**Supplementary Table 1.** 2-fold or more upregulated genes after siRNA mediated knockdown of either hPop1 or Rpp40 in HEp-2 cells compared to control transfected cells.

symbolImage: SymbolImage: SymbolRSAD2Viperin3,62,0defense response to virusSYPL1Synaptophysin-like protein 13,22,5transport / synaptic transmissionNT5C3Cytosolic 5'-nucleotidase 33,1n.s.pyrimidine nucleoside metabolic processTRIM22Tripartite motif-containing protein 222,91,4response to virus / immune response / regulation of transcription, DNA-dependeDAZAP2DAZ-associated protein 22,61,9?MUC13Mucin-13 precursor2,6n.s.?INDOIndolearnine 2,3-dioxygenase2,5n.s.Immune responseLIMA1Epithelial protein lost in neoplasm2,5n.s.Immune responseGBP3Guanylate-binding protein 32,5n.s.Immune responsePARP12Poly [ADP-ribose] polymerase 122,51,5?GSTA1Glutathione S-transferase A12,51,2glutathione metabolic process	
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GSTA1 Glutathione S-transferase A1 2,5 1,2 glutathione metabolic process	
ARPC1A Actin-related protein 2/3 complex subunit 1A 2,5 2,9 actin cytoskeleton organization	
CASP7 Caspase-7 precursor 2,5 2,1 release of cytochrome c from mitochondr	a /
proteolysis / apoptosis / heart developme	nt
H3F3A Histone H3.3 2,5 2,9 nucleosome assembly	
TNFSF10     Tumor necrosis factor ligand superfamily     2,5     1,4     apoptosis / immune response /	
member cell-cell signaling / signal transduction /	
pos. reg. I-kappaB kinase/NF-kappaB ca	scade
BTBD3 BTB/POZ domain-containing protein 2,4 n.s. ? Protein binding (mol. Function Go term)	
USP41 Putative ubiquitin carboxyl-terminal hydrolase 2,4 1,6 ubiquitin-dependent protein catabolic pro-	ess
DDT     D-dopachrome decarboxylase     2,4     2,4     melanin biosynthetic process from tyrosin	е
HCP5 HLA class I histocompatibility antigen protein 2,4 1,2 ?	
BAG2 BAG family molecular chaperone regulator 2 2,4 1,8 protein folding / apoptosis / prot. metaboli	c process
CAPNS1Calpain small subunit 12,32,0positive regulation of cell proliferation	
FAM8A1     Protein FAM8A1     2,3     1,7     G-protein coupled receptor protein signal	ng
HIST1H2AC Histone H2A type 1-C 2,2 n.s. nucleosome assembly	
SAMD9   Sterile alpha motif domain-containing protein 9   2,2   1,4   ? Localized to cytosol     Data   Butyrophilin subfamily 3 member A1   200   1.4   1.4   1.4	
BTN3A1 precursor 2,2 1,4 lipid metabolic process	
PARP10 Poly [ADP-ribose] polymerase 10 2,2 1,2 nucleic acid bindig (mol go term),	
may play a role in cell proliferation	
OGFR     Opioid growth factor receptor     2,2     1,3     regulation of cell growth       C44 rf(00     UN/4 exception of participants     2.4     n.2     Auxiety of the duration of the durati	
C14orf100 JNK1-associated membrane protein 2,1 n.s. ? May be a regulator of the duration of M.	
act. in resp. to various stress stimuli (By s	• /
IER3IP1 Immediate early response 3-interacting 2,1 1,8 ? May be involved in protein transport be	
protein 1 endoplasm. Reticul. and Golgi app. (By s	milarity)
TTC35 Tetratricopeptide repeat protein 35 2,1 1,5 ?   FDV000 F have an two protein 20 2.4 1.4 which in the protein and the	
FBX028 F-box only protein 28 2,1 1,4 ubiquitin-dependent protein catabolic protein cata	ess
GHITM Growth hormone-inducible transmembrane 2,1 1,6 ?	
protein Probable ATP-dependent RNA helicase   DDX58 DDX58   2,1 1,4   response to virus / innate immune response	se
ISG15 Interferon-induced 17 kDa protein precursor 2,1 1,4 protein modification process /	
ubiquitin-dependent protein catabolic pro	cess/
cell-cell signaling/ response to virus /	

		I		modification-dependent protein catabolic process /
				ISG15-protein conjugation /
HLA-F	major histocompatibility complex, class I	2.1	1.4	interspecies interaction between organisms
nla-r	major histocompatibility complex, class I,	2,1	1,4	antigen processing and presentation of peptide
15125	F isoform 3 precursor	2.1	<b>n</b> 0	antigen via MHC class I / immune response /
IFI35	Interferon-induced 35 kDa protein	2,1	n.s.	immune response / response to virus
SLC22A4	Solute carrier family 22 member 4	2,1	1,6	triacylglycerol metabolic process / ion transport /
				body fluid secretion / carnitine metabolic process
PRKD1	Serine/threonine-protein kinase D1	2,1	1,2	protein amino acid phosphorylation /
				intracellular signaling cascade / cell proliferation
TRIM5	Tripartite motif-containing protein 5	2,0	1,2	ubiquitin-dependent protein catabolic process /
				response to virus / interspecies interaction
PPBP	Platelet basic protein precursor	2,0	1,2	chemotaxis / immune response / cell proliferation /
				glucose transport / defense response to bacterium
IFI27	Interferon alpha-inducible protein 27	2,0	1,4	aging / response to virus
FLJ11286	UPF0515 protein C19orf66	2,0	1,2	?
	Interferon-induced helicase C domain-			
IFIH1	containing	2,0	1,4	response to virus / regulation of apoptosis /
	protein 1			interspecies interaction between organisms /
				innate immune response
ID3	DNA-binding protein inhibitor ID-3	2,0	-1,2	negative regulation of transcription /
				epithelial cell differentiation / positive regulation of
				apoptosis / regulation of DNA replication /
				multicellular organismal development /
				heart development / response to wounding /
				neuron differentiation
HSPB8	Heat shock protein beta-8	2,0	n.s.	response to heat
SLC15A3	Solute carrier family 15 member 3	2,0	n.s.	oligopeptide transport / protein transport
ZBTB38	Zinc finger and BTB domain-containing	2,0	1,3	positive regulation of transcription
201000	protein 38	2,0	1,0	
ER01L	ERO1-like protein alpha precursor	2,0	1,8	protein modification process / protein thiol-disulfide
ERGIE		2,0	1,0	exchange / transport / response to temperature /
				electron transport chain / endoplasmic reticulum
				unfolded protein response /
				chaperone cofactor-dependent protein folding
AGXT2L1	Alanineglyoxylate aminotransferase 2-like 1	2.0	<b>n</b> 0	
		2,0	n.s.	amino acid metabolic process
PLEKHA2	Pleckstrin homology domain-containing	2,0	1,4	? May recruit other proteins to the plasma
	family A member 2			membrane (By similarity)
MAL2	Protein MAL2	n.s.	2,5	?The protein is a component of lipid rafts and, in polarized cells, it primarily localizes to endosomal
				structures beneath the apical membrane. It is
				required for transcytosis, an intracellular transport
				pathway used to deliver membrane-bound proteins
				and exogenous cargos from the basolateral to the
				apical surface.
CNOT6	CCR4-NOT transcription complex subunit 6	1,5	2,3	transcription
RAD51AP1	RAD51-associated protein 1	1,2	2,1	double-strand break repair via homologous
				recombination / nucleosome assembly
UHMK1	Serine/threonine-protein kinase Kist	1,6	2,0	protein amino acid phosphorylation / cell cycle
		,-	-, -	arrest / regulation of protein export from nucleus
CAB39	Calcium-binding protein 39	1,8	2,0	Akt/PKB signaling pathway (CST) /
0		1,0	2,0	mTor signaling (KEGG)
AP2B1	AP-2 complex subunit beta-1	1,6	2,0	vesicle-mediated transport / defense resp. to virus
		.,0	,0	

<sup>a</sup> Only genes more than 2-fold up- or down-regulated by both the hPop1 and Rpp40 knock-downs are shown.

<sup>b</sup>GO-terms listed are from the Gene Onthology Consortium [36].

n.s.: not significant (P>0.05)

## **Supplementary Table 2.** 2-fold or more downregulated genes after siRNA mediated knockdown of either hPop1 or Rpp40 in HEp-2 cells compared to control transfected cells.

gene	description	hPop1 <sup>ª</sup>	Rpp40 <sup>a</sup>	GO-term biological process <sup>b</sup>
symbol				
NQO1	NAD(P)H dehydrogenase [quinone] 1	-4,6	-3,0	xenobiotic metabolic process / nitric oxide biosynth.
				process / response to oxidative stress / synaptic
				cholinergic / toxin resp. / neg. regulation of catal.
				activity / oxidation reduction
HMOX1	Heme oxygenase 1	-3,5	-3,5	heme oxidation
NAT13	N-acetyltransferase 13	-2,7	n.s.	N-terminal protein amino acid acetylation /
				metabolism
TRIM16	Tripartite motif-containing protein 16	-2,6	-1,8	May play a role in the reg. of keratinocyte diff.
FTL	Ferritin light chain	-2,5	-1,2	iron ion transport / cellular iron ion homeostasis
TRIB3	Tribbles homolog 3	-2,5	-1,6	transcription / aa phosphorylation / neg. reg.
				protein kinase activity / stress response /
	Radiation-inducible immediate-early gene IEX-			regulation of MAP kinase activity / apoptosis
IER3	1	-2,4	-1,8	apoptosis / anti-apoptosis / anatom. struct. morph.
ТКТ	Transketolase	-2,4	-1,7	regulation of growth
		-		chemotaxis / inflammatory response / immune
CXCL2	C-X-C motif chemokine 2 precursor	-2,3	-1,5	resp.
YWHAZ	14-3-3 protein zeta/delta	-2,3	-1,3	protein targeting / anti-apoptosis / signal transduct.
IL18	Interleukin-18 precursor	-2,3	-1,7	angiogenesis / immune response /
				T-helper 1 and 2 type immune response /
				positive regulation of activated T cell proliferation
IL8	Interleukin-8 precursor	-2,3	-3,4	angiogenesis / immune response / cell motion /
				inflammatory response / cell-cell signaling / neg.
				regulation of cell proliferation / cell adhesion
FAM129A	Protein Niban	-2,3	-1,6	regulation of protein amino acid phosphorylation /
-				stress response / positive regulation of translation
TXNRD1	Thioredoxin reductase 1, cytoplasmic	-2,3	-1,6	mesoderm formation / signal transduction /
				response to oxidative stress /
01/04000			4.0	cell proliferation / electron transport chain
CYBASC3		-2,3	-1,3	transport / electron transport chain
MKNK2	MAP kinase-interacting serine/threonine-protein	-2,3	n.s.	reg. of translation /amino acid phosphorylation
	kinase 2			/ stress resp. / cell surf. receptor signal transduct.
ALPK3	Alpha-protein kinase 3	-2,2	-1,4	protein amino acid phosphorylation / multicellular
	Alde Late as destants from the 4 meanshire Q4	0.4	4.0	organismal development / heart development
AKR1C1	Aldo-keto reductase family 1 member C1	-2,1	-1,2	xenobiotic metabolic process / digestion /
	Mussia 40	0.4		cholesterol homeostasis / oxidation reduction
MYH10	Myosin-10	-2,1	n.s.	cytokinesis post mitosis / in utero embryo develop.
	Ovella demondent bings to this test OA	0.1		cell proliferation / actin filament-based movement
CDKN2A	Cyclin-dependent kinase inhibitor 2A,	-2,1	n.s.	G1/S transition of mitotic cell cycle /

	isoforms 1/2/3			rRNA processing / caspase activation
OLR1	Oxidized low-density lipoprotein receptor 1	-2,1	-1,9	proteolysis / inflammatory resp. / immune resp. cell adhesion / blood circulation
HEATR5A	HEAT repeat-containing protein 5A	-2,1	-1,5	reg. of transcription, DNA-dependent / pathogen.
CUL1	Cullin-1	-2,1	n.s.	G1/S trans. of mitotic cell cycle /
				ubiquitin-dependent protein catabolic process
				/ apoptosis
	Pleckstrin homology domain-containing family	2.0	4.0	
PLEKHA3	A member 3	-2,0	-1,9	?
GCLM	Glutamatecysteine ligase regulatory subunit	-2,0	-2,1	cysteine metabolic proc. /
GCLIM	Glutamatecysteine ligase regulatory subulit	-2,0	-2,1	glutathione metabolic process / neg. regulation of
				apoptosis / regulation of blood vessel size
	Nuclear receptor subfamily 1 group D member			apoptosis / regulation of blood vessel size
NR1D2	2	-2,0	-1,4	transcription
INHBB	Inhibin beta B chain precursor	-2,0	-1,9	ovarian follicle development / defense response / cell differentiation
SKP1A	S-phase kinase-associated protein 1	-2,0	n.s.	ubiquitin-dependent protein catabolic process /
				positive regulation of ubiquitin-protein ligase
				activity during mitotic cell cycle
AP3S1	AP-3 complex subunit sigma-1	-2,0	n.s.	intracellular protein transport / insulin receptor
				signaling pathway / vesicle-mediated transport
JAG1	Protein jagged-1 precursor	-2,0	-1,5	angiogenesis / cell fate determination / regulation of
				proliferation / Notch signaling pathway
GDF15	Growth/differentiation factor 15 precursor	-1,8	-3,0	transforming growth factor beta receptor signaling
				pathway / cell-cell signaling
ADRB3	Beta-3 adrenergic receptor	-1,2	-2,4	G-protein coupled receptor prot. signaling pathway
				energy reserve metabolic process/
				neg. regulation of multicellular organism growth
AXL	Tyrosine-protein kinase receptor UFO	n.s.	-2,4	protein amino acid phosphorylation /
	precursor			signal transduct.(stimulation of cell proliferation)
SLC11A2	Natural resistance-associated macrophage protein 2	n.s.	-2,3	cobalt ion transport / iron ion transport
CDKN1A	Cyclin-dependent kinase inhibitor 1	n.s.	-2,3	G1/S transition of mitotic cell cycle / G2/M transition
				of mitotic cell cycle / cell cycle arrest
EIF2A	Eukaryotic translation initiation factor 2A	-1,6	-2,2	regulation of translation / protein amino acid
				phosphorylation / ribosome assembly
RPP40	Ribonuclease P protein subunit p40	n.s.	-2,2	tRNA processing
NDUFB5	NADH dehydrogenase [ubiquinone] 1	n.s.	-2,0	mitochondrial electron transport,
	beta subcomplex subunit 5,			NADH to ubiquinone
	mitochondrial precursor			
HIGD1A	HIG1 domain family member 1A	n.s.	-2,0	response to stress

<sup>a</sup> Only genes more than 2-fold up- or down-regulated by both the hPop1 and Rpp40 knock-downs are

shown.

<sup>b</sup>GO-terms listed are from the Gene Onthology Consortium [36].

n.s.: not significant (P>0.05)