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Supplemental Information

Targeting of the Dosage-Compensated Male X-Chromosome during Early *Drosophila* Development

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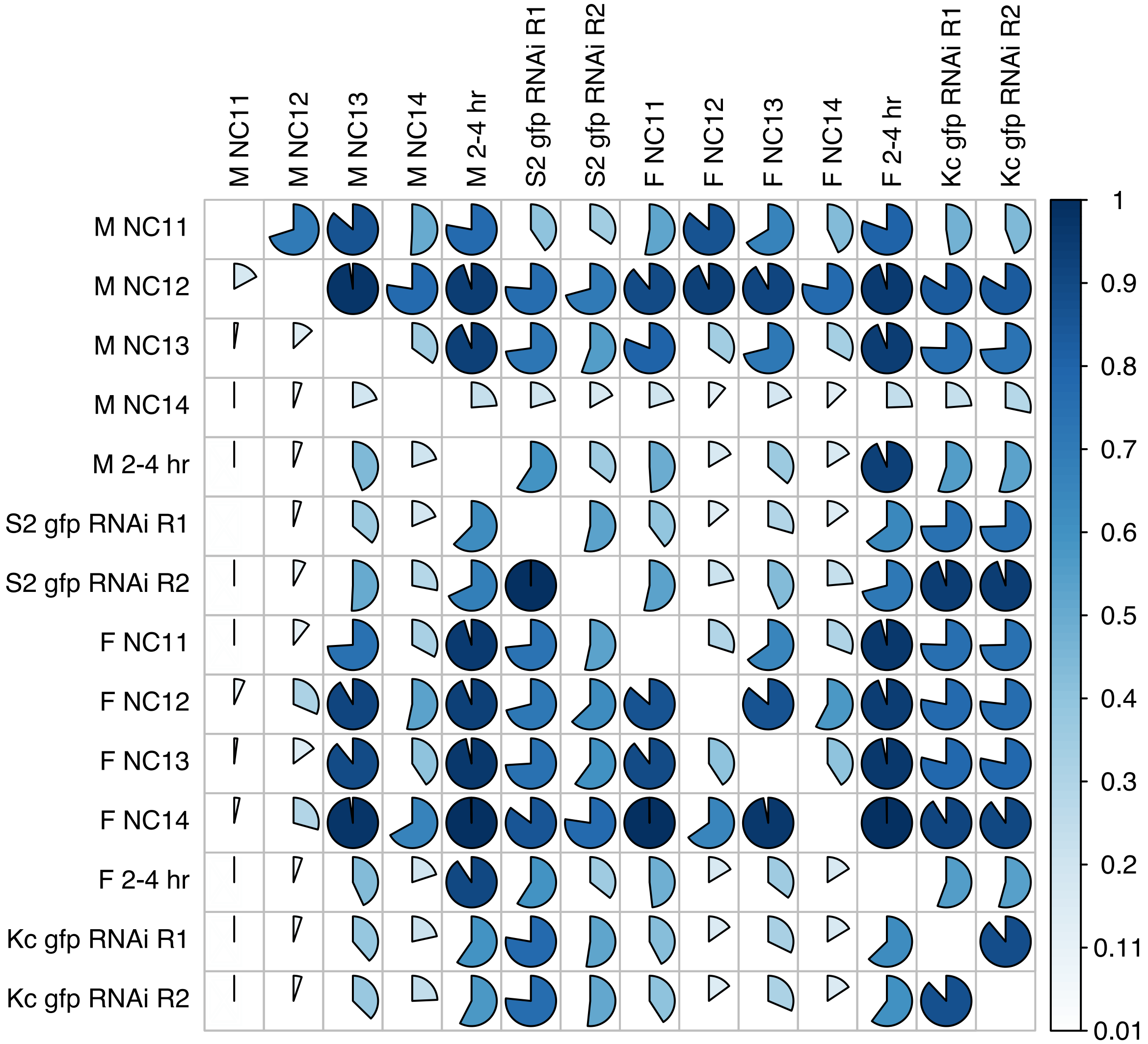


Figure S1 (related to Figure 2). Percent overlap of CLAMP ChIP-seq peaks between all samples from the current study and previous cell culture CLAMP ChIP-seq samples. Cell culture (S2, male; Kc, female) CLAMP ChIP-seq data from Soruco et al. 2013, NCBI accession number GSE39271.

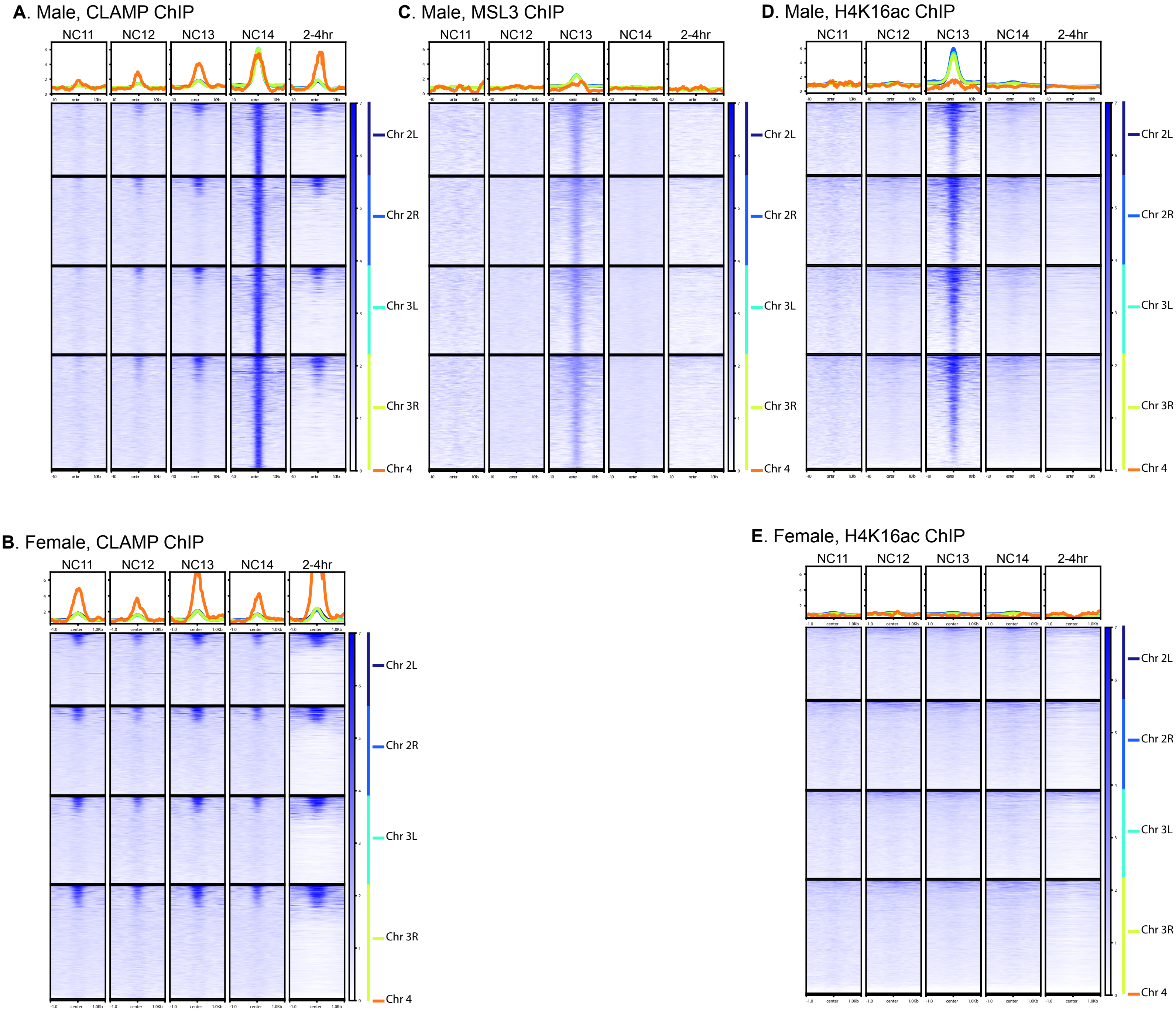
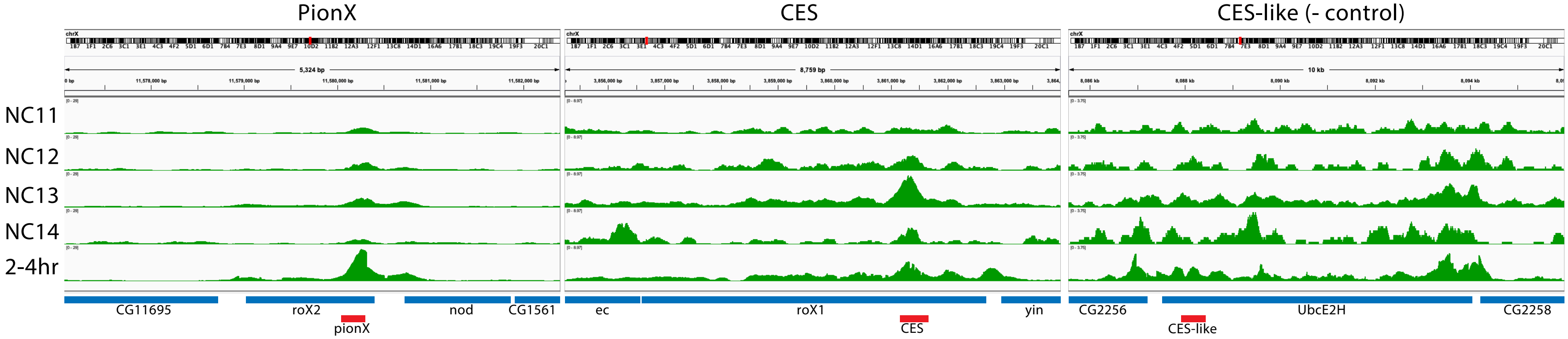
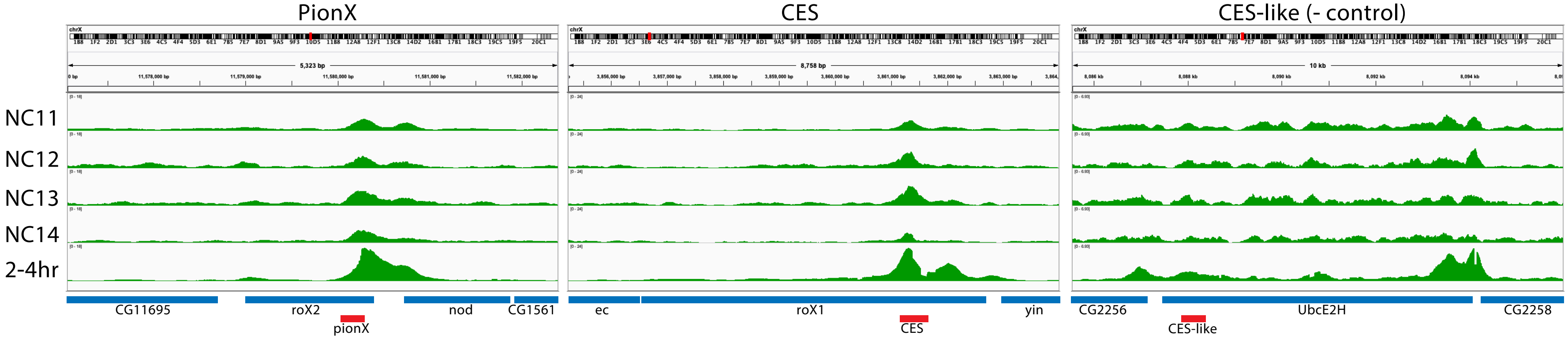


Figure S2 (related to Figure 2). Staged, sexed ChIP-seq heat maps at autosomal CLAMP sites. Data are mapped over autosomal CLAMP sites and broken into chromosomes: 2L, dark blue; 2R, light blue; 3L, teal; 3R, light green; 4, orange. (A) CLAMP ChIP-seq from male embryos. (B) CLAMP ChIP-seq from female embryos. (C) MSL3 ChIP-seq from male embryos. (D) H4K16ac ChIP-seq from male embryos. (E) H4K16ac ChIP-seq from female embryos.

A. Male, CLAMP ChIP



B. Female, CLAMP ChIP



C. Male, MSL3 ChIP

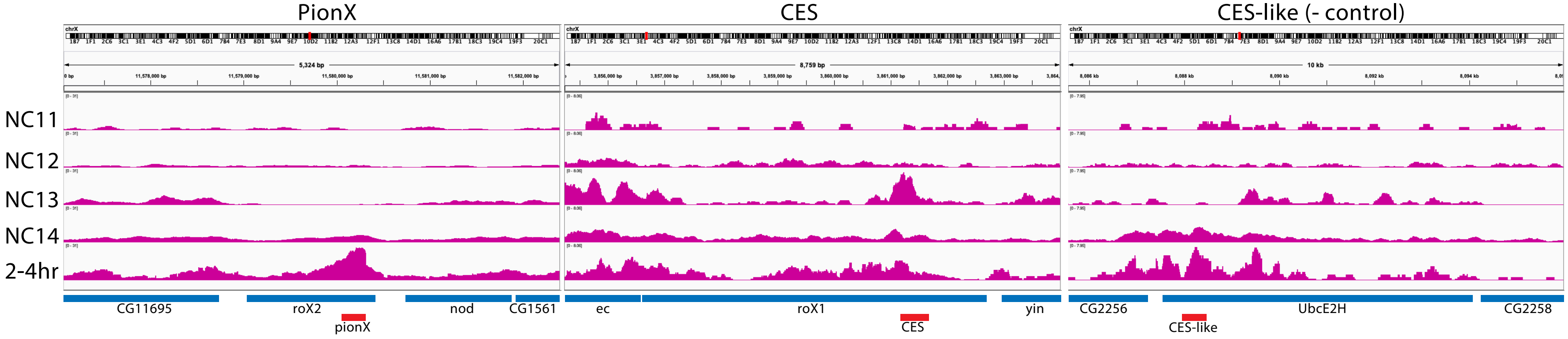


Figure S3 (related to Figure 2). CLAMP (A and B) and MSL3 (C) ChIP-seq profiles over individual loci representative of classes in **Figure 2**, including *roX2* (PionX; Villa et al. 2016), *roX1* (CES; Soruco et al. 2013, Alekseyenko et al. 2008), and *UbcE2H* (CES-like; Soruco et al. 2013, Alekseyenko et al. 2008). Nearby genes are represented in blue and PionX, CES, and CES-like sites in red. Profiles generated in Integrative Genomics Viewer. Data are group autoscaled.