SUPPLEMENTAL FIGURES

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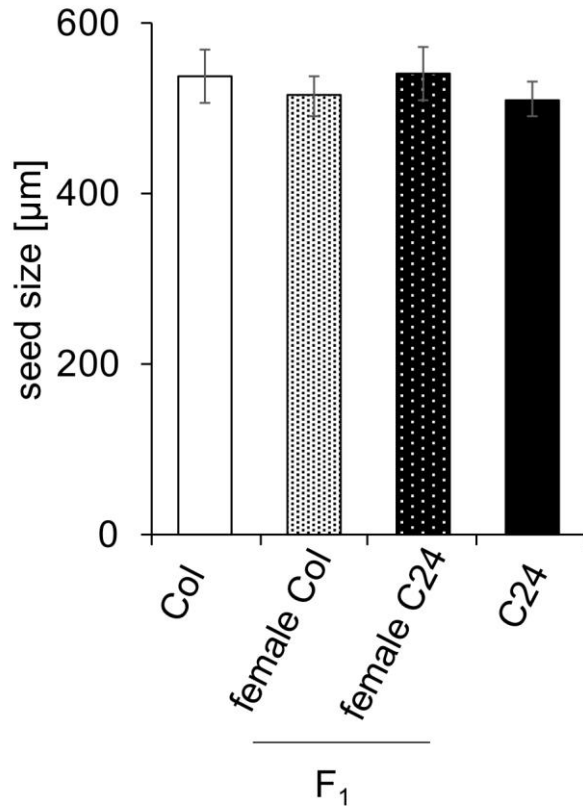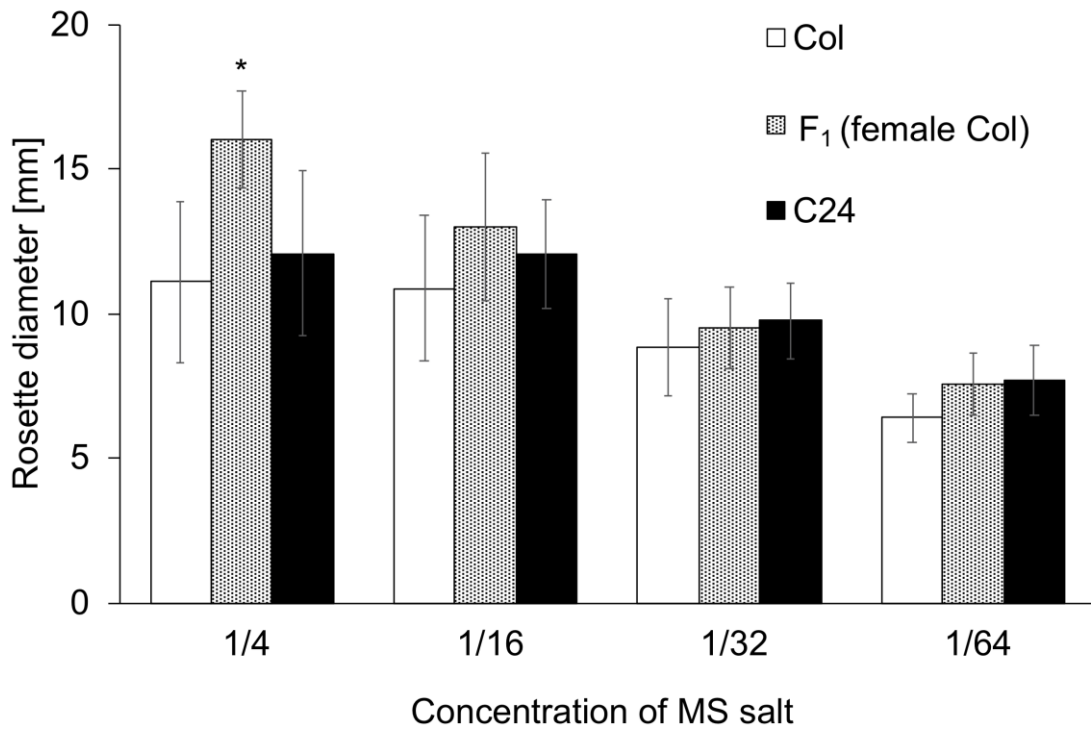5 **Supplementary Figure S1. The average seed sizes of Col, C24 and their F$_1$ hybrids.**

6 The major axis of each seed was measured using ImageJ software. $n \geq 53$.

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14 **Supplementary Figure S2. Rosette diameter of F$_1$ hybrid and parents in N-limited**

15 **condition**. MS salt concentrations were modified for each condition. Rosette diameters

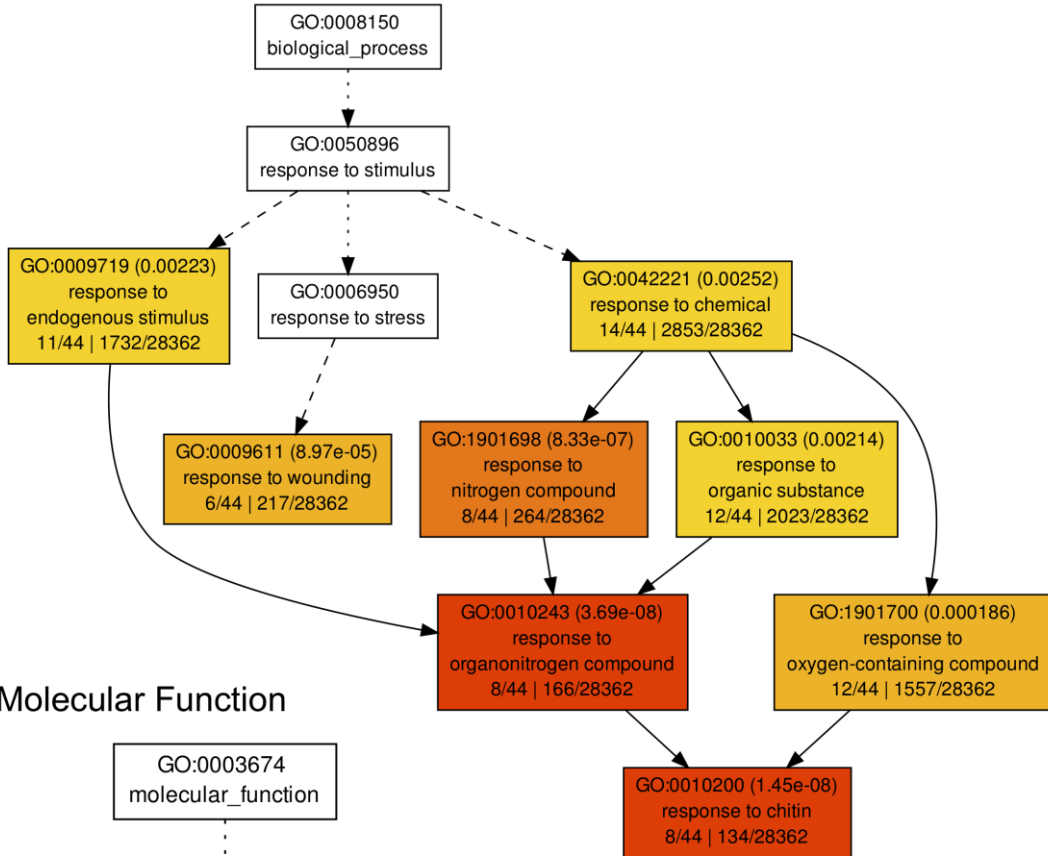16 of Col, C24, and F$_1$ hybrid (female Col) plants were measured at 14 DAS. $n \geq 13$.

17 Asterisks (*) indicate significant differences between F$_1$ hybrid values and MPV based

18 on Student's *t*-test ($p < 0.05$).
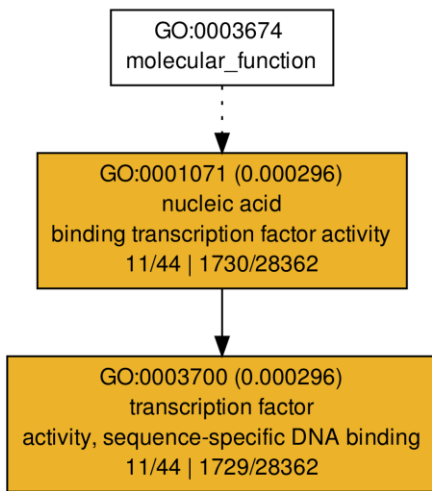
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A: Biological Process

B: Molecular Function

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Supplementary Figure S3. Overview of singular enrichment analysis (SEA) of the

up-regulated transcript profiles in F₁ hybrid compared with parents (log₂FC ≥

25   **0.58, FDR < 0.05).** SEA was performed using agriGO (bioinfo.cau.edu.cn/agriGO/). A:

26   The "Biological Process" for each GO term was used for the hierarchical graph. B:

27   "Molecular Function" of the GO term was used for the hierarchical graph. Solid arrows

28   represent relationships between the two enriched GO terms. Dashed arrows represent

29   relationships between the enriched and un-enriched terms. Dotted arrows represent

30   relationships between un-enriched terms. Significantly enriched GO terms are colored

31   on a spectrum from white to red according to their corresponding FDR adjusted p-value.
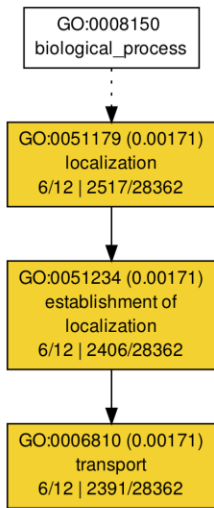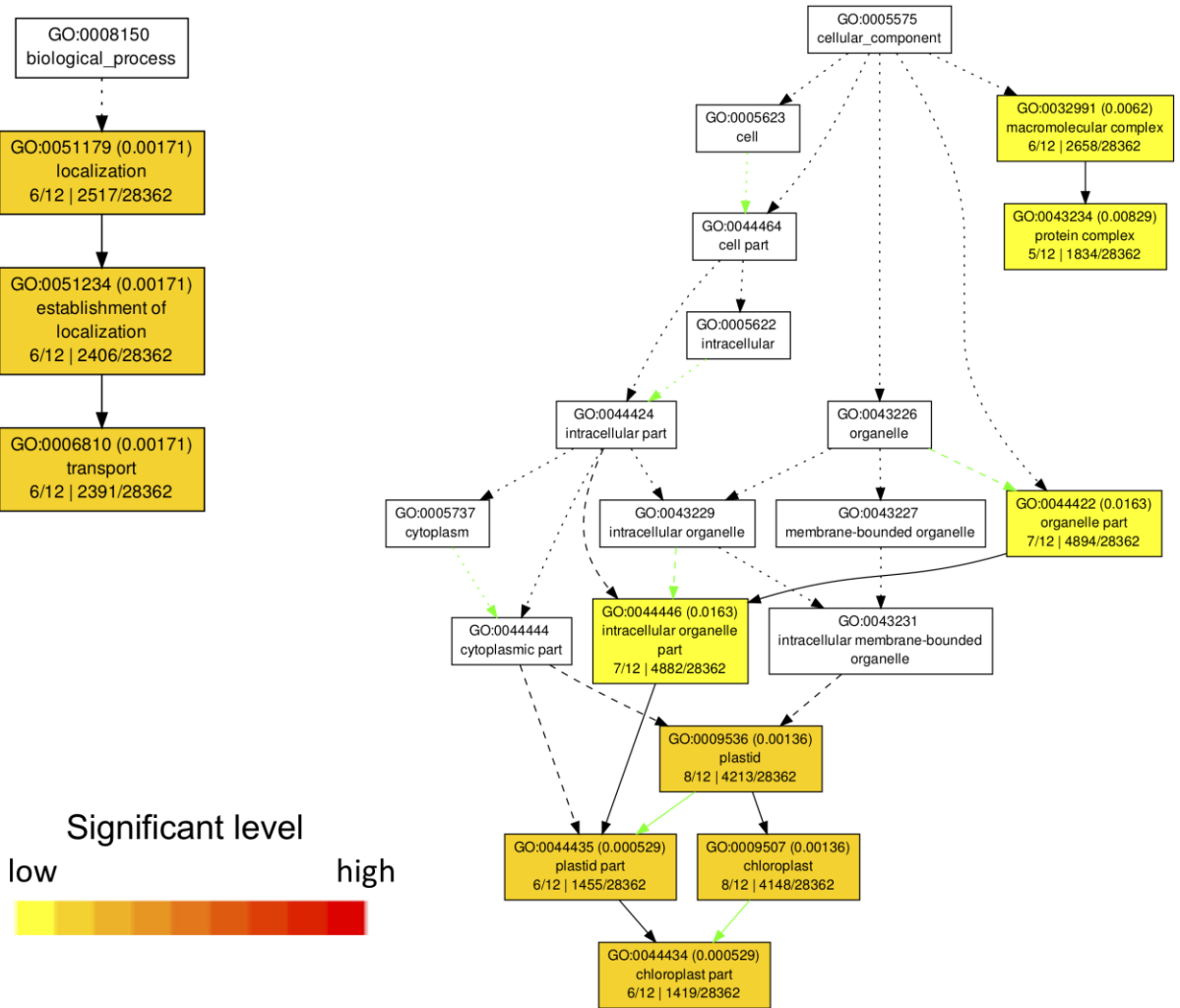
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A: Biological Process

GO:0008150
biological_process

GO:0051179 (0.00171)
localization
6/12 | 2517/28362

GO:0051234 (0.00171)
establishment of
localization
6/12 | 2406/28362

GO:0006810 (0.00171)
transport
6/12 | 2391/28362

B: Cellular Component

GO:0005575
cellular_component

GO:0005623
cell

GO:0032991 (0.0062)
macromolecular complex
6/12 | 2658/28362

GO:0043234 (0.00829)
protein complex
5/12 | 1834/28362

GO:0044464
cell part

GO:0005622
intracellular

GO:0044424
intracellular part

GO:0043226
organelle

GO:0005737
cytoplasm

GO:0043229
intracellular organelle

GO:0043227
membrane-bounded organelle

GO:0044422 (0.0163)
organelle part
7/12 | 4894/28362

GO:0044444
cytoplasmic part

GO:0044446 (0.0163)
intracellular organelle
part
7/12 | 4882/28362

GO:0043231
intracellular membrane-bounded
organelle

GO:0009536 (0.00136)
plastid
8/12 | 4213/28362

GO:0044435 (0.000529)
plastid part
6/12 | 1455/28362

GO:0009507 (0.00136)
chloroplast
8/12 | 4148/28362

GO:0044434 (0.000529)
chloroplast part
6/12 | 1419/28362

Significant level

low — high

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Supplementary Figure S4. Overview of singular enrichment analysis (SEA) of down-regulated transcript profiles in F_1 hybrid compared with parents ($log_2FC \leqq$ -0.58, FDR<0.05). SEA was performed using agriGO (bioinfo.cau.edu.cn/agriGO/). A:

46   The "Biological Process" for each GO term was used for the hierarchical graph. B:

47   "Cellular Component" of the GO term was used for the hierarchical graph. Solid arrows

48   represent relationships between two enriched GO terms. Dashed arrows represent

49   relationships between enriched and un-enriched terms. Dotted arrows represent

50   relationships between un-enriched terms. Green dotted arrows represent negative

51   regulation. Significantly enriched GO terms are colored on a spectrum from white to red

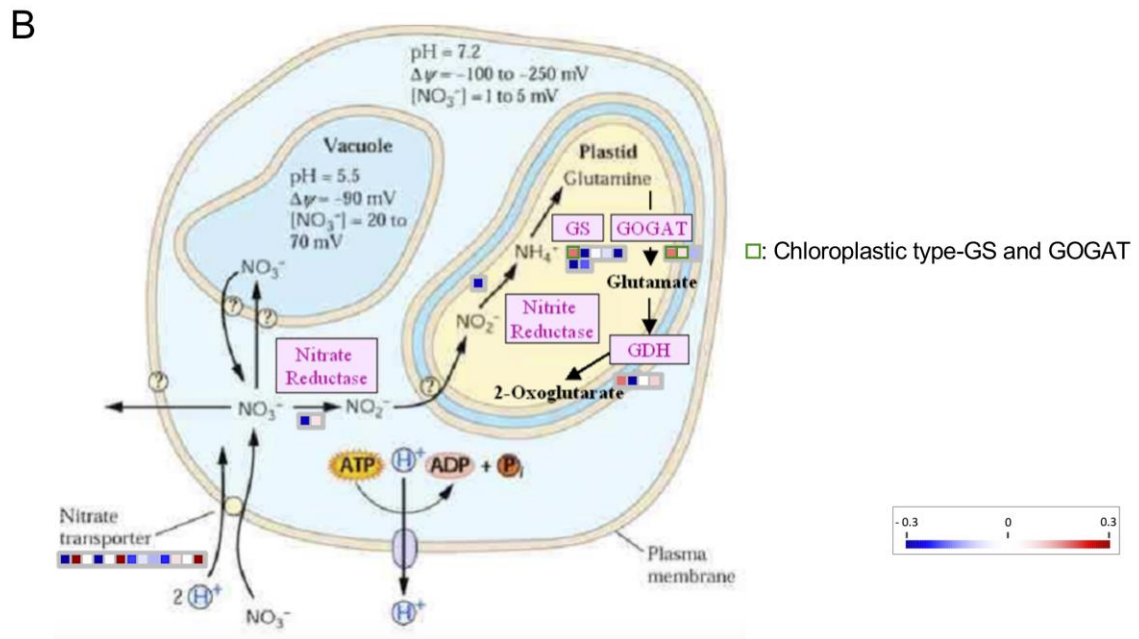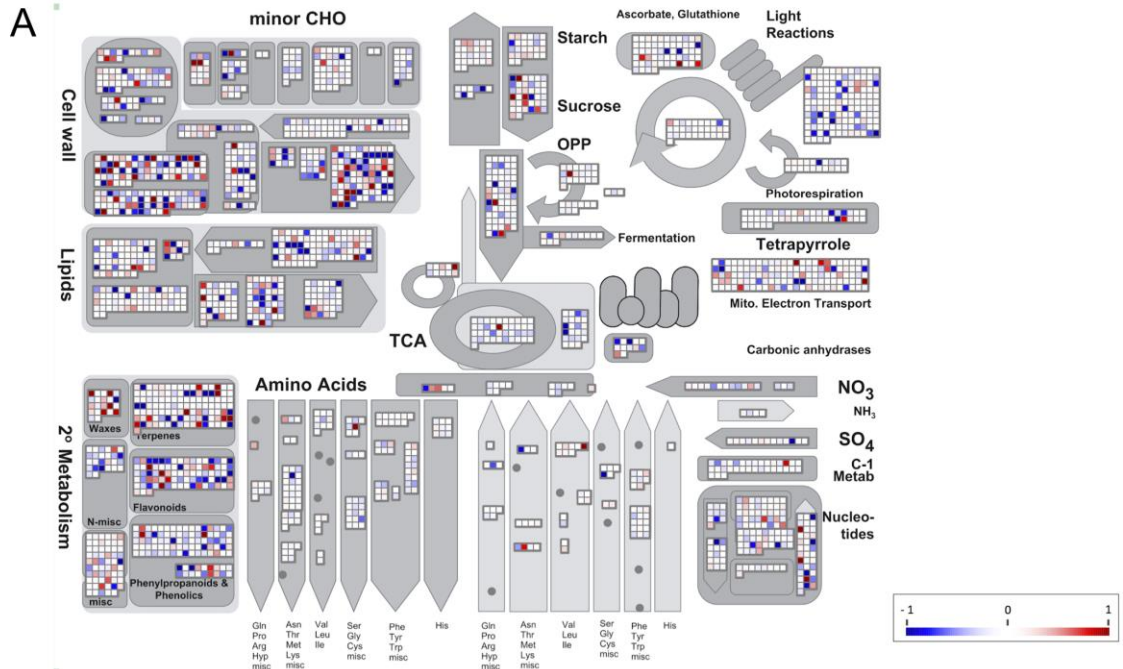52   according to their corresponding FDR adjusted p-values.

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Supplementary Figure S5. Overview of metabolic transcript differences for whole

rosette samples of F_1 hybrid compared with parental plants generated using the

66   **MapMan tool.** Differences in F_1 hybrid transcript levels vs MPV based on probe sets

67   classified as "metabolism overview" (A) and "N-metabolism" (B) are shown. Red and

68   blue colors indicate that transcript levels are increased or decreased, respectively, in F_1

69   hybrid compared to parents. All values indicate $\log_2$ ratios (F_1/MPV) at 15 DAS

70   produced using the Arabidopsis ATH1 Array. The MapMan tool was used for

71   visualization of gene expression differences between F_1 hybrid transcript levels and

72   MPV. The number of biological replicates is three.