

Table S1 dsRNAs targeting the 76 nt sequence of collagen genes elicit the superdumpy phenotype in *eri-1(mg366)* animals. L1 animals of *eri-1(mg366)* mutants were fed with dsRNAs and the phenotypes were scored 3 days later. +++, superdumpy; -, no dumpy.

<i>RNAi (76mer)</i>	<i>superdumpy</i>
<i>no RNAi</i>	-
<i>dpy-13</i>	++++
<i>sqt-3</i>	++++
<i>col-93a</i>	++++
<i>col-93c</i>	++++
<i>col-43</i>	++++
<i>col-94</i>	++++
<i>col-122</i>	++
<i>col-179</i>	-

Tables S2-S7

Available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.159780/-/DC1>

Table S2 The number of reads of NRDE-3-associated siRNAs targeting collagen genes.

Table S3 Candidate-based RNAi screening to search for genes by which the silencing were strongly depended on *nrde* pathway. 168 genes present in operons were selected from the Ahringer RNAi library with reported phenotype in either N2 or *rrf-3* strain. The 168 operon genes are unlikely to be repetitive based on the criteria of >90% nt identity in a stretch of >200 nt sequence to one or more of the other genes or genomic loci. 28 RNAi clones targeting multi-gene families were selected from the Ahringer RNAi library. NRDE-dependent silencing was observed when feeding animals with dsRNA targeting of histones, homeobox genes, and GPCR.

Table S4 Off-target gene silencing preferentially requires the *Nrde* pathway. *eri-1(mg366);MAGO12* was crossed with *eri-1(mg366)*. Eight independent F2 animals were selected that suppressed the *dpy-13* RNAi-induced superdumpy. The F2 suppressors were then genotyped for the twelve Argonaute genes. *nrde-3(tm1116)*, but not other eleven *wago* alleles, is linked to superdumpy suppression.

Table S5 Deep sequencing identified 178 NRDE-3 targets that exhibit at least ten raw reads and two fold enrichment between *FLAG::GFP::NRDE-3* and *eri-1(mg366);dpy-13(e458);FLAG::GFP::NRDE-3;(dpy-13 RNAi)* strains.

Table S6 Sixty-three genomic loci were identified to display most NRDE-associated siRNA reads. Most of these loci are homologous in sequence to another region in the genome.

Table S7 The primers used for quantitative real time PCR analysis.