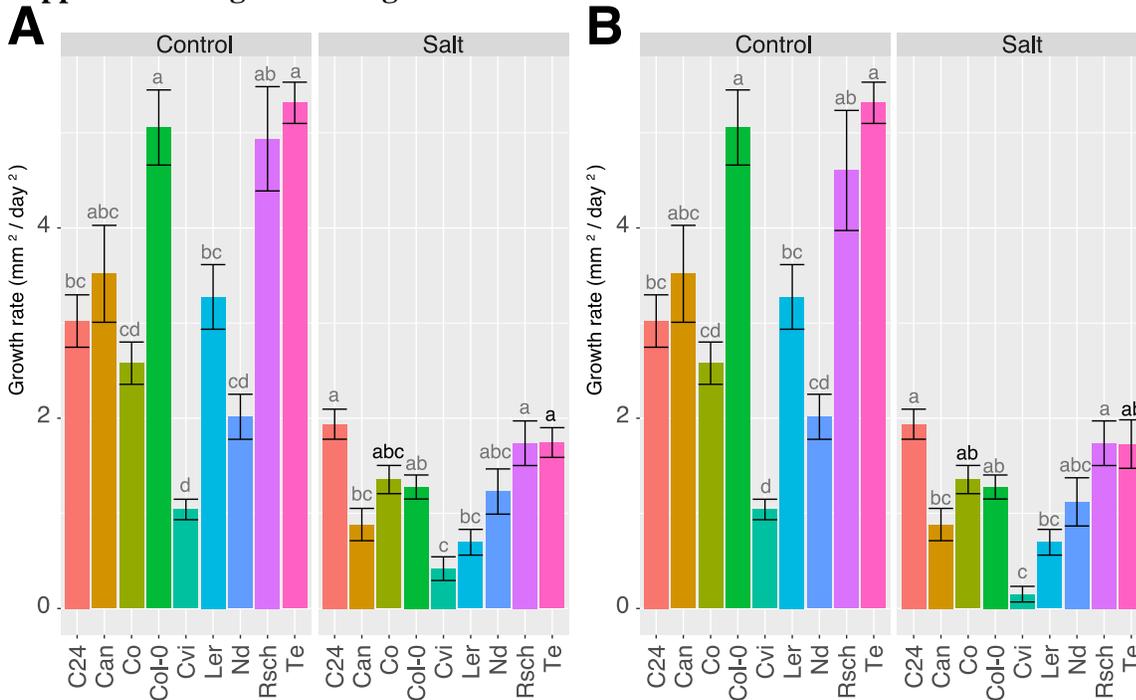
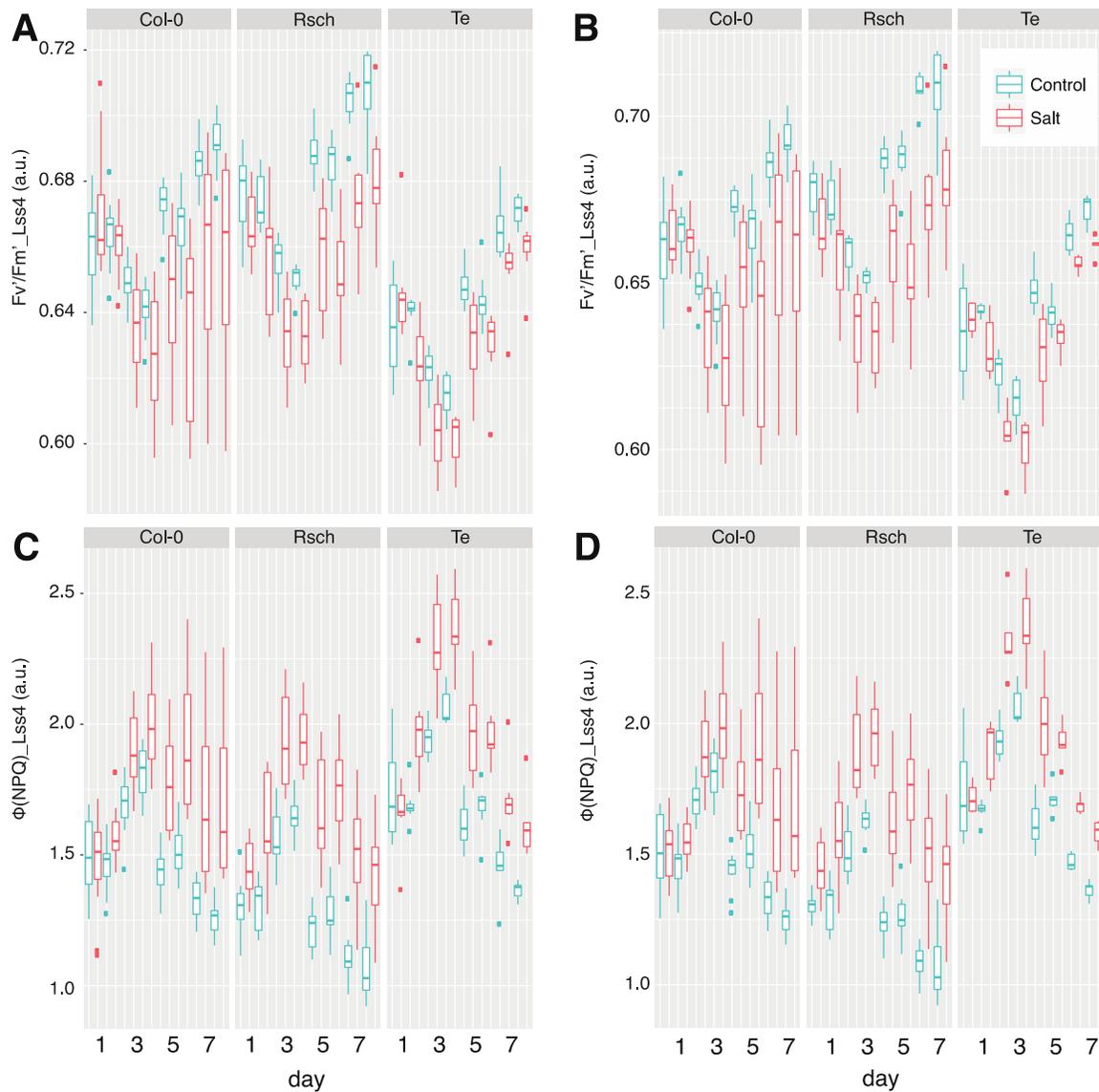


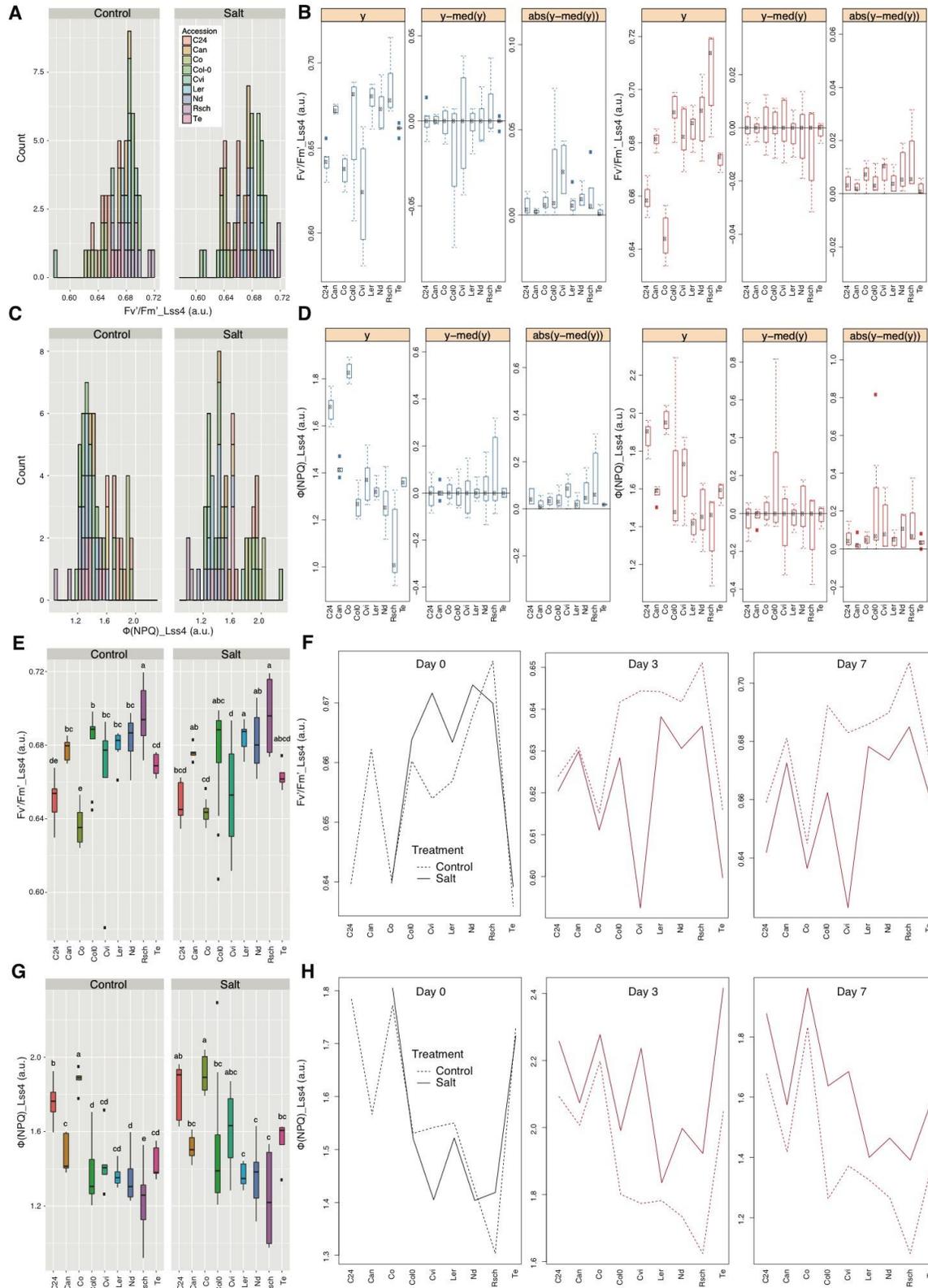
1 **Supplemental Figures & Legends:**



2
3 **Supplemental Figure S1. Effect of outliers identified using R^2 on the differences observed**
4 **between genotypes.** The summary of the growth dynamics among predefined groups was
5 calculated using (A) curated and (B) non-curated data. The ANOVA test, complemented by
6 Tukey's HSD pairwise test, was used to examine significant differences between pre-selected
7 groups. The bars represent the average growth rate fitted with a quadratic function, calculated
8 from 9 replicates. The error bars represent the standard error. The letters indicate significantly
9 different groups, as identified by Tukey's HSD pairwise test, with a p-value threshold of 0.05.
10 The data were curated based on the fit of the quadratic function to the observed data. The
11 samples with R^2 values below 0.7 were eliminated from the dataset.
12
13



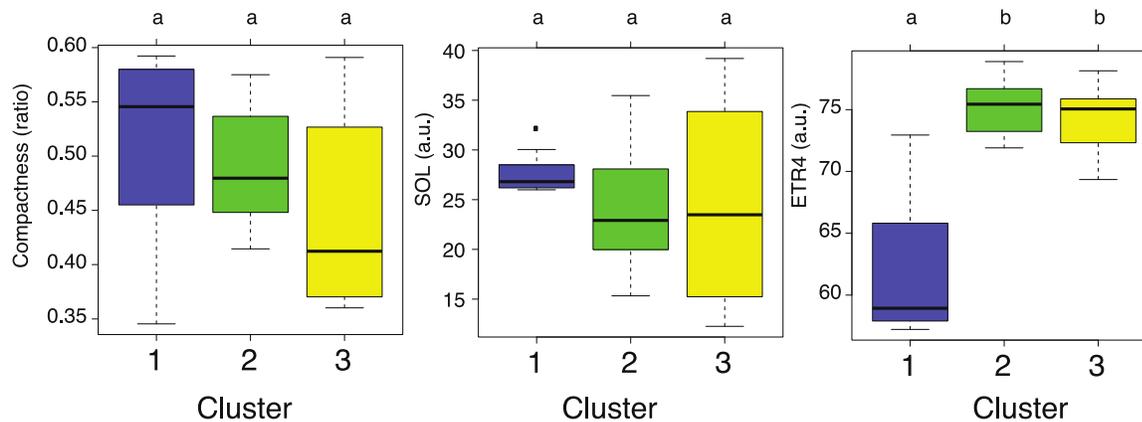
14
 15 **Supplemental Figure S2. Data curation assisted with visual inspection.** The box plots
 16 represent the maximum quantum yield in a light-adapted state (F_v'/F_m') both (A) before and (B)
 17 after data curation, and non-photochemical quenching at the highest light intensity measured
 18 [$\Phi(NPQ)$] at the highest photon irradiance ($L_{ss4} = 440 \mu\text{mol m}^{-2} \text{s}^{-1}$) using arbitrary units (a.u.)
 19 both (C) before and (D) after data curation. The “non-curated data” (A and C) were curated
 20 using the quadratic fit (samples with R^2 values below 0.7 were removed). For the “curated data”
 21 (B and D), the outliers were identified and removed using the $1.5 \cdot \text{IQR}$ method on all the
 22 measured traits, with at least twelve outlying traits necessary to qualify a sample as an outlier.
 23 The changes in the photosynthetic traits of three studied accessions throughout time are
 24 presented using blue and red box plots, indicating the trait value under control and salt-stress
 25 conditions, respectively, both before (A and C) and after (B and D) the 28 samples identified as
 26 outliers were removed. The average number of replicates per genotype, condition and day is 9 in
 27 (A) and (C) and 6.74 in (B) and (D).
 28



29
 30 **Supplemental Figure S3. Hypothesis testing including assumptions for ANOVA.** MVA
 31 allows users to visually inspect the distribution of phenotypic data using histograms, and to test
 32 for a normal distribution using the Shapiro-Wilk test. (A) The histogram represents the number

33 of samples (y-axis) observed for maximum quantum yield under the light-adapted state
34 (F_v'/F_m') (x-axis) at the highest photon irradiance ($L_{ss4} = 440 \mu\text{mol m}^{-2} \text{s}^{-1}$) using arbitrary
35 units (a.u.) under control and salt-stress conditions (left and right panel, respectively), measured
36 seven days after applying the salt treatment. The values observed for different genotypes are
37 represented by different colors stacked on top of each other. The equal variance between the
38 samples was tested using both Levene's and Bartlett's tests, and **(B)** visually inspected using box
39 plots for the observed data (y), the subtracted median [$y - \text{med}(y)$] and the absolute deviation
40 from the median [$\text{abs}(y - \text{med}(y))$]. The blue and red box plots indicate the variance in
41 $F_v'/F_m'_{Lss4}$ between plants grown under control and salt-stress conditions, respectively. The
42 **(C)** normal distribution and **(D)** equal variance were also examined using histograms and box
43 plots, respectively, for non-photochemical quenching [$\Phi(\text{NPQ})$] at the highest photon irradiance
44 ($L_{ss4} = 440 \mu\text{mol m}^{-2} \text{s}^{-1}$) using arbitrary units (a.u.), also measured on the seventh day after salt
45 treatment. Significant differences among the predefined groups were tested using ANOVA and
46 Tukey's HSD pairwise tests for **(E)** $F_v'/F_m'_{Lss4}$ and **(F)** $\Phi(\text{NPQ})_{Lss4}$. The interaction
47 between two predefined factors (genotype and treatment) was tested using two-way ANOVA for
48 **(G)** $F_v'/F_m'_{Lss4}$ and **(H)** $\Phi(\text{NPQ})_{Lss4}$, and then visually represented using interaction plots
49 for data subsets of the measurements zero, three and seven days after treatment. The red lines
50 represent a significant interaction between genotype and treatment, as identified by two-way
51 ANOVA with a p-value threshold of 0.05. The data used in all the plots were curated for outliers
52 in all the measured traits using the $1.5 \cdot \text{IQR}$ method. A data point was considered an outlier if the
53 sample was identified as an outlier in at least twelve traits.

54
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56
 57 **Figure S4. Hierarchical clusters validation.** The box plots represent rosette compactness,
 58 slenderness of leaves (SOL) and electron-transport rate moving beyond photosystem II (ETR4),
 59 respectively grouped into hierarchical clusters based on area, maximum quantum yield in a light-
 60 adapted state (F_v'/F_m' _Lss4) and non-photochemical quenching ($\Phi(NPQ)$ _Lss4) measured
 61 under the highest light intensity. The letters above the box plots indicate significantly different
 62 groups, as identified by Tukey's HSD pairwise test with a p-value < 0.05. The hierarchical
 63 clusters were calculated using only data collected on the last (seventh) day after salt-treatment
 64 application from the curated dataset. The data used in all the plots were curated for outliers
 65 across all the measured traits using the $1.5 \times IQR$ method. A data point was considered an outlier
 66 if the sample was identified as an outlier in at least twelve traits. The data were additionally
 67 curated using the quadratic fit (samples with R^2 values below 0.7 were removed).

68
 69

70 **Supplemental Dataset legends:**

71
72 **Supplemental Dataset S1.** A dataset from Awlia et al. (2016) is used to exhibit the functions of
73 MVApp. Detailed descriptions of the measured phenotypic traits are listed in Supplemental
74 Dataset S2.

75
76 **Supplemental Dataset S2.** List of all the measured traits used for the data analysis in
77 Supplemental Dataset S1.

78
79 **Supplemental Dataset S3.** The R^2 values for different models included in MVApp, reflecting
80 their fit to the increase in rosette area under control and salt-stress conditions.

81
82 **Supplemental Dataset S4.** Outliers identified using the fit of quadratic function to rosette area
83 in MVApp. DELTA represents plant growth (mm^2/day^2); INTERCEPT represents the starting
84 value of each plant. The goodness of fit of the linear model used to fit the square root
85 transformed rosette area is represented by r_squared.

86
87 **Supplemental Dataset S5.** List of samples identified as outliers by the 1.5*IQR method, based
88 on all traits. A data point was considered an outlier if the sample was identified as an outlier in at
89 least twelve traits.

90
91 **Supplemental Dataset S6.** Correlation between individual traits measured for plants grown
92 under salt-stress and control conditions. The correlation coefficients were calculated using
93 curated data, with a total number of 966 samples. The outliers were identified using the 1.5*IQR
94 method on all the measured traits; a sample qualified as an outlier if it was outlying in at least
95 twelve traits. The data was additionally curated using the quadratic fit (samples with R^2 values
96 below 0.7 were removed).

97
98 **Supplemental Dataset S7.** Eigen values PCA using all measured traits and curated dataset. The
99 data were scaled prior to PCA and subset by "treatment". PCA was performed after the outliers
100 were removed from the curated data. The outliers were identified using the 1.5*IQR method on
101 all the measured traits; a sample qualified as an outlier if it was outlying in at least twelve traits.
102 The data were additionally curated using the quadratic fit (samples with R^2 values below 0.7
103 were removed).

104
105 **Supplemental Dataset S8.** Contributions (%) of the individual measured traits to the PCs under
106 control and salt-stress conditions. The data were scaled prior to PCA and subset by "treatment".
107 PCA was performed after the outliers were removed from the curated data. The outliers were
108 identified using the 1.5*IQR method on all the measured traits; a sample qualified as an outlier if
109 it was outlying in at least twelve traits. The data were additionally curated using the quadratic fit
110 (samples with R^2 values below 0.7 were removed).

111
112 **Supplemental Dataset S9.** Clustering of the phenotypes of nine Arabidopsis accessions using
113 hierarchical clustering with the Ward method and Area, FvFm_Lss4 and NPQ_Lss4 as the major
114 determinants. Clustering was performed after the outliers were removed from the curated and
115 scaled data. The outliers were identified using the 1.5*IQR method on all the measured traits; a

116 sample qualified as an outlier if it was outlying in at least twelve traits. The data were
117 additionally curated using the quadratic fit (samples with R^2 values below 0.7 were removed).

118
119 **Supplemental Dataset S10.** Quantile regression of various traits of major interest, calculated
120 using MVApp. The p-values from the regression analysis were calculated using MVApp for each
121 quantile of a trait of major interest. The significant contributions are highlighted in red. The
122 chlorophyll fluorescence traits are scored at increasing light intensities, which are marked by
123 Lss1, Lss2, Lss3 and Lss4. The contributions of a trait of major interest to itself are not
124 applicable (n.a.) and are marked as such in the table. The quantile regression was calculated
125 using raw data separated by day of measurement and treatment.

126
127 **Supplemental Dataset S11.** Broad-sense heritability estimations calculated for all individual
128 traits by day of experiment and treatment for nine Arabidopsis accessions with an average of
129 nine biological replicates. The heritability was calculated using raw data.

130