



Supplement Figure S3. Multiple sequence alignment of the 5 (including isoforms of each) novel *A. perfoliata* Heat Shock Protein 90 alpha (HSP90 alpha/α) sequences with recognised HSP90 alpha isoforms BLAST hits sequences. The secondary protein structure prediction the HSP90 alpha characteristic structure using the PSIPRED Protein Analysis Workbench (presented below the alignment). Each β-strand or α-helix is numbered and shaded in yellow (β-strand) and pink (α-helix). The domain analysis of C-terminal and N-terminal domains of HSP90 alpha isoforms using SMART tools is boxed in blue and red, respectively. Unique cytosolic HSP90, MEEVD peptide sequences are in green type and the unique cytosolic HSP90 alpha, LIP and EDD peptide sequences are shaded in green (Chen et al., 2006; Skantar & Carta, 2004).



	610	620	630	640	650	660	670	680	690	700
	HSP90									
NP_005339 HsapHSP90α	IEPIDEYCVQ	QLKEFEGKTL	VSVTKEGLEL	PED-----	-----EEKK	KQEE-----	KKTKFENLCK	IMKDI-LEKK	VEKVVVSNRL	VTSPCCIVTS
NP_034610 MmusHSP90α	IEPIDEYCVQ	QLKEFEGKTL	VSVTKEGLEL	PED-----	-----EEKK	KQEE-----	KKTKFENLCK	IMKDI-LEKK	VEKVVVSNRL	VTSPCCIVTS
Q9GKX7 EcabHSP90α	IEPIDEYCVQ	QLKEFEGKTL	VSVTKEGLEL	PED-----	-----EEKK	KQEE-----	KKTKFENLCK	IMKDI-LEKK	VEKVVVSNRL	VTSPCCIVTS
THD20903 FhepHSP90α	LDPIDEYAVT	QLREYDGKKL	VCVTKEGLQL	PED-----	-----EEKK	EFEE-----	LKAAYEPLCK	QIQEI-LGKR	VEKVAVSNRM	TSSPCCIVTS
TPP59511 FgigHSP90α	LDPIDEYAVT	QLREYDGKKL	VCVTKEGLQL	PED-----	-----EEKK	EFEE-----	LKAAYEPLCK	QIQEI-LGKR	VEKVAVSNRM	TSSPCCIVTS
XP_024345770 EgrahHSP90α	VDPIDEYAVP	QLREYDGKKL	VCVTKEGLEL	PED-----	-----EEKK	RFEE-----	VKASFEPTCK	KIKDI-LGNK	VEKVTVSNRL	TSSPCCIVTS
CDI70178 EgrahHSP90α	VDPIDEYAVP	QLREYDGKKL	VCVTKEGLEL	PED-----	-----EEKK	RFEE-----	VKASFEPTCK	KIKDI-LGNK	VEKVTVSNRL	TSSPCCIVTS
CDS25067 EgrahHSP90	VDFMDEYVNV	AMTEYLGKSL	VCVSRDLQL	PEEKVEAVVA	E----E-EKG	TTTQGEWMEC	VVADFESTCG	KMKEI-LGER	VESVRVSSRL	TSSPCCVITS
CDS39694 EmulHSP90	VDFMDEYVNV	AMTEYLGKSL	VCVSRDLQL	PEERVEAVVA	EAAAAEEERK	TTTQGEWMEC	VVADFESTCG	KMKEI-LGER	VESVRVSSRL	TSSPCCVITS
CDS28179 HmichHSP90	QGETRQRIIG	MVISYEDMEL	VDVSKMTREP	ENNLN----	-----EDYS	KILD-----	---EYRFMLE	KIKEL-LGDK	IVDLKISQVP	LDVPCICIST-
ApHSP90-1.1	DTVIDQYIAD	LIVSYADKKL	VDVSATNFEM	STDLEQ----	-----DENL	RISS-----	---EFESTCK	SVRAI-LADQ	VEGVIVSNKL	CDAPCCISAS
ApHSP90-1.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ApHSP90-2.1	NTKIDQSIQV	MIVSYDNKEL	VDVSATNFEM	LNDLEQ----	-----KENDK	RISS-----	---EFESTCK	SIKKI-LANE	VEDVVVSNKI	SYTPCCICISTS
ApHSP90-2.2	NTKIDQSIQV	MIVSYDNKEL	VDVSATNFEM	LNDLEQ----	-----KENDK	RISS-----	---EFESTCK	SIKKI-LANE	VEDVVVSNKI	SYTPCCICISTS
ApHSP90-3	SNPADYSFIC	DKNCYKLYKI	RSVGSYANIK	ELS-----	-----KEEER	EYRES-----	-CVEFASTCS	TMENY-YEGG	HASVVRVSRRL	VNSPCCAFVG
ApHSP90-4	CDPIDEYAVT	QLREYDGKKL	VCVTKEGLEL	PED-----	-----DEEKK	RFEE-----	VKAAPFEPTCK	KIKDI-LGNK	VEKVVVSNRL	VSSPCCIVTS
ApHSP90-5.1	TEPMDEYVMQ	ALSEVKGKKT	QNLAKGGLDL	KLE-----	-----KESKE	KFEE-----	QERAFKPLTD	WLRDKGLSGK	IKDAKISQRL	DSSPCALVAD
ApHSP90-5.2	TEPMDEYVMQ	ALSEVKGKKT	QNLAKGGLDL	KLE-----	-----KESKE	KFEE-----	QERAFKPLTD	WLRDKGLSGK	IKDAKISQRL	DSSPCALVAD
	α20	β14				α21		β15		β16
	710	720	730	740	750	760	770	780	790	800
	HSP90									
NP_005339 HsapHSP90α	TYGWTANMER	IMKAQALR--	-DNSTMGYMA	AKKHLEINPD	HSIIETLRQK	AEA-DKNDKS	VKDLVILLYE	TALLSSGFSL	EDPQTHANRI	YRMIKLGLGI
NP_034610 MmusHSP90α	TYGWTANMER	IMKAQALR--	-DNSTMGYMA	AKKHLEINPD	HSIIETLRQK	AEA-DKNDKS	VKDLVILLYE	TALLSSGFSL	EDPQTHANRI	YRMIKLGLGI
Q9GKX7 EcabHSP90α	TYGWTANMER	IMKAQALR--	-DNSTMGYMA	AKKHLEINPD	HSIIETLRQK	AEA-DKNDKS	VKDLVILLYE	TALLSSGFSL	EDPQTHANRI	YRMIKLGLGI
THD20903 FhepHSP90α	EFGWSANMER	IMKAQALR--	-DSSTMGYMA	AKKHLEINPR	HKIVQSLKSL	FEK-GESNKL	AKDLVFLLYS	TALLSSGFSL	EDPKVHSGRI	HQLISMCLDI
TPP59511 FgigHSP90α	EFGWSANMER	IMKAQALR--	-DSSTMGYMA	AKKHLEINPR	HKIVQSLKSL	FEK-GESNKL	AKDLVFLLYS	TALLSSGFSL	EDPKVHSGRI	HQLISMCLDI
XP_024345770 EgrahHSP90α	TFGWSANMER	IMKAQALR--	-DSSTMGYMS	AKKHLEINPD	HKVMIRLKEM	LSAEGEPNKI	CKDLINMLFS	TALLASGFTL	EDPKAHANKI	HELISMCLDI
CDI70178 EgrahHSP90α	TFGWSANMER	IMKAQALR--	-DSSTMGYMS	AKKHLEINPD	HKVMIRLKEM	LSAEGEPNKI	CKDLINMLFS	TALLASGFTL	EDPKAHANKI	HELISMCLDI
CDS25067 EgrahHSP90	TFGWSANMQR	IGKAQALR--	-NPHSLRNNS	AKKHLEINAN	DSIIIGLKKM	LSATEGMPNKI	SRDMLEILYN	TALLDSGFVL	KEPKTHTNTI	HALIRMFLEI
CDS39694 EmulHSP90	TFGWSANMQR	IGKAQALR--	-NPHSLRNNS	AKKHLEINAN	DSIIIGLKKM	LSATEGMPNKI	SRDMLEILYN	TALLDSGFVL	KEPKTHTNTI	HALIRMFLEI
CDS28179 HmichHSP90	VEEVEVNV	-----	-----	-----	-----	-----	-----	-----	-----	-----
ApHSP90-1.1	TEGISLNMAR	ILKSQ-RG--	-GDSSTTEKPA	SKKYFEINAK	HPMINWLKKT	LDQEEESPSTA	SKNLVNMLYS	AALLRSGNTL	ERPRSFTKLM	YSFINMYLKE
ApHSP90-1.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ApHSP90-2.1	TEDASLNRVIS	ILKSPGRG--	-DSSSTTKKPA	SKKYFEINPK	DPIINRLKKM	LDQGESPNTS	SKNIVNMLYS	AALLRSGKTL	ERPHSFTKLM	YNFVNMCLKE
ApHSP90-2.2	TEDASLNRVIS	ILKSPGRG--	-DSSSTTKKPA	SKKYFEINPK	DPIINRLKKM	LDQGESPNTS	SKNIVNMLYS	AALLRSGKTL	ERPHSFTKLM	YNFVNMCLKE
ApHSP90-3	-----	GK LPFGEPLK--	-----	PSSPRE	EEVNFNPN	HEVLIRLKEK	CCNNDGNLNA	YAPIINILLE	TALIDSGFMP	PDPIRYADMV
ApHSP90-4	TFGWSANMER	IMKAQALR--	-DSSTMGYMS	AKKHLEINPD	HKVMIRLKEM	LSADGEPNKI	CKDLINMLFS	TALLTSGFTL	EDPKAHANKI	HELISMCLDI
ApHSP90-5.1	EYMASGNFQK	VMLSQAYGSI	DPATNAYYLN	QRTLEVNP	HPLIKKLNEL	VQN-DPNDV	AKENTMLLYD	TAVLRSGFIM	QDLVGFAERI	ERELRKNLVD
ApHSP90-5.2	EYMASGNFQK	VMLSQAYGSI	DPATNAYYLN	QRTLEVNP	HPLIKKLNEL	VQN-DPNDV	AKENTMLLYD	TAVLRSGFIM	QDLVGFAERI	ERELRKNLVD
	α22		β17		α23		α24		α25	
	810	820	830	840						
	HSP90									
NP_005339 HsapHSP90α	DEDDPTA--D	DTSAAVTTEE--	--MPFLEGDD	DTSRMEEVD--	-----	-----	-----	-----	-----	-----
NP_034610 MmusHSP90α	DEDDPTV--D	DTSAAVTTEE--	--MPFLEGDD	DTSRMEEVD--	-----	-----	-----	-----	-----	-----
Q9GKX7 EcabHSP90α	DEDDPTA--D	DSSAAVTTEE--	--MPFLEGDD	DTSRMEEVD--	-----	-----	-----	-----	-----	-----
THD20903 FhepHSP90α	PTDDEMKT--T	DTPEVPSST--	--ATPAEAGD	D-AGMEEVD--	-----	-----	-----	-----	-----	-----
TPP59511 FgigHSP90α	PTDDEMKT--T	DTPEVPSST--	--ATPAEAGD	D-AGMEEVD--	-----	-----	-----	-----	-----	-----
XP_024345770 EgrahHSP90α	PEDETMTK--E	EEKNTASSD--	-VAAPVEAGD	DGAAMEEVD--	-----	-----	-----	-----	-----	-----
CDI70178 EgrahHSP90α	PEDETMTK--E	EEKNTASSD--	-VAAPVEAGD	DGAAMEEVD--	-----	-----	-----	-----	-----	-----
CDS25067 EgrahHSP90	PECESVK--D	AEQVTADSD--	-EAALVQAGD	DGGAMGEVG--	-----	-----	-----	-----	-----	-----
CDS39694 EmulHSP90	PECESVK--D	AEQVTADSD--	-EAALVQAGD	DGGAMGEVG--	-----	-----	-----	-----	-----	-----
CDS28179 HmichHSP90	VKLTYSVDAE	-----SKDE	INYEIDSSPM	NRLA-----	-----	-----	-----	-----	-----	-----
ApHSP90-1.1	HKEIMKATKE	GIDEERSPGE	FNFEIDSCPM	NVLL-----	-----	-----	-----	-----	-----	-----
ApHSP90-1.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
ApHSP90-2.1	QKEIKVATKE	LLNENRSPKE	FSLGINHCPK	IVRKEKKSSW	VRIYF	-----	-----	-----	-----	-----
ApHSP90-2.2	HKEIMKATKE	GIDEERSPGE	FNFEIDSCPM	NVLL-----	-----	-----	-----	-----	-----	-----
ApHSP90-3	SKTTEMPKET	EERALYSEST	--SSPFLAAD	KGGDVCCTP--	-----	-----	-----	-----	-----	-----
ApHSP90-4	PEDETMTKDV	EEKANATTEG	GATAPIEAGD	DGAAMEEVD--	-----	-----	-----	-----	-----	-----
ApHSP90-5.1	DVAEQVEPDD	SIPEPVEDEK	-KEESSEQAE	PMDVKEEL--	-----	-----	-----	-----	-----	-----
ApHSP90-5.2	DVAEQVEPDD	SIPEPVEDEK	-KEESSEQAE	PMDVKEEL--	-----	-----	-----	-----	-----	-----

Supplement Figure S3-Continued 3. Multiple sequence alignment of the 5 (including isoforms of each) novel *A. perfoliata* Heat Shock Protein 90 alpha (HSP90 alpha/α) sequences with recognised HSP90 alpha isoforms BLAST hits sequences. The secondary protein structure prediction the HSP90 alpha characteristic structure using the PSIPRED Protein Analysis Workbench (presented below the alignment). Each β-strand or α-helix is numbered and shaded in yellow (β-strand) and pink (α-helix). The domain analysis of C-terminal and N-terminal domain of HSP90 alpha isoforms using SMART tools is boxed in blue and red, respectively. Unique cytosolic HSP90, MEEVD peptide sequences are in green type and the unique cytosolic HSP90 alpha, LIP and EDD peptide sequences are shaded in green (Chen et al., 2006; Skantar & Carta, 2004).