



Supplementary Data 1. Statistics of transcriptome sequencing data for leaves, flowers, stems, seedling roots, and seedling shoots of six flax cultivars/lines: #3896, Alizee, Atlant, Diplomat, LM98, and Universal. Reads were mapped to the NCBI representative *L. usitatissimum* genome (GenBank assembly: GCA_000224295.2) using STAR and plots were generated by MultiQC.