



**Supplemental Figure 2.** Predicted structure of wild-type and M11 versions of the MPMV constitutive transport element (CTE). Secondary structures were predicted by RNAfold, where two guanosine bases in the wild-type CTE (A, see arrows) were mutated to cytosines in the M11 mutant (B, arrows) to perturb the structure of the NXF1-binding region. The heat color gradation indicates the base-pairing probability from 0 to 1.