Jedlicka *et al. Mobile DNA* (2020) 11:3
https://doi.org/10.1186/s13100-019-0199-7

Mobile DNA

CORRECTION Open Access

Correction to: Nested plant LTR retrotransposons target specific regions of other elements, while all LTR retrotransposons often target palindromes and nucleosome-occupied regions: in silico study

Pavel Jedlicka[1], Matej Lexa[2], Ivan Vanat[2], Roman Hobza[1] and Eduard Kejnovsky[1*]

Correction to: Mobile DNA
https://doi.org/10.1186/s13100-019-0186-z

Following publication of the original article [1], the authors spotted an error in Table 2.

- t-test pvalue in penultimate row = "0.61" should not be bold
- the asterisks with significance levels should be as follows: "(* for p < 0.1, ** for p < 0.01 and *** for p < 0.001)"

The original article has been corrected. The correct presentation of Table 2 is shown below.

Author details
[1]Department of Plant Developmental Genetics, Institute of Biophysics of the Czech Academy of Sciences, Kralovopolska 135, 61200 Brno, Czech Republic. [2]Faculty of Informatics, Masaryk University, Botanicka 68a, 60200 Brno, Czech Republic.

Published online: 07 January 2020

Reference
1. Jedlicka, et al. Nested plant LTR retrotransposons target specific regions of other elements, while all LTR retrotransposons often target palindromes and nucleosome-occupied regions: in silico study. Mobile DNA. 2019;10:50. https://doi.org/10.1186/s13100-019-0186-z.

The original article can be found online at https://doi.org/10.1186/s13100-019-0186-z

* Correspondence: kejnovsk@ibp.cz
[1]Department of Plant Developmental Genetics, Institute of Biophysics of the Czech Academy of Sciences, Kralovopolska 135, 61200 Brno, Czech Republic
Full list of author information is available at the end of the article

Table 2 Palindromes within sequences flanking the insertion site. We used the paldpl program to detect approximate palindromes of at least 3 bp with no more than 30% mismatches or indels. This analysis was done in native flanking sequences identified in plant genomes and their randomized (permutated) counterparts, to control for base content effects. We carried out a paired t-test for difference in calculated stem lengths of the native and randomized palindromes. Significant values after Benjamini-Hochberg correction for multiple family testing are marked with an asterisk and printed in bold (* for $p < 0.1$, ** for $p < 0.01$ and *** for $p < 0.001$). Three families with increased mean palindrome stem length after randomization are marked with a tilde

Group	Count	Palindrome length		Paired t-test *p*-value
		native	*random*	
ALL	14,813	5.5	5.4	**0.000004*** **
nested	*830*	*5.2*	*5.3*	*0.50~*
non-nested	*13,983*	*5.5*	*5.4*	***0.000001*****
Ale	1314	5.5	5.5	0.93
Alesia	21	5.8	5.7	0.75
Angela	91	5.3	5.3	0.93
Athila	1088	5.5	5.3	**0.008** **
Bianca	*443*	*6.0*	*6.1*	*0.97~*
Bryco	*29*	*5.8*	*5.9*	*0.95~*
CRM	482	5.3	5.2	0.53
Galadriel	49	5.4	5.1	0.40
Ikeros	348	5.5	5.3	0.10
Ivana	1018	5.5	5.3	**0.008** **
Ogre	1520	5.5	5.4	0.64
Phygy	285	5.3	5.3	0.94
Reina	852	5.4	5.4	0.67
Retand	2078	5.4	5.3	0.37
Sire	1225	5.4	5.2	**0.001** **
Tcn1	1947	5.5	5.4	**0.001** **
TAR	477	5.5	5.4	0.14
Tekay	1029	5.4	5.4	0.61
Tork	*517*	*5.6*	*5.8*	***0.05*~***