Curated Genes with the Greatest Up or Down Regulation

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
aagr-2	R05F9.12			1.63		Upregulated with infection of three bacterial pathogens (Serratia marcescens, Enterococcus faecalis and otorhabdus luminescens), and Harposporium(Engelmann et al., 2011). Exhibits alpha-1,4-glucosidase activity. Is involved in glycogen catabolic process. Human ortholog(s) of this gene are implicated in congenital sucrase-isomaltase deficiency and glycogen storage disease II. Is an ortholog of human MGAM (maltase-glucoamylase). Affected by >15 chemicals. GO Terms: carbohydrate binding, lysosome, membrane, metabolic process (WormBase, 2021).
aak-1	PAR2.3				1.51	Up 2.17X with 7.5uM meHgCl exposure (McElwee et al., 2013). aak-1 activity is required, in parallel with aak-2 and downstream of daf-2, daf-7, and par-4, for negative regulation of germline proliferation during dauer development. Predicted to localize to cytoplasm and nucleus. Human ortholog(s) of this gene implicated in Huntington's disease; breast cancer; colon cancer; and type 2 diabetes mellitus. Orthologous to human PRKAA1 and PRKAA2. GO Terms: ATP Binding, nucleus, cytoplasm, phosphorylation, transferase activity (Wormbase, 2021). Transgenerational Reproductive Defects Arise in Post-L1 Diapause AMPK/aak-1/aak-2 Mutants. H3K4me3 Levels Are Abnormally High in the PGCs of Post-L1 Diapause AMPK/aak-1/aak-2 Mutants (Demoinet et al., 2017). aak-1 and aak-2 affect paraquat sensitivity of adult *C. elegans* worms (Lee et al., 2008). AMPK catalytic subunit (*aak-1*) (Narbonne and Roy, 2009). there are two α isoforms of AMP-activated protein kinase in C. elegans, AAK-1 and AAK-2 (Kuo et al., 2020).
aass-1	R02D3.1			1.63		Is predicted to have oxidoreductase activity. Is expressed in gonadal sheath cell and hypodermal cell. Human ortholog(s) of this gene are implicated in hyperlysinemia. Is an ortholog of human AASS (aminoadipate-semialdehyde synthase). Affected by eleven chemicals. GO Terms: cytoplasm, catalytic activity, metabolic process, oxidoreductase activity, saccaropine dehydrogenase (Wormbase, 2021).
abf-2	C50F2.10	-2.01				*abf-2* is expressed in excretory cell, marginal cell, and pharyngeal neurons, affected by 13 chemicals, involved in defense response to Gram-negative and Gram-positive bacteria (Wormbase, 2021). Down with *P. aeruginosa* (Evans et al., 2008). Up 1.8x w *M. nematophilum* (O'Rourke et al., 2006). "*abf-2*, was previously shown to have *in vitro* activity against the pathogenic fungus *Candida krusei*" (Pukkila-Worley et al., 2011).
abhd-11.1	F32B4.6	-2.21				*abhd-11.1* is enriched in male, affected by 6 chemicals, a close homolog of human ABHD11 and is predicted to have hydrolase activity, GO Term: mitochondrion (Wormbase, 2021).

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abtm-1	Y74C10AR.3			1.58		Is predicted to have ATP binding activity; ATPase activity; and ATPase-coupled transmembrane transporter activity. Is involved in cellular iron ion homeostasis. Localizes to mitochondrion. Is expressed in coelomocyte; hypodermis; intestine; and spermatheca. Is used to study X-linked sideroblastic anemia with ataxia. Human ortholog(s) of this gene are implicated in X-linked sideroblastic anemia with ataxia. Is an ortholog of human ABCB7 (ATP binding cassette subfamily B member 7). Affected by paraquat and antimycin. GO Terms: ATP binding, integral component of membrane, mitochondrion (Wormbase, 2021). Disruption of the ATP-binding Cassette B7 (ABTM-1/ABCB7) Induces Oxidative Stress and Premature Cell Death in Caenorhabditis elegans (González-Cabo et al., 2011). worms with downregulated levels of abtm-1 by RNAi are viable, although have increased oxidative stress and ferric iron accumulation (Mora-Lorca et al., 2016).
acd-1	C24G7.2		2.56			*acd-1* is expressed in AMshL and AMshR neurons, affected by > 10 chemicals, predicted to have sodium channel activity, involved in response to acidic pH and sodium ion transport, close human homologs ASIC1, ASIC2, and ASIC4 are implicated in autosomal recessive pseudohypoaldosteronism type 1 and bronchiectasis 3, GO terms: integral component of plasma membrane, sodium ion transport, response to acidic pH (Wormbase, 2021). Down 30% w *M. nematophilum* in Ce (O'Rourke et al., 2006). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Down 1.7x w NaAsO2 (this study).
acd-2	C24G7.4		1.85			*acd-2* is enriched in germ line and hypodermis, affected by 10 chemicals, predicted to have sodium channel activity, a close homolog of human ASIC1 and ASIC4, GO Terms: integral component of plasma membrane, ion transport, sodium ion transmembrane transport (Wormbase, 2021). Down 2.0x w meHgCl (McElwee et al., 2013).
acly-1	D1005.1			1.55		Up 2.5X with 24h Drechmeria coniospora infection (Pujol et al., 2008a). Is predicted to have ATP binding activity; ATP citrate synthase activity; and metal ion binding activity. Is an ortholog of human ACLY (ATP citrate lyase). Affected by >10 chemicals. GO Terms: ATP binding, acetyl-CoA biosynthetic process, cytoplasm, fatty acid biosynthetic process, lipid process, metal ion process, transferase activity (Wormbase, 2021). Expressed in the mitochondria (Zhu et al., 2020).
acp-3	F14E5.3				-2.12	Is enriched in AVK, amphid sheath cell, somatic gonad precursor, and in male based on RNA-seq studies. Is affected by ten chemicals including methylmercuric chloride, manganese chloride, and D-glucose based on microarray and RNA-seq studies. Human ACP4 exhibits protein tyrosine phosphatase activity and receptor tyrosine kinase binding activity. Is predicted to encode a protein with the following domains: Histidine phosphatase superfamily (branch 2), Histidine phosphatase superfamily, clade-2, and Histidine phosphatase superfamily. Is an ortholog of human ACP2 (acid phosphatase 2,

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						lysosomal), ACP3 (acid phosphatase 3), and ACP4 (acid phosphatase 4). GO Terms: integral component of membrane (Wormbase, 2021). Up 3X with 7.5uM meHgCl (McElwee et al., 2013).
adbp-2	T17A3.9			-2.31		Is affected by five chemicals including Psoralens, allantoin, and metformin based on RNA-seq studies (Wormbase, 2021).
adss-1	C37H5.6			1.84		Up 2.1X with meHgCl (McElwee et al., 2013). Is predicted to have GTP binding activity; adenylosuccinate synthase activity; and magnesium ion binding activity. Is expressed in several structures, including intestine; nervous system; non-striated muscle; pharynx; and reproductive system. Is an ortholog of human ADSS1 (adenylosuccinate synthase 1) and ADSS2 (adenylosuccinate synthase 2). GO Terms: AMP biosynthetic process, magnesium ion binding (Wormbase, 2021).
afd-1	W03F11.6			1.52		Down 0.5 with 12h D. Coniospora infection (Pujol et al., 2008a). Is enriched in AB; germ line; head mesodermal cell; mechanosensory neurons; and muscle cell based on microarray and RNA-seq studies. Is affected by twelve chemicals including rotenone; Cry5B; and Psoralens based on RNA-seq and microarray studies. Human AFDN exhibits Ras GTPase binding activity and actin filament binding activity. Is an ortholog of human AFDN. GO Terms: Cell adhesion, protein binding (Wormbase, 2021). Housekeeping gene.
alp-1	T11B7.4				-2.04	Is predicted to have metal ion binding activity. Is involved in determination of adult lifespan and pharyngeal pumping. Localizes to several cellular components, including actin filament bundle, basal part of cell, and striated muscle dense body. Is expressed in body wall musculature, hypodermis, marginal cell, and pharyngeal muscle cell. Is used to study cardiomyopathy and myopathy. Human ortholog(s) of this gene are implicated in dilated cardiomyopathy 1C, myofibrillar myopathy 4, and osteoporosis. Is an ortholog of human LDB3 (LIM domain binding 3). Affected by 15 chemicals. GO Terms: actin binding, cytoplasm, determination of adult lifespan, metal ion binding, nucleus, muscle structure development (Wormbase, 2021).
aqp-8	K02G10.7		2.25			*aqp-8* is enriched in cephalic sheath cell, coelomocyte, excretory cell, hypodermis, PVD, OLL and somatic gonad precursor, predicted to have channel activity, localizes to cell surface, expressed in excretory system; germ line; intestinal cell; non-striated muscle; and ray, close homolog of human AQP9, GO term: integral component of membrane (Wormbase, 2021). Up 1.6x w *M. nematophilum* in Ce (O'Rourke et al., 2006). Down ~25% w *D. coniospora* and *E. carotovora* in Ce (Pujol et al., 2008b; Wong et al., 2007). Up 5x w *S. aureus* in Ce (Irazoqui et al., 2010). Expressed in osmoregulatory tissues and involved in water transport, "*aqp-8* mRNA levels increase approximately eightfold during hypertonic

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						stress" (Huang et al., 2007). Up 1.7x w Ag+ (Hunt et al., 2014). Up w glucose, has two DAF-16 binding sites (Lee et al., 2009). Ethanol response gene (Kwon et al., 2004).
asp-14	K10C2.3	2.28	2.28			*asp-14* is enriched in intestine and head mesodermal cell, involved in innate immune response, affected by > 20 chemicals, predicted to have aspartic-type endopeptidase activity, a close homolog of human CTSE (cathepsin E), PGA3 (pepsinogen A3), and PGA4 (pepsinogen A4) (Wormbase, 2021). Up ~3x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 40% w *E. faecalis* in Ce (Wong et al., 2007). Upregulated by SKN-1 (Oliveira et al., 2009). Up 5x w *Y. pestis* and regulated by PMK-1/p38 MAPK in Ce (Bolz et al., 2010). K10C2.3 is a stress response gene regulated by "AAK-2, the *C. elegans* homolog of an alpha subunit of AMP-activated protein kinase (AMPK) is an intracellular fuel sensor that regulates cellular energy homeostasis and functions in stress resistance and lifespan extension" (Shin et al., 2011). Up 2x w 7.5µM HgCl2 in Ce (McElwee et al., 2013). Induced by NaAsO2 and paraquat in Ce (Sahu et al., 2013).
avr-14	B0207.12	2.04	2.56	1.59		*avr-14* is enriched in neurons and head mesodermal cell, affected by 7 chemicals, exhibits drug binding activity and extracellularly glutamate-gated chloride channel activity, involved in locomotory behavior, regulation of pharyngeal pumping, and response to drug, localizes to membrane, expressed in neurons and somatic nervous system, close human homologs GLRA3 and GLRA4 are implicated in hyperekplexia 2, GO terms: nervous system process, response to drug, integral component of plasma membrane, ion transmembrane transport, locomotion involved in locomotory behavior (Wormbase, 2021). Up 1.8x w *S. marcescens* in Ce (Wong et al., 2007).
bath-25	T27C10.4	-1.96				*bath-25* is affected by nine chemicals (Wormbase, 2021). Down 1.6x w DMA (this study).
bro-1	F56A3.5			-2.79		Down 2X with DMA in this study. Down 2.8X with 2uM meHgCl (McElwee et al., 2013). Upregulated with D. coniospora infection (Engelmann et al., 2011). Is predicted to have transcription coactivator activity. Is involved in nematode male tail tip morphogenesis and stem cell population maintenance. Localizes to nucleus. Is expressed in hypodermis; muscle cell; pharyngeal neurons; ray precursor cell; and uterine seam cell. Human ortholog(s) of this gene are implicated in acute myeloid leukemia. Is an ortholog of human CBFB. GO Terms: DNA binding, male tip morphogenesis, nucleus, Transcription coregulator activity. Affected by >10 chemicals (Wormbase, 2021).
bxc-41	C32B5.11				1.97	Affected by 9 chemicals. Is enriched in NSM; neurons; and ventral nerve cord based on tiling array and microarray studies (Wormbase, 2021). -1.6X with DMA in this study.
cbl-1	C12C8.2	2.06				*cbl-1* is enriched in PVD and OLL neurons and intestine, affected by > 15 chemicals, encodes a putative cystathionine gamma-lyase (Wormbase, 2021). Down 40% w *M. nematophilum* in Ce (O'Rourke et al., 2006). Down 30% w *P. luminescens* in Ce (Wong et

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						al., 2007). Down 2.6x w *S. aureus* in Ce (Irazoqui et al., 2010). Up w *Harposporium* + 3 bacterial species in Ce (Engelmann et al., 2011). Up 4.2x w NaAsO2 (Sahu et al., 2013). Down ~40% w Ag+ in Ce (Hunt et al., 2014). Up w acrylamide in Ce (Hasegawa et al., 2008). Upregulated by SKN-1 & needed for NaAsO2 resistance (Oliveira et al., 2009).
ccm-2	K07A9.3			-2.40		Is enriched in AVK, coelomocyte, head mesodermal cell, and intestine based on tiling array and RNA-seq studies. Is affected by seven chemicals including tryptophan, rotenone, and stavudine based on microarray and RNA-seq studies. Is predicted to encode a protein with the following domain: PH-like domain superfamily (Wormbase, 2021).
cct-7	T10B5.5			1.94		Is predicted to have ATP binding activity and unfolded protein binding activity. Is expressed in anchor cell; head; non-striated muscle; and tail. Is an ortholog of human CCT7 (chaperonin containing TCP1 subunit 7). CCT-7 is required for normal transgene repression and subcellular localization, embryonic and larval viability, fertility, vulval development, and normal locomotion. Affected by five chemicals (Wormbase, 2021).
cdk-9	H25P06.2			1.68		Is involved in several processes, including germ cell development; nematode larval development; and regulation of protein modification process. Localizes to chromosome. Is expressed in several structures, including germ line. Human ortholog(s) of this gene are implicated in congestive heart failure. Is an ortholog of human CDK9 (cyclin dependent kinase 9). GO Terms: nucleus, development, kinase activity, regulation of cell cycle, regulation of histone H3-K36 trimethylation (Wormbase, 2021).
cdr-1	F35E8.11		4.96			*cdr-1* is enriched in intestine, ASER and PLM neurons, affected by > 20 chemicals, involved in stress response to cadmium ion, localizes to lysosome in intestine (Liao et al., 2002), homolog of human FAXC, GO term: integral component of membrane, lysosome (Wormbase, 2021). "The Cd-responsive protein CDR-1 further improves Cd resistance, possibly by pumping Cd2+ into lysosomes" (Liao et al., 2002). Predicted direct target of DAF-16 and downregulated in *daf-16* mutants = upregulated by DAF-16 (McElwee et al., 2003). Upregulated by SKN-1 and arsenic (Oliveira et al., 2009). Up 2-3x w *P. aeruginosa* in Ce (Evans et al., 2008; Troemel et al., 2006). Up with 3 bacterial species in Ce (Engelmann et al., 2011). Up 73x w Cd in Ce (Cui et al., 2007). Up with Cd and high NaAsO2 in Ce (Sahu et al., 2013).
cec-2	C50A2.2	2.37				*cec-2* is enriched in neurons, germ line, male distal tip cell, and somatic gonad precursor, affected by eight chemicals (Wormbase, 2021).
ced-1	Y47H9C.4			1.55		Upregulated after Harposporium infection (Engelmann et al., 2011). Exhibits scavenger receptor activity. Is involved in several processes, including cytoskeleton organization; left/right axis specification; and phagocytosis. Localizes to several cellular components, including phagocytic cup; phagocytic vesicle membrane; on the plasma membrane,

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						engulfing pseudopodia, and nascent phagosomesand. Is expressed in body wall musculature; engulfing cell; hyp7 syncytium; and muscle cell. Human ortholog(s) of this gene are implicated in early-onset myopathy-areflexia-respiratory distress-dysphagia syndrome. Is an ortholog of human MEGF10 (multiple EGF like domains 10) (Wormbase, 2021). Unfolded protein response genes, regulated in a CED-1-dependent manner, are involved in the C. elegans immune response to live bacteria (Haskins et al., 2008). Induced by graphene oxide (Zhao et al., 2016). Induced by several aneugenic compounds (Prochloraz, Benfiocarb, Thiabendazole, TCMTB, Maneb, Parathion, Dicofol, Norflurazon, Triflumizide) (Allard et al., 2013). A subset of chromatin modifiers inhibit apoptosis (CED-1::GFP) in the heterogametic germ line (set-2, met-1, met-2, L4440) (Checchi and Engebrecht, 2011).
ceh-45	ZK993.1			-2.18		Is predicted to have DNA binding activity. Is expressed in pharynx and spermatheca. Is an ortholog of human GSC (goosecoid homeobox). Affected by twelve chemicals. GO Terms: DNA-binding transcription factor activity, nucleus, nuclear chromatin, RNA polymerase specific (Wormbase, 2021).
ceh-87	F34D6.2	-1.87				*ceh-87* is enriched in body wall muscle cell, affected by 6 chemicals, close homolog of human ZHX1, GO Terms: DNA-binding transcription repressor activity, negative regulation of transcription by RNA polymerase II, neuron differentiation, nucleus (Wormbase, 2021).
ces-1	F43G9.11		-3.42			*ces-1* is involved in negative regulation of programmed cell death and negative regulation of transcription by RNA polymerase II, exhibits RNA polymerase II regulatory region sequence-specific DNA binding activity, close homolog of human SCRT1 and SCRT2, GO Terms: negative regulation of transcription by RNA polymerase II, nucleus (Wormbase, 2021). *ces-1* regulates glutamatergic behaviors (spontaneous locomotion reversals and mechanosensory nose-touch response) independently of cell death regulation (Park et al., 2021). Down 2x w 20µM HgCl2 and down 5x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
ces-2	ZK909.4		-3.45			*ces-2* is expressed in excretory duct cell, involved in apoptotic process and positive regulation of programmed cell death, exhibits RNA polymerase II regulatory region DNA binding activity and sequence-specific double-stranded DNA binding activity, used to study acute lymphoblastic leukemia, close homolog of human DBP and TEF, GO Terms: regulation of transcription, DNA-templated, nucleus (Wormbase, 2021). Down 3.8x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
cfi-1	T23D8.8		2.13			CFI-1 exhibits sequence-specific DNA binding activity, enriched in neurons, affected by 6 chemicals, involved in cell fate commitment; neuron differentiation; and regulation of transcription by RNA polymerase II, localizes to nucleus, expressed in ganglia; head

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						muscle; neurons; and pharyngeal muscle cell, close homolog of human ARID3A and ARID3C, GO Terms: negative regulation of transcription by RNA polymerase II, nucleus, cell fate commitment, sequence-specific DNA binding (Wormbase, 2021). Up 1.7x w NaAsO2 (this study).
chaf-2	Y71G12B.1				1.58	Is enriched in several structures, including Z4.a; germ line; head mesodermal cell; intestine; and male distal tip cell based on RNA-seq studies. Is affected by several genes including daf-16; age-1; and daf-12 based on microarray and RNA-seq studies. Is affected by four chemicals including Alovudine; stavudine; and Zidovudine based on RNA-seq and microarray studies. Is predicted to have histone binding activity. Human ortholog(s) of this gene are implicated in several diseases, including glioblastoma; oral squamous cell carcinoma; and skin melanoma. Is an ortholog of human CHAF1B (chromatin assembly factor 1 subunit B). GO Terms: Nucleus (Wormbase, 2021).
cit-1.2	F44B9.3			1.85		Is predicted to have cyclin-dependent protein serine/threonine kinase regulator activity. Is involved in embryo development and regulation of phosphorylation of RNA polymerase II C-terminal domain. Localizes to nucleus. Is expressed in several structures, including intestine, pharynx, and head. Is an ortholog of human CCNT1 (cyclin T1). Affected by four chemicals. GO Terms: embryo development, nucleus, regulation of transcription, cycle-dependent protein serine/threonine kinase activator activity (Wormbase, 2021). H2O2 affected the transcription process cit-1.2 (Aan et al 2019)
clec-105	Y18D10A.24		2.20			*clec-105* is enriched in NSM neurons, predicted to have carbohydrate binding activity (Wormbase, 2021).
clec-143	ZK673.9	2.76				*clec-143* is enriched in intestine, affected by > 15 chemicals, predicted to have carbohydrate binding activity (Wormbase, 2021). Up 10x w NaAsO2 in Ce (Sahu et al., 2013). Up 4x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up w *Harposporium* + 3 bacterial species in Ce (Engelmann et al., 2011). Up 2x w 2µM meHg in Ce (McElwee et al., 2013). Upregulated by SKN-1 (Oliveira et al., 2009).
clec-154	F10F2.5				1.65	Up 7.9X with 7.5uM meHgCl (McElwee et al., 2013). Is enriched in germline and in male based on RNA-seq studies. Is affected by several genes including daf-2; eat-2; and pgl-1 based on RNA-seq and microarray studies. Is affected by five chemicals including methylmercuric chloride; allantoin; and Sirolimus based on microarray and RNA-seq studies (Wormbase, 2021).
clec-162	C07A9.1	-2.25				*clec-162* is enriched in neuronal support cells, affected by 5 chemicals, predicted to have carbohydrate binding activity, GO Terms: extracellular region, carbohydrate binding, signaling receptor activity (Wormbase, 2021). Down 2.7x w DMA in Ce (this study).

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clec-168	F38A1.7		-3.52		-2.29	*clec-168* is affected by 3 chemicals, predicted to have carbohydrate binding activity (Wormbase, 2021). Down 2.3x w meHgCl in Ce (this study).
clec-169	F38A1.14		-6.46		-4.00	*clec-169* is enriched in intestine, Z4 and Z1, affected by 20 chemicals, predicted to have carbohydrate binding activity (Wormbase, 2021). Down 6x w 7.5µM meHg in Ce (McElwee et al., 2013).
clec-193					1.54	Is predicted to have carbohydrate binding activity. Affected by 7 chemicals (Wormbase, 2021). C-type lectin (clec-193) was upregulated at 48 Fusarium hpi (hours post infection) (Nag et al., 2017).
clec-196	F26D10.12		-3.29			*clec-196* is predicted to have carbohydrate binding activity, close homolog of human KLRF2 (killer cell lectin like receptor F2) (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Down 12x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
clec-2	B0454.7	7.11	3.77			*clec-2* is predicted to have carbohydrate binding activity, affected by 20 chemicals (Wormbase, 2021). Up 17x w NaAsO2 in Ce (Sahu et al., 2013). Up 7x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up w HgCl2 and meHg in Ce (McElwee et al., 2013). Down 35% w Ag+ in Ce (Hunt et al., 2014).
clec-230	C29F3.5		-4.68			*clec-230* is enriched in germline precursor cell, hypodermis and pharyngeal muscle cell, affected by > 20 chemicals, predicted to have carbohydrate binding activity (Wormbase, 2021). Down 24% w *M. nematophilum* in Ce (O'Rourke et al., 2006). Down 26% w *P. luminescens* in Ce (Wong et al., 2007). Up w *D. coniospora* in Ce (Engelmann et al., 2011).
clec-236	Y70C5C.5	-2.36				*clec-236* pseudogene is enriched in NSM neurons and in male, affected by daf-2; hsf-1; and clk-1 affected by eleven chemicals (Wormbase, 2021). Up 6.4x w 7.5µM meHgCl in Ce (McElwee et al., 2013).
clec-249	Y51A2A.7	-1.98				*clec-249* is predicted to have carbohydrate binding activity (Wormbase, 2021).
clec-3	C41H7.7	9.91	5.81			*clec-3* is enriched in intestine, affected by >20 chemicals, predicted to have carbohydrate binding activity (Wormbase, 2021). Up w *P. aeruginosa* (Evans et al., 2008; Muir and Tan, 2008; Troemel et al., 2006). Up with Harposporum in Ce (Engelmann et al., 2011). Up 42x w NaAsO2 (Sahu et al., 2013).
clec-34					1.87	Down 1.5X with NaAsO2 in this study. Affected by 5 chemicals. GO Terms: Carbohydrate binding, integral component of membrane (Wormbase, 2021).
clec-42	F16H6.1		-3.74			*clec-42* is expressed in neurons, enriched in PVD, OLL, intestine, head mesodermal cell and male-specific anatomical entity, affected by > 15 chemicals, predicted to have carbohydrate binding activity (Wormbase, 2021). Ethanol response gene (Kwon et al., 2004). Up 1.8x w *M. nematophilum* in Ce (O'Rourke et al., 2006). Up w three bacterial species in Ce (Engelmann et al., 2011).

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clec-60	ZK666.6	-2.21				*clec-60* is expressed in intestine, enriched in PVD and OLL neurons, affected by > 20 chemicals, GO Term: defense response to Gram-positive bacterium (Wormbase, 2021). Down ~2-3x w 3 concentrations of meHgCl in Ce (McElwee et al., 2013). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Up 6.6x w *M. nematophilum* (O'Rourke et al., 2006). Up 8.3x w *S. aureus* in Ce (Irazoqui et al., 2010). Down w Ag+ and AgNP in Ce (Hunt et al., 2014). Downregulated by SKN-1 under normal conditions (Oliveira et al., 2009). Down 2.2x w DMA in Ce (this study).
clec-70	Y46C8AL.3		-8.61		-5.64	*clec-70* is enriched in intestine, affected by > 20 chemicals, involved in defense response to Gram-positive bacterium, predicted to have carbohydrate binding activity (Wormbase, 2021). Up 4.4x w *M. nematophilum* in Ce (O'Rourke et al., 2006). Up 4.3x w *S. aureus* in Ce (Irazoqui et al., 2010). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up w cadmium and w high NaAsO2 in Ce (Sahu et al., 2013). Up 5.8x w 7.5µM HgCl2 in Ce (McElwee, 2010). Down 5.6x w meHgCl (this study).
clec-77	Y46C8AR.3				2.32	Is affected by twelve chemicals including Tunicamycin; multi-walled carbon nanotube; and Psoralens based on microarray and RNA-seq studies (Wormbase, 2021).
clh-3	E04F6.11			1.67		Is predicted to have voltage-gated chloride channel activity. Localizes to plasma membrane. Is expressed in egg-laying apparatus; epithelial cell; excretory cell; intestine; and muscle cell. Human ortholog(s) of this gene are implicated in several diseases, including Bartter disease (multiple); idiopathic generalized epilepsy 11; and myotonia congenita. Is an ortholog of human CLCN2 (chloride voltage-gated channel 2). Affected by nine chemicals. GO Terms: chloride transmembrane transport, integral component of membrane, ion transport, plasma membrane (Wormbase, 2021). A mutation in a CLC anion channel alters serotonergic neuronal activity in *C. elegans* (Branicky et al., 2012).
clpp-1	ZK970.2	-1.82				*clpp-1* is enriched in intestine, body wall muscle cell, germline precursor cell, ASER, germ line and somatic gonad precursor, affected by 5 chemicals, localizes to mitochondrial matrix, close homolog human CLPP is implicated in Perrault syndrome, GO Terms: mitochondrial matrix, mitochondrial unfolded protein response, mitochondrion, protein quality control for misfolded or incompletely synthesized proteins, proteolysis (Wormbase, 2021). X
cnc-9	R13D7.11		2.10		-2.07	*cnc-9* is enriched in amphid sheath cell, affected by Colistin and nitroguanidine (Wormbase, 2021). Down 1.9x w HgCl2 (this study).
cogc-3	Y71F9AM.4	1.79				*cogc-3* is enriched in NSM and germ line, affected by 7 chemicals, involved in gonad morphogenesis and regulation of cell migration, localizes to Golgi apparatus and endoplasmic reticulum, expressed in intestine; pharynx; seam cell; and vulva, close

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						homolog of human COG3, GO Terms: intra-Golgi vesicle-mediated transport, gonad morphogenesis, endoplasmic reticulum (Wormbase, 2021).
col-121	F56D5.1		-3.87			*col-121* is enriched in hypodermis, predicted to be a structural constituent of cuticle, GO term: integral component of membrane, structural constituent of cuticle (Wormbase, 2021). *col-121* encodes a cuticle collagen required for resistance to bisphenol A and mutations in *col-121* increase cuticle permeability without altering lifecycle (Watanabe et al., 2005). Down w zearalenone in Ce (Yang et al., 2018b). Down 3.3x w 2µM meHgCl and 23x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
col-55	T05E7.2			1.63		Is affected by several genes including daf-2; eat-2; and sir-2.1 based on microarray and RNA-seq studies. Is affected by resveratrol; fluoranthene; and Sirolimus based on microarray studies. GO Term: Collagen Trimer (Wormbase, 2021). *col-55* gene expression decreased in *daf-2* mutants = gene is upregulated with DAF-2 activity (Halaschek-Wiener et al., 2005).
comt-4	Y40B10A.6		-4.54			*comt-4* is enriched in intestine, affected by > 20 chemicals, a close homolog of human COMTD1 predicted to have O-methyltransferase activity (Wormbase, 2021). Upregulated by glucose, contains two DAF-16 binding sites (Lee et al., 2009). "*comt-4* which encodes an enzyme with putative catechol-O-methyltransferase activity involved in dopamine degradation" (Rodriguez-Ramos et al., 2017). Up 3.7x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 3.8x w cadmium in Ce (Cui et al., 2007). Up 3.3x w *S. aureus* in Ce (Irazoqui et al., 2010). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Up w AgNP and Ag+ in Ce (Hunt et al., 2014).
coq-2	F57B9.4	-1.84				*coq-2* is enriched in body wall muscle cell, ASER, germ line and intestine, affected by 2 chemicals, close homolog human COQ2 is implicated in primary coenzyme Q10 deficiency 1, GO Terms: integral component of mitochondrial inner membrane, 4-hydroxybenzoate decaprenyltransferase activity, mitochondrion (Wormbase, 2021). *coq-2* encodes an enzyme in the ubiquinone synthesis pathway.
cpg-18	C45E5.4			-2.24		Is enriched in OLL, PVD, and pharynx based on tiling array and RNA-seq studies. Is affected by sixteen chemicals including Heme, Mercuric Chloride, and rotenone based on microarray and RNA-seq studies (Wormbase, 2021). Up 2.4X with 20uM HgCl2 (McElwee et al., 2013). Up 1.5X with 24h Ag+ (Hunt et al., 2014). Upregulated with Harposporium infection (Engelmann et al., 2011).
cpg-20	K08B4.2		-3.32			*cpg-20* is affected by seventeen chemicals including 1-methylnicotinamide; methylmercuric chloride; and Mianserin (Wormbase, 2021). Down 8x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
cpg-20	K08B4.2				-2.07	Is affected by seventeen chemicals including 1-methylnicotinamide, methylmercuric chloride, and Mianserin based on RNA-seq and microarray studies (Wormbase, 2021). Down 3.3X with DMA, down 2X with HgCl2. Down 8X with 7.5uM meHgCl (McElwee et al., 2013).
crh-1	Y41C4A.4			-2.53		Exhibits transcription coactivator binding activity. Is involved in several processes, including determination of adult lifespan, positive regulation of transcription by RNA polymerase II, and thermosensory behavior. Is expressed in several structures, including germ line, gonad, head ganglion, intestine, and neurons. Human homologs of this gene are implicated in Pick's disease and schizophrenia. Is an ortholog of human ATF1 (activating transcription factor 1), CREB1 and CREM. GO Terms: determination of adult lifespan, DNA binding, nucleus, positive regulation of transcription by RNA polymerase II (Wormbase, 2021).
cri-1	K07A1.7		2.05			*cri-1* is expressed in amphid neurons, intestine, marginal cell, and rectal gland cell, affected by 4 chemicals, a close homolog of human HECA (Wormbase, 2021).
ctsa-4.1	K10B2.2	1.90				*K10B2.2* is enriched in PVD, OLL neurons and intestine, affected by > 15 chemicals, predicted to have serine-type carboxypeptidase activity, close human homolog CTSA is implicated in galactosialidosis (Wormbase, 2021). Up 4x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 1.6x w *E. faecalis* in Ce (Wong et al., 2007). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 3x w 7.5µM HgCl2 in Ce (McElwee et al., 2013). Up w Cd and high NaAsO2 in Ce (Sahu et al., 2013). Upregulated by SKN-1 and As stress (Oliveira et al., 2009). Candidate lysosomal cathepsin (Xu et al., 2014).
cubn-1	ZC116.3	-2.72			-2.47	*ZC116.4* is a dead gene name, now called *ZC116.3 = cubn-1*, which is enriched in pharynx, germ line, body wall musculature, vulval muscle, intestine, anal depressor muscle, coelomocyte, male-specific anatomical entity, neuron and seam cell, affected by 14 chemicals, predicted to have calcium ion binding activity, expressed in tail close human homolog CUBN is implicated in megaloblastic anemia, GO Terms: lipid metabolic process, protein transport, extracellular region, calcium ion binding (Wormbase, 2021). "the only *C. elegans* homolog of the intrinsic factor-vitamin B12 receptor cubilin (Kozyraki et al., 1998, Seetharam et al., 1997)" (Zhang et al., 2020a). Listed as ZC116.4, down 1.7x w DMA in Ce (this study).
cutl-2	Y53C12B.6		-3.77			*cutl-2* is enriched in hypodermis, affected by eighteen chemicals (Wormbase, 2021). Down 2.6x w 2µM meHgCl and 15x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
cutl-8	ZK265.8		-3.33			*cutl-8* is enriched in PLM, affected by fifteen chemicals (Wormbase, 2021).
cyb-3	T06E6.2				1.53	Exhibits cyclin-dependent protein serine/threonine kinase regulator activity. Involved in several processes, including chromosome organization; oocyte maturation; and

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						pronuclear migration. Localizes to cytoplasm and nucleus. Is expressed in several structures, including AB; EM, and germ line. Orthologous to human CCNB3 (cyclin B3). Affected by >10 chemicals. (Wormbase, 2021). Expression level of cyb-3 significantly reduced with Triptolide (diterpenoid epoxide which is produced by the thunder god vine) (Ruan et al., 2017). Among cell cycle regulators required for male gonadal fates were the cyclin-dependent kinase cdk-1 and its cognate cyclin cyb-3 (Kalis et al., 2010).
cyk-1	F11H8.4				-2.28	Is predicted to have Rho GTPase binding activity and actin binding activity. Is involved in pronuclear migration. Localizes to cleavage furrow and cytoplasmic side of plasma membrane. Colocalizes with actomyosin contractile ring. Is expressed in body wall musculature. Human ortholog(s) of this gene are implicated in autosomal dominant auditory neuropathy 1, autosomal dominant nonsyndromic deafness 1, and premature ovarian failure. Is an ortholog of human DIAPH3 (diaphanous related formin 3) (Wormbase, 2021).
cyp-13A3	T10B9.5	-1.79				*cyp-13A3* is enriched in somatic gonad precursor, affected by 10 chemicals, a close homolog of human genes CYP3A4, CYP3A43, and CYP3A7-CYP3A51P, which are implicated in essential hypertension and platelet-type bleeding disorder 14, GO Terms: oxidoreductase activity, metal ion binding, heme binding, iron ion binding (Wormbase, 2021).
cyp-14A4	R04D3.1		4.56			*cyp-14A4* is affected by > 10 chemicals, predicted to have heme binding, iron ion binding, and oxidoreductase activity, expressed in intestine, homolog of human CYP2U1 implicated in hereditary spastic paraplegia 56, GO term: metal ion binding (Wormbase, 2021). Up 15x w Cd in Ce (Cui et al., 2007). Up 8x w caffeine in Ce (Min et al., 2015). Up with two fungi + three bacterial species (Engelmann et al., 2011).
cyp-35B3	K07C6.2		1.89			*cyp-35B3* is affected by 6 chemicals, GO Terms: exogenous drug catabolic process, xenobiotic metabolic process, intracellular membrane-bounded organelle, metal ion binding, oxidoreductase activity, close human homolog CYP2U1 is implicated in hereditary spastic paraplegia 56 (Wormbase, 2021).
cyp-35D1	F14H3.10		5.57			*cyp-35D1* is enriched in PVD, OLL and intestine, affected by > 10 chemicals, close human CYP2U1 is implicated in hereditary spastic paraplegia 56, predicted to have heme binding activity, iron ion binding activity, and oxidoreductase activity, GO terms: xenobiotic metabolic process, drug catabolic process (Wormbase, 2021). Up 3x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 2.5x w *P. luminescens* in Ce (Wong et al., 2007). Required for thiabendazole (anthelmintic) resistance in Ce (Jones et al., 2015). Down w glucose in Ce (Garcia et al., 2015).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
daf-3	F25E2.5		-2.38		-2.33	Exhibits cis-regulatory region sequence-specific DNA binding activity. Is involved in several processes, including determination of adult lifespan, positive regulation of dauer larval development, and regulation of pharyngeal pumping. Localizes to condensed chromosome, cytoplasm, and nucleus. Is expressed in several structures, including P1, P2, hermaphrodite distal tip cell, hypodermal cell, and neurons. Human ortholog(s) of this gene are implicated in juvenile polyposis syndrome, juvenile polyposis-hereditary hemorrhagic telangiectasia syndrome, and pancreatic carcinoma. Is an ortholog of human SMAD4 (SMAD family member 4) GO Terms: transforming growth factor beta receptor signaling pathway, condensed chromosome, cytoplasm, defense response to Gram-negative bacterium, metal ion binding, regulation of transcription (Wormbase, 2021). *daf-3* mutants are dauer defective = they don't form dauers. "In *C. elegans*, DAF-7 is a TGFβ homolog that is secreted by ASI sensory neurons in response to environmental cues, such as pheromones and food. The canonical DAF-7 TGFβ pathway signals through the DAF-1 Type I and DAF-4 Type II receptors to downstream DAF-8 and DAF-14. These R-SMADs translocate into the nucleus to inhibit the Co-SMAD DAF-3 [8,20]" (Hu et al., 2020b). "The dauer constitutive and fat storage phenotypes caused by mutations in these upstream TGF-β signalling genes are suppressed by null mutations in *daf-3*, which also encodes a SMAD protein8 (Fig. 2). Thus *daf-3* acts in this TGF-β pathway analogously to *daf-16* in the insulin-like pathway: *daf-3* gene activity is negatively regulated by upstream TGF-β signalling" (Ogg et al., 1997). Down 1.6X with DMA in this study.
daf-38	Y105C5A.23				1.61	Up 1.6X with NaAsO2 and up 1.7X with DMA in this study. Exhibits protein heterodimerization activity. Is involved in G protein-coupled receptor signaling pathway involved in dauer larval development. Is expressed in chemosensory neurons and head neurons. GO Terms: G protein-coupled receptor activity involved in dauer activity, integral component of the membrane, neuropeptide signaling pathway, signal transduction. (Wormbase, 2021).
dct-19	C32H11.13				-2.27	Is affected by paraquat based on RNA-seq studies. Is predicted to encode a protein with the following domains: CUB-like domain and CUB-like domain. Affected by three chemicals (Wormbase, 2021). Down with 24h Ag+ (Hunt et al., 2014).
deb-1				1.60		Is a structural constituent of cytoskeleton. Is involved in cytoskeletal anchoring at plasma membrane and positive regulation of ovulation. Localizes to several cellular components, including cytoskeleton; dense body; and striated muscle dense body. Is expressed in gonad. Human ortholog(s) of this gene are implicated in dilated cardiomyopathy 1W and hypertrophic cardiomyopathy 15. Is an ortholog of human VCL (vinculin). Is affected by 15 chemicals (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
del-4	T28B8.5		-3.84			*del-4* is expressed in ganglia and neurons, affected by 6 chemicals, predicted to have sodium channel activity, close human homolog SCNN1G is implicated in bronchiectasis and renal tubular transport disease, GO terms: sodium ion transport, ligand-gated sodium channel activity, integral component of plasma membrane (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). T28B8.5::GFP (pmk-1/P38 reporter) was induced in worms exposed to all 5 *P. aeruginosa* isolates (Vasquez-Rifo et al., 2020). X
dhhc-8	Y39E4B.7			1.53		Is predicted to have protein-cysteine S-palmitoyltransferase activity. Predicted to localize to Golgi apparatus and endoplasmic reticulum. Is an ortholog of human ZDHHC5 and ZDHHC8. Affected by rotenone. GO Terms: ER, golgi apparatus, integral component of membrane, transferase activity, protein targeting to membrane (Wormbase, 2021).
dhs-8	K10H10.3	1.77	4.28			*dhs-8* is enriched in PLM and pharynx, affected by twenty-three chemicals, close human homolog WWOX is implicated in spinocerebellar ataxia 12; early infantile epileptic encephalopathy 28; and esophageal cancer, GO term: oxidoreductase activity (Wormbase, 2021). Up 3x w acrylamide in Ce (Hasegawa et al., 2008). Up 5x w juglone in Ce (Przybysz et al., 2009). Upregulated by SKN-1 & up w NaAsO2 in Ce (Oliveira et al., 2009). Up w NaAsO2 in Ce (Sahu et al., 2013). Up w HgCl2 and w meHgCl in Ce (McElwee et al., 2013).
dnj-12	F39B2.10			1.64		Is predicted to have heat shock protein binding activity; metal ion binding activity; and unfolded protein binding activity. Is expressed in several structures, including anal depressor muscle; excretory cell; intestine; pharynx; and reproductive system. Is an ortholog of human DNAJA1 (DnaJ heat shock protein family (Hsp40) member A1). Affected by four chemicals. (Wormbase 2021.)
dod-17	K10D11.1	6.41	2.58			*dod-17* is enriched in pharynx, intestine and head mesodermal cell, affected by > 20 chemicals, involved in innate immune response (Wormbase, 2021). Up 27x w NaAsO2 in Ce (Sahu et al., 2013). Up 6x w *P. aeruginosa* in Ce (Troemel et al., 2006). Down 3x w *S. aureus* in Ce (Irazoqui et al., 2010). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 5x w 20µM HgCl2 (McElwee et al., 2013). Upregulated by SKN-1 (Oliveira et al., 2009). Repressed in *daf-12(rh273)* and *daf-2* (Fisher and Lithgow, 2006). Up 3x w X-rays & 4.5x w gamma rays in Ce (Greiss et al., 2008). Pdod-17::rfp transcriptional reporter is expressed mainly in the intestine (i) of wild-type and is downregulated in the intestine of *daf-2(−)* mutants and upregulated in daf-16(−); daf-2(−) mutants (Zhang et al., 2013).
dod-22	F55G11.5		-4.16			*dod-22* is expressed in head neurons and rectal gland cell, enriched in neurons and intestine, affected by > 20 chemicals, involved in defense response to Gram-negative bacterium and innate immune response (Wormbase, 2021). Up 7x w *Y. pestis* in Ce (Bolz et al., 2010). Upregulated by UVC (Boyd et al., 2010). Activated by *elt-2* and induced by at

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						least five pathogens (Yang et al., 2016). Up 5x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 1.6x w *M. nematophilum* in Ce (O'Rourke et al., 2006). Up 34% w *E. carotovora* in Ce (Wong et al., 2007). Up 2x w Ag+ in Ce (Hunt et al., 2014). Upregulated by SKN-1 (Oliveira et al., 2009). Downregulated by DAF-16 (Tepper et al., 2013; Watanabe et al., 2020). Down 4x w 2µM meHgCl and 8x w 7.5µM meHgCl in Ce (McElwee et al., 2013). X
dod-24	C32H11.12	5.31				*dod-24* is enriched in DA neuron, VA neuron, and intestine, involved in defense response to Gram-negative bacterium, affected by > 20 chemicals (Wormbase, 2021). Up 4x w *P. aeruginosa* in Ce (Troemel et al., 2006). "predicted to be strongly induced by *P. aeruginosa* (31, 35, 41)" (Kim and Mylonakis, 2012). Up with Yersinia pestis (Bolz et al., 2010). Up 4.6x w 7.5µM HgCl2 only in Ce (McElwee et al., 2013). Upregulated by SKN-1 (Oliveira et al., 2009). Repressed in *daf-12(rh273)* and *daf-2* (Fisher and Lithgow, 2006). *dod-24* is a DAF-16 Class II (Downregulated) gene (Tepper et al., 2013). Up 6x w NaAsO2 in Ce (Sahu et al., 2013). Up 3x w X-rays & w gamma rays w X-rays in Ce (Greiss et al., 2008). Up 1.7x w DMA (this study).
dpy-7	F46C8.6		-4.13			*dpy-7* encodes a cuticular collagen, enriched in hypodermis, intestine and male-specific anatomical entity, affected by > 20 chemicals, a structural constituent of collagen and cuticulin-based cuticle involved in cuticle development, collagen and cuticulin-based cuticle molting cycle and post-embryonic body morphogenesis, GO Term: structural constituent of cuticle (Wormbase, 2021). Down 55% w *D. coniospora* in Ce (Pujol et al., 2008). Up w three bacterial species in Ce (Engelmann et al., 2011). Up w meHgCl and required for meHgCl resistance (Rudgalvyte et al., 2013).
drp-1	T12E12.4			1.59		Is predicted to have GTP binding activity. Is involved in apoptotic mitochondrial changes; embryo development; and mitochondrial fission. Localizes to mitochondrion. Is expressed in several structures, including germ line; non-striated muscle; preanal ganglion; rectal muscle; and somatic nervous system. Is used to study Parkinson's disease. Human ortholog(s) of this gene are implicated in encephalopathy due to defective mitochondrial and peroxisomal fission 1 and optic atrophy 5. Is an ortholog of human DNM1L (dynamin 1 like). Affected by nine chemicals. GO Terms: apoptotic mitochondrial changes, cytoplasm, GTP binding, membrane (Wormbase, 2021). Drp-1 mutants showed defects in larval growth after exposure to 2.4 DNP, Acrolein, Cadmium, Paraquat when compared to controls. deficiencies in fission and fusion sensitized nematodes to arsenite-induced lethality throughout aging (Luz et al., 2017). Drp-1 Is Essential for CoCl2-Induced Mitochondrial Fission and ROS Generation (Zheng et al., 2020).
dsl-6	H02I12.4		-4.55			*dsl-6* is enriched in hypodermis, hermaphrodite-specific anatomical entity, affected by eighteen chemicals, GO term: integral component of plasma membrane (Wormbase,

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						2021). Decreased LAG-2, DOS-1 or DSL-6 results in resistance to aldicarb and their loss phenocopies *glp-1(lf)* (Sorkac et al., 2018). Down in dose response to 31x w 7.5µM meHg in Ce (McElwee et al., 2013).
dyn-1	C02C6.1			1.50		Exhibits GTPase activity. Is involved in several processes, including phagosome maturation involved in apoptotic cell clearance; positive regulation of necrotic cell death; receptor-mediated endocytosis, and the CED-1 pathway that regulates engulfment and degradation of apoptotic cells. Localizes to several cellular components, including periciliary membrane compartment; pseudopodium; and spindle microtubule. Is expressed in several structures, including neurons; non-striated muscle; pharyngeal-intestinal valve; rectal valve cell; and somatic nervous system, hermaphrodite gonad. Human ortholog(s) of this gene are implicated in Charcot-Marie-Tooth disease dominant intermediate B; centronuclear myopathy 1; and early infantile epileptic encephalopathy 31. Is an ortholog of human DNM1; DNM2; and DNM3. GO Terms: (Wormbase, 2021). Increased expression with Au-NP exposure (Tsyusko et al., 2012). Decreased expression in shn-1 mutant and C. albicans infection (Innate immunity pathway) (Sun et al., 2020).
eat-6	B0365.3			2.18		Exhibits sodium:potassium-exchanging ATPase activity. Localizes to membrane. Is expressed in several structures, including coelomocyte; intestine; neurons; pharynx; and vulval muscle. Is used to study alcohol use disorder. Is an ortholog of human ATP1A3 (ATPase Na+/K+ transporting subunit alpha 3). Affected by 11 chemicals. GO Terms: ion transport, integral component of the membrane, metal ion binding, plasma membrane, reproduciton (Wormbase, 2021). RNAi of eat-6 stimulates hypodermal and intestinal expression of a gst-4::GFP (Melo and Ruvkun, 2012b). Percent increase of life expectancy varies with gene and allele, eat-6(ad792) mutant, 36 percent (Henderson et al., 2005). 1.7X increase with UV-treatment (DNA damage) (Edifizi et al., 2017).
egas-2	Y69H2.12	2.16				*egas-2* is enriched in NSM, affected by 5 chemicals, predicted to have calcium ion binding activity and sodium channel activity, GO Terms: sodium ion transmembrane transport, integral component of plasma membrane, calcium ion binding (Wormbase, 2021).
emb-4	Y80D3A.2	1.91				*emb-4* is enriched in germ line, AVK and intestine, expressed in embryonic cell, localizes to nucleus, affected by 9 chemicals, close homolog of human AQR, GO Term: nucleus, spliceosomal complex, mRNA processing (Wormbase, 2021). "*emb-4* encodes a highly conserved protein with orthologs in fly, mouse, and human and has a subtle role in Notch signaling … mutations in the maternal-effect gene *emb-4* cause defects in both PIE-1 degradation and germline-specific chromatin remodeling" (Checchi and Kelly, 2006).
eri-12	B0001.6			1.59		Affected by 6 chemicals. Localizes to cytoplasm. GO Terms: cytoplasm, protein binding (Wormbase, 2021). Up 1.6X with P. luminescens infection (Wong et al., 2007).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
far-4	F15B9.2		2.41			*far-4* encodes a fatty acid and retinol-binding protein, is affected by 15 chemicals, predicted to have lipid binding activity (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Up 2x w 20µM HgCl2 and 5-6x w 2 and 7.5µM meHgCl in Ce (McElwee et al., 2013). Up w AgNP and Ag+ in Ce (Hunt et al., 2014).
far-5	F15B9.3				-2.12	Is predicted to have lipid binding activity. Is expressed in male. Affected by 14 chemicals (Wormbase, 2021).
fbxa-103	F09C3.4		-3.97			*fbxa-103* is affected by eleven chemicals (Wormbase, 2021). Down 6.3x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013). Down 1.9x w HgCl2 in Ce (this study).
fbxa-178	F17A9.1		2.40			*fbxa-178* pseudogene is enriched in germ line, affected by four chemicals (Wormbase, 2021).
fbxa-214	Y38A10A.4	2.12				*fbxa-214* is affected by five chemicals (Wormbase, 2021).
fbxa-224	ZK1290.9			-2.35		Is enriched in NSM based on tiling array studies. Is affected by ten chemicals including methylmercuric chloride, Tunicamycin, and multi-walled carbon nanotube based on microarray and RNA-seq studies. Is predicted to encode a protein with the following domains: FTH domain, HTH domain in Mos1 transposase, F-box domain, F-box domain, Domain of unknown function DUF38 (Wormbase, 2021).
fbxa-81	T24C2.4			-2.21		Is enriched in neurons based on microarray studies. Is affected by five chemicals including Psoralens, allantoin, and Sirolimus based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: FTH domain, F-box domain, F-box domain, Domain of unknown function DUF38, Caenorhabditis species, F-box-like domain superfamily, and F-box A protein FB155\/FB224.) Wormbase 2021). Down 1.9X with meHgCl in this study.
fbxb-45	M01D1.10		-3.22			*fbxb-45* is enriched in NSM neuron; Z4.a; germ line; male distal tip cell; and somatic gonad precursor, affected by thirteen chemicals including hydrogen sulfide; 1-methylnicotinamide; and methylmercuric chloride (Wormbase, 2021). Down 3x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
fbxb-66	Y40B1B.3		-3.84			*fbxb-66* is enriched in hypodermis and pharynx, affected by seventeen chemicals (Wormbase, 2021). Down 2.2x w 7.5µM meHgCl in Ce (McElwee et al., 2013). Down 1.8x w HgCl2 and down 1.6 w meHgCl in Ce (this study).
fbxc-34	R07C3.5		-4.09			*fbxc-34* is enriched in pharynx, hypodermis, intestine, pharyngeal muscle cell and head mesodermal cell, affected by seventeen chemicals (Wormbase, 2021). Down 7.1x w meHgCl in Ce (McElwee et al., 2013).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
fbxc-35	R07C3.14			-2.27		Is enriched in head mesodermal cell based on RNA-seq studies. Is affected by six chemicals including metformin, Sirolimus, and Psoralens based on RNA-seq and microarray studies (Wormbase, 2021).
fer-1	F43G9.6	2.49				*fer-1* is expressed in spermatid and spermatocyte, affected by 15 chemicals, predicted to have calcium-dependent phospholipid binding activity, close human homolog DYSF (dysferlin) is associated with nonsyndromic deafness 9 and muscular dystrophy, GO Terms: amoeboid sperm motility, spermatogenesis, integral component of plasma membrane, integral component of organelle membrane (Wormbase, 2021). Up 2.7x w 7.5µM meHg in Ce (McElwee et al., 2013). Down 1.5x w DMA (this study).
fipr-10	C50H2.12	-1.87				*fipr-10* is enriched in germ line, affected by 6 chemicals (Wormbase, 2021). Down 1.7x w HgCl2 in Ce (this study).
flp-33	T07D10.6	2.06				*flp-33* is enriched in NSM and dopaminergic neurons, affected by eight chemicals (Wormbase, 2021).
gadr-1	F58D2.1			-2.83	-2.07	Enriched in NSM, affected by methylmercuric chloride, bisphenol S, Zidovudine, allantoin, Sirolimus, Psoralens and Rifampin (Wormbase, 2021). Down 9X with 7.5uM meHgCl (McElwee et al., 2013). Down 2X with DMA in this study.
gba-4	Y4C6B.6				-4.73	Down 2X with 0.75uM, down 2.9X with 2uM, Down 5.4X with 7.5uM meHgCl in Ce (McElwee et al., 2013). GO Terms: Lipid metabolic process, glucosylceramidase activity. Human ortholog(s) of this gene are implicated in Gaucher's disease (multiple); Lewy body dementia; and late onset Parkinson's disease. Is an ortholog of human GBA (glucosylceramidase beta) (Wormbase, 2021).. Downregulated with B. thuringiensis Bt247 and Bt679 exposure (Zárate-Potes et al., 2020). (McElwee, Ho et al. 2013). Downregulated with activated mitochondrial Nrf/SKN-1 (Paek et al., 2012).
gcs-1	F37B12.2	1.77				*gcs-1* is enriched in PVD and OLL neurons, germ line, hypodermis, germline precursor cell, affected by 15 chemicals, encodes the *C. elegans* ortholog of gamma-glutamine cysteine synthetase heavy chain GCS-1 which is associated with glutamate-cysteine ligase deficiency, GCS-1 is predicted to function in a conserved oxidative stress response pathway as a phase II detoxification enzyme that catalyzes the rate-limiting first step in glutathione biosynthesis, predicted to have ATP binding activity and glutamate-cysteine ligase activity, GO Terms: glutathione biosynthetic process, response to reactive oxygen species, response to superoxide, response to arsenic-containing substance, response to heat (Wormbase, 2021). Upregulated by juglone, has DAF-16 (but was not downregulated in *daf-16* mutants) and SKN-1 binding sites (Przybysz et al., 2009). Upregulated by SKN-1 and up with acrylamide (Hasegawa et al., 2008). Up w NaAsO2 (Sahu et al., 2013) Up with

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						NaAsO2 in a SKN-1 dependent manner (Oliveira et al., 2009). Up 2x w HgCl2 (McElwee et al., 2013). Up 1.6x w DMA (this study).
gcy-27	C06A12.4			-2.23		Is predicted to have guanylate cyclase activity, protein kinase activity, and purine ribonucleoside triphosphate binding activity. Is involved in chemosensory behavior and sensory perception of bitter taste. Is expressed in amphid neurons. Human ortholog(s) of this gene are implicated in Leber congenital amaurosis 1, choroidal sclerosis, and cone-rod dystrophy 6. Is an ortholog of human GUCY2D (guanylate cyclase 2D, retinal) and GUCY2F (guanylate cyclase 2F, retinal). GO Terms: chemosensory behavior, integral component of membrane, plasma membrane, sensory perception of bitter taste (Wormbase, 2021). Upregulated with D. coniospora infection (Engelmann et al., 2011).
gcy-3	R134.1	1.83				*gcy-3* is expressed in neurons, affected by 4 chemicals, close human homologs GUCY2D and GUCY2F are implicated in Leber congenital amaurosis 1; choroidal sclerosis; and cone-rod dystrophy 6, GO Terms: integral component of membrane, plasma membrane, cyclic nucleotide biosynthetic process, signal transduction (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011).
gei-1	F45H7.2				-2.10	Is predicted to have lipid binding activity. Human ortholog(s) of this gene are implicated in colorectal cancer. Is an ortholog of human DLC1 (DLC1 Rho GTPase activating protein) and STARD13 (StAR related lipid transfer domain containing 13). Affected by fifteen chemicals. GO Terms: lipid binding, GTPase activity, signal transduction, actin cytoskeleton organization (Wormbase, 2021).
glb-9	C28F5.2	-2.20				*glb-9* is expressed in neurons and somatic nervous system, affected by 3 chemicals, GO Terms: heme binding, metal ion binding, oxygen carrier activity (Wormbase, 2021). X
glrx-3	D2063.3	2.04				*glrx-3* is enriched in PLM and germ line, localizes to striated muscle dense body, affected by 3 chemicals, a close homolog of human GLRX3, predicted to have electron transfer activity and protein disulfide oxidoreductase activity, GO Terms: nucleus, electron transport chain, cellular iron ion homeostasis, metal ion binding, striated muscle dense body (Wormbase, 2021).
gly-12	F48E3.1			2.32		Exhibits alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity. Is involved in protein N-linked glycosylation. Localizes to perinuclear region of cytoplasm. Is expressed in body wall musculature, ganglia, hypodermis, and intestine. GO Terms: golgi medial cisterna, integral component of the membrane, metal ion binding, transferase activity (Wormbase, 2021).
gnrr-1	F54D7.3			1.84		Is expressed in intestine; neurons; oocyte; pharynx; and sperm. Human ortholog(s) of this gene are implicated in hypogonadotropic hypogonadism 7 with or without anosmia. Is an ortholog of human GNRHR (gonadotropin releasing hormone receptor). Affected by 6

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						chemicals. GO Terms: G protein coupled receptor activity, integral component of membrane, plasma membrane(Wormbase, 2021).
grd-7	F46H5.6			-3.31		-13X with 7.5uM meHgCl (McElwee et al., 2013). GRD-7 is expressed in three to four posterior DA motorneurons of the ventral nerve cord; GRD-7 is weakly required for normal molting; GRD-7 is also required for normal growth to full size, cuticle adhesion, locomotion, and vulval morphogenesis; all of these requirements may reflect common defects in cholesterol-dependent hedgehog-like signalling or in vesicle trafficking. Affected by 6 chemicals. GO Terms: cell communication, protein binding, extracellular region, signaling receptor binding (Wormbase, 2021).
grl-19	R02D3.6		2.31		1.60	*grl-19* encodes a hedgehog-like protein, is expressed in excretory duct and excretory pore, enriched in dopaminergic neurons, affected by 9 chemicals (Wormbase, 2021). Expressed in intestine (Agilent Array info). Involved in OxStr response and aging, upregulated by DAF-16 (Kim and Sun, 2007). Down 43x w 7.5µM meHg in Ce (McElwee et al., 2013).
grl-24	F11E6.2		-4.58			*grl-24* is enriched in hypodermis, affected by eight chemicals including (Wormbase, 2021). Germline Interactome ORF (Walhout et al., 2002). Down 2.6x w 7.5µM meHg in Ce (McElwee et al., 2013). X
grl-30	T24A6.3	2.02				*grl-30* is affected by several genes including daf-12; eri-1; and lin-15B (Wormbase, 2021).
grl-31	T24A6.19			-2.32		Is expressed in vulF. Is predicted to encode a protein with the following domains: Ground-like domain and Ground-like domain. Affected by 4 chemicals (Wormbase, 2021).
gst-10	Y45G12C.2	2.11	2.12			*gst-10* is involved in heat acclimation and response to UV-C, expressed in head and tail, affected by > 20 chemicals, used to study obesity, close homolog human GSTP1 is implicated in obesity, GO Terms: determination of adult lifespan, response to hydrogen peroxide, response to UV-C (Wormbase, 2021). Down w *M. nematophilum* in Ce (O'Rourke et al., 2006). Down w *S. aureus* in Ce (Irazoqui et al., 2010). Up w methanol extracts from velvet antler (Wang et al., 2020). Down w depleted uranium in Ce (Lu et al., 2020b). Required for resistance to 4-hydroxynon-2-enal in Ce (Ayyadevara et al., 2007). Upregulated by SKN-1 (Oliveira et al., 2009). Upregulated by SKN-1 (Tullet et al., 2008b). Up 2.5x w aspirin in Ce (Ayyadevara et al., 2013). Down w glucose in Ce (Li et al., 2018). Down w LiCl and Li2CO3 in Ce (Inokuchi et al., 2015). Upregulated by SKN-1 and up w OxStr (Park et al., 2009). Up w Chlorpyrifos and Diazinon in Ce (Vinuela et al., 2010). Up 2x w Al2O3 NPs (Zhang et al., 2020b). Up 1.6x w NaAsO2 (Sahu et al., 2013).
gst-12	F37B1.2	3.84	5.89			*gst-12* is enriched in pharynx, amphid sheath cell, germ line and neurons, affected by 20 chemicals, a close homolog off human HPGDS (Wormbase, 2021). Up 32x w NaAsO2 (Sahu et al., 2013). Up 5x w juglone in Ce (Przybysz et al., 2009). Upreg by SKN-1 & up 9x w O2

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						in Ce (Park et al., 2009). Up 2x w acrylamide in Ce (Hasegawa et al., 2008). Reg by SKN-1 & up w 25µM meHg in Ce (Vanduyn et al., 2010). Up w TiO2 NPs in Ce (Hu et al., 2020a). Up w Ag+ & AgNP in Ce (Hunt et al., 2014). Up in dose response to 39x w meHgCl in Ce (McElwee, 2010). Upregulated by SKN-1 & up w NaAsO2 in Ce (Oliveira et al., 2009).
gst-13	T26C5.1		2.01			*gst-13* is predicted to have transferase activity, involved in innate immune response, a close homolog of human HPGDS (Wormbase, 2021). Up 2.9x w *P. aeruginosa* in Ce (Troemel et al., 2006). Likely SKN-1 target, up w juglone in Ce (Przybysz et al., 2009). Upreg by SKN-1 (Park et al., 2009). Upregulated by SKN-1 under normal conditions (Oliveira et al., 2009). Up 7.5x w NaAsO2 in Ce (Sahu et al., 2013). Up 1.6x w NaAsO2 (this study).
gst-14	F37B1.3	2.79	3.98			*gst-14* is expressed in neurons, intestine and pharynx, affected by > 15 chemicals, close homolog of human HPGDS (Wormbase, 2021). Up w *D. coniospora* & *Harposporium* in Ce (Engelmann et al., 2011). Up w AgNP in Ce (Hunt et al., 2014). Upreg by SKN-1 & up w O2 in Ce (Park et al., 2009). Upregulated by SKN-1 & up w NaAsO2 in Ce (Oliveira et al., 2009). Up 2x w acrylamide in Ce (Hasegawa et al., 2008). Down w resveratrol in Ce (Aranaz et al., 2020). Up 28x w meHg in Ce (McElwee et al., 2013). Up 5.8x w NaAsO2 in Ce (Sahu et al., 2013).
gst-16	F37B1.5	5.75	6.8			*gst-16* is affected by > 20 chemicals, predicted to have transferase activity, a close homolog of human HPGDS (Wormbase, 2021). Up 17x w NaAsO2 (Sahu et al., 2013). Up 5x w juglone and upregulated by SKN-1 in Ce (Przybysz et al., 2009). Up 3x w acrylamide in Ce (Hasegawa et al., 2008). Up 3x w Al2O3 NPs (Zhang et al., 2020b). Up 3x w selenium in Ce (Boehler et al., 2014). Up w heme in Ce (Severance et al., 2010). Up w HgCl2 & meHg (McElwee et al., 2013).
gst-19	F37B1.8	-2.20			-3.19	*gst-19* is enriched in coelomocyte, affected by > 15 chemicals, predicted to have transferase activity, close homolog of human HPGDS, GO Terms: glutathione metabolic process, glutathione transferase activity (Wormbase, 2021). Negatively regulated by SKN-1/Nrf2 in Ce "*skn-1* can act to negatively regulate the expression of genes involved in the response to some oxidative stresses (Oliveira et al., 2009)" (Miller et al., 2011). Down 4-6x w 3 concentrations of meHgCl in Ce (McElwee et al., 2013). Down 2.2x w DMA in Ce (this study).
gst-25	F37F2.3	6.90	10.4			*gst-25* is affected by 10 chemicals, predicted to have glutathione transferase activity, close homolog of human GSTP1 (Wormbase, 2021). Up 30x w NaAsO2 (Sahu et al., 2013). Up 5x w juglone in Ce (Przybysz et al., 2009). Down w cinnamaldehyde in Ce (Lu et al., 2020a). Has SKN-1 binding site but expression not reduced with *skn-1* RNAi, up w

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						dazomet (Jones et al., 2013). Upregulated by DAF-16 (Minniti et al., 2009). Up in dose response to 26x w meHgCl in Ce (McElwee et al., 2013).
gst-30	ZK546.11	5.27	7.5			*gst-30* is expressed in head tail and vulva, predicted to have transferase activity, enriched in body wall muscle cell, NSM and head mesodermal cell, affected by > 20 chemicals, close homolog of human HPGDS (Wormbase, 2021). Up w AgNO3 in Ce (Starnes et al., 2019). Up 64x w NaAsO2 (Sahu et al., 2013). Has SKN-1 binding site and expression is reduced with SKN-1 RNAi, up w juglone in Ce (Przybysz et al., 2009). Up 2x w AgNP (Hunt et al., 2014). Up 2x w HgCl2 and 4x w meHg (McElwee, 2010). d w cinnamaldehyde in Ce (Lu et al., 2020a). Has SKN-1 binding site, up w dazomet (Jones et al., 2013). Up 5x w acrylamide (Hasegawa et al., 2008). Up 50% w Al2O3 NPs (Zhang et al., 2020b).
gst-35	Y1H11.2	2.06	6.38			*gst-35* is enriched in male and hypodermis, affected by > 15 chemicals, predicted to have transferase activity, a close homolog of human HPGDS (Wormbase, 2021). Up 3x w 20µM HgCl2 and dose response to 39x w meHgCl in Ce (McElwee, 2010). Upregulated by SKN-1 & needed for NaAsO2 resistance (Oliveira et al., 2009).
gst-37	Y32G9A.1		10.4			*gst-37* is expressed in neurons, gonad, head and tail, affected by 9 chemicals, predicted to have transferase activity, close homolog of human HPGDS, regulated by DAF-12 (Wormbase, 2021). Up 100x w meHg in Ce (McElwee, 2010). Up 2x w acrylamide in Ce (Hasegawa et al., 2008). Req for NaAsO2 resistance (Sahu et al., 2013).
gst-5	R03D7.6		3.02			*gst-5* is expressed in neurons, intestine and nerve ring, is affected by > 20 chemicals, involved in innate immune response, inhibits CEP-1- and HUS-1-dependent germline apoptosis, close human homolog HPGDS (Wormbase, 2021). Upregulated by SKN-1 and arsenic (Oliveira et al., 2009). Upregulated by SKN-1 and pathogens (Hoeven et al., 2011). Up 3x w juglone (Przybysz et al., 2009). Up 2x w Al2O3 NPs (Zhang et al., 2020b). Up 2x w *P. luminescens* in Ce (Wong et al., 2007). Up 2-4x w *P. aeruginosa* in Ce (Evans et al., 2008; Troemel et al., 2006). Up 2x w AgNP in Ce (Hunt et al., 2014). Up 4x w acrylamide in Ce (Hasegawa et al., 2008). Up 12x w meHgCl in Ce (McElwee et al., 2013). Up 13x w NaAsO2 in Ce (Sahu et al., 2013). X
gsto-2	C02D5.3	4.08	5.27			*gsto-2* (C02D5.3, not C02D5.3a) is enriched in pharynx and muscle cell, affected by 11 chemicals, predicted to have glutathione dehydrogenase (ascorbate), glutathione transferase, and methylarsonate reductase activity, expressed in head intestine and tail, close homolog of human GSTO1 and GSTO2, GO Terms: cellular oxidant detoxification, methylarsonate reductase activity, oxidoreductase activity (Wormbase, 2021). Up w gengnianchun (TCM) in Ce (Meng et al., 2018). Up w probiotic (CBM 588) in Ce (Kato et al., 2018). Up w acrylamide in Ce (Hasegawa et al., 2008). Upregulated by SKN-1 and

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						arsenic (Oliveira et al., 2009). Up ~2.7x w 20µM HgCl2 or w 7.5µM meHgCl (McElwee et al., 2013).
gyf-1	C18H9.2			-2.17		Is enriched in germ line and neurons based on tiling array and RNA-seq studies. Is affected by several genes including daf-16; daf-2; and glp-1 based on microarray; tiling array; RNA-seq; and proteomic studies. Is affected by seven chemicals including rotenone; Zidovudine; and Sirolimus based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: GYF domain; GYF domain; and GYF-like domain superfamily. Is an ortholog of human GIGYF1 (GRB10 interacting GYF protein 1) and GIGYF2 (GRB10 interacting GYF protein 2) (Wormbase, 2021).
haf-8	Y57G11C.1	-2.27				*haf-8* is affected by 10 chemicals, predicted to have ATP binding activity; ATPase activity; and ATPase-coupled transmembrane transporter activity, close human homolog TAP2 is implicated in MHC class I deficiency, GO Terms: integral component of membrane, ATPase-coupled transmembrane transporter activity, transmembrane transport (Wormbase, 2021). Down 1.5x w HgCl2, and down 1.9x w meHgCl in Ce (this study).
hgap-1	Y18H1A.3			1.51		Is predicted to have GTPase activator activity. Is involved in determination of adult lifespan. Is an ortholog of human RALGAPA1 and RALGAPA2. Affected by six chemicals. GO Terms: cytoplasm, nucleus, GTPase activator activity, determination of adult lifespan (Wormbase, 2021). RNAi-mediated knockdown of *C. elegans hgap-1* and *hgap*-2 RalGAP subunits decreases lifespan in daf-2(e1370) reduced function InsR animals ($p < 0.0001$) (Martin et al., 2014).
hlh-34	T01D3.2		-3.72		-2.08	*hlh-34* is enriched in neurons, affected by 7 chemicals, a close homolog of human NPAS1 implicated in obesity, expressed in AVJL and AVJR neurons, predicted to have DNA binding activity, GO Terms: regulation of DNA-templated transcription, multicellular organism development, nervous system development, "nucleus, nuclear chromatin, DNA binding (Wormbase, 2021).
hpo-33	F28B1.1				2.7908	Is enriched in male-specific anatomical entity and in male based on RNA-seq and microarray studies. (Wormbase, 2021).
hrg-3	F58E6.7	-1.86				*hrg-3* is enriched in intestine and head mesodermal cell, affected by > 20 chemicals, GO Terms: defense response to Gram-negative bacterium, heme transmembrane transporter activity (Wormbase, 2021). Up 2.1x w 7.5µM HgCl2 in Ce (McElwee et al., 2013). Down 1.9x w HgCl2, down 2.0x w meHgCl, and down 2.3x w DMA in Ce (this study).
hsp-3	C15H9.6			1.68		0.5X downreg after 12h Drechmeria coniospora infection (Pujol et al., 2008a). Is involved in IRE1-mediated unfolded protein response. Is expressed in several structures, including germ line; intestine; pharyngeal gland cell; pharyngeal-intestinal valve; and tail. Is an ortholog of human HSPA5 (heat shock protein family A (Hsp70) member 5). Affected by

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						>10 chemicals. GO Terms: cellular response to unfolded protein, ER chaperone complex, heat shock protein binding, membrane, misfolded protein binding, nucleus (Wormbase, 2021). Triclosan and BPA increase hsp-3::GFP (García-Espiñeira et al., 2018b). Hsp-3::GFP increase after HgCl2 exposure (8-24hr), Zn2+, Cd2+, Cu2+, Fe3+ (De Pomerai et al., 2010). Herbicides Glyphosate and Atrazine also increase hsp-3::GFP (García-Espiñeira et al., 2018a).
ift-139	ZK328.7	-1.93				*ift-139* is enriched in neurons, affected by > 10 chemicals, close homolog human TTC21B is implicated in asphyxiating thoracic dystrophy 4 and nephronophthisis 12 and used to study nephronophthisis, GO Term: intraciliary retrograde transport (Wormbase, 2021). Nephronophthisis-related gene *ift-139* in *Caenorhabditis elegans* "was exclusively expressed in ciliated neurons in *C. elegans*. Genetic and cellular analyses suggest that *ift-139* plays a role in retrograde intraflagellar transport and is required for cilia formation. A homologous point mutation that causes ciliopathy disrupted the function of *ift-139* in *C. elegans*. *ift-139* is an orthologue of human *TTC21B*, mutations in which are known to cause nephronophthisis 12 and short-rib thoracic dysplasia 4. These results suggest that *ift-139* is evolutionarily conserved and fundamental to the formation of cilia." (Niwa, 2016)
ins-19	T10D4.13	-1.92				*ins-19* is enriched in male-specific anatomical entity, affected by 13 chemicals, GO Terms: hormone activity, signal transduction (Wormbase, 2021). INS-19 is a neuropeptide = "short sequences of amino acids that function either directly or indirectly to modulate synaptic activity" (Li and Kim, 2008). *ins-19* is a "core hypoxic response gene" (Kruempel et al., 2020). Down 1.8x w DMA in Ce (this study).
ins-5	ZK84.3	1.81	2.32		2.28	*ins-5* encodes an insulin-like peptide, affected by 7 chemicals, is involved in dauer larval development, expressed coelomocyte; head muscle; neurons; somatic nervous system; and vulva, predicted to have hormone activity (Wormbase, 2021). Up 1.4x w *E. carotovora* in Ce (Wong et al., 2007). "In the promoter region of *ins-5*, a SKN-1 binding site is located at 84 base pairs (bp) upstream of the first exon [18] … functions as a putative agonist of DAF-2, at least in part, and is transcriptionally regulated via the p38 MAPK signaling … the insulin peptide gene *ins-5*, partially mediates the expression of DAF-16 targets via p38 MAPK signaling [29] … findings support the view that *ins-5* is a target gene of SKN-1 and its expression is upregulated via the p38 MAPK signaling" (Yanase et al., 2020). *ins-5* expression is upregulated by DAF-16 (Kaplan et al., 2019). Down 1.8x w HgCl2 (this study).
ins-7	ZK1251.2	-1.87				*ins-7* is enriched in excretory cell, intestine, PVD and OLL neurons, affected by > 20 chemicals, GO Terms: hormone activity, olfactory learning, signal transduction (Wormbase, 2021). INS-7 is an insulin-like neuropeptide (Li and Kim, 2008). SKN-1/Nrf2

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						downregulates *ins-7* and RNAi knockdown of *ins-7* extends lifespan (Oliveira et al., 2009). The insulin-like peptide (ILP) "ins-6 acts from ASI sensory neurons to enable learning by repressing the transcription of another ILP, *ins-7*, specifically in URX neurons. A high level of INS-7 from URX disrupts learning by antagonizing the insulin receptor-like homolog DAF-2 in the postsynaptic neurons RIA, which play an essential role in the neural circuit underlying olfactory learning" (Chen et al., 2013). Down 2.3x w 7.5µM meHgCl in Ce (McElwee et al., 2013). Up w high NaAsO2 and cadmium (Sahu et al., 2013). Down 1.9x w DMA in Ce (this study).
ins-8	ZK1251.11	-2.69				*ins-8* is expressed in egg-laying apparatus, gonad, head muscle, neurons, and somatic nervous system, affected by 6 chemicals, predicted to have hormone activity, GO Terms: signal transduction, hormone activity, extracellular region (Wormbase, 2021). Target of Notch receptor GLP-1 (Liu et al., 2021) Down 2.6x w DMA (this study).
ints-8	Y48G10A.4			1.54	1.55	Is enriched in germ line and germline precursor cell, affected by several genes including daf-16; dpy-10; and eat-2 based on RNA-seq; microarray; and proteomic studies. Is affected by five chemicals including rotenone; Zidovudine; and antimycin based on RNA-seq and microarray studies. Is an ortholog of human INTS8 (integrator complex subunit 8). GO Terms: nucleus (Wormbase, 2021). Silencing of C. elegans integrator subunits (including ints-8) disrupts snRNA processing, causes aberrant pre-mRNA splicing, and induces the heat shock response, and is induced by Cadmium (Wu et al., 2019).
irg-5	F35E12.5	1.90	2.72			*irg-5* (infection response gene) is enriched in pharynx, cephalic sheath cell, ventral nerve cord, intestine, neurons, affected by > 20 chemicals, involved in defense response to Gram-positive bacterium (Wormbase, 2021). Up w harmane in Ce (Jakobsen et al., 2013). *F35E12.5* "is involved in the transcriptional response towards several bacterial pathogens, including *P. aeruginosa*" (Bolz et al., 2010; O'Rourke et al., 2006; Pukkila-Worley et al., 2012; Troemel et al., 2006). Up 3.8x w M. nematophilum (O'Rourke et al., 2006). Up w chlorpromazine in Ce (Cao and Aballay, 2016). Repressed in *daf-12(rh273)* and *daf-2* (Fisher and Lithgow, 2006). Up at 25°C in Ce (Gomez-Orte et al., 2018). Up w *C. albicans* in Ce (Pukkila-Worley et al., 2011). F35H12.5::GFP is "primarily induced in the intestine" (Melo and Ruvkun, 2012a). Upregulated by SKN-1 under normal conditions (Oliveira et al., 2009). Up w 20µM HgCl2 and in dose response to 32x w 7.5µM meHg in Ce (McElwee, 2010). Up w Ag+ in Ce (Hunt et al., 2014).
irk-1	R03E9.4		2.12			*irk-1* is expressed in egg-laying apparatus and neurons, IRK-1 exhibits inward rectifier potassium channel activity, involved in regulation of G protein-coupled receptor signaling pathway and regulation of oviposition, localizes to neuron projection and neuronal cell body, close homolog of human KCNJ14, KCNJ18 and KCNJ4 which are implicated in

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						diabetes mellitus (multiple); heart conduction disease (multiple); and long QT syndrome (multiple), GO terms: potassium ion transport, integral component of membrane, plasma membrane (Wormbase, 2021). Protein expression altered with *E. coli*, *S. aureus*, and *V. alginolyticus* in Ce (Sharika et al., 2018).
jkk-1	F35C8.3			1.90		Exhibits JUN kinase kinase activity, involved in hyperosmotic response and locomotion, localizes to axon; cytoplasm; and neuronal cell body, expressed in neurons. Is an ortholog of human MAP2K7 (mitogen-activated protein kinase kinase 7). Affected by 4 chemicals. GO Terms: Activation of MAPK activity, hyperosmotic response, locomotion, metal ion binding, neuronal cell body (Wormbase, 2021). Asenite-induced germline apoptosis was blocked in loss-of-function allele c-Jun N-terminal kinase (jkk-1) (Pei et al., 2008), similar effects after Cu and Ni exposure (Caito et al., 2012). Upregulated with D. coniospora infection (Engelmann et al., 2011).
jmjd-1.1	F43G6.6			-2.13		Is predicted to have metal ion binding activity. Human ortholog(s) of this gene are implicated in syndromic X-linked intellectual disability Siderius type. Is an ortholog of human KDM7A (lysine demethylase 7A). Affected by nine chemicals. GO Terms: chromatin organization, metal ion binding, nucleus, oxidation-reduction process, oxidoreductase activity (Wormbase, 2021). Up 3.6X with meHgCl (McElwee et al., 2013).
kcc-1	R13A1.2			-2.14		Exhibits potassium:chloride symporter activity. Is involved in chloride transport and potassium ion transport. Is expressed in several structures, including hermaphrodite distal tip cell, pharyngeal muscle cell, tail neurons, ventral nerve cord, and vulva. Human ortholog(s) of this gene are implicated in agenesis of the corpus callosum with peripheral neuropathy, early infantile epileptic encephalopathy 34, and idiopathic generalized epilepsy 14. Is an ortholog of human SLC12A4 (solute carrier family 12 member 4), SLC12A5 (solute carrier family 12 member 5), and SLC12A7 (solute carrier family 12 member 7). GO Terms: chloride ion homeostasis, integral component of membrane, synapse (Wormbase, 2021).
kel-8	W02G9.2				1.54	Is involved in protein ubiquitination and ubiquitin-dependent protein catabolic process. Is expressed in command interneuron and intestine. Is an ortholog of human KLHL8 (kelch like family member 8). GO Terms: neuronal cell body, synapse, protein ubiquitination (Wormbase, 2021). Kel-8 protects C. elegans from cadmium toxicity in a mek-1 (MAPKK)-dependent manner (Cui et al., 2007).
ketn-1	F54E2.3	-2.27				*F54E2.4 is dead! Merged into -> ketn-1* is expressed in anal depressor muscle, body wall musculature, male gonad, and pharyngeal muscle cell, enriched in pharynx, germ line, body wall musculature, vulval muscle, ventral nerve cord, nerve ring, dorsal nerve cord, somatic neuron, tail neuron, lateral nerve cord, body wall muscle cell, head mesodermal

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						cell, hermaphrodite-specific anatomical entity and muscle cell, affected by 14 chemicals, exhibits actin filament binding activity, close human homolog MYOT is implicated in myofibrillar myopathy 3 and spheroid body myopathy, GO Terms: muscle contraction, actin filament binding (Wormbase, 2021). Down 2.1x w *P. aeruginosa* in Ce (McElwee et al., 2013). Down 20% w *D. coniospora* in Ce (Pujol et al., 2008b).
kin-30	M01B2.1				-3.33	Is predicted to have protein tyrosine kinase activity. Predicted to localize to integral component of plasma membrane and receptor complex. Human ortholog(s) of this gene are implicated in several diseases, including adult-onset leukoencephalopathy with axonal spheroids and pigmented glia; basal ganglia calcification; and hematologic cancer (multiple). Is an ortholog of several human genes including KIT, PDGFRA, and PDGFRB (Wormbase, 2021).
lat-1	B0457.1			1.65		Up 1.5X with NaAsO2 in this study. Exhibits endopeptidase activity and protein homodimerization activity. Is involved in several processes, including anterior/posterior pattern specification; embryo development; and self proteolysis. Localizes to integral component of plasma membrane. lat-1 is required for embryonic elongation, pharyngeal development, and sperm development and/or function; LAT-1 is expressed in developing epithelia, and also in pharyngeal muscles and neurons, and in the nerve ring;. Is an ortholog of human ADGRL3 (adhesion G protein-coupled receptor L3). Affected by >10 chemicals. Human ortholog(s) of this gene are implicated in glioblastoma and hypertrophic cardiomyopathy. GO Terms: Carbohydrate binding, embryo development ending in birth or egg hatching, G protein coupled receptor activity, integral component of membrane, integral component of plasma membrane, sexual reproduction (Wormbase, 2021). Latrophilin is required for toxicity of black widow spider venom (Mee et al., 2004).
lbp-8	T22G5.6		6.8			*lbp-8* is affected by > 20 chemicals, localizes to lysosome and nucleus, enriched in intestine, AFD, ASER and male-specific anatomical entity, encodes a lipid binding protein involved in long-chain fatty acid transport, close human homologs FABP5, FABP9 and PMP2 are implicated in Charcot-Marie-Tooth disease type 1G, GO Terms: long-chain fatty acid transporter activity, lysosome, nucleus (Wormbase, 2021). “the lysosomal acid lipase LIPL-4 triggered nuclear translocalization of a lysosomal lipid chaperone LBP-8, which promoted longevity by activating the nuclear hormone receptors NHR-49 and NHR-80.” (Folick et al., 2015). “SKN-1 upregulates *lipl-3* and *lbp-8* in WT and GSC(−) animals” (Steinbaugh et al., 2015).
ldb-1	F58A3.1			1.63		Exhibits DNA-binding transcription factor activity and LIM domain binding activity. Is involved in mechanosensory behavior; synapse assembly; and vulval development. Is

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						expressed in several structures, including AIY; body wall musculature; gonad; neurons; and vulval muscle. Is an ortholog of human LDB1 (LIM domain binding 1) and LDB2 (LIM domain binding 2). Affected by 9 chemicals. GO Terms: DNA-binding transcription factor activity, locomotion, mechanosensory behavior, nervous system development, nucleus, synapse assembly, vulval development (Wormbase, 2021). Inactivation of *ldb-1* (by RNAi) shortened life span, *ldb-1* is a DAF-16 target gene (Wook Oh et al., 2006). Up 1.6X with M. nematophilum infection (O'Rourke et al., 2006).
lea-1	K08H10.1			1.52		Is predicted to have lipid binding activity. Is involved in hyperosmotic response; response to desiccation; and response to heat. Is expressed in several structures, including body wall musculature; gonad; head neurons; and tail neurons. Is an ortholog of human PLIN4 (perilipin 4). Affected by >20 chemicals. GO Terms: hyperosmotic response, lipid binding, lipid transport, response to heat (Wormbase, 2021). SKN-1 downregulated gene, decreases As resistance (Oliveira et al., 2009).
let-765	F20H11.2				1.54	Is involved in several processes, including nematode male tail tip morphogenesis; positive regulation of Ras protein signal transduction; and vulval cell fate specification. Predicted to have chromatin DNA binding activity and histone binding activity. Localizes to nucleus. Is an ortholog of human SBNO1. GO Terms: chromatin DNA binding, histone binding, male tip morphogenesis, nucleus, vulval fate specification (Wormbase, 2021).
lgc-9	C04C3.2		1.90			*C04C3.2* is enriched in neurons, affected by 7 chemicals, GO Terms: integral component of plasma membrane, ion transmembrane transport, nervous system process (Wormbase, 2021).
lim-9	F25H5.1				-2.17	Exhibits protein domain specific binding activity. Localizes to M band. Is expressed in several structures, including body wall musculature, excretory canal, non-striated muscle, spermatheca, and vulva. Is an ortholog of human FHL2 (four and a half LIM domains 2). GO Terms: metal ion binding, nucleus, protein binding. Affected by >15 chemicals. Is an ortholog of human FHL2 (four and a half LIM domains 2). (Wormbase, 2021). Down 2.2X with DMA in this study.
lst-4	Y37A1B.2			1.92		3.07X upreg after 24h infection with Drechmeria coniospora (Pujol et al., 2008a). Exhibits enzyme binding activity; phosphatidylinositol phosphate binding activity; and protein self-association. Is involved in execution phase of apoptosis and phagosome-lysosome fusion involved in apoptotic cell clearance. Localizes to early phagosome. Is expressed in embryonic cell; gonad; and gonadal sheath cell. Is an ortholog of human SNX18 (sorting nexin 18) and SNX33 (sorting nexin 33). Affected by nine chemicals. GO Terms: GTPase binding, lipid binding, membrane, apoptosis, protein binding, protein transport, phagosome (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
lurp-2	F25H9.1				-2.60	Is affected by six chemicals including metformin, Sirolimus, and Psoralens based on RNA-seq and microarray studies (Wormbase, 2021).
magi-1	K01A6.2			1.57		Exhibits beta-catenin binding activity and glutamate receptor binding activity. Is involved in habituation; long-term memory; and regulation of protein localization. Localizes to adherens junction and synapse. Is expressed in several structures, including anus; egg-laying apparatus; intestine; neurons; and pharynx. Human ortholog(s) of this gene are implicated in nephrotic syndrome type 15. Is an ortholog of human MAGI2 and MAGI3. Affected by eight chemicals. GO Terms: cell junction, membrane, cytoplasm, synapse (Wormbase, 2021). Graphene oxide disrupts the protein-protein interaction between Neuroligin/NLG-1 and DLG-1 or MAGI-1 in nematode Caenorhabditis elegans (Zhao et al., 2020).
mask-1	R11A8.7			1.82		Up 2.8X with 24h D.c infection (Pujol et al., 2008a). Is predicted to have RNA binding activity. Predicted to localize to cytoplasm. Is expressed in several structures, including hypodermis; intestine; nervous system; pharynx; head and vulva. Is an ortholog of human ANKHD1-EIF4EBP3 (ANKHD1-EIF4EBP3 readthrough) and ANKRD17 (ankyrin repeat domain 17). Affected by 10 chemicals (Wormbase, 2021).
mbl-1	K02H8.1	-1.99	1.90			*mbl-1* is expressed in excretory cell, enriched in intestine, neurons and retrovesicular ganglion, affected by 10 chemicals, close human homologs MBNL1, MBNL2, and MBNL3, GO Terms: metal ion binding, nucleus, regulation of alternative mRNA splicing (Wormbase, 2021). *C. elegans* Muscleblind homolog *mbl-1* functions in neurons to regulate synapse formation (Spilker et al., 2012). Loss of "MBL-1 (the sole ortholog of mammalian MBNLs), which is known to be required for normal lifespan, shortens lifespan by decreasing the activity of p38 MAPK/PMK-1 as well as the function of transcription factors ATF-7 and SKN-1", also "mitochondrial stress caused by knockdown of mitochondrial electron transport chain components promotes the longevity of mbl-1 mutants in a partially PMK-1-dependent manner" (Matilainen et al., 2021).
mca-2	R05C11.3			1.51		Is predicted to have ATP binding activity and calcium transmembrane transporter activity, phosphorylative mechanism. Is expressed in hypodermis. Human ortholog(s) of this gene are implicated in X-linked spinocerebellar ataxia 1 and autosomal recessive nonsyndromic deafness 12. Is an ortholog of several human genes including ATP2B2, ATP2B3, and ATP2B4. Affected by >10 chemicals. GO Terms: ATP binding, calcium ion transmembrane transport, integral component of the membrane (Wormbase, 2021).
mcd-1	Y51H1A.6			1.64		Is predicted to have metal ion binding activity. Is involved in nematode larval development; positive regulation of growth rate; and programmed cell death. Affected by 5 chemicals. GO Terms: apoptotic process, metal ion binding (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
mcm-7	F32D1.10				1.55	Is predicted to have ATP binding activity; DNA binding activity; and DNA helicase activity. Is involved in MCM complex assembly and localizes in nucleus; embryo development; and mitotic sister chromatid segregation. Is expressed in head; intestine; tail, and body wall musculature. Human ortholog(s) of this gene implicated in hepatocellular carcinoma. Is an ortholog of human MCM7 (minichromosome maintenance complex component 7). GO Terms: ATP Binding, DNA binding, double-strand break repair via break-induced replication, nucleus, MCM complex activity (Wormbase, 2021). MCM-7 was decreased in abundance upon UV treatment (Edifizi et al., 2017). Decreased after valproate exposure (Munasinghe, 2015).
mec-1	T07H8.4			1.60		Down 1.7X with NaAsO2, down 1.5X with DMA in this study. Is predicted to have calcium ion binding activity and serine-type endopeptidase inhibitor activity. Is involved in detection of mechanical stimulus involved in sensory perception of touch; extracellular structure organization; and mechanosensory behavior. Is expressed in PVT; cholinergic neurons; intestinal muscle; and touch receptor neurons. Is an ortholog of human TFPI2 (tissue factor pathway inhibitor 2). uniform MEC-1 localization requires the activity of him-4. Affected by eight chemicals. GO Terms: calcium ion binding, sensory perception, negative reg of endopeptidase activity (Wormbase, 2021).
meg-1	K02B9.1	1.82				MEG-1 is involved in P granule disassembly and germ cell proliferation, expressed in embryonic founder cells, germline precursor cell and germ line, affected by > 15 chemicals, GO Terms: germ cell proliferation, reproduction (Wormbase, 2021). Up 1.2x w *D. coniospora* in Ce (Pujol et al., 2008b). Up 1.4x w *M. nematophilum* in Ce (O'Rourke et al., 2006).
mes-1	F54F7.5			1.79		Is required for unequal cell divisions in the early embryonic germline; during embryonic cell divisions, mes-1 is involved in positioning of the early mitotic spindle and of associated P granules. Is involved in asymmetric protein localization involved in cell fate determination; establishment of mitotic spindle localization; and left/right axis specification. Localizes to plasma membrane. Affected by >10 chemicals. GO Terms: Cell fate specification, gamete generation, integral component of membrane, embryonic digestive tract morphogenesis (Wormbase, 2021). mes-1 mutant nematodes that are fertile survive as long as wild-type when exposed to P. aeruginosa, whereas mes-1 mutant nematodes that are sterile are much more resistant (Alper et al., 2010).
mig-15	ZC504.4				-2.13	Is predicted to have ATP binding activity and protein serine/threonine kinase activity. Is involved in several processes, including body morphogenesis, dorsal/ventral axon guidance, and regulation of GABAergic synaptic transmission. Is expressed in several structures, including QL, QR, body wall musculature, pharynx, and somatic nervous

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						system. Is used to study epilepsy. Is an ortholog of human MINK1 (misshapen like kinase 1) and TNIK (TRAF2 and NCK interacting kinase). Affected by six chemicals. GO Terms: activation of protein kinase activity, ATP binding, dorsal /ventral axon guidance, neuron projection morphogenesis, reproduction (Wormbase, 2021).
mlc-7	K08E3.10				1.78	GO Term: Calcium ion binding. Affected by >10 chemicals. Human ortholog(s) of this gene are implicated in hypertrophic cardiomyopathy 8. (Wormbase, 2021).
mltn-2	Y52B11A.7	1.84				*mltn-2* is enriched in intestine, germ line, AVK and head mesodermal cell, affected by four chemicals, predicted to encode a protein with the following domains: Moulting cycle and Moulting cycle MLT-10-like protein, GO Term: integral component of membrane (Wormbase, 2021).
mob-2	F09A5.4			1.62		Down 0.2X with 24h Drechmeria coniospora infection (Pujol et al., 2008a). Is enriched in intestine and neurons based on proteomic and microarray studies. Is affected by six chemicals including Tunicamycin; Atrazine; and cadmium based on RNA-seq and microarray studies. Is an ortholog of human MOB2 (MOB kinase activator 2) (Wormbase, 2021).
mrp-6	F20B6.3			2.67		Is predicted to have ATP binding activity; ATPase activity; and ATPase-coupled xenobiotic transmembrane transporter activity. Affected by 7 chemicals. GO Terms: Integral component of the membrane, xenobiotic transport, nucleotide binding (Wormbase, 2021). Expressed in intestine, neurons, nerve cord (Hunt-Newbury 2007). RNAi phenotype: egg laying defect (Sheps et al., 2004). Knockdown, cold induced longevity (Lee et al., 2019).
mrp-7	Y43F8C.12	1.89		1.77	1.77	*mrp-7* is expressed in DA neuron, enriched in intestine, neurons, germline precursor cell, body wall musculature, affected by > 15 chemicals, involved in response to methylmercury, predicted to have ATP binding activity; ATPase activity; and ATPase-coupled transmembrane transporter activity, close human homolog ABCC2 is implicated in Dubin-Johnson syndrome; arterial calcification of infancy; and pseudoxanthoma elasticum, GO Terms: response to methylmercury, integral component of membrane (Wormbase, 2021). Regulated by NaAsO2 exposure (Sahu et al., 2013). Loss of the *mrp-7* caused Hg sensitivity and 2x increase in Hg levels in the nematode compared to wild type (Sedensky and Morgan, 2018). Inhibits MeHg-induced GST and heat-shock protein (HSP) gene expression and animal toxicity (VanDuyn and Nass, 2014). Up 1.9X with NaAsO2 in this study.
mup-2	T22E5.5.1			1.55		Is involved in several processes, including axonal fasciculation; cell positioning, regulated muscle contraction in larval and adult body wall muscle, epidermal morphogenesis, and is required for proper function of the hermaphrodite nonstriated oviduct myoepithelial

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						sheath, proper growth, fertility, and sarcomere organization. Human ortholog(s) of this gene are implicated in intrinsic cardiomyopathy (multiple) and muscle tissue disease (multiple). Is an ortholog of human TNNT1 tiar(troponin T1, slow skeletal type) and TNNT3 (troponin T3, fast skeletal type). Affected by >10 chemicals. GO Terms: axonal fasciculation, embryonic morphogenesis, larval somatic muscle development, muscle contraction, ovulation (Wormbase, 2021). 1.63X upreg of TNNT1 in HepaRG cells treated with NaAsO2 (Dreval et al., 2018). MUP-2 contains at least one significantly peroxide-sensitive cysteine (target of peroxide stress) (Kumsta et al., 2010). Increased expression with organophosphate dichlorvos exposure (Lewis et al., 2013).
nas-14	F09E8.6			-2.19		Is predicted to have metalloendopeptidase activity and zinc ion binding activity. Is expressed in marginal cell and pharyngeal muscle cell. Is an ortholog of human ASTL (astacin like metalloendopeptidase). Affected by ten chemicals. GO Terms: extracellular region, metal ion binding, hydrolase activity, zinc ion binding (Wormbase, 2021). Down 1.8X with DMA in this study.
nas-21	T11F9.5		2.05			*nas-21* is expressed in gonad, hyp7 syncytium, intestine, and uterine seam cell, affected by 11 chemicals, predicted to have metalloendopeptidase activity and zinc ion binding activity, GO Terms: molting cycle, collagen and cuticulin-based cuticle, zinc ion binding (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
nas-23	R10H1.5		-6.67			*nas-23* is expressed in hyp7 syncytium; intestine; pharyngeal muscle cell; and rectum, affected by 8 chemicals, predicted to have metalloendopeptidase activity and zinc ion binding activity, GO Terms: metal ion binding, zinc ion binding, metalloendopeptidase activity, (Wormbase, 2021). Up w three bacterial species in Ce (Engelmann et al., 2011).
nas-27	T23F4.4				-2.37	Is predicted to have metalloendopeptidase activity and zinc ion binding activity. Is expressed in hyp7 syncytium, intestine, and rectal epithelium. GO Terms: extracellular region, metal ion binding, molting cycle, collagen and cuticulin-based cuticle, proteolysis (Wormbase, 2021).
nfki-1	C33A11.1			1.54		Is predicted to have transcription factor binding activity. Is expressed in RMGL; RMGR; and nervous system. Is an ortholog of human NFKBIZ (NFKB inhibitor zeta). Affected by seven chemicals. GO Terms: apoptotic process, positive regulation of cell differentiation, regulation of transcription by RNA polymerase, transcription (Wormbase, 2021).
nhr-127	T13F3.3		-4.05		-2.02	*nhr-127* is expressed in seam cell, enriched in hypodermis, affected by 14 chemicals, predicted to have DNA-binding transcription factor activity; sequence-specific DNA binding activity; and zinc ion binding activity, GO terms: regulation of transcription, DNA-templated, nucleus, DNA binding, DNA-binding transcription factor activity, zinc ion

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						binding (Wormbase, 2021). Down 29% w *P. luminescens* in Ce (Wong et al., 2007). Required for lifespan extension with probiotic *L. fermentum* JDFM216 (Park et al., 2018).
nhr-147	C03G6.8				-2.06	Is predicted to have DNA-binding transcription factor activity, sequence-specific DNA binding activity, and zinc ion binding activity. Human ortholog(s) of this gene are implicated in maturity-onset diabetes of the young type 1 and type 2 diabetes mellitus. Is an ortholog of human HNF4A (hepatocyte nuclear factor 4 alpha) and HNF4G (hepatocyte nuclear factor 4 gamma). GO Terms: anatomical structure development, metal ion binding, nucleus, regulation of transcription, regulation of transcription by RNA polymerase II. Is affected by 12 chemicals (Wormbase, 2021). Down 3X with DMA, down 2X with HgCl2 in this study. Up 1.5X with 4h Ag+ (Hunt et al., 2014).
nhr-214	T07C5.3		-4.40			*nhr-214* is expressed in head neurons, affected by 6 chemicals, predicted to have DNA-binding transcription factor activity; sequence-specific DNA binding activity; and zinc ion binding activity, GO terms: nucleus, DNA-binding transcription factor activity, regulation of transcription, zinc ion binding (Wormbase, 2021). Up 5.5x w 7.5µM meHg in Ce (McElwee et al., 2013).
nhr-218	T13F3.2		-3.78			*nhr-218* is enriched in NSM neurons, homolog of human PPARA (peroxisome proliferator activated receptor alpha), affected by 9 chemicals, predicted to have DNA-binding transcription factor activity; sequence-specific DNA binding activity; and zinc ion binding activity, GO Terms: regulation of transcription, DNA-templated, nucleus, DNA binding transcription factor activity, zinc ion binding (Wormbase, 2021). Down 3.6x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
nhr-229	Y116A8C.18				-2.63	Is predicted to have DNA-binding transcription factor activity, sequence-specific DNA binding activity, and zinc ion binding activity. Affected by Sirolimus according to microarray. GO Terms: Metal ion binding, nucleus, DNA binding, zinc ion binding, regulation of translation (Wormbase, 2021).
nhr-23	C01H6.5	1.78				*nhr-23* is enriched in PVD and OLL neurons, germ line, hypodermis, germline precursor cell and head mesodermal cell, expressed in gonad head neurons, and oocyte, affected by 8 chemicals, exhibits RNA polymerase II regulatory region sequence-specific DNA binding activity, involved in molting cycle and positive regulation of transcription, close human homolog RORC is implicated in idiopathic generalized epilepsy 15 (Wormbase, 2021).
nhr-30	C25E10.1			-2.49		Down 1.5X with DMA in this study. Upregulated with Harposporium infection (Engelmann et al., 2011). Is predicted to have DNA-binding transcription factor activity, sequence-specific DNA binding activity, and zinc ion binding activity. Is expressed in head. GO Terms: DNA binding, metal ion binding, nucleus, regulation of transcription. Affected by six chemicals. (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
nhr-37	F44C4.2				-2.19	Is predicted to have DNA-binding transcription factor activity, sequence-specific DNA binding activity, and zinc ion binding activity. Is expressed in neurons and seam cell. Is an ortholog of human PPARA (peroxisome proliferator activated receptor alpha). Affected by five chemicals. GO Terms: DNA binding, metal ion binding, regulation of transcription (Wormbase, 2021).
nhr-66	T09A12.4			1.55		Is predicted to have DNA-binding transcription factor activity; sequence-specific DNA binding activity; and zinc ion binding activity. Predicted to localize to nucleus. Is expressed in several structures, including ganglia; hypodermis; intestine; spermatheca; and terminal bulb. Microarray analysis indicates that expression of nhr-66 in neurons and seam cells is upregulated in response to exposure to cholesterol (Wormbase, 2021). Decreased mRNA expression with 1ug/L nanopolystyrene exposure (Qiu et al., 2020).
nhr-81	C47F8.8	1.94				*nhr-81* is predicted to have DNA-binding transcription factor activity; sequence-specific DNA binding activity; and zinc ion binding activity, expressed in seam cell, GO Terms: metal ion binding, regulation of transcription, DNA-templated, zinc ion binding, nucleus (Wormbase, 2021).
nit-1	ZK1058.6	3.64	2.21			*nit-1* is enriched in germline precursor cell, hypodermis, intestine and muscle cell, a predicted nitrilase, affected by >20 chemicals (WormBase 20201). Down 2x w *S. aureus* in Ce (Irazoqui et al., 2010). Down 26% w M. nematophelium (O'Rourke et al., 2006). Regulated by PMK-1 (Keshet et al., 2017). Up 3.1x w 7.5µM meHg in Ce (McElwee et al., 2013). Up w Cd and up 8x w NaAsO2 in Ce (Sahu et al., 2013). Upregulated by SKN-1 in Ce (Oliveira et al., 2009). Up w juglone in Ce (Przybysz et al., 2009). Up w H2S and upregulated by SKN-1 in Ce (Miller et al., 2011). Up >4x w acrylamide in Ce (Hasegawa et al., 2008).
nkat-1	F28H6.3		2.10			*nkat-1* is expressed in neurons, affected by 7 chemicals, predicted to have catalytic activity and pyridoxal phosphate binding activity, close homolog of human KYAT3, GO Terms: mitochondrion (Wormbase, 2021). X
nkcc-1	Y37A1C.1			1.53		Predicted to have sodium:potassium:chloride symporter activity. Predicted to be involved in cell volume homeostasis; inorganic ion homeostasis; and inorganic ion transmembrane transport. Predicted to localize to integral component of membrane. Is expressed in body wall musculature; intestine; neurons; oocyte; and vulval muscle. Y37A1C.1A protein is predicted to be mitochondrial with 52% accuracy. Human ortholog(s) of this gene are implicated in Bartter disease type 1 and Gitelman syndrome. Is an ortholog of human SLC12A2 and SLC12A3. Affected by 15 chemicals. GO Terms: chloride ion homeostasis, chloride transmembrane transport, integral component of membrane, ion transport (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
nlp-49	H05L03.3				-2.19	Is expressed in nerve ring neurons. Affected by eight chemicals (Wormbase, 2021).
nlp-81	Y67D8B.4			-2.29		Is enriched in neurons and retrovesicular ganglion based on microarray and tiling array studies. Is affected by six chemicals including allantoin, Sirolimus, and Rifampin based on RNA-seq and microarray studies (Wormbase, 2021). Up 2X with 8h S. aureus infection (Irazoqui et al., 2010).
nos-3	Y53C12B.3			2.12	2.30	Up 1.79X increase with12h D.c (natural fungal pathogen Drechmeria coniospora) infection, 2.27X increase after 24h D.c infection (Pujol et al., 2008a). 1.5X increase after M. nematophilum infection (O'Rourke et al., 2006). Is involved in positive regulation of meiotic nuclear division. RNA-binding, localizes to cytoplasm. Is expressed in several structures, including Psub3; Psub4; Z2; Z3; and germ line, GO Term: regulation of translation (Wormbase, 2021). Down 2X with DMA in this study.
npp-13	Y37E3.15			1.95		Is involved in several processes, including regulation of mitotic cell cycle. Human ortholog(s) of this gene are implicated in nephrotic syndrome type 12. Is an ortholog of human NUP93 (nucleoporin 93). GO Terms: embryo development, membrane, nucleus, protein transport. Affected by three chemicals (Wormbase, 2021). Knockdown of npp-3 causes a reduction in nuclear size reflects diminished nuclear import (Galy et al.2003). Upon heat shock in C. elegans, NPP-13 also interacts with Pol II-transcribed heat-responsive genes (hsp-16.2/41 promoter) at the pore (Rohner et al., 2013).
npr-33	F31B9.1			-2.30		Is predicted to have G protein-coupled receptor activity. Human ortholog(s) of this gene are implicated in essential hypertension. Affected by five chemicals. GO Terms: integral component of membrane, G protein-coupled receptor activity (Wormbase, 2021).
nprt-1	Y54G2A.17	1.84				*nprt-1* is a close homolog of human NAPRT (nicotinate phosphoribosyltransferase) predicted to have nicotinate phosphoribosyltransferase activity, GO Terms: metal ion binding (Wormbase, 2021).
nrfl-1				1.60		Exhibits protein membrane adaptor activity. Localizes to apical plasma membrane. Is expressed in excretory canal; pharyngeal muscle cell; intestine and tail. Affected by 11 chemicals. Human ortholog(s) of this gene are implicated in hypophosphatemic nephrolithiasis/osteoporosis 2. in C. elegans, nrfl-1 is required for normally short lifespan and for normal acetylcholine neurotransmission. Is an ortholog of human SLC9A3R1 (SLC9A3 regulator 1) (Wormbase, 2021).
nspa-1	H12D21.1	10.7	8.7			*nspa-1* is affected by nine chemicals (Wormbase, 2021). Upregulated when DAF-16 is activated + putative direct target of DAF-16 (McElwee et al., 2003). Up 2.6x w meHgCl in Ce (McElwee et al., 2013).
nspa-5	ZC412.6	9.44	7.5			*nspa-5* is enriched in amphid sheath cell, neurons, and in male, affected by nineteen chemicals including (Wormbase, 2021). Upregulated by SKN-1 & up w NaAsO2 in Ce

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						(Oliveira et al., 2009). Up w *D. coniospora* and *Harposporium* in Ce (Engelmann et al., 2011).
nspa-8	W06A7.5	34.0	21.8			*nspa-8* is enriched in amphid sheath cell and in male, affected by fifteen chemicals (Wormbase, 2021). Upregulated by SKN-1 & up w NaAsO2 in Ce (Oliveira et al., 2009).
nspd-8	Y23H5B.9	-1.83				*nspd-8* is affected by five chemicals (Wormbase, 2021). Down 1.8x w HgCl2 in Ce (this study).
nspd-9	F26A1.10		2.07			*nspd-9* is expressed in head, enriched in neurons, germ line and male, affected by 18 chemicals (Wormbase, 2021). Up w *D. coniospora* & *Harposporium* in Ce (Engelmann et al., 2011). Up 2.4x w 7.5µM meHg in Ce (McElwee et al., 2013). Up 1.5x w NaAsO2 (this study).
oac-36	F56H6.12	2.28				*oac-36* is enriched in germ line, affected by 2 chemicals, predicted to have transferase activity for acyl groups other than amino-acyl groups, GO Terms: cellular polysaccharide biosynthetic process, integral component of membrane (Wormbase, 2021).
oac-51	W03B1.7		-3.83			*oac-51* is enriched in hypodermis and somatic gonad precursor, affected by 18 chemicals, GO Terms: cellular polysaccharide biosynthetic process, integral component of membrane (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
oac-57	K09E10.1	-1.93				*oac-57* is enriched in intestine, head mesodermal cell and neurons, affected by 12 chemicals, GO Terms: cellular polysaccharide biosynthetic process, integral component of membrane, transferring acyl groups other than amino-acyl groups (Wormbase, 2021). Up w meHgCl (McElwee, 2013) and up w D. coniospora + Harposporium (Engelman 2011) and up w P. luminescens (O'Rourke, 2006).
oac-58	K09E10.2	-1.97				*oac-58* is enriched in intestine, affected by 5 chemicals, predicted to have transferase activity, transferring acyl groups other than amino-acyl groups, GO Term: integral component of membrane (Wormbase, 2021). Up 3.2x w meHgCl (McElwee 2013) and up w exposure to 3 bacterial species (Engelman 2011).
pam-1	F49E8.3			1.54		0.6X downreg after M. nematophilum infection (O'Rourke et al., 2006). Exhibits metalloaminopeptidase activity. Is involved in several processes, including exit from meiosis; first cell cycle pseudocleavage; and regulation of oocyte maturation. Localizes to condensed chromosome; cytoplasm; and mitotic spindle pole. Is expressed in amphid process; intestine; male-specific anatomical entity; nerve ring; and tail neurons. in vitro, PAM-1 exhibits metal-dependent aminopeptidase activity, hydrolyzing the N-terminal amino acid from various peptide substrates. Is an ortholog of human NPEPPS (aminopeptidase puromycin sensitive). Affected by 4 chemicals. GO Terms: cell differentiation, condensed chromosome, embryo development, metal ion binding, oogenesis, zinc ion binding (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
pde-6	Y95B8A.10				-2.18	Is predicted to have 3',5'-cyclic-AMP phosphodiesterase activity. Is involved in negative regulation of oocyte maturation. Human ortholog(s) of this gene are implicated in primary pigmented nodular adrenocortical disease and striatonigral degeneration. Is an ortholog of human PDE8A (phosphodiesterase 8A) and PDE8B (phosphodiesterase 8B). Affected by 10 chemicals. GO Terms: hydrolase activity, metal ion binding, negative regulation of oocyte maturation, signal transduction (Wormbase, 2021).
pdk-1	H42K12.1			1.52		Up 1.5X with DMA in this study. Exhibits protein kinase activity PDK-1 is a component of the DAF-2/insulin receptor-like signaling pathway and accordingly, functions to regulate such processes as dauer larvae formation, longevity, and salt chemotaxis learning; genetic analyses indicate that, in regulating dauer arrest, PDK-1 acts downstream of AGE-1/PI3K and upstream of the AKT-1 and AKT-2 kinases; a PDK-1::GFP fusion protein is expressed broadly beginning in late stage embryos and continuing on through adulthood; expression is seen in head, tail, and ventral cord motor neurons, pharyngeal tissues, hypodermal cells, the intestine, and the somatic gonad; in neurons, the PDK-1::GFP localizes to cell bodies and processes, with occasional expression seen in some neuronal nuclei. Is an ortholog of human PDPK1 (3-phosphoinositide dependent protein kinase 1). Human ortholog(s) of this gene implicated in prostate cancer. Affected by nine chemicals. GO Terms: ATP binding, axon, cytoplasm, learning or memory, nucleus, regulation of chemotaxis (Wormbase, 2021). PDK-1/PDK1 (gain of function mutation) negatively regulated the arsenite-induced apoptosis (Wang et al., 2014). SKN-1 downregulates genes that encode the IIS pathway kinase PDK-1 and the DAF-2 agonist INS-7 (Oliveira et al., 2009). insulin signaling pathway, PDK-1 and AKT-1/2, were identified as part of this emerging pathway. The insulin signaling pathway has been shown to be involved in both aging and the oxidative stress response in *C. elegans* (Kaletsky and Murphy, 2010). "AKT-1/AKT-2/SGK-1 have been isolated from whole-worm extracts showing they form a protein complex that transduces the PI 3-kinase signals via PDK-1 to control the localization and activation of DAF-16 by direct phosphorylation (Hertweck et al., 2004)" (Tissenbaum, 2018).
pdxk-1	F57C9.1	2.01	2.00			*pdxk-1* is enriched in BAG, excretory cell, GABAergic neuron, hypodermis and germ line, affected by 6 chemicals, a close homolog of human PDXK (pyridoxal kinase), predicted to have ATP binding activity; metal ion binding activity; and pyridoxal kinase activity, GO term: metal ion binding (Wormbase, 2021). Has SKN-1 binding site, up 2x w juglone in Ce (Przybysz et al., 2009). Up 2x w 7.5µM meHg in Ce (McElwee et al., 2013). "the pdxk-1 mutant was readily paralyzed by levamisole suggests a presynaptic role for *pdxk-1* in the

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						nervous system" (Nordquist et al., 2018). Upregulated by SKN-1 and As stress (Oliveira et al., 2009).
pgph-2	F44E7.2				1.87	Is affected by >15 chemicals. GO Terms: Cytoplasm, dephosphorylation, phosphatase activity. Is expressed in hypodermis; intestinal muscle; and nervous system. Is an ortholog of human PDXP (pyridoxal phosphatase) and PGP (phosphoglycolate phosphatase) (Wormbase, 2021).
pho-11	C05C10.4		2.22			*pho-11* is affected by > 15 chemicals, predicted to have acid phosphatase activity (Wormbase, 2021). Down 56% w *M. nematophilum* in Ce (O'Rourke et al., 2006). Up 5x w *Y. pestis* in Ce (Bolz et al., 2010). Up 2.2x w *P. aeruginosa* in Ce at 4h but down at 8h (Troemel et al., 2006). Up 1.5x w *E. faecalis* in Ce (Wong et al., 2007). Down w *P. aeruginosa* in Ce (Evans et al., 2008). Direct target of DAF-16 and downregulated in *daf-16*- mutants = upregulated by DAF-16 (McElwee et al., 2003). Ethanol response gene (Kwon et al., 2004). Up 1.6x w NaAsO2 (this study).
pigw-1	Y110A2AL.12	-1.85				*pigw-1* is enriched in NSM, germline precursor cell and somatic gonad precursor, affected by 5 chemicals, predicted to have transferase activity, transferring acyl groups, a close homolog of human PIGW, GO Terms: integral component of endoplasmic reticulum membrane, glucosaminyl-phosphatidylinositol O-acyltransferase activity (Wormbase, 2021). Down 1.6x w HgCl2 in Ce (this study).
pitr-5	F09G2.3		-3.24			PITR-5 is predicted to have inorganic phosphate transmembrane transporter activity, close human homologs SLC20A1 and SLC20A2 are implicated in basal ganglia calcification, GO Terms: phosphate ion transmembrane transport, integral component of plasma membrane (Wormbase, 2021). Up 3x w diethyl hydrogen phosphite (DEHP) in Ce (Roh et al., 2007). Down 4x w *P. aeruginosa* in Ce (Evans et al., 2008).
plc-1	F31B12.1	-2.12				*plc-1* is enriched in body wall musculature, vulval muscle, ventral nerve cord, nerve ring, dorsal nerve cord, somatic neuron, tail neuron, lateral nerve cord, pharynx, affected by 12 chemicals, exhibits GTPase inhibitor activity, close homolog of human PLCE1 implicated in nephrotic syndrome type 3, GO Terms: activation of immune response, defense response to Gram-positive bacterium, GTPase inhibitor activity, lipid catabolic process, metal ion binding, negative regulation of GTPase activity (Wormbase, 2021). X
pmr-1	ZK256.1b			1.51		Exhibits calcium transmembrane transporter activity, phosphorylative mechanism and manganese transmembrane transporter activity, phosphorylative mechanism. Is involved in several processes, including metal ion transport; response to calcium ion; and response to manganese ion. Localizes to Golgi apparatus and membrane. Is expressed in male gonad; seam cell; and spermatheca. Is expressed in gonad; intestine; nervous system; pharyngeal-intestinal valve; and seam cell. Human ortholog(s) of this gene are implicated

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						in Hailey-Hailey disease. Is an ortholog of human ATP2C1 Affected by 10 chemicals. GO Terms: ATP binding, calcium ion transport, endoplasmic reticulum, golgi apparatus, integral component of membrane, plasma membrane, responsive to oxidative stress (Wormbase, 2021). *pmr-1* knock down causes animals to become resistant to oxidative stress and suppresses high reactive oxygen species sensitivity of smf-3 RNA-mediated interference and daf-16 worms (Cho et al., 2005). Observations indicate *pmr-1* as a candidate gene implicated in mediating the worm's innate immune response (Schifano et al., 2019). HSP-16. 1 localizes to the medial Golgi and functions together with PMR-1 to mediate the protective effect of preconditioning against heat stroke "PMR-1 deficiency suppresses preconditioning-acquired resistance to heat stroke (Fig. 2d). Importantly, overexpression of PMR-1 is sufficient to promote survival after heat stroke even without preconditioning, bypassing the requirement for both HSF-1 and HSP-16.1" (Kourtis et al., 2012).
pms-2	H12C20.2				-2.54	Is predicted to have ATP binding activity, ATPase activity, and mismatched DNA binding activity. Human ortholog(s) of this gene are implicated in hereditary nonpolyposis colorectal cancer type 4. Is an ortholog of human PMS2 (PMS1 homolog 2, mismatch repair system component). Affected by nine chemicals. GO Terms: ATP binding, cellular response to DNA damage stimulus, mismatch repair (Wormbase, 2021).
pqn-11	C09G1.1				1.75	Up 1.7X with NaAsO2 in this study. Is enriched in male-specific anatomical entity based on microarray studies. PQN-11 encodes an unfamiliar protein with a glutamine/asparagine-rich domain that is dispensable for viability and gross morphology. Is affected by six chemicals including Psoralens; allantoin; and Sirolimus based on RNA-seq and microarray studies (Wormbase, 2021).
prom-1	F26H9.1	1.76				*prom-1* is germline precursor cell, germ line, neurons, affected by thirteen chemicals (Wormbase, 2021).
ptr-12	K07A3.2	1.91			1.98	*ptr-12* is enriched in neurons, hypodermis, germ line, somatic gonad precursor and muscle cell, involved in molting cycle, affected by 9 chemicals, close homolog of human PTCHD3, GO Terms: endocytosis, molting cycle, collagen and cuticulin-based cuticle, integral component of membrane, plasma membrane, cytoplasmic vesicle membrane (Wormbase, 2021). Upregulated after mechanical whole body stretching (Zuela-Sopilniak, Dorfman et al. 2019).
ptr-17	Y18D10A.7				2.09	Affected by >10 chemicals. Go Terms: Integral component of plasma membrane. Is enriched in PLM based on RNA-seq studies. Human ortholog(s) of this gene are implicated in autistic disorder. Is an ortholog of human PTCHD3 (patched domain containing 3) (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
ptr-4	C45B2.7		-4.02			*ptr-4* is enriched in PVD, OLL, hypodermis, intestine, PLM and somatic gonad precursor, affected by > 20 chemicals, involved in endocytosis; molting cycle; and nematode male tail tip morphogenesis, close homolog of human PTCHD3 (may play a role in sperm development or sperm function), GO terms: integral component of membrane, cytoplasmic vesicle membrane, plasma membrane, molting cycle, collagen and cuticulin-based cuticle (Wormbase, 2021).
pyk-1	F25H5.3			1.88		Is predicted to have kinase activity; metal ion binding activity; and pyruvate kinase activity. Human ortholog(s) of this gene are implicated in pyruvate kinase deficiency of red cells. Is an ortholog of human PKLR (pyruvate kinase L/R) and PKM (pyruvate kinase M1/2). Is expressed in body wall musculature and reproductive system. Human ortholog(s) of this gene implicated in Gaucher's disease; congenital nonspherocytic hemolytic anemia; malaria; pyruvate kinase deficiency of red cells; and type 2 diabetes mellitus. Affected by >10 chemicals. GO Terms: metal ion binding, kinase activity, transferase activity (Wormbase, 2021). Pyk-1 mutants live longer than N2, and live even longer with 4,4'-diaminodiphenylsulfone treatment (Cho et al., 2010).
rbm-5	T08B2.5			1.72		Up 1.6X with NaAsO2 in this study. Is expressed in CAN; head neurons; intestinal cell; muscle cell; and ventral nerve cord. Human ortholog(s) of this gene are implicated in TARP syndrome. Is an ortholog of human RBM5 (RNA binding motif protein 5). GO Terms: metal ion binding activity, nucleus (Wormbase, 2021).
rgef-1	F25B3.3				-3.12	Down 2.8X with HgCl2 in this study. Exhibits Rap guanyl-nucleotide exchange factor activity. Is involved in chemotaxis and positive regulation of Ras protein signal transduction. Localizes to cytoplasm and intracellular membrane-bounded organelle. Is expressed in nervous system and neurons, body wall musculature, vulval muscle. Human ortholog(s) of this gene are implicated in platelet-type bleeding disorder 18. Is an ortholog of human RASGRP3 (RAS guanyl releasing protein 3). GO Terms: Ca ion binding, intracellular membrane-bound organelle. Affected by seven chemicals (Wormbase, 2021).
rgef-1	F25B3.3			-2.81		Down 3X with meHgCl in this study. Exhibits Rap guanyl-nucleotide exchange factor activity. Is involved in chemotaxis and positive regulation of Ras protein signal transduction. Localizes to cytoplasm and intracellular membrane-bounded organelle. Is expressed in nervous system and neurons, body wall musculature, vulval muscle. Human ortholog(s) of this gene are implicated in platelet-type bleeding disorder 18. Is an ortholog of human RASGRP3. Affected by allantoin, Sirolimus, metformin, Rifampin, resveratrol, Ag nanoparticles and triclosan. GO Terms: calcium ion binding, chemotaxis, cytoplasm, intracellular membrane-bound organelle, Ras (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
rha-2	C06E1.10			1.8321		Is predicted to have ATP binding activity; RNA binding activity; and RNA helicase activity. Human ortholog(s) of this gene are implicated in 46,XY sex reversal. Is an ortholog of human DHX37 (DEAH-box helicase 37). rha-2 functions in a number of different biological processes, including germline development, body wall muscle organization, and adult lifespan determination. Affected by five chemicals. GO Terms: Nucleus, ATP binding, RNA binding (Wormbase, 2021).
rict-1	F29C12.3			1.76		Is involved in mesendoderm development. Localizes to TORC2 complex. rict-1 activity is required for regulation of fat metabolism, feeding, growth, and life span. Is expressed in several structures, including head neurons; intestine; pharynx; spermatheca; and ventral nerve cord. Is an ortholog of human RICTOR (RPTOR independent companion of MTOR complex 2). Affected by 10 chemicals. GO Terms: TOR signaling, actin cytoskeleton reorganization (Wormbase, 2021). *rict-1* is a major player in TOR signaling "Rictor (Rapamycin-Insensitive Companion of mTOR) … TORC2 is defined as the complex containing LET-363/TOR and RICT-1/Rictor … RICT-1-SGK-1 pathway appears to act in the intestine to regulate fat metabolism independently of DAF-16/FoxO" (Blackwell et al., 2019). "*rict-1* also regulates fat in parallel to insulin-like signaling through daf-2, akt-1, and daf-16 … rict-1;daf-16 double mutants demonstrate shorter life span than either single mutant, indicating that rict-1 does not shorten life span only via regulation of the DAF-16/FOXO transcriptional outputs of insulin signaling" (Soukas et al., 2009). TORC2/rict-1 animals show dysregulation of H4K20 mono- and tri-methyl silencing epigenetic marks (Webster et al., 2013). Oxidative stress transcriptomic response is induced by chronic gamma irradiation (differential regulation of rict-1) (Maremonti et al., 2020). 10ug/L (L1-adult) Ractopamine increased expression levels of daf-15 and rict-1 (Zhuang et al., 2014). RICT-1/mTORC2 is required for activation of the SGK-1 kinase [99], [103], [104], which phosphorylates and inhibits SKN-1 (Tullet et al., 2008a).
rpl-24.1	D1007.12	1.93				*rpl-24.1* is enriched in germ line, body wall musculature, vulval muscle, intestine, pharynx, anal depressor muscle and somatic gonad precursor, affected by seven chemicals, close human homolog RPL24 exhibits RNA binding activity and cadherin binding activity, GO Terms: ribosomal large subunit assembly, structural constituent of ribosome, translation (Wormbase, 2021).
rrf-1	F26A3.8			1.84		Up 1.96X with 24 h Drechmeria coniospora infection (Pujol et al., 2008a). Exhibits DEAD/H-box RNA helicase binding activity and RNA-directed 5'-3' RNA polymerase activity. Is involved in hermaphrodite genitalia morphogenesis and production of siRNA involved in RNA interference. Localizes to mutator focus; nucleus; and polysome. Affected by five chemicals. GO Terms: gene silencing by RNA, hermaphrodite genitalia

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						morphogenesis, nucleus, production of siRNA involved in RNA interference, transcription (Wormbase, 2021). Long-Term Silencing Is Transmitted in a Non-Mendelian Manner and Requires the RNA-Dependent RNA Polymerase rrf-1 (Rechavi et al., 2011).
rrn-3.1	F31C3.9			-3.19		Is affected by several genes including daf-16; npr-1; and lin-28 based on RNA-seq studies. Is affected by four chemicals including rotenone; multi-walled carbon nanotube; and sesamin based on RNA-seq and microarray studies (Wormbase, 2021).
rskn-1	T01H8.1			1.53		Is predicted to have ATP binding activity; magnesium ion binding activity; and protein serine/threonine kinase activity. Human ortholog(s) of this gene are implicated in Coffin-Lowry syndrome and non-syndromic X-linked intellectual disability. Is an ortholog of human RPS6KA1 (ribosomal protein S6 kinase A1). Affected by >10 chemicals. GO Terms: ATP Binding, magnesium ion biding, determination of adult lifespan, transferase activity (Wormbase, 2021). rskn-1 RNAi suppressed spermatocyte dedifferentiation and instead induced meiotic divisions (Cha et al., 2012). Up 2X with 24 h D. coniospora infection ((Pujol et al., 2008a)
sams-3	C06E7.1			1.66		Is expressed in several structures, including enteric muscle; intestine; nervous system; pharynx; and reproductive system. Human ortholog(s) of this gene implicated in hypermethioninemia. Is an ortholog of human MAT1A (methionine adenosyltransferase 1A) and MAT2A (methionine adenosyltransferase 2A). Affected by >10 chemicals. GO Terms: metal ion binding, methionine adenosyltransferase activity, ATP binding (Wormbase, 2021). Reduced SAM synthetase levels (Sams-3 RNAi) releases perinuclear arrays of heterochromatin (Towbin et al., 2012). Up with Harposporium infection (Engelmann et al., 2011).
scl-11	F49E11.6				-5.22	Is enriched in dopaminergic neurons and intestine based on tiling array and RNA-seq studiesIs affected by seven chemicals including cholesterol; lathosterol; and Diazinon based on microarray studies. Is an ortholog of human CRISP2 (cysteine rich secretory protein 2) and GLIPR1 (GLI pathogenesis related 1) (Wormbase, 2021).
sdz-23	F58G4.4	-3.41				*sdz-23* is expressed in embryonic cells, GO Term: integral component of membrane (Wormbase, 2021). Wnt signaling target (Lezzerini and Budovskaya, 2014). Down 2.3x w HgCl2, and down 2.7x w meHgCl, and down 2.6x w DMA in Ce (this study).
sdz-23	F58G4.4			-2.31	-2.70	Expressed in embryonic cells, GO Term: integral component of membrane (Wormbase, 2021). Wnt signaling target (Lezzerini and Budovskaya, 2014). Down 3.4X with NaAsO2, down 2.6X with DMA in this study.
sdz-8	C55A6.5		2.25			*sdz-8* is enriched in body wall muscle cell, affected by thirty-three chemicals, close human homolog CBR3 exhibits NADPH binding activity and carbonyl reductase (NADPH) activity (Wormbase, 2021). Up 15x w NaAsO2 in Ce (Sahu et al., 2013). Upregulated by SKN-1 and

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						As stress (Oliveira et al., 2009). Has SKN-1 binding element(s) and up w juglone in Ce (Przybysz et al., 2009). Up w AgNP and Ag+ in Ce (Hunt et al., 2014). Up w HgCl2 & meHgCl in Ce (McElwee, 2010). Up 3x w acrylamide in Ce (Hasegawa et al., 2008).
ser-1	F59C12.2	-2.08				*ser-1* is enriched in ventral nerve cord and head mesodermal cell, affected by 5 chemicals, exhibits G protein-coupled serotonin receptor activity and serotonin binding activity, close human homolog HTR2B is implicated in alcohol dependence, GO Terms: G protein-coupled serotonin receptor signaling pathway, integral component of plasma membrane, neurotransmitter receptor activity, response to heat (Wormbase, 2021).
set-25	Y43F4B.3			1.77		Is predicted to have metal ion binding activity and methyltransferase activity. Localizes to nuclear heterochromatin. Is expressed in hypodermis; intestine; muscle cell; and neurons. set-25 encodes a putative histone H3 lysine-9 methyltransferase, with a C-terminal SET domain but no obvious non-nematode orthologs EPI. Affected by 9 chemicals. GO Terms: Methyltransferase activity, metal ion binding, nucleus (Wormbase, 2021). High temperature inhibits SET-25–mediated repression in the germ line, causing loss of H3K9me3 (loss of repression) (Klosin et al., 2017).
sftb-1	T08A11.2			1.71		Is predicted to have mRNA binding activity. Is involved in negative regulation of gene expression. large-scale RNAi assays indicate that T08A11.2 activity is essential for a number of processes including embryonic development, normal adult lifespan, vulval morphogenesis, locomotion. ortholog(s) of this gene are implicated in myelodysplastic syndrome. Is an ortholog of human SF3B1 (splicing factor 3b subunit 1). Affected by 4 chemicals. GO Terms: negative regulation of gene expression, nucleus, spliceosome (Wormbase, 2021). Used as a nuclear marker (Serrat et al., 2019). Up 2.5X with D. coniospora infection (Pujol et al., 2008a).
skn-1	T19E7.2				1.51	Exhibits Hsp70 protein binding activity and RNA polymerase II regulatory region sequence-specific DNA binding activity. Is involved in several processes, including endoplasmic reticulum unfolded protein response; positive regulation of cellular response to manganese ion; and positive regulation of transcription from RNA polymerase II promoter in response to heat stress. n Human ortholog(s) of this gene implicated in Alzheimer's disease; cataract; hepatocellular carcinoma; and macular degeneration. during postembryonic development, SKN-1 functions in the p38 MAPK pathway to regulate the oxidative stress response and in parallel to DAF-16/FOXO in the DAF-2-mediated insulin/IGF-1-like signaling pathway to regulate adult lifespan (Wormbase, 2021). The expressions of GCS-1, GSS-1, and SKN-1 were induced by NaAsO2 exposure. Induced 24 and 26% after 1mM and 5mM respectively. SKN-1, orthologue of Nrf2, activates expression of phase 2 genes, including gamma-glutamylcysteine synthetase

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						(GCS-1), which catalyzes the rate-limiting step of glutathione synthesis (Zhang et al., 2020c). Induced by Nickel exposure (Ijomone et al., 2020). SKN-1 is expressed in C. elegans DA neurons, and genetic knockdown renders the neurons vulnerable to MeHg-induced cell death (Vanduyn et al., 2010).
smf-2	K11G12.3				-2.08	Is predicted to have transition metal ion transmembrane transporter activity. Is involved in iron ion homeostasis, manganese ion homeostasis, and response to manganese ion. Localizes to apical plasma membrane. Is expressed in dopaminergic neurons, gonadal sheath cell, marginal cell, and pharyngeal-intestinal valve. Human ortholog(s) of this gene are implicated in hypochromic microcytic anemia. Is an ortholog of human SLC11A1 (solute carrier family 11 member 1) and SLC11A2 (solute carrier family 11 member 2). Affected by seven chemicals. GO Terms: apical plasma membrane, cadmium ion transmembrane transport, cytoplasmic vesicle membrane, integral component of membrane, ion transport, metal ion transport (Wormbase, 2021).
smk-1	F41E6.4			-2.20		Is involved in several processes, including defense response to bacterium, negative regulation of mitotic DNA damage checkpoint, and response to X-ray. Localizes to nucleus. Is expressed in hypodermis, intestine, and tail. Is an ortholog of human PPP4R3A (protein phosphatase 4 regulatory subunit 3A) and PPP4R3B (protein phosphatase 4 regulatory subunit 3B). Affected by nine chemicals. GO Terms: cellular response to DNA damage stimulus, defense to bacterium, nucleus, response to UV, response to X-ray, negative regulation of mitotic DNA damage checkpoint (Wormbase, 2021). "DAF-16-mediated immunity in adults requires SMK-1, a regulatory subunit of the PP4 protein phosphatase complex. Our data suggest that as the function of one branch of the innate immune system of *C. elegans* (PMK-1) declines over time, DAF-16-mediated immunity ramps up to become the predominant means of protecting adults from infection" (McHugh et al., 2020).
sms-1	H21P03.3b			1.50		Is predicted to have ceramide cholinephosphotransferase activity. integral component of endoplasmic reticulum membrane; and integral component of plasma membrane. Is expressed in several structures, including body wall musculature; pharyngeal cell; rectal muscle; ventral nerve cord; vulval muscle, spermatheca. Human ortholog(s) of this gene implicated in calvarial doughnut lesions with bone fragility. Is an ortholog of human SGMS2 (sphingomyelin synthase 2). Affected by >10 chemicals. GO Terms: ceramide biosynthetic process, golgi apparatus, integral component of ER membrane, integral component of membrane, lipid metabolic process, transferase activity (Wormbase, 2021). sms-1, is a strong suppressor of clozapine-induced effects (Hao et al., 2017).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
snf-2	F55H12.1				2.12	Is affected by >10 chemicals. Is predicted to have neurotransmitter:sodium symporter activity. Human ortholog(s) of this gene are implicated in creatine transporter deficiency. GO Terms: sodium ion transmembrane transporter, integral component of membrane, plasma membrane (Wormbase, 2021).
snf-5	Y46G5A.30	2.10				*snf-5* is affected by > 20 chemicals, predicted to have metal ion binding activity and neurotransmitter:sodium symporter activity, expressed in amphid neurons, intestinal cell, pharyngeal neurons, and rectal gland cell, close human homologs SLC6A8, SLC6A12, and SLC6A13 are implicated in creatine transporter deficiency, GO Terms: integral component of membrane, plasma membrane, metal ion binding (Wormbase, 2021). Up 2x w *D. coniospora* in Ce (Pujol et al., 2008b). Up 2.6x w meHg in Ce (McElwee et al., 2013).
snf-6	M01G5.5			1.57		Sodium neurotransmitter symporter Family 6. Exhibits PDZ domain binding activity and acetylcholine transmembrane transporter activity. Is involved in acetylcholine transport; choline transport; and positive regulation of locomotion. Predicted to localize to plasma membrane. Is expressed in body wall musculature; enteric muscle; neurons; and vulval muscle. Is used to study Duchenne muscular dystrophy. Human ortholog(s) of this gene are implicated in hyperekplexia 3. Is an ortholog of human SLC6A14 (solute carrier family 6 member 14). Affected by four chemicals. GO Terms: amino acid: sodium symporter activity, integral component of membrane, neuromuscular synaptic transmission, plasma membrane, positive regulation of locomotion (Wormbase, 2021).
snx-14	Y48E1B.14			1.87		Is predicted to have phosphatidylinositol binding activity. Human ortholog(s) of this gene are implicated in autosomal recessive spinocerebellar ataxia 20. Is an ortholog of human SNX14 (sorting nexin 14). GO Terms: Integral component of the membrane. Affected by 7 chemicals, and 4 MAPK-R P genes (Wormbase, 2021).
spe-29	F25H8.7			-2.44		Down 3X with DMA in this study. GO Terms: integral component in membrane, spermatid development (Wormbase, 2021). Upregulated with Harposporium infection (Engelmann et al., 2011).
spp-21	T25C12.4				-2.62	Down 2.7X with DMA in this study. Is affected by thirteen chemicals. Is predicted to encode a protein with the following domains: Saposin B type domain and Saposin-like (Wormbase, 2021).
spp-7	ZK616.9		-4.39			*spp-7* is expressed in ALM and PLM, head neurons, intestine, affected by 15 chemicals, encodes an antimicrobial peptide that belongs to the SPP-protein family (WormBse 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). Down 2.6x w 7.5µM meHg in Ce (McElwee et al., 2013).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
sprr-1	R03A10.6	1.83	2.21			*sprr-1* is enriched in neurons, affected by 7 chemicals, predicted to have G protein-coupled receptor activity, GO Terms: G protein-coupled receptor signaling pathway, integral component of membrane (Wormbase, 2021). Up 1.8x w NaAsO2 (this study).
sra-16	AH6.13			2.80		Down 1.5X with NaAsO2 in this study. Is affected by Microcystin-LR based on microarray studies (Wormbase, 2021). A fragment of an sra-like gene (chemosensory, G-protein-coupled receptor) (Troemel et al., 1995).
sra-17	F28C12.1	-4.60	-4.51			*sra-17* is expressed in neurons, predicted to have G protein-coupled receptor activity, GO terms: integral component of membrane, sensory perception of chemical stimulus, G protein-coupled receptor signaling pathway (Wormbase, 2021).
sra-30	Y40H7A.6	-2.02				*sra-30* is affected by 3 chemicals, GO Terms: G protein-coupled receptor signaling pathway, integral component of membrane, sensory perception of chemical stimulus (Wormbase, 2021).
srb-8	F37C12.15	-1.88				*srb-8* is affected by five chemicals (Wormbase, 2021).
srbc-13	K09C6.5				-2.63	Is affected by aldicarb, dafa, and adsorbable organic bromine compound based on microarray studies. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srbc and 7TM GPCR, serpentine receptor class bc (Srbc) (Wormbase, 2021).
srbc-16	C45H4.1		3.80			*srbc-16* is affected by four chemicals, GO term: integral component of membrane (Wormbase, 2021).
srbc-32	C02A12.5	-1.86				*srbc-23* is affected by mir-34 and drh-3, affected by Rifampin, Psoralens and Sirolimus, GO Term: integral component of membrane (Wormbase, 2021).
srbc-36	C02A12.6		2.34			*srbc-36* GO term: integral component of membrane (Wormbase, 2021).
srbc-51	F54B8.9		-4.03	-2.73		*srbc-51* is affected by six chemicals, GO term: integral component of membrane (Wormbase, 2021).
srd-12	C39H7.6	-1.88				*srd-12* is affected by drh-3, GO Term integral component of membrane (Wormbase, 2021).
srd-52	K02A2.4	-1.89				*srd-52* is affected by six chemicals (Wormbase, 2021). X
sre-19	Y39C12A.6			-2.17		Is affected by allantoin based on microarray studies. Is predicted to encode a protein with the following domains: C. elegans Sre G protein-coupled chemoreceptor and 7TM GPCR, serpentine receptor class e (Sre). GO Terms: Integral component of membrane, sensory perception of chemical stimulus (Wormbase, 2021).
sre-3	C07D10.3	-2.02				*sre-3* is enriched in hypodermis, affected by multi-walled carbon nanotube and allantoin, GO Terms: integral component of membrane, sensory perception of chemical stimulus (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
sre-50	C50E10.11				-2.05	Is enriched in body wall musculature and ray based on microarray studies. Is affected by eight chemicals including Psoralens, allantoin, and metformin based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: C. elegans Sre G protein-coupled chemoreceptor and 7TM GPCR, serpentine receptor class e (Sre). GO Terms: integral component of membrane, sensory perception of chemical stimulus (Wormbase, 2021). Down 1.8X with DMA, down 1.7X with HgCl2 in this study.
srg-11	T04A8.2			-2.14	-2.07	Is predicted to have transmembrane signaling receptor activity. GO Terms: integral component of membrane, sensory perception of chemical stimulus. Affected by allantoin according to microarray (Wormbase, 2021). Down 1.5X with NaAsO2 in this study.
srg-25	T09D3.5	-1.83				*srg-25* is expressed in ciliated neurons, affected by 0 chemicals, GO Terms: integral component of membrane, sensory perception of chemical stimulus, transmembrane signaling receptor activity (Wormbase, 2021).
srg-40	T19C4.4	-2.82				*srg-40* is predicted to have transmembrane signaling receptor activity, GO Terms: sensory perception of chemical stimulus, integral component of membrane, transmembrane signaling receptor activity (Wormbase, 2021).
srg-5	T12A2.11				-2.20	Is predicted to have transmembrane signaling receptor activity. Is expressed in head neurons and ray. GO Terms: integral component of membrane. Affected by three chemicals. (Wormbase, 2021).
srg-50	Y43B11AR.2			-3.16		Is predicted to have transmembrane signaling receptor activity. Predicted to be involved in sensory perception of chemical stimulus. Predicted to localize to integral component of membrane. Enriched in neuron, AFD, ASER and PLM according to tiling array and RNA-seq. Affected by aldicarb according to microarray (Wormbase, 2021).
srg-61	C24B9.11	-2.36			-2.00	*srg-61* is enriched in NSM neurons, affected by adsorbable organic bromine compound, predicted to have transmembrane signaling receptor activity, GO Terms: sensory perception of chemical stimulus, integral component of membrane, transmembrane signaling receptor activity (Wormbase, 2021). Down 2.1x w DMA in Ce (this study).
srh-101	F31F4.10	-3.72		-2.19		*srh-101* pseudogene is affected by clk-1 and sir-2.1 (Wormbase, 2021).
srh-128	Y47G7B.1			2.1748		Is enriched in AVK based on RNA-seq studies. Is affected by Rifampin; allantoin; and adsorbable organic bromine compound based on RNA-seq and microarray studies (Wormbase, 2021). >1.5X increase in Microcystis aeruginosa-enriched batch culture (MC-BA)(Saul et al., 2015).
srh-171	Y60A3A.5	-1.82				*srh-171* is affected by 2 chemicals, GO Term: integral component of membrane (Wormbase, 2021). Down 3.4x w 7.5µM meHgCl in Ce (McElwee et al., 2013). Down 1.9x w HgCl2, and down 1.7x w meHgCl or DMA in Ce (this study).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
srh-189	C03G6.20		4.08			*srh-189* is affected by clk-1, daf-12, daf-16, mrps-5, lin-14 and lin-4, affected by resveratrol (Wormbase, 2021).
srh-265	T06E6.9	-2.32				*srh-265* is affected by clk-1; sir-2.1; and ahr-1, affected by four chemicals, GO Term: integral component of membrane (Wormbase, 2021).
srh-307	Y59A8B.5		-5.04	-3.86		*srh-307* pseudogene is enriched in muscle cell, affected by six chemicals (Wormbase, 2021).
srh-308	F58E10.6		-4.12	-2.34		*srh-308* is affected by six chemicals, GO term: integral component of membrane (Wormbase, 2021). Down 2.1x w meHgCl in Ce (this study).
srh-42	Y54G11A.15	-2.31		-2.15		*srh-42* is affected by mir-34 and drh-3, GO Term: integral component of membrane (Wormbase, 2021). Down 1.8x w meHgCl or DMA (this study).
srh-61	T21B4.8		-4.47	-2.19	-2.38	*srh-61* is enriched in NSM, affected by Sirolimus and resveratrol, GO term: integral component of membrane (Wormbase, 2021).
srh-95	F21H7.11		-5.34			*srh-95* is enriched in germ line, affected by rsr-2 and clk-1 only, GO term: integral component of membrane (Wormbase, 2021). Down ~20% w *E. carotovora* in Ce (Wong et al., 2007).
sri-2	F36G9.9	-2.32				*sri-2* is enriched in neurons, affected by sir-2.1; ain-1; and ain-2, affected by resveratrol, GO Term: integral component of membrane (Wormbase, 2021). Down 2.1x w HgCl2, and down 1.6x w meHgCl in Ce (this study).
sri-26	C41G6.14	-2.03				*sri-26* is expressed in chemosensory neurons, affected by fluoranthene, GO Term: integral component of membrane (Wormbase, 2021). Up w 3 bacterial species in Ce (Engelmann et al., 2011).
sri-61	F34D6.6	1.86				*sri-61* is expressed in ADLL and ADLR, enriched in germ line and somatic gonad precursor, affected by 8 chemicals, GO Term: integral component of membrane (Wormbase, 2021).
sri-67	Y60A3A.22		-3.44	-2.74		*sri-67* is affected by five chemicals including Psoralens; allantoin; and metformin, GO Term: integral component of membrane (Wormbase, 2021).
sri-8	ZK666.10	-1.79				*sri-8* is enriched in germ line, affected by five chemicals (Wormbase, 2021).
sri-9	Y102A5C.29	-2.29				*sri-9* is expressed in ADLL and ADLR (amphid neurons), affected by 2 chemicals, GO Term: integral component of membrane (Wormbase, 2021).
srj-1	ZK829.8				-2.69	Is affected by resveratrol based on microarray studies. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srj and 7TM GPCR, serpentine receptor class j (Srj) (Wormbase, 2021).
srj-51	C31B8.10				1.8827	Up 1.8X with DMA exposure. Is affected by adr-1; eat-2; and sir-2.1 based on RNA-seq and microarray studies (Wormbase, 2021).
srm-2	T28H11.3				-2.10	Is expressed in neurons. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Str and 7TM GPCR, serpentine receptor class r

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						(Str). GO Terms: integral component of membrane. Affected by tryptophan, resveratrol and Diazinon according to microarray (Wormbase, 2021).
srr-10	T05B11.6			-2.61		Is expressed in ganglia, head neurons, and rectal gland cell. Is predicted to encode a protein with the following domains: Caenorhabditis protein of unknown function, DUF267 (Wormbase, 2021). Up with Harposporium infection (Engelmann et al., 2011).
srt-18	R03H4.4				-2.36	Is affected by Tunicamycin and resveratrol based on microarray studies. GO Terms: Integral component of membrane (Wormbase2021).
srt-61	T27C10.1			-2.49		Is affected by resveratrol based on microarray studies. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srt and 7TM GPCR, serpentine receptor class t (Srt). GO Terms: integral component of membrane (Wormbase, 2021).
srt-70	B0238.6				-2.03	Is expressed in ADFL, ADFR, PHBL, and PHBR. Is predicted to encode a protein with the following domain: 7TM GPCR, serpentine receptor class t (Srt). Affected by Ag nanoparticles according to microarray. GO Terms: Integral component of membrane (Wormbase, 2021). Down 1.5X with NaAsO2, down 1.6X with HgCl2 in this study.
sru-20	T04A11.7		-6.88			*sru-20* is affected by thirteen chemicals, GO term: integral component of membrane (Wormbase, 2021). Down 2.5x w 2µM and 4.4x w 7.5µM meHgCl in Ce (McElwee et al., 2013). Down 1.9x w HgCl2 (this study).
sru-22				-2.67		0.56X with meHgCl in Ce. 0.52X with DMA in Ce. Up w D. coniospora in Ce (Engelmann et al., 2011). Is affected by several genes including daf-2; glp-1; and let-60 based on tiling array; microarray; and RNA-seq studies. Is affected by five chemicals including tryptophan; Sodium Chloride; and Atrazine based on microarray and RNA-seq studies (Wormbase, 2021).
sru-31	C50C10.4			1.73		Is affected by Atrazine and fluoranthene based on microarray studies. Is expressed in hypodermis; intestine; nervous system; and pharynx. GO Terms: Integral component of the membrane (Wormbase, 2021).
srv-10	F53F1.9			-3.14		Is affected by drh-3 based on RNA-seq studies. Is affected by four chemicals including metformin; Sirolimus; and Rifampin based on RNA-seq studies. Integral component of the membrane (Wormbase, 2021).
srv-8	F53F1.7				-2.12	Is expressed in ASKL, ASKR, PHCL, PHCR, and sensory neurons. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srv and 7TM GPCR, serpentine receptor class v (Srv). GO Terms: Integral component of membrane (Wormbase, 2021). Down 1.7X with NaAsO2, down 2.2X with DMA in this study.

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
srw-140	C03A7.3			-2.19		Is predicted to have G protein-coupled peptide receptor activity. GO Terms: G protein-coupled receptor signaling pathway, integral component of membrane (Wormbase, 2021).
srw-16	T10H4.5	-3.07				SRW-16 is predicted to have G protein-coupled peptide receptor activity, GO Terms: G protein-coupled receptor signaling pathway, integral component of membrane (Wormbase, 2021).
srw-19	T10H4.8	-1.91				*srw-19* is affected by 2 chemicals, predicted to have G protein-coupled peptide receptor activity, GO Terms: G protein-coupled receptor signaling pathway, integral component of membrane (Wormbase, 2021).
srw-25	T09F5.14	-1.84				*srw-25* is affected by 3 genes and 2 chemical (Wormbase, 2021). Down 1.9x w HgCl2, and down 1.6x w DMA in Ce (this study).
srw-54	Y32B12C.2				-2.55	Is predicted to have G protein-coupled peptide receptor activity. GO terms: membrane (Wormbase, 2021).
srw-63	Y37A1B.10	-1.81				*srw-63* is affected by rsr-2 and spc-1, predicted to have G protein-coupled peptide receptor activity, GO Terms: G protein-coupled receptor signaling pathway, integral component of membrane (Wormbase, 2021).
srw-81	Y51A2B.7			-2.71		Enriched in germline (Wormbase, 2021). Up 4X with meHgCl in Ce. (McElwee et al., 2013).
srx-46	E02C12.2				-2.16	Is affected by Sirolimus based on microarray studies. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srx and 7TM GPCR, serpentine receptor class x (Srx). GO Terms: Integral component of membrane (Wormbase, 2021). Down 2.3X with DMA in this study.
srx-67	K07C6.10	-2.16				*srx-67* is enriched in neurons, affected by six chemicals, GO Term: integral component of membrane (Wormbase, 2021).
srx-78	C01G10.3			-2.47		Up 2.5X with meHgCl (McElwee et al., 2013). Is affected by methylmercuric chloride and nitroguanidine based on microarray studies. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srx and 7TM GPCR, serpentine receptor class x (Srx) (Wormbase, 2021).
srx-82	F43A11.6	-2.16				*srx-82* is affected by rsr-2 and clk-1, GO Term: integral component of membrane (Wormbase, 2021).
srx-92	F10G2.6		1.94			*srx-92* is enriched in NSM, affected by 3 chemicals, GO Terms: integral component of membrane (Wormbase, 2021). Up 2.9x w 2µM meHgCl (McElwee et al., 2013).
srx-97	F19B10.7	-2.09				*srx-97* is enriched in neurons, affected by nine chemicals, GO Term: integral component of membrane (Wormbase, 2021). G-protein-coupled receptor (GPCR) "*srx-97* promoter drives expression specifically in the head ASH and tail PHB chemosensory neurons of *C. elegans*. Moreover, the SRX-97 protein localizes to the ciliary ends of the ASH neurons.

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						… *srx-97* mutants present defects in chemotaxis behavior, more specifically toward high concentrations of benzaldehyde. Moreover, the mutant phenotype could be rescued by both endogenous and neuron-specific expression of the wild-type *srx-97* gene, suggesting concentration-dependent behavioral plasticity for odors in *C. elegans* through the SRX-97 GPCR." (Kadam et al., 2021). Down 2.0x w DMA in Ce (this study).
srxa-15	Y44A6B.2				-2.69	Down 2.6X with DMA in this study. Is affected by Rifampin, allantoin, and glycine based on RNA-seq studies. Is predicted to encode a protein with the following domains: Caenorhabditis serpentine receptor-like protein, class xa and 7TM GPCR, serpentine receptor class xa (Srxa) (Wormbase, 2021).
srxa-16	F44G3.5	-2.55		-2.56		*srxa-16* is affected by drh-3; cyc-1; and mir-34, affected by paraquat, GO Term: integral component of membrane (Wormbase, 2021). Down 2.6x w HgCl2 in Ce (this study).
srz-60	C04C3.1		-4.40		-2.13	*srz-60* is affected by Psoralens; Rifampin; and Sirolimus, GO term: integral component of membrane (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). Down 2.3x w HgCl2 in Ce (this study).
srz-7	T17A3.11		3.02			*srz-7* pseudogene is enriched in neurons, affected by Acrylamide; Chlorpyrifos; and adsorbable organic bromine compound (Wormbase, 2021).
srz-81	C09G12.13			-2.28		Is affected by four chemicals including Rifampin, allantoin, and Sirolimus based on RNA-seq studies (Wormbase, 2021).
str-125	T05E12.1				-2.55	Is expressed in head neurons and interneuron. GO Terms: detection of chemical stimulus involved in sensory perception of smell, G protein-coupled olfactory receptor activity, integral component of membrane. Affected by two chemicals (Wormbase, 2021).
str-135	F21F8.10		2.01			*str-135* is enriched in FLP, affected by resveratrol; Atrazine; and fluoranthene, predicted to encode an integral plasma membrane serpentine receptor, GO Term: integral component of plasma membrane, detection of chemical stimulus involved in sensory perception of smell, olfactory behavior, G protein-coupled receptor signaling pathway (Wormbase, 2021).
str-139	ZC513.9		-3.35	-2.36		*str-139* is affected by four chemicals including Rifampin; Sirolimus; and resveratrol, GO Terms: detection of chemical stimulus involved in sensory perception of smell, G protein-coupled olfactory receptor activity, integral component of membrane, integral component of plasma membrane (Wormbase, 2021). Down 1.8X with meHgCl in this study.
str-163	Y9C9A.3			-2.29		Localizes to non-motile cilium. Is expressed in AWBL and AWBR. Enriched in ASER according to RNA-seq. Affected by rsr-2, ubc-9, npr-1, jmjd-3.1, dpy-21, mir-34, mir-71, cox-5B, dpy-7, alg-1, sek-1, aak-1, aak-2, spc-1, unc-70, skn-1 and sir-2.1 according to tiling array, microarray and RNA-seq. Affected by Tunicamycin, Rifampin, Psoralens, Sirolimus,

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						allantoin, paraquat, Ag nanoparticles and silicon dioxide nanoparticle according to microarray and RNA-seq. GO associations: sensory perception, G protein coupled olfactory receptor activity, integral component of membrane (Wormbase, 2021).
str-19	T23D5.7	-2.08				*str-19* is affected by resveratrol, adsorbable organic bromine compound and nitroguanidine, GO Term: integral component of membrane (Wormbase, 2021).
str-209	F26G5.5				-2.49	Is affected by four chemicals. GO Terms: G protein-coupled olfactory receptor activity, integral component of membrane, integral component of plasma membrane (Wormbase, 2021).
str-216	K02H11.5	-2.71				*str-216* pseudogene is affected by smg-2; daf-2; and eat-2 (Wormbase, 2021). X
str-225	C07G3.6	1.96				*str-225* is enriched in coelomocyte, affected by four chemicals, GO Terms: detection of chemical stimulus involved in sensory perception of smell, olfactory behavior, integral component of plasma membrane, G protein-coupled receptor signaling pathway (Wormbase, 2021). Up 1.7x w DMA (this study).
str-229	C17E7.11	-1.87				*str-229* is enriched in NSM neurons, affected by dibromoacetic acid, GO Terms: detection of chemical stimulus involved in sensory perception of smell, G protein-coupled olfactory receptor activity, integral component of plasma membrane, olfactory behavior (Wormbase, 2021).
str-249	C42D4.12				-2.56	Is expressed in PVT and head neurons. Affected by 3 chemicals. GO Terms: detection of chemical stimulus involved in sensory perception of smell, G protein-coupled olfactory receptor activity, integral component of membrane, integral component of plasma membrane, olfactory behavior (Wormbase, 2021).
str-29	C18B10.9		2.20			*str-29* is a pseudogene (Wormbase, 2021).
str-31	C54F6.10		-4.84			*str-31* is expressed in PVT neurons, hypodermis, rectal epithelial cell, and vulva, enriched in hypodermis and muscle cell, affected by 15 chemicals, GO term: integral component of membrane (Wormbase, 2021). Down ~20% w *P. luminescens* in Ce (Wong et al., 2007). Down 2.1x w HgCl2 in Ce (this study).
str-39	F37B4.12				-2.32	Down 2.1X with DMA in this study. Is enriched in NSM based on tiling array studies. Is affected by adsorbable organic bromine compound based on microarray studies. GO Terms: Integral component of membrane (Wormbase, 2021).
str-48	C34D4.8	-2.67			-2.07	*str-48* is enriched in germ line, affected by Atrazine; fluoranthene; and dibromoacetic acid, GO Term: integral component of membrane (Wormbase, 2021). Down 2.1x w meHgCl in Ce (this study).
swt-2	C54F6.4	5.40				*swt-2* is affected by seven chemicals, involved in carbohydrate transport, human homolog SLC50A1, GO Terms: carbohydrate transport, Golgi membrane, plasma membrane,

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						integral component of membrane (Wormbase, 2021). Up 5x w 2µM meHgCl and 25x w 7.5µM meHgCl in Ce (McElwee et al., 2013).
sygl-1	T27F6.4	2.05				*sygl-1* is expressed in germ cell, germ line, gonad, head mesodermal cell, and DD neuron, affected by 10 chemicals (Wormbase, 2021). Up 2x w 2µM meHg in Ce (McElwee et al., 2013). GLP-1/Notch target gene specifically for germ-line stem cell maintenance (Kershner et al., 2014).
tag-52	C02F12.4			-2.43		Up 1.6X with DMA in this study. Is predicted to have guanyl-nucleotide exchange factor activity. Is expressed in anchor cell, gonad, spermatheca, and uterine toroidal epithelial cell. Is an ortholog of human ARHGEF39 (Rho guanine nucleotide exchange factor 39). Affected by 11 chemicals. GO Terms: cytoplasm, rho guanyl-nucleotide exchange factor activity (Wormbase, 2021).
tba-5	F16D3.1				1.82	Localizes to axonemal microtubule. Is expressed in amphid neurons and phasmid neurons. GO Terms: Cytoplasm, axonemal microtubule, GTP binding, mitotic cell cycle, structural component of cytoskeleton, nucleotide binding. Is an ortholog of human TUBAL3 (tubulin alpha like 3) (Wormbase, 2021).
tbx-8	T07C4.2			-2.34		Is predicted to have DNA-binding transcription factor activity, RNA polymerase II-specific. Is involved in embryonic body morphogenesis. Localizes to nucleus. Is expressed in several structures, including Eal, Ear, Epl, Epr, and intestine. Human ortholog(s) of this gene are implicated in asthma, nasal polyps, and aspirin intolerance. Is an ortholog of human EOMES (eomesodermin) and TBR1 (T-box brain transcription factor 1). Affected by ten chemicals, GO Terms: DNA binding, transcription factor activity, embryonic body morphogenesis, nucleus (Wormbase, 2021).
tiar-1	C18A3.5			1.76		Is predicted to have RNA binding activity. Is involved in several processes, including determination of adult lifespan; nematode larval development; and response to UV. Localizes to P granule; cytoplasmic stress granule; and nucleus. Is expressed in several structures, including germ line; hypodermis; mechanosensory neurons; somatic cell; and tail. Is an ortholog of human TIA1 and TIAL1. Affected by eight chemicals. GO Terms: cytoplasm, aging, larval development, nucleus, regulation of locomotion, reproduction, response to oxidative stress, response to UV, RNA binding, stress granule (Wormbase, 2021). Protects the germline from the adverse effects of heat shock (Huelgas-Morales et al., 2016). TIAR-1 is required to induce germ cell apoptosis under different conditions, including starvation, heat shock, osmotic, oxidative stress, and UV irradiation (Carlos Giovanni and Rosa, 2013). -3.2X after dosing with aspirin (Huang et al., 2017).
try-8	F25E5.10	2.04				*try-8* is enriched in germ line, male and muscle cell, affected by 8 chemicals, predicted to have serine-type endopeptidase activity (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
ttr-13	Y44A6B.4	1.80				*ttr-13* is affected by six chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
twk-17	C44E12.3	1.91				*twk-17* is expressed in neurons, affected by 8 chemicals, predicted to have potassium channel activity, GO Terms: potassium ion transmembrane transport, integral component of plasma membrane (Wormbase, 2021).
uaf-1	Y92C3B.2				1.57	Exhibits pre-mRNA 3'-splice site binding activity. Is involved in several processes, including embryonic body morphogenesis; mRNA 3'-splice site recognition; and nematode larval development. Localizes to nucleoplasm. Is an ortholog of human U2AF2 (U2 small nuclear RNA auxiliary factor 2). Affected by 7 chemicals. GO Terms: developmental growth, germ cell development, nucleus, RNA binding (Wormbase, 2021). analyzed RAD-51 foci in a strain harboring a temperature-sensitive allele of the basal splicing factor U2AF (uaf-1 n4588), and showed that pre-mRNA splicing is dispensable for nutrient-dependent DNA damage to form in Z2/Z3 (Butuči et al., 2015).
ubc-26	Y110A2AM.3			-2.36		Is affected by Rifampin, Psoralens, and Sirolimus based on RNA-seq studies. Human UBE2J2 exhibits ubiquitin conjugating enzyme activity and ubiquitin protein ligase binding activity. Is predicted to encode a protein with the following domains: Ubiquitin-conjugating enzyme, Ubiquitin-conjugating enzyme E2, and Ubiquitin-conjugating enzyme\/RWD-like. Is an ortholog of human UBE2J2 (ubiquitin conjugating enzyme E2 J2). GO Terms: endoplasmic reticulum, integral component of membrane, nucleus, ubiquitin conjugating enzyme activity (Wormbase, 2021).
ubxn-6	H06H21.6			1.58		Is expressed in nervous system and pharynx. Is an ortholog of human UBXN6 (UBX domain protein 6). Affected by nine chemicals (Wormbase, 2021). Caenorhabditis elegans UBX cofactors for CDC-48/p97 control spermatogenesis (Sasagawa et al., 2010).
ugt-10	T19H12.11	4.51				*ugt-10* is enriched in intestine and neuron, affected by 11 chemicals, predicted to have UDP-glycosyltransferase activity, human homolog(s) UGT1A9, UGT2B17, and UGT2B28 are implicated in Crigler-Najjar syndrome and Gilbert syndrome, GO Terms: integral component of membrane, intracellular membrane-bounded organelle (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Down 40% x w Ag+ (Hunt et al., 2014).
ugt-13	H23N18.1	2.27				*ugt-13* is affected by > 20 chemicals, close human homologs UGT1A1, UGT2B28 and UGT2B7 are implicated in Crigler-Najjar syndrome and Gilbert syndrome, GO Terms: integral component of membrane, intracellular membrane-bounded organelle (Wormbase, 2021). Up 3.4x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up w juglone in Ce (Przybysz et al., 2009). Down 2.5x w *S. aureus* in Ce (Irazoqui et al., 2010). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 4.6x w 20µM HgCl2 in Ce (McElwee et al., 2013). Up 10x w NaAsO2 in Ce (Sahu et al., 2013). Induced by allyl isothiocyanate (in

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						wasabi) and upregulated by SKN-1 (Hasegawa et al., 2010). Induced by thiabendazole and dazomet and upregulated by SKN-1 (Jones et al., 2013). Up 2.5x w acrylamide in Ce (Hasegawa et al., 2008).
ugt-34	F29F11.2		94.5			*ugt-34* is enriched in neurons, affected by >15 chemicals, predicted to have UDP-glycosyltransferase activity, close human homologs UGT1A8, UGT2A3, and UGT2B15 are implicated in Crigler-Najjar syndrome and Gilbert syndrome, GO Term: integral component of membrane (Wormbase, 2021). Up 52x w 7.5µM meHg in Ce (McElwee, 2010). Up w acrylamide in Ce (Hasegawa et al., 2008).
unc-7	R07D5.1	2.08				UNC-7 is affected by 10 chemicals, exhibits gap junction channel activity, involved in: oviposition; regulation of neuronal signal transduction; and spicule insertion, localizes to gap junction and neuron projection membrane, expressed in OL socket cell; g1AR; muscle cell; neurons; and pharyngeal gland cell, GO Terms: cellular response to dopamine, ion transmembrane transport, regulation of locomotion involved in locomotory behavior, spicule insertion, regulation of male mating behavior, integral component of membrane, plasma membrane (Wormbase, 2021). Involved in ivermectin resistance (Dent et al., 2000).
vab-10	T02G6.2		2.04		2.89	*T02G6.2* is a dead sequence, see *ZK1151.1 = vab-10* is enriched in hypodermis and neural support cells and somatic gonad precursor, affected by > 15 chemicals, predicted to have actin filament binding activity, involved in epidermis morphogenesis, colocalizes with intermediate filament, expressed in body wall musculature; gonad; intestinal lumen; nerve ring; and pharynx, close homolog of human DST (dystonin) which is implicated in several diseases, GO Terms: wound healing, actin binding, microtubule, plasma membrane (Wormbase, 2021). Up 1.7x w NaAsO2 (this study).
vps-28	Y87G2A.10				-2.15	Is involved in receptor catabolic process. Localizes to ESCRT I complex. Is an ortholog of human VPS28 (VPS28 subunit of ESCRT-I). GO Terms: endosome, protein transport, receptor catabolic process. Affected by six chemicals (Wormbase, 2021).
wac-1.2	Y40B1A.1			-2.14		Is enriched in germ line and somatic gonad precursor based on RNA-seq studies. Is affected by four chemicals including rotenone, stavudine, and Rifampin based on RNA-seq studies. Is predicted to encode a protein with the following domains: WW domain, WW domain, WW domain superfamily, and WW domain-containing adapter protein with coiled-coil. GO Terms: chromatin organization (Wormbase, 2021).
zfh-2	ZC123.3			1.53		Down 0.47X with 24h D. coniospora infection (Pujol et al., 2008a). Is predicted to have DNA binding activity and zinc ion binding activity, predicted to localize to nucleus. Is expressed in anal depressor muscle; anal sphincter muscle; body wall musculature; nerve ring; and vulval muscle. Human ortholog(s) of this gene are implicated in congenital ptosis

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						and prostate cancer. Is an ortholog of human ZFHX3 (zinc finger homeobox 3). Affected by six chemicals. GO Terms: negative regulation of transcription, nucleus, zinc ion binding (Wormbase, 2021).
zif-1	F59B2.6	1.79				*zif-1* is enriched in germline precursor cell, hypodermis, pharyngeal muscle cell, germ line, and somatic gonad precursor, affected by > 10 chemicals, involved in embryo development and ubiquitin-dependent protein catabolic process (Wormbase, 2021). Up 2x w 2uM meHgCl in Ce (McElwee et al., 2013).
znf-236	Y48G8AL.10				1.85	Is enriched in AVK and germ line based on RNA-seq studies. Is affected by eleven chemicals including rotenone; Alovudine; and Zidovudine based on RNA-seq and microarray studies. GO Terms: Nucleus, DNA-binding transcription factor activity. Human ortholog(s) of this gene are implicated in autosomal dominant non-syndromic intellectual disability 21 and immunodeficiency-centromeric instability-facial anomalies syndrome 2. Is an ortholog of several human genes including ZNF729 (zinc finger protein 729); ZNF845 (zinc finger protein 845); and ZNF99 (zinc finger protein 99) (Wormbase 2021.)7X increase after BPA exposure (Camacho, Truong et al. 2018).
	B0207.2	-1.87				*B0207.2* is enriched in AFD and dopaminergic neurons, affected by six chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	B0207.5	2.23				*B0207.5* is expressed in vas deferens valve cell, enriched in germ line and male, affected by 10 chemicals (Wormbase, 2021).
	B0207.7		1.88			*B0207.7* is expressed in neurons, enriched in germline, affected by > 15 chemicals, GO Terms: nucleus, protein kinase activity (Wormbase, 2021). Up 3.2x w meHgCl (McElwee et al., 2013).
	B0348.1			-2.83		GO Terms: Integral component of membrane, metal ion binding. Is enriched in AVK based on RNA-seq studies. Is affected by multi-walled carbon nanotube; Cry5B; and Triclosan based on RNA-seq and microarray studies. (Wormbase, 2021).
	B0524.7	1.78				*B0524.7* is affected by daf-12, dpy-21, lin-22, mina-1 and mrps-5 according to tiling array and RNA-seq (Wormbase, 2021).
	C01B9.3		1.94			*C01B9.3* pseudogene is affected by adr-1 and daf-2 (Wormbase, 2021).
	C01G12.7		1.91			*C01G12.7* is enriched in neurons, affected by 8 chemicals, GO Terms: integral component of membrane (Wormbase, 2021).
	C03C10.5		-4.05			C03C10.5 is enriched in intestine and pharynx, affected by eighteen chemicals (Wormbase, 2021). Up 1.4x w *E. faecalis* in Ce (Wong et al., 2007). Down 2x w 2µg/mL meHgCl and 18x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	C04B4.2	1.89				C04B4.2 is expressed in head, enriched in intestine and neurons, affected by 12 chemicals, GO Term: negative regulation of gene expression (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	C04C3.1			-2.27		Is affected by Psoralens, Rifampin, and Sirolimus based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: Serpentine type 7TM GPCR chemoreceptor Srz and 7TM GPCR, serpentine receptor class z (Srz). GO Terms: integral component of membrane (Wormbase, 2021). Down 2.1X with meHgCl in this study. Up with Harposporium infection (Engelmann et al., 2011).
	C04E6.8	-2.04				*C04E6.8* is enriched in neurons, affected by nine chemicals (Wormbase, 2021). Down 2.1x w HgCl2 in Ce (Wormbase, 2021).
	C04E6.8			-2.14		Is enriched in neurons based on tiling array, RNA-seq, and microarray studies. Is affected by nine chemicals including Tunicamycin, Psoralens, and allantoin based on microarray and RNA-seq studies. Is predicted to encode a protein with the following domain: NTF2-like domain superfamily (Wormbase, 2021). Down 2X with NaAsO2 in this study. Up with D. coniospora infection (Engelmann et al., 2011).
	C04F5.2			-2.30	-2.24	Is enriched in GABAergic neurons, germ line, and ventral nerve cord based on tiling array and RNA-seq studies. Is affected by adsorbable organic bromine compound based on microarray studies. GO Terms: integral component of membrane (Wormbase, 2021).
	C06C3.5		2.02			*C06C3.5* pseudogene is enriched in head mesodermal cell, affected by six chemicals (Wormbase, 2021).
	C07A9.9		2.48			*C07A9.9* is enriched in hypodermis and neurons, affected by eleven chemicals (Wormbase, 2021).
	C07C7.1			-2.21		Is enriched in AFD, ASER, AVK, PLM, and neurons based on tiling array and RNA-seq studies. Is affected by five chemicals including metformin, Sirolimus, and Psoralens based on RNA-seq studies. GO Terms: integral component of membrane (Wormbase, 2021). Down 2.2X with DMA, down 1.7X with NaAsO2, down 1.7X with meHgCl in this study.
	C07D8.5		1.85			*C07D8.5* is enriched in ventral nerve cord, affected by resveratrol and Sirolimus, a close homolog of human AKR1C8P (aldo-keto reductase family 1 member C8, pseudogene), GO Terms: oxidoreductase activity (Wormbase, 2021). Up 1.6x w NaAsO2 (this study).
	C07G3.8	-2.75				*C07G3.8* is enriched in amphid sheath cell, affected by Tunicamycin; Alovudine; and Sirolimus (Wormbase, 2021).
	C08A9.3				-2.04	Is predicted to have RNA transmembrane transporter activity. Is an ortholog of human SIDT1 (SID1 transmembrane family member 1) and SIDTy112 (SID1 transmembrane family member 2). GO Terms: integral component of membrane, lysosome, plasma membrane, RNA transport. Affected by seven chemicals (Wormbase, 2021). Down 1.6X with NaAsO2 in this study.

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	C09B9.4		1.93			*C09B9.4* is enriched in germ line and AFD, predicted to have ATP binding activity and protein kinase activity, affected by > 20 chemicals, GO Terms: nucleus (2021 WormBase). Up 4.0x w meHgCl in Ce (McElwee et al., 2013).
	C10G11.10				1.52	Up 1.6X with NaAsO2 in this study. Up 2.65X with 7.5uM meHgCl (McElwee et al., 2013). Is enriched in NSM and in male based on tiling array and RNA-seq studies. Is affected by several genes including daf-2; eat-2; and pgl-1 based on microarray; tiling array; and RNA-seq studies. Is affected by eight chemicals including methylmercuric chloride; antimycin; and fluoranthene based on microarray and RNA-seq studies. GO Terms: Integral component of membrane (Wormbase, 2021).
	C11H1.5	1.81				*C11H1.5* is affected by fifteen chemicals, GO Terms: actin cytoskeleton reorganization, plasma membrane (Wormbase, 2021).
	C12D12.7	-1.82				*C12D12.7* is affected by 2 genes only (Wormbase, 2021). Down 1.5x w HgCl2 in Ce (this study).
	C12D5.10	-2.40				*C12D5.10* is enriched in amphid sheath cell, affected by multi-walled carbon nanotube; antimycin; and Chlorpyrifos (Wormbase, 2021).
	C12D8.2		1.89			*C12D8.2* is affected by daf-2 and eat-2, affected by Triclosan (Wormbase, 2021).
	C12D8.9				-2.31	Down 1.8X with HgCl2 in this study. Is enriched in ASER based on RNA-seq studies. Is affected by five chemicals including methylmercuric chloride, Cry5B, and paraquat based on microarray studies.
	C15B12.8		25.4			*C15B12.8* is enriched in body wall muscle cell, intestine and head mesodermal cell, affected by 14 chemicals, predicted to have oxidoreductase activity, localizes to peroxisome, close human homolog PIPOX (Wormbase, 2021). Up 43x w HgCl2 & in dose response up to 14x w meHg in Ce (McElwee, 2010). "Very few genes were similarly affected by both HgCl2 and MeHgCl exposures" but C15B12.8 was one (McElwee et al., 2013).
	C15C8.8		-3.91			*C15C8.8* is enriched in germline precursor cell, affected by clk-1; dpy-7; and pry-1 (Wnt signaling), affected by five chemicals (Wormbase, 2021).
	C16B8.2				1.6177	Up 1.5X with DMA in this study. Upregulated after D. coniospora infection (Engelmann et al., 2011). 2.6X upreg after 20uM HgCl2 exposure (McElwee et al., 2013). Is enriched in PLM based on RNA-seq studies. Is affected by several genes including daf-16; daf-2; and daf-12 based on microarray and RNA-seq studies. Is affected by eleven chemicals including Mercuric Chloride; rotenone; and stavudine based on microarray and RNA-seq studies (Wormbase, 2021).
	C16C8.10	1.77				*C16C8.10* is enriched in male and male-specific anatomical entity, affected by 8 chemicals (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	C17B7.10		3.05			C17B7.10 is enriched in germ line, affected by five chemicals (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Up 2x w 20µM HgCl2 and 7x w 7.5µM meHg in Ce (McElwee et al., 2013).
	C17B7.12		4.37			*C17B7.12* is enriched in neurons, affected by ten chemicals (Wormbase, 2021).
	C17B7.7	2.20				*C17B7.7* is not considered a gene (Wormbase, 2021). *C17B7.7* is a putative direct target of DAF-16 (McElwee et al., 2003).
	C17F4.12	-2.57				*C17F4.12* is enriched in hypodermis, affected by five chemicals (Wormbase, 2021).
	C17H12.6	2.25				*C17H12.6* is enriched in intestine, somatic gonad precursor, neurons, affected by > 20 chemicals, involved in innate immune response (Wormbase, 2021). Up 14x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 4x w 20µM HgCl2 in Ce (McElwee et al., 2013). Up 6.9x w NaAsO2 in Ce (Sahu et al., 2013). Up w Ag+ and AgNP in Ce (Hunt et al., 2014). Up 4x w X-rays & gamma rays in Ce (Greiss et al., 2008). Upregulated by SKN-1 & up w NaAsO2 in Ce (Oliveira et al., 2009).
	C17H12.8		-3.76			*C17H12.8* is enriched in OLL and PVD neurons, head mesodermal cell; intestine; and pharyngeal muscle cell, affected by twenty-seven chemicals, GO Term: innate immune response (Wormbase, 2021). Up 5x w *Y. pestis* and required for resistance in Ce (Bolz et al., 2010). Up 2.9x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 2.6x w *M. nematophilum* in Ce (O'Rourke et al., 2006). Strongly downregulated four hours after *C. albicans* infection (Pukkila-Worley et al., 2011). Up 7x w X-rays & gamma rays in Ce (Greiss et al., 2008). Up 2x w Ag+ in Ce (Hunt et al., 2014). Up w NaAsO2 and paraquat (Sahu et al., 2013). Down 2.9x w 2µM or 7.5µM meHgCl (McElwee et al., 2013).
	C18C4.7				-2.53	Is enriched in coelomocyte, male-specific anatomical entity, and neurons based on microarray and tiling array studies. Is affected by eighteen chemicals (Wormbase, 2021). Up with D. coniospora + Harposporium infection (Engelmann et al., 2011).
	C24H12.12		-3.33			*C24H12.12* pseudogene is affected by eat-2; pgl-1; and dpy-21, affected by six chemicals including indole; Psoralens; and allantoin (Wormbase, 2021).
	C24H12.3			-2.25		Affected by chd-3, let-418, glh-4, glh-1, pgl-1, pgl-3, alg-1, dlc-1, eat-2, daf-2, sin-3 and wdr-5.1 according to RNA-seq and microarray. Affected by Psoralens, allantoin, metformin, Sirolimus and Rifampin according to RNA-seq (Wormbase, 2021).
	C24H12.9			-2.68		Is affected by five chemicals including Alovudine; metformin; and Sirolimus based on RNA-seq and microarray studies (Wormbase, 2021). Up with D. coniospora infection (Engelmann et al., 2011).
	C25F6.8		-3.43			*C25F6.8* is affected by seven chemicals including Sodium Chloride; allantoin; and Sirolimus (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	C30B5.6				-2.55	Is enriched in GABAergic neurons, coelomocyte, excretory cell, and neurons based on tiling array and microarray studies. Is affected by fifteen chemicals including methylmercury hydroxide, Tunicamycin, and D-glucose based on RNA-seq and microarray studies. GO Terms: membrane (Wormbase, 2021).
	C32B5.15		-3.33			C32B5.15 is enriched in NSM; Z1; and Z4 neurons, affected by twelve chemicals including methylmercuric chloride; Mianserin; and multi-walled carbon nanotube (Wormbase, 2021). Down 3.5x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	C32H11.3	10.1	6.6			*C32H11.3* is enriched in neurons, affected by nineteen chemicals (Wormbase, 2021). Up 4.6x w NaAsO2 (Sahu et al., 2013). Upregulated by SKN-1 & needed for NaAsO2 resistance (Oliveira et al., 2009). Up 3x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Up 10.1x w NaAsO2 in Ce (this study).
	C32H11.4	11.7	6.7			*C32H11.4* is enriched in intestine, PVD and OLL neurons and head mesodermal cell, affected by >20 chemicals, involved in innate immune response (Wormbase, 2021). Innate immune responder to 5 pathogens (Yang et al., 2016) (Muir and Tan, 2008) (Troemel et al., 2006). Up ~3x w X-rays and gamma-rays (Greiss et al., 2008). Down w Ag+ in Ce (Hunt et al., 2014). Upregulated by SKN-1 & needed for NaAsO2 resistance (Oliveira et al., 2009). Up 12x w NaAsO2 (Sahu et al., 2013). Upregulated by DAF-12 and DAF-2 (Fisher and Lithgow, 2006), downregulated by DAF-16 (Li et al., 2008; Tepper et al., 2013).
	C35E7.7				-3.16	Is enriched in male based on RNA-seq studies. Is affected by several genes including rrf-3; clk-1; and eat-2 based on tiling array; microarray; and RNA-seq studies. Is affected by nine chemicals including Tunicamycin; Alovudine; and stavudine based on microarray and RNA-seq studies (Wormbase, 2021).
	C37A5.6		5.17			*C37A5.6* is affected by fourteen chemicals, GO Term: innate immune response (Wormbase, 2021).
	C37C3.10	-2.01				*C37C3.10* is enriched in intestine, affected by sixteen chemicals (Wormbase, 2021). Up w 3 bacterial species in Ce (Engelmann et al., 2011). Down 2.3x w DMA in Ce (this study).
	C38C10.3		3.02			*C38C10.3* is affected by fourteen chemicals (Wormbase, 2021). Up 4.2x w meHg in Ce (McElwee et al., 2013).
	C39D10.1		2.01			*C39D10.1* is affected by clk-1; rsr-2; and rrf-2, affected by aldicarb (Wormbase, 2021).
	C40A11.2		-3.23			*C40A11.2* is enriched in DA neuron; VA neuron; hypodermis; and pharynx, affected by ten chemicals including 1-methylnicotinamide; methylmercuric chloride; and multi-walled carbon nanotube, close human homolog TNFAIP1 exhibits GTP-Rho binding activity and identical protein binding activity, also has high homology to KCTD10 (potassium channel tetramerization domain containing 10) and KCTD13 (potassium channel tetramerization

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						domain containing 13) (Wormbase, 2021). Down 8.7x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	C40A11.6		-3.26			C40A11.6 is enriched in CEPshDL; CEPshDR; CEPshVL; CEPshVR; and pharynx, affected by twelve chemicals including 1-methylnicotinamide; methylmercuric chloride; and bisphenol S, close homolog human TNFAIP1 exhibits GTP-Rho binding activity and identical protein binding activity, also has high homology to KCTD10 (potassium channel tetramerization domain containing 10); KCTD13 (potassium channel tetramerization domain containing 13) (Wormbase, 2021). Down 9.2x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	C41G6.13		-5.45			*C41G6.13* is enriched in hypodermis, affected by seven chemicals (Wormbase, 2021).
	C43D7.4				-2.09	Is affected by five chemicals including Mercuric Chloride, Rifampin, and allantoin based on microarray and RNA-seq studies (Wormbase, 2021).
	C43H6.6				1.72	Down 1.5X with NaAsO2 in this study. Upregulated with bacteria Serratia marcescens, Enterococcus faecalis, otorhabdus luminescens, and fungal *Harposporium* infection (Engelmann et al., 2011). Is enriched in BAG; dopaminergic neurons; and neurons based on tiling array and microarray studies. Is affected by several genes including daf-2; rrf-3; and eat-2 based on microarray; tiling array; and RNA-seq studies. Is affected by seven chemicals including stavudine; Zidovudine; and Cry5B based on RNA-seq and microarray studies. Go Terms: extracellular space, integral component of membrane, negative regulation of inflammatory response (Wormbase, 2021).
	C44H9.7			-2.13		Is enriched in intestine and pharyngeal muscle cell based on tiling array studies. Is affected by fourteen chemicals including 1-methylnicotinamide, methylmercuric chloride, and Zidovudine based on RNA-seq and microarray studies. GO Terms: integral component of membrane (Wormbase, 2021). Down 3.7X with DMA in this study. Down 2.8X with 2uM, and down 6.6X with 7.5uM meHgCl (McElwee et al., 2013).
	C45B11.6		-3.65			C45B11.6 is enriched in AVA neurons, affected by 15 chemicals, predicted to have cis-stilbene-oxide hydrolase activity, a close homolog of human EPHX1 (epoxide hydrolase 1), GO term: integral component of endoplasmic reticulum membrane (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
	C45B2.3	-2.09			-2.01	*C45B2.3* is enriched in excretory cell and hypodermis, affected by thirteen chemicals (Wormbase, 2021). Up 25x w 20µM HgCl2 in Ce (McElwee et al., 2013). Down 3.0x w DMA in Ce (this study).
	C46A5.4		-4.42			*C46A5.4* is enriched in intestine, affected by > 20 chemicals, predicted to have heme binding activity and peroxidase activity, GO Terms: heme binding, response to oxidative stress (Wormbase, 2021). Required in Ce for *E. faecalis* resistance (Tiller and Garsin,

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						2014). Up 36% w *E. carotovora* in Ce (Wong et al., 2007). Down 9.7x w 7.5µM meHg in Ce (McElwee et al., 2013).
	C47A4.3				-2.03	Is predicted to have phosphoprotein phosphatase activity. Is an ortholog of human PPP1CA (protein phosphatase 1 catalytic subunit alpha). Affected by eleven chemicals. GO Terms: cytoplasm, hydrolase activity, nucleus, protein dephosphorylation (Wormbase, 2021).
	C47E12.13			-2.36		Is affected by nine chemicals including methylmercuric chloride, Alovudine, and stavudine based on microarray and RNA-seq studies (Wormbase, 2021). Down 3.1X with DMA, down 1.9X with meHgCl in this study. Down 3.4X with 7.5uM meHgCl (McElwee et al., 2013).
	C50H11.13		2.23			*C50H11.13* is enriched in neurons, GO term: integral component of membrane (Wormbase, 2021).
	C50H2.4	-1.92				*C50H2.4* is enriched in male distal tip cell, and somatic gonad precursor, affected by seven chemicals (Wormbase, 2021). Down to 0.64x in Ce exposed to *E. carotovora* or *P. luminescens* (Wong et al., 2007).
	C53A5.9		-3.21			*C53A5.9* is enriched in body wall muscle cell; intestine; neurons; and retrovesicular ganglion, affected by skn-1; rrf-3; and elt-2, affected by thirteen chemicals including methylmercuric chloride; Mercuric Chloride; and allantoin (Wormbase, 2021). Up 3-4x w HgCl2 and meHgCl in Ce (McElwee et al., 2013).
	C56C10.4		-3.94			*C56C10.4* is enriched in ASER and PLM neurons, and amphid sheath cell, affected by fourteen chemicals (Wormbase, 2021). Up w three bacterial species in Ce (Engelmann et al., 2011). Down 2.6x w 7.5µM meHgCl in Ce (McElwee et al., 2013).
	C56G3.2	2.18	2.64			*C56G3.2* is enriched in intestine, affected by Tunicamycin, paraquat and allantoin, predicted to have oxidoreductase activity (Wormbase, 2021).
	D1044.6	2.12				*D1044.6* is enriched in germ line, germline precursor cell, and somatic gonad precursor, affected by seventeen chemicals, a close homolog of human ZNF318, GO Terms: nucleoplasm, regulation of transcription, DNA-templated (Wormbase, 2021). Up 20x w BPA in Ce (Camacho, 2019).
	D1054.3				-2.09	Is enriched in body wall muscle cell, germ line, germline precursor cell, intestine, and muscle cell, affected by eight chemicals, predicted to encode a protein with the following domains: SGS domain and SGS domain. Is an ortholog of human SUGT1 (SGT1 homolog, MIS12 kinetochore complex assembly cochaperone). GO Terms: protein stabilization (Wormbase, 2021).
	E02C12.9	-2.23				*E02C12.9* is affected by Chlorpyrifos and Diazinon (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	EGAP9.4				-2.68	Down 2.5X with DMA in this study. Is enriched in NSM and head mesodermal cell based on tiling array and RNA-seq studies. Is affected by Psoralens, allantoin, and Rifampin based on RNA-seq studies (Wormbase, 2021).
	F01D5.2	4.86	3.06			*F01D5.2* is enriched in intestine, affected by twenty-four chemicals (Wormbase, 2021). Up 8.8x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up w *Harposporium* in Ce (Engelmann et al., 2011). Upregulated by DKF-2, an innate immune regulator (Ren et al., 2009). Down 3x w *S. aureus* (Irazoqui et al., 2010).
	F01D5.3	3.42	3.28			*F01D5.3* is enriched in intestine, affected by > 20 chemicals, involved in innate immune response (Wormbase, 2021). Upregulated by DKF-2, an innate immune regulator (Ren et al., 2009). Upregulated by SKN-1 (Oliveira et al., 2009). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 4x w meHg in Ce (McElwee et al., 2013).
	F01D5.5	2.88				*F01D5.5* is enriched in PVD and OLL neurons, intestine and head mesodermal cell, affected by > 20 chemicals, involved in innate immune response (Wormbase, 2021). Up 5.8x w *P. aeruginosa* in Ce (Troemel et al., 2006). Up 1.6x w *M. nematophilum* in Ce (O'Rourke et al., 2006). Up w *Harposporium* in Ce (Engelmann et al., 2011). Upregulated by DKF-2, an innate immune regulator (Ren et al., 2009). Down w *C. albicans* in Ce (Pukkila-Worley et al., 2011). Upregulated by SKN-1 (Oliveira et al., 2009). Up w NaAsO2 and Cd in Ce (Sahu et al., 2013).
	F01G4.6			1.53		Is enriched in NSM and muscle cell based on Chronogram; RNA-seq; and microarray studies. Is affected by ten chemicals including Zidovudine; Rifampin; and Psoralens based on RNA-seq and microarray studies. Predicted to localize to integral component of mitochondrial inner membrane. Is expressed in body wall musculature; intestine; and pharynx. Is an ortholog of human SLC25A3 (solute carrier family 25 member 3). GO Terms: integral component of membrane, integral component of mitochondrial membrane, mitochondrion, phosphate ion transport (Wormbase, 2021).
	F07C4.6		-3.45		-5.62	*F07C4.6* is enriched in intestine, affected by seven chemicals including methylmercuric chloride; antimycin; and Ethanol (Wormbase, 2021). Down 27X with meHgCl (McElwee et al., 2013).
	F07H5.13	-1.89	-3.37			*F07H5.13* is enriched in AVK and NSM neurons, body wall muscle cell, and intestine, affected by seventeen chemicals including methylmercury hydroxide, 1-methylnicotinamide, and methylmercuric chloride (Wormbase, 2021). Down 4.7x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013). Down 2.1x w HgCl2 and down 1.9x w meHgCl in Ce (this study).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F10C1.1				1.52	Is enriched in NSM based on tiling array studies. Is affected by rsr-2 and drh-3 based on tiling array and RNA-seq studies. Is affected by dafa#1 and Sirolimus based on microarray studies (Wormbase, 2021).
	F10D2.16			-3.16		Is enriched in neurons based on microarray studies. Is affected by resveratrol based on microarray studies. integral component of membrane (Wormbase, 2021).
	F11C1.4			1.54		1.6X upreg with dichlorvos exposure (Lewis et al., 2009). Upreg with *D. coniospora* infection (Engelmann et al., 2011). Is enriched in DA neuron; VA neuron; and neurons based on tiling array and RNA-seq studies. Is affected by four chemicals including Rifampin; Psoralens; and Sirolimus based on RNA-seq and microarray studies. Is an ortholog of human LDAH (lipid droplet associated hydrolase). GO Terms: lipid droplet, lipid storage (Wormbase, 2021). Up 1.5x with DMA (this study).
	F11E6.9		-3.85			*F11E6.9* is affected by twelve chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). Down 24% w *E. carotovora* in Ce (Wong et al., 2007). Down w HgCl2 in Ce (this study).
	F13B12.4		-4.24			F13B12.4.2 is enriched in germline precursor cell, hypodermis, and neurons, affected by sixteen chemicals (Wormbase, 2021). Up w three bacterial species in Ce (Engelmann et al., 2011). Down 3.6x w 7.5µM meHg in Ce (McElwee et al., 2013).
	F13C5.3			-2.56		Is enriched in dopaminergic neurons based on tiling array studies. Is affected by eleven chemicals including multi-walled carbon nanotube, stavudine, and Zidovudine based on RNA-seq and microarray studies (Wormbase, 2021). Down 3.1X with NaAsO2, Down 1.5 with meHgCl in this study.
	F14D7.1		2.27			*F14D7.1* is enriched in FLP, germ line, male and intestine, affected by eight chemicals (Wormbase, 2021). Up 2.9x w 7.5µM meHgCl in Ce (McElwee et al., 2013).
	F14D7.11	-1.91				*F14D7.11* is enriched in neurons, affected by nitroguanidine, GO Term: plasma membrane (Wormbase, 2021). Extracellular vesicle (EV) releasing neurons (EVN) act in sensory signaling and "F14D7.11::GFP localized in cilia and secreted EVs from all 27 EVNs" (Wang et al., 2015).
	F14D7.5	-2.00				*F14D7.5* is enriched in amphid sheath cell and dopaminergic neurons, affected by six chemicals (Wormbase, 2021). Down 2.0x w DMA in Ce (this study).
	F15B9.8		-5.09			*F15B9.8* is enriched in germline precursor cell, hypodermis, Z4, Z1, intestine, AFD and NSM neurons, and somatic gonad precursor, affected by twenty-eight chemicals (Wormbase, 2021). Down 2x w 2µM and 7.5µM meHg in Ce (McElwee et al., 2013). Up w paraquat and NaAsO2 (Sahu et al., 2013).
	F17A2.4	2.29				*F17A2.4* pseudogene is affected by eat-2 and daf-2 (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F17B5.4	-2.18				*F17B5.4* is enriched in seam cell, affected by 4 chemicals, GO Terms: chondroitin sulfate biosynthetic process, integral component of membrane, positive regulation of response to oxidative stress (Wormbase, 2021). Down ~2.5x w 2µM and w 7.5µM meHgCl in Ce (McElwee et al., 2013).
	F17B5.8	3.07	2.75			*F17B5.8* is enriched in neurons and intestine, affected by thirteen chemicals (Wormbase, 2021).
	F17C11.15			-3.73	-3.13	Is affected by several genes including clk-1; pgl-1; and prg-1 based on RNA-seq and microarray studies (Wormbase, 2021).
	F18C5.9		-3.78			*F18C5.9* is affected by ten chemicals (Wormbase, 2021). Down 2.5x w 2µM meHgCl and 4.6x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	F19B10.11	2.07				*F19B10.11* pseudogene is affected by seven chemicals (Wormbase, 2021). Up 33% w *E. faecalis* in Ce (Wong et al., 2007). X
	F19D8.2			1.69	1.71	Up 1.7X with meHgC in this study. Upregulated after *D. coniospora* infection (Engelmann et al., 2011). Is enriched in Z1.p; Z4.a; male distal tip cell; neurons; and retrovesicular ganglion based on RNA-seq and microarray studies. Is affected by six chemicals including Psoralens; allantoin; and Sirolimus based on RNA-seq and microarray studies (Wormbase, 2021).
	F20A1.8	-2.31				*F20A1.8* is enriched in muscle cell, affected by five chemicals (Wormbase, 2021). Up 2.1x w 2µM meHgCl in Ce (McElwee et al., 2013). Down 1.7x w DMA in Ce (this study).
	F21A3.7			1.94		Predicted to be involved in several processes, including chemical synaptic transmission; nervous system process; and regulation of membrane potential. Predicted to localize to integral component of plasma membrane; neuron projection; and synapse. Affected by five chemicals. GO Terms: extracellular ligand-gated ion channel activity, integral component of membrane, ion transport, nervous system process (Wormbase, 2021).
	F21C10.9		4.35			*F21C10.9* is enriched in PVD, OLL, ASER, PLM, hypodermis and intestine, affected by > 20 chemicals, predicted to have transferase activity (Wormbase, 2021). Upregulated by glucose in Ce (Lee et al., 2009). Up 8x w nitric oxide in Ce (Gusarov et al., 2013). Up 14x w 20µM HgCl2 and 2.3x w 7.5µM meHgCl (McElwee, 2010). Up w Cd and high NaAsO2 (Sahu et al., 2013).
	F21F8.5	1.78				*F21F8.5* is enriched in germ line and intestine, by four chemicals including multi-walled carbon nanotube; Zidovudine; and resveratrol (Wormbase, 2021).
	F21H12.2	2.19				*F21H12.2* pseudogene is enriched in neurons (Wormbase, 2021).
	F21H12.3	2.12				*F21H12.3* is by four chemicals including Tunicamycin; Cry5B; and Colistin (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F23C8.11		2.16			*F23C8.12* is dead, refer to *F23C8.11* pseudogene is enriched in AVE, affected by aak-2; alg-1; and mex-3, affected by Mianserin (Wormbase, 2021).
	F23C8.12				1.87	Dead gene, integrated into F23C8.11. Is enriched in AVE based on tiling array studies. Affected by Mianserin according to RNA-seq (Wormbase, 2021).
	F23F12.3		-3.66			*F23F12.3* is enriched in Z4, Z1, intestine and somatic gonad precursor, GO term: integral component of membrane, a close homolog of human SLC22A14 predicted to have transmembrane transporter activity (Wormbase, 2021). Downregulated by SKN-1 (Oliveira et al., 2009). Down 5.2x w 7.5µM meHg in Ce (McElwee et al., 2013).
	F25C8.1		2.03			*F25C8.1* pseudogene is affected by eleven chemicals (Wormbase, 2021).
	F26A10.2			-2.30		Is enriched in Psub1, head mesodermal cell, neurons, and pharynx based on microarray and RNA-seq studies. Is affected by eleven chemicals including 1-methylnicotinamide, rotenone, and D-glucose based on RNA-seq and microarray studies. Human ZNF148 exhibits DNA-binding transcription repressor activity, RNA polymerase II-specific and RNA polymerase II cis-regulatory region sequence-specific DNA binding activity. Is predicted to encode a protein with the following domains: Zinc finger C2H2-type and Zinc finger C2H2 superfamily. Is an ortholog of human ZNF148 (zinc finger protein 148) (Wormbase, 2021).
	F26C11.4				-2.45	Is enriched in male based on RNA-seq studies. Is affected by eight chemicals including Alovudine, stavudine, and Zidovudine based on RNA-seq studies (Wormbase, 2021).
	F26D2.3				1.97	Upregulated with bacteria Serratia marcescens, Enterococcus faecalis and otorhabdus luminescens, and two fungal pathogens Drechmeria coniospora and Harposporium sp. Infection (Engelmann et al., 2011). Is affected by nine chemicals. Human ortholog(s) of this gene are implicated in cataract 13 with adult i phenotype. Is an ortholog of several human genes including GCNT1 (glucosaminyl (N-acetyl) transferase 1); GCNT3 (glucosaminyl (N-acetyl) transferase 3, mucin type); and GCNT7 (glucosaminyl (N-acetyl) transferase family member 7). GO Terms: Golgi membrane, Integral component of membrane, trasferase activity (Wormbase, 2021).
	F26G1.10		-3.53			*F26G1.10* is enriched in intestine, PLM neurons, and head mesodermal cell, affected by ten chemicals (Wormbase, 2021).
	F26G1.9		-5.33			*F26G1.9* is enriched in germline precursor cell, hypodermis and PLM neurons, affected by five chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
	F27C1.11	1.89				*F27C1.11* is enriched in AFD, ASER, PLM and other neurons, affected by ten chemicals, close human homolog LOXHD1 is implicated in autosomal recessive nonsyndromic deafness 77, GO Term: intracellular signal transduction (Wormbase, 2021).
	F28A10.2		-4.54			*F28A10.2* pseudogene is enriched in male, affected by five chemicals (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F30A10.2		-3.23			*F30A10.2* is enriched in germline precursor cell; hypodermis; intestine; and somatic gonad precursor, affected by sixteen chemicals including methylmercury hydroxide; 1-methylnicotinamide; and methylmercuric chloride (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Down 2.2x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	F30H5.5			-3.04		Down 2.3X with DMA in this study. Upregulated with Harposporium infection (Engelmann et al., 2011). Enriched in AFD, ASER and germ line according to RNA-seq. Affected by mir-34, elli-1, hpl-2, daf-2, mex-1, mex-3 and spn-4 according to microarray and RNA-seq. Affected by multi-walled carbon nanotube according to RNA-seq (Wormbase, 2021).
	F31C3.14			3.10		Up 2.4X with treatment with 500 µg/mL Lonicera japonica (Yang et al., 2018a).
	F35B3.4		-3.21			F35B3.4 is enriched in DA neuron; VA neuron; hypodermis; and intestine, affected by twenty-two chemicals including Heme; hydrogen sulfide; and Nitric Oxide based on microarray and RNA-seq studies (Wormbase, 2021).
	F35E2.10			-7.73		Is enriched in male based on RNA-seq studies. Is affected by five chemicals including multi-walled carbon nanotube; Hydrolyzable Tannins; and paraquat based on RNA-seq and microarray studies (Wormbase, 2021).
	F36D1.10			2.24		Is affected by rsr-2 and dpy-21 based on tiling array and RNA-seq studies (Wormbase, 2021).
	F36H5.7			-2.67		Affected by metformin and Psoralens based on RNA-seq studies (Wormbase, 2021).
	F36H9.5		1.88			*F36H9.5* is enriched in germline precursor cell and hypodermis, affected by eleven chemicals, GO Terms: endoplasmic reticulum membrane, Golgi membrane, integral component of membrane (Wormbase, 2021).
	F37A4.4		-3.55			*F37A4.4* is enriched in germ line, hypodermis, muscle cell, and in male, affected by twenty-four chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 3.4x w 7.5µM meHgCl in Ce (McElwee et al., 2013).
	F37D6.4			-2.36		Is affected by seven chemicals including D-glucose, stavudine, and Psoralens based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: F-box associated and F-box associated domain, type 2. GO Terms: integral component of membrane (Wormbase, 2021). Down 1.7x with DMA in this study.
	F38B6.8			-2.20		Is enriched in CEM, HOB, IL2 neuron, and ray neuron type B based on RNA-seq studies (Wormbase, 2021). Down 1.8x with DMA in this study.
	F39B2.3	1.91	2.04			*F39B2.3* is enriched in germ line, intestine and muscle cell, affected by 11 chemicals, predicted to have oxidoreductase activity, close homolog of human CRYZ, GO Terms: mRNA 3'-UTR binding, cytosol (Wormbase, 2021). Up 2.5x w 7.5µM meHgCl in Ce (McElwee et al., 2013). Has a SKN-1 binding site in promoter, up >4x w acrylamide in Ce

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						(Hasegawa et al., 2008). Upregulated by SKN-1 and As stress (Oliveira et al., 2009). Up 2.0x w DMA (this study).
	F42F12.11			-3.11		Down 2.3X with DMA in this study. Affected by metformin, Psoralens, allantoin, Sirolimus and Rifampin according to RNA-seq. (Wormbase, 2021).
	F44D12.10	-2.61				*F44D12.10* is affected by drh-3, GO Term: metal ion binding (Wormbase, 2021). Down 1.9x w HgCl2 in Ce (this study).
	F46B3.19	2.02				*F46B3.19* pseudogene is enriched in NSM and hypodermis, affected by Colistin (Wormbase, 2021).
	F46B3.22	-1.82				*F46B3.22* is affected by four chemicals (Wormbase, 2021). Down 1.7x w meHgCl in Ce (this study).
	F46B3.22				-2.55	Down 1.5X with NaAsO2 in this study. Is affected by four chemicals including multi-walled carbon nanotube, Atrazine, and Colistin based on RNA-seq and microarray studies (Wormbase, 2021).
	F47B3.7		2.57			*F47B3.7* is enriched in germ line and male, affected by > 15 chemicals, predicted to have protein tyrosine phosphatase activity (Wormbase, 2021). Up 1.6x w *P. luminescens* in Ce (Wong et al., 2007). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 4.8x w 7.5µM meHg in Ce (McElwee et al., 2013). X
	F48C1.8		2.25			*F48C1.8* is affected by eight chemicals (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Down 1.5x w meHgCl (this study).
	F48E3.9	2.16				*F48E3.9* is enriched in BAG (sensory neuron), affected by thirteen chemicals (Wormbase, 2021). Up w *D. coniospora* and *Harposporium* in Ce (Engelmann et al., 2011).
	F48E8.2	-1.80				*F48E8.2* is enriched in germ line, germline precursor cell, AVK and somatic gonad precursor, affected by nine chemicals, close homolog of human EAPP, GO Terms: nucleus, positive regulation of cell population proliferation (Wormbase, 2021). X
	F49C5.11		4.67			*F49C5.11* is enriched in neurons and hypodermis, affected by six chemicals (Wormbase, 2021).
	F49D11.3	-2.00			-2.90	*F49D11.3* is affected by 3 chemicals, predicted to have chondroitin 4-sulfotransferase activity, GO Terms: chondroitin sulfate biosynthetic process, integral component of membrane, positive regulation of response to oxidative stress (Wormbase, 2021). Down 2.0x w HgCl2 or DMA (this study).
	F49F1.10		-6.07			*F49F1.10* is enriched in germline precursor cell and male-specific anatomical entity, affected by 3 chemicals, a close homolog of human LGALSL (galectin like) predicted to have carbohydrate binding activity (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Down 3.6x w HgCl2 (this study).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F49F1.10			-3.58		Down 6X with DMA in this study. F49F1.10 is a close homolog of human LGALSL (galectin like) predicted to have carbohydrate binding activity. Affected by three genes. GO Terms: carbohydrate binding (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011).
	F49F1.11		-4.31			*F49F1.11* is enriched in neurons, affected by 7 chemicals, a close homolog of human LGALSL (galectin like) predicted to have carbohydrate binding activity (Wormbase, 2021).
	F52D2.6	1.90			1.75	*F52D2.6* is affected by several genes including daf-2; eat-2; and sma-2, affected by 6 chemicals including Chlorpyrifos and Diazinon (Wormbase, 2021).
	F52F12.9	4.98	3.71			*F52F12.9* is enriched in male, affected by five chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 5x w NaAsO2 in Ce (this study).
	F53B7.4			-3.51		Is enriched in AVA; AVE; neurons; and ventral nerve cord based on tiling array and microarray studies. GO Terms: integral component of membrane. Is affected by copper sulfate based on microarray studies (Wormbase, 2021).
	F53F10.2			2.12		Is predicted to have catalytic activity. Predicted to be involved in polyamine biosynthetic process. Affected by three chemicals (Wormbase, 2021). Putative Antizyme Inhibitor AZI activity (Stegehake et al., 2015).
	F53F4.2		-3.48			*F53F4.2* is affected by rrf-3; elt-2; and aak-2, affected by seven chemicals including metformin; Psoralens; and allantoin (Wormbase, 2021).
	F53G2.2	2.70				*F53G2.2* is enriched in germ line and pharynx, affected by eight chemicals (Wormbase, 2021).
	F53H2.3			1.65		Is expressed in gonad and intestine. Enriched in coelomocyte. (Wormbase, 2021).
	F54B11.10		-3.64			*F54B11.10* is enriched in ASER, NSM, and PLM neurons, hypodermis, and intestine, affected by nineteen chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011). Down 2.1x w HgCl2 and 1.9x w meHgCl in Ce (this study).
	F54D12.9		-3.92			*F54D12.9* is enriched in male, affected by seven chemicals (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
	F54H12.4	2.10				*F54H12.4* is affected by Rifampin and resveratrol (Wormbase, 2021). Up 33% w *S. marcescens* in Ce (Wong et al., 2007). Protein level altered w *E. coli* in Ce (Sharika et al., 2018).
	F55C12.5			1.58		Is predicted to have lipid binding activity. Is expressed in AIYL and AIYR. Predicted to be involved in lipid transport. Predicted to localize to endoplasmic reticulum. Is an ortholog of human TEX2 (testis expressed 2). Affected by >10 chemicals. GO Terms: endoplasmic reticulum, integral component of membrane, lipid binding, lipid transport (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F55G11.2	10.4	2.90			*F55G11.2* is regulated by the ELT-2 GATA transcription factor, enriched in intestine, affected by > 20 chemicals, involved in innate immune response (Wormbase, 2021). Up 47x w NaAsO2 in Ce (Sahu et al., 2013). Up 5-17x w *P. aeruginosa* in Ce (Evans et al., 2008; Troemel et al., 2006). Up w *Harposporium* in Ce (Engelmann et al., 2011). Up 5x w HgCl2 in Ce (McElwee et al., 2013). Up w chlorpyrifos and diazinon in Ce (Vinuela et al., 2010). Upregulated by SKN-1 (Oliveira et al., 2009).
	F55G11.3		5.58			*F55G11.3* pseudogene is affected by five chemicals (Wormbase, 2021).
	F56D5.3	3.07				*F56D5.3* is enriched in AFD neuron, affected by > 20 chemicals, predicted to have FMN binding activity and oxidoreductase activity (Wormbase, 2021). Up w juglone in Ce (Przybysz et al., 2009). Up w 20mM HgCl2 and dose response to 7x w meHg in Ce (McElwee et al., 2013). Upregulated by SKN-1 (Oliveira et al., 2009). Up 43x w NaAsO2 in Ce (Sahu et al., 2013). OxStr resp gene upregulated by SKN-1 (Park et al., 2009). Down 22% w *M. nematophilum* (O'Rourke et al., 2006). Up 1.8x w DMA (this study).
	F57H12.6		-3.44			*F57H12.6* is enriched in OLL and PVD neurons, hypodermis; intestine; and male-specific anatomical entity, affected by twenty-five chemicals including Nitric Oxide; methylmercury hydroxide; and 1-methylnicotinamide (Wormbase, 2021). Up 39% w *D. coniospora* in Ce (Pujol et al., 2008). Up w *D. coniospora* in Ce (Engelmann et al., 2011). Up w fungal infection (Omi et al., 2021). Up w Ag+ and AgNP in Ce (Hunt et al., 2014).
	F58A6.5			-2.35		Is enriched in germ line and in male based on RNA-seq studies. Is affected by nineteen chemicals including nicotinic acid, methylmercuric chloride, and Tunicamycin based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: Interactor of ZYG-11 and Protein of unknown function DUF856, Caenorhabditis species. GO Terms: Integral component of membrane (Wormbase, 2021). Down 1.6X with DMA, down 1.9X with meHgCl in this study. Up with 7.5uM meHgCl (McElwee et al., 2013).
	F58B6.1			-2.37		Is enriched in intestine based on RNA-seq studies. Is affected by seven chemicals including Tunicamycin, Mianserin, and bisphenol A based on microarray and RNA-seq studies. Is predicted to encode a protein with the following domains: Lipase (class 3), Fungal lipase-like domain, and Alpha\/Beta hydrolase fold. GO Terms: lipid metabolic process (Wormbase, 2021). Down 2.8X with DMA in this study. Down 3.2X with P. aeruginosa infection (Troemel et al., 2006).
	F58D2.3			-3.02		Down 2.8X with DMA in this study. Is affected by several genes including daf-2, eat-2, and lin-54 based on microarray and RNA-seq studies. Is affected by five chemicals including Psoralens, allantoin, and Sirolimus based on RNA-seq and microarray studies (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	F58F9.10		-3.40		-2.45	*F58F9.10* is a pseudogene affected by clk-1, smg-2, and drh-3 (Wormbase, 2021).
	F58H7.5	2.12				*F58H7.5* is enriched in germ line, neurons, and retrovesicular ganglion, affected by ten chemicals (Wormbase, 2021). Heat inducible (Ni et al., 2016).
	F59A1.15				2.08	Affected by >10 chemicals. Go Terms: Integral component of membrane, olfactory behavior, detection of chemical stimulus involved in sensory perception of smell, G protein-coupled olfactory receptor activity. Is predicted to encode a protein with the following domain: MFS transporter superfamily. 3.2X increase with 7.5 uM MeHgCl (McElwee et al., 2013).
	F59A6.10		-3.23			F59A6.10 is enriched in excretory cell and hypodermis, affected by skn-1; clk-1; and eat-2, affected by eleven chemicals including Tunicamycin; nanoparticle; and Alovudine (Wormbase, 2021). Up w *Harposporium* in Ce (Engelmann et al., 2011).
	H01G02.4	-1.84				*H01G02.4* is enriched in germ line, NSM and intestine, affected by seven chemicals (Wormbase, 2021).
	H10D12.2			2.55		Is affected by eleven chemicals including multi-walled carbon nanotube; Zidovudine; and Sodium Chloride based on RNA-seq and microarray studies (Wormbase, 2021).
	H11E01.3			1.50		Is enriched in body wall musculature; intestine; nerve ring neurons; and neurons based on microarray; RNA-seq; and proteomic studies. Is affected by eight chemicals including stavudine; Zidovudine; and Rifampin based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domain: Protein of unknown function DUF4590 (Wormbase, 2021).
	H12I13.5	1.80			1.74	*H12I13.5* is affected by Tunicamycin, allantoin and Sirolimus (Wormbase, 2021). Up w *D. coniospora* & *Harposporium* in Ce (Engelmann et al., 2011). Up 1.7x w meHgCl (this study).
	H20J04.7	1.88				*H20J04.7* is affected by rsr-2 and drh-3, GO Term: integral component of membrane (Wormbase, 2021).
	H25K10.1	1.91				*H25K10.1* is enriched in AFD neurons and intestine, affected by > 15 chemicals, predicted to have acid phosphatase activity and metal ion binding activity, close homolog of human ACP7, GO Term: metal ion binding (Wormbase, 2021). Ethanol response gene (Kwon et al., 2004). Upregulated by SKN-1 (Oliveira et al., 2009). Up w *Harposporium* + 3 bacterial species in Ce (Engelmann et al., 2011).
	H38K22.7	-1.90				*H38K22.7* is enriched in amphid sheath cell, affected by four chemicals (Wormbase, 2021).
	K01A2.4			-2.17		Is enriched in AFD, PLM, body wall musculature, and head mesodermal cell based on RNA-seq and microarray studies. Is affected by fourteen chemicals including Heme, 1-methylnicotinamide, and Zidovudine based on microarray and RNA-seq studies. Is

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						predicted to encode a protein with the following domain: Phosphorylation site. GO Terms: integral component of membrane (Wormbase, 2021). Down 2.9X with DMA in this study. Up 1.7X with M. nematophilum infection (O'Rourke et al., 2006).
	K02D3.1	-3.30				*K02D3.1* is enriched in AVK and neurons, affected by eight chemicals (Wormbase, 2021). Down 2.3x w *S. aureus* in Ce (Irazoqui et al., 2010). Down 2.1x w *P. aeruginosa* in Ce (Troemel et al., 2006).
	K02E11.5	-2.22				*K02E11.5* is enriched in AFD neurons, amphid sheath cell, arcade cell, pharyngeal-intestinal valve cell, and somatic gonad precursor, affected by nine chemicals (Wormbase, 2021). Down 2.9x w meHgCl in Ce (McElwee et al., 2013). Down 2.0x w DMA in Ce (this study).
	K02E11.7	-2.26				*K02E11.7* is enriched in PLM, amphid sheath cell, and hypodermis, affected by ten chemicals (Wormbase, 2021). Down 3.5x w 7.5µM meHgCl in Ce (McElwee et al., 2013). Down 2.8x w DMA (this study).
	K02E11.9	-2.23				*K02E11.9* pseudogene is enriched in amphid sheath cell, arcade cell, and pharyngeal-intestinal valve cell, affected by methylmercuric chloride (Wormbase, 2021). Down 3.4x w meHgCl in Ce (McElwee et al., 2013). Down 2.1x w DMA in Ce (this study).
	K02E7.7		-3.30	-2.38		*K02E7.7* is affected by eight chemicals including Psoralens; allantoin; and metformin (Wormbase, 2021).
	K02F6.6		2.04			*K02F6.6* is affected by several genes including daf-2; pgl-1; and glh-1 (Wormbase, 2021).
	K06C4.7	3.19				This gene is dead (Wormbase, 2021).
	K07C11.12			-2.40		Is affected by several genes including pgl-1, cep-1, and glh-1 based on RNA-seq studies (Wormbase, 2021).
	K08C9.5		-3.34			*K08C9.5* is enriched in CEM, FLP, HOB, IL2 neuron, and ray neuron type B, affected by several genes including age-1; rrf-3; and eat-2, affected by eight chemicals including aldicarb; multi-walled carbon nanotube; and Psoralens (Wormbase, 2021).
	K08E4.8	-2.19			-2.12	*K08E4.8* is predicted to encode a protein with an F-box associated domain, type 2 (Wormbase, 2021).
	K08F4.13	4.65	5.20			*K08F4.13* pseudogene is affected by wdr-23, daf-16, hsf-1, fog-2, daf-2 and eat-2 (no chemicals listed) (Wormbase, 2021).
	K09E3.7	1.76				*K09E3.7* is enriched in germ line, affected by sixteen chemicals (Wormbase, 2021).
	K09E4.1				-2.10	Is enriched in germ line and in male based on RNA-seq studies. Is affected by eighteen chemicals including Ethanol, nicotinic acid, and methylmercuric chloride based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domain: Protein kinase-like domain superfamily (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	K09E9.4				-2.01	Is predicted to have cAMP-dependent protein kinase inhibitor activity. Is an ortholog of human PKIA (cAMP-dependent protein kinase inhibitor alpha), PKIB (cAMP-dependent protein kinase inhibitor beta), and PKIG (cAMP-dependent protein kinase inhibitor gamma). GO Terms: cytoplasm, negative regulation of protein kinase activity, nucleus, cAMP-dependent protein kinase inhibitor activity. Affected by four chemicals (Wormbase, 2021). Down 1.7X with HgCl2 in this study.
	K10C2.6	-2.25				*K10C2.6* is enriched in NSM, affected by tryptophan (Wormbase, 2021).
	K10C9.9		2.27			*K10C9.9* is enriched in ASER neuron and muscle cell, affected by eight chemicals (Wormbase, 2021).
	K10H10.6		3.98			*K10H10.6* is enriched in ASER and RID neurons, affected by eight chemicals, close human homolog WWOX (WW domain containing oxidoreductase) implicated in autosomal recessive spinocerebellar ataxia (Wormbase, 2021). Up w HgCl2 and w meHgCl in Ce (McElwee et al., 2013). Up 1.8x w NaAsO2 in Ce (this study).
	K12C11.6	-1.99			-2.39	*K12C11.6* is enriched in intestine and head mesodermal cell, affected by 8 chemicals, a close homolog of human SLC31A1, GO Terms: copper ion transmembrane transporter activity, integral component of membrane, plasma membrane (Wormbase, 2021). Up 1.5X with Ag+ (Hunt et al., 2014). Down 1.9x w HgCl2 and 1.7x w DMA in Ce (this study).
	M01B12.4			1.57		Up 1.94X with 24h D. coniospora infection (Pujol et al., 2008a). Is enriched in germ line; intestine; and neurons based on microarray and RNA-seq studiesF. Is affected by five chemicals including bisphenol S; Zidovudine; and Hydrolyzable Tannins based on RNA-seq and microarray studies (Wormbase, 2021).
	M01G12.2			-2.47		Up 4.6X with HgCl2 (McElwee et al., 2013). Down 2.8X with DMA in this study. Is affected by clk-1 and sir-2.1 based on microarray studies. Is affected by Mercuric Chloride and nitroguanidine based on microarray studies. Is predicted to encode a protein with the following domains: Serpin (serine protease inhibitor), Serpin family, Serpin domain, and Serpin superfamily. (Wormbase, 2021).
	M03D4.4		-3.32			*M03D4.4* is expressed in pharyngeal muscle cell, close homolog human ZNF653 exhibits several functions, including AF-2 domain binding activity; transcription corepressor activity; and transcription factor binding activity, GO Terms: DNA-binding transcription factor activity, RNA polymerase II-specific, nucleus (Wormbase, 2021).
	M04B2.8	2.16				*M04B2.8* is a pseudogene (Wormbase, 2021). Down 2.0x w HgCl2, down 2.2x w DMA (this study).
	M04C9.2		2.11			*M04C9.2* is affected by four chemicals, close homolog of human PGPEP1 (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	M04C9.2				-2.34	Is affected by four chemicals including multi-walled carbon nanotube, Sodium Chloride, and Ag nanoparticles based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: Putative pyroglutamyl peptidase. GO Terms: cysteine-type peptidase activity, hydrolase activity, proteolysis. Is an ortholog of human PGPEP1 (pyroglutamyl-peptidase I) (Wormbase, 2021). Up 2.2X with DMA, Down 2.2X with HgCl2 in this study.
	M110.7	2.29	2.20			*M110.7* is enriched in germ line, NSM and male, affected by 15 chemicals, predicted to have hydrolase activity and be involved in lipid metabolism, a close homolog of human PNPLA7, GO Terms: lipid metabolic process, endoplasmic reticulum, integral component of membrane (Wormbase, 2021). Up 4.2x w 7.5µM meHg in Ce (McElwee et al., 2013). M110.7 is a homolog of vertebrate secondary organophosphate target, NTE (Lewis et al., 2009).
	M163.11			-2.56		Is affected by four chemicals including Psoralens, allantoin, and Rifampin based on RNA-seq studies. Is predicted to encode a protein with the following domains: ShK domain-like and ShKT domain. Affected by four chemicals. (Wormbase, 2021). Down 3.1X with DMA in this study. Upregulated with infection of three bacterial pathogens (Serratia marcescens, Enterococcus faecalis and otorhabdus luminescens) (Engelmann et al., 2011).
	M163.9				-2.32	GO Terms: integral component of membrane (Wormbase, 2021).
	M195.4		2.11			*M195.4* pseudogene is affected by sir-2.1; ubc-9; and jmjd-3.1 (Wormbase, 2021).
	M199.9	-1.93				*M199.9* is enriched in cephalic sheath cell, affected by ten chemicals (Wormbase, 2021).
	R01H2.8			-2.16		Is enriched in BAG and neurons based on tiling array and microarray studies. Is affected by multi-walled carbon nanotube and Colistin based on RNA-seq and microarray studies. GO Terms: integral component of membrane (Wormbase, 2021). Down 1.8X with DMA, down 1.6X with meHgCl in this study. Up with Harposporium infection (Engelmann et al., 2011).
	R03H10.4	1.76				*R03H10.4* is expressed in seminal vesicle, germ line, male and male-specific anatomical entity, affected by 9 chemicals (Wormbase, 2021). Male enriched reporter gene expression in seminal vesicle (Thoemke et al., 2005).
	R04B5.11		2.58			*R04B5.11* is enriched in germ line and in male, affected by nine chemicals (Wormbase, 2021). Up w *D. coniospora* & *Harposporium* in Ce (Engelmann et al., 2011). Up 3x w 7.5µM meHg in Ce (McElwee et al., 2013).
	R05H10.3				2.07	Affected by 9 chemicals. Is enriched in germ line; germline precursor cell; and somatic gonad precursor based on RNA-seq studies, and is affected by 3 germline genes. (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	R07B1.7		-3.54			*R07B1.7* is enriched in OLL and PVD neurons, and coelomocyte, affected by eight chemicals (Wormbase, 2021). Down 2.1x w HgCl2 and down 1.7x w meHgCl in Ce (this study).
	R07C3.3	-1.86				*R07C3.3* is enriched in AVK and germ line, affected by Sirolimus, close human homologs GCNT1, GCNT3, and GCNT7 are implicated in cataract 13 with adult i phenotype, GO Terms: Golgi membrane, transferring glycosyl groups (Wormbase, 2021).
	R08E5.3				-2.34	Is expressed in intestine. Is predicted to encode a protein with the following domains: Methyltransferase domain. Affected by >20 chemicals (Wormbase, 2021). Down 1.7X with NaAsO2, Down 2.2X with DMA in this study. Down with 20nM Ag, 20nM Au (Hunt et al., 2014). Down 2.7X with 7.5uM meHg (McElwee et al., 2013).
	R09H10.5			2.13		Upregulated with infection of three bacterial pathogens (Serratia marcescens, Enterococcus faecalis and otorhabdus luminescens) (Engelmann et al., 2011). Is enriched in coelomocyte and head mesodermal cell based on tiling array and RNA-seq studies. Is affected by thirteen chemicals including rotenone; D-glucose; and Zidovudine based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: EGF-like domain and MD domain (Wormbase, 2021).
	R186.8	-1.84				*R186.8* is enriched in ASER, germ line, somatic gonad precursor, male-specific anatomical entity and intestine, affected by 2 chemicals, GO Term: ribosome (Wormbase, 2021). Down 1.7x w DMA in Ce (this study).
	T01B6.1	2.06				*T01B6.1* is enriched in GABAergic neurons OLL and PVD neurons, head mesodermal cell and muscle cell, affected by fourteen chemicals, a close homolog of human SAPCD2 (Wormbase, 2021). Up w *D. coniospora* & *Harposporium* in Ce (Engelmann et al., 2011).
	T02E9.6		-4.33			*T02E9.6* is enriched in male, affected by eat-2; alg-1; and rsr-2, affected by Psoralens; allantoin; and Sirolimus (Wormbase, 2021).
	T04B2.8	-2.15				*T04B2.8* is enriched in body wall muscle cell and in male, affected by nine chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	T05A7.11		-3.50			T05A7.11 is enriched in NSM neurons, affected by 12 chemicals, predicted to have fucosyltransferase activity, GO Term: protein glycosylation (Wormbase, 2021).
	T05A8.7	1.76				*T05A8.7* is enriched in male-specific anatomical entity, AVK neurons and somatic gonad precursor, affected by 4 chemicals, GO Term: integral component of membrane (Wormbase, 2021). Up 1.6x w DMA (this study).
	T05H10.3		-3.77			T05H10.3 is enriched in dopaminergic neurons, germline precursor cell, and intestine, affected by 26 chemicals (Wormbase, 2021). Down 9.9x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	T06E4.12			-2.35	-2.02	Is enriched in intestine, affected by ten chemicals including Ethanol, tryptophan, and methylmercury hydroxide based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domain: Pistil-specific extensin-like protein (Wormbase, 2021). Down 1.7X with NaAsO2, down 2.8X with DMA in this study.
	T06G6.11				1.75	Is affected by several genes including daf-16; clk-1; and nhr-25 based on microarray and RNA-seq studies. Is affected by six chemicals including Psoralens; allantoin; and Sirolimus based on RNA-seq and microarray studies (Wormbase, 2021). Down 5.6X after 48h with 25 mg/l Atrazine (Reichert and Menzel, 2005).
	T07C12.4			-2.58		Is affected by clk-1 based on microarray studies (Wormbase, 2021). Down 2.7X with DMA in this study.
	T07G12.14			-2.27		Is affected by several genes including eat-2, pgl-1, and dpy-21 based on RNA-seq studies (Wormbase, 2021).
	T07G12.8	1.86				*T07G12.8* pseudogene is enriched in germ line and somatic gonad precursor, affected by eight chemicals (Wormbase, 2021).
	T08G11.1			1.71		Up 2.5X with 24h Drechmeria coniospora infection (Pujol et al., 2008a). Is expressed in vulval muscle, body wall musculature. Predicted to localize to extrinsic component of membrane. Human ortholog(s) of this gene are implicated in Parkinson's disease 23 and choreaacanthocytosis. Is an ortholog of human VPS13A (vacuolar protein sorting 13 homolog A). Affected by nine chemicals. Go Terms: extrinsic component of membrane, protein retention in Golgi aparatus (Wormbase, 2021).
	T08G5.7	2.20				*T08G5.7* is enriched in ASER neuron, predicted to encode a Zinc finger C2H2-type protein (Wormbase, 2021).
	T09F5.1		-3.73		-2.20	*T09F5.1* is affected by > 15 chemicals, a close homolog of B3GALT4, predicted to have transferase activity, transferring glycosyl groups, GO Terms: integral component of membrane, Golgi membrane (Wormbase, 2021). Up 30-46% w *E. carotovora* and *P. luminescens* in Ce (Wong et al., 2007).
	T10B10.3				1.59	Is expressed in anterior gonad arm. Predicted to be involved in several processes, including Golgi organization; lysosome localization; and positive regulation of membrane tubulation. Predicted to localize to endosome membrane. GO Terms: Endosome membrane, Golgi organization, lysosome localization (Wormbase, 2021).
	T10B5.8		3.12			*T10B5.8* is affected by > 10 chemicals, predicted to have FMN binding activity and oxidoreductase activity (WormBase 20201).
	T10D4.15	-2.04				*T10D4.15* is enriched in male, affected by seven chemicals, regulated by TRA-1 (involved in sex determination) (Wormbase, 2021). Down 2.9x w DMA in Ce (this study).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	T10H4.13	-2.36				*T10H4.13* is enriched in amphid sheath cell, affected by dpy-21; smg-2; and unc-70, close human homolog PHYHIP exhibits protein tyrosine kinase binding activity (Wormbase, 2021).
	T15D6.12	-1.85				*T15D6.12* is affected by 6 chemicals, predicted to have transferase activity, transferring glycosyl groups, GO Term: integral component of membrane (Wormbase, 2021).
	T19H5.6		-3.46			T19H5.6 is predicted to have chitin binding activity, GO Term: integral component of membrane (Wormbase, 2021).
	T20D4.20		3.24			*T20D4.20* pseudogene is enriched in NSM and body wall muscle, affected by four chemicals (Wormbase, 2021).
	T21E12.5				-2.25	Is enriched in male based on RNA-seq studies. Is affected by nine chemicals including methylmercury hydroxide, methylmercuric chloride, and Tunicamycin based on RNA-seq and microarray studies. GO Terms: Integral component of membrane (Wormbase, 2021).
	T22B2.5			-2.91	-3.04	Is affected by seven chemicals. GO Terms: Integral component of the membrane (Wormbase, 2021).
	T22B2.6	1.79				*T22B2.6* is enriched in DA and VA neurons, affected by fourteen chemicals (Wormbase, 2021). Down 3.5x w 20µM HgCl2 in Ce (McElwee et al., 2013).
	T24D5.1	1.96				*T24D5.1* is affected by 3 chemicals (Wormbase, 2021). Up w *D. coniospora* in Ce (Engelmann et al., 2011).
	T24D5.2	2.27	2.28			*T24D5.2* is enriched in neurons, affected by six chemicals (Wormbase, 2021).
	T26C11.8			-2.37		Is enriched in NSM based on tiling array studies. Is affected by six chemicals including Psoralens, allantoin, and metformin based on RNA-seq and microarray studies. GO Terms: Integral component of the membrane (Wormbase, 2021).
	T26E4.2			-2.37		Is affected by methylmercuric chloride based on microarray studies (Wormbase, 2021). Down 2.8X with meHgCl (McElwee et al., 2013).
	T27A3.8	-1.94				*T27A3.8* is enriched in intestine, affected by eleven chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	T27E4.5		-3.33			T27E4.5 is predicted to have peptidase inhibitor activity (Wormbase, 2021).
	T28A11.18		2.80			*T28A11.18* is enriched in muscle cells, affected by eight chemicals (Wormbase, 2021).
	T28A11.2		3.55			*T28A11.2* is enriched in PLM, body wall muscle cell, and muscle cell, affected by ten chemicals (Wormbase, 2021). Up w dichlorvos and w fenamiphos in Ce (Lewis et al., 2009). Up w *D. coniospora* and w *Harposporium* (Engelmann et al., 2011).
	T28A11.20		2.63			*T28A11.20* is affected by nine chemicals (Wormbase, 2021). Up 2.9x w 7.5µM meHg in Ce (McElwee et al., 2013).
	T28A11.6		2.19			*T28A11.6* pseudogene is enriched in DA neuron; VA neuron; body wall muscle cell; and hypodermis, affected by seven chemicals (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	VY10G11R.1		-3.74			VY10G11R.1 is affected by 7 chemicals, predicted to have ATP binding activity and protein kinase activity, close homolog of human HASPIN (histone H3 associated protein kinase), GO Terms: mitotic cell cycle, nucleus, histone H3-T3 phosphorylation (Wormbase, 2021).
	W01A11.7	-1.79				*W01A11.7* is enriched in dopaminergic and AFD neurons, excretory cell, and ventral nerve cord, affected by twelve chemicals (Wormbase, 2021).
	W01D2.6	-2.14				*W01D2.6* is enriched in arcade cell and pharyngeal-intestinal valve cell, affected by multi-walled carbon nanotube, GO Term: integral component of membrane (Wormbase, 2021).
	W02B3.7				-2.18	Is enriched in male-specific anatomical entity and in male. Is affected by Rifampin, Sirolimus, and fluoranthene. Human ortholog(s) of this gene are implicated in dilated cardiomyopathy 1X and muscular dystrophy (multiple). Is predicted to encode a protein with the following domain: Fukutin-related. Is an ortholog of human FKTN (fukutin). GO Terms: integral component of membrane (Wormbase, 2021).
	W04G5.13		-4.10			*W04G5.13* pseudogene is enriched in head mesodermal cell, affected by five chemicals (Wormbase, 2021).
	W06H8.2	4.91	4.38			*W06H8.2* is enriched in germ line and muscle cell, affected by > 20 chemicals, predicted to have FMN binding activity and oxidoreductase activity (Wormbase, 2021). Up 92x w NaAsO2 in Ce (Sahu et al., 2013). Up 6x w juglone, has DAF-16 and SKN-1 binding elements (expression not changed in *daf-16* mutants), and *skn-1* RNAi reduces expression (Przybysz et al., 2009). Up 2.4x w HgCl2 and dose response up to 29x w meHgCl in Ce (McElwee et al., 2013). Up 48x w ethanol in Ce (Patananan et al., 2015). Up w Ag+ and AgNP in Ce (Hunt et al., 2014).
	W08F4.10	-2.23				*W08F4.10* is affected by clk-1; hpl-2; and spn-4, affected by Sirolimus (Wormbase, 2021).
	W09G12.3	-1.93				*W09G12.3* is affected by five chemicals (Wormbase, 2021).
	W10D9.1		-3.58			*W10D9.1* is enriched in pharynx, affected by Rifampin and allantoin, GO Term: integral component of membrane (Wormbase, 2021). Down 1.9x w meHgCl in Ce (this study).
	Y105C5B.11	2.03				*Y105C5B.11* is enriched in male, affected by eleven chemicals, GO Terms: innate immune response, metal ion binding (Wormbase, 2021). Down ~25% w *S. marcescens* and *P. luminescens* in Ce (Wong et al., 2007). Up 4.6x w 7.5µM meHgCl in Ce (McElwee et al., 2013).
	Y105C5B.3		-7.56			*Y105C5B.3* is affected by 10 chemicals, a close homolog of human ACP7 predicted to have acid phosphatase activity and metal ion binding activity, GO term: metal ion binding (Wormbase, 2021). 1.25x w *E. faecalis* in Ce (Wong et al., 2007).
	Y105C5B.7		-6.81			*Y105C5B.7* pseudogene is affected by seven chemicals (Wormbase, 2021). Down 24% w *S. marcescens* in Ce (Wong et al., 2007).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	Y108F1.1			1.88		Is affected by several genes including daf-16; sek-1; and isp-1 based on RNA-seq and microarray studies. Is affected by cadmium; Sirolimus; and allantoin based on microarray studies (Wormbase, 2021).
	Y110A2AL.4		-4.60			*Y110A2AL.4* is enriched in excretory cell, hypodermis, intestine and head mesodermal cell, affected by twenty-three chemicals (Wormbase, 2021). Down to 0.2x w high glucose (Yan et al., 2017). Down 2.7x w 7.5µM meHg in Ce (McElwee et al., 2013).
	Y111B2A.10			-2.37	-2.60	Is enriched in germ line and neurons based, affected by eleven chemicals. Is an ortholog of human ZNF689 (zinc finger protein 689). GO Terms: Nucleus, transcriptional regulation (Wormbase, 2021). Down 1.7X with DMA in this study.
	Y116F11A.3	-2.05				*Y116F11A.3* is enriched in AVK, affected by four chemicals (Wormbase, 2021).
	Y116F11B.7				2.02	2.77X upregulated after 7.5uM meHg (McElwee et al., 2013). Affected by 10 chemicals (Wormbase, 2021).
	Y14H12A.2			-2.17		Is enriched in head mesodermal cell and intestine based on tiling array and RNA-seq studies. Is affected by six chemicals including Tunicamycin, multi-walled carbon nanotube, and stavudine based on microarray and RNA-seq studies (Wormbase, 2021). Down 1.7X with DMA in this study.
	Y18D10A.27			-2.46		Is affected by four chemicals including Psoralens, allantoin, and Rifampin based on RNA-seq studies (Wormbase, 2021).
	Y23H5A.8				1.77	Is enriched in intestine and somatic gonad precursor based on RNA-seq studies. Is affected by nine chemicals including rotenone; Alovudine; and Psoralens based on RNA-seq and microarray studies (Wormbase, 2021).
	Y24D9A.9				-2.23	Is enriched in germ line based on RNA-seq studies. Is affected by bisphenol A and glycine based on RNA-seq studies (Wormbase, 2021). Down 1.7X with HgCl2 in this study.
	Y26D4A.18	-1.85				*Y26D4A.18* is affected by clk-1 (Wormbase, 2021).
	Y26D4A.3	-1.95				*Y26D4A.3* is enriched in intestine, affected by six chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	Y37A1A.4				-2.06	Is enriched in Z4.a, excretory cell, male distal tip cell, neurons, and somatic gonad precursor, affected by 18 chemicals including 1-methylnicotinamide, rotenone, and D-glucose. Human ortholog(s) of this gene are implicated in autosomal recessive nonsyndromic deafness 104. Human RIPOR2 exhibits 14-3-3 protein binding activity. (Wormbase, 2021). Down 1.5X with NaAsO2 with this study.
	Y37A1B.7		-3.94			*Y37A1B.7* is enriched in germline precursor cell; hypodermis; intestine; mechanosensory neurons; and somatic gonad precursor, affected by twenty chemicals (Wormbase, 2021). Down ~2x w 2µM and 7.5µM meHgCl in Ce (McElwee et al., 2013). X

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	Y37H2A.13	-1.88				*Y37H2A.13* is enriched in AVA neurons, affected by seventeen chemicals (Wormbase, 2021).
	Y38E10A.9		-4.89			*Y38E10A.9* is enriched in GABAergic neurons, affected by eleven chemicals (Wormbase, 2021).
	Y38H6C.23				-2.02	Is enriched in OLL, PVDand intestine based on tiling array and RNA-seq studies. Is affected by seven chemicals including 1-methylnicotinamide, D-glucose, and Alovudine based on RNA-seq and microarray studies (Wormbase, 2021). Down 2X with DMA, down 2.6X with HgCl2 in this study. Up with Harposporium infection (Engelmann et al., 2011).
	Y38H6C.23			-2.60		Is enriched in OLL, PVD, and intestine based on tiling array and RNA-seq studies. Is affected by seven chemicals (Wormbase, 2021). Down 2X with DMA, down 2X with meHgCl in this study. Up with Harposporium infection (Engelmann et al., 2011).
	Y38H8A.1		-4.00			*Y38H8A.1* is enriched in hypodermis and somatic gonad precursor, affected by thirteen chemicals, GO term: integral component of membrane (Wormbase, 2021).
	Y38H8A.2				-2.03	Is predicted to have metal ion binding activity. Affected by ten chemicals (Wormbase, 2021).
	Y39B6A.25				1.65	4.5X upreg after 7.5uM meHgCl (McElwee et al., 2013). Is enriched in male based on RNA-seq studies. Is affected by several genes including clk-1; eat-2; and npr-1 based on microarray and RNA-seq studies. Is affected by twelve chemicals including methylmercuric chloride; manganese chloride; and multi-walled carbon nanotube based on microarray and RNA-seq studies(Wormbase, 2021).
	Y39F10A.2	-2.23			-2.53	*Y39F10A.2* pseudogene is affected by adsorbable organic bromine (Wormbase, 2021).
	Y40A1A.2			1.88		Down 1.6X with NaAsO2 in this study. Is affected by several genes including age-1; eat-2; and mex-3 based on microarray; tiling array; and RNA-seq studies. Is affected by four chemicals including Psoralens; allantoin; and Sirolimus based on RNA-seq studies (Wormbase, 2021).
	Y41D4A.1		-3.60			*Y41D4A.1* is enriched in male, affected by ten chemicals (Wormbase, 2021). Up 4.2x w meHgCl in Ce (McElwee et al., 2013).
	Y45G12C.10	2.17				*Y45G12C.10* is affected by methylmercuric chloride, GO Terms: integral component of plasma membrane, G protein-coupled olfactory receptor activity, detection of chemical stimulus involved in sensory perception of smell (Wormbase, 2021). Up 4x w 2µM and 5.4x w 7.5µM meHg in Ce (McElwee et al., 2013).
	Y45G12C.3	2.20	2.11			*Y45G12C.3* is enriched in intestine and pharynx, affected by five chemicals, a close homolog of human GSTP1, GO Term: glutathione metabolic process (Wormbase, 2021).
	Y45G5AM.4		-3.99	-2.29		*Y45G5AM.4* is enriched in AFD, ASER, and PLM neurons, arcade cell, and pharyngeal-intestinal valve cell, affected by five chemicals (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	Y46G5A.36	-1.81	-3.29			*Y46G5A.36* is enriched in AFD neuron, affected by eight chemicals including methylmercury hydroxide; manganese chloride; and Cry5B (Wormbase, 2021).
	Y46G5A.37	2.28				*Y46G5A.37* is affected by daf-2; rrf-3; and eat-2, affected by multi-walled carbon nanotube and Colistin (Wormbase, 2021).
	Y48G1C.10				1.56	Is enriched in OLL; PVD; germ line; and somatic gonad precursor based on microarray and RNA-seq studies. Predicted to localize to nucleus. Is affected by rotenone; Alovudine; and Chlorpyrifos based on RNA-seq and microarray studies. Is an ortholog of human MTMR10 (myotubularin related protein 10) and MTMR12 (myotubularin related protein 12). Human ortholog(s) of this gene are implicated in autosomal dominant non-syndromic intellectual disability 21 and immunodeficiency-centromeric instability-facial anomalies syndrome 2 (Wormbase, 2021).
	Y51H4A.5				-3.29	Is enriched in PLM and intestine based on tiling array and RNA-seq studies. Is affected by several genes including daf-16; daf-2; and glp-1 based on microarray and RNA-seq studies. Is affected by >15 chemicals. GO annotation: Lipid metabolic process (Wormbase, 2021). Down 0.4X with 4h Ag+ (Hunt et al., 2014). Down 2.9X with 2uM, 6.5X with 7.5uM meHgCl (McElwee et al., 2013).
	Y51H7C.10		-3.69			*Y51H7C.10* is affected by eight chemicals, GO term: integral component of membrane (Wormbase, 2021). X
	Y53C10A.15				-2.23	Is predicted to have DNA-binding transcription factor activity and sequence-specific DNA binding activity. Affected by seven chemicals (Wormbase, 2021).
	Y53G8AL.3				-2.78	Is enriched in CEM, HOB, IL2 neuron, NSM, and ray neuron type B based on tiling array and RNA-seq studies. Is affected by Atrazine and Sirolimus based on microarray studies (Wormbase, 2021).
	Y54B9A.1			-2.53	-2.19	Is enriched in OLL and PVD based on microarray studies. Is affected by six chemicals including sesamin, Psoralens, and allantoin based on microarray and RNA-seq studies. Is predicted to encode a protein with the following domains: GETHR pentapeptide repeat (5 copies) and GETHR pentapeptide repeat (Wormbase, 2021).
	Y54E2A.4			-2.22		Is predicted to have ATP binding activity and nucleic acid binding activity. Is an ortholog of human ASCC3 (activating signal cointegrator 1 complex subunit 3). GO Terms: nucleus, hydrolase activity, ATP binding, RNA binding. Affected by seven chemicals. (Wormbase, 2021). Up 2.2X with meHgCl (McElwee et al., 2013).
	Y54E5A.2				1.63	Is enriched in male based on RNA-seq studies. Is affected by several genes including daf-16; daf-2; and eat-2 based on tiling array; microarray; and RNA-seq studies. Is affected by nine chemicals including manganese chloride; Rifampin; and allantoin based on RNA-seq

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
						and microarray studies. GO Terms: integral component of the membrane (Wormbase, 2021). Up 1.7X with NaAsO2 in this study.
	Y55H10A.2		3.26			*Y55H10A.2* is enriched in neurons, affected by four chemicals, GO term: integral component of membrane (Wormbase, 2021).
	Y56A3A.28			-2.43		Is enriched in germ line based on RNA-seq studies. Is affected by seven chemicals including rotenone, Alovudine, and stavudine based on RNA-seq and microarray studies. Is predicted to encode a protein with the following domains: C2H2-type zinc-finger domain, Zinc finger superfamily. GO Terms: Nucleus, positive regulation of transcription, DNA binding transcription activator activity (Wormbase, 2021).
	Y57A10C.8	1.81				*Y57A10C.8* is enriched in FLP neurons, affected by four chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	Y57G11C.41		2.68			*Y57G11C.41* is enriched in body wall muscle cell, affected by Tunicamycin and Colistin (Wormbase, 2021).
	Y61A9LA.12	-2.18				*Y61A9LA.12* is enriched in head mesodermal cell, affected by five chemicals (Wormbase, 2021). X
	Y64G10A.7				-2.95	Is predicted to have calcium ion binding activity. Is an ortholog of human MEGF6 (multiple EGF like domains 6). Is affected by ten chemicals. GO Terms: Calcium ion binding (Wormbase, 2021).
	Y66D12A.25	-2.24				*This gene is dead* (Wormbase, 2021).
	Y68A4A.10				1.93	Is affected by Chlorpyrifos based on microarray studies (Wormbase, 2021). 4X Upregulated Fuku natural organic material, 10X upregulated HS1500 (Menzel et al., 2005).
	Y68A4B.4				1.66	Is enriched in coelomocyte and ventral nerve cord based on tiling array studies. Is affected by several genes including clk-1; daf-19; and ubc-9 based on tiling array and microarray studies. Is affected by six chemicals including Tunicamycin; sucrose; and stearic acid based on microarray and RNA-seq studies (Wormbase, 2021).
	Y69H2.17	-2.22				*Y69H2.17* is enriched in AVK and neurons, affected by four chemicals (Wormbase, 2021). Down 1.6x w HgCl2 in Ce (this study).
	Y6G8.6	-2.32				*Y6G8.6* is enriched in DA neuron and VA neuron, affected by 4 chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	Y70G10A.3				-2.36	Is expressed in excretory cell and hypodermis. Is an ortholog of human SLCO4A1 (solute carrier organic anion transporter family member 4A1). Is affected by ten chemicals. GO Terms: integral component of membrane, integral component of plasma membrane, ion transport (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	Y71G12B.31	-1.82			-2.41	*Y71G12B.31* is enriched in GABAergic neurons, GO Terms: integral component of membrane, protein tyrosine phosphatase activity (Wormbase, 2021). Down 1.7x w HgCl2 in Ce (this study).
	Y71H10B.1			1.57		Is predicted to have metal ion binding activity. Is expressed in anal depressor muscle; hypodermis; pharynx; reproductive system, and tail. Human ortholog(s) of this gene are implicated in hereditary spastic paraplegia 45. Is an ortholog of human NT5C2 (5'-nucleotidase, cytosolic II). Affected by seven chemicals. GO Terms: metal ion binding, dephosphorylation, hydrolase activity (Wormbase, 2021). Induces *gcs-1* expression in a *skn-1* independent manner (Wang et al., 2010).
	Y73B6BL.14	2.14	2.02			*Y73B6BL.14* is predicted to have DNA binding activity and DNA ligase (ATP) activity, GO Terms: DNA Repair, DNA replication, nucleus, mitochondrion (Wormbase, 2021). Down 16% w *D. coniospora* (a nematophagous fungi) in Ce (Pujol et al., 2008). Down 24% w *P. luminescens* in Ce (Wong et al., 2007). Upregulated by SKN-1 & up w NaAsO2 in Ce (Oliveira et al., 2009).
	Y73B6BL.22	-2.35				*Y73B6BL.22* is enriched in head mesodermal, affected by several genes including daf-2; clk-1; and aak-2, affected by five chemicals, GO Term: integral component of membrane (Wormbase, 2021).
	Y75B12B.3	-2.49			-2.29	*Y75B12B.3* is enriched in intestine, affected by ten chemicals (Wormbase, 2021). Up with *D. coniospora* + *Harposporium* in Ce (Engelmann et al., 2011). Down 2.3x w meHgCl in Ce (this study).
	Y75D11A.3				1.6468	Up 1.5X with NaAsO2 in this study. Is enriched in germ line and germline precursor cell based on RNA-seq studies. Is affected by several genes including daf-2; glp-1; and skn-1 based on microarray; tiling array; and RNA-seq studies. Is affected by ten chemicals including hydrogen sulfide; 4-bromodiphenyl ether; and Alovudine based on microarray and RNA-seq studies (Wormbase, 2021).
	Y80D3A.8			3.07		Up 3.8X with meHgCl in Ce (McElwee et al., 2013). Predicted to have protein tyrosine phosphatase activity. GO Terms: Integral component of membrane. Affected by 8 chemicals (Wormbase, 2021) (Fatima et al., 2018). 1 fold change with exposure to Gram-positive pathogen Enterococcus faecalis (seeded on plate) (Liu et al., 2020).
	Y87G2A.16	-2.09				*Y87G2A.16* is enriched in AFD and intestine, affected by 13 chemicals, predicted to have chondroitin 4-sulfotransferase activity, GO Terms: chondroitin sulfate biosynthetic process, integral component of membrane, membrane, positive regulation of response to oxidative stress (Wormbase, 2021). Down 1.8x w DMA in Ce (this study).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	Y9C9A.5		-3.29			*Y9C9A.5* is enriched in NSM neuron, affected by six chemicals including methylmercuric chloride; Psoralens; and allantoin, GO Terms: integral component of plasma membrane (Wormbase, 2021). Down 4.3x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	ZC15.1	-1.89				*ZC15.1* is enriched in AVE, AVK and head mesodermal cell, affected by 3 chemicals (Wormbase, 2021).
	ZC15.3			1.73		Is enriched in head mesodermal cell based on RNA-seq studies. Is affected by seven chemicals including Tunicamycin; metformin; and Sirolimus based on microarray and RNA-seq studies (Wormbase, 2021). Upregulated with D. coniospora infection (Engelmann et al., 2011).
	ZC190.6				-2.89	Is affected by four chemicals including Rifampin. Sirolimus, and allantoin based on RNA-seq studies (Wormbase, 2021).
	ZC196.8	-1.84				*ZC196.8* is enriched in neurons, affected by dafa#1, GO Term: integral component of membrane (Wormbase, 2021).
	ZC21.3			-2.74		Is enriched in head mesodermal cell based on RNA-seq studies. Is affected by fifteen chemicals (Wormbase, 2021).
	ZC443.7		2.01			*ZC443.7* is affected by Colistin, predicted to encode an integral plasma membrane serpentine receptor, GO Term: integral component of membrane (Wormbase, 2021).
	ZK1073.1			1.50		Is enriched in germ line; neurons; and retrovesicular ganglion based on microarray; tiling array; and RNA-seq studies. Is affected by nine chemicals including rotenone; D-glucose; and nicotine based on RNA-seq; proteomic; and microarray studies. Human ortholog(s) of this gene are implicated in Charcot-Marie-Tooth disease type 4D. Human NDRG1 exhibits Rab GTPase binding activity; cadherin binding activity; and cytoskeletal protein binding activity. Is an ortholog of human NDRG1, NDRG2, NDRG3 (Wormbase, 2021).
	ZK1225.1	-2.08			-2.54	*ZK1225.1* is affected by nine chemicals (Wormbase, 2021). Up w 3 bacterial species in Ce (Engelmann et al., 2011).
	ZK1248.20		5.08			*ZK1248.20* is enriched in amphid sheath cell and in male, affected by seven chemicals, GO term: integral component of membrane (Wormbase, 2021).
	ZK1251.3		-5.14			*ZK1251.3* is enriched in NSM and male, affected by 13 chemicals, a close homolog of human SRD5A1 predicted to have 3-oxo-5-alpha-steroid 4-dehydrogenase activity and cholestenone 5-alpha-reductase activity, GO terms: lipid metabolic process, integral component of membrane, organelle membrane, oxidoreductase activity, steroid biosynthetic process (Wormbase, 2021). Up 2.6x w 7.5µM meHg in Ce (McElwee et al., 2013).
	ZK380.4	2.12				*ZK380.4* is enriched in NSM, affected by eight chemicals (Wormbase, 2021).

Gene	REFSEQ	NaAsO2	DMA	HgCl2	meHgCl	Notes and References
	ZK381.2		-4.13			ZK381.2 is enriched in hypodermis and intestine, affected by 15 chemicals, predicted to have transferase activity, transferring glycosyl groups, GO term: integral component of membrane (Wormbase, 2021). Down 3.3x w 7.5µM meHgCl (McElwee et al., 2013).
	ZK39.9	-1.98				*ZK39.9* is affected by hpl-2 and rsr-2 (Wormbase, 2021). Down 1.7x w DMA in Ce (this study).
	ZK402.2			-2.20		Is predicted to encode a protein with the following domains: Domain of unknown function (DUF545) and SPK domain (Wormbase, 2021).
	ZK418.11			-2.92		Is enriched in AFD; ASER; and PLM based on RNA-seq studies. Is affected by five chemicals including tryptophan; Rifampin; and allantoin based on microarray and RNA-seq studies. GO Terms: Nucleus (Wormbase, 2021).
	ZK616.8		2.25			*ZK616.8* is enriched in NSM neuron and in male, affected by eight chemicals (Wormbase, 2021). Up 1.4x w *S. marcescens* and 1.3x w *E. faecalis* in Ce (Wong et al., 2007). Up 2.7x w 7.5µM meHg in Ce (McElwee, 2010).
	ZK675.4		-3.52			*ZK675.4* is enriched in intestine, affected by sixteen chemicals (Wormbase, 2021). Up 2.0x w 2µM HgCl2 but down 2.1x w 2µg/mL meHgCl and down 9.8x w 7.5µg/mL meHgCl in Ce (McElwee et al., 2013).
	ZK742.4	2.32	3.79			*ZK742.4* is regulated by the DAF-16, affected by > 20 chemicals, predicted to play a role in lipid metabolism, predicted to have FMN binding activity and oxidoreductase activity (Wormbase, 2021). Up 14x w NaAsO2 in Ce (Sahu et al., 2013). Up 6x w juglone (Przybysz et al., 2009). Up w Ag+ and AgNP 2014 (Hunt et al., 2014). Up w HgCl2 & meHgCl in Ce (McElwee et al., 2013). Predicted direct target of DAF-16 and upregulated in *daf-2*-mutants = up when DAF-16 is active (McElwee et al., 2003). Upregulated by SKN-1 and arsenic (Oliveira et al., 2009). Up >4x w acrylamide in Ce (Hasegawa et al., 2008).
	ZK813.6		-3.21			ZK813.6 is enriched in intestine, affected by thirteen chemicals (Wormbase, 2021).
	ZK892.5			-2.28		Is enriched in GABAergic neurons and in male based on RNA-seq studies. Is affected by seventeen chemicals including manganese chloride, D-glucose, and stavudine based on RNA-seq and microarray studies. GO Terms: integral component of the membrane (Wormbase, 2021). Down 1.6X with NaAsO2, down 1.6X with HgCl2.
	ZK930.6		-3.56			ZK930.6 is enriched in male and somatic gonad precursor, affected by 15 chemicals, predicted to have ATP-dependent peptidase activity and serine-type endopeptidase activity (Wormbase, 2021). Down 2.0x w HgCl2 and down 1.7x w meHgCl in Ce (this study).

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