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* about emPAI: in 2005 Ishihama et al. (Molecular & Cellular Proteomics 4:1265-1272, 2005) showed that emPAI can be used to obtain an estimate of protein abundance. It was already known that respective protein abundance roughly corresponded to the number of matched spectra. However, since tryptic cleavage of proteins yields different number of detectable peptides for each protein (depending on protein sequence length and physicochemical properties of the generated peptides) it was necessary to calculate a Protein Abundance Index (PAI) that takes these factors into account. Protein abundance expressed as PAI (or emPAI) can thus be used to compare protein abundance between samples and different proteins thanks to this correction.

PAI is calculated as: Nobserved / Ntheoretical

Where Nobserved is the number of unique precursor identification from all peptides of an identified protein and Ntheoretical is the total number of theoretically detectable peptides for that protein.
Proteomic analysis employing LCMSMS identified the tabulated mitoribosomal proteins as co-precipitants with ICT1. Analysis was performed as described in the Supplemental Experimental Procedures.
Supp Fig 1 si-ICT1B does not affect the growth of rho0 cells.
Equal numbers (~6000) of HeLa or 143B rho0 rhod cancer cell lines were grown in DMEM supplemented with 50 μg/ml-1 uridine in independent wells of a 96 well plate and exposed to 3 different siRNAs designed against the indicated transcripts or to the non-targeting control. After 3 days, medium was aspirated and 200 μl per well of 0.5 mg/ml MTT in DMEM medium was added. Plates were incubated for 3 h at 37 °C, MTT solution removed and 200 μl DMSO added to dissolve formazan crystals and incubation at 37 °C for 5 min. Absorbance was measured at 550 nm in a microplate reader (Bio-Tek). In two cases, (TUFM and TRNT1) no effect on growth of either cell line was noted for one siRNA and consequently data is not shown. All siRNAs were assayed from quadruplicate wells in one plate except for si-ICTB, where quadruplicates were performed in two independent plates (B1 and B2). Results are shown normalised to the growth of cells treated with the non-targeting siRNA from which the mean absorbance was taken. Transcripts were designed against the RefSeq accession numbers given.

Supp Fig 2 Standard curve of si-ICT1B.
To determine the concentration of si-ICT1B that caused depletion of endogenous ICT1 and which resulted in similar steady state levels of inducibly expressed ICT1 to natural endogenous levels, lysates were produced from HEK293T cells uninduced (lane 1, 2) or after 3 days expression of ICT1-Flag (lanes 3-6, 1 μg/ml-1 tet as inducer) in the presence of no (lane 1) or varying concs of si-ICT1B (5 - 30 nM, lanes 2-6). Anti-ICT1 and anti-β-actin antibodies are used.