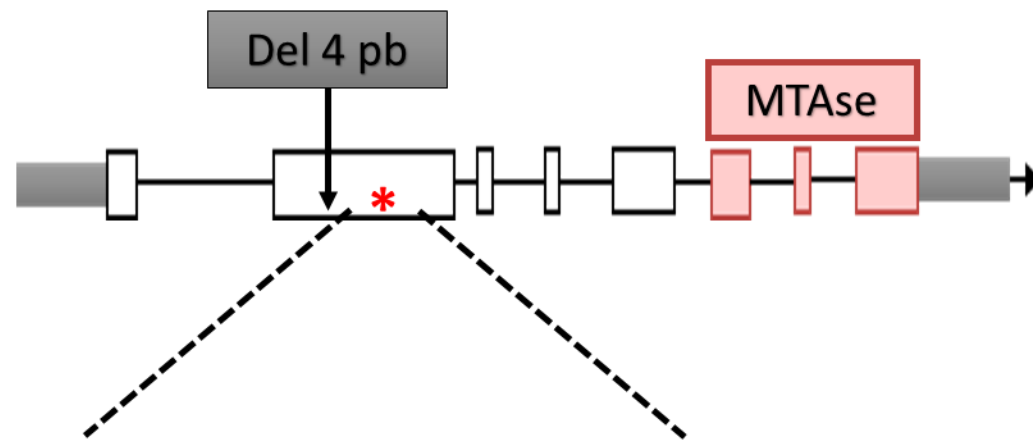


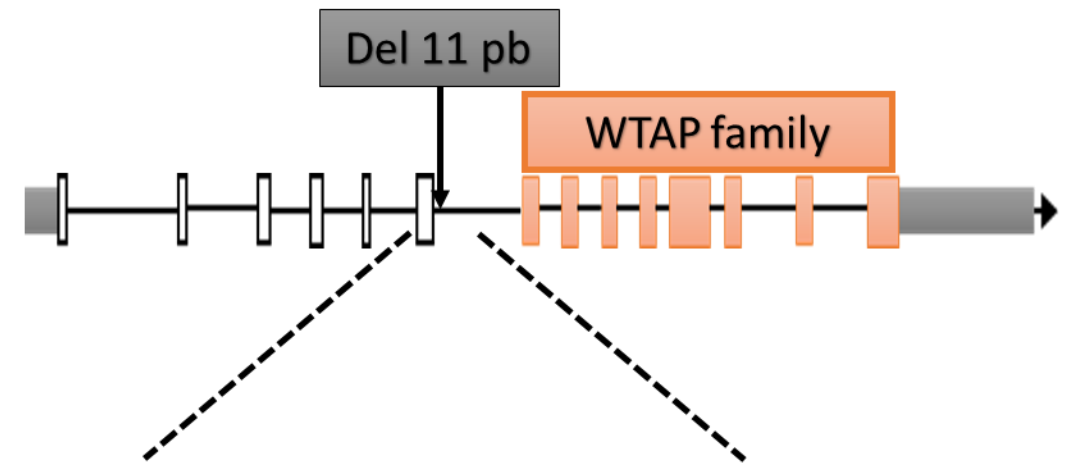
PpMTA



WT CTAGATTGCCTGGGGATTCCCT

Ppmta and QM CTAGATTGCC - - - - GATTCCCT

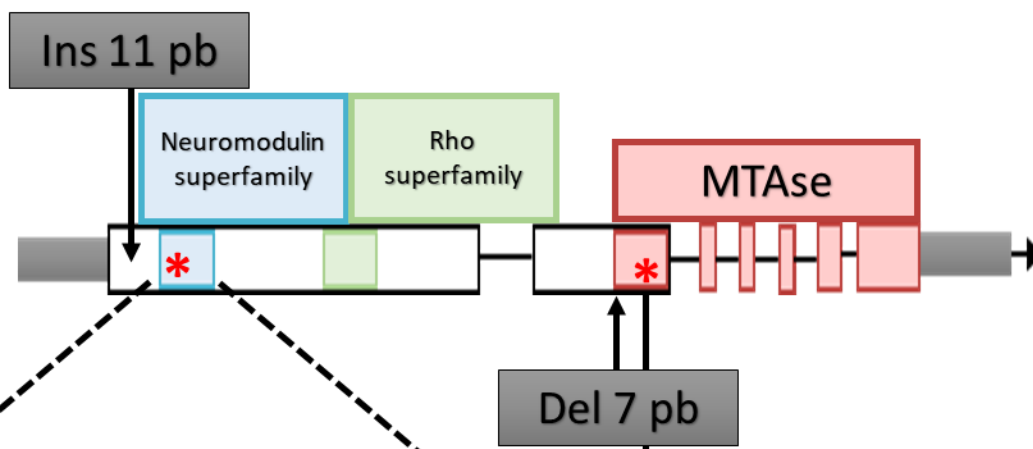
PpFIP37



WT ACTCAATCTACGGGGATCATAGTACTTG

Ppfip37 and QM ACTCAAT - - - - - TAGTACTTG

PpMTB1



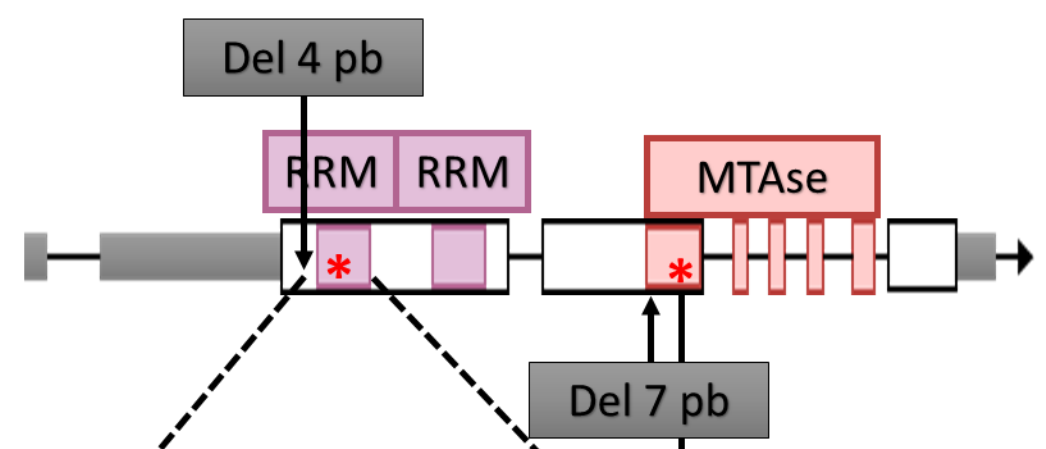
WT ACGAAGGTGAGTAGCAGGAGCGA

Ppmtb1 GCAGGAGCAGG

WT CCAAAGCTGAAAGAGCTGA

QM CCAAAG - - - - - GCTGA

PpMTB2



WT TTGGATGAGTGGGAG

Ppmtb2 TTGGATG - - - - - GGAG

WT CCAAAGCTGAAAGAGCTGA

QM CCAAAG - - - - - GCTGA

Figure S1. CRISPR/Cas9 edition of MTC genes caused frameshift mutations

Diagrams show the genomic structure of the *PpMTA*, *PpFIP37*, *PpMTB1* and *PpMTB2* genes analyzed in this work. The annotated protein domains were obtained using NCBI Conserved Domain Search Tool, and are indicated in colors within exons, introns are represented by thin black lines and 5'UTR, and 3'UTR are shown in grey rectangles. MTase: methyl-transferase domain, RRM: RNA-recognition motif. *PpMTB1* and *PpMTB2* proteins have different domains at their N-terminus, *PpMTB1* has the Neuromodulin and the Rho domains, while *PpMTB2* has two RRMs. The mutations generated by CRISPR/Cas9 are indicated in the schemes by grey boxes above the genes, the position of the premature stop codon generated by frameshift is shown by a red asterisk. Insertions and deletions caused by genome editing are indicated for each mutant. *PpMTB1* and *PpMTB2* alleles present in the quadruple mutant (*QM*) are also indicated.