

Table S1.

<u>ER Stress and ER homeostasis</u>		
<u>Gene ID</u>	<u>Function</u>	<u>SKN-1 target study</u>
<i>abu-8</i>	alternative unfolded protein response [51]	this study
<i>abu-11</i>	alternative unfolded protein response [51]	this study
<i>acl-4</i>	Phospholipid biosynthesis gene, ER stress upregulated [8]	ChIP [34]
<i>arf-1.1</i>	GTP-binding ADP-ribosylation factor, ER stress upregulated [51]	ChIP [34]
<i>atf-5</i>	ER and oxidative stress transcription factor ATF4 [8,15]	ChIP [34], microarray [21]
<i>atf-6</i>	ER transcription factor [8]	ChIP [34]
<i>B0348.2</i>	LPS-induced tumor necrosis factor alpha factor, integral to membrane [8]	microarray [21]
<i>C47E12.3</i>	putative EDEM factor (ERAD) [8]	ChIP (operon) [34]
<i>cdc-48.2</i>	ERAD ATPase, p97 [8]	ChIP [34]
<i>cdr-4</i>	membrane bound gst, ER stress upregulated [8,51]	ChIP [34]
<i>cebp-2</i>	C48E7.11, putative C/EBP β , ER stress regulated [81]	ChIP [34]
<i>cept-1</i>	PtdCho synthesis, ER membrane integrity [80,88]	ChIP [34]
<i>cka-1</i>	PtdCho synthesis, ER membrane integrity [80,88]	ChIP [34]
<i>ckb-4</i>	PtdCho synthesis, up with ER stress [8] and oxidative [21], ER membrane integrity [80,88]	ChIP [34], microarray [21]
<i>cnb-1</i>	calcineurin, UPR [64], interacts with PERK [65], not predicted to increase with ER stress [8]	ChIP [34]
<i>crt-1</i>	calreticulin, mataintenance of ER [66], up with ER stress (this study)	ChIP [34]
<i>dnj-28</i>	ER chaperone, regulated with ER stress [8]	ChIP [34]
<i>E04D5.1</i>	putative eIF2 α (Wormbase), PERK phosphorylation target during ER stress [89]	ChIP [34]
<i>erd-2</i>	putative ER lumen protein retaining receptor similar to yeast <i>erd2</i> [67]	ChIP [34], microarray [21]
<i>ero-1</i>	ER oxidoreductase, upregulated with ER stress [8,15]	ChIP [34]
<i>F41B4.3</i>	Membrane bound, ER stress upregulated [51]	ChIP [34]
<i>F42G8.8</i>	putative serine/threonine specific PP1 [68] (by homology, Wormbase)	microarray [21]
<i>F47A4.5</i>	Phospholipase, ER stress upregulated [8]	ChIP [34]

<i>F55E10.6</i>	putative corticosteroid beta-dehydrogenase (by homology, Wormbase), most likely resides in ER [82]	microarray [21]
<i>fzo-1</i>	Mito/ER connector (Mfn1/Mfn2) essential for mitochondrial-associated membrane (MAM) formation [70]	ChIP [34]
<i>hsp-16.11</i>	chaperone, ER stress upregulated [51]	ChIP [34]
<i>hsp-16.2</i>	chaperone, ER stress upregulated [51]	ChIP [34]
<i>hsp-16.41</i>	chaperone, ER stress upregulated [51]	ChIP [34]
<i>hsp-3</i>	ER chaperone, BiP homolog, upregulated with ER stress [8,51]	ChIP [34]
<i>hsp-4</i>	ER chaperone, BiP homolog, upregulated with ER stress [8,51,90]	this study
<i>ire-1</i>	ER signaling factor [90]	ChIP [34]
<i>larp-1</i>	homologous to La protein, stabilizes yeast Hac1(<i>xbp-1</i>) transcript [71]	ChIP [34]
<i>larp-5</i>	homologous to La protein, stabilizes yeast Hac1 (<i>xbp-1</i>) transcript [71]	ChIP [34]
<i>lgg-1</i>	homologous to LC3/Atg8, regulated by ER stress factor ATF4 [72]	ChIP [34]
<i>lgg-3</i>	homologous to ATG12, regulated by ATF4 during ER stress [73]	ChIP [34]
<i>lin-15B</i>	negatively regulates G1 progression, ER stress upregulated [51]	ChIP [34]
<i>lpd-2</i>	regulates <i>lpd</i> genes, modulates ER stress [74,83]	ChIP (operon) [34]
<i>memb-2</i>	Sec22 SNARE protein, ER stress upregulated [8]	ChIP [34]
<i>pcp-2</i>	Prolyl Carboxy Peptidase like, IRE-1 dependent [8], up with oxidative stress	microarray [21]
<i>pcyt-1</i>	CCT enzyme for PtdCho synthesis, ER membrane integrity [80,88]	ChIP [34]
<i>pdi-2</i>	ER Protein disulfide isomerase, upregulated with ER stress [8,51]	ChIP [34]
<i>pdi-3</i>	ER protein disulfide isomerase [75]	ChIP [34]
<i>pek-1</i>	ER signaling factor, kinase [8]	ChIP [34]
<i>psd-1</i>	flow of phospholipid mito to ER, MAM associated [76]	ChIP [34]
<i>R05G6.7</i>	VDAC, MAM associated [52], not predicted to increase with ER stress [8]	ChIP [34]
<i>R12E2.13</i>	Mannosyltransferase, upregulated with ER stress [8]	ChIP [34]
<i>sca-1</i>	SERCA, calcium homeostasis, upregulated with ER stress [8]	ChIP [34]
<i>sec-22</i>	Sec22 SNARE protein, ER stress upregulated [8]	ChIP [34]
<i>sel-1</i>	HMG-CoA Reductase, ERAD complex, upregulated with ER stress [8]	ChIP [34]

<i>skn-1</i>	ER stress factor, up with ER stress (this study, [8])	ChIP [34]
<i>T05E11.3</i>	HSP90 chaperone [66], up with ER stress (this study)	ChIP [34]
<i>T14G8.3</i>	HSP70-like ER resident, ER stress upregulated [51]	ChIP [34]
<i>tag-320</i>	cell redox homeostasis, thioredoxin, ER stress upregulated [51]	ChIP [34]
<i>vha-13</i>	vacuolar proton-translocating ATPase (V-ATPase), regulated by calcineurin/calreticulin [77]	ChIP [34], microarray [21]
<i>xbp-1</i>	ER transcription factor, up with ER stress (this study, [90])	ChIP [34]
<i>Y40B10A.2</i>	O-methyltransferase, ER stress upregulated [51]	ChIP [34]
<i>Y41C4A.11</i>	Similar to COPI, WD repeat family, ER stress upregulated [8,51]	ChIP [34], microarray [21]
<i>Y51B9A.9</i>	putative MAPK9 like kinase (JNK pathway, by homology, Wormbase) [84]	microarray [21]

Endobiotic and Xenobiotic metabolism, predicted to be ER-localized

<u>Gene ID</u>	<u>Function</u>	<u>SKN-1 target study</u>
<i>C35D10.10</i>	putative TMX thioredoxin-like protein, ER Golgi transport, MAM (by homology, Wormbase) [78]	microarray [21]
<i>C46H11.2</i>	Flavin-containing monooxygenase, most likely ER localized [55]	microarray [21]
<i>cyp-13A1</i>	cytochrome p450, most likely ER localized [55]	ChIP [34]
<i>cyp-13B1</i>	cytochrome p450, most likely ER localized [55]	microarray [21]
<i>cyp-14A1</i>	cytochrome p450, most likely ER localized [55]	microarray [21]
<i>cyp-25A4</i>	cytochrome p450, most likely ER localized [55]	ChIP [34]
<i>cyp-33C4</i>	cytochrome p450, most likely ER localized [55]	ChIP [34]
<i>cyp-33C7</i>	cytochrome p450, most likely ER localized [55]	ChIP [34]
<i>cyp-33C8</i>	cytochrome p450, most likely ER localized [55]	ChIP [34]
<i>cyp-43A1</i>	cytochrome p450, most likely ER localized [55]	ChIP [34]
<i>F17A9.4</i>	potential NADH oxidase, predicted SR localized [85,86]	ChIP [34], microarray [21]
<i>F17A9.5</i>	potential NADH oxidase, predicted SR localized [85,86]	microarray [21]
<i>F56D5.3</i>	potential NADH oxidase, predicted SR localized [85,86]	microarray [21]
<i>hpo-19</i>	NADH-cytochrome b-5 reductase, integral to membrane, predicted ER localized [87]	ChIP (operon) [34], microarray [21]
<i>K04A8.10</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	microarray [21]

<i>ugt-1</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	microarray [21]
<i>ugt-11</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34]
<i>ugt-13</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34]
<i>ugt-16</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	microarray [21]
<i>ugt-20</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34]
<i>ugt-22</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34], microarray [21]
<i>ugt-23</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	microarray [21]
<i>ugt-31</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34], microarray [21]
<i>ugt-46</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	microarray [21]
<i>ugt-48</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	microarray [21]
<i>ugt-58</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34], microarray [21]
<i>ugt-64</i>	UDP-Glucuronosyl Transferase, ER lumen [79]	ChIP [34]
ZK742.4	potential NADH oxidase, predicted SR localized [85,86]	ChIP [34], microarray [21]