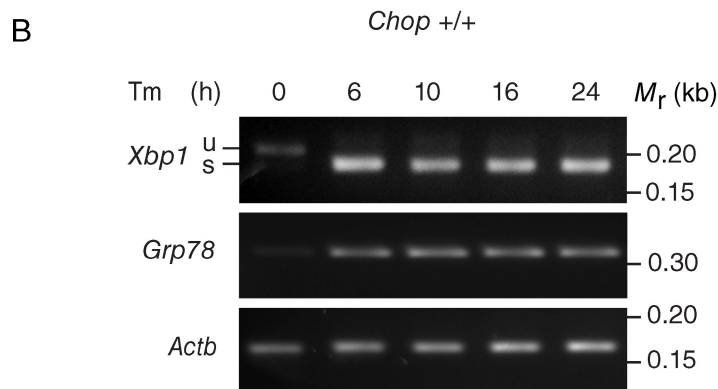
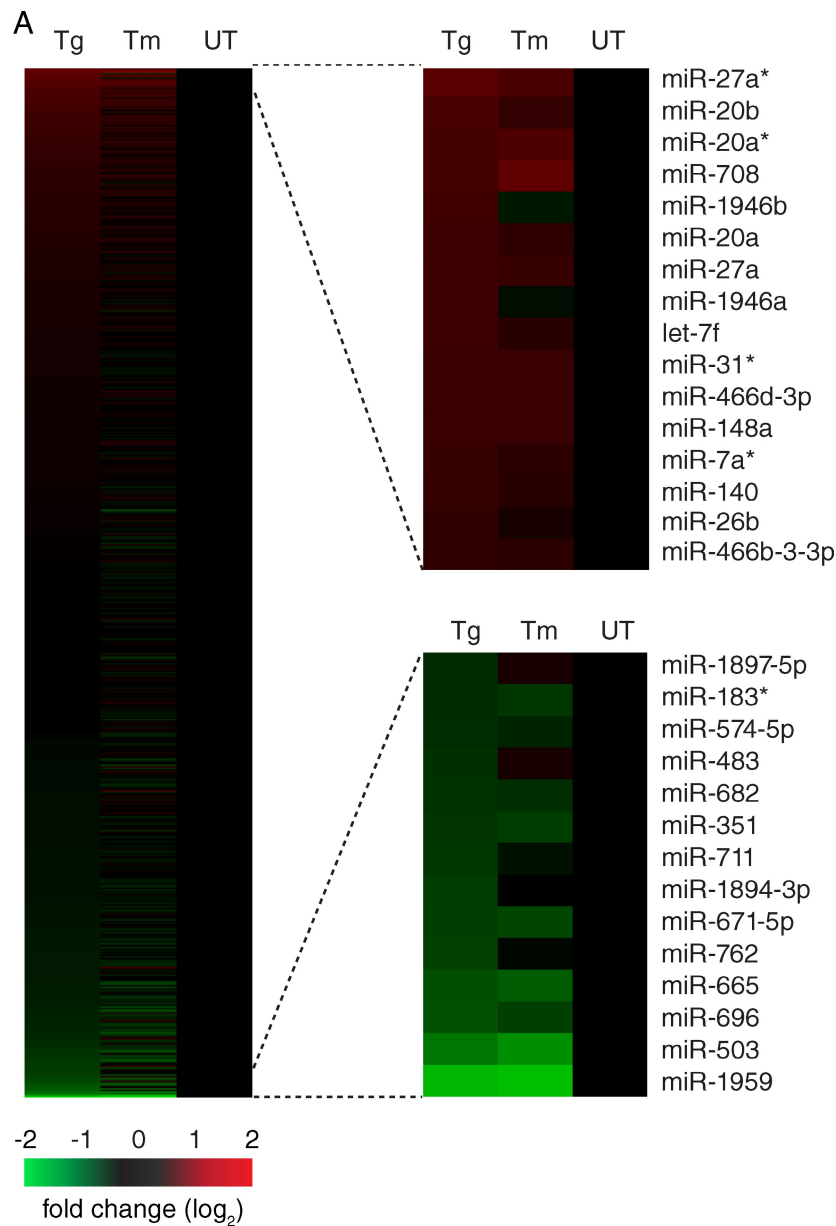


Behrman et al., <http://www.jcb.org/cgi/content/full/jcb.201010055/DC1>

Figure S1. Inconspicuous changes in the expression of miRNAs in 3T3 fibroblasts exposed to ER stress for 10 h. (A) Heat map of miRNA expression from 3T3 cells treated with either 5 μ g/ml Tm or 500 nM Tg for 10 h. The applied criterium for differential expression was a more than twofold change in treated versus untreated (UT) conditions, represented as logarithmic values. Red, increase in differential expression during ER stress; Green, decrease in differential expression. Only miR-1959 and miR-503 showed a decrease in differential expression. No miRNAs showed an increase in differential expression. Asterisks indicate the passenger strand of the miRNA. (B) RT-PCR assay of *Chop*^{+/+} MEFs showing splicing of *Xbp1* mRNA and accumulation of the *Grp78* transcript. s, spliced form of *Xbp1*; u, unspliced variant. The loading control used was β -actin (*Actb*).



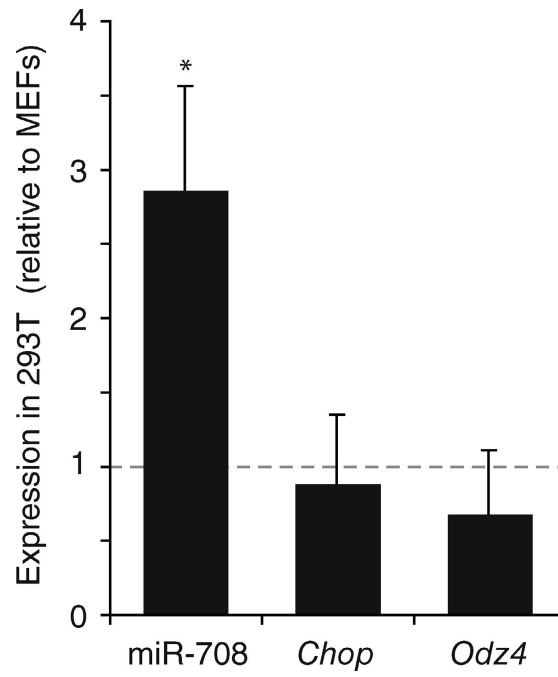


Figure S2. **Expression of miR-708, *Chop*, and *Odz4* in 293T cells compared with MEFs.** Quantitative RT-PCR assay of *Chop*, *Odz4*, and TaqMan miRNA assay for miR-708 in MEFs and 293T cells. The dashed line indicates the expression level of the transcripts in MEFs. The loading controls used were β -actin and U6 small nuclear RNA. Error bars are SEMs of six independent experiments. *, $P > 0.0001$. P-values were derived from a *t* test for independent samples.

Table S1. Top 30 candidate target genes of miR-708 defined by TargetScan

| Gene symbol | Gene name | Score | Function/process |
|-------------------|---|--------------|---|
| <i>SHPRH</i> | SNF2 histone linker plant homeodomain RING helicase | −0.82 | DNA repair |
| <i>KIAA0355</i> | KIAA0355 | −0.68 | Unknown |
| <i>GPM6A</i> | glycoprotein M6A | −0.44 | Neuronal processes |
| <i>BAMBI</i> | BMP and activin membrane-bound inhibitor | −0.43 | TGF- β receptor signaling |
| <i>NNAT</i> | neuronatin | −0.42 | Brain development |
| <i>AAK1</i> | AP2-associated kinase 1 | −0.41 | Receptor-mediated endocytosis |
| <i>IQSEC2</i> | IQ motif and Sec7 domain 2 | −0.40 | ADP ribosylation factor guanyl-nucleotide exchange factor |
| <i>EN2</i> | engrailed homeobox 2 | −0.40 | Nervous system development |
| <i>HOXB3</i> | homeobox B3 | −0.38 | Development |
| <i>RAP1B</i> | RAP1B, member of Ras oncogene family | −0.37 | GTPase activity |
| <i>hCG1757335</i> | hCG1757335 | −0.37 | Unknown |
| <i>FOXJ3</i> | forkhead boxJ3 | −0.37 | Transcription |
| <i>CHL</i> | cell adhesion molecule with homology to L1CAM | −0.34 | Neural cell adhesion |
| <i>ETF1</i> | eukaryotic translation termination factor 1 | −0.33 | Translation |
| <i>TMEM200B</i> | transmembrane protein 200B | −0.33 | Unknown |
| <i>TNS3</i> | tensin 3 | −0.32 | Cell migration/proliferation |
| <i>RPGRIP1L</i> | RPGRIP1-like | −0.32 | Development |
| <i>DKK3</i> | dickkopf homolog 3 (<i>Xenopus laevis</i>) | −0.32 | Inhibitor of Wnt signaling pathway |
| <i>DGCR14</i> | DiGeorge syndrome critical region gene 14 | −0.30 | RNA splicing/nervous system development |
| <i>SETDB1</i> | SET domain, bifurcated 1 | −0.29 | Chromatin modification |
| <i>SLAMF6</i> | SLAM family member 6 | −0.29 | Natural killer cell activation |
| <i>RHO</i> | rhodopsin | −0.28 | Phototransduction |
| <i>RPP14</i> | RNase P/mitochondrial RNA processing 14-kD subunit | −0.28 | tRNA processing |
| <i>GRIA4</i> | glutamate receptor, ionotropic, AMPA 4 | −0.28 | Synaptic transmission |
| <i>SRPRB</i> | signal recognition particle receptor, B subunit | −0.27 | Putative co-translation |
| <i>C14ORF101</i> | chromosome 14 ORF 101 | −0.27 | Unknown |
| <i>CNTFR</i> | ciliary neurotrophic factor receptor | −0.26 | Nervous system development |
| <i>RNF165</i> | ring finger protein 165 | −0.24 | Metal ion binding |
| <i>RCVRN</i> | recoverin | −0.24 | Phototransduction |
| <i>C12orf101</i> | chromosome 12 ORF | −0.24 | Unknown |

Top 30 predicted target genes of miR-708 defined by TargetScan. Gene symbols, names, total context scores, and manually curated gene function/process for each candidate are indicated. Bold highlights rhodopsin. Gene symbols are human homologues. Score is the context score as assigned by TargetScan.