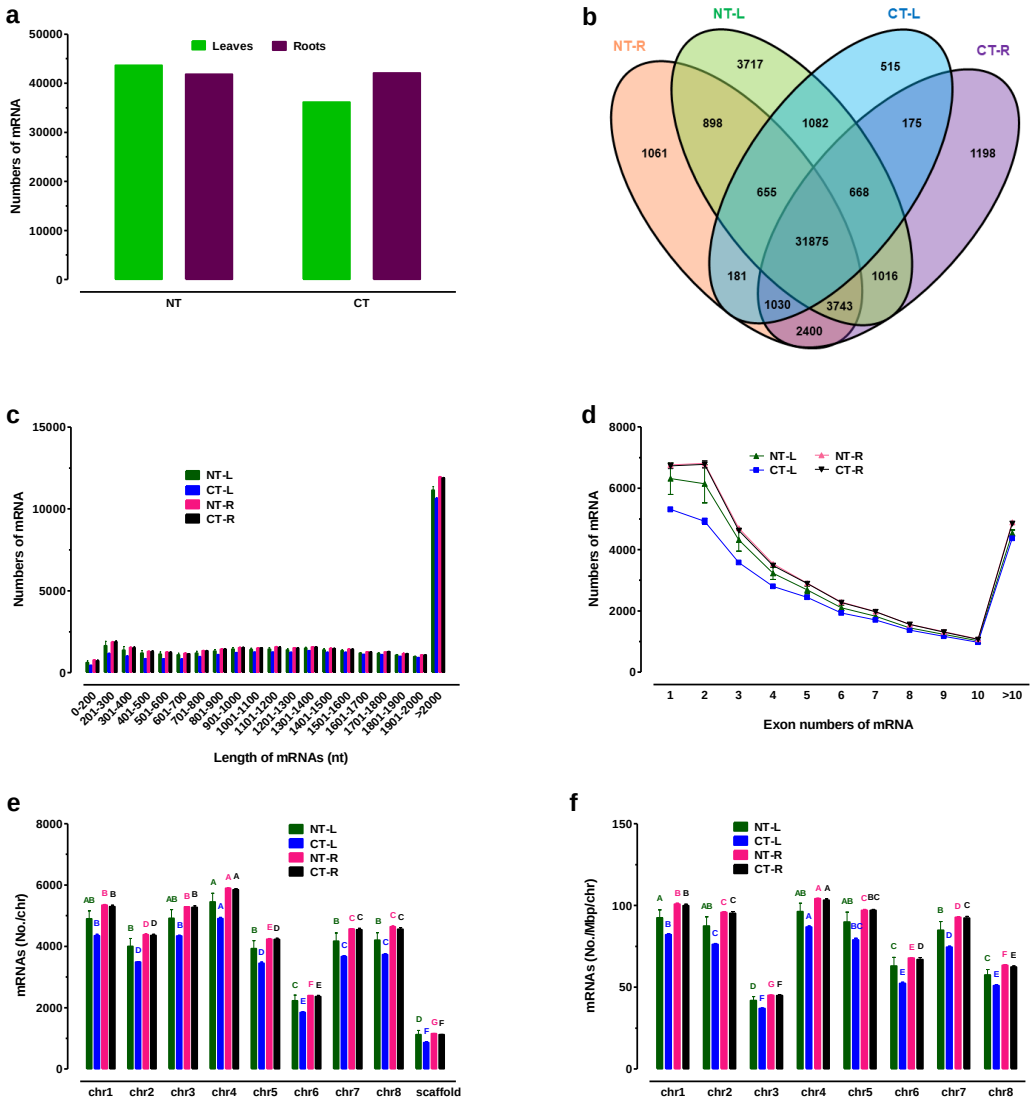


**Figure S3.** Identification of mRNAs by high-throughput sequencing in *M. truncatula* seedlings. (**a**) Total numbers of mRNA identified in leaves and roots. (**b**) Numbers of common/specific mRNA identified in NT-L, CT-L, NT-R and CT-R. The values shown in (**a**) and (**b**) were obtained from three independent RNAseq experiments. (**c**) Length distribution of mRNAs in leaves and roots. (**d**) Numbers of mRNA containing different numbers of exon in NT-L, CT-L, NT-R and CT-R. (**e**) Number distribution of mRNAs on eight chromosomes of leaves and roots with and without cold treatment. (**f**) Density distribution of mRNAs on eight chromosomes of leaves and roots with and without cold treatment. Capital letters indicate significant difference at $P<0.05$ according to the *t*-test between chromosomes in the same treatment samples. Values

shown in (**c**) (**d**) (**e**) and (**f**) were means ± SE with three independent RNAseq experiments. NT: non-cold treated; CT: cold treated; L: leaves; R: roots.