



**Figure S8 Agronomic traits of *BnLECI*, *BnLECI17A* and *BnLECI17D* overexpression transgenic *Brassica napus*.** (A) RT-qPCR analysis of *BnLECI* expression in 25 DAP seeds of *BnLECI*, *BnLECI17A* and *BnLECI17D* transgenic plants. (B) Assay of oil and protein contents in seeds of *BnLECI*, *BnLECI17A* and *BnLECI17D* transgenic plants. The seeds of 10 plants in each line (T3 generation) planted in the field were used for the assay. (C) Assay of agronomic traits of *BnLECI*, *BnLECI17A* and *BnLECI17D* transgenic plants. More than 10 plants in each line (T3 generation) planted in the field were used for analyzing plant height, pod number per plant, seed number per pod and seed weight. Three biological replicates were performed, and means  $\pm$  SE are shown (Fisher's Least Significant Difference (LSD) test, \* $P < 0.05$ , \*\* $P < 0.01$ ). (D) Phenotype of wild type and *BnLECI* transgenic plants. WT, wild type; CK, the null transgenic lines; OLW1-18, *BnLECI* transgenic lines; OLA1-19, *BnLECI17A* transgenic lines; OLD1-18, *BnLECI17D* transgenic lines; DAP, day after pollination.