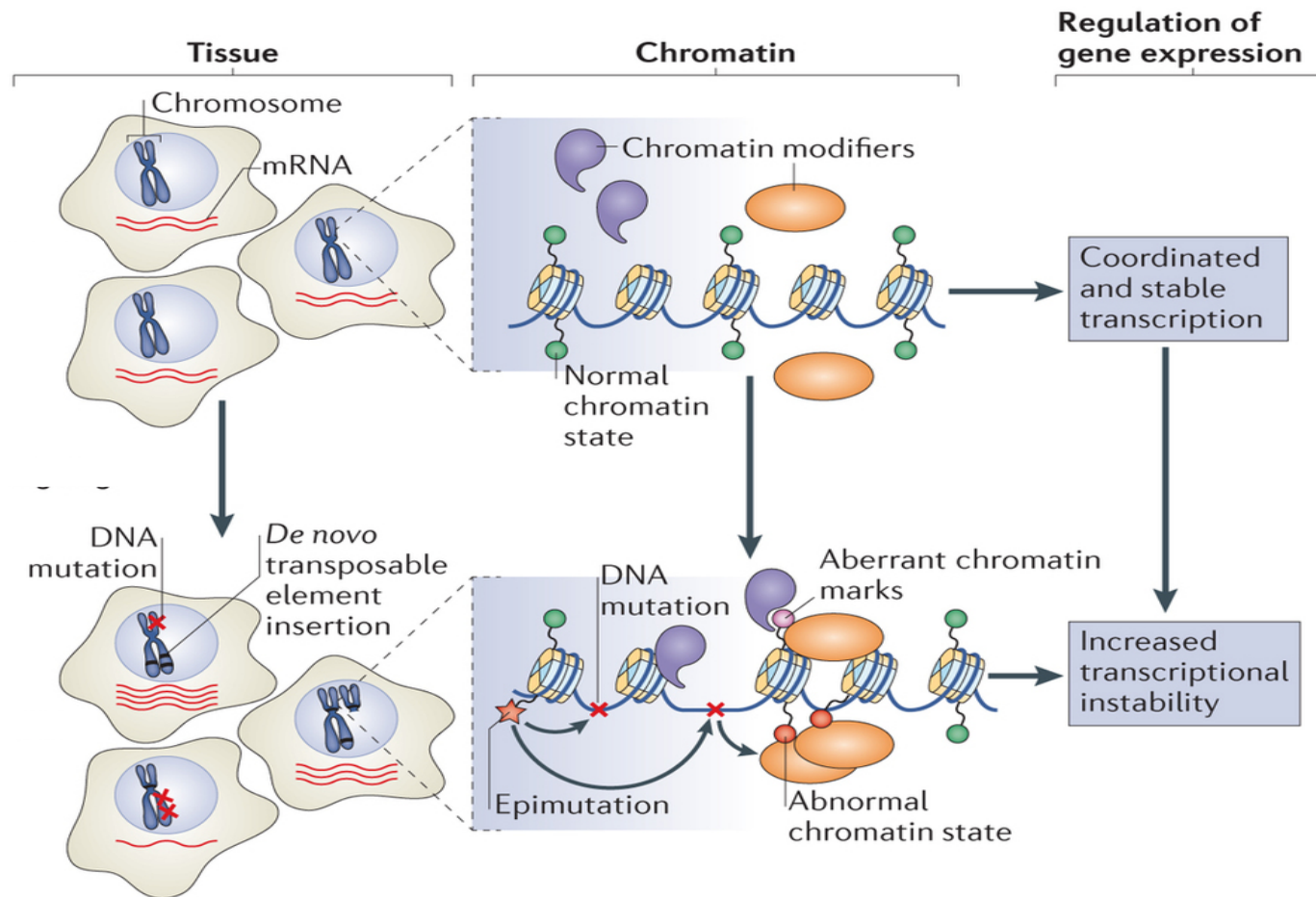


(Epi)genomic environmental response in Drosophila

Cristina Vieira

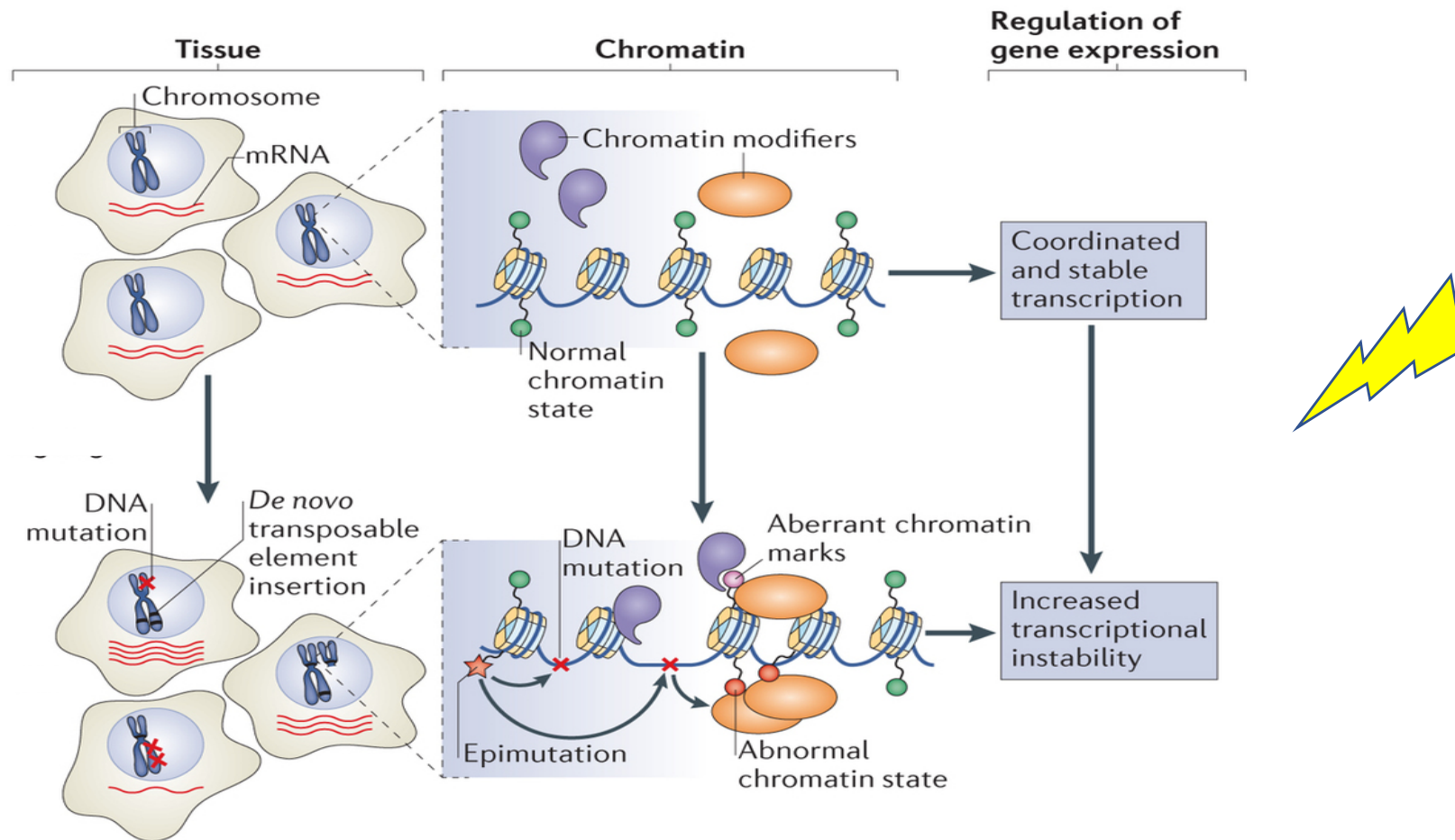
Genome stability



Nature Reviews | [Molecular Cell Biology](#)

Benayoun et al. 2015

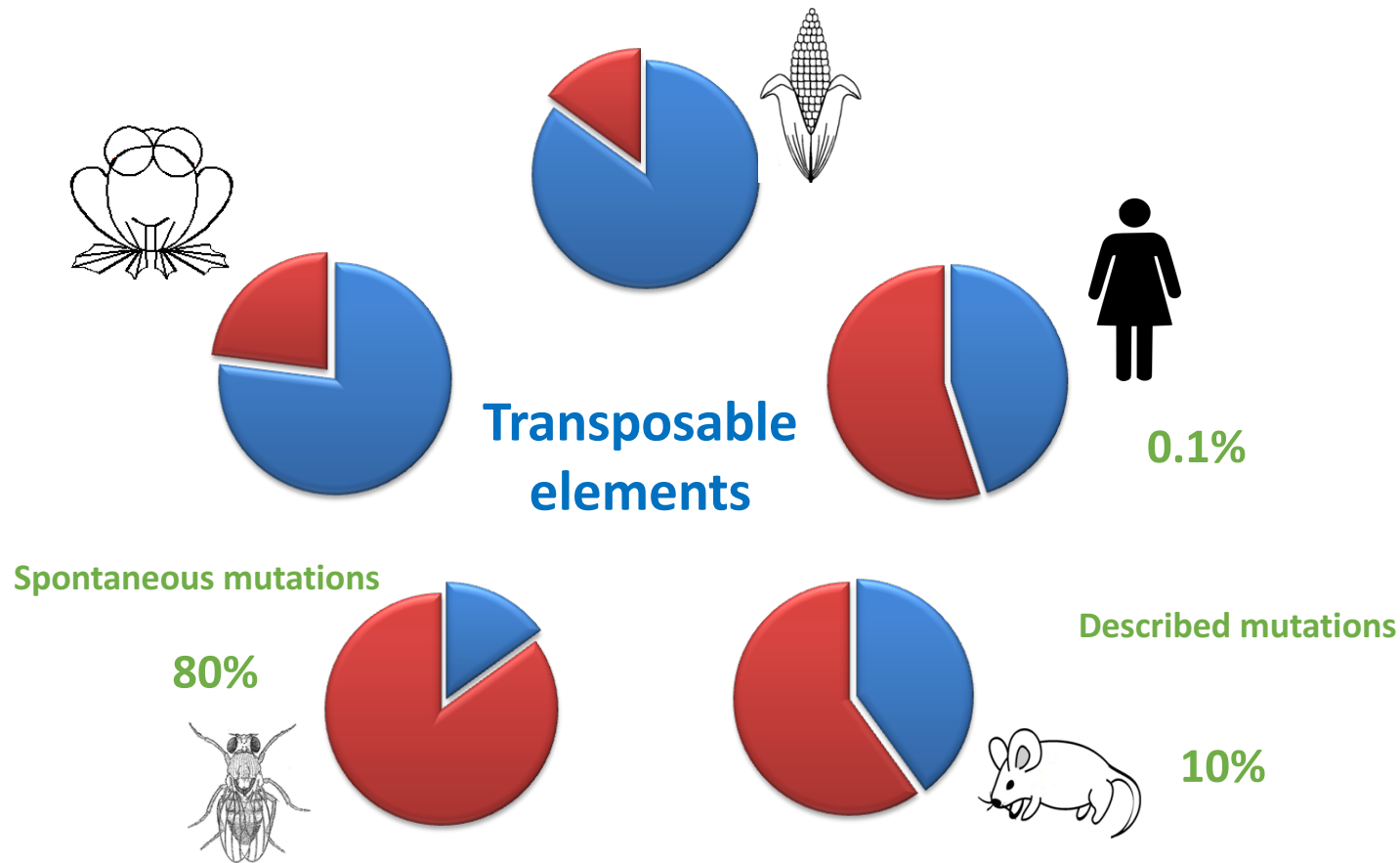
Genome stability



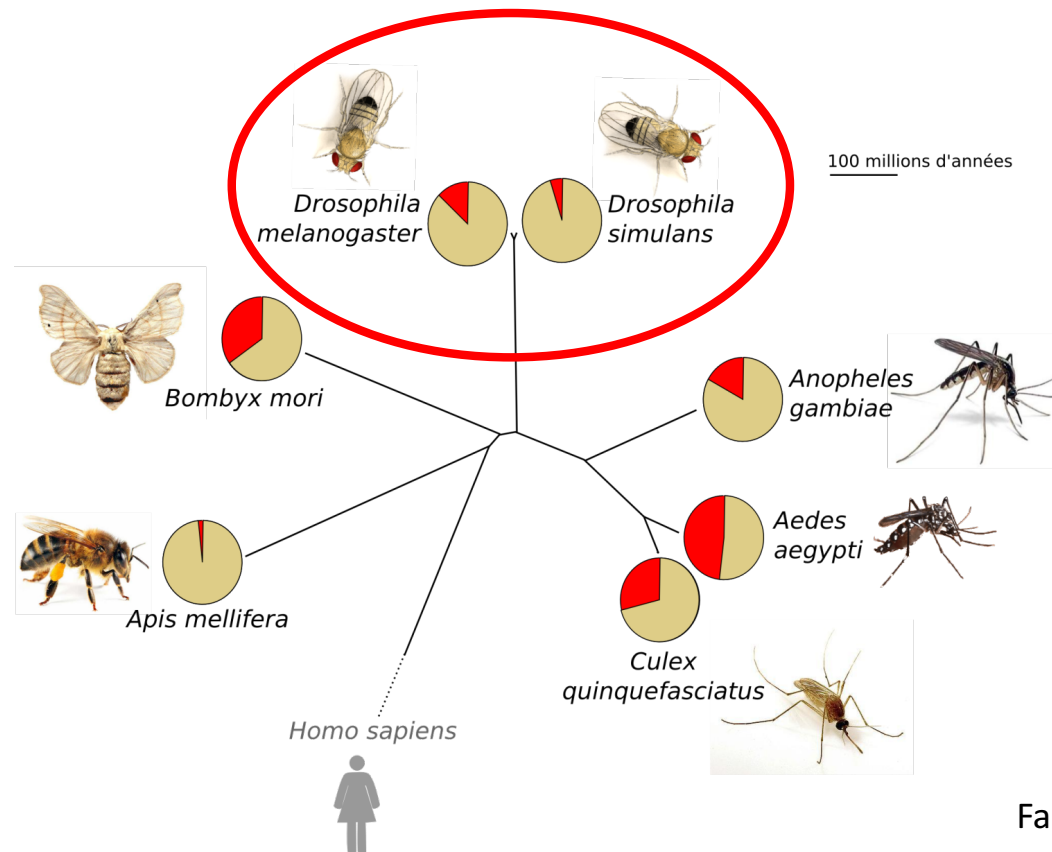
Nature Reviews | [Molecular Cell Biology](#)

Benayoun et al. 2015

TE proportions in some sequenced genomes

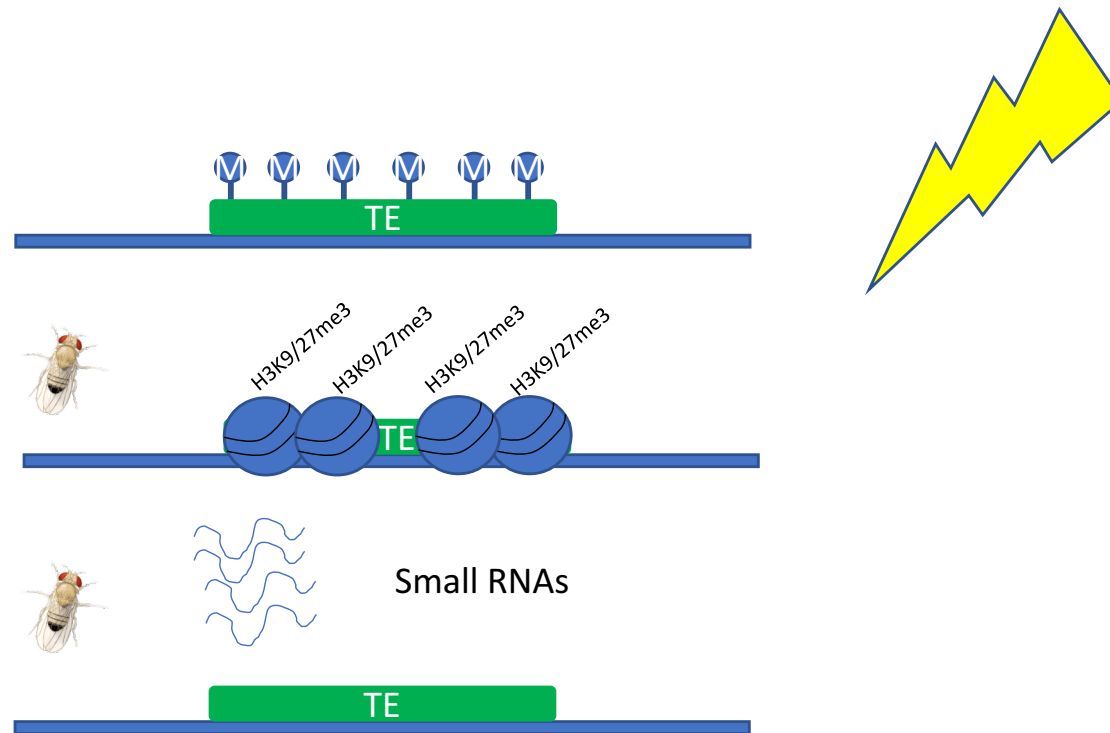


Proportion of TE in some sequenced genomes

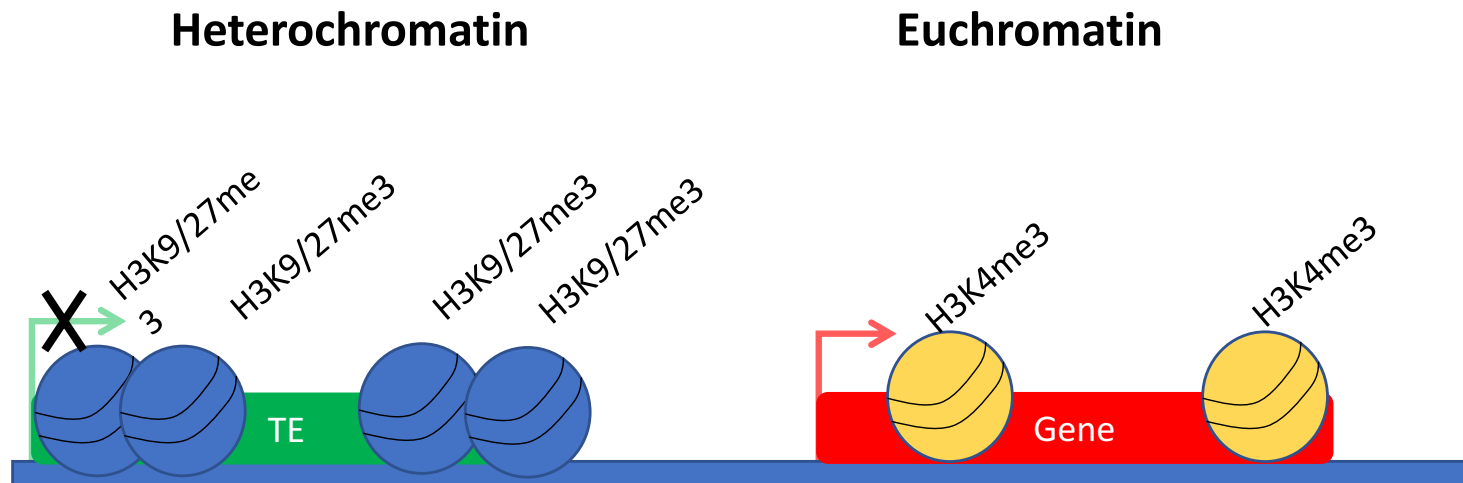


Fablet and Vieira 2011

Does environmental changes affect the stability of the genome mediated by TEs?



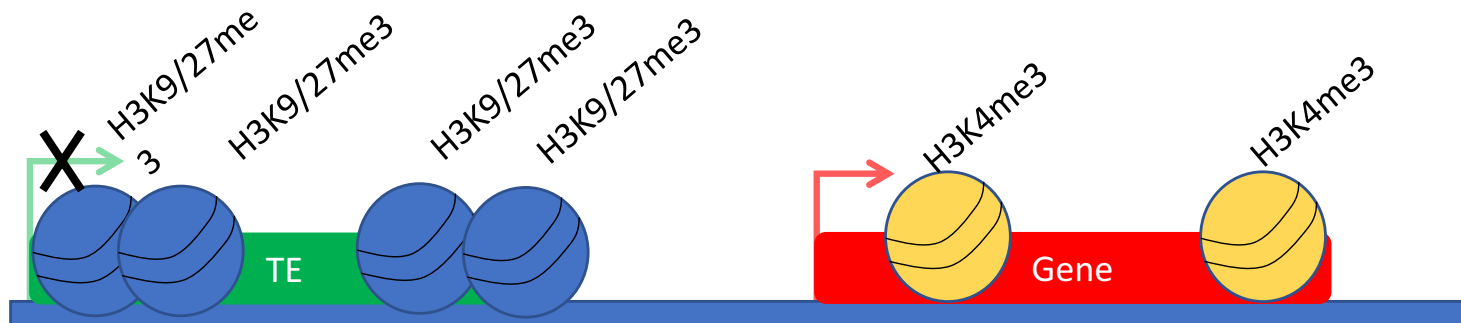
Genome Homeostasis



Genome Homeostasis → Genome instability?
With or without environmental external
changes?

Heterochromatin???

Euchromatin ???



“controlling elements”

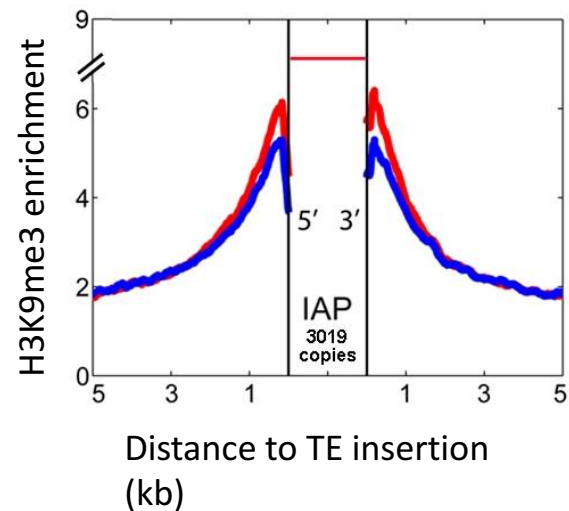


Barbara McClintock
(1902-1992)



Retrotransposon-Induced Heterochromatin Spreading in the Mouse Revealed by Insertional Polymorphisms

Rita Rebollo^{1,2}, Mohammad M. Karimi², Misha Bilenky³, Liane Gagnier^{1,2}, Katharine Miceli-Royer^{1,2}, Ying Zhang^{1,2}, Preeti Goyal², Thomas M. Keane⁴, Steven Jones^{2,3}, Martin Hirst³, Matthew C. Lorincz^{2*}, Dixie L. Mager^{1,2*}

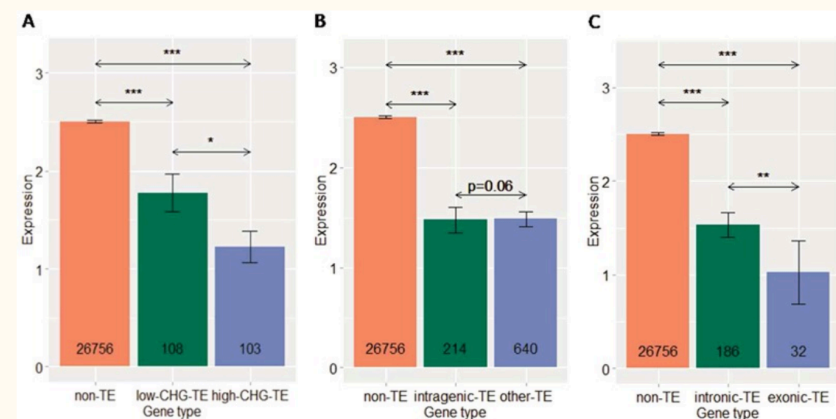


Published online 26 March 2015

Nucleic Acids Research, 2015, Vol. 43, No. 8 3911–3921
doi: 10.1093/nar/gkv258

Epigenetic regulation of intragenic transposable elements impacts gene transcription in *Arabidopsis thaliana*

Tu N. Le¹, Yuji Miyazaki¹, Shohei Takuno² and Hidetoshi Saze^{1,*}

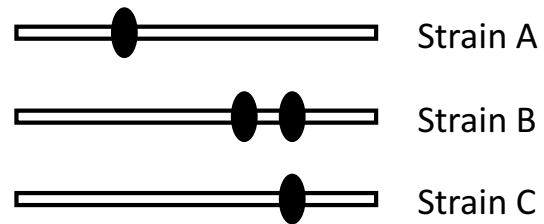


Are TE genome expression modifiers with environmental changes?

- We need:
 - TE insertion polymorphism and gene expression
 - Stress disturbing genome homeostasis
- Different approaches
 - Candidate genes
 - Genome wide

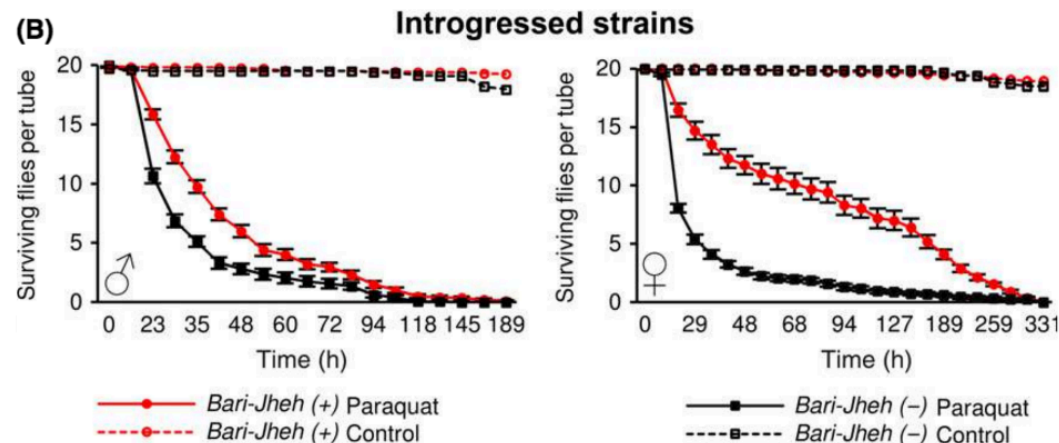
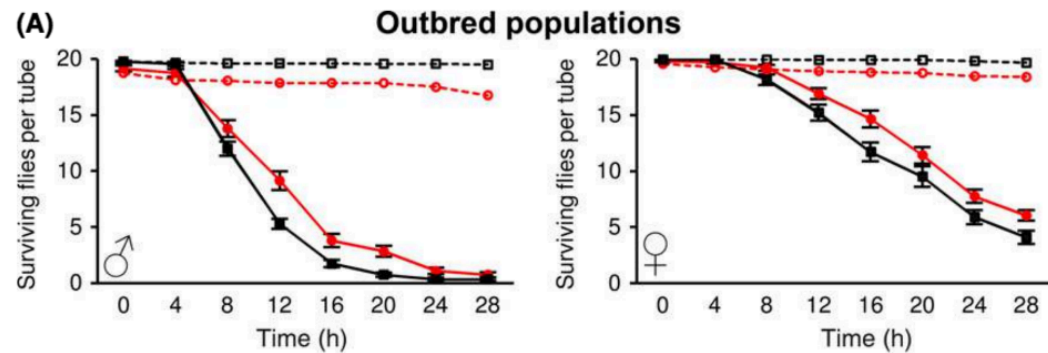
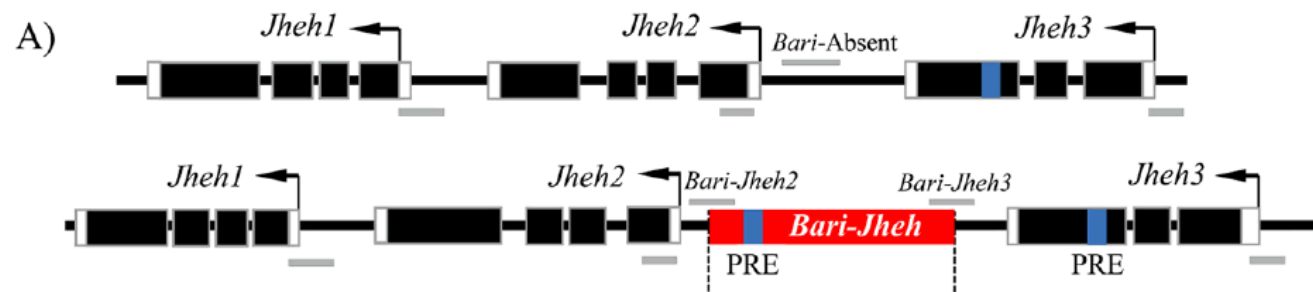
Genome expression modifiers

- TE insertion polymorphism and gene expression



TE insertion polymorphism and gene expression

The case of Bari-Jheh (Juvenile hormone epoxy hydrolase)

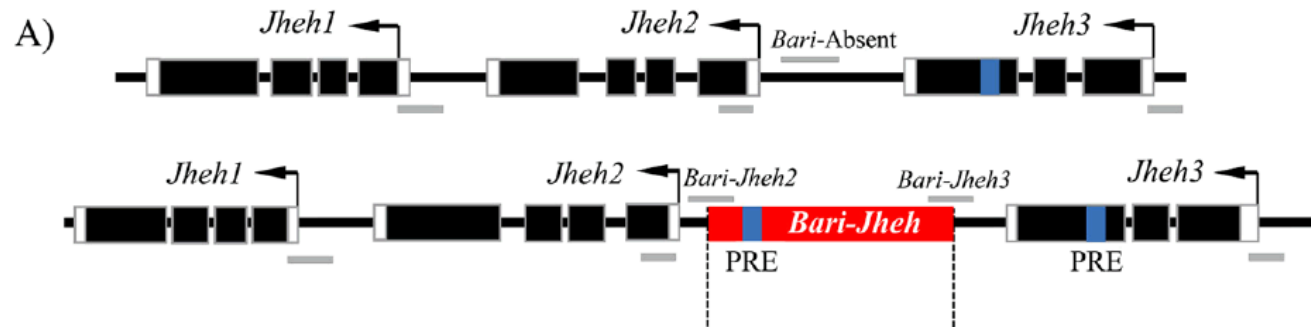


expression

	Non stress	Stress
Jheh1	=	up
Jheh2	down	up
Jheh3	down	down

Guio et al 2014 (JG lab)

The case of Bari-Jheh



- Is Bari affecting the chromatin structure?

Predictions:

Trithorax group Response Elements (TREs) that recruit H3K4 methyltransferases,

Polycomb group Response Elements (PREs) that recruit H3K27 methyltransferases

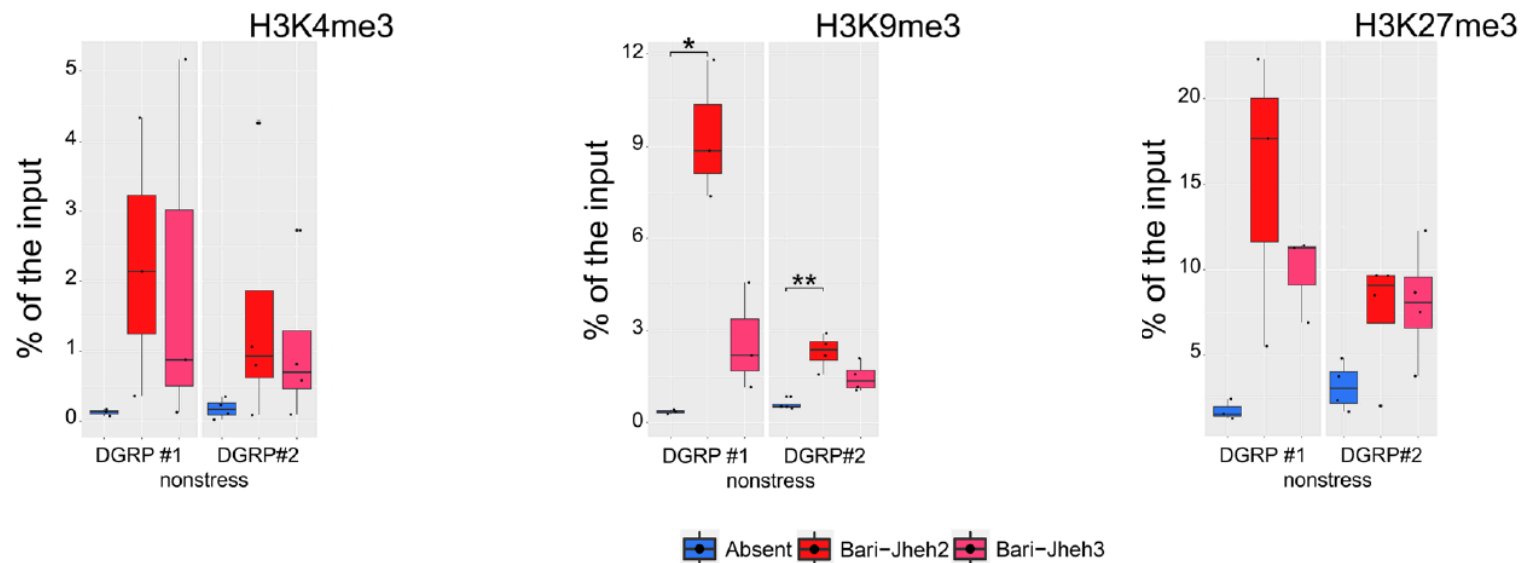
no TRE, one PRE in the Bari-Jheh sequence, and one PRE in the coding region of *Jheh3*

The case of Bari-Jheh

- Two genetic backgrounds
- Three histone marks:
 - H3K4m3 – associated with active chromatine
 - H3K9m3 – repressive mark associated with TEs
 - H3K27m3 – associated with facultative heterochromatin (silenced or repressed promoters and enhancers)

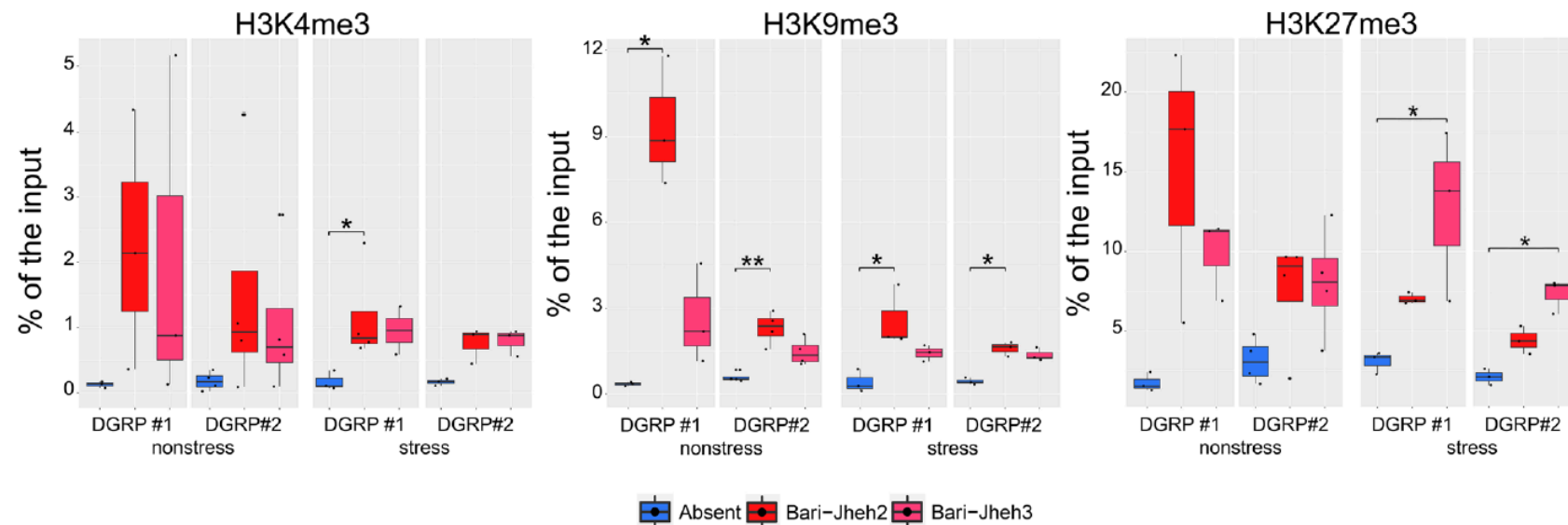
The case of Bari-Jheh

- Bari-Jheh is associated with an enrichment of H3K9me3 histone mark in nonstress conditions.



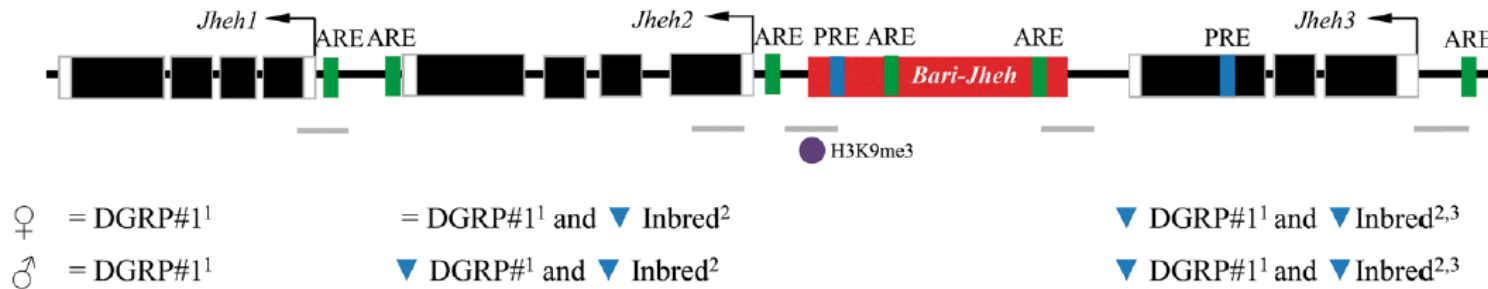
The case of Bari-Jheh

- Bari-Jheh is also associated with an enrichment for H3K4me3 and H3K27me3 chromatin marks in oxidative stress conditions.

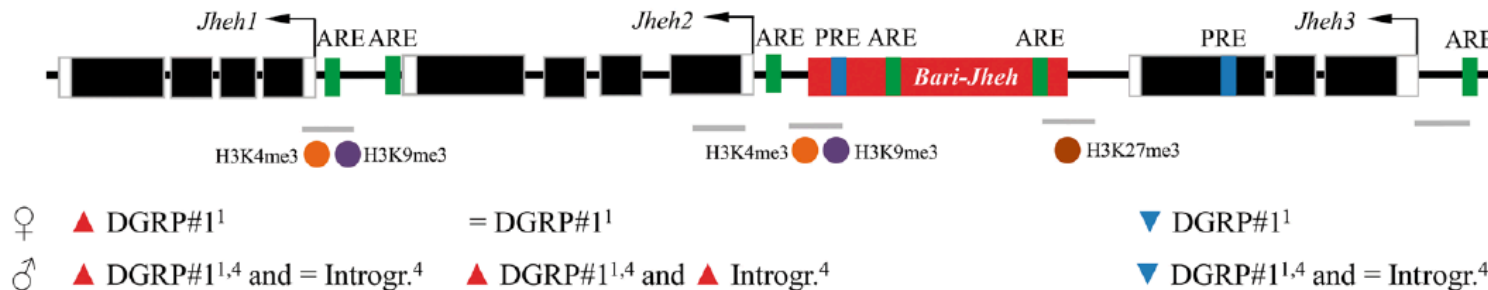


Summary of the histone enrichments found in the Bari-Jheh genomic region.

A) nonstress conditions



B) stress conditions



Are TE genome expression modifiers with environmental changes?

- We need:
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- Different approaches
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 - Genome wide

Is stress disturbing genome homeostasis? (McClintock)

- Response to environment with different recently wild-type strains of *Drosophila*
 - *D. melanogaster* and *D. simulans*

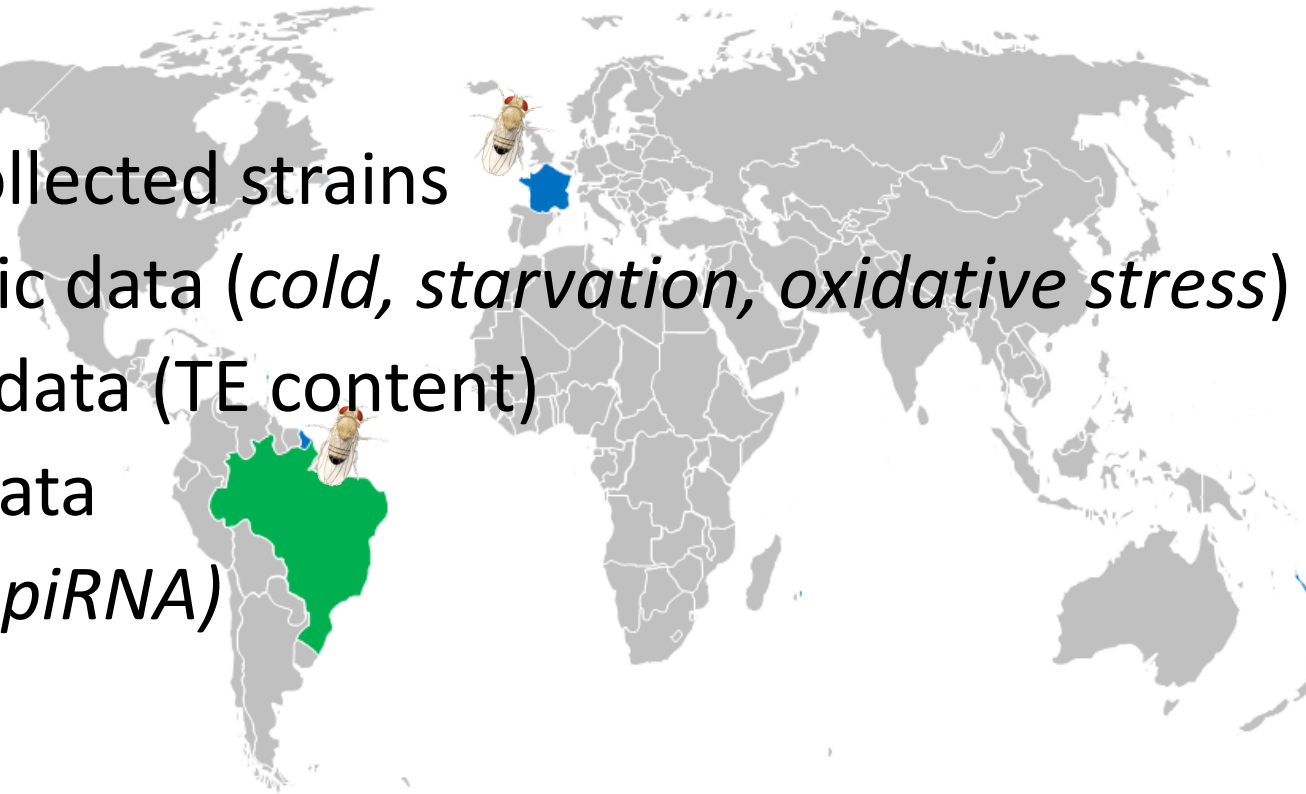
Environment effects



Judit Salces-Ortiz



- Freshly collected strains
- Phenotypic data (*cold, starvation, oxidative stress*)
- Genomic data (TE content)
- RNAseq data
- (*ChIPseq+piRNA*)





Marie Fablet



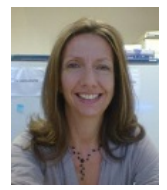
Nelly Burlet



Judit Salces-Ortiz



Sonia Martinez



Bianca Menezes

Environment effects

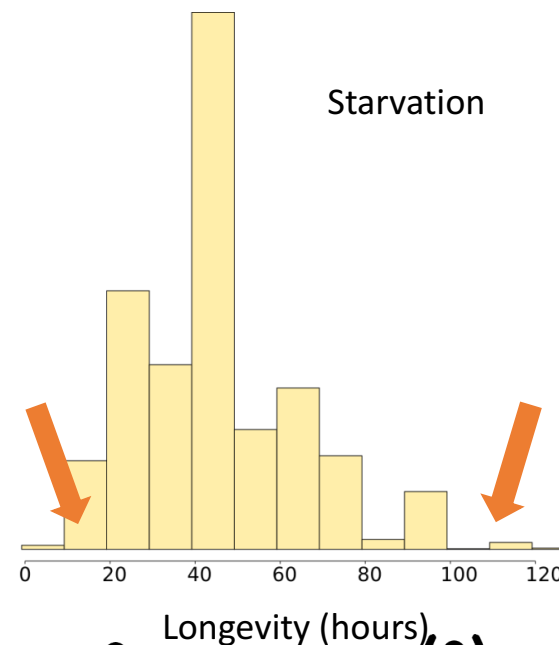
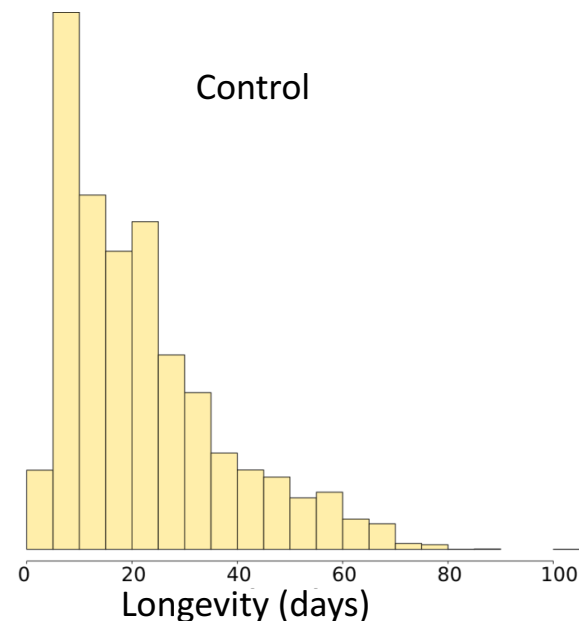
- Phenotypic measures in different environments (30 inbred lines/condition): longevity, starvation, cold, oxidative stress

Selection of a total of 8 lines

-2 species

-2 populations

-2 lines



Environment effects: gene expression

- How to measure the expression of TEs or piRNAs without losing information due to the repetitive nature of TE sequences?
- Development of specific software: TE tools (Lerat et al 2017)



TE tools



- **TE sequences (fasta file)**
 - Annotated or non annotated genomes
- **“rosette” file (text file allowing different levels of analyses)**

chromosome	insertion	type	family	class	expression	etc
2L_1 (21346122..21346196) LTR/Gypsy	297_Dsi_1	297_Dsi	Gypsy	LTR	somatic	
2L_1 (21681877..21682629) LTR/Gypsy	297_Dsi_2	297_Dsi	Gypsy	LTR	somatic	
2L_1 (21699675..21700427) LTR/Gypsy	297_Dsi_3	297_Dsi	Gypsy	LTR	somatic	
2R_1 (120098..120414) LTR/Gypsy	297_Dsi_31	297_Dsi	Gypsy	LTR	somatic	
2R_1 (1236902..1237012) LTR/Gypsy	297_Dsi_32	297_Dsi	Gypsy	LTR	somatic	
2R_1 (412736..413170,413270..413270) LTR/Gypsy	ACCORD2_Dmel_12	ACCORD2_Dmel	Gypsy	LTR	germline	
2R_1 (427330..428124) LTR/Gypsy	ACCORD2_Dmel_13	ACCORD2_Dmel	Gypsy	LTR	germline	
2R_1 (996594..996745) LTR/Gypsy	ACCORD2_Dmel_14	ACCORD2_Dmel	Gypsy	LTR	germline	
2R_1 (1077913..1080665,1082958..1082958) LINE/LOA	BAGGINS1_69	BAGGINS1	LOA	LINE	germline	
2R_1 (1080987..1081517) LINE/LOA	BAGGINS1_70	BAGGINS1	LOA	LINE	germline	
2R_1 (1094723..1094905) LINE/LOA	BAGGINS1_71	BAGGINS1	LOA	LINE	germline	

TE tools



- **Takes into account of the multicopy status and thus the diversity of TEs at the copy level**
 - => we can work on TE families not present in the reference genome
 - => better mapping of reads on copy rather than on consensus
-
- **Differential expression analysis with DESeq2**
 - **mRNA and small RNA**

TE tools



- **Available**

- <https://github.com/l-modolo/TEtools>
- Or by the web site lbbe.univ-lyon1.fr



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