

## **New Phytologist Supporting Information**

Article title: Plasticity, pleiotropy and fitness tradeoffs in Arabidopsis genotypes with different telomere lengths

Authors: Brandon E. Campitelli, Samsad Razzaque, Borja Barbero, Liliia R. Abdulkina, Mitchell H. Hall, Dorothy E. Shippen, Thomas E. Juenger and Eugene V. Shakirov.

Article acceptance date: 14 November 2021

### **Supplemental Data 5**

Below we show the output of the different methods we used to explore differences from wildtype (Col-0), where each separate grid of 9 panels represents one of the seven traits we apply this analysis to in our manuscript (i.e., there are 7 grids representing traits from Figure 3 and Supplemental Figure 7). Each grid is organized such that three columns represent the three experimental treatments and the three rows represent the three methods for calculating the “difference from the wildtype” as follows:

#### **[1] Absolute difference from wildtype (as presented in the main text):**

$$y = |\text{Phenotype}(\text{mutant}) - \text{MeanPhenotype}(\text{Col-0})|$$

We first calculated the mean trait value for Col-0 for each phenotype in each of the three treatments to generate a matrix of wild type phenotypes. We then estimated the difference from the wild type by subtracting the observed phenotypic value for each individual from the mean value for Col-0 in the appropriate treatment. We then estimated the absolute value by transforming all of the difference from wild type estimates to positive values.

#### **[2] Fold difference from wildtype:**

$$y = |\text{Phenotype}(\text{mutant}) - \text{MeanPhenotype}(\text{Col-0})| / \text{MeanPhenotype}(\text{Col-0})$$

Next, to estimate the fold difference, we simply divided the absolute difference from wildtype from 1 above by the mean phenotypic value for wildtype (Col-0) from the appropriate treatment.

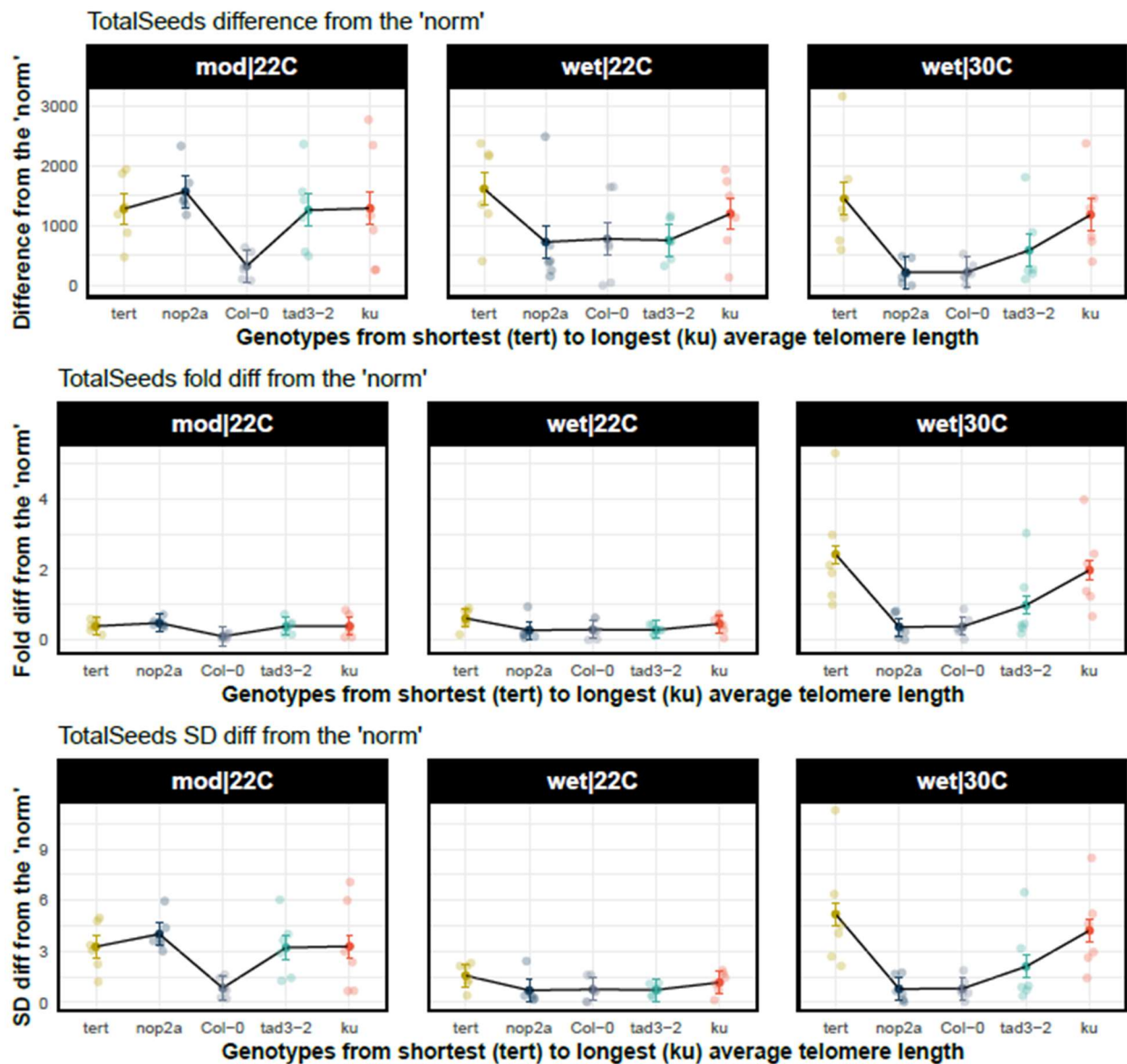
#### **[3] Standard deviation from wildtype:**

$$y = |\text{Phenotype}(\text{mutant}) - \text{MeanPhenotype}(\text{Col-0})| / \text{StandardDeviation}(\text{Col-0})$$

Finally, we converted the absolute difference from wildtype into units of standard deviation by dividing the absolute difference from wildtype values from 1 above by the standard deviation for wildtype (Col-0) from the appropriate treatment.

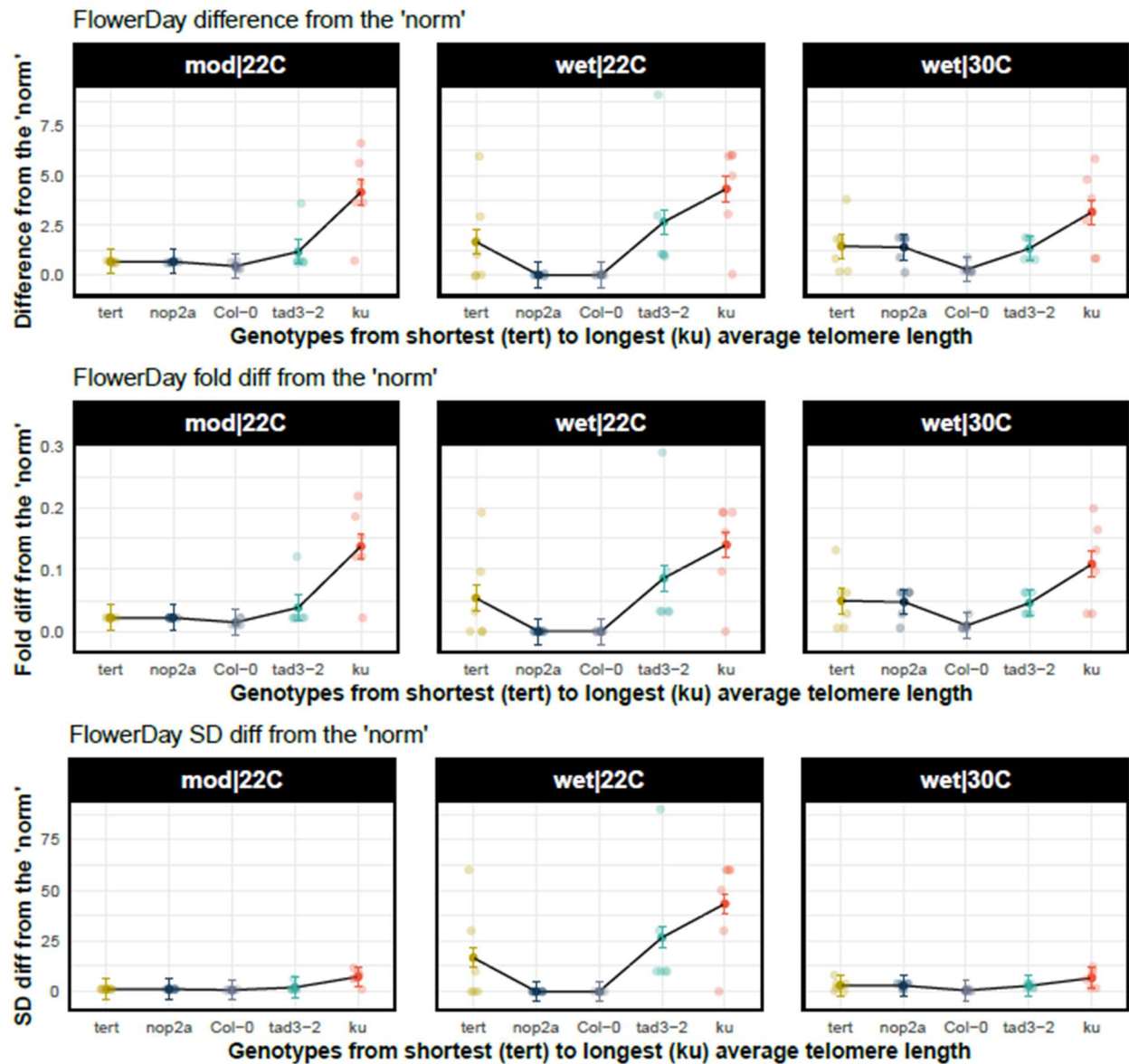
Following the transformations performed above, we analyzed these data using linear mixed model ANOVAs using PROC MIXED in SAS, and below we present least-squared means and standard errors estimates produced by these models.

**Grid 1: Reproductive fitness (total seed)**



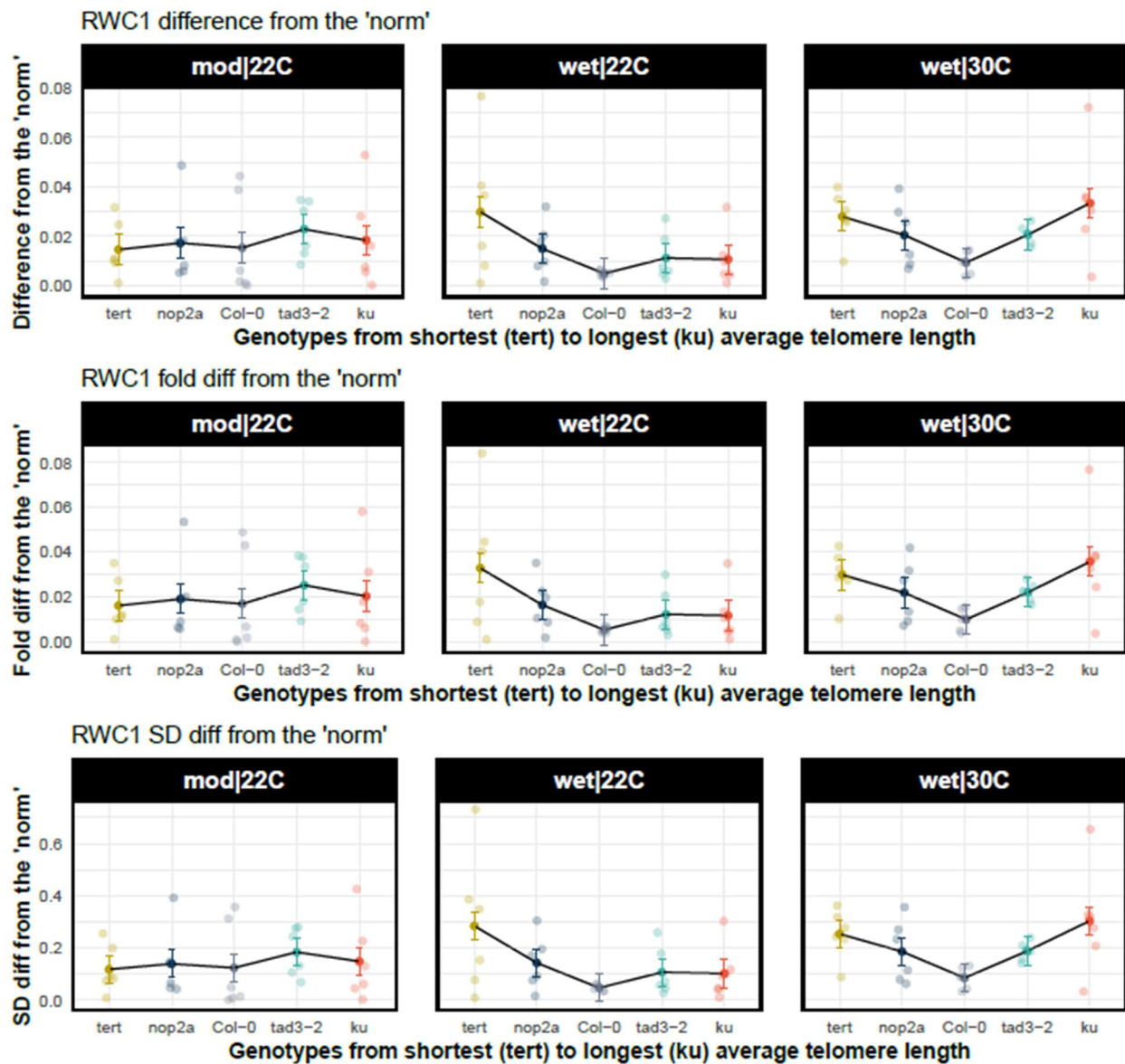
**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for Reproductive fitness. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.

**Grid 2: Flowering times (days to first flower)**



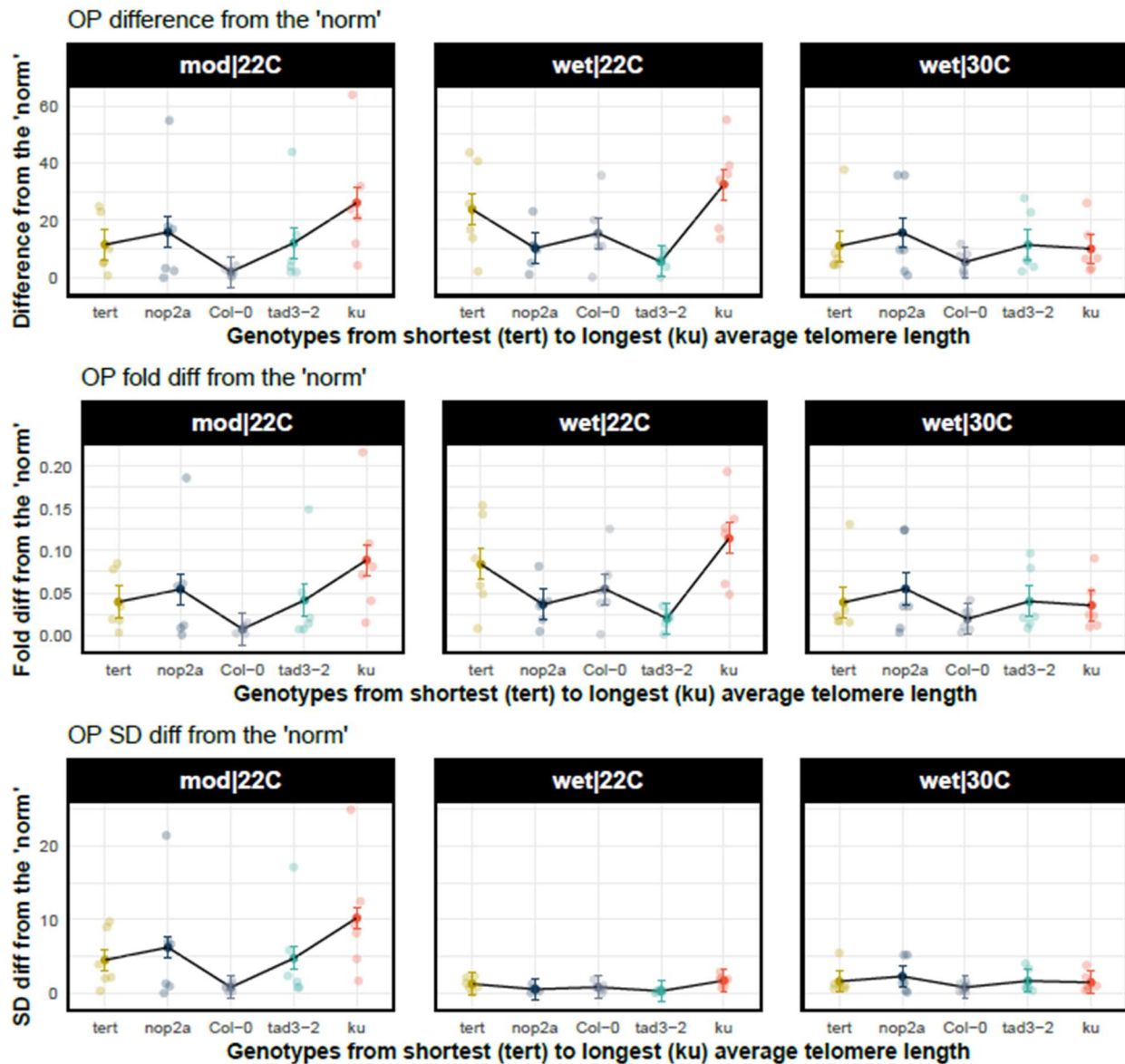
**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for Flowering time. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.

Grid 3: Relative water content ((Fresh weight – Dry weight)/(Turgid weight – Dry weight))



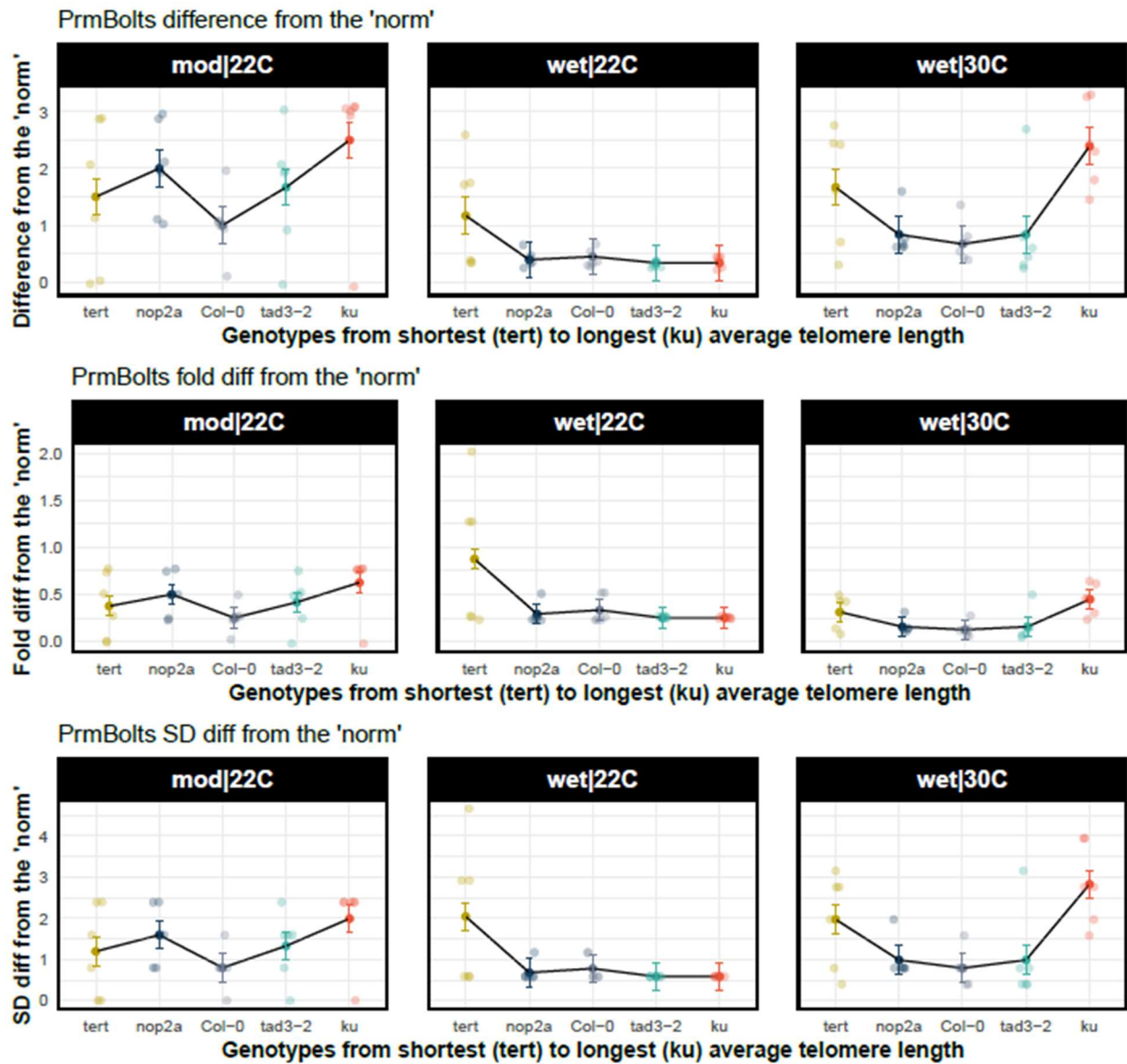
**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for RWC. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.

**Grid 4: Osmotic potential (mmol solute / kg tissue)**



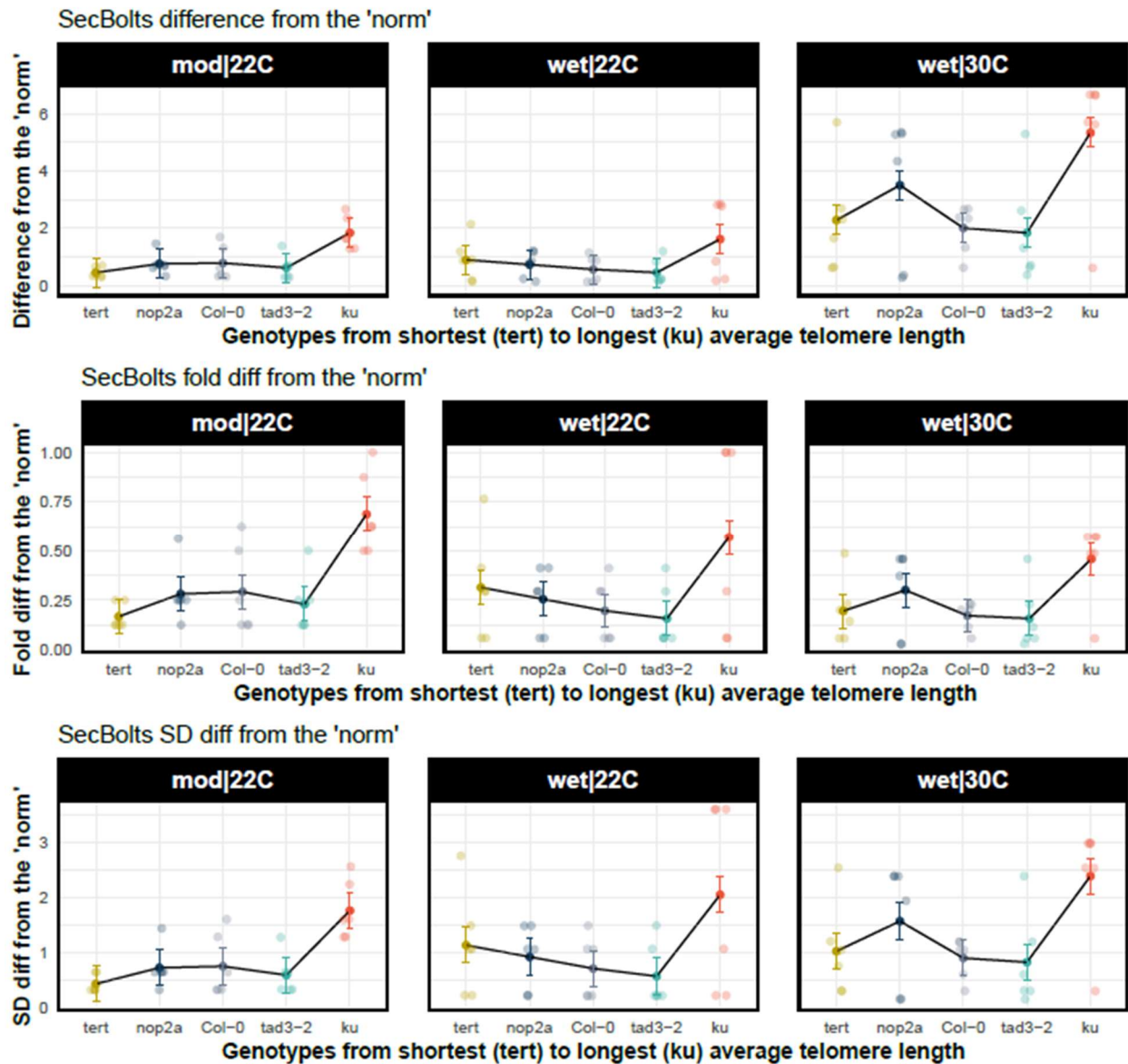
**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for OP. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.

**Grid 5: Number of primary bolts**



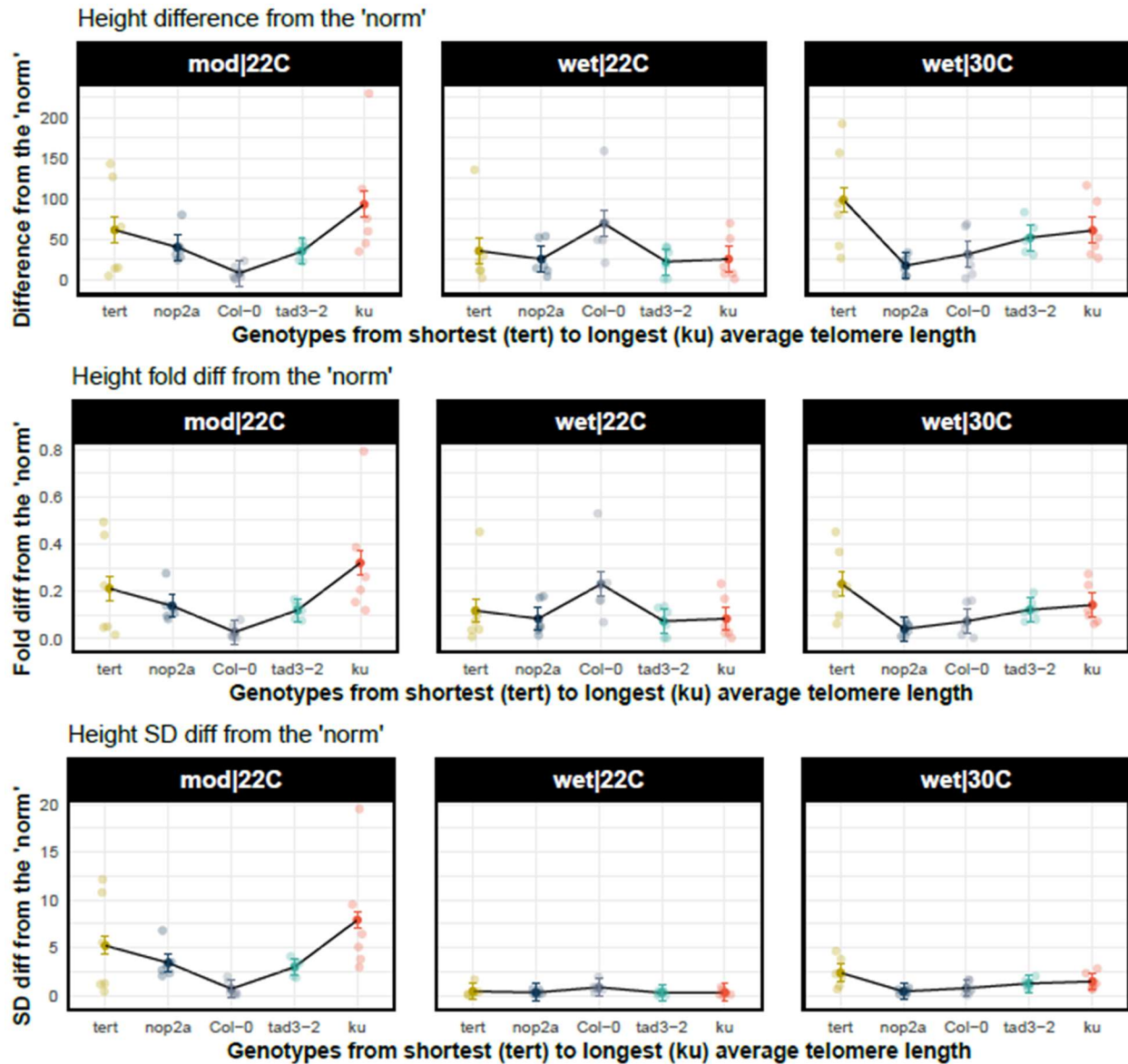
**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for the number of primary bolts. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.

## Grid 6: Number of secondary bolts



**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for the number of secondary bolts. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.

**Grid 7: Height (mm)**



**Analysis of strength response in *Arabidopsis thaliana* plant traits.** Response strength is defined as the absolute (positive or negative) variation from the Col-0 wild type trait values. Response strength was analyzed for height. Trait values of Col-0 genotype were subtracted from corresponding values for all other genotypes, transformed to positive values and plotted, with genotypes from left to right arranged from the shortest (*tert*) to the longest (*ku70*) telomere length. Points show least-squared means  $\pm$  standard error.