

Mix and Match

In this tab you can select up to eight genotypes to compare in different conditions, which are presented in individual sub-tabs.

The boxplots represent the selected phenotype of eight chosen accessions, and the letters above the graphs represent the significant groups as calculated using Tukey pair-wise comparison with p-value < 0.05.

DISCLAIMER: As the results presented in here are based only on four biological replicates, the significant differences between the accessions should be interpreted with caution.

Chose a phenotype to display

average Lateral Root Length

Genotype 1

Col-0

Genotype 5

Tsu-0

Genotype 2

C24

Genotype 6

Sav-0a

Genotype 3

Cvi-0

Genotype 7

Gr-5

Genotype 4

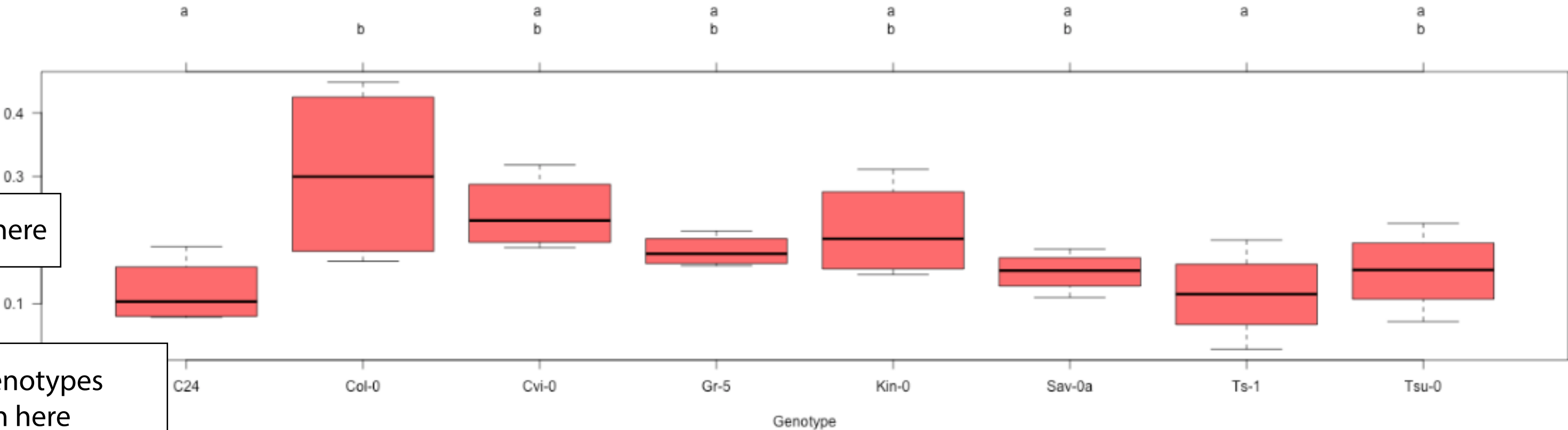
Kin-0

Genotype 8

Ts-1

0 mM NaCl 75 mM NaCl 125 mM NaCl

Examine the differences between genotypes at different conditions



Change the phenotype here

Change the genotypes for comparison here