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Supplemental information

Transcriptome regulation by PARP13 in basal and antiviral states in human cells

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Figure S1: RNA-seq and qPCR quality control assessments related to Figure 1. A. Scatter plots of RNA-seq counts between all samples. Plot depicting replicates are shown in red. The R value for each pairwise correlation is in the upper left corner of each plot. B. Bar plots of qPCR from Fig. 1C of selected gene expression relative to WTss gene levels normalized to GAPDH. Each point represents a replicate. Error bars are +/- 1 sd.

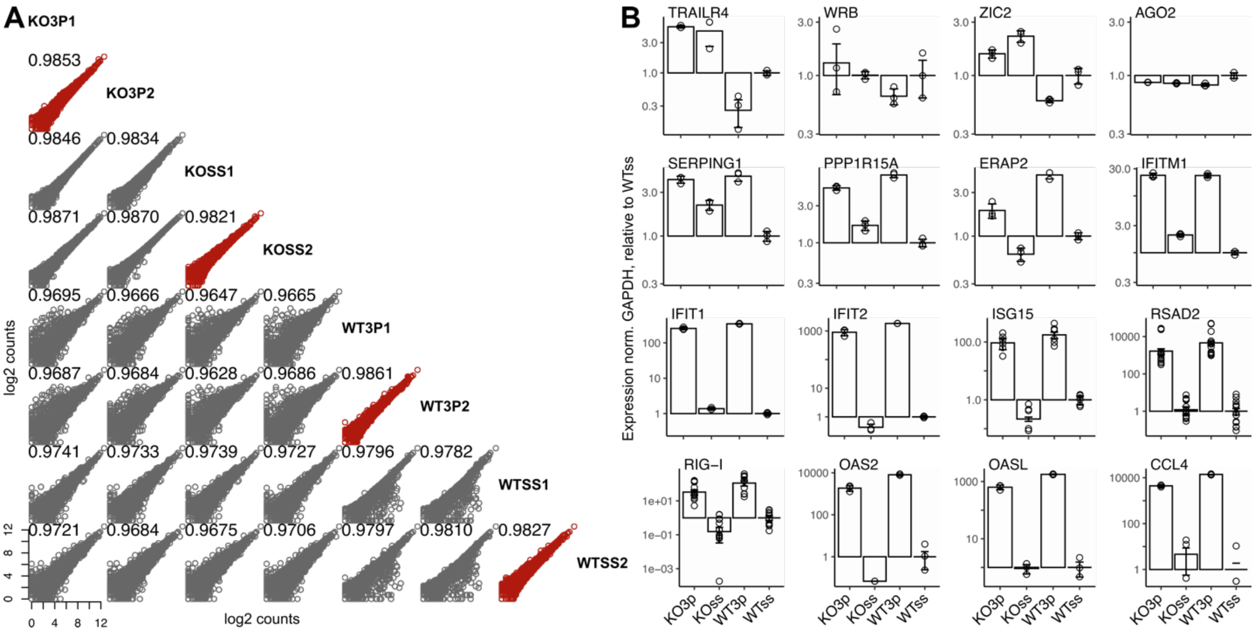

Figure S2: Extended images of Western blots shown in A. Figure 2E, B. Figure 4C, and C. Figure 5I. KO = PARP13 KO cells

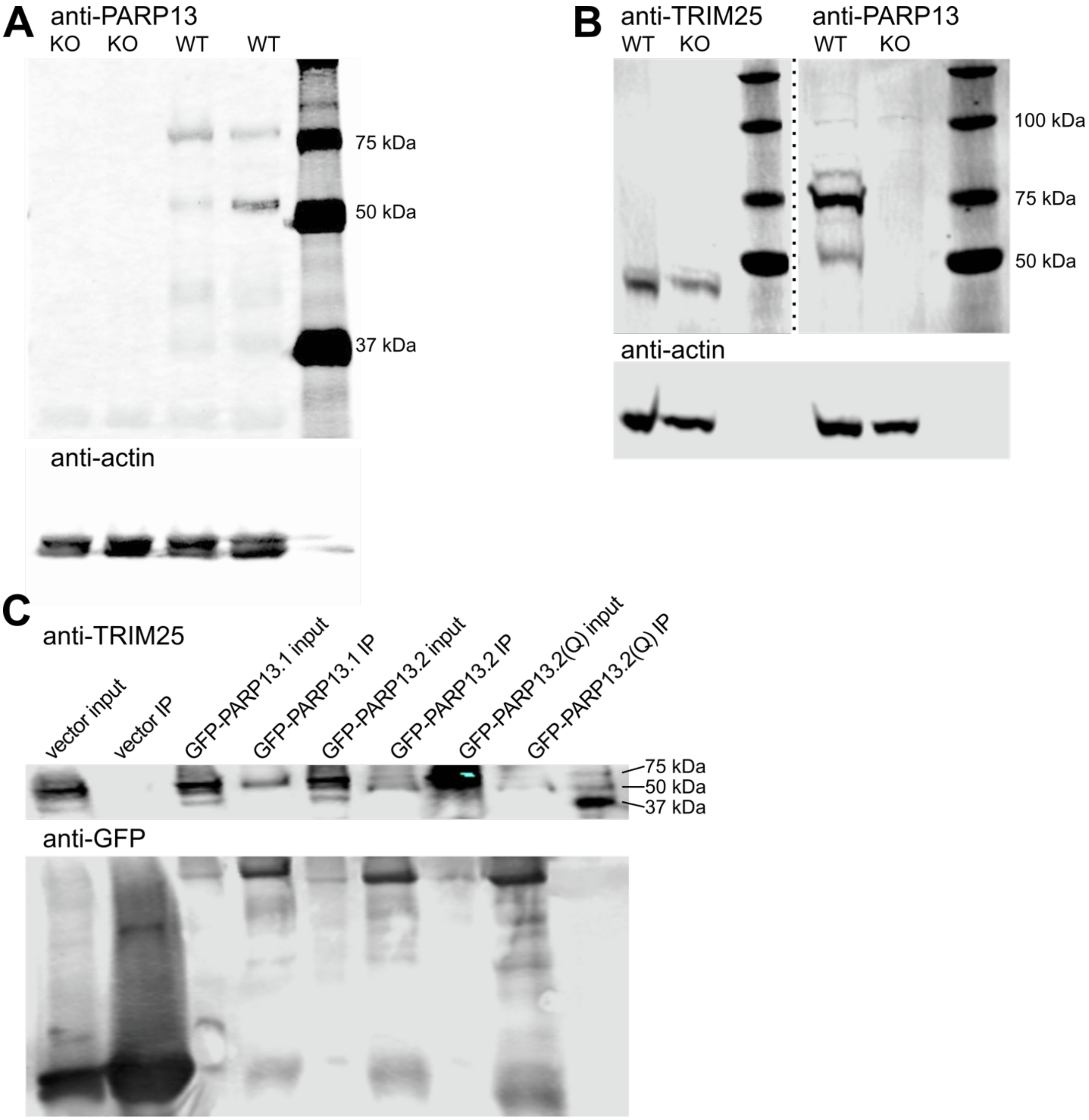

Table S1: Relative expression of twelve genes that are downregulated in PARP13 KO cells compared to WT cells at basal states and up-regulated upon 3p-RNA treatment in WT cells. Related to Figure 1 and 4A.

Gene	KO/WT SS log2FC	KO/WT SS padj	P3/SS WT log2FC	P3/SS WT padj	KO/WT 3P log2FC	KO/WT 3P padj	ISGylation
CSF1	-1.3826637	0.01880959	2.29278472	1.34E-16	-3.400768	3.34E-34	
DDX58 (RIGI)	-2.1582511	0.07511729	7.0016834	2.93E-146	-6.3531339	1.33E-16	Y
ISG15	-1.2700558	0.06613593	6.06966307	1.06E-135	-5.7254932	3.29E-26	Y
LY6E	-0.5485837	0.09399252	1.22268526	6.79E-08	-1.6528347	1.66E-18	
OAS3	-3.0691376	4.97E-07	5.46489459	2.66E-148	-7.7654887	2.32E-157	
PHF11	-6.2162958	0.00737596	2.60329592	9.50E-07	-7.6680384	2.12E-06	
PPP1R15A	-2.354659	6.60E-17	1.20630142	0.00011046	-3.3921319	7.06E-66	
SHISA5	-0.8316249	0.00478896	1.58005666	4.86E-10	-2.248933	7.77E-34	
UBE2L6	-1.0642208	0.06614123	4.11120005	6.43E-79	-5.0439383	1.11E-106	Y
USP18	-1.3250928	0.00039169	3.40742688	2.63E-62	-4.4255337	1.81E-103	Y
USP41	-1.4939115	0.02008495	3.33861735	7.26E-38	-4.4309707	1.45E-57	Y
WARS	-0.4781476	0.06303628	1.82677446	6.67E-25	-2.2762076	2.61E-40	
ZC3HAV1 (PARP13)	-1.4342847	6.00E-06	2.02628388	6.58E-21	-3.4079062	2.43E-59	

Table S2: qPCR primer sequences. Related to Figures 1C, S1B, 2C, 2G, 4B, and 4D.

TARGET	SEQUENCE	COMMENTS
AGO2_F	CCATGTACTCGGGAGCCG	
AGO2_R	CCCAAAGTCGGGTCTAGGTG	
ATP6AP1_F	TGAGTTACAATGACACCGCTC	
ATP6AP1_R	AGTCGTTCATAGGTCAGTGAGA	
CCL4_F	GCTTCCTCGCAACTTTGTGG	
CCL4_R	TCACTGGGATCAGCACAGAC	
EIF1_F	GAAACGGCAGGAAGACCCTTA	
EIF1_R	CGGATGCTCAATTACAGTACCAT	
ERAP2_F	TGGGGGAAAATGCAGAGGTC	
ERAP2_R	GGAGTGAACACCCGTCTTGT	
GAPDH_F	TTCGACAGTCAGCCGCATCTTCTT	
GAPDH_R	GCCCAATACGACCAAATCCGTTGA	
HDAC3_F	GGCAACTTCCACTACGGAGC	
HDAC3_R	GCATATTGGTGGGGCTGACT	
HERC5_F	CAACTGGGAGAGCCTTGTGGTT	
HERC5_R	CTGGACCAGTTTGCTGAAAGTGG	
IFIT1_F	AGAACGGCTGCCTAATTTACA	
IFIT1_R	GCTCCAGACTATCCTTGACCTG	
IFIT2_F	GCCGAACAGCTGAGAATTGC	
IFIT2_R	TTAGTTGCCGTAGGCTGCTC	
IFITM1_F	CTCTTCTTGAACTGGTGCTGTC	
IFITM1_R	GTCACGTCGCCAACCATCTTC	
ISG15_F	AGAGGCAGCGAACTCATCTTT	
ISG15_R	CAGCATCTTCACCGTCAGGTC	
JF_585_F	ACTGGGCAGGTGTCCACTC	psiCHECK-3 Forward for both luciferases (spans intron)
JF_586_R	GTTTGCGTTGCTCGGGGTC	psiCHECK-3 Reverse for hRluc (modifed)
JF_587_R	GAAGGGAGCAGGGCCCTTC	psiCHECK-3 Reverse for luciferase (control)
OAS2_F	TCCTGGAGCTGGTCACACAA	
OAS2_R	CGGCTGGGTCCAAGATCAC	
OASL_F	CTGAGAAGGCAGCTCACGAA	
OASL_R	CTCCAACCCTTTGGGTCTCC	
PARP13.1_F	TCAAAACCGCTGTCATGGCCCC	
PARP13.1_R	GCCAGAGTGGCTTGCGCAGAA	
PARP13.2_F	GCAGCAGATGAAGAGAGGGCCA	
PARP13.2_R	TGAGCCCAGGGCATGAACATCT	
PPP1R15A_F	TGAGACTCCCCTAAAGGCCA	
PPP1R15A_R	CCAGACAGCCAGGAAATGGA	

RIG-I_F	AGAGCACTTGTGGACGCTTT
RIG-I_R	TGTTTTGCCACGTCCAGTCA
RSAD2_F	TCCTGCTTGGTGCCTGAATC
RSAD2_R	AGCTTCTTCTACACCAACATCCA
SERPING1_F	TCTCCTAACACTACCCCGCA
SERPING1_R	CAGCCCACACAGGTTAAGGT
SLC3A2_F	TGAATGAGTTAGAGCCCGAGA
SLC3A2_R	GTCTTCCGCCACCTTGATCTT
STT3A_F	TTGGGACGAATCATTGGAGGA
STT3A_R	GTAAGGTGGTACGTGACGATG
TBP_F	GAGAGCCACGAACCACGGCA
TBP_R	TGCTGCCAGTCTGGACTGTTCT
TMED3_F	TCACCCAGATGGAGTCCGC
TMED3_R	AATCGTCTCGCCAACAGACC
TRAILR4_F	TTAAGTTCGTCGTCTTCATC
TRAILR4_R	TCTGATCTATGAGATCCTGC
TRIM25_F	CGAGAGCACTGGATGATGTGA
TRIM25_R	CTGCTCCACCTTTCTGTTTGC
UBE2L6_F	CTGGAAGCCTTGCACCAAGA
UBE2L6_R	GAACATGAGTTAGGAGGGCCG
USP18_F	CTCCTTGATTCAGGTGTTCGTAA
USP18_R	AGGGCACGTTGCACTTCTG
USP41_F	TGGAGGGCAGTATGAGCTTTTT
USP41_R	ATGACCGGAGTCTGCCATTC
WRB_F	GGTTGCTGGTGCTCAGCTTC
WRB_R	CCGCTCTCATCTGTGACTCC
XBP1_F	CCCTCCAGAACATCTCCCCAT
XBP1_R	ACATGACTGGGTCCAAGTTGT
ZIC2_F	CACGTCCACACCTCCGATAA
ZIC2_R	CTCATGGACCTTCATGTGCT