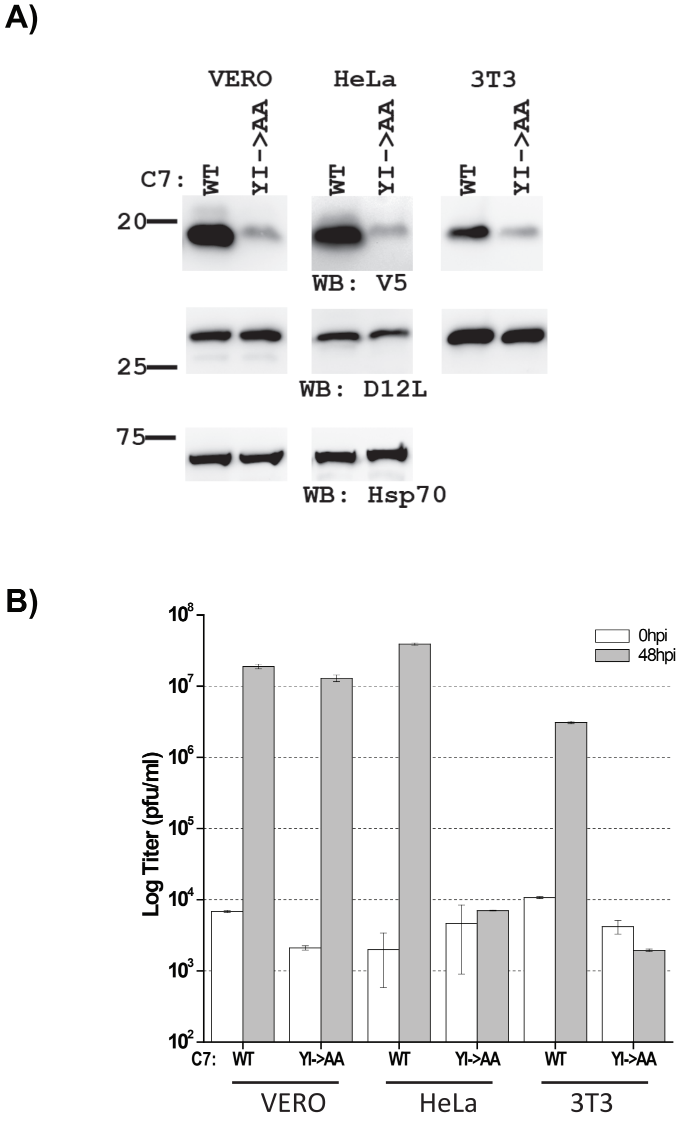

Supplemental figure 1. Tyr135 and Ile136 are critical for the function of VACV C7. **(A)** A recombinant VACV was generated by introducing to vK1L$^-$C7L$^-$ a C7L with alanine substitutions at Tyr135 and Ile136. This virus (C7:YI->AA) or vVACV-C7L (C7:WT) were used to infect the indicated cell lines at a MOI of 5. At 8 hpi, Western blot were performed as described in legend to Fig. 2B. **(B).** The cells were infected by the indicated viruses at a MOI of 0.5 PFU/cell. Virus titers at 0 and 48 hpi were determined by plaque assay on the permissive VERO cells.

Supplementary Table 1. Large scale ISG screens for VACV WT-GFP$^+$ and vK1L$^-$C7L$^-$/GFP$^+$. This table shows complete data sets from large scale ISG screens. For both viruses, replication levels, normalized to Fluc control, are shown with *z* scores. Data are ranked by differential *z* score, with genes preferentially inhibiting vK1L$^-$C7L$^-$/GFP$^+$ ranked first. The 100% normalization value was determined from the average of 3 independent preparations of Fluc.ires.TagRFP lentiviral pseudoparticles. Common ISG aliases: BST2 - tetherin, C19orf66 - FLJ11286, DDX58 - RIG-I, DDX60 - FLJ20035, DHX58 - LGP2, EIF2AK2 - PKR, IDO1 - INDO, IFI6 - G1P3 / 6-16, IFIH1 - MDA5, IFIT1 - ISG56, IFIT2 - ISG54, IFIT3 - ISG50, IFIT5 - ISG58, IFITM1 - 9-27, IFITM2 - 1-8D, IFITM3 - 1-8U, PSMB8 - LMP7, PSMB9 - LMP2, PSMB10 - MECL1, NAMPT - PBEF1, RSAD2 - viperin, ZBP1 - DAI, ZC3HAV1- ZAP.

Supplementary Table 1. Large scale ISG screen:VACV WT-GFP+ and vK1L-C7L-/GFP+ in Huh7 cells (Page 1 of 4)

	VACV WT-GFP+		vK1L-C7L-/GFP+				VACV WT-GFP+		vK1L-C7L-/GFP+		
Gene	**Percent Infected**	***Z* score**	**Percent Infected**	***Z* score**	**Differential *Z* score**	**Gene**	**Percent Infected**	***Z* score**	**Percent Infected**	***Z* score**	**Differential *Z* score**
TRIM25	140.9	3.13	73.7	-3.39	**-6.52**	**KIAA1618**	113.3	0.56	103.7	-0.37	**-0.93**
IRF1	120.4	1.22	87.7	-1.98	**-3.21**	**CEBPD**	107.3	0.00	98.1	-0.93	**-0.93**
IRF2	137.9	2.85	109.9	0.24	**-2.61**	**DDIT4**	100.7	-0.62	92.3	-1.52	**-0.90**
PRKD2	134.1	2.50	108.1	0.06	**-2.43**	**DDX58**	150.8	4.05	138.9	3.16	**-0.90**
THOC4	119.4	1.13	96.3	-1.11	**-2.24**	**MT1G**	98.4	-0.83	90.5	-1.70	**-0.87**
MT1F	118.6	1.06	96.1	-1.14	**-2.20**	**CD69**	118.4	1.03	109.1	0.17	**-0.87**
ERLIN1	117.6	0.96	97.1	-1.04	**-2.00**	**Fluc**	100.7	-0.62	92.8	-1.47	**-0.85**
STAT2	111.8	0.42	92.0	-1.55	**-1.97**	**HERC6**	111.0	0.35	102.5	-0.50	**-0.85**
FLJ39739	118.1	1.01	99.4	-0.81	**-1.82**	**PUS1**	111.0	0.35	102.7	-0.47	**-0.82**
CCNA1	124.5	1.60	105.5	-0.19	**-1.79**	**PNPT1**	104.7	-0.24	96.9	-1.06	**-0.82**
PPM1K	120.7	1.25	102.2	-0.52	**-1.77**	**PI4K2B**	102.4	-0.45	94.8	-1.27	**-0.81**
ADM	114.8	0.70	97.6	-0.99	**-1.69**	**DHX58**	116.1	0.82	107.6	0.01	**-0.81**
C1S	124.5	1.60	106.8	-0.06	**-1.66**	**ABLIM3**	113.1	0.54	104.8	-0.27	**-0.81**
RNF19B	112.8	0.51	96.3	-1.11	**-1.63**	**MKX**	117.6	0.96	109.1	0.17	**-0.80**
CCR1	122.7	1.43	106.0	-0.14	**-1.58**	**OAS2**	124.7	1.62	116.0	0.86	**-0.77**
UNC84B	113.1	0.54	97.4	-1.01	**-1.55**	**NCF1**	104.2	-0.29	97.1	-1.04	**-0.75**
IFITM3	115.6	0.77	99.9	-0.76	**-1.53**	**BLVRA**	102.4	-0.45	95.8	-1.16	**-0.71**
ZNF385B	117.9	0.99	102.5	-0.50	**-1.49**	**IL15**	100.7	-0.62	94.3	-1.32	**-0.70**
TAP1	125.2	1.67	109.6	0.22	**-1.45**	**HEG1**	120.4	1.22	112.7	0.52	**-0.70**
IL1RN	117.1	0.92	102.2	-0.52	**-1.44**	**MCOLN2**	107.5	0.02	100.7	-0.68	**-0.70**
C5orf39	120.2	1.20	105.3	-0.22	**-1.42**	**HLA-C**	98.7	-0.81	92.5	-1.50	**-0.69**
NOD2	111.6	0.40	97.4	-1.01	**-1.41**	**CCND3**	96.1	-1.04	90.2	-1.73	**-0.68**
MT1M	115.6	0.77	101.4	-0.60	**-1.38**	**GMPR**	108.5	0.11	102.0	-0.55	**-0.66**
ARHGEF3	116.1	0.82	102.0	-0.55	**-1.37**	**SPSB1**	113.8	0.61	107.1	-0.04	**-0.65**
HSH2D	122.9	1.46	108.6	0.11	**-1.34**	**CYP1B1**	111.8	0.42	105.3	-0.22	**-0.64**
TNFAIP3	114.8	0.70	101.2	-0.63	**-1.33**	**IFI35**	112.3	0.47	105.8	-0.17	**-0.63**
LIPA	109.0	0.16	96.1	-1.14	**-1.30**	**FUT4**	117.6	0.96	110.9	0.34	**-0.62**
TIMP1	122.2	1.39	108.3	0.09	**-1.30**	**FNDC4**	101.4	-0.55	95.8	-1.16	**-0.62**
SCARB2	115.9	0.80	102.5	-0.50	**-1.30**	**FAM134B**	106.2	-0.10	100.4	-0.70	**-0.60**
SAMD4A	114.3	0.66	101.2	-0.63	**-1.28**	**DUSP5**	107.0	-0.03	101.2	-0.63	**-0.60**
C5orf27	113.1	0.54	100.4	-0.70	**-1.24**	**TBX3**	130.5	2.17	123.1	1.57	**-0.59**
CRY1	96.1	-1.04	84.9	-2.26	**-1.22**	**TNFAIP6**	114.3	0.66	108.1	0.06	**-0.59**
NPAS2	116.6	0.87	104.0	-0.35	**-1.21**	**SNN**	121.2	1.29	114.4	0.70	**-0.59**
IRF7	113.6	0.59	101.4	-0.60	**-1.19**	**NUP50**	119.9	1.18	113.4	0.60	**-0.57**
UPP2	120.9	1.27	108.6	0.11	**-1.16**	**STAP1**	110.3	0.28	104.5	-0.29	**-0.57**
HLA-F	115.6	0.77	103.7	-0.37	**-1.15**	**CRP**	117.6	0.96	111.4	0.40	**-0.57**
C4orf32	119.4	1.13	107.3	-0.01	**-1.14**	**LGALS9**	111.8	0.42	106.0	-0.14	**-0.56**
G6PC	120.4	1.22	108.3	0.09	**-1.13**	**GCH1**	115.1	0.73	109.1	0.17	**-0.56**
RSAD2	107.3	0.00	96.3	-1.11	**-1.11**	**P2RY6**	116.4	0.84	110.4	0.29	**-0.55**
GBP4	108.3	0.09	97.4	-1.01	**-1.10**	**ATF3**	107.0	-0.03	101.7	-0.58	**-0.55**
IL6ST	124.7	1.62	112.7	0.52	**-1.10**	**CD163**	126.0	1.74	119.5	1.21	**-0.53**
PTMA	111.8	0.42	100.7	-0.68	**-1.10**	**NAPA**	100.2	-0.67	95.6	-1.19	**-0.52**
ULK4	118.6	1.06	107.3	-0.01	**-1.07**	**CLEC2B**	106.7	-0.05	101.7	-0.58	**-0.52**
MICB	103.5	-0.36	93.3	-1.42	**-1.06**	**RGS1**	103.7	-0.34	98.9	-0.86	**-0.52**
EHD4	101.9	-0.50	92.0	-1.55	**-1.05**	**C10orf10**	113.6	0.59	108.1	0.06	**-0.52**
NMI	100.7	-0.62	91.0	-1.65	**-1.03**	**TAGAP**	123.9	1.55	117.8	1.04	**-0.52**
PIM3	110.8	0.33	100.7	-0.68	**-1.00**	**HK2**	115.3	0.75	109.9	0.24	**-0.51**
KIAA0082	112.1	0.44	102.0	-0.55	**-0.99**	**RIK2**	119.6	1.15	113.9	0.65	**-0.50**
MTHFD2L	101.7	-0.52	92.5	-1.50	**-0.97**	**APOL2**	116.9	0.89	111.4	0.40	**-0.50**
CX3CL1	112.6	0.49	102.7	-0.47	**-0.96**	**GLRX**	120.2	1.20	114.4	0.70	**-0.50**

Supplementary Table 1. Large scale ISG screen:VACV WT-GFP+ and vK1L-C7L-/GFP+ in Huh7 cells (Page 2 of 4)

	VACV WT-GFP+		vK1L-C7L-/GFP+				VACV WT-GFP+		vK1L-C7L-/GFP+		
Gene	**Percent Infected**	***Z* score**	**Percent Infected**	***Z* score**	**Differential *Z* score**	**Gene**	**Percent Infected**	***Z* score**	**Percent Infected**	***Z* score**	**Differential *Z* score**
GBP5	105.0	-0.22	100.4	-0.70	**-0.49**	**MT1H**	91.3	-1.49	91.8	-1.57	**-0.08**
TMEM51	118.4	1.03	112.9	0.55	**-0.48**	**SIRPA**	101.4	-0.55	101.2	-0.63	**-0.08**
FAM125B	121.7	1.34	116.0	0.86	**-0.48**	**CES1**	108.5	0.11	108.1	0.06	**-0.05**
SLC16A1	108.8	0.14	104.0	-0.35	**-0.48**	**FCGR1A**	109.0	0.16	108.6	0.11	**-0.05**
ISG20	115.9	0.80	110.6	0.32	**-0.48**	**UNC93B1**	104.2	-0.29	104.2	-0.32	**-0.03**
GAK	104.5	-0.26	100.2	-0.73	**-0.47**	**IL17RB**	117.4	0.94	116.5	0.91	**-0.03**
LMO2	127.7	1.91	121.8	1.44	**-0.46**	**HLA-E**	101.2	-0.57	101.4	-0.60	**-0.03**
LRG1	89.5	-1.66	86.4	-2.11	**-0.45**	**SERPINB9**	91.6	-1.47	92.5	-1.50	**-0.03**
HES4	96.4	-1.02	93.0	-1.45	**-0.43**	**COMMD3**	108.3	0.09	108.1	0.06	**-0.03**
MAX	101.7	-0.52	98.1	-0.93	**-0.41**	**TYMP**	93.1	-1.33	94.1	-1.34	**-0.02**
NT5C3	99.9	-0.69	97.1	-1.04	**-0.35**	**SLC25A28**	100.2	-0.67	100.7	-0.68	**-0.01**
FAM46A	106.7	-0.05	103.5	-0.40	**-0.35**	**ALDH1A1**	109.0	0.16	109.1	0.17	**0.01**
SLC25A30	116.6	0.87	112.7	0.52	**-0.34**	**Fluc**	106.0	-0.12	106.3	-0.12	**0.01**
DNAPTP6	113.8	0.61	110.1	0.27	**-0.34**	**TRIM14**	97.6	-0.90	98.6	-0.88	**0.02**
IFITM3	112.1	0.44	108.6	0.11	**-0.33**	**SERPINE1**	99.9	-0.69	100.9	-0.65	**0.04**
STAT1	112.6	0.49	109.1	0.17	**-0.33**	**HPSE**	100.9	-0.59	102.0	-0.55	**0.04**
SLC15A3	99.7	-0.71	97.1	-1.04	**-0.32**	**PDGFRL**	105.2	-0.19	106.0	-0.14	**0.05**
CCL2	107.5	0.02	104.5	-0.29	**-0.31**	**SECTM1**	106.0	-0.12	106.8	-0.06	**0.06**
FBXO6	112.3	0.47	109.1	0.17	**-0.30**	**WARS**	96.4	-1.02	97.9	-0.96	**0.06**
HLA-G	103.5	-0.36	100.9	-0.65	**-0.29**	**ATP10D**	103.2	-0.38	104.2	-0.32	**0.06**
GBP2	107.3	0.00	104.5	-0.29	**-0.29**	**LAP3**	103.2	-0.38	104.2	-0.32	**0.06**
PRIC285	101.4	-0.55	99.2	-0.83	**-0.28**	**AXUD1**	110.3	0.28	110.9	0.34	**0.07**
CD38	111.6	0.40	108.6	0.11	**-0.28**	**USP18**	97.4	-0.93	98.9	-0.86	**0.07**
ADFP	101.9	-0.50	99.7	-0.78	**-0.28**	**GBP3**	107.3	0.00	108.1	0.06	**0.07**
JUNB	97.1	-0.95	95.3	-1.22	**-0.27**	**GCA**	107.3	0.00	108.1	0.06	**0.07**
PSCD1	97.4	-0.93	95.6	-1.19	**-0.26**	**CFB**	118.4	1.03	118.5	1.11	**0.08**
C4orf33	114.3	0.66	111.4	0.40	**-0.26**	**IFNGR1**	125.5	1.69	125.1	1.78	**0.08**
ZBP1	111.3	0.37	108.6	0.11	**-0.26**	**PNRC1**	97.4	-0.93	99.2	-0.83	**0.09**
MAFB	114.8	0.70	111.9	0.45	**-0.26**	**IFIT1**	99.7	-0.71	101.4	-0.60	**0.11**
C9orf91	103.2	-0.38	101.2	-0.63	**-0.25**	**ANGPTL1**	106.2	-0.10	107.6	0.01	**0.11**
RARRES3	106.0	-0.12	104.0	-0.35	**-0.22**	**FAM46C**	117.1	0.92	117.8	1.04	**0.12**
IRF9	109.8	0.23	107.6	0.01	**-0.22**	**ISG15**	94.6	-1.18	96.9	-1.06	**0.12**
C9orf19	136.3	2.71	132.3	2.49	**-0.22**	**BST2**	122.2	1.39	122.6	1.52	**0.13**
BTN3A3	112.1	0.44	109.9	0.24	**-0.20**	**GJA4**	109.8	0.23	111.1	0.37	**0.14**
CASP7	109.5	0.21	107.6	0.01	**-0.20**	**AMPH**	114.6	0.68	115.7	0.83	**0.15**
GTPBP2	107.0	-0.03	105.3	-0.22	**-0.19**	**WHDC1**	95.1	-1.14	97.6	-0.99	**0.15**
PSMB9	121.2	1.29	118.5	1.11	**-0.18**	**TAP2**	104.2	-0.29	106.3	-0.12	**0.17**
CSDA	99.2	-0.76	98.1	-0.93	**-0.17**	**NRN1**	105.7	-0.15	107.8	0.04	**0.18**
ARG2	105.7	-0.15	104.2	-0.32	**-0.17**	**OPTN**	97.1	-0.95	99.9	-0.76	**0.19**
B4GALT5	109.8	0.23	108.1	0.06	**-0.17**	**VEGFC**	94.1	-1.23	97.1	-1.04	**0.20**
RASSF4	107.3	0.00	105.8	-0.17	**-0.16**	**BAG1**	104.0	-0.31	106.3	-0.12	**0.20**
MARCKS	112.3	0.47	110.6	0.32	**-0.15**	**ADAMDEC1**	97.6	-0.90	100.4	-0.70	**0.20**
GK	107.0	-0.03	105.8	-0.17	**-0.14**	**OASL**	134.1	2.50	134.3	2.70	**0.20**
PCTK2	113.6	0.59	111.9	0.45	**-0.14**	**LGALS3**	99.2	-0.76	102.0	-0.55	**0.21**
SAMHD1	107.5	0.02	106.3	-0.12	**-0.13**	**SSBP3**	96.1	-1.04	99.2	-0.83	**0.21**
XAF1	115.3	0.75	113.7	0.63	**-0.12**	**ETV7**	92.3	-1.40	95.8	-1.16	**0.23**
STARD5	105.7	-0.15	104.8	-0.27	**-0.12**	**MX1**	113.3	0.56	115.5	0.81	**0.24**
AKT3	90.6	-1.56	91.0	-1.65	**-0.09**	**PBEF1**	108.3	0.09	111.1	0.37	**0.28**
ANKRD22	116.9	0.89	115.5	0.81	**-0.09**	**IL28RA**	99.4	-0.74	103.0	-0.45	**0.29**
RAB27A	107.5	0.02	106.8	-0.06	**-0.08**	**JAK2**	113.3	0.56	116.2	0.88	**0.32**

Supplementary Table 1. Large scale ISG screen:VACV WT-GFP+ and vK1L-C7L-/GFP+ in Huh7 cells (Page 3 of 4)

	VACV WT-GFP+		vK1L-C7L-/GFP+				VACV WT-GFP+		vK1L-C7L-/GFP+		
Gene	Percent Infected	*Z* score	Percent Infected	*Z* score	Differential *Z* score	Gene	Percent Infected	*Z* score	Percent Infected	*Z* score	Differential *Z* score
NFIL3	98.4	-0.83	102.5	-0.50	**0.33**	**LAMP3**	96.9	-0.97	104.2	-0.32	**0.65**
EIF3EIP	105.2	-0.19	108.8	0.14	**0.33**	**FLJ23556**	94.4	-1.21	102.0	-0.55	**0.66**
SLFN5	121.7	1.34	124.1	1.67	**0.33**	**TXNIP**	111.3	0.37	118.0	1.06	**0.69**
IMPA2	103.2	-0.38	107.1	-0.04	**0.34**	**TREX1**	96.1	-1.04	104.0	-0.35	**0.70**
IGFBP2	98.9	-0.78	103.2	-0.42	**0.36**	**AGPAT9**	90.3	-1.59	98.6	-0.88	**0.70**
SP110	104.0	-0.31	108.1	0.06	**0.37**	**MAFF**	117.6	0.96	124.1	1.67	**0.71**
STEAP4	97.6	-0.90	102.2	-0.52	**0.38**	**MYD88**	92.1	-1.42	100.4	-0.70	**0.72**
IFI44	100.9	-0.59	105.3	-0.22	**0.38**	**ETV6**	96.4	-1.02	104.5	-0.29	**0.72**
MAB21L2	110.8	0.33	114.4	0.70	**0.38**	**EXT1**	112.1	0.44	119.3	1.19	**0.74**
CCDC109B	104.7	-0.24	108.8	0.14	**0.38**	**PSMB8**	112.6	0.49	119.8	1.24	**0.75**
APOBEC3A	111.8	0.42	115.5	0.81	**0.38**	**THBD**	87.5	-1.85	96.6	-1.09	**0.76**
TNFSF10	122.4	1.41	125.4	1.80	**0.39**	**SOCS1**	97.4	-0.93	105.8	-0.17	**0.76**
CXCL9	107.8	0.04	111.9	0.45	**0.40**	**PRAME**	90.1	-1.61	99.2	-0.83	**0.78**
ADAR	111.3	0.37	115.2	0.78	**0.41**	**SOCS2**	106.5	-0.08	114.4	0.70	**0.78**
GALNT2	95.1	-1.14	100.2	-0.73	**0.41**	**RBCK1**	89.3	-1.68	98.6	-0.88	**0.80**
IFI30	95.9	-1.07	100.9	-0.65	**0.41**	**PADI2**	96.4	-1.02	105.3	-0.22	**0.80**
CD74	96.1	-1.04	101.2	-0.63	**0.42**	**AIM2**	97.4	-0.93	106.3	-0.12	**0.81**
CD80	116.1	0.82	119.8	1.24	**0.42**	**ZNF313**	128.5	1.98	135.3	2.80	**0.82**
CPT1A	99.2	-0.76	104.2	-0.32	**0.44**	**BCL3**	93.6	-1.28	103.2	-0.42	**0.86**
UBE2L6	101.4	-0.55	106.5	-0.09	**0.46**	**CCL5**	103.5	-0.36	112.4	0.50	**0.86**
PML	109.0	0.16	113.7	0.63	**0.47**	**SPTLC2**	103.5	-0.36	112.4	0.50	**0.86**
TMEM140	119.6	1.15	123.6	1.62	**0.47**	**PMAIP1**	97.6	-0.90	107.1	-0.04	**0.86**
C22orf28	100.2	-0.67	105.5	-0.19	**0.47**	**S100A8**	95.1	-1.14	104.8	-0.27	**0.87**
MSR1	114.8	0.70	119.3	1.19	**0.49**	**ABTB2**	118.6	1.06	126.7	1.93	**0.87**
TRIM5	92.1	-1.42	98.1	-0.93	**0.49**	**EPAS1**	119.9	1.18	128.0	2.06	**0.88**
TNFRSF10A	122.2	1.39	126.2	1.88	**0.49**	**GBP1**	101.4	-0.55	110.9	0.34	**0.89**
C6orf150	99.4	-0.74	105.0	-0.24	**0.49**	**PFKFB3**	99.4	-0.74	109.1	0.17	**0.90**
IFI27	106.5	-0.08	111.6	0.42	**0.50**	**CXCL10**	112.1	0.44	121.1	1.37	**0.92**
IFI44L	126.5	1.79	130.2	2.29	**0.50**	**PXK**	92.6	-1.37	103.0	-0.45	**0.93**
PPM1K	103.7	-0.34	109.1	0.17	**0.50**	**PHF15**	114.1	0.63	123.1	1.57	**0.94**
IFI6	107.5	0.02	112.9	0.55	**0.53**	**TDRD7**	111.8	0.42	121.1	1.37	**0.95**
IFIT5	95.1	-1.14	101.4	-0.60	**0.54**	**DCP1A**	118.9	1.08	127.7	2.03	**0.95**
TNSF13B	108.3	0.09	113.7	0.63	**0.54**	**APOL1**	97.4	-0.93	107.8	0.04	**0.96**
GTPBP1	99.7	-0.71	105.8	-0.17	**0.55**	**SCO2**	95.6	-1.09	106.3	-0.12	**0.97**
IL15RA	106.2	-0.10	111.9	0.45	**0.55**	**LY6E**	113.1	0.54	122.6	1.52	**0.98**
NDC80	112.8	0.51	118.0	1.06	**0.55**	**ACSL1**	101.4	-0.55	111.9	0.45	**0.99**
SLC1A1	99.9	-0.69	106.0	-0.14	**0.55**	**MCL1**	88.3	-1.77	100.2	-0.73	**1.04**
AQP9	91.6	-1.47	98.4	-0.91	**0.56**	**KIAA0040**	105.2	-0.19	116.0	0.86	**1.05**
TRIM21	95.1	-1.14	101.7	-0.58	**0.56**	**B2M**	97.6	-0.90	109.1	0.17	**1.07**
IFIT2	99.4	-0.74	105.8	-0.17	**0.57**	**PLEKHA4**	101.7	-0.52	113.2	0.57	**1.10**
CD274	87.3	-1.87	94.6	-1.29	**0.58**	**MT1X**	100.7	-0.62	112.4	0.50	**1.12**
SMAD3	98.4	-0.83	105.0	-0.24	**0.59**	**IL1R**	97.6	-0.90	109.6	0.22	**1.12**
VAMP5	103.0	-0.41	109.3	0.19	**0.60**	**TRAFD1**	92.8	-1.35	105.3	-0.22	**1.13**
LGMN	97.1	-0.95	104.0	-0.35	**0.60**	**CCL8**	96.6	-1.00	109.1	0.17	**1.16**
AHNAK2	97.9	-0.88	104.8	-0.27	**0.61**	**OGFR**	81.7	-2.39	95.3	-1.22	**1.17**
CLEC4E	83.2	-2.25	91.2	-1.62	**0.62**	**CLEC4D**	91.8	-1.44	104.8	-0.27	**1.17**
Fluc	93.3	-1.30	100.7	-0.68	**0.62**	**GEM**	96.4	-1.02	109.3	0.19	**1.21**
SAT3	108.8	0.14	115.2	0.78	**0.64**	**ARNTL**	75.9	-2.93	90.5	-1.70	**1.23**
NCOA3	121.9	1.36	127.4	2.01	**0.64**	**CD9**	108.8	0.14	121.1	1.37	**1.23**
GZMB	113.1	0.54	119.3	1.19	**0.65**	**CCL19**	107.3	0.00	119.8	1.24	**1.24**

Supplementary Table 1. Large scale ISG screen:VACV WT-GFP+ and vK1L-C7L-/GFP+ in Huh7 cells (Page 4 of 4)

	VACV WT-GFP+		vK1L-C7L-/GFP+				VACV WT-GFP+		vK1L-C7L-/GFP+		
Gene	**Percent Infected**	***Z* score**	**Percent Infected**	***Z* score**	**Differential *Z* score**	**Gene**	**Percent Infected**	***Z* score**	**Percent Infected**	***Z* score**	**Differential *Z* score**
GPX2	99.9	-0.69	113.2	0.57	**1.26**						
CTCFL	99.2	-0.76	112.7	0.52	**1.28**						
CCDC75	113.8	0.61	126.4	1.90	**1.30**						
HESX1	107.8	0.04	120.8	1.34	**1.30**						
ENPP1	118.6	1.06	131.0	2.37	**1.31**						
TMEM49	94.1	-1.23	108.6	0.11	**1.35**						
TRIM34	92.6	-1.37	107.3	-0.01	**1.36**						
ANKFY1	132.0	2.31	144.0	3.67	**1.36**						
DEFB1	109.5	0.21	123.1	1.57	**1.36**						
PDK1	92.1	-1.42	107.1	-0.04	**1.38**						
CMAH	102.4	-0.45	116.7	0.93	**1.39**						
PMM2	97.1	-0.95	112.1	0.47	**1.42**						
SAA1	94.1	-1.23	109.3	0.19	**1.42**						
DYNLT1	101.9	-0.50	116.7	0.93	**1.43**						
LEPR	104.5	-0.26	119.5	1.21	**1.48**						
RPL22	103.5	-0.36	119.5	1.21	**1.57**						
CCL4	96.4	-1.02	113.2	0.57	**1.59**						
INDO	91.3	-1.49	108.8	0.14	**1.63**						
SERPING1	95.9	-1.07	113.9	0.65	**1.72**						
TRIM38	91.3	-1.49	110.1	0.27	**1.76**						
CDKN1A	112.3	0.47	129.7	2.24	**1.77**						
C15orf48	103.7	-0.34	122.1	1.47	**1.81**						
LINCR	90.6	-1.56	110.6	0.32	**1.88**						
IFITM2	89.8	-1.63	110.6	0.32	**1.95**						
CREB3L3	90.1	-1.61	111.6	0.42	**2.03**						
PLSCR1	108.3	0.09	128.7	2.14	**2.05**						
FKBP5	100.4	-0.64	122.6	1.52	**2.16**						
C2orf31	97.4	-0.93	122.3	1.50	**2.42**						
MAP3K5	109.8	0.23	137.6	3.03	**2.80**						
CHMP5	111.8	0.42	139.9	3.26	**2.84**						