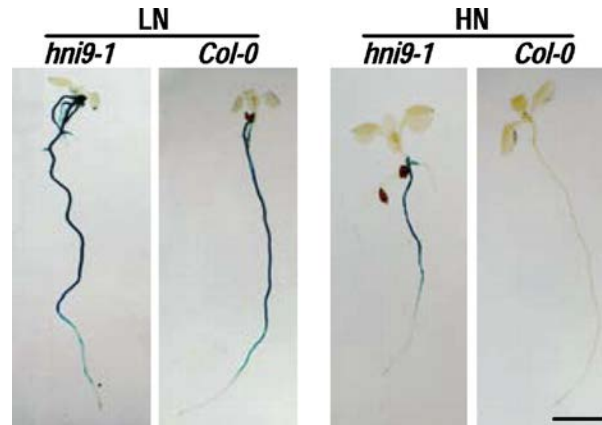
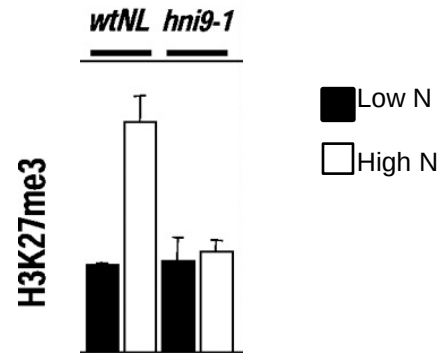


Chromatin dynamics in response to variations of nutritional environment in *Arabidopsis*

Chromatin dynamics in response to variations of nutritional environment in Arabidopsis

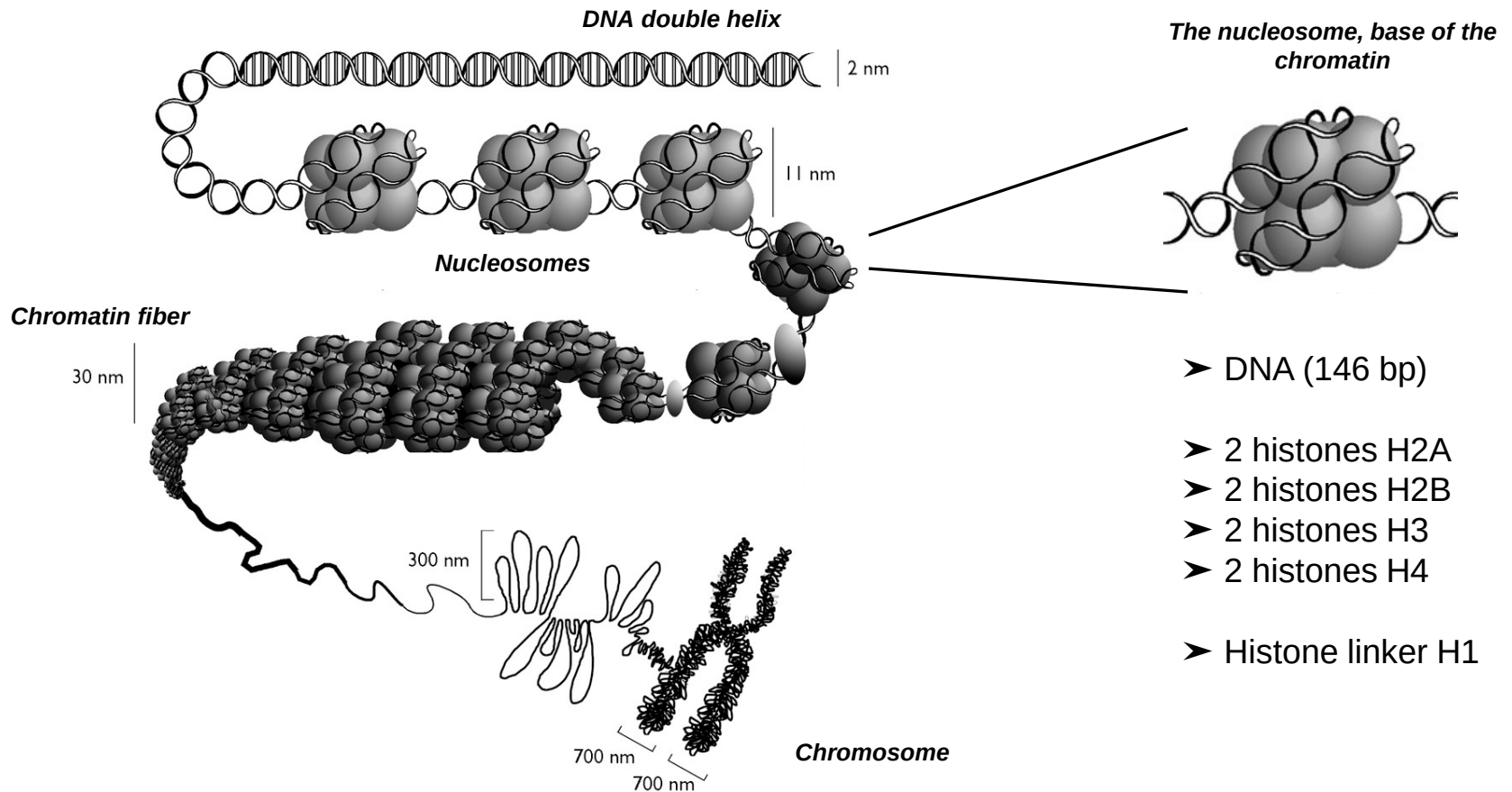


Widiez et al. PNAS (2011)

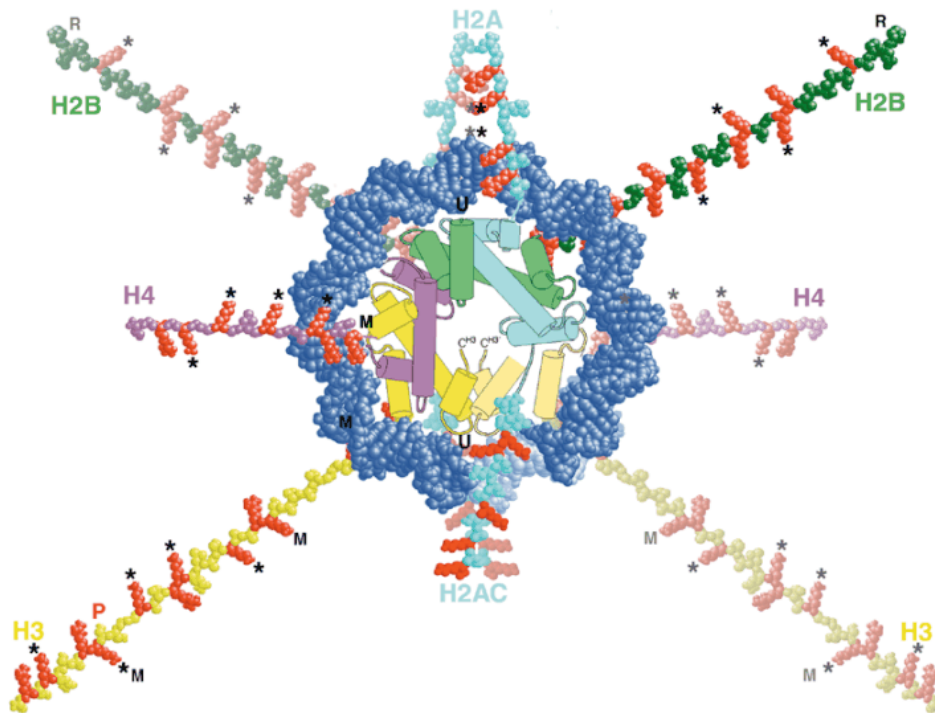


Transcriptional repression of *NRT2.1* by high N supply is associated with chromatin changes

Chromatin, the packaging structure of the genome



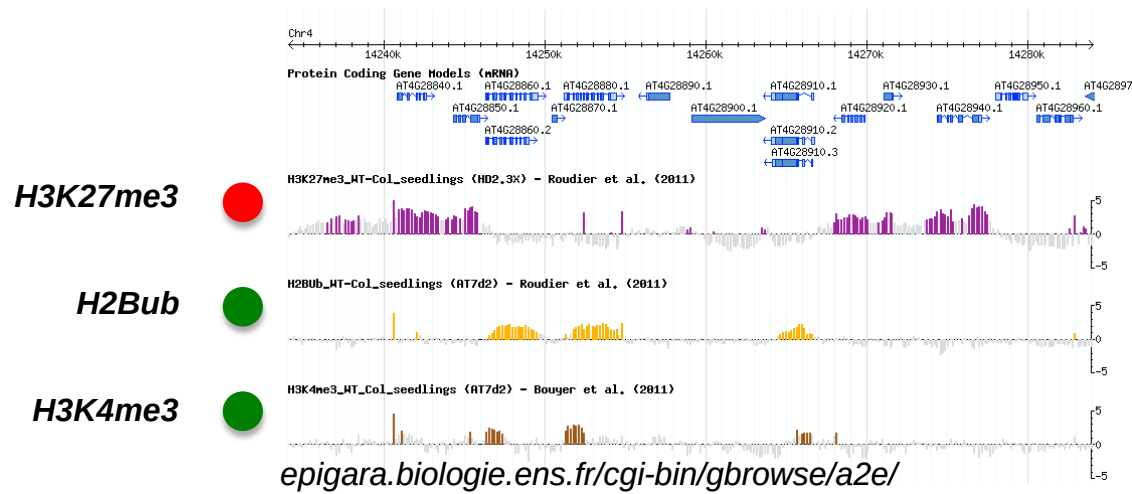
Chromatin-level control of genome activity relies on a variety of modifications



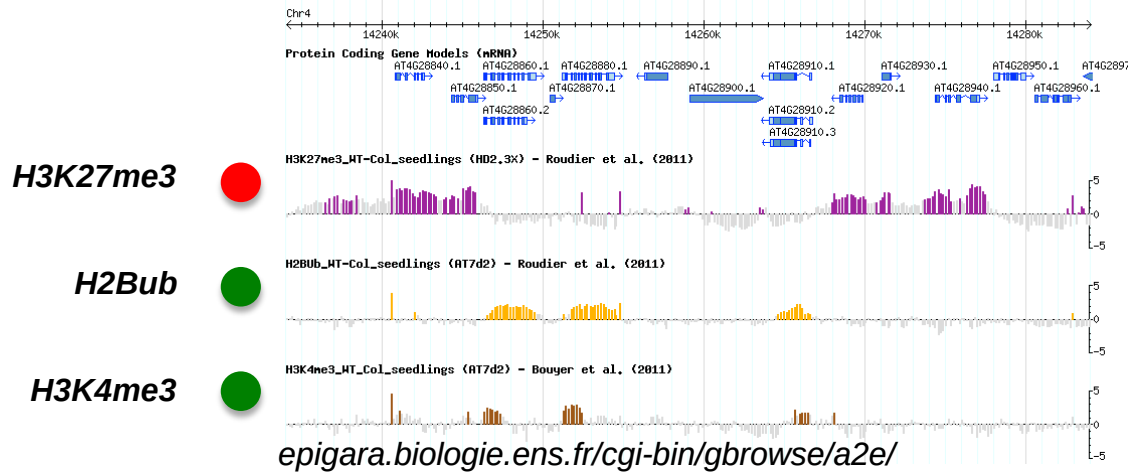
- Histones post-translational modifications:
 - methylation
 - acetylation
 - ubiquitination
 - ...
- DNA methylation
- Histone variants
- Chromatin remodelers
- Non-coding RNAs

Chromatin marks define chromatin states with distinct functional properties

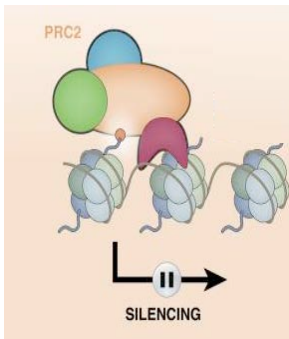
H3K27me3 is associated with actively repressed genes



H3K27me3 is associated with actively repressed genes



H3K27me3 is established by Polycomb group (PcG) complexes



Fly

Differentiation
Proliferation
Cell memory
Cancer development

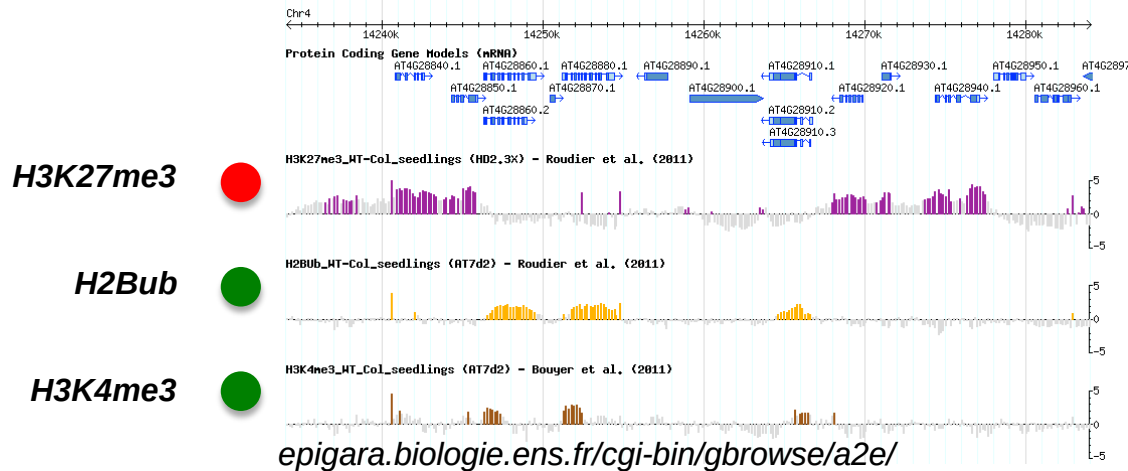
...

Plants

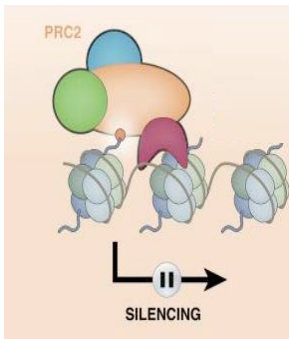
Imprinting
Embryo development
Flowering

...

H3K27me3 is associated with actively repressed genes



H3K27me3 is established by Polycomb group (PcG) complexes



Fly

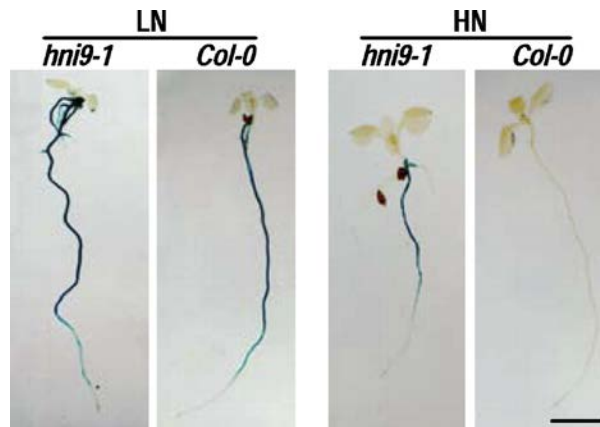
Differentiation
Proliferation
Cell memory
Cancer development

...

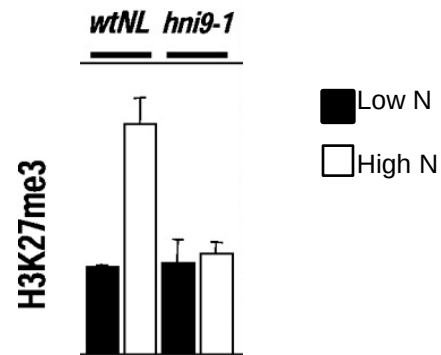
Plants

Imprinting
Embryo development
Flowering
...

H3K27me3/PcG pathways can establish concerted genomic responses



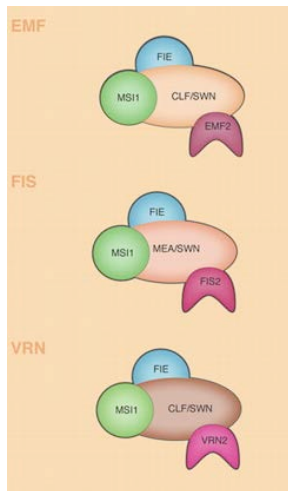
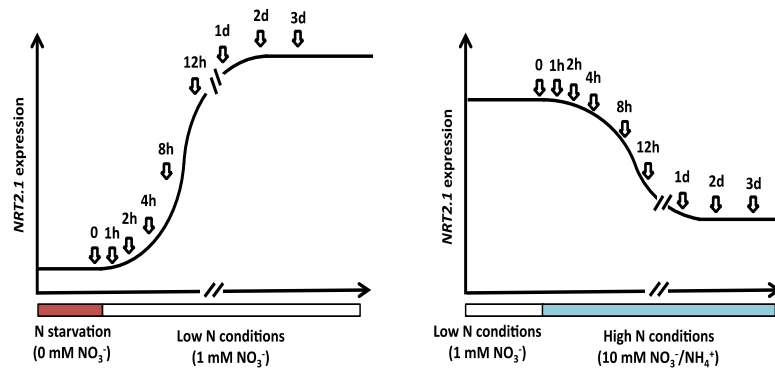
Widiez et al. PNAS (2011)



H3K27me3 dynamics contribution to stress response?

Role of H3K27me3 and related pathways in *NRT2.1* transcriptional regulation

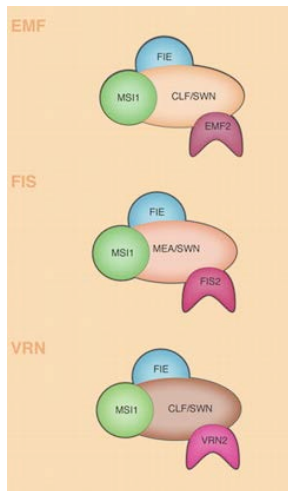
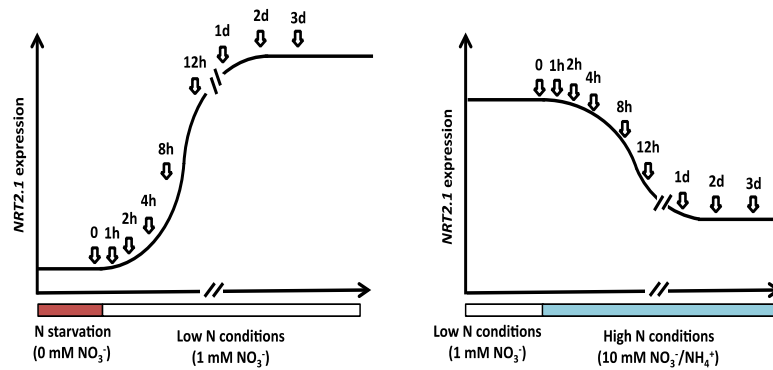
Contribution of H3K27me3 to *NRT2.1* transcription regulation



-*clf*
 -*swn*
 -*msi1*
 ...
 -*lhp1*
 -*ring1a/b*
 -*bim1a/b*

Role of H3K27me3 and related pathways in *NRT2.1* transcriptional regulation

Contribution of H3K27me3 to *NRT2.1* transcription regulation



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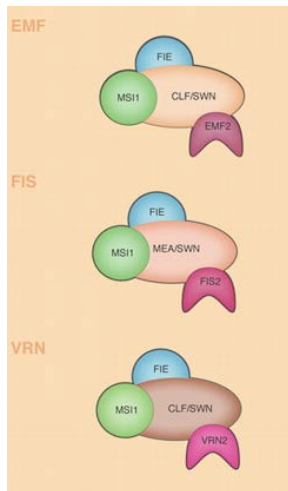
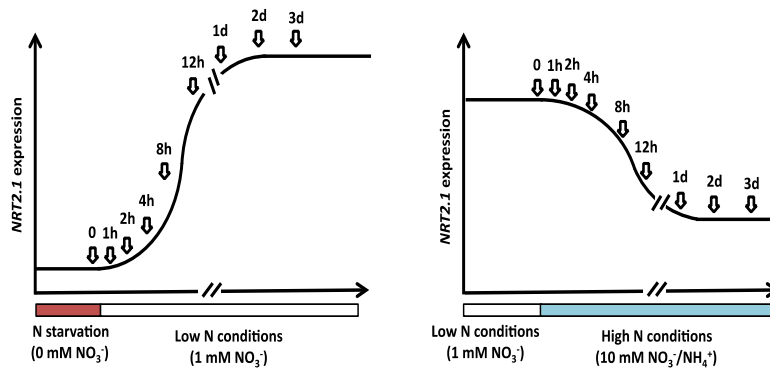
An antisense RNA at the *NRT2.1* locus



- role in *NRT2.1* regulation
- implication in H3K27me3 dynamics
- association with PcG complexes

Role of H3K27me3 and related pathways in *NRT2.1* transcriptional regulation

Contribution of H3K27me3 to *NRT2.1* transcription regulation



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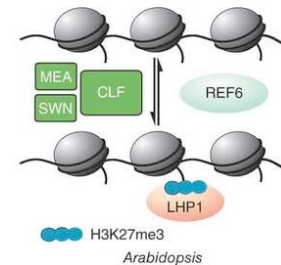
An antisense RNA at the *NRT2.1* locus



- role in *NRT2.1* regulation
- implication in H3K27me3 dynamics
- association with PcG complexes

Dynamics/reversibility of H3K27me3 regulation

-H3K27me3 demethylation (*REF6*)

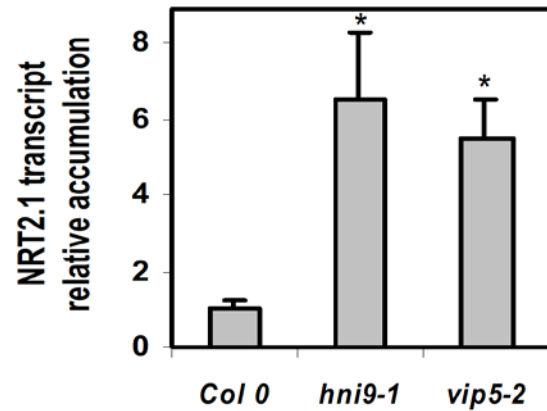


- SWN2/SNF2 proteins
- Cell divisions

Characterization of ordered chromatin changes during adaptation to nutritional environment

H2B mono-ubiquitination

IWS1/HNI9 is associated with the *PAF1* complex



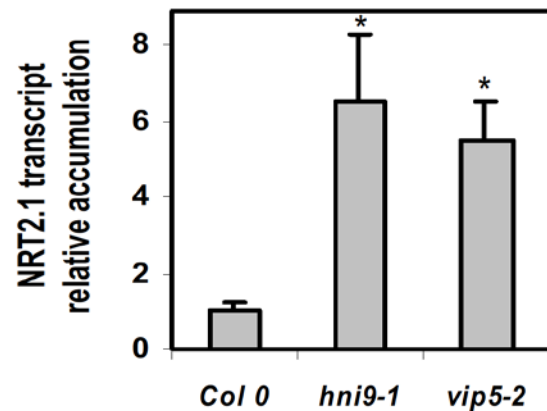
H2Bub levels during *NRT2.1* transcriptional regulation

Impact on H3K27me3

Characterization of ordered chromatin changes during adaptation to nutritional environment

H2B mono-ubiquitination

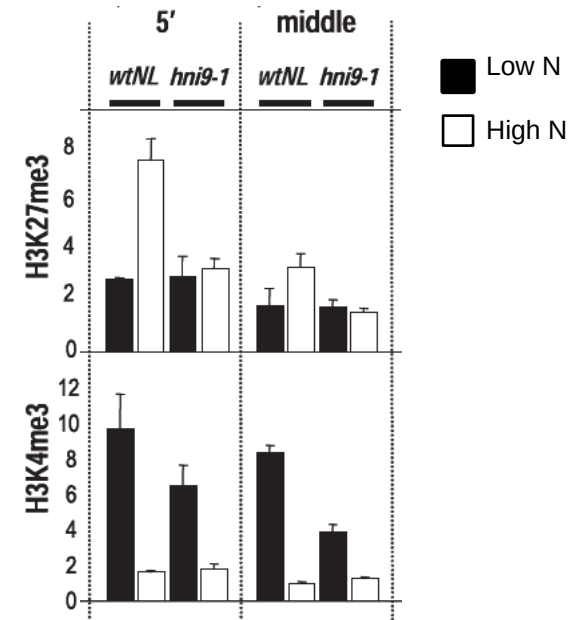
IWS1/HNI9 is associated with the *PAF1* complex



H2Bub levels during *NRT2.1* transcriptional regulation

Impact on H3K27me3

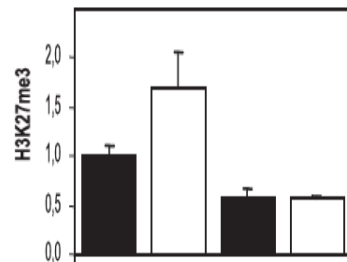
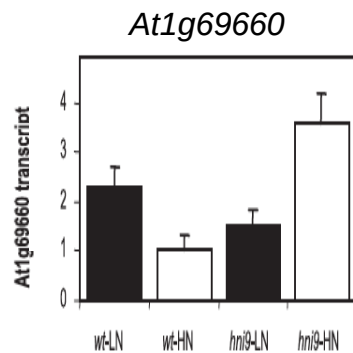
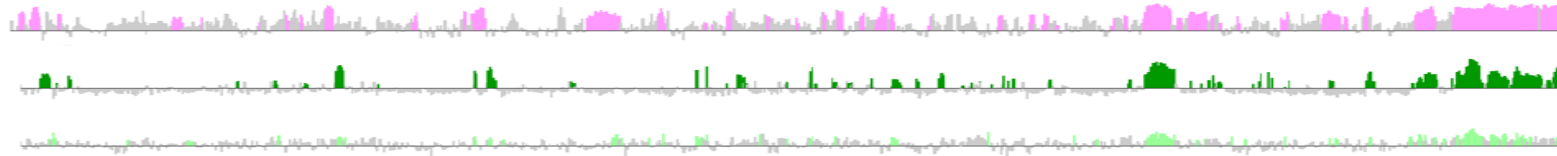
H3K4 methylation



Role of H3K4 demethylation in the establishment of *NRT2.1* silencing

Genome-wide relevance and extension of the model

Epigenomic map of H3K27me3 in contrasting nutritional environment

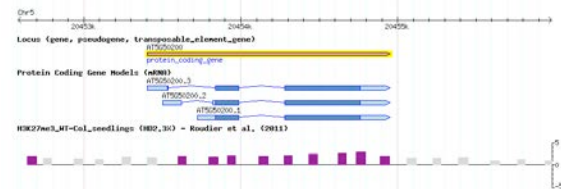


■ Low N
□ High N

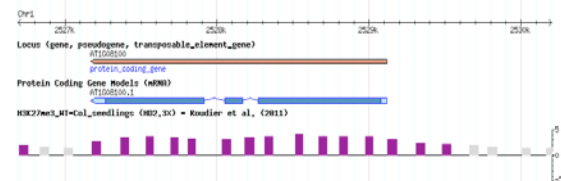
Locus
Gene model
H3K27me3

Locus
Gene model
H3K27me3

NAR2.1



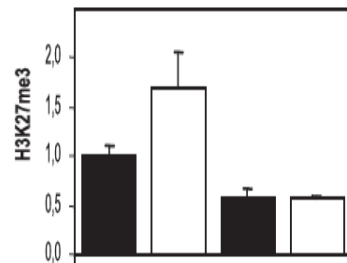
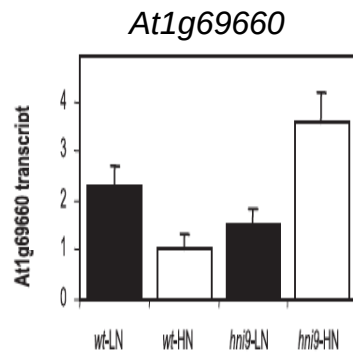
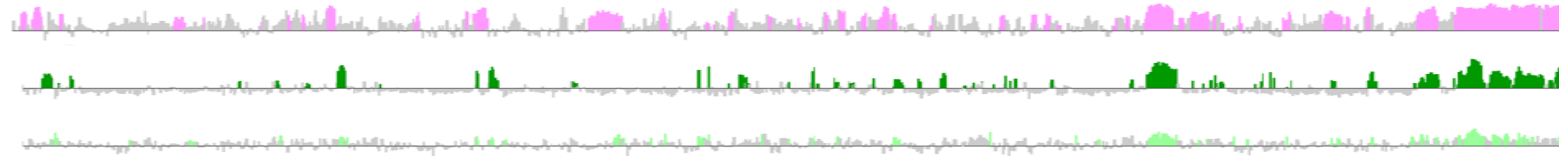
NRT2.2



epigara.biologie.ens.fr/cgi-bin/gbrowse/a2e/

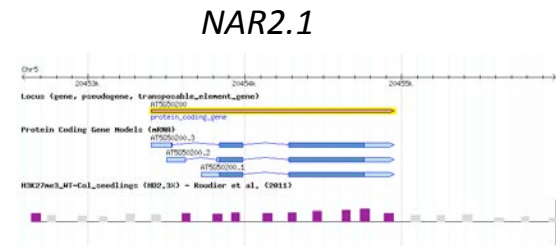
Genome-wide relevance and extension of the model

Epigenomic map of H3K27me3 in contrasting nutritional environment

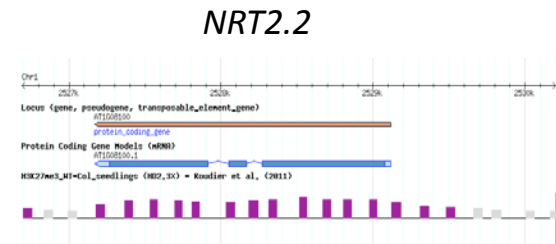


■ Low N
□ High N

Locus
Gene model
H3K27me3



Locus
Gene model
H3K27me3



epigara.biologie.ens.fr/cgi-bin/gbrowse/a2e/

Implication of H3K27me3 and PcG complexes in adaptation to other stress

- nutritional
- drought
- heat
- ...