

Genome-wide association study of maize resistance to *Pythium aristosporum* stalk rot

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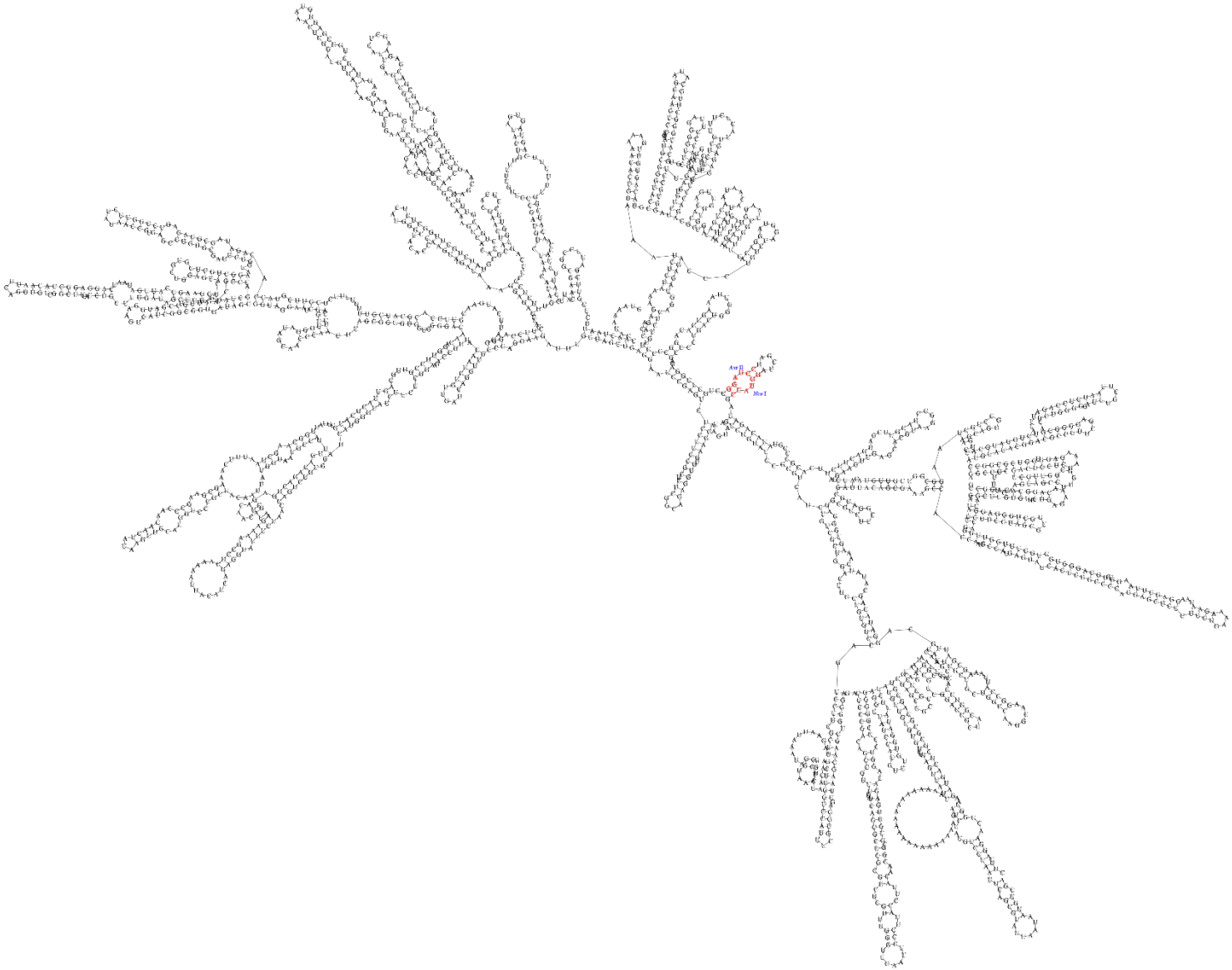
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A



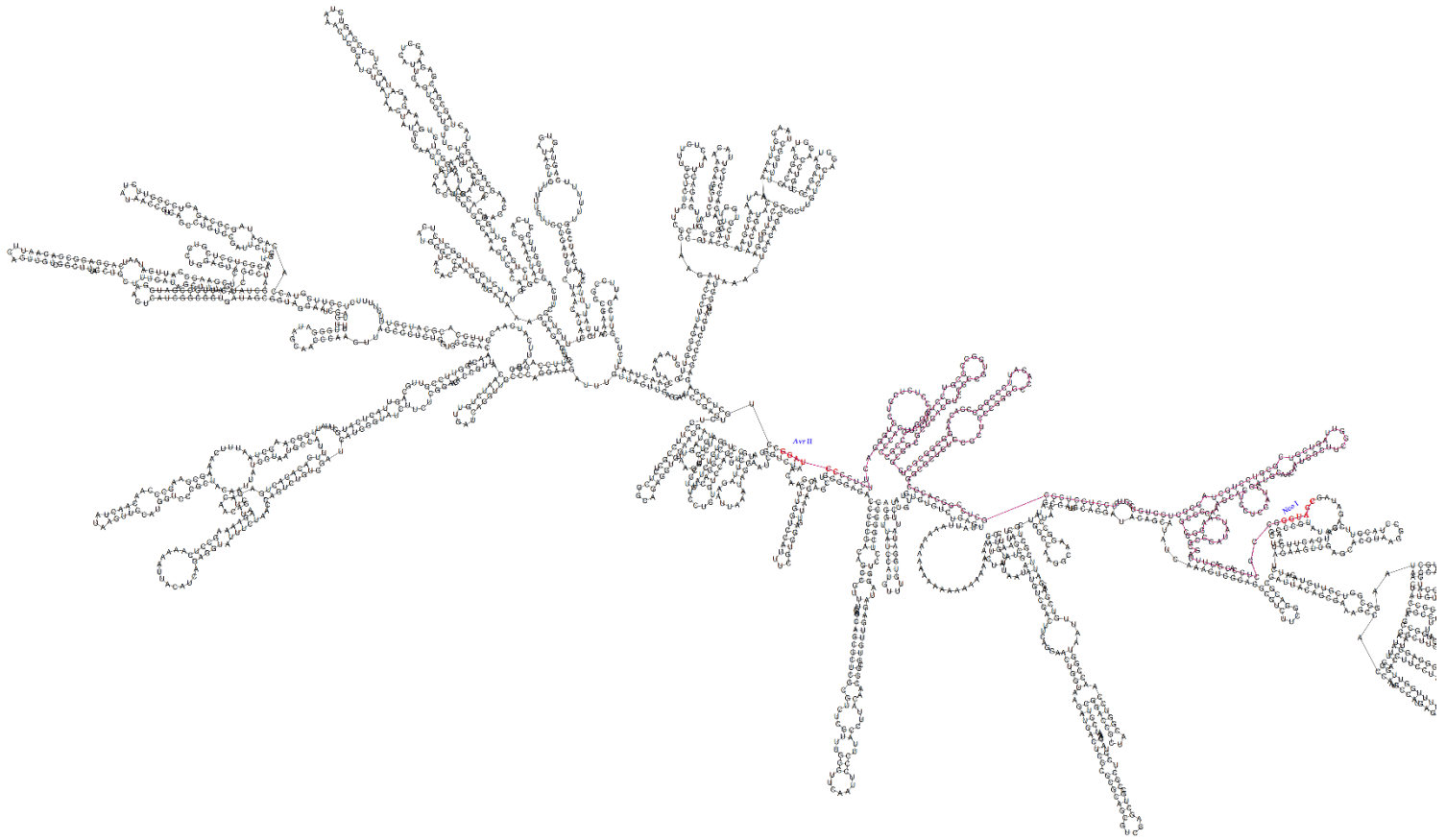
B

FIGURE S1 | Deep learning predicted BMVCP5 (+) strand RNA3 second structure without and with *Zm00001d051313* gene-specific fragment inserts. Full length (+) stands of BMV RNA3, without (A) or with gene fragment inserts representing *Zm00001d051313* (B) were folded with the MXFold2 Web server (<http://www.dna.bio.keio.ac.jp/mxfold2/>). Locations of the two cloning sites are indicated. Gene-specific fragment inserts were shown with magenta dashed lines.

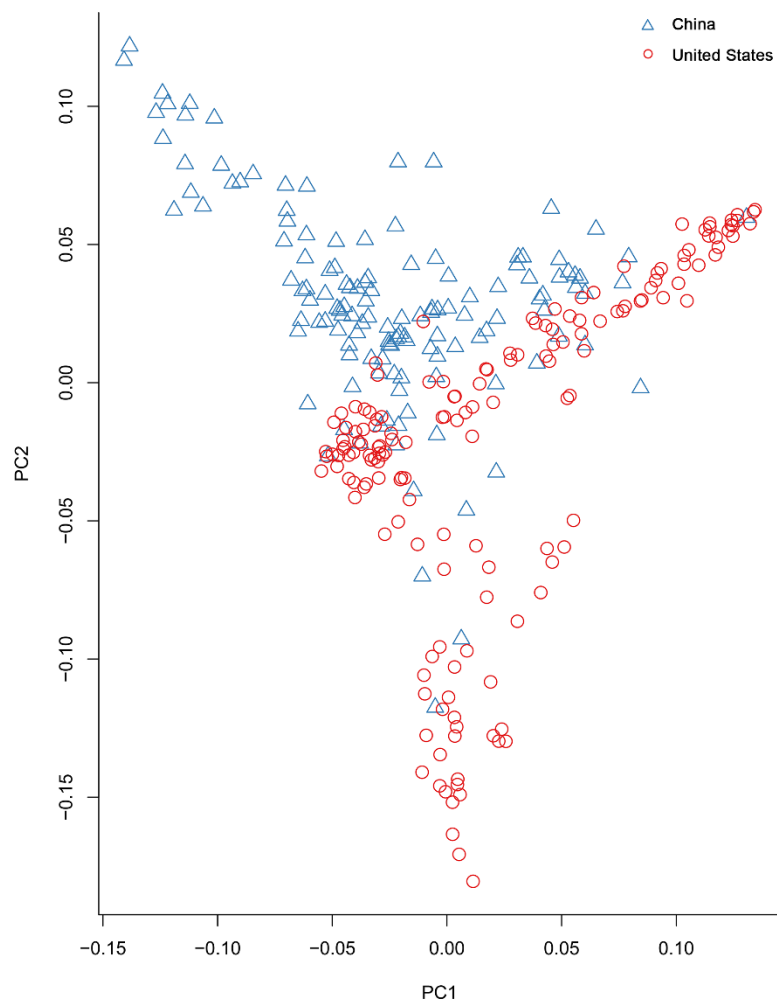


FIGURE S2 | Principal component (PC) analysis based on SNP genotypic data. Blue triangles and red circles indicate inbred lines that collected from China, and United States, respectively.

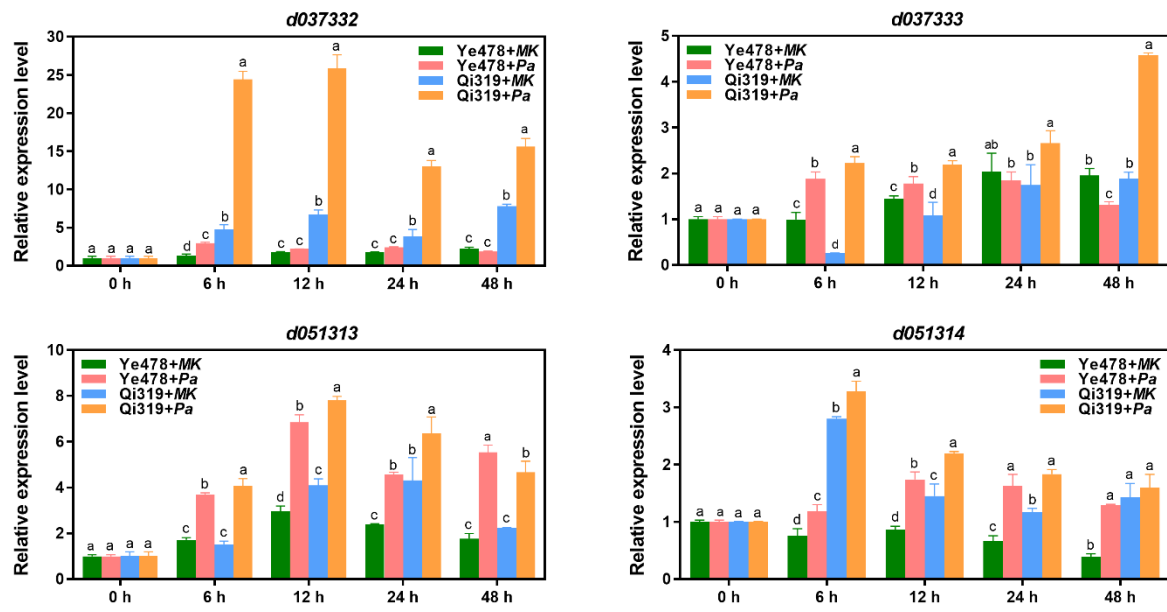


FIGURE S3 | Expression of the four candidate genes was quantified by qRT-PCR in two control inbred lines post *Pythium aristosporum* infection. Different letters on the columns show a significant difference ($P < 0.05$) as determined by the Tukey-Kramer test.

