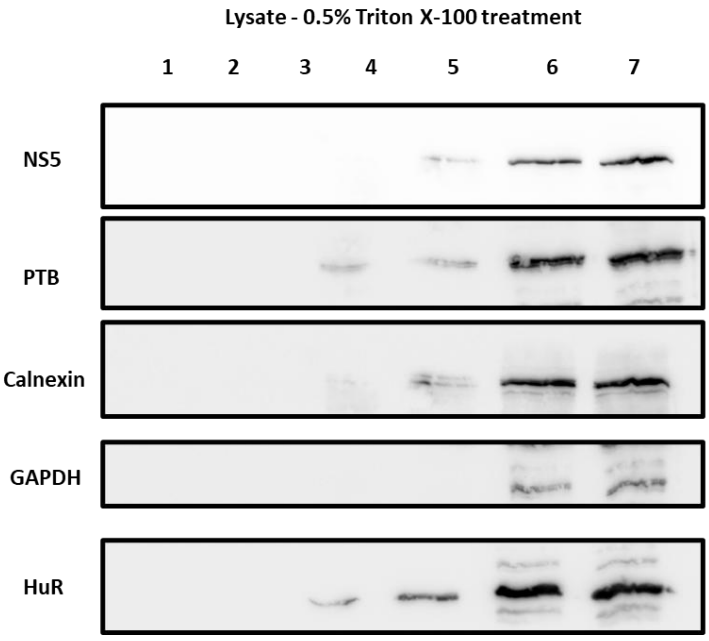
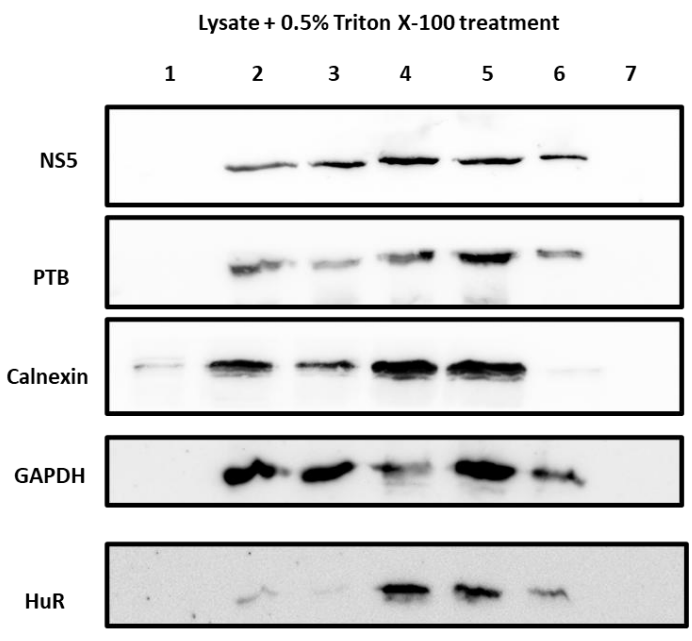
Supplementary Figure 1 –

a.

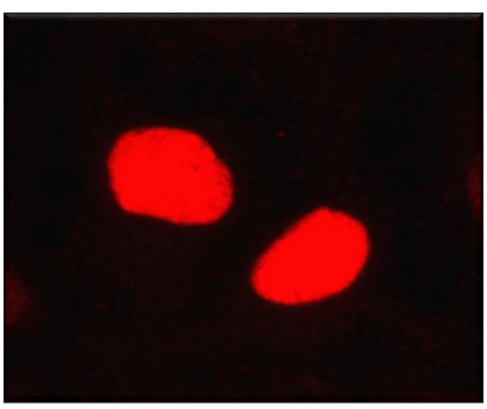




Lysate - 0.5% Triton X-100 treatment							
	1	2	3	4	5	6	7
NS5	0	0	0	0	892.527	17455.296	33782.673
PTB	0	0	0	601.113	1330.598	7745.104	8481.518
Calnexin	0	0	0	456.899	2050.376	7961.125	8960.368
GAPDH	0	0	0	0	0	891.113	1168.77
HuR	0	0	0	511.92	2423.891	7068.154	6715.347

Lysate + 0.5% Triton X-100 treatment							
	1	2	3	4	5	6	7
NS5	0	2865.184	3724.134	5728.205	4728.426	2394.234	0
PTB	0	3679.497	1432.062	4173.841	7354.912	2112.355	0
Calnexin	349.506	5770.79	3154.426	8478.276	9302.397	254.849	0
GAPDH	0	10241.13	8837.175	5170.64	11416.78	4213.326	0
HuR	0	1046.234	332.849	9516.296	7800.175	2427.912	0

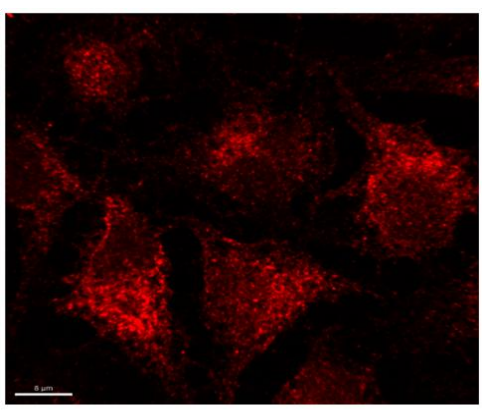
b.



NS5

0.1% Triton X 100

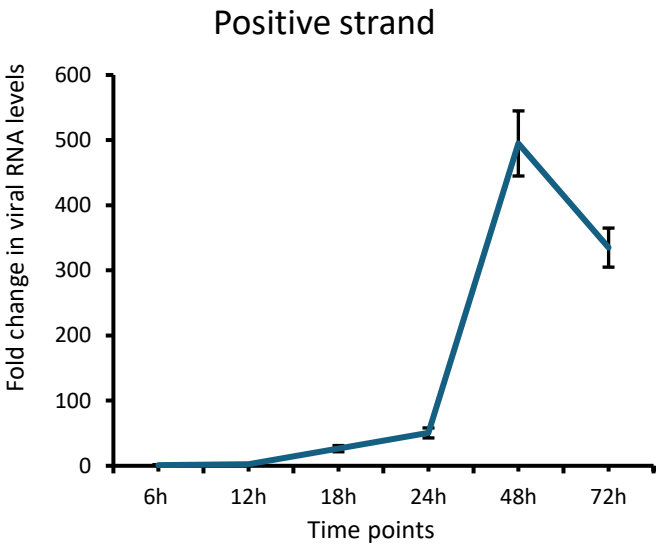
c.



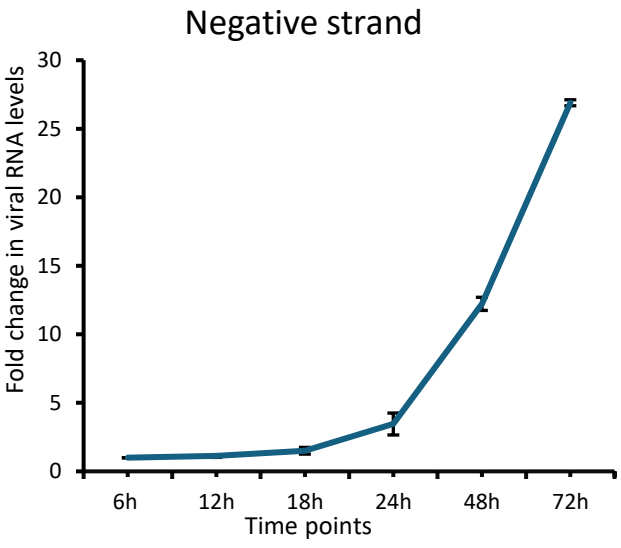
NS5

10ug/ml Digitonin

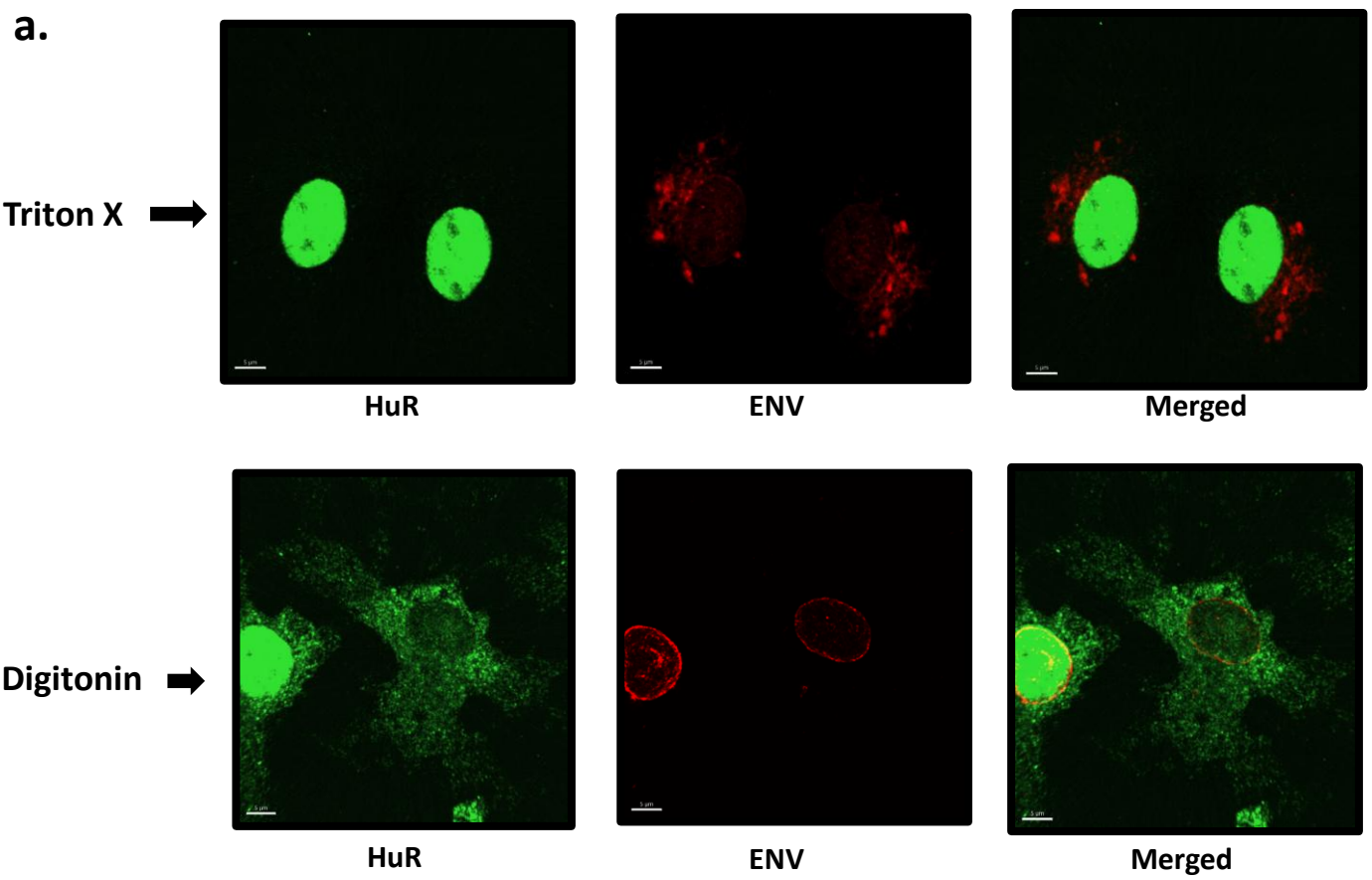
d.

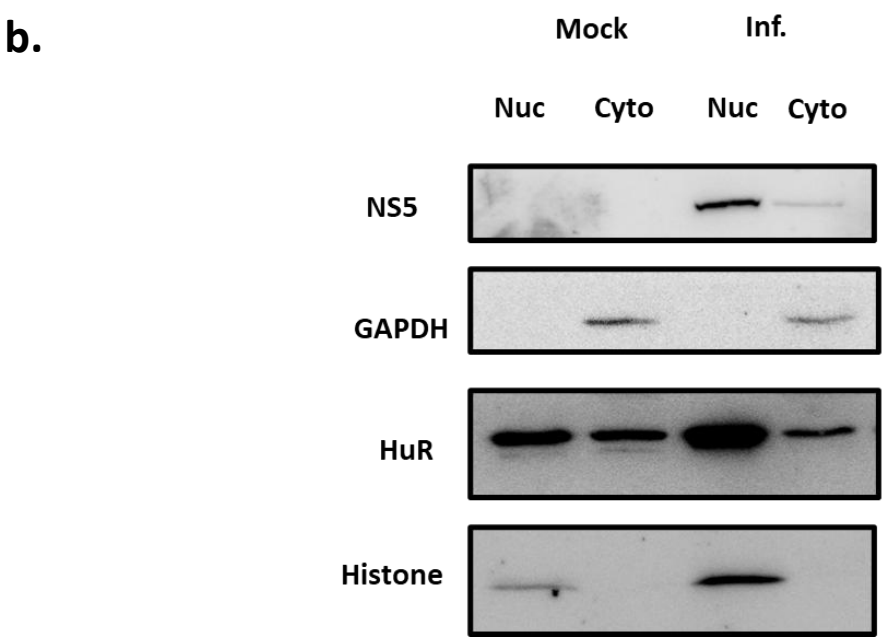

Positive strand
Fold change in viral RNA levels
600
500
400
300
200
100
0
6h
12h
18h
24h
48h
72h
Time points

e.

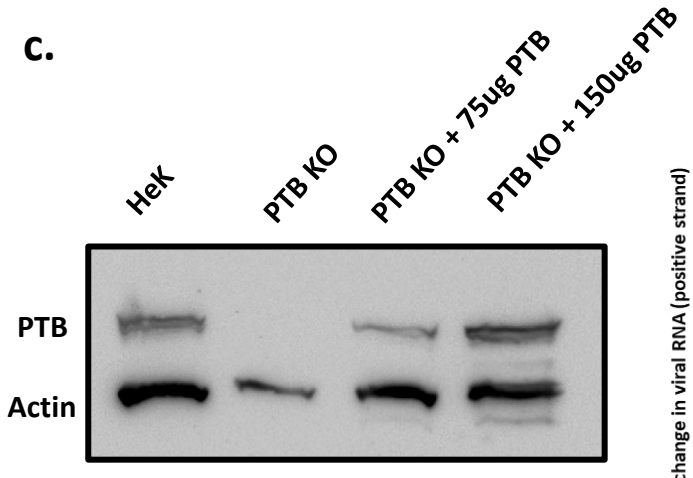

Negative strand
Fold change in viral RNA levels
30
25
20
15
10
5
0
6h
12h
18h
24h
48h
72h
Time points

Supplementary Figure 2 –

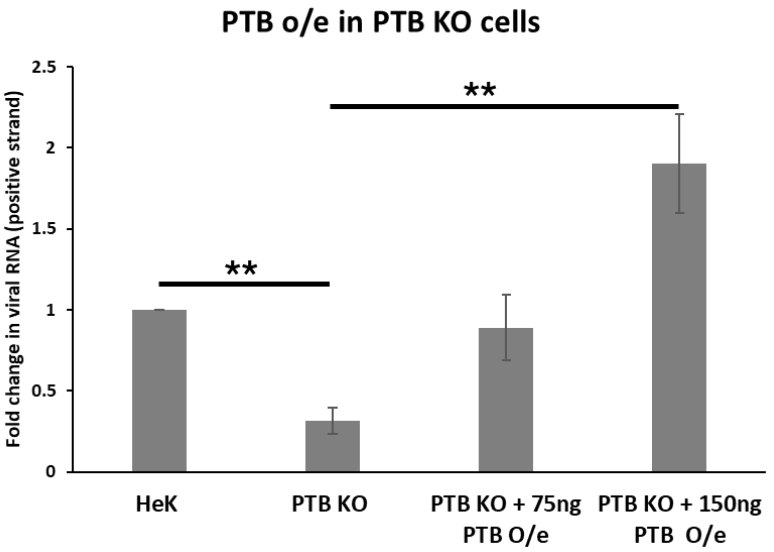




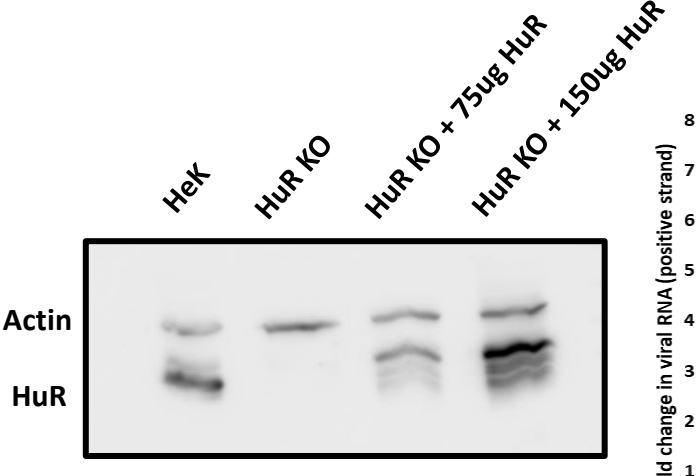
c.


HeK
PTB KO
PTB KO + 75ug PTB
PTB KO + 150ug PTB
PTB
Actin

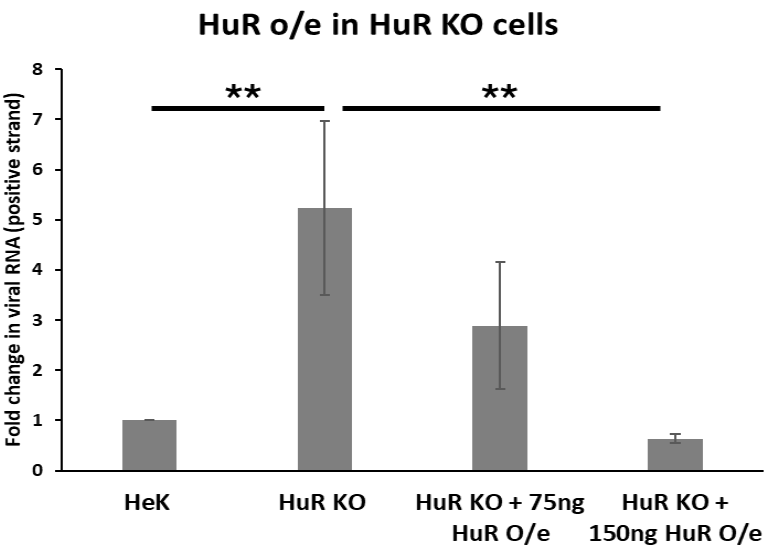
d.


PTB o/e in PTB KO cells
Fold change in viral RNA (positive strand)
2.5
2
1.5
1
0.5
0
**
**
HeK
PTB KO
PTB KO + 75ng PTB O/e
PTB KO + 150ng PTB O/e

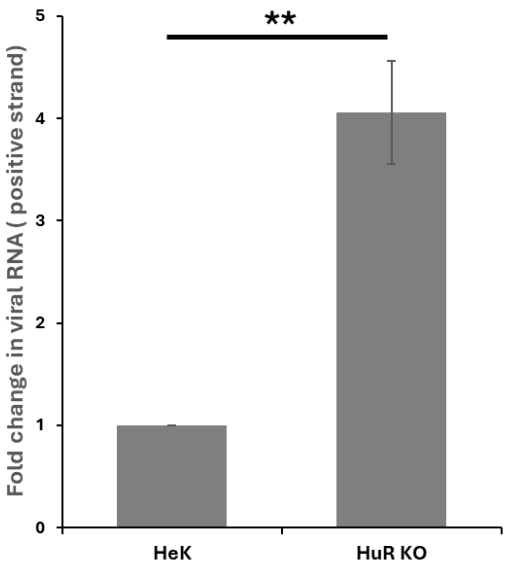
e.


HeK
HuR KO
HuR KO + 75ug HuR
HuR KO + 150ug HuR
Actin
HuR

f.

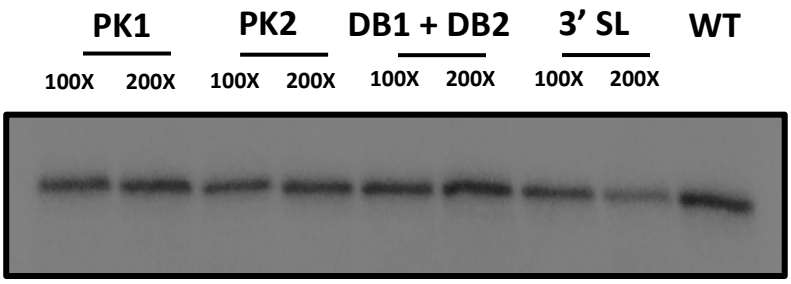

HuR o/e in HuR KO cells
Fold change in viral RNA (positive strand)
8
7
6
5
4
3
2
1
0
**
**
HeK
HuR KO
HuR KO + 75ng HuR O/e
HuR KO + 150ng HuR O/e

g.


Fold change in viral RNA (positive strand)
5
4
3
2
1
0
**
HeK
HuR KO

Supplementary Figure 3 –

a.



b.

AAAGCAAAACUAACAUGAAACAAGGCUAGAAGUCAGGUCGGAU
UAAGCCAUAGUACGGAAAAAACUAUGCUACCUGUGAGCCCCG
UCCAAGGACGUUAAAAGAAGUCAGGCCAUCAUAAAUGCCAUA
GCUUGAGUAAACUAUGCAGCCUGUAGCUCCACCUGAGAAGG
UGUAAAAAAUCCGGGAGGCCACAAACCAUGGAAGCUGUACGC
AUGGCGUAGUGGACUAGCGGUUAGAGGAGACCCCUCCCUUA
CAAAUCGCAGCAACAAUGGGGGCCCAAGGCGAGAUGAAGCUG
UAGUCUCGCUGGAAGGACUAGAGGUUAGAGGAGACCCCCCC
GAAACAAAAAACAGCAUAUUGACGCUGGGAAAGACCAGAGAUC
CUGCUGUCUCCCUCAGCAUCAUUCCAGGCACAGAACGCCAGA
AAAUGGAAUGGUGCUGUUGAAUCAACAGGUUCU

Polypyrimidine track binding sites – CCCUCCCUU and UCUCCU

Human Antigen R binding sites – AUU

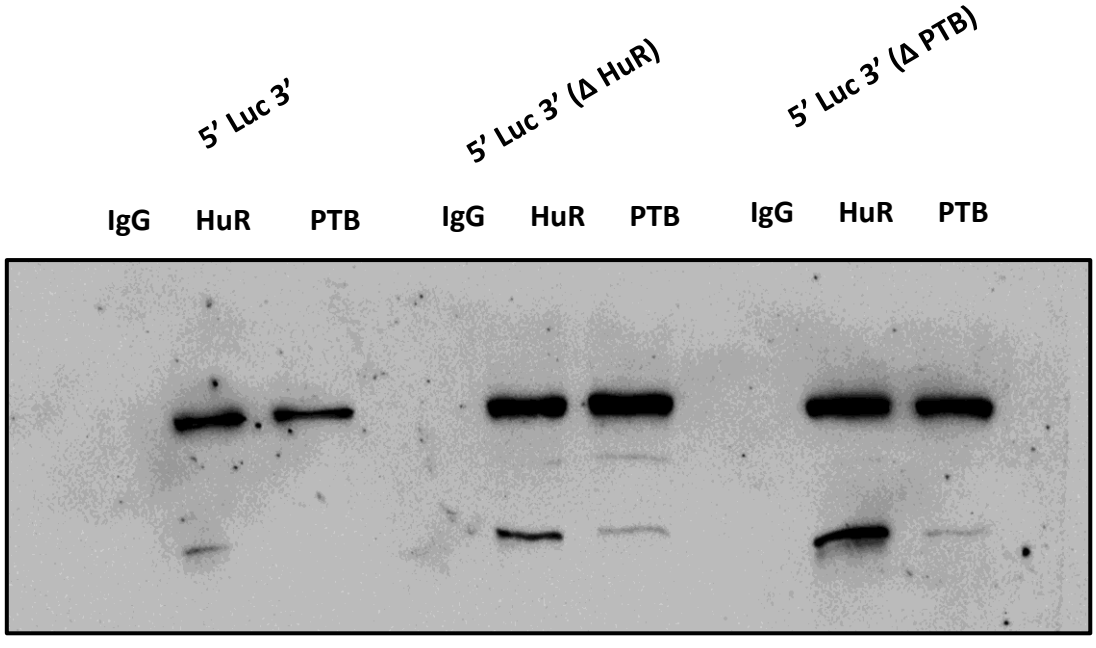
3' UTR cyclisation sequence – CAGCAUAUUGA

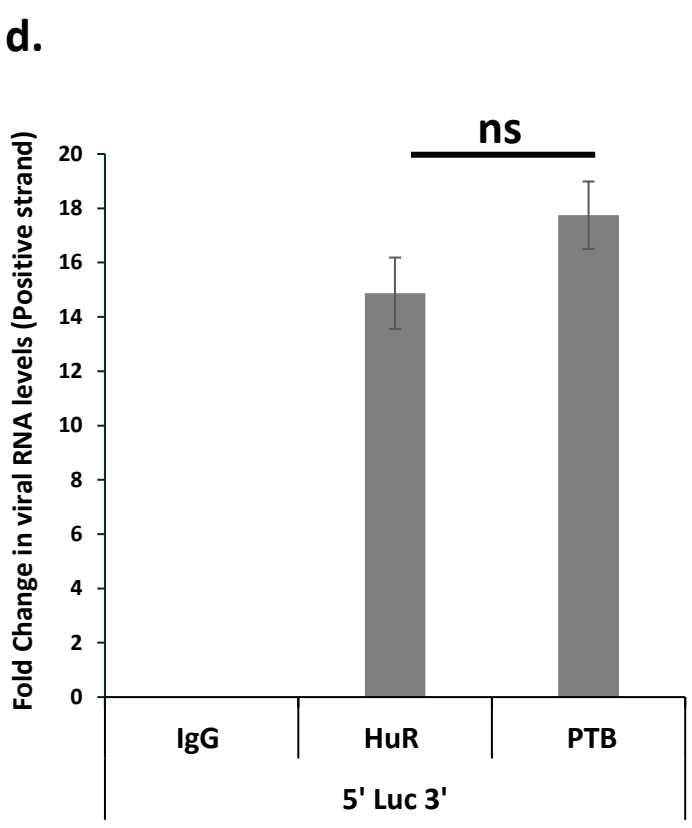
3' SL -

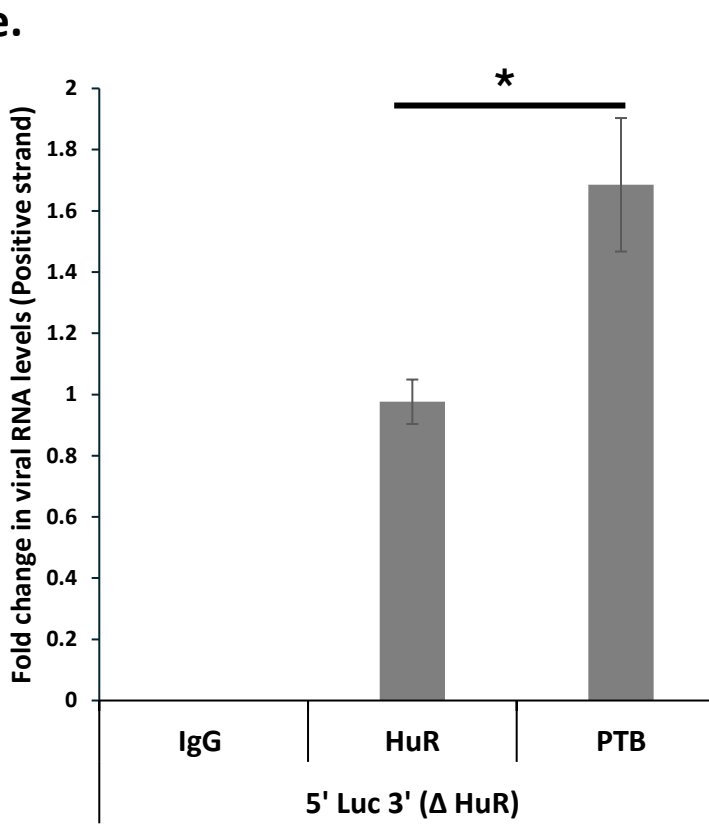
HuR binding mutant – AUU to AGG

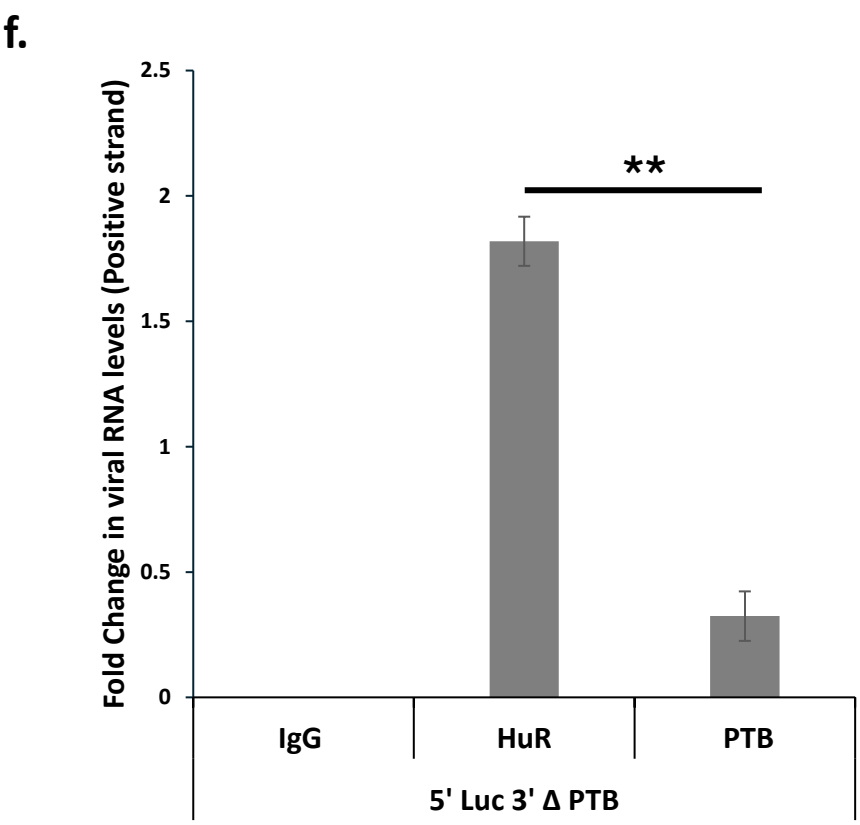
PTB binding mutant – UCUCCU to UAUAAU

c.

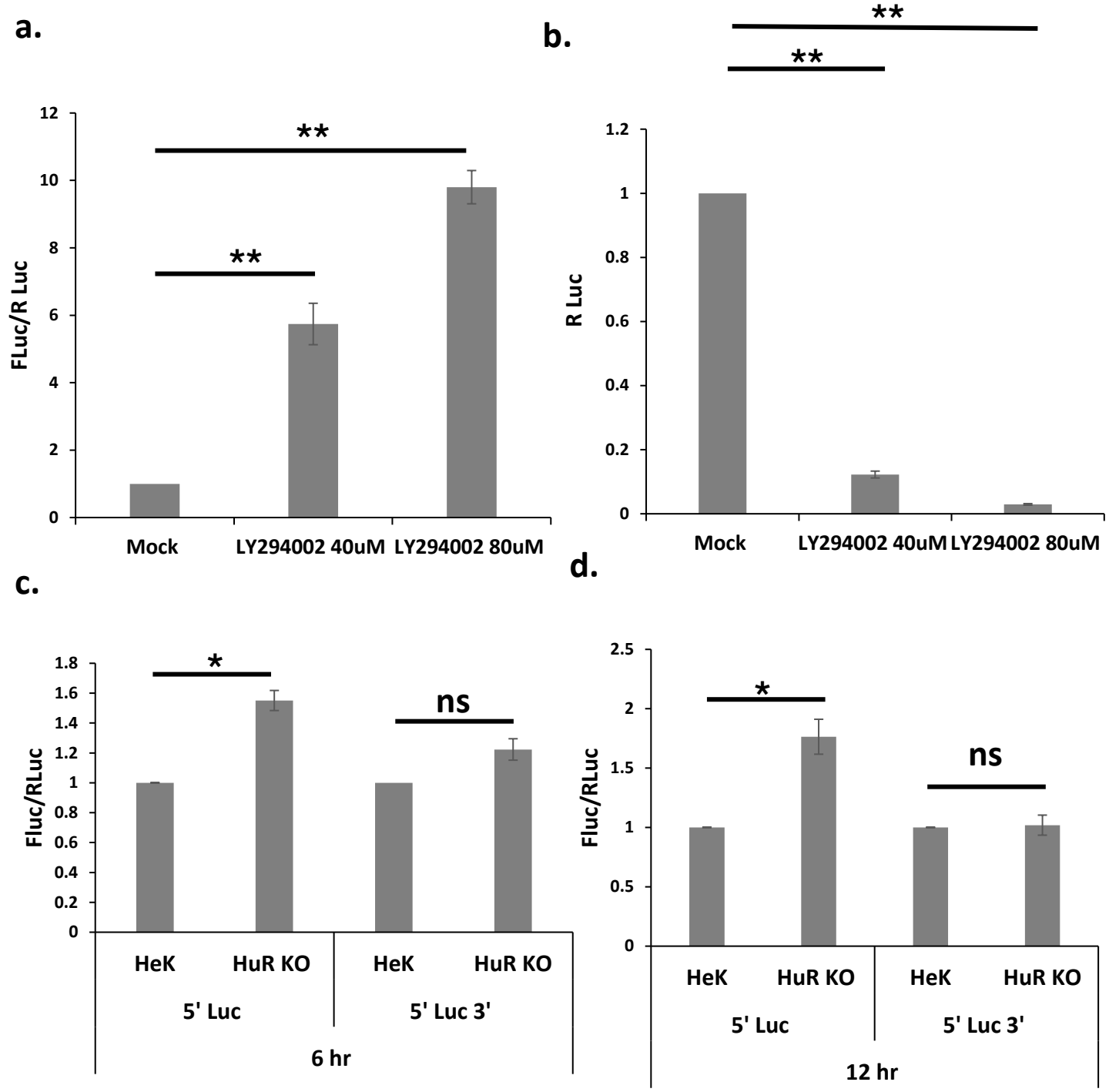


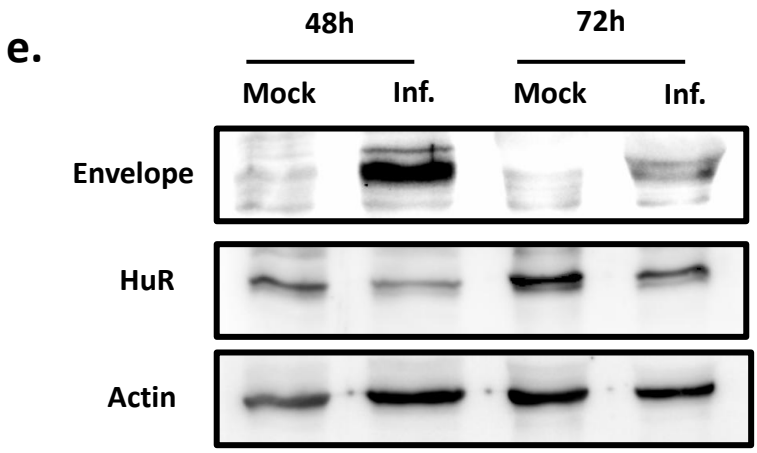

d.
ns
Fold Change in viral RNA levels (Positive strand)
20
18
16
14
12
10
8
6
4
2
0
IgG
HuR
PTB
5' Luc 3'


e.
*
Fold change in viral RNA levels (Positive strand)
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
IgG
HuR
PTB
5' Luc 3' (Δ HuR)

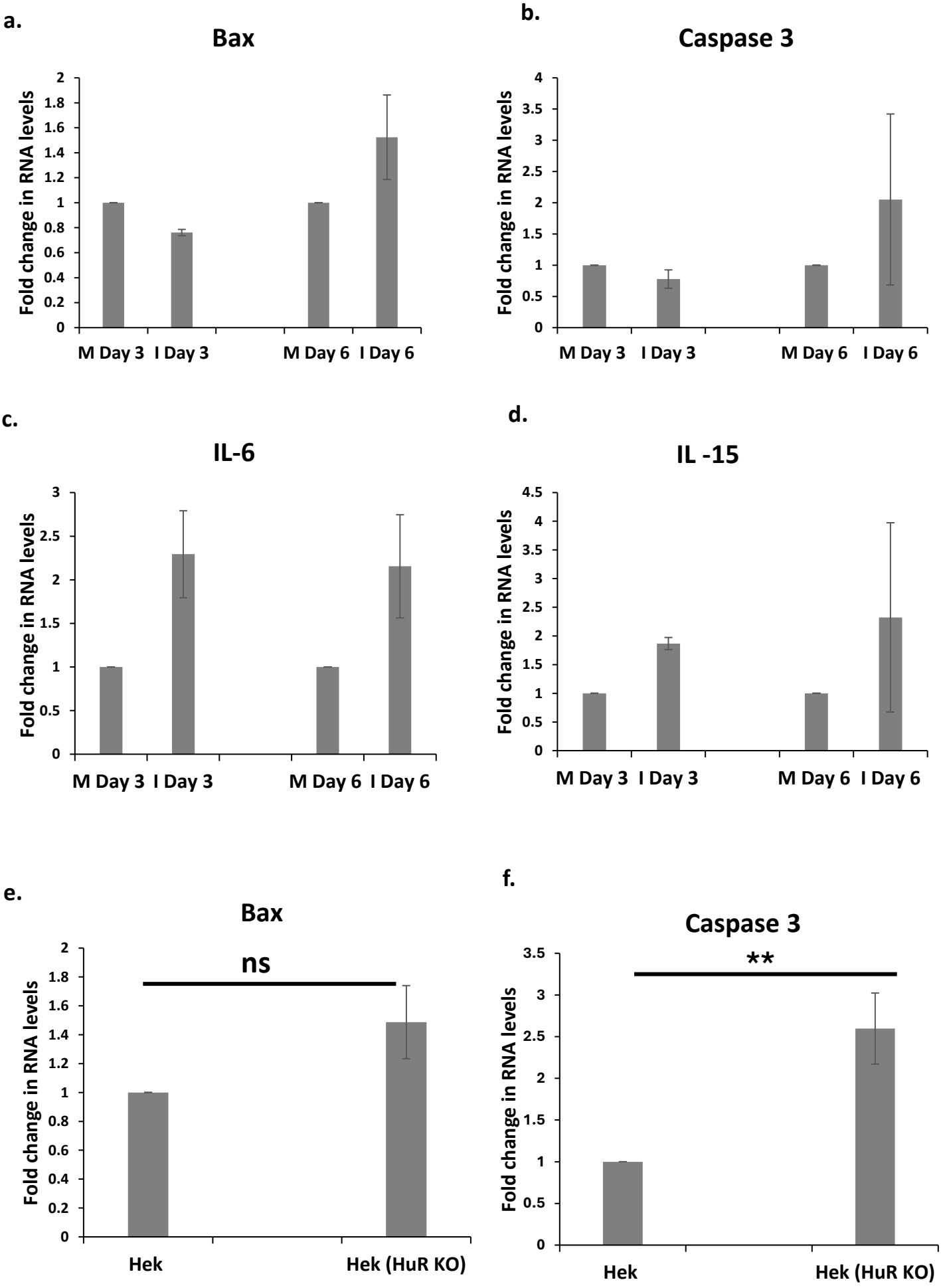

f.
**
Fold Change in viral RNA levels (Positive strand)
2.5
2
1.5
1
0.5
0
IgG
HuR
PTB
5' Luc 3' Δ PTB

Supplementary Figure 4 –

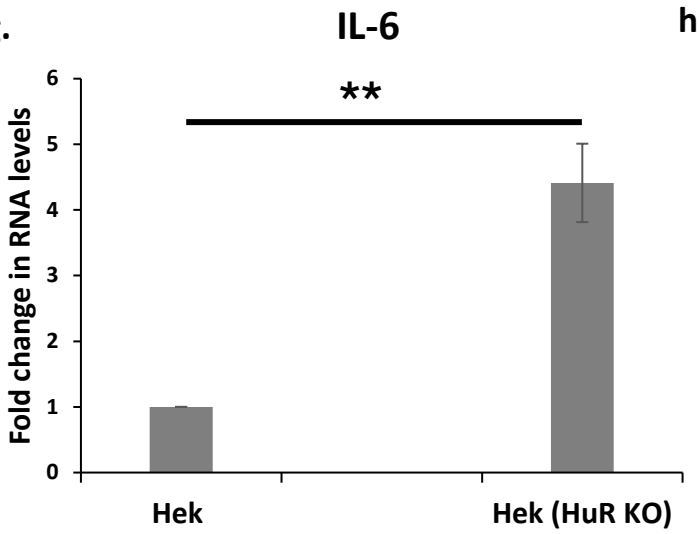




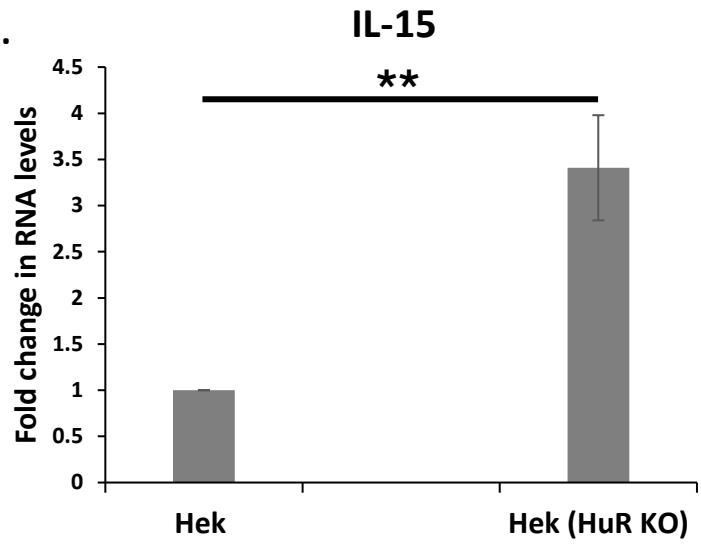
Supplementary Figure 5 –



g.


IL-6
**
Fold change in RNA levels
0
1
2
3
4
5
6
Hek
Hek (HuR KO)

h.


IL-15
**
Fold change in RNA levels
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
Hek
Hek (HuR KO)

Supplementary Table 1 –

List of Primers used in this study:

1	DV NS5 Fwd	GCCCTTCTGTTCACACCATT
2	DV NS5 Rev	CCACATTTGGGCGTAAGACT
3	GAPDH Fwd	CAGCCTAGGATCATCAGCAAT
4	GAPDH Rev	GGTCATGAGTCCTTCCACGA
5	DV fwd mice	TCAAT ATGCTGAAACGCGCGAGAAACCG
6	DV rev mice	AACGCCACAAGGGCCATGAACA
7	TNF-alpha mouse fwd	GGTGCCTATGTCTCAGCCTCTT
8	TNF-alpha mouse rev	GCCATAGAACTGATGAGAGGGAG
9	TNF-alpha human fwd	CTCTTCTGCCTGCTGCACTTTG
10	TNF-alpha human rev	ATGGGCTACAGGCTTGTCACTC
11	CXCL-15 mouse fwd	GGTGATATTCGAGACCATTTACTG
12	CXCL-15 mouse rev	GCCAACAGTAGCCTTCACCCAT
13	IL8 human fwd	GAGAGTGATTGAGAGTGGACCAC
14	IL8 human rev	CACAACCCTCTGCACCCAGTTT
15	IL6 mouse fwd	TACCACTTCACAAGTCGGAGGC
16	IL6 mouse rev	CTGCAAGTGCATCATCGTTGTTC
17	IL6 human fwd	AGACAGCCACTCACCTCTTCAG
18	IL6 human rev	TTCTGCCAGTGCCTCTTTGCTG
19	IL15 mouse fwd	GTAGGTCTCCCTAAAACAGAGGC
20	IL15 mouse rev	TCCAGGAGAAAGCAGTTCATTGC
21	IL15 human fwd	AACAGAAGCCAACTGGGTGAATG
22	IL15 human rev	CTCCAAGAGAAAGCACTTCATTGC
23	BAX mouse fwd	AGGATGCGTCCACCAAGAAGCT
24	BAX mouse rev	TCCGTGTCCACGTCAGCAATCA
25	BAX human fwd	TCAGGATGCGTCCACCAAGAAG
26	BAX human rev	TGTGTCCACGGCGGCAATCATC
27	caspase 3 mouse fwd	GGAGTCTGACTGGAAAGCCGAA
28	caspase 3 mouse rev	CTTCTGGCAAGCCATCTCCTCA
29	caspase 3 human fwd	GGAAGCGAATCAATGGACTCTGG
30	caspase 3 human rev	GCATCGACATCTGTACCAGACC

Supplementary Table 2

Accession	Description	Coverage [%]	Abundances (Normalized): F1: Sample	Found in Sample: [S1] F1: Sample
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1	20	923162.4135	High
P0DMV9	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1	19	777036.3769	High
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	14	1531640.426	High
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1 SV=2	15	900301.6044	High
Q32P51	Heterogeneous nuclear ribonucleoprotein A1-like 2 OS=Homo sapiens OX=9606 GN=HNRNPA1L2 PE=2 SV=2	5	422245.8188	High
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2	5	187123.3736	High
O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2	5	94005.78835	High
P04792	Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2	13	207068.1558	High
P57721	Poly(rC)-binding protein 3 OS=Homo sapiens OX=9606 GN=PCBP3 PE=1 SV=2	7	121155.3283	High
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1 SV=2	4	94886.9427	High
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=5	18	1004340.153	High
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=3	9	349956.4274	High
Q58FF8	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens OX=9606 GN=HSP90AB2P PE=1 SV=2	16	120081.1901	Peak Found
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1	15	242303.5254	High
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1	15	364155.2026	High
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	11	166464.7394	Peak Found
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNPC PE=1 SV=4	4	137053.7877	High
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	3	75545.65176	High
Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens OX=9606 GN=ERP44 PE=1 SV=1	6	47071.45084	Peak Found
Q9UHX1	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1	3	40913.36328	Peak Found
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=GPD2 PE=1 SV=3	1	18784.00186	Not Found
O75083	WD repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=WDR1 PE=1 SV=4	1	115040.5156	High
Q9BU61	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens OX=9606 GN=NDUFAF3 PE=1 SV=1	6	52506.60131	High
P48741	Putative heat shock 70 kDa protein 7 OS=Homo sapiens OX=9606 GN=HSPA7 PE=5 SV=2	7	292934.0938	High
Q9NZT1	Calmodulin-like protein 5 OS=Homo sapiens OX=9606 GN=CALML5 PE=1 SV=2	10	65140.49369	Peak Found
P11021	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2	27	3500457.14	High
P14618	Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4	44	3438158.517	High
P60709	Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	43	8215127.942	High
P63261	Actin, cytoplasmic 2 OS=Homo sapiens OX=9606 GN=ACTG1 PE=1 SV=1	43		High
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1	36	3312732.144	High
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	54	5734473.763	High
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2	34	1689507.672	High

P68363	Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1	28	2053326.427	High
P06733	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	43	2197073.682	High
P02545	Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1	25	1095177.619	High
P07355	Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2	39	1347426.877	High
Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=2	22	343339.1645	High
P49327	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3	6	915028.0545	High
P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens OX=9606 GN=KRT8 PE=1 SV=7	15	301904.8713	High
P09211	Glutathione S-transferase P OS=Homo sapiens OX=9606 GN=GSTP1 PE=1 SV=2	62	2139169.21	High
P26641	Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G PE=1 SV=3	22	959639.999	High
P07237	Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=3	18	738023.0329	High
P23528	Cofilin-1 OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=3	50	1598176.131	High
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=2	26	1415612.916	High
P62805	Histone H4 OS=Homo sapiens OX=9606 GN=H4C1 PE=1 SV=2	41	3348960.748	High
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens OX=9606 GN=AHNAK PE=1 SV=2	7	964703.848	High
P19338	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	11	833835.7543	High
P14625	Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	14	817551.8997	High
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=1	17	827489.7642	High
P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens OX=9606 GN=KRT15 PE=1 SV=3	13	46737.79386	High
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2	20	931086.918	High
P60174	Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=4	20	546316.3201	High
P13639	Elongation factor 2 OS=Homo sapiens OX=9606 GN=EEF2 PE=1 SV=4	7	370346.6627	High
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV=1	17	413015.5572	High
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3	19	462624.6089	High
Q01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTBN1 PE=1 SV=2	2	405615.7794	High
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3	10	310983.662	High
Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens OX=9606 GN=SPTAN1 PE=1 SV=3	3	416143.8029	High
P07437	Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2	16	516444.6011	High
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	7	471388.1563	High
P04083	Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2	14	295156.3228	High
P68371	Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1	12	119013.6374	High
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1	6	672903.5446	High
P35579	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4	5	478464.2972	High
P16403	Histone H1.2 OS=Homo sapiens OX=9606 GN=H1-2 PE=1 SV=2	23	246545.3741	High
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6	5	253988.8699	High

P07195	L-lactate dehydrogenase B chain OS=Homo sapiens OX=9606 GN=LDHB PE=1 SV=2	14	325127.8074	High
Q16777	Histone H2A type 2-C OS=Homo sapiens OX=9606 GN=H2AC20 PE=1 SV=4	22	769772.7644	High
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=3	21	342122.2374	High
P08195	4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=3	9	230456.5877	High
P00533	Epidermal growth factor receptor OS=Homo sapiens OX=9606 GN=EGFR PE=1 SV=2	5	212410.0257	High
P10412	Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2	22	863559.2046	High
Q06830	Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1	32	816844.2567	High
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4	16	544740.5719	High
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=2	25	559604.0099	High
P06703	Protein S100-A6 OS=Homo sapiens OX=9606 GN=S100A6 PE=1 SV=1	29	459911.0006	High
Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=5	2	292804.0967	High
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3	14	277469.4911	High
P05783	Keratin, type I cytoskeletal 18 OS=Homo sapiens OX=9606 GN=KRT18 PE=1 SV=2	11	488584.3126	High
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3	4		High
P10599	Thioredoxin OS=Homo sapiens OX=9606 GN=TXN PE=1 SV=3	35	365184.6318	High
P09382	Galectin-1 OS=Homo sapiens OX=9606 GN=LGALS1 PE=1 SV=2	39	417566.9837	High
P07737	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2	31	442825.904	High
P0DP25	Calmodulin-3 OS=Homo sapiens OX=9606 GN=CALM3 PE=1 SV=1	20	351591.084	High
P63104	14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1	14	241477.9732	High
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens OX=9606 GN=PPIB PE=1 SV=2	18	365608.4572	High
P61604	10 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPE1 PE=1 SV=2	25	250116.0055	High
P81605	Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2	23	320814.1765	High
P05387	60S acidic ribosomal protein P2 OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1	39	320949.2138	High
P29692	Elongation factor 1-delta OS=Homo sapiens OX=9606 GN=EEF1D PE=1 SV=5	16	226893.1097	High
Q07020	60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=2	14	150432.7437	High
P08865	40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=4	10	136590.211	High
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens OX=9606 GN=GANAB PE=1 SV=3	3	204278.4298	High
P06454	Prothymosin alpha OS=Homo sapiens OX=9606 GN=PTMA PE=1 SV=2	14	336870.5226	High
P15144	Aminopeptidase N OS=Homo sapiens OX=9606 GN=ANPEP PE=1 SV=4	2	242371.7307	High
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=2	23	173425.1906	High
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1	7	225945.1657	High