

Figure S1: Percentage of differentially expressed genes (DEGs) identified ($\log_2 \text{FC} > |0.58|$; $\text{FDR} \leq 0.05$) by RNA-Seq analysis from the comparison between NO_3^- or NH_4^+ supplied maize seedlings for 24 h with respect to the control (-N, nitrogen deficient solution). Data are shown as percentage of genes differentially expressed in response to each treatment in $+\text{NO}_3^-$ (A) and $+\text{NH}_4^+$ (B) treatments on the total amount of DEGs. DEGs were classified as up-regulated according to their \log_2 fold change values (a $\log_2\text{FC}$ threshold $> |0.58|$ was set, corresponding to a 1.5-fold change increase or decrease in expression). Among the up- and downregulated DEGs, several ranges of induction or repression are shown as \log_2 of the gene expression fold changes.

