Supplementary Figure Legend

Supplementary Figure 1. Chromosome mapping of helicase-like genes in *C. elegans* and pairs and clusters of homologous genes in each subfamily.

Helicase-like genes in each subfamily were mapped onto the six C. elegans chromosomes (abbreviated Chr I to V and Chr X) based on the "genomic position" described in WormBase (WS159). The genes were classified into the following subfamilies: DEAD-box (A), DEAH-box (B), SWI2/SNF2 (C), SKI2 (D), UPF1 (E), MCM (F), PIF1 (G), MPH1 (H), RAD3/RECQ (I), and others (J). Each position on the chromosome is indicated by a triangle pin and a gene name based on the genomic position (bp). The color of the gene name indicates the phenotype of the corresponding RNAi-treated nematode: embryonic lethal (red), larval arrest (orange), slow growth (yellow), wild-type, i.e. no growth-defect phenotype (green), and no data (gray). Reported pseudogenes (H03G16.3, T08D2.3, Y57A10A.6, Y73B3B.5, Y106G6D.5, ZK250.10) are indicated in blue, italic letters. The gene pair and cluster members were identified as described in the legend of Supplementary Table 4 and indicated with colored lines, boxes and pins in the map as follows: *E*-values of 0 to $1.0 \times e^{-100}$ in the BLASTN analyses for both genomic DNA and mRNA sequences in red for significantly homologous genes that are likely to have generated from a putative common ancestor gene by duplications. Three gene pairs (*Y67D2.6* and *Y108F1.5*, *T23H2.3* and *F59A7.8*, and *R03D7.2* and *K08D10.5*) are also in pink indicating closely related genes. Nucleotide sequences of these genes share significant similarities, although they do not completely meet the criteria described above (Supplementary Table 4).

Note: The *C. elegans*-specific SNF2-like genes and *Helitrons* closely localized on the terminal region of each chromosome. However, the genes from each gene pair were not always co-localized on chromosomes and co-localized genes were not always homologous genes. The gene pairs *F57B9.3* and *inf-1*, *mut-14* and *ZC317.1*, *Y46G5A.4* and *Y46G5A.6*, *drh-1* and *drh-2* co-localized, however, members from other pairs did not. The genes from gene pairs *C44H9.2* and *C44H9.4*, *xnp-1* and *tag-192*, *csb-1* and *F53H4.6*, and *F01G4.3* and *C08F8.2* were mapped very closely on the same chromosome, but they did not share any significant sequence homologies.

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