

1 **SUPPLEMENTAL METHODS**

2 **Functional Enrichment Analysis**

3 g:Profiler (<http://biit.cs.ut.ee/gprofiler/>) webtool was used for finding enriched GO terms in
4 the DEGs at 1.5 hrs with Best per parent (moderate filtering) setting from g:Profiler for
5 “Hierarchical filtering” option in order to select only the most statistically significant term
6 from a particular hierarchical group. A score above 1.3 for negative log of adjusted p-values
7 was considered significant.

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9 **Motif Enrichment Analysis**

10 Webtool (<https://www.arabidopsis.org/tools/bulk/motiffinder/index.jsp>) was used for
11 identifying motif overrepresentation (using hypergeometric test) within the 1000 bp
12 upstream sequences (relative to Transcription Start Site) of genes.

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14 **MapMan Photosynthesis Genes**

15 Mappings excel sheet “Ath_AFFY_ATH1_TAIR10” at ([http://mapman.gabipd.org/
16 web/quest/mapmanstore](http://mapman.gabipd.org/web/quest/mapmanstore)) was used to assign photosynthesis genes to the different
17 categories in Supplemental Table S1.

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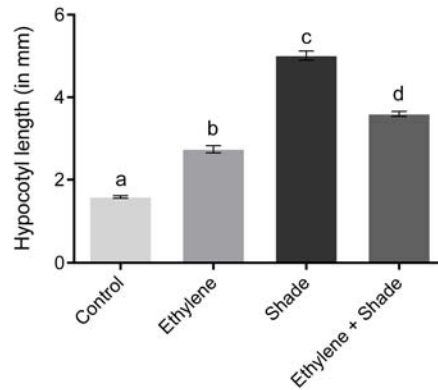
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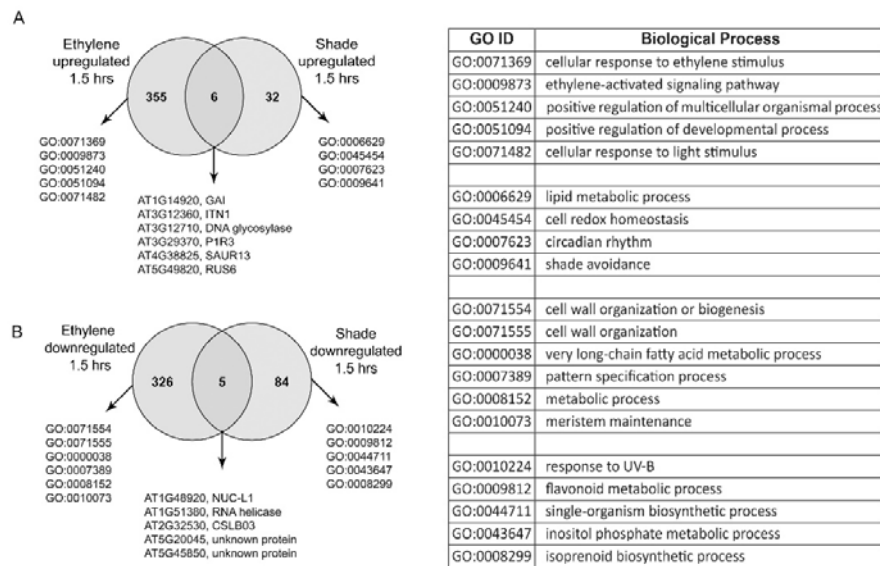
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SUPPLEMENTAL FIGURES AND TABLES



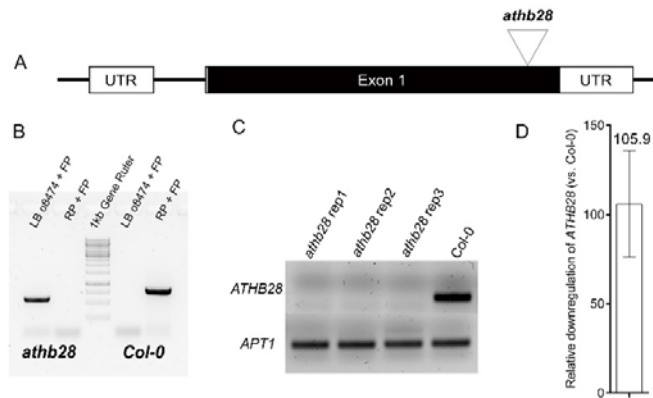
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Supplemental Figure S1. Effect of 7 d control, ethylene, shade and combination (ethylene + shade) treatments on hypocotyl length of *Arabidopsis* seedlings in short day photoperiod (9 h light / 15 h dark). Data represents mean ± S.E. (n=30-50). Different letters above the bars indicate significant differences (1-way ANOVA followed by Post-Hoc pairwise comparison).



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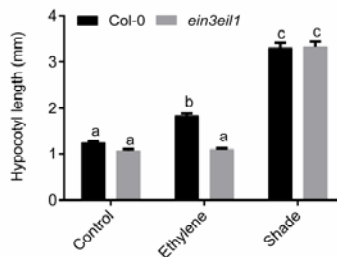
Supplemental Figure S2. g:Profiler analysis for enriched Gene ontology (GO) IDs (adj. p-value ≤ 0.05) or genes for DEGs (A) up- or (B) down- regulated at 1.5 hrs in the hypocotyl in response to ethylene or shade. Biological process (BP) terms corresponding to enriched GO IDs have been tabulated on the right side.



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54 **Supplemental Figure S3.** Genotyping and transcript level verification. A, T-DNA insertion position in GABI-
 55 KAT line GK-326G12 (*athb28*) B, Genotyping of *athb28*, (C) and (D) Null transcript and downregulation level
 56 of ATHB28 in *athb28* (vs. Col-0). Abbreviations: In (B) LP: left primer, RP: right primer, LBo8474: GABI-KAT
 57 sequencing primer.

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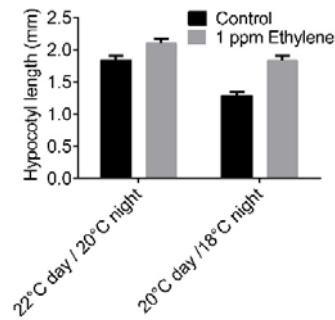
60 **Supplemental Figure S4.** Ethylene signalling mutant *ein3eil1* shows hypocotyl elongation response similar to
 61 wild-type in response to shade but totally lacks elongation in response to ethylene. Hypocotyl length was
 62 measured following 96 h of ethylene and shade. Mean \pm S.E. was calculated for 60 seedlings. Different letters
 63 indicate significant differences from a 2-way ANOVA followed by Tukey's HSD Post-Hoc pairwise comparison.

Motifs over-represented in TAIR Motif analysis					
Gene set	Top 2 motifs	Relevance	% Gene Set	% Genome	p-value
Common Up	CACATG	HUD type E-box or PBE-box	51	36	3.94e ⁻²²
	TAATTA	homeodomain binding site	72	60	3.85e ⁻¹⁵
Common Down	CACGTG	G-box	22	15	5.62e ⁻⁰⁹
	ACGTGG	ABA-responsive element (ACGTGG/TC).	28	21	1.39e ⁻⁰⁷

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66 **Supplemental Figure S5.** TAIR motif analysis and functional validation of PIFs and MYCs in hypocotyl
 67 elongation. TAIR motif overrepresentation (Lamesch et al., 2012). Top 2 hexamer motifs are shown for each
 68 set along with the name of motifs (relevance). % Microarray and % Genome indicate percentage of genes
 69 with the motif relative to the total number of genes in the gene set and in the genome respectively.
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72 **Supplemental Figure S6.** Hypocotyl length of Landsberg erecta ecotype of *Arabidopsis thaliana* under
 73 control and 1 μL^{-1} ethylene conditions when grown at 22°C day / 20°C night and 20°C day / 18°C night
 74 temperature regime.

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Photosynthesis category	Ethylene specific	Common Down	Shade specific
Light reaction. Photosystem II	53.33	20.00	1.67
Light reaction. Photosystem I	62.96	7.41	3.70
Light reaction. Other bins	36.07	13.11	3.28
Photorespiration	22.73	45.45	4.55
Calvin cycle	28.13	56.25	3.13

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78 **Supplemental Table S1.** Proportion of photosynthesis genes in different gene sets from the Venn diagram of
 79 negative clusters. Numbers in the table denote the % of total Mapman-assigned genes for the different
 80 photosynthetic processes. Bold numbers indicate top 3 photosynthetic categories.

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82 LITERATURE CITED

83 **J. Reimand, M. Kull, H. Peterson, J. Hansen, J. Vilo (2007).** g:Profiler - a web-based
 84 toolset for functional profiling of gene lists from large-scale experiments *NAR.* **35:**
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86 **Nagel, A., Thimm, O., Redestig, H., Blaesing, O.E., Steinhauser, D., Gibon, Y.,**
 87 **Morcuende, R., Weicht, D., Meyer, S., and Stitt, M. (2005).** Extension of the
 88 Visualization Tool MapMan to Allow Statistical Analysis of Arrays, Display of
 89 Corresponding Genes, and Comparison with Known Responses. *Plant Physiol.* **138:**
 90 1195–1204.

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