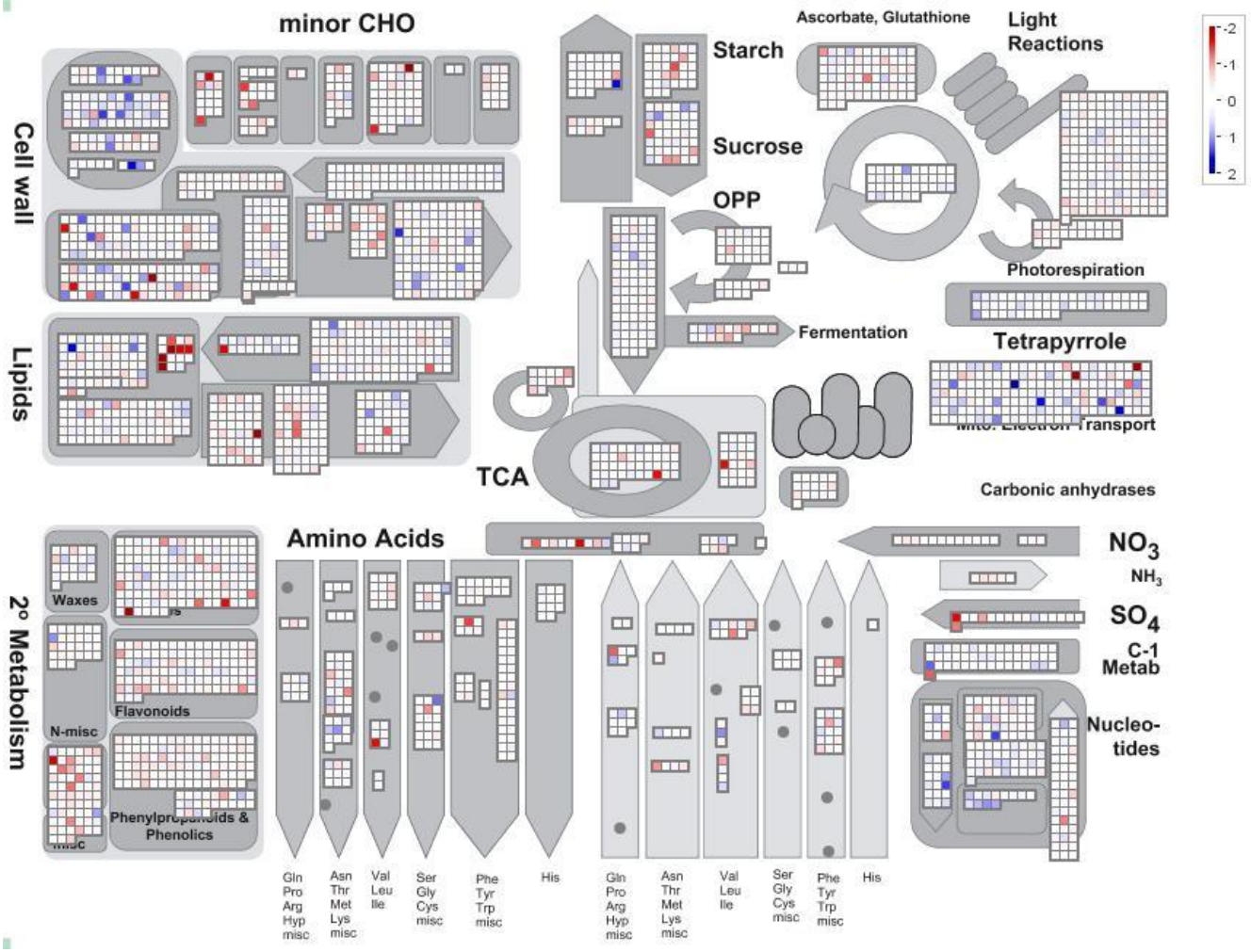

Fig. S1: Mapman representation of the relative gene expression profile and related metabolic processes in *rpoTmp* dark-grown seedlings. Microarray data sets were processed using the RobiNA web tool and implemented into the MapMan visualization mask according to the recommendations on the website. Gene up-regulation is given by blue squares, gene down-regulation by red squares. A corresponding color code is indicated in the top right corner of the plot. Values refer to log2 fold changes.

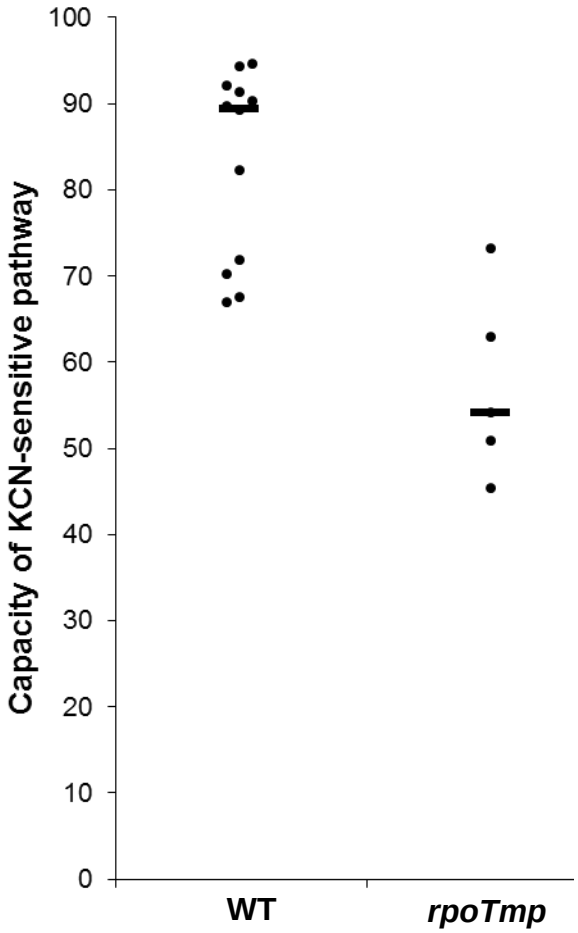

Fig. S2: Capacity of the KCN-sensitive pathway in etiolated seedlings. Capacity of the KCN-sensitive pathway was calculated upon addition of 1 mM SHAM into the measurement cell (final concentration). The figure presents the ratio in percentage of the KCN-sensitive O_2 consumption rate to the total consumption rate. Median values (thick horizontal lines) of N independent measurements (full circles) were scatter-plotted for WT (N=12) and *rpoTmp* (N=5).

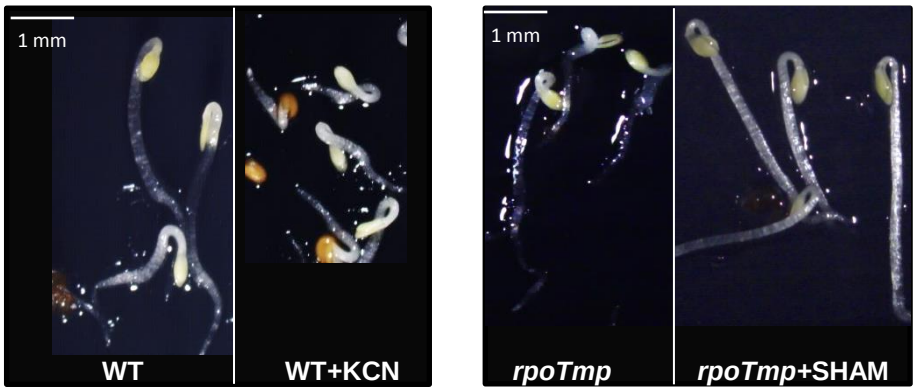

Fig. S3: Images of etiolated inhibitor-treated plants. Phenotype of the WT and *rpoTmp* grown in absence or in presence of 1 mM KCN (left panel) and 1mM SHAM (right panel), respectively. Scale bar corresponds to 1 mm.

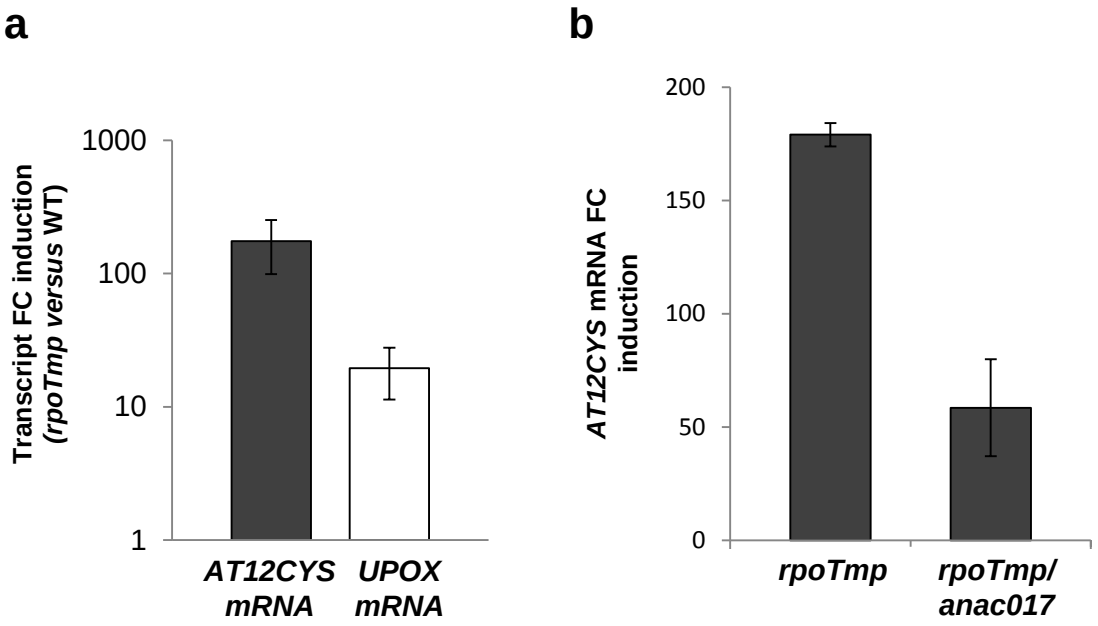

Fig. S4: Expression changes of oxidative stress marker genes in etiolated mutant plants compared to WT. **a**) Linear fold change (FC) induction of *AT12CYS* and *UPOX* transcripts in *rpoTmp* plants *versus* WT. Transcript expression levels were determined by RT-qPCR and normalized with the mean of *ACTIN* 2-8 expression, used as reference gene. The mean values of three technical replicates are plotted. Error bars correspond to standard errors. **b**) Linear fold change (FC) induction of *AT12CYS* transcripts in *rpoTmp* and *rpoTmp/anac017* plants *versus* WT. The mean values of two biological RT-qPCR replicates are plotted.

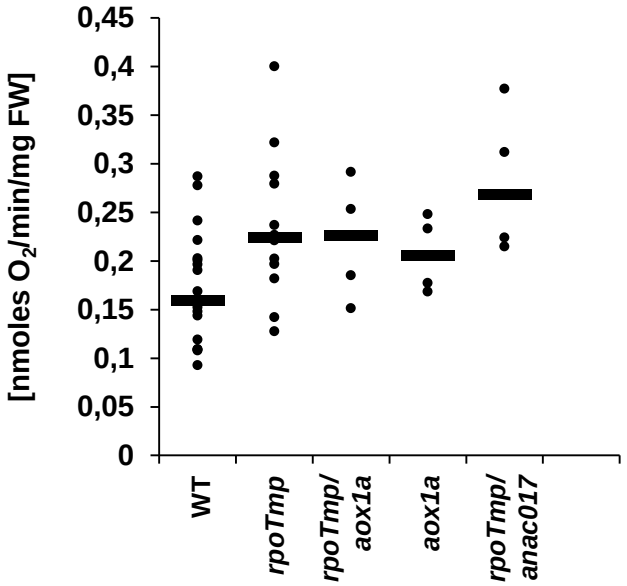

Fig. S5: Total O_2 consumption rate in etiolated mutant plants. Median values (thick horizontal lines) of N independent measurements (full circles) were scatter-plotted for WT (N=19), *rpoTmp* (N=12), *rpoTmp/aox1a* (N=5), *aox1a* (N=4), *rpoTmp/anac017* (N=4).

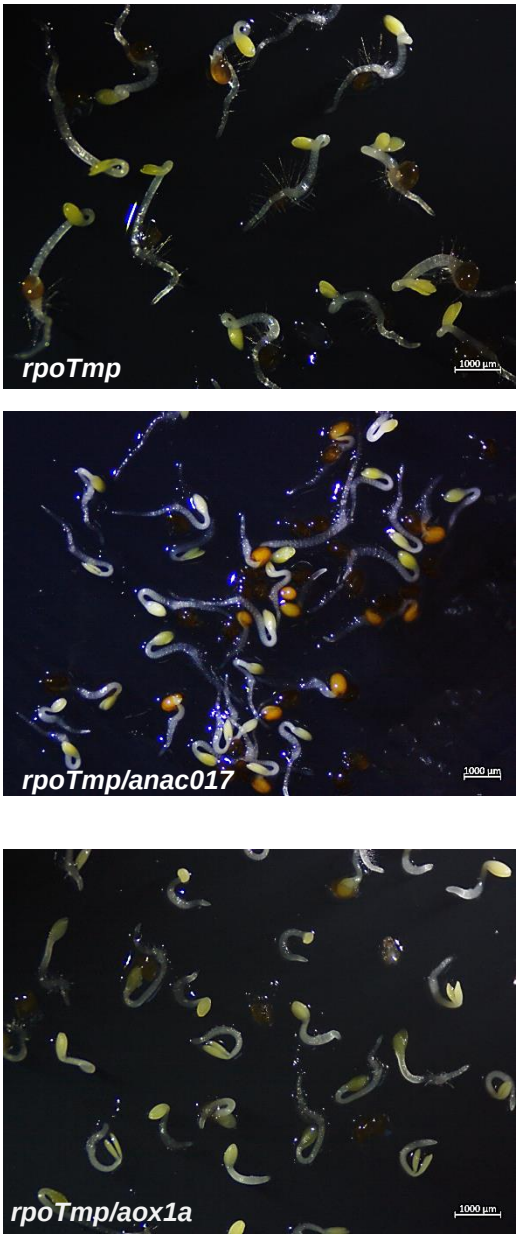

Fig. S6: Images of etiolated *rpoTmp, rpoTmp/anac017* and *rpoTmp/aox1a* mutant plants. Scale bar corresponds to 1 mm.

qPCR primers	
AOX1a FWD	GACGGTCCGTACGGTTTCG
AOX1a REV	CTTCTGATTCGCGTCCTCCTCCT
AT12CYS2 FWD	GCCTCCTCAATCTGTGAACC
AT12CYS2 REV	CCAAATGCAGTTCCAGTACC
UPOX FWD	CCGAGAACCCGCCAAAACC
UPOX REV	GCTTCTCTGCAACTGCCTC
ACT 2.8 FWD	GGTAACATTGTGCTCAGTGGTGG
ACT 2.8 REV	AACGACCTTAATCTTCATGCTGC

Table S1: Primers used in qPCR for expression analyses.