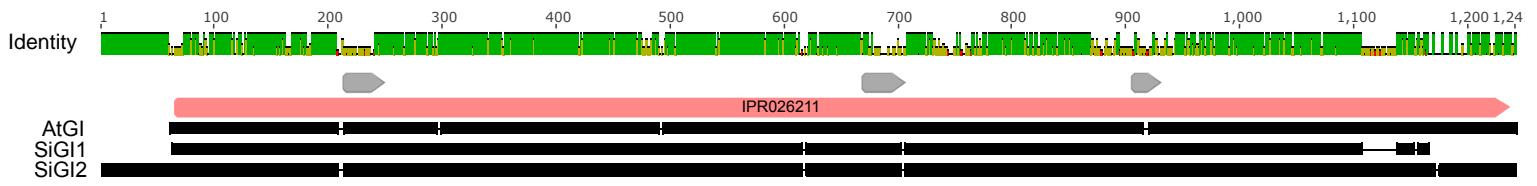
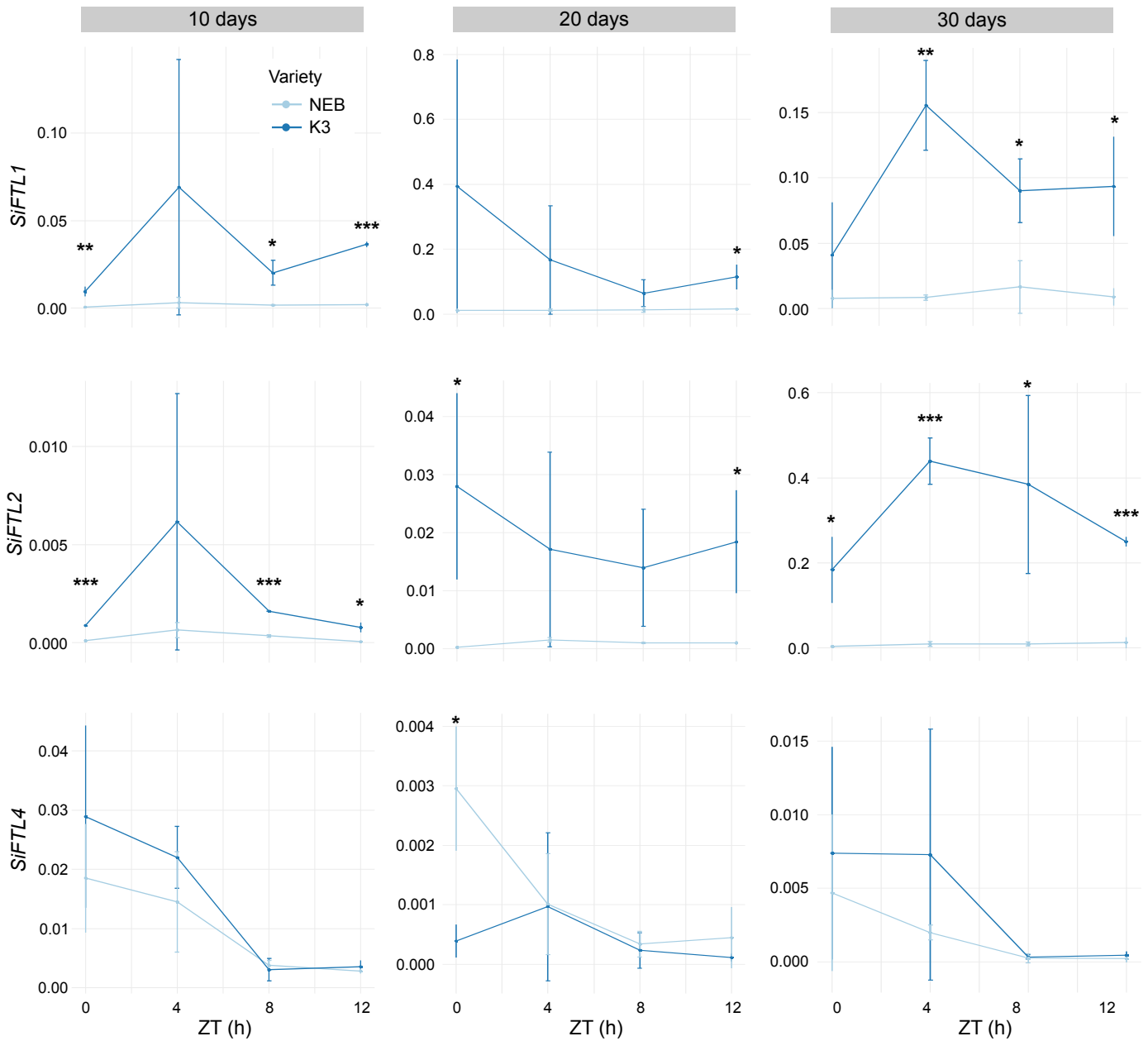


Supplementary Fig. S1 Full-length amino acids sequence alignment of AtFT (AT1G65480) from *A. thaliana* and the four FT-like proteins of sesame (a). The conserved phosphatidylethanolamine-binding protein (PEBP) domain is indicated by the red pentagon. b) Phylogenetic tree of FT-like proteins from *A. thaliana* (AtFT and AtTSF [AT4G20370]), rice (OsHd3a [LOC_Os06g06320], RFT1 [LOC_Os06g06300] and OsFTL1 [LOC_Os01g11940]), and sesame. Phylogenetic tree was constructed based on the alignment of the full-length protein sequences and the neighbor-joining method. Numbers on the nodes indicate the bootstrap values based on 1000 replicates. c) Schematic representation of the chromosome 11 region where *SiFTL2* and *SiFTL3* (red pentagons) are located. These two genes are organized in a head-to-tail tandem array.



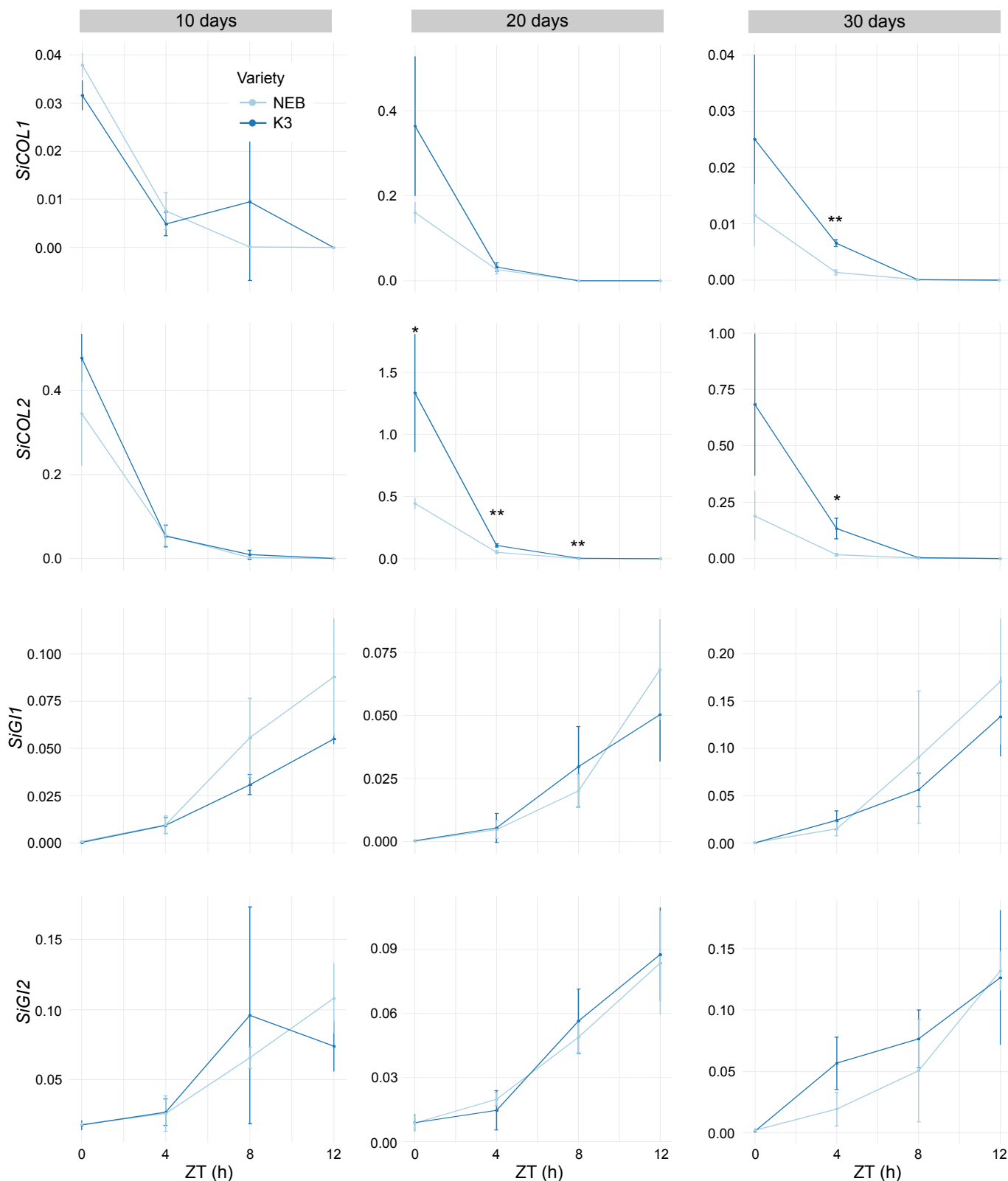
Supplementary Fig. S2 Full-length amino acids sequence alignment of AtGI (AT1G22770) from *A. thaliana* and the two homologous proteins of sesame. The conserved domain related to GIGANTEA (InterPro entry IPR026211) is indicated by the red pentagon. Intrinsically disordered regions (predicted by InterProScan using MobiDB) are indicated by gray pentagons.

Growth stage



Supplementary Fig. S3 Comparison of the expression level of *SiFTL1* (up), *SiFTL2* (middle), and *SiFTL4* (bottom) genes between the early flowering variety ‘K3’ (blue lines) and late flowering variety ‘NEB’ (light blue lines). RNA was extracted from leaves at three growth stages: 10 days (left column), 20 days (middle column), and 30 days post-emergence (right column). Zeitgeber time (ZT) 0 indicates the beginning of the light phase (lights on). The beginning of the dark phase (lights off) was at ZT 12, i.e. photoperiod of 12 h light and 12 h darkness. Data are mean \pm standard deviation of three individuals. * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$ based on Student's *t*-test.

Growth stage



Supplementary Fig. 4 Comparison of the expression level of *SiCOL1* (first row), *SiCOL2* (second row), *SiG11* (third row), and *SiG12* (last row) genes between the early flowering variety ‘K3’ (blue lines) and late flowering variety ‘NEB’ (light blue lines). RNA was extracted from leaves at three growth stages: 10 days (left column), 20 days (middle column), and 30 days post-emergence (right column). Zeitgeber time (ZT) 0 indicates the beginning of the light phase (lights on). The beginning of the dark phase (lights off) was at ZT 12, i.e. photoperiod of 12 h light and 12 h darkness. Data are mean \pm standard deviation of three individuals. * $P < 0.05$ and ** $P < 0.01$ based on Student's *t*-test.