Online Resource 1. Bioinformatics pipeline based on *de novo* assembly of unmapped reads used for discovery of maize yellow mosaic virus in maize RNA-seq data. (a) Raw reads were assessed with FastQC, trimmed with Trimmomatic based on the FastQC results, and aligned to the reference genomes of maize and *C. zeina* to collect unmapped reads. (b) Unmapped reads were assembled using Trinity, their protein sequences predicted with TransDecoder and compared against the NCBI nr database using BLASTP.