

Table S1. Analysis of variance table of traits evaluated.

Trait	Source of variation	df	p-value
Shoot dry weight	Genotype	9	4.54e-10 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.535
Root dry weight	Genotype	9	4.54e-10 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.535
Root shoot ratio	Genotype	9	2.21e-06 ***
	Treatment	1	1.84e-14 ***
	Genotype * Treatment	9	0.56
Root length	Genotype	9	1.08e-08 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.464
Root area	Genotype	9	1.04e-08 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.605
Root volume	Genotype	9	1.61e-07 ***
	Treatment	1	4.00e-11 ***
	Genotype * Treatment	9	0.131
Relative water content	Genotype	9	3.32e-08 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	4.36e-09 ***
Chlorophyll content	Genotype	9	< 2e-16 ***
	Treatment	1	8.16e-12 ***
	Genotype * Treatment	9	0.00471 **
Stomatal conductance	Genotype	9	0.23471
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.00432 **
Stomata number	Genotype	9	5.28e-14 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.000446 ***
Seed weight	Genotype	9	< 2e-16 ***
	Treatment	1	< 2e-16 ***
	Genotype * Treatment	9	0.00113 **

The table shows standard anova for all traits except for relative water content and stomatal conductance). Relative water content and stomatal conductance shows the non-parametric analysis of variance with ARTool package. Df: degree of freedom. Significant codes: 0 '\*\*\*' 0.001 '\*\*' 0.01.