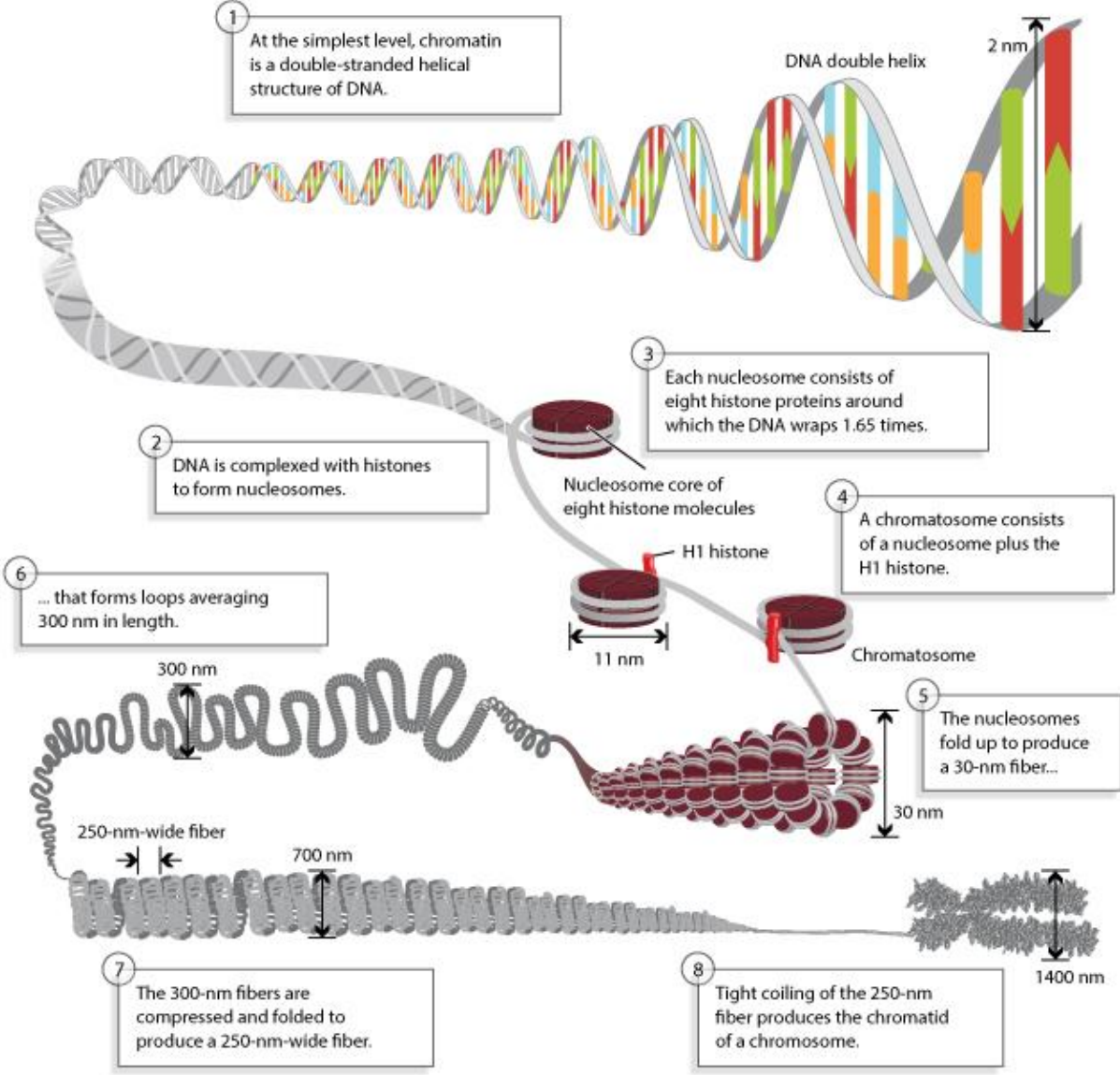


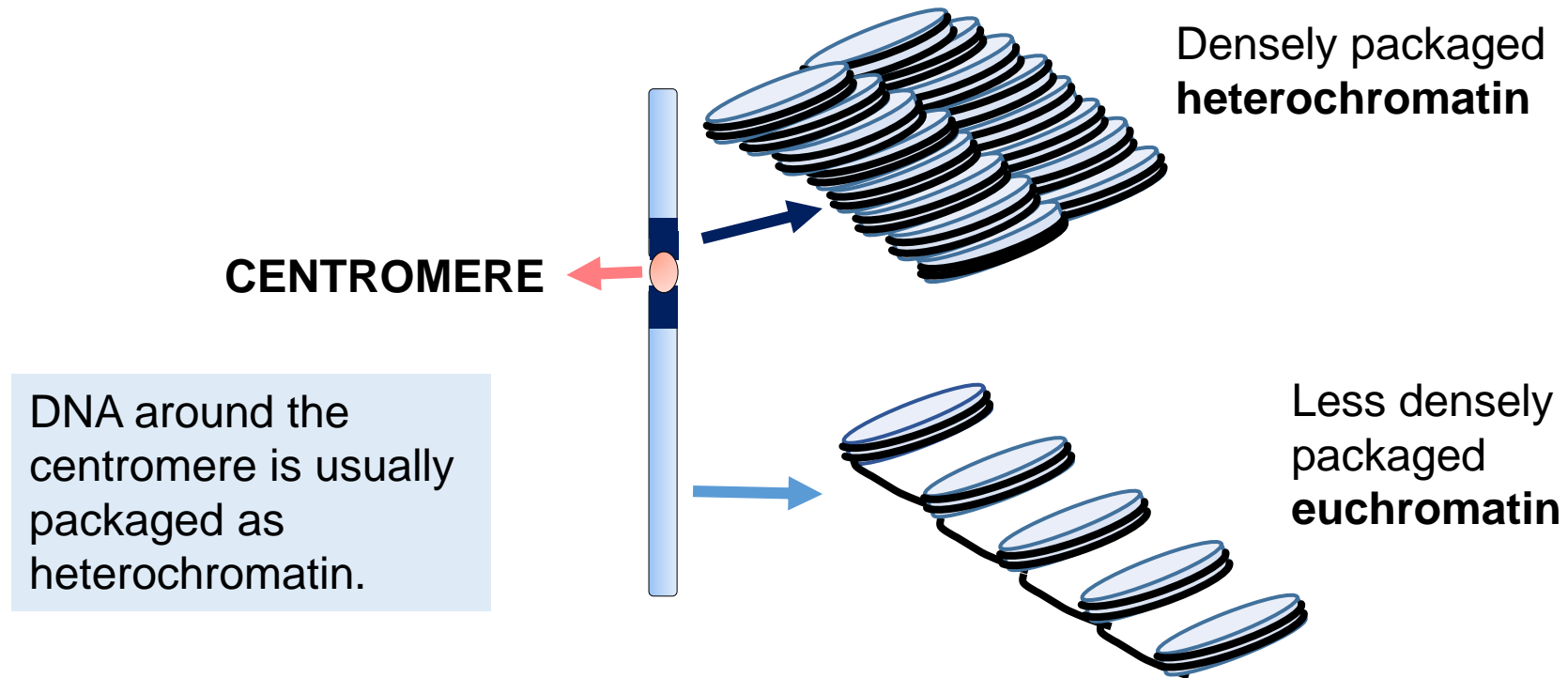
Chromatin modifications, reshuffling and restructuring

Sotirios (Akis) Fragkostefanakis
fragkost@bio.uni-frankfurt.de

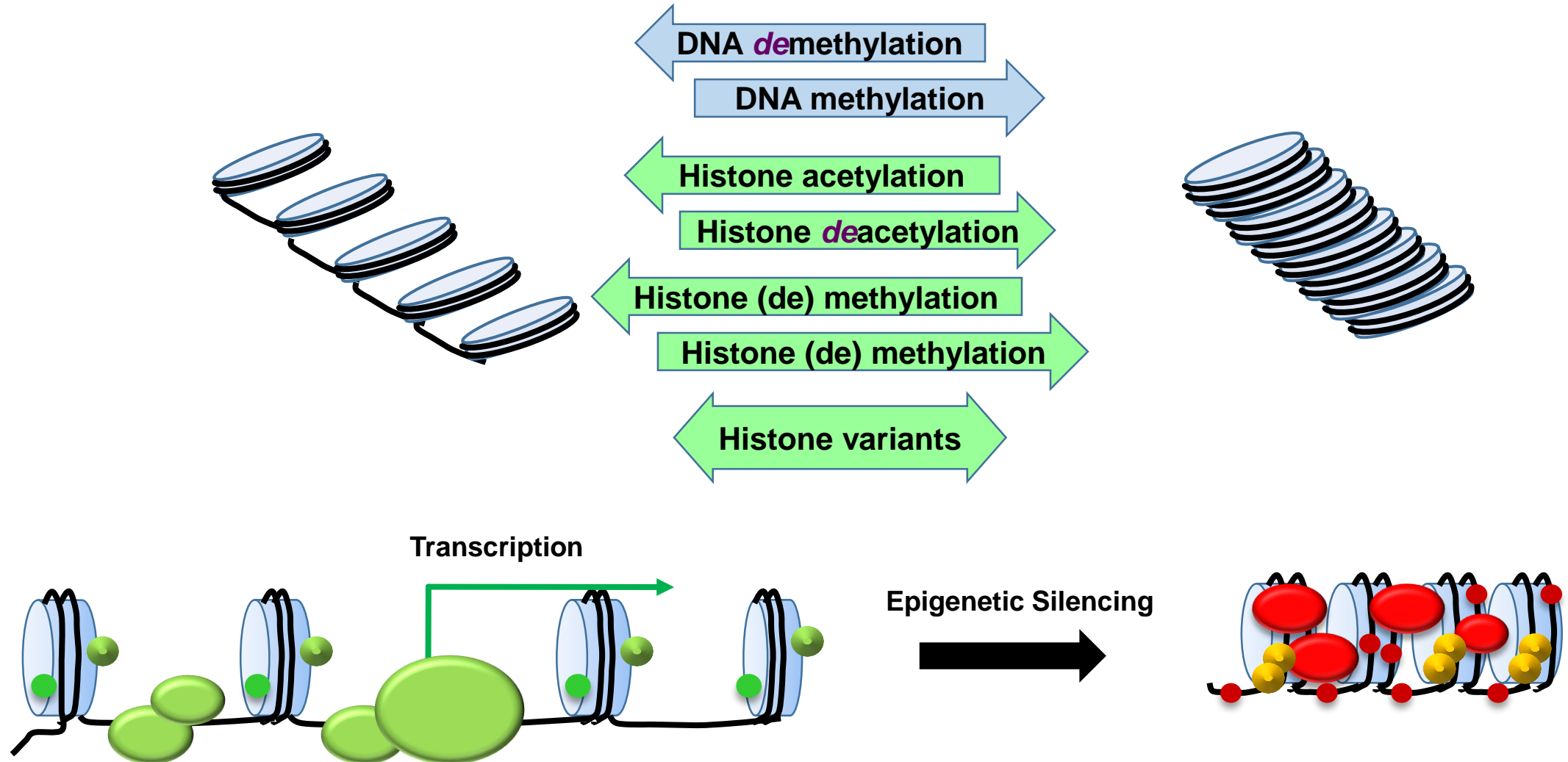
DNA Packaging: Nucleosomes and Chromatin



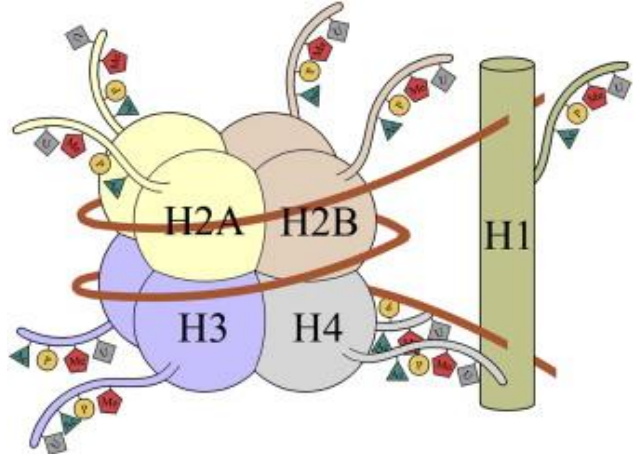
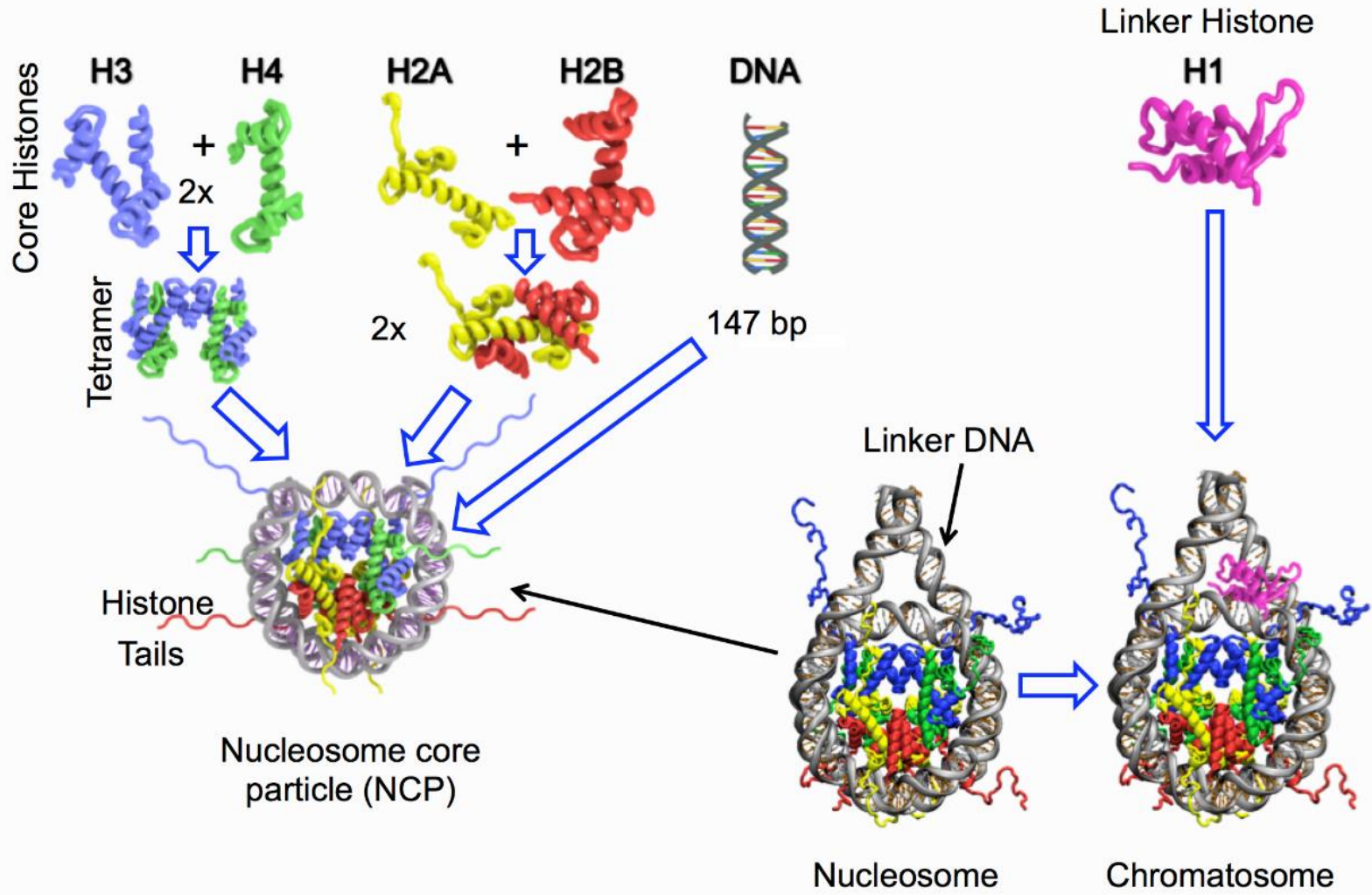
Chromosomes consist of heterochromatin and euchromatin



Chromosomes consist of heterochromatin and euchromatin



Histone complex



Histone variants in plants

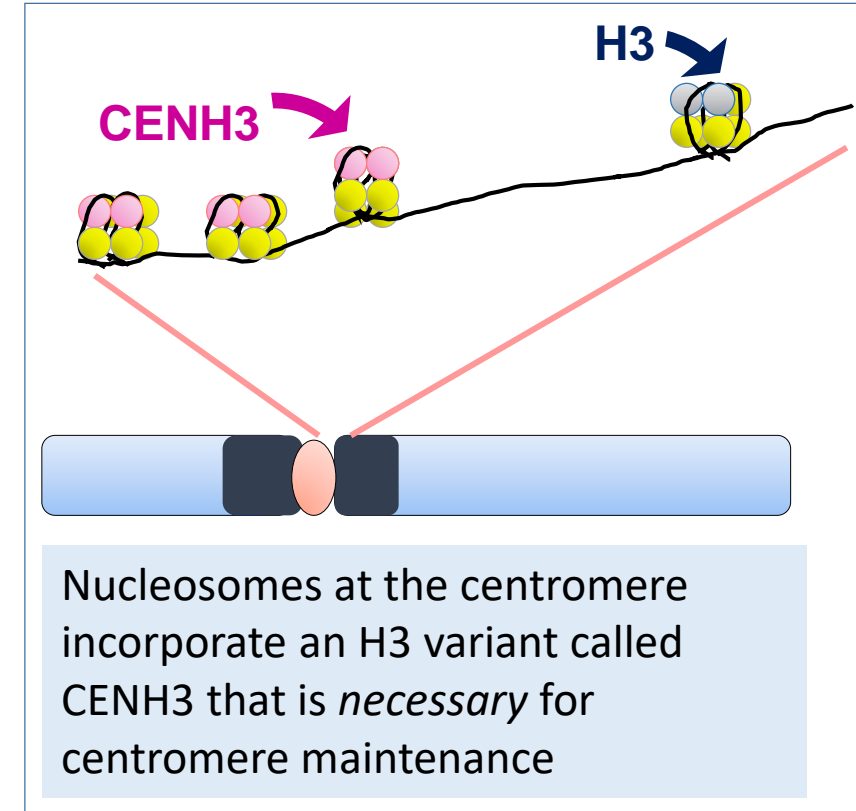
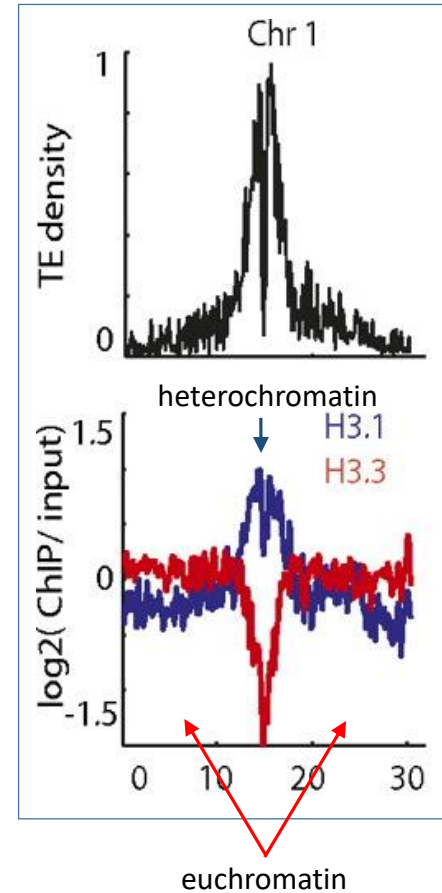
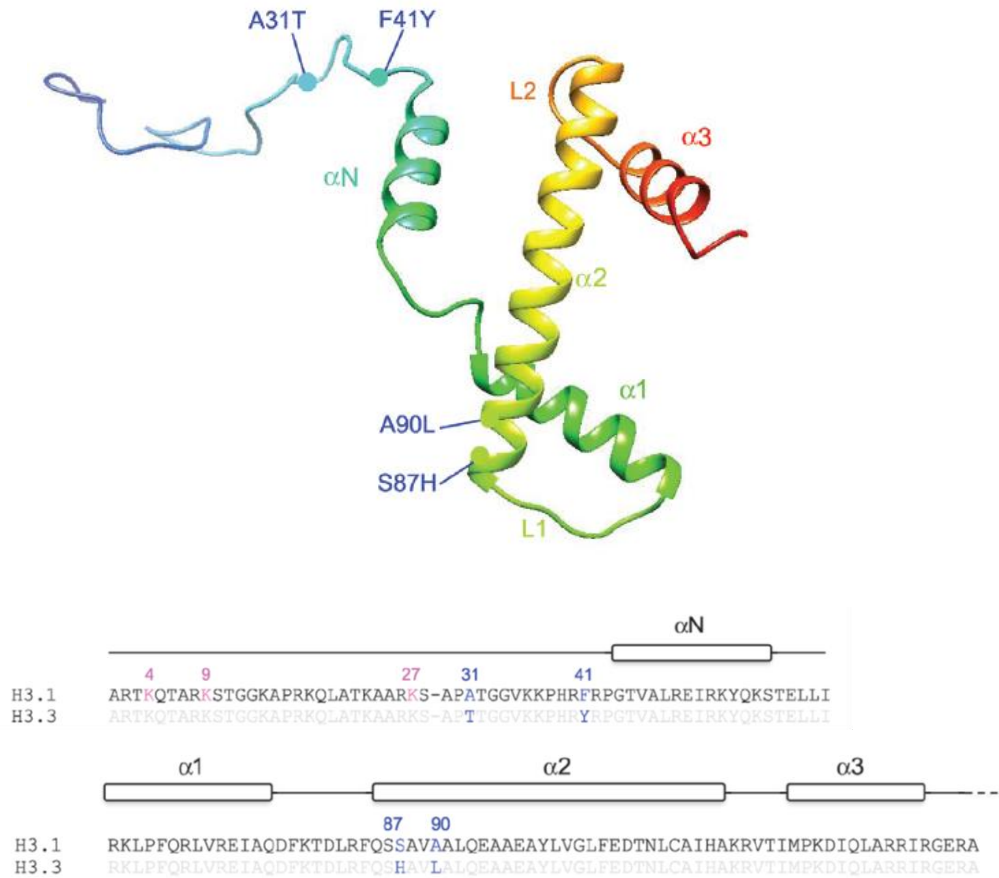
Arabidopsis thaliana histone-coding genes

Histone H3	Gene	Histone H4	Histone H2A	Histone H2B
Histone H3		H4	H2A.1	H2B.1
H3.1	<i>At5g65360, HTR1</i>	<i>At3g46320</i>	<i>At5g54640, HTA1</i>	<i>At1g07790, HTB1</i>
	<i>At1g09200, HTR2</i>	<i>At5g59690</i>	H2A.2	<i>At5g22880, HTB2</i>
	<i>At3g27360, HTR3</i>	<i>At2g28740</i>	H2A.10	<i>At2g28720, HTB3</i>
	<i>At5g10400, HTR9</i>	<i>At1g07820</i>	<u>H2A.13</u>	<i>At5g59910, HTB4</i>
	<u><i>At5g10390, HTR13</i></u>	<i>At3g53730</i>	H2A.X.3	<i>At2g37470, HTB5</i>
H3.3	<i>At4g40030, HTR4</i>	<i>At5g59970</i>	H2A.X.5	<i>At3g53650, HTB6</i>
	<i>At4g40040, HTR5</i>	<i>At3g45930</i>	H2A.W.6	<i>At3g09480, HTB7</i>
	<i>At5g10980, HTR8</i>	<i>At1g07660</i>	H2A.W.7	<i>At1g08170, HTB8</i>
H3.6	<i>At1g13370, HTR6</i>		H2A.W.12	<i>At3g45980, HTB9</i>
H3.7	<i>At1g75610, HTR7</i>		H2A.Z.4	<i>At5g02570, HTB10</i>
H3.10	<i>At1g19890, HTR10</i>		H2A.Z.8	<i>At3g46030, HTB11</i>
H3.11	<i>At5g65350, HTR11</i>		H2A.Z.9	
CenH3	<i>At1g01370, HTR12</i>		H2A.Z.11	
H3.14	<i>At1g75600, HTR14</i>			
H3.15	<i>At5g12910, HTR15</i>			

Replicative/canonical: expressed during S-phase and deposited during DNA replication in a DNA-synthesis-dependent manner

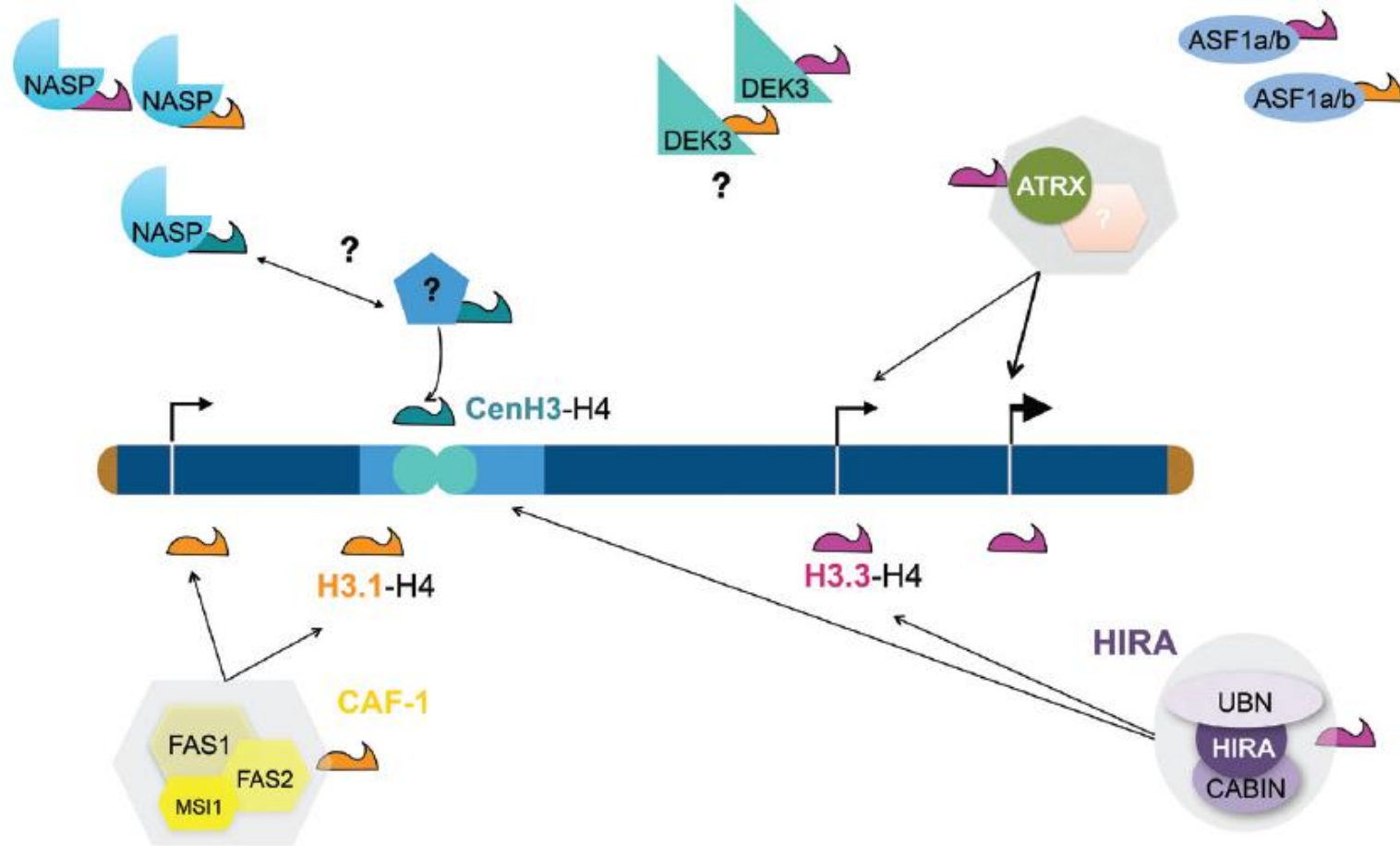
Replacement: expressed throughout the cell-cycle and are deposited in a DNA-synthesis-independent manner

Three main H3 variants: H3.1, H3.3 & CenH3



Deposition of H3 variants by histone chaperones

ASF: Anti Silencing Factor



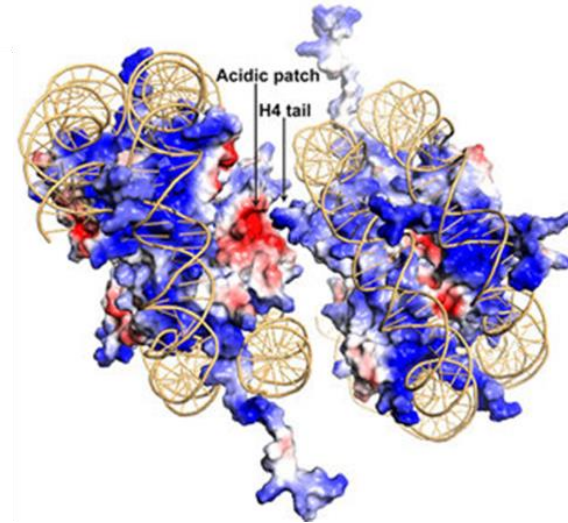
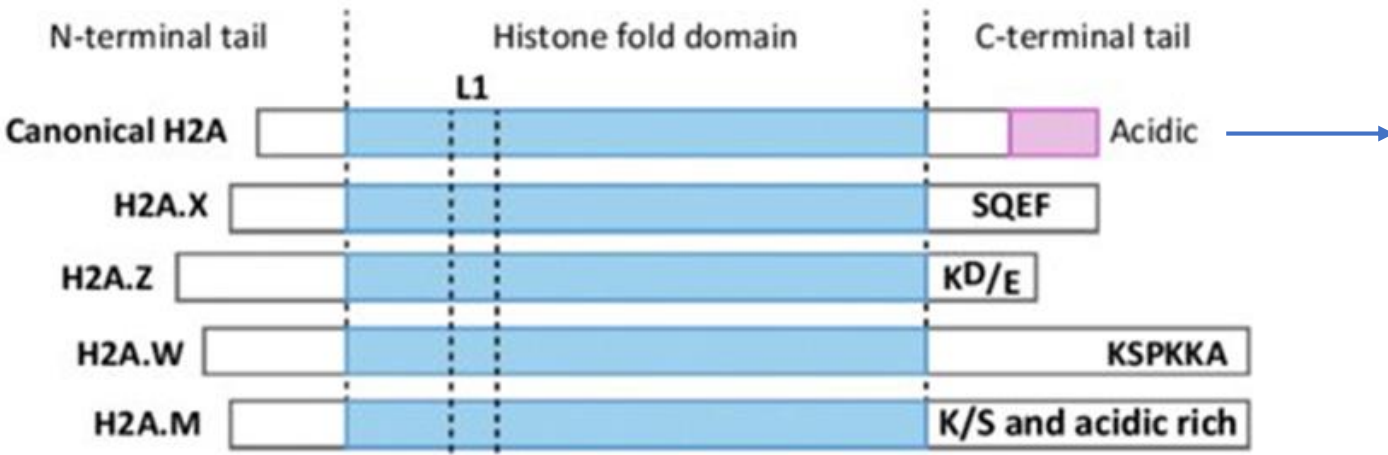
NASP: Nuclear Autoantigenic Sperm Protein

CAF-1: Chromatin assembly factor 1
 FAS: Fasciata
 MSI: Multicopy Suppressor of IRA

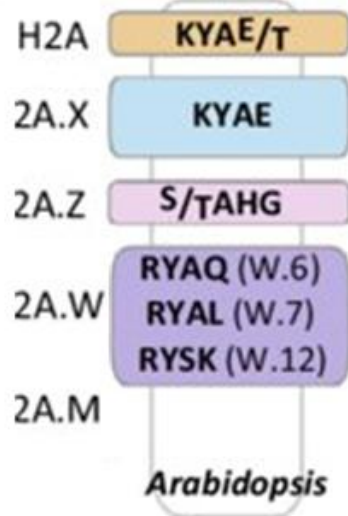
HIRA: Histone Regualtor A
 UBN: Ubinuclein
 CABIN: Calcineurin Binding Protein

Histone H2A variants

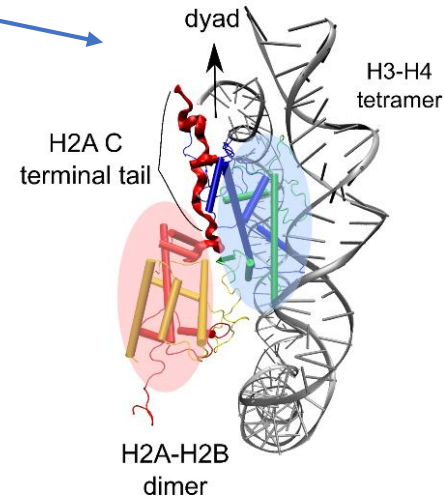
Nucleosome array compaction



Dhall et al. 2014, J. Biol. Chem.

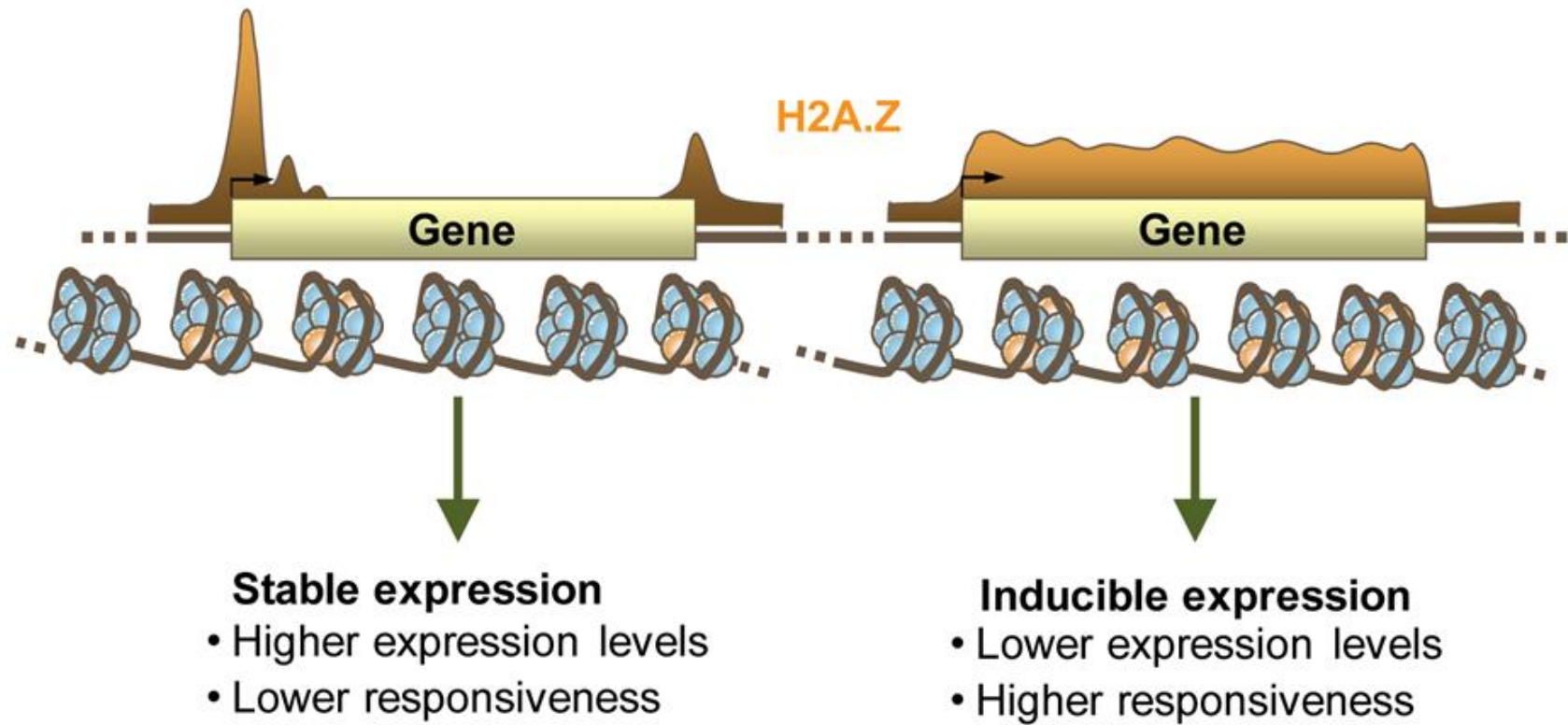


Dimer formation
Nucleosome stability

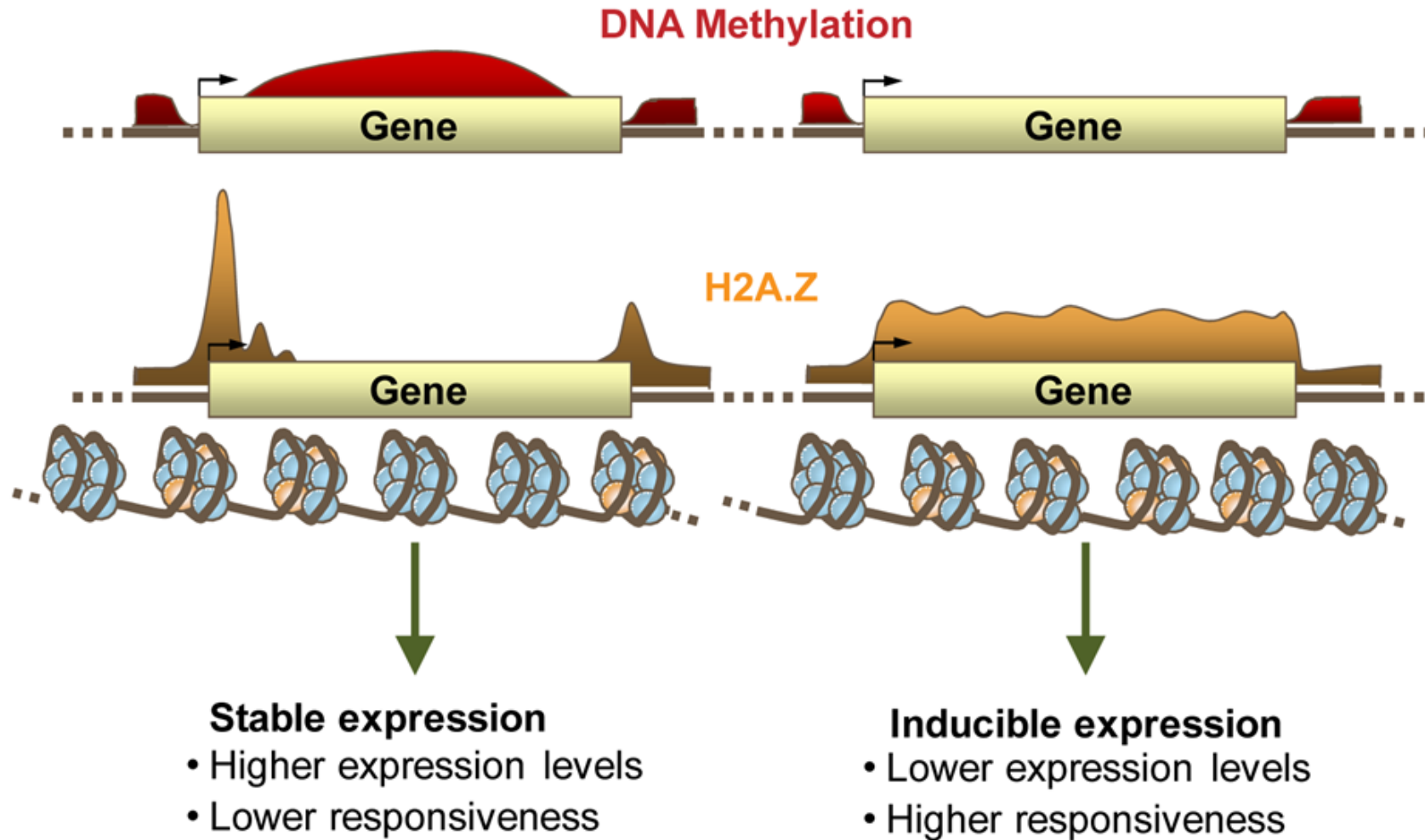


Biswas et al. 2011, PLOS Comp. Biol.

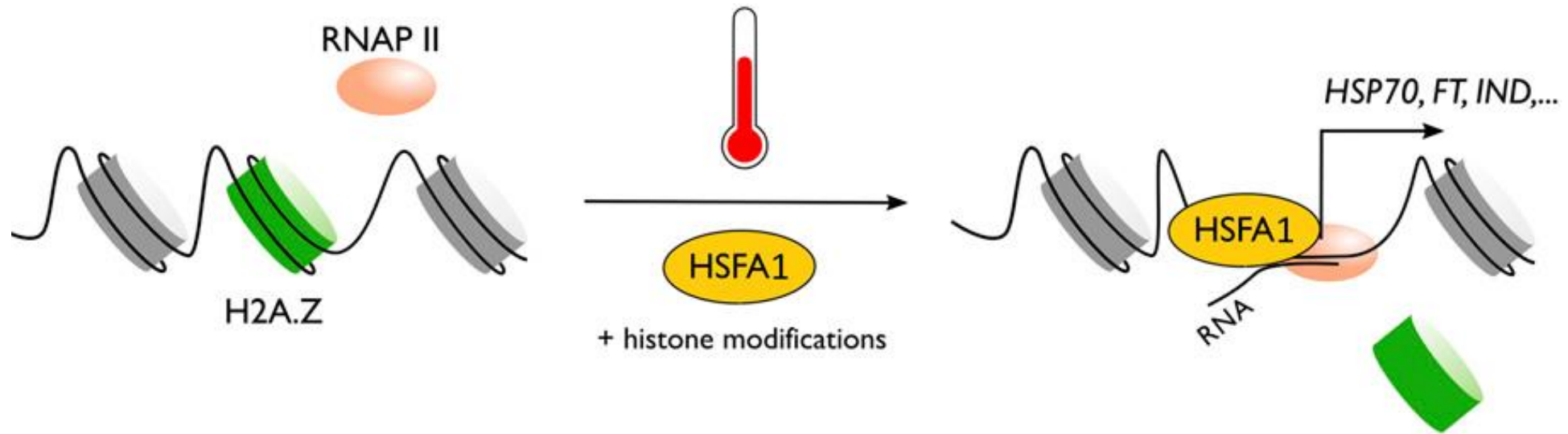
H2A.Z and expression patterning



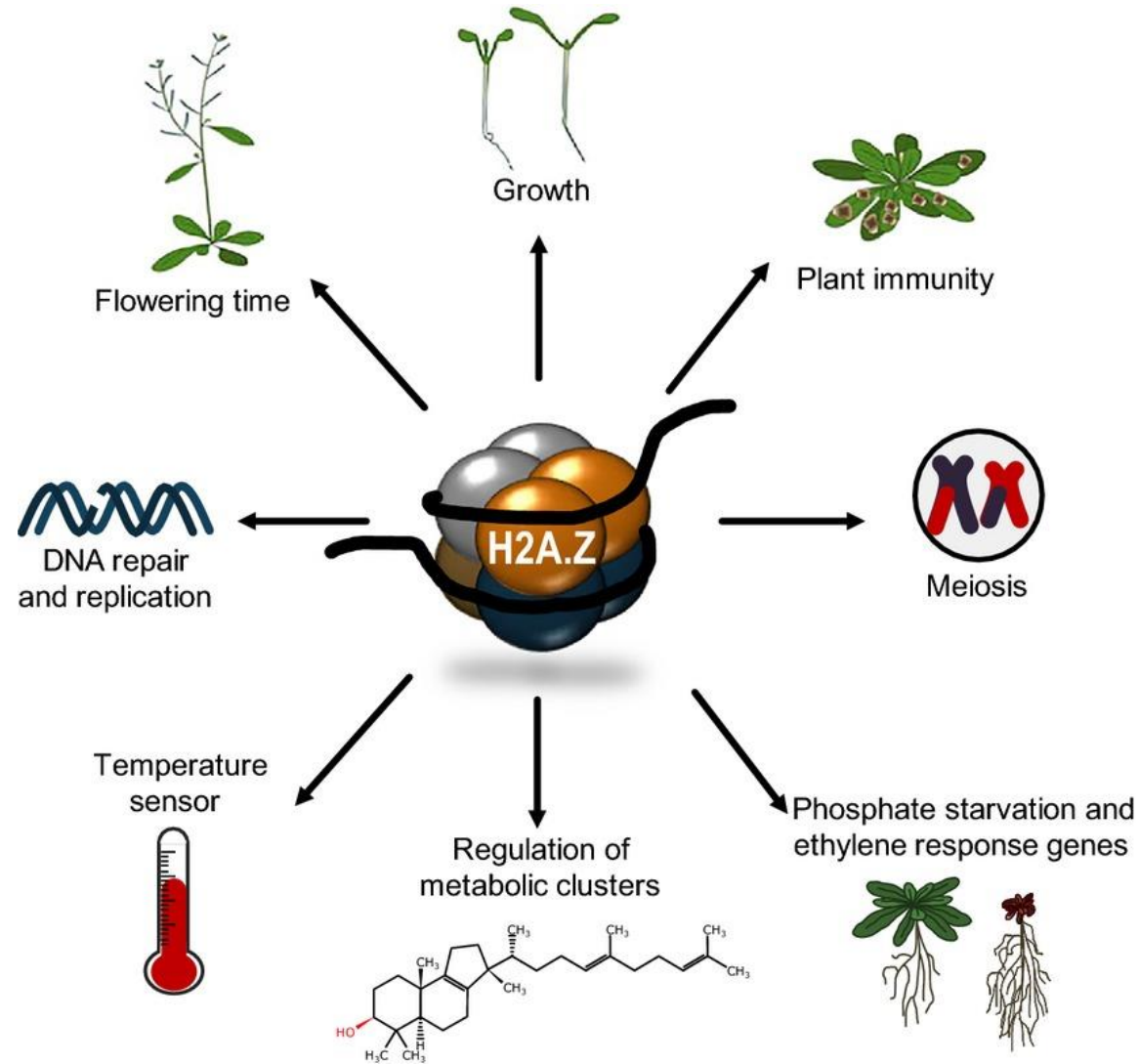
H2A.Z and expression patterning



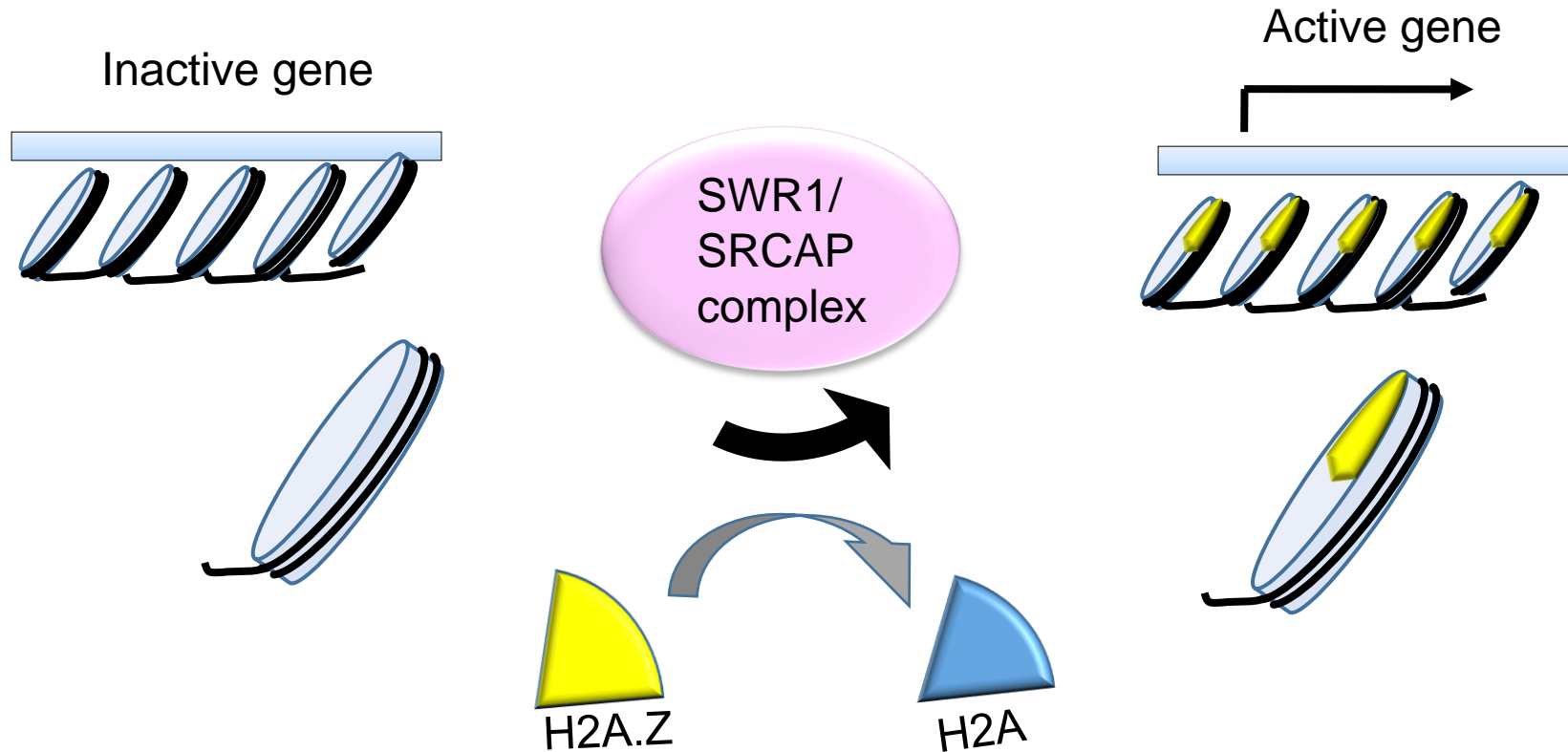
H2A.Z regulates the responsiveness of heat stress induced genes



H2A.Z in plant development and stress responses

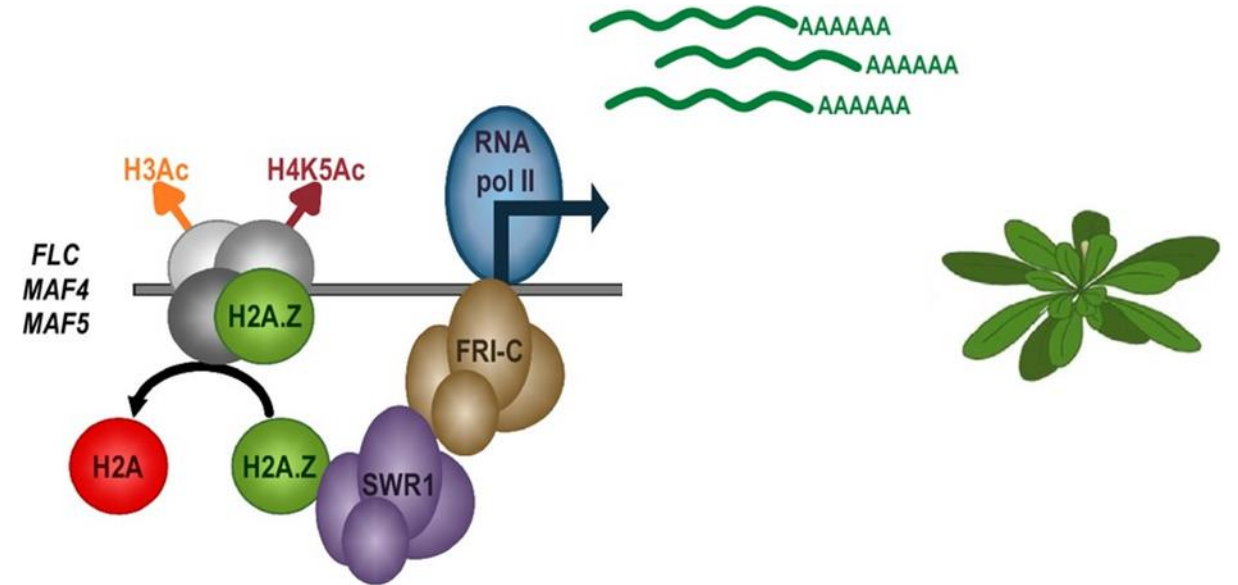
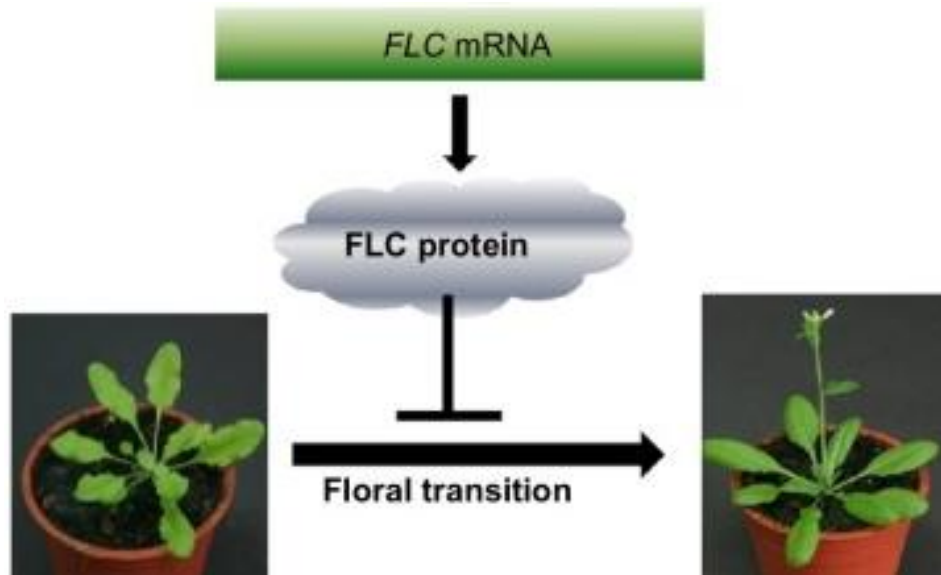


Remodelling of chromatin by SWR1

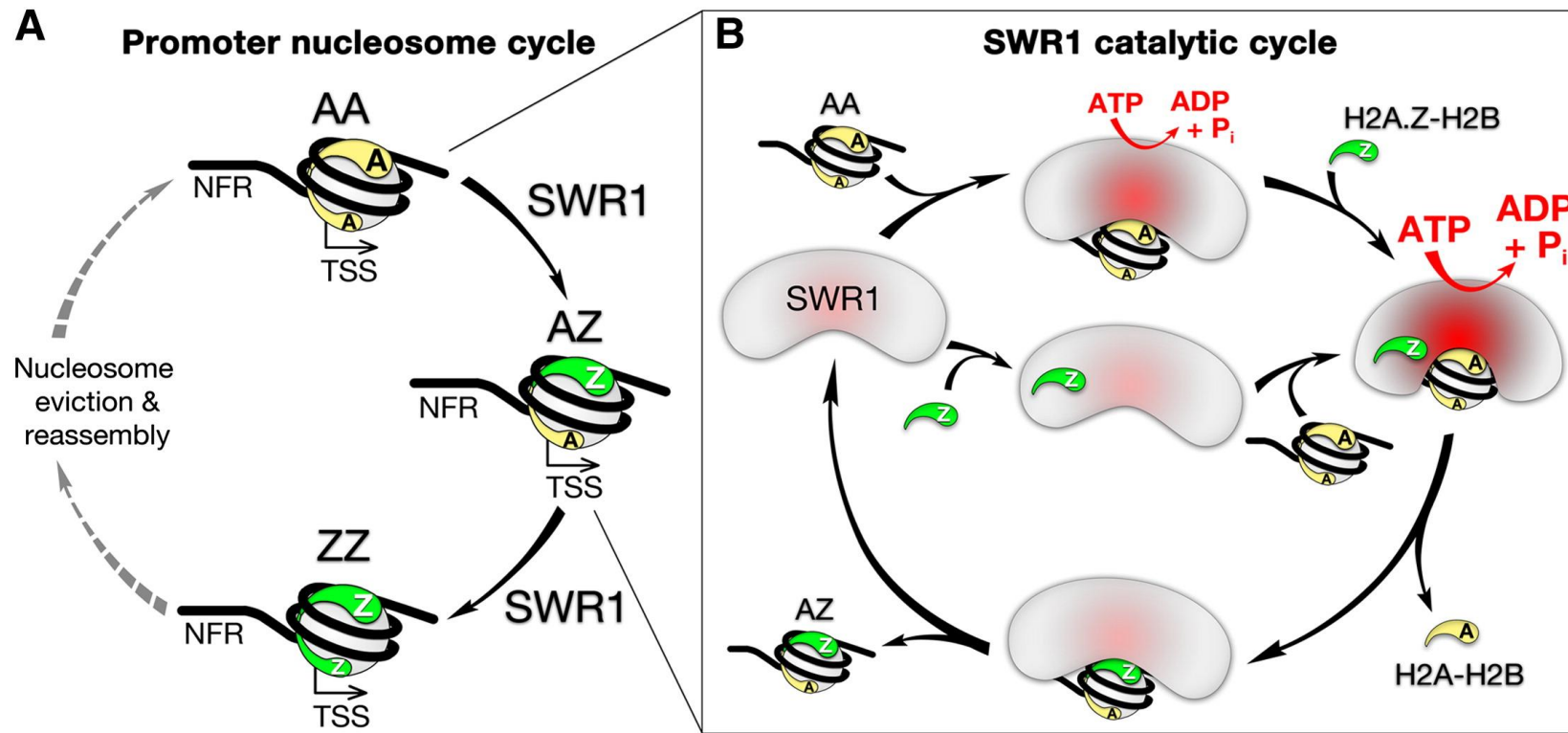


The histone variant H2A.Z promotes transcription and is swapped into the nucleosome by the SWR1/SRCAP complex.

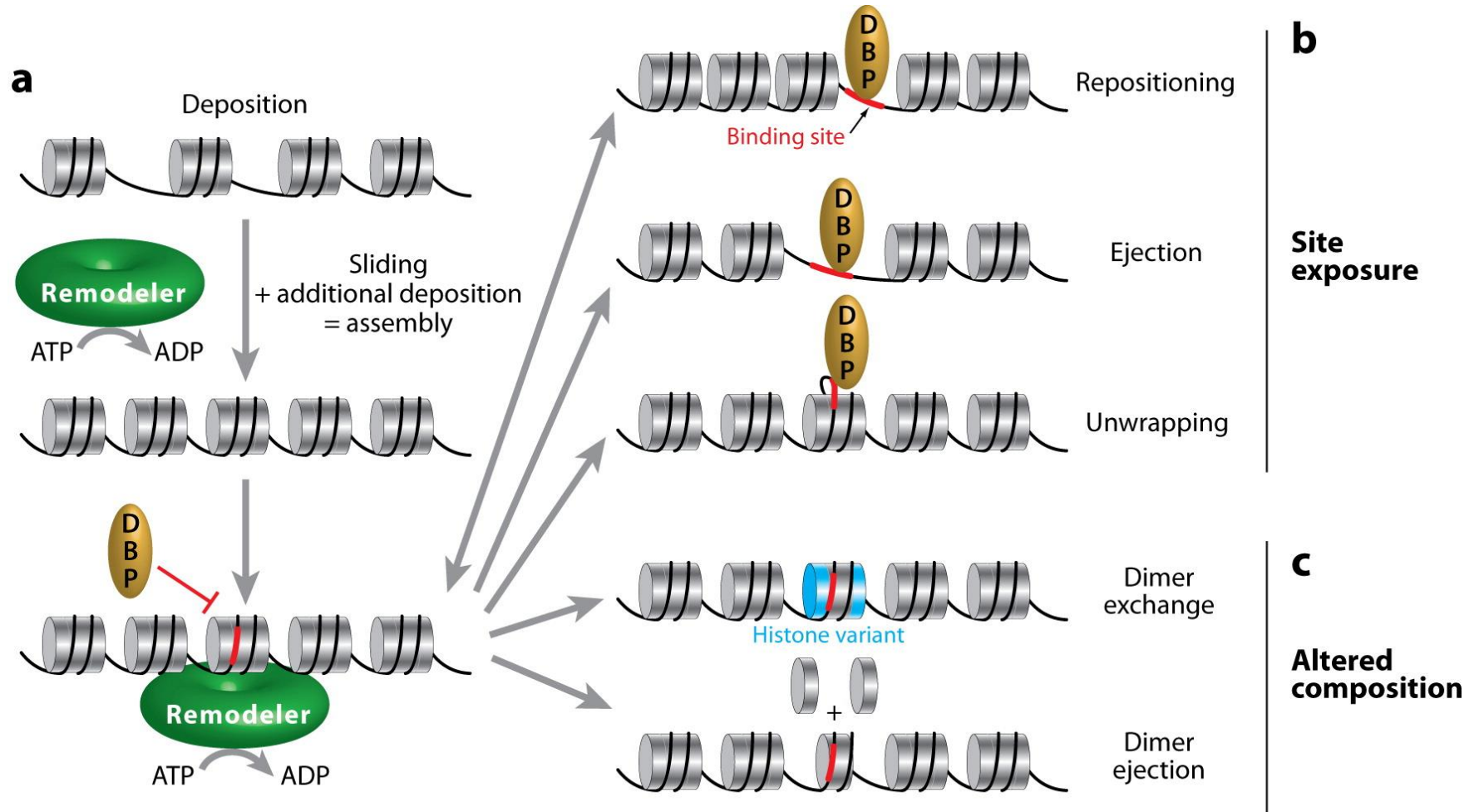
H2A.Z deposition by SWR1 complex



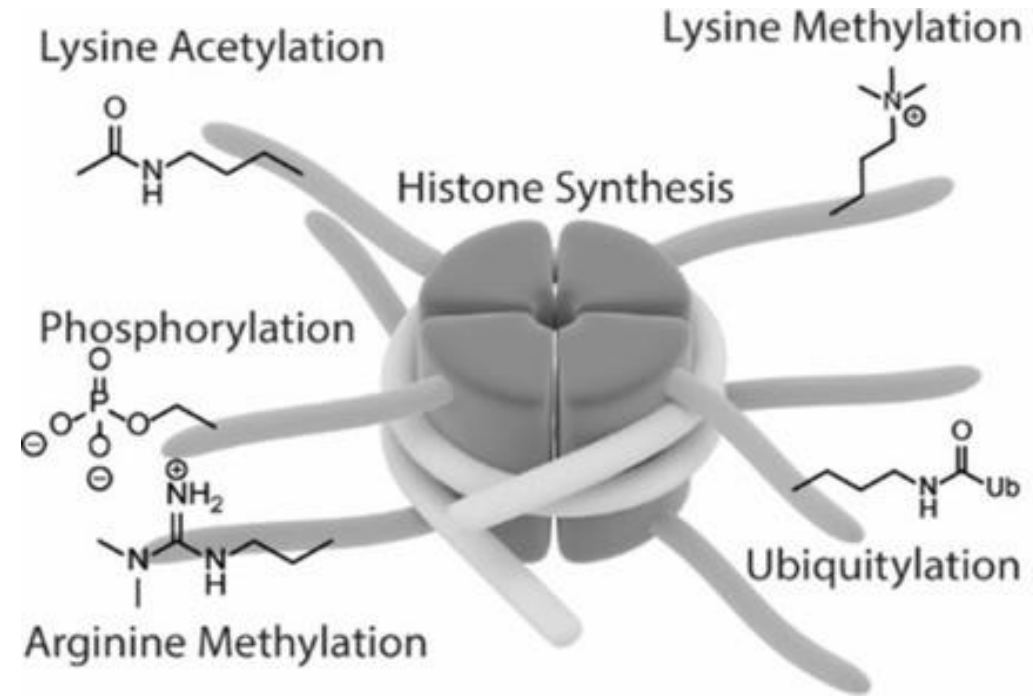
Remodelling of chromatin by SWR1



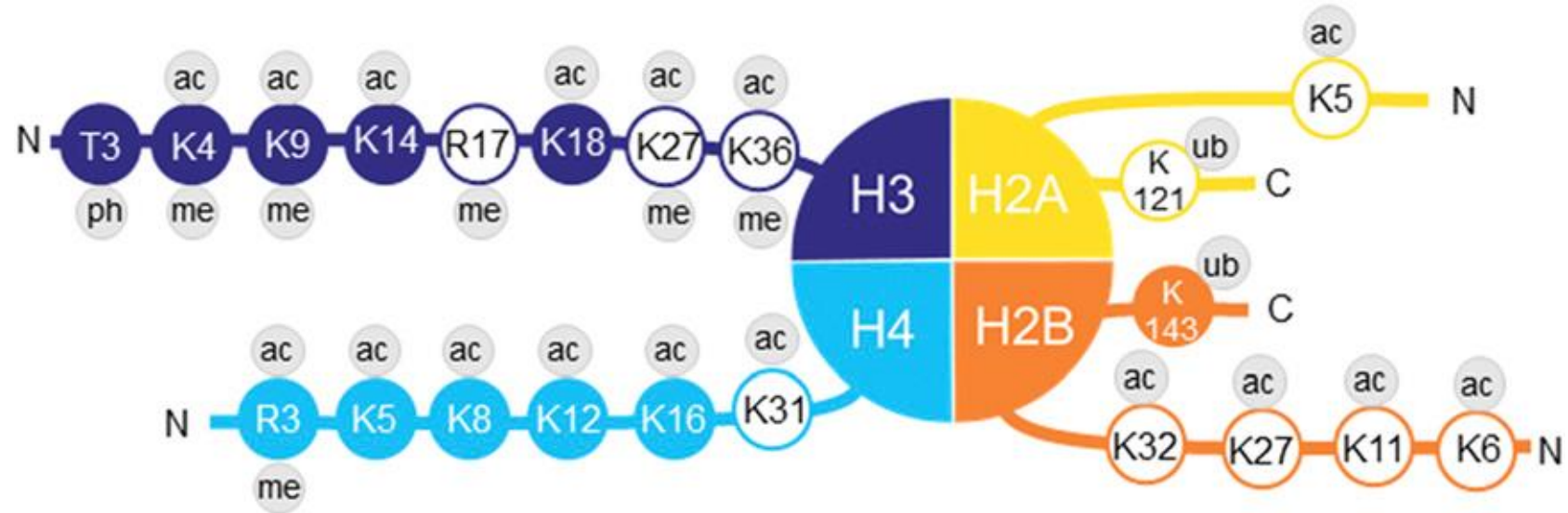
Remodelers use energy to move/alter histone octamers



Post-translational modifications of histones



Histone modifications in plants



Active marks

Histone acetylations, H2Bub
H3K4me3, H3K36me2/3

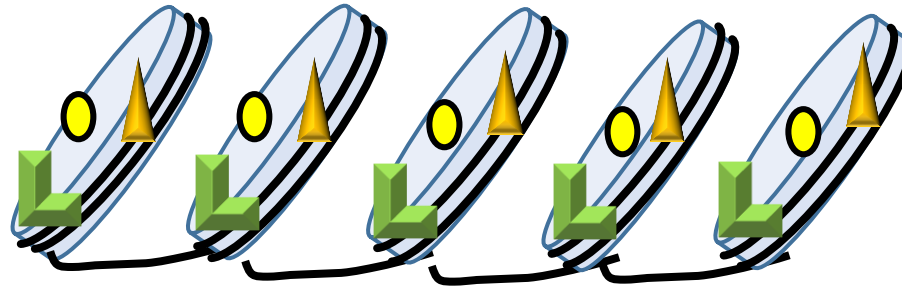
Repressive marks

H3K9me2/3, H3K27me3, H3T3ph,
H2Aub, symmetric H4R3

Histone modification affects chromatin structure

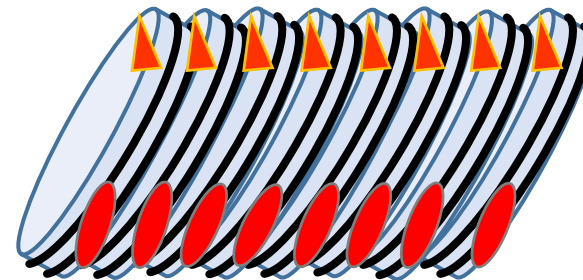
Open configuration

H3	Me	P	Ac
	K4	S10	K14



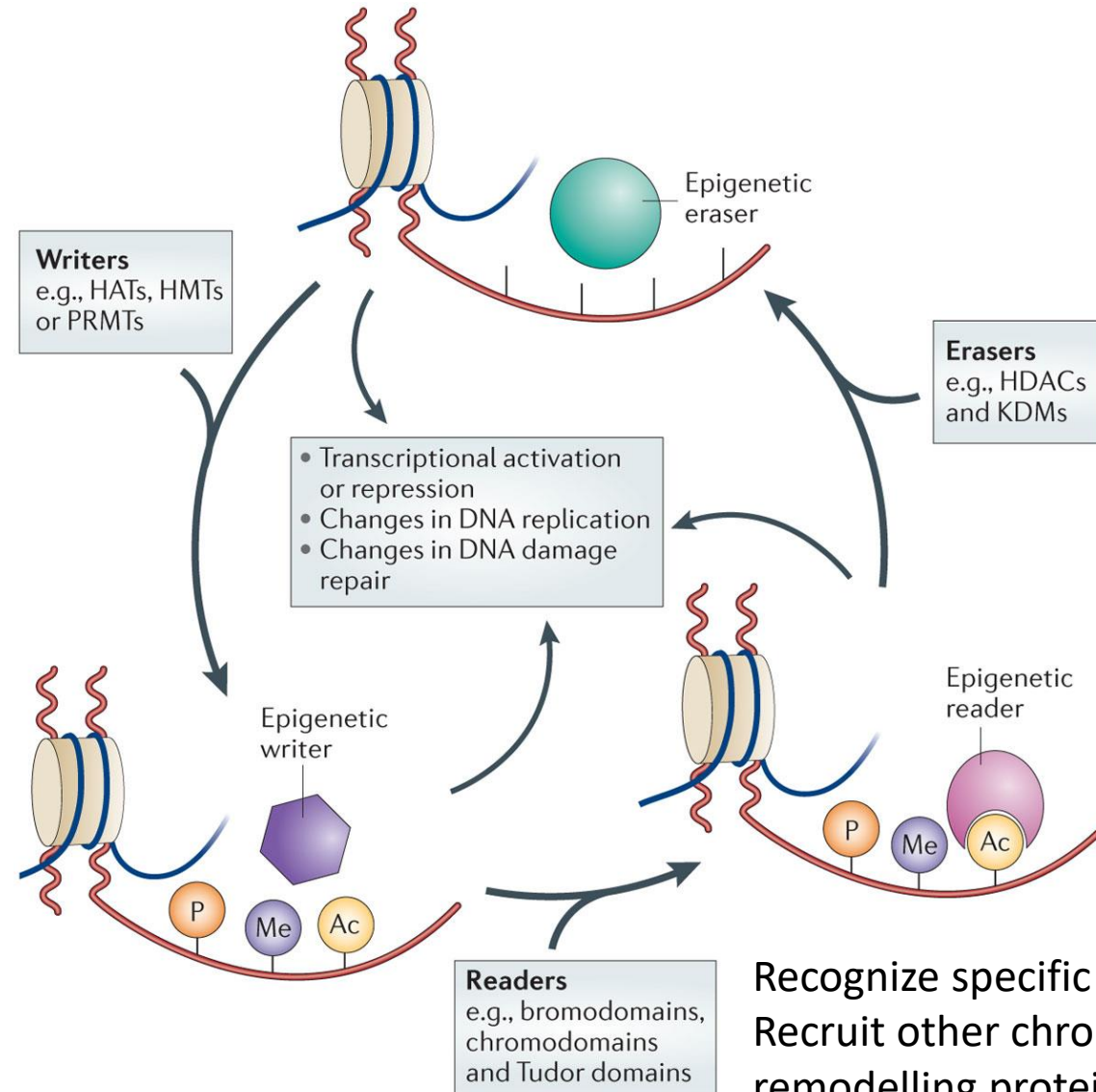
Closed configuration

H3	Me	Me P
	K9	K27 S28



Writers, erasers and readers

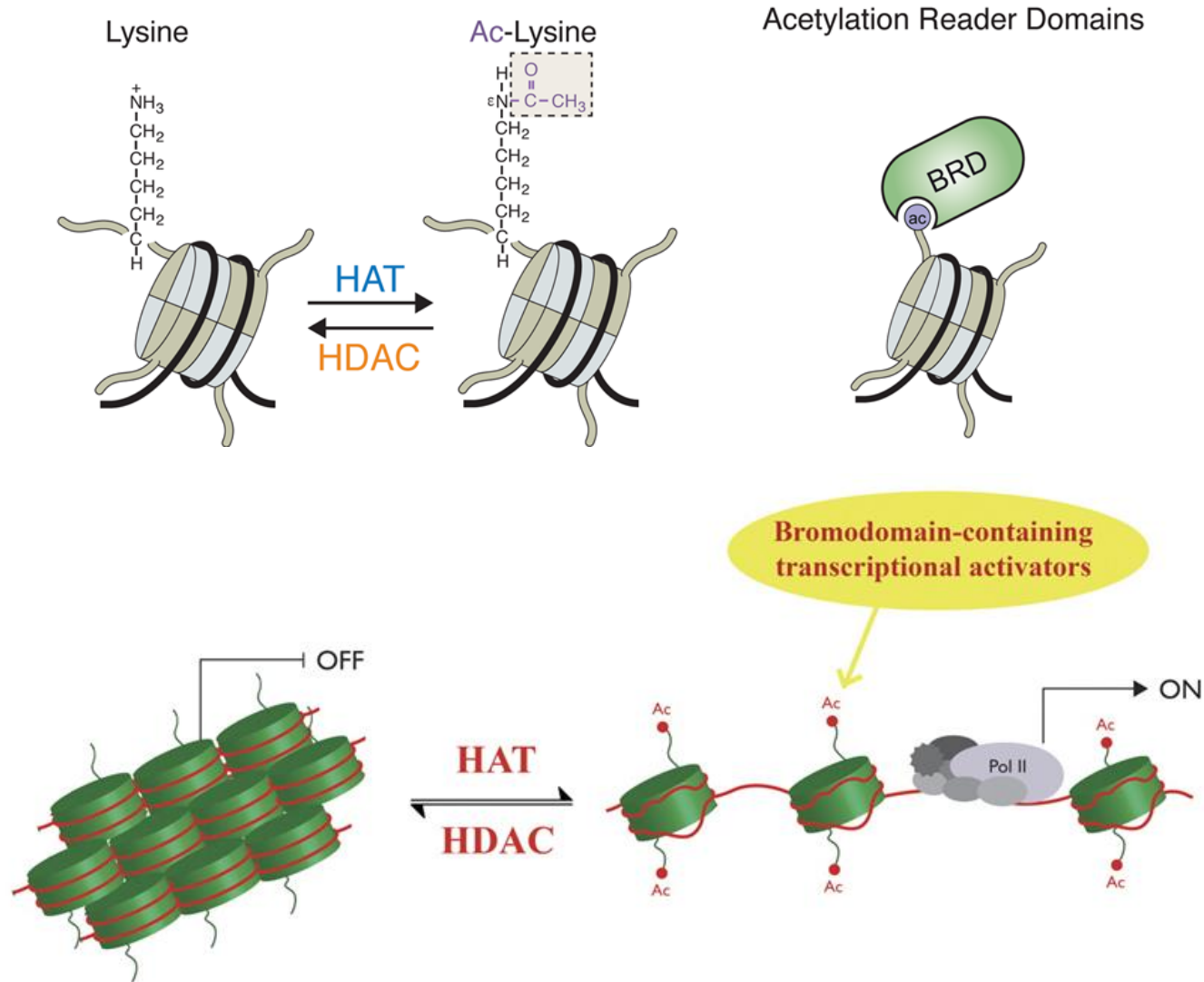
Acetyltransferases
Methyltransferases
Kinases
Ubiquitinases



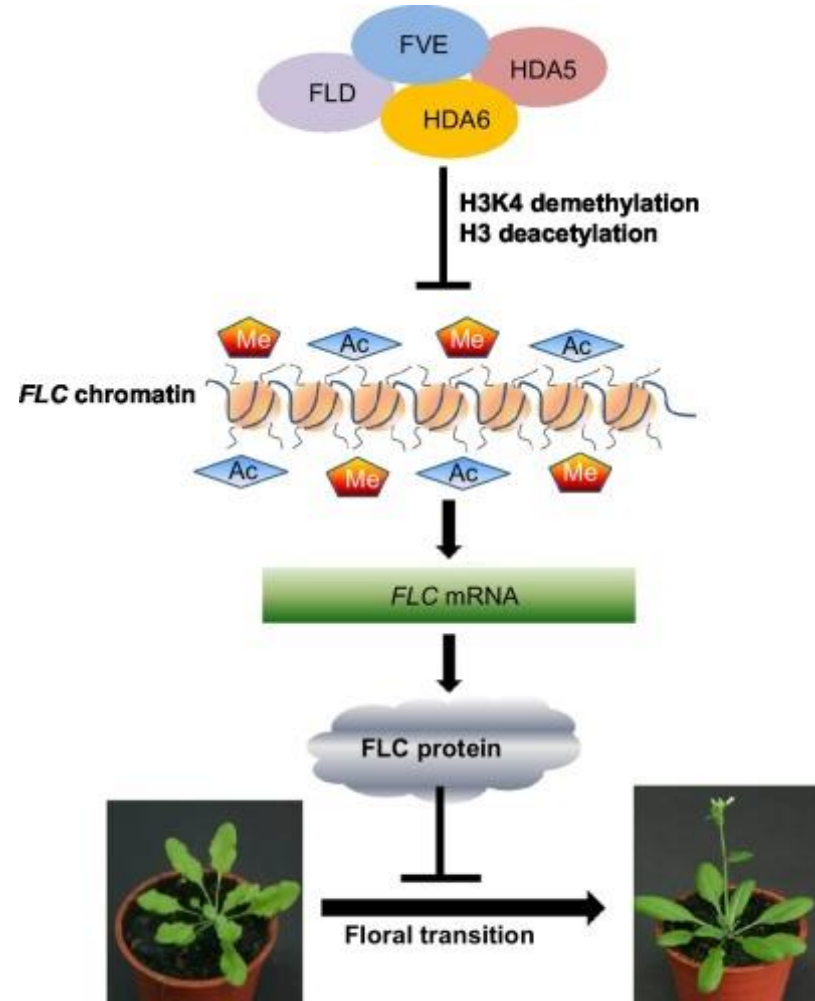
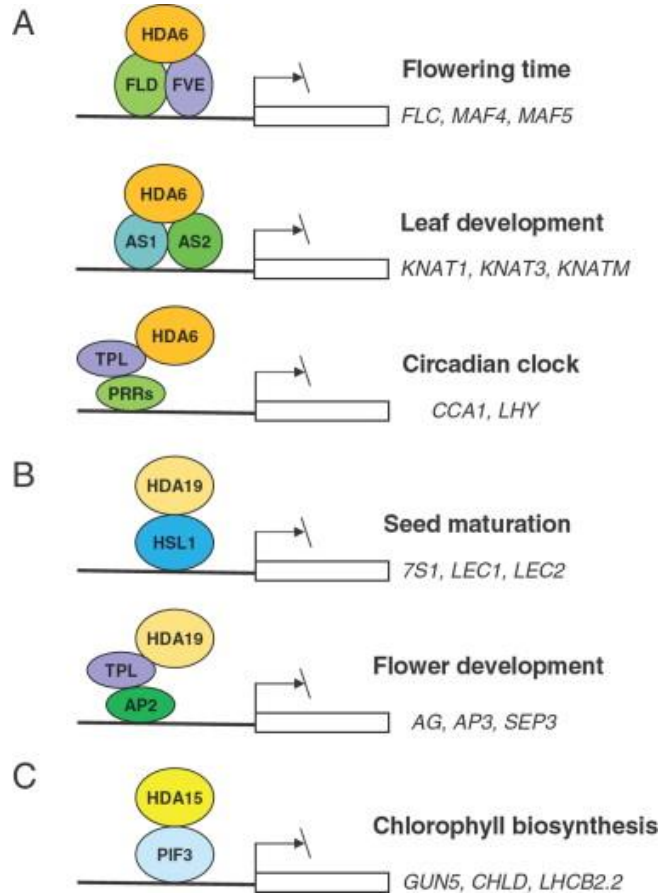
Deacetylases
Demethylases
Phosphatases
Deubiquitinases

Recognize specific histone marks
Recruit other chromatin modifiers and
remodelling proteins to alter
chromatin architecture and function.

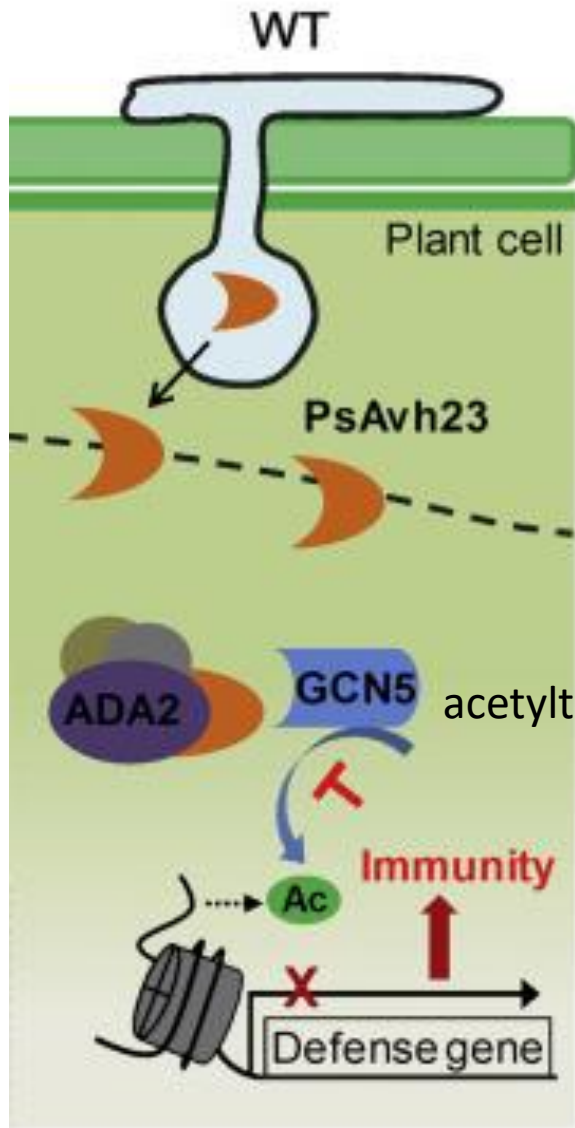
Acetylation of histone lysine is associated to transcription



Transcriptional regulation by histone acetylation



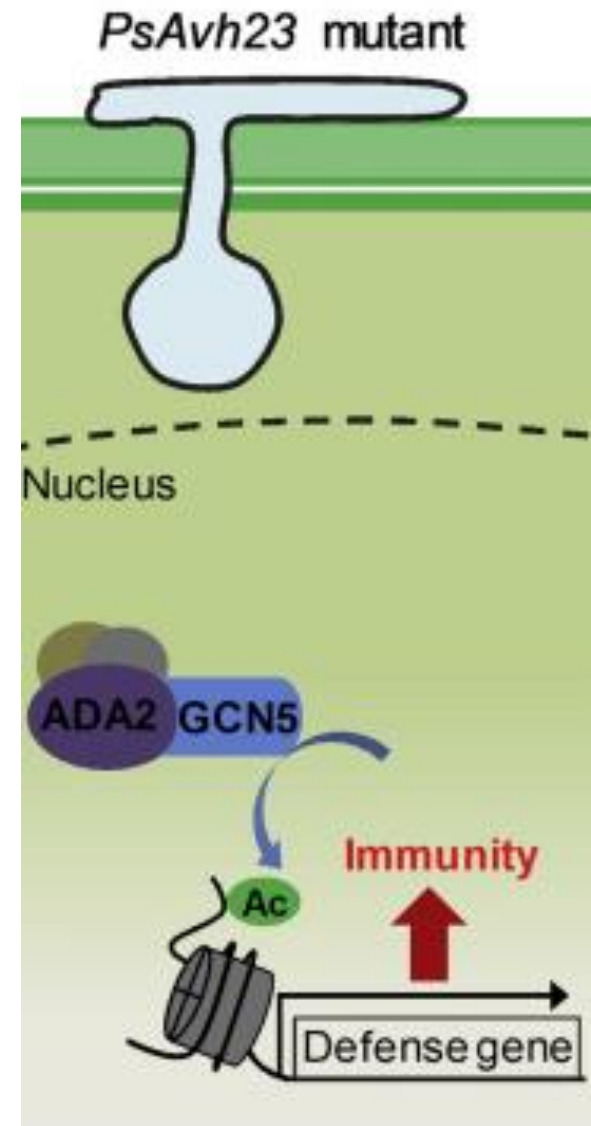
Importance of histone acetylation for plant immunity



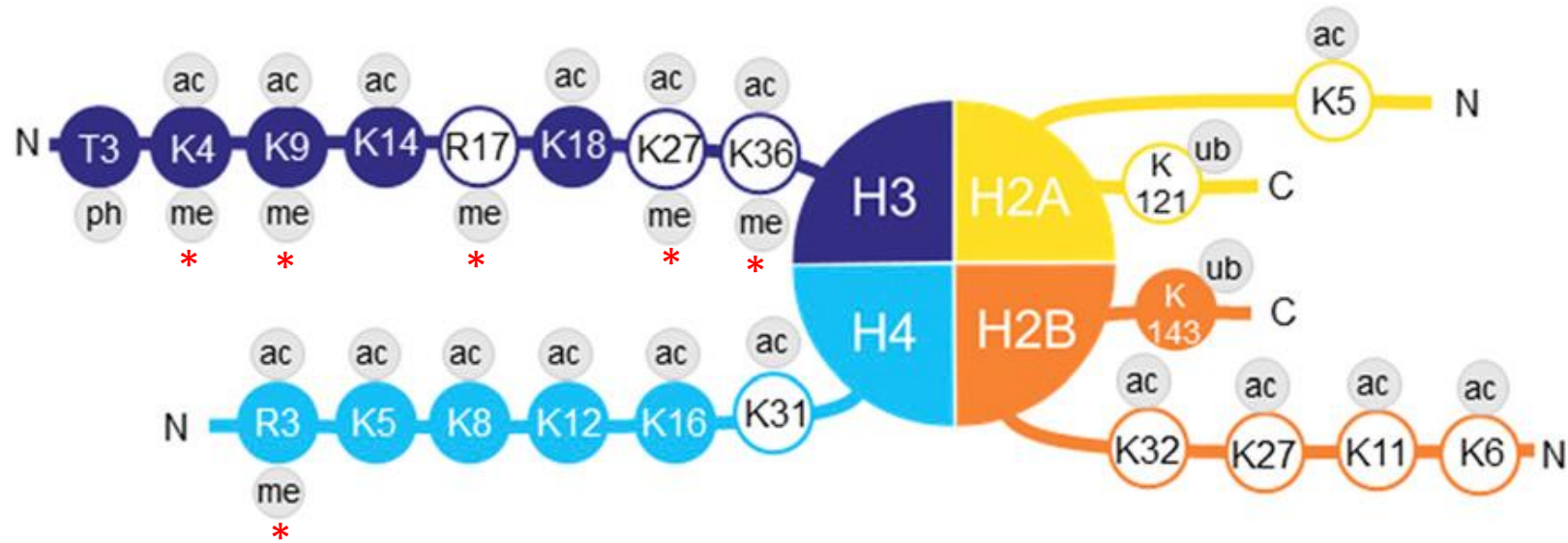
Phytophthora sojae

SAGA
Spt-Ada-Gcn5 Acetyltransferase

suppression H3K9 acetylation



Histone methylation



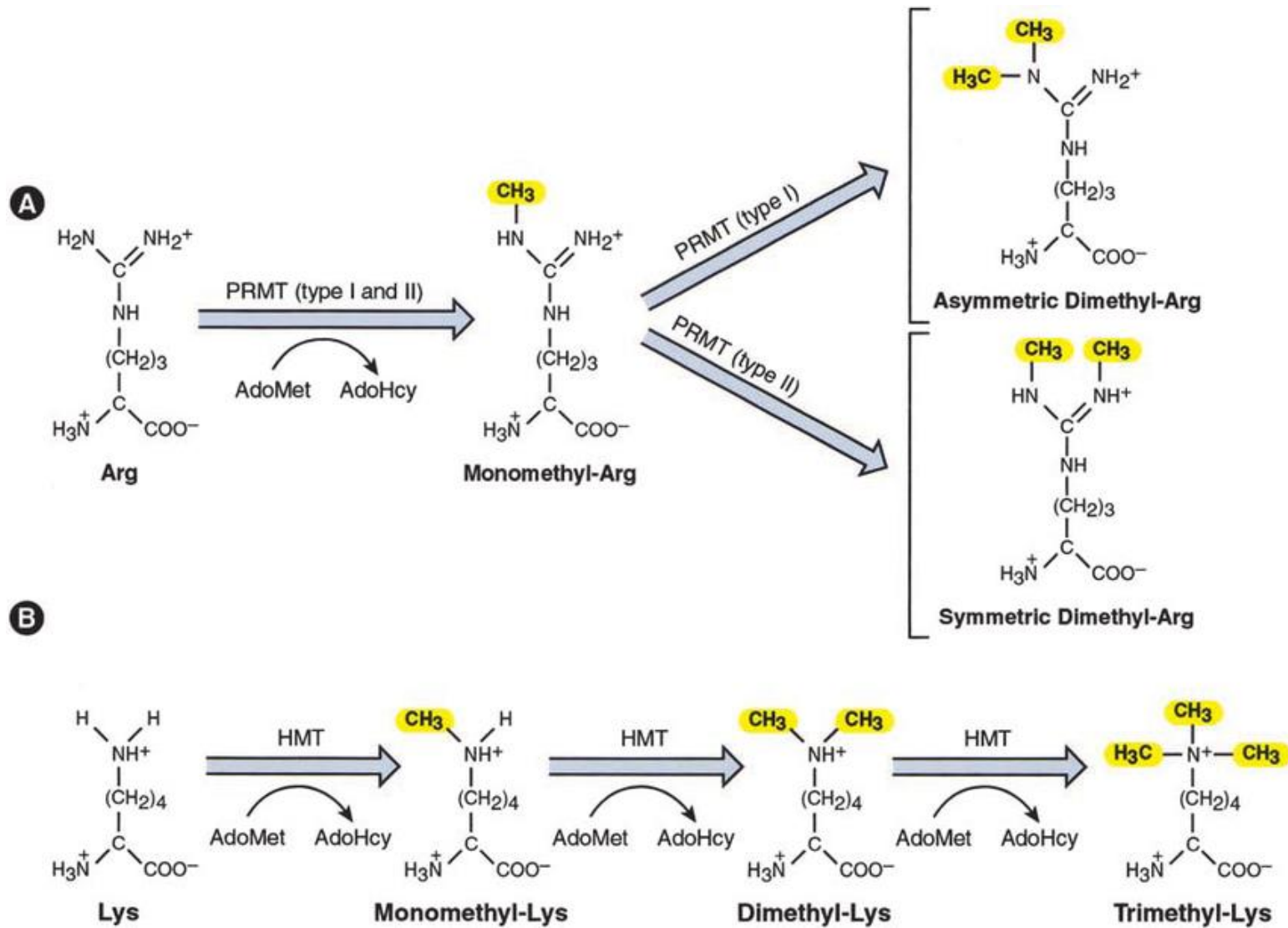
Active marks

Histone acetylations, H2Bub
H3K4me3, H3K36me2/3

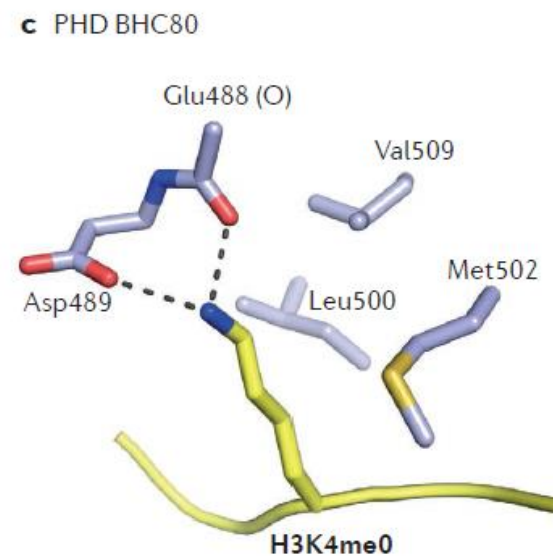
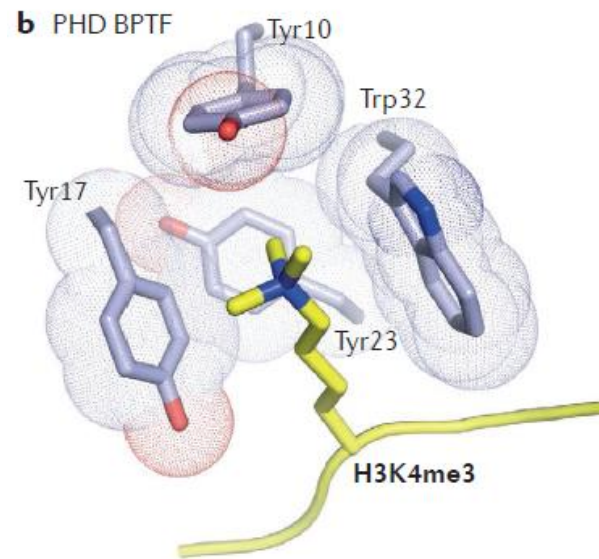
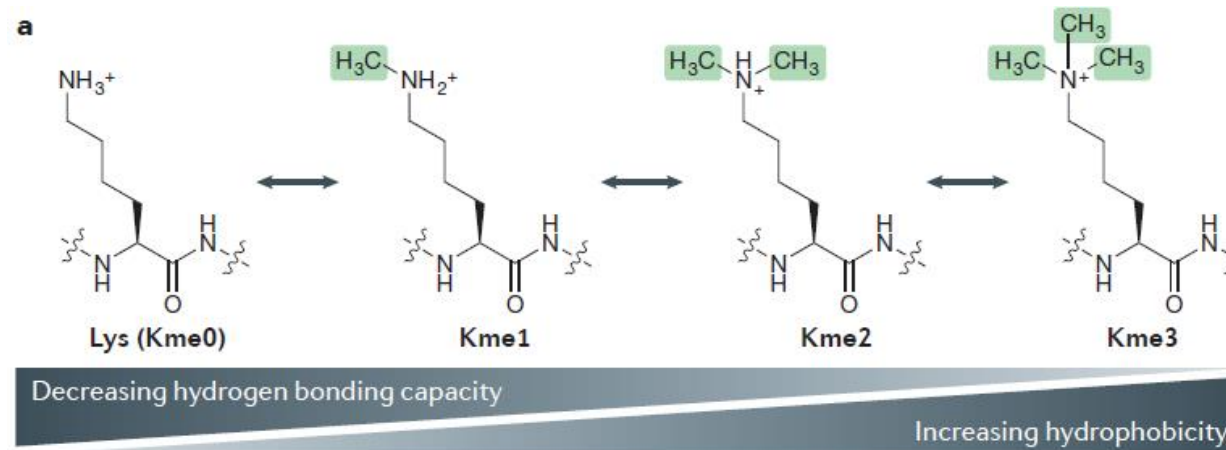
Repressive marks

H3K9me2/3, H3K27me3, H3T3ph,
H2Aub, symmetric H4R3

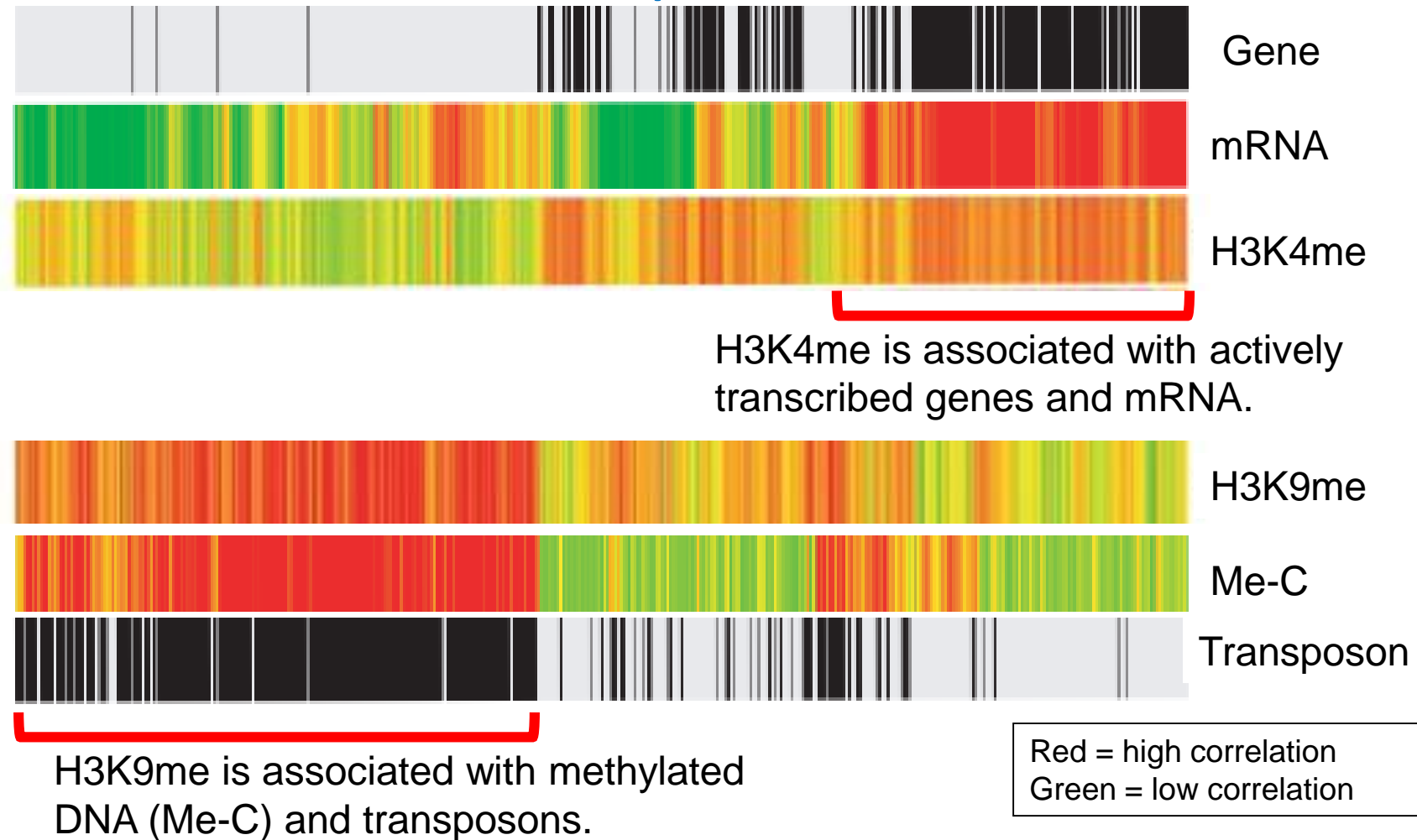
Arginine and Lysine methylation



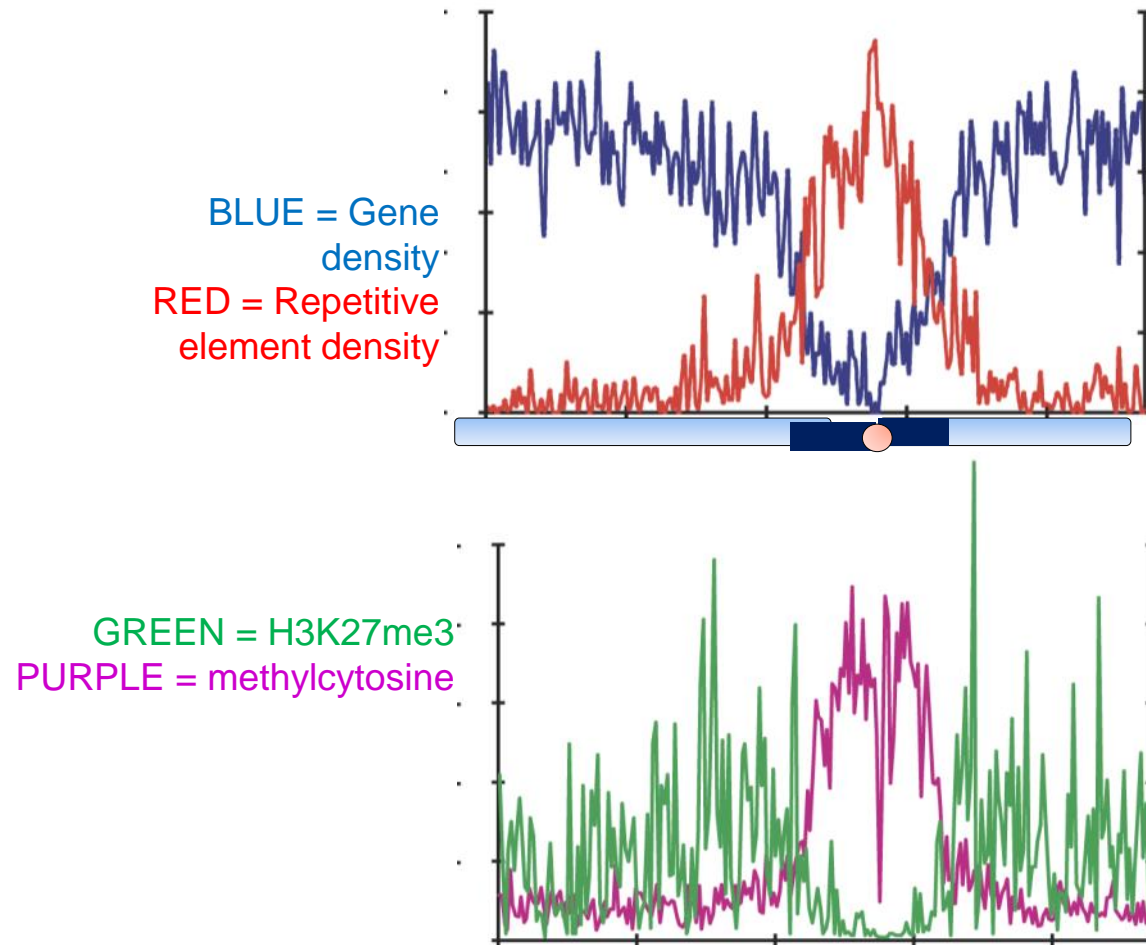
Effect of histone methylation



Histone modifications are associated with genes and transposons

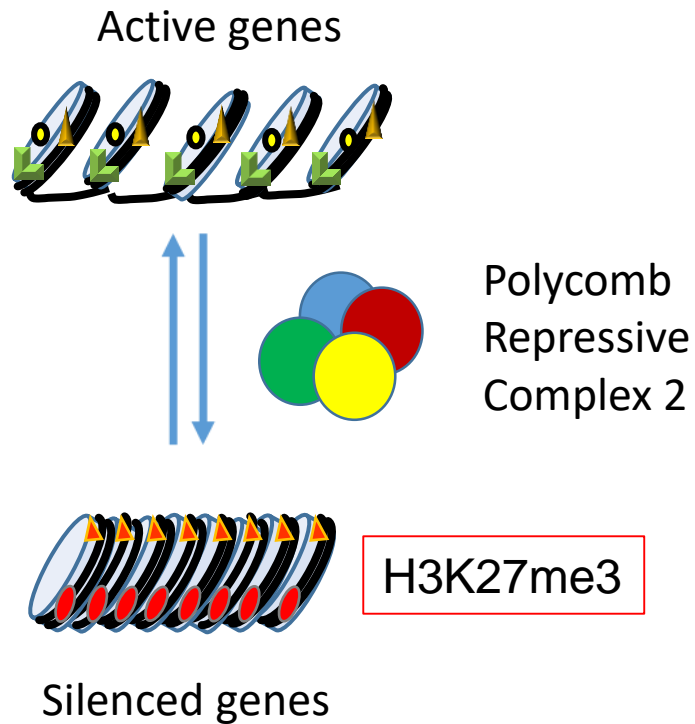


H3K27me3 is associated with genes



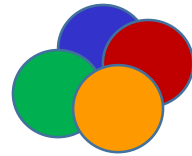
H3K27me3 in Arabidopsis is present within the gene-rich region, not the repeat-rich region.

H3K27me3 methylation by Polycomb Repressive Complex 2



Drosophila PRC2			
E(Z) (methylase)	ESC	SU(Z)12	NURF55
Arabidopsis PRC2			
CURLY LEAF (CLF)	FERTILIZATION INDEPENDENT ENDOSPERM (FIE)	FERTILIZATION-INDEPENDENT SEED 2 (FIS2)	MULTICOPY SUPPRESSOR OF IRA1 (MSI1,2,3,4,5)
MEDEA (MEA)		EMBRYONIC FLOWER 2 (EMF2)	
SWINGER (SWN)		VERNALIZATION 2 (VRN2)	

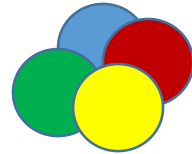
Plants make multiple PRC2 complexes with different targets



MEA + FIS2 complex



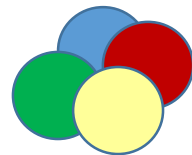
Seed development



CLF/SWN + VRN2 complex



Transition to flowering

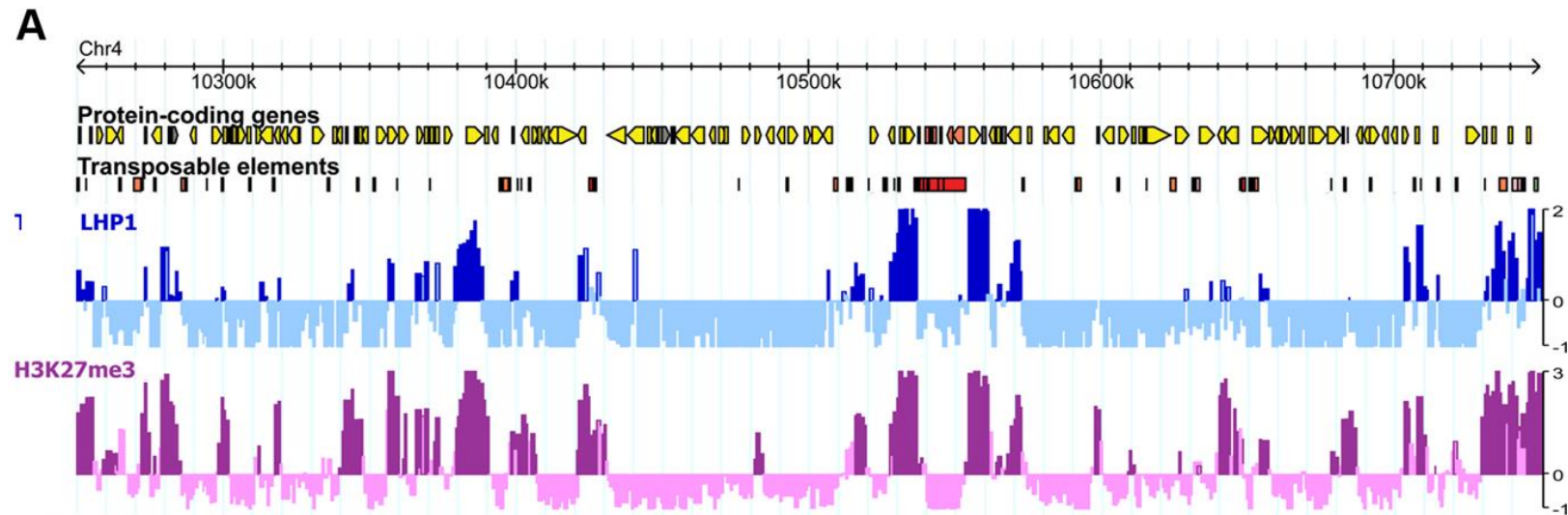
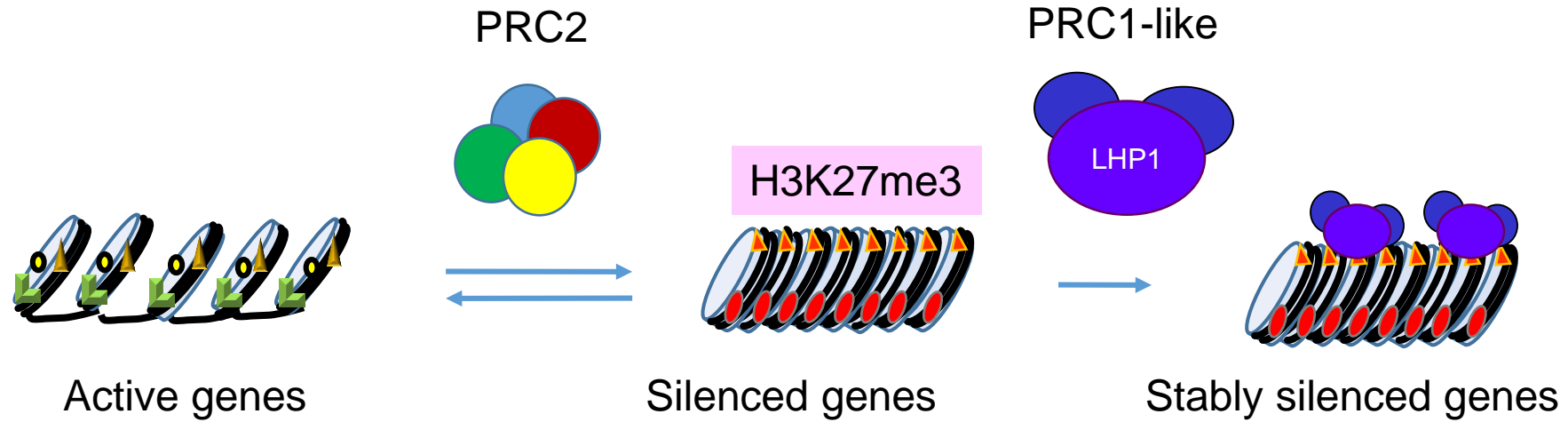


CLF/SWN + EMF2 complex



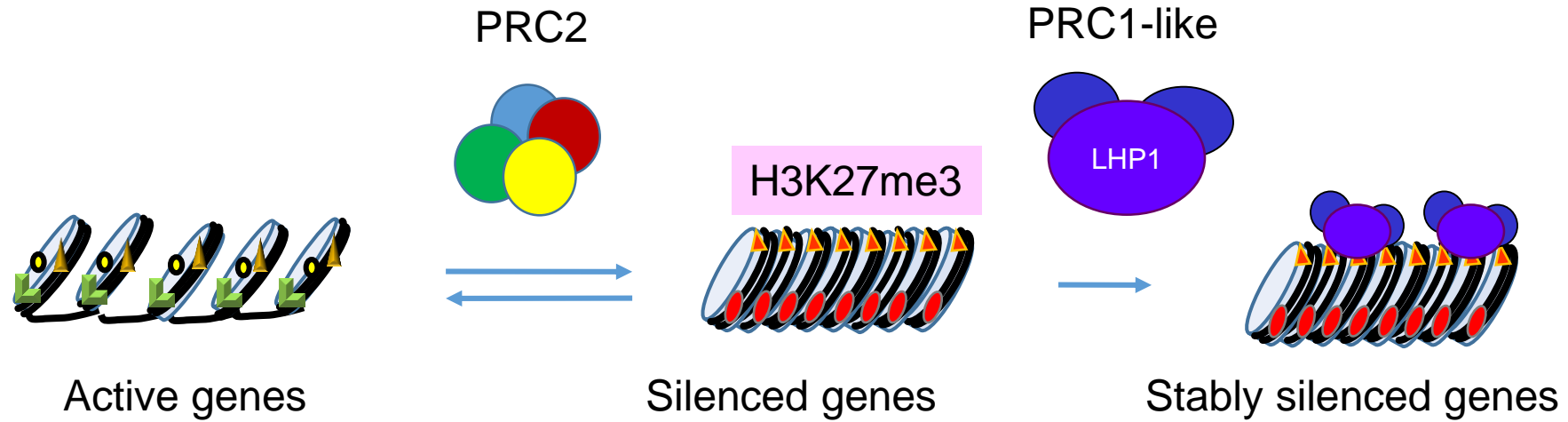
Floral organogenesis

LHP1 co-localizes with H3K27me3



LHP1 binds specifically to H3K27me3

In plants LHP1 maintains H3K27me3



Maintenance of silenced state
of FLC after vernalization!!!

Control of flowering by epigenetic reprogramming

Resetting *FLC* expression:

Silenced during gamete formation

Reactivated during fertilization or early embryogenesis

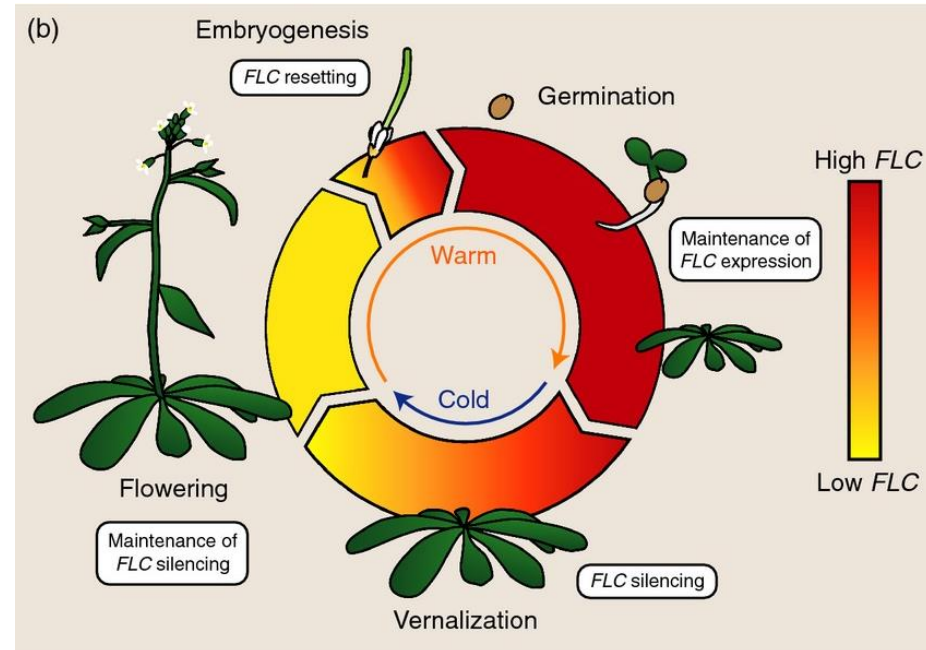
SWR1 incorporates H2A.Z variant

FLC maintained silenced:

Association with LHP1

FT is expressed

Flowering is induced



FLC expression:

H4 acetylation, H3K4me,
H3K36me, H2A.Z incorporation

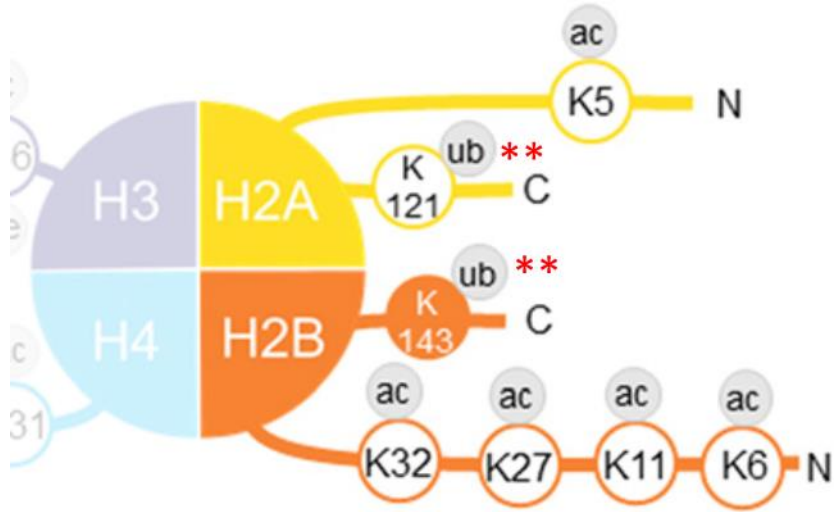
FLC silencing

Expression of the VRN3 gene (part of VRN2-PRC2 complex)

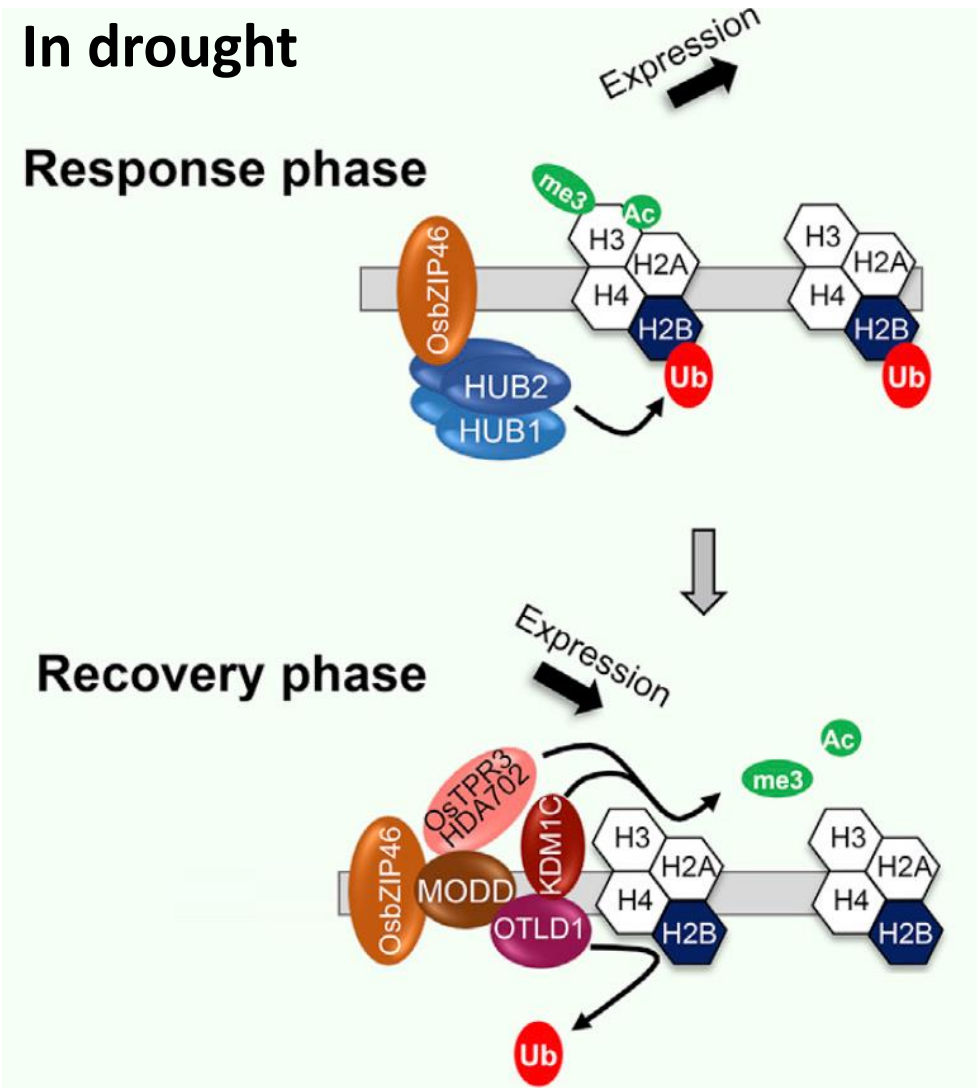
Activating marks removed

Silencing marks (H3K9me, H3K27me3) added

Histone Ubiquitination



Ueda and Seki 2020, Plant Phys





epicatch

Thank you