So you think you can cluster?

In our paper we clustered the accessions based on the ratios of: average Lateral Root Length per Main Root Length, Lateral Root Length per Main Root Length, and Main Root Length per Total Root Size in all conditions studied. However, we realize that such a cluster analysis can be performed for any set of chosen traits. Therefore, in this tab we integrated our dataset so that you can perform your own cluster analysis on the traits of your interest.

Let's cluster   Step 1   Step 2   Step 3   Step 4

Compare the clusters by clicking on the tab >> Cluster Validation << to examine significant differences between your clusters.

DISCLAIMER: Note that the differences between the clusters may be due to the unequal distribution of the accessions between the samples. Therefore, the results presented in here should be interpreted with caution.

Below please select the trait for which you wish to validate your cluster analysis

chose a trait to test

Number of Lateral Roots 75 mM NaCl

Depth 75 mM NaCl
Depth 125 mM NaCl
Main Root Vector Angle 0 mM NaCl
Main Root Vector Angle 75 mM NaCl
Main Root Vector Angle 125 mM NaCl
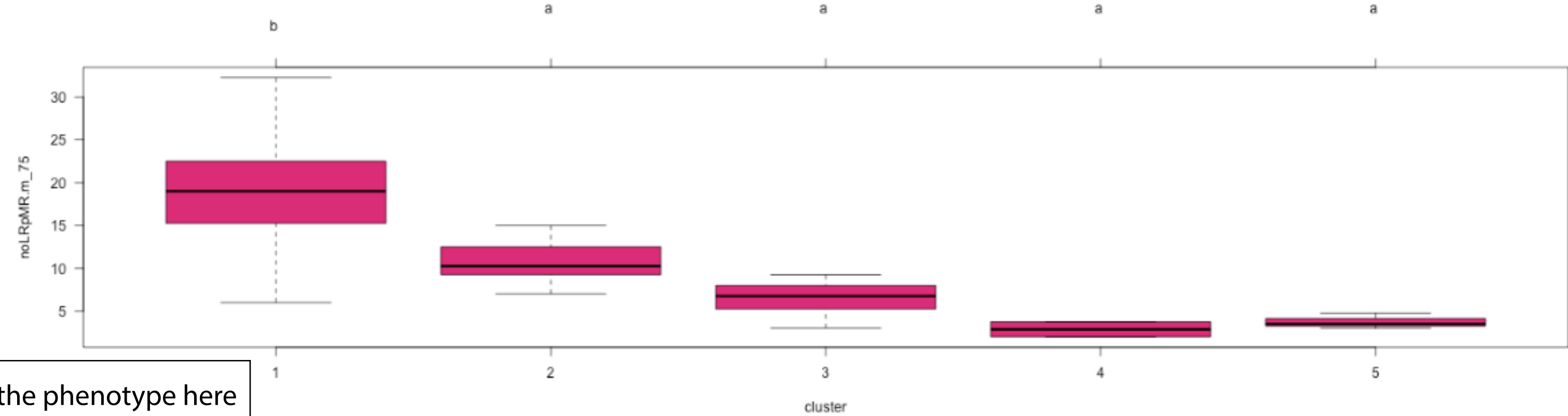Number of Lateral Roots 0 mM NaCl
Number of Lateral Roots 75 mM NaCl

Clustering Heat Map   Accession Dendrogram   Cluster Validation

Perform cluster validation

Change the phenotype here

The boxplot represents the phenotype value chosen in **Step 3** per cluster. The average values per accessions were pulled depending on the cluter cut-off value determined in **Step 2** . The letters above the graph represent the significant groups as calculated using Tukey pair-wise comparison with p-value < 0.05.