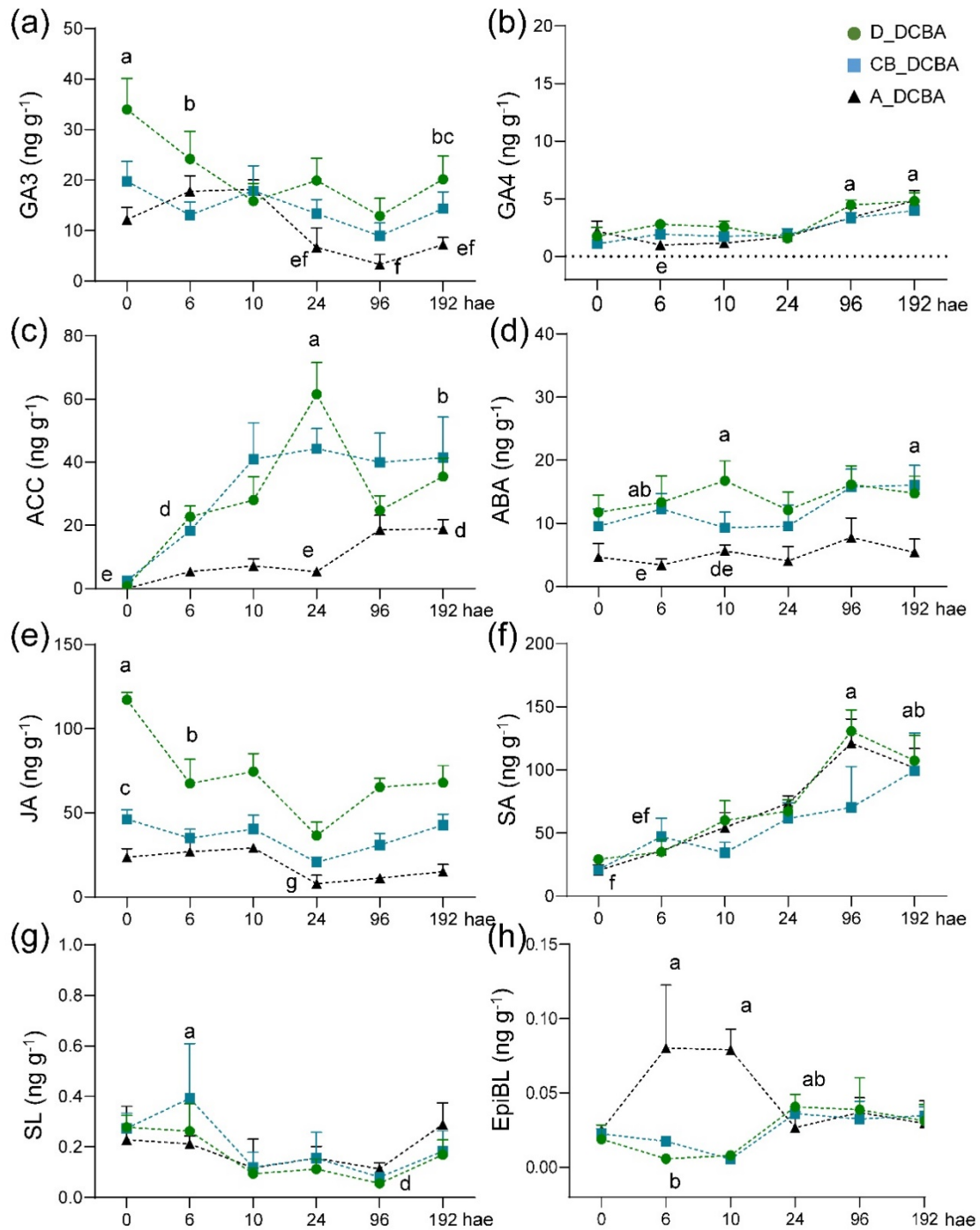
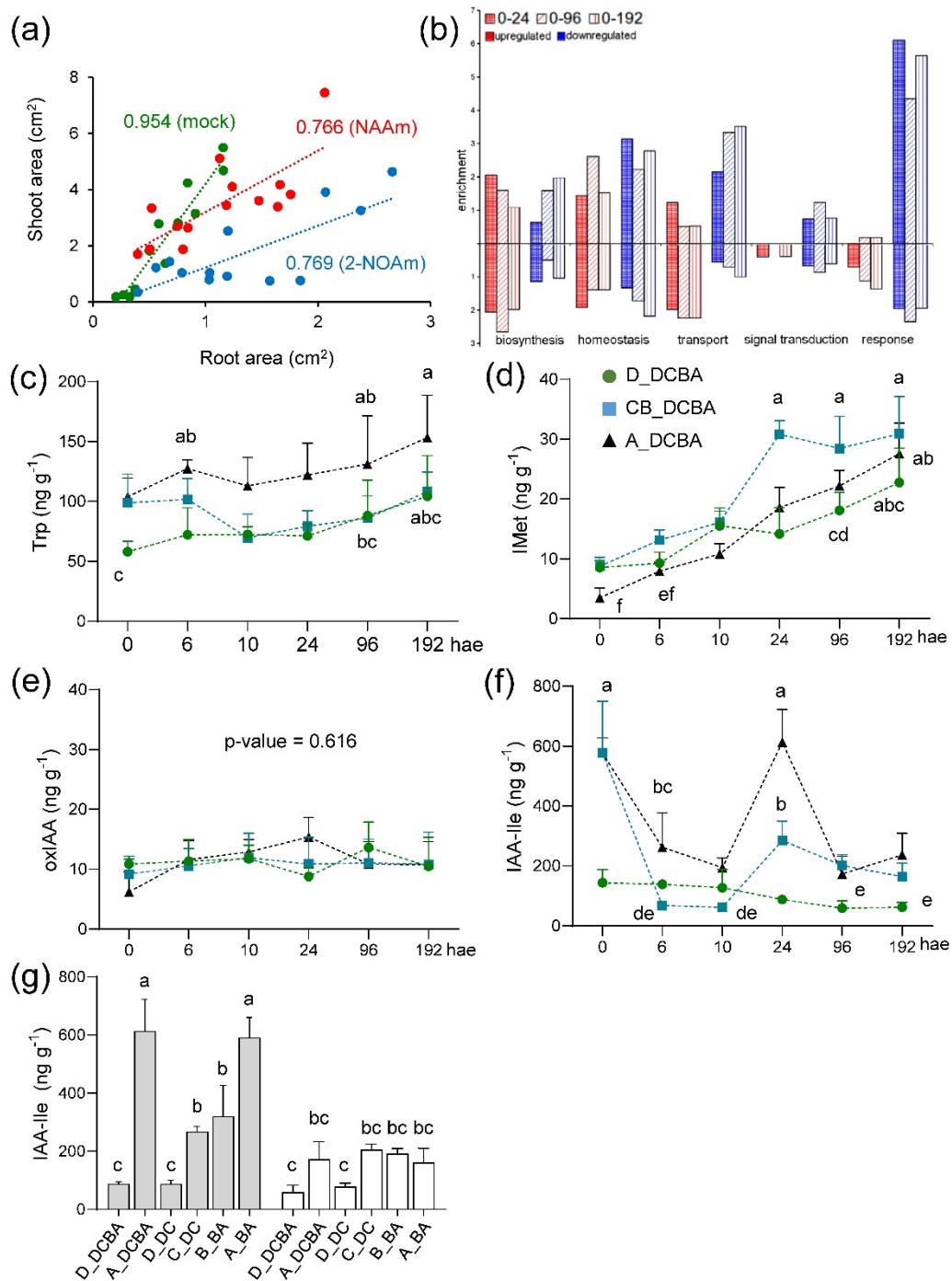


**Figure S1**



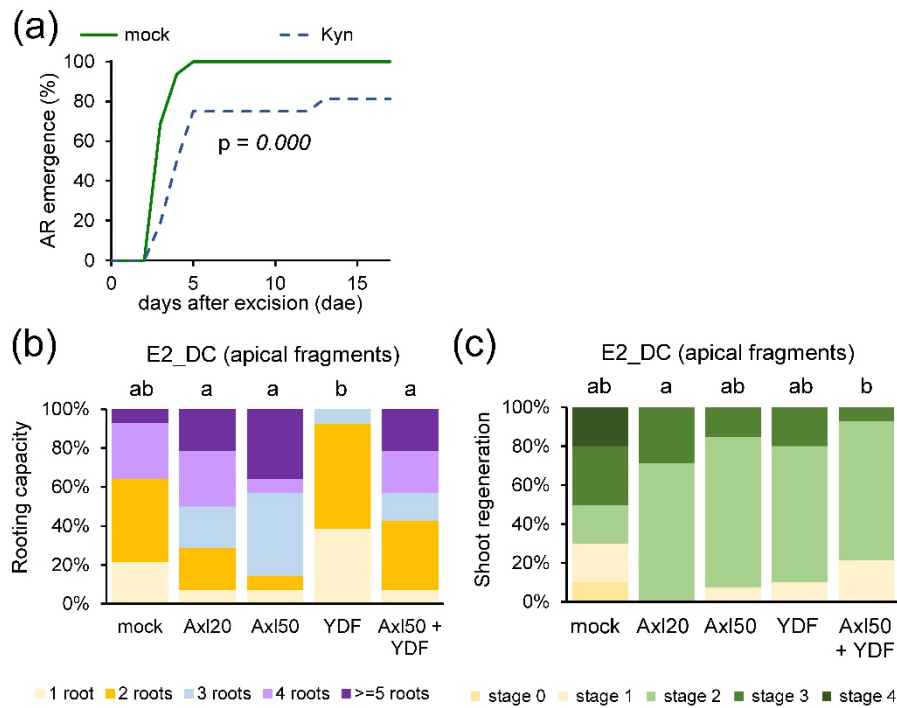
**Figure S1.** Endogenous hormone levels during de novo organ formation (cont.). (a) GA3, (b) GA4, (c) the ethylene precursor 1-aminocyclopropane-1-carboxylic acid (ACC), (d) abscisic acid (ABA), (e) jasmonic acid (JA), (f) salicylic acid (SA), (g) solanacol (SL), and (h) epibrassinolide (EpiBL). Different letters indicate significant differences ( $p < 0.001$ ) between samples.

**Figure S2**



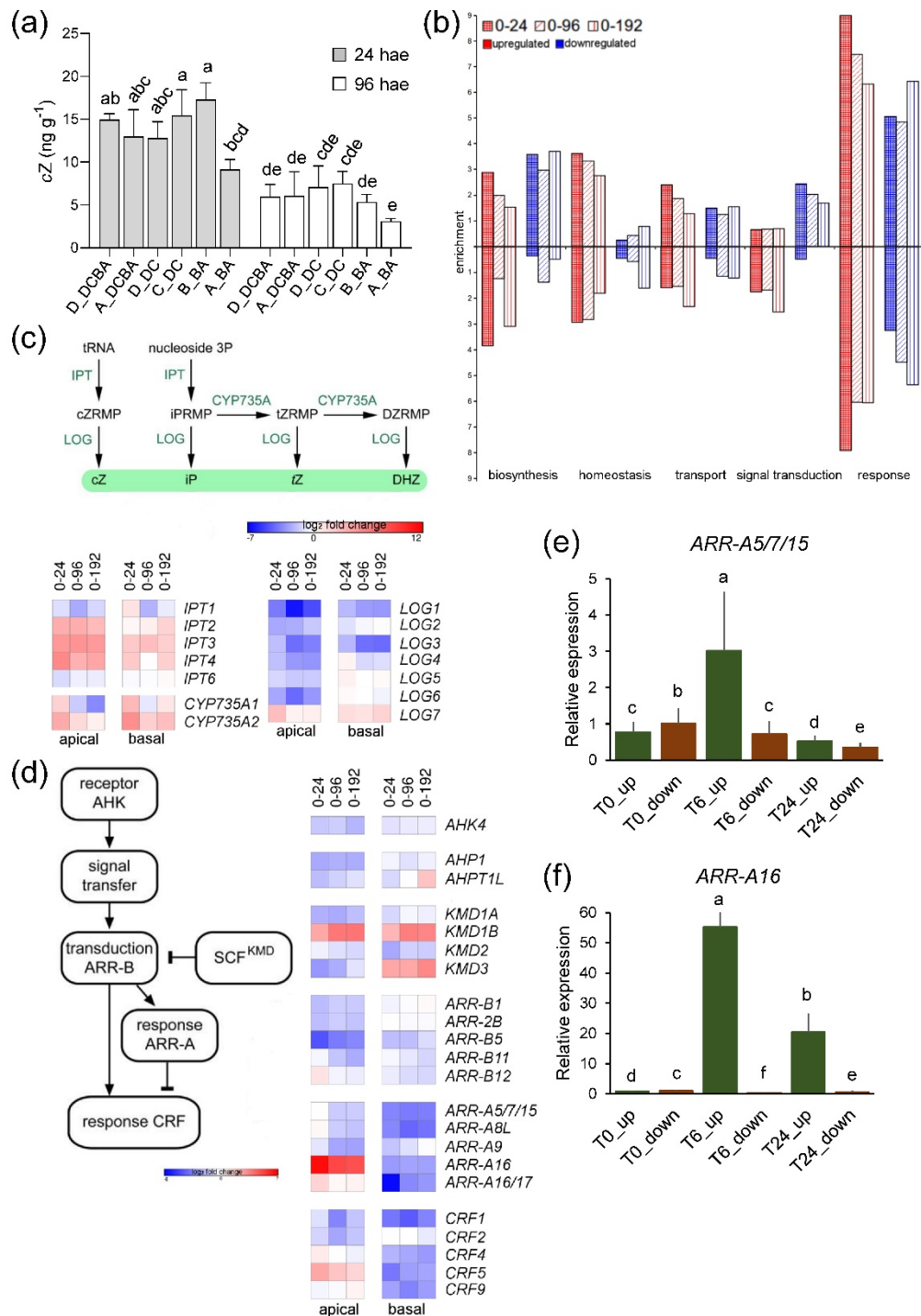
**Figure S2.** Endogenous levels of auxin metabolites during de novo organ formation. **(a)** Relationship between root area and shoot area at 21 dae. Numbers indicate Person's correlation coefficient in the studied samples. **(b)** Enrichment of DEGs in different auxin subcategories (see **Materials and Methods**). **(c-f)** Accumulation of auxin metabolites during de novo organ formation: **(c)** Tryptophan (Trp), **(d)** indole-3-methanol (IMet), **(e)** oxyndole-3-acetic acid (oxIAA), and **(f)** indole-3-acetyl-L-isoleucine (IAA-Ile). **(g)** Endogenous levels of IAA-Ile at 24 and 96 hae in apical (D) and basal (A) regions of whole (DCBA) or half-sectioned (DC and BA) hypocotyl explants. Different letters in c-g indicate significant differences (p-value < 0.001, otherwise indicated) between samples.

**Figure S3**



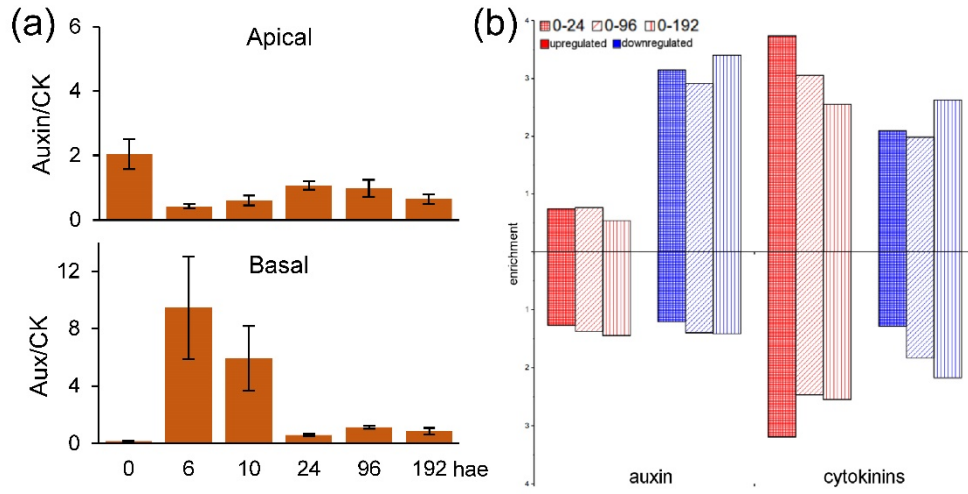
**Figure S3.** Auxin regulation during de novo organ formation (cont.). **(a)** AR emergence of whole hypocotyl explants in response to the indicated treatment; Kyn: 25  $\mu$ M L-kynurenine added to the growing medium. **(b)** Rooting capacity of apical hypocotyl explants at 17 dae. **(c)** Shoot regeneration stages of 'Micro-Tom' explants at 17 dae. Explants in b, c were continuously incubated with 20  $\mu$ M auxinole (Axl20), 50  $\mu$ M auxinole (Axl50), 50  $\mu$ M yucasin DF (YDF), or 50  $\mu$ M auxinole and 50  $\mu$ M yucasin DF. Different letters in b, c indicate significant differences (p-value < 0.001) between treatments.

**Figure S4**



**Figure S4.** Regulation of CK pathway genes during de novo organ formation. **(a)** Endogenous levels of cZ at 24 and 96 hae in apical (D) and basal (A) regions of whole (DCBA) or half-sectioned (DC and BA) hypocotyl explants. **(b)** Enrichment of DEGs in different CK subcategories. Expression values of DEGs were in log<sub>2</sub> fold change relative to 0 hae according to the scale bars in figure (FDR < 0.01). **(c)** Schematic diagram of CK biosynthesis and DEGs found in this pathway. **(d)** Schematic diagram of CK transduction pathway and DEGs found in this pathway. **(e-f)** Relative expression of *ARR-A5/7/15* (e) and *ARR-A16* (f) at 0, 6 and 24 hae in apical (green bars) and basal (brown bars) regions of the hypocotyl. Different letters in e, f indicate significant differences (p-value < 0.001) between samples.

**Figure S5**



**Figure S5.** Auxin-to-CK ratio regulates de novo organ formation (cont.). **(a)** IAA-to-CK ratio in the apical (D) and the basal (A) region of whole (DCBA) hypocotyl explants during the studied time course. **(b)** Enrichment of DEGs in different auxin and CK subcategories (see **Materials and Methods**).

**Table S1.** Raw data for hormonal measurements (ng/mL). **(a)** Results from whole hypocotyl explants (DCBA fragments). **(b)** Results from half-sectioned hypocotyl explants (DC and BA fragments).

**Table S2.** Annotation and classification of genes associated to auxin biosynthesis, homeostasis, transport, and response in tomato. SolycID and ITAG4.0 annotation were retrieved from SolGenomics (<https://solgenomics.net/>). Putative *Arabidopsis thaliana* orthologs were identified from the Ensembl Plants database using BioMart. Legend: %id. Target *A. thaliana*, percentage of identity of target *A. thaliana* gene identical to tomato gene; %id. tomato gene, percentage of identity of target tomato gene identical to *A. thaliana* gene; confidence, orthology confidence score from the Ensembl Plants database. KEGG identifiers and annotations were retrieved using an RBBH strategy (see **Materials and Methods**).

**Table S3.** Annotation and classification of genes associated to CK biosynthesis, homeostasis, transport, and response in tomato. See legend from **Table S2**.

**Table S4.** Primers for qRT-PCR validation of RNA-seq data. Gene name and gene identifier in ITAG4.0 annotation (Solyc ID) are included. Nucleotide sequence of the forward and reverse primers and amplicon size (cDNA) are indicated.