Supplementary data

Supplementary Table S1. Primer list for PCR and real time PCR

Primer name	**Primer sequence**
NPTII-Fw:	5’- ATGATTGAACAAGATGGATTGCAC -3’
NPTII-Rv:	5’- TCAGAAGAACTCGTCAAGAAGGCG -3’
HSP70-Fw:	5’- CAAAATGCCTAACCCGAAGCC -3’
HSP70-Rv:	5’- CGTAGTCCCCAAA-TCAATTCCGA -3’
UBQ-Fw:	5'- CACCAAGCCAAAGAAGATCA -3'
UBQ-Rv:	5'- TCAGCATTAGGGCACTCCTT -3'
DELLA-Fw:	5’- CTGATATGGCTGGTTGGGTACA -3’
DELLA-Rv:	5’- AGAAGAAGAAGAACCACAACCAG -3’
IAA9-Fw:	5’- TTGGTGTTGGGGAGGAGGAG -3’
IAA9-Rv:	5’- AGGGCAAGTCTCCTCACCTC -3’

Supplementary Table S2. List of genes that was obtained product names at Panther (http://pantherdb.org/) in the nearest neighbouring gene group of *SlIAA9*. IDs are based on iTAG 2.3.

Mapped ID	Gene Name / Gene Symbol	PANTHER Family/Subfamily	PANTHER Protein Class
Solyc12g056840	Uncharacterized protein	Phosphopantothenate--cysteine ligase (pthr12290: sf2)	Ligase (PC00142)
Solyc03g019730	Uncharacterized protein	Sumo-activating enzyme subunit 1 (pthr10953: sf162)	Ligase (PC00142) transfer/carrier protein (PC00219)
Solyc03g098730	Uncharacterized protein	Cysteine protease inhibitor wscp-related (pthr33107: sf11)	protease inhibitor (PC00191)
Solyc10g084920	PRA1 family protein	Pra1 family protein (pthr12859: sf0)	Amino acid transporter (PC00046)
Solyc11g011910	Transmembrane 9 superfamily member	Transmembrane 9 superfamily member-related (pthr10766: sf14)	Transporter (PC00227)
Solyc09g075000	Uncharacterized protein	Wd repeat-containing protein 89 (pthr22889: sf0)	
Solyc11g017300	Uncharacterized protein	Cop9 signalosome complex subunit 5 (pthr10410: sf6)	Metalloprotease (PC00153)
Solyc09g083150	Uncharacterized protein	Nad(p)h-quinone oxidoreductase subunit n	Chloroplastic (PTHR35515:SF1)
Solyc04g077970	Uncharacterized protein	Adenine phosphoribosyltransferase 1	Chloroplastic (PTHR11776:SF8)
Solyc02g062680	Anaphase-promoting complex subunit 10	Anaphase-promoting complex subunit 10 (pthr12936: sf0)	Enzyme modulator (PC00095) Ligase (PC00142)
Solyc05g018410	Uncharacterized protein	3-hydroxyisobutyryl-coa hydrolase-like protein 3	Mitochondrial-related (PTHR43176:SF5) Acetyltransferase (PC00038) Acyltransferase (PC00042) Dehydrogenase(PC00092) Epimerase/Racemase(PC00096) Hydratase(PC00120) Ligase(PC00142)
Solyc03g097750	Uncharacterized protein	Translocon-associated protein subunit beta (pthr12861: sf3)	

Solyc04g081770	Uncharacterized protein	Gdsl esterase/lipase exl1-related (pthr45642: sf25)	
Solyc01g005470	Uncharacterized protein	Plac8-like protein 1 (pthr15907: sf21)	
Solyc04g078850	Protein DCL	Ortholog	DCL Protein (DUF3223) (PTHR33415:SF2)
Solyc02g085500	Uncharacterized protein	Transcription repressor ofp10-related (pthr33057: sf68)	
Solyc02g030300	Uncharacterized protein	Subfamily not named (pthr27002: sf359)	
Solyc05g049950	Small nuclear ribonucleoprotein-associated protein	Small nuclear ribonucleoprotein-associated protein b' (pthr10701: sf0)	mRNA splicing factor (PC00148)
Solyc04g076850	Auxin-responsive protein	Subfamily not named (pthr31734: sf18)	
Solyc08g028690	Uncharacterized protein	Subfamily not named (pthr43180: sf1)	
Solyc05g009390	Uncharacterized protein	Alpha/beta-hydrolases superfamily protein (pthr11614: sf94)	Phospholipase (PC00186) serine protease (PC00203)
Solyc02g081160	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta 1-related (pthr43650: sf1)	carbohydrate kinase (PC00065)
Solyc10g083570	Fructose-bisphosphate aldolase	Subfamily not named (pthr11627: sf41)	
Solyc11g028020	TAGL11 transcription factor	Agamous-like mads-box protein agl11 (pthr11945: sf170)	MADS box transcription factor (PC00250)
Solyc12g056100	UBC8	Ubiquitin-conjugating enzyme e2 29-related (pthr24068: sf78)	
Solyc06g064840	Uncharacterized protein	Agamous-like mads-box protein agl11 (pthr11945: sf170)	MADS box transcription factor (PC00250)
Solyc07g041970	Uncharacterized protein	Subtilisin-like protease sbt1.8 (pthr10795: sf335)	protease inhibitor (PC00191) serine protease (PC00203)

Supplementary Table S3. The distance from *SlHSP70-1* to *SlIAA9* and *SlDELLA* in their co-expression network

Gene ID	Shortest distance to *SlIAA9* (Solyc04g076850.2)	Shortest distance to *SlDELLA* (Solyc11g011260.1)
Solyc10g086410.2	3	2
Solyc06g076020.2 (*SlHSP70-1*)	3	1
Solyc07g043560.2	3	3
Solyc01g106260.2	2	3
Solyc01g106210.2	2	2
Solyc09g010630.2	3	3
Solyc11g066100.1	3	3
Solyc08g082820.2	3	3
Solyc09g075950.1	3	3

Supplementary Table S4. GO enrichment analysis of *SlIAA9* gene on the network ($p < 0.05$ adjusted by FDR)

Adjusted PValue_iaa9_1st2nd	description_iaa91st2nd	Name (GO_ID)	N_iaa91st2nd	nn_iaa91st2nd	X_iaa91st2nd	xx_iaa91st2nd
2.44E-05	protein binding	5515	19542	3768	983	259
2.80E-03	copper ion binding	5507	19542	75	983	15
4.69E-03	endopeptidase complex	1905369	19542	13	983	6
4.69E-03	proteasome complex	502	19542	13	983	6
4.69E-03	proteasome core complex	5839	19542	13	983	6
4.69E-03	peptidase complex	1905368	19542	13	983	6
5.92E-03	protein peptidyl-prolyl isomerization	413	19542	9	983	5
5.92E-03	peptidyl-prolyl cis-trans isomerase activity	3755	19542	9	983	5
1.01E-02	cis-trans isomerase activity	16859	19542	10	983	5
1.49E-02	oxidoreductase activity, acting on the CH-NH2 group of donors, disulfide as acceptor	16642	19542	3	983	3
1.49E-02	glycine dehydrogenase (decarboxylating) activity	4375	19542	3	983	3
1.49E-02	cytoplasm	5737	19542	699	983	58
2.64E-02	peptidyl-proline modification	18208	19542	19	983	6
3.18E-02	poly-pyrimidine tract binding	8187	19542	36	983	8
3.18E-02	poly(U) RNA binding	8266	19542	36	983	8
3.30E-02	proteasome core complex, alpha-subunit complex	19773	19542	8	983	4

4.46E-02	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	16810	19542	68	983	11
4.61E-02	NADH dehydrogenase (ubiquinone) activity	8137	19542	22	983	6

Supplementary Table S5. GO enrichment analysis of *SlDELLA* gene on the network (p < 0.05 adjusted by FDR)

Adjusted PValue_della1st2nd	description_della1st2nd	Name (GO_ID)	N_della1st2nd	nn_della1st2nd	X_della1st2nd	xx_della1st2nd
3.04E-05	endopeptidase complex	1905369	19542	13	216	5
3.04E-05	proteasome complex	502	19542	13	216	5
3.04E-05	proteasome core complex	5839	19542	13	216	5
3.04E-05	peptidase complex	1905368	19542	13	216	5
4.05E-03	unfolded protein binding	51082	19542	55	216	6
9.10E-03	protein binding	5515	19542	3768	216	65
2.92E-02	protein N-acetylglucosaminyltransferase activity	16262	19542	3	216	2
2.92E-02	soluble NSF attachment protein activity	5483	19542	3	216	2

Supplementary Table S6. List of *SlHSP70* genes identified in tomato genome[*]

No.	Gene ID	Organism	Transcript Name	Location	Direction	Description
1	Solyc01g060400.1	*S. lycopersicum*	Solyc01g060400.1.1	SL2.50ch01:70789203..70789569	reverse	Heat shock protein (AHRD V1 **-- Q8IB24_PLAF7); contains Interpro domain(s) IPR013126 Heat shock protein 70
2	Solyc01g099660.2	*S. lycopersicum*	Solyc01g099660.2.1	SL2.50ch01:89839013..89842124	forward	Heat shock protein (AHRD V1 ***- Q84KP8_CYAME); contains Interpro domain(s) IPR013126 Heat shock protein 70
3	Solyc01g103450.2	*S. lycopersicum*	Solyc01g103450.2.1	SL2.50ch01:92060728..92065237	forward	Chaperone DnaK (AHRD V1 ***- Q1SKX2_MEDTR); contains Interpro domain(s) IPR012725 Chaperone DnaK
4	Solyc01g106210.2	*S. lycopersicum*	Solyc01g106210.2.1	SL2.50ch01:94157485..94161397	forward	Chaperone DnaK (AHRD V1 ***- A2Q199_MEDTR); contains Interpro domain(s) IPR012725 Chaperone DnaK
5	Solyc01g106260.2	*S. lycopersicum*	Solyc01g106260.2.1	SL2.50ch01:94215968..94220340	forward	Chaperone DnaK (AHRD V1 ***- A2Q199_MEDTR); contains Interpro domain(s) IPR012725 Chaperone DnaK
6	Solyc02g080470.2	*S. lycopersicum*	Solyc02g080470.2.1	SL2.50ch02:44673835..44685301	forward	Heat shock protein 4 (AHRD V1 ***- B6U237_MAIZE); contains Interpro domain(s) IPR013126 Heat shock protein 70
7	Solyc03g082920.2	*S. lycopersicum*	Solyc03g082920.2.1	SL2.50ch03:52794869..52798836	reverse	Heat shock protein (AHRD V1 ***- Q84KP8_CYAME); contains Interpro domain(s) IPR013126 Heat shock protein 70
8	Solyc03g117620.2	*S. lycopersicum*	Solyc03g117620.2.1	SL2.50ch03:66722304..66723457	reverse	Heat shock protein (AHRD V1 *-*- Q801X9_CARAU); contains Interpro domain(s) IPR013126 Heat shock protein 70
9	Solyc03g117630.1	*S. lycopersicum*	Solyc03g117630.1.1	SL2.50ch03:66724560..66726524	reverse	Heat shock protein (AHRD V1 ***- B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
10	Solyc04g011440.2	*S. lycopersicum*	Solyc04g011440.2.1	SL2.50ch04:3894918..3898067	forward	heat shock protein (AHRD V1 ***- B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70

11	Solyc06g005440.1	*S. lycopersicum*	Solyc06g005440.1.1	SL2.50ch06:441236..441592	forward	heat shock protein (AHRD V1 ***-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
12	Solyc06g052050.2	*S. lycopersicum*	Solyc06g052050.2.1	SL2.50ch06:35713191..35716219	forward	Heat shock protein (AHRD V1 ***-Q84KP8_CYAME); contains Interpro domain(s) IPR013126 Heat shock protein 70
13	Solyc06g076020.2	*S. lycopersicum*	Solyc06g076020.2.1	SL2.50ch06:47192489..47195586	reverse	heat shock protein (AHRD V1 ***-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
14	Solyc07g005820.2	*S. lycopersicum*	Solyc07g005820.2.1	SL2.50ch07:655717..659235	reverse	heat shock protein (AHRD V1 ***-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
15	Solyc07g043560.2	*S. lycopersicum*	Solyc07g043560.2.1	SL2.50ch07:57457649..57465996	reverse	Heat shock protein 4 (AHRD V1 ***-B6U237_MAIZE); contains Interpro domain(s) IPR013126 Heat shock protein 70
16	Solyc08g082820.2	*S. lycopersicum*	Solyc08g082820.2.1	SL2.50ch08:65489311..65493585	forward	Heat shock protein (AHRD V1 ***-Q84KP8_CYAME); contains Interpro domain(s) IPR013126 Heat shock protein 70
17	Solyc09g010630.2	*S. lycopersicum*	Solyc09g010630.2.1	SL2.50ch09:3965253..3968837	forward	heat shock protein (AHRD V1 ***-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
18	Solyc09g075950.1	*S. lycopersicum*	Solyc09g075950.1.1	SL2.50ch09:67581791..67583521	forward	Heat shock protein 1 (AHRD V1 ***-B6SXY0_MAIZE); contains Interpro domain(s) IPR013126 Heat shock protein 70
19	Solyc10g086410.2	*S. lycopersicum*	Solyc10g086410.2.1	SL2.50ch10:65236863..65240232	forward	Heat shock protein 70-3 (AHRD V1 ***-Q67BD0_TOBAC); contains Interpro domain(s) IPR013126 Heat shock protein 70
20	Solyc11g020040.1	*S. lycopersicum*	Solyc11g020040.1.1	SL2.50ch11:10015582..10019521	forward	Chaperone DnaK (AHRD V1 ***-Q1SKX2_MEDTR); contains Interpro domain(s) IPR012725 Chaperone DnaK
21	Solyc11g066060.1	*S. lycopersicum*	Solyc11g066060.1.1	SL2.50ch11:51740558..51743431	forward	heat shock protein (AHRD V1 ***-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70

22	Solyc11g066100.1	*S. lycopersicum*	Solyc11g066100.1.1	SL2.50ch11:51773141..51775439	reverse	heat shock protein (AHRD V1 ***-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
23	Solyc12g042560.1	*S. lycopersicum*	Solyc12g042560.1.1	SL2.50ch12:39980666..39981646	forward	heat shock protein (AHRD V1 *-*-B2D2G5_CAPSN); contains Interpro domain(s) IPR013126 Heat shock protein 70
24	Solyc12g043110.1	*S. lycopersicum*	Solyc12g043110.1.1	SL2.50ch12:39110693..39115806	forward	Heat shock protein 4 (AHRD V1 ***-B6U237_MAIZE); contains Interpro domain(s) IPR013126 Heat shock protein 70
25	Solyc12g043120.1	*S. lycopersicum*	Solyc12g043120.1.1	SL2.50ch12:39096307..39100382	forward	Heat shock protein 4 (AHRD V1 ***-B6U237_MAIZE); contains Interpro domain(s) IPR013126 Heat shock protein 70

* Data extracted from Phytozome database (https://phytozome.jgi.doe.gov/pz/portal.html#)

Supplementary Table S7. Gene expression level of targeted *SlHSP70-1* in each tissues of tomato *S. lycopersicum* M82 *and S. pennellii* *

Species	Tissue	Expression Level	Standard Deviation	Samples
Solanum lycopersicum var. M82	Floral	12.83	0	M82.floral,
Solanum lycopersicum var. M82	Stem	62.5	0	M82.stem,
Solanum lycopersicum var. M82	Leaf	12.22	0	M82.leaf,
Solanum lycopersicum var. M82	Vegetative meristem	8.45	0	M82.veg,
Solanum lycopersicum var. M82	Seedling	22.44	0	M82.sdling,
Solanum lycopersicum var. M82	Root	29.62	0	M82.root,
Solanum lycopersicum var. M82	Mature Fruit	50.18	0	M82.MatureFruit,
Solanum lycopersicum var. M82	Developing Fruit	431.67	0	M82.Developing Fruit,
Solanum pennellii	Floral	5.47	0	penn.floral,
Solanum pennellii	Stem	9.12	0	penn.stem,
Solanum pennellii	Leaf	3.1	0	penn.leaf,
Solanum pennellii	Vegetative meristem	19.57	0	penn.veg,
Solanum pennellii	Seedling	22.88	0	penn.sdling,
Solanum pennellii	Root	34.35	0	penn.root,
Solanum pennellii	Mature Fruit	232.5	0	penn.Mature Fruit,
Solanum pennellii	Developing Fruit	313.29	0	penn.Developing Fruit,

The seedling sample was collected at 3 days then grown on plate at 22°C under a mixture of cool-white and far-red fluorescent light. Shoot and root tissue was collected from seedling 10 days after sowing on plates. Vegetative meristems were collected when the 3rd leaf reached 1 mm (30-37 days post germination). Stem between 4th and 5th leaves and inflorescent meristem were collected when meristems were fully formed (50 days post germination for *S. lycopersicum* var. M82 and 56 days post germination for *S. pennellii*). Young green fruits and mature fruits were collected from plants in the greenhouse. Data were extracted from Tomato eFp browsers, available on website http://bar.utoronto.ca/efp_tomato/cgi-bin/efpWeb.cgi.

*Koenig et al 2013. PNAS July 9, 110 (28) E2655-E2662;
https://doi.org/10.1073/pnas.1309606110,
Data extracted from tomato eFP browsers http://bar.utoronto.ca/efp_tomato/cgi-bin/efpWeb.cgi)

Legends of Supplementary Figures

Supplementary Figure S1. The phylogenetic tree and genomic structure analysis of tomato *SlHSP70* family genes

A) The phylogenetic analysis was inferred using the Neighbor-Joining method. The phylogenetic tree was constructed by MEGA7 software, with 1000 replicates for bootstrap test, using amino acid sequences. B) Genomic structure description of *SlHSP70*. The structures were visualized by Gene Structure Display Server (GSDS) ver. 2.0 based on genomic sequence. The position of each gene was rearranged following the position of amino acid in the phylogenetic tree.

Supplementary Figure S2. The expression level of *SlHSP70-1* in ovaries of T0 generation of transgenic plants.

Ovaries were collected at the day of flowering. S1-13 were the 13 lines of transformants. The relative expression level of *SlHSP70-1* was calculated by following the Ct method. Wild type (WT) plants were used as control. Tomato *Ubiquitin* (*SlUBQ*) was used as the internal reaction control to normalize the level of *SlHSP70-1* between different samples. Bar indicates the mean value ± SD from 2 biological replications

Supplementary Figure S3. The shoot height of the *SlHSP70-1* overexpressing line of S10

A) The visible phenotype of the *SlHSP70-1* overexpressing line of S10 (*SlHSP70*-OE-S10) and WT plants at 60 DAF. B) Mean values of plant height of the *SlHSP70*-OE-S10 and WT. Asterisks representative for significant difference with $^{*}P<0.05$, $^{**}P<0.01$ according to Student's *t*-test carried out on raw data. Bar indicates mean values of six biological replicates ± SD.

Supplementary Figure S4. Comparison of the internode length of *SlHSP70*-OE-S10 and WT plants

A) Morphological phenotypes of 5th and 6th internodes of WT at 60 DAS. B) Morphological phenotypes of 5th and 6th internodes of *SlHSP70*-OE-S10 plant at 60 DAS. C) Comparison the length of internode of *SlHSP70*-OE-S10 and WT by each internode position. Internode position was set from cotyledon (the first) to top (the 9th) of the plant. Bar indicates the mean value of the internode length of the six independent plants for each genotype ± SD. D)

Comparison of the *SlHSP70-1* expression level in the internode of *SlHSP70*-OE-S10 and WT. Bar indicates the mean value of the three biological replications for each genotype ± SD. (*), (**), (****) representative for significant difference at P-value less than 0.05, 0.01 and 0.001 by Student's *t*-test, respectively.

Supplementary Figure S5. Comparison of the plant height of the *SlHSP70*-OE, the *Sliaa9*, and WT plants

A) The length of tomato plant at 60 DAS. B) Mean values of plant heights were compared between *HSP70*-OE, *Sliaa9* mutant, and WT. Bar indicated mean values of 6 biological replicates ± SD Asterisks representative for significant difference with *P<0.05, **P<0.01, ***P<0.001 according to Student's *t-test* carried out on raw data.

Supplementary Figure S6. Comparison of leaf descriptions between *SlHSP70*-OE S13 and WT plants

A) Morphological phenotypes of the leaves of the sixth position of *SlHSP70*-OE and WT plants at 30 DAS. Bar scale at 1 cm. B) Expression levels of *SlHSP70-1* in the young leaf of *SlHSP70*-OE and WT at 17 DAS. Bar indicates the mean value of internode length of the three biological replications ± SD C) Comparison of leaf length of *SlHSP70*-OE and WT plants according to each leaf position. Bar indicates the mean value ± SD of the six independent plants for each genotype. (*) showed the significance at $p<0.05$, by Student's *t*-test.

Supplementary Figure S7. Comparison of leaf descriptions between *SlHSP70*-S10 and WT plants A) Morphological phenotypes of the leaves of the sixth position of *SlHSP70*-OE and WT plants at 30 DAS. Bar scale at 1 cm. B) Expression levels of *SlHSP70-1* in the young leaf of *SlHSP70*-OE and WT at 17 DAS. Bar indicates the mean value of internode length of the three biological replications ± SD. C) Comparison of leaf length of *SlHSP70*-OE and WT plants according to each leaf position. Bar indicates the mean value ± SD of the six independent plants for each genotype. (*) showed the significance at P<0.05, by Student's *t*-test.

Supplementary Figure S8. Phenotypes related to reproductive development of *SlHSP70*-OE and WT plants

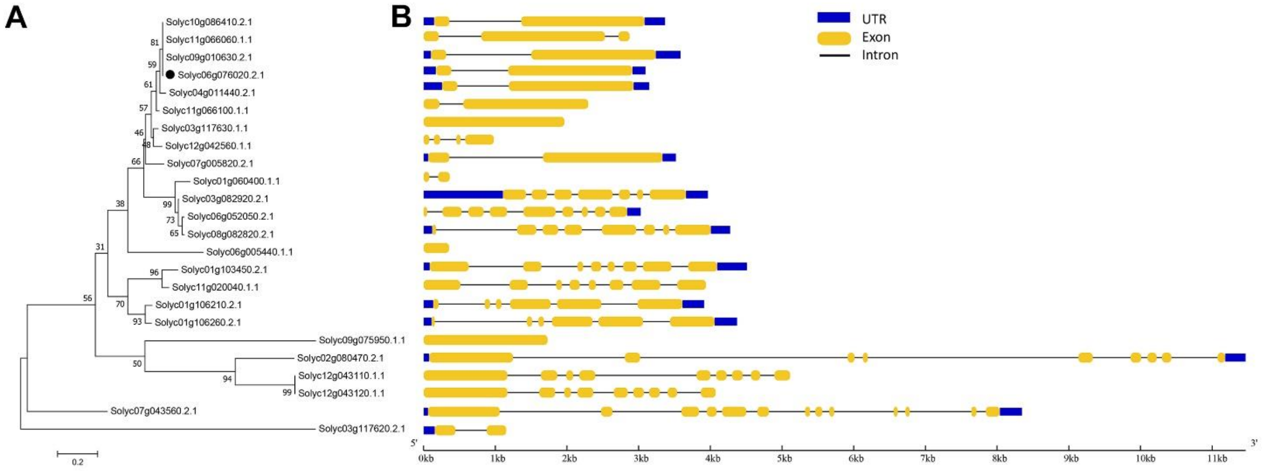
Comparison of A) time of first flowering, B) number of flowers, C) number of fruits and fruit set rate D). Bar indicates the mean value ± SD from six independent plants for each genotype. (*), (**) showed the significance at $p<0.05$, $p<0.001$ by Student's *t*-test.

Supplementary Figure S9. Fruit development of the *SlHSP70*-OE tomato

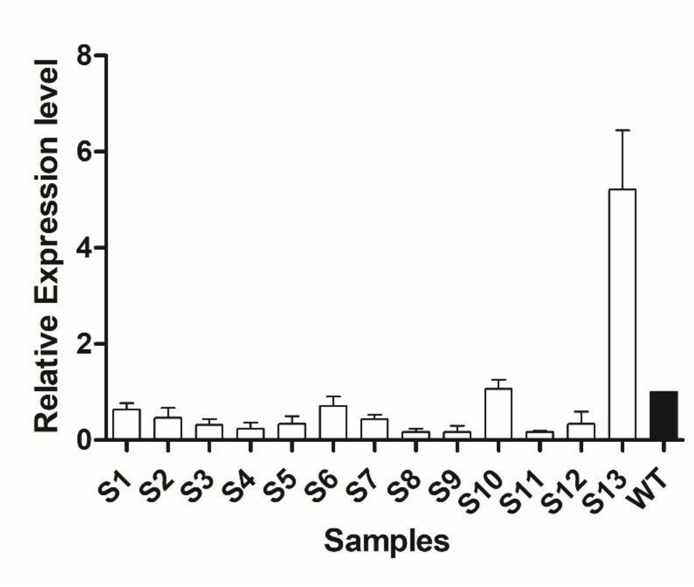
A) Ovaries of *SlHSP70*-OE and WT at 0, 2, 4 DAF, respectively. Ovaries were observed under microscope with 50 times magnification. Photos were taken with bar scale at 1 mm. B) The expression levels of *SlHSP70-1* in the ovaries of *SlHSP70*-OE and WT at □2, 0, 2, 4 DAF, respectively. Bar indicates the mean value of the *SlHSP70-1* gene expression from three biological replications ± SD C, D) Comparison of diameter and vertical size of the *SlHSP70*-OE and WT fruits at 0, 2, 4 DAF, respectively. Bar indicates the mean of 36 fruits sizes of the six independent plants for each genotype ± SD E, F) Comparison of diameter and vertical size of *SlHSP70*-OE and WT fruit at 12 DAF and 30 DAF, respectively. Bar indicates the mean of 36 fruits size values of the six independent plants for each genotype ± SD (***) showed the significance at $p<0.001$, by Student *t*-test.

Supplementary Figure S10. The expression level of *SlHSP70-1* in each tissue of tomato *S. lycopersicum* M82 and that of *S. pennellii*

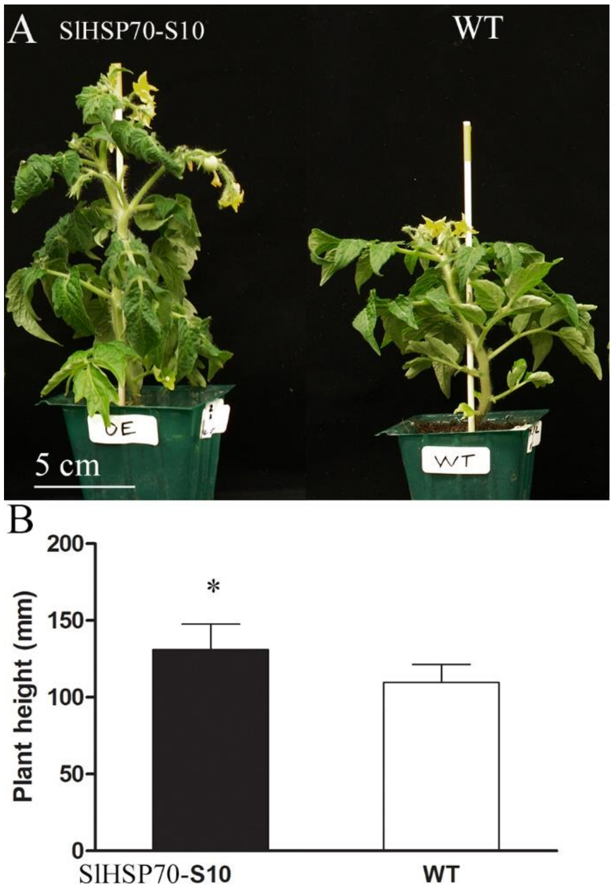
The seedling sample was collected at three days then grown on plate at 22°C under a mixture of cool-white and far-red fluorescent light. Shoot and root tissue was collected from seedling 10 DAF on plates. Vegetative meristems were collected when the 3rd leaf reached 1 mm (30-37 days post germination). Stem between the 4th and the 5th leaves and inflorescent meristems were collected when meristems were fully formed (50 days post germination for *S. lycopersicum* var. M82 and 56 days post germination for *S. pennellii*). Young green fruits and mature fruits were collected from plants in the greenhouse. Data were extracted from Tomato eFp browsers, available on website http://bar.utoronto.ca/efp_tomato/cgi-bin/efpWeb.cgi.



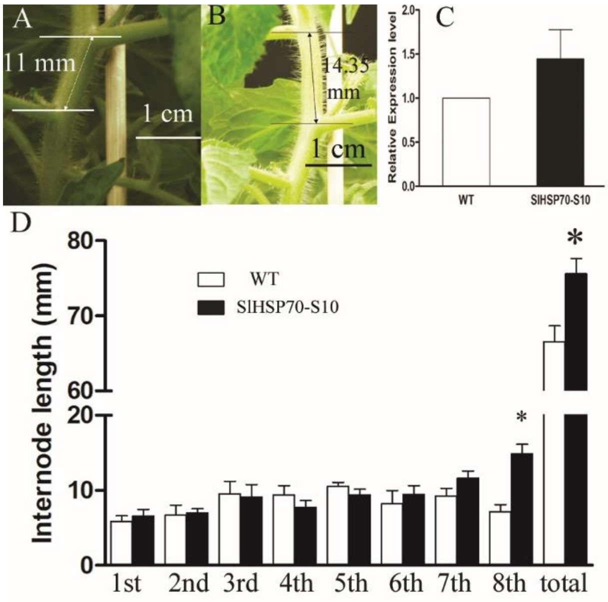
Supplementary Figure S1. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



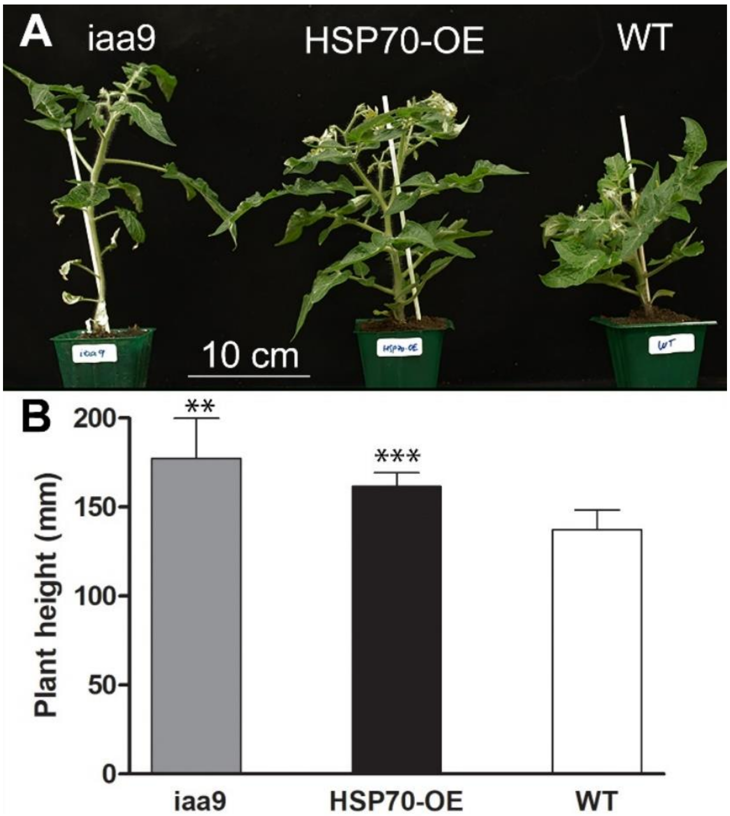
Supplementary Figure S2. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



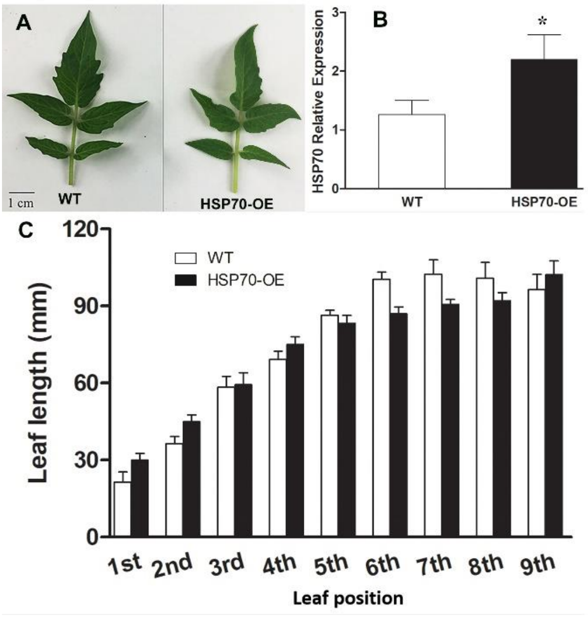
Supplementary Figure S3. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



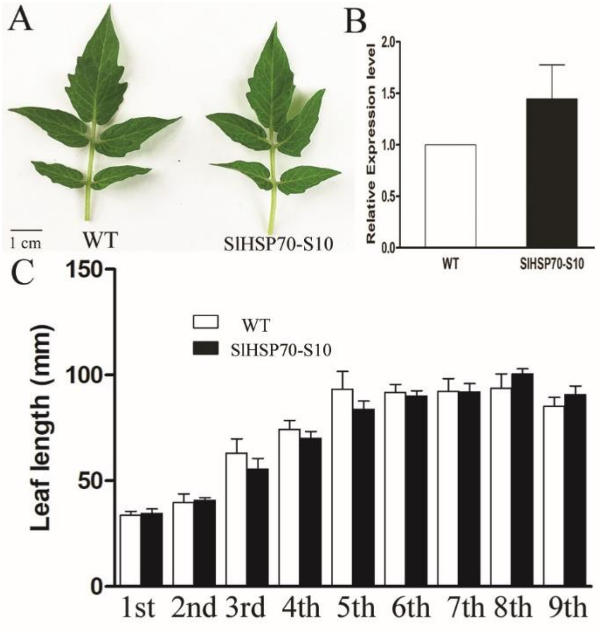
Supplementary Figure S4. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



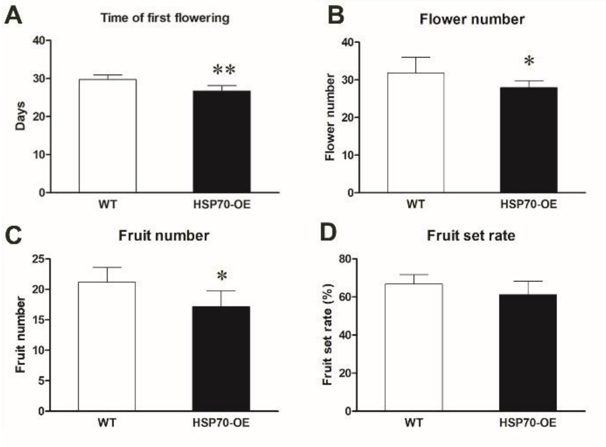
Supplementary Figure S5. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



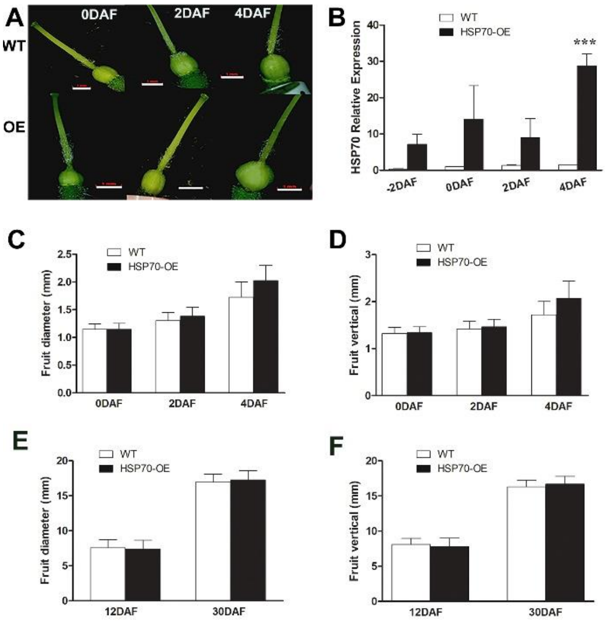
Supplementary Figure S6. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



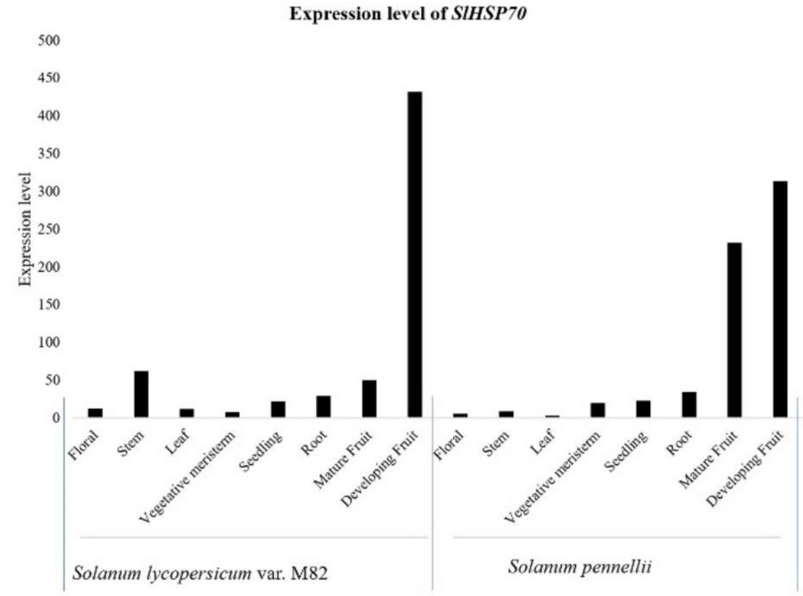
Supplementary Figure S7. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



Supplementary Figure S8. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



Supplementary Figure S9. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano



Supplementary Figure S10. Nam Tuan Vu, Ken Kamiya, Atsushi Fukushima, Shuhei Hao, Wang Ning, Tohru Ariizumi, Hiroshi Ezura, and Miyako Kusano