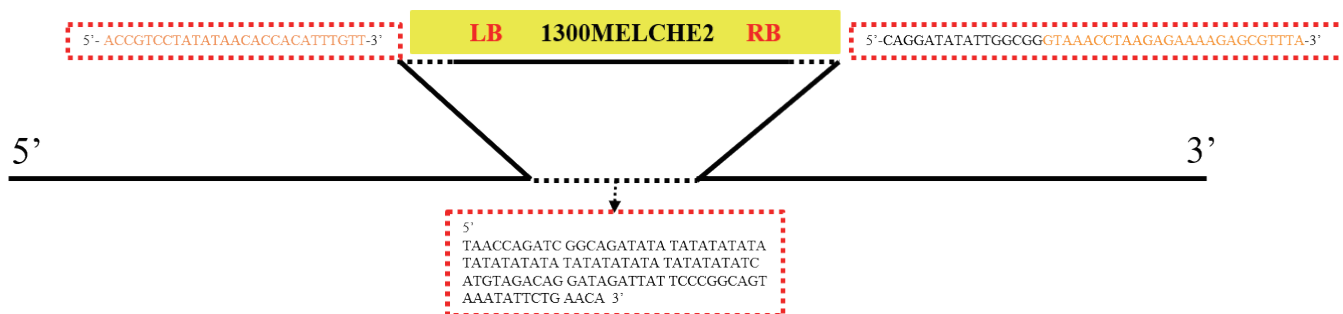




3'

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 GTCAAATTTATTCAACTTAATATC AAAATTTAGTATTTTCTCACAGGATTTCATATTTAAGCTTTCTGGCTACGCGCTGGACTGCATATGCAAAATCGAGGCACT
 CCAGATGAGGTTTTAAGGCCTCAAAAGTACATAATATATAAAAAAATAAGTGATGACCCCTTCGAGTCGTCACAAATAACCAACCTACGCATGCTCTCATGTGTG
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 TTTTTTAATTCAAACCAACRB 1300MELCHE2 LBAT AATGTTGATTCTTGATTCTTCGTTTCTTTTTTAAATATTGATGAGCCCGAGCAAGTTTCTAACATATAGT
 ATATGAATAATATCATCAGTAACATACATAAAAGTTAGACAGTAGTGTAGTATTACTCTCTTTTTTCTCTTTGTATATCGTTTCTTATTAATTAAATAGGTCTT
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 GCACTGATACAAAGTGCTGAGATATACGTACGTTGCTAGACAAAACTTTGAAGCAAGTTTAAAGCTTTAAGGTAAAATTAAAATAGCTATACGTGGTGGAAACAG
 ATCCAAGAAGTCTACAGCTTAACTAAACTCGTCCCTGTTAGAATAAATATATCATTGAAAGCAATCATACAATTTATTCTATGTGTAATCAAACAATTAA
 CACATGCAAAAATTATATGAGTTATCTTTTGAAC 5'

Supplementary Figure S1. The nucleotide sequence of the insertion site of the MELCHE2 construct.

It was predicted that approximately 104 nucleotides were deleted by insertion of the construct and additional 16 nucleotides around right border (RB) were eliminated, as indicated by red boxes. While green letters display the nucleotide sequence of the *Nicotiana benthamiana* contig, Niben101Scf08318Ctg002, that matched with the sequence obtained from the RB iPCR product, blue letters show Niben101Scf08318Ctg003 that matched with the sequence obtained from the left border (LB) iPCR product.