Table S1 Primers used in this work

Name	Sequence (5' to 3')	Purpose
HSP90.5GWFullF	GGGGACAAGTTTGTACAAAAAGC AGGCTCCATGGCTCCTGCTTTGAGTAGAAGT	Used to amplify the AtHSP90.5 full length cDNA for BP reaction to generate
HSP90.5GWFullR	GGGGACCACTTTGTACAAGAAAGCTGGGTTTA <u>CTTGTCATC</u> <u>ATCGTCCTTATAGTC</u> ATCTTGCCAAGGATCACTCTC	entry vector. The underlined represent the FLAG-tag coding sequence.
HSP90.5K478F	CAAGAAATCTCTGAGAGTGAA	Transgene detection
HSP90.5K625R	TTGCAACTTTGTCACCGAGC	
HSP90.5D62F	GCAACCATGGACGCCGCCGTGGCGGAG	
HSP90.5D780FLAG R	CCGTTCTAGATTACTTGTCATCATCGTCCTT	tagged and non-tagged mature form (D62-D780) into
HSP90.5D780R	CCGTTCTAGATCAATCTTGCCAAGGATCACTCTC	pProEXHTb vector
HSP90.5-qF	GTGGATTCACTCCTGATAGC	Forward primer for qPCR
HSP90.5-qEndo-R	CACTGCAAACAAAGAAGG	Reverse primer for endogenous gene (3' UTR) for qPCR
HSP90.5-qTotal-R	GCCAAGGATCACTCTCTGCC	Reverse primer for both endogenous and transgene for qPCR
ACTIN7F	TCACAGAGGCACCTCTTAACC	Reference gene for qPCR
ACTIN7R	CCCTCGTAGATTGGCACAG	



Figure S1. The Arabidopsis HSP90.5 gene structure with relative positions of primers used for this study. The numbered boxes represent exons. The relative positions of translation initiation codon ATG and stop codon TGA are also labelled.



Figure S2. PCR amplification of transgene fragments from Arabidopsis genomic DNA to genotype transgenic plants. A, A typical PCR analysis for primary transgenic plants. B, A typical PCR analysis of the F2 generation plants from backcrossed heterozygous transgenic lines. PCR amplification using HSP90.5K478F and HSP90.5K625R produced a 722bp fragment from endogenous HSP90.5 gene and a 481bp fragment from transgene.

Figure S2



Figure S3. Chlorophyll a and b contents in rosette leaves of HSP90.5 cosuppression lines. 5-week-old plants were grown at 110 μ mol.m².sec⁻¹ with 16/8 hr light/dark cycle.Error bars represent standard deviation with three independent assays. *denotes significantly different (P < 0.05) compared to WT values by student t-test. C*a*: Chlorophyll *a*. C*b*: Chlorophyll *b*.

- A, Entire rosette leaves of transgenic plants were analyzed for chlorophyll content.
- B, For Wild type (WT) and no. 3 alino plants, the leaves were sectioned into proximal (albino) and distal portions for chlorophyll extraction to differentiate the albinism.

Figure S4.

AtHSP90.5	611	LLCDWIKQQLGDKVAKVQVSNRLSSSPCVLVSGKFGWSANMERLMKAQALGDTSSLEFMRGRRILEINPD	680
PtHSP90C	619	LLCDWIKQQLGEKVAKVQVSKRLSSSPCVLVSGKFGWSANMERLMKAQALGDQSSLEFMRGRRILEINPD	688
GmHSP90C	620	LLCDWIKQQLGDKVAKVQISNRLSSSPCVLVSGKFGWSANMERLMKAQALGDTASLEFMRGRRILEINAD	689
OsHSP90C	611	LLCDWVKQQLGDKVAKVQISKRLSLSPCVLVSGKFGWSANMERLMKAQTLGDTSSLEFMRGRRIFEINPD	680
ZmHSP90C	618	LLCDWVKQQLGDKVAKVQISKRLSSSPCVLVSGKFGWSANMERLMKAQTLGDTSSLEFMRGRRIFEINPD	687
PpHSP90C	664	LLCDWMKQNLGDKVAKVTVSKRISSSPCVLVSGKFGWSANMERIMKAQTLGDNSQMEFMRGRRILEINPN	733
SmHSP90C	640	YCCDWIKQILGEKVASVGISNRLSTSPCVLVTGKHGWSANMERIMKAQALGDTSQLDYMRGKRILEINPQ	709
CrHSP90C	629	PVVDFLKKALGERVEKVTVSNRLLDSPCALVTSKFGWSANMERIMRSQALGDARAMEYMKGRKIMEINPN	698
		::: **::* .* :*:*: ****: ************	
AtHSP90.5	681	HPIIKDLNAACKNAPESTEATRVVDLLYDTAIISSGFTPDSPAELGNKIYEMMAMAVGGRWGRVEEEEES	750
PtHSP90C	689	HPIIKDLNAACKNAPDSSDAKRAVDLLYDTALISSGFTPDSPAELGGKIYEMMAMALGGRWGRSDGDEAE	758
GmHSP90C	690	HPIIKDLSAACKNAPDSSEAKRAVDLLYDTALISSGFSPDSPAELGNKIYEMMALALGGRWGRSEEEEGD	759
OsHSP90C	681	HPIVKDLNAACKNEPESTEAKRAVELLYETALISSGYTPDSPAELGGKIYEMMTIALGGRWGRSDTETEA	750
ZmHSP90C	688	HPIIKDLSAACKNEPESTEARRAVELLYEAALISSGYTPESPAELGGKIYEMMAIALGGRWGRSDMEEAE	757
PpHSP90C	734	HPIIQDLNVACKDTPNNPRAQAMVNLLHETALLSSGFTPENPAEFGARVYEMMGLALIGKQGGEEKAESV	803
SmHSP90C	710	HPIIASLNEACKSSPHDTRAQEIVELLYETAHVSSGFTPDNASEFGARIYDMIGVALGGRQVLSGQEEEY	779
CrHSP90C	699	HDIIAGIKTLLKEKDED-RARDLSELLYETALITSGFQVDSPKDYASKVFTLMKIALGYDILSEAEEQAA	767
		* *: .:. * * :**:::* ::**: : : . ::: :*:	
AtHSP90.5	751	STVNEGDDKSGESDPWQD 780	
PtHSP90C	759	DNAEESDANASETSEPQVIEPSEVRTESDPWQD 791	
GmHSP90C	760	ASVEAADSSTSEESDPWTTD- 794	
OsHSP90C	751	ATTGDASTETGSSEATVTEVIEPSEVRPESDPWRD 785	
ZmHSP90C	758	ASTGEASAEADSESDPWRDQ- 793	
PpHSP90C	804	EQSTPSEEGATSBRDPWQS 836	
SmHSP90C	780	SAPSAPQVDYSQGYSGGYGVSPPPPEASAATPPPPPATEAEVVVEPSEVREGDPWKS 836	
CrHSP90C	768	AAAPQAAEAAAAPKAAEAAAVPKVEATPVDAEVVSDDPWKKSA 810	
		*.: * . ***	

Figure S4. Sequence alignment of the C-terminal fragments of chloroplast HSP90C isoforms from different species.

The alignment was performed using CLUSTALW (<u>http://npsa-pbil.ibcp.fr/cgi-bin/align_clustalw.pl</u>) and only partial C-terminal fragments are shown. The HSP90C isoforms are as following with accession numbers included in the brackets: AtHSP90.5, *Arabidopsis thaliana* HSP90.5 (Q9SIF2); PtHSP90C, *Populus trichocarpa* HSP90C (XP_002311417); GmHSP90C, *Glycine max* HSP90C (XP_0035188021); OsHSP90C, *Oryza sativa* HSP90C (B8BC47); ZmHSP90C, *Zea mays* HSP90C (AFW651291); PpHSP90C, *Physcomitrella patens* HSP90C (XP_0017798941); SmHSP90C, *Selaginella moellendorffii* HSP90C (D8TAK0); CrHSP90C: *Chlamydomonas reinhardtii* HSP90C (Q66T67). The relative positions of the amino acids are also labelled for each isoforms. "*" represents identical amino acids. "." and ":" represent weak and strong similarity respectively.