

Figure S1. Workflow for the identification of DRPPs.

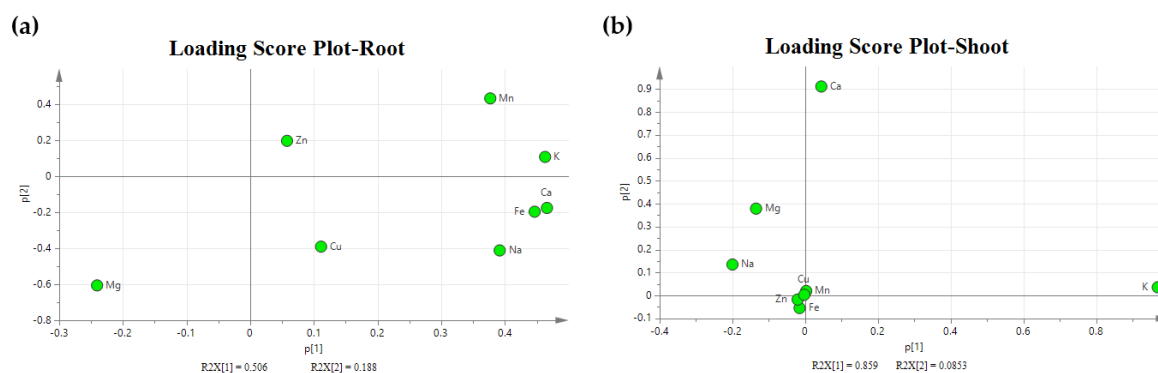
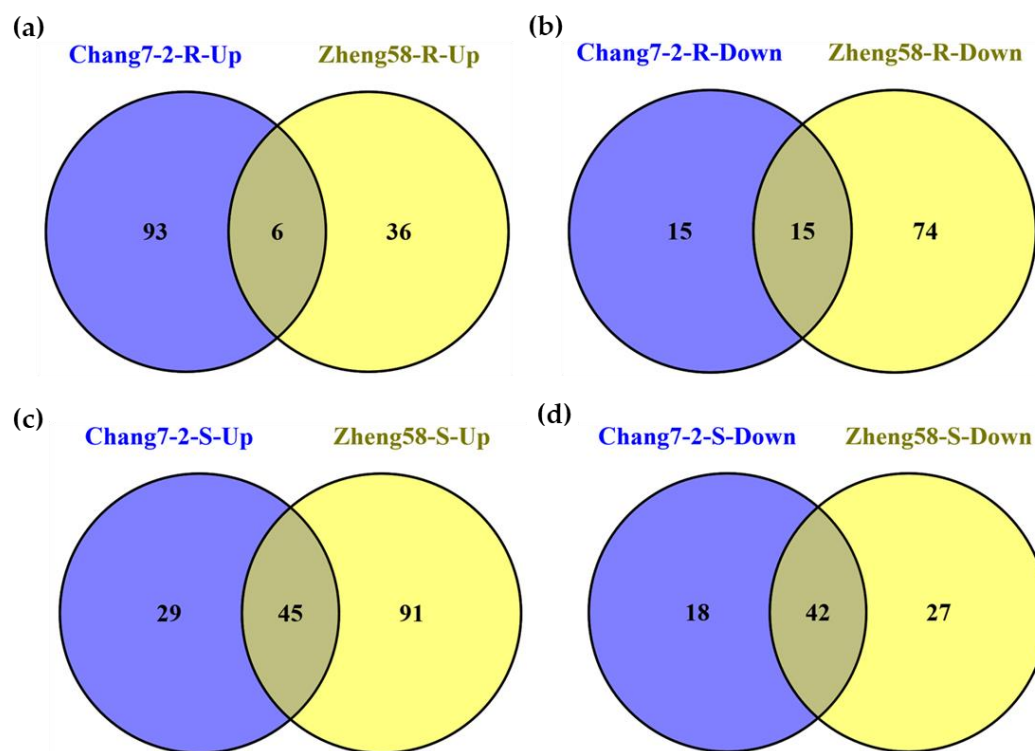
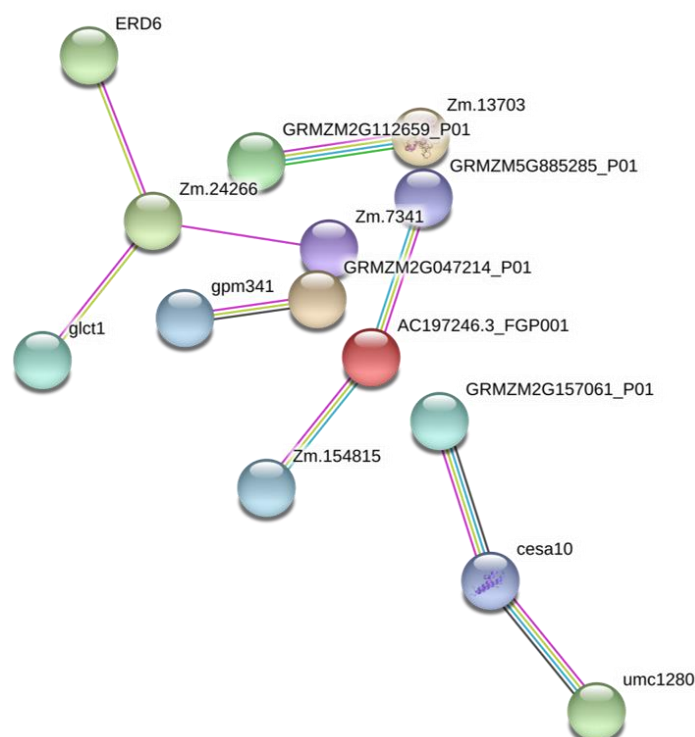


Figure S2. Loading score plot for metal elements determination in roots (a) and shoots (b) of Chang7-2 and Zheng58 after salt treatment for 0.5 h and 2 h.



**Figure S3.** Numbers of up-regulated and down-regulated phosphoproteins in Chang7-2 and Zheng58 after salt treatment for 0.5 h and 2 h. Numbers of up-regulated and down-regulated phosphoproteins in roots (a,b) and shoots (c,d) of Chang7-2 and Zheng58.



**Figure S4.** Protein interaction network of DRPPs in Chang7-2 root.

**Table S1.** Ion contents in roots and shoots of Chang7-2 and Zheng58 at three different salt treatment points (Unit: mg.g<sup>-1</sup> DW).

Tissue	Genotype	Time	K	Na	Ca	Mg	Mn	Fe	Zn	Cu
root	Chang7-2	0 h	15.094	1.943	2.549	8.258	0.235	0.601	0.087	0.017
		0.5 h	14.413	3.059	1.946	8.216	0.252	0.705	0.104	0.016
		2 h	13.743	3.018	2.005	7.602	0.155	0.401	0.068	0.018
	Zheng58	0 h	20.779	1.466	2.494	4.351	0.499	0.479	0.089	0.016
		0.5 h	25.754	4.454	19.417	6.512	0.529	1.042	0.098	0.020
		2 h	31.408	5.175	13.218	5.811	0.402	1.080	0.075	0.016
shoot	Chang7-2	0 h	47.722	1.314	6.334	5.086	0.114	0.067	0.054	0.014
		0.5 h	51.729	1.519	6.197	4.730	0.105	0.085	0.042	0.015
		2 h	44.795	2.016	7.038	4.127	0.075	0.052	0.037	0.008
	Zheng58	0 h	72.088	0.523	6.895	3.679	0.096	0.050	0.027	0.010
		0.5 h	57.291	0.506	6.626	3.707	0.098	0.049	0.028	0.012
		2 h	56.704	1.055	8.407	4.476	0.102	0.039	0.028	0.014

**Table S2.** Numbers of identified or quantified PSMs, unique phosphopeptides, phosphoproteins and phosphorylation sites in roots and shoots.

	Root	Shoot	Overlap	Total
Phosphoproteins PSMs (1% FDR)	36635	40119	—	—
Proteins identified	3432	3482	2108	—
Phosphoproteins quantified	3084	2986	1954	4116
Unique phosphopeptides quantified	9772	11062	5375	—
Unique phosphorylation sites	7175	7394	5121	9448