Supplemental Table 1

Large Scale ISG Screen: EboV trVLP in HEK293T cells – p1 and p2 values (Page 1 of 4)

Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score	Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score
P2RY6	0.4	-1.24	41.5	-1.23	**MCOLN**	28.0	-0.89	40.4	-1.25
BST2/THN	0.5	-1.24	91.8	-0.18	**ZNF313**	28.1	-0.89	53.5	-0.98
CCL5	0.5	-1.24	106.0	0.11	**PDGFRL**	28.3	-0.89	100.0	-0.01
NMI	0.6	-1.24	0.4	-2.08	**PNPT1**	28.7	-0.88	103.6	0.06
APOL6	0.6	-1.24	188.5	1.83	**PHF15**	28.7	-0.88	119.2	0.39
ARHGAP17	1.9	-1.22	57.9	-0.88	**GBP5**	28.9	-0.88	116.9	0.34
WHDC1	2.3	-1.21	32.0	-1.42	**JAK2**	29.6	-0.87	96.8	-0.08
B2M	2.8	-1.21	108.2	0.16	**ATF3**	30.3	-0.86	116.4	0.33
OAS1	2.9	-1.21	76.4	-0.50	**C10orf10**	30.5	-0.86	41.8	-1.22
CTCFL	3.3	-1.20	55.6	-0.93	**AIM2**	30.5	-0.86	70.3	-0.63
DNAPTP6	3.4	-1.20	58.4	-0.88	**CCL19**	30.6	-0.86	78.0	-0.47
PPM1K	4.2	-1.19	35.0	-1.36	**RAB27A**	30.9	-0.86	58.7	-0.87
MT1G	4.3	-1.19	57.1	-0.90	**IFI35**	31.1	-0.85	174.6	1.54
IFIH1 / MDA5	4.3	-1.19	17.9	-1.72	**FBXO6**	31.4	-0.85	52.3	-1.00
FNDC4	8.1	-1.14	142.9	0.88	**UNC93B1**	31.9	-0.84	28.2	-1.50
C5orf39	8.3	-1.14	15.0	-1.78	**HLA-E**	32.1	-0.84	66.7	-0.70
SOCS2	8.5	-1.14	77.3	-0.48	**GTPBP2**	32.5	-0.84	184.2	1.74
FCGR1A	10.1	-1.12	148.1	0.99	**GLRX**	32.8	-0.83	60.9	-0.82
MCL1	11.2	-1.10	124.4	0.50	**CX3CL1**	33.1	-0.83	212.9	2.33
ARHGEF3	11.4	-1.10	15.9	-1.76	**TAP2**	33.2	-0.83	145.1	0.92
FLT1	11.7	-1.10	67.9	-0.68	**XAF1**	33.4	-0.82	55.0	-0.95
MAP3K14	11.9	-1.09	63.6	-0.77	**WARS**	33.7	-0.82	112.2	0.24
OASL	12.1	-1.09	123.2	0.47	**IFNGR1**	34.1	-0.82	51.7	-1.01
TNK2	12.4	-1.09	165.0	1.34	**SLC25A28**	34.5	-0.81	105.1	0.10
GBP2	13.2	-1.08	74.2	-0.55	**VIPERIN**	34.7	-0.81	98.2	-0.05
GALNT2	13.7	-1.07	133.9	0.69	**ZBP1**	34.9	-0.81	54.1	-0.96
FFAR2	14.9	-1.06	43.0	-1.20	**MYD88**	35.4	-0.80	46.4	-1.12
CCDC92	15.0	-1.06	79.8	-0.43	**CASP7**	35.5	-0.80	71.3	-0.61
LMO2	15.4	-1.05	80.7	-0.41	**NDC80**	35.6	-0.80	66.9	-0.70
SLC15A3	16.0	-1.04	174.0	1.53	**MAFF**	36.0	-0.79	97.5	-0.06
HERC5	16.6	-1.04	77.1	-0.49	**APOBEC3A**	36.5	-0.79	56.2	-0.92
TXNIP	16.6	-1.03	80.5	-0.42	**ZNF385B**	36.6	-0.78	61.2	-0.82
UBA7	17.5	-1.02	55.8	-0.93	**DEFB1**	37.1	-0.78	80.9	-0.41
PIM3	17.5	-1.02	87.6	-0.27	**XRN**	37.1	-0.78	88.0	-0.26
TRIM25	17.7	-1.02	25.4	-1.56	**SAMD4A**	38.3	-0.76	62.5	-0.79
TRIM56	19.2	-1.00	25.6	-1.56	**SMAD3**	38.7	-0.76	80.5	-0.42
SLFN12	19.4	-1.00	56.1	-0.92	**STAT2**	39.9	-0.74	105.0	0.09
STEAP4	19.8	-1.00	86.3	-0.30	**PUS1**	39.9	-0.74	120.3	0.41
CXCL10	19.8	-0.99	90.5	-0.21	**IFIT3**	40.9	-0.73	92.5	-0.17
MAB21L2	19.9	-0.99	130.6	0.62	**C15orf48**	41.2	-0.73	63.9	-0.76
FAM46C	20.6	-0.99	38.6	-1.29	**IFITM1**	41.3	-0.73	109.3	0.18
MX2	21.6	-0.97	49.9	-1.05	**GK**	41.4	-0.72	67.8	-0.68
GBP1	21.8	-0.97	78.6	-0.46	**SAT1**	42.4	-0.71	93.9	-0.14
PABPC4	22.0	-0.97	20.4	-1.67	**KIAA0082**	42.5	-0.71	50.9	-1.03
SERPINE1	22.3	-0.96	52.2	-1.00	**TNFRSF10A**	43.7	-0.70	177.3	1.59
SERPING1	23.2	-0.95	68.0	-0.68	**TNFAIP3**	44.3	-0.69	182.0	1.69
C5orf27	23.5	-0.95	81.9	-0.39	**IL28RA**	44.4	-0.69	80.4	-0.42
SERPINB9	23.8	-0.94	155.3	1.14	**NFIL3**	45.0	-0.68	78.1	-0.47
IRF1	24.0	-0.94	33.2	-1.40	**RARRES3**	45.1	-0.68	97.0	-0.07
HCP5	24.5	-0.94	110.4	0.21	**BIRC3**	46.4	-0.66	67.0	-0.70
ODC1	24.6	-0.93	151.4	1.06	**HEG1**	46.5	-0.66	74.1	-0.55
TRIM14	24.7	-0.93	65.9	-0.72	**C9ofr19**	46.5	-0.66	85.1	-0.32
CLEC4D	25.3	-0.93	68.9	-0.66	**HSPA6**	46.6	-0.66	124.7	0.50
IFIT1	25.4	-0.92	96.3	-0.09	**USP18**	47.4	-0.65	52.6	-1.00
CNP	25.5	-0.92	156.1	1.15	**DDX60**	47.7	-0.65	87.9	-0.26
NCF1	26.8	-0.91	92.8	-0.16	**EPAS1**	48.0	-0.64	193.5	1.93
CD274	26.9	-0.91	88.2	-0.26	**SAMHD1**	48.2	-0.64	55.7	-0.93
IFI27	27.5	-0.90	95.5	-0.10	**FAM125B**	48.4	-0.64	60.8	-0.82
CEACAM1	27.6	-0.90	59.7	-0.85	**STAP1**	49.1	-0.63	50.5	-1.04

Large Scale ISG Screen: EboV trVLP in HEK293T cells – p1 and p2 values (Page 2 of 4)

Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score	Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score
DYNLT1	49.5	-0.62	77.0	-0.49	**ISG20**	68.1	-0.39	44.7	-1.16
SSBP3	49.5	-0.62	51.2	-1.03	**TRAFD1**	68.1	-0.39	126.7	0.54
RBM43	49.7	-0.62	75.9	-0.51	**MX1**	68.2	-0.39	72.0	-0.59
AKT3	49.8	-0.62	109.0	0.18	**HLA-F**	68.4	-0.39	125.4	0.52
ANGPTL1	50.5	-0.61	97.3	-0.07	**TAP1**	68.6	-0.38	98.8	-0.04
FAM70A	50.7	-0.61	75.8	-0.51	**LGALS3**	69.9	-0.37	85.9	-0.30
UPP2	50.7	-0.61	50.0	-1.05	**HLA-C**	70.2	-0.36	123.5	0.48
SIRPA	51.0	-0.60	38.2	-1.29	**CASP1**	70.4	-0.36	43.4	-1.19
CCND3	52.1	-0.59	163.9	1.32	**RPL22**	70.8	-0.35	116.2	0.33
RNF19B	52.2	-0.59	82.5	-0.37	**APOL3**	71.2	-0.35	75.3	-0.52
MTHFD2L	52.5	-0.59	73.4	-0.56	**PSCD1**	72.4	-0.34	67.5	-0.69
EIF3EIP	53.2	-0.58	147.1	0.97	**SCO2**	72.6	-0.33	166.5	1.37
THBD	53.3	-0.57	201.1	2.09	**TRIM38**	73.4	-0.32	116.5	0.33
NT5C3	53.5	-0.57	84.5	-0.33	**IFI44**	75.2	-0.30	79.5	-0.44
PSMB8	53.6	-0.57	80.4	-0.42	**IFI44L**	75.7	-0.29	30.0	-1.47
MS4A4A	54.0	-0.57	52.2	-1.00	**AXUD1**	75.9	-0.29	90.9	-0.20
SECTM1	54.0	-0.57	45.8	-1.14	**MAFF**	76.4	-0.28	102.4	0.04
ABLIM3	54.5	-0.56	53.7	-0.97	**ARNTL**	76.6	-0.28	154.5	1.12
FAM46A	54.9	-0.55	52.3	-1.00	**TLR3**	76.9	-0.28	106.4	0.12
RTP4	55.1	-0.55	87.1	-0.28	**CXCL9**	77.0	-0.28	85.2	-0.32
CMAH	55.2	-0.55	115.0	0.30	**C9orf91**	77.0	-0.28	120.6	0.42
MT1M	55.9	-0.54	148.2	0.99	**IFI16**	77.7	-0.27	94.9	-0.12
SOCS1	56.6	-0.53	108.5	0.17	**PSMB9**	77.7	-0.27	126.0	0.53
DDX58	57.1	-0.53	33.2	-1.40	**IFITM3**	78.3	-0.26	64.8	-0.74
BAG1	57.2	-0.53	122.4	0.45	**ALDH1A1**	78.9	-0.25	69.4	-0.65
UNC84B	57.3	-0.52	96.8	-0.08	**ERLIN1**	79.2	-0.25	72.9	-0.57
C19orf66	57.4	-0.52	96.9	-0.08	**CCL8**	79.3	-0.25	51.3	-1.02
B4GALT5	57.9	-0.52	104.5	0.08	**INDO**	79.8	-0.24	88.7	-0.25
SPTLC2	58.1	-0.51	88.3	-0.25	**RNASE4**	80.1	-0.24	161.0	1.26
BUB1	58.6	-0.51	74.2	-0.55	**AGPAT9**	80.2	-0.24	69.0	-0.66
MOV10	59.1	-0.50	513.4	8.58	**DCP1A**	82.3	-0.21	108.3	0.16
SAMD9L	59.4	-0.50	66.9	-0.70	**HERC6**	82.5	-0.21	124.0	0.49
TMEM51	60.0	-0.49	104.9	0.09	**IL17RB**	82.9	-0.20	152.4	1.08
VAMP5	60.2	-0.49	65.5	-0.73	**JUNB**	84.0	-0.19	115.9	0.32
BLZF1	60.2	-0.49	109.1	0.18	**N4BP1**	84.5	-0.18	59.3	-0.86
PRKD2	60.4	-0.49	150.6	1.04	**EPSTI1**	84.6	-0.18	90.3	-0.21
CHMP5	60.6	-0.48	126.8	0.55	**TGFB1**	85.1	-0.18	126.1	0.53
DDX3X	60.6	-0.48	59.7	-0.85	**SAA1**	85.1	-0.18	204.6	2.16
TMEM49	60.9	-0.48	118.1	0.36	**PFKFB3**	85.6	-0.17	137.3	0.76
SP110	61.2	-0.48	131.9	0.65	**C2orf31**	85.9	-0.17	125.1	0.51
CCNA1	62.6	-0.46	128.5	0.58	**PCTK3**	86.5	-0.16	113.5	0.27
IRF9	62.9	-0.46	90.5	-0.21	**PARP12**	86.7	-0.16	103.0	0.05
PARP10	63.6	-0.45	98.6	-0.04	**STARD5**	87.4	-0.15	115.0	0.30
SLC1A1	63.7	-0.45	51.9	-1.01	**FER1L3**	87.5	-0.15	69.5	-0.65
ANKRD22	64.0	-0.44	110.6	0.21	**ISG15**	87.6	-0.14	135.4	0.72
C4orf32	64.0	-0.44	91.9	-0.18	**MT1L**	87.7	-0.14	84.7	-0.33
BCL3	64.0	-0.44	128.9	0.59	**IFI6**	87.9	-0.14	47.4	-1.10
MAFF	64.1	-0.44	64.8	-0.74	**IFITM2**	88.1	-0.14	86.1	-0.30
C4orf33	64.4	-0.44	76.6	-0.50	**PMAIP1**	88.5	-0.13	61.8	-0.81
C1S	64.5	-0.43	50.3	-1.04	**NOS2A**	89.7	-0.12	76.5	-0.50
APOL2	64.6	-0.43	87.8	-0.26	**PLEKHA4**	90.0	-0.11	83.1	-0.36
TRIM21	65.5	-0.42	56.4	-0.92	**STAT3**	90.7	-0.11	61.9	-0.80
HESX1	65.9	-0.42	97.7	-0.06	**EIF2AK2**	91.0	-0.10	67.4	-0.69
SNN	66.7	-0.41	57.6	-0.89	**ELF1**	91.5	-0.10	32.8	-1.41
LIPA	66.7	-0.41	107.0	0.13	**PBEF1**	92.3	-0.09	127.7	0.56
LAMP3	67.1	-0.40	107.0	0.13	**RIPK2**	92.6	-0.08	28.7	-1.49
CCDC109B	67.2	-0.40	51.7	-1.02	**DUSP5**	93.1	-0.08	142.8	0.88
OPTN	67.8	-0.39	77.9	-0.47	**CSDA**	93.8	-0.07	164.4	1.33
DDIT4	68.0	-0.39	130.1	0.61	**OGFR**	94.1	-0.06	106.3	0.12

Large Scale ISG Screen: EboV trVLP in HEK293 cells – p1 and p2 values (Page 3 of 4)

Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score	Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score
EXT1	94.2	-0.06	99.2	-0.03	**SLC25A30**	128.3	0.37	157.1	1.18
RBM25	95.1	-0.05	77.9	-0.47	**S100A8**	128.4	0.37	96.7	-0.08
BCL2L14	95.1	-0.05	60.0	-0.84	**SP100**	129.2	0.38	82.8	-0.37
PRAME	95.9	-0.04	177.4	1.60	**CRY1**	130.9	0.40	115.4	0.31
GEM	95.9	-0.04	80.8	-0.41	**ATP10D**	131.8	0.41	102.7	0.04
BTN3A3	96.1	-0.04	106.2	0.12	**IL1RN**	132.0	0.41	175.7	1.56
TBX3	96.4	-0.03	168.5	1.41	**IFI30**	132.5	0.42	107.7	0.15
MICB	98.2	-0.01	63.5	-0.77	**APOBEC3G**	132.8	0.42	68.1	-0.67
GPX2	98.9	0.00	114.8	0.30	**TDRD7**	132.9	0.42	123.3	0.47
CD74	100.2	0.01	130.0	0.61	**PTMA**	133.0	0.42	99.1	-0.03
STAT1	101.6	0.03	115.6	0.31	**LINCR**	134.5	0.44	83.8	-0.35
RNF24	102.2	0.04	91.1	-0.20	**MT1F**	134.6	0.44	49.9	-1.05
GZMB	102.2	0.04	75.8	-0.51	**GCA**	134.7	0.45	98.5	-0.04
CYP1B1	102.4	0.04	202.7	2.12	**CD163**	136.0	0.46	174.2	1.53
LEPR	102.4	0.04	116.0	0.32	**CPT1A**	136.6	0.47	161.5	1.27
ADAMDEC1	103.3	0.05	101.6	0.02	**TCF7L2**	136.7	0.47	138.7	0.79
NPAS2	103.6	0.06	133.9	0.69	**SLC16A1**	137.5	0.48	46.8	-1.12
ADFP	104.0	0.06	103.1	0.05	**PMM2**	139.5	0.51	103.8	0.07
ANKFY1	104.0	0.06	92.6	-0.17	**MAFB**	139.6	0.51	214.0	2.36
ABTB2	104.7	0.07	144.1	0.90	**THOC4**	140.0	0.51	105.6	0.10
CD69	105.2	0.08	108.9	0.17	**HES4**	140.8	0.52	149.2	1.01
ZNF295	106.3	0.09	115.1	0.30	**TIMP1**	143.6	0.56	76.6	-0.50
AQP9	106.6	0.09	51.1	-1.03	**IRF7**	143.7	0.56	186.1	1.78
NCOA3	107.0	0.10	104.8	0.09	**TAGAP**	143.7	0.56	153.9	1.11
CCDC75	107.9	0.11	88.5	-0.25	**LGMN**	145.4	0.58	113.9	0.28
RGS1	108.4	0.12	183.2	1.72	**PADI2**	146.2	0.59	278.6	3.70
FKBP5	108.8	0.12	78.9	-0.45	**BLVRA**	146.5	0.59	86.8	-0.29
FLJ39739	108.8	0.12	104.5	0.08	**SQLE**	146.9	0.60	118.5	0.37
CXCL11	109.6	0.13	85.0	-0.32	**NOD2**	147.4	0.61	169.5	1.43
CLEC2B	109.7	0.13	142.8	0.88	**GBP3**	148.4	0.62	145.5	0.93
PXK	110.1	0.14	68.8	-0.66	**MKX**	148.7	0.62	69.7	-0.64
CCL2	111.2	0.15	43.0	-1.19	**COMMD3**	149.6	0.63	64.9	-0.74
IRF2	111.4	0.15	145.1	0.93	**BATF2**	150.7	0.65	109.8	0.19
TLK2	112.3	0.16	92.1	-0.17	**DHX58**	153.6	0.68	100.6	0.00
APOL1	112.5	0.17	70.4	-0.63	**GCH1**	154.0	0.69	57.1	-0.90
GAK	112.8	0.17	121.8	0.44	**CDKN1A**	154.2	0.69	153.5	1.10
PCTK2	113.3	0.18	95.6	-0.10	**ENPP1**	154.9	0.70	106.5	0.12
ZNF107	113.5	0.18	103.5	0.06	**IL1R**	155.1	0.70	46.7	-1.12
MARCK	114.2	0.19	276.4	3.65	**UBE2L6**	155.3	0.70	86.3	-0.29
CEBPD	115.1	0.20	116.2	0.33	**PFKFB3**	155.7	0.71	275.7	3.64
TYMP	115.7	0.21	96.6	-0.08	**RBCK1**	158.7	0.75	140.3	0.83
CES1	115.9	0.21	130.3	0.62	**HSH2D**	158.8	0.75	178.5	1.62
KIAA1618	116.4	0.22	134.5	0.70	**RIPK2**	159.8	0.76	79.2	-0.44
TREX1	116.4	0.22	99.7	-0.02	**NAPA**	160.1	0.76	75.3	-0.53
G6PC	116.9	0.22	133.4	0.68	**CFB**	161.7	0.78	107.0	0.13
IMPA2	117.4	0.23	97.7	-0.06	**CLEC4A**	162.0	0.79	109.9	0.19
DDX60	117.5	0.23	78.6	-0.46	**IFIT5**	162.7	0.80	106.0	0.11
C22orf28	119.4	0.25	98.5	-0.04	**FNDC3B**	163.2	0.80	103.6	0.06
ABCA9	120.2	0.26	154.0	1.11	**KIAA0082**	164.0	0.81	64.6	-0.75
MT1H	120.9	0.27	153.7	1.10	**CD38**	167.2	0.85	77.4	-0.48
SPSB1	121.0	0.27	120.4	0.41	**HK2**	167.7	0.86	149.8	1.02
SCARB2	121.0	0.27	57.4	-0.90	**ETV6**	168.2	0.87	97.4	-0.07
PPM1K	122.1	0.29	63.1	-0.78	**LY6E**	168.4	0.87	66.6	-0.71
MAP3K5	122.7	0.29	5.3	-1.98	**TFEC**	170.4	0.89	98.1	-0.05
CRP	124.0	0.31	98.4	-0.04	**SLFN5**	170.5	0.89	64.6	-0.75
IRF2	124.9	0.32	59.8	-0.85	**LAP3**	172.5	0.92	110.1	0.20
RGL-1	125.8	0.33	153.1	1.09	**NRN1**	172.7	0.92	91.3	-0.19
GMPR	126.4	0.34	93.6	-0.14	**ZNF107**	174.4	0.94	86.4	-0.29
CCL4	127.4	0.35	72.7	-0.58	**PDK1**	174.5	0.94	94.9	-0.12

Large Scale ISG Screen: EboV trVLP in HEK293 cells – p1 and p2 values (Page 4 of 4)

Gene	P2 Replication (% control)	Z score	P1 Replication (% control)	Z score
LGALS9	175.7	0.96	166.6	1.37
IL6ST	176.3	0.97	106.9	0.13
RASGEF1B	179.1	1.00	72.8	-0.58
RASSF4	183.0	1.05	118.3	0.37
DTX3L	188.2	1.12	110.6	0.21
CCR1	189.7	1.13	70.7	-0.62
CREB3L3	192.2	1.17	152.9	1.09
LOC400759	193.2	1.18	85.1	-0.32
IL15	193.6	1.18	55.3	-0.94
NUP50	196.4	1.22	87.3	-0.27
IGFBP2	197.3	1.23	141.9	0.86
GJA4	198.1	1.24	104.7	0.09
HLA-G	198.5	1.25	82.1	-0.38
FUT4	199.1	1.25	234.5	2.78
PNRC1	200.1	1.27	80.6	-0.41
LAMP3	206.0	1.34	143.4	0.89
EHD4	206.6	1.35	77.7	-0.47
SIGLEC1	206.9	1.35	177.7	1.60
C6orf150	213.1	1.43	142.6	0.87
FAM134B	217.7	1.49	94.5	-0.12
PLSCR1	221.2	1.53	63.1	-0.78
GBP4	223.4	1.56	92.3	-0.17
ADM	223.6	1.56	124.9	0.51
VEGFC	224.7	1.57	134.0	0.69
ETV7	225.2	1.58	80.0	-0.43
AMPH	228.5	1.62	190.9	1.88
IL15RA	229.8	1.64	135.0	0.72
LRG1	246.4	1.85	132.9	0.67
TLR7	248.7	1.88	63.9	-0.76
ADAR	250.4	1.90	180.5	1.66
TNFSF10	255.5	1.96	99.2	-0.03
CD80	262.4	2.05	63.1	-0.78
ARG2	269.5	2.14	132.9	0.67
TRIM34	271.6	2.16	103.1	0.05
HPSE	273.0	2.18	109.3	0.18
ZC3HAV1	273.6	2.19	70.7	-0.62
PML	277.0	2.23	267.3	3.46
PI4K2B	278.1	2.24	99.9	-0.01
MASTL	280.4	2.27	161.7	1.27
FLJ23556	291.6	2.41	99.0	-0.03
PAK3	295.7	2.46	59.2	-0.86
TNFSF13B	306.0	2.59	90.3	-0.21
ULK4	312.9	2.68	90.2	-0.21
MSR1	317.5	2.74	124.4	0.50
TNFAIP6	323.0	2.81	127.8	0.57
MAX	331.3	2.91	146.1	0.95
KIAA0040	345.5	3.09	121.8	0.44
OAS3	371.0	3.41	148.0	0.99
IFIT2	406.4	3.85	103.0	0.05
AHNAK2	408.6	3.88	125.6	0.52
TRIM5	410.9	3.91	80.4	-0.42
OAS2	433.0	4.19	104.0	0.07
CD9	491.6	4.92	188.2	1.82