## **Supplementary Information**

## <u>Supplementary Data Set 1</u>

**Table S1:** List and description of differentially downregulated genes ( $\geq$ 2-fold; *P*<0.05) in *Arabidopsis thaliana* plants under L treatment. FC: Absolute fold-change between L and Control-L (CL) treatments. (P): putative genes.

**Table S2:** List and description of differentially upregulated genes ( $\geq$ 2-fold; *P*<0.05) in *Arabidopsis thaliana* plants under L treatment. FC: Absolute fold-change between L and Control-L (CL) treatments. (P): putative genes.

**Table S3:** List and description of differentially downregulated genes ( $\geq$ 2-fold; *P*<0.05) in *Arabidopsis thaliana* plants under H treatment. FC: Absolute fold-change between H and Control-H (CH) treatments. (P): putative genes.

**Table S4:** List and description of differentially upregulated genes ( $\geq$ 2-fold; *P*<0.05) in *Arabidopsis thaliana* plants under H treatment. FC: Absolute fold-change between H and Control-H (CH) treatments. (P): putative genes.

## <u>Supplementary Data Set 2</u>

**Table S5:** Downregulated genes in *Arabidopsis thaliana* plants shared by both metal (L: low and H: high) treatments. The "Score" was obtained after the sum of gene foldchange (FC) position in each treatment. (P): putative genes. In bold, genes selected for RT-qPCR validation. **Table S6:** Upregulated genes in *Arabidopsis thaliana* plants shared by both metal (L: low and H: high) treatments. The "Score" was obtained after the sum of gene fold-change (FC) position in each treatment. (P): putative genes. In bold, genes selected for RT-qPCR validation.