

Nitrate regulates maize root transcriptome through nitric oxide dependent and independent mechanisms

Laura Ravazzolo ¹, Sara Trevisan ¹, Silvia Iori ², Cristian Forestan ³, Mario Malagoli ¹ and Silvia Quaggiotti ^{1,*}

Supplementary Materials: The following are available online at <https://www.mdpi.com/article/10.3390/ijms22179527/s1>:

Figure S1: KEGG Search&Color Pathway representation of the pathway 'Plant hormone signal transduction' (zma04075). The analysis was defined by setting cluster 2 in brown (down-regulated by nitrate, NO-independent), cluster 3 in red (down-regulated by nitrate, NO-modulated), cluster 4 in violet (up-regulated by nitrate, NO-dependent), cluster 5 in yellow (up-regulated by nitrate, NO-independent) and cluster 6 in blue (up-regulated by nitrate, NO-modulated). In this pathway, no terms were found for cluster 1 (down-regulated by nitrate, NO-dependent).

Table S1: Summary of gene expression values (expressed as Reads Per Kb per Million, RPKM) for all treatments analyzed (-N; +NO₃⁻; +NO₃⁻ +cPTIO).

Table S2: Summary of gene expression values (expressed as Reads Per Kb per Million, RPKM) for DEGs in the six clusters analyzed: Cluster 1, DEGs down-regulated by nitrate provision and NO-dependent; cluster 2, DEGs down-regulated by nitrate and NO-independent; cluster 3, DEGs down-regulated by nitrate and NO-modulated; cluster 4, DEGs up-regulated by nitrate provision and NO-dependent; cluster 5, genes up-regulated by nitrate provision and NO-independent; cluster 6, DEGs up-regulated by nitrate and NO-modulated.

Table S3: Complete Gene Ontology (GO) enrichments for each of the six clusters.

Table S4: Complete KEGG Reconstruction Pathways results for each of the six clusters.

Table S5: List of genes and primers used to validate RNA-seq dataset with Real-time PCR.

Table S6: Summary statistics of RNA-Seq read sequencing, quality trimming and mapping. For each condition (-N; +NO₃⁻; +NO₃⁻ +cPTIO) three biological replicates were processed (R1, R2, R3). Replicate R1 for the +NO₃⁻ +cPTIO treatment (highlighted in grey) did not correlate with the other replicates of the same treatment and was therefore excluded from further differential expression analysis.

Supplementary Dataset 1: Cuffdiff complete results of pairwise differential expression analyses (-N vs +NO₃⁻ +cPTIO)

Supplementary Dataset 2: Cuffdiff complete results of pairwise differential expression analyses (+NO₃⁻ vs +NO₃⁻ +cPTIO)