



Figure S4. Verification of the transcriptomic analysis by RT-qPCR of selected DEGs from the C and N metabolism. Relative expression levels of *SISPS* (A), *SISUT1* (B), *SIADPG* (C), *SINR* (D), *SIGS2* (E) and *SIASN2* (F) genes in leaves and roots at optimal (8 mM N, dark coloured bars) and sub-optimal (4 mM N, light coloured bars) conditions. Each value (\pm SE) is mean of three different determinations. For each organ, different letters indicate significant differences ($P < 0.05$). NS: not significant. (G) Heatmap displaying the log2 fold-change of the values from RT-qPCR and transcriptome in leaf samples.