Supporting Information for

"Lyssavirus P protein isoforms diverge significantly in subcellular interactions underlying mechanisms of interferon antagonism"

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Figure S1. Live cell CLSM images of HeLa cells expressing the indicated GFP-fused P protein isoforms, of Nishigahara (upper panel) and Ni-CE (lower panel). Images are representative of cells from \geq 5 fields of view.



Figure S2. CLSM images of COS-7 cells expressing the indicated GFP-fused Ni-P isoforms. Cells were fixed and immunostained for β -tubulin following treatment without (left panels) or with Taxol (center panels) or Nocodazole (right panels). Images are representative of cells from \geq 4 fields of view.



Figure S3. Super-resolution imaging of immunolabelled MTs in fixed COS-7 cells treated with Taxol or Nocodazole. dSTORM images indicate expected stimulation of microtubule filament assembly by Taxol and disassembly by Nocodazole (resulting in loss of networks except for MT-organizing centres). Scale bars = 10 μ m (top) and 3 μ m (bottom).



Figure S4. Live cell CLSM images of HeLa cells expressing GFP-fused P3 of the indicated lyssaviruses, following treatment with or without Taxol. Images are representative of cells from \geq 5 fields of view (except GFP, 3 fields of view).



Figure S5. CLSM images of COS-7 cells expressing the indicated GFP-fused lyssavirus P3 proteins. Cells were fixed and immunostained for b-tubulin following treatment without (left panel) or with Taxol (centre panel) or Nocodazole (right panel). Images are representative of cells from \geq 3 fields of view.



Figure S6. Western blot analysis of lysates of COS-7 cells using the indicated antibodies. Irrelevant intervening lanes have been removed.



Figure S7. Amino acid alignment of lyssavirus P3. (A) Protein sequence comparisons of lyssavirus P3 proteins used in this study using Clustal Omega (EMBL-EBI). Regions of P3 protein shown to be important to its functions are indicated, including the N-NLS (localised to the NTR, normal text), S-AD (pink), MTAS (undefined sequence localised within the CTD, underlined text), STAT1-binding (red), S₂₁₀ phosphorylation site (yellow), C-NLS (blue) and C-NES (green). Splice site for Ni/MOKV chimeric P3 proteins are labelled by an arrow. Residue numbers correspond to the full length P1 protein of RABV (CVS/Ni). (B) Percent similarity of indicated lyssavirus full-length P proteins (P1) compared to that of Ni.