Day 14 DEG modules**

<b>Module 1</b>	ANLN, ASPM, AURKB, BIRC5, BUB1, CCNB2, CDC25A, CDC45, CDCA2, CDCA5, CDK1, CENPA, CEP55, CXCL9, DTL, E2F1, E2F8, HIST1H1B, HIST1H2AB, HIST1H2AH, HIST1H2AJ, HIST1H2AL, HIST1H2BE, HIST1H2BI, HIST1H2BL, HIST1H2BM, HIST1H2BO, HIST1H3B, HIST1H3C, HIST1H3F, HIST1H3G, HIST1H3J, HIST2H3A, HIST2H3C, HMMR, IGHV2-5, IGHV4-39, IGHV5-51, IGKV1D-16, IGKV2-28, IGLC1, IGLC2, IGLV1-40, IGLV1-44, IGLV1-47, IGLV1-51, IGLV2-23, IGLV2-8, IGLV3-1, IGLV3-21, IGLV3-25, IGLV6-57, IGLV8-61, JCHAIN, KIF4A, KIFC1, MCM10, MKI67, MYBL2, MZB1, NCAPG, NUSAP1, PBK, PYCR1, RRM2, SDC1, TOP2A, TPX2, TYMS
<b>Module 2</b>	ANKRD22, ANO5, ANXA10, ATF3, BATF2, C1QA, C1QB, C1QC, CARD17, CMPK2, CXCL11, CXCR2P1, DDX60, DHX58, EIF2AK2, ELOVL3, EPSTI1, ETV7, FAM72B, FBXO39, FBXO6, FRMD3, GBP1, GBP1P1, GBP4, GBP5, GPR84, HERC5, HERC6, HNRNPCP4, IFI27, IFI35, IFI44, IFI44L, IFI6, IFIT1, IFIT2, IFIT3, IFITM3, IRF7, KCTD14, LAP3, LIF, LY6E, MT1E, MT2A, MX1, MYOF, NAT8, NEURL3, NMRAL1P1, OAS1, OAS2, OAS3, OASL, OR52M2P, PDCD1LG2, PLSCR1, PXT1, RMI2, RNASE1, RP4-641G12.3, RPL37P6, RSAD2, RTP4, RUFY4, SAMD4A, SCO2, SERPING1, SF3A3P2, SIGLEC1, SMTNL1, SOCS1, SPATS2L, STAT1, TCN2, TMEM51, TMPRSS2, UBE2L6, USP18, XAF1, ZDHHC4P1
<b>Module 3</b>	ADAMTS5, AGMO, ALPL, ANGPT1, ARHGEF40, CNTNAP3, CNTNAP3B, CXCL6, ENTPD2, FABP6, INHBB, MTCYBP11, OTX1, PDZD3, PHF24, RAB36, RBM17P1, RP11-34P1.2, RP11-435F17.3, RP4-673D20.4, RSPH14, SCRT2, SDC2, TGM3, THBD, TSPEAR

**Table S13: GO term enrichment, module 1**

p_value	term_id	source	term_name
1.95E-15	GO:0000278	GO:BP	mitotic cell cycle
9.38E-14	GO:0051301	GO:BP	cell division
9.38E-14	GO:1903047	GO:BP	mitotic cell cycle process
2.66E-13	GO:0022402	GO:BP	cell cycle process
4.30E-12	GO:0007049	GO:BP	cell cycle
6.26E-12	GO:0002250	GO:BP	adaptive immune response
2.24E-11	GO:0000280	GO:BP	nuclear division
7.99E-11	GO:0048285	GO:BP	organelle fission
7.55E-10	GO:0140014	GO:BP	mitotic nuclear division
1.49E-08	GO:0051726	GO:BP	regulation of cell cycle
5.37E-08	GO:0010564	GO:BP	regulation of cell cycle process
5.37E-08	GO:0007059	GO:BP	chromosome segregation
9.42E-08	GO:0007346	GO:BP	regulation of mitotic cell cycle
1.37E-06	GO:0051225	GO:BP	spindle assembly
1.94E-06	GO:0002376	GO:BP	immune system process
2.09E-06	GO:0000819	GO:BP	sister chromatid segregation
2.81E-06	GO:0006955	GO:BP	immune response
5.60E-06	GO:1902850	GO:BP	microtubule cytoskeleton organization involved in mitosis
7.92E-06	GO:0030261	GO:BP	chromosome condensation
1.19E-05	GO:0000070	GO:BP	mitotic sister chromatid segregation
1.41E-05	GO:0061640	GO:BP	cytoskeleton-dependent cytokinesis
1.44E-05	GO:0000226	GO:BP	microtubule cytoskeleton organization
1.44E-05	GO:0140694	GO:BP	non-membrane-bounded organelle assembly
1.44E-05	GO:0000910	GO:BP	cytokinesis
1.75E-05	GO:0007051	GO:BP	spindle organization

1.75E-05	GO:0098813	GO:BP	nuclear chromosome segregation
2.41E-05	GO:1901987	GO:BP	regulation of cell cycle phase transition
2.41E-05	GO:0044770	GO:BP	cell cycle phase transition
2.83E-05	GO:0090307	GO:BP	mitotic spindle assembly
3.54E-05	GO:1901990	GO:BP	regulation of mitotic cell cycle phase transition
3.80E-05	GO:0044772	GO:BP	mitotic cell cycle phase transition
5.15E-05	GO:0000281	GO:BP	mitotic cytokinesis
6.37E-05	GO:0090068	GO:BP	positive regulation of cell cycle process
9.46E-05	GO:0050896	GO:BP	response to stimulus
1.59E-04	GO:0000075	GO:BP	cell cycle checkpoint signaling
3.01E-04	GO:0007088	GO:BP	regulation of mitotic nuclear division
3.01E-04	GO:0007017	GO:BP	microtubule-based process
3.08E-04	GO:0010948	GO:BP	negative regulation of cell cycle process
3.17E-04	GO:0051782	GO:BP	negative regulation of cell division
3.54E-04	GO:0045787	GO:BP	positive regulation of cell cycle
3.88E-04	GO:0007052	GO:BP	mitotic spindle organization
4.18E-04	GO:0007076	GO:BP	mitotic chromosome condensation
6.05E-04	GO:0099024	GO:BP	plasma membrane invagination
7.29E-04	GO:0051783	GO:BP	regulation of nuclear division
7.37E-04	GO:0010324	GO:BP	membrane invagination
7.91E-04	GO:0071459	GO:BP	protein localization to chromosome, centromeric region
8.84E-04	GO:0051276	GO:BP	chromosome organization
9.70E-04	GO:0010971	GO:BP	positive regulation of G2/M transition of mitotic cell cycle
0.0010789	GO:0045786	GO:BP	negative regulation of cell cycle
0.0010789	GO:1901988	GO:BP	negative regulation of cell cycle phase transition
0.00125181	GO:1902751	GO:BP	positive regulation of cell cycle G2/M phase transition
0.00125181	GO:0070925	GO:BP	organelle assembly
0.00140546	GO:1901992	GO:BP	positive regulation of mitotic cell cycle phase transition
0.00153578	GO:0044839	GO:BP	cell cycle G2/M phase transition
0.00155144	GO:0051983	GO:BP	regulation of chromosome segregation
0.00166382	GO:0006260	GO:BP	DNA replication
0.00193684	GO:0034502	GO:BP	protein localization to chromosome
0.00205423	GO:0008315	GO:BP	G2/M transition of meiotic cell cycle
0.00220075	GO:0006910	GO:BP	phagocytosis, recognition
0.00254143	GO:0006959	GO:BP	humoral immune response
0.00264175	GO:0050864	GO:BP	regulation of B cell activation
0.00268621	GO:0032466	GO:BP	negative regulation of cytokinesis
0.00276358	GO:0007010	GO:BP	cytoskeleton organization
0.00276358	GO:0006958	GO:BP	complement activation, classical pathway
0.00286226	GO:0032506	GO:BP	cytokinetic process
0.00300647	GO:1903046	GO:BP	meiotic cell cycle process
0.00303171	GO:1901989	GO:BP	positive regulation of cell cycle phase transition
0.00326051	GO:0051256	GO:BP	mitotic spindle midzone assembly
0.0032657	GO:0045931	GO:BP	positive regulation of mitotic cell cycle
0.00333016	GO:0010389	GO:BP	regulation of G2/M transition of mitotic cell cycle
0.00387243	GO:0002455	GO:BP	humoral immune response mediated by circulating immunoglobulin
0.0038989	GO:0000022	GO:BP	mitotic spindle elongation
0.0038989	GO:0090306	GO:BP	meiotic spindle assembly
0.0043505	GO:1902749	GO:BP	regulation of cell cycle G2/M phase transition
0.00448759	GO:0006956	GO:BP	complement activation
0.00448759	GO:0007080	GO:BP	mitotic metaphase plate congression
0.00448759	GO:0031570	GO:BP	DNA integrity checkpoint signaling
0.00448759	GO:0006911	GO:BP	phagocytosis, engulfment
0.00448759	GO:0050853	GO:BP	B cell receptor signaling pathway
0.00448759	GO:0051231	GO:BP	spindle elongation
0.00448759	GO:0006323	GO:BP	DNA packaging
0.00521537	GO:0051640	GO:BP	organelle localization
0.00521537	GO:0007093	GO:BP	mitotic cell cycle checkpoint signaling
0.00591555	GO:0051653	GO:BP	spindle localization



0.00603928	GO:0051255	GO:BP	spindle midzone assembly
0.00603928	GO:0044771	GO:BP	meiotic cell cycle phase transition
0.00714536	GO:0051656	GO:BP	establishment of organelle localization
0.00717054	GO:0009411	GO:BP	response to UV
0.00721605	GO:0051321	GO:BP	meiotic cell cycle
0.00756291	GO:0050871	GO:BP	positive regulation of B cell activation
0.00804108	GO:0051310	GO:BP	metaphase plate congression
0.00877466	GO:0000086	GO:BP	G2/M transition of mitotic cell cycle
0.00884349	GO:0009263	GO:BP	deoxyribonucleotide biosynthetic process
0.00998382	GO:0000212	GO:BP	meiotic spindle organization
0.01355175	GO:0007096	GO:BP	regulation of exit from mitosis
0.01355175	GO:0010972	GO:BP	negative regulation of G2/M transition of mitotic cell cycle
0.01355175	GO:1903083	GO:BP	protein localization to condensed chromosome
0.01355175	GO:0006996	GO:BP	organelle organization
0.01355175	GO:0034501	GO:BP	protein localization to kinetochore
0.01426945	GO:1902750	GO:BP	negative regulation of cell cycle G2/M phase transition
0.01426945	GO:0051303	GO:BP	establishment of chromosome localization
0.01500357	GO:0050000	GO:BP	chromosome localization
0.01500357	GO:0140013	GO:BP	meiotic nuclear division
0.01534299	GO:0007063	GO:BP	regulation of sister chromatid cohesion
0.01534299	GO:0071103	GO:BP	DNA conformation change
0.01534299	GO:0016064	GO:BP	immunoglobulin mediated immune response
0.01534299	GO:1901991	GO:BP	negative regulation of mitotic cell cycle phase transition
0.01544809	GO:0033044	GO:BP	regulation of chromosome organization
0.01580012	GO:0019724	GO:BP	B cell mediated immunity
0.01580012	GO:0033043	GO:BP	regulation of organelle organization
0.01616134	GO:0042113	GO:BP	B cell activation
0.01616134	GO:0034644	GO:BP	cellular response to UV
0.01616134	GO:0006259	GO:BP	DNA metabolic process
0.01654379	GO:2001251	GO:BP	negative regulation of chromosome organization
0.0203386	GO:0051304	GO:BP	chromosome separation
0.02078715	GO:0042742	GO:BP	defense response to bacterium
0.0228951	GO:0008283	GO:BP	cell population proliferation
0.02485926	GO:0008037	GO:BP	cell recognition
0.02646739	GO:0045769	GO:BP	negative regulation of asymmetric cell division
0.02646739	GO:1902977	GO:BP	mitotic DNA replication preinitiation complex assembly
0.02646739	GO:0031938	GO:BP	obsolete regulation of chromatin silencing at telomere
0.02646739	GO:1905116	GO:BP	positive regulation of lateral attachment of mitotic spindle microtubules to
0.02646739	GO:1905115	GO:BP	regulation of lateral attachment of mitotic spindle microtubules to kinetochore
0.02646739	GO:0007344	GO:BP	pronuclear fusion
0.02646739	GO:0000741	GO:BP	karyogamy
0.02646739	GO:0033301	GO:BP	cell cycle comprising mitosis without cytokinesis
0.02646739	GO:0000921	GO:BP	septin ring assembly
0.02775825	GO:0010458	GO:BP	exit from mitosis
0.02918043	GO:0045930	GO:BP	negative regulation of mitotic cell cycle
0.03093824	GO:0007143	GO:BP	female meiotic nuclear division
0.03268183	GO:0000077	GO:BP	DNA damage checkpoint signaling
0.03268183	GO:0016043	GO:BP	cellular component organization
0.03298054	GO:0071482	GO:BP	cellular response to light stimulus
0.03298054	GO:0007095	GO:BP	mitotic G2 DNA damage checkpoint signaling
0.03298054	GO:0006270	GO:BP	DNA replication initiation
0.03298054	GO:0006974	GO:BP	cellular response to DNA damage stimulus
0.03298054	GO:0042542	GO:BP	response to hydrogen peroxide
0.03583736	GO:0050851	GO:BP	antigen receptor-mediated signaling pathway
0.03627251	GO:0040001	GO:BP	establishment of mitotic spindle localization
0.03768625	GO:0016572	GO:BP	histone phosphorylation
0.03768625	GO:0045740	GO:BP	positive regulation of DNA replication
0.0388357	GO:0007094	GO:BP	mitotic spindle assembly checkpoint signaling
0.0388357	GO:0071173	GO:BP	spindle assembly checkpoint signaling

0.0388357	GO:0071174	GO:BP	mitotic spindle checkpoint signaling
0.04053506	GO:0031577	GO:BP	spindle checkpoint signaling
0.04084731	GO:0061982	GO:BP	meiosis I cell cycle process
0.0419691	GO:0045841	GO:BP	negative regulation of mitotic metaphase/anaphase transition
0.04233104	GO:0033048	GO:BP	negative regulation of mitotic sister chromatid segregation
0.04233104	GO:0044786	GO:BP	cell cycle DNA replication
0.04233104	GO:0033046	GO:BP	negative regulation of sister chromatid segregation
0.04233104	GO:1902100	GO:BP	negative regulation of metaphase/anaphase transition of cell cycle
0.04233104	GO:0032877	GO:BP	positive regulation of DNA endoreduplication
0.04233104	GO:0099607	GO:BP	lateral attachment of mitotic spindle microtubules to kinetochore
0.04233104	GO:1904170	GO:BP	regulation of bleb assembly
0.04233104	GO:1904172	GO:BP	positive regulation of bleb assembly
0.04233104	GO:0071840	GO:BP	cellular component organization or biogenesis
0.04233104	GO:0009262	GO:BP	deoxyribonucleotide metabolic process
0.04233104	GO:2000816	GO:BP	negative regulation of mitotic sister chromatid separation
0.04233104	GO:0045870	GO:BP	positive regulation of single stranded viral RNA replication via double stranded DNA
0.04233104	GO:0031106	GO:BP	septin ring organization
0.04569513	GO:0051985	GO:BP	negative regulation of chromosome segregation
0.04569513	GO:1905819	GO:BP	negative regulation of chromosome separation
0.04740585	GO:0033047	GO:BP	regulation of mitotic sister chromatid segregation
0.04913496	GO:0044818	GO:BP	mitotic G2/M transition checkpoint

**Table S14: GO term enrichment, module 2**

p_value	term_id	source	term_name
4.01E-23	GO:0044419	GO:BP	biological process involved in interspecies interaction between organisms
1.11E-22	GO:0140546	GO:BP	defense response to symbiont
1.11E-22	GO:0051607	GO:BP	defense response to virus
1.20E-21	GO:0009615	GO:BP	response to virus
1.20E-21	GO:0043207	GO:BP	response to external biotic stimulus
1.20E-21	GO:0051707	GO:BP	response to other organism
2.20E-21	GO:0009607	GO:BP	response to biotic stimulus
9.69E-20	GO:0098542	GO:BP	defense response to other organism
5.59E-19	GO:0045087	GO:BP	innate immune response
8.36E-17	GO:0006952	GO:BP	defense response
2.21E-16	GO:0006955	GO:BP	immune response
1.85E-14	GO:0048525	GO:BP	negative regulation of viral process
3.91E-14	GO:0009605	GO:BP	response to external stimulus
2.04E-13	GO:0045071	GO:BP	negative regulation of viral genome replication
2.61E-13	GO:0002376	GO:BP	immune system process
2.78E-13	GO:0050792	GO:BP	regulation of viral process
3.72E-13	GO:0034097	GO:BP	response to cytokine
9.18E-13	GO:0034340	GO:BP	response to type I interferon
1.53E-12	GO:1903900	GO:BP	regulation of viral life cycle
1.17E-11	GO:0045069	GO:BP	regulation of viral genome replication
1.51E-11	GO:0002831	GO:BP	regulation of response to biotic stimulus
1.51E-11	GO:0071357	GO:BP	cellular response to type I interferon
1.51E-11	GO:0016032	GO:BP	viral process
1.51E-11	GO:0006950	GO:BP	response to stress
2.12E-11	GO:0019079	GO:BP	viral genome replication
4.19E-11	GO:0071345	GO:BP	cellular response to cytokine stimulus
5.65E-11	GO:0019058	GO:BP	viral life cycle
3.55E-10	GO:0070106	GO:BP	interleukin-27-mediated signaling pathway
5.86E-10	GO:0060337	GO:BP	type I interferon signaling pathway
9.63E-08	GO:0050776	GO:BP	regulation of immune response
1.49E-07	GO:0050896	GO:BP	response to stimulus
1.80E-07	GO:0045088	GO:BP	regulation of innate immune response

2.73E-07	GO:0098586	GO:BP	cellular response to virus
3.24E-07	GO:0060700	GO:BP	regulation of ribonuclease activity
3.43E-07	GO:0035455	GO:BP	response to interferon-alpha
4.47E-07	GO:0002682	GO:BP	regulation of immune system process
1.39E-06	GO:0039530	GO:BP	MDA-5 signaling pathway
1.46E-06	GO:0032481	GO:BP	positive regulation of type I interferon production
1.68E-06	GO:0010033	GO:BP	response to organic substance
1.85E-06	GO:0019221	GO:BP	cytokine-mediated signaling pathway
1.85E-06	GO:0035456	GO:BP	response to interferon-beta
2.03E-06	GO:0031347	GO:BP	regulation of defense response
2.82E-06	GO:0039528	GO:BP	cytoplasmic pattern recognition receptor signaling pathway in response to virus
2.82E-06	GO:0002221	GO:BP	pattern recognition receptor signaling pathway
5.07E-06	GO:0071310	GO:BP	cellular response to organic substance
5.53E-06	GO:0002684	GO:BP	positive regulation of immune system process
5.97E-06	GO:0032101	GO:BP	regulation of response to external stimulus
6.80E-06	GO:0032728	GO:BP	positive regulation of interferon-beta production
1.07E-05	GO:0062208	GO:BP	positive regulation of pattern recognition receptor signaling pathway
1.82E-05	GO:0032069	GO:BP	regulation of nuclease activity
1.83E-05	GO:0042221	GO:BP	response to chemical
1.84E-05	GO:0034341	GO:BP	response to interferon-gamma
1.92E-05	GO:0032479	GO:BP	regulation of type I interferon production
1.92E-05	GO:0032606	GO:BP	type I interferon production
2.06E-05	GO:0070887	GO:BP	cellular response to chemical stimulus
2.66E-05	GO:0062207	GO:BP	regulation of pattern recognition receptor signaling pathway
3.02E-05	GO:0032608	GO:BP	interferon-beta production
3.02E-05	GO:0032648	GO:BP	regulation of interferon-beta production
3.85E-05	GO:0002753	GO:BP	cytoplasmic pattern recognition receptor signaling pathway
5.11E-05	GO:0039529	GO:BP	RIG-I signaling pathway
5.61E-05	GO:0002833	GO:BP	positive regulation of response to biotic stimulus
6.68E-05	GO:0001817	GO:BP	regulation of cytokine production
7.14E-05	GO:0045824	GO:BP	negative regulation of innate immune response
7.14E-05	GO:0001816	GO:BP	cytokine production
8.59E-05	GO:0002764	GO:BP	immune response-regulating signaling pathway
1.02E-04	GO:0071346	GO:BP	cellular response to interferon-gamma
1.15E-04	GO:0060338	GO:BP	regulation of type I interferon-mediated signaling pathway
1.22E-04	GO:0098883	GO:BP	synapse pruning
1.22E-04	GO:1900246	GO:BP	positive regulation of RIG-I signaling pathway
1.53E-04	GO:0002683	GO:BP	negative regulation of immune system process
1.58E-04	GO:0035457	GO:BP	cellular response to interferon-alpha
2.03E-04	GO:0080134	GO:BP	regulation of response to stress
2.11E-04	GO:0010628	GO:BP	positive regulation of gene expression
3.65E-04	GO:0050778	GO:BP	positive regulation of immune response
3.65E-04	GO:0001819	GO:BP	positive regulation of cytokine production
3.73E-04	GO:0140374	GO:BP	antiviral innate immune response
4.38E-04	GO:0048519	GO:BP	negative regulation of biological process
4.61E-04	GO:0009617	GO:BP	response to bacterium
4.76E-04	GO:0002832	GO:BP	negative regulation of response to biotic stimulus
5.42E-04	GO:0051701	GO:BP	biological process involved in interaction with host
6.01E-04	GO:0060339	GO:BP	negative regulation of type I interferon-mediated signaling pathway
6.16E-04	GO:0071659	GO:BP	negative regulation of IP-10 production
6.29E-04	GO:0044403	GO:BP	biological process involved in symbiotic interaction
7.83E-04	GO:0150146	GO:BP	cell junction disassembly
7.83E-04	GO:0039535	GO:BP	regulation of RIG-I signaling pathway
0.00112004	GO:0071658	GO:BP	regulation of IP-10 production
0.00112004	GO:0071612	GO:BP	IP-10 production
0.00112004	GO:1900245	GO:BP	positive regulation of MDA-5 signaling pathway
0.00112004	GO:2000342	GO:BP	negative regulation of chemokine (C-X-C motif) ligand 2 production

0.00112004	GO:0039531	GO:BP	regulation of viral-induced cytoplasmic pattern recognition receptor signaling pathway
0.00118058	GO:0048583	GO:BP	regulation of response to stimulus
0.00150829	GO:0050688	GO:BP	regulation of defense response to virus
0.00180684	GO:0001959	GO:BP	regulation of cytokine-mediated signaling pathway
0.00190682	GO:0046718	GO:BP	viral entry into host cell
0.00234777	GO:0044409	GO:BP	entry into host
0.00246814	GO:0060759	GO:BP	regulation of response to cytokine stimulus
0.00258734	GO:0032020	GO:BP	ISG15-protein conjugation
0.0031419	GO:0052126	GO:BP	movement in host environment
0.00343763	GO:0072307	GO:BP	regulation of metanephric nephron tubule epithelial cell differentiation
0.00343763	GO:0039533	GO:BP	regulation of MDA-5 signaling pathway
0.00343763	GO:0072257	GO:BP	metanephric nephron tubule epithelial cell differentiation
0.00343763	GO:0003339	GO:BP	regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis
0.00352417	GO:0002252	GO:BP	immune effector process
0.00410363	GO:0048584	GO:BP	positive regulation of response to stimulus
0.00418121	GO:0060333	GO:BP	interferon-gamma-mediated signaling pathway
0.00440146	GO:0046719	GO:BP	regulation by virus of viral protein levels in host cell
0.00441951	GO:0050777	GO:BP	negative regulation of immune response
0.00560744	GO:0016064	GO:BP	immunoglobulin mediated immune response
0.00566795	GO:0006958	GO:BP	complement activation, classical pathway
0.00591302	GO:0019724	GO:BP	B cell mediated immunity
0.00605792	GO:0046596	GO:BP	regulation of viral entry into host cell
0.00694385	GO:0032103	GO:BP	positive regulation of response to external stimulus
0.00709934	GO:0051240	GO:BP	positive regulation of multicellular organismal process
0.00839844	GO:0002455	GO:BP	humoral immune response mediated by circulating immunoglobulin
0.008592	GO:0002224	GO:BP	toll-like receptor signaling pathway
0.0088856	GO:0052372	GO:BP	modulation by symbiont of entry into host
0.00932234	GO:0003337	GO:BP	mesenchymal to epithelial transition involved in metanephros morphogenesis
0.00985089	GO:0002449	GO:BP	lymphocyte mediated immunity
0.0105796	GO:0006956	GO:BP	complement activation
0.01071979	GO:0072182	GO:BP	regulation of nephron tubule epithelial cell differentiation
0.01102776	GO:0002460	GO:BP	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
0.01141035	GO:0007166	GO:BP	cell surface receptor signaling pathway
0.01166089	GO:0031348	GO:BP	negative regulation of defense response
0.01170067	GO:0071639	GO:BP	positive regulation of monocyte chemotactic protein-1 production
0.01170067	GO:0010273	GO:BP	detoxification of copper ion
0.01170067	GO:1990169	GO:BP	stress response to copper ion
0.01170067	GO:0048518	GO:BP	positive regulation of biological process
0.01170067	GO:0043903	GO:BP	regulation of biological process involved in symbiotic interaction
0.01326574	GO:0072160	GO:BP	nephron tubule epithelial cell differentiation
0.01326574	GO:0072283	GO:BP	metanephric renal vesicle morphogenesis
0.01467806	GO:2000341	GO:BP	regulation of chemokine (C-X-C motif) ligand 2 production
0.01467806	GO:0006878	GO:BP	cellular copper ion homeostasis
0.01467806	GO:0061687	GO:BP	detoxification of inorganic compound
0.01467806	GO:0072567	GO:BP	chemokine (C-X-C motif) ligand 2 production
0.01520813	GO:0051716	GO:BP	cellular response to stimulus
0.01587883	GO:0045089	GO:BP	positive regulation of innate immune response
0.01623744	GO:2000696	GO:BP	regulation of epithelial cell differentiation involved in kidney development
0.01771245	GO:0048585	GO:BP	negative regulation of response to stimulus
0.01771245	GO:0032722	GO:BP	positive regulation of chemokine production
0.01771245	GO:0097501	GO:BP	stress response to metal ion
0.01771245	GO:0072077	GO:BP	renal vesicle morphogenesis
0.01797994	GO:0034121	GO:BP	regulation of toll-like receptor signaling pathway
0.01814177	GO:0030522	GO:BP	intracellular receptor signaling pathway
0.01858735	GO:0002253	GO:BP	activation of immune response

0.01869491	GO:1900225	GO:BP	regulation of NLRP3 inflammasome complex assembly
0.01869491	GO:0055070	GO:BP	copper ion homeostasis
0.01869491	GO:0001960	GO:BP	negative regulation of cytokine-mediated signaling pathway
0.01869491	GO:0072087	GO:BP	renal vesicle development
0.01869491	GO:0070373	GO:BP	negative regulation of ERK1 and ERK2 cascade
0.01994172	GO:0009968	GO:BP	negative regulation of signal transduction
0.02001478	GO:0001818	GO:BP	negative regulation of cytokine production
0.02001478	GO:0071637	GO:BP	regulation of monocyte chemotactic protein-1 production
0.02001478	GO:0060231	GO:BP	mesenchymal to epithelial transition
0.02001478	GO:0072234	GO:BP	metanephric nephron tubule development
0.02001478	GO:0071605	GO:BP	monocyte chemotactic protein-1 production
0.020532	GO:0060761	GO:BP	negative regulation of response to cytokine stimulus
0.020532	GO:0048644	GO:BP	muscle organ morphogenesis
0.02111015	GO:0030097	GO:BP	hemopoiesis
0.02142648	GO:0044546	GO:BP	NLRP3 inflammasome complex assembly
0.02308519	GO:0072170	GO:BP	metanephric tubule development
0.02308519	GO:0046597	GO:BP	negative regulation of viral entry into host cell
0.02308519	GO:0140632	GO:BP	inflammasome complex assembly
0.02427936	GO:0032682	GO:BP	negative regulation of chemokine production
0.02427936	GO:0045649	GO:BP	regulation of macrophage differentiation
0.02427936	GO:0032727	GO:BP	positive regulation of interferon-alpha production
0.02427936	GO:0072243	GO:BP	metanephric nephron epithelium development
0.02427936	GO:0035458	GO:BP	cellular response to interferon-beta
0.02427936	GO:0002443	GO:BP	leukocyte mediated immunity
0.02427936	GO:0071294	GO:BP	cellular response to zinc ion
0.02490294	GO:0048523	GO:BP	negative regulation of cellular process
0.0259085	GO:0048534	GO:BP	hematopoietic or lymphoid organ development
0.0259085	GO:0042832	GO:BP	defense response to protozoan
0.0275832	GO:0072273	GO:BP	metanephric nephron morphogenesis
0.0275832	GO:0001562	GO:BP	response to protozoan
0.0275832	GO:0072202	GO:BP	cell differentiation involved in metanephros development
0.02812297	GO:0051239	GO:BP	regulation of multicellular organismal process
0.02889737	GO:1901676	GO:BP	positive regulation of histone H3-K27 acetylation
0.02889737	GO:0035393	GO:BP	chemokine (C-X-C motif) ligand 9 production
0.02889737	GO:0075512	GO:BP	clathrin-dependent endocytosis of virus by host cell
0.02889737	GO:1903901	GO:BP	negative regulation of viral life cycle
0.02889737	GO:0035394	GO:BP	regulation of chemokine (C-X-C motif) ligand 9 production
0.02889737	GO:0018003	GO:BP	peptidyl-lysine N6-acetylation
0.02889737	GO:0035395	GO:BP	negative regulation of chemokine (C-X-C motif) ligand 9 production
0.02889737	GO:0072207	GO:BP	metanephric epithelium development
0.02889737	GO:0072308	GO:BP	negative regulation of metanephric nephron tubule epithelial cell differentiation
0.02889737	GO:0071280	GO:BP	cellular response to copper ion
0.02981727	GO:0006959	GO:BP	humoral immune response
0.02991582	GO:0032642	GO:BP	regulation of chemokine production
0.02991582	GO:0032602	GO:BP	chemokine production
0.02991582	GO:0010648	GO:BP	negative regulation of cell communication
0.02998196	GO:0023057	GO:BP	negative regulation of signaling
0.03148319	GO:0034123	GO:BP	positive regulation of toll-like receptor signaling pathway
0.03330831	GO:0009966	GO:BP	regulation of signal transduction
0.03330831	GO:0032607	GO:BP	interferon-alpha production
0.03330831	GO:0032647	GO:BP	regulation of interferon-alpha production
0.03355252	GO:0032760	GO:BP	positive regulation of tumor necrosis factor production
0.03380045	GO:0002520	GO:BP	immune system development
0.03547261	GO:0045637	GO:BP	regulation of myeloid cell differentiation
0.03550895	GO:0051241	GO:BP	negative regulation of multicellular organismal process
0.03674117	GO:1903557	GO:BP	positive regulation of tumor necrosis factor superfamily cytokine production
0.03869676	GO:0002573	GO:BP	myeloid leukocyte differentiation

0.03894546	GO:0003338	GO:BP	metanephros morphogenesis
0.0397397	GO:0008219	GO:BP	cell death
0.04344946	GO:0006915	GO:BP	apoptotic process
0.04608565	GO:1902532	GO:BP	negative regulation of intracellular signal transduction
0.04617162	GO:0046916	GO:BP	cellular transition metal ion homeostasis
0.04749094	GO:0019060	GO:BP	intracellular transport of viral protein in host cell
0.04749094	GO:0043007	GO:BP	maintenance of rDNA
0.04749094	GO:0043377	GO:BP	negative regulation of CD8-positive, alpha-beta T cell differentiation
0.04749094	GO:0009197	GO:BP	pyrimidine deoxyribonucleoside diphosphate biosynthetic process
0.04749094	GO:0009196	GO:BP	pyrimidine deoxyribonucleoside diphosphate metabolic process
0.04749094	GO:0034127	GO:BP	regulation of MyD88-independent toll-like receptor signaling pathway
0.04749094	GO:0072183	GO:BP	negative regulation of nephron tubule epithelial cell differentiation
0.04749094	GO:0030581	GO:BP	symbiont intracellular protein transport in host
0.04749094	GO:0001868	GO:BP	regulation of complement activation, lectin pathway
0.04749094	GO:0002274	GO:BP	myeloid leukocyte activation
0.04749094	GO:0046072	GO:BP	dTDP metabolic process
0.04749094	GO:0071276	GO:BP	cellular response to cadmium ion
0.04749094	GO:0001869	GO:BP	negative regulation of complement activation, lectin pathway
0.04749094	GO:0061394	GO:BP	regulation of transcription from RNA polymerase II promoter in response to arsenic-containing substance
0.04749094	GO:0046077	GO:BP	dUDP metabolic process
0.04749094	GO:0006233	GO:BP	dTDP biosynthetic process
0.04749094	GO:0006227	GO:BP	dUDP biosynthetic process
0.04749094	GO:0003340	GO:BP	negative regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis
0.04749094	GO:0046725	GO:BP	negative regulation by virus of viral protein levels in host cell
0.04749094	GO:0002761	GO:BP	regulation of myeloid leukocyte differentiation
0.04828234	GO:1903706	GO:BP	regulation of hemopoiesis
0.04830707	GO:0006882	GO:BP	cellular zinc ion homeostasis
0.04848604	GO:0012501	GO:BP	programmed cell death