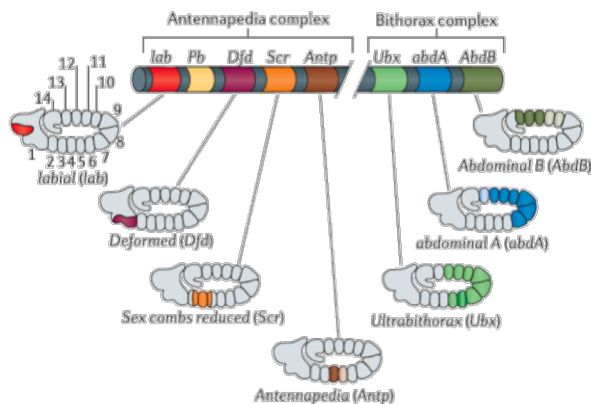
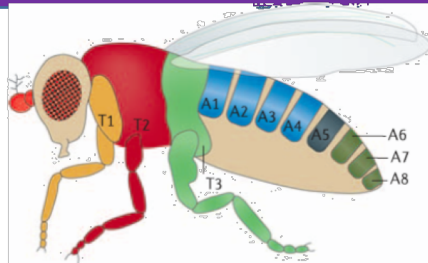


**Post-transcriptional gene regulation by  
Polycomb and Trithorax group genes**

## Polycomb group genes were first defined in *Drosophila melanogaster*

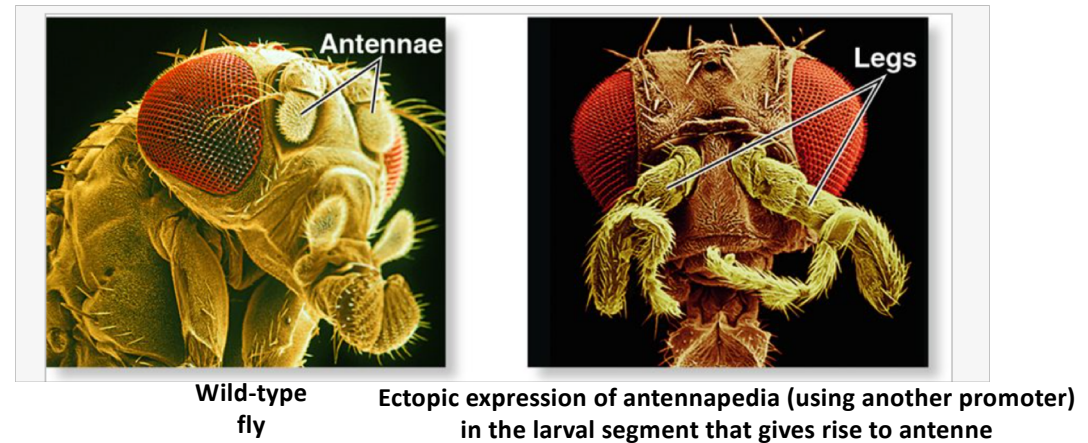


### Body patterning in *D. melanogaster* is controlled by Hox genes

Antennapedia and Bithorax complexes are gene clusters that encode a series of homeotic genes

Hox genes show body segment specific gene expression and are essential to define the gene expression patterns of each body segment

- Expression is specific in the larvae but also
- in the body segment that has been developed from the larval segment

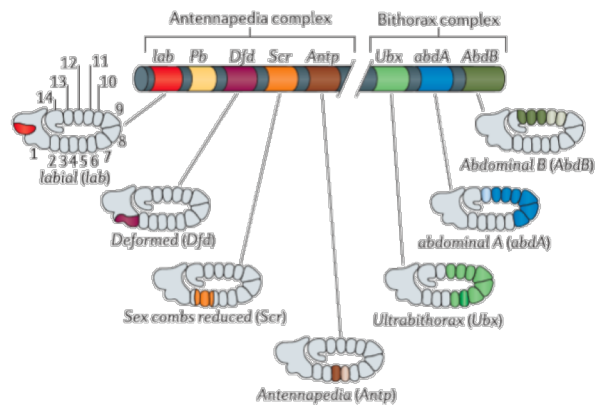
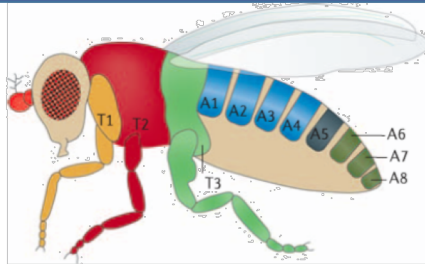


Colinearity – posterior/anterior gene arrangement corresponds with posterior/anterior gene expression (conserved in vertebrates – Hox gene cluster)

Polycomb silencers control cell fate, development and cancer

**Homeotic transformation: a normal body part is replaced by a body part which is regularly found in other regions.**

## Polycomb group genes were first defined in *Drosophila melanogaster*



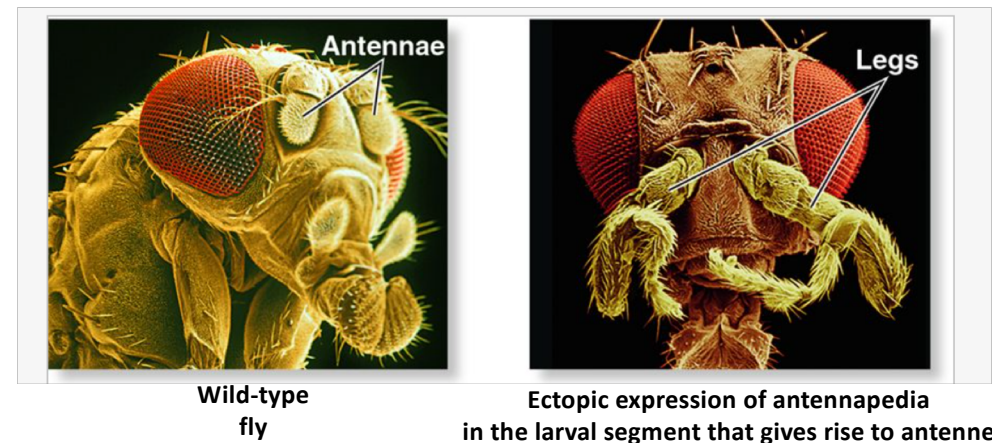
Colinearity – posterior/anterior gene arrangement corresponds with posterior/anterior gene expression (conserved in vertebrates – Hox gene cluster)

Polycomb silencers control cell fate, development and cancer

Antennapedia activates the “leg” gene expression program in the antennae

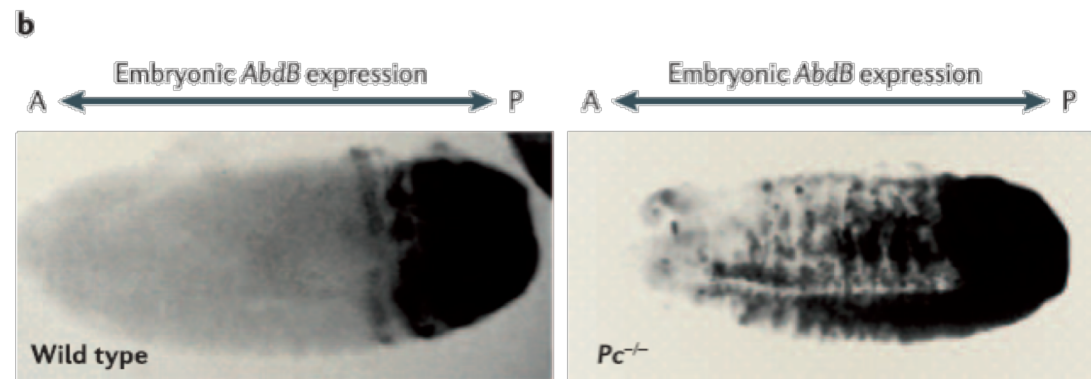
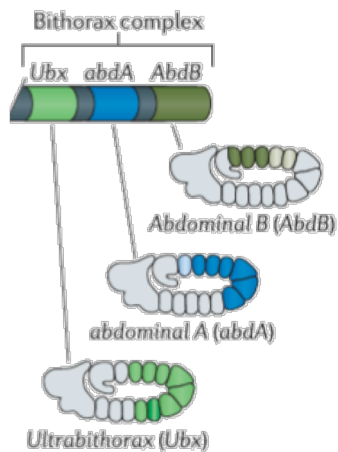
**HOWEVER:**

Other fly mutations were isolated that did not impact on Antennapedia or Bithorax complexes but caused homeotic transformations!!!



**Homeotic transformation: a normal body part is replaced by a body part which is regularly found in other regions.**

## Mutations in Pc (Polycomb) and other related genes results in aberrant expression of abdominal B in larvae

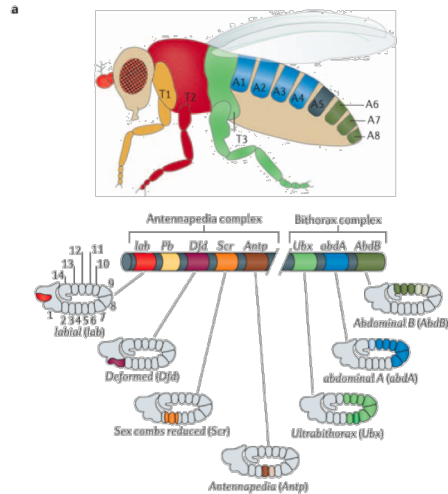


Polycomb (Pc) is required to limit the gene expression of Hox genes to the relevant larval segment

- Pc does represses Hox genes in segments where respective Hox gene should not activate its respective gene expression program
- Pc is not the only gene that has this function: several gene exist: **POLYCOMB GROUP GENES (PcG)**
- **IMPORTANT: Pc mutations can recapitulate a gain of function phenotype of a Hox gene**

Polycomb silencers control cell fate, development and cancer

## PcG mutations can recapitulate a gain of function phenotype of a Hox gene



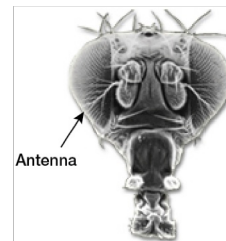
Wild-type fly



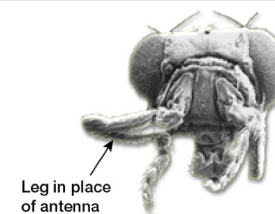
Ectopic expression of antennapedia in the larval segment that gives rise to antennae

### Polycomb mutants recapitulate Hox gene mutations

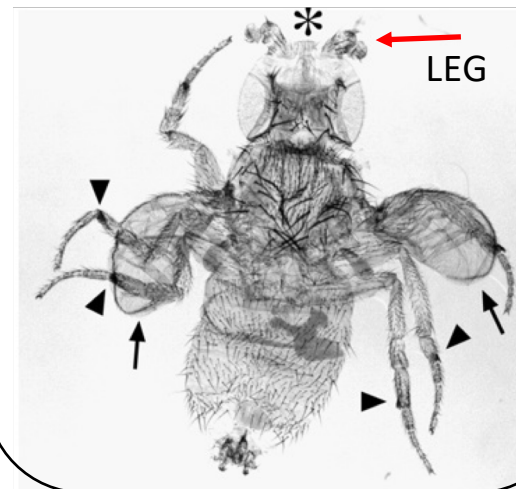
Wild type



Mutation in Antennapedia gene



Su(z)12 mutant (polycomb group gene) with antennapedia phenotype



**Important:**

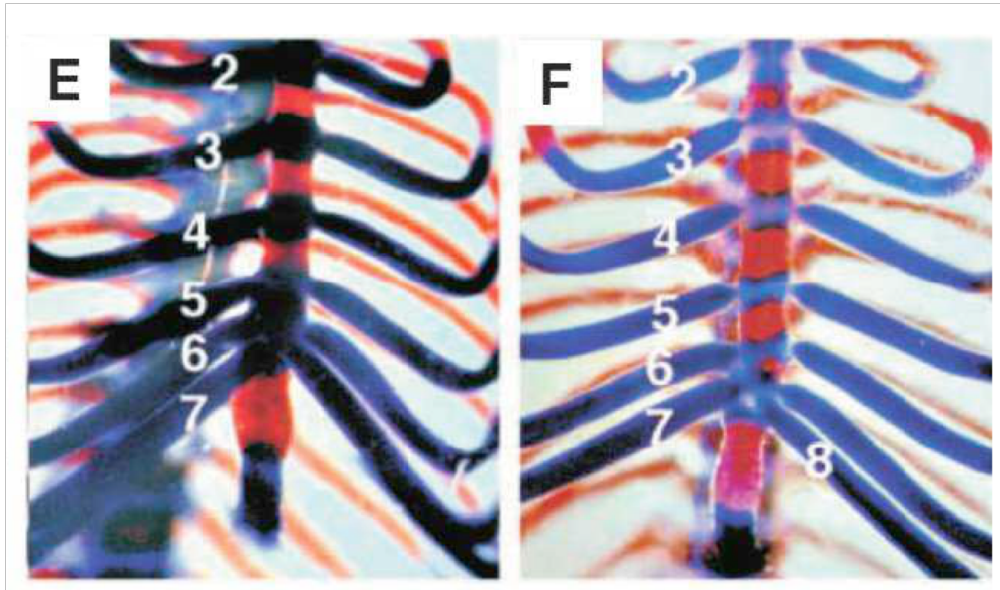
**PcG phenotypes are complex, several body segments can be affected.**

**→ PcG group proteins regulate many genes and maintain gene expression programs**

**PcG group genes are key regulators of gene expression that repress silence genes on the epigenetic level**

**Polycomb group genes are highly conserved!**

## Polycomb group genes are conserved regulators of development



**Homeotic transformation of vertebrae:  
Ring 1A<sup>-/-</sup> mice (PcG gene)**

8 instead of 7 vertebrae

Polycomb group genes are key regulators of

- Development
- Disease

## Polycomb group genes are conserved in evolution

DNA binding

Polycomb repressive complex 2 (PRC2)

Polycomb repressive complex 1 (PRC1)

<i>Drosophila melanogaster</i>			<i>Mus musculus</i>	<i>Arabidopsis thaliana</i>	<i>Caenorhabditis elegans</i>
<b>PcG DNA binding proteins</b>					
PHO	Pleiohomeotic	Zinc finger	YY1		
PHOL	Pleiohomeotic-like	Zinc finger			
PSQ	Pipsqueak	BTB-POZ domain			
DSP1	Dorsal switch protein 1	HMG domain protein	HMGB2		
<b>PRC2 core proteins</b>					
ESC	Extra sex combs	WD 40 repeats	EED	FIE	MES-6
E(Z)	Enhancer of zeste	SET domain	EZH1/ENX2 EZH2/ENX1	CLF MEA SWN	MES-2
SU(Z)12	Suppressor of zeste 12	Zinc finger VEFS box	SU(Z)12	FIS2 VRN2 EMF2	
p55	p55	Histone-binding domain	RBAP48 RBAP46	MSI1 (MSI2/3/4/5)	
<b>PRC1 core proteins</b>					
PC	Polycomb	Chromodomain	CBX2/M33 CBX4/MPC2 CBX6 CBX7 CBX8/MPC3		
PH	Polyhomeotic	Zinc finger SAM/SPM domain	EDR1/MPH1/RAE28 EDR2/MPH2 (EDR3)		SOP-2
PSC	Posterior sex combs	Zinc finger HTH domain	BMI1 MEL18/RNF110/ZFP144	AtBMI1A AtBMI1B AtBMI1C	MIG-32
SCE/dRING	Sex combs extra/dRing	RING zinc finger	RING1/RING1A RNF2/RING1B	AtRING1A AtRING1B	SPAT-3

Epigenetic writers

PcG mutations can recapitulate a gain of function phenotype of a Hox gene

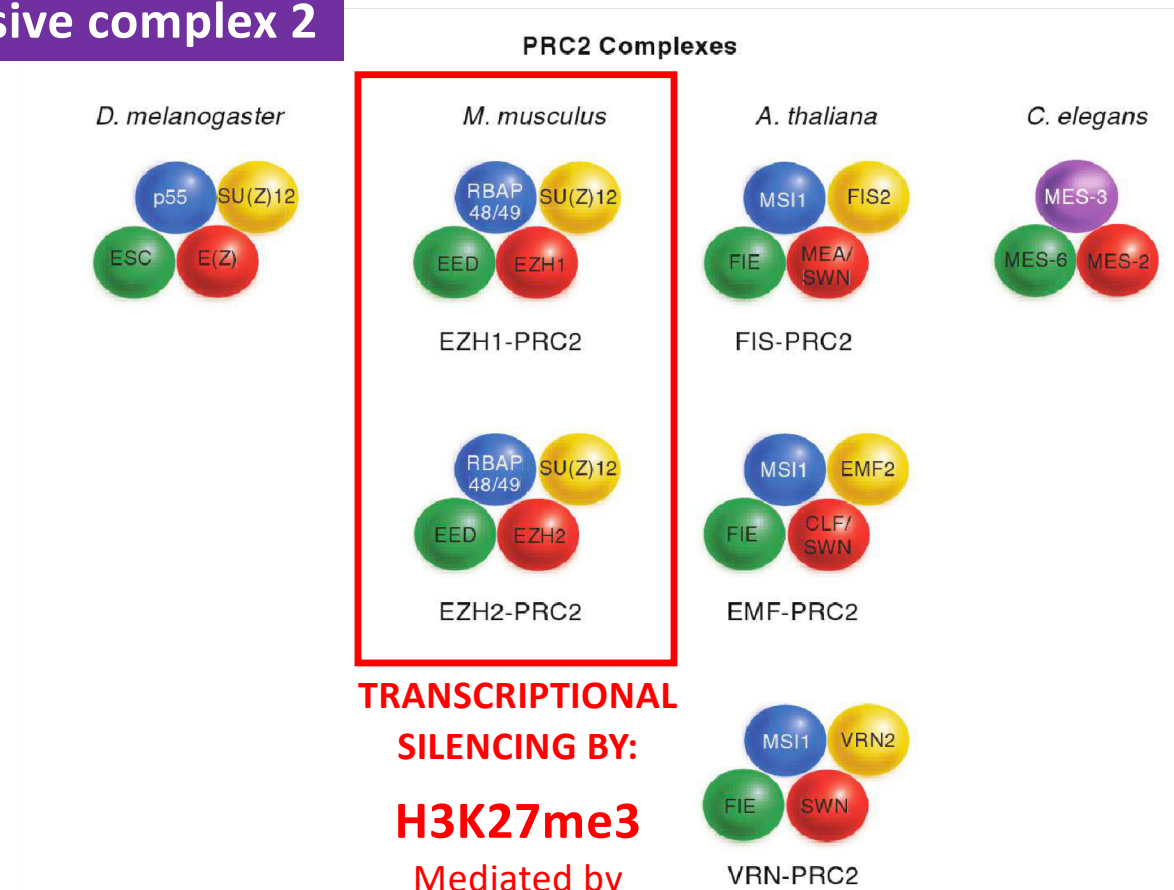
*PcG loss of function gives complex phenotypes, many PcG genes have been discovered in mutational screens*

*→ might function as complex?*

***HOW CAN I PURIFY THE POLYCOMB PROTEIN IN A COMPLEX??***

## Polycomb complexes induce histone modifications

### PRC2 – Polycomb repressive complex 2



**TRANSCRIPTIONAL  
SILENCING BY:**

**H3K27me3**

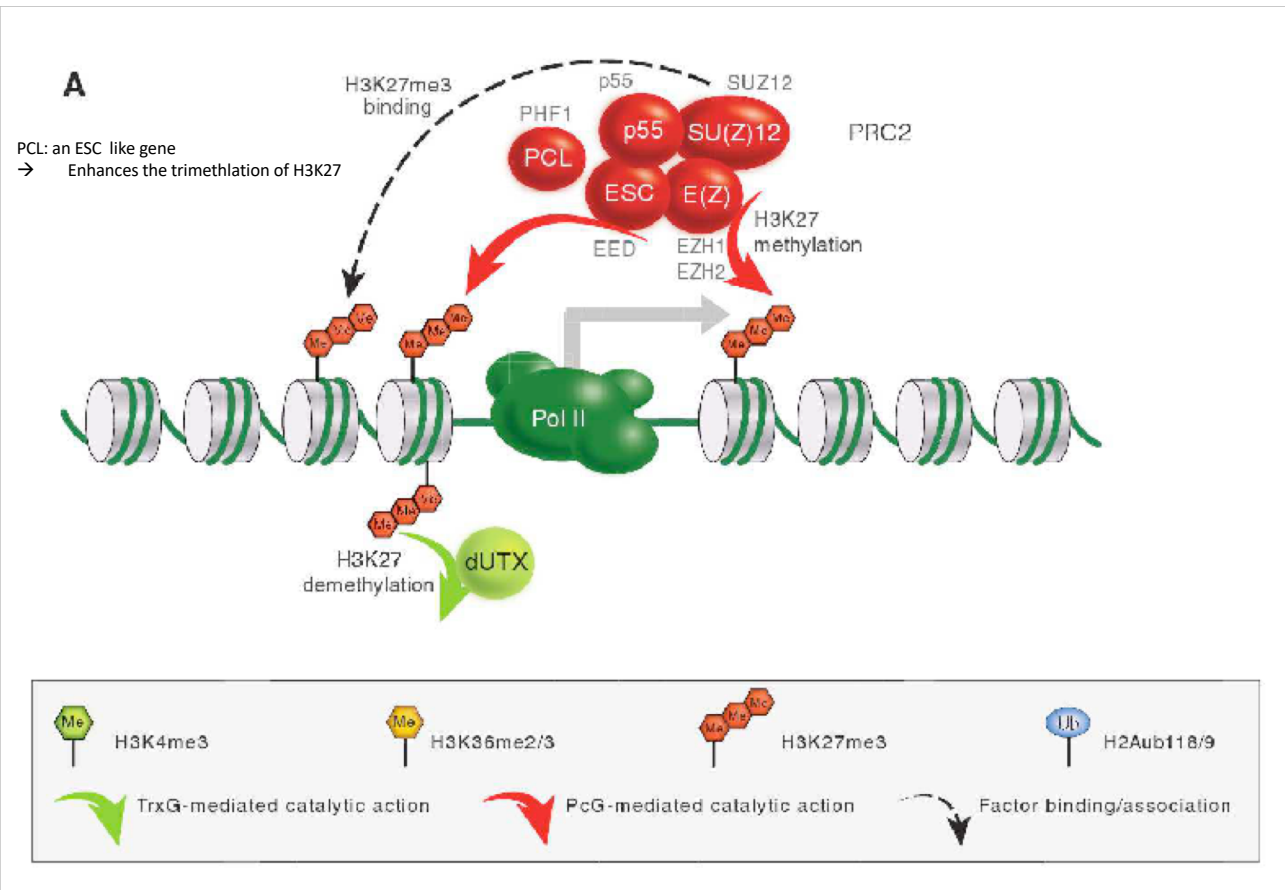
Mediated by

**EZH1** or **EZH2**

(EZH2 is more

important; EZH1 has rather low expression)

## PRC2 – Polycomb repressive complex 2



PRC2 imposes H3K27me3, however the direct structural impact of H3K27me3 on chromatin structure is not known.

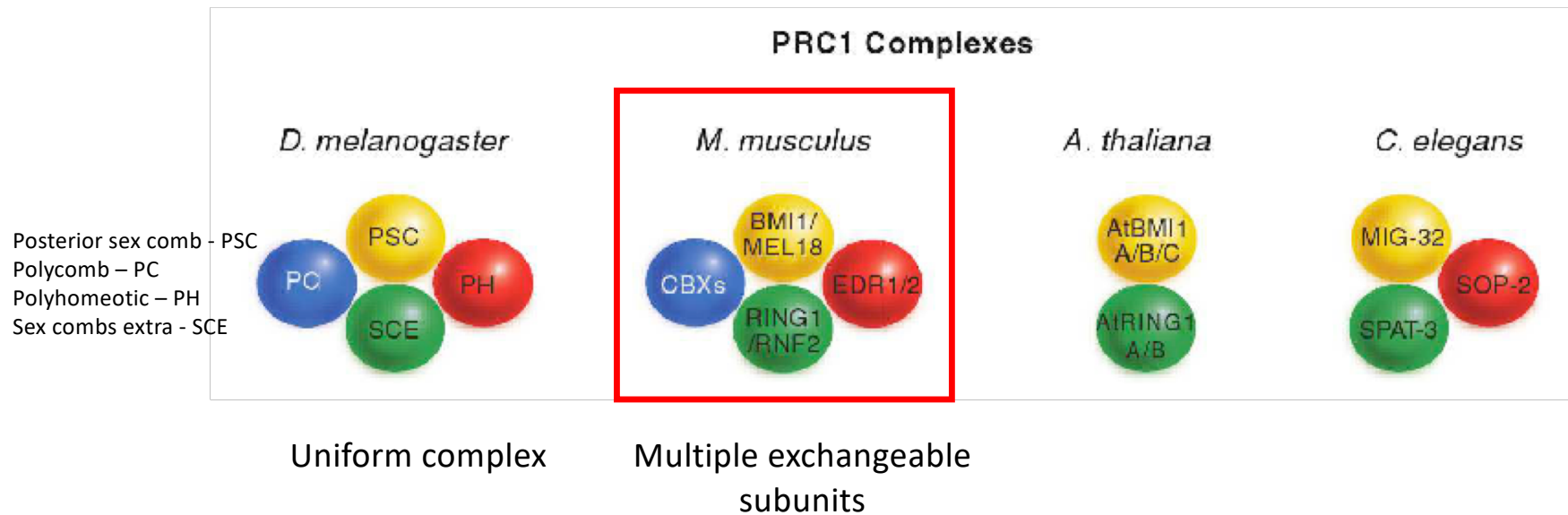
H3K27me3 form a platform for binding of EED → entire PRC2 complex is stabilized → EZH induces more H3K27me3 → **self reinforcing loop**.  
→ Heredity of gene silencing

→ H3K27me3 is also a binding platform for PRC1 complex

UTX is a de-methylase of the TRITHORAX group

→ **Antagonism Polycomb - Trithorax**

## Polycomb complexes induce histone modifications



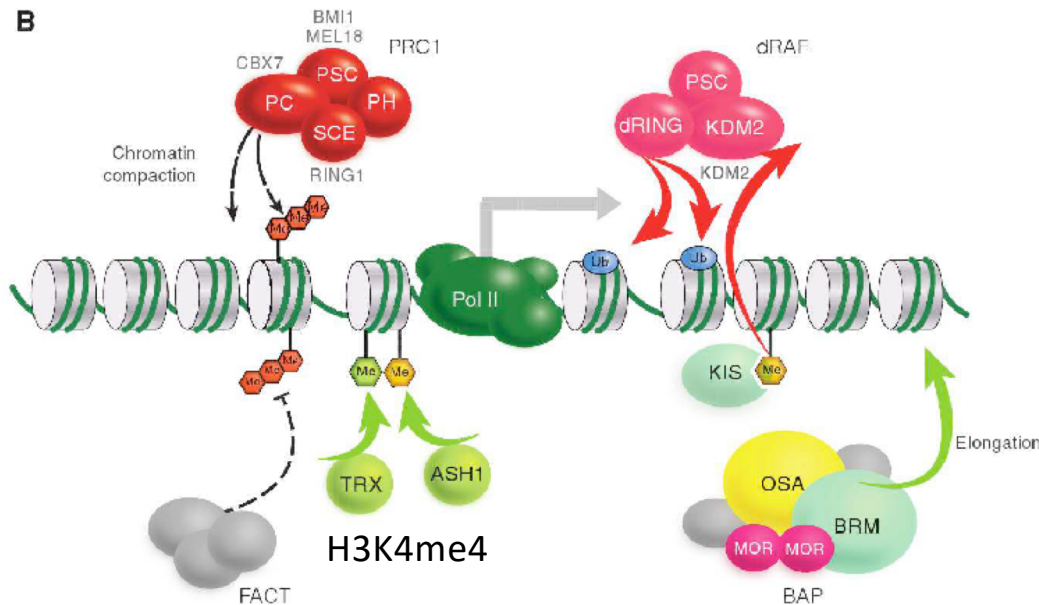
**Heterogeneity of PRC1 complex components**

**TRANSCRIPTIONAL  
SILENCING “MEASURABLE” BY:**

**ubH2AK119 and ubH2AK118**

**Mediated by  
Ring1a/Ring1b Ubiquitin ligases**

## PRC1 – Polycomb repressive complex 1



**Figure 5.** Schematic representation of the core PcG and TrxG protein complexes and their functions at promoters. *Drosophila* PcG proteins are depicted as red ovals with selected mammalian orthologs indicated in gray text. (A) Components and function of the PRC2 and counteracting activities of TrxG proteins (light green). (B) Components and functions of PRC1 and dRING-associated factor (dRAF) and the counteracting activities of the BAP SWI/SNF, facilitates chromatin transcription (FACT) remodeling complexes, and SET-domain histone KMTs TRX and ASH1. The TrxG protein Kismet-L is a member of the chromatin-helicase-DNA-binding (CHD) sub-family of chromatin-remodeling factors, stimulating elongation of Pol II. (Adapted from [Enderle 2011](#).)

The FACT complex has been shown to destabilize the interaction between the H2A/H2B dimer and the H3/H4 tetramer of the nucleosome, thus reorganizing the structure of the nucleosome. In this way, the FACT complex may play a role in DNA replication and other processes that traverse the chromatin, as well as in transcription elongation.

### PRC1 is recruited by H3K27me3

→ PRC1 restricts access of RNA Pol II and SNI/SNF chromatin remodeling complexes → impede gene activation.

### Role of ubH2A118/119:

- Inhibit the recruitment of the FACT chromatin remodeling complex

### The PSC/dRING containing dRAF complex

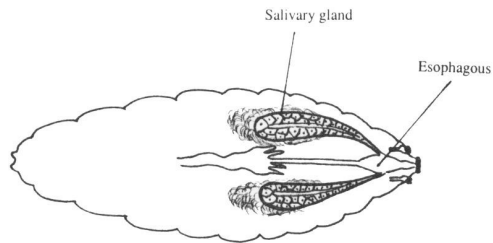
dRAF complex contains PRC1 proteins and the KDM2 jumonji domain protein

- dRING makes ubH2AK118/119  
- KDM2 demethylates H3K36me; Kismet-L loosens access

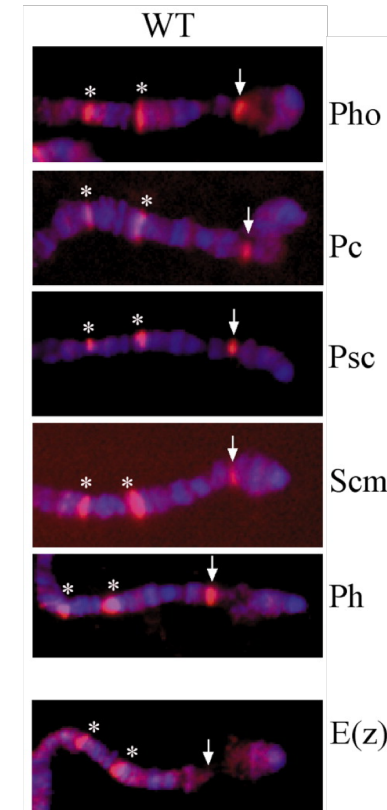
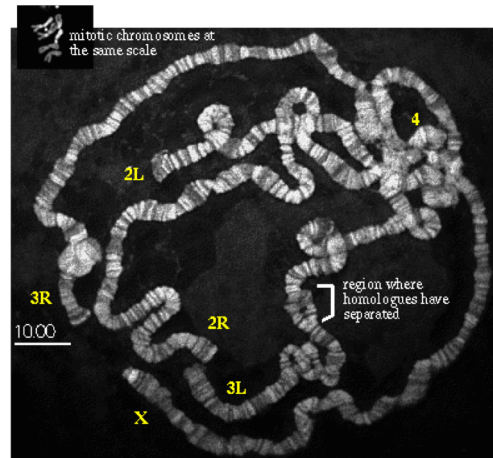
### → Antagonism Polycomb – Trithorax

TRX and ASH1 place active methylation marks; Kismet-L binds active methylation mark and stimulates transcriptional elongation

# PRC2 and PRC1 gene silencing is highly relevant for gene expression on the entire genome level

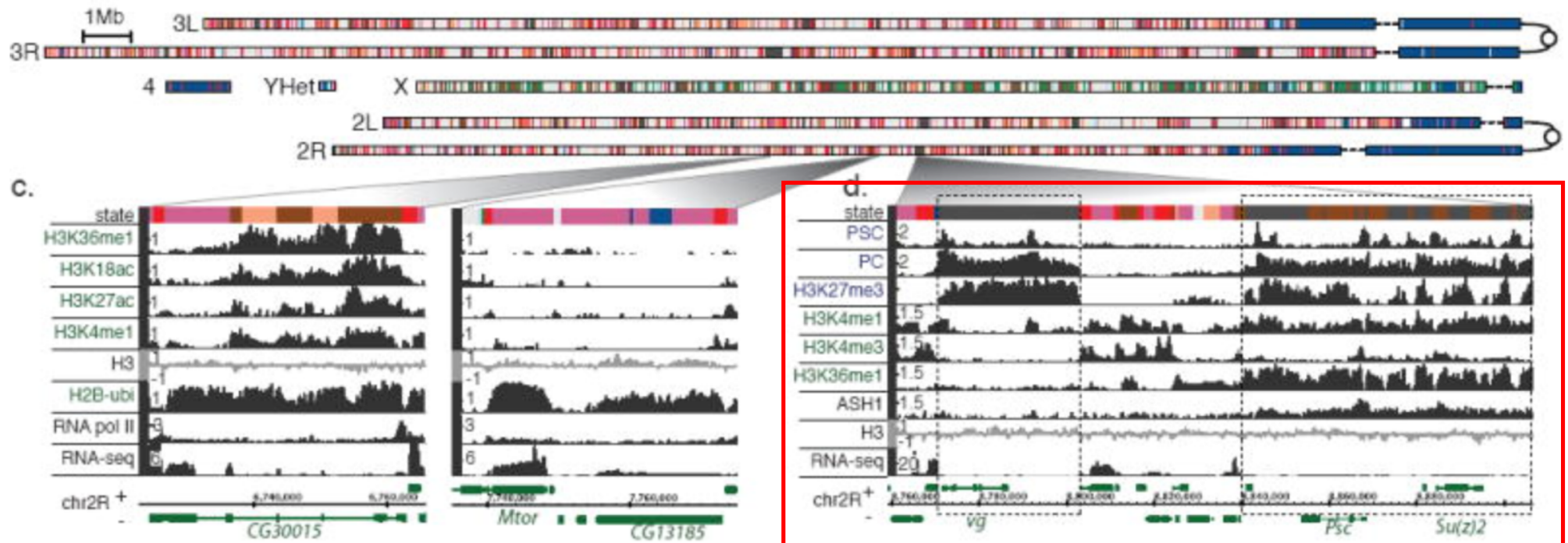


Un cromosoma politenico è un cromosoma gigante. I cromosomi politenici si formano in seguito a vari cicli di replicazione che producono molte copie (anche centinaia) di cromatidi fratelli che rimangono uniti. La formazione dei cromosomi politenici ha la funzione di aumentare il volume cellulare ma può anche comportare un vantaggio metabolico dato che l'elevato numero di copie di geni permette un alto livello di espressione genica. In *Drosophila melanogaster*, per esempio, i cromosomi delle ghiandole salivari delle larve subiscono numerosi cicli di endoreplicazione, e questo consente di produrre grandi quantità di secreto prima dell'impupamento.



## *D. Melanogaster polythene chromosomes*

# PRC2 and PRC1 gene silencing is highly relevant for gene expression on the entire genome level



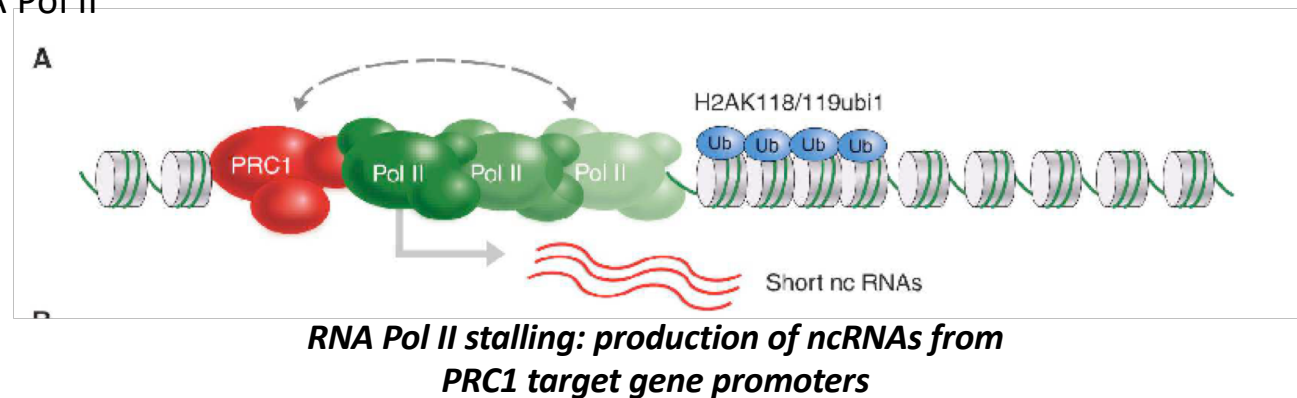
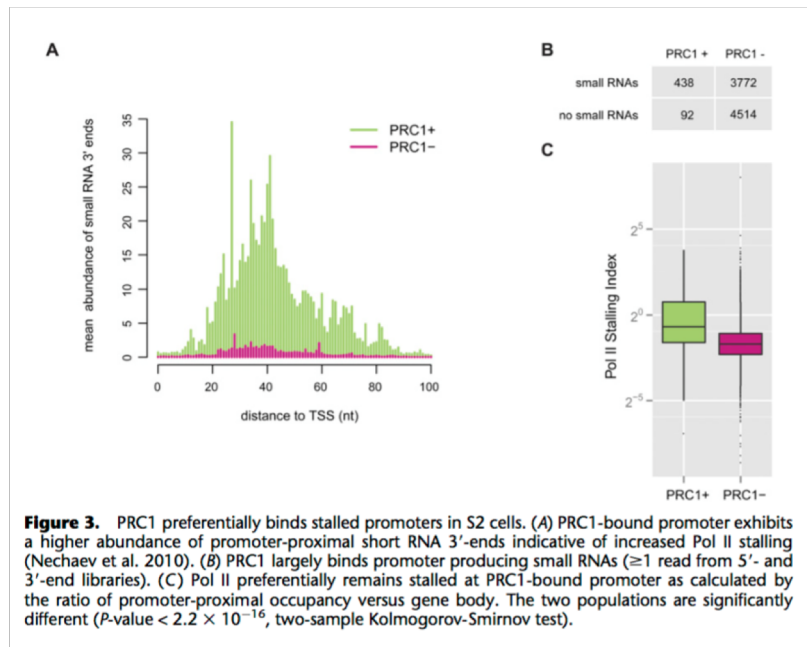
*D. Melanogaster* chromatin map

# POLYCOMB GROUP GENE- DEPENDENT SILENCING

## 1. PRC1 induces a stalling of RNA Polymerase at promoters of Polycomb target genes (in drosophila)

### What is a stalled RNA Polymerase II?

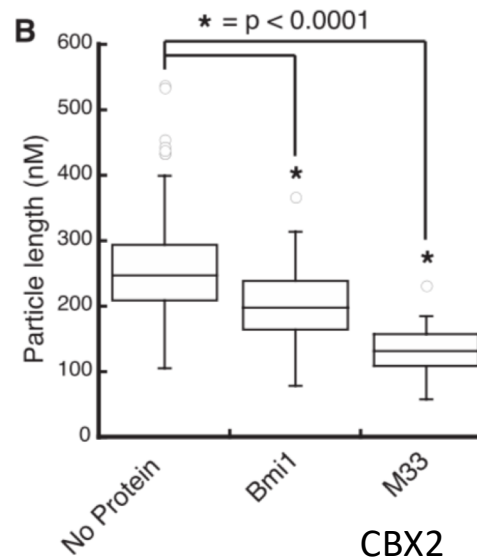
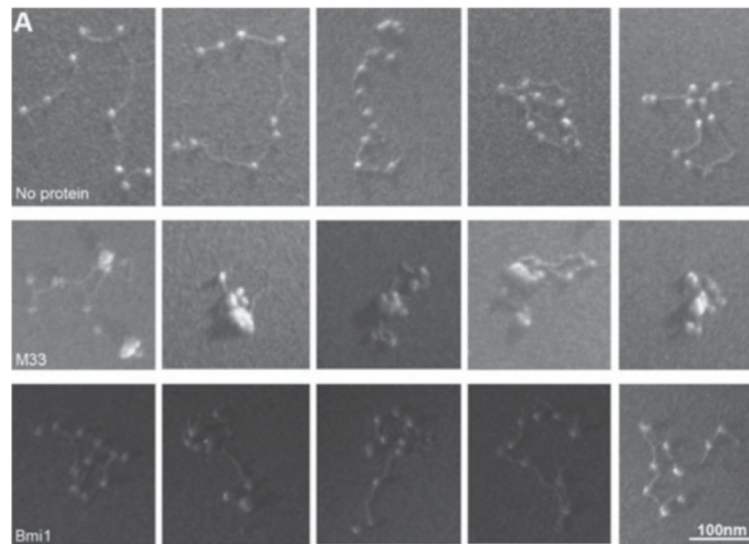
- Replication, transcription, and translation stress all lead to stalling of their respective polymerases
- When stalling at promoters RNA Polymerase produces a significant amount of short ncRNAs → detectable by RNA-Seq
- Important: Overlapping RNA-Seq data and Polycomb ChIP seq revealed that many PRC1 target genes produce short ncRNAs from promoters → PRC1 stalls RNA Pol II



Transcription elongation is not a smooth ride along the DNA railway. For proofreading, the polymerase is made to back-up, erase some of the RNA it has already made and have another go at transcription. In general, RNA polymerase does not transcribe through a gene at a constant pace. Rather it pauses periodically at certain sequences, sometimes for long periods of time before resuming transcription. In extreme cases, for example, when the polymerase encounters a damaged nucleotide, it comes to a complete halt. More often, an elongating polymerase is stalled near the promoter. Promoter-proximal pausing during early elongation is a commonly used mechanism for regulating genes poised to be expressed rapidly or in a coordinated fashion.

## POLYCOMB GROUP GENE- DEPENDENT SILENCING

### 2. PRC1 induces chromatin compaction

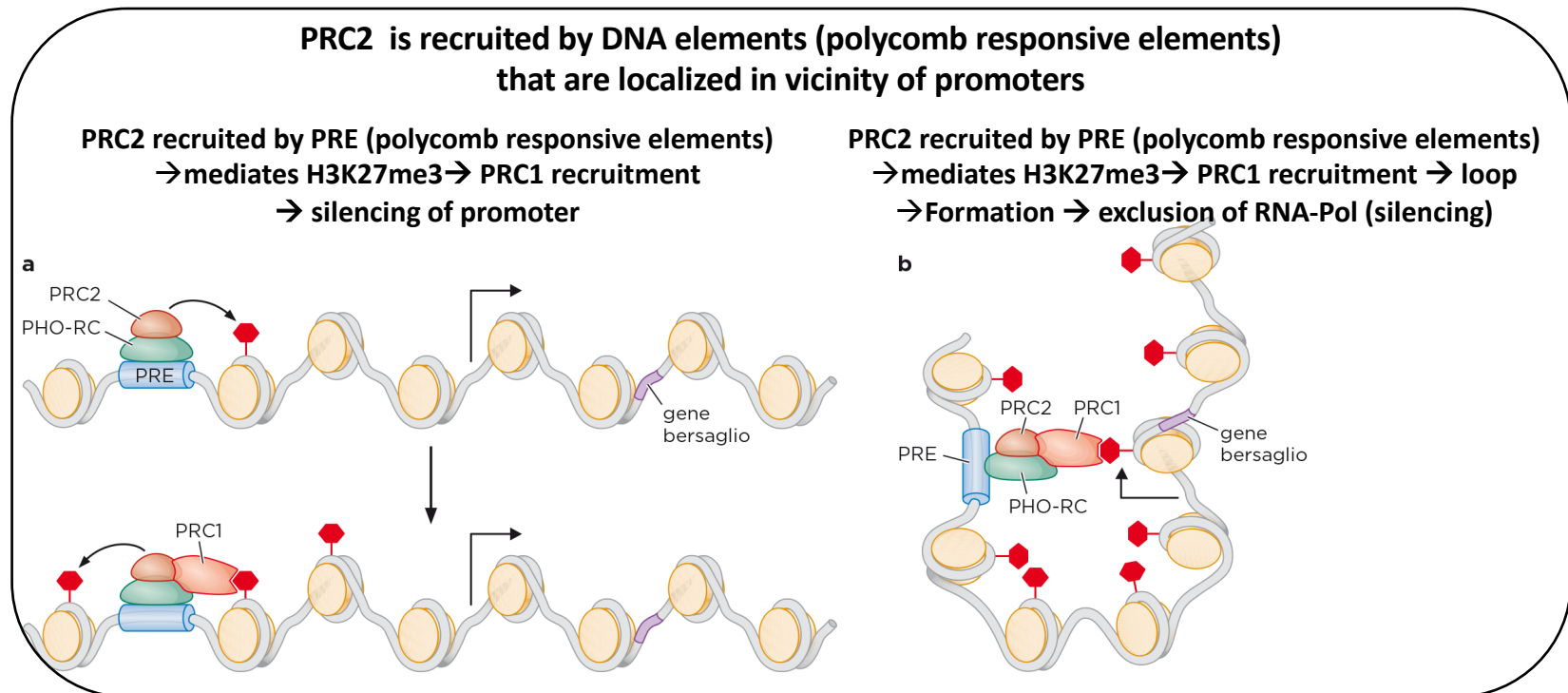


**Figure 5.** Compaction of nucleosomal arrays by mouse PcG proteins. (A) Representative EM images of nucleosomal arrays incubated with the indicated PcG protein. (B) Box plot representation of the measured maximal diameter of nucleosomal array particles. Particle length is the diameter of the smallest circle that can entirely surround one nucleosomal array. The box represents the upper and lower quartile, and the line splitting the box represents the mode. The open circles represent outliers, and the asterisks indicate a  $P$ -value of  $<0.0001$  using Student's  $t$ -test. No protein,  $n = 72$ ; Bmi1,  $n = 50$ ; M33,  $n = 30$ .

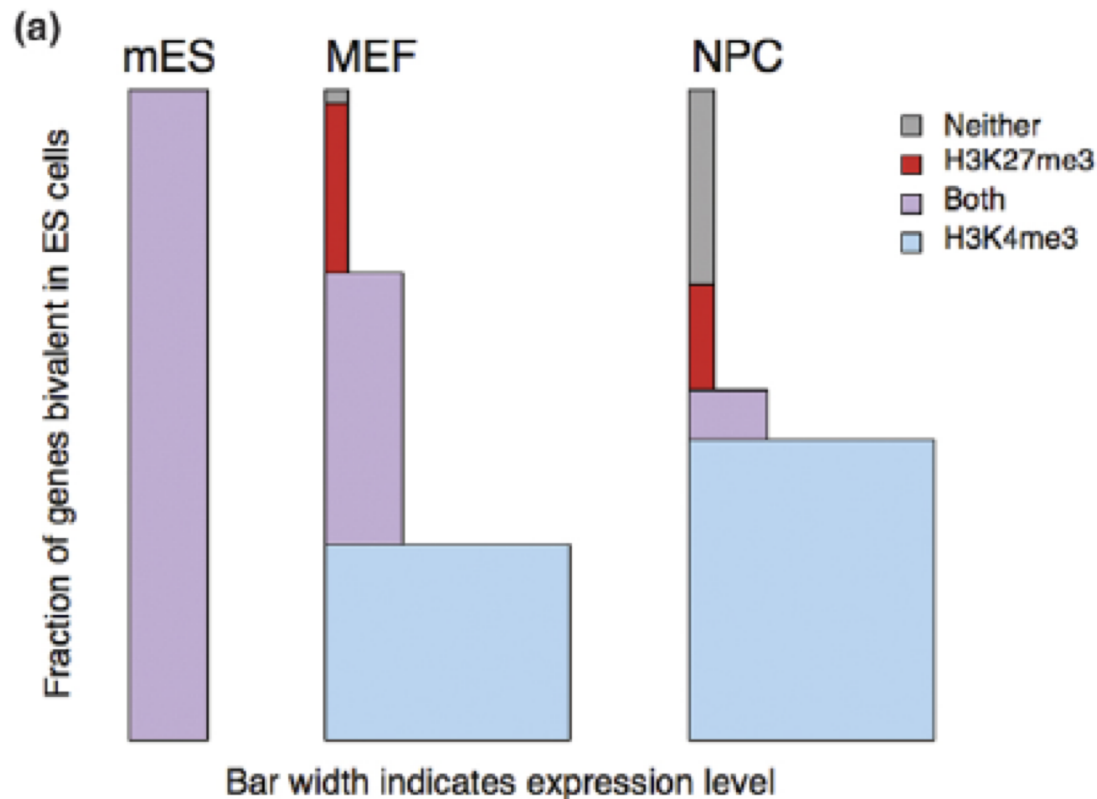
Purified nucleosomal arrays incubate with recombinant polycomb proteins  
→ Arrays are compacted

## Polycomb repressive complexes organize chromatin in a loop structure → repression

### 3. PRC2 - PRC1 induces chromatin looping – RNA polymerase exclusion



## PRC2 is essential for gene expression control in development/differentiation/disease



(b)

Genes involved in	ES	MEF	NPC
Haematopoiesis	Bivalent	K27 or neither	K27 or neither
Mesenchyme	Bivalent	K4	K27 or neither
Adipogenesis	Bivalent	Bivalent	K27 or neither
Neurogenesis	Bivalent	K27 or neither	Bivalent

mES: mouse embryonic stem cells  
MEFs: Mouse embryonic fibroblasts  
NPC: neuronal progenitor cells

**Stem cell regulation by polycomb repressors:  
postponing commitment**

Alexandra M Pietersen and Maarten van Lohuizen

Current Opinion in Cell Biology 2008, 20:201–207

## HOW ARE PcG PROTEINS RECRUITED TO TARGET GENES? – POLYCOMB RESPONSE ELEMENTS

Polycomb repressive complex 1/2 interacts with defined DNA sequences = PRE Polycomb responsive elements

PRE elements were discovered in *Drosophila* → enrichment of PRC1/2 components at PRE sites

PRC2 and PRC1 components do not have DNA binding domains

PRC2 and PRC1 interact with specialized PcG group proteins that bind PREs

*D.melanogaster*: PHO Pleiohomeotic; PHO-L Pleiohomeotic like → form PhoRC complex

PhoRC complex at app 45% of all PRC1/2 target genes; other sites: PRC1/PRC2 interacts with other DNA binding proteins

## Polycomb group genes are conserved in evolution

DNA binding

Polycomb repressive complex 2 (PRC2)

Polycomb repressive complex 1 (PRC1)

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PcG DNA binding proteins						
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PHOL	Pleiohomeotic-like	Zinc finger				
PSQ	Pipsqueak	BTB-POZ domain				
DSP1	Dorsal switch protein 1	HMG domain protein	HMGB2			
PRC2 core proteins						
ESC	Extra sex combs	WD 40 repeats	EED	FIE	MES-6	
E(Z)	Enhancer of zeste	SET domain	EZH1/ENX2 EZH2/ENX1	CLF MEA SWN	MES-2	
SU(Z)12	Suppressor of zeste 12	Zinc finger VEFS box	SU(Z)12	FIS2 VRN2 EMF2		
p55	p55	Histone-binding domain	RBAP48 RBAP46	MSI1 (MSI2/3/4/5)		
PRC1 core proteins						
PC	Polycomb	Chromodomain	CBX2/M33 CBX4/MPC2 CBX6 CBX7 CBX8/MPC3			
PH	Polyhomeotic	Zinc finger SAM/SPM domain	EDR1/MPH1/RAE28 EDR2/MPH2 (EDR3)		SOP-2	
PSC	Posterior sex combs	Zinc finger HTH domain	BMI1 MEL18/RNF110/ZFP144	AtBMI1A AtBMI1B AtBMI1C	MIG-32	Epigenetics
SCE/dRING	Sex combs extra/dRing	RING zinc finger	RING1/RING1A RNF2/RING1B	AtRING1A AtRING1B	SPAT-3	

PRE BINDING PROTEINS

Epigenetic writers

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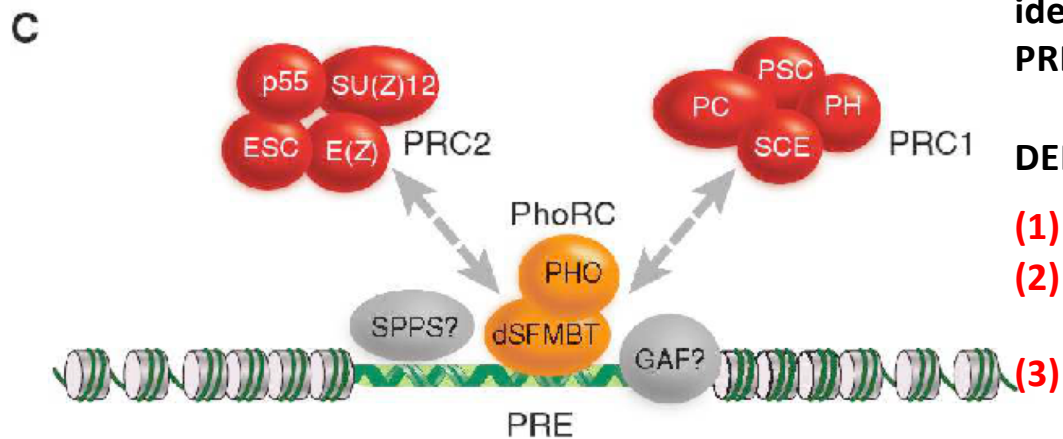
*D. melanogaster*: PHO Pleiohomeotic; PHO-L Pleiohomeotic like → form PhoRC complex = Pho repressive complex

PhoRC complex at app 45% of all PRC1/2 target genes; other sites: PRC1/PRC2 interacts with other DNA binding proteins

**PRE elements well defined in *Drosophila***  
(mathematical prediction/consensus sequences identify many (but not all) PREs)

## DEFINITION OF PRE ELEMENTS:

- (1) **PREs attract H3K27me<sub>3</sub>,**
- (2) **they should form a new binding site for PcG proteins when inserted at a new location within the genome, and**
- (3) **they confer PcG-based repression to a reporter gene.**



# PREs have many binding sites for certain TFs – not only for Pho/Phol

Development 134, 223-232 (2007) doi:10.1242/dev.02723

## Polycomb/Trithorax response elements and epigenetic memory of cell identity

Leonie Ringrose<sup>1</sup> and Renato Paro<sup>2</sup>

**PREs consist of modules of sequences that can recruit multiple transcriptional regulators that interact Polycomb group proteins.**

**The set of transcription factors available for binding to PRE elements is defined by the cell-identity (gene expression Profile of the respective cell)**

**(NOTE: also TrxG proteins can be found at PREs)**

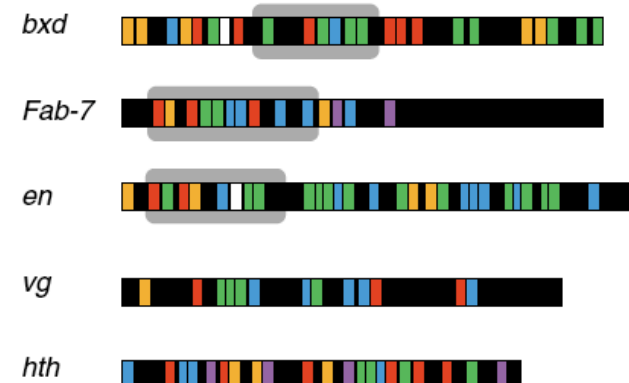
### A PRE motifs

Pho/Phol	GCCAT
Dsp1	GAAAA
GAF/Psq	GAGAG
Zeste	YGAGYG
Grh	TGTTTTT
Sp1/KLF	RRGGYGY

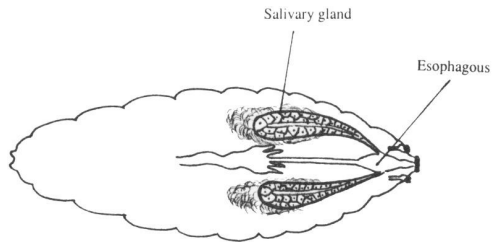
### B Motif occurrence in non-PREs



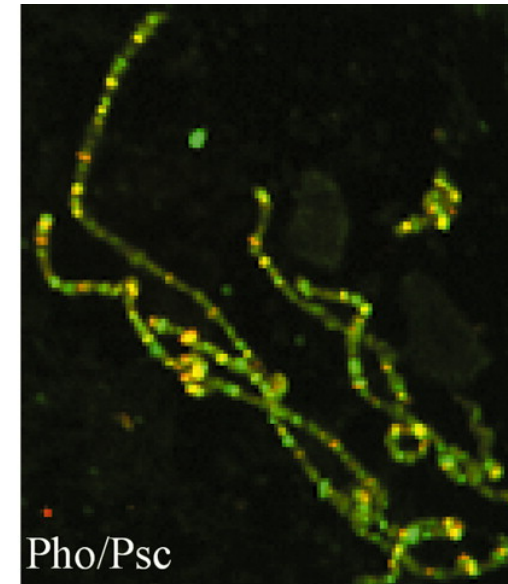
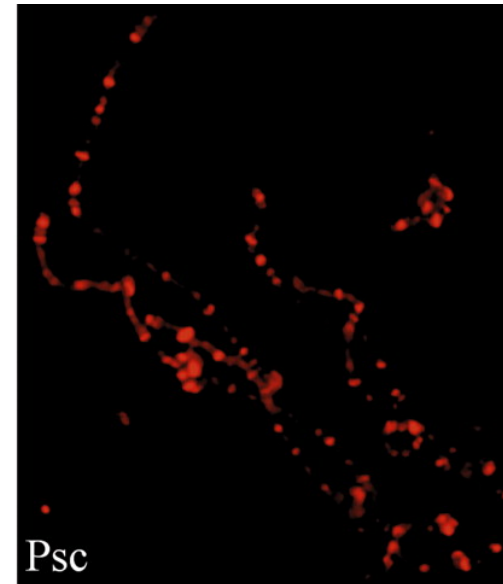
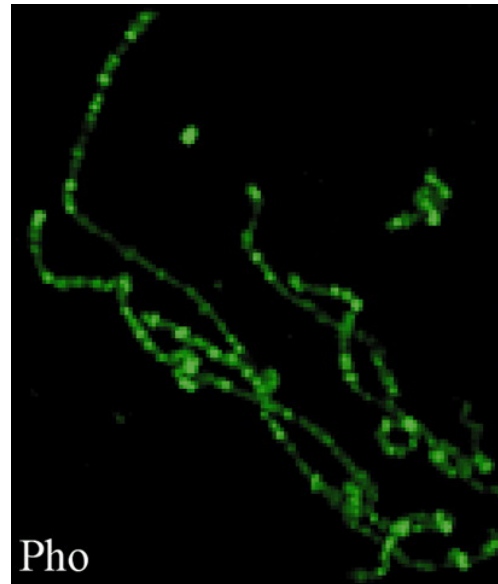
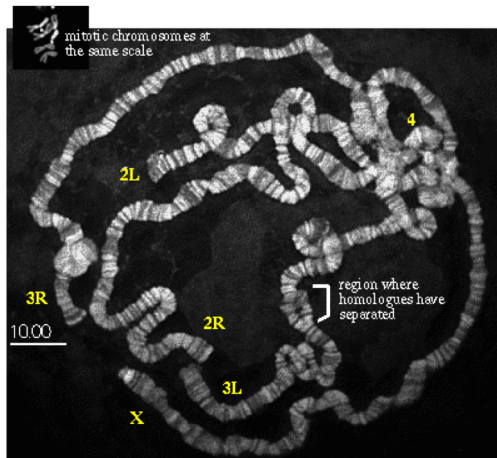
### C Motif occurrence in PREs



# Pho RECRUITS POLYCOMB PROTEINS TO DEFINED GENES



Un cromosoma politenico è un cromosoma gigante. I cromosomi politenici si formano in seguito a vari cicli di replicazione che producono molte copie (anche centinaia) di cromatidi fratelli che rimangono uniti. La formazione dei cromosomi politenici ha la funzione di aumentare il volume cellulare ma può anche comportare un vantaggio metabolico dato che l'elevato numero di copie di geni permette un alto livello di espressione genica. In *Drosophila melanogaster*, per esempio, i cromosomi delle ghiandole salivari delle larve subiscono numerosi cicli di endoreplicazione, e questo consente di produrre grandi quantità di secreto prima dell'impupamento.



# HOW ARE PcG PROTEINS RECRUITED TO TARGET GENES? – POLYCOMB RESPONSE ELEMENTS

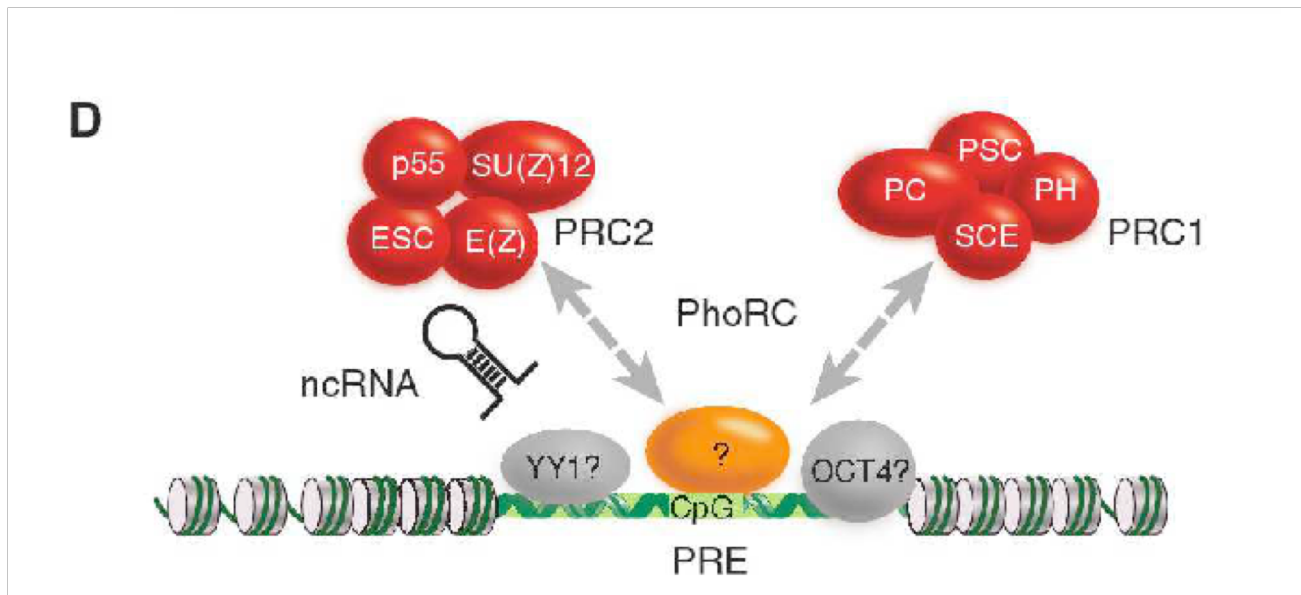
**PREs are ill defined: a "consensus PRE site" does not exist**

Polycomb proteins accumulate around gene promoters

PRC2/PRC1 target sites can be defined by ChIP Seq

Often YY1 co-localizes with PRC1/2; however there is no defined mechanism that explains PRC1/2 complex recruitment to PRC1/PRC2 target genes → multiple transcription factors can interact with PRC1/2 (i.e. OCT4)

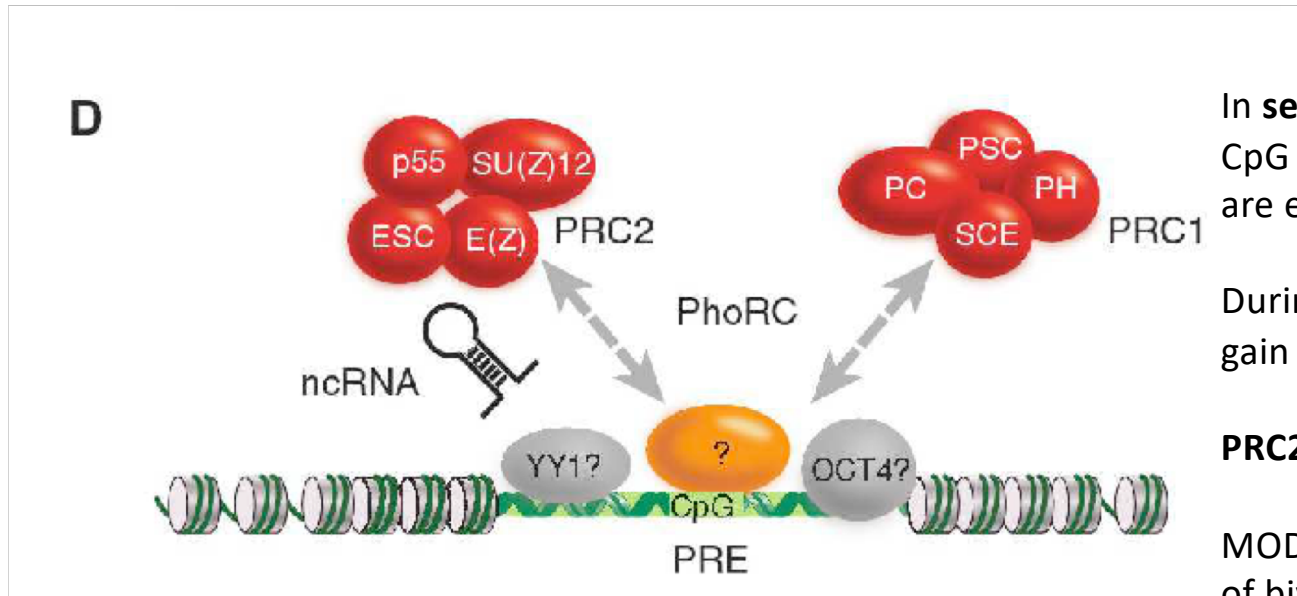
V  
e  
r  
t  
e  
b  
r  
a  
t  
e  
s



# HOW ARE PcG PROTEINS RECRUITED TO TARGET GENES? – POLYCOMB RESPONSE ELEMENTS

## A LINK BETWEEN H3K27me3 – PRC1 – PRC2 – CpG DNA METHYLATION

V  
e  
r  
t  
e  
b  
r  
a  
t  
e  
s



In **self-renewing embryonic stem cells**






CpG islands show low DNA methylation but are enriched for H3K27me3

During differentiation most H3K27me3 CpGs gain DNA methylation

**PRC2 interact with DNMTs (IP)**

MODEL: H3K27me3 (PRC1/2) at CpG islands of bivalent genes mediate the inactivation of the gene by DNA methylation during differentiation

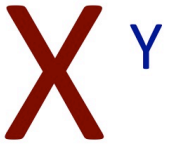

## DOSAGE COMPENSATION IN VERTEBRATES: X chromosome inactivation (XCI)

	Male	Female	
<i>Drosophila melanogaster</i>	 Y AA	XX AA	rox lncRNA
<i>Homo sapiens</i>	 Y AA	  AA	Xist lncRNA - POLYCOMB
<i>Caenorhabditis elegans</i>	 AA	 AA	

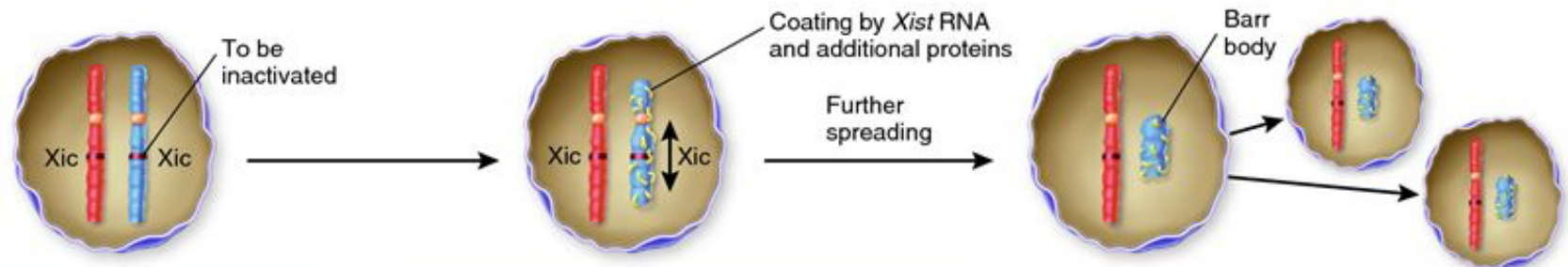
## PRC1/2 CAN INTERACT WITH ncRNA

X chromosome inactivation  
in vertebrate species

### Dosage Compensation

Male	Female
	
Y chromosome lost most of the ancestral genes	Silence most of the genes on one X chromosome

Xic: (X inactivation  
center)  
Encodes a series  
of ncRNAs that are  
involved in **choice** and  
**silencing** of one X.  
**Xist** drives the  
silencing of an entire  
X chromosome



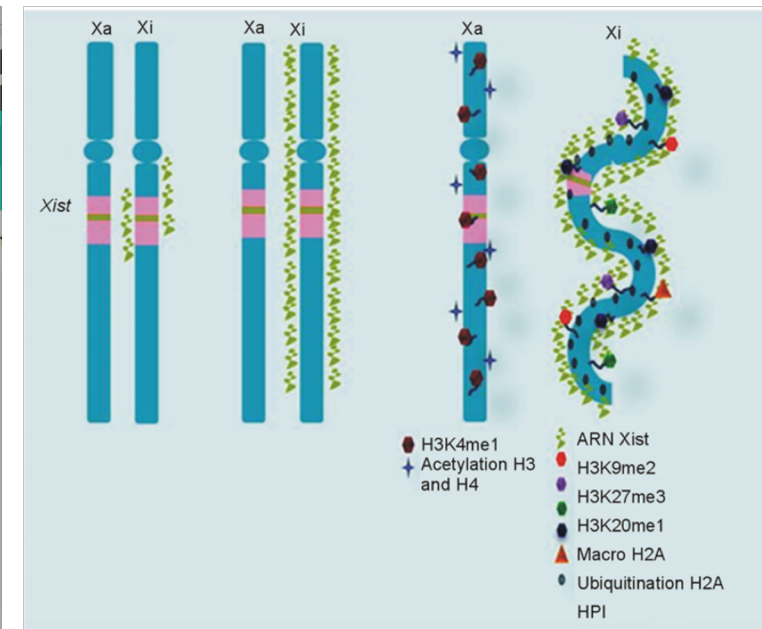
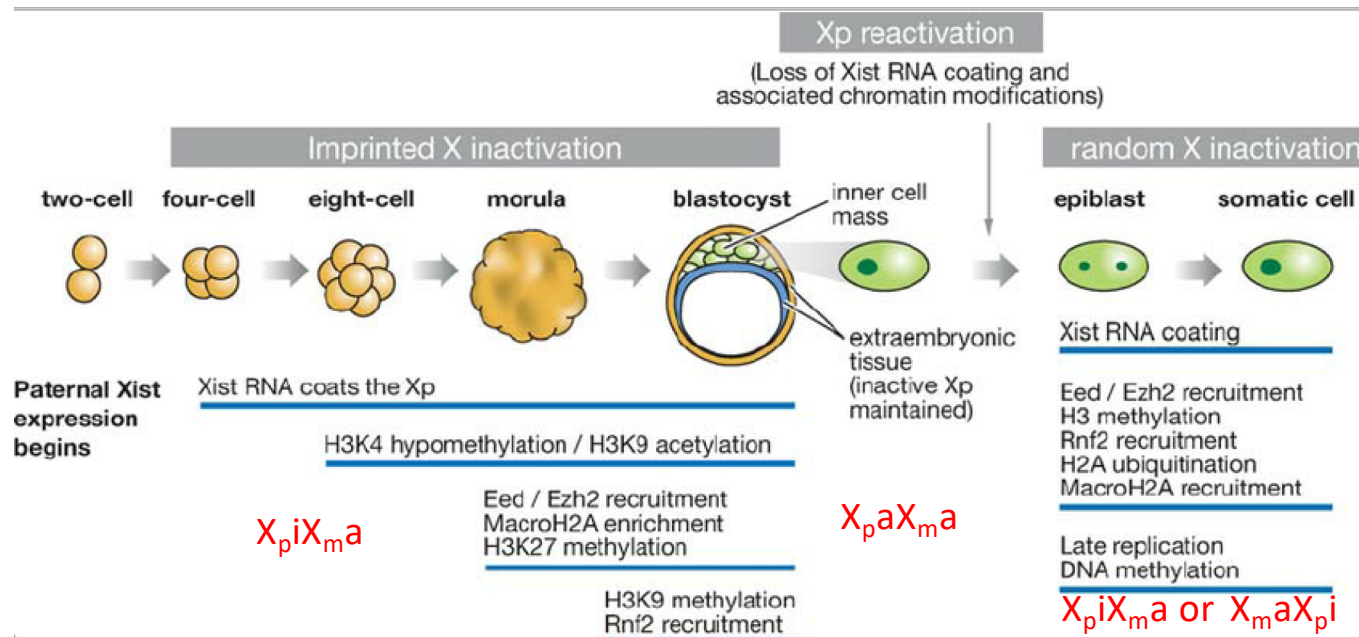
1 **Initiation:** Occurs during embryonic development. The X inactivation centres (Xics) are counted and one of the X chromosomes is targeted for inactivation.

2 **Spreading:** Occurs during embryonic development. It begins at the Xic and progresses toward both ends until the entire chromosome is inactivated. The *Xist* gene, located within the Xic, encodes an RNA that coats the X chromosome and promotes its compaction into a Barr body.

3 **Maintenance:** Occurs from embryonic development through adult life. The inactivated X chromosome is maintained as a Barr body during subsequent cell divisions.

# PRC1/2 CAN INTERACT WITH ncRNA

## Xist and PRC2



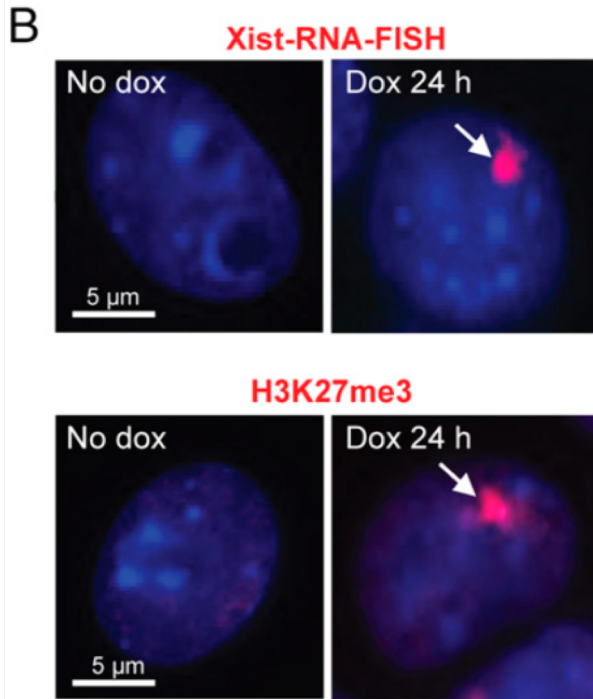
Inner cell mass = epiblast cells: BOTH X chromosomes are active in female cells

Embryonic stem cells are cultivated from the inner cell mass and contain active X chromosome chromatin

A. Female ES cells:  $X_a X_a \rightarrow$  Differentiation in vitro  $\rightarrow X_a X_i$  (random X inactivation)

B. Male ES cell:  $X_a Y \rightarrow X_a$  has active chromatin. NOTE: when Xist is ectopically expressed from X  $\rightarrow$  silencing  $\rightarrow$  male ES cell dies

## PRC1/2 CAN INTERACT WITH ncRNA



**C**

Male embryonic stem cell with a doxycyclin inducible Xist Transgene

Addition of Doxycyclin to the medium mediates Xist expression

A stem-loop repeat motif of the Xist lncRNA recruits PRC2 to the future Xi

Xist RNA spreads along the entire X chromosome (model: Xist expression from inducible Promoter)

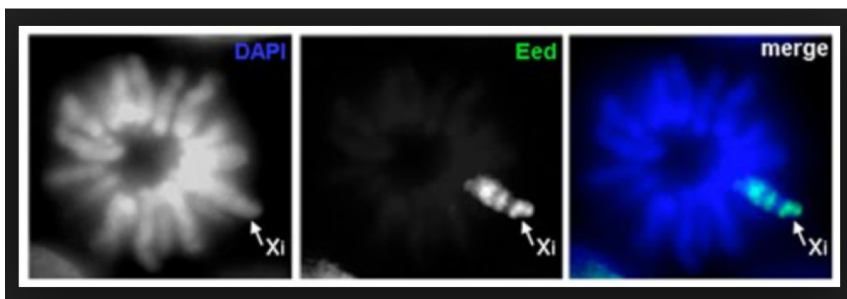
Also PRC2 components (i.e. Eed) spread across the future Xi

PRC2 (Ezh2) mediates chromosome wide H3K27me3 methylation

PRC1 is also recruited to the Xi (PRC2 independent) H2AK119 ubiquitination

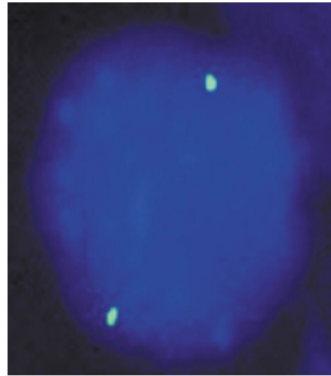
Imposition of DNA methylation  
Incorporation of histone variants

CHROMOSOME WIDE GENE SILENCING

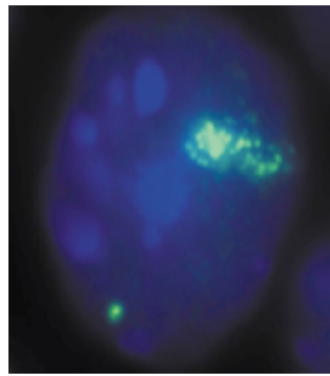


## Xist spreads along the future X chromosome

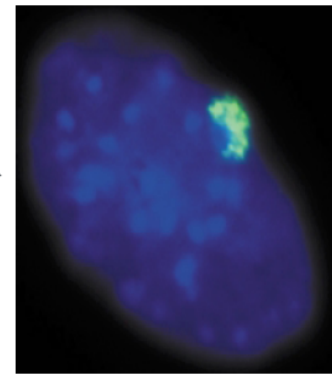
Xist RNA-FISH on female embryonic stem cells that initiate X inactivation



2 X chromosomes  
Express Xist at low levels  
(both X active)



1 X chromosome  
Express Xist at high levels  
(choice,  
silencing of 1 X chromosome)



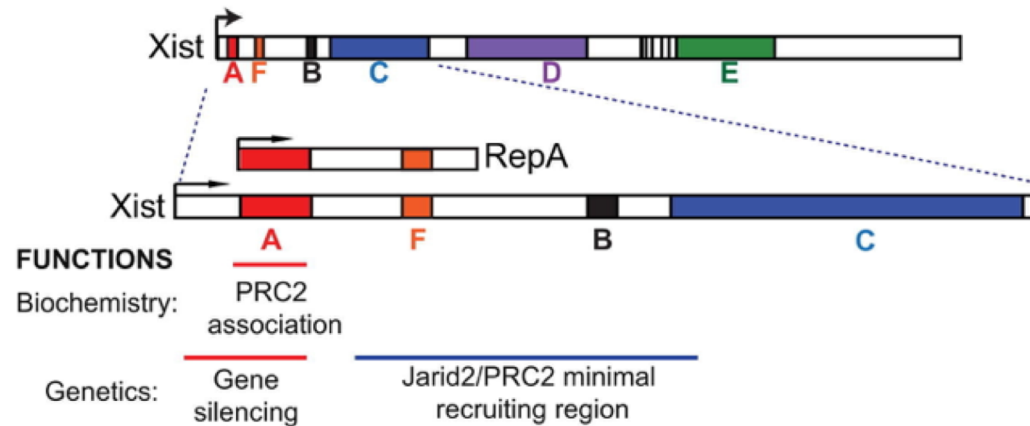
1 X chromosome  
Express Xist at high levels  
(silencing of 1 X chromosome)  
Other X chromosome has silenced  
completely its Xist gene

48 hours

## PRC1/2 CAN INTERACT WITH ncRNA

Gene

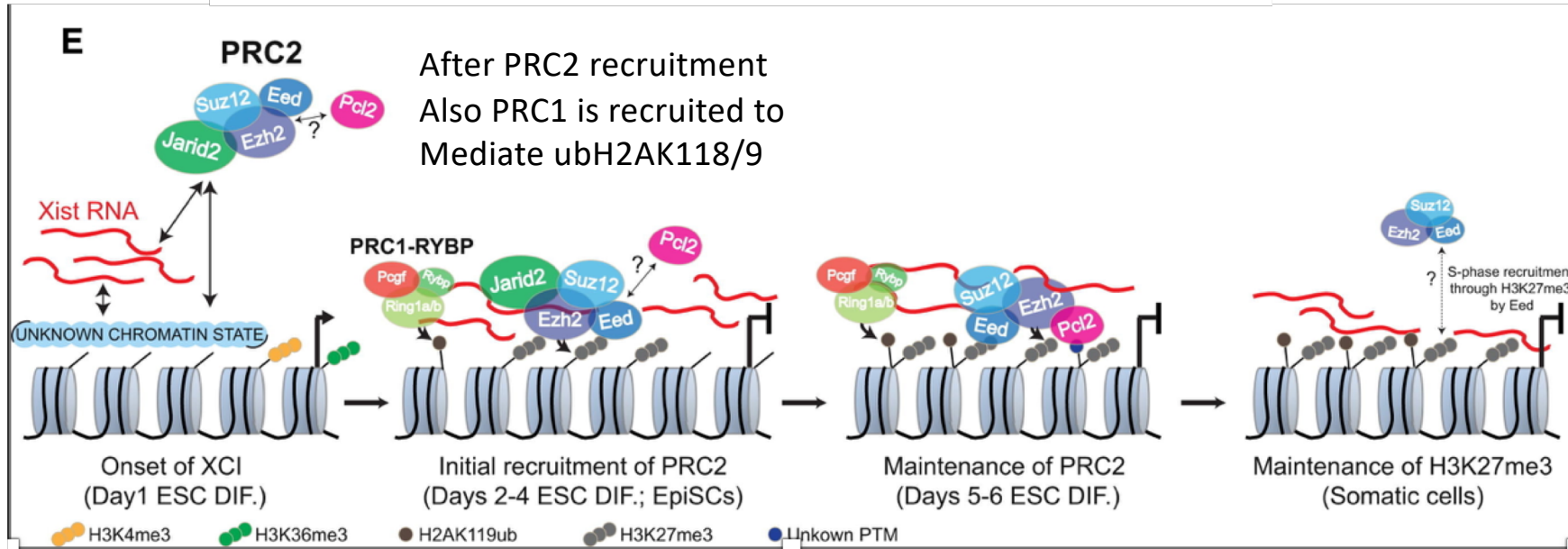
Function of  
relevant Xist RNA region



Xist contains RNA regions that:

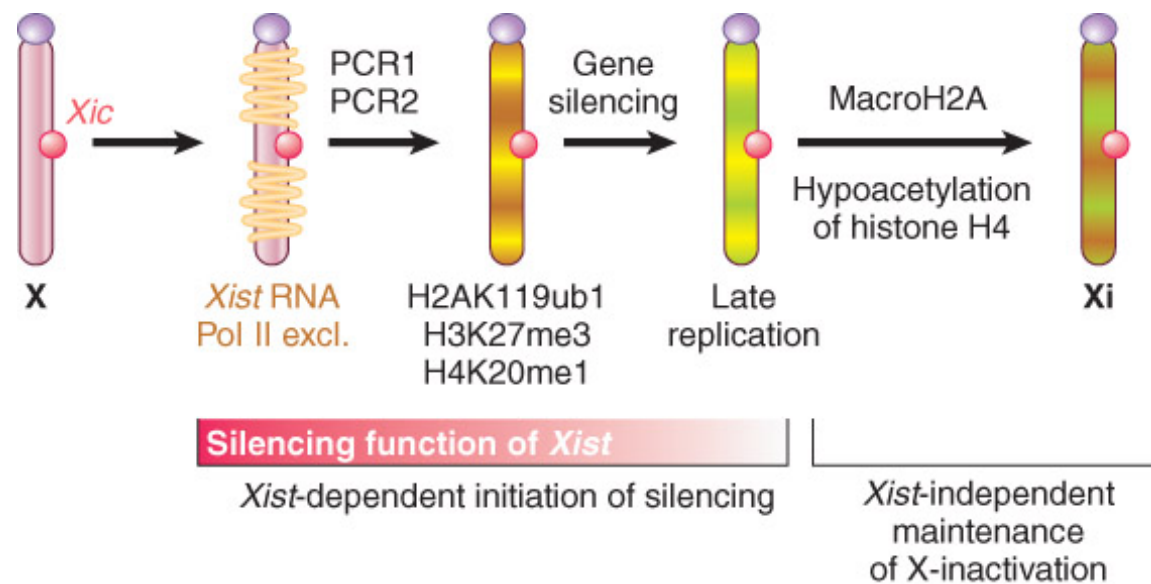
- Recruit PRC2
- interact with the PRC2 co-factor Jared2

(important: Jared helps PRC2 to interact with chromatin → general function of Jared2 in PRC2 complex)



## PRC1/2 CAN INTERACT WITH ncRNA

- *Xist* recruits Polycomb complexes, which modify histones on the inactive X



*Xist* RNA produced from the *Xic* locus accumulates on the future inactive X (Xi).

Adapted from A. Wutz and J. Gribnau, Curr. Opin. Genet. Dev. 17 (2007): 387-393.

# PRC1/2 CAN INTERACT WITH ncRNA

HOTAIR lncRNA interacts with PRC2 → DIRECTS PRC2 TO TARGET GENES (i.e Hox4)

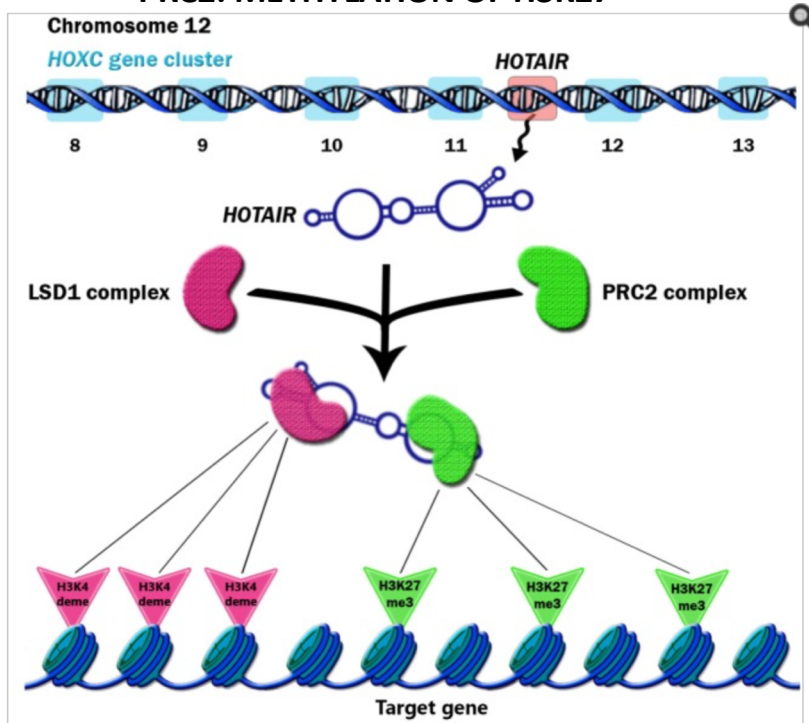
HOTAIR lncRNA is overexpressed in tumors → → altered gene expression → → tumorformation and progression

HOTAIR lncRNA expression is a prognostic marker (poor survival)

HOTAIR Complexes with LSD1 and PRC2

LSD1: DEMTHYLATION OF H3K4

PRC2: METHYLATION OF H3K27



## HOTAIR IS OVEREXPRESSED IN HUMAN CANCER

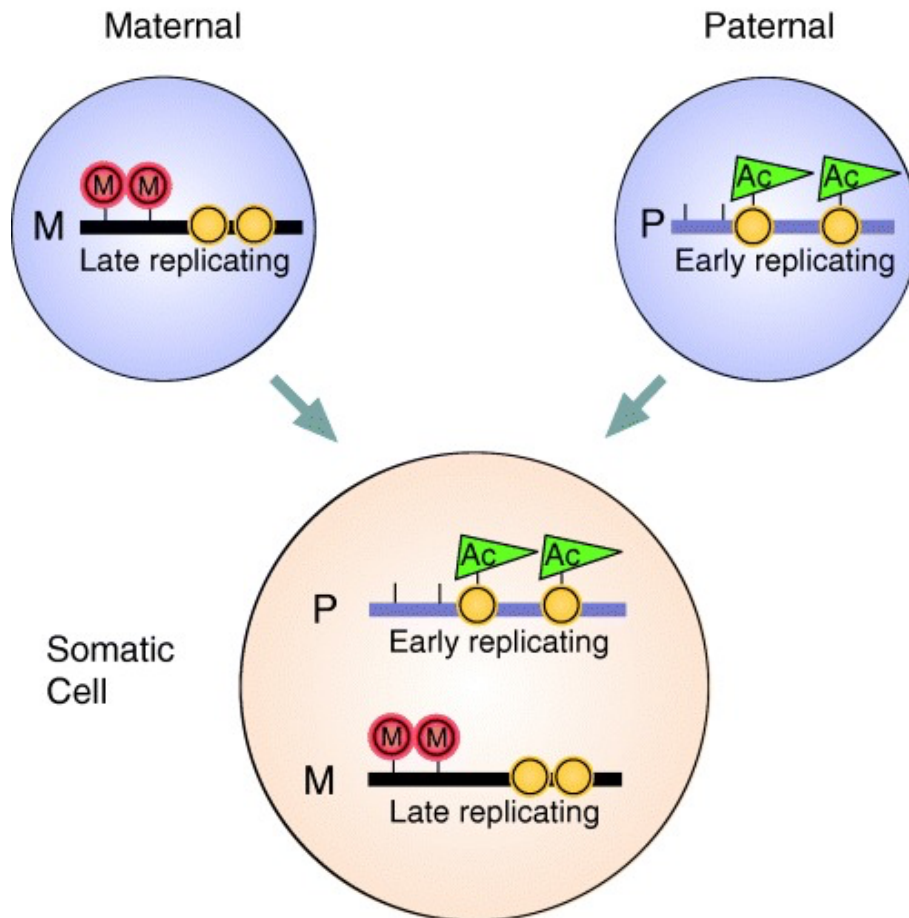
Table 1

Overexpression of *HOTAIR* in different cancers

Type	Overexpression of <i>HOTAIR</i>	References
Breast cancer	Poor prognosis, metastasis, invasion, and short overall survival	<a href="#">21-35</a>
Esophageal squamous cell carcinoma (ESCC)	Poor prognosis, high TNM stage, invasion, metastasis, and short overall survival	<a href="#">36-37</a>
Gastric cancer	Tumor staging, venous infiltration, and lymph node metastasis	<a href="#">38-39</a>
Hepatocellular carcinoma	Invasion of HCC cells, possibility of recurrence	<a href="#">40-44</a>
Colorectal cancer	Poor prognosis, low survival, and metastasis promotion	<a href="#">45-47</a>
Gallbladder cancer (GBC)	Promoting carcinogenesis	<a href="#">29</a>
Bladder cancer (BC)	Poor prognosis and high recurrence rate	<a href="#">48</a>
Renal carcinoma	Proliferation, invasion, and promotion of tumor growth	<a href="#">49</a>
Cervical cancer	FIGO stage, aggression, and lymph node metastasis	<a href="#">30</a>
Epithelial ovarian cancer	Poor prognosis, FIGO stage, lymph node metastasis, overall survival, and metastatic stage of EOC	<a href="#">50</a>
Endometrial carcinoma	Poor prognosis, lymph node metastasis, EC grade, and overall survival	<a href="#">51-52</a>
Lung cancer	Invasion and metastasis	<a href="#">53</a>
Non-small cell lung cancer	Promotion of lymph node metastasis	<a href="#">54-55</a>
Small-cell lung cancer	Poor prognosis, proliferation and invasion	<a href="#">56</a>
Nasopharyngeal carcinoma	Poor prognosis, overall survival, proliferation, invasion, and promotion of tumor stage	<a href="#">31</a>
Melanoma	Invasion and metastasis	<a href="#">57</a>
Glioma	Poor prognosis, cell cycle progression, and glioma grade	<a href="#">58</a>
Pancreatic cancer	Proliferation and aggression of tumors	<a href="#">59</a>

## PRC1/2 CAN INTERACT WITH ncRNA – genomic imprinting

### Imprinting



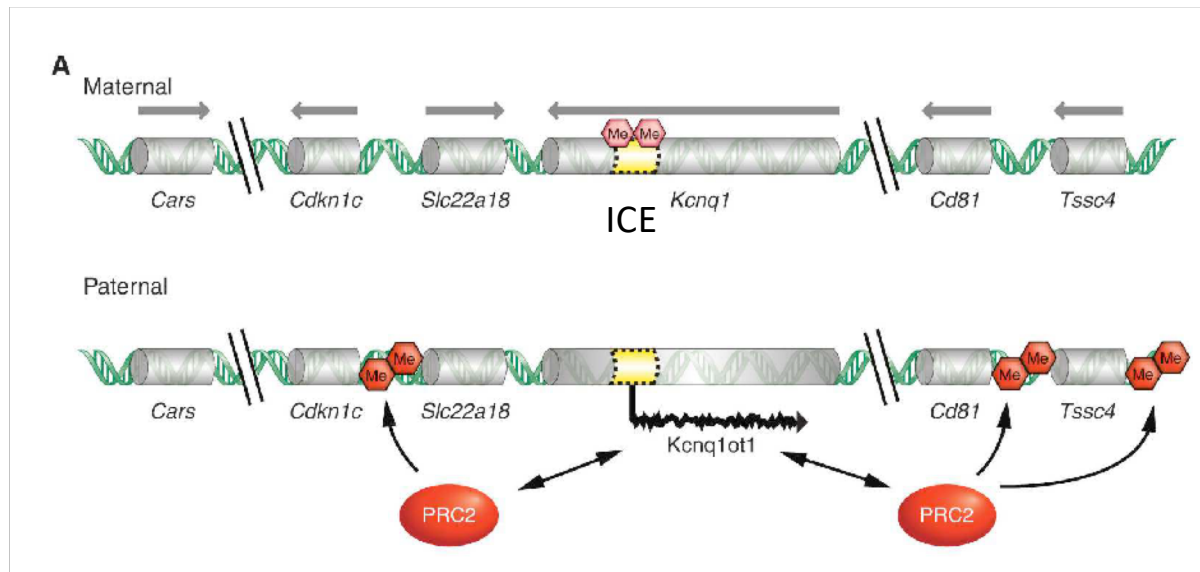
Epigenetic information is not erased from all genes after fertilization.  
Some genes maintain the epigenetic information from the paternal/maternal chromosomes

**= IMPRINTED GENES**

- Exclusive expression of the maternal or paternal gene
- For example imprinted XCI

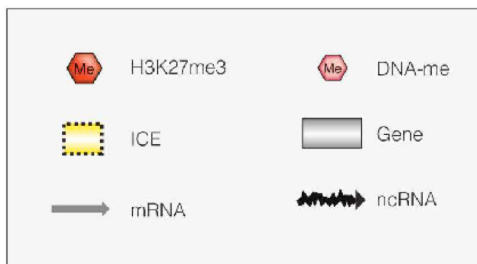
## PRC1/2 CAN INTERACT WITH ncRNA

### Genomic Imprinting: *Kcnq1* LOCUS IN MOUSE



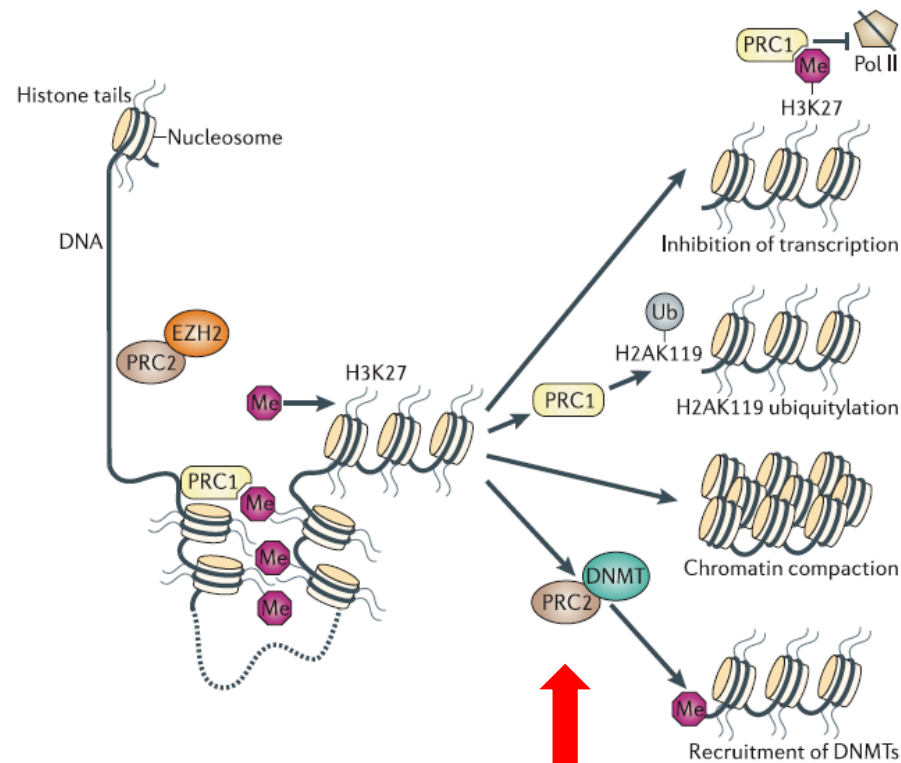
**Maternal allele:** ACTIVE – expression of protein coding genes around *Kcnq1*.  
 WHY: *Kcnq1* lncRNA has ICE (CpG island) methylation at promoter (ICE: Imprinting control element) → *Kcnq1* is silenced

**Paternal allele:** INACTIVE – genes around *Kcnq1* are silenced.  
 WHY: *Kcnq1* CpG island is unmethylated. *Kcnq1* lncRNA is expressed.  
**lncRNA recruits PRC2 that silences nearby genes**



**Figure 8.** Interplay of PcG-mediated repression and DNA methylation regulates genomic imprinting in plants and mammals. (A) Regulation of genomic imprinting at the *Kcnq1* domain on distal chromosome 7. The imprinting control element (ICE) is maternally methylated and prevents the transcription of the lncRNA *Kcnq1ot1* from the maternal chromosome. The paternally expressed *Kcnq1ot1* associates with chromatin and recruits chromatin modifying complexes, such as PRC2, to mediate and maintain transcriptional silencing of several paternal, protein-coding alleles. (B) In *Arabidopsis* seeds, the paternally

# OVERVIEW: IMPACT OF POLYCOMB ON GENE EXPRESSION

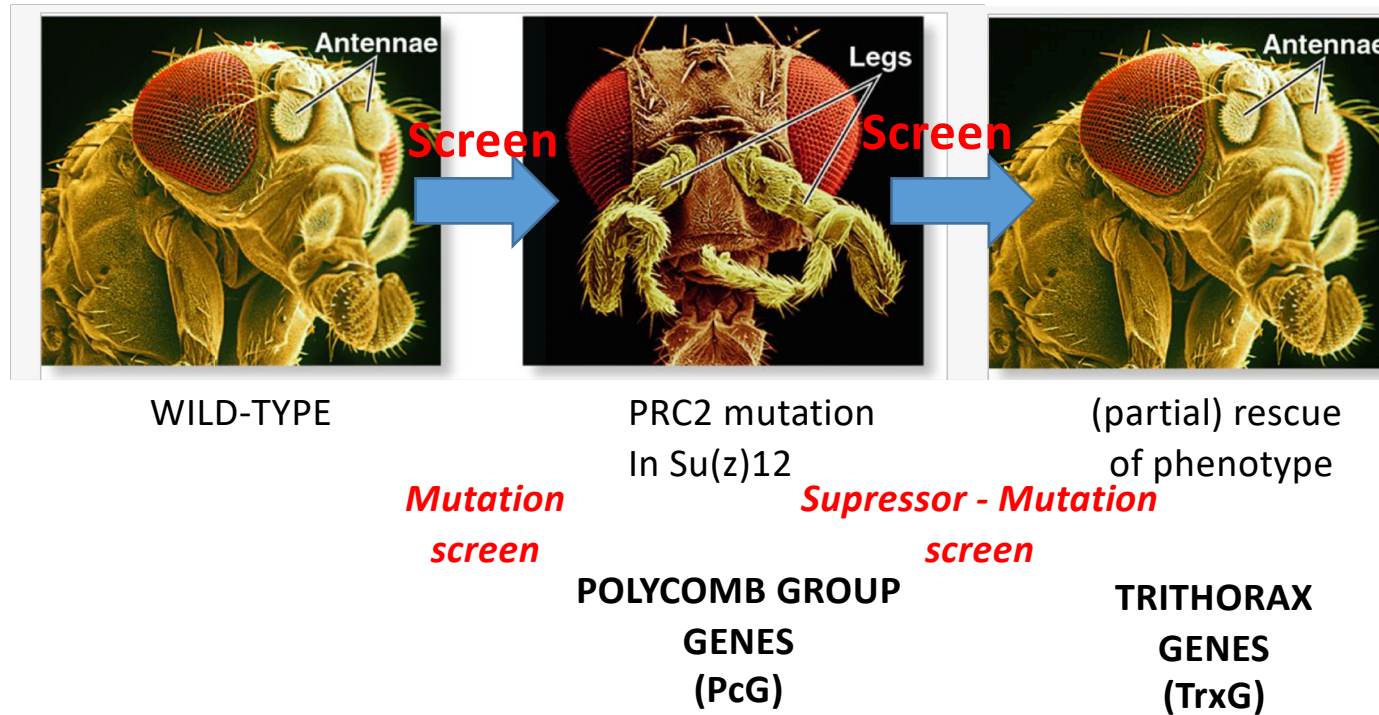


- Chromatin remodeling (i.e. FACT)
- H3K36me3 (i.e. KDM2)

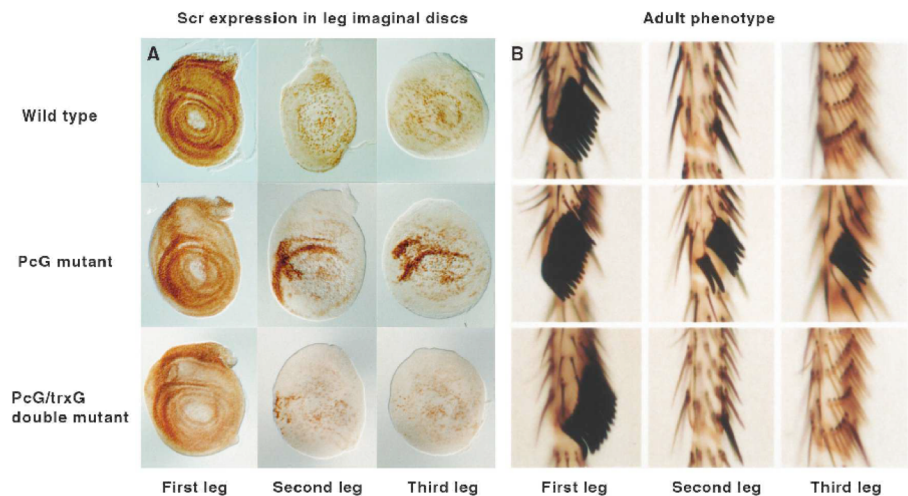
Polycomb silencers control cell fate, development and cancer

## EXPERIMENTAL APPROACH IN DROSOPHILA:

**A SUPPRESSOR MUTATION SCREEN TO IDENTIFY  
EPIGENETIC REGULATORS THAT ACTIVATE GENE EXPRESSION  
--- TRITHORAX GROUP GENES ---**



# A SUPPRESSOR MUTATION SCREEN TO IDENTIFY EPIGENETIC REGULATORS THAT ACTIVATE GENE EXPRESSION --- TRITHORAX GROUP GENES ---



**Figure 4.** trxB mutations block the derepression of Hox genes in PcG mutants. (A) Leg imaginal discs stained with antibodies against the protein encoded by the Hox gene, *Scr*, which specifies the identity of the labial and first thoracic segments, including the first leg. (B) Basitarsal segments of the legs of wild-type and mutant adults. Note the presence of sex comb teeth on the first leg, but not the second and third legs of wild-type adults. The *Scr* gene is partially derepressed in the second and third leg discs, in which it is normally silent, in individuals heterozygous for mutations in PcG genes leading to the appearance of ectopic sex comb teeth on the second and third legs. These phenotypes are suppressed by mutations in *brm* and many other trxB genes. (A, Reprinted, with permission, from [Tamkun et al. 1992](#), © Elsevier; B, portion modified, with permission, from Kennison 2003, © Elsevier.)

**Table 1.** Biochemical functions of trxB proteins

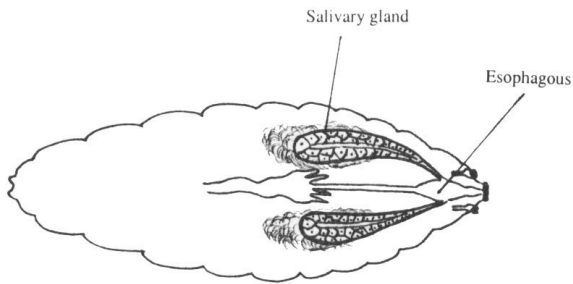
Known function	Organism			
	<i>Drosophila</i>	Human	Yeast	Complexed with non-trxB proteins?
ATP-dependent chromatin remodeling	BRM	BRG1/HBRM	Swi2/Snf2, Sth1	Yes (5–10) <sup>a</sup>
	OSA	BAF250	Swi1/Adr6	Yes (5–10)
	MOR	BAF155, BAF170	Swi3, Rsc8	Yes (5–10)
	SNR1	hSNF5/INI1	Snf5, Sfh1	Yes (5–10)
	Kismet (KIS)	CHD7	–	NK
Histone methyltransferases	Trithorax (TRX)	MLL1, MLL3	MLL2, Set1	Yes (5–20)
	Absent, small or homeotic 1 (ASH1)	MLL4, hASH1	hSET1 –	NK
Mediator subunits	Kohtalo (KTO)	TRAP230	Srb8	Yes (13–24)
	Skuld (SKD)	TRAP240	Srb9	Yes (13–24)
Cohesin subunit	Verthandi (VTD)	Rad21	Scc1/Rad21	Yes (>3)
Transcription factor	Trithorax-like (TRL)	BTBD14B	–	No
Growth factor receptor	Breathless (BTL)	FGFR3	–	NK
Other	Sallimus (SLS)	Titin	–	NK

*Drosophila* males use their sex combs to grasp the females' abdomen and genitalia and to spread their wings prior to copulation.

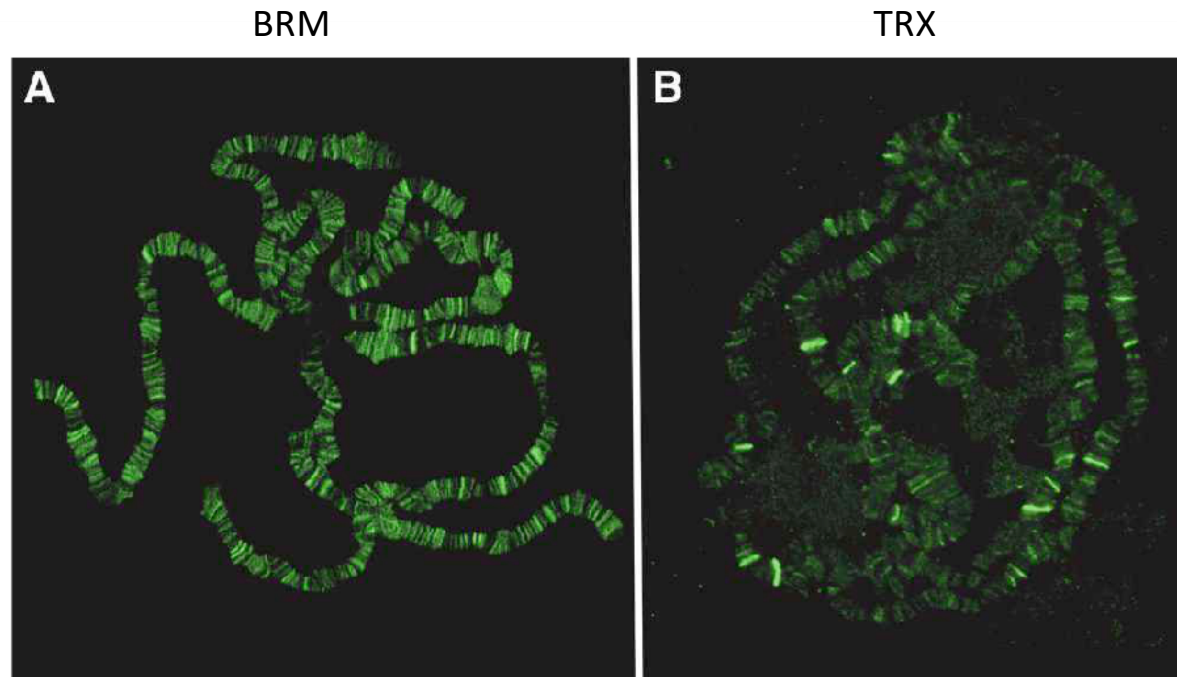
## TRITHORAX GROUP GENES TrxG

Selected <i>D. melanogaster</i> TrxG proteins	Mammalian homologues	Biochemical role(s)	
Trithorax	Myeloid/lymphoid or mixed-lineage leukaemia proteins 1–3	SET domain subunit of a methyltransferase for H3K4	CHROMATIN MODIFICATION H3K4 METHYLATION
Absent small and homeotic disks protein 1 (ASH1)	ASH1-like	SET domain subunit of a methyltransferase for H3K4 and/or H3K36	CHROMATIN MODIFICATION H3K4 – H3K36 METHYLATION
Brahma (BRM)	BRM (also known as SMARCA2) and BRG1 (also known as SMARCA4)	ATPase subunit of a SWI/SNF-type nucleosome remodelling complex	CHROMATIN REMODELLING
Kismet	Chromodomain helicase DNA-binding protein 7	ATPase subunit of a presumed chromodomain-type nucleosome remodelling complex, which functions in transcription elongation	CHROMATIN REMODELLING
Nejire (also known as CBP)	?	Subunit of the TAC1 complex, which mediates histone acetylation	CHROMATIN MODIFICATION

## TRITHORAX GROUP GENES ARE LOCALIZED TO DEFINED POSTIONS IN THE GENOME

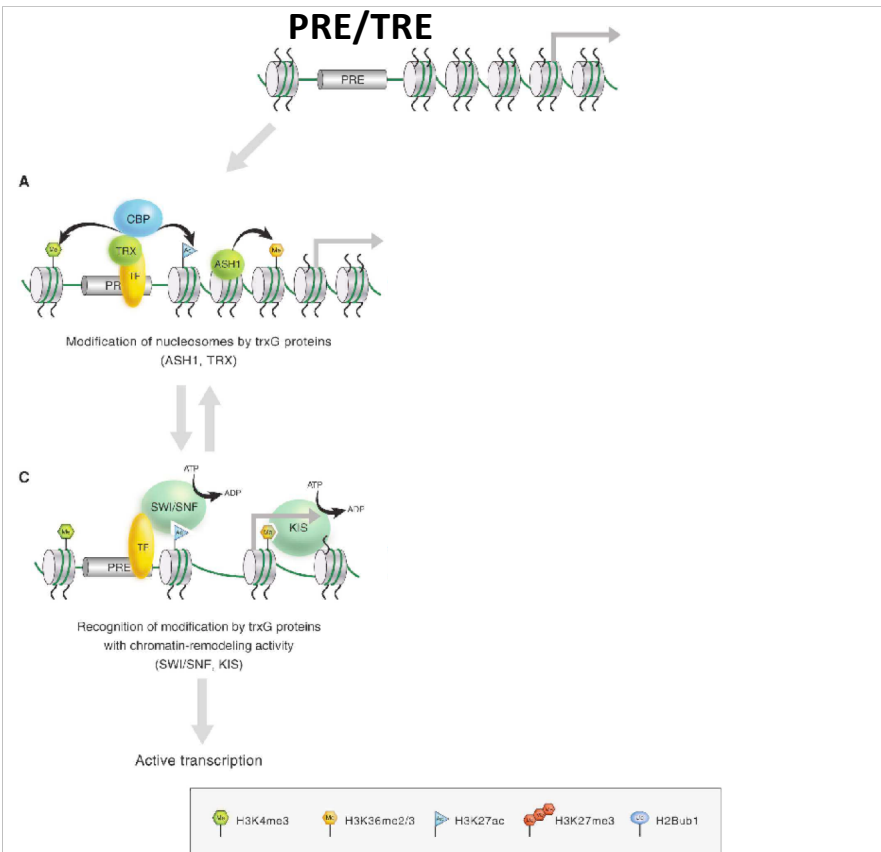


Un cromosoma politenico è un cromosoma gigante. I cromosomi politenici si formano in seguito a vari cicli di replicazione che producono molte copie (anche centinaia) di cromatidi fratelli che rimangono uniti. La formazione dei cromosomi politenici ha la funzione di aumentare il volume cellulare ma può anche comportare un vantaggio metabolico dato che l'elevato numero di copie di geni permette un alto livello di espressione genica. In *Drosophila melanogaster*, per esempio, i cromosomi delle ghiandole salivari delle larve subiscono numerosi cicli di endoreplicazione, e questo consente di produrre grandi quantità di secreto prima dell'impupamento.



**Figure 6.** Chromosomal distribution of *trxG* proteins. The genome-wide distribution of *trxG* proteins was examined by staining *Drosophila* salivary gland polytene chromosomes with antibodies against BRM (A) or TRX (B). Consistent with a relatively global role in transcriptional activation, BRM is associated with hundreds of sites in a pattern that overlaps extensively with RNA Pol II. In contrast, strong TRX signals are detected at a much smaller number of sites on polytene chromosomes.

# 1. TRITHORAX GROUP GENES COVALENTLY MODIFY HISTONES



**Figure 7.** trxG and PcG functions and interactions. Both trxG and PcG families include proteins that covalently modify histones and those that noncovalently modify chromatin. Covalent modifications on histones can promote or block the binding or activity of trxG complexes (e.g., SWI/SNF and KIS), PcG complexes (e.g., PRC1 and PRC2), or other factors involved in the maintenance of active or repressed states. Binding by these latter complexes has the potential to lead to further covalent modification, thus leading to iterative cycles of covalent modification and recognition of the covalent marks.

Fly **TRX** has 6 HKMTs homologs in humans:

- hSET1A
  - hSET1B
  - MLL1
  - MLL2
  - MLL3
  - MLL4
- COMPASS complex components: H3K4 methylation and promotion of shift from transcriptional initiation to elongation; in general H3K4me associates with active transcription
- H3K4me associates with active transcription

Fly **ASH1** has 1 HKMT homolog in humans:

- hASH1
- H3K4me and H3K36 methylation → activation of transcription

**REMEMBER THE LINK BETWEEN H3K4me and DNA methylation**

## 2. A LINK BETWEEN TrxG PROTEINS AND HISTONE ACETYLATION

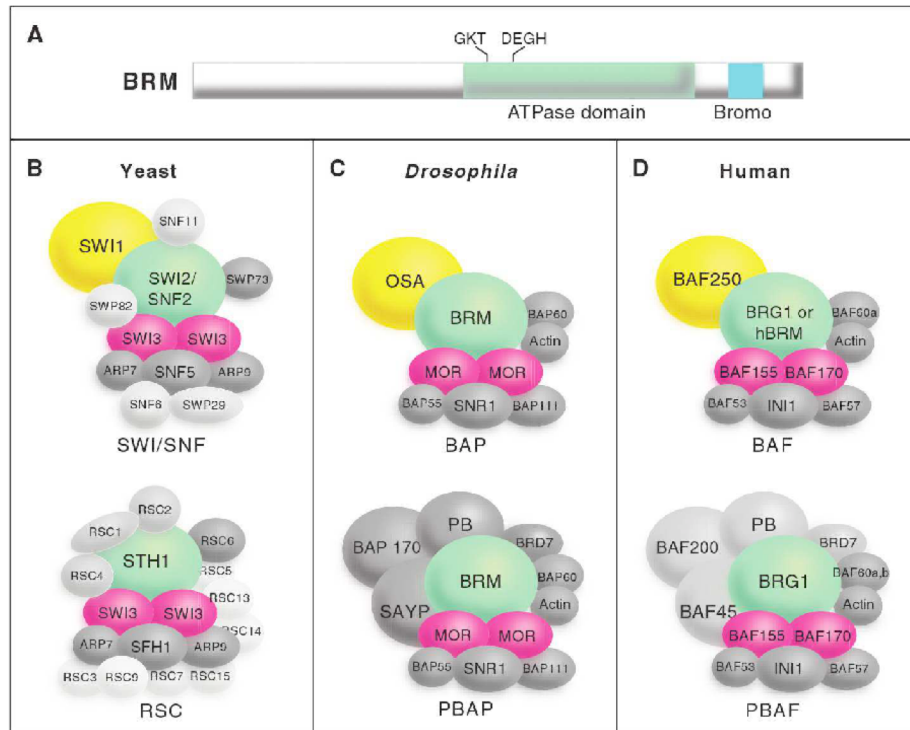
Fly: -

TRX is associated with dCBP: a histone lysine acetyl transferase (dCBP is not a TrxG gene) (humans: CBP/p300 HAT complex!!!). Recruitment of TrxG proteins by transcription factor brings HAT and leads to:

- TrxG protein kismet (kis) contains a helicase domain is recruited after ASH1 activity → chromatin remodeling

- H3K4 methylation, H3K36 methylation
  - H3 and H4 acetylation
  - Reduced H3K9 methylation
  - Reduced H3K27 methylation
  - Reduced DNA methylation (humans)
- EPIGENETIC ACTIVATION OF GENE EXPRESSION**

### 3. TRITHORAX GROUP PROTEINS ARE CENTRAL CHROMATIN REMODELERS



**Figure 5.** The SWI/SNF family of remodeling complexes. Each complex contains a member of SNF2/SWI2 family of ATPases and at least eight other subunits. (A) Schematic diagram of the BRM protein showing the location of the ATPase domain and carboxy-terminal bromodomain (which shows affinity to acetylated lysine residues in histone tails), which are conserved in all SNF2/SWI2 family members. SWI/SNF complexes in yeast (B), *Drosophila* (C), and humans (D) are shown. *Drosophila* trxG proteins (BRM, MOR, and OSA) and their counterparts in other organisms are shown in color. Further information about these complexes and their subunits may be found in [Mohrmann and Verrijzer \(2005\)](#).

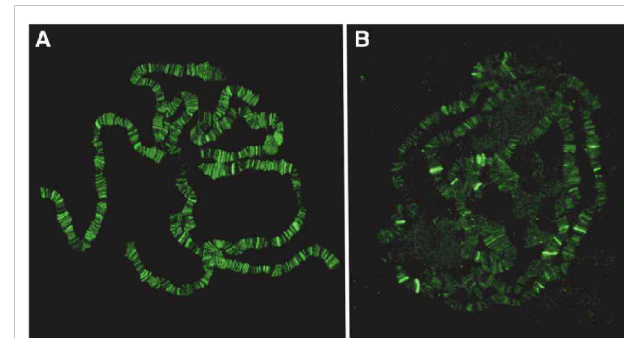
Trithorax group proteins BRM (fly) BRG1 (human) belong to the SWI/SNF family of chromatin remodelers.

SWI/SNF family chromatin remodeling complexes contain up to 18 subunits and can shift nucleosomes to increase the accessibility of regulatory sequences

Chromatin remodelers are recruited by transcription factors but are also recruited during transcriptional elongation.

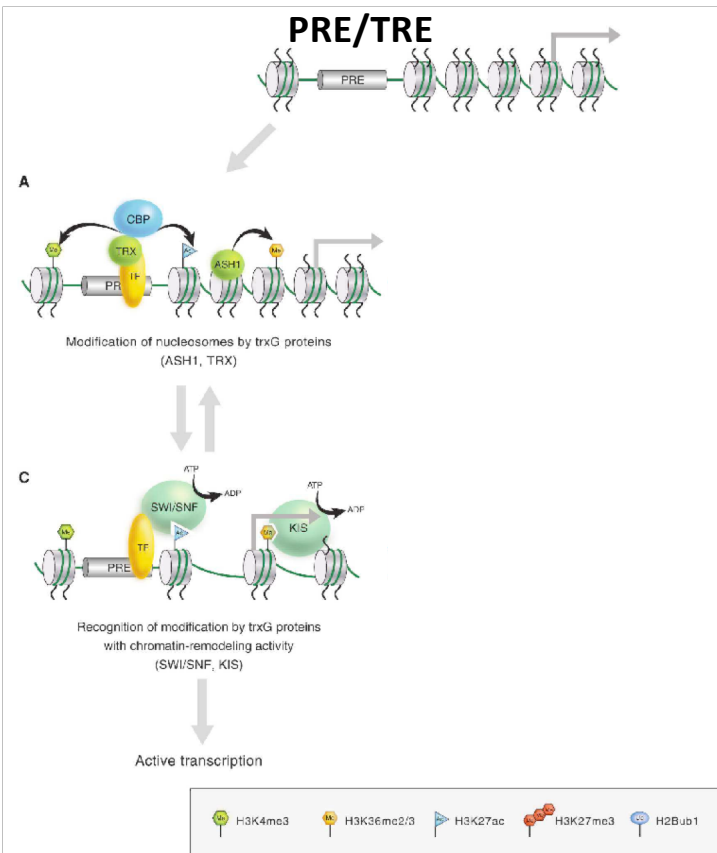
→ Chromatin remodeling is essential during all phases of transcription

→ #25000 complexes in a human cell: highly important for gene expression control



**Figure 6.** Chromosomal distribution of trxG proteins. The genome-wide distribution of trxG proteins was examined by staining *Drosophila* salivary gland polytene chromosomes with antibodies against BRM (A) or TRX (B). Consistent with a relatively global role in transcriptional activation, BRM is associated with hundreds of sites in a pattern that overlaps extensively with RNA Pol II. In contrast, strong TRX signals are detected at a much smaller number of sites on polytene chromosomes.

### 3. TRITHORAX GROUP PROTEINS ARE CENTRAL CHROMATIN REMODELERS



**Figure 7.** trxG and PcG functions and interactions. Both trxG and PcG families include proteins that covalently modify histones and those that noncovalently modify chromatin. Covalent modifications on histones can promote or block the binding or activity of trxG complexes (e.g., SWI/SNF and KIS), PcG complexes (e.g., PRC1 and PRC2), or other factors involved in the maintenance of active or repressed states. Binding by these latter complexes has the potential to lead to further covalent modification, thus leading to iterative cycles of covalent modification and recognition of the covalent marks.

Kismet (fly) CHD7 (human) has affinity for H3K36methylated chromatin  
 → Chromatin remodelling complex (multiprotein)  
 → Associated with RNA polymerase

**Table 1.** Biochemical functions of trxG proteins

Known function	Organism			Complexed with non-trxG proteins?
	<i>Drosophila</i>	Human	Yeast	
ATP-dependent chromatin remodeling	BRM	BRG1/HBRM	Swi2/Snf2, Sth1	Yes (5–10) <sup>a</sup>
	OSA	BAF250	Swi1/Adr6	Yes (5–10)
	MOR	BAF155, BAF170	Swi3, Rsc8	Yes (5–10)
	SNR1	hSNF5/INI1	Snf5, Sfh1	Yes (5–10)
	Kismet (KIS)	CHD7	–	NK
Histone methyltransferases	Trithorax (TRX)	MLL1, MLL3	MLL2, Set1	Yes (5–20)
	Absent, small or homeotic 1 (ASH1)	MLL4, hASH1	hSET1 –	NK
Mediator subunits	Kohtalo (KTO)	TRAP230	Srb8	Yes (13–24)
	Skuld (SKD)	TRAP240	Srb9	Yes (13–24)
Cohesin subunit	Verthandi (VTD)	Rad21	Scc1/Rad21	Yes (>3)
Transcription factor	Trithorax-like (TRL)	BTBD14B	–	No
Growth factor receptor	Breathless (BTL)	FGFR3	–	NK
Other	Sallimus (SLS)	Titin	–	NK

# CHARGE SYNDROME IS CAUSED BY MUTATION IN HUMAN *kis* (CHD7)

CHARGE syndrome (formerly known as CHARGE association), is a syndrome caused by a genetic disorder. It was first described in 1979. In 1981, the term "CHARGE" came into use as an acronym for the set of unusual congenital features seen in a number of newborn children.[1] The letters stand for: coloboma of the eye, heart defects, atresia of the nasal choanae, retardation of growth and/or development, genital and/or urinary abnormalities, and ear abnormalities and deafness. These features are no longer used in making a diagnosis of CHARGE syndrome, but the name remains. CHARGE syndrome is the leading cause of congenital deafblindness.

CHARGE syndrome was formerly referred to as CHARGE association, which indicates a non-random pattern of congenital anomalies that occurs together more frequently than one would expect on the basis of chance. Very few people with CHARGE will have 100% of its known features. In 2004, mutations on the CHD7 gene (located on Chromosome 8) were found in 10 of 17 patients in a study conducted in the Netherlands, making CHARGE an official syndrome. A further study in the US of 110 individuals with CHARGE syndrome showed that 60% of those tested had a mutation of the CHD7 gene.[6] CHD7 is a member of the chromodomain helicase DNA-binding (CHD) protein family that plays a role in transcription regulation by chromatin remodeling.[7]

1/10000 births

500 different mutations in CDH7 identified

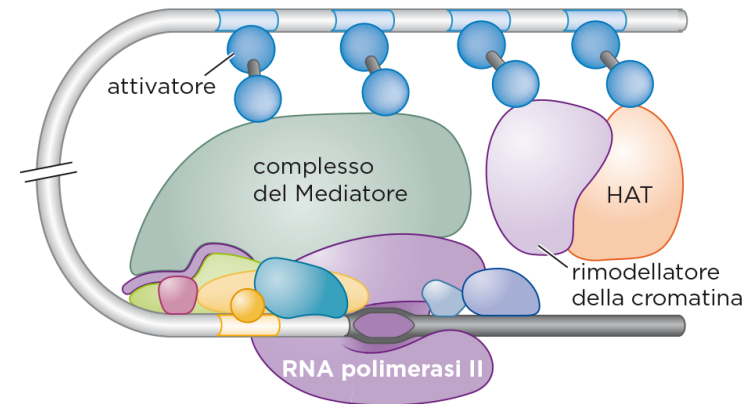


## Major Features of CHARGE Syndrome (very common in CHARGE and relatively rare in other conditions)

FEATURE	INCLUDES	FREQUENCY
Coloboma of the eye	Coloboma (sort of like a cleft) of the iris, retina, choroid, macula or disc (not the eyelid); microphthalmos (small eye) or anophthalmos (missing eye): CAUSES VISION LOSS <a href="#">Pictures</a>	80%-90%
Choanal atresia or stenosis	The choanae are the passages that go from the back of the nose to the throat. They can be narrow (stenosis) or blocked (atresia). It can be unilateral (one-sided) or bilateral (both sides), bony or membranous.  <b>Unilateral atresia or stenosis can be difficult to diagnose</b> <a href="#">Pictures</a>	50%-60%
Cranial nerve abnormality	I - Missing or decreased sense of smell	90-100%
	IX/X - Swallowing difficulties, aspiration - <a href="#">Pictures</a>	70%-90%
	VII - Facial palsy (one side or both) - <a href="#">Pictures</a>	40%
CHARGE outer ear	Short, wide ear with little or no lobe, "snipped off" helix (outer fold), prominent antihelix (inner fold) which is discontinuous with tragus, triangular concha, decreased cartilage (floppy), often stick out, usually asymmetric - <a href="#">Pictures</a>	>50%
CHARGE middle ear	Malformed bones of the middle ear (ossicles): CAUSES CONDUCTIVE HEARING LOSS	Common
CHARGE inner ear	Malformed cochlea (Mondini defect); small or absent semicircular canals: CAUSE HEARING LOSS AND BALANCE PROBLEMS - <a href="#">Pictures</a>	90%

## 4. TRITHORAX GROUP PROTEINS ARE ASSOCIATED WITH THE TRANSCRIPTIONAL COMPLEX

- The mediator complex is a large protein complex (<20 proteins) that communicates between the basal transcription factors and activating regulatory elements.
- Essential for the initiation of transcription!!



## 5. TRITHORAX GROUP PROTEINS ARE LINKED WITH LONG-RANGE CHROMATIN INTERACTION

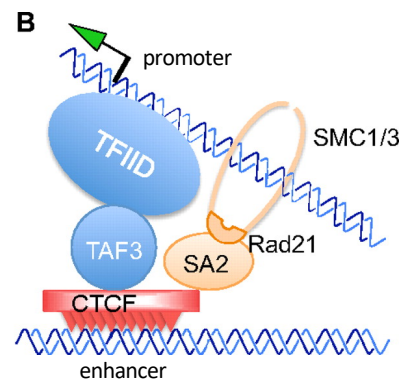
Rad21 is member of trithorax group genes!  
Has a role in long range chromatin interaction  
Links enhancers with promoters via loop formation

**Table 1.** Biochemical functions of trxG proteins

Known function	Organism			Complexed with non-trxG proteins?
	<i>Drosophila</i>	Human	Yeast	
ATP-dependent chromatin remodeling	BRM	BRG1/HBRM	Swi2/Snf2, Sth1	Yes (5–10) <sup>a</sup>
	OSA	BAF250	Swi1/Adr6	Yes (5–10)
	MOR	BAF155, BAF170	Swi3, Rsc8	Yes (5–10)
	SNR1	hSNF5/INI1	Snf5, Sfh1	Yes (5–10)
	Kismet (KIS)	CHD7	–	NK
Histone methyltransferases	Trithorax (TRX)	MLL1, MLL3	MLL2, Set1	Yes (5–20)
	Absent, small or homeotic 1 (ASH1)	MLL4, hASH1	hSET1 –	NK
Mediator subunits	Kohtalo (KTO)	TRAP230	Srb8	Yes (13–24)
	Skuld (SKD)	TRAP240	Srb9	Yes (13–24)
Cohesin subunit	Verthandi (VTD)	Rad21	Scc1/Rad21	Yes (>3)
Transcription factor	Trithorax-like (TRL)	BTBD14B	–	No
Growth factor receptor	Breathless (BTL)	FGFR3	–	NK
Other	Sallimus (SLS)	Titin		NK

## 5. TRITHORAX GROUP PROTEINS ARE LINKED WITH LONG-RANGE CHROMATIN INTERACTION

Rad21 is member of trithorax group genes!  
Has a role in long range chromatin interaction  
Links enhancers with promoters via loop formation



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Growth factor receptor	Breathless (BTL)	FGFR3	–	NK
Other	Sallimus (SLS)	Titin	–	NK

# Trithorax group proteins are recruited by TRE – Trithorax response elements

## DROSOPHILA

TRE elements are concentrated DNA binding sites for Trithorax group proteins

→ Recruitment function

NOTE: MOST TRE elements overlap with PRE elements

For example: GAF/Psq and Zeste have an important role in Trithorax recruitment  
And gene activation.

However, sites are located in PREs

→ Cell type specific transcription program (type and dosage of expressed transcription factors  
co-ordinate balance of Polycomb/Trithorax function

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## Polycomb/Trithorax response elements and epigenetic memory of cell identity

Leonie Ringrose<sup>1</sup> and Renato Paro<sup>2</sup>

PRE/TRE motifs and flexibility of PRE/TRE design. (A) DNA motifs shown to be important for PRE/TRE function. The Grh (Grainy head) protein binds to several different PRE/TRE sites. The motif shown is that found in PRE/TREs by Blastyak et al. (Blastyak et al., 2006). The Dsp1 protein also has broad DNA-binding specificity (Brickman et al., 1999). The motif shown is that used by Dejardin et al. (Dejardin et al., 2005). Gaf binds the same target sequence as Pipsqueak (Psq), suggesting that the two proteins may compete or cooperate at closely spaced sites. (B) Many of these motifs are important for regulating genes that do not have PRE/TREs, for example the *Drosophila* white gene which is regulated by the Zeste protein (600 bp of upstream regulatory region are shown). These motifs are also short and occur randomly in DNA, such as in the bacterial LacZ gene (the first 600 bp of the coding sequence are shown). (C) PRE/TREs have different combinations of motifs, with no preferred order or number. Shown here are ~600 bp of the *bxd* and *Fab-7* PREs from the *Drosophila* Bithorax complex, and of PRE/TREs from the *Drosophila* engrailed (*en*), vestigial (*vg*) and homothorax (*hth*) loci. **Grey boxes show minimal PRE/TREs where these have been defined (Dejardin et al., 2005; Brown et al., 2005).** Flanking sequences contain additional motif clusters which may contribute to the function of these PRE/TREs in their endogenous context.

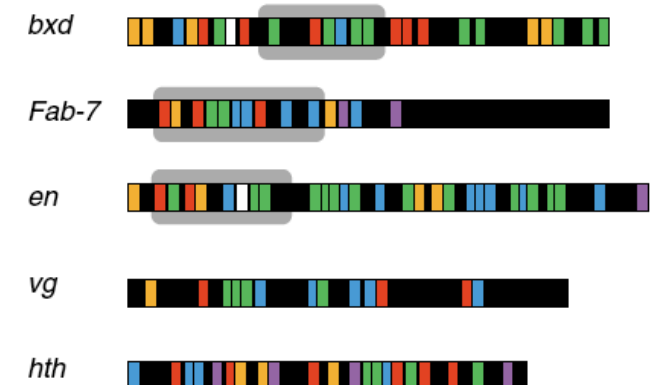
### A PRE motifs

	Pho/Phol	GCCAT
	Dsp1	GAAAA
	GAF/Psq	GAGAG
	Zeste	YGAGYG
	Grh	TGTTTTT
	Sp1/KLF	RRGGYGY

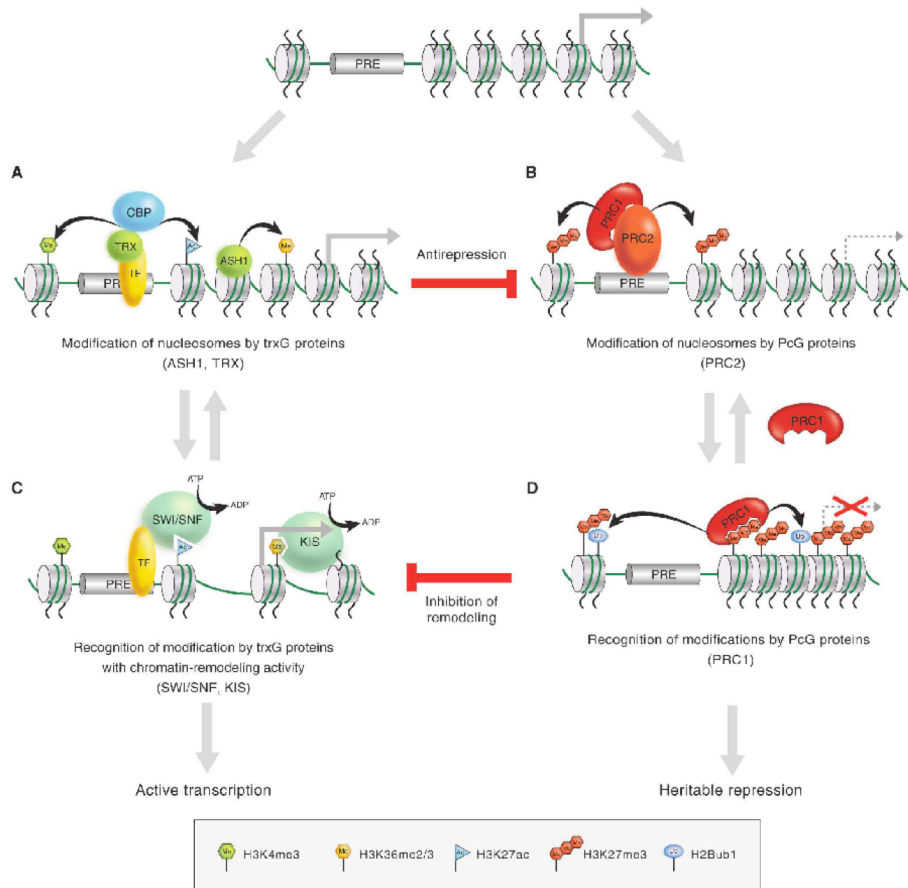
### B Motif occurrence in non-PREs



### C Motif occurrence in PREs



## COMPETEING FUNCTION OF POLYCOMB AND TRITHORAX GROUP PROTEINS AT PRE/TREs



**Figure 7.** TrxG and PcG functions and interactions. Both TrxG and PcG families include proteins that covalently modify histones and those that noncovalently modify chromatin. Covalent modifications on histones can promote or block the binding or activity of TrxG complexes (e.g., SWI/SNF and KIS), PcG complexes (e.g., PRC1 and PRC2), or other factors involved in the maintenance of active or repressed states. Binding by these latter complexes has the potential to lead to further covalent modification, thus leading to iterative cycles of covalent modification and recognition of the covalent marks.

- ASH1 mediates H3K4me3 and H3K36me3
- H3K36 methylation enhances transcriptional elongation
- TRX/CBP complex mediates H3K4methylation and H3K27acetylation
- H3K27acetylation prevents H3K27methylation by E(z)
- H3K4me3 inhibits the recruitment of PRC2
- H3K36methylation inhibits the activity of PRC2

**FUNCTIONAL ANTAGONISM + PREVENTION OF SPREADING OF PcG and TrxG TYPE OF CHROMATIN**

**REMEMBER: TRANSCRIPTION FACTORS CONTROL THE EQUILIBRIUM BETWEEN PcG and TrxG**

## EXPERIMENTAL APPROACH IN DROSOPHILA:

### A SUPPRESSOR MUTATION SCREEN TO IDENTIFY EPIGENETIC REGULATORS THAT ACTIVATE GENE EXPRESSION --- TRITHORAX GROUP GENES ---

