Supplementary Table S2. Differentially Expressed Genes with Response to Stress Activity

M60.2	1.68	M60.2
hsp-17	1.66	Heat Shock Protein
his-10	1.60	HIStone
pqm-1	1.53	ParaQuat (Methylviologen) responsive
lea-1	1.43	Plant late embryo abundant (LEA) related
skr-3	1.41	SKp1 Related (ubiquitin ligase complex component)
skr-3	1.36	SKp1 Related (ubiquitin ligase complex component)
his-37	1.31	HIStone
catalase	1.41	Y54G11A.13
ftn-1	1.41	FerriTiN
mtl-1	1.27	MeTaLlothionein
mtl-2	1.27	MeTaLlothionein
coq-3	1.26	COenzyme Q (ubiquinone) biosynthesis
sod-4	1.20	SOD (superoxide dismutase)
gst-5	1.20	Glutathione S-Transferase
mev-1	1.16	Succinate dehydrogenase cytochrome b chain
gst-4	1.15	Glutathione S-Transferase
R05H10	1.10	Glutathione peroxidases
gcs-1	−1.45	Gamma GlutamylCysteine Synthetase
daf-18	−1.47	abnormal DAuer Formation
mpk-1	−1.48	MAP Kinase
mre-11	−1.49	Human MRE11 protein like
dnj-8	−1.5	DNaJ domain (prokaryotic heat shock protein)
F23C8.9	−1.5	F23C8.9
thn-1	−1.56	Arabidopsis pathogenesis-related protein 5 like
F08F8.4	−1.77	F08F8.4
gst-10	−2.03	Glutathione S-Transferase
clk-1	−1.17	CLocK (biological timing) abnormality
coq-1	−1.23	COenzyme Q (ubiquinone) biosynthesis
coq-2	−1.31	COenzyme Q (ubiquinone) biosynthesis

Microarray data showing significantly ($p < 0.05$) changed genes in GO class representing response to stress from GYY4137-exposed (100 μM) *C. elegans*.