Table 2. Description of regulators of gpdh-1 expression (*rgpd*) genes

			Homologs§			
Sequence/gene name*	Causes protein aggregation†	Description (expression pattern)‡	*Hs*	*Dm*	*Cb*	*Sc*
Protein homeostasis						
K04G2.1	Y	Translation initiation factor 2, beta subunit	🟩	🟩	🟩	🟨
B0511.10/*eif-3.E*	Y	Translation initiation factor 3, subunit e (I, H, O)	🟩	🟩	🟩	
Y39G10AR.8	Y	Translation initiation factor 2, gamma subunit (I, O)	🟩	🟩	🟩	🟩
F22B5.2/*eif-3.G*		Translation initiation factor 3, subunit g	🟨	🟨	🟩	🟨
D2085.3		Translation initiation factor 2B, epsilon subunit (I, H, O)	🟨	🟨	🟩	🟨
D2013.7/*eif-3.F*		Translation initiation factor 3, subunit f	🟨	🟨	🟩	
Y54E2A.11/*eif-3.B*		Translation initiation factor 3, subunit b (O)	🟩	🟩	🟩	🟩
F57B9.3	Y	Translation initiation factor 4F, helicase subunit	🟩	🟩	🟩	🟩
C27D11.1/*egl-45*	Y	Translation initiation factor 3, subunit a	🟩	🟩	🟩	🟩
C37C3.2	Y	Translation initiation factor 5	🟩	🟩	🟩	🟩
F22D6.3/*nrs-1*		Asparaginyl-tRNA synthetase	🟩	🟩	🟩	🟩

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
T08B2.9/*frs-1*		Phenylalanyl-tRNA synthetase, beta subunit	🟩	🟩	🟩	🟩
T02G5.9/*krs-1*		Lysyl-tRNA synthetase (I, H, O)	🟩	🟩	🟩	🟩
F22B5.9/*frs-2*	Y	Phenylalanyl-tRNA synthetase	🟩	🟩	🟩	🟩
R74.1/*lrs-1*		Leucyl-tRNA synthetase	🟩	🟩	🟩	🟩
F26F4.10/*rrt-1*		Arginyl-tRNA synthetase	🟩	🟩	🟩	🟩
T10F2.1/*grs-1*		Glycyl-tRNA synthetase	🟩	🟩	🟩	🟩
C47E12.1/*srs-2*		Seryl-tRNA synthetase	🟩	🟩	🟩	🟩
R11A8.6/*irs-1*		Isoleucyl-tRNA synthetase (H, O)	🟩	🟩	🟩	🟩
Y80D3A.1/*wrs-1*		Tryptophanyl-tRNA synthetase	🟩	🟩	🟩	🟩
C32E8.11		N-end rule pathway, recognition component UBR1	🟩	🟩	🟩	🟨
C36B1.4/*pas-4*	Y	20S proteasome, regulatory subunit alpha type (O)	🟩	🟩	🟩	🟩
Y46G5A.6[¶]	Y	RNA helicase BRR2, DEAD-box superfamily	🟩	🟩	🟩	🟩

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
ZK20.5/*rpn-12*		26S proteasome regulatory complex, subunit RPN12/PSMD8	🟨	🟨	🟩	🟨
C23G10.4/*rpn-2*		26S proteasome regulatory complex (I, H, O)	🟩	🟩	🟩	🟩
F57B9.10/*rpn-6*	Y	26S proteasome regulatory complex	🟩	🟩	🟩	🟩
T22D1.9/*rpn-1*		26S proteasome regulatory complex	🟩	🟩	🟩	🟩
C35B1.1/*ubc-1*		Ubiquitin-protein ligase (I, H, O)	🟩	🟩	🟩	🟩
CD4.6/*pas-6*	Y	20S proteasome, regulatory subunit alpha type	🟩	🟩	🟩	🟩
Y53C10A.12/*hsf-1*	Y	Heat shock transcription factor	🟨	🟨	🟩	🟨
W08F4.8/*cdc-37*		Cell division cycle 37 protein, CDC37	🟩	🟩	🟩	
K01C8.10/*cct-4*	Y	Chaperonin complex component, TCP-1 δ-subunit (I, O)	🟩	🟩	🟩	🟩
T21B10.7/*cct-2*	Y	Chaperonin complex component, TCP-1 β-subunit (H,O)	🟩	🟩	🟩	🟩
F26D10.3/*hsp-1*	Y	Molecular chaperones HSP70/HSC70, HSP70 superfamily (I,O)	🟩	🟩	🟩	🟩
Y55F3AR.3/*cct-8*		Chaperonin complex component, TCP-1 θ-subunit	🟩	🟩	🟩	🟩

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
T10B5.5/*cct-7*	Y	Chaperonin complex component, TCP-1 η-subunit (O)	🟩	🟩	🟩	🟩
T21G5.5/*star-2*		RNA-binding protein Sam68 and related KH domain proteins	🟩	🟩	🟩	🟨
F37E3.1		Nuclear cap-binding complex, subunit NCBP1/CBP80	🟩	🟩	🟩	🟨
Y110A7A.8	Y	mRNA splicing factor PRP31	🟩	🟩	🟩	🟨
K02F2.3/*tag-203*	Y	Splicing factor 3b, subunit 3	🟩	🟩	🟩	🟩
W08E3.1/*snr-2*	Y	U1 snRNP component	🟨	🟨	🟩	🟨
Y71F9B.4/*snr-7*	Y	Small nuclear ribonucleoprotein G	🟨	🟨	🟨	🟨
F26A3.2		Nuclear cap-binding protein complex, subunit CBP20, RRM superfamily	🟩	🟩	🟩	🟨
W07E6.4/*prp-21*		Splicing factor 3a, subunit 1	🟩	🟩	🟩	🟨
T13H5.4	Y	Splicing factor 3a, subunit 3	🟩	🟩	🟩	🟨
T28D9.10/*snr-3*	Y	Small nuclear ribonucleoprotein SMD1 and related snRNPs	🟨	🟨	🟩	🟨
C18D11.4/*rsp-8*		RRM domain; splicing factor (I, O)	🟨	🟨	🟩	🟨

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
T08A11.2	Y	Splicing factor 3b, subunit 1	🟩	🟩	🟩	🟩
ZK652.1/*snr-5*	Y	Small nuclear ribonucleoprotein (snRNP) SMF (I, H, O)	🟨	🟨	🟨	🟨
W08D2.7		Nuclear exosomal RNA helicase MTR4, DEAD-box superfamily (I, O)	🟩	🟩	🟩	🟩
F19F10.9		U4/U6.U5 snRNP associated protein	🟩	🟩	🟩	🟨
Y59A8B.6		HAT repeat protein	🟩	🟩	🟩	🟩
K07C5.6		RNA splicing factor Slu7p	🟩	🟩	🟩	🟨
Y116A8C.42/*snr-1*	Y	Small nuclear ribonucleoprotein Sm D3 (H, O)	🟨	🟨	🟩	🟨
Extracellular matrix						
T14B4.7/*dpy-10*[¶]		Collagens (type IV and type XIII) and related proteins	🟨	🟨	🟩	
T21D12.2/*dpy-9*[¶]		Collagens (type IV and type XIII) and related proteins	🟨	🟨	🟩	
C31H2.2/*dpy-8*[¶]		Collagens (type IV and type XIII) and related proteins	🟨	🟨	🟩	
F46C8.6/*dpy-7*[¶]		Collagens (type IV and type XIII) and related proteins (H)	🟨	🟨	🟩	

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
M60.2[¶]		Placental protein 11	🟨	🟨	🟩	
Signalling						
ZK849.2		PDZ domain	🟩	🟨	🟩	
T08G11.4		Methylase	🟩	🟨	🟩	🟨
R06A10.2/*gsa-1*		G protein subunit Galphas, small G protein superfamily (I, O)	🟩	🟩	🟩	🟩
F26H9.6/*rab-5*	Y	GTPase Rab5/YPT51 and related small G protein superfamily GTPases	🟩	🟩	🟨	🟩
EGAP2.3/*pho-1*[¶]		Lysosomal and prostatic acid phosphatases (I)	🟨	🟨	🟩	
M110.5/*dab-1*	Y	Adaptor protein disabled (I, H, O)	🟨	🟨	🟩	
Y110A2AL.8/*ptc-3*	Y	Membrane protein patched/PTCH	🟩	🟩	🟩	🟨
C54A12.1/*ptr-6*		Predicted membrane protein, patched superfamily	🟨	🟩	🟩	🟨
B0285.1		Cdc2-related protein kinase (I, H, O)	🟩	🟩	🟩	🟩
F20H11.2/*nsh-1*		Nuclear helicase MOP-3/SNO, DEAD-box superfamily	🟩	🟨	🟩	🟨

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
Y11D7A.9		FGF activating protein 1		🟨	🟩	
F33D4.2/*itr-1*		Inositol 1,4,5-trisphosphate receptor (I, O)	🟩	🟩	🟩	
C07G1.5/*hgrs-1*		Membrane trafficking and cell signaling protein HRS, contains VHS and FYVE domains	🟩	🟩	🟩	🟨
F38H4.9/*let-92*		Serine/threonine protein phosphatase 2A, catalytic subunit (I, O)	🟩	🟩	🟩	🟨
F58E2.9/*srz-23*[¶]		7-transmembrane receptor			🟨	
Metabolism						
T10E9.9		Short-chain acyl-CoA dehydrogenase	🟩	🟩	🟩	
F32H2.5		Animal-type fatty acid synthase and related proteins	🟩	🟩	🟩	🟨
Y105E8B.5		Hypoxanthine-guanine phosphoribosyltransferase	🟨		🟩	
F42A8.2/*tag-55*		Succinate dehydrogenase, Fe-S protein subunit (I, H, O)	🟩	🟩	🟩	🟩
C06A8.1		5,10-methylenetetrahydrofolate reductase (I, H, O)	🟩	🟨	🟩	🟩
C01F1.3	Y	Putative NAD^+-dependent epimerases	🟨	🟨	🟩	

			Homologs§			
Sequence/gene name*	Causes protein aggregation†	Description (expression pattern)‡	*Hs*	*Dm*	*Cb*	*Sc*
C28H8.11		Tryptophan 2,3-dioxygenase (H, O)	🟩	🟩	🟩	🟨
C03G5.1		Succinate dehydrogenase, flavoprotein subunit (I, H, O)	🟩	🟩	🟩	🟩
H13N06.3/*gob-1*		Trehalose phosphate synthase			🟩	
Protein trafficking						
R06A4.4/*imb-2*		Nuclear transport receptor karyopherin-β2/transportin, importin β superfamily	🟩	🟩	🟩	🟩
F38E11.5		Vesicle coat complex COPI, β' subunit	🟩	🟩	🟩	🟩
F55C5.8		Signal recognition particle, subunit Srp68 (I, O)	🟩	🟩	🟩	🟨
C37C3.3¶	Y	Protein involved in glucose derepression and prevacuolar endosome protein sorting (O)	🟩	🟩	🟩	🟨
C02C6.1/*dyn-1*		Vacuolar sorting protein VPS1, dynamin, and related proteins (I, O)	🟩	🟩	🟩	🟩
R160.1/*dpy-23*		Adaptor complexes medium subunit family	🟩	🟩	🟩	🟩
Transcriptional regulation						
C01H6.5/*nhr-23*		Steroid hormone nuclear receptor (I, O)	🟩	🟩	🟩	

			Homologs[§]			
Sequence/gene name*	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
F57B9.2/*ntl-1*	Y	Negative regulator of transcription	🟩	🟩	🟩	🟩
C55A6.9		Putative RNA polymerase II regulator	🟩	🟩	🟩	🟨
C01B10.5/*hil-7*		Histone H1.1 isoform				
K08E4.1/*spt-5*		RNA polymerase II transcription elongation factor DSIF/SUPT5H/SPT5 (I, O)	🟩	🟩	🟩	🟩
ZC518.3/*ccr-4*		Glucose-repressible alcohol dehydrogenase transcriptional effector CCR4 and related proteins	🟩	🟩	🟩	🟩
T22D1.10/*ruvb-2*		DNA helicase TIP49, TBP-interacting protein	🟩	🟩	🟩	🟩
T28F12.2/*unc-62*		Transcription factor MEIS1 and related HOX domain proteins	🟩	🟩	🟩	🟨
C27H6.2/*ruvb-1*		DNA helicase, TBP-interacting protein	🟩	🟩	🟩	🟩
No assigned function						
T26C5.2[¶]		Unnamed protein. Contains a PAN domain that mediates protein–protein and protein–carbohydrate interactions			🟩	
ZC328.1		Unnamed protein			🟩	
Y110A7A.11		Predicted membrane protein	🟨		🟩	

			Homologs[§]			
Sequence/gene name[*]	Causes protein aggregation[†]	Description (expression pattern)[‡]	*Hs*	*Dm*	*Cb*	*Sc*
C32E12.3/*osr-1*[¶]		Unnamed protein (I, H)			🟩	
F23F1.4		Unnamed protein				
C50D2.1[¶]		Unnamed protein			🟩	
C38C6.3[¶]		Unnamed protein			🟩	
ZK1067.7/*pqn-95*[¶]		Uncharacterized protein (O)	🟨	🟨	🟩	
M88.6/*pan-1*[¶]		Leucine rich repeat protein	🟨	🟨	🟩	🟨
C23G10.8		Unnamed protein (I, O)			🟩	
F20H11.6		Unnamed protein				
ZK1128.3		Unnamed protein			🟩	
Y111B2A.14/*pqn-80*		Ubinuclein, nuclear protein interacting with cellular and viral transcription factors	🟨	🟨	🟩	🟨
T05D4.4[¶]		Unnamed protein		🟨	🟩	
W07B3.2/*gei-4*		Unnamed protein		🟨	🟩	

			Homologs§			
Sequence/gene name*	Causes protein aggregation†	Description (expression pattern)‡	*Hs*	*Dm*	*Cb*	*Sc*
F49C12.12¶	Y	Unnamed protein		🟨	🟨	
B0035.11		Uncharacterized conserved protein	🟩	🟩	🟩	🟨
F52B11.3/*noah-1*¶	Y	Unnamed protein		🟨	🟩	
Y57G11C.31		Uncharacterized protein			🟩	
Y39B6A.1		Uncharacterized protein	🟩	🟨	🟩	🟨
E01B7.1	Y	Uncharacterized protein	🟨	🟨	🟩	
F14H3.9		Uncharacterized protein				
Y39B6A.12		Uncharacterized protein			🟩	
F11C7.5¶		Unnamed protein			🟩	

*Sequence/gene name of gene targeted by RNAi.

†RNAi gene inactivations identified to cause protein aggregation by Nollen *et al*. (1).

‡Predicted functions were based mainly on KOG (eukaryotic orthologous groups) annotations as described in Wormbase. In some cases, function was inferred from the known function of homologs in other organisms. Expression patterns were determined based on information available in Wormbase; I, intestine (including foregut); H, hypodermis; O, other.

[§] Homologs were identified based on BLASTP analysis as implemented in Wormbase. *Hs*, *Homo sapiens*; *Dm*, *Drosophila melanogaster*; *Cb*, *Caenorhabditis briggsae*; *Sc*, *Sacchromyces cerevisea*. Green, strong homology (BLAST e < –50); yellow, weak homology (BLAST e > –50); white, no homologs.

[¶] Possible secreted protein. Prediction based on presence of signal peptide identified by using SignalP 3.0 (www.cbs.dtu.dk/services/SignalP).

1. Nollen, E. A., Garcia, S. M., van Haaften, G., Kim, S., Chavez, A., Morimoto, R. I. & Plasterk, R. H. (2004) *Proc. Natl. Acad. Sci USA* **101,** 6403–6408.