Figure S1. Related to Figure 1. Comparison of the amino acid sequence conservation between *C. elegans* DEAD-box helicase proteins, Drosophila Vasa and human DDX4 in A) the flanking domain B) the negatively charged C terminal tryptophan domain. C) The phylogenomic tree showing the conservation of the CCHC zinc-knuckle motif (orange) across Vasa proteins has been updated from (Figure 1C in Gustafson and Wessel, 2010) using phyloT (phylot.biobyte.de) and NCBI taxonomy data. Dashed lines indicate loss of the motif in some species.

Figure S2. Related to Figure 3. All images (now condensed) used to quantify granularity and expression in Figure 3. The domain location of the mutation, strain name, allele name and mutation type is indicated. Ten worms analyzed for each genotype.

Figure S3. Related to Figure 6. GLH-1 Immunoprecipitation. Left: Microscope images of control non-antigen exposed anti-DYKDDDDK agarose beads compared to beads exposed to lysate from the GLH-1::GFP::3xFLAG expressing strain. Right: Western blot comparing GLH-1 expression in the input, unbound and elute fraction after immunoprecipitation with protein lysate from the GLH-1::GFP::3xFLAG expressing strain. Results were replicated three times.

Table S1: CRISPR/Cas9 reagents for generating *glh-1* alleles

Table S2: Proteins with enhanced or depleted GLH-1 association in wild type (DEAD) and GLH-1 mutants (DAAD & DQAD)

2505 proteins identified by FLAG-IP LC/MS/MS of 3xFLAG-tagged GLH-1 (and mutant GLH-1) *C. elegans* lysates compared to control (large supplemental spreadsheet file). Proteomics data used to generate this spreadsheet have been uploaded to the PRIDE proteomics repository, project accession PXD014135.

Table S3: Protein classes with enriched or depleted GLH-1 associations

Excel table (attached) showing protein classes identified by gene ontology analysis.