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Supplementary Data

Differentially expressed proteins in sugarcane leaves in response to water deficit stress

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Supplementary table 1. Identification of water stress-responsive proteins in sugarcane leaves (cv. Khon Kaen 3). The proteins were identified by LC-ESI-IT-MS/MS and the Mascot and OMSSA search engines.

Spot number	Magnitude of change (fold)	Experiment		Theoretical		Protein accession numbers	Protein homologs	Species	Mascot			OMSSA	
		pI	M_r	pI	M_r				Score	Hits	Cov (%)	Hits	E-value
							Photosynthesis						
D02	1.6	4.86	33	5.5	30	gi|162461137	chlorophyll a/b-binding apoprotein CP26 precursor	*Zea mays*	185	4	11	1	2.44E-03
U04	1.6	6.0	27	5.84	27	gi|75265661	Chlorophyll a-b binding protein 1B-21, chloroplastic	*Hordeum vulgare*	107	2	5	1	7.48E-07
U07	1.9	6.93	29	5.59	35	gi|195619530	oxygen-evolving enhancer protein 1	*Zea mays*	368	7	11	1	2.14E-08
U12	1.3	5.28	63	5.31	54	gi|75324213	ATP synthase subunit beta, chloroplastic (EC=3.6.3.14)	*Saccharum* hybrid	528	17	35	10	1.58E-04 to 3.25E-09
U13	1.5	5.48	63	5.31	54	gi|48478778	ATP synthase CF1 beta subunit (EC=3.6.3.14)	*Saccharum* hybrid	1,373	26	50	24	2.86E-05 to 1.08E-14
U14	1.4	5.84	64	5.87	56	gi|90110817	ATP synthase subunit alpha, chloroplastic (EC=3.6.3.14)	*Saccharum* hybrid	544	9	21	6	3.28E-3 to 8.66E-10
U15	1.6	6.03	64	5.87	56	gi|90110817	ATP synthase subunit alpha, chloroplastic (EC=3.6.3.14)	*Saccharum* hybrid	549	9	21	6	1.72E-03 to 6.89E-09
							Defense						
D01	2.0	5.16	23	6.47	24	gi|54299342	heat shock protein hsp22 precursor, mitochondrial	*Zea mays*	44	1	4	1	1.54E-02
U01	3.8	6.19	18	6.77	17	gi|226504442	16.9 kDa class I heat shock protein 1	*Zea mays*	113	2	14	1	2.10E-01
U02	1.4	4.98	19	5.31	19	gi|269993586	chloroplastic Cu/Zn superoxide dismutase (EC=1.15.1.1)	*Zea mays*	230	3	21	1	1.54E-02

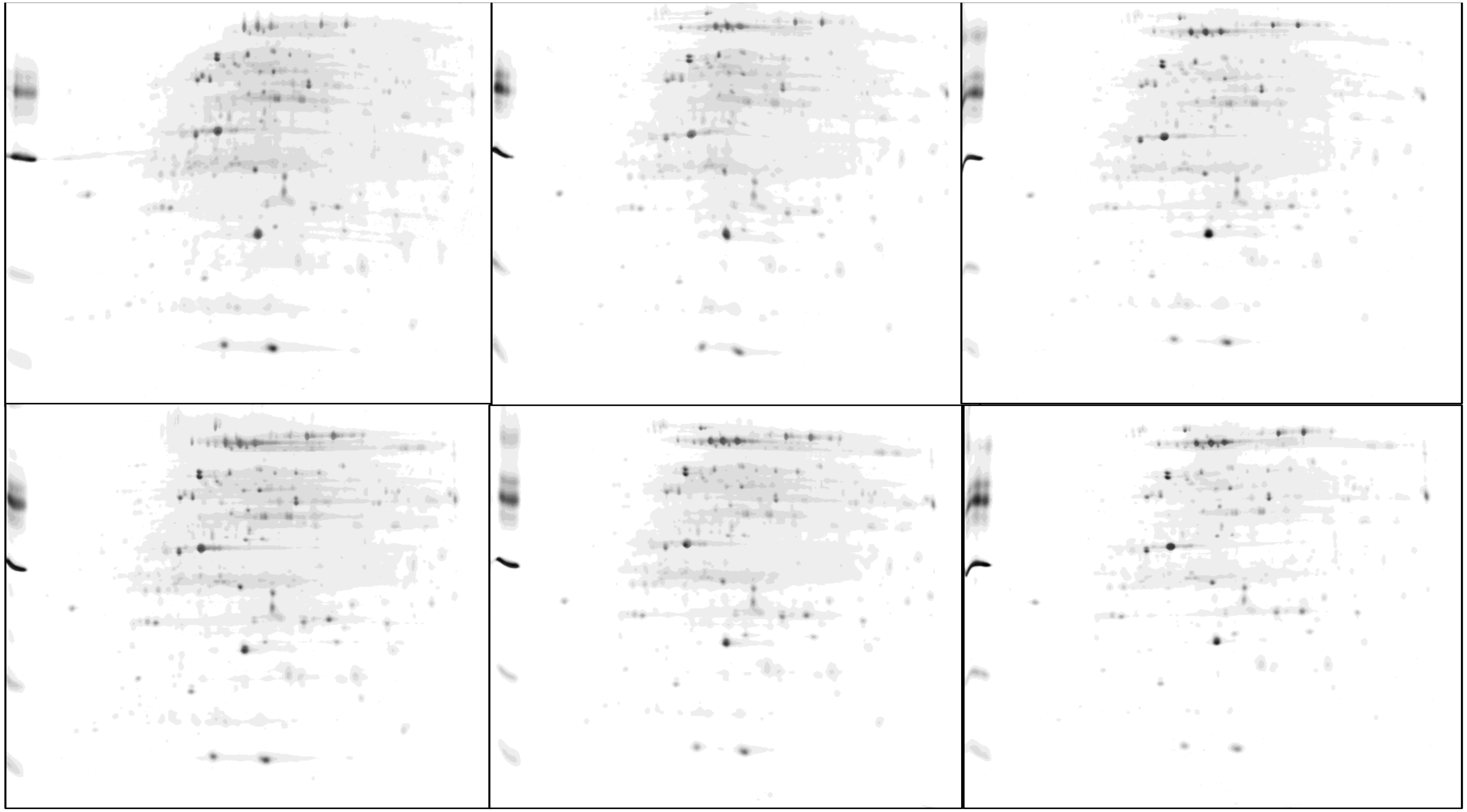
Supplementary table 1. (continued)

Spot number	Magnitude of change (fold)	Experiment		Theoretical		Protein accession number	Protein homolog	Species	Mascot			OMSSA	
		pI	M_r	pI	M_r				Score	Hits	Cov (%)	Hits	E-value
U05	1.6	6.37	28	7.11	25	gi|162461288	superoxide dismutase [Mn] 3.1, mitochondrial precursor (EC=1.15.1.1)	*Zea mays*	61	1	6	1	5.83E-03
U06	1.5	6.13	28	6.71	25	gi|212722004	superoxide dismutase [Mn] 3.4, mitochondrial precursor (EC=1.15.1.1)	*Zea mays*	282	5	23	5	1.32E-03 to 3.80E-08
U03	1.3	4.72	26	5.81	28	gi|195626524	2-cysteine peroxiredoxin BAS1	*Zea mays*	154	3	11	1	9.63E-03
U09	2.1	6.67	44	6.27	35	gi|17297979	26S proteasome regulatory particle non-ATPase subunit8	*Oryza sativa* Japonica Group	153	2	7	1	1.42E-04
U10	1.7	5.76	55	6.07	53	gi|226508704	elongation factor Tu	*Zea mays*	173	2	6	1	1.54E-10
U11	2.5	5.90	55	5.07	50	gi|226508704	elongation factor Tu	*Zea mays*	112	3	5	1	2.27E-07
							Miscellaneous						
D03	1.6	5.10	41	5.11	54	gi|11583	ATPase, beta subunit	*Hordeum vulgare*	70	1	3	1	1.17E-11
D04	1.6	5.0	50	6.07	50	gi|226530482	phosphoglycerate kinase (EC 2.7.2.3)	*Zea mays*	160	2	5	1	4.98E-05
U08	1.2	5.41	40	5.69	33	gi|162461348	Isoflavone reductase homolog IRL(EC=1.3.1.-)	*Zea mays*	228	3	11	1	1.88E-06

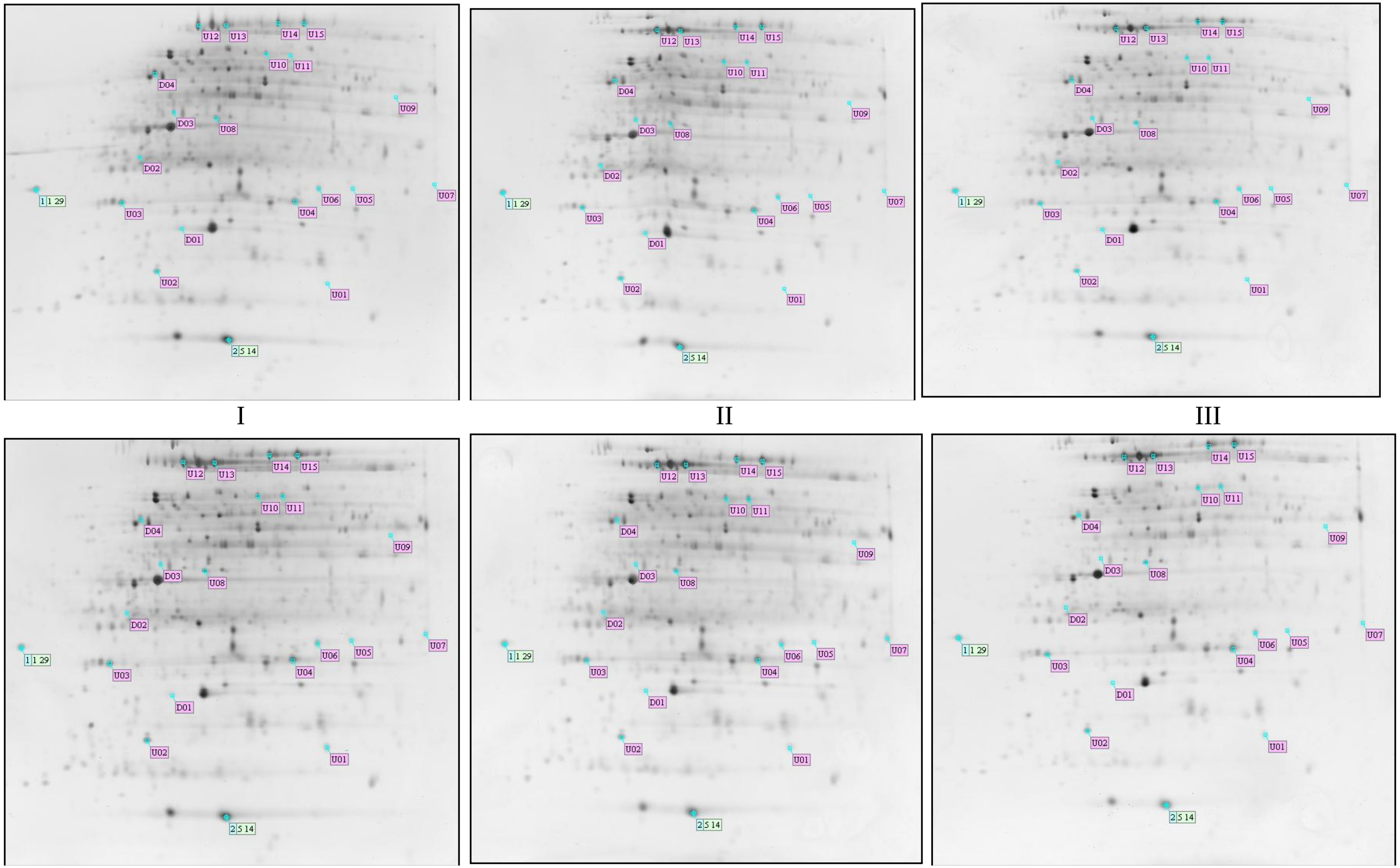
Criteria: M_r: molecular weight; pI: isoelectric point; Species: organism in which the protein has been identified; Score: identified score obtained with Mascot; Hits: the number of MS/MS spectra that were matched to an orthologous protein; Cov (%): percentage of orthologous protein sequence coverage obtained with the Mascot-identified peptides; E-value: a significant hit in OMSSA.

Mascot website: http://www.matrixscience.com/search_form_select.html

OMSSA website:http://pubchem.ncbi.nlm.nih.gov/omssa/index.htm



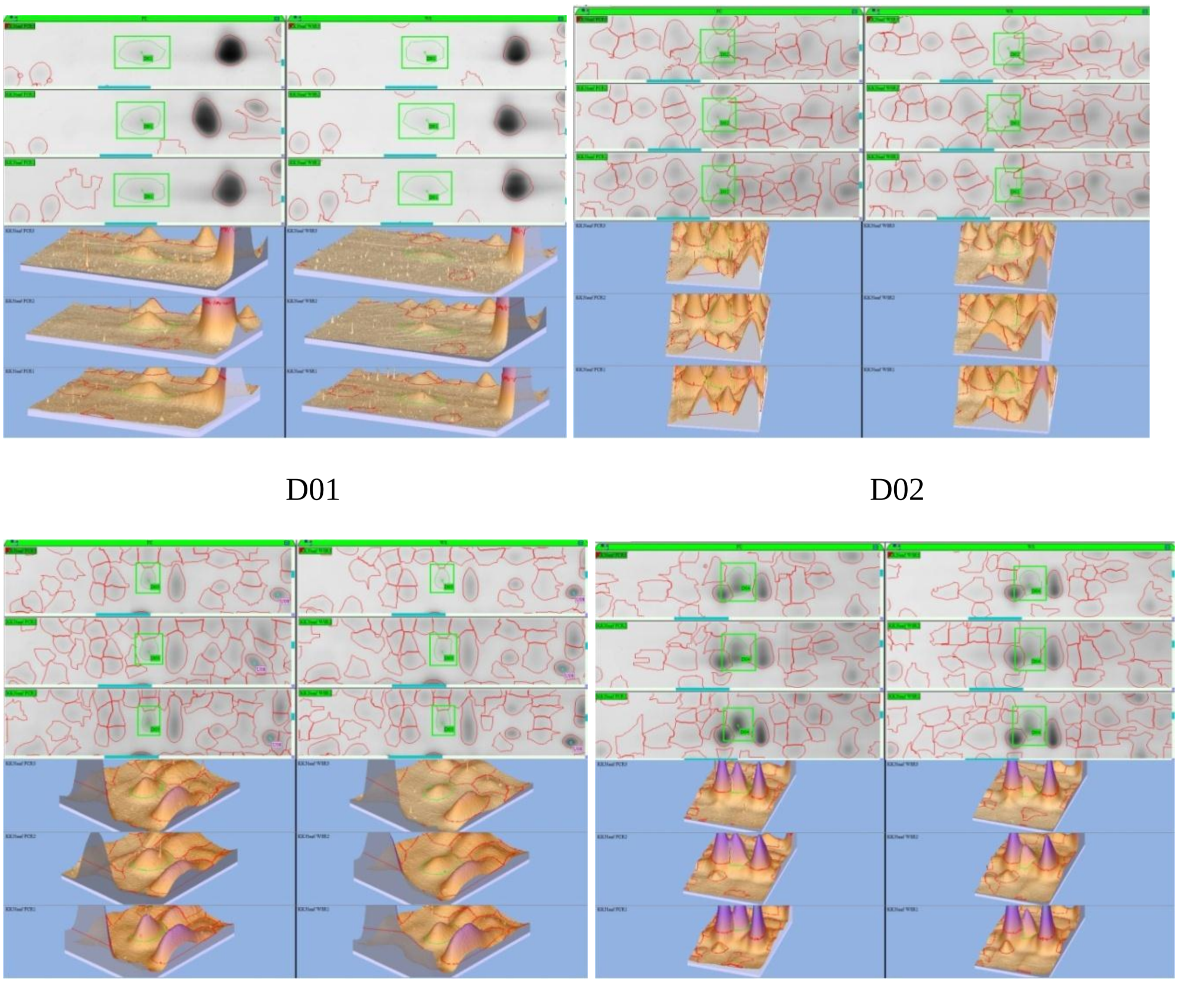
Supplementary fig 1. The reproducibility of the protein separation using 2-DE. Proteins from plants with an adequate water supply (Upper row) and from water-stressed plants (lower row) were separated into three replicates (column1 to column 3). Proteins with known molecular weight were also separated in each gel and are shown on the left-hand side of each gel.



I II III

I II III

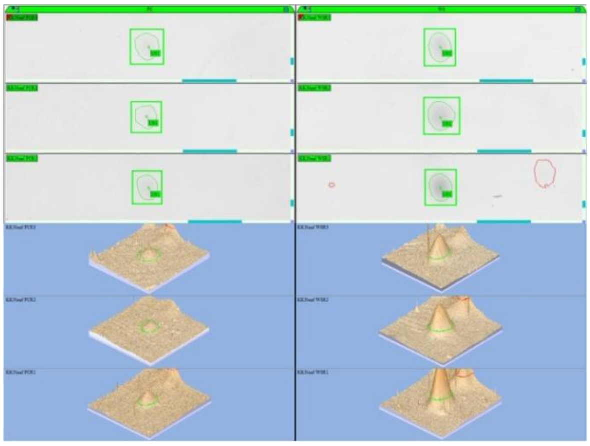
Supplementary fig 2. Image analysis of proteins in 2-DE gels. Proteins from sugarcane leaves under adequate water supply (upper row) or water stress (lower row) were separated into three replicates (I, II and III). Four proteins (U01-U04) were down- and fifteen proteins (U01-U15) up-regulated.



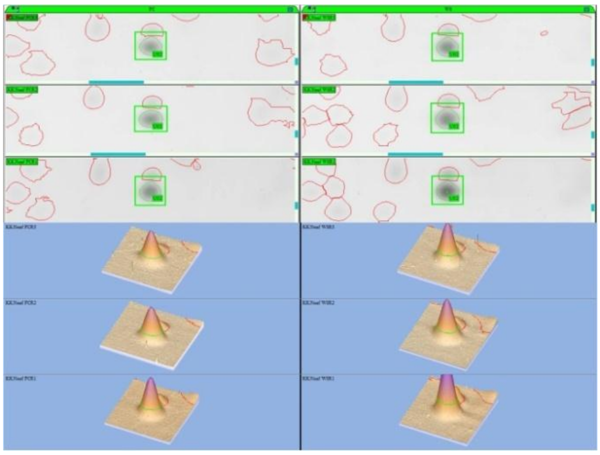
D01 D02

D03 D04

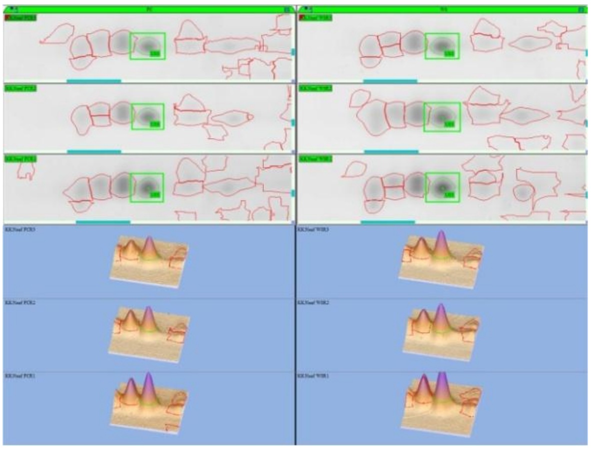
Supplementary fig 3. Two- and three-dimensional views of proteins down-regulated (D01-D04) under water deficit stress. For each protein spot, the left column represents the adequate water supply treatment,and the right column represents the water stress treatment. The upper three rows are 2Dviews and the lower three rows are 3D views of the protein spots. Each row represents a view from one replicate.



U01



U02



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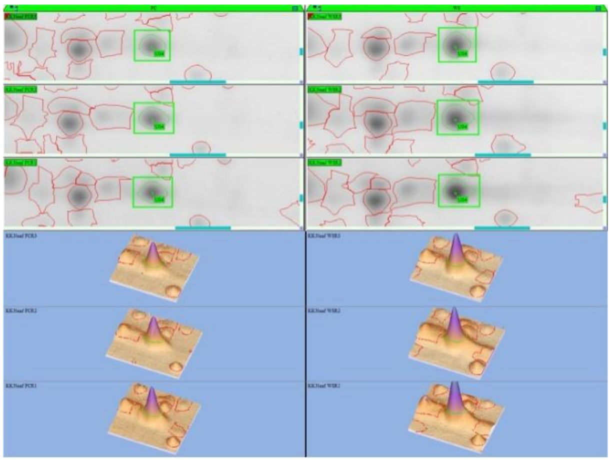
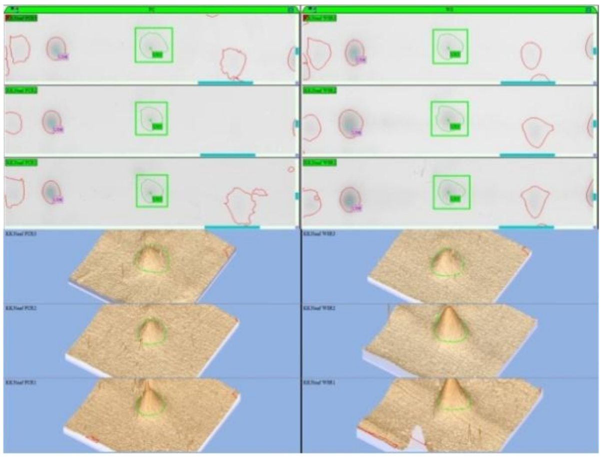
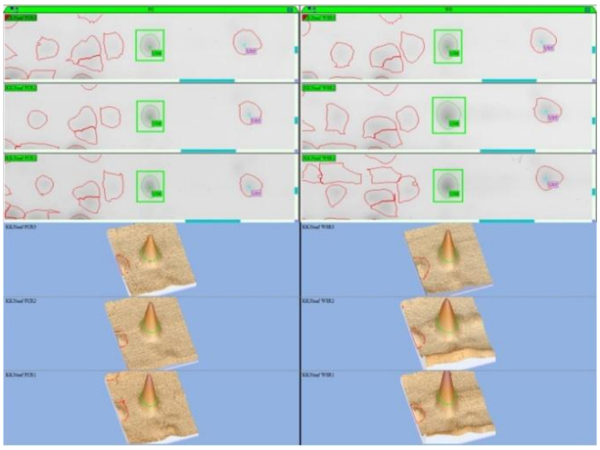


U04

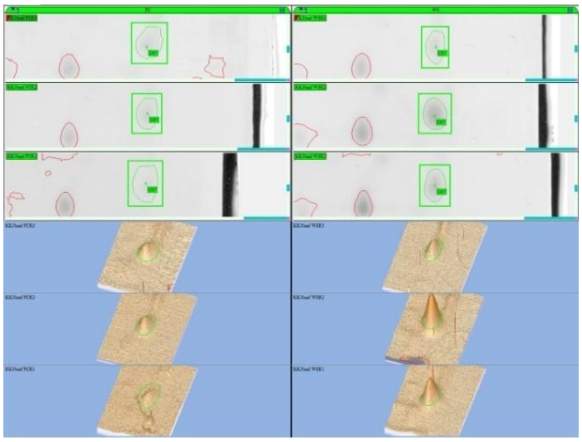


U05

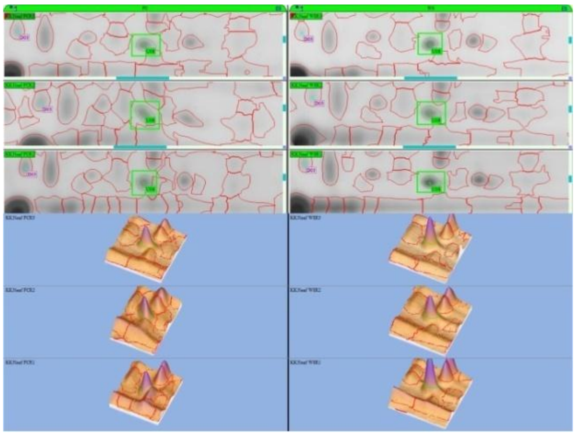


U06

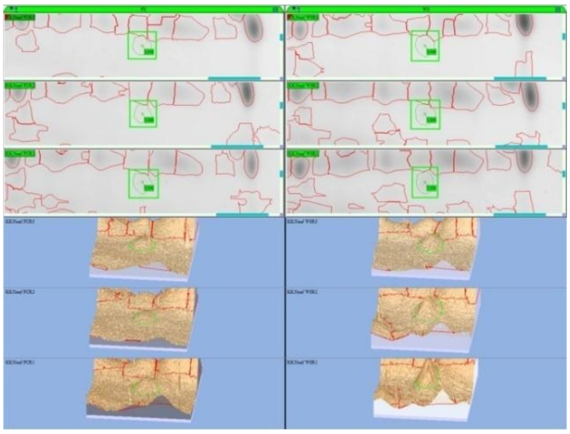
Supplementary fig 4. Two- and three-dimensional views of proteins up-regulated (U01-U15) under water deficit stress. For each protein spot, the left column represents the adequate water supply treatment, and the right column represents the water stress treatment. The upper three rows are 2Dviews and the lower three rows are 3D views of the protein spots. Each row represents a view from one replicate.



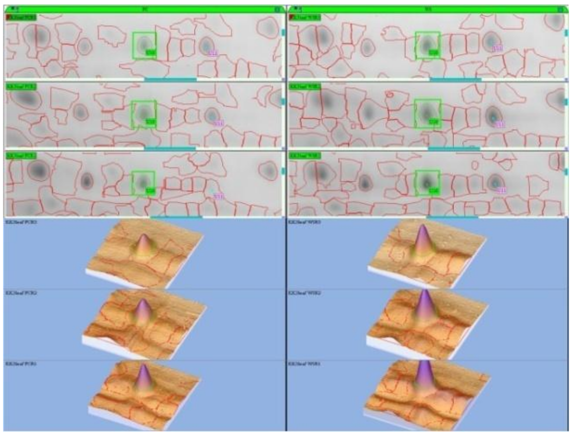
U07



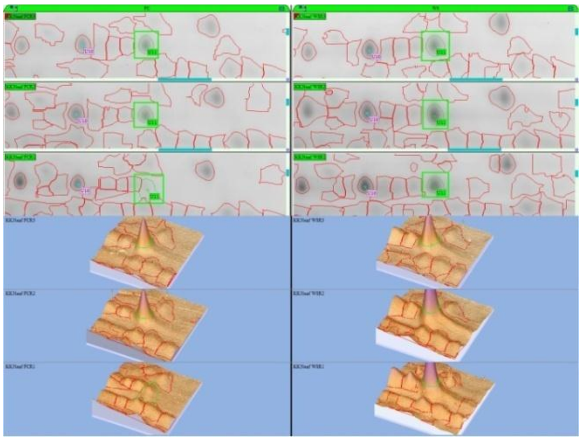
U08



U09



U10



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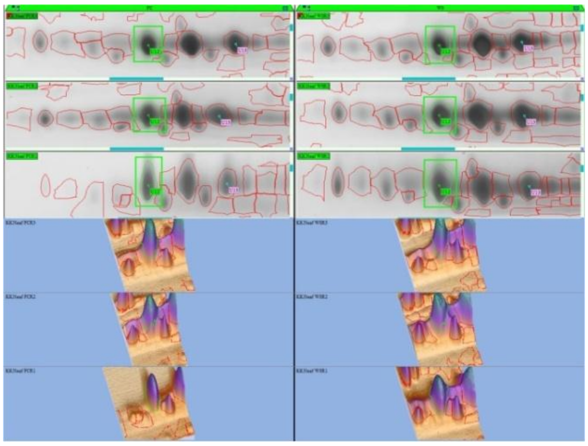
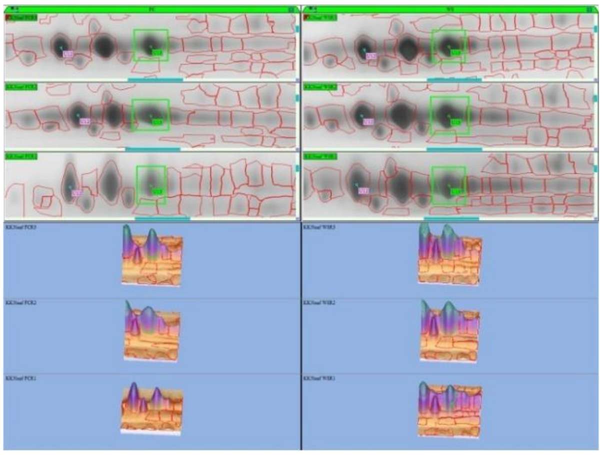
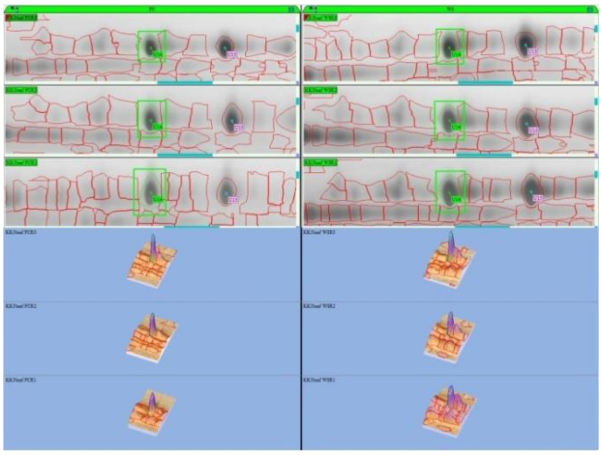


U12

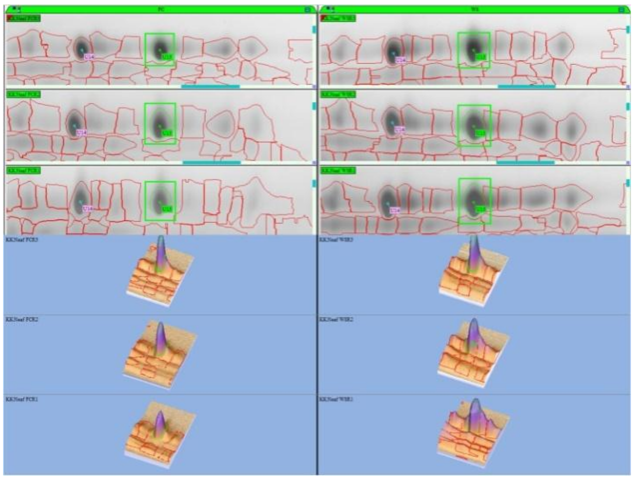
Supplementary fig 4. (continued)



U13



U14



U15

Supplementary fig 4. (continued)