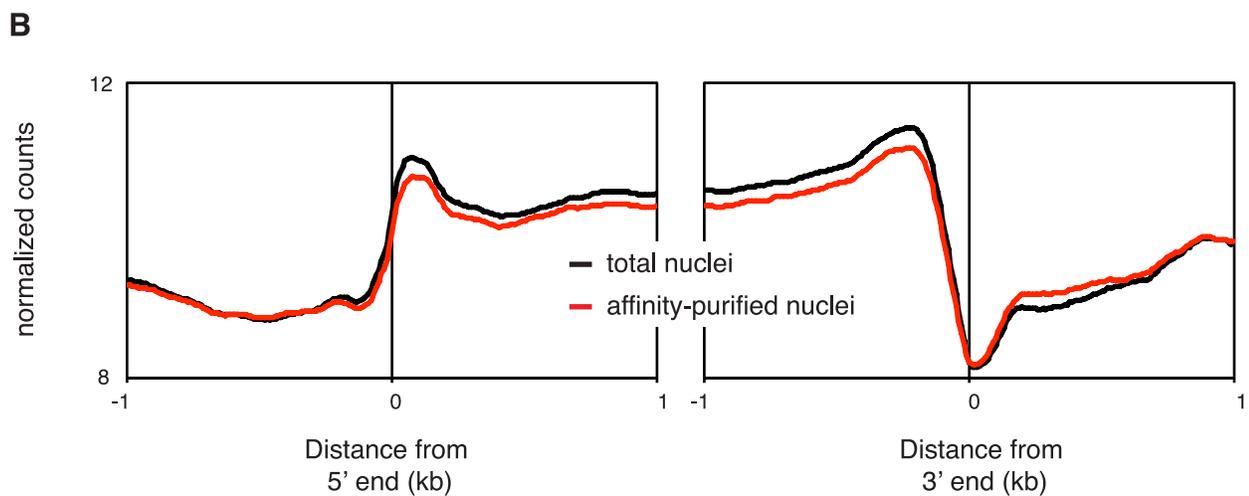
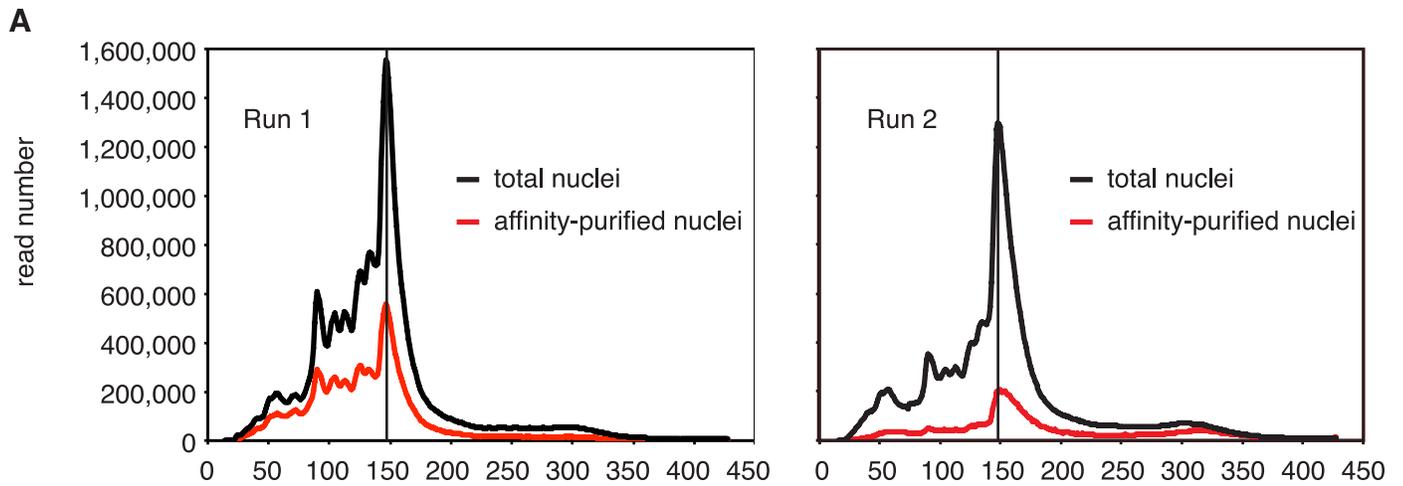


Supplemental Figure 1. Correlation between total and nuclear RNA pools. RNA from total adult worms or total nuclei isolated from adult worms was converted to cDNA, amplified, labeled and analyzed on Roche NimbleGen whole-genome tiling microarrays. Averaged data from two biological replicates for total RNA and four biological replicates for nuclear RNA is shown.



Supplemental Figure 2. (A) *C. elegans* read numbers from the Illumina paired-end sequencing runs plotted by size. Read numbers for both total nuclei (black) and affinity-purified (red) nuclei samples peak at a fragment length corresponding to mononucleosomes. (B) Ends analysis of Illumina paired-end sequencing reads. Genes were aligned at the 5' and 3' end and average normalized read counts were plotted for total nuclei (black) and affinity-purified nuclei (red).