

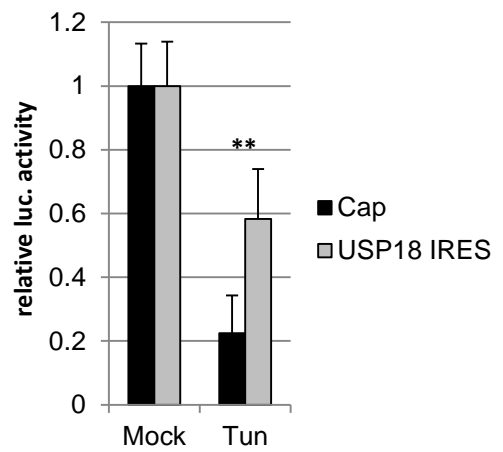
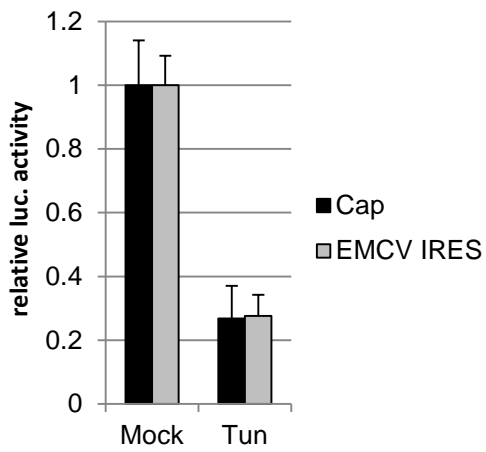
**A**

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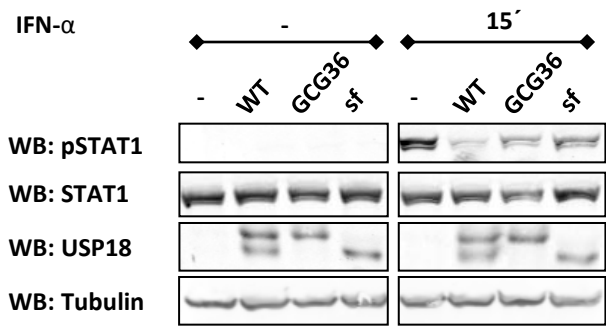
**B**

human	GAGTGATCAC	GAATGAGCAA	GCGTTTTGGG	CTCCTGAGGC	AAATCTGTCA
pongo abelii	GAGTGATCAC	GAATGAGCAA	GCGTTTTGGG	CTCCTGAGAC	AAACCTGTCA
mus musculus	GTGTGATCAC	TAATGGGCAA	GGGTTTTGGG	CTCCTGAGGA	AACCCTGCCA
rattus norvegicus	GTGTGATCAC	TAATGGGCAA	AGGGTTTTGGG	CTCCTGAGGA	AAACCTGCCA
	▼▼▼				
human	GTCCATCCTG	GCTGAGTCCT	CGCAGTCCCC	GGCAGATCTT	GAAGAAAAGA
pongo abelii	GTCCATCCTG	GCTGAGTCTC	CGCAGTCCCC	GGCAGATCTT	GAAGAAAAGA
mus musculus	GTCAGTTGTG	GCTGAGCCGC	AGCAGTACTC	AGC...GCTG	GAGGAAGAGA
rattus norvegicus	GTCAGTTGTG	GCTAATCCTC	AGCAGCACTC	AGC...TCTG	GAGGAAGAGA
		***			
human	AGGAAGAAGA	CAGCAACATG	AAGAGAGAGC	AGCCCAGAGA	GCGTCCCAGG
pongo abelii	AGGAAGAAGA	CAGCAACATG	AAGAGAGAGC	AGCCCAGAGA	GCGTCCCAGG
mus musculus	GGAC.....	CATGAAGAGG	AAGAGAGTGC	TGTCTAGAGA	CCTCTGCAGT
rattus norvegicus	AGAA.....	CATGAAGAGG	AAGAGAGTGC	TGTCTAGAGA	GCTCTGCAGT
human	GCCTGGGACT	ACCCTCATGG	CCTGGTTGGT	TTACACAACA	TTGGACAGAC
pongo abelii	GCCTGGGACT	ACCCTCATGG	CCTGGTTGGT	TTACACAACA	TTGGACAGAC
mus musculus	GCCTGGGACA	GCCCTCATGG	TCTGGTTGGT	TTACACAACA	TCGGACAGAC
rattus norvegicus	GCCTGGGACC	GCCCTCATGG	TTTCGTTGGG	TTACACAACA	TCGGTCAGAC

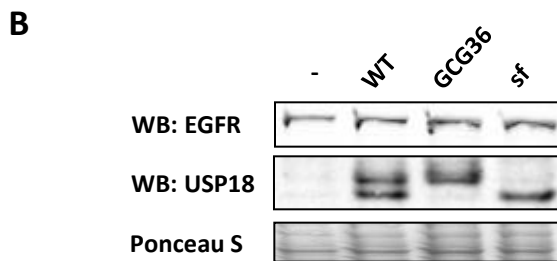
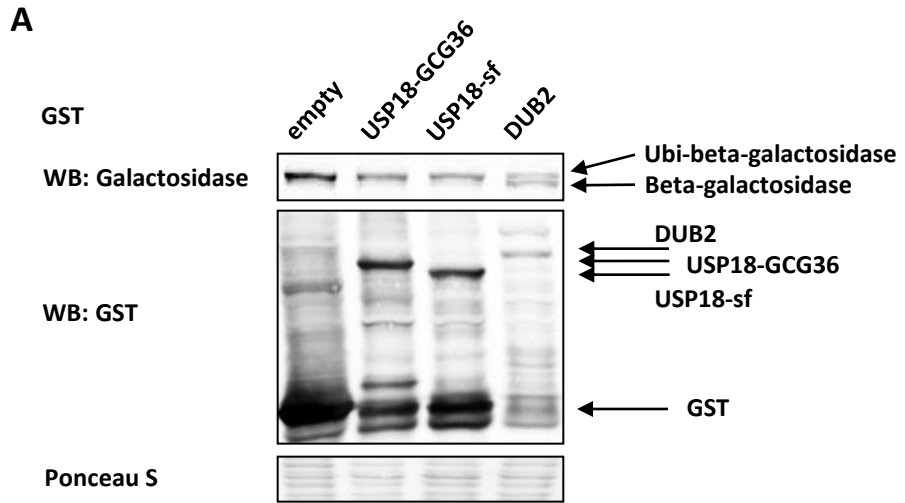
### Supplementary Figure S1



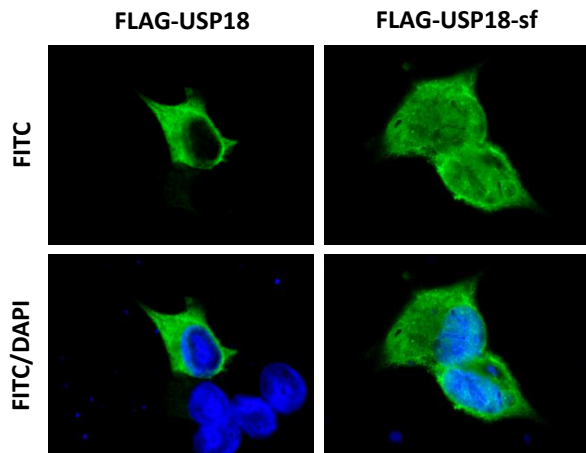
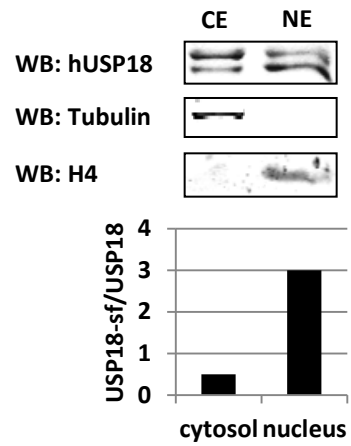
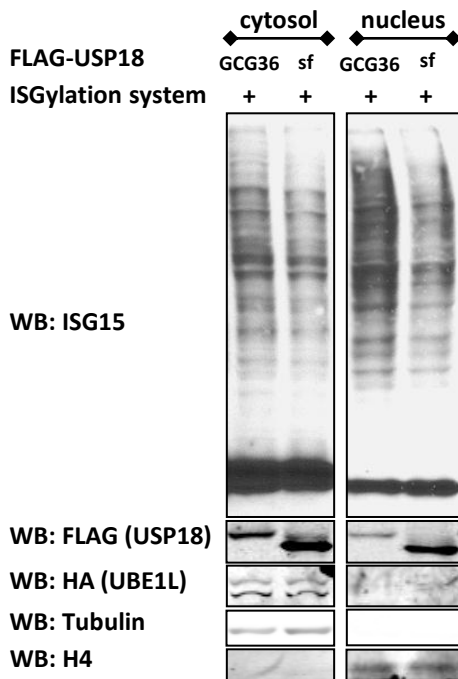
**Supplementary Figure S2**



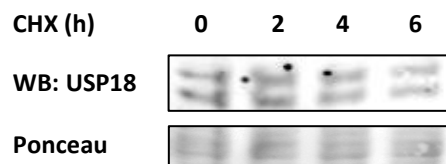
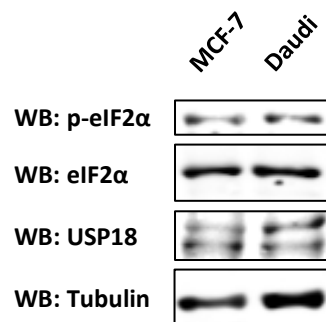
**Supplementary Figure S3**



Supplementary Figure S4

**A****B****C**

**Supplementary Figure S5**

**A****B****Supplementary Figure S6**

**Supplementary Figure S1: Deduced protein sequence of human *USP18* starting from CTG16 and cross species alignment of the 5' region of *USP18* coding sequence.**

- A) Predicted amino acid sequence of human *USP18*. *USP18*-sf translation initiation site (Met36) is marked with an asterisk and active site cysteine (Cys49) with a square. Conserved domains of UBP family members are indicated as follows: Cys box; QQDAQEEF motif; LPOILVIHLKRF consensus; His box.
- B) Human, orangutan, mouse and rat *USP18* sequences were aligned. In-frame ATGs and CTGs are highlighted gray. Kozak consensus is underlined. Primary translation initiation site of human *USP18* (CTG16) is marked with arrows and ATG36 marked with asterisks.

**Supplementary Figure S2: *USP18* IRES activity is relatively resistant to Tunicamycin induced translational stress**

Dicistronic plasmids depicted in *Figure 3A* containing either EMCV or *USP18* IRES were transiently transfected into HeLa cells. 24h post-transfection cells were treated with 2.5  $\mu\text{g/ml}$  Tunicamycin (Tun) or carrier (Mock) for 14h before analysis. Luciferase activities corresponding to firefly luciferase (IRES) and renilla luciferase (Cap) were measured. Shown are relative luciferase activities of three independent experiments. Asterisks indicate statistical significance (t-test) of  $P < 0.05$ .

**Supplementary Figure S3: Both *USP18* isoforms downregulate type I interferon induced JAK/STAT signaling in MCF-7 cells.**

MCF-7 cells stably expressing *USP18*, *USP18*-GCG36 or *USP18*-sf were treated with 10 ng/ml hIFN- $\alpha$  for 15min. Cells were lysed and protein lysates subjected to *USP18*, STAT1 as well as phospho-STAT1 Western Blotting. Tubulin was used as loading control.

**Supplementary Figure S4: *USP18* isoforms do not show significant De-ubiquitin activity or upregulation of EGFR expression.**

- A) *E. Coli* (BL21) were cotransformed with GST-h*USP18* constructs and a construct coding for Ubiquitin- $\beta$ -galactosidase. Bacterial cell lysates were subjected to GST and Galactosidase Western Blotting. Only the positive control DUB2 shows significant cleavage of ubiquitin. Ponceau S staining was used as loading control.
- B) Whole cell lysates from HeLa cells stably expressing *USP18*, *USP18*-GCG36 or *USP18*-sf were probed for EGFR and *USP18* by Western Blotting. Ponceau S staining was used as loading control.

**Supplementary Figure S5: *USP18*-sf is the dominant isoform in the nucleus of MCF-7 cells and *USP18*-sf transfected cells show reduced protein ISGylation in the nucleus.**

- A) MCF-7 cells were transfected with FLAG-*USP18* or FLAG-*USP18*-sf. Immunostaining of MeOH fixed cells shows that FLAG-*USP18*-sf is localized in the nucleus and the cytosol whereas FLAG-*USP18* is mostly excluded from the nucleus.
- B) MCF-7 cells were treated with 10 ng/ml IFN- $\alpha$  for 36h to induce expression of *USP18*. Cells were then lysed and nuclear/cytosolic fractions prepared. Each subcellular fraction was probed for *USP18* as well as nuclear and cytosolic markers. *USP18*-sf/*USP18* ratio was quantified with *Li-Cor* Odyssey system.
- C) MCF-7 cells were transiently transfected with ISGylation system and either FLAG-*USP18*-GCG36 or FLAG-*USP18*-sf. 36h after transfection cytosolic and nuclear extracts were prepared and probed for ISG15, *USP18*, UBE1L as well as nuclear and cytosolic markers.

**Supplementary Figure S6: USP18 isoforms do not show a difference in protein turnover and expression of USP18-sf does not correlate with phosphorylation of eIF2 $\alpha$ .**

- A) MCF-7 cells stably expressing USP18 were treated with 20 $\mu$ g/ml of cycloheximide (CHX) and USP18 protein levels at indicated time points analyzed by Western Blotting. Ponceau S staining was used as loading control.
- B) MCF-7 and Daudi cells stably expressing USP18 were analyzed for eIF2 $\alpha$  phosphorylation and expression of the two USP18 isoforms by Western Blotting. Tubulin was used as loading control.