



Supplemental Figure S1 Bioinformatics analysis of MsGSTU17. (a) Analysis of conserved domains within the MsGSTU17 protein sequence. (b) Prediction of the MsGSTU17 protein structure, with the modeling template derived from [PDB I3S5Q9.1.A]. Each color corresponds to a different protein fold. (c) Identification of *cis*-acting elements in the promoter region of *MsGSTU17* in alfalfa.