

Supplementary Fig. 1. Mean and standard deviation of the average expression level (absolute intensity) of all genes, belonging to the three groups of biosynthetic/non-allosteric, biosynthetic/allosteric and the enzymes catalyzing the first catabolic step of the amino acids, over the entire set of abiotic stresses analyzed in this study,-

Supplementary Fig. 2. The degree of fluctuation of mRNA levels of individual genes from the entire sets of biosynthetic/non-allosteric (black histograms), biosynthetic/allosteric (blue histograms) and the enzymes catalyzing the first catabolic step of the amino acids (red histograms) genes of the seven metabolic pathways described in Fig. 1 in response to the eight different abiotic stresses (both in shoots and roots). The degree of fluctuation of the mRNA levels was estimated using standard deviation of expression (\log_2 ratio of treatments vs. controls) and the individual genes are set in order from highest (top) to lowest (bottom) standard deviation of expression. The names of the enzymes encoded by the individual genes, as provided in Table 1, are given on top of the histograms.

Supplementary Fig. 3. Response of shoot mRNA levels of genes encoding biosynthetic/allosteric enzymes (blue lines) and the enzymes catalyzing the first catabolic step of the amino acids (red lines) of six representative metabolic modules to the eight different abiotic stresses. Columns represent the different modules as indicated on the left, while rows represent the different stresses as indicated on top. The time course of the different stresses is indicated in the bottom. The changes in mRNA levels are given in \log_2 ratios of treatments versus controls (Y axes on the left).

Supplementary Fig. 4. Response of root mRNA levels of genes encoding biosynthetic/allosteric enzymes (blue lines) and the enzymes catalyzing the first catabolic step of the amino acids (red lines) of six representative metabolic modules to the eight different abiotic stresses. Columns represent the different modules as

indicated on the left, while rows represent the different stresses as indicated on top. The time course of the different stresses is indicated in the bottom. The changes in mRNA levels are given in \log_2 ratios of treatments versus controls (Y axes on the left).

Supplementary Fig. 5. (8 figure pages) The responses of combined isozymic mRNA levels of genes encoding isozymes of representative metabolic pathways to representative stress conditions in shoots. The combined isozymic mRNA levels of genes encoding biosynthetic/allosteric enzymes, biosynthetic/non-allosteric enzymes and enzymes catalyzing the first catabolic steps of the amino acids are indicated by blue, black and red lines, respectively. The names of the enzymes encoded by the different isozymic genes, as provided in Table 1, are given in the boxes of each panel. Each page contains the response of the eight different modules to a different stress condition. The combined isozymic mRNA levels are given in \log_2 ratios of treatments versus controls (Y axes on the left). Only values greater than 2-fold increase or 2-fold decrease in combined isozymic mRNA levels (broken horizontal lines) were considered as significant changes.

Supplementary Fig. 6. (8 figure pages) The responses of combined isozymic mRNA levels of genes encoding isozymes of representative metabolic pathways to representative stress conditions in roots. The combined isozymic mRNA levels of genes encoding biosynthetic/allosteric enzymes, biosynthetic/non-allosteric enzymes and enzymes catalyzing the first catabolic steps of the amino acids are indicated by blue, black and red lines, respectively. The names of the enzymes encoded by the different isozymic genes, as provided in Table 1, are given in the boxes of each panel.

Each page contains the response of the eight different modules to a different stress condition. The combined isozymic mRNA levels are given in \log_2 ratios of treatments versus controls (Y axes on the left). Only values greater than 2-fold increase or 2-fold decrease in combined isozymic mRNA levels (broken horizontal lines) were considered as significant changes.

Supplementary Fig. 7. The mean mRNA levels (\log_2 ratio of treatment versus control) of the subset of genes encoding annotated proteases that are induced in response to senescence and programmed cell death (PCD) in roots (A) and shoots (B) of plants exposed to the eight different abiotic stresses. The mean mRNA levels of the same subset of genes upon exposure to senescence and PCD are given in broken lines marked by arrows over the entire stresses.