

File S4. The alignment of the MITE in the duplication with the representative MITE

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SE220500133  --GGCCTTGTTTCGTTTCTGCCGGATTGGTGGGTCGGAACGATTCCCTGACCGGATTGCTT 57
SQ225117734  TAAGATCTTGTTTCGTTTGTGTCGAATTGGTGGGTCGGAAAGATTCCCTAGCCGGATTGCTA 60
                *  *****  ** ** *****  *****  *****
SE220500133  CTCTAATTTATATAAACTTTGATTAGCTGGAACGATTCCGGGTGCAATCCGACGAAAACG 117
SQ225117734  CTCTAATTTATATAAACTTTGATTAGCTGTAACGATTCCGGGTGCAATCCGACAAAACG 120
                *****  *****
SE220500133  AACAAGGC--- 126
SQ225117734  AACATGGCCTAA 132
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The MITE sequences in the duplication of AC234515.1 (indexed as SQ225117734 by Chen, *et al.* 2014) were aligned with the representative sequences SE220500133 by ClustalW 2.1. The sequences are listed from 5'TIR to 3'TIR (TIR sequences are boxed), including the "TAA" (in bold) as the 3-bp target site duplications.