

**Supplemental Fig. S1** Genome-wide identification and characterization of the differentially expressed genes (DEGs) that were responsive to nitrogen (N) limitations in the shoots and roots of *B. napus* seedlings through high-throughput transcriptome sequencing. (A) *Pearson* correlation coefficients (R) of the RNA-seq data between each pair of biological replicates. (B-C) Venn diagram showing intersection analysis (B) and gene ontology (GO) term annotations (C) of the DEGs. In the word cloud, the font sizes indicate the GO term numbers. The bigger the fonts are, the more the corresponding GO terms are. For the RNA-seq experiment, the rapeseed plants were grown under 9.0 mM NO3- for 10 d, which were then transferred to 0.30 mM NO3-, and the shoots and roots were individually sampled at 0 h, 3 h and 72 h. False discovery rate (FDR) ≤ 0.05 and log2 (fold-change) ≥1 are used as the thresholds to identify DEGs.