

Table S1. qRT-PCR primer sequences of candidate genes.

GENE ID	Primer sequence (Upstream)	Primer sequence (Downstream)
Tua-5	F:GCGGCACCTATCTGTTTGTTT	R:ACACCTTGACCTCAACACAGT
<i>Glyma.14g029100</i>	F:GCCCAGGCACTCAGGTATCT	R:ATGGATGCAACAAGAGGGCT
<i>Glyma.14g029500</i>	F:CTTGATGAGGTCATTCAGGAAGGTG	R:TCACAGGCAACACCATATATGACA
<i>Glyma.14g030100</i>	F:TCGAGGTGCTCAGGTGTATG	R:AGTGCCACGTGTCATAGCAA
<i>Glyma.14g030500</i>	F:TTGCAATCACCGCACAAA	R:TATCATCGCAGGACTTGGTGA
<i>Glyma.14g030600</i>	F:CTGGGGGAATCATATCATCACAAA	R:CTGCAGCTCGCGGAAG
<i>Glyma.14g030700</i>	F:TCCATGGGATCTTCCAATGAGTT	R:AGGCTTGTCAATCCCTGTGG

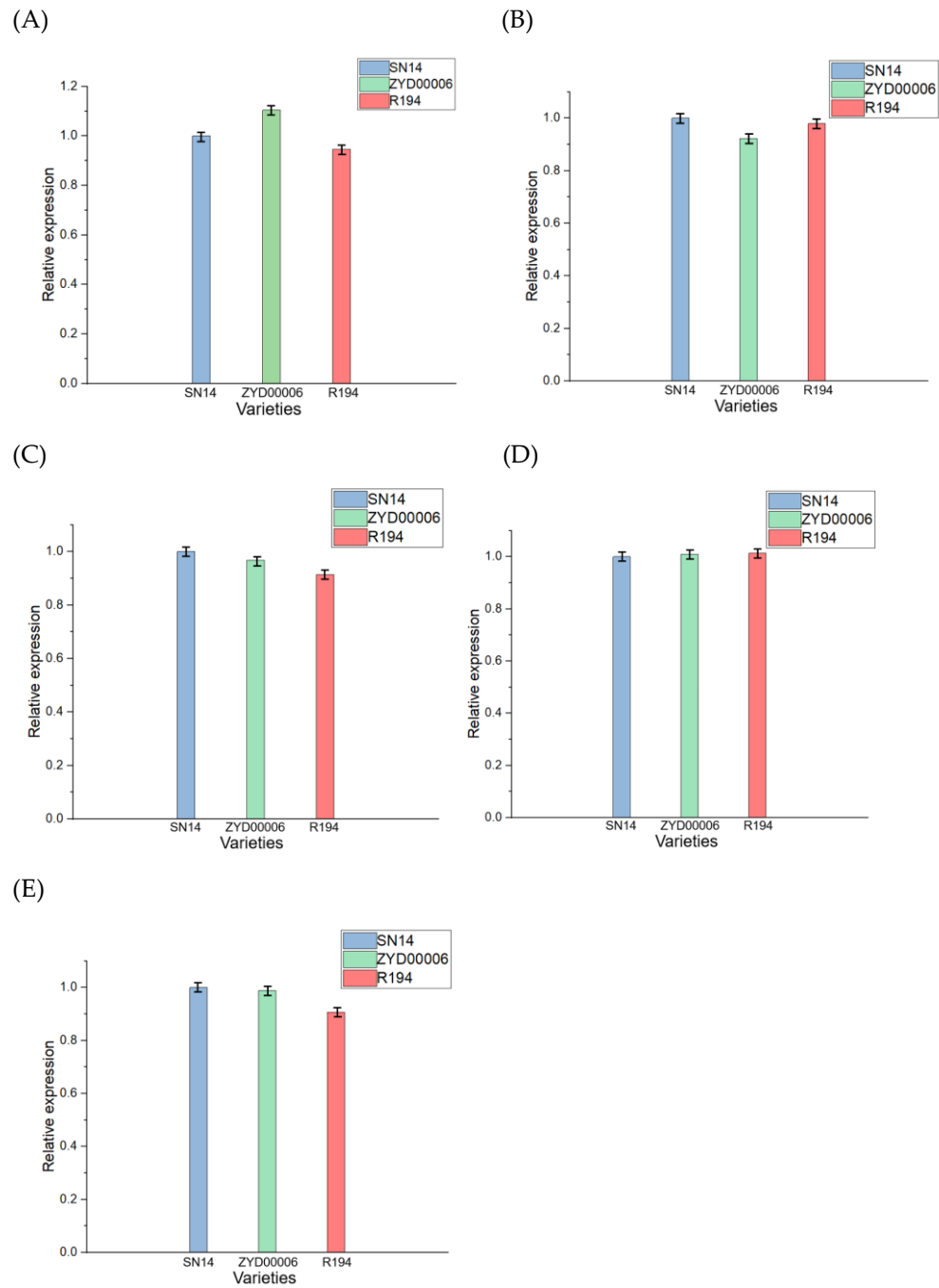


Figure S1. The relative transcription level of other candidate genes in leaves of parents and lines with high sucrose content at V4 stage. (A): *GLYMA.14G029500*; (B): *GLYMA.14G030100*; (C): *GLYMA.14G030500*; (D): *GLYMA.14G030600*; (E): *GLYMA.14G030700*.