

Chromatin Compaction by Small RNAs and the Nuclear RNAi Machinery in *C. elegans*

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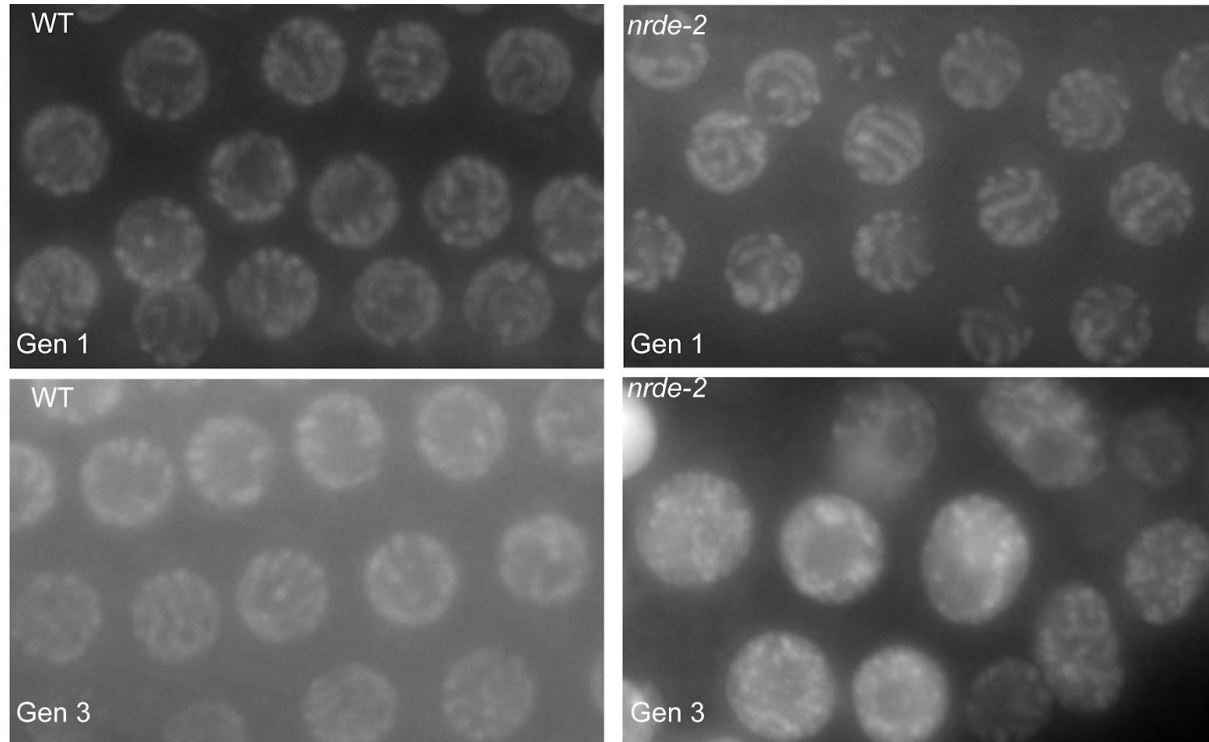
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77 Avenue Louis Pasteur

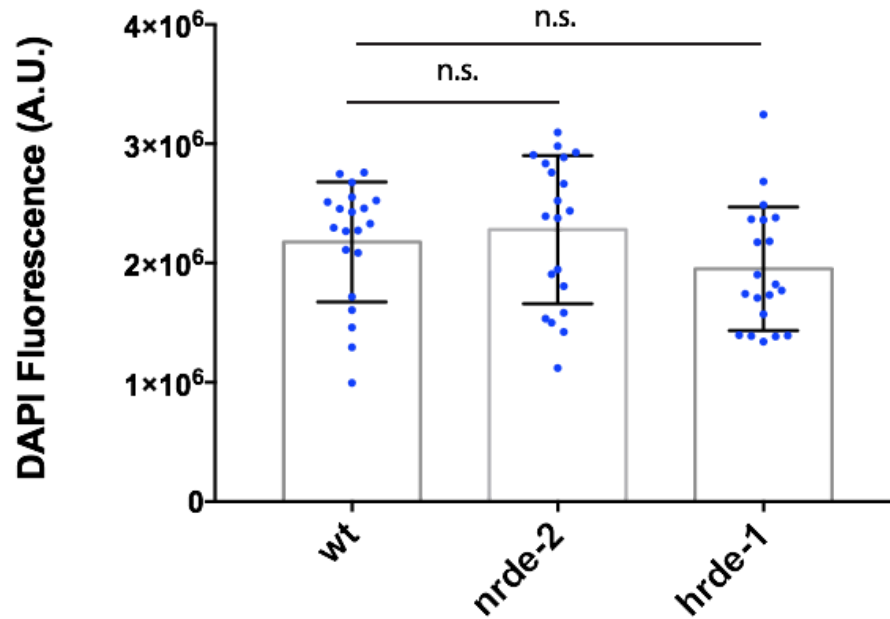
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Boston, MA. 02215

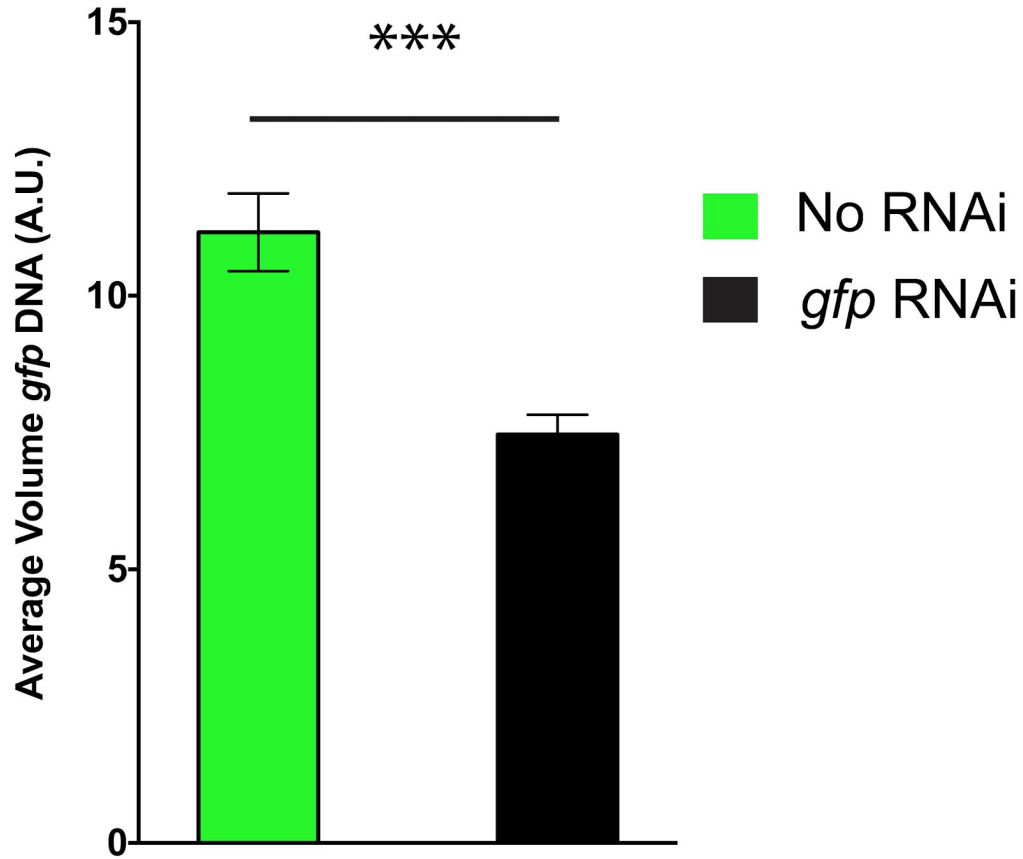
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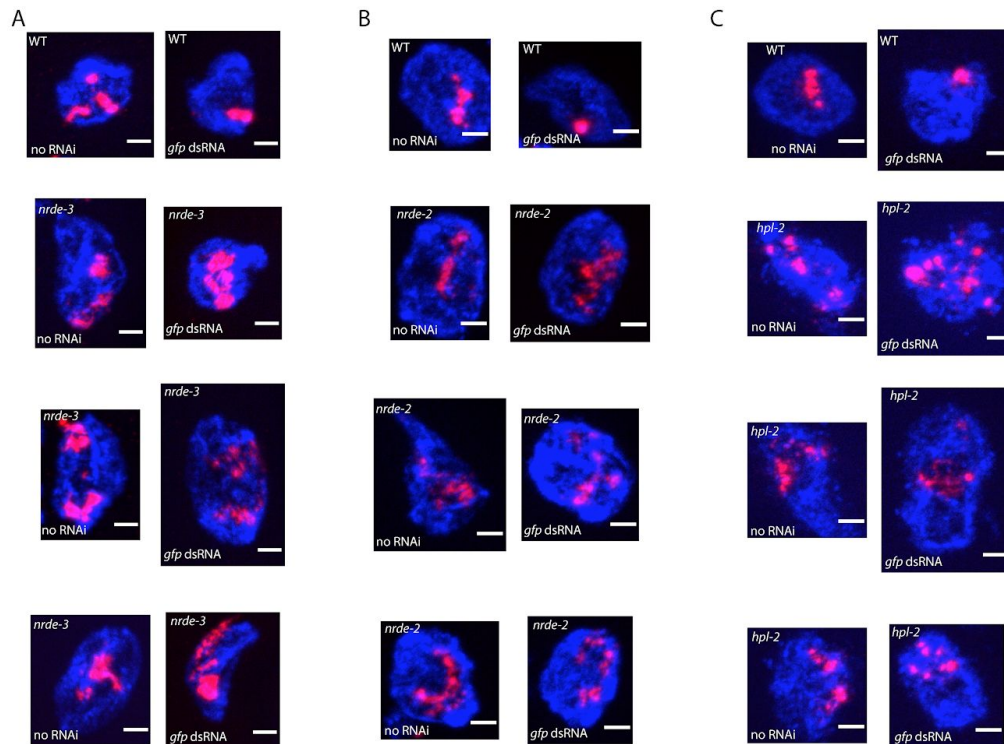
Supplementary Figure 1. Late generation *nrde-2*(-) animals display enlarged/disorganized germline chromatin. Fluorescent micrograph of pachytene germ cells of animals expressing a *gfp::h2b* transgene in the germline. Wild type or *nrde-2*(*gg091*) animals were maintained at 25°C for three generations. Images are to same scale.



Supplementary Figure 2. Wild-type, *nrde-2*(-) and *hrde-1*(-) nuclei possess similar amounts of DNA. Fluorescent DAPI intensity measurements were made from individual germ cells of wild type, *nrde-2*(*gg091*), and *hrde-1*(*tm1200*) animals grown at 25°C for three generations. Each data point represents one germ cell nuclei. Data points were collected from four different animals per genotype. p-value was calculated using a student's two tailed t-test. n.s. = not significant.



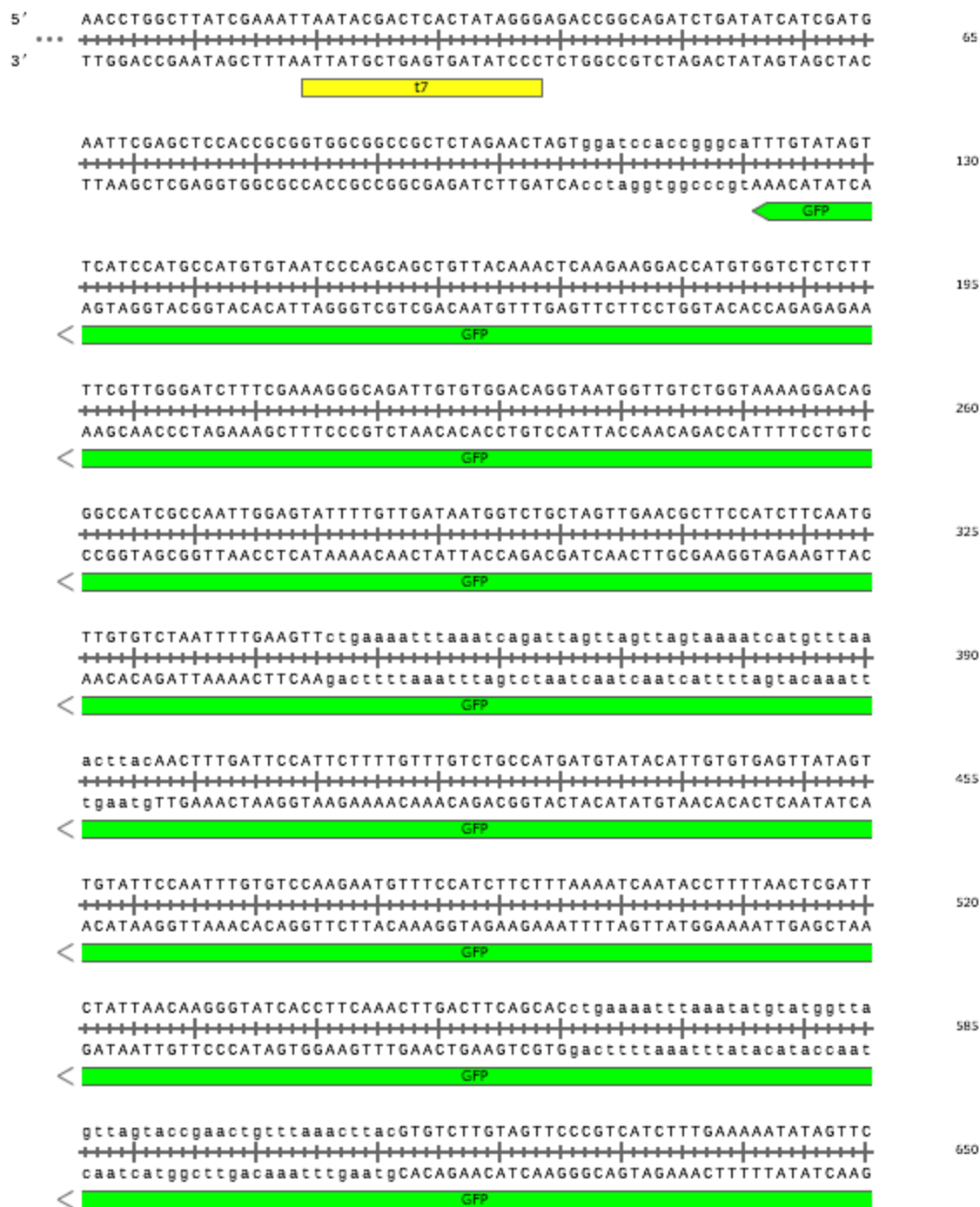
Supplementary Figure 3. Volume quantifications of the *sur-5::gfp* transgene. Volume quantifications for animals exposed to *gfp* RNAi (right) or no RNAi (left). p-value was calculated using a student's two tailed t-test. *** = p-value <0.005.

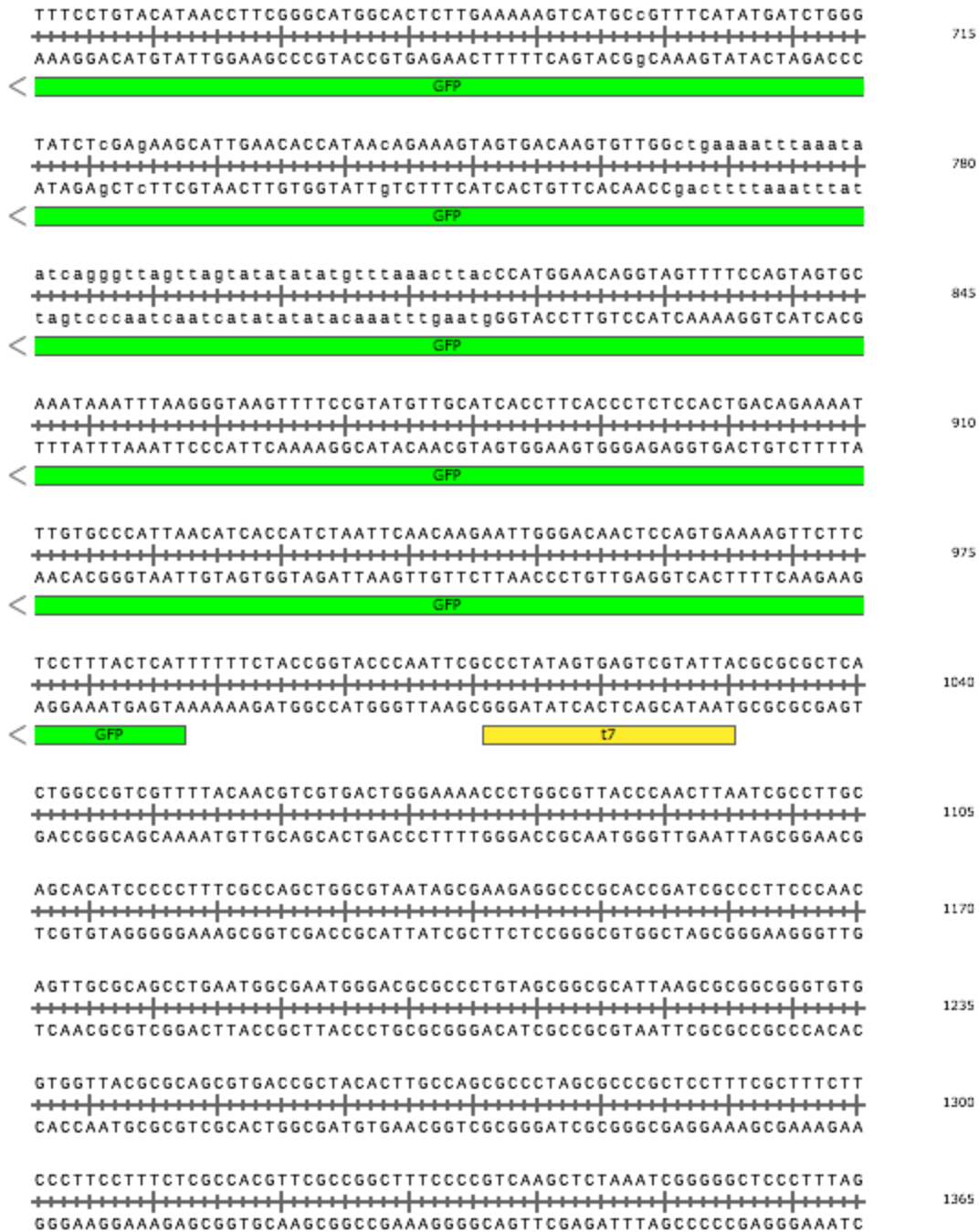


Supplementary Figure 4. Representative images of chromatin compaction in wild-type, *nrde-3*, *nrde-2*, and *hpl-2* animals. Fluorescent micrographs of intestinal nuclei from animals possessing a multicopy *sur-5::gfp* transgene stained with DNA FISH probes targeting *gfp* DNA (red) and DAPI (blue) in wild type or *nrde-3*(*gg066*) (A), wild type or *nrde-2*(*gg091*) (B), and wild type or *hpl-2*(*tm1489*) (C) mutant animals exposed to no RNAi (left) or *gfp* RNAi (right). Images are to same scale. Scale bars = 3 um.

Movie 1. 3D reconstructions of GFP::H2B fluorescence in wild type and *nrde-2*(-) mutant animals. 3D reconstructions of confocal Z-slices for wild type and *nrde-2(gg091)* animals expressing a *gfp::h2b* reporter in the germline and maintained at 25°C for three generations. Z-slices were gathered at 0.3 um intervals. 3D reconstructions were generated using Nikon Imaging software. Images are to same scale.

Sequence: Sup_File_1_gfp_RNAi_plasmid.dna (Circular / 3579 bp)
 Features: 3 total





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AAGC      3'
+++++    *** 3579
TTCG      5'

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