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► **To cite this version:**

Dagmara Robakowska Hyzorek, Marie Mirouze, Pierre Larmande. Integration and Visualization of Epigenome and Mobilome Data in Crops. JOBIM: Journées Ouvertes Biologie Informatique Mathématiques, Jun 2016, Lyon, France. , 2016. hal-01411668

HAL Id: hal-01411668

<https://hal.science/hal-01411668>

Submitted on 9 Dec 2016

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Integration and Visualization of Epigenome and Mobilome Data in Crops

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Transposable elements (TEs) in plant genomes

Introduction:

In the coming years, the study of the interaction between the epigenome and the mobilome is likely to give insights on the role of TEs on genome stability and evolution.

In the present project we have created tools to collect epigenetic datasets from different laboratories and databases and translate them to a standard format to be integrated, analyzed and finally visualized.

Visualization:

For data visualization we used Circos, a powerful standalone tool. The circular layout representations greatly enhance the visualization of scientific results.

Data Integration:

We aim to integrate our data in online epigenome and mobilome database for the rice and arabidopsis data.

- GBrowse graphical interface: 1 : pop up menu 2 : part of detailed report, both available for each feature.

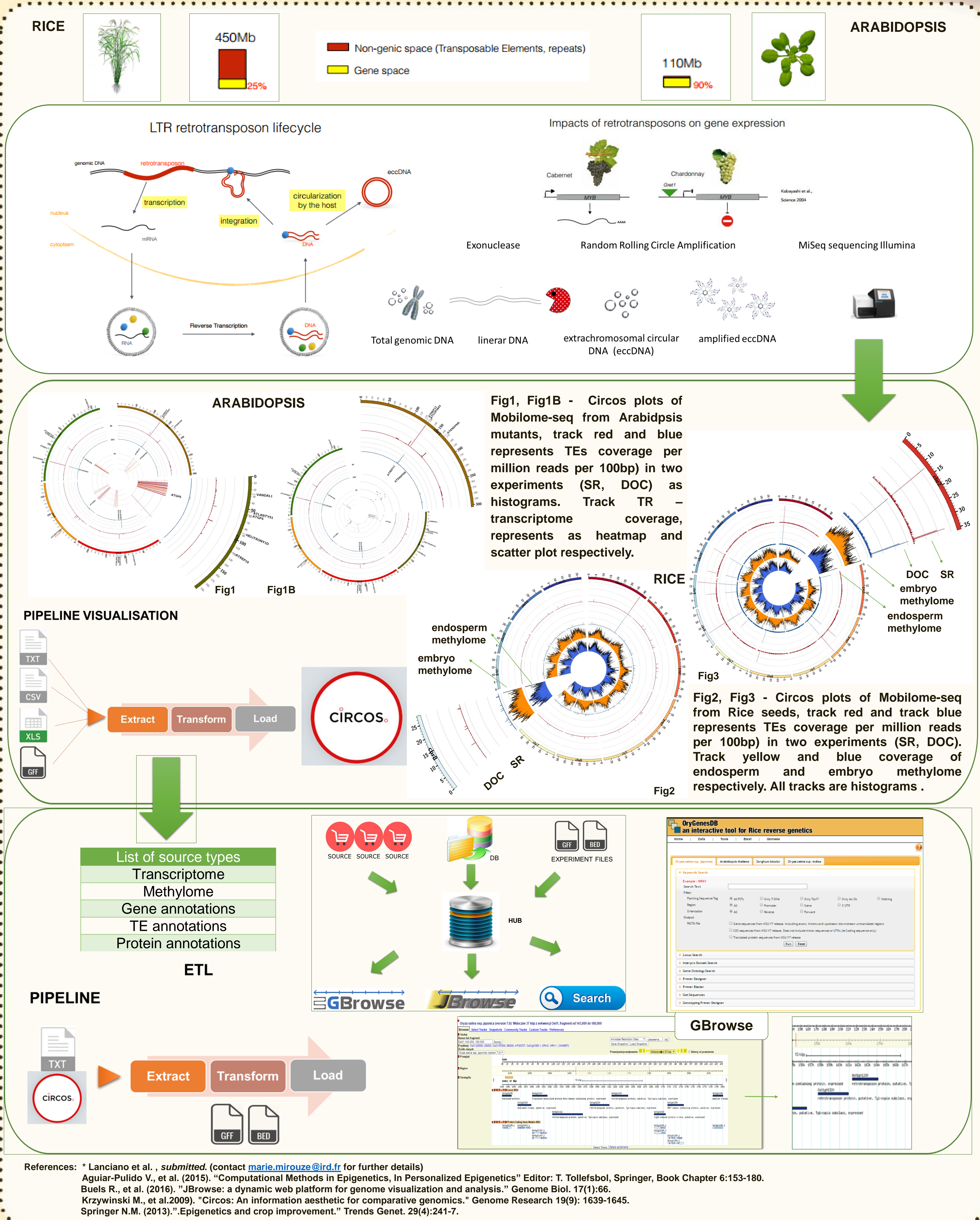
- Quick search: search through all databases and display search results as tables.

Conclusion:

Playing on different filter parameters and tools, this versatile workflow will be useful in the detection of active transposable elements. It has already been run on different data sets, from *Arabidopsis thaliana* and *Oryza sativa*.

Perspectives:

This tool will be adapted to other crops (maize, potato etc..)



References: * Lanciano et al., *submitted*. (contact marie.mirouze@ird.fr for further details)
 Aguiar-Pulido V., et al. (2015). "Computational Methods in Epigenetics, In Personalized Epigenetics" Editor: T. Tollefsbol, Springer, Book Chapter 6:153-180.
 Buels R., et al. (2016). "JBrowse: a dynamic web platform for genome visualization and analysis." *Genome Biol.* 17(1):66.
 Krzywinski M., et al. (2009). "Circos: An information aesthetic for comparative genomics." *Genome Research* 19(9): 1639-1645.
 Springer N.M. (2013). "Epigenetics and crop improvement." *Trends Genet.* 29(4):241-7.