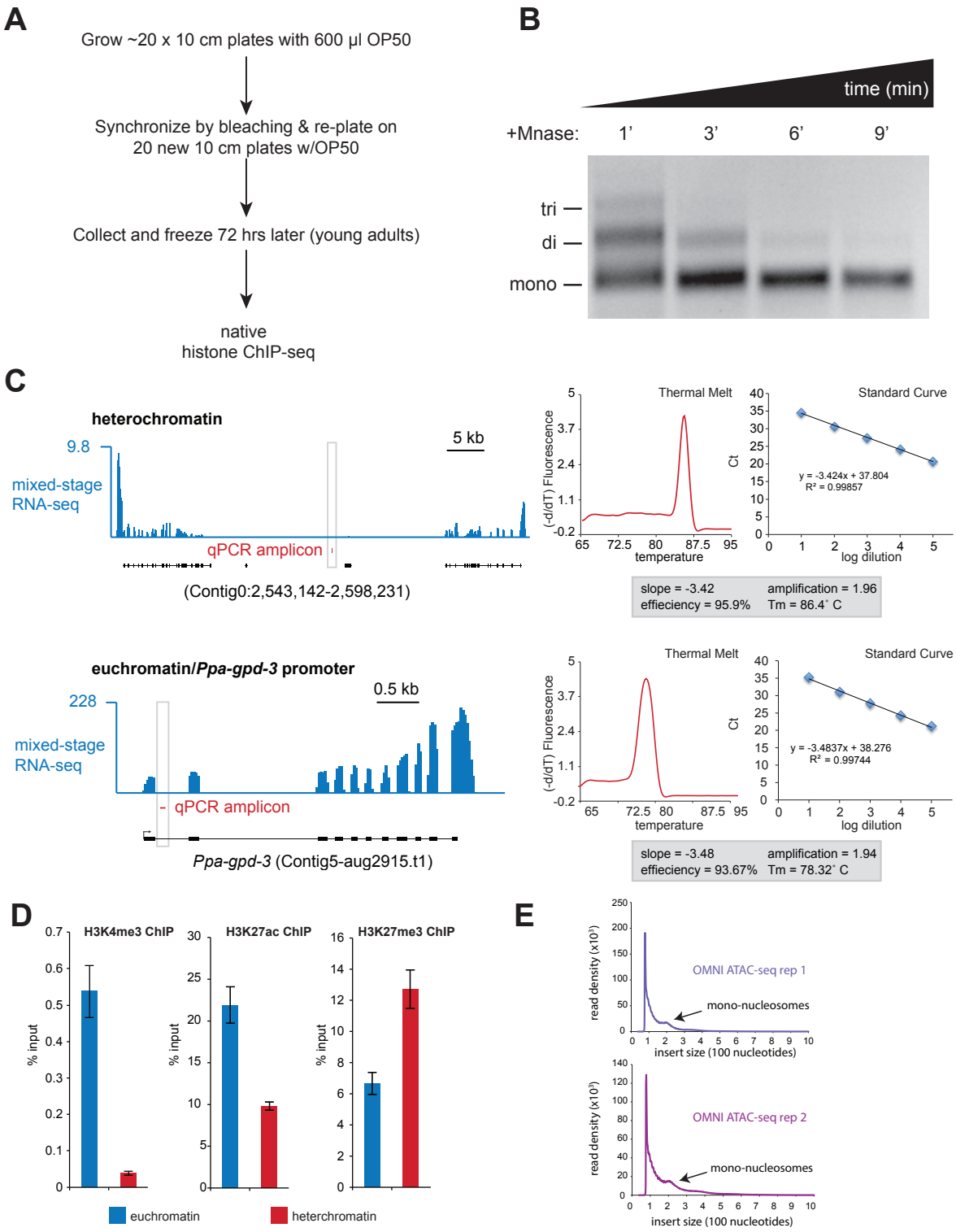

Supplemental Figure S2. ChIP and ATAC-seq methodology and quality control. (*A*) Strategy for biological sample collection and processing. (*B*) Mnase digestion of purified native nuclei results in time-dependent nucleosome fragmentation. Shown is an agarose gel of purified DNA incubated at 37° C for the indicated times with MNase (NEB). We chose 5 min. for subsequent chromatin fragmentation. (*C*) Genomic loci of qPCR Primers (Supplemental Table S3) used for verifying ChIP-seq specificity. The heterochromatin pair was designed in a gene 'desert' devoid of RNA-seq expression, and the euchromatin primer pair was designed near the *Ppa-gpd-3/gapdh* promoter. Also shown are thermal melts and a 5-log titration to demonstrate primer specificity, assessed on a LightCycler 480 (Roche). RNA-seq reads and coordinates apply to the Hybrid 1 Genome (http://pristionchus.org/download/), and genes correspond to the Augustus 2013 annotation. (*D*) ChIP-qPCR with indicated antibodies shows specificity of histone marks for euchromatin (H3K4me3, H3K27ac) and heterochromatin (H3K27me3) enrichment. Data is presented as percent input ($100x2^{\Delta Ct}$). (*E*) Sequencing read density of OMNI ATAC by size for two replicates. Reads less than 100 nucleoties are considered sub-nucleosomal integration events (Buenrostro et al., 2013).