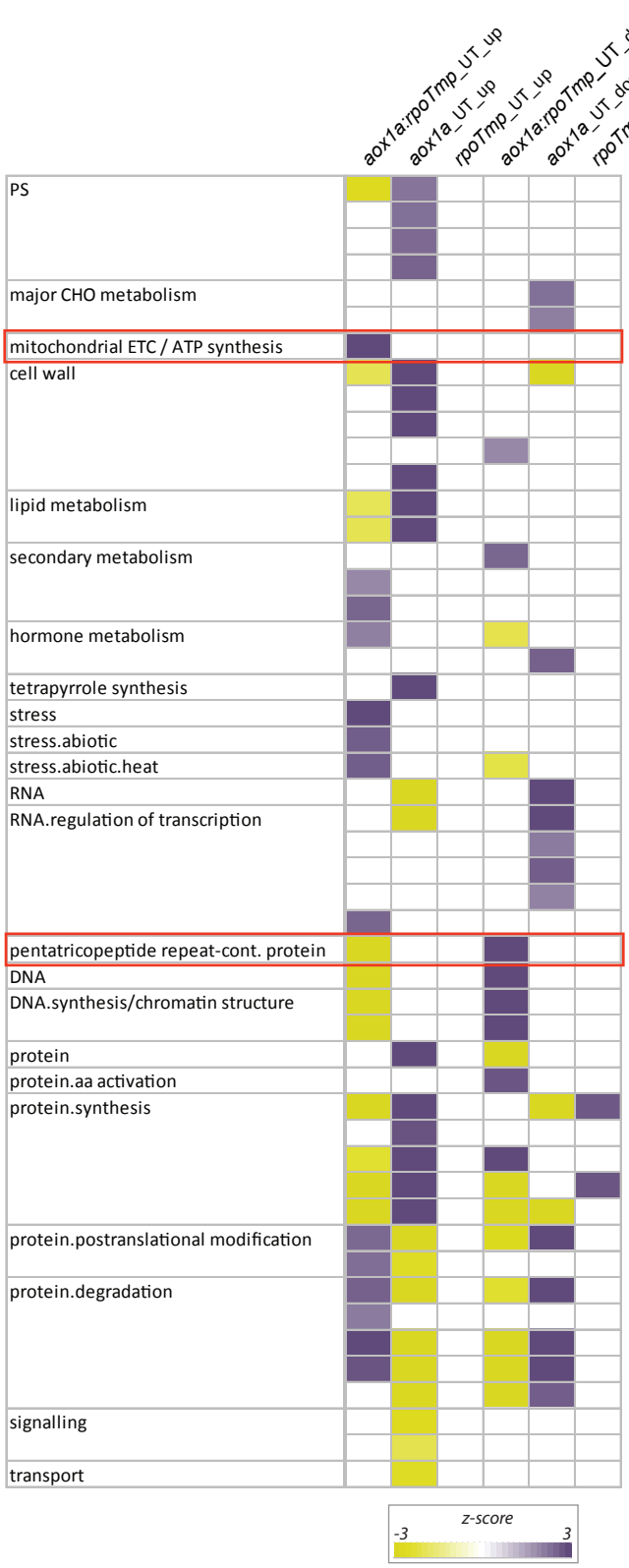
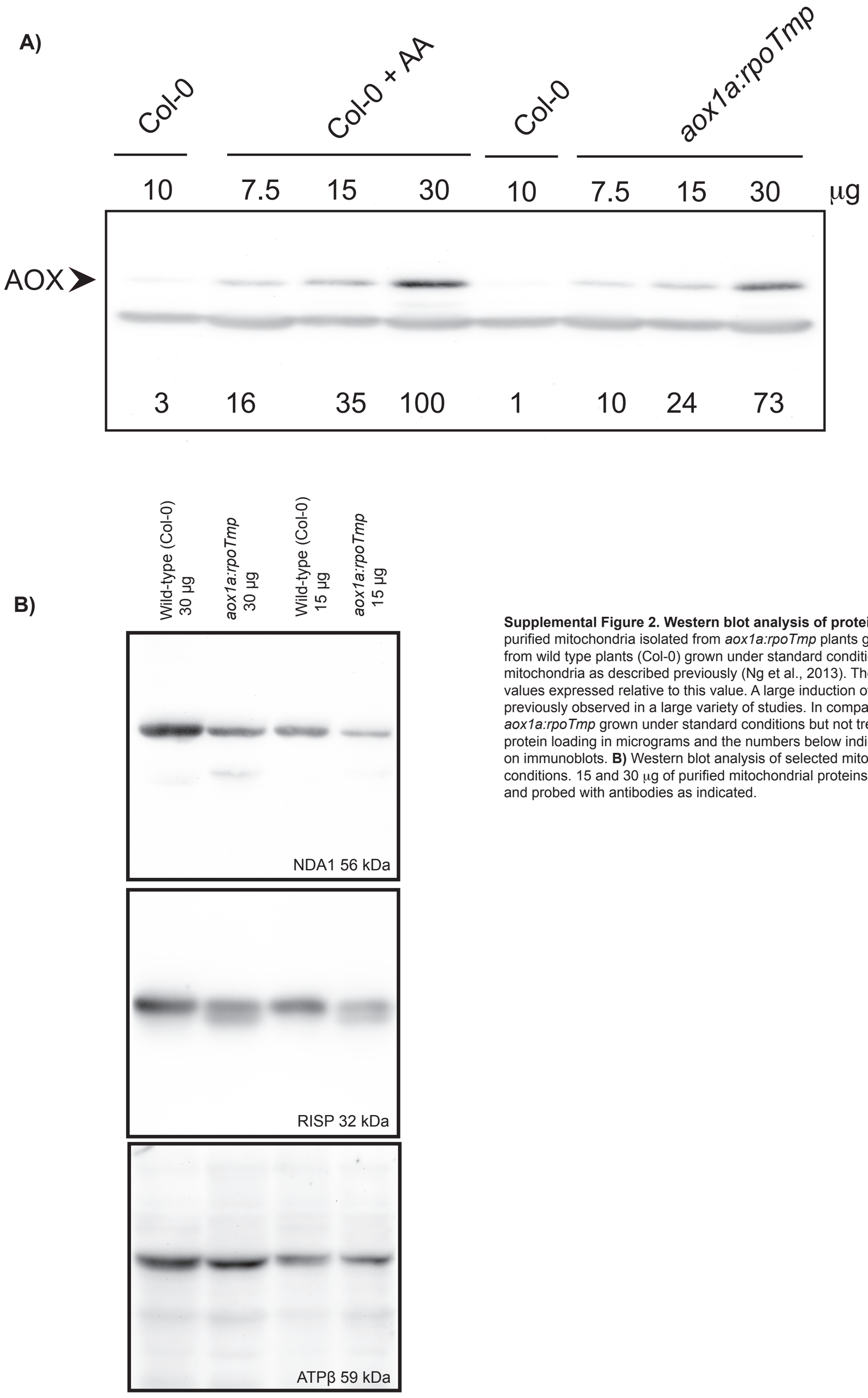
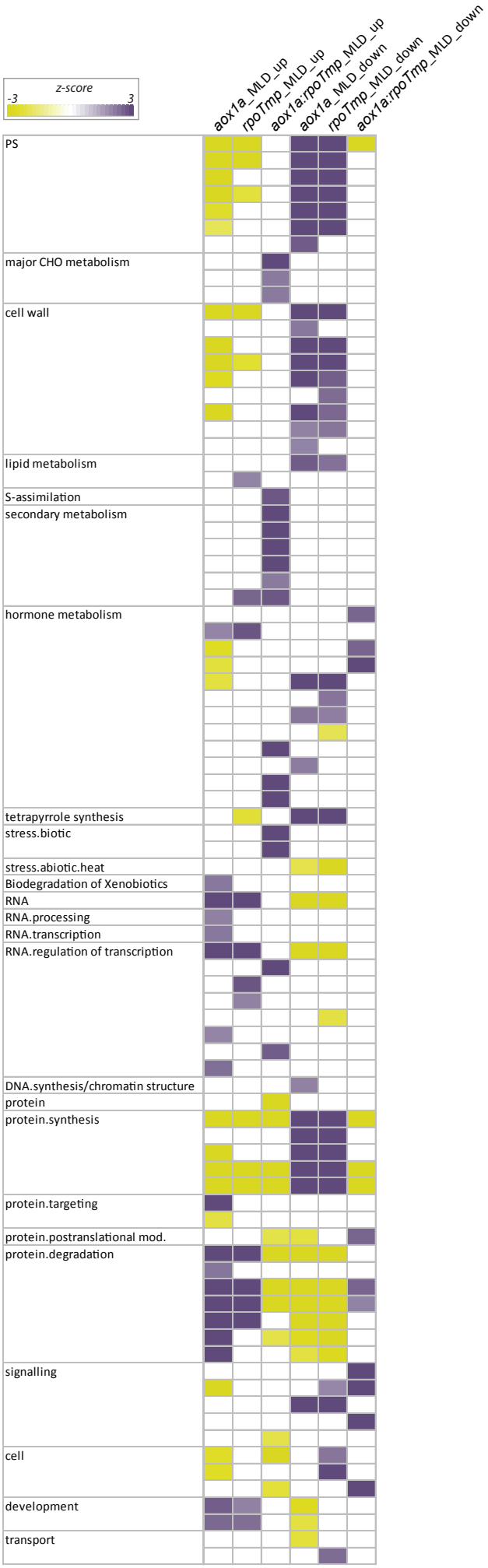


Supplemental Figure 1. Pageman representation of the functional categories that are over-represented (purple) or under-represented (yellow) among genes whose transcripts changed in abundance in *aox1a, rpoTmp* and *aox1a:rpoTmp* grown under standard conditions. Boxed in red are the functional categories of mitochondrial electron transport/ATP synthesis that is over-represented in genes whose transcripts increase in abundance in *aox1a:rpoTmp* grown under standard conditions, and PPR proteins that are over-represented in genes whose transcripts decrease in abundance in *aox1a:rpoTmp* grown under standard conditions.

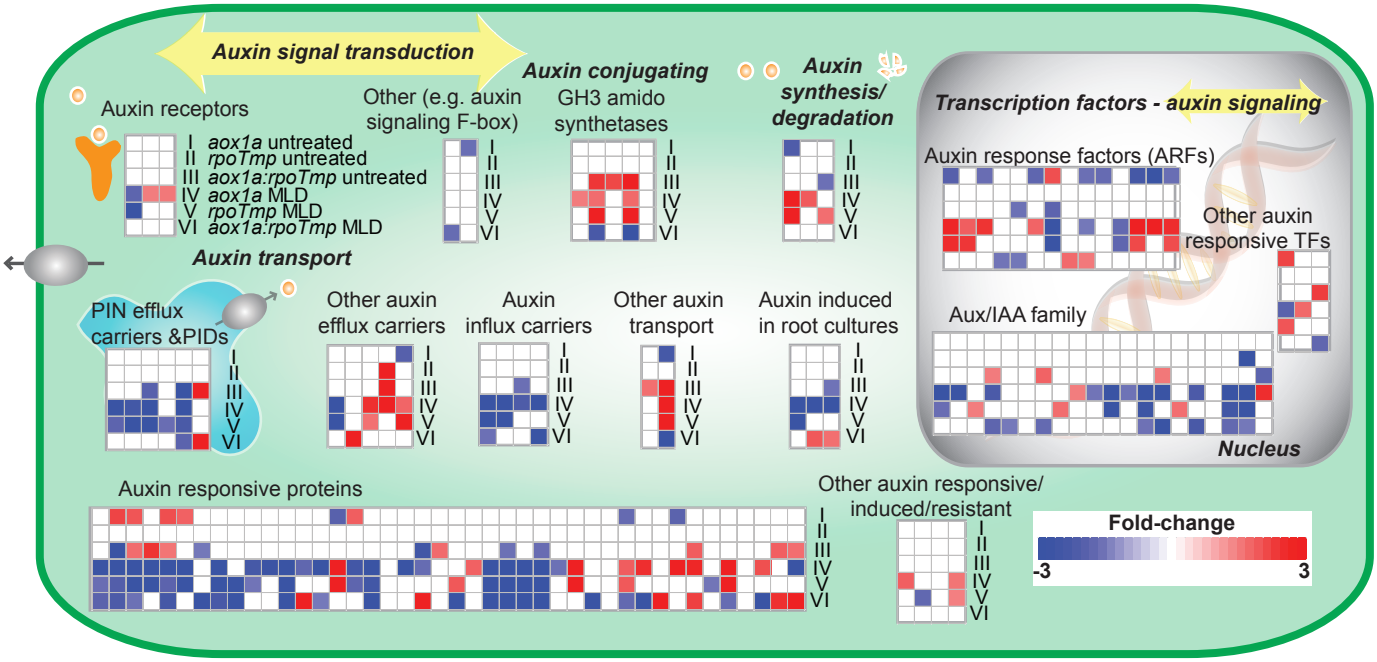
Supplementary Figure 1



Supplemental Figure 2. Western blot analysis of protein abundance in *aox1a:rpoTmp*. A) The amount of AOX in purified mitochondria isolated from *aox1a:rpoTmp* plants grown under standard conditions was compared to that isolated from wild type plants (Col-0) grown under standard conditions, but treated with antimycin A (AA) 6h prior to isolation of mitochondria as described previously (Ng et al., 2013). The highest signal detected for AOX was set to 100 and all other values expressed relative to this value. A large induction of AOX from Col-0 plants with antimycin A was observed as previously observed in a large variety of studies. In comparison the amount of AOX detected in purified mitochondria from *aox1a:rpoTmp* grown under standard conditions but not treated with AA was similar. The numbers on top indicate the protein loading in micrograms and the numbers below indicate the normalised signal intensity of the AOX band detected on immunoblots. **B)** Western blot analysis of selected mitochondrial proteins in *aox1a:rpoTmp* under standard growth conditions. 15 and 30 µg of purified mitochondrial proteins were isolated from wild type (Col-0) and *aox1a:rpoTmp* plants and probed with antibodies as indicated.



Supplemental Figure 3. A Pageman visualisation showing the over-represented functional categories for all differentially expressed genes in all three mutants grown under MLD stress.



Supplemental Figure 4. Transcript abundance changes of auxin related gene ontologies in *aox1a, rpoTmp* and *aox1a rpoTmp* under standard (untreated) and adverse (MLD) growth conditions. Responses are shown as significant fold-changes relative to mock/untreated samples (p<0.05, PPDE>0.95; genes - columns, treatments -rows).