

Salmonid Double-stranded RNA–Dependent Protein Kinase Activates Apoptosis and Inhibits Protein Synthesis

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Abstract (250 words)

 The dsRNA-dependent protein kinase (PKR) is a key factor of innate immunity. It is involved in translation inhibition, apoptosis and enhancement of the proinflammatory and interferon responses. However, how these antiviral functions are conserved during evolution remains largely unknown. Overexpression and knockout studies in a Chinook salmon (*Oncorhynchus tshawytscha*) cell line were conducted to assess the role of salmonid PKR in the antiviral response. Three distinct mRNA isoforms from a unique *pkr* gene, named *pkr-fl* (full length), *pkr-ml* (medium length) and *pkr-sl* (short 25 length), were cloned and a *pkr^{-/-}* clonal fish cell line was developed using CRISPR/Cas9 genome editing. PKR-FL includes an N-terminal dsRNA-binding domain and a C-terminal kinase domain, while PKR-ML and PKR-SL display a truncated or absent kinase domain, respectively. PKR-FL is induced during IFNA2 stimulation but not during viral hemorrhagic septicemia virus (VHSV) infection. Overexpression experiments showed that only PKR-FL possesses antiviral functions including activation of apoptosis and inhibition of *de novo* protein synthesis. Knockout experiments confirmed that PKR is involved in apoptosis activation during late stage of VHSV infection. Endogenous PKR also plays a critical role in translation inhibition upon poly(I:C) transfection after IFNA2 treatment. It is, however, not involved in translational arrest during VHSV infection. Extra- and intracellular titrations showed that endogenous PKR does not directly inhibit viral replication but apparently favors virion release into the supernatant, likely by triggering late apoptosis. Altogether, our data confirm that salmonid PKR has conserved molecular functions, that VHSV appears to bypass with subversion strategies.

Key points (85 characters including spaces/sentence)

- Three isoforms of Chinook salmon PKR are present in CHSE-EC cells
- Full-length PKR triggers apoptosis and inhibits *de novo* protein synthesis
- Endogenous PKR is not involved in translational arrest during VHSV infection
- Endogenous PKR favors virion release into the supernatant at a late infection stage

 Keywords: PKR, EIF2AK2, Chinook salmon, *Oncorhynchus tshawytscha,* interferon response, apoptosis, translational arrest, antiviral activity

Introduction

 The host innate immunity is the first line of defense against viral infections. Rapid and efficient detection of viruses is critical to mount an immune response capable of limiting virus replication and propagation to neighboring cells. It is well established that pathogen-associated molecular patterns (PAMPs) are recognized by sensors called pattern recognition receptors (PRRs). Activation of PRRs triggers signaling cascades, which subsequently leads to the production of host defense molecules, including type I interferons (IFNs), proinflammatory cytokines and chemokines. Type I IFNs induce the transcription of hundreds of IFN-stimulated genes (*ISGs*), including effector genes, which can have direct antiviral actions or modulate cell physiology to inhibit viral infection, replication and 54 propagation $¹$.</sup>

 Eukaryotic translation initiation factor 2 alpha kinase 2 (EIF2AK2), better known as dsRNA- dependent protein kinase (PKR), is one of the most studied proteins encoded by an *ISG*. It is recognized as a multifunctional key factor of innate immunity, as it acts both as a sensor and an effector in response to viral infections. Mammalian PKR is constitutively and ubiquitously expressed at low levels in all tissues and as all *ISG* products, its expression is induced by a variety of stress 60 associated responses, including type I IFNs, LPS stimulation and viral infections $2,3$. Structurally, PKR contains an N-terminal regulatory region with two dsRNA-binding motifs (dsRBMs) and a C-62 terminal kinase domain 2.4 . PKR requires an activation step to be fully catalytically functional 5.6 . This activation is primarily mediated by binding to dsRNA, which is produced during the replication cycle 64 of RNA viruses ⁶. Interactions with dsRNA occur through its dsRBMs, leading to homodimer 65 formation mediated by the N-terminal lobe of the kinase domain 4.7 . PKR dimerization induces conformational changes that allow the *trans* autophosphorylation of the activation loop at critical 67 conserved threonine residues ⁷. Once activated, PKR phosphorylates the α -subunit of the eIF2 68 complex, which is required for the initiation of mRNA translation. Phosphorylation of eIF2 α blocks the recycling of inactive eIF2-GDP complex by the GTP exchange factor eIF2B, resulting in the 70 inhibition of the cell translation machinery .

 Although PKR is best described for its effect on protein translation, it is also involved in many other antiviral mechanisms. Overexpression of mammalian PKR is known for promoting apoptosis in 73 transfected cells via both the intrinsic mitochondrial and extrinsic death receptor pathways $9-12$ while 74 *Pkr^{-/-}* mouse embryonic fibroblasts (MEFs) or *PKR^{-/-}* Hela cells displayed resistance to apoptosis in 75 response to dsRNA, TNF- α , or LPS 13,14 . The molecular mechanisms underlying PKR-mediated 76 apoptosis involve eIF2 α phosphorylation-dependent induction of specific stress response genes $14-18$

77 and activation of transcription factors NF- κ B and p53^{19–21}. PKR was also reported to modulate the inflammatory and the type I IFN responses, by activating mitogen-activated protein kinases (MAPKs)-dependent^{22–24} and NF- κ B signaling pathways^{20,25} and enhancing type I IFN production 80 upon infection with some but not all viruses $21,26-29$. In most cases, the precise role of PKR in the activation of these different pathways remains elusive and whether PKR acts directly or indirectly has not been fully clarified. The importance of PKR role in the antiviral response is further emphasized by the numerous subversion strategies developed by viruses to antagonize PKR-mediated 84 antiviral mechanisms, as recently reviewed by Cesaro and Michiels .

 Orthologs of mammalian *PKR* have been found in fish genomes, in cartilaginous fish as well as bony fish 31 . Some teleost fish families, including cyprinids, salmonids and clupeids, also possess a fish-87 specific paralog of *pkr*, called *pkz*, which encodes a Z-DNA-dependent protein kinase ³². *pkz* genes 88 in fish were isolated before fish *pkr* genes, in Crucian carp 33 , zebrafish 34 and Atlantic salmon 35 , among other species. Although most studies on fish PKR did not dissect the structure-function relationship as extensively as in mammals, they indicate that most antiviral functions attributed to mammalian PKR are overall conserved in these organisms. Briefly, a few studies have reported that Fish PKR (and PKZ) are able to phosphorylate eIF2 α and inhibit *de novo* protein synthesis ^{36–40}, trigger 93 apoptosis $38,41,42$, modulate the NF- κ B signaling pathway $36,43$ and the production of type I IFN $44,45$, although the molecular mechanisms have not been investigated. Of note, in fish, most studies were performed using overexpression approaches, which generally lead to unnaturally high levels of the protein of interest. A few other studies have also used knock-down approaches based on morpholino 97 oligonucleotides , short interfering RNAs 40 or chemical inhibition $44,47$ but to the best of our knowledge, no knockout *in cellulo* fish models have been developed so far.

 In this study, we identified and cloned three different isoforms of *pkr* in a salmonid cell line from Chinook salmon (*Oncorhynchus tshawytscha*). To investigate their respective antiviral functions, we used both overexpression and knockout approaches. For this purpose, we developed the first *pkr* knockout clonal fish cell line using CRISPR/Cas9 genome editing. We showed that PKR is involved in apoptosis activation and plays a major role in translational arrest upon poly(I:C) stimulation but not during VHSV infection. Our data further suggest that PKR favors the release of VHSV virions into the supernatant at a late infectious stage, likely by triggering apoptosis. Taken together, our results indicate that salmonid PKR exhibits conserved molecular functions but the endogenous protein does not have a major antiviral effect against VHSV, likely due to evasion strategies evolved 108 by the virus.

Material and methods

1. Cell lines, culture conditions and viruses

 The *Epithelioma papulosum cyprinid* (EPC) cell line was grown in Leibovitz's L-15 medium (Gibco) supplemented with 10% fetal bovine serum (FBS, Eurobio) and penicillin (100 U/mL)-streptomycin (100 μg/mL) (P/S) (BioValley). The Chinook salmon (*Oncorhynchus tshawytscha)* embryo (CHSE- 214) cell line was maintained in Glasgow's modified Eagle's medium (GMEM) containing 25 mM HEPES (Biosera) supplemented with 10% FBS, 2 mM L-glutamine (Eurobio), and penicillin (100 U/mL)-streptomycin (100 μg/mL). The CHSE-EC cell line, that was previously genetically 117 modified to stably express a monomeric enhanced green fluorescence protein (mEGFP)⁴⁸, as well as 118 its derivatives were grown in L-15 medium supplemented with 10% FBS, penicillin (100 U/mL)- streptomycin (100 μg/mL), 500 μg/mL G418 (Invivogen), 30 μg/mL hygromycin B Gold 120 (Invivogen). All cell lines were maintained at 20° C without CO₂.

 Recombinant viral hemorrhagic septicemia virus expressing tomato red fluorescent protein (rVHSV- Tomato) was a kind gift from Dr. Stéphane Biacchesi (Université Paris-Saclay, INRAE, UVSQ, VIM, 123 Jouy-en-Josas, France)⁴⁹. rVHSV-Tomato was propagated in EPC cells (multiplicity of infection (MOI) of 1): briefly, the virus was adsorbed onto the cells for 1h at 14°C with regular gentle shaking; L-15+2% heat-inactivated FBS was added afterwards and the supernatants were collected at 5 days post-infection, 0.2 µm-filtered, aliquoted and stored at -80°C. Golden shiner virus (GSV) was propagated in CHSE-214 (MOI 1.5) at 22°C in GMEM+2% FBS, as described above for rVHSV- Tomato. At 10 days post-infection, the remaining cells were scraped and the cell suspension was bath- sonicated (4 x 1 min at ~40 kHz) (EMAG AG), clarified at 400 g for 5 min, 0.2 µm-filtered, aliquoted and stored at -80°C. rVHSV-Tomato and GSV titers were determined by plaque assay (as described in section 11).

2. Development and validation of a *pkr^{-/-}* **cell line**

 The previously established CHSE-EC cell line (hereafter referred to as EC) was used to develop a 134 pkr^{-/-} cell line. Four single guide RNAs (sgRNAs) were designed within the first and second coding 135 exons of the *pkr* gene (LOC112253229, LG24), using CRISPOR v5.01 web tool (Table I)⁵⁰. To ensure the specificity of the sgRNAs, care was taken that no off-target genes with more than 3 mismatches in the first 12 bp adjacent to the PAM (most likely off-targets) were identified in the Chinook salmon genome (Otsh_v2.0, NCBI RefSeq assembly GCF_018296145.1). A sgRNA targeting the *mEGFP* gene was also used as previously designed ⁴⁸.

 The sgRNAs were synthesized using the T7 RiboMAX™ Express Large Scale RNA Production System kit (Promega) using 0.5 µg of each primer, incubated with 1µL of RQ1 DNase (Promega) for 1h at 37°C and purified using TRIzol™ reagent (Invitrogen), according the manufacturers' instructions. The sgRNAs were resuspended in RNase- and DNase-free water and quantified using a Nanodrop spectrophotometer. The purity of the sgRNAs was checked on a 2% agarose-EtBr gel before or after a 30 min treatment with RNase A (Qiagen) at room temperature. Each sgRNA was 146 mixed with recombinant TrueCut™ Cas9 Protein v2 (Invitrogen) at a 1:1 molar ratio (0.2 µg sgRNA 147 and 1 µg rCas9 ie. 6.1 pmol each in 2 µL) and incubated at room temperature for 20 min. The sgRNA- mEGFP/Cas9 complex was mixed with each sgRNA-PKR/Cas9 complex at 1:1 volume ratio in resuspension buffer R (Neon™ Transfection System kit, Invitrogen) (1 µL of each complex in a final 150 volume of 5 μ L). The mix was transfected into EC cells using the NeonTM Transfection System (Invitrogen): EC cells were prepared as described in section 4 and 5 μ L of cell suspension at 2 x 10⁷ 152 cells/mL was mixed with 5 μ L of sgRNA/Cas9 complex (ie. 1 x 10⁵ cells, 6.1 pmol of Cas9 and 6.1 pmol of sgRNA per 10 µL of transfection reaction). The cells were transfected using the same 154 conditions established for plasmids, as described in section 4. All transfected cells $({\sim}5 \times 10^5 \text{ cells})$ 155 were mixed in 5 mL L-15+10%FBS+P/S in a 25 cm² flask (Sarstedt) and incubated at 20 $^{\circ}$ C for 3-4 weeks.

157 Once the cell population reached confluency, the transfected cells were passaged (surface ratio 1:4), 158 and \sim 2 x 10⁶ cells were used for genomic DNA extraction using NucleoSpin Tissue Mini kit (Macherey-Nagel), according to the manufacturer's instructions. Genomic DNA segments containing the targeted sites were amplified by PCR using GoTaq® G2 Flexi DNA Polymerase (Promega) using the following genotyping primers: PKR-gen1-F/PKR-gen1-R and PKR-gen2-F/PKR-gen2-R for *pkr* coding exon 1 and exon 2, respectively [\(Table I](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6612602/table/tI/)). The PCR cycling program was performed in a thermal cycler (Eppendorf) and was as follows: 94°C for 3 min then 35 cycles of 94°C for 15 s, 58°C 164 for 15 sec, 72°C for 40 sec, and a final extension of 72°C for 5 min. The PCR products were purified using NucleoSpin Gel and PCR Clean-up Mini kit (Macherey-Nagel) and directly sequenced using the same amplification primers (Sanger sequencing service, Eurofins) (Table I). Sequences were 167 analyzed using Synthego ICE analysis tool v3 (Synthego)⁵¹ to assess the percentage of mutated cells in the transfected cell populations (bulks). sgRNA-PKR2-4 failed to show any genome editing at the targeted sites so only the bulks transfected with sgRNA-PKR1 were further used for clonal isolation.

 Cells from two independent cell populations transfected with sgRNA-PKR1 were either manually 171 isolated or sorted by FACS, respectively. For manual isolation, \sim 1 x 10⁵ cells were seeded in a 6-well plate and serially diluted (6-fold dilutions) in duplicates. Three to four weeks post-seeding, clonal

 cell patches were marked, analyzed under a fluorescent Axio Observer Z1 microscope (Zeiss, Oberkochen, Germany) and ~50 mEGFP-deficient clones were selected, detached mechanically by scraping with a pipette tip and sub-cultured into 48-well plates. After 3-4 weeks, 22 clones were sub-176 cultured and propagated in 25 cm² flasks and their genotype was characterized as described above. For FACS-sorted clones, cells were detached by trypsin-EDTA action and mEGFP-deficient single 178 cells at a density of ~4 x 10⁶ cells/mL were individualized by a BD FACSAriaTM Fusion Flow Cytometer (Institut Pasteur, Paris, France) using a 100 µm nozzle into a 96-well plate (Sarstedt) in L- 15 supplemented with 10% FBS, penicillin (200 U/mL)-streptomycin (200 μg/mL), 500 μg/mL G418 and 30 μg/mL hygromycin B Gold. Seven weeks later, 5 clones were sub-cultured and propagated in 25 cm² flasks and their genotype was characterized as described above.

 Two manually isolated clones, EC-PKR-C19 and EC-PKR-C28, presenting a 1-nt insertion (29_30insT resulting in V11fsX22, KO) and a 6-nt deletion (30_35delGTGCGA, resulting in C11_E12del, WT-like) at the sgRNA targeted site respectively, and two FACS-sorted clones, EC- PKR-C3 and EC-PKR-C5, presenting the same 1-nt insertion (29_30insT resulting in V11fsX22, KO) at the targeted site, were kept for knock-out validation by western blot. For this purpose, these clones 188 and the WT EC cell line were seeded into 6-well plates at a density of 1.2 x 10^6 cells/well in L- 15+2%FBS+P/S. The next day, cells were stimulated in triplicates with *Salmo salar* IFNA2 supernatant (produced as described in section 5) diluted to 1:10 in L-15+2%FBS+P/S or left untreated and incubated at 20°C. At 72h post-stimulation, medium was removed, cells were washed once with ice-cold DPBS, scraped in 1 mL ice-cold DPBS supplemented with 2.5 mM EDTA and centrifuged at 1500 g at 4°C for 5 min. The cell pellets were drained, resuspended in 100 µL NP-40 lysis buffer (50 mM Tris-HCl pH 7.4, 150 mM NaCl, 2 mM EDTA, 0.5% NP40, 1 mM DTT, 10% glycerol, cOmplete™ protease inhibitor (Merck), PhosSTOP™ phosphatase inhibitor (Merck)) and lysed for 45 min at 4°C under gentle shaking. The cell lysates were clarified by centrifugation at 5000 g at 4°C for 5 min and stored at -80°C until use for western blot analysis as described in section 7.

3. Plasmid constructions

 Chinook salmon *pkr* open reading frame (ORF) sequences were identified *in silico* using NCBI Reference Otsh_v2.0 Primary Assembly and predicted transcripts XM_042305680.1 and $\text{KM}_{042305681.1}$. Total RNA from 1.5 x 10^6 EC cells infected with rVHSV-Tomato (MOI 1) at 48 and 72hpi in triplicates was extracted using the QiaShredder and RNeasy mini kits(Qiagen) according to the manufacturer's instructions. RNA (1 µg) was used as template for reverse transcription and generation of cDNA using the QuantiTect Reverse Transcription kit (Qiagen) with random primers.

 The cDNA was diluted two-fold with RNase-free water and used as template to amplify the *pkr* ORF sequence. Nested PCR amplifications were performed using Q5 2X High-Fidelity mastermix (New England Biolabs) and 2 sets of specific primers according to the manufacturer's instructions: OtPKR- R0-F/ OtPKR-R0-R and OtPKR-R0bis-F/OtPKR-R0bis-R were used for the first PCR round while OtPKR-P2A-F and OtPKR-HindIII-R were used for the second PCR round (Table I). The PCR cycling programs were performed in a thermal cycler (Eppendorf) and were as follows: 98°C for 30 211 sec followed by 35 cycles of 98°C for 15 s, 66°C (1st round) or 60°C (2nd round) for 15 sec, 72°C for 90 sec, and a final extension of 72°C for 2 min. PCR products were purified with the NucleoSpin Gel and PCR Clean-up Mini kit (Macherey-Nagel) and sent to sequencing. Purified PCR products were digested with HindIII enzymes (Thermofisher), cloned into HindIII/EcoRV-digested pcDNA3.1-Zeo- BFP vector using T4 DNA ligase (New England Biolabs) according to the manufacturer's instructions and fully sequenced. The pcDNA3.1-Zeo-BFP vector was initially obtained by subcloning the BFP 217 gene amplified from pCite-P-BFP 52 into a pcDNA3.1-(-)-Zeo backbone (Invitrogen) using BFP- F/BFP-R primers (Table I) followed by XhoI/HindIII digestion. The pCite-PBFP plasmid was a kind gift from Dr. Hortense Decool (Université Paris-Saclay, INRAE, UVSQ, VIM, France). All plasmids were produced in Stellar™ Competent Cells (Takara) and were purified using NucleoBond Xtra Maxi EF (Macherey-Nagel) according to the manufacturer's instructions.

4. Transfections

 Transfections were performed by electroporation using the Neon™ Transfection System (Invitrogen) 224 as described previously ⁴⁸. Briefly, the cells were washed in DPBS (Sigma-Aldrich), detached by trypsin-EDTA action, resuspended in L-15+10%FBS+P/S and centrifuged at 400 g for 5 min. The cell pellet was drained, resuspended in L-15 without Phenol Red (Gibco), centrifuged at 13 000g for 227 30 sec, and resuspended again in L-15 without Phenol Red. The cell concentration was adjusted to 2×10^7 cells/mL. Depending on the experiment, the cell suspension was mixed with various plasmid 229 constructs (Table II) to reach a final concentration of 0.5 μ g/1 x 10⁵ cells in 10 μ L of transfection reaction. A fluorescent vector (mEGFP or RFP-KDEL) was added to verify and/or normalize transfection efficiency between each condition.

 The cells were then transfected using the same conditions established for plasmids for CHSE-214 233 cells or EPC cells ⁵³. Briefly, transfections were carried out in an electroporator MPK5000 (NeonTM Transfection System, Invitrogen) using either a 10 μL or a 100 µL transfection kit (Neon™ Transfection System, Invitrogen) set to two pulses for 20 ms at 1300 V (CHSE-214 and derivatives) 236 or 1400 V (EPC). All transfected cells were mixed in L-15+10%FBS+P/S, split into flasks or plates

(depending on the experiment) and incubated at 20°C for a time determined for each experiment.

5. Production of Salmo salar IFNA2 supernatant

239 In order to produce IFNA2-containing supernatant, 44×10^6 EPC cells were transfected with 240 pcDNA3.1-Zeo-ssIFNA2 54 or pcDNA3.1-Zeo-mEGFP (control) using the conditions described in section 3. The transfected cells were pooled in 24 mL of $L15+10\%$ FBS+P/S, split into two 75 cm² flasks and incubated at 20°C. At 48h post-transfection, supernatants were collected and clarified by centrifugation 400 g, 5 min, 0.2 µm filtered, aliquoted and stored at -80°C until use. The RTG-P1 cell line (ATCC CRL-2829), which constitutively expresses the firefly luciferase gene under the promoter 245 of the IFN-induced mx_l gene ⁵⁵, was used to determine the IFN activity of the IFNA2 supernatants 246 produced. Briefly, 1:4 serial dilutions in L-15 of the harvested supernatants were applied onto 4.5 x 247 10⁴ RTG-P1 cells in 96-well plates in quadruplicates and cells were incubated at 20°C. At 30h post- stimulation, medium was removed and 75 µL of Steady-Glo® Luciferase Assay System (Promega) was added in each well and the cell lysates were processed as described in section 8.

6. Real-time quantitative PCR

251 EC (WT) cells were seeded in 6-well plates to a final density of 1.5 x 10^6 cells/well in L- 15+2%FBS+P/S. The next day, cells in triplicates or quadruplicates were infected with rVHSV- Tomato (MOI 1) at 14°C for 8 or 24h, stimulated with recombinant *Salmo salar* IFNA2 supernatant (produced as described in section 5) diluted to 1:10 in L-15+2%FBS+P/S for 72h or left untreated.

 Total RNA was extracted from cells in individual P6 wells in triplicates or quadruplicates using QiaShredder and RNeasy mini kits (Qiagen) in accordance with the manufacturer's instructions. Quality control of the samples was determined using a Nanodrop spectrophotometer. The cDNA was 258 generated from 1.5 µg of total RNA using the iScript™ Advanced cDNA Synthesis Kit for RT-qPCR (BioRad) and the synthesis was performed in a thermal cycler (Eppendorf) as recommended by the manufacturer. cDNA was diluted to 1:3 in DNase- and RNase-free water and stored at -20°C until use. "No RT" control reactions were made by omitting the reverse transcriptase. The cDNA was mixed with TB Green qPCR Premix Ex Taq (Tli RNaseH Plus) (Takara) along with forward and 263 reverse primers (Table III) at a final concentration of 210 nM each in Twin.tec[®] real-time PCR plates (Eppendorf). Amplification was performed using a CFX Connect cycler (BioRad) using the following cycling program: initial denaturation at 95°C for 30 sec followed by 40 cycles of 10 sec at 95°C and 30 sec at 60°C. For each biological replicate, mean Cq values of target genes were calculated based

267 on technical duplicate reactions and then normalized using the geometric mean of Cq values of 3 housekeeping genes (*otelf1α, otrps29, otgapdh3*). The relative expression of each target gene (*otpkr-fl*, *otpkr-ml*, *otpkr-fl* and *otmx123*) was expressed as 2^{−∆Cq}, which was then used to calculate their respective fold change in comparison to non-stimulated cells.

 For each set of primers, the efficiency was calculated by linear regression obtained by using ten-fold serial dilutions of plasmid containing the target sequence (target genes) or of a pool of cDNA (housekeeping genes) and the qPCR products were validated by gel migration and sequencing. For the primers targeting each PKR isoform, the specificity of each primer set was validated by checking their cross-reactivity using plasmid constructs developed in this study.

7. Immunoblotting

 Aliquots of 60 μL of cell lysates (obtained as described in sections 2 and 8) were mixed with 30 μL Laemmli buffer (45 mM Tris, 345 mM glycine, 38% glycerol, 4.8% SDS, 20% β-mercaptoethanol, 0.04% bromophenol blue) and incubated at 100°C for 5 min.

 A volume of 8 µL of cell lysates was loaded on 10% or 12% polyacrylamide gels and protein samples were separated by electrophoresis in Tris-glycine buffer (25 mM Tris, 192 mM glycine, pH 8,3). Proteins were then transferred onto a nitrocellulose membrane (BioRad) using the mixed molecular weight program from the Trans-Blot® Turbo™ Transfer System (BioRad). The blots were blocked either with 5% non-fat milk or 5% BSA in TBST (10 mM Tris pH 7.4, 150 mM NaCl, 0.1% Tween 285 20) for 1h at room temperature and then incubated with primary antibodies overnight at 4° C. The following primary antibodies were used with the dilution factors and buffers indicated in Table VI: rabbit anti-PKR antiserum, mouse monoclonal anti-GFP, rabbit polyclonal anti-eIF2α-P, mouse monoclonal anti-puromycin, mouse monoclonal anti-VHSV N, rabbit anti-GSV antiserum, rabbit anti-Mx123 antiserum. The custom-made anti-PKR antibody, initially raised again *Salmo salar* PKR $⁴⁷$, was a generous gift from Pr. Øystein Evensen (NMBU, Oslo, Norway). The anti-VHSV N</sup> antibody was a kind gift from Dr. Stéphane Biacchesi (Université Paris-Saclay, INRAE, UVSQ, VIM, 292 Jouy-en-Josas, France). The anti-Mx123 antibody, raised against rainbow trout Mx3 56 , was a generous gift from Dr. Marta Alonso-Hearn (Department of Animal Health, NEIKER-Basque Institute for Agricultural Research and Development, Basque Research and Technology Alliance, Derio, Spain) and Pr. Jorunn Jorgensen (UiT The Arctic University of Norway, Tromsø, Norway). The blots were washed 5 times in TBST, incubated with horseradish peroxidase (HRP)-conjugated anti-mouse or anti-rabbit (1:4000) secondary antibodies (SeraCare), washed 4 times in TBST and 298 once in PBS. Western blots were developed using ClarityTM Western ECL substrate (BioRad) and detected using ChemiDoc Touch Imaging System (BioRad). After the first detection, the membrane was washed twice with TBST, stripped for 15 min at 37°C using Restore™ Plus buffer (Thermo Scientific), washed twice in TBST, saturated with TBST-5% non-fat milk for 1h and re-probed with a new primary antibody for 2.5h-3h and developed as described above. The following primary antibodies were used for the second round of detection: mouse monoclonal anti-α-tubulin antibody, rabbit polyclonal anti-actin, mouse monoclonal anti-eIF2α (Table IV). Densitometric analysis of the blots was performed using Image Lab software (v 6.1.0, Biorad).

8. Assays for assessing translation inhibition activity of Chinook salmon PKR

 The translation inhibition activity of Chinook salmon PKR was assessed by luciferase assay and immunoblotting. Luciferase assay is a method commonly used for detecting protein synthesis 309 inhibition activity of PKR in mammalian models and other vertebrates $36-38,40,46,57,58$ and was adapted to quantify the translation inhibition activity of PKR isoforms. For this purpose, EC-PKR-C19 cells 311 were co-transfected with pcDNA3.1-Hyg-RFP-KDEL $(0.2 \mu g/10 \mu L)$, pcDNA3-Neo-Luc (0.25 µg/10 µL) and either pcDNA3.1-Zeo-BFP or pcDNA3.1-Zeo-BFP-P2A-PKR-FL/ML/SL 313 (0.25 μ g/10 μ L) or mock transfected, split into 96-well plates (~1 x 10⁴ cells/well in 16 wells per 314 condition) and incubated at 20°C. At 24h post-transfection, medium was removed, 100 µL DPBS was added into each well and RFP fluorescence was measured using a fluorometer (Tecan Infinite M200PRO) with excitation and emission wavelengths of 544 and 603 nm, respectively. Then, DPBS was removed, 75 µL of Steady-Glo® Luciferase Assay System (Promega) was added in each well and the cell lysates were incubated in the dark at room temperature for 5 min. Cell lysates were transferred into a flat-bottom white-walled plate (Greiner Bio-One) and luminescence was measured using a Tecan Infinite M200 Pro luminometer over an integration period of 1000 ms (Tecan, Männedorf, Switzerland). The luminescence value from each well was corrected by subtracting the mean values obtained from the wells containing medium (blank), normalized to the corrected fluorescence value from each well and graphed as fold change relative to the BFP transfected cells.

 In a similar fashion, the protein synthesis inhibition activity of PKR isoforms was assessed by western blot using mEGFP as a reporter system and puromycin as a marker of de novo protein synthesis. For 326 this purpose, EC-PKR-C19 cells were co-transfected with pcDNA3-Hyg-mEGFP $(0.2 \mu g/10 \mu L)$ and either pcDNA3.1-Zeo-BFP or pcDNA3.1-Zeo-BFP-P2A-PKR-FL/ML/SL (0.5 µg/10 µL) or mock 328 transfected, split into 6-well plates $(-1.5 \times 10^6 \text{ cells/well}$ in quadruplicates) and incubated at 20°C for 329 30h. In parallel, cells were either treated with cycloheximide (CHX, 50 µg/mL, Thermofisher) for

 24h or treated with thapsigargin (Tg, 2 µM, Merck) for 30 min. Both drugs are well-established 331 translation inhibitors were used as positive controls for translational inhibition $59,60$. At 30h post- transfection, cells were pulsed with 5 µg/mL puromycin (Gibco) diluted in growth medium for 15 min at 20°C. The cells were then processed as described in section 2, with a lysis step performed in 75 µL NP-40 lysis buffer, and cell lysates were stored at -80°C until use for western blot analysis as described in section 7.

 For knockout experiments, poly(I:C) treatment and virus infections were carried out. Poly(I:C) transfections and not simple incubation were performed, as CHSE-214 are known for not responding 338 to extracellular poly(I:C)⁶¹. Non-stimulated or IFN-pretreated EC, EC-PKR-C28 and EC-PKR-C19 were transfected with high molecular weight poly(I:C)-rhodamine (Invivogen) at a final 340 concentration of 0.15 µg per 1 x $10⁵$ cells per 10 µL of transfection reaction. Transfected cells were 341 split into 12-well plates $(\sim 3.3 \times 10^5 \text{ cells/well}$ in triplicates), incubated at 20 $^{\circ}$ C for 24h. For virus infections, EC, EC-PKR-C28 and EC-PKR-C19 were seeded in 6-well plates to a final density of 343 1.5x10⁶ cells/well in L-15+2%FBS+P/S. The next day, cells were infected in triplicates with rVHSV- Tomato or GSV at MOI 1 or left uninfected and incubated at 14°C or 22°C, respectively. At 24h post- transfection or 16, 24 and 40h post-infection, cells were pulsed with puromycin and processed as described above until use for western blot analysis.

9. Apoptosis assay

 Apoptosis was assessed by genomic DNA (gDNA) fragmentation and by measuring enzymatic activity of caspase 3/7, caspase 8 and caspase 9.

 For the gDNA fragmentation assay, EC-PKR-C19 cells were co-transfected with pcDNA3.1-Hyg- RFP-KDEL (2 µg/100 µL) and either pcDNA3.1-Zeo-BFP or pcDNA3.1-Zeo-BFP-P2A-PKR-352 FL/ML/SL (5 μ g/100 μ L). Around 4 x 10⁶ transfected cells were seeded in 25 cm² flasks incubated at 20°C. At 6hpt, growth medium was removed, cells were washed three times in PBS to eliminate dead cells and new growth medium was added into each flask. At 72 hpt, growth medium was collected, pooled with trypsinized cells and centrifuged at 400 g for 5 min. The cell pellets were drained and used for genomic DNA extraction using NucleoSpin Tissue Mini kit (Macherey-Nagel), according to the manufacturer's instructions. For each condition, 3 µg of gDNA was loaded onto a 1.5% agarose-EtBr gel for each condition.

 The enzymatic activity of caspase 3/7, caspase 8 and caspase 9 was measured by using the Caspase-Glo[®] $3/7$ assay kit (Promega), in accordance with the manufacturer's instructions. For overexpression

 experiments, EC-PKR-C19 cells were co-transfected with pcDNA3.1-Hyg-RFP-KDEL (0.2 µg/10 µL) and either pcDNA3.1-Zeo-BFP or pcDNA3.1-Zeo-BFP-P2A-PKR-FL/ML/SL (0.5 µg/10 µL) or mock transfected with water instead of plasmid. A volume of 75 µL of transfected 364 cells was seeded in 96-well plates (Sarstedt) to a final density of $1x10⁵$ cells/well and incubated at 20°C. In parallel, EC-PKR-C19 cells were stimulated with staurosporine (STS, 1µM, Santa Cruz) or infected with GSV (MOI 1) and incubated at 22°C for 24h. At 72h post-transfection or 24h post-367 treatment (STS or GSV), 75 µL of either Caspase-Glo[®] 3/7, Caspase-Glo[®] 8 or Caspase-Glo[®] 9 reagent was added to each well (8 and 4 technical replicates per condition for transfection and treatment conditions, respectively). The plates were gently shaken on a plate shaker for 30 sec and incubated in the dark at room temperature for 30 min. The luminescence levels in the cell lysates were measured as described above in section 8. For knockout experiments, EC, EC-PKR-C28, EC- PKR-C19, EC-PKR-C3 and EC-PKR-C5 cells were seeded in 96-well plates to a final density of 5 x 10^4 cells/well in L-15+2%FBS+P/S. The next day, the growth medium was removed and the cells were infected in quadruplicates with 75 µL of rVHSV-Tomato suspension at MOI 10, MOI 1 or MOI 0.1 or left uninfected and incubated at 14°C. At 24, 48 and 72 hpi, cells were lysed with 50 µL of 376 Caspase Glo[®] 3/7 reagent and the same protocol described above was applied for luminescence measurement.

10. rVHSV-Tomato fluorescence monitoring

 The replication of rVHSV-Tomato in cells expressing PKR isoforms or in knockout cell lines was monitored by sequential fluorescence measurement. For overexpression experiments, EC-PKR-C19 381 cells were co-transfected with pcDNA3.1-Pur-mEGFP (0.2 µg/10 µL) and either pcDNA3.1-Zeo- BFP or pcDNA3.1-Zeo-BFP-P2A-PKR-FL/ML/SL (0.5 µg/10 µL) or mock transfected and split in quadruplicates in 96-well plates and incubated at 20°C for 24h. For knockout experiments, EC, EC- PKR-C28, EC-PKR-C19, EC-PKR-C3 and EC-PKR-C5 cells were seeded in 96-well plates to a final 385 density of $5x10^4$ cells/well in L-15+2%FBS+P/S. The next day, the medium was removed and cells were infected in quadruplicates (overexpression experiment) or octuplicates (KO experiment) with rVHSV-Tomato at MOI 0.1, 1 or 10 in L-15 without Phenol Red (Gibco)+2%FBS+P/Sor left uninfected. At 24, 32, 48, 56, 72, 80 and 96h post-infection, the tomato red fluorescence was measured using a fluorometer (Tecan Infinite M200PRO) with excitation and emission wavelengths of 548 and 593 nm, respectively. The fluorescence values were corrected by subtracting the mean values obtained from the non-infected wells.

11. Virus titration in extracellular supernatants and intracellular sonicates

EC, EC-PKR-C28, EC-PKR-C19 cells were seeded in 25 cm² flasks to a final density of $4x10^6$ cells/flask in L-15+2%FBS+P/S. The next day, cells were infected in quadruplicates with rVHSV- Tomato at MOI 1 incubated at 14°C. At 96 h post-infection, the supernatants (4 mL) were collected and kept on ice. The remaining cells were washed 3 times in cold DPBS, scrapped in 2 mL of new growth medium and bath-sonicated (4 x 1 min~40 kHz) (EMAG AG). Supernatants and sonicates were clarified by centrifugation at 400 g for 5 min and virus titers were determined by plaque assay on EPC cells under a carboxymethylcellulose overlay (0.75% in MEM (Eurobio) supplemented with 400 25 mM HEPES, 2 mM L-glutamine, 350 mg/L NaHCO₃, 2.5% FBS and P/S. At 3 to 4 dpi, cell monolayers were fixed with 3.7% formol for 1h at room temperature, stained with 0.5% crystal violet and plaque forming units (PFU) were counted.

12. Statistical analysis

 Results shown in each figure were derived from at least two independent experiments; the data 405 presented are means \pm standard deviation (SD). Statistical tests used are indicated in the legend of each. All statistical analyses were performed using GraphPad Prism software version 9.5.1.

Results

Diversity of pkr mRNA isoforms in salmonid EC cells

 In addition to the two rounds of whole genome duplication (WGD) events that occurred during the early evolution of chordates and vertebrates, the genomes of salmonid fish have undergone two supplementary WGD rounds, including a teleost-specific third WGD that dates back to 225-333 413 million years ago and a salmonid-specific WGD ~80-100 million years ago $62-64$. As a consequence, for each single-copy gene in tetrapods, up to four copies can be found in distinct loci in salmonids, if all have been retained. In reality, following WGD events, duplicated genes can either be lost, 416 pseudogenized, sub- or neo-functionalized, with frequent additional tandem duplication events ⁶⁵. In 417 mammals and birds, the *pkr* gene is typically unique ^{31,32}. In contrast, two or three *pkr* paralogs have been reported in amphibians (e.g. *Xenopus laevis* and *X. tropicalis*) ³² . Similarly, several fish genomes also comprise two or more *pkr* paralogs and several ancient paralogs including *pkz* (Ensembl release 110). In salmonids, tBlastn analysis revealed a unique *pkr* gene in species belonging to genus *Salmo* and *Oncorhynchus*. In the genome of Chinook salmon (*Oncorhynchus tshawytscha*), the *pkr* gene was found at the locus LOC112253229 on LG24. The sequences of predicted isoforms 423 XP_042161614.1 and XP_042161615.1, which result from alternative splicing, contain 729 and 728 amino acids, and share 34.5%, 33.6% and 35.2% identity with human PKR (NP_001129123.1), 425 chicken PKR (NP_989818.3) and amphibian PKR (NP_001091256.1), respectively.

426 We first analyzed the diversity of *pkr* mRNAs in CHSE-EC cells (hereafter referred to as EC) ⁴⁸. Amplification of the full-length CDS using cDNA of rVHSV-Tomato-infected EC cells resulted in 3 distinct products of 2187 bp 1122 bp and 464 bp, respectively (Figure 1A, Table V). In the following paragraphs, these three products will be referred to as *pkr-fl* (full length), *pkr-ml* (medium length) and *pkr-sl* (short length). The *pkr-fl* product matched the predicted *pkr*transcript (XM_042305681.1) with 99.95% identity. It spans 19 exons, which corresponds to NCBI's predicted model, and encodes a 728 aa polypeptide matching the predicted PKR protein (XP_042161615.1) with 99.86% identity. In contrast, the two shorter 1122 pb (*pkr-ml*) and 464 pb (*pkr-sl*) products covered 51% and 21% of the sequence, respectively, and comprise 9 exons and 6 exons only. Of note, missing exons from *pkr-ml* were also absent in *pkr-sl* and were all located in the middle part of the ORF. *pkr-ml* and *pkr-sl* are likely products of alternative splicing and encode polypeptides of 373 aa and 107 aa, respectively.

437 Using SMART (Simple Modular Architecture Research Tool)^{66,67} and InterProScan database, three double-stranded RNA binding motifs (dsRBM1-3) and a kinase domain were identified in the N-

terminal and C-terminal domains of PKR-FL, respectively (Figure 1C). This organization of

 functional domains is generally shared by PKR of other vertebrates. Indeed, although only two dsRBMs are found in mammalian and amphibian PKR, the numbers of dsRBMs present in fish PKR 442 actually varies from one to three ³². Importantly, PKR-ML only contains one complete dsRBM and the N-terminal portion of a second dsRBM fused to a truncated kinase domain, while PKR-SL only comprises one dsRBM and no kinase domain.

 Several important structural features known in mammalian PKR are conserved in Chinook salmon PKR. The dsRBM(s) of all PKR isoforms are highly conserved, as shown by the alignment with 447 human PKR dsRBMs and consensus motif reported by Masliah et al. ⁶⁸. In particular, the three motifs 448 of PKR-FL contain most of the residues involved in the canonical $\alpha_1 - \beta_1 - \beta_2 - \beta_3 - \alpha_2$ fold and/or dsRNA binding (Figure 1D). In addition, dsRBM1 matches dsRBM consensus more closely than dsRBM2 450 and dsRBM3, as also observed for dsRBM1 and dsRBM2 in human PKR ⁶⁹.

 The primary structure of PKR-FL kinase domain contains the 11 conserved kinase subdomains 452 described by Hanks et al. 70 , as mammalian PKR and other protein kinases (Figure 1E). In particular, ATP binding motifs can be found, including the canonical Gly-X-Gly-X-X-Gly in subdomain I, Asp- Leu-Lys-Pro-Ser-Asn in subdomain VI and Asp-Phe-Gln in subdomain VII, which are predicted to 455 interact with ATP through Mg^{2+} salt bridges ². Subdomain II contains at position 461 the invariant 456 lysine residue that is directly involved in the transfer of the phosphate from ATP to its substrate . 457 Equivalents of the two threonine residues Thr446 Thr451 in human PKR 71 , which are key autophosphorylation sites involved in PKR activation, namely, are also present in the so-called activation loop of PKR-FL (Thr616 and Thr621). Finally, PKR-FL also contains features specific to eIF2α kinases, including an acidic kinase insert, that spans subdomain V and continues in the inter-461 region between subdomains V and VI, and a conserved eIF2 α kinase motif located a few amino acids 462 away from the kinase insert, that is required for PKR kinase activity $32,57$. On the other hand, PKR- ML is missing the first 78 amino acids of a full-length kinase domain, which comprise domains I to V. The invariant lysine residue of subdomain II is also absent from PKR-ML kinase domain. This 465 residue is required for mammalian PKR kinase activity $71,72$. Therefore, the catalytic activity of PKR- ML is expected to be limited or absent. PKR-SL lacks the entire kinase catalytic domain and is expected to be catalytically inactive.

PKR-FL is induced following IFN stimulation but not during VHSV or GSV infections

 The expression profiles of PKR isoforms in response to different stimuli were characterized by western blot and RT-qPCR on EC cells stimulated with recombinant *Salmo salar* IFNA2 or infected with two different viruses: viral hemorrhagic septicemia virus (VHSV), an enveloped negative-sense single-stranded RNA virus belonging to the genus *novirhabdovirus*, and golden shiner virus (GSV), a naked, double-stranded RNA virus belonging to the genus *aquareovirus*. A recombinant VHSV encoding the fluorescent protein tdTomato, rVHSV-Tomato, was used to facilitate the monitoring of 475 the infection before each sampling timepoint . For both viruses, CPE appearance was also visually checked and the progression of the infection was verified by western blot using specific antibodies (data not shown).

 At the protein level, PKR-FL was constitutively expressed at low levels in non-treated EC cells and its expression was significantly induced in IFNA2-stimulated cells at the protein level from 48h post- stimulation (~1.7-fold increase) to 72h post-stimulation (~2.4-fold increase) (Figure 2A,B). However, no induction of PKR-FL was detected during viral infections with either rVHSV-Tomato or GSV at any of the time points examined (16-40h post-infection). These results correlate with *pkr-fl* expression at the transcript level: a strong induction of *pkr-fl* mRNA expression was observed after at 72h post- stimulation compared to non-stimulated cells (~31-fold increase) (Figure 2D) but no significant induction was detected in rVHSV-Tomato-infected cells at 8 or 24hpi. Remarkably, a similar response was observed with transcripts of *mx1/2/3*, which are well-known IFN stimulated genes both 487 in mammals and fish 73,74 . A ~5 log-fold increase in relative expression was observed upon IFNA2 stimulation, while no induction was detected in rVHSV-Tomato infected cells.

 Although recombinant PKR-ML was detected by western blot using the same polyclonal anti-PKR serum used to detect PKR-FL, endogenous PKR-ML could not be detected at the protein level in EC cells in response to IFNA2 stimulation or virus infection (Figure 2A). However, *pkr-ml* mRNA was amplified by RT-qPCR. Although its expression was lower than *pkr-fl* at the steady state (Figure 2C), it displayed a modest but significant induction at 24h post-infection with rVHSV-Tomato and upon IFNA2 stimulation (5-fold and 3.8-fold increase, respectively) (Figure 2D).

 Endogenous PKR-SL expression could not be assessed by western blot, as recombinant PKR-SL was not detected by our polyclonal anti-PKR antibody. RT-qPCR data revealed a very low expression of *pkr-sl* compared to *pkr-ml* or *pkr-fl* (Figure 2C) and no induction was observed upon rVHSV-Tomato infection or IFNA2 treatment.

 Overall, our observations show that PKR-FL expression is predominant at both transcript and protein levels and is strongly induced by type I IFN but not viral infection in EC cells. On the other hand, *pkr-ml* mRNA expression is slightly induced by both type I IFN and viral infection, contrary to *pkr-sl*, which is not induced in all contexts.

 CRISPR/Cas9-based edition of the pkr gene leads to null mutation and abolishes PKR expression in EC cells

 To further characterize Chinook salmon PKR function in the antiviral response, we disrupted the unique *pkr* gene in EC cells, using CRISPR/Cas9 technology. In the following study, four isolated clones were further characterized. Three of them, namely EC-PKR-C19; EC-PKR-C3 and EC-PKR- C5 presented a 1-nt insertion at the targeted cut site leading to a frameshift resulting in the introduction of a premature codon at position 22 (29_30insT resulting in V11fsX22) (Figure 3A). A fourth clone, EC-PKR-C28, exhibited a 6-nt deletion leading to the deletion of two amino acids, Cys11 and Glu12 (30_35delGTGCGA, resulting in C11_E12del). This clone was considered "WT- like" and it was used as an additional positive control for further experiments. As previous experiments showed that IFNA2 was a fast and potent inducer of PKR-FL in EC cells, the PKR expression status in each clone was validated by western blot using IFNA2 stimulated cells. Our results confirm that PKR-FL was strongly expressed in WT EC cells and WT-like EC-PKR-C28 cells 516 stimulated with IFNA2 for 72h, while no induction of PKR-FL was observed in $pkr^{-/-}$ EC-PKR-C19 517 and -C3 and -C5 clones (Figure 3B,C).

Chinook salmon PKR triggers apoptosis during viral infection

The functional role of mammalian PKR in apoptosis has been widely described in the literature ^{9,11,13} 520 and has also been reported in fish $38,39,41$. However, the contribution of PKR to apoptotic reaction during viral infection remains poorly defined especially in non-mammalian models. We therefore characterized the activation of the caspase cascade in EC cells by gain and loss-of-function experiments after viral infection. For this purpose, we performed a genomic DNA laddering test, which is a hallmark of apoptosis, and used a luminescence-based enzymatic assay to quantify the catalytic activity of specific caspases, including Caspase 3/7, Caspase 8 and Caspase 9. Caspase3/7 is an executioner caspase that is activated downstream of the caspase cascade upon apoptosis signaling. It can either be activated by (1) the extrinsic pathway via extracellular signals or (2) the intrinsic pathway aka. mitochondrial pathway upon intracellular signals and stresses. Caspase 8 is known for being activated by the extrinsic pathway while caspase 9 is mainly activated by the intrinsic 530 pathway 75 .

 Overexpression of PKR-FL induces apoptosis. To avoid inadvertent activation of endogenous PKR 532 in transfected cells, the ability of PKR isoforms to trigger apoptosis was assessed in *pkr^{-/-}* EC-PKR- C19 cells transfected with the corresponding expression plasmids. Cells stimulated with staurosporine 534 (STS), a well-known activator of apoptosis $76,77$ or infected with GSV, a lytic virus known for

 inducing apoptosis (unpublished data), were included as positive controls. Electrophoresis results show gDNA laddering in GSV-infected cells and, to a lesser extent, in STS-stimulated cells, suggesting that apoptosis was triggered by both treatments (Figure 4A, right panel). These qualitative results were confirmed by measuring caspase enzymatic activity: indeed, caspase3/7 was activated upon stimulation with STS or GSV (3.6-fold and 6.5-fold increase, respectively), thereby validating the assay (Figure 4B). For cells transfected with PKR-FL but not with PKR-ML and PKR-SL, a faint gDNA fragmentation was visible, suggesting the presence of apoptotic cells following overexpression of PKR-FL (Figure 4A, left panel). Similarly, transfection of PKR-FL but not PKR-ML or PKR-SL 543 triggered the activation of caspase3/7 in *pkr^{-/-}* EC-PKR-C19 cells, with a 2.6-fold increase of activity compared to BFP transfected cells (Figure 4B).

 To decipher if both extrinsic and intrinsic pathways are involved in PKR-FL-mediated Caspase3/7 activation, the activation of Caspase 8 and Caspase 9 was assessed after overexpression of PKR isoforms (Figure 4C,D). Our data show that both caspase 8 and caspase 9 were activated upon overexpression of PKR-FL but not with PKR-ML or PKR-SL, although caspase 8 activation was less pronounced (1.2-fold increase for caspase 8 compared to 1.6 fold-increase for caspase 9). Of note, caspase 9 but not caspase 8 was activated in EC cells treated with STS, which is known to primarily 551 trigger apoptosis *via* the intrinsic pathway 78,79 .

Loss of function experiment in *pkr-/-* **cells show that endogenous PKR triggers apoptosis during VHSV infection.** Although PKR-FL was not induced during rVHSV-Tomato infection (Figure 2A,B), constitutively expressed endogenous PKR could play a role in apoptosis activation during 555 viral infection. To test this hypothesis, WT EC cells, WT-like EC-PKR-C28 cells and *pkr^{-/-}* EC-PKR- C19, -C3 and -C5 clones were infected with rVHSV-Tomato at two different MOI (MOI 1 or MOI 0.1) and caspase3/7 activity was measured at 24h, 48h and 72h post-infection.

 Our results show that the caspase 3/7 activity observed in WT EC and WT-like EC-PKR-C28 was 559 almost fully abolished in all *pkr^{-/-}* clones starting from 48h post-infection at MOI 1 (Figure 5A). A similar but delayed response was observed at MOI 0.1, with a significantly higher caspase3/7 signal 561 in WT EC and WT-like EC-PKR-C28 cells compared to *pkr^{-/-}* clones that occurred at 72h post- infection (Figure 5B). Interestingly, caspase 3/7 signal was significantly lower in WT-like EC-PKR- C28 compared to WT EC cells at 48h post-infection at MOI 1 (Figure 5A) and this difference was even more marked at MOI 10 (data not shown). Two hypotheses can explain this discrepancy: (1) the 6-nt deletion resulting in a 2-aa deletion (Cys11 and Glu12) might alter PKR ability to induce apoptosis; (2) as shown in Figure 3C, PKR-FL is slightly but significantly less induced in WT-like

- EC-PKR-C28 upon IFNA2, suggesting that endogenous PKR-FL expression level is somewhat lower
- in this clone for a reason independent from the 2-aa deletion (clonal effect) and as a consequence,
- apoptosis might be slightly less activated. The fact that PKR-FL-C11_E12del isolated from EC-PKR-
- C28 exhibits a similar translation inhibition activity that WT PKR-FL supports the second hypothesis
- (Figure S2).
- Our data illustrate that PKR-FL induces apoptosis *via* the caspase 8 and caspase 9 pathways and that it plays a key role in the activation of apoptosis during rVHSV-Tomato infection.

Chinook salmon PKR is involved in host translational arrest

- PKR is also known for its role in host translation inhibition in virus infected cells *via* phosphorylation of eIF2α. The role of PKR in protein synthesis inhibition in EC cells was investigated by western blot using two different approaches: overexpression of PKR isoforms and activation of endogenous PKR 578 with poly $(I:C)$.
- **Overexpression of PKR-FL induces a cellular shutoff of host protein translation.** To examine 580 the role of Chinook salmon PKR isoforms on host protein translation, *pkr^{-/-}* EC-PKR-C19 cells were co-transfected with expression vectors encoding PKR isoforms and with a plasmid featuring a reporter gene encoding either mEGFP or firefly luciferase. Protein synthesis was assessed by quantification of mEGFP expression by western blot or by luciferase luminescence assay, 584 respectively. Importantly, in contrast to WT EC cells, *pkr^{-/-}* EC-PKR-C19 cells do not constitutively express mEGFP, as the disruption of the transgene is our screening criterion for successful gene edition (see Material and Methods, data not shown). Therefore, the GFP signal only corresponds to the mEGFP encoded by the transiently transfected plasmid. Co-transfections with plasmids encoding PKR-FL but not PKR-ML or PKR-SL resulted in a drastic reduction of GFP signal intensity (Figure 6A,B). Similar results were obtained with luciferase as a reporter gene (Figure 6D). A similar assay was performed to compare luciferase activity upon transfection with WT PKR-FL and mutated PKR- FL-C11_E12del isolated from WT-like EC-PKR-C28 (Figure S2). Our results showed that co- transfection with PKR-FL-C11_E12del expression plasmid resulted in a severe decrease in luciferase activity, as WT PKR-FL overexpression, indicating that they exhibit similar translation inhibition. These observations further suggest that the loss of Cys11 and Glu12 in WT-like EC-PKR-C28 does not affect drastically the protein functions.
- Since these assays only assess the expression of exogenous reporter genes and not on endogenous cellular proteins, we also evaluated the impact of each PKR isoform on the translation of endogenous

 proteins. For this purpose, transfected cells were pulsed with puromycin, an aminonucleoside which is incorporated into nascent peptides, leading to premature chain termination and spontaneous 600 dissociation from the ribosome $80,81$. Puromycylated nascent chains can be detected by western blot 601 using anti-puromycin antibodies. Puromycin can therefore replace radioactive tracers such as S^{35} 602 methionine and be used as a metabolic probe to measure *de novo* protein synthesis ⁸⁰. Cycloheximide and thapsigargin were used are positive controls, since these drugs are well-established translation inhibitors ^{59,60}. Consistent with reporter gene experiments, western blot analysis showed that the levels of puromycin incorporated into newly synthetized proteins decreased significantly with PKR- FL but not with PKR-ML or PKR-SL overexpression (Figure 6A,C). These results suggest that PKR-FL overexpression is able to inhibit host protein translation in the absence of any PKR activator.

Translation shutoff induced by type I IFN and $poly(I:C)$ **is abolished in** $pkr^{-/-}$ **cells.** In order to confirm the role of endogenous PKR in host translation inhibition, we compared the response of WT 610 and WT-like cells (EC and EC-PKR-C28, respectively) and *pkr*^{-/-} EC-PKR-C19 cells upon 611 transfection with poly(I:C), a synthetic analog of dsRNA. Poly(I:C) was used as a viral dsRNA mimic to activate PKR, while simultaneously avoiding the potential viral subversion mechanisms that can occur during viral infections. Before transfection, all cells were either pretreated with IFNA2 for 48h in order to induce PKR expression or left untreated. Western blot analysis showed no differences in puromycin signal intensity after poly(I:C) transfection between non-pretreated cell lines (Figure 7A,B, left panel). In contrast, when cells were pretreated with IFNA2, the levels of puromycin incorporated into newly synthetized proteins significantly decreased upon poly(I:C) transfection in 618 WT EC and WT-like EC-PKR-C28 cells (37% and 48% reduction, respectively) but not in *pkr*^{-/-} EC- PKR-C19 cells (Figure 7A and 7B, right panel). Taken together, these results show that endogenous PKR expression is required for the inhibition of host translation induced by poly(I:C).

 Endogenous PKR is not the main driver of protein synthesis shutoff induced by rVHSV-Tomato infection

 To assess the role of endogenous PKR in translation inhibition in a context of viral infection, which is intrinsically more complex than poly(I:C) stimulation, we compared the response of WT EC and 625 WT-like EC-PKR-C28 cells with that of *pkr*^{-/-} EC-PKR-C19 cells during rVHSV-Tomato infection. In all cell lines, the puromycin signal intensity decreased as early as 24h post-infection and drastically 627 dropped at 40h post-infection (Figure 8A and 8D). These data negatively correlate with eIF2 α phosphorylation, which increased at 24h and peaked at 40h post-infection (Figure 8A and 8C). Interestingly, VHSV N was expressed as early as 16h post-infection and expression levels increased over time (24-40h post-infection), despite the decrease in host *de novo* protein synthesis (Figure 631 8A,B). However, no significant differences between WT, WT-like and *pkr^{-/-}* cell lines were detected at all infection time points examined. These results indicate that VHSV-induced phosphorylation of 633 eIF2 α closely correlates with a decrease in host translation, while viral protein synthesis continued to increase during the shutoff of host protein synthesis. The absence of differences between cell lines shows this phenomenon involves a PKR-independent mechanism.

 To further verify those results, all cell lines were pretreated with IFNA2 before rVHSV-Tomato infection. However, there were, once again, no differences between cell lines despite high levels of PKR expression (Figure S3). These findings further confirm the hypothesis that phosphorylation of eIF2α and host translation inhibition is not mediated by PKR during rVHSV-Tomato infection. Similar results were obtained with GSV, a dsRNA virus. Indeed, although GSV infection led to decreased levels of puromycin incorporated into proteins and increased phosphorylation of eIF2α at 24h post-infection, no differences between cell lines could be observed (Figure S3).

Chinook salmon PKR can play antagonistic roles in virus replication

644 Immunoblots showing a similar expression of VHSV N protein in WT, WT-like and $pkr^{-/-}$ cell lines were indicative that PKR had little to no effect on VHSV replication at an early stage of infection. To investigate further PKR role in virus replication and production, we used rVHSV-Tomato, in which the expression cassette encoding tdTomato was inserted in the N-P intergenic region of VHSV 648 genome and is therefore expressed only during its viral replication cycle . The use of this virus enabled us to monitor viral replication using fluorescence as a non-invasive proxy for viral replication.

 Overexpression of PKR-FL inhibits rVHSV-Tomato replication. To assess whether Chinook 652 salmon PKR is involved in the inhibition of viral replication, $pkr^{-/-}$ EC-PKR-C19 cells were transfected with plasmids encoding different PKR isoforms and subsequently infected with rVHSV- Tomato. The fluorescence of rVHSV-Tomato was monitored from 24h to 96h post-infection. A modest but constant reduction in measured fluorescence was observed in PKR-FL transfected cells from 48h post-transfection to 96h post-transfection (Figure 9A). Once normalized to the mean fluorescence measured in BFP-transfected cells at each time point, this represents a decrease of around 30% (Figure 9B). Similarly, overexpression of PKR-FL but not PKR-ML or PKR-SL resulted in a limited but significant decrease in viral titer in the supernatants at 96h post-infection (Figure 9C). 660 Consistent with previous fluorescence results, this constitutes a drop of \approx 25% (calculated on the basis of non-log transformed titers) compared to BFP-transfected cells. Taken together, these results suggest that overexpression of PKR-FL but not other isoforms inhibits rVHSV-Tomato replication.

 Endogenous PKR favors the release of virus into the supernatants. The role of endogenous PKR during rVHSV-Tomato infection was investigated by comparing the evolution of the red fluorescence 665 in WT EC, WT-like EC-PKR-C28 and *pkr^{-/-}* EC-PKR-C19 cell lines from 24h to 96h post-infection. 666 The fluorescence signal was significantly higher in $pkr^{-/-}$ EC-PKR-C19 compared to the WT and WT- like cell lines and this difference was more pronounced at a high MOI: significant differences between 668 pkr^{-/-} and WT cell lines started to appear as early as 48h, 72h and 96h post-infection at MOI 10, MOI 1 and MOI 0.1, respectively (Figure 10A-C). Importantly, a similar trend was observed in other *pkr*- ^{/-} clones (EC-PKR-C3 and EC-PKR-C5), excluding the hypothesis of a clone-specific effect (Figure S4). Because tdTomato is not present in newly formed virions, supernatants of infected cells were titrated by plaque assay. Surprisingly, viral titers in the supernatants were slightly but significantly 673 Iower in *pkr*^{-/-} EC-PKR-C19 cells compared to WT EC and WT-like EC-PKR-C28 cells (Figure 10D), which was inconsistent with our fluorescence data, indicative of the intracellular level of tdTomato. Because our previous results showed that PKR was involved in apoptosis at a late stage of viral infection, we hypothesized that absence of PKR could inhibit virion release. If this were true, virions would accumulate in the infected cells and a higher intracellular viral titer could be expected. To clarify this point, after supernatant collection, remaining infected cells were washed three times, sonicated and the sonicates were titrated by plaque assay. Our results show that intracellular viral 680 titers were weakly but significantly higher in pkr^{-1} EC-PKR-C19 cells compared to WT EC cells 681 (Figure 10E). However, there was no difference between *pkr*^{-/-} EC-PKR-C19 and WT-like EC-PKR- C28 cells. As mentioned earlier, this discrepancy may be explained by the fact that PKR is less expressed in WT-like EC-PKR-C28 compared to WT EC.

 Whilst there are differences in extracellular and intracellular titers between cell lines, the "total titer", ie. the total amount of extracellular and intracellular infectious virions produced by each cell line, was not significantly modified by *pkr* disruption. These results suggest that endogenous PKR does

not affect viral replication *per se*, but rather favors the release of viral particles into the supernatant.

Discussion

 In this study, we have identified and cloned three isoforms of a unique Chinook salmon *pkr* gene, named *pkr-fl*, *pkr-ml* and *pkr-sl*, the last two lacking important catalytic regions. Using complementary *in cellulo* approaches based on overexpression and knockout studies, we showed that salmonid PKR is involved in apoptosis activation and plays a major role in translational arrest upon poly(I:C) stimulation but not during VHSV infection. Our data further indicate that PKR favors the release of VHSV virions into the supernatant at a late infectious stage, likely by triggering apoptosis. Taken together, our results demonstrate that salmonid PKR has conserved molecular functions compared to their mammalian counterparts. However, the endogenous protein did not have a major antiviral effect against VHSV, likely due to subversion strategies evolved by the virus.

698 In line with previous studies on mammalian and fish cell lines 2.47 both RT-qPCR and western blot analysis revealed a constitutive but modest expression of PKR-FL in EC cells, which was strongly induced after IFNA2 treatment. In contrast, neither *pkr-fl* nor *mx1/2/3* expression was induced during infection with either rVHSV-Tomato or GSV, both at transcript and protein levels. Comparable results were previously obtained in the rainbow trout RTG-P1 cell line, which expresses the firefly 703 luciferase gene under the control of the *mx1* gene promoter ⁵⁵. These observations suggest that the IFN response was limited in the epithelial-like salmonid EC cells during rVHSV-Tomato infection, 705 due to virus-mediated IFN suppression mechanisms, possibly *via* its NV protein ^{82–85}.

 Although endogenous PKR was not induced in EC cells during rVHSV-Tomato infection, we still investigated the potential antiviral activity of PKR *via* overexpression and loss-of-function 708 approaches. In line with other overexpression studies in fish models $37,45,46$, we observed that overexpression of PKR-FL but not PKR-ML or PKR-SL resulted in a limited but significant decrease in rVHSV-Tomato titers in the supernatant. Using a knockout approach, we further showed that VHSV extracellular titers were slightly but significantly lower, while intracellular titers were higher 712 in the pkr^{-1} cell line, compared to the WT cell line. Our results therefore suggest that endogenous PKR does not affect viral replication and virion assembly *per se*, but favors the release of viral particles into the supernatant. In contrast, it was recently reported that chemical inhibition of PKR in rainbow trout RTG2 and RTGill cells lines did not have any impact on extracellular VHSV titers in 716 comparison to untreated cells ⁴⁴. Differences between our results and this study may arise from remanent PKR activity following chemical inhibition, which may downplay the full effect observed in our study.

 Enzymatic assays also showed that PKR plays a preponderant role in the activation of apoptosis and triggers it at a relatively late stage of VHSV infection. Based on previous titration results, we propose that *pkr* knockout could reduce virion release by limiting apoptosis activation at a late infection stage. In contrast, PKR-FL antiviral activity upon overexpression would mainly occur through early activation of apoptosis, when it is detrimental to efficient virus replication. Interestingly, the kinetics of caspase 3 activation correlated with apoptotic kinetics described in the literature for 725 novirhabdoviruses ⁸⁶. This relatively late activation of apoptosis has been attributed to VHSV NV protein, which inhibits apoptosis at the early stage of viral infection and prevents infected cells from 727 undergoing cell death before mature viral particles are produced . On the other hand, apoptosis can 728 be advantageous at the late stage of viral replication to facilitate viral release and dissemination $87,88$. Precisely, while VHSV NV protein has an "early" anti-apoptotic function, the matrix (M) protein of 730 novirhabdoviruses is known for its pro-apoptotic properties ⁸⁹. At a late stage of infection, it has been suggested that abundant proapoptotic M protein takes over and triggers a late apoptosis activation, 732 which facilitates viral release and spread ⁸⁶. It is therefore tempting to speculate that VHSV has evolved a NV-driven strategy which takes advantage of PKR-mediated apoptosis.

 Besides apoptosis, a key antiviral mechanism of PKR is the inhibition of the translation machinery *via* phosphorylation of eIF2α. By using reporter genes and quantifying puromycin incorporation into newly synthetized proteins, we further demonstrated that both overexpressed PKR-FL and endogenous poly(I:C)-activated PKR were able to inhibit host *de novo* protein synthesis. These results are in line with several studies on mammalian and fish PKR, as recently reviewed by Chaumont et al. 739 ³¹. In a context of viral infection, we showed that VHSV-induced phosphorylation of eIF2 α closely correlates with a decrease in host protein translation. However, no differences were observed between 741 WT and $pkr^{-/-}$ cell lines, revealing that this phenomenon is PKR-independent. Importantly, PKR is 742 not the only kinase that can trigger host translational arrest; eIF2 α can be phosphorylated by four other kinases: PERK (PKR-like ER kinase), GCN2 (general control non-derepressible 2), HRI (heme-744 regulated inhibitor) and PKZ (Z-DNA-dependent protein kinase) $34,90$. Although each eIF2 α kinase primarily responds to specific stresses, several studies provide evidence that they may have 746 cooperative functions. For instance, eIF2 α phosphorylation can be mediated by PKR but also PERK 747 and GCN2 during viral infections ^{91,92}. A recent study using chemical inhibitors showed that eIF2 α phosphorylation and shutoff of host translation was mediated by PERK and not PKR during VHSV 749 infection $44,93$. Using *pkr^{-/-}* cell lines instead of chemical inhibitors, our results confirm that PKR is not to be the main driver of host translational arrest during VHSV infection. These results suggest that VHSV is able to bypass PKR-mediated translation inhibition but not an alternative host signaling 752 pathway activated by another eIF2 α kinase.

 Besides PKR-FL, we have also identified and cloned two other isoforms expressed in EC cells during VHSV infection, namely PKR-ML and PKR-SL, which are splice variants of PKR-FL. We demonstrated that PKR-ML and PKR-SL do not mediate apoptosis and inhibition of translation, most likely because that they both lack important catalytic regions and are defective in kinase activity. The fact that these two isoforms exist but do not retain any of the typical antiviral functions established for PKR-FL raises the question of their physiological role(s) in the cell. Interestingly, weakly 759 expressed splice variants have been reported for mammalian PKR $94-96$ as well as for zebrafish PKZ ^{34,97}. Li and Koromilas reported a splice variant (PKR Δ E7), in which exon 7 was spliced out, resulting in a truncated 174-aa protein containing only dsRNA binding domains. Interestingly, PKRΔE7 exhibited a dominant negative function, as co-expression of both isoforms relieved PKR-mediated 763 translation inhibition ⁹⁵. Because PKR-SL also contains dsRBM1 and a truncated dsRBM2, it might have a similar dominant negative activity as human PKRΔE7. Abraham et al. also reported that murine lymphocytic leukemia cells expressed a *Pkr* transcript presenting an in-frame deletion of 579 bp. The resulting truncated protein is strikingly similar to PKR-ML: in both cases, the in-frame deletion occurred within dsRBM2 and in the C-terminal portion of the acidic kinase insert of the kinase domain. Abraham et al. showed that this truncated protein was able to form dimers with 769 endogenous PKR and to bind dsRNA . Whether PKR-ML possesses similar characteristics remains to be determined.

 In conclusion, our results establish that salmonid PKR has conserved molecular functions, including apoptosis activation and inhibition of protein synthesis. However, endogenous PKR does not play a major antiviral role during VHSV infection. It seems that VHSV has evolved a strategy to subvert PKR antiviral action, by limiting early PKR induction and evading PKR-mediated translational arrest. VHSV also appeared to take advantage of PKR-mediated apoptosis to favor viral spread at a late stage of infection.

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Table legends

- Table I: Primers used in this study
- Table II: Plasmids used in this study
- Table III: qPCR primers used in this study
- Table IV: List of primary antibodies used for Western blots in this study
- Table V: Molecular characteristics of Chinook salmon PKR isoforms isolated in this study

Figure legends

 Figure 1: Isolation of three Chinook salmon PKR isoforms expressed during rVHSV-Tomato infection in EC cells. (**A**) Electrophoresis on 1.5% agar gel (100 V, 60 min) of PKR isoforms (FL = 1146 full length, ML = medium length, SL = short length) amplified from cDNA of EC cells infected with rVHSV-Tomato (MOI 1). (**B**) Chromosomal localisation of Chinook salmon PKR (LOC112253229) and schematic representation of the 3 isolated PKR isoforms at the transcript level. Boxes represent exons and straight lines represent introns. The transcripts of PKR-FL, PKR-ML and PKR-SL are represented in black and untranscripted regions are in grey. (**C**) Schematic representation of the 3 isolated PKR isoforms at the protein level. dsRBM = dsRNA binding motif, KD = kinase domain. The location of each predicted domain or motif was obtained using SMART (Simple Modular Architecture Research Tool). (**D**) Sequence alignment of dsRNA binding motifs from Chinook salmon PKR isoforms and human PKR. The sequence consensus identified in most dsRNA-binding motifs from other proteins and the corresponding residues conserved for the fold and/or dsRNA binding are taken from Masliah et al. and drawn below the alignment. The canonical secondary 1157 structured elements are shown above the alignment $68,69$. The circles above the sequences show 1158 residues that have identified as important for dsRNA binding in human PKR 71,72 . (**E**) Schematic representation of human PKR (hPKR) and Chinook salmon PKR-FL and PKR-ML kinase domains. 1160 The different subdomains (I-XI) conserved in kinase proteins were taken from Hanks et al. 70 and 1161 Meurs et al.². Motifs involved in ATP binding are represented by a black line, the invariant lysine residue involved in the phosphoryl transfer reaction is represented by an inverted white triangle, 1163 autophosphorylation sites described for hPKR 71 are represented by inverted black triangles and are located in the activation loop (black dotted line). The acidic kinase insert is indicated by a black double arrow and the eIF2α kinase conserved motif is represented by a grey line; both features are conserved in eIF2α kinases.

 Figure 2: Expression profile of the three PKR isoforms in EC cells during IFNA2 stimulation or virus infection determined by western blot (A;B) and by RT-qPCR (C;D). (**A**) EC cells were stimulated with *S. salar* IFNA2 supernatant for (24-72h), infected with rVHSV-Tomato (16-40 hpi), GSV (16-24hpi) or left untreated (Ctrl). Negative and positive controls are EC cells transfected with pcDNA3.1-Zeo-BFP or plasmids encoding PKR isoforms (PKR-SL, -ML, -FL), respectively. Cell lysates were separated by SDS-PAGE and immunoblotted with antibodies against *S. salar* PKR and α-tubulin (α-tub). PKR-SL was not detected by the anti-PKR antibody and was therefore not represented. Endogenous PKR-ML was not detected following IFNA2 stimulation and viral infections; the double bands present on the blot are believed to be non-specific bands. (**B**) Densitometric quantification of (A). PKR-FL signal intensity normalized to α-tubulin signal intensity 1177 and graphed as fold change relative to non-stimulated or non-infected cells. Bars show means \pm SD from 2 pooled independent experiments (n=3 for each experiment); ns, non-significant (*p* > 0.05), *, *p* < 0.05, ****, *p* < 0.0001, Kruskal-Wallis test with Dunn's post-hoc multiple comparison tests. (**C;D**) EC cells were stimulated with *S. salar* IFNA2 supernatant for 72h, infected with rVHSV- Tomato (8-24 hpi) or left untreated (Ctrl). (**C**) Relative expression levels of *pkr* isoforms and *mx123* genes. (**D**) Expression fold change relative to non-stimulated and non-infected controls. Bars show 1183 means \pm SD from 2 pooled independent experiments (n=3 or n=4 for each experiment); \ast , *p* < 0.05, 1184 ****, $p < 0.0001$, ordinary one-way ANOVA with Tukey's post-hoc multiple comparison tests.

Figure 3: Development and validation of a *pkr***^{** \prime **} cell line. (A) Genotype of EC cells (WT), EC-** PKR-C28 (6-nt deletion, 30_35delGTGCGA, resulting in C11_E12del, WT-like) and EC-PKR-C19, 1187 EC-PKR-C3 and EC-PKR-C5 (1-nt insertion, 29_30insT resulting in V11fsX22, *pkr^{-/-}*) obtained from sequencing of purified PCR products amplified from genomic DNA from each cell line. The location of the sgRNA is underlined, the protospacer adjacent motif is in dark grey, the start codon and the premature stop codon are highlighted in black, the 1-nt insertion in EC-PKR-C19, -C3 and -C5 is in light grey. The corresponding chromatograms are available in Figure S1. (**B**) EC and EC-PKR clones were stimulated with *S. salar* IFNA2 supernatant for 72h; positive and negative controls are EC-PKR- C19 cells transfected with pcDNA3.1-Zeo-BFP or pcDNA3.1-Zeo-BFP-P2A-PKR-FL, respectively. Cell lysates were separated by SDS-PAGE and immunoblotted with antibodies against PKR and α- tubulin (α-tub). (**C**) Densitometric quantification of (B). PKR signal intensity normalized to α-tubulin 1196 signal intensity and graphed as fold change relative to non-stimulated cells. Bars show means \pm SD 1197 from 3 pooled independent experiments (n=3 or n=4 for each experiment); $*, p < 0.05, ***, p <$ 0.0001, ordinary two-way ANOVA with Bonferroni's post-hoc multiple comparison tests.

Figure 4: Overexpression of PKR-FL induces apoptosis. $pkr^{-/-} EC-PKR-C19$ **cells were transfected** with plasmids encoding BFP or different PKR isoforms (PKR-SL, -ML, -FL); at 72hpt, gDNA was extracted for gDNA laddering assay or caspase activity was measured. In parallel, EC-PKR-C19 cells 1202 were either stimulated with staurosporine (STS, 1 μ M) for 24h, infected with GSV (MOI 1) for 24- 48h or left untreated, as positive and negative controls, respectively. (**A**) Electrophoresis on 1.5% agar gel (50V, 60 min) of gDNA from transfected cells (left, 3000 ng/well) or GSV-infected and STS- stimulated cells (right, 600 ng/well). Gels are representative of 2 independent experiments. (**B**) Caspase 3/7 activity (**C**) Caspase 8 activity and (**D**) Caspase 9 activity signal graphed as fold change

- relative to cells transfected with BFP-encoding plasmid (left) or left untreated (right). Dotplots show 1208 means \pm SD from two pooled independent experiments (n=8 for transfection experiments; n=4 for stimulation experiments); ns, non-significant (p > 0.05), ****, p < 0.0001, ordinary one-way ANOVA with Tukey's post-hoc multiple comparison tests.
- **Figure 5: Endogenous Chinook salmon PKR triggers apoptosis during rVHSV-Tomato** 1212 **infection.** EC (WT), EC-PKR-C28 (WT-like) and EC-PKR-C19, -C3 and -C5 (*pkr^{-/-}*) were infected 1213 with rVHSV-Tomato at (A) MOI 1 or (B) MOI 0.1 and caspase $3/7$ activity was measured at 24, 48 1214 and 72 h post-infection. Bars show means \pm SD from two pooled independent experiments (n=4 for each experiment); ns, non-significant (*p* > 0.05), *, *p* < 0.05, **, *p* < 0.01, ****, *p* < 0.0001, ordinary two-way ANOVA with Tukey's post-hoc multiple comparison tests.
- 1217 **Figure 6: Overexpression of PKR-FL inhibits host translation. (A)** $pkr^{-/-}$ **EC-PKR-C19 cells were** cotransfected with pcDNA3.1-Hyg-mEGFP and plasmids encoding BFP or different PKR isoforms (PKR-SL, -ML, -FL). At 8 hpt, mock transfected cells were treated with cycloheximide (CHX, 50 µg/mL, 24h) or thapsigargin (Tg, 2 µM, 45 min). At 30 hpt, cells were pulsed with puromycin (5 µg/mL) for 15 min and cell lysates were separated by SDS-PAGE and immunoblotted with antibodies against PKR, GFP, puromycin (puro) or actin. (**A,B**) Densitometric quantification of (A). (**B**) GFP signal intensity normalized to actin signal intensity and graphed as fold change relative to BFP 1224 transfected cells. Bars show means \pm SD from two pooled independent experiments (n=3 or n=4 for each experiment), *, *p* < 0.05; **, *p* < 0.01, ****, *p* < 0.0001, ordinary one-way ANOVA with Tukey's post-hoc multiple comparison tests. (**C**) Puromycin signal intensity normalized to actin 1227 signal intensity and graphed as fold change relative to BFP transfected cells. (D) pkr^{-1} EC-PKR-C19 cells were cotransfected with pcDNA3-G418-Luc and plasmids encoding BFP or different PKR isoforms (PKR-SL, -ML, -FL). At 24 hpt, luciferase activity was measured. Luminescence signal 1230 intensity graphed as fold change relative to BFP transfected cells. Data shown are means \pm SD (n=16) and are representative of 2 independent experiments; ****, *p* < 0.0001, ordinary one-way ANOVA with Tukey's post-hoc multiple comparison tests.

Figure 7: Endogenous Chinook salmon PKR inhibits host translation upon transfection with

poly(I:C). (**A**) Non-stimulated or ssIFNA2-pretreated EC (WT), EC-PKR-C28 (WT-like) and EC-

1235 PKR-C19 (*pkr^{-/-}*) cells were transfected with rhodamine-labeled poly(I:C)-HMW (pIC) or mock

- transfected (Ctl). At 24 hpt, cells were pulsed with puromycin (5 µg/mL) for 15 min and cell lysates
- 1237 were separated by SDS-PAGE and immunoblotted with antibodies against PKR, puromycin and α-
- 1238 tubulin. **(B)** Densitometric quantification of (A). Puromycin signal intensity normalised to α -tubulin 1239 signal intensity and graphed as fold change relative to mock transfected cells. Bars show means \pm SD 1240 from two pooled independent experiments ($n=3$ for each experiment), ns, non-significant ($p > 0.05$);
- *, *p* < 0.05; **, *p* < 0.01, two-way ANOVA with Bonferroni's post-hoc multiple comparison tests.
- **Figure 8: Endogenous Chinook salmon PKR is not the main driver of protein synthesis inhibition during rVHSV-Tomato infection.** (**A**) EC (WT), EC-PKR-C28 (WT-like) and EC-PKR-1244 C19 (pkr^{-/-}) cells were either infected with rVHSV-Tomato at MOI 1, left uninfected (Ctrl) or stimulated with cycloheximide (CHX, 50 µg/mL) for 24h. At 16, 24 or 40 hpi, cells were pulsed with 1246 puromycin (5 µg/mL) for 15 min and cell lysates were separated by SDS-PAGE and immunoblotted 1247 with antibodies against VHSV N, eIF2α-P, eIF2α, puromycin (puro), actin, PKR and α-tubulin (α- tub). (**B,C,D**) Densitometric quantification of (A). (**B**) VHSV N signal intensity normalized to actin signal intensity. (**C**) eIF2α-P signal intensity normalised to eIF2α signal intensity and graphed as fold change relative to control cells. (**D**) Puromycin signal intensity normalized to actin signal intensity 1251 and graphed as fold change relative to control cells. Bars show means \pm SD from two pooled independent experiments (n=3 for each experiment); ns, non-significant (*p* > 0.05), ordinary two-way ANOVA with Tukey's post-hoc multiple comparison tests.
- 1254 Figure 9: Overexpession of PKR-FL inhibits rVHSV-Tomato replication. *pkr*¹- EC-PKR-C19 cells were transfected with pcDNA3.1-Zeo-BFP or plasmids encoding PKR isoforms. At 24hpt, cells were infected with rVHSV-Tomato (MOI 1) and fluorescence was measured at different time points post-infection. (**A**) Fluorescence signal intensity measured over time; data shown are means ± SD from 6 independent experiments (n=4 for each experiment); two-way ANOVA with Tukey's post- hoc multiple comparison tests were performed on log-transformed data: *, *p* < 0.05; **, *p* < 0.01, comparison to BFP. (**B**) Fluorescence signal intensity graphed as fold change relative to BFP transfected cells; *, *p* < 0.05, two-way RM ANOVA with Tukey's post-hoc multiple comparison tests. (**C**) Supernatant was collected at 96hpi, pooled (4 wells per condition) and titrated by plaque 1263 assay. Data shown are means \pm SD from 6 independent experiments (n=1 for each experiment, 4 pooled wells); *, *p* < 0.05; **, *p* < 0.01, ordinary one-way ANOVA with Tukey's post-hoc multiple comparison tests.

Figure 10: Endogenous Chinook salmon PKR favors the release of rVHSV-Tomato particles

into the supernatant. (**A;B;C**) EC (WT), EC-PKR-C28 (WT-like) and EC-PKR-C19 (*pkr-*/-) cells

were infected with rVHSV-Tomato at (**A**) MOI 10, (**B**) MOI 1 or (**C**) MOI 0.1 and fluorescence was

- measured at different time points post-infection. Graphs show means ± SD from 4 independent experiments (n=8 for each experiment). two-way RM ANOVA with Tukey's post-hoc multiple comparison tests were performed on each log-transformed data set: (A) *, *p* < 0.05 starting from
- 48 hpi ; (B) *, *p* < 0.05 starting from 72 hpi ; (C) *, *p* < 0.05 at 96 hpi. (**D;E;F**) EC (WT), EC-PKR-
- 1273 C28 (WT-like) and EC-PKR-C19 (*pkr^{-/-}*) cells were infected with rVHSV-Tomato at MOI 1;
- supernatants were collected at 96 hpi and the remaining cells were scraped and sonicated; both
- supernatants and sonicates were titrated by plaque assay. Log-transformed plaque forming unit (PFU)
- counts from (**D**) supernatants, (**E**) sonicated cells and (**F**) total sum of both values of EC, EC-PKR-
- 1277 C28, EC-PKR-C19 cells (4 x 10⁶ cells) infected with rVHSV-Tomato for 96 hpi. Bars show means \pm
- SD from two pooled independent experiments (n=4 for each experiment), *, *p* < 0.05; **, *p* < 0.01,
- Kruskal-Wallis test with Dunn's post-hoc multiple comparison tests on log-transformed data.