**Virologica Sinica**

**Supplementary Data**

**Human cytomegalovirus RNA2.7 inhibits RNA polymerase II (Pol II) Serine-2 phosphorylation by reducing the interaction between Pol II and phosphorylated cyclin-dependent kinase 9 (pCDK9)**

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**Supplementary Table S1** Genes involved host gene activation.

|  |  |  |  |
| --- | --- | --- | --- |
| Symbol | Entrez gene name | Fold Changes | |
| HAN | HAN  ΔRNA2.7 |
| EPCAM | Epithelial cell adhesion molecule | 24.76 | 47.13 |
| ATF3 | Activating transcription factor 3 | 17.35 | 34.09 |
| IFI27 | Interferon, alpha-inducible protein 27 | 27.68 | 32.66 |
| WT1 | Wilms tumor 1 | 10.05 | 30.75 |
| TRIB3 | Tribbles pseudokinase 3 | 10.67 | 20.94 |
| ZNF367 | Zinc finger protein 367 | 8.14 | 20.09 |
| FZD5 | Frizzled class receptor 5 | 9.90 | 19.75 |
| ONECUT2 | One cut homeobox 2 | 14.09 | 16.40 |
| HDAC9 | Histone deacetylase 9 | 6.31 | 10.49 |
| TFAP2C | Transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma) | 6.04 | 10.38 |
| RORA | RAR-related orphan receptor A | 6.54 | 10.23 |
| DDIT3 | DNA-damage-inducible transcript 3 | 3.91 | 9.18 |
| CEBPA | CCAAT/enhancer binding protein (C/EBP), alpha | 6.67 | 9.05 |
| GRHL1 | Grainyhead-like 1 (Drosophila) | 4.41 | 8.59 |
| SOX17 | SRY (sex determining region Y)-box 17 | 4.90 | 6.26 |
| MXD1 | MAX dimerization protein 1 | 4.01 | 6.13 |
| CEBPG | CCAAT/enhancer binding protein (C/EBP), gamma | 3.70 | 6.00 |
| PRKCB | Protein kinase C, beta | 3.16 | 5.77 |
| POLR3G | Polymerase (RNA) III (DNA directed) polypeptide G (32kD) | 3.46 | 5.68 |
| F2RL1 | Coagulation factor II (thrombin) receptor-like 1 | 2.50 | 5.26 |
| TEAD4 | TEA domain family member 4 | 4.33 | 5.16 |
| MEF2C | Myocyte enhancer factor 2C | 5.52 | 5.06 |
| GATA3 | GATA binding protein 3 | 2.42 | 5.03 |
| HES1 | Hes family bHLH transcription factor 1 | 5.77 | 4.92 |
| KLF7 | Kruppel-like factor 7 (ubiquitous) | 3.50 | 4.92 |
| CCRN4L | CCR4 carbon catabolite repression 4-like (S. cerevisiae) | 2.49 | 4.71 |
| NHLH2 | Nescient helix loop helix 2 | 3.42 | 4.63 |
| PAWR | PRKC, apoptosis, WT1, regulator | 4.06 | 4.63 |
| TCF19 | Transcription factor 19 | 2.04 | 4.51 |
| EOMES | Eomesodermin | 4.02 | 4.47 |
| ELK4 | ETS-domain protein (SRF accessory protein 1) | 4.65 | 4.45 |
| GABPB1 | GA binding protein transcription factor | 2.85 | 4.35 |
| IL6 | Interleukin 6 | 4.01 | 4.26 |
| LRRFIP1 | Leucine rich repeat (in FLII) interacting protein 1 | 3.41 | 4.16 |
| RUNX3 | Runt-related transcription factor 3 | 3.93 | 3.99 |
| KLF15 | Kruppel-like factor 15 | 2.32 | 3.98 |
| DDX58 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 58 | 4.14 | 3.83 |
| SP4 | Sp4 transcription factor | 2.34 | 3.81 |
| KLF5 | Kruppel-like factor 5 (intestinal) | 3.18 | 3.66 |
| GCFC2 | GC-rich sequence DNA-binding factor 2 | 2.37 | 3.57 |
| NR2C2 | Nuclear receptor subfamily 2, group C, member 2 | 2.57 | 3.54 |
| KLF2 | Kruppel-like factor 2 | 2.72 | 3.51 |
| FOXO1 | Forkhead box O1 | 2.94 | 3.47 |
| TNFSF11 | Tumor necrosis factor (ligand) superfamily, member 11 | 4.05 | 3.32 |
| FNIP1 | Folliculin interacting protein 1 | 2.32 | 3.31 |
| SUV39H2 | Suppressor of variegation 3-9 homolog 2 (Drosophila) | 2.26 | 3.15 |
| TFEB | Transcription factor EB | 2.62 | 3.14 |
| INSM1 | Insulinoma-associated 1 | 4.08 | 3.07 |
| OTUD7B | OTU deubiquitinase 7B | 2.02 | 3.02 |
| ZNF174 | Zinc finger protein 174 | 2.87 | 2.98 |
| CXCL10 | Chemokine (C-X-C motif) ligand 10 | 3.38 | 2.97 |
| NFYA | Nuclear transcription factor Y, alpha | 2.05 | 2.97 |
| POLR2D | Polymerase (RNA) II (DNA directed) polypeptide D | 2.03 | 2.79 |
| HEY1 | Hes-related family bHLH transcription factor with YRPW motif 1 | 3.23 | 2.78 |
| FGF2 | Fibroblast growth factor 2 (basic) | 3.20 | 2.74 |
| BMP6 | Bone morphogenetic protein 6 | 5.56 | 2.73 |
| NACC2 | NACC family member 2, BEN and BTB (POZ) domain containing | 2.10 | 2.72 |
| SETD8 | SET domain containing (lysine methyltransferase) 8 | 2.05 | 2.72 |
| BHLHE40 | Basic helix-loop-helix family, member e40 | 3.22 | 2.69 |
| ZNF141 | Zinc finger protein 141 | 2.19 | 2.68 |
| STAT1 | Signal transducer and activator of transcription 1, 91kDa | 3.38 | 2.61 |
| CSRNP1 | Cysteine-serine-rich nuclear protein 1 | 2.99 | 2.56 |
| RFX3 | Regulatory factor X, 3 (influences HLA class II expression) | 2.26 | 2.56 |
| ARNTL | Aryl hydrocarbon receptor nuclear translocator-like | 2.14 | 2.54 |
| LIF | Leukemia inhibitory factor | 2.45 | 2.50 |
| NPAS2 | Neuronal PAS domain protein 2 | 2.83 | 2.49 |
| VEGFA | Vascular endothelial growth factor A | 2.54 | 2.36 |
| MEF2D | Myocyte enhancer factor 2D | 2.35 | 2.35 |
| KLF12 | Kruppel-like factor 12 | 2.07 | 2.19 |
| GATA2 | GATA binding protein 2 | 3.06 | 2.18 |
| PID1 | Phosphotyrosine interaction domain containing 1 | 2.14 | 2.17 |
| XBP1 | X-box binding protein 1 | 2.53 | 2.15 |
| ETV5 | Ets variant 5 | 2.06 | 2.12 |
| MDM2 | MDM2 proto-oncogene, E3 ubiquitin protein ligase | 2.22 | 2.10 |
| MEF2A | Myocyte enhancer factor 2A | 2.37 | 2.10 |
| SPEN | Spen family transcriptional repressor | 2.28 | 2.05 |
| BMP2 | Bone morphogenetic protein 2 | 2.34 | 2.04 |
| ARNTL2 | Aryl hydrocarbon receptor nuclear translocator-like 2 | 2.05 | 2.03 |
| TSC22D1 | TSC22 domain family, member 1 | 2.57 | 2.00 |
| SUB1 | SUB1 homolog (S. cerevisiae) | −2.64 | −2.02 |
| ZFHX3 | Zinc finger homeobox 3 | −2.49 | −2.05 |
| SMAD3 | SMAD family member 3 | −2.34 | −2.10 |
| VEZF1 | Vascular endothelial zinc finger 1 | −2.19 | −2.10 |
| TCF12 | Transcription factor 12 | −2.22 | −2.22 |
| MED17 | Mediator complex subunit 17 | −2.28 | −2.27 |
| CDKN2A | Cyclin-dependent kinase inhibitor 2A | −2.06 | −2.36 |
| BPTF | Bromodomain PHD finger transcription factor | −2.44 | −2.37 |
| NR1H3 | Nuclear receptor subfamily 1, group H, member 3 | −2.18 | −2.46 |
| EID1 | EP300 interacting inhibitor of differentiation 1 | −2.75 | −2.54 |
| NFIX | Nuclear factor I/X (CCAAT-binding transcription factor) | −2.31 | −2.67 |
| CTNNB1 | Catenin (cadherin-associated protein), beta 1, 88kDa | −2.06 | −2.68 |
| TRIM27 | Tripartite motif containing 27 | −2.20 | −2.69 |
| EDNRB | Endothelin receptor type B | −2.23 | −2.70 |
| MYOCD | Myocardin | −3.62 | −2.70 |
| PIR | Pirin (iron-binding nuclear protein) | −3.41 | −2.74 |
| TAF9B | TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor | −2.05 | −2.74 |
| NFIA | Nuclear factor I/A | −2.80 | −2.94 |
| CEBPD | CCAAT/enhancer binding protein (C/EBP), delta | −2.17 | −3.26 |
| SOX11 | SRY (sex determining region Y)-box 11 | −2.08 | −3.34 |
| ELP2 | Elongator acetyltransferase complex subunit 2 | −4.23 | −3.75 |
| IGF1 | Insulin-like growth factor 1 (somatomedin C) | −4.36 | −3.82 |
| TADA2A | Transcriptional adaptor 2A | −8.34 | −3.93 |
| MEOX2 | Mesenchyme homeobox 2 | −4.71 | −3.98 |
| TCF25 | Transcription factor 25 (basic helix-loop-helix) | −4.19 | −3.98 |
| DKK1 | Dickkopf WNT signaling pathway inhibitor 1 | −2.93 | −4.37 |
| SNCA | Synuclein, alpha (non A4 component of amyloid precursor) | −2.43 | −4.42 |
| BMP5 | Bone morphogenetic protein 5 | −2.66 | −4.44 |
| TPR | Translocated promoter region, nuclear basket protein | −2.85 | −4.54 |
| RGCC | Regulator of cell cycle | −2.50 | −4.67 |
| DDX5 | DEAD (Asp-Glu-Ala-Asp) box helicase 5 | −4.19 | −4.78 |
| CHD3 | Chromodomain helicase DNA binding protein 3 | −2.26 | −8.75 |
| AFF4 | AF4/FMR2 family, member 4 | −2.34 | 3.49 |
| HMGA2 | High mobility group AT-hook 2 | 3.71 | −2.04 |
| PAX6 | Paired box 6 |  | 93.44 |
| MNX1 | Motor neuron and pancreas homeobox 1 |  | 16.60 |
| SOX2 | SRY (sex determining region Y)-box 2 |  | 10.65 |
| GATA5 | GATA binding protein 5 |  | 9.72 |
| USP2 | Ubiquitin specific peptidase 2 |  | 8.52 |
| MYBL2 | V-myb avian myeloblastosis viral oncogene homolog-like 2 |  | 8.20 |
| HOXC6 | Homeobox C6 |  | 7.78 |
| HNF4G | Hepatocyte nuclear factor 4, gamma |  | 7.41 |
| CD40 | CD40 molecule, TNF receptor superfamily member 5 |  | 7.35 |
| MESP1 | Mesoderm posterior basic helix-loop-helix transcription factor 1 |  | 6.69 |
| PROX1 | Prospero homeobox 1 |  | 6.64 |
| PGR | Progesterone receptor |  | 5.56 |
| CNOT1 | CCR4-NOT transcription complex, subunit 1 |  | 5.30 |
| GTF2A1 | General transcription factor IIA, 1, 19/37kDa |  | 5.17 |
| BATF3 | basic leucine zipper transcription factor, ATF-like 3 |  | 5.01 |
| MET | MET proto-oncogene, receptor tyrosine kinase |  | 4.16 |
| LRP6 | Low density lipoprotein receptor-related protein 6 |  | 4.08 |
| ETV7 | Ets variant 7 |  | 4.04 |
| E2F7 | E2F transcription factor 7 |  | 3.93 |
| GABPA | GA binding protein transcription factor, alpha subunit 60kDa |  | 3.86 |
| ARRB2 | Arrestin, beta 2 |  | 3.31 |
| IRF4 | Interferon regulatory factor 4 |  | 3.31 |
| EZH2 | Enhancer of zeste 2 polycomb repressive complex 2 subunit |  | 3.30 |
| PPARGC1B | Peroxisome proliferator-activated receptor gamma, coactivator 1 beta |  | 3.23 |
| CKAP2 | Cytoskeleton associated protein 2 |  | 3.18 |
| HOXA10 | Homeobox A10 |  | 3.18 |
| NCOA3 | Nuclear receptor coactivator 3 |  | 3.18 |
| TAL1 | T-cell acute lymphocytic leukemia 1 |  | 3.18 |
| BRCA1 | Breast cancer 1, early onset |  | 3.17 |
| RPS6KA1 | Ribosomal protein S6 kinase, 90kDa, polypeptide 1 |  | 3.11 |
| MED30 | Mediator complex subunit 30 |  | 3.01 |
| ZNF593 | Zinc finger protein 593 |  | 2.94 |
| TAF5L | TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor |  | 2.93 |
| CHCHD3 | Coiled-coil-helix-coiled-coil-helix domain containing 3 |  | 2.91 |
| TAF1A | TATA box binding protein (TBP)-associated factor, RNA polymerase I, A |  | 2.90 |
| POU4F2 | POU class 4 homeobox 2 |  | 2.88 |
| PLK3 | polo-like kinase 3 |  | 2.84 |
| BCL11B | P-cell CLL/lymphoma 11B (zinc finger protein) |  | 2.80 |
| TET2 | Tet methylcytosine dioxygenase 2 |  | 2.79 |
| NFAT5 | Nuclear factor of activated T-cells 5, tonicity-responsive |  | 2.72 |
| NUFIP1 | Nuclear fragile X mental retardation protein interacting protein 1 |  | 2.70 |
| SETX | Senataxin |  | 2.70 |
| GTF2H2 | General transcription factor IIH, polypeptide 2, 44kDa |  | 2.69 |
| DR1 | Down-regulator of transcription 1, TBP-binding (negative cofactor 2) |  | 2.60 |
| FOXA3 | Forkhead box A3 |  | 2.60 |
| FOXK2 | Forkhead box K2 |  | 2.59 |
| ELP4 | Elongator acetyltransferase complex subunit 4 |  | 2.58 |
| VPRBP | Vpr (HIV-1) binding protein |  | 2.58 |
| NCOA1 | Nuclear receptor coactivator 1 |  | 2.57 |
| PITX2 | Paired-like homeodomain 2 |  | 2.53 |
| CPEB3 | Cytoplasmic polyadenylation element binding protein 3 |  | 2.51 |
| BUD31 | BUD31 homolog (S. cerevisiae) |  | 2.50 |
| HOXD8 | Homeobox D8 |  | 2.49 |
| CBX4 | Chromobox homolog 4 |  | 2.47 |
| PHIP | Pleckstrin homology domain interacting protein |  | 2.44 |
| TFAM | Transcription factor A, mitochondrial |  | 2.44 |
| FNIP2 | Folliculin interacting protein 2 |  | 2.41 |
| HSF2 | Heat shock transcription factor 2 |  | 2.41 |
| KLF11 | Kruppel-like factor 11 |  | 2.41 |
| CRY1 | Cryptochrome circadian clock 1 |  | 2.40 |
| HHEX | Hematopoietically expressed homeobox |  | 2.38 |
| BEX1 | Brain expressed, X-linked 1 |  | 2.34 |
| DNMT3B | DNA (cytosine-5-)-methyltransferase 3 beta |  | 2.34 |
| E2F1 | E2F transcription factor 1 |  | 2.33 |
| TET3 | Tet methylcytosine dioxygenase 3 |  | 2.33 |
| ZNF354A | Zinc finger protein 354A |  | 2.31 |
| IVNS1ABP | Influenza virus NS1A binding protein |  | 2.30 |
| KAT2B | K(lysine) acetyltransferase 2B |  | 2.29 |
| TNKS | Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase |  | 2.29 |
| ALX1 | ALX homeobox 1 |  | 2.28 |
| CHD1 | Chromodomain helicase DNA binding protein 1 |  | 2.27 |
| NFATC3 | Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 |  | 2.26 |
| CIAO1 | Cytosolic iron-sulfur assembly component 1 |  | 2.25 |
| TCEB3 | Transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A) |  | 2.25 |
| SUV39H1 | Suppressor of variegation 3-9 homolog 1 (Drosophila) |  | 2.23 |
| CGGBP1 | CGG triplet repeat binding protein 1 |  | 2.21 |
| ELP3 | Elongator acetyltransferase complex subunit 3 |  | 2.21 |
| CAMTA2 | Calmodulin binding transcription activator 2 |  | 2.20 |
| MED13 | Mediator complex subunit 13 |  | 2.20 |
| MITF | Microphthalmia-associated transcription factor |  | 2.20 |
| BLZF1 | Basic leucine zipper nuclear factor 1 |  | 2.17 |
| FOXA1 | Forkhead box A1 |  | 2.17 |
| TRIM24 | Tripartite motif containing 24 |  | 2.17 |
| MAFF | V-maf avian musculoaponeurotic fibrosarcoma oncogene homolog F |  | 2.15 |
| ATF5 | Activating transcription factor 5 |  | 2.13 |
| HMGB2 | High mobility group box 2 |  | 2.13 |
| SMAD2 | SMAD family member 2 |  | 2.12 |
| CREBRF | CREB3 regulatory factor |  | 2.08 |
| CRLF3 | Cytokine receptor-like factor 3 |  | 2.08 |
| MYO6 | Myosin VI |  | 2.08 |
| EPC1 | Enhancer of polycomb homolog 1 (Drosophila) |  | 2.07 |
| NFATC1 | Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 |  | 2.05 |
| FOSL1 | FOS-like antigen 1 |  | 2.04 |
| CDC73 | Cell division cycle 73 |  | 2.03 |
| HCFC2 | Host cell factor C2 |  | 2.03 |
| HIRA | Histone cell cycle regulator |  | 2.03 |
| RIPK1 | Receptor (TNFRSF)-interacting serine-threonine kinase 1 |  | 2.02 |
| ASXL2 | Additional sex combs like transcriptional regulator 2 |  | 2.01 |
| RITA1 | RBPJ interacting and tubulin associated 1 |  | 2.01 |
| ATF7 | Activating transcription factor 7 |  | 2.00 |
| CBX6 | Chromobox homolog 6 |  | −2.01 |
| MLX | MLX, MAX dimerization protein |  | −2.01 |
| RNASEL | Ribonuclease L (2',5'-oligoisoadenylate synthetase-dependent) |  | −2.01 |
| MAML2 | Mastermind-like 2 (Drosophila) |  | −2.02 |
| MZF1 | Myeloid zinc finger 1 |  | −2.03 |
| NR2F1 | Nuclear receptor subfamily 2, group F, member 1 |  | −2.04 |
| SNAPC3 | Small nuclear RNA activating complex, polypeptide 3, 50kDa |  | −2.04 |
| ETS2 | V-ets avian erythroblastosis virus E26 oncogene homolog 2 |  | −2.05 |
| PRDM16 | PR domain containing 16 |  | −2.06 |
| MED16 | Mediator complex subunit 16 |  | −2.07 |
| HEXIM1 | Hexamethylene bis-acetamide inducible 1 |  | −2.08 |
| HDAC4 | Histone deacetylase 4 |  | −2.10 |
| ORC2 | Origin recognition complex, subunit 2 |  | −2.10 |
| RXRA | Retinoid X receptor, alpha |  | −2.10 |
| ZHX1 | Zinc fingers and homeoboxes 1 |  | −2.10 |
| UBE2I | Ubiquitin-conjugating enzyme E2I |  | −2.11 |
| SOX4 | SRY (sex determining region Y)-box 4 |  | −2.12 |
| TCF4 | Transcription factor 4 |  | −2.12 |
| FHL2 | Four and a half LIM domains 2 |  | −2.13 |
| TEF | Thyrotrophic embryonic factor |  | −2.13 |
| FST | Follistatin |  | −2.14 |
| H2AFY | H2A histone family, member Y |  | −2.15 |
| ZBTB1 | Zinc finger and BTB domain containing 1 |  | −2.16 |
| SNAI2 | Snail family zinc finger 2 |  | −2.18 |
| TBX5 | T-box 5 |  | −2.18 |
| SATB1 | SATB homeobox 1 |  | −2.22 |
| HMGB1 | High mobility group box 1 |  | −2.24 |
| NR2F2 | Nuclear receptor subfamily 2, group F, member 2 |  | −2.24 |
| TGFB1I1 | Transforming growth factor beta 1 induced transcript 1 |  | −2.24 |
| TBL1XR1 | Transducin (beta)-like 1 X-linked receptor 1 |  | −2.25 |
| PRDM5 | PR domain containing 5 |  | −2.28 |
| IL33 | Interleukin 33 |  | −2.31 |
| CCND1 | Cyclin D1 |  | −2.32 |
| ARID5B | AT rich interactive domain 5B (MRF1-like) |  | −2.35 |
| GLI2 | GLI family zinc finger 2 |  | −2.38 |
| BRD3 | Bromodomain containing 3 |  | −2.40 |
| ATRX | Alpha thalassemia/mental retardation syndrome X-linked |  | −2.42 |
| MECP2 | Methyl CpG binding protein 2 |  | −2.48 |
| CSRNP3 | Cysteine-serine-rich nuclear protein 3 |  | −2.49 |
| BCL11A | B-cell CLL/lymphoma 11A (zinc finger protein) |  | −2.52 |
| SMAD4 | SMAD family member 4 |  | −2.55 |
| MSC | Musculin |  | −2.56 |
| TCF3 | Transcription factor 3 |  | −2.57 |
| CBX2 | Chromobox homolog 2 |  | −2.63 |
| TCF21 | Transcription factor 21 |  | −2.80 |
| FOXF1 | Forkhead box F1 |  | −2.97 |
| DBP | D site of albumin promoter (albumin D-box) binding protein |  | −3.05 |
| PPARGC1A | Peroxisome proliferator-activated receptor gamma, coactivator 1 alpha |  | −3.07 |
| STAT6 | Signal transducer and activator of transcription 6, interleukin-4 induced |  | −3.15 |
| KANK2 | KN motif and ankyrin repeat domains 2 |  | −3.39 |
| FOXJ2 | Forkhead box J2 |  | −3.82 |
| H2AFY2 | H2A histone family, member Y2 |  | −3.85 |
| HOXA5 | Homeobox A5 |  | −3.99 |
| RBPJ | Recombination signal binding protein for immunoglobulin kappa J region |  | −4.05 |
| MAVS | Mitochondrial antiviral signaling protein |  | −5.27 |

**Supplementary Table S2** Sequences of primers used in this study.

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| --- | --- | --- |
| Name | Primer Sequence | Product sizes (bp) |
| RNA2.7rt | Forward: ACGGATAAGTAGAGTGTAGGC  Reverse: ATGCATGCAAACTTCTCATT | 701 |
| RNA2.7D | Forward: ACGACGATGATTCCTTACCG  Reverse: TCTCGGGTTCTTTTTGTTGG | 231 |
| UL83 | Forward: CTGATCCTGGTGTCGCAGTA  Reverse: GCTCTTTCCACTGGTTCTGC | 370 |
| RL1 | Forward: ATAGGCGAGGGC  Reverse: CGATGCGGTGGAT | 428 |
| RL6 | Forward: CCGAACCAACGAGACAG  Reverse: ATTACGCATAGGAAAGAT | 212 |
| RL8A | Forward: CGCTGTTTCTGTTGTGGC  Reverse: CATGTGAGGGCTTGTTGC | 208 |
| RL9A | Forward: AAACAGCACGTAGGTCAGG  Reverse: TAGATGCCGCCAGCCAC | 131 |
| UL123 (IE1) | Forward: GCTCTGCATAGTTAGCCCAATA  Reverse: GCCGAAGAATCCCTCAAAAAC | 282 |
| UL44 | Forward: GTGCGCGCCCGATTTCAATATG  Reverse: GCTTTCGCGCACAATGTCTTGA | 69 |
| UL55 | Forward: TACGTGCAGTACGGTCAACTGG  Reverse: ACATTCCTCAGTGCGGTGGTTG | 68 |
| UL99 | Forward: ACTCCGCGCCAAAAGAAGAT  Reverse: TTAAAAGGGCAAGGAGGCGG | 78 |
| pRNA2.7 | Forward: CCGCTCGAGAGATCGCTGCTGCTCCGGCGTTC  Reverse: CCCAAGCTTGCATGCAAACTTCTCATTTATTG | 2499 |
| pRNA2.7A | Forward: CCGCTCGAGAGATCGCTGCTGCTCCGGCGTTC  Reverse: CCCAAGCTTGGCTGCTGACCGACGCGTCAGGA | 883 |
| pRNA2.7B | Forward: CCGCTCGAGACCGCGATCTCCGTATAGGTAGA  Reverse: CCCAAGCTTATGACTCCTTCGTGTCCAGGGAG | 868 |
| pRNA2.7C | Forward: CCGCTCGAGACAACATCATCATCGGAGACCAT  Reverse: CCCAAGCTTGCATGCAAACTTCTCATTTATTG | 952 |
| pRNA2.7C1 | Forward: CCGCTCGAGACAACATCATCATCGGAGA  Reverse: CCCAAGCTTCTAGGTGTACTTTGATGCT | 391 |
| pRNA2.7C2 | Forward: CCGCTCGAGCACATCAACACAGCGA  Reverse: CCCAAGCTTTGTGGATCCTAAGAGGT | 370 |
| pRNA2.7C3 | Forward: CCGCACGAGGAGATTCGCACTTGAA  Reverse: CCCAAGCTTGCATGCAAACTTCTCA | 304 |
| pRNA2.7C2a | Forward: CCGCTCGAGCACATCAACACAGCGA  Reverse: CCCAAGCTTATATCCGAGTATCTGT | 151 |
| pRNA2.7C2b | Forward: CCGCTCGAGACCGTCCTTACGAGAA  Reverse: CCCAAGCTTCGAGGGACATCACGAT | 160 |
| pRNA2.7C2c | Forward: CCGCTCGAGGACTTCATCGCAACGA  Reverse: CCCAAGCTTTGTGGATCCTAAGAGGT | 163 |
| T7RNA2.7C2c | Forward: taatacgactcactatagggGACTTCATCGCAACGA  Reverse: GTGGATCCTAAGAGGT | 165 |
| MCM2 | Forward: CCAGCGTATCCCAATCCA  Reverse: TTCGCTGTGCCAGGGTCT | 468 |
| MCM4 | Forward: GAGGAGCAGGCAGAGGAGGA  Reverse: TCCCGATGGAGGCGTTTGG | 281 |
| MCM5 | Forward: GGCTCCCTGATGGACTTACT  Reverse: CATGGCTTCGTGGATTGC | 296 |
| Cdt1 | Forward: AAGGATCCCGCCTACCAGCGCTTCC  Reverse: CCAAGCTTGAAGGTGGGGACACTG | 288 |
| Cdc6 | Forward: AAGGATCCCGAATACCAGCGCTTCC  Reverse: CCAAGCTTGAAGGTGGGGACACTG | 271 |
| GAPDH | Forward: TGGTGAAGACGCCAGTGGA  Reverse: GCACCGTCAAGGCTGAGAAC | 137 |

Sequences recognized by restriction endonucleases are underlined; T7 promoter sequence is indicated with lowercase letters.

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**Supplementary Fig. S1** Construction of HCMV RNA2.7 deleted mutant. **A** Schematic diagram showing genomic location of HCMV RNA2.7. RNA2.7 is indicated in black bar. **B** Schematic diagram showing the deletion of HCMV RNA2.7 by homologous reconbination. A kanamycin resistance gene was inserted into the RNA2.7 locus. **C** Viral genomes were assessed with restriction endonuclease *Eco*R I and *Spe* I. M, marker. **D** Validationof RNA2.7 deletion. Transcription of RNA2.7 could not be detected in HELF cells infected with HANΔRNA2.7. HCMV UL83 was amplified as a positive control. **E** Quantitative PCR of selected viral genes. HELF cells were infected with HAN or HANΔRNA2.7 (MOI = 1.0). Transcriptions of RNA2.7 flanking genes (*RL1*, *RL6*, *RL8A* and *RL9A*), viral immediate early (*UL123*), early (*UL44* and *UL55*) and late (*UL83* and *UL99*) genes were measured. Data are presented as mean ± SEM.

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**Supplementary Fig. S2** No interaction between RNA2.7C2c and phospho-CDK9 protein.No change was found after competitive RNA or anti-pCDK9 antibody was added into the EMSA systems.

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**Supplementary Fig. S3** Pathway analysis indicating effects of RNA2.7 on cell cycle control. **A** Results of pathway analysis indicating effects of RNA2.7 on pathways involved in cell cycle regulation. **B** Heatmap showing that 11 genes involved in cell cycle control of chromosomal replication are increased in cells infected with HANΔRNA2.7.