

Supplementary Figure 1. Prediction of TRIP-Br1 mitochondrial localization. MitoProt software program, a computational method to predict mitochondrial localization of target protein, was used to predict the possibility of TRIP-Br1 mitochondrial localization using the full-length TRIP-Br1 amino acid sequence. The MitoProt software is available at <ftp://ftp.biologie.ens.fr/pub/molbio>. Based on the protein localization prediction program (TargetP 1.1 Server), VDCA1, a well-known mitochondrial protein with the number of amino acid residues similar to TRIP-Br1, was used as a control. VDCA1 has a high probability of export into mitochondria. However, TRIP-Br1 does not carry the typical mitochondrial leader sequence. Therefore, it has a low possibility of mitochondrial translocation.

Supplementary Figure 2. A,B MCF7^{WT-TRIP-Br1} and MCF7^{KD-TRIP-Br1} cells were cultured in a confocal dish for 24 h, followed by staining with Mitotracker dye (100 nM) for 30 min. TRIP-Br1 localization in mitochondria was determined via two-color immunofluorescence microscopy using anti-TRIP-Br1 (yellow) and Mitotracker dyes (red). These cells were visualized under a confocal microscope. Representative fluorescent images are visualized with confocal microscopy (scale bar, 20 μ m).

Supplementary Figure 3. Mice strains were genotyped via PCR as described previously [63].

Supplementary Figure 4. Potential phosphorylation sites amino acid sequences of TRIP-Br1 protein predicted with NetPhos 2.0 Server. Targeted potential phosphorylation sites were mutated by changing serine to alanine. Mitochondrial TRIP-Br1 levels are shown after STS treatment.

Supplementary Figure 1

TRIP-Br1

Input sequence length : 233 aa

VALUES OF COMPUTED PARAMETERS

Net charge of query sequence : -28
 Analysed region : 10
 Number of basic residues in targeting sequence : 5
 Number of acidic residues in targeting sequence : 0
Cleavage site : not predictable
 Cleaved sequence :

HYDROPHOBIC SCALE USED

	GES	KD	GVH1	ECS
H17	1.176	1.353	0.185	0.551
MesoH	-0.031	0.468	-0.183	0.295
MuHd_075	16.929	13.174	4.465	4.026
MuHd_095	16.679	11.844	5.013	4.232
MuHd_100	14.339	11.578	4.121	3.290
MuHd_105	18.576	12.091	5.196	3.839
Hmax_075	-25.083	-7.233	-7.833	-2.063
Hmax_095	-21.000	-4.987	-7.951	-1.015
Hmax_100	-26.800	-7.600	-8.948	-1.800
Hmax_105	-22.400	-4.783	-8.199	-1.237

Probability of export to mitochondria: 0.0608

Supplementary Figure 2



