Figure S4 Regulatory networks from interaction analysis of TFs and candidate genes were visualized by Cytoscape. (a) Key TFs interacted with *GA2ox* (EVM0019043). (b) Key TFs interacted with *GASA* (EVM0003383). (c) Key TFs interacted with *AGPase* (EVM0014895). (d) Key TFs interacted with *AGPase* (EVM0016620). (e) Key TFs interacted with *SSS* (EVM0005345). (f) Key TFs interacted with SSS (EVM0021407). (g) Key TFs interacted with *SBE* (EVM0024297). (h) Key TFs interacted with *ISA* (EVM0012578). (i) Key TFs interacted with *CYC* (EVM0027628). (j) Key TFs interacted with CDKI (EVM0023713). (k) Key TFs interacted with *XTH* (EVM0010814). (l) Key TFs interacted with expansin (EVM0023051). The Pearson correlation coefficient was colored in red and blue for high and low correlation, respectively. * represents the co-expression level with P-value≤0.05, and ** represent the co-expression level with P-value≤0.01.