

Strigolactones are positive regulators of light harvesting genes in tomato

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Supplementary Material

Supplementary Figures S1-S2

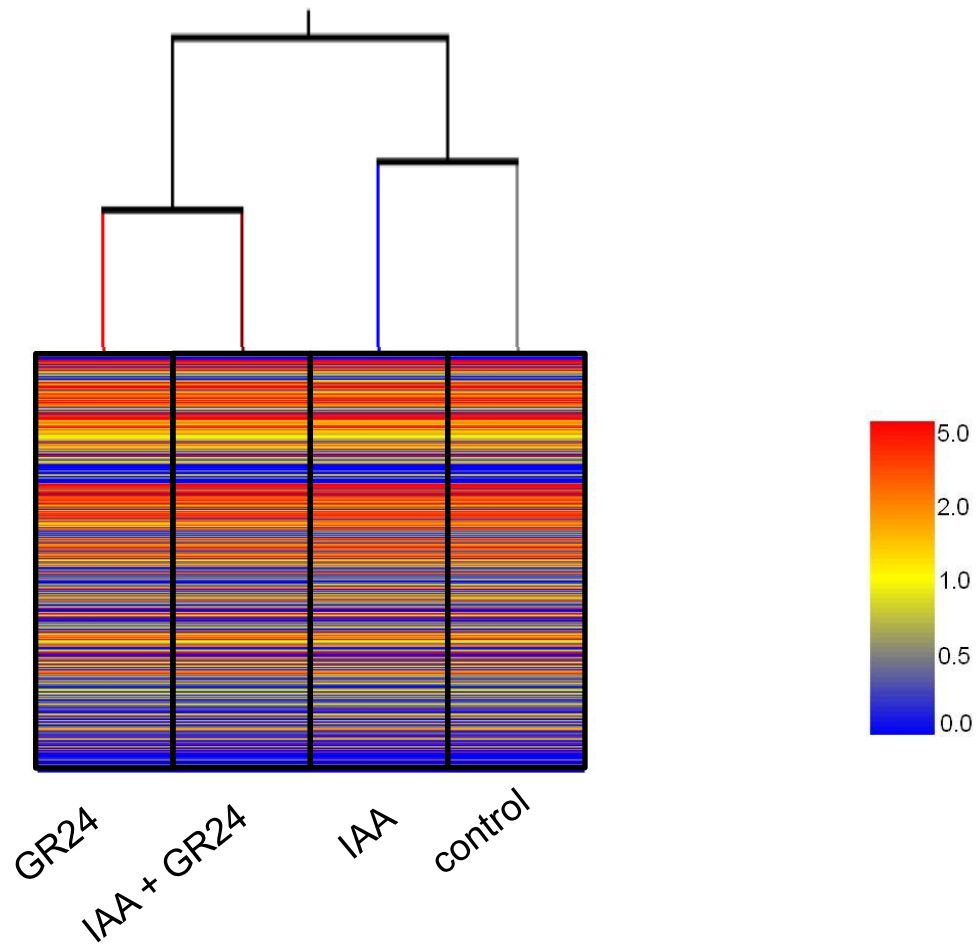


Fig S1. Hierarchical clustering of microarray hybridization gene-expression data of roots exposed to GR24 and IAA treatments: IAA (10^{-8} M), IAA (10^{-8} M) + GR24 (13.5 μ M), GR24 (27 μ M) and non-treated controls. Color scale represents fold change in gene expression in treatments versus controls.

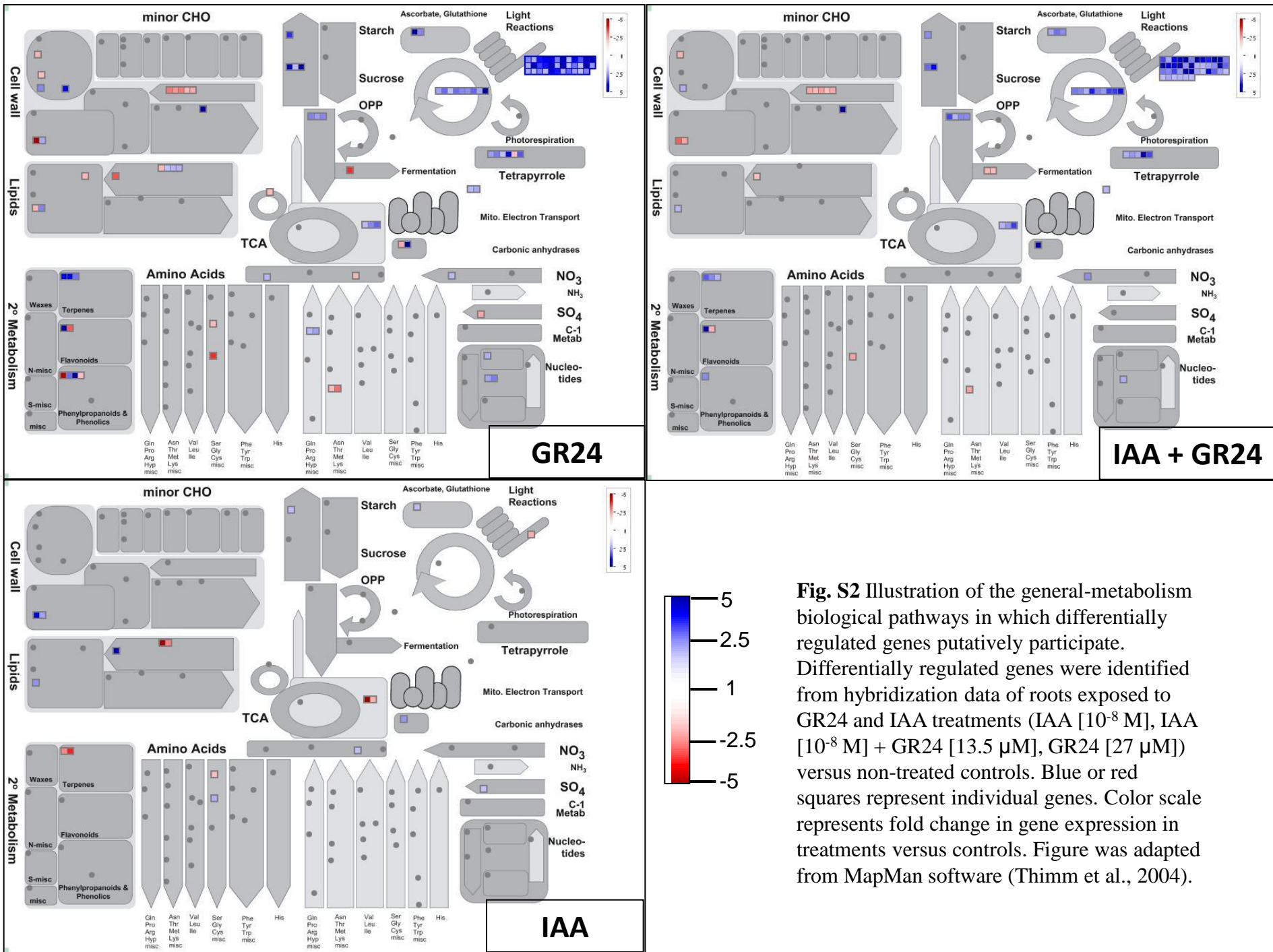


Fig. S2 Illustration of the general-metabolism biological pathways in which differentially regulated genes putatively participate. Differentially regulated genes were identified from hybridization data of roots exposed to GR24 and IAA treatments (IAA [10^{-8} M], IAA [10^{-8} M] + GR24 [$13.5 \mu\text{M}$], GR24 [$27 \mu\text{M}$]) versus non-treated controls. Blue or red squares represent individual genes. Color scale represents fold change in gene expression in treatments versus controls. Figure was adapted from MapMan software (Thimm et al., 2004).