



**Online Resource 5.** RNA-dependent RNA polymerase-based phylogenetic analysis of maize yellow mosaic virus and related Poleroviruses. The evolutionary history was inferred from the RNA-dependent RNA polymerase nucleotide sequences by using the Maximum Likelihood method with the GTRGAMMA model. Bootstrap consensus values are shown at the nodes. The sequences were extracted from complete genome sequences with the following NCBI accession numbers: RSA BR1A (MG570476), RSA SCM (MN943641), Kenya KALRO (MH205607), Kenya MYDV-like (MF974579), Tanzania 76 (MG664790.1), Ethiopia (MF684369), Nigeria (KY684356.1), China Y11 (KU248489.1), China Y1 (KU179221.1), China MYDV-RMV2 (KT992824.1), China SC (MK652149), Brazil (KY940544.1), Ecuador (KY052793), BVG Gimje (KT962089.1) and MYDV-RMV (KC921392.1). The latter two were used as outgroups. The scale bar indicates the number of nucleotide substitutions per site.