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Widespread activation of developmental gene expression characterized by PRC1-dependent chromatin looping

V. Loubiere, G. L. Papadopoulos, Q. Szabo, A.-M. Martinez*, G. Cavalli*

Polycomb repressive complexes 1 and 2 have been historically described as transcriptional repressors, but recent reports suggest that PRC1 might also support activation, although the underlying mechanisms remain elusive. Here, we show that stage-specific PRC1 binding at a subset of active promoters and enhancers during Drosophila development coincides with the formation of three-dimensional (3D) loops, an increase in expression during development and repression in PRC1 mutants. Dissection of the dachshund locus indicates that PRC1-anchored loops are versatile architectural platforms that persist when surrounding genes are transcriptionally active and fine-tune their expression. The analysis of RING1B binding profiles and 3D contacts during neural differentiation in mice suggests that this role is conserved in mammals.

RESULTS

PRC1 binds a subset of active regulatory elements in eye discs

First, we characterized the three-dimensional (3D) epigenome of Drosophila eye-antennal imaginal discs (EDs) by producing chromatin immunoprecipitation–sequencing (ChIP-seq) maps for a comprehensive set of active (H3K4me2/3, H3K36me3, and H4K20me1), enhancer-related (H3K4me1), PRC2-mediated (H3K27me1/2), and PRC1-mediated (H2AK118Ub) posttranslational modifications (PTMs) that were analyzed in addition to our previously published ChIP-seq data for H3K27me3 and H3K27Ac (3). Furthermore, we generated a high-resolution Hi-C map from EDs (~1.25-kb resolution; fig. S1, see Materials and Methods). Genome-wide clustering of PTM ChIP-seq signals using self-organizing maps (SOMs) (Fig. 1A, fig. S2, and table S1) identified five distinct chromatin types that exhibit hallmarks of active transcription start sites (aTSSs), active transcription termination sites (aTTSs), enhancers, PcG-repressed, and the previously described null chromatin state (Fig. 1B and fig. S2) (10, 11). While aTSS and aTTS bins are essentially transcriptionally active, PcG-repressed bins are mostly silent, as expected (fig. S3). Moreover, aTSS and enhancer bins show high ATAC-seq (assay for transposable-accessible chromatin–sequencing) levels, as expected for these regulatory elements, which are known to be nucleosome depleted (fig. S3). Markedly, a subset of active enhancer bins found in the vicinity of transcriptionally active genes also show consistent enrichment for the PRC1-mediated H2AK118Ub mark without the PRC2-mediated H3K27me3 repressive mark (Fig. 1B and figs. S2 and S4). For instance, the grainy head gene is ubiquitously expressed in the ED (12) and retains detectable H2AK118Ub enrichment (fig. S4). Although previous studies using S2 cells suggest that the H2AK118Ub is virtually absent from active sites (11), our analysis suggests that catalytically active PRC1 complex binds to a subset of active enhancers in the developing ED. Further studies will be needed to address whether H2AK118Ub can genuinely mark active genes or whether the colocalization observed here might reflect the coexistence of multiple cell types in ED. Future investigations should also address the dynamics of PRC1 binding at these active sites, and whether it coincides with ongoing transcription.

PRC1 binding is associated with increased enhancer-promoter 3D contact frequencies in the ED

The five chromatin types (Fig. 1A) were used to segment the Hi-C map (Fig. 1C), and the results show that each type preferentially interacts with itself (Fig. 1, D and E) (13). In addition, aTSS and aTTS bins interact with each other, while they are segregated from PcG and null repressed chromatin at long-range distances (250 kb to 5 Mb) (Fig. 1D) (14). Enhancer bins behave like active chromatin at long-range distances, namely, they interact preferentially with themselves and with aTSS bins (Fig. 1D). The fact that they show no preferential short-range interactions with aTSS bins (25 to 250 kb) (Fig. 1E) is consistent with the possibility that enhancers only interact with a small subset of all surrounding promoters. To identify this subset, we complemented preexisting ChIP-seq data for the canonical PRC1 members PC (Polycomb) and PH (Polyhomeotic) (3) with a ChIP-seq for the PRC1 member PSC (Posterior Sex Combs), and ranked aTSS and enhancer bins based on PRC1 enrichment. We found
Fig. 1. PRC1 binding is associated with increased enhancer/promoter contacts in ED. (A) Schematic view of the workflow used for the genome-wide stratification of PTMs using self-organizing maps. (B) Heatmap showing the average PTM z scores for each chromatin type (indicated at the bottom). (C) Hi-C screenshot of a ~1.4-Mb region on the chromosome 3R. Genome-wide stratification of the ED epigenome is reported at the bottom. (D and E) Log2(observed (o)/expected (e)) average interaction frequencies between each chromatin type at long- (250 kb to 5 Mb) and short-range (25 to 250 kb) distances, respectively. (F) Log2(o/e) average interaction frequencies between aTSS and enhancer bins (25 to 250 kb) ranked by increasing PH enrichment. (G) Bar graph showing the ontologies of the top interacting aTSS bins from (F). (H) k-Means clustering of PTM ChIP-seq around a stringent set of PRC1 (PH and/or PC and/or PSC) binding sites (±2.5 kb). Clusters are shown on the left, together with PRC1 (PH, PC, and PSC) ChIP-seq tracks. (I and J) Log2(o/e) aggregate interactions within 25-kb windows centered on PRC1-bound (PRC1+) or PRC1-depleted (PRC1−) aTSS and enhancer (Enh.) sites between 25 to 250 kb (I) and 250 kb to 5 Mb (J). Corresponding quantifications of the Hi-C score (±2.5 kb) are shown on the right. Wilcoxon, ***p < 1 × 10^{-5}. 

that high PRC1 levels are predictive of increased contact frequencies at both short- and long-range distances (Fig. 1F and figs. S5 and S6). Hence, the strength of enhancer-promoter contacts at genes involved in growth, imaginal disc morphogenesis, and eye development unexpectedly correlates with PRC1 binding to both elements (Fig. 1, F and G, and table S2).

To identify PRC1-bound TSSs and enhancers genome wide, we clustered PTM ChIP-seq signals around a stringent set of PRC1 peaks (see Materials and Methods and table S3). Notably, 60% of PRC1 sites lack detectable H3K27me3 in the ED and are decorated with the H3K27Ac active mark (Fig. 1H and fig. S7). In contrast with canonical H3K27me3-enriched Polycomb loci, these sites lie in the vicinity of transcriptionally active genes (fig. S8A and tables S4 and S5; see Materials and Methods) and correspond to either H3K4me3-enriched aTSSs (>76% at less than 500 bp; fig. S8E) or H3K4me1-decorated enhancer-like binding sites (Fig. 1H and fig. S7). The 858 H3K27Ac-enriched putative enhancer sites lie in open chromatin regions (fig. S8B) (15, 16) that substantially overlap with previous mapping of developmental enhancers by STARR-seq (self-transcribing active regulatory region sequencing) in BG3 cells (fig. S8C) (17, 18), suggesting that they correspond to active enhancers.

PRC1-bound enhancers are located near critical genes regulating growth, imaginal disc, and eye development (fig. S8D and table S6). To test whether PRC1 binding mediates preferential interactions between active enhancer and promoter elements, we produced aggregate plots of the interaction frequencies centered on PRC1-bound aTSSs and enhancers. The results (Fig. 1, I and J) show that PRC1 binding induces stronger 3D contacts than control sets of aTSSs and enhancers characterized by similar pairwise distances, by similar ATAC-seq enrichments, and by the absence of PRC1 peaks (fig. S9; see Materials and Methods), both at short- and long-range distances. In contrast, PRC1-bound enhancers do not contact the TSSs of the corresponding genes. Therefore, PRC1 binding is associated with increased 3D contact frequencies between a subset of active regulatory elements in ED (Fig. 1, I and J and figs. S10 and S11).

**PRC1-anchored enhancer-promoter loops are developmentally dynamic**

To test whether PRC1-anchored enhancer-promoter loops are developmentally dynamic, we analyzed the difference between late embryos (16 to 18 hours) and larval EDs. Sixty-three percent of PRC1 enhancers, which we named stage-specific enhancers (SSEs), show no detectable PRC1 peaks (Fig. 2, A to C, and fig. S12, A to C), lower H3K4me1 and H3K27Ac (Fig. S12, D and E), and generally do not form enhancer-promoter loops in embryos (Fig. 2, D and E, and fig. S12, F and G). Unexpectedly, SSE target genes are transcriptionally up-regulated during development and down-regulated in EDs bearing PRC1 mutant clones (Fig. 2F and table S7). To eliminate the possibility that these transcriptional changes arise from a compensatory response by remaining heterozygous cells, we used an RNA interference (RNAi) system that allowed us to knock down ph in about 90% of the cells within the ED and reproduce the tumorigenic phenotype associated with ph mutation (fig. S13) (3). The ph RNAi transriptome is skewed toward down-regulation at ph-bound enhancers, including SSEs (fig. S14). Consistent with the lack of H3K27me3 on these genes, mutations affecting the PRC2 methyltransferase E(z) or its PRC1 reader Pc have a much weaker transcriptional effect than ph and Psc mutations (Fig. 2F). These results suggest a previously unknown role for PRC1 in promoting SSE-promoter 3D contacts at active genes enriched for H3K27Ac to favor their transcriptional induction during development (Fig. 2G).

**PREs in the dac/CG5888 locus are required for faithful gene activation**

Although the finding of PRC1-anchored repressive loops at H3K27me3-enriched loci is not unprecedented (7, 8), the presence of PRC1 loops at fully active sites (Fig. 2G) was unknown. It was recently suggested that a subset of Polycomb response elements (PREs) might be marked by H3K27me3 to maintain silencing in some cells, while they may switch to function as developmental enhancers in other cells (19), but the chromatin conformation of these elements in the active or the repressed state was not directly analyzed. We therefore tested the alternative possibility that a subset of canonical PREs contains enhancers that may activate transcription via PRC1-mediated looping. Clustering analysis shows that the Polycomb cluster can be subdivided into two subclusters, characterized by differential transcription, chromatin marking, and 3D looping frequencies. Polycomb cluster A (Fig. 1H) is characterized by higher transcription (fig. S8A) and H3K4me1 levels (fig. S7) than the Polycomb cluster B (Fig. 1H and fig. S7), suggesting that developmental enhancers in the Polycomb A cluster are in a poised state (20). We found that Polycomb A sites form stronger loops between them and are marked by higher H2AK118Ub levels than Polycomb B sites (fig. S15). Some of these sites are located at key developmental gene loci that show increased H3K4me1 and 3D contacts in EDs compared with embryos (Fig. 3A). One of these loci includes the dan and danr promoters (21), which exhibit stage-specific H3K4me3 peaks and are up-regulated in the ED (×5.0 and ×7.6, respectively; Fig. 3A). Furthermore, a significant fraction of genes from the H2AK118Ub-enriched Polycomb cluster A is down-regulated in ph and Psc mutants (Fig. 3B) and in ph RNAi EDs (fig. S14). Down-regulated genes include the core members of the Retinal Determination Gene Network (twin of eyeless, eyegeone, sine oculis, eyes absent, and tiptop) (table S7 and fig. S14), which are major determinants of eye development (22). These data suggest that PRC1 might sustain transcriptional activation in the expression domains at a subset of targets, which are otherwise marked by the canonical PRC2-mediated H3K27me3 mark in their silencing domains.

To directly test whether PRC1-anchored sites, which form repressive chromatin loops in the cells where genes are silent, might also play an activating role in the normal gene expression domain, we focused on the PRC1 loop located near the uncharacterized CG5888 gene and the eye selector gene dachshund (dac) (8). We found that this loop is maintained in the ED, although the spreading of the H3K4me1 and H3K27Ac marks coincides with increased dac transcription (by 4.5-fold) (Fig. 3A). To overcome the problem of cell heterogeneity in the ED, we took a microscopy-based approach focusing on the dac gene in its active expression domain (a broad stripe of cells including the morphogenetic furrow (MF), as well as its anterior and posterior neighbors) and in its repressed state (anterior to the MF) (fig. S16, A and B). CRISPR-mediated deletion of the two PRC1-binding sites located in the dac/CG5888 locus (Fig. 4A and fig. S16C) (8) leads to reduced dac expression (Fig. 4, A and B, and fig. S16, A and B). Because the dac TSS-proximal binding site is close to the dac promoter (fig. S16C) and might therefore dampen its expression via close cis-regulatory effects, we tested the impact of the sole removal of the 3′ dac TSS-distal PRC1 binding site. No transcriptional impact on dac transcripts was found in this mutant condition (Fig. 4, A and B). Furthermore, in a line where the
Fig. 2. Reinforced PRC1 binding is associated with increased interactions and transcriptional activation at the larval stage. (A) PH, H3K4me1, and H3K27Ac ChIP-seq tracks centered on stage-specific enhancer (SSE) sites that only overlap with PRC1 peaks at the larval stage (±2.5 kb). (B and C) PH ChIP-seq average tracks in a 2-kb window centered on SSEs at embryonic (in gray) and larval stages (in orange). Corresponding quantifications (±500 bp) are shown in (C). Wilcoxon, ****P < 1 × 10−5. (D and E) Log2(α/ε) aggregate interactions within 25-kb windows centered on PRC1-bound aTSSs and SSEs between 25 and 250 kb in embryos (left) and EDs (right). Corresponding quantifications (±2.5 kb) are shown in (E). Wilcoxon, ****P < 1 × 10−5. (F) Percentage of significantly up- (top) and down-regulated (bottom) SSE-assigned genes during development (on the left) or between control and PRC2 [E(z)731] or PRC1 (PcXT109, ph505, and Psc1.B8) mutant EDs (on the right, padjust cutoff = 0.001). Hypergeometric test, ****P < 1 × 10−5; ***P < 1 × 10−3; **P < 1 × 10−2; N.S., not significant. (G) Screenshots of Hi-C maps centered on developmentally regulated enhancer-promoter loops anchored at active PRC1 binding sites in embryo (top panels) and ED (middle panels). PRC1 peaks from ED and their assigned clusters are shown below Hi-C screenshots (legend on the upper left) and projected on the maps as white squares. At the bottom, PTM ChIP-seq tracks are shown for embryos (black) and EDs (red).
insertion of a gypsy insulator sequence (8) blocks the interaction between the two PRC1-binding sites (Fig. 4, A and C), dac expression is not affected (Fig. 4B). Three-dimensional fluorescence in situ hybridization (3D FISH) measurements using DNA probes located next to the PRC1 anchor sites (Fig. 4, C and D, and fig. S16C) indicate that the loop is normally present not only in the silent cells but also in the cells where dac is transcribed, and it is disrupted in both regions upon CRISPR-mediated deletion of both PRC1 binding
sites or the dac TSS-distal 3′ site only (Fig. 4D). These data suggest that PRC1 does induce a loop in the dac/CG5888 locus both in the silent and in the active part of the tissue, but disruption of the loop does not play a major transcriptional role for the dac gene in this stage.

We therefore tested whether the CG5888 gene might be affected. In contrast to dac, deletion of the two PRC1-binding sites induced CG5888 expression, suggesting that loss of silencing in complete absence of Polycomb proteins (8) might be the dominant effect for this gene. Markedly, however, CG5888 expression is reduced upon deletion of the 3′ PRC1 binding site, as well as upon insertion of a gypsy insulator sequence (Fig. 4, A and B). These data suggest that the loop in the dac/CG5888 plays an instructive role for expression of CG5888, whereas it is not required for transcription of dac in normal conditions. In the case of silencing, the PRC1-dependent loop was shown to play an instructive role for the dac gene in sensitized genetic conditions. Whether this is true also for activation remains to be studied.

**Dynamic PRC1-Anchored enhancer-promoter loops form during in vitro differentiation of mouse neural progenitor stem cells**

We note that the results described above differ from the case of the Meis2 locus in mice, in which the activation of the gene involves the disruption of a RING1B-dependent tripartite interaction between the promoter of the gene, a distal repressive site, and a tissue-specific enhancer (23). Therefore, we analyzed high-resolution Hi-C maps from synchronized populations of mouse embryonic stem cells (ESCs) and neural progenitor stem cells (NPCs) obtained from an in vitro differentiation system (24) to address whether PRC1 also mediates enhancer-promoter contacts in mammalian cells. NPCs are characterized by a
Fig. 5. PRC1 redeployment at developmental enhancers correlates with transcriptional activation and increased enhancer-promoter loops during NPC specification in mouse cells. (A) k-Means clustering of RING1B, H3K4me3, H3K27Ac, H3K4me1, and H3K27me3 ChIP-seq signals from NPCs centered on RING1 peaks from NPCs (±2.5 kb). Clusters are depicted on the left. Corresponding ChIP-seq tracks from ESCs are shown for comparison. (B) Violin plot of the log 2(FPKM + 1) of the genes assigned to each cluster in NPCs. (C) Bar graph of the percentage of significantly up- (top) and down-regulated (bottom) genes between ESCs and NPCs (padjust cutoff = 0.001). Hypergeometric test, ****P < 1 × 10−5; **P < 1 × 10−2. (D) Comparative Gene Ontology (GO) analysis of the genes assigned to each cluster. (E and F) Log2(o/e) aggregate interactions within 100-kb windows centered on RING1B-bound aTSS and enhancer sites between 50 kb and 5 Mb in ESCs (left) and NPCs (right). Corresponding quantifications are shown in (F) (±10 kb). Wilcoxon, ****P < 1 × 10−5. (G) Screenshots of Hi-C maps centered on developmentally regulated enhancer-promoter loops anchored at active RING1B binding sites in ESCs (top panels) and NPCs (middle panels). RING1B peaks from NPCs, and their assigned clusters are shown below Hi-C screenshots (see legend on the upper left) and are projected on the maps as white squares. On the bottom panels, PTM ChIP-seq tracks are shown for ESCs (black) and NPCs (red).
DISCUSSION

PRC1 plays important roles during normal physiology and in cancer (1–3), but how it might play a dual silencing and an activating role is a matter of great interest. The data provided here suggest that, rather than behaving as transcriptional repressors, PRC1-mediated loops establish versatile architectural platforms that can induce repression and activation. In the absence of transcription factors, PRC1 might cooperate with PRC2 to establish repressive loops and to form silent Polycomb domains, whereas the binding of developmental transcription factors might exploit PRC1-dependent enhancer-promoter contacts to coordinate the timely induction of cognate genes during development. The net effect of looping appears to be gene specific since expression of the CG5888 gene is more sensitive to disruption of a PRC1-dependent loop than the neighboring dac gene. At dac, one of the PRC1 binding sites is within a few hundred base pairs (bp) from the TSS, whereas the PRC1-binding site closest to the two alternative CG5888 alternative promoters is located, respectively, around 16 and 25 kb away. One possibility is therefore that the relative location of regulatory elements might modulate the effects of PRC1-dependent loops. In addition to the role in 3D looping, recent work has shown that PRC1 might assist transcription by modulating occupancy and phosphorylation of RNA polymerase II, as well as association of the pausing-elongation factor Spt5 to enhancers and promoters (4). In future studies, it will be important to analyze the relative role and the interplay of these mechanisms in individual cells at the onset of silencing, as well as during transcriptional activation to understand the chain of molecular events that triggers this dual function for Polycomb-bound regions.

MATERIALS AND METHODS

Fly stocks and handling

Flies were raised on standard corn meal yeast extract medium at 25°C. The Oregon-R w1118 line, referred to as wild type (WT), was obtained from R. Paro [Zentrum für Molekulare Biologie der Universität Heidelberg (ZMBH), University of Heidelberg, Germany]. For the transcriptome of PcXT109 and enhancer (H3K4me1) sites (Fig. 5A), RING1B and H3K4me1 are sharply increased at enhancer sites in NPCs compared with ESCs and exhibit weak but significant H3K27Ac enrichments with H3K27me3-repressed sites (Fig. 5A and fig. S17). Accordingly, genes flanking these sites show higher transcription (Fig. 5B) and up-regulation in NPCs (Fig. 5C) and are enriched for neural-related ontologies (Fig. 5D). Furthermore, RING1B enhancer sites form stage-specific loops with RING1B-bound promoters in NPCs (Fig. 5, E to G). These observations confirm the data from Drosophila and suggest that PRC1-anchored active enhancer-promoter contacts are an evolutionary conserved feature in metazoans.

ChIP-seq from EDs or whole Drosophila embryos

ChIP from ED or whole 14- to 16-hour embryos were performed in duplicate as previously described (27). Briefly, ~200 EDs from wandering larvae were used per replicate for PTM ChIP-seq and ~500 for PSC ChIP-seq [PSC antibody is described in (28)]. For each replicate of PTM ChIP-seq from 14- to 16-hour embryos, 2-hour collections were performed at 25°C with about 500 flies. When necessary, several batches of dissection/collection were snap frozen in liquid nitrogen and stored at ~80°C to collect enough material. Samples were then transferred into a tight Tenbrock and cross-linked for 15 min at room temperature (RT) using 1.8% formaldehyde and contained in storage before being lysed on ice for 2 hours with 1% SDS lysis buffer 2 [see (27)]. Chromatin was sonicated using a Bioruptor (Diagenode) for 18 cycles (settings, 30 s on and 30 s off; high power), and the quality of the sonication was checked on a 1.5% agarose gel (~300-bp fragments). Then, samples were precleared overnight (O/N) using 15 µl of protein A Dynabeads (Thermo Fisher Scientific, catalog no. 10001D) at 4°C, and an aliquot was kept apart to constitute the INPUT. Antibodies were added (table S8) 4 hours before the addition of 30 µl of protein A Dynabeads and O/N incubation at 4°C. Last, the beads were washed, and the precipitated chromatin was eluted before O/N de-cross-linking at 65°C, protease K treatment, phenol/chloroform purification, and O/N ethanol precipitation. Libraries were prepared using TruSeq ChIP Sample Preparation kit from Illumina following the manufacturer’s instructions. PSC ChIP-seq libraries were subjected to 50-bp single-end sequencing on a HiSeq 2500, PTM ChIP-seq libraries from ED were subjected to 50-bp paired-end sequencing on a HiSeq 2000, and PTM ChIP-seq from 14- to 16-hour embryos were subjected to 75-bp paired-end sequencing on a HiSeq 2000 (~50 to 100 million reads per replicate).

Hi-C from EDs or whole Drosophila embryos

Hi-C experiments from ED and 16- to 18-hour embryos were conducted as previously described by Ogiyama et al. (8). For larval Hi-C triplicates, ~200 EDs were quickly dissected (<1 hour) from wandering larvae at RT in Schneider’s insect medium before being directly processed. Briefly, formaldehyde was added to reach a 2% final concentration, and the samples were homogenized for 3 min using a tight tenbrock at RT and transferred on a rotating wheel (total time for fixation was 10 min). Then, cell membranes were lysed on ice, and nuclei were subjected to Dpn II treatment O/N at 37°C. The next day, restriction sites were end repaired and biotinylated.
RNA-seq from Drosophila EDs

About 150 EDs were dissected from wandering larvae on ice, and total RNA was extracted using TRIzol reagent. Total RNA was purified using the RNA clean and concentrator kit from Zymo Research (catalog no. R1015). Then, poly-A RNAs were selected, and libraries were prepared using the TruSeq Stranded mRNA Sample Preparation kit from Illumina (PCXT109) or the NEBNext Ultra RNA Library Prep Kit for Illumina (ph RNAi) and subjected to either 50-bp single-end sequencing (PXT109 mutant EDs, ~50 million reads per replicate, two replicates) or 150-bp paired-end sequencing (white UAS-RNAi and polyhomeotic UAS-RNAi, ~40 million reads per replicate, four replicates) on a HiSeq 2000.

Three-dimensional fluorescence in situ hybridization

To generate the DNA probes for 3D FISH in the 
ad locus, genomic DNA of Drosophila was PCR amplified twice using the PCR primers that were designed in (8) and are available in table S9. PCR products were purified using the QIAquick PCR purification kit (QIAGEN, catalog no. 28104), and the probes were labeled with Alexa Fluor 555 and 647 dyes using the FISH Tag DNA Multicolor Kit (Invitrogen Life Technologies, catalog no. MP32951). Then, FISH experiments on ED were conducted as previously described by Bantignies and Cavalli (29). Briefly, ~20 EDs were quickly dissected (<20 min) from wandering larvae and fixed for 20 min at RT using a 4% formaldehyde dilution in PBTr [phosphate-buffered saline (PBS) + 0.1% Tween 20]. EDs were treated with RNase A (200 μg/ml) for 2 hours and permeabilized in PBTr (PBS + 0.3% Triton X-100) for 1 hour at RT. Then, EDs were progressively transferred into a prehybridization mixture [50% formamide, 4× saline–sodium citrate (SSC) buffer, 100 mM NaH2PO4 (pH 7.0), and 0.1% Tween 20], and DNA was denatured for 15 min at 80°C. EDs were subsequently transferred into FISH buffer [50% formamide, 10% dextran sulfate, 2× SSC, and Salmon sperm DNA (0.5 mg/ml)] containing ~30 ng of each DNA FISH fluorescent probe and hybridized for 14 to 20 hours at 37°C while protected from light. The following day, DNA was counterstained with 4′,6-diamidino-2-phenylindole (DAPI), and EDs were washed before being mounted on microscope slides using ProLong Gold antifade reagent (Invitrogen, catalog no. P36930). Images were acquired on a Leica SP8 confocal microscope (63× objective, 59-nm pixel size, 300-nm z-steps), and microscopy pictures were mounted using the Fiji software (30).

Microscopy image analysis

3D FISH analysis was conducted using the “Image Processing Toolbox” in MATLAB (version R2018a). Briefly, the channels were smoothed using 2D Gaussian filters (σ = 3 and 1 for DAPI and FISH channels, respectively) and segmented in 3D; FISH objects that were smaller than 50 voxels or located outside of the segmented DAPI were discarded. Last, 3D distances between the centroids of FISH objects were calculated, and only the mutual nearest neighbors that were closer than 0.8 μm were considered.

For measuring the area of DAPI- and green fluorescent protein (GFP)-positive cells in eye discs, images of individual discs were smoothed using Gaussian filter (σ = 6) and segmented using Otsu’s method. Holes within segmented discs were filled using the imfill function before area measurement. Last, a DAPI mask was applied to the GFP segmentation before calculating the GFP/DAPI overlapping fraction.

Reverse transcription quantitative PCR

Wandering larvae were collected and briefly washed with 70% ethanol. Then, ~30 EDs were quickly dissected (<30 min) on ice in Schneider’s medium, and total RNA was extracted using TRIzol reagent. Total RNA was purified using the RNA clean and concentrator kit from Zymo Research (catalog no. R1015) following the manufacturer’s instructions and using the DNase I from AMBIION (catalog no. AM2222). Purified RNA was quantified on a NanoDrop, and 250 ng of RNA was used for the reverse transcription using the SuperScript III First-Strand Synthesis System kit from Thermo Fisher Scientific (catalog no. 18080051) following the manufacturer’s recommendations. Last, reverse transcription quantitative PCR (RT-qPCR) was performed on a LightCycler480 (Roche). PCR primers are listed in table S9.

Immunostainings

For DAC immunostainings in WT (W1118) and pre-mutant EDs, experiments were systematically performed in parallel. Wandering larvae were collected, and EDs were quickly dissected at RT in 1× PBS before being fixed for 20 min in 4% Formaldehyde. EDs were permeabilized for 1 hour in 1× PBS + 0.5% Triton X-100 and blocked for 1 hour in 3% bovine serum albumin (BSA) PBTr (1× PBS + 0.025% Triton X-100). Then, primary antibodies were added (table S8) in 1% BSA PBTr and incubated O/N at 4°C on a rotating wheel. The following day, discs were washed in PBTr, and secondary antibodies or rhodamine phalloidin was added (table S8) and incubated for 2 hours at RT on a rotating wheel. Then, nuclei were counterstained with DAPI, and EDs were washed in PBTr before being mounted on microscope slides using ProLong Gold antifade reagent (Invitrogen, catalog no. P36930). Last, images were acquired on a Zeiss Axioimager Z2 Apotome Leica SP8 confocal microscope using the same settings for both genotypes, and images were mounted using the Fiji software (30).

Alignment, peak calling, and visualization of ChIP-seq, ATAC-seq, and FAIRE-seq from Drosophila

After initial quality checks of newly generated data using fastqc, paired-end and single-end .fastq files were aligned to the dm6 version of the Drosophila genome using bowtie 2 with default parameters.
[v2.1.0; (31)]. Newly generated and publicly available data used in this study are listed in table S10. Reads with low mapping quality (mapq, <30) were discarded using samtools (32). As a control, ChIP-seq duplicates generated for this study were clustered together on the basis of their Pearson correlation coefficients (fig. 18). Peak calling was performed on each replicate separately and on the merged replicates using MACS2 (v2.1.1.20160309) (33) with the following parameters: -g dm --nomodel --keep-dup 1 --extsize 200. For the visualization and the quantification of ChIP-seq tracks, reads per kilo base per million mapped reads (RPKM)–normalized bigWig binary files were generated using the bamCoverage function from DeepTools2 (v2.5.1) (34) with the following parameters: -o = bigwig --samFlagInclude 128 --ignoreDuplicates -e 200 --normalizeUsingRPKM. Last, replicates were merged using the bigWigMerge and bedGraphToBigWig tools from the University of California, Santa Cruz (35), with default parameters. For the visualization of the tracks, the Integrative Genomics Viewer (36) and the “seqplots” R package (v1.20.0) (37) were used.

**k-Means clustering of PTM ChIP-seq signals around PRC1 peaks in ED**

Highly confident PRC1 peaks in ED were defined as the union of nonoverlapping PH, PC, and PSC peaks that (i) were detected in the two biological replicates with a q value of at least 2 and (ii) had a q value of at least 25 when using merged replicates (see the previous section for the details regarding the peak calling with MACS2). Average ChIP-seq signals were computed around PRC1 peak summits (±2.5 kb) for H3K4me3, H3K4me2, H3K36me3, H3K27Ac, H4K20me1, H3K4me1, H3K27me1, H3K27me3, H2AK118Ub, and H3K27me2 in ED using bwtools (38). Then, ChIP-seq signals were scaled and stratified into seven clusters using the “kmeans” function in R (R version 3.5.1, www.R-project.org). Last, PRC1 enhancer sites from ED that did not overlap with the PRC1 peaks from late embryos (±1 kb) were defined as SSE sites. Heatmaps and average tracks were plotted using the “seqplots” R package (v1.20.0) (37).

**k-Means clustering of PTM ChIP-seq signals around ATAC-seq peaks in ED**

For the clustering of ATAC-seq peaks in ED, only the ATAC-seq peaks with a -log_{10} P value of at least 25 were considered. Then, clustering was performed with the same approach as for the PRC1 peak summits (see previous paragraph). Last, the ATAC-seq peak summits from the “aTSS” and “enhancer” clusters that do not overlap with highly confident PRC1 peak summits (defined in the previous section) ±2.5 kb were used as PRC1-depleted control sets.

**Genome-wide clustering of PTM ChIP-seq signals from ED using SOMs**

SOMs have been previously shown to be a powerful method to identify complex relationships between genomic data (9). This algorithm relies on a machine learning–based process that trains for a given number of iterations to build a model, which is used to produce intuitively readable maps. Average ChIP-seq enrichments were computed genome wide (2.5-kb bins) for H3K4me3, H3K4me2, H3K36me3, H3K27Ac, H4K20me1, H3K4me1, H3K27me1, H3K27me3, H2AK118Ub, and H3K27me2 in ED using bwtools (38). The resulting matrix was scaled and used to train an 80 × 80 toroidal SOM for 100 iterations using the “kohonen” R package (v3.0.7) (39, 40). Then, we overimposed a k-means clustering directly on the SOM nodes using the “kmeans” function in R (R version 3.5.1, www.R-project.org; fig. S2). Last, the maps were plotted using an in-house R script.

**Hi-C analysis from ED or whole Drosophila embryos**

Raw Hi-C sequencing data were processed using the “sHiC2” pipeline (41). Construction of expected models, Hi-C contact scoring, and Hi-C aggregate plots were performed using the “shamran” R package [https://bitbucket.org/tanaylab/shamran, (42)]. Hi-C replicates generated for this study cluster together and show high Pearson correlation coefficients (fig. S18). Moreover, our newly generated Hi-C replicates from whole 16- to 18-hour embryos cluster with the two replicates generated in (8) and show high Pearson correlation coefficients (fig. S18). Therefore, these three replicates were merged to increase the resolution of the maps. Hi-C map visualization, segmented interaction frequencies, and downstream analyses were conducted using in-house R scripts using the “misha” package (https://github.com/msuria/misha-package).

Moreover, to facilitate the visualization of newly generated Hi-C maps, raw sequencing data were processed using the Hi-C–Pro pipeline (version 2.11.1, REF: 26619908) with default parameters and normalized at 2-, 5-, and 10-kb resolutions using the ice_norm flag. Last, the hicpro2juicebox utility was used to convert the allValidPairs output of the pipeline into Juicebox.hic format at fragment resolution. These processed files are available in the GEO database repository.

**Alignment and differential expression analysis of Drosophila RNA-seq**

After initial quality checks of newly generated data using fastqc, paired-end and single-end .fastq files were aligned to the dm6 version (dmel_r6.15 annotation) of the *Drosophila* genome using STAR with default parameters (v2.4.0i) (43). Then, the reads were counted using htseq-count (44), and the differential expression analysis was performed using the “DESeq2” R package (v1.22.1) (45).

**Collection and alignment of ESC and NPC datasets**

Raw ChIP-seq data for RING1B from ESCs and NPCs, H3K4me1, H3K4me3, H3K27Ac, and H3K27me3 from NPCs were collected (table S10) and aligned to the mm10 version of the mouse genome using bowtie 2 with default parameters [v2.1.0; (31)]. For the visualization and the quantification of ChIP-seq signals, RPKM-normalized bigWig binary files were generated with the same method used for *Drosophila* ChIP-seq (see upper sections). H3K4me1, H3K4me3, H3K27Ac, and H3K27me3 ChIP-seq datasets from ESCs, RNA-seq, and Hi-C data from ESCs and NPCs were taken from (46) (table S10).

**k-Means clustering of RING1B peaks from NPCs**

RING1B PRC1 peak coordinates reported in (25) were lifted over to the mm10 version of the mouse genome, and the peaks that were closer than 500 bp have been merged. Average ChIP-seq enrichments for RING1B, H3K4me3, H3K27Ac, H3K4me1, and H3K27me3 from NPCs were computed around RING1B peaks from NPCs (±2.5 kb), mean normalized, and stratified using the kmeans function in R (k = 4).

**Hi-C analysis from ESCs and NPCs**

Hi-C quantification, aggregate plots, and Hi-C maps visualization were generated with the same methods as for *Drosophila* Hi-C (see upper sections).
Gene assignment strategy and Gene Ontology analysis
For each cluster, PRC1 peaks were assigned to overlapping genes. In the case where a peak does not overlap with any gene, it was assigned to the gene corresponding to the closest annotated TSS. To identify and visualize enriched Gene Ontologies [DAVID database, “Biological Process” (BP) ontologies (46)], the “clusterProfiler” R package (47) has been used. For mammalian data, the same methods were used as for Drosophila.

Manipulation of genomic coordinate files
Computations on genomic coordinate files (.bed) were conducted using the “BEDTools” suite (v2.26.0) (48).

SUPPLEMENTARY MATERIALS
Supplementary material for this article is available at http://advances.sciencemag.org/cgi/suppl/2020/6/eaax4001/DC1

REFERENCES AND NOTES

fluorescent in different compositions at different target genes. C. J. R. W.


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