

**File S5. The alignment between the 3'TIR of the duplicated MITE (SQ225117735) with a compatible MITE 5'TIR in the genome.**

```

SQ225005122   TAAGGCCATGTTTCGTTTCTGTCGGATTGGTGGGTCGGAACGATTCCGAGCCGG--ATTGC 58
SQ225117735   TTAGGCCATGTTTCGTTTGTGTCGGATTG--CACCCGGAATCGTTAC-AGCTAATCAAAGT 57
* ******* * * * * * * * * * * * * * * * * * * * * * * * * * * *

SQ225005122   TTCTCTAATTTATATAAAC--TTGATTAACCGAAACGATTCCGGGTG--TAATCCGATG 114
SQ225117735   TTATATAAATTAGAGTAGCAATCCGGCTA---GGAATCTTTCGACCCACCAATTCGACA 114
* * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

SQ225005122   TAACCGAACAAGACCTAA 132
SQ225117735   CAAACGAACAAGATCTTA 132
* * ***** * * *

```

An example (SQ225005122) of the MITE with a compatible 5' TIR with the 3' TIR of the duplicated MITE (SQ225117735) in the RET reaction is shown. SQ225005122 is shown from 5' to 3' and SQ225117735 is from 3' to 5'. The compatible TIR of RET is enclosed in black box. The 3-bp TSD sequences are in bold. The MITE sequences were indexed in Chen, *et al.* 2014. The alignment was calculated by ClustalW 2.1.