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## Investigating the involvement of the chromatin state in the control of gene expression in *Leptosphaeria maculans*

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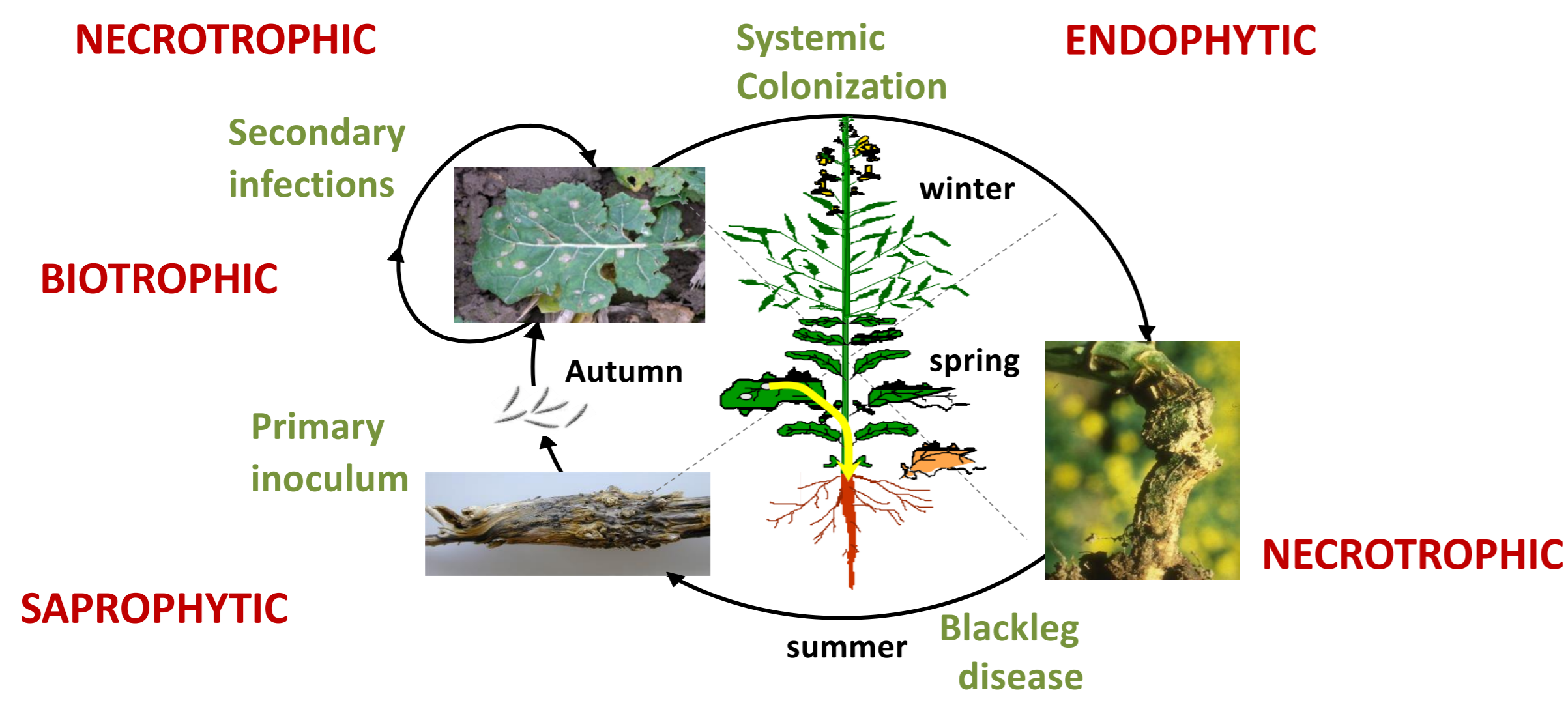
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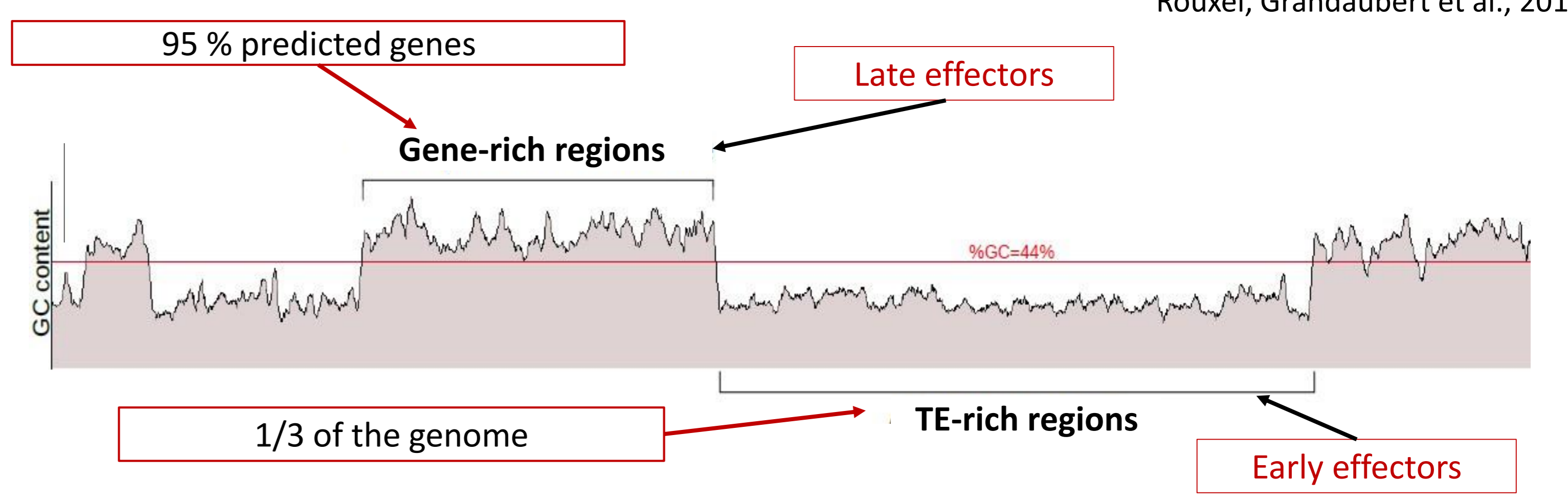


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## 1/Context: *Leptosphaeria* life cycle and control of effector gene expression



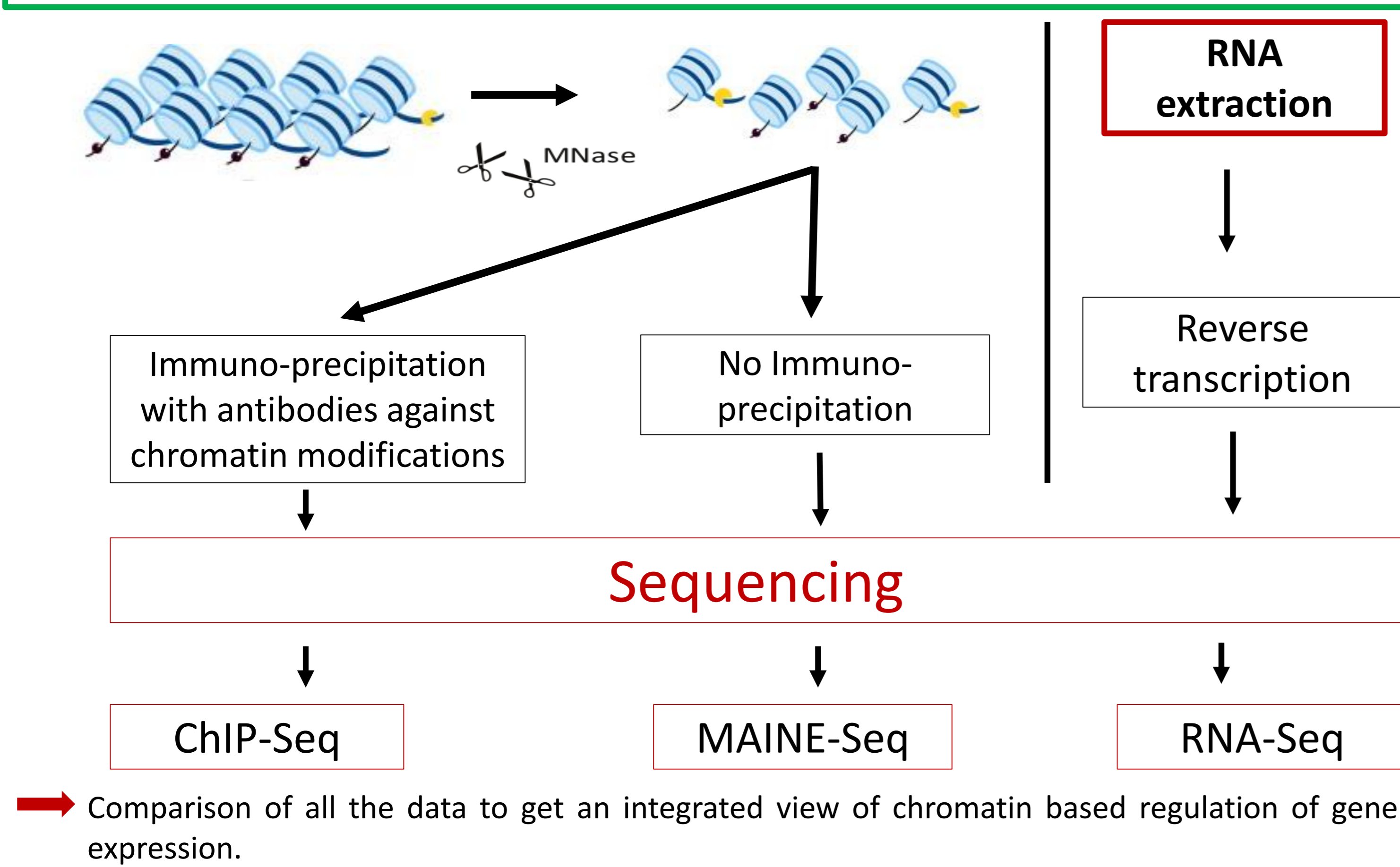
*Leptosphaeria maculans*, a hemibiotrophic fungus responsible for stem canker, colonizes oilseed rape in two stages: an early stage of cotyledon or leaf colonization, and a late colonization stage during which the fungus colonizes, systemically, without visible symptom, the plant before stem canker appears.



Rouxel, Grandaubert et al., 2011

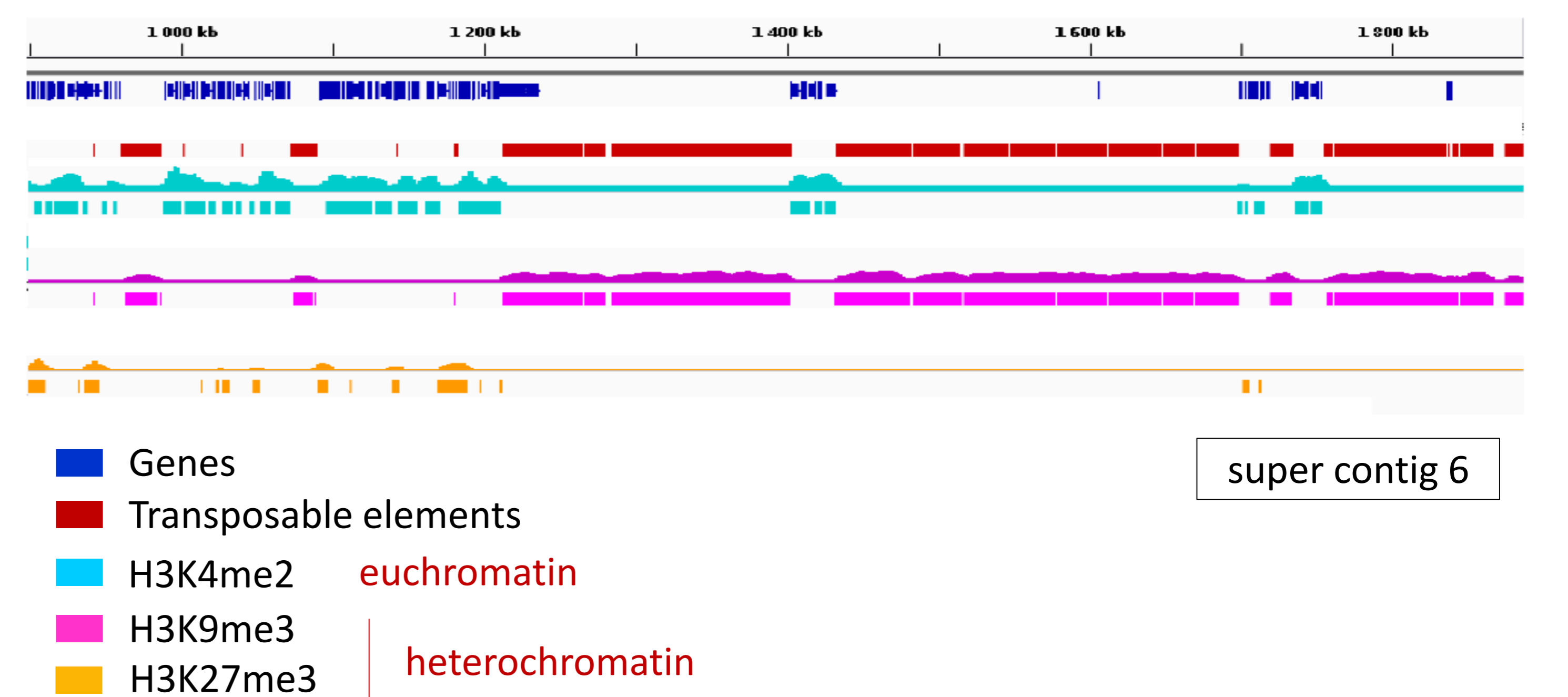
*L. maculans* presents a bipartite genome structure alternating gene-rich and transposable element (TE)-rich regions. TE-rich regions are enriched in putative effector-encoding genes that are expressed specifically in an early stage of infection ('early effectors'). In contrast, gene-rich regions were recently reported to contain putative effector-encoding genes specifically expressed during the late stages of stem infection ('late effectors').

## 2/Strategy to decipher the role of chromatin structure on effector gene expression *in vitro*



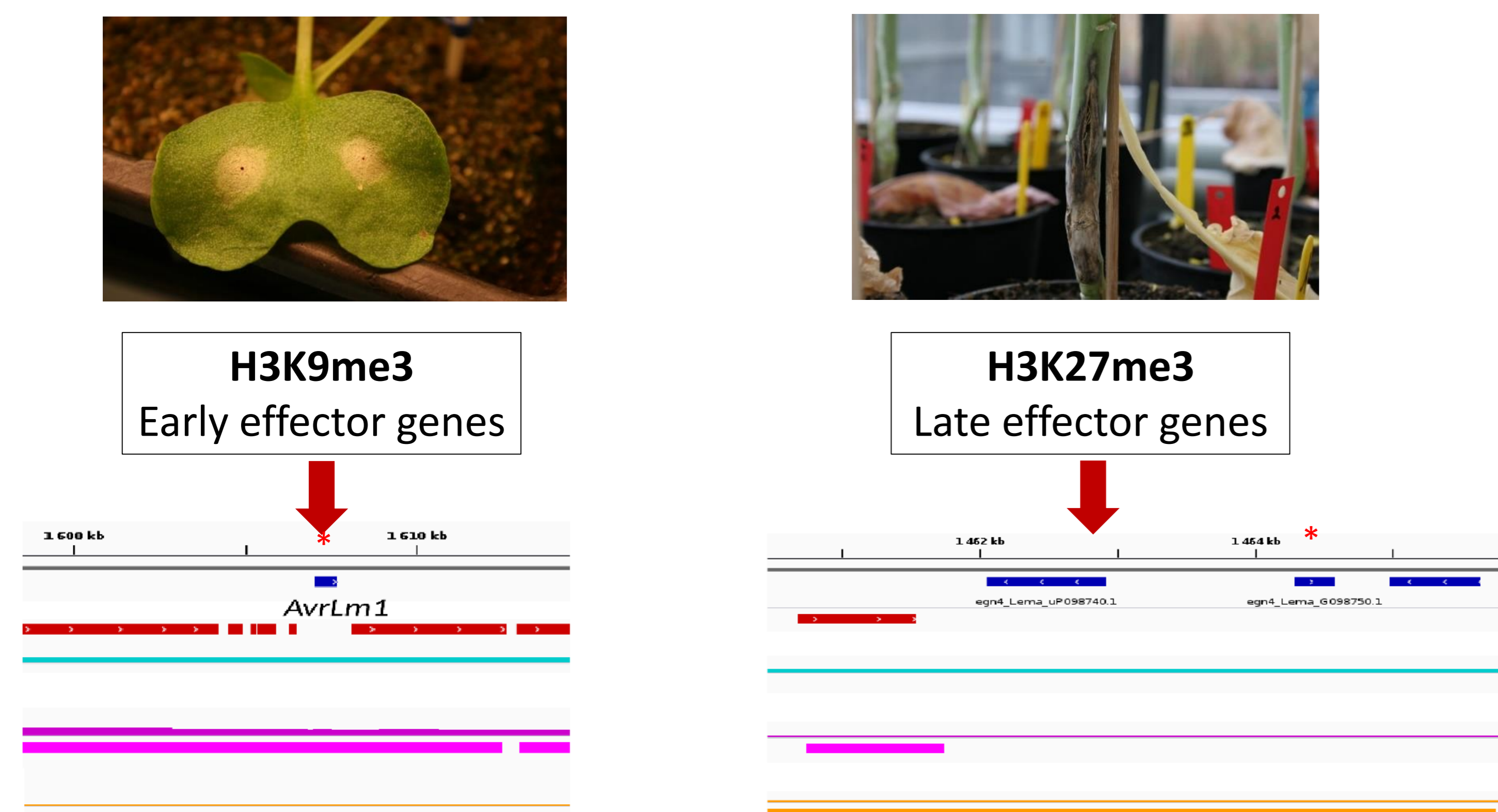
## 3/Localization of chromatin marks on *Leptosphaeria* genome

Soyer et al., unpublished



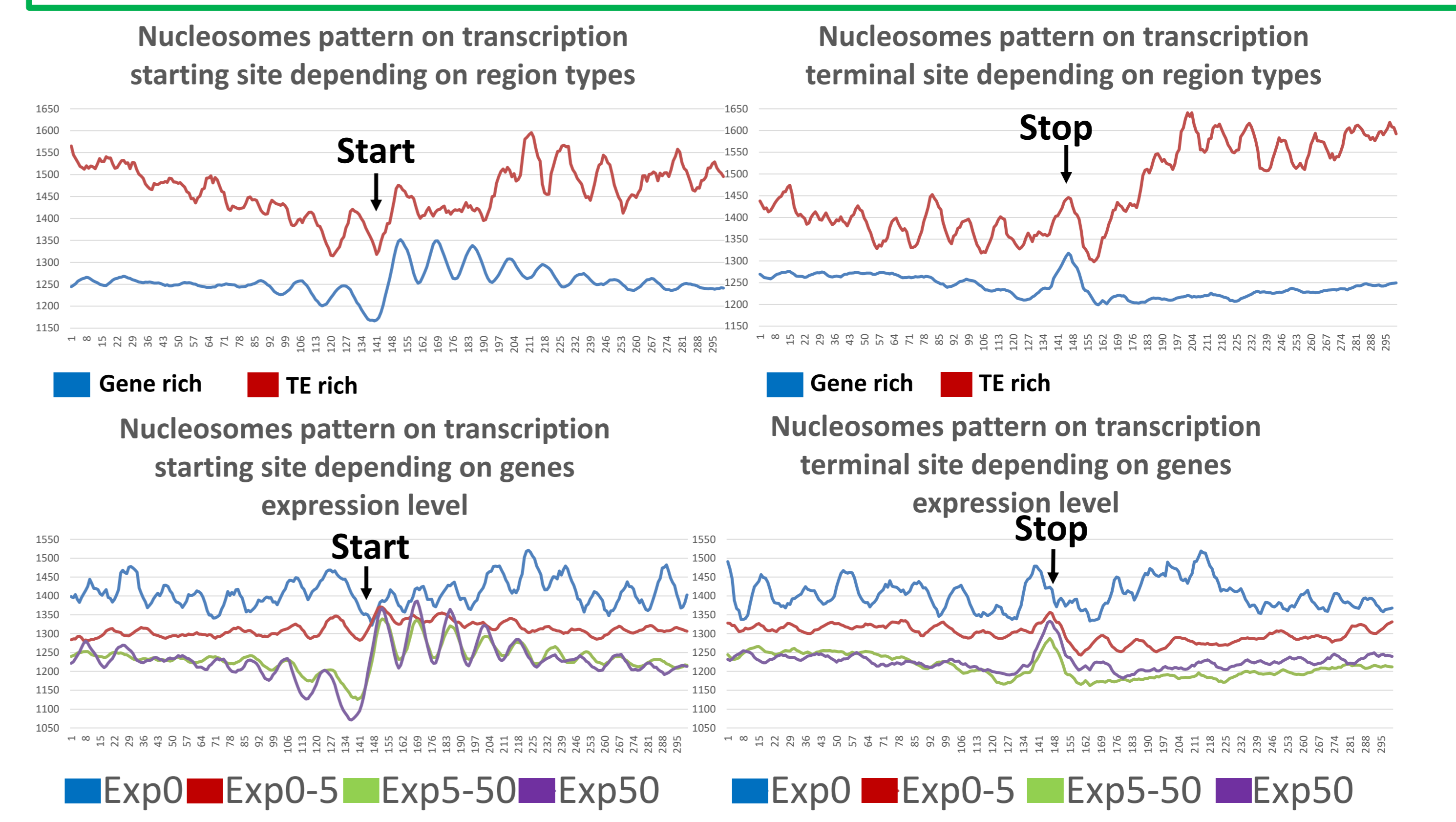
Gene-rich regions are enriched in an euchromatin mark, H3K4me2. Both TE-rich and gene-rich regions are enriched in heterochromatin marks, but these marks are distinct. While TE-rich regions are enriched in H3K9me3, gene-rich regions are enriched in H3K27me3.

## 4/Chromatin marks at late and early effector loci



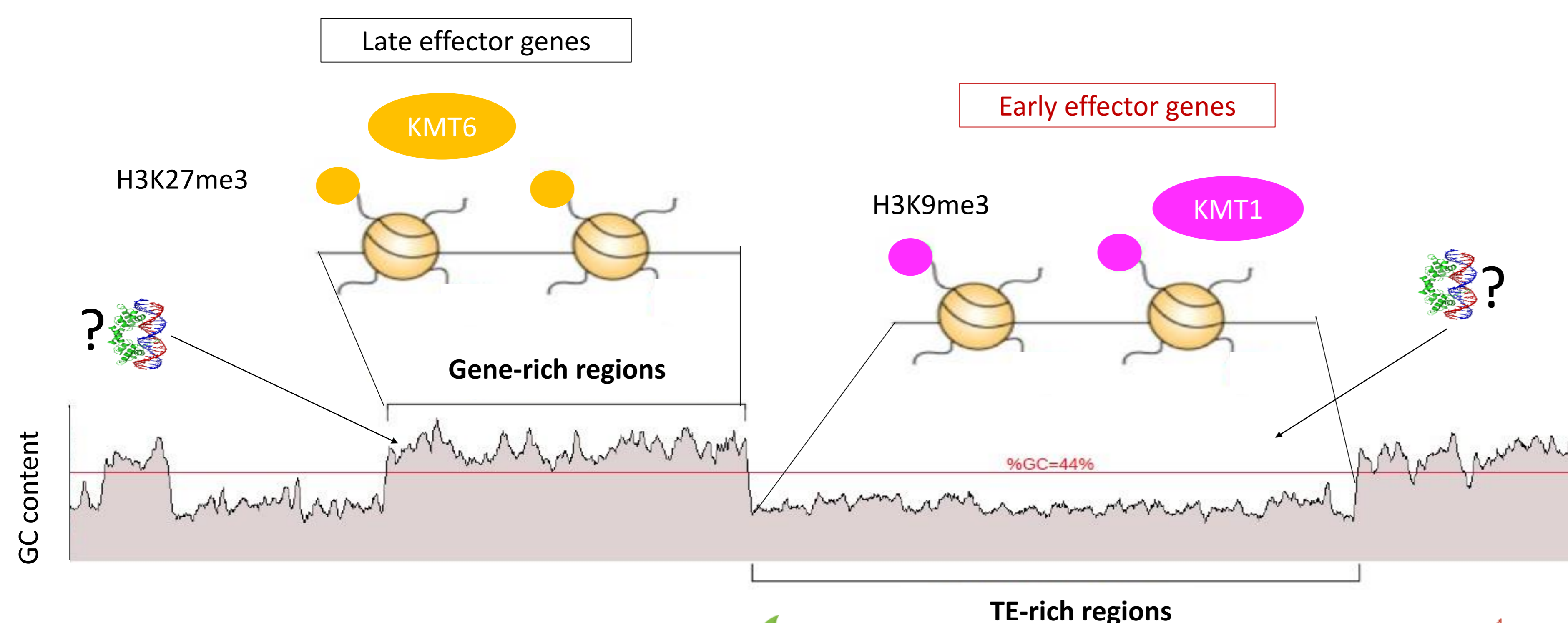
Early effector genes are statistically associated to H3K9me3 compartments. Late effector genes on the contrary are specifically associated to H3K27me3 compartments. The differential time of expression of these genes sets can be led by these different type of marks.

## 5/Nucleosome positioning on genes depending on regions and expression level



Nucleosomes have well defined positions on transcription starting site and stop of gene-rich regions unlike nucleosomes on TE-rich regions. Nucleosomes have also better positioning on well expressed genes than on poorly expressed genes. These observations are clearer on nucleosomes localized just after the start which are crucial for transcription efficiency. With Exp corresponding to expression level in TPM (transcript per million).

## 6/Effector concerted expression model and perspectives



Repression of Early effector is maintained by KMT1 responsible for H3K9me3 methylation (Soyer *et al.* 2014). Chromatin remodeling leads to a decondensation at effector gene loci, rendering their promoters accessible to specific transcription factors. The late effector expression mechanism would be similar. But the repression should be maintained by KMT6 responsible for H3K27me3.

### Next stages:

Inactivation of KMT1 and KMT6 to assess the specific regulation of early and late effector genes.

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