

Supplementary Figure

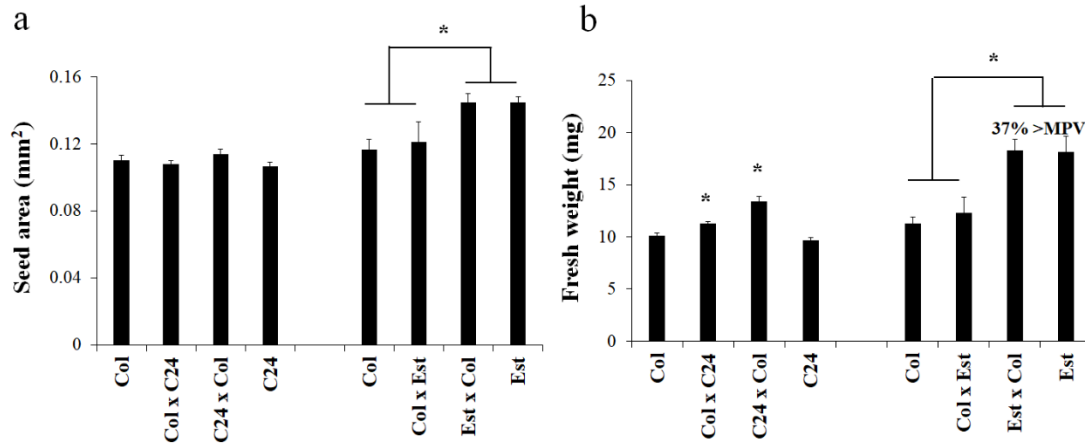


Figure S1. Seed area and fresh weight of C24 and Est crossed to Col. (a) Seed area and (b) fresh weight of Col/C24 and Col/Est. Seed area data were an average of at least 100 seeds collected from at least five individual plants $\pm$ SE. Fresh weight data collected in 15 DAS ($n \geq 12$), mg/plant $\pm$ SE; SE, standard error. Significant value compared with BPV in Col/C24 combination and grouped comparison on Col/Est combination (* $P < 0.001$ by Student's t -test).

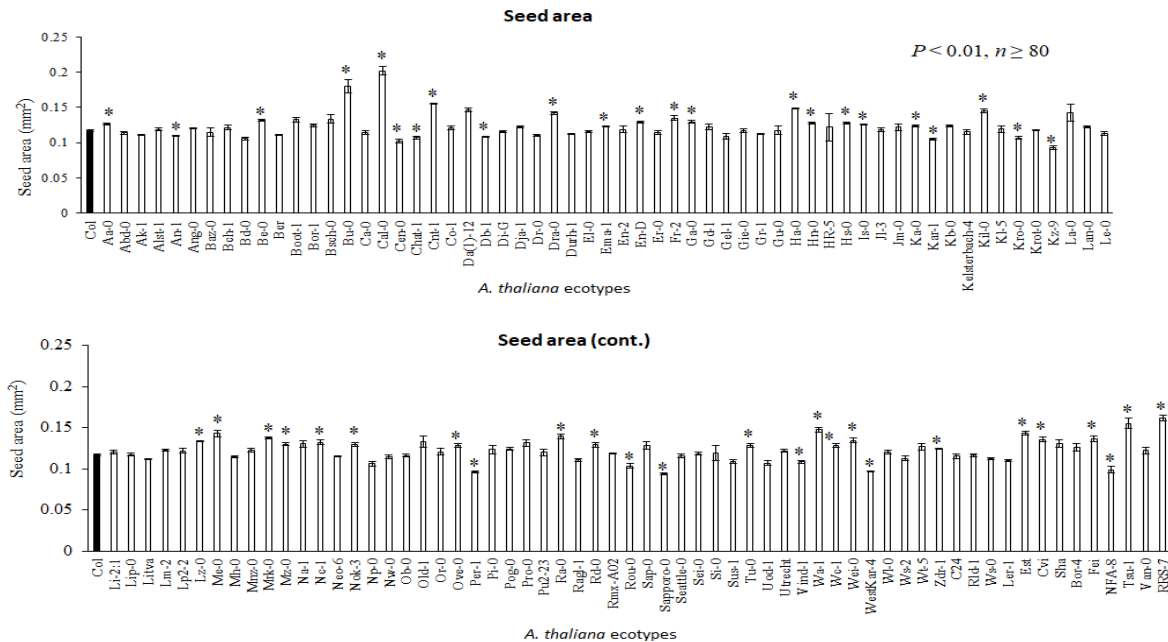
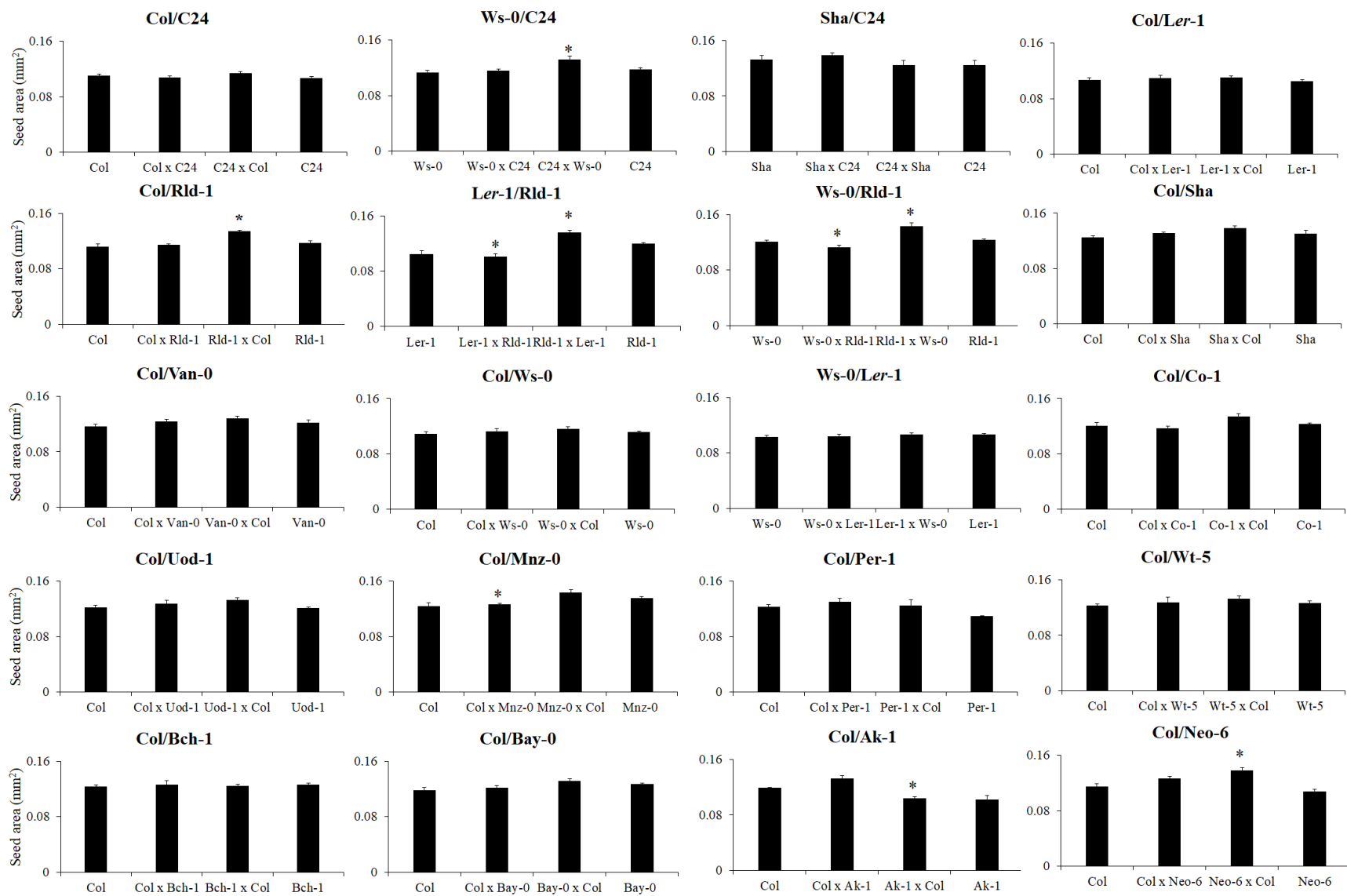


Figure S2. Seed area of Arabidopsis accessions.

Data were average $\pm$ SE; SE, standard error ($n \geq 80$ seeds of three individuals). The black bar is data of Col as the control line for comparison test (*, $P < 0.01$ by Student's t -test).



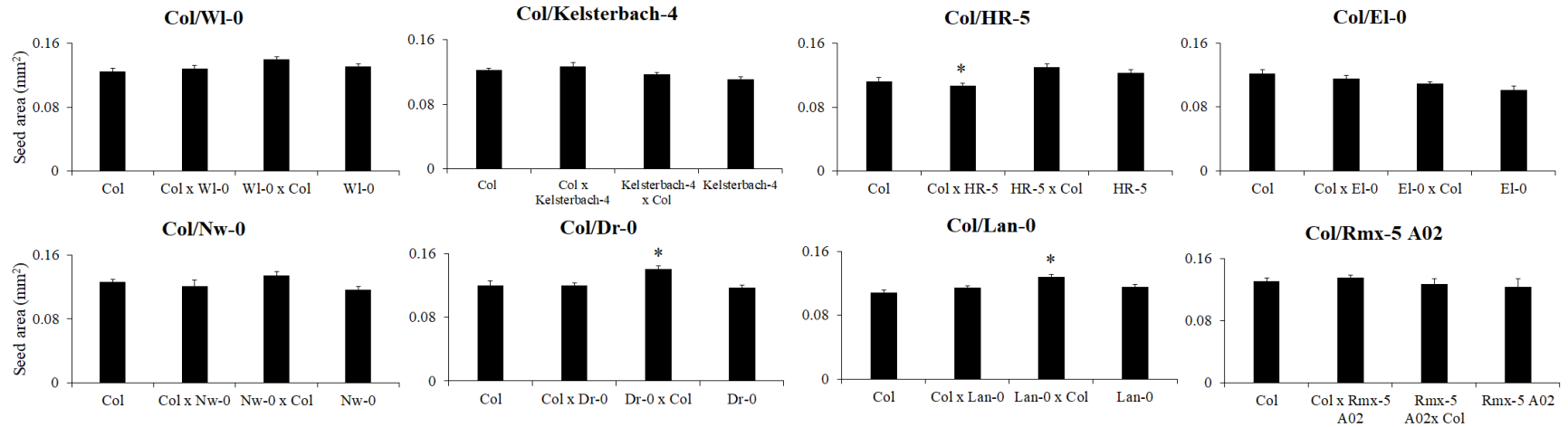
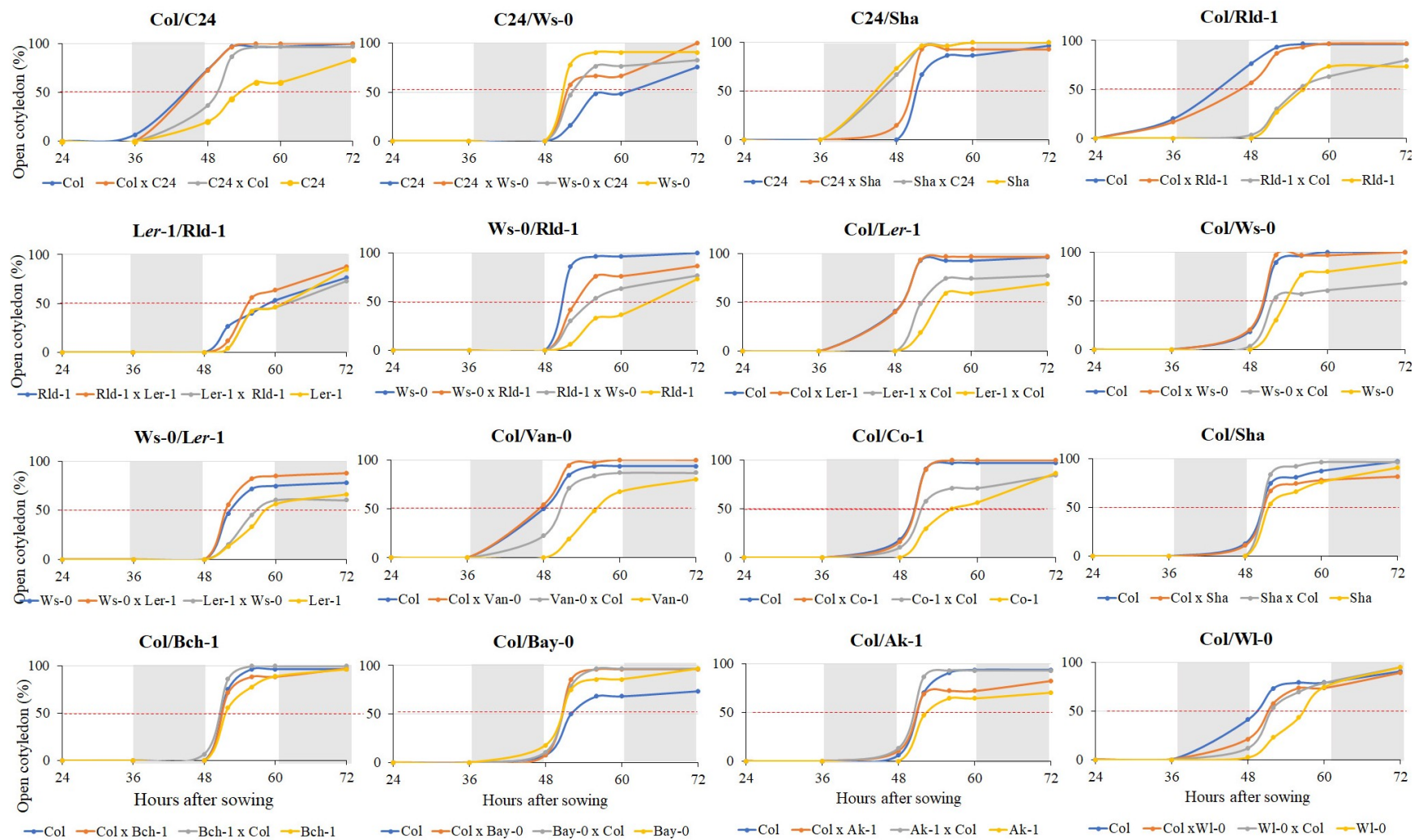


Figure S3. Measurements of seed area of differential parental combinations.

Statistical comparisons between two reciprocal hybrids and their BPV with $P < 0.01$ (Student's t -test), $n \geq 100$ seeds collected at least three individual plants. All error bars are standard error.



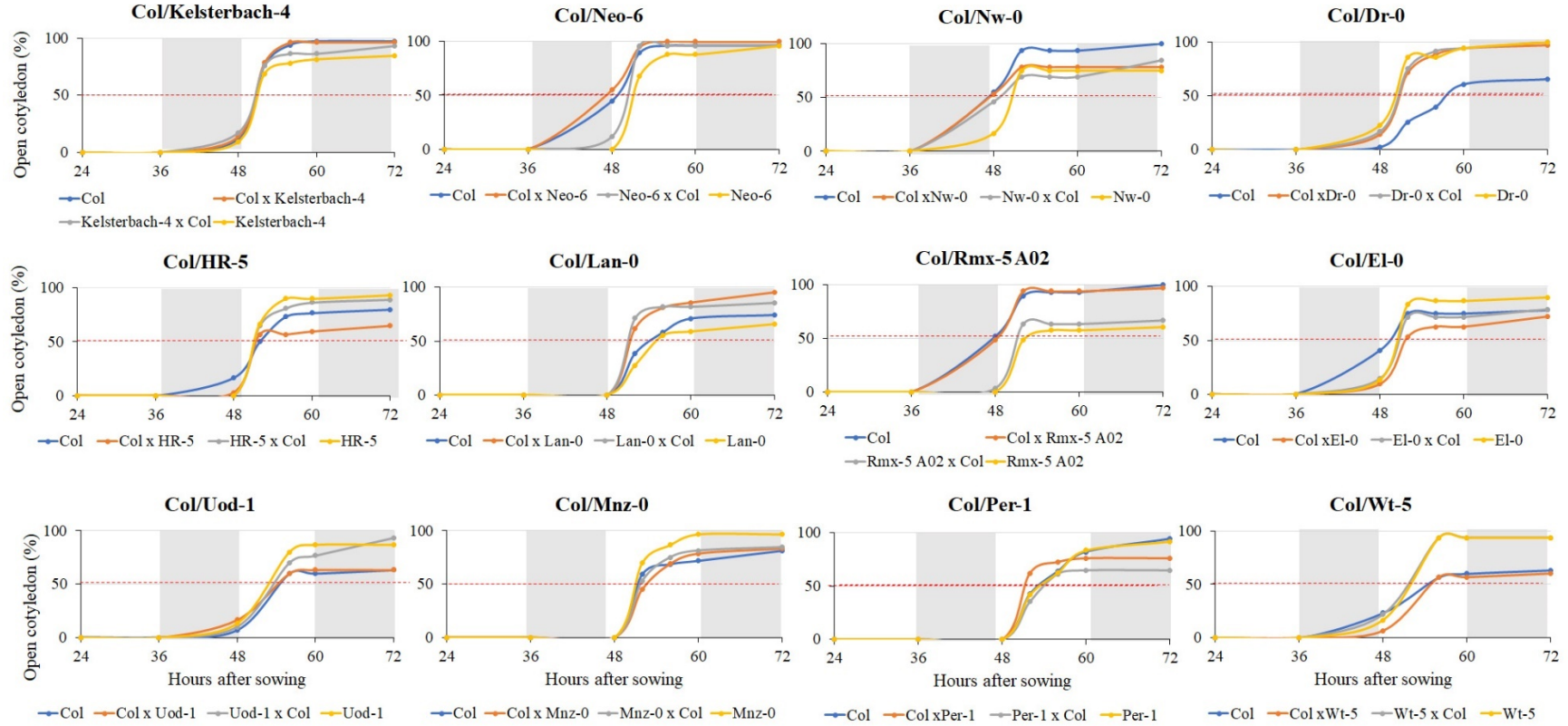
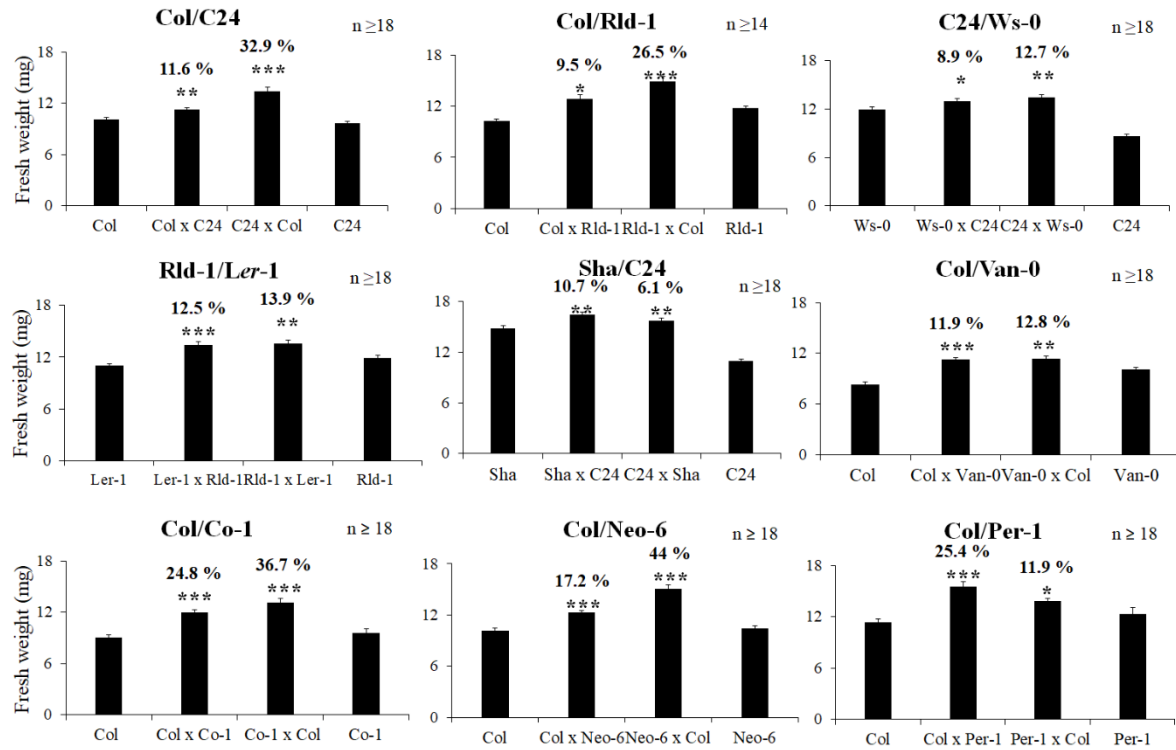


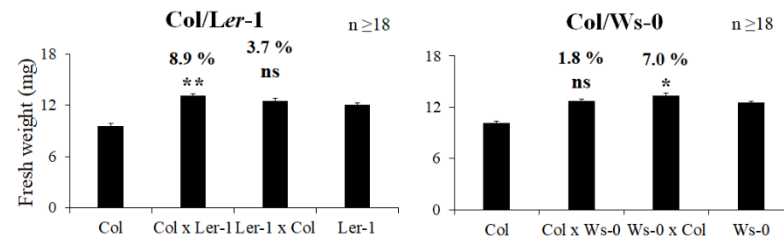
Figure S4. Seed germination time of intraspecific hybrids and their parents.

The percentage of fully open cotyledons was tracked between 24 and 72 HAS. Gray blocks represent the dark phase of a day. Red horizontal lines mean seed germination time (the time of 50% fully open cotyledons).

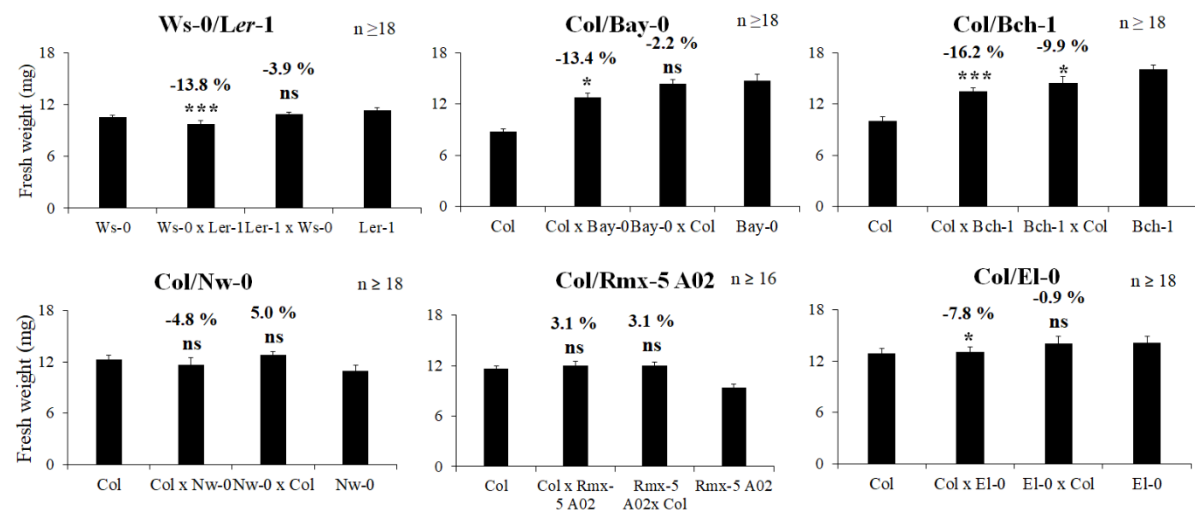
a. High heterosis



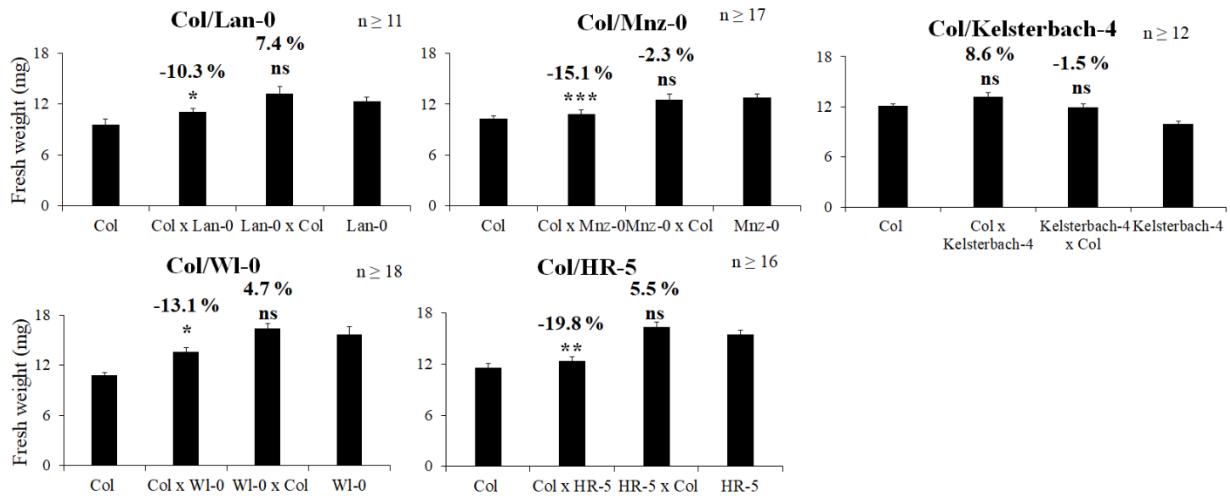
b. Low heterosis



c. No heterosis



c. No heterosis (Cont.)



d. Unclassified combinations

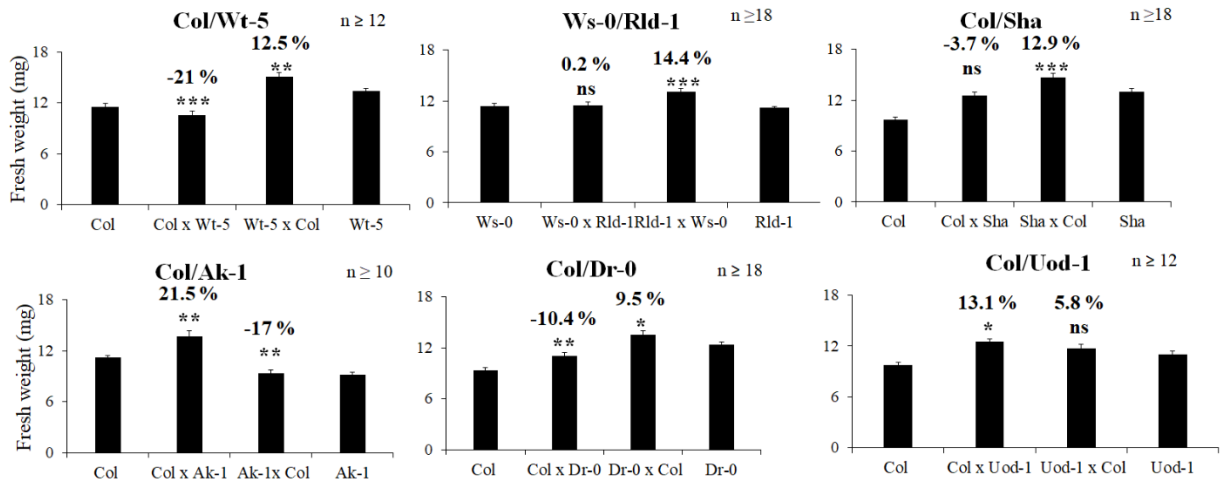
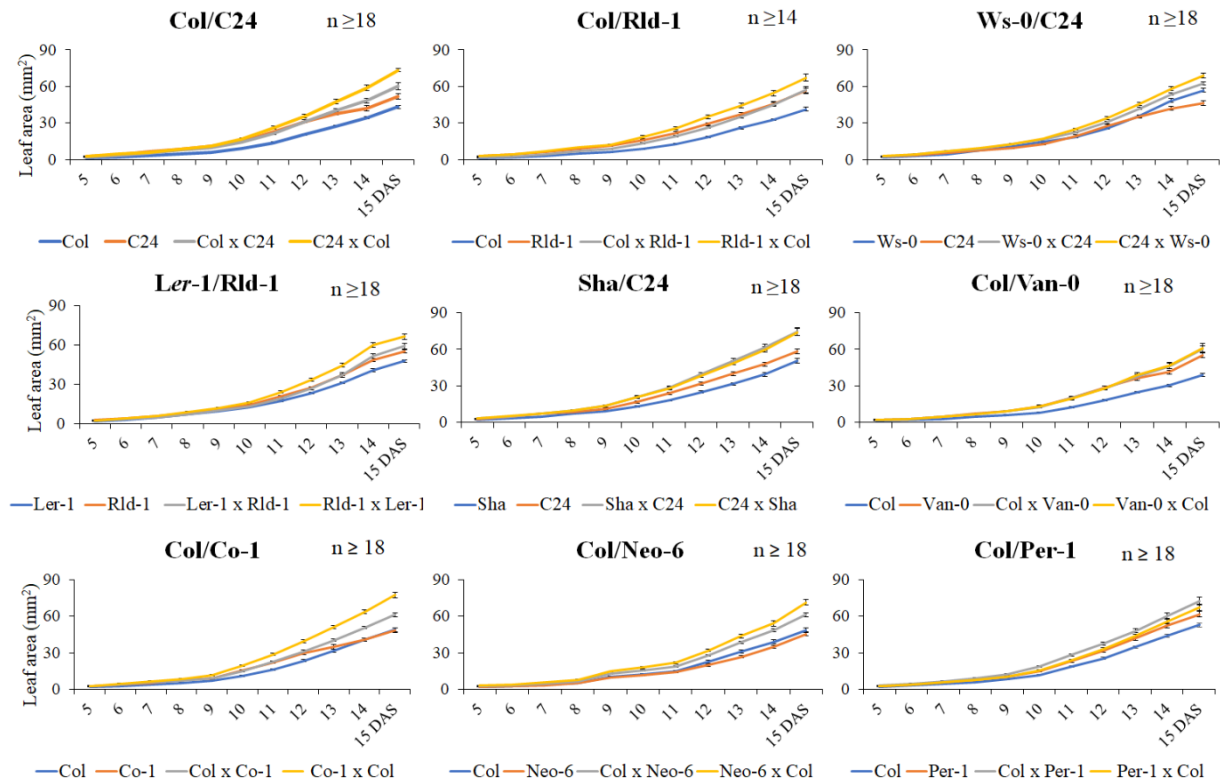


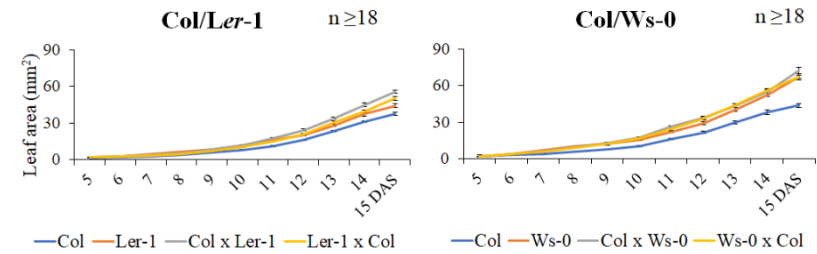
Figure S5. Fresh weight of 28 hybrid combinations at 15 DAS.

High heterosis (a), low heterosis (b), no heterosis (c), and unclassified combinations (d). Numbers above each hybrid's bar represents a level from BPV. Black asterisks show above BPV; ns: not significant, * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, Student's t -test. n represents in detail the number of plants collected from each combination. Data indicate the average and error bar (standard error).

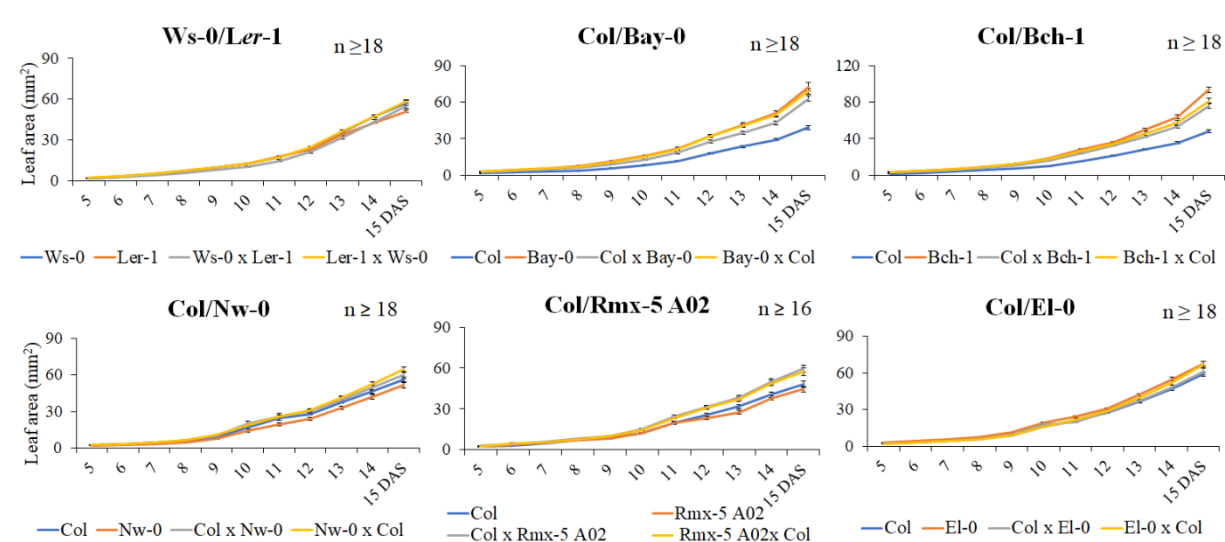
a. High heterosis



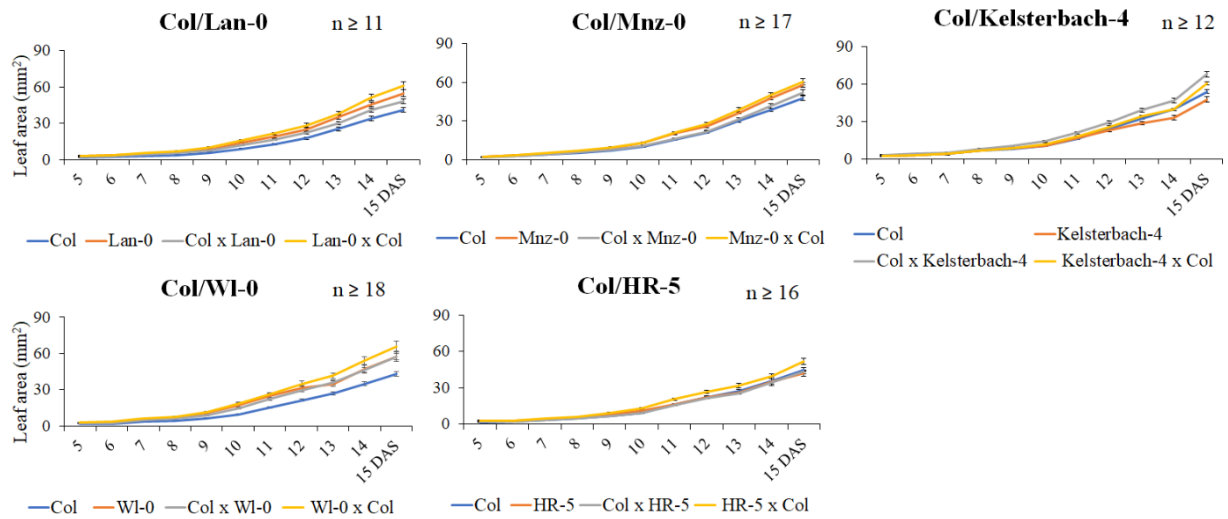
b. Low heterosis



c. No heterosis



c. No heterosis (Cont.)



d. Unclassified combinations

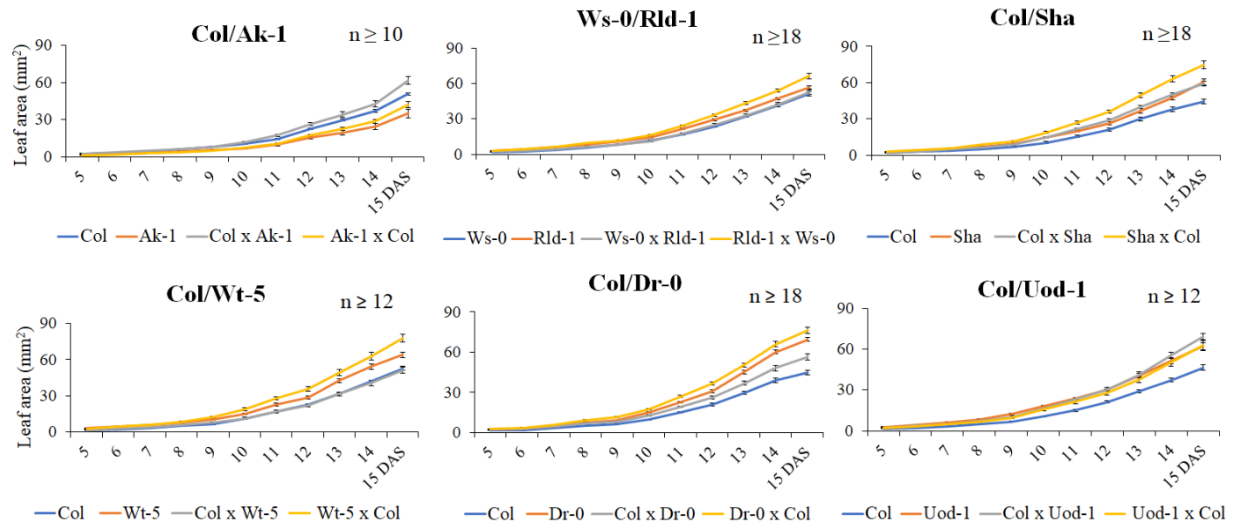


Figure S6. Leaf area of 28 hybrid combinations at 15 DAS. High heterosis (a), low heterosis (b), no heterosis (c), and unclassified combinations (d). n represents the number of plants collected from each combination. Data indicate average and error bar standard error.

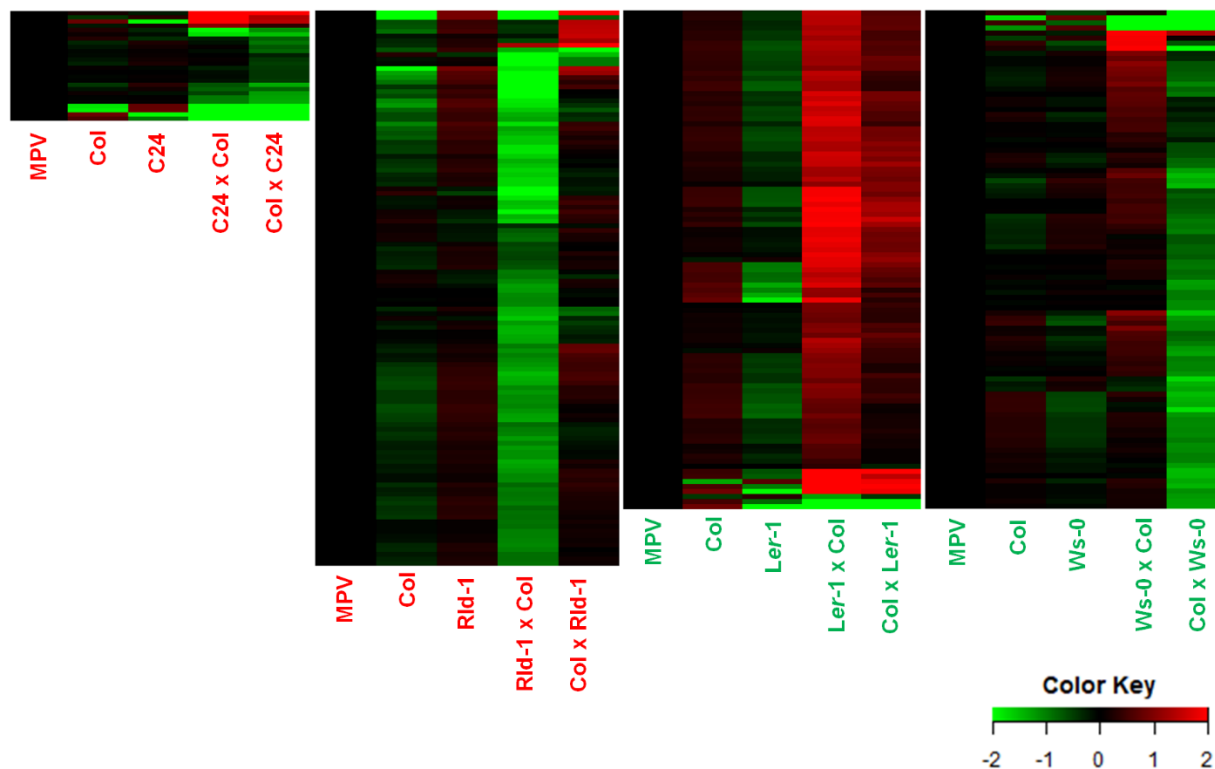


Figure S7. Heat map represents significantly altered metabolites in at least one reciprocal F₁ hybrid from combinations.

Significant comparisons were performed by multiple *t*-test (FDR < 0.05), increased/decreased metabolites compared with both parents. Differences of red/green colors exhibit the log₂ fold change (up/down) normalized to MPV (control: MPV as 0 in log₂ fold change). Red/green words mean the name of high/low-biomass heterosis.

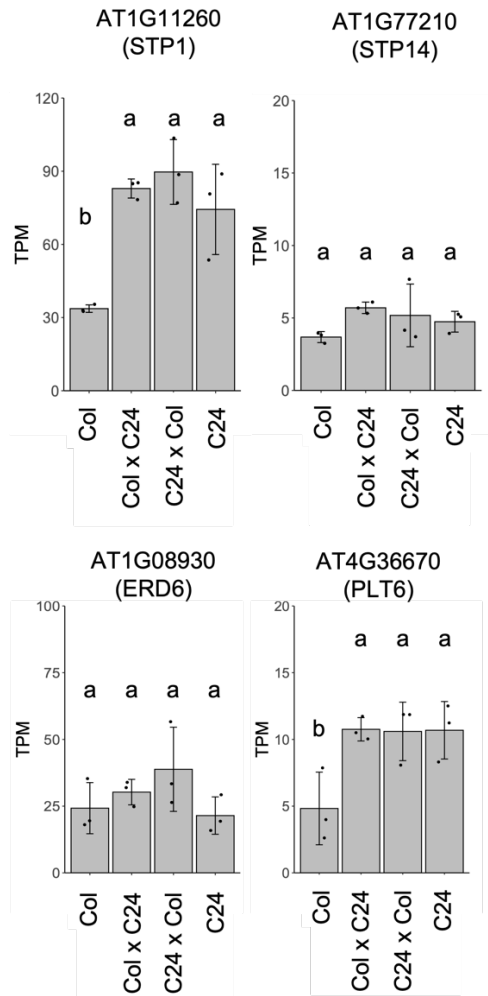
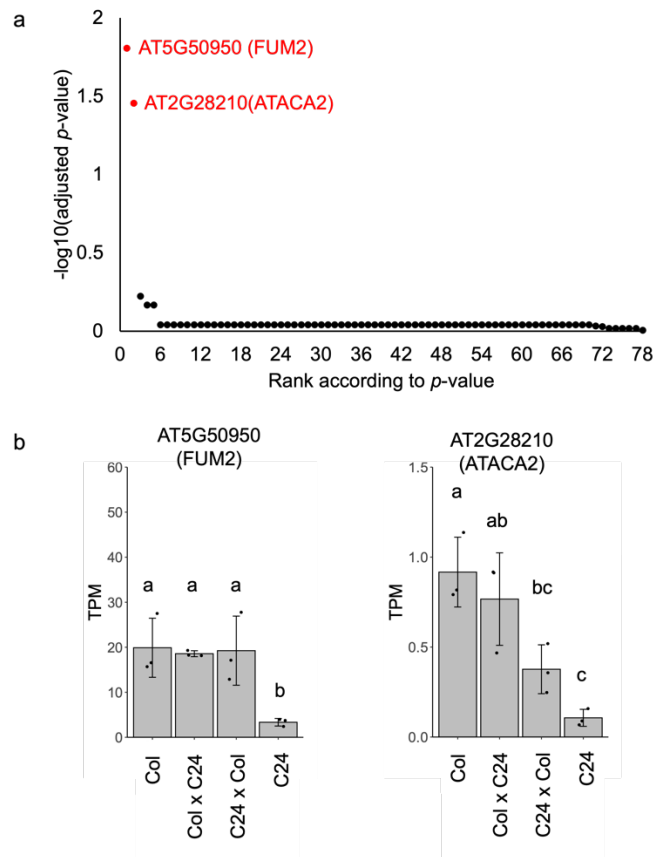


Figure S8. Expression pattern of sugar metabolism-related genes in Col, C24, and their reciprocal F₁ hybrids

Expression patterns of sugar transporters mentioned in Groszmann et al. 2015. Different letters indicate significant differences based on Tukey's test ($p < 0.05$). Error bars represent the SD of three biological replicates.

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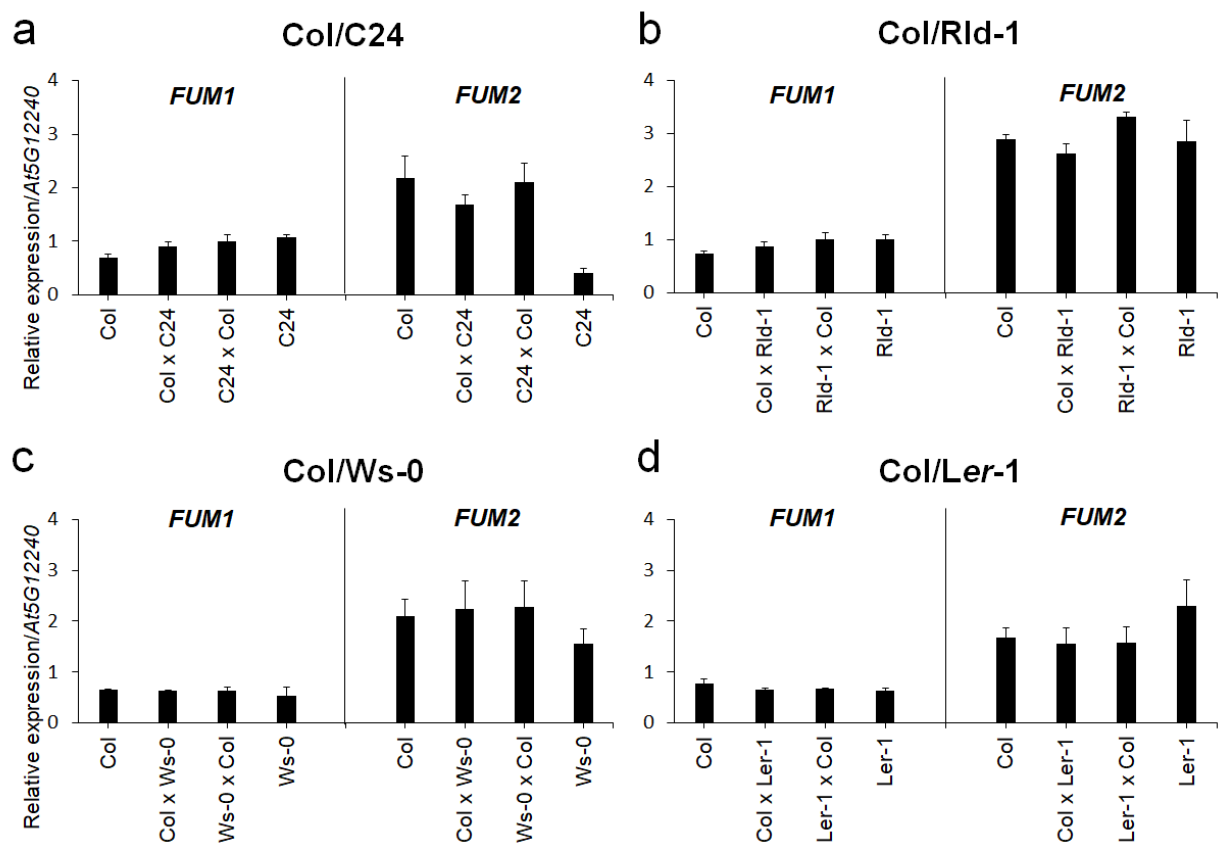
58 **Figure S9.** Expression patterns of genes related to TCA cycle in Col, C24 and their reciprocal F₁ hybrids

59 a: Overview of statistical analysis in TCA cycle-related genes. One-way ANOVA were performed among
 60 Col, C24, and their F₁ hybrids to calculate raw p -value. FDR-adjusted p -values were calculated by R
 61 software.

62 b: Differentially expressed genes related to TCA cycle. Different letters indicate significant differences
 63 based on Tukey's test ($p < 0.05$). Error bars represent the SD of three biological replicates.

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68 **Figure S10.** Gene expression of *FUM1* and *FUM2* in the different combinations.

69 The hybrids and parents of (a) Col/C24, (b) Col/Rld-1, (c) Col/Ws-0, and (d) Col/Ler-1 combination.

70 Data represent the average of three biological replicates and standard error.