Quantitative *in vivo* analysis of chromatin binding of Polycomb and Trithorax group proteins reveals retention of ASH1 on mitotic chromatin

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**ABSTRACT**

The Polycomb (PcG) and Trithorax (TrxG) group proteins work antagonistically on several hundred developmentally important target genes, giving stable mitotic memory, but also allowing flexibility of gene expression states. How this is achieved in quantitative terms is poorly understood. Here, we present a quantitative kinetic analysis in living *Drosophila* of the PcG proteins Enhancer of Zeste, (E(Z)), Pleiohomeotic (PHO) and Polycomb (PC) and the TrxG protein absent, small or homeotic discs 1 (ASH1). Fluorescence recovery after photobleaching and fluorescence correlation spectroscopy reveal highly dynamic chromatin binding behaviour for all proteins, with exchange occurring within seconds. We show that although the PcG proteins substantially dissociate from mitotic chromatin, ASH1 remains robustly associated with chromatin throughout mitosis. Finally, we show that chromatin binding by ASH1 and PC switches from an antagonistic relationship in interphase, to a cooperative one during mitosis. These results provide quantitative insights into PcG and TrxG chromatin-binding dynamics and have implications for our understanding of the molecular nature of epigenetic memory.

**INTRODUCTION**

The highly conserved Polycomb (PcG) and Trithorax (TrxG) group proteins constitute a gene regulatory system that is essential for maintaining the correct identity of both stem cells and differentiated cells (1,2). The PcG and TrxG proteins share several hundred developmentally important target genes (3–5). These two groups of proteins work antagonistically to maintain a balance between silencing (PcG) and activation (TrxG) of their targets (6). For several target genes, reporter assays have shown that the PcG and TrxG can maintain mitotically heritable stable states of both silent (7,8) and activated gene expression (9–11) depending on the initial transcriptional status of the target gene. Thus, these proteins have the capacity to maintain stable epigenetic memory of transcriptional decisions, in the absence of the initial determining transcription factors. However, this regulatory system also has an inherent flexibility, allowing PcG and TrxG target genes to switch their transcriptional status dynamically on developmental or experimental cues (9,12). The PcG and TrxG proteins function in several large multiprotein complexes, and in *Drosophila*, are recruited to their targets via multiple sequence-specific DNA-binding proteins (13,14). Thus, many chromatin-binding components work together, giving a dynamic balance between stable mitotic propagation of transcriptional states and flexibility of these states to allow developmental transitions.

Live imaging studies have given important insights into the dynamic nature of chromatin binding for some components of this system (15–17). The Polycomb repressive complex 1 (PRC1) contains several proteins, including Polycomb (PC) and Polyhomeotic (PH). In flies, both of these proteins have been shown to bind dynamically to chromatin, with exchange of bound molecules occurring within seconds (17). These studies demonstrate that PRC1 complexes bind chromatin by simple chemical equilibria (15). Given this observation, it has been proposed that developmental transitions in PcG and TrxG regulation may be a matter of quantitative, rather than qualitative change (18). To understand dynamic aspects of regulation by PcG and TrxG proteins, it is crucial to gain quantitative information about their absolute molecule numbers, molar concentrations and kinetic chromatin-binding properties in living animals. We have recently reported a quantitative analysis of these parameters for the PRC1 proteins PC and PH in living *Drosophila* (17). However, for other components of the PcG/TrxG system, such as
PRC2 proteins, DNA-binding proteins and the TrxG proteins, whether they also bind dynamically to chromatin, and whether different proteins have different kinetics, is unknown. Furthermore, quantitative information on molecule numbers and cellular concentrations is lacking. This puts limits on modelling and systems biology approaches aiming at the understanding of Polycomb and Trithorax group proteins as a complex and dynamic system.

To understand PcG and TrxG function, quantitative knowledge of chromatin-binding dynamics is essential not only in interphase but also throughout the cell cycle, where the most important challenges for the propagation of epigenetic memory are at replication and mitosis. Recent studies have shown that some PcG and TrxG proteins can bind to newly replicated chromatin, providing models for propagation of information at the replication fork (19–23). However, the behaviour of these proteins during mitosis is less well studied. Live imaging and immunofluorescence studies have demonstrated substantial dissociation of PRC1 proteins during mitosis (17,24,25). Different immunofluorescence studies of the human TrxG protein MLL have reported dissociation from mitotic chromatin (26) or robust association (27).

We have recently shown by quantitative live imaging that a small fraction of Drosophila PC molecules remains bound to mitotic chromatin in both neuroblasts (NBs) and sensory organ precursor cells (SOPs) (17). Remarkably, this subpopulation of molecules binds mitotic chromatin with up to 300-fold longer residence times than in interphase, indicating that the nature of the PC–chromatin interaction is profoundly altered at mitosis. Importantly, the extent and strength of PC binding to mitotic chromatin is highly cell-type specific, suggesting that regulation of this mitotic association may be important for epigenetic memory and cell identity. A comprehensive understanding of the regulation of mitotic chromatin association requires quantitative analysis of more components of the PcG and TrxG system, in terms of whether and how they bind mitotic chromatin in living animals, and how they interact with each other.

Here, we present a quantitative live imaging analysis of the Drosophila PRC2 protein enhancer of Zeste (E(Z)), the DNA-binding protein Pleiohomeotic (PHO) and the TrxG protein absent, small or homeotic discs 1 (ASH1). These proteins represent several different functions within the PcG/TrxG regulatory system; thus, we envisaged that they may have specific kinetic properties related to their functions. We quantify absolute molecule numbers, cellular concentrations and kinetic chromatin-binding properties of all three proteins in living animals, and we compare them with those of PC. We show that all of the proteins bind remarkably dynamically to interphase chromatin, exchanging like PC, within seconds. We quantify different extents of mitotic dissociation for each protein, with ASH1 showing the most robust and abundant association with metaphase chromatin in several cell types. Finally, we present the surprising finding that although ASH1 limits the residence time of PC on interphase chromatin, it is required for the long residence time of PC in metaphase, indicating a switch from an antagonistic to a cooperative relationship between these two proteins during mitosis. In summary, this study constitutes a quantitative kinetic analysis of key components of an epigenetic system, providing several unexpected insights into their dynamics and interdependence of chromatin binding and the potential molecular nature of mitotic memory.

MATERIALS AND METHODS

Transgenic fly lines expressing EGFP fusion proteins

Generation of PcG/TrxG enhanced green fluorescent protein (EGFP) fusion protein fly lines is described in detail in Supplementary Methods. Constructs, sequences, plasmid maps and fly lines are available on request. For details of fly strains and crosses and ash1 knockdown experiments, see Supplementary Methods.

Quantification of protein expression levels and molecule numbers

Quantification of PC, PHO and ASH1 was performed on nuclear extracts, and quantification of E(Z) expression levels was performed on whole-cell extracts, as described in Supplementary Materials and Methods. Ratios were calculated as described in the legend of Figure 1. Calculation of molecule numbers via virus-like particle (VLP) calibration of EGFP was performed as described previously (17) and as given in the legend of Supplementary Table S1. Calculation of molecule numbers via fluorescence correlation spectroscopy (FCS)-based calibration of EGFP is described under FCS later in the text.

Live imaging

Live imaging of SOP and NB lineages was performed as described previously (17), see also Supplementary Methods. For embryo live imaging, embryos were collected on apple juice–agar plates for 60 min and dechorionated using a 50% solution of household bleach (2.8% hypochlorite) for 2 min. Embryos were lined up on a filter and transferred onto a No. 1.5 coverslip (Menzel) coated with embryo glue (28) and covered with Voltalef 10S oil. Live imaging of PcG/TrxG proteins during embryogenesis was performed at room temperature on a Zeiss Confocal Laser Scanning Microscope LSM780 with a 40×/NA 1.3 oil immersion objective. Z-stacks were recorded every 15 s to generate a time-lapse movie of early nuclear divisions. Image planes of 512 × 512 px were acquired with a zoom of 4.3 resulting in a voxelsize of 100 × 100 x 800 nm. EGFP was excited with an Argon laser at 488 nm [acousto-optical tunable filter (AOTF): PC: 0.5%, E(Z): 1%, ASH1: 2%, PHO: 3%] and detected between 490–578 nm (Gain: PC, E(Z): 650V, ASH1: 700V, PHO: 750V). The pinhole was set to 90 μm. Images were deconvolved using Huygens Core (SVI) with the Classic Maximum Likelihood Estimation (CLME) method and 40 iterations and a theoretical point spread function (PSF). Maximum intensity projections were calculated from the deconvolved z-stacks. To analyse mitotic chromatin attachment, average line
Figure 1. Generation of transgenic EGFP-tagged PcG/TrxG fly lines. (A) Schematic representation of EGFP fusion proteins. Shown are domains according to UNIPROT (light grey), the position of the EGFP tag (dark grey) and the size of the fusion protein in kDa. Proteins are drawn to scale. EGFP::PHO, EGFP::E(Z), EGFP::ASH1, this study; PC::EGFP (25). (B) Transgenes were generated with different promoters as shown. All of the lines shown gave viable homozygous stocks. The table shows whether the fusion protein was visible by fluorescence microscopy in larval salivary glands and embryos, and whether it was able to rescue lethal combinations of mutant alleles as follows: EGFP::PHO expressed under the aTubulin promoter rescued pho1/pho1. (1) flies carrying Actin5c driven EGFP::PHO with appropriate balancers (Supplementary Figure S1) could not be generated, see ‘Materials and Methods’ section. (2) PC::EGFP rescued Pc3/PcXL5 but not Pc3/Pc3 (17,25). EGFP::E(Z) driven by the endogenous or aTubulin promoters rescued E(z)731/E(z)63E11. (3) Rescue was not performed with Actin5c driven EGFP::E(Z), as the aTubulin promoter gave full rescue. EGFP::ASH1 driven by the aTubulin promoter rescued three combinations of alleles: ash110/ash122, ash122/(3L)Exel9011 and ash110/Df(3L)Exel9011. (C) For selected lines, percentage of rescue is calculated for heterozygous (light grey) or homozygous (dark grey) transgenes (Supplementary Figure S1 and ‘Materials and Methods’ section). EGFP::ASH1 rescue is shown for ash122/(3L)Exel9011. Mean and standard deviations of two independent experiments are shown. Numbers of scored flies: 1115 (PHO), 1346 (E(Z)p.Tub), 1115 (E(Z)p.E(z), 235 (ASH1) (ASH1 rescues performed with other allele combinations see Supplementary Figure S1). (D–G) Left: western blot using antibodies against endogenous proteins. Extracts were prepared from 2- to 3-h-old embryo collections. PHO, PC and ASH1: nuclear extracts, E(Z): whole cell extract. ‘WT’ the parental landing site line. ‘Tg’ homozygous transgenic line. Right: quantification of expression levels. Black: (WT): endogenous protein in WT line is set to 1. Grey: levels of the endogenous and EGFP fusion protein in the transgenic line are shown relative to the endogenous protein in WT. Mean and standard error from at least three independent extracts are shown.
profiles were generated by measuring lines (140 px) perpendicular to the mitotic chromatin in nine nuclei per image.

Fluorescence recovery after photobleaching

Fluorescence recovery after photobleaching (FRAP) in SOP and type I NB lineages was performed as described previously (17). In embryos, FRAP experiments were performed similarly to our previous study (17) with the following modifications: FRAP was performed on a Zeiss LSM710 using 40×/NA 1.3 lens and a pinhole of 100 μm. Zoom factor 10 results in images with a pixel size of 42 nm. Images (512 × 75 px) were acquired every 16–25 ms. EGFP was excited with an Argon laser at 488 nm (AOTF: 0.5–1%) and detected between 490–600 nm (Gain: 500–700V). In general, laser intensities were kept as low as possible to minimize unintentional photobleaching. A circular region with a radius of 15 px in the centre of the image was bleached using 2 bleach pulses with 100% of the 488 nm Argon laser. Intensity measurements of the bleached region and a control region for background correction, as well as a control image series without bleach for normalization of unintentional photobleaching, were performed using an in-house developed MATLAB script, which uses the function tiffread.m (29) (code available on request). A reaction–diffusion model (30) was used to extract kinetic parameters from FRAP recovery curves as described in detail previously (17).

Fluorescence correlation spectroscopy

FCS experiments were performed on a Zeiss LSM780 microscope using a 40×/NA 1.3 lens. EGFP was excited using the 488 nm line of an Argon laser with the AOTF set to 0.2% and a pinhole of 1 airy unit. Auto-correlation curves (ACFs) were acquired using the microscope software ZEN from intensity fluctuations measured for 5 s. Multiple measurements per nucleus were averaged to generate an ACF that was then used to extract kinetic parameters in MATLAB using a reaction–diffusion model (31). The FCS measurement volume (V = 0.104 ± 0.042 μm³) was calibrated using FCS measurements of a fluorescein concentration series by measuring concentrations between 5 and 100 nM and determining n from the ACF using Df = 425 μm²/s (32). Extrapolation of molecule numbers in the whole nucleus was done by multiplication of n determined from the ACF with the ratio Vnucleus/VFCS = 2145. The average volume of a nucleus during cycle 12 of embryogenesis (Vnucleus) was determined by measuring volumes of five nuclei in a 3D reconstruction of H2B::red fluorescent protein (RFP)-marked chromatin (Vnucleus = 222.6 ± 7.5 μm³).

RESULTS

EGFP fusions of Polycomb and Trithorax group proteins: tools for live imaging

The PRC1 proteins PC and PH have been shown to bind dynamically to chromatin in embryos (15) and in larval and pupal cells (15,17). To investigate kinetic properties of other PcG and TrxG proteins, we generated transgenic flies carrying EGFP fusions of selected proteins (Figure 1A). We chose the DNA-binding protein PHO, the PRC2 protein E(Z) and the Trithorax group protein ASH1. The PHO protein recruits other PcG proteins to DNA via its sequence-specific DNA-binding activity (33–36). The E(Z) protein is a histone methyltransferase that methylates histone H3 on lysine 27, creating a binding platform for PRC1 (37). ASH1 is a histone methyltransferase that methylates Histone H3 on lysine 36 (38). This modification has been shown to antagonize PRC2-mediated H3K27 methylation (39). ChIP profiling shows co-localization of these proteins with PRC1 proteins at many target sites (3–5). In summary, the selected proteins not only interact with DNA and/or chromatin via different platforms but also interact with each other by distinct mechanisms. Thus, we reasoned that a comparison of their dynamic chromatin-binding properties may be highly informative.

To screen for optimal expression levels for both viability and live imaging, each EGFP fusion was cloned downstream of three different promoters, namely, Actin5C, αTubulin and the presumed endogenous promoter, defined as the region upstream of the gene of interest, extending to the next adjacent annotated gene region (see ‘Materials and Methods’ section). For comparison, the published PC::EGFP transgene, under control of the endogenous PC promoter, was included in the analysis [Figure 1A; (25)]. EGFP::PHO, EGFP::EZ and EGFP::ASH1 transgenes were inserted at the same landing site using ΦC31-mediated site-specific integration (40).

Transgenes were recovered from all injected constructs (Figure 1B). To ascertain their usefulness for live imaging, all transgenic lines were evaluated for their EGFP expression levels in larval salivary glands and embryos, showing that with the exception of EGFP::ASH1 and EGFP::PHO under control of the presumed endogenous promoters, all lines gave a visible EGFP signal (Figure 1B). To determine whether these PHO, E(Z) and ASH1 fusion proteins are functional, as well as visible, each was tested for its ability to rescue lethal combinations of alleles of the respective gene (Figure 1B and C, Supplementary Figure S1 and ‘Materials and Methods’ section). Each of the three fusions was able to rescue lethality, with the extent of rescue depending on the expression strategy used (Figure 1C). The apparent rescue to >100% for E(Z) and ASH1 under the αTubulin promoter arises from underrepresentation of other genotypes in the progeny of the rescue cross (Supplementary Figure S1). This analysis demonstrates that all three of the novel fusion proteins are able to fulfill the functions of their endogenous counterparts.

To determine the expression levels of the fusion proteins in relation to those of the endogenous proteins, we performed quantitative western blots on embryos (Figure 1D–G and Supplementary Figure S2) and in third instar larval brains (Supplementary Figure S3). Quantification of signals revealed that the fusion proteins were expressed at between 0.3- and 4.8-fold compared with the endogenous protein. Each protein
was expressed at similar levels in embryos (Figure 1D–G) and in larval brains (Supplementary Figure S3), and levels were relatively stable throughout embryonic development (Supplementary Figure S2). Interestingly, the presence of the E(Z) transgene under its own promoter led to substantial upregulation of the endogenous E(Z) protein (Figure 1F). Cross-regulation between PC::EGFP and PH::EGFP transgenes has been observed previously, where the presence of the transgene led to downregulation of the endogenous copy [(15,17), this effect is also visible in Figure 1E]. In summary, we have generated three novel transgenic PcG and TrxG fusion proteins that have ideal properties as tools for live imaging: they are expressed at moderate levels in transgenic animals, but nevertheless give sufficient signal for imaging in living tissues.

The TrxG protein ASH1 binds mitotic chromatin in embryos

Early Drosophila embryogenesis provides an ideal system to study mitosis. The nuclei of the syncytial embryo divide 13 times synchronously before cellularization (blastoderm). Divisions occur rapidly within 9–21 min (41) and are characterized by an altered cell cycle with severely shortened G1/G2 phases. Zygotic transcription starts just before blastoderm, and proteins observed before this stage are, therefore, maternally contributed, either as proteins or mRNAs.

To investigate the behaviour of PHO, E(Z) and ASH1 during the cell cycle, and to compare it with that of PC, we performed time-lapse confocal microscopy of preblastoderm mitotic divisions in living transgenic embryos. The αTubulin driven constructs are used in this and all subsequent experiments unless otherwise stated. This analysis revealed characteristic behaviour of each EGFP::fusion protein. EGFP::PHO was undetectable by the onset of prophase, and it did not reappear until the next interphase (Figure 2A), suggesting complete dissociation from mitotic chromatin in early embryos. However, we note that EGFP::PHO showed the lowest EGFP levels of all fusion proteins; thus, we cannot exclude that mitotic binding is present but undetectable. PC::EGFP was detectable in the vicinity of chromatin throughout mitosis, but did not show specific localization to mitotic chromosomes (compare Figures 2B and D). This is consistent with previous observations of mitotic behaviour of PC in embryos (24,25). EGFP::E(Z) was essentially undetectable

![Figure 2. Time-lapse microscopy of PcG/TrxG EGFP fusion proteins during blastoderm embryogenesis. Left: Living blastoderm embryos were imaged using confocal microscopy to visualize expression and localization of PcG/TrxG fusion proteins (A–D) and EGFPnls (E) during cleavage cycles 10–13 of embryogenesis. Shown are individual timepoints corresponding to different cell cycle phases, as indicated. Images are maximum-intensity projections of z-stacks from deconvolved time-lapse experiments. Scale bar represents 10 μm and is the same for all images. Right: averaged line profiles through nine individual nuclei within the maximum-intensity projections at metaphase shown in images (left) were measured. The line was chosen to be perpendicular to the mitotic chromatin plate. The y-axis shows the raw average intensity along the lines.](image-url)
during metaphase and anaphase, suggesting complete disassociation (Figure 2C). Metaphase lasts for 3–5 min, suggesting that degradation and re-synthesis of proteins is unlikely to explain the observed protein re-localization after mitosis. Consistent with this, quantification of EGFP intensities for all fusion proteins in other cell types revealed little or no reduction in protein levels during mitosis (Supplementary Table S1, row B), again arguing against mitotic degradation of specific proteins. Thus, we reason that the dissociation of PcG proteins from chromatin during prophase would lead to the redistribution of the protein throughout the syncytial embryo. In contrast, EGFP::ASH1 showed robust association with chromatin throughout the entire mitotic cycle (Figure 2D). To determine whether mitotic association is a common feature of TrxG proteins, we performed immunofluorescence analysis of the TrxG proteins TRX and OSA, showing that TRX, but not OSA, was detectable on mitotic chromatin (Supplementary Figure S4).

In summary, this analysis shows that although the PcG proteins substantially dissociate from chromatin and re-associate at different times during the mitotic cycle, the TrxG proteins ASH1 and TRX remain associated with chromatin throughout mitosis.

**Quantitative kinetic analysis reveals highly dynamic chromatin-binding behaviour for all proteins**

To determine whether PHO, EZ and ASH1 EGFP fusion proteins show dynamic chromatin binding, we performed quantitative kinetic analysis on preblastoderm embryos and compared the binding kinetics of these three proteins with those of PC::EGFP. We have previously measured interphase kinetics of the same PC::EGFP fusion protein in NBs and SOPs, showing residence times of a few seconds (17). To obtain several independent measures of binding kinetics, we performed and compared both FRAP (Supplementary Figure S5) and FCS (Figure 3 and Supplementary Figures S6 and S7). FCS was performed in preblastoderm embryos, at cleavage cycles 10–13. (A–D) Auto-correlation curves of EGFP::PHO, PC::EGFP, EGFP::E(Z) and EGFP::ASH1. G(τ): auto-correlation; τ: correlation time [s]. All transgenes except PC::EGFP are under aTubulin promoter control. (E) Bound fractions were calculated from mean values of $k_{on}^*$ and $k_{off}$ shown in Supplementary Figure S6 and Supplementary Table S1, as $k_{on}^* / (k_{on}^* + k_{off})$. (F) Residence times were calculated as $1 / k_{off}$. Mean and cumulative standard errors of at least nine nuclei in at least two different embryos are shown.

Figure 3. *In vivo* kinetics of chromatin binding of PcG and TrxG proteins measured by FCS in embryos. FCS was performed in preblastoderm embryos, at cleavage cycles 10–13. (A–D) Auto-correlation curves of EGFP::PHO, PC::EGFP, EGFP::E(Z) and EGFP::ASH1. G(τ): auto-correlation; τ: correlation time [s]. All transgenes except PC::EGFP are under aTubulin promoter control. (E) Bound fractions were calculated from mean values of $k_{on}^*$ and $k_{off}$ shown in Supplementary Figure S6 and Supplementary Table S1, as $k_{on}^* / (k_{on}^* + k_{off})$. (F) Residence times were calculated as $1 / k_{off}$. Mean and cumulative standard errors of at least nine nuclei in at least two different embryos are shown.
These models enable extraction of values for the diffusion coefficient, \( D_f \) the pseudo first order association rate \( k^*_{\text{on}} \) and the dissociation rate \( k_{\text{off}} \). Comparison of different fitting procedures showed contributions of binding to the kinetics of all four proteins (data not shown), and FRAP data showed a contribution of diffusion to the recovery kinetics of the three proteins thus studied (Supplementary Figure S8). Thus, the full model with all three parameters was used for analysis of all data, enabling comparisons both between the techniques and between the different proteins. A full list of kinetic parameters for each protein is given in Supplementary Table S1.

To control for the effects of fusion protein overexpression on kinetic behaviour, we used two strategies. First, we compared the kinetics of EGFP::E(Z) under the control of the \( \alpha \text{Tubulin} \) and \( \text{Actin5C} \) promoters, which gave different levels of EGFP::E(Z) protein. Analysis of parameters extracted from both FRAP and FCS data revealed no significant differences in the values of \( k^*_{\text{on}} \) and \( k_{\text{off}} \); thus, the expression level of EGFP::E(Z) does not detectably affect the inherent kinetic properties of the fusion protein [Supplementary Figures S5G–N and S6, compare E(Z) \( p.\text{Tub} \) and E(Z) \( p.\text{Actin} \)]. Second, we compared the kinetics of EGFP::ASH1 under control of the \( \alpha \text{Tubulin} \) promoter in flies wild-type for endogenous \( \text{ash1} \), to the same transgenic protein in an \( \text{ash1} \) mutant background. Strikingly, the kinetic behaviour of the EGFP::ASH1 protein measured by FRAP was identical in these two genetic backgrounds (Supplementary Figure S5G–N, compare ASH1 and ASH1 rescue), indicating again that the overexpression of protein in the wild-type background has no detectable effect on its kinetic behaviour.

Analysis by FRAP and FCS revealed that all four proteins bind chromatin dynamically (Figure 3 and Supplementary Figure S5). The extracted diffusion coefficients given by FCS and FRAP were in reasonably good agreement with each other, with the exception of EGFP::ASH1, for which a slower diffusion coefficient \( k_{\text{diff}} \) was detected. However, the ratio \( k^*_{\text{on}} \) to \( k_{\text{off}} \) calculated from FRAP data was remarkably similar to that measured for other proteins by FCS (Supplementary Figure S5B, D and F). Thus, the values extracted from FCS and FRAP may be considered as giving upper and lower limits to the true values of \( k^*_{\text{on}} \) and \( k_{\text{off}} \). Importantly, the relationship between \( k^*_{\text{on}} \) and \( k_{\text{off}} \) was stringently constrained (Supplementary Figure S5B, D and F) and was reproducible between the two techniques and between different proteins (Supplementary Figure S7C and D). This is best seen in the calculated bound fractions \[ = \frac{k^*_{\text{on}}(k^*_{\text{on}}+k_{\text{off}})}{(k^*_{\text{on}}+k_{\text{off}})(k^*_{\text{on}}+k_{\text{off}})+k_{\text{off}}}, \] which were identical for FCS and FRAP (Figure 3E and Supplementary Figure S7F).

This analysis showed the highest bound fraction for EGFP::ASH1 of \( \sim50\% \) compared with \( 14\% \) for the other three proteins (Figure 3E and Supplementary Figure S7F). EGFP::ASH1 also showed the longest residence time with both techniques, at \( \sim2\text{-fold longer than} \) PC::EGFP and EGFP::E(Z) (Figure 3F and Supplementary Figure S7E). We have previously measured the kinetics of PC::EGFP by FRAP, using identical fitting procedures to those used here, in larval NBs and pupal SOPs (17). Interestingly, the residence time measured here by FRAP in embryos (Supplementary Figure S5N) was essentially identical to that measured in SOPs previously (17) (embryos 1.27 s, SOPs 1.39 s), but longer than that measured in NBs (0.46 s).

In summary, this quantitative kinetic analysis demonstrates that all four proteins tested show substantial binding to chromatin in early embryos, and that this binding is highly dynamic, with exchange between bound and free proteins occurring within seconds.

**Absolute quantification reveals similar numbers of chromatin-bound molecules for all proteins**

The kinetic analysis described earlier in the text measures relative quantities. Conversion of relative values to absolute numbers gives insights into concentrations of endogenous proteins and numbers of chromatin-bound molecules (17,18). To gain an estimate of absolute numbers of endogenous molecules, we used EGFP calibration in combination with quantitative western blotting (Figures 1D–G and 4). To obtain independent measurements of EGFP numbers, we used two methods of EGFP calibration, namely, imaging of EGFP-containing VLPs (43) and direct measurement of molecule numbers by FCS (Figure 4A and Supplementary Figure S9). Measurements were performed in preblastoderm embryos at syncytial division cycles 10–13. The average calculated numbers of EGFP molecules per nucleus were in excellent agreement between the two techniques, giving only 1.02-, 1.49- and 1.42-fold difference (VLP/FCS) for EGFP::PC, EGFP::E(Z) and EGFP::ASH1, respectively (Figure 4A). Thus, both EGFP calibration methods provide a robust basis for further calculations. We note that calibration by FCS has the advantage that both kinetic analysis and quantification are performed in the same cell. A full list of quantitative measurements for each protein is given in Supplementary Table S1.

EGFP numbers were converted to endogenous molecule numbers in wild-type flies via quantitative western blots as described previously (17) (Figure 1D–G). As a control for
Remarkably, despite a difference of ~10-fold in the EGFP numbers between the two transgenes (Figure 4B), the resulting calculated numbers of wild-type endogenous E(Z) molecules were highly similar, with only 1.42-fold difference $[p.E(z)/p.Tub]$, Figure 4C). This demonstrates that quantification by EGFP calibration and western blotting is robust over a wide range of signal intensities.

Further calculations taking into account the interphase nuclear volume and the chromatin-bound fractions measured by kinetic analysis in embryos estimated the molar concentrations and numbers of chromatin-bound molecules for each endogenous protein (Figure 4D). This analysis revealed that although the estimated concentrations of the different proteins were different by up to 3.75-fold (between 40 and 150 nM), the calculated numbers of chromatin-bound molecules were nevertheless remarkably similar at between 1700 and 4000. Taken together, these results demonstrate that independent calibration techniques give reliable measurement of molecule numbers, revealing highly consistent chromatin-bound quantities of the different proteins, despite their different kinetic characteristics.

ASH1 and PHO bind mitotic chromatin in neuroblasts

The live imaging analysis presented earlier in the text shows that the EGFP::ASH1 protein binds mitotic chromatin in embryos (Figure 2), and kinetic analysis defines quantitative parameters for chromatin binding in interphase (Figure 3). However, because of rapid chromatin movements and the short time of mitosis in preblastoderm embryos, it was not possible to perform kinetic analysis of metaphase chromatin. We have previously shown that larval NB and pupal SOP lineages are amenable to FRAP analysis in metaphase (17), identifying bound molecules that are not readily detectable by image analysis alone. This study reported the surprising finding that a small population of PC::EGFP molecules binds to both NB and SOP chromatin in metaphase with 10- and 300-fold longer residence times, respectively, than in interphase.

To determine whether a fraction of the PHO and E(Z) fusion proteins do indeed bind mitotic chromatin, and to study their kinetic behaviour, we performed live imaging and FRAP in type I NBs at interphase and metaphase (Figure 5, see also Figure 6A). Histone H2A fused to GFP (H2A::GFP) was used to mark chromatin and served as a guide for bleach spot placement on metaphase chromatin. The bound fraction of molecules was calculated as described earlier in the text for embryos, using the values of $k_{on}$ and $k_{off}$ extracted from FRAP data, $[\text{bound fraction} = k_{on}/(k_{on}+k_{off})]$. See Supplementary Table S1 for full listing of parameters and calculations. Analysis of metaphase FRAP data for EGFP::PHO revealed a bound fraction of ~1%, similar to that previously reported for PC::EGFP (Figure 5D and Supplementary Table S1). In contrast, no bound fraction
Figure 5. Quantification of chromatin binding in NB lineage. (A–C) Deconvolved confocal laser scanning images of EGFP::PHO (A), EGFP::E(Z) (B) and EGFP::ASH1 (C) in NB interphase (top row in each panel) and metaphase (bottom row in each panel). (Left) Diagrams identify NB and ganglion mother cells (GMCs) in images. H2A::RFP was used as a marker for chromatin. Merge panels show EGFP in green and H2A::RFP in red. Mask panels show the volumes occupied by EGFP in blue and the volume occupied by H2A::RFP in yellow. All EGFP:: fusion proteins shown were expressed under the βTubulin promoter. (D) Fraction of bound EGFP molecules calculated for PHO, PC and E(Z) using the values of \( k_{\text{on}} \) and \( k_{\text{off}} \) extracted from FRAP data [bound fraction = \( \frac{k_{\text{on}}}{k_{\text{on}} + k_{\text{off}}} \)]. See Supplementary Table S1 for full listing of parameters and calculations. For ASH1, bound fraction was calculated by image analysis, see Supplementary Table S1. (E) Residence times measured by FRAP for EGFP::PHO, (continued)
was detected for EGFP::E(Z), suggesting complete displacement from metaphase chromatin (Figure 5D and Supplementary Table S1). The low level of EGFP::ASH1 expression in NBs did not allow FRAP analysis in these cells. However, analysis of images showed that similarly to embryos, ASH1 was robustly detectable on metaphase chromatin in the NB lineage, representing 43% of the total protein. (Figure 5C and D and Supplementary Table S1).

To determine whether metaphase chromatin binding for EGFP::PHO and EGFP::ASH1 undergoes changes in kinetic properties, we examined residence times in interphase and metaphase. As aforementioned, because of the low level of EGFP::ASH1 in interphase (Figure 5C), it was not possible to perform FRAP on EGFP::ASH1 in NBs. However, kinetic parameters were extracted from FRAP performed in the SOP lineage, in which EGFP::ASH1 also visibly bound mitotic chromatin (Supplementary Figure S10). Neither EGFP::ASH1 nor EGFP::PHO protein showed a significant difference in residence time between interphase and metaphase (Figure 5E), thus the fold increase observed for PC::EGFP seems to be unique for this protein (17). However, the mitotic residence times of both PHO and ASH1 were longer than for PC, indicating that each protein has specific and distinct behaviour.

To calculate the number of endogenous chromatin-bound molecules for each protein in metaphase, we performed VLP-mediated EGFP calibration and quantitative western blotting (Supplementary Figure S3). This analysis indicated that ~600 endogenous ASH1 molecules were bound to metaphase chromatin in NBs, in contrast to 207 for PHO and 347 for PC (17). In SOPs, in which EGFP::ASH1 is more highly expressed, we estimated the number of chromatin-bound ASH1 molecules at ~4000 (Supplementary Table S1), whereas PHO and E(Z) showed essentially identical behaviour as in NBs (data not shown). In summary, this analysis demonstrates that both EGFP::ASH1 and EGFP::PHO bind to mitotic chromatin in the NB lineage, and it indicates that substantially more ASH1 molecules remain bound than PHO or PC.

**ASH1 and PC switch from an antagonistic to a cooperative relationship during mitosis**

We have previously shown that the majority of PC::EGFP dissociates from NB chromatin at the onset of mitosis. Those molecules that do remain bound show 10-fold increase in their residence time (17). Here, we have shown that EGFP::ASH1 binds robustly to mitotic chromatin. PC and ASH1 share many chromatin targets (4), raising the possibility that they may bind mitotic chromatin by related mechanisms. To gain insight into the relationship between PC and ASH1 in interphase and mitosis, we performed RNAi-mediated knockdown of ashl in NBs and analysed the kinetic behaviour of PC::EGFP (Figure 6). PcG genes have been shown to be essential for NB survival (44). To determine whether ash1 is also required for NB integrity, we asked whether ash1 knockdown affects NB survival. ash1 RNAi using the inscutable GAL4 driver, which is expressed in all NBs (45), was lethal. In contrast, limiting ash1 knockdown to only the type II NB lineage (Figure 6A and Supplementary Methods) gave viable flies, enabling examination of NB lineages in third instar larval brains. This analysis showed that the depletion of ash1 led to a pronounced loss of NBs from the type II lineage, demonstrating that, like PcG genes, ash1 is required for NB survival (Figure 6B and C). As RNAi was performed only in specific cell lineages, it was not possible to evaluate the knockdown efficiency in these cells. Instead, the efficiency of ash1 knockdown was evaluated in late embryos using the ubiquitous Actin5C GAL4 driver, showing ~7-fold reduction of ash1 transcript levels on RNAi knockdown (Figure 6D).

To investigate the effects of ash1 knockdown on PC::EGFP kinetics, it was necessary to use transient RNAi expression to enable NB survival. For genetic reasons, it was not possible to achieve this specifically in the type II lineage (see Supplementary Methods). Instead, we performed ash1 RNAi over a limited time window in all third instar larval NBs by transient induction of RNAi using the inscutable GAL4 driver (see Supplementary Methods). Imaging and FRAP analysis was performed in type I NBs (Figure 6A), allowing comparison with previous results obtained from the same cell type ([17]; Figure 5).

Analysis of fluorescence intensity showed that PC::EGFP protein levels themselves were unaffected by ash1 knockdown (Figure 6E and F). PC::EGFP kinetics were analysed by FRAP. Calculation of the fraction of bound PC::EGFP molecules showed only modest changes in interphase and metaphase on ash1 knockdown (Figure 6G and H; see also Supplementary Table S2). Surprisingly, ash1 knockdown had opposite effects on PC::EGFP residence times in interphase and mitosis. In interphase, depletion of ash1 led to a 2.5-fold increase in PC::EGFP residence time, consistent with an antagonistic relationship between the two proteins (Figure 6I). In contrast, in metaphase, ash1 depletion resulted in a substantial decrease of PC::EGFP residence time, of ~3.7-fold (Figure 6J).

This change in residence time reflects a change in the parameter $k_{off}$ (see Figure 6J), whereas the absence of substantial change in bound molecule numbers reflects the fact that both $k_{on}$ and $k_{off}$ change in the knockdown [Bound fraction $= k_{on} / (k_{on} + k_{off})$]. The full set of kinetic parameters and calculations is given in Supplementary Table S2. As both the PC::EGFP protein levels and the numbers of bound molecules were largely...
unaffected by ash1 knockdown (Figure 6E–H), we reason that the differences in residence time reflect inherent properties of the PC::EGFP–chromatin interaction.

In summary, these results demonstrate that ash1 is required for the increase in residence time of PC::EGFP on chromatin on the interphase to metaphase transition and suggest that the two proteins may switch from an antagonistic to a cooperative relationship during mitosis.

DISCUSSION

We have performed a quantitative live imaging analysis of the Drosophila PRC2 protein E(Z), the DNA-binding protein PHO and the TrxG protein ASH1, and compared their properties with those previously described for the PRC1 protein PC. By comparing key components involved in recruitment, activation and silencing, this study gives quantitative insights into dynamic aspects of
PcG and TrxG regulation and the molecular nature of mitotic memory.

In the course of this study, we generated and characterized three novel transgenic PcG and TrxG fusion proteins. All three can substitute for the in vivo function of their endogenous counterparts, are expressed at moderate levels in transgenic animals and give sufficient signal for imaging in living tissues; thus, these transgenes widen the repertoire of tools available for live imaging of PcG and TrxG proteins, which has previously been limited to PC (25) and PH (15). The expression levels of the fusion proteins are in the range of 1- to 5-fold compared with those of their endogenous counterparts. These levels of overexpression do not interfere with the physiological function of the proteins, and we did not observe any aberrant phenotypes in flies expressing the fusion proteins. In contrast, although heterozygous mutants in Pcg and trxG genes are viable, they do show homeotic phenotypes (46). Together these observations suggest that the PcG and TrxG system is more sensitive to a reduction in protein levels than to an increase. However, there may be effects of the additional protein copies that are not readily detectable in terms of viability or phenotype.

Using these novel fusion proteins, we show that all of the proteins studied show highly dynamic chromatin binding, exchanging within seconds. We show that analysis of kinetics by FRAP and FCS shows excellent agreement in terms of the relative differences between proteins (Supplementary Figure S7E and F), which are the quantities of interest here. Chromatin-binding kinetics determined with fusion proteins expressed at different levels or in a mutant background (Supplementary Figure S5G, I, M and N) result in similar estimates, indicating that kinetic parameters are not influenced by the expression level of the fusion protein; thus, we reason that the kinetic measurements reported here are relevant to the wild-type situation in which lower levels of protein are present.

We have also performed absolute quantification of molecule numbers, giving estimates of cellular concentrations and chromatin-bound numbers in both interphase and mitosis, of both transgenic and endogenous molecules. Measurements of the numbers of EGFP fusion proteins showed excellent agreement between different techniques (Figure 4A). Estimations of endogenous molecule numbers, based on the ratio of fusion protein to endogenous protein determined from cell extracts, also showed good agreement between calculations based on different expression strategies (Figure 4B and C). Thus, we reason that we have obtained robust estimates for the total amount of endogenous protein per cell. This analysis revealed that the endogenous PcG and TrxG proteins are present in embryonic nuclei at around 150 nM (Figure 4D) and increase to between 200 and 400 nM in NBs (Supplementary Table S1). Knowledge of intracellular concentrations of these molecules is an essential step towards quantitative models of their function and places important constraints on the required affinity and abundance of binding sites for a productive interaction by mass action kinetics (18).

We used these measures of total molecule numbers in combination with bound fractions extracted from FRAP and FCS, to estimate numbers of endogenous chromatin-bound molecules (Figure 4D). These estimates have the limitation that they are based on the assumption that the bound fraction of fusion protein faithfully reflects the bound fraction of endogenous molecules. The fact that different expression levels of EGFPLASH1 and EGFPLASH1:E(Z) did not significantly affect the bound fraction of transgenic molecules, (Supplementary Figures S5M and S6) suggests that this may indeed be the case for these proteins. However, as there is currently no method to directly test whether endogenous molecules are differently distributed between bound and free fractions than the GFP:fusion proteins, this remains a caveat. We note that potential uncertainty of the endogenous bound fraction will affect second order kinetic processes (on rates), but first order processes (off rates and, therefore, residence times) will be unaffected.

Despite these potential limitations, the comparison of different proteins yields valuable insights. For example, in early preblastoderm (2–3 h) embryos, we detected a robust fraction of chromatin-bound molecules for all four proteins (between 1700 and 4000 endogenous bound molecules, Figure 4D). This is consistent with ChIP-based observations of PcG and TrxG binding to Hox genes in the first 5 h of embryogenesis (47) and suggests early regulatory roles for the PcG and TrxG proteins. The residence times of all proteins were several seconds or less. This is comparable with residence times measured by similar methods for transcription factors and remodelers, but substantially shorter than those for promoter-bound and initiating polymerase II, [reviewed in (18)], raising questions about how the PcG and TrxG proteins interact in quantitative terms, in real-time, with the transcription machinery. Using the quantitative measurements of kinetic properties and molecular quantities presented here and elsewhere (18), it should be feasible in future to generate accurate mathematical models to address these issues.

The quantitative analysis presented here reveals not only similarities but also clear differences between the proteins that may be important for their distinct functions. For example, the DNA-binding protein PHO has up to 10-fold longer residence times than either PC or E(Z) in both embryos and NBs (Figure 3F and 5E). PHO has been shown to directly recruit complexes containing both E(Z) (35) and PC (34); thus, the longer residence time of PHO may reflect a more stable binding platform, which is ‘visited’ dynamically by the other PcG proteins. Like PC, the majority of chromatin-bound PHO molecules dissociate from mitotic chromatin, but several hundred molecules remain bound (Figures 5F and 7A). In contrast to PC, we did not observe a significant increase in the residence time of this bound population of PHO molecules. However, the mitotic residence time of PHO was still longer than for PC, again suggesting that PHO may provide a relatively stable binding platform for PC during mitosis, and that it may not change its mode of binding to chromatin on the interphase–metaphase transition. However, it will be important in future to determine whether PHO does indeed bind the same sites in
interphase and mitosis, and whether it is required for anchoring PC to its binding sites during mitosis (34), or whether the increased residence time of PC reflects binding to chromatin via a different molecular interaction. Recent ChIP analysis of the PRC1 protein PSC shows that it binds to different sites on mitotic chromatin in interphase and mitosis (48). Similar analysis for PC and PHO may bring light to the interdependence of these proteins for mitotic binding. Surprisingly, RNAi knockdown of \textit{pho} in NBs had no detectable effect on the kinetics of PC-ASH1 interaction (\textit{ash1} knockdown experiments indicate an antagonistic or competitive relationship between ASH1 and PC for chromatin binding in interphase, which switches to a cooperative one in metaphase. See ‘Discussion’ section for details.

In contrast to PHO and PC, the E(Z) protein showed complete dissociation from mitotic chromatin (Figure 7A). Imaging of embryos (Figure 2C), SOPs (data not shown) and NBs (Figure 5B) showed no detectable bound protein. This result was confirmed by FRAP analysis of EGFP::E(Z) in metaphase NBs (Figure 5D). The complete dissociation of E(Z) from mitotic chromatin demonstrates that the physical presence of E(Z) is not required in mitosis for the binding of PC. It has been proposed that E(Z) is required for PC binding, by methylating lysine 27 of Histone H3 (H3K27me3), creating a binding platform for the PC chromodomain [for review see (37)]. It is possible that the E(Z)-independent binding of PC that we observe in metaphase is mediated by anchorage to H3K27me3 tails that persist through mitosis. However, we have recently shown that in both NBs and SOPs, there is a robust accumulation of H3S28 phosphorylation adjacent to sites of H3K27me3 at the onset of mitosis, which would preclude PC binding to H3K27me3 (17). This, in combination with the increased residence time of PC in mitosis, suggests that mitotic binding of PC is E(Z) and H3K27me3 independent, consistent with several reports of alternative mechanisms of PC binding to chromatin in vivo and at other cell cycle stages (20, 22, 23, 34).

Surprisingly, the TrxG protein ASH1 showed the longest residence time of all proteins measured (Figure 3F and Supplementary Figures S5N and S7E). ASH1 has been shown genetically to act as an ‘anti-repressor’ to PcG action (6). Our results suggest that ASH1 may fulfil its functions not only by modifying the chromatin template (38) but also by its physical presence on chromatin. The behaviour of ASH1 in mitosis was strikingly different to that of the other proteins. In all cell types studied, EGFP::ASH1 was robustly and visibly bound to mitotic chromatin (Figures 2D, 5C and 7A and Supplementary Figure S10). Quantification by FRAP, FCS and direct image analysis indicates that although 51–62% of EGFP::ASH1 molecules are bound in interphase, between 36 and 51% of total molecules remain bound in metaphase (Supplementary Table S1). Indeed, we estimate that the fraction of bound ASH1 is reduced by no more than ∼30% in any cell type, in strong contrast to the reduction in bound fraction of 92–100% observed for PHO, PC and E(Z) (Supplementary Table S1). The lower bound fraction of PcG proteins during mitosis suggests a role of mitotic chromatin retention of ASH1 for maintenance of active gene expression states. Such a role is consistent with models in which silencing is the default state (14), and genes that need to be reactivated are ‘bookmarked’. The human TrxG protein MLL has been shown to bind mitotic chromatin in HeLa cells, whereas the ASH1 protein is evicted (27). The authors propose that mitotic bookmarking by MLL may facilitate inheritance of active gene expression states during cell division. Our results suggest that ASH1 may play an analogous role in \textit{Drosophila}. Because of the complexity of TRX regulation, we were not able to address the TRX protein by live imaging. The transcript is alternatively spliced, and the protein itself is cleaved to N- and C-terminal parts, which have different, although incompletely characterized roles in gene regulation (4). However, TRX was detectable on mitotic chromatin by immunofluorescence staining; thus, in \textit{Drosophila}, ASH1 and TRX may both be required for the mitotic memory of active states.

The fact that both PcG and TrxG proteins remain bound to mitotic chromatin, albeit to different extents (Figure 7A), is intriguing in light of a recent study reporting that both PcG and TrxG proteins, but not modified histones, remain associated with newly replicated chromatin in \textit{Drosophila} embryos (22). Furthermore, the PRC1 protein PSC has recently been shown to be lost from PcG targets during mitosis but to be retained on a subset of sites that the authors propose may be important for
re-establishment of binding sites after mitosis (48). In light of these and our own findings, we propose that the ‘default silencing’ model may be an oversimplification, and that both TrxG and PcG proteins may be retained at specific sites both during replication and mitosis. It will be essential in future to determine whether these targets are different in different cell types.

By taking advantage of the genetic tools available in Drosophila, we have addressed interactions between different proteins, using cell-type-specific RNAi of one protein in combination with kinetic analysis of another. Surprisingly, knockdown of ash1 in NBs had opposite effects on PC chromatin-binding kinetics in interphase and in metaphase, consistent with a switch in the functional relationship between ASH1 and PC during mitosis. These effects may be indirect, caused by loss of activation of ASH1 targets that are required to regulate PC binding. However, as ASH1 and PC share many chromatin targets (4), it is also likely that the effects of ash1 knockdown on PC kinetics involve direct molecular interactions between the two proteins and the chromatin template (Figure 7B).

In interphase, depletion of ash1 led to an increase in PC residence time on chromatin, suggesting an antagonistic relationship between the two proteins, consistent with genetic studies (6). The two proteins may compete directly for the same binding sites, for example, by competition for access to histones, to DNA or to DNA-binding proteins (Figure 7B). Interestingly, PHO has been shown to bind through different domains both to PC and to the BRM (Brahma) remodelling complex (34). It would be of great interest in future to determine whether PHO also binds ASH1. Alternatively, ASH1 may antagonize PC binding by modifying the chromatin template. ASH1 methylates Histone H3 on lysine 36 (38), which has been shown to antagonize PRC2-mediated H3K27 methylation (39). Thus, loss of ASH1 may lead to an increase in H3K27 methylation, which could lead to an increase in global PC-binding stability, reflected in a longer residence time.

The antagonistic relationship between ASH1 and PC that we observe for interphase chromatin binding is not surprising, given their opposite roles in activation and silencing. In contrast, for mitotic chromatin binding, ash1 knockdown led to a decrease in PC residence time, indicating that the relationship between the two proteins switches from antagonistic to cooperative during mitosis (Figure 7B). Thus, the time for which PC is retained on mitotic chromatin depends on ASH1. This dependence may reflect a direct interaction between ASH1 and PC, for example, mediated by post-translational modifications of one or both proteins at mitosis, such that their affinity for each other increases (50). Alternatively, we envisage that the robust binding of ASH1 to mitotic chromatin may modify the template in such a way that binding sites for PC become available. In addition to histone templates, these sites may also include single-stranded DNA and non-coding RNAs [reviewed in (14)]. Finally, several histone-modifying enzymes have been shown to have additional non-histone targets (51,52), and ASH1 may be no exception. Thus, ASH1 may modify PC itself, in a cell cycle-specific manner, thereby altering its chromatin-binding properties. The molecular mechanisms by which ASH1 interacts with mitotic chromatin and influences PC will be key questions for future studies.

In summary, these findings suggest that mitotic memory of transcriptional states may involve active cooperation between PcG and TrxG proteins throughout the critical time window of mitosis. Why might such cooperativity be required? Correct maintenance of transcriptional states in interphase requires the dynamic and antagonistic interaction of both the PcG and TrxG proteins, ensuring flexibility of the system (53). However, during mitosis, transcriptional activity is globally shut down (54) (Figure 7A); thus, the PcG and TrxG are no longer required for transcriptional regulation. We envisage that it may be essential to maintain both the PcG and TrxG proteins on their chromatin target sites during mitosis to ensure their concerted presence at the next interphase. The requirement for both to be present may be met by cooperative binding to mitotic chromatin.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online: Supplementary Tables 1 and 2, Supplementary Figures 1–10, Supplementary Methods and Supplementary References [55–64].

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