**Supplemental methods (detailed descriptions)**

**RNA library preparation and sequencing**

The total RNA input amounts used for ribo-depletion were 200 ng for leaf (Ribo-Zero rRNA Removal Kit (Plant Leaf), Illumina) and 1 µg for root samples (Ribo-Zero rRNA Removal Kit (Plant Seed/Root), Illumina). Directional sequencing libraries were constructed using Illumina’s ScriptSeq RNA Library Prep Kit. For this purpose, both mRNA and long non-coding RNA were sequenced from the samples. The resulting libraries were multiplexed and sequenced on an Illumina NovaSeq S1 flow cell 300 cycle flow cell (2x151 bp paired-end reads).

**Assembly, transcript annotation and model construction**

The genome-guided Trinity *de novo* assembly (Haas et al., 2013) was constructed with the NCBI reference genome DPV01 (Khalas) using default parameters and resulted in 82,472 transcripts. The transcripts were annotated by the AHRD pipeline (https://github.com/groupschoof/AHRD) and MapMan BINs (Schwacke et al., 2019).

With EdgeR (Robinson et al., 2010), a generalized linear model (GLM) using the design “model.matrix(~0+Group)” was applied to identify differences between root (root\_salt\_K – root\_ctrl\_K) and leaves (shoot\_salt\_K – shoot\_ctrl\_K). Genes were considered as differentially expressed when the adjusted p-value (FDR, False Discovery Rate) was below 0.05.

**Enrichment of MapMan BINs, GO and KEGG terms**

We analyzed the affected metabolic pathways and Gene Ontology (GO) terms (MapMan: Table S1; KEGG and GO: Table S4) to provide further information for the reader. The KEGG (Kyoto Encyclopedia of Genes and Genomes) pathway enrichment was performed with EdgeR (Robinson et al., 2010) using orthologous *Arabidopsis* gene IDs. The gene ontology (GO) term enrichment was done with the R-package topGO (Alexa et al., 2006) using the methods *elim*, *classic* and *weight*. The *elim* method was applied for the final enrichment. Heatmaps were drawn with the R-package pheatmap (<https://www.rdocumentation.org/packages/pheatmap/versions/1.0.12/topics/pheatmap>) using colors according to -log10(p-value) for significant terms.

**Flame photometry sample preparation**

The plant material was dried for 2 days at 60°C and the dry weight was measured. After grinding, 50 mg of each sample were used for acid digestion with 5 ml of 0.5 M HNO3. For extracting the ions, samples were incubated at 80°C for 1 h (Munns et al., 2010). After acid digestion, samples were centrifuged at 4,000 g for 20 min. Supernatants were transferred into new tubes and diluted before measurement.

Each sample was measured three times and the values averaged. By measuring standard solutions, the concentration was calculated and related to dry weight.

**Element analysis**

Freeze dried tissue samples were placed in an oven at 70°C overnight before analysis. About 50 mg dried subsamples were weighed and digested in closed vessels using a microwave digester (MARS Xpress; CEM Microwave Technology, Buckingham, UK). Samples were first digested with 3 ml concentrated HNO3 before the addition of 1 ml of 30% H2O2 to complete digestion. Digested samples were diluted to 50 ml with sterile MilliQ water before element analyses. Total K, Ca, Mg, P, S, Na, Cl, Fe, Mn, Zn, Cu and Ni concentrations were determined on digested material by ICP-MS (Nexion 1000, PerkinElmer, Waltham, MA, USA). Blank digestions were performed to determine background concentrations of elements and a tomato leaf standard (Reference 1573a; National Institute of Standards and Technology, NIST, Gaithersburg, MD, USA) was used as an analytical control.

**Biochemical analyses**

Quantification of total soluble protein and sugar, and determination of anions

Total soluble protein was quantified using the Bradford assay (Du et al., 2014). Soluble sugar was extracted and determined after conversion with the anthrone reagent as described previously (Du et al., 2018). The anions nitrate (NO3-), phosphate (PO43-) and sulphate (SO42-) were determined in aqueous extracts by automated anion chromatography and pulsed amperometric detection (Peuke et al., 2006).

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