

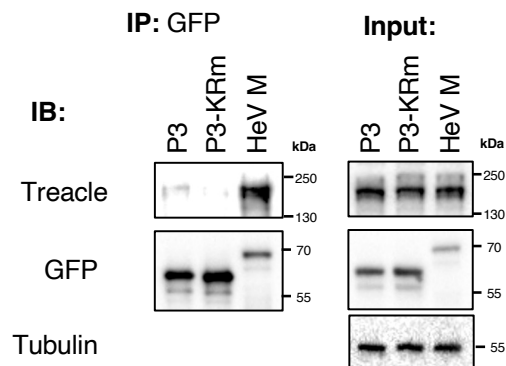
Figure S1

MOJV	-----MEATSDFKDATWQDGGLLKSIDAELEQGYMPIKYRVIN	39
KV	-----MEAITNFMFYTWFEFGSLNKVEPELDENGSMIPKVRVLN	39
CEDV	MDPSDLRRIIMEDDKSLVNNDDSTETDFLEKTWREGSKIDKITPEVDENGNMVKYVVFN	60
HEV	MDF-----SVSDNLDDPIEGVSDFSPTSWENGGYLDKVEPEIDKHGSMIPKYKIYT	51
NIV	MEP-----DIKSISSEMEGVSDFSFSSWENGGYLDKVEPEIDENGSMIPKYKIYT	51
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MOJV	PGGNERKTMGYMYLIAYGFVEDVLNDHKTQQKPKIRTVAAYPFVGVSSDSSPEDLLKSAC	99
KV	PGYNDKSSGYQYLICYGFVEDIRSESNKDKKPTIRTTASFPLGVGRSDASPENLLDEVC	99
CEDV	PGKNERKTSGYQYMICYGFIEDGPIGSPRVKGNIRTTASFPLGVGKTYSSPEEILQELT	120
HEV	PGANERKFNNMYMICYGFVEDVERSPESGRKKKIRTTAAYPLGVGKSTSHPQDLLEELC	111
NIV	PGANERKYNMYMICYGFVEDVERTPETGKRKKKIRTTAAYPLGVGKSASHPQDLLEELC	111
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MOJV	ALDVSVRTAGATEKIVMGARTLGLCLAPWSSVLNNGAIFNASKICNNVDLIQLGTPQRL	159
KV	KLSITVRRTAGAEEKIVYGVSGGILYLDPWKKVLKNGAIFTATKVCNIECVLVDKHQSL	159
CEDV	TLKITVRRTAGSNEKLVYGITGPLNHLYPWKVLTGGSIFSAVKVCRNVDQILLDRPQIL	180
HEV	SLKVTVRRTAGATEKIVFGSSGPLHLLPWKKILTGGSI FNAVKVCRNVDQIQLEKQQL	171
NIV	SLKVTVRRTAGSTEKVVFGSSGPLNHLVPWKVLTGGSIFNAVKVCRNVDQIQLDKHQAL	171
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MOJV	RIFFLSITLLTDKGIYKPKTVLEFRESNAVAFNLLVSLRIDTDLTRAGMKGIVDKEGRR	219
KV	RIFFLSITKLTDRGYTIPRRMLEFRYNNAIANLLVTLAISTDTTKSGVRGKKNEDGFT	219
CEDV	RVFFLSITKLTDRGVYMI PKSVLDFRSDNSMAFNLLVYLKIDTDTKAGIRGIVNKEGER	240
HEV	RIFFLSITKLNDSGIYMI PRMTLEFRNNAIAFNLLVYLKIDADLAKAGIQGSFDKDGTK	231
NIV	RIFFLSITKLNDSGIYMI PRMTLEFRNNAIAFNLLVYLKIDADLSKMGIQGSLDKDGFK	231
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MOJV	LATFMLHIGNFVRRGRKPYSEYCKKKVENMALIFSLGAVGGLSLHVRFTGKLSKRLIAS	279
KV	LVTFMTHMGNFQRRAGKTYSEYCSRRKVDKMKMKSFLGAIIGLSFHVRIDGVI SKRLFAE	279
CEDV	ITSFMLHIGNFTRRGKHYSEYCKRKIDMKMLTFALGTIGGLSLHIRIDGRISKRLQAQ	300
HEV	VASFMLHLGNFVRRAGKYSEYCKRKIDRMKQLQSLGSIIGGLSLHIKINGVISKRLFAQ	291
NIV	VASFMLHLGNFVRRAGKYSDVYCKRKIDRMKQLQSLGSIIGGLSLHIKINGVISKRLFAQ	291
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MOJV	MRFHRNICFSLMDINPGLNKLWNHECEIQKITAVFQPSIPKDFKIYDDVLDINTGKILK	339
KV	MGFRRNICYCLIDINPWINKLWNTCEIRNVAAVLQPSVPRDFMIYDDVFDINTGKILP	339
CEDV	VGFQRNICYSLMDTNPWLNKLWNNSCEIHKVTAVIQPSVPKDFMLEDILIDINTGKILK	360
HEV	MGFQKNLCFSLMDINPWLNRLWNNSCEISRVAAVLQPSVPREFMIYDDVFDINTGKILK	351
NIV	MGFQKNLCFSLMDINPWLNRLWNNSCEISRVAAVLQPSVPREFMIYDDVFDINTGRILK	351
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MOJV	N---	340
KV	SKHA	343
CEDV	----	360
HEV	G---	352
NIV	G---	352

Supplementary Figure S1 Sequence alignment of henipavirus M proteins used in study.

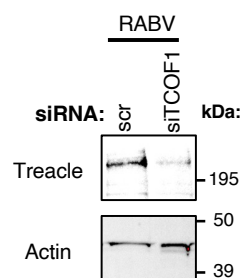
Alignment using Clustal Omega (version 1.2.4) of HeV M (Accession number: AEB21196.1), NiV M (AAV43914.1), CedV M (AFP87277.1), MojV M (AHM23775.1) and KV M (YP_009091836). Positions with an absolutely conserved residue (*); residues with strong similarity (:); Residues with weak similarity (.). Key residues of the bipartite NLS (two clusters of basic residues) are highlighted in red font; K258 residue (bold underlined) is absolutely conserved across all species.

Figure S2



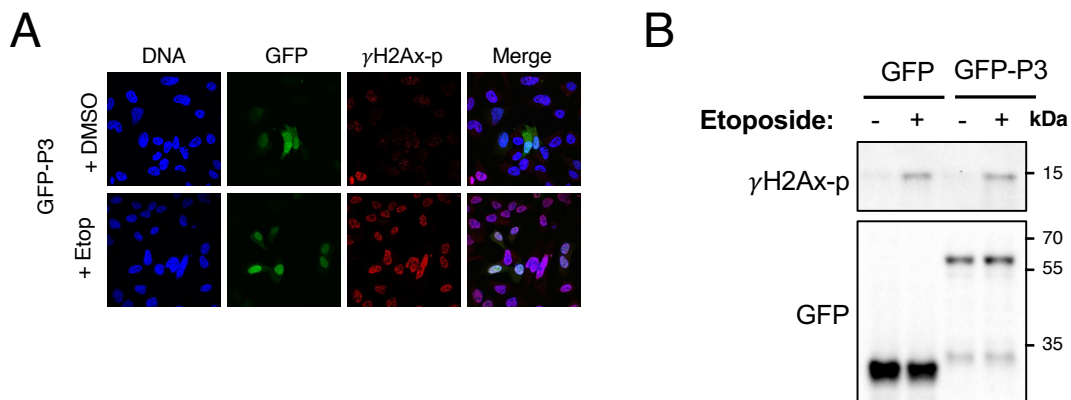
Supplementary Figure S2 **HeV M co-precipitates Treacle to a greater extent than P3.** HEK-293T cells were transfected to express the indicated GFP-fused proteins, prior to lysis and IP with GFP-Trap beads (as performed in Figs. 3A & 5A). IP and input samples were analysed by IB and probed with the indicated antibodies.

Figure S3



Supplementary Figure S3 Confirmation of the effectiveness of siRNA knockdown. HEK-293 cells were transfected with siRNA (scr or siTCOF1) for 48 h (see Materials and Methods for details) prior to infection by RABV (MOI 0.01). Cells were lysed at 48 h p.i. and analysed by IB using the indicated antibodies.

Figure S4



Supplementary Figure S4 **Expression of RABV P3 does not induce DNA-damage in HeLa cells.**

HeLa cells transfected to express GFP-P3 protein were treated without (DMSO) or with etoposide at 21 h p.t. for 3 h prior to (A) fixation and immunostaining for γ H2AX phosphorylated at S139 (γ H2AX-p), and imaging by CLSM (images representative of 10 fields of view taken from two independent experiments) or (B) lysed and analysed for IB analysis using the indicated antibodies.