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

Please select three phenotypes that you would like to take into consideration for the cluster analysis. You will see the heat-map of the chosen phenotypes appear in the first tab. The value of the phenotypes is normalized with z-Fisher transformation, so the color scale is normalized for each phenotype

Trait 1

Main Root Length 75 mM NaCl ▼

Trait 2

average Lateral Root Length 75 mM NaCl ▼

Trait 3

Number of Lateral Roots 75 mM NaCl ▼

Change the phenotype here

Clustering Heat Map	Accession Dendrogram	Cluster Validation

This graph represents the clustering of the accessions based on three selected traits. The colors represent the phenotype value which has been normalized per trait with Z-Fisher transformation. Please note that the data per accession is based on the average trait value collected from 4 replicas only.