

SUPPLEMENTAL DATASETS AND TABLES

Dataset S1: Microarray dataset comparing gene transcript levels following exposure to tunicamycin versus control. Dataset S1 lists mRNAs that increased after 1 hr, 10 μ M treatment of extracellular tachyzoites with tunicamycin ($p < 0.05$ and FDR < 0.05). Data represents three biological replicates that were filtered for statistical significance ($p \leq 0.05$ and FDR < 0.05).

Dataset S2: List of genes as defined by probesets that are suggested to be subject to preferential translation in response to tunicamycin. Data represents probe sets that showed a statistically significant ($p \leq 0.02$) increase in gene transcripts associated with polysomes following a 1 hour treatment with 10 μ M tunicamycin as compared to non-stressed conditions.

Table S1: Quantitative PCR confirmation of select microarray analyses of induced and repressed gene transcripts in response to ER stress.

Gene ID	Function	Microarray	qPCR
ENHANCED			
TGME49_077230	Calreticulin-family member domain	3.44	11.37
TGME49_017160	Derlin-1	6.97	13.63
TGME49_095670	E3 ligase	2.8	4.74
TGME49_014170	RAB geranylgeranyl transferase	4.14	3.28
REPRESSED			
TGME49_226930	hypothetical protein	-2.91	-2.15
TGME49_268560	RAD2 endonuclease-related	-4.45	-3.11
TGME49_218590	protein phosphatase 2C, putative	-3.23	-2.44
TGME49_268830	hypothetical protein	-2.6	-1.89

Four enhanced or repressed genes were examined following exposure to tunicamycin. In each case, the trend in gene expression as measured by qPCR was similar to that reported in the microarray data.

Table S2: Quantitative PCR confirmation of select microarray analyses of induced and repressed polysomal RNA association in response to ER stress.

Product	ToxoDB Version 5 ID	Microarray	qPCR
ENHANCED			
AP2X-9	TGME49_015150	23%	9 ± 0.4%
AP2IV-5	TGME49_011720	49%	31 ± 1.2%
AP2VIIb-3	TGME49_055220	25%	12 ± 0.7%
AP2XII-4	TGME49_047700	20%	18 ± 0.7%
TgGCN5-B	TGME49_043440	33%	37 ± 0.9%
TgGCN1	TGME49_031480	30%	26 ± 1.5%
REPRESSED			
TgDHFR-TS	TGME49_049180	-23%	-11 ± 0.8%
Protein Phosphatase Inhibitor 2	TGME49_032760	-31%	-21 ± .6%
N-term Cyclin	TGME49_066900	-30%	-29 ± 1.1%

Changes in mRNA association with polysomes were measured by qPCR for 6 enhanced and 3 repressed genes following exposure to tunicamycin. In each case, the microarray and qPCR data showed similar trends.

Table S3: Primers used for quantitative PCR

Primer sequence (5' to 3')	Primer name	Use
GAGGCCGACGACCTAGAAGA	Calreticulin qF	measure changes in transcript levels
AACCCACTGCGTCTCTAAAGAAA	Calreticulin qF	measure changes in transcript levels
ATCTTTGGCGTCGGTTCGTA	Derlin 1 qF	measure changes in transcript levels
ACAAACGCGTACTCGGATTCC	Derlin 1 qR	measure changes in transcript levels
CGACGGTGGAAAGTCGGTAGA	E3 ligase prot qF	measure changes in transcript levels
CAAGGGTGGCCACAGAAGAA	E3 ligase prot qR	measure changes in transcript levels
GCACTCGAGCCTTCTTGCA	geranylgeranyl transferase qF	measure changes in transcript levels
CGTTTGTTGTCGAGAGAGATTG	geranylgeranyl transferase qR	measure changes in transcript levels
AAAGTCGAGAGGATGGGAGTTG	hypothetical_226930 qF	measure changes in transcript levels
AAGCCCCAGAAGCTTTTTTCG	hypothetical_226930 qR	measure changes in transcript levels
GCCTCCGGTACTCAGATCA	RAD2 endonuclease qF	measure changes in transcript levels
GGTCGGACTCATCGGCATAT	RAD2 endonuclease qR	measure changes in transcript levels
GCGACGGAGTCTGGGACTT	Protein phosphatase 2C qF	measure changes in transcript levels
GCACGAGCTGCTCTGTCTT	Protein phosphatase 2C qR	measure changes in transcript levels
AGTTCGGTTCGGTCGTTTGT	hypothetical_268830 qF	measure changes in transcript levels
CTTGCGTCCCGTTTAAAG	hypothetical_268830 qR	measure changes in transcript levels
GTGCTCGTTACCCGCTGAGT	AP2X-9 qF	measure changes in translation efficiency
GGAAACCTTGCGGAGTATCG	AP2X-9 qR	measure changes in translation efficiency
CGAAGCACGACAGTGAAGCA	AP2IV-5 qF	measure changes in translation efficiency
AGGGATCGTGGCTGTGTTTC	AP2IV-5 qR	measure changes in translation efficiency
AGCGTTTTCTGCAAGTATCG	AP2Viiib-3 qF	measure changes in translation efficiency
TCGTTGTTGGTCGGCACAT	AP2Viiib-3 qR	measure changes in translation efficiency
CTGCACCCGTTCTGTAAAGGA	AP2XII-4 qR	measure changes in translation efficiency
AACACCACCACTCGCATCTG	AP2XII-4 qF	measure changes in translation efficiency
ACGAAGTTCAGTTGATGTTCAAGAA	GCN5-B qR	measure changes in translation efficiency
GTTACGGAACTTGCCAGCTCGTT	GCN5-B qF	measure changes in translation efficiency
ATGCGATCTGGCGTCTTTGT	GCN1 qF	measure changes in translation efficiency
CCGAAACGCGAAGAGCATAG	GCN1 qR	measure changes in translation efficiency
GAGACCGTTCCCATTTGTGA	DHFR qF	measure changes in translation efficiency
CGTAGCCACGACCTCAAAA	DHFR qR	measure changes in translation efficiency
ATGTGGAGACGGCAGTTTCC	Protein Phosphatase Inhib 2 qF	measure changes in translation efficiency
CAAGAGAGCTCCGAAAATCG	Protein Phosphatase Inhib 2 qR	measure changes in translation efficiency
ACTGGAAGGCCGAGACAATG	N-term cyclin qR	measure changes in translation efficiency
TGCGTGGGAGCTGAAAGAA	N-term cyclin qF	measure changes in translation efficiency
GGAGTTTTCGGCATTGTTA	RNA Spike qF	normalize data
GCATTTTCTTTCACAGCTTCGA	RNA Spike qR	normalize data

List of primers used to confirm the fidelity of the microarray analysis.