

Um *et al.*, Supplementary Figure 1

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Gm10 Ra  FLKGHEDLRQDE RVMQLFGLVNTLLSENS PKTAEKDLS IQRYAVI PL SPNSGLI EWVPNC 2139
Gm10 Fb  FLKGHEDLRQDE RVMQLFGLVNTLLSENS PKTAEKDLS IQRYAVI PL SPNSGLI EWVPNC 2139
At10 R   FLKGHEDLRQDE RVMQLFGLVNTLLSENS PKTAEKDLS IQRYAVI PL SPNSGLI EWVPNC 2123
*****

Gm10 Ra  DTLHLH IREYRDA RKITL NQEHKCM LSEA PDYDHLPLI AKVEVEE HADLNTEGNDLARVIL 2199
Gm10 Fb  DTLHLH IREYRDA RKITL NQEHKCM LSEA PDYDHLPLI AKVEVEE HADLNTEGNDLARVIL 2199
At10 R   DTLHLH IREYRDA RKITL NQEHKCM LSEA PDYDHLPLI AKVEVEE HADLNTEGNDLARVIL 2183
*****

Gm10 Ra  WLKSR TSETWLER RTNYTRS LA VMSMVGYLL GLGDRHP SNLM LHRFS GKILLHID EGDCEE 2259
Gm10 Fb  WLKSR TSETWLER RTNYTRS LA VMSMVGYLL GLGDRHP SNLM LHRFS GKILLHID EGDCEE 2259
At10 R   WLKSR TSETWLER RTNYTRS LA VMSMVGYLL GLGDRHP SNLM LHRFS GKILLHID EGDCEE 2243
*****

Gm10 Ra  ASMNRE KEPEKVP FRITRML VKAMEVSGI EGNFRSTCE NVMQVLR TNKD SVMAMMEAFVH 2319
Gm10 Fb  ASMNRE KEPEKVP FRITRML VKAMEVSGI EGNFRSTCE NVMQVLR TNKD SVMAMMEAFVH 2319
At10 R   ASMNRE KEPEKVP FRITRML VKAMEVSGI EGNFRSTCE NVMQVLR TNKD SVMAMMEAFVH 2303
*****

Gm10 Ra  DPLI NWRLFNENE VP QMSMLTSN---HVPP VVNSEE---SAPNREL DHPQRGARE RELLQF 2374
Gm10 Fb  DPLI NWRLFNENE VP QMSMLTSN---HVPP VVNSEE---SAPNREL DHPQRGARE RELLQF 2374
At10 R   DPLI NWRLFNENE VP QMSMLTSN---HVPP VVNSEE---SAPNREL DHPQRGARE RELLQF 2363
*****

Gm10 Ra  VNQLGD ANEVLNE RA VVVMARM SNKLTGR DE STCSSVSNSSPQHA VD HS SLI SCDTREV 2432
Gm10 Fb  VNQLGD ANEVLNE RA VVVMARM SNKLTGR DE STCSSVSNSSPQHA VD HS SLI SCDTREV 2432
At10 R   VNQLGD ANEVLNE RA VVVMARM SNKLTGR DE STCSSVSNSSPQHA VD HS SLI SCDTREV 2417
*****

Gm10 Ra  HRLS VKLQVQKLI IQASHE NL CQNYVGVCP EW 2468
Gm10 Fb  HRLS VKLQVQKLI IQASHE NL CQNYVGVCP EW 2468
At10 R   HRLS VKLQVQKLI IQASHE NL CQNYVGVCP EW 2453
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Um *et al.*, Supplementary Figure 2

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GmS6 K1a  FEELKVVGQGAERKUYQVRKNEFS ELYAMKVMRKDKIMKKNHAEYMKAEERDILT KIDHPF 209
GmS6 K1b  FEELKVVGQGAERKUYQVRKNEFS ELYAMKVMRKDKIMKKNHAEYMKAEERDILT KIDHPF 209
GmS6 K1c  FEELKVVGQGAERKUYQVRKNEFS ELYAMKVMRKDKIMKKNHAEYMKAEERDILT KIDHPF 209
At S6 K1   FEELKVVGQGAERKUYQVRKNEFS ELYAMKVMRKDKIMKKNHAEYMKAEERDILT KIDHPF 193
**      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

GmS6 K1a  VVQLRYSEQTKYR LYLVLDFVNGGHLEFQ LYHQGLFRE DLARTYT AEIVCAVSHLHANGI 269
GmS6 K1b  VVQLRYSEQTKYR LYLVLDFVNGGHLEFQ LYHQGLFRE DLARTYT AEIVSAVSHLHANGI 269
GmS6 K1c  VVQLRYSEQTKYR LYLVLDFVNGGHLEFQ LYHQGLFRE DLARTYT AEIVCAVSHLHANGI 269
At S6 K1   IVQLRYSEQTKYR LYLVLDFVNGGHLEFQ LYHQGLFRE DLARTYT AEIVSAVSHLHANGI 253
*      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

GmS6 K1a  MHRDLKPENILLD ADGHVMLTD EGLAKQF EE STRSNMCGTLEYMAP EITLGRGHDKARD 329
GmS6 K1b  MHRDLKPENILLD ADGHVMLTD EGLAKQF EE STRSNMCGTLEYMAP EITLGRGHDKARD 329
GmS6 K1c  MHRDLKPENILLD ADGHVMLTD EGLAKQF EE STRSNMCGTLEYMAP EITLGRGHDKARD 329
At S6 K1   MHRDLKPENILLD ADGHVMLTD EGLAKQF EE STRSNMCGTLEYMAP EITLGRGHDKARD 313
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

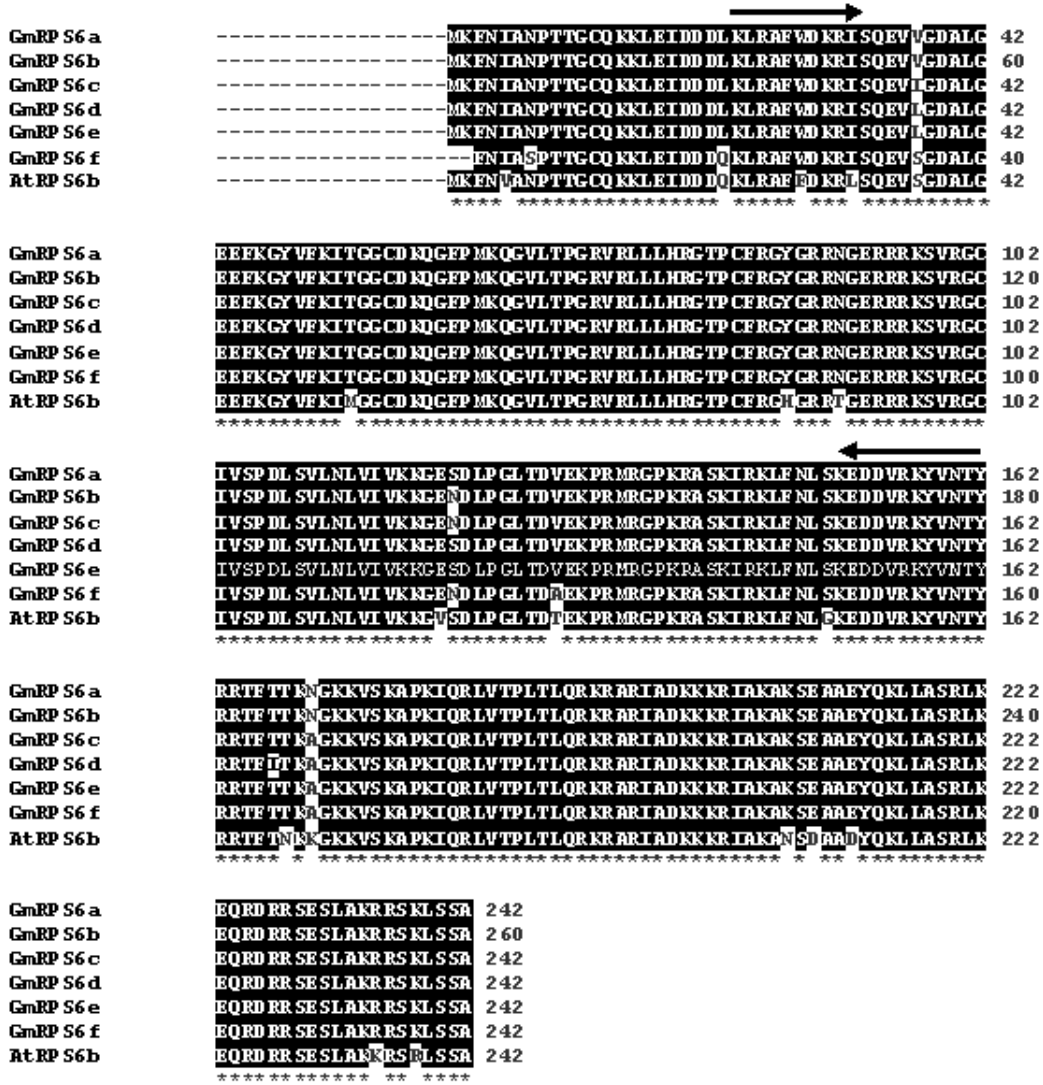
GmS6 K1a  WWSVGLLLYEMLT GKPPFCGGRDKIQOKIVKDKIKLP AFLSSEAHSLKGLLQKEPERR 389
GmS6 K1b  WWSVGLLLYEMLT GKPPFCGGRDKIQOKIVKDKIKLP AFLSSEAHSLKGLLQKEPERR 389
GmS6 K1c  WWSVGLLLYEMLT GKPPFCGGRDKIQOKIVKDKIKLP AFLSSEAHSLKGLLQKEPERR 389
At S6 K1   WWSVGLLLYEMLT GKPPFCGGRDKIQOKIVKDKIKLP AFLSSEAHSLKGLLQKEPERR 372
***** * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

GmS6 K1a  LGCGRGVVEETKSHKWEKPI NQKLEARE IQPSRPEVAGVQCVA NE EKRWTDMPVVDSF 449
GmS6 K1b  LGCGRGVVEETKSHKWEKPI NQKLEARE IQPSRPEVAGVQCVA NE EKRWTDMPVVDSF 449
GmS6 K1c  LGCGRGVVEETKSHKWEKPI NQKLEARE IQPSRPEVAGVQCVA NE EKRWTDMPVVDSF 449
At S6 K1   LGCGRGVVEETKSHKWEKPI NQKLEARE IQPSRPEVAGVQCVA NE EKRWTDMPVVDSF 432
**      * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

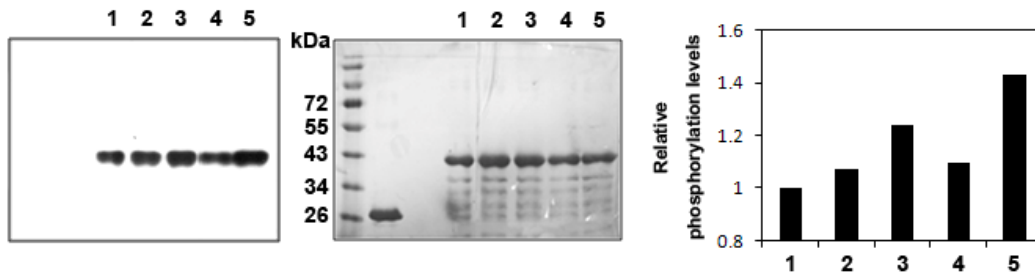
GmS6 K1a  RASPNG 455
GmS6 K1b  RASPNG 455
GmS6 K1c  RASPNG 455
At S6 K1   RASPSS 438
*      * *

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Um *et al.*, Supplementary Figure 3



Um *et al.*, Supplementary Figure 4



Um *et al.*, Supplementary Figure 5

Spot #1,3: cytosolic glutamine synthetase GSbeta1 [Glycine max]

1	MSLLSDLINL	NLSDTTEKVI	AEYIWIGGSG	MDLRSKARTL	PGPVSDPSEL
51	PKWNYDGSST	GQAPGEDSEV	ILYPQAIFRD	PFRRGNNILV	ICDAYTPAGE
101	PIPTNKRHAA	AKVFSHPDVV	AEVPWYGIEQ	EYTLLQKDIQ	WPLGWPVGGF
151	PGPQGPYYCG	VGADKAFGRD	IVDAHYKACI	YAGINISGIN	GEVMPGQWEF
201	QVGPSVGISA	GDEIWAARYI	LER ITEIAGV	VVSFDPKPIK	GDWNGAGAHT
251	NYSTK SMRED	GGYEVIKAAI	DKLGKKHKEH	IAAYGEGNER	RLTGRHETAD
301	INTFLWGVAN	RGASVRVGRD	TEKAGKGYFE	DRRPASNMDP	YVVTSMIADT
351	TILWKP				

Spot #2: cytosolic glutamine synthetase beta2 [Glycine max]

1	MSLLSDLINL	NLSDTTEKVI	AEYIWIGGSG	MDLRSKARTL	PGPVSDPSKL
51	PKWNYDGSST	GQAPGEDSEV	LIYPQAIFRD	PFRRGNNILV	ICDITYTPAGE
101	PIPTNKRHDA	AKVFSHPDVV	AEETWYGIEQ	EYTLLQKDIQ	WPLGWPVGGF
151	PGPQGPYYCG	VGADKAFGRD	IVDAHYKACL	YAGINISGIN	GEVMPGQWEF
201	QVGPSVGISA	GDEVWAARYI	LER IIIEIAGV	VVSFDPKPIQ	GDWNGAGAHT
251	NYSTK SMRND	GGYEVIKTAI	EKLGKRHKEH	IAAYGEGNER	RLTGRHETAD
301	INTFLWGVAN	RGASVRVGRD	TEKAGKGYFE	DRRPASNMDP	YVVTSMIADT
351	TILWKP				

Spot #4,5: heat shock protein 90-2 [Glycine max]

1	MASETETFAF	QAEINQLLSL	IINTFYNSKE	IFL RELISNA	SDALDKIRFE
51	SLTDKSKLDA	QPELFIHIIP	DKTNNTLSII	DSGIGMTKAD	LVNNLGTIAR
101	SGTKEFMEAL	AAGADVSMIG	QFGVGFYSAY	LVADKIVVTT	KHNDDEQYVW
151	ESHAGGSFTV	TRDTSGENLG	RGTKITLFLK	EDQLEYLEER	RLKDLIKHS
201	EFISYPISLW	IEKTTEKEIS	DDEDEEEKKD	EEGKVEDVDE	DKEKEEKKKK
251	TI KEVSHEWS	LVNKQKPIWM	RKPEEITKEE	YAAFYKSLTN	DWEEHLAVKH
301	FSVEGQLEFK	AVLFIKRAP	FDLFDTKKKP	NNIKLYVRRV	FIMDNCEELM
351	PEYLSFVKGI	VDSEDLPLNI	SREMLQQNKI	LKVIRKNLVK	KCIEMFFEIA
401	ENKEDYNKFY	EAFSKNLKLG	IHEDSQNKTK	LAELLYRHST	KSGDEMTSLK
451	DYVTRMKEGQ	NDIYYITGES	KKAVENSPFL	EKLKKKGFEV	LYMVDAIDY
501	AVGQLKEFEG	KKLVSATKEG	LKLDESEDEK	KKKEELKEKF	EGLCHVIKDV
551	LGDKVEKVVV	SDRVVDSPPC	LVTGEYGWTA	NMERIMKAQA	LRDSSMAGYM
601	SSKKTMEINP	ENPIMEELRK	RADADKNDKS	VKDLVLLLF	TALLTSGFSL
651	DDPNTFGNRI	HRMLKLGLSI	DEDAGEADAD	MPPLEDADAD	AEGSKMEEVD

Spot #6: early-responsive to dehydration 2 [*Arabidopsis halleri* subsp.]

1 MAGKGEGPAI GIDLGTYSYSC VGVWQHDRV E I IANDQGNRT TPSYVAFTDS
51 ERLIGDAAKN QVAMNPVNTV FDAKRLIGRI FSNASVQSDM KLWPFKIIPG
101 QEDKPMILVN YKGEEKQFAA EEISSMVLVK MREIAEAYLG SSIKNAVVTV
151 PAYFNDSQRQ ATKDAGVIAG LNVLRIINEP TAAAIAYGLD KKATSVGNKN
201 VLIFDLGGGT FDVSLLTIEE GIFEVKATAG DTHLGGEDFD NRMVNHVQVE
251 FKRKNKKDIS GNPRALRRLR TACERAKRTL SSTAQTTEIEV DSLFEGIDFY
301 SPITRARFEE MNMDLFRKCM EPVEKCLRDA **NMNKNTIHDV** **VLVGGSTRIP**
351 **KVQQLLQNF** **NGKELCKSIN** **PDEAVAYGAA** **VQAALLSGEG** **NEKVQDLLLL**
401 DVTPLSLGIE TVGGVMTTLI QRNTTIPTKK EQVFTTNADN QPGVLIQVYE
451 GERARTKDNN ILGKFELSGI PPAPRGVPQF TVCFDIDSNG IILNVAEDMA
501 TGKKNKITIT NGKGRLSKDD IEKMQDAEK YKYEDEEHKK NVEAKNRLEN
551 YAYNMRNTIC DIGDKLPAVD KKKIEDSIEE AMQWLDGNQL AEAEDEFEDKM
601 KELESVYNPI ITKMYQGGMD EE

Spot #7: putative TCP-1/cpn60 chaperonin family protein (ISS) [*Ostreococcus tauri*]

1 XXRLASFVGA MAIGDLVKST LGPKGMDKIL QSVQKGRQVT VTNDGATILK
51 SIYVDNPAAK VLVDISKAQD DEVGDGTTSV VVFASELLRQ AEQLVAQHVH
101 PMTIIQGFRE ACEAAKAALE ETARDNAGSK EKFEEDLMNI AKTTLSSKIL
151 THDKHEHFARL **AVDAVLR**LKG SGDLEMIQVI QKPGGNLKDS FLDEGFILDK
201 RFGVGVQPKRI ENAKILIAN T PMDTDKIKIY GARVVRVDSMA KVADIEQAER
251 EKMKRKCEKI IGYGINCFIN RQLIYNYPEQ IFTEAGVAAI EHADF DGIER
301 LALVTGGDIC STFDNPEVDQ LGGCDLIEEI MIGEDRLIRF SGVAKGEACT
351 IVLRGASEHI LGEAERSLHD ALCVLTSTVK DSRVIYGGGC SEMIMSKAVE
401 ELAAKTPGKR SLAMECFKA L **RAIPTIICD** **NAGLDSADIV** **SQMR**AAHAEG
451 DKKAGVNVLT GEVGDMMQCG VVECFRVKQQ VLLSATEAAE MIIRVDDIIK
501 STPRQRE

Spot #8: glyceraldehyde-3-phosphate dehydrogenase [*Glycine max*]

1 MGKVKIGING FGRIGRLVAR VALQRDDVEL VAVNDPFITT DYMTYMFKYD
51 SVHGHWKHHD VTKVDEK**TLL** **FGDKPVTIFG** **HRNPEEIPWG** STGADIIVES
101 TGVFTDKDKA AAHLKGGAKK **VIISAPSKDA** PMFVVG VNEH EYKPELDIIS
151 NASCTTNCLA PLAKVINDRF **GIVEGLMTTV** **HSITATQKT**TV DGPSAKDWRG
201 **GRAASFNIIP** **SSTGA**AKAVG **KVLPALNGKL** TGMAFR**VPTV** **DVSVVDLTVR**
251 LEKEASYDEI KNAIKEESEG KLKGILGYTE DDVVSTDFIG DSRSSIFDAK
301 AGIALNKNFV KLVSWYDNEW GYSSRVIDLL VVFAKKS L

Spot #9: putative auxin efflux carrier [Zea mays]

1	MITGTDFYHV	MTAMVPLYVA	MILAYGSRVW	WRIFTPDQCS	GINRFVALFA
51	VPLLSFHFI	TNNPYTMNIR	FIAADTLQKL	IVLALLTAW	YLSRRGCLEW
101	TITLFSLSL	PNTLVMGIP	LKGMYGDFSG	SLMVQIVVLQ	CIIWYTLMLF
151	MFEYRGARIL	ITEQFPDTAG	AIASIVVDPD	VVSLDGRNDA	IETEAEVKED
201	GKIHVTVRRS	NASRSDIYSR	RSMGFSSTTP	RPSNLTNAEI	YSLQSSRNPT
251	PRGSSFNHTD	FYSMVGRSSN	FAAGDAFGLR	TGATPRPSNY	EEDPQ GKANK
301	YGQYPAPNPA	MAAQPAKGLK	KAANGQAKGE	DGKDLHMFVW	SSSASPVS DV
351	FGNGAAEYND	AAAVKEVRMA	VASPRKVAAD	GRKERGEDFA	ERDDFSFGNR
401	GAAERDAEAG	DEKAAAAAA	AQGNAGAVAA	PAAMPPTSVM	TRLILIMVWR
451	KLIRNPNTYS	SLIGLIWSLV	CFRWNFEMPA	IILKISISILS	DAGLGMAMFS
501	LGLFMALQPR	IIACGNKVAT	FAMAVRFLTG	PAVMAAASFA	VGLRGTL LHV
551	AIVQAALPQG	IVPFVFAKEY	GVHPDILSTA	VIFGMLIALP	ITLVYYILMG
601	L				

Um *et al.*, Supplementary Figure 6

A. Spot #6: early-responsive to dehydration 2, identity: 92% (60/65)

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AhHsp70      DFNENENTLIDVVLVGGSTRI PKVQQLIQEENCKELCKSINPD EAVYGARVQRAILSG
Gm18g52610  DEKMDISSTVLDVVLVGGSTRI PKVQQLIQEENCKELCKSINPD EAVYGARVQRAILSG
*****

AhHsp70      EGNEK
Gm18g52610  EGNEK
*****
    
```

B. Spot #7: putative TCP-1/cpn60 chaperonin family protein, identity: 80% (25/31)

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OsTCP-1      LAVDRAVLR-----RIPITLIDNAGLDSRDI VSQMR
Gm12g09250  LAVDRAVLR-----RIPITLIDNAGLDSRELISQLR
***** **
    
```

C. Spot #9: putative auxin efflux carrier, identity: 69% (22/32)

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ZmPIN      RARRAAAGQCNRGAVADRRAMPPT SVMTRLLILM VWR
Gm19g30900 -RELHPKQCE S----RPTSMPT SVMTRLLILM VWR
*      ***      *      *****
    
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