

## **Supplementary Table Legends**

**Supplementary Table S1** Quantitative PCR [ $\log_2$  relative change [ddc(t)] in WRKY expression and primer sequences.

**Supplementary Table S2** Significant ( $1 \times 10^{-8}$ ) enriched GO terms (biological processes) from differentially expressed gene data sets in T200 and TME3 at 12, 32 and 67 days post *South African cassava mosaic* virus infection.

**Supplementary Table S3** Differentially expressed (DE) interacting gene partners (and their GO functions) associated with *Arabidopsis* homologs (AtWRKY33 and 53 in T200 and AtWRKY40 and 70 in TME3) of upregulated *MeWRKY* TFs in enriched SA, ET, JA or ABA hormone pathways post-SACMV infection.

GOs associated with *Arabidopsis* homologs of differentially expressed (DE) *MeWRKY*s and their DE interacting gene partners in a central AtWRKY 33, 40, 53 and 70 protein-protein network.

**Supplementary Table S4** AtWRKY28 (*MeWRKY*81 homolog) interacting partners and their functions.

**Supplementary Table S5** Log<sub>2</sub> fold expression of *AtWRKY* homologs in susceptible and resistant plant host-geminivirus infections at different stages of infection.