

Supplementary data for Baquero Forero and Cvrčková: SH3Ps – evolution and diversity of a family of proteins engaged in plant cytokinesis

The supplementary materials consist of the following:

Supplementary Figure S1: A maximum likelihood phylogenetic tree of seed plant SH3P2 protein sequences (in this file).

Supplementary Figure S2: Alignment of all full-length angiosperm SH3P sequences (in this file).

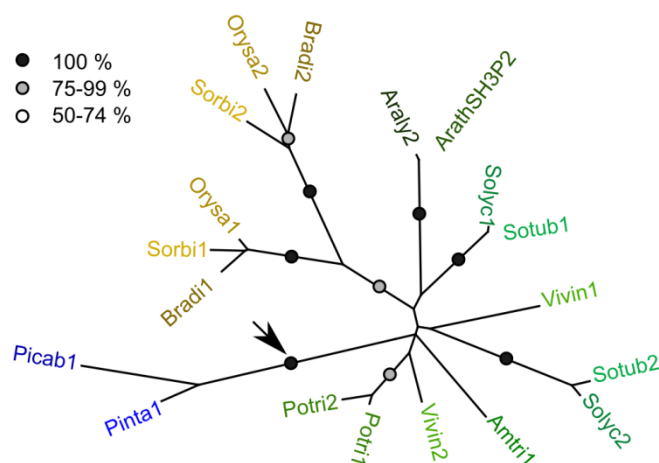
Supplementary Table S1: Inventory of SH3P homologs in selected plant species (in a separate MS Excel spreadsheet file TableS1.xls).

Supplementary Table S2: List of primers used for cloning into yeast two hybrid vectors (in this file).

Supplementary Table S3: List of primers used for cloning into Gateway™ compatible vectors.

Supplementary Data S1: Structural models of Arabidopsis SH3P1, SH3P2 and SH3P3 in the standard PDB format (in a separate Zip archive file DataS1.zip). Recommended viewer: DeepView (see Ref. [64], available at <https://spdbv.vital-it.ch/>).

Supplementary Figure S1. A maximum likelihood phylogenetic tree of seed plant SH3P2 protein sequences. Symbols at branches denote bootstrap support (no symbols for support below 50 %), the arrow marks the position of the root of the angiosperm SH3P2 clade (with the gymnosperms serving as an outgroup). For species color-coding see Figure 1, for accession numbers of all sequences see Supplementary Table S1.



Supplementary Figure S2. Alignment of all full-length angiosperm SH3P sequences. Positions where amino acid category is conserved across all sequences are highlighted in green, those with amino acid category shared by all members of at least one clade and present in at least one member of another clade are shown on yellow background, clade-specific positions (i.e. those where amino acid type is shared by all members of one clade but not with other clades) are highlighted in turquoise. For amino acid categories definition see legend to Figure 3, for sequence description see Supplementary Table S1. Incomplete sequences or those lacking parts of well-conserved domains (possibly because of imperfect splicing prediction) have been omitted (*continued on next page*).

	10	20	30	40	50	60	70	80
ArathSH3P1	MDAIRKQAAKLRQ	QVARQQQAVLKHL	--GHV-NADAVVVDEELHCH	QKLDLIS	STKAARKRLRN	IVRGLEGF	FIATG	YK
Potri3	MDAIKKQATRLRQ	QVARQQQAVLKHL	--GHF-SNEGIIIVDEAELQCY	QHLQNLN	NSRAAKHF	QKNIVRG	AEGFV	SSK
Potri4	MDAEFKQATRLRQ	QVARQQQAVLKHL	--GHL-SNEGIIIVDEAELQCY	QHLQNLN	NSRTAKHF	QKNIVRG	VEGFV	SSK
Vivin3	MDAIRKQASKLRQ	QVARQQQAVLKQL	--GHF-GIETVVVDEAQ	---ROLQNL	INSTRAKHF	QKDIVRG	IEGFV	STSSK
Solyc3	MDAIKKQATKLRQ	QVARQQQAVLKQL	--GHL-GHESVMVDEAELEI	QRLQEL	YMSRAAKHF	QORDIVRG	VEGYI	STSSK
Sotub3	MDAIKKQATKLRQ	QVARQQQAVLKQL	--GHL-GHESVMVDEAELEI	QRLQEL	YMSRAAKHF	QORDIVRG	VEGYI	STSSK
Amtri2	MDTLKQASKFRQ	QVSKQQQAVLKQF	--STHG-GNDTVITDEAEVRC	HKLES	LSISTRAKHF	QKDVVRG	IEGLI	STSSK
Bradi3	MDTLKQASKLRQ	QVARQQQAVRKTF	--STRY-NQDTSIVDEAELEC	HNLR	LNSTRAKHF	QORTIVRG	VEGFV	AVSSK
Sorbi3	MDALKQASKLRQ	QVARQQQAVLKQF	--SARY-NQDPSIVDEAELEC	QNLQRL	LNSTRAKHF	QORNIVRG	VEGFIA	ISSK
Orysa3	MDTLKQASKLRQ	QVARQQQAVRKQF	--SARY-NQDPSIVDEAELEC	QNLQRL	LNSTRAKHF	QORSIVRG	VEGFIA	VS
ArathSH3P2	MDAIRKQASRLRQ	QVARQQQAVFKQFGGGGY	--GSG--LADAEALNQ	QKLEKLY	ISTRAKHY	QORDIVRG	VEGYI	VTSSK
Amtri1	MDAIRKQATKLRQ	QVARQQQAVFKQFGGGGY	--GSG--LADAEALNQ	QKLEKLY	ISTRAGKH	QFORDIVRG	VEGFIV	VTSSK
Bradi1	MDAIRKQASKLRQ	QVARQQQAVLKQF	--GGGY-GADSVFADEGEAQ	QHTKLEKLY	ISTRAAKH	QFORDIVRG	VEGYI	VTSSK
Bradi2	MDALWQASRLKQ	QVAR--QGVFRQF	--GGAYGNSDNAFTDESEV	KLQRL	EKLILSTRAAKH	QFORDIVRG	VEGYI	VTSSK
Orysa1	MDAIRKQASKLRQ	QVARQQQAVMKQF	--GGGY-GADGAFADAEACQ	MSKLEKLY	ISTRAAKH	QFORDIVRG	VEGYI	VTSSK
Orysa2	MDALWQASRLKQ	QVSR--QGVFKQF	--GAAYGNSDNAFTDESEV	NLQRL	EKLILSTRAAKH	QFORDIVRG	VEGYI	VTSSK
Potri1	MDAIRKQATKLRQ	QVARQQQAVLKQFGGGGY	--GSG--LADAEALNQ	QKLEKLY	ISTRAGKH	QFORDIVRG	VEGYI	VTSSK
Potri2	MDAIRKQATKLRQ	QVARQQQAVLKQFGAGGY	--GSD--LVTDEAEMQ	QHKLERLY	ISTRAGKH	QFORDIVRG	VEGYI	VTSSK
Solyc1	MDAIRKQATRLRQ	QVARQQQAVLKQFGAGGY	--GSD--LVTDEAEMQ	QHKLERLY	ISTRAGKH	QFORDIVRG	VEGYI	VTSSK
Solyc2	MSIRKQATKLRQ	QVARQQQAVFKQF	--SSGLGGPDNSVTDEVEL	QOQKLEKLY	ISTRAGKH	QFORDIVRG	VEGYI	ITSSK
Sotub1	MDAIRKQATRLRQ	QVARQQQAVLKQFGAGGY	--GSD--LVTDEAEMQ	QHKLERLY	ISTRAGKH	QFORDIVRG	VEGYI	VTSSK
Sotub2	MDSIRKQATKLRQ	QVARQQQAVFKQF	--SSGLGGPDNSVTDEVEL	QOQKLEKLY	ISTRAGKH	QFORDIVRG	VEGYI	ITSSK
Sorbi1	MDAIRKQASKLRQ	QVARQQQAVMKQF	--GGGY-GADGVFADEGEAQ	MSKLEKLY	ISTRAAKH	QFORDIVRG	VEGYI	VTSSK
Sorbi2	MDALWQASRLKQ	QVAR--QGVFKQF	--GYGNSDNAFTDESEV	KLQRL	EKLILSTRAAKH	QFORDIVRG	VEGYI	VTSSK
Vivin1	MDAIRKQATKIIQ	QVARQQQAVLKQFGGGGY	--GSD--LVTDEAEMQ	QHKLERLY	ISTRAGKH	QFORDIVRG	VEGFIV	VTSSK
Vivin2	MDAIRKQASKFRQ	QVARQQQAVLKQFGGGGY	--GSD--LVTDEAEMQ	QHKLERLY	ISTRAGKH	QFORDIVRG	VEGFIV	VTSSK
ArathSH3P3	MDAFRRQASKLRQ	QVARQQQAVIKQFSGTG	YESSDMVIDE	LEMQHQLDKL	RSTRSAKE	QFORDIVR	GAFTAI	SVK
Bradi4	MDAIRKQASKFKQ	QVARQQQAVIKQFSTTG	YERSDSVVIDE	LEMQHQLDKL	SSRSGRDF	QKDIVR	AGFVSI	SSK
Orysa4	MDVLRKQASKFKQ	QVARQQQAVIKQFSTTG	YEHSDAVVIDE	LEMQHQLDKL	SSRSGRDF	QKDIVR	AGFVSI	SSK
Potri5	MDALRQASKLRQ	QVARQQQAVIKQFSSTG	YESSDMVIDE	LEMQHQLDKL	SSRSGRDF	QKDIVR	AGFVSI	SSK
Solyc4	MDALRQASKLRQ	QVARQQQAVIKQFSATG	YESSDMVIDE	LEMQHQLDKL	SSRSGRDF	QKDIVR	AGFVSI	SSK
Sotub4	MDALRQASKLRQ	QVARQQQAVIKQFSATG	YESSDMVIDE	LEMQHQLDKL	SSRSGRDF	QKDIVR	AGFVSI	SSK
Sorbi4	MDALRQASKFKQ	QVARQQQAVIKQFSTTG	YERSDSVVIDE	LEMQHQLDKL	SSRSGRDF	QKDIVR	AGFVSI	SSK
Vivin4	MDALRQASKFRQ	QVARQQQAVIKQFGGTG	YESSDMVIDE	LEMQHQLDKL	RSTRAGK	DFQDIVR	AGFVSI	SSK
ArathSH3P1	VVEIGLKF	FAEDFKKYG	DENPDA--NTP--LSRVA	HHFGTHYKSV	EGERETLL	GVLSQVCE	IRTM	YISABIEDARHLVNH
Potri3	QMEILRL	LADECKKYG	AEHQSE--NNY--VARTV	LQFGASHNL	MENKEILL	GVLDQVSK	LRALIT	GABIEDARHLTHRY
Potri4	QMEMLRL	LADECKKYG	AEHQSE--NNY--VARAV	LQFGASHNL	MENKETIV	GVLDQVSK	LRALIT	GABIEDARRLTHH
Vivin3	QMEIVRMA	EDCKKYG	ETENQST--GSP--LARAALY	FGNTHSSMEK	RETL	GVFCQVSE	LRVLIT	GABIEDARHLTHRY
Solyc3	QVEIAR	KLVDNCKYK	GEIQNG--PST--LQKVA	VEGTHHAAMED	REIM	GVLSQVCE	LRASIH	GABIEDARHLTHSY
Sotub3	QVEIAR	KLVDNCKYK	GEIQNG--PST--LQKVA	VEGTHHAAMED	REIM	GVLSQVCE	LRASIH	GABIEDARHLTHSY
Amtri2	QMEIATK	LADDECKKYG	ENESHSS--NTT--LASAS	RQFCTRN	SMESREN	LRRILSTQVSE	LRAMVM	GABIEDARLLTHRY
Bradi3	QMEIVK	LAEDECKKYG	NNNQNL--GFV--LGIAS	VEFGKHTQ	MEIREK	LLKVLGEQVFE	LRREMIM	SABIEDARLLITYRY
Sorbi3	QMEIVK	LAEDECKKYG	CNDNQHF--GFA--LARASEE	FGKHQ	QIEKRED	LLKSLGEQVFE	LRREMIM	SABIEDARLLITYRY
Orysa3	QMEIVK	LAEDECCR	YGNNDNQF--GFI--LARAS	VEFGNTHSQMEK	REN	LLKFLGEQVFE	LRREMIM	SABIEDARLLITYRY
ArathSH3P2	QVEIGTK	LSEDSRKYG	ENCTCTSGNT--LTRAALN	YGRARAQMEK	RGNNL	KALGTQVAE	LRAMVL	GABIEDARHLAORY
Amtri1	QVEIGTK	LSEDSRKYG	ENCTCTSGGT--LAKAALS	YGRARAQTEK	RGNNL	HKALGTQVAE	LRAMVL	GABIEDARHLAORY
Bradi1	QVEIGNK	LCEDEGKKYG	VENTCTSGST--LSRAALS	YGRARSRLMEK	RGNNL	KAFGTQVAE	LRAMVM	GABIEDARHLAORY
Bradi2	QVEIGNK	LCEDEGKKYG	VENTCTSGNT--LSKAATY	YGRARSRLMEK	RGNNL	KAFGTQVAE	LRAMVM	GABIEDARHLAORY
Orysa1	QVEIGNK	LCEDEGKKYG	VENTCTSGST--LSKAALC	YGRARSRLMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Orysa2	QVEIGNK	LSDDEGKKYG	ENTCTCTSGNT--LSKAAMY	YGRARSRLMEK	RGNNL	RAFGTQVAE	LRAMVM	GABIEDARHLAORY
Potri1	QVEIGTK	FSEDSRKYG	ENCTCTSGNT--LSKAAVN	YGRARAQMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Potri2	QVEIGTR	FSEDSRKYG	ENCTCTSGNT--LSKAAVN	YGRARAQMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Solyc1	QVEIGTK	LSEDSRKYG	ENCTCTSGTT--LSKAALG	YGRARAQMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Solyc2	QVEIGTK	LSEDSRKYG	ENKCTSGST--LSKAALS	YGRARAQTEK	RED	LLKALGTQVAE	LRAMV	GABIEDARHLAORY
Sotub1	QVEIGTK	LSEDSRKYG	ENCTCTSGTT--LSKAALG	YGRARAQMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Sotub2	QVEIGTK	LSEDSRKYG	ENCTCTSGST--LSKAALS	YGRARAQTEK	RED	LLKSLGTQVAE	LRAMV	GABIEDARHLAORY
Sorbi1	QVEIGNK	LCEDEGKKYG	ENTCTCTSGST--LSKAALS	YGRARSRLMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Sorbi2	QVEIGNK	LSDDEGKKYG	ENTCTCTSGTT--LSKAATY	YGRARSRLMEK	RGNNL	KAFGTQVAE	LRAMVM	GABIEDARHLAORY
Vivin1	QVEIGTK	LSEDSRKYG	ENCTCTSGST--LSKAALS	YGRARAQMEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
Vivin2	QVEIGTK	LSEDSRKYG	ENTCTCTSGNT--LSKAALN	YGRARAQTEK	RGNNL	KALGTQVAE	LRAMVM	GABIEDARHLAORY
ArathSH3P3	HIVAGTK	LSEDCCR	YGNENQNDENI--LAKAA	ATVCDARKH	VDKQED	FNKLLASQVLD	LRAMV	AGSABIEDARHLAORY
Bradi4	HIVVGTK	FSEDCFR	YGENNAD--EEA--LAKAAS	LGGALRN	VEKYEYED	FSRTLSSQTID	LRAMAT	CVABIEDARGLAORY
Orysa4	HIVVGTK	FSEDCFR	YGENNAD--EEA--LAKAAS	LGGALRN	VEKYEYED	FSRTLSSQTID	LRAMAT	CVABIEDARGLAORY
Potri5	HIVAGTK	LSEDCCR	YGTENIN--ENI--LAKAA	ATVCDARKH	VEQED	LNLLFSQILD	LRAMIT	DSABIEDARHLAORY
Solyc4	HIVAGTK	LSEDCCR	YGTENIN--DEV--LAKAAS	ITVCDARKH	VEQED	LNLLFSQILD	LRAMV	AGSABIEDARHLAORY
Sotub4	HIVTGTK	LSEDCCR	YGTENIN--DEV--LAKAAS	ITVCDARKH	VEQED	LNLLFSQILD	LRAMV	AGSABIEDARHLAORY
Sorbi4	HIVVGTK	FSEDCFR	YGTENIN--DEA--LAKAAS	LGGALRN	IEKYEYED	FSRTLSSQTID	LRSMAM	AGSABIEDARGLAORY
Vivin4	QIVTGTK	LSEDCCR	YGTENIN--DNI--LAKAAS	ITVCDARKH	IAQED	LNLLSSQILD	LRAMV	TGABIEDARHLAORY

	170	180	190	200	210	220	230	240
ArathSH3P1	DRLRQEV	LAQATDVLRRRSKLKESDIS	EAYIKLKN	ESRLAELKSSMKTLC	ETKINLE	VOD	QONV	YSORIRALVE
Potri3	DKLRLQEV	LAQAAEVLRRSKTRDSEIS	ASCMKLQAP	EARLT	TELKSTVMALGR	ETAMSSSV	ENQOE	ETACRLFSMDA
Potri4	DKLQRAV	VQAAEVLRCRSTKTRDSEIS	ASCTKLRA	EARL	ELKSTVMALGR	ETAMSSSV	ENQOE	ETACRLFSMDA
Vivin3	ERLRQEV	LSQAADVLRRQAKFRPATSA	SSIKLQSE	AKLSE	ELKSTVMALGR	ETAMSSSV	ENQOE	ETACRLFSMDA
Solyc3	DRMRQEF	FSQATEVIRROSKFRE	--ASTSLAKLKN	ETRLSELK	SVLVLGKE	TDMLSV	EEBQOE	ETFOKLLIMVDA
Sotub3	DRMRQEF	FSQATEVIRROSKFRE	--ASTSLAKLKN	ETRLSELK	SVLVLGKE	TDMLSV	EEBQOE	ETFOKLLIMVDA
Amtri2	DRIRQEV	LAQVAEVRRLQAKLKEP	GANASAYKLQNE	FMKLS	ELKSSLSALGKE	ATAAMSSV	EAQOE	ETACRLFSMDA
Bradi3	QRIRQDM	FSQIADVMRKQLKSKESSEN	SD-SLKLQH	ESKLSEL	RTTLAALGR	ETAMSSSV	EAQOE	ETACRLFSMDA
Sorbi3	QRIRQDM	FSQIADVMRKQLKSKESSEN	NTNSVKLQH	ESKLSEL	RTTLAALGR	ETAMSSSV	EAQOE	ETACRLFSMDA
Orysa3	QRIRQDM	FSQIADVMRKQLKSKESSEN	NTNSVKLQH	ESKLSEL	RTTLAALGR	ETAMSSSV	EAQOE	ETACRLFSMDA
ArathSH3P2	DRMRQEA	LAQATEVARQAKARE	ESQGNPILMKLES	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE	ETACRLFSMDA
Amtri1	DRMRQEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Bradi1	DRMRQEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Bradi2	DRMRQEA	LAQAVV	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Orysa1	DRMRQEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Orysa2	DRMRQEA	LAQAV	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Potri1	DRMRQEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Potri2	DRMRQEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Solyc1	DRMRQEA	LAQAV	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Solyc2	DRVRQEA	LAQAI	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Sotub1	DRMRQEA	LAQAV	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Sotub2	DRVRQEA	LAQAI	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Sorbi1	DRMRQEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Sorbi2	DRMRQEA	LAQAVV	EVSRQONVRE	ESAGNGE	VISKLEA	EYKLE	ELKSNM	VGLCKE
Vivin1	ERMRMEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
Vivin2	ERMRMEA	LAQAI	EVSKROMVRE	EGTGNVNSAKLDA	EAKLHOLK	ENMTILCKE	ASALASV	EDQOE
ArathSH3P3	SRMRQEA	THATEVSRQONVRE	-API	ENVAKLQ	ELKSNM	VGLCKE	ASALASV	EDQOE
Bradi4	SRMRHEA	ILSAEIAARKAVRE	-SPIA	NTTKLQ	ELKSNM	VGLCKE	ASALASV	EDQOE
Orysa4	SRMRHEA	ILSAEIAARKAVRE	-APLA	HTTKLQ	ELKSNM	VGLCKE	ASALASV	EDQOE
Potri5	SRMRHEA	ILSAEIAARKAVRE	-SPIA	NTTKLQ	ELKSNM	VGLCKE	ASALASV	EDQOE
Solyc4	SKMRQEA	ILQATEVSRQONVRE	-API	ENVAKLH	ELKSNM	VGLCKE	ASALASV	EDQOE
Sotub4	SKMRQEA	ILQATEVSRQONVRE	-API	ENVAKLH	ELKSNM	VGLCKE	ASALASV	EDQOE
Sorbi4	SRMRHEA	ILSAEIAARKAVRE	-API	HTTKLQ	ELKSNM	VGLCKE	ASALASV	EDQOE
Vivin4	SRMRHEA	ILQATEVSRQONVRE	-API	ENVAKLH	ELKSNM	VGLCKE	ASALASV	EDQOE

	330	340	350	360	370	380	390	400
ArathSH3P1	TKPSPKDEMKSSPQEE	TKSNHQKEIKSSPQEE	IKKSN	GSDDHHNHQLLSQ	NDSEFLAKVHPFDAQ	PGELSLAVDDYVI		
Potri3					DALYIAKVIHPFDAQ	EGELSLFIDDFVV		
Potri4					DGLFLAKVIHPFDAQ	EGELSLSVDDFVV		
Vivin3					GSYFLAKVIHPFDAQ	DGELSLSVDDYVV		
Solyc3					PTYFLAKVMHSEDAQ	DGELSLLEVGDYVV		
Sotub3					PTYFLAKVMHSEDAQ	DGELSLLEVGDYVV		
Amtri2					AMYFLAEVLHPFDAQ	EGELSLSVGDYVV		
Bradi3	SEPTR				NSQEVHVEVHPFDAQ	DGELINISVGDYVV		
Sorbi3	SESTG				NSQEVQVEVHPFDAQ	DGELISLAVGEYVV		
Orysa3	SEPTR				NGQEVHVEVHPFDAQ	DGELISISVGDYVV		
ArathSH3P2					MGYFLCEVLFPPYHGV	DVELSLSTGEYVV		
Amtri1					SSYFLCEVMHPYRAE	DVELISLSVGDYVV		
Bradi1					VEHFLAEALQSYRAE	ETELINLSLSTGEYIV		
Bradi2					VDFFLCEALDSFKAE	ESELINLSLGDIVI		
Orysa1					VEFLAEALQSYRAE	ETELINLAAGDYIV		
Orysa2					VDFFLCEALDSFKAE	ESELINLSAGDIIV		
Potri1					ISYFLCEVMHSTQGG	DVELTILSIGDYVV		
Potri2					MGYFLCEVMHSTQGG	DVELTILSIGDFVV		
Solyc1					MGYFLCEVMYPYQAE	DVELINLSVGEYIV		
Solyc2					TTYFLAEVHPYEA	DVELTLLIGDYVV		
Sotub1					MGYFLCEVMYPYQAE	DVELINLSVGEYIV		
Sotub2					TTYFLAEVHPYEA	DVELTLLIGDYVV		
Sorbi1					VEYFLAEALQSYRAE	ETELINLSAGDYIV		
Sorbi2					VDFFLCEALDSFKAE	ESELINLSAGDIIV		
Vivin1					MGYFLCEVMHSEQAE	DVELINLSVGDHVV		
Vivin2					ISYFLCEVMHSTQAE	DVELINLSIGDFVV		
ArathSH3P3					TSYFLAEVLHPPESAA	EKELDLKGDYIV		
Bradi4					AQYFLAEAMHNFGT	EKELSLIVGDYIV		
Orysa4					AQYFLAEAMHNFGT	EKELSLIVGDYVV		
Potri5					TTYFLAEAMHPIAE	EKELSLAVGDCIV		
Solyc4					TKYFLAEAMHSEAE	EKELSLSVGDYVV		
Sotub4					TKYFLAEAMHSEAE	EKELSLSVGDYVV		
Sorbi4					AQYFLAEAMHNFGT	EKELSLIVGDYVV		
Vivin4					TMYFLAEAMHESAA	EKELSLNVGDYVV		

	410	420	430	440	450
ArathSH3P1	VRQVAGTGNSEGEKKGWFS	SAYVEKQEKAPASKI	-VESNSKQQ		
Potri3	VRKVAPTGNSEGECKKKGWFS	SAYTEKHAKAPASKI	-MEESSTP		
Potri4	VRQVAPTGNSEGECKKKGWFS	SAYTEKHENSPERAT	-SVSELLKAIPSGMV		
Vivin3	VRQVAPNGNSEGECKKTAGWFS	SAYVERROKAPASVI	-NEEASLAMIPN		
Solyc3	VRQVAPNGNSEGECKKKGWFS	SAYAVMSDEVAASKM	-VETDTTP		
Sotub3	VRQVAPNGNSEGECKKTAGWFS	SAYAVKSDEVAASKM	-VETDTTP		
Amtri2	VRQVAPAGNSEGECKKKGWFS	SAYTELROKAPASKI	-SDIDPQS		
Bradi3	VRQVARNNGNSEGECKKKGWFS	SAYVQORDKAPASKV	-IEPGLLTA		
Sorbi3	VRQVAPANGNSEGECKKKGWFS	SAYVEQROKAPASKV	-IEPGLLTT		
Orysa3	VRQVAPNGNSEGECKKKGWFS	SAYVEQROKAPASKV	-IEPGLLTT		
ArathSH3P2	VRKVAGSGNAGEGECKKKGWFS	YGYIERRERV LASKV	-SEVF		
Amtri1	VRKVARTGNAGEGECKKKGWFS	SDYIERRERV LANKV	-AEVF		
Bradi1	VRKVSNNGNAGEGECKKKGWFS	SEYIEKRORV LASKV	-AQVF		
Bradi2	VRKVSNNGNAGEGECKKKGWFS	HAYIERRERV LASKV	-PHIF		
Orysa1	VRKVSNNGNAGEGECKKKGWFS	YDYIEKRORV LASKV	-AQVF		
Orysa2	VRKVSTNGNAGEGECKKKGWFS	HGYIERRERV LASKV	-PHIF		
Potri1	VRKVSNNGNAGEGECKKKGWFS	YGYIERRORV LASKI	-AEVF		
Potri2	VRKVSNNGNAGEGECKKKGWFS	YGYIERRORV LASKI	-AEVF		
Solyc1	IRKVSNNGNAGEGECKKKGWFS	FGYIERRORV LASKV	-AEVF		
Solyc2	VRKVSNNGNAGEGECKKKGWFS	FGYVERRERILATKV	-AEVF		
Sotub1	IRKVSNNGNAGEGECKKKGWFS	FGYIERRORV LASKV	-AEVF		
Sotub2	VRKVSNNGNAGEGECKKKGWFS	FGYVERRERILATKV	-AEVF		
Sorbi1	VRKVSNNGNAGEGECKKKGWFS	YDYIEKRERV LASKV	-AQVF		
Sorbi2	VRKVSNNGNAGEGECKKKGWFS	HAYIERQERV LASKV	-PHIF		
Vivin1	IRKVSNNGNAGEGECKKKGWFS	VGYIERRERV LASKI	-V		
Vivin2	VRKVSNNGNAGEGECKKKGWFS	FGYIEKRERV LASKM	-AEVF		
ArathSH3P3	VRKVAPQTGNAGEGECKKKGWFS	MAAYIEKRORLPTTNFAAEVY			
Bradi4	VRQVAPNGNAGEGECKKKGWFS	AGYVERRENIPP NKVFPQA			
Orysa4	VRQVAPNGNAGEGECKKKGWFS	AAAYVERRENIPP NKVFPQA			
Potri5	VRKVAPPTGNAGEGECKKKGWFS	SAAYIEKRORMSTSLA-AQAY			
Solyc4	VRKVAPQGNAGEGECKKKGWFS	SEAYIEKRORVPTSN GATEAY			
Sotub4	VRKVAPQGNAGEGECKKKGWFS	SEAYIEKRORVPTSN GATEVY			
Sorbi4	VRQVAPNGNAGEGECKKKGWFS	AAAYVERRENIPP NKVFPQA			
Vivin4	VRKVAPHTGNAGEGECKKKGWFS	SEAYIAKRORLPTSNVAAEVY			

Supplementary Table S2: List of primers used for restriction enzyme-based cloning into yeast two hybrid vectors with restriction enzymes used and names indicating final destination vectors

Gene	Primer sequence 5' - 3'	Enzyme	Primer name
SH3P2	TTGGATCCGCAGAAACCCGCATCAACTC	BamHI	SH3P2_pGAD_for
	TTGAATTCTGTGAATAGCTCTTGATCTGGTGA	EcoRI	SH3P2_pGAD_rev
SH3P3	TTCTCGAGGTAGTTTGTGGGGACAGGACA	XhoI	SH3P3_pGAD_for
	TTGAATTCGGGAAATCAAGAGGAGAAGTGAC	EcoRI	SH3P3_pGAD_rev
FH5	TTCATATGTACTCTGTTGGTTCCTCCATCAA	NdeI	FH5_pGBKT7_for
	TTCTGCAGAACTAGACTGATCCACGCGTCT	PstI	FH5_pGBKT7_rev
	TTCATATGTACTCTGTTGGTTCCTCCATCAA	NdeI	FH5_pGAD_for
	TTCCCGGGAAGCTAGACTGATCCACGCGTCT	XmaI	FH5_pGAD_rev

Supplementary Table S3: List of primers used for cloning into Gateway™ compatible vectors, PCR amplification of coding sequence with recombination sites and cloning into donor vectors for creating vectors for transient expression experiments. Primers M13for and M13rev were used for amplification of coding sequences of all three genes with recombination sites from pDONOR221 vectors for recombination into target vectors.

Gene	Primer sequence 5' - 3'	Vector (target)	Primer name
SH3P1	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAAGCTATAAGAAAGCAAGCTG	pDONOR221 (pGBKT7gw, pGADT7gw)	SH3P1_CDSgw for
	GGGGACCACTTTGTACAAAGAAAGCTGGGTACTGTTGCTTGGAGTTTGATTCCA		SH3P1_CDSgw rev
SH3P2	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATGCAATTAGAAAACAAGC	pDONOR221 (pGBKT7gw)	SH3P2_for_gw
	GGGGACCACTTTGTACAAAGAAAGCTGGGTATCAGAAACTTCGGACACTTT		SH3P2_rev_gw
SH3P3	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGATGCGTTTAGAAGACAAGC	pDONOR221 (pB7m34GW)	SH3P3 cds for gw
	GGGGACCACTTTGTACAAAGAAAGCTGGGTATCAGTAACTTCAGCAGCAAAGTT		SH3P3 cds rev gw
FH5	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGTTGGAATGATTCGAGGAGG	pDONOR221 (pB7m34GW)	FH5_for_gw
	GGGGACCACTTTGTACAAAGAAAGCTGGGTAGTCTGAATCTGAACTAGACTGATCCAC		FH5_rev_gw
DRP1A	GGGGACAAGTTTGTACAAAAAAGCAGGCTTAATGGAAAATCTGATCTCTCTGGTT	pDONOR221 (pGBKT7gw)	DRP1_for_gw
	GGGGACCACTTTGTACAAAGAAAGCTGGGTATCACTTGGACCAAGCAACA		DRP1_rev_gw
All	GTAAACGACGGCCAGT AACAGCTATGACCAT	pGBKT7gw	M13for M13rev