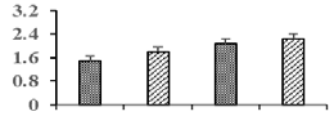
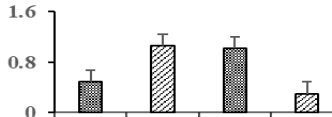
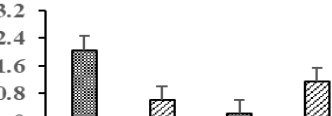
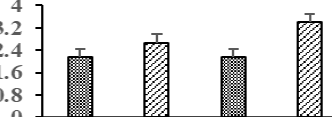
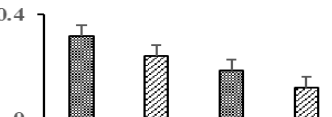
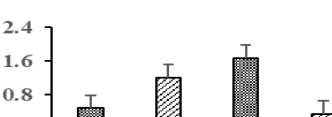

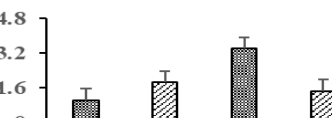
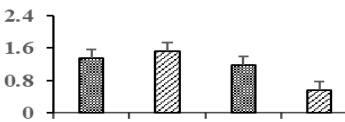
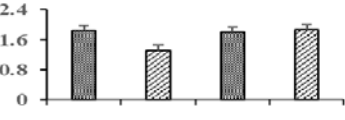
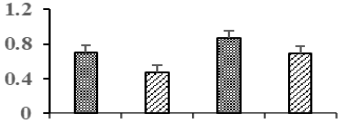
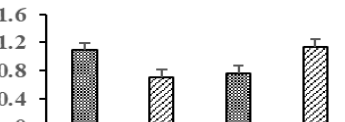
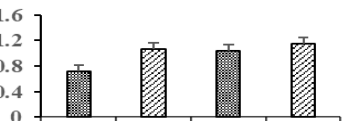
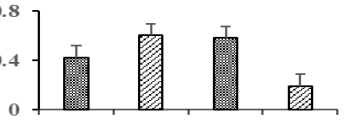
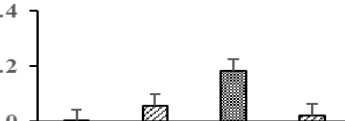
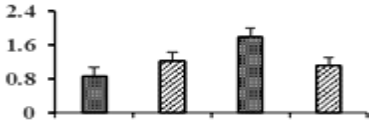
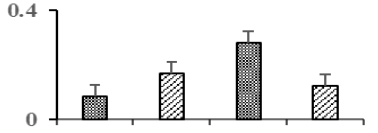
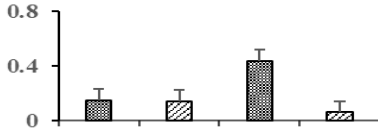


23	A0A2C9VRW1	Glyceraldehyde 3-phosphate dehydrogenase	<i>Dorcoceras hygrometrium</i>	cyt	41/5.9	42/6.58	6	20	
17	A0A0K9QST5	Malate dehydrogenase	<i>Spinacia oleracea</i>	pTP	37/6.9	38/7.44	7	31	
Photosynthesis-related proteins									
20	Q8L5T3	Rubisco activase	<i>C. quinoa</i>	cyt	41/6.8	47.8/7.05	21	47	
21	A0A438FB46	Oxygen evolving enhancer protein 1, OEE1	<i>Vitis vinifera</i>	cTP	40/5.8	39.7/5.63	7	20	
9	Q8WK19	Ribulose biphosphate carboxylase large chain	<i>Derbesia marina</i>	cTP	55/6.1	48.1/6.92	1	30	
16	A0A2P2LRA9	Uncharacterized protein	<i>Spinacia oleracea</i>	cTP	28/5.9	31.4/5.6	2	11	
ROS (reactive oxygen species) scavenging and detoxification									
24	A0A2K3PPT5	Glutamine synthetase	<i>Spinacia oleracea</i>		43/5.1	39/5.48	13	30	
13	B8XF08	Carbonic anhydrase /Ascorbate peroxidase	<i>Arabis alpine</i>	cTP	34/5.2	27.4/5.5	4	20	

19	A0A397XKU3	Germin-like protein	<i>Gossypium raimondii</i>	22/6.9	26.4/6.52	1	11	
22	D8T1R0	Domain Thioredoxin Containing protein (Fragment)	<i>Selaginella moellendorffii</i>	42/5.7	25.6/6	2	60	
10	A0A067GWV4	Lactoylglutathione lyase	<i>Spinacia oleracea</i>	41/5.6	39.6/6.7	6	20	
Stress defense and heat shock proteins								
1	O50036	Heat shock 70 protein	<i>Spinacia oleracea</i>	72/5.1	76.1/5.3	14	28	
2	A0A0K9RYB1	Protein disulfide-isomerase	<i>Morus notabilis</i>	60/5.2	56.1/4.89	5	15	
Enzyme activation								
11	A0A0K9QK04	14_3_3 domain Containing protein	<i>Spinacia oleracea</i>	30/5.1	29.6/4.88	4	25	
12	A0A0K9QK04	14_3_3 domain containing protein	<i>Spinacia oleracea</i>	35/4,6	29.4/4.87	2	11	
ATPases								

3	H2BBA4	ATP synthase subunit alpha, chloroplastic	<i>C. quinoa</i>	cTP	5.5/57	55.3/5.27	4	16	
4	H2BBA4	ATP synthase subunit alpha, chloroplastic	<i>C. quinoa</i>	cTP	56/5.6	55.5/5.27	11	37	
5	H2BBA4	ATP synthase subunit alpha, chloroplastic	<i>C. quinoa</i>	cTP	57/5.1	55.3/5.27	16	44	

^a Spot number as indicated on the 2D-PAGE master gels (see Fig. 5)

^b Accession number is assigned from UniProtKB database.

^c Peptide signal according to ‘TargetP’ software: mTP, mitochondrial transit peptide; pTP, plast transit peptide; cyt, cytoplasm; SP, secreted protein.

^d Experimental pI and mass (kDa) of identified proteins. Experimental values were computed by Progenesis Software.

^e Theoretical pI and mass (kDa) of identified proteins.

^f Number of peptides matching to the unigene sequence.

^g Sequence coverage percentage.

^h Changes in the protein abundance in leaves of UDEC-5 (Q4) and Kcoito (Q3) genotypes under NaCl salt treatment (0 and 300 mM). Data on the Y axis represent the relative volume of each spot (means of 3 replicates± standard error).