

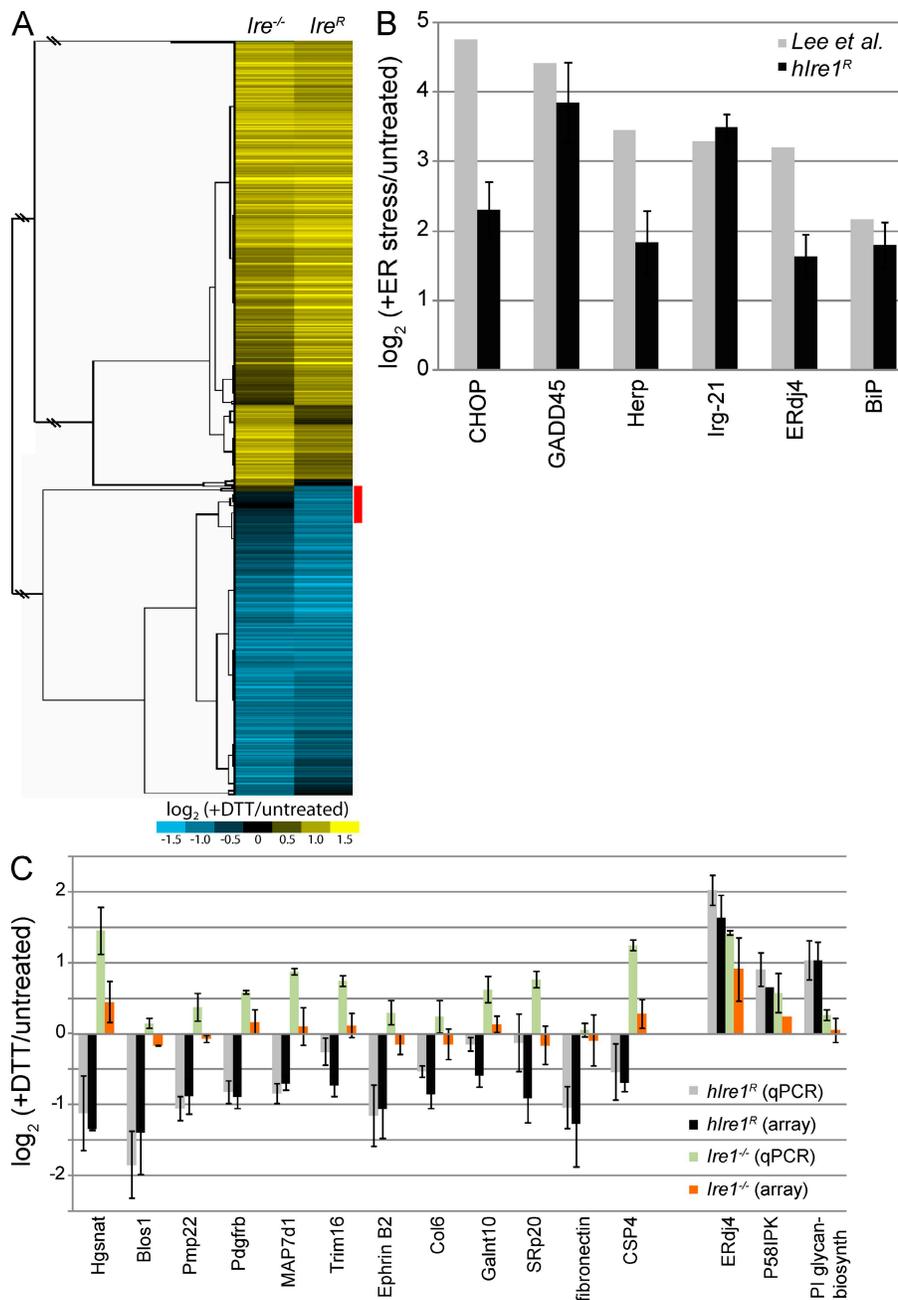
Hollien et al., <http://www.jcb.org/cgi/content/full/jcb.200903014/DC1>

Figure S1. **Microarray analysis reveals *Ire1*-dependent down-regulation.** (A) Hierarchical clustering result from MEEBO array data. The 2,458 spots passing all quality control measures and for which at least one of the two cell lines displayed a change in mRNA abundance of 1.5-fold upon treatment with DTT are shown. The red bar indicates the cluster used for further analysis of *Ire1*-dependent RNA decay. (B) Comparison of UPR target gene regulation between our MEEBO data and previously published results (Lee et al. 2003. *Mol. Cell. Biol.* 23:7448–7459). Genes that were strongly up-regulated in response to ER stress in Lee et al. (2003) and for which our arrays displayed data passing quality control measures are shown. (C) Confirmation of regulation of RIDD candidates measured by qPCR. For full gene names and reference identifications, see Table I. PI, phosphatidylinositol. (B and C) Error bars represent the SDs of two to three independent experiments.

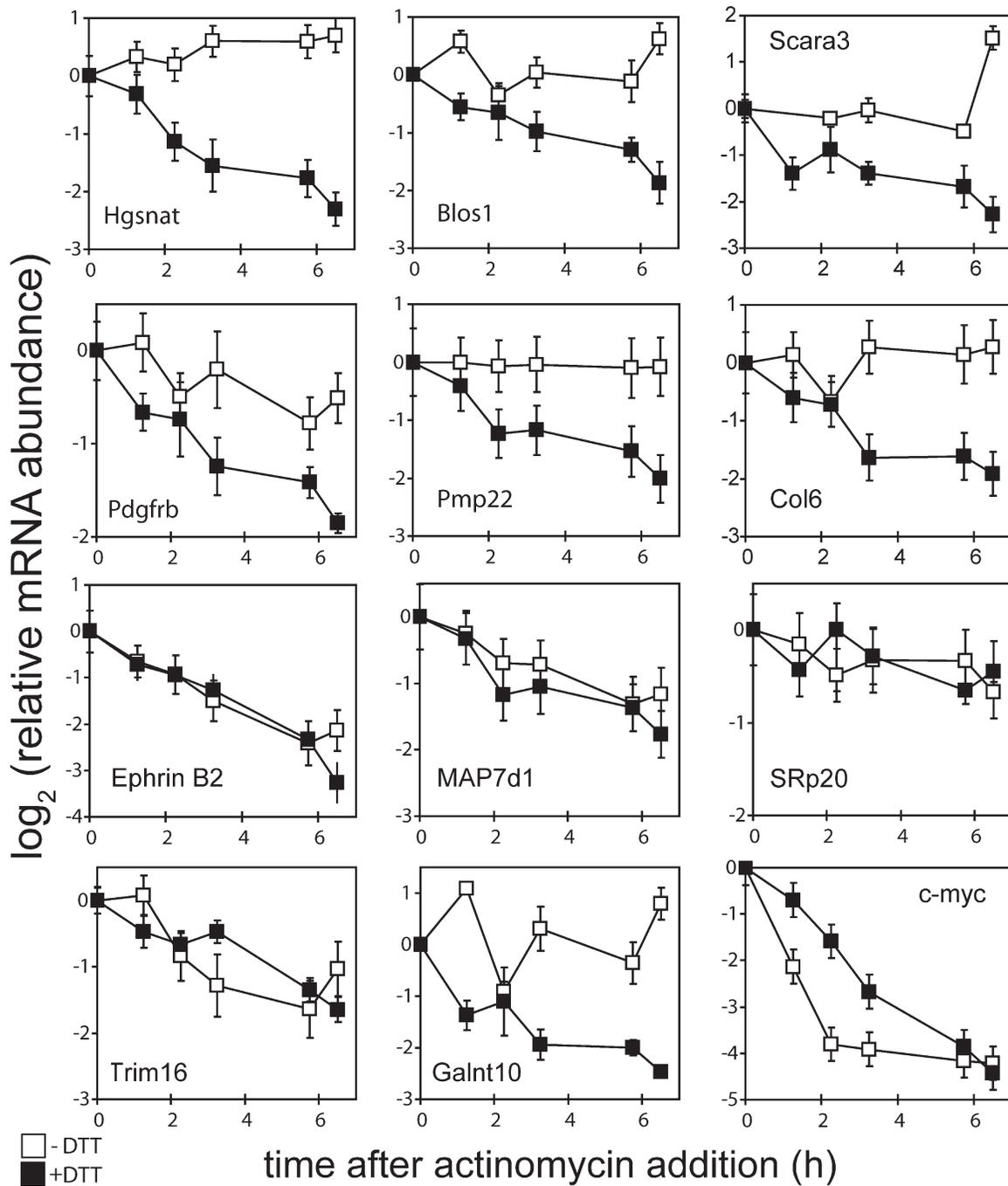


Figure S2. **Decay rate measurements for RIDD candidate mRNAs.** *hlre1^R* cells were treated with 1 $\mu\text{g}/\text{ml}$ actinomycin D with or without 2 mM DTT, and relative mRNA abundance was monitored over time by qPCR. RNA levels were normalized to those of Rpl19 and to untreated controls from time 0. *c-myc* is shown as a control for effective blocking of transcription by actinomycin D. For full gene names, see Table I. Error bars represent the SDs of qPCR replicates.

Table S1. Primers used for qPCR

Target	Primer 1	Primer 2
Hgsnat	5'-TCTCCGCTTCTCCATTTG-3'	5'-CGCATACACGTGGAAAGTCA-3'
Blos1	5'-CAAGGAGCTGCAGGAGAAGA-3'	5'-GCCTGGTTGAAGTTCTCCAC-3'
Scara3	5'-TGCATGGATACTGACCCTGA-3'	5'-GCCGTGTTACCAGCTTCTTC-3'
Pdgfrb	5'-AACCCCTTACAGCTGCCT-3'	5'-TAATCCCGTCAGCATCTCC-3'
Pmp22	5'-TGCGATACAGCAGAAATGGAG-3'	5'-TTGGTGGCCAATACAAGTCA-3'
Col6	5'-TGCTCAACATGAAGCAGACC-3'	5'-TTGAGGGAGAAAGCTCTGGA-3'
Ephrin B2	5'-CGTCTATGGATTCGGGTGT-3'	5'-CAGCAATTTGGCAACCTTTT-3'
MAP7d1	5'-CGCACCTTACAGACTGGTGA-3'	5'-TACCCGCCTCTCCACATAG-3'
SRp20	5'-TTTTCCCTTTGCTTGTCAC-3'	5'-TATGCATGCCTCCATTCAA-3'
Trim16	5'-CGGACCTCCCCAGTAGATT-3'	5'-TGTGAACTCCTCCCCATTCC-3'
Galnt10	5'-CCTTAGAGATGCTGGGATCG-3'	5'-TGAGGACTCAACTCCCCTTG-3'
ERdj4	5'-GGATGGTTCTAGTAGACAAAGG-3'	5'-CTTCGTTGAGTGACAGTCCTGC-3'
BiP	5'-TCAGCATCAAGCAAGGATTG-3'	5'-AAGCCGTGGAGAAGATCTGA-3'
Rpl19 (housekeeping control)	5'-CTGATCAAGGATGGGCTGAT-3'	5'-GCCGCTATGTACAGACACGA-3'
XBP-1 (splicing)	5'-TTACGGGAGAAAACCTACGGC-3'	5'-GGGTCCAACCTTGCCAGAATGC-3'