

A unity of opposites in between Nrf1- and Nrf2-mediated responses to the endoplasmic reticulum stressor tunicamycin

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Supplementary tables:

Table S1. ARE and AP1-binding sites in -5 kbp to TSS and also to TIS of ER-stress gene promoters

Gene ID	Name	ARE/EpRE (5'-TGAC/GnnnGC-3')	TRE/AP1 site (5'-TGAC/GTCA-3')
3309	BIP/GRP78	TGGC GCAATCTCAGCTC (-4344 to -4328) ATTT TGACCAGGCTGGT (-3811 to -3795) TGGT GCGATCTCAGCTC (-2848 to -2832) TAAG TGACTGTGCTTTG (-2480 to -2464) GAGC TGAGATTGCACTA (-1339 to -1323)	CTCT TGAGTCA CCAG (-2104 to -2090) GTACT TGAGTCA CAGG (-2048 to -2034)
9451	PERK	GGTT TGAGTTCGCTCAT (-2728 to -2712) TCTAG CAAAC TCATATA (-1844 to -1828) GCGT GCCAGGTCAGAGT (-719 to -703) CCAAT TGAGAGAGCAAAC (+60 to +76)	
2081	IRE1	ACCC GCCACCTCAGCCT (-4079 to -4063) TGAG TGACTTGGCCGTG (-692 to -676) AGTCT TGACGCGGCAGGT (-370 to -354) TGAG GCTCGGTCA CCGC (+26 to +42)	
22926	ATF6	TCTT GCTCTGTCA CCCA (-3459 to -3443) GAGCT TGAGATGGCTCCA (-2054 to -2038) GTTCT TGAGATAGCCACG (-343 to -327)	
1649	CHOP	CACAG CTTGGTCA TGTC (-4521 to -4505) AAGGG CTACCTCAGTCA (-4384 to -4368) AGGC GCCCTGTCA CCCA (-2780 to -2764) TCTC GCTCTGTCA CCCA (-935 to -919) AAGCT TGAGTTGGCCAGG (+2219 to +2235)	CGCAT TGACTCA CCCA (-242 to -228)
7494	XBP1	TCCC TGACCGAGCTGGT (-4419 to -4403) CACT GCAGCCTCAATCT (-4205 to -4189) CTCAG CCTCCTCAGTAG (-3987 to -3971) ATGT TGACCAGGCTGGT (-3901 to -3885) CTGT TGACCAGGCTGGA (-2943 to -2927) CTGG TGACAGAGCCTGA (-869 to -853) AAAT GCACGCTCATAGT (-701 to -685)	GGCAT TGAGTCA CCGT (-4306 to -4292)
468	ATF4	CTGC TGAGATTGCAGTA (-4933 to -4917) ATCT TGAGAGAGCTCAT (-4449 to -4433) ACCA TGACTGGGCAAGC (-3612 to -3596) TTGC TGACTGTGCTCCC (-3105 to -3089) GGACT TGACTTGGCTGAG (-2940 to -2924) ATTT GCACAGTCATCTG (-2230 to -2214) CCTC TGAGGCAGCAGGA (-1788 to -1773) CCAT GCAGACTCAGCCG (-893 to -877)	GGCG TGAGTCA AGGG (+513 to +527)

Note: TSS, transcriptional start signal and TIS, translation initiation signal.

Table S2. The primer pairs used for qRT-PCR analysis

Name	Forward primer (5' to 3')	Reverse primer (5' to 3')
β-actin	CATGTACGTTGCTATCCAGGC	CTCCTTAATGTCACGCACGAT
Nrf1	GCTGGACACCATCCTGAATC	CCTTCTGCTTCATCTGTGCG
Nrf2	TCAGCGACGGAAAGAGTATGA	CCACTGGTTTCTGACTGGATGT
GCLM	GTGTGATGCCACCAGATTTGAC	CACAATGACCGAATACCGCAGT
HO-1	CAGAGCCTGGAAGACACCCTAA	AAACCACCCCAACCCTGCTAT
Chop	GGAAACAGAGTGGTCATTCCC	CTGCTTGAGCCGTTCAATTCTC
Bip	GAACGTCTGATTGGCGATGC	ACCACCTTGAACGGCAAGAA
ATF6	AGCAGCACCCAAGACTCAAAC	GCATAAGCGTTGGTACTGTCTGA
ATF4	CCCTTCACCTTCTTACAACCTC	TGCCCAGCTCTAAACTAAAGGA
XBP1	CCCTCCAGAACATCTCCCCAT	ACATGACTGGGTCCAAGTTGT
IRE1	GAGACCCTGCGCTATCTGAC	CTTGGCCTCTGTCTCCTTGG
PERK	CTTCCAGTGGGACCAAGACC	CGAGGTCCGACAGCTCTAAC
PSMB6	TCAAGAAGGAGGGCAGGTGT	GTAAGTGGCAACGGCGAA
PSMA1	ATTCATCAAATTGAATATGCAAT	CTCTGATTGCGCCCTTTTCAA
PSMA4	TTGCTGTACATTGGCTGGGA	ACACAGCTGCAGCGCTATTA
PSMA7	TACATCACCCGCTACATCGC	AGAGCCTAGGAGTGCCATCA
PSMB7	CTGTGTGCGGTGTATGCTCCA	TGCCAGTTTTCCGGACCTTT
PSMC1	ACAAGGTGCATGCCGTGATA	CTGTGCCAGGTGGACCATAG