Visual ModuleOrganizer: a graphical interface for the detection and comparative analysis of repeat DNA modules

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Abstract

Background: DNA repeats, such as transposable elements, minisatellites and palindromic sequences, are abundant in sequences and have been shown to have significant and functional roles in the evolution of the host genomes. In a previous study, we introduced the concept of a repeat DNA module, a flexible motif present in at least two occurrences in the sequences. This concept was embedded into ModuleOrganizer, a tool allowing the detection of repeat modules in a set of sequences. However, its implementation remains difficult for larger sequences.

Results: Here we present Visual ModuleOrganizer, a Java graphical interface that enables a new and optimized version of the ModuleOrganizer tool. To implement this version, it was recoded in C++ with compressed suffix tree data structures. This leads to less memory usage (at least 120-fold decrease in average) and decreases by at least four the computation time during the module detection process in large sequences. Visual ModuleOrganizer interface allows users to easily choose ModuleOrganizer parameters and to graphically display the results. Moreover, Visual ModuleOrganizer dynamically handles graphical results through four main parameters: gene annotations, overlapping modules with known annotations, location of the module in a minimal number of sequences, and the minimal length of the modules. As a case study, the analysis of FoldBack4 sequences clearly demonstrated that our tools can be extended to comparative and evolutionary analyses of any repeat sequence elements in a set of genomic sequences. With the increasing number of sequences available in public databases, it is now possible to perform comparative analyses of repeated DNA modules in a graphic and friendly manner within a reasonable time period.

Availability: Visual ModuleOrganizer interface and the new version of the ModuleOrganizer tool are freely available at: http://lcb.cnrs-mrs.fr/spip.php?rubrique313.

Keywords: Compressed suffix tree, Maximal repeats, Repeat modules, Graphical interface

Background

Repeated sequences (e.g. transposable elements, minisatellites, ...) are present in all living organisms studied until date [1]. They are evolutionary conserved sequences and have been shown to have a significant functional importance [2]. Recent studies show the role of transposable elements in the evolution of host genomes [3-5], including transposable elements domestication (neogene), exaptation, and transcription regulators [1,6,7]. A number of tools has been described for the search of repeated elements in a genome. However, most of them (RepeatMasker [8], Censor [9], and ISFinder [10]) are BLAST-like tools that detect repeats (such as transposable elements) using a library of consensus sequences. Except for phylogeny analysis, there are few bioinformatic tools (VISTA [11], GATA [12], GraphDNA [13], Recon [14] and DomainOrganizer [15]) that facilitate the analysis of relationships and variations between the copies of a given family of repeats [16,17].

In a previous study, we developed ModuleOrganizer that indexed all maximal repeats (MR) of sequences via a suffix tree in order to detect conserved modules within the repeated sequences [18]. Indeed, the algorithm recursively associates two MR if the spacer between them is smaller than the size of the largest maximal repeat and if
the edit distance between spacers of all occurrences is not greater than the size of the smallest maximal repeat. The MR association yields to the formation of modules under restrictions defined by the user such as the minimal length of the module (MinSizeModule) and the minimal number of sequences (MinSequences) [18].

Although the previous version of the ModuleOrganizer tool can efficiently detect repeated modules within sequences of smaller sizes (<100 Kbp), its implementation with larger sequences remains problematic. This is often because memory usage becomes bottleneck. Since ModuleOrganizer command lines are the limiting factors for its use, a graphical interface should be useful for launching and analyzing ModuleOrganizer results. To overcome these difficulties, we propose an optimized version of the ModuleOrganizer software with its corresponding graphical interface called Visual ModuleOrganizer.

Implementation

Since the previous algorithm was written in C language, the new version of ModuleOrganizer [18] was first completely recoded in C++ which drives better memory management. Then, as using a standard suffix tree [19] to compute and store all maximal repeats (MR) leads to a high memory usage during the process of ModuleOrganizer, a data structure based on the compressed suffix tree Välimäki [20] was applied to the new algorithm version.

Therefore, the final re-implementation of the new version contains options of the previous algorithm such as search of palindromic modules, search of exact repeats, search of truncated modules, creation of a classification tree file, search in a minimal number of sequences and association distance between MR. In addition, new options were also developed including the ‘-limit integer’ option which stops the ModuleOrganizer run process after the detection of integer modules, and the ‘-f MinSizeMR’ option that selects MR of equal or greater size than MinSizeMR bp before the formation of the module. This option decreases the ModuleOrganizer run time but have little effects on the sensitivity/specificity of module detection (data not shown). Finally, the new option ‘-p m’ prints each m minute the approximative progress of the software.

As the input, ModuleOrganizer needs FASTA file containing the nucleotide sequence(s) (input-file1, mandatory). It can also use a FASTA reference (input-file2, optional) file. This reference sequence file must contain a unique sequence. The ‘-REF input-file2’ option limits the module detection to MR present in both input and reference sequences.

ModuleOrganizer creates one mandatory output file (named ‘Module File’) that contains the list of detected modules in a tabular format as follows:

```bash
>seq1_name length_seq1
START1 END1 MODULE x nb_sequence orientation
START2 END2 MODULE y nb_sequence orientation ...
>seq2_name length_seq2
START3 END3 MODULE x nb_sequence orientation
START4 END4 MODULE y nb_sequence orientation ...
```

where START1, START2, START3 and START4 (END1, END2, END3 and END4) correspond to the start (end) location of modules within the sequences. x and y represent the identification number of modules. nb_sequence is the number of sequences in which the module is present and orientation gives the orientation of the module in sequences (letter ‘d’ for the direct strand and letter ‘c’ for the reverse strand).

If the input file contains three or more sequences, ModuleOrganizer creates an Unweighted Pair Group Method with Arithmetic Mean (UPGMA)-based tree from the matrix of presence/absence of modules in sequences. This tree is then saved as a second output file, with ‘upgma’ extension name. The ‘-MR’ option writes out (in a tabular format) the list of detected MR (see Additional file 1). The option ‘-SVG’ allows the creation of an optional output file in Scalar Vector Graphics (SVG) format, a XML-based vector language that grants modifications with any Scalar Vector Graphics-enabled image processing tool.

The new ModuleOrganizer version was successfully compiled and tested on Linux 64 bits, Windows 7 32/64 bits, and MacOsX 64 bits. The Visual ModuleOrganizer interface was coded and compiled with Java version 1.6.

Results and discussion

Data-processing improvements

During the run process of the previous algorithm, positions of the selected MR are first copied in the computer memory space before the building of all potential modules. By consequence, this method might lead to high memory usage and therefore slows down the detection process. In order to improve the efficiency of ModuleOrganizer memory usage, the new algorithm directly reads the MR positions through the compressed suffix tree data structure. As shown in Figure 1, this change (from suffix tree to compressed suffix tree) dramatically decreases the memory usage of ModuleOrganizer, particularly for large sequences. Indeed, in the previous and the new version, artificial random sequences from 10 to 240 Kbp exhibit a memory usage of 29 to 5326 Mb and 13 to 25 Mb, respectively. As shown in Figure 1, the expected required memory space for a 1 Mbp genome should be about 21 Gb with the previous program (>8 Gb of RAM memory...
Figure 1 Memory usage comparison between old and new versions of the ModuleOrganizer algorithm. The blue (red) line corresponds to the old (new) version of the algorithm. The size range of the sequences is from 10 Kbp to 1000 Kbp. Experienced and expected results are displayed with plain and dotted lines, respectively.

for a standard computer) while it should only require 98 Mb with the new version. Interestingly, a typical running process with the new version of ModuleOrganizer reduces the required memory space by at least 120 times in average when compared to the old version. Moreover, the new ModuleOrganizer version is faster than the previous one, especially for sequences greater than 200 Kbp (Additional file 2). Indeed, for a 240-Kbp sequence, the new tool is 4.8 times faster than the previous version (57 and 277 minutes, respectively). For larger sequences (about 1 Mb), the expected running time do not exceed four hours with the new algorithm of ModuleOrganizer.

The visual ModuleOrganizer graphical interface

For an user-friendly ModuleOrganizer and results easily handle, a Visual ModuleOrganizer interface was created and divided into two main areas as described below.

The visual ModuleOrganizer tool parameters

Through Visual ModuleOrganizer, ModuleOrganizer parameters (Area 1 in Figure 2) can be used in two different ways: (i) ModuleOrganizer is launched by selecting ‘No’ on the ‘Using Previous Results’ button; or (ii) previous results from ModuleOrganizer are displayed by selecting ‘Yes’ with the same button.

In the first case, the two first mandatory parameters are the ‘Input: FASTA File’ button, which selects the input file, and the ‘Output: Module File’, in which ModuleOrganizer results are written and displayed by the Visual ModuleOrganizer interface. The third mandatory parameter (e.g. MinSizeModule) is the minimal size of the module, which is chosen from a list (Figure 2). Therefore, a module is detected and selected by the algorithm if its size is equal or longer than MinSizeModule. By default (with ‘Automatic’ size), ModuleOrganizer proposes to set MinSizeModule to the minimal value of x such that it does not exists a word of size x in the sequence(s).

In addition to the three mandatory parameters, Visual ModuleOrganizer has the seven optional parameters. The three first parameters (‘Palindromic modules’, ‘Truncated modules’, and ‘Exact repeats’) provide binary choices and were described in the previous version [18]. Four others were computed in the new version of ModuleOrganizer. ‘Minimal number of sequences’ (e.g. MinSequences) and ‘Maximal number of modules’ (e.g. MaxModules) options require an integer value x, and limit the detection of modules in at least x sequences and to a maximal number of modules x in the whole set of sequences, respectively. The option ‘Module located in a reference’ refers to detected modules located in the reference sequence as well as in the mandatory ‘Input FASTA File’ sequences. The last option, labeled ‘Annotations’, opens a new frame (see upper right frame in Figure 2) that allows the user to add genomic annotations from Genbank [21], EMBL [22], AB- BLAST [23], or NCBI-BLAST [24] and/or repeat annotations from RepeatMasker [8], Censor [9], and Repet [25] formats within the graphical interface. It is noteworthy that each annotation should be added independently for each sequence. Interestingly, the user can add its own annotation in a tabular format.

In the second case, when the button ‘Yes’ from ‘Using Previous Results’ is selected (see upper left frame in Figure 2), ModuleOrganizer parameters become invisible. They are replaced by a mandatory parameter ‘Input: ModuleOrganizer File’ and two optional parameters labeled ‘Option: Tree file’ from an upgma-based tree and ‘Annotations’ as described above. Both ‘Input: ModuleOrganizer File’ and ‘Option: Tree file’ use the result file created from a previous ModuleOrganizer run.

In both cases, once all the parameters are selected, the user launches the ModuleOrganizer algorithm with the ‘RUN ModuleOrganizer’ button. Detailed information about parameters and graphical options are available with the ‘HELP’ button (Additional file 3).
**Graphical display and optional parameters**

A graphical display of the ModuleOrganizer results is illustrated in Figure 2 (Area 2). By default, each sequence (e.g. SEQ_3) is represented by two lines: one corresponds to a graduated ruler along the sequence (from 5’ to 3’) and the other consists of modules (boxes with different textures). Identical modules are displayed with the same texture to facilitate intra- and inter-sequence comparisons. A reverse module is indicated by a black triangle (e.g. module 9 in SEQ_3) while a truncated module (e.g. module 3 in SEQ_3) is shown by a dark grey diagonal line within the texture. When an user clicks on a graphical element, a menu with the detailed information (nature of the genetic object and its location) is displayed (e.g. a detailed information is shown for a repeat on SEQ_2 in Figure 2).

Similar pop-up menu (e.g. module 9 in SEQ_3) allows the user to display the nucleotide sequence of a particular or all copies of repeated modules (with their co-ordinates along each sequence), which can be useful for further analysis. It is noteworthy that the sequence order is based on upgma-based tree (by default) instead of alphabetical name order.

Above the graphical panel, four options are provided allowing the user to dynamically add or remove elements (from results or annotations) in the graph. The ‘Draw annotations’ option displays or removes annotations on graph based on the selected item thanks to the ‘Annotations Menu’ menu. When genomic or repeat annotations are displayed, one or two additional lines, corresponding to genetic objects and repeat annotations from ‘Annotations’ files, are added between the module and the ruler lines (Figure 2, see SEQ_1 and SEQ_2 with respectively...
two and one additional lines, in the context of ‘ALL
annotations’ item). The genomic annotations include six
different items: ‘Genes’, ‘Exons’, ‘Introns’, ‘5’ ‘3’ UTRs’,
‘Pseudos’ (pseudogenes), ‘MiscRNAs’; that can be selected
independently. Their orientations are shown by an arrow
shape while repeat annotation orientations are indicated
by a black triangle. The ‘NO Annotation’ item removes all
annotations.

The ‘Draw Overlapping Modules’ menu displays or
removes detected modules based on their overlap or not
with visible annotations (genomic or repeat). ‘All Modules’
item draws modules wherever the annotations (Figure 2,
Area 2), while ‘Overlap with Annotations’ and ‘NO Over-
lap with Annotations’ (see Additional file 4), respectively
draws and removes the modules that overlap the annota-
tion positions.

‘Draw Modules present in at least M Sequences’ and
‘Draw Modules by Size’ sliders display modules located
within a minimal number of sequences and with a min-
imal length, respectively. Minimum and maximum val-
ues of the two sliders are automatically taken from the
ModuleOrganizer process with the ‘M Sequences’ ranges
from 1 to total number of sequences and the ‘Size’
ranges from minimal and maximal length of the detected
modules.

Under the graph, four buttons facilitate the modification
of the graphical view: ‘Zoom in’ and ‘Zoom out’ but-
tons increase and decrease by a factor 2 the graph width,
respectively. ‘Global view’ button adjusts the graph width
(including the graph elements) according to the largest
sequence. The last button, labeled ‘Enlarge Graph’, (or
‘Reduce Graph’ after a click on it) removes the parameter
area (Figure 2, Area 1) (or displays it) from the interface.

Finally, the ‘Save results’ combo-list saves the graph
(whole graph or viewed graph in a PNG format) for exter-
nal use. All graphical options can be changed and associ-
ated at any moment and the graph dynamically displays
the elements based on the user choices. Detailed informa-
tion about parameters and graphical options are available
through the ‘HELP’ button (Additional file 3).

A case study: the FoldBack4 transposable element family
of Drosophila melanogaster
FoldBack elements are a family of transposable elements
described in Drosophila melanogaster. Structurally, the
members of this dispersed repetitive family have long
inverted terminal repeats and a central loop between the
repeats. The lengths of these repeats and loops vary from
element to element [26,27]. The inverted repeats of all the
family members are homologous [27] and carry a peculiar
organization of sequences with highly conserved complex
sequences at the termini [28]. Several families of Fold-
Back, including the FoldBack4 (FB4) family, are known to
be non-autonomous transposable elements [26,27].

For this study, 10 FB4 sequence elements ranging from
627 to 2266 bp were chosen. These elements are gen-
erally highly variable in their internal sequence, includ-
ing numerous insertions, deletions, and repetitions, but
share consensus palindromic extremities in all their copies
because they are necessary for the transposition [28]. With
a MinSizeModule settled to 25 bp, ‘Palindromic modules’
and ‘Truncated modules’ options selected, the Module-
Organizer algorithm discovered 23 modules (Figure 3A).
Palindromic structures of the FB4 sequences are described
by modules 1-5 that should correspond to Terminal
Inverted Repeat (TIR). Internal sequences are mainly
composed of the modules 8-10 which are repeated in tandem,
looking like minisatellites. Those are often present in
the internal sequence of non-autonomous transpos-
able elements [1,28]. According to the module composi-
tion, the upgma-based tree clusters the FB4 sequences in
4 distinct groups: Group1 = FB4_3, FB4_8, and FB4_4;
Group2 = FB4_1, FB4_9, and FB4_5; Group 3 = FB4_10
and FB4_11; Group4 = FB4_2 and FB4_7, allowing inter-
and intra-groups comparison of the detected modules.
Indeed, the reverse occurrence of modules 3 and 4 were
deleted in FB4_2 and FB4_7 (from Group4) and reverse
modules 2-5 were absent in FB4_10 and FB4_11 (from
Group3). These findings clearly suggest that partial dele-
tions of these palindromic structures would impair the
transposition of these FB4 sequences.

Through the Visual ModuleOrganizer interface, the
‘Draw Modules present in at least M Sequences’ slider was
settled to 9, allowing only the display of modules present
in at least nine of the ten FB4 sequences. As a result, the
palindromic modules (module 1 to 5) and the module 9
from the internal sequence are still displayed (Figure 3B),
indicating that those palindromic modules are evolu-
tionary conserved within the FB4 family and might be
essential for the transposition. This observation also puts
forward that the ‘Draw Modules present in at least M
Sequences’ option can be useful for comparative analysis
(insertions, deletions, repetitions, rearrangements, ...) of
modules in a given set of a sequence family. In a similar
way, when the ‘Draw Modules by Size’ slider is set to 58
(e.g the displayed modules are equal or longer than 58 bp),
only modules 1, 4, 5 and 15 are displayed in Figure 3C,
therefore allowing the identification of large conserved
modules.

Altogether, the case study of FB4 spotlights the abil-
ity of Visual ModuleOrganizer for comparative analysis of
highly complex and variant repeat structures in a given
set of sequences. These complex repeat features include
biological known repeat structures (palindromes, min-
satellites, ...) that are usually not observable by standard
analysis tools such as VISTA [11], GATA [12], GraphDNA
[13], and Recon [14]. Indeed, it has been shown that
these software which combine multiple alignment with
Figure 3 Identification and comparative analysis of repeat DNA modules in FoldBack4 sequences using Visual ModuleOrganizer. From the ten FoldBack4 sequences, a *MinSizeModule* of 25, *Palindrome modules*’ and *Truncated modules*’ options, the ModuleOrganizer algorithm detects 23 modules. Graphical displays of the results: (A) default graphical options, (B) *Draw Modules present in at least M Sequences*’ slider sets to 9 and (C) *Draw Modules by Size*’ slider sets to 58 bp.
graphical tools fail to retrieve a good organization of the non-autonomous elements for a typical family such as FB4 [18]. Therefore, ModuleOrganizer remains the sole algorithm that is able to identify distinct structural repeats such as duplicated, palindromic and truncated modules, allowing the user to infer putative functional role of these modules.

Conclusion
We have described Visual ModuleOrganizer, a novel graphical interface with a new optimized implementation of the ModuleOrganizer tool. The key features of these tools are: (1) detection of modules within larger sequences and with efficient low memory usage; (2) user-friendly handling of ModuleOrganizer thanks to a graphical interface; and (3) dynamic graphical parameters that tune the visualization of the results based on the user needs. In addition, Visual ModuleOrganizer will be useful to investigate evolutionary and comparative analysis (modules insertions, deletions, rearrangements, ...) from all type of DNA repeats (transposable elements, CRISPR, minisatellites, ...). ModuleOrganizer remains applicable in principle to any set of nucleic sequences sharing some similarities and for which a multiple alignment fails to correctly retrieve the architecture of conserved blocks in the sequences. With the increasing number of sequence data available in biological databases, these features in the Visual ModuleOrganizer interface clearly provide new opportunities for inter- and intra-sequence comparative analysis of repeat DNA modules in an easy, user-friendly manner within a reasonable time.

Additional files

Additional file 1: Example maximal repeat (MR) output file in a tabular format. Each file shows six columns: the maximal repeat word, the identification number in the suffix tree, the MR size, the occurrence number, the number of sequences where the MR is present and the list of start positions.

Additional file 2: Run time comparison between old and new versions of ModuleOrganizer. The blue (red) line represents running time process observed with old (new) version of ModuleOrganizer. The size range of the sequences is from 10 Kbp to 1000 Kbp. Experienced and expected results are displayed with plain and dotted lines, respectively.

Additional file 3: Screenshoot of the HELP interface.

Additional file 4: Module display when the ‘NO Overlay with Notations’ item is selected. Some modules (e.g. Module 1 and 2) became invisible when the ‘NO Overlay with Notations’ item is selected.

Abbreviations
CRISPR: Clustered regularly interspaced short palindromic repeats; FB4: FoldBack4; MR: Maximal repeats; RAM: Random access memory; SVG: Scalar vector graphics; UPGMA: Unweighted pair group method with arithmetic mean.

Competing interests
The authors declare that they have no competing interests.

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Authors' contributions
ST and ET conceived the study, analyzed the results and wrote the paper. ST performed the computational implementations. All the authors read and approved the final manuscript.

References
1. Bigot Y: Mobile genetic elements, protocols and genomic applications, 2012. ISBN 978-1-61779-602-9.
2. Romanish MT, Nakamura H, Lai CR, Wang Y, Mager DL: A novel protein isoform of the multicopy human naip gene derives from intragenic alu sine promoters. PLoS One 2009, 4(5):761.
3. Joly-Lopez Z, Forczek E, Hoen DR, N J, Bureau TE: A gene family derived from transposable elements during early angiosperm evolution has reproductive fitness benefits in arabidopsis thaliana. PLoS Genet 2012, 8(10):e1002951.
4. Li Y, Li C, J X, Jin Y: Domestication of transposable elements into microRNA genes in plants. PLoS One 2011, 6:19212.
5. Siddique A, Buisine N, Chalmers R: The transposon-like corelia elements encode numerous strong promoters and provide a potential new mechanism for phase variation in the meningococcus. PLoS Genet 2011, 7(10):e1001277.
6. Hayward A, Ghazal A, Andersson G, Andersson L, Jern P: Zbed evolution: repeated utilization of dna transposons as regulators of diverse host functions. PLoS One 2013, 8(3):e59940.
7. Rebollo R, Fairvar S, Mager DL: C-gate - catalogue of genes affected by transposable elements. Mob DNA 2012, 3(1):9.
8. Smit AFA, Hubley R, Green P: RepeatMasker Open-3.0. http://www.repeatmasker.org.
9. Pavlicek A, Kohany O, Jurka J: Repeat Mining: Basic Tools for Detection and Analysis. In Analytical Tools for DNA, Genes and Genomes Nuts and Bolts. Edited by Markoff A. Eagleville: DNA Press; 2005.
10. Siguier P, Perochon J, Lestrade L, Mahillon J, Chandler M: Isfinder: the reference centre for bacterial insertion sequences. Nucleic Acids Res 2006, 34(1):32–36.
11. Dubchak I, Poliakov A, Kishlyuk A, Brudno M: Multiple whole-genome alignments without a reference organism. Genome Res 2009, 19(4):682–9.
12. Nix DA, Eisen MB: Gata: a graphic alignment tool for comparative sequence analysis. BMC Bioinformatics 2005, 6(9).
13. Thomas JA, Horstpool D, Brown B, Tcherepanov V, Upton C: GraphDNA: a java program for graphical display of dna composition analyses. BMC Bioinformatics 2007, 8(2):1.
14. Bao Z, Eddy SR: Automated de novo identification of repeat sequence families in sequenced genomes. Genome Res 2002, 12(1):1269–1276.
15. Tempel S, Giraud M, Lavenier D, Lerman IC, Valin AS, CouéeI, Amrani AE, Nicolas J: Domain organization within repeated dna sequences: application to the study of a family of transposable elements. Bioinformatics 2006, 22:1948–54.
16. Böhne B, Zhou Q, Darras D, Schmidt C, Schartl M, Galiana-Amoux D, Volf JN: Zisupton-a novel superfamly of dna transposable elements recently active in fish. Mol Biol Evol 2012, 29(2):631–45.
17. Maio M, Bello X, Puig XM, Ruiz A: Striking structural dynamism and nucleotide sequence variation of the transposon galileo in the genome of drosophila mojavensis. Mol DNA 2013, 411(6).
18. Tempel S, Rousseau C, Tahir F, Nicolas J: Moduleorganizerdetecting modules in families of transposable elements. BMC Bioinformatics 2010, 11:474.
19. Gusfield D: Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology. Cambridge University Press; 1997. ISBN 0-521-58519-8.
20. Valimäki V, Gerlach N abd, Dixit K, Makinen V: Compressed suffix tree-a basis for genome-scale sequence analysis. Bioinformatics 2010, 23:629–630.
21. Benson DA, Cavanaugh M, Clark K, Karsch-Mizrachi I, Lipman DJ, Ostell J, Sayers EW: Genbank. Nucleic Acids Res 2013, 41(D1):36–42.
22. Kulikova T, Akhtar R, Aldebert P, Althorpe Nea: Embl nucleotide sequence database in 2006. *Nucleic Acids Res* 2007, 35(1):16–20.
23. Gish W: AB-BLAST. http://blast.advbiocomp.com
24. Johnson M, Zaretskaya I, Raytselis Y, Merezhuk Y, McGinnis S, Madden TL: Ncbi blast: a better web interface. *Nucleic Acids Res* 2008, 36:5–9.
25. Flutre T, Duprat S, Feuillet C, Quesneville H: Considering transposable element diversification in de novo annotation approaches. *PLoS ONE* 2011, 6(1):16526.
26. Brierley H, Potter S: Distinct characteristics of loop sequences of two drosophila foldback transposable elements. *Nucleic Acids Res* 1985, 13(2):485–500.
27. Silber J, Bazin C, Lemeunier F, Aulard S, Volovitch M: Distribution and conservation of the foldback transposable element in drosophila. *J Mol Evol* 1989, 28(3):220–4.
28. Potter SS: Dna sequence of a foldback transposable element in drosophila. *Nature* 1982, 297:201–204.

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