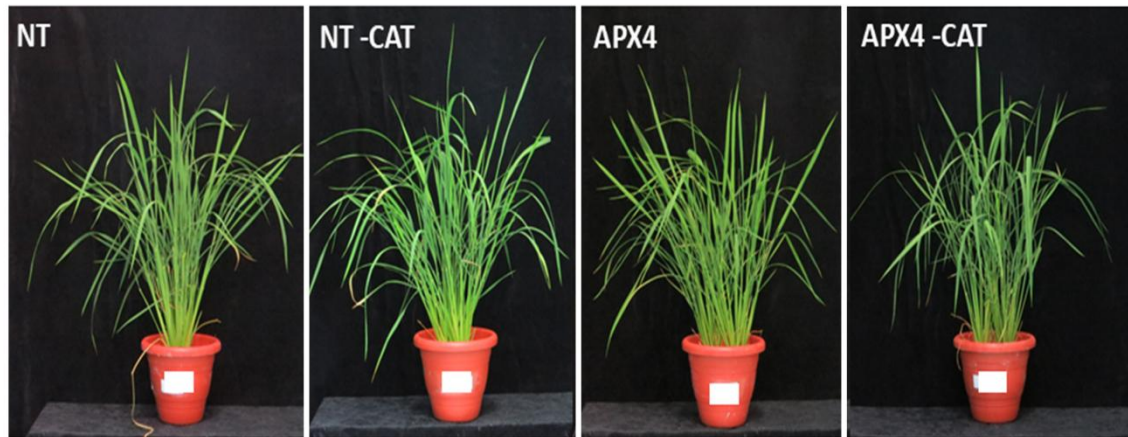


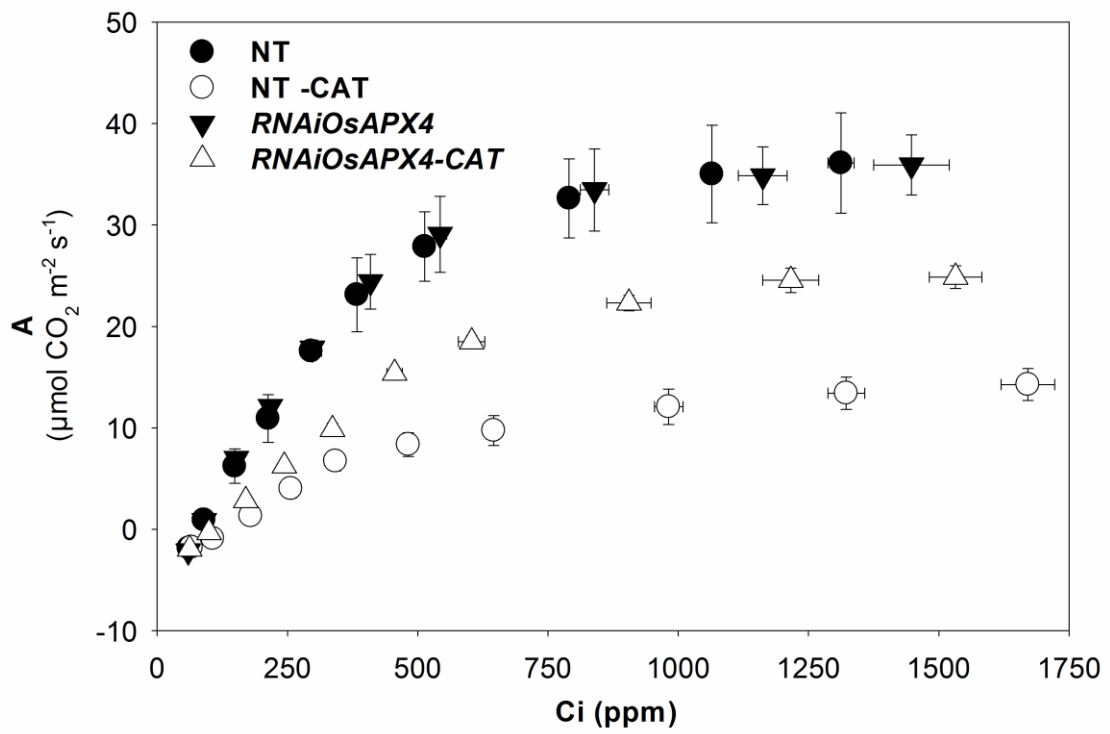
**Impairment of peroxisomal APX and CAT activities increases protection of  
photosynthesis under oxidative stress conditions**

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Alencar<sup>1</sup>, Danilo M. Daloso<sup>1</sup>, Marcia Margis-Pinheiro<sup>3</sup>, Setsuko Komatsu<sup>4</sup> & Joaquim A.  
G. Silveira<sup>1\*</sup>

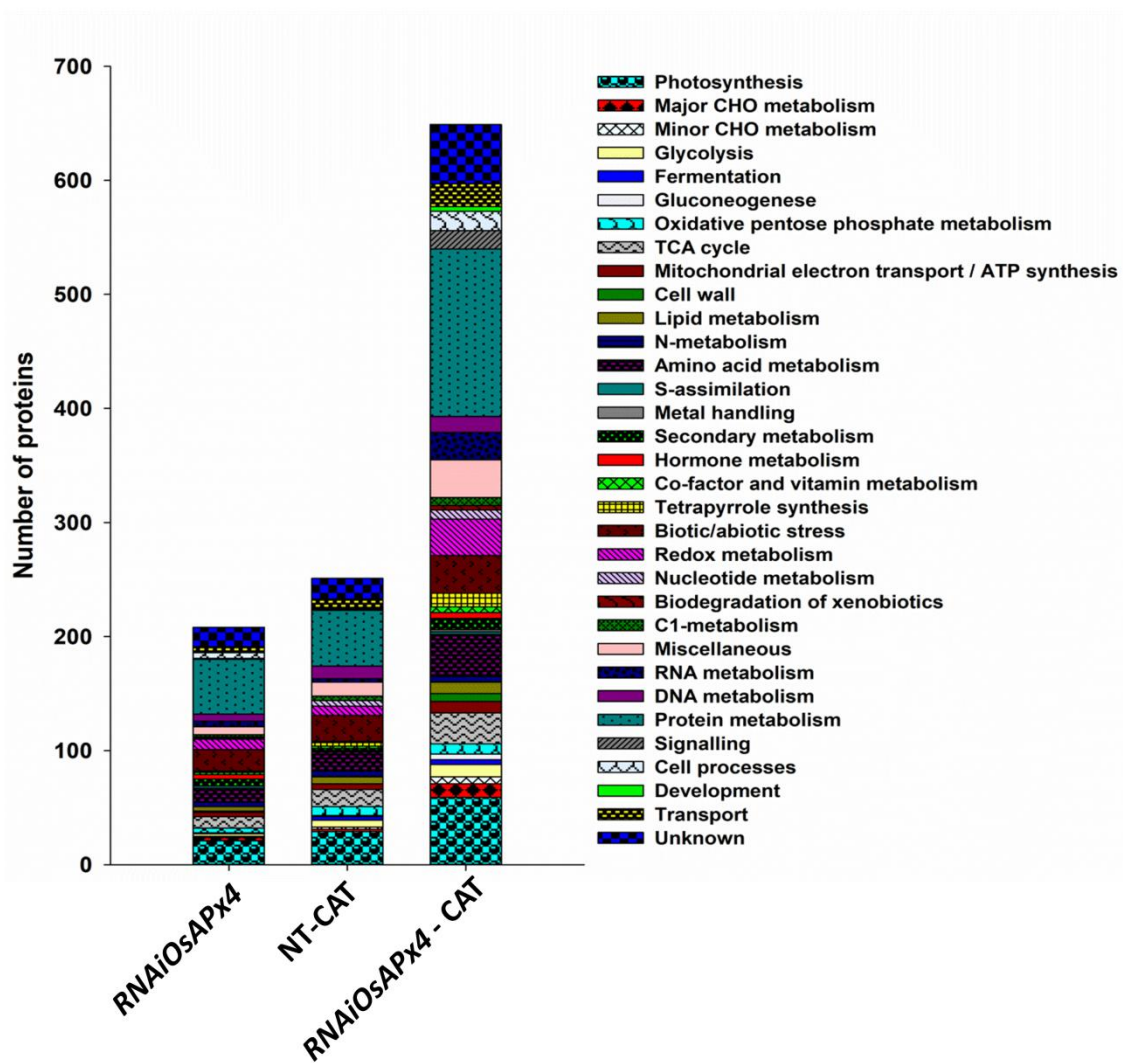
**SUPPLEMENTARY MATERIAL**



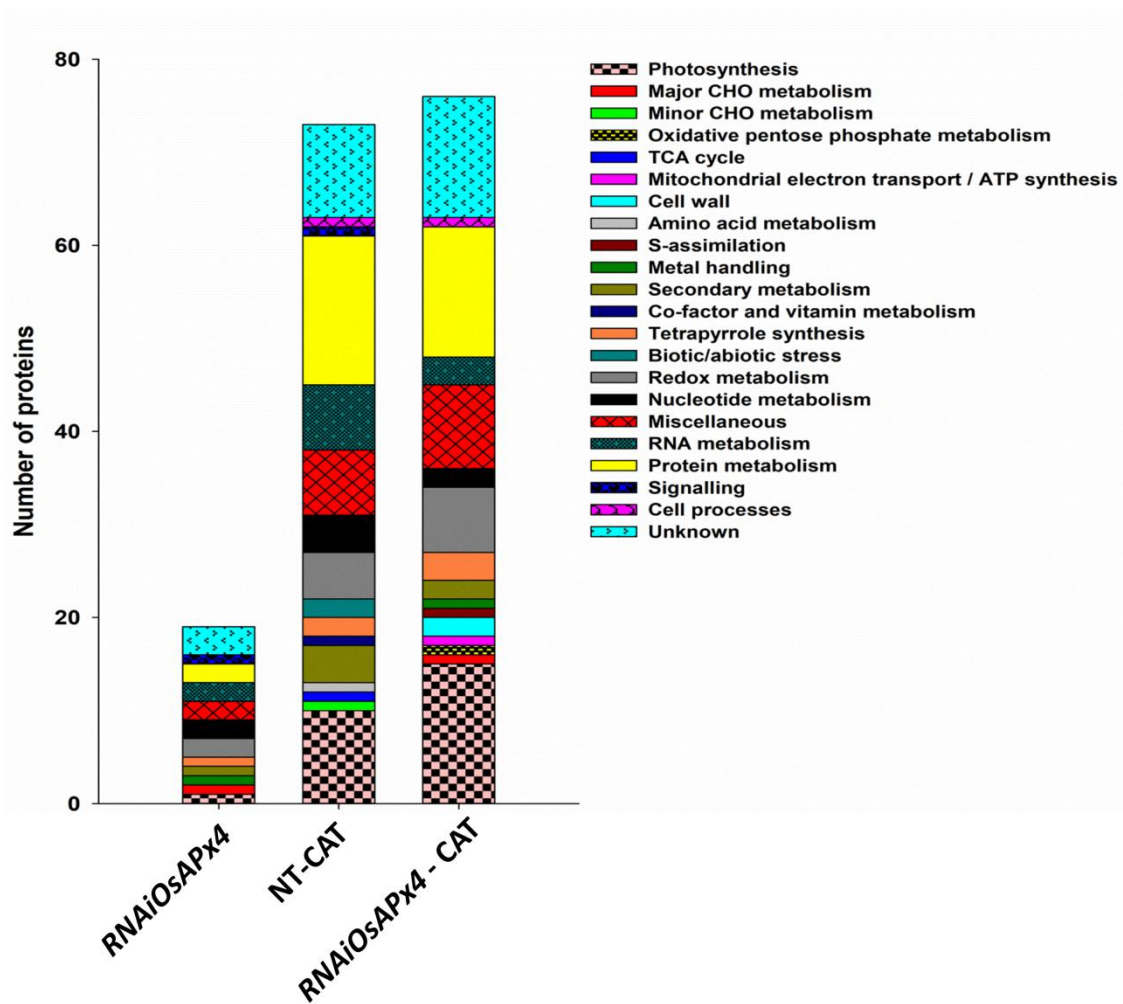
**Supplementary figure 1.** Morphological aspects of shoots of non-transformed (NT) and *RNAiOsAPX4* rice plants exposed 10 mM 3-AT (-CAT) and control. Plants are the most representative from four biological replicates.



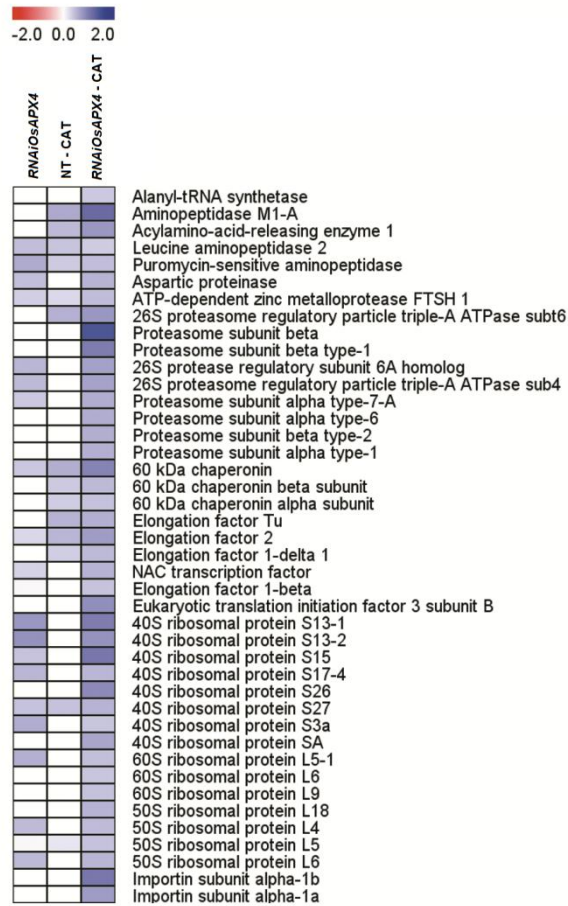
**Supplementary figure 2.**  $P_N/C_i$  curves non-transformed (NT) and *RNAiOsAPX4* rice plants exposed 10 mM 3-AT (-CAT) and control. The points represent means of four replicates  $\pm$ SD.



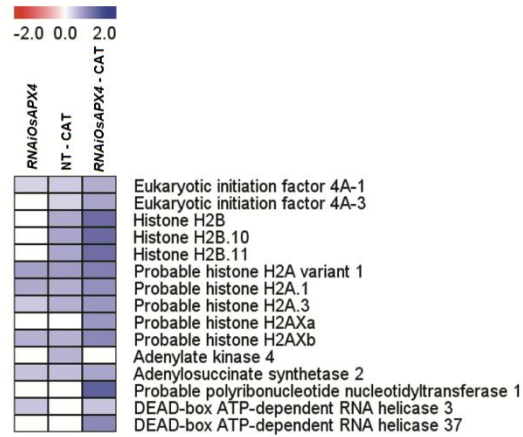
**Supplementary figure 3.** Functional classification of proteins with increased abundance. The amount of each protein in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT) were all compared to the respective protein amount found in NT control plants. Each protein content was considered increased if the log<sub>2</sub> value was higher than 0.5. Proteins were classified by the software (MapMan) according to their involvement in each metabolic process.



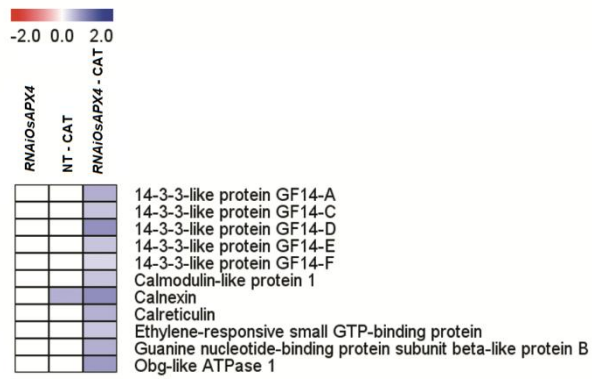
**Supplementary figure 4.** Functional classification of proteins with decreased abundance. The amount of each protein in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT) were all compared to the respective protein amount found in NT control plants. Each protein content was considered increased if the log<sub>2</sub> value was higher than 0.5. Proteins were classified by the software (MapMan) according to their involvement in each metabolic process.



**Supplementary figure 5.** Heatmap of differently expressed proteins related to protein metabolism in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT), all compared to the respective protein amount in NT control plants. The fold change from proteomics was plotted into a heatmap using MEV software framework.

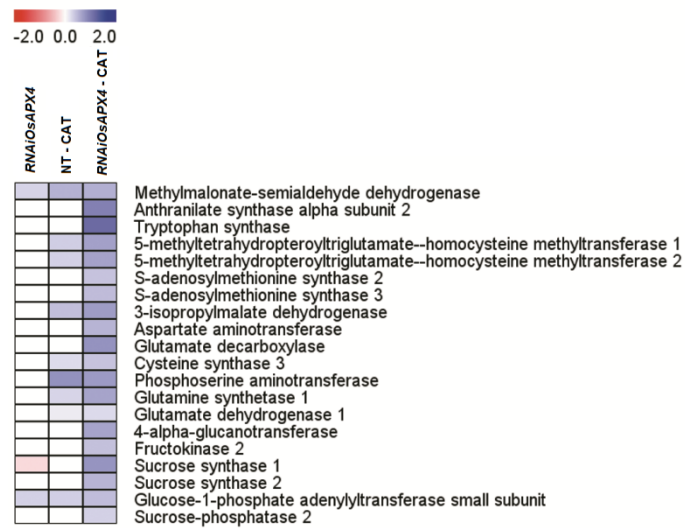


**Supplementary figure 6.** Heatmap of differently expressed proteins related to nuclear metabolism in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT), all compared to the respective protein amount in NT control plants. The fold change from proteomics was plotted into a heatmap using MEV software framework.

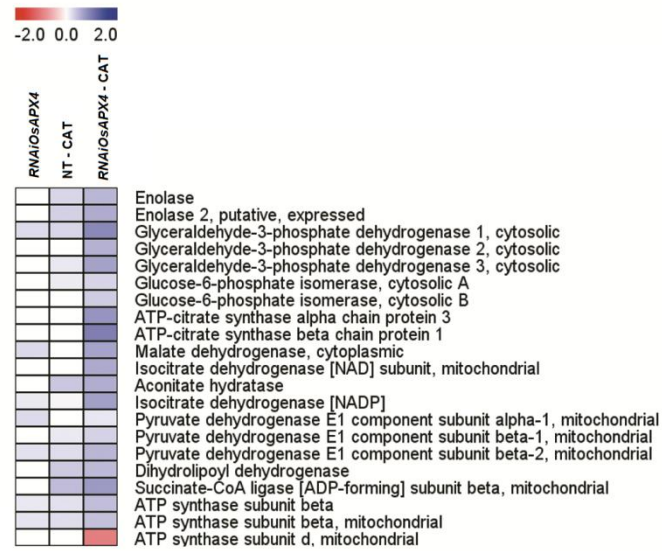


**Supplementary figure 7.** Heatmap of differently expressed proteins related to signalling metabolism in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT), all compared to the respective protein amount in NT control plants. The fold change from proteomics was plotted into a heatmap using MEV software framework.





**Supplementary figure 8.** Heatmap of differently expressed proteins related to amino acid and sugar metabolism in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT), all compared to the respective protein amount in NT control plants. The fold change from proteomics was plotted into a heatmap using MEV software framework.



**Supplementary figure 9.** Heatmap of differently expressed proteins related to respiratory metabolism in leaves of *RNAiOsAPX4* under normal growth condition and in non-transformed (NT) and *RNAiOsAPX4* plants exposed to 10 mM 3-AT (-CAT), all compared to the respective protein amount in NT control plants. The fold change from proteomics was plotted into a heatmap using MEV software framework.