

**File S6. 5' TIRs with perfect complementarity to the 3' TIR of the duplication-associated MITE SQ225117735 are found in multiple MITEs in the maize B73 genome.**

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SQ225158225      TTAGGCCATGTTTCGTTTTTTGTGTCAATCCATGGGGATTGAGGGGGAACAAATCCCCTATAA
SQ225163989      TTAGGCCATGTTTCGTTTTTTGTGCCAATCCATAGGGATTGAGGGGGATTAAATCCCCTACAA
RC_SQ225030358    TTAGGCCATGTTTCGTTTTTTGTGCCAATCCATAGGGATTGAGGGGGATTAAATCCCCTACAA
RC_SQ225082017    TTAGGCCATGTTTCGTTTTTTGTGCCAATCCATAGGGATTGAGGGGGATTAAATCCCCTACAA
SQ225027317      TTAGGCCATGTTTCGTTTTTTGTGCCAATCCATAGGGATTGAGGGGGATTAAATCCCCTACAA
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SQ225158225      GTCAAAATCCCCTCAATCCCTTCCAATCCCCTCAATCCCCTATGGTTTGGGGATGAAAC
SQ225163989      GTCAA-ATCCTCTCCAATCCCTTCCAATCCCCTCAATCCCTATGGTTTGGGGATCAAC
RC_SQ225030358    GTCAAAATCCTCTCCAATCCCTTCCAATCCCCTCAATCCCTATGGTTTGGGGATCAAC
RC_SQ225082017    GTCAAAATCCTCTCCAATCCCTTCCAATCCCCTCAATCCCTATGGTTTGGGGATAAAC
SQ225027317      GTCAAAATCCTCTCCAATCCCTTCCAATCCCCTCAATCCCTATGGTTTGGGGATAAAC
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SQ225158225      GAACATGGCCTTA
SQ225163989      GAACATGGCCTTA
RC_SQ225030358    GAACATGGCCTTA
RC_SQ225082017    GAACATGGCCTTA
SQ225027317      GAACATGGCCTTA
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Alignment of maize genomic MITEs with perfectly complementary 5' and 3' termini (enclosed in boxes). The perfect MITEs have 5' TIRs complementary to the 3' TIR of the duplication-associated MITE SQ225117735 and are flanked by 3-bp TSDs (in bold). The MITE sequences are all indexed by Chen, *et al.* 2014 with SQ numbers.