

Figure S5. Analysis of the predicted protein StGDSL1 from *Stenocereus thurberi*. (a, b) Signal peptide and topology of StGDSL1 amino acid sequence. (a) The amino acid sequence corresponding to the signal peptide (red, orange, and yellow) and the cleavage site (CS; green dashed line) were determined by Signal P 6.0 software. (b) The signal peptide (orange) and outside (blue) region of the protein sequence were determined by deepTMHMM software. (c) Predicted protein domains contained in StGDSL1 amino acid sequences were determined by InterProScan.