

Table 1 Suppl. Identification of drought-responsive proteins in two maize genotypes under control and drought stress conditions. ^a - Spot ID numbers correspond to the spots in Fig. 1. ^b - The significantly matched proteins. Only a higher protein score and the number of matched peptides and the protein score confidence interval (C.I.) $\geq 95\%$ were reported as candidate drought-responsive proteins. ^c - The matched protein number in NCB databases. ^d - The matched protein score. ^e - Experimental or theoretical mass (M) [kDa] and pI of identified proteins. Experimental values were calculated with the *Image master* software. Theoretical values were retrieved from the protein database. ^g - The number of matched peptides. ^h - Up- (↑) or down-regulation (↓) of spots during drought stress.

Spots ID ^a	Significantly matched proteins ^b	Accession No. ^c	Protein score ^d	Exp. (pI/M) ^e	Theor. (pI/M) ^f	NMP ^g	Regulation ^h
1	ribulose biphosphate carboxylase small chain, chloroplastic	P05348	252	7.3/13	9.1/19.1	13	↑
2	ribulose 1,5-bisphosphate carboxylase/oxygenase thylakoid lumenal 16.5 kDa protein chloroplastic	CAA68419	243	7.3/13	9.1/19.0	12	
	oxygen evolving enhancer protein 3 containing protein	AQK66951	212	4.5/16	8.87/25.4	5	↓
	photosynthetic NDH subunit of lumenal location 3 chloroplastic	ACG48907	154	4.5/16	7.66/25.3	8	
		ONM50900	144	4.5/16	7.66/28.3	7	
3	light-harvesting complex I 11 kDa protein	O65101	147	8.5/11	10.1/14.9	4	↓
4	chlorophyll <i>a-b</i> binding protein 6A	ACG35952	135	5.1/23	6.3/26.6	4	↓
5	oxygen evolving complex 33 kDa subunit	AQK81304	255	5.2/30	5.59/34.5	18	↓
	oxygen-evolving enhancer protein 1	ACG31595	255	5.2/30	5.59/34.5	18	
6	glyceraldehyde-3-phosphate dehydrogenase 1	AQK50979	107	7.2/41	6.46/36.5	10	↑
	glyceraldehyde-3-phosphate dehydrogenase 2	Q09054	94	7.2/41	6.41/36.5	8	
7	malate dehydrogenase 2	NP_001142100	269	6.1/36	8.23/35.3	9	↑
8	nucleoside diphosphate kinase 1	NP_001296954	280	6.9/16	6.3/16.5	6	↑
9	nucleotide diphosphate kinase 1	NP_001167891	170	7.3/15	6.84/16.8	8	↑
10	fructose-bisphosphate aldolase	AQK39564	434	5.7/35	7.63/41.7	13	↓
11	ATP synthase Δ chain	ACG39343	241	4.0/25	4.98/26.6	9	↓
	H(+)-transporting ATP synthase, partial	CAA46804	231	4.0/25	4.35/20.2	7	
	ATP synthase delta chain, chloroplastic	NP_001307779	211	4.0/25	4.98/26.6	9	
12	proteasome subunit alpha type	AQL09261	285	6.8/26	6.11/27.5	15	↑
	maize 20 S proteasome α subunit	CAC19494	197	6.8/26	6.1/27.4	13	
13	50 S ribosomal protein L1	NP_001150277	221	6.8/26	8.69/37.2	16	↑
14	polynucleotidyl transferase ribonuclease H-like superfamily protein	AQK97097	296	4.2/19	8.32/47.1	11	↓
	50 S ribosomal protein L12-1	ACN34791	289	4.2/19	5.4/19.1	6	
15	FKBP-type peptidyl-prolyl <i>cis-trans</i> isomerase 4	NP_001148233	244	6.2/15	9.51/21.9	9	↓
16	germin-like protein precursor	NP_001140857	91	5.2/21	6.02/21.9	4	↓
17	chloroplastic Cu/Zn superoxide dismutase	BAI50561	256	4.7/17	5.31/18.7	5	↓
18	ribulose biphosphate carboxylase small chain C	ACG37749	238	5.4/13	8.98/19.1	9	↑
	ribulose 1,5-bisphosphate carboxylase/oxygenase	CAA68419	161	5.4/13	9.1/19.0	12	
19	ribulose biphosphate carboxylase small chain	P05348	192	7.2/12	9.1/19.1	12	↑
	ribulose 1,5-bisphosphate carboxylase/oxygenase	CAA68419	183	7.2/12	9.1/19.0	11	
20	oxygen-evolving enhancer protein 2	XP_008652004	300	5.8/25	9.5/31.8	11	↓
21	thylakoid lumenal 19 kDa protein	NP_001148434	81	4.7/23	5.48/27.2	9	↓
22	Thylakoid lumenal 17.4 kDa protein	AQK64808	161	4.5/16	7.44/23.6	13	↓
23	chloroplast ribulose biphosphate carboxylase/oxygenase activase, partial	Q9ZT00	247	5.3/43	6.29/47.9	19	↓
24	plastocyanin	XP_008648719	141	3.4/13	5.62/15.9	2	↓
25	chain A, crystal structure of Psbp	4RTH_A	379	5.9/25	5.96/20.1	11	↓
	oxygen-evolving enhancer protein 2	ONM27748	355	5.9/25	8.97/27.2	12	
26	glyceraldehyde-3-phosphate dehydrogenase 2	Q09054	143	6.9/39	6.41/36.5	11	↑
	glyceraldehyde-3-phosphate dehydrogenase 1	AQK50979	110	6.9/39	6.46/36.5	10	
27	glyceraldehyde-3-phosphate dehydrogenase 1	NP_001105413	194	6.8/25	6.46/36.5	11	↑
	glyceraldehyde-3-phosphate dehydrogenase 2	AQK78441	138	6.8/25	6.4/32.0	11	
28	glyceraldehyde-3-phosphate dehydrogenase 2	AQK78441	362	7.3/39	6.4/32.0	12	↑
	glyceraldehyde-3-phosphate dehydrogenase 1	AQK50979	277	7.3/39	6.46/36.5	12	

29	glyceraldehyde-3-phosphate dehydrogenase 2	Q09054	196	7.2/39	6.41/36.5	10	↑
	glyceraldehyde-3-phosphate dehydrogenase 1	AQK50979	120	7.2/39	6.46/36.5	9	
30	malate dehydrogenase	NP_001105420	81	5.3/43	5.79/46.8	12	↓
	malate dehydrogenase 1	ACG28169	74	5.3/43	6.49/46.8	11	
31	glyceraldehyde-3-phosphate dehydrogenase 1	AQK50981	149	5.4/39	6.45/32.0	6	↓
	glyceraldehyde-3-phosphate dehydrogenase 2	AQK78441	145	5.4/39	6.4/32.0	5	
32	fructose-bisphosphate aldolase	ACG36798	288	6.0/37	7.63/41.8	12	↓
33	fructose-bisphosphate aldolase	AQK39564	312	6.0/37	7.63/41.7	14	↓
34	fructose-bisphosphate aldolase	AQK39564	197	5.7/37	7.63/41.7	16	↓
35	peptidyl-prolyl cis-trans isomerase	NP_001149265	282	6.6/19	9.28/26.2	8	↑
36	50 S ribosomal protein L10	ONL96805	288	6.0/23	8.96/24.3	15	↑
37	Tat pathway signal sequence family protein	ONM33764	83	6.4/24	9.71/23.0	6	↑
	50 S ribosomal protein L21	ACG44073	82	6.4/24	9.34/22.9	7	
38	peptidyl-prolyl <i>cis-trans</i> isomerase	NP_001149265	237	5.9/19	9.28/26.2	6	↑
39	lipase-like	AQL01995	156	7.4/35	7.88/39.0	9	↑
	50 S ribosomal protein L1	NP_001150277	68	7.4/35	8.69/37.2	12	
40	peptidyl-prolyl <i>cis-trans</i> isomerase	AQK79627	585	7.2/19	9.4/26.4	11	↑
41	50 S ribosomal protein L1	NP_001150277	319	7.2/35	8.69/37.2	14	↑
42	NAD(P)-binding Rossmann-fold superfamily protein	AQK95531	545	7.1/27	9.11/31.8	16	↑
	NAD-dependent epimerase/dehydratase	ONM10952	243	7.1/27	9.44/22.3	8	
43	NAD-dependent epimerase/dehydratase	ACG33645	166	7.1/28	6.77/27.8	13	↑
44	proteasome subunit β type-6	AQK80294	137	5.8/24	5.48/26.1	12	↑
45	α/β -hydrolases superfamily protein	AQK52092	140	7.3/29	6.31/28.6	10	↑
46	β -D-glucosidase precursor	AEM17055	314	6.3/57	6.75/63.2	20	↓
	β -glucosidase2	AQK40582	243	6.3/57	6.75/64.1	21	
45	endo-1,3-1,4- β -D-glucanase	AAC69757	112	7.3/29	6.75/33.1	7	↑
47	superoxide dismutase	AQK93195	325	6.3/23	6.71/25.2	8	↑
	Mn-superoxide dismutase (mitochondrion)	AAA72020	171	6.3/23	6.23/25.3	4	
48	glutathione S-transferase 3	NP_001105111	281	7.0/25	5.96/23.9	6	↑
45	retrotransposon protein Ty1-copia subclass	ACG38448	146	7.3/29	6.5/30.0	11	↑
49	opaque endosperm 1	AQK56217	74	6.8/21	9.52/103	27	↑

Table 2 Suppl. A list of peptide sequences from the identified drought-responsive proteins in two maize genotypes under control and drought stress conditions. ^a - Spot ID numbers correspond to the spots in Fig. 1. ^b - Only a higher protein score and the number of matched peptides and the protein score confidence interval (C.I.) ≥ 95 % were reported as candidate drought-responsive proteins. ^c - The matched protein number in *NCB* databases. ^d - The protein score confidence interval (C.I.). ^e - The number of matched peptides.

Spots ID ^a	Significantly matched proteins ^b	Accession No. ^c	C.I. [%] ^d	NMP ^e	Sequence of identified peptides
1	ribulose biphosphate carboxylase small chain, chloroplastic	P05348	100	13	STASLPVAR,VIGFDNIK,QVDYLLR,YWTMWK,SYPDAFHR,SLGNVSNNGGRIR,NGWIPCLEFSK,ENSTSPCYYDGR,LPMFGCNDATQVYK,QTQCVSFIAYKPPGSD,FETLSYLPPLSTDDLLK,KFETLSYLPPLSTDDLLK,LPMFGCNDATQVYK
	ribulose 1,5-bisphosphate carboxylase/oxygenase	CAA68419	100	12	STASLPVAR,VIGFDNIK,YWTMWK,SYPDAFHR,SLGNVSNNGGRIR,NGWIPCLEFSK,ENSTSPCYYDGR,LPMFGCNDATQVYK,QTQCVSFIAYKPPGSD,FETLSYLPPLSTDDLLK,KFETLSYLPPLSTDDLLK,LPMFGCNDATQVYK
2	thylakoid lumenal 16.5 kDa chloroplastic protein	AQK66951	100	5	LSSSPEQR,SAFVSSATALEK,WIALAGLGGQLK,NVVDNSSLATLFTSVSK,QGISSSGAETGYLQDLIYR
	oxygen evolving enhancer protein 3 containing protein	ACG48907	100	8	LILQELMAK,EINNAETGTR,STFMYDFDK,STAFDLLALEDLLGK,LFDSFETLQEAFTAK,LISAAEDKPPFVDLANR,NGIYMADIGPSFAAHAYR,NGIYMADIGPSFAAHAYR
	photosynthetic NDH subunit of luminal location 3 chloroplastic	ONM50900	100	7	LILQELMAK,STFMYDFDK,STAFDLLALEDLLGK,LFDSFETLQEAFTAK,LISAAEDKPPFVDLANR,NGIYMADIGPSFAAHAYR,NGIYMADIGPSFAAHAYR
3	light-harvesting complex I 11 kDa protein	O65101	100	4	GPQEPQPGPR,KGPQEPQPGPR,FFETFAAPFTK,FFETFAAPFTK
4	lorophyll <i>a-b</i> binding protein 6A	ACG35952	100	4	ESEVYHCR,FKESVYHCR,YPGGAFDPLGFSR,KYPGGAFDPLGFSR
5	oxygen evolving complex 33 kDa subunit	AQK81304	100	18	NAPPEFQK,VPFLFTVK,RLTYDEIQSK,LCLEPTSFTVK,KLCLEPTSFTVK,GDEEELQKENIK,NAASSTGNITLSVTK,GGSTGYDNAVALPAGGR,DGIDYAAVTVQLPgger,ITCSLQDVASRCVDAK,GTGTANQCPTIDG
	oxygen-evolving enhancer protein 1	ACG31595	100	18	GVESFPFK,IGGRAPFASLPSRPSSQLACR,QLVATGKPESFGGPFLVPSYR,LAGFALATSALLVSGASAEGTPKR,FEEKDGIDYAAVTVQLPgger,GGSTGYDNAVALPAGGRGDEEELQK,SNPETGEVIGVFESVQPSDTDLGAK,QLVATGKPESFGGPFLVPSYR
6	glyceraldehyde-3-phosphatedehydrogenase 1	AQK50979	100	10	NAPPEFQK,VPFLFTVK,RLTYDEIQSK,LCLEPTSFTVK,KLCLEPTSFTVK,GDEEELQKENIK,NAASSTGNITLSVTK,GGSTGYDNAVALPAGGR,DGIDYAAVTVQLPgger,ITCSLQDVASRCVDAK,GTGTANQCPTIDG
	glyceraldehyde-3-phosphatedehydrogenase 2	Q09054	99.99	8	GVESFPFK,IGGRAPFASLPSRPSSQLACR,QLVATGKPESFGGPFLVPSYR,LAGFALATSALLVSGASAEGTPKR,FEEKDGIDYAAVTVQLPgger,GGSTGYDNAVALPAGGRGDEEELQK,SNPETGEVIGVFESVQPSDTDLGAK,QLVATGKPESFGGPFLVPSYR
7	malate dehydrogenase 2	NP_001142100	100	9	LTGMSFR,HSDITLK,LTGMSFR,IGINGFGR,YDTVHGHWK,AGIALNDHFVK,VPTVDVSVVDLTVR,TLLFGDKPVTVFGR,LVSWYDNEWGYSNR,GIMGYAEDLVSTDFLGDSR
					LTGMSFR,IGINGFGR,YDTVHGWQK,AGIALNDHFIK,VPTVDVSVVDLTVR,LVSWYDNEWGYSNR,GIMGYVEDLVSTDFTGDSR,LVSWYDNEWGYSNR
					GELKSSIDK,LFGVTTLDVVR,DDLNFNAGIVK,KLFGVTTLDVVR,RTQDGGTEVVEAK,NGVEEVGLGLGELNEFEK,GFMGDDQLGEALEGSDVVIIPAGVPR,GFMGDDQLGEALEGSDVVIIPAGVPR

8	nucleoside diphosphate kinase 1	NP_0012969 100 54	6	GDFAVDIGR, GLIGEHSR, NVIHGSDSIESANK, IIGAT NPLASEPGTIR, KIIGATNPLASEPGTIR, KIIGATNPLA SEPGTIR
9	nucleotide diphosphate kinase 1	NP_0011678 100 91	8	GLIGDIISR, GDYAVEVGR, GMKFMNVER, SNLHPWI YEA, IIGATRPWEAAPGTIR, KEIALWFPPEGVAQWK, R IIGATRPWEAAPGTIR, IIGATRPWEAAPGTIR
10	fructose-bisphosphate aldolase	AQK39564 100	13	TWGGQPDK, AAQDALLR, EAAYYQQGAR, ATPEQ VAAYTLK, LASIGLENTEANR, TVVSIPNGPSELAVK, RLASIGLENTEANR, IVDILAEQGIVPGIK, ALQNTCL KTWGGQPDK, TIASPGRGILAMDESATCGK, GLVP LAGSNNESWCQGLDGLASR, YAAISQDNGLVPIVEP EILLDGEHGIER, YAAISQDNGLVPIVEPEILLDGEHG IER
11	ATP synthase delta chain	ACG39343 100	9	MTGAKNVR, AELIGEIAK, DGSNLIDMSVR, SASFSS VARGLPSLR, TQLDPALIAGFTVQYGR, IFSDEAVAEF FDNPTVPR, LKTQLDPALIAGFTVQYGR, SSELQPHV VNFLNVVVDNFR, AAAEAAAESYASALSEVAVENG TLEQTVSDLEK
	H(+)-transporting ATP synthase, partial	CAA46804 100	7	MTGAKNVR, AELIGEIAK, DGSNLIDMSVR, TQLDPA LIAGFTVQYGR, IFSDEAVAEFFDNPTVPR, LKTQLDP ALIAGFTVQYGR, SSELQPHVVNFLNVVVDNFR
	ATP synthase delta chain, chloroplastic	NP_0013077 100 79	9	MTGAKNVR, AELIGEIAK, DGSNLIDMSVR, SASFSS VARGLPSLR, TQLDPALIAGFTVQYGR, IFADAVAEF FDNPTVPR, LKTQLDPALIAGFTVQYGR, SSELQPHV VNFLNVVVDNFR, AAAEAAAESYASALSEVAVENG TLEQTVSDLEK
12	proteasome subunit alpha type	AQL09261 100	15	EERLFR, SAGVTSIGVR, ATEIEVGVVR, HITIFSPEGR, LYQVEYAFK, GADSVCCVVTQK, EQEAINFLEK, GADS VCVVTQKK, CDPAGHFFGHK, WGYEMPVDVLAK, Y VGLLATGLTADAR, LLDQTSVTHLPITK, VLTTEEID QHLTAISER, VLTTEEIDQHLTAISERD, VLTTEEIDQH LTAISER
	maize 20 S proteasome α subunit	CAC19494 100	13	SAGVTSIGVR, ATEIEVGVVR, HITIFSPEGR, LYQVEY AFK, GADSVCCVVTQK, EQEAINFLEK, GADSVCCVVT QKK, CDPAGHFFGHK, WGYEMPVDVLAK, LLDQTS VTHLPITK, ALTTEEIDQHLTAISER, ALTTEEIDQHL TAISERD, ALTTEEIDQHLTAISERD
13	50 S ribosomal protein L1	NP_0011502 100 77	16	YNDQQLR, SGIVHIPFGK, LIASPDMMPK, FVESAEA HFR, TAYLCSSMGPSIK, KDYDVPTAISLMK, MNLDP KYNDQQLR, LIASPDMMPKVAGLGK, AAGADIVGG EDLIEQIK, LNIKEMLDYGLESD, AGTVSSNITQAI EFKK, TAYLCSSMGPSIKLNIK, QMSSAKFVESAEAH FR, TAYLCSSMGPSIKLNIK, VDFPEEDLIANFMSVVR , GIYWK TAYLCSSMGPSIK
14	polynucleotidyl transferase ribonuclease H- like superfamily	AQK97097 100	11	NLVDHLQER, MAVLQLCVGH, EVMGVEIEKPK, AV TVASTATESPK, FVGVVDVDVRLR, TEFDVVEEV PSSAR, CDCNIVNNTVDLR, VLELGDITAGLTLEEA R, QLEEVGAKCECDMLK, LGVTAAAFAPA AVVAAPG AGGGAAAEAPVEK, VLELGDITAGLTLEEAR
	50 S ribosomal protein L12-1	ACN34791 100	6	NLVDHLQER, AVTVASTATESPK, TEFDVVEEVPSA R, VLELGDITAGLTLEEAR, LGVTAAAFAPA AVVAAP GAGGGAAAEAPVEK, VLELGDITAGLTLEEAR
15	FKBP-type peptidyl-prolyl <i>cis-trans</i> isomerase 4	NP_0011482 100 33	9	GKPLTFR, LPPALAYGEK, LEDGTVFDSSYK, VVG TGAAGQQLIR, LEDGTVFDSSYK, GWDQGIVGGEG IPPMLAGGK, AHYTGRLEDGTVFDSSYK, GWEPTSC VIPPNSTLLFDVEYVGR, VVG TGAAGQQLIR
16	germin-like protein precursor	NP_0011408 99.98 57	4	VTFLDDAQVKK, SSVTANDFYFHGLAGQGK, AAVTP AFVGQFPGVNGLGISAAR, SSVTANDFYFHGLAGQG K

17	chloroplastic Cu/Zn superoxide dismutase	BAI50561	100	5	GGHELSTGNAGGR,AFVVHELEDDLK,GASEVE GVVTLTQDDDGPTTVNVR,AFVVHELEDDLKGGH ELSLSTGNAGGR,HAGDLGNIVANAEGIAEATIVDT QIPLTGPNSVVGR
18	ribulose biphosphate carboxylase small chain C	ACG37749	100	9	VIGFDNVR,YWTMWK,ENSTSPCYDGR,CMQVWP AYGNKK,ENSTSPCYDGR,ELQEIAAYPDAFHR,Q TQCVSFIAYKPPGSE,FETLSYLPPLSTDDLK,KFET LSYLPPLSTDDLK
	ribulose 1,5-bisphosphate carboxylase/oxygenase	CAA68419	100	12	STASLPVAR,VIGFDNIK,YWTMWK,SYPDAFHR,ENS TSPCYDGR,CMQVWPAYGNKK,ENSTSPCYDGR, LPMFGCNDATQVYK,QTQCVSFIAYKPPGSD,ELQE AKSYPDFAHR,FETLSYLPPLSTDDLK,KFETLSYL PPLSTDDLK
19	ribulose biphosphate carboxylase small chain	P05348	100	12	STASLPVAR,VIGFDNIK,QVDYLLR,YWTMWK,SYP DAFHR,ENSTSPCYDGR,IRCMQVWPAYGNK,LPM FGCNDATQVYK,QTQCVSFIAYKPPGSD,FETLSYLP PLSTDDLK,KFETLSYLPPLSTDDLK,ENSTSPCY DGR
	ribulose 1,5-bisphosphate carboxylase/oxygenase	CAA68419	100	11	STASLPVAR,VIGFDNIK,YWTMWK,SYPDAFHR,ENS TSPCYDGR,IRCMQVWPAYGNK,LPMFGCNDATQ VYK,QTQCVSFIAYKPPGSD,FETLSYLPPLSTDDLK ,KFETLSYLPPLSTDDLK,VIGFDNIK
20	oxygen-evolving enhancer protein 2	XP_0086520 04	100	11	EFPGQVLR,QYYAVSVLTR,EREFGQVLR,HQLIAAT VSDGK,ASTEYIAYS GDGFK,TADGDEGGKHQLIAA TVSDGK,YEDNFDANSNVSVIIQPTSK,TIADYGSPEE FLSQVDYLLGR,KTIADYGSPEEFLSQVDYLLGR,TD SEGGFETGAVATANVLESSTPVVDGK,EFPGQVLR
21	thylakoid luminal 19 kDa protein	NP_0011484 34	99.78	9	EYLTFLSGIR,GTNGTDSEFFNPR,AEKEYLTFLSGIR, DTAEYVYDVPEGWK,LYAHFVTAPNAEWSR,KDTA EYVYDVPEGWK,ADGAGQVYVEYEVAGASAHSLIS VTCAR,ALAPLSAVLDNLALSDVGLLDQISSADDVR ,EYLTFLSGIR
22	thylakoid luminal 17.4 kDa protein	AQK64808	100	13	FCDYTNEK,SLAAALMSEAK,LPPLSTEPNR,GTDF NAVIDR,LCTNTSISPDAR,NTVLSGSTFDDAK,GTDF TNAVIDRVNFEK,MASSSCLASPGATLCRPR,MDDV VFEDTIIGYIDLQK,AFVGNTIGQANGVYDKPLDLR, ADLTGAIFKNTVLSGSTFDDAK,LACGVLAAWSVAS ASNPVIAASQR,LPPLSTEPNR
23	chloroplast ribulose bisphosphate carboxylase/oxygenase activase, partial	Q9ZT00	100	19	VYDDEVVR,FYWAPTR,VYDDEVRR,QTDEDRWK,NF MTLPNIK,EGPPTFEQPK,SFQCELVFAK,MEKFYWAP TR,WVSETGVENIAR,GFMDKLVVHLSK,MSCLFIND LDAGAGR,AAAFSSTVGAPASTPTR,MSCLFINDLDA GAGR,GLAYDISDDQQDITR,SYNFDNMMDGFYIAK ,LLEYGHMLVAEQENVK,LLEYGHMLVAEQENVKR, VPIIVTGNDFSTLYAPLIR,TDGVDEEHVVQLVDTFP GQSIDFFGALR,
24	plastocyanin	XP_0086487 19	100	2	NNAGFPHNVVFEDEVPSGVDATK,NNAGFPHNVV FDEVPSGVDATK
25	chain A, crystal structure of Psbp	4RTH_A	100	11	EFPGQVLR,AYGEAANVFGK,EREFGQVLR,QYYSI TVLTR,HQLITATVSDGK,NTDFISYVGDGFK,KNTDF ISYVGDGFK,TADGDEGGKHQLITATVSDGK,YEDN FDANSNVSVIIQPTSK,AITEYGSPEEFLSQVDYLLG K,TDSEGGFETDAVATANVLESSTPVVDGK
	oxygen-evolving enhancer protein 2	ONM27748	100	12	EFPGQVLR,SAQLFVCK,SAQLFVCKAQK,EREFGQ VLR,QYYISITVLTR,HQLITATVSDGK,NTDFISYVGD GFK,KNTDFISYVGDGFK,TADGDEGGKHQLITATVS DGK,YEDNFDANSNVSVIIQPTSK,AITEYGSPEEFLS QVDYLLGK,TDSEGGFETDAVATANVLESSTPVVDG K

26	glyceraldehyde-3-phosphatedehydrogenase 2	Q09054	100	11	IGINGFGR,YDTVHGWQWK,AGIALNDHFIK,AVGKVL PELNGK,VPTVDVSVVDLTVR,TLLFGEKPVTVFGIR, LVSWYDNEWGYSNR,GIMGYVEEDLVSTDFTGDSR ,VIHDNFGIIEGLMTTVHAITATQK,NPEEIPWGEAGA EYVVESTGVFTDKDK,GIMGYVEEDLVSTDFTGDSR
	glyceraldehyde-3-phosphatedehydrogenase 1	AQK50979	100	10	IGINGFGR,YDTVHGHWK,AGIALNDHFVK,VPTVD VSVVDLTVR,TLLFGDKPVTVFGIR,LVSWYDNEWG YSNR,YDTVHGHWKHSDITLK,GIMGYAEEDLVSTD FLGDSR,NPEEIPWGEAGA EYVVESTGVFTDKDK,L VSWYDNEWGYSNR
27	glyceraldehyde-3-phosphatedehydrogenase 1	NP_0011054 13	100	11	LTGMSFR,IGINGFGR,GASYEDIKK,YDTVHGHWK, AGIALNDHFVK,AASFNIIPSSSTGAAK,VPTVDVSVV DLTVR,TLLFGDKPVTVFGIR,LVSWYDNEWGYSNR, GIMGYVEEDLVSTDFLGDSR,LVSWYDNEWGYSNR
	glyceraldehyde-3-phosphatedehydrogenase 2	AQK78441	100	11	GASYEEIK,YDTVHGWQWK,AGIALNDHFIK,AASFNI PSSSTGAAK,VPTVDVSVVDLTVR,TLLFGEKPVTVFG IR,LVSWYDNEWGYSNR,TYMFKYDTVHGWQWK,GI MGYVEEDLVSTDFTGDSR,AGIALNDHFIKLVSWYD NEWGYSNR,LVSWYDNEWGYSNR
28	glyceraldehyde-3-phosphatedehydrogenase 2	AQK78441	100	12	LTGMSFR,GASYEEIKK,YDTVHGWQWK,AGIALNDH FIK,DAPMFVVGVNEDK,VPTVDVSVVDLTVR,TLLF GEKPVTVFGIR,LVSWYDNEWGYSNR,TYMFKYDT VHGWQWK,GIMGYVEEDLVSTDFTGDSR,NPEEIPWG EAGA EYVVESTGVFTDK,NPEEIPWGEAGA EYVVE STGVFTDKDK
	glyceraldehyde-3-phosphatedehydrogenase 1	AQK50979	100	12	HSDITLK,LTGMSFR,IGINGFGR,YDTVHGHWK,AGI ALNDHFVK,DAPMFVVGVNEDK,VPTVDVSVVDLT VR,TLLFGDKPVTVFGIR,LVSWYDNEWGYSNR,GI MGYAEEDLVSTDFLGDSR,NPEEIPWGEAGA EYVVE STGVFTDK,NPEEIPWGEAGA EYVVESTGVFTDKD K
29	glyceraldehyde-3-phosphatedehydrogenase 2	Q09054	100	10	LTGMSFR,IGINGFGR,GASYEEIKK,YDTVHGWQWK, AGIALNDHFIK,DAPMFVVGVNEDK,VPTVDVSVVD LTVR,TLLFGEKPVTVFGIR,LVSWYDNEWGYSNR,G IMGYVEEDLVSTDFTGDSR
	glyceraldehyde-3-phosphatedehydrogenase 1	AQK50979	100	9	LTGMSFR,IGINGFGR,YDTVHGHWK,AGIALNDHFV K,DAPMFVVGVNEDK,VPTVDVSVVDLTVR,TLLFG DKPVTVFGIR,LVSWYDNEWGYSNR,GIMGYAEEDL VSTDFLGDSR
30	malate dehydrogenase	NP_0011054 20	99.77	12	RGGVLIQK,SSAASTAVSIVDAIR,ECFGVFCTTYDLK ,LASGEVFGDQPIALK,QAQDGVATAVATEAPASR,K ECFGVFCTTYDLK,ECFGVFCTTYDLKAEDK,GDGD YELASDVLMDDFLWER,SFQALEGVAMELEDSLYP LLR,VSNVTIWGNHSTTQVPDFLNAK,SKGDGDYEL ASDVLMDDFLWER,SSAASTAVSIVDAIR
	malate dehydrogenase 1	ACG28169	98.78	11	RGGVLIQK,SSAASTAVSIVDAIR,ECFGVFCTTYDLK ,QAQDGVATAVATEAPASR,KECFGVFCTTYDLK,ECF GVFCTTYDLKAEDK,GDGDYELASDVLMDDFLWE R,SFQALEGVAMELEDSLYPLLR,VSNVTIWGNHSTT QVPDFLNAK,SKGDGDYELASDVLMDDFLWER,SS AASTAVSIVDAIR
31	glyceraldehyde-3-phosphate dehydrogenase 1	AQK50981	100	6	HSDITLKDSK,VPTVDVSVVDLTVR,TLLFGDKPVTV FGIR,LVSWYDNEWGYSNR,GIMGYAEEDLVSTDFL GDSR,LVSWYDNEWGYSN
	glyceraldehyde-3-phosphate dehydrogenase 2	AQK78441	100	5	VPTVDVSVVDLTVR,TLLFGEKPVTVFGIR,LVSWYD NEWGYSNR,LVSWYDNEWGYSNR,GIMGYVEEDLV STDFTGDSR
32	fructose-bisphosphate aldolase	ACG36798	100	12	AAQDALLLR,EAAYYQQGAR,ATPEQVAAYTLK,LA SIGLENTEANR,TVVSSIPNGPSELAVK,RLASIGLEN TEANR,IVDILVEQGIVPGIK,ALQNTCLKTWGGQPD K,SEWGATRQAAAPRPPTVSMVVR,GLVPLAGSNNE WCQGLDGLASR,YAAISQDNLVPIVEPEILLDGEH GIER,AAQDALLLR

33	fructose-bisphosphate aldolase	AQK39564	100	14	EAAWGLAR,TWGGQDPDK,AAQDALLLR,EAAYYQQGAR,ATPEQVAAYTLK,LASIGLENTEANR,TVVSIPNGPSELAVK,RLASIGLENTEANR,IVDILAEQGIVPGIK,ALQNTCLKTWGGQDPDK,SEWGATRQAAAPRPPTVSMVVR,GLVPLAGSNNESWCQGLDGLASR,YAAISQDNGLVPIVEPEILLDGEHGIER,AAQDALLLR
34	fructose-bisphosphate aldolase	AQK39564	100	16	TWGGQDPDK,AAQDALLLR,ASAYADELVK,YTSDGEAAEAK,EAAYYQQGAR,ATPEQVAAYTLK,LASIGLENTEANR,GILAMDESNATCGK,TVVSIPNGPSELAVK,RLASIGLENTEANR,IVDILAEQGIVPGIK,ALQNTCLKTWGGQDPDK,GLVPLAGSNNESWCQGLDGLASR,SEWGATRQAAAPRPPTVSMVVR,GLVPLAGSNNESWCQGLDGLASR,YAAISQDNGLVPIVEPEILLDGEHGIER
35	peptidyl-prolyl cis-trans isomerase	NP_001149265	100	8	TFKDENFK,VYFDISIGNPVGK,VISDFMIQGGDFDK,ITNKVYFDISIGNPVGK,IVIGLYGDDVPQTTFENFR,VISDFMIQGGDFDKGNGTGGK,HVVFGQVLEGMDVVSLIESQETDR,VYFDISIGNPVGK
136	50 S ribosomal protein L10	ONL96805	100	15	DALPDTCR,ALETMPSR,AFQKEER,FYGPGRDFK,EETVTTVR,DALPDTCR,KEETVTTVR,DVVAVLSAYVR,DALPDTCRLLVAK,EQLEGCYLLAGIK,VEETNDFVGAVFEGK,AIEGTPWEALKPCMK,EQLEGCYLLAGIKYEGLTVK,GMNAWLFVHTEEVPAALKPYR,AEVYATLLGALQGPATSLVATLQAPAR
37	Tat pathway signal sequence family protein	ONM33764	99.87	6	LFVIVAPVR,VPGLSEPDENGWR,ALASAAVASVLGFAGR,AAAVTCFSGPSLSVGR,VPDGWDEVVPVSADLGGTEIDLR,VPGLSEPDENGWR
	50 S ribosomal protein L21	ACG44073	99.82	7	QYIVMPGR,TLTLSTLPSLR,GANVNDQIILNK,DADIFAVVMIGSR,DADIFAVVMIGSR,AYIGMPVVTNAAVHAVVEEQGR,AYIGMPVVTNAAVHAVVEEQGRDDK
38	peptidyl-prolyl cis-trans isomerase	NP_001149265	100	6	TFKDENFK,VYFDISIGNPVGK,VISDFMIQGGDFDK,IVIGLYGDDVPQTTFENFR,HVVFGQVLEGMDVVSLIESQETDR,VISDFMIQGGDFDK
39	lipase-like	AQL01995	100	9	YNYQNSAR,VIPDFLCR,FGLPFLPPSK,VIPDFLCR,CSDGRVIPDFLCR,IMYADFYSAVYDMVK,GANMAITGATAMDAPFFR,FNDLSTNHNAQLQAQISALQAK,KFNDLSTNHNAQLQAQISALQAK
	50 S ribosomal protein L1	NP_001150277	95.96	12	YNDQQLR,SGIVHIPFGK,LIASPDMMPK,FVESAEAHFR,DYDVPTAISLMK,TAYLCSSMGPSIK,LIASPDMPKVAGLGK,AAGADIVGGEDLIEQIK,AGTVSSNITQAIEEFKK,TAYLCSSMGPSIKLNIK,QMSSAKFVESA EAHFR,VDFPEEDLIANFMSVVR
40	peptidyl-prolyl cis-trans isomerase	AQK79627	100	11	TPWLDGR,TFKDENFK,LIESQETDR,VYFDISIGNPVGK,VISDFMIQGGDFDK,LIESQETDRGDRPK,HVVFGQVVEGMDIVR,ITNKVYFDISIGNPVGK,IVIGLYGDVVPQTAENFR,VISDFMIQGGDFDKGNGTGGK,LVHTGPGVVSMANAGPNTNGSQFFICTVK
41	50 S ribosomal protein L1	NP_001150277	100	14	YNDQQLR,IAVLTQGEK,SGIVHIPFGK,LIASPDMMPK,FVESAEAHFR,ILGPRGLMPNPK,DYDVPTAISLMK,TAYLCSSMGPSIK,KDYDVPTAISLMK,AGTVSSNITQAIEEFKK,AAGADIVGGEDLIEQIK,AGTVSSNITQAIEEFKK,VDFPEEDLIANFMSVVR,VDFPEEDLIANFMSVVR
42	NAD(P)-binding Rossmann-fold superfamily protein	AQK95531	100	16	TVLVTGAGGR,ALFAQVNSR,MKPGFDPSK,EREGQFVGR,LGNANILVWK,ALFAQVNSRF,AGGLQDKDGLR,IGGGDDVVFVGDIR,ELIVGKDDEILK,AEQYLADSLPYTHIR,ADVAEVCIQALLFEESK,KAQYLADSLPYTHIR,HIVLVGSMGGTDINHPLNK,AFDLASKPEGETPTTDFR,GGRPEFYFEEGSYEQVDWIGQK,IGGGDDVVFVGDIR

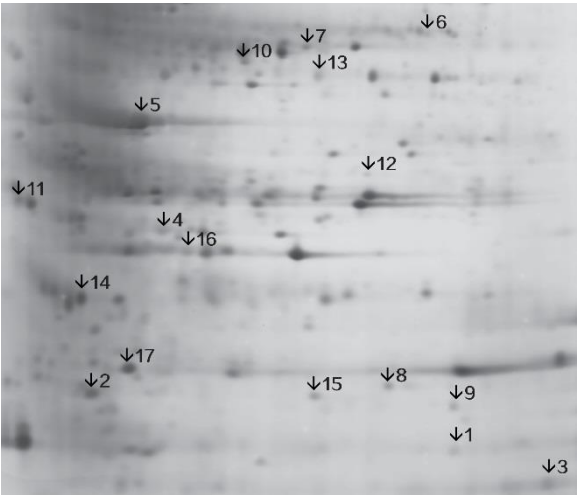
	NAD-dependent epimerase/dehydratase	ONM10952	100	8	MKPGFDPSK,ERSEQFVAR,IGAAGDVYVADIR,AEQYLADSGIPYTIIR,KAEQYLADSGIPYTIIR,LAPAVQGVDALIILTSAPK,MADSATSRPTVLVTGAGGRTGQIVYNK,MKPGFDPSK
43	NAD-dependent epimerase/dehydratase	ACG33645	100	13	ALFSQITAR,ALFSQITARF,IGAAGDVYVADIR,AFDLASKPEGVGTPTK,ADSATSRPTVLVTGAGGR,ELLVGKDDELLQTDTK,ADVAEVCVQALQYEEAK,LAPAVQGVDAIILTSAPK,AEQYLADSGIPYTIIRPGGLQDK,KAEQYLADSGIPYTIIRPGGLQDK,GGRPEFYEDGMYPEQVDWLQK,MADSATSRPTVLVTGAGGRTGQIVYNK,IGAAGDVYVADIR
44	proteasome subunit β type-6	AQK80294	100	12	NFYPGDK,VVSLAMAR,LLAYQNK,RNFYPGDK,TVTINADGVK,TSTGMVYANR,ITQLTDNVYVCR,SGSADTQVISDYVR,YEGGQIFSVPLGGTILK,ASDKITQLTDNVYVCR,YFLHQHTIQLGQPATVK,ITQLTDNVYVCR
45	endo-1,3-1,4- β -D-glucanase	AQK52092	100	10	AYVSGAASSSR,ERHEVPYYAK,AAEDAKPLFAALK,AGYFVVVPDFLK,IFQGVHGFACR,EGKSVAVGGYCWGGK,QLAEAGEVVHDLPGGLR,AVCLSHPYSVTADDMK,AVVLASDVFGYEAPLLR,AVVLASDVFGYEAPLLR
46	β -D-glucosidase precursor	AEM17055	100	20	FSISWPR,RLDYIQR,EMGMDAYR,GDYPFSMR,YYKGENGR,EMGMDAYR,IGLAFDVMGR,VCFDNFGDK,ERLPFFSDK,VPYGTSLDEQAK,EKPLPMEAALNDYK,GTVEGGINQDGIDYK,EKPLPMEAALNDYKR,SMDINLGWFLEPVVR,VGNENGVLQSPSEIPR,GESNWDHFCHNFPER,GTVEGGINQDGIDYK,GESNWDHFCHNFPER,IMDGSNADIGANSYHMYK,IGLAFDVMGR
	β -glucosidase 2	AQK40582	100	21	FSISWPR,RLDYIQR,EMGMDAYR,GDYPFSMR,YGIVYVDR,YYKGENGR,EMGMDAYR,IGLAFDVMGR,VCFDNFGDK,ERLPFFSDK,VPYGTSLDEQAK,EKPLPMEAALNDYK,GTVEGGINQDGIDYK,EKPLPMEAALNDYKR,SMDINLGWFLEPVVR,VGNQNGVQLLSPSEIPR,GESNWDHFCHNFPER,GTVEGGINQDGIDYK,IMDGSNADIGANSYHMYK,YGNPPIYITENIGDVIDTK,NKYGNPPIYITENIGDVIDTK
45	endo-1,3-1,4- β -D-glucanase	AAC69757	100	7	AAEDAKPLFAALK,AGYFVVVPDFLK,EGKSVAVGGYCWGGK,QLAEAGEVVHDLPGGLR,AVCLSHPYSVTADDMK,AVVLASDVFGYEAPLLR,AVVLASDVFGYEAPLLR
47	superoxide dismutase	AQK93195	100	8	YAGEVYENVLA,HHATYVANYNK,GDASAVVQLQGAIK,NVRPDYLNNIWK,FNGGGHVNHSIFWK,NLKPISEGGEPHKG,NLKPISEGGEPHKG,LGWAIDEDFGSFEALVK
	Mn-superoxide dismutase (mitochondrion)	AAA72020	100	4	GDASAVVQLQGAIK,NVRPDYLNNIWK,NVRPDYLNNIWK,LGWAIDEDFGSFEALVK
48	glutathione S-transferase 3	NP_001105111	100	6	VLDVYEAHLAR,LYGMPLSPNVVR,YASEGTDLLPATASAAK,GLDFEIVPVDLTGAHK,YLAGDEFTLADANHASYLLYLSK,GLDFEIVPVDLTGAHK
45	retrotransposon protein Ty1-copia subclass	ACG38448	100	11	AYVSGAASSSR,ERHEVPYYAK,AAEDAKPLFAALK,AGYFVVVPDFLK,IFQGVHGFACR,EGKSVAVGGYCWGGK,YNTTDPFAVQDRR,QLAEAGEVVHDLPGGLR,AVCLSHPYSVTADDMK,AVVLASDVFGYEAPLLR,ERHEVPYYAK

49	opaque endosperm 1	AQK56217	98.78	27	SRLPVER,SAAQNEHAK,AEILDNAAR,TYAEFVDR,E TAAAVIVQK,MMTKGILEK,SNGLFTTPSR,HIYESPT PTK,IFGQLRDNLK,EASISIQAYCR,AGQIILDMRR, QATVAIQCSWR,ETAAAVIVQKYVR,EISPLLNCIQA PK,QDLCPSLSVRQIYR,HEQNHEILLRCIK,QQLTAC VEKIFGQLR,QIYRICSMYWDDK,EVEGKCNHLQQN LDK,LPVERHEQNHEILLR,QKAFNMPTMNNLSVAP K,AHLQACLAALLIQSYIR,RAHLQACLAALLIQSYI R,DGKPVAACIIYKCLLHWR,AFNMPTMNNLSVAPK TLSEK,FAVLVPELMIGSYDEKMMTK,
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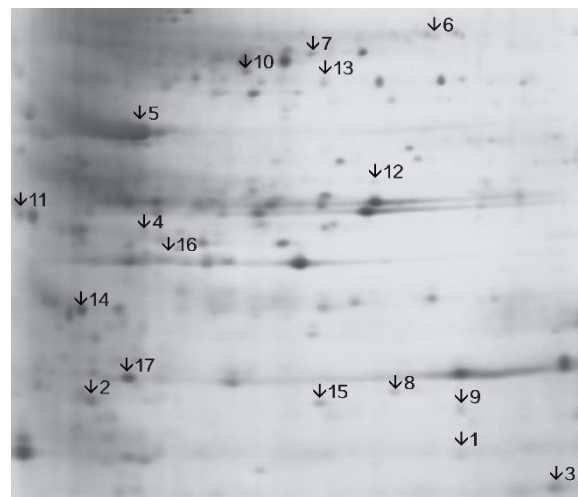
DH-CK1 (Denghai 605-control 1)



DH-DK2 (Denghai 605-control 2)



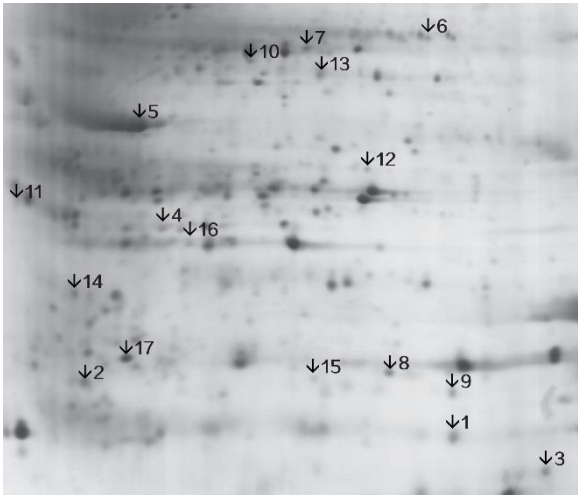
DH-DK3 (Denghai 605-control 3)



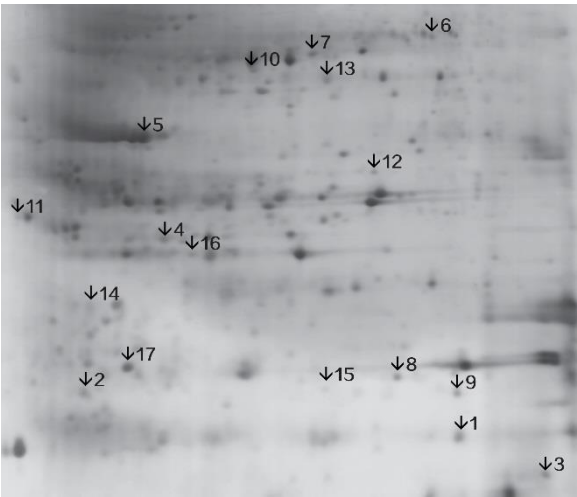
DH-DS1 (Denghai 605-drought stress 1)



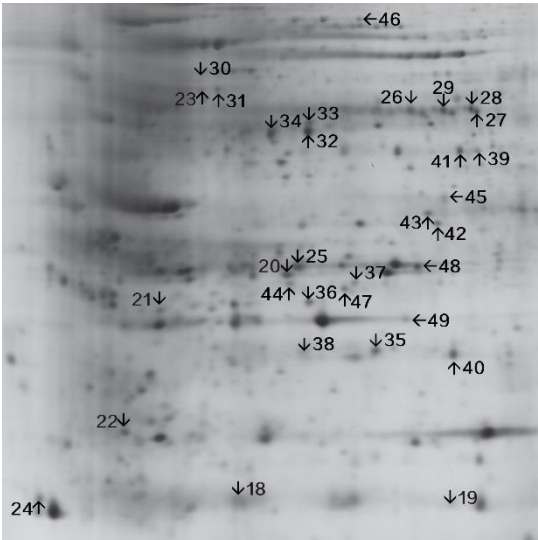
DH-DS2 (Denghai 605-drought stress 2)



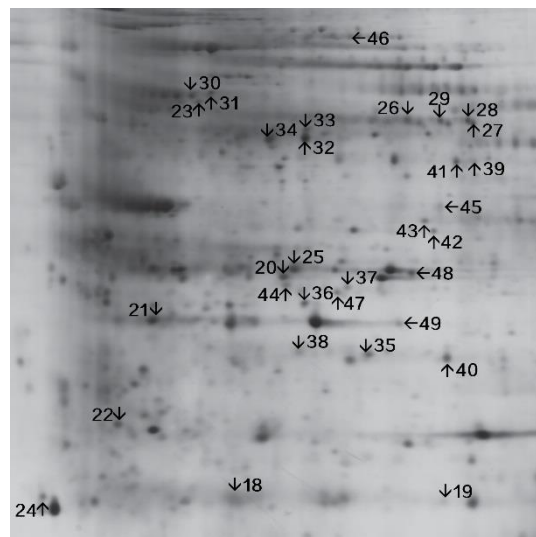
DH-DS3 (Denghai 605-drought stress 3)



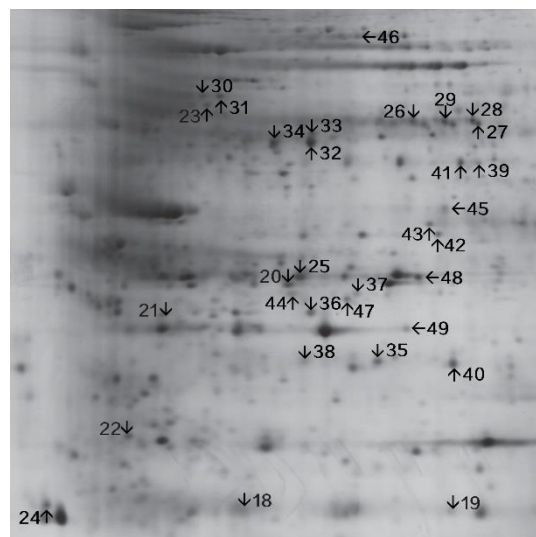
LY-CK1 (Liyu 35-control 1)



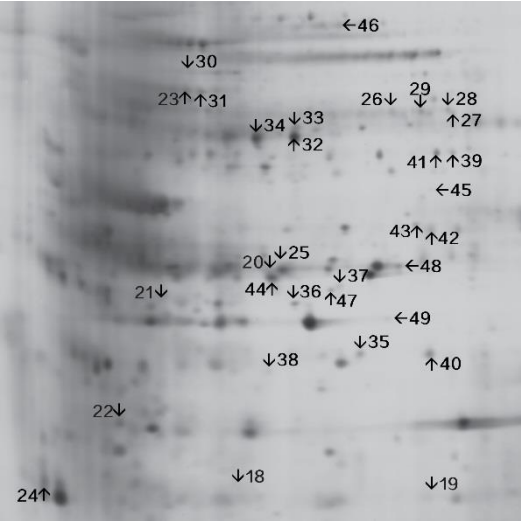
LY-CK2 (Liyu 35-control 2)



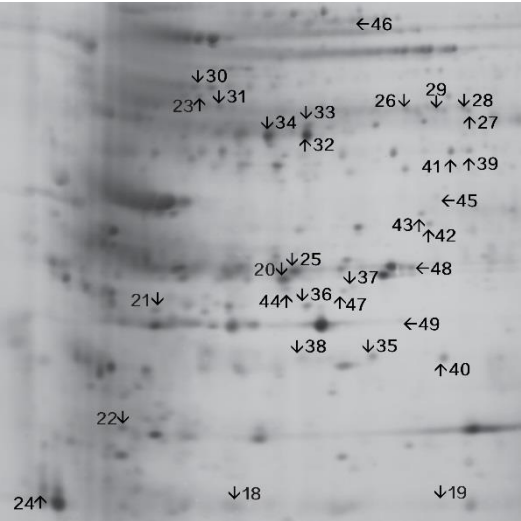
LY-CK3 (Liyu 35-control 3)



LY-DS1 (Liyu 35-drought stress 1)



LY-DS2 (Liyu 35-drought stress 2)



LY-DS-3 (Liyu 35-drought stress 3)

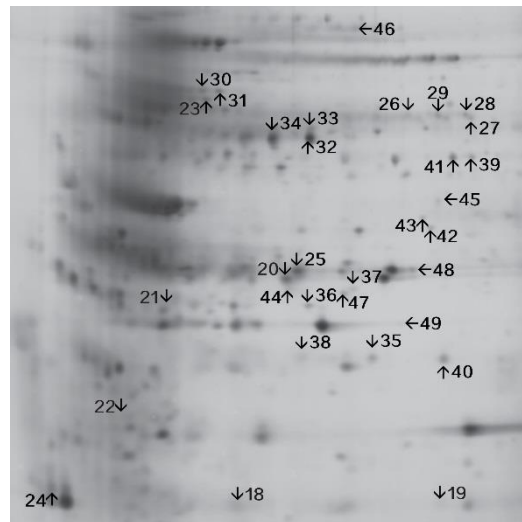


Fig. 1 Suppl. The images of all two-dimensional gel electrophoresis gels showing the leaf proteomes of drought-stressed and control plants of two maize genotypes. Three gels, three independent biological replicates in each treatment.