

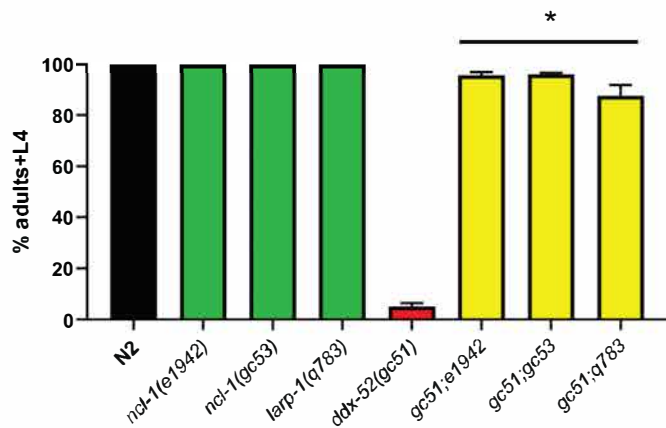
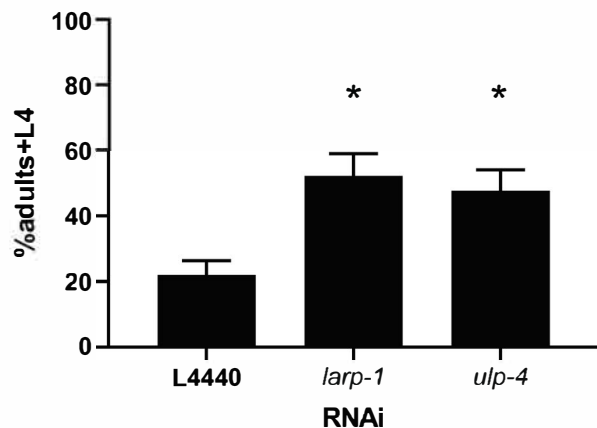
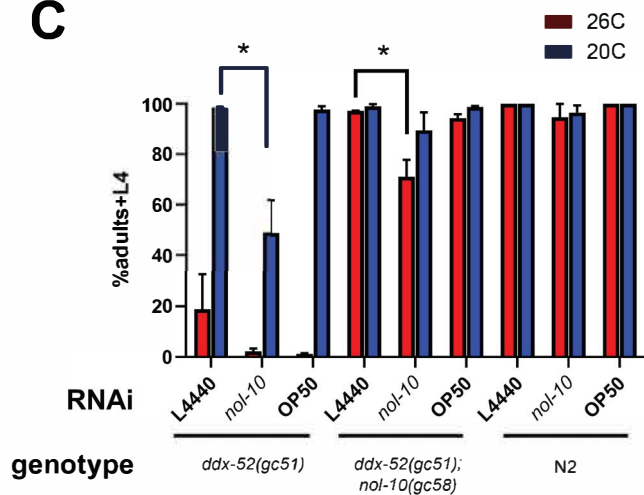
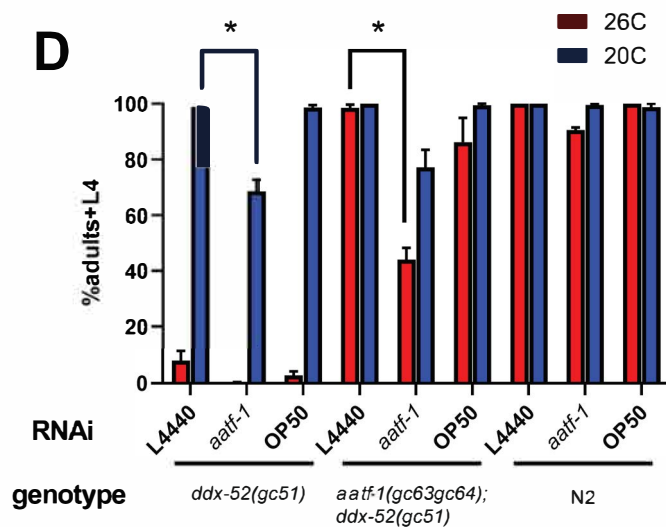
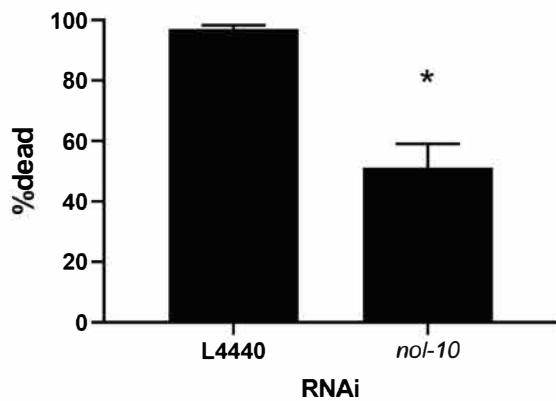
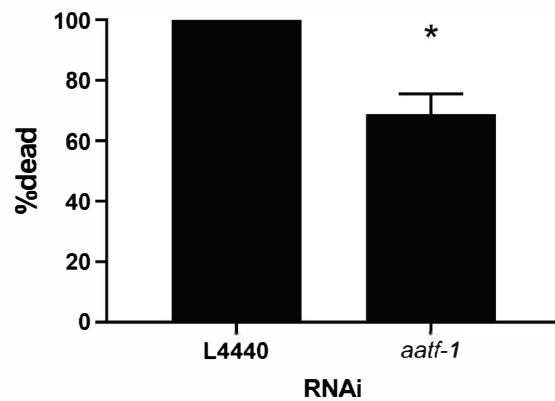
A**B****C****D****E****F**

Figure S1. Gene Identification of Suppressor Mutations, Related to Figure 2. (A) *ncl-1(lf)* and *larp-1(lf)* suppress *ddx-52(gc51)* developmental arrest. % of adults/L4 larvae were scored after growth at 26°C for 72 hours, mean +/- s.e.m (N≥5). *-p<0.05 for all panels, unpaired, 2-sided t-test. (B) *ulp-4(RNAi)* and *larp-1(RNAi)* partially suppress *ddx-52(gc51)* developmental arrest. *ddx-52(gc51)* animals were fed the indicated RNAi and scored for development to adults/L4 larvae at 26°C after 72 hours, mean +/- s.e.m (N≥8). L4440 is an empty vector containing bacteria and serves a normal hypoxic sensitivity negative control for all RNAi experiments. (C) *nol-10(RNAi)* partially arrest *ddx-52(gc51)* and *ddx-52(gc51);nol-10(gc58)* development. Animals of the indicated genotype were fed the indicated RNAi, L4440 or OP50 control bacteria and scored for development to adults/L4 larvae at 20°C and at 26°C after 72 hours. mean +/- s.e.m (N=4). (D) *aatf-1(RNAi)* partially arrest *ddx-52(gc51)* and *aatf-1(gc63gc64) ddx-52(gc51)* development. Animals of the indicated genotype were fed the indicated RNAi, L4440 or OP50 control bacteria and scored for development to adults/L4 larvae at 20°C and at 26°C after 72 hours. mean +/- s.e.m (N=3). (E) *nol-10(RNAi)* causes hypoxia resistance. Wild type animals were fed the indicated RNAi at 20°C. % death after recovery from 24 hours hypoxia. mean +/- s.e.m (N=3). (F) *aatf-1(RNAi)* causes hypoxia resistance. Wild type animals were fed the indicated RNAi at 20°C. % death after recovery from 20 hours hypoxia. mean +/- s.e.m (N=3).

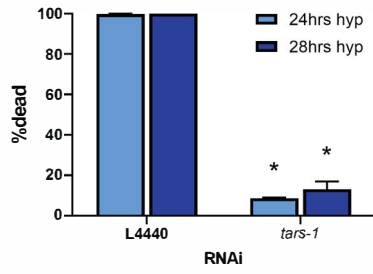
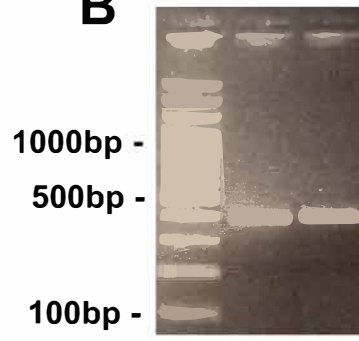
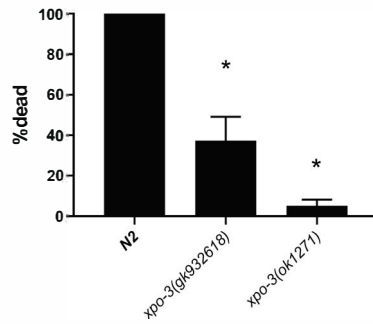
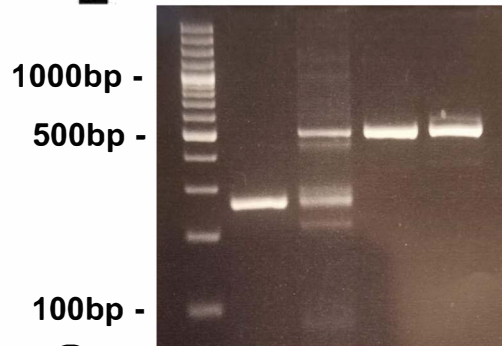
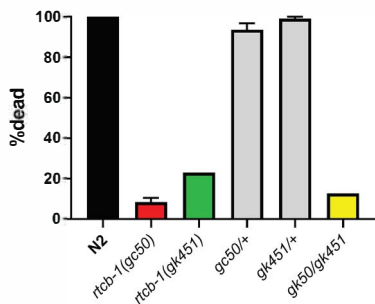
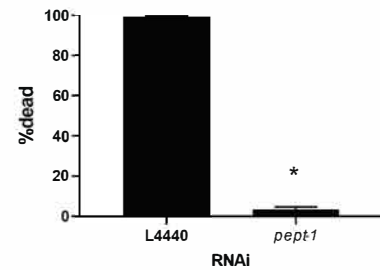
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Figure S2. tRNA pathway and *pept-1* mutants, Related to Table 1, Figure 3 (A) Wild type animals were fed the indicated RNAi at 20°C. % death after recovery from hypoxia. mean +/- s.e.m (N=3). * p<0.01 vs L4440 (B) RTPCR agarose gel electrophoresis. Lanes 1: 100 bp ladder, 2: wild type partial cDNA, 3: *tars-1(gc52)* partial cDNA. (C) cDNA sequence. *tars-1(gc52)* cDNA sequencing trace on top. N2 cDNA sequencing trace on bottom. Black line indicates start of exon 2. (D) Effect of independent *xpo-3(lf)* alleles on hypoxic death. 20 hrs of hypoxia, 24 hrs recovery. N=3, * - p<0.01 vs N2 (E) *gc50* reduces *rctb-1(RNA)* splicing. RTPCR agarose gel electrophoresis lanes 1: 100 bp ladder, 2: wild type partial cDNA, 3: *rctb-1(gc50)* partial cDNA, 4: N2 partial genomic DNA, 5: *rctb-1(gc50)* partial genomic DNA. (F) *rctb-1(lf)* produces hypoxia resistance. 20 hrs of hypoxia, 24 hrs recovery. N=3 except *rctb-1(gk451)* and *gc50/gk451* = one trial. (G) *pept-1(RNAi)* causes hypoxia resistance. Wild type animals were fed the indicated RNAi at 20°C. % death after recovery from hypoxia. mean +/- s.e.m (N=6). * p<0.01 vs L4440

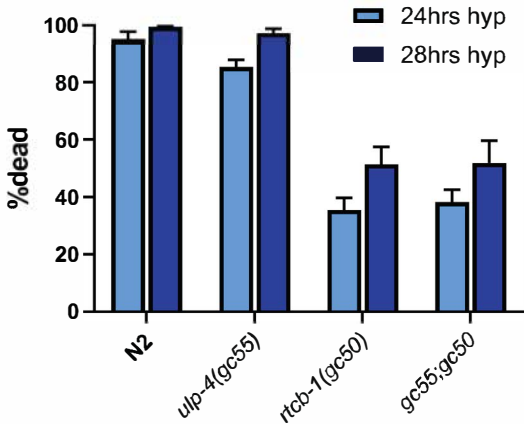


Figure S3. Lack of effect of *ulp-4(rf)* on *rtcb-1(rf)* hypoxia resistance, Related to Figure 3.

% death after 24-hour recovery from 24 or 28 hour hypoxic incubation time. Data are mean +/- s.e.m (N≥3). There are no significant differences between *rtcb-1(rf)* and *ulp-4(rf);rtcb-1(rf)* at either of the incubation times. N2 is the wild type control.

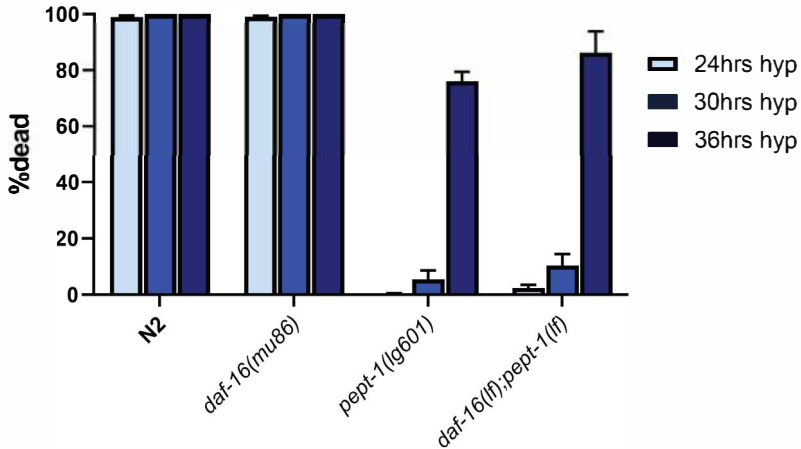


Figure S4. Loss of PEPT-1 causes hypoxia resistance in a DAF-16 independent manner, Related to Figure 3.

% death after 24 hour recovery from hypoxia at 24 , 30, and 36 hours incubation time. Data are mean +/- s.e.m (N=3) . There are no significant differences between *pept-1(lg601)* and *daf-16(lf);pept-1(lg601)* at any of the incubation times. N2 is the wild type control.

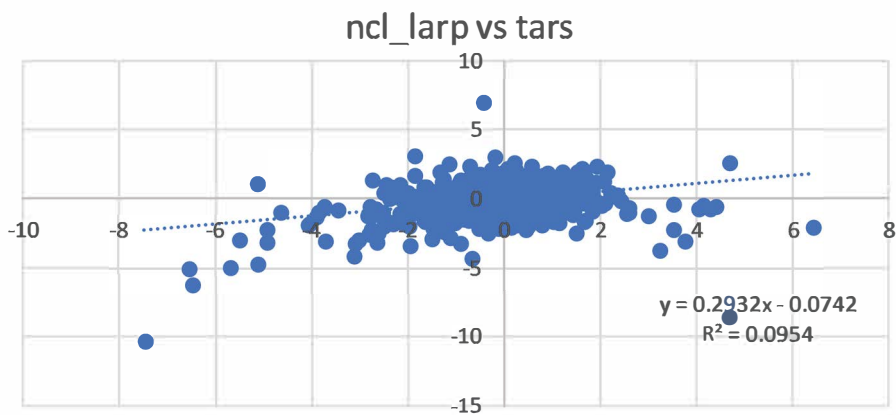
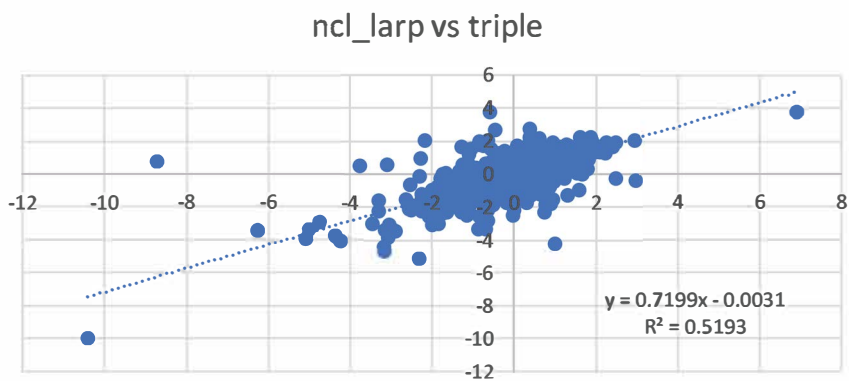
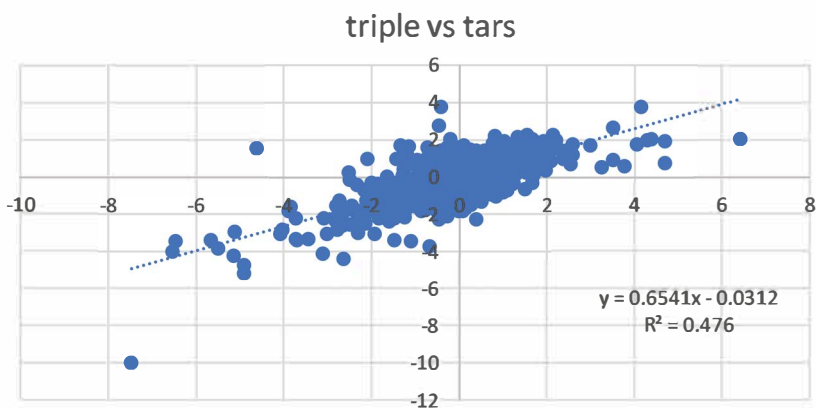
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Figure S5. Correlation of proteomes, Related to Figure 5. Ratio of protein abundance of mutant/N2 in TMT proteomes. **(A)** *larp-1(q783) ncl-1(gc53)* vs *tars-1(gc52)* ; **(B)** *tars-1(gc52);larp-1(q783) ncl-1(gc53)* vs *larp-1(q783) ncl-1(gc53)* ; **(C)** *tars-1(gc52);larp-1(q783) ncl-1(gc53)* vs *tars-1(gc52)*

Table S1. *ddx-52(gc51)* ts phenotype, Related to Figure 1

genotype	development at 26°C
N2	adults/L4
<i>ddx-52(gc51)</i>	arrest+dead
<i>ddx-52(gk409936)</i>	arrest+dead
<i>gc51</i> /+	adults/L4
<i>gk409936</i> /+	adults/L4
<i>gc51/gk409936</i>	arrest+dead
<i>gc51</i> Ex[DDX-52::GFP]	adults/L4

development scored for > 100 animals/replicate

minimum of 3 biological replicates/strain

For a given strain, all animals scored in all replicates

had the developmental phenotype noted

Table S2. suppressors of *ddx-52(gc51)*, Related to Figure 2

gene	alleles	predicted allele effect	predicted gene function
<i>ncl-1</i>	<i>gc53</i>	deletion, lf	Repressor of rRNA transcription
<i>larp-1</i>	<i>gc56</i> and <i>gc57</i>	missense, lf or rf	Represses translation of 5'-TOP mRNAs
<i>ulp-4</i>	<i>gc54</i> and <i>gc55</i>	missense, rf	Removes SUMO
<i>nol-10</i>	<i>gc58</i>	missense, gf	Promotes ribosome biogenesis
<i>aatf-1</i>	<i>gc63gc64</i>	missense, gf	Promotes ribosome biogenesis, apoptosis antagonizing