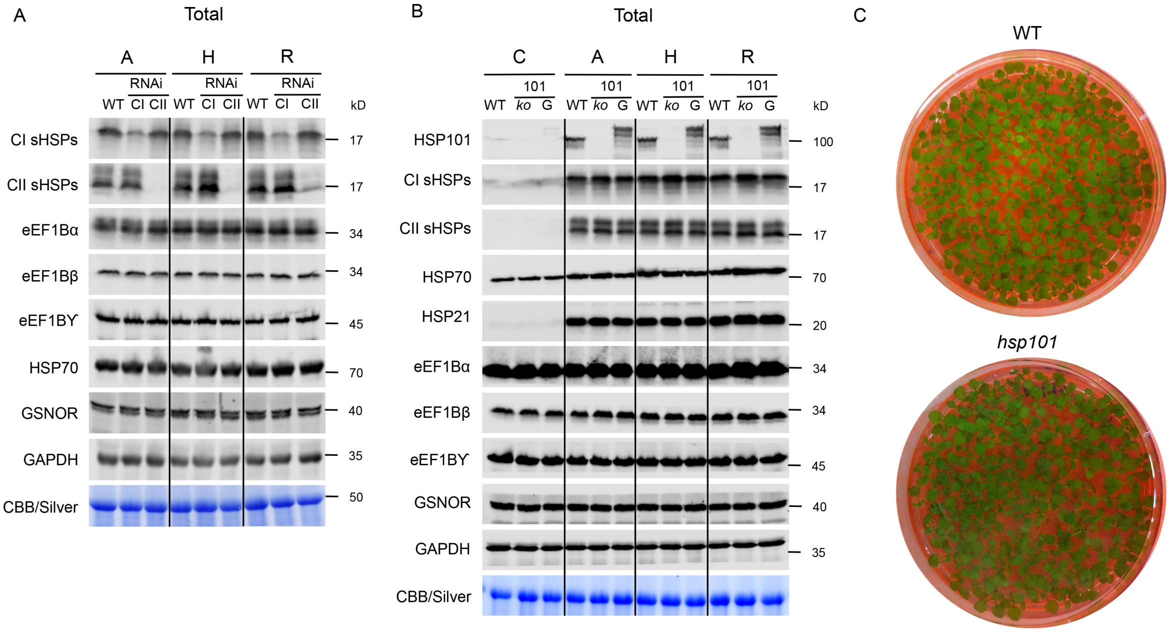

Figure S1. Abundance of sHSP-interacting proteins remains unaltered during heat stress, and *hsp101* mutant seedlings are able to survive the heat stress treatment. Total protein representing an equivalent fraction of the samples used for the analysis of soluble and insoluble proteins shown in Figure 4 **(A)** or Figure 5 **(B)** was separated by SDS-PAGE and analyzed by immunoblotting with the indicated antibodies. The total amount of the proteins analyzed was not noticeably altered during the heat stress treatments. Therefore, the increase or decrease in the insoluble fraction is not due to changes in total protein abundance. **C.** Pictures of the seedlings were taken of the plants 5 days after the same heat stress treatment.

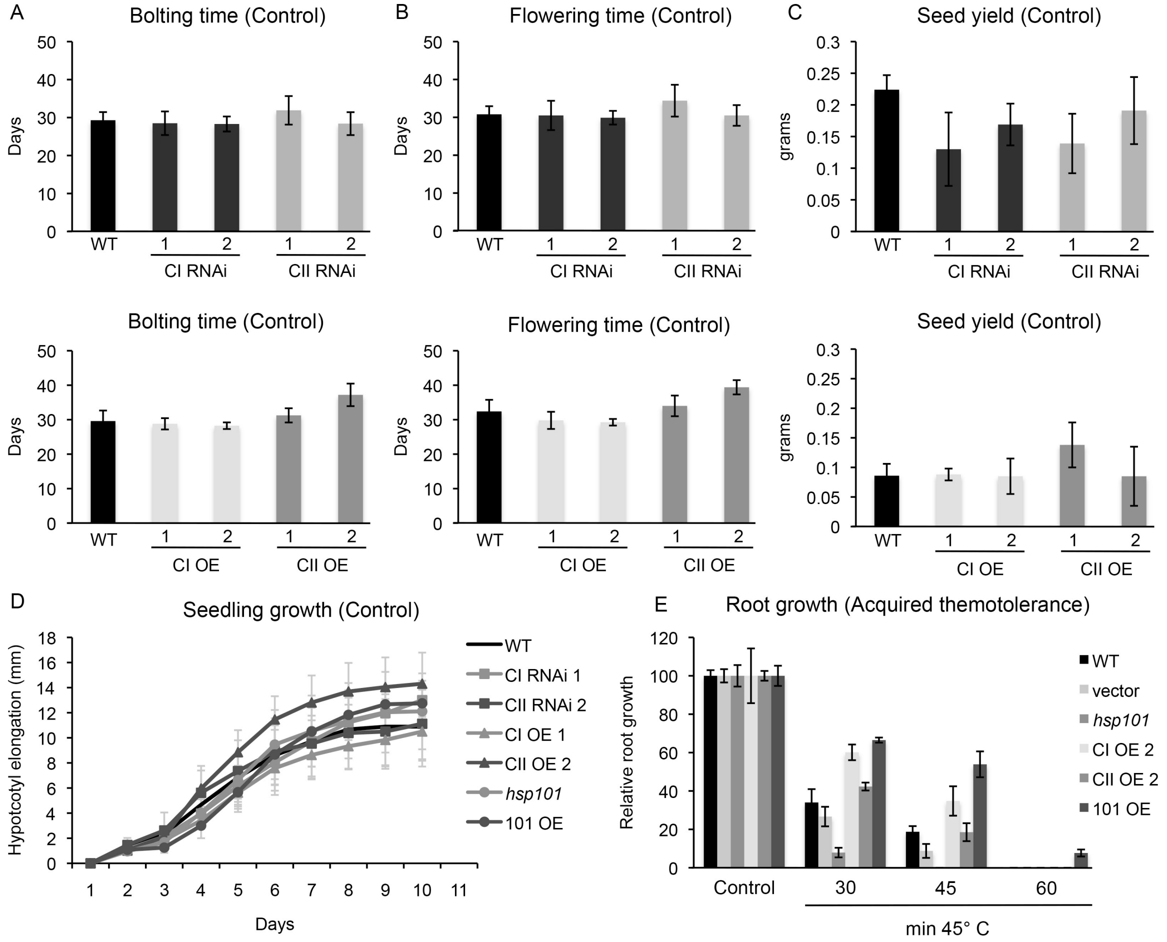

Figure S2. CI and CII sHSP RNAi and overexpression (OE) lines develop normally under control conditions and show reduced root growth after heat stress.

A. The average bolting and **B.** flowering time was determined for the same lines in long day conditions 16h light/8hrs dark, 21°C at 80 μmol m^{-2} s^{-1}. Error bars represent the standard deviation (n=15-18). **C.** The average seed yield was weighed per plant. Error bars represent the standard deviation (n=13-15). **D.** Hypocotyl elongation of dark grown seedlings was monitored for CI and CII RNAi and overexpression lines daily for 10 days. Error bars represent the standard deviation (n=10-15). **E.** CI and CII sHSP OE lines are important for the maintenance of root growth during heat stress recovery. Seedlings were grown on plates in the light for 4 days, acclimated and heat stressed at 45°C for 30, 45 or 60 min. Seedlings were returned to 22°C and root growth after heat stress was quantified after 5 days. Root growth is normalized to growth of untreated seedlings (Control). Error bars represent the standard deviation (n=18 per line).

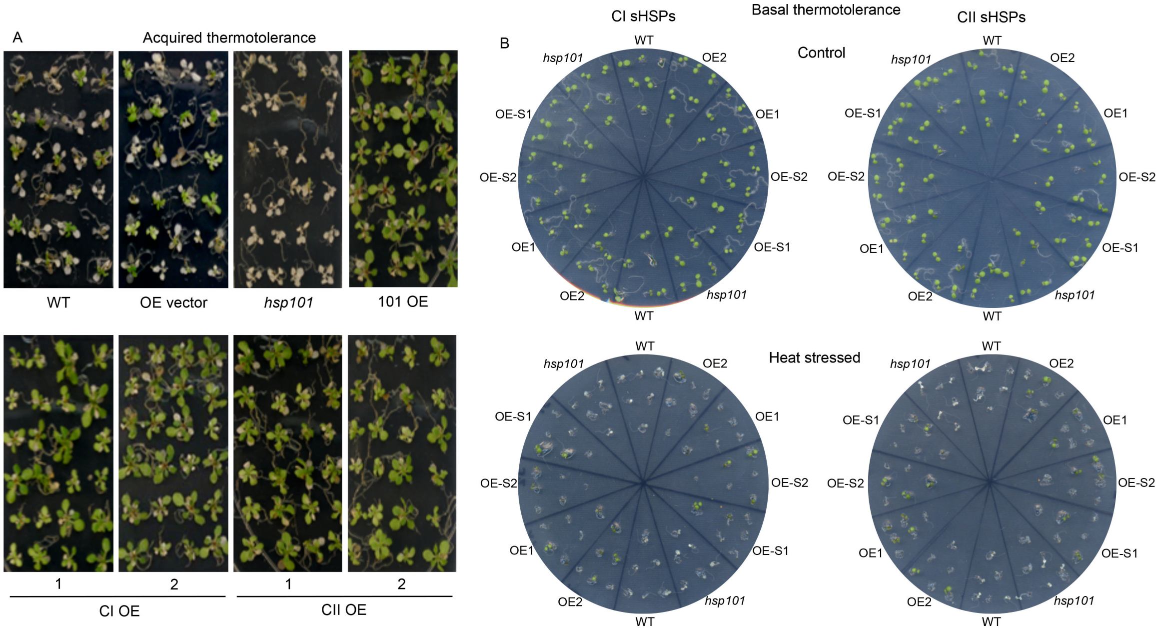

Fig. S3. Overexpression of sHSPs increases heat stress tolerance. A. Pictures of the plants used for the data graphed in Fig. 1E were taken 7 days after the heat stress treatment. **B.** Comparison of heat stress tolerance of the CI and CII OE lines with the CI-Strep and CII-Strep OE lines (OE-S1 and S2). The hsp101 null mutant was included as an additional heat sensitive control. Arabidopsis seedlings were grown for 4 days and either maintained at 22 ^{o}C or heat stressed at 44°C for 90 min. Pictures were taken 5 days after the heat stress.

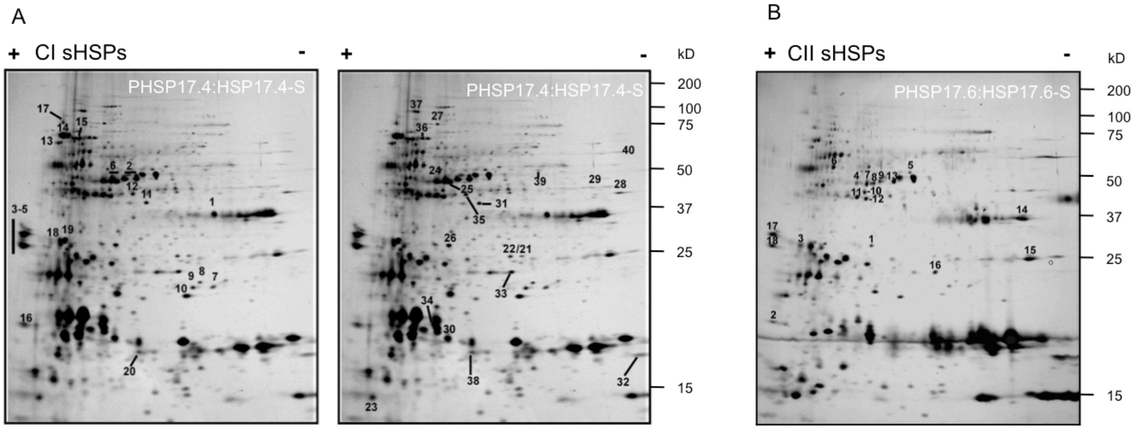

Figure S4. sHSP-interacting proteins for which peptide data were obtained by mass spectrometry. A, B. 2D-PAGE of affinity samples as shown in Figure 3 for CI (**B**) or CII (**C**) sHSPs. The numbers indicate the spots that were excised and analyzed using mass spectrometry and that correspond to the protein identities listed in Tables S1 (for CI) and S2 (for CII).

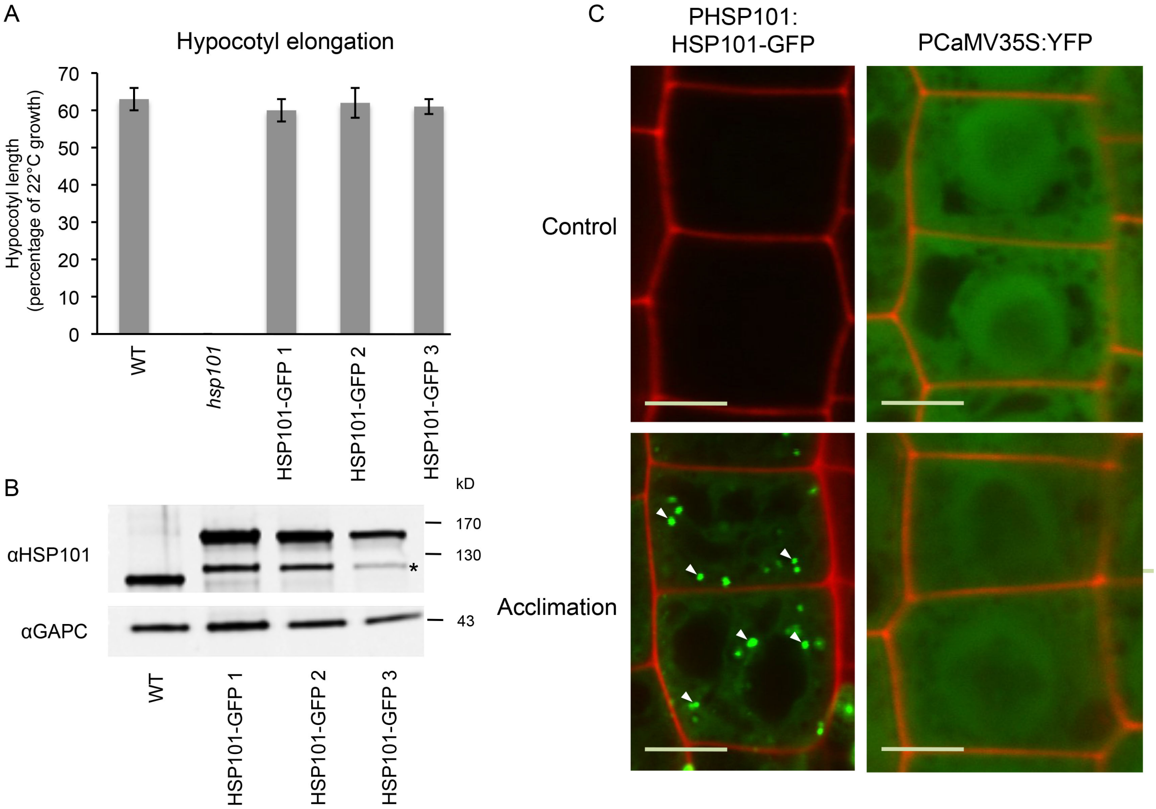

Figure S5. PHSP101:HSP101-GFP is heat induced, complements the *hsp101* null phenotype and accumulates in cytosolic foci during heat stress. A. Hypocotyl elongation assays were conducted on wild type, *hsp101* and three independent PHSP101:HSP101-GFP recombinant lines. Seedlings were dark-grown for 2.5 days, acclimated (38°C, 90 min, 21°C, 2 hrs) and subsequently heat stressed at 45°C for 2hrs. Hypocotyl elongation was determined 2.5 days after the heat stress. Values are shown as percentages relative to elongation without heat treatment. Error bars indicate standard error of the mean (n=11-15). All the PHSP101:HSP101-GFP recombinant lines tested were able to rescue the wild type, heat tolerant phenotype. **B.** Wild type and HSP101-GFP transgenic plants were heat stressed as in A, and crude protein extracts isolated. Samples were separated using SDS-PAGE and immunoblot analysis was performed using an antibody directed against the HSP101 N-terminal domain. HSP101-GFP migrated at the expected size. The * indicates a degradation product of HSP101-GFP. GAPDH was used as a loading control. **C.** HSP101-GFP expression is induced by heat and localized to punctate structures during acclimation conditions (white arrowheads). As a control for non-specific, heat-induced localization, plants expressing free YFP (PCaMV35S:YFP) were subjected to control and acclimation (1.5hr 38°C and recovered for 2hrs at 22°C); free YFP showed no accumulation in cytosolic foci.

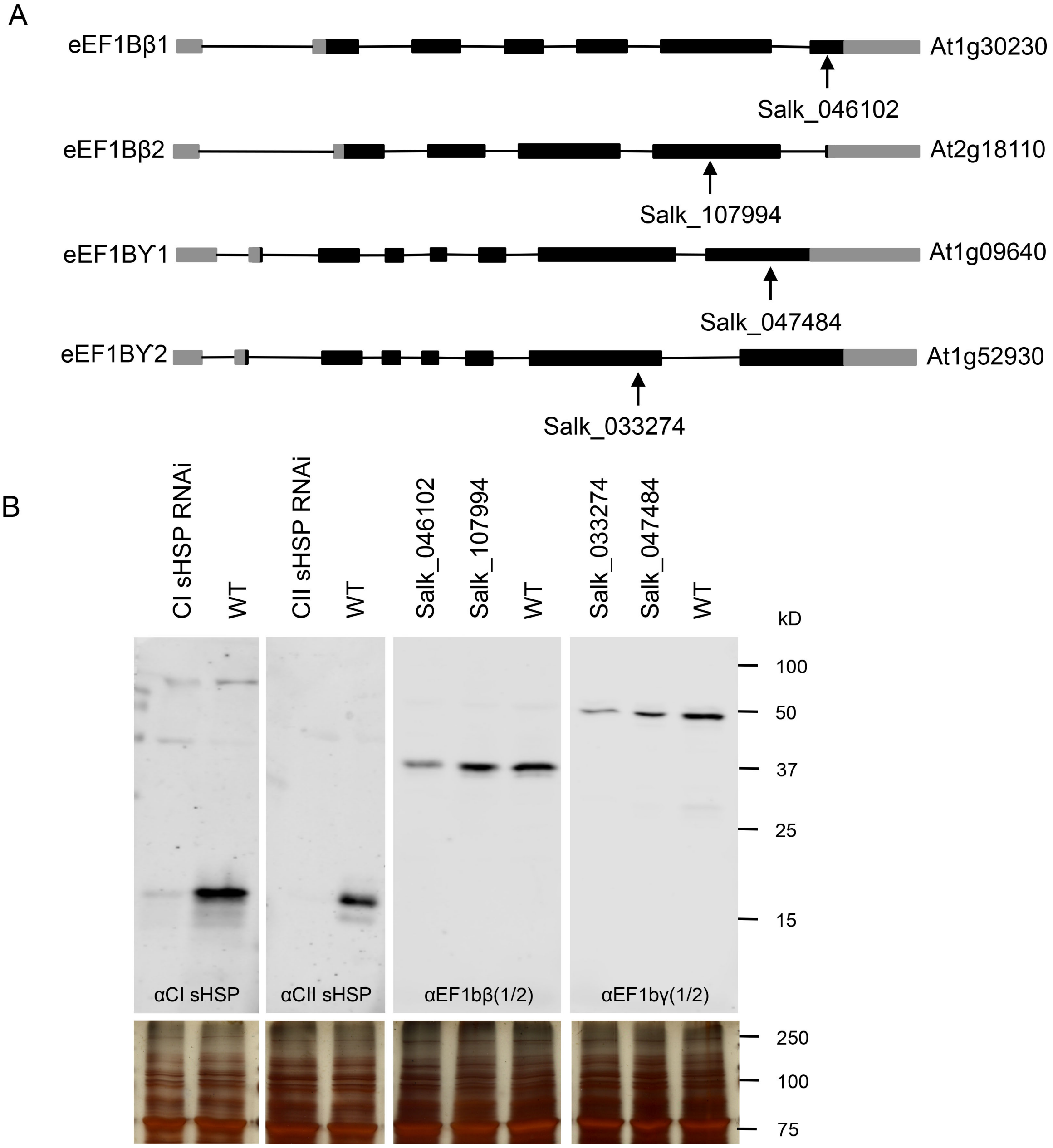

Figure S6. Location of T-DNA insertions in eEF1Bβ1 and 2, eEF1B γ1 and 2, and the specificity of the EF1B β and γ antibodies. A. Homozygous T-DNA insertion lines were selected for the two isoforms of both eEF1Bβ (1 and 2) and eEF1Bγ (1 and 2). UTRs are depicted in gray and introns are indicated by a line. The location of the T-DNA insertions is indicated by an arrow. **B.** CI sHSPs accumulate in cytosolic foci in the sHSP CII RNAi lines **C.** Homozygous lines were selected and grown on PNS plates together with wild type. Total proteins were extracted from heat acclimated seedlings, separated by SDS-PAGE and further processed for immunoblot analysis. The Salk lines eEF1bβ1 and eEF1Bγ2 both showed a reduced signal, indicating that these isoforms contribute the most to the signal observed in wild type. These mutants were used to determine the specificity of the signal observed in the immunolocalization experiments in Figure 6, Panels H and I.

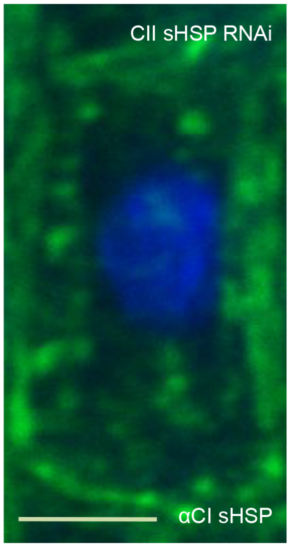

Figure S7. CI sHSPs accumulate in punctate structures in the CII sHSP RNAi during heat stress acclimation. Arabidopsis CII sHSP RNAi seedlings were heat acclimated (90min, 38°C and 2hrs, 21°C), fixed and processed for immunolocalization using the CI sHSP polyclonal antibody and were detected using a secondary antibody coupled to Alexa594. The image was taken in an Arabidopsis root cortex cell.

Table S1. CI sHSP-interacting proteins

	Protein name		PI	MW	AGI
1	Fructose bisphosphate aldolase 8	K.GILAADESTGTIGK.R K.EGGVLPGIK.V K.AAQEALYVR.C	6.4	38.5	At3g52930
2	Eukaryotic translation elongation factor 1B, gamma 1, 2	K.ALIAAEYAGVK.I I.AAEYAGVK.I	5.4 5.1	46.4 46.7	At1g57720 At1g09640

		K.IEESADFQMGVTNK.S K.VPVLETPEGPIFESNAIAR.Y R.MGYAPFSAPAEEAAISALK.R A.PAEEAAISALK.R K.FTSAFPHVER.Y A.PVAEAPKPAEEEEAPKPK.A K.PAEEEEAPKPK.A K.YNDENMVSFVTLNK.V K.MLICGSEGPFK.V R.VSQMIEDAEPFEGEALLDAK.C			
3	Eukaryotic translation elongation factor 1B, alpha 2	M.AVTFSDLHTEEGVK.S V.TFSDLHTEEGVK.S K.TYISGDQLSVDDVK.V K.VYAAVPVKPSDAFPNASK.W K.WYESVASQLAK.S R.GVEMPGLFWGASK.L M.PGLFWGASK.L R.GVEMPGLFWGASK.L	4.2	24.2	At5g19510
4	Eukaryotic translation elongation factor 1B, beta 1	F.AALAKPPTSQYVNASR.W R.WYNHIDALLR.I F.PNLNSDAGLK.K K.SSVLIDIKPWDDETDMK.K	4.2	25.1	At1g30230
5	Eukaryotic translation elongation factor 1B, beta 1, 2	K.KLDEHLLTR.S K.LDEHLLTR.S R.SYITGYQASK.D R.SIQMEGLFWGASK.L	4.2 4.2	25.1 25.3	At1g30230 At2g18110
6	Eukaryotic translation initiation factor 4A-1/DEA (D/H)-box RNA helicase (eIF4A-3)	K.GLDVIQQAQSGTGK.T K.MFVLDEADEMLSR.G K.RDELTLEGIK.Q R.DELTLEGIK.Q R.VLITTDLLAR.G K.GVAINFVTR.D	5.4 4.9	46.7 46.8	At3g13920 At1g72730
	Eukaryotic translation elongation factor 1B, gamma 1	K.VPVLETPEGSVFESNAIAR.Y	5.1	46.7	At1g09640
	Eukaryotic translation initiation factor 4A-2	K.GVAINFVTLDDQR.M	5.3	46.8	At1g54270
7	Glutathione S-transferase 11	K.VPAFEDGDFK.L	6.6	23.6	At1g02920
8	Glutathione S transferase phi 2	R.YENQGTNLLQTDSK.N	6.3	24.1	At4g02520
9	Glutathione S-transferase 11	K.VPAFEDGDFK.L	6.6	23.6	At1g02920
10	Heat shock protein HSP23.6 (mitochondrial)	K.LALEQDTLVIR.G	7.0	23.6	At4g25200
11	O-methyltransferase 1	R.LLTSYSVLTCSNR.K R.IYGLGPVCK.Y K.NEDGVSIAALCLMNQDK.V	5.8	39.6	At5g54160
12	S-adenosylmethionine synthase	K.ANVDYEQIVR.K K.TQVTIEYINESGAMVPVR.V K.SIVASGLAR.R	5.6	42.8	At3g17390
13	Heat shock cognate protein 70.1	R.FSDSSVQSDMK.L K.DAGVIAGLNVMR.I R.MVNHFVQEFK.R R.FEELNMDLFR.K K.STVHDVVLVGGSTR.I K.VQQLLQDFFNGK.E K.NALENYAYNMR.N K.ELESICNPIIAK.M	4.7	71.4	At5g02500
	Heat shock protein 70T-1	K.NQVAMNPVNTVFDAK.R	5.0	68.4	At1g56410
14	Heat shock protein 70	K.NQVAMNPTNTVFDAK.R K.DAGVISGLNVMR.I	4.9	71.1	At3g12580
15	Heat shock protein 70	K.NQVALNPQNTVFDAK.R	4.9	71.1	At3g12580
16	Translationally controlled tumor protein	K.VVDIVDTFR.L K.LSEEDQAVFK.K L.SEEDQAVFK.K K.EGSTNPTFLYFAH.G K.EIENGILWEVEGK.W	4.3	18.9	At3g16640
17	Cell division cycle 48	K.LAEDVDLER.I R.SENPEAMEEDGVDEVSEIK.A K.YQAFAQTLQQSR.G	4.9	89.4	At3g09840

18	Plasma-membrane associated cation-binding protein 1	K.KEEATPAPAVVETPVKEPETTTTAPVAEPPKP.	4.7	24.6	At4g20260
19	Plasma-membrane associated cation-binding protein 1	K.KEEATPAPAVVETPVK.E	4.7	24.6	At4g20260
20	Eukaryotic elongation factor 5A-2	K.LPTDDGLTAQMR.L	5.8	17.1	At1g26630
21	Vacuolar H+-ATPase subunit E isoform 3 Vacuolar H+-ATPase subunit E isoform 1	K.IDYSMQLNASR.I K.VLQAQDDIVNAMK.D	6.3 6.1	26.1 27.1	At4g11150 At1g64200
22	Nucleotide-rhamnose synthase/epimerase-reductase	K.LCEAQGITYTYGSGR.L K.NYENVCTLR.V	5.8	33.6	At1g63000
23	Profilin 2	K.PAEIAGINK.D K.YMVVQGEAGAVIR.G	4.7	14.0	At4g29350
24	Eukaryotic translation initiation factor 1B, gamma 1	Y.SAPAEEGAISTLK.R K.EAPVAEAPK.L K.LAEEEEAPKPK.A K.VPVLETPEGSVFESNAIAR.Y	5.1	46.7	At1g09640
25	Eukaryotic translation initiation factor 4A-1/DEA (D/H)-box RNA helicase (eIF4A-3) Eukaryotic translation elongation factor 1B, gamma chain Eukaryotic translation initiation factor 4A-2	K.GLDVIQQAQSGTGK.T K.MFVLDEADEMLSR.G K.GVAINFVTR.D K.RDELTLEGIK.Q R.DELTLEGIK.Q R.VLITTDLLAR.G K.VPVLETPEGSVFESNAIAR.Y K.GVAINFVTLDDQR.M	5.4 4.9 5.1 5.3	46.7 46.8 46.7 46.8	At3g13920 At1g72730 At1g09640 At1g54270
26	Jacalin-related lectin 30	K.VYVGQAQDGISAVK.F K.SPEEVTGEEHGK.S K.IFGSDGSVITMLR.F K.GANLWDDGSTHDAVTK.I Y.FAPLTTTTPLTPAK.Q	5.6	32.2	At3g16420
27	Jacalin-related lectin 34	K.LEAQGNSTGGTSWDDGSDYDGVTK.I N.STGGTSWDDGSDYDGVTK.I K.IYASYGGEGIQYVK.F K.LTAEGGETGAVWDDGSHDDVK.K K.VYVGQGQDGVAAVK.F K.NGSQVVFGDER.G Y.LAPSGTTPLTPATQSQK.L K.FGVHVAPITK.-	5.2	72.5	At3g16460
28	Aminoacyl synthase complex-interacting multifunctional protein 1 (ARC1)	K.ITPGLYTDENGVATYK.G	7.5	42.1	At2g40660
29	Cyclase associated protein 1 (CAP1)	K.IGGPVLDVTK.I K.DSLETAITTAK.S	6.6	51.0	At4g34490
30	Heat shock protein 17.6 (CII)	R.KFQLPDNADLEK.I	5.4	17.7	At5g12030
31	O-methyltransferase 1	K.DAILDGGIPFNK.A R.LLTSYSVLTCSNR.K R.IYGLGPVCK.Y K.NEDGVSIAALCLMNQDK.V	5.8	39.6	At5g54160
32	Cytosolic cyclophilin ROC1	K.VYFDMTIDGQPAGR.I	8.0	18.4	At4g38740
33	Ascorbate peroxidase 1	K.DIVALSGAHTLGR.C K.EGLLQLVSDK.A	6.0	27.6	At1g07890
34	HSP17.4 (CI)	K.VEVEDGNILQISGER.S K.ASMENGVLSVTVPK.V	4.9	17.4	At3g46230
35	S-adenosylmethionine synthase	K.ANVDYEQIVR.K R.FVIGGPHGDAGLTGR.K	5.6	42.8	At3g17390
36	FK506 binding protein 62	K.TDEEQVVDGLDR.A	5.0	61.5	At3g25230
37	Cell division cycle 48	R.LDDVGYDDVGGVR.K K.LAEDVDLER.I R.SENPEAMEEDGVDEVSEIK.A K.YQAFAQTLQQSR.G	4.9	89.4	At3g09840
38	Eukaryotic elongation factor 5A-2	K.LPTDDGLTAQMR.L	5.8	17.1	At1g26630
39	GTP-binding protein	K.IGIVGLPNVGK.S R.DLETITEELR.L K.PVVYLINLNER.D	6.8	44.5	At1g30580
40	3-methylcrotonyl-CoA carboxylase	R.IGIMGGAQAAGVLTQIER.A	8.7	64.0	At4g34030

Table S2. CII sHSP interacting proteins

	Protein name		PI	MW	ACC
1	Jacalin-related lectin 30	K.VYVGQAQDGISAVK.F K.IFGSDGSVITMLR.F	5.6	32.2	At3g16420
2	Translationally controlled tumor protein	K.LSEEDQAVFK.K K.VVDIVDTFR.L K.EGSTNPTFLYFAH.G	4.3	18.9	At3g16640
3	DNA-damage-repair/toleration protein 112 (chloroplast)	A.IEVLLGGGDGSLAFIPNDFSIAK.G	4.8	17.0	At1g20340
4	DEA (D/H)-box RNA helicase (eIF4A-3)	K.GLDVIQQAQSGTGK.T K.MFVLDEADEMLSR.G	4.9	46.8	At1g72730
5	S-Adenosyl-L-homocysteinase	K.AGIIVLAEGR.L	5.8	53.4	At4g13940
6	ATPase alpha subunit (chloroplast)	R.ADEISNIIR.E K.IAQIPVSEAYLGR.V I.PVSEAYLGR.V R.VINALANPIDGR.G R.LIESPAPGIISR.R K.ASSVAQVVTSLQER.G R.EQHTLIIYDDLSK.Q R.EAYPGDVFYLHSR.L K.TNKPQFQEIIASTK.T K.TLTAEAESFLK.E	4.9	55.3	AtCg00120
7	Eukaryotic translation initiation factor 4A-1	R.GIYAYGFEK.P K.IQVGVFSATMPPEALEITR.K R.GIYAYGFEKPSAIQQR.G R.ALGDYLGVK.A K.MFVLDEADEMLSR.G K.RDELTLEGIK.Q R.VLITTDLLAR.G	5.3	49.9	At3g13920
	Eukaryotic translation initiation factor 4A-2	R.KGVAINFVTLDDQR.M	5.3	46.8	At1g54270
8	Eukaryotic translation elongation factor 1B, gamma 2	R.VSQMIEDAEPFEGEALLDAK.C	5.4	46.4	At1g57720
9	Eukaryotic translation elongation factor 1B, gamma 2	K.ALIAAEYAGVK.I K.IEESADFQMGVTNK.S K.YNDENMVSFVTLNK.V R.VSQMIEDAEPFEGEALLDAK.C	5.4	46.4	At1g57720
10	RAB GTPase homolog E1b	K.KYDEIDAAPEER.A R.GITINTATVEYETENR.H K.QVGVPDMVVFLNK.E K.VGETVDLVGLR.E R.SYTVTGVEMFQK.I K.ILDEALAGDNVGLLLR.G	6.1	51.6	At4g20360
11	Actin 8	R.IAPEEHPVLLTEAPLNPK.A K.LSFVAVDYEQEMETSK.T K.AEYDEAGPGIVHR.K R.DLTDYLMK.I	5.3	41.9	At1g49240
	Actin 7	R.TTGIVLDSGDGVSH.T R.GYMFTTTAER.E	5.2	41.7	At5g09810
12	11 results				
13	Eukaryotic translation elongation factor 1B, gamma 2	K.ALIAAEYAGVK.I K.IEESADFQMGVTNK.S K.VPVLETPEGPIFESNAIAR.Y A.PAEEAAISALK.R K.FTSAFPHVER.Y K.AAPVAEAPKPAEEEEAPKPK.A K.YNDENMVSFVTLNK.V K.MLICGSEGPFK.V R.VSQMIEDAEPFEGEALLDAK.C	5.4	46.4	At1g57720
14	Glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC)	K.DAPMFVVGVNEHEYK.S R.AASFNIIPSSTGAAK.A R.VVDLIVHMSK.A	7.1	36.9	AT3g04120
15	BCCP-like protein 3	K.SSTTTISDGSSDASVSDGKK.T K.VGDFEMNLK.R	9.0	29.6	AT3g56130
16	Ascorbate peroxidase 1	K.DIVALSGAHTLGR.C	6.0	27.6	At1g07890
17	Eukaryotic translation elongation factor 1B, beta 2	R.SIQMEGLFWGASK.L	4.2	25.3	At2g18110
18	Eukaryotic translation elongation factor 1B, alpha 2	M.AVTFSDLHTEEGVK.S K.TYISGDQLSVDDVK.V K.VYAAVPVKPSDAFPNASK.W	4.2	24.2	At5g19510

		K.WYESVASQLAK.S			

Table S3 CI/CII sHSP interacting proteins of which the orthologues are present in stress granules in *S. cerevisiae* and human cells.

CI spot	CII spot	Protein ID	AGI	Heat induction (mRNA)	Yeast	Yeast stress granules	Human	Human stress granules
2 6 24 25	8 9 13	Eukaryotic translation elongation factor 1B, gamma chain	At1g09640 At1g57720	No No	YKL081W TEF4 EFC1	Jain *et al.* 2016 Cherkasov *et al.* 2015 Wallace *et al.* 2015	EEF1G EF1G GIG35	Not detected
3 4 5	17 18	Eukaryotic translation elongation factor 1B, alpha, beta	At1g30230 At2g18110 At5g19510	2x 2x <1.5x	YAL003W TEF5 EFB1	Cherkasov *et al.* 2015	EEF1B	Not detected
6, 25	4 7	Eukaryotic translation initiation factor 4A1/4A2/DEA (D/H)-box RNA helicase	At1g54270 At1g72730 At3g13920	No No No	YKR059W TIF1 YJL138C TIF2	Jain *et al.* 2016	EIF4A2 BM-010 DDX2B EIF4A3	Jain *et al.* 2016
12 35	-	S-adenosylmethionine synthase	At3g17390	0.5x	YLR180W YDR502C	Jain *et al.* 2016	SAMS1 MAT1A SAMS2 MAT2A	Not detected
13 14 15	1D*	Heat shock cognate protein 70/70.1/70T-1	At1g56410 At3g12580 At5g02500	No 10x 2x	SSA1-4 SSB2	Walters *et al.* 2015 Jain *et al.* 2016 (SSA3,SSB2) Cherkasov *et al.* 2015 (SSA1,SSA2)	HSPA1AB HSPA2,6,8	Not detected
16	2	Translationally controlled tumor protein	At3g16640	No	YKL056C TMA19 MMI1	Jain *et al.* 2016 Cherkasov *et al.* 2015 Rinnerthaler *et al.* 2013	TPT1 HRF TCTP	Jain *et al.* 2016
17 37	-	Cell division cycle 48	At3g09840	<2x	YDL126C CDC48	Not detected	VCP CDC48 p97	Jain *et al.* 2016
20 38	-	Eukaryotic initiation factor 5A-2	At1g26630	No	YEL034 HYP2 TIF51A	Cherkasov *et al.* 2015	EIF5A2	Not detected
21	-	V-type H+-transporting ATPase subunit E	At4g11150	No	YOR332W VMA4	Jain *et al.* 2016 **	ATP6E1 VMA4	Not detected
23	-	Profilin 2	At4g29350	No	YOR122C PFY1 CLS5 PRF1	Figley *et al.* 2014	PFN PFN2	Jain *et al.* 2016***
28	-	Aminoacyl synthase complex-interacting multifunctional protein 1 (ARC1)	At2g40660	No	YGL105W ARC1	Jain *et al.* 2016 Cherkasov*et al.* 2015 Wallace *et al.* 2015	AIMP1 EMAP2 EMAPII HLD3 SCYE1 p43	Not detected
32	-	Cytosolic cyclophilin ROC1	At4g38740	<2x	YDR155C CPR1 CPH1 CYP1	Cherkasov *et al.* 2015	PPIF CYP3	Not detected
36	-	FK506 binding protein 62	At3g25230	8x	YNL135C FPR1 FKB1 RBP1	Cherkasov *et al.* 2015	FKBP4 FKBP51 FKBP52 FKBP59 HBI Hsp56 PPIase	Not detected
39	-	GTP-binding protein	At1g30580	No	YBR025C OLA1 YHL014C YLF2	Cherkasov *et al.* 2015 Wallace *et al.* 2015	OLA1 DOC45 GBP45 GTBP9	Not detected

*Identified in a 1D CII sHSP–affinity gel
**Not Detected; VMA2, subunit of same ATPase detected

***PFN2 was detected

Table S4 Percentage insoluble proteins of an independent experiment

% insoluble	Acclimation				Heat stressed				Recovery			
	WT	CI	CII	*hsp101*	WT	CI	CII	*hsp101*	WT	CI	CII	*hsp101*
CI sHSPs	1		3	9	47		45	46	13		51	80
CII sHSPs	2	4		5	6	10		28	3	9		8
HSP101	2	2	2		4	4	5		5	5	6	
HSP70	14	18	16	35	44	45	45	42	30	37	38	38
eEF1bα	9	18	16	32	57	63	61	65	38	60	43	55
eEF1Bβ	4	4	5	29	64	65	61	59	26	42	33	53
eEF1Bγ	0	3	3	26	69	72	72	76	41	55	50	66
GSNOR	19	18	19	21	73	70	59	68	67	66	58	56
GAPDH	1	1	0	0	0	0	0	0	0	2	2	2

Table S5 Primers

1	Gen. HSP17.4I-Strep F	TCGAAAAATAAGAGGAACTCTGAAGTTG
2	Gen. HSP17.4I-Strep R	ACTGCGGGTGGCTCCAACCAGAGATATCAATGGACTTG
3	OE HSP17.4I-Strep F	CATTCGAAGAGAATTCTAG
4	OE HSP17.4I-Strep R	CAACGAGATCTGTGATTAC
5	Gen. 17.6II F	GTCGCTTAAGTTTGTTTGTGATCGTG
6	Gen. 17.6II R	GAAGTCAACGTTGATATCCATACTGATG
7	Gen. 17.6-II strep F	TCGAAAAATGAGTTCGTTTTGGTGATTGTGTG
8	OE 17.6II strep F	TCGAAAAATGAGTTTGTTTTTCTAGAGTCCGC
9	Gen. 17.6-II strep R OE17.6-II strep R	ACTGCGGGTGGCTCCAAGCAACTTGAACTTGAATTGTC
10	Ds17.4-I F	GGACTAGTGGCGCGCCAGAGTAAGCGAAACGATGTC
11	Ds17.4-I R	CGGGATCCATTTAAATCAGAGTTCCTCTTAACCAGAGA
12	Ds17.6-II F	GGACTAGTGGCGCGCCAATGGATTTAGGAAGGTTTCC
13	Ds17.6-II R	CGGGATCCATTTAAATCCAACACACAATCACAAAACAA
14	GFP F	GGCTCGAGATGAGTAAAGGAGAAGAA
15	GFP R	TCTCTAGATTATTTGTATAGTTCATCCATGC
16	eEF1Bα1CDS F	AAAAAAACATATGGCGGTTACATTTTCTGATCTCC
17	eEF1Bα1CDS R	AAAAAAAGGATCCCTAAATCTTGTTAAAAGCG
18	eEF1Bβ1CDS F	AAAAAAACATATGGCAGCATTCCCTAACCTTAAC
19	eEF1Bβ1CDS R	AAAAAAACTCGAGCTACAAAAACTTGGGAAACTG
20	eEF1Bγ1CDS F	AAAAAAACATATGGCTTTGGTCTTGCACACG
21	eEF1Bγ1CDS R	AAAAAAACTCGAGTCACTTGAAGCACTTGGCGTC
22	Salk_046102 F	CCTTTGTGCTTAACTCGATTGAG
23	Salk_046102 R	GTTGACCTTTTCGGAGAGGAG
24	Salk_107994 F	AAGTCATCTCCATTCCCATTC
25	Salk_107994 R	TGCTGAAGAGAGAGCAGCTTC
26	Salk_047484 F	TCAATCAAGGCAAAATTACCG
27	Salk_047484 R	GTCCCTCCTATTGCTTCCAAG
28	Salk_033274 F	TTTCACTTAAAGCATTTGGCG
29	Salk_033274 R	GGCAATTTCTGCATTGAAGAG
30	Salk_BP	TGGTTCACGTAGTGGGCCATCG