

Supplementary Figure S1: The results of five genes expression compared RNA-seq and qRT-PCR in fanni (a) and longya10 (b), respectively. * $p < 0.05$.

Supplementary Figure S2: The expression of genes related to photosynthesis-related pathways in leaves of flax under saline stress.

Supplementary Table S1: The overview of RNA-seq data.

Supplementary Table S2: The data of GO analysis.

Supplementary Table S3: The data of phytohormones related genes expression analysis.

Supplementary Table S4: The data of transcription factors related genes expression analysis.

Supplementary Table S5: The data of ionic transport related genes expression analysis.

Supplementary Table S6: The data of epigenetic modification related genes expression analysis.

Supplementary Table S7: The list of primers for qRT-PCR.